

Characterization of the Cofactor Utilisation and Regulation of Key Enzymes in Central  
Catabolism in *Ruminiclostridium thermocellum*

By

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University of Manitoba, 2017

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## Abstract

*Ruminiclostridium thermocellum*, an anaerobic Gram-positive thermophile capable of direct lignocellulosic hydrolysis producing ethanol, H<sub>2</sub>, CO<sub>2</sub>, acetate, formate, and lactate being as major end products. The high rate of cellulose hydrolysis combined with the ability to produce ethanol makes *R. thermocellum* a very attractive organism for the generation of ethanol via consolidated bioprocessing. However, the branched nature of the *R. thermocellum* central catalysis limits the carbon and electrons available for ethanol production, therefore limiting its industrial potential when compared to current ethanol production technologies and current fossil fuel prices.

Due to the branched nature of the *R. thermocellum*, understanding of the carbon and electron flux regulation is vital in understanding the metabolism associated with ethanol production. The understanding of flux also opens important doors in terms of genetic modifications increasing ethanol yields and cell growth rates making a more industrially competitive strain of *R. thermocellum*. The transcript of *R. thermocellum* showed that the transcription of end product synthesis genes do not necessarily correlate with the presence of the particular function in the cell. Rather, the carbon and electron flux in the cells seem to be regulated by the presence of small high-energy metabolites such as PPi since the presence of PPi directly regulates the activity of key central catabolism proteins such as the glucokinase, phosphofructokinase, and the malic enzyme, as well as being a phosphate group donor replacing the reliance ATP as an energy carrier. The glucokinase and phosphoglycerate kinase



display a regulation that favors relatively low levels of cofactor, GTP or ATP, by having substrate inhibition leading to decreases in activity based on increase cofactor concentrations.

The importance of small molecule regulation is reinforced by the intracellular concentrations observed in *R. thermocellum* and closely related organisms. The concentration of PPi increases rapidly upon inoculation with a slow decrease reaching a minimum at the onset of stationary phase. The PPi replaces ATP as the indicator for the energetic state of the cell influencing various cellular mechanisms by direct modulation of enzyme activity or by the activation of transcriptional regulators.



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## Dedication

To my parents, Richard and Claudette, my brother Christian, and my sister Chantal.

Thank you for the unwavering support throughout my long years of study.

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And to my wife, Charushi

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## List of Abbreviations

3PG	3-phosphoglycerate
6PGD	6-phosphogluconate dehydratase
AADC	Acetoacetate decarboxylase
ABE	Acetone butanol ethanol
ACAT	Acetyl-CoA acetyltransferase
AcoAT	Acetate-acetoacetate CoA transferase
ADH	Alcohol dehydrogenase
ADHE	Bifunctional aldehyde/alcohol dehydrogenase
ADP	Adenosine diphosphate
AK	Acetate kinase
ALDH	Aldehyde dehydrogenase
ALDO	Aldolase
AMP	Adenosine monophosphate
ATCC	American type culture collection
ATK	Acetate thiokinase
ATP	Adenosine triphosphate



AMW	Acetonitrile/methanol/water
BCDH	Butyryl-CoA dehydrogenase
BCoAT	Butyrate-acetoacetate CoA transferase
BDH	Butanol dehydrogenase
BiH <sub>2</sub> ase	Bifurcating hydrogenase
BK	Butyrate kinase
BLAST	Basic Local Alignment Tool
BLDH	Butyraldehyde dehydrogenase
CcpA	Carbon control protein A
CCR	Carbon catabolite repression
CO <sub>2</sub>	Carbon dioxide
CRISPR	Clustered regulatory interspaced short palindromic repeats
CRT	Crotonase
CTP	Cytosine triphosphate
DNA	Deoxyribonucleic acid
DSM	Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (German collection of microorganisms and cell cultures)
DTT	Dithiothreitol



Ech	Energy conserving hydrogenase
ED	Entner-Doudoroff pathway
EMP	Embden-Meyerhof-Parnas pathway
ENO	Enolase
ePPx	exopolyphosphatase
FADH	Flavin adenine dinucleotide
FBP	Fructose 1,6-bisphosphate
Fd	Ferredoxin
Fd-H <sub>2</sub> ase	Ferredoxin-dependent hydrogenase
G6PDH	Glucose 6-phosphate dehydrogenase
GAPDH	Glyceraldehyde 3-phosphate dehydrogenase
GAPDHN	Non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase
GAPOR	Glyceraldehyde 3-phosphate oxidoreductase
GDP	Guanosine diphosphate
GEM	Genome-scale metabolic model
GK	Glucokinase
GMP	Guanosine monophosphate



GppA	ppGpp phosphohydrolase
GTP	Guanosine triphosphate
H <sup>+</sup> -PPase	H <sup>+</sup> -translocating V-type pyrophosphatase
H <sub>2</sub>	Hydrogen gas
H <sub>2</sub> ase	Hydrogenase
HBDH	Hydroxybutyryl-CoA dehydrogenase
HK	Hexokinase
HPLC	High performance liquid chromatography
HPRR	HPr response regulator
IPTG	Isopropyl-β-D-thiogalactoside
KDGA	2-keto-3-deoxygluconate-6-phosphate aldolase
LDH	Lactate dehydrogenase
MalE	Malic enzyme
MDH	Malate dehydrogenase
MOPS	3-(N-morpholino) propanesulfonic acid
Na <sup>+</sup> -H <sub>2</sub> ase	Na <sup>+</sup> -translocating V-type pyrophosphatase
NAD(H)	Nicotinamide adenine dinucleotide



NADP(H)	Nicotinamide adenine dinucleotide phosphate
NADPH-H <sub>2</sub> ase	NADPH hydrogenase
NfnAB	NADH-dependent reduced Ferredoxin: NADP <sup>+</sup> oxidoreductase
NFOR	NADH ferredoxin oxidoreductase
OAA	Oxaloacetate
OAADC	Oxaloacetate decarboxylase
PAS	Per Arnt Sim domain
PCR	Polymerase chain reaction
PDC	Pyruvate decarboxylase
PDH	Pyruvate dehydrogenase
PEP	Phosphoenolpyruvate
PEPCK	Phosphoenolpyruvate decarboxylase
PFK	Phosphofructokinase
PFL	Pyruvate formate lyase
PGD	Phosphogluconate dehydratase
PGI	Phosphoglucose isomerase
PGK	Phosphoglycerate kinase



PGL	6-phosphogluconolactonase
PGM	Phosphoglycerate mutase
P <sub>i</sub>	Inorganic phosphate
PK	Pyruvate kinase
polyP	Poly-phosphate
POR	Pyruvate ferredoxin oxidoreductase
Ppase	Pyrophosphatase
PPaX	HPr associated pyrophosphatase
PPDK	Pyruvate phosphate dikinase
ppGpp	Guanosine tetraphosphate
PPi	Pyrophosphate
PPP	Pentose phosphate pathway
PEPs	Phosphoenolpyruvate synthase
PTA	Phosphotransacetylase
PTB	Phosphobutyrylase
PTS	Phosphotransferase system
RNA	Ribonucleic acid



RNAseq	Ribonucleic acid sequencing
RNF	<i>Rhodobacter</i> nitrogen fixing
ROK	Repressor/open reading frames of unknown function/sugar kinases
RPE	Ribulose-5-phosphate 3-epimerase
RPI	Ribose-5-phosphate isomerase
SDS-PAGE	Sodium dodecyl sulfate polyacrylamide gel electrophoresis
TAL	Transaldolase
TCA	Tri-carboxylic acid cycle
THF	Tetrahydrofolate
TKT	Transketolase
UTP	Uracil triphosphate



# 1 Literature review<sup>1</sup>

## 1.1 Introduction

Microbial fermentations have been used in the preparations of various forms of foods and beverages for thousands of years with evidence of fermented rice, honey, and fruit found as far back as 8000 BC (McGovern et al. 2004). While beverages draw flavors from the chemicals produced during fermentation, such as lactic acid, acetic acid, ethanol, and CO<sub>2</sub> these chemicals have also become the direct interest for chemical industries. While many of these chemicals can be synthesized via various chemical processes such as the carbonylation of methanol for acetic acid production, many of these processes rely on petroleum-based precursors for synthesis rendering them unsustainable and reliant of increasingly hard to access fossil fuels sources (Rogers, Chen, and Zidwick 2013). Anaerobic organisms can naturally produce many valuable chemicals using renewable biomass sources.

One of the first non-food industrial applications of biological fermentation processes was caused by greatly increased demand for acetone during World War I by the British Government for the production of cordite. This led to the development of alternative means of acetone synthesis (Ross 1961; Jones and Woods 1986). *Clostridium acetobutylicum*, also known as the Weizmann Organism, produces acetone through the Acetone-Butanol-Ethanol fermentation process (ABE) and was widely used for acetone production starting in 1916 (Ross 1961; Jones and Woods 1986; Gabriel 1928). *C. acetobutylicum* produces acetone, butanol, and ethanol in a 6:3:1 ratio using various sugars as a biomass feedstock. The ABE process relies on the 2 phases of *C.*

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<sup>1</sup> Contributing authors: Marcel Taillefer and Richard Sparling. Glycolysis as the Central Core of Fermentation. *Advances in Biochemical Engineering/Biotechnology*. (2015): 1-23



*acetobutylicum* growth: Phase 1, the acidogenic phase in which *C. acetobutylicum* consumes sugars producing acetic acid and butyric acid. The acids produced in the acidogenic phase cause a drop in pH, which causes a metabolic shift to Phase 2, the solventogenic phase. In the solventogenic phase, the organism will continue to utilize sugars but will also take up the acetic acid and butyric acid which are then converted into acetone, butanol, and ethanol (Jones and Woods 1986; Gottschalk 1986; Thauer, Jungermann, and Decker 1977; Häggström 1985). The production of acetone and butanol via the ABE process remained readily used in industry until the 1950s when the production of acetone and butanol from fossil fuels became more economically viable when compared to fermentation (Ross 1961; Jones and Woods 1986). The branched nature of the ABE process limits the yields of acetone or butanol therefore limiting its industrial potential.

Nevertheless, the current issues surrounding the potential for petroleum shortages as well as greenhouse gasses from our extensive combustion of petroleum productions has revived interest in biological alternatives to petrochemicals (Demain, Newcomb, and Wu 2005). This revival has been taking full advantage of recent advances in our understanding of bacterial fermentation through genomic and other high-throughput techniques (Bao et al. 2014; Linville et al. 2013). As well, the possibility for genetic manipulation (Olson, Sparling, and Lynd 2015) has caused researchers to revisit dark fermentation processes for biofuel production. There is special interest in the direct fermentation of the sugar content from inexpensive, but complex carbon feedstocks such as lignocellulose (McKendry 2002; Hamelinck, Van Hooijdonk, and Faaij 2005; Carroll and Somerville 2009), since many industrially relevant anaerobic bacteria have the capabilities of utilizing various carbon sources and also harbor the capability of degrading



complex materials such as lignocellulosic biomass (Table 1.1) (Lamed and Zeikus 1980; Tracy et al. 2012; Lynd et al. 2002; Lynd et al. 2005). While many anaerobic organisms have the potential to be utilized for various industrial processes, a wide number of organisms have branched metabolic pathways, using pyruvate as a major metabolic intermediate, leading to the simultaneous production of multiple chemicals of more or lesser value (Figure 1.1), which leads to the need of increased downstream processing.

Since most of the fermentative products of interest are the direct products of central metabolism associated with sugar fermentation (both hexoses and pentoses) for the conservation of usable energy an understanding of the core metabolism of these organisms is important in order to better exploit the wide range of fermentative organisms available. This is the primary purpose of the current review and will be done in light of the most recent knowledge based on genomic approaches.

## 1.2 Fermentation: variations on glycolytic pathways to pyruvate

The conservation of chemical energy, generally in the form of ATP, is essential for growth of both aerobic and anaerobic bacteria (Stouthamer 1973; Schneider and Gourse 2004). Both aerobic and anaerobic organisms will oxidize sugars to pyruvate and NADH. Aerobic organisms can utilize the TCA cycle in order to completely oxidize pyruvate to CO<sub>2</sub> and utilize the NADH and FADH for oxidative phosphorylation via the electron transport chain. Anaerobic organisms rely on substrate level phosphorylation, or the direct chemical phosphorylation, for ATP generation during oxidation of sugars to pyruvate, while NADH and pyruvate are converted



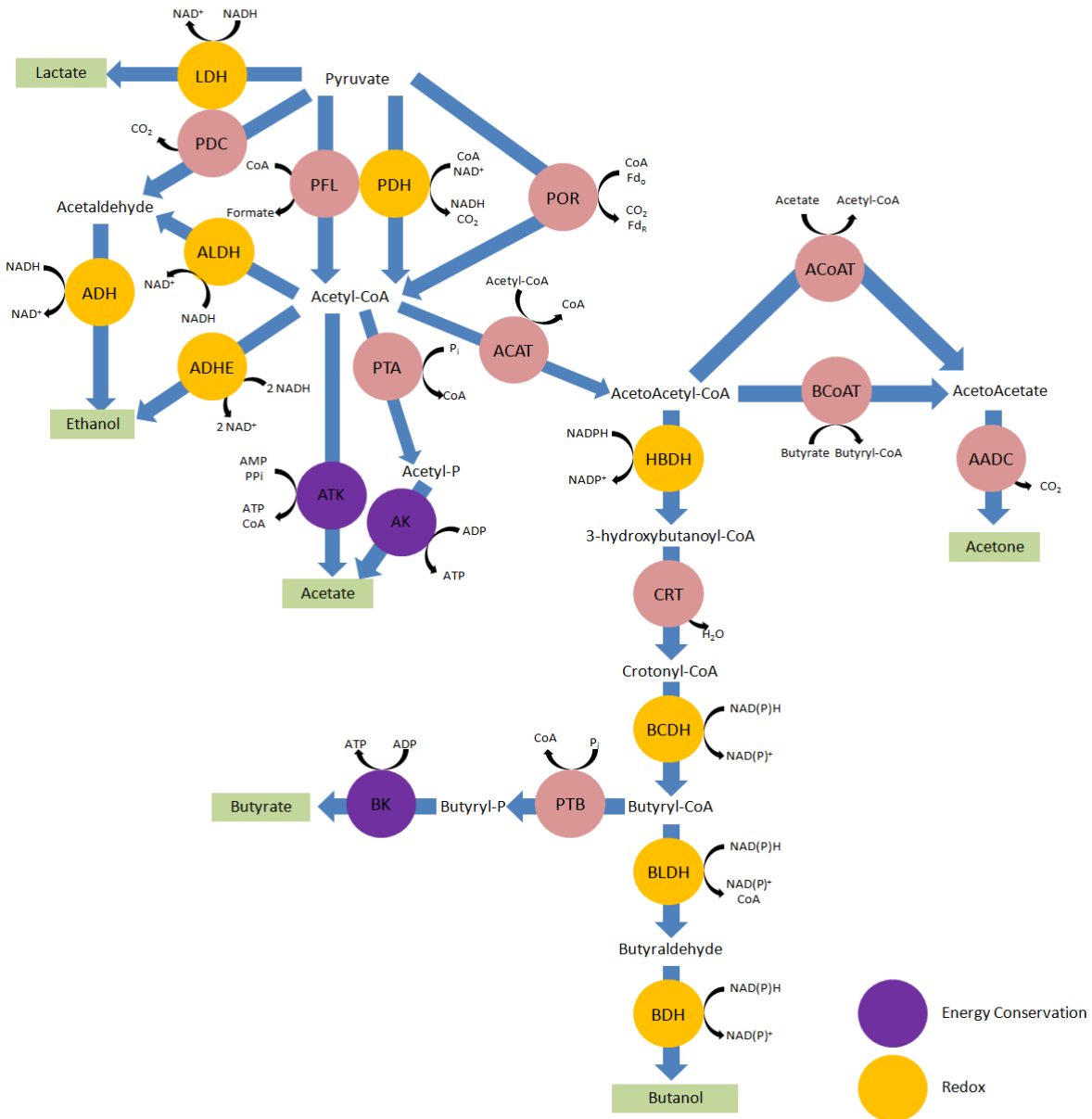
Table 1.1 : Industrially relevant Firmicutes producing bioenergy products from inexpensive renewable sources <sup>2</sup>

Organism	Growth temperature	Bioenergy products	Carbon source	Reference
<i>Ruminiclostridium thermocellum</i>	60	Ethanol H <sub>2</sub>	Lignocellulosic	(Lynd 1996)
<i>Ruminiclostridium termitidis</i>	37	Ethanol H <sub>2</sub>	Lignocellulosic	(Hethener, Brauman, and Garcia 1992)
<i>Ruminiclostridium cellulolyticum</i>	37	Ethanol H <sub>2</sub>	Lignocellulosic	(Ren et al. 2007)
<i>Ruminiclostridium stercorarium</i>	60	Ethanol	Lignocellulosic	(Schellenberg et al. 2014)
<i>Clostridium ljungdahlii</i>	37	Ethanol	CO <sub>2</sub> , CO, H <sub>2</sub> (Syngas)	(J. R. Phillips et al. 1993)
<i>Clostridium acetobutylicum</i>	37	Acetone Butanol Ethanol	Lignocellulosic, Starch	(Ross 1961; Gabriel 1928)
<i>Clostridium tyrobutyricum</i>	37	Butanol	Maltose Starch	(Yu et al. 2011)
<i>Clostridium beijerinckii</i>	35	Acetone Butanol Ethanol	Lignocellulosic	(Bellido et al. 2015)
<i>Lachnoclostridium phytofermentans</i>	37	Ethanol	Lignocellulosic	(Warnick, Methé, and Leschine 2002)
<i>Thermoanaerobacter ethanolicus</i>	70	Ethanol	Glucose Xylose	(Wiegel and Ljungdahl 1981)
<i>Thermoanaerobacter pseudethanolicus</i>	65	Ethanol	Glucose Xylose	(Hemme et al. 2011)
<i>Thermoanaerobacterium saccharolyticum</i>	55	Ethanol Butanol	Xylose	(Shaw et al. 2008; Bhandiwad et al. 2014)
<i>Caldicellulosiruptor bescii</i>	75	Ethanol	Lignocellulosic	(Chung et al. 2014)
<i>Caldicellulosiruptor saccharolyticus</i>	70	H <sub>2</sub>	Lignocellulosic	(Bielen and Verhaart 2013)

<sup>2</sup> Nomenclature of the organisms used in Table 1.1 are based on the re-classification of the *Clostridium* based on Yutin and Galperin 2013



Figure 1.1 : Various end product synthesis pathways. LDH, lactate dehydrogenase; PDC, pyruvate decarboxylase; PFL, pyruvate formate lyase; PDH, pyruvate dehydrogenase; POR, pyruvate ferredoxin oxidoreductase; ALDH, acetaldehyde dehydrogenase; ADH, alcohol dehydrogenase; ADHE, bifunctional acetaldehyde alcohol dehydrogenase; PTA, phosphotransacetylase; AK, acetate kinase; ATK, acetate thiokinase; ACAT, acetyl-CoA acetyltransferase; BCoAT, butyrate-acetoacetate CoA-transferase; ACoAT, acetate-acetoacetate CoA-transferase; AADC, acetoacetate decarboxylase; HBDH, hydroxybutyryl-CoA dehydrogenase; CRT, crotonase; BCDH, butyryl-CoA dehydrogenase; BLDH, butyraldehyde dehydrogenase; BDH, butanol dehydrogenase; PTB, phosphobutyrylase; BK, butyrate kinase





into various end products such as lactate, acetate, and ethanol (Prescott, Harley, and Klein 2005), which may not necessarily be associated with further energy conservation.

In general, anaerobic bacteria will employ the Embden-Meyerhof-Parnas (EMP) pathway for sugar utilization (Gottschalk 1986). The traditional EMP pathway can be divided into two sections. The upper section or investment phase utilizes ATP as a phosphate group donor to phosphorylate glucose and fructose-6-phosphate. The lower section or pay-off phase produces ATP through the phosphoglycerate kinase and pyruvate kinase. Therefore, through the EMP pathway, it is possible to produce a net of 2 ATP molecules and 2 NADH per glucose (Prescott, Harley, and Klein 2005).

An alternative for the EMP pathway for growth on hexoses would be the Entner-Doudoroff (ED) pathway. The traditional ED pathway, originally characterized in *Pseudomonas*, is found generally in Gram-negative facultative anaerobes (Entner and Doudoroff 1952; Conway 1992) including the ethanol producer *Zymomonas* (Barker and Hillier 1912; Swings and De Ley 1977). However, slight alterations to the ED have been identified in all three domains of life: Bacteria, Eukarya, and Archaea (Conway 1992; Andreesen and Gottschalk 1969; Romano and Conway 1996). Some *Clostridia* can utilize a semi-phosphorylative ED pathway in which glucose is converted to gluconate by gluconate dehydrogenase. The gluconate is converted to 2-keto-3-deoxy-gluconate which is then phosphorylated into 2-keto-3-deoxy-6-phosphogluconate via gluconate dehydratase and 2-keto-3-deoxy-gluconate kinase (Conway 1992; Bender, Andreesen, and Gottschalk 1971). Some hyper-thermophilic archaea will utilize another alternative to the ED pathway known as the non-phosphorylated ED pathway (Conway 1992; Ahmed et al. 2005). The traditional, semi-phosphorylated, and non-phosphorylated ED pathway lead to a net



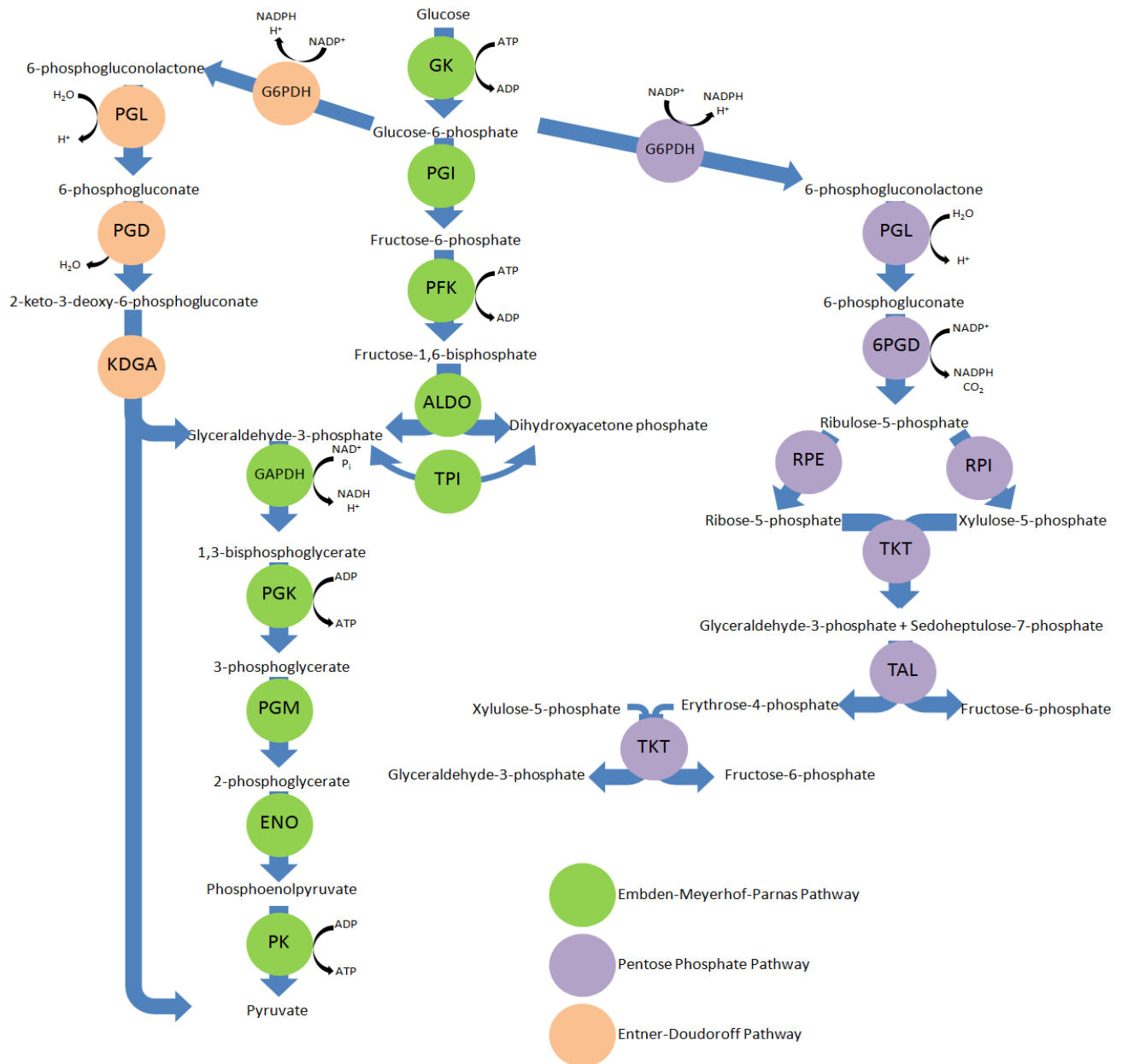
production of only one ATP and 2 NAD(P)H per glucose (Entner and Doudoroff 1952; Conway 1992; Andreesen and Gottschalk 1969; Ahmed et al. 2005).

The Pentose Phosphate pathway (PPP) can utilize both hexoses and pentoses. The PPP also allows for the interconversion of hexoses and pentoses. The PPP can be separated into 2 branches, the oxidative branch and non-oxidative branch. In the oxidative phase, glucose-6-phosphate is converted to ribulose-5-phosphate through various steps producing NADPH. This oxidative branch is viewed as a very important contributor to the production of the biosynthetic molecule NADPH (Prescott, Harley, and Klein 2005; Boyle 2005). The non-oxidative phase produces various biosynthetic precursors such as ribose-5-phosphate and erythrose-4-phosphate. For all the pathways above, pyruvate is produced and electrons are transferred to an electron carrier, typically nicotinamide. These various pathways are contrasted in Figure 1.2.

During fermentation, various compounds, primarily derived from pyruvate can be utilized as terminal electron acceptors to produce various chemicals such as lactic acid and butanol (Gottschalk 1986; Prescott, Harley, and Klein 2005). The reoxidation of electron carriers, generally NADH, is essential for glycolysis to continue, specifically phosphorylation of glyceraldehyde-3-phosphate to 1,3-bisphosphoglycerate, and therefore a careful balance is achieved between the reduction of  $\text{NAD}^+$  and the oxidation of NADH during anaerobic growth.



Figure 1.2 : Conventional pathways for glycolysis. GK, glucokinase; PGI, phosphate glucose isomerase; PFK, phosphofructokinase; ALDO, fructose-1,6-bisphosphate aldolase; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; PGK, phosphoglycerate kinase; PGM, phosphoglycerate mutase; ENO, enolase; PK, pyruvate kinase; G6PDH, glucose-6-phosphate dehydrogenase; PGL, 6-phosphogluconolactonase; PGD, phosphogluconate dehydratase; KDGA, 2-keto-3-deoxygluconate-6-phosphate aldolase; 6PGD, 6-phosphogluconate dehydrogenase; RPE, ribulose-5-phosphate 3-epimerase; RPI, ribose-5-phosphate isomerase; TKT, transketolase; TAL, transaldolase





### 1.3 Variations in Cofactor Specificity in the Embden-Meyerhof-Parnas Pathway

Focusing on the EMP-pathway, the variations in pathways that hexoses can take is compounded by the differences in cofactor specificity of key enzymes in glycolysis as used by different organisms.

#### 1.3.1 Glucokinase

Glucokinase (GK) catalyzes the phosphorylation of glucose into glucose-6-phosphate, generally using ATP as a phosphate group donor. Bacterial GK however, share no homologies with the less specific hexokinases found throughout the domain Eukarya and also differ from hexokinases by being specific for glucose, nevertheless, despite their lack of homology the affinity for glucose binding ( $K_m$ ) of bacterial GK is similar to that of eukaryotic hexokinases (Ronimus and Morgan 2003; Cárdenas, Cornish-Bowden, and Ureta 1998). GK in prokaryotes can be further divided into three major groups, ATP-dependent, ADP-dependent, and polyphosphate (polyP)-dependent (Ronimus and Morgan 2003; Ito et al. 2001; Labes and Schonheit 2003; Holwerda et al. 2014; N. F. Phillips, Horn, and Wood 1993; Hsieh, Kowalczyk, and Phillips 1996). ATP-dependent GK are found in all Domains of life ranging from human, yeast, Bacteria, and Archaea and have a very conserved structure (Anderson, Stenkamp, and Steitz 1978; Rosano et al. 1999; Aleshin et al. 1998). ADP-dependent GK are found extensively in thermophilic archaea especially in the phylum *Euryarchaeota* (Koga et al. 2000; Dörr et al. 2003). The prevalence of ADP-dependent GK in thermophilic archaea is believed to be due to the increased thermostability of ADP at higher temperatures. This, along with the possibility of recycling ADP generated from ATP hydrolysis used in anabolic reactions as a high-energy phosphate donor can lead to more efficient energy conservation during growth. However,



despite the increased thermostability and the possible increase in net ATP generation, no functional ADP-dependent GKs have been identified in thermophiles within the domain Bacteria. Polyphosphate (polyP)-dependent GKs were believed to have evolved early in the evolution of life since it is believed that polyP was already available in prebiotic times (Kornberg 1995). Therefore, it is believed that the primitive polyP-dependent GK evolved through time to utilize nucleotide triphosphates or nucleotide diphosphates since many polyP-GK are not specific for polyP but can often utilize ATP, CTP, UTP, or GTP as phosphate group donors as well as PolyP (Szymona and Widomski 1974; N. F. Phillips, Hsieh, and Kowalczyk 1999).

### 1.3.2 Phosphofructokinase

Phosphofructokinase (PFK) catalyzes the phosphorylation of fructose-6-phosphate into fructose-1,6-bisphosphate generally using ATP as a phosphate donor in organisms ranging from *E. coli* to mammals. ATP-dependent PFK plays a pivotal role in the regulation of carbon flux through glycolysis as the first irreversible reaction of glycolysis (Moreno-Sánchez et al. 2008). Therefore, it was believed that ATP-dependent PFK is conserved throughout the tree of life and essential for glycolysis. However, pyrophosphate (PPi)-dependent PFKs have been found in lower eukaryotes such as *Entamoeba histolytica* and *Toxoplasma gondii*, in plants, in Archaea, and in some Bacteria (Mertens 1991; Mertens et al. 1998; Peng and Mansour 1992; Wood, O'Brien, and Micheales 1977). PFKs can be organized into three main phylogenetically distinct-but-related families. Family A PFK includes the ATP-dependent PFK from higher eukaryotes, ATP- and PPi-dependent PFK from bacteria, PPi-dependent from some Archaea, and the PPi-dependent from plants (Mertens et al. 1998; Michels et al. 1997; Siebers, Klenk, and Hensel 1998; Wu et al. 1991; Ding, Ronimus, and Morgan 2000). Family A PPi-dependent PFK can further be divided into Type



I, which are not regulated by fructose-2,6-bisphosphate and found predominantly in anaerobic bacteria, and Type II which are activated by the presence of fructose -2,6-bisphosphate similar to ATP-dependent PFK found in higher eukaryotes and are generally only found in plants (Ronimus and Morgan 2003; Mertens et al. 1998). P<sub>PPi</sub>-dependent PFK, unlike ATP-dependent PFK, is reversible and can also be utilized for gluconeogenesis essentially replacing fructose-1,6-bisphosphatase. Family B PFKs are ATP-dependent and found generally in Enterobacteria such as *E. coli* (Ronimus and Morgan 2003; Kotlarz and Buc 1982; Ronimus and Morgan 2001). Family B PFKs have demonstrated the potential of phosphorylating various substrates such as fructose, fructose-1-phosphate, adenosine, and ribose (Sigrell et al. 1998). Family C are ADP-dependent PFKs that have only been identified in thermophilic Archaea and some mesophilic methanogenic Archaea (Ronimus and Morgan 2001; Verhees et al. 2001; Tuininga et al. 1999).

### 1.3.3 Glyceraldehyde-3-Phosphate Dehydrogenase and Phosphoglycerate Kinase

Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) catalyzes the reversible phosphorylation of glyceraldehyde-3-phosphate utilizing NAD<sup>+</sup> and inorganic phosphate (P<sub>i</sub>) into 1,3-bisphosphoglycerate and NADH. Some plants and photosynthetic cyanobacteria have NADP-dependent GAPDH which is utilized for gluconeogenesis involved in CO<sub>2</sub> assimilation (Fothergill-Gilmore and Michels 1993; Brinkmann et al. 1989; Valverde, Losada, and Serrano 1997). Phosphoglycerate kinase (PGK) catalyzes the transfer of a phosphate group from 1,3-bisphosphoglycerate onto ADP forming ATP and 3-phosphoglycerate. Most PGKs can utilize other purine nucleotides such as GDP/GTP with similar affinities as ADP/ATP but with much lower catalytic (<50%) rates making ATP/ADP the preferred substrates (Krietsch and Bücher 1970; Kuntz and Krietsch 1982; Encalada et al. 2009).



At this point in the glycolytic pathway, many thermophilic Archaea utilize variants of the typical EMP pathway such as a tungsten dependent glyceraldehyde-3-phosphate ferredoxin oxidoreductase (GAPOR). This bypasses the transfer of the phosphate group onto ADP catalyzed by PGK yielding a lower net ATP gained directly from glycolysis. GAPOR catalyzes the direct irreversible conversion of glyceraldehyde-3-phosphate into 3-phosphoglycerate using ferredoxin as an electron acceptor, bypassing the need for GAPDH and PGK (Ronimus and Morgan 2003; Reher, Gebhard, and Schönheit 2007; Van Der Oost et al. 1998). There has been no GAPOR orthologs found in Bacteria, however, some bacteria will have an enzyme similar to GAPOR in the form of a non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase (GAPDHN). GAPDHN, like GAPOR, directly and irreversibly catalyzes the conversion of glyceraldehyde-3-phosphate into 3-phosphoglycerate, but using  $\text{NADP}^+$  as an electron acceptor rather than ferredoxin (Boyd, Cvitkovitch, and Hamilton 1995; A. T. Brown and Wittenberger 1971). Once believed to be found exclusively in plants, GAPDHN have been identified in many bacteria including some Firmicutes such as *Clostridium acetobutylicum* (Iddar et al. 2005). However, in *C. acetobutylicum* the activity of the GAPDHN was roughly 100-fold lower than the GAPDH activity under the conditions tested, and therefore its role in metabolism remains unclear (Iddar et al. 2002).

#### 1.3.4 Pyruvate Kinase

The final step of the traditional EMP pathway is the conversion of phosphoenolpyruvate (PEP) into pyruvate. Generally, this final step is catalyzed by pyruvate kinase (PK) transferring the phosphate onto ADP creating ATP. PKs can be generally assembled into type I and type II based on their regulatory mechanisms. Type I PKs are activated by various sugar phosphates such



as fructose-1,6-bisphosphate and are generally found in Bacteria and eukaryotes. Type II PKs are regulated by energy intermediates such as AMP and ATP rather than sugar phosphates and are found throughout Bacteria and Archaea (Ronimus and Morgan 2003; Schramm et al. 2000). The conversion of PEP into pyruvate can also be catalyzed by a pyruvate phosphate dikinase (PPDK) or pyruvate water dikinase (PPS) rather than PK. PPDK utilizes PEP, AMP, and PPi to produce pyruvate, ATP, and P<sub>i</sub>. PPS is similar to PPDK but utilizes PEP, AMP, and P<sub>i</sub> producing pyruvate and ATP. However, pyruvate production through PK is expected to be favored over PPDK and PPS because it is a more thermodynamically favorable reaction (Thauer, Jungermann, and Decker 1977). Despite PK being thermodynamically favorable, some organisms will utilize PPDK or PPS over PK even if both are present in the genome. In the thermophilic Archaea *Thermococcus kodakarensis*, PK and PPS are utilized during glycolysis. The PPS is the main contributor of pyruvate flux with the PK being activated under high ADP concentrations in order to regulate the internal concentration of ADP (Imanaka et al. 2006). This regulatory mechanism might be specific to Archaea, specifically, the *Thermococcales*, since many Archaea utilize ADP-dependent GK and PFK over ATP- or PPi-dependent versions that are employed in bacteria. Another Archaea however, *Thermoproteus tenax*, utilizes ATP-dependent GK and PPi-dependent PFK rather than ADP-dependent versions and employs similar means of pyruvate kinase regulation. In the *T. tenax* genome, PK, PPDK, and PPS are all encoded, with PK being expressed only during heterotrophic growth and PPS only being expressed during autotrophic growth, while the PPDK is expressed under all conditions. During heterotrophic growth, both PK and PPDK are utilized for glycolysis with the activity of the PPDK regulated by the ratio of ATP/AMP while the PK activity is regulated by the concentration of ADP (Tjaden et al. 2006). A further example of regulation



can be found in *Caldicellulosiruptor saccharolyticus*. During growth, *C. saccharolyticus* will utilize both PPK and a type II PK that is regulated by the presence of PPi, AMP, and ADP during growth (Bielen et al. 2010; Feng et al. 2008). All of these proposed regulatory mechanisms demonstrate the importance of energy carriers as direct regulators of pyruvate synthesis.

Taken together, alternative co-factor utilization can offer various advantages such as flexibility in cofactor utilization, allowing organisms to adapt to various conditions, and the recycling of by-products from anabolic reactions for catabolic reactions in order to increase the net ATP gained from glycolysis. The utilization of alternative cofactors can alter the regulation of glycolytic flux by alteration of key regulatory steps such as PFK (PPi versus ATP). Increased energy efficiency in modified glycolysis pathways could offer advantages to strictly fermentative organisms such as bacteria from the class Clostridia. Studying these variations in greater depth is of importance since several fermentative organisms with industrial potential show differences in cofactor utilization observed through both genomic studies and recent physiological studies.

#### 1.4 The Variant glycolytic pathway of *Ruminiclostridium thermocellum*

The genus *Clostridium* contains a wide variety of obligatory anaerobic sporulating organisms, several of which have the potential to generate industrially relevant fermentative end-products. From a phylogenetic point of view it encompasses a rather wide range of distinct clades. A recent phylogenetic re-evaluation has broken up the genus, redistributing many of the species into 6 new genera (Yutin and Galperin 2013). For example, *C. acetobutylicum* and several other acetone-butanol producers stay in the genus *Clostridium*, while several of the better-



studied ethanol producing, cellulose degrading clostridia have been moved to the *Ruminococcaceae*, a family which includes the cellulolytic ethanol producing *Ruminococcus albus*, into the genus *Ruminiclostridium*. The type species for this new genus is *Ruminiclostridium thermocellum* (formally *Clostridium thermocellum*), a well-studied thermophile capable of growth on crystalline cellulose and candidate for commercial bioethanol production via consolidated bioprocessing of lignocellulosic biomass (Demain, Newcomb, and Wu 2005; Lynd et al. 2002; Yutin and Galperin 2013). However, wild-type *R. thermocellum* strains undergo mixed-acid fermentations producing lactate, formate, acetate, ethanol, H<sub>2</sub>, and CO<sub>2</sub> which limits the production of bioethanol due to diversion of carbon and electrons by the branched metabolic pathways (Rydzak et al. 2009; Rydzak et al. 2011; Carere et al. 2008; Islam et al. 2006; Lynd, Grethlein, and Wolkin 1989; Ellis et al. 2012). *R. thermocellum* has all of the genes required for a functional EMP pathway with the exception of a PK, and the required proteins are transcribed and translated during growth (Roberts et al. 2010; Raman et al. 2011; Rydzak et al. 2012; Burton and Martin 2012). Therefore, it was believed that *R. thermocellum* had a classical glycolysis pathway, with the PK assumed to be present, but somehow missing from the annotation. While PK activity was reported in *R. thermocellum* strain 651 in the 1970's, no gene could be linked to this activity (Patni and Alexander 1971). None of the currently sequenced strains of *R. thermocellum* have any annotated PK gene. Explanations for the discrepancies are that the PK activity was linked to a specific strain of *R. thermocellum* strain 651, and subsequently this particular strain was lost, or that the *R. thermocellum* strain 651 described in the 1970's could have been contaminated with various saccharolytic organisms such as bacteria from the genus



*Thermoanaerobacter* (Zhou et al. 2013; Golovchenko, Chuvilskaya, and Akimenko 1986; Erbezniik et al. 1997).

Looking at glycolysis in greater detail, cell extracts of *R. thermocellum* ATCC 27405 and DSM 1313 display very low or undetectable ATP-dependent GK activity (Zhou et al. 2013; S. V. Nochur et al. 1992). Instead, *R. thermocellum* displayed GK activity with a strong preference for GTP (50 fold higher than ATP) as a phosphate group donor. GTP-dependent GK has been identified in other organisms such as *Fibrobacter succinogenes*, *Fibrobacter intestinalis*, and *Ruminococcus albus* (Glass and Sherwood 1994; Lou, Dawson, and Strobel 1997). Both *R. thermocellum* and *R. albus* fall under the family *Ruminococcaceae*. Interestingly, these organisms all utilize cellulosic materials as a carbon source during growth in their natural environments. The GTP-dependent GK activity from *F. intestinalis*, *R. albus*, and *R. thermocellum* were not specific for GTP but all displayed lower activity with ATP when measured in cell extracts similar to the partially purified GTP-dependent GK from *F. succinogenes* (Zhou et al. 2013; Glass and Sherwood 1994; Lou, Dawson, and Strobel 1997). This indicates that GTP-dependent GK share similarities with the polyP-dependent GK in that they have a preferred phosphate donor but are not specific to one phosphate donor. While PPi was tested as a putative phosphate group donor for GK in the *R. thermocellum* cell extract, no activity was detectable (Zhou et al. 2013).

The reaction catalyzed by ATP-dependent PFK is often viewed as the first commitment step in glycolysis since it is essentially irreversible under biological conditions. However, *R. thermocellum* does not exhibit any detectable ATP-dependent PFK activity but instead utilizes a PPi-dependent PFK for fructose-6-phosphate phosphorylation when grown on cellobiose (Zhou et al. 2013). The *R. thermocellum* genome contains a copy of both ATP- and PPi-dependent PFK



genes and both are transcribed and translated. However, the levels of PPI-dependent PFK in the proteome and transcriptome is much greater than that of the ATP-dependent PFK (Raman et al. 2011; Rydzak et al. 2012; Burton and Martin 2012). Utilization of PPI-dependent PFK offers a net increase of 1 ATP per glucose during glycolysis by recycling PPI generated as a by-product of various anabolic reactions in order to phosphorylate fructose-6-phosphate (Mertens et al. 1998; Bielen et al. 2010; M Müller 1992; Miklós Müller et al. 2001).

In the absence of PK, *R. thermocellum* must utilize alternative means of pyruvate generation. Possible alternatives include PPDK, phosphoenolpyruvate carboxykinase (PEPCK), oxaloacetate decarboxylase (OADC), or a malate shunt, all of which are present in the genome, transcribed and translated (Raman et al. 2011; Rydzak et al. 2012; Burton and Martin 2012). PPDK are believed to play a role in gluconeogenesis rather than glycolysis in many organisms (Hutchins, Holden, and Adams 2001; Chao et al. 1993). However, *Trypanosoma cruzi* utilizes the internal concentrations of PPI in order to control phosphoenolpyruvate (PEP) utilization. Under high internal concentrations of PPI, PEP utilization shifts from PK to PPDK for the production of pyruvate and ATP (Acosta et al. 2004). While this provides precedence for PPDK use in *R. thermocellum*, it was observed that the deletion of the PPDK gene had little effect on the growth rate or final culture density (Zhou et al. 2013). Pyruvate may also be produced indirectly through a malate shunt. Phosphoenolpyruvate is converted to oxaloacetate via the GDP-dependent phosphoenolpyruvate carboxykinase (PEPCK). The oxaloacetate can then be converted to malate and finally pyruvate by NADH-dependent malate dehydrogenase (MDH) and NADP<sup>+</sup>-dependent malic enzyme (MalE) (Figure 1.3Figure 1.3). MDH catalyzes the reduction of oxaloacetate into malate with NADH as a preferred cofactor. MalE catalyzes the decarboxylation of malate into

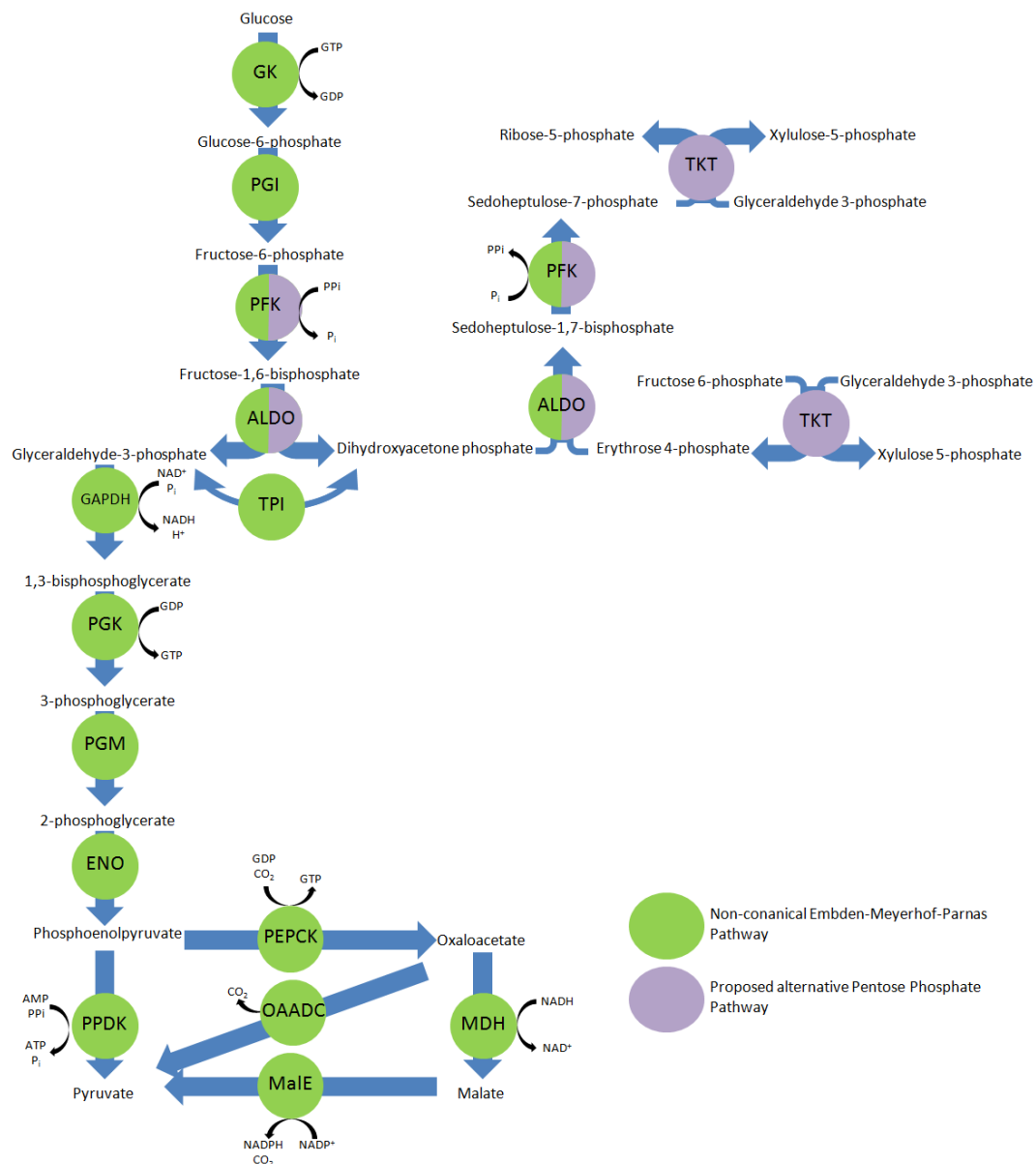


pyruvate utilizing  $\text{NADP}^+$  as a cofactor (Lamed and Zeikus 1981; Taillefer et al. 2015). Overall, the indirect conversion of phosphoenolpyruvate into pyruvate via the malate shunt produces GTP rather than ATP and a transfer of electrons between NADH and  $\text{NADP}^+$ . Conversely, oxaloacetate can be directly decarboxylated into pyruvate using a proton-translocating, membrane-bound OAADC. Either way, GTP produced through PEPCK could be used to recharge GDP discharged from the GK thus linking the malate shunt with the initiation of glycolysis. PPDK is expected to be activated by  $\text{PPi}$  (Tjaden et al. 2006), the MalE, and therefore the malate shunt, is inhibited by the presence of  $\text{PPi}$  (Glass and Sherwood 1994). High concentrations of  $\text{PPi}$  would be expected to direct carbon flux through PPDK while low concentrations of  $\text{PPi}$  redirects carbon through OAADC and the malate shunt ultimately regulating the production of pyruvate (Taillefer et al. 2015).

However, based on theoretical calculations, the amount of  $\text{PPi}$  generated as a by-product from various reactions would not be able to account for the  $\text{PPi}$  requirement for  $\text{PPi}$ -dependent PFK and PPDK during active growth (Zhou et al. 2013; Heinonen 2001; Willquist and Van Niel 2010). Therefore, the active generation of  $\text{PPi}$  seems to be a requirement for glycolysis during growth using  $\text{PPi}$ -dependent PFK and PPDK. The active generation of  $\text{PPi}$  can possibly be done through multiple means in *R. thermocellum* such as the utilization of a membrane-bound  $\text{H}^+$ -translocating V-type inorganic pyrophosphatase (V-type PPase), modified pentose phosphate pathway via the  $\text{PPi}$ -dependent PFK (Figure 1.3), and glycogen cycling (Heinonen 2001; M. Baltscheffsky, Schultz, and Baltscheffsky 1999; Hungate 1963; Guedon, Desvaux, and Petitdemange 2000).



Figure 1.3 : Proposed *R. thermocellum* central catalysis pathways. GK, glucokinase; PGI, phosphate glucose isomerase; PFK, phosphofructokinase; ALDO, fructose-1,6-bisphosphate aldolase; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; PGK, phosphoglycerate kinase; PGM, phosphoglycerate mutase; ENO, enolase; PPDK, pyruvate phosphate dikinase; PEPC, phosphoenolpyruvate carboxykinase; MDH, malate dehydrogenase; MalE, malic enzyme; OAADC, oxaloacetate decarboxylase; TKT, transketolase





In *R. thermocellum*, the genome does not encode a soluble inorganic pyrophosphatase, rather it encodes for one V-type PPase that is transcribed and translated throughout the growth indicating that it is active during growth (Raman et al. 2011; Rydzak et al. 2012; Burton and Martin 2012). Generally, V-type PPase utilizes the breakdown of PPi into P<sub>i</sub> in order to pump H<sup>+</sup> across the membrane. Due to the need for active generation of PPi however, the V-type PPase could utilize the proton motor force in order to synthesize PPi, similar to how ATP is generated through ATP synthase (Heinonen 2001; M. Baltscheffsky, Schultz, and Baltscheffsky 1999).

*R. thermocellum* does not have a complete pentose phosphate pathway as it lacks the enzymes for the oxidative branch (glucose-6-phosphate dehydrogenase, gluconolactonase, and 6-phosphogluconate dehydrogenase) and also the transaldolase for the non-oxidative branch (Rydzak et al. 2012). Rather, the pentose phosphate pathway of *R. thermocellum* is predicted to rely on intermediates produced by the EMP pathway, fructose-6-phosphate and glyceraldehyde-3-phosphate, in order to feed into the pentose phosphate pathway for the production of pentose intermediates. In the absence of a transaldolase, *R. thermocellum* possibly employs a novel mechanism for pentose generation that has been demonstrated in several parasitic protists such as *Entamoeba histolytica* and in *Escherichia coli* (Rydzak et al. 2012; Mertens 1993; Mertens, De Jonckheere, and Van Schaftingen 1993; Susskind, Warren, and Reeves 1982; Nakahigashi et al. 2009). This mechanism involves the aldolase and PPi-dependent PFK from the EMP pathway along with the transketolase. The aldolase converts dihydroxyacetone phosphate and erythrose-4-phosphate into sedoheptulose-1,7-bisphosphate. The sedoheptuloase-1,7-bisphosphate is then dephosphorylated by PPi-dependent PFK into sedoheptulose-7-phosphate producing PPi. And finally the sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate are converted into



xylulose-5-phosphate and ribose-5-phosphate (Rydzak et al. 2012; Susskind, Warren, and Reeves 1982). Therefore, the conversion of hexoses to pentoses could help supply the PPi required for growth in *R. thermocellum*. The lack of an oxidative phase of the PPP also removes the NADPH-generating reactions of the PPP required for many biosynthetic reactions. However, this lack of NADPH generation could be alleviated by flux through the transhydrogenation reaction of the malate shunt or by the activity of an NADH-dependent reduced ferredoxin:NADP<sup>+</sup> oxidoreductase (NfnAB) which simultaneously utilizes both NADH and reduced ferredoxin producing NADPH (Rydzak et al. 2014; S. Wang et al. 2010). This also raises an interesting regulation based on the production of a biosynthetic by-product, PPi, and a biosynthetic requirement, NADPH.

PPi can also be produced during glycogen cycling, more specifically by glucose-1-phosphate adenylyltransferase. The simultaneous production and consumption of glycogen has been observed in some related cellulolytic organisms such as *Ruminiclostridium cellulolyticum* and *R. albus* (Hungate 1963; Guedon, Desvaux, and Petitdemange 2000). The proteome of *R. thermocellum* supports simultaneous production and consumption of glycogen since both glycogen synthesis and breakdown proteins are detectable throughout growth (Rydzak et al. 2012). However, uncontrolled cycling would result in a futile cycle of production and consumption. But it is possible that glycogen cycling could be regulated by the internal concentrations of PPi and ATP. At high concentrations of ATP, glucose-1-phosphate adenylyltransferase would utilize ATP and glucose-1-phosphate to produce PPi and ADP-glucose, while at low ATP concentrations, the flux through glucose-1-phosphate adenylyltransferase would be greatly reduced limiting PPi production.



Therefore, despite the requirement for *R. thermocellum* to produce PPi for glycolysis, utilization of a PPi-dependent PFK and PPDK leads to a net increase in the conservation of chemical energy due to the recycling of PPi from various biosynthetic reactions such as the synthesis of nucleic acids, amino acids, fatty acids, and lipids (Willquist and Van Niel 2010). The utilization of PPi-dependent enzymes in glycolysis could reflect the strict fermentative lifestyle of *R. thermocellum* where efficient energy generation is a requirement for its growth and survival.

### 1.5 Ruminiclostridium glycolysis a widespread model?

When compared to the traditional *E. coli* model, it would seem that the *R. thermocellum* central catabolism is not canonical in the sense that it may rely on enzymes (GK, PFK, PGK, PPDK) that utilize alternative cofactors during growth, and adapt alternative strategy for a functional non-oxidative pentose phosphate pathway (Rydzak et al. 2012; Zhou et al. 2013). An analysis of the genome of some Firmicutes and other phyla, especially thermophiles, revealed that many species of *Ruminiclostridium*, *Caldicellulosiruptor*, *Thermotoga*, and *Thermoanaerobacter* have a PPi-dependent PFK and an ATP-dependent PFK in their genomes (Bielen et al. 2010; Carere et al. 2012; Baptiste, Moreira, and Philippe 2003). While both ATP- and PPi-dependent PFK have been annotated in *R. stercorarium* based on sequence homology with the *R. thermocellum* PFK, the proteome of *R. stercorarium* shows significantly higher expression of the PPi-dependent PFK versus the ATP-dependent PFK (Schellenberg et al. 2014). A further role of PPi-dependent PFK in *Ruminiclostridium* may be to compensate for the missing transaldolase gene for PPP in for example *R. stercorarium* (Schellenberg et al. 2014) and *R. termitidis* (Munir et al. 2016)(Figure 1.3), organisms that can use xylose, a pentose, as sole carbon and energy source.



While *R. thermocellum* does not contain a PK gene, most other organisms do encode a PK in their genome. Despite the presence of a PK gene in their genomes, *C. saccharolyticus*, *R. termitidis*, and *R. stercorarium* seem to prefer the utilization of their PPDK based on expression levels and/or enzyme activities (Bielen et al. 2010; Schellenberg et al. 2014; Munir et al. 2016). The presence of both a PPDK and PK is expected to be regulated by the internal concentrations of PPi since PK activity is strongly inhibited by PPi (Bielen et al. 2010; Acosta et al. 2004). Since the internal concentrations of PPi were found to be relatively high (4 mM) during exponential growth in *C. saccharolyticus*, it would seem that PPDK will be utilized over PK during active growth showing a strong preference for PPDK even with an active PK present (Bielen et al. 2010). Therefore, the regulation of pyruvate generation seems to be similar to what is proposed in *R. thermocellum* in which the malate shunt is inhibited by the internal concentration of PPi leading to PPDK utilization during high internal PPi concentrations (Taillefer et al. 2015).

With the absence of the oxidative branch of the PPP, production of NADPH can be done through the malate shunt or through the NfnAB. Similarly to *R. thermocellum*, *R. stercorarium* and *R. termitidis* are lacking a complete oxidative branch and therefore would rely on alternative means to produce NADPH such as the malate shunt (Schellenberg et al. 2014; Munir et al. 2016). This also correlates with the phylogenetic grouping of the *R. thermocellum*, *R. termitidis*, and *R. stercorarium* Male hinting at a similar regulation by PPi (Taillefer et al. 2015). Taken together, the central catalysis of *R. thermocellum* is different from the "conventional" model, however, it seems to be similar to various other Firmicutes especially within the genus *Ruminiclostridium*. This also raises the importance of PPi for *Ruminiclostridium* as not only a putative energy-recycling source but also as a regulatory molecule regulating pyruvate synthesis and NADPH



generation. Aspects of this pathway variant are likely to extend to other genera, for example in the *Caldicellulosiruptor*.

## 1.6 Conclusion

Utilization of inexpensive renewable biomass sources is of interest making anaerobic organisms of particular interest due to their ability for utilization of various and complex substrates without requiring extensive pre-treatments. However, the branched nature of the central catalysis of many anaerobic bacteria diminishes the industrial potential of this process.

As the bioenergy products are produced directly from glycolysis products and intermediates, the careful understanding of glycolysis is essential in the development of strategies for increasing product yields and therefore increasing industrial potential. While the *R. thermocellum* glycolysis differs in cofactor preference when compared to the 'traditional' *E.coli*/yeast model employed by the other Clostridia such as *C. acetobutylicum*, it seems to be a representative model of the metabolism found in various Firmicutes, especially in the genus *Ruminiclostridium*. Alterations in cofactor utilization such as the preference for PPi rather than ATP as the phosphate group donor for PFK can render the reaction reversible, dampening the regulatory role of PFK in controlling the glycolytic flux. Insights into the cofactor utilization of *R. thermocellum* have also revealed PPi as a very important putative regulator of many essential reactions such as the control of pyruvate production and NADPH production. However, the importance of PPi as a putative regulator of catabolic and anabolic reactions is not strictly a phenomenon of *R. thermocellum* metabolism but seems widespread among the genus



*Ruminiclostridium* and other related Firmicutes. Therefore, *R. thermocellum* glycolysis appears as a valid alternative model for many industrially relevant anaerobic bacteria.

Furthermore, the diversity of potential variations in pathways described in the current review reemphasizes the importance of refining annotation on the basis of biochemical characterization of key enzymes in central metabolism in relevant organisms, especially with respect to cofactor specificity and allosteric regulation. The presence within the genome of multiple genes putatively coding for the same annotated function, and even their expression in the transcriptome and proteome reminds us of the further importance of allostery in regulating the flux of intermediates through these enzymes. There is a potential interplay of high energy phosphate carriers (ATP, GTP, PPI) and electron carriers (NADH, NADPH, and ferredoxin), making the measurement of in vivo concentrations of these co-factors crucial in understanding not only central metabolism but also end product selection in industrially relevant fermentative organisms (Table 1.1).

## 1.7 Thesis objectives

The objective of this thesis was to evaluate the biochemical properties of central catalysis in *R. thermocellum* in order to assess the effect of small high-energy metabolites such as PPI and ATP. Further, the importance of PPI as a phosphate group donor and flux regulator of central catalysis is assessed using biochemical and genomic analyses. Overall, the thesis goals were focused on gaining a better understanding of the mechanisms regulating carbon and electron flux through central catalysis and end-product synthesis pathways.

The specific aims were



1. To evaluate the important central catabolism genes and putative flux regulatory nodes (GK, PFK, PGK, PPK, MDH, and MalE) in order to gain a better understanding of the enzyme kinetics associated with the particular proteins (Chapter 2, 4)
2. To evaluate the regulatory effects of small high energy metabolites such as ATP, and PPi on the enzyme activity of key central catalysis proteins in order to better understand the putative regulatory role of PPi (Chapter 2, 4)
3. To assess the variety of PPi metabolism genes found through industrially relevant Firmicutes in order to gain an idea of the diversity of PPi metabolism and to assess possible trends in terms of gene presence (Chapter 3)
4. To investigate the genetic and expression differences observed in 3 strains of *R. thermocellum* which produce 3 different end-product ratios in order to gain a better understanding of the regulatory mechanisms controlling the amount of specific end products (Chapter 5)



## 2 Reassessment of the Transhydrogenase/Malate Shunt Pathway in *Ruminiclostridium thermocellum* ATCC 27405 through Kinetic Characterization of Malic Enzyme and Malate Dehydrogenase<sup>3</sup>

### 2.1 Introduction

*Ruminiclostridium thermocellum* is a Gram-positive, anaerobic, thermophile capable of one of the highest growth rates on crystalline cellulose (Lynd et al. 2002; Demain, Newcomb, and Wu 2005). Furthermore, given its native ability to produce ethanol and H<sub>2</sub>, *R. thermocellum* is seen as an attractive microorganism for the production of biofuels via consolidated bioprocessing of lignocellulosic biomass. Unfortunately, current yields and production rates of ethanol and/or H<sub>2</sub> are low due to branched product pathways (Rydzak et al. 2009; Rydzak et al. 2011; Carere et al. 2008) which redirect carbon and electron flux away from the desired biofuel. These unwanted products include lactate, formate, and/or acetate (Islam et al. 2006; Carere et al. 2012; Lynd, Grethlein, and Wolkin 1989), as well as secreted amino acids (Ellis et al. 2012; Y. Deng et al. 2013). Thus, redirecting carbon and electron flux away from these secreted products towards either ethanol or H<sub>2</sub> may improve the economic viability of biofuels production using *R. thermocellum*.

A key pathway node involved in the interconversion of phosphoenolpyruvate (PEP) and pyruvate, which may catalyze either substrate level phosphorylation or transhydrogenation reactions between NADH to NADP<sup>+</sup>, has been re-visited in *R. thermocellum* (Y. Deng et al. 2013; Lamed and Zeikus 1980). The inter-conversion of PEP and pyruvate may be catalyzed using a

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<sup>3</sup> Contributing authors: Marcel Taillefer, Thomas Rydzak, David Levin, Ivan Oresnik, and Richard Sparling. *Applied and Environmental Microbiology* 81, No 7 (2015): 2423-2432



number of different putative enzymes. In contrast to most clostridia and other fermentative ethanol and/or H<sub>2</sub> producing organisms (Carere et al. 2012), *R. thermocellum* ATCC 27405 (GenBank accession number CP00568.1) does not encode a pyruvate kinase, which catalyzes PEP to pyruvate with the concomitant production of ATP from ADP and P<sub>i</sub>. Thus, an alternative means to generate pyruvate during glycolysis must be employed. Instead, *R. thermocellum* encodes two pyruvate dikinases (Cthe\_1308 and Cthe\_1253), which can potentially convert PEP to pyruvate and produce ATP from AMP and PP<sub>i</sub>. However, pyruvate dikinases are believed to play a role in gluconeogenesis, producing of PEP, rather than catabolizing it, in many organisms (Hutchins, Holden, and Adams 2001; Chao et al. 1993). Alternatively, pyruvate production in *R. thermocellum* could follow an alternative route involving phosphoenolpyruvate carboxykinase (PEPCK) (Cthe\_2874), a putative malate dehydrogenase (MDH) (Cthe\_0345), and malic enzyme (MalE) (Cthe\_0344) (Figure 2.7A). This pathway, referred to as the ‘malate shunt’, may be capable of a transhydrogenation reaction, during which electrons are transferred from NADH to NADP<sup>+</sup> (Lamed and Zeikus 1980). However, cofactor specificity of both MDH and MalE varies from organism to organism, and thus the specificity of these enzymes must be elucidated to verify the impact they may have on *R. thermocellum* metabolism.

MDHs, which can catalyze the reversible oxidation of malate to oxaloacetate (OAA), play a critical role in many biological processes such as the tricarboxylic acid cycle, amino acid synthesis, maintenance of reduction/oxidation pools, metabolic stress response, and gluconeogenesis (Ge et al. 2010; Goward and Nicholls 1994; Dong and Somero 2009; Zaitseva, Meneely, and Lamb 2009). They can be divided into two main groups based on cofactor preference: NAD<sup>+</sup>-dependent (EC 1.1.1.37) or NADP<sup>+</sup>-dependent (EC 1.1.1.82). Plants have a



chloroplastic NADP<sup>+</sup>-dependent MDH essential for malate shuttling in C<sub>3</sub> plants and carbon fixation in C<sub>4</sub> plants (Sheen 1999). MDHs have been identified in both dimeric and tetrameric oligomeric states. The tetrameric MDHs, also known as [LDH-like] MDH, have a quaternary protein structure similar to that of lactate dehydrogenase (LDH). MDH shares a common ancestry with LDH rendering the annotation of LDH or MDH based on amino acid sequence unreliable (Goward and Nicholls 1994). A mutation of a single amino acid in the *E.coli* MDH can convert its substrate specificity from oxaloacetate to pyruvate, essentially converting the MDH to an LDH (Yin and Kirsch 2007). This leads to increased uncertainty pertaining to the annotation of LDH or MDH based on amino acid sequence homology and warrants further biochemical characterization in each species of interest.

Like MDH, MalE, which catalyzes the oxidative decarboxylation of malate to pyruvate and CO<sub>2</sub>, can be classified into three different categories based on the cofactor specificity and the ability to decarboxylate OAA. These include: (i) NAD<sup>+</sup>-dependent, but not OAA-decarboxylating, MalE (1.1.1.39), typically utilized in carbon fixation in plants, (ii), NAD<sup>+</sup>-dependent OAA-decarboxylating MalE (EC 1.1.1.38), and (iii) NADP<sup>+</sup>-dependent OAA-decarboxylating MalE (1.1.1.40) (Bologna, Andreo, and Drincovich 2007). While the non-OAA decarboxylating MalE enzyme is incapable of converting OAA to pyruvate, the two latter enzymes can catalyze either malate or OAA, to pyruvate, thereby potentially bypassing the malate shunt/transhydrogenase pathway in the case of the latter. Furthermore, cofactor dependence of OAA-decarboxylating malic enzymes can also determine if transhydrogenation from NADH to NADP<sup>+</sup> occurs using the malate shunt. Thus, characterization of enzyme kinetics and cofactor specificity is critical in validating the proposed transhydrogenation pathway in *R. thermocellum*.



Recent evidence has indeed supported that PEP is likely converted to pyruvate via the malate shunt in *R. thermocellum*. Transcriptomic (Raman et al. 2011) and proteomic (Rydzak et al. 2012) studies have shown that Cthe\_2874, Cthe\_0345, and Cthe\_0344 are highly expressed in *R. thermocellum*, suggesting that they play a key role in pyruvate metabolism. Furthermore, *in vitro* crude cell extract enzyme activities demonstrated that MDH activity is strictly NADH-dependent whereas MalE activity is strictly NADPH-dependent in *R. thermocellum* strain DSM 1313 in cell-free extracts (Y. Deng et al. 2013). Similar observations were made in *R. thermocellum* strains AS39 and LQRI, reporting NADH-dependent MDH activity and an ammonium activated NADP<sup>+</sup>-dependent MalE-like activity in crude cell extracts (Lamed and Zeikus 1980). Subsequent purification of MalE from *R. thermocellum* AS39 revealed this NADP<sup>+</sup>-dependent MalE activity was NH<sub>4</sub><sup>+</sup> and Mn<sup>+2</sup> dependent (Lamed and Zeikus 1981).

To date, however, no one has directly shown which annotated putative genes encoding MDH and MalE are responsible for the assayed enzyme activities in *R. thermocellum*. While NADH-dependent MDH activity has been demonstrated, current GenBank annotation of the gene Cthe\_0345 lists it as a lactate dehydrogenase (LDH) belonging to the malate/lactate dehydrogenase PFAM. Furthermore, despite evidence that there is a MalE is NADP<sup>+</sup>-dependent via enzyme activities in *R. thermocellum*, the one annotated is indicated as an NAD<sup>+</sup>-dependent OAA-decarboxylating MalE (EC 1.1.1.38). Furthermore, there have been no studies demonstrating MalE OAA-decarboxylating activity in *R. thermocellum*. We have therefore cloned, purified, and characterized the putative MDH (Cthe\_0345) and MalE (Cthe\_0344) to determine cofactor specificity and enzyme kinetics to validate their presence and elucidate their possible role in the malate shunt and their potential role in *R. thermocellum* biofuels metabolism.



## 2.2 Materials and Methods

### 2.2.1 Strains and reagents.

*Ruminiclostridium thermocellum* ATCC 27405 genomic DNA was purchased from the American Type Culture Collection. *E. coli* DH5 $\alpha$  was used as the host for plasmid construction and screening. *E. coli* BL21 (DE3) was used as the expression strain for recombinant protein expression. The plasmids used for protein expression were pRSET-A (Life Technologies Corp.) and pET-28a (+) (Millipore Ltd.). All antibiotics used were purchased from Sigma-Aldrich. All PCR reactions were done using iProof™ High-Fidelity DNA polymerase (Biorad Laboratories Ltd). PCR purification was done using QIAquick PCR Purification Kit (Qiagen Inc.) All restriction enzymes used were purchased from New England Biolabs. Plasmids were extracted using Qiagen Plasmid Mini Kit (Qiagen Inc.). Recombinant proteins were purified using HiTrap™ chelating column (GE Healthcare Bio-Sciences Corp.). Malic acid, OAA, NADP<sup>+</sup>, NADPH, ATP, ADP, AMP, pyrophosphate (PPi), and all buffers used were from Sigma-Aldrich.

### 2.2.2 Primers and plasmid construction

Primers for MDH and MalE were designed using the corresponding gene sequence from Integrated Microbial Genomics (Markowitz et al. 2012). MDH (Cthe\_0345) was amplified by PCR using the sense primer 5'-ATATGGATCCCATGGAAATGGTAAAAAGTAGGTC-3' and antisense primer 5'-ATATGAATTCTTATAAATTCTTAACCTCGTTCAATAC-3'. The PCR product was purified and digested using BamHI and EcoRI restriction enzymes. The digested product was then ligated into pRSET-A by T4 DNA ligase (PROMEGA) to create the recombinant plasmid pAHCT345. MalE (Cthe\_0344) was amplified by PCR using the sense primer 5'-CATATGGATTACAGAAAGAATCACTAAG-3' and the antisense primer 5'-



CGGCCGTTATATTCTTGCAACTCCGGTTTTTC-3'. The PCR was purified and digested using NdeI and EagI. The digested product was then ligated into pET-28a (+) to create the recombinant plasmid pKHCT344. Plasmid constructs were verified via sequencing (Macrogen Corp.)

### 2.2.3 Overexpression and recombinant protein isolation

*E. coli* BL21 (DE3) containing either the pAHCT345 or pKHCT344 plasmid was cultured overnight in LB medium containing ampicillin (100 µg/mL) for pAHCT345 or kanamycin (30 µg/mL) for pKHCT344 at 37°C. Overnight cultures were re-inoculated into fresh LB medium containing the proper antibiotic and grown aerobically at 37°C until an OD<sub>600</sub> of 0.5-0.7. Isopropyl β-D-1-thiogalactopyranoside (IPTG) was then added to a final concentration of 1 mM. The cultures were grown for an additional 12 hours at 30°C. Cells were harvested and resuspended in buffer containing 20 mM NaH<sub>2</sub>PO<sub>4</sub> (pH 7.4), 0.5 M NaCl, and 20 mM imidazole. Cells were lysed at 37°C after 15 minutes incubation with 1 mg/mL lysozyme, 1% Triton X-100, 5 µg/mL DNase, 5 µg/mL RNase, and 5 mM MgCl<sub>2</sub> (Sambrook, Fritsh, and Maniatis 1982). Cell lysates were centrifuged at 4500 RPM for 30 minutes at 4°C. Supernatants were filtered through a 0.22 µm filter prior to being loaded on a Ni<sup>2+</sup> HiTrap metal affinity column and purified following the manufacturer's instructions (GE Healthcare Bio-Sciences Corp.). The recombinant His<sub>6</sub>-tagged proteins were eluted using a stepwise imidazole gradient. Imidazole and NaCl were removed from the protein samples using HiTrap<sup>TM</sup> Desalting Column eluting with 20 mM NaH<sub>2</sub>PO<sub>4</sub> (pH 7.4). Enzyme purity was verified by SDS-PAGE with a 12% resolving gel and a 5% stacking gel. Visualization of the proteins was done by staining the gels with Coomassie Brilliant Blue R-250. Protein concentration was measured by the Bradford assay using bovine serum albumin as a protein standard (Bradford 1976).



#### 2.2.4 Enzyme assays

All enzyme activities were measured in a 300  $\mu$ l well with a total reaction volume of 200  $\mu$ l up to 50°C. MDH activity was measured in a standard reaction containing 100 mM 3-(N-morpholino)propanesulfonic acid (MOPS) (pH 7.0), 10 mM dithiothreitol (DTT), 2 mM OAA, 0.2 mM NADH. MalE activity was measured in a standard reaction containing 100 mM MOPS (pH 7.0), 10 mM DTT, 2 mM malate, 0.2 mM NADP<sup>+</sup>, 5 mM MnCl<sub>2</sub>, 20 mM NH<sub>4</sub>Cl (Issakidis et al. 1992). LDH activity was measured in a standard reaction containing 100 mM MOPS (pH 7.0), 10 mM DTT, 10 mM pyruvate, 0.2 mM NADH, and 0.005 mM fructose-1-6-bisphosphate (Lamed and Zeikus 1980). Changes in cofactor (NADH, NADP<sup>+</sup>) concentration were monitored at 340 nm using BioTek Synergy 4 plate reader with a molar extinction coefficient of 6220 M<sup>-1</sup>cm<sup>-1</sup> (adjusted for light path during calculations).

#### 2.2.5 Kinetic properties

The kinetic properties for MDH and MalE were determined by varying substrate or cofactor concentration while keeping the concentration of all other constituents at saturating levels at 25°C and 50°C for the MDH and 50°C for the MalE and pH 7.0. Inhibition assays were performed using standard reaction conditions with varying inhibitor concentration at 50°C. All kinetic parameters were determined by fitting the data to the Michaelis-Menten equation using Sigma-Plot 11.0 (Systat Software Inc.).

#### 2.2.6 Effects of pH and temperature

Thermostability was determined by incubating aliquots of recombinant enzyme in the standard reaction conditions excluding NADH or NADP<sup>+</sup>. The aliquots were cooled on ice and



tested for residual activity at 50°C using the standard conditions. The optimal pH was measured in the following buffers: cacodylic acid (pH 5.6-6.5), MOPS (pH 6.5-7.5), and Tris-HCl (pH 7.5-8.6).

#### 2.2.7 Phylogenetic analysis

The evolutionary history of both Cthe\_0345 (MDH) and Cthe\_0344 (MalE) were inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura and Nei 1993). The tree with the highest log-likelihood (-29200.6535) (MDH) and (-22585.0304) (MalE) are shown. Initial trees for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log-likelihood value (Bootstrap values for 1000 replicates were calculated). The trees are drawn to scale, with branch lengths measured in the number of substitutions per site. The analyses involved 38 (MDH) and 31 (MalE) nucleotide sequences respectively. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 796 (MDH) and 849 (MalE) positions in the final datasets. Evolutionary analyses were conducted in MEGA5 (Tamura et al. 2011).

### 2.3 Results

The monomeric molecular weight of the cloned and purified His-tagged MalE and MDH were approximately 48 kDa and 40 kDa, respectively, corresponding to the predicted molecular masses of both proteins containing the 6xHis-tag. Both enzymes were found to be stable, retaining over 90% activity at 4°C, when stored in desalted elution buffer for a month. However, when the enzymes were stored in the presence of 0.02% or 0.04% sodium azide at 4°C, the activity was reduced by 50 % over the same time period. A 30% reduction in activity was observed when the enzymes were stored in the presence of 15% glycerol at -20°C for a month.



### 2.3.1 Effect of pH and temperature on malate dehydrogenase

The optimal pH for OAA reduction by MDH was found to be 6.8 when using MOPS as a buffer (Figure 2.1). Although MDH-dependent oxidation of malate has been shown in other organisms, typically at a higher pH optima than that of OAA reduction (Eprintsev, Falaleeva, and Parfyonova 2005; Janiczek et al. 1993), recombinant *R. thermocellum* MDH did not oxidize malate in the presence of either NAD<sup>+</sup> or NADP<sup>+</sup> as cofactors within the pH range tested (pH 5.6-10.5). The MDH was stable at 37°C for 10 hours with a 10 % reduction in activity. However, after incubation at 60°C for 1 hour, 54% of the initial activity of the purified enzyme was detectable with none of the initial activity detectable after 4 hours (Figure 2.2a).

### 2.3.2 Malate dehydrogenase kinetics

Kinetic parameters for the recombinant MDH are summarized in Table 2.1. The  $K_m$  for OAA at 25°C was 0.20 mM using NADH as a cofactor. The  $K_{cat}$  for oxaloacetate reduction was 45.8 s<sup>-1</sup> with NADH as a cofactor. When NADPH was used as a cofactor, the  $K_{cat}$  was reduced to 14.9 s<sup>-1</sup> and the  $K_m$  for oxaloacetate increased to 0.77 mM resulting in a 12-fold decrease in the catalytic efficiency ( $K_{cat}/K_m$ ). High concentrations of oxaloacetate inhibited the activity of the MDH with a 30% reduction in activity at 7 mM and a 99% reduction in activity at 25 mM. The addition of ATP, ADP, AMP, or PPi had no observable effect on MDH activity. MDH was also not affected by the addition of fructose 1,6-bisphosphate. No detectable LDH activity was found under any of the conditions tested.



Table 2.1 : The catalytic values for the MDH from *Ruminiclostridium thermocellum* (25°C and 50°C), *Vulcanithermus medioatlanticus*, *Paracoccus denitrificans*, *Beggiatoa leptomitiformis*, *Streptomyces coelicolor*, *Corynebacterium glutamicum*, and *Streptomyces aureofaciens*.

	$K_{cat} (s^{-1})$	$K_m(OAA)$ (mM)	$K_m(NADH)$ (mM)	Catalytic Efficiency ( $mM^{-1}s^{-1}$ )	Ref
<i>R. thermocellum</i> (25)	45.82	0.20	ND	230.25	(Taillefer et al. 2015)
<i>R. thermocellum</i> (50)	389.43	0.44	0.164	879.08	(Taillefer et al. 2015)
<i>V. medioatlanticus</i>	14.72	0.048	0.0014	306.76	(Eprintsev, Falaleeva, and Parfyonova 2005)
<i>P. denitrificans</i>	184	ND	ND	ND	(Janiczek et al. 1993)
<i>B. leptomitiformis</i>	60.51	0.02	0.017	3025.3	(Eprintsev et al. 2003)
<i>S. coelicolor</i>	1870	0.19	0.083	9894	(Ge et al. 2010)
<i>C. glutamicum</i>	510	0.057	0.041	8947	(Genda, Nakamatsu, and Ozak 2003)
<i>S. aureofaciens</i>	ND	0.1	0.085	ND	(Mikulášová et al. 1998)



Figure 2.1 : The relative activity of the recombinant Cthe\_0344 (MalE) (■) and Cthe\_0345 (MDH) (▲) at various pH values with standard assays conditions at 50°C (MalE) and 25°C (MDH).

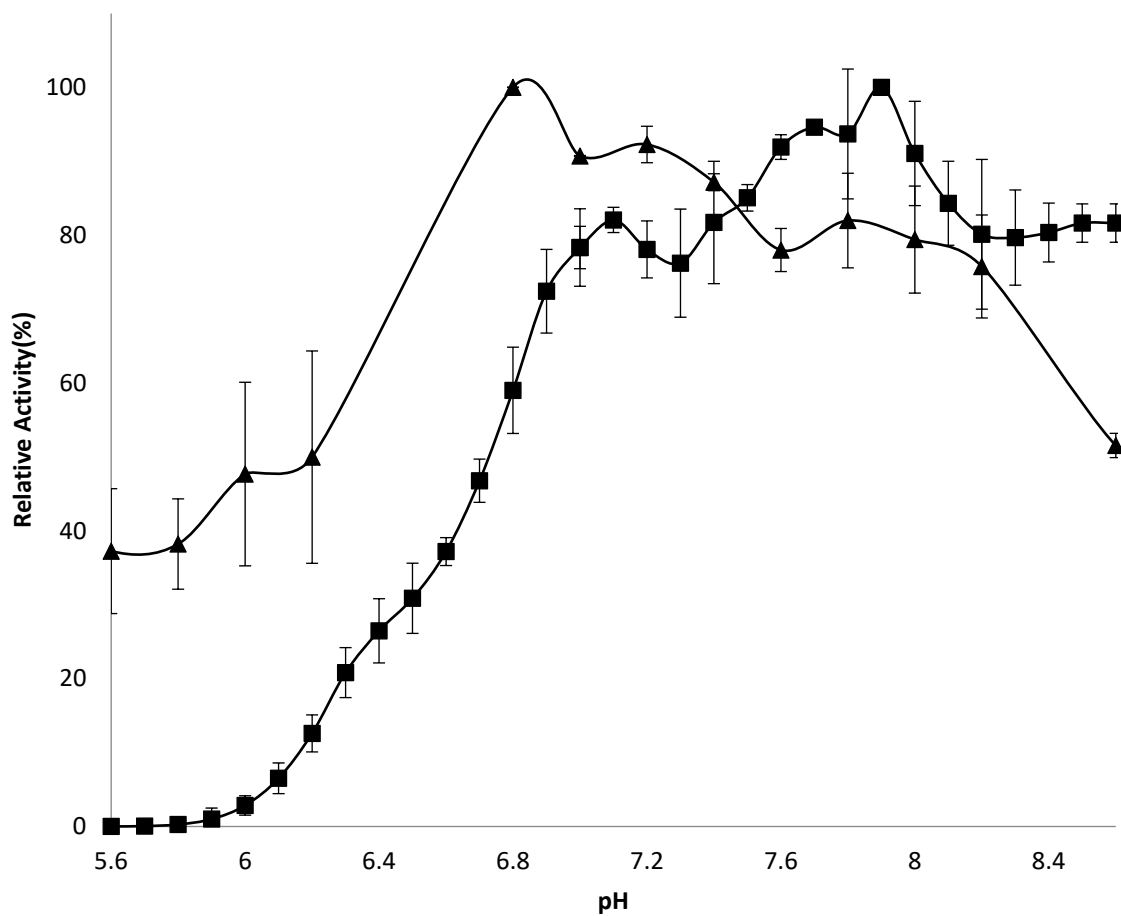
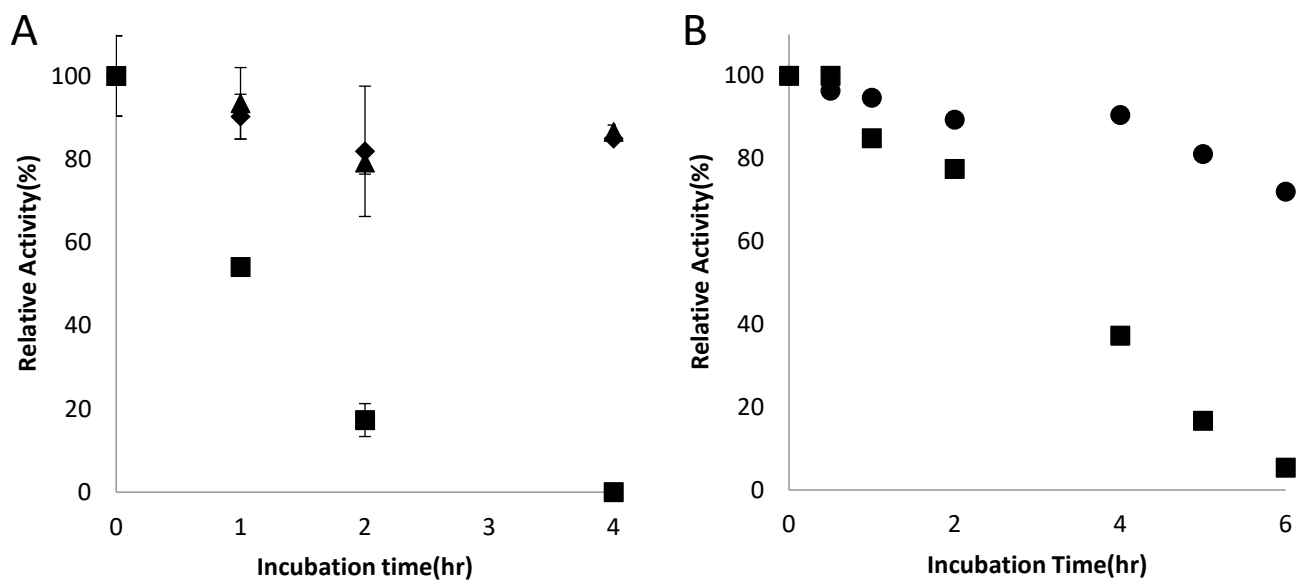




Figure 2.2 : Thermostability profile of A) Cthe\_0345(MDH) at 4°C (▲), 25°C (◆), and 60°C (■) and B) Cthe\_0344(MaE) at 37°C (●) and 60°C (■) under standard assay conditions at pH 7.0 with 20 mM  $\text{NH}_4^+$  and 5 mM  $\text{Mn}^{2+}$ .





### 2.3.3 Effect of pH and temperature on malic enzyme activity

The optimal pH for malate decarboxylation for the recombinant MalE was found to be 7.9 with a plateau of high relative activity between pH 7.1 and 8.5 (Figure 2.1). The MalE was stable at 37°C for 4 hours retaining 90.5% of its initial activity. Incubation at 60°C for 4 hours led to a 63% reduction in activity (Figure 2.2b).

### 2.3.4 Malic enzyme kinetics

Kinetic parameters for the recombinant MalE are summarized in Table 2.2. The  $K_m$  for malate was 0.20 mM using  $\text{NADP}^+$  as a cofactor with a  $K_{cat}$  of  $520.8 \text{ s}^{-1}$  at a temperature of 50°C. No malate decarboxylation activity was detected when  $\text{NAD}^+$  was used in place of  $\text{NADP}^+$  as a cofactor. The recombinant MalE did not decarboxylate OAA. Pyruvate carboxylation activity was measurable in the presence of NADPH with a  $K_m$  for pyruvate of 0.438 mM and a  $K_{cat}$   $71.83 \text{ s}^{-1}$ , indicating this enzyme is reversible. The addition of  $\text{NH}_4^+$  and  $\text{Mg}^{2+}$  or  $\text{Mn}^{2+}$  increased the activity of the MalE, with  $\text{Mn}^{2+}$  being the preferred divalent cation. The activation effect of  $\text{NH}_4^+$  saturated at approximately 15 mM (Figure 2.3a). The addition of ATP or AMP resulted in a small decrease in activity of 15% and 7% respectively at 1 mM concentrations. The addition of PPi, however, led to a sharp decrease in MalE activity with a calculated  $K_i$  of 0.036 mM at 50°C with saturating  $\text{NH}_4^+$  and  $\text{Mn}^{2+}$  (Figure 2.3b). The addition of PPi had no effect on the  $K_m$  for malate but decreased the  $V_{max}$  fairly sharply.

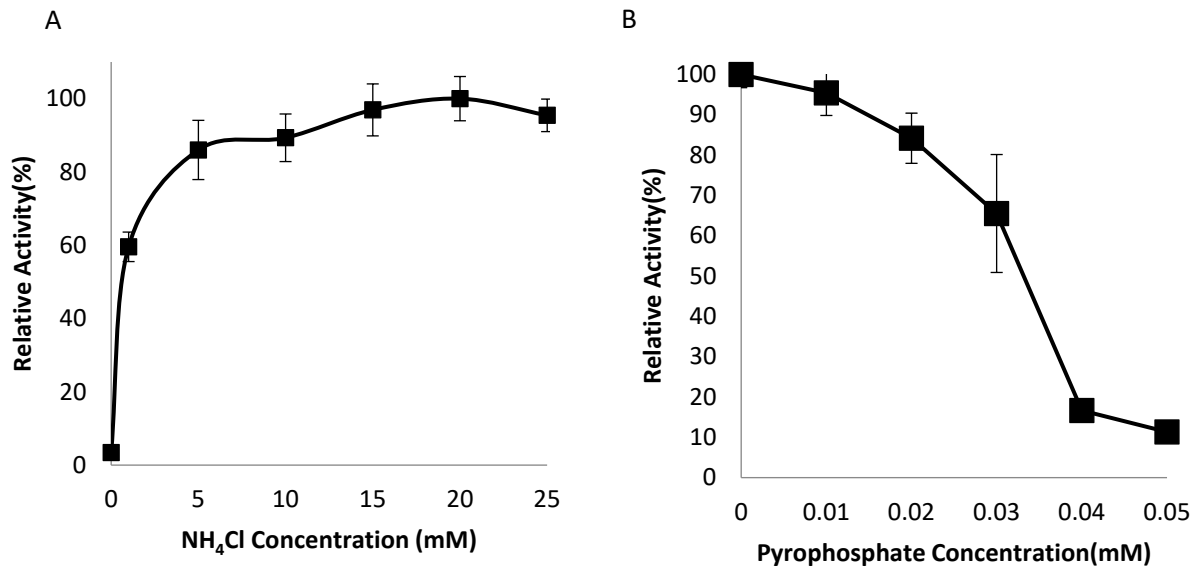


Table 2.2 : The catalytic values for the MalE from *Ruminiclostridium thermocellum*, *Streptococcus bovis*, *Escherichia coli*, and *Sulfolobus solfataricus*.

		$K_{cat} (s^{-1})$	$K_m(malate)$ (mM)	$K_m(NADP)$ (mM)	Catalytic Efficiency ( $mM^{-1}s^{-1}$ )	Ref
<i>R. thermocellum</i>	Tetramer	520.8	0.20	0.035	2622.36	(Taillefer et al. 2015)
<i>S. bovis</i>	Dimer	90.7	0.63	ND	143.97	(Kawai et al. 1996)
<i>E. coli</i> (SfcA)	Tetramer	NAD : 82.7 NADP : 12.4	0.66	1	NAD : 125.30 NADP : 18.79	(Bologna, Andreo, and Drincovich 2007)
<i>E. coli</i> (MaeB)	Octamer	NAD : ND NADP : 66.6	3.41	0.0415	NADP : 19.53	(Bologna, Andreo, and Drincovich 2007)
<i>S. solfataricus</i>	Dimer	31.5	0.018	0.003	1750.00	(Bartolucci et al. 1987)



Figure 2.3 : The relative activities of recombinant Cthe\_0344(MaE) at pH 7.0 in the presence of (a) varying concentrations of  $\text{NH}_4\text{Cl}$  with 5 mM  $\text{Mn}^{2+}$  and (b) varying concentrations of PPI with 20 mM  $\text{NH}_4^+$  and 5 mM  $\text{Mn}^{2+}$





### 2.3.5 Phylogenetic analysis

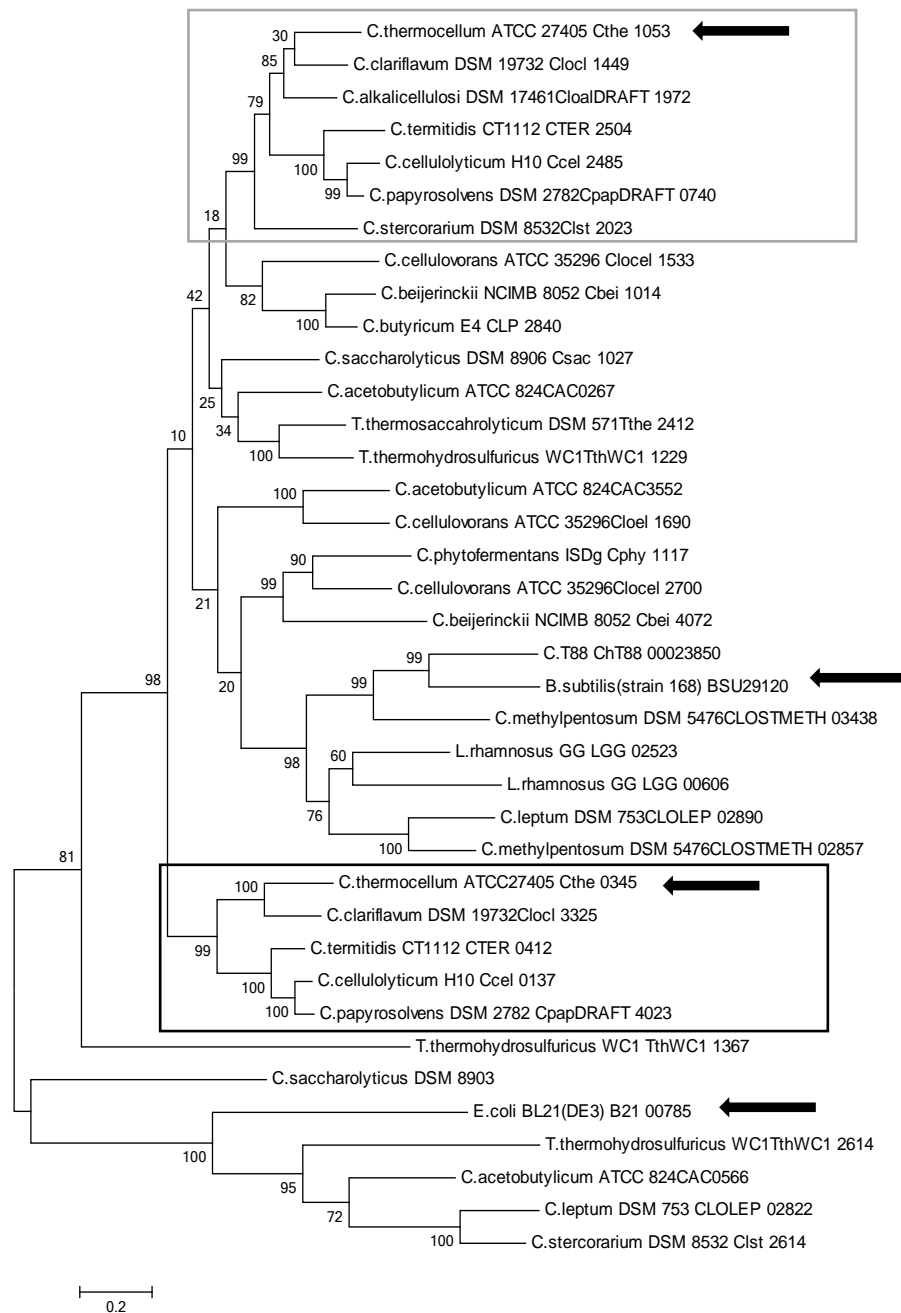
Phylogenetic analysis of the putative MDH and LDH from various Clostridia showed that, while they appear to be derived from a common ancestor, the MDH and LDH from *R. thermocellum* were separated into different groups (Figure 2.4). The grouping around Cthe\_0345 (MDH) contains MDHs with the characteristic of having a neighboring malic enzyme gene. The malic enzyme from these organisms have also been found to group with Cthe\_0344 (Figure 2.5). The alignment of Cthe\_0345 (MDH) with the *E. coli* K-12 MG1655 MDH showed that at position 86, based on Cthe\_0345 (MDH) amino acid position, both *E. coli* and Cthe\_0345 (MDH) contained an arginine. However, in positions 18, 90, 212, and 216 the amino acids differed with Cthe\_0345 (MDH) having valine, glutamic acid, aspartic acid, and isoleucine rather than isoleucine, methionine, glycine, and valine in *E. coli* (Figure 2.6).

## 2.4 Discussion

The conversion of PEP to pyruvate can be viewed as an essential step in the *R. thermocellum* metabolism. However, the lack of pyruvate kinase forces the use of an alternate means of pyruvate production. It has been suggested that pyruvate production is done through a PEPCK, MDH, and MalE or "malate shunt" resulting in the transfer electrons between NADH and NADP<sup>+</sup> and the generation of GTP and pyruvate (Y. Deng et al. 2013; Raman et al. 2011; Rydzak et al. 2012). Enzyme assays in cell-free extract have shown MDH activity along with NH<sub>4</sub><sup>+</sup> activated MalE activity (Y. Deng et al. 2013; Lamed and Zeikus 1980). However, to date, no genes had been proven to encode the MDH and MalE. We have therefore cloned, purified, and



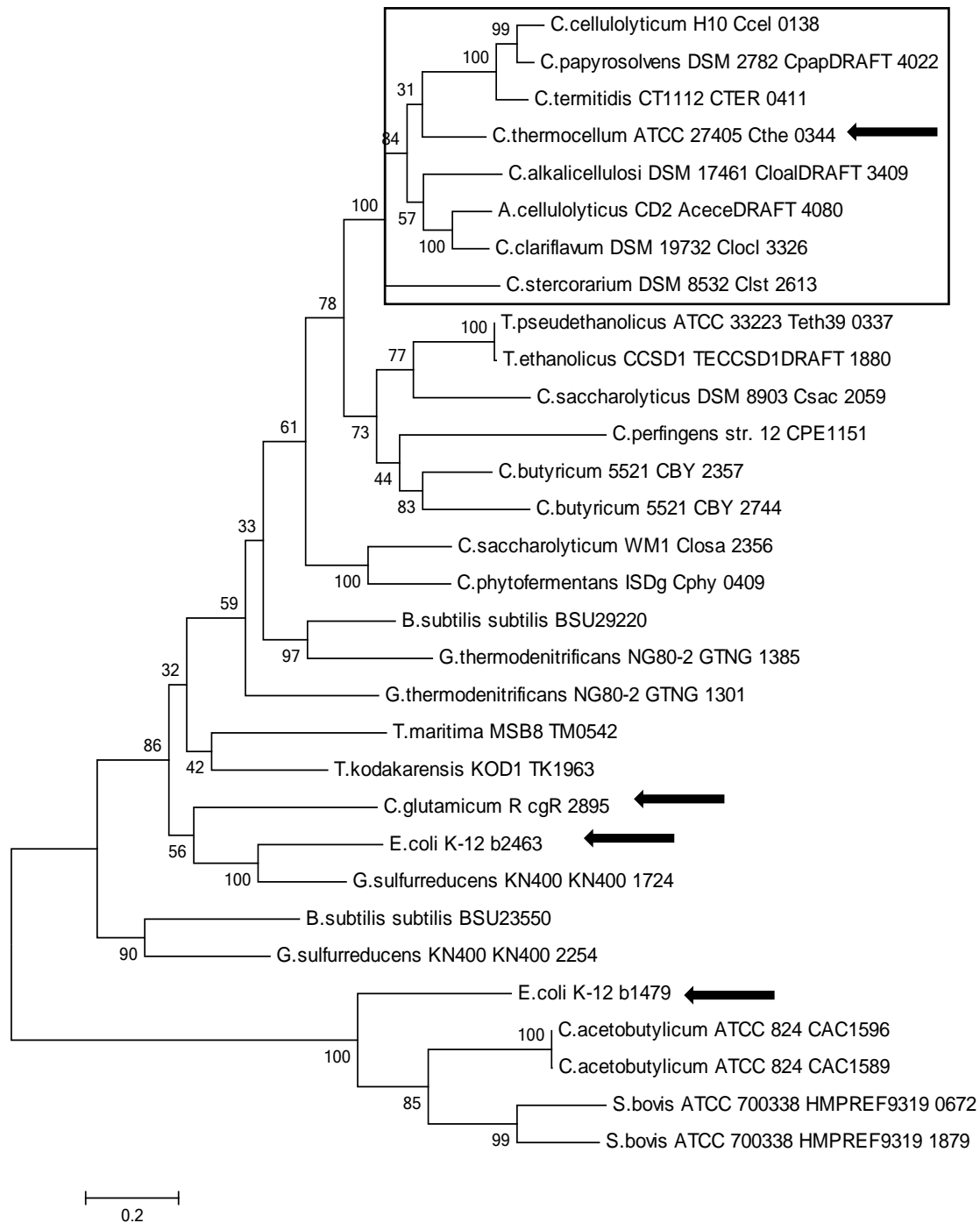
Figure 2.4 : Molecular Phylogenetic analysis of Cthe\_0345 (MDH) by Maximum Likelihood method. The gray box indicates a grouping of putative LDH coding genes. The black box indicates a grouping of MDH genes which have a neighboring MalE gene. Arrows indicate sequences for which corresponding enzymes have been purified and characterized (LDH and MDH). The unrooted tree is drawn to scale, with branch lengths measured in the number of substitutions per site.<sup>4</sup>



<sup>4</sup> Nomenclature utilised for phylogenetic tree was prior to reclassification by Yutin and Galparin (2013).



Figure 2.5 : Molecular Phylogenetic analysis of Cthe\_0344 (MalE) by Maximum Likelihood method. The box indicates the group of MalE with a neighboring MDH gene. Arrows indicate sequences for which corresponding enzymes have been purified and characterized. The unrooted tree is drawn to scale, with branch lengths measured in the number of substitutions per site<sup>5</sup>.



<sup>5</sup> Nomenclature utilised for phylogenetic tree was prior to reclassification by Yutin and Galparin (2013).



Figure 2.6 : Amino acid alignment of Cthe\_0345 (MDH) and Cthe\_1053 (LDH) from *R. thermocellum* and b3236 (MDH) from *E. coli* K-12 MG1655. Shaded areas indicate positions 18, 86, 90, 212, and 216 based on the amino acid positions of Cthe\_0345 (MDH).

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Cthe_0345 (MDH) MEMVKSRKVAIIGAGFVGASAAFTMALRQTA---NELVLIDVFKEKAIG
Cthe_1053 (LDH) MNNKVIKKVTVVGAGFVGSTTAYTLMLSGLI---SEIVLIDINAKGADG
E.coli MDH      -----MKVAVLGAA-CGIGQALALLKTLQPSGSELSLYDI-APVTPG

Cthe_0345 (MDH) EAMDNHGLPFMQMSLYAGD--YSDVKDCDVIVVTAGANRKPGETRIDL
Cthe_1053 (LDH) EVMDLNHGMPFVRPVEIYRGD--YKDCAGSDIVIITAGANRKEGETRIDL
E.coli MDH      VAVDLSH-IPTAVKIKGFGSGEDATPALEGADVVLISAGVARKPGMDRSDL

Cthe_0345 (MDH) AKKNVMIKEVTQNMKYNNHGVILVSNPVD----IITYMIQKWSGLPV
Cthe_1053 (LDH) VKRNTEVEFKNIINEIVKYNNDICILLVVTNPVD----ILTYVTYKLSGFPK
E.coli MDH      FNVNAGIVKNLVQQVAKTCPKACIGIITNPVNTTVAIAAEVLKKAGVYDK

Cthe_0345 (MDH) GKVIGSGTVLDSIRFRYLLSEKLGVDVRNVHGYIIEGH-GDSQLPLWSCT
Cthe_1053 (LDH) NKVIGSGCTVLDARFRYLLSEHVKVDARNVHAYIIEGH-GDTEVAAWSLA
E.coli MDH      NKLFCV-TTLDIIRSNTFVAELKKGQPGVEVPVIGHSGVTILPL--LS

Cthe_0345 (MDH) HIAGKNINEYIDDPKCNFTTEEDK--KIAEDVKTAGATIINKK---GATY
Cthe_1053 (LDH) NIAGIPMDRYCDE--CHQCEEQISRNKIYESVKNAAYEIIRNK---GATY
E.coli MDH      QVPG-----VSFTEQVA--DITKRIQNAGTEVVEAKAGGGSAT

Cthe_0345 (MDH) YGIAVSINT----IVETLLKNQNTIRTVGTVINQMYGIEDVAISLPSIVN
Cthe_1053 (LDH) YAVALAVRR----IVEAIVRNENSILTVSSLLEGQYGLSDVCLSVPTIVG
E.coli MDH      LSMQQAARFGLSLVRALQGEQGVVECAAYVEGDGQYA---RFFSQPLLLG

Cthe_0345 (MDH) SEGVOEVLQF-NLTPEEEEALRFSAEQVKKVL---NEVKNL
Cthe_1053 (LDH) VNGIEEILNV-PFNDEEIQLLRKSGNTLKEII----KTLDI
E.coli MDH      KNGVEERKSIGTLSAFEQNALEGMLDTLKKDIALGEFVNK

```



characterized the putative MDH (Cthe\_0345) and MalE (Cthe\_0344) to determine cofactor specificity and enzyme kinetics to validate their presence and elucidate their role in the malate shunt and their potential role in *R. thermocellum* biofuels metabolism. The optimal pH for the MDH-dependent OAA reduction was 6.8, which agrees with the reported values from many thermophilic MDHs (Eprintsev, Falaleeva, and Parfyonova 2005). MDH-dependent oxidation of malate is generally found to be optimal at higher pH than that of OAA reduction. However, *R. thermocellum* MDH did not have any detectable malate oxidation activity regardless of the pH (5.6-10.5) or any conditions used during the assays. This seems to indicate that the MDH from *R. thermocellum* greatly favors oxaloacetate reduction under physiological pH and under all tested conditions. The MDH from *R. thermocellum* was found to be thermostable retaining over 50% activity after a one-hour incubation at 60°C. This is higher than what is observed in the hyperthermophilic *B. candolyticus* which lost 50% of its activity after a 1 minute incubation at 59°C, but similar to the values for *V. mediatlanticus* which retained over 75% activity after 15 minutes of incubation at 60°C (Eprintsev, Falaleeva, and Parfyonova 2005; Kristjansson and Ponnampereuma 1980). The  $K_m$  for OAA was significantly higher than many characterized MDHs such as the ones from *V. mediatlanticus* (0.048 mM), *C. glutamicum* (0.057 mM), and *S. aureofaciens* (0.1 mM) (Eprintsev, Falaleeva, and Parfyonova 2005; Genda, Nakamatsu, and Ozak 2003; Mikulášová et al. 1998). The  $K_{cat}$  for OAA reduction was similar to previously published values from *V. mediatlanticus* (14.72 s<sup>-1</sup>) and *B. leptomitiformis* (60.51 s<sup>-1</sup>) but significantly lower than the published  $K_{cat}$  for *P. infestans* (3496.2 s<sup>-1</sup>) (Eprintsev, Falaleeva, and Parfyonova 2005; Eprintsev et al. 2003; Maloney et al. 2004; López-Calcano et al. 2009). The MDH from *R. thermocellum* preferred the utilization of NADH over NADPH with a 12 fold reduction in the catalytic efficiency



( $K_{cat}/K_m$ ) with NADPH as a cofactor. This is similar to what was observed in *S. avermitilis*, *C. glutamicum*, and *T. flavus* (Genda, Nakamatsu, and Ozak 2003; Z.-D. Wang et al. 2011; Tomita et al. 2006).

The monomeric molecular mass of the MalE is much smaller than most Gram-negative and eukaryotic MalE but is similar in size to both Gram-positive and archaeal MalEs (Bologna, Andreo, and Drincovich 2007; Gourdon et al. 2000; Kobayashi et al. 1989; Moreadith and Lehninger 1984; Boles, De Jong-Gubbels, and Pronk 1998; Bartolucci et al. 1987). The MalE consists of a 170 kDa tetramer consisting of four 40 kDa monomers (Lamed and Zeikus 1981). The optimal pH was found to be rather high at 7.9. However, high levels of activity were found between pH 7.1 and 8.5. These values agreed with previously reported values for *R. thermocellum* (Lamed and Zeikus 1981) and are similar to various MalE from other gram-positive organisms (Gourdon et al. 2000; Kawai et al. 1996). The  $K_m$  for malate from the MalE was found to be lower than the MalE from *S. bovis* (0.63 mM) and *E. coli* (0.66 mM) but significantly higher than the reported value for the MalE from *S. sulfataricus* (0.018 mM) (Bologna, Andreo, and Drincovich 2007; Bartolucci et al. 1987; Kawai et al. 1996). The MalE from *R. thermocellum* differed from previously reported MalEs in that it was not inhibited to a significant extent by the presence of ATP and AMP, whereas in *S. bovis*, the addition of 1 mM ATP and 1 mM ADP reduced the MalE activity by 90% and 49% respectively (Kawai et al. 1996). The recombinant *R. thermocellum* MalE was inhibited in the presence of relatively low concentrations of PPi. PPi did not seem to affect the binding affinity of malate or NADP<sup>+</sup>. However, the addition of PPi affected the velocity of the enzyme leading to a lower  $V_{max}$  value. Therefore, this indicated that PPi is a non-competitive inhibitor of MalE. In *T. cruzi*, high levels of PPi induce a shift in

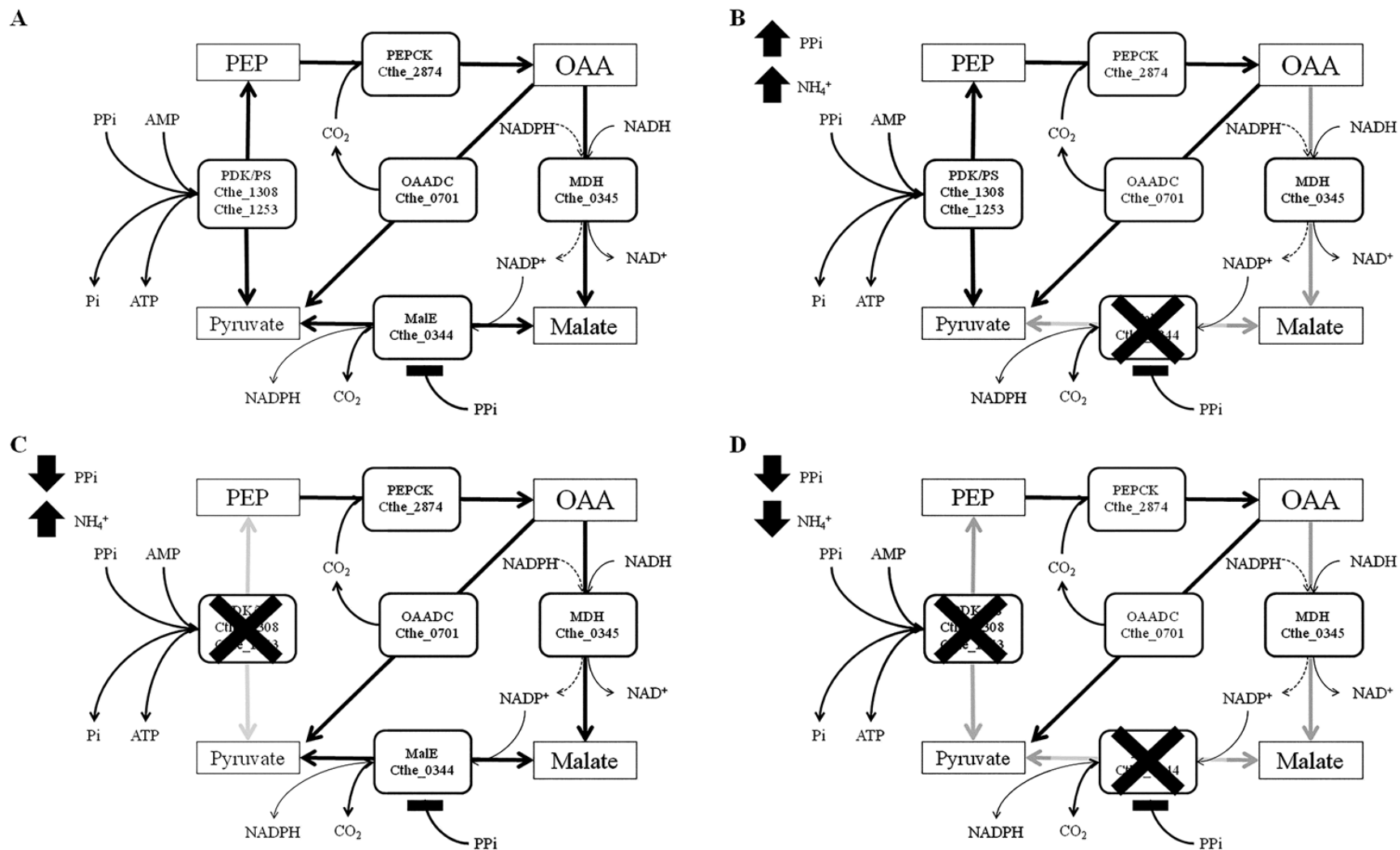


phosphoenolpyruvate (PEP) utilization from pyruvate kinase and PEP carboxykinase to pyruvate dikinase (PPDK) (Acosta et al. 2004). In *R. thermocellum*, the levels of PPDK and MalE were found to be high in both the transcriptome and proteome during growth (Raman et al. 2011; Rydzak et al. 2012; Burton and Martin 2012). Therefore, *R. thermocellum* could utilize intracellular PPi concentration as a signal for directing carbon flow from PEP. Both Burton and Martin (2012) and Rydzak et al. (2012) have suggested an important role for PPi in exponential phase in this organism (Rydzak et al. 2012; Burton and Martin 2012). In *Caldicellulosiruptor saccharolyticus* (Bielen et al. 2010), another cellulolytic thermophilic relative of the clostridia, high levels of PPi have been observed during exponential growth. Increased concentrations of PPi would inhibit the MalE leading to carbon flowing through the PPDK in order to produce pyruvate. However, deletion of the PPDK gene in *R. thermocellum* caused no decrease in growth rate or final culture density (Zhou et al. 2013). Together, this indicates that *R. thermocellum* utilizes a robust redundant system of pyruvate generation that can easily adapt to intracellular conditions (Figure 2.7). Under high concentrations of PPi, the carbon flow would proceed through the PPDK or PEPCK and a membrane-associated OAA decarboxylase complex (OAADC) (Cthe\_0699-0701) (Figure 2.7b). Once PPi concentration fall, then the carbon flow would be redirected through the malate shunt and/or the OAADC (Figure 2.7c). However, under conditions of both low PPi and low NH<sub>4</sub>, then the carbon would be forced through the OAADC solely for pyruvate generation (Figure 2.7d).

The phylogenetic analysis of the Cthe\_0345 protein seems to indicate that some MDHs can be distinguished from LDHs based on their phylogenetic grouping despite the ambiguity in the



Figure 2.7 : (A) Putative pyruvate producing pathways in *R. thermocellum* under (B) high intracellular PPi and NH<sub>4</sub><sup>+</sup>, (C) low intracellular PPi and high NH<sub>4</sub><sup>+</sup>, (D) low PPi and NH<sub>4</sub><sup>+</sup>.

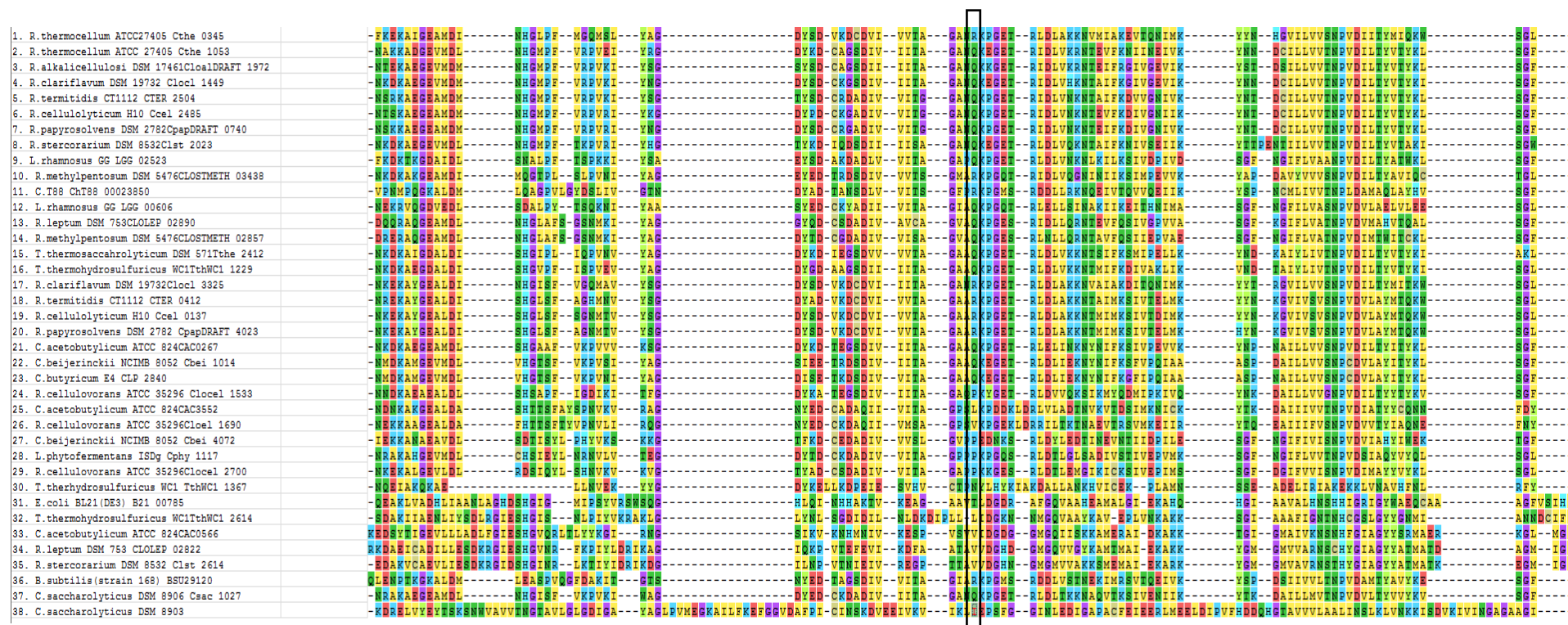




annotation of MDH and LDH (Figure 2.4). Therefore, the presence of a neighboring MalE gene next to a putative MDH/LDH gene would seem to indicate MDH/LDH gene is likely an MDH. However, the phylogenetic analysis also showed that most MDHs and LDHs are indistinguishable from one another from a phylogenetic point of view. The MalE phylogenetic analysis showed a distinct group MalE which have neighboring MDHs of which the MalE from *R. thermocellum* is the first representative from this group to be characterized. The substrate specificity of the MDH in *E. coli* can be modified by a single amino acid change, arginine to glutamine, at position 81 (Nicholls et al. 1992). Furthermore, the substrate specificity of the *E. coli* MDH can be completely shifted to pyruvate with a total of 5 amino acid substitutions (Yin and Kirsch 2007). Interestingly, when the amino acid sequence of Cthe\_0345 (MDH) was compared with the *E. coli* MDH the amino acids at positions 18, 90, and 216 (based on Cthe\_0345 amino acid positions) were found to be valine, glutamic acid, and isoleucine rather than isoleucine, methionine, and valine in *E. coli* MDH. The amino acids at these positions in Cthe\_0345 (MDH) are identical to the amino acid in the same positions for the Cthe\_1053 (LDH) and the substitutions made by Yin and Kirsch (2007) which shifted substrate specificity from OAA to pyruvate. However, the Cthe\_0345 (MDH) and Cthe\_1053 (LDH) differ at positions 86 and 212. At positions 86, the Cthe\_0345 (MDH) contains the expected arginine based on the *E. coli* MDH whereas the Cthe\_1053 (LDH) contains a glutamine. Therefore, similar to *E. coli*, the substrate specificity of the Cthe\_0345 (MDH) may be governed by the presence of either an arginine (MDH) or glutamine (LDH) at position 86. However, only 26 of the 38 sequences used in the phylogenetic tree (Figure 2.4) had an arginine or glutamine at position 86 when aligned with Cthe\_0345 (MDH) (Figure 2.8). While the amino



Figure 2.8: Amino acid alignment of putative MDH and LDH sequences. The box indicates amino acid position 86 of the Cthe\_0345 (MDH) from *R. thermocellum*





acid at position 86 can hint at the associated activity, it cannot be used reliably to distinguish an MDH from a LDH since not all aligned MDHs and LDHs contain arginine or glutamine at position 86.

## 2.5 Conclusion

The characterization of the biochemical properties of the MDH and MalE from *R. thermocellum* has provided insight into their possible catabolic role in this organism and possibly other closely related clostridia. The lack of malate oxidation activity by the MDH under the experimental conditions would indicate that the MDH greatly favors oxaloacetate reduction, therefore primarily producing malate, and has a higher affinity for NADH rather than NADPH. It has been suggested that the activation of MalE by  $\text{NH}_4^+$  is used by *R. thermocellum* as a signal for the production of cofactors required for biosynthesis (Lamed and Zeikus 1981). Likewise, fluctuating levels of PPi could also possibly be utilized as a signal for *R. thermocellum* to increase the production of biosynthetic cofactors GTP and NADPH by utilization of the PEPCK and the malate shunt over PPDK. The regulation of the MalE by both  $\text{NH}_4^+$  and PPi indicates that high energy intermediates and  $\text{NH}_4^+$  may play a major role in the regulation of carbon flux through competing pyruvate producing pathways. Hence, further metabolomic analysis of *R. thermocellum* would help determine the role of the metabolome as a possible regulator of carbon and electron flux through competing pathways. The combination of biochemical data with metabolomic and proteomic analysis could lead to better understanding of carbon and electron flux regulation in *R. thermocellum* leading to the determination of prime candidate genes for genetic engineering.



### 3 *In silico* genomic analysis reinforces the importance of PPi as a regulatory molecule in the genus *Ruminiclostridium*

#### 3.1 Introduction

Many organisms belonging to the class Clostridia have arisen as having great potential for industrial chemical production, ranging from acetone production by *Clostridium acetobutylicum* to ethanol production in *Ruminiclostridium thermocellum* (Ross 1961; Jones and Woods 1986; Gabriel 1928; Olson, Sparling, and Lynd 2015). As outlined in Chapter 1: Table 1.1, many Clostridia play important roles in the industrial production of a multitude of products. However, most of the organisms observed in Chapter 1: Table 1.1 are also predicted to have variations in the central catabolism of various carbohydrate sources such as alternative cofactor utilization (Taillefer and Sparling 2015; Taillefer et al. 2015; Rydzak et al. 2012).

High energy compounds have been shown to regulate the activity of many catabolic enzymes such as hexokinase (HK), phosphofructokinase (PFK), enolase (ENO), 3-phosphoglycerate mutase (PGAM) (Figure 1.2) (Moreno-Sánchez et al. 2008). Studies have also shown that the activity of the lactate dehydrogenase (LDH) from *Caldicellulosiruptor saccharolyticus* can be directly regulated by the presence of high energy carriers namely ATP and pyrophosphate (PPi) (Willquist and Van Niel 2010). Therefore, it was predicted that intracellular ATP and PPi could directly regulate lactate production by directly modulating LDH activity. PPi is produced in cells by various different sources mainly metabolic reactions with the largest contributor to PPi synthesis being nucleotide incorporation in nucleic acid synthesis (Heinonen 2001). PPi has been suggested as a primitive high energy bond donor since many primitive organisms such as anaerobic bacteria and primitive protists contain variants of HK, pyruvate phosphate dikinase



(PPDK), phosphoglycerate kinase (PGK), and PFK which utilize PPi as a phosphate group donor rather than the traditional ATP (Kulaev and Vagabov 1983). Therefore, it was suggested that the more predominant ATP-utilizing glycolytic enzymes evolved from a primitive PPi based system. However, in a more recent study, it was stated that the PPi-dependent variant of the glycolytic enzymes evolved from a more ancient ATP based systems (Chi and Kemp 2000). Indeed, the active site of the PPi-dependent phosphofructokinase from *Entamoeba histolytica* could be altered to fit the much larger ATP instead of PPi by the mutation of a single amino acid, aspartic acid to glycine at position 175, within the active site. This indicates the possibility of having a pre-existing nucleotide binding domain predating the pyrophosphate binding for this enzyme. Therefore, it was hypothesized that the primitive kinases utilized a nucleotide-based energy donor. This hypothesis is based on the theory that the earliest forms of life were self-replicating nucleic acids. Therefore, the primitive proteins would have evolved around the interaction with nucleotides leading to primitive nucleotide specificity with ATP, and PPi dependent variants evolving at a later point (Chi and Kemp 2000).

PPi metabolism has been previously described in plants and highly derived eukaryotes. However, there has been very limited information published on the PPi dependence and PPi metabolism of fermentative prokaryotes (Bielen et al. 2010). In many protists such as *Toxoplasma gondii*, *Trichomonas vaginalis*, and *Entamoeba histolytica* some of the ATP-dependent core glycolysis enzyme are missing and replaced with a PPi dependent variant (Mertens et al. 1998; Peng and Mansour 1992; Reeves and Guthrie 1975). In *E. histolytica* the ATP-dependent PFK, phosphoenolpyruvate carboxykinase (PEPCK), and acetate kinase (AK) are all absent and replaced with PPi dependent variants (Reeves and South 1974; Reeves 1970;



Reeves and Guthrie 1975). *E. histolytica* also lacks any detectable pyruvate kinase (PK) activity, which deviates from the traditional glycolysis model. Instead, *E. histolytica* utilizes a PPI dependent PPDK for the production of pyruvate (Reeves 1968). Using PPI dependent enzymes can increase the net gain of ATP by substrate level phosphorylation since less ATP is consumed as a result of using PPI-dependent phosphofructokinase. However, utilization of the PPI-dependent PFK and PPDK over the ATP –dependent PFK and PK can remove two of the major glycolysis carbon flux regulators, leading to a less stringent regulation of the commitment steps of glycolysis (Mertens 1993).

Organisms employing a traditional ATP-dependent metabolism regulate the intracellular concentration of PPI via the use inorganic pyrophosphatase (PPase) enzyme. The absence of PPases would result in very high intracellular accumulation of PPI leading to PPI becoming toxic to the organism. Pyrophosphatase can be classified into 2 major classes, the soluble PPase and membrane-bound PPase. The soluble PPase can be found in all domains of life. The soluble PPases hydrolyze PPI into two inorganic phosphates (Pi) molecules leading to the energy obtained by cleaving the PPI bond to be dissipated as heat (Cooperman, Baykov, and Lahti 1992). Soluble PPase has been shown to be essential in both *E.coli* and yeast in order to prevent the rapid toxic build-up of PPI which would otherwise inhibit many biosynthetic enzymes (Chen et al. 1990; Lundin, Baltscheffsky, and Ronne 1991). In *E. coli*, it was calculated that the concentration of PPI would rise to over 3 M within an hour in actively growing cells lacking any active PPase. However, the presence of the soluble PPase controls the concentrations of PPI and keeps it at approximately 1 mM throughout growth (Klemme 1976). The amino acid sequences of the active site of soluble PPase is very conserved for both prokaryotes and eukaryotes with 24 amino acids



being conserved throughout the tree of life. Fifteen of the 17 polar amino acids within the active site are highly conserved in both prokaryotes and eukaryotes. Despite the highly conserved active site, the remainder of the amino acid sequence differs greatly in prokaryotes and eukaryotes (Cooperman, Baykov, and Lahti 1992).

Another family of PPase is the membrane bound V-type PPase. These can be grouped into H<sup>+</sup>-translocating or Na<sup>+</sup>-translocating V-type PPases. The H<sup>+</sup>-PPases can be found in all domains of life except in animals and fungi. H<sup>+</sup>-PPase can further be classified into two different types, K<sup>+</sup>-stimulated and K<sup>+</sup>-independent. The K<sup>+</sup>-stimulated H<sup>+</sup>-PPase have been traditionally found only in lower eukaryotes. However, studies have demonstrated the presence of a K<sup>+</sup>-stimulated H<sup>+</sup>-PPase in *Thermotoga maritima* opening the possibilities of finding more K<sup>+</sup>-stimulated H<sup>+</sup>-PPase in bacteria (Pérez-Castiñeira et al. 2001). H<sup>+</sup>-PPase catalyze the hydrolysis of PPi to two Pi with the energy generated from the hydrolysis being utilized to pump protons across a membrane thereby creating a cross membrane proton potential (Rea et al. 1992), which can be utilized by an F<sub>0</sub>F<sub>1</sub> ATP synthase to produce ATP. It has been suggested that generation of ATP through PPi hydrolysis would occur at a stoichiometry of 8 PPi per ATP produced (M. Baltscheffsky, Schultz, and Baltscheffsky 1999). Therefore, it can be predicted that strictly fermentative organisms can utilize a V-type H<sup>+</sup>-PPase in order to increase the efficiency in energy conservation by recycling a biosynthetic by-product to generate proton motor force. However, this system can be viewed as inefficient since 8 PPi (-33 kJ/mol each PPi hydrolyzed) is required for pumping out the 4 H<sup>+</sup> required to produce 1 ATP (30.5 kJ/mol) through the F<sub>0</sub>F<sub>1</sub> ATP synthase. Thus, this would result in a loss of energy of 237.5 kJ/mol of ATP synthesized by the F<sub>0</sub>F<sub>1</sub> ATP synthase (Thauer, Jungermann, and Decker 1977; Gottschalk 1986).



Taken together, this suggests that despite the lack of knowledge on bacterial PPI metabolism, PPI may play a very significant role during bacterial growth both as a secondary energy carrier and also as a possible regulator of many cellular processes. Therefore, we measured the intracellular concentration of PPI in *R. thermocellum* in order to access changes in intracellular levels throughout growth. Combining the intracellular measurements of PPI with an in silico genomic comparison of closely related organisms could shed light on the means of PPI hydrolysis and intracellular PPI could alter central catalysis and metabolism regulation.

## 3.2 Methods

### 3.2.1 Organisms and media preparation

Fresh cultures of *R. thermocellum* ATCC 27405, *Ruminiclostridium stercorarium* DSM 8532, and *Ruminiclostridium termitidis* DSM 5398 were maintained by routinely transferring 5% (v/v) mid-exponential phase inoculum into complex 1191 medium containing 2 g/L cellobiose or  $\alpha$ -cellulose (Levin et al. 2006; Rydzak et al. 2009). Cultures were grown at 60°C for *R. thermocellum* and *R. stercorarium* or 37°C for *R. termitidis* and stored anaerobically at 4°C until analysis. All chemicals were obtained from Sigma Chemical Co. (St. Louis, MO) and all gasses were purchased from Welder's Supply (Winnipeg, MB). Experiments were carried out anaerobically in sealed Corning bottles (1.1 L) containing 500 mL of 1191 medium adjusted to pH 7.2 with cellobiose or  $\alpha$ -cellulose as a carbon source. Preparation of the Corning bottles and inoculation protocols were followed as previously described by Islam *et al* 2006 (Levin et al. 2006).

### 3.2.2 Intracellular PPI measurements

Extraction of intracellular PPI was done via the acetonitrile:methanol:water extraction adapted from Bennett *et al* 2009 (Bennett et al. 2009). All cells were grown in complex 1191



media with 2 g/L cellobiose (Islam et al. 2006). Cells were quickly separated from the growth media using a 0.45 µm nylon filter via vacuum filtration. The filters were quickly submerged in 0.75 mL of ice-cold 40:40:20 mixture of acetonitrile:methanol:water (AMW). The submerged nylon filters and AMW were incubated at -20°C for 1 hour. The nylon filter was removed and the AMW was centrifuged at 12 000 RPM in order to remove any insoluble components. The samples were stored at -80°C until analyzed. P<sub>i</sub> concentrations were determined using a Pyrophosphate Assay Kit (P<sub>i</sub>PER™, Life Technologies Corp.). The ATP concentration was measured using a Molecular Probes ATP determination Kit (Fisher Scientific, Ottawa, ON) with a BioTek Synergy 4 plate reader. The intracellular volume of the cells were determined by cell measurements using the negative stain Nigrosin and Nikon Eclipse Ti Microscope with a Nikon DS-Fi1C camera (Nikon Corp., Tokyo, Japan) (Mackinnon and Hawes 1961; Kaltenbach, Kaltenbach, and Lyons 1958).

### 3.2.3 *Insilico genomic and phylogenetic analysis*

The cofactor and K<sup>+</sup>-dependence of the V-type PPase were determined as outlined by Luoto *et al* 2011. The *R. thermocellum* V-type PPase (Cthe\_1425) was aligned with the V-type PPase sequence from *Chlorobium limicola* (Clim\_1173). The amino acid positions 180, 242, 246, 478, and 481 in *C. limicola* (Clim\_1173) corresponded to positions 173, 239, 243, 464, and 467 in *R. thermocellum* (Cthe\_1425). The cofactor specificity of the PFKs were predicted using the alignment of key residues as outlined by Baptiste *et al.* (2003) and Bielen *et al.* (2010).

The evolutionary history of the PPases, PFK, and PPDK were inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura and Nei 1993). The tree with the highest log likelihood (-3253.1595) (PPase), (-27726.0828) (PFK), (-39513.34) (PPDK) and is shown. The percentage of trees in which the associated taxa clustered together is shown next



to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value (Bootstrap values with 1000 replicates are calculated). The unrooted tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. Evolutionary analyses were conducted in MEGA6 (Tamura et al. 2011).

### 3.3 Results and Discussion

#### 3.3.1 Intracellular PPI concentrations

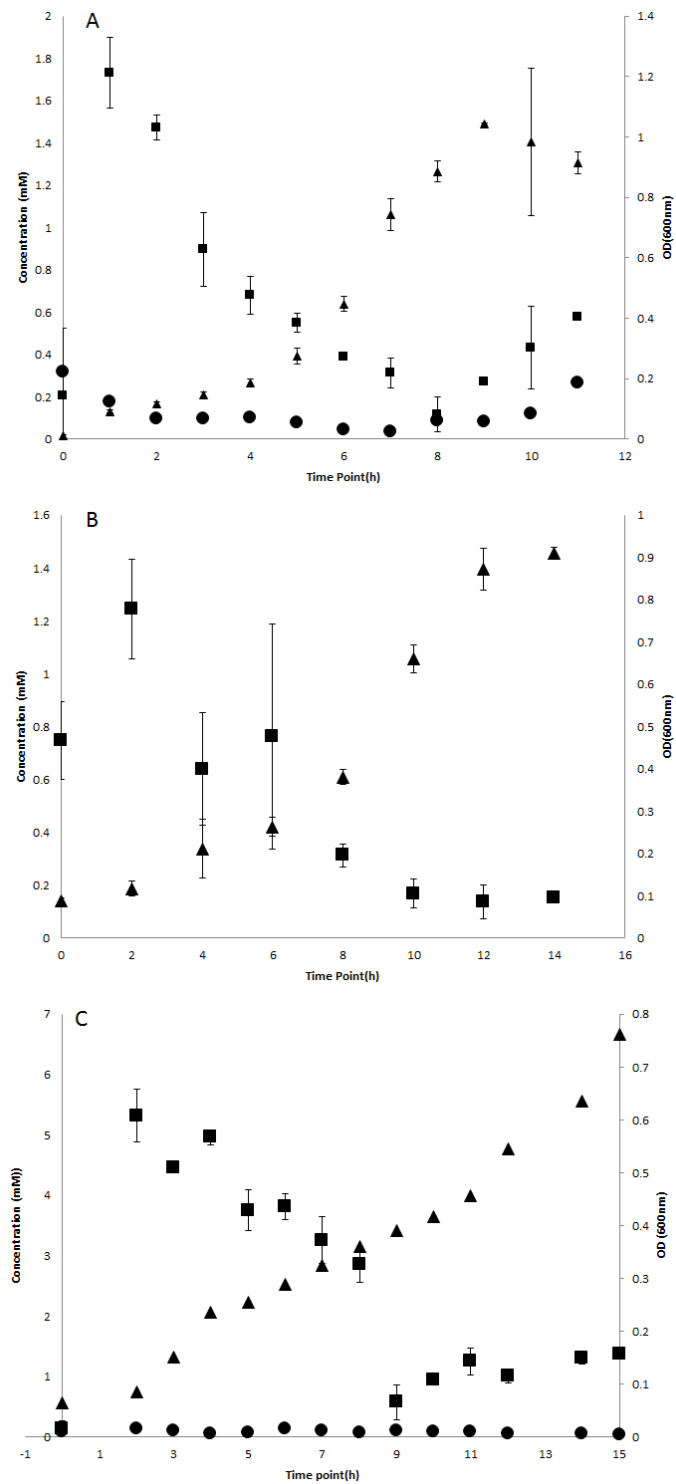
The intracellular concentration measured in *R. thermocellum*, *R. stercorarium*, and *R. termitidis* displayed an initial buildup of PPI at the beginning of growth followed by a steady decline in PPI concentration until a minimum is reached near the onset of stationary phase (Figure 3.1). This trend agrees with previous reports in *Caldicellulosiruptor saccharolyticus* which showed a general decrease in internal PPI concentrations throughout exponential phase (Bielen et al. 2010). While the general trend of internal PPI concentration were similar in *R. thermocellum*, *R. stercorarium*, and *R. termitidis*, the concentrations of PPI differed between the organisms with *R. termitidis* having the largest PPI concentration (5.32 mM) followed by *R. thermocellum* (1.73 mM) and *R. stercorarium* (1.24 mM) (Figure 3.1). In *R. thermocellum* and *R. termitidis*, the concentration of ATP is found to be much lower than the intracellular PPI except for the onset of stationary phase.

#### 3.3.2 Inorganic Pyrophosphatase (EC: 3.6.1.1)

The genomic analysis of various organism of the class *Clostridia* and *Thermotogae*, chosen due to their industrial potential, revealed that there is a large variation in the total



Figure 3.1: Intracellular P<sub>i</sub> concentrations (■) and ATP concentrations (●) throughout growth (▲) of A) *R. thermocellum*, B) *R. stercorarium*, and C) *R. termitidis*





number of PPase (Soluble and V-type) found in each organism, ranging from 1 PPase in *R. thermocellum* to 5 PPases in *R. cellulovorans* (Table 3.1). *Thermotoga maritima* was chosen for the genomic analysis due to both its V-type PPase and PPi-dependent PFK being isolated and characterized, forming a good basis for genomic analysis (Ding, Ronimus, and Morgan 2001; Pérez-Castiñeira et al. 2001). With the number of PPases varying from organisms to organisms, the ion specificity of the V-type PPase also varied between organisms with some utilizing  $K^+$  over  $H^+$  based on sequence analysis. 50% of the analyzed genomes have been found to contain both a V-type PPase as well as a soluble PPase (Table 3.1). V-type PPases are found in the majority of the analyzed genomes in both mesophiles and thermophiles. However, organisms containing only soluble PPases are found to be almost exclusively mesophilic. This seems to indicate that, as expected, the generation of heat via PPi hydrolysis is not favorable in thermophilic organisms. The finding of V-type PPase in the vast majority of analyzed genomes in both mesophilic and thermophilic *Clostridia* indicates that a strong prevalence of V-type PPase in fermentative Firmicutes, which could help offset the relatively low levels of ATP synthesis during fermentation by salvaging energy from biosynthetic reactions such as nucleic acid and protein synthesis. However, the presence of V-type PPase could also apply for the production of PPi utilized in central glycolysis rather than strictly for PPi hydrolysis by harnessing the proton motor force across the membrane. This prevalence also indicates the possibilities of internal levels of PPi playing a very important level in terms of carbon and electron flux regulation such as malate shunt regulation and lactate production (Chapter 2; Bielen et al. 2010).



Table 3.1: List of all annotated pyrophosphatase in various Clostridia and Thermotogae with their respective locus tags and pyrophosphatase type.

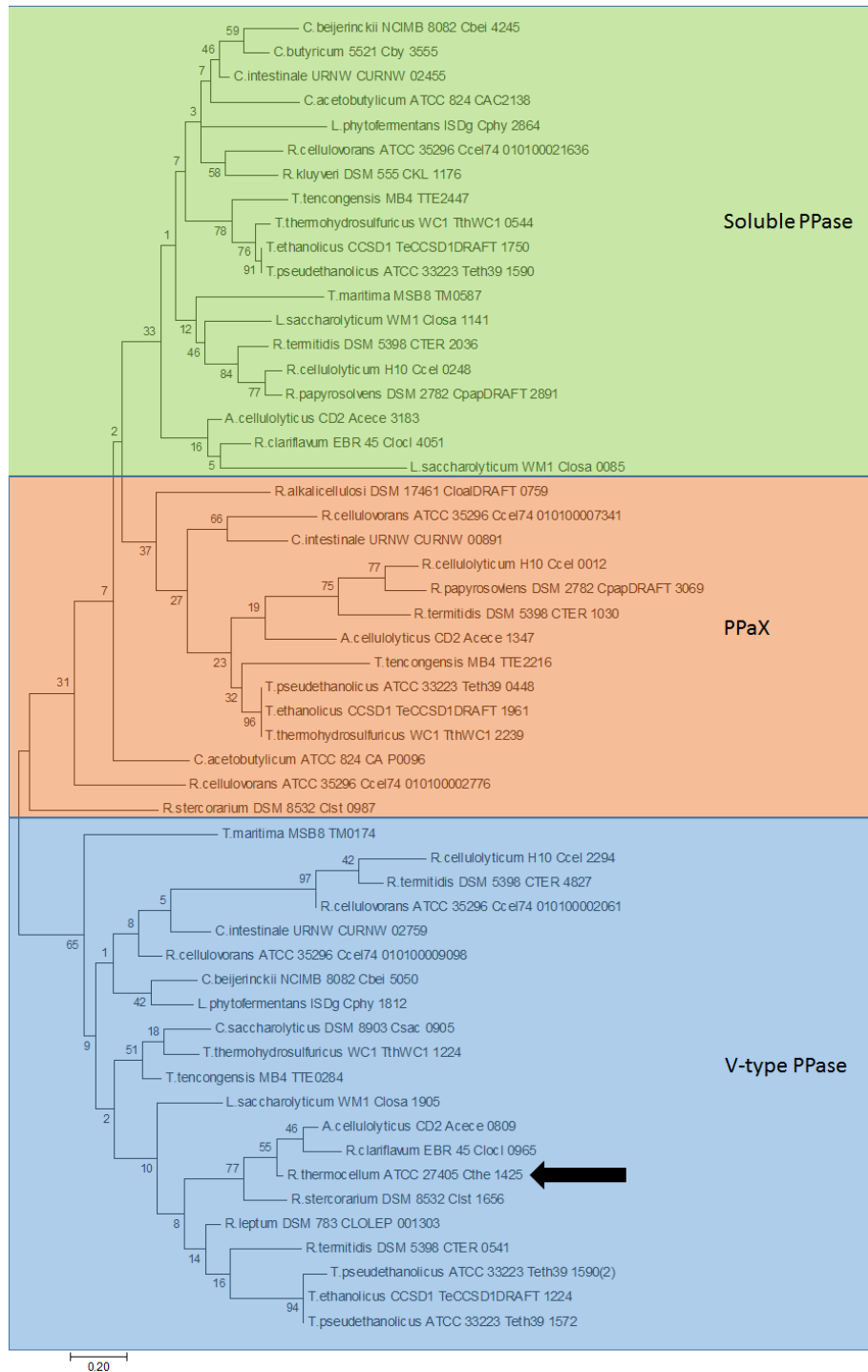
Inorganic Pyrophosphatase(3.6.1.1)		
<b><i>Ruminiclostridium thermocellum</i> ATCC 27405</b>	Cthe_1425	V-type
<b><i>Ruminiclostridium clariflavum</i> EBR 45</b>	Clocl_0965	V-type
	Clocl_4051	Soluble
<b><i>Ruminiclostridium stercorarium</i> DSM 8532</b>	Clst_1656	V-type
	Clst_0987	PPax
<b><i>Ruminiclostridium cellulovorans</i> ATCC 35296</b>	Ccel74_010100002061	V-type
	Ccel74_010100002776	PPax
	Ccel74_010100007341	PPax
	Ccel74_010100009098	V-type
	Ccel74_010100021636	Soluble
<b><i>Ruminiclostridium termitidis</i> DSM 5398</b>	CTER_0541	V-type
	CTER_2036	Soluble
	CTER_1030	PPax
	CTER_4827	V-type
<b><i>Ruminiclostridium cellulolyticum</i> H10</b>	Ccel_2294	V-type
	Ccel_0012	PPax
	Ccel_0248	Soluble
<b><i>Ruminiclostridium papyrosolvens</i> DSM 2782</b>	CpapDRAFT_2891	Soluble
	CpapDRAFT_3069	PPax
<b><i>Ruminiclostridium alkalicellulosi</i> DSM 17461</b>	CloalDRAFT_0759	PPax
<b><i>Ruminiclostridium leptum</i> DSM 753</b>	CLOLEP_00103	V-type
<b><i>Ruminiclostridium kluyveri</i> DSM 555</b>	CKL_1176	Soluble
<b><i>Lachnoclostridium saccharolyticum</i> WM1</b>	Closa_0085	Soluble
	Closa_1141	Soluble
	Closa_1905	V-type
<b><i>Lachnoclostridium phytofermentans</i> ISDg</b>	Cphy_2864	Soluble
	Cphy_1812	V-type
<b><i>Clostridium acetobutylicum</i> ATCC 824</b>	CA_P0096	PPax
	CAC2138	Soluble
<b><i>Clostridium intestinale</i> URNW</b>	CURNW_00891	PPax
	CURNW_02455	Soluble
	CURNW_02759	V-type
<b><i>Clostridium beijerinckii</i> NCIMB 8082</b>	Cbei_4245	Soluble
	Cbei_5050	V-type
<b><i>Clostridium butyricum</i> 5521</b>	Cby_3555	Soluble
<b><i>Clostridium tyrobutyricum</i> DSM 2637</b>	K932DRAFT_00448	Soluble
<b><i>Thermoanaerobacter ethanolicus</i> CCSD1</b>	TeCCSD1DRAFT_1224	V-type
	TeCCSD1DRAFT_1750	Soluble



	TeCCSD1DRAFT_1961	PPax
<b>Thermoanaerobacter pseudethanolicus ATCC 33223</b>	Teth39_1590	Soluble
	Teth39_0448	PPax
	Teth39_1572	V-type
	Teth39_1590	V-type
<b>Thermoanaerobacter thermohydrosulfuricus WC1</b>	TthWC1_0544	Soluble
	TthWC1_1224	V-type
	TthWC1_2239	PPax
<b>Thermoanaerobacterium saccharolyticum</b>	Ga0059259_00703	Soluble
	Ga0059259_01234	V-type
<b>Acetivibrio cellulolyticus CD2</b>	Acece_1437	PPax
	Acece_3183	Soluble
	Acece_0809	V-type
<b>Caldicellulosiruptor saccharolyticus DSM 8903</b>	Csac_0905	V-type
<b>Caldicellulosiruptor bescii DSM 6725</b>	Athe_0756	V-type
<b>Caldanaerobacter subterraneus tencongensis</b>	TTE0284	V-type
	TTE2216	PPax
	TTE2447	Soluble
<b>Thermotoga maritima MSB8</b>	TM0174	V-type
	TM0587	Soluble



Figure 3.2: The evolutionary history of the pyrophosphatase inferred by using the Maximum Likelihood method. The percentage of trees in which the associated taxa clustered together is shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The arrows indicate the *R. thermocellum* Cthe\_1425 V-type PPase.





Sodium-dependent inorganic V-type pyrophosphatases ( $\text{Na}^+$ -PPase) have been fairly recently discovered in both mesophilic and thermophilic organisms (Malinen et al. 2007).  $\text{Na}^+$ -PPase are very similar to  $\text{H}^+$ -PPase with the exception of a requirement of both  $\text{K}^+$  and  $\text{Na}^+$  while  $\text{H}^+$ -PPase do not have a strict requirement for  $\text{K}^+$ . The differentiation between  $\text{Na}^+$  and  $\text{H}^+$  -PPase can be done by the analysis of the amino acids at positions 173, 239, 243, 464, and 467 (Luoto et al. 2011). These positions correspond to the binding domains for  $\text{H}^+$  or  $\text{Na}^+$  and  $\text{K}^+$ . The  $\text{K}^+$  dependence specifically was determined by the identity of the amino acid at position 464 which is lysine for  $\text{K}^+$  independence and alanine for  $\text{K}^+$  dependence (Luoto et al. 2011). The key amino acids for  $\text{Na}^+$ -PPase distinction are glycine, alanine, glycine at positions 243, 464, and 467, respectively. Seven of the 20  $\text{H}^+$ -PPase in Table 3.2 were found to actually contain the  $\text{Na}^+$ -PPase signature. However, the current annotations of the genomes do not take into account the difference between  $\text{Na}^+$ -PPase and  $\text{H}^+$ -PPase (Table 3.2). Interestingly, based on the consensus amino acid sequence, only the  $\text{H}^+$ -PPase (Ccel74\_010100009098) from *R. cellulovorans* is found to be  $\text{K}^+$  dependent showing a large preference for  $\text{K}^+$  independence in *Clostridia*. The sequence analysis revealed a clear separation between  $\text{H}^+$  and  $\text{Na}^+$  dependent V-type PPase with a larger group belonging to the  $\text{H}^+$  V-type PPase (Table 3.2).

### 3.3.3 HPr kinase/phosphorylase

Of the 23 analyzed genomes, only 6 genomes were found to have only one gene encoding a PPase, with 3 of those genomes, *R. thermocellum*, *R. leptum*, and *C. saccharolyticus*, having only a V-type PPase. Interestingly, *R. alkalicellulosi* does not contain any putative gene encoding for either a soluble PPase or a  $\text{H}^+$ -PPase. It does, however, have a gene encoding for a smaller pyrophosphatase known as a PPaX pyrophosphatase (PPaX). PPaX catalyzes the hydrolysis of  $\text{PPi}$



Table 3.2: Analysis of substrate specificity and potassium dependence. The amino acid positions correspond to the amino acid position of the *R. thermocellum* ATCC 27405

Cthe\_1425 gene.

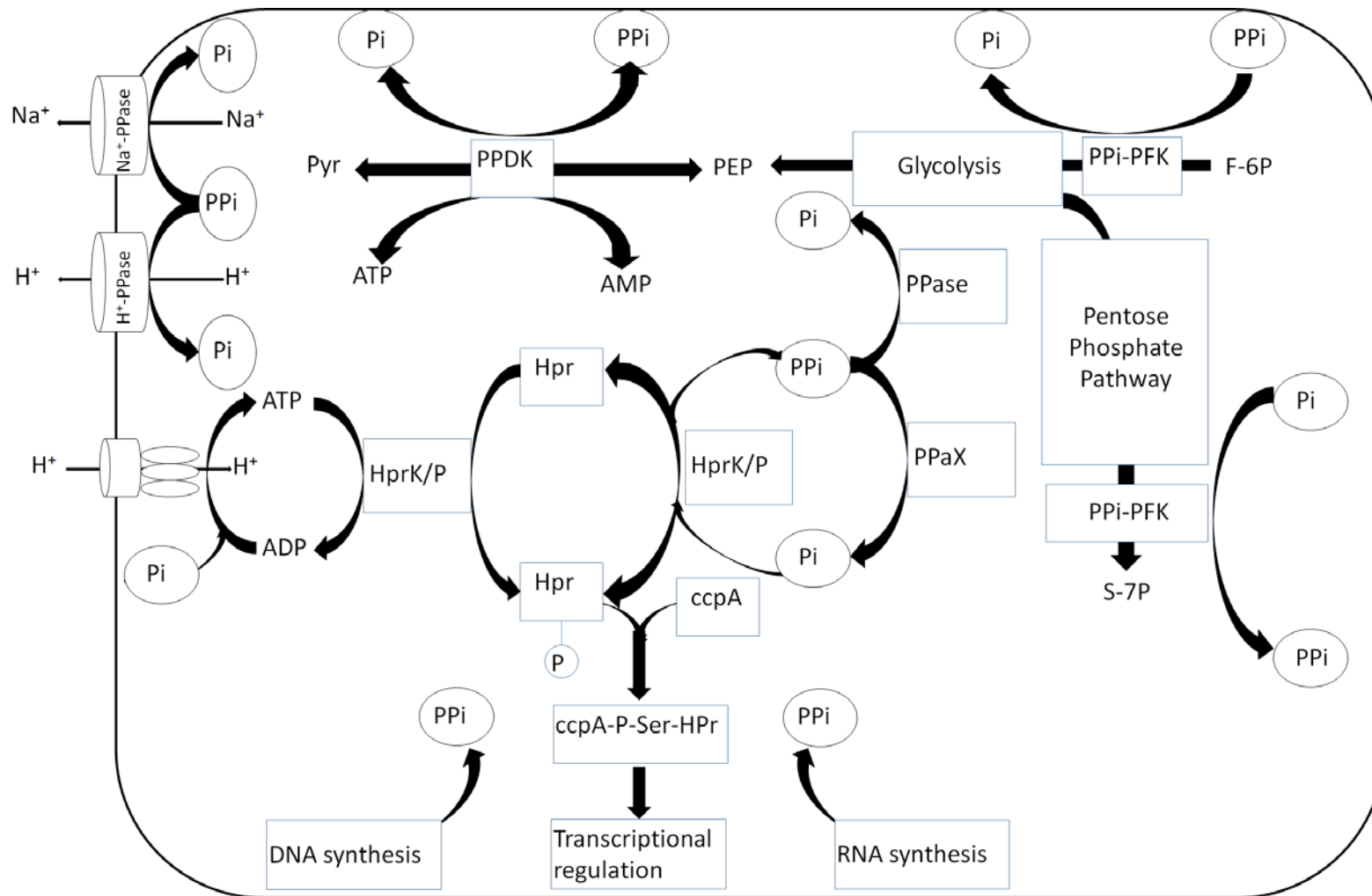
	Locus Tag		K-dependence	173	239	243	464	467
<b>Ruminiclostridium thermocellum ATCC 27405</b>	Cthe_1425	H	-	S	D	A	K	T
<b>Ruminiclostridium clariflavum EBR 45</b>	Clocl_0965	H	-	S	D	A	K	T
<b>Ruminiclostridium stercorarium DSM 8532</b>	Clst_1656	H	-	S	D	A	K	T
<b>Ruminiclostridium cellulovorans ATCC 35296</b>	Ccel74_010100002061	H	-	A	E	V	K	A
	Ccel74_010100009098	H	+	G	E	G	A	A
<b>Ruminiclostridium termitidis DSM 5398</b>	CTER_0541	H	-	G	E	V	K	T
	CTER_4827	H	-	A	E	V	K	A
<b>Ruminiclostridium cellulolyticum H10</b>	Ccel_2294	H	-	A	E	V	K	A
<b>Clostridium beijerinckii NCIMB 8082</b>	Cbei_5050	H	-	G	E	A	K	T
<b>Caldanaerobacter subterraneus tencongensis</b>	TTE0284	H	-	G	E	A	K	T
<b>Thermoanaerobacter thermohydrosulfuricus WC1</b>	TthWC1_1224	H	-	G	E	A	K	T
<b>Acetivibrio cellulolyticus CD2</b>	Acece_0809	H	-	S	D	A	K	T
<b>Caldicellulosiruptor saccharolyticus DSM 8903</b>	Csac_0905	H	-	G	E	A	K	T
<b>Lachnoclostridium saccharolyticum WM1</b>	Closa_1905	Na	+	S	E	G	A	G
<b>Clostridium intestinale URNW</b>	CURNW_02759	Na	+	G	E	G	A	G
<b>Lachnoclostridium phytofermentans ISDg</b>	Cphy_1812	Na	+	G	E	G	A	G
<b>Ruminiclostridium leptum</b>	CLOLEP_00103	Na	+	G	E	G	A	G
<b>Thermoanaerobacter ethanolicus CCSD1</b>	TeCCSD1DRAFT_1224	Na	+	A	E	G	A	G
<b>Thermotoga maritima MSB8</b>	TM0174	Na	+	A	E	G	A	G
<b>Thermoanaerobacter pseudethanolicus ATCC 33223</b>	Teth39_1572	Na	+	A	E	G	A	G
	Teth39_1590	Na	+	A	E	G	A	G



to Pi in a similar manner to the soluble PPase. However, PPaX have been found to be associated with the hydrolysis of the PPi resulting from the dephosphorylation of P-Ser-HPr protein by HPr kinase/phosphorylase (HPr K/P). The HPr K/P protein is related to the carbon catabolite repression (CCR) system, which is generally triggered by the uptake of rapidly metabolizable carbohydrates. In Gram-positive organisms, CCR is generally done through the action of the catabolite control protein A (CcpA) (Mijakovic et al. 2002) (Figure 3.3). CcpA can be activated by the binding of the phosphocarrier protein HPr, phosphorylated at the serine at position 46. This differs from the role of HPr in the phosphotransferase system (PTS) which requires the phosphorylation of HPr at histidine 15 by E1 protein of the PTS system (Kotrba, Inui, and Yukawa 2001). The HPr K/P phosphorylates HPr specifically at Ser-46 thus blocking the phosphorylation of the His-15 preventing the unintended activation of the PTS system. The phosphorylation of HPr allows the binding of HPr(Ser-46)-P to CcpA thus activating the transcriptional regulator. In Gram-positive, it is estimated that the CcpA is capable of modulating the transcription of over 10% of the genome with relevant targets including PFK, PK, LDH, PEPCK, AK, and AdhE (Yoshida et al. 2001; Luesink et al. 1998; Grundy and Waters 1993; Antunes et al. 2012). The HPr K/P was found to be regulated by many compounds including ATP, GTP, fructose-1,6-bisphosphate, and phosphate (Galinier et al. 1998; Kravanja et al. 1999; Reizer et al. 1998). The choice of phosphate donor by HPr K/P is controlled based on the local concentrations of either ATP or PPi allowing for utilization of both depending on which concentration is highest (Mijakovic et al. 2002). Putative KPr K/P are found in all of the analyzed genomes except for *T. maritima*, which had no putative HPr K/P nor any HPr (Table 3.3). While all other organisms contain only a single putative HPr K/P gene, a larger variation in the number of putative HPr genes were predicted ranging from none



Figure 3.3: Overview of enzymes related to maintenance of intracellular PPi levels. HPr K/P: bifunctional HPr kinase/phosphorylase, PPase: Soluble pyrophosphatase, H<sup>+</sup>-PPase: H<sup>+</sup>-dependent V-type pyrophosphatase, Na<sup>+</sup>-PPase: Na<sup>+</sup>-dependent V-type pyrophosphatase, PPaX: HPr associated PPase, PPDk: pyruvate phosphate dikinase, PPi-PFK: PPi-dependent PFK.





being found in *C. butyricum* and *T. maritima* to six in *L. saccharolyticum* (Table 3.3). Most of the sequences analyzed were found to contain both the His-15 and Ser-46 allowing for utilization for both CCR and PTS. Overall, there is an agreement between the lack of a His-15 site and the predicted lack of a PTS system (Table 3.3). In *R. thermocellum*, 2 putative HPr have been identified (Cthe\_2735 and Cthe\_0117). Both were found to have Ser-46 but Cthe\_2735 did not contain the His-15 (Figure 3.4). The proteome of *R. thermocellum* however, showed that the Cthe\_2735 was found in much high levels than Cthe\_0117 showing a clear preference for Cthe\_2735 under standard conditions (Rydzak et al. 2012). Therefore, the preference for Cthe\_2735 over Cthe\_0117 reinforces the prediction of no active PTS system in *R. thermocellum*. Interestingly, some of the butyrate producers, *C. acetobutylicum*, *C. beijerinckii*, and *C. intestinale* URNW processed a much larger putative HPr like protein along with a more standard HPr. These large HPr-response regulators (HPRR) like proteins appear as a fusion between HPr, 2 PAS subunits, and an ATPase domain creating a protein approximately 10 times larger than HPr alone. The precise function of the HPRR is currently unknown, the presence of the PAS subunits suggests that the protein functions to sense the redox potential of the cells or directly sensing oxygen (Taylor and Zhulin 1999; Kotrba, Inui, and Yukawa 2001). The ATPase domains would suggest the ability to autophosphorylate allowing for direct response to stimuli without the need of axillary proteins such as the HPr K/P.

### 3.3.4 Pyruvate phosphate dikinase (EC: 2.7.9.1)

Of the analyzed organisms, only three, *R. cellulolyticum*, *C. acetobutylicum*, and *R. papyrosolvans* had no annotated PPDK genes (Table 3.4). All three of these organisms have a soluble PPase gene. Organisms containing a soluble PPase generally keep intracellular PPi



Table 3.3: List of annotated HPr kinase/phosphorylase, HPr, and prediction of the presence of a PTS system. ND: no annotated gene corresponding to the enzyme was found.

	HPr K/P	HPr	PTS
<b>Ruminiclostridium thermocellum ATCC 27405</b>	Cthe_0110	Cthe_2735 Cthe_0117	-
<b>Ruminiclostridium clariflavum EBR 45</b>	Clocl_1131	Clocl_0666 Clocl_1138	-
<b>Ruminiclostridium stercorarium DSM 8532</b>	Clst_1366	Clst_2316	-
<b>Ruminiclostridium cellulovorans ATCC 35296</b>	Clocl_1671	Clocl_2058	+
<b>Ruminiclostridium termitidis DSM 5398</b>	CTER_4826	CTER_3631 CTER_1040	-
<b>Ruminiclostridium cellulolyticum H10</b>	Ccel_2293	Ccel_0806	-
<b>Ruminiclostridium papyrosolvens DSM 2782</b>	CpapDRAFT_3810	CpapDRAFT_2128	+
<b>Ruminiclostridium alkalicellulosi DSM 17461</b>	CloalDRAFT_2938	CloalDRAFT_0024 CloalDRAFT_2932	-
<b>Ruminiclostridium leptum DSM 753</b>	CLOLEP_00065	CLOLEP_02181	-
<b>Ruminiclostridium kluyveri DSM 555</b>	CKL_1489	CKL_1452	+
<b>Lachnoclostridium saccharolyticum WM1</b>	Closa_1084	Closa_2486	+
		Closa_1250	
		Closa_1088	
		Closa_1508	
		Closa_2170 Closa_0012	
<b>Lachnoclostridium phytofermentans ISDg</b>	Cphy_0328	Cphy_0333 Cphy_1769 Cphy_3549	-
<b>Clostridium acetobutylicum ATCC 824</b>	CAC1089	CAC1820 CAC3088*	+
<b>Clostridium intestinale URNW</b>	CINTURNW_2854	CINTURNW_2085 CINTURNW_2508*	+
<b>Clostridium beijerinckii NCIMB 8082</b>	Cbei_1408	Cbei_1219 Cbei_2147*	+
<b>Clostridium butyricum 5521</b>	CBY_0045	ND	+
<b>Clostridium tyrobutyricum DSM 2637</b>	K932DRAFT_00553	K932DRAFT_00831	+
<b>Thermoanaerobacter ethanolicus CCSD1</b>	TeCCSD1DRAFT_0066	TeCCSD1DRAFT_1782	+
<b>Thermoanaerobacter pseudethanolicus ATCC 33223</b>	Teth39_0576	Teth39_0679	+
<b>Thermoanaerobacter thermohydrosulfuricus WC1</b>	TthWC1_1297	TthWC1_1711	+
<b>Thermoanaerobacterium saccharolyticum</b>	Ga0059259_00543	Ga0059259_01825	+
<b>Acetivibrio cellulolyticus CD2</b>	Acece_1027	Acece_2127 Acece_1034	-
<b>Caldicellulosiruptor saccharolyticus DSM 8903</b>	Csac_1186	Csac_2438 Csac_1163	-
<b>Caldicellulosiruptor bescii DSM 6725</b>	Athe_0364	Athe_0323 Athe_0150	-
<b>Caldanaerobacter subterraneus tencongensis</b>	TTE1964	TTE1820	+
<b>Thermotoga maritima MSB8</b>	ND	ND	-

\*HPRR like



Figure 3.4: Amino acid sequence analysis of the HPr highlighting the His-15 and Ser-46 sites.

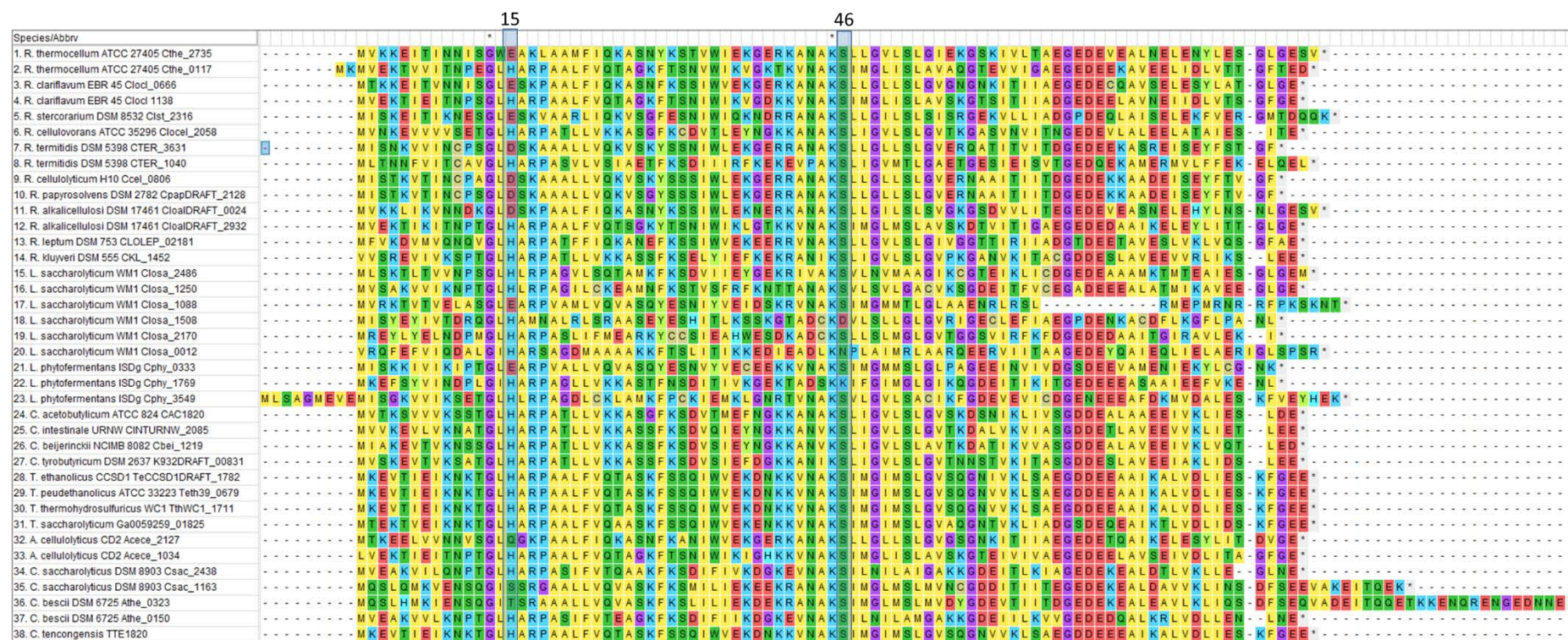




Table 3.4: List of annotated pyruvate phosphate dikinase and pyruvate kinase with their respective locus tags. ND: no annotated gene corresponding to the enzyme was found.

	<b>PPDK(2.7.9.1)</b>	<b>PK(2.7.1.40)</b>
<b>Ruminiclostridium thermocellum ATCC 27405</b>	Cthe_1308	ND
<b>Ruminiclostridium clariflavum EBR 45</b>	Clocl_2755	Clocl_1090
<b>Ruminiclostridium stercorarium DSM 8532</b>	Clst_0708	Clst_0418
<b>Ruminiclostridium cellulovorans ATCC 35296</b>	Ccel74_010100014661	Ccel74_010100010268
<b>Ruminiclostridium termitidis DSM 5398</b>	CTER_0809	CTER_0649
<b>Ruminiclostridium cellulolyticum H10</b>	ND	Ccel_2569
<b>Ruminiclostridium papyrosolvens DSM 2782</b>	ND	CpapDRAFT_0002
<b>Ruminiclostridium alkalicellulosi DSM 17461</b>	CloalDRAFT_3958	CloalDRAFT_0484
<b>Ruminiclostridium leptum DSM 753</b>	CLOLEP_00303	CLOLEP_03925
<b>Ruminiclostridium kluyveri DSM 555</b>	CKL_0920	CKL_3558
<b>Lachnoclostridium saccharolyticum WM1</b>	Closa_0915	Closa_0670
<b>Lachnoclostridium phytofermentans ISDg</b>	Cphy_0651	Cphy_0741 Cphy_2900
<b>Clostridium acetobutylicum ATCC 824</b>	ND	CAC0518 CAC1036
<b>Clostridium intestinale URNW</b>	CURNW_02380	CURNW_00429
<b>Clostridium beijerinckii NCIMB 8082</b>	Cbei_0849	Cbei_0485 Cbei_4851 Cbei_1412
<b>Clostridium butyricum 5521</b>	CBY_3510	CBY_0049 CBY_1825 CBY_3982
<b>Clostridium tyrobutyricum DSM 2637</b>	K932DRAFT_02703	K932DRAFT_00307
<b>Thermoanaerobacter ethanolicus CCSD1</b>	TeCCSD1DRAFT_1370	TECCSD1DRAFT_1788
<b>Thermoanaerobacter pseudethanolicus ATCC 33223</b>	Teth39_1358	Teth39_0684
<b>Thermoanaerobacter thermohydrosulfuricus WC1</b>	TthWC1_2295	TthWC1_1706
<b>Thermoanaerobacterium saccharolyticum</b>	Ga0059259_01049	Ga0059259_01830
<b>Acetivibrio cellulolyticus CD2</b>	Acece_4511	Acece_0975
<b>Caldicellulosiruptor saccharolyticus DSM 8903</b>	Csac_1955	Csac_1831
<b>Caldicellulosiruptor bescii DSM 6725</b>	Athe_1409	Ath_1266
<b>Caldanaerobacter subterraneus tencongensis</b>	TTE0981	TTE1815
<b>Thermotoga maritima MSB8</b>	TM0272	TM0208



concentrations low and static through rapid and steady hydrolysis of PPi (Heinonen and Drake 1988). Therefore, the lower intracellular concentrations of PPi associated with soluble PPase utilization may render flux through PPDK for ATP production unfavorable.

In some anaerobic organisms containing both a PPDK and pyruvate kinase gene, it has been observed that the PPDK is expressed at higher levels than the pyruvate kinase (Rydzak et al. 2012; Munir et al. 2016; Burton and Martin 2012; Van De Werken et al. 2008). ATP efficiency has been suggested as a motive for the preferential expression of the ATP conserving reversible PPDK versus the irreversible pyruvate kinase (Liapounova et al. 2006). The presence of PPi could also be employed as a direct switch between PK and PPDK utilization since pyruvate kinase has been shown to be inhibited in the presence of PPi. The fluctuation pattern of internal PPi concentration would favor flux through pyruvate kinase in the later phase of exponential phase when the internal concentrations of PPi are lower while flux through PPDK would be favored at the beginning of growth when PPi levels are high (Bielen et al. 2010; Heinonen and Drake 1988). Interestingly, *R. thermocellum* does not contain an annotated PK in the genome nor has any PK activity been detected (Rydzak et al. 2009; Zhou et al. 2013). In *R. thermocellum*, an alternative malate transhydrogenase pathway has been proposed as a putative pathway for pyruvate production, therefore, bypassing the need for PK (Chapter 2) (Taillefer et al. 2015; Rydzak et al. 2012; Carere et al. 2012). The purified malic enzyme was inhibited by PPi indicating its importance as a major contributor to the regulation of carbon and electron flux of the pyruvate generating pathways (Chapter 2) (Taillefer et al. 2015). High levels of PPi would inhibit the malic enzyme while simultaneously acting as a substrate for the PPDK. However, no PPDK activity has been published in cell-free extract despite high levels in both the proteome and transcriptome



raising the importance of protein characterization (Zhou et al. 2013; Rydzak et al. 2012; Burton and Martin 2012; Raman et al. 2011). Further, isolation and characterization of the PPDK gene product did not yield any in-vitro activity under the conditions tested so far (Chapter 4). However, recent work has demonstrated PPDK activity in cell-free extracts of *R. thermocellum* requiring the addition of  $\text{NH}_3$  as an activator (Olson et al. personal communication).

The phylogenetic analysis of the PPDK revealed an interesting division in the analyzed PPDK (Figure 3.5). The PPDK separated into 2 major groups with one group containing mostly the PPDK from the *Ruminiclostridium* and *Lachnoclostridium* while the other group contained mostly the PPDK from the *Thermoanaerobacter*, *Thermoanaerobacterium*, *Clostridium*, and *Caldicellulosiruptor*. While 2 groups can be seen in the phylogenetic analysis, the biochemical distinction between cannot be assessed due to the lack of closely related isolated and purified PPDK. The closest related organism with a purified PPDK was *Lachnoclostridium symbiosus* (Formerly *Bacteroides symbiosus*) which displayed a much greater affinity for AMP and  $\text{PPi}$  when compared to the affinity of ATP and  $\text{P}_i$  (Milner, Michaels, and Wood 1975). Therefore, this would suggest that its primary role is pyruvate and ATP generation rather than PEP generation which has been suggested as the primary role for the PPDK found in both groups in the phylogenetic analysis (Bielen et al. 2010; Van De Werken et al. 2008; Rydzak et al. 2012; Taillefer et al. 2015).

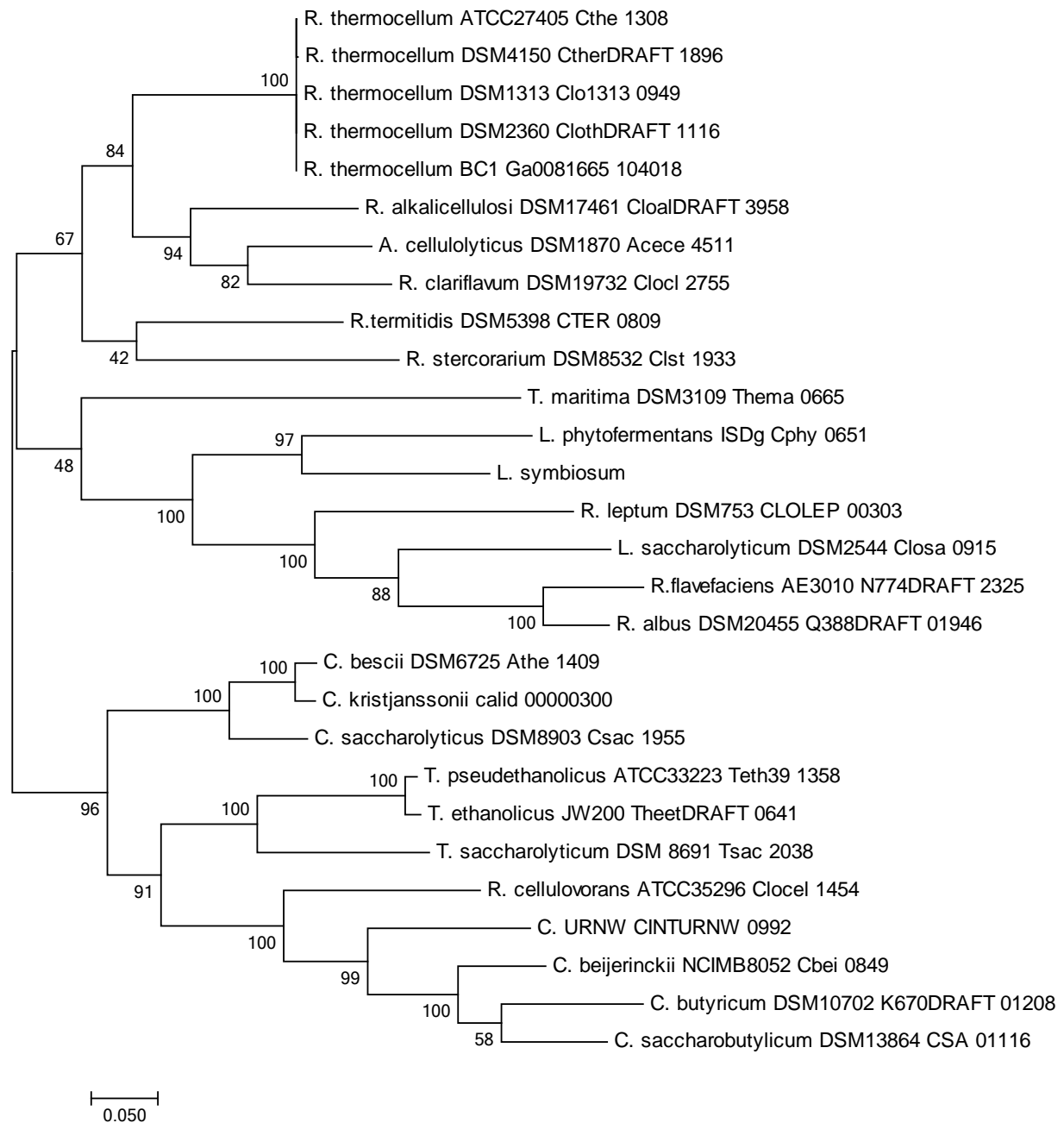
### 3.3.5 Phosphofructokinase (EC: 2.7.1.11)

PFK is one of the key enzymes of glycolysis and therefore, as expected, every organism analyzed has at least one annotated PFK gene with only 4 organisms analyzed not containing more than one annotated PFK (Table 3.5). Of all the observed PFK genes, only TM0289 gene from *T.*



Figure 3.5: The evolutionary history of the pyruvate phosphate dikinase inferred by using the Maximum Likelihood method.

The percentage of trees in which the associated taxa clustered together is shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.





*maritima* has been annotated as a P<sub>i</sub> dependant PFK. Recent proteomics studies in *R. thermocellum* have shown that the expression of the putative P<sub>i</sub>-dependant PFK (Cthe\_0347) was much higher than the 2 putative ATP-dependent PFK (Cthe\_0389<sup>6</sup> and Cthe\_1261) (Rydzak et al. 2012; Raman et al. 2011; Burton and Martin 2012). The utilization of P<sub>i</sub>-dependent PFK is viewed as a means of increasing the ATP efficiency in many organisms (Bielen et al. 2010; Mertens 1993). However, based on theoretical calculations in *R. thermocellum*, the production of P<sub>i</sub> via biosynthesis would be insufficient for P<sub>i</sub>-dependent PFK glycolysis (Zhou et al. 2013). Therefore, this seems to indicate that despite the possible ATP conservation of utilization of P<sub>i</sub>-dependent PFK, the limitation of the amount of P<sub>i</sub> available for glycolysis would lead to the utilization of ATP and/or GTP in order to produce P<sub>i</sub> via ATP-pyrophosphatase (Cthe\_0716). However, the transcriptome and proteomes of *R. thermocellum* show no detectable levels of Cthe\_0716 protein during growth on cellulose or cellobiose (Burton and Martin 2012; Raman et al. 2011; Rydzak et al. 2012). Production of P<sub>i</sub> could also be achieved using proton motor force via a V-type PPase as done in *Rhodospirillum rubrum* and various plants (M. Baltscheffsky, Schultz, and Baltscheffsky 1999; Heinonen 2001). While the generation of P<sub>i</sub> using the proton motor force seems plausible, there is no biochemical data to support this possibility in *R. thermocellum*. Five of the organisms observed had PFKs that did not fit into any cofactor specificity based on their amino acid sequence (Table 3.5). While the function or cofactor specificity of these PFKs remains unclear, it has been proposed that these would correspond to either regulatory subunits capable

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<sup>6</sup> Cthe\_0389 predicted to be P<sub>i</sub> dependent in Figure 3.6

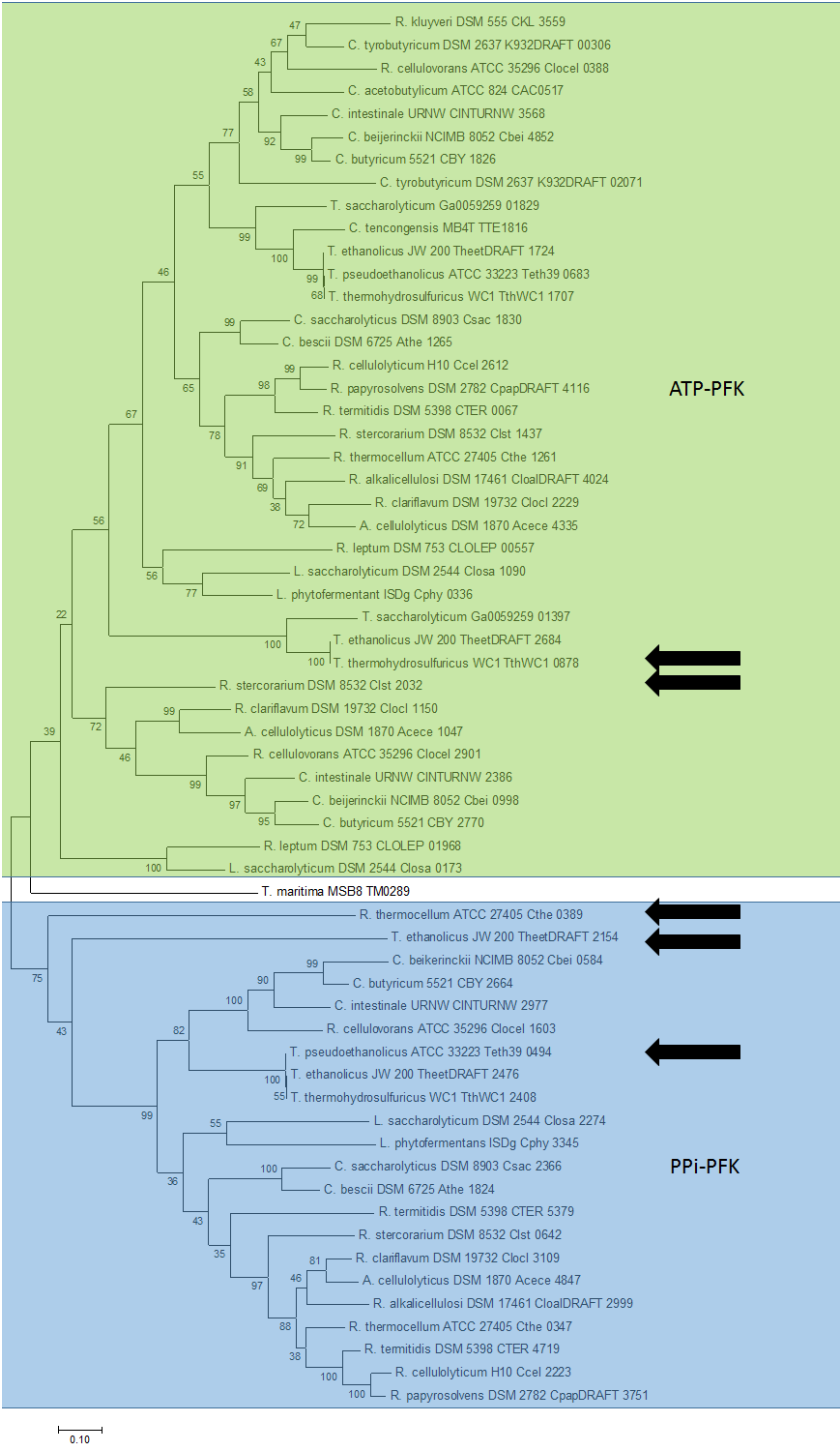


Table 3.5: List of annotated ATP-dependent phosphofructokinase and PPi-dependent phosphofructokinase.

	ATP-dependent Phosphofructokinase (2.7.1.11)	PPi-dependent Phosphofructokinase (2.7.1.90)	Unknown
<b>Ruminiclostridium thermocellum ATCC 27405</b>	Cthe_1261	Cthe_0347	Cthe_0389
<b>Ruminiclostridium clariflavum EBR 45</b>	ClocI_1150 ClocI_2229	ClocI_3109	
<b>Ruminiclostridium stercorarium DSM 8532</b>	Clst_1437	Clst_0642	Clst_2032
<b>Ruminiclostridium cellulovorans ATCC 35296</b>	Clocel_2901 Clocel_0388	Clocel_1603	
<b>Ruminiclostridium termitidis DSM 5398</b>	CTER_0067	CTER_5379 CTER_4719	
<b>Ruminiclostridium cellulolyticum H10</b>	Ccel_2612	Ccel_2223	
<b>Ruminiclostridium papyrosolvens DSM 2782</b>	CpapDRAFT_4116	CpapDRAFT_3751	
<b>Ruminiclostridium alkalicellulosi DSM 17461</b>	CloalDRAFT_4024	CloalDRAFT_2999	
<b>Ruminiclostridium leptum DSM 753</b>	CLOLEP_01968 CLOLEP_00557		
<b>Ruminiclostridium kluyveri DSM 555</b>	CKL_3559		
<b>Lachnoclostridium saccharolyticum WM1</b>	Closa_1090 Closa_0173	Closa_2274	
<b>Lachnoclostridium phytofermentans ISDg</b>	Cphy_0336	Cphy_3345	
<b>Clostridium acetobutylicum ATCC 824</b>	CAC0517		
<b>Clostridium intestinale URNW</b>	CINTURNW_3568 CINTURNW_2386	CINTURNW_2977	
<b>Clostridium beijerinckii NCIMB 8082</b>	Cbei_4852 Cbei_0998	Cbei_0584	
<b>Clostridium butyricum 5521</b>	CBY_1826 CBY_2770	CBY_3664	
<b>Clostridium tyrobutyricum DSM 2637</b>	K932DRAFT_00306 K932DRAFT_02071		
<b>Thermoanaerobacter ethanolicus CCSD1</b>	TheetDRAFT_2684 TheetDRAFT_1724	TheetDRAFT_2476	TheetDRAFT_2154
<b>Thermoanaerobacter pseudethanolicus ATCC 33223</b>	Teth39_0683		Teth39_0494
<b>Thermoanaerobacter thermohydrosulfuricus WC1</b>	TthWC1_1707	TthWC1_2408	TthWC1_0878
<b>Thermoanaerobacterium saccharolyticum</b>	Ga0059259_01397 Ga0059259_01829		
<b>Acetivibrio cellulolyticus CD2</b>	Acece_1047 Acece_4335	Acece_4847	
<b>Caldicellulosiruptor saccharolyticus DSM 8903</b>	Csac_1830	Csac_2366	
<b>Caldicellulosiruptor bescii DSM 6725</b>	Athe_1265	Athe_1824	
<b>Caldanaerobacter subterraneus tencongensis MB4T</b>	TTE1816		
<b>Thermotoga maritima MSB8</b>		TM0289	



Figure 3.6: The evolutionary history of the phosphofructokinase inferred by using the Maximum Likelihood method. The percentage of trees in which the associated taxa clustered together is shown next to the branches. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. Arrows indicate the sequences that could not be identified based on amino acid sequence.





of PFK regulation or are evolutionary transitions between PPi and ATP-dependent PFK leading to ambiguity in their cofactor utilization (Baptiste, Moreira, and Philippe 2003; Bielen et al. 2010). The phylogenetic analysis of the annotated PFKs shows a grouping of both PPi-dependent and ATP-dependent PFK allowing for prediction of cofactor specificity (Figure 3.6). The distinct separation of the groups allows for the prediction of cofactor utilization of PFK containing an unknown cofactor-binding signature. Based on the phylogenetic analysis, Cthe\_0389, TheetDRAFT\_2154, and Teth39\_0494 are predicted to be PPi-dependent while Clst\_2032 and TthWC1\_0878 are ATP-dependent (Figure 3.6). The prediction of PPi-dependence in Cthe\_0389 agrees very well with the cell lysate enzyme assay displaying only PPi-dependent activity (Zhou et al. 2013). Further, the proteome and transcriptome of *R. thermocellum* display very high levels of Cthe\_0389 comparable to the PPi-dependent PFK (Cthe\_0347) indicating a putatively important role in the phosphorylation of F-6P (Rydzak et al. 2012, Chapter 5).

### 3.3.6 Pyrophosphate

Taken together, these patterns suggest that PPi plays a major role not only as a means of energy conservation but also as a regulatory molecule for flux regulation within some Clostridia. Therefore, the variation in PPi concentration in organisms containing a V-type PPase could dictate the current energy state of the cells. In *R. thermocellum*, *R. stercorarium*, and *R. termitidis* we found that the internal concentration of PPi was high at the beginning of growth with a steady decrease in concentration as the cells multiply with a minimum reached at the onset of the stationary phase (Figure 3.1). The values and patterns observed are very similar to the closely related *C. saccharolyticus* (Bielen et al. 2010). However, *R. thermocellum*, *R. stercorarium*, and *R. termitidis* all possess different profiles in terms of PPase present with only a single V-type PPase



in *R. thermocellum*, a single V-type PPase and PPaX in *R. stercorarium*, and two V-types PPase, one soluble PPase, and one PPaX in *R. termitidis*. The re-evaluation of the raw transcriptomic and proteomic data from Munir et al. indicates that the expression of both V-types PPase and the soluble PPase in *R. termitidis* were found to be relatively high indicating possible utilization of both PPase. Therefore, the pattern of internal PPI concentrations does not rely on the presence of specific PPase as the same pattern is observed, regardless of PPase profile. The patterns in PPI concentrations regardless of PPase profile reinforces the importance PPI as a regulator of central catalysis by both directly interacting with glycolytic enzymes such as the GK (Chapter 4) and the malic enzyme (Chapter 2) or indirectly by modulation of the transcription of various genes through the HPr/CcpA system (Figure 3.3) (Chapter 2) (Taillefer et al. 2015). Therefore, further knowledge on the mechanism of sensing and controlling internal PPI concentrations would shed insights into the extent and importance of intracellular PPI in Firmicutes.

### 3.4 Conclusion

PPI metabolism in Clostridia, and more broadly throughout the Domain Bacteria is poorly understood. Generally, only thought as a by-product of biosynthesis quickly degraded by PPase, it would appear to play a much greater role as an energy carrier or as a regulatory molecule. Despite variations in the PPase profile, *R. thermocellum*, *R. stercorarium*, and *R. termitidis* possess very similar patterns of internal PPI concentrations that are consistent with other closely related organisms. This reinforces the idea that PPI in the genus *Ruminiclostridium*, and more broadly the Clostridia plays a greater role as both an energy carrier and a regulatory molecule influencing carbon and electron flux. However, a greater understanding of the concentration sensing and



regulation mechanism would provide great insight into the role of PPI in *Ruminiclostridium* allowing for the discovery of novel genetic engineering target to control internal PPI concentrations in order to be able to modulate carbon and electron flux.



## 4 Regulation of key enzymes of glycolysis showing influence of pyrophosphate as a key regulatory intermediate

### 4.1 Introduction

*Ruminiclostridium thermocellum* is a Gram-positive, anaerobic, thermophilic, Firmicute capable of one of the highest growth rates on crystalline cellulose while producing ethanol and H<sub>2</sub> as key fermentative products (Lynd et al. 2002; Demain, Newcomb, and Wu 2005). Therefore, *R. thermocellum* is viewed a very attractive model for the development of industrially viable biofuel production via consolidated bioprocessing of lignocellulose biomass. However, the current yields and production rates ethanol are low due to the presence of branched product pathways leading to industrially less favourable products such as lactic acid, acetic acid, and formic acid (Zhou et al. 2013; Rydzak et al. 2009; Carere et al. 2008; Islam et al. 2006; Lynd, Grethlein, and Wolkin 1989). While the pathways utilized for end product generation are rather well understood, the regulatory mechanisms dictating end-product flux are poorly understood (Zhou et al. 2013; Taillefer et al. 2015; Rydzak et al. 2014).

Glycolysis in *R. thermocellum*, as with many organisms, is the key to energy conservation and organic carbon assimilation (Gottschalk 1986; Lamed and Zeikus 1980). However, recent work has demonstrated that central catalysis in *R. thermocellum* deviates from the “typical” model of glycolysis (Zhou et al. 2013; Taillefer et al. 2015; Rydzak et al. 2012). Contrary to most ethanol and H<sub>2</sub> producing organisms, *R. thermocellum* ATCC 27405 (GenBank accession number CP00568.1) does not encode for any putative pyruvate kinase nor has any pyruvate kinase activity been identified (Carere et al. 2012; Rydzak et al. 2009; Zhou et al. 2013). Alternatively to the pyruvate kinase, an alternative pathway in the form of the malate shunt has been proposed and



evaluated (Taillefer et al. 2015; Zhou et al. 2013; Rydzak et al. 2012). Several other alterations to the “typical” model of glycolysis have been proposed previously by Rydzak et al. (2012), such as utilization of GTP-dependent glucokinase (GK) and pyrophosphate (PPi) dependent phosphofructokinase (PFK). Both of these activities have been confirmed through enzymatic assays (Zhou et al. 2013). However, as the assays were carried out in cell-free extract, the putative function could not be tied with a particular gene, and the kinetics and possible allosteric enzyme regulation could not be accurately measured. These particular reactions have been demonstrated to be key contributors to the control of metabolic flux through glycolysis and therefore a greater understanding towards cofactor preference and biochemical regulation would shed insight into the regulation of metabolic flux in glycolysis as a whole (Moreno-Sánchez et al. 2008; Saavedra et al. 2007).

Glucokinase (GK) (EC 2.4.1.2) catalyzes the phosphorylation of glucose into glucose-6-phosphate typically utilizing ATP as a phosphate group donor. Bacterial specific GK however, do not share any homology with the non-specific hexokinases from the Eukaryota. However, despite the lack of homology, the affinity for glucose and cofactor are similar in both Eukaryotic hexokinases and bacterial GK (Ronimus and Morgan 2003; Cárdenas, Cornish-Bowden, and Ureta 1998). In prokaryotes, GK can generally be divided into 2 major groups, GK belonging to the repressor/open reading frames of unknown function/sugar kinases (ROK) family and GK that do not have the ROK motif (Titgemeyer et al. 1994). Prokaryotic GK can further be divided into 3 groups based on cofactor preference ATP-dependent, ADP-dependent, and polyphosphate (polyP)-dependent (Ronimus and Morgan 2003; Ito et al. 2001; Labes and Schonheit 2003; Holwerda et al. 2014; N. F. Phillips, Horn, and Wood 1993; Hsieh, Kowalczyk, and Phillips 1996).



Despite the presence of a GK in the *R. thermocellum* genome (Cthe\_2938), very low to absent activities of ATP-dependent GK were demonstrated in cell-free extracts (Ng and Zeikus 1982; S. V. Nochur et al. 1992; Golovchenko, Chuvilskaya, and Akimenko 1986), suggesting it belongs to one of the other groups of prokaryotic GK.

Phosphofructokinase (PFK) (2.7.1.11) catalyzes the phosphorylation of fructose-6-phosphate into fructose-1,6-bisphosphate (FBP) generally utilizing ATP as a phosphate group donor. While ATP-dependent PFK have been identified in all the branches of the tree of life, some alternatives to the ATP-dependence have been identified in Archaea and Bacteria (Mertens 1991; Mertens et al. 1998; Peng and Mansour 1992; Wood, O'Brien, and Micheales 1977). In *R. thermocellum*, 3 putative PFK have been annotated: an ATP-dependent PFK (Cthe\_1261), PPi-dependent PFK (Cthe\_0347), and ATP-dependent PFKb (Cthe\_0389). All three putative PFK are detected in the proteome with the PPi-dependent PFK (Cthe\_0347) having the highest protein levels (Rydzak et al. 2012; Burton and Martin 2012). While ATP-dependent PFK activity had been previously described in *R. thermocellum* (Patni and Alexander 1971), recent studies were only able to detect PPi-dependent PFK activity in cell-free extracts (Zhou et al. 2013).

Phosphoglycerate kinase (PGK) (2.7.2.3) catalyzes the reversible dephosphorylation of 1,3-bisphosphoglycerate into 3-phosphoglycerate using ADP as a phosphate group acceptor. Most characterized PGK have been shown to also utilize various other nucleotide phosphate group acceptors such as GDP and CDP. Despite being capable of utilizing various nucleotides, ADP appears to be the preferred substrate having the highest catalytic rates (Krietsch and Bücher 1970; Kuntz and Krietsch 1982; Encalada et al. 2009). The *R. thermocellum* contains one annotated PGK (Cthe\_0138) gene, and it is expressed at high levels throughout growth (Rydzak



et al. 2012; Raman et al. 2011; Burton and Martin 2012). In cell-free extracts, both ADP and GDP dependent PGK have been measured with similar specific activities in cell-free extracts displaying an alternative to the typical PGK cofactor preference (Zhou et al. 2013; Patni and Alexander 1971).

The interconversion of phosphoenolpyruvate (PEP) into pyruvate in *R. thermocellum* differs from various organisms due to the lack of a pyruvate kinase (PK) gene. Pyruvate phosphate dikinase (PPDK) (2.7.9.1) can catalyze the interconversion of PEP into pyruvate similar to PK using PPi and AMP rather than ADP as cofactors. Due to the lack of the PK, alternatives for pyruvate generations have been proposed in *R. thermocellum* such as the PPDK and the malate shunt (Rydzak et al. 2012; Taillefer et al. 2015). While PPDK utilization for glycolysis has been demonstrated closely related organisms such as *Caldicellulosiruptor saccharolyticus* and in various thermophilic archaea such as *Thermococcus kodakorensis* and *Thermoproteus tenax*, the role of PPDK in the *R. thermocellum* glycolysis remains unclear (Chapter 2) (Bielen et al. 2010; Tjaden et al. 2006; Imanaka et al. 2006; Feng et al. 2008).

Glycolysis is key for the breakdown of sugars and energy conservation in most fermentative Firmicutes such as *R. thermocellum*. The regulation of glycolysis can be viewed as a bottleneck for energy conservation and therefore a careful understanding of the main contributors of carbon flux through glycolysis is vital for a thorough understanding. We have therefore cloned, purified, and characterized the putative GK (Cthe\_2938), PFK (Cthe\_0347), PGK (Cthe\_0138), and PPDK (Cthe\_1308) in order to confirm their cofactor specificity and to evaluate their putative functions and allosteric regulation by the presence of internal metabolites. Taken



together, this would shed light on some putative regulatory mechanisms dictating carbon and electron flux through glycolysis in *R. thermocellum*.

## 4.2 Materials and Methods

### 4.2.1 Strains and reagent

*E. coli* DH5 $\alpha$  was used as the host for plasmid screening. *E. coli* T7 Shuffle (Life Technologies Corp.) was used as the expression strain for recombinant protein expression. PCR purification was done using QIAquick PCR Purification Kit (Qiagen Inc.). All restriction enzymes used were purchased from New England Biolabs. Plasmids were extracted using Qiagen Plasmid Mini Kit (Qiagen Inc.). Recombinant proteins were purified using HiTrap<sup>TM</sup> chelating column (GE Healthcare Bio-Sciences Corp.). Glucose, fructose-6-phosphate (F6P), 3-phosphoglyceric acid (3PG), phosphoenolpyruvate (PEP), NADP<sup>+</sup>, NADPH, NAD<sup>+</sup>, NADH, ATP, ADP, AMP, GTP, PPi, and all buffers used were from Sigma-Aldrich.

### 4.2.2 Plasmid preparation

Plasmids were designed using the corresponding gene sequence for the PPDK (Cthe\_1308), GK (Cthe\_2938), PFK (Cthe\_0347), and PGK (Cthe\_0138) from Integrated Microbial Genomics (Markowitz et al. 2012). The plasmids were synthesized by GeneArt (Life Technologies Corp.) using a pRSET-A backbone to form the recombinant plasmids pAHCT1308 (PPDK), pAHCT2938 (GK), pAHCT0347 (PFK), and pAHCT0138 (PGK). The recombinant plasmids were transformed and confirmed by restriction digest and sequencing in *E. coli* DH5 $\alpha$ . The confirmed plasmids were transformed into *E. coli* T7 Shuffle (New England Biolabs) for recombinant protein expression.



#### 4.2.3 Overexpression and recombinant protein isolation

*E. coli* T7 Shuffle containing one of the plasmids (pAHCT1308, pAHCT2938, pAHCT0347, or pAHCT0138) was cultured overnight in TB medium containing ampicillin (100 µg/mL) at 30°C. Overnight cultures were re-inoculated into fresh TB medium containing ampicillin (100 µg/mL) and grown aerobically at 30°C until an OD<sub>600</sub> of 0.5-0.7. Isopropyl β-D-1-thiogalactopyranoside (IPTG) was then added to a final concentration of 0.5 mM. The cultures were grown for an additional 12 hours at 30°C. Cells were harvested and resuspended in buffer containing 20 mM NaH<sub>2</sub>PO<sub>4</sub> (pH 7.4), 0.5 M NaCl, and 20 mM imidazole. Cells were lysed at 37°C after 15 minutes incubation with 1 mg/mL lysozyme, 1% Triton X-100, 5 µg/mL DNase, 5 µg/mL RNase, and 5 mM MgCl<sub>2</sub> (Sambrook, Fritsh, and Maniatis 1982). Cell lysates were centrifuged at 10 000 RPM for 30 minutes at 4°C in a Fiberlite F13-14x50cy rotor. Supernatants were filtered through a 0.22 µm filter prior to being loaded on a Ni<sup>2+</sup> HiTrap™ metal affinity column and purified following the manufacturer's instructions (GE Healthcare Bio-Sciences Corp.). The recombinant His<sub>6</sub>-tagged proteins were eluted using a stepwise imidazole gradient. Imidazole and NaCl were removed from the recombinant protein samples using HiTrap™ Desalting Column eluting with 20 mM NaH<sub>2</sub>PO<sub>4</sub> (pH 7.4). Enzyme purity was verified by SDS-PAGE with a 12% resolving gel and a 5% stacking gel. Visualization of the recombinant proteins was done by staining the gels with Coomassie Brilliant Blue R-250. Protein concentration was measured by the Bradford assay using bovine serum albumin as a protein standard (Bradford 1976).

#### 4.2.4 Enzyme assays

All enzyme activities were measured in a 300 µl well with a total reaction volume of 200 µl up to 50°C. GK activity was measured in a standard reaction containing 100 mM Tris-HCl (pH 7.0), 10 mM dithiothreitol (DTT), 50 mM KCl, 5 mM MgCl<sub>2</sub>, 2 mM NADP, 1 U/mL glucose-6-



phosphate dehydrogenase (G6PDH). Glucose and phosphate donor concentrations were varied. The assay was started by addition of the phosphate donor (ATP or GTP) (Takahashi et al. 1995). PFK activity was measured in a standard reaction containing 100 mM Tris-HCl (pH 7.0), 10 mM DTT, 5 mM MgCl<sub>2</sub>, 2 mM NADH, 3 U/mL aldolase, 1 U/mL triosephosphate isomerase, 1 U/mL  $\alpha$ -glycerophosphate dehydrogenase. Fructose-6-phosphate and phosphate donor concentrations were varied. The assay was started by addition of P<sub>Pi</sub> (De Jong-Gubbels et al. 1995). PGK activity was measured in a standard reaction containing 100 mM Tris-HCl (pH 7.0), 5 mM MgCl<sub>2</sub>, 2 mM NADH, 2 mM EDTA, 1 U/mL glyceraldehyde-3-phosphate dehydrogenase. 3-phosphoglycerate and phosphate donor concentrations were varied. The assay started by addition of the phosphate donor (ATP or GTP) (van Hoek, Van Dijken, and Pronk 1998). PPDK activity was measured in a standard reaction containing 100 mM Tris-HCl (pH 7.0), 5 mM MgCl<sub>2</sub>, 2 mM NADH, 1 U/mL lactate dehydrogenase. Phosphoenolpyruvate, P<sub>Pi</sub>, and AMP concentrations were varied. The assay was started by addition of P<sub>Pi</sub>. 10 mM pyruvate, 0.2 mM NADH, and 0.005 mM fructose-1,6-bisphosphate (De Jong-Gubbels et al. 1995). Changes in cofactor (NADH, NADP<sup>+</sup>) concentration were monitored at 340 nm using BioTek Synergy 4 plate reader with a molar extinction coefficient of 6220 M<sup>-1</sup>cm<sup>-1</sup> (adjusted for light path during calculations).

#### 4.2.5 Kinetic properties

The kinetic properties for the recombinant GK, PFK, PGK, and PPDK were determined by varying substrate or cofactor concentrations while keeping the concentration of all other constituents at saturating levels at 50°C and pH 7.0. Inhibition assays were performed using the standard reaction conditions above, but with varying inhibitor concentration at 50°C. All kinetic



parameters were determined by fitting the data to the Michaelis-Menten equation using Sigma-Plot (Systat Software Inc.).

#### 4.2.6 Phylogenetic Analysis

The evolutionary history of the GK was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura and Nei 1993). The tree with the highest log likelihood, -21202.9453, is shown. Initial tree(s) for the heuristic search were obtained by applying the Neighbor-Joining method to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach (Bootstrap values with 1000 replicates were calculated). The unrooted tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 nucleotide sequences. All positions containing gaps and missing data were eliminated. There was a total of 475 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 (Tamura et al. 2013).

### 4.3 Results

#### 4.3.1 Glucokinase (Cthe\_2938)

The monomeric molecular mass of the cloned and purified His-tagged GK was approximately 38 kDa corresponding to the predicted molecular mass of the GK protein containing the 6xHis tag. The GK was found to be stable at 4°C for 2 weeks when stored in desalted elution buffer with 10 mM DTT.

GK activity was found to be specific for glucose with no detectable activity with other hexoses including fructose, mannose, galactose, and sorbose. The recombinant GK was found to utilize both GTP and ATP as phosphate group donors with  $K_m$  of  $0.43 \pm 0.09$  mM and  $0.54 \pm 0.04$  mM respectively (Table 4.1, Figure 4.1). With ATP as a phosphate donor, positive cooperative



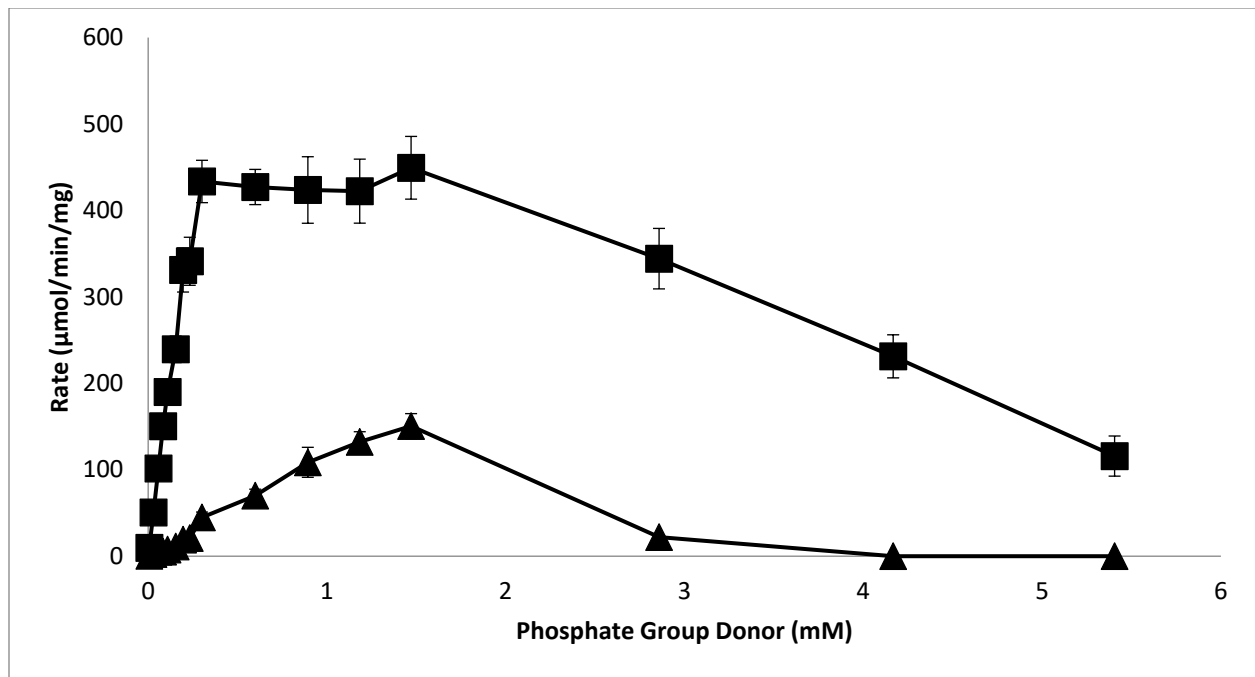
Table 4.1: Kinetic values of the recombinant Cthe\_2938 (GK), Cthe\_0347 (PFK), Cthe\_0138 (PGK), and Cthe\_1308 (PPDK)

	Monomeric molecular mass (kDa)	K <sub>m</sub> (mM)	V <sub>max</sub> ( $\frac{\mu\text{mol}}{\text{min mg}}$ )	K <sub>cat</sub> (s <sup>-1</sup> )	Catalytic efficiency (mM <sup>-1</sup> s <sup>-1</sup> )
Cthe_2938(GK)	38	GTP: 0.43 ATP: 0.54*	GTP: 1023.2 ATP: 128.9	GTP: 577.1 ATP: 72.7	GTP: 1342.1 ATP: 134.6
Cthe_0347(PFK)	50	PPi: 0.23	39.7	30.14	131.1
Cthe_0138(PGK)	43	GTP: 0.25 ATP: 0.17	GTP: 103 ATP: 87	GTP: 73.3 ATP: 61.9	GTP: 293.2 ATP: 364.2
Cthe_1308(PPDK)	100	X	X	X	X

\* Hill coefficient = 2.1



Figure 4.1: Activity of the Recombinant GK with (■) GTP or (▲) ATP as phosphate group donor.





binding was observed with a Hill coefficient of 2.1. No GK activity was detectable with PPI as the sole phosphate group donor. However, the addition of PPI to the reaction increased the recombinant GK activity, with a 100% increase in activity at 8 mM PPI (Figure 4.2). Increased concentrations of both GTP ( $K_i = 1.21 \pm 0.28$ ) and ATP led to substrate inhibition, with peak activities at concentrations of approximately 1.5 mM of the respective phosphate group donor (Figure 4.1). When GTP was used as a phosphate group donor, the  $K_{cat}$  was calculated to be  $577.1 \text{ s}^{-1}$  resulting in a catalytic efficiency ( $K_{cat}/K_m$ ) of  $1342.1 \text{ mM}^{-1}\text{s}^{-1}$ .

The phylogenetic analysis of Cthe\_2938 GK suggests the presence of a GTP preferring ROK GK group containing the Cthe\_2938 (GK) gene (Figure 4.3). The amino acid sequence analysis of the GK (Cthe\_2938) revealed the presence of the putative ROK consensus sequence (CXCGXXGCXE) (Concha and León 2000; Hofmann et al. 1999). The ROK consensus sequence was also detected in 31 of the 51 analyzed amino acids sequences analyzed during the phylogenetic analysis.

#### 4.3.2 Phosphofructokinase (Cthe\_0347)

The monomeric molecular mass of the cloned and purified His-tagged PFK was approximately 50 kDa corresponding to the predicted molecular mass of the GK protein containing the 6xHis Tag. The PFK was found to be stable for 7 days when stored in desalted elution buffer.

Recombinant PFK activity was found to utilize solely PPI as a phosphate group donor with no detectable activity with ATP, GTP, PEP, and ADP. The recombinant PFK displayed very low levels PFK activity with a  $V_{max}$  of  $39.7 \text{ } \mu\text{mol min}^{-1}\text{mg}^{-1}$  and a calculated  $K_{cat}$  of  $30.14 \text{ s}^{-1}$  (Table 4.1). The PFK showed high affinity for PPI as a phosphate group donor with a  $K_m$  of  $0.23 \pm 0.09$



Figure 4.2: Effects of PPI on the recombinant glucokinase activity

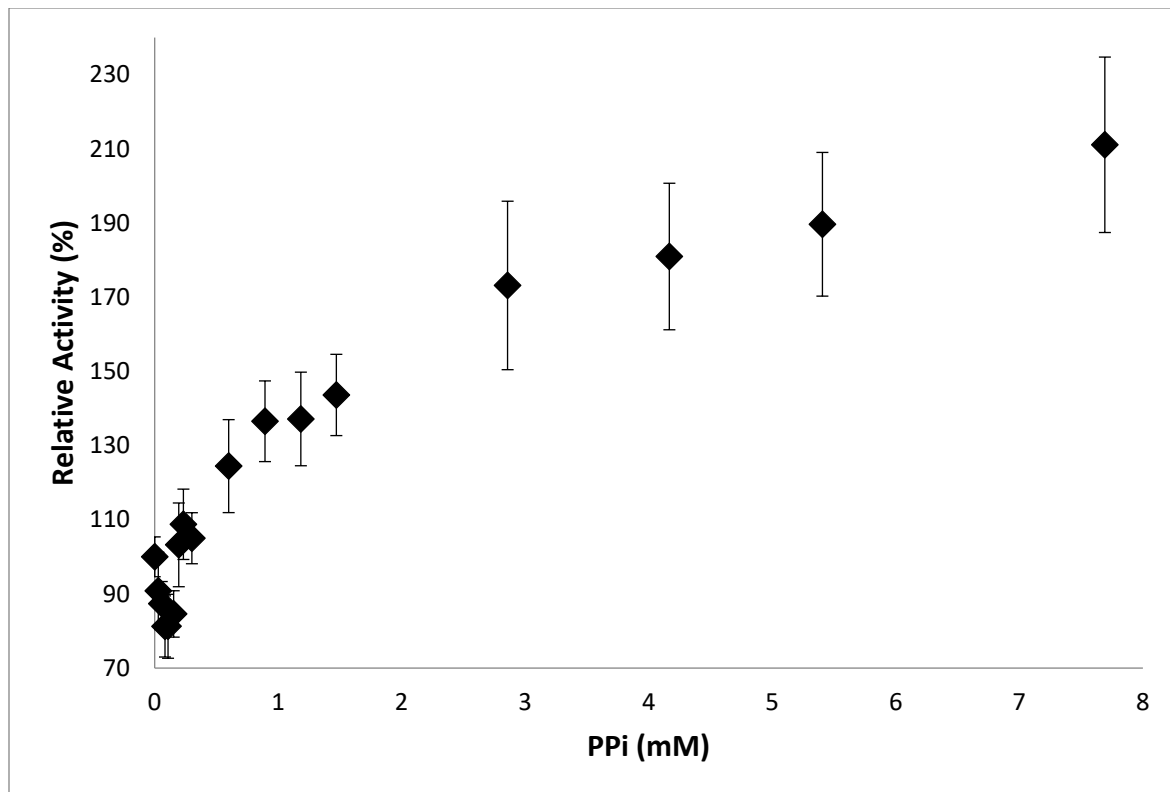
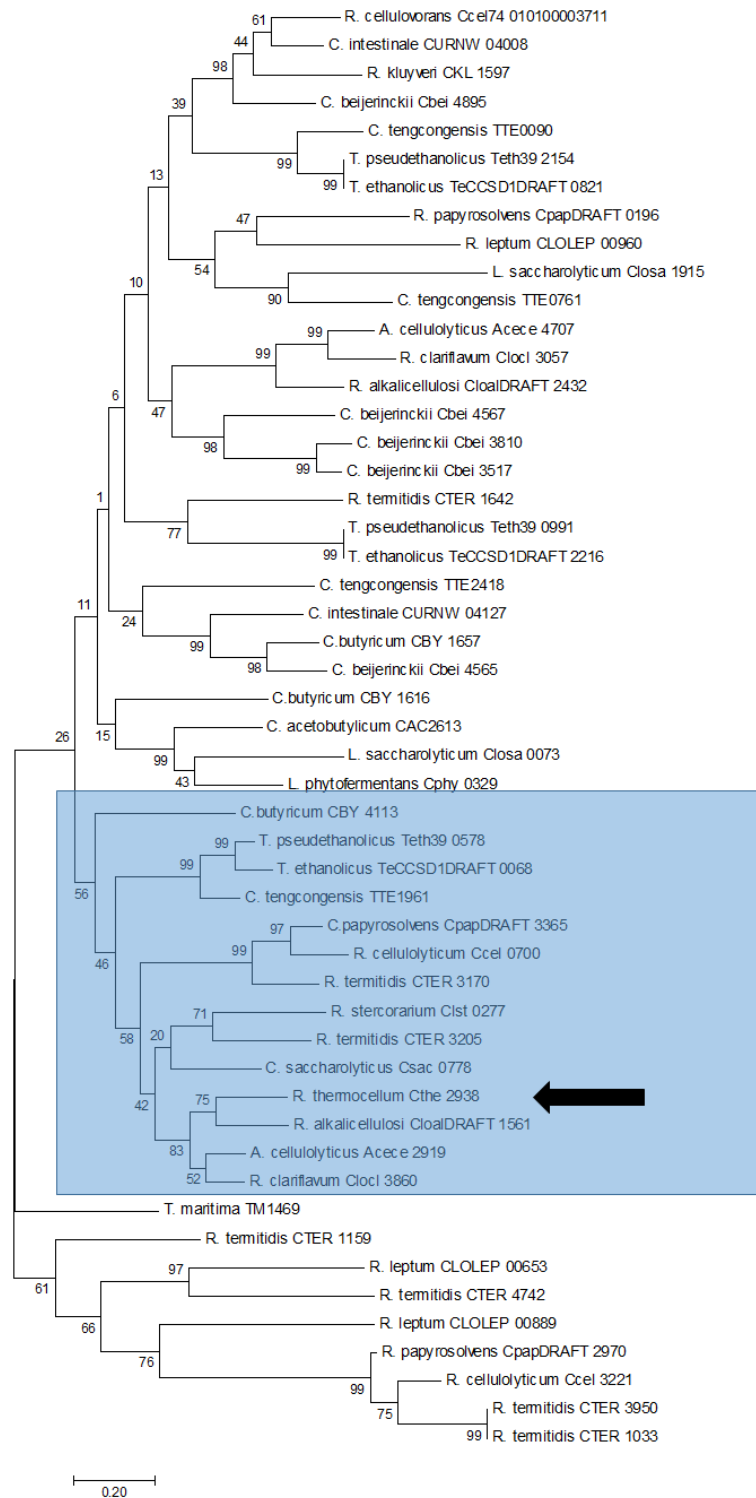




Figure 4.3: Molecular Phylogenetic analysis of the *R. thermocellum* GK (Cthe\_2938) by Maximum Likelihood method. The box indicates a putative GTP-dependent GK group. The arrow indicates the *R. thermocellum* Cthe\_2938 GK. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site





mM. Substrate inhibition was also observed as the increase in PPi concentration led to inhibition of the recombinant PFK with a  $K_i$  of  $1.38 \pm 0.5$  mM (Figure 4.4). The addition of 1 mM ADP, AMP, GTP, GMP, and PEP had no significant effect on recombinant PFK activity. However, the addition of 1 mM ATP led to 60 % decrease in activity when compared to the control.

#### 4.3.3 Phosphoglycerate Kinase (Cthe\_0138)

The monomeric molecular mass of the cloned and purified His-tagged PGK was approximately 47 kDa corresponding to the predicted molecular mass of the PGK protein containing the 6xHis Tag. The recombinant PGK was able to utilize both GTP and ATP as phosphate group donors with  $K_m$  of  $0.25 \pm 0.08$  mM and  $0.17 \pm 0.08$  mM respectively. The calculated  $V_{max}$  of the recombinant PGK was found to be very similar with both GTP ( $103 \pm 14$   $\mu\text{mol min}^{-1}\text{mg}^{-1}$ ) and ATP ( $87 \pm 10$   $\mu\text{mol min}^{-1}\text{mg}^{-1}$ ) as phosphate donors. When GTP was used as a phosphate donor, the recombinant PGK followed Michaelis-Menten kinetics. However, when ATP was used as a phosphate donor, the addition of higher concentrations of ATP led to substrate inhibition with a peak at approximately 1 mM (Figure 4.5). The addition of PPi had no measurable effect on the recombinant PGK activity and was not able to be utilized as a phosphate group donor.

#### 4.3.4 Pyruvate phosphate dikinase (Cthe\_1308)

The monomeric molecular mass of the cloned and purified His-tagged PPDK was approximately 100 kDa corresponding to the predicted molecular mass of the PPDK protein containing the 6xHis Tag. Under all of the conditions tested, no measurable PPDK activity was observed.



Figure 4.4: Specific activity of the recombinant PFK.

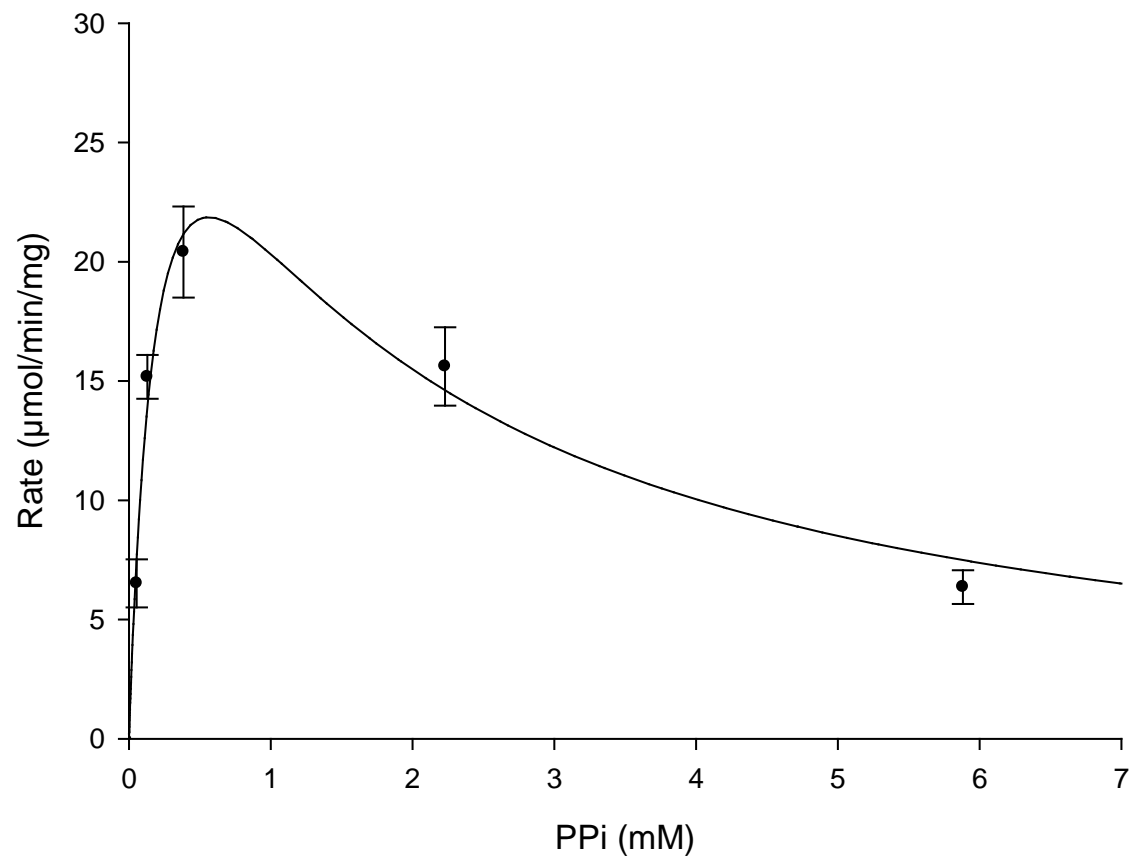
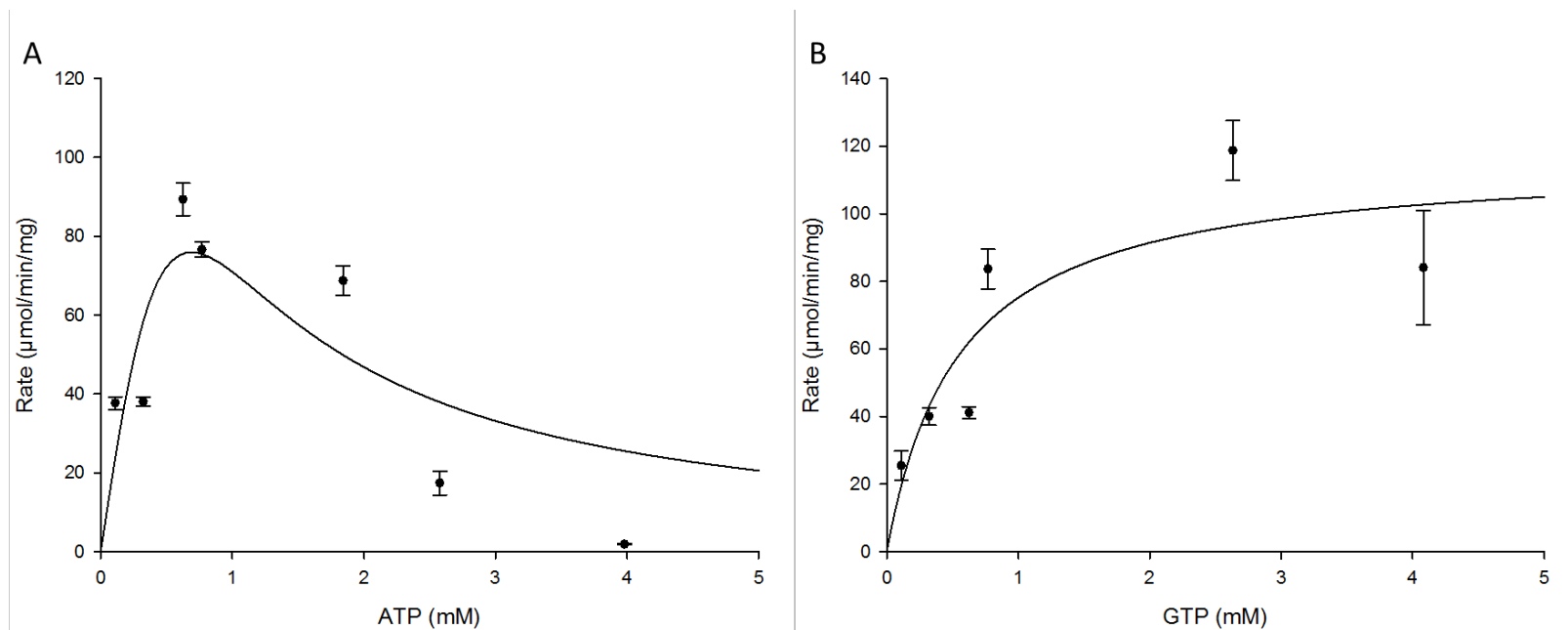




Figure 4.5: Specific activity of the recombinant PGK A) with ATP fitted using substrate inhibition equation and B) with GTP fitted using the Michaelis-Menten equation.





#### 4.4 Discussion

The breakdown of larger more complex sugars is essential in order to conserve the chemical energy associated with sugar catabolism (Stouthamer 1973; Schneider and Gourse 2004). Therefore, the thorough understanding of the central catalysis can be viewed as vital in order to determine proper engineering strategies of genetic engineering for increased end product synthesis in various Firmicutes (Lynd 1996; Olson, Sparling, and Lynd 2015; Zhou et al. 2013). While it has been suggested that the central catalysis of *R. thermocellum* is atypical when compared to traditional models such as *E. coli* (Zhou et al. 2013; Taillefer and Sparling 2015), these suggestions were made based on genome annotation and cell-free extract enzyme assays. While displaying the predicted activity, the exact activity or substrate specificity of the functions could not be attributed to a specific gene. We have therefore cloned, purified and characterized key metabolic flux regulators of central catalysis in order to determine their cofactor specificity and enzyme kinetics in order to elucidate their putative roles in central catalysis and the potential as central catalysis flux regulators.

The GK activity was specific for glucose which is consistent with bacterial glucokinases such as the GK from *Bacillus subtilis*, *Thermotoga maritima*, and *E. coli* (Skarlatos and Dahl 1998; Hansen and Schönheit 2003; Meyer et al. 1997). As previously measured by Zhou et al (2013) the GK displayed both GTP and ATP-dependent activity with a very strong preference for the GTP over ATP (Zhou et al. 2013). While the differences in the rate of reaction might differ greatly, the affinity for both ATP and GTP are quite similar at 0.54 mM and 0.43 mM respectively. This means that despite the similarity in affinity for both ATP and GTP, the great differences in reaction velocity leads to GTP being favored over ATP as a phosphate group donor for the recombinant



GK. Interestingly, GTP-dependent GK activity has been previously described in various bacteria such as *Fibrobacter succinogenes*, *Ruminococcus albus*, and *Actinomyces naeslundii* (Lou, Dawson, and Strobel 1997; Glass and Sherwood 1994; Takahashi et al. 1995). The presence of GTP-dependent GK activity in both *R. albus* and *R. thermocellum* reinforces the reclassification of this clostridial species by Yutin and Galperin (2013) into the family *Ruminococcaceae*, incidentally, the same family as *R. albus* (Yutin and Galperin 2013). This also indicates an important regulatory mechanism based on the intracellular concentrations of both ATP and GTP since both co-factors induce substrate inhibition beyond approximately 1.5 mM concentration. Therefore, it would seem that the cofactor utilized would be dependent on the intracellular levels of these co-factors. This regulatory mechanism would also contribute to the maintenance of the low intracellular ATP and GTP concentrations. High concentrations of ATP and GTP could lead to a decrease in the metabolic flux through the GK, which would lead, in turn, to an overall decreased flux through glycolysis. This mechanism would contribute to the maintenance of the overall intracellular concentration below 1.5 mM of high energy nucleotides as observed in *R. thermocellum* (Figure 3.1) and in some closely related organisms such as *Caldicellulosiruptor saccharolyticus* (Bielen et al. 2010) and *C. acetobutylicum* in the solventogenic phase (Amador-Noguez et al. 2011). These values are found to be much lower than intracellular concentrations found in *E. coli* with values of 9.6 mM and 4.9 mM for ATP and GTP respectively (Bennett et al. 2009). The recombinant GK was also activated by the presence of PPi with a 50% increase in activity at peak (2 mM) (Figure 4.2) intracellular PPi concentrations, reinforcing the importance of PPi as an important regulator of flux in *R. thermocellum* and other closely related Firmicutes



as was previously predicted (Chapter 1,2,3) (Bielen et al. 2010; Taillefer et al. 2015; Rydzak et al. 2012; Zhou et al. 2013).

While the GK displayed flexibility in its phosphate group donor selection, the recombinant PFK was found to be specific for PPI as predicted by amino acid sequence analysis (Rydzak et al. 2012). The activity of the PFK was found to be substantially lower than the recombinant GK at  $39.7 \mu\text{mol min}^{-1}\text{mg}^{-1}$  and  $1023.2 \mu\text{mol min}^{-1}\text{mg}^{-1}$  respectively. The  $V_{\text{max}}$  of the recombinant PFK differs greatly from other characterized PFK such as the PPI-PFK from *Thermotoga maritima*, *Spirochaeta thermophila*, *Thermoproteus tenax*, and *Entamoeba histolytica* ( $203 - 438 \mu\text{mol min}^{-1}\text{mg}^{-1}$ ) (Siebers, Klenk, and Hensel 1998; Z. Deng et al. 1998; Ronimus et al. 2001; Ding, Ronimus, and Morgan 2001). The smaller values of  $V_{\text{max}}$  measured in the recombinant PFK could be reflective of the isolation method used. However, the activities could also imply that the primary function in the cell of this specific PFK is not for the phosphorylation of F6P. *R. thermocellum* is predict to have an alternative pentose phosphate pathway (PPP) as it lacks any transaldolase gene along with the genes required for the oxidative branch of the PPP (Rydzak et al. 2012; Taillefer and Sparling 2015). Therefore, this *R. thermocellum* requires an alternative in order to generate pentose sugars such as ribose-5-phosphate and xylose-5-phosphate. A novel mechanism has been proposed in *R. thermocellum* and demonstrated in *Entamoeba histolytica* and other parasitic protist which utilize the phosphofructokinase and fructose-1,6-bisphosphate aldolase in the non-oxidative branch of the PPP (Mertens 1993; Mertens, De Jonckheere, and Van Schaftingen 1993; Susskind, Warren, and Reeves 1982; Rydzak et al. 2012). The fructose-1,6-bisphosphate aldolase converts erythrose-4-phosphate and dihydroxyacetone phosphate into sedoheptulose-1,7-bisphosphate which gets further dephosphorylated into sedoheptulose-7-



phosphate by the PFK (Figure 1.3). Therefore, in *R. thermocellum*, the protein encoded by Cthe\_0347 could be utilized primarily in the PPP rather than glycolysis or gluconeogenesis with PFK (Cthe\_1261) and PFKb (Cthe\_0389) accounting for the majority of the PFK activity measured in cell-free extract (Zhou et al. 2013). While both Cthe\_1261 and Cthe\_0389 are annotated as being ATP-dependent, no measurable ATP-dependent PFK activity has been found in cell-free extract despite the proteome indicating similar levels of expression of Cthe\_1261 and Cthe\_0389 when compared to other kinases such as the GK (Zhou et al. 2013; Rydzak et al. 2012). Increased levels of PFKb have been associated with increased PPi-dependent PFK activities in cell-free extracts in *R. thermocellum* adapted for higher growth rate and higher ethanol yields (Tian et al. 2016). Therefore, taken together this would indicate that PFKb is a major contributor to the interconversion of F6-P into F1,6-P.

The recombinant PGK displayed properties similar to the recombinant GK in that it can utilize both GTP and ATP as a phosphate group donor. While the  $K_m$  of ATP was actually lower than that of the GTP, increased levels of ATP actually led to substrate inhibition, however, increased concentrations of GTP did not lead to substrate inhibition. At lower concentrations of ATP, the catalytic efficiency of the recombinant PGK was higher with ATP as a phosphate donor over GTP (Figure 4.5) displaying a putative slight preference for ATP at lower energy carrier concentrations. The internal concentrations of ATP have been previously measured in *R. thermocellum* and were found to be below 1 mM throughout growth (Figure 3.1), similar to closely related organisms such as *Caldicellulosiruptor saccharolyticus* leading to a slight preference of ATP over GTP (Bielen et al. 2010). However, the wider optimal activity found with



GTP would allow the enzyme to better respond to variations in GTP concentrations without having any effects on PGK activity.

Since glycolysis is the main contributor of energy conservation, regulation of carbon and electron flux through glycolysis via substrate inhibition would lead to direct control of the intracellular concentration of various internal high energy metabolites such as GTP, ATP, and PPi. The presence of substrate inhibition in glycolysis allows *R. thermocellum* to regulate the flux through glycolysis based on energy consumption inside of the cells, and therefore creating an energy balance optimal for glycolysis and biosynthesis (Reed, Lieb, and Nijhout 2010; Uyeda, Furuya, and Luby 1981). The presence of PPi has also been shown to modulate malic enzyme leading to inhibition of the malate shunt limiting carbon and electron flux towards pyruvate (Chapter 2) (Taillefer et al. 2015). While previously believed that high concentrations of PPi would induce PPDK activity, no recombinant PPDK was observable (Figure 2.7). These findings are consistent with enzyme assays done in cell-free extracts that do not have any measurable PPDK activity (Zhou et al. 2013) despite elevated levels of PPDK in both transcript (Raman et al. 2011)(Chapter 5) and protein (Rydzak et al. 2012; Burton and Martin 2012) levels. However, recent experiments in cell-free extracts have shown PPDK activity when induced with relatively high concentrations of NH<sub>3</sub> (Olson *et al.* personal communication).

## 4.5 Conclusions

The characterization of the biochemical properties of the GK, PFK, PGK, and PPDK from *R. thermocellum* has provided valuable insight into the putative regulatory mechanisms of key flux regulators of glycolysis in *R. thermocellum* and other closely related organisms. The substrate inhibition of the GK by both GTP and ATP, along with the substrate inhibition of the PGK by ATP



reveal interesting regulatory mechanisms which would favor constant levels of both ATP and GTP below 1.5 mM. When taken together with previous studies showing pyrophosphate inhibition of the malic enzyme (Taillefer et al. 2015, Chapter 2), the activation of GK by PPi demonstrates the importance of the intracellular concentrations of PPi in the cells acting as a signal of the current cell state. Therefore, with the low activities of the recombinant PFK, this reinforces that the current understanding of the central catalysis of *R. thermocellum* requires further refining in order to create viable genetic engineering strategies in order to increase the flux of glucose through glycolysis allowing for faster ethanol generation. This knowledge would increase the commercial viability of not only *R. thermocellum*, but also of all commercially relevant *Ruminiclostridium* species.



## 5 Transcriptomic and genomic analysis of three *R. thermocellum* strains producing different ratios of end products.

### 5.1 Introduction

The genus *Ruminiclostridium* hold great potential in terms of industrial ethanol production via consolidated bioprocessing allowing for the generation of fuels from renewable abundant biomass sources along with minimizing the requirement of extensive and expensive pre-treatments (Olson et al. 2012; Lynd et al. 2005; Olson, Sparling, and Lynd 2015; Demain, Newcomb, and Wu 2005; Lynd, Grethlein, and Wolkin 1989). *Ruminiclostridium thermocellum* has been extensively studied and represents a good model not only for other members of the genus *Ruminiclostridium* but for many other fermentative Firmicutes (Chapter 1) (Taillefer and Sparling 2015).

The type strain of *R. thermocellum* ATCC 27405 (DSM 1237) has been extensively studied for many years as an organism with great industrial potential (Patni and Alexander 1971; Lynd 1996; Lynd, Grethlein, and Wolkin 1989; Levin et al. 2006; Rydzak et al. 2009; Wiegel, Ljungdahl, and Demain 1985; Zeikus 1980). *R. thermocellum* ATCC 27405 produces approximately equimolar amounts of both ethanol and acetate (~ 4 mM) with concentrations of formate at approximately 2 mM and trace amounts of lactate. The ratio of CO<sub>2</sub> to H<sub>2</sub> is also measured at a ratio of 1.5:1 (6:4 mM) (Rydzak et al. 2009; Islam et al. 2006; Sparling et al. 2006). Others strains of *R. thermocellum* have been characterized and generally differ based on the amounts of end products generated and carbohydrate utilization. *R. thermocellum* DSM 2360 (LQRI) produces a much greater acetate to ethanol ratio of 3:1 compared to the 1:1 of *R. thermocellum* ATCC 27405 in continuous and batch cultures (Strobel 1995; Lamed, Lobos, and Su 1988). However, many previous experiments done with *R. thermocellum* displayed the ability to grow on glucose as a



carbon source (Strobel 1995). This has been questioned, as the currently available strains of *R. thermocellum* are incapable of growing on glucose, raising questions on the purity of the strains utilized during these previous experiments. Therefore, it is believed that the ability to grow on glucose could be attributed to contamination from other organisms such as *Thermoanaerobacter* (Erbeznik et al. 1997). It was also stated that multiple mutations were required in order to have cultures of *R. thermocellum* capable of growing on glucose (Saraswathy V. Nochur, Roberts, and Demain 1990).

*R. thermocellum* DSM 4150 (JW20) was originally found to be quite interesting due to its apparent native capability to grow glucose and fructose along with cellobiose and cellulose without the prolonged adaptation procedure required other strains to grown on glucose (Saraswathy V. Nochur, Roberts, and Demain 1990; Strobel 1995). DSM 4150 produced an acetate to ethanol ratio of 0.2 and a CO<sub>2</sub> to H<sub>2</sub> ratio of 2.9 (Freier, Mothershed, and Wiegel 1988). This would make DSM 4150 the best ethanol producer when compared to other available strains of *R. thermocellum*. However, nearly 20 years after its isolation and characterization, it was found that the commercially available strain of DSM 4150 was found to in fact be a co-culture between DSM 4150 and *Thermoanaerobacter ethanolicus* (Erbeznik et al. 1997). This puts into question the validity of the results obtained prior to 1997 especially since currently available strains of *R. thermocellum* are not capable of growth on glucose as a sole carbon source.

Therefore, we decided to grow *R. thermocellum* strains ATCC 27405, DSM 4150, and DSM 2360 side by side in the same medium in order to measure the differences in end products produced during growth. We also wanted to observe the variations in the annotated genomes along with the transcription of central catalysis genes in order to correlate differences in



expression with differences in end-product synthesis in these closely related but genetically non-identical strains. This could potentially reveal novel genetic engineering targets focus on natural variations among different strains of *R. thermocellum*.

## 5.2 Materials and methods

### 5.2.1 Organisms and media preparation

Fresh cultures of *R. thermocellum* ATCC 27405, DSM 4150, and DSM 2360 were maintained by routinely transferring 5% (v/v) mid-exponential phase inoculum into complex 1191 medium containing 2 g/L cellobiose or  $\alpha$ -cellulose (Levin et al. 2006; Rydzak et al. 2009). Cultures were grown at 60°C and stored anaerobically at 4°C until analysis to stop end-product synthesis. All chemicals were obtained from Sigma Chemical Co. (St. Louis, MO) and all gasses were purchased from Welder's Supply (Winnipeg, MB). Experiments were carried out anaerobically in sealed Corning bottles (1.1 L) containing 500 mL of 1191 medium adjusted to pH 7.2 with cellobiose or  $\alpha$ -cellulose as a carbon source. Preparation of the Corning bottles and inoculation protocols were followed as previously described by Islam *et al.* 2006.

### 5.2.2 Cell growth and end product analysis

Cell growth was monitored spectrophotometrically at 600 nm using a Biochrom Novaspec II spectrophotometer. Samples were collected using a 1 mL syringe (Becton, Dickinson, and Company, Franklin Lakes, NJ) with a 22G hypodermic needle (Fisher Scientific, Ottawa, ON). Samples were centrifuged at 12 000 RPM for 10 mins in a Fiberlite F13-14x50cy rotor and the supernatant containing soluble end-products was removed. Soluble end product analysis was carried out by high-performance liquid chromatography (HPLC) (Dionex ICS-3000, Thermo Fisher Scientific, MA, USA) equipped with a refractive index detector and an ion exclusion column (Aminex HPX-87H; Bio-Rad laboratories, CA, USA) using a 5mM sulphuric acid mobile phase. H<sub>2</sub>



and CO<sub>2</sub> concentrations were measured using a Varian 490-GC gas chromatograph system (Varian Medical Systems Inc., CA, USA), equipped with a Thermal Conductivity Detector (TCD).

### 5.2.3 RNA isolation and RNA sequencing

One mL of cell cultures were sampled from *R. thermocellum* ATCC 27405, DSM 2360, and DSM 4150 during exponential growth (OD ~ 0.45) and centrifuged immediately at 10 000 x g in order to pellet cells. The cell pellet was washed with phosphate buffered saline solution (pH 7). Total RNA was extracted from the washed cell pellet using the PureLink® RNA Mini Kit (Ambion, Life technologies, CA, USA). The concentration of isolated RNA was determined via Nanodrop 1000 spectrophotometer and Qubit 2.0 Fluorometer (Fisher Scientific, Ottawa, ON). The purified RNA samples were stored at –80°C and shipped on dry ice where the cDNA libraries were created and sequenced by the McGill University and Génome Québec Innovation Centre (Montréal, Québec) using Illumina HiSeq 2000 platform.

### 5.2.4 Data analysis

The data from the RNAseq was gathered and analyzed using an in-house 'Omics data analysis system called UNITY (McQueen et al. 2015; Munir et al. 2016; Fu et al. 2015). RNAseq reads were identified and mapped based on the Integrated Microbial Genomics (IMG) annotation of the *R. thermocellum* ATCC 27405 genome (GenBank accession number [NC 009012.1](#)). Expression level was determined as the log2 sum of 100-mer alignment fragments per gene to allow for cross strain comparison. The cross strain comparisons were done as described by Verbeke *et al.* (2014). The differences in expression levels between biological replicates ( $R1=A2-A1$ ), where Ax are biological replicates and between strains ( $Z=AY-AX$ ), where Y and X are difference strains were determined. Four values are determined per comparison comprised of



$R1=A2-A1$ ,  $R2=B2-B1$ ,  $Z1=B1-A1$ , and  $Z2=B2-A2$ . Further transformation of the data combines the differences of measurements into a unified expression value (W). Firstly, the expression values for all the samples were normalized to a mean of zero and a standard deviation of 1. Vectors were then computed as the distance from the origin to the mapped coordinates determined by the coordinates determined by (R1, R2) or (Z1, Z2). The differences between the magnitudes of the vectors were scaled by the ratio of their respective populations. The up or down regulation of the W value was computed using the angle from the X-axis to the (Z1, Z2) coordinate such that angles between  $315^\circ$  and  $135^\circ$  are positive while all other angles represent negative regulation. Finally, the unified expression value was normalized to have a mean of 0 and a standard deviation of 1 to form Wnet. The Wnet values were validated on a transcript-to-transcript basis using the mean of the standard deviations of the biological replicates and cross strain comparisons. The signal to noise (S/N) is the ratio of the magnitude of the vectors scaled by the overall system S/N. A false discovery rate of  $< 10\%$  was used to define a S/N cut-off of 2.8 (Wstats) using a Monte-Carlo Model. The Wstats allow for the reliable comparison of relatively small changes in expression levels given the variability between biological replicates were sufficiently smaller. However, elimination of any Wstats below 2.8 would eliminate the vast majority of the transcript, therefore analysis was performed despite having Wstats values below 2.8 for many of the transcripts analyzed.

## 5.3 Results and Discussion

### 5.3.1 Strain growth

The growth of all three strains of *R. thermocellum* was consistent with previously reported values on cellobiose and cellulose. However, some deviations in the ethanol to acetate ratios were observed in DSM 2360. Previous reports have shown an approximately 3:1 ratio whereas



in the results obtained in the present study were found to be much closer to 1:1 (Figure 5.1) (Strobel 1995; Lamed, Lobos, and Su 1988). The acetate to ethanol ratio in DSM 4150 was found to be 0.7, which differs greatly from the previously reported 0.2 (Freier, Mothershed, and Wiegel 1988). Contrary to the previous report, none of the strains were capable of growth on glucose as the sole carbon source. This seems to indicate that the previous reports of growth on glucose were done with contaminated cultures with a another organism capable of growth on glucose, multiple mutations in the genome allowing for the growth on glucose, or that the particular strains used were capable of growth on glucose but were however subsequently lost as was suggested for other discrepancies such as the cofactor utilisation of the GK and presence of PK activity (Zhou et al. 2013).

### 5.3.2 RNA Sequencing

RNA sequencing and transcriptomic analyses were done in three strains of *R. thermocellum* in order to assess what differences in expression profile could account for the variations in the amount of end products produced by each strain. The linear regression of the log2 of the sum of 100-mer elements between biological replicates showed a good correlation ( $R^2 > 0.9$ ) indicating the reproducibility of the biological replicates (Figure 5.2). The transcripts of *R. thermocellum* ATCC 27405, DSM 2360, and DSM 4150 covered over 90% of the protein-coding genes in their respective genomes (Table 5.1). Overall, the transcriptomes across the three strains were found to be very conserved with very little changes in the expression of the central glycolysis and end-product synthesis pathways. Many of the transcripts agree with previous



Figure 5.1: End Product profile of strains ATCC 27405, DSM 2360, and DSM 4150 grown on cellobiose at the time of sampling for transcriptomic analysis.

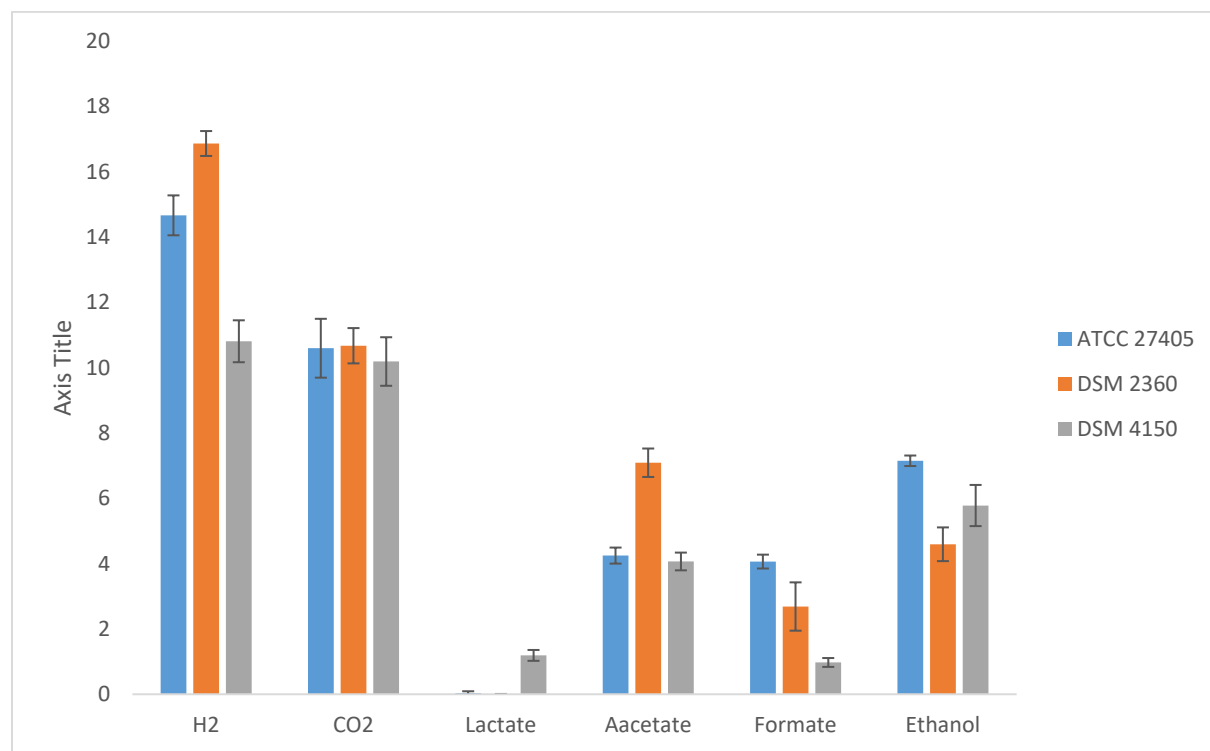




Figure 5.2: Inter-replicate correlation of the 100-mer reads of the ATCC 27405, DSM 2360, and DSM 4150 strains. A) ATCC 27405 on cellobiose, B) DSM 2360 on cellobiose, C) DSM 4150 on cellobiose, D) ATCC 27405 on  $\alpha$ -cellulose, E) DSM 2360 on  $\alpha$ -cellulose, and F) DSM 4150 on  $\alpha$ -cellulose. The axis represents the 100-mer reads of the biological replicates.

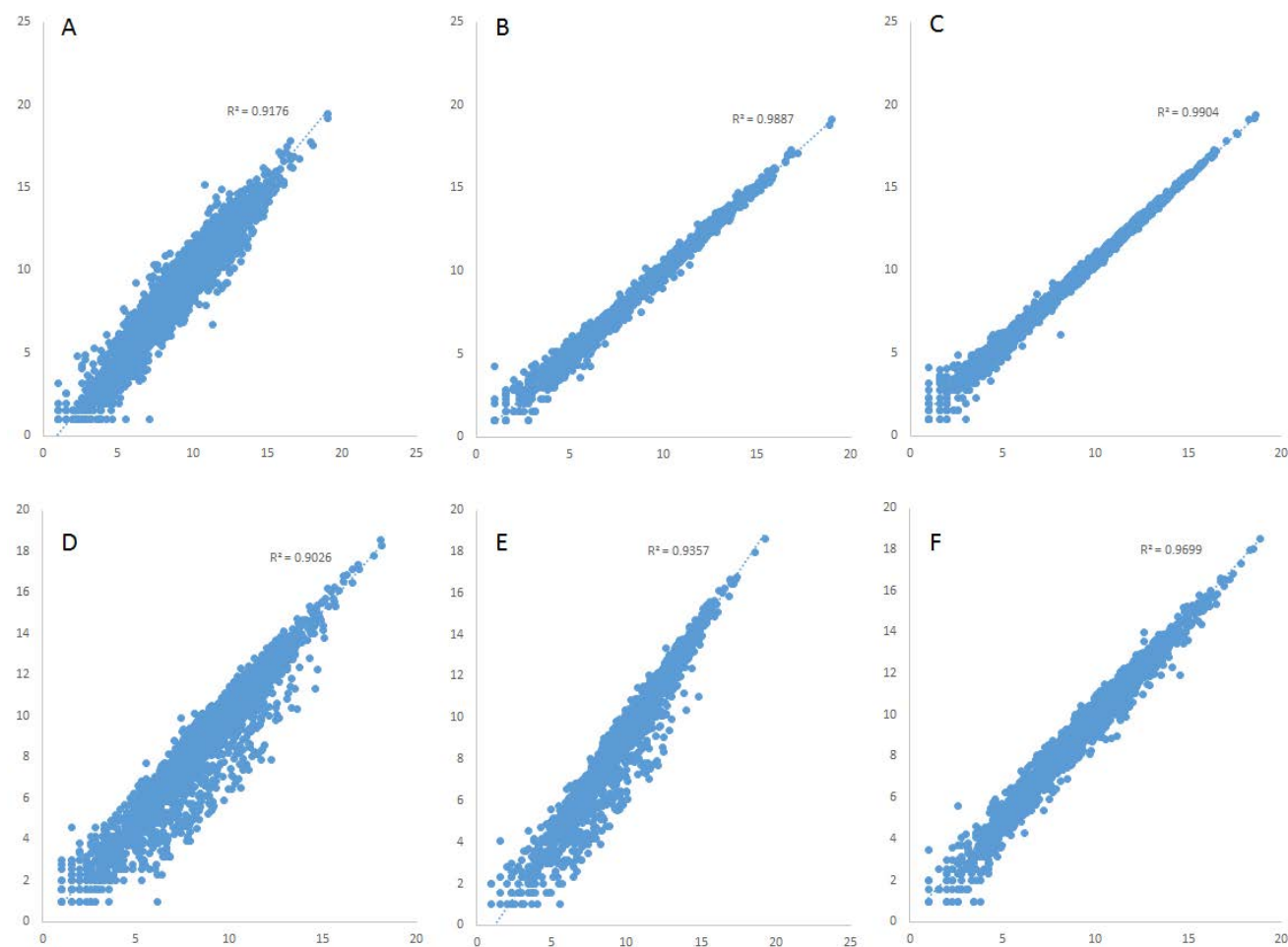




Table 5.1: General RNAseq and genome comparison results

	Accession	Genome size	GC%	Genes	Protein coding genes	rRNA	tRNA	Symmetric identity	Transcripts Detected	% protein coding genes detected
ATCC 27405	NC_009012.1	3.84	39	3376	3224	12	56	NA	3149	97.67
DSM 2360	NZ_ACVX000000000.1	3.58	39.2	3111	3012	12	53	91.92	2790	92.63
DSM 4150	NZ_ABVG000000000.2	3.77	39.1	3270	3069	12	56	91.8	2845	92.70

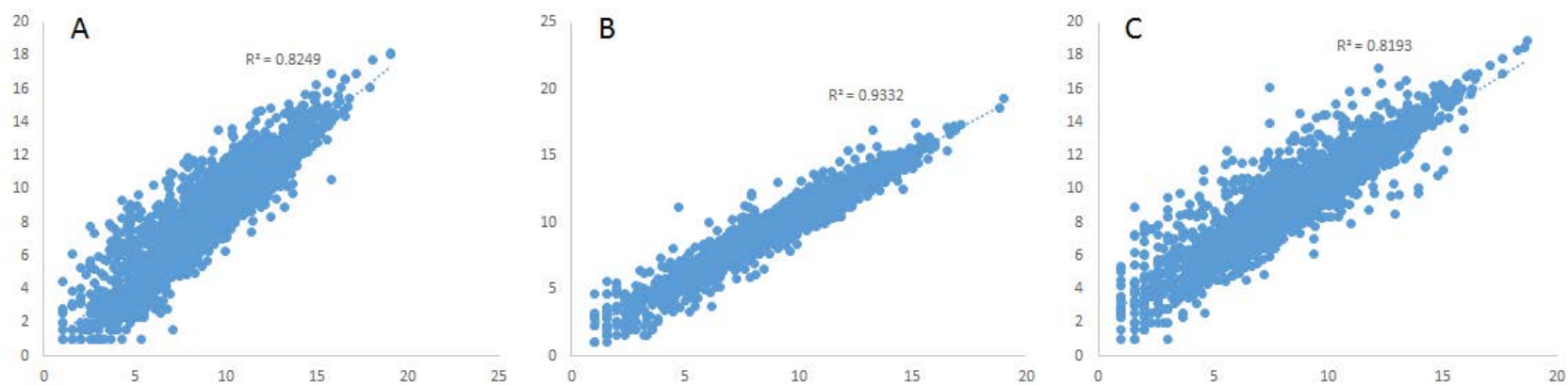


proteomic analysis in terms of specific gene preference (Rydzak et al. 2012; Burton and Martin 2012). However, the stability of the transcriptomes across the three strains does not insinuate that the transcript levels do not affect the end-product patterns observed in the three different stains. Small changes in the transcripts, especially in redox centered reactions, could have small changes in terms of metabolite concentrations that over the span of the cellular metabolism might cause significant changes that alter carbon and electron flow thus modulating end product synthesis.

RNA sequencing was also done on all three strains grown on 2 g/L cellulose in order to assess the differences in expression between cellobiose-grown cells and cellulose-grown cells. The expression pattern of cellobiose and cellulose grown cells were extremely similar with an overall  $R^2$  of 0.83, 0.93, and 0.83 over a span of 3120, 2778, and 2832 transcripts for ATCC 27405, DSM 2360, and DSM 4150 respectively (Figure 5.3). This shows a very high correlation similar to values obtained from replicates indicating a very high degree of stability in the transcript across the two different conditions. These values agree with similar results in *R. termitidis* which showed relatively small changes in expression patterns with growth on cellobiose versus cellulose (Munir et al. 2015). The relatively small changes in expression between cellobiose and cellulose grown cells was expected, as the overall metabolism of the cells would be identical with variations in the flux through pathways since the substrate are nearly identical but resulting in different growth rates. Therefore, this would reinforce the idea that central catalysis regulation and end products synthesis is not reliant on differential expression patterns but rather variations in internal metabolites present despite the differences in growth rates observed between the 2 major carbon and energy substrate selected.



Figure 5.3: Correlation between cellobiose-grown cells and  $\alpha$ -cellulose grown cells in strains A) ATCC 27405, B) DSM 2360, and C) DSM 4150. The x-axis represents the 100-mer reads of the cells grown on cellobiose and the y-axis represents the 100-mer reads for the cells grown on  $\alpha$ -cellulose.





### 5.3.3 Glycolysis

The expression of the genes associated with glycolysis were found to be highly expressed in all three organisms as expected from the previous proteomes by Rydzak *et al* (2012) and Burton *et al* (2012). The expression of the 3 putative phosphofructokinases (PFK) was found to be high with the PPI-PFK (Cthe\_0347) being expressed at much higher levels than the putative ATP-dependent PFK as predicted by the proteome (Rydzak *et al.* 2012). However, the expression of the putative PPI-dependent PFKb (Cthe\_0389) was found to be expressed at levels similar to the PPI-dependent PFK, except for DSM 4150, which displayed lower levels of Cthe\_0389 compared to the other two strains (Table 5.2). The absence of ATP-dependent PFK activity in cell-free extracts reinforces the preferential expression of the PPI-dependent PFK (Zhou *et al.* 2013). However, recombinant PPI-dependent PFK enzyme assays displayed low activity in terms of fructose-6-phosphate phosphorylation suggesting that the Cthe\_1261 and/or Cthe\_0389 could be PPI-dependent despite the annotation (Chapter 4). The sequence analysis in Chapter 3 predicted that the Cthe\_1261 is ATP-dependent but was inconclusive in terms of the Cthe\_0389 gene, which did not fall into either PPI or ATP-dependent groups (Table 3.5). However, the Cthe\_0389 did group with the PPI-dependent group during the phylogenetic analysis predicting that Cthe\_0389 could exhibit similar PPI-dependence as the Cthe\_0347 (Figure 3.6). However, further biochemical analysis would be required in order to elucidate the specific kinetic properties along with the specific cofactor preferences.

Upon the comparison between the cells grown on cellobiose versus the cells grown on  $\alpha$ -cellulose, we can see a large change in expression in the PPI-dependent PFK with an approximate 14-fold reduction in expression in *R. thermocellum* ATCC 27405 grown in  $\alpha$ -cellulose compared



Table 5.2: Expression of glycolysis related genes growing on cellobiose.

			Average log2 100-mer reads			Wnet		Wstats			
	EC number	R. thermocellum ATCC 27405	ATCC 27405	DSM 2360	DSM 4150	27405 vs 2360 (Wnet)	27405 vs 4150 (Wnet)	2360 vs 4150 (Wnet)	27405 vs 2360	27405 vs 4150	2360 vs 4150
Cellobiose phosphorylase	2.4.1.20	Cthe_0275	14.33	12.86	13	0.13	0.14	0.01	1	1.1	0.6
Hexokinase	2.7.1.1	Cthe_2938	11.58	11.59	10.58	-0.37	0.01	0.55	1.5	0.6	5.5
Phosphoglucose mutase	5.4.2.2	Cthe_1265	13.34	13.04	12.23	-0.23	0.06	0.46	1.1	0.8	5.7
Hexophosphate isomerase	5.3.1.9	Cthe_0217	13.37	12.66	13.32	-0.07	-0.3	-0.3	0.6	2.1	8
Phosphofructokinase	2.7.1.90	Cthe_0347	15.52	15.88	15.93	-0.59	-0.5	0.04	3	4.1	0.2
	2.7.1.11	Cthe_1261	11.72	11.52	11.42	-0.23	-0.1	0.05	0.9	0.9	0.8
	2.7.1.11	Cthe_0389	15.47	15.5	13.4	-0.24	0.41	1.16	0.8	1.3	9.6
Fructose 1,6-bisphosphate aldolase	4.1.2.13	Cthe_0349	16.42	15.79	16.56	-0.11	-0.4	-0.3	1	4.7	4.7
Triosephosphate isomerase	5.3.1.1	Cthe_0139	14.93	14.22	15.53	-0.09	-0.6	-0.7	0.8	5.1	15
Glyceraldehyde dehydrogenase	1.2.1.12	Cthe_0137	17.81	16.97	17.93	-0.11	-0.4	-0.4	0.2	7.4	4.5
Phosphoglycerate kinase	2.7.2.3	Cthe_0138	15.65	15.02	16.15	-0.13	-0.6	-0.6	1.2	5.3	12
Phosphoglycerate mutase	5.4.2.1	Cthe_0140	14.72	14.94	15.97	-0.47	-0.9	-0.5	2	4	11
		Cthe_0707	11.15	9.92	10.49	0.13	-0.1	-0.2	7.7	0.3	2.1
		Cthe_0946	10.42	10.14	10.2	-0.25	-0.1	0	1.5	0.9	0.6
		Cthe_1292	13.19	12.99	12.8	-0.2	-0.1	0.09	0.9	0.9	0.9
		Cthe_1435	8.81	8	6.76	-0.08	0.46	0.68	0.4	2.1	5.8
		Cthe_2449	7.35	6.22	6.82	0.01	-0.1	-0.2	0.8	0.9	2.2
		Cthe_3153	7.83	6.86	9.24	-0.04	-1	-1.2	0.6	4.4	7.6



Enolase	4.2.1.11	Cthe_0143	14.85	14.66	16.62	-0.29	-1.2	-1	1.7	7.1	7.3
Pyruvate Kinase	2.7.1.40	NA									
Pyruvate Phosphate Dikinase	2.7.9.1	Cthe_1308	13.99	12.43	15.18	0.22	-0.9	-1.4	2.1	12	16
Pyruvate Water dikinase	2.7.9.2	Cthe_1253	10.47	10.4	9.89	-0.41	-0.1	0.24	5.1	0.4	1.7
Phosphoenolpyruvate carboxykinase	4.1.1.49	Cthe_2874	16.43	15.47	15.24	0.15	0.06	0.05	0.2	0.7	0.6
Malate dehydrogenase	1.1.1.37	Cthe_0345	16.36	14.7	13.19	0.19	1.01	0.84	1.1	3.7	7.6
Malic Enzyme	1.1.1.40	Cthe_0344	16.7	15.27	13.8	0.05	0.81	0.8	0.7	2.2	6.8
Oxaloacetate decarboxylase	4.1.1.3	Cthe_0699	14.18	14.69	13.8	-0.62	-0.1	0.44	2.5	0.6	2.5
		Cthe_0700	11.99	12.55	11.07	-0.42	0.09	0.7	1	0.3	2.3
		Cthe_0701	14.54	16.06	16.46	-0.98	-1.1	-0.1	2	2.6	1



to cellobiose ( $W_{net} = 4.8$ ). Interestingly, in DSM 2360 and DSM 4150, the change in expression of the PPI-dependent PFK is greatly reduced with  $W_{net}$  of 1.32 and 0.98 respectively. The change in the expression profile of the PPI-dependent PFK could be attributed to the presence of a transposase belonging to the IS30 family just upstream of the Cthe\_0347 gene which is not present in DSM 4150 and DSM 2360.

As is a common trait in *R. thermocellum*, all three strains analyzed lacked the presence of a putative pyruvate kinase gene in their respective genomes. As previously described (Chapter 2), the presence of all of the genes required for the malate transhydrogenase pathway is present and expressed highly in all three strains (Table 5.2). However, in DSM 4150, the expression of the pyruvate phosphate dikinase (PPDK) is higher (15.18) than what is expressed in both ATCC 27405 (13.99) and DSM 2360 (12.43). The increased expression of the PPDK is accompanied by lower expression of the remainder of the malate shunt with the greatest expression change found in the malate dehydrogenase (MDH). In Chapter 4, we isolated and characterized the PPDK from *R. thermocellum* ATCC 27405 and were not able to detect any activity similar to what was shown in cell-free extracts (Zhou et al. 2013). The PPDK gene in DSM 4150 is nearly identical to the PPDK gene of ATCC 27405 with 882 of 883 amino acids being identical (417 T to A). Therefore, the slight preference of utilization of the PPDK over the malate transhydrogenase shunt might increase the NADH/NADPH ratio. The increase in NADH versus NADPH could activate LDH activity increasing the lactate production in DSM 4150 versus DSM 2360 and ATCC 27405.

The expression of the malate transhydrogenase pathway did not significantly change between cells grown on cellobiose and  $\alpha$ -cellulose while the expression of the PPDK was increased in  $\alpha$ -cellulose grown cells. This result disagrees with the observations of Burton and



Martin (2012) which showed a 0.6-fold decrease in PPDK. However, the MDH and ME were both detected in their proteome but were not quantified but it was predicted that it would be increased due to a 1.6 fold increase expression of the phosphoenolpyruvate carboxykinase (PEPCK) along with a 0.6 fold decrease in oxaloacetate decarboxylase (OAADC) levels (Burton and Martin 2012).

#### 5.3.4 Pentose phosphate pathway

As previously described in Chapter 1, *R. thermocellum* lacks a complete pentose phosphate pathway (PPP). Specifically, the oxidative branch is missing in the genome of all three strains. The expression of the modified PPP is consistent across the three strains with the Cthe\_2704-2705 transketolase being favored. As mentioned previously, the three strains expressed the PPI-dependent PFK at very high levels supporting the possibility of the PPI-dependent PFK being utilized in the modified PPP (Chapter 1, Chapter 3) (Mertens, De Jonckheere, and Van Schaftingen 1993).

#### 5.3.5 End product synthesis

The production of end products is essential for the regeneration of reducing equivalent to allow for the continuation of glycolysis (Gottschalk 1986). The amount of end products being produced by the three strains differed slightly with DSM 2360 producing the most H<sub>2</sub>, ATCC 27405 producing the most ethanol, and DSM 4150 producing small amounts of lactate prior to stationary phase (Figure 5.1). However, the expression of the end-product synthesis genes was found to be consistent throughout the three strains. The expression of the pyruvate formate lyase gene (PFL) was found to be higher in DSM 4150 when compared to ATCC 27405 and DSM



2360 with Wnet of 1.34 and 0.8 respectively. However, despite the increased expression of PFL in DSM 4150, the amount of formate generated is lower than both ATCC 27405 and DSM 2360.

The bifunctional ADHE has been accredited as the main contributor to the production of ethanol. Therefore, it is not surprising to find that the expression of the AdhE was relatively high (Table 5.3). The expression of AdhE was increased in DSM 2360 with Wnet of 1.32 and 1.35 relative to ATCC 27405 and DSM 4150 respectively (Table 5.3). However, the expression of the Fe-containing alcohol dehydrogenase (Cthe\_0394) was found to be expressed at levels approximately 4-fold higher than the ADHE. These values differ from the proteome done by Ryzak et al. (2012) which showed a much higher expression of the AdhE protein, showing a putative translational regulation of the Fe-containing ADH.

Analysis of the transcript for the various hydrogenases showed that despite differences in the amount of H<sub>2</sub> produced, very small variations in hydrogenase transcripts were observed. All types of hydrogenase and electron shuffling enzymes present in the genome were expressed in the transcriptome including the energy conserving Ech-like Ferredoxin-dependent hydrogenase (Fd-H<sub>2</sub>ase), *Rhodobacter* nitrogen fixing (RNF)-like NADH:ferredoxin oxidoreductase (NFOR), the bifurcating hydrogenase (BiH<sub>2</sub>ase), NADPH reduced ferredoxin: NADPH oxidoreductase (NFNAB), and NADPH-dependent hydrogenase (NADPH-H<sub>2</sub>ase) (Table 5.4). The highest expressed H<sub>2</sub>ase or electron shuffling enzyme in ATCC 27405 was found to be the NADPH-H<sub>2</sub>ase (14.56) with the lowest overall expression being the Fd-H<sub>2</sub>ase (11.05). Interestingly, the BiH<sub>2</sub>ase (14.71) was found to be the highest expressed H<sub>2</sub>ase/electron shuffling enzyme in DSM



Table 5.3: Expression of end product synthesis associated genes growing on cellobiose.

	EC number	R. thermocellum ATCC 27405	Average log <sub>2</sub> 100-mer reads			Wnet		Wstats			
			ATCC 27405	DSM 2360	DSM 4150	27405 vs 2360	27405 vs 4150	2360 vs 4150	27405 vs 2360	27405 vs 4150	2360 vs 4150
Lactate Dehydrogenase	1.1.1.27	Cthe_1053	11.61	12.28	11.33	-0.77	-0.22	0.53	5.59	2.52	6.92
Pyruvate Formate Lyase	2.3.1.54	Cthe_0505	13.62	14.3	15.89	-0.66	-1.34	-0.8	1.95	4.01	10.05
Pyruvate Formate Lyase AE		Cthe_0506	11.49	12.28	13.46	-0.64	-1.1	-0.53	1.52	2.44	3.8
Pyruvate Ferredoxin Oxidoreductase	1.2.7.1	Cthe_2390	12.89	12.93	10.99	-0.48	0.4	1.04	6.04	2.2	7.03
		Cthe_2391	10.71	10.91	7.81	-0.53	0.86	1.67	3.85	3.38	9.24
		Cthe_2392	12.74	14.23	12.05	-1.11	-0.08	1.19	3.74	0.32	8.3
		Cthe_2393	12.78	14.63	12.41	-1.25	-0.09	1.22	3.52	0.7	9.13
		Cthe_0866	12.05	11.81	11.6	-0.22	-0.09	0.15	0.95	0.72	4.1
		Cthe_0614	11.26	10.76	10.01	-0.11	0.1	0.41	0.66	0.83	4.6
		Cthe_2794	2.16	1.58	2.75	-0.17	-0.56	-0.52	2.19	2.46	3.47
		Cthe_2795	1	1	1	-0.06	-0.2	-0.14	0.49	0.65	0.33
		Cthe_2796	3.35	2.75	3.64	-0.5	-0.29	-0.16	0.11	0.89	0.75
		Cthe_2797	8.08	7.75	11.36	-0.15	-1.94	-1.88	0.82	12.75	11.7
Fused Pyruvate ferredoxin oxidoreductase	1.2.7.1	Cthe_3120	14.8	13.87	15.01	0.01	-0.26	-0.46	0.39	0.95	2.35
Aldehyde dehydrogenase	1.2.1.10	Cthe_2238	8.48	7.31	8.2	-0.02	-0.18	-0.38	0.43	1.06	2.73
Alcohol dehydrogenase	1.1.1.1	Cthe_0394	17.19	17.06	15.43	-0.05	0.22	0.8	0.5	0.87	2.95
		Cthe_0101	12.43	12.04	11.74	-0.25	-0.04	0.16	3.33	0.39	1.75
		Cthe_2579	10.73	11.46	11.42	-0.8	-0.68	0.07	5.32	5.57	3
Bifunctional aldehyde/alcohol dehydrogenase		Cthe_0423	14.64	16.81	14.29	-1.32	-0.1	1.35	2.65	0.72	7
Acetate Thiokinase	6.2.1.1	Cthe_0551	13.51	12.21	12.81	0.06	-0.04	-0.21	0.93	0.33	1.96



Phosphotransacetylase	2.3.1.8	Cthe_1029	10.39	10.69	10.26	-0.5	-0.23	0.28	2.02	1.32	11.3
Acetate Kinase	2.7.2.1	Cthe_1028	10.91	11.61	11.53	-0.69	-0.58	0.08	2.3	2.32	1.72



Table 5.4: Expression of hydrogenase and electron shuffling related genes during growth on cellobiose

		Average log <sub>2</sub> 100-mer reads			Wnet		Wstats				
	EC number	R. thermocellum ATCC 27405	ATCC 27405	DSM 2360	DSM 4150	27405 vs 2360	27405 vs 4150	2360 vs 4150	27405 vs 2360	27405 vs 4150	2360 vs 4150
Ferredoxin-dependent Hydrogenase		Cthe_3020	11.4	11.17	12.92	-0.14	-0.88	-0.88	0.62	1.86	11.69
		Cthe_3021	9.95	8.92	10.66	0.04	-0.57	0.88	0.65	1.79	6.48
		Cthe_3022	9.01	8.56	7.29	-0.07	0.09	0.61	0.52	0.6	2.52
		Cthe_3023	10.83	9.95	8.99	-0.04	0.2	0.46	0.49	0.8	2.3
		Cthe_3024	12.95	11.1	10.46	0.37	0.74	0.38	2.37	4.9	6.46
		Cthe_3025	2.91	3.35	4.54	-0.33	-1.14	-0.44	0.86	9.7	1.56
NADH-ferredoxin oxidoreductase		Cthe_2430	12.09	12.15	14.26	-0.45	-1.32	-1.04	2.57	4.73	5.75
		Cthe_2431	11.28	11.46	13.38	-0.49	-1.25	-0.93	2.69	3.84	4.84
		Cthe_2432	10.41	11.02	12.69	-0.63	-1.34	-0.77	2.06	4.01	4.08
		Cthe_2433	10.46	10.87	12.59	-0.53	-1.21	-0.79	1.79	3.01	3.52
		Cthe_2434	10.1	10.91	12.18	-0.67	-1.19	-0.56	1.75	2.97	3.54
		Cthe_2435	9.79	10.68	11.79	-0.73	-1.18	-0.51	1.95	3.08	4.66
Bifurcating Hydrogenase		Cthe_0340	10.71	11.94	10.49	-0.87	-0.18	0.79	2.04	0.87	5.6
		Cthe_0341	13	14.46	13.22	-0.9	-0.3	0.67	1.65	0.95	4.71
		Cthe_0342	13.89	15.21	13.97	-0.78	-0.24	0.66	1.37	0.83	4.18
		Cthe_0428	10.66	13.16	10.95	-1.23	-0.23	1.12	1.52	0.72	4.07
		Cthe_0429	12.46	14.92	12.80	-1.17	-0.27	1.09	1.43	0.74	5.85
		Cthe_0430	13.41	16.05	14.03	-1.48	-0.6	1.03	1.36	0.81	9.52
NADPH-dependent Hydrogenase		Cthe_3003	14.56	13.54	13.88	0.14	-0.08	-0.02	0.31	0.42	0.39
		Cthe_3004	14.62	12.56	13.29	0.25	0.07	-0.19	0.95	0.7	1.12
NADH reduced ferredoxin: NADPH oxidoreductase		Cthe_0372	11.38	10.95	10.95	-0.15	-0.12	0.02	0.87	0.99	0.48
		Cthe_0373	11.2	10.79	10.59	-0.2	-0.07	0.12	1.33	1.31	1.59



2360 and a slight increase in the transcripts associated with NFOR in DSM 4150 (Wnet 1.25 when compared to ATCC 27405). Upon comparison with published proteomes, the expression of the Fd-H<sub>2</sub>ase and the NFOR differed from the proteome levels. The proteome by Rydzak *et al.* (2012) was unable to detect the presence of 3 of the 6 subunits of the NFOR and 3 of the 6 subunits for the Fd-H<sub>2</sub>ase, we were able to detect all 6 of both the NFOR and Fd-H<sub>2</sub>ase at relatively high levels (Rydzak et al. 2012). The discrepancies could be caused by the inherent difficulties of detecting membrane proteins during proteomic analysis or could be indicative of translational regulation. The expression of the NFOR was slightly elevated in DSM 4150 when compared to ATCC 27405 with an average Wnet difference of 1.25 (Table 5.4).

DSM 2360 produced a higher level of H<sub>2</sub> while producing a slightly lower amount of ethanol when compared to both DSM 4150 and ATCC 27405 (Figure 5.1). The differences in the amount of H<sub>2</sub> produces in DSM 2360 versus ATCC 27405 could not, however, be explained by differences in transcript levels (Table 5.4). The differences in H<sub>2</sub> and ethanol generation could, however, be attributed to the fusion of the NADPH hydrogenase in DSM 2360 along with a slight increase in BiH<sub>2</sub>ase expression. The NADPH hydrogenase forms a heterodimer containing the catalytic domain and the ferredoxin containing domain, which are encoded respectively by Cthe\_3003 and Cthe\_3004 in ATCC 27405. However, in DSM 2360, both the domains are fused into a single transcript due to a mutation in the stop site of the Cthe\_3003, which replaces the stop codon with a codon coding for glutamine (Figure 5.4). This mutation fuses both genes while keeping the Cthe\_3004 in-frame with the Cthe\_3003. The fusion of the NADPH hydrogenase could impact its ability to utilize H<sub>2</sub> in order to reduce NADP limiting the amount of NADPH utilized in the generation of ethanol via the AdhE resulting in lower amounts of ethanol being



produced, despite a slight increase in the transcript levels of AdhE in DSM 2360 compared to ATCC 27405. Overall, the expression levels of the H<sub>2</sub>ase were consistent throughout the three strains with slight variations. Despite the apparent small changes in expression, the alteration to redox balances could create a cascade effect altering the internal metabolite concentrations influencing end product synthesis. However, further work regarding internal metabolite concentrations would be required to understand the effect of the changes in the redox systems within these three strains.

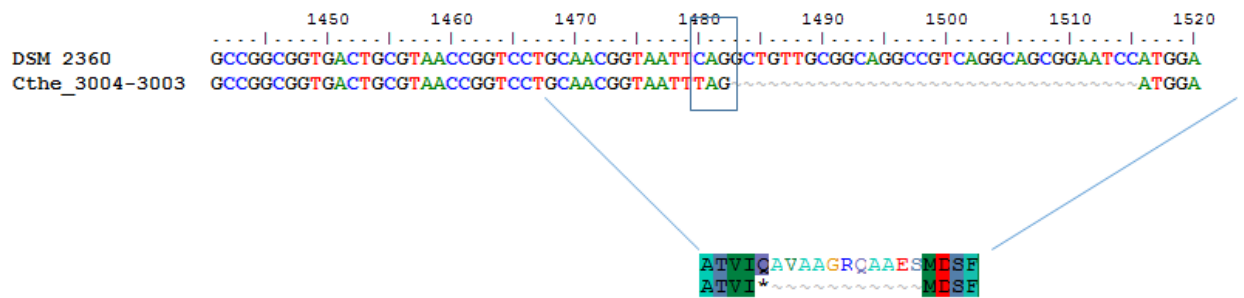
#### 5.3.6 Pyrophosphate metabolism and regulation

The expression of the V-type PPase was consistent through the three strains with a very small increase in expression in ATCC 27405 when compared to DSM 4150 and DSM 2360. However, the difference in expression was below the statistical significance threshold, with a Wstats value well below 2.8. The expression of the PPase agrees well with the intracellular concentrations of PPi, which decrease throughout growth in all three strains (Figure 3.1). As predicted by Zhou *et al.* (2013), this seems to indicate that the amount of PPi produced as a by-product of biosynthesis is not sufficient to supply the requirements for PPi by central glycolysis leading to a steady decrease in PPi concentrations until a minimum is reached at the onset of stationary phase.

The expression of the entire HPr regulatory mechanism as described in Chapter 3 was detected in all three strains. The expression of HPr and the HPr Kinase/phosphorylase (Cthe\_0117 and Cthe\_0110) were found to be slightly higher in ATCC 27405 when compared with both DSM 2360 and DSM 4150. However, these differences were very small with Wnet



sequence.





differences of 0.2 and 0.1 respectively showing relatively little changes across the three strains with regards to transcriptional regulation due to changes in HPr levels.

Another putatively important source of PPI in the cells would be from glycogen cycling as described in Chapter 1 (Hungate 1963; Guedon, Desvaux, and Petitdemange 2000). The expression of the glycogen-cycling enzymes were relatively highly expressed in all three strains. However, the expression of the glycogen-cycling genes were found to be increased in DSM 4150 when compared against ATCC 27405 with an average Wnet difference of 1.13. The slight increase in the expression of the glycogen synthesis genes could help with the PPI supply in DSM 4150 due to an increase in the PPDK gene. Therefore, leading to an increased flux towards pyruvate without the transhydrogenation of the NADH to NADPH of the malate shunt resulting in increased lactate production in DSM 4150 when compared to ATCC 27405.

#### 5.3.7 Cellobiose versus cellulose

The overall expression of the gene involved in central catabolism were found to be consistent with an over  $R^2$  of 0.8 in all three strains (Figure 5.3). We can see a relatively small increase in the transcription of most glycolysis and end-product synthesis genes in cells grown on cellobiose versus cells grown on  $\alpha$ -cellulose (Table 5.5). Interestingly, in DSM 4150, the expression of the generally extremely highly expressed alcohol dehydrogenase (Cthe\_0394) was found to be expressed much lower in the  $\alpha$ -cellulose grown cells with a Wnet of 4.25 while having a slight increase in the bifunctional aldehyde/alcohol dehydrogenase (Cthe\_0423) (Table 5.5). The transcript of the H<sub>2</sub>ase gene and electron shuffling genes show a general decrease in transcript levels with cells grown on  $\alpha$ -cellulose versus cells grown on cellobiose (Table 5.6).



Table 5.5: Expression of glycolysis and end-product synthesis related genes growing on cellobiose and  $\alpha$ -cellulose

	EC number	R. thermocellum ATCC 27405	ATCC 27405					DSM 2360					DSM 4150				
			Average 100-mer reads - CB	Average 100-mer reads - AC	Zmag (CB vs AC)	Wnet (CB vs AC)	Wstats (CB vs AC)	Average 100-mer reads - CB	Average 100-mer reads - AC	Zmag (CB vs AC)	Wnet (CB vs AC)	Wstats (CB vs AC)	Average 100-mer reads - CB	Average 100-mer reads - AC	Zmag (CB vs AC)	Wnet (CB vs AC)	Wstats (CB vs AC)
Cellobiose phosphorylase	2.4.1.20	Cthe_0275	14.33	10.12	1.46	1.49	1.1	12.86	13.10	-0.13	-0.08	0.4	13.00	13.44	-0.01	-0.01	0.5
Hexokinase	2.7.1.1	Cthe_2938	11.58	10.44	0.74	0.46	0.7	11.59	11.05	1.03	1.21	2.9	10.58	10.04	0.75	0.86	9.3
Phosphoglucose mutase	5.4.2.2	Cthe_1265	13.34	12.60	0.25	0.47	0.3	13.04	13.70	-0.50	-0.5	1.4	12.23	11.66	0.77	0.86	5.8
Hexophosphate isomerase	5.3.1.9	Cthe_0217	13.37	12.24	0.71	0.39	0.7	12.66	12.47	0.57	0.69	3.9	13.32	12.50	0.97	1.15	18.0
Phosphofructokinase	2.7.1.90	Cthe_0347	15.52	11.46	4.15	4.8	1.4	15.88	15.30	1.07	1.32	4.2	15.93	15.23	0.88	0.98	5.6
	2.7.1.11	Cthe_1261	11.72	10.77	0.53	0.32	0.4	11.52	11.57	0.27	0.18	0.7	11.42	11.07	0.59	0.67	8.0
	2.7.1.11	Cthe_0389	15.47	15.64	-0.77	-0.01	0.5	15.50	15.23	0.66	0.7	2.2	13.40	9.44	3.56	4.12	9.6
Fructose 1,6-bisphosphate aldolase	4.1.2.13	Cthe_0349	16.42	14.72	1.35	1.48	1.2	15.79	15.14	1.16	1.45	4.4	16.56	15.77	0.95	0.97	3.0
Triosephosphate isomerase	5.3.1.1	Cthe_0139	14.93	13.34	1.27	1.67	1.8	14.22	13.97	0.65	0.7	2.0	15.53	14.19	1.40	1.6	8.3
Glyceraldehyde dehydrogenase	1.2.1.12	Cthe_0137	17.81	16.31	1.15	1.58	2.0	16.97	16.79	0.56	0.47	1.2	17.93	16.70	1.31	1.41	4.0
Phosphoglycerate kinase	2.7.2.3	Cthe_0138	15.65	14.07	1.25	1.56	1.6	15.02	14.75	0.68	0.78	2.7	16.15	14.65	1.53	1.8	14.7
Phosphoglycerate mutase	5.4.2.1	Cthe_0140	14.72	13.74	0.58	0.41	0.7	14.94	14.35	1.08	1.4	7.5	15.97	16.05	0.25	0.16	0.8
		Cthe_0707	11.15	9.96	0.78	1.37	10.7	9.92	10.81	-0.80	-0.92	2.6	10.49	10.57	0.22	0.13	0.7
		Cthe_0946	10.42	9.60	0.27	0.42	0.3	10.14	9.73	0.88	0.82	1.2	10.20	8.38	1.80	1.91	4.0
		Cthe_1292	13.19	12.05	0.73	0.28	0.6	12.99	12.63	0.78	0.75	1.7	12.80	12.45	0.59	0.66	7.0
		Cthe_1435	8.81	8.17	-0.02	0.03	0.5	8.00	8.32	-0.07	-0.03	0.6	6.76	6.81	0.26	0.19	1.2
		Cthe_2449	7.35	6.67	0.22	0.41	0.3	6.22	6.56	-0.12	-0.09	0.7	6.82	7.01	0.15	0.03	0.6
		Cthe_3153	7.83	6.97	0.42	0.28	0.7	6.86	7.69	-0.73	-0.88	3.5	9.24	8.36	1.02	1.06	3.0
Enolase	4.2.1.11	Cthe_0143	14.85	13.80	0.64	1	2.4	14.66	13.70	1.52	1.63	2.0	16.62	15.53	1.20	1.3	4.3
Pyruvate Kinase	2.7.1.40	NF															
Pyruvate Phosphate Dikinase	2.7.9.1	Cthe_1308	13.99	12.73	0.88	1.41	3.4	12.43	11.82	1.07	1.12	1.9	15.18	13.96	1.31	1.45	5.2
Pyruvate Water dikinase	2.7.9.2	Cthe_1253	10.47	10.25	-0.40	-0.38	1.2	10.40	10.19	0.58	0.71	4.4	9.89	10.30	-0.03	-0.02	0.5
Phosphoenolpyruvate carboxykinase	4.1.1.49	Cthe_2874	16.43	14.80	1.37	0.39	0.6	15.47	16.22	-0.64	-0.25	0.7	15.24	16.01	-0.33	-0.25	1.1



Malate dehydrogenase	1.1.1.37	Cthe_0345	16.36	15.42	0.52	0.16	0.5	14.70	15.19	-0.27	-0.09	0.5	13.19	13.07	0.40	0.42	4.2
Malic Enzyme	1.1.1.40	Cthe_0344	16.70	15.72	0.57	0.89	0.3	15.27	15.39	0.19	0.09	0.4	13.80	13.88	0.24	0.25	3.0
Oxaloacetate decarboxylase	4.1.1.3	Cthe_0699	14.18	13.49	0.22	0.19	0.6	14.69	14.26	0.87	0.99	2.9	13.80	13.91	0.22	0.14	0.8
		Cthe_0700	11.99	11.16	0.40	0.63	0.3	12.55	11.66	1.445	1.47	1.8	11.07	12.07	-0.515	-0.41	1.4
		Cthe_0701	14.54	14.10	-0.09	-1.29	0.1	16.06	15.38	1.19	1.41	3.4	16.46	16.59	0.2	0.15	0.9
Lactate Dehydrogenase	1.1.1.27	Cthe_1053	11.61	10.94	0.13	0.19	0.3	12.28	12.12	0.525	0.48	1.5	11.33	10.76	0.77	0.88	7.4
Pyruvate Formate Lyase	2.3.1.54	Cthe_0505	13.62	12.87	0.29	0.56	0.3	14.3	13.46	1.4	1.84	7.6	15.89	15.75	0.425	0.34	1.2
Pyruvate Formate Lyase AE		Cthe_0506	11.49	10.79	0.26	0.95	0.3	12.28	11.3	1.565	2.15	31.2	13.46	13.32	0.42	0.35	1.2
Pyruvate Ferredoxin Oxidoreductase	1.2.7.1	Cthe_2390	12.89	11.52	1.01	1.44	2.2	12.93	12.49	0.885	1.16	8.7	10.99	11.32	0.025	0.16	0.2
		Cthe_2391	10.71	9.46	0.87	1.2	1.9	10.91	10.18	1.23	1.28	1.9	7.81	8.225	-0.04	-0.19	0.2
		Cthe_2392	12.74	11.51	0.88	0.77	0.9	14.23	13.4	1.365	1.63	3.5	12.05	12.75	-0.28	-0.13	0.8
		Cthe_2393	12.78	11.60	0.80	0.2	0.6	14.63	13.72	1.47	1.69	2.7	12.41	13.3	-0.435	-0.4	1.9
		Cthe_0866	12.05	11.25	0.35	0.35	0.4	11.81	11.63	0.555	0.67	3.5	11.6	11.03	0.76	0.77	2.8
		Cthe_0614	11.26	10.89	-0.15	-0.27	0.4	10.76	11.03	-0.015	-0.03	0.4	10.01	10.09	0.225	0.13	0.7
		Cthe_2794	2.16	1.58	0.84	0.38	0.4	1.58	0	2.36	2.76	2.7	2.75	1.5	1.27	.63	0.7
		Cthe_2795	1.00	1.58	-1.16	-0.05	0.5	1	0	1.03	0.52	0.7	1	0	1.11	0.89	1.4
		Cthe_2796	3.35	3.41	-0.51	-0.19	0.5	2.745	2	1.265	0.42	0.7	3.64	3.695	0.25	0.07	0.4
		Cthe_2797	8.08	6.03	1.81	2.7	2.8	7.75	5.475	3.225	4.16	6.11	11.36	9.875	1.52	1.67	4.55
Fused Pyruvate ferredoxin oxidoreductase	1.2.7.1	Cthe_3120	14.80	13.42	1.04	0.13	0.52	13.87	12.82	1.665	1.96	3.08	15.01	14.72	0.545	0.45	1.21
Aldehyde dehydrogenase	1.2.1.10	Cthe_2238	8.48	7.09	0.92	0.77	0.83	7.305	7.18	0.495	0.36	1.02	8.2	8.015	0.46	0.41	1.47
Alcohol dehydrogenase	1.1.1.1	Cthe_0394	17.19	16.86	-0.17	-1	0.26	17.06	16.96	0.435	0.06	0.56	15.43	10.64	4.245	4.77	5.81
		Cthe_0101	12.43	11.51	0.43	0.27	0.7	12.04	12.06	0.29	0.29	1.89	11.74	11.12	0.8	0.78	2.38
		Cthe_2579	10.73	9.95	0.32	0.37	0.9	11.46	10.75	1.21	1.1	1.36	11.42	10.04	1.43	1.7	18.77
Bifunctional aldehyde/alcohol dehydrogenase		Cthe_0423	14.64	14.29	-0.21	-1.05	0.16	16.81	16.4	0.845	0.7	1.25	14.29	15.66	-0.83	-0.88	3.56
Acetate Thiokinase	6.2.1.1	Cthe_0551	13.51	12.39	0.69	0.85	1.43	12.21	12.47	-0.005	-0.28	0.04	12.81	12.18	0.82	0.91	5.59
Phosphotransacetylase	2.3.1.8	Cthe_1029	10.39	8.98	1.04	0.33	0.59	10.69	10.17	0.985	1.34	16.76	10.26	9.435	0.97	1.07	5
Acetate Kinase	2.7.2.1	Cthe_1028	10.91	9.39	1.18	0.38	0.6	11.61	11.18	0.87	1.17	14	11.53	10.41	1.22	1.41	10.28



Table 5.6: Expression of hydrogenase and electron shuffling related genes growing on cellobiose and  $\alpha$ -cellulose

EC number	R. thermocellum ATCC 27405	ATCC 27405					DSM 2360					DSM 4150				
		Average 100-mer reads - CB	Average 100-mer reads - AC	Zmag (CB vs AC)	Wnet (CB vs AC)	Wstats (CB vs AC)	Average 100-mer reads - CB	Average 100-mer reads - AC	Zmag (CB vs AC)	Wnet (CB vs AC)	Wstats (CB vs AC)	Average 100-mer reads - CB	Average 100-mer reads - AC	Zmag (CB vs AC)	Wnet (CB vs AC)	Wstats (CB vs AC)
Ferredoxin-dependent Hydrogenase	Cthe_3020	11.40	10.66	0.30	1.59	0.18	11.17	10.86	0.75	0.51	0.86	12.92	12.37	0.755	0.84	5.48
	Cthe_3021	9.95	9.09	0.42	0.99	0.24	8.92	8.35	1.08	1.08	1.36	10.66	9.94	0.89	0.94	3.29
	Cthe_3022	9.01	8.05	0.65	1.56	0.28	8.56	8.36	0.6	0.43	0.89	7.285	7.69	-0.035	-0.3	0.15
	Cthe_3023	10.83	9.49	1.02	0.75	0.37	9.945	9.99	0.295	0.05	0.54	8.985	9.1	0.205	0.09	0.37
	Cthe_3024	12.95	11.39	1.20	0.84	0.8	11.1	11.77	-0.49	-0.09	0.53	10.46	10.73	0.075	0.03	0.58
	Cthe_3025	2.91	2.20	0.07	0.67	0.32	3.35	5	0.065	0.67	0.32	4.54	3.95	0.79	0.84	3.51
NADH-ferredoxin oxidoreductase	Cthe_2430	12.09	9.97	1.86	2.52	1.94	12.15	10.79	2.05	2.74	12.18	14.26	13.68	0.785	0.72	1.61
	Cthe_2431	11.28	9.68	1.29	1.34	1.15	11.46	10.18	1.94	2.61	14.85	13.38	12.92	0.69	0.61	1.45
	Cthe_2432	10.41	9.09	0.96	0.44	0.65	11.02	9.81	1.85	2.31	4.74	12.69	12.11	0.78	0.75	1.98
	Cthe_2433	10.46	9.14	0.95	0.25	0.57	10.87	9.895	1.56	1.97	5.15	12.59	12.01	0.79	0.71	1.55
	Cthe_2434	10.10	8.83	0.92	0.1	0.48	10.91	10.04	1.435	1.83	5.98	12.18	11.49	0.87	0.86	2.21
	Cthe_2435	9.79	8.74	0.63	0.77	0.31	10.68	9.72	1.535	2.03	9.43	11.79	11.13	0.855	0.85	2.33
Bifurcating Hydrogenase	Cthe_0340	10.71	10.35	-0.15	-0.33	0.36	11.94	11.47	0.915	1.02	2.46	10.49	10.85	0	-0.02	0.54
	Cthe_0341	13.00	12.45	0.11	0.84	0.3	14.46	13.53	1.495	1.73	2.88	13.22	13.5	0.065	0.04	0.37
	Cthe_0342	13.89	13.29	0.19	0.95	0.3	15.21	14.32	1.425	1.57	2.27	13.97	14.41	-0.06	-0.06	2.29
	Cthe_0428	10.66	9.97	0.40	0.62	0.4	13.16	12.79	0.795	0.5	0.93	10.95	12.06	-0.61	-0.49	1.48
	Cthe_0429	12.46	11.69	0.61	0.53	0.4	14.92	14.32	1.085	1.19	2.37	12.8	13.73	-0.465	-0.28	1
	Cthe_0430	13.44	12.76	0.55	0.71	0.4	16.05	15.75	0.725	0.63	1.26	14.03	14.9	-0.415	-0.34	1.57
NADPH-dependent Hydrogenase	Cthe_3003	14.56	12.82	1.55	0.18	0.52	13.54	12.95	1.075	0.69	0.94	13.88	13.39	0.705	0.66	2.01
	Cthe_3004	14.62	12.62	1.80	1.47	0.89	12.56	12.05	0.985	0.64	0.94	13.29	12.69	0.8	0.84	3.31
NADH reduced ferredoxin: NADPH oxidoreductase	Cthe_0372	11.38	10.31	0.64	0.06	0.51	10.95	10.75	0.59	0.44	0.97	10.95	10.41	0.735	0.77	3.45
	Cthe_0373	11.20	10.20	0.51	0.15	0.57	10.79	10.4	0.815	0.98	3.69	10.59	9.95	0.82	0.73	1.76



Some small deviations to the general decrease are observed. In DSM 2360, the average  $W_{net}$  between cellobiose and  $\alpha$ -cellulose grown cells for the  $H_2$ ase and electron shuffling gene is 0.69. However, the NFOR had an average  $W_{net}$  of 2.25 showing a much greater decrease in cells grown on  $\alpha$ -cellulose possibly related to a decrease in overall growth rate. In DSM 4150, there was a very small increase in the  $BiH_2$ ase in cells grown on  $\alpha$ -cellulose with an average  $W_{net}$  of -0.2.

## 5.4 Conclusion

We have analyzed the transcriptomes of three strains of *R. thermocellum* grown on both cellobiose and  $\alpha$ -cellulose which shows very consistent results with previous proteomic analyses except for a few discrepancies such as the increase expression of the PEPCCK when cells were growing on cellulose as a carbon source (Rydzak et al. 2012; Burton and Martin 2012). The transcriptomes also displayed a very conserved expression pattern regardless of cellobiose or  $\alpha$ -cellulose being used a sole carbon source which even with respect to cellulosome specific proteins such as CipA. Interestingly, the expression patterns often did not agree with the amount of end products being produced such as increase PFL expression in DSM 4150 despite a lower amount of formate being produced. Overall, this shows that the glycolytic pathways along with end product synthesis pathways are regulated by the presence of small metabolites, rather than transcriptional or translational regulation. Therefore, a careful understanding of the regulatory mechanisms modulating the activity of key glycolytic enzymes is required in order to better understand the mechanisms of carbon and electron flux regulation in glycolysis. Thereby allowing for the development novel genetic modification strategies centered around modulation of



internal metabolite concentrations to form favorable concentrations optimized for carbon and electron flux through glycolysis.



## 6 General Discussion

*R. thermocellum* as an industrial ethanol producing organism is very attractive due to its high cellulose utilization and developed genetic modification systems (Olson, Sparling, and Lynd 2015). However, the branched nature of the central catalysis of *R. thermocellum* limits the generation of ethanol due to funneling of carbon and electrons towards undesirable end products such as acetate and H<sub>2</sub>. Therefore, this limits the viability of *R. thermocellum* when compared to the current technologies of liquid fuel generation. The elimination of competing pathways can be utilized to force carbon and electrons through the ethanol-generating pathways. Many of the competing pathways in *R. thermocellum* have been modified in the search for increased ethanol production.

### 6.1 Effects of elimination of competing end product synthesis pathways

The elimination of lactate generation by knockout of the lactate dehydrogenase (LDH) gene showed a very small increase in ethanol generation when compared to wild-type strains of *R. thermocellum* (Biswas et al. 2014). However, this particular mutation was combined with a mutation in the AdhE gene, which reduced ethanol generation but increased ethanol tolerance. The single mutation of LDH did not fare any better in terms of ethanol generation with no significant increase in ethanol with an LDH knockout (Argyros et al. 2011). Similar results were obtained with the elimination of acetate generation by phosphotransacetylase (Pta) knockout. The Pta mutant showed no significant increase in ethanol generation when compared to wild-type despite the complete elimination of acetate generation (Argyros et al. 2011; Tripathi et al. 2010). A double knockout of Pta and LDH fared no better with very little increases in ethanol generation combined with pyruvate secretion. However, the evolution of the double knockout



for 2000 hours led to an approximate doubling in ethanol generation with no pyruvate being secreted from the cells (Argyros et al. 2011).

A very important factor for ethanol generation is the availability of electrons generated by central catalysis. Therefore, the elimination of  $H_2$  production as an electron sink would increase the available electrons for ethanol generation. However, the hydrogenase systems in *R. thermocellum* are fairly complex, redundant mechanisms requiring many subunits to form a functional hydrogenase. Many of the hydrogenases require a maturase protein system (HydEFG) in order to ensure proper folding of the Fe-containing active centers of the hydrogenase (Mulder et al. 2011). Therefore, elimination of the maturase gene would not prevent the transcription or translation of the hydrogenase genes but would render them incapable of proper function due to improper folding. However, the HydEFG system is limited to FeFe hydrogenase and not required for the maturation of NiFe containing hydrogenase systems such as the Fd-dependent hydrogenase (Ech). Therefore, a double mutant of the HydG and all the genes associated with the Fd-dependent hydrogenase were required to eliminate  $H_2$  generation in *R. thermocellum* DSM 1313. The elimination of  $H_2$  coupled with a mutation in AdhE allowing for simultaneous utilization of NADH and NADPH as electron donors led to an approximate doubling in ethanol generation (Biswas et al. 2015). In *R. thermocellum* DSM 1313, the ADH activity is reliant on NADH as a cofactor whereas in *R. thermocellum* ATCC 27405, both NADH and NADPH can be utilized with almost equivalent activities in cell-free extract (Biswas et al. 2015; Rydzak et al. 2009). Interestingly, despite having identical sequences for the AdhE gene, a mutation of the AdhE gene in DSM 1313 is required for NADPH utilization while ATCC 27405 does not require a mutation for NADPH utilization based on the ability for ATCC 27405 cell-free extracts to display



NADPH-dependent ADH activity (Rydzak et al. 2009). DSM 1313 and ATCC 27405 also share 100% identity with 2 (Cthe\_0394 and Cthe\_0101) of the 3 predicted ADH. The Cthe\_2579 ADH, however, has one small mutation modifying an arginine to glycine at position 29. This mutation falls very close to the predicted NAD(P)H binding site. However, in the proteome, the acetaldehyde dehydrogenase (Aldh) and the Cthe\_2579 ADH are not detectable (Rydzak et al. 2012). The transcriptome does, however, show modest expression of both the Aldh and the Cthe\_2579 hinting at a possibility of Cthe\_2579 being responsible for NADPH -dependent ADH activity (Chapter 5). This small example highlights the importance of biochemical knowledge of specific proteins, in this case the ADHs, in order to be able to better create hypotheses on the effects of mutations. While the utilization of proteomic and transcriptomic tools allows for the generation of hypothesis, the deviations between transcriptomics and proteomics (Chapter 5, Rydzak et al. 2012; Raman et al. 2011; Burton and Martin 2012) raises questions about the stability of the techniques utilized for analysis. Thus increasing the importance of biochemical data in order to develop better predictive models capable of predicting flux by using a combination of both protein levels and biochemical data.

The mutations of the carbon and electron utilizing pathways have redirected carbon and electrons towards ethanol with mixed results regarding ethanol generation (Argyros et al. 2011; Biswas et al. 2014; Biswas et al. 2015; S. D. Brown et al. 2011). One factor that remained relatively constant was the growth rate of *R. thermocellum*. Therefore, this indicates that not only carbon and electron flux towards competing products are responsible for lower ethanol yields, but the limitation associated with flux through central catalysis indirectly limits ethanol generation by limiting growth rate. A careful understanding of the regulatory mechanisms modulating carbon



and electron flux through central catalysis would allow for the development of novel strategies to improve growth rate and subsequent ethanol generation.

## 6.2 Pyrophosphate and Global Cell Regulation

Polyphosphate (polyP) varies greatly in *E. coli* as a response to many factors including environmental stress such as high salts and nutrient limitations resulting in rapid accumulation and/or consumption of polyP (Kornberg, Rao, and Ault-Riché 1999). PolyP is a chain of tens to hundreds of phosphates linked by high energy phosphoanhydride bonds similar to those found between the phosphates of ATP (H. Baltscheffsky 1981). In *E. coli*, the transfer from a rich media into induces a rapid build-up in polyP concentration followed by a steady decrease through growth (Ault-Riché et al. 1998). This pattern is similar to the pattern obtained from PPi during inoculation of actively growing cells into new media. However, the shift in PPi was observed during a transfer from a depleted media to fresh media, the reverse of what was seen with the polyP in *E. coli*. The inverse relationship between polyP and PPi could be the result of the breakdown of polyP into PPi by exopolyphosphatase (ePPX) which is capable of cleaving polyP but cannot hydrolyze polyP beyond PPi (Keasling, Bertsch, and Kornberg 1993). The accumulation of polyP in bacteria is reliant on the presence of a polyphosphate kinase (PPK) gene in order to hydrolyse ATP adding the phosphates to the growing polyP (Keasling, Bertsch, and Kornberg 1993; Kornberg, Rao, and Ault-Riché 1999; Ault-Riché et al. 1998). However, *R. thermocellum* along with other *Ruminiclostridium* do not contain any putative PPK gene rendering the accumulation of polyP uncertain along with the absence of a dedicated ePPX gene. In *R. thermocellum*, a bifunctional ePPX/ppGpp phosphohydrolase (GppA) (Cthe\_2578) is predicted based on BLAST analysis. However, the bifunctional ePPX/GppA also appears to



contain a CRISPR-associated endonuclease Cas3-HD like domain. Hence, it would appear that Cthe\_2578 might not be an ePPX but rather be utilized as a response protein capable of interaction with polyP/PPi and ppGpp as signaling molecules. Therefore, in *R. thermocellum*, an alternative regulatory mechanism revolving around PPi may be utilized due to the absence of polyP metabolism genes. The signaling molecule ppGpp has been shown to inhibit ePPX activity when present allowing for the accumulation of polyP under amino acid or phosphate-limited conditions in *E. coli* (Kuroda et al. 1997).

During the late exponential phase of growth, the absence of various nutrients, mainly amino acids could induce activation of the RelA gene (Cthe\_1344) in *R. thermocellum* activating the formation of the regulatory molecule ppGpp. Therefore, the inoculation of late exponential phase cells into fresh media would result in inhibition of the PPi hydrolysing enzymes by ppGpp allowing for the increase in intracellular PPi levels. The increase in PPi continues to increase until the inactivation of ppGpp into GDP and PPi by SpoT. The buildup of PPi is then sufficient to induce glycolysis and restrict MalE activity favoring energy conservation over biosynthetic intermediate buildup. However, extensive study would be required to confirm the putative regulatory role of ppGpp on PPi accumulation in *R. thermocellum*. Further, in the absence of PPK, what role would PPi play in response to induction through various environmental stress?

### 6.3 Proposed regulation of carbon and electron flux through central glycolysis by pyrophosphate

The lack of a pyruvate kinase gene or any pyruvate kinase in *R. thermocellum* causes a deviation from the 'traditional' view of central catalysis (Rydzak et al. 2009; Zhou et al. 2013), thus reinforcing the apparent importance of the malate transhydrogenase pathway specifically



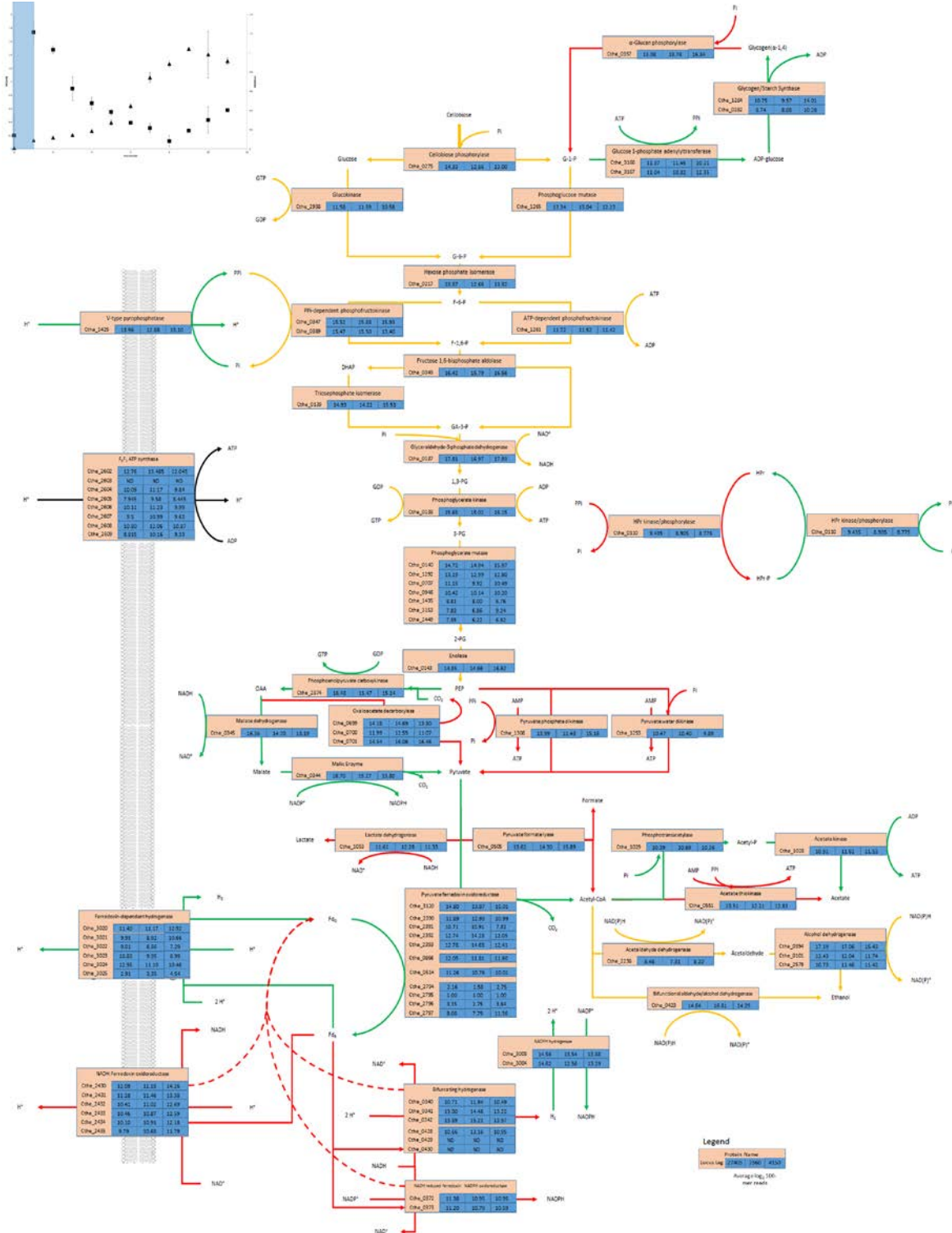
regarding the MalE and MDH (Chapter 2). The unidirectional activity of the MDH along with its expression pattern in both the transcriptome and proteome indicates its importance in central catalysis (Chapter 2, 5 Rydzak et al. 2012). Similarly, the MalE expression along with its activity support its putative role in central catalysis. However, the activation by  $\text{NH}_3$  along with the inhibition by PPI raises important questions about the regulatory mechanisms of carbon and electron flux regulation around the generation of pyruvate. The proposed mechanism of regulation based on intracellular PPI levels agrees with the measured concentrations of PPI in growing *R. thermocellum* cells (Chapter 3).

#### 6.3.1 Phase 1: Initial inoculation phase

The initial inoculation of late exponential cells results in a low initial intracellular PPI concentration due to low intracellular PPI concentrations in the inoculum (Figure 6.1). However, the high concentration of nutrients induces the accumulation of PPI and the rapid inactivation of ppGpp. The initial low concentrations of PPI are insufficient to induce the activity of the glucokinase (GK) and the PPI-dependent phosphofructokinase (PPI-PFK) therefore reducing the carbon flux through the remainder of glycolysis (Figure 4.2, Figure 4.4). Glycogen synthesis would be induced due to an increased concentration of glucose and more importantly glucose 1 phosphate (G-1-P) caused by slower flux through GK and PPI-PFK thus creating a storage of glycogen along with generating PPI. The low levels of PPI would not inhibit the malic enzyme (MalE) thus activating the malate shunt while limiting the pyruvate phosphate dikinase (PPDK) activity. Therefore, this would increase the available GTP and NADPH present due to NADH transhydrogenation. The utilization of the pyruvate ferredoxin oxidoreductase (POR) leads to increases in reduced ferredoxin. The reduced ferredoxin buildup would be offset by increased



Figure 6.1: Proposed metabolic flux of *R. thermocellum* during the initial inoculation phase. The green arrows indicate high flux. The yellow arrows indicate medium flux. The red arrows indicate low or absent flux based on allosterory and measured PPI concentrations. The average expression of each particular gene is present for strains ATCC 27405, DSM 2360, and DSM 4150.





NiFe-ferredoxin-dependent hydrogenase (Fd-H<sub>2</sub>ase) activity. The increased Fd-H<sub>2</sub>ase is important in order to generate the proton motor force required for the V-type pyrophosphatase (PPase) in order to generate PPi. The H<sub>2</sub> generated by the Fd-H<sub>2</sub>ase is harnessed by the NADPH-H<sub>2</sub>ase thus further increasing the levels of NADPH. The increases in NADPH and GTP along with the inactivation of the HPr system would trigger increased biosynthesis leading to the transcription and translation of the components required for active growth. The increased biosynthesis of proteins, DNA, RNA, lipids, and lipopolysaccharides along with PPi generation through the V-type PPase results in a rapid increase in intracellular PPi concentration (Figure 3.1). The utilisation of the V-type PPase in order to produce is hypothesized based on the relatively low energy conservation of PPi hydrolysis followed by ATP synthesis by the ATP synthase (Chapter 3) and by the calculations showing the inability of *R. thermocellum* to produce enough PPi to supply the PPi-PFK during growth (Zhou et al. 2013).

### 6.3.2 Phase 2: Initial growth phase

The increase in PPi and GTP in the previous phase reaches a peak, now increasing the activity of the GK and PPi-PFK. The increased flux through GK and PPi-PFK induce an increase in flux through glycolysis (Figure 6.2). The increase rate of glycolysis is further increased by the breakdown of glycogen producing G-1-P. The increase in G-1-P can further increase the PPi-PFK by increasing the supply of fructose 6-phosphate (F-6-P)/ glucose 6-phosphate (G-6-P) available. The trickle-down effect of the increased activity of the GK and PPi-PFK leads to a general increase in flux through glycolysis. The presence of high concentrations of PPi would inhibit the malate shunt thus forcing the flux through the PPDK thus maintaining high levels of NADH rather than NADPH. Despite the increased levels of NADH, the lactate dehydrogenase (LDH) remains inactive



The yellow arrows indicate medium flux. The red arrows indicate low or absent flux based on allosteric and measured PPI concentrations. The average expression of the particular gene is present for strains ATCC 27405, DSM 2360, and DSM 4150.





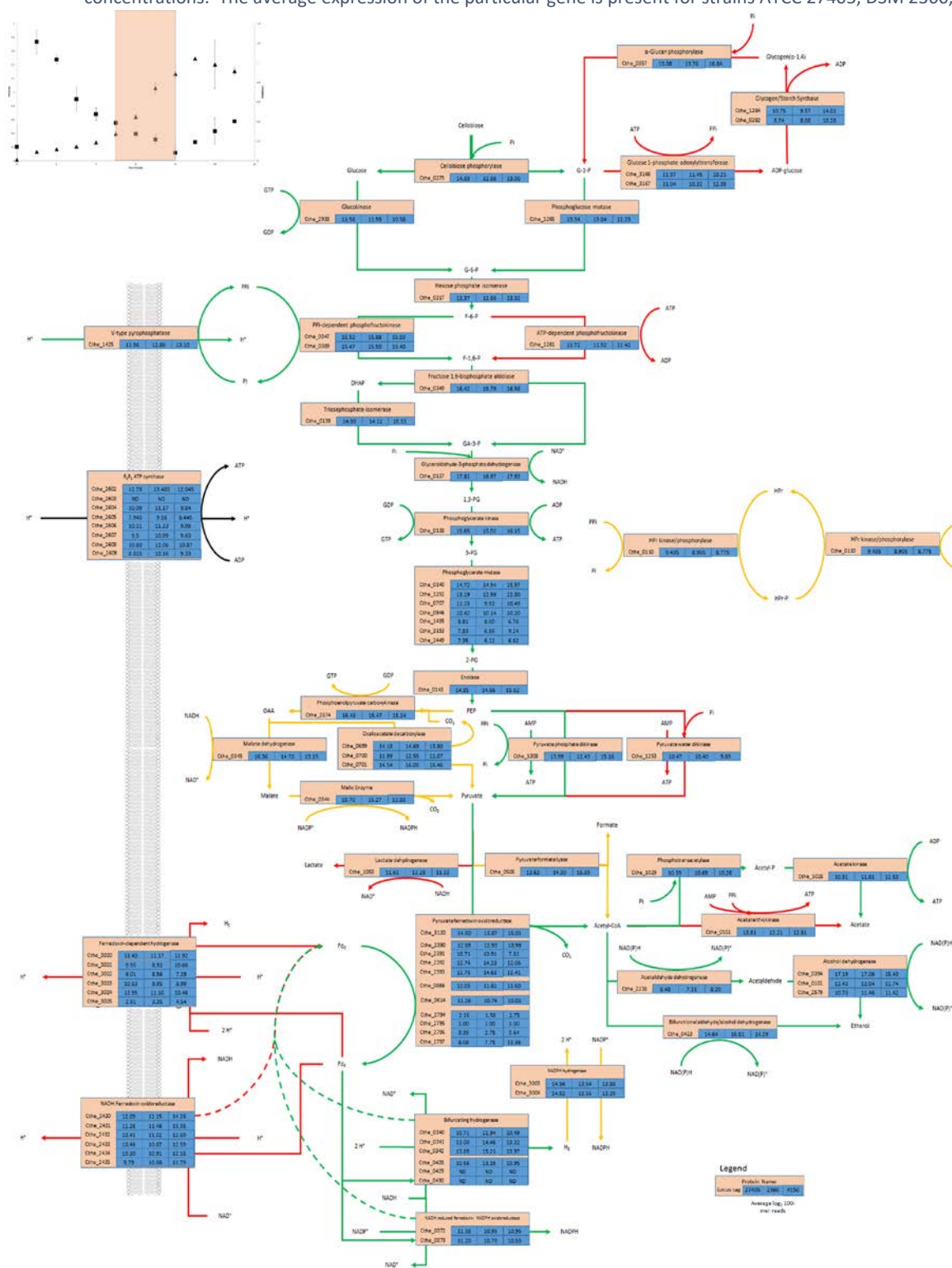
due to the still relatively high concentration of PPi as was measured in *C. saccharolyticus* (Willquist and Van Niel 2010). Reduced ferredoxin from the POR would be oxidized by both the NADH-ferredoxin oxidoreductase (NFOR) and the bifurcating (BiH<sub>2</sub>ase) H<sub>2</sub>ase in order to both maintain the proton motor force across the membrane while still producing the H<sub>2</sub> that is observed in the end products (Figure 5.1). While the Fd-H<sub>2</sub>ase would be able to achieve both the proton motor force generation as well as the H<sub>2</sub> generation, its lower expression in the transcriptome and proteome favors alternative to the Fd-H<sub>2</sub>ase (Chapter 5, Rydzak et al. 2012). The relatively high levels of PPi prefer acetate production via the acetate thiokinase (ATK) over the usual phosphotransacetylase (PTA)/acetate kinase (AK). During this phase, the high levels of PPi, indicating a high-energy state for the cell, induce the activation of the HPr/CcpA transcriptional regulation system. The V-type PPase along with biosynthesis of proteins, DNA, RNA, lipids, and lipopolysaccharides continue to produce during this phase but are no longer able to produce sufficient PPi in order to compensate for the high PPi usage of the PPi-PFK, PPDK, and ATK. Thus leading to a slow decrease in the intracellular concentrations of PPi. Overall, the initial growth phase focuses on rapid glycolytic flux along with increased energy conservation by ATP generation through PPDK and ATK (Figure 6.2).

### 6.3.3 Phase 3: Growth phase

Throughout growth, the intracellular concentration of PPi continues due to higher consumption (PPi-PFK, PPDK, and ATK) over production (V-type PPase and biosynthesis). The drop in PPi concentration no longer inhibits the MalE allowing for utilization of the malate shunt along with the PPDK allowing flexibility in the pathway utilization (Figure 6.3). During the growing



Figure 6.3: Proposed metabolic flux of *R. thermocellum* during the growth phase. The green arrows indicate high flux. The yellow arrows indicate medium flux. The red arrows indicate low or absent flux based on allostery and measured PPI concentrations. The average expression of the particular gene is present for strains ATCC 27405, DSM 2360, and DSM 4150.





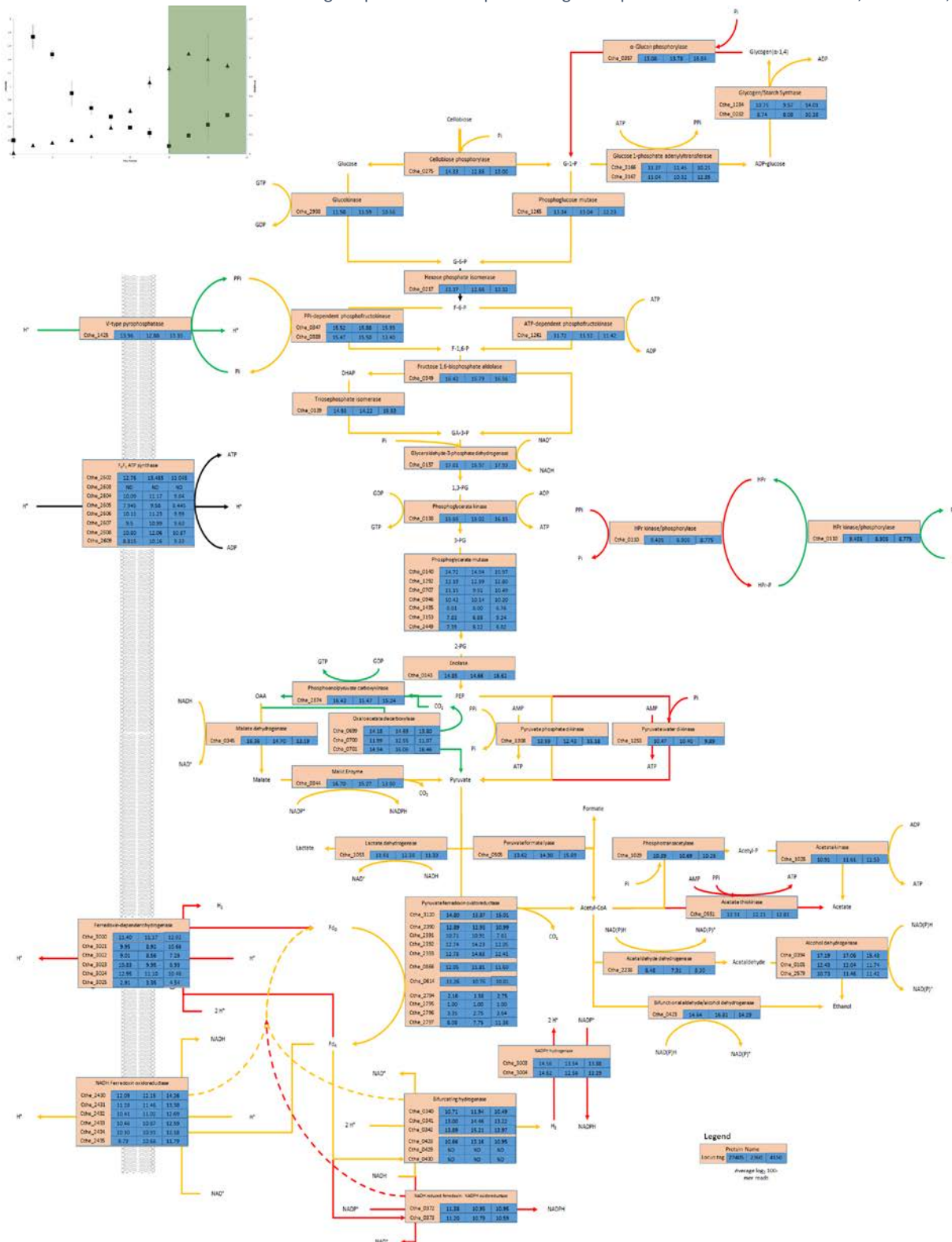
phase, acetate generation would be mediated by the PTA and AK over the ATK system due to the drop in PPI concentration making the utilization of PPI for ATP generation less favorable. Similar to the initial growth phase, the focus of the growth phase is on the conservation of energy along with a high glycolytic rate. The growth phase differs from the initial growth phase by having multiple pyruvate synthesis pathways allowing for the cells to adapt to any changes in environmental conditions. The appearance of formate as an end product is generally seen later during growth (Sparling et al. 2006), therefore, in the growth phase the flux through the pyruvate formate lyase (PFL) would increase to coincide with the appearance of formate as an end product. The increased flux through PFL would also putatively allow for increase amino acid synthesis by increasing the C1 availability for tetrahydrofolate (THF) cycling allowing for greater availability for amino acid biosynthetic precursors (Rydzak, Lynd, and Guss 2015).

#### 6.3.4 Phase 4: Stationary phase

At the onset of the stationary phase, the PPI concentrations reach a minimum indicating a low energy state of the cell. The low energy state induces a slowdown of the overall glycolysis due to a decrease in GK and PPI-PFK activity due to low PPI concentrations. Also, the low PPI concentrations limit the capabilities of the PPDK, therefore, forcing an alternative to pyruvate synthesis. The absence of various nutrients, mainly amino acids could induce activation of the RelA gene (Cthe\_1344) in *R. thermocellum* activating the formation of the regulatory molecule ppGpp and limiting flux through MalE due to low NH<sub>3</sub> concentrations. Thus this would force the flux through the putative oxaloacetate decarboxylase (OAADC) system. The low energy state of the cells induces the dephosphorylation of the HPr system leading to inactivation of the catabolite



Figure 6.4: Proposed metabolic flux of *R. thermocellum* during the stationary phase. The green arrows indicate high flux. The yellow arrows indicate medium flux. The red arrows indicate low or absent flux based on allosteric and measured PPI concentrations. The average expression of the particular gene is present for strains ATCC 27405, DSM 2360, and DSM 4150.





co-repression (CCR) system preparing the cells for the stationary phase of life their life cycle (Figure 6.4). Flux towards lactate is increased due to the removal of the PPi inhibition of LDH activity. In this particular model, it is proposed that the small flux through LDH is utilized as a means of rebalancing NADH/NAD<sup>+</sup> ratio putatively due to an increased flux through the NFOR throughout growth.

In the previous model, the importance of PPi as a phosphate group donor in central catalysis as well as a regulatory molecule modulating carbon and electron flux. While the previous model was derived for *R. thermocellum*, very similar regulatory mechanisms would be expected in *R. termitidis*, *R. stercorarium*, and *C. saccharolyticus* based on similar trends in intracellular PPi measurements (Figure 3.1) (Bielen et al. 2010). However, these organisms differ from *R. thermocellum* in that they all contain and express pyruvate kinase (PK) genes (Munir et al. 2016; Schellenberg et al. 2014). Low levels of PPi would allow for flux through the malate shunt, but would also allow for flux through PK leading to rapid ATP generation and therefore, putatively alter the NADH/NADPH levels by bypassing the transhydrogenase of the malate shunt.

#### 6.4 Extend of the *R. thermocellum* like metabolism

*R. thermocellum* has an atypical metabolism as previously described in Chapter 1 when compared to the traditional *E. coli* model. The extent of the *R. thermocellum* metabolism seems to be prevalent across the *Ruminiclostridium* and various other closely related families such as *Caldicellulosiruptor* and *Ruminococcus*. The genomic analysis of various industrially attractive Firmicutes reveals many organisms demonstrating similar central glycolysis associated enzymes based on sequence analysis (Chapter 1, 3). The extent of putative PPi-PFK in the Firmicutes raises interesting questions regarding the evolution of PFK co-factor utilization (Figure 3.6). The



modification of one amino acid in the PPi-PFK cofactor binding site allows for the binding of ATP would suggest that ATP-PFK form the ancient line of PFK evolution concurrent with the theory of early self-replicating nucleotides (Chi and Kemp 2000). The divergent from ATP utilization to PPi utilization in fermentative organisms appears to be an evolutionary adaptation allowing for increase energy conversion. However, the prevalence of PPi-PFK in thermophilic archaea and thermophilic bacteria raises an interesting question regarding the evolutionary ancestor of PFK as thermophilic archaea are viewed as more closely resembling primordial organisms (Siebers, Klenk, and Hensel 1998). Regardless of the evolutionary origins, the PPi-PFK appears to be a vital fixture in many Firmicutes, especially in the family *Ruminiclostridium*.

The reclassification of the family *Clostridium* has been proposed by Yutin and Galperin (2013), which reclassifies many *Clostridium* into new families. While the adoption of the new nomenclature has been met with much resistance, the biochemical and phylogenetic data from the proteins associated with central catalysis agree with the new classification. The phylogenetic analysis of the MDH (Figure 2.4), MalE (Figure 2.5), GK (Figure 4.3), PFK (Figure 3.6), and PPDK (Figure 3.5) all support the reclassification of the *Clostridium* into separate family by showing clear grouping of the new *Ruminiclostridium*, *Lachnoclostridium*, and the traditional *Clostridium*. Therefore, while they originally appeared as a single family, the reclassification of the *Clostridium* agrees very well with the predicted biochemistry and phylogeny of their proteins.



## 7 Conclusions and Future Directions

### 7.1 Thesis conclusions

The development of environmentally friendly alternatives to the current dependence on fossil fuel is vital for the reduction of greenhouse gas emission contributing to the climate change currently being observed. The production of liquid fuels via consolidated bioprocessing is an important stepping-stone in offsetting a portion of the liquid fossil fuels usage. The production of liquid fuels through consolidated bioprocessing also has the attractive alternative of increasing energy security allowing for the production of fuel without reliance on the presence of fossil fuels deposits. *R. thermocellum* is a very attractive organism for consolidated bioprocessing due to its high rate of cellulose hydrolysis along with its native ability to generate ethanol. However, the branched nature of the *R. thermocellum* central catalysis limits the viability of *R. thermocellum* as an industrial organism due to diverting carbon and electrons away from the desired end product of ethanol into lactate, acetate, formate, and H<sub>2</sub>. Genetic engineering studies have successfully removed some of the competing pathways yielding higher concentrations of ethanol through growth. However, these genetic modifications do not always have the predicted effects and rarely have any effect on the growth rate of *R. thermocellum*.

The aim of this thesis was to address some key central catalysis proteins in order to assess their particular role in glycolytic flux regulation along with their general kinetic properties.

Aim 1: To evaluate the important central catabolism genes and putative flux regulatory nodes (GK, PFK, PGK, PPK, MDH, and MalE) in order to gain a better understanding of the enzyme kinetics associated with the particular proteins (Chapter 2, 4)



- 1) We found relatively high levels of activity in purified MDH (NADH) and MalE (NADPH) when compared to related organisms (Taillefer et al. 2015)
- 2) We detected high activities for the cloned and purified GK (GTP and ATP) and PGK (GDP and ADP)<sup>7</sup>
- 3) The activity of the GK was reliant on the concentration of GTP or ATP present. Increases in nucleotide concentrations resulted in decreases in activity
- 4) Similar to the GK, the PGK displayed substrate inhibition with increasing concentration of ADP but did not have inhibition with GDP
- 5) We detected relatively low activities of the cloned and purified PPI-PFK
- 6) We were not able to detect the activity of the cloned and purified PPDK

Aim 2: To evaluate the regulatory effects of small high-energy metabolites such as ATP, and PPI on the enzyme activity of key central catalysis proteins in order to better understand the putative regulatory role of PPI (Chapter 2, 4)

- 1) We found that the presence of PPI was a strong inhibitor of MalE activity (Taillefer et al. 2015)
- 2) We found that the presence of NH<sub>3</sub> was a strong activator of MalE activity (Taillefer et al. 2015)
- 3) We found that the presence of PPI was an activator of GK activity<sup>7</sup>
- 4) We found that the presence of ATP was an inhibitor of PPI-PFK activity<sup>7</sup>

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<sup>7</sup> Coauthors of manuscript in progress : R. Sparling, A. Froese, and D. Levin



Aim 3: To assess the diversity of PPi metabolism genes found through industrially relevant Firmicutes in order to gain an idea of the diversity of PPi metabolism and to assess possible trends in terms of gene presence (Chapter 3)

- 1) The intracellular concentration of PPi in *R. thermocellum*, *R. termitidis*, and *R. stercorarium* all follow the same pattern of a sharp increase at the beginning of growth followed by a gradual decrease in PPi until reaching a minimum at the onset of stationary phase
- 2) Most of the industrially relevant Firmicutes possess more than one type of PPase in their genome showing diversity in the PPi regulating mechanisms
- 3) Most of the industrially relevant Firmicutes contain both PPi and ATP-PFK allowing for flexibility in cofactor utilization
- 4) Some of the cofactor specificity of the putative PFK could not be determined via sequence analysis. However, phylogenetic analysis has hinted at their cofactor preference
- 5) Many HPr proteins in the analyzed organisms did not contain the amino acid residue required for PTS activity thus primarily utilized for CCR

Aim 4: To assess the differences between 3 *R. thermocellum* strains in order to gain a better understanding of the regulatory mechanisms controlling the amount of specific end products through transcriptomic analysis (Chapter 5)

- 1) Overall, the transcriptome across the different strains was found to be very stable



- 2) The transcriptome across the different conditions (CB vs  $\alpha$ -cellulose) was very stable with high correlation
- 3) The level of transcription did not always correlate with the changes in end product amount observed in the different strains
- 4) Various transcripts not detected by the proteome were detected by RNAseq showing a putative bias in the proteomic extraction protocol

Taken as a whole, this thesis reinforces the notion that end product synthesis is not regulated by transcription level of certain genes in *R. thermocellum*. But rather end product synthesis is regulated by the presence of small metabolites modulating carbon and electron flux through central catalysis and end-product synthesis pathways. This thesis also elaborates on the importance of PPi as a phosphate group donor and as a signaling molecule in *R. thermocellum* and other closely related organisms especially the *Ruminiclostridium*. Therefore, novel strains of *R. thermocellum* could be developed centered around controlling the intracellular PPi thus allowing for increased flux through glycolysis and therefore putatively increasing overall growth rate.

## 7.2 Future directions

### 7.2.1 Metabolic modelling

The development of genome-scale metabolic models can be a very powerful tool in order to assess putative genetic engineering targets in silico allowing for rapid screening without the requirement for extensive genetic manipulation. Many genome-scale metabolic models (GEM) have been previously developed focused on adapting genome content into a valid model (Roberts et al. 2010; Gowen and Fong 2010; Dash, Ng, and Maranas 2016; Thompson et al. 2016;



Thompson et al. 2015). However, due to the lack of complete understanding of central catalysis in *R. thermocellum*, some constraints had to be implemented into their models, which limit their accuracy. The lack of pyruvate kinase (PK) gene and activity has been confirmed by genomic, proteomic, and enzymatic analyses (Carere et al. 2012; Rydzak et al. 2009; Rydzak et al. 2012; Zhou et al. 2013). However, in a previous model, the presence of PK had to be forced into the model in order for their predictive model to function (Roberts et al. 2010). This constraint does not allow the model to reflect the central catalysis of *R. thermocellum* as the addition of PK removes the regulation of transhydrogenation by the malate shunt and the energy conservation by the PPDK. However, recent work has predicted the pathways utilized for pyruvate generation in *R. thermocellum* allowing for the refinement of the GEM (Rydzak et al. 2012; Taillefer et al. 2015; Zhou et al. 2013).

Further, early GEM did not take into account differential expression of proteins, hence, presence in the genome indicates activity. Therefore, further refinement to the GEM was done by overlaying the transcriptome of *R. thermocellum* in order to create a model that has the constraints of relative expression leading to an increase in the predictive capabilities of the particular GEM (Gowen and Fong 2010). While the addition of the transcriptome to the model increased its predictive accuracy, the presence of a transcript or protein does not guarantee the corresponding function. In both the proteome and transcriptome of *R. thermocellum* we can observe proteins that are expressed at relatively high levels that do not have the corresponding flux such as for example the LDH (Rydzak et al. 2012; Raman et al. 2011, Chapter 5).

The addition of pathway flux is the next step in the refinement of GEM. The addition of biochemical data for key flux contributors allows for the predictive model to take into



account allosteric regulation by the input of restrictions in flux based on biochemical data. For example, the addition of a constraint to GK, which is modulated based on intracellular PPI levels allows to modify the flux going through GK, and ultimately glycolysis, based on the conditions. Therefore, the addition of biochemical data to the GEM allows for greater predictive power by allowing the analyses of the changes in metabolites based on in silico genetic modification. Interestingly, a new GEM for *R. thermocellum* DSM 1313 has been created by creating a scaffold using the genome with refinement by transcriptomic, and experimental data such as end-product synthesis and growth rate (Thompson et al. 2016). Without the addition of biochemical constraints, this GEM was able to predict the importance of PPI and the malate shunt such as activation of the PPDK and inhibition of the MalE as was confirmed in Chapter 2. Therefore, while the GEM can predict putative control point regulation, however, the addition of biochemical data for a greater number of key glycolytic proteins would allow for prediction beyond a single control point. Allowing predictions of global regulatory effects on electron and carbon flux. Therefore, the future biochemical characterisation of all the glycolytic proteins along with the end product synthesis proteins would be invaluable to the development of robust, accurate predictive models capable of generating valuable genetic engineering targets regardless of the particular outcome required (ethanol production, H<sub>2</sub> production, growth rate, etc.). Hence, the development of a GEM that is more driven by metabolic knowledge would clear the road for intensive strain development leading to the greater industrial capabilities for *R. thermocellum*.

### 7.2.2 Strain development

The development of novel industrial *R. thermocellum* strains would be greatly increased by the development of accurate predictive models. Predictions of an “ideal” strain for ethanol

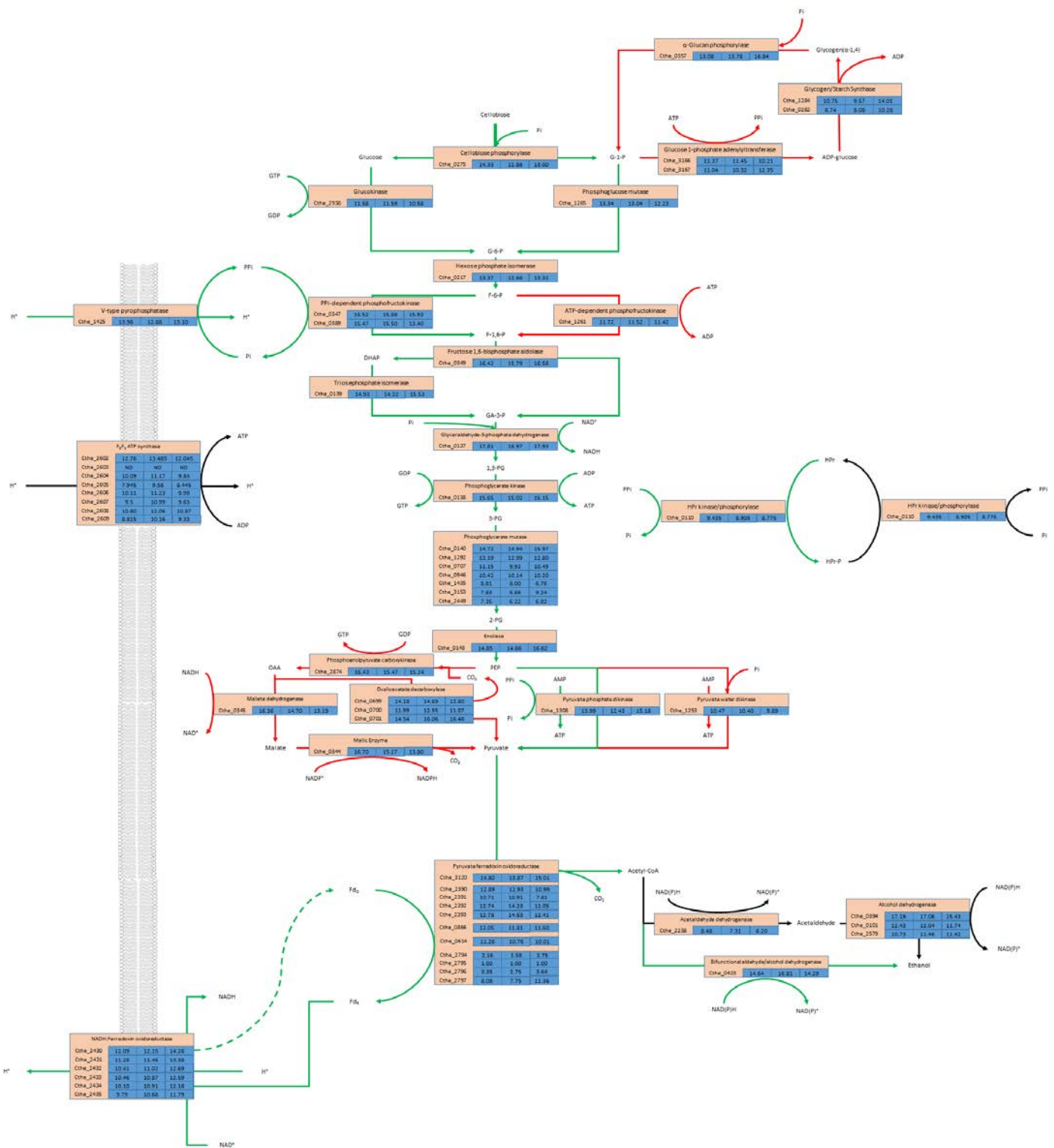


generation could be made based on the biochemical data obtained in Chapter 2 and 4 along with putative PPI regulatory mechanisms proposed in Chapter 3, 5, and 6. The combination of multiple genetic manipulations previously done would be essential in the development of an ideal strain. The deletion of the competing pathways (( $\Delta$ hydG,  $\Delta$ pfl,  $\Delta$ pta-ack, and  $\Delta$ ldh) in *R. thermocellum* DSM 1313 have been shown to be able to increase ethanol by almost 100% (Papanek et al. 2015). However, when grown on increasing concentration of Avicel PH105, the production of ethanol peaked at 20 g/L at approximately 75 mM. Further, growth at 50 g/L Avicel PH105 caused a 20 mM decrease in ethanol generation. Surprisingly, the increased concentration of substrate resulted in lactate generation despite the knockout of the LDH gene. The small amount of lactate is predicted to be produced by the promiscuous behavior of the MDH (Li et al. 2012) despite the lack of LDH activity in the cloned and characterized MDH (Chapter 2). Regardless, the increase in substrate concentration seemingly causes an overflow of metabolites resulting in the requirement for lactate generation in response to the build-up of excess NADH and the need for NAD<sup>+</sup> regeneration. Therefore, an increase in glycolytic flux resulting from the increase in substrate concentration causes a bottleneck at the conversion of pyruvate to acetyl-CoA similar to what it observed with pyruvate in *R. cellulolyticum* (Guedon et al. 1999).

The ideal strain would require specific ethanol generation at nearly 100% theoretical yield of 2 moles of ethanol per glucose consumed. The genetic manipulations outlined above are a very good starting for the creation of the ideal strain (Papanek et al. 2015). The elimination of competing pathways eliminates many issues in terms of carbon and electron diversion (Figure 7.1). The knockout of the competing pathways eliminates lactate, acetate, formate, and most of the H<sub>2</sub>. Further, the overexpression of the V-type PPase leads to increased internal



is present for strains ATCC 27405, DSM 2360, and DSM 4150.





concentrations of P<sub>Pi</sub>. The constant high levels of P<sub>Pi</sub> lead to an increase glycolytic flux through glycolysis due to activation of the GK and P<sub>Pi</sub>-PFK. The increase P<sub>Pi</sub> levels lead to utilization of the PPDK over the malate shunt in terms of pyruvate generation leading to a more rapid flux to pyruvate. However, increases in glycolytic flux have been shown to cause a bottleneck in pyruvate to acetyl-CoA interconversion in *R. thermocellum* causing an overflow towards lactate generation despite the knockout of LDH (Papanek et al. 2015). To alleviate any issues of overflow due to increasing glycolytic flux, POR could be overexpressed thus allowing for more rapid flux away from pyruvate preventing overflow metabolism. However, the overexpression and increased flux through POR would increase Fd<sub>R</sub> concentration requiring rapid rebalancing. The overexpression of the NFOR plays a few vital roles in the ideal strain. The NFOR would firstly oxidize the Fd<sub>R</sub> reducing NADH in the process. Thus, the extra NADH produced through Fd oxidation would directly be utilized by AdhE in order to produce ethanol. Secondly, the oxidation of Fd results in the pumping out of protons leading to the generation of proton motor force. The proton motor force generated could further be harnessed by the V-type PPase maintaining the high concentration of P<sub>Pi</sub> required for increase glycolytic flux. The remaining H<sub>2</sub>ase would need to be knocked out in order to eliminate the competition for Fd<sub>R</sub> generated by the POR. The knock of the maturase protein HydG (Cthe\_0625) eliminates the NADPH H<sub>2</sub>ase and the BiH<sub>2</sub>ase followed by the knockout of the Fd-H<sub>2</sub>ase and the NfnAB proteins. Therefore, the ideal strain would have the removal of all competing pathways for carbon and electron while having increased flux through glycolysis due to increased intracellular P<sub>Pi</sub> concentrations. The increase in glycolytic flux would be offset by the overexpression of the POR and NFOR leading to the theoretical yield



of 2 ethanol and 2 CO<sub>2</sub> per glucose consumed or 648 mL of ethanol per kg of glucose equivalents consumed.

However, one issue that remains is the ethanol tolerance of *R. thermocellum*. Increased production of ethanol is irrelevant if the organism is incapable of surviving in the environment. The key to ethanol tolerance appears to be with the cofactor specificity of AdhE (S. D. Brown et al. 2011). The native *R. thermocellum* is capable of tolerating approximately 2% ethanol prior to slowing growth. Strains with a mutated AdhE, preferring NADPH over NADH, are capable of uninhibited growth up to 4 % (Biswas et al. 2014). However, 4% is still much lower than many of the industrial yeast strains (~20%) (Costa et al. 1997). The increase in ethanol tolerance is generally attributed to changes in membrane lipids (Ingram 1990). Therefore, strain evolution on increasing concentrations of ethanol would allow for the discovery of novel ethanol resistant *R. thermocellum* strains allowing for increased ethanol generation prior to growth inhibition. The evolved ethanol-tolerant strain would then be a valuable candidate as the platform for the genetic modifications outlined (Table 7.1).

As we can see, the development of a commercially viable strain of *R. thermocellum* would require extensive strain evolution and genetic modifications. However, the innate ability for *R. thermocellum* to readily degrade lignocellulosic material increased its industrial potential by removing the reliance on extensive pre-treatments or expensive substrates. Therefore, *R. thermocellum* remains a very alluring candidate for the development of economically viable consolidated bioprocessing systems aimed at industrial scale production of ethanol.



Table 7.1: Proposed and successful deletions and genetic modification required for the creation of the “ideal” strain of R.

thermocellum. X: gene knockout, -: decreased gene expression, and +: increased gene expression.

Function	Protein	Gene	Genetic manipulation	
Lactate production	Lactate dehydrogenase	Cthe_1053	X	(Biswas et al. 2014; Argyros et al. 2011)
Formate production	Pyruvate formate lyase	Cthe_0505	X	(Rydzak et al. 2015)
Acetate production	Phosphotransacetylase	Cthe_1028	X	(Argyros et al. 2011;
	Acetate Kinase	Cthe_1029	X	Tripathi et al. 2010)
H <sub>2</sub> production	Fd-dependent hydrogenase	Cthe_3020-3025	X	(Biswas, et al. 2015)
	FeFe active site maturase	Cthe_0654	X	
Ferredoxin oxidation	NADH reduced ferredoxin: NADPH oxidoreductase	Cthe_0372-0373	-	
	NADH:ferredoxin oxidoreductase	Cthe_2430-2435	+	
PPi generation	V-type pyrophosphatase	Cthe_1425	+	
Pyruvate metabolism	Pyruvate ferredoxin oxidoreductase	Cthe_3120	+	



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# Supplementary Figures and Tables

Supplementary Table 1: Raw transcriptomic data for *R. thermocellum* ATCC 27405, DSM 2360, and DMS 4150 growing on cellobiose



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Cthe_00612 55S sodium solute/transporter superfamily	14.9	14.9	12	12.1	12.8	11.4	-0.07	-0.1	-0.62	2.92	2.89	2.1	1.55	-0.82	-1.34	-0.31	-0.28	0	0.85	0.99	0.41	0.49	-0.5	-0.5	1.2	0.57	-0.68	0.93	0.44	-0.52	6.25	4.68	8.6
Cthe_02376 DNA gyrase, B subunit	13.8	13.9	10.9	11	13.3	11.8	-0.06	-0.06	-0.52	2.87	2.87	0.5	0.04	-2.37	-2.83	-0.3	-0.16	0.33	0.83	0.98	-0.3	-0.2	-1.2	-1.3	1.2	-0.23	-1.75	0.89	-0.2	-1.35	7.55	1.69	16.41
Cthe_01721 phage portal protein, HK97 family	4.52	2.58					1.94			4.52	2.58	4.52	2.58		2.17			1.54	0.84	1.46	0.94			1.21	1.26		0.93	0.99		1.62	1.82		
Cthe_02461 transcriptional regulator, XRE family	4.17	2.58					1.59			4.17	2.58	4.17	2.58		1.74			1.39	0.84	1.31	0.94			1.19	1.23		0.92	0.97		1.87	2.11		
Cthe_01740 BRD-like protein	4.09	2.58					1.51			4.09	2.58	4.09	2.58		1.74			1.35	0.84	1.27	0.94			1.18	1.22		0.91	0.96		1.94	2.19		
Cthe_01704 toxin secretion/phage lysis holin	3.7	2.58	0				1.12	0		3.7	2.58	3.7	2.58		0	1.16	0.03	1.19	0.84	1.1	0.94	0.18		1.17	1.19	0.18	0.9	0.94	0.16	2.51	2.83	20	
Cthe_02770 transposase IS116/IS110/IS902	2.58	4.09			6.04	5.98	-1.51		0.06	2.58	4.09	-3.46	-1.89	-6.04	-5.98	-2.09		2.27	0.7	1.54	-2	-1	-2.9	-3	1.17	-1.57	-3.87	0.9	-1.27	-3.01	1.62	1.65	6.19
Cthe_02743 putative metalloendopeptidase, glycoprotease	12.8	12.3	9.69	9.66	9.34	9.98	0.46	0.03	-0.64	3.07	2.64	3.42	2.32	0.35	-0.32	0.35	0.12	-0.07	0.91	0.87	0.98	0.82	0.07	0.01	1.17	1.2	0.05	0.9	0.94	0.05	6.81	8.14	1.7
Cthe_01533 transposase, mutator type	3.46	2.58				0	0.88			0	3.46	2.58	3.46	2.58	0	0.88		2.07	1.08	0.84	1	0.94		0.18	1.15	0.88	0.13	0.89	0.69	0.12	3.18	1.39	0.19



Chb_02294 transposase	3.32	2.58	3.32	2.58	0.69	0.00	0.84	0.94	0.94	1.15	1.18	0.89	0.93	3.83	4.38
Chb_02500 carboxyl phosphate synthase, small subunit	11.9	11.8	8.95	8.95	10.3	0.74	-0.02	-0.7	2.91	2.81	1.84	-0.55	-1.68	-2.36	-2.00
Chb_02502 carboxyl phosphate synthase, large subunit	11.5	11.7	8.95	8.95	10.3	0.74	-0.02	-0.7	2.92	2.81	1.84	-0.55	-1.68	-2.36	-2.00
Chb_02503 transposase, mutator type	9.74	8.53	6.11	6.11	7.7	1.21	0	0.29	3.63	3.42	3.03	1.53	-0.6	-0.89	1.27
Chb_02504 transposase, mutator type, TnA/B-like family	11.9	11.7	7.48	7.48	9.7	0.76	-0.02	-0.7	2.91	2.81	1.84	-0.55	-1.68	-2.36	-2.00
Chb_02505 FtsK	12.5	11.9	9.24	9.24	11.2	0.86	0.27	0.75	4.02	3.73	0.5	-1.21	-2.92	-3.34	0.96
Chb_02506 cellulose enzyme, docked type 1	9.95	8.3	5.83	6.04	7.72	8.4	1.65	-0.21	0.76	4.12	2.26	2.23	-0.18	-1.89	-2.44
Chb_02506 protein of unknown function, family 2047	12.5	11.9	9.24	9.24	11.2	0.86	0.27	0.75	4.02	3.73	0.5	-1.21	-2.92	-3.34	0.96
Chb_02508 type II secretion system inner membrane B	12.5	11	8.64	8.75	7.3	8.0	0.7	1.45	-0.11	0.77	3.85	2.29	5.19	2.97	1.34
Chb_02508 type II secretion system inner membrane B	12.5	11	8.64	8.75	7.3	8.0	0.7	1.45	-0.11	0.77	3.85	2.29	5.19	2.97	1.34
Chb_02511 NLP/PG	9.4	2.32	0.61	0.61	8.92	0.1	0.12	-0.67	2.46	2.36	1.66	1	-1.44	-2.23	-0.3
Chb_02518 N-acetylmannosyl-L-alanine amidase	8.73	8.2	5.61	5.61	4.86	4.8	0.41	-0.61	0.05	3.73	2.71	3.87	3.51	0.14	0.8
Chb_02519 GCM-related N-acetyltransferase	11.5	11.5	8.61	8.61	9.4	0.8	0.09	-0.63	2.49	2.36	2.55	0.05	-0.47	-0.5	0.1
Chb_02520 ornithine 5'-phosphate dehydratase	11.4	9.99	7.72	7.72	9.47	1.0	1.44	0.26	-0.66	2.71	2.53	2.06	-0.04	-1.65	-2.57
Chb_02521 Chek signal transduction histidine kinases	10.2	8.29	5.83	6.25	6.41	7.0	1.88	-0.42	0.63	4.34	2.04	3.76	1.25	-0.58	-0.79
Chb_02522 Chek signal transduction histidine kinases	10.2	8.29	5.83	6.25	6.41	7.0	1.88	-0.42	0.63	4.34	2.04	3.76	1.25	-0.58	-0.79
Chb_02523 Radical SAM	10.6	10.2	7.91	7.91	8.2	8.6	0.42	0	-0.4	2.67	2.25	2.38	1.56	-0.29	-0.69
Chb_02524 amino acid efflux carrier	10.6	10.2	7.91	7.91	8.2	8.6	0.42	0	-0.4	2.67	2.25	2.38	1.56	-0.29	-0.69
Chb_02525 hypothetical protein	8.03	7.3	5.04	4.86	9.71	10.5	0.73	0.18	-0.78	2.99	2.44	-1.68	-1.39	-4.67	-5.63
Chb_02526 Radial SAM	10.6	10.2	7.91	7.91	8.2	8.6	0.42	0	-0.4	2.67	2.25	2.38	1.56	-0.29	-0.69
Chb_02527 response regulator receiver modulated CheR	12.4	11	8.41	8.63	7.29	7.9	0.42	-0.22	0.63	2.97	2.33	4.09	3.04	1.12	0.71
Chb_02528 pyruvate carboxylase	12.2	11.2	9.55	9.69	9.54	10.3	0.03	-0.14	0.8	2.62	2.45	2.63	1.8	0.01	-0.65
Chb_02529 pyruvate carboxylase	12.2	11.2	9.55	9.69	9.54	10.3	0.03	-0.14	0.8	2.62	2.45	2.63	1.8	0.01	-0.65
Chb_02530 response regulator receiver modulated CheR	12.4	11	8.41	8.63	7.29	7.9	0.42	-0.22	0.63	2.97	2.33	4.09	3.04	1.12	0.71
Chb_02531 polychaete ABC transporter	12.4	11	8.41	8.63	7.29	7.9	0.42	-0.22	0.63	2.97	2.33	4.09	3.04	1.12	0.71
Chb_02532 sulfite ABC transporter, inner membrane subunit	3.91	3	1.28	1.32	2.32	2.81	0.91	1.59	-0.49	2.04	1.42	1.59	0.19	-0.85	-1.23
Chb_02533 ABC transporter related protein	3.91	3	1.28	1.32	2.32	2.81	0.91	1.59	-0.49	2.04	1.42	1.59	0.19	-0.85	-1.23
Chb_02534 histidine ATP-binding protein	3.91	3	1.28	1.32	2.32	2.81	0.91	1.59	-0.49	2.04	1.42	1.59	0.19	-0.85	-1.23
Chb_02535 MATE efflux family protein	10.2	9.7	7.36	7.82	8.59	4.05	-0.12	-0.57	2.79	2.22	2.13	1.11	-0.86	-1.11	0.33
Chb_02536 Methyltransferase, type 11	9.09	8.86	0	1.58	0.98	0.3	-0.18	-0.58	1.23	1.18	0.63	0.1	-0.23	-0.05	-0.4
Chb_02537 short-chain dehydrogenase/reductase SDR	8.02	8.7	5.75	5.93	7.97	8.4	-1.13	-0.18	-0.43	2.32	3.27	0.1	0.8	-2.22	-2.47
Chb_02538 Radial SAM	7.02	6.07	3.71	3.81	5.34	6.34	0.95	-0.64	0.91	3.85	2.26	1.59	-0.27	-2.23	-0.95
Chb_02539 short-chain dehydrogenase/reductase SDR	8.02	8.7	5.75	5.93	7.97	8.4	-1.13	-0.18	-0.43	2.32	3.27	0.1	0.8	-2.22	-2.47
Chb_02540 short-chain dehydrogenase/reductase SDR	8.02	8.7	5.75	5.93	7.97	8.4	-1.13	-0.18	-0.43	2.32	3.27	0.1	0.8	-2.22	-2.47
Chb_02541 RNA polymerase, sigma 28 subunit	9.74	8.7	6.49	6.63	8.8	10.4	0.76	0.52	1.72	1.66	1.41	-0.47	-0.99	-1.1	0.88
Chb_02542 short-chain dehydrogenase/reductase SDR	8.02	8.7	5.75	5.93	7.97	8.4	-1.13	-0.18	-0.43	2.32	3.27	0.1	0.8	-2.22	-2.47
Chb_02543 diphosphate 4-epimerase	9.84	8.13	5.17	6.09	6.81	7.64	1.71	0.92	0.83	4.07	2.04	3.03	4.09	-1.64	-1.55
Chb_02544 hypothetical protein	9.84	8.13	5.17	6.09	6.81	7.64	1.71	0.92	0.83	4.07	2.04	3.03	4.09	-1.64	-1.55
Chb_02545 glycine kinase	11	11.5	9.62	8.45	8.56	8.4	0.43	0.02	-0.42	2.74	2.14	0.07	-0.29	-0.3	0.19
Chb_02546 transposase, mutator type	3.81	2	0.61	0.61	2.81	2	1.85	0.2	3.81	2	3.81	2	0.61	0.61	2.81
Chb_02547 binding protein transducer transport systems	11.5	11.2	7.85	7.73	11	1	1.65	0.12	0	3.62	2.09	10.47	8.85	0.73	1.81
Chb_02548 hypothetical protein	11.5	11.2	7.85	7.73	11	1	1.65	0.12	0	3.62	2.09	10.47	8.85	0.73	1.81
Chb_02549 two component transport system, ArcA	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02550 two component transport system, ArcB	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02551 two component transport system, ArcC	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02552 two component transport system, ArcD	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02553 two component transport system, ArcE	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02554 two component transport system, ArcF	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02555 two component transport system, ArcG	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02556 two component transport system, ArcH	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02557 two component transport system, ArcI	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02558 two component transport system, ArcJ	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02559 two component transport system, ArcK	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02560 two component transport system, ArcL	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02561 two component transport system, ArcM	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02562 two component transport system, ArcN	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02563 two component transport system, ArcO	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02564 two component transport system, ArcP	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02565 two component transport system, ArcQ	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02566 two component transport system, ArcR	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02567 two component transport system, ArcS	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02568 two component transport system, ArcT	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02569 two component transport system, ArcU	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02570 two component transport system, ArcV	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02571 two component transport system, ArcW	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02572 two component transport system, ArcX	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02573 two component transport system, ArcY	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02574 two component transport system, ArcZ	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02575 two component transport system, ArcA	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02576 two component transport system, ArcB	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02577 two component transport system, ArcC	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02578 two component transport system, ArcD	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02579 two component transport system, ArcE	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02580 two component transport system, ArcF	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02581 two component transport system, ArcG	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02582 two component transport system, ArcH	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02583 two component transport system, ArcI	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02584 two component transport system, ArcJ	12.9	12.8	10.6	10.5	9.81	10.3	0.09	0.08	0.44	2.3	2.29	3.11	2.58	0.81	0.29
Chb_02585 two component transport system, ArcK	12.9	12.8													



Che_00780 HAD superfamily hydrolase, subfamily 1A, variant	9	8.74	7.34	7.3	6.41	6.99	0.26	0.04	-0.56	1.66	1.44	2.57	1.75	0.91	0.31	0.1	0.16	0.2	0.31	0.31	0.61	0.58	0.33	0.34	0.38	0.79	0.44	0.26	0.62	0.36	0.47	8.56	6.17	
Che_01381 inner membrane translocator	2.98	6.17	3.41	4.75	5.17	0.47	-0.24	-0.83	-0.42	2.78	2.19	1.2	1.02	-1.58	-1.17	-0.52	-2.51	0.67	0.79	0.88	0.02	0.28	-0.5	-0.5	0.38	-0.07	-0.56	0.26	0.36	0.09	0.79	0.1	1.2	
Che_01384 hypothetical protein	11	11.2	9.54	9.45	9.2	7.4	1.22	-0.46	-1.2	1.09	0.3	0.2	0.2	-1.09	0.3	0.2	0.2	0.37	0.2	0.37	0.07	0.5	-0.5	0.34	-0.07	-0.56	0.26	0.36	0.09	0.79	0.1	1.2		
Che_02306 ABC efflux family protein	11	11.6	9.8	9.72	9.38	10.1	-0.39	0.08	-0.73	1.45	1.92	1.87	1.53	-0.42	-0.39	-0.7	0.28	0.37	0.38	0.12	0.31	0.48	0.1	-0	0.38	0.4	-0.03	0.26	0.3	0.04	1.51	1.64	0.75	
Che_02504 hypothetical protein	15	12.4	12.4	12.4	12.4	12.4	-0.17	-0.17	-0.17	0.11	0.26	0.17	0.17	-0.17	-0.17	-0.17	0.11	0.26	0.17	0.17	0.17	0.17	0.17	-0.17	0.11	0.26	0.17	0.17	0.17	0.17	0.17	0.17		
Che_04714 cytochrome haemolysin, family 5	112	103.9	120.9	120.8	120.2	8.63	0.34	-0.17	-0.61	1.91	1.4	3.18	2.23	1.27	0.83	0.2	-0.5	0.03	0.41	0.29	0.88	0.78	0.5	0.62	0.37	1.13	0.72	0.25	0.89	0.58	1.87	13.21	5.3	
Che_05004 ferredoxin	14	15	12.4	12.8	12.9	13.7	-0.67	-0.42	-0.8	1.93	2.18	1.39	1.26	-0.54	-0.52	-1.08	-1.28	0.64	0.46	0.66	0.1	0.36	0.4	-0.3	0.37	1.11	-0.26	0.25	0.07	-0.19	0.95	0.7	1.12	
Che_05234 DNA replication and repair protein RecF	112	103.9	120.9	120.8	120.2	8.63	0.34	-0.17	-0.61	1.91	1.4	3.18	2.23	1.27	0.83	0.2	-0.5	0.03	0.41	0.29	0.88	0.78	0.5	0.62	0.37	1.13	0.72	0.25	0.89	0.58	1.87	13.21	5.3	
Che_05319 translocator protein, GltI family	119	122.8	103.5	103.6	103.8	11.5	-0.92	-0.1	-0.77	1.38	1.2	1.17	1.32	-0.21	-0.88	-1.36	-0.28	-0.57	0.16	0.07	0.39	0.2	-0.3	0.35	0.07	-0.26	0.24	0.04	-0.19	1	0.61	0.22		
Che_05231 Methionine adenosyltransferase	112	113	96.5	97.4	96.6	11.1	-0.06	-0.09	-0.14	1.57	1.54	0.65	0.17	-0.92	-1.37	-0.1	-0.25	0.27	0.28	0.36	0.2	-0.1	-0.5	-0.6	0.35	-0.16	-0.72	0.24	-0.14	-0.55	2.27	1.39	6.88	
Che_05274 nucleotide reductase	111	111	97.6	98.5	101.7	11.7	-0.18	-0.18	-0.18	1.57	1.54	0.65	0.17	-0.92	-1.37	-0.1	-0.25	0.27	0.28	0.36	0.2	-0.1	-0.5	-0.6	0.35	-0.16	-0.72	0.24	-0.14	-0.55	2.27	1.39	6.88	
Che_02759 translocator protein, ArcZ family	9.89	10.2	8.46	8.31	7.97	10.2	-0.3	0.15	-0.38	1.43	1.88	1.02	0.04	-1.31	-1.84	-0.59	0.5	0.8	0.2	0.52	-0.5	-0.2	-0.7	-0.8	0.36	-0.26	-0.94	0.24	-0.22	0.72	1.44	1.09	3.81	
Che_05270 hypothetical protein	9.83	8.06	6.67	6.75	7.74	8.51	-0.47	-0.08	-0.77	1.86	1.31	0.79	-0.45	-1.07	-1.76	-0.36	-0.22	0.5	0.8	0.2	0.52	-0.5	-0.2	-0.7	-0.8	0.36	-0.26	-0.94	0.24	-0.22	0.72	1.44	1.09	3.81
Che_05214 binding protein-dependent transport systems	112	103.9	120.9	120.8	120.2	8.63	0.34	-0.17	-0.61	1.91	1.4	3.18	2.23	1.27	0.83	0.2	-0.5	0.03	0.41	0.29	0.88	0.78	0.5	0.62	0.37	1.13	0.72	0.25	0.89	0.58	1.87	13.21	5.3	
Che_05178 SAMase	6.44	6.69	4.75	4.95	4.38	5.55	-0.25	-0.2	-1.16	1.69	1.74	2.05	1.14	0.36	-0.6	-0.53	-0.59	-1.8	0.32	0.45	0.39	0.31	0.08	-0.1	0.35	0.09	-0.12	0.24	0.06	-0.08	1.39	0.6	0.28	
Che_00926 signal recognition particle docking protein FstY	11.14	11.5	9.92	9.77	10.5	11.2	-0.18	0.15	-0.66	1.43	1.76	0.85	0.17	-0.58	-1.39	-0.44	0.5	-0.13	0.2	0.46	-0.1	-0.4	-0.6	0.34	-0.03	-0.6	0.23	0.04	-0.45	1.51	0.65	0.48		
Che_00861 AT controlled adenoviral protein Btu(C)Csd(Cb)	9.61	9.39	7.86	8.08	9.61	10.7	-0.17	-0.53	-1.75	1.39	0.63	-0.02	-1.12	-1.61	-0.05	-0.1	0.05	0.34	0.29	0.3	-0.6	-0.7	-0.7	0.34	-0.3	-0.86	0.23	0.43	0.26	2.16	14.12	7.46		
Che_01427 branched-chain amino acid transporter	8.04	7.95	6.21	6.44	5.61	6.46	-0.09	-0.23	-0.85	1.83	1.51	2.43	1.49	0.6	-0.02	-1.11	-0.69	-0.77	0.38	0.34	0.55	0.46	0.19	0.17	0.34	0.55	0.1	0.23	0.42	-0.09	1.46	2.1	0.82	
Che_02267 Sodium transpore two-sector ATPase	11.4	12.7	10.1	10.2	11.5	12.4	-1.26	-0.12	-1.49	1.31	2.45	-0.12	0.24	-1.43	-1.21	-1.78	-0.34	-0.93	0.15	0.78	0.6	-0.1	-0.8	-1	0.34	-0.12	-1.12	-0.11	-0.86	0.88	0.64	0.28	0.8	
Che_02790 ABC transporter-related protein	13	13.7	11.2	11.5	11.9	12.7	-0.1	-1.42	-3.17	1	1	1	1	-2.58	-0.02	-1.09	-2.67	0.58	0.58	0.57	0.3	-0.5	-1.3	-1.4	0.34	-0.07	-1.33	-0.23	-0.46	-1.02	0.72	0.56	1.58	
Che_02791 binding protein-dependent transport systems	4	4.46	2	1.28	3.32	4.75	0.54	0.42	-1.43	2	1.88	0.88	-1.29	-1.32	-1.37	-0.44	1.34	-0.23	0.45	0.52	-0.2	-0.7	-0.7	-1.5	0.34	-0.17	-1.23	-0.23	-0.15	-0.95	0.98	0.64	1.86	
Che_01308 pyruvate, phosphate dikinase	10.2	12.8	13.5	14.9	15.5	15.2	-0.02	-0.13	-0.66	1.64	1.49	-0.85	-1.53	-2.49	-3.02	-0.2	0.38	-1.27	0.69	0.33	0.39	-0.8	-1.3	-1.4	0.33	-1.16	-1.86	-0.22	-0.94	-1.44	2.05	115.2	15.4	
Che_02239 polye amino acid ABC transporter, inner membrane	9.52	9.68	8.08	8.02	8.13	9.15	0.74	-0.04	0.06	-0.62	1.44	1.54	0.39	-0.19	-1.05	-1.73	-0.27	0.22	0	0.21	0.36	0.3	-0.6	-0.8	0.33	-0.36	-0.92	-0.2	-0.3	-0.7	2.39	3.54	14.46	
Che_05079 Ragulator biosynthesis	8.97	8.09	6.73	6.92	6.98	7.22	-0.88	-0.19	-0.24	2.24	1.17	1.99	0.87	-0.25	-0.3	0.86	-0.56	1.27	0.55	0.36	0.19	0.2	0.02	0.33	0.07	0	0.22	0.04	0.02	1.13	0.6	0.51	0.1	
Che_02276 AAA ATPase, central region	14.4	14	12.4	12.7	11.3	12	0.36	0.1	-0.69	1.94	1.32	1.95	1.36	-0.87	-0.22	-0.28	-0.32	0.54	0.24	0.58	0.55	0.53	0.33	0.33	0.07	0.67	0.22	0.76	0.54	2.34	7.41	6.7		
Che_03013 hydrogense expression/formation protein HygE	0.31	10.2	8.61	8.17	7.82	8.84	-0.05	-0.5	-1.07	0.7	1.04	0.56	0.33	-0.14	-0.71	-1.26	-1.33	-1.5	-0.1	0.13	-0.3	-0.2	-0.2	0.37	0.07	-0.67	0.22	0.15	-0.04	0.17	0.31	0.4	0.1	
Che_00699	7.54	6.67	5.14	5.21	3.56	5.81	-0.87	-0.22	-0.45	2.11	1.46	2.18	0.86	0.07	-0.6	0.85	0.72	0.57	0.5	0.32	0.44	0.19	-0.1	-0.1	0.32	0.25	-0.01	0.21	0.18	0.05	1.07	1.06	0.55	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98	0.87	-0.22	-0.4	0.31	0.58	0.62	0.58	0.13	0.3	0.39	0.49	0.39	0.32	0.31	0.79	0.21	0.95	0.54	1.09	10.42	29.14	
Che_01551	0.31	9.41	8.01	8.25	8.91	9.87	-0.22	-0.25	-1.16	1.08	1.02	1.98																						



Che_03661 Nucleotidyl transferase	128	12.5	11.6	12	13	13.7	0.27	-0.4	0.87	1.23	0.56	-1.07	-2.21	-2.3	-2.77	0.11	-1.22	-0.83	0.12	-1	-1.1	-1.2	-1.3	0.15	-1.31	-1.53	0.07	-1.06	-1.18	0.26	4.06	3.97		
Che_04240 transcriptional regulator, GntR family	119	12.6	11.8	11.6	10.8	11.1	1.31	-0.18	-0.87	2.16	0.87	3.35	1.46	1.18	0.19	0.14	-0.53	0.15	0.37	0.18	0.1	0.1	0.1	0.15	0.17	0.08	0.07	0.35	0.7	1.7	4.86			
Che_05212 RNA-directed RNA polymerase sigma factor	105	12.5	10.6	10.9	10.5	10.2	1.16	-0.35	-0.61	0.27	1.15	0.87	2.85	1.36	0.27	-1.2	-1.06	-0.13	0.35	0.73	1.48	1.12	0.17	0.13	0.17	0.18	0.07	0.32	1.3	0.38	1.1			
Che_05208 transcriptional regulator, Lac family	8.58	7.97	7.34	7.02	7.79	8.46	0.61	0.32	0.67	1.24	0.95	0.79	0.49	-0.45	-1.44	0.53	1.03	-0.17	0.12	0.08	-0.2	-0.3	-0.6	-0.15	-0.3	-0.51	-0.07	-0.26	-0.38	0.25	1.72	2.13		
Che_05101 cist envelope protein, sigma factor	8.95	7.75	7.37	7.57	8.29	8.46	0.74	-0.19	-0.36	0.76	1.06	0.74	0.34	-0.24	-1.40	0.26	0.76	-0.27	0.17	0.12	0.07	0.1	0.1	0.15	0.17	0.17	0.07	0.26	0.41	2.33	0.84			
Che_05746 binding protein-dependent transport systems	9.79	9.97	8.61	8.69	9.44	10.1	-0.18	-0.08	-0.62	1.18	1.28	0.35	-0.09	-0.83	-1.37	-0.44	-0.22	0	0.124	0.04	-0.2	-0.5	-0.6	-0.14	-0.32	-0.17	-0.07	-0.27	0.54	1.06	2.14	1.27		
Che_01796 Prephenate dehydrogenase	13.4	14.5	13.3	13.6	13	13.8	0.24	-0.25	-0.78	0.86	0.95	1.27	0.73	0.31	-0.22	-0.52	0.75	-0.53	0.24	0.18	0.31	0.05	0.06	0.15	0.02	0.06	0.07	0	0.06	0.18	0.43	0.28		
Che_02082 hypothetical protein	13.5	11.9	12.9	12.3	11.6	11.4	-0.43	-0.36	-0.71	1.37	1.45	1.16	1.1	0.1	-0.17	-0.17	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	0.15	-0.18	-0.5	0.07	0.16	0.54	1.15	1.15	3.17		
Che_01839 Radical SAM	13.9	14.3	12.7	12.8	12.1	11.8	-0.36	-0.17	-0.61	1.27	1.46	2.74	2.49	1.47	1.03	-0.67	-0.5	0.013	0.13	0.32	0.68	0.9	0.6	0.73	0.14	0.99	0.87	0.78	0.7	0.83	3.84	6.29		
Che_05230 glutamate 1-semialdehyde 2,1-aminomutase	4.58	3.81	3.7	3.2	4.95	2.99	0.77	0.68	0.34	1.58	1.49	-0.37	-1.48	-1.95	-2.97	0.71	2.16	0.89	0.27	0.33	0.7	-0.8	-1	-1.4	-0.14	-0.8	-1.38	-0.07	-0.46	-1.06	0.37	2.04	2.46	
Che_01961 Nucleotidyl transferase	13.5	11.9	12.9	12.3	11.6	11.4	-0.43	-0.36	-0.71	1.37	1.45	1.16	1.1	0.1	-0.17	-0.17	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	0.15	-0.18	-0.5	0.07	0.16	0.54	1.15	1.15	3.17		
Che_00808 metal dependent phosphohydrolase	8.09	8.29	7.13	6.83	8.82	7.4	1.3	0.28	-0.58	1.48	1.46	1.77	-0.11	-0.29	-0.57	1.38	0.91	0.13	0.23	0.1	0.27	-0.2	0.04	-0.1	0.14	0.05	0	0.02	0.02	0.33	0.58	0.49		
Che_02382 hypothetical protein	9.48	10.3	8.99	9.18	7.88	8.61	-0.84	-0.29	-0.73	0.59	1.14	1.16	1.71	1.01	0.57	-1.26	-0.87	-0.37	-0.17	0.19	0.56	1.88	0.48	0.15	0.3	0.47	0.07	0.22	0.38	0.3	1.02	2.16		
Che_02107 membrane protein-like protein	8.95	7.75	7.37	7.57	8.29	8.46	0.74	-0.19	-0.36	0.76	1.06	0.74	0.34	-0.24	-1.40	0.26	0.76	-0.27	0.17	0.12	0.07	0.1	0.1	0.15	0.17	0.17	0.07	0.26	0.41	2.33	0.84			
Che_01845 Heavy metal transport/ detoxification protein	8.43	7.74	6.78	6.82	7.93	8.75	0.69	-0.04	-0.82	1.65	0.92	0.5	-1.01	-1.15	-1.93	0.63	-0.09	-0.67	0.33	0.7	-0.3	-0.6	-0.6	-0.9	-0.15	-0.48	-0.97	-0.07	-0.4	-0.74	0.97	1.69	5.29	
Che_02676 GntM	13.6	13.5	12.3	12.8	12.4	13.4	0.1	-0.12	-0.53	1.33	1.11	0.8	0.17	-0.53	-0.94	-0.1	0.34	0.3	0.16	0.16	-0.2	-0.1	-0.3	-0.3	0.14	-0.12	-0.41	-0.07	-0.11	-0.3	1.28	1.4	3.48	
Che_05044 glyoxylate-AMC synthetase	13.1	13	11.8	11.9	11.2	11.9	-0.1	-0.1	-0.46	1.32	1.1	1.6	0.02	-0.71	-1.06	-0.07	-0.28	0.35	0.16	0.15	-0.2	-0.1	-0.4	0.15	-0.18	-0.5	0.07	0.16	0.54	1.15	1.15	3.17		
Che_01961 Nucleotidyl transferase	12.8	12.5	11.6	12	13.9	14.7	0.27	-0.4	0.87	1.23	0.56	-1.07	-2.21	-2.3	-2.77	0.11	-1.22	-0.83	0.12	-1	-1.1	-1.2	-1.3	0.15	-1.31	-1.53	0.07	-1.06	-1.18	0.26	4.06	3.97		
Che_05425 inorganic phosphatase	14	13.9	12.7	13.1	12.8	13.4	0.03	-0.36	-0.51	1.27	0.88	1.13	0.59	-0.14	-0.29	0.19	-1.09	0.37	0.13	0.05	0	0.07	-0.2	0.02	0.14	0.02	-0.01	0.07	0	0.01	0.25	0.39	0.47	
Che_03480 Heavy metal transport/ detoxification protein	8.43	7.74	6.78	6.82	7.93	8.75	0.69	-0.04	-0.82	1.65	0.92	0.5	-1.01	-1.15	-1.93	0.63	-0.09	-0.67	0.33	0.7	-0.3	-0.6	-0.6	-0.9	-0.15	-0.48	-0.97	-0.07	-0.4	-0.74	0.97	1.69	5.29	
Che_02382 major facilitator superfamily MFS_1	10.9	10.7	9.71	10	9.24	9.83	0.18	-0.32	-0.59	1.19	0.89	1.66	0.88	-0.09	0.47	0.2	0	0.97	0.1	0	0	0.2	0.2	0.13	0.28	0.13	0.28	0.16	0.06	0.21	0.34	0.22	6.76	1.06
Che_01713 dihydroxy acid dehydratase	12.6	13.5	11.9	12.2	12.3	13.2	-0.19	-0.31	-0.94	0.71	1.3	0.27	0.23	-0.44	-1.07	-1.33	0.94	-1.01	-0.1	0.25	0.4	-0.1	-0.4	-0.3	-0.02	-0.29	-0.06	0.03	-0.21	0.34	0.53	1.17	1.17	
Che_01735 outer domain-containing protein	7.77	7.42	6.77	6.55	6.09	6.75	0.35	0.22	-0.66	1	0.87	1.68	0.7	0.68	-0.2	0.21	0.72	-0.13	0.02	0.05	0.23	0.11	0.23	0.07	0.13	0.2	0.13	0.06	0.14	0.12	0.14	2.35	1.1	
Che_01955 RNA binding S1	10.7	11.1	9.37	9.61	8.81	10.16	-0.32	-0.24	-0.76	1.37	1.45	0.93	0.49	-0.44	-0.96	-0.62	-0.72	-0.47	0.18	0.32	-0.1	0.03	0.3	-0.3	0.13	0.07	-0.32	0.06	-0.07	-0.23	0.77	0.3	1.76	
Che_01962 dihydrodipicolinate synthase	13.3	14.8	12.2	12.5	12.1	12	-1.54	-0.3	-0.78	1.06	2.3	2.05	2.81	0.99	-0.51	-2.12	-0.91	-0.53	0.04	0.71	0.39	1.03	0.7	0.45	0.13	0.62	0.42	0.06	0.48	0.34	0.62	1.15	1.84	
Che_01791 3-phosphoglycerate 1-carboxyvinyltransferase	14.4	14.8	13.5	13.8	13.5	14.7	-0.37	-0.36	-0.76	0.93	1.04	0.97	0.58	0.04	-0.46	-0.68	-0.78	-0.47	-0.13	0.11	0.07	-0.1	-0.1	0.13	0.08	-0.01	0.06	-0.08	-0.01	0.25	0.29	0.39	0.9	
Che_01713 dihydroxy acid dehydratase	12.6	13.5	11.9	12.2	12.3	13.2	-0.19	-0.31	-0.94	0.71	1.3	0.27	0.23	-0.44	-1.07	-1.33	0.94	-1.01	-0.1	0.25	0.4	-0.1	-0.4	-0.3	-0.02	-0.29	-0.06	0.03	-0.21	0.34	0.53	1.17	1.17	
Che_01011 aminotransferase, class I and II	8.85	10	7.92	8.05	6.21	6.57	-1.18	-0.13	-0.36	0.93	1.88	2.64	3.46	1.71	-1.18	-1.68	-0.88	-0.67	0.56	0.64	1.32	0.71	0.97	0.13	1.05	1.06	0.28	0.82	0.84	0.65	1.76	4.22		
Che_05316 transposase, mutator type	9.29	7.64	6.79	7.2	6.89	8.05	-1.05	-0.45	-1.7	2.34	1.44	2.44	-0.91	-1.1	-1.8	-0.68	-0.48	-0.2	0.36	0.41	-0.1	-0.4	0.13	-0.08	-0.01	0.06	0.4	0.65	0.81	0.45	0.48	1.49		
Che_01613 Ribonuclease H	11.3	10.9	9.64	9.88	9.05	9.66	0.34	-0.24	-0.61	1.62	1.04	2.21	1.26	0.59	0.22	0.2	0.72	0.03	0.29	0.14	0.46	0.36	0.18	0.29	0.13	0.54	0.23	0.06	0.42	0.2	0.85	1.56	1.68	
Che_01512 flagellin-like protein	6.57	6.13	4.97	4.58	4.25	4.75	1.44	-0.41	-0.5	2.4	0.55	2.32	0.88	-0.08	-0.17	-1.56	-1.25	0.48	-0.27	-0.13	0.5	-0.1	-0.09	0.13	0.15	-0.04	0.06	0.1	-0.02	0.63	0.71	0.4		
Che_05316 methyl-accepting chemotaxis sensory transducer	8.1	7.38	6.48	6.43	5.32	5.29	0.77	0.05	-0.3	1.62	0.95	1.42	0.78	0.29	0.05	0.03	0.06	0.29	0.38	0.37	0.3	-0.5	0.7	0.12	0.15	0.08	0.07	0.07	0.07	0.07	0.07	0.07		
Che_00962 dihydrodipicolinate synthase	13.3	14.8	12.2	12.5	12.1	12	-1.54	-0.3	-0.78	1.06	2.3	2.05	2.81	0.99	-0.51	-2.12	-0.91	-0.53	0.04	0.71	0.39	1.03	0.7	0.45	0.13	0.62	0.42	0.06	0.48	0.34	0.62	1.15	1.84	
Che_03036 methyl-accepting chemotaxis sensory transducer	8.1	7.38	6.48	6.43	5.32	5.29	0.77	0.05	-0.3	1.62	0.95	1.42	0.78	0.29	0.05	0.03	0.06	0.29	0.38	0.37	0.3	-0.5	0.7	0.12	0.15	0.08	0.07	0.07	0.07	0.07	0.07	0.07		
Che_05315 sulfate ABC transporter, periplasmic	8.58	7.97	7.34	7.02	7.79	8.46	0.61	0.32	0.67	1.24	0.95	0.79	0.49	-0.45	-1.44	0.53	1.03	-0.17	0.12	0.08	-0.2	-0.3	-0.6	-0.15	-0.3	-0.51	-0.07	-0.26	-0.38	0.25	1.72	2.13		
Che_05551 AMP-dependent synthetase and ligase	13.5	13.5	12.1	12.3	12.5	13.2	0.02	-0.19	-0.72	1.41	1.2	1.07	0.33	0.34	-0.87	-0.2	-0.56	-0.33	0.19	0.2	0	-0	-0.3	-0.3	0.13	0.2	-0.29	-0.06	-0.04	-0.21	0.93	0.33	1.96	
Che_01572 beta-lactamase-like protein	9.77	7.89	7.29	7.62	7	4.32	1.80	-0.33	-1.32	2.48	0.27	0.67	3.57	4.29	5.3	2.1	-1	-2.38	0.66	0.14	0.28	1.93	1.94	0.12	-2.1	2.36	0.19	1.86	1.86	1.6	2.02	3.6		
Che_01470 RNA polymerase sigma 24-subunit, ECF family	10.2	9.58	8.76	8.86	8.08	8.54	-0.15	-0.22	-0.62	1.44	1.12	1.02	1.04	0.02	-0.4	-0.4	0.02	0.4	0.11	0.09	0.46	0.83	0.45	0.12	0.16	0.13	0.06	0.07	0.07	0.07	0.07	0.07		
Che_05316 hypothetical protein	10.3	10.2	8.87	9.06	7.64	7.92	0.11	-0.19	-0.46	1.43	1.13	2.84	2.27	1.41	1.14	0.09	-0.56	0.33	0.22	0.17	0.73	0.8	0.17	0.12	0.06	0.06	0.05	0.07	0.09	0.63	4.58	4.21		
Che_02308 CheC-like protein	6.78	6.32	5.32	5.13	4.07	8.79	0.46	-0.19	-0.27	1.46	1.19	-1.29	-2.47	-2.75	-1.68	0.85	-0.62	-0.38	0.22	0.12	-0.1	-0.1	-0.14	-0.18	-0.12	-0.15	-0.15	-0.15	-1.66	0.84	7.77	10.72		
Che_02947 dihydroacet																																		



Che_00874 glutamine amidotransferase of anthranilate	8.34	9.93	7.61	7.98	7.88	8.04	-1.59	-0.37	-0.16	0.73	1.95	0.46	1.89	-0.27	-0.06	-0.29	-1.12	1.53	-0.1	0.55	-0.3	0.64	0.2	0.14	0.06	0.12	-0.02	0	0.08	0	0.45	0.6	0.46	
Che_02821 response regulator receiver modulated CheB	7.48	7.29	5.98	6.25	5.67	6.29	0.19	-0.27	-0.48	1.5	1.04	1.45	1.1	-0.21	-0.04	0.00	-0.81	0	0.23	0.13	0.26	0.25	0.05	0.16	0.06	0.37	0.05	0	0.28	0.01	0.45	0.63	0.81	0.69
Che_03550 catalase terminal protein	9.39	10.2	8.56	9.21	8.83	9.21	0.11	-0.22	-0.14	0.38	0.83	0.37	1.15	-0.22	-0.04	0.00	-0.48	0.027	0	0.13	0.21	0	0	0	0	0.17	0.05	0	0.11	0.01	0.31	0.76	0.81	0.76
Che_02821 response regulator receiver modulated CheB	7.48	7.29	5.98	6.25	5.67	6.29	0.19	-0.27	-0.62	1.5	1.04	1.81	1	0.31	-0.04	0.01	-0.81	0	0.23	0.13	0.28	0.25	0.05	0.16	0.06	0.37	0.05	0	0.28	0.05	0.65	0.83	0.69	
Che_02820 SEC C-terminal protein	11.2	10.2	9.55	10.11	9.57	10.17	0.19	-0.22	-0.33	0.71	0.83	0.67	0.83	0.12	-0.04	0.01	-0.48	0.02	0	0.13	0.21	0	0	0	0	0.17	0.05	0	0.11	0.01	0.33	0.62	0.81	0.69
Che_01573 hypothetical protein	10.05	10.5	8.95	9.19	9.01	9.64	-0.24	-0.24	-0.63	1.28	1.28	1.28	1.28	-0.03	-0.06	-0.46	-0.52	-0.72	-0.03	0.14	0.06	0.43	0.18	-0.1	-0.1	0.06	0.07	0	0.04	-0.01	0.63	0.8	0.62	
Che_01172 protein of unknown function DUF362	12.6	12.5	11.4	11.6	11.97	10.7	-0.08	-0.24	-0.7	1	1	1	1	0.96	-0.12	-0.72	-0.27	-0.21	0.1	0.24	0.04	0.62	0.18	0.69	0.06	0.83	0.79	0	0.65	0.63	0.34	0.85	0.91	
Che_01517 phage putative tail completion protein	10.05	10.5	8.95	9.19	9.01	9.64	-0.24	-0.24	-0.7	1	1	1	1	0.96	-0.12	-0.72	-0.27	-0.21	0.1	0.24	0.04	0.62	0.18	0.69	0.06	0.83	0.79	0	0.65	0.63	0.34	0.85	0.91	
Che_01410 canal diffusion factor binding protein	10	11.6	9.94	9.81	10.1	10.7	-1.61	-0.13	-0.69	0.08	1.82	-0.03	0.89	-0.11	-0.03	-0.21	-0.44	-0.23	-0.4	0.49	0.5	0.2	-0.2	-0.3	0.06	-0.07	-0.28	0	0.07	-0.2	0.55	0.57	0.37	
Che_02081 small Cif-binding protein	9.25	9.45	8.16	8.28	8.33	9.02	-0.42	-0.12	-0.69	1.09	1.17	0.92	0.43	-0.17	-0.74	-0.47	-0.34	-0.23	0.06	0.19	-0.1	-0.1	-0.2	-0.2	0.05	-0.02	-0.22	-0.01	-0.03	-0.16	0.69	0.43	0.26	
Che_00318 Glutamine synthetase (NADH)	8.88	8.88	6.02	6.32	6.22	6.32	-0.46	-0.3	-0.46	0.3	0.3	0.3	0.3	-0.05	-0.17	-0.05	-0.3	-0.05	-0.17	-0.05	-0.3	-0.05	-0.3	-0.05	0.03	-0.17	-0.05	-0.3	-0.05	-0.3	0.16	0.74	1.17	
Che_01513 Holliday junction tensionase YagH	7.85	7.62	6.77	6.88	5.55	5.83	0.19	-0.11	-0.28	0.14	0.74	2.26	1.79	1.22	-1.05	0.01	-0.31	1.13	0.08	0	0.48	0.58	0.48	0.74	0.05	0.51	0.71	-0.01	0.39	0.57	0.2	1.53	2.51	
Che_01504 amino acid acetylation domain	9.59	9.25	4.39	4.47	5.95	6.49	0.08	0.22	-0.34	1.54	1.08	-0.02	-1.24	-1.56	-1.22	0.62	0.72	0.27	0.25	0.14	-0.5	-0.7	-0.8	-1.1	-0.05	0.73	-1.23	-0.01	0.46	-0.95	0.6	2.97	5.84	
Che_02339 glycol transferase	11.9	12.8	9.18	9.1	9.19	10.9	-0.17	-0.11	-0.36	0.71	0.83	0.67	0.71	-0.11	-0.46	-0.07	-0.18	0.01	0.01	0.12	0.13	0.27	0.13	0.25	0.03	0.19	0.17	-0.02	0.34	0.15	0.7	1.1	1.87	
Che_01213 penicillinic sensor signal transduction histidine	9.27	8.85	7.68	7.78	7.88	8.4	0.62	-0.01	-0.47	1.39	0.76	1.49	0.17	0.1	-0.59	-0.54	0	-0.27	0.19	0	0.14	-0.1	-0.1	-0.1	-0.05	0.01	-0.11	-0.02	-0.02	-0.07	0.7	0.67	1.84	
Che_02584 penicillinic sensor signal transduction histidine	11.1	9.2	9.14	9.28	8.38	8.65	1.92	-0.14	-0.47	1.98	0.08	2.94	0.55	0.96	0.63	2.15	-0.41	0	-0.44	-0.4	0.77	0.06	0.36	0.51	-0.05	0.29	0.53	-0.01	0.22	0.43	0.54	0.8	3.22	
Che_02318 predicted ATPase of the PP-loop superfamily	12.1	9.04	8.67	8.77	9.45	9.45	1.15	-0.2	-0.78	1.86	0.05	2.86	0.05	0.53	-0.12	0.66	-0.02	0.39	0.07	0.74	0.22	0.17	0.17	0.17	-0.05	0.48	-0.01	-0.27	0.38	1.18	1.67	1.84		
Che_01106 twitching motility protein	11.3	11.1	11.5	11.9	12.4	11.1	0.01	-0.36	-0.61	1.55	1.18	0.62	0	-0.89	-1.18	-0.21	-0.09	0.26	0.19	-0.2	-0.2	-0.5	-0.5	-0.5	0.04	-0.25	-0.53	-0.02	-0.22	-0.4	0.58	3.13	2.13	
Che_01022 RNA (guanine N7)-O <sup>6</sup> -methyltransferase	10.03	9.85	8.92	9.29	8.92	9.48	0.03	-0.53	-0.41	0.63	0.94	-0.07	-0.47	-0.37	-0.91	-0.03	0.19	0.1	-0.1	-0.2	-0.3	-0.2	-0.2	0.04	-0.13	-0.23	-0.02	-0.12	-0.16	0.41	1.11	1.31		
Che_00751 Cif-binding protein	13.4	11.5	10.7	10.7	10.7	10.7	0.38	-0.36	-0.11	0.67	2.57	1.93	1.47	1.03	-0.17	0.82	0.03	0.87	0.06	0.61	0.65	0.65	0.77	0.77	0.03	0.17	0.85	-0.02	0.54	0.68	1.02	2.31	3.74	
Che_01423 protein of unknown function UPP0118	11.3	10.8	9.96	9.78	9.18	9.64	0.44	-0.17	-0.46	1.32	1.05	2.1	1.2	0.78	0.15	0.32	0.56	0.38	0.16	0.13	0.41	0.34	0.27	0.26	0.04	0.4	0.26	-0.02	0.33	0.22	0.64	1.96	1.62	
Che_02034 serine/threonine protein kinase	9.48	9.87	8.09	8.26	7.9	8.57	0.51	-0.17	-0.67	1.39	0.71	1.58	0.4	0.19	-0.31	-0.41	-0.5	-0.17	0.19	0	0.18	0	0	0.01	0.03	0.08	0.07	-0.02	0.05	0.07	0.59	0.92	0.06	
Che_02036 methyltransferase	12.1	12.2	11.1	11.1	10.8	11.1	-0.09	-0.04	-0.5	0.98	1.03	1.46	1.05	0.48	-0.02	-0.33	-0.09	0.4	0.01	0.12	0.13	0.27	0.13	0.25	0.03	0.19	0.17	-0.02	0.34	0.15	0.7	1.1	1.87	
Che_02343 GCN5-related N acetyltransferase	7.77	8.9	7.5	7.45	8.64	9	-1.13	0.05	-0.36	0.27	1.45	-0.87	-0.1	-1.14	-1.55	-1.62	-1.19	0.87	-0.1	0.32	-0.9	-0.2	-0.6	-0.7	-0.51	-0.51	-1.77	-0.02	-0.42	-0.59	0.54	1.12	3.39	
Che_02788 histone protein	2.85	1.58	1	2.81	4	1.23	-1	-1.19	2.81	0.58	0	-2.42	-2.81	3	1.3	-3.09	-1.9	0.8	-0.1	0.5	-1.2	-1.4	-1.4	-1.4	0.03	-0.82	-1.47	-0.02	-0.67	1.13	0.48	1.31	1.85	
Che_01453	7.01	6.71	5.71	5.95	5.21	5.73	0.3	-0.22	-0.34	1.38	0.76	1	1	0.96	-0.32	0.13	-0.66	0.27	0.14	0	0.28	0.31	0.15	0.28	0.03	0.29	0.21	-0.02	0.22	0.38	0.41	2.67	1.48	
Che_00319 class II adolabax/aducan-like protein	9.53	9.81	8.57	8.71	8.71	9.13	-0.28	-0.14	-0.43	0.96	1	1	0.83	0.68	-0.42	-0.57	-0.41	0.63	0	0.15	0.1	0.11	-0.2	-0.1	-0.01	-0.01	-0.05	-0.02	-0.02	-0.43	0.48	0.74	0.74	
Che_00395 RhoB or Huc1 transducer	18.7	16.7	15.8	16.1	14.3	14.9	-0.46	-0.3	-0.62	1.42	0.66	2.93	1.85	-1.51	1.39	-0.35	-0.91	0	0.2	0.1	0.77	0.62	0.62	0.81	0.04	0.91	-0.08	-0.02	0.71	0.7	0.42	6.42	3.74	
Che_00751 transcriptional regulator, XRE family with cognate	8.01	8.78	8.28	8.37	8.95	1.07	-0.05	-0.48	-0.77	0.65	1.08	-0.07	-0.69	-1.32	1.39	-0.12	0.38	-0.1	0.2	0.38	-0.1	-0.1	-0.4	-0.4	-0.03	-0.04	-0.06	-0.44	-0.22	-0.48	0.36	0.93	0.66	
Che_01006 glycol transferase, family 28	6.71	6.29	4.58	5.09	4.63	6.87	1.42	-0.51	-0.44	2.13	0.2	0.28	-1.58	-1.87	-1.38	-1.53	-1.66	0.6	0.51	-0.3	-0.4	-0.9	-1	-0.8	-0.03	-0.59	-0.99	-0.02	-0.49	-0.76	0.53	1.31	2.48	
Che_01120 transcriptional regulator, Lac family	11.6	11.3	10.3	10.5	9.43	10.1	0.26	-0.16	-0.44	1.28	0.86	2.15	1.25	-0.87	-0.39	0.1	-0.47	-0.74	0.34	0.04	0.43	0.36	0.32	0.39	0.03	0.53	-0.43	-0.02	-0.41	-0.63	0.61	1.044	3.54	
Che_00344 serine/threonine protein kinase	9.48	9.87	8.09	8.26	7.9	8.57	0.51	-0.17	-0.67	1.39	0.71	1.58	0.4	0.19	-0.31	-0.41	-0.5	-0.17	0.19	0	0.18	0	0	0.01	0.03	0.08	0.07	-0.02	0.05	0.07	0.59	0.92	0.06	
Che_02762 transcriptional regulator like protein	9.13	9.32	8.17	8.17	8.78	9.37	-0.19	0.1	-0.59	0.86	1.15	0.35	0.05	-0.51	-1	-0.46	0.34	-0.1	-0.18	-0.4	-0.2	-0.3	-0.5	-0.4	-0.03	-0.52	-0.02	-0.26	-0.39	0.64	1.95	5.4		
Che_01250 spermidine/putrescine ABC transporter ATPase	10.2	9.99	8.07	8.72	10	10.6	-0.25	0.35	-0.56	1.49	-1.07	1.27	0.23	-0.58	-0.94	-1.85	-0.09	1.12	0	0.09	0.23	-0.4	-0.4	-0.5	-0.8	-0.03	-0.54	-0.48	-0.02	-0.45	-0.61	0.44	6.09	2.85
Che_02061 isopantetheinase protein	9.56	9.43	8.5	8.59	8.29	8.12	0.13	-0.36	-0.41	0.79	1.2	1.3	0.3	0.27	-0.3	-0.43	-0.27	0.1	0.17	0.12	0.1	0.09	0.13	0.13	0.03	0.25	-0.02	-0.03	-0.16	0.38	3.13	1.02		
Che_02113 3-isopropylmalate dehydratase, large subunit	12.3	11.4	11.3	11.7	12.5	11.3	-1.05	-0.38	-0.77	1.04	1.71	-0.2	0.08	-1.24	-1.63	-1.52	-1.16	-0.5	0.07	0.16	0.06	-0.6	-0.2	-0.7	0.04	-0.26	-0.79	-0.02	-0.22	-0.6	0.46	0.86	2.28	
Che_02278 extracellular sulfo-binding protein, family 3	10.53	11.5	12.5	12.5	5.36	6.3	-0.57	0.05	-0.49	1.33	0.81	8.53	7.02	1.2	6.21	6.48	1.07	0.13	0.08	0.02	0.2	2.86	3.5	3.5	0.03	0.43	4.65	-0.02	1.23	3.65	0.62	8.32	14.75	
Che_02061 isopantetheinase protein	9.56	9.43	8.5	8.59	8.29	8.12	0.13	-0.36	-0.41	0.79	1.2	1.3	0.3	0.27	-0.3	-0.43	-0.27	0.1	0.17	0.12	0.1	0.09	0.13	0.13	0.03	0.25	-0.02	-0.03	-0.16	0.38	3.13	1.02		
Che_02034 serine/threonine protein kinase	9.48	9.87	8.09	8.26	7.9	8.57	0.51	-0.17	-0.67	1.39	0.71	1.58	0.4	0.19	-0.31	-0.41	-0.5	-0.17	0.19	0	0.18	0	0	0.01	0.03	0.08	0.07	-0.02	0.05	0.07	0.59	0.92	0.06	
Che_01120 twitching motility protein	11.3	11.1	11.5	11.9	12.4	11.1	0.01	-0.36	-0.61	1.55	1.18	0.62	0	-0.89	-1.18	-0.2																		



Che_00712 cytidylate kinase	13	13.4	12.4	12.5	12.1	6.7	-0.46	-0.04	-0.53	0.52	0.94	0.9	0.83	0.38	-0.11	-0.79	-0.09	0.3	-0.02	0.08	-0.1	0.18	0.08	0.12	-0.01	0.03	0.1	0.06	0.01	0.09	0.52	0.57	1.53
Che_01291 UvrC/Protein	11.6	10.5	10.4	10.2	11.2	11.9	1.14	0.09	-0.69	1.15	1.1	-1.1	-0.43	-0.75	-1.53	1.19	0.31	-0.23	0.08	-0.3	-0.4	-0.5	-0.46	-0.01	-0.6	-0.07	-0.6	-0.06	-0.3	-0.55	0.52	1.62	6.76
Che_01515 MspZ/Start transporter	9.21	9.29	8.9	8.04	8.7	8.8	-0.79	-0.18	-0.34	-0.29	0.1	0.14	-0.34	-0.39	-0.54	0.37	0.19	0.57	0.08	-0.2	0.43	0.0	0.13	-0.01	-0.37	-0.19	-0.7	-0.13	0.31	0.3	0.89	0.89	
Che_01510 RNA modification enzyme, MAb family	9.33	9.21	8.53	8.76	10.4	11.2	0.12	-0.23	-0.76	0.8	0.45	-0.07	-1.95	-1.87	-2.4	0.07	-0.69	-0.47	0.1	-0.2	-1	-1	-1	-1	-0.01	-0.31	-1.36	-0.06	-1.06	-1.05	0.48	6.77	5.91
Che_02601 4-6 ferredoxin-like protein	8.11	7.43	7.1	6.88	7.3	7.5	-0.17	-0.33	-0.08	0.08	1.35	-0.17	-0.81	-0.87	-0.98	0.1	0.01	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	
Che_02795 pyruvate ferredoxin/NADoxin oxidoreductase	11.2	11.7	10.6	10.6	11	11.5	-0.47	0.01	-0.48	0.6	1.08	0.21	0.2	-0.39	-0.88	-0.38	0.06	-0.47	0.14	0.4	-0.1	-0.3	-0.3	-0.01	-0.23	-0.23	-0.36	-0.19	-0.24	0.53	1.03	2.84	
Che_01232 AMP-dependent kinase	11.7	11.7	11.9	11.9	12.2	12.6	0.14	0.03	-0.15	-0.14	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1		
Che_04049 flagellar signal protein FljI	6.54	6.15	5.76	5.61	5.64	5.7	0.39	0.17	-0.06	0.76	0.54	0.9	0.45	0.14	-0.09	0.26	0.56	1.87	-0.1	-0.1	-0.01	0	0.13	-0.01	-0.3	0.16	-0.06	-0.26	0.14	0.46	0.13	0.23	
Che_00530 heat shock protein Hsp90	9.85	9.14	8.82	8.73	9.07	10.4	0.71	0.09	-0.41	1.03	0.41	-0.12	-1.24	-1.15	-1.65	0.65	0.31	0.7	0.01	-0.2	-0.6	-0.7	-0.6	-0.7	-0.01	-0.7	-0.84	-0.06	-0.58	0.64	0.48	2.17	4.16
Che_00809 lipopolysaccharide transferase	9.15	9.15	9.12	9.02	9.02	9.7	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11	-0.11		
Che_00024 biotin biosynthesis protein BiotC	5.21	6.13	5.04	5.09	6.43	7.04	-0.92	-0.05	-0.61	0.17	1.04	-1.22	-0.91	-1.39	-1.95	-1.36	-0.12	0.03	-0.3	-0.1	-0.6	-0.8	0.09	-0.02	-0.88	-1.1	-0.07	-0.72	0.87	0.53	1.97	30.95	
Che_00033 small GTP-binding protein	8.61	9.41	9.42	9.21	7.58	8.11	-0.8	-0.07	-0.53	0.47	1.2	1.03	1.3	0.56	0.1	-1.21	-0.19	0.3	0.2	-0.2	-0.1	-0.38	0.17	0.23	-0.01	0.11	0.23	-0.07	0.27	0.47	0.7	2.68	
Che_00377 hypothetical protein	9.98	9.12	9.06	9.06	9.08	9.17	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06	-0.06		
Che_00599 thapsigargin-binding protein Thst	10.2	10.7	9.75	9.9	9.2	10.2	-0.48	-0.17	-1.01	0.48	0.79	1.01	0.48	0.53	-0.31	-0.81	-0.5	-1.3	-0.2	-0.01	-0.1	0.38	0.16	0.01	-0.02	-0.28	0.05	-0.07	-0.22	0.05	0.44	0.11	0.38
Che_01052 competence/damage inducible protein CnaK	10.3	10.6	8.87	10.1	8	8.85	-0.33	-0.24	-0.85	0.43	0.52	2.3	1.78	1.87	1.26	-0.63	-0.72	-0.77	-0.27	-0.1	0.5	0.39	0.79	0.85	-0.02	0.55	1	0.07	0.42	0.8	0.54	1.77	3.67
Che_01188 protein of unknown function DUF990	9.31	10.7	9.84	8.59	9.19	-1.42	-0.36	-0.08	-0.17	0.79	1	1.4	1.7	1.95	1.98	-1.09	-0.23	-0.3	0.01	0.57	0.5	0.68	0.01	-0.02	0.14	-0.08	-0.07	0.3	0.47	0.66	1.54		
Che_01841 hypothetical protein	9.87	10.9	9.81	9.85	10.6	11.4	-1.07	-0.04	-0.8	0.06	1.09	-0.7	-0.43	-0.76	-1.52	-1.54	-0.09	-0.6	-0.4	0.15	-0.8	-0.4	-0.5	-0.6	-0.03	-0.53	-0.69	-0.07	-0.44	-0.52	0.54	1.22	4.3
Che_02523 thapsigargin family protein	9.83	9.3	8.64	8.62	8.18	8.7	-0.08	-0.04	-0.75	1.04	0.7	1.56	0.43	0.52	-0.27	0.25	0.16	-0.43	0.05	0	0.17	0.31	0.25	-0.03	-0.03	0.06	-0.07	0.03	0.08	0.29	0.78	1.11	
Che_02453 hypothetical protein	10.5	9.57	9.27	9.27	9.26	9.54	0.05	-0.07	-0.78	1.52	0.13	2.36	0.03	1.04	0.53	0.85	-0.19	0.53	0.16	-0.2	0.52	0.05	0.25	-0.03	-0.29	0.45	-0.07	0.02	0.36	1.1	3.15		
Che_02688 polyphosphate biosynthesis protein	9.98	9.5	9.26	9.04	8.23	8.63	-0.48	0.22	-0.4	0.72	0.46	1.75	0.87	1.03	0.41	0.37	0.72	0.73	-0.1	0.1	0.26	0.19	0.39	-0.04	-0.14	0.4	-0.07	0.1	0.33	0.43	0.89	1.82	
Che_02973 sugar fermentation stimulation protein	10.5	10.5	9.7	9.62	12.2	12.9	-0.15	-0.08	-0.75	0.66	0.89	-1.81	-2.47	-2.47	-3.3	-0.41	0.28	-0.43	0.1	0.06	-1.3	-1.3	-1.6	-0.02	-0.16	-0.4	-0.07	-0.14	-0.17	0.54	0.82	1.61	
Che_03074 Col like hydrolase	8.79	9.4	8.24	8.2	8.57	8.9	-0.55	0.04	-0.1	0.55	1.14	0.22	0.16	-0.33	-0.78	-0.59	0.16	0.7	0.27	0.17	0.4	-0.1	-0.3	-0.2	-0.02	-0.16	-0.24	-0.07	-0.14	0.17	0.54	0.82	1.61
Che_03133 alpha/beta hydrolase fold	9.64	9.85	9.1	9.27	8.04	8.64	-0.21	-0.17	-0.6	0.54	0.58	1.6	1.21	1.06	-0.63	-0.48	-0.5	0.07	-0.2	0.1	0.19	0.34	0.41	0.51	-0.03	0.28	0.58	0.07	0.21	0.47	0.58	1.82	3.42
Che_03155 beta-lactamase like protein	10.4	9.09	9.15	10.3	10.8	10.3	-0.03	-0.06	-0.55	1.34	0.25	0.17	-1.41	-1.17	-1.66	1.05	0.16	0.23	0.16	-0.4	-0.8	-0.7	0.07	-0.02	-0.66	-0.92	-0.07	-0.54	-0.7	0.54	1.9	11.45	
Che_03211 Glucose-6-phosphate isomerase	13.1	13.5	12.6	12.7	13.6	14.6	-0.23	-0.05	-0.58	0.62	1.8	0.22	-0.13	-0.4	-0.93	-0.51	-0.12	0.13	-0.1	0.01	0.4	-0.2	0.3	0.3	-0.02	-0.36	-0.4	-0.07	-0.3	0.37	2.05	8.01	
Che_03814 NADH kinase	12.5	12.7	11.6	11.5	10.3	11	0.23	0.02	-0.71	0.89	0.68	2.16	1.22	1.27	-0.54	0.06	0.09	-0.3	0	-0.43	0.35	0.5	0.47	-0.02	-0.49	0.64	-0.07	0.38	0.32	0.92	4.12	7.3	
Che_01018 binding protein dependent transport systems	15.6	16	15.2	15.4	15.3	15.9	-0.45	-0.2	-0.59	0.38	0.63	0.28	0.41	-0.1	-0.49	-0.78	-0.59	-0.1	-0.1	-0.1	-0.4	-0.1	-0.1	-0.1	-0.02	-0.23	-0.08	-0.07	-0.2	-0.05	0.33	1.15	0.93
Che_01218 extracellular sulfate-binding protein	7.38	6.57	6.39	6.25	6.77	6.6	-0.81	-0.06	-0.6	0.12	0.61	0.06	-0.06	-0.18	-0.78	0.16	0.13	-0.1	0.2	-0.1	0.6	-0.5	-0.6	-0.6	-0.01	-0.43	-0.55	-0.07	-0.36	0.41	0.38	1.72	8.42
Che_01404 inner-membrane transporter	7.36	7.52	6.81	6.81	7.67	8.29	-0.16	-0.14	-0.62	0.69	0.71	-0.31	-0.77	-1	-1.48	-0.42	-0.41	-0	-0.1	-0	-0.6	-0.5	-0.6	-0.6	-0.02	-0.73	-0.77	-0.07	-0.6	0.59	0.42	4.46	6.79
Che_02089 glycylglycine transporter 36	15.3	15.1	14.1	14.3	13.6	13.4	-1.22	-0.26	-0.74	-0.17	0.79	-0.27	0.15	0.44	-0.04	-1.73	-0.78	-0.4	-0.5	0.01	-0.4	0.14	0.11	0.16	-0.02	-0.02	0.06	-0.07	-0.03	0.06	0.52	0.33	0.13
Che_02850 RNA polymerase (sigma 38 subunit, RpoD)	10.3	10.3	11.9	12.3	11.9	12.3	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	-0.13	
Che_02852 DNA-directed RNA polymerase, alpha subunit	13.4	14.8	13.9	14.5	13.4	13.4	-1.39	-0.61	-0.56	-0.53	0.25	0.03	0.76	0.5	0.51	-1.94	-1.88	-0.07	-0.7	0.2	-0.5	0.14	0.45	-0.02	-0.11	0.19	-0.07	-0.1	0.16	0.51	0.63	0.84	
Che_02950 transcribed regulatory protein, GntK family	7.09	7.57	6.23	6.32	6.54	6.4	-0.39	-0.22	-0.88	-0.21	0.77	-0.84	-0.81	-0.44	-0.63	1.49	0.97	1.35	-0	-0.5	-0.2	-0.6	-0.4	-0.02	-0.14	-0.03	-0.07	-0.13	-0.01	0.52	0.66	0.44	
Che_02974 Glucuronide dehydrogenase (NADPH)	12.1	12.6	12.6	12.7	13.1	13.1	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	-0.16	
Che_01795 phospho-2-hydroxy-3-deoxyheptulate kinase	14.3	14.2	13.4	13.5	13.1	13.6	0.1	-0.09	-0.55	0.02	0.63	1.17	0.52	0.3	-0.1	-0.25	-0.23	-0.1	0.1	0.04	0.07	0.12	-0.02	-0.02	0.02	0.09	-0.07	0	0.09	0.08	0.36	1.36	
Che_01822 Extracellular ligand-binding protein	6.98	5.04	4.86	5.17	5.46	6.41	-0.46	-0.71	-1.35	0.12	0.13	0.22	0.3	1	0.56	-0.79	-1.29	-2.45	0.4	-0.1	-0.1	0.38	0.37	-0.03	-0.48	0.04	-0.07	0.4	0.05	0.48	0.07	0.54	
Che_01838 histidine junction (Dna helicase subunit)	9.45	9.45	9.45	9.45	9.45	9.45	-0.24	-0.05	-0.18	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	0.04	
Che_00758 protein of unknown function UPP0202	8.75	8.12	7.86	7.71	6.89	7.49	0.63	0.15	-0.6	0.89	0.41	1.86	0.63	0.97	0.22	0.56	0.5	0.07	-0.2	0.3	0.08	0.36	0.29	-0.02	0.19	0.39	-0.07	0.14	0.32	0.46	1.26	3.05	
Che_01014 Msd2 family protein	11.8	12.1	11.2	11.1	11	11.5	-0.3	-0.07	-0.35	0.52	0.67	0.04	0.55	0.22	-0.42	-0.59	0.25	0.17	-0.2	0.02	0.2	0.08	0.01	-0.01	-0.02	-0.03	-0.01	-0.04	0.01	0.57	0.6	0.36	
Che_01511 DNA-stem-loop binding protein	8.75	9.12	8.56	8.45	8.19	8.2	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	
Che_02449 helicase, RecT/TrfA family	9.29	9.21	8.62	8.92	9.08	9.82																											



Che_02556 Radial SAM	6.99	5.75	5.64	5.46	7.01	7.58	1.24	0.18	0.57	1.35	0.29	-0.02	-1.83	-1.37	-2.12	1.31	0.59	0.17	0.17	0.2	0.5	-1.07	-1.08	-0.81	-1.12	-0.11	-0.66	-0.86	0.39	1.89	6.78		
Che_02557 glyceraldehyde 3-phosphate dehydrogenase, type I	1.73	1.67	1.69	1.76	1.82	1.62	0.16	-0.15	0.57	1.1	0.07	-0.05	-0.48	-0.75	-1.17	0.03	-0.47	0.17	0.02	-0.1	0.43	-0.5	-0.07	-0.52	-0.57	-0.11	-0.48	-0.43	0.72	7.42	4.5		
Che_02558 Fucose 4-epimerase	8.64	8.32	8.58	8.18	8.88	8.31	0.18	-0.15	0.57	1.04	0.01	-0.05	-0.48	-0.75	-1.17	0.03	-0.47	0.17	0.02	-0.1	0.43	-0.5	-0.07	-0.52	-0.57	-0.11	-0.48	-0.43	0.72	7.42	4.5		
Che_02559 inner membrane translocator	14.9	15.8	14.9	15	12.9	13.6	-0.09	-0.15	0.68	-0.04	0.74	1.94	2.16	1.98	1.45	-1.33	-0.44	-0.2	-0.4	0.34	0.75	0.84	0.59	-0.08	0.53	1.2	-0.11	0.41	0.95	0.62	1.39	8.75	
Che_02561 NAD-dependent deaminase/dehydratase	11.5	11.5	11.8	11.2	11.2	11.9	0.01	-0.15	0.68	-0.04	0.74	1.94	2.16	1.98	1.45	-1.33	-0.44	-0.2	-0.4	0.34	0.75	0.84	0.59	-0.08	0.53	1.2	-0.11	0.41	0.95	0.62	1.39	8.75	
Che_02564 transcriptional regulator, Deaf family	115	104	104	104	8.84	10.3	1.02	-0.04	-0.45	1.13	0.08	1.61	0.15	0.04	-0.07	1.02	-0.09	0.57	0.07	-0.3	0.2	-0.13	0.21	-0.07	0.16	-0.11	0.0	0.14	0.64	0.45	1.43		
Che_02572 glyceraldehyde, hydrolase family 5	13.9	14.8	13.6	13.8	12.7	13.5	-0.02	-0.23	0.77	0.29	0.88	1.16	1.31	0.87	0.33	-1.36	-0.69	0.5	0.3	0.1	0.39	0.32	0.07	-0.07	0.07	0.35	-0.11	0.04	0.29	0.4	0.81	1.86	
Che_02577 phase shock protein C, PspC	6.34	6.34	6.46	7.28	6.28	6.9	0.13	-0.04	-0.14	0.34	0.29	0.33	0.17	0.13	0.17	0.13	0.17	0.13	0.17	0.13	0.17	0.13	-0.07	0.07	0.35	-0.11	0.04	0.29	0.4	0.81	1.86		
Che_02586 histone kinase	7.64	7.89	7.74	7.16	5.86	6.15	-0.25	-0.02	-0.29	0.5	0.73	1.78	1.74	1.28	1.01	-0.53	-0.03	0.11	0.2	-0.23	0.57	0.51	0.72	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67	
Che_02544 transcriptional regulator, Deaf family	115	104	104	104	8.84	10.3	1.02	-0.04	-0.45	1.13	0.08	1.61	0.15	0.04	-0.07	1.02	-0.09	0.57	0.07	-0.3	0.2	-0.13	0.21	-0.07	0.16	-0.11	0	0.14	0.64	0.45	1.43		
Che_02524 transcriptional regulator, Deaf family	115	104	104	104	8.84	10.3	1.02	-0.04	-0.45	1.13	0.08	1.61	0.15	0.04	-0.07	1.02	-0.09	0.57	0.07	-0.3	0.2	-0.13	0.21	-0.07	0.16	-0.11	0	0.14	0.64	0.45	1.43		
Che_02567 transcriptional regulator, TetR family	6.52	6.61	5.46	5.49	4.75	5.83	0.91	-0.03	-1.08	1.06	1.12	1.77	-0.22	0.71	-0.34	0.9	-0.06	-1.33	0.04	0.3	0.27	-0.13	0.24	-0.08	0	0.1	-0.11	-0.02	0.07	0.5	0.52		
Che_02572 Chromatin synthase	13.3	11.9	13	13	15.2	15.9	-0.08	0	-0.68	-0.27	0.85	-1.91	-0.21	-2.18	-0.86	-0.94	0.03	-0.2	-0.04	-1.3	0.11	-1.14	-0.07	-1.48	-1.72	-0.11	-1.33	0.64	0.41	28.91	1.9		
Che_02588 carboxyl phosphate kinase, large subunit	11.2	11.2	11.8	11.2	11.8	11.6	-0.03	-0.13	0.54	0.17	0.18	0.17	0.18	0.17	0.18	0.17	0.18	0.17	0.18	0.17	0.18	0.17	-0.07	0.16	-0.11	0.04	0.29	0.4	0.81	1.86	1.9		
Che_02583 ribose phosphate pyrophosphatase	11.9	12.1	11.4	11.1	11.6	-0.09	-0.03	-0.51	0.53	0.69	0.79	0.47	0.26	-0.22	-0.46	-0.06	-0.37	0.2	-0.2	0.02	0.03	0.06	-0.08	-0.03	-0.01	-0.11	-0.04	0.02	0.84	0.62	0.6		
Che_02583 DNA-directed DNA polymerase	8.73	7.93	7.71	7.72	6.27	7.11	0.78	-0.01	-0.84	1	0.21	2.44	0.82	1.44	0.61	0.74	0	0.73	0.02	-0.3	0.16	0.17	0.08	-0.05	-0.36	0.66	-0.11	0.27	0.53	0.7	1.28	3.5	
Che_02200 undecylenyl phosphatase	11.2	11.8	11.1	11.2	11.8	11.6	-0.03	-0.13	0.54	0.17	0.18	0.17	0.18	0.17	0.18	0.17	0.18	0.17	0.18	0.17	0.18	0.17	-0.07	0.16	-0.11	0.04	0.29	0.4	0.81	1.86	1.9		
Che_02582 peptidase A24A-like protein	11.9	12.3	11.5	11.1	11.6	-0.04	0.02	-0.52	0.37	0.79	0.73	0.61	0.36	-0.18	-0.72	-0.09	0.33	-0.1	0.01	0.2	0.08	0.08	-0.08	-0.03	-0.06	-0.11	-0.04	0.06	0.72	0.59	1.1		
Che_03161 NAD-dependent epimerase/dehydratase	11.8	12.6	11.7	11.8	1	-0.79	-0.05	1	0.1	0.84	30.8	12.59	10.7	11.75	-1.2	-0.12	0.54	0.3	0.003	-0.2	0.78	4.95	0.41	-0.07	0.46	4.16	-0.11	0.35	0.27	0.62	0.31	3.07	
Che_02511 Nucleo-Mechano-sensor (non channel)	8.73	8.03	7.61	7.48	5.98	6.93	0.7	0.13	-1.07	1.12	0.55	2.87	1.1	1.75	0.55	0.64	0.54	0.07	-0.1	0.24	0.22	0.47	-0.07	0.44	0.63	-0.11	0.23	0.51	0.31	1.11	1.85		
Che_03012 Carbohydrate binding family 6	9.14	9.03	8.18	8.33	9.25	10.1	-0.11	-0.15	-0.81	0.96	0.7	-0.11	-1.03	-1.07	-1.73	-0.09	-0.44	-0.63	0	0	-0.6	-0.6	-0.8	-0.08	-0.7	-0.85	-0.11	-0.38	-0.65	0.13	2.99	4.17	
Che_03046 anaerobic ribonucleoside triphosphate reductase	14.1	12.4	12.7	12.5	11.8	12.6	1.68	0.25	0.78	1.35	-0.08	2.27	0.19	0.92	-0.11	1.85	0.81	-0.53	0.17	0.4	0.48	0.13	0.14	-0.07	0.12	0.22	-0.11	0.08	0.19	0.43	0.64	1.24	
Che_03088 carboxymethyl phosphate synthase, large subunit	12.7	11.7	12.8	12.8	9.9	10.7	1.07	-0.17	-0.8	0.91	1.16	2.84	0.07	1.93	2.13	0.1	-1.09	0.6	0	0.9	0.73	0.24	0.82	1.35	-0.08	-0.49	1.08	-0.11	0.38	0.86	0.55	1.9	1.65
Che_02085 deoxydinucleoside 5'-triphosphate nucleotidyltransferase	8.89	9.12	8.35	7.96	7.66	8.5	-0.23	0.39	-0.84	0.54	1.16	1.23	0.62	0.69	-0.54	-0.51	1.25	-0.77	-0.2	0.18	0.03	0.23	-0.1	-0.08	0.1	0.04	-0.11	0.06	0.05	0.38	0.24	0.59	
Che_02520 CMP/UMP deaminase, zinc-binding	12	10.2	10.6	10.5	10.1	10.5	1.78	0	0.45	1.37	-0.41	1.87	-0.36	0.5	1.98	0.03	0.57	0.18	-0.6	0.09	0.13	0.14	0.2	-0.08	-0.01	0.16	-0.11	-0.02	0.14	0.38	0.51	1.43	
Che_02583 ribose phosphate pyrophosphatase	11.9	12.1	11.4	11.4	11.6	-0.19	-0.03	-0.51	0.53	0.69	0.79	0.47	0.26	-0.22	-0.46	-0.06	-0.37	0.2	-0.2	0.02	0.03	0.06	-0.08	-0.03	-0.01	-0.11	-0.04	0.02	0.84	0.62	0.6		
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577 phase shock protein C, PspC	6.74	7.68	7.28	7.38	5.98	6.79	1.83	0.4	-0.81	1.09	-0.34	2.79	0.15	1.7	0.49	2.04	1.28	-0.68	0.06	-0.5	0.71	-0.1	0.71	0.44	-0.07	0.36	0.72	-0.11	0.27	0.58	0.76	1.17	2.67
Che_02577																																	



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Che_01342 beta-lactamase-like protein	8.7	9.25	8.75	8.91	8.46	8.95	-0.55	-0.16	-0.49	-0.05	0.34	0.24	0.3	0.29	-0.04	-0.19	-0.47	0.43	-0.4	-0.2	-0.4	-0.1	0.04	0.16	-0.23	-0.18	0.07	-0.24	-0.16	0.07	0.95	0.92	0.86
Che_01115 glycogen debranching enzyme, putative	9.99	11	10.4	10.4	10.1	11	-1.02	0	-0.47	-0.42	-1.18	-0.34	0.01	0.08	-0.09	0.08	0.03	-0.17	-0.61	-0.7	-0.2	-0.1	-0.1	-0.24	-0.35	-0.15	-0.34	-0.3	-0.09	0.82	1.03	0.94	
Che_02388 P85	14.9	16	15.4	15.6	13.7	15.7	-0.05	-0.47	-0.47	0.4	1.82	-0.37	0.05	0.19	1.52	-0.47	0.18	0.2	-0.6	-0.2	-0.2	0.02	0.08	-0.15	-0.2	-0.4	-0.7	-0.2	-0.18	1.12	1.08	1.18	
Che_02559 sugar phosphatase isoenzymes, RplK/Lac/LacB	11.8	12	11.6	11.4	12.1	-0.2	0.04	-0.72	0.21	0.45	-0.43	-0.09	0.22	-0.54	-0.47	0.16	-0.33	-0.3	-0.2	-0.3	-0.2	0.01	-0.1	-0.23	-0.26	-0.06	-0.24	-0.22	-0.03	1.42	1.54	1	
Che_02507 glycosyl hydrolase, alpha-L-fucosidase	7.97	7.31	7.31	7.39	7.16	7.71	-0.06	-0.47	-0.47	0.07	0.16	-0.07	0.02	-0.09	0.07	0.08	0.07	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.05	-0.04	-0.05	-0.04	-0.05	0.05	0.05	0.1	1.1	
Che_03573 two component transcriptional regulator, winged	8.32	8.82	8.88	8.28	7.32	7.68	0.5	0.1	-0.36	-0.06	0.54	1	1.14	1.06	0.6	0.84	0.34	0.87	0.4	-0.1	-0.1	0.31	0.41	0.5	-0.23	0.05	-0.51	-0.24	0.02	0.41	1	0.6	0.31
Che_01813 urease accessory protein UreG	3.16	3.47	3.46	3.7	4.7	5.29	-0.29	0.17	-0.39	0	0.46	-1.53	-1.83	-1.53	-2.29	-0.58	0.56	0.1	-0.4	-0.1	-1.2	0.8	-1.1	-0.24	-0.39	-1.25	-0.24	-1.13	-0.96	1.1	5.87	7.81	
Che_02886 DNA polymerase III, beta subunit	9.94	10.9	10.3	10.4	11.3	11.83	-0.03	-0.47	-0.47	0.07	0.16	-0.07	0.02	-0.09	0.07	0.08	0.07	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.05	-0.04	-0.05	-0.04	-0.05	0.05	0.05	0.1	1.1	
Che_06828 deoxyribose-5-phosphate synthase	8.16	7.18	11.5	11.5	11.3	11.8	-0.36	0	-0.48	0.1	0.46	0.26	0.14	0.16	-0.32	-0.67	0.03	0.47	-0.4	-0.4	-0.1	-0.1	0.01	-0.23	-0.23	-0.05	-0.24	-0.2	-0.02	1.18	1.13	0.16	
Che_02303	11.59	13.4	7.69	7.77	6.32	7.01	1.25	-0.08	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	-0.49	0.9	
Che_01714 14-12 acyl-CoA oxidase, long-chain	9.42	10.17	14.7	14.2	14.2	14.5	-0.42	-0.07	-0.47	-0.47	0.07	0.16	-0.07	0.02	-0.09	0.07	0.08	0.07	-0.4	-0.4	-0.4	-0.4	-0.4	-0.4	-0.05	-0.04	-0.05	-0.04	-0.05	0.05	0.05	0.1	
Che_01590 Phosphoglycerate-binding domain 1	13.6	13.2	13.3	11.3	11.6	14.2	-0.46	0.22	-0.6	0.29	0.05	0.13	-0.26	-0.18	-0.34	0.35	0.72	0.07	-0.3	-0.3	-0.5	-0.6	-0.2	-0.4	-0.24	-0.72	-0.35	-0.24	-0.59	-0.26	1.1	5.08	2.1
Che_02773 metal dependent phosphoglycerate	11.6	11.3	11.1	11.2	10.9	11.5	0.29	-0.17	-0.59	0.34	0.08	0.05	-0.23	-0.11	-0.31	0.14	0.5	0.1	-0.2	-0.2	-0.2	-0.3	-0.05	-0.24	-0.32	-0.04	-0.24	-0.27	0.02	1.41	4.7	0.27	
Che_02537 two component transcriptional regulator, winged	8.12	8.12	7.36	7.38	7.14	6.5	0.1	-0.36	-0.06	0.54	1	1.14	1.06	0.6	0.84	0.34	0.87	0.4	-0.1	-0.1	0.31	0.41	0.5	-0.23	0.05	-0.51	-0.24	0.02	0.41	1	0.6	0.31	
Che_03583 periplasmic sensor signal transduction histidine	8.34	8.07	8.64	8.54	7.19	7.55	-0.7	0	-0.36	-0.2	0.53	1.5	1.52	1.35	0.99	-1.12	0.03	0.87	-0.5	-0.5	-0.5	-0.5	-0.5	-0.23	-0.17	0.76	-0.24	0.12	0.61	0.91	0.77	3.42	
Che_00684 Polynucleotide phosphorylase region	11	10.9	10.6	10.9	9.22	9.9	0.11	-0.24	-0.68	0.38	0.03	1.79	1	1.41	0.97	0.09	0.72	-0.2	-0.3	-0.3	-0.3	-0.3	-0.3	-0.24	-0.32	-0.79	-0.24	0.24	0.61	1.36	3.81	4.03	
Che_02052 hypothetical protein	13.1	13	12.7	12.7	12.1	12.7	0.1	-0.57	-0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	-0.24	-0.32	-0.79	-0.24	0.24	0.61	1.36	3.81	4.03	
Che_02052 protein of unknown function DUF1312	9.35	9.24	8.84	8.89	8.44	8.97	-0.11	-0.05	-0.53	0.51	0.35	0.91	0.27	0.4	-0.08	-0.09	-0.12	0.3	-0.2	-0.2	-0.1	-0.1	0.09	0.13	-0.24	-0.06	0.11	-0.24	-0.06	0.1	3.68	0.91	1.63
Che_04043 gid protein	10.9	11.5	11	10.9	11.3	12.2	-0.57	0.09	-0.84	-0.11	0.55	-0.43	-0.7	-0.32	-1.25	0.93	0.31	-0.75	-0.5	-0.7	-0.7	-0.5	-0.3	-0.23	-0.58	-0.43	-0.24	-0.48	-0.32	0.96	1.62	2.31	
Che_02634 Polynucleotide deoxyribosyltransferase region	14.1	14.7	14.2	14.2	14.1	14.6	-0.02	-0.07	-0.44	0.03	0.17	0.4	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	-0.23	-0.09	0.01	-0.24	-0.02	0.01	0.86	1.04	0.08	
Che_01014 14-12 acyl-CoA oxidase, long-chain	10.1	14.7	14.2	14.2	14.1	14.5	-0.62	-0.48	-0.11	-0.44	-0.11	0.47	0.17	0.14	-0.27	-0.19	-0.19	-0.47	-0.5	-0.2	-0.5	-0.1	-0.03	-0.23	-0.26	-0.03	-0.24	-0.22	-0.01	0.96	1.04	0.28	
Che_00558 quinine tRNA-ribosyltransferase	9.93	10.4	9.89	10.1	8.82	9.49	-0.43	-0.19	-0.67	0.04	0.28	1.11	0.87	1.07	0.59	0.75	0.56	-0.17	-0.4	-0.2	-0.19	-0.41	-0.49	-0.23	-0.02	0.55	-0.24	0	0.45	0.99	0.56	0.34	
Che_01952 pseudotetrasaccharide synthase, Rhu family	11.2	11.5	10.9	11.5	11.5	12.3	-0.11	-0.18	-0.75	0.29	0.27	0.3	-0.04	-0.19	-1.16	0.36	-0.53	-0.43	-0.3	-0.3	-0.6	-0.6	-0.4	-0.23	-0.74	-0.47	-0.24	-0.61	0.35	1.27	1.5	2.81	
Che_02044 ribosomal protein L4/L1e	11.2	12.1	11.6	11.8	9.6	10	-0.96	-0.26	-0.41	-0.4	0.3	1.56	2.1	1.96	1.81	-1.44	-0.78	-0.7	-0.6	-0.2	-0.17	0.73	0.14	-0.23	0.4	0.125	0.24	-0.3	0.99	0.78	1.08	4.48	
Che_02045 codA codon division protein Flz2	11.5	12.1	11.6	11.6	11.6	12.2	-0.6	-0.07	-0.61	0.4	0.53	-0.07	-0.08	0.07	-0.61	-0.96	-0.25	0.05	-0.5	-0.5	-0.5	-0.2	-0.1	-0.2	-0.24	-0.36	-0.12	-0.24	-0.3	0.99	0.99	1.36	2.14
Che_02026 hypothetical protein	11.7	12.2	11.7	11.7	10.8	11.4	-0.43	0.01	-0.74	0.03	0.47	1.09	0.78	1.06	0.31	0.75	0.06	-0.4	-0.4	-0.1	0.34	0.41	0.34	-0.24	-0.02	-0.47	-0.24	0.38	1.11	0.44	4.39	0.4	
Che_01768 Nrf1-related domain containing protein	9.55	9.21	11.1	11	9.86	10.4	-1.2	0.07	-0.34	-0.59	-0.68	0.62	1.28	1.21	0.6	-1.7	-0.25	-0.27	-0.7	-0.7	-0.7	-0.7	-0.7	-0.24	-0.06	-0.44	-0.24	-0.03	0.52	0.78	0.88	6.28	
Che_02405 Heme metal transport/detoxification protein	10.3	12.3	9.34	9.01	7.61	8.15	0.32	0.13	-0.54	0.41	0.22	1.94	1.08	1.33	0.86	0.17	0.44	-0.27	-0.2	-0.2	-0.3	-0.3	-0.3	-0.24	-0.38	-0.82	-0.24	-0.29	0.66	1.5	3.18	5.8	
Che_00314 hydroxymethylated phenylphosphonate synthase	14.1	14.7	14.2	14.2	14.1	14.6	-0.02	-0.07	-0.44	0.03	0.17	0.4	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	-0.23	-0.09	0.01	-0.24	-0.02	0.01	0.86	1.04	0.08	
Che_06828 deoxyribose-5-phosphate synthase	11.6	11.9	11.5	11.5	11.3	11.8	-0.36	0	-0.48	0.1	0.46	0.26	0.14	0.16	-0.32	-0.67	0.03	0.47	-0.4	-0.4	-0.1	-0.1	0.01	-0.23	-0.23	-0.05	-0.24	-0.2	-0.02	1.18	1.13	0.16	
Che_01813 urease accessory protein UreG	3.17	3.46	3.37	3.7	4.7	5.29	-0.29	0.17	-0.39	0	0.46	-1.53	-1.83	-1.53	-2.29	-0.58	0.56	0.1	-0.4	-0.1	-1.2	0.8	-1.1	-0.24	-0.39	-1.25	-0.24	-1.13	-0.96	1.1	5.87	7.81	
Che_02387 60 kDa inner membrane protein	11.7	12.5	12.1	12.1	11.3	11.7	-0.25	-0.03	-0.47	0.25	0.13	-0.23	-0.17	-0.25	-0.23	0.15	0.43	0.23	-0.2	-0.2	-0.1	-0.1	0.01	-0.23	-0.23	-0.05	-0.24	-0.2	-0.02	1.18	1.13	0.16	
Che_01519 putative RNA methylase	11.7	11.4	11.3	11.5	11.3	8.83	0.31	-0.28	-0.53	0.47	-0.12	0.42	2.58	2.95	2.7	0.16	0.84	0.3	0.7	0.07	0.4	0.88	0.94	1.3	1.62	1.28	1.94	-0.25	1.01	1.53	1.08	0.76	7.7
Che_01300 Phosphoglycerate-binding UreG	9.77	11.4	10.6	10.8	8.78	9.37	-1.44	-0.23	-0.59	-0.79	0.42	0.99	1.84	1.78	1.42	-0.69	0.1	-0.8	-0.2	-0.1	0.61	0.75	0.94	-0.25	0.17	1	1.1	0.12	-0.82	0.08	0.7	5.75	
Che_02046 Phosphoglycerate-binding UreG	9.77	11.4	10.6	10.8	8.78	9.37	-1.44	-0.23	-0.59	-0.79	0.42	0.99	1.84	1.78	1.42	-0.69	0.1	-0.8	-0.2	-0.1	0.61	0.75	0.94	-0.25	0.17	1	1.1	0.12	-0.82	0.08	0.7	5.75	
Che_01519 putative RNA methylase	11.7	11.4	11.3	11.5	11.3	8.83	0.31	-0.28	-0.53	0.47	-0.12	0.42	2.58	2.95	2.7	0.16	0.84	0.3	0.7	0.07	0.4	0.88	0.94	1.3	1.62	1.28	1.94	-0.25	1.01	1.53	1.08	0.76	7.7
Che_01300 Phosphoglycerate-binding UreG	9.77	11.4	10.6	10.8	8.78	9.37	-1.44	-0.23	-0.59	-0.79	0.42	0.99	1.84	1.78	1.42	-0.69	0.1	-0.8	-0.2	-0.1	0.61	0.75	0.94	-0.25	0.17	1	1.1	0.12	-0.82	0.08	0.7	5.75	
Che_02046 Phosphoglycerate-binding UreG	9.77	11.4	10.6	10.8	8.78	9.37	-1.44	-0.23	-0.59	-0.79	0.42	0.99	1.84	1.78	1.42	-0.69	0.1	-0.8	-0.2	-0.1	0.61	0.75	0.94	-0.25	0.17	1	1.1	0.12	-0.82	0.08	0.7	5.75	
Che_01519 putative RNA methylase	11.7	11.4	11.3	11.5	11.3	8.83	0.31	-0.28	-0.53	0.47	-0.12	0.42	2.58	2.95	2.7	0.16	0.84	0.3	0.7	0.07	0.4	0.88	0.94	1.3	1.62	1.28	1.94	-0.25	1.01	1.53	1.08	0.76	7.7
Che_01300 Phosphoglycerate-binding UreG	9.77	11.4	10.6	10.8	8.78	9.37	-1.44	-0.23	-0.59	-0.79	0.42	0.99	1.84	1.78	1.42	-0.69	0.1	-0.8	-0.2	-0.1	0.61	0.75	0.94	-0.25	0.17	1	1.1	0.12	-0.82	0.08	0.7	5.75	
Che_02046 Phosphoglycerate-binding UreG	9.77	11.4	10.6	10.8	8.78	9.37	-1.44	-0.23	-0.59	-0.79																							



Chb_02420 Hsp superfamily phospholipases-like protein	13.3	12.4	12.8	12.8	11.8	12.3	0.93	0.03	0.56	0.52	-0.38	1.56	0.07	1.04	0.45	0.93	0.12	0.2	0.2	0.5	0.17	0.2	0.4	0.42	0.33	0.02	0.55	-0.32	0	0.45	1.2	0.54	8.29
Chb_02712 Peptide lyase/AmoA alleloin	7.03	7.22	6.94	7.03	6.94	7.15	0.2	-0.09	-0.07	-0.08	-0.12	-7.26	-7.76	-7.25	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	-6.86	
Chb_02717 Transposase, non-retro type	8.46	8.17	8.37	8.37	8.46	8.09	0.29	0.15	0.14	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15	0.15		
Chb_04040 DNA topoisomerase I	11.2	11.6	11.3	11.4	12.1	12.8	0.04	-0.09	0.73	0.13	0.22	-0.88	-1.17	-0.75	-1.39	-0.77	-0.25	0.37	0.53	0.3	0.7	-0.5	-0.6	-0.33	0.94	-0.66	-0.32	-0.77	-0.5	1.33	3	5.42	
Chb_02552 chitinase-like protein	8.21	8.38	8.08	8.04	8.21	8.04	0.09	-0.07	0.24	0.13	0.27	-0.34	-0.37	-0.17	-0.34	-0.17	-0.34	-0.17	-0.34	-0.17	-0.34	-0.17	-0.34	-0.17	-0.34	-0.17	-0.34	-0.17	-0.34	-0.17	-0.34		
Chb_00808 MCP methyltransferase, Chp7	7.77	7.75	7.71	7.77	7.74	8.52	1.02	-0.16	-0.58	0.66	-0.52	-0.17	-1.77	-0.83	-1.25	1.04	-0.47	0.13	-0.1	0.6	-0.6	-1	-0.5	-0.33	-0.88	-0.62	-0.32	-0.72	-0.47	1.08	2.41	4.74	
Chb_01244 glycolyl transferase, family 2	11.9	10.8	11.2	11.6	10.7	11.3	1.18	-0.38	-0.63	0.72	-0.84	1.26	-0.55	0.54	-0.29	1.23	-1.16	0.03	-0.18	0.04	-0.4	-0.16	-0.33	-0.33	-0.15	-0.19	-0.32	-0.14	0.16	0.9	0.78	1.05	
Chb_02611 UDP-N-acetylglucosamine 6-phosphate 4-epimerase	11.1	11.7	10.9	10.9	11.1	10.9	0.09	-0.01	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17	0.17		
Chb_00573 protein synthetase/threonine phosphatases	11.7	11.6	11.4	11.4	11.3	11.9	0.09	-0.01	0.57	0.36	-0.26	-0.39	-0.67	-0.03	-0.11	0	0.17	0.3	-0.2	-0.3	-0.3	-0.1	-0.1	-0.33	-0.4	-0.11	-0.32	-0.34	0.07	0.43	0.51	2.67	
Chb_00808 MCP methyltransferase, Chp7	7.77	7.75	7.71	7.77	7.74	8.52	1.02	-0.16	-0.58	0.66	-0.52	-0.17	-1.77	-0.83	-1.25	1.04	-0.47	0.13	-0.1	0.6	-0.6	-1	-0.5	-0.33	-0.88	-0.62	-0.32	-0.72	-0.47	1.08	2.41	4.74	
Chb_02532 putative signal transduction protein with CDS	8.36	8.66	8.59	8.39	8.17	12.3	0.3	0.2	-0.59	-0.27	-1.38	-1.67	-1.35	-1.34	-0.59	0.66	0.1	0.5	-0.2	-1.8	-1.6	-1.59	-0.35	-2.52	-2.39	-0.33	-0.03	-0.85	1.28	10.06	12.46		
Chb_02970 ABC transporter related protein	8.25	7.84	8.08	7.57	8.19	0.39	-0.24	-0.62	0.41	-0.22	0.68	-0.33	-0.77	-0.11	0.26	0.72	0	-0.2	0.5	-0.2	-0.3	-0.03	-0.12	-0.33	-0.33	-0.02	-0.32	-0.28	0.03	1.36	0.35	1.7	
Chb_00300 signal peptide 1	11.5	11.7	11.5	10.1	10.7	12.3	0.23	-0.61	-0.22	0.24	1.4	1.02	1.62	0.78	0.51	0.75	0.03	-0.5	-0.1	0.3	0.26	0.67	0.19	0.34	0.17	0.78	-0.33	-0.12	0.62	1.25	1.24	3.96	
Chb_00436 Tetraacylglycerol_TPS_2	12.2	12.7	11.8	11.8	12.2	11.7	0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17	-0.17		
Chb_00504 ATPase associated with various cellular	12.2	12.5	12.3	12.3	10.8	10.7	-0.07	-0.08	-0.61	-0.09	0.2	1.95	1.71	2.04	1.51	-0.48	-0.22	0.03	-0.5	0.3	0.56	0.87	0.98	-0.35	0.51	1.28	-0.33	0.39	1.02	1.47	2.19	19.67	
Chb_01609 protein of unknown function DUF5454	9.51	10	9.7	9.8	10.2	10.7	-0.52	-0.09	0.49	-0.2	0.23	-0.71	-0.68	-0.51	-0.86	-0.25	0.43	-0.5	0.3	0.8	-0.5	-0.3	-0.34	-0.73	-0.38	-0.33	-0.6	0.28	1.25	2.23	3.03		
Chb_00484 open coat protein	9.46	9.06	9.24	9.09	9.59	6.46	0.39	0.15	-0.53	-0.01	0.352	1.6	3.11	2.76	0.38	0.55	0.3	-0.4	1.03	0.98	0.4	0.4	0.4	-0.35	1.31	2.07	-0.33	1.03	1.61	7.98	12.14		
Chb_01079 Nucleotidyl transferase	9.06	7.52	8.39	8.37	10.7	11.5	1.54	0.02	-0.8	0.67	-0.85	-1.68	-4.02	-2.35	-1.17	1.68	0.09	-0.6	-0.1	0.2	-1.9	-1.2	-1.5	-0.34	-1.89	-1.85	-0.33	-1.53	1.43	0.9	2.9	10.64	
Chb_01957 extracellular subunit-binding protein, family 1	9.49	9.33	9.22	9.36	9.16	9.92	0.36	-0.74	0.37	-0.23	0.33	-0.79	-0.04	-0.56	0.22	0.72	-0.47	-0.33	-0.5	0.4	-0.5	-0.1	-0.1	-0.35	-0.52	-0.03	-0.33	-0.43	0.01	1.43	2.77	0.63	
Chb_02698 putative transcriptional regulator, Copic family	10.27	9.29	10.3	10.1	9.41	9.99	1.57	0.23	-0.58	-0.76	1.25	-0.67	-0.89	0.08	0.47	0.75	0.13	-0.3	0.7	0.04	-0.5	0.33	0.22	-0.35	-0.16	-0.28	-0.33	-0.43	0.21	0.93	10.94	15.74	
Chb_01811 transglutaminase-like protein	10.2	10.6	10.3	10.3	10.5	11.1	-0.42	0.02	-0.66	-0.14	-0.3	-0.3	-0.54	-0.16	-0.84	-0.74	0.09	-0.13	-0.5	0.2	-0.6	-0.4	-0.2	-0.3	-0.34	-0.59	-0.3	-0.33	-0.49	0.22	1.42	2.29	6.73
Chb_00309 extracellular ABC_8 subunit	12	12.6	12.3	12.5	12.9	13.8	-0.63	-0.16	-0.88	-0.32	0.15	-0.91	-1.16	-0.59	-1.31	1	0.47	-0.87	-0.6	-0.5	-0.7	-0.4	-0.5	-0.35	-0.84	-0.49	-0.33	-0.49	0.37	1.13	1.93	2.15	
Chb_00806 8-oxoguanine DNA glycosylase-like protein	8.36	8.66	8.59	8.39	8.17	12.3	0.3	0.2	-0.59	-0.27	-1.38	-1.67	-1.35	-1.34	-0.59	0.66	0.1	0.5	-0.2	-1.8	-1.6	-1.59	-0.35	-2.52	-2.39	-0.33	-0.03	-0.85	1.28	10.06	12.46		
Chb_01808 phase SP01 DNA polymerase-related protein	8.55	8.9	8.82	8.72	10.2	10.7	-0.61	-0.11	-0.47	-0.38	0.34	-1.17	-1.03	-0.79	-1.37	-0.98	0.38	-0.5	0.6	-0.2	-1	-0.6	-0.5	-0.35	-0.95	-0.64	-0.33	-0.78	0.48	1.17	2.46	3.88	
Chb_01878 protein of unknown function DUF342	10.9	10.9	10.7	10.8	13.4	14.3	0.04	-0.13	-0.85	0.24	0.07	-2.5	-3.39	-2.74	-3.46	-1.07	-0.38	-0.77	-0.1	0.3	-1.6	-1.7	-1.4	-0.7	-0.35	-2.12	-2.04	-0.33	-1.71	2.18	6.6	8.43	
Chb_01440 Methyltransferase type 12	9.46	9.06	9.24	9.09	9.59	6.46	0.39	0.15	-0.53	-0.01	0.352	1.6	3.11	2.76	0.38	0.55	0.3	-0.4	1.03	0.98	0.4	0.4	0.4	-0.35	1.31	2.07	-0.33	1.03	1.61	7.98	12.14		
Chb_00436 Tetraacylglycerol_TPS_2	11.4	12.7	11.7	11.8	12.4	13	-0.57	-0.12	-0.34	-0.27	0.18	-1.01	-0.98	-0.74	-1.16	-0.93	-0.34	0.27	0.5	-0.3	-0.9	-0.6	-0.4	-0.4	-0.35	-0.91	-0.56	-0.33	-0.74	0.42	1.2	2.63	4.78
Chb_00744 copper amine oxidase-like protein	10.3	10.1	9.88	9.9	9.91	13.3	-0.03	-0.52	-0.38	0.22	-0.87	0.22	0.49	0	0.06	0.06	0.33	-0.3	-0.3	-0.1	-0.1	-0.14	-0.18	-0.34	-0.08	-0.18	-0.33	-0.08	0.16	8.5	10.7	2.27	
Chb_01079 Nucleotidyl transferase	9.06	7.52	8.39	8.37	10.7	11.5	1.54	0.02	-0.8	0.67	-0.85	-1.68	-4.02	-2.35	-1.17	1.68	0.09	-0.6	-0.1	0.2	-1.9	-1.2	-1.5	-0.34	-1.89	-1.85	-0.33	-1.53	1.43	0.9	2.9	10.64	
Chb_01805 glycolyl transferase, group 1	1.67	5.7	5.55	5.46	4.09	5	-0.03	0.09	-0.91	-0.12	0.24	1.58	0.7	1.46	0.46	-0.26	0.31	-0.97	-0.4	0.3	0.18	0.12	0.59	0.42	0.34	0	0.57	-0.33	-0.02	0.46	2.17	0.49	2.37
Chb_01162 glucosamine-Fructose-6-phosphate 1-phosphotransferase, group 1	11.2	11.3	11.6	10.8	11.5	11.6	-0.43	-0.14	-0.63	-0.11	0.38	-0.43	0.56	0.67	0.18	-2.22	-0.41	-0.03	-0.9	0.2	-0.37	0.02	0.27	0.34	-0.2	0.29	-0.33	-0.18	0.34	0.8	0.71	2.82	
Chb_01301 glycolyl transferase, group 1	11.1	11.3	11.2	11.4	11.1	11.6	-0.02	-0.14	-0.14	-0.11	0.6	-0.21	-0.47	-0.02	-0.14	-0.02	-0.14	-0.02	-0.14	-0.02	-0.14	-0.02	-0.14	-0.02	-0.14	-0.02	-0.14	-0.02	-0.14	0.02	0.14	0.02	
Chb_02885 phosphatidylinositol-4-phosphate-3-kinase	11.9	12	11.8	12.1	11.4	11.9	0.09	-0.29	-0.56	0.07	-0.13	0.5	0.03	0.43	0.16	-0.33	-0.87	0.2	0.4	-0.4	0.3	-0.2	-0.11	0.26	0.34	-0.25	0.15	-0.33	-0.22	0.13	1.23	1.98	1.05
Chb_00621 putative transduction initiation factor, pfl_289	11.9	11.9	12.4	12.5	12.3	13	-0.81	-0.11	-0.7	-0.46	-0.24	-0.36	-0.25	-0.41	-1.22	-0.31	-0.27	-0.6	-0.7	-0.3	-0.1	-0.1	-0.1	-0.34	-0.45	-0.04	-0.33	-0.38	-0.02	1.05	1.31	0.83	
Chb_00722 rRNA	12.2	12.9	12.8	12.7	12.9	12.9	0.12	-0.08	-0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	
Chb_01079 Nucleotidyl transferase	9.06	7.52	8.39	8.37	10.7	11.5	1.54	0.02	-0.8	0.67	-0.85	-1.68	-4.02	-2.35	-1.17	1.68	0.09	-0.6	-0.1	0.2	-1.9	-1.2	-1.5	-0.34	-1.89	-1.85	-0.33	-1.53	1.43	0.9	2.9	10.64	
Chb_01959 arginyl-RNA transferase	12.2	12.9	12.8	12.7	12.9	12.9	0.12	-0.08	-0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	0.12	
Chb_02386 ribonuclease E protein component	12.1	12.1	12.1	12.1	12.1	12.1	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	
Chb_00860 Rubrerythrin	12.1	12.1	12.1	12.1	12.1	12.1	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02	
Chb_01094 Radical SAM-like protein	11.4	12	11.8	12	13.9	14.7	-0.39	-0.21	-0.77	-0.13	-0.05	-2.31	-2.69	-1.28	-1.27	-0.67	-0.62	-0.5	-0.5	-1.5	-1.4	-1.3	-0.6	-0.34	-1.02	-0.59	-0.33	-0.83	-0.45	1.51			



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Che_00360 thiorodan	11	9.83	111	10.8	131	13.6	1.12	0.29	-0.5	-0.14	-0.97	-2.17	-3.79	-2.03	-2.82	1.16	0.94	0.4	0.5	-0.8	-1.5	-1.8	-1.1	-1.3	-0.57	-2.06	-1.54	-0.51	-1.66	-1.19	1.26	4.31	5.53	
Che_00279 signal peptide 1	12.5	11.9	12.5	12.4	10.7	11.3	0.58	0.1	-0.6	-0.4	-1.81	0.61	1.81	1.09	0.45	0.3	0	0	0.4	-0.8	0.28	0.8	0.76	0.76	0.57	-0.58	-0.18	-1.02	-0.51	-0.13	0.81	2.1	1.35	0.40
Che_01421 signal peptide periplasmic SS3, 36k	12.1	12.4	12.5	12.5	12.5	12.5	0.06	0	-0.4	-0.6	-0.14	0.06	0	-0.14	0.06	0	0	0	0	0	0	0	0	0	0	-0.17	-0.4	-0.1	-0.1	0.3	0.1	3.2	0.8	1.7
Che_01787 glycose hydrolase 156, 38k	11.4	11.6	11.7	11.8	10.7	11.3	0.19	-0.66	-0.3	-0.2	0.75	0.28	1.05	-0.88	-0.46	-0.25	-0.13	-0.6	-0.5	-0.2	-0.1	0.4	0.43	0.58	-0.08	-0.55	-0.52	-0.08	-0.45	-2.71	0.9	6.95	0.85	
Che_00353 Polymyxin resistance	9.5	10.1	9.61	9.63	9.63	9.63	0.07	0	-0.2	-0.2	-0.1	0.07	0	-0.2	0.07	0	0	0	0	0	0	0	0	0	-0.12	-0.1	-0.1	-0.1	0.07	0.07	0.07	0.07	0.07	
Che_00276 translocation elongation factor 2 [B]-27/67k	14.3	15.5	15.6	15.6	14.5	15.2	-0.23	-0.48	-0.68	-1.29	-0.54	-0.22	0.33	1.07	0.87	1.74	-1.47	-0.2	-1.0	-0.6	0	0	0.64	0.64	-0.58	-0.22	-0.54	-0.52	-0.19	-0.44	1.01	0.78	1.71	
Che_00083 cell cycle protein	9.94	10.2	10.5	10.3	9.76	10.2	-0.25	0.18	-0.4	-0.57	-0.14	0.18	0.03	0.75	0.17	0.53	0.59	0.73	0.4	-0.4	-0.2	0.26	0.27	0.58	-0.26	-0.23	-0.22	-0.22	0.2	1.97	1.16	1.33		
Che_02401 4-phosphoprotein 2C methylesterase	10.1	10.1	10.1	10.1	10.1	10.1	0.12	0	-0.4	-0.1	0.12	0	0	-0.4	0.12	0	0	0	0	0	0	0	0	0	-0.17	-0.4	-0.1	-0.1	0.12	0.12	0.12	0.12	0.12	
Che_01421 signal peptide periplasmic SS3, 36k type	12.3	12.4	12.5	12.5	11.9	12.6	0.06	0	-0.4	-0.2	0.14	0.38	-0.2	0.58	-0.06	-0.3	0.03	-0.5	-0.4	-0.3	-0.3	0.14	0.14	-0.58	-0.17	-0.22	-0.52	-0.31	-0.19	-0.43	3.2	9.88	0.4	
Che_01102 fibrinall assembly protein	11.1	11.6	11.7	11.8	10.6	11.2	-0.43	-0.16	-0.38	-0.33	-0.26	-0.48	0.33	1.01	0.59	0.75	-0.47	0.13	-0.7	-0.5	-0.3	-0.38	0.49	-0.58	-0.14	-0.55	-0.33	-0.13	-0.45	1.83	0.9	4.24		
Che_01104 hypothetical protein	9.69	9.99	10.1	10.1	9.6	10.4	-0.3	-0.18	-0.38	-0.18	-0.1	-0.24	0.3	0.03	0.12	0.1	0.12	0.12	0.12	0.12	0.12	0.12	0.12	-0.12	-0.12	-0.12	-0.12	-0.12	-0.12	-0.12	-0.12	-0.12		
Che_00832 exoenzyme B, small subunit	6.36	6.97	7.17	7.04	5.04	6.25	-0.61	-0.13	-1.21	-0.81	-0.07	1.32	0.72	2.13	0.99	-0.98	0.44	-1.97	-0.8	-0.4	0.07	0.31	0.91	0.6	-0.59	0.34	0.79	-0.33	-0.26	0.63	1.61	0.15	1.8	
Che_01102 fibrinall assembly protein	11.1	11.6	11.7	11.8	10.6	11.2	-0.43	-0.16	-0.38	-0.33	-0.26	-0.48	0.33	1.01	0.59	0.75	-0.47	0.13	-0.7	-0.5	-0.3	-0.38	0.49	-0.58	-0.14	-0.55	-0.33	-0.13	-0.45	1.83	0.9	4.24		
Che_00981 5-deoxyadenosine triphosphatase M3p/4	10.1	10.1	10.1	10.1	10.1	10.1	0.12	0	-0.4	-0.1	0.12	0	0	-0.4	0.12	0	0	0	0	0	0	0	0	0	-0.17	-0.4	-0.1	-0.1	0.12	0.12	0.12	0.12	0.12	
Che_02204 cyclophosphin synthase	6.74	5.98	6.61	6.7	6.02	6.95	0.76	0.22	-0.93	-0.18	-0.72	0.72	0.72	0.97	-0.25	0.72	0.72	-1.03	-0.5	-0.2	-0.2	-0.6	0.33	0.04	-0.59	-0.35	-0.14	-0.53	-0.12	1.66	1.14	0.88		
Che_00568 methionine tRNA formyltransferase	10	10.9	11	11.1	10.1	10.7	-0.91	-0.18	-0.55	-0.95	-0.22	-0.13	0.23	0.82	0.45	-1.35	0.53	-0.23	-0.8	-0.5	-0.6	0.1	0.29	0.42	-0.59	-0.26	-0.42	-0.33	-0.22	0.34	1.31	0.94	2.94	
Che_02391 pyruvate formate lyase	10.2	10.2	10.2	10.2	10.2	10.2	0.03	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36		
Che_02443 electron transport complex, RefA/RBCDCE type, E	10.2	10.7	10.8	10.9	10.21	11.1	-0.49	-0.13	-0.94	-0.59	-0.23	-1.91	-2.36	-1.32	-1.13	-0.83	-0.38	-1.07	-0.5	-1.3	-1.2	-0.7	0.1	-0.59	-1.49	-1.03	-0.53	-1.21	-0.79	1.79	3.01	3.52		
Che_01848 copper translocating P-type ATPase	10.8	10.7	10.7	10.9	11	13.9	1.46	0.02	-0.69	-0.12	-0.21	-1.31	-3.86	-3.03	-3.65	-0.2	-0.19	-0.23	-0.5	-0.5	-1.9	-1.9	-1.5	-1.8	-0.59	-2.56	-2.3	-0.33	-2.06	1.78	4.77	19.61	26.15	
Che_01518 hypothetical protein	9.69	9.99	10.1	10.1	11.8	12.4	-0.3	-0.03	-0.52	-0.05	-0.15	-0.2	-2.36	-1.72	-2.21	-0.59	-0.06	-0.3	-0.6	-0.4	-1.7	-0.9	0.1	-0.59	-1.72	-1.31	-0.53	-0.03	-1.03	2.49	6.28	13.51		
Che_00191 proteasome inhibitor 14, serpin	9.94	9.51	9.9	9.93	9.91	7.5	7.92	0.43	-0.01	-0.37	0.04	0	2.39	1.59	2.35	1.99	0.31	0	0.83	0.4	-0.3	0.53	0.51	1.01	1.24	-0.59	0.54	1.47	-0.53	-0.42	1.36	4.34	1.89	6.42
Che_01097 peptidease S14, ClpP	6.49	7.89	7.83	8.17	8.96	9.75	-1.34	-0.32	-0.79	-1.36	-0.34	-0.47	-1.92	-1.11	-1.58	-1.88	-0.97	-0.57	-1.05	-1.6	-1.6	-1.6	-1.6	-0.57	-1.44	-0.74	-1.17	-0.56	-1.07	2.17	2.7	0.7		
Che_01718 proteasome inhibitor, Serp subunit	12.6	13.3	13.3	10.5	10.5	10.4	-0.13	0.03	-0.36	-0.77	0.3	0.69	0.06	0.23	-0.03	-0.1	-0.4	-0.5	-0.2	-0.1	0.21	0.21	0.21	0.21	-0.61	-0.11	-0.3	-0.44	-0.26	0.29	5.71	3.9	9.84	
Che_02704 Transketolase-like protein	12.6	13.3	13.3	10.4	13.2	14	-0.7	0.09	-0.78	-0.86	-0.07	-0.61	-0.69	-0.25	-0.62	-1.09	-0.31	-0.53	-0.8	-0.4	-0.5	-0.02	-0.2	-0.6	-0.4	-0.07	-0.54	-0.53	-0.04	1.55	1.7	0.88		
Che_01378 response regulator receiver modulated met	5.29	5.91	5.93	5.32	6.82	7.26	1.38	0.61	0.44	-0.64	-1.41	-1.53	-3.35	-0.89	-1.94	1.48	1.94	0.6	-0.7	-1.2	-1.6	-1.5	-0.9	-0.61	-1.66	-0.7	-0.54	-1.34	-0.53	-1	2.86	1.64	0.4	
Che_02728 phosphatase M1.6, aminopeptidase 1	12.4	12	12.3	12.4	11.7	12.3	0.37	-0.02	-0.65	-0.3	-0.36	0.72	0.3	0.69	0.06	0.23	-0.03	-0.1	-0.4	-0.5	-0.2	-0.1	0.21	0.21	-0.61	-0.11	-0.3	-0.44	-0.26	0.29	5.71	3.9	9.84	
Che_01170 dihydropyridine reductase	9.79	8.59	9.74	8.63	8.97	8.3	1.2	0.11	-0.33	0.05	-1.04	0.82	0.71	0.77	0.33	1.26	0.38	0.97	0.4	-0.8	-0.2	-0.57	0.35	-0.6	-0.16	-0.29	-0.14	-0.14	0.24	1.41	0.71	1.41		
Che_00062 sulfolip	12.5	12.7	12.7	12.3	12.7	12.7	-0.07	-0.11	-0.52	-0.42	-0.26	0.29	0.04	0.71	0.3	0.56	-0.11	-0.33	-0.6	-0.5	-0.4	-0.2	0.24	0.34	-0.61	-0.27	-0.35	-0.14	-0.23	0.29	2.4	1.44	3.06	
Che_00184 UDP-glucose 4-epimerase	11.1	11	11.2	11.2	11.9	12.6	0.05	0.03	-0.17	-0.18	-0.14	0.67	-0.17	0.03	0.17	0.03	0.17	0.03	-0.4	-0.9	-0.4	0.1	0.1	0.1	-0.16	-0.36	-0.04	-0.34	0.63	0.51	11.77	11.1	0.7	
Che_02629 UDP-N-acetylglucosamine phosphorylase	10.6	10.9	11	11.1	10.4	11	-0.26	-0.07	-0.61	-0.41	-0.22	0.2	0.15	0.61	0.07	0.54	0.19	0.03	-0.6	-0.4	-0.3	0.19	0.21	-0.61	-0.37	-0.25	-0.14	-0.31	-0.21	2.61	2.05	4.91		
Che_01378 response regulator receiver modulated met	5.29	5.91	5.93	5.32	6.82	7.26	1.38	0.61	0.44	-0.64	-1.41	-1.53	-3.35	-0.89	-1.94	1.48	1.94	0.6	-0.7	-1.2	-1.6	-1.5	-0.9	-0.61	-1.66	-0.7	-0.54	-1.34	-0.53	-1	2.86	1.64	0.4	
Che_00568 protein of unknown function DUF1865	9.69	9.99	10.1	10.1	11.8	12.4	-0.3	-0.03	-0.52	-0.05	-0.15	-0.2	-2.36	-1.72	-2.21	-0.59	-0.06	-0.3	-0.6	-0.4	-1.7	-0.9	0.1	-0.59	-1.72	-1.31	-0.53	-0.03	-1.03	2.49	6.28	13.51		
Che_01383 Tetraacycline resistance TPR 2	11.1	11.4	11.6	11.5	10.5	11.1	-0.3	0.03	-0.65	-0.47	-0.14	0.67	0.32	1.14	0.67	0.32	1.14	0.67	0.32	1.14	0.67	0.32	1.14	0.67	-0.08	-0.58	-0.14	-0.58	-0.47	2.49	0.81	12.98		
Che_02717 ribosomal protein L33	7.4	7.59	8.2	7.86	7.3	8.01	-0.19	0.35	-0.69	-0.8	-0.26	0.08	-0.42	0.88	-0.16	-0.46	1.12	-0.23	-0.45	-0.5	-0.5	-0.4	0.04	0.04	-0.6	-0.08	-0.16	-0.54	-0.4	0.14	1.48	2.62	0.97	
Che_02542 binding protein of unknown transport systems	10.2	10.2	10.2	10.2	10.2	10.2	0.03	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36	-0.36		
Che_00665 HicA	8.14	7.19	8.29	8.29	7.68	8.38	0.95	-0.3	-0.69	0.15	-1.1	0.45	-1.19	0.3	0.99	0.95	-0.91	-0.23	-0.4	-0.3	-0.4	-0.05	0.13	-0.61	-0.55	-0.0	-0.54	-0.46	-0.02	1.43	1.78	0.49		
Che_01097 peptidease S14, ClpP	6.49	7.89	7.83	8.17	8.96	9.75	-1.34	-0.32	-0.79	-1.36	-0.34	-0.47	-1.92	-1.11	-1.58	-1.88	-0.97	-0.57	-1.05	-1.6	-1.6	-1.6	-1.6	-0.57	-1.44	-0.74	-1.17	-0.56	-1.07	2.17	2.7	0.7		
Che_01316 proteasome S8 and S53, subunit, knase	11.5	12.4	12.5	12.6	13.2	13.9	-0.89	-0.44	-0.71	-0.99	-0.24	-1.71	-1.53	-2.72	-1.92	-1.32	-1.41	-0.38	-0.5	-1.3	-0.8	-0.4	0.5	-0.62	-1.21	-0.59	-0.58	-0.45	-0.39	1.39	2.53	4.48		
Che_01253 Xanthine/xanthine dehydrogenase C, C-terminal	11.5	13.2	13.2	10.7	11.6	11.6	-0.75	-0.35	-0.94	-1.73	-0.33	-0.78	-1.59	-2.32	-1.92	-1.38	-1.06	-1.07	-1.2	-1.5	-0.2	0.53	1.09	1.2	-0.62	-1.04	-1.35	-0.02	1.11	0.97	4.07	3.59	0.4	
Che_02942 transcriptional regulator, C-terminal	10.1	10.1	10.1	10.1	10.1	10.1	0.12	0	-0.4	-0.1	0.12	0	0	-0.4	0.12	0	0	0	0	0	0	0	0	0	-0.17	-0.4	-0.1	-0.1	0.12	0.12	0.12	0.12	0.12	
Che_00458 exoenzyme B, small subunit	6.36	6.97	7.17</																															



Chc_02720 ABC transporter related protein	9.41	9.3	9.79	9.79	8.89	9.63	0.11	0	1.74	-0.38	-0.49	-0.52	-0.33	0.9	0.16	-0.09	0.03	-0.4	0.6	0.6	-0.3	-0.3	0.26	-0.8	-0.34	0.36	0.7	-0.29	0.3	17.44	2.36	3.49		
Chc_06009 peptidase M48	8.64	8.07	8.74	8.74	8.47	10.3	-1.11	-0.08	-0.77	-1.5	-0.48	-0.87	-2.39	-1.33	-0.17	-1.59	-0.06	0.83	-1.1	0.6	-1.7	-1.0	0.17	-0.8	-1.77	-1.09	0.7	-1.43	0.84	1.5	2.74	4.87		
Chc_02050 CHRSP-associated RAMP protein, SS02435 family	8.82	9.37	9.82	9.82	9.82	9.82	-0.55	-0.03	-0.73	-0.78	-0.48	-0.65	-0.83	-0.77	-0.11	-1.98	-0.09	0.37	-0.93	-0.6	-0.8	-0.13	0.12	-0.81	-0.65	-0.16	-0.71	0.54	1.32	1.25	6.22			
Chc_02054 PspA protein	5.99	4.17	6	6.04	5.52	6.15	-1.78	-0.04	0.63	-0.05	-1.87	-0.43	-1.98	-0.48	-0.11	1.98	-0.09	-0.03	-0.4	-1.2	0.3	-1.1	-0.12	-0.81	-0.65	-0.16	-0.71	0.54	1.32	1.25	6.22			
Chc_02051 Ribonuclease A	9.13	10.5	10.2	10.2	9.89	10.2	-0.12	-0.11	0.74	-0.12	-0.75	-0.18	-0.48	-0.12	-0.11	1.98	-0.09	-0.03	-0.4	-1.2	0.3	-1.1	-0.12	-0.81	-0.65	-0.16	-0.71	0.54	1.32	1.25	6.22			
Chc_02055 phosphoserine aminotransferase	12.7	13.7	14.3	14.3	13.1	13.8	-0.94	-0.21	0.73	-1.34	-0.61	-0.32	-1.11	1.02	0.5	1.38	-0.62	-0.07	-0.3	-1.0	-0.6	-0.2	-0.39	0.44	-0.81	-0.37	-0.48	-0.71	0.31	0.39	1.57	1.08	2.71	
Chc_02146 single-stranded DNA specific exonuclease Rct1	11.7	12.1	12.5	12.6	10.9	11.5	-0.35	-0.03	0.6	-0.81	-0.49	-0.79	-0.54	-1.6	1.03	-0.65	-0.06	-0.07	-0.8	-0.2	-0.2	-0.06	0.66	-0.81	-0.02	-0.97	-0.71	0.03	0.77	2.97	0.98	35.58		
Chc_02025 phosphoserine phosphatase	12.7	13.7	14.3	14.3	13.1	13.8	-0.94	-0.21	0.73	-1.34	-0.61	-0.32	-1.11	1.02	0.5	1.38	-0.62	-0.07	-0.3	-1.0	-0.6	-0.2	-0.39	0.44	-0.81	-0.37	-0.48	-0.71	0.31	0.39	1.57	1.08	2.71	
Chc_02056 type IV sodium/calcium exchanger membrane region	1.98	4.86	6.1	6.04	5.27	5.49	-1.12	-0.25	0.79	-0.13	-1.5	-1.28	-0.63	-1.41	-0.87	1.36	-0.75	-0.37	-0.51	-1.0	-0.5	-0.37	-0.54	-0.81	-0.67	-0.72	-0.71	0.13	0.58	1.48	0.8	1.35		
Chc_02170 ABC transporter related protein	9.13	10.5	10.2	10.2	9.89	10.2	-0.12	-0.11	0.74	-0.12	-0.75	-0.18	-0.48	-0.12	-0.11	1.98	-0.09	-0.03	-0.4	-1.2	0.3	-1.1	-0.12	-0.81	-0.65	-0.16	-0.71	0.54	1.32	1.25	6.22			
Chc_02056 type IV sodium/calcium exchanger protein PIM	14.3	14.5	15.1	15	14.3	15.1	-0.28	-0.03	0.75	-0.8	-0.49	-0.77	-0.54	-1.34	0.73	-0.05	-0.37	-0.12	-0.43	-0.8	-0.6	-0.5	-0.4	-0.25	0.15	-0.82	-0.52	-0.22	-0.72	-0.43	0.19	0.3	2.15	1.18
Chc_02160 histidine triad (HTI) protein	10.7	10.5	11.3	11.2	11.2	11.9	-0.21	0.11	0.64	-0.33	-0.63	-0.49	-1.34	-0.04	-0.71	0.04	0.38	-0.07	-0.7	-0.7	-0.8	-1.2	-0.2	-0.82	-0.10	-0.16	-0.72	-0.84	-0.11	4.81	29.51	1.86		
Chc_02058 App-1 protein	7.96	7.86	7.96	7.96	7.96	7.96	-0.07	-0.07	0.79	-0.79	-0.79	-0.79	-0.79	-0.79	-0.79	0.04	-0.07	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	
Chc_02070 protein of unknown function DUF21	10.4	10.2	10.8	10.8	11	8.36	0.93	0.26	-0.14	-0.67	-0.41	-2.05	1.12	2.46	1.93	0.1	-0.41	-0.17	-0.6	-0.7	-0.39	0.13	-0.70	1.21	-0.83	-0.45	1.55	-0.72	0.34	1.23	4.45	0.67	12.13	
Chc_02077 phosphoglycerate kinase	10.2	10.6	11.1	11.2	10	10.7	-0.35	-0.07	0.64	-0.85	-0.57	-0.22	-0.07	1.07	0.5	0.65	-0.19	-0.07	-0.8	-0.6	-0.4	-0.2	-0.41	-0.84	-0.83	-0.32	-0.57	-0.72	-0.27	0.46	2.94	1.6	9.9	
Chc_02160 histidine triad (HTI) protein	10.7	10.5	11.3	11.2	11.9	11.9	-0.07	-0.07	0.79	-0.79	-0.79	-0.79	-0.79	-0.79	-0.79	0.04	-0.07	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	
Chc_02031 transposase S220-like protein	9.8	9.84	10.1	10.1	8.71	9.46	-0.68	0.04	0.75	-0.32	-1.14	1.09	-0.52	1.41	0.62	0.84	-0.16	-0.48	-0.6	-0.9	-0.4	-0.57	0.51	-0.83	-0.45	1.55	-0.72	0.34	1.23	4.45	0.67	12.13		
Chc_02056 type IV polyubiquitin protein PIM	14.3	14.5	15.1	15	14.3	15.1	-0.28	-0.03	0.75	-0.8	-0.49	-0.77	-0.54	-1.34	0.73	-0.05	-0.37	-0.12	-0.43	-0.8	-0.6	-0.5	-0.4	-0.25	0.15	-0.82	-0.52	-0.22	-0.72	-0.43	0.19	0.3	2.15	1.18
Chc_02051 histidine triad (HTI) protein	10.7	10.5	11.3	11.2	11.9	11.9	-0.07	-0.07	0.79	-0.79	-0.79	-0.79	-0.79	-0.79	-0.79	0.04	-0.07	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	-0.7	
Chc_02182 diglycylate cyclase with GAP sensor	11.4	12	12.5	12.7	11.4	12.1	-0.59	-0.23	-0.69	-1.08	-0.72	-0.03	-0.07	1.11	0.65	-0.95	-0.69	-0.23	-0.9	-0.7	-0.4	-0.2	-0.52	-0.82	-0.32	-0.57	-0.72	-0.27	0.46	1.9	1.24	3.09		
Chc_02047 cytoskeleton protein	5.09	4.09	5.32	5.39			1	0.07	-1	-0.23	-1.3	5.09	4.09	5.32	5.39	1.01	-0.19	0.5	-1	1.71	1.59	2.42	0.36	-0.83	-2.11	3.87	-0.72	1.67	1.04	2.12	5.25	68.44		
Chc_02186 alpha/beta hydrolase fold 4	10.1	9.7	10.1	10.5	9.6	10.8	-0.48	-0.01	-1	-0.32	-0.76	-0.47	-1.46	-0.78	0.3	0.31	1	-1.6	-0.8	-0.7	-0.3	-0.8	-0.28	-0.82	-0.35	0.04	-0.72	-0.3	0.05	5.39	0.99	0.58		
Chc_02149 aminoacyl-histidine dipeptidase	8.49	9.66	10.1	10.1	9.04	9.55	-1.17	-0.02	0.51	-1.63	-0.48	-0.55	-1.1	1.08	-0.99	-1.67	-0.03	-0.37	-1.1	-0.6	-0.7	-0.1	-0.42	0.49	-0.84	-0.38	-0.59	-0.73	-0.32	0.48	1.51	1	5.8	
Chc_02083 2-amino-4-hydroxy-6	9.44	9.58	10.1	10.2	9.48	10.1	-0.14	-0.11	0.62	-0.68	-0.65	-0.4	-0.52	0.64	0.13	0.4	-0.31	0	-0.7	-0.5	-0.4	-0.21	0.25	-0.87	-0.07	-0.28	-0.73	-0.47	0.23	3.83	3.76	3.51		
Chc_02052 dimethylallyltransferase	8.50	9.43	9.89	9.86	8.26	8.72	-0.68	-0.07	-0.46	-1.34	-0.33	-0.29	-0.71	1.63	1.24	-1.31	-0.19	0.33	-1	-0.6	-0.4	-0.31	0.67	0.84	-0.84	-0.09	0.99	-0.73	-0.09	0.79	1.78	0.65	6.36	
Chc_02043 electron transport complex, hnfAEC02 type B	9.41	10.2	10.7	10.7	11.4	12.2	-0.76	-0.04	-1.18	-1.25	-0.33	-1.99	-2.01	-2.4	-1.48	-1.16	-0.09	-0.53	-1	-0.6	-1.4	-1.1	-0.4	-0.6	-0.84	-1.45	-0.67	-0.73	-1.18	0.51	1.95	0.88	4.66	
Chc_02060 ABC transporter related protein-like	10.4	10.5	11.2	11.1	9.87	10.6	-0.04	0.11	-0.68	-0.45	-0.58	-0.69	-0.49	-0.48	-1.34	-0.55	-0.17	0.38	-0.2	-0.6	-0.2	-0.2	-0.54	0.47	-0.84	-0.22	-0.65	-0.71	-0.19	0.52	4.32	2.89	5.56	
Chc_02021 dehydrobinase synthase	4.92	4.95	5.46	5.49	4.84	5.81	-0.63	0	1.7	-1.17	-0.34	-0.62	-0.83	0.5	1	0.03	1.83	-0.9	-0.6	-0.4	-0.2	-0.11	0.79	-0.85	-0.39	0.04	-0.74	-0.33	0.05	2.21	1.05	3.6		
Chc_02027 purine operon repressor, Prr	11.5	11.5	12.1	12.1	10.3	11.1	-0.02	0.05	0.34	-0.63	-0.56	-1.04	0.52	1.67	1.08	-0.25	-0.19	-0.27	-0.6	-0.1	-0.04	-0.08	0.75	-0.85	-0.02	-0.97	-0.74	-0.03	0.77	5.91	0.4	10.29		
Chc_02099 anti-sigma factor antagonist	10.8	10.7	11.3	11.3	9.74	10.4	-0.1	0.08	0.63	-0.58	-0.6	1.05	0.34	1.63	0.94	-0.11	0.28	-0.03	-0.7	-0.6	-0.1	-0.57	0.68	-0.85	-0.04	-0.91	-0.74	-0.05	0.77	6.23	1.27	11.3		
Chc_02235 protein of unknown function DUF115	10.8	10.7	11.3	11.3	9.74	10.4	-0.1	0.08	0.63	-0.58	-0.6	1.05	0.34	1.63	0.94	-0.11	0.28	-0.03	-0.7	-0.6	-0.1	-0.57	0.68	-0.85	-0.04	-0.91	-0.74	-0.05	0.77	6.23	1.27	11.3		
Chc_02051 Ribosomal protein L29	8.97	9.74	10.3	10.8	8.14	8.76	-1.17	-0.49	-0.62	-1.69	-1.01	-0.43	0.98	2.12	1.99	-1.67	-1.5	0	-1.2	-0.8	-0.3	0.24	0.91	1.24	-0.86	-0.03	1.31	-0.75	0.04	1.04	1.26	0.54	3.42	
Chc_02022 ribosomal protein L35	10.6	10.2	12.5	13.1	10.9	11.6	-1.39	-0.56	-0.73	-1.91	-1.08	-0.57	-1.38	1.03	1.45	-1.94	-1.72	-0.37	-1.2	-0.9	-0.6	-0.6	-0.66	0.84	-0.86	-0.21	-0.88	-0.75	-0.18	0.7	1.16	0.74	2.18	
Chc_02091 protein of unknown function DUF448	8.56	8.52	9.35	9.37	8.24		-0.09	-0.4	-0.57	-0.82	-0.73	-0.48	-0.35	1.05	1.35	0.63	-0.46	-0.09	-0.8	-0.7	-0.2	-0.18	0.58	-0.86	-0.06	-0.16	-0.6	-0.5	-0.1	0.6	2.39	0.6	6.02	
Chc_02186 single-strand binding protein	12.8	13.5	14	14.1	12	12.3	-0.62	-0.03	0.33	-1.18	-0.59	-0.88	1.17	2.06	1.76	-0.99	-0.66	-0.07	-0.9	-0.6	-0.1	-0.33	-0.88	1.12	-0.88	-0.04	1.28	-0.76	0.02	1.02	2.27	0.56	4.68	
Chc_02079 UTP-N-acetyluridylyl transferase	9.64	10.1	10.7	10.9	9.88	10.5	-0.48	-0.22	-0.61	-1.76	-1.04	-0.57	-1.38	1.03	1.45	-1.94	-1.72	-0.37	-1.2	-0.9	-0.6	-0.6	-0.6	-0.6	-0.86	-0.21	-0.88	-0.75	-0.18	0.7	1.16	0.74	2.18	
Chc_02097 hypothetical bacterial protein	8.56	8.52	9.35	9.37	8.24		-0.09	-0.4	-0.57	-0.82	-0.73	-0.48	-0.35	1.05	1.35	0.63	-0.46	-0.09	-0.8	-0.7	-0.2	-0.18	0.58	-0.86	-0.06	-0.16	-0.6	-0.5	-0.1	0.6	2.39	0.6	6.02	
Chc_02087 protein of unknown function DUF322	8.86	9.81	7.28	9.03	7.58	8.11	0.73	0.25	0.33	-0.67	-1.15	1.03	-0.23	1.7	0.92	0.68	0.81	0.3	0.8	-0.7	-0.1	-0.31	0.77	-0.87	-0.12	-0.85	-0.76	-0.11	0.68	2.15	0.88	3.77		
Chc_02029 ribosomal protein S13	8.86	9.4	10.3	10.7	9.31	9.82	-0.88	-0.39	-0.51	-1.47	-1.05	-0.46	-0.88	0.99	0.87	-1.51	-1.37	-0.11	-0.37	-0.7	-0.8	-1.2	-0.37	0.64	-0.87	-0.43	-0.55	-0.76	-0.36	0.45	1.48	1.23	1.86	
Chc_02186 cell division/interphase	10.1	10.1	11.4	11.4	10.7	11.4	-0.14	-0.07	-0.37	-0.82	-0.73	-0.48	-0.35	1.05	1.35	0.63	-0.46	-0.09	-0.8	-0.7	-0.2	-0.18	0.58	-0.86	-0.06	-0.16	-0.6	-0.5						



Che_0026 Grx/GreB family elongation factor	9.38	10.2	11.2	11.3	12	-0.98	-0.02	0.72	-2	-1.04	-2.07	1.81	-0.07	-0.77	-1.43	-0.03	-0.33	-1.3	-0.8	-1.4	-1	-0.1	0.2	-1.17	-1.38	-0.22	-1	-1.12	-0.6	2.14	2.64	2.75	
Che_0082 ATP phosphoribosyltransferase	2.46	5.32	6.19	6.49	8.39	-1.86	-1.3	-0.53	-2.73	-1.12	-1.4	-0.07	1.33	-1.1	-2.52	-0.91	-0.1	-0.81	-1.1	-0.3	0.53	0.76	-1.17	-0.57	0.78	-1	-0.47	0.62	1.31	1.01	3.22		
Che_02327 Two component transcriptional regulator, LuxR	1.81	2.32	3.17	3.58	4.09	5	-1.49	-0.91	0.64	-0.74	-0.28	2.68	0.92	4.62	5	-0.97	-0.1	-0	-0.6	-1.3	0.5	1.17	-1.07	-1.07	-1.1	-0.87	-0.1	-0.7	0.05	1.78	1.13		
Che_00299 ribosomal protein L24yL30yL32yL50yL52yL54yL55y	5.26	7.01	8.14	7.92	8.14	8.54	-1.34	0.22	-0.4	-2.47	-0.91	-2.47	-1.53	0	0.62	-1.88	0.72	0.73	-1.5	-0.8	-1.6	-0.1	-0.2	-1.17	-1.35	-0.03	-1	-1.11	0.01	1.66	2.02	0.6	
Che_02323 ribosomal protein L20	1.58	11.5	12.3	12.18	13.4	14.7	-0.64	-0.1	-0.42	-1.2	-0.34	-0.3	-0.43	-0.18	-0.27	-0.36	-0.1	-0.2	-0.3	-1.1	-0.3	-0.6	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	1.73	1.98		
Che_02443 GNCS-related N acetyltransferase	6.51	6.04	7.38	7.52	8.81	10.2	0.47	-0.14	-0.35	-0.87	-1.48	-3.3	-41.2	-2.43	-2.64	0.36	-0.41	0.9	0.8	-1.1	-1.9	-2	-1.2	-1.2	-1.18	-2.55	-1.61	-1.01	-2.06	-1.24	4.82	6.48	5.91
Che_00444 Transketolase-like protein	5.58	5.25	6.55	6.49	7.17	4.17	-0.33	0.06	-1	-0.97	-1.24	2.41	1.08	3.38	2.32	0.19	-0.22	-1.27	-0.8	0.9	0.4	0.29	1.5	1.42	-1.18	-0.33	1.87	-1.01	0.25	1.48	8.62	10.8	5.34
Che_02558 transcriptional activator, BcdR/Nr22 family	10.1	10.1	11.6	11.4	11.7	11.8	-0.04	-0.1	-0.14	-0.11	-0.17	1.1	0.07	0.14	-0.16	-0.14	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	1.23	1.49	1.39	
Che_01229 Spore germination protein-like protein	10.5	11	12.1	12.1	10.2	10.8	-0.49	-0.09	-0.55	-1.57	-1.17	0.27	0.21	0.14	1.18	0.82	-0.25	0.23	-1.1	-0.9	0.4	-0.1	0.77	0.91	-1.2	-0.21	-1.14	-1.02	-0.18	0.91	3.28	1.06	11.7
Che_01283 endonuclease III, NAD-dependent	9.49	9.66	10.8	10.9	9.62	10.2	-0.17	-0.15	-0.58	-1.28	-1.26	-0.13	0.54	1.15	0.72	0.43	0.44	-0.13	-1.1	-0.9	-0.6	-0.4	0.5	0.56	-1.2	-0.6	0.65	-1.02	0.52	4.39	3.54	5.22	
Che_02543 Nucleotide transferase	10.1	10.1	11.2	11.3	11.7	11.8	-0.04	-0.1	-0.14	-0.11	-0.17	1.1	0.07	0.14	-0.16	-0.14	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	1.23	1.49	1.39	
Che_00771 putative helix-turn-helix protein, TMM3/p13-like	10.1	10.1	11.4	11.7	8.1	8.9	-0.05	-0.33	-0.76	-1.29	-1.57	1.91	1.2	3.2	2.77	-0.28	-1	-0.47	-1	-1.1	0.33	0.34	1.46	-1.2	0.35	-0.22	0.26	1.59	2.81	1.97	6.59		
Che_00643 Nucleotide transferase	4.25	3.46	5.21	5.13	1.58	2	0.79	0.08	-0.42	-0.96	-1.67	2.67	1.46	3.63	1.33	0.75	0.28	0.67	-0.8	-1.1	0.66	0.45	1.62	1.85	-1.2	0.58	2.35	-1.02	0.45	1.85	3.5	1.81	11.29
Che_02091 hydro-lyase, Fe-type, tartaric/nicotinic	12.9	12.9	12.9	12.8	13.4	14.7	-0.04	-0.1	-0.14	-0.11	-0.17	1.1	0.07	0.14	-0.16	-0.14	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	-0.1	1.23	1.49	1.39	
Che_00937 fatty acid/phospholipid synthesis protein PlsX	12.9	12.9	12.4	14	11.5	12.1	-0.06	-0.03	-0.62	-1.15	-1.12	1.38	0.82	2.53	1.94	-0.3	-0.06	0	0.9	-0.9	0.1	0.37	1.1	1.21	-1.19	0.13	-0.63	-1.02	0.09	1.29	8.28	14.9	90.85
Che_01283 endonuclease III	12.4	12.8	14	13.9	12.3	13	-0.4	0.11	-0.66	-1.61	-1.1	0.04	0.22	1.65	0.88	0.72	0.38	-0.13	-1.1	-0.9	-0.5	-0.3	0.88	0.65	-1.21	-0.4	0.88	-1.03	-0.34	0.7	3.46	1.75	7.81
Che_02067 DNA segregation Phase III/SpolIIE and related	10.1	10.1	11.2	11.3	11.7	12.1	0.05	-0.04	-0.61	-1.08	-1.17	-1.56	-2.22	-0.48	-1.05	-0.16	-0.09	0.03	-0.9	-0.9	-1.2	-1.1	-1.3	1.24	-1.21	-1.6	-0.49	-1.03	-0.27	13.71	22.91	17.73	
Che_01229 putative anti-sigma regulatory factor	10.6	10.9	12.3	12.9	4.75	5.7	-0.27	-0.64	-0.95	-1.65	-2.02	5.87	7.52	7.21	-0.56	-1.97	-1.1	-1.3	-2.05	2.06	3.45	0.83	-1.21	-0.63	-1.21	-0.63	-1.21	-0.63	-1.21	1.68	5.35	7.84	
Che_02256 replicative DNA helicase	12	12.6	13.7	13.8	12.5	13.4	-0.54	-0.07	-0.92	-1.65	-1.18	-0.43	0.81	1.22	0.37	0.89	0.19	-1	-1.1	-0.9	-0.5	0.48	0.37	-1.22	-0.58	-0.45	-1.04	-0.48	0.37	3.19	1.48	1.88	
Che_02076 periplasmic sensor signal transduction histidine kinase	8.45	8.9	10	10.1	11.7	12.3	-0.45	-0.18	-0.65	-1.29	-1.2	-3	-1.64	-2.11	-0.78	-0.53	-0.1	-1.1	-1	-1.9	-1.7	-1.9	-1.9	-1.22	-2.34	-1.21	-1.04	-1.18	0.93	3.08	7.27	7.96	
Che_02899 putative anti-sigma regulatory factor	10.4	10.3	11.5	11.5	9.92	10.6	0.12	0.04	-0.65	-1.08	-1.16	0.49	-0.28	1.57	0.88	-0.07	0.16	-0.1	-0.9	-0.3	-0.3	-0.5	0.65	-1.22	-0.39	0.89	-1.04	-0.33	0.71	14.41	7.17	16.24	
Che_00533 hypothetical protein	0.84	0.32	6.64	6.32	6.11	7.09	0.84	0.32	-0.98	-1.28	-1.18	-0.75	-2.57	0.53	-0.77	0.81	1.03	-1.2	-1.2	-1.2	-1.1	0.16	-0.2	-1.22	-1.22	-1.05	-1.04	-0.99	-0.02	2.36	2.41	0.61	
Che_01203 SpoIIE	9.94	10.6	11.7	11.7	11.5	14.4	-0.61	-0.07	-0.86	-1.78	-1.1	-3.58	-3.83	-1.4	-2.73	-0.98	0.25	-0.8	-1.2	-0.9	-1.1	1.8	-0.9	-1.22	-2.48	-1.46	-1.04	-2	1.12	2.92	4.86	6.32	
Che_02207 isopentenyl diphosphate	4.32	5.3	5.39	5.32	6.17	7.27	1.52	0.07	-1	-0.87	-2.32	-1.65	-4.27	-0.78	-1.95	1.88	0.25	-1.6	-1.4	-1.2	-2	-0.5	0.9	-1.23	-1.86	-0.74	-1.05	-1.5	-0.56	1.97	2.34	2.03	
Che_02283 methyl-accepting chemotaxis sensory transducer	5.88	5.29	6.62	6.81	5.49	6.6	0.59	0.09	-1.11	-1.04	-1.54	0.39	-1.31	1.43	0.23	0.51	0.31	-1.63	-0.8	-1.1	-0.3	0.58	0.33	-1.23	-0.44	-1.05	-0.37	0.33	4.62	1.09	1.31		
Che_02285 methyl-accepting chemotaxis sensory transducer	5.88	5.29	6.62	6.81	5.49	6.6	0.59	0.09	-1.11	-1.04	-1.54	0.39	-1.31	1.43	0.23	0.51	0.31	-1.63	-0.8	-1.1	-0.3	0.58	0.33	-1.23	-0.44	-1.05	-0.37	0.33	4.62	1.09	1.31		
Che_02255 (HNAIIE) hydrolase	11.8	12.1	13.2	13.3	12.5	13.4	-0.25	-0.07	-0.86	-1.38	-1.2	-0.71	-1.32	0.67	-0.12	0.53	-0.19	-0.8	-0.9	-0.8	0.22	0.11	-1.23	-0.89	-0.12	-0.75	-0.11	-0.45	2.61	1	1		
Che_01011 Pectinolytic glycosyltransferase	7.41	7.55	8.27	8.81	8.31	9.1	-1.14	-0.09	-0.79	-1.31	-1.26	-0.9	-1.55	0.41	-0.29	-0.4	-0.25	-0.57	-1	-0.9	-0.9	-0.9	0.1	0.02	-1.24	-1.08	-1.01	-0.68	0.02	3.76	0.04	0.55	
Che_02744 LysC transglycosylase, catalytic	9.76	9.71	11	11.4	8.97	9.67	-0.07	-0.18	-0.65	-1.28	-1.05	-0.69	-0.04	2.07	1.49	0.36	0.97	-0.27	-1.1	-1	-0.2	-0.2	0.88	1.04	-0.16	-1.34	-1.06	-1.14	0.98	1.03	1.64	0.41	
Che_00936 O-acetyl (acyl carrier protein) synthase II	11.1	11.9	13.1	13.2	10.3	11.1	-0.86	-0.1	-0.8	-1.97	-2.11	0.75	0.81	2.72	2.02	-1.28	-0.28	-0.6	-1.39	-0.2	0.77	1.19	1.28	-1.24	-0.06	-1.63	-1.06	-1.06	1.29	2.39	0.4	8.73	
Che_01564 GNCS-related N acetyltransferase	9.03	9.36	10.7	10.7	9.48	6.34	-0.33	-0.14	-0.88	-1.5	-1.31	3.57	1.02	5.07	4.33	-0.63	-0.41	-0.87	-1.1	-1.09	1.33	2.49	1.25	-1.31	3.25	-1.07	1.03	2.55	1.82	3.26	11.75		
Che_01569 O-acetylhomoserine aminocarbonyltransferase	9.03	9.36	10.7	10.7	9.48	6.34	-0.33	-0.14	-0.88	-1.5	-1.31	3.57	1.02	5.07	4.33	-0.63	-0.41	-0.87	-1.1	-1.09	1.33	2.49	1.25	-1.31	3.25	-1.07	1.03	2.55	1.82	3.26	11.75		
Che_00679 Serine-type D-Ala-D-Ala carbonyltransferase	10.1	10.6	11.8	11.8	10.4	11.1	-0.45	-0.07	-0.7	-1.62	-1.24	-0.26	0.51	1.36	0.73	0.78	-0.19	-0.27	-1.1	-0.9	-0.6	0.4	0.55	0.57	-1.26	-0.56	-0.74	-1.07	-0.46	5.99	3.63	20.3	
Che_01205 putative serine kinase, PfkA	11.5	11.8	13	13	13.5	16.2	-0.31	0	-0.72	-1.51	-1.2	-4.02	-4.43	-2.51	-3.23	-0.6	-0.03	-0.33	-1.1	-0.9	-2.3	-1.1	-1.3	-1.6	-1.26	-2.39	-1.96	-1.07	-2.36	-1.52	4.7	10.22	20.22
Che_01573 nitrogenase protein	8.99	9.78	11	11.2	12.7	14.9	-0.71	-0.25	-0.86	-1.26	-1.2	-4.02	-4.43	-2.51	-3.23	-0.6	-0.03	-0.33	-1.1	-0.9	-2.3	-1.1	-1.3	-1.6	-1.26	-2.39	-1.96	-1.07	-2.36	-1.52	4.7	10.22	20.22
Che_01309 Radical SAM	9.58	8.6	10.5	10.6	12.5	13.2	-0.98	-0.08	-0.65	-0.93	-1.99	-2.93	-4.56	-2	-2.57	-0.99	-0.22	-0.1	-1.3	-1.8	-2.2	-1	-1.2	-1.27	-2.55	-1.55	-1.08	-2.08	-1.2	6.39	21.9		
Che_01082 histidinol dehydrogenase	5.88	7.21	8.46	9.19	7.67	8.36	-1.33	-0.73	-0.69	-1.58	-1.79	-1.15	-1.79	0.83	-1.86	-2.25	-0.25	-1.5	-1.3	-1.7	-1.7	0.28	0.62	-1.27	-1.04	-0.34	-1.08	-0.85	0.28	1.2	1.76	1	
Che_00902 3-methyl-2-oxobutanoic acid dehydrogenase	5.88	7.21	8.46	9.19	7.67	8.36	-1.33	-0.73	-0.69	-1.58	-1.79	-1.15	-1.79	0.83	-1.86	-2.25	-0.25	-1.5	-1.3	-1.7	-1.7	0.28	0.62	-1.27	-1.04	-0.34	-1.08	-0.85	0.28	1.2	1.76	1	
Che_01973 Transcription factor Tfr_2	10.4	10.2	11.5	11.7	12.4	12.9	-0.21	-0.12	-0.53	-1.12	-1.45	-1.93	-2.67	0.81	-1.22	0.04	0.34	0.3	-0.9	-1	-1.3	-1.3	-0.5	0.5	-1.28	-1.83	-0.61	-1.09	-1.48	-0.46	7.99	14.23	4.99
Che_01041 N-acetylaminoadenine-9-phosphate synthase	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Che_01565 Nitrogenase	9.04	10.1	11.5	11.7	11.8	13.9	-0.57	-0.1	-0.47	-1.26	-1.46	-0	-0.58	2.46	1.88	1.01	3.16	-3.47	-1.5	-1.5	-0.5	1.48	1.18	-1									







		log2 100-mer reads				Intersample variability (R)				Intersample variability (Rnet)						
locus	locus-description	Cellobiose		α-cellulose		CB vs αC(Z)		Cellobiose α-cellulose		CB vs αC(Znet)		Cellobiose α-cellulose		W	Wnet	Wstats
Cthe_01492	NAD(P)H dehydrogenase (quinone)	11.39	11.42	8.65	8.61	2.74	2.81	-0.03	0.04	2.07	3.54	-0.22	0.32	3.76	4.8	5.93
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_01493	transcriptional regulator, PadR-like family	9.79	9.75	7.02	6.98	2.77	2.77	0.04	0.04	2.1	3.49	-0.14	0.32	3.76	4.8	6.55
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_00347	phosphofructokinase	15.77	15.26	10.59	12.32	5.18	2.94	0.51	-1.73	4.56	3.74	0.45	-2.36	3.76	4.8	1.38
Cthe_01490	RNA related	8.29	7.67	4.95	5.21	3.34	2.46	0.62	-0.26	2.68	3.03	0.59	-0.14	3.51	4.48	3.75
Cthe_01491	transcriptional regulator, PadR-like family	6.77	6.3	2.81	3.81	3.96	2.49	0.47	-1	3.32	3.07	0.4	-1.26	3.35	4.28	1.91
Cthe_02982	hypothetical protein	9.48	10.32	7.75	7.29	1.73	3.03	-0.84	0.46	1.04	3.87	-1.24	0.95	2.62	3.35	1.44
Cthe_02982	hypothetical protein	9.48	10.32	7.75	7.29	1.73	3.03	-0.84	0.46	1.04	3.87	-1.24	0.95	2.62	3.35	1.44
Cthe_01156	zinc finger, CHC2-type	5.29	3.32	4.32	3	0.97	0.32	1.97	1.32	0.27	-0.12	2.27	2.26	2.56	3.28	0.05
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
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Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
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Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
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Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0.14	0.53	2.41	3.09	2.97
Cthe_01575	purine nucleoside phosphorylase	7.3	7.04	5.13	4.95	2.17	2.09	0.26	0.18	1.49	2.49	0				



Cthe_01428	glycoside hydrolase, family 1	7.84	7.64	5.36	6.04	2.48	1.6	0.2	-0.68	1.81	1.76	0.06	-0.77	1.84	2.37	1.84
Cthe_00024	biotin biosynthesis protein BioC	5.21	6.13	4.39	5.7	0.82	0.43	-0.92	-1.31	0.11	0.04	-1.34	-1.73	1.83	2.35	0.03
Cthe_01429	hypothetical protein	2.32	1	1.58	0	0.74	1	1.32	1.58	0.03	0.88	1.46	2.65	1.81	2.33	0.16
Cthe_01812	Urease accessory protein UreD	4.32	3.17	3.81	2.32	0.51	0.85	1.15	1.49	-0.2	0.66	1.25	2.52	1.81	2.33	0.14
Cthe_01385	preprotein translocase, SecA subunit	12.08	13.86	11.33	12.8	0.75	1.06	-1.78	-1.47	0.04	0.97	-2.41	-1.97	1.8	2.32	0.18
Cthe_01385	preprotein translocase, SecA subunit	12.08	13.86	11.33	12.8	0.75	1.06	-1.78	-1.47	0.04	0.97	-2.41	-1.97	1.8	2.32	0.18
Cthe_01851	protein of unknown function DUF1113	11.22	10.08	10.68	9.36	0.54	0.72	1.14	1.32	-0.17	0.47	1.24	2.26	1.79	2.3	0.11
Cthe_01245	phosphoribosylamine-glycine ligase	9.37	11.1	8.84	10.15	0.53	0.95	-1.73	-1.31	-0.18	0.81	-2.35	-1.73	1.77	2.28	0.16
Cthe_01245	phosphoribosylamine-glycine ligase	9.37	11.1	8.84	10.15	0.53	0.95	-1.73	-1.31	-0.18	0.81	-2.35	-1.73	1.77	2.28	0.16
Cthe_01245	phosphoribosylamine-glycine ligase	9.37	11.1	8.84	10.15	0.53	0.95	-1.73	-1.31	-0.18	0.81	-2.35	-1.73	1.77	2.28	0.16
Cthe_01245	phosphoribosylamine-glycine ligase	9.37	11.1	8.84	10.15	0.53	0.95	-1.73	-1.31	-0.18	0.81	-2.35	-1.73	1.77	2.28	0.16
Cthe_01245	phosphoribosylamine-glycine ligase	9.37	11.1	8.84	10.15	0.53	0.95	-1.73	-1.31	-0.18	0.81	-2.35	-1.73	1.77	2.28	0.16
Cthe_01245	phosphoribosylamine-glycine ligase	9.37	11.1	8.84	10.15	0.53	0.95	-1.73	-1.31	-0.18	0.81	-2.35	-1.73	1.77	2.28	0.16
Cthe_00513	DNA binding domain, excisionase family	2.32	1.58			2.32	1.58	0.74		1.64	1.74	0.74		1.73	2.23	1.82
Cthe_00782	putative methyl-accepting chemotaxis sensory	4.81	4.86	3.17	3.32	1.64	1.54	-0.05	-0.15	0.95	1.68	-0.25	0.03	1.71	2.2	4.31
Cthe_00694	spermidine synthase	13.37	13.24	11.04	11.71	2.33	1.53	0.13	-0.67	1.65	1.66	-0.02	-0.76	1.66	2.14	1.73
Cthe_02281	response regulator receiver modulated CheB	11.38	10.96	7.45	9.22	3.93	1.74	0.42	-1.77	3.29	1.97	0.34	-2.42	1.66	2.14	0.88
Cthe_02281	response regulator receiver modulated CheB	11.38	10.96	7.45	9.22	3.93	1.74	0.42	-1.77	3.29	1.97	0.34	-2.42	1.66	2.14	0.88
Cthe_00694	spermidine synthase	13.37	13.24	11.04	11.71	2.33	1.53	0.13	-0.67	1.65	1.66	-0.02	-0.76	1.66	2.14	1.73
Cthe_00694	spermidine synthase	13.37	13.24	11.04	11.71	2.33	1.53	0.13	-0.67	1.65	1.66	-0.02	-0.76	1.66	2.14	1.73
Cthe_00694	spermidine synthase	13.37	13.24	11.04	11.71	2.33	1.53	0.13	-0.67	1.65	1.66	-0.02	-0.76	1.66	2.14	1.73
Cthe_02281	response regulator receiver modulated CheB	11.38	10.96	7.45	9.22	3.93	1.74	0.42	-1.77	3.29	1.97	0.34	-2.42	1.66	2.14	0.88
Cthe_00694	spermidine synthase	13.37	13.24	11.04	11.71	2.33	1.53	0.13	-0.67	1.65	1.66	-0.02	-0.76	1.66	2.14	1.73
Cthe_01616	phage minor structural protein	4	3.81	2.32	1.58	1.68	2.23	0.19	0.74	0.99	2.69	0.05	1.38	1.64	2.11	1.17
Cthe_02519	2-isopropylmalate synthase/homocitrate synthase	13.03	14.64	12.71	13.83	0.32	0.81	-1.61	-1.12	-0.4	0.6	-2.2	-1.44	1.62	2.09	0.15
Cthe_01870	GCN5-related N-acetyltransferase	11.34	10.23	10.66	9.58	0.68	0.65	1.11	1.08	-0.03	0.37	1.2	1.89	1.62	2.09	0.09
Cthe_02519	2-isopropylmalate synthase/homocitrate synthase	13.03	14.64	12.71	13.83	0.32	0.81	-1.61	-1.12	-0.4	0.6	-2.2	-1.44	1.62	2.09	0.15
Cthe_02519	2-isopropylmalate synthase/homocitrate synthase	13.03	14.64	12.71	13.83	0.32	0.81	-1.61	-1.12	-0.4	0.6	-2.2	-1.44	1.62	2.09	0.15
Cthe_02519	2-isopropylmalate synthase/homocitrate synthase	13.03	14.64	12.71	13.83	0.32	0.81	-1.61	-1.12	-0.4	0.6	-2.2	-1.44	1.62	2.09	0.15
Cthe_02519	2-isopropylmalate synthase/homocitrate synthase	13.03	14.64	12.71	13.83	0.32	0.81	-1.61	-1.12	-0.4	0.6	-2.2	-1.44	1.62	2.09	0.15
Cthe_01384	FoIC bifunctional protein	9.88	11.62	9.53	10.68	0.35	0.94	-1.74	-1.15	-0.37	0.79	-2.36	-1.48	1.61	2.08	0.18
Cthe_01384	FoIC bifunctional protein	9.88	11.62	9.53	10.68	0.35	0.94	-1.74	-1.15	-0.37	0.79	-2.36	-1.48	1.61	2.08	0.18
Cthe_01384	FoIC bifunctional protein	9.88	11.62	9.53	10.68	0.35	0.94	-1.74	-1.15	-0.37	0.79	-2.36	-1.48	1.61	2.08	0.18
Cthe_01384	FoIC bifunctional protein	9.88	11.62	9.53	10.68	0.35	0.94	-1.74	-1.15	-0.37	0.79	-2.36	-1.48	1.61	2.08	0.18
Cthe_01384	FoIC bifunctional protein	9.88	11.62	9.53	10.68	0.35	0.94	-1.74	-1.15	-0.37	0.79	-2.36	-1.48	1.61	2.08	0.18
Cthe_01384	FoIC bifunctional protein	9.88	11.62	9.53	10.68	0.35	0.94	-1.74	-1.15	-0.37	0.79	-2.36	-1.48	1.61	2.08	0.18
Cthe_01384	FoIC bifunctional protein	9.88	11.62	9.53	10.68	0.35	0.94	-1.74	-1.15	-0.37	0.79	-2.36	-1.48	1.61	2.08	0.18
Cthe_02279	polar amino acid ABC transporter, inner membrane	12.22	11.98	9.48	10.44	2.74	1.54	0.24	-0.96	2.07	1.68	0.11	-1.2	1.59	2.05	1.24
Cthe_02279	polar amino acid ABC transporter, inner membrane	12.22	11.98	9.48	10.44	2.74	1.54	0.24	-0.96	2.07	1.68	0.11	-1.2	1.59	2.05	1.24
Cthe_00564	Trans-hexaprenyltransferase	11.18	11.04	8.64	9.5	2.54	1.54	0.14	-0.86	1.87	1.68	-0.01	-1.05	1.58	2.04	1.34
Cthe_01500	ABC transporter related protein	8.23	8.04	6.58	6.74	1.65	1.3	0.19	-0.16	0.96	1.32	0.05	0.02	1.58	2.04	17.03
Cthe_00564	Trans-hexaprenyltransferase	11.18	11.04	8.64	9.5	2.54	1.54	0.14	-0.86	1.87	1.68	-0.01	-1.05	1.58	2.04	1.34
Cthe_00564	Trans-hexaprenyltransferase	11.18	11.04	8.64	9.5	2.54	1.54	0.14	-0.86	1.87	1.68	-0.01	-1.05	1.58	2.04	1.34
Cthe_00696	putative rRNA methylase	12.91	13.15	10.56	11.41	2.35	1.74	-0.24	-0.85	1.67	1.97	-0.49	-1.03	1.57	2.03	1.27
Cthe_02967	major facilitator superfamily MFS_1	8.94	8.61	6.41	7.18	2.53	1.43	0.33	-0.77	1.86	1.51	0.23	-0.91	1.56	2.01	1.43
Cthe_02799	Cystathionine gamma-synthase	10.29	10.33	8.75	8.86	1.54	1.47	-0.04	-0.11	0.85	1.57	-0.24	0.09	1.56	2.01	3.91
Cthe_01627	uncharacterized phage protein	3.7	2.32	0	1	3.7	1.32	1.38	-1	3.05	1.35	1.54	-1.26	1.56	2.01	0.94
Cthe_02799	Cystathionine gamma-synthase	10.29	10.33	8.75	8.86	1.54	1.47	-0.04	-0.11	0.85	1.57	-0.24	0.09	1.56	2.01	3.91
Cthe_02799	Cystathionine gamma-synthase	10.29	10.33	8.75	8.86	1.54	1.47	-0.04	-0.11	0.85	1.57	-0.24	0.09	1.56	2.01	3.91
Cthe_02799	Cystathionine gamma-synthase	10.29	10.33	8.75	8.86	1.54	1.47	-0.04	-0.11	0.85	1.57	-0.24	0.09	1.56	2.01	3.91
Cthe_02799	Cystathionine gamma-synthase	10.29	10.33	8.75	8.86	1.54	1.47	-0.04	-0.11	0.85	1.57	-0.24	0.09	1.56	2.01	3.91
Cthe_02799	Cystathionine gamma-synthase	10.29	10.33	8.75	8.86	1.54	1.47	-0.04	-0.11	0.85	1.57	-0.24	0.09	1.56	2.01	3.91
Cthe_02974	hypothetical protein	9.68	9.26	7.39	7.92	2.29	1.34	0.42	-0.53	1.61	1.38	0.34	-0.55	1.55	2	1.84
Cthe_01628	phage major capsid protein, HK97 family	6.09	4.52	2.81	3	3.28	1.52	1.57	-0.19	2.62	1.65	1.77	-0.03	1.52	1.96	0.98
Cthe_00695	putative agmatinase	13.53	13.75	11.12	12.03	2.41	1.72	-0.22	-0.91	1.73	1.94	-0.46	-1.12	1.52	1.96	1.21
Cthe_01501	ABC transporter, transmembrane region	8.77	7.89	6.38	6.39	2.39	1.5	0.88	-0.01	1.71	1.62	0.91	0.24	1.52	1.96	1.41
Cthe_00695	putative agmatinase	13.53	13.75	11.12	12.03	2.41	1.72	-0.22	-0.91	1.73	1.94	-0.46	-1.12	1.52	1.96	1.21
Cthe_00695	putative agmatinase	13.53	13.75	11.12	12.03	2.41	1.72	-0.22	-0.91	1.73	1.94	-0.46	-1.12	1.52	1.96	1.21
Cthe_00695	putative agmatinase	13.53	13.75	11.12	12.03	2.41	1.72	-0.22	-0.91	1.73	1.94	-0.46	-1.12	1.52	1.96	1.21
Cthe_00695	putative agmatinase	13.53	13.75	11.12	12.03	2.41	1.72	-0.22	-0.91	1.73	1.94	-0.46	-1.12	1.52	1.96	1.21
Cthe_00208	single-stranded-DNA-specific exonuclease RecJ	9.86	10.58	9.05	10.18	0.81	0.4	-0.72	-1.13	0.1	0	-1.09	-1.45	1.51	1.95	0.03
Cthe_00208	single-stranded-DNA-specific exonuclease RecJ	9.86	10.58	9.05	10.18	0.81	0.4	-0.72	-1.13	0.1	0	-1.09	-1.45	1.51	1.95	0.03
Cthe_01868	carbamoyl-phosphate synthase, large subunit	12.74	11.67	11.97	11.17	0.77	0.5	1.07	0.8	0.06	0.15	1.15	1.47	1.5	1.94	0.05
Cthe_01868	carbamoyl-phosphate synthase, large subunit	12.74	11.67	11.97	11.17	0.77	0.5	1.07	0.8	0.06	0.15	1.15	1.47	1.5	1.94	0.05
Cthe_01868	carbamoyl-phosphate synthase, large subunit	12.74	11.67	11.97	11.17	0.77	0.5	1.07	0.8	0.06	0.15	1.15	1.47	1.5	1.94	0.05
Cthe_01868	carbamoyl-phosphate synthase, large subunit	12.74	11.67	11.97	11.17	0.77	0.5	1.07	0.8	0.06	0.15	1.15	1.47	1.5	1.94	0.05
Cthe_01868	carbamoyl-phosphate synthase, large subunit	12.74	11.67	11.97	11.17	0.77	0.5	1.07	0.8	0.06	0.15	1.15	1.47	1.5	1.94	0.05
Cthe_01868	carbamoyl-phosphate synthase, large subunit	12.74	11.67	11.97	11.17	0.77	0.5	1.07	0.8	0.06	0.15	1.15	1.47	1.5	1.94	0.05
Cthe_01868	carbamoyl-phosphate synthase, large subunit	12.74	11.67	11.97	11.17	0.77	0.5	1.07	0.8	0.06	0.15	1.15	1.47	1.5	1.94	0.05
Cthe_03018	hydrogenase expression/synthesis, HypA	7.75	9.43	7.42	8.49	0.33	0.94	-1.68	-1.07	-0.39	0.79	-2.29	-1.36	1.49	1.92	0.19
Cthe_03017	hydrogenase accessory protein HypB	8.99	10.63	8.77	9.78	0.22	0.85	-1.64	-1.01	-0.5	0.66	-2.24	-1.27	1.46	1.89	0.18
Cthe_00683	diaminopimelate decarboxylase	10.71	12.08	10.15	11.25	0.56	0.83	-1.37	-1.1	-0.15	0.63	-1.9	-1.41	1.46	1.89	0.15
Cthe_01609	Recombinase	2.81	2	2.58	1	0.23	1	0.81	1.58	-0.49	0.88	0.82	2.65	1.46	1.89	0.2
Cthe_01448	MATE efflux family protein	10.15	9.7	7.52	8.35	2.63	1.35	0.45	-0.83	1.96	1.4	0.38	-1	1.46	1.89	1.26
Cthe_03017	hydrogenase accessory protein HypB	8.99	10.63	8.77	9.											



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Cthe_00482	flagellar biosynthetic protein FLIQ	9.64	8.78	7.32	7.64	2.32	1.14	0.86	-0.32	1.64	1.09	0.89	-0.23	1.15	1.49	1.2
Cthe_01342	beta-lactamase-like protein	8.7	9.25	7.88	8.8	0.82	0.45	-0.55	-0.92	0.11	0.07	-0.88	-1.14	1.15	1.49	0.05
Cthe_01551		10.28	9.41	7.73	8.32	2.55	1.09	0.87	-0.59	1.88	1.01	0.9	-0.64	1.15	1.49	1.09
Cthe_00275	glycosyltransferase 36	14.11	14.55	12.27	12.95	1.84	1.6	-0.44	-0.68	1.15	1.76	-0.74	-0.77	1.15	1.49	1.11
Cthe_01551		10.28	9.41	7.73	8.32	2.55	1.09	0.87	-0.59	1.88	1.01	0.9	-0.64	1.15	1.49	1.09
Cthe_00750	spermidine/putrescine ABC transporter ATPase	10.24	9.99	8.78	8.86	1.46	1.13	0.25	-0.08	0.77	1.07	0.12	0.14	1.15	1.49	4.02
Cthe_00482	flagellar biosynthetic protein FLIQ	9.64	8.78	7.32	7.64	2.32	1.14	0.86	-0.32	1.64	1.09	0.89	-0.23	1.15	1.49	1.2
Cthe_00750	spermidine/putrescine ABC transporter ATPase	10.24	9.99	8.78	8.86	1.46	1.13	0.25	-0.08	0.77	1.07	0.12	0.14	1.15	1.49	4.02
Cthe_00275	glycosyltransferase 36	14.11	14.55	12.27	12.95	1.84	1.6	-0.44	-0.68	1.15	1.76	-0.74	-0.77	1.15	1.49	1.11
Cthe_00750	spermidine/putrescine ABC transporter ATPase	10.24	9.99	8.78	8.86	1.46	1.13	0.25	-0.08	0.77	1.07	0.12	0.14	1.15	1.49	4.02
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_02235	protein of unknown function DUF115	5.86	5.32	5.75	3.81	0.11	1.51	0.54	1.94	-0.61	1.63	0.49	3.2	1.14	1.48	0.3
Cthe_01331	aspartyl-tRNA synthetase	11.68	12.86	11.32	12.15	0.36	0.71	-1.18	-0.83	-0.36	0.46	-1.66	-1	1.14	1.48	0.17
Cthe_02970	ABC transporter related protein	8.25	7.86	6.51	6.79	1.74	1.07	0.39	-0.28	1.05	0.99	0.3	-0.17	1.14	1.48	2.35
Cthe_02873	hypothetical protein	10.94	10.69	8.75	9.49	2.19	1.2	0.25	-0.74	1.51	1.18	0.12	-0.86	1.14	1.48	1.24
Cthe_01931	S-layer-like domain containing protein	11.11	10.83	9.5	9.77	1.61	1.06	0.28	-0.27	0.92	0.97	0.16	-0.15	1.14	1.48	3.42
Cthe_02970	ABC transporter related protein	8.25	7.86	6.51	6.79	1.74	1.07	0.39	-0.28	1.05	0.99	0.3	-0.17	1.14	1.48	2.35
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_01331	aspartyl-tRNA synthetase	11.68	12.86	11.32	12.15	0.36	0.71	-1.18	-0.83	-0.36	0.46	-1.66	-1	1.14	1.48	0.17
Cthe_01331	aspartyl-tRNA synthetase	11.68	12.86	11.32	12.15	0.36	0.71	-1.18	-0.83	-0.36	0.46	-1.66	-1	1.14	1.48	0.17
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_01331	aspartyl-tRNA synthetase	11.68	12.86	11.32	12.15	0.36	0.71	-1.18	-0.83	-0.36	0.46	-1.66	-1	1.14	1.48	0.17
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_01331	aspartyl-tRNA synthetase	11.68	12.86	11.32	12.15	0.36	0.71	-1.18	-0.83	-0.36	0.46	-1.66	-1	1.14	1.48	0.17
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_01331	aspartyl-tRNA synthetase	11.68	12.86	11.32	12.15	0.36	0.71	-1.18	-0.83	-0.36	0.46	-1.66	-1	1.14	1.48	0.17
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-bisphosphate aldolase, class II	16.57	16.26	14.35	15.08	2.22	1.18	0.31	-0.73	1.54	1.15	0.2	-0.85	1.14	1.48	1.24
Cthe_00349	fructose-1,6-b															



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Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.34	13.11	11.38	12.4	0.96	0.71	-0.77	-1.02	0.26	0.46	-1.15	-1.29	1.01	1.32	0.17
Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.34	13.11	11.38	12.4	0.96	0.71	-0.77	-1.02	0.26	0.46	-1.15	-1.29	1.01	1.32	0.17
Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.34	13.11	11.38	12.4	0.96	0.71	-0.77	-1.02	0.26	0.46	-1.15	-1.29	1.01	1.32	0.17
Cthe_02073	amidohydrolase	10.58	10.15	8.77	9.15	1.81	1	0.43	-0.38	1.12	0.88	0.35	-0.32	1	1.3	1.69
Cthe_01090	hypothetical protein	11.03	12.21	10.52	11.34	0.51	0.87	-1.18	-0.82	-0.2	0.69	-1.66	-0.98	1	1.3	0.21
Cthe_02721	ribosomal protein L1	12.93	14.19	12.22	13.18	0.71	1.01	-1.26	-0.96	0	0.9	-1.76	-1.2	1	1.3	0.24
Cthe_00064	Na/PI-cotransporter II-related protein	15.07	14.58	12.8	13.54	2.27	1.04	0.49	-0.74	1.59	0.94	0.42	-0.86	1	1.3	1.08
Cthe_00232	hypothetical protein	9.82	11.05	9.29	10.13	0.53	0.92	-1.23	-0.84	-0.18	0.76	-1.72	-1.02	1	1.3	0.22
Cthe_02721	ribosomal protein L1	12.93	14.19	12.22	13.18	0.71	1.01	-1.26	-0.96	0	0.9	-1.76	-1.2	1	1.3	0.24
Cthe_02073	amidohydrolase	10.58	10.15	8.77	9.15	1.81	1	0.43	-0.38	1.12	0.88	0.35	-0.32	1	1.3	1.69
Cthe_02721	ribosomal protein L1	12.93	14.19	12.22	13.18	0.71	1.01	-1.26	-0.96	0	0.9	-1.76	-1.2	1	1.3	0.24
Cthe_02073	amidohydrolase	10.58	10.15	8.77	9.15	1.81	1	0.43	-0.38	1.12	0.88	0.35	-0.32	1	1.3	1.69
Cthe_01905	glycosyl transferase, family 28	6.25	4.86	4.86	4	1.39	0.86	1.39	0.86	0.69	0.68	1.55	1.56	0.99	1.29	0.25
Cthe_01905	glycosyl transferase, family 28	6.25	4.86	4.86	4	1.39	0.86	1.39	0.86	0.69	0.68	1.55	1.56	0.99	1.29	0.25
Cthe_02665	Zn-finger containing protein	8.14	6.81	6.94	6.54	1.2	0.27	1.33	0.4	0.5	-0.19	1.48	0.86	0.99	1.29	0.18
Cthe_00922	diaminopimelate dehydrogenase	10.78	10.54	9.42	9.48	1.36	1.06	0.24	-0.06	0.66	0.97	0.11	0.17	0.99	1.29	3.26
Cthe_00922	diaminopimelate dehydrogenase	10.78	10.54	9.42	9.48	1.36	1.06	0.24	-0.06	0.66	0.97	0.11	0.17	0.99	1.29	3.26
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	11.77	12.65	10.89	11.86	0.88	0.79	-0.88	-0.97	0.17	0.57	-1.29	-1.21	0.98	1.28	0.19
Cthe_01341	Radical SAM	10.17	10.62	9.37	10.18	0.8	0.44	-0.45	-0.81	0.09	0.06	-0.75	-0.97	0.98	1.28	0.05
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	11.77	12.65	10.89	11.86	0.88	0.79	-0.88	-0.97	0.17	0.57	-1.29	-1.21	0.98	1.28	0.19
Cthe_02947	prolyl-tRNA synthetase	11.16	11.6	9.21	10.06	1.95	1.54	-0.44	-0.85	1.27	1.68	-0.74	-1.03	0.98	1.28	0.93
Cthe_00079	hypothetical protein	9.01	7.65	7.69	7.21	1.32	0.44	1.36	0.48	0.62	0.06	1.51	0.98	0.98	1.28	0.19
Cthe_02947	prolyl-tRNA synthetase	11.16	11.6	9.21	10.06	1.95	1.54	-0.44	-0.85	1.27	1.68	-0.74	-1.03	0.98	1.28	0.93
Cthe_01341	Radical SAM	10.17	10.62	9.37	10.18	0.8	0.44	-0.45	-0.81	0.09	0.06	-0.75	-0.97	0.98	1.28	0.05
Cthe_02947	prolyl-tRNA synthetase	11.16	11.6	9.21	10.06	1.95	1.54	-0.44	-0.85	1.27	1.68	-0.74	-1.03	0.98	1.28	0.93
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	11.77	12.65	10.89	11.86	0.88	0.79	-0.88	-0.97	0.17	0.57	-1.29	-1.21	0.98	1.28	0.19
Cthe_01341	Radical SAM	10.17	10.62	9.37	10.18	0.8	0.44	-0.45	-0.81	0.09	0.06	-0.75	-0.97	0.98	1.28	0.05
Cthe_02947	prolyl-tRNA synthetase	11.16	11.6	9.21	10.06	1.95	1.54	-0.44	-0.85	1.27	1.68	-0.74	-1.03	0.98	1.28	0.93
Cthe_02947	prolyl-tRNA synthetase	11.16	11.6	9.21	10.06	1.95	1.54	-0.44	-0.85	1.27	1.68	-0.74	-1.03	0.98	1.28	0.93
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	11.77	12.65	10.89	11.86	0.88	0.79	-0.88	-0.97	0.17	0.57	-1.29	-1.21	0.98	1.28	0.19
Cthe_01341	Radical SAM	10.17	10.62	9.37	10.18	0.8	0.44	-0.45	-0.81	0.09	0.06	-0.75	-0.97	0.98	1.28	0.05
Cthe_02847	phage / plasmid primase, P4 family	4.58	4	2.32	3	2.26	1	0.58	-0.68	1.58	0.88	0.54	-0.77	0.97	1.27	1.08
Cthe_00720	aminotransferase, class V	14.13	14.21	12.47	13.01	1.66	1.2	-0.08	-0.54	0.97	1.18	-0.29	-0.56	0.97	1.27	1.36
Cthe_02180	Cl- channel, voltage gated	10.25	9.83	7.91	8.76	2.34	1.07	0.42	-0.85	1.66	0.99	0.34	-1.03	0.97	1.27	1
Cthe_02612	Fibronectin, type III	8.01	7.38	6.04	6.39	1.97	0.99	0.63	-0.35	1.29	0.87	0.6	-0.27	0.97	1.27	1.33
Cthe_00720	aminotransferase, class V	14.13	14.21	12.47	13.01	1.66	1.2	-0.08	-0.54	0.97	1.18	-0.29	-0.56	0.97	1.27	1.36
Cthe_00720	aminotransferase, class V	14.13	14.21	12.47	13.01	1.66	1.2	-0.08	-0.54	0.97	1.18	-0.29	-0.56	0.97	1.27	1.36
Cthe_00616	amino acid-binding ACT	11.09	11.86	10.33	11.18	0.76	0.68	-0.77	-0.85	0.05	0.41	-1.15	-1.03	0.96	1.25	0.15
Cthe_00081	arginine biosynthesis bifunctional protein ArgJ	12.89	12.94	11.34	11.79	1.55	1.15	-0.05	-0.45	0.86	1.1	-0.25	-0.42	0.96	1.25	1.6
Cthe_01816	urease, alpha subunit	5.75	5.04	5.25	3.46	0.5	1.58	0.71	1.79	-0.21	1.74	0.7	2.97	0.96	1.25	0.32
Cthe_00169	dehydrogenase (flavoproteins)	7.83	7.32	7.57	6.32	0.26	1	0.51	1.25	-0.46	0.88	0.45	2.15	0.96	1.25	0.25
Cthe_02981	hypothetical protein	13.04	12.67	11.58	11.49	1.46	1.18	0.37	0.09	0.77	1.15	0.27	0.39	0.96	1.25	1.64
Cthe_00081	arginine biosynthesis bifunctional protein ArgJ	12.89	12.94	11.34	11.79	1.55	1.15	-0.05	-0.45	0.86	1.1	-0.25	-0.42	0.96	1.25	1.6
Cthe_01816	urease, alpha subunit	5.75	5.04	5.25	3.46	0.5	1.58	0.71	1.79	-0.21	1.74	0.7	2.97	0.96	1.25	0.32
Cthe_00081	arginine biosynthesis bifunctional protein ArgJ	12.89	12.94	11.34	11.79	1.55	1.15	-0.05	-0.45	0.86	1.1	-0.25	-0.42	0.96	1.25	1.6
Cthe_00081	arginine biosynthesis bifunctional protein ArgJ	12.89	12.94	11.34	11.79	1.55	1.15	-0.05	-0.45	0.86	1.1	-0.25	-0.42	0.96	1.25	1.6
Cthe_00081	arginine biosynthesis bifunctional protein ArgJ	12.89	12.94	11.34	11.79	1.55	1.15	-0.05	-0.45	0.86	1.1	-0.25	-0.42	0.96	1.25	1.6
Cthe_00081	arginine biosynthesis bifunctional protein ArgJ	12.89	12.94	11.34	11.79	1.55	1.15	-0.05	-0.45	0.86	1.1	-0.25	-0.42	0.96	1.25	1.6
Cthe_00081	arginine biosynthesis bifunctional protein ArgJ	12.89	12.94	11.34	11.79	1.55	1.15	-0.05	-0.45	0.86	1.1	-0.25	-0.42	0.96	1.25	1.6
Cthe_01816	urease, alpha subunit	5.75	5.04	5.25	3.46	0.5	1.58	0.71	1.79	-0.21	1.74	0.7	2.97	0.96	1.25	0.32
Cthe_00253	ATPase associated with various cellular	9.19	10.15	8.72	9.45	0.47	0.7	-0.96	-0.73	-0.24	0.44	-1.39	-0.85	0.95	1.24	0.17
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_03019	4Fe-4S ferredoxin, iron-sulfur binding	8.09	9.56	7.73	8.51	0.36	1.05	-1.47	-0.78	-0.36	0.96	-2.02	-0.92	0.95	1.24	0.26
Cthe_01705	hypothetical protein	6.58	5.21	5.36	5	1.22	0.21	1.37	0.36	0.52	-0.28	1.53	0.8	0.95	1.24	0.19
Cthe_01911	Carbohydrate binding family 6	11.28	12.14	10.6	11.42	0.68	0.72	-0.86	-0.82	-0.03	0.47	-1.26	-0.98	0.95	1.24	0.17
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00253	ATPase associated with various cellular	9.19	10.15	8.72	9.45	0.47	0.7	-0.96	-0.73	-0.24	0.44	-1.39	-0.85	0.95	1.24	0.17
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00253	ATPase associated with various cellular	9.19	10.15	8.72	9.45	0.47	0.7	-0.96	-0.73	-0.24	0.44	-1.39	-0.85	0.95	1.24	0.17
Cthe_00179	Argininosuccinate synthase	12.83	11.42	11.42	10.9	1.41	0.52	1.41	0.52	0.71	0.18	1.57	1.05	0.95	1.24	0.22
Cthe_00253	ATPase associated with various cellular	9.19	10.15	8.72	9.45	0.47	0.7	-0.96	-0.73	-0.24	0.44	-1.39	-0.85	0.95	1.24	0.17
Cthe_00253	ATPase associated with various cellular	9.19	10.15	8.72	9.45	0.47	0.7	-0.96	-0.73	-0.24	0.44	-1.39	-0.85	0.95	1.24	0.17
Cthe_00253	ATPase associated with various cellular	9.19	10.15	8.72	9.45	0.47	0.7	-0.96	-0.73	-0.24	0.44	-1.39	-0.85	0.95	1.24	0.17
Cthe_01799	ABC transporter related protein	13.6	12.89	10.86	11.89	2.74	1	0.71	-1.03	2.07	0.88	0.7	-1.3	0.94	1.23	0.86
Cthe_02236	flagellin-like protein	6.61	6.52	5	5.46	1.61	1.06	0.09	-0.46	0.92	0.97	-0.07	-0.44	0.94	1.23	1.69
Cthe_00063	Rubredoxin-type Fe(Cys)4 protein	14.7	14.2	12.53	13.21	2.17	0.99	0.5	-0.68	1.49	0.87	0.44	-0.77	0.94	1.23	1.09
Cthe_00907	hypothetical protein	11.91	10.98	9.75	9.87	2.16	1.11	0.93	-0.12	1.48	1.04	0.97	0.08	0.94	1.23	1.04
Cthe_03007	ErkK/YbiS/YcfS/YnhG	5.39	4.17	3	2.81	2.39	1.36	1.22	0.19	1.71	1.41	1.34	0.55	0.93	1.22	0.86
Cthe_00755	aminotransferase, class I and II	13.35	14.6	12.31	13.47	1.04	1.13	-1.25	-1.16	0.34	1.07	-1.75	-1.5	0.93	1.22	0.27
Cthe_01479	hypothetical protein	3.32	4.32	2	3.32	1.32	1	-1	-1.32	0.62	0.88	-1.44	-1.			



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Cthe_01386	hypothetical protein	11.11	12.22	9.77	11.09	1.34	1.13	-1.11	-1.32	0.64	1.07	-1.57	-1.74	0.84	1.1	0.3
Cthe_01634	hypothetical protein	1.58	1.58	0	1.58	1.58	0	0	-1.58	0.89	-0.59	-0.19	-2.14	0.84	1.1	0.28
Cthe_02064	spore germination B3 GerAC like	7.71	7.52	6.48	6.58	1.23	0.94	0.19	-0.1	0.53	0.79	0.05	0.11	0.84	1.1	4.42
Cthe_01879	hypothetical protein	8.06	7.37	7.34	6.69	0.72	0.68	0.69	0.65	0.01	0.41	0.67	1.24	0.84	1.1	0.16
Cthe_01425	Inorganic diphosphatase	13.97	13.94	12.82	12.95	1.15	0.99	0.03	-0.13	0.45	0.87	-0.15	0.06	0.84	1.1	3.41
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B subunit	7.29	9.16	6.64	7.63	0.65	1.53	-1.87	-0.99	-0.06	1.66	-2.52	-1.24	0.84	1.1	0.33
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B subunit	7.29	9.16	6.64	7.63	0.65	1.53	-1.87	-0.99	-0.06	1.66	-2.52	-1.24	0.84	1.1	0.33
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B subunit	7.29	9.16	6.64	7.63	0.65	1.53	-1.87	-0.99	-0.06	1.66	-2.52	-1.24	0.84	1.1	0.33
Cthe_02989	glycosyltransferase 36	13.91	15.13	13.75	14.34	0.16	0.79	-1.22	-0.59	-0.56	0.57	-1.71	-0.64	0.83	1.09	0.25
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_00952	dihydroorotase, multifunctional complex type	13.67	11.93	10.3	11.09	3.37	0.84	1.74	-0.79	2.71	0.65	1.99	-0.94	0.83	1.09	0.71
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_00952	dihydroorotase, multifunctional complex type	13.67	11.93	10.3	11.09	3.37	0.84	1.74	-0.79	2.71	0.65	1.99	-0.94	0.83	1.09	0.71
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_00952	dihydroorotase, multifunctional complex type	13.67	11.93	10.3	11.09	3.37	0.84	1.74	-0.79	2.71	0.65	1.99	-0.94	0.83	1.09	0.71
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
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Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
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Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82	0.92	0.56	-0.48	-0.84	0.21	0.24	-0.79	-1.02	0.83	1.09	0.14
Cthe_02108	Orn/Lys/Arg decarboxylase, major region	10.9	11.38	9.98	10.82											



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Cthe_00285	isocitrate dehydrogenase, NADP-dependent	15.14	14.94	13.74	14.06	1.4	0.88	0.2	-0.32	0.7	0.71	0.06	-0.23	0.79	1.04	2.36
Cthe_03100	Diaminopimelate epimerase	7.18	7.48	6	7.04	1.18	0.44	-0.3	-1.04	0.48	0.06	-0.56	-1.32	0.79	1.04	0.19
Cthe_00285	isocitrate dehydrogenase, NADP-dependent	15.14	14.94	13.74	14.06	1.4	0.88	0.2	-0.32	0.7	0.71	0.06	-0.23	0.79	1.04	2.36
Cthe_01423	protein of unknown function UPF0118	11.28	10.84	9.55	9.97	1.73	0.87	0.44	-0.42	1.04	0.69	0.36	-0.38	0.78	1.03	1.34
Cthe_03112	glycosidase, PH1107-related	9.88	8.99	9.02	7.36	0.86	1.63	0.89	1.66	0.15	1.81	0.92	2.77	0.78	1.03	0.35
Cthe_00635	protein serine/threonine phosphatases	10.98	10.65	9.19	9.74	1.79	0.91	0.33	-0.55	1.1	0.75	0.23	-0.58	0.78	1.03	1.2
Cthe_03118	hemerythrin-like metal-binding protein	12.29	11.98	10.68	11.1	1.61	0.88	0.31	-0.42	0.92	0.71	0.2	-0.38	0.78	1.03	1.52
Cthe_01390	alpha/beta hydrolase fold	10.34	11.16	9.49	10.34	0.85	0.82	-0.82	-0.85	0.14	0.62	-1.21	-1.03	0.78	1.03	0.22
Cthe_00396	ABC transporter related protein	11.17	11.63	9.46	10.21	1.71	1.42	-0.46	-0.75	1.02	1.5	-0.76	-0.88	0.78	1.03	0.88
Cthe_00718	hypothetical protein	6.74	5.61	5.49	4.91	1.25	0.7	1.13	0.58	0.55	0.44	1.22	1.14	0.78	1.03	0.24
Cthe_01525	protein of unknown function DUF214	8.1	7.5	7.38	7.07	0.72	0.43	0.6	0.31	0.01	0.04	0.56	0.73	0.78	1.03	0.03
Cthe_01725	hypothetical protein	4.95	3.91	3.81	3	1.14	0.91	1.04	0.81	0.44	0.75	1.11	1.48	0.78	1.03	0.26
Cthe_02507	peptidase U57, YabG	4.58	3.91	3.81	3.32	0.77	0.59	0.67	0.49	0.06	0.28	0.65	1	0.78	1.03	0.13
Cthe_00635	protein serine/threonine phosphatases	10.98	10.65	9.19	9.74	1.79	0.91	0.33	-0.55	1.1	0.75	0.23	-0.58	0.78	1.03	1.2
Cthe_02210	3-isopropylmalate dehydratase, small subunit	11.49	12.86	10.52	11.59	0.97	1.27	-1.37	-1.07	0.27	1.28	-1.9	-1.36	0.77	1.01	0.31
Cthe_02702	polysaccharide pyruvyl transferase	12.17	12.14	10.43	11.08	1.74	1.06	0.03	-0.65	1.05	0.97	-0.15	-0.73	0.77	1.01	1.08
Cthe_01919	MgtC/SapB transporter	9.23	8.29	8.19	7.86	1.04	0.43	0.94	0.33	0.34	0.04	0.99	0.76	0.77	1.01	0.15
Cthe_02702	polysaccharide pyruvyl transferase	12.17	12.14	10.43	11.08	1.74	1.06	0.03	-0.65	1.05	0.97	-0.15	-0.73	0.77	1.01	1.08
Cthe_02234	hypothetical protein	4.09	2.58	2.58	2.32	1.51	0.26	1.51	0.26	0.82	-0.21	1.7	0.65	0.77	1.01	0.26
Cthe_01755	hypothetical protein	14.82	13.86	13.86	13.58	0.96	0.28	0.96	0.28	0.26	-0.18	1.01	0.68	0.77	1.01	0.15
Cthe_00364	transcriptional regulator, XRE family	10.35	8.97	9.07	8.84	1.28	0.13	1.38	0.23	0.58	-0.4	1.54	0.61	0.77	1.01	0.24
Cthe_02210	3-isopropylmalate dehydratase, small subunit	11.49	12.86	10.52	11.59	0.97	1.27	-1.37	-1.07	0.27	1.28	-1.9	-1.36	0.77	1.01	0.31
Cthe_00813	peptidase S55, SpoIVB	8.27	7.48	7.37	6.78	0.9	0.7	0.79	0.59	0.19	0.44	0.8	1.15	0.77	1.01	0.19
Cthe_02210	3-isopropylmalate dehydratase, small subunit	11.49	12.86	10.52	11.59	0.97	1.27	-1.37	-1.07	0.27	1.28	-1.9	-1.36	0.77	1.01	0.31
Cthe_02210	3-isopropylmalate dehydratase, small subunit	11.49	12.86	10.52	11.59	0.97	1.27	-1.37	-1.07	0.27	1.28	-1.9	-1.36	0.77	1.01	0.31
Cthe_02210	3-isopropylmalate dehydratase, small subunit	11.49	12.86	10.52	11.59	0.97	1.27	-1.37	-1.07	0.27	1.28	-1.9	-1.36	0.77	1.01	0.31
Cthe_02210	3-isopropylmalate dehydratase, small subunit	11.49	12.86	10.52	11.59	0.97	1.27	-1.37	-1.07	0.27	1.28	-1.9	-1.36	0.77	1.01	0.31
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_02231	Methyltransferase type 11	4.86	3.7	3.58	3.17	1.28	0.53	1.16	0.41	0.58	0.19	1.26	0.88	0.76	1	0.22
Cthe_01849	Heavy metal transport/detoxification protein	8.43	7.74	6.61	6.83	1.82	0.91	0.69	-0.22	1.13	0.75	0.67	-0.08	0.76	1	1.13
Cthe_01444	GCN5-related N-acetyltransferase	9.56	8.57	8.52	8.24	1.04	0.33	0.99	0.28	0.34	-0.1	1.05	0.68	0.76	1	0.16
Cthe_00283	aldo/keto reductase	12.76	12.7	10.87	11.63	1.89	1.07	0.06	-0.76	1.2	0.99	-0.11	-0.89	0.76	1	0.97
Cthe_01849	Heavy metal transport/detoxification protein	8.43	7.74	6.61	6.83	1.82	0.91	0.69	-0.22	1.13	0.75	0.67	-0.08	0.76	1	1.13
Cthe_02306	MATE efflux family protein	11.25	11.64	9.21	10.21	2.04	1.43	-0.39	-1	1.36	1.51	-0.68	-1.26	0.76	1	0.8
Cthe_03013	hydrogenase expression/formation protein HypE	9.31	10.15	8	9.2	1.31	0.95	-0.84	-1.2	0.61	0.81	-1.24	-1.56	0.76	1	0.29
Cthe_01190	hypothetical protein	8.15	7.73	6.71	6.79	1.44	0.94	0.42	-0.08	0.74	0.79	0.34	0.14	0.76	1	1.65
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
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Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
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Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.11	0.99	-0.03	-0.15	0.41	0.87	-0.22	0.03	0.76	1	2.43
Cthe_00143	Phosphopyruvate hydratase	14.83	14.86	13.72	13.87	1.										







Cthe_01376	Homoserine dehydrogenase	10.17	10.38	7.97	9.06	2.2	1.32	-0.21	-1.09	1.52	1.35	-0.45	-1.39	0.73	0.96	0.78
Cthe_03072	acyl-ACP thioesterase	10.39	10.39	9.31	9.42	1.08	0.97	0	-0.11	0.38	0.84	-0.19	0.09	0.73	0.96	2.46
Cthe_00127	RNA methyltransferase, TrmH family, group 2	8.78	8.28	7.08	7.44	1.7	0.84	0.5	-0.36	1.01	0.65	0.44	-0.29	0.73	0.96	1.28
Cthe_00127	RNA methyltransferase, TrmH family, group 2	8.78	8.28	7.08	7.44	1.7	0.84	0.5	-0.36	1.01	0.65	0.44	-0.29	0.73	0.96	1.28
Cthe_00127	RNA methyltransferase, TrmH family, group 2	8.78	8.28	7.08	7.44	1.7	0.84	0.5	-0.36	1.01	0.65	0.44	-0.29	0.73	0.96	1.28
Cthe_00127	RNA methyltransferase, TrmH family, group 2	8.78	8.28	7.08	7.44	1.7	0.84	0.5	-0.36	1.01	0.65	0.44	-0.29	0.73	0.96	1.28
Cthe_00127	RNA methyltransferase, TrmH family, group 2	8.78	8.28	7.08	7.44	1.7	0.84	0.5	-0.36	1.01	0.65	0.44	-0.29	0.73	0.96	1.28
Cthe_02399	Formate--tetrahydrofolate ligase	12.38	12.66	10.82	11.43	1.56	1.23	-0.28	-0.61	0.87	1.22	-0.54	-0.67	0.73	0.96	0.98
Cthe_00127	RNA methyltransferase, TrmH family, group 2	8.78	8.28	7.08	7.44	1.7	0.84	0.5	-0.36	1.01	0.65	0.44	-0.29	0.73	0.96	1.28
Cthe_00236	aldo/keto reductase	11.51	12.4	10.94	11.6	0.57	0.8	-0.89	-0.66	-0.14	0.59	-1.3	-0.74	0.72	0.95	0.23
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_03105	exsB protein	11.14	11.01	9.92	10.17	1.22	0.84	0.13	-0.25	0.52	0.65	-0.02	-0.12	0.72	0.95	3.84
Cthe_01739	SNF2-related protein	5.55	4.75	2.81	3.91	2.74	0.84	0.8	-1.1	2.07	0.65	0.81	-1.41	0.72	0.95	0.75
Cthe_00761	Ribonuclease H	11.26	10.92	8.67	9.88	2.59	1.04	0.34	-1.21	1.92	0.94	0.24	-1.58	0.72	0.95	0.75
Cthe_01739	SNF2-related protein	5.55	4.75	2.81	3.91	2.74	0.84	0.8	-1.1	2.07	0.65	0.81	-1.41	0.72	0.95	0.75
Cthe_00355	hypothetical protein	10.2	9.92	8.87	9.1	1.33	0.82	0.28	-0.23	0.63	0.62	0.16	-0.09	0.72	0.95	2.71
Cthe_01006	ribosomal protein S2	13.83	14.1	11.67	12.75	2.16	1.35	-0.27	-1.08	1.48	1.4	-0.53	-1.38	0.72	0.95	0.77
Cthe_02269	V-type ATPase, D subunit	11.04	12	9.6	10.91	1.44	1.09	-0.96	-1.31	0.74	1.01	-1.39	-1.73	0.72	0.95	0.32
Cthe_00506	pyruvate formate-lyase activating enzyme	11	11.98	10.46	11.12	0.54	0.86	-0.98	-0.66	-0.17	0.68	-1.41	-0.74	0.72	0.95	0.25
Cthe_02990	peptide methionine sulfoxide reductase	6.78	8.59	6.79	7.29	-0.01	1.3	-1.81	-0.5	-0.73	1.32	-2.45	-0.5	0.72	0.95	0.34
Cthe_02291	hypothetical protein	1.58	0	0	1.58	1.58	1.58	0	0.89	1.79	0.26	0.72	0.95	0.28	0.95	0.28
Cthe_01006	ribosomal protein S2	13.83	14.1	11.67	12.75	2.16	1.35	-0.27	-1.08	1.48	1.4	-0.53	-1.38	0.72	0.95	0.77
Cthe_02269	V-type ATPase, D subunit	11.04	12	9.6	10.91	1.44	1.09	-0.96	-1.31	0.74	1.01	-1.39	-1.73	0.72	0.95	0.32
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_01006	ribosomal protein S2	13.83	14.1	11.67	12.75	2.16	1.35	-0.27	-1.08	1.48	1.4	-0.53	-1.38	0.72	0.95	0.77
Cthe_02269	V-type ATPase, D subunit	11.04	12	9.6	10.91	1.44	1.09	-0.96	-1.31	0.74	1.01	-1.39	-1.73	0.72	0.95	0.32
Cthe_00506	pyruvate formate-lyase activating enzyme	11	11.98	10.46	11.12	0.54	0.86	-0.98	-0.66	-0.17	0.68	-1.41	-0.74	0.72	0.95	0.25
Cthe_00761	Ribonuclease H	11.26	10.92	8.67	9.88	2.59	1.04	0.34	-1.21	1.92	0.94	0.24	-1.58	0.72	0.95	0.75
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_02990	peptide methionine sulfoxide reductase	6.78	8.59	6.79	7.29	-0.01	1.3	-1.81	-0.5	-0.73	1.32	-2.45	-0.5	0.72	0.95	0.34
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_02269	V-type ATPase, D subunit	11.04	12	9.6	10.91	1.44	1.09	-0.96	-1.31	0.74	1.01	-1.39	-1.73	0.72	0.95	0.32
Cthe_00342	hydrogenase, Fe-only	13.2	14.58	13.01	13.56	0.19	1.02	-1.38	-0.55	-0.53	0.91	-1.91	-0.58	0.72	0.95	0.3
Cthe_02973	sugar fermentation stimulation protein	10.36	10.51	7.94	9.19	2.42	1.32	-0.15	-1.25	1.74	1.35	-0.37	-1.64	0.71	0.94	0.74
Cthe_02890	putative transcriptional regulator	10.13	10.85	9	10.01	1.13	0.84	-0.72	-1.01	0.43	0.65	-1.09	-1.27	0.71	0.94	0.26
Cthe_02657	histone-like DNA-binding protein	14.01	12.24	12.18	11.98	1.83	0.26	1.77	0.2	1.14	-0.21	2.02	0.56	0.71	0.94	0.31
Cthe_00039	methyl-accepting chemotaxis sensory transducer	6.86	5.13	4.95	4.17	1.91	0.96	1.73	0.78	1.22	0.82	1.98	1.44	0.71	0.94	0.34
Cthe_00039	methyl-accepting chemotaxis sensory transducer	6.86	5.13	4.95	4.17	1.91	0.96	1.73	0.78	1.22	0.82	1.98	1.44	0.71	0.94	0.34
Cthe_02351	hypothetical protein	7.72	7.55	6.58	6.39	1.14	1.16	0.17	0.19	0.44	1.12	0.03	0.55	0.71	0.94	1.23
Cthe_02404	transcriptional regulator, GntR family	11.19	11.09	9.39	10.09	1.8	1	0.1	-0.7	1.11	0.88	-0.06	-0.8	0.7	0.92	0.99
Cthe_03035	D-isomer specific 2-hydroxyacid dehydrogenase,	15.38	15.49	14.15	14.47	1.23	1.02	-0.11	-0.32	0.53	0.91	-0.33	-0.23	0.7	0.92	1.47
Cthe_01901	transposase, mutator type	5.58	4.09	4.25	4.09	1.33	0	1.49	0.16	0.63	-0.59	1.68	0.5	0.7	0.92	0.28
Cthe_03035	D-isomer specific 2-hydroxyacid dehydrogenase,	15.38	15.49	14.15	14.47	1.23	1.02	-0.11	-0.32	0.53	0.91	-0.33	-0.23	0.7	0.92	1.47
Cthe_01431	hypothetical protein	12.54	13.21	11.4	12.4	1.14	0.81	-0.67	-1	0.44	0.6	-1.02	-1.26	0.7	0.92	0.26
Cthe_03035	D-isomer specific 2-hydroxyacid dehydrogenase,	15.38	15.49	14.15	14.47	1.23	1.02	-0.11	-0.32	0.53	0.91	-0.33	-0.23	0.7	0.92	1.47
Cthe_03035	D-isomer specific 2-hydroxyacid dehydrogenase,	15.38	15.49	14.15	14.47	1.23	1.02	-0.11	-0.32	0.53	0.91	-0.33	-0.23	0.7	0.92	1.47
Cthe_03035	D-isomer specific 2-hydroxyacid dehydrogenase,	15.38	15.49	14.15	14.47	1.23	1.02	-0.11	-0.32	0.53	0.91	-0.33	-0.23	0.7	0.92	1.47
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_01510	short-chain dehydrogenase/reductase SDR	8.07	9.2	7.73	8.3	0.34	0.9	-1.13	-0.57	-0.38	0.74	-1.6	-0.61	0.69	0.91	0.27
Cthe_02212	transcriptional regulator, AraC family	10.6	10.51	8.77	9.5	1.83	1.01	0.09	-0.73	1.14	0.9	-0.07	-0.85	0.69	0.91	0.96
Cthe_01510	short-chain dehydrogenase/reductase SDR	8.07	9.2	7.73	8.3	0.34	0.9	-1.13	-0.57	-0.38	0.74	-1.6	-0.61	0.69	0.91	0.27
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_03110	UBA/THIF-type NAD/FAD binding fold	10.27	9.85	8.29	8.99	1.98	0.86	0.42	-0.7	1.3	0.68	0.34	-0.8	0.69	0.91	0.95
Cthe_03126	NUDIX hydrolase	8.53	7.04	6.88	6.48	1.65	0.56	1.49	0.4	0.96	0.24	1.68	0.86	0.69	0.91	0.29
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_01510	short-chain dehydrogenase/reductase SDR	8.07	9.2	7.73	8.3	0.34	0.9	-1.13	-0.57	-0.38	0.74	-1.6	-0.61	0.69	0.91	0.27
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0.69	0.91	0.99
Cthe_00548	ABC transporter related protein	10.23	10.28	9.29	8.8	0.94	1.48	-0.05	0.49	0.23	1.59	-0.25	1	0.69	0.91	0.88
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrogenase,	10.11	10.45	8.71	9.22	1.4	1.23	-0.34	-0.51	0.7	1.22	-0.61	-0.52	0		



Cthe_03159	transcriptional regulator, GntR family	11.92	12.84	10.4	11.14	1.52	1.7	-0.92	-0.74	0.83	1.91	-1.34	-0.86	0.67	0.89	0.73
Cthe_00597	thiamine biosynthesis protein ThiS	5.52	5.61	4.52	4.58	1	1.03	-0.09	-0.06	0.3	0.93	-0.3	0.17	0.67	0.89	1.59
Cthe_02968	4Fe-4S ferredoxin, iron-sulfur binding	9.34	9.45	7.83	8.39	1.51	1.06	-0.11	-0.56	0.82	0.97	-0.33	-0.59	0.67	0.89	1.06
Cthe_00344	Malate dehydrogenase	16.24	17.16	15.25	16.18	0.99	0.98	-0.92	-0.93	0.29	0.85	-1.34	-1.15	0.67	0.89	0.29
Cthe_02968	4Fe-4S ferredoxin, iron-sulfur binding	9.34	9.45	7.83	8.39	1.51	1.06	-0.11	-0.56	0.82	0.97	-0.33	-0.59	0.67	0.89	1.06
Cthe_02934	ABC transporter related protein	9.6	10.41	8.38	9.46	1.22	0.95	-0.81	-1.08	0.52	0.81	-1.2	-1.38	0.67	0.89	0.3
Cthe_01475	hypothetical protein	10.59	10.43	9.3	9.61	1.29	0.82	0.16	-0.31	0.59	0.62	0.01	-0.21	0.67	0.89	2.29
Cthe_02934	ABC transporter related protein	9.6	10.41	8.38	9.46	1.22	0.95	-0.81	-1.08	0.52	0.81	-1.2	-1.38	0.67	0.89	0.3
Cthe_02934	ABC transporter related protein	9.6	10.41	8.38	9.46	1.22	0.95	-0.81	-1.08	0.52	0.81	-1.2	-1.38	0.67	0.89	0.3
Cthe_00144	preprotein translocase, SecG subunit	14.26	14.31	13.03	13.35	1.23	0.96	-0.05	-0.32	0.53	0.82	-0.25	-0.23	0.67	0.89	1.61
Cthe_00344	Malate dehydrogenase	16.24	17.16	15.25	16.18	0.99	0.98	-0.92	-0.93	0.29	0.85	-1.34	-1.15	0.67	0.89	0.29
Cthe_00344	Malate dehydrogenase	16.24	17.16	15.25	16.18	0.99	0.98	-0.92	-0.93	0.29	0.85	-1.34	-1.15	0.67	0.89	0.29
Cthe_00903	protein-export membrane protein SecF	13.17	14.3	12.79	13.36	0.38	0.94	-1.13	-0.57	-0.34	0.79	-1.6	-0.61	0.66	0.87	0.28
Cthe_00196	glutamine synthetase, catalytic region	11.26	11.08	9.25	10.1	2.01	0.98	0.18	-0.85	1.33	0.85	0.04	-1.03	0.66	0.87	0.86
Cthe_00596	GTP-binding protein	8.81	8.31	6.77	7.49	2.04	0.82	0.5	-0.72	1.36	0.62	0.44	-0.83	0.66	0.87	0.89
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_03036	methyl-accepting chemotaxis sensory transducer	8.1	7.38	6.38	6.43	1.72	0.95	0.72	-0.05	1.03	0.81	0.71	0.18	0.66	0.87	1.01
Cthe_00091	Peptidoglycan glycosyltransferase	11.31	11.19	9.5	10.22	1.81	0.97	0.12	-0.72	1.12	0.84	-0.04	-0.83	0.66	0.87	0.95
Cthe_01486	NUDIX hydrolase	8.02	7.97	6.98	7.06	1.04	0.91	0.05	-0.08	0.34	0.75	-0.12	0.14	0.66	0.87	2.51
Cthe_01583	deoxyribose-phosphate aldolase	6.49	6.36	5.17	5.52	1.32	0.84	0.13	-0.35	0.62	0.65	-0.02	-0.27	0.66	0.87	1.86
Cthe_03036	methyl-accepting chemotaxis sensory transducer	8.1	7.38	6.38	6.43	1.72	0.95	0.72	-0.05	1.03	0.81	0.71	0.18	0.66	0.87	1.01
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_00903	protein-export membrane protein SecF	13.17	14.3	12.79	13.36	0.38	0.94	-1.13	-0.57	-0.34	0.79	-1.6	-0.61	0.66	0.87	0.28
Cthe_01583	deoxyribose-phosphate aldolase	6.49	6.36	5.17	5.52	1.32	0.84	0.13	-0.35	0.62	0.65	-0.02	-0.27	0.66	0.87	1.86
Cthe_01486	NUDIX hydrolase	8.02	7.97	6.98	7.06	1.04	0.91	0.05	-0.08	0.34	0.75	-0.12	0.14	0.66	0.87	2.51
Cthe_00196	glutamine synthetase, catalytic region	11.26	11.08	9.25	10.1	2.01	0.98	0.18	-0.85	1.33	0.85	0.04	-1.03	0.66	0.87	0.86
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_01583	deoxyribose-phosphate aldolase	6.49	6.36	5.17	5.52	1.32	0.84	0.13	-0.35	0.62	0.65	-0.02	-0.27	0.66	0.87	1.86
Cthe_00196	glutamine synthetase, catalytic region	11.26	11.08	9.25	10.1	2.01	0.98	0.18	-0.85	1.33	0.85	0.04	-1.03	0.66	0.87	0.86
Cthe_01486	NUDIX hydrolase	8.02	7.97	6.98	7.06	1.04	0.91	0.05	-0.08	0.34	0.75	-0.12	0.14	0.66	0.87	2.51
Cthe_01486	NUDIX hydrolase	8.02	7.97	6.98	7.06	1.04	0.91	0.05	-0.08	0.34	0.75	-0.12	0.14	0.66	0.87	2.51
Cthe_01486	NUDIX hydrolase	8.02	7.97	6.98	7.06	1.04	0.91	0.05	-0.08	0.34	0.75	-0.12	0.14	0.66	0.87	2.51
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_01486	NUDIX hydrolase	8.02	7.97	6.98	7.06	1.04	0.91	0.05	-0.08	0.34	0.75	-0.12	0.14	0.66	0.87	2.51
Cthe_00196	glutamine synthetase, catalytic region	11.26	11.08	9.25	10.1	2.01	0.98	0.18	-0.85	1.33	0.85	0.04	-1.03	0.66	0.87	0.86
Cthe_01583	deoxyribose-phosphate aldolase	6.49	6.36	5.17	5.52	1.32	0.84	0.13	-0.35	0.62	0.65	-0.02	-0.27	0.66	0.87	1.86
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_00196	glutamine synthetase, catalytic region	11.26	11.08	9.25	10.1	2.01	0.98	0.18	-0.85	1.33	0.85	0.04	-1.03	0.66	0.87	0.86
Cthe_00196	glutamine synthetase, catalytic region	11.26	11.08	9.25	10.1	2.01	0.98	0.18	-0.85	1.33	0.85	0.04	-1.03	0.66	0.87	0.86
Cthe_02714	acetolactate synthase, large subunit,	12.63	13.53	12	12.67	0.63	0.86	-0.9	-0.67	-0.08	0.68	-1.31	-0.76	0.66	0.87	0.25
Cthe_00196	glutamine synthetase, catalytic region	11.26	11.08	9.25	10.1	2.01	0.98	0.18	-0.85	1.33	0.85	0.04	-1.03	0.66	0.87	0.86
Cthe_02096	methionyl-tRNA synthetase	12.08	12.17	10.74	11.17	1.34	1	-0.09	-0.43	0.64	0.88	-0.3	-0.39	0.65	0.86	1.24
Cthe_01442	ATP-dependent transcriptional regulator-like	6.51	6.23	4.52	5.32	1.99	0.91	0.28	-0.8	1.31	0.75	0.16	-0.95	0.65	0.86	0.88
Cthe_02719	NusG antitermination factor	11.82	12.5	10.86	11.7	0.96	0.8	-0.68	-0.84	0.26	0.59	-1.04	-1.02	0.65	0.86	0.25
Cthe_00814	DNA repair protein RecN	10.16	10.63	9.46	10.06	0.7	0.57	-0.47	-0.6	-0.01	0.25	-0.77	-0.65	0.65	0.86	0.14
Cthe_01200	adenosylhomocysteinase	11.23	11.81	10.13	10.44	1.1	1.37	-0.58	-0.31	0.4	1.43	-0.91	-0.21	0.65	0.86	0.89
Cthe_01804	cell wall hydrolase/autolysin	9.63	8.75	8.56	8.12	1.07	0.63	0.88	0.44	0.37	0.34	0.91	0.92	0.65	0.86	0.22
Cthe_02312	hypothetical protein	9.66	8.48	8.48	8.31	1.18	0.17	1.18	0.17	0.48	-0.34	1.29	0.52	0.65	0.86	0.24
Cthe_02096	methionyl-tRNA synthetase	12.08	12.17	10.74	11.17	1.34	1	-0.09	-0.43	0.64	0.88	-0.3	-0.39	0.65	0.86	1.24
Cthe_00031	putative membrane transporter	7.13	6.07	5.04	5.04	2.09	1.03	1.06	0	1.41	0.93	1.14	0.26	0.65	0.86	0.81
Cthe_02937	cobalt transport protein	8.87	9.03	7.11	7.88	1.76	1.15	-0.16	-0.77	1.07	1.1	-0.39	-0.91	0.65	0.86	0.87
Cthe_02523	hypothetical protein	12.28	11.39	9.97	10.64	2.31	0.75	0.89	-0.67	1.63	0.51	0.92	-0.76	0.65	0.86	0.8
Cthe_02096	methionyl-tRNA synthetase	12.08	12.17	10.74	11.17	1.34	1	-0.09	-0.43	0.64	0.88	-0.3	-0.39	0.65	0.86	1.24
Cthe_02937	cobalt transport protein	8.87	9.03	7.11	7.88	1.76	1.15	-0.16	-0.77	1.07	1.1	-0.39	-0.91	0.65	0.86	0.87
Cthe_02096	methionyl-tRNA synthetase	12.08	12.17	10.74	11.17	1.34	1	-0.09	-0.43	0.64	0.88	-0.3	-0.39	0.65	0.86	1.24
Cthe_02937	cobalt transport protein	8.87	9.03	7.11	7.88	1.76	1.15	-0.16	-0.77	1.07	1.1	-0.39	-0.91	0.65	0.86	0.87
Cthe_01200	adenosylhomocysteinase	11.23	11.81	10.13	10.44	1.1	1.37	-0.58	-0.31	0.4	1.43	-0.91	-0.21	0.65	0.86	0.89
Cthe_01200	adenosylhomocysteinase	11.23	11.81	10.13	10.44	1.1	1.37	-0.58	-0.31	0.4	1.43	-0.91	-0.21	0.65	0.86	0.89
Cthe_02096	methionyl-tRNA synthetase	12.08	12.17	10.74	11.17	1.34	1	-0.09	-0.43	0.64	0.88	-0.3	-0.39	0.65	0.86	1.24
Cthe_01804	cell wall hydrolase/autolysin	9.63	8.75	8.56	8.12	1.07	0.63	0.88	0.44	0.37	0.34	0.91	0.92	0.65	0.86	0.22
Cthe_01200	adenosylhomocysteinase	11.23	11.81	10.13	10.44	1.1	1.37	-0.58	-0.31	0.4	1.43	-0.91	-0.21	0.65	0.86	0.89
Cthe_01200	adenosylhomocysteinase	11.23	11.81	10.13	10.44	1.1	1.37	-0.58	-0.31	0.4	1.43	-0.91	-0.21	0.65	0.86	0.89
Cthe_02096	methionyl-tRNA synthetase	12.08	12.17	10.74	11.17	1.34	1	-0.09	-0.43	0.64	0.88	-0.3	-0.39	0.65	0.86	1.24
Cthe_01375	aspartate kinase	11.39	11.87	10.34	11.2	1.05	0.67	-0.48	-0.86	0.35	0.4	-0.79	-1.05	0.64	0.85	0.23
Cthe_00562	protein of unknown function DUF1312	9.35	9.24	7.89	8.36	1.46	0.88	0.11	-0.47	0.77	0.71	-0.05	-0.45	0.64	0.85	1.3
Cthe_00648	glutamyl-tRNA synthetase	13.07	12.95	11.63	12.08	1.44	0.87	0.12	-0.45	0.74	0.69	-0.04	-0.42	0.64	0.85	1.35
Cthe_00860	Rubrythrin	12.13	12.07	10.69	11.16	1.44	0.91	0.06	-0.47	0.74	0.75	-0.11	-0.45	0.64	0.85	1.28
Cthe_00551	AMP-dependent synthetase and ligase	13.52	13.5	12.19	12.59	1.33	0.91	0.02	-0.4	0.63	0.75	-0.16	-0.35	0.64	0.85	1.43
Cthe_01375	aspartate kinase	11.39	11.87	10.34	11.2	1.05	0.67	-0.48	-0.86	0.35	0.4					



Cthe_02551	Radical SAM	5.98	6.17	4.7	5.73	1.28	0.44	-0.19	-1.03	0.58	0.06	-0.42	-1.3	0.63	0.84	0.24
Cthe_02553	Radical SAM	7.02	6.07	4.86	5.29	2.16	0.78	0.95	-0.43	1.48	0.56	1	-0.39	0.63	0.84	0.83
Cthe_00944	SMC protein-like protein	10.29	10.49	9.18	10.06	1.11	0.43	-0.2	-0.88	0.41	0.04	-0.44	-1.08	0.63	0.84	0.2
Cthe_01092	hypothetical protein	9.56	10.08	9	9.53	0.56	0.55	-0.52	-0.53	-0.15	0.22	-0.84	-0.55	0.63	0.84	0.15
Cthe_02256	replicative DNA helicase	12.04	12.58	11.03	11.87	1.01	0.71	-0.54	-0.84	0.31	0.46	-0.86	-1.02	0.63	0.84	0.23
Cthe_00025	adenosylmethionine-8-amino-7-oxononanoate	6.38	6.99	5.64	6.29	0.74	0.7	-0.61	-0.65	0.03	0.44	-0.95	-0.73	0.63	0.84	0.21
Cthe_00341	NADH dehydrogenase (quinone)	12.39	13.6	12.21	12.68	0.18	0.92	-1.21	-0.47	-0.54	0.76	-1.7	-0.45	0.63	0.84	0.3
Cthe_03024	NADH dehydrogenase (quinone)	12.84	13.05	10.94	11.84	1.9	1.21	-0.21	-0.9	1.21	1.19	-0.45	-1.11	0.63	0.84	0.8
Cthe_03024	NADH dehydrogenase (quinone)	12.84	13.05	10.94	11.84	1.9	1.21	-0.21	-0.9	1.21	1.19	-0.45	-1.11	0.63	0.84	0.8
Cthe_00025	adenosylmethionine-8-amino-7-oxononanoate	6.38	6.99	5.64	6.29	0.74	0.7	-0.61	-0.65	0.03	0.44	-0.95	-0.73	0.63	0.84	0.21
Cthe_00256	replicative DNA helicase	12.04	12.58	11.03	11.87	1.01	0.71	-0.54	-0.84	0.31	0.46	-0.86	-1.02	0.63	0.84	0.23
Cthe_00341	NADH dehydrogenase (quinone)	12.39	13.6	12.21	12.68	0.18	0.92	-1.21	-0.47	-0.54	0.76	-1.7	-0.45	0.63	0.84	0.3
Cthe_00025	adenosylmethionine-8-amino-7-oxononanoate	6.38	6.99	5.64	6.29	0.74	0.7	-0.61	-0.65	0.03	0.44	-0.95	-0.73	0.63	0.84	0.21
Cthe_00341	NADH dehydrogenase (quinone)	12.39	13.6	12.21	12.68	0.18	0.92	-1.21	-0.47	-0.54	0.76	-1.7	-0.45	0.63	0.84	0.3
Cthe_00341	NADH dehydrogenase (quinone)	12.39	13.6	12.21	12.68	0.18	0.92	-1.21	-0.47	-0.54	0.76	-1.7	-0.45	0.63	0.84	0.3
Cthe_00341	NADH dehydrogenase (quinone)	12.39	13.6	12.21	12.68	0.18	0.92	-1.21	-0.47	-0.54	0.76	-1.7	-0.45	0.63	0.84	0.3
Cthe_00341	NADH dehydrogenase (quinone)	12.39	13.6	12.21	12.68	0.18	0.92	-1.21	-0.47	-0.54	0.76	-1.7	-0.45	0.63	0.84	0.3
Cthe_00341	NADH dehydrogenase (quinone)	12.39	13.6	12.21	12.68	0.18	0.92	-1.21	-0.47	-0.54	0.76	-1.7	-0.45	0.63	0.84	0.3
Cthe_02524	transcriptional regulator, BadM/Rrf2 family	8.78	8.88	6.89	7.76	1.89	1.12	-0.1	-0.87	1.2	1.06	-0.31	-1.06	0.62	0.82	0.81
Cthe_00617	AAA ATPase, central region	12.54	13.35	11.77	12.49	0.77	0.86	-0.81	-0.72	0.06	0.68	-1.2	-0.83	0.62	0.82	0.26
Cthe_00110	HPr kinase	9.48	9.39	7.28	8.33	2.2	1.06	0.09	-1.05	1.52	0.97	-0.07	-1.33	0.62	0.82	0.76
Cthe_00858	protein of unknown function DUF1432	13.46	13.41	11.97	12.49	1.49	0.92	0.05	-0.52	0.8	0.76	-0.12	-0.53	0.62	0.82	1.14
Cthe_02810	Na/Pi-cotransporter II-related protein	10.24	10.84	8.93	10.02	1.31	0.82	-0.6	-1.09	0.61	0.62	-0.94	-1.39	0.62	0.82	0.29
Cthe_03117	zinc/iron permease	13.65	13.16	11.93	12.39	1.72	0.77	0.49	-0.46	1.03	0.54	0.42	-0.44	0.62	0.82	1.07
Cthe_01000	phosphatidate cytidylyltransferase	11.14	12.2	10.74	11.29	0.4	0.91	-1.06	-0.55	-0.32	0.75	-1.51	-0.58	0.62	0.82	0.28
Cthe_02693	hypothetical protein	11.53	11.32	10.24	10.54	1.29	0.78	0.21	-0.3	0.59	0.56	0.07	-0.2	0.62	0.82	2.16
Cthe_03002	hypothetical protein	11.37	12.11	10.83	11.39	0.54	0.72	-0.74	-0.56	-0.17	0.47	-1.11	-0.59	0.62	0.82	0.22
Cthe_01000	phosphatidate cytidylyltransferase	11.14	12.2	10.74	11.29	0.4	0.91	-1.06	-0.55	-0.32	0.75	-1.51	-0.58	0.62	0.82	0.28
Cthe_01000	phosphatidate cytidylyltransferase	11.14	12.2	10.74	11.29	0.4	0.91	-1.06	-0.55	-0.32	0.75	-1.51	-0.58	0.62	0.82	0.28
Cthe_00040	Cellulase, Cellulose 1,4-beta-cellobiosidase	10.54	10.49	8.81	9.51	1.73	0.98	0.05	-0.7	1.04	0.85	-0.12	-0.8	0.62	0.82	0.93
Cthe_00110	HPr kinase	9.48	9.39	7.28	8.33	2.2	1.06	0.09	-1.05	1.52	0.97	-0.07	-1.33	0.62	0.82	0.76
Cthe_00110	HPr kinase	9.48	9.39	7.28	8.33	2.2	1.06	0.09	-1.05	1.52	0.97	-0.07	-1.33	0.62	0.82	0.76
Cthe_00040	Cellulase, Cellulose 1,4-beta-cellobiosidase	10.54	10.49	8.81	9.51	1.73	0.98	0.05	-0.7	1.04	0.85	-0.12	-0.8	0.62	0.82	0.93
Cthe_01000	phosphatidate cytidylyltransferase	11.14	12.2	10.74	11.29	0.4	0.91	-1.06	-0.55	-0.32	0.75	-1.51	-0.58	0.62	0.82	0.28
Cthe_00110	HPr kinase	9.48	9.39	7.28	8.33	2.2	1.06	0.09	-1.05	1.52	0.97	-0.07	-1.33	0.62	0.82	0.76
Cthe_01000	phosphatidate cytidylyltransferase	11.14	12.2	10.74	11.29	0.4	0.91	-1.06	-0.55	-0.32	0.75	-1.51	-0.58	0.62	0.82	0.28
Cthe_00040	Cellulase, Cellulose 1,4-beta-cellobiosidase	10.54	10.49	8.81	9.51	1.73	0.98	0.05	-0.7	1.04	0.85	-0.12	-0.8	0.62	0.82	0.93
Cthe_00110	HPr kinase	9.48	9.39	7.28	8.33	2.2	1.06	0.09	-1.05	1.52	0.97	-0.07	-1.33	0.62	0.82	0.76
Cthe_00110	HPr kinase	9.48	9.39	7.28	8.33	2.2	1.06	0.09	-1.05	1.52	0.97	-0.07	-1.33	0.62	0.82	0.76
Cthe_00110	HPr kinase	9.48	9.39	7.28	8.33	2.2	1.06	0.09	-1.05	1.52	0.97	-0.07	-1.33	0.62	0.82	0.76
Cthe_01000	phosphatidate cytidylyltransferase	11.14	12.2	10.74	11.29	0.4	0.91	-1.06	-0.55	-0.32	0.75	-1.51	-0.58	0.62	0.82	0.28
Cthe_01055	protein of unknown function DUF58	11.16	11.86	10.49	11.11	0.67	0.75	-0.7	-0.62	-0.04	0.51	-1.06	-0.68	0.61	0.81	0.23
Cthe_02540	Mov34/MPN/PAD-1	3	2.32	1	1.58	2	0.74	0.68	-0.58	1.32	0.5	0.66	-0.62	0.61	0.81	0.88
Cthe_02448	inner-membrane translocator	7.36	7.52	6	6.48	1.36	1.04	-0.16	-0.48	0.66	0.94	-0.39	-0.47	0.61	0.81	1.06
Cthe_00201	glutamate synthase, alpha subunit-like protein	8.36	8.2	7.29	7.3	1.07	0.9	0.16	-0.01	0.37	0.74	0.01	0.24	0.61	0.81	1.93
Cthe_01181	transglutaminase-like protein	10.17	10.59	9.08	9.95	1.09	0.64	-0.42	-0.87	0.39	0.35	-0.71	-1.06	0.61	0.81	0.23
Cthe_00181	Holliday junction DNA helicase RuvA	9.26	9.49	7.76	8.37	1.5	1.12	-0.23	-0.61	0.81	1.06	-0.47	-0.67	0.61	0.81	0.92
Cthe_00970	transposase, mutator type	5.46	4	4.09	4	1.37	0	1.46	0.09	0.67	-0.59	1.64	0.39	0.61	0.81	0.3
Cthe_00440	Domain of unknown function DUF1727	12.67	12.59	11.64	11.74	1.03	0.85	0.08	-0.1	0.33	0.66	-0.09	0.11	0.61	0.81	2.92
Cthe_00504	Putative enzyme of poly-gamma-glutamate	13.33	12.96	11.84	12.2	1.49	0.76	0.37	-0.36	0.8	0.53	0.27	-0.29	0.61	0.81	1.36
Cthe_02511	MscS Mechanosensitive ion channel	8.73	8.03	6.99	7.2	1.74	0.83	0.7	-0.21	1.05	0.63	0.69	-0.06	0.61	0.81	0.99
Cthe_00827	hemolysin A	9.25	9.72	8.69	9.21	0.56	0.51	-0.47	-0.52	-0.15	0.16	-0.77	-0.53	0.61	0.81	0.13
Cthe_02255	tRNA(Ile)-lysidine synthetase	11.81	12.06	10.89	11.59	0.92	0.47	-0.25	-0.7	0.21	0.1	-0.5	-0.8	0.61	0.81	0.14
Cthe_01719	phage major capsid protein, HK97 family	5.81	4.39	3.17	3.58	2.64	0.81	1.42	-0.41	1.97	0.6	1.59	-0.36	0.61	0.81	0.71
Cthe_02448	inner-membrane translocator	7.36	7.52	6	6.48	1.36	1.04	-0.16	-0.48	0.66	0.94	-0.39	-0.47	0.61	0.81	1.06
Cthe_02255	tRNA(Ile)-lysidine synthetase	11.81	12.06	10.89	11.59	0.92	0.47	-0.25	-0.7	0.21	0.1	-0.5	-0.8	0.61	0.81	0.14
Cthe_00484	flagellar biosynthetic protein FlhB	12.4	11.6	10.16	10.88	2.24	0.72	0.8	-0.72	1.56	0.47	0.81	-0.83	0.6	0.8	0.79
Cthe_00033	small GTP-binding protein	8.61	9.41	7.67	8.5	0.94	0.91	-0.8	-0.83	0.23	0.75	-1.19	-1	0.6	0.8	0.28
Cthe_00863	glutamine synthetase, catalytic region	12.4	13.67	12.34	12.75	0.06	0.92	-1.27	-0.41	-0.66	0.76	-1.77	-0.36	0.6	0.8	0.31
Cthe_02335	polysaccharide biosynthesis protein	10.09	10.5	8.93	9.85	1.16	0.65	-0.41	-0.92	0.46	0.37	-0.7	-1.14	0.6	0.8	0.25
Cthe_02142	recombination protein RecR	12.1	12.47	11.09	11.88	1.01	0.59	-0.37	-0.79	0.31	0.28	-0.65	-0.94	0.6	0.8	0.21
Cthe_00484	flagellar biosynthetic protein FlhB	12.4	11.6	10.16	10.88	2.24	0.72	0.8	-0.72	1.56	0.47	0.81	-0.83	0.6	0.8	0.79
Cthe_02406	hypothetical protein	10.52	10.62	8.64	9.51	1.88	1.11	-0.1	-0.87	1.19	1.04	-0.31	-1.06	0.6	0.8	0.8
Cthe_00033	small GTP-binding protein	8.61	9.41	7.67	8.5	0.94	0.91	-0.8	-0.83	0.23	0.75	-1.19	-1	0.6	0.8	0.28
Cthe_02658	RNA-binding S4	9.79	8.39	8.22	8	1.57	0.39	1.4	0.22	0.88	-0.01	1.56	0.59	0.6	0.8	0.3
Cthe_00068	Peptidylprolyl isomerase	12.99	12.63	10.83	11.75	2.16	0.88	0.36	-0.92	1.48	0.71	0.26	-1.14	0.6	0.8	0.79
Cthe_00323	hypothetical protein	7.6	7.94	6.79	7.41	0.81	0.53	-0.34	-0.62	0.1	0.19	-0.61	-0.68	0.6	0.8	0.13
Cthe_01524	hypothetical protein	8.07	7.59	6.11	6.81	1.96	0.78	0.48	-0.7	1.28	0.56	0.41	-0.8	0.6	0.8	0.87
Cthe_00068	Peptidylprolyl isomerase	12.99	12.63	10.83	11.75	2.16	0.88	0.36	-0.92	1.48	0.71	0.26	-1.14	0.6	0.8	0.79
Cthe_00863	glutamine synthetase, catalytic region	12.4	13.67	12.34	12.75	0.06	0.92	-1.27	-0.41	-0.66	0.76	-1.77	-0.36	0.6	0.8	0.31
Cthe_00863	glutamine synthetase, catalytic region	12.4	13.67	12.34	12.75	0.06	0.92	-1.27	-0.41	-0.66	0.76	-1.77	-0.36	0.6	0.8	0.31
Cthe_00863	glutamine synthetase, catalytic region	12.4	13.67	12.34	12.75	0.06	0.92	-1.27	-0.41	-0.66	0.76	-1.77	-0.36	0.6	0.8	0.31
Cthe_00863	glutamine synthetase, catalytic region	12.4	13.67	12.34	12.75	0.06	0.92	-1.27	-0.41	-0.66	0.76	-1.77	-0.36	0.6	0.8	0.31
Cthe_00863	glutamine synthetase, catalytic region	12.4	13.67	12.34	12.75	0.06	0.92	-1.27	-0.41	-0.66	0.76	-1.77	-0.36	0.6	0.8	0.31
Cthe_00863	glutamine synthetase, catalytic region	12.4	13.67	12.34	12.75	0.06	0.92	-1.27	-0.41	-0.66	0.76	-1.77	-0.36			



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Cthe_02800	aminotransferase, class I and II	9.11	9.64	7.58	8.3	1.53	1.34	-0.53	-0.72	0.84	1.38	-0.85	-0.83	0.56	0.75	0.76
Cthe_02800	aminotransferase, class I and II	9.11	9.64	7.58	8.3	1.53	1.34	-0.53	-0.72	0.84	1.38	-0.85	-0.83	0.56	0.75	0.76
Cthe_02800	aminotransferase, class I and II	9.11	9.64	7.58	8.3	1.53	1.34	-0.53	-0.72	0.84	1.38	-0.85	-0.83	0.56	0.75	0.76
Cthe_02800	aminotransferase, class I and II	9.11	9.64	7.58	8.3	1.53	1.34	-0.53	-0.72	0.84	1.38	-0.85	-0.83	0.56	0.75	0.76
Cthe_02556	Radical SAM	6.99	5.75	5.55	5.39	1.44	0.36	1.24	0.16	0.74	-0.06	1.36	0.5	0.55	0.73	0.29
Cthe_02888	imidazoleglycerol phosphate synthase, cyclase	7.99	8.83	7.09	7.88	0.9	0.95	-0.84	-0.79	0.19	0.81	-1.24	-0.94	0.55	0.73	0.3
Cthe_01455	hypothetical protein	8.65	8.52	7.47	7.76	1.18	0.76	0.13	-0.29	0.48	0.53	-0.02	-0.18	0.55	0.73	2.22
Cthe_03108	phage SPO1 DNA polymerase-related protein	8.55	9.16	7.6	8.37	0.95	0.79	-0.61	-0.77	0.24	0.57	-0.95	-0.91	0.55	0.73	0.26
Cthe_00491	CheW protein	9.09	8.88	7.58	8.98	1.51	-0.1	0.21	-1.4	0.82	-0.74	0.07	-1.86	0.55	0.73	0.33
Cthe_00714	hydroxymethylbutenyl pyrophosphate reductase	14.05	14.67	13.6	14.07	0.45	0.6	-0.62	-0.47	-0.27	0.29	-0.96	-0.45	0.55	0.73	0.21
Cthe_00491	CheW protein	9.09	8.88	7.58	8.98	1.51	-0.1	0.21	-1.4	0.82	-0.74	0.07	-1.86	0.55	0.73	0.33
Cthe_00215	phenylalanyl-tRNA synthetase, beta subunit	10.5	11.65	9.73	10.5	0.77	1.15	-1.15	-0.77	0.06	1.1	-1.62	-0.91	0.55	0.73	0.33
Cthe_00278	pseudouridine synthase	10.29	10.5	8.57	9.37	1.72	1.13	-0.21	-0.8	1.03	1.07	-0.45	-0.95	0.55	0.73	0.79
Cthe_00714	hydroxymethylbutenyl pyrophosphate reductase	14.05	14.67	13.6	14.07	0.45	0.6	-0.62	-0.47	-0.27	0.29	-0.96	-0.45	0.55	0.73	0.21
Cthe_00714	hydroxymethylbutenyl pyrophosphate reductase	14.05	14.67	13.6	14.07	0.45	0.6	-0.62	-0.47	-0.27	0.29	-0.96	-0.45	0.55	0.73	0.21
Cthe_03107	Radical SAM	9.53	10	8.41	8.78	1.12	1.22	-0.47	-0.37	0.42	1.21	-0.77	-0.3	0.55	0.73	0.87
Cthe_00297	hypothetical protein	8.39	8.47	6.83	7.47	1.56	1	-0.08	-0.64	0.87	0.88	-0.29	-0.71	0.55	0.73	0.91
Cthe_02888	imidazoleglycerol phosphate synthase, cyclase	7.99	8.83	7.09	7.88	0.9	0.95	-0.84	-0.79	0.19	0.81	-1.24	-0.94	0.55	0.73	0.3
Cthe_00215	phenylalanyl-tRNA synthetase, beta subunit	10.5	11.65	9.73	10.5	0.77	1.15	-1.15	-0.77	0.06	1.1	-1.62	-0.91	0.55	0.73	0.33
Cthe_00215	phenylalanyl-tRNA synthetase, beta subunit	10.5	11.65	9.73	10.5	0.77	1.15	-1.15	-0.77	0.06	1.1	-1.62	-0.91	0.55	0.73	0.33
Cthe_00714	hydroxymethylbutenyl pyrophosphate reductase	14.05	14.67	13.6	14.07	0.45	0.6	-0.62	-0.47	-0.27	0.29	-0.96	-0.45	0.55	0.73	0.21
Cthe_00714	hydroxymethylbutenyl pyrophosphate reductase	14.05	14.67	13.6	14.07	0.45	0.6	-0.62	-0.47	-0.27	0.29	-0.96	-0.45	0.55	0.73	0.21
Cthe_00215	phenylalanyl-tRNA synthetase, beta subunit	10.5	11.65	9.73	10.5	0.77	1.15	-1.15	-0.77	0.06	1.1	-1.62	-0.91	0.55	0.73	0.33
Cthe_00278	pseudouridine synthase	10.29	10.5	8.57	9.37	1.72	1.13	-0.21	-0.8	1.03	1.07	-0.45	-0.95	0.55	0.73	0.79
Cthe_03108	phage SPO1 DNA polymerase-related protein	8.55	9.16	7.6	8.37	0.95	0.79	-0.61	-0.77	0.24	0.57	-0.95	-0.91	0.55	0.73	0.26
Cthe_02888	imidazoleglycerol phosphate synthase, cyclase	7.99	8.83	7.09	7.88	0.9	0.95	-0.84	-0.79	0.19	0.81	-1.24	-0.94	0.55	0.73	0.3
Cthe_00714	hydroxymethylbutenyl pyrophosphate reductase	14.05	14.67	13.6	14.07	0.45	0.6	-0.62	-0.47	-0.27	0.29	-0.96	-0.45	0.55	0.73	0.21
Cthe_02888	imidazoleglycerol phosphate synthase, cyclase	7.99	8.83	7.09	7.88	0.9	0.95	-0.84	-0.79	0.19	0.81	-1.24	-0.94	0.55	0.73	0.3
Cthe_00714	hydroxymethylbutenyl pyrophosphate reductase	14.05	14.67	13.6	14.07	0.45	0.6	-0.62	-0.47	-0.27	0.29	-0.96	-0.45	0.55	0.73	0.21
Cthe_02888	imidazoleglycerol phosphate synthase, cyclase	7.99	8.83	7.09	7.88	0.9	0.95	-0.84	-0.79	0.19	0.81	-1.24	-0.94	0.55	0.73	0.3
Cthe_00215	phenylalanyl-tRNA synthetase, beta subunit	10.5	11.65	9.73	10.5	0.77	1.15	-1.15	-0.77	0.06	1.1	-1.62	-0.91	0.55	0.73	0.33
Cthe_00113	Uncharacterized P-loop ATPase protein UPF0042	9.7	9.99	8.82	8.88	0.88	1.11	-0.29	-0.06	0.17	1.04	-0.55	0.17	0.54	0.72	1.03
Cthe_02208	LexA DNA-binding region containing protein	15.55	14.92	12.92	14.13	2.63	0.79	0.63	-1.21	1.96	0.57	0.6	-1.58	0.54	0.72	0.68
Cthe_02535	adenylsulfate reductase, thioredoxin dependent	2.32	1	0	2.32	1	1.32	0	1.64	0.88	1.46	0.26	0.54	0.72	0.71	0.71
Cthe_03216	transposase, mutator type	4.32	4.25	2.58	3.32	1.74	0.93	0.07	-0.74	1.05	0.78	-0.1	-0.86	0.54	0.72	0.85
Cthe_02535	adenylsulfate reductase, thioredoxin dependent	2.32	1	0	2.32	1	1.32	0	1.64	0.88	1.46	0.26	0.54	0.72	0.71	0.71
Cthe_02345	DegT/DnrJ/EryC1/StrS aminotransferase	11.31	11.84	10.12	11.06	1.19	0.78	-0.53	-0.94	0.49	0.56	-0.85	-1.17	0.54	0.72	0.29
Cthe_02208	LexA DNA-binding region containing protein	15.55	14.92	12.92	14.13	2.63	0.79	0.63	-1.21	1.96	0.57	0.6	-1.58	0.54	0.72	0.68
Cthe_02185	ribosomal protein S18	12.43	12.59	11.18	11.6	1.25	0.99	-0.16	-0.42	0.55	0.87	-0.39	-0.38	0.54	0.72	1.06
Cthe_02902	ribosomal protein S10	11.39	11.84	9.85	11.06	1.54	0.78	-0.45	-1.21	0.85	0.56	-0.75	-1.58	0.54	0.72	0.33
Cthe_02791	binding-protein-dependent transport systems	4	3.46	3.32	2.32	0.68	1.14	0.54	1	-0.03	1.09	0.49	1.77	0.54	0.72	0.33
Cthe_03189	hypothetical protein	11.25	11.52	10.28	10.99	0.97	0.53	-0.27	-0.71	0.27	0.19	-0.53	-0.82	0.54	0.72	0.19
Cthe_02902	ribosomal protein S10	11.39	11.84	9.85	11.06	1.54	0.78	-0.45	-1.21	0.85	0.56	-0.75	-1.58	0.54	0.72	0.33
Cthe_02791	binding-protein-dependent transport systems	4	3.46	3.32	2.32	0.68	1.14	0.54	1	-0.03	1.09	0.49	1.77	0.54	0.72	0.33
Cthe_02185	ribosomal protein S18	12.43	12.59	11.18	11.6	1.25	0.99	-0.16	-0.42	0.55	0.87	-0.39	-0.38	0.54	0.72	1.06
Cthe_02902	ribosomal protein S10	11.39	11.84	9.85	11.06	1.54	0.78	-0.45	-1.21	0.85	0.56	-0.75	-1.58	0.54	0.72	0.33
Cthe_02535	adenylsulfate reductase, thioredoxin dependent	2.32	1	0	2.32	1	1.32	0	1.64	0.88	1.46	0.26	0.54	0.72	0.71	0.71
Cthe_02208	LexA DNA-binding region containing protein	15.55	14.92	12.92	14.13	2.63	0.79	0.63	-1.21	1.96	0.57	0.6	-1.58	0.54	0.72	0.68
Cthe_02535	adenylsulfate reductase, thioredoxin dependent	2.32	1	0	2.32	1	1.32	0	1.64	0.88	1.46	0.26	0.54	0.72	0.71	0.71
Cthe_00219	5-nitroimidazole antibiotic resistance protein	7.73	7.29	6.27	6.58	1.46	0.71	0.44	-0.31	0.77	0.46	0.36	-0.21	0.53	0.71	1.21
Cthe_01199	amidohydrolase	10.49	11.59	10.12	10.61	0.37	0.98	-1.1	-0.49	-0.35	0.85	-1.56	-0.48	0.53	0.71	0.32
Cthe_02691	galactoside O-acetyltransferase	8.93	8.53	6.97	7.75	1.96	0.78	0.4	-0.78	1.28	0.56	0.31	-0.92	0.53	0.71	0.81
Cthe_00951	orotidine 5'-phosphate decarboxylase	11.43	9.99	8.65	9.36	2.78	0.63	1.44	-0.71	2.11	0.34	1.61	-0.82	0.53	0.71	0.66
Cthe_01199	amidohydrolase	10.49	11.59	10.12	10.61	0.37	0.98	-1.1	-0.49	-0.35	0.85	-1.56	-0.48	0.53	0.71	0.32
Cthe_01495	pyridoxamine 5'-phosphate oxidase-related,	11.54	10.64	9.53	9.91	2.01	0.73	0.9	-0.38	1.33	0.49	0.94	-0.32	0.53	0.71	0.8
Cthe_01312	glycyl-tRNA synthetase	12.99	13.72	12.14	12.86	0.85	0.86	-0.73	-0.72	0.14	0.68	-1.1	-0.83	0.53	0.71	0.28
Cthe_00317	hypothetical protein	12.18	12.08	10.92	11.29	1.26	0.79	0.1	-0.37	0.56	0.57	-0.06	-0.3	0.53	0.71	1.47
Cthe_02549	cellulosome enzyme, dockerin type I	9.33	9.22	7.48	8.29	1.85	0.93	0.11	-0.81	1.16	0.78	-0.05	-0.97	0.53	0.71	0.81
Cthe_01547	hypothetical protein	10.82	9.52	9.46	9.41	1.36	0.11	1.3	0.05	0.66	-0.43	1.44	0.33	0.53	0.71	0.3
Cthe_02849	hypothetical protein	1.58	0	1.58	0	1.58	0	1.58	0.89	-0.59	1.79			0.53	0.71	0.34
Cthe_01312	glycyl-tRNA synthetase	12.99	13.72	12.14	12.86	0.85	0.86	-0.73	-0.72	0.14	0.68	-1.1	-0.83	0.53	0.71	0.28
Cthe_01312	glycyl-tRNA synthetase	12.99	13.72	12.14	12.86	0.85	0.86	-0.73	-0.72	0.14	0.68	-1.1	-0.83	0.53	0.71	0.28
Cthe_00951	orotidine 5'-phosphate decarboxylase	11.43	9.99	8.65	9.36	2.78	0.63	1.44	-0.71	2.11	0.34	1.61	-0.82	0.53	0.71	0.66
Cthe_01312	glycyl-tRNA synthetase	12.99	13.72	12.14	12.86	0.85	0.86	-0.73	-0.72	0.14	0.68	-1.1	-0.83	0.53	0.71	0.28
Cthe_00951	orotidine 5'-phosphate decarboxylase	11.43	9.99	8.65	9.36	2.78	0.63	1.44	-0.71	2.11	0.34	1.61	-0.82	0.53	0.71	0.66
Cthe_01199	amidohydrolase	10.49	11.59	10.12	10.61	0.37	0.98	-1.1	-0.49	-0.35	0.85	-1.56	-0.48	0.53	0.71	0.32
Cthe_01199	amidohydrolase	10.49	11.59	10.12	10.61	0.37	0.98	-1.1	-0.49	-0.35	0.85	-1.56	-0.48	0.53	0.71	0.32
Cthe_01199	amidohydrolase	10.49	11.59	10.12	10.61	0.37	0.98	-1.1	-0.49	-0.35	0.85	-1.56	-0.48	0.53	0.71	0.32
Cthe_01199	amidohydrolase	10.49	11.59	10.12	10.61	0.37	0.98	-1.1	-0.49	-0.35	0.85	-1.56	-0.48	0.53	0.71	0.32
Cthe_01312	glycyl-tRNA synthetase	12.99	13.72	12.14	12.86	0.85	0.86	-0.73	-0.72	0.14	0.68	-1.1	-0.83	0.53	0.71	0.28
Cthe_01199	amidohydrolase	10.49	11.59	10.12	10.61	0.37	0.98	-1.1	-0.49	-0.35	0.85	-1.56	-0.48	0.53	0.71	0.32
Cthe_02718	preprotein translocase, SecE subunit	10.2	10.33	9.15	9.92	1.05	0.41	-0.13	-0.77	0.35	0.01	-0.35	-0.91	0.52	0.7	0.2
Cthe_01052	competence/damage-inducible protein ClnA	10.3	10.63	8.61	9.43	1.69	1.2	-0.33	-0.82	1	1.18	-0.6	-0.98	0.52	0.7	0.76
Cthe_01284	glycogen/starch synthases, ADP-glucose type	11.06	10.43	9.52	9.58	1.54	0.85	0.63	-0.06	0.85	0.66	0.6	0.17	0.52	0.7	0.97
Cthe_00377	peptidase M56, BlaR1	7	6.77	5.17	6.61	1.83	0.16	0.23	-1.44	1.14</						



Cthe_00509	sodium ion-translocating decarboxylase, beta	14.01	13.84	12.18	12.96	1.83	0.88	0.17	-0.78	1.14	0.71	0.03	-0.92	0.52	0.7	0.82
Cthe_00022	8-amino-7-oxononanoate synthase	4.58	5.39	3.81	3.91	0.77	1.48	-0.81	-0.1	0.06	1.59	-1.2	0.11	0.52	0.7	0.74
Cthe_01259	CDP-alcohol phosphatidyltransferase	10.76	10.39	9.07	9.65	1.69	0.74	0.37	-0.58	1	0.5	0.27	-0.62	0.52	0.7	0.93
Cthe_00509	sodium ion-translocating decarboxylase, beta	14.01	13.84	12.18	12.96	1.83	0.88	0.17	-0.78	1.14	0.71	0.03	-0.92	0.52	0.7	0.82
Cthe_01022	Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	10.7	11.35	10.11	10.63	0.59	0.72	-0.65	-0.52	-0.12	0.47	-1	-0.53	0.52	0.7	0.24
Cthe_03113	Nucleotidyl transferase	9.12	8.75	8.64	7.6	0.48	1.15	0.37	1.04	-0.23	1.1	0.27	1.83	0.52	0.7	0.34
Cthe_01284	glycogen/starch synthases, ADP-glucose type	11.06	10.43	9.52	9.58	1.54	0.85	0.63	-0.06	0.85	0.66	0.6	0.17	0.52	0.7	0.97
Cthe_02743	putative metalloendopeptidase, glycoprotease	12.76	12.3	11.1	11.59	1.66	0.71	0.46	-0.49	0.97	0.46	0.39	-0.48	0.52	0.7	0.98
Cthe_02887	phosphoribosylformimino-5-aminoimidazole	8.89	9.46	7.76	8.65	1.13	0.81	-0.57	-0.89	0.43	0.6	-0.9	-1.09	0.52	0.7	0.29
Cthe_00577	thiamine pyrophosphokinase	9.85	10.21	8.77	9.58	1.08	0.63	-0.36	-0.81	0.38	0.34	-0.64	-0.97	0.52	0.7	0.25
Cthe_00509	sodium ion-translocating decarboxylase, beta	14.01	13.84	12.18	12.96	1.83	0.88	0.17	-0.78	1.14	0.71	0.03	-0.92	0.52	0.7	0.82
Cthe_01022	Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	10.7	11.35	10.11	10.63	0.59	0.72	-0.65	-0.52	-0.12	0.47	-1	-0.53	0.52	0.7	0.24
Cthe_02887	phosphoribosylformimino-5-aminoimidazole	8.89	9.46	7.76	8.65	1.13	0.81	-0.57	-0.89	0.43	0.6	-0.9	-1.09	0.52	0.7	0.29
Cthe_01022	Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	10.7	11.35	10.11	10.63	0.59	0.72	-0.65	-0.52	-0.12	0.47	-1	-0.53	0.52	0.7	0.24
Cthe_03113	Nucleotidyl transferase	9.12	8.75	8.64	7.6	0.48	1.15	0.37	1.04	-0.23	1.1	0.27	1.83	0.52	0.7	0.34
Cthe_01284	glycogen/starch synthases, ADP-glucose type	11.06	10.43	9.52	9.58	1.54	0.85	0.63	-0.06	0.85	0.66	0.6	0.17	0.52	0.7	0.97
Cthe_01284	glycogen/starch synthases, ADP-glucose type	11.06	10.43	9.52	9.58	1.54	0.85	0.63	-0.06	0.85	0.66	0.6	0.17	0.52	0.7	0.97
Cthe_01259	CDP-alcohol phosphatidyltransferase	10.76	10.39	9.07	9.65	1.69	0.74	0.37	-0.58	1	0.5	0.27	-0.62	0.52	0.7	0.93
Cthe_01259	CDP-alcohol phosphatidyltransferase	10.76	10.39	9.07	9.65	1.69	0.74	0.37	-0.58	1	0.5	0.27	-0.62	0.52	0.7	0.93
Cthe_01259	CDP-alcohol phosphatidyltransferase	10.76	10.39	9.07	9.65	1.69	0.74	0.37	-0.58	1	0.5	0.27	-0.62	0.52	0.7	0.93
Cthe_00509	sodium ion-translocating decarboxylase, beta	14.01	13.84	12.18	12.96	1.83	0.88	0.17	-0.78	1.14	0.71	0.03	-0.92	0.52	0.7	0.82
Cthe_00509	sodium ion-translocating decarboxylase, beta	14.01	13.84	12.18	12.96	1.83	0.88	0.17	-0.78	1.14	0.71	0.03	-0.92	0.52	0.7	0.82
Cthe_00509	sodium ion-translocating decarboxylase, beta	14.01	13.84	12.18	12.96	1.83	0.88	0.17	-0.78	1.14	0.71	0.03	-0.92	0.52	0.7	0.82
Cthe_03113	Nucleotidyl transferase	9.12	8.75	8.64	7.6	0.48	1.15	0.37	1.04	-0.23	1.1	0.27	1.83	0.52	0.7	0.34
Cthe_03113	Nucleotidyl transferase	9.12	8.75	8.64	7.6	0.48	1.15	0.37	1.04	-0.23	1.1	0.27	1.83	0.52	0.7	0.34
Cthe_03113	Nucleotidyl transferase	9.12	8.75	8.64	7.6	0.48	1.15	0.37	1.04	-0.23	1.1	0.27	1.83	0.52	0.7	0.34
Cthe_00577	thiamine pyrophosphokinase	9.85	10.21	8.77	9.58	1.08	0.63	-0.36	-0.81	0.38	0.34	-0.64	-0.97	0.52	0.7	0.25
Cthe_01022	Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	10.7	11.35	10.11	10.63	0.59	0.72	-0.65	-0.52	-0.12	0.47	-1	-0.53	0.52	0.7	0.24
Cthe_00022	8-amino-7-oxononanoate synthase	4.58	5.39	3.81	3.91	0.77	1.48	-0.81	-0.1	0.06	1.59	-1.2	0.11	0.52	0.7	0.74
Cthe_01259	CDP-alcohol phosphatidyltransferase	10.76	10.39	9.07	9.65	1.69	0.74	0.37	-0.58	1	0.5	0.27	-0.62	0.52	0.7	0.93
Cthe_01301	protein of unknown function DUF795	9.77	8.93	7.88	8.19	1.89	0.74	0.84	-0.31	1.2	0.5	0.86	-0.21	0.51	0.68	0.82
Cthe_02557	glycosyl transferase, family 2	6.07	4.46	4.25	4.17	1.82	0.29	1.61	0.08	1.13	-0.16	1.82	0.38	0.51	0.68	0.34
Cthe_00706	transcriptional regulator, RpiR family	12.01	11.48	10.49	10.76	1.52	0.72	0.53	-0.27	0.83	0.47	0.47	-0.15	0.51	0.68	1.09
Cthe_01843	transcriptional regulator, BadM/Rrf2 family	9.92	10.03	8.92	9.12	1	0.91	-0.11	-0.2	0.3	0.75	-0.33	-0.05	0.51	0.68	1.36
Cthe_02681	serine phosphatase	7.17	7.13	7.14	5.88	0.03	1.25	0.04	1.26	-0.69	1.25	-0.14	2.17	0.51	0.68	0.37
Cthe_00615	Phenylacetate-CoA ligase	12.51	13.16	11.99	12.47	0.52	0.69	-0.65	-0.48	-0.19	0.43	-1	-0.47	0.51	0.68	0.24
Cthe_01016	cell wall hydrolase/autolysin	7.93	6.89	6.61	6.21	1.32	0.68	1.04	0.4	0.62	0.41	1.11	0.86	0.51	0.68	0.3
Cthe_02627	purine operon repressor, PurR	11.5	11.52	10.36	10.68	1.14	0.84	-0.02	-0.32	0.44	0.65	-0.21	-0.23	0.51	0.68	1.42
Cthe_02681	serine phosphatase	7.17	7.13	7.14	5.88	0.03	1.25	0.04	1.26	-0.69	1.25	-0.14	2.17	0.51	0.68	0.37
Cthe_02944	periplasmic sensor signal transduction histidine	11.12	9.2	9.07	9.14	2.05	0.06	1.92	-0.07	1.37	-0.5	2.21	0.15	0.51	0.68	0.37
Cthe_00158	ribonuclease, Rne/Rng family	10.55	10.65	9.59	10.31	0.96	0.34	-0.1	-0.72	0.26	-0.09	-0.31	-0.83	0.51	0.68	0.17
Cthe_03161	Pseudouridine synthase, Rsu	9.37	9.43	7.7	8.44	1.67	0.99	-0.06	-0.74	0.98	0.87	-0.26	-0.86	0.51	0.68	0.82
Cthe_00092	septum site-determining protein MinC	9.52	9.91	7.95	9.16	1.57	0.75	-0.39	-1.21	0.88	0.51	-0.68	-1.58	0.51	0.68	0.33
Cthe_00560	FAD-dependent pyridine nucleotide-disulphide	14.48	14.74	13.52	13.71	0.96	1.03	-0.26	-0.19	0.26	0.93	-0.51	-0.03	0.51	0.68	1.06
Cthe_00941	CDP-diacylglycerol-glycerol-3-phosphate	11.2	11.67	10.53	11.05	0.67	0.62	-0.47	-0.52	-0.04	0.32	-0.77	-0.53	0.51	0.68	0.19
Cthe_00941	CDP-diacylglycerol-glycerol-3-phosphate	11.2	11.67	10.53	11.05	0.67	0.62	-0.47	-0.52	-0.04	0.32	-0.77	-0.53	0.51	0.68	0.19
Cthe_00158	ribonuclease, Rne/Rng family	10.55	10.65	9.59	10.31	0.96	0.34	-0.1	-0.72	0.26	-0.09	-0.31	-0.83	0.51	0.68	0.17
Cthe_03161	Pseudouridine synthase, Rsu	9.37	9.43	7.7	8.44	1.67	0.99	-0.06	-0.74	0.98	0.87	-0.26	-0.86	0.51	0.68	0.82
Cthe_00615	Phenylacetate-CoA ligase	12.51	13.16	11.99	12.47	0.52	0.69	-0.65	-0.48	-0.19	0.43	-1	-0.47	0.51	0.68	0.24
Cthe_02681	serine phosphatase	7.17	7.13	7.14	5.88	0.03	1.25	0.04	1.26	-0.69	1.25	-0.14	2.17	0.51	0.68	0.37
Cthe_00560	FAD-dependent pyridine nucleotide-disulphide	14.48	14.74	13.52	13.71	0.96	1.03	-0.26	-0.19	0.26	0.93	-0.51	-0.03	0.51	0.68	1.06
Cthe_00615	Phenylacetate-CoA ligase	12.51	13.16	11.99	12.47	0.52	0.69	-0.65	-0.48	-0.19	0.43	-1	-0.47	0.51	0.68	0.24
Cthe_00615	Phenylacetate-CoA ligase	12.51	13.16	11.99	12.47	0.52	0.69	-0.65	-0.48	-0.19	0.43	-1	-0.47	0.51	0.68	0.24
Cthe_00941	CDP-diacylglycerol-glycerol-3-phosphate	11.2	11.67	10.53	11.05	0.67	0.62	-0.47	-0.52	-0.04	0.32	-0.77	-0.53	0.51	0.68	0.19
Cthe_00941	CDP-diacylglycerol-glycerol-3-phosphate	11.2	11.67	10.53	11.05	0.67	0.62	-0.47	-0.52	-0.04	0.32	-0.77	-0.53	0.51	0.68	0.19
Cthe_00941	CDP-diacylglycerol-glycerol-3-phosphate	11.2	11.67	10.53	11.05	0.67	0.62	-0.47	-0.52	-0.04	0.32	-0.77	-0.53	0.51	0.68	0.19
Cthe_00941	CDP-diacylglycerol-glycerol-3-phosphate	11.2	11.67	10.53	11.05	0.67	0.62	-0.47	-0.52	-0.04	0.32	-0.77	-0.53	0.51	0.68	0.19
Cthe_01054	ATPase associated with various cellular	12.16	12.53	11.28	11.92	0.88	0.61	-0.37	-0.64	0.17	0.31	-0.65	-0.71	0.5	0.67	0.21
Cthe_02365	tRNA modification GTPase TrmE	9.44	9	7.82	8.3	1.62	0.7	0.44	-0.48	0.93	0.44	0.36	-0.47	0.5	0.67	0.98
Cthe_02900	RNA polymerase, sigma 28 subunit	9.5	10.01	8.98	9.43	0.52	0.58	-0.51	-0.45	-0.19	0.26	-0.82	-0.42	0.5	0.67	0.2
Cthe_00026		8.25	8.11	7.07	7.38	1.18	0.73	0.14	-0.31	0.48	0.49	-0.01	-0.21	0.5	0.67	1.83
Cthe_02737	excinuclease ABC, C subunit	10.39	10.66	9	9.57	1.39	1.09	-0.27	-0.57	0.69	1.01	-0.53	-0.61	0.5	0.67	0.85
Cthe_00026		8.25	8.11	7.07	7.38	1.18	0.73	0.14	-0.31	0.48	0.49	-0.01	-0.21	0.5	0.67	1.83
Cthe_02708	hypothetical protein	10.61	12.1	9.97	10.7	0.64	1.4	-1.49	-0.73	-0.07	1.47	-2.05	-0.85	0.5	0.67	0.37
Cthe_01023	protein of unknown function DUF205	9.66	10.17	8.58	9.41	1.08	0.76	-0.51	-0.83	0.38	0.53	-0.82	-1	0.5	0.67	0.28
Cthe_01504	Linocin_M18 bacteriocin protein	16.7	16.18	14.95	15.49	1.75	0.69	0.52	-0.54	1.06	0.43	0.46	-0.56	0.5	0.67	0.89
Cthe_02595	translation factor SUA5	10.98	12.2	10.5	11.06	0.48	1.14	-1.22	-0.56	-0.23	1.09	-1.71	-0.59	0.5	0.67	0.35
Cthe_02931	ribosomal protein S4	12.37	13.45	11.6	12.33	0.77	1.12	-1.08	-0.73	0.06	1.06	-1.54	-0.85	0.5	0.67	0.34
Cthe_03185	tRNA-guanine transglycosylases, various	8.71	9.87	7.92	8.68	0.79	1.19	-1.16	-0.76	0.08	1.16	-1.64	-0.89	0.5	0.67	0.35
Cthe_01848	copper-translocating P-type ATPase	10.76	10.74	9.64	9.94	1.12	0.8	0.02	-0.3	0.42	0.59	-0.16	-0.2	0.5	0.67	1.59
Cthe_03025	hypothetical protein	3	2.81	1.58	2.81	1.42	0	0.19	-1.23	0.72	-0.59	0.05	-1.61	0.5	0.67	0.32
Cthe_03162	SAM dependent methyltransferase	9.91	10.7	8.68	9.69	1.23	1.01	-0.79	-1.01	0.53	0.9	-1.18	-1.27	0.5	0.67	0.34
Cthe_02613	S-layer-like domain containing protein	10.9	9.11	8.85	8.73	2.05	0.38	1.79	0.12	1.37	-0.03	2.05	0.44	0.5	0.67	0.37
Cthe_02931	ribosomal protein S4	12.37	13.45	11.6	12.33	0.77	1.12	-1.08	-0.73	0.06	1.06	-1.54	-0.85	0.5	0.67	0.34
Cthe_01023	protein of unknown function DUF205	9.66														



Cthe_01505	S-layer-like domain containing protein	10.02	9.68	8.78	8.97	1.24	0.71	0.34	-0.19	0.54	0.46	0.24	-0.03	0.49	0.66	1.65
Cthe_02085	deoxyuridine 5'-triphosphate nucleotidohydrolase	8.89	9.12	8.02	8.62	0.87	0.5	-0.23	-0.6	0.16	0.15	-0.47	-0.65	0.49	0.66	0.15
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/CobO/Cob	9.61	9.39	7.31	8.45	2.3	0.94	0.22	-1.14	1.62	0.79	0.09	-1.47	0.49	0.66	0.69
Cthe_02085	deoxyuridine 5'-triphosphate nucleotidohydrolase	8.89	9.12	8.02	8.62	0.87	0.5	-0.23	-0.6	0.16	0.15	-0.47	-0.65	0.49	0.66	0.15
Cthe_00816	NAD(+) kinase	12.45	12.22	11.22	11.52	1.23	0.7	0.23	-0.3	0.53	0.44	0.1	-0.2	0.49	0.66	1.73
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/CobO/Cob	9.61	9.39	7.31	8.45	2.3	0.94	0.22	-1.14	1.62	0.79	0.09	-1.47	0.49	0.66	0.69
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/CobO/Cob	9.61	9.39	7.31	8.45	2.3	0.94	0.22	-1.14	1.62	0.79	0.09	-1.47	0.49	0.66	0.69
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/CobO/Cob	9.61	9.39	7.31	8.45	2.3	0.94	0.22	-1.14	1.62	0.79	0.09	-1.47	0.49	0.66	0.69
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/CobO/Cob	9.61	9.39	7.31	8.45	2.3	0.94	0.22	-1.14	1.62	0.79	0.09	-1.47	0.49	0.66	0.69
Cthe_00816	NAD(+) kinase	12.45	12.22	11.22	11.52	1.23	0.7	0.23	-0.3	0.53	0.44	0.1	-0.2	0.49	0.66	1.73
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/CobO/Cob	9.61	9.39	7.31	8.45	2.3	0.94	0.22	-1.14	1.62	0.79	0.09	-1.47	0.49	0.66	0.69
Cthe_02085	deoxyuridine 5'-triphosphate nucleotidohydrolase	8.89	9.12	8.02	8.62	0.87	0.5	-0.23	-0.6	0.16	0.15	-0.47	-0.65	0.49	0.66	0.15
Cthe_02085	deoxyuridine 5'-triphosphate nucleotidohydrolase	8.89	9.12	8.02	8.62	0.87	0.5	-0.23	-0.6	0.16	0.15	-0.47	-0.65	0.49	0.66	0.15
Cthe_00816	NAD(+) kinase	12.45	12.22	11.22	11.52	1.23	0.7	0.23	-0.3	0.53	0.44	0.1	-0.2	0.49	0.66	1.73
Cthe_02356	quinolinate synthetase complex, A subunit	13.97	13.59	12.62	12.9	1.35	0.69	0.38	-0.28	0.65	0.43	0.29	-0.17	0.48	0.65	1.3
Cthe_02075	protein of unknown function DUF28	12.26	11.93	10.9	11.24	1.36	0.69	0.33	-0.34	0.66	0.43	0.23	-0.26	0.48	0.65	1.27
Cthe_00324	valyl-tRNA synthetase	12.46	13.75	11.09	11.87	1.37	1.88	-1.29	-0.78	0.67	2.18	-1.8	-0.92	0.48	0.65	0.63
Cthe_02381	seryl-tRNA synthetase	12.56	12.47	11.36	11.71	1.2	0.76	0.09	-0.35	0.5	0.53	-0.07	-0.27	0.48	0.65	1.47
Cthe_02305	putative undecaprenol kinase	11.56	12.08	10.77	11.37	0.79	0.71	-0.52	-0.6	0.08	0.46	-0.84	-0.65	0.48	0.65	0.25
Cthe_02348	Ig-related protein	19.02	19.46	18.15	18.29	0.87	1.17	-0.44	-0.14	0.16	1.13	-0.74	0.05	0.48	0.65	0.86
Cthe_02611	Fibronectin, type III	7.87	7.71	6.87	6.77	1	0.94	0.16	0.1	0.3	0.79	0.01	0.41	0.48	0.65	1.16
Cthe_01623	phage major tail protein, phi13 family	5	5.09	4.17	4	0.83	1.09	-0.09	0.17	0.12	1.01	-0.3	0.52	0.48	0.65	0.95
Cthe_00324	valyl-tRNA synthetase	12.46	13.75	11.09	11.87	1.37	1.88	-1.29	-0.78	0.67	2.18	-1.8	-0.92	0.48	0.65	0.63
Cthe_02381	seryl-tRNA synthetase	12.56	12.47	11.36	11.71	1.2	0.76	0.09	-0.35	0.5	0.53	-0.07	-0.27	0.48	0.65	1.47
Cthe_00324	valyl-tRNA synthetase	12.46	13.75	11.09	11.87	1.37	1.88	-1.29	-0.78	0.67	2.18	-1.8	-0.92	0.48	0.65	0.63
Cthe_02381	seryl-tRNA synthetase	12.56	12.47	11.36	11.71	1.2	0.76	0.09	-0.35	0.5	0.53	-0.07	-0.27	0.48	0.65	1.47
Cthe_02356	quinolinate synthetase complex, A subunit	13.97	13.59	12.62	12.9	1.35	0.69	0.38	-0.28	0.65	0.43	0.29	-0.17	0.48	0.65	1.3
Cthe_00324	valyl-tRNA synthetase	12.46	13.75	11.09	11.87	1.37	1.88	-1.29	-0.78	0.67	2.18	-1.8	-0.92	0.48	0.65	0.63
Cthe_02381	seryl-tRNA synthetase	12.56	12.47	11.36	11.71	1.2	0.76	0.09	-0.35	0.5	0.53	-0.07	-0.27	0.48	0.65	1.47
Cthe_02356	quinolinate synthetase complex, A subunit	13.97	13.59	12.62	12.9	1.35	0.69	0.38	-0.28	0.65	0.43	0.29	-0.17	0.48	0.65	1.3
Cthe_02305	putative undecaprenol kinase	11.56	12.08	10.77	11.37	0.79	0.71	-0.52	-0.6	0.08	0.46	-0.84	-0.65	0.48	0.65	0.25
Cthe_02381	seryl-tRNA synthetase	12.56	12.47	11.36	11.71	1.2	0.76	0.09	-0.35	0.5	0.53	-0.07	-0.27	0.48	0.65	1.47
Cthe_02381	seryl-tRNA synthetase	12.56	12.47	11.36	11.71	1.2	0.76	0.09	-0.35	0.5	0.53	-0.07	-0.27	0.48	0.65	1.47
Cthe_02356	quinolinate synthetase complex, A subunit	13.97	13.59	12.62	12.9	1.35	0.69	0.38	-0.28	0.65	0.43	0.29	-0.17	0.48	0.65	1.3
Cthe_00324	valyl-tRNA synthetase	12.46	13.75	11.09	11.87	1.37	1.88	-1.29	-0.78	0.67	2.18	-1.8	-0.92	0.48	0.65	0.63
Cthe_02381	seryl-tRNA synthetase	12.56	12.47	11.36	11.71	1.2	0.76	0.09	-0.35	0.5	0.53	-0.07	-0.27	0.48	0.65	1.47
Cthe_00261	HAD-superfamily hydrolase, subfamily IA, variant	9.78	9.03	7.85	8.38	1.93	0.65	0.75	-0.53	1.24	0.37	0.75	-0.55	0.47	0.63	0.78
Cthe_01841	hypothetical protein	9.87	10.94	9.04	9.8	0.83	1.14	-1.07	-0.76	0.12	1.09	-1.52	-0.89	0.47	0.63	0.35
Cthe_02429	protein of unknown function UFP0118	9.4	9.96	8.48	8.71	0.92	1.25	-0.56	-0.23	0.21	1.25	-0.89	-0.09	0.47	0.63	0.8
Cthe_01408	two component transcriptional regulator, winged	7.9	7.88	6.43	7.01	1.47	0.87	0.02	-0.58	0.78	0.69	-0.16	-0.62	0.47	0.63	0.91
Cthe_02211	3-isopropylmalate dehydratase, large subunit	12.31	13.36	11.33	12.19	0.98	1.17	-1.05	-0.86	0.28	1.13	-1.5	-1.05	0.47	0.63	0.36
Cthe_02963	oligopeptide/dipeptide ABC transporter, ATPase	9.94	9.59	7.56	9.35	2.38	0.24	0.35	-1.79	1.7	-0.24	0.25	-2.45	0.47	0.63	0.39
Cthe_00878	CheW protein	12.3	11.01	10.82	10.79	1.48	0.22	1.29	0.03	0.79	-0.26	1.43	0.3	0.47	0.63	0.32
Cthe_01758	protein of unknown function DUF583	11.88	11.5	10.05	10.76	1.83	0.74	0.38	-0.71	1.14	0.5	0.29	-0.82	0.47	0.63	0.8
Cthe_00878	CheW protein	12.3	11.01	10.82	10.79	1.48	0.22	1.29	0.03	0.79	-0.26	1.43	0.3	0.47	0.63	0.32
Cthe_01408	two component transcriptional regulator, winged	7.9	7.88	6.43	7.01	1.47	0.87	0.02	-0.58	0.78	0.69	-0.16	-0.62	0.47	0.63	0.91
Cthe_00070	asparaginyl-tRNA synthetase	12.47	13.04	11.7	12.29	0.77	0.75	-0.57	-0.59	0.06	0.51	-0.9	-0.64	0.47	0.63	0.26
Cthe_00767	16S rRNA processing protein RimM	9.58	10.2	8.95	9.46	0.63	0.74	-0.62	-0.51	-0.08	0.5	-0.96	-0.52	0.47	0.63	0.26
Cthe_02963	oligopeptide/dipeptide ABC transporter, ATPase	9.94	9.59	7.56	9.35	2.38	0.24	0.35	-1.79	1.7	-0.24	0.25	-2.45	0.47	0.63	0.39
Cthe_00700	biotin/lipoyl attachment protein	11.57	12.41	10.85	11.47	0.72	0.94	-0.84	-0.62	0.01	0.79	-1.24	-0.68	0.47	0.63	0.31
Cthe_00070	asparaginyl-tRNA synthetase	12.47	13.04	11.7	12.29	0.77	0.75	-0.57	-0.59	0.06	0.51	-0.9	-0.64	0.47	0.63	0.26
Cthe_02211	3-isopropylmalate dehydratase, large subunit	12.31	13.36	11.33	12.19	0.98	1.17	-1.05	-0.86	0.28	1.13	-1.5	-1.05	0.47	0.63	0.36
Cthe_02963	oligopeptide/dipeptide ABC transporter, ATPase	9.94	9.59	7.56	9.35	2.38	0.24	0.35	-1.79	1.7	-0.24	0.25	-2.45	0.47	0.63	0.39
Cthe_00070	asparaginyl-tRNA synthetase	12.47	13.04	11.7	12.29	0.77	0.75	-0.57	-0.59	0.06	0.51	-0.9	-0.64	0.47	0.63	0.26
Cthe_02211	3-isopropylmalate dehydratase, large subunit	12.31	13.36	11.33	12.19	0.98	1.17	-1.05	-0.86	0.28	1.13	-1.5	-1.05	0.47	0.63	0.36
Cthe_00700	biotin/lipoyl attachment protein	11.57	12.41	10.85	11.47	0.72	0.94	-0.84	-0.62	0.01	0.79	-1.24	-0.68	0.47	0.63	0.31
Cthe_02211	3-isopropylmalate dehydratase, large subunit	12.31	13.36	11.33	12.19	0.98	1.17	-1.05	-0.86	0.28	1.13	-1.5	-1.05	0.47	0.63	0.36
Cthe_00261	HAD-superfamily hydrolase, subfamily IA, variant	9.78	9.03	7.85	8.38	1.93	0.65	0.75	-0.53	1.24	0.37	0.75	-0.55	0.47	0.63	0.78
Cthe_00070	asparaginyl-tRNA synthetase	12.47	13.04	11.7	12.29	0.77	0.75	-0.57	-0.59	0.06	0.51	-0.9	-0.64	0.47	0.63	0.26
Cthe_00261	HAD-superfamily hydrolase, subfamily IA, variant	9.78	9.03	7.85	8.38	1.93	0.65	0.75	-0.53	1.24	0.37	0.75	-0.55	0.47	0.63	0.78
Cthe_02211	3-isopropylmalate dehydratase, large subunit	12.31	13.36	11.33	12.19	0.98	1.17	-1.05	-0.86	0.28	1.13	-1.5	-1.05	0.47	0.63	0.36
Cthe_00700	biotin/lipoyl attachment protein	11.57	12.41	10.85	11.47	0.72	0.94	-0.84	-0.62	0.01	0.79	-1.24	-0.68	0.47	0.63	0.31
Cthe_00070	asparaginyl-tRNA synthetase	12.47	13.04	11.7	12.29	0.77	0.75	-0.57	-0.59	0.06	0.51	-0.9	-0.64	0.47	0.63	0.26
Cthe_02211	3-isopropylmalate dehydratase, large subunit	12.31	13.36	11.33	12.19	0.98	1.17	-1.05	-0.86	0.28	1.13	-1.5	-1.05	0.47	0.63	0.36
Cthe_00606	DNA internalization-related competence protein	10.51	11.23	10.06	10.49	0.45	0.74	-0.72	-0.43	-0.27	0.5	-1.09	-0.39	0.46	0.62	0.28
Cthe_00751	transcriptional regulator, XRE family with cupin	10.05	8.78	7.83	7.86	2.22	0.92	1.27	-0.03	1.54	0.76	1.4	0.21	0.46	0.62	0.68
Cthe_00376	transcriptional repressor, CopY family	6.36	6.11	4.7	6	1.66	0.11	0.25	-1.3	0.97	-0.43	0.12	-1.71	0.46	0.62	0.35
Cthe_01600	two component transcriptional regulator, winged	10.41	10.21	9.16	9.51	1.25	0.7	0.2	-0.35	0.55	0.44	0.06	-0.27	0.46	0.62	1.43
Cthe_02355	L-aspartate oxidase	11.34	11.86	10.45	11.11	0.89	0.75	-0.52	-0.66	0.18	0.51	-0.84	-0.74	0.46	0.62	0.27
Cthe_01498	methyl-accepting chemotaxis sensory transducer	5.98	4.64	4.39	4.32	1.59	0.32	1.34	0.07	0.9	-0.12	1.49	0.36	0.46	0.62	0.33
Cthe_01498	methyl-accepting chemotaxis sensory transducer	5.98	4.64	4.39	4.32	1.59	0.32	1.34	0.07	0.9	-0.12	1.49	0.36	0.46	0.62	0.33
Cthe_01600	two component transcriptional regulator, winged	10.41	10.21	9.16	9.51	1.25	0.7	0.2	-0.35	0.55	0.44	0.06	-0.27	0.46	0.62	1.43
Cthe_00328	peptide chain release factor 3	12.24	13.16	11.28	11.63	0.96	1.53	-0.92	-0.35	0.26	1.66	-1.34	-0.27	0.46	0.62	0.69
Cthe_00769	ribosomal protein S16	8.31	8.97	7.71	8.21	0.6	0.76	-0.66	-0.5							



Cthe_01207	membrane protein-like protein	13.46	13.89	12.38	13.17	1.08	0.72	-0.43	-0.79	0.38	0.47	-0.72	-0.94	0.45	0.61	0.29
Cthe_00621	putative translation initiation factor, aIF-2B1	11.92	12.73	11.03	11.76	0.89	0.97	-0.81	-0.73	0.18	0.84	-1.2	-0.85	0.45	0.61	0.33
Cthe_03160	putative RNA methylase, NOL1/NOP2/sun family	10.2	11.25	8.28	9.47	1.92	1.78	-1.05	-1.19	1.23	2.03	-1.5	-1.55	0.45	0.61	0.62
Cthe_02946	2C-methyl-D-erythritol 2,4-cyclodiphosphate	11.08	10.04	8.55	9.48	2.53	0.56	1.04	-0.93	1.86	0.24	1.11	-1.15	0.45	0.61	0.66
Cthe_00220	transposase, IS4	13.44	12.79	12.5	12.38	0.94	0.41	0.65	0.12	0.23	0.01	0.62	0.44	0.45	0.61	0.17
Cthe_01197	intein	7.89	6.75	6.48	6.38	1.41	0.37	1.14	0.1	0.71	-0.04	1.24	0.41	0.45	0.61	0.31
Cthe_00859	hypothetical protein	12.67	12.63	11.19	11.78	1.48	0.85	0.04	-0.59	0.79	0.66	-0.14	-0.64	0.45	0.61	0.88
Cthe_00621	putative translation initiation factor, aIF-2B1	11.92	12.73	11.03	11.76	0.89	0.97	-0.81	-0.73	0.18	0.84	-1.2	-0.85	0.45	0.61	0.33
Cthe_02946	2C-methyl-D-erythritol 2,4-cyclodiphosphate	11.08	10.04	8.55	9.48	2.53	0.56	1.04	-0.93	1.86	0.24	1.11	-1.15	0.45	0.61	0.66
Cthe_02946	2C-methyl-D-erythritol 2,4-cyclodiphosphate	11.08	10.04	8.55	9.48	2.53	0.56	1.04	-0.93	1.86	0.24	1.11	-1.15	0.45	0.61	0.66
Cthe_01183	ATPase associated with various cellular	11.43	11.58	10.23	10.65	1.2	0.93	-0.15	-0.42	0.5	0.78	-0.37	-0.38	0.45	0.61	0.98
Cthe_00212	Beta-glucosidase	12.03	12.46	11.05	11.76	0.98	0.7	-0.43	-0.71	0.28	0.44	-0.72	-0.82	0.45	0.61	0.27
Cthe_00621	putative translation initiation factor, aIF-2B1	11.92	12.73	11.03	11.76	0.89	0.97	-0.81	-0.73	0.18	0.84	-1.2	-0.85	0.45	0.61	0.33
Cthe_00212	Beta-glucosidase	12.03	12.46	11.05	11.76	0.98	0.7	-0.43	-0.71	0.28	0.44	-0.72	-0.82	0.45	0.61	0.27
Cthe_02946	2C-methyl-D-erythritol 2,4-cyclodiphosphate	11.08	10.04	8.55	9.48	2.53	0.56	1.04	-0.93	1.86	0.24	1.11	-1.15	0.45	0.61	0.66
Cthe_00212	Beta-glucosidase	12.03	12.46	11.05	11.76	0.98	0.7	-0.43	-0.71	0.28	0.44	-0.72	-0.82	0.45	0.61	0.27
Cthe_01183	ATPase associated with various cellular	11.43	11.58	10.23	10.65	1.2	0.93	-0.15	-0.42	0.5	0.78	-0.37	-0.38	0.45	0.61	0.98
Cthe_00212	Beta-glucosidase	12.03	12.46	11.05	11.76	0.98	0.7	-0.43	-0.71	0.28	0.44	-0.72	-0.82	0.45	0.61	0.27
Cthe_01183	ATPase associated with various cellular	11.43	11.58	10.23	10.65	1.2	0.93	-0.15	-0.42	0.5	0.78	-0.37	-0.38	0.45	0.61	0.98
Cthe_01183	ATPase associated with various cellular	11.43	11.58	10.23	10.65	1.2	0.93	-0.15	-0.42	0.5	0.78	-0.37	-0.38	0.45	0.61	0.98
Cthe_01183	ATPase associated with various cellular	11.43	11.58	10.23	10.65	1.2	0.93	-0.15	-0.42	0.5	0.78	-0.37	-0.38	0.45	0.61	0.98
Cthe_00621	putative translation initiation factor, aIF-2B1	11.92	12.73	11.03	11.76	0.89	0.97	-0.81	-0.73	0.18	0.84	-1.2	-0.85	0.45	0.61	0.33
Cthe_00542	protein of unknown function DUF45	8.07	8.47	6.55	7.69	1.52	0.78	-0.4	-1.14	0.83	0.56	-0.69	-1.47	0.44	0.59	0.35
Cthe_01109	permease	6.67	5.95	5.64	5.29	1.03	0.66	0.72	0.35	0.33	0.38	0.71	0.79	0.44	0.59	0.27
Cthe_02445	Alcohol dehydrogenase GroES-like protein	5.36	5.67	4.7	4.46	0.66	1.21	-0.31	0.24	-0.05	1.19	-0.57	0.62	0.44	0.59	0.79
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_02441	transcriptional regulator, DeoR family	11.45	10.44	10.17	10.06	1.28	0.38	1.01	0.11	0.58	-0.03	1.07	0.42	0.44	0.59	0.28
Cthe_02441	transcriptional regulator, DeoR family	11.45	10.44	10.17	10.06	1.28	0.38	1.01	0.11	0.58	-0.03	1.07	0.42	0.44	0.59	0.28
Cthe_02445	Alcohol dehydrogenase GroES-like protein	5.36	5.67	4.7	4.46	0.66	1.21	-0.31	0.24	-0.05	1.19	-0.57	0.62	0.44	0.59	0.79
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_02554	glycosyl transferase, group 1	6.94	6.13	5.25	5.29	1.69	0.84	0.81	-0.04	1	0.65	0.82	0.2	0.44	0.59	0.79
Cthe_01345	adenine phosphoribosyltransferase	10.78	11.34	9.79	10.53	0.99	0.81	-0.56	-0.74	0.29	0.6	-0.89	-0.86	0.44	0.59	0.3
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_03191	ATPase involved in chromosome partitioning-like	13.52	13.63	12.72	13.22	0.8	0.41	-0.11	-0.5	0.09	0.01	-0.33	-0.5	0.44	0.59	0.08
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_02463	DNA binding domain, excisionase family	7.35	7.1	5.86	6.38	1.49	0.72	0.25	-0.52	0.8	0.47	0.12	-0.53	0.44	0.59	0.96
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_01345	adenine phosphoribosyltransferase	10.78	11.34	9.79	10.53	0.99	0.81	-0.56	-0.74	0.29	0.6	-0.89	-0.86	0.44	0.59	0.3
Cthe_01345	adenine phosphoribosyltransferase	10.78	11.34	9.79	10.53	0.99	0.81	-0.56	-0.74	0.29	0.6	-0.89	-0.86	0.44	0.59	0.3
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_02445	Alcohol dehydrogenase GroES-like protein	5.36	5.67	4.7	4.46	0.66	1.21	-0.31	0.24	-0.05	1.19	-0.57	0.62	0.44	0.59	0.79
Cthe_01345	adenine phosphoribosyltransferase	10.78	11.34	9.79	10.53	0.99	0.81	-0.56	-0.74	0.29	0.6	-0.89	-0.86	0.44	0.59	0.3
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_01345	adenine phosphoribosyltransferase	10.78	11.34	9.79	10.53	0.99	0.81	-0.56	-0.74	0.29	0.6	-0.89	-0.86	0.44	0.59	0.3
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_01961	Nucleotidyl transferase	12.79	12.52	11.47	11.84	1.32	0.68	0.27	-0.37	0.62	0.41	0.15	-0.3	0.44	0.59	1.25
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01345	adenine phosphoribosyltransferase	10.78	11.34	9.79	10.53	0.99	0.81	-0.56	-0.74	0.29	0.6	-0.89	-0.86	0.44	0.59	0.3
Cthe_00864	pyruvate ferredoxin/flavodoxin oxidoreductase	12.5	13.16	11.73	12.33	0.77	0.83	-0.66	-0.6	0.06	0.63	-1.01	-0.65	0.44	0.59	0.3
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.27	12.91	11.47	12.09	0.8	0.82	-0.64	-0.62	0.09	0.62	-0.99	-0.68	0.44	0.59	0.29
Cthe_01855	Methyltransferase type 11	8.99	8.85	7.54	8.08	1.45	0.77	0.14	-0.54	0.76	0.54	-0.01	-0.56	0.43	0.58	0.94
Cthe_01554	methylated-DNA--protein-cysteine	10.4	9.95	9.1	9.21	1.3	0.74	0.45	-0.11	0.6	0.5	0.38	0.09	0.43	0.58	1.12
Cthe_02144	DNA polymerase III, subunits gamma and tau	9.68	10.66	8.99	9.61	0.69	1.05	-0.98	-0.62	-0.02	0.96	-1.41	-0.68	0.43	0.58	0.34



Cthe_00492	CheC, inhibitor of MCP methylation	9.51	9.09	7.75	9.14	1.76	-0.05	0.42	-1.39	1.07	-0.66	0.34	-1.85	0.42	0.57	0.38
Cthe_01269	hypothetical protein	11.99	11.92	10.53	11.11	1.46	0.81	0.07	-0.58	0.77	0.6	-0.1	-0.62	0.42	0.57	0.87
Cthe_00088	cell shape determining protein, MreB/Mri family	10.47	10.04	9.14	9.37	1.33	0.67	0.43	-0.23	0.63	0.4	0.35	-0.09	0.42	0.57	1.16
Cthe_00930	Radical SAM	9.52	10.08	8.66	9.29	0.86	0.79	-0.56	-0.63	0.15	0.57	-0.89	-0.7	0.42	0.57	0.29
Cthe_02789	NLPA lipoprotein	4	2.81	2.58	2.58	1.42	0.23	1.19	0	0.72	-0.25	1.3	0.26	0.42	0.57	0.32
Cthe_00293	hypothetical protein	8.79	8.23	7.97	7.89	0.82	0.34	0.56	0.08	0.11	-0.09	0.51	0.38	0.42	0.57	0.13
Cthe_02789	NLPA lipoprotein	4	2.81	2.58	2.58	1.42	0.23	1.19	0	0.72	-0.25	1.3	0.26	0.42	0.57	0.32
Cthe_01580	inner-membrane translocator	5.17	5.78	4.75	4.32	0.42	1.46	-0.61	0.43	-0.3	1.56	-0.95	0.91	0.42	0.57	0.68
Cthe_01821	inner-membrane translocator	4	3.32	3	2.81	1	0.51	0.68	0.19	0.3	0.16	0.66	0.55	0.42	0.57	0.22
Cthe_00350	signal peptidase I	11.51	11.74	10.29	11.14	1.22	0.6	-0.23	-0.85	0.52	0.29	-0.47	-1.03	0.41	0.56	0.3
Cthe_00483	type III secretion system inner membrane R	12.49	11.04	9.96	10.4	2.53	0.64	1.45	-0.44	1.86	0.35	1.62	-0.41	0.41	0.56	0.64
Cthe_02036	amidohydrolase 2	9.11	8.1	7.77	7.24	1.34	0.86	1.01	0.53	0.64	0.68	1.07	1.06	0.41	0.56	0.35
Cthe_00609	peptidase M42	6.64	7.75	6.52	6.81	0.12	0.94	-1.11	-0.29	-0.6	0.79	-1.57	-0.18	0.41	0.56	0.35
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.55	11.19	10.13	10.54	1.42	0.65	0.36	-0.41	0.72	0.37	0.26	-0.36	0.41	0.56	1.02
Cthe_00749	binding-protein-dependent transport systems	9.77	10.02	8.69	9.05	1.08	0.97	-0.25	-0.36	0.38	0.84	-0.5	-0.29	0.41	0.56	0.9
Cthe_00483	type III secretion system inner membrane R	12.49	11.04	9.96	10.4	2.53	0.64	1.45	-0.44	1.86	0.35	1.62	-0.41	0.41	0.56	0.64
Cthe_02107	thymidylate kinase	10	10.24	8.55	9.59	1.45	0.65	-0.24	-1.04	0.76	0.37	-0.49	-1.32	0.41	0.56	0.34
Cthe_00505	formate acetyltransferase	13.29	13.94	12.61	13.13	0.68	0.81	-0.65	-0.52	-0.03	0.6	-1	-0.53	0.41	0.56	0.3
Cthe_02687	thioesterase superfamily	9.65	9.76	8.55	8.9	1.1	0.86	-0.11	-0.35	0.4	0.68	-0.33	-0.27	0.41	0.56	1.04
Cthe_01980	hypothetical protein	7.38	6.58	5.64	5.88	1.74	0.7	0.8	-0.24	1.05	0.44	0.81	-0.11	0.41	0.56	0.78
Cthe_00749	binding-protein-dependent transport systems	9.77	10.02	8.69	9.05	1.08	0.97	-0.25	-0.36	0.38	0.84	-0.5	-0.29	0.41	0.56	0.9
Cthe_02107	thymidylate kinase	10	10.24	8.55	9.59	1.45	0.65	-0.24	-1.04	0.76	0.37	-0.49	-1.32	0.41	0.56	0.34
Cthe_00505	formate acetyltransferase	13.29	13.94	12.61	13.13	0.68	0.81	-0.65	-0.52	-0.03	0.6	-1	-0.53	0.41	0.56	0.3
Cthe_00350	signal peptidase I	11.51	11.74	10.29	11.14	1.22	0.6	-0.23	-0.85	0.52	0.29	-0.47	-1.03	0.41	0.56	0.3
Cthe_00609	peptidase M42	6.64	7.75	6.52	6.81	0.12	0.94	-1.11	-0.29	-0.6	0.79	-1.57	-0.18	0.41	0.56	0.35
Cthe_02107	thymidylate kinase	10	10.24	8.55	9.59	1.45	0.65	-0.24	-1.04	0.76	0.37	-0.49	-1.32	0.41	0.56	0.34
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.55	11.19	10.13	10.54	1.42	0.65	0.36	-0.41	0.72	0.37	0.26	-0.36	0.41	0.56	1.02
Cthe_00505	formate acetyltransferase	13.29	13.94	12.61	13.13	0.68	0.81	-0.65	-0.52	-0.03	0.6	-1	-0.53	0.41	0.56	0.3
Cthe_00505	formate acetyltransferase	13.29	13.94	12.61	13.13	0.68	0.81	-0.65	-0.52	-0.03	0.6	-1	-0.53	0.41	0.56	0.3
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.55	11.19	10.13	10.54	1.42	0.65	0.36	-0.41	0.72	0.37	0.26	-0.36	0.41	0.56	1.02
Cthe_00609	peptidase M42	6.64	7.75	6.52	6.81	0.12	0.94	-1.11	-0.29	-0.6	0.79	-1.57	-0.18	0.41	0.56	0.35
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.55	11.19	10.13	10.54	1.42	0.65	0.36	-0.41	0.72	0.37	0.26	-0.36	0.41	0.56	1.02
Cthe_02107	thymidylate kinase	10	10.24	8.55	9.59	1.45	0.65	-0.24	-1.04	0.76	0.37	-0.49	-1.32	0.41	0.56	0.34
Cthe_00505	formate acetyltransferase	13.29	13.94	12.61	13.13	0.68	0.81	-0.65	-0.52	-0.03	0.6	-1	-0.53	0.41	0.56	0.3
Cthe_02107	thymidylate kinase	10	10.24	8.55	9.59	1.45	0.65	-0.24	-1.04	0.76	0.37	-0.49	-1.32	0.41	0.56	0.34
Cthe_00505	formate acetyltransferase	13.29	13.94	12.61	13.13	0.68	0.81	-0.65	-0.52	-0.03	0.6	-1	-0.53	0.41	0.56	0.3
Cthe_02107	thymidylate kinase	10	10.24	8.55	9.59	1.45	0.65	-0.24	-1.04	0.76	0.37	-0.49	-1.32	0.41	0.56	0.34
Cthe_00505	formate acetyltransferase	13.29	13.94	12.61	13.13	0.68	0.81	-0.65	-0.52	-0.03	0.6	-1	-0.53	0.41	0.56	0.3
Cthe_00904	protein-export membrane protein SecD	13.03	13.96	12.23	12.9	0.8	1.06	-0.93	-0.67	0.09	0.97	-1.35	-0.76	0.4	0.54	0.35
Cthe_00574	serine/threonine protein kinase	12.06	12.66	11.4	11.89	0.66	0.77	-0.6	-0.49	-0.05	0.54	-0.94	-0.48	0.4	0.54	0.29
Cthe_03064	polysaccharide biosynthesis protein	11.58	11.73	10.04	10.75	1.54	0.98	-0.15	-0.71	0.85	0.85	-0.37	-0.82	0.4	0.54	0.75
Cthe_00574	serine/threonine protein kinase	12.06	12.66	11.4	11.89	0.66	0.77	-0.6	-0.49	-0.05	0.54	-0.94	-0.48	0.4	0.54	0.29
Cthe_02171	type III restriction enzyme, res subunit	10.36	11.08	9.84	10.27	0.52	0.81	-0.72	-0.43	-0.19	0.6	-1.09	-0.39	0.4	0.54	0.31
Cthe_03144	transcriptional regulator, AraC family	8.22	7.08	6.11	6.36	2.11	0.72	1.14	-0.25	1.43	0.47	1.24	-0.12	0.4	0.54	0.68
Cthe_02214	hypothetical protein	11.82	11.04	9.95	10.43	1.87	0.61	0.78	-0.48	1.18	0.31	0.79	-0.47	0.4	0.54	0.75
Cthe_00574	serine/threonine protein kinase	12.06	12.66	11.4	11.89	0.66	0.77	-0.6	-0.49	-0.05	0.54	-0.94	-0.48	0.4	0.54	0.29
Cthe_02171	type III restriction enzyme, res subunit	10.36	11.08	9.84	10.27	0.52	0.81	-0.72	-0.43	-0.19	0.6	-1.09	-0.39	0.4	0.54	0.31
Cthe_02539	UBA/THIF-type NAD/FAD binding fold	4.39	4.09	3.32	3	1.07	1.09	0.3	0.32	0.37	1.01	0.19	0.74	0.4	0.54	0.79
Cthe_03050	Fibronectin, type III	9.9	8.73	8.39	8.14	1.51	0.59	1.17	0.25	0.82	0.28	1.27	0.64	0.4	0.54	0.34
Cthe_00574	serine/threonine protein kinase	12.06	12.66	11.4	11.89	0.66	0.77	-0.6	-0.49	-0.05	0.54	-0.94	-0.48	0.4	0.54	0.29
Cthe_01846	periplasmic sensor signal transduction histidine	7.91	8.76	7.12	7.76	0.79	1	-0.85	-0.64	0.08	0.88	-1.25	-0.71	0.4	0.54	0.35
Cthe_00574	serine/threonine protein kinase	12.06	12.66	11.4	11.89	0.66	0.77	-0.6	-0.49	-0.05	0.54	-0.94	-0.48	0.4	0.54	0.29
Cthe_00461	gid protein	10.88	11.45	10.07	10.66	0.81	0.79	-0.57	-0.59	0.1	0.57	-0.9	-0.64	0.4	0.54	0.29
Cthe_01543	aspartyl-tRNA synthetase	9.69	10.94	9.07	9.68	0.62	1.26	-1.25	-0.61	-0.09	1.26	-1.75	-0.67	0.4	0.54	0.38
Cthe_02925	methionine aminopeptidase, type I	13.57	13.45	12.35	12.74	1.22	0.71	0.12	-0.39	0.52	0.46	-0.04	-0.33	0.4	0.54	1.17
Cthe_01860	cell division ATP-binding protein FtsE	11.34	11.5	10.03	10.94	1.31	0.56	-0.16	-0.91	0.61	0.24	-0.39	-1.12	0.4	0.54	0.31
Cthe_00279	hypothetical protein	7.39	7.52	6.48	6.66	0.91	0.86	-0.13	-0.18	0.2	0.68	-0.35	-0.02	0.4	0.54	1.14
Cthe_01615	hypothetical protein	1	1	1	1	1	1	-1	-1	0.88	-1.44	-1.44	-1.44	0.4	0.54	0.34
Cthe_02193	Carbohydrate binding family 6	10.58	11.45	9.9	10.47	0.68	0.98	-0.87	-0.57	-0.03	0.85	-1.27	-0.61	0.4	0.54	0.34
Cthe_01860	cell division ATP-binding protein FtsE	11.34	11.5	10.03	10.94	1.31	0.56	-0.16	-0.91	0.61	0.24	-0.39	-1.12	0.4	0.54	0.31
Cthe_01543	aspartyl-tRNA synthetase	9.69	10.94	9.07	9.68	0.62	1.26	-1.25	-0.61	-0.09	1.26	-1.75	-0.67	0.4	0.54	0.38
Cthe_01543	aspartyl-tRNA synthetase	9.69	10.94	9.07	9.68	0.62	1.26	-1.25	-0.61	-0.09	1.26	-1.75	-0.67	0.4	0.54	0.38
Cthe_00904	protein-export membrane protein SecD	13.03	13.96	12.23	12.9	0.8	1.06	-0.93	-0.67	0.09	0.97	-1.35	-0.76	0.4	0.54	0.35
Cthe_01543	aspartyl-tRNA synthetase	9.69	10.94	9.07	9.68	0.62	1.26	-1.25	-0.61	-0.09	1.26	-1.75	-0.67	0.4	0.54	0.38
Cthe_00574	serine/threonine protein kinase	12.06	12.66	11.4	11.89	0.66	0.77	-0.6	-0.49	-0.05	0.54	-0.94	-0.48	0.4	0.54	0.29
Cthe_02925	methionine aminopeptidase, type I	13.57	13.45	12.35	12.74	1.22	0.71	0.12	-0.39	0.52	0.46	-0.04	-0.33	0.4	0.54	1.17
Cthe_01543	aspartyl-tRNA synthetase	9.69	10.94	9.07	9.68	0.62	1.26	-1.25	-0.61	-0.09	1.26	-1.75	-0.67	0.4	0.54	0.38
Cthe_02190	N-acetylglucosamine-6-phosphate deacetylase	10.06	9.16	8.9	8.87	1.16	0.29	0.9	0.03	0.46	-0.16	0.94	0.3	0.39	0.53	0.28
Cthe_02443	Transketolase-like protein	6.17	5.55	5.21	4.91	0.96	0.64	0.62	0.3	0.26	0.35	0.59	0.71	0.39	0.53	0.27
Cthe_02462	BRO-like protein	8.23	7.36	7.02	6.82	1.21	0.54	0.87	0.2	0.51	0.21	0.9	0.56	0.39	0.53	0.29
Cthe_00964	amino acid-binding ACT	11.94	13.63	11.19	11.99	0.75	1.64	-1.69	-0.8	0.04	1.82	-2.3	-0.95	0.39	0.53	0.41
Cthe_01014	MutS2 family protein	11.79	12.09	10.28	11.01	1.51	1.08	-0.3	-0.73	0.82	1	-0.56	-0.85	0.39	0.53	0.71
Cthe_02418	ATPase	12.38	12.41	11.2	11.61	1.18	0.8	-0.03	-0.41	0.48	0.59	-0.22	-0.36	0.39	0.53	1.01
Cthe_02672	transposase, mutator type	6.98	5.83	4.7	5.25	2.28	0.58	1.15	-0.55	1.6	0.26	1.25	-0.58	0.39	0.53	0.66
Cthe_00186	UDP-glucose 4-epimerase	11.06	11.01	10.08	10.31	0.98	0.7	0.05	-0.23	0.28	0.44	-0.12	-0.09	0.39	0.53	1.95
Cthe_02589	hypothetical protein	11.12	11.13	10.19	10.37	0.93	0.76	-0.01	-0.1							



Cthe_00964	amino acid-binding ACT	11.94	13.63	11.19	11.99	0.75	1.64	-1.69	-0.8	0.04	1.82	-2.3	-0.95	0.39	0.53	0.41
Cthe_02443	Transketolase-like protein	6.17	5.55	5.21	4.91	0.96	0.64	0.62	0.3	0.26	0.35	0.59	0.71	0.39	0.53	0.27
Cthe_02443	Transketolase-like protein	6.17	5.55	5.21	4.91	0.96	0.64	0.62	0.3	0.26	0.35	0.59	0.71	0.39	0.53	0.27
Cthe_02190	N-acetylglucosamine-6-phosphate deacetylase	10.06	9.16	8.9	8.87	1.16	0.29	0.9	0.03	0.46	-0.16	0.94	0.3	0.39	0.53	0.28
Cthe_02443	Transketolase-like protein	6.17	5.55	5.21	4.91	0.96	0.64	0.62	0.3	0.26	0.35	0.59	0.71	0.39	0.53	0.27
Cthe_02443	Transketolase-like protein	6.17	5.55	5.21	4.91	0.96	0.64	0.62	0.3	0.26	0.35	0.59	0.71	0.39	0.53	0.27
Cthe_00964	amino acid-binding ACT	11.94	13.63	11.19	11.99	0.75	1.64	-1.69	-0.8	0.04	1.82	-2.3	-0.95	0.39	0.53	0.41
Cthe_00186	UDP-glucose 4-epimerase	11.06	11.01	10.08	10.31	0.98	0.7	0.05	-0.23	0.28	0.44	-0.12	-0.09	0.39	0.53	1.95
Cthe_00186	UDP-glucose 4-epimerase	11.06	11.01	10.08	10.31	0.98	0.7	0.05	-0.23	0.28	0.44	-0.12	-0.09	0.39	0.53	1.95
Cthe_00964	amino acid-binding ACT	11.94	13.63	11.19	11.99	0.75	1.64	-1.69	-0.8	0.04	1.82	-2.3	-0.95	0.39	0.53	0.41
Cthe_00964	amino acid-binding ACT	11.94	13.63	11.19	11.99	0.75	1.64	-1.69	-0.8	0.04	1.82	-2.3	-0.95	0.39	0.53	0.41
Cthe_00186	UDP-glucose 4-epimerase	11.06	11.01	10.08	10.31	0.98	0.7	0.05	-0.23	0.28	0.44	-0.12	-0.09	0.39	0.53	1.95
Cthe_00964	amino acid-binding ACT	11.94	13.63	11.19	11.99	0.75	1.64	-1.69	-0.8	0.04	1.82	-2.3	-0.95	0.39	0.53	0.41
Cthe_02443	Transketolase-like protein	6.17	5.55	5.21	4.91	0.96	0.64	0.62	0.3	0.26	0.35	0.59	0.71	0.39	0.53	0.27
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_01579	ABC transporter related protein	6.41	6.87	5.93	5.52	0.48	1.35	-0.46	0.41	-0.23	1.4	-0.76	0.88	0.38	0.52	0.69
Cthe_02664	ABC-1	9.97	9.41	9.08	8.74	0.89	0.67	0.56	0.34	0.18	0.4	0.51	0.77	0.38	0.52	0.27
Cthe_02736	phosphoenolpyruvate-protein phosphotransferase	12.27	12.26	10.88	11.44	1.39	0.82	0.01	-0.56	0.69	0.62	-0.17	-0.59	0.38	0.52	0.85
Cthe_00198	Glutamate synthase (NADPH)	6.92	7.88	5.73	6.69	1.19	1.19	-0.96	-0.96	0.49	1.16	-1.39	-1.2	0.38	0.52	0.39
Cthe_00945	metallophosphoesterase	10.92	10.86	9.55	10.5	1.37	0.36	0.06	-0.95	0.67	-0.06	-0.11	-1.18	0.38	0.52	0.32
Cthe_02186	single-strand binding protein	12.84	13.46	11.07	12.08	1.77	1.38	-0.62	-1.01	1.08	1.44	-0.96	-1.27	0.38	0.52	0.64
Cthe_02322	DNA recombinase	6.15	5	3.32	4.52	2.83	0.48	1.15	-1.2	2.16	0.12	1.25	-1.56	0.38	0.52	0.61
Cthe_00477	flagellar motor switch protein FlIM	12.94	11.35	10.38	10.54	2.56	0.81	1.59	-0.16	1.89	0.6	1.8	0.02	0.38	0.52	0.62
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_02598	uracil phosphoribosyltransferase	12.98	13	11.82	12.21	1.16	0.79	-0.02	-0.39	0.46	0.57	-0.21	-0.33	0.38	0.52	1.05
Cthe_03093	Adenylosuccinate synthase	10.54	11.1	9.77	10.32	0.77	0.78	-0.56	-0.55	0.06	0.56	-0.89	-0.58	0.38	0.52	0.3
Cthe_00367	NADP oxidoreductase, coenzyme F420-dependent	9.71	9.43	8.43	8.79	1.28	0.64	0.28	-0.36	0.58	0.35	0.16	-0.29	0.38	0.52	1.15
Cthe_00160	ribosomal protein L21	12.69	12.73	11.07	11.82	1.62	0.91	-0.04	-0.75	0.93	0.75	-0.24	-0.88	0.38	0.52	0.74
Cthe_00765	ribosomal protein L19	14.15	13.68	12.67	13.07	1.48	0.61	0.47	-0.4	0.79	0.31	0.4	-0.35	0.38	0.52	0.9
Cthe_01026	ribosomal protein L32	12.23	12.27	10.83	11.41	1.4	0.86	-0.04	-0.58	0.7	0.68	-0.24	-0.62	0.38	0.52	0.82
Cthe_00235	Glutaredoxin-like protein, YruB-family	10.04	10.01	8.6	9.19	1.44	0.82	0.03	-0.59	0.74	0.62	-0.15	-0.64	0.38	0.52	0.83
Cthe_01002	hypothetical protein	9.44	9.43	8.38	8.69	1.06	0.74	0.01	-0.31	0.36	0.5	-0.17	-0.21	0.38	0.52	1.28
Cthe_00636	hypothetical protein	10.35	10.06	9.09	9.43	1.26	0.63	0.29	-0.34	0.56	0.34	0.17	-0.26	0.38	0.52	1.18
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_03093	Adenylosuccinate synthase	10.54	11.1	9.77	10.32	0.77	0.78	-0.56	-0.55	0.06	0.56	-0.89	-0.58	0.38	0.52	0.3
Cthe_01579	ABC transporter related protein	6.41	6.87	5.93	5.52	0.48	1.35	-0.46	0.41	-0.23	1.4	-0.76	0.88	0.38	0.52	0.69
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_00160	ribosomal protein L21	12.69	12.73	11.07	11.82	1.62	0.91	-0.04	-0.75	0.93	0.75	-0.24	-0.88	0.38	0.52	0.74
Cthe_00765	ribosomal protein L19	14.15	13.68	12.67	13.07	1.48	0.61	0.47	-0.4	0.79	0.31	0.4	-0.35	0.38	0.52	0.9
Cthe_01026	ribosomal protein L32	12.23	12.27	10.83	11.41	1.4	0.86	-0.04	-0.58	0.7	0.68	-0.24	-0.62	0.38	0.52	0.82
Cthe_02664	ABC-1	9.97	9.41	9.08	8.74	0.89	0.67	0.56	0.34	0.18	0.4	0.51	0.77	0.38	0.52	0.27
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_01579	ABC transporter related protein	6.41	6.87	5.93	5.52	0.48	1.35	-0.46	0.41	-0.23	1.4	-0.76	0.88	0.38	0.52	0.69
Cthe_02598	uracil phosphoribosyltransferase	12.98	13	11.82	12.21	1.16	0.79	-0.02	-0.39	0.46	0.57	-0.21	-0.33	0.38	0.52	1.05
Cthe_00198	Glutamate synthase (NADPH)	6.92	7.88	5.73	6.69	1.19	1.19	-0.96	-0.96	0.49	1.16	-1.39	-1.2	0.38	0.52	0.39
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_00198	Glutamate synthase (NADPH)	6.92	7.88	5.73	6.69	1.19	1.19	-0.96	-0.96	0.49	1.16	-1.39	-1.2	0.38	0.52	0.39
Cthe_03093	Adenylosuccinate synthase	10.54	11.1	9.77	10.32	0.77	0.78	-0.56	-0.55	0.06	0.56	-0.89	-0.58	0.38	0.52	0.3
Cthe_02736	phosphoenolpyruvate-protein phosphotransferase	12.27	12.26	10.88	11.44	1.39	0.82	0.01	-0.56	0.69	0.62	-0.17	-0.59	0.38	0.52	0.85
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_02598	uracil phosphoribosyltransferase	12.98	13	11.82	12.21	1.16	0.79	-0.02	-0.39	0.46	0.57	-0.21	-0.33	0.38	0.52	1.05
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_02598	uracil phosphoribosyltransferase	12.98	13	11.82	12.21	1.16	0.79	-0.02	-0.39	0.46	0.57	-0.21	-0.33	0.38	0.52	1.05
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_00198	Glutamate synthase (NADPH)	6.92	7.88	5.73	6.69	1.19	1.19	-0.96	-0.96	0.49	1.16	-1.39	-1.2	0.38	0.52	0.39
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_03093	Adenylosuccinate synthase	10.54	11.1	9.77	10.32	0.77	0.78	-0.56	-0.55	0.06	0.56	-0.89	-0.58	0.38	0.52	0.3
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_00198	Glutamate synthase (NADPH)	6.92	7.88	5.73	6.69	1.19	1.19	-0.96	-0.96	0.49	1.16	-1.39	-1.2	0.38	0.52	0.39
Cthe_00198	Glutamate synthase (NADPH)	6.92	7.88	5.73	6.69	1.19	1.19	-0.96	-0.96	0.49	1.16	-1.39	-1.2	0.38	0.52	0.39
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_00198	Glutamate synthase (NADPH)	6.92	7.88	5.73	6.69	1.19	1.19	-0.96	-0.96	0.49	1.16	-1.39	-1.2	0.38	0.52	0.39
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.72	0.09	-0.4	0.51	0.47	-0.07	-0.35	0.38	0.52	1.09
Cthe_00716	Nucleoside-diphosphate kinase	11.56	10.16	10.05	10.16	1.51	0	1.4	-0.11	0.82	-0.59	1.56	0.09	0.38	0.52	0.36
Cthe_03093	Adenylosuccinate synthase	10.54	11.1	9.77	10.32	0.77	0.78	-0.56	-0.55	0.06	0.56	-0.89	-0.58	0.38	0.52	0.3
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	10.58	10.49	9.37	9.77	1.21	0.7									



Cthe_02603	ATP synthase F0, C subunit	8.57	8.8	7.78	8.26	0.79	0.54	-0.23	-0.48	0.08	0.21	-0.47	-0.47	0.37	0.51	0.19
Cthe_02603	ATP synthase F0, C subunit	8.57	8.8	7.78	8.26	0.79	0.54	-0.23	-0.48	0.08	0.21	-0.47	-0.47	0.37	0.51	0.19
Cthe_02820	MCP methyltransferase, CheR-type	7.38	6.82	5.29	6.83	2.09	-0.01	0.56	-1.54	1.41	-0.6	0.51	-2.08	0.37	0.51	0.4
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00850		7.95	8.21	7.21	7.66	0.74	0.55	-0.26	-0.45	0.03	0.22	-0.51	-0.42	0.37	0.51	0.19
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_00856	branched-chain amino acid aminotransferase	15.12	14.51	13.5	13.91	1.62	0.6	0.61	-0.41	0.93	0.29	0.57	-0.36	0.37	0.51	0.81
Cthe_02603	ATP synthase F0, C subunit	8.57	8.8	7.78	8.26	0.79	0.54	-0.23	-0.48	0.08	0.21	-0.47	-0.47	0.37	0.51	0.19
Cthe_00909	lipoprotein signal peptidase	10.07	9.56	8.65	8.94	1.42	0.62	0.51	-0.29	0.72	0.32	0.45	-0.18	0.36	0.49	0.91
Cthe_02166	putative PAS/PAC sensor protein	12.92	11.57	10.52	10.97	2.4	0.6	1.35	-0.45	1.72	0.29	1.5	-0.42	0.36	0.49	0.63
Cthe_00726	peptidase M18, aminopeptidase I	12.37	12	11.64	11.59	0.73	0.41	0.37	0.05	0.02	0.01	0.27	0.33	0.36	0.49	0.03
Cthe_00747	extracellular solute-binding protein, family 1	11.38	11.49	10.48	11.02	0.9	0.47	-0.11	-0.54	0.19	0.1	-0.33	-0.56	0.36	0.49	0.19
Cthe_01325	putative oxygen-independent coproporphyrinogen	10.03	10.38	8.79	9.33	1.24	1.05	-0.35	-0.54	0.54	0.96	-0.62	-0.56	0.36	0.49	0.74
Cthe_02983	methyl-accepting chemotaxis sensory transducer	7.36	6.63	6.32	5.55	1.04	1.08	0.73	0.77	0.34	1	0.72	1.42	0.36	0.49	0.37
Cthe_00909	lipoprotein signal peptidase	10.07	9.56	8.65	8.94	1.42	0.62	0.51	-0.29	0.72	0.32	0.45	-0.18	0.36	0.49	0.91
Cthe_02166	putative PAS/PAC sensor protein	12.92	11.57	10.52	10.97	2.4	0.6	1.35	-0.45	1.72	0.29	1.5	-0.42	0.36	0.49	0.63
Cthe_02983	methyl-accepting chemotaxis sensory transducer	7.36	6.63	6.32	5.55	1.04	1.08	0.73	0.77	0.34	1	0.72	1.42	0.36	0.49	0.37
Cthe_00552	transcriptional regulator, XRE family with cupin	11.74	11.8	10.54	10.98	1.2	0.82	-0.06	-0.44	0.5	0.62	-0.26	-0.41	0.36	0.49	0.92
Cthe_01481	membrane protein-like protein	8.63	8.32	6.91	7.63	1.72	0.69	0.31	-0.72	1.03	0.43	0.2	-0.83	0.36	0.49	0.73
Cthe_01514	protein of unknown function DUF125,	11.51	11.15	9.56	10.44	1.95	0.71	0.36	-0.88	1.27	0.46	0.26	-1.08	0.36	0.49	0.68
Cthe_02635	pyridoxamine 5'-phosphate oxidase-related,	9.88	8.26	7.29	7.48	2.59	0.78	1.62	-0.19	1.92	0.56	1.84	-0.03	0.36	0.49	0.61
Cthe_01403	FeoA	2.58	2.32	1.58	1	1	1.32	0.26	0.58	0.3	1.35	0.14	1.14	0.36	0.49	0.68
Cthe_01578	Radical SAM	6.44	6.69	5.91	5.09	0.53	1.6	-0.25	0.82	-0.18	1.76	-0.5	1.5	0.36	0.49	0.63
Cthe_01767	hypothetical protein	11.86	13.24	10.24	11.63	1.62	1.61	-1.38	-1.39	0.93	1.78	-1.91	-1.85	0.36	0.49	0.42
Cthe_02346	O-antigen polymerase	12.18	12.72	10.64	11.78	1.54	0.94	-0.54	-1.14	0.85	0.79	-0.86	-1.47	0.36	0.49	0.38
Cthe_03040	hypothetical protein	7.79	7.95	7.08	6.91	0.71	1.04	-0.16	0.17	0	0.94	-0.39	0.52	0.36	0.49	0.81
Cthe_00883	flagellar protein	8.72	8.35	8	7.91	0.72	0.44	0.37	0.09	0.01	0.06	0.27	0.39	0.36	0.49	0.07
Cthe_01325	putative oxygen-independent coproporphyrinogen	10.03	10.38	8.79	9.33	1.24	1.05	-0.35	-0.54	0.54	0.96	-0.62	-0.56	0.36	0.49	0.74
Cthe_00747	extracellular solute-binding protein, family 1	11.38	11.49	10.48	11.02	0.9	0.47	-0.11	-0.54	0.19	0.1	-0.33	-0.56	0.36	0.49	0.19
Cthe_01325	putative oxygen-independent coproporphyrinogen	10.03	10.38	8.79	9.33	1.24	1.05	-0.35	-0.54	0.54	0.96	-0.62	-0.56	0.36	0.49	0.74
Cthe_01578	Radical SAM	6.44	6.69	5.91	5.09	0.53	1.6	-0.25	0.82	-0.18	1.76	-0.5	1.5	0.36	0.49	0.63
Cthe_00726	peptidase M18, aminopeptidase I	12.37	12	11.64	11.59	0.73	0.41	0.37	0.05	0.02	0.01	0.27	0.33	0.36	0.49	0.03
Cthe_00909	lipoprotein signal peptidase	10.07	9.56	8.65	8.94	1.42	0.62	0.51	-0.29	0.72	0.32	0.45	-0.18	0.36	0.49	0.91
Cthe_01325	putative oxygen-independent coproporphyrinogen	10.03	10.38	8.79	9.33	1.24	1.05	-0.35	-0.54	0.54	0.96	-0.62	-0.56	0.36	0.49	0.74
Cthe_01553	hypothetical protein	11.05	10.47	9.56	9.86	1.49	0.61	0.58	-0.3	0.8	0.31	0.54	-0.2	0.35	0.48	0.84
Cthe_02288	PEBP	10.02	8.29	7.1	7.82	2.92	0.47	1.73	-0.72	2.26	0.1	1.98	-0.83	0.35	0.48	0.59
Cthe_01112	transcriptional regulator, ArsR family	7.77	7.72	6.94	6.75	0.83	0.97	0.05	0.19	0.12	0.84	-0.12	0.55	0.35	0.48	0.85
Cthe_02333	two component transcriptional regulator, winged	10.39	9.97	9.04	9.36	1.35	0.61	0.42	-0.32	0.65	0.31	0.34	-0.23	0.35	0.48	0.99
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_00148	transposase, mutator type	12.82	11.66	11.45	11.53	1.37	0.13	1.16	-0.08	0.67	-0.4	1.26	0.14	0.35	0.48	0.35
Cthe_00304	Integrase, catalytic region	9.19	9.23	8.16	8.46	1.03	0.77	-0.04	-0.3	0.33	0.54	-0.24	-0.2	0.35	0.48	1.14
Cthe_01904	amino acid adenylation domain	5.93	5.25	4.91	4.39	1.02	0.86	0.68	0.52	0.32	0.68	0.66	1.05	0.35	0.48	0.34
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_02333	two component transcriptional regulator, winged	10.39	9.97	9.04	9.36	1.35	0.61	0.42	-0.32	0.65	0.31	0.34	-0.23	0.35	0.48	0.99
Cthe_01772	protein of unknown function DUF218	10.75	10.22	9.32	9.6	1.43	0.62	0.53	-0.28	0.73	0.32	0.47	-0.17	0.35	0.48	0.9
Cthe_02257	ribosomal protein L9	11.06	11.07	10.16	10.71	0.9	0.36	-0.01	-0.55	0.19	-0.06	-0.2	-0.58	0.35	0.48	0.18
Cthe_02593	peptide chain release factor 1	11.99	12.53	11.13	11.73	0.86	0.8	-0.54	-0.6	0.15	0.59	-0.86	-0.65	0.35	0.48	0.32
Cthe_01270	proteinase inhibitor I4, serpin	11	11.25	9.94	10.31	1.06	0.94	-0.25	-0.37	0.36	0.79	-0.5	-0.3	0.35	0.48	0.84
Cthe_01441	hypothetical protein	4.25	4.09	3.17	3.46	1.08	0.63	0.16	-0.29	0.38	0.34	0.01	-0.18	0.35	0.48	1.59
Cthe_02257	ribosomal protein L9	11.06	11.07	10.16	10.71	0.9	0.36	-0.01	-0.55	0.19	-0.06	-0.2	-0.58	0.35	0.48	0.18
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_00949	carbamoyl-phosphate synthase, large subunit	12.75	13.04	10.8	11.89	1.95	1.15	-0.29	-1.09	1.27	1.1	-0.55	-1.39	0.35	0.48	0.63
Cthe_00685	peptidase M50	10.84	10.53	10.23	9.88	0.61	0.65	0.31	0.35	-0.1	0.37	0.2	0.79	0.34	0.47	0.26
Cthe_01182	protein of unknown function DUF58	10.66	10.95	9.5	10.28	1.16	0.67	-0.29	-0.78	0.46	0.4	-0.55	-0.92	0.34	0.47	0.32
Cthe_00117	HPNtr domain containing protein	10.03	9.62	8.85	8.88	1.18	0.74	0.41	-0.03	0.48	0.5	0.33	0.21	0.34	0.47	1
Cthe_01265	phosphoglucosyltransferase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_00815	arginine repressor, ArgR	9.58	10.11	9.05	9.42	0.53	0.69	-0.53	-0.37	-0.18	0.43	-0.85	-0.3	0.34	0.47	0.29
Cthe_03127	peptidase M56, BlaR1	9.02	8.02													



Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_02518	ketol-acid reductoisomerase	14.95	15.37	13.36	14.2	1.59	1.17	-0.42	-0.84	0.9	1.13	-0.71	-1.02	0.34	0.47	0.65
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_02518	ketol-acid reductoisomerase	14.95	15.37	13.36	14.2	1.59	1.17	-0.42	-0.84	0.9	1.13	-0.71	-1.02	0.34	0.47	0.65
Cthe_02518	ketol-acid reductoisomerase	14.95	15.37	13.36	14.2	1.59	1.17	-0.42	-0.84	0.9	1.13	-0.71	-1.02	0.34	0.47	0.65
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01231	Serine-type D-Ala-D-Ala carboxypeptidase	9.75	8.94	8.13	8.13	1.62	0.81	0.81	0	0.93	0.6	0.82	0.26	0.34	0.47	0.72
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_03075	GMP synthase, large subunit	13.71	13.86	12.25	12.93	1.46	0.93	-0.15	-0.68	0.77	0.78	-0.37	-0.77	0.34	0.47	0.72
Cthe_02518	ketol-acid reductoisomerase	14.95	15.37	13.36	14.2	1.59	1.17	-0.42	-0.84	0.9	1.13	-0.71	-1.02	0.34	0.47	0.65
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_03075	GMP synthase, large subunit	13.71	13.86	12.25	12.93	1.46	0.93	-0.15	-0.68	0.77	0.78	-0.37	-0.77	0.34	0.47	0.72
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_01231	Serine-type D-Ala-D-Ala carboxypeptidase	9.75	8.94	8.13	8.13	1.62	0.81	0.81	0	0.93	0.6	0.82	0.26	0.34	0.47	0.72
Cthe_01265	phosphoglucomutase/phosphomannomutase	13.16	13.52	12.34	12.86	0.82	0.66	-0.36	-0.52	0.11	0.38	-0.64	-0.53	0.34	0.47	0.27
Cthe_02263	H+-transporting two-sector ATPase, C subunit	10.88	11.38	9.11	10.11	1.77	1.27	-0.5	-1	1.08	1.28	-0.81	-1.26	0.34	0.47	0.63
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00677	phosphopentomutase	10.23	10.58	9.66	9.46	0.57	1.12	-0.35	0.2	-0.14	1.06	-0.62	0.56	0.33	0.46	0.72
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_00371	transposase, mutator type	3.46	3.17	2.32	2.58	1.14	0.59	0.29	-0.26	0.44	0.28	0.17	-0.14	0.33	0.46	1.33
Cthe_01550	transposase IS116/IS110/IS902	12.29	11.83	10.57	11.23	1.72	0.6	0.46	-0.66	1.03	0.29	0.39	-0.74	0.33	0.46	0.72
Cthe_02325	Recombinase	11.35	11.39	10.3	10.95	1.05	0.44	-0.04	-0.65	0.35	0.06	-0.24	-0.73	0.33	0.46	0.26
Cthe_02361	DNA gyrase, A subunit	11.84	12.24	10.96	11.53	0.88	0.71	-0.4	-0.57	0.17	0.46	-0.69	-0.61	0.33	0.46	0.3
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.29	9.29	8.18	8.55	1.11	0.74	0	-0.37	0.41	0.5	-0.19	-0.3	0.33	0.46	1.02
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_01274	nucleoside recognition	12.04	11.05	10.19	10.3	1.85	0.75	0.99	-0.11	1.16	0.51	1.05	0.09	0.33	0.46	0.68
Cthe_02326	protein of unknown function DUF163	10.4	10.45	8.99	9.6	1.41	0.85	-0.05	-0.61	0.71	0.66	-0.25	-0.67	0.33	0.46	0.76
Cthe_02492	Baseplate J-like protein	8.09	7.36	5.52	6.77	2.57	0.59	0.73	-1.25	1.9	0.28	0.72	-1.64	0.33	0.46	0.6
Cthe_02730	translation elongation factor 1A (EF-1A/EF-Tu)	16.78	16.9	15.44	16.02	1.34	0.88	-0.12	-0.58	0.64	0.71	-0.34	-0.62	0.33	0.46	0.76
Cthe_02531	sulfate ABC transporter, periplasmic	4.95	4.25	4	4	0.95	0.25	0.7	0	0.24	-0.22	0.69	0.26	0.33	0.46	0.25
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00703	hypothetical protein	13.27	11.48	11.27	11.57	2	-0.09	1.79	-0.3	1.32	-0.72	2.05	-0.2	0.33	0.46	0.41
Cthe_01898	hypothetical protein	9.87	9.39	8.21	8.8	1.66	0.59	0.48	-0.59	0.97	0.28	0.41	-0.64	0.33	0.46	0.75
Cthe_02531	sulfate ABC transporter, periplasmic	4.95	4.25	4	4	0.95	0.25	0.7	0	0.24	-0.22	0.69	0.26	0.33	0.46	0.25
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.29	9.29	8.18	8.55	1.11	0.74	0	-0.37	0.41	0.5	-0.19	-0.3	0.33	0.46	1.02
Cthe_02361	DNA gyrase, A subunit	11.84	12.24	10.96	11.53	0.88	0.71	-0.4	-0.57	0.17	0.46	-0.69	-0.61	0.33	0.46	0.3
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.29	9.29	8.18	8.55	1.11	0.74	0	-0.37	0.41	0.5	-0.19	-0.3	0.33	0.46	1.02
Cthe_02730	translation elongation factor 1A (EF-1A/EF-Tu)	16.78	16.9	15.44	16.02	1.34	0.88	-0.12	-0.58	0.64	0.71	-0.34	-0.62	0.33	0.46	0.76
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_00677	phosphopentomutase	10.23	10.58	9.66	9.46	0.57	1.12	-0.35	0.2	-0.14	1.06	-0.62	0.56	0.33	0.46	0.72
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00677	phosphopentomutase	10.23	10.58	9.66	9.46	0.57	1.12	-0.35	0.2	-0.14	1.06	-0.62	0.56	0.33	0.46	0.72
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.29	9.29	8.18	8.55	1.11	0.74	0	-0.37	0.41	0.5	-0.19	-0.3	0.33	0.46	1.02
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.29	9.29	8.18	8.55	1.11	0.74	0	-0.37	0.41	0.5	-0.19	-0.3	0.33	0.46	1.02
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11												



Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.29	9.29	8.18	8.55	1.11	0.74	0	-0.37	0.41	0.5	-0.19	-0.3	0.33	0.46	1.02
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_02938	putative glucokinase, ROK family	11.4	11.75	10.16	10.71	1.24	1.04	-0.35	-0.55	0.54	0.94	-0.62	-0.58	0.33	0.46	0.72
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00852	peptidase A24A-like protein	11.85	12.25	11.01	11.55	0.84	0.7	-0.4	-0.54	0.13	0.44	-0.69	-0.56	0.33	0.46	0.29
Cthe_00677	phosphopentomutase	10.23	10.58	9.66	9.46	0.57	1.12	-0.35	0.2	-0.14	1.06	-0.62	0.56	0.33	0.46	0.72
Cthe_00893	protein of unknown function DUF633	8.91	9.26	7.76	8.24	1.15	1.02	-0.35	-0.48	0.45	0.91	-0.62	-0.47	0.32	0.44	0.73
Cthe_01291	amidohydrolase 2	11.77	11.28	10.11	10.7	1.66	0.58	0.49	-0.59	0.97	0.26	0.42	-0.64	0.32	0.44	0.74
Cthe_01986	phage / plasmid primase, P4 family	4.52	3.17	1.58	2.81	2.94	0.36	1.35	-1.23	2.28	-0.06	1.5	-1.61	0.32	0.44	0.58
Cthe_01305	Cupin 2, conserved barrel	10.24	9.4	9.1	9.12	1.14	0.28	0.84	-0.02	0.44	-0.18	0.86	0.23	0.32	0.44	0.3
Cthe_00822	IstB-like ATP-binding protein	7.86	5.98	4.86	5.49	3	0.49	1.88	-0.63	2.34	0.13	2.16	-0.7	0.32	0.44	0.58
Cthe_03150	cobalamin biosynthesis protein CobD	11.31	11.43	10.5	10.95	0.81	0.48	-0.12	-0.45	0.1	0.12	-0.34	-0.42	0.32	0.44	0.16
Cthe_03172	protein of unknown function DUF214	7.88	7.6	7.29	7.11	0.59	0.49	0.28	0.18	-0.12	0.13	0.16	0.53	0.32	0.44	0.18
Cthe_02023	response regulator receiver and ANTAR domain	8.63	8.88	7.55	7.95	1.08	0.93	-0.25	-0.4	0.38	0.78	-0.5	-0.35	0.32	0.44	0.8
Cthe_00479	response regulator receiver protein	10.37	8.84	7.94	8.01	2.43	0.83	1.53	-0.07	1.76	0.63	1.73	0.15	0.32	0.44	0.6
Cthe_00054	protein of unknown function DUF187	10.29	11.07	9.2	10.02	1.09	1.05	-0.78	-0.82	0.39	0.96	-1.16	-0.98	0.32	0.44	0.38
Cthe_01630	phage portal protein, HK97 family	7.48	5.75	4.81	4.95	2.67	0.8	1.73	-0.14	2	0.59	1.98	0.05	0.32	0.44	0.59
Cthe_00803	pseudouridine synthase, RluA family	12.55	11.08	10	10.57	2.55	0.51	1.47	-0.57	1.88	0.16	1.65	-0.61	0.32	0.44	0.6
Cthe_02267	Sodium-transporting two-sector ATPase	11.42	12.68	9.91	11.17	1.51	1.51	-1.26	-1.26	0.82	1.63	-1.76	-1.65	0.32	0.44	0.42
Cthe_02432	electron transport complex, RnfABCDGE type, G	10.2	10.62	8.69	9.48	1.51	1.14	-0.42	-0.79	0.82	1.09	-0.71	-0.94	0.32	0.44	0.65
Cthe_02801	carbon-monoxide dehydrogenase, catalytic subunit	5.32	5.7	4.75	4.58	0.57	1.12	-0.38	0.17	-0.14	1.06	-0.66	0.52	0.32	0.44	0.71
Cthe_00794	aluminium resistance protein	10.26	9.96	9.2	9.32	1.06	0.64	0.3	-0.12	0.36	0.35	0.19	0.08	0.32	0.44	1.37
Cthe_01447	hypothetical protein	9.94	9.39	8.44	8.82	1.5	0.57	0.55	-0.38	0.81	0.25	0.5	-0.32	0.32	0.44	0.8
Cthe_03180	hypothetical protein	9.32	9.65	7.99	8.61	1.33	1.04	-0.33	-0.62	0.63	0.94	-0.6	-0.68	0.32	0.44	0.7
Cthe_01059	hypothetical protein	13.85	13.51	12.54	12.92	1.31	0.59	0.34	-0.38	0.61	0.28	0.24	-0.32	0.32	0.44	0.94
Cthe_02267	Sodium-transporting two-sector ATPase	11.42	12.68	9.91	11.17	1.51	1.51	-1.26	-1.26	0.82	1.63	-1.76	-1.65	0.32	0.44	0.42
Cthe_03150	cobalamin biosynthesis protein CobD	11.31	11.43	10.5	10.95	0.81	0.48	-0.12	-0.45	0.1	0.12	-0.34	-0.42	0.32	0.44	0.16
Cthe_02267	Sodium-transporting two-sector ATPase	11.42	12.68	9.91	11.17	1.51	1.51	-1.26	-1.26	0.82	1.63	-1.76	-1.65	0.32	0.44	0.42
Cthe_03150	cobalamin biosynthesis protein CobD	11.31	11.43	10.5	10.95	0.81	0.48	-0.12	-0.45	0.1	0.12	-0.34	-0.42	0.32	0.44	0.16
Cthe_00803	pseudouridine synthase, RluA family	12.55	11.08	10	10.57	2.55	0.51	1.47	-0.57	1.88	0.16	1.65	-0.61	0.32	0.44	0.6
Cthe_02801	carbon-monoxide dehydrogenase, catalytic subunit	5.32	5.7	4.75	4.58	0.57	1.12	-0.38	0.17	-0.14	1.06	-0.66	0.52	0.32	0.44	0.71
Cthe_03150	cobalamin biosynthesis protein CobD	11.31	11.43	10.5	10.95	0.81	0.48	-0.12	-0.45	0.1	0.12	-0.34	-0.42	0.32	0.44	0.16
Cthe_03150	cobalamin biosynthesis protein CobD	11.31	11.43	10.5	10.95	0.81	0.48	-0.12	-0.45	0.1	0.12	-0.34	-0.42	0.32	0.44	0.16
Cthe_03150	cobalamin biosynthesis protein CobD	11.31	11.43	10.5	10.95	0.81	0.48	-0.12	-0.45	0.1	0.12	-0.34	-0.42	0.32	0.44	0.16
Cthe_02801	carbon-monoxide dehydrogenase, catalytic subunit	5.32	5.7	4.75	4.58	0.57	1.12	-0.38	0.17	-0.14	1.06	-0.66	0.52	0.32	0.44	0.71
Cthe_02267	Sodium-transporting two-sector ATPase	11.42	12.68	9.91	11.17	1.51	1.51	-1.26	-1.26	0.82	1.63	-1.76	-1.65	0.32	0.44	0.42
Cthe_01576	basic membrane lipoprotein	8.52	8.21	7.93	7.06	0.59	1.15	0.31	0.87	-0.12	1.1	0.2	1.58	0.31	0.43	0.39
Cthe_02102	methyltransferase small	10.57	10.03	8.81	9.47	1.76	0.56	0.54	-0.66	1.07	0.24	0.49	-0.74	0.31	0.43	0.69
Cthe_02252	thioesterase family protein	9.68	9.3	7.92	9.13	1.76	0.17	0.38	-1.21	1.07	-0.34	0.29	-1.58	0.31	0.43	0.39
Cthe_02696	carbohydrate kinase, YjeF related protein	10.63	10.62	9.05	9.79	1.58	0.83	0.01	-0.74	0.89	0.63	-0.17	-0.86	0.31	0.43	0.7
Cthe_00553	transcriptional regulator, LysR family	8.44	8.25	6.95	7.56	1.49	0.69	0.19	-0.61	0.8	0.43	0.05	-0.67	0.31	0.43	0.76
Cthe_01362	NusG antitermination factor	11.57	12.03	11.1	11.42	0.47	0.61	-0.46	-0.32	-0.24	0.31	-0.76	-0.23	0.31	0.43	0.28
Cthe_00963	Dihydrodipicolinate reductase	12.48	14.27	11.71	12.51	0.77	1.76	-1.79	-0.8	0.06	2	-2.42	-0.95	0.31	0.43	0.43
Cthe_03088		14.49	13.19	12.25	12.54	2.24	0.65	1.3	-0.29	1.56	0.37	1.44	-0.18	0.31	0.43	0.62
Cthe_01266	methyl-accepting chemotaxis sensory transducer	7.17	6.27	5.88	5.43	1.29	0.84	0.9	0.45	0.59	0.65	0.94	0.94	0.31	0.43	0.37
Cthe_01757	peptidase M23B	13.64	13.11	11.54	12.5	2.1	0.61	0.53	-0.96	1.42	0.31	0.47	-1.2	0.31	0.43	0.63
Cthe_01960	Peptidoglycan-binding domain 1	13.63	13.17	12.07	12.6	1.56	0.57	0.46	-0.53	0.87	0.25	0.39	-0.55	0.31	0.43	0.75
Cthe_02328	UDP-N-acetylglucosamine	12.27	12.03	11.01	11.42	1.26	0.61	0.24	-0.41	0.56	0.31	0.11	-0.36	0.31	0.43	0.96
Cthe_01266	methyl-accepting chemotaxis sensory transducer	7.17	6.27	5.88	5.43	1.29	0.84	0.9	0.45	0.59	0.65	0.94	0.94	0.31	0.43	0.37
Cthe_02106	protein of unknown function DUF327	9.61	9.58	8.45	9.18	1.16	0.4	0.03	-0.73	0.46	0	-0.15	-0.85	0.31	0.43	0.3
Cthe_02240	protein of unknown function DUF180	9.22	7.92	7.74	7.9	1.48	0.02	1.3	-0.16	0.79	-0.56	1.44	0.02	0.31	0.43	0.38
Cthe_02696	carbohydrate kinase, YjeF related protein	10.63	10.62	9.05	9.79	1.58	0.83	0.01	-0.74	0.89	0.63	-0.17	-0.86	0.31	0.43	0.7
Cthe_02723	ribosomal protein L7/L12	11.92	12.8	10.75	11.36	1.17	1.44	-0.88	-0.61	0.47	1.53	-1.29	-0.67	0.31	0.43	0.62
Cthe_00087	maf protein	10.1	9.29	8.95	8.95	1.15	0.34	0.81	0	0.45	-0.09	0.82	0.26	0.31	0.43	0.3
Cthe_00613	thiamine pyrophosphate enzyme-like TPP-binding	13.25	13.67	12.76	13.08	0.49	0.59	-0.42	-0.32	-0.22	0.28	-0.71	-0.23	0.31	0.43	0.27
Cthe_00016	Ferritin and Dps	14.44	13.71	13.46	13.47	0.98	0.24	0.73	-0.01	0.28	-0.24	0.72	0.24	0.31	0.43	0.27
Cthe_01593	NUDIX hydrolase	10.84	9.93	9.67	9.73	1.17	0.2	0.91	-0.06	0.47	-0.29	0.95	0.17	0.31	0.43	0.32
Cthe_02250	hypothetical protein	4.39	4.09	3.91	2	0.48	2.09	0.3	1.91	-0.23	2.49	0.19	3.15	0.31	0.43	0.45
Cthe_00704	hypothetical protein	13.22	11.44	11.1	11.33	2.12	0.11	1.78	-0.23	1.44	-0.43	2.04	-0.09	0.31	0.43	0.41
Cthe_00851	hypothetical protein	9.56	10.05	8.93	9.34	0.63	0.71	-0.49	-0.41	-0.08	0.46	-0.8	-0.36	0.31	0.43	0.3
Cthe_02357	hypothetical protein	12.8	12.87	11.48	12.04	1.32	0.83	-0.07	-0.56	0.62	0.63	-0.27	-0.59	0.31	0.43	0.77
Cthe_00613	thiamine pyrophosphate enzyme-like TPP-binding	13.25	13.67	12.76	13.08	0.49	0.59	-0.42	-0.32	-0.22	0.28	-0.71	-0.23	0.31	0.43	0.27
Cthe_00963	Dihydrodipicolinate reductase	12.48	14.27	11.71	12.51	0.77	1.76	-1.79	-0.8	0.06	2	-2.42	-0.95	0.31	0.43	0.43
Cthe_02723	ribosomal protein L7/L12	11.92	12.8	10.75	11.36	1.17	1.44	-0.88	-0.61	0.47	1.53	-1.29	-0.67	0.31	0.43	0.62
Cthe_00963	Dihydrodipicolinate reductase	12.48	14.27	11.71	12.51	0.77	1.76	-1.79	-0.8	0.06	2	-2.42	-0.95	0.31	0.43	0.43
Cthe_02328	UDP-N-acetylglucosamine	12.27	12.03	11.01	11.42	1.26	0.61	0.2								







Cthe_01421	signal peptide peptidase SppA, 36K type	12.3	12.36	10.85	11.52	1.45	0.84	-0.06	-0.67	0.76	0.65	-0.26	-0.76	0.29	0.41	0.7
Cthe_02893	response regulator receiver protein	11.86	10.52	10.17	10.32	1.69	0.2	1.34	-0.15	1	-0.29	1.49	0.03	0.29	0.41	0.39
Cthe_00378	hypothetical protein	6.15	6.15	5.29	5.46	0.86	0.69	0	-0.17	0.15	0.43	-0.19	0	0.29	0.41	1.35
Cthe_01998	intein	7.98	6.69	6.27	5.73	1.71	0.96	1.29	0.54	1.02	0.82	1.43	1.08	0.29	0.41	0.41
Cthe_03092	conserved hypothetical protein, CF-27 family	13.57	13.01	12.68	12.69	0.89	0.32	0.56	-0.01	0.18	-0.12	0.51	0.24	0.29	0.41	0.22
Cthe_00452	cellulosome anchoring protein, cohesion region	10.86	10.17	9.8	9.77	1.06	0.4	0.69	0.03	0.36	0	0.67	0.3	0.29	0.41	0.28
Cthe_00018	hypothetical protein	8.39	8.54	7.69	8.05	0.7	0.49	-0.15	-0.36	-0.01	0.13	-0.37	-0.29	0.29	0.41	0.16
Cthe_00230	hypothetical protein	12.22	12.78	11.45	11.96	0.77	0.82	-0.56	-0.51	0.06	0.62	-0.89	-0.52	0.29	0.41	0.34
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00162	ribosomal protein L27	12.67	12.83	11.23	11.91	1.44	0.92	-0.16	-0.68	0.74	0.76	-0.39	-0.77	0.29	0.41	0.69
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_01311	signal transduction histidine kinase regulating	11.1	10.96	9.96	10.71	1.14	0.25	0.14	-0.75	0.44	-0.22	-0.01	-0.88	0.29	0.41	0.31
Cthe_01004	uridylate kinase	9.04	9.34	8.15	8.69	0.89	0.65	-0.3	-0.54	0.18	0.37	-0.56	-0.56	0.29	0.41	0.29
Cthe_00673	ribonuclease H	8.66	8.9	7.75	8.29	0.91	0.61	-0.24	-0.54	0.2	0.31	-0.49	-0.56	0.29	0.41	0.28
Cthe_01421	signal peptide peptidase SppA, 36K type	12.3	12.36	10.85	11.52	1.45	0.84	-0.06	-0.67	0.76	0.65	-0.26	-0.76	0.29	0.41	0.7
Cthe_03190	helicase, RecD/TraA family	11.03	11.67	9.94	10.71	1.09	0.96	-0.64	-0.77	0.39	0.82	-0.99	-0.91	0.29	0.41	0.38
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_01004	uridylate kinase	9.04	9.34	8.15	8.69	0.89	0.65	-0.3	-0.54	0.18	0.37	-0.56	-0.56	0.29	0.41	0.29
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.66	-0.27	0.29	0.41	0.73
Cthe_02449	Phosphoglycerate mutase	7.48	7.22	6.91	6.43	0.57	0.79	0.26	0.48	-0.14	0.57	0.14	0.98	0.29	0.41	0.33
Cthe_00140	phosphoglycerate mutase,	14.53	14.91	13.56	13.91	0.97	1	-0.38	-0.35	0.27	0.88	-0.				



Cthe_00600	thiamine biosynthesis protein ThiF	8.86	9.47	8.29	8.29	0.57	1.18	-0.61	0	-0.14	1.15	-0.95	0.26	0.28	0.39	0.66
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00600	thiamine biosynthesis protein ThiF	8.86	9.47	8.29	8.29	0.57	1.18	-0.61	0	-0.14	1.15	-0.95	0.26	0.28	0.39	0.66
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00600	thiamine biosynthesis protein ThiF	8.86	9.47	8.29	8.29	0.57	1.18	-0.61	0	-0.14	1.15	-0.95	0.26	0.28	0.39	0.66
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00600	thiamine biosynthesis protein ThiF	8.86	9.47	8.29	8.29	0.57	1.18	-0.61	0	-0.14	1.15	-0.95	0.26	0.28	0.39	0.66
Cthe_01943	deoxyribose-phosphate aldolase	10.9	11.14	9.32	10.14	1.58	1	-0.24	-0.82	0.89	0.88	-0.49	-0.98	0.28	0.39	0.64
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00105	riboflavin synthase, alpha subunit	10.33	10.44	9.6	9.59	0.73	0.85	-0.11	0.01	0.02	0.66	-0.33	0.27	0.28	0.39	0.87
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00600	thiamine biosynthesis protein ThiF	8.86	9.47	8.29	8.29	0.57	1.18	-0.61	0	-0.14	1.15	-0.95	0.26	0.28	0.39	0.66
Cthe_01943	deoxyribose-phosphate aldolase	10.9	11.14	9.32	10.14	1.58	1	-0.24	-0.82	0.89	0.88	-0.49	-0.98	0.28	0.39	0.64
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00217	Glucose-6-phosphate isomerase	13.25	13.48	11.93	12.54	1.32	0.94	-0.23	-0.61	0.62	0.79	-0.47	-0.67	0.28	0.39	0.69
Cthe_00105	riboflavin synthase, alpha subunit	10.33	10.44	9.6	9.59	0.73	0.85	-0.11	0.01	0.02	0.66	-0.33	0.27	0.28	0.39	0.87
Cthe_00163	GTP1/OBG subdomain containing protein	12.55	12.64	10.66	11.68	1.89	0.96	-0.09	-1.02	1.2	0.82	-0.3	-1.29	0.27	0.38	0.62
Cthe_01480	hypothetical protein	6.04	5.49	4.17	4.95	1.87	0.54	0.55	-0.78	1.18	0.21	0.5	-0.92	0.27	0.38	0.64
Cthe_01688	Radical SAM	11.15	10.69	9.98	9.85	1.17	0.84	0.46	0.13	0.47	0.65	0.39	0.45	0.27	0.38	0.76
Cthe_02552	Radical SAM	6.75	6.09	5.29	5.46	1.46	0.63	0.66	-0.17	0.77	0.34	0.64	0	0.27	0.38	0.74
Cthe_00269	glycoside hydrolase, family 8	14.91	15.15	14.25	14.6	0.66	0.55	-0.24	-0.35	-0.05	0.22	-0.49	-0.27	0.27	0.38	0.23
Cthe_02446	ABC-type sugar transport system periplasmic	9.5	8.51	7.58	7.97	1.92	0.54	0.99	-0.39	1.23	0.21	1.05	-0.33	0.27	0.38	0.64
Cthe_02597	sugar-phosphate isomerases, RpiB/LacA/LacB	11.84	12.04	10.68	11.16	1.16	0.88	-0.2	-0.48	0.46	0.71	-0.44	-0.47	0.27	0.38	0.74
Cthe_01278	ATP-dependent DNA helicase RecG	8.92	9.19	8.03	8.29	0.89	0.9	-0.27	-0.26	0.18	0.74	-0.53	-0.14	0.27	0.38	0.78
Cthe_01653	SNF2-related protein	6.23	5.04	4	4.58	2.23	0.46	1.19	-0.58	1.55	0.09	1.3	-0.62	0.27	0.38	0.61
Cthe_02066	serine O-acetyltransferase	10.08	10.42	9.11	9.46	0.97	0.96	-0.34	-0.35	0.27	0.82	-0.61	-0.27	0.27	0.38	0.73
Cthe_02964	binding-protein-dependent transport systems	11.47	9.82	8.13	9.6	3.34	0.22	1.65	-1.47	2.68	-0.26	1.88	-1.97	0.27	0.38	0.56
Cthe_00309	exonuclease ABC, B subunit	12	12.63	11.42	11.8	0.58	0.83	-0.63	-0.38	-0.13	0.63	-0.97	-0.32	0.27	0.38	0.35
Cthe_01278	ATP-dependent DNA helicase RecG	8.92	9.19	8.03	8.29	0.89	0.9	-0.27	-0.26	0.18	0.74	-0.53	-0.14	0.27	0.38	0.78
Cthe_01653	SNF2-related protein	6.23	5.04	4	4.58	2.23	0.46	1.19	-0.58	1.55	0.09	1.3	-0.62	0.27	0.38	0.61
Cthe_02410	protein of unknown function DUF342	10.92	10.9	9.77	10.47	1.15	0.43	0.02	-0.7	0.45	0.04	-0.16	-0.8	0.27	0.38	0.31
Cthe_00421	flavoprotein	8.2	8.6	7.65	7.97	0.55	0.63	-0.4	-0.32	-0.16	0.34	-0.69	-0.23	0.27	0.38	0.29
Cthe_00674	NUDIX hydrolase	10.37	10.44	8.97	9.61	1.4	0.83	-0.07	-0.64	0.7	0.63	-0.27	-0.71	0.27	0.38	0.7
Cthe_01287	periplasmic sensor signal transduction histidine	10.88	10.57	9.57	10	1.31	0.57	0.31	-0.43	0.61	0.25	0.2	-0.39	0.27	0.38	0.85
Cthe_01166	protein of unknown function DUF147	12.06	12.17	11.14	11.65	0.92	0.52	-0.11	-0.51	0.21	0.18	-0.33	-0.52	0.27	0.38	0.25
Cthe_01503	hypothetical protein	15.4	14.67	13.68	14.17	1.72	0.5	0.73	-0.49	1.03	0.15	0.72	-0.48	0.27	0.38	0.68
Cthe_02380	TPR repeat domain containing protein	11.02	10.95	10.01	10.31	1.01	0.64	0.07	-0.3	0.31	0.35	-0.1	-0.2	0.27	0.38	1.17
Cthe_00847	translation elongation factor P (EF-P)	13.49	13.56	12.1	12.73	1.39	0.83	-0.07	-0.63	0.69	0.63	-0.27	-0.7	0.27	0.38	0.7
Cthe_01003	ribosome recycling factor	11.08	11.26	9.98	10.41	1.1	0.85	-0.18	-0.43	0.4	0.66	-0.41	-0.39	0.27	0.38	0.77
Cthe_01005	translation elongation factor Ts (EF-Ts)	12.51	13.01	11.28	11.88	1.23	1.13	-0.5	-0.6	0.53	1.07	-0.81	-0.65	0.27	0.38	0.65
Cthe_02726	ribosomal protein L7Ae/L30e/S12e/Gadd45	11.93	11.62	10.23	10.98	1.7	0.64	0.31	-0.75	1.01	0.35	0.2	-0.88	0.27	0.38	0.67
Cthe_01028	acetate kinase	10.65	11.17	8.86	9.91	1.79	1.26	-0.52	-1.05	1.1	1.26	-0.84	-1.33	0.27	0.38	0.6
Cthe_02103	4Fe-4S ferredoxin, iron-sulfur binding	14.98	14.2	13.41	13.5	1.57	0.7	0.78	-0.09	0.88	0.44	0.79	0.12	0.27	0.38	0.69
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_02964	binding-protein-dependent transport systems	11.47	9.82	8.13	9.6	3.34	0.22	1.65	-1.47	2.68	-0.26	1.88	-1.97	0.27	0.38	0.56
Cthe_03129	Citrate transporter	8.5	9.39	7.79	8.32	0.71	1.07	-0.89	-0.53	0	0.99	-1.3	-0.55	0.27	0.38	0.39
Cthe_03184	caption transporter	9.26	10.15	8.16	8.73	1.1	1.42	-0.89	-0.57	0.4	1.5	-1.3	-0.61	0.27	0.38	0.61
Cthe_01775	peptidase M22, glycoprotease	9.94	9.84	8.64	9.15	1.3	0.69	0.1	-0.51	0.6	0.43	-0.06	-0.52	0.27	0.38	0.79
Cthe_02015	hypothetical protein	8.05	6.39	5.52	5.58	2.53	0.81	1.66	-0.06	1.86	0.6	1.89	0.17	0.27	0.38	0.58
Cthe_01416	hypothetical protein	4.86	4.91	3.81	4.17	1.05	0.74	-0.05	-0.36	0.35	0.5	-0.25	-0.29	0.27	0.38	0.9
Cthe_01028	acetate kinase	10.65	11.17	8.86	9.91	1.79	1.26	-0.52	-1.05	1.1	1.26	-0.84	-1.33	0.27	0.38	0.6
Cthe_01028	acetate kinase	10.65	11.17	8.86	9.91	1.79	1.26	-0.52	-1.05	1.1	1.26	-0.84	-1.33	0.27	0.38	0.6
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_02597	sugar-phosphate isomerases, RpiB/LacA/LacB	11.84	12.04	10.68	11.16	1.16	0.88	-0.2	-0.48	0.46	0.71	-0.44	-0.47	0.27	0.38	0.74
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_02597	sugar-phosphate isomerases, RpiB/LacA/LacB	11.84	12.04	10.68	11.16	1.16	0.88	-0.2	-0.48	0.46	0.71	-0.44	-0.47	0.27	0.38	0.74
Cthe_02964	binding-protein-dependent transport systems	11.47	9.82	8.13	9.6	3.34	0.22	1.65	-1.47	2.68	-0.26	1.88	-1.97	0.27	0.38	0.56
Cthe_02066	serine O-acetyltransferase	10.08	10.42	9.11	9.46	0.97	0.96	-0.34	-0.35	0.27	0.82	-0.61	-0.27	0.27	0.38	0.73
Cthe_02446	ABC-type sugar transport system periplasmic	9.5	8.51	7.58	7.97	1.92	0.54	0.99	-0.39	1.23	0.21	1.05	-0.33	0.27	0.38	0.64
Cthe_02597	sugar-phosphate isomerases, RpiB/LacA/LacB	11.84	12.04	10.68	11.16	1.16	0.88	-0.2	-0.48	0.46	0.71	-0.44	-0.47	0.27	0.38	0.74
Cthe_02726	ribosomal protein L7Ae/L30e/S12e/Gadd45	11.93	11.62	10.23	10.98	1.7	0.64	0.31	-0.75	1.01	0.35	0.2	-0.88	0.27	0.38	0.67
Cthe_02597	sugar-phosphate isomerases, RpiB/LacA/LacB	11.84	12.04	10.68	11.16	1.16	0.88	-0.2	-0.48	0.46	0.71	-0.44	-0.47	0.27	0.38	0.74
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32</									



Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_02597	sugar-phosphate isomerases, RpiB/LacA/LacB	11.84	12.04	10.68	11.16	1.16	0.88	-0.2	-0.48	0.46	0.71	-0.44	-0.47	0.27	0.38	0.74
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_01028	acetate kinase	10.65	11.17	8.86	9.91	1.79	1.26	-0.52	-1.05	1.1	1.26	-0.84	-1.33	0.27	0.38	0.6
Cthe_02794	pyruvate/ketoisovalerate oxidoreductase, gamma	2.32	2	1.58	2.32	0.42	0.32	-1.58	1.64	0.03	0.21	-2.14	0.27	0.38	0.43	
Cthe_02597	sugar-phosphate isomerases, RpiB/LacA/LacB	11.84	12.04	10.68	11.16	1.16	0.88	-0.2	-0.48	0.46	0.71	-0.44	-0.47	0.27	0.38	0.74
Cthe_00957	preprotein translocase, YajC subunit	10.46	10.01	9.06	9.47	1.4	0.54	0.45	-0.41	0.7	0.21	0.38	-0.36	0.26	0.37	0.78
Cthe_00792	Protein of unknown function UPF0001	8.54	8.52	7.74	8.17	0.8	0.35	0.02	-0.43	0.09	-0.07	-0.16	-0.39	0.26	0.37	0.15
Cthe_01024	small GTP-binding protein	10.96	11.14	9.56	10.47	1.4	0.67	-0.18	-0.91	0.7	0.4	-0.41	-1.12	0.26	0.37	0.38
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_01589	transcriptional repressor, CopY family	6.94	6.25	5.98	6.02	0.96	0.23	0.69	-0.04	0.26	-0.25	0.67	0.2	0.26	0.37	0.29
Cthe_01655	hypothetical protein	8.77	7.34	6.52	6.48	2.25	0.86	1.43	0.04	1.57	0.68	1.6	0.32	0.26	0.37	0.59
Cthe_02040	ATP-dependent exonuclease synthesis protein Add	9.65	9.81	8.22	8.91	1.43	0.9	-0.16	-0.69	0.73	0.74	-0.39	-0.79	0.26	0.37	0.66
Cthe_02363	methyltransferase GidB	9.73	10.62	8.83	9.5	0.9	1.12	-0.89	-0.67	0.19	1.06	-1.3	-0.76	0.26	0.37	0.4
Cthe_02596	protein tyrosine phosphatase	10.23	10.96	9.52	10.01	0.71	0.95	-0.73	-0.49	0	0.81	-1.1	-0.48	0.26	0.37	0.38
Cthe_02373	RNA-binding S4	8.48	8.53	7.06	7.71	1.42	0.82	-0.05	-0.65	0.72	0.62	-0.25	-0.73	0.26	0.37	0.69
Cthe_01237	leucyl-tRNA synthetase	13.5	14.19	12.64	13.23	0.86	0.96	-0.69	-0.59	0.15	0.82	-1.05	-0.64	0.26	0.37	0.38
Cthe_02769	protein of unknown function DUF542, ScdA-like	7.55	7.34	6.32	6.74	1.23	0.6	0.21	-0.42	0.53	0.29	0.07	-0.38	0.26	0.37	0.88
Cthe_01094	Radical SAM-like protein	11.62	12.01	10.71	11.02	0.91	0.99	-0.39	-0.31	0.2	0.87	-0.68	-0.21	0.26	0.37	0.7
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_01873	HMG-I and HMG-Y, DNA-binding	11.07	10.36	10	10.04	1.07	0.32	0.71	-0.04	0.37	-0.12	0.7	0.2	0.26	0.37	0.3
Cthe_01545	hypothetical protein	6.77	7.31	5.95	6.21	0.82	1.1	-0.54	-0.26	0.11	1.03	-0.86	-0.14	0.26	0.37	0.67
Cthe_00195	RNA polymerase, sigma-24 subunit, ECF subfamily	9.07	7.59	6.77	6.71	2.3	0.88	1.48	0.06	1.62	0.71	1.66	0.35	0.26	0.37	0.59
Cthe_01954	hypothetical protein	9.78	10.26	8.94	9.2	0.84	1.06	-0.48	-0.26	0.13	0.97	-0.79	-0.14	0.26	0.37	0.69
Cthe_02277	hypothetical protein	10.45	9.93	8.76	9.4	1.69	0.53	0.52	-0.64	1	0.19	0.46	-0.71	0.26	0.37	0.68
Cthe_02999	hypothetical protein	10.2	9.18	8.18	8.71	2.02	0.47	1.02	-0.53	1.34	0.1	1.09	-0.55	0.26	0.37	0.62
Cthe_01237	leucyl-tRNA synthetase	13.5	14.19	12.64	13.23	0.86	0.96	-0.69	-0.59	0.15	0.82	-1.05	-0.64	0.26	0.37	0.38
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_01237	leucyl-tRNA synthetase	13.5	14.19	12.64	13.23	0.86	0.96	-0.69	-0.59	0.15	0.82	-1.05	-0.64	0.26	0.37	0.38
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_00957	preprotein translocase, YajC subunit	10.46	10.01	9.06	9.47	1.4	0.54	0.45	-0.41	0.7	0.21	0.38	-0.36	0.26	0.37	0.78
Cthe_01237	leucyl-tRNA synthetase	13.5	14.19	12.64	13.23	0.86	0.96	-0.69	-0.59	0.15	0.82	-1.05	-0.64	0.26	0.37	0.38
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02363	methyltransferase GidB	9.73	10.62	8.83	9.5	0.9	1.12	-0.89	-0.67	0.19	1.06	-1.3	-0.76	0.26	0.37	0.4
Cthe_02596	protein tyrosine phosphatase	10.23	10.96	9.52	10.01	0.71	0.95	-0.73	-0.49	0	0.81	-1.1	-0.48	0.26	0.37	0.38
Cthe_02040	ATP-dependent exonuclease synthesis protein Add	9.65	9.81	8.22	8.91	1.43	0.9	-0.16	-0.69	0.73	0.74	-0.39	-0.79	0.26	0.37	0.66
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_00576	Ribulose-phosphate 3-epimerase	10.19	10.55	8.77	9.73	1.42	0.82	-0.36	-0.96	0.72	0.62	-0.64	-1.2	0.26	0.37	0.39
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9
Cthe_02579	iron-containing alcohol dehydrogenase	10.67	10.79	9.91	9.99	0.76	0.8	-0.12	-0.08	0.05	0.59	-0.34	0.14	0.26	0.37	0.9



Cthe_00866	pyruvate flavodoxin/ferredoxin	11.76	12.34	11.01	11.49	0.75	0.85	-0.58	-0.48	0.04	0.66	-0.91	-0.47	0.25	0.35	0.36
Cthe_01276	panetheine-phosphate adenyllyltransferase	10.76	10.41	9.56	9.87	1.2	0.54	0.35	-0.31	0.5	0.21	0.25	-0.21	0.25	0.35	0.93
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.76	12.34	11.01	11.49	0.75	0.85	-0.58	-0.48	0.04	0.66	-0.91	-0.47	0.25	0.35	0.36
Cthe_00601	thiamine-phosphate pyrophosphorylase	9.16	9.87	8.76	8.62	0.4	1.25	-0.71	0.14	-0.32	1.25	-1.07	0.47	0.25	0.35	0.62
Cthe_00854	shikimate 5-dehydrogenase	11.1	11.15	10.03	10.65	1.07	0.5	-0.05	-0.62	0.37	0.15	-0.25	-0.68	0.25	0.35	0.31
Cthe_01276	panetheine-phosphate adenyllyltransferase	10.76	10.41	9.56	9.87	1.2	0.54	0.35	-0.31	0.5	0.21	0.25	-0.21	0.25	0.35	0.93
Cthe_01774	ribosomal-protein-alanine acetyltransferase	8.41	8.21	7.29	8.06	1.12	0.15	0.2	-0.77	0.42	-0.37	0.06	-0.91	0.25	0.35	0.34
Cthe_01599	multi-sensor signal transduction histidine	11.18	11.37	9.76	10.45	1.42	0.92	-0.19	-0.69	0.72	0.76	-0.42	-0.79	0.25	0.35	0.66
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_00854	shikimate 5-dehydrogenase	11.1	11.15	10.03	10.65	1.07	0.5	-0.05	-0.62	0.37	0.15	-0.25	-0.68	0.25	0.35	0.31
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_01276	panetheine-phosphate adenyllyltransferase	10.76	10.41	9.56	9.87	1.2	0.54	0.35	-0.31	0.5	0.21	0.25	-0.21	0.25	0.35	0.93
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_00854	shikimate 5-dehydrogenase	11.1	11.15	10.03	10.65	1.07	0.5	-0.05	-0.62	0.37	0.15	-0.25	-0.68	0.25	0.35	0.31
Cthe_00601	thiamine-phosphate pyrophosphorylase	9.16	9.87	8.76	8.62	0.4	1.25	-0.71	0.14	-0.32	1.25	-1.07	0.47	0.25	0.35	0.62
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.76	12.34	11.01	11.49	0.75	0.85	-0.58	-0.48	0.04	0.66	-0.91	-0.47	0.25	0.35	0.36
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_00601	thiamine-phosphate pyrophosphorylase	9.16	9.87	8.76	8.62	0.4	1.25	-0.71	0.14	-0.32	1.25	-1.07	0.47	0.25	0.35	0.62
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.76	12.34	11.01	11.49	0.75	0.85	-0.58	-0.48	0.04	0.66	-0.91	-0.47	0.25	0.35	0.36
Cthe_01389	metal dependent phosphohydrolase	11.48	12.12	10.13	11.09	1.35	1.03	-0.64	-0.96	0.65	0.93	-0.99	-1.2	0.25	0.35	0.41
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.76	12.34	11.01	11.49	0.75	0.85	-0.58	-0.48	0.04	0.66	-0.91	-0.47	0.25	0.35	0.36
Cthe_00399	protein of unknown function DUF477	10.96	11.35	10.34	10.68	0.62	0.67	-0.39	-0.34	-0.09	0.4	-0.68	-0.26	0.24	0.34	0.32
Cthe_00763	GTP-binding protein	11.78	11.5	10.09	10.86	1.69	0.64	0.28	-0.77	1	0.35	0.16	-0.91	0.24	0.34	0.64
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_00099	5,10-methylenetetrahydrofolate reductase	11.3	10.48	10.17	10.27	1.13	0.21	0.82	-0.1	0.43	-0.28	0.84	0.11	0.24	0.34	0.34
Cthe_00541	peptidase M24	9.01	8.98	7.64	8.24	1.37	0.74	0.03	-0.6	0.67	0.5	-0.15	-0.65	0.24	0.34	0.7
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransferase	14.44	14.81	13.23	13.8	1.21	1.01	-0.37	-0.57	0.51	0.9	-0.65	-0.61	0.24	0.34	0.65
Cthe_00112	UDP-N-acetylenolpyruvoylglucosamine reductase	9.4	9.56	8.82	8.49	0.58	1.07	-0.16	0.33	-0.13	0.99	-0.39	0.76	0.24	0.34	0.66
Cthe_02414	Monogalactosyldiaclylglycerol synthase	8.58	8.86	8.1	7.7	0.48	1.16	-0.28	0.4	-0.23	1.12	-0.54	0.86	0.24	0.34	0.63
Cthe_00443	protein of unknown function DUF1290	10.32	9.99	9.29	9.31	1.03	0.68	0.33	-0.02	0.33	0.41	0.23	0.23	0.24	0.34	0.91
Cthe_02802	NLPA lipoprotein	5.91	4.95	4.09	4.39	1.82	0.56	0.96	-0.3	1.13	0.24	1.01	-0.2	0.24	0.34	0.63
Cthe_02804	ABC transporter related protein	5.73	5.95	5.13	5.43	0.6	0.52	-0.22	-0.3	-0.11	0.18	-0.46	-0.2	0.24	0.34	0.24
Cthe_02891	chaperonin Cpn10	9.22	8.96	8.28	7.98	0.94	0.98	0.26	0.3	0.23	0.85	0.14	0.71	0.24	0.34	0.68
Cthe_01779	hypothetical protein	9.54	8.26	7.83	7.88	1.71	0.38	1.28	-0.05	1.02	-0.03	1.41	0.18	0.24	0.34	0.4
Cthe_02241	hypothetical protein	9.86	8.98	8.03	8.5	1.83	0.48	0.88	-0.47	1.14	0.12	0.91	-0.45	0.24	0.34	0.63
Cthe_02030	intein	10.36	9.2	8.78	8.84	1.58	0.36	1.16	-0.06	0.89	-0.06	1.26	0.17	0.24	0.34	0.39
Cthe_02994	hypothetical protein	11.63	11.2	10.23	10.68	1.4	0.52	0.43	-0.45	0.7	0.18	0.35	-0.42	0.24	0.34	0.74
Cthe_00194	hypothetical protein	10.15	8.5	7.55	7.95	2.6	0.55	1.65	-0.4	1.93	0.22	1.88	-0.35	0.24	0.34	0.57
Cthe_00099	5,10-methylenetetrahydrofolate reductase	11.3	10.48	10.17	10.27	1.13	0.21	0.82	-0.1	0.43	-0.28	0.84	0.11	0.24	0.34	0.34
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransferase	14.44	14.81	13.23	13.8	1.21	1.01	-0.37	-0.57	0.51	0.9	-0.65	-0.61	0.24	0.34	0.65
Cthe_02802	NLPA lipoprotein	5.91	4.95	4.09	4.39	1.82	0.56	0.96	-0.3	1.13	0.24	1.01	-0.2	0.24	0.34	0.63
Cthe_02804	ABC transporter related protein	5.73	5.95	5.13	5.43	0.6	0.52	-0.22	-0.3	-0.11	0.18	-0.46	-0.2	0.24	0.34	0.24
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_02414	Monogalactosyldiaclylglycerol synthase	8.58	8.86	8.1	7.7	0.48	1.16	-0.28	0.4	-0.23	1.12	-0.54	0.86	0.24	0.34	0.63
Cthe_00541	peptidase M24	9.01	8.98	7.64	8.24	1.37	0.74	0.03	-0.6	0.67	0.5	-0.15	-0.65	0.24	0.34	0.7
Cthe_00112	UDP-N-acetylenolpyruvoylglucosamine reductase	9.4	9.56	8.82	8.49	0.58	1.07	-0.16	0.33	-0.13	0.99	-0.39	0.76	0.24	0.34	0.66
Cthe_00099	5,10-methylenetetrahydrofolate reductase	11.3	10.48	10.17	10.27	1.13	0.21	0.82	-0.1	0.43	-0.28	0.84	0.11	0.24	0.34	0.34
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransferase	14.44	14.81	13.23	13.8	1.21	1.01	-0.37	-0.57	0.51	0.9	-0.65	-0.61	0.24	0.34	0.65
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransferase	14.44	14.81	13.23	13.8	1.21	1.01	-0.37	-0.57	0.51	0.9	-0.65	-0.61	0.24	0.34	0.65
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_00112	UDP-N-acetylenolpyruvoylglucosamine reductase	9.4	9.56	8.82	8.49	0.58	1.07	-0.16	0.33	-0.13	0.99	-0.39	0.76	0.24	0.34	0.66
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransferase	14.44	14.81	13.23	13.8	1.21	1.01	-0.37	-0.57	0.51	0.9	-0.65	-0.61	0.24	0.34	0.65
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_00099	5,10-methylenetetrahydrofolate reductase	11.3	10.48	10.17	10.27	1.13	0.21	0.82	-0.1	0.43	-0.28	0.84	0.11	0.24	0.34	0.34
Cthe_02414	Monogalactosyldiaclylglycerol synthase	8.58	8.86	8.1	7.7	0.48	1.16	-0.28	0.4	-0.23	1.12	-0.54	0.86	0.24	0.34	0.63
Cthe_00112	UDP-N-acetylenolpyruvoylglucosamine reductase	9.4	9.56	8.82	8.49	0.58	1.07	-0.16	0.33	-0.13	0.99	-0.39	0.76	0.24	0.34	0.66
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_00112	UDP-N-acetylenolpyruvoylglucosamine reductase	9.4	9.56	8.82	8.49	0.58	1.07	-0.16	0.33	-0.13	0.99	-0.39	0.76	0.24	0.34	0.66
Cthe_00099	5,10-methylenetetrahydrofolate reductase	11.3	10.48	10.17	10.27	1.13	0.21	0.82	-0.1	0.43	-0.28	0.84	0.11	0.24	0.34	0.34
Cthe_02359	metal dependent phosphohydrolase	10.9	10.54	9.29	9.96	1.61	0.58	0.36	-0.67	0.92	0.26	0.26	-0.76	0.24	0.34	0.67
Cthe_00099	5,10-methylenetetrahydrofolate reductase	11.3	10.48	10.17	10.27	1.13	0.21	0.82	-0.1	0.43	-0.28	0.84	0.11	0.24	0.34	0.34
Cthe_00459	DNA protecting protein DprA	10.82	11.09	9.7	10.18	1.12	0.91	-0.27	-0.48	0.42	0.75	-0.53</				



Cthe_03151	Adenosylcobinamide-phosphate guanylyltransferas	8.43	7.9	6.87	7.41	1.56	0.49	0.53	-0.54	0.87	0.13	0.47	-0.56	0.23	0.33	0.68
Cthe_01592	Glycerate kinase	11.01	10.58	9.71	10.06	1.3	0.52	0.43	-0.35	0.6	0.18	0.35	-0.27	0.23	0.33	0.8
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_02253	ATP-dependent metalloprotease FtsH	13.97	14.16	12.95	13.54	1.02	0.62	-0.19	-0.59	0.32	0.32	-0.42	-0.64	0.23	0.33	0.33
Cthe_01592	Glycerate kinase	11.01	10.58	9.71	10.06	1.3	0.52	0.43	-0.35	0.6	0.18	0.35	-0.27	0.23	0.33	0.8
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_03151	Adenosylcobinamide-phosphate guanylyltransferas	8.43	7.9	6.87	7.41	1.56	0.49	0.53	-0.54	0.87	0.13	0.47	-0.56	0.23	0.33	0.68
Cthe_03151	Adenosylcobinamide-phosphate guanylyltransferas	8.43	7.9	6.87	7.41	1.56	0.49	0.53	-0.54	0.87	0.13	0.47	-0.56	0.23	0.33	0.68
Cthe_03151	Adenosylcobinamide-phosphate guanylyltransferas	8.43	7.9	6.87	7.41	1.56	0.49	0.53	-0.54	0.87	0.13	0.47	-0.56	0.23	0.33	0.68
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01029	phosphate acetyltransferase	10.18	10.6	8.5	9.46	1.68	1.14	-0.42	-0.96	0.99	1.09	-0.71	-1.2	0.23	0.33	0.59
Cthe_01592	Glycerate kinase	11.01	10.58	9.71	10.06	1.3	0.52	0.43	-0.35	0.6	0.18	0.35	-0.27	0.23	0.33	0.8
Cthe_02752	beta-lactamase-like protein	9.77	7.89	7.06	7	2.71	0.89	1.88	0.06	2.04	0.72	2.16	0.35	0.22	0.32	0.56
Cthe_00095	methylglyoxal synthase	11.81	11.5	10.4	10.94	1.41	0.56	0.31	-0.54	0.71	0.24	0.2	-0.56	0.22	0.32	0.71
Cthe_00661	Ricin B lectin	11.24	11.38	10.37	10.62	0.87	0.76	-0.14	-0.25	0.16	0.53	-0.36	-0.12	0.22	0.32	0.82
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_02179	Pectate lyase/Amb allergen	7.03	7.23	5.88	6.57	1.15	0.66	-0.2	-0.69	0.45	0.38	-0.44	-0.79	0.22	0.32	0.37
Cthe_02203	GTP cyclohydrolase I	11.99	11.53	10.6	11.02	1.39	0.51	0.46	-0.42	0.69	0.16	0.39	-0.38	0.22	0.32	0.73
Cthe_01085	glycosyl transferase, group 1	5.67	5.7	5.43	4.75	0.24	0.95	-0.03	0.68	-0.48	0.81	-0.22	1.29	0.22	0.32	0.4
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_02701	glycosyl transferase, WecB/TagA/Cpsf family	9.95	10.53	8.17	9.25	1.78	1.28	-0.58	-1.08	1.09	1.29	-0.91	-1.38	0.22	0.32	0.57
Cthe_02599	CMP/dCMP deaminase, zinc-binding	12.03	12.41	10.75	11.39	1.28	1.02	-0.38	-0.64	0.58	0.91	-0.66	-0.71	0.22	0.32	0.63
Cthe_02258	phosphoesterase, RecJ-like protein	11.55	11.67	10.67	11.13	0.88	0.54	-0.12	-0.46	0.17	0.21	-0.34	-0.44	0.22	0.32	0.27
Cthe_02722	ribosomal protein L10	12.38	13.5	11.51	12.19	0.87	1.31	-1.12	-0.68	0.16	1.34	-1.59	-0.77	0.22	0.32	0.43
Cthe_01601	phosphate uptake regulator, PhoU	11	10.55	9.75	10.02	1.25	0.53	0.45	-0.27	0.55	0.19	0.38	-0.15	0.22	0.32	0.8
Cthe_02276	AAA ATPase, central region	14.32	13.96	12.75	13.4	1.57	0.56	0.36	-0.65	0.88	0.24	0.26	-0.73	0.22	0.32	0.66
Cthe_02712	hypothetical protein	10.52	10.54	9.61	9.87	0.91	0.67	-0.02	-0.26	0.2	0.4	-0.21	-0.14	0.22	0.32	1
Cthe_02555	methyltransferase FkbM family	6.23	5.88	5.46	5.25	0.77	0.63	0.35	0.21	0.06	0.34	0.25	0.58	0.22	0.32	0.31
Cthe_03053	hypothetical protein	9.86	8.89	8.46	8.52	1.4	0.37	0.97	-0.06	0.7	-0.04	1.02	0.17	0.22	0.32	0.38
Cthe_01871	Tn7-like transposition protein D	9.4	8.65	8.21	8.17	1.19	0.48	0.75	0.04	0.49	0.12	0.75	0.32	0.22	0.32	0.35
Cthe_00497	RNA related	4.64	3.7	2.58	4.17	2.06	-0.47	0.94	-1.59	1.38	-1.28	0.99	-2.15	0.22	0.32	0.45
Cthe_01878	hypothetical protein	8.61	8.13	7.69	7.62	0.92	0.51	0.48	0.07	0.21	0.16	0.41	0.36	0.22	0.32	0.27
Cthe_02722	ribosomal protein L10	12.38	13.5	11.51	12.19	0.87	1.31	-1.12	-0.68	0.16	1.34	-1.59	-0.77	0.22	0.32	0.43
Cthe_02261	hypothetical protein	11.73	11.36	10.39	10.84	1.34	0.52	0.37	-0.45	0.64	0.18	0.27	-0.42	0.22	0.32	0.75
Cthe_02203	GTP cyclohydrolase I	11.99	11.53	10.6	11.02	1.39	0.51	0.46	-0.42	0.69	0.16	0.39	-0.38	0.22	0.32	0.73
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_02722	ribosomal protein L10	12.38	13.5	11.51	12.19	0.87	1.31	-1.12	-0.68	0.16	1.34	-1.59	-0.77	0.22	0.32	0.43
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_02261	hypothetical protein	11.73	11.36	10.39	10.84	1.34	0.52	0.37	-0.45	0.64	0.18	0.27	-0.42	0.22	0.32	0.75
Cthe_00095	methylglyoxal synthase	11.81	11.5	10.4	10.94	1.41	0.56	0.31	-0.54	0.71	0.24	0.2	-0.56	0.22	0.32	0.71
Cthe_02701	glycosyl transferase, WecB/TagA/Cpsf family	9.95	10.53	8.17	9.25	1.78	1.28	-0.58	-1.08	1.09	1.29	-0.91	-1.38	0.22	0.32	0.57
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_02599	CMP/dCMP deaminase, zinc-binding	12.03	12.41	10.75	11.39	1.28	1.02	-0.38	-0.64	0.58	0.91	-0.66	-0.71	0.22	0.32	0.63
Cthe_02203	GTP cyclohydrolase I	11.99	11.53	10.6	11.02	1.39	0.51	0.46	-0.42	0.69	0.16	0.39	-0.38	0.22	0.32	0.73
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_02203	GTP cyclohydrolase I	11.99	11.53	10.6	11.02	1.39	0.51	0.46	-0.42	0.69	0.16	0.39	-0.38	0.22	0.32	0.73
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_02701	glycosyl transferase, WecB/TagA/Cpsf family	9.95	10.53	8.17	9.25	1.78	1.28	-0.58	-1.08	1.09	1.29	-0.91	-1.38	0.22	0.32	0.57
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_01261	6-phosphofructokinase	11.44	12	10.44	11.09	1	0.91	-0.56	-0.65	0.3	0.75	-0.89	-0.73	0.22	0.32	0.39
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_02203	GTP cyclohydrolase I	11.99	11.53	10.6	11.02	1.39	0.51	0.46	-0.42	0.69	0.16	0.39	-0.38	0.22	0.32	0.73
Cthe_02261	hypothetical protein	11.73	11.36	10.39	10.84	1.34	0.52	0.37	-0.45	0.64	0.18	0.27	-0.42	0.22	0.32	0.75
Cthe_02600	glycosyl transferase, family 4	12.59	13.23	11.34	12.01	1.25	1.22	-0.64	-0.67	0.55	1.21	-0.99	-0.76	0.22	0.32	0.6
Cthe_01188	protein of unknown function DUF990	9.31	10.73	8.38	9.17	0.93	1.56	-1.42	-0.79	0.22	1.71	-1.96	-0.94	0.21	0.3	0.45
Cthe_02747	PHP-like protein	9.91	9.93	9.07	9.27	0.84	0.66	-0.02	-0.2	0.13	0.38	-0.21	-0.05	0.21	0.3	1.05
Cthe_03075	von Willebrand factor, type A	9.49	9.91	8.59	9.13	0.9	0.78	-0.42	-0.54	0.19	0.56	-0.71	-0.56	0.21	0.3	0.37
Cthe_02197	Carbohydrate binding family 6	5.32	4.17	3.7	3.58	1.62	0.59	1.15	0.12	0.93	0.28	1.25	0.44	0.21	0.3	0.41
Cthe_02548	Alpha-N-arabinofuranosidase	10.83	10.98	9.62	10.16	1.21	0.82	-0.15	-0.54	0.51	0.62	-0.37	-0.56	0.21	0.3	0.67
Cthe_00688	putative transcriptional regulator	10.89	11.31	9.51	10.43	1.38	0.88	-0.42	-0.92	0.68	0.71	-0.71	-1.14	0.21	0.3	0.41
Cthe_02634	transcriptional regulator, AraC family	11.26	9.77	9.37	9.72	1.89	0.05	1.49	-0.35	1.2	-0.51	1.68	-0.27	0.21	0.3	0.43
Cthe_01513	DNA adenine methylase	9.32	9.52	8.63	8.96	0.69	0.56	-0.2	-0.33	-0.02	0.24	-0.44	-0.24	0.21	0.3	



Cthe_02548	Alpha-N-arabinofuranosidase	10.83	10.98	9.62	10.16	1.21	0.82	-0.15	-0.54	0.51	0.62	-0.37	-0.56	0.21	0.3	0.67
Cthe_01218	Leucyltransferase	9.46	10.11	8.53	8.94	0.93	1.17	-0.65	-0.41	0.22	1.13	-1	-0.36	0.21	0.3	0.61
Cthe_02197	Carbohydrate binding family 6	5.32	4.17	3.7	3.58	1.62	0.59	1.15	0.12	0.93	0.28	1.25	0.44	0.21	0.3	0.41
Cthe_02332	multi-sensor signal transduction histidine	10.75	10.75	9.38	10	1.37	0.75	0	-0.62	0.67	0.51	-0.19	-0.68	0.21	0.3	0.67
Cthe_02537	sulfate adenylyltransferase, large subunit	4	3.91	3.58	3	0.42	0.91	0.09	0.58	-0.3	0.75	-0.07	1.14	0.21	0.3	0.4
Cthe_02537	sulfate adenylyltransferase, large subunit	4	3.91	3.58	3	0.42	0.91	0.09	0.58	-0.3	0.75	-0.07	1.14	0.21	0.3	0.4
Cthe_02197	Carbohydrate binding family 6	5.32	4.17	3.7	3.58	1.62	0.59	1.15	0.12	0.93	0.28	1.25	0.44	0.21	0.3	0.41
Cthe_02537	sulfate adenylyltransferase, large subunit	4	3.91	3.58	3	0.42	0.91	0.09	0.58	-0.3	0.75	-0.07	1.14	0.21	0.3	0.4
Cthe_02537	sulfate adenylyltransferase, large subunit	4	3.91	3.58	3	0.42	0.91	0.09	0.58	-0.3	0.75	-0.07	1.14	0.21	0.3	0.4
Cthe_02537	sulfate adenylyltransferase, large subunit	4	3.91	3.58	3	0.42	0.91	0.09	0.58	-0.3	0.75	-0.07	1.14	0.21	0.3	0.4
Cthe_02197	Carbohydrate binding family 6	5.32	4.17	3.7	3.58	1.62	0.59	1.15	0.12	0.93	0.28	1.25	0.44	0.21	0.3	0.41
Cthe_02537	sulfate adenylyltransferase, large subunit	4	3.91	3.58	3	0.42	0.91	0.09	0.58	-0.3	0.75	-0.07	1.14	0.21	0.3	0.4
Cthe_02537	sulfate adenylyltransferase, large subunit	4	3.91	3.58	3	0.42	0.91	0.09	0.58	-0.3	0.75	-0.07	1.14	0.21	0.3	0.4
Cthe_02366	single-stranded nucleic acid binding R3H	11.11	11.35	10.38	10.74	0.73	0.61	-0.24	-0.36	0.02	0.31	-0.49	-0.29	0.2	0.29	0.31
Cthe_01394	two component transcriptional regulator, winged	8.02	8.22	7.34	7.66	0.68	0.56	-0.2	-0.32	-0.03	0.24	-0.44	-0.23	0.2	0.29	0.27
Cthe_02198	transposase	6.19	5	4.52	4.39	1.67	0.61	1.19	0.13	0.98	0.31	1.3	0.45	0.2	0.29	0.42
Cthe_02371	chromosomal replication initiator protein DnaA	12.59	12	11.29	11.34	1.3	0.66	0.59	-0.05	0.6	0.38	0.55	0.18	0.2	0.29	0.69
Cthe_00622	methylthioadenosine phosphorylase	11.77	12.41	10.34	11.34	1.43	1.07	-0.64	-1	0.73	0.99	-0.99	-1.26	0.2	0.29	0.43
Cthe_01394	two component transcriptional regulator, winged	8.02	8.22	7.34	7.66	0.68	0.56	-0.2	-0.32	-0.03	0.24	-0.44	-0.23	0.2	0.29	0.27
Cthe_01172	protein of unknown function DUF362	12.6	12.52	10.8	11.74	1.8	0.78	0.08	-0.94	1.11	0.56	-0.09	-1.17	0.2	0.29	0.6
Cthe_00417	ribosomal protein S15	14.08	13.76	12.82	13.24	1.26	0.52	0.32	-0.42	0.56	0.18	0.21	-0.38	0.2	0.29	0.76
Cthe_02264	H+-transporting two-sector ATPase, E subunit	11.42	12.05	9.88	10.97	1.54	1.08	-0.63	-1.09	0.85	1	-0.97	-1.39	0.2	0.29	0.44
Cthe_02408	phage shock protein A, PspA	13.61	13.17	12.48	12.52	1.13	0.65	0.44	-0.04	0.43	0.37	0.36	0.2	0.2	0.29	0.77
Cthe_00470	hypothetical protein	8.12	7.63	6.38	7.49	1.74	0.14	0.49	-1.11	1.05	-0.38	0.42	-1.42	0.2	0.29	0.42
Cthe_00366	hypothetical protein	12.27	10.9	10.04	10.34	2.23	0.56	1.37	-0.3	1.55	0.24	1.53	-0.2	0.2	0.29	0.57
Cthe_00417	ribosomal protein S15	14.08	13.76	12.82	13.24	1.26	0.52	0.32	-0.42	0.56	0.18	0.21	-0.38	0.2	0.29	0.76
Cthe_02264	H+-transporting two-sector ATPase, E subunit	11.42	12.05	9.88	10.97	1.54	1.08	-0.63	-1.09	0.85	1	-0.97	-1.39	0.2	0.29	0.44
Cthe_00622	methylthioadenosine phosphorylase	11.77	12.41	10.34	11.34	1.43	1.07	-0.64	-1	0.73	0.99	-0.99	-1.26	0.2	0.29	0.43
Cthe_00417	ribosomal protein S15	14.08	13.76	12.82	13.24	1.26	0.52	0.32	-0.42	0.56	0.18	0.21	-0.38	0.2	0.29	0.76
Cthe_02264	H+-transporting two-sector ATPase, E subunit	11.42	12.05	9.88	10.97	1.54	1.08	-0.63	-1.09	0.85	1	-0.97	-1.39	0.2	0.29	0.44
Cthe_00622	methylthioadenosine phosphorylase	11.77	12.41	10.34	11.34	1.43	1.07	-0.64	-1	0.73	0.99	-0.99	-1.26	0.2	0.29	0.43
Cthe_02264	H+-transporting two-sector ATPase, E subunit	11.42	12.05	9.88	10.97	1.54	1.08	-0.63	-1.09	0.85	1	-0.97	-1.39	0.2	0.29	0.44
Cthe_01800	Peptidoglycan-binding LysM	9.77	11.21	9.58	9.8	0.19	1.41	-1.44	-0.22	-0.53	1.49	-1.99	-0.08	0.19	0.28	0.45
Cthe_02169	metallophosphoesterase	9.19	8.91	7.7	8.34	1.49	0.57	0.28	-0.64	0.8	0.25	0.16	-0.71	0.19	0.28	0.65
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_03153	Phosphoglycerate mutase	7.92	7.73	7.07	6.86	0.85	0.87	0.19	0.21	0.14	0.69	0.05	0.58	0.19	0.28	0.68
Cthe_00583	response regulator receiver protein	12.06	12	10.88	11.35	1.18	0.65	0.06	-0.47	0.48	0.37	-0.11	-0.45	0.19	0.28	0.73
Cthe_01853	cold-shock DNA-binding domain protein	12.71	12.39	11.7	11.85	1.01	0.54	0.32	-0.15	0.31	0.21	0.21	0.03	0.19	0.28	0.99
Cthe_01766	glutamate 5-kinase	11.34	11.73	10.6	11	0.74	0.73	-0.39	-0.4	0.03	0.49	-0.68	-0.35	0.19	0.28	0.36
Cthe_02039	UvrD/REP helicase	7.22	8.05	6.44	6.97	0.78	1.08	-0.83	-0.53	0.07	1	-1.22	-0.55	0.19	0.28	0.42
Cthe_02581	dihydropterolate synthase	10.03	10.53	9.1	9.49	0.93	1.04	-0.5	-0.39	0.22	0.94	-0.81	-0.33	0.19	0.28	0.62
Cthe_01953	cell wall hydrolase, SleB	8.64	9.39	8.48	8.07	0.16	1.32	-0.75	0.41	-0.56	1.35	-1.12	0.88	0.19	0.28	0.58
Cthe_02222	glycosyltransferase 28-like protein	7.29	7.64	6.57	6.74	0.72	0.9	-0.35	-0.17	0.01	0.74	-0.62	0	0.19	0.28	0.67
Cthe_01201	purine nucleoside phosphorylase I, inosine and	11.32	11.93	10.82	11.1	0.5	0.83	-0.61	-0.28	-0.21	0.63	-0.95	-0.17	0.19	0.28	0.39
Cthe_00409	ACT domain-containing protein	8.62	8.52	7.84	7.85	0.78	0.67	0.1	-0.01	0.07	0.4	-0.06	0.24	0.19	0.28	0.92
Cthe_00583	response regulator receiver protein	12.06	12	10.88	11.35	1.18	0.65	0.06	-0.47	0.48	0.37	-0.11	-0.45	0.19	0.28	0.73
Cthe_01935	arginyl-tRNA synthetase	12.16	12.87	11.77	12	0.39	0.87	-0.71	-0.23	-0.33	0.69	-1.07	-0.09	0.19	0.28	0.4
Cthe_02065	cysteinyI-tRNA synthetase	11.24	11.73	10.41	10.9	0.83	0.83	-0.49	-0.49	0.12	0.63	-0.8	-0.48	0.19	0.28	0.39
Cthe_02815	lysyl-tRNA synthetase	14.49	15.07	13.33	13.93	1.16	1.14	-0.58	-0.6	0.46	1.09	-0.91	-0.65	0.19	0.28	0.59
Cthe_01025	protein of unknown function DUF512	11.49	11.38	9.97	10.69	1.52	0.69	0.11	-0.72	0.83	0.43	-0.05	-0.83	0.19	0.28	0.63
Cthe_02215	Mg2+ transporter protein, CorA-like protein	12.62	11.9	10.95	11.47	1.67	0.43	0.72	-0.52	0.98	0.04	0.71	-0.53	0.19	0.28	0.62
Cthe_03136	peptidase S8 and S53, subtilisin, kexin,	11.19	10.62	9.76	10.15	1.43	0.47	0.57	-0.39	0.73	0.1	0.52	-0.33	0.19	0.28	0.67
Cthe_01766	glutamate 5-kinase	11.34	11.73	10.6	11	0.74	0.73	-0.39	-0.4	0.03	0.49	-0.68	-0.35	0.19	0.28	0.36
Cthe_02581	dihydropterolate synthase	10.03	10.53	9.1	9.49	0.93	1.04	-0.5	-0.39	0.22	0.94	-0.81	-0.33	0.19	0.28	0.62
Cthe_01935	arginyl-tRNA synthetase	12.16	12.87	11.77	12	0.39	0.87	-0.71	-0.23	-0.33	0.69	-1.07	-0.09	0.19	0.28	0.4
Cthe_02065	cysteinyI-tRNA synthetase	11.24	11.73	10.41	10.9	0.83	0.83	-0.49	-0.49	0.12	0.63	-0.8	-0.48	0.19	0.28	0.39
Cthe_02815	lysyl-tRNA synthetase	14.49	15.07	13.33	13.93	1.16	1.14	-0.58	-0.6	0.46	1.09	-0.91	-0.65	0.19	0.28	0.59
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_01935	arginyl-tRNA synthetase	12.16	12.87	11.77	12	0.39	0.87	-0.71	-0.23	-0.33	0.69	-1.07	-0.09	0.19	0.28	0.4
Cthe_02065	cysteinyI-tRNA synthetase	11.24	11.73	10.41	10.9	0.83	0.83	-0.49	-0.49	0.12	0.63	-0.8	-0.48	0.19	0.28	0.39
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_03153	Phosphoglycerate mutase	7.92	7.73	7.07	6.86	0.85	0.87	0.19	0.21	0.14	0.69	0.05	0.58	0.19	0.28	0.68
Cthe_02815	lysyl-tRNA synthetase	14.49	15.07	13.33	13.93	1.16	1.14	-0.58	-0.6	0.46	1.09	-0.91	-0.65	0.19	0.28	0.59
Cthe_01766	glutamate 5-kinase	11.34	11.73	10.6	11	0.74	0.73	-0.39	-0.4	0.03	0.49	-0.68	-0.35	0.19	0.28	0.36
Cthe_02065	cysteinyI-tRNA synthetase	11.24	11.73	10.41	10.9	0.83	0.83	-0.49	-0.49	0.12	0.63	-0.8	-0.48	0.19	0.28	0.39
Cthe_03153	Phosphoglycerate mutase	7.92	7.73	7.07	6.86	0.85	0.87	0.19	0.21	0.14	0.69	0.05	0.58	0.19	0.28	0.68
Cthe_02581	dihydropterolate synthase	10.03	10.53	9.1	9.49	0.93	1.04	-0.5	-0.39	0.22	0.94	-0.81	-0.33	0.19	0.28	0.62
Cthe_02039	UvrD/REP helicase	7.22	8.05	6.44	6.97	0.78	1.08	-0.83	-0.53	0.07	1	-1.22	-0.55	0.19	0.28	0.42
Cthe_01935	arginyl-tRNA synthetase	12.16	12.87	11.77	12	0.39	0.87	-0.71	-0.23	-0.33	0.69	-1.07	-0.09	0.19	0.28	0.4
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_01953	cell wall hydrolase, SleB	8.64	9.39	8.48	8.07	0.16	1.32	-0.75	0.41	-0.56	1.35	-1.12	0.88	0.19	0.28	0.58
Cthe_01201	purine nucleoside phosphorylase I, inosine and	11.32	11.93	10.82	11.1	0.5	0.83	-0.61	-0.28	-0.21	0.63	-0.95	-0.17	0.19	0.28	0.39
Cthe_01201	purine nucleoside phosphorylase I, inosine and	11.32	11.93	10.82	11.1	0.5	0.83	-0.61	-0.28	-0.21	0.63	-0.95	-0.17	0.19	0.28	0.39
Cthe_01201	purine nucleoside phosphorylase I, inosine and	11.32	11.93	10.82	11.1	0.5	0.83	-0.61	-0.28	-0.21	0.63	-0.95	-0.17	0.19	0.28	0.39
Cthe_																



Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_01201	purine nucleoside phosphorylase I, inosine and	11.32	11.93	10.82	11.1	0.5	0.83	-0.61	-0.28	-0.21	0.63	-0.95	-0.17	0.19	0.28	0.39
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_01201	purine nucleoside phosphorylase I, inosine and	11.32	11.93	10.82	11.1	0.5	0.83	-0.61	-0.28	-0.21	0.63	-0.95	-0.17	0.19	0.28	0.39
Cthe_02581	dihydropterate synthase	10.03	10.53	9.1	9.49	0.93	1.04	-0.5	-0.39	0.22	0.94	-0.81	-0.33	0.19	0.28	0.62
Cthe_01201	purine nucleoside phosphorylase I, inosine and	11.32	11.93	10.82	11.1	0.5	0.83	-0.61	-0.28	-0.21	0.63	-0.95	-0.17	0.19	0.28	0.39
Cthe_01292	proposed homoserine kinase	13.02	13.36	11.72	12.38	1.3	0.98	-0.34	-0.66	0.6	0.85	-0.61	-0.74	0.19	0.28	0.61
Cthe_01933	Zn-dependent hydrolase of the beta-lactamase	11.21	11.09	10.31	10.79	0.9	0.3	0.12	-0.48	0.19	-0.15	-0.04	-0.47	0.18	0.27	0.29
Cthe_02101	Protein of unknown function UPF0011	9.85	9.6	8.93	9.06	0.92	0.54	0.25	-0.13	0.21	0.21	0.12	0.06	0.18	0.27	1.24
Cthe_02327	beta-lactamase-like protein	10.79	10.87	9.58	10.28	1.21	0.59	-0.08	-0.7	0.51	0.28	-0.29	-0.8	0.18	0.27	0.38
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate aldolase	14.25	14.15	13.15	13.55	1.1	0.6	0.1	-0.4	0.4	0.29	-0.06	-0.35	0.18	0.27	0.78
Cthe_00523	Resolvase-like protein	7.98	7	6.02	6.64	1.96	0.36	0.98	-0.62	1.28	-0.06	1.04	-0.68	0.18	0.27	0.58
Cthe_00886	DNA polymerase I	9.96	10.89	9.36	9.77	0.6	1.12	-0.93	-0.41	-0.11	1.06	-1.35	-0.36	0.18	0.27	0.43
Cthe_01313	phosphopantothenoicysteine	11.13	12.05	10.2	10.86	0.93	1.19	-0.92	-0.66	0.22	1.16	-1.34	-0.74	0.18	0.27	0.43
Cthe_02620	protein of unknown function DUF1078-like protein	7.14	7.91	5.95	6.78	1.19	1.13	-0.77	-0.83	0.49	1.07	-1.15	-1	0.18	0.27	0.43
Cthe_02821	response regulator receiver modulated CheB	7.48	7.29	6.21	6.94	1.27	0.35	0.19	-0.73	0.57	-0.07	0.05	-0.85	0.18	0.27	0.38
Cthe_02821	response regulator receiver modulated CheB	7.48	7.29	6.21	6.94	1.27	0.35	0.19	-0.73	0.57	-0.07	0.05	-0.85	0.18	0.27	0.38
Cthe_02676	GumN	13.63	13.53	12.78	12.99	0.85	0.54	0.1	-0.21	0.14	0.21	-0.06	-0.06	0.18	0.27	1.67
Cthe_00445	cell division protein FtsZ	11.5	12.1	10.3	10.94	1.2	1.16	-0.6	-0.64	0.5	1.12	-0.94	-0.71	0.18	0.27	0.58
Cthe_02619	cell shape determining protein, MreB/Mri family	13.36	13.63	11.93	12.84	1.43	0.79	-0.27	-0.91	0.73	0.57	-0.53	-1.12	0.18	0.27	0.42
Cthe_00101	iron-containing alcohol dehydrogenase	12.45	12.41	11.27	11.75	1.18	0.66	0.04	-0.48	0.48	0.38	-0.14	-0.47	0.18	0.27	0.7
Cthe_01485	beta-lactamase-like protein	11.29	11.49	10.12	10.65	1.17	0.84	-0.2	-0.53	0.47	0.65	-0.44	-0.55	0.18	0.27	0.64
Cthe_02164	Rubredoxin-type Fe(Cys)4 protein	11.48	10.37	9.47	9.96	2.01	0.41	1.11	-0.49	1.33	0.01	1.2	-0.48	0.18	0.27	0.58
Cthe_00547	periplasmic solute binding protein	9.94	9.8	9.42	8.97	0.52	0.83	0.14	0.45	-0.19	0.63	-0.01	0.94	0.18	0.27	0.39
Cthe_01333	hypothetical protein	9.79	9.71	9.03	8.96	0.76	0.75	0.08	0.07	0.05	0.51	-0.09	0.36	0.18	0.27	0.78
Cthe_01452	KWC repeat containing protein	10.89	11.48	9.83	10.52	1.06	0.96	-0.59	-0.69	0.36	0.82	-0.92	-0.79	0.18	0.27	0.41
Cthe_01778	copper amine oxidase-like protein	13.7	13.83	12.29	13.16	1.41	0.67	-0.13	-0.87	0.71	0.4	-0.35	-1.06	0.18	0.27	0.41
Cthe_03096	hypothetical protein	14.16	13.77	12.88	13.29	1.28	0.48	0.39	-0.41	0.58	0.12	0.3	-0.36	0.18	0.27	0.71
Cthe_02986	hypothetical protein	8.34	6.52	6.02	6.43	2.32	0.09	1.82	-0.41	1.64	-0.46	2.09	-0.36	0.18	0.27	0.45
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate aldolase	14.25	14.15	13.15	13.55	1.1	0.6	0.1	-0.4	0.4	0.29	-0.06	-0.35	0.18	0.27	0.78
Cthe_00547	periplasmic solute binding protein	9.94	9.8	9.42	8.97	0.52	0.83	0.14	0.45	-0.19	0.63	-0.01	0.94	0.18	0.27	0.39
Cthe_01313	phosphopantothenoicysteine	11.13	12.05	10.2	10.86	0.93	1.19	-0.92	-0.66	0.22	1.16	-1.34	-0.74	0.18	0.27	0.43
Cthe_01313	phosphopantothenoicysteine	11.13	12.05	10.2	10.86	0.93	1.19	-0.92	-0.66	0.22	1.16	-1.34	-0.74	0.18	0.27	0.43
Cthe_01313	phosphopantothenoicysteine	11.13	12.05	10.2	10.86	0.93	1.19	-0.92	-0.66	0.22	1.16	-1.34	-0.74	0.18	0.27	0.43
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate aldolase	14.25	14.15	13.15	13.55	1.1	0.6	0.1	-0.4	0.4	0.29	-0.06	-0.35	0.18	0.27	0.78
Cthe_00886	DNA polymerase I	9.96	10.89	9.36	9.77	0.6	1.12	-0.93	-0.41	-0.11	1.06	-1.35	-0.36	0.18	0.27	0.43
Cthe_02821	response regulator receiver modulated CheB	7.48	7.29	6.21	6.94	1.27	0.35	0.19	-0.73	0.57	-0.07	0.05	-0.85	0.18	0.27	0.38
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate aldolase	14.25	14.15	13.15	13.55	1.1	0.6	0.1	-0.4	0.4	0.29	-0.06	-0.35	0.18	0.27	0.78
Cthe_01313	phosphopantothenoicysteine	11.13	12.05	10.2	10.86	0.93	1.19	-0.92	-0.66	0.22	1.16	-1.34	-0.74	0.18	0.27	0.43
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate aldolase	14.25	14.15	13.15	13.55	1.1	0.6	0.1	-0.4	0.4	0.29	-0.06	-0.35	0.18	0.27	0.78
Cthe_00764	signal peptidase I	12.3	11.74	10.77	11.31	1.53	0.43	0.56	-0.54	0.84	0.04	0.51	-0.56	0.17	0.25	0.62
Cthe_03049	TPR repeat domain containing protein	11.67	11.64	10.84	11.21	0.83	0.43	0.03	-0.37	0.12	0.04	-0.15	-0.3	0.17	0.25	0.21
Cthe_00042	small GTP-binding protein	12.66	12.25	11.8	11.87	0.86	0.38	0.41	-0.07	0.15	-0.03	0.33	0.15	0.17	0.25	0.24
Cthe_03155	beta-lactamase-like protein	10.43	9.4	8.94	9.07	1.49	0.33	1.03	-0.13	0.8	-0.1	1.1	0.06	0.17	0.25	0.41
Cthe_01638	ParB-like nuclease	3.7	3.32	1	2.58	2.7	0.74	0.38	-1.58	2.03	0.5	0.29	-2.14	0.17	0.25	0.54
Cthe_02287	transcriptional regulator, AraC family	11.35	9.83	9.49	9.97	1.86	-0.14	1.52	-0.48	1.17	-0.79	1.71	-0.47	0.17	0.25	0.45
Cthe_00295	phosphoserine aminotransferase	12.73	13.67	12.15	12.54	0.58	1.13	-0.94	-0.39	-0.13	1.07	-1.36	-0.33	0.17	0.25	0.43
Cthe_00728	phage integrase	8.52	7.87	7.4	7.25	1.12	0.62	0.65	0.15	0.42	0.32	0.62	0.48	0.17	0.25	0.38
Cthe_01277	putative methyltransferase	10.24	10.32	9.06	9.73	1.18	0.59	-0.08	-0.67	0.48	0.28	-0.29	-0.76	0.17	0.25	0.38
Cthe_01638	ParB-like nuclease	3.7	3.32	1	2.58	2.7	0.74	0.38	-1.58	2.03	0.5	0.29	-2.14	0.17	0.25	0.54
Cthe_01735	phage DNA polymerase	10.58	9.51	8.75	8.85	1.83	0.66	1.07	-0.1	1.14	0.38	1.15	0.11	0.17	0.25	0.58
Cthe_00295	phosphoserine aminotransferase	12.73	13.67	12.15	12.54	0.58	1.13	-0.94	-0.39	-0.13	1.07	-1.36	-0.33	0.17	0.25	0.43
Cthe_01532	flagellin-like protein	6.57	5.13	4.64	4.91	1.93	0.22	1.44	-0.27	1.24	-0.26	1.61	-0.15	0.17	0.25	0.44
Cthe_01899	Serine-type D-Ala-D-Ala carboxypeptidase	11.61	11.33	10.07	10.76	1.54	0.57	0.28	-0.69	0.85	0.25	0.16	-0.79	0.17	0.25	0.62
Cthe_02183	UTP-glucose-1-phosphate uridylyltransferase	12.62	12.53	11.77	12.18	0.85	0.35	0.09	-0.41	0.14	-0.07	-0.07	-0.36	0.17	0.25	0.24
Cthe_02433	electron transport complex, RnfABCDGE type, E	10.21	10.7	8.7	9.57	1.51	1.13	-0.49	-0.87	0.82	1.07	-0.8	-1.06	0.17	0.25	0.57
Cthe_02943	ABC-2 type transporter	9.5	9.8	8.36	8.89	1.14	0.91	-0.3	-0.53	0.44	0.75	-0.56	-0.55	0.17	0.25	0.62
Cthe_01573	nitrogenase iron protein	8.99	9.78	8.82	8.91	0.17	0.87	-0.79	-0.09	-0.55	0.69	-1.18	0.12	0.17	0.25	0.42
Cthe_01658	potassium uptake protein, TrkH family	9.48	10.23	8.6	9.01	0.88	1.22	-0.75	-0.41	0.17	1.21	-1.12	-0.36	0.17	0.25	0.58
Cthe_02943	ABC-2 type transporter	9.5	9.8	8.36	8.89	1.14	0.91	-0.3	-0.53	0.44	0.75	-0.56	-0.55	0.17	0.25	0.62
Cthe_01217	ATP-dependent Clp protease, ATP-binding subunit	10.42	11.05	10.05	10.24	0.37	0.81	-0.63	-0.19	-0.35	0.6	-0.97	-0.03	0.17	0.25	0.4
Cthe_01614	hypothetical protein	0	1	0	0	0	1	-1	0	-0.72	0.88	-1.44	0.26	0.17	0.25	0.44
Cthe_01487	hypothetical protein	9.15	8.54	7.71	8.08	1.44	0.46	0.61	-0.37	0.74	0.09	0.57	-0.3	0.17	0.25	0.65
Cthe_02202	hypothetical protein	12.11	11.91	10.86	11.35	1.25	0.56	0.2	-0.49	0.55	0.24	0.06	-0.48	0.17	0.25	0.7
Cthe_02482	hypothetical protein	8.13	6.74	5.43	6.55	2.7	0.19	1.39	-1.12	2.03	-0.31	1.55	-1.44	0.17	0.25	0.55
Cthe_02491	hypothetical protein	5.17	4.75	3.32	4.46	1.85	0.29	0.42	-1.14	1.16	-0.16	0.34	-1.47	0.17	0.25	0.44
Cthe_00524	hypothetical protein	8.33	7.59	6.51	7.2	1.82	0.39	0.74	-0.69	1.13	-0.01	0.74	-0.79	0.17	0.25	0.59
Cthe_02183	UTP-glucose-1-phosphate uridylyltransferase	12.62	12.53	11.77	12.18	0.85	0.35	0.09	-0.41	0.14	-0.07	-0.07	-0.36	0.17	0.25	0.24
Cthe_00295	phosphoserine aminotransferase	12.73	13.67	12.15	12.54	0.58	1.13	-0.94	-0.39	-0.13	1.07	-1.36	-0.33	0.17	0.25	0.43
Cthe_01573	nitrogenase iron protein	8.99	9.78	8.82	8.91	0.17	0.87	-0.79	-0.09	-0.55	0.69	-1.18	0.12	0.17	0.25	0.42
Cthe_02943	ABC-2 type transporter	9.5	9.8	8.36	8.89	1.14	0.91	-0.3	-0.53	0.44	0.75	-0.56	-0.55	0.17	0.25	0.62
Cthe_02183	UTP-glucose-1-phosphate uridylyltransferase	12.62	12.53	11.77	12.18	0.85	0.35	0.09	-0.41	0.14	-0.07	-0.07	-0.36	0.17	0.25	0.24
Cthe_00295	phosphoserine aminotransferase	12.73	13.67	12.15	12.54	0.58	1.13	-0.94	-0.39	-0.13	1.07	-1.36	-0.33	0.17	0.25	0.43
Cthe_02183	UTP-glucose-1-phosphate uridylyltransferase	12.62	12.53	11.77	12.18	0.85	0.35	0.09	-0.41							



Cthe_00660	glycoside hydrolase, family 81	7.79	7.76	7.43	7.07	0.36	0.69	0.03	0.36	-0.36	0.43	-0.15	0.8	0.16	0.24	0.39
Cthe_00490	CheA signal transduction histidine kinases	11.61	11.07	10.08	11.04	1.53	0.03	0.54	-0.96	0.84	-0.54	0.49	-1.2	0.16	0.24	0.43
Cthe_00905	metal dependent phosphohydrolase	8.98	9.98	8.28	8.77	0.7	1.21	-1	-0.49	-0.01	1.19	-1.44	-0.48	0.16	0.24	0.44
Cthe_01039	ribosomal protein S20	16.08	15.2	14.45	14.63	1.63	0.57	0.88	-0.18	0.94	0.25	0.91	-0.02	0.16	0.24	0.6
Cthe_01451	GCN5-related N-acetyltransferase	6.75	5.39	5.17	5.55	1.58	-0.16	1.36	-0.38	0.89	-0.82	1.51	-0.32	0.16	0.24	0.44
Cthe_02265	H+-transporting two-sector ATPase, C (AC39)	11.82	12.55	10.06	11.33	1.76	1.22	-0.73	-1.27	1.07	1.21	-1.1	-1.67	0.16	0.24	0.45
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransferase	12.35	12.71	11.32	11.78	1.03	0.93	-0.36	-0.46	0.33	0.78	-0.64	-0.44	0.16	0.24	0.61
Cthe_00381	hypothetical protein	9.35	8.29	7.83	8.04	1.52	0.25	1.06	-0.21	0.83	-0.22	1.14	-0.06	0.16	0.24	0.42
Cthe_02493	phage-like element PB5X protein	7.08	6.13	4.81	5.81	2.27	0.32	0.95	-1	1.59	-0.12	1	-1.26	0.16	0.24	0.56
Cthe_00308	hypothetical protein	13.25	13.69	11.57	12.71	1.68	0.98	-0.44	-1.14	0.99	0.85	-0.74	-1.47	0.16	0.24	0.45
Cthe_02265	H+-transporting two-sector ATPase, C (AC39)	11.82	12.55	10.06	11.33	1.76	1.22	-0.73	-1.27	1.07	1.21	-1.1	-1.67	0.16	0.24	0.45
Cthe_01840	cysteine synthase A	11.63	12.34	10.62	11.29	1.01	1.05	-0.71	-0.67	0.31	0.96	-1.07	-0.76	0.16	0.24	0.43
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransferase	12.35	12.71	11.32	11.78	1.03	0.93	-0.36	-0.46	0.33	0.78	-0.64	-0.44	0.16	0.24	0.61
Cthe_01039	ribosomal protein S20	16.08	15.2	14.45	14.63	1.63	0.57	0.88	-0.18	0.94	0.25	0.91	-0.02	0.16	0.24	0.6
Cthe_02265	H+-transporting two-sector ATPase, C (AC39)	11.82	12.55	10.06	11.33	1.76	1.22	-0.73	-1.27	1.07	1.21	-1.1	-1.67	0.16	0.24	0.45
Cthe_00490	CheA signal transduction histidine kinases	11.61	11.07	10.08	11.04	1.53	0.03	0.54	-0.96	0.84	-0.54	0.49	-1.2	0.16	0.24	0.43
Cthe_01840	cysteine synthase A	11.63	12.34	10.62	11.29	1.01	1.05	-0.71	-0.67	0.31	0.96	-1.07	-0.76	0.16	0.24	0.43
Cthe_00605	NLP/P60	14.47	14.35	13.57	14.02	0.9	0.33	0.12	-0.45	0.19	-0.1	-0.04	-0.42	0.16	0.24	0.29
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransferase	12.35	12.71	11.32	11.78	1.03	0.93	-0.36	-0.46	0.33	0.78	-0.64	-0.44	0.16	0.24	0.61
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransferase	12.35	12.71	11.32	11.78	1.03	0.93	-0.36	-0.46	0.33	0.78	-0.64	-0.44	0.16	0.24	0.61
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransferase	12.35	12.71	11.32	11.78	1.03	0.93	-0.36	-0.46	0.33	0.78	-0.64	-0.44	0.16	0.24	0.61
Cthe_01840	cysteine synthase A	11.63	12.34	10.62	11.29	1.01	1.05	-0.71	-0.67	0.31	0.96	-1.07	-0.76	0.16	0.24	0.43
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransferase	12.35	12.71	11.32	11.78	1.03	0.93	-0.36	-0.46	0.33	0.78	-0.64	-0.44	0.16	0.24	0.61
Cthe_02265	H+-transporting two-sector ATPase, C (AC39)	11.82	12.55	10.06	11.33	1.76	1.22	-0.73	-1.27	1.07	1.21	-1.1	-1.67	0.16	0.24	0.45
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransferase	12.35	12.71	11.32	11.78	1.03	0.93	-0.36	-0.46	0.33	0.78	-0.64	-0.44	0.16	0.24	0.61
Cthe_00768	nucleic acid binding protein, containing KH	10.02	10.44	9.3	9.51	0.72	0.93	-0.42	-0.21	0.01	0.78	-0.71	-0.06	0.15	0.23	0.62
Cthe_01027	protein of unknown function DUF177	14.02	14.33	12.47	13.34	1.55	0.99	-0.31	-0.87	0.86	0.87	-0.57	-1.06	0.15	0.23	0.57
Cthe_00175	polysaccharide deacetylase	12.89	13.21	12.24	12.54	0.65	0.67	-0.32	-0.3	-0.06	0.4	-0.59	-0.2	0.15	0.23	0.36
Cthe_00202	glutamine synthetase, type I	9.68	10.18	8.64	9.14	1.04	1.04	-0.5	-0.5	0.34	0.94	-0.81	-0.5	0.15	0.23	0.59
Cthe_03086	3-phosphoshikimate 1-carboxyvinyltransferase	11.88	12.29	11.26	11.56	0.62	0.73	-0.41	-0.3	-0.09	0.49	-0.7	-0.2	0.15	0.23	0.38
Cthe_00515	transposase IS66	11.84	11.38	10.53	10.93	1.31	0.45	0.46	-0.4	0.61	0.07	0.39	-0.35	0.15	0.23	0.66
Cthe_01854	methylated-DNA--protein-cysteine	7.39	7.06	5.91	6.54	1.48	0.52	0.33	-0.63	0.79	0.18	0.23	-0.7	0.15	0.23	0.62
Cthe_00471	flagellar hook-length control protein	11.27	10.56	9.07	10.43	2.2	0.13	0.71	-1.36	1.52	-0.4	0.7	-1.8	0.15	0.23	0.46
Cthe_01923	CTP synthase	11.5	12.54	10.88	11.31	0.62	1.23	-1.04	-0.43	-0.09	1.22	-1.49	-0.39	0.15	0.23	0.45
Cthe_02502	CMP/dCMP deaminase, zinc-binding	11.95	10.17	8.92	10.09	3.03	0.08	1.78	-1.17	2.37	-0.47	2.04	-1.52	0.15	0.23	0.53
Cthe_02978	transcriptional regulator, Crp/Fnr family	8.07	7.38	6.58	6.94	1.49	0.44	0.69	-0.36	0.8	0.06	0.67	-0.29	0.15	0.23	0.62
Cthe_00157	hypothetical protein	10.23	10.47	8.57	9.65	1.66	0.82	-0.24	-1.08	0.97	0.62	-0.49	-1.38	0.15	0.23	0.44
Cthe_01850	hypothetical protein	6.36	5.7	4.52	5.64	1.84	0.06	0.66	-1.12	1.15	-0.5	0.64	-1.44	0.15	0.23	0.45
Cthe_02512	protein of unknown function DUF951	4.25	3.17	1	2.81	3.25	0.36	1.08	-1.81	2.59	-0.06	1.16	-2.48	0.15	0.23	0.53
Cthe_02502	CMP/dCMP deaminase, zinc-binding	11.95	10.17	8.92	10.09	3.03	0.08	1.78	-1.17	2.37	-0.47	2.04	-1.52	0.15	0.23	0.53
Cthe_02741	ATP-dependent Clp protease, ATP-binding subunit	14.09	14.71	13.41	13.8	0.68	0.91	-0.62	-0.39	-0.03	0.75	-0.96	-0.33	0.15	0.23	0.42
Cthe_00307	hypothetical protein	13.73	13.72	11.85	12.9	1.88	0.82	0.01	-1.05	1.19	0.62	-0.17	-1.33	0.15	0.23	0.56
Cthe_02966	hypothetical protein	5.25	4.09	3.58	3.46	1.67	0.63	1.16	0.12	0.98	0.34	1.26	0.44	0.15	0.23	0.44
Cthe_01680	DNA polymerase, beta-like region	7.58	6.34	5.67	5.17	1.91	1.17	1.24	0.5	1.22	1.13	1.36	1.02	0.15	0.23	0.55
Cthe_02008	conserved hypothetical protein, CF-22 family	8.18	6.89	6.39	6.69	1.79	0.2	1.29	-0.3	1.1	-0.29	1.43	-0.2	0.15	0.23	0.44
Cthe_00918	cellulosome enzyme, dockerin type I	9.21	9.5	8.2	8.77	1.01	0.73	-0.29	-0.57	0.31	0.49	-0.55	-0.61	0.15	0.23	0.4
Cthe_03086	3-phosphoshikimate 1-carboxyvinyltransferase	11.88	12.29	11.26	11.56	0.62	0.73	-0.41	-0.3	-0.09	0.49	-0.7	-0.2	0.15	0.23	0.38
Cthe_01923	CTP synthase	11.5	12.54	10.88	11.31	0.62	1.23	-1.04	-0.43	-0.09	1.22	-1.49	-0.39	0.15	0.23	0.45
Cthe_00202	glutamine synthetase, type I	9.68	10.18	8.64	9.14	1.04	1.04	-0.5	-0.5	0.34	0.94	-0.81	-0.5	0.15	0.23	0.59
Cthe_01923	CTP synthase	11.5	12.54	10.88	11.31	0.62	1.23	-1.04	-0.43	-0.09	1.22	-1.49	-0.39	0.15	0.23	0.45
Cthe_03086	3-phosphoshikimate 1-carboxyvinyltransferase	11.88	12.29	11.26	11.56	0.62	0.73	-0.41	-0.3	-0.09	0.49	-0.7	-0.2	0.15	0.23	0.38
Cthe_00202	glutamine synthetase, type I	9.68	10.18	8.64	9.14	1.04	1.04	-0.5	-0.5	0.34	0.94	-0.81	-0.5	0.15	0.23	0.59
Cthe_03086	3-phosphoshikimate 1-carboxyvinyltransferase	11.88	12.29	11.26	11.56	0.62	0.73	-0.41	-0.3	-0.09	0.49	-0.7	-0.2	0.15	0.23	0.38
Cthe_03086	3-phosphoshikimate 1-carboxyvinyltransferase	11.88	12.29	11.26	11.56	0.62	0.73	-0.41	-0.3	-0.09	0.49	-0.7	-0.2	0.15	0.23	0.38
Cthe_00202	glutamine synthetase, type I	9.68	10.18	8.64	9.14	1.04	1.04	-0.5	-0.5	0.34	0.94	-0.81	-0.5	0.15	0.23	0.59
Cthe_01923	CTP synthase	11.5	12.54	10.88	11.31	0.62	1.23	-1.04	-0.43	-0.09	1.22	-1.49	-0.39	0.15	0.23	0.45
Cthe_00202	glutamine synthetase, type I	9.68	10.18	8.64	9.14	1.04	1.04	-0.5	-0.5	0.34	0.94	-0.81	-0.5	0.15	0.23	0.59
Cthe_00202	glutamine synthetase, type I	9.68	10.18	8.64	9.14	1.04	1.04	-0.5	-0.5	0.34	0.94	-0.81	-0.5	0.15	0.23	0.59
Cthe_00202	glutamine synthetase, type I	9.68	10.18	8.64	9.14	1.04	1.04	-0.5	-0.5	0.34	0.94	-0.81	-0.5	0.15	0.23	0.59
Cthe_02367	60 kDa inner membrane insertion protein	12.3	12.47	11.36	11.84	0.94	0.63	-0.17	-0.48	0.23	0.34	-0.4	-0.47	0.14	0.22	0.37
Cthe_01009	O-methyltransferase, family 3	10.68	11.14	9.48	10.11	1.2	1.03	-0.46	-0.63	0.5	0.93	-0.76	-0.7	0.14	0.22	0.57
Cthe_01252	Auxin Efflux Carrier	12.55	12.71	10.27	11.68	2.28	1.03	-0.16	-1.41	1.6	0.93	-0.39	-1.88	0.14	0.22	0.54
Cthe_01729	DNA methylase N-4/N-6	4.52	4.39	4	3.32	0.52	1.07	0.13	0.68	-0.19	0.99	-0.02	1.29	0.14	0.22	0.44
Cthe_02059	RNA polymerase, sigma-24 subunit, ECF subfamily	11.41	9.96	9.11	9.54	2.3	0.42	1.45	-0.43	1.62	0.03	1.62	-0.39	0.14	0.22	0.55
Cthe_00027	hypothetical protein	6.46	5.25	4.32	4.95	2.14	0.3	1.21	-0.63	1.46	-0.15	1.32	-0.7	0.14	0.22	0.55
Cthe_03101	aminotransferase, class I and II	8.85	10.03	7.45	8.39	1.4	1.64	-1.18	-0.94	0.7	1.82	-1.66	-1.17	0.14	0.22	0.54
Cthe_01040	DNA polymerase III, delta subunit	10.89	10.29	9.63	9.6	1.26	0.69	0.6	0.03	0.56	0.43	0.56	0.3	0.14	0.22	0.62
Cthe_01729	DNA methylase N-4/N-6	4.52	4.39	4	3.32	0.52	1.07	0.13	0.68	-0.19	0.99	-0.02	1.29	0.14	0.22	0.44
Cthe_00027	hypothetical protein	6.46	5.25	4.32	4.95	2.14	0.3	1.21	-0.63	1.46	-0.15	1.32	-0.7	0.14	0.22	0.55
Cthe_00288	MCP methyltransferase, CheR-type	12.21	11.35	10.49	10.96	1.72	0.39	0.86	-0.47	1.03	-0.01	0.89	-0.45	0.14	0.22	0.58
Cthe_00472	flagellar hook capping protein	10.39	9.58	8.25	9.57	2.14	0.01	0.81	-1.32	1.46	-0.57	0.82	-1.74	0.14	0.22	0.46
Cthe_00976	phospho-N-acetylmuramoyl-pentapeptide-	10.39	10.47	10.13	9.67	0.26	0.8	-0.08	0.46	-0.46	0.59	-0.29	0.95	0.14	0.22	0.42
Cthe_00288	MCP methyltransferase, CheR-type	12.21	11.35	10.49	10.96	1.72	0.39	0.86	-0.47	1.03	-0.01	0.89	-0.45	0.14	0.22	0.58
Cthe_00183	protein of unknown function DUF208	8.78	8.63	7.23	7.99	1.55	0.64	0.15	-0.76	0.86	0.35	0	-0.89	0.14	0.22	0.59



Cthe_01302	hypothetical protein	11.18	12.19	10.2	10.77	0.98	1.42	-1.01	-0.57	0.28	1.5	-1.45	-0.61	0.13	0.2	0.54
Cthe_01690	Radical SAM	9.62	8.95	7.94	8.58	1.68	0.37	0.67	-0.64	0.99	-0.04	0.65	-0.71	0.13	0.2	0.58
Cthe_02822	oxidoreductase-like protein	13.16	12.36	11.57	11.94	1.59	0.42	0.8	-0.37	0.9	0.03	0.81	-0.3	0.13	0.2	0.59
Cthe_01163	phosphoglucosamine mutase	10	10.22	8.96	9.53	1.04	0.69	-0.22	-0.57	0.34	0.43	-0.46	-0.61	0.13	0.2	0.4
Cthe_01847	two component transcriptional regulator, winged	7.58	8.29	6.63	7.11	0.95	1.18	-0.71	-0.48	0.24	1.15	-1.07	-0.47	0.13	0.2	0.56
Cthe_02588	putative transcriptional activator, Baf family	9.33	9.43	8.71	8.69	0.62	0.74	-0.1	0.02	-0.09	0.5	-0.31	0.29	0.13	0.2	0.67
Cthe_03102	cell envelope-related transcriptional attenuator	8.89	9.73	9.03	8.21	-0.14	1.52	-0.84	0.82	-0.87	1.65	-1.24	1.5	0.13	0.2	0.54
Cthe_01842	O-acetylhomoserine/O-acetylserine sulphydrylase	11.03	11.78	9.82	10.52	1.21	1.26	-0.75	-0.7	0.51	1.26	-1.12	-0.8	0.13	0.2	0.55
Cthe_02304	hypothetical protein	10.3	10.19	8.63	9.5	1.67	0.69	0.11	-0.87	0.98	0.43	-0.05	-1.06	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02583	2-amino-4-hydroxy-6-	9.44	9.58	8.5	8.97	0.94	0.61	-0.14	-0.47	0.23	0.31	-0.36	-0.45	0.13	0.2	0.38
Cthe_00489	response regulator receiver modulated CheB	10.12	9.31	8.16	9.35	1.96	-0.04	0.81	-1.19	1.28	-0.65	0.82	-1.55	0.13	0.2	0.46
Cthe_01858	peptidase M23B	12.2	12.52	10.98	11.71	1.22	0.81	-0.32	-0.73	0.52	0.6	-0.59	-0.85	0.13	0.2	0.43
Cthe_00489	response regulator receiver modulated CheB	10.12	9.31	8.16	9.35	1.96	-0.04	0.81	-1.19	1.28	-0.65	0.82	-1.55	0.13	0.2	0.46
Cthe_01847	two component transcriptional regulator, winged	7.58	8.29	6.63	7.11	0.95	1.18	-0.71	-0.48	0.24	1.15	-1.07	-0.47	0.13	0.2	0.56
Cthe_00766	tRNA (guanine-N1)-methyltransferase	10.35	10.92	9.56	10.01	0.79	0.91	-0.57	-0.45	0.08	0.75	-0.9	-0.42	0.13	0.2	0.43
Cthe_01962	pseudouridine synthase, RluA family	11.2	11.31	9.68	10.61	1.52	0.7	-0.11	-0.93	0.83	0.44	-0.33	-1.15	0.13	0.2	0.44
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_01842	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_00508	hypothetical protein	6.23	7.19	5.91	5.88	0.32	1.31	-0.96	0.03	-0.4	1.34	-1.39	0.3	0.13	0.2	0.55
Cthe_03163	Carbohydrate binding family 25	12.98	12.38	11.96	12.11	1.02	0.27	0.6	-0.15	0.32	-0.19	0.56	0.03	0.13	0.2	0.37
Cthe_01738	hypothetical protein	3.32	1.58	1	1	2.32	0.58	1.74	0	1.64	0.26	1.99	0.26	0.13	0.2	0.46
Cthe_01877	hypothetical protein	5.64	5.49	5.09	4.46	0.55	1.03	0.15	0.63	-0.16	0.93	0	1.21	0.13	0.2	0.44
Cthe_02481	hypothetical protein	7.75	6.07	5.55	6.09	2.2	-0.02	1.68	-0.54	1.52	-0.62	1.91	-0.56	0.13	0.2	0.46
Cthe_02016	RNA related	6.87	6.38	5.32	5.95	1.55	0.43	0.49	-0.63	0.86	0.04	0.42	-0.7	0.13	0.2	0.59
Cthe_00321	TPR repeat domain containing protein	9.87	10.09	9.12	9.32	0.75	0.77	-0.22	-0.2	0.04	0.54	-0.46	-0.05	0.13	0.2	0.66
Cthe_02417	Abortive infection protein	11.62	11.99	11.19	11.36	0.43	0.63	-0.37	-0.17	-0.29	0.34	-0.65	0	0.13	0.2	0.39
Cthe_01233	hypothetical protein	3.7	2.58	1.58	2.32	2.12	0.26	1.12	-0.74	1.44	-0.21	1.21	-0.86	0.13	0.2	0.55
Cthe_00476	hypothetical protein	12.67	10.72	10.14	10.02	2.53	0.7	1.95	0.12	1.86	0.44	2.25	0.44	0.13	0.2	0.47
Cthe_01290	hypothetical protein	11.95	10.89	9.85	10.63	2.1	0.26	1.06	-0.78	1.42	-0.21	1.14	-0.92	0.13	0.2	0.55
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02583	2-amino-4-hydroxy-6-	9.44	9.58	8.5	8.97	0.94	0.61	-0.14	-0.47	0.23	0.31	-0.36	-0.45	0.13	0.2	0.38
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02588	putative transcriptional activator, Baf family	9.33	9.43	8.71	8.69	0.62	0.74	-0.1	0.02	-0.09	0.5	-0.31	0.29	0.13	0.2	0.67
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02588	putative transcriptional activator, Baf family	9.33	9.43	8.71	8.69	0.62	0.74	-0.1	0.02	-0.09	0.5	-0.31	0.29	0.13	0.2	0.67
Cthe_02583	2-amino-4-hydroxy-6-	9.44	9.58	8.5	8.97	0.94	0.61	-0.14	-0.47	0.23	0.31	-0.36	-0.45	0.13	0.2	0.38
Cthe_01302	hypothetical protein	11.18	12.19	10.2	10.77	0.98	1.42	-1.01	-0.57	0.28	1.5	-1.45	-0.61	0.13	0.2	0.54
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_01962	pseudouridine synthase, RluA family	11.2	11.31	9.68	10.61	1.52	0.7	-0.11	-0.93	0.83	0.44	-0.33	-1.15	0.13	0.2	0.44
Cthe_00766	tRNA (guanine-N1)-methyltransferase	10.35	10.92	9.56	10.01	0.79	0.91	-0.57	-0.45	0.08	0.75	-0.9	-0.42	0.13	0.2	0.43
Cthe_00489	response regulator receiver modulated CheB	10.12	9.31	8.16	9.35	1.96	-0.04	0.81	-1.19	1.28	-0.65	0.82	-1.55	0.13	0.2	0.46
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_01163	phosphoglucosamine mutase	10	10.22	8.96	9.53	1.04	0.69	-0.22	-0.57	0.34	0.43	-0.46	-0.61	0.13	0.2	0.4
Cthe_01842	O-acetylhomoserine/O-acetylserine sulphydrylase	11.03	11.78	9.82	10.52	1.21	1.26	-0.75	-0.7	0.51	1.26	-1.12	-0.8	0.13	0.2	0.55
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02588	putative transcriptional activator, Baf family	9.33	9.43	8.71	8.69	0.62	0.74	-0.1	0.02	-0.09	0.5	-0.31	0.29	0.13	0.2	0.67
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_01842	O-acetylhomoserine/O-acetylserine sulphydrylase	11.03	11.78	9.82	10.52	1.21	1.26	-0.75	-0.7	0.51	1.26	-1.12	-0.8	0.13	0.2	0.55
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13		



Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_01163	phosphoglucosamine mutase	10	10.22	8.96	9.53	1.04	0.69	-0.22	-0.57	0.34	0.43	-0.46	-0.61	0.13	0.2	0.4
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02393	thiamine pyrophosphate enzyme-like TPP-binding	12.51	13.05	11.25	11.95	1.26	1.1	-0.54	-0.7	0.56	1.03	-0.86	-0.8	0.13	0.2	0.56
Cthe_00107	Riboflavin synthase	10.06	10.04	9.33	9.6	0.73	0.44	0.02	-0.27	0.02	0.06	-0.16	-0.15	0.13	0.2	0.16
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_02428	modification methylase, HemK family	9.85	10.54	9	9.39	0.85	1.15	-0.69	-0.39	0.14	1.1	-1.05	-0.33	0.13	0.2	0.57
Cthe_00926	signal recognition particle-docking protein FtsY	11.35	11.53	9.99	10.8	1.36	0.73	-0.18	-0.81	0.66	0.49	-0.41	-0.97	0.12	0.19	0.44
Cthe_00572	radical SAM enzyme, Cfr family	11.71	11.57	10.63	11.17	1.08	0.4	0.14	-0.54	0.38	0	-0.01	-0.56	0.12	0.19	0.38
Cthe_00780	HAD-superfamily hydrolase, subfamily IA, variant	9	8.74	8.25	8.26	0.75	0.48	0.26	-0.01	0.04	0.12	0.14	0.24	0.12	0.19	0.26
Cthe_03073	HAD-superfamily hydrolase, subfamily IA, variant	7.5	7.25	6.57	6.78	0.93	0.47	0.25	-0.21	0.22	0.1	0.12	-0.06	0.12	0.19	1.01
Cthe_00311	excinuclease ABC, A subunit	10.26	11.05	9.55	9.98	0.71	1.07	-0.79	-0.43	0	0.99	-1.18	-0.39	0.12	0.19	0.45
Cthe_00516	IS66 Orf2 like	5.21	4.39	3.32	4.46	1.89	-0.07	0.82	-1.14	1.2	-0.69	0.84	-1.47	0.12	0.19	0.46
Cthe_01884	transposase IS116/IS110/IS902	8.75	8.06	7.08	7.71	1.67	0.35	0.69	-0.63	0.98	-0.07	0.67	-0.7	0.12	0.19	0.57
Cthe_01777	amidohydrolase	11.42	11.12	10.2	10.65	1.22	0.47	0.3	-0.45	0.52	0.1	0.19	-0.42	0.12	0.19	0.65
Cthe_01907	amino acid adenylation domain	7.01	6.3	5.67	5.32	1.34	0.98	0.71	0.35	0.64	0.85	0.7	0.79	0.12	0.19	0.57
Cthe_00106	GTP cyclohydrolase II	10.23	10.46	9.32	9.67	0.91	0.79	-0.23	-0.35	0.2	0.57	-0.47	-0.27	0.12	0.19	0.63
Cthe_00420	dipicolinate synthase	8.67	8.93	8.09	8.32	0.58	0.61	-0.26	-0.23	-0.13	0.31	-0.51	-0.09	0.12	0.19	0.36
Cthe_01380	response regulator receiver protein	10.67	10.1	9.42	9.56	1.25	0.54	0.57	-0.14	0.55	0.21	0.52	0.05	0.12	0.19	0.63
Cthe_01937	glutamate racemase	9.98	10.36	9.45	9.47	0.53	0.89	-0.38	-0.02	-0.18	0.72	-0.66	0.23	0.12	0.19	0.6
Cthe_00053	ribonucleoside-diphosphate reductase,	13.27	14.16	12.64	13.03	0.63	1.13	-0.89	-0.39	-0.08	1.07	-1.3	-0.33	0.12	0.19	0.45
Cthe_01293	metal dependent phosphohydrolase	13.19	11.22	10.66	11.32	2.53	-0.1	1.97	-0.66	1.86	-0.74	2.27	-0.74	0.12	0.19	0.47
Cthe_01380	response regulator receiver protein	10.67	10.1	9.42	9.56	1.25	0.54	0.57	-0.14	0.55	0.21	0.52	0.05	0.12	0.19	0.63
Cthe_02113	periplasmic sensor signal transduction histidine	9.27	8.65	7.94	8.15	1.33	0.5	0.62	-0.21	0.63	0.15	0.59	-0.06	0.12	0.19	0.61
Cthe_00103	protein of unknown function UPF0047	7.97	7.4	6.97	7.11	1	0.29	0.57	-0.14	0.3	-0.16	0.52	0.05	0.12	0.19	0.37
Cthe_01422	RDD domain containing protein	12.13	12.26	11.17	11.65	0.96	0.61	-0.13	-0.48	0.26	0.31	-0.35	-0.47	0.12	0.19	0.39
Cthe_01494	protein of unknown function DUF6, transmembran	5.93	6.91	5.86	5.86	0.07	1.05	-0.98	0	-0.65	0.96	-1.41	0.26	0.12	0.19	0.45
Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_01783	ribosomal protein L13	10.71	10.41	9.39	10.11	1.32	0.3	0.3	-0.72	0.62	-0.15	0.19	-0.83	0.12	0.19	0.42
Cthe_02935	methyltransferase small	10.39	10.17	9.15	9.65	1.24	0.52	0.22	-0.5	0.54	0.18	0.09	-0.5	0.12	0.19	0.63
Cthe_00156	Radical SAM	12.44	12.36	10.99	11.7	1.45	0.66	0.08	-0.71	0.76	0.38	-0.09	-0.82	0.12	0.19	0.58
Cthe_01053	L-lactate dehydrogenase	11.78	11.43	10.93	10.95	0.85	0.48	0.35	-0.02	0.14	0.12	0.25	0.23	0.12	0.19	0.3
Cthe_03090	hydro-lyases, Fe-S type, tartrate/fumarate	8.21	8.18	7.23	7.7	0.98	0.48	0.03	-0.47	0.28	0.12	-0.15	-0.45	0.12	0.19	0.36
Cthe_01659	TrkA-N	8.08	8.97	7.57	7.87	0.51	1.1	-0.89	-0.3	-0.2	1.03	-1.3	-0.2	0.12	0.19	0.45
Cthe_00699	carboxyl transferase	14.07	14.28	13.45	13.52	0.62	0.76	-0.21	-0.07	-0.09	0.53	-0.45	0.15	0.12	0.19	0.64
Cthe_01947	Redoxin	10.72	11.03	9.69	10.16	1.03	0.87	-0.31	-0.47	0.33	0.69	-0.57	-0.45	0.12	0.19	0.59
Cthe_02384	S-layer-like domain containing protein	13.8	12.8	12.29	12.47	1.51	0.33	1	-0.18	0.82	-0.1	1.06	-0.02	0.12	0.19	0.44
Cthe_00427	serine phosphatase	13.34	14.51	12.61	13.01	0.73	1.5	-1.17	-0.4	0.02	1.62	-1.65	-0.35	0.12	0.19	0.54
Cthe_01154	transcriptional regulator, XRE family	9.52	8.68	8.34	8.58	1.18	0.1	0.84	-0.24	0.48	-0.44	0.86				



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Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_00572	radical SAM enzyme, Cfr family	11.71	11.57	10.63	11.17	1.08	0.4	0.14	-0.54	0.38	0	-0.01	-0.56	0.12	0.19	0.38
Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_00699	carboxyl transferase	14.07	14.28	13.45	13.52	0.62	0.76	-0.21	-0.07	-0.09	0.53	-0.45	0.15	0.12	0.19	0.64
Cthe_03090	hydro-lyases, Fe-S type, tartrate/fumarate	8.21	8.18	7.23	7.7	0.98	0.48	0.03	-0.47	0.28	0.12	-0.15	-0.45	0.12	0.19	0.36
Cthe_00053	ribonucleoside-diphosphate reductase,	13.27	14.16	12.64	13.03	0.63	1.13	-0.89	-0.39	-0.08	1.07	-1.3	-0.33	0.12	0.19	0.45
Cthe_03090	hydro-lyases, Fe-S type, tartrate/fumarate	8.21	8.18	7.23	7.7	0.98	0.48	0.03	-0.47	0.28	0.12	-0.15	-0.45	0.12	0.19	0.36
Cthe_00572	radical SAM enzyme, Cfr family	11.71	11.57	10.63	11.17	1.08	0.4	0.14	-0.54	0.38	0	-0.01	-0.56	0.12	0.19	0.38
Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_00572	radical SAM enzyme, Cfr family	11.71	11.57	10.63	11.17	1.08	0.4	0.14	-0.54	0.38	0	-0.01	-0.56	0.12	0.19	0.38
Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_00572	radical SAM enzyme, Cfr family	11.71	11.57	10.63	11.17	1.08	0.4	0.14	-0.54	0.38	0	-0.01	-0.56	0.12	0.19	0.38
Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_00572	radical SAM enzyme, Cfr family	11.71	11.57	10.63	11.17	1.08	0.4	0.14	-0.54	0.38	0	-0.01	-0.56	0.12	0.19	0.38
Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_00572	radical SAM enzyme, Cfr family	11.71	11.57	10.63	11.17	1.08	0.4	0.14	-0.54	0.38	0	-0.01	-0.56	0.12	0.19	0.38
Cthe_01320	ribosomal protein L11 methyltransferase	8.91	9.25	8.46	8.37	0.45	0.88	-0.34	0.09	-0.27	0.71	-0.61	0.39	0.12	0.19	0.59
Cthe_00770	signal recognition particle protein	11.56	11.72	10.78	11.01	0.78	0.71	-0.16	-0.23	0.07	0.46	-0.39	-0.09	0.11	0.18	0.65
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_02249	helicase, RecD/TraA family	9.29	9.21	8.2	8.63	1.09	0.58	0.08	-0.43	0.39	0.26	-0.09	-0.39	0.11	0.18	0.66
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_02219	flagellar protein FlaG protein	5.73	6.09	5.17	5.39	0.56	0.7	-0.36	-0.22	-0.15	0.44	-0.64	-0.08	0.11	0.18	0.4
Cthe_02628	SpoVG	14.85	13.57	13.15	13.63	1.7	-0.06	1.28	-0.48	1.01	-0.68	1.41	-0.47	0.11	0.18	0.46
Cthe_02076	periplasmic sensor signal transduction histidine	8.45	8.9	7.93	7.97	0.52	0.93	-0.45	-0.04	-0.19	0.78	-0.75	0.2	0.11	0.18	0.58
Cthe_00116	protein of unknown function DUF199	11.07	11.23	10.05	10.48	1.02	0.75	-0.16	-0.43	0.32	0.51	-0.39	-0.39	0.11	0.18	0.61
Cthe_00331	hypothetical protein	8.7	8.12	7.63	7.77	1.07	0.35	0.58	-0.14	0.37	-0.07	0.54	0.05	0.11	0.18	0.39
Cthe_01165	YbbR-like protein	11.94	11.97	11.06	11.45	0.88	0.52	-0.03	-0.39	0.17	0.18	-0.22	-0.33	0.11	0.18	0.35
Cthe_02104	PSP1	11.35	11.74	10.04	10.75	1.31	0.99	-0.39	-0.71	0.61	0.87	-0.68	-0.82	0.11	0.18	0.56
Cthe_01759	hypothetical protein	8.45	8.88	8.25	7.62	0.2	1.26	-0.43	0.63	-0.52	1.26	-0.72	1.21	0.11	0.18	0.54
Cthe_02440	hypothetical protein	10.38	10.24	9.79	9.67	0.59	0.57	0.14	0.12	-0.12	0.25	-0.01	0.44	0.11	0.18	0.35
Cthe_00689	RDD domain containing protein	11.38	11.25	9.79	10.6	1.59	0.65	0.13	-0.81	0.9	0.37	-0.02	-0.97	0.11	0.18	0.56
Cthe_00760	hypothetical protein	12.56	11.87	11.11	11.48	1.45	0.39	0.69	-0.37	0.76	-0.01	0.67	-0.3	0.11	0.18	0.58
Cthe_00100	hypothetical protein	11.57	11.76	10.96	11.19	0.61	0.57	-0.19	-0.23	-0.1	0.25	-0.42	-0.09	0.11	0.18	0.35
Cthe_01042	hypothetical protein	12.05	12.09	11.3	11.59	0.75	0.5	-0.04	-0.29	0.04	0.15	-0.24	-0.18	0.11	0.18	0.29
Cthe_01941	putative regulatory protein, FmdB family	8.31	7.6	6.57	7.27	1.74	0.33	0.71	-0.7	1.05	-0.1	0.7	-0.8	0.11	0.18	0.56
Cthe_01116	HMG-I and HMG-Y, DNA-binding	5.32	5	4.39	4.17	0.93	0.83	0.32	0.22	0.22	0.63	0.21	0.59	0.11	0.18	0.6
Cthe_02707	ABC-type transport system involved in	8.96	10.23	8.33	8.8	0.63	1.43	-1.27	-0.47	-0.08	1.51	-1.77	-0.45	0.11	0.18	0.47
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_00770	signal recognition particle protein	11.56	11.72	10.78	11.01	0.78	0.71	-0.16	-0.23	0.07	0.46	-0.39	-0.09	0.11	0.18	0.65
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_02249	helicase, RecD/TraA family	9.29	9.21	8.2	8.63	1.09	0.58	0.08	-0.43	0.39	0.26	-0.09	-0.39	0.11	0.18	0.66
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_03003	hydrogenase, Fe-only	13.84	15.28	12.22	13.41	1.62	1.87	-1.44	-1.19	0.93	2.16	-1.99	-1.55	0.11	0.18	0.52
Cthe_01093	Methenyltetrahydrofolate cyclohydrolase	10.99	11.31	9.99	10.44	1	0.87	-0.32	-0.45	0.3	0.69	-0.59	-0.42	0.11	0.18	0.58
Cthe_02444	Transketolase-like protein	5.58	5.25	4.46	4.81	1.12	0.44	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_00403	DNA-directed RNA polymerase sigma factor	10.75	10.2	9.7	9.82	1.05	0.48	0.33	-0.35	0.42	0.06	0.23	-0.27	0.11	0.18	0.67
Cthe_01058	Glycine hydroxymethyltransferase	13.81	13.08	12.2	12.76	1.61	0.32	0.73	-0.56	0.92	-0.12	0.72	-0.59	0.1	0.16	0.56
Cthe_01458	extracellular solute-binding protein, family 3	9.2	10.46	8.41	9	0.79	1.46	-1.26	-0.59	0.08	1.56	-1.76	-0.64	0.1	0.16	0.47
Cthe_03124	AMP-dependent synthetase and ligase	13.32	13.89	12.12	12.79	1.2	1.1	-0.57	-0.67	0.5	1.03	-0.9	-0.76	0.1	0.16	0.55
Cthe_00561	AppE-like lipoprotein	11.26	11.08	9.91	10.52	1.35	0.56	0.18	-0.61	0.						



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Cthe_00681	IMP dehydrogenase/GMP reductase	14.96	14.32	13.59	13.92	1.37	0.4	0.64	-0.33	0.67	0	0.61	-0.24	0.09	0.15	0.57
Cthe_00305	DNA topoisomerase (ATP-hydrolyzing)	10.73	10.61	9.7	10.08	1.03	0.53	0.12	-0.38	0.33	0.19	-0.04	-0.32	0.09	0.15	0.66
Cthe_00180	crossover junction endonuclease RuvC	9.75	8.98	8.21	8.63	1.54	0.35	0.77	-0.42	0.85	-0.07	0.77	-0.38	0.09	0.15	0.56
Cthe_01946	FAD-dependent pyridine nucleotide-disulphide	10.94	11.5	9.82	10.51	1.12	0.99	-0.56	-0.69	0.42	0.87	-0.89	-0.79	0.09	0.15	0.46
Cthe_00917	glutamyl-tRNA synthetase	13.48	13.67	12.41	12.9	1.07	0.77	-0.19	-0.49	0.37	0.54	-0.42	-0.48	0.09	0.15	0.58
Cthe_02601	UDP-N-acetylglucosamine 2-epimerase	12.01	12.51	10.82	11.55	1.19	0.96	-0.5	-0.73	0.49	0.82	-0.81	-0.85	0.09	0.15	0.46
Cthe_02713	dihydroxy-acid dehydratase	12.57	13.47	11.62	12.25	0.95	1.22	-0.9	-0.63	0.24	1.21	-1.31	-0.7	0.09	0.15	0.47
Cthe_00958	queuine tRNA-ribosyltransferase	9.93	10.36	9.1	9.53	0.83	0.83	-0.43	-0.63	0.12	0.63	-0.72	-0.39	0.09	0.15	0.44
Cthe_00373	oxidoreductase FAD/NAD(P)-binding	11.21	11.18	9.88	10.52	1.33	0.66	0.03	-0.64	0.63	0.38	-0.15	-0.71	0.09	0.15	0.57
Cthe_01211	pyridoxal-phosphate dependent TrpB-like enzyme	15.22	15.32	14.49	14.67	0.73	0.65	-0.1	-0.18	0.02	0.37	-0.31	-0.02	0.09	0.15	0.67
Cthe_00373	oxidoreductase FAD/NAD(P)-binding	11.21	11.18	9.88	10.52	1.33	0.66	0.03	-0.64	0.63	0.38	-0.15	-0.71	0.09	0.15	0.57
Cthe_02713	dihydroxy-acid dehydratase	12.57	13.47	11.62	12.25	0.95	1.22	-0.9	-0.63	0.24	1.21	-1.31	-0.7	0.09	0.15	0.47
Cthe_02713	dihydroxy-acid dehydratase	12.57	13.47	11.62	12.25	0.95	1.22	-0.9	-0.63	0.24	1.21	-1.31	-0.7	0.09	0.15	0.47
Cthe_02713	dihydroxy-acid dehydratase	12.57	13.47	11.62	12.25	0.95	1.22	-0.9	-0.63	0.24	1.21	-1.31	-0.7	0.09	0.15	0.47
Cthe_02601	UDP-N-acetylglucosamine 2-epimerase	12.01	12.51	10.82	11.55	1.19	0.96	-0.5	-0.73	0.49	0.82	-0.81	-0.85	0.09	0.15	0.46
Cthe_02601	UDP-N-acetylglucosamine 2-epimerase	12.01	12.51	10.82	11.55	1.19	0.96	-0.5	-0.73	0.49	0.82	-0.81	-0.85	0.09	0.15	0.46
Cthe_02601	UDP-N-acetylglucosamine 2-epimerase	12.01	12.51	10.82	11.55	1.19	0.96	-0.5	-0.73	0.49	0.82	-0.81	-0.85	0.09	0.15	0.46
Cthe_00917	glutamyl-tRNA synthetase	13.48	13.67	12.41	12.9	1.07	0.77	-0.19	-0.49	0.37	0.54	-0.42	-0.48	0.09	0.15	0.58
Cthe_00681	IMP dehydrogenase/GMP reductase	14.96	14.32	13.59	13.92	1.37	0.4	0.64	-0.33	0.67	0	0.61	-0.24	0.09	0.15	0.57
Cthe_02713	dihydroxy-acid dehydratase	12.57	13.47	11.62	12.25	0.95	1.22	-0.9	-0.63	0.24	1.21	-1.31	-0.7	0.09	0.15	0.47
Cthe_00681	IMP dehydrogenase/GMP reductase	14.96	14.32	13.59	13.92	1.37	0.4	0.64	-0.33	0.67	0	0.61	-0.24	0.09	0.15	0.57
Cthe_00681	IMP dehydrogenase/GMP reductase	14.96	14.32	13.59	13.92	1.37	0.4	0.64	-0.33	0.67	0	0.61	-0.24	0.09	0.15	0.57
Cthe_00681	IMP dehydrogenase/GMP reductase	14.96	14.32	13.59	13.92	1.37	0.4	0.64	-0.33	0.67	0	0.61	-0.24	0.09	0.15	0.57
Cthe_02713	dihydroxy-acid dehydratase	12.57	13.47	11.62	12.25	0.95	1.22	-0.9	-0.63	0.24	1.21	-1.31	-0.7	0.09	0.15	0.47
Cthe_01946	FAD-dependent pyridine nucleotide-disulphide	10.94	11.5	9.82	10.51	1.12	0.99	-0.56	-0.69	0.42	0.87	-0.89	-0.79	0.09	0.15	0.46
Cthe_02601	UDP-N-acetylglucosamine 2-epimerase	12.01	12.51	10.82	11.55	1.19	0.96	-0.5	-0.73	0.49	0.82	-0.81	-0.85	0.09	0.15	0.46
Cthe_02740	ATP-dependent Clp protease, proteolytic subunit	13.27	13.46	12.51	12.83	0.76	0.63	-0.19	-0.32	0.05	0.34	-0.42	-0.23	0.08	0.14	0.4
Cthe_00870	NADPH-dependent FMN reductase	11.8	11.25	10.34	10.9	1.46	0.35	0.55	-0.56	0.77	-0.07	0.5	-0.59	0.08	0.14	0.56
Cthe_01896	metallophosphoesterase	10.95	10.01	9.29	9.57	1.66	0.44	0.94	-0.28	0.97	0.06	0.99	-0.17	0.08	0.14	0.54
Cthe_02561	CDP-glucose 4,6-dehydratase	10.64	9.98	8.67	9.63	1.97	0.35	0.66	-0.96	1.29	-0.07	0.64	-1.2	0.08	0.14	0.53
Cthe_00289	DEAD_2	10.67	10.83	9.17	10.07	1.5	0.76	-0.16	-0.9	0.81	0.53	-0.39	-1.11	0.08	0.14	0.46
Cthe_00740	transcriptional regulator, GntR family	13.91	12.6	11.84	12.18	2.07	0.42	1.31	-0.34	1.39	0.03	1.45	-0.26	0.08	0.14	0.53
Cthe_01478	transcriptional regulator, TetR family	9.77	9.34	8.7	8.85	1.07	0.49	0.43	-0.15	0.37	0.13	0.35	0.03	0.08	0.14	0.63
Cthe_00711	chorismate mutase	11.99	12.3	11.25	11.58	0.74	0.72	-0.31	-0.33	0.03	0.47	-0.57	-0.24	0.08	0.14	0.43
Cthe_00715	Adenosylmethionine decarboxylase	11.47	11.86	9.69	10.79	1.78	1.07	-0.39	-1.1	1.09	0.99	-0.68	-1.41	0.08	0.14	0.53
Cthe_00731	Shikimate kinase	10.62	10.73	9.58	10.03	1.04	0.7	-0.11	-0.45	0.34	0.44	-0.33	-0.42	0.08	0.14	0.58
Cthe_02459	protein of unknown function DUF955	10.22	8.88	8.1	8.48	2.12	0.4	1.34	-0.38	1.44	0	1.49	-0.32	0.08	0.14	0.53
Cthe_00289	DEAD_2	10.67	10.83	9.17	10.07	1.5	0.76	-0.16	-0.9	0.81	0.53	-0.39	-1.11	0.08	0.14	0.46
Cthe_01432	transposase IS200-like protein	11.81	11.66	10.64	11.13	1.17	0.53	0.15	-0.49	0.47	0.19	0	-0.48	0.08	0.14	0.59
Cthe_00174	sulfatase	12.07	12.55	11.38	11.71	0.69	0.84	-0.48	-0.33	-0.02	0.65	-0.79	-0.24	0.08	0.14	0.44
Cthe_00185	cell wall hydrolase/autolysin	12.38	10.93	10.35	10.92	2.03	0.01	1.45	-0.57	1.35	-0.57	1.62	-0.61	0.08	0.14	0.48
Cthe_00272	Serine-type D-Ala-D-Ala carboxypeptidase	10.8	10.96	10.23	10.24	0.57	0.72	-0.16	-0.01	-0.14	0.47	-0.39	0.24	0.08	0.14	0.6
Cthe_00441	UDP-N-acetylglucosamine	10.43	10.4	9.94	9.73	0.49	0.67	0.03	0.21	-0.22	0.4	-0.15	0.58	0.08	0.14	0.43
Cthe_01041	UDP-N-acetylmuramoylalanine--D-glutamate ligase	12.09	12.76	11.42	11.68	0.67	1.08	-0.67	-0.26	-0.04	1	-1.02	-0.14	0.08	0.14	0.55
Cthe_02550	glycosyltransferase sugar-binding region	6.49	5.91	5.17	5.52	1.32	0.39	0.58	-0.35	0.62	-0.01	0.54	-0.27	0.08	0.14	0.58
Cthe_02561	CDP-glucose 4,6-dehydratase	10.64	9.98	8.67	9.63	1.97	0.35	0.66	-0.96	1.29	-0.07	0.64	-1.2	0.08	0.14	0.53
Cthe_02694	O-antigen polymerase	12.17	12.82	11.38	11.82	0.79	1	-0.65	-0.44	0.08	0.88	-1	-0.41	0.08	0.14	0.46
Cthe_00784	hypothetical protein	9.86	9.89	9.15	9.3	0.71	0.59	-0.03	-0.15	0	0.28	-0.22	0.03	0.08	0.14	0.71
Cthe_00410	protein of unknown function DUF711	11.94	12.13	10.99	11.46	0.95	0.67	-0.19	-0.47	0.24	0.4	-0.42	-0.45	0.08	0.14	0.43
Cthe_01075	protein of unknown function DUF881	10.87	10.72	9.76	10.2	1.11	0.52	0.15	-0.44	0.41	0.18	0	-0.41	0.08	0.14	0.61
Cthe_01208	GCNS-related N-acetyltransferase	6.71	6.09	5.61	5.83	1.1	0.26	0.62	-0.22	0.4	-0.21	0.59	-0.08	0.08	0.14	0.43
Cthe_02933	ribosomal protein L17	13.49	14.47	12.83	13.15	0.66	1.32	-0.98	-0.32	-0.05	1.35	-1.41	-0.23	0.08	0.14	0.53
Cthe_00193	sodium/hydrogen exchanger	7.08	6.27	5.39	6	1.69	0.27	0.81	-0.61	1	-1.19	0.82	-0.67	0.08	0.14	0.54
Cthe_01556	binding-protein-dependent transport systems	9.72	9.87	9.14	9.17	0.58	0.7	-0.15	-0.03	-0.13	0.44	-0.37	0.21	0.08	0.14	0.61
Cthe_02740	ATP-dependent Clp protease, proteolytic subunit	13.27	13.46	12.51	12.83	0.76	0.63	-0.19	-0.32	0.05	0.34	-0.42	-0.23	0.08	0.14	0.4
Cthe_00320	hypothetical protein	10.27	10.7	9.65	9.81	0.62	0.89	-0.43	-0.16	-0.09	0.72	-0.72	0.02	0.08	0.14	0.57
Cthe_00705	hypothetical protein	9.32	8.34	7.94	8.34	1.38	0	0.98	-0.4	0.68	-0.59	1.04	-0.35	0.08	0.14	0.46
Cthe_02379	hypothetical protein	9.58	9.52	8.81	9.08	0.77	0.44	0.06	-0.27	0.06	0.06	-0.11	-0.15	0.08	0.14	0.26
Cthe_01651	hypothetical protein	4.58	3.32	2.81	2	1.77	1.32	1.26	0.81	1.08	1.35	1.39	1.48	0.08	0.14	0.48
Cthe_01219	hypothetical protein	12.16	12.39	11.12	11.67	1.04	0.72	-0.23	-0.55	0.34	0.47	-0.47	-0.58	0.08	0.14	0.44
Cthe_01418	hypothetical protein	7.39	6.89	5.86	6.51	1.53	0.38	0.5	-0.65	0.84	-0.03	0.44	-0.73	0.08	0.14	0.55
Cthe_00697	type IV pilus assembly PilZ	10.13	9.53	9	9.02	1.13	0.51	0.6	-0.02	0.43	0.16	0.56	0.23	0.08	0.14	0.43
Cthe_01275	H+-ATPase subunit H	11.71	10.8	10.03	10.45	1.68	0.35	0.91	-0.42	0.99	-0.07	0.95	-0.38	0.08	0.14	0.54
Cthe_01414	hypothetical protein	7.39	7.19	6.19	6.79	1.2	0.4	0.2	-0.6	0.5	0	0.06	-0.65	0.08	0.14	0.43
Cthe_01552	MAEBL, putative	11	9.84	9.27	9.46	1.73	0.38	1.16	-0.19	1.04	-0.03	1.26	-0.03	0.08	0.14	0.46
Cthe_00731	Shikimate kinase	10.62	10.73	9.58	10.03	1.04	0.7	-0.11	-0.45	0.34	0.44	-0.33	-0.42	0.08	0.14	0.58
Cthe_00711	chorismate mutase	11.99	12.3	11.25	11.58	0.74	0.72	-0.31	-0.33	0.03	0.47	-0.57	-0.24	0.08	0.14	0.43
Cthe_00715	Adenosylmethionine decarboxylase	11.47	11.86	9.69	10.79	1.78	1.07	-0.39	-1.1	1.09	0.99	-0.68	-1.41	0.08	0.14	0.53
Cthe_00715	Adenosylmethionine decarboxylase	11.47	11.86	9.69	10.79	1.78	1.07	-0.39	-1.1	1.09	0.99	-0.68	-1.41	0.08	0.14	0.53
Cthe_02933	ribosomal protein L17	13.49	14.47	12.83	13.15	0.66	1.32	-0.98	-0.32	-0.05	1.35	-1.41	-0.23	0.08	0.14	0.53
Cthe_01556	binding-protein-dependent transport systems	9.72	9.87	9.14	9.17	0.58	0.7	-0.15	-0.03	-0.13	0.44	-0.37	0.21	0.08	0.14	0.61
Cthe_00289	DEAD_2	10.67	10.83	9.17	10.07	1.5	0.76	-0.16	-0.9	0.81	0.53	-0.39	-1.11	0.08	0.14	0.46
Cthe_00711	chorismate mutase	11.99	12.3	11.25	11.58	0.74	0.72	-0.31	-0.33	0.03	0.47	-0.57	-0.24	0.08	0.14	0.43
Cthe_00272	Serine-type D-Ala-D-Ala carboxypeptidase	10.8	10.96	10.23	10.24	0.57	0.72	-0.16	-0.01	-0.14	0.47	-0.39	0.24	0.08	0.14	0.6
Cthe_00711	chorismate mutase	11.99														



Cthe_00715	Adenosylmethionine decarboxylase	11.47	11.86	9.69	10.79	1.78	1.07	-0.39	-1.1	1.09	0.99	-0.68	-1.41	0.08	0.14	0.53
Cthe_00711	chorismate mutase	11.99	12.3	11.25	11.58	0.74	0.72	-0.31	-0.33	0.03	0.47	-0.57	-0.24	0.08	0.14	0.43
Cthe_01051	integral membrane protein MvIN	9.49	10.39	8.11	9.07	1.38	1.32	-0.9	-0.96	0.68	1.35	-1.31	-1.2	0.07	0.13	0.48
Cthe_02220	NAD-dependent epimerase/dehydratase	7.34	7.86	6.58	6.89	0.76	0.97	-0.52	-0.31	0.05	0.84	-0.84	-0.21	0.07	0.13	0.55
Cthe_02232	polysaccharide biosynthesis protein CapD	5.21	4.32	3.81	4.17	1.4	0.15	0.89	-0.36	0.7	-0.37	0.92	-0.29	0.07	0.13	0.46
Cthe_02770	transposase IS116/IS110/IS902	2.58	4.09	2.58	2.58	0	1.51	-1.51	0	-0.72	1.63	-2.07	0.26	0.07	0.13	0.48
Cthe_00717	MCP methyltransferase, CheR-type	11.55	10.4	9.83	9.8	1.72	0.6	1.15	0.03	1.03	0.29	1.25	0.3	0.07	0.13	0.47
Cthe_02818	CheA signal transduction histidine kinases	10.17	8.29	7.99	8.87	2.18	-0.58	1.88	-0.88	1.5	-1.44	2.16	-1.08	0.07	0.13	0.48
Cthe_02819	methyl-accepting chemotaxis sensory transducer	8.65	7.48	6.49	7.72	2.16	-0.24	1.17	-1.23	1.48	-0.94	1.27	-1.61	0.07	0.13	0.48
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_02220	NAD-dependent epimerase/dehydratase	7.34	7.86	6.58	6.89	0.76	0.97	-0.52	-0.31	0.05	0.84	-0.84	-0.21	0.07	0.13	0.55
Cthe_02232	polysaccharide biosynthesis protein CapD	5.21	4.32	3.81	4.17	1.4	0.15	0.89	-0.36	0.7	-0.37	0.92	-0.29	0.07	0.13	0.46
Cthe_02626	UDP-N-acetylmuramate-alanine ligase	11.08	12.12	11.13	11	-0.05	1.12	-1.04	0.13	-0.78	1.06	-1.49	0.45	0.07	0.13	0.48
Cthe_00712	cytidylate kinase	12.95	13.41	12.2	12.49	0.75	0.92	-0.46	-0.29	0.04	0.76	-0.76	-0.18	0.07	0.13	0.55
Cthe_02885	phosphoribosylaminoimidazole-succinocarboxamid	11.86	11.95	10.83	11.27	1.03	0.68	-0.09	-0.44	0.33	0.41	-0.3	-0.41	0.07	0.13	0.58
Cthe_00717	MCP methyltransferase, CheR-type	11.55	10.4	9.83	9.8	1.72	0.6	1.15	0.03	1.03	0.29	1.25	0.3	0.07	0.13	0.47
Cthe_02818	CheA signal transduction histidine kinases	10.17	8.29	7.99	8.87	2.18	-0.58	1.88	-0.88	1.5	-1.44	2.16	-1.08	0.07	0.13	0.48
Cthe_02819	methyl-accepting chemotaxis sensory transducer	8.65	7.48	6.49	7.72	2.16	-0.24	1.17	-1.23	1.48	-0.94	1.27	-1.61	0.07	0.13	0.48
Cthe_00418	Polyribonucleotide nucleotidyltransferase	14.05	14.34	12.02	13.3	2.03	1.04	-0.29	-1.28	1.35	0.94	-0.55	-1.68	0.07	0.13	0.52
Cthe_02541	nitrite and sulphite reductase 4Fe-4S region	5.78	4.7	4	4.17	1.78	0.53	1.08	-0.17	1.09	0.19	1.16	0	0.07	0.13	0.54
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_03120	pyruvate flavodoxin/ferredoxin	14.4	15.19	12.96	13.88	1.44	1.31	-0.79	-0.92	0.74	1.34	-1.18	-1.14	0.07	0.13	0.52
Cthe_01321	chaperone protein DnaI	9.63	9.51	9.02	9.02	0.61	0.49	0.12	0	-0.1	0.13	-0.04	0.26	0.07	0.13	0.35
Cthe_02497	hypothetical protein	3	1.58	1	0	2	1.58	1.42	1	1.32	1.74	1.59	1.77	0.07	0.13	0.52
Cthe_02480	hypothetical protein	8.07	6.63	5.67	6.51	2.4	0.12	1.44	-0.84	1.72	-0.41	1.61	-1.02	0.07	0.13	0.52
Cthe_00526	hypothetical protein	9.14	7.92	7.33	7.74	1.81	0.18	1.22	-0.41	1.12	-0.32	1.34	-0.36	0.07	0.13	0.47
Cthe_01015	hypothetical protein	9.66	8.5	7.92	7.99	1.74	0.51	1.16	-0.07	1.05	1.16	1.26	0.15	0.07	0.13	0.47
Cthe_02490	hypothetical protein	7.98	6.93	5.83	6.78	2.15	0.15	1.05	-0.95	1.47	-0.37	1.12	-1.18	0.07	0.13	0.52
Cthe_02483	hypothetical protein	7.94	6.75	5.13	6.61	2.81	0.14	1.19	-1.48	2.14	-0.38	1.3	-1.98	0.07	0.13	0.52
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_02885	phosphoribosylaminoimidazole-succinocarboxamid	11.86	11.95	10.83	11.27	1.03	0.68	-0.09	-0.44	0.33	0.41	-0.3	-0.41	0.07	0.13	0.58
Cthe_00712	cytidylate kinase	12.95	13.41	12.2	12.49	0.75	0.92	-0.46	-0.29	0.04	0.76	-0.76	-0.18	0.07	0.13	0.55
Cthe_02626	UDP-N-acetylmuramate-alanine ligase	11.08	12.12	11.13	11	-0.05	1.12	-1.04	0.13	-0.78	1.06	-1.49	0.45	0.07	0.13	0.48
Cthe_00418	Polyribonucleotide nucleotidyltransferase	14.05	14.34	12.02	13.3	2.03	1.04	-0.29	-1.28	1.35	0.94	-0.55	-1.68	0.07	0.13	0.52
Cthe_00717	MCP methyltransferase, CheR-type	11.55	10.4	9.83	9.8	1.72	0.6	1.15	0.03	1.03	0.29	1.25	0.3	0.07	0.13	0.47
Cthe_03120	pyruvate flavodoxin/ferredoxin	14.4	15.19	12.96	13.88	1.44	1.31	-0.79	-0.92	0.74	1.34	-1.18	-1.14	0.07	0.13	0.52
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_02885	phosphoribosylaminoimidazole-succinocarboxamid	11.86	11.95	10.83	11.27	1.03	0.68	-0.09	-0.44	0.33	0.41	-0.3	-0.41	0.07	0.13	0.58
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_02885	phosphoribosylaminoimidazole-succinocarboxamid	11.86	11.95	10.83	11.27	1.03	0.68	-0.09	-0.44	0.33	0.41	-0.3	-0.41	0.07	0.13	0.58
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_03091	hydro-lyases, Fe-S type, tartrate/fumarate	11.6	11.54	10.44	10.95	1.16	0.59	0.06	-0.51	0.46	0.28	-0.11	-0.52	0.07	0.13	0.57
Cthe_02626	UDP-N-acetylmuramate-alanine ligase	11.08	12.12	11.13	11	-0.05	1.12	-1.04	0.13	-0.78	1.06	-1.49	0.45	0.07	0.13	0.48
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.82	12.42	1.13	0.97	-0.44	-0.6	0.43	0.84	-0.74	-0.65	0.07	0.13	0.54
Cthe_01760	penicillin-binding protein, 1A family	12.95	13.39	11.												



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Cthe_02105	DNA-directed DNA polymerase	9.51	9.45	8.2	8.89	1.31	0.56	0.06	-0.69	0.61	0.24	-0.11	-0.79	0.05	0.1	0.46
Cthe_02374	DNA replication and repair protein RecF	9.67	10.09	8.19	9.12	1.48	0.97	-0.42	-0.93	0.79	0.84	-0.71	-1.15	0.05	0.1	0.48
Cthe_00948	oxidoreductase FAD/NAD(P)-binding	10.47	10.94	8.68	9.82	1.79	1.12	-0.47	-1.14	1.1	1.06	-0.77	-1.47	0.05	0.1	0.52
Cthe_00478	CheC, inhibitor of MCP methylation	12.86	11.28	10.64	10.82	2.22	0.46	1.58	-0.18	1.54	0.09	1.79	-0.02	0.05	0.1	0.48
Cthe_00229	NAD-dependent epimerase/dehydratase	10.82	10.78	9.74	10.2	1.08	0.58	0.04	-0.46	0.38	0.26	-0.14	-0.44	0.05	0.1	0.56
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	12.53	12.19	11.6	11.55	0.93	0.64	0.34	0.05	0.22	0.35	0.24	0.33	0.05	0.1	0.57
Cthe_00478	CheC, inhibitor of MCP methylation	12.86	11.28	10.64	10.82	2.22	0.46	1.58	-0.18	1.54	0.09	1.79	-0.02	0.05	0.1	0.48
Cthe_00573	protein serine/threonine phosphatases	11.73	11.64	10.77	11.18	0.96	0.46	0.09	-0.41	0.26	0.09	-0.07	-0.36	0.05	0.1	0.42
Cthe_01590	peptidase M56, BlaR1	10.3	9.22	8.63	8.75	1.67	0.47	1.08	-0.12	0.98	0.1	1.16	0.08	0.05	0.1	0.48
Cthe_02313	protein of unknown function DUF218	9.46	9.32	8.47	8.89	0.99	0.43	0.14	-0.42	0.29	0.04	-0.01	-0.38	0.05	0.1	0.43
Cthe_00722	tRNA	12.13	13.36	11.17	11.81	0.96	1.55	-1.23	-0.64	0.26	1.69	-1.72	-0.71	0.05	0.1	0.52
Cthe_01751	RNA methyltransferase, TrmA family	7.59	6.79	6.07	6.48	1.52	0.31	0.8	-0.41	0.83	-0.13	0.81	-0.36	0.05	0.1	0.53
Cthe_02224	putative methionyl-tRNA formyltransferase	6.74	7.15	6.21	6.38	0.53	0.77	-0.41	-0.17	-0.18	0.54	-0.7	0	0.05	0.1	0.46
Cthe_00948	oxidoreductase FAD/NAD(P)-binding	10.47	10.94	8.68	9.82	1.79	1.12	-0.47	-1.14	1.1	1.06	-0.77	-1.47	0.05	0.1	0.52
Cthe_02434	electron transport complex, RnfABCDGE type, A	9.72	10.48	8.38	9.27	1.34	1.21	-0.76	-0.89	0.64	1.19	-1.14	-1.09	0.05	0.1	0.48
Cthe_01602	phosphate ABC transporter, ATPase subunit	7.43	7.25	6.63	6.82	0.8	0.43	0.18	-0.19	0.09	0.04	0.04	-0.03	0.05	0.1	1.11
Cthe_03000	phosphate transporter	12.75	13.24	11.31	12.22	1.44	1.02	-0.49	-0.91	0.74	0.91	-0.8	-1.12	0.05	0.1	0.48
Cthe_01415	ABC transporter related protein	7.08	6.38	5.61	6.09	1.47	0.29	0.7	-0.48	0.78	-0.16	0.69	-0.47	0.05	0.1	0.54
Cthe_00857	protein of unknown function DUF107	11.08	11.46	10.38	10.68	0.7	0.78	-0.38	-0.3	-0.01	0.56	-0.66	-0.2	0.05	0.1	0.46
Cthe_01189	ABC transporter related protein	9.42	10.18	8.35	8.98	1.07	1.2	-0.76	-0.63	0.37	1.18	-1.14	-0.7	0.05	0.1	0.52
Cthe_00229	NAD-dependent epimerase/dehydratase	10.82	10.78	9.74	10.2	1.08	0.58	0.04	-0.46	0.38	0.26	-0.14	-0.44	0.05	0.1	0.56
Cthe_01602	phosphate ABC transporter, ATPase subunit	7.43	7.25	6.63	6.82	0.8	0.43	0.18	-0.19	0.09	0.04	0.04	-0.03	0.05	0.1	1.11
Cthe_02105	DNA-directed DNA polymerase	9.51	9.45	8.2	8.89	1.31	0.56	0.06	-0.69	0.61	0.24	-0.11	-0.79	0.05	0.1	0.46
Cthe_01796	Prephenate dehydrogenase	14.29	14.53	13.2	13.73	1.09	0.8	-0.24	-0.53	0.39	0.59	-0.49	-0.55	0.05	0.1	0.54
Cthe_00290	Homoserine dehydrogenase	11.68	11.92	10.33	11.07	1.35	0.85	-0.24	-0.74	0.65	0.66	-0.49	-0.86	0.05	0.1	0.53
Cthe_00290	Homoserine dehydrogenase	11.68	11.92	10.33	11.07	1.35	0.85	-0.24	-0.74	0.65	0.66	-0.49	-0.86	0.05	0.1	0.53
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	12.53	12.19	11.6	11.55	0.93	0.64	0.34	0.05	0.22	0.35	0.24	0.33	0.05	0.1	0.57
Cthe_01796	Prephenate dehydrogenase	14.29	14.53	13.2	13.73	1.09	0.8	-0.24	-0.53	0.39	0.59	-0.49	-0.55	0.05	0.1	0.54
Cthe_00290	Homoserine dehydrogenase	11.68	11.92	10.33	11.07	1.35	0.85	-0.24	-0.74	0.65	0.66	-0.49	-0.86	0.05	0.1	0.53
Cthe_02224	putative methionyl-tRNA formyltransferase	6.74	7.15	6.21	6.38	0.53	0.77	-0.41	-0.17	-0.18	0.54	-0.7	0	0.05	0.1	0.46
Cthe_01602	phosphate ABC transporter, ATPase subunit	7.43	7.25	6.63	6.82	0.8	0.43	0.18	-0.19	0.09	0.04	0.04	-0.03	0.05	0.1	1.11
Cthe_02105	DNA-directed DNA polymerase	9.51	9.45	8.2	8.89	1.31	0.56	0.06	-0.69	0.61	0.24	-0.11	-0.79	0.05	0.1	0.46
Cthe_00722	tRNA	12.13	13.36	11.17	11.81	0.96	1.55	-1.23	-0.64	0.26	1.69	-1.72	-0.71	0.05	0.1	0.52
Cthe_00573	protein serine/threonine phosphatases	11.73	11.64	10.77	11.18	0.96	0.46	0.09	-0.41	0.26	0.09	-0.07	-0.36	0.05	0.1	0.42
Cthe_00229	NAD-dependent epimerase/dehydratase	10.82	10.78	9.74	10.2	1.08	0.58	0.04	-0.46	0.38	0.26	-0.14	-0.44	0.05	0.1	0.56
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	12.53	12.19	11.6	11.55	0.93	0.64	0.34	0.05	0.22	0.35	0.24	0.33	0.05	0.1	0.57
Cthe_01796	Prephenate dehydrogenase	14.29	14.53	13.2	13.73	1.09	0.8	-0.24	-0.53	0.39	0.59	-0.49	-0.55	0.05	0.1	0.54
Cthe_00722	tRNA	12.13	13.36	11.17	11.81	0.96	1.55	-1.23	-0.64	0.26	1.69	-1.72	-0.71	0.05	0.1	0.52
Cthe_00722	tRNA	12.13	13.36	11.17	11.81	0.96	1.55	-1.23	-0.64	0.26	1.69	-1.72	-0.71	0.05	0.1	0.52
Cthe_00229	NAD-dependent epimerase/dehydratase	10.82	10.78	9.74	10.2	1.08	0.58	0.04	-0.46	0.38	0.26	-0.14	-0.44	0.05	0.1	0.56
Cthe_00229	NAD-dependent epimerase/dehydratase	10.82	10.78	9.74	10.2	1.08	0.58	0.04	-0.46	0.38	0.26	-0.14	-0.44	0.05	0.1	0.56
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	12.53	12.19	11.6	11.55	0.93	0.64	0.34	0.05	0.22	0.35	0.24	0.33	0.05	0.1	0.57
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	12.53	12.19	11.6	11.55	0.93	0.64	0.34	0.05	0.22	0.35	0.24	0.33	0.05	0.1	0.57
Cthe_00290	Homoserine dehydrogenase	11.68	11.92	10.33	11.07	1.35	0.85	-0.24	-0.74	0.65	0.66	-0.49	-0.86	0.05	0.1	0.53
Cthe_00370	conserved hypothetical radical SAM protein	9.45	10.28	8.73	9.14	0.72	1.14	-0.83	-0.41	0.01	1.09	-1.22	-0.36	0.04	0.09	0.48
Cthe_00634	serine/threonine protein kinase	12.5	12.35	11.16	11.8	1.34	0.55	0.15	-0.64	0.64	0.22	0	-0.71	0.04	0.09	0.54
Cthe_01482	Cof-like hydrolase	10.23	10.11	9.14	9.64	1.09	0.47	0.12	-0.5	0.39	0.1	-0.04	-0.5	0.04	0.09	0.45
Cthe_02162	peptidase C26	8.84	8.82	8.09	8.29	0.75	0.53	0.02	-0.2	0.04	0.19	-0.16	-0.05	0.04	0.09	0.65
Cthe_02580	phosphodiesterase, MJ0936 family	8.5	9.23	7.94	8.14	0.56	1.09	-0.73	-0.2	-0.15	1.01	-1.1	-0.05	0.04	0.09	0.52
Cthe_00357	alpha-glucan phosphorylases	13.1	13.06	12.55	12.45	0.55	0.61	0.04	0.1	-0.16	0.31	-0.14	0.41	0.04	0.09	0.45
Cthe_03167	glucose-1-phosphate adenylyltransferase, GlgD	11.11	10.97	10	10.47	1.11	0.5	0.14	-0.47	0.41	0.15	-0.01	-0.45	0.04	0.09	0.54
Cthe_00634	serine/threonine protein kinase	12.5	12.35	11.16	11.8	1.34	0.55	0.15	-0.64	0.64	0.22	0	-0.71	0.04	0.09	0.54
Cthe_01825	multi-sensor hybrid histidine kinase	5.78	5.39	4.46	5.09	1.32	0.3	0.39	-0.63	0.62	-0.15	0.3	-0.7	0.04	0.09	0.47
Cthe_00962	dihydrodipicolinate synthase	13.25	14.79	12.33	13.05	0.92	1.74	-1.54	-0.72	0.21	1.97	-2.11	-0.83	0.04	0.09	0.49
Cthe_02260	Prephenate dehydratase	11.52	11.64	10.27	10.91	1.25	0.73	-0.12	-0.64	0.55	0.49	-0.34	-0.71	0.04	0.09	0.53
Cthe_00001	Recombinase	11.53	11.28	10.63	10.88	0.9	0.4	0.25	-0.25	0.19	0	0.12	-0.12	0.04	0.09	0.63
Cthe_00634	serine/threonine protein kinase	12.5	12.35	11.16	11.8	1.34	0.55	0.15	-0.64	0.64	0.22	0	-0.71	0.04	0.09	0.54
Cthe_03207	transposase, mutator type			1.58		-1.58	2	-2	1.58	-2.34	2.35	-2.69	2.65	0.04	0.09	0.49
Cthe_01679	Methyltransferase type 11	7.29	6.67	4.91	6.25	2.38	0.42	0.62	-1.34	1.7	0.03	0.59	-1.77	0.04	0.09	0.51
Cthe_00962	dihydrodipicolinate synthase	13.25	14.79	12.33	13.05	0.92	1.74	-1.54	-0.72	0.21	1.97	-2.11	-0.83	0.04	0.09	0.49
Cthe_02562	glucose-1-phosphate cytidylyltransferase	10.6	10.19	8.86	9.75	1.74	0.44	0.41	-0.89	1.05	0.06	0.33	-1.09	0.04	0.09	0.52
Cthe_00741	adenylosuccinate lyase	12	12.62	10.77	11.5	1.23	1.12	-0.62	-0.73	0.53	1.06	-0.96	-0.85	0.04	0.09	0.52
Cthe_02254	hypoxanthine phosphoribosyltransferase	11.17	10.62	9.77	10.31	1.4	0.31	0.55	-0.54	0.7	-0.13	0.5	-0.56	0.04	0.09	0.53
Cthe_00634	serine/threonine protein kinase	12.5	12.35	11.16	11.8	1.34	0.55	0.15	-0.64	0.64	0.22	0	-0.71	0.04	0.09	0.54
Cthe_01825	multi-sensor hybrid histidine kinase	5.78	5.39	4.46	5.09	1.32	0.3	0.39	-0.63	0.62	-0.15	0.3	-0.7	0.04	0.09	0.47
Cthe_01944	protein of unknown function DUF458	14.25	13.32	12.54	13.12	1.71	0.2	0.93	-0.58	1.02	-0.29	0.97	-0.62	0.04	0.09	0.52
Cthe_02368	protein of unknown function DUF37	10.03	9.86	8.97	9.44	1.06	0.42	0.17	-0.47	0.36	0.03	0.03	-0.45	0.04	0.09	0.45
Cthe_02562	glucose-1-phosphate cytidylyltransferase	10.6	10.19	8.86	9.75	1.74	0.44	0.41	-0.89	1.05	0.06	0.33	-1.09	0.04	0.09	0.52
Cthe_01145	N-6 DNA methylase	9.73	10.25	9.27	9.4	0.46	0.85	-0.52	-0.13	-0.26	0.66	-0.84	0.06	0.04	0.09	0.47
Cthe_00455	Mg chelatase, subunit ChlI	10.16	10.03	8.71	9.45	1.45	0.58	0.13	-0.74	0.76	0.26	-0.02	-0.86	0.04	0.09	0.52
Cthe_01401	hypothetical protein	10.97	10.08	9.31	10.22	1.66	-0.14	0.89	-0.91	0.97	-0.79	0.92	-1.12	0.04	0.09	0.48
Cthe_01994	hypothetical protein	6.04	5	3.91	5.04	2.13	-0.04	1.04	-1.13	1.45	-0.65	1.11	-1.45	0.04	0.09	0.49
Cthe_00940	hypothetical protein	7.81	7.51	6.73	7.12	1.08	0.39	0.3	-0.39	0.38	-0.01	0.19	-0.33	0.04	0.09	0.56
Cthe_02009	intein	6.81	5.86	5.29	5.73	1.52	0.13	0.95	-0.44	0.83	-0.4	1	-0.41	0.04	0.09	0.48
Cthe_01624	hypothetical protein	2.58	2	1.58	0	1	2	0.58	1.58	0.3	2.35	0.54	2.65	0.04	0.09	0.49



Cthe_00962	dihydrodipicolinate synthase	13.25	14.79	12.33	13.05	0.92	1.74	-1.54	-0.72	0.21	1.97	-2.11	-0.83	0.04	0.09	0.49
Cthe_02254	hypoxanthine phosphoribosyltransferase	11.17	10.62	9.77	10.31	1.4	0.31	0.55	-0.54	0.7	-0.13	0.5	-0.56	0.04	0.09	0.53
Cthe_00741	adenylosuccinate lyase	12	12.62	10.77	11.5	1.23	1.12	-0.62	-0.73	0.53	1.06	-0.96	-0.85	0.04	0.09	0.52
Cthe_00741	adenylosuccinate lyase	12	12.62	10.77	11.5	1.23	1.12	-0.62	-0.73	0.53	1.06	-0.96	-0.85	0.04	0.09	0.52
Cthe_00357	alpha-glucan phosphorylases	13.1	13.06	12.55	12.45	0.55	0.61	0.04	0.1	-0.16	0.31	-0.14	0.41	0.04	0.09	0.45
Cthe_00357	alpha-glucan phosphorylases	13.1	13.06	12.55	12.45	0.55	0.61	0.04	0.1	-0.16	0.31	-0.14	0.41	0.04	0.09	0.45
Cthe_00741	adenylosuccinate lyase	12	12.62	10.77	11.5	1.23	1.12	-0.62	-0.73	0.53	1.06	-0.96	-0.85	0.04	0.09	0.52
Cthe_00962	dihydrodipicolinate synthase	13.25	14.79	12.33	13.05	0.92	1.74	-1.54	-0.72	0.21	1.97	-2.11	-0.83	0.04	0.09	0.49
Cthe_02260	Prephenate dehydratase	11.52	11.64	10.27	10.91	1.25	0.73	-0.12	-0.64	0.55	0.49	-0.34	-0.71	0.04	0.09	0.53
Cthe_01546	4Fe-4S ferredoxin, iron-sulfur binding	9.97	10.41	9.24	9.56	0.73	0.85	-0.44	-0.32	0.02	0.66	-0.74	-0.23	0.03	0.08	0.48
Cthe_02453	hypothetical protein	10.52	9.57	8.99	8.94	1.53	0.63	0.95	0.05	0.84	0.34	1	0.33	0.03	0.08	0.48
Cthe_01826	response regulator receiver sensor signal	12.01	11.33	10.57	11.07	1.44	0.26	0.68	-0.5	0.74	-0.21	0.66	-0.5	0.03	0.08	0.52
Cthe_01456	ABC transporter related protein	8.87	10.44	7.57	8.6	1.3	1.84	-1.57	-1.03	0.6	2.12	-2.15	-1.3	0.03	0.08	0.49
Cthe_02630	ribose-phosphate pyrophosphokinase	11.91	12.1	11.3	11.43	0.61	0.67	-0.19	-0.13	-0.1	0.4	-0.42	0.06	0.03	0.08	0.55
Cthe_02886	imidazole glycerol phosphate synthase, glutamine	10.05	10.26	9.08	9.55	0.97	0.71	-0.21	-0.47	0.27	0.46	-0.45	-0.45	0.03	0.08	0.47
Cthe_00585	Integrase, catalytic region	13.66	13.38	12.7	13.1	0.96	0.28	0.28	-0.4	0.26	-0.18	0.16	-0.35	0.03	0.08	0.46
Cthe_00757	DNA repair protein RadC	9.44	9	8.41	8.41	0.3	0.52	0.44	-0.07	0.33	0.18	0.36	0.15	0.03	0.08	0.54
Cthe_02376	DNA gyrase, B subunit	13.81	13.87	12.53	13.21	1.28	0.66	-0.06	-0.68	0.58	0.38	-0.26	-0.77	0.03	0.08	0.48
Cthe_02858	transposase, mutator type	4.09	4.39	3.58	3.7	0.51	0.69	-0.3	-0.12	-0.2	0.43	-0.56	0.08	0.03	0.08	0.47
Cthe_02308	CheC-like protein	6.78	6.32	5.17	6	1.61	0.32	0.46	-0.83	0.92	-0.12	0.39	-1	0.03	0.08	0.49
Cthe_03005	Peptidoglycan-binding LysM	5	3.32	2.58	3.32	2.42	0	1.68	-0.74	1.74	-0.59	1.91	-0.86	0.03	0.08	0.49
Cthe_00954	Uracil phosphoribosyltransferase	13.13	11.23	10.51	11.01	2.62	0.22	1.9	-0.5	1.95	-0.26	2.19	-0.5	0.03	0.08	0.49
Cthe_02630	ribose-phosphate pyrophosphokinase	11.91	12.1	11.3	11.43	0.61	0.67	-0.19	-0.13	-0.1	0.4	-0.42	0.06	0.03	0.08	0.55
Cthe_01826	response regulator receiver sensor signal	12.01	11.33	10.57	11.07	1.44	0.26	0.68	-0.5	0.74	-0.21	0.66	-0.5	0.03	0.08	0.52
Cthe_00052	hypothetical protein	13.23	12.96	12.21	12.57	1.02	0.39	0.27	-0.36	0.32	-0.01	0.15	-0.29	0.03	0.08	0.55
Cthe_00150	RNA modification enzyme, MiaB family	9.33	9.21	8.61	8.8	0.72	0.41	0.12	-0.19	0.01	0.01	-0.04	-0.03	0.03	0.08	0.16
Cthe_00723	tyrosyl-tRNA synthetase	12.2	12.93	11.18	11.77	1.02	1.16	-0.73	-0.59	0.32	1.12	-1.1	-0.64	0.03	0.08	0.51
Cthe_00626	hypothetical protein	11.73	12.16	11.15	11.31	0.58	0.85	-0.43	-0.16	-0.13	0.66	-0.72	0.02	0.03	0.08	0.52
Cthe_02181	predicted ATPase of the PP-loop superfamily	11.53	10.38	9.65	10.09	1.88	0.29	1.15	-0.44	1.19	-0.16	1.25	-0.41	0.03	0.08	0.51
Cthe_02405	Heavy metal transport/detoxification protein	9.55	9.23	8.72	8.35	0.83	0.88	0.32	0.37	0.12	0.71	0.21	0.82	0.03	0.08	0.48
Cthe_01424	hypothetical protein	13.19	12.53	11.57	12.29	1.62	0.24	0.66	-0.72	0.93	-0.24	0.64	-0.83	0.03	0.08	0.51
Cthe_00525	hypothetical protein	9.09	7.83	7.18	7.49	1.91	0.34	1.26	-0.31	1.22	-0.09	1.39	-0.21	0.03	0.08	0.49
Cthe_01296	hypothetical protein	11.43	9.93	9.24	9.77	2.19	0.16	1.5	-0.53	1.51	-0.35	1.69	-0.55	0.03	0.08	0.49
Cthe_01577	hypothetical protein	8.25	8.28	7.8	7.22	0.45	1.06	-0.03	0.58	-0.27	0.97	-0.22	1.14	0.03	0.08	0.49
Cthe_02485	hypothetical protein	8.59	7.18	6.43	7.4	2.16	-0.22	1.41	-0.97	1.48	-0.91	1.57	-1.21	0.03	0.08	0.49
Cthe_00041	hypothetical protein	8.38	7.53	6.91	6.94	1.47	0.59	0.85	-0.03	0.78	0.28	0.87	0.21	0.03	0.08	0.52
Cthe_02465	hypothetical protein	6.98	6.02	5.43	5.95	1.55	0.07	0.96	-0.52	0.86	-0.49	1.01	-0.53	0.03	0.08	0.49
Cthe_02200	hypothetical protein	6.07	5.73	4.91	5.43	1.16	0.3	0.34	-0.52	0.46	-0.15	0.24	-0.53	0.03	0.08	0.47
Cthe_00264	hypothetical protein	6.27	4.81	4.09	4.91	2.18	-0.1	1.46	-0.82	1.5	-0.74	1.64	-0.98	0.03	0.08	0.49
Cthe_02886	imidazole glycerol phosphate synthase, glutamine	10.05	10.26	9.08	9.55	0.97	0.71	-0.21	-0.47	0.27	0.46	-0.45	-0.45	0.03	0.08	0.47
Cthe_00723	tyrosyl-tRNA synthetase	12.2	12.93	11.18	11.77	1.02	1.16	-0.73	-0.59	0.32	1.12	-1.1	-0.64	0.03	0.08	0.51
Cthe_02630	ribose-phosphate pyrophosphokinase	11.91	12.1	11.3	11.43	0.61	0.67	-0.19	-0.13	-0.1	0.4	-0.42	0.06	0.03	0.08	0.55
Cthe_00723	tyrosyl-tRNA synthetase	12.2	12.93	11.18	11.77	1.02	1.16	-0.73	-0.59	0.32	1.12	-1.1	-0.64	0.03	0.08	0.51
Cthe_01456	ABC transporter related protein	8.87	10.44	7.57	8.6	1.3	1.84	-1.57	-1.03	0.6	2.12	-2.15	-1.3	0.03	0.08	0.49
Cthe_02886	imidazole glycerol phosphate synthase, glutamine	10.05	10.26	9.08	9.55	0.97	0.71	-0.21	-0.47	0.27	0.46	-0.45	-0.45	0.03	0.08	0.47
Cthe_00150	RNA modification enzyme, MiaB family	9.33	9.21	8.61	8.8	0.72	0.41	0.12	-0.19	0.01	0.01	-0.04	-0.03	0.03	0.08	0.16
Cthe_02376	DNA gyrase, B subunit	13.81	13.87	12.53	13.21	1.28	0.66	-0.06	-0.68	0.58	0.38	-0.26	-0.77	0.03	0.08	0.48
Cthe_02630	ribose-phosphate pyrophosphokinase	11.91	12.1	11.3	11.43	0.61	0.67	-0.19	-0.13	-0.1	0.4	-0.42	0.06	0.03	0.08	0.55
Cthe_00954	Uracil phosphoribosyltransferase	13.13	11.23	10.51	11.01	2.62	0.22	1.9	-0.5	1.95	-0.26	2.19	-0.5	0.03	0.08	0.49
Cthe_01456	ABC transporter related protein	8.87	10.44	7.57	8.6	1.3	1.84	-1.57	-1.03	0.6	2.12	-2.15	-1.3	0.03	0.08	0.49
Cthe_00723	tyrosyl-tRNA synthetase	12.2	12.93	11.18	11.77	1.02	1.16	-0.73	-0.59	0.32	1.12	-1.1	-0.64	0.03	0.08	0.51
Cthe_00954	Uracil phosphoribosyltransferase	13.13	11.23	10.51	11.01	2.62	0.22	1.9	-0.5	1.95	-0.26	2.19	-0.5	0.03	0.08	0.49
Cthe_02886	imidazole glycerol phosphate synthase, glutamine	10.05	10.26	9.08	9.55	0.97	0.71	-0.21	-0.47	0.27	0.46	-0.45	-0.45	0.03	0.08	0.47
Cthe_02630	ribose-phosphate pyrophosphokinase	11.91	12.1	11.3	11.43	0.61	0.67	-0.19	-0.13	-0.1	0.4	-0.42	0.06	0.03	0.08	0.55
Cthe_02886	imidazole glycerol phosphate synthase, glutamine	10.05	10.26	9.08	9.55	0.97	0.71	-0.21	-0.47	0.27	0.46	-0.45	-0.45	0.03	0.08	0.47
Cthe_01456	ABC transporter related protein	8.87	10.44	7.57	8.6	1.3	1.84	-1.57	-1.03	0.6	2.12	-2.15	-1.3	0.03	0.08	0.49
Cthe_00954	Uracil phosphoribosyltransferase	13.13	11.23	10.51	11.01	2.62	0.22	1.9	-0.5	1.95	-0.26	2.19	-0.5	0.03	0.08	0.49
Cthe_00723	tyrosyl-tRNA synthetase	12.2	12.93	11.18	11.77	1.02	1.16	-0.73	-0.59	0.32	1.12	-1.1	-0.64	0.03	0.08	0.51
Cthe_01456	ABC transporter related protein	8.87	10.44	7.57	8.6	1.3	1.84	-1.57	-1.03	0.6	2.12	-2.15	-1.3	0.03	0.08	0.49
Cthe_02886	imidazole glycerol phosphate synthase, glutamine	10.05	10.26	9.08	9.55	0.97	0.71	-0.21	-0.47	0.27	0.46	-0.45	-0.45	0.03	0.08	0.47
Cthe_01456	ABC transporter related protein	8.87	10.44	7.57	8.6	1.3	1.84	-1.57	-1.03	0.6	2.12	-2.15	-1.3	0.03	0.08	0.49
Cthe_00145	metal dependent phosphohydrolase	12.97	12.58	12.04	12.29	0.93	0.29	0.39	-0.25	0.22	-0.16	0.3	-0.12	0.02	0.06	0.47
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_01229	Spore germination protein-like protein	10.48	10.97	10.19	10.11	0.29	0.86	-0.49	0.08	-0.43	0.68	-0.8	0.38	0.02	0.06	0.51
Cthe_00607	peptidase M42	8.49	8.54	7.43	7.91	1.06	0.63	-0.05	-0.48	0.36	0.34	-0.25	-0.47	0.02	0.06	0.52
Cthe_01844	transcriptional regulator, BadM/Rrf2 family	10.2	10.28	9.43	9.68	0.77	0.6	-0.08	-0.25	0.06	0.29	-0.29	-0.12	0.02	0.06	0.53
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_00610	histidinol-phosphate aminotransferase	8.53	9.19	7.75	8.16	0.78	1.03	-0.66	-0.41	0.07	0.93	-1.01	-0.36	0.02	0.06	0.49
Cthe_00672	pyrroline-5-carboxylate reductase	10.82	10.26	9.69	9.95	1.13	0.31	0.56	-0.26	0.43	-0.13	0.51	-0.14	0.02	0.06	0.48
Cthe_01457	polar amino acid ABC transporter, inner membrane	9.11	10.45	7.33	8.67	1.78	1.78	-1.34	-1.34	1.09	2.03	-1.86	-1.77	0.02	0.06	0.5
Cthe_02509	DNA topoisomerase	9.14	8.37	7.85	8.31	1.29	0.06	0.77	-0.46	0.59	-0.5	0.77	-0.44	0.02	0.06	0.49
Cthe_01063	thiamine biosynthesis/trRNA modification protein	11.63	11.84	10.76	11.12	0.87	0.72	-0.21	-0.36	0.16	0.47	-0.45	-0.29	0.02	0.06	0.52
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimidazole	6.52	6.57	5.55	5.98	0.97	0.59	-0.05	-0.43	0.27	0.28	-0.25	-0.39	0.02	0.06	0.47
Cthe_02582	dihydroneopterin aldolase	8.23	8.31	7.63	7.71	0.6	0.6	-0.08	-0.08	-0.11	0.29	-0.29	0.14	0.02	0.06	0.54
Cthe_02621	protein of unknown function DUF1078-like protein	7.26	7.62	5.81	6.67	1.45	0.95	-0.36	-0.86	0.76	0.81	-0.64	-1.05</			



Cthe_00610	histidinol-phosphate aminotransferase	8.53	9.19	7.75	8.16	0.78	1.03	-0.66	-0.41	0.07	0.93	-1.01	-0.36	0.02	0.06	0.49
Cthe_02582	dihydroneopterin aldolase	8.23	8.31	7.63	7.71	0.6	0.6	-0.08	-0.08	-0.11	0.29	-0.29	0.14	0.02	0.06	0.54
Cthe_00610	histidinol-phosphate aminotransferase	8.53	9.19	7.75	8.16	0.78	1.03	-0.66	-0.41	0.07	0.93	-1.01	-0.36	0.02	0.06	0.49
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimidazole	6.52	6.57	5.55	5.98	0.97	0.59	-0.05	-0.43	0.27	0.28	-0.25	-0.39	0.02	0.06	0.47
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimidazole	6.52	6.57	5.55	5.98	0.97	0.59	-0.05	-0.43	0.27	0.28	-0.25	-0.39	0.02	0.06	0.47
Cthe_02582	dihydroneopterin aldolase	8.23	8.31	7.63	7.71	0.6	0.6	-0.08	-0.08	-0.11	0.29	-0.29	0.14	0.02	0.06	0.54
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_00607	peptidase M42	8.49	8.54	7.43	7.91	1.06	0.63	-0.05	-0.48	0.36	0.34	-0.25	-0.47	0.02	0.06	0.52
Cthe_00672	pyrroline-5-carboxylate reductase	10.82	10.26	9.69	9.95	1.13	0.31	0.56	-0.26	0.43	-0.13	0.51	-0.14	0.02	0.06	0.48
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_00610	histidinol-phosphate aminotransferase	8.53	9.19	7.75	8.16	0.78	1.03	-0.66	-0.41	0.07	0.93	-1.01	-0.36	0.02	0.06	0.49
Cthe_00672	pyrroline-5-carboxylate reductase	10.82	10.26	9.69	9.95	1.13	0.31	0.56	-0.26	0.43	-0.13	0.51	-0.14	0.02	0.06	0.48
Cthe_00610	histidinol-phosphate aminotransferase	8.53	9.19	7.75	8.16	0.78	1.03	-0.66	-0.41	0.07	0.93	-1.01	-0.36	0.02	0.06	0.49
Cthe_02582	dihydroneopterin aldolase	8.23	8.31	7.63	7.71	0.6	0.6	-0.08	-0.08	-0.11	0.29	-0.29	0.14	0.02	0.06	0.54
Cthe_00672	pyrroline-5-carboxylate reductase	10.82	10.26	9.69	9.95	1.13	0.31	0.56	-0.26	0.43	-0.13	0.51	-0.14	0.02	0.06	0.48
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimidazole	6.52	6.57	5.55	5.98	0.97	0.59	-0.05	-0.43	0.27	0.28	-0.25	-0.39	0.02	0.06	0.47
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimidazole	6.52	6.57	5.55	5.98	0.97	0.59	-0.05	-0.43	0.27	0.28	-0.25	-0.39	0.02	0.06	0.47
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimidazole	6.52	6.57	5.55	5.98	0.97	0.59	-0.05	-0.43	0.27	0.28	-0.25	-0.39	0.02	0.06	0.47
Cthe_00607	peptidase M42	8.49	8.54	7.43	7.91	1.06	0.63	-0.05	-0.48	0.36	0.34	-0.25	-0.47	0.02	0.06	0.52
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimidazole	6.52	6.57	5.55	5.98	0.97	0.59	-0.05	-0.43	0.27	0.28	-0.25	-0.39	0.02	0.06	0.47
Cthe_00672	pyrroline-5-carboxylate reductase	10.82	10.26	9.69	9.95	1.13	0.31	0.56	-0.26	0.43	-0.13	0.51	-0.14	0.02	0.06	0.48
Cthe_00672	pyrroline-5-carboxylate reductase	10.82	10.26	9.69	9.95	1.13	0.31	0.56	-0.26	0.43	-0.13	0.51	-0.14	0.02	0.06	0.48
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_00672	pyrroline-5-carboxylate reductase	10.82	10.26	9.69	9.95	1.13	0.31	0.56	-0.26	0.43	-0.13	0.51	-0.14	0.02	0.06	0.48
Cthe_00372	glutamate synthase (NADPH), homotetrameric	11.23	11.53	9.95	10.66	1.28	0.87	-0.3	-0.71	0.58	0.69	-0.56	-0.82	0.02	0.06	0.51
Cthe_01985	phage major capsid protein, HK97	4.09	3	2.32	2.81	1.77	0.19	1.09	-0.49	1.08	-0.31	1.18	-0.48	0.01	0.05	0.5
Cthe_00015	alpha-L-arabinofuranosidase B	10.06	8.72	8.01	8.6	2.05	0.12	1.34	-0.59	1.37	-0.41	1.49	-0.64	0.01	0.05	0.5
Cthe_01838	glycoside hydrolase, family 10	15.56	15.12	14.45	14.91	1.11	0.21	0.44	-0.46	0.41	-0.28	0.36	-0.44	0.01	0.05	0.49
Cthe_02382	major facilitator superfamily MFS_1	10.9	10.72	9.63	10.23	1.27	0.49	0.18	-0.6	0.57	0.13	0.04	-0.65	0.01	0.05	0.5
Cthe_02735	HPNtr domain containing protein	7.77	7.42	6.81	7.16	0.96	0.26	0.35	-0.35	0.26	-0.21	0.25	-0.27	0.01	0.05	0.51
Cthe_00315	DNA-directed RNA polymerase sigma factor	7.06	6.89	6.3	6.52	0.76	0.37	0.17	-0.22	0.05	-0.04	0.03	-0.08	0.01	0.05	0.42
Cthe_00644	Vitamin B12 dependent methionine synthase,	8.56	8.88	7.58	8.07	0.98	0.81	-0.32	-0.49	0.28	0.6	-0.59	-0.48	0.01	0.05	0.49
Cthe_01569	O-acetylhomoserine aminocarboxypropyltransferase	10.64	11.02	10.31	10.27	0.33	0.75	-0.38	0.04	-0.39	0.51	-0.66	0.32	0.01	0.05	0.49
Cthe_00458	exodeoxyribonuclease III Xth	11.59	11.56	10.87	11.06	0.72	0.5	0.03	-0.19	0.01	0.15	-0.15	-0.03	0.01	0.05	0.55
Cthe_00460	DNA topoisomerase I	11.19	11.63	10.2	10.72	0.99	0.91	-0.44	-0.52	0.29	0.75	-0.74	-0.53	0.01	0.05	0.5
Cthe_01066	DNA repair protein RecO	10.38	10.18	9.54	9.79	0.84	0.39	0.2	-0.25	0.13	-0.01	0.06	-0.12	0.01	0.05	0.55
Cthe_00062	sulfatase	12.47	12.74	12.22	11.89	0.25	0.85	-0.27	0.33	-0.47	0.66	-0.53	0.76	0.01	0.05	0.49
Cthe_02615	UDP-N-acetylglucosamine	10.68	11.03	10.05	10.25	0.63	0.78	-0.35	-0.2	-0.08	0.56	-0.62	-0.05	0.01	0.05	0.51
Cthe_02901	putative anti-sigma regulatory factor,	10.34	9.98	9.38	9.73	0.96	0.25	0.36	-0.35	0.26	-0.22	0.26	-0.27	0.01	0.05	0.51
Cthe_01235	Cellulose 1,4-beta-cellobiosidase	10.6	10.2	9.53	9.95	1.07	0.25	0.4	-0.42	0.37	-0.22	0.31	-0.38	0.01	0.05	0.49
Cthe_01936	hypothetical protein	8.23	8.79	7.88	7.88	0.35	0.91	-0.56	0	-0.37	0.75	-0.89	0.26	0.01	0.05	0.51
Cthe_01557	ABC transporter related protein	10.2	10.26	9.71	9.46	0.49	0.8	-0.06	0.25	-0.22	0.59	-0.26	0.64	0.01	0.05	0.51
Cthe_02386	VanW	11.52	12.06	11.13	11.17	0.39	0.89	-0.54	-0.04	-0.33	0.72	-0.86	0.2	0.01	0.05	0.5
Cthe_03230	hypothetical protein	11.28	11.82	10.43	10.86	0.85	0.96	-0.54	-0.43	0.14	0.82	-0.86	-0.39	0.01	0.05	0.49
Cthe_01872	Tn7-like transposition protein C	10.27	9.67	9.09	9.01	1.18	0.66	0.6	0.08	0.48	0.38	0.56	0.38	0.01	0.05	0.51
Cthe_02422	hypothetical protein	14.82	14.43	13.86	13.96	0.96	0.47	0.39	-0.1	0.26	0.1	0.3	0.11	0.01	0.05	0.49
Cthe_01474	hypothetical protein	5	3.58	2.81	3.46	2.19	0.12	1.42	-0.65	1.51	-0.41	1.59	-0.73	0.01	0.05	0.5
Cthe_00939	hypothetical protein	7.9	7.57	6.58	7.18	1.32	0.39	0.33	-0.6	0.62	-0.01	0.23	-0.65	0.01	0.05	0.51
Cthe_01557	ABC transporter related protein	10.2	10.26	9.71	9.46	0.49	0.8	-0.06	0.25	-0.22	0.59	-0.26	0.64	0.01	0.05	0.51
Cthe_01838	glycoside hydrolase, family 10	15.56	15.12	14.45	14.91	1.11	0.21	0.44	-0.46	0.41	-0.28	0.36	-0.44	0.01	0.05	0.49
Cthe_00458	exodeoxyribonuclease III Xth	11.59	11.56	10.87	11.06	0.72	0.5	0.03	-0.19	0.01	0.15	-0.15	-0.03	0.01	0.05	0.55
Cthe_02615	UDP-N-acetylglucosamine	10.68	11.03	10.05	10.25	0.63	0.78	-0.35	-0.2	-0.08	0.56	-0.62	-0.05	0.01	0.05	0.51
Cthe_00460	DNA topoisomerase I	11.19	11.63	10.2	10.72	0.99	0.91	-0.44	-0.52	0.29	0.75	-0.74	-0.53	0.01	0.05	0.5
Cthe_02901	putative anti-sigma regulatory factor,	10.34	9.98	9.38	9.73	0.96	0.25	0.36	-0.35	0.26	-0.22	0.26	-0.27	0.01	0.05	0.51
Cthe_01235	Cellulose 1,4-beta-cellobiosidase	10.6	10.2	9.53	9.95	1.07	0.25	0.4	-0.42	0.37	-0.22	0.31	-0.38	0.01	0.05	0.49
Cthe_01569	O-acetylhomoserine aminocarboxypropyltransferase	10.64	11.02	10.31	10.27	0.33	0.75	-0.38	0.04	-0.39	0.51	-0.66	0.32	0.01	0.05	0.49
Cthe_01569	O-acetylhomoserine aminocarboxypropyltransferase	10.64	11.02	10.31	10.27	0.33	0.75	-0.38	0.04	-0.39	0.51	-0.66	0.32	0.01	0.05	0.49
Cthe_02615	UDP-N-acetylglucosamine	10.68	11.03	10.05	10.25	0.63	0.78	-0.35	-0.2	-0.08	0.56	-0.62	-0.05	0.01	0.05	0.51
Cthe_02615	UDP-N-acetylglucosamine	10.68	11.03	10.05	10.25	0.63	0.78	-0.35	-0.2	-0.08	0.56	-0.62	-0.05	0.01	0.05	0.51
Cthe_00652	4-oxalocrotonate tautomerase	6.21	5.93	5.36	5.49	0.85	0.44	0.28	-0.13	0.14	0.06	0.16	0.06	0	0.04	0.5
Cthe_01798	CoA-binding protein	13.25	12.79	12.23	12.61	1.02	0.18	0.46	-0.38	0.32	-0.32	0.39	-0.32	0	0.04	0.5
Cthe_03168	hypothetical protein	9.69	9.99	8.52	9.15	1.17	0.84	-0.3	-0.63	0.47	0.65	-0.56	-0.7	0	0.04	0.5
Cthe_02112	two component transcriptional regulator, winged	9.69	8.88	8.23	8.71	1.46	0.17	0.81	-0.48	0.77	-0.34	0.82	-0.47	0	0.04	0.5
Cthe_00732	Chorismate synthase	13.29	13.87	11.9	12.77	1.39	1.1	-0.58	-0.87	0.69	1.03	-0.91	-1.06	0	0.04	0.5
Cthe_00306	DNA gyrase/topoisomerase IV, subunit A	9.74	10.21	9.46	9.39	0.28	0.82	-0.47	0.07	-0.44	0.62	-0.77	0.36	0	0.04	0.5
Cthe_00832	exodeoxyribonuclease VII, small subunit	6.36	6.97	6.43	6.91	-0.07	0.06	-0.61	-0.48	-0.8	-0.5	-0.95	-0.47	0	0.04	0.5
Cthe_02004	transposase	9.59	8.2	7.58	7.38	2.01	0.82	1.39	0.2	1.33	0.62	1.55	0.56	0	0.04	0.5
Cthe_00462	flagellar basal-body rod protein FlgB	12.2	11.36	12.2	11.65	0	-0.29	0.84	0.55	-0.72	-1.01	0.86	1.09	0	0.04	0.5
Cthe_02112	two component transcriptional regulator, winged	9.69	8.88	8.23	8.71	1.46	0.17	0.81	-0.48	0.77	-0.34	0.82	-0.47	0	0.04	0.5
Cthe_00060	SEC-C motif containing protein	11.24	10.94	9.84	10.51	1.4	0.43	0.3	-0.67	0.7	0.04	0.19	-0.76	0	0.04	0.5
Cthe_00242	hypothetical protein	13.04	12.51	11.91	12.3	1.13	0.21	0.53	-0.39	0.43	-0.28	0.47	-0.33	0	0.04	0.5
Cthe_00369	protein of unknown function DUF111	9.68	10.54	8.67	9.3	1.01	1.24	-0.86	-0.63	0.31	1.24	-1.26	-0.7	0	0.04	0.5
Cthe_01555	NLPA lipoprotein	10.65	10.72	10.2												



Cthe_00732	Chorismate synthase	13.29	13.87	11.9	12.77	1.39	1.1	-0.58	-0.87	0.69	1.03	-0.91	-1.06	0	0.04	0.5
Cthe_00652	4-oxalocrotonate tautomerase	6.21	5.93	5.36	5.49	0.85	0.44	0.28	-0.13	0.14	0.06	0.16	0.06	0	0.04	0.5
Cthe_00732	Chorismate synthase	13.29	13.87	11.9	12.77	1.39	1.1	-0.58	-0.87	0.69	1.03	-0.91	-1.06	0	0.04	0.5
Cthe_00652	4-oxalocrotonate tautomerase	6.21	5.93	5.36	5.49	0.85	0.44	0.28	-0.13	0.14	0.06	0.16	0.06	0	0.04	0.5
Cthe_00732	Chorismate synthase	13.29	13.87	11.9	12.77	1.39	1.1	-0.58	-0.87	0.69	1.03	-0.91	-1.06	0	0.04	0.5
Cthe_00652	4-oxalocrotonate tautomerase	6.21	5.93	5.36	5.49	0.85	0.44	0.28	-0.13	0.14	0.06	0.16	0.06	0	0.04	0.5
Cthe_03169	short-chain dehydrogenase/reductase SDR	12.86	13.1	12.2	12.4	0.66	0.7	-0.24	-0.2	-0.05	0.44	-0.49	-0.05	0	0.04	0.51
Cthe_00652	4-oxalocrotonate tautomerase	6.21	5.93	5.36	5.49	0.85	0.44	0.28	-0.13	0.14	0.06	0.16	0.06	0	0.04	0.5
Cthe_03169	short-chain dehydrogenase/reductase SDR	12.86	13.1	12.2	12.4	0.66	0.7	-0.24	-0.2	-0.05	0.44	-0.49	-0.05	0	0.04	0.51
Cthe_03169	short-chain dehydrogenase/reductase SDR	12.86	13.1	12.2	12.4	0.66	0.7	-0.24	-0.2	-0.05	0.44	-0.49	-0.05	0	0.04	0.51
Cthe_03133	alpha/beta hydrolase fold	9.64	9.85	10.28	9.46	-0.64	0.39	-0.21	0.82	-1.38	-0.01	-0.45	1.5	-0.01	0.03	0.5
Cthe_01435	Phosphoglycerate mutase	9.19	8.42	7.87	8.46	1.32	-0.04	0.77	-0.59	0.62	-0.65	0.77	-0.64	-0.01	0.03	0.5
Cthe_01787	glycoside hydrolase 15-related	11.43	11.62	11.08	10.98	0.35	0.64	-0.19	0.1	-0.37	0.35	-0.42	0.41	-0.01	0.03	0.49
Cthe_01697	transcriptional regulator, ArsR family	8.96	8.81	10.91	8.98	-1.95	-0.17	0.15	1.93	-2.71	-0.84	0	3.18	-0.01	0.03	0.5
Cthe_01809	RNA polymerase, sigma-24 subunit, ECF subfamily	12.77	12.97	14.31	12.79	-1.54	0.18	-0.2	1.52	-2.3	-0.32	-0.44	2.56	-0.01	0.03	0.5
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_02243	flagellar hook-associated protein FlgK	7.17	7.58	7.01	7.61	0.16	-0.03	-0.41	-0.6	-0.56	-0.63	-0.7	-0.65	-0.01	0.03	0.5
Cthe_00488	type IV pilus assembly PilZ	8.24	7.55	6.89	7.64	1.35	-0.09	0.69	-0.75	0.65	-0.72	0.67	-0.88	-0.01	0.03	0.49
Cthe_00775	tRNA delta(2)-isopentenylpyrophosphate	11.19	10.76	11.2	10.73	-0.01	0.03	0.43	0.47	-0.73	-0.54	0.35	0.97	-0.01	0.03	0.49
Cthe_01893	hypothetical protein	8.28	8.3	8.39	7.96	-0.11	0.34	-0.02	0.43	-0.84	-0.09	-0.21	0.91	-0.01	0.03	0.51
Cthe_01565	Nitrogenase	9.68	10.25	9.83	9.59	-0.15	0.66	-0.57	0.24	-0.88	0.38	-0.9	0.62	-0.01	0.03	0.49
Cthe_02457	hypothetical protein	10.63	9.81	9.82	9.93	0.81	-0.12	0.82	-0.11	0.1	-0.76	0.84	0.09	-0.01	0.03	0.51
Cthe_00590	transposase IS3/IS911	7.86	7.58	6.98	7.38	0.88	0.2	0.28	-0.4	0.17	-0.29	0.16	-0.35	-0.01	0.03	0.49
Cthe_02781	hypothetical protein	8.86	8.52	7.95	8.33	0.91	0.19	0.34	-0.38	0.2	-0.31	0.24	-0.32	-0.01	0.03	0.52
Cthe_01987	hypothetical protein	8.47	7.57	9.63	8.15	-1.16	-0.58	0.9	1.48	-1.91	-1.44	0.94	2.5	-0.01	0.03	0.5
Cthe_01462	transcriptional regulator, XRE family	8.8	8.12	10.05	8.54	-1.25	-0.42	0.68	1.51	-2	-1.21	0.66	2.55	-0.01	0.03	0.5
Cthe_02245	hypothetical protein	5.95	6.54	6	6.48	-0.05	0.06	-0.59	-0.48	-0.78	-0.5	-0.92	-0.47	-0.01	0.03	0.5
Cthe_01669	DNA recombinase, putative	2.58	1	1	1.58	1.58	-0.58	-0.58	0.89	-1.44	1.79	-0.62	-0.01	0.03	0.5	
Cthe_03083	hypothetical protein	7.35	6.41	8.43	7	-1.08	-0.59	0.94	1.43	-1.83	-1.46	0.99	2.42	-0.01	0.03	0.5
Cthe_01856	small acid-soluble spore protein beta	8.02	7.8	7.77	7.56	0.25	0.24	0.22	0.21	-0.47	-0.24	0.09	0.58	-0.01	0.03	0.51
Cthe_01140	hypothetical protein	8.62	9.41	8.9	9.22	-0.28	0.19	-0.79	-0.32	-1.01	-0.31	-1.18	-0.23	-0.01	0.03	0.49
Cthe_02843	hypothetical protein	5.91	5.17	4.7	5.17	1.21	0	0.74	-0.47	0.51	-0.59	0.74	-0.45	-0.01	0.03	0.51
Cthe_01565	Nitrogenase	9.68	10.25	9.83	9.59	-0.15	0.66	-0.57	0.24	-0.88	0.38	-0.9	0.62	-0.01	0.03	0.49
Cthe_01435	Phosphoglycerate mutase	9.19	8.42	7.87	8.46	1.32	-0.04	0.77	-0.59	0.62	-0.65	0.77	-0.64	-0.01	0.03	0.5
Cthe_01435	Phosphoglycerate mutase	9.19	8.42	7.87	8.46	1.32	-0.04	0.77	-0.59	0.62	-0.65	0.77	-0.64	-0.01	0.03	0.5
Cthe_01435	Phosphoglycerate mutase	9.19	8.42	7.87	8.46	1.32	-0.04	0.77	-0.59	0.62	-0.65	0.77	-0.64	-0.01	0.03	0.5
Cthe_01435	Phosphoglycerate mutase	9.19	8.42	7.87	8.46	1.32	-0.04	0.77	-0.59	0.62	-0.65	0.77	-0.64	-0.01	0.03	0.5
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_01565	Nitrogenase	9.68	10.25	9.83	9.59	-0.15	0.66	-0.57	0.24	-0.88	0.38	-0.9	0.62	-0.01	0.03	0.49
Cthe_00775	tRNA delta(2)-isopentenylpyrophosphate	11.19	10.76	11.2	10.73	-0.01	0.03	0.43	0.47	-0.73	-0.54	0.35	0.97	-0.01	0.03	0.49
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_01435	Phosphoglycerate mutase	9.19	8.42	7.87	8.46	1.32	-0.04	0.77	-0.59	0.62	-0.65	0.77	-0.64	-0.01	0.03	0.5
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	



Cthe_03084	putative RNA methylase	10.19	10.37	9.91	9.88	0.28	0.49	-0.18	0.03	-0.44	0.13	-0.41	0.3	-0.01	0.03	0.51
Cthe_01435	Phosphoglycerate mutase	9.19	8.42	7.87	8.46	1.32	-0.04	0.77	-0.59	0.62	-0.65	0.77	-0.64	-0.01	0.03	0.5
Cthe_01473	NADPH-dependent FMN reductase	12.2	11.68	11.25	11.55	0.95	0.13	0.52	-0.3	0.24	-0.4	0.46	-0.2	-0.02	0.01	0.52
Cthe_01517	type I phosphodiesterase/nucleotide	10.55	10.62	10.06	10.18	0.49	0.44	-0.07	-0.12	-0.22	0.06	-0.27	0.08	-0.02	0.01	0.45
Cthe_01564	GCN5-related N-acetyltransferase	9.03	9.36	9.09	8.82	-0.06	0.54	-0.33	0.27	-0.79	0.21	-0.6	0.67	-0.02	0.01	0.51
Cthe_02309	Nitrilase/cyanide hydratase and apolipoprotein	7.33	6.51	5.83	6.67	1.5	-0.16	0.82	-0.84	0.81	-0.82	0.84	-1.02	-0.02	0.01	0.49
Cthe_03076	Radical SAM	11.77	11.42	11.18	11.2	0.59	0.22	0.35	-0.02	-0.12	-0.26	0.25	0.23	-0.02	0.01	0.47
Cthe_03092	inner-membrane translocator	14.85	15.75	15.28	15.31	-0.43	0.44	-0.9	-0.03	-0.16	0.06	-1.31	0.21	-0.02	0.01	0.49
Cthe_00861	cell envelope-related transcriptional attenuator	12.48	12.47	11.9	12.3	0.58	0.17	0.01	-0.4	-0.13	-0.34	-0.17	-0.35	-0.02	0.01	0.53
Cthe_02763	hypothetical protein	9.17	8.91	8.65	8.63	0.52	0.28	0.26	0.02	-0.19	-0.18	0.14	0.29	-0.02	0.01	0.46
Cthe_01381	threonine synthase	13.9	14.14	13.58	13.52	0.32	0.62	-0.24	0.06	-0.4	0.32	-0.49	0.35	-0.02	0.01	0.48
Cthe_01559	Cystathionine gamma-synthase	10.71	11.76	11.7	10.97	-0.99	0.79	-1.05	0.73	-1.73	0.57	-1.5	1.36	-0.02	0.01	0.51
Cthe_01684	transposase IS3/IS911	9.19	8.25	7.79	8.34	1.4	-0.09	0.94	-0.55	0.7	-0.72	0.99	-0.58	-0.02	0.01	0.49
Cthe_02324	Resolvase-like protein	5.43	4	3.46	4.58	1.97	-0.58	1.43	-1.12	1.29	-1.44	1.6	-1.44	-0.02	0.01	0.5
Cthe_02750	IstB-like ATP-binding protein	8.87	9.63	9.21	9.16	-0.34	0.47	-0.76	0.05	-1.07	0.1	-1.14	0.33	-0.02	0.01	0.51
Cthe_02538	thiamine biosynthesis protein ThiS	0		1.58		-1.58		0	1.58	-2.34		-0.19	2.65	-0.02	0.01	0.49
Cthe_01938	D-alanine--D-alanine ligase	10.08	10.51	9.91	9.75	0.17	0.76	-0.43	0.16	-0.55	0.53	-0.72	0.5	-0.02	0.01	0.49
Cthe_03171	S-layer domain-like protein	6.71	5.95	6.94	6.21	-0.23	-0.26	0.76	0.73	-0.96	-0.97	0.76	1.36	-0.02	0.01	0.49
Cthe_02578	Ppx/GppA phosphatase	11.95	11.84	11.58	11.5	0.37	0.34	0.11	0.08	-0.35	-0.09	-0.05	0.38	-0.02	0.01	0.53
Cthe_02578	Ppx/GppA phosphatase	11.95	11.84	11.58	11.5	0.37	0.34	0.11	0.08	-0.35	-0.09	-0.05	0.38	-0.02	0.01	0.53
Cthe_00937	fatty acid/phospholipid synthesis protein PlsX	12.86	12.92	12.62	12.49	0.24	0.43	-0.06	0.13	-0.48	0.04	-0.26	0.45	-0.02	0.01	0.52
Cthe_01446	peptidase S1 and S6, chymotrypsin/Hap	12.71	13.23	12.75	12.85	-0.04	0.38	-0.52	-0.1	-0.77	-0.03	-0.84	0.11	-0.02	0.01	0.51
Cthe_02842	hypothetical protein	7.32	6.29	6.52	6.58	0.8	-0.29	1.03	-0.06	0.09	-1.01	1.1	0.17	-0.02	0.01	0.51
Cthe_03237	Relaxase/mobilization nuclease domain containing	9.11	9.69	9.54	8.99	-0.43	0.7	-0.58	0.55	-1.16	0.44	-0.91	1.09	-0.02	0.01	0.49
Cthe_02170	hypothetical protein	9	9.76	9.72	9.08	-0.72	0.68	-0.76	0.64	-1.46	0.41	-1.14	1.23	-0.02	0.01	0.51
Cthe_03165	PpC-type peptidyl-prolyl cis-trans isomerase	11.11	11.16	10.6	10.79	0.51	0.37	-0.05	-0.19	-0.2	-0.04	-0.25	-0.03	-0.02	0.01	0.46
Cthe_00630	hypothetical protein	11.2	11.9	11.4	11.73	-0.2	0.17	-0.7	-0.33	-0.93	-0.34	-1.06	-0.24	-0.02	0.01	0.51
Cthe_03067	membrane spanning protein	10.76	11.23	10.93	10.56	-0.17	0.67	-0.47	0.37	-0.9	0.4	-0.77	0.82	-0.02	0.01	0.49
Cthe_00937	fatty acid/phospholipid synthesis protein PlsX	12.86	12.92	12.62	12.49	0.24	0.43	-0.06	0.13	-0.48	0.04	-0.26	0.45	-0.02	0.01	0.52
Cthe_00392	inner-membrane translocator	14.85	15.75	15.28	15.31	-0.43	0.44	-0.9	-0.03	-0.16	0.06	-1.31	0.21	-0.02	0.01	0.49
Cthe_01559	Cystathionine gamma-synthase	10.71	11.76	11.7	10.97	-0.99	0.79	-1.05	0.73	-1.73	0.57	-1.5	1.36	-0.02	0.01	0.51
Cthe_01381	threonine synthase	13.9	14.14	13.58	13.52	0.32	0.62	-0.24	0.06	-0.4	0.32	-0.49	0.35	-0.02	0.01	0.48
Cthe_01559	Cystathionine gamma-synthase	10.71	11.76	11.7	10.97	-0.99	0.79	-1.05	0.73	-1.73	0.57	-1.5	1.36	-0.02	0.01	0.51
Cthe_00937	fatty acid/phospholipid synthesis protein PlsX	12.86	12.92	12.62	12.49	0.24	0.43	-0.06	0.13	-0.48	0.04	-0.26	0.45	-0.02	0.01	0.52
Cthe_01381	threonine synthase	13.9	14.14	13.58	13.52	0.32	0.62	-0.24	0.06	-0.4	0.32	-0.49	0.35	-0.02	0.01	0.48
Cthe_01559	Cystathionine gamma-synthase	10.71	11.76	11.7	10.97	-0.99	0.79	-1.05	0.73	-1.73	0.57	-1.5	1.36	-0.02	0.01	0.51
Cthe_01938	D-alanine--D-alanine ligase	10.08	10.51	9.91	9.75	0.17	0.76	-0.43	0.16	-0.55	0.53	-0.72	0.5	-0.02	0.01	0.49
Cthe_02578	Ppx/GppA phosphatase	11.95	11.84	11.58	11.5	0.37	0.34	0.11	0.08	-0.35	-0.09	-0.05	0.38	-0.02	0.01	0.53
Cthe_00937	fatty acid/phospholipid synthesis protein PlsX	12.86	12.92	12.62	12.49	0.24	0.43	-0.06	0.13	-0.48	0.04	-0.26	0.45	-0.02	0.01	0.52
Cthe_00937	fatty acid/phospholipid synthesis protein PlsX	12.86	12.92	12.62	12.49	0.24	0.43	-0.06	0.13	-0.48	0.04	-0.26	0.45	-0.02	0.01	0.52
Cthe_01938	D-alanine--D-alanine ligase	10.08	10.51	9.91	9.75	0.17	0.76	-0.43	0.16	-0.55	0.53	-0.72	0.5	-0.02	0.01	0.49
Cthe_01559	Cystathionine gamma-synthase	10.71	11.76	11.7	10.97	-0.99	0.79	-1.05	0.73	-1.73	0.57	-1.5	1.36	-0.02	0.01	0.51
Cthe_00937	fatty acid/phospholipid synthesis protein PlsX	12.86	12.92	12.62	12.49	0.24	0.43	-0.06	0.13	-0.48	0.04	-0.26	0.45	-0.02	0.01	0.52
Cthe_01938	D-alanine--D-alanine ligase	10.08	10.51	9.91	9.75	0.17	0.76	-0.43	0.16	-0.55	0.53	-0.72	0.5	-0.02	0.01	0.49
Cthe_01559	Cystathionine gamma-synthase	10.71	11.76	11.7	10.97	-0.99	0.79	-1.05	0.73	-1.73	0.57	-1.5	1.36	-0.02	0.01	0.51
Cthe_01559	Cystathionine gamma-synthase	10.71	11.76	11.7	10.97	-0.99	0.79	-1.05	0.73	-1.73	0.57	-1.5	1.36	-0.02	0.01	0.51
Cthe_01330	signal peptidase I	10.96	10.55	10.12	10.36	0.84	0.19	0.41	-0.24	0.13	-0.31	0.33	-0.11	-0.03	0	0.54
Cthe_00570	peptidase, membrane zinc metallopeptidase,	10.37	10.62	10.05	10.37	0.32	0.25	-0.25	-0.32	-0.4	-0.22	-0.5	-0.23	-0.03	0	0.47
Cthe_00521	helicase-like protein	9.85	10.16	9.9	9.54	-0.05	0.62	-0.31	0.36	-0.78	0.32	-0.57	0.8	-0.03	0	0.48
Cthe_00496	Integrase, catalytic region															
Cthe_00510	Integrase, catalytic region															
Cthe_00521	helicase-like protein	9.85	10.16	9.9	9.54	-0.05	0.62	-0.31	0.36	-0.78	0.32	-0.57	0.8	-0.03	0	0.48
Cthe_00588	Integrase, catalytic region															
Cthe_00692	Integrase, catalytic region															
Cthe_00698	Integrase, catalytic region															
Cthe_00879	Integrase, catalytic region															
Cthe_01193	transposase, mutator type															
Cthe_01206	Integrase, catalytic region															
Cthe_01242	Integrase, catalytic region															
Cthe_01392	Integrase, catalytic region															
Cthe_01469	Integrase, catalytic region															
Cthe_01496	Integrase, catalytic region															
Cthe_01656	Integrase, catalytic region															
Cthe_01661	Integrase, catalytic region															
Cthe_01674	Integrase, catalytic region															
Cthe_01676	Integrase, catalytic region															
Cthe_01683	Integrase, catalytic region															
Cthe_01687	Integrase, catalytic region															
Cthe_01691	Integrase, catalytic region															
Cthe_01712	Integrase, catalytic region															
Cthe_01881	Integrase, catalytic region															
Cthe_01889	transposase, mutator type															
Cthe_01976	Integrase, catalytic region															
Cthe_01993	Integrase, catalytic region															
Cthe_01999	Integrase, catalytic region															
Cthe_02000	Integrase, catalytic region															
Cthe_02012	Integrase, catalytic region															
Cthe_02017	transposase, mutator type															
Cthe_02114	Integrase, catalytic region															
Cthe_02135	Integrase, catalytic region															
Cthe_02153	Integrase, catalytic region															
Cthe_02173	Integrase, catalytic region															
Cthe_02188	Integrase, catalytic region															
Cthe_02201	transposase, mutator type															
Cthe_02715	Integrase, catalytic region															
Cthe_02716	Integrase, catalytic region															
Cthe_02816	transposase, mutator type															
Cthe_02830	IstB-like ATP-binding protein															
Cthe_02831	transposase															
Cthe_03051	transposase, mutator type															
Cthe_03181	Integrase, catalytic region															
Cthe_03182	Integrase, catalytic region															
Cthe_01295	5-formyltetrahydrofolate cyclo-ligase	9.88	9.28	8.88	9.22	1	0.06	0.6	-0.34	0.3	-0.5	0.56	-0.26	-0.03	0	0.53
Cthe_00808	MCP methyltransferase, CheR-type	7.77	6.75	7.43	7.09	0.34	-0.34	1.02	0.34	-0.38	-1.09	1.09	0.77	-0.03	0	0.49
Cthe_00977	UDP-N-acetylmuramoylalanine-D-glut															



Cthe_01647	hypothetical protein	5.09	4.09	3.7	4.17	1.39	-0.08	1	-0.47	0.69	-0.71	1.06	-0.45	-0.03	0	0.48
Cthe_02504	hypothetical protein	9.57	9.21	8.68	9.03	0.89	0.18	0.36	-0.35	0.18	-0.32	0.26	-0.27	-0.03	0	0.55
Cthe_02631	Aminoacyl-tRNA hydrolase	8.07	8.43	7.91	7.75	0.16	0.68	-0.36	0.16	-0.56	0.41	-0.64	0.5	-0.03	0	0.48
Cthe_02624		6.49	6.13	5.46	5.98	1.03	0.15	0.36	-0.52	0.33	-0.37	0.26	-0.53	-0.03	0	0.47
Cthe_00312	ATPase AAA-2	11.1	11.54	11.03	10.97	0.07	0.57	-0.44	0.06	-0.65	0.25	-0.74	0.35	-0.03	0	0.48
Cthe_00666	HfIC protein	8.4	7.73	7.51	7.73	0.89	0	0.67	-0.22	0.18	-0.59	0.65	-0.08	-0.03	0	0.53
Cthe_00187	hypothetical protein	9.08	9.65	9.47	8.95	-0.39	0.7	-0.57	0.52	-1.12	0.44	-0.9	1.05	-0.03	0	0.49
Cthe_02329	hypothetical protein	10.87	9.55	9.61	9.94	1.26	-0.39	1.32	-0.33	0.56	-1.16	1.46	-0.24	-0.03	0	0.49
Cthe_01610	hypothetical protein															
Cthe_01468	hypothetical protein	9.84	9.39	8.7	9.32	1.14	0.07	0.45	-0.62	0.44	-0.49	0.38	-0.68	-0.03	0	0.47
Cthe_01894	hypothetical protein	9.21	9.14	9.61	8.94	-0.4	0.2	0.07	0.67	-1.13	-0.29	-0.1	1.27	-0.03	0	0.51
Cthe_02856	hypothetical protein	6.48	6.07	6.48	6.04	0	0.03	0.41	0.44	-0.72	-0.54	0.33	0.92	-0.03	0	0.52
Cthe_00239	cellulosome enzyme, dockerin type I	9.25	10.47	10.05	10.21	-0.8	0.26	-1.22	-0.16	-1.54	-0.21	-1.71	0.02	-0.03	0	0.51
Cthe_01143	hypothetical protein	9.13	9.33	8.77	8.83	0.36	0.5	-0.2	-0.06	-0.36	0.15	-0.44	0.17	-0.03	0	0.46
Cthe_02192	hypothetical protein	10.09	10.14	11.13	9.98	-1.04	0.16	-0.05	1.15	-1.79	-0.35	-0.25	2	-0.03	0	0.51
Cthe_01125	hypothetical protein	4.32	2.58	5.04	3.7	-0.72	-1.12	1.74	1.34	-1.46	-2.24	1.99	2.29	-0.03	0	0.5
Cthe_01677	Abortive infection protein	7.48	7.14	7.31	7.02	0.17	0.12	0.34	0.29	-0.55	-0.41	0.24	0.7	-0.03	0	0.52
Cthe_00824	copper amine oxidase-like protein	12.45	12.59	12.06	12.29	0.39	0.3	-0.14	-0.23	-0.33	-0.15	-0.36	-0.09	-0.03	0	0.55
Cthe_03238	hypothetical protein															
Cthe_02624		6.49	6.13	5.46	5.98	1.03	0.15	0.36	-0.52	0.33	-0.37	0.26	-0.53	-0.03	0	0.47
Cthe_00808	MCP methyltransferase, CheR-type	7.77	6.75	7.43	7.09	0.34	-0.34	1.02	0.34	-0.38	-1.09	1.09	0.77	-0.03	0	0.49
Cthe_01330	signal peptidase I	10.96	10.55	10.12	10.36	0.84	0.19	0.41	-0.24	0.13	-0.31	0.33	-0.11	-0.03	0	0.54
Cthe_01295	5-formyltetrahydrofolate cyclo-ligase	9.88	9.28	8.88	9.22	1	0.06	0.6	-0.34	0.3	-0.5	0.56	-0.26	-0.03	0	0.53
Cthe_02631	Aminoacyl-tRNA hydrolase	8.07	8.43	7.91	7.75	0.16	0.68	-0.36	0.16	-0.56	0.41	-0.64	0.5	-0.03	0	0.48
Cthe_00977	UDP-N-acetylmuramoylalananyl-D-glutamyl-2,	8.09	8.64	8.71	8.06	-0.62	0.58	-0.55	0.65	-1.36	0.26	-0.88	1.24	-0.03	0	0.51
Cthe_00666	HfIC protein	8.4	7.73	7.51	7.73	0.89	0	0.67	-0.22	0.18	-0.59	0.65	-0.08	-0.03	0	0.53
Cthe_00977	UDP-N-acetylmuramoylalananyl-D-glutamyl-2,	8.09	8.64	8.71	8.06	-0.62	0.58	-0.55	0.65	-1.36	0.26	-0.88	1.24	-0.03	0	0.51
Cthe_01295	5-formyltetrahydrofolate cyclo-ligase	9.88	9.28	8.88	9.22	1	0.06	0.6	-0.34	0.3	-0.5	0.56	-0.26	-0.03	0	0.53
Cthe_00977	UDP-N-acetylmuramoylalananyl-D-glutamyl-2,	8.09	8.64	8.71	8.06	-0.62	0.58	-0.55	0.65	-1.36	0.26	-0.88	1.24	-0.03	0	0.51
Cthe_00977	UDP-N-acetylmuramoylalananyl-D-glutamyl-2,	8.09	8.64	8.71	8.06	-0.62	0.58	-0.55	0.65	-1.36	0.26	-0.88	1.24	-0.03	0	0.51
Cthe_01295	5-formyltetrahydrofolate cyclo-ligase	9.88	9.28	8.88	9.22	1	0.06	0.6	-0.34	0.3	-0.5	0.56	-0.26	-0.03	0	0.53
Cthe_00465	flagellar M-ring protein FlIF	12.14	11.64	11.39	11.53	0.75	0.11	0.5	-0.14	0.04	-0.43	0.44	0.05	-0.04	-0.01	0.55
Cthe_02034	serine/threonine protein kinase	9.48	8.97	10.19	9.13	-0.71	-0.16	0.51	1.06	-1.45	-0.82	0.45	1.86	-0.04	-0.01	0.49
Cthe_02077	CoA-binding protein	9.39	9.28	8.97	8.94	0.42	0.34	0.11	0.03	-0.3	-0.09	-0.05	0.3	-0.04	-0.01	0.58
Cthe_02586	amidohydrolase 2	10.8	10.5	10.46	10.28	0.34	0.22	0.3	0.18	-0.38	-0.26	0.19	0.53	-0.04	-0.01	0.46
Cthe_00032	glycoside hydrolase, family 26	12.77	12.19	11.77	12.03	1	0.16	0.58	-0.26	0.3	-0.35	0.54	-0.14	-0.04	-0.01	0.46
Cthe_00389	PfkB	14.94	15.99	15.56	15.71	-0.62	0.28	-1.05	-0.15	-1.36	-0.18	-1.5	0.03	-0.04	-0.01	0.51
Cthe_00806	PAS/PAC sensor hybrid histidine kinase	6.87	6.25	6.51	6.27	0.36	-0.02	0.62	0.24	-0.36	-0.62	0.59	0.62	-0.04	-0.01	0.47
Cthe_02034	serine/threonine protein kinase	9.48	8.97	10.19	9.13	-0.71	-0.16	0.51	1.06	-1.45	-0.82	0.45	1.86	-0.04	-0.01	0.49
Cthe_01650	DNA-directed DNA polymerase	4.58	3.58	3.32	3.7	1.26	-0.12	1	-0.38	0.56	-0.76	1.06	-0.32	-0.04	-0.01	0.48
Cthe_01808	transposase IS116/IS110/IS902	9.61	9.93	11.27	9.65	-1.66	0.28	-0.32	1.62	-2.42	-0.18	-0.59	2.71	-0.04	-0.01	0.49
Cthe_02034	serine/threonine protein kinase	9.48	8.97	10.19	9.13	-0.71	-0.16	0.51	1.06	-1.45	-0.82	0.45	1.86	-0.04	-0.01	0.49
Cthe_02585	biotin-acetyl-CoA-carboxylase ligase	10.25	9.87	9.54	9.63	0.71	0.24	0.38	-0.09	0	-0.24	0.29	0.12	-0.04	-0.01	0.43
Cthe_00465	flagellar M-ring protein FlIF	12.14	11.64	11.39	11.53	0.75	0.11	0.5	-0.14	0.04	-0.43	0.44	0.05	-0.04	-0.01	0.55
Cthe_00258	cellulosome enzyme, dockerin type I	9.53	9.26	8.9	8.99	0.63	0.27	0.27	-0.09	-0.08	-0.19	0.15	0.12	-0.04	-0.01	0.6
Cthe_00806	PAS/PAC sensor hybrid histidine kinase	6.87	6.25	6.51	6.27	0.36	-0.02	0.62	0.24	-0.36	-0.62	0.59	0.62	-0.04	-0.01	0.47
Cthe_02034	serine/threonine protein kinase	9.48	8.97	10.19	9.13	-0.71	-0.16	0.51	1.06	-1.45	-0.82	0.45	1.86	-0.04	-0.01	0.49
Cthe_00783	RNA modification enzyme, MiaB family	9.94	10.24	9.68	9.87	0.26	0.37	-0.3	-0.19	-0.46	-0.04	-0.56	-0.03	-0.04	-0.01	0.46
Cthe_00258	cellulosome enzyme, dockerin type I	9.53	9.26	8.9	8.99	0.63	0.27	0.27	-0.09	-0.08	-0.19	0.15	0.12	-0.04	-0.01	0.6
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.64	9.06	8.66	8.9	0.98	0.16	0.58	-0.24	0.28	-0.35	0.54	-0.11	-0.04	-0.01	0.46
Cthe_00665	HfIK protein	8.14	7.19	6.91	7.38	1.23	-0.19	0.95	-0.47	0.53	-0.87	1	-0.45	-0.04	-0.01	0.52
Cthe_02532	sulfate ABC transporter, inner membrane subunit	3.91	3	3.17	3.17	0.74	-0.17	0.91	0	0.03	-0.84	0.95	0.26	-0.04	-0.01	0.48
Cthe_00520	hypothetical protein	8.36	8.58	7.94	8.01	0.42	-0.57	-0.22	-0.07	-0.3	0.25	-0.46	0.15	-0.04	-0.01	0.45
Cthe_00400	hypothetical protein	11.57	11.62	11.04	11.17	0.53	0.45	-0.05	-0.13	-0.18	0.07	-0.25	0.06	-0.04	-0.01	0.42
Cthe_01142	hypothetical protein	7.87	8.64	8.13	8.14	-0.26	0.5	-0.77	-0.01	-0.99	0.15	-1.15	0.24	-0.04	-0.01	0.48
Cthe_02094	hypothetical protein	7.27	8.15	7.69	7.03	-0.42	1.12	-0.88	0.66	-1.15	1.06	-1.29	1.26	-0.04	-0.01	0.49
Cthe_02466	hypothetical protein	7.18	6.43	6.07	6.38	1.11	0.05	0.75	-0.31	0.41	-0.51	0.75	-0.21	-0.04	-0.01	0.47
Cthe_01196	hypothetical protein	7.45	6.09	6.7	6.61	0.75	-0.52	1.36	0.09	0.04	-1.35	1.51	0.39	-0.04	-0.01	0.49
Cthe_01434	hypothetical protein	8.78	7.95	7.65	7.96	1.13	-0.01	0.83	-0.31	0.43	-0.6	0.85	-0.21	-0.04	-0.01	0.47
Cthe_01595	hypothetical protein	7.95	7.18	7.23	7.24	0.72	-0.06	0.77	-0.01	0.01	-0.68	0.77	0.24	-0.04	-0.01	0.47
Cthe_00379	hypothetical protein	6.48	6.48	5.86	6.49	0.62	-0.01	0	-0.63	-0.09	-0.6	-0.19	-0.7	-0.04	-0.01	0.47
Cthe_00868	type IV pilus assembly PilZ	10.09	10.11	9.58	9.8	0.51	0.31	-0.02	-0.22	-0.2	-0.13	-0.21	-0.08	-0.04	-0.01	0.6
Cthe_00271	type 3a, cellulose-binding	12.13	12.77	12.38	12.29	-0.25	0.48	-0.64	0.09	-0.98	0.12	-0.99	0.39	-0.04	-0.01	0.52
Cthe_02532	sulfate ABC transporter, inner membrane subunit	3.91	3	3.17	3.17	0.74	-0.17	0.91	0	0.03	-0.84	0.95	0.26	-0.04	-0.01	0.48
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.64	9.06	8.66	8.9	0.98	0.16	0.58	-0.24	0.28	-0.35	0.54	-0.11	-0.04	-0.01	0.46
Cthe_02585	biotin-acetyl-CoA-carboxylase ligase	10.25	9.87	9.54	9.63	0.71	0.24	0.38	-0.09	0	-0.24	0.29	0.12	-0.04	-0.01	0.43
Cthe_00389	PfkB	14.94	15.99	15.56	15.71	-0.62	0.28	-1.05	-0.15	-1.36	-0.18	-1.5	0.03	-0.04	-0.01	0.51
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.64	9.06	8.66	8.9	0.98	0.16	0.58	-0.24	0.28	-0.35	0.54	-0.11	-0.04	-0.01	0.46
Cthe_01650	DNA-directed DNA polymerase	4.58	3.58	3.32	3.7	1.26	-0.12	1	-0.38	0.56	-0.76	1.06	-0.32	-0.04	-0.01	0.48
Cthe_00071	Cellulose 1,4-beta-cellobiosidase	11.46	11.86	11.33	11.33	0.13	0.53	-0.4	0	-0.59	0.19	-0.69	0.26	-0.04	-0.01	0.47
Cthe_00665	HfIK protein	8.14	7.19	6.91	7.38	1.23	-0.19	0.95	-0.47	0.53	-0.87	1	-0.45	-0.04	-0.01	0.52
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.64	9.06	8.66	8.9	0.98	0.16	0.58	-0.24	0.28	-0.35	0.54	-0.11	-0.04	-0.01	0.46
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.64	9.06	8.66	8.9	0.98	0.16	0.58	-0.24	0.28	-0.35	0.54	-0.11	-0.04	-0.01	0.46
Cthe_00389	PfkB	14.94	15.99	15.56	15.71	-0.62	0.28	-1.05	-0.15	-1.36	-0.18	-1.5	0.03	-0.04	-0.01	0.51
Cthe_00389	PfkB	14.94	15.99	15.56	15.71	-0.62	0.28	-1.05	-0.15	-1.36	-0.18	-1.5	0.03	-0.04	-0.01	0.51
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.64	9.06	8.66	8.9	0.98	0.16	0.58	-0.24	0.28	-0.35	0.54	-0.11	-0.04	-0.01	0.46
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.64	9.06	8.66	8.9	0.98	0.16	0.58	-0.24	0.28	-0.35	0.54	-0.11	-0.04	-0.01	0.46



Cthe_02807	glycoside hydrolase, family 5	7.87	7.31	9.72	7.79	-1.85	-0.48	0.56	1.93	-2.61	-1.29	0.51	3.18	-0.05	-0.03	0.51
Cthe_00072	phage shock protein C, PspC	8.77	6.94	9.52	8.17	-0.75	-1.23	1.83	1.35	-1.49	-2.4	2.1	2.3	-0.05	-0.03	0.51
Cthe_00074	RNA polymerase, sigma-24 subunit, ECF subfamily	0		1.58	0	-1.58	0	1.58	-2.34	-0.59	-0.19	2.65	-0.05	-0.03	0.51	
Cthe_00777	DNA mismatch repair protein MutS	11.36	11.49	10.89	11.01	0.47	0.48	-0.13	-0.12	-0.24	0.12	-0.35	0.08	-0.05	-0.03	0.42
Cthe_03048	DNA repair protein RadC	7.85	8.86	8.49	8.42	-0.64	0.44	-1.01	0.07	-1.38	0.06	-1.45	0.36	-0.05	-0.03	0.52
Cthe_01177	putative nicotinate phosphoribosyltransferase	8.2	7.88	8.16	7.78	0.04	0.1	0.32	0.38	-0.68	-0.44	0.21	0.83	-0.05	-0.03	0.53
Cthe_00463	flagellar basal-body rod protein FlgC	11.73	11.16	11.82	11.23	-0.09	-0.07	0.57	0.59	-0.82	-0.69	0.52	1.15	-0.05	-0.03	0.48
Cthe_00332	phosphoribulokinase/uridine kinase	11.71	11.68	11.07	11.46	0.64	0.22	0.03	-0.39	-0.07	-0.26	-0.15	-0.33	-0.05	-0.03	0.42
Cthe_00072	phage shock protein C, PspC	8.77	6.94	9.52	8.17	-0.75	-1.23	1.83	1.35	-1.49	-2.4	2.1	2.3	-0.05	-0.03	0.51
Cthe_03187	putative anti-sigma regulatory factor,	10.48	8.78	9.37	9.49	1.11	-0.71	1.7	-0.12	0.41	-1.63	1.94	0.08	-0.05	-0.03	0.49
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01420	protein of unknown function DUF204	10.12	10.06	9.61	9.69	0.51	0.37	0.06	-0.08	-0.2	-0.04	-0.11	0.14	-0.05	-0.03	0.64
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	8.11	7.18	7.01	7.27	1.1	-0.09	0.93	-0.26	0.4	-0.72	0.97	-0.14	-0.05	-0.03	0.47
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_02757	sodium/hydrogen exchanger	10.06	10.01	9.42	9.64	0.64	0.37	0.05	-0.22	-0.07	-0.04	-0.12	-0.08	-0.05	-0.03	0.31
Cthe_02941	2-C-methyl-D-erythritol 4-phosphate	7.26	7.52	6.92	7.01	0.34	0.51	-0.26	-0.09	-0.38	0.16	-0.51	0.12	-0.05	-0.03	0.44
Cthe_01173	type IV pilus assembly PilZ	11.97	10.89	10.72	11.07	1.25	-0.18	1.08	-0.35	0.55	-0.85	1.16	-0.27	-0.05	-0.03	0.48
Cthe_01932	S-layer-like domain containing protein	5.21	5.36	4.91	4.95	0.3	0.41	-0.15	-0.04	-0.42	0.01	-0.37	0.2	-0.05	-0.03	0.56
Cthe_02319	restriction endonuclease (HaeIII)	12.53	12.71	12.21	12.38	0.32	0.33	-0.18	-0.17	-0.4	-0.1	-0.41	0	-0.05	-0.03	0.56
Cthe_02997	hypothetical protein	8.08	7	7.55	7.34	0.53	-0.34	1.08	0.21	-0.18	-1.09	1.16	0.58	-0.05	-0.03	0.48
Cthe_00651	hypothetical protein	7.85	6.95	6.94	7.07	0.91	-0.12	0.9	-0.13	0.2	-0.76	0.94	0.06	-0.05	-0.03	0.47
Cthe_01147	hypothetical protein	5.93	5.43	4.91	5.39	1.02	0.04	0.5	-0.48	0.32	-0.53	0.44	-0.47	-0.05	-0.03	0.54
Cthe_02259	hypothetical protein	10.98	10.63	10.16	10.32	0.82	0.31	0.35	-0.16	0.11	-0.13	0.25	0.02	-0.05	-0.03	0.38
Cthe_00216	small acid-soluble spore protein, alpha/beta	7.34	7.98	8.57	7.46	-1.23	0.52	-0.64	1.11	-1.98	0.18	-0.99	1.94	-0.05	-0.03	0.51
Cthe_02458	hypothetical protein	11.7	10.56	10.78	10.87	0.92	-0.31	1.14	-0.09	0.21	-1.04	1.24	0.12	-0.05	-0.03	0.48
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	8.11	7.18	7.01	7.27	1.1	-0.09	0.93	-0.26	0.4	-0.72	0.97	-0.14	-0.05	-0.03	0.47
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	8.11	7.18	7.01	7.27	1.1	-0.09	0.93	-0.26	0.4	-0.72	0.97	-0.14	-0.05	-0.03	0.47
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	8.11	7.18	7.01	7.27	1.1	-0.09	0.93	-0.26	0.4	-0.72	0.97	-0.14	-0.05	-0.03	0.47
Cthe_02928	ribosomal protein L36	6.02	6.78	6.07	5.86	-0.05	0.92	-0.76	0.21	-0.78	0.76	-1.14	0.58	-0.05	-0.03	0.48
Cthe_02941	2-C-methyl-D-erythritol 4-phosphate	7.26	7.52	6.92	7.01	0.34	0.51	-0.26	-0.09	-0.38	0.16	-0.51	0.12	-0.05	-0.03	0.44
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	8.11	7.18	7.01	7.27	1.1	-0.09	0.93	-0.26	0.4	-0.72	0.97	-0.14	-0.05	-0.03	0.47
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_02191	1,4-alpha-glucan branching enzyme	11.5	11.76	11.39	11.09	0.11	0.67	-0.26	0.3	-0.61	0.4	-0.51	0.71	-0.05	-0.03	0.47
Cthe_02941	2-C-methyl-D-erythritol 4-phosphate	7.26	7.52	6.92	7.01	0.34	0.51	-0.26	-0.09	-0.38	0.16	-0.51	0.12	-0.05	-0.03	0.44
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_02807	glycoside hydrolase, family 5	7.87	7.31	9.72	7.79	-1.85	-0.48	0.56	1.93	-2.61	-1.29	0.51	3.18	-0.05	-0.03	0.51
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01177	putative nicotinate phosphoribosyltransferase	8.2	7.88	8.16	7.78	0.04	0.1	0.32	0.38	-0.68	-0.44	0.21	0.83	-0.05	-0.03	0.53
Cthe_00332	phosphoribulokinase/uridine kinase	11.71	11.68	11.07	11.46	0.64	0.22	0.03	-0.39	-0.07	-0.26	-0.15	-0.33	-0.05	-0.03	0.42
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7</				



Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	8.11	7.18	7.01	7.27	1.1	-0.09	0.93	-0.26	0.4	-0.72	0.97	-0.14	-0.05	-0.03	0.47
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	8.11	7.18	7.01	7.27	1.1	-0.09	0.93	-0.26	0.4	-0.72	0.97	-0.14	-0.05	-0.03	0.47
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_03027	Citrate (Si)-synthase	14.57	14.75	14.51	14.32	0.06	0.43	-0.18	0.19	-0.66	0.04	-0.41	0.55	-0.05	-0.03	0.54
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_01319	protein of unknown function DUF558	9.04	9.45	9.21	8.94	-0.17	0.51	-0.41	0.27	-0.9	0.16	-0.7	0.67	-0.05	-0.03	0.53
Cthe_00028	uncharacterized protein, YcgL-like protein	10.03	9.01	9.08	9.29	0.95	-0.28	1.02	-0.21	0.24	-1	1.09	-0.06	-0.06	-0.04	0.53
Cthe_00986	peptidase M16-like protein	10.62	11.44	10.92	10.82	-0.3	0.62	-0.82	0.1	-1.03	0.32	-1.21	0.41	-0.06	-0.04	0.47
Cthe_00971		9.97	8.75	9.15	9.13	0.82	-0.38	1.22	0.02	0.11	-1.15	1.34	0.29	-0.06	-0.04	0.47
Cthe_00795	alpha amylase, catalytic region	9.32	8.68	8.87	8.69	0.45	-0.01	0.64	0.18	-0.27	-0.6	0.61	0.53	-0.06	-0.04	0.46
Cthe_02698	putative transcriptional regulator, CopG family	10.66	9.29	10.43	9.97	0.23	-0.68	1.37	0.46	-0.49	-1.59	1.53	0.95	-0.06	-0.04	0.52
Cthe_00833	exodeoxyribonuclease VII, large subunit	9.68	10.1	9.66	9.75	0.02	0.35	-0.42	-0.09	-0.7	-0.07	-0.71	0.12	-0.06	-0.04	0.55
Cthe_03220	CRISPR-associated protein Cas4	8.21	7.27	7.24	7.4	0.97	-0.13	0.94	-0.16	0.27	-0.78	0.99	0.02	-0.06	-0.04	0.47
Cthe_02663	methyl-accepting chemotaxis sensory transducer	9.83	8.17	9.21	8.94	0.62	-0.77	1.66	0.27	-0.09	-1.72	1.89	0.67	-0.06	-0.04	0.48
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_00978	UDP-N-acetylmuramyl-tripeptide synthetases	9.64	10.12	9.79	9.28	-0.15	0.84	-0.48	0.51	-0.88	0.65	-0.79	1.03	-0.06	-0.04	0.47
Cthe_01824	two component transcriptional regulator, AraC	5.21	4.58	4.75	4.58	0.46	0	0.63	0.17	-0.26	-0.59	0.6	0.52	-0.06	-0.04	0.46
Cthe_02663	methyl-accepting chemotaxis sensory transducer	9.83	8.17	9.21	8.94	0.62	-0.77	1.66	0.27	-0.09	-1.72	1.89	0.67	-0.06	-0.04	0.48
Cthe_02775	transcriptional regulator, Crp/Fnr family	8.17	8.08	7.46	7.81	0.71	0.27	0.09	-0.35	0	-0.19	-0.07	-0.27	-0.06	-0.04	0.38
Cthe_03062	signal transduction histidine kinase regulating	9.75	10.78	10.27	10.1	-0.52	0.68	-1.03	0.17	-1.26	0.41	-1.47	0.52	-0.06	-0.04	0.48
Cthe_00771	putative helix-turn-helix protein, YlxM/p13-like	10.08	10.13	9.61	9.85	0.47	0.28	-0.05	-0.24	-0.24	-0.18	-0.25	-0.11	-0.06	-0.04	0.62
Cthe_01509	protein of unknown function DUF438	10.56	10.93	10.36	10.52	0.2	0.41	-0.37	-0.16	-0.52	0.01	-0.65	0.02	-0.06	-0.04	0.45
Cthe_00338	NADH-quinone oxidoreductase, E subunit	11.88	12.08	11.49	11.74	0.39	0.34	-0.2	-0.25	-0.33	-0.09	-0.44	-0.12	-0.06	-0.04	0.42
Cthe_03066	ABC transporter related protein	11.17	11.36	10.94	10.64	0.23	0.72	-0.19	0.3	-0.49	0.47	-0.42	0.71	-0.06	-0.04	0.46
Cthe_02761	glycoside hydrolase, family 9	10.14	10.28	9.64	10.38	0.5	-0.1	-0.14	-0.74	-0.21	-0.74	-0.36	-0.86	-0.06	-0.04	0.46
Cthe_00154	protein of unknown function DUF1292	8.42	7.58	7.52	7.73	0.9	-0.15	0.84	-0.21	0.19	-0.81	0.86	-0.06	-0.06	-0.04	0.54
Cthe_03082	hypothetical protein	5.29	4	4.52	4.52	0.77	-0.52	1.29	0	0.06	-1.35	1.43	0.26	-0.06	-0.04	0.52
Cthe_02168	Propeptide, PepSY amd peptidase M4	12.04	11.31	11.28	11.32	0.76	-0.01	0.73	-0.04	0.05	-0.6	0.72	0.2	-0.06	-0.04	0.45
Cthe_01088	hypothetical protein	9.13	9.93	10.27	9.31	-1.14	0.62	-0.08	0.96	-1.89	0.32	-1.19	1.71	-0.06	-0.04	0.52
Cthe_02134	RNA related	6.51	5.95	6.38	6.02	0.13	-0.07	0.56	0.36	-0.59	-0.69	0.51	0.8	-0.06	-0.04	0.54
Cthe_02140	hypothetical protein	8.25	8.95	8.34	9.23	-0.09	-0.28	-0.7	-0.89	-0.82	-1	-1.06	-1.09	-0.06	-0.04	0.48
Cthe_01836	hypothetical protein	8.82	8.35	9.89	8.6	-1.07	-0.25	0.47	1.29	-1.82	-0.96	0.4	2.21	-0.06	-0.04	0.51
Cthe_01398	cellulosome enzyme, dockerin type I	13.09	12.41	12.03	12.44	1.06	-0.03	0.68	-0.41	0.36	-0.63	0.66	-0.36	-0.06	-0.04	0.54
Cthe_00753	hypothetical protein	8.03	7.52	7.28	7.43	0.75	0.09	0.51	-0.15	0.04	-0.46	0.45	0.03	-0.06	-0.04	0.58
Cthe_02836	hypothetical protein	4.09	3.46	4.52	3.7	-0.43	-0.24	0.63	0.82	-1.16	-0.94	0.6	1.5	-0.06	-0.04	0.52
Cthe_01784	hypothetical protein	14.25	13.48	13.8	13.59	0.45	-0.11	0.77	0.21	-0.27	-0.75	0.77	0.58	-0.06	-0.04	0.46
Cthe_03066	ABC transporter related protein	11.17	11.36	10.94	10.64	0.23	0.72	-0.19	0.3	-0.49	0.47	-0.42	0.71	-0.06	-0.04	0.46
Cthe_03066	ABC transporter related protein	11.17	11.36	10.94	10.64	0.23	0.72	-0.19	0.3	-0.49	0.47	-0.42	0.71	-0.06	-0.04	0.46
Cthe_00338	NADH-quinone oxidoreductase, E subunit	11.88	12.08	11.49	11.74	0.39	0.34	-0.2	-0.25	-0.33	-0.09	-0.44	-0.12	-0.06	-0.04	0.42
Cthe_02225	Glyoxalase/bleomycin resistance	5.39	5.98	5.32	5.21	0.07	0.77	-0.59	0.11	-0.65	0.54	-0.92	0.42	-0.06	-0.04	0.47
Cthe_02225	Glyoxalase/bleomycin resistance	5.39	5.98	5.32	5.21	0.07	0.77	-0.59	0.11	-0.65	0.54	-0.92	0.42	-0.06	-0.04	0.47
Cthe_02225	Glyoxalase/bleomycin resistance	5.39	5.98	5.32	5.21	0.07	0.77	-0.59	0.11	-0.65	0.54	-0.92	0.42	-0.06	-0.04	0.47
Cthe_00833	exodeoxyribonuclease VII, large subunit	9.68	10.1	9.66	9.75	0.02	0.35	-0.42	-0.09	-0.7	-0.07	-0.71	0.12	-0.06	-0.04	0.55
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_02225	Glyoxalase/bleomycin resistance	5.39	5.98	5.32	5.21	0.07	0.77	-0.59	0.11	-0.65	0.54	-0.92	0.42	-0.06	-0.04	0.47
Cthe_00338	NADH-quinone oxidoreductase, E subunit	11.88	12.08	11.49	11.74	0.39	0.34	-0.2	-0.25	-0.33	-0.09	-0.44	-0.12	-0.06	-0.04	0.42
Cthe_00978	UDP-N-acetylmuramyl-tripeptide synthetases	9.64	10.12	9.79	9.28	-0.15	0.84	-0.48	0.51	-0.88	0.65	-0.79	1.03	-0.06	-0.04	0.47
Cthe_02225	Glyoxalase/bleomycin resistance	5.39	5.98	5.32	5.21	0.07	0.77	-0.59	0.11	-0.65	0.54	-0.92	0.42	-0.06	-0.04	0.47
Cthe_02225	Glyoxalase/bleomycin resistance	5.39	5.98	5.32	5.21	0.07	0.77	-0.59	0.11	-0.65	0.54	-0.92	0.42	-0.06	-0.04	0.47
Cthe_00338	NADH-quinone oxidoreductase, E subunit	11.88	12.08	11.49	11.74	0.39	0.34	-0.2	-0.25	-0.33	-0.09	-0.44	-0.12	-0.06	-0.04	0.42
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_00338	NADH-quinone oxidoreductase, E subunit	11.88	12.08	11.49	11.74	0.39	0.34	-0.2	-0.25	-0.33	-0.09	-0.44	-0.12	-0.06	-0.04	0.42
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_00978	UDP-N-acetylmuramyl-tripeptide synthetases	9.64	10.12	9.79	9.28	-0.15	0.84	-0.48	0.51	-0.88	0.65	-0.79	1.03	-0.06	-0.04	0.47
Cthe_00978	UDP-N-acetylmuramyl-tripeptide synthetases	9.64	10.12	9.79	9.28	-0.15	0.84	-0.48	0.51	-0.88	0.65	-0.79	1.03	-0.06	-0.04	0.47
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_00338	NADH-quinone oxidoreductase, E subunit	11.88	12.08	11.49	11.74	0.39	0.34	-0.2	-0.25	-0.33	-0.09	-0.44	-0.12	-0.06	-0.04	0.42
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_00978	UDP-N-acetylmuramyl-tripeptide synthetases	9.64	10.12	9.79	9.28	-0.15	0.84	-0.48	0.51	-0.88	0.65	-0.79	1.03	-0.06	-0.04	0.47
Cthe_00978	UDP-N-acetylmuramyl-tripeptide synthetases	9.64	10.12	9.79	9.28	-0.15	0.84	-0.48	0.51	-0.88	0.65	-0.79	1.03	-0.06	-0.04	0.47
Cthe_00884	Lytic transglycosylase, catalytic	8.39	8.93	8.25	8.19	0.14	0.74	-0.54	0.06	-0.58	0.5	-0.86	0.35	-0.06	-0.04	0.46
Cthe_02225	Glyoxalase/bleomycin resistance	5.39	5.98	5.32	5.21	0.07	0.77	-0.59	0.11	-0.65	0.54	-0.92	0.42	-0.06	-0.04	0.47
Cthe_00338	NADH-quinone oxidoreductase, E subunit	11.88	12.08	11.49	11.74	0.39	0.34	-0.2	-0.25	-0.33	-0.09	-0.44	-0.12	-0.06	-0.04	0.42
Cthe_00468	flagellar protein export ATPase FliI	9.77	9.42	8.86	9.52	0.91	-0.1	0.35	-0.66	0.2	-0.74	0.25	-0.74	-0.07	-0.05	0.55
Cthe_01764	Outer membrane protein-like protein	10.19	10.84	10												



Cthe_01258	copper amine oxidase-like protein	9.93	9.26	10.25	9.51	-0.32	-0.25	0.67	0.74	-1.05	-0.96	0.65	1.38	-0.07	-0.05	0.52
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_00468	flagellar protein export ATPase FliI	9.77	9.42	8.86	9.52	0.91	-0.1	0.35	-0.66	0.2	-0.74	0.25	-0.74	-0.07	-0.05	0.55
Cthe_02369	ribonuclease P protein component	12.32	12.11	11.59	11.83	0.73	0.28	0.21	-0.24	0.02	-0.18	0.07	-0.11	-0.07	-0.05	0.78
Cthe_01958	UV-endonuclease UvdE	7.91	8.55	8.35	7.71	-0.44	0.84	-0.64	0.64	-1.17	0.65	-0.99	1.23	-0.07	-0.05	0.48
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02079	signal peptidase I	12.46	11.88	11.88	11.88	0.58	0	0.58	0	-0.13	-0.59	0.54	0.26	-0.07	-0.05	0.57
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_00566	primosomal protein N'	10.28	10.17	9.65	9.83	0.63	0.34	0.11	-0.18	-0.08	-0.09	-0.05	-0.02	-0.07	-0.05	1.26
Cthe_00503	2'-5' RNA ligase	8.93	8.78	9.33	8.58	-0.4	0.2	0.15	0.75	-1.13	-0.29	0	1.39	-0.07	-0.05	0.47
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02369	ribonuclease P protein component	12.32	12.11	11.59	11.83	0.73	0.28	0.21	-0.24	0.02	-0.18	0.07	-0.11	-0.07	-0.05	0.78
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_00468	flagellar protein export ATPase FliI	9.77	9.42	8.86	9.52	0.91	-0.1	0.35	-0.66	0.2	-0.74	0.25	-0.74	-0.07	-0.05	0.55
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoreductase,	0	2	1.58	1.58	-1.58	0.42	-2	0	-2.34	0.03	-2.69	0.26	-0.07	-0.05	0.49
Cthe_01069	protein of unknown function UPF0054	9.51	10.03	9.46	9.59	0.05	0.44	-0.52	-0.13	-0.67	0.06	-0.84	0.06	-0.08	-0.06	0.45
Cthe_00251	transglutaminase-like protein	10.21	10.59	10.13	10.32	0.08	0.27	-0.38	-0.19	-0.64	-0.19	-0.66	-0.03	-0.08	-0.06	0.57
Cthe_00511	histidine kinase	10.01	9.29	9.02	9.21	0.99	0.08	0.72	-0.19	0.29	-0.47	0.71	-0.03	-0.08	-0.06	0.44
Cthe_02605	ATP synthase F1, delta subunit	7.58	8.31	7.84	8.24	-0.26	0.07	-0.73	-0.4	-0.99	-0.49	-1.1	-0.35	-0.08	-0.06	0.54
Cthe_02666	ATPase, P-type (transporting), HAD superfamily,	8.99	9.43	9.04	9.04	-0.05	0.39	-0.44	0	-0.78	-0.01	-0.74	0.26	-0.08	-0.06	0.56
Cthe_00518	type III restriction enzyme, res subunit	10.23	11.04	10.48	10.79	-0.25	0.25	-0.81	-0.31	-0.98	-0.22	-1.2	-0.21	-0.08	-0.06	0.46
Cthe_02177	hypothetical protein	7.27	6.64	6.43	6.54	0.84	0.1	0.63	-0.11	0.13	-0.44	0.6	0.09	-0.08	-0.06	0.42
Cthe_00627	hypothetical protein	10.74	11.32	10.95	10.9	-0.21	0.42	-0.58	0.05	-0.94	0.03	-0.91	0.33	-0.08	-0.06	0.55
Cthe_00402	copper amine oxidase-like protein	14.06	14.59	14.2	14.21	-0.14	0.38	-0.53	-0.01	-0.87	-0.03	-0.85	0.24	-0.08	-0.06	0.55
Cthe_03209	hypothetical protein	6.66	7.18	6.61	6.71	0.05	0.47	-0.52	-0.1	-0.67	0.1	-0.84	0.11	-0.08	-0.06	0.45
Cthe_02514	hypothetical protein	5.64	5.04	5.98	5.17	-0.34	-0.13	0.6	0.81	-1.07	-0.78	0.56	1.48	-0.08	-0.06	0.47
Cthe_02733	hypothetical protein	6.19	5.09	6.32	5.64	-0.13	-0.55	1.1	0.68	-0.86	-1.4	1.19	1.29	-0.08	-0.06	0.53
Cthe_00869	hypothetical protein	11.74	11.61	11.19	11.28	0.55	0.33	0.13	-0.09	-0.16	-0.1	-0.02	0.12	-0.08	-0.06	0.87
Cthe_02475	phage portal protein, SPP1 family	9.07	8.07	8.09	8.34	0.98	-0.27	1	-0.25	0.28	-0.99	1.06	-0.12	-0.08	-0.06	0.54
Cthe_01220	hypothetical protein	12.94	12.91	12.5	12.55	0.44	0.36	0.03	-0.05	-0.28	-0.06	-0.15	0.18	-0.08	-0.06	0.69
Cthe_00412	glycoside hydrolase, family 9	14.76	16.17	15.63	16.25	-0.87	-0.08	-1.41	-0.62	-1.61	-0.71	-1.95	-0.68	-0.08	-0.06	0.48
Cthe_01544	hypothetical protein	6.93	6.85	6.41	6.34	0.52	0.51	0.08	0.07	-0.19	0.16	-0.09	0.36	-0.08	-0.06	0.38
Cthe_02472	hypothetical protein	9.4	8.5	8.71	8.65	0.69	-0.15	0.9	0.06	-0.02	-0.81	0.94	0.35	-0.08	-0.06	0.45
Cthe_02605	ATP synthase F1, delta subunit	7.58	8.31	7.84	8.24	-0.26	0.07	-0.73	-0.4	-0.99	-0.49	-1.1	-0.35	-0.08	-0.06	0.54
Cthe_02605	ATP synthase F1, delta subunit	7.58	8.31	7.84	8.24	-0.26	0.07	-0.73	-0.4	-0.99	-0.49	-1.1	-0.35	-0.08	-0.06	0.54
Cthe_02605	ATP synthase F1, delta subunit	7.58	8.31	7.84	8.24	-0.26	0.07	-0.73	-0.4	-0.99	-0.49	-1.1	-0.35	-0.08	-0.06	0.54
Cthe_02666	ATPase, P-type (transporting), HAD superfamily,	8.99	9.43	9.04	9.04	-0.05	0.39	-0.44	0	-0.78	-0.01	-0.74	0.26	-0.08	-0.06	0.56
Cthe_00518	type III restriction enzyme, res subunit	10.23	11.04	10.48	10.79	-0.25	0.25	-0.81	-0.31	-0.98	-0.22	-1.2	-0.21	-0.08	-0.06	0.46
Cthe_02605	ATP synthase F1, delta subunit	7.58	8.31	7.84	8.24	-0.26	0.07	-0.73	-0.4	-0.99	-0.49	-1.1	-0.35	-0.08	-0.06	0.54
Cthe_01271	Carbohydrate binding family 6	9.66	8.63	8.63	8.94	10.3	-0.31	1.03	-0.31	0.33	-1.04	1.1	-0.21	-0.09	-0.08	0.55
Cthe_01862	ABC transporter related protein	14.26	14.51	14.99	14.19	-0.73	0.32	-0.25	0.8	-1.47	-0.12	-0.5	1.47	-0.09	-0.08	0.53
Cthe_02378	parB-like partition protein	10.15	10.12	9.81	9.78	0.34	0.34	0.03	0.03	-0.38	-0.09	-0.15	0.3	-0.09	-0.08	0.65
Cthe_02808	transcriptional regulator, LacI family	8.58	7.97	10.34	8.4	-1.76	-0.43	0.61	1.94	-2.52	-1.22	0.57	3.2	-0.09	-0.08	0.48
Cthe_01304	PhoH-like protein	8.37	9.24	8.54	8.37	-0.17	0.87	-0.87	0.17	-0.9	0.69	-1.27	0.52	-0.09	-0.08	0.46
Cthe_01318	response regulator receiver protein	7.77	7.92	7.58	7.53	0.19	0.39	-0.15	0.05	-0.53	-0.01	-0.37	0.33	-0.09	-0.08	0.6
Cthe_02163	anti-sigma-factor antagonist	9.11	8.47	8.34	8.5	0.77	-0.03	0.64	-0.16	0.06	-0.63	0.61	0.02	-0.09	-0.08	0.58
Cthe_00982	MraZ protein	13.46	13.05	13.51	12.97	-0.05	0.08	0.41	0.54	-0.78	-0.47	0.33	1.08	-0.09	-0.08	0.45
Cthe_02450	hypothetical protein	7.96	6.49	8.05	7.24	-0.09	-0.75	1.47	0.81	-0.82	-1.69	1.65	1.48	-0.09	-0.08	0.48
Cthe_01387	hypothetical protein	10.63	10.53	10.32	10.12	0.31	0.41	0.1	0.2	-0.41	0.01	-0.06	0.56	-0.09	-0.08	0.41
Cthe_00238	hypothetical protein	5.91	6.93	6.66	6.43	-0.75	0.5	-1.02	0.23	-1.49	0.15	-1.46	0.61	-0.09	-0.08	0.53
Cthe_01594	hypothetical protein	7.43	6.32	6.29	6.52	1.14	-0.2	1.11	-0.23	0.44	-0.88	1.2	-0.09	-0.09	-0.08	0.46
Cthe_00109	cellulosome enzyme, dockerin type I	6.11	5.17	6.95	5.75	-0.84	-0.58	0.94	1.2	-1.58	-1.44	0.99	2.08	-0.09	-0.08	0.52
Cthe_01912	copper amine oxidase-like protein	15.26	15.28	14.63	14.83	0.63	0.45	-0.02	-0.2	-0.08	0.07	-0.21	-0.05	-0.09	-0.08	0.28
Cthe_02464	hypothetical protein	5.21	3.7	4.32	4.39	0.89	-0.69	1.51	-0.07	0.18	-1.6	1.7	0.15	-0.09	-0.08	0.53
Cthe_02499	hypothetical protein	4.39	3	2.81	3.58	1.58	-0.58	1.39	-0.77	0.89	-1.44	1.55	-0.91	-0.09	-0.08	0.53
Cthe_00653	putative transcriptional regulator, CopG family	13.39	12.47	12.77	12.65	0.62	-0.18	0.92	0.12	-0.09	-0.85	0.96	0.44	-0.09	-0.08	0.45
Cthe_01732	hypothetical protein	5.83	5.09	5.58	5.21	0.25	-0.12	0.74	0.37	-0.47	-0.76	0.74	0.82	-0.09	-0.08	0.45
Cthe_01862	ABC transporter related protein	14.26	14.51	14.99	14.19	-0.73	0.32	-0.25	0.8	-1.47	-0.12	-0.5	1.47	-0.09	-0.08	0.53
Cthe_01862	ABC transporter related protein	14.26	14.51	14.99	14.19	-0.73	0.32	-0.25	0.8	-1.47	-0.12	-0.5	1.47	-0.09	-0.08	0.53
Cthe_01785	protein of unknown function DUF147	11.46	11.14	11.38	10.96	0.08	0.18	0.32	0.42	-0.64	-0.32	0.21	0.89	-0.1		



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Cthe_01533	transposase, mutator type	3.46	2.58	2.58	2.81	0.88	-0.23	0.88	-0.23	0.17	-0.93	0.91	-0.09	-0.13	-0.13	0.58
Cthe_01562	protein of unknown function DUF214	10.93	11.15	11.35	10.82	-0.42	0.33	-0.22	0.53	-1.15	-0.1	-0.46	1.06	-0.13	-0.13	0.56
Cthe_01282	diguanylate cyclase with GAF sensor	11.4	11.99	11.72	11.58	-0.32	0.41	-0.59	0.14	-1.05	0.01	-0.92	0.47	-0.13	-0.13	0.57
Cthe_01238	iojap-like protein	9.37	9.45	9.08	9.12	0.29	0.33	-0.08	-0.04	-0.43	-0.1	-0.29	0.2	-0.13	-0.13	0.7
Cthe_03044	protein of unknown function DUF975	10.54	10.63	11.26	10.27	-0.72	0.36	-0.09	0.99	-1.46	-0.06	-0.3	1.76	-0.13	-0.13	0.46
Cthe_00494	hypothetical protein	8.4	7.75	6.91	8.16	1.49	-0.41	0.65	-1.25	0.8	-1.19	0.62	-1.64	-0.13	-0.13	0.46
Cthe_03143	hypothetical protein	7.61	7.14	6.82	7.08	0.79	0.06	0.47	-0.26	0.08	-0.5	0.4	-0.14	-0.13	-0.13	0.67
Cthe_00014	hypothetical protein	8.11	6.27	6.67	6.95	1.44	-0.68	1.84	-0.28	0.74	-1.59	2.11	-0.17	-0.13	-0.13	0.47
Cthe_03038	hypothetical protein	9.25	8.03	10.75	8.86	-1.5	-0.83	1.22	1.89	-2.26	-1.81	1.34	3.12	-0.13	-0.13	0.48
Cthe_02032	hypothetical protein	10.13	9.71	9.92	9.57	0.21	0.14	0.42	0.35	-0.51	-0.38	0.34	0.79	-0.13	-0.13	0.42
Cthe_01621	hypothetical protein	6.15	5.7	6.07	5.73	0.08	-0.03	0.45	0.34	-0.64	-0.63	0.38	0.77	-0.13	-0.13	0.59
Cthe_01562	protein of unknown function DUF214	10.93	11.15	11.35	10.82	-0.42	0.33	-0.22	0.53	-1.15	-0.1	-0.46	1.06	-0.13	-0.13	0.56
Cthe_01560	Pyridoxal-5'-phosphate-dependent enzyme, beta	10.18	10.95	11.06	10.03	-0.88	0.92	-0.77	1.03	-1.62	0.76	-1.15	1.82	-0.13	-0.13	0.47
Cthe_00153	Holliday junction resolvase YagF	7.81	7.62	7.12	7.47	0.69	0.15	0.19	-0.35	-0.02	-0.37	0.05	-0.27	-0.13	-0.13	0.76
Cthe_01560	Pyridoxal-5'-phosphate-dependent enzyme, beta	10.18	10.95	11.06	10.03	-0.88	0.92	-0.77	1.03	-1.62	0.76	-1.15	1.82	-0.13	-0.13	0.47
Cthe_01560	Pyridoxal-5'-phosphate-dependent enzyme, beta	10.18	10.95	11.06	10.03	-0.88	0.92	-0.77	1.03	-1.62	0.76	-1.15	1.82	-0.13	-0.13	0.47
Cthe_00464	flagellar hook-basal body complex subunit FlIE	10.52	9.9	10.36	9.92	0.16	-0.02	0.62	0.44	-0.56	-0.62	0.59	0.92	-0.14	-0.14	0.43
Cthe_01903	polysaccharide deacetylase	5.29	4.25	4.09	4.32	1.2	-0.07	1.04	-0.23	0.5	-0.69	1.11	-0.09	-0.14	-0.14	0.43
Cthe_01956	Tagatose-6-phosphate kinase	9.76	9.94	9.46	9.79	0.3	0.15	-0.18	-0.33	-0.42	-0.37	-0.41	-0.24	-0.14	-0.14	0.66
Cthe_01057	phage shock protein C, PspC	8.29	7.32	8.4	7.79	-0.11	-0.47	0.97	0.61	-0.84	-1.28	1.02	1.18	-0.14	-0.14	0.55
Cthe_01664	transcriptional regulator, MerR family	6.67	6.54	5.83	6.29	0.84	0.25	0.13	-0.46	0.13	-0.22	-0.02	-0.44	-0.14	-0.14	0.33
Cthe_00676	tyrosine recombinase XerD	11.61	11.11	13.28	11.41	-1.67	-0.3	0.5	1.87	-2.43	-1.03	0.44	3.09	-0.14	-0.14	0.48
Cthe_00776	DNA mismatch repair protein MutL	11.13	11.35	10.66	10.87	0.47	0.48	-0.22	-0.21	-0.24	0.12	-0.46	-0.06	-0.14	-0.14	0.32
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_01959	Methyltransferase type 11	6.92	7.46	6.75	6.85	0.17	0.61	-0.54	-0.1	-0.55	0.31	-0.86	0.11	-0.14	-0.14	0.41
Cthe_00464	flagellar hook-basal body complex subunit FlIE	10.52	9.9	10.36	9.92	0.16	-0.02	0.62	0.44	-0.56	-0.62	0.59	0.92	-0.14	-0.14	0.43
Cthe_02029	glycosyltransferase	7.11	7.24	6.58	7.12	0.53	0.12	-0.13	-0.54	-0.18	-0.41	-0.35	-0.56	-0.14	-0.14	0.38
Cthe_02141	metal-dependent phosphohydrolase, HD subdomain	7.4	8.39	7.94	8.61	-0.54	-0.22	-0.99	-0.67	-1.28	-0.91	-1.42	-0.76	-0.14	-0.14	0.55
Cthe_00339	histidine kinase	11.94	12.5	11.86	12	0.08	0.5	-0.56	-0.14	-0.64	0.15	-0.89	0.05	-0.14	-0.14	0.41
Cthe_01057	phage shock protein C, PspC	8.29	7.32	8.4	7.79	-0.11	-0.47	0.97	0.61	-0.84	-1.28	1.02	1.18	-0.14	-0.14	0.55
Cthe_00337	PHP-like protein	9.75	9.72	9.21	9.79	0.54	-0.07	0.03	-0.58	-0.17	-0.69	-0.15	-0.62	-0.14	-0.14	0.63
Cthe_02577	adenylate cyclase	10.03	10.05	9.63	9.74	0.4	0.31	-0.02	-0.11	-0.32	-0.13	-0.21	0.09	-0.14	-0.14	0.85
Cthe_00351	PpiC-type peptidyl-prolyl cis-trans isomerase	11.4	11.29	10.59	11.03	0.81	0.26	0.11	-0.44	0.1	-0.21	-0.05	-0.41	-0.14	-0.14	0.32
Cthe_02002	hypothetical protein	6.82	6.3	5.98	6.07	0.84	0.23	0.52	-0.09	0.13	-0.25	0.46	0.12	-0.14	-0.14	0.33
Cthe_00752	hypothetical protein	6.23	5.32	5.04	5.64	1.19	-0.32	0.91	-0.6	0.49	-1.06	0.95	-0.65	-0.14	-0.14	0.57
Cthe_02661	Septum formation initiator	12.36	11.11	11.25	11.4	1.11	-0.29	1.25	-0.15	0.41	-1.01	1.38	0.03	-0.14	-0.14	0.44
Cthe_02857	hypothetical protein	8.34	7.73	7.62	7.77	0.72	-0.04	0.61	-0.15	0.01	-0.65	0.57	0.03	-0.14	-0.14	0.64
Cthe_03228	copper amine oxidase-like protein	8.89	8.88	8.39	8.7	0.5	0.18	0.01	-0.31	-0.21	-0.32	-0.17	-0.21	-0.14	-0.14	0.8
Cthe_02839	hypothetical protein	9.23	7.75	8.97	8.55	0.26	-0.8	1.48	0.42	-0.46	-1.76	1.66	0.89	-0.14	-0.14	0.54
Cthe_02477	hypothetical protein	6.63	4.86	5.25	5.49	1.38	-0.63	1.77	-0.24	0.68	-1.51	2.02	-0.11	-0.14	-0.14	0.46
Cthe_02141	metal-dependent phosphohydrolase, HD subdomain	7.4	8.39	7.94	8.61	-0.54	-0.22	-0.99	-0.67	-1.28	-0.91	-1.42	-0.76	-0.14	-0.14	0.55
Cthe_01956	Tagatose-6-phosphate kinase	9.76	9.94	9.46	9.79	0.3	0.15	-0.18	-0.33	-0.42	-0.37	-0.41	-0.24	-0.14	-0.14	0.66
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_01956	Tagatose-6-phosphate kinase	9.76	9.94	9.46	9.79	0.3	0.15	-0.18	-0.33	-0.42	-0.37	-0.41	-0.24	-0.14	-0.14	0.66
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_01956	Tagatose-6-phosphate kinase	9.76	9.94	9.46	9.79	0.3	0.15	-0.18	-0.33	-0.42	-0.37	-0.41	-0.24	-0.14	-0.14	0.66
Cthe_00737	Phosphopantethiene-protein transferase	10.57	10.61	10.11	10.48	0.46	0.13	-0.04	-0.37	-0.26	-0.4	-0.24	-0.3	-0.14	-0.14	0.7
Cthe_01048	Rhomboid-like protein	10.73	11.01	10.77	10.64	-0.04	0.37	-0.28	0.13	-0.77	-0.04	-0.54	0.45	-0.15	-0.15	0.62
Cthe_01353	polysaccharide biosynthesis protein	10.99	11.9	11.54	11.72	-0.55	0.18	-0.91	-0.18	-1.29	-0.32	-1.32	-0.02	-0.15	-0.15	0.57
Cthe_00993	protein of unknown function DUF448	6.71	8.06	7.49	7.5	-0.78	0.56	-1.35	-0.01	-1.52	0.24	-1.88	0.24	-0.15	-0.15	0.46
Cthe_00849	3-dehydroquinate dehydratase, type II	6.34	6.82	6.13	6.27	0.21	0.55	-0.48	-0.14	-0.51	0.22	-0.79	0.05	-0.15	-0.15	0.39
Cthe_01064	aminotransferase, class V	11.95	11.53	11.12	11.21	0.83	0.32	0.42	-0.09	0.12	-0.12	0.34	0.12	-0.15	-0.15	0.26
Cthe_01845	Homoserine O-succinyltransferase	12.22	12.09	11.78	11.81	0.44	0.28	0.13	-0.03	-0.28	-0.18	-0.02	0.21	-0.15	-0.15	0.89
Cthe_02832	transposase, mutator type	2.32	1	2	2.32	-1	1.32	-2	1.64	-2.06	1.46	-2.77	-0.15	-0.15	-0.15	0.47
Cthe_02189	diguanylate cyclase with GAF sensor	13.55	12.63	12.61	12.69	0.94	-0.06	0.92	-0.08	0.23	-0.68	0.96	0.14	-0.15	-0.15	0.42
Cthe_02609	ATP synthase F1, epsilon subunit	8.37	9.26	8.61	9.54	-0.24	-0.28	-0.89	-0.93	-0.97	-1	-1.3	-1.15	-0.15	-0.15	0.45
Cthe_01563	ABC transporter related protein	8.96	9.47	9.53	9.03	-0.57	0.44	-0.51	0.5	-1.31	0.06	-0.82	1.02	-0.15	-0.15	0.56
Cthe_02547	hypothetical protein	10.91	10.3	10.21	10.35	0.7	-0.05	0.61	-0.14	-0.01	-0.66	0.57	0.05	-0.15	-0.15	0.65
Cthe_01436	RNA related	7.31	5.67	6.94	6.43	0.37	-0.76	1.64	0.51	-0.35	-1.71	1.86	1.03	-0.15	-0.15	0.46
Cthe_00228	hypothetical protein	9.13	9.06	8.57	8.9	0.56	0.16	0.07	-0.33	-0.15	-0.35	-0.1	-0.24	-0.15	-0.15	0.82
Cthe_01832	hypothetical protein	10.24	10.84	10.37	11.02	-0.13	-0.18	-0.6	-0.65	-0.86	-0.85	-0.94	-0.73	-0.15	-0.15	0.57
Cthe_02760	glycoside hydrolase, family 9	11.09	10.45	10.01	10.76	1.08	-0.31	0.64	-0.75	0.38	-1.04	0.61	-0.88	-0.15	-0.15	0.58
Cthe_02175	hypothetical protein	11.39	9.48	10.34	10.3	1.05	-0.82	1.91	0.04	0.35	-1.79	2.2	0.32	-0.15	-0.15	0.46
Cthe_02669	hypothetical protein	8.67	7.89	8.55	8.17	0.12	-0.28	0.78	0.38	-0.6	-1	0.79	0.83	-0.15	-0.15	0.57
Cthe_00849	3-dehydroquinate dehydratase, type II	6.34	6.82	6.13	6.27	0.21	0.55	-0.48	-0.14	-0.51	0.22	-0.79	0.05	-0.15	-0.15	0.39
Cthe_01563	ABC transporter related protein	8.96	9.47	9.53	9.03	-0.57	0.44	-0.51	0.5	-1.31	0.06	-0.82	1.02	-0.15	-0.15	0.56
Cthe_02609	ATP synthase F1, epsilon subunit	8.37	9.26	8.61	9.54	-0.24	-0.28	-0.89	-0.93	-0.97	-1	-1.3	-1.15	-0.15	-0.15	0.45
Cthe_02609	ATP synthase F1, epsilon subunit	8.37	9.26	8.61	9.54	-0.24	-0.28	-0.89	-0.93	-0.97	-1	-1.3	-1.15	-0.15	-0.15	0.45
Cthe_01845	Homoserine O-succinyltransferase	12.22	12.09	11.78	11.81	0.44	0.28	0.13	-0.03	-0.28	-0.18	-0.02	0.21	-0.15	-0.15	0.89
Cthe_02609	ATP synthase F1, epsilon subunit	8.37	9.26	8.61	9.54	-0.24	-0.28	-0.89	-0.93	-0.97	-1	-1.3	-1.15	-0.15	-0.15	0.45
Cthe_01845	Homoserine O-succinyltransferase	12.22	12.09	11.78	11.81	0.44	0.28	0.13	-0.03	-0.28	-0.18	-0.02	0.21	-0.15	-0.15</	



Cthe_01536	ABC transporter related protein	6.38	7.41	6.77	6.78	-0.39	0.63	-1.03	-0.01	-1.12	0.34	-1.47	0.24	-0.16	-0.16	0.44
Cthe_00469	flagellar export protein FliJ	6.54	6.15	5.64	6.61	0.9	-0.46	0.39	-0.97	0.19	-1.26	0.3	-1.21	-0.16	-0.16	0.57
Cthe_02622	hypothetical protein	12.88	11.68	12.21	12.2	0.67	-0.52	1.2	0.01	-0.04	-1.35	1.31	0.27	-0.16	-0.16	0.57
Cthe_02121	hypothetical protein	10.58	9.91	10.39	9.95	0.19	-0.04	0.67	0.44	-0.53	-0.65	0.65	0.92	-0.16	-0.16	0.42
Cthe_01141	hypothetical protein	9.34	10.17	9.51	9.61	-0.17	0.56	-0.83	-0.1	-0.9	0.24	-1.22	0.11	-0.16	-0.16	0.43
Cthe_00084	hypothetical protein	11.61	10.33	11.46	11	0.15	-0.67	1.28	0.46	-0.57	-1.57	1.41	0.95	-0.16	-0.16	0.55
Cthe_02614	hypothetical protein	11.69	11.49	11.11	11.06	0.58	0.43	0.2	0.05	-0.13	0.04	0.06	0.33	-0.16	-0.16	0.23
Cthe_01574	hypothetical protein	11.7	11.6	10.87	11.34	0.83	0.26	0.1	-0.47	0.12	-0.21	-0.06	-0.45	-0.16	-0.16	0.3
Cthe_02314	hypothetical protein	10.77	10.37	9.98	10.31	0.79	0.06	0.4	-0.33	0.08	-0.5	0.31	-0.24	-0.16	-0.16	0.73
Cthe_00735	cellulosome anchoring protein, cohesion region	11.66	10.93	10.72	11.09	0.94	-0.16	0.73	-0.37	0.23	-0.82	0.72	-0.3	-0.16	-0.16	0.61
Cthe_01536	ABC transporter related protein	6.38	7.41	6.77	6.78	-0.39	0.63	-1.03	-0.01	-1.12	0.34	-1.47	0.24	-0.16	-0.16	0.44
Cthe_00910	extracellular solute-binding protein, family 5	9.64	9.81	9.56	9.48	0.08	0.33	-0.17	0.08	-0.64	-0.1	-0.4	0.38	-0.16	-0.16	0.66
Cthe_01224	ribosomal protein L35	10.07	10.15	9.67	10.05	0.4	0.1	-0.08	-0.38	-0.32	-0.44	-0.29	-0.32	-0.16	-0.16	0.71
Cthe_02536	phosphoadenosine phosphosulfate reductase	2.58	3.17	3	2	-0.42	1.17	-0.59	1	-1.15	1.13	-0.92	1.77	-0.16	-0.16	0.45
Cthe_01035	DNA ligase, NAD-dependent	9.49	9.66	9.56	9	-0.07	0.66	-0.17	0.56	-0.8	0.38	-0.4	1.11	-0.16	-0.16	0.42
Cthe_00556	asparagine synthase (glutamine-hydrolyzing)	8.95	8.87	8.8	8.43	0.15	0.44	0.08	0.37	-0.57	0.06	-0.09	0.82	-0.16	-0.16	0.39
Cthe_02536	phosphoadenosine phosphosulfate reductase	2.58	3.17	3	2	-0.42	1.17	-0.59	1	-1.15	1.13	-0.92	1.77	-0.16	-0.16	0.45
Cthe_00556	asparagine synthase (glutamine-hydrolyzing)	8.95	8.87	8.8	8.43	0.15	0.44	0.08	0.37	-0.57	0.06	-0.09	0.82	-0.16	-0.16	0.39
Cthe_02536	phosphoadenosine phosphosulfate reductase	2.58	3.17	3	2	-0.42	1.17	-0.59	1	-1.15	1.13	-0.92	1.77	-0.16	-0.16	0.45
Cthe_02536	phosphoadenosine phosphosulfate reductase	2.58	3.17	3	2	-0.42	1.17	-0.59	1	-1.15	1.13	-0.92	1.77	-0.16	-0.16	0.45
Cthe_02536	phosphoadenosine phosphosulfate reductase	2.58	3.17	3	2	-0.42	1.17	-0.59	1	-1.15	1.13	-0.92	1.77	-0.16	-0.16	0.45
Cthe_02536	phosphoadenosine phosphosulfate reductase	2.58	3.17	3	2	-0.42	1.17	-0.59	1	-1.15	1.13	-0.92	1.77	-0.16	-0.16	0.45
Cthe_02081	small GTP-binding protein	9.25	9.45	9.34	8.74	-0.09	0.71	-0.2	0.6	-0.82	0.46	-0.44	1.17	-0.17	-0.18	0.42
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_01606		4.91	3	3.46	3.7	1.45	-0.7	1.91	-0.24	0.76	-1.62	2.2	-0.11	-0.17	-0.18	0.46
Cthe_00974	UDP-N-acetylglucosamine--N-acetylmuramyl-	9.3	10.27	9.59	9.62	-0.29	0.65	-0.97	-0.03	-1.02	0.37	-1.4	0.21	-0.17	-0.18	0.43
Cthe_01076	protein of unknown function DUF881	9.93	9.49	9.3	9.42	0.63	0.07	0.44	-0.12	-0.08	-0.49	0.36	0.08	-0.17	-0.18	0.76
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_03046	cell cycle protein	7.42	9.06	8.41	8.04	-0.99	1.02	-1.64	0.37	-1.73	0.91	-2.24	0.82	-0.17	-0.18	0.46
Cthe_02823	hypothetical protein	9.4	8.73	9.77	9.04	-0.37	-0.31	0.67	0.73	-1.1	-1.04	0.65	1.36	-0.17	-0.18	0.56
Cthe_03211	protein of unknown function DUF324	5.98	6.52	6.78	6.11	-0.8	0.41	-0.54	0.67	-1.54	0.01	-0.86	1.27	-0.17	-0.18	0.56
Cthe_01882	hypothetical protein	4.91	3.81	2.81	4.58	2.1	-0.77	1.1	-1.77	1.42	-1.72	1.19	-2.42	-0.17	-0.18	0.46
Cthe_00662	hypothetical protein	6.87	6.99	6.3	6.55	0.57	0.44	-0.12	-0.25	-0.14	0.06	-0.34	-0.12	-0.17	-0.18	0.24
Cthe_02668	hypothetical protein	7.06	5.86	6.83	6.46	0.23	-0.6	1.2	0.37	-0.49	-1.47	1.31	0.82	-0.17	-0.18	0.56
Cthe_00974	UDP-N-acetylglucosamine--N-acetylmuramyl-	9.3	10.27	9.59	9.62	-0.29	0.65	-0.97	-0.03	-1.02	0.37	-1.4	0.21	-0.17	-0.18	0.43
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11.22	10.58	10.92	0.01	0.3	-0.63	-0.34	-0.71	-0.15	-0.97	-0.26	-0.17	-0.18	0.41
Cthe_00571	sun protein	10.59	11													



Cthe_03235	hypothetical protein	13.28	11.73	13.06	12.44	0.22	-0.71	1.55	0.62	-0.5	-1.63	1.75	1.2	-0.18	-0.19	0.45
Cthe_02894	hypothetical protein	11.36	9.94	10.15	10.3	1.21	-0.36	1.42	-0.15	0.51	-1.12	1.59	0.03	-0.18	-0.19	0.43
Cthe_02824	hypothetical protein	0	1	1.58		-1.58	1	-1	1.58	-2.34	0.88	-1.44	2.65	-0.18	-0.19	0.47
Cthe_01151	hypothetical protein	9.13	8.8	8.6	8.5	0.53	0.3	0.33	0.1	-0.18	-0.15	0.23	0.41	-0.18	-0.19	0.28
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_02796	pyruvate flavodoxin/ferredoxin	3	3.7	4	2.81	-1	0.89	-0.7	1.19	-1.74	0.72	-1.06	2.06	-0.18	-0.19	0.46
Cthe_00058	RNA polymerase sigma factor	10.48	9.1	9.08	9.35	1.4	-0.25	1.38	-0.27	0.7	-0.96	1.54	-0.15	-0.19	-0.2	0.43
Cthe_00890	RNA polymerase, sigma-24 subunit, ECF subfamily	7.59	6.94	6.78	7.06	0.81	-0.12	0.65	-0.28	0.1	-0.76	0.62	-0.17	-0.19	-0.2	0.67
Cthe_02530	glutamate-1-semialdehyde-2,1-aminomutase	4.58	3.81	2.81	4.17	1.77	-0.36	0.77	-1.36	1.08	-1.12	0.77	-1.8	-0.19	-0.2	0.45
Cthe_00809	CheW protein	6.25	5.04	6.11	5.67	0.14	-0.63	1.21	0.44	-0.58	-1.51	1.32	0.92	-0.19	-0.2	0.56
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.23	6.15	6.23	5.73	0	0.42	0.08	0.5	-0.72	0.03	-0.09	1.02	-0.19	-0.2	0.4
Cthe_00897	putative deoxyguanosinetriphosphate	8.84	7.02	7.62	7.7	1.22	-0.68	1.82	-0.08	0.52	-1.59	2.09	0.14	-0.19	-0.2	0.45
Cthe_00809	CheW protein	6.25	5.04	6.11	5.67	0.14	-0.63	1.21	0.44	-0.58	-1.51	1.32	0.92	-0.19	-0.2	0.56
Cthe_01268	histidine kinase	3.91	2.81	3	3	0.91	-0.19	1.1	0	0.2	-0.87	1.19	0.26	-0.19	-0.2	0.41
Cthe_02662	RNA binding S1	14.27	13.9	13.51	13.87	0.76	0.03	0.37	-0.36	0.05	-0.54	0.27	-0.29	-0.19	-0.2	0.77
Cthe_01588	extracellular solute-binding protein, family 1	9.44	7.79	10.17	8.77	-0.73	-0.98	1.65	1.4	-1.47	-2.03	1.88	2.38	-0.19	-0.2	0.46
Cthe_00936	3-oxoacyl-(acyl-carrier-protein) synthase III	11.08	11.94	11.29	11.62	-0.21	0.32	-0.86	-0.33	-0.94	-0.12	-1.26	-0.24	-0.19	-0.2	0.42
Cthe_00657	hypothetical protein	11.79	11.38	11.58	11.2	0.21	0.18	0.41	0.38	-0.51	-0.32	0.33	0.83	-0.19	-0.2	0.38
Cthe_01535	hypothetical protein	5.7	6.57	5.88	6.02	-0.18	0.55	-0.87	-0.14	-0.91	0.22	-1.27	0.05	-0.19	-0.2	0.41
Cthe_00936	3-oxoacyl-(acyl-carrier-protein) synthase III	11.08	11.94	11.29	11.62	-0.21	0.32	-0.86	-0.33	-0.94	-0.12	-1.26	-0.24	-0.19	-0.2	0.42
Cthe_01588	extracellular solute-binding protein, family 1	9.44	7.79	10.17	8.77	-0.73	-0.98	1.65	1.4	-1.47	-2.03	1.88	2.38	-0.19	-0.2	0.46
Cthe_02530	glutamate-1-semialdehyde-2,1-aminomutase	4.58	3.81	2.81	4.17	1.77	-0.36	0.77	-1.36	1.08	-1.12	0.77	-1.8	-0.19	-0.2	0.45
Cthe_00936	3-oxoacyl-(acyl-carrier-protein) synthase III	11.08	11.94	11.29	11.62	-0.21	0.32	-0.86	-0.33	-0.94	-0.12	-1.26	-0.24	-0.19	-0.2	0.42
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.23	6.15	6.23	5.73	0	0.42	0.08	0.5	-0.72	0.03	-0.09	1.02	-0.19	-0.2	0.4
Cthe_00936	3-oxoacyl-(acyl-carrier-protein) synthase III	11.08	11.94	11.29	11.62	-0.21	0.32	-0.86	-0.33	-0.94	-0.12	-1.26	-0.24	-0.19	-0.2	0.42
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.23	6.15	6.23	5.73	0	0.42	0.08	0.5	-0.72	0.03	-0.09	1.02	-0.19	-0.2	0.4
Cthe_00936	3-oxoacyl-(acyl-carrier-protein) synthase III	11.08	11.94	11.29	11.62	-0.21	0.32	-0.86	-0.33	-0.94	-0.12	-1.26	-0.24	-0.19	-0.2	0.42
Cthe_00897	putative deoxyguanosinetriphosphate	8.84	7.02	7.62	7.7	1.22	-0.68	1.82	-0.08	0.52	-1.59	2.09	0.14	-0.19	-0.2	0.45
Cthe_01268	histidine kinase	3.91	2.81	3	3	0.91	-0.19	1.1	0	0.2	-0.87	1.19	0.26	-0.19	-0.2	0.41
Cthe_02530	glutamate-1-semialdehyde-2,1-aminomutase	4.58	3.81	2.81	4.17	1.77	-0.36	0.77	-1.36	1.08	-1.12	0.77	-1.8	-0.19	-0.2	0.45
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.23	6.15	6.23	5.73	0	0.42	0.08	0.5	-0.72	0.03	-0.09	1.02	-0.19	-0.2	0.4
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.23	6.15	6.23	5.73	0	0.42	0.08	0.5	-0.72	0.03	-0.09	1.02	-0.19	-0.2	0.4
Cthe_00936	3-oxoacyl-(acyl-carrier-protein) synthase III	11.08	11.94	11.29	11.62	-0.21	0.32	-0.86	-0.33	-0.94	-0.12	-1.26	-0.24	-0.19	-0.2	0.42
Cthe_00936	3-oxoacyl-(acyl-carrier-protein) synthase III	11.08	11.94	11.29	11.62	-0.21	0.32	-0.86	-0.33	-0.94	-0.12	-1.26	-0.24	-0.19	-0.2	0.42
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.23	6.15	6.23	5.73	0	0.42	0.08	0.5	-0.72	0.03	-0.09	1.02	-0.19	-0.2	0.4
Cthe_02530	glutamate-1-semialdehyde-2,1-aminomutase	4.58	3.81	2.81	4.17	1.77	-0.36	0.77	-1.36	1.08	-1.12	0.77	-1.8	-0.19	-0.2	0.45
Cthe_00855	HAD superfamily (subfamily IIA) phosphatase,	10.33	10.21	9.44	10.01	0.89	0.2	0.12	-0.57	0.18	-0.29	-0.04	-0.61	-0.2	-0.22	0.31
Cthe_02427	protein of unknown function DUF1385	11.3	11.83	11.13	11.35	0.17	0.48	-0.53	-0.22	-0.55	0.12	-0.85	-0.08	-0.2	-0.22	0.37
Cthe_01346	single-stranded-DNA-specific exonuclease RecJ	11.71	12.06	11.38	11.71	0.33	0.35	-0.35	-0.33	-0.39	-0.07	-0.62	-0.24	-0.2	-0.22	0.33
Cthe_02850	transposase IS116/IS110/IS902	4.58	2.81	3	3.32	1.58	-0.51	1.77	-0.32	0.89	-1.34	2.02	-0.23	-0.2	-0.22	0.44
Cthe_00928	4-hydroxythreonine-4-phosphate dehydrogenase	8.6	8.74	8.27	8.82	0.33	-0.08	-0.14	-0.55	-0.39	-0.71	-0.36	-0.58	-0.2	-0.22	0.67
Cthe_00979	Peptidoglycan glycosyltransferase	10.17	10.47	10.65	9.79	-0.48	-0.68	-0.3	0.86	-1.21	0.41	-0.56	1.56	-0.2	-0.22	0.43
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_03085	response regulator receiver protein	11.53	11.85	11.47	11.65	0.06	0.2	-0.32	-0.18	-0.66	-0.29	-0.59	-0.02	-0.2	-0.22	0.69
Cthe_02991	NADH:flavin oxidoreductase/NADH oxidase	7.67	8.1	8.45	7.37	-0.78	0.73	-0.43	1.08	-1.52	0.49	-0.72	1.89	-0.2	-0.22	0.44
Cthe_02991	NADH:flavin oxidoreductase/NADH oxidase	7.67	8.1	8.45	7.37	-0.78	0.73	-0.43	1.08	-1.52	0.49	-0.72	1.89	-0.2	-0.22	0.44
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_00928	4-hydroxythreonine-4-phosphate dehydrogenase	8.6	8.74	8.27	8.82	0.33	-0.08	-0.14	-0.55	-0.39	-0.71	-0.36	-0.58	-0.2	-0.22	0.67
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_01346	single-stranded-DNA-specific exonuclease RecJ	11.71	12.06	11.38	11.71	0.33	0.35	-0.35	-0.33	-0.39	-0.07	-0.62	-0.24	-0.2	-0.22	0.33
Cthe_00928	4-hydroxythreonine-4-phosphate dehydrogenase	8.6	8.74	8.27	8.82	0.33	-0.08	-0.14	-0.55	-0.39	-0.71	-0.36	-0.58	-0.2	-0.22	0.67
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.8	0.14	0.48	-0.56	-0.22	-0.58	0.12	-0.89	-0.08	-0.2	-0.22	0.37
Cthe_01352	UDP-glucose 6-dehydrogenase	11.72	12.28	11.58	11.											



Cthe_01138	protein of unknown function DUF87	8.23	8.96	8.28	8.92	-0.05	0.04	-0.73	-0.64	-0.78	-0.53	-1.1	-0.71	-0.22	-0.24	0.4
Cthe_01620	Protein of unknown function DUF132	11.75	11.62	12	11.28	-0.25	0.34	0.13	0.72	-0.98	-0.09	-0.02	1.35	-0.22	-0.24	0.41
Cthe_02656	MazG family protein	10.65	10.78	10.36	10.61	0.29	0.17	-0.13	-0.25	-0.43	-0.34	-0.35	-0.12	-0.22	-0.24	0.83
Cthe_02749	hypothetical protein	10.89	11.03	10.82	10.75	0.07	0.28	-0.14	0.07	-0.65	-0.18	-0.36	0.36	-0.22	-0.24	0.74
Cthe_02515	Guanine deaminase	9.13	9.2	8.89	8.93	0.24	0.27	-0.07	-0.04	-0.48	-0.19	-0.27	0.2	-0.22	-0.24	0.86
Cthe_00637	protein of unknown function DUF909	15.07	14.57	14.89	14.65	0.18	-0.08	0.5	0.24	-0.54	-0.71	0.44	0.62	-0.22	-0.24	0.66
Cthe_01168	Extradiol ring-cleavage dioxygenase, class III	8.9	9.18	8.8	9	0.1	0.18	-0.28	-0.2	-0.62	-0.32	-0.54	-0.05	-0.22	-0.24	0.72
Cthe_03042	hypothetical protein	12.68	11.62	12.32	12.11	0.36	-0.49	1.06	0.21	-0.36	-1.31	1.14	0.58	-0.22	-0.24	0.6
Cthe_02515	Guanine deaminase	9.13	9.2	8.89	8.93	0.24	0.27	-0.07	-0.04	-0.48	-0.19	-0.27	0.2	-0.22	-0.24	0.86
Cthe_02717	ribosomal protein L33	7.4	7.59	6.89	7.42	0.51	0.17	-0.19	-0.53	-0.2	-0.34	-0.42	-0.55	-0.22	-0.24	0.32
Cthe_00545	prepilin peptidase CpaA	7.99	7.35	7.46	7.48	0.53	-0.13	0.64	-0.02	-0.18	-0.78	0.61	0.23	-0.22	-0.24	0.69
Cthe_01167	Radical SAM	9.11	9.35	8.66	9.13	0.45	0.22	-0.24	-0.47	-0.27	-0.26	-0.49	-0.45	-0.22	-0.24	0.32
Cthe_00862	hypothetical protein	9.83	10.03	9.85	9.74	-0.02	0.29	-0.2	0.11	-0.74	-0.16	-0.44	0.42	-0.22	-0.24	0.7
Cthe_00221	hypothetical protein	7.77	7.32	7.67	7.18	0.1	0.14	0.45	0.49	-0.62	-0.38	0.38	1	-0.22	-0.24	0.38
Cthe_00433	glycoside hydrolase, family 9	11.81	12.24	11.83	12.22	-0.02	0.02	-0.43	-0.39	-0.74	-0.56	-0.72	-0.33	-0.22	-0.24	0.66
Cthe_00802	hypothetical protein	6.86	5.86	6.67	6.13	0.19	-0.27	1	0.54	-0.53	-0.99	1.06	1.08	-0.22	-0.24	0.42
Cthe_02717	ribosomal protein L33	7.4	7.59	6.89	7.42	0.51	0.17	-0.19	-0.53	-0.2	-0.34	-0.42	-0.55	-0.22	-0.24	0.32
Cthe_00545	prepilin peptidase CpaA	7.99	7.35	7.46	7.48	0.53	-0.13	0.64	-0.02	-0.18	-0.78	0.61	0.23	-0.22	-0.24	0.69
Cthe_02515	Guanine deaminase	9.13	9.2	8.89	8.93	0.24	0.27	-0.07	-0.04	-0.48	-0.19	-0.27	0.2	-0.22	-0.24	0.86
Cthe_01167	Radical SAM	9.11	9.35	8.66	9.13	0.45	0.22	-0.24	-0.47	-0.27	-0.26	-0.49	-0.45	-0.22	-0.24	0.32
Cthe_02515	Guanine deaminase	9.13	9.2	8.89	8.93	0.24	0.27	-0.07	-0.04	-0.48	-0.19	-0.27	0.2	-0.22	-0.24	0.86
Cthe_02515	Guanine deaminase	9.13	9.2	8.89	8.93	0.24	0.27	-0.07	-0.04	-0.48	-0.19	-0.27	0.2	-0.22	-0.24	0.86
Cthe_02515	Guanine deaminase	9.13	9.2	8.89	8.93	0.24	0.27	-0.07	-0.04	-0.48	-0.19	-0.27	0.2	-0.22	-0.24	0.86
Cthe_02119	glycoside hydrolase, family 10	11.06	11.35	11.16	11.06	-0.1	0.29	-0.29	0.1	-0.83	-0.16	-0.55	0.41	-0.23	-0.25	0.69
Cthe_00519	DNA methylase N-4/N-6	10.43	10.78	10.03	10.3	0.4	0.48	-0.35	-0.27	-0.32	0.12	-0.62	-0.15	-0.23	-0.25	0.3
Cthe_02959		10.72	9.66	11.83	10.45	-1.11	-0.79	1.06	1.38	-1.86	-1.75	1.14	2.35	-0.23	-0.25	0.55
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.48	11.06	10.29	10.49	0.19	0.57	-0.58	-0.2	-0.53	0.25	-0.91	-0.05	-0.23	-0.25	0.36
Cthe_00817	diguanylate cyclase	7.9	7.3	7.12	7.42	0.78	-0.12	0.6	-0.3	0.07	-0.76	0.56	-0.2	-0.23	-0.25	0.72
Cthe_00205	hypothetical protein	11.17	11.66	10.88	11.11	0.29	0.55	-0.49	-0.23	-0.43	0.22	-0.8	-0.09	-0.23	-0.25	0.34
Cthe_02044	hypothetical protein	6.32	5.36	5.52	5.73	0.8	-0.37	0.96	-0.21	0.09	-1.13	1.01	-0.06	-0.23	-0.25	0.63
Cthe_01670	Recombinase	5.32	3.81	4	4.17	1.32	-0.36	1.51	-0.17	0.62	-1.12	1.7	0	-0.23	-0.25	0.42
Cthe_00386	hypothetical protein	8.16	6.25	7.89	7.2	0.27	-0.95	1.91	0.69	-0.45	-1.99	2.2	1.3	-0.23	-0.25	0.45
Cthe_00501	hypothetical protein	10.84	9.35	9.95	10.12	0.89	-0.77	1.49	-0.17	0.18	-1.72	1.68	0	-0.23	-0.25	0.58
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.48	11.06	10.29	10.49	0.19	0.57	-0.58	-0.2	-0.53	0.25	-0.91	-0.05	-0.23	-0.25	0.36
Cthe_00519	DNA methylase N-4/N-6	10.43	10.78	10.03	10.3	0.4	0.48	-0.35	-0.27	-0.32	0.12	-0.62	-0.15	-0.23	-0.25	0.3
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.48	11.06	10.29	10.49	0.19	0.57	-0.58	-0.2	-0.53	0.25	-0.91	-0.05	-0.23	-0.25	0.36
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.48	11.06	10.29	10.49	0.19	0.57	-0.58	-0.2	-0.53	0.25	-0.91	-0.05	-0.23	-0.25	0.36
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.48	11.06	10.29	10.49	0.19	0.57	-0.58	-0.2	-0.53	0.25	-0.91	-0.05	-0.23	-0.25	0.36
Cthe_00436	Tetratricopeptide TPR_2	11.4	11.97	11.86	11.65	-0.46	0.32	-0.57	0.21	-1.19	-0.12	-0.9	0.58	-0.24	-0.27	0.63
Cthe_01472	Carbohydrate binding family 11	11.81	10.58	11.15	11.17	0.66	-0.59	1.23	-0.02	-0.05	-1.46	1.35	0.23	-0.24	-0.27	0.6
Cthe_03041	UbiA prenyltransferase	10.54	10.65	10.47	10.39	0.07	0.26	-0.11	0.08	-0.65	-0.21	-0.33	0.38	-0.24	-0.27	0.76
Cthe_00436	Tetratricopeptide TPR_2	11.4	11.97	11.86	11.65	-0.46	0.32	-0.57	0.21	-1.19	-0.12	-0.9	0.58	-0.24	-0.27	0.63
Cthe_03097	glycosyl transferase, family 2	13.25	13.44	13.12	13.2	0.13	0.24	-0.19	-0.08	-0.59	-0.24	-0.42	0.14	-0.24	-0.27	0.81
Cthe_00051	hypothetical protein	4.86	4.25	5.58	4.39	-0.72	-0.14	0.61	1.19	-1.46	-0.79	0.57	2.06	-0.24	-0.27	0.44
Cthe_01203	SpoVR	9.94	10.55	11.1	10.2	-1.16	0.35	-0.61	0.9	-1.91	-0.07	-0.95	1.62	-0.24	-0.27	0.57
Cthe_00614	pyruvate ferredoxin/ferredoxin oxidoreductase	10.96	11.56	10.78	10.99	0.18	0.57	-0.6	-0.21	-0.54	0.25	-0.94	-0.06	-0.24	-0.27	0.35
Cthe_02602	ATP synthase FO, A subunit	12.79	12.73	12.76	12.55	0.03	0.18	0.06	0.21	-0.69	-0.32	-0.11	0.58	-0.24	-0.27	0.72
Cthe_02086	peptidase U32	9.85	10.39	10.02	10.32	-0.17	0.07	-0.54	-0.3	-0.9	-0.49	-0.86	-0.2	-0.24	-0.27	0.65
Cthe_03142	hypothetical protein	10.12	9.39	9.59	9.37	0.53	0.02	0.73	0.22	-0.18	-0.56	0.72	0.59	-0.24	-0.27	0.36
Cthe_00921	hypothetical protein	6.51	6.09	7.6	6.15	-1.09	-0.06	0.42	1.45	-1.84	-0.68	0.34	2.45	-0.24	-0.27	0.45
Cthe_02751	hypothetical protein	6.66	7.01	6.67	6.83	-0.01	0.18	-0.35	-0.16	-0.73	-0.32	-0.62	0.02	-0.24	-0.27	0.72
Cthe_01198	hypothetical protein	6.48	5.39	5.43	5.49	1.05	-0.1	1.09	-0.06	0.35	-0.74	1.18	0.17	-0.24	-0.27	0.39
Cthe_01926	intein	8.02	6.79	7.55	7.17	0.47	-0.38	1.23	0.38	-0.24	-1.15	1.35	0.83	-0.24	-0.27	0.42
Cthe_00614	pyruvate ferredoxin/ferredoxin oxidoreductase	10.96	11.56	10.78	10.99	0.18	0.57	-0.6	-0.21	-0.54	0.25	-0.94	-0.06	-0.24	-0.27	0.35
Cthe_02602	ATP synthase FO, A subunit	12.79	12.73	12.76	12.55	0.03	0.18	0.06	0.21	-0.69	-0.32	-0.11	0.58	-0.24	-0.27	0.72
Cthe_02602	ATP synthase FO, A subunit	12.79	12.73	12.76	12.55	0.03	0.18	0.06	0.21	-0.69	-0.32	-0.11	0.58	-0.24	-0.27	0.72
Cthe_02602	ATP synthase FO, A subunit	12.79	12.73	12.76	12.55	0.03	0.18	0.06	0.21	-0.69	-0.32	-0.11	0.58	-0.24	-0.27	0.72
Cthe_00614	pyruvate ferredoxin/ferredoxin oxidoreductase	10.96	11.56	10.78	10.99	0.18	0.57	-0.6	-0.21	-0.54	0.25	-0.94	-0.06	-0.24	-0.27	0.35
Cthe_01472	Carbohydrate binding family 11	11.81	10.58	11.15	11.17	0.66	-0.59	1.23	-0.02	-0.05	-1.46	1.35	0.23	-0.24	-0.27	0.6
Cthe_02086	peptidase U32	9.85	10.39	10.02	10.32	-0.17	0.07	-0.54	-0.3	-0.9	-0.49	-0.86	-0.2	-0.24	-0.27	0.65
Cthe_01472	Carbohydrate binding family 11	11.81	10.58	11.15	11.17	0.66	-0.59	1.23	-0.02	-0.05	-1.46	1.35	0.23	-0.24	-0.27	0.6
Cthe_02602	ATP synthase FO, A subunit	12.79	12.73	12.76	12.55	0.03	0.18	0.06	0.21	-0.69	-0.32	-0.11	0.58	-0.24	-0.27	0.72
Cthe_00270	glycoside hydrolase, family 18	10.36	10.97	10.66	10.82	-0.3	0.15	-0.61	-0.16	-1.03	-0.37	-0.95	0.02	-0.25	-0.28	0.65
Cthe_01813	urease accessory protein UreG	3.17	3.46	3.46	2.58	-0.29	0.88	-0.29	0.88	-1.02	0.71	-0.55	1.59	-0.25	-0.28	0.41
Cthe_00197	glutamine amidotransferase, class-II	7.89	8.31	7.55	7.83	0.34	0.48	-0.42	-0.28	-0.38	0.12	-0.71	-0.17	-0.25	-0.28	0.31
Cthe_02884	Imidazoleglycerol-phosphate dehydratase	10.86	10.81	10.02	10.52	0.84	0.29	0.05	-0.5	0.13	-0.16	-0.12	-0.5	-0.25	-0.28	0.23
Cthe_01700	Recombinase	5.43	4.17	4.17	4.32	1.26	-0.15	1.26	-0.15	0.56	-0.81	1.39	0.03	-0.25	-0.28	0.4
Cthe_03210	protein of unknown function DUF324	4.86	5.55	5.61	5.17	-0.75	0.38	-0.69	0.44	-1.49	-0.03	-1.05	0.92	-0.25	-0.28	0.6
Cthe_00466	flagellar motor switch protein FlgI	10.35	9.96	9.57	10.11	0.78	-0.15	0.39	-0.54	0.07	-0.81	0.3	-0.56	-0.25	-0.28	0.72
Cthe_01349	Undecaprenyl-phosphate galactose	12.07	11.59	11.7	11.63	0.37	-0.04	0.48	0.07	-0.35	-0.65	0.41	0.36	-0.25	-0.28	0.76
Cthe_01807	hypothetical protein	11.36	13.07	13.75	12.37	-2.39	0.7	-1.71	1.38	-3.16	0.44	-2.32	2.35	-0.25	-0.28	0.54
Cthe_00779	copper amine oxidase-like protein	9.88	9.45	9.17	9.15	0.71	0.3	0.43	0.02	0	-0.15	0.35	0.29	-0.25	-0.28	0.19
Cthe_01406	hypothetical protein	4.25	4.46	3.7	4	0.55	0.46	-0.21	-0.3	-0.16	0.09	-0.45	-0.2	-0.25	-0.28	0.21
Cthe_02790	ABC transporter related protein	3.17	3	2.58	2.81	0.59	0.19	0.17	-0.23	-0.12	-0.31	0.03	-0.09	-0.25	-0.28	1.97
Cthe_01813	urease accessory protein UreG	3.17	3.46	3.46	2.58	-0.29	0.88	-0.29	0.88	-1.02	0.71	-0.55	1.59	-0.25	-0.28	0.41



Cthe_01741	hypothetical protein			1	0	-1	0	1	-1.74	-0.59	1.77	-0.26	-0.29	0.58		
Cthe_02010	hypothetical protein	7.69	6.69	7.01	7.11	0.68	-0.42	1	-0.1	-0.03	-1.21	1.06	0.11	-0.26	-0.29	0.64
Cthe_00066	hypothetical protein	6.23	6.67	7.15	5.93	-0.92	0.74	-0.44	1.22	-1.66	0.5	-0.74	2.11	-0.26	-0.29	0.44
Cthe_00896	DNA primase	12.49	11.51	11.6	11.92	0.89	-0.41	0.98	-0.32	0.18	-1.19	1.04	-0.23	-0.26	-0.29	0.63
Cthe_00807	response regulator receiver modulated CheB	7.73	6.3	7.09	7.06	0.64	-0.76	1.43	0.03	-0.07	-1.71	1.6	0.3	-0.26	-0.29	0.59
Cthe_00896	DNA primase	12.49	11.51	11.6	11.92	0.89	-0.41	0.98	-0.32	0.18	-1.19	1.04	-0.23	-0.26	-0.29	0.63
Cthe_00896	DNA primase	12.49	11.51	11.6	11.92	0.89	-0.41	0.98	-0.32	0.18	-1.19	1.04	-0.23	-0.26	-0.29	0.63
Cthe_00896	DNA primase	12.49	11.51	11.6	11.92	0.89	-0.41	0.98	-0.32	0.18	-1.19	1.04	-0.23	-0.26	-0.29	0.63
Cthe_00896	DNA primase	12.49	11.51	11.6	11.92	0.89	-0.41	0.98	-0.32	0.18	-1.19	1.04	-0.23	-0.26	-0.29	0.63
Cthe_00774	RNA chaperone Hfq	11	9.9	10.96	10.26	0.04	-0.36	1.1	0.7	-0.68	-1.12	1.19	1.32	-0.27	-0.3	0.41
Cthe_02275	hypothetical protein	8.9	8.55	8.63	8.52	0.27	0.03	0.35	0.11	-0.45	-0.54	0.25	0.42	-0.27	-0.3	0.81
Cthe_00895	RNA polymerase, sigma 38 subunit, RpoS	12.85	12.34	12.11	12.42	0.74	-0.08	0.51	-0.31	0.03	-0.71	0.45	-0.21	-0.27	-0.3	0.8
Cthe_01538	transcriptional regulator, XRE family	7.94	8.88	8.67	8.68	-0.73	0.2	-0.94	-0.01	-1.47	-0.29	-1.36	0.24	-0.27	-0.3	0.61
Cthe_00292	transposase, mutator type	11.92	10.9	10.75	10.86	1.17	0.04	1.02	-0.11	0.47	-0.53	1.09	0.09	-0.27	-0.3	0.36
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.58	11.94	11.16	11.46	0.42	0.48	-0.36	-0.3	-0.3	0.12	-0.64	-0.2	-0.27	-0.3	0.27
Cthe_02139	alpha-L-arabinofuranosidase B	8.12	8.09	7.3	7.89	0.82	0.2	0.03	-0.59	0.11	-0.29	-0.15	-0.64	-0.27	-0.3	0.27
Cthe_03045	FHA domain containing protein	7.32	8.18	8.35	7.77	-1.03	0.41	-0.86	0.58	-1.78	0.01	-1.26	1.14	-0.27	-0.3	0.59
Cthe_00093	septum site-determining protein MinD	12.53	12.7	11.98	12.39	0.55	0.31	-0.17	-0.41	-0.16	-0.13	-0.4	-0.36	-0.27	-0.3	0.22
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.58	11.94	11.16	11.46	0.42	0.48	-0.36	-0.3	-0.3	0.12	-0.64	-0.2	-0.27	-0.3	0.27
Cthe_01096	hypothetical protein	3.91	4.7	4.46	4.52	-0.55	0.18	-0.79	-0.06	-1.29	-0.32	-1.18	0.17	-0.27	-0.3	0.63
Cthe_01128	hypothetical protein	4.58	4.17	4.58	4.25	0	-0.08	0.41	0.33	-0.72	-0.71	0.33	0.76	-0.27	-0.3	0.69
Cthe_02360	glycoside hydrolase, family 9	8.83	8.78	8.34	8.97	0.49	-0.19	0.05	-0.63	-0.22	-0.87	-0.12	-0.7	-0.27	-0.3	0.71
Cthe_03080	cellulosome anchoring protein, cohesion region	12.16	13.68	13.42	13.81	-1.26	-0.13	-1.52	-0.39	-2.01	-0.78	-2.09	-0.33	-0.27	-0.3	0.57
Cthe_02331	hypothetical protein	14.19	12.97	13.52	13.28	0.67	-0.31	1.22	0.24	-0.04	-1.04	1.34	0.62	-0.27	-0.3	0.4
Cthe_02438	hypothetical protein	9.39	8.73	9.24	8.97	0.15	-0.24	0.66	0.27	-0.57	-0.94	0.64	0.67	-0.27	-0.3	0.67
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.58	11.94	11.16	11.46	0.42	0.48	-0.36	-0.3	-0.3	0.12	-0.64	-0.2	-0.27	-0.3	0.27
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.58	11.94	11.16	11.46	0.42	0.48	-0.36	-0.3	-0.3	0.12	-0.64	-0.2	-0.27	-0.3	0.27
Cthe_02633	hypothetical protein	13.77	12.74	12.94	12.86	0.83	-0.12	1.03	0.08	0.12	-0.76	1.1	0.38	-0.27	-0.3	0.37
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.58	11.94	11.16	11.46	0.42	0.48	-0.36	-0.3	-0.3	0.12	-0.64	-0.2	-0.27	-0.3	0.27
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.58	11.94	11.16	11.46	0.42	0.48	-0.36	-0.3	-0.3	0.12	-0.64	-0.2	-0.27	-0.3	0.27
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.58	11.94	11.16	11.46	0.42	0.48	-0.36	-0.3	-0.3	0.12	-0.64	-0.2	-0.27	-0.3	0.27
Cthe_01070	metal dependent phosphohydrolase	11.67	12.31	11.38	11.62	0.29	0.69	-0.64	-0.24	-0.43	0.43	-0.99	-0.11	-0.28	-0.32	0.34
Cthe_01471	glycoside hydrolase, family 5	11.2	10.86	11.03	10.58	0.17	0.28	0.34	0.45	-0.55	-0.18	0.24	0.94	-0.28	-0.32	0.34
Cthe_00067	Silent information regulator protein Sir2	10.82	11.02	10.29	10.66	0.53	0.36	-0.2	-0.37	-0.18	-0.06	-0.44	-0.3	-0.28	-0.32	0.2
Cthe_00210	transcriptional regulator, LacI family	11.58	11.32	10.93	11.36	0.65	-0.04	0.26	-0.43	-0.06	-0.65	0.14	-0.39	-0.28	-0.32	0.89
Cthe_00495	RNA polymerase, sigma 28 subunit	9.74	8.7	8.5	9.34	1.24	-0.64	1.04	-0.84	0.54	-1.53	1.11	-1.02	-0.28	-0.32	0.6
Cthe_03026	GreA/GreB family elongation factor	9.18	10.16	9.82	10.33	-0.64	-0.17	-0.98	-0.51	-1.38	-0.84	-1.41	-0.52	-0.28	-0.32	0.6
Cthe_01587	ABC transporter related protein	5.29	4.32	6.71	5.13	-1.42	-0.81	0.97	1.58	-2.17	-1.78	1.02	2.65	-0.28	-0.32	0.56
Cthe_01874	transposase, mutator type	4.95	4.25	4.09	4.09	0.86	0.16	0.7	0	0.15	-0.35	0.69	0.26	-0.28	-0.32	0.29
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_02244	flagellar hook-associated protein FlgK	7.14	7.76	7.04	7.79	0.1	-0.03	-0.62	-0.75	-0.62	-0.63	-0.96	-0.88	-0.28	-0.32	0.38
Cthe_01204	protein of unknown function DUF444	9.2	9.91	10.3	9.54	-1.1	0.37	-0.71	0.76	-1.85	-0.04	-1.07	1.41	-0.28	-0.32	0.59
Cthe_02078	protein of unknown function UPF0029	9.2	9.16	8.77	8.96	0.43	0.2	0.04	-0.19	-0.29	-0.29	-0.14	-0.03	-0.28	-0.32	1.61
Cthe_00628	hypothetical protein	10.81	11.61	10.82	11.02	-0.01	0.59	-0.8	-0.2	-0.73	0.28	-1.19	-0.05	-0.28	-0.32	0.37
Cthe_00788	DivIVA	10.37	10.23	10.19	10.08	0.18	0.15	0.14	0.11	-0.54	-0.37	-0.01	0.42	-0.28	-0.32	0.88
Cthe_00134	hypothetical protein	8.38	9.63	9.32	9.84	-0.94	-0.21	-1.25	-0.52	-1.68	-0.9	-1.75	-0.53	-0.28	-0.32	0.59
Cthe_01192	hypothetical protein	10.04	10.07	11.9	10.24	-1.86	-0.17	-0.03	1.66	-2.62	-0.84	-0.22	2.77	-0.28	-0.32	0.56
Cthe_02828	hypothetical protein	8.7	8.25	7.95	8.37	0.75	-0.12	0.45	-0.42	0.04	-0.76	0.38	-0.38	-0.28	-0.32	0.8
Cthe_01640	hypothetical protein	1	0			1	0	1	0.3	-0.59	1.06			-0.28	-0.32	0.35
Cthe_01781	hypothetical protein	9.51	8.71	8.9	8.99	0.61	-0.28	0.8	-0.09	-0.1	-1	0.81	0.12	-0.28	-0.32	0.69
Cthe_01587	ABC transporter related protein	5.29	4.32	6.71	5.13	-1.42	-0.81	0.97	1.58	-2.17	-1.78	1.02	2.65	-0.28	-0.32	0.56
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_01512	Type II site-specific deoxyribonuclease	7.92	8.86	7.94	8.08	-0.02	0.78	-0.94	-0.14	-0.74	0.56	-1.36	0.05	-0.28	-0.32	0.38
Cthe_00067	Silent information regulator protein Sir2	10.82	11.02	10.29	10.66	0.53	0.36	-0.2	-0.37	-0.18	-0.06	-0.44	-0.3	-0.28	-0.32	0.2
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_01587	ABC transporter related protein	5.29	4.32	6.71	5.13	-1.42	-0.81	0.97	1.58	-2.17	-1.78	1.02	2.65	-0.28	-0.32	0.56
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_00067	Silent information regulator protein Sir2	10.82	11.02	10.29	10.66	0.53	0.36	-0.2	-0.37	-0.18	-0.06	-0.44	-0.3	-0.28	-0.32	0.2
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_00067	Silent information regulator protein Sir2	10.82	11.02	10.29	10.66	0.53	0.36	-0.2	-0.37	-0.18	-0.06	-0.44	-0.3	-0.28	-0.32	0.2
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_02528	uroporphyrin-III C-methyltransferase	5.75	5.95	5.17	6.13	0.58	-0.18	-0.2	-0.96	-0.13	-0.85	-0.44	-1.2	-0.28	-0.32	0.38
Cthe_00067	Silent information regulator protein Sir2	10.82	11.02	10.29	10.66	0.53	0.36	-0.2	-0.37	-0.18	-0.06	-0.44	-0.3	-0.28	-0.32	0.2
Cthe_00067	Silent information regulator protein Sir2	10.82	11.02	10.29	10.66	0.53	0.36	-0.2	-0.37	-0.18	-0.06	-0.44	-0.3	-0.28	-0.32	0.2
Cthe_01379	oxidoreductase-like protein	8.77	8.55	8.38	8.08	0.39	0.47	0.22	0.3	-0.33	0.1	0.09	0.71	-0.29	-0.33	0.27
Cthe_03087	response regulator receiver protein	12.71	12.91	12.75	12.67	-0.04	0.24	-0.2	0.08	-0.77	-0.24	-0.44	0.38	-0.29	-0.33	0.78
Cthe_00880	phospho-2-dehydro-3-deoxyheptonate aldolase	9.73	10.26	9.4	9.67	0.33	0.59	-0.53	-0.27	-0.39	0.28	-0.85	-0.15	-0.29	-0.33	0.31
Cthe_02498	N-acetylmuramoyl-L-alanine amidase	4	2.32	2	3.81	2	-1.49	1.68	-1.81	1.32	-2.78	1.91	-2.48	-0.29	-0.33	0.55
Cthe_03087	response regulator receiver protein	12.71	12.91	12.75	12.67	-0.04	0.24	-0.2	0.08	-0.77	-0.24	-0.44	0.38	-0.29	-0.33	0.78
Cthe_00029	hypothetical protein	9.17	8.31	8.33	8.28	0.84	0.03	0.86	0.05	0.13	-0.54	0.89	0.33	-0.29	-0.33	0.33
Cthe_00584	protein of unknown function DUF503	8.64	8	7.85	8.2	0.79	-0.2	0.64	-0.35	0.08	-0.88	0.61	-0.27	-0.29	-0.33	0.74
Cthe_01466	protein of unknown function DUF1706	5.95	5.73	5.55	5.58	0.4	0.15	0.22	-0.03	-0.32	-0.37	0.09	0.21	-0.29	-0.33	1.2
Cthe_02092	dimethyladenosine transferase	8.55	9.43	8.71	9.08	-0.16	0.35	-0.88	-0.37	-0.89	-0.07	-1.29	-0.3			



Cthe_02083	DNA-directed DNA polymerase	8.71	7.93	8.65	8.29	0.06	-0.36	0.78	0.36	-0.66	-1.12	0.79	0.8	-0.3	-0.34	0.65
Cthe_02320	DNA-cytosine methyltransferase	12.8	12.62	12.24	12.44	0.56	0.18	0.18	-0.2	-0.15	-0.32	0.04	-0.05	-0.3	-0.34	3.1
Cthe_01068	cytidine deaminase	9.52	9.9	9.1	9.42	0.42	0.48	-0.38	-0.32	-0.3	0.12	-0.66	-0.23	-0.3	-0.34	0.26
Cthe_00885	dephospho-CoA kinase	8.3	8.93	8.05	8.31	0.25	0.62	-0.63	-0.26	-0.47	0.32	-0.97	-0.14	-0.3	-0.34	0.33
Cthe_01068	cytidine deaminase	9.52	9.9	9.1	9.42	0.42	0.48	-0.38	-0.32	-0.3	0.12	-0.66	-0.23	-0.3	-0.34	0.26
Cthe_01068	cytidine deaminase	9.52	9.9	9.1	9.42	0.42	0.48	-0.38	-0.32	-0.3	0.12	-0.66	-0.23	-0.3	-0.34	0.26
Cthe_01942	hypothetical protein	11.58	11.82	11.78	10.81	-0.2	1.01	-0.24	0.97	-0.93	0.9	-0.49	1.73	-0.31	-0.35	0.4
Cthe_02897	transcription elongation factor GreA	15.11	14.75	14.53	14.71	0.58	0.04	0.36	-0.18	-0.13	-0.53	0.26	-0.02	-0.31	-0.35	1.18
Cthe_00262	gamma-glutamyl phosphate reductase	12.78	13.15	12.84	13.03	-0.06	0.12	-0.37	-0.19	-0.79	-0.41	-0.65	-0.03	-0.31	-0.35	0.77
Cthe_00810	CheA signal transduction histidine kinases	8.08	7.01	8.09	7.34	-0.01	-0.33	1.07	0.75	-0.73	-1.07	1.15	1.39	-0.31	-0.35	0.4
Cthe_00273	metal dependent phosphohydrolase	11.56	11.27	11.19	11.19	0.37	0.08	0.29	0	-0.35	-0.47	0.17	0.26	-0.31	-0.35	1.06
Cthe_00810	CheA signal transduction histidine kinases	8.08	7.01	8.09	7.34	-0.01	-0.33	1.07	0.75	-0.73	-1.07	1.15	1.39	-0.31	-0.35	0.4
Cthe_02746	protein of unknown function DUF402	9.68	9.31	9.06	9.29	0.62	0.02	0.37	-0.23	-0.09	-0.56	0.27	-0.09	-0.31	-0.35	1.12
Cthe_00631	hypothetical protein	11.07	11.58	11.24	11.59	-0.17	-0.01	-0.51	-0.35	-0.9	-0.6	-0.82	-0.27	-0.31	-0.35	0.7
Cthe_00262	gamma-glutamyl phosphate reductase	12.78	13.15	12.84	13.03	-0.06	0.12	-0.37	-0.19	-0.79	-0.41	-0.65	-0.03	-0.31	-0.35	0.77
Cthe_00810	CheA signal transduction histidine kinases	8.08	7.01	8.09	7.34	-0.01	-0.33	1.07	0.75	-0.73	-1.07	1.15	1.39	-0.31	-0.35	0.4
Cthe_00262	gamma-glutamyl phosphate reductase	12.78	13.15	12.84	13.03	-0.06	0.12	-0.37	-0.19	-0.79	-0.41	-0.65	-0.03	-0.31	-0.35	0.77
Cthe_00262	gamma-glutamyl phosphate reductase	12.78	13.15	12.84	13.03	-0.06	0.12	-0.37	-0.19	-0.79	-0.41	-0.65	-0.03	-0.31	-0.35	0.77
Cthe_00262	gamma-glutamyl phosphate reductase	12.78	13.15	12.84	13.03	-0.06	0.12	-0.37	-0.19	-0.79	-0.41	-0.65	-0.03	-0.31	-0.35	0.77
Cthe_01895	transcriptional regulator, PadR-like family	9.5	9.48	9.5	8.85	0	0.63	0.02	0.65	-0.72	0.34	-0.16	1.24	-0.32	-0.37	0.36
Cthe_03028	Pyridoxal-dependent decarboxylase	13.75	14.03	13.28	13.68	0.47	0.35	-0.28	-0.4	-0.24	-0.07	-0.54	-0.35	-0.32	-0.37	0.22
Cthe_01216	ATP-dependent Clp protease adaptor protein ClpS	8.12	8.36	8.15	8.15	-0.03	0.21	-0.24	0	-0.76	-0.28	-0.49	0.26	-0.32	-0.37	0.82
Cthe_00702	hypothetical protein	9.5	8.72	9.06	9.03	0.44	-0.31	0.78	0.03	-0.28	-1.04	0.79	0.3	-0.32	-0.37	0.72
Cthe_00796	hypothetical protein	6.58	5.43	5.75	6	0.83	-0.57	1.15	-0.25	0.12	-1.43	1.25	-0.12	-0.32	-0.37	0.64
Cthe_01891	hypothetical protein	6.41	5.13	5.73	5.46	0.68	-0.33	1.28	0.27	-0.03	-1.07	1.41	0.67	-0.32	-0.37	0.39
Cthe_03028	Pyridoxal-dependent decarboxylase	13.75	14.03	13.28	13.68	0.47	0.35	-0.28	-0.4	-0.24	-0.07	-0.54	-0.35	-0.32	-0.37	0.22
Cthe_03028	Pyridoxal-dependent decarboxylase	13.75	14.03	13.28	13.68	0.47	0.35	-0.28	-0.4	-0.24	-0.07	-0.54	-0.35	-0.32	-0.37	0.22
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_02352	putative signal-transduction protein with CBS	9.87	9.88	9.8	9.1	0.07	0.78	-0.01	0.7	-0.65	0.56	-0.2	1.32	-0.33	-0.38	0.36
Cthe_00438	cellulosome enzyme, dockerin type I	5.36	4.25	4.75	4.46	0.61	-0.21	1.11	0.29	-0.1	-0.9	1.2	0.7	-0.33	-0.38	0.37
Cthe_00255	hypothetical protein	6.97	7.71	6.97	7.7	0	0.01	-0.74	-0.73	-0.72	-0.57	-1.11	-0.85	-0.33	-0.38	0.37
Cthe_00754	hypothetical protein	8.13	8.68	8.74	8.41	-0.61	0.27	-0.55	0.33	-1.35	-0.19	-0.88	0.76	-0.33	-0.38	0.66
Cthe_01520	hypothetical protein	8.57	8.6	8.28	8.41	0.29	0.19	-0.03	-0.13	-0.43	-0.31	-0.22	0.06	-0.33	-0.38	1.31
Cthe_02041	hypothetical protein	3.81	2.58	3.7	3	0.11	-0.42	1.23	0.7	-0.61	-1.21	1.35	1.32	-0.33	-0.38	0.4
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_00555	Pp1C-type peptidyl-prolyl cis-trans isomerase	12.43	12.61	12.26	12.52	0.17	0.09	-0.18	-0.26	-0.55	-0.46	-0.41	-0.14	-0.33	-0.38	0.93
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_01253	phosphoenolpyruvate synthase	10.48	10.45	10.24	10.26	0.24	0.19	0.03	-0.02	-0.48	-0.31	-0.15	0.23	-0.33	-0.38	1.17
Cthe_01236	Fibronectin, type III	10.54	10.15	10.43	10.22	0.11	-0.07	0.39	0.21	-0.61	-0.69	0.3	0.58	-0.34	-0.39	0.79
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02972	glycoside hydrolase, family 11	13.87	13.33	13.15	13.5	0.72	-0.17	0.54	-0.35	0.01	-0.84	0.49	-0.27	-0.34	-0.39	0.84
Cthe_00442	Polypeptide-transport-associated, FtsQ-type	12.18	11.5	11.3	11.27	0.88	0.23	0.68	0.03	0.17	-0.25	0.66	0.3	-0.34	-0.39	0.23
Cthe_02560	dTDP-4-dehydrodihydroxamate 3,5-epimerase	9.84	8.13	8.16	8.4	1.68	-0.27	1.71	-0.24	0.99	-0.99	1.95	-0.11	-0.34	-0.39	0.4
Cthe_01619	transcriptional regulator, AbrB family	11.09	10.78	11.33	10.52	-0.24	0.26	0.31	0.81	-0.97	-0.21	0.2	1.48	-0.34	-0.39	0.37
Cthe_02436	hypothetical protein	5.7	6.21	6.93	5.39	-1.23	0.82	-0.51	1.54	-1.98	0.62	-0.82	2.59	-0.34	-0.39	0.43
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02560	dTDP-4-dehydrodihydroxamate 3,5-epimerase	9.84	8.13	8.16	8.4	1.68	-0.27	1.71	-0.24	0.99	-0.99	1.95	-0.11	-0.34	-0.39	0.4
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_02704	Transketolase-like protein	12.63	13.33	12.54	12.88	0.09	0.45	-0.7	-0.34	-0.63	0.07	-1.06	-0.26	-0.34	-0.39	0.33
Cthe_00467	Flagellar biosynthesis/type III secretory	9.68	9.3	8.96	9.63	0.72	-0.33	0.38	-0.67	0.01	-1.07	0.29	-0.76	-0.35	-0.41	0.74
Cthe_00268	hypothetical protein	10.49	10.07	10.36	10.16	0.13	-0.09	0.42	0.2	-0.59	-0.72	0.34	0.56	-0.35	-0.41	0.8
Cthe_02031	transposase IS200-like protein	9.8	8.94	8.8	8.79	1	0.15	0.86	0.01	0.3	-0.37	0.89	0.27	-0.35	-0.41	0.29
Cthe_02778	cytidyltransferase-related domain	8.32	8.29	7.91	8.22	0.41	0.07	0.03	-0.31	-0.31	-0.49	-0.15	-0.21	-0.35	-0.41	1.26
Cthe_00467	Flagellar biosynthesis/type III secretory	9.68	9.3	8.96	9.63	0.72	-0.33	0.38	-0.67	0.01	-1.07	0.29	-0.76	-0.35	-0.41	0.74
Cthe_00984	prolipoprotein diacylglycerol transferase	9.26	10.37	9.5	9.7	-0.24	0.67	-1.11	-0.2	-0.97	0.4	-1.57	-0.05	-0.35	-0.41	0.38
Cthe_00569	protein of unknown function DUF116	9.62	10.12	9.27	9.61	0.35	0.51	-0.5	-0.34	-0.37	0.16	-0.81	-0.26	-0.35	-0.41	0.27
Cthe_01696	hypothetical protein	9.73	9.38	11.31	9.43	-1.58	-0.05	0.35	1.88	-2.34	-0.66	0.25	3.11	-0.35	-0.41	0.44
Cthe_01794	translation elongation factor 2 (EF-2/EF-G)	12.54	10.58	11.64	11.78	0.9	-1.2	1.96	-0.14	0.19	-2.35	2.26	0.05	-0.35	-0.41	0.59
Cthe_02674	hypothetical protein	6.04	5.58	5.61	5.64	0.43	-0.06	0.46	-0.03	-0.29	-0.68	0.39	0.21	-0.35	-0.41	0.94
Cthe_01119	hypothetical protein	8.27	7.94	8.44	7.68	-0.17	0.26	0.33	0.76	-0.9	-0.21	0.23	1.41	-0.35	-0.41	0.36
Cthe_02576	hypothetical protein	11.81	11.89	11.8	11.71	0.01	0.18	-0.08	0.09	-0.71	-0.32	-0.29	0.39	-0.35	-0.41	0.9
Cthe_01356	glycosyltransferase	11.47	12.66	11.84	12.06	-0.37	0.6	-1.19	-0.22	-1.1	0.29	-1.67	-0.08	-0.35	-0.41	0.38
Cthe_02018	hypothetical protein	9.96	8.99	9.84	9.51	0.12	-0.52	0.97	0.33	-0.6	-1.35</					



Cthe_00243	copper amine oxidase-like protein	12.61	12.59	11.7	12.39	0.91	0.2	0.02	-0.69	0.2	-0.29	-0.16	-0.79	-0.37	-0.43	0.25
Cthe_03205	hypothetical protein	8.8	10.32	9.59	10.25	-0.79	0.07	-1.52	-0.66	-1.53	-0.49	-2.09	-0.74	-0.37	-0.43	0.41
Cthe_03077	cellulosome anchoring protein, cohesion region	15.83	17.13	16.9	17.32	-1.07	-0.19	-1.3	-0.42	-1.82	-0.87	-1.81	-0.38	-0.37	-0.43	0.61
Cthe_01130	hypothetical protein	4.25	6.09	6.15	5.86	-1.9	0.23	-1.84	0.29	-2.66	-0.25	-2.49	0.7	-0.37	-0.43	0.58
Cthe_01149	hypothetical protein	6.85	6.19	6.44	6.09	0.41	0.1	0.66	0.35	-0.31	-0.44	0.64	0.79	-0.37	-0.43	0.3
Cthe_00565	hypothetical protein	13.1	12.24	13.01	12.69	0.09	-0.45	0.86	0.32	-0.63	-1.25	0.89	0.74	-0.37	-0.43	0.68
Cthe_01957	extracellular solute-binding protein, family 1	9.49	9.13	8.81	9.39	0.68	-0.26	0.36	-0.58	-0.03	-0.97	0.26	-0.62	-0.37	-0.43	0.81
Cthe_01568	Radical SAM	7.73	8.96	8.13	8.4	-0.4	0.56	-1.23	-0.27	-1.13	0.24	-1.72	-0.15	-0.38	-0.44	0.38
Cthe_02474	phage terminase, large subunit, PBSX family	10.25	9.61	9.59	9.85	0.66	-0.24	0.64	-0.26	-0.05	-0.94	0.61	-0.14	-0.38	-0.44	0.84
Cthe_03146	peptidase M56, BlaR1	9.17	9.13	9.24	8.48	-0.07	0.65	0.04	0.76	-0.8	0.37	-0.14	1.41	-0.38	-0.44	0.35
Cthe_01511	DNA methylase N-4/N-6	8.41	9.42	8.35	8.59	0.06	0.83	-1.01	-0.24	-0.66	0.63	-1.45	-0.11	-0.38	-0.44	0.35
Cthe_02767	Methyltransferase type 12	8.16	8.08	8.59	8.08	-0.43	0	0.08	0.51	-1.16	-0.59	-0.09	1.03	-0.38	-0.44	0.71
Cthe_02945	histidine kinase	9.66	8.39	8.38	8.44	1.28	-0.05	1.27	-0.06	0.58	-0.66	1.4	0.17	-0.38	-0.44	0.35
Cthe_03146	peptidase M56, BlaR1	9.17	9.13	9.24	8.48	-0.07	0.65	0.04	0.76	-0.8	0.37	-0.14	1.41	-0.38	-0.44	0.35
Cthe_00151	protein of unknown function DUF965	11.3	10.64	11.32	10.96	-0.02	-0.32	0.66	0.36	-0.74	-1.06	0.64	0.8	-0.38	-0.44	0.71
Cthe_02604	ATP synthase F0, B subunit	9.74	10.44	9.58	9.92	0.16	0.52	-0.7	-0.34	-0.56	0.18	-1.06	-0.26	-0.38	-0.44	0.3
Cthe_02955	hypothetical protein	5.43	4.39	4.32	4.32	1.11	0.07	1.04	0	0.41	-0.49	1.11	0.26	-0.38	-0.44	0.31
Cthe_02007	RNA related	7.64	5.88	7.34	6.64	0.3	-0.76	1.76	0.7	-0.42	-1.71	2.01	1.32	-0.38	-0.44	0.41
Cthe_02592	hypothetical protein	9.32	9.57	8.77	9.42	0.55	0.15	-0.25	-0.65	-0.16	-0.37	-0.5	-0.73	-0.38	-0.44	0.26
Cthe_01631	hypothetical protein	12.01	12.16	12.73	12.08	-0.72	0.08	-0.15	0.65	-1.46	-0.47	-0.37	1.24	-0.38	-0.44	0.67
Cthe_03206	hypothetical protein	9.07	10.16	9.4	10.01	-0.33	0.15	-1.09	-0.61	-1.06	-0.37	-1.55	-0.67	-0.38	-0.44	0.37
Cthe_00019	regulatory protein, P-II family	11.02	10.97	10.61	10.93	0.41	0.04	0.05	-0.32	-0.31	-0.53	-0.12	-0.23	-0.38	-0.44	1.33
Cthe_01280	hypothetical protein	4.25	4.17	3.91	4	0.34	0.17	0.08	-0.09	-0.38	-0.34	-0.09	0.12	-0.38	-0.44	1.91
Cthe_01892	RNA related	5.43	5.46	5.61	4.75	-0.18	0.71	-0.03	0.86	-0.91	0.46	-0.22	1.56	-0.38	-0.44	0.36
Cthe_01257	Carbohydrate-binding, CenC-like protein	10.13	9.53	10.77	9.94	-0.64	-0.41	0.6	0.83	-1.38	-1.19	0.56	1.52	-0.38	-0.44	0.63
Cthe_01194	hypothetical protein	9.84	9.11	9.25	9.4	0.59	-0.29	0.73	-0.15	-0.12	-1.01	0.72	0.03	-0.38	-0.44	0.79
Cthe_02151	hypothetical protein	12.06	12.73	11.94	12.39	0.12	0.34	-0.67	-0.45	-0.6	-0.09	-1.02	-0.42	-0.38	-0.44	0.31
Cthe_02604	ATP synthase F0, B subunit	9.74	10.44	9.58	9.92	0.16	0.52	-0.7	-0.34	-0.56	0.18	-1.06	-0.26	-0.38	-0.44	0.3
Cthe_02604	ATP synthase F0, B subunit	9.74	10.44	9.58	9.92	0.16	0.52	-0.7	-0.34	-0.56	0.18	-1.06	-0.26	-0.38	-0.44	0.3
Cthe_02604	ATP synthase F0, B subunit	9.74	10.44	9.58	9.92	0.16	0.52	-0.7	-0.34	-0.56	0.18	-1.06	-0.26	-0.38	-0.44	0.3
Cthe_02604	ATP synthase F0, B subunit	9.74	10.44	9.58	9.92	0.16	0.52	-0.7	-0.34	-0.56	0.18	-1.06	-0.26	-0.38	-0.44	0.3
Cthe_02623	Exopolysaccharide biosynthesis protein	8.68	8.58	8.22	8.87	0.46	-0.29	0.1	-0.65	-0.26	-1.01	-0.06	-0.73	-0.39	-0.46	0.8
Cthe_00781	GCN5-related N-acetyltransferase	9.42	8.9	8.98	9.03	0.44	-0.13	0.52	-0.05	-0.28	-0.78	0.46	0.18	-0.39	-0.46	0.94
Cthe_00758	protein of unknown function UPF0102	8.75	8.12	8.25	8.34	0.5	-0.22	0.63	-0.09	-0.21	-0.91	0.6	0.12	-0.39	-0.46	0.86
Cthe_03178	protein of unknown function DUF342	10.92	10.88	10.65	10.72	0.27	0.16	0.04	-0.07	-0.45	-0.35	-0.14	0.15	-0.39	-0.46	1.56
Cthe_02777	nicotinamide mononucleotide transporter PnuC	8.65	8.26	8.09	8.3	0.56	-0.04	0.39	-0.21	-0.15	-0.65	0.3	-0.06	-0.39	-0.46	1.22
Cthe_01176	CheC-like protein	11.63	9.95	11.49	10.68	0.14	-0.73	1.68	0.81	-0.58	-1.66	1.91	1.48	-0.39	-0.46	0.41
Cthe_00544	protein serine/threonine phosphatases	9.8	9.19	9.16	8.99	0.64	0.2	0.61	0.17	-0.07	-0.29	0.57	0.52	-0.39	-0.46	0.22
Cthe_02898	anti-sigma-factor antagonist	10.79	10.69	10.53	10.55	0.26	0.14	0.1	-0.02	-0.46	-0.38	-0.06	0.23	-0.39	-0.46	1.41
Cthe_00899	hypothetical protein	8.14	6.79	8.26	7.32	-0.12	-0.53	1.35	0.94	-0.85	-1.37	1.5	1.68	-0.39	-0.46	0.4
Cthe_02845	hypothetical protein	9.94	8.45	9.26	8.91	0.68	-0.46	1.49	0.35	-0.03	-1.26	1.68	0.79	-0.39	-0.46	0.38
Cthe_01407	hypothetical protein	5.21	4	4.58	4.25	0.63	-0.25	1.21	0.33	-0.08	-0.96	1.32	0.76	-0.39	-0.46	0.36
Cthe_01065	type IV pilus assembly PilZ	11.43	10.67	11.14	10.66	0.29	0.01	0.76	0.48	-0.43	-0.57	0.76	0.98	-0.39	-0.46	0.32
Cthe_00586	transposase IS3/IS911	12.75	12.35	12.15	12.42	0.6	-0.07	0.4	-0.27	-0.11	-0.69	0.31	-0.15	-0.39	-0.46	1.14
Cthe_00544	protein serine/threonine phosphatases	9.8	9.19	9.16	8.99	0.64	0.2	0.61	0.17	-0.07	-0.29	0.57	0.52	-0.39	-0.46	0.22
Cthe_01067	GTP-binding protein Era	10.87	11.12	10.32	10.75	0.55	0.37	-0.25	-0.43	-0.16	-0.04	-0.5	-0.39	-0.4	-0.47	0.15
Cthe_00223	hypothetical protein	7.77	6.95	7.62	7.01	0.15	-0.06	0.82	0.61	-0.57	-0.68	0.84	1.18	-0.4	-0.47	0.34
Cthe_00247	DNA mismatch repair protein MutS-like protein	10.9	10.74	11.1	10.28	-0.2	0.46	0.16	0.82	-0.93	0.09	0.01	1.5	-0.4	-0.47	0.35
Cthe_01178	isochorismatase hydrolase	6.85	6	6.64	6.07	0.21	-0.07	0.85	0.57	-0.51	-0.69	0.87	1.12	-0.4	-0.47	0.34
Cthe_03063	Acetyl xylan esterase	8.55	10.01	8.94	9.05	-0.39	0.96	-1.46	-0.11	-1.12	0.82	-2.01	0.09	-0.4	-0.47	0.39
Cthe_00640	cellulosome enzyme, dockerin type I	10.14	9.62	9.35	9.28	0.79	0.34	0.52	0.07	0.08	-0.09	0.46	0.36	-0.4	-0.47	0.12
Cthe_00811	response regulator receiver protein	4.09	3.32	4.95	3.91	-0.86	-0.59	0.77	1.04	-1.6	-1.46	0.77	1.83	-0.4	-0.47	0.61
Cthe_00152	aldo/keto reductase	12.17	11.61	11.61	11.78	0.56	-0.17	0.56	-0.17	-0.15	-0.84	0.51	0	-0.4	-0.47	0.94
Cthe_02854	intein	11.79	10.46	11.58	11.28	0.21	-0.82	1.33	0.3	-0.51	-1.79	1.48	0.71	-0.4	-0.47	0.64
Cthe_03063	Acetyl xylan esterase	8.55	10.01	8.94	9.05	-0.39	0.96	-1.46	-0.11	-1.12	0.82	-2.01	0.09	-0.4	-0.47	0.39
Cthe_02754	beta-lactamase-like protein	7.67	7.63	7.62	7.52	0.05	0.11	0.04	0.1	-0.67	-0.43	-0.14	0.41	-0.41	-0.48	1.03
Cthe_01267	two component transcriptional regulator, LuxR	3.81	2.32	2.58	2.58	1.23	-0.26	1.49	0	0.53	-0.97	1.68	0.26	-0.41	-0.48	0.37
Cthe_02632	transcription-repair coupling factor	8.57	9.79	8.9	9.15	-0.33	0.64	-1.22	-0.25	-1.06	0.35	-1.71	-0.12	-0.41	-0.48	0.37
Cthe_02793	aminotransferase, class I and II	7.4	6.88	7.12	6.67	0.28	0.21	0.52	0.45	-0.44	-0.28	0.46	0.94	-0.41	-0.48	0.28
Cthe_00913	transposase IS116/IS110/IS902	13.48	13.77	15.07	13.79	-1.59	-0.02	-0.29	1.28	-2.35	-0.62	-0.55	2.2	-0.41	-0.48	0.6
Cthe_02632	transcription-repair coupling factor	8.57	9.79	8.9	9.15	-0.33	0.64	-1.22	-0.25	-1.06	0.35	-1.71	-0.12	-0.41	-0.48	0.37
Cthe_03057	transposase	7.19	5.49	7.9	6.41	-0.71	-0.92	1.7	1.49	-1.45	-1.94	1.94	2.52	-0.41	-0.48	0.43
Cthe_00401	methyl-accepting chemotaxis sensory transducer	11.68	11.34	12.65	11.65	-0.97	-0.31	0.34	1	-1.71	-1.04	0.24	1.77	-0.41	-0.48	0.63
Cthe_00401	methyl-accepting chemotaxis sensory transducer	11.68	11.34	12.65	11.65	-0.97	-0.31	0.34	1	-1.71	-1.04	0.24	1.77	-0.41	-0.48	0.63
Cthe_00891	response regulator receiver protein	12.14	10.2	10.39	10.6	1.75	-0.4	1.94	-0.21	1.06	-1.18	2.24	-0.06	-0.41	-0.48	0.4
Cthe_01267	two component transcriptional regulator, LuxR	3.81	2.32	2.58	2.58	1.23	-0.26	1.49	0	0.53	-0.97	1.68	0.26	-0.41	-0.48	0.37
Cthe_01721	phage portal protein, HK97 family	4.52	2.58	2.81	3	1.71	-0.42	1.94	-0.19	1.02	-1.21	2.24	-0.03	-0.41	-0.48	0.4
Cthe_00291	protein of unknown function DUF255	6.02	6.13	7.07	5.61	-1.05	0.52	-0.11	1.46	-1.8	0.18	-0.33	2.47	-0.41	-0.48	0.41
Cthe_00222	hypothetical protein	6.77	6.34	6.57	6.07	0.2	0.27	0.43	0.5	-0.52	-0.19	0.35	1.02	-0.41	-0.48	0.29
Cthe_00263	hypothetical protein	3.58	3.17	2	3.46	1.58	-0.29	0.41	-1.46	0.89	-1.01	0.33	-1.95	-0.41	-0.48	0.38
Cthe_02011	RNA related	7.85	6.54	6.87	6.75	0.98	-0.21	1.31	0.12	0.28	-0.9	1.45	0.44	-0.41	-0.48	0.35
Cthe_02863	intein	9.02	8.31	8.11	8.05	0.91	0.26	0.71	0.06	0.2	-0.21	0.7	0.35	-0.41	-0.48	0.21
Cthe_02683	hypothetical protein	9.87	9.4	9.34	9.11	0.53	0.29	0.47	0.23	-0.18	-0.16	0.4	0.61	-0.41	-0.48	0.19
Cthe_01036	hypothetical protein	7.97	7.91	8.19	7.33	-0.22	0.58	0.06	0.86	-0.95	0.26	-0.11	1.56	-0.41	-0.48	0.35
Cthe_02793	aminotransferase, class I and II	7.4	6.88	7.12	6.67	0.28	0.21	0.52	0.45	-0.44	-0.28	0.46	0.94	-0.41	-0.48	0.28
Cthe_02632	transcription-repair coupling factor	8.57	9.79	8.9	9.15	-0.33	0.64	-1.22	-0.25	-1.06	0.					



Cthe_01857	carboxyl-terminal protease	11.9	11.55	11.31	11.09	0.59	0.46	0.35	0.22	-0.12	0.09	0.25	0.59	-0.42	-0.49	0.13
Cthe_00529	RNA related		0				0	0			-0.59	-0.19		-0.42	-0.49	1.74
Cthe_00013	hypothetical protein	6.83	6.15	6.79	6.49	0.04	-0.34	0.68	0.3	-0.68	-1.09	0.66	0.71	-0.42	-0.49	0.74
Cthe_03132	cellulosome enzyme, dockerin type I	10.7	10.9	11	10.76	-0.3	0.14	-0.2	0.24	-1.03	-0.38	-0.44	0.62	-0.42	-0.49	0.81
Cthe_02019	intein	9.5	8.21	9.54	9.05	-0.04	-0.84	1.29	0.49	-0.77	-1.82	1.43	1	-0.42	-0.49	0.64
Cthe_02961	extracellular solute-binding protein, family 5	9.76	10.47	10.22	10.58	-0.46	-0.11	-0.71	-0.36	-1.19	-0.75	-1.07	-0.29	-0.42	-0.49	0.71
Cthe_02370	ribosomal protein L34	8.57	8.15	7.98	8.26	0.59	-0.11	0.42	-0.28	-0.12	-0.75	0.34	-0.17	-0.42	-0.49	1.12
Cthe_01857	carboxyl-terminal protease	11.9	11.55	11.31	11.09	0.59	0.46	0.35	0.22	-0.12	0.09	0.25	0.59	-0.42	-0.49	0.13
Cthe_02686	type IV pilus assembly protein PilM	14.18	13.9	14.35	13.99	-0.17	-0.09	0.28	0.36	-0.9	-0.72	0.16	0.8	-0.43	-0.51	0.79
Cthe_02686	type IV pilus assembly protein PilM	14.18	13.9	14.35	13.99	-0.17	-0.09	0.28	0.36	-0.9	-0.72	0.16	0.8	-0.43	-0.51	0.79
Cthe_01815	UreE urease accessory-like protein	4.32	2.58	4.09	3.32	0.23	-0.74	1.74	0.77	-0.49	-1.68	1.99	1.42	-0.43	-0.51	0.4
Cthe_01358	glycosyltransferase	11.47	12.51	11.61	11.92	-0.14	0.59	-1.04	-0.31	-0.87	0.28	-1.49	-0.21	-0.43	-0.51	0.34
Cthe_00335	hydrogenase large subunit-like protein	9.8	10.16	9.34	9.94	0.46	0.22	-0.36	-0.6	-0.26	-0.26	-0.64	-0.65	-0.44	-0.52	0.23
Cthe_01617	phage putative tail component	1	1		1.58	1	-0.58	0	-1.58	0.3	-1.44	-0.19	-2.14	-0.44	-0.52	0.38
Cthe_01228	threonyl-tRNA synthetase	12.78	13.22	12.31	12.71	0.47	0.51	-0.44	-0.4	-0.24	0.16	-0.74	-0.35	-0.44	-0.52	0.2
Cthe_01144	restriction modification system DNA specificity	8.25	8.76	8.63	8.66	-0.38	0.1	-0.51	-0.03	-1.11	-0.44	-0.82	0.21	-0.44	-0.52	0.79
Cthe_01228	threonyl-tRNA synthetase	12.78	13.22	12.31	12.71	0.47	0.51	-0.44	-0.4	-0.24	0.16	-0.74	-0.35	-0.44	-0.52	0.2
Cthe_01228	threonyl-tRNA synthetase	12.78	13.22	12.31	12.71	0.47	0.51	-0.44	-0.4	-0.24	0.16	-0.74	-0.35	-0.44	-0.52	0.2
Cthe_01144	restriction modification system DNA specificity	8.25	8.76	8.63	8.66	-0.38	0.1	-0.51	-0.03	-1.11	-0.44	-0.82	0.21	-0.44	-0.52	0.79
Cthe_01228	threonyl-tRNA synthetase	12.78	13.22	12.31	12.71	0.47	0.51	-0.44	-0.4	-0.24	0.16	-0.74	-0.35	-0.44	-0.52	0.2
Cthe_01228	threonyl-tRNA synthetase	12.78	13.22	12.31	12.71	0.47	0.51	-0.44	-0.4	-0.24	0.16	-0.74	-0.35	-0.44	-0.52	0.2
Cthe_00629	type II secretion system protein E	12.19	12.99	12.02	12.37	0.17	0.62	-0.8	-0.35	-0.55	0.32	-1.19	-0.27	-0.45	-0.53	0.29
Cthe_00994	NusA antitermination factor	10.92	12.16	11.09	11.33	-0.17	0.83	-1.24	-0.24	-0.9	0.63	-1.74	-0.11	-0.45	-0.53	0.35
Cthe_01350	single-strand binding protein	10.6	10.93	10.7	10.9	-0.1	0.03	-0.33	-0.2	-0.83	-0.54	-0.6	-0.05	-0.45	-0.53	0.92
Cthe_01033	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_01011	Peptidoglycan glycosyltransferase	7.41	7.55	8.31	6.92	-0.9	0.63	-0.14	1.39	-1.64	0.34	-0.36	2.36	-0.45	-0.53	0.39
Cthe_00623	transcriptional regulators, TraR/DksA family	11.53	9.77	10.07	10.12	1.46	-0.35	1.76	-0.05	0.77	-1.1	2.01	0.18	-0.45	-0.53	0.37
Cthe_00567	peptide deformylase	8.48	9.42	8.58	9.08	-0.1	0.34	-0.94	-0.5	-0.83	-0.09	-1.36	-0.5	-0.45	-0.53	0.32
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_02293	hypothetical protein	1.58		1	1	0.58	-1	1.58	0	-0.13	-2.06	1.79	0.26	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_01011	Peptidoglycan glycosyltransferase	7.41	7.55	8.31	6.92	-0.9	0.63	-0.14	1.39	-1.64	0.34	-0.36	2.36	-0.45	-0.53	0.39
Cthe_00567	peptide deformylase	8.48	9.42	8.58	9.08	-0.1	0.34	-0.94	-0.5	-0.83	-0.09	-1.36	-0.5	-0.45	-0.53	0.32
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_01011	Peptidoglycan glycosyltransferase	7.41	7.55	8.31	6.92	-0.9	0.63	-0.14	1.39	-1.64	0.34	-0.36	2.36	-0.45	-0.53	0.39
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_01011	Peptidoglycan glycosyltransferase	7.41	7.55	8.31	6.92	-0.9	0.63	-0.14	1.39	-1.64	0.34	-0.36	2.36	-0.45	-0.53	0.39
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_01011	Peptidoglycan glycosyltransferase	7.41	7.55	8.31	6.92	-0.9	0.63	-0.14	1.39	-1.64	0.34	-0.36	2.36	-0.45	-0.53	0.39
Cthe_00133	AMP-dependent synthetase and ligase	8.71	10.01	9.86	10.17	-1.15	-0.16	-1.3	-0.31	-1.9	-0.82	-1.81	-0.21	-0.45	-0.53	0.64
Cthe_02692	glycosyl transferase, group 1	10.88	10.7	10.78	10.09	0.1	0.61	0.18	0.69	-0.62	0.31	0.04	1.3	-0.46	-0.54	0.3
Cthe_01571	binding-protein-dependent transport systems	8.6	9.97	8.9	9.11	-0.3	0.86	-1.37	-0.21	-1.03	0.68	-1.9	-0.06	-0.46	-0.54	0.36
Cthe_01786	DNA repair protein RadA	10.08	11.13	10.05	10.35	0.03	0.78	-1.05	-0.3	-0.69	0.56	-1.5	-0.2	-0.46	-0.54	0.33
Cthe_00663	hypothetical protein	8.01	7.66	8.98	7.52	-0.97	0.14	0.35	1.46	-1.71	-0.38	0.25	2.47	-0.46	-0.54	0.4
Cthe_00972	hypothetical protein	6.74	6.25	6.74	6.04	0	0.21	0.49	0.7	-0.72	-0.28	0.42	1.32	-0.46	-0.54	0.31
Cthe_00772	Peptidoglycan-binding LysM	10.67	9.55	11.3	10.39	-0.63	-0.84	1.12	0.91	-1.37	-1.82	1.21	1.64	-0.46	-0.54	0.63
Cthe_01571	binding-protein-dependent transport systems	8.6	9.97	8.9	9.11	-0.3	0.86	-1.37	-0.21	-1.03	0.68	-1.9	-0.06	-0.46	-0.54	0.36
Cthe_01106	twitching motility protein	13.06	13.05	13.02	12.96	0.04	0.09	0.01	0.06	-0.68	-0.46	-0.17	0.35	-0.47	-0.56	1.19
Cthe_00900	aspartate 1-decarboxylase	8.65	8.05	9.6	8.57	-0.95	-0.52	0.6	1.03	-1.69	-1.35	0.56	1.82	-0.47	-0.56	0.64
Cthe_01106	twitching motility protein	13.06	13.05	13.02	12.96	0.04	0.09	0.01	0.06	-0.68	-0.46	-0.17	0.35	-0.47	-0.56	1.19
Cthe_00643	hypothetical protein	5.58	4.17	4.25	4.25	1.33	-0.08	1.41	0	0.63	-0.71	1.57	0.26	-0.47	-0.56	0.34
Cthe_00830	acid phosphatase/vanadium-dependent	8.32	8.76	7.93	8.58	0.39	0.18	-0.44	-0.65	-0.33	-0.32	-0.74	-0.73	-0.47	-0.56	0.25
Cthe_00611	RNA-metabolising metallo-beta-lactamase	11.73	10.93	10.98	11.38	0.75	-0.45	0.8	-0.4	0.04	-1.25	0.81	-0.35	-0.47	-0.56	0.8
Cthe_00959	S-adenosylmethionine-tRNA-ribosyltransferase-	10.48	10.76	9.92	10.5	0.56	0.26	-0.28	-0.58	-0.15	-0.21	-0.54	-0.62	-0.47	-0.56	0.18
Cthe_01508	hypothetical protein	9.22	8.36	9.16	8.44	0.06	-0.08	0.86	0.72	-0.66	-0.71	0.89	1.35	-0.47	-0.56	0.34
Cthe_01917	ATPase, P-type (transporting), HAD superfamily,	9.11	10.92	10.05	10.29	-0.94	0.63	-1.81	-0.24	-1.68	0.34	-2.45	-0.11	-0.47	-0.56	0.39
Cthe_02841	hypothetical protein	7.45	6.58	6.93	7.04	0.52	-0.46	0.87	-0.11	-0.19	-1.26	0.9	0.09	-0.47	-0.56	0.79
Cthe_03227	copper amine oxidase-like protein	7.67	7.12	7.07	6.85	0.6	0.27	0.55	0.22	-0.11	-0.19	0.5	0.59	-0.47	-0.56	0.16
Cthe_03055	hypothetical protein	1	1		1	1	0	0	-1	0.3	-0.59	-0.19	-1.26	-0.47	-0.56	0.29
Cthe_01806	cellulosome enzyme, dockerin type I	10.31	9.65	9.46	10.28	0.85	-0.63	0.66	-0.82	0.14	-1.51	0.64	-0.98	-0.47	-0.56	0.73
Cthe_01717	hypothetical protein	4.52	3.32	4.09	3.58	0.43	-0.26	1.2	0.51	-0.29	-0.97	1.31	1.03	-0.47	-0.56	0.34
Cthe_00938	regulatory protein, DeoR	13.53	13.22	13.23	12.74	0.3	0.48	0.31	0.49	-0.42	0.12	0.2	1	-0.47	-0.56	0.24
Cthe_00900	aspartate 1-decarboxylase	8.65	8.05	9.6	8.57	-0.95	-0.52	0.6	1.03	-1.69	-1.35	0.56	1.82	-0.47	-0.56	0.64
Cthe_00959	S-adenosylmethionine-tRNA-ribosyltransferase-	10.48	10.76	9.92	10.5	0.56	0.26	-0.28	-0.58	-0.15	-0.21	-0.54	-0.62	-0.47	-0.56	0.18
Cthe_01508	hypothetical protein	9.22	8.36	9.16	8.44	0.06	-0.08	0.86	0.72	-0.66	-0.71	0.89	1.35	-0.47	-0.56	0.34
Cthe_01917	ATPase, P-type (transporting), HAD superfamily,	9.11	10.92	10.05	10.29	-0.94	0.63	-1.81	-0.24	-1.68	0.34	-2.45	-0.11	-0.47	-0.56	0.39
Cthe_00900	aspartate 1-decarboxylase	8.65	8.05	9.6	8.57	-0.95	-0.52	0.6	1.03	-1.69	-1.35	0.56	1.82	-0.47	-0.56	0.64
Cthe_01508	hypothetical protein	9.22	8.36	9.16	8.44	0.06	-0.08	0.86	0.72	-0.66	-0.71	0.89	1.35	-0.47	-0.56	0.34
Cthe_00900	aspartate 1-decarboxylase	8.65	8.05	9.6	8.57	-0.95	-0.52	0.6	1.03	-1.69	-1.35					



Cthe_01357	glycosyl transferase, group 1	10.75	12.1	11.19	11.54	-0.44	0.56	-1.35	-0.35	-1.17	0.24	-1.88	-0.27	-0.5	-0.59	0.35
Cthe_01582	cytidine deaminase	2.58	4.25	3	3.17	-0.42	1.08	-1.67	-0.17	-1.15	1	-2.27	0	-0.5	-0.59	0.38
Cthe_01347	Gat5/VqeY	14.53	14.38	14.37	14.34	0.16	0.04	0.15	0.03	-0.56	-0.53	0	0.3	-0.5	-0.59	1.44
Cthe_02227	phosphopantetheine-binding	4.86	3.81	4	3.81	0.86	0	1.05	0.19	0.15	-0.59	1.12	0.55	-0.5	-0.59	0.27
Cthe_01518	hypothetical protein	3.46	3.91	3	3.46	0.46	0.45	-0.45	-0.46	-0.26	0.07	-0.75	-0.44	-0.5	-0.59	0.17
Cthe_02779	hypothetical protein	5.81	6.25	5.39	5.93	0.42	0.32	-0.44	-0.54	-0.3	-0.12	-0.74	-0.56	-0.5	-0.59	0.2
Cthe_01121	hypothetical protein	6.38	5.32	5.49	5.32	0.89	0	1.06	0.17	0.18	-0.59	1.14	0.52	-0.5	-0.59	0.28
Cthe_00055	hypothetical protein	6.75	6.54	8.48	6.97	-1.73	-0.43	0.21	1.51	-2.49	-1.22	0.07	2.55	-0.5	-0.59	0.61
Cthe_01137	hypothetical protein	6.74	7.54	7.4	7.61	-0.66	-0.07	-0.8	-0.21	-1.4	-0.69	-1.19	-0.06	-0.5	-0.59	0.74
Cthe_00987	riboflavin biosynthesis protein RibF	10.15	10.87	10.02	10.62	0.13	0.25	-0.72	-0.6	-0.59	-0.22	-1.09	-0.65	-0.5	-0.59	0.28
Cthe_01582	cytidine deaminase	2.58	4.25	3	3.17	-0.42	1.08	-1.67	-0.17	-1.15	1	-2.27	0	-0.5	-0.59	0.38
Cthe_00987	riboflavin biosynthesis protein RibF	10.15	10.87	10.02	10.62	0.13	0.25	-0.72	-0.6	-0.59	-0.22	-1.09	-0.65	-0.5	-0.59	0.28
Cthe_00987	riboflavin biosynthesis protein RibF	10.15	10.87	10.02	10.62	0.13	0.25	-0.72	-0.6	-0.59	-0.22	-1.09	-0.65	-0.5	-0.59	0.28
Cthe_01582	cytidine deaminase	2.58	4.25	3	3.17	-0.42	1.08	-1.67	-0.17	-1.15	1	-2.27	0	-0.5	-0.59	0.38
Cthe_00987	riboflavin biosynthesis protein RibF	10.15	10.87	10.02	10.62	0.13	0.25	-0.72	-0.6	-0.59	-0.22	-1.09	-0.65	-0.5	-0.59	0.28
Cthe_00987	riboflavin biosynthesis protein RibF	10.15	10.87	10.02	10.62	0.13	0.25	-0.72	-0.6	-0.59	-0.22	-1.09	-0.65	-0.5	-0.59	0.28
Cthe_01582	cytidine deaminase	2.58	4.25	3	3.17	-0.42	1.08	-1.67	-0.17	-1.15	1	-2.27	0	-0.5	-0.59	0.38
Cthe_00987	riboflavin biosynthesis protein RibF	10.15	10.87	10.02	10.62	0.13	0.25	-0.72	-0.6	-0.59	-0.22	-1.09	-0.65	-0.5	-0.59	0.28
Cthe_01107	type II secretion system protein E	13.36	13.53	13.65	13.45	-0.29	0.08	-0.17	0.2	-1.02	-0.47	-0.4	0.56	-0.51	-0.61	0.92
Cthe_03149	aminoacyl-histidine dipeptidase	8.49	9.66	8.49	8.82	0	0.84	-1.17	-0.33	-0.72	0.65	-1.65	-0.24	-0.51	-0.61	0.33
Cthe_01107	type II secretion system protein E	13.36	13.53	13.65	13.45	-0.29	0.08	-0.17	0.2	-1.02	-0.47	-0.4	0.56	-0.51	-0.61	0.92
Cthe_00538	Serine-type D-Ala-D-Ala carboxypeptidase	10.14	10.59	11.69	9.77	-1.55	0.82	-0.45	1.92	-2.31	0.62	-0.75	3.17	-0.51	-0.61	0.41
Cthe_00789	periplasmic sensor signal transduction histidine	8.34	9.07	8.08	8.5	0.26	0.57	-0.73	-0.42	-0.46	0.25	-1.1	-0.38	-0.51	-0.61	0.25
Cthe_00914	RNA-binding S4	11.69	11.61	11.65	11.57	0.04	0.04	0.08	0.08	-0.68	-0.53	-0.09	0.38	-0.51	-0.61	1.24
Cthe_01062	hypothetical protein	12.19	13.26	12.18	12.53	0.01	0.73	-1.07	-0.35	-0.71	0.49	-1.52	-0.27	-0.51	-0.61	0.31
Cthe_02610	VanW	13.15	11.73	12.42	12.06	0.73	-0.33	1.42	0.36	0.02	-1.07	1.59	0.8	-0.51	-0.61	0.34
Cthe_02877	hypothetical protein	9.16	8.99	9.36	8.45	-0.2	0.54	0.17	0.91	-0.93	0.21	0.03	1.64	-0.51	-0.61	0.33
Cthe_03174	S-layer-like domain containing protein	9.36	9.52	9.33	9.47	0.03	0.05	-0.16	-0.14	-0.69	-0.51	-0.39	0.05	-0.51	-0.61	1.23
Cthe_01419	hypothetical protein	5.43	4.7	5.86	4.75	-0.43	-0.05	0.73	1.11	-1.16	-0.66	0.72	1.94	-0.51	-0.61	0.36
Cthe_02732	hypothetical protein	8.46	8.63	7.77	8.26	0.69	0.37	-0.17	-0.49	-0.02	-0.04	-0.4	-0.48	-0.51	-0.61	0.04
Cthe_01047	hypothetical protein	10.21	9.8	11.02	10.17	-0.81	-0.37	0.41	0.85	-1.55	-1.13	0.33	1.55	-0.51	-0.61	0.68
Cthe_00679	Serine-type D-Ala-D-Ala carboxypeptidase	13.33	12.8	13.06	13.02	0.27	-0.22	0.53	0.04	-0.45	-0.91	0.47	0.32	-0.51	-0.61	1
Cthe_03149	Serine-type D-Ala-D-Ala carboxypeptidase	10.14	10.59	11.69	9.77	-1.55	0.82	-0.45	1.92	-2.31	0.62	-0.75	3.17	-0.51	-0.61	0.41
Cthe_00679	aminoacyl-histidine dipeptidase	8.49	9.66	8.49	8.82	0	0.84	-1.17	-0.33	-0.72	0.65	-1.65	-0.24	-0.51	-0.61	0.33
Cthe_00679	Serine-type D-Ala-D-Ala carboxypeptidase	10.14	10.59	11.69	9.77	-1.55	0.82	-0.45	1.92	-2.31	0.62	-0.75	3.17	-0.51	-0.61	0.41
Cthe_00679	Serine-type D-Ala-D-Ala carboxypeptidase	10.14	10.59	11.69	9.77	-1.55	0.82	-0.45	1.92	-2.31	0.62	-0.75	3.17	-0.51	-0.61	0.41
Cthe_00532	hydrolase (HAD superfamily)-like protein	7.52	7.29	7.14	7.26	0.38	0.03	0.23	-0.12	-0.34	-0.54	0.1	0.08	-0.52	-0.62	2.8
Cthe_02420	HD superfamily phosphohydrolases-like protein	13.32	12.39	12.54	12.32	0.78	0.07	0.93	0.22	0.07	-0.49	0.97	0.59	-0.52	-0.62	0.24
Cthe_00969		7.54	6.67	6.61	6.48	0.93	0.19	0.87	0.13	0.22	-0.31	0.9	0.45	-0.52	-0.62	0.21
Cthe_03208	Integrase, catalytic region	5.93	5.36	5.61	5.61	0.32	-0.25	0.57	0	-0.4	-0.96	0.52	0.26	-0.52	-0.62	1
Cthe_01351	acetobutylicum phosphotransbutyrylase	9.57	10.49	9.49	9.88	0.08	-0.61	-0.92	-0.39	-0.64	0.31	-1.34	-0.33	-0.52	-0.62	0.29
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_01521	hypothetical protein	7.45	7.62	7.6	7.54	-0.15	0.08	-0.17	0.06	-0.88	-0.47	-0.4	0.35	-0.52	-0.62	1.05
Cthe_00073	hypothetical protein	9.36	8.08	11.04	9.29	-1.68	-1.21	1.28	1.75	-2.44	-2.37	1.41	2.91	-0.52	-0.62	0.59
Cthe_01152	hypothetical protein	8.37	7.48	8.32	8.03	0.05	-0.55	0.89	0.29	-0.67	-1.4	0.92	0.7	-0.52	-0.62	0.75
Cthe_00316	PA14	6.97	7.29	7.04	7.42	-0.07	-0.13	-0.32	-0.38	-0.8	-0.78	-0.59	-0.32	-0.52	-0.62	0.94
Cthe_02274	hypothetical protein	6.87	6.6	6.44	6.6	0.43	0	0.27	-0.16	-0.29	-0.59	0.15	0.02	-0.52	-0.62	2.44
Cthe_02311	hypothetical protein	14.08	13.77	13.85	13.83	0.23	-0.06	0.31	0.02	-0.49	-0.68	0.2	0.29	-0.52	-0.62	1.34
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_03059	phosphotransferase KptA/Tpt1	9.38	8.54	9.03	8.52	0.35	0.02	0.84	0.51	-0.37	-0.56	0.86	1.03	-0.52	-0.62	0.28
Cthe_01124	phenazine biosynthesis protein PhzF family	7.36	7.25	8.53	7.5	-1.17	-0.25	0.11	1.03	-1.92	-0.96	-0.05	1.82	-0.53	-0.63	0.66
Cthe_00322	glycoside hydrolase, family 3-like protein	10.73	10.88	9.98	10.52	0.75	0.36	-0.15	-0.54	0.04	-0.06	-0.37	-0.56	-0.53	-0.63	0.06
Cthe_01332	histidyl-tRNA synthetase	10.53	11.94	10.97	11.31	-0.44	0.63	-1.41	-0.34	-1.17	0.34	-1.95	-0.26	-0.53	-0.63	0.35
Cthe_02111	protein of unknown function DUF214	6.3	7.12	6.02	6.44	0.28	0.68	-0.82	-0.42	-0.44	0.41	-1.21	-0.38	-0.53	-0.63	0.27
Cthe_01139	hypothetical protein	8.18	9.16	8.29	8.92	-0.11	0.24	-0.98	-0.63	-0.84	-0.24	-1.41	-0.7	-0.53	-0.63	0.31
Cthe_03203	CRISPR-associated protein Cas5, Hmari subtype	10.61	12.07	12.02	12.25	-1.41	-0.18	-1.46	-0.23	-2.16	-0.85	-2.01	-0.09	-0.53	-0.63	0.65
Cthe_01332	histidyl-tRNA synthetase	10.53	11.94	10.97	11.31	-0.44	0.63	-1.41	-0.34	-1.17	0.34	-1.95	-0.26	-0.53	-0.63	0.35
Cthe_01332	histidyl-tRNA synthetase	10.53	11.94	10.97	11.31	-0.44	0.63	-1.41	-0.34	-1.17	0.34	-1.95	-0.26	-0.53	-0.63	0.35
Cthe_00322	glycoside hydrolase, family 3-like protein	10.73	10.88	9.98	10.52	0.75	0.36	-0.15	-0.54	0.04	-0.06	-0.37	-0.56	-0.53	-0.63	0.06
Cthe_01332	histidyl-tRNA synthetase	10.53	11.94	10.97	11.31	-0.44	0.63	-1.41	-0.34	-1.17	0.34	-1.95	-0.26	-0.53	-0.63	0.35
Cthe_00322	glycoside hydrolase, family 3-like protein	10.73	10.88	9.98	10.52	0.75	0.36	-0.15	-0.54	0.04	-0.06	-0.37	-0.56	-0.53	-0.63	0.06
Cthe_01332	histidyl-tRNA synthetase	10.53	11.94	10.97	11.31	-0.44	0.63	-1.41	-0.34	-1.17	0.34	-1.95	-0.26	-0.53	-0.63	0.35
Cthe_00322	glycoside hydrolase, family 3-like protein	10.73	10.88	9.98	10.52	0.75	0.36	-0.15	-0.54	0.04	-0.06	-0.37	-0.56	-0.53	-0.63	0.06
Cthe_00620	iron (metal) dependent repressor, DtxR family	12.17	11.79	12.42	12.02	-0.25	-0.23	0.38	0.4	-0.98	-0.93	0.29	0.86	-0.54	-0.65	0.84
Cthe_02731	RNA polymerase, sigma-24 subunit, ECF subfamily	10.6	9.93	11.08	10.43	-0.48	-0.5	0.67	0.65	-1.21	-1.32	0.65	1.24	-0.54	-0.65	0.72
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00189	non-canonical purine NTP pyrophosphatase,	9.89	9.99	10.25	9.96	-0.36	0.03	-0.1	0.29	-1.09	-0.54	-0.31	0.7	-0.54	-0.65	0.89
Cthe_00837	protein of unknown function DUF322	8.61	7.88	8.42	7.8	0.19	0.08	0.73	0.62	-0.53	-0.47					



Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_00363	aminotransferase, class I and II	11.56	13.08	11.92	12.17	-0.36	0.91	-1.52	-0.25	-1.09	0.75	-2.09	-0.12	-0.54	-0.65	0.36
Cthe_01084	spore coat protein	5.39	5.17	5.75	4.7	-0.36	0.47	0.22	1.05	-1.09	0.1	0.09	1.85	-0.55	-0.66	0.33
Cthe_01811	transcriptional repressor, CopY family	5	3.91	5.13	4.17	-0.13	-0.26	1.09	0.96	-0.86	-0.97	1.18	1.71	-0.55	-0.66	0.35
Cthe_01153	diguanylate cyclase	6.64	6.3	6.13	6.48	0.51	-0.18	0.34	-0.35	-0.2	-0.85	0.24	-0.27	-0.55	-0.66	1.36
Cthe_01383	Tetratricopeptide TPR_2	11.14	11.44	10.55	11.2	0.59	0.24	-0.3	-0.65	-0.12	-0.24	-0.56	-0.73	-0.55	-0.66	0.16
Cthe_01636	hypothetical protein	0				0		0		-0.72		-0.19		-0.55	-0.66	2.13
Cthe_01989	RNA related	11.92	10.42	11.05	10.75	0.87	-0.33	1.5	0.3	0.16	-1.07	1.69	0.71	-0.55	-0.66	0.33
Cthe_00361	hypothetical protein	12.08	10.68	11.45	11.6	0.63	-0.92	1.4	-0.15	-0.08	-1.94	1.56	0.03	-0.55	-0.66	0.7
Cthe_02038	cellulosome enzyme, dockerin type I	9.07	8.14	9.92	8.41	-0.85	-0.27	0.93	1.51	-1.59	-0.99	0.97	2.55	-0.56	-0.67	0.39
Cthe_02838	intein	9.71	7.93	9.44	8.63	0.27	-0.7	1.78	0.81	-0.45	-1.62	2.04	1.48	-0.56	-0.67	0.37
Cthe_02021	hypothetical protein	8.18	7.2	9.95	8.22	-1.77	-1.02	0.98	1.73	-2.53	-2.09	1.04	2.88	-0.56	-0.67	0.6
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00734	peptidase M23B	11.48	11.1	11.11	11.22	0.37	-0.12	0.38	-0.11	-0.35	-0.76	0.29	0.09	-0.57	-0.68	1.55
Cthe_01030	3-oxoacyl-(acyl-carrier-protein) synthase	11.01	11.36	11.71	11.3	-0.7	0.06	-0.35	0.41	-1.44	-0.5	-0.62	0.88	-0.57	-0.68	0.8
Cthe_01977	hypothetical protein	9.33	8.24	8.87	8.37	0.46	-0.13	1.09	0.5	-0.26	-0.78	1.18	1.02	-0.57	-0.68	0.3
Cthe_02825	intein	10.6	9.3	9.95	9.53	0.65	-0.23	1.3	0.42	-0.06	-0.93	1.44	0.89	-0.57	-0.68	0.31
Cthe_01030	3-oxoacyl-(acyl-carrier-protein) synthase	11.01	11.36	11.71	11.3	-0.7	0.06	-0.35	0.41	-1.44	-0.5	-0.62	0.88	-0.57	-0.68	0.8
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_01030	3-oxoacyl-(acyl-carrier-protein) synthase	11.01	11.36	11.71	11.3	-0.7	0.06	-0.35	0.41	-1.44	-0.5	-0.62	0.88	-0.57	-0.68	0.8
Cthe_01030	3-oxoacyl-(acyl-carrier-protein) synthase	11.01	11.36	11.71	11.3	-0.7	0.06	-0.35	0.41	-1.44	-0.5	-0.62	0.88	-0.57	-0.68	0.8
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_01030	3-oxoacyl-(acyl-carrier-protein) synthase	11.01	11.36	11.71	11.3	-0.7	0.06	-0.35	0.41	-1.44	-0.5	-0.62	0.88	-0.57	-0.68	0.8
Cthe_01030	3-oxoacyl-(acyl-carrier-protein) synthase	11.01	11.36	11.71	11.3	-0.7	0.06	-0.35	0.41	-1.44	-0.5	-0.62	0.88	-0.57	-0.68	0.8
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00831	Polyprenyl synthetase	9.05	9.51	8.58	9.08	0.47	0.43	-0.46	-0.5	-0.24	0.04	-0.76	-0.5	-0.57	-0.68	0.15
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_00388	Alcohol dehydrogenase GroES-like protein	18.05	17.55	17.72	17.77	0.33	-0.22	0.5	-0.05	-0.39	-0.91	0.44	0.18	-0.57	-0.68	1.17
Cthe_01256	glycoside hydrolase, family 3-like protein	9.66	8.75	10.21	9.46	-0.55	-0.71	0.91	0.75	-1.29	-1.63	0.95	1.39	-0.58	-0.7	0.69
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_02950	Pectate lyase/Amb allergen	7.6	6.27	7.85	6.73	-0.25	-0.46	1.33	1.12	-0.98	-1.26	1.48	1.95	-0.58	-0.7	0.37
Cthe_02506	S-layer-like domain containing protein	11.4	10.58	11.84	10.67	-0.44	-0.09	0.82	1.17	-1.17	-0.72	0.84	2.03	-0.58	-0.7	0.35
Cthe_02685	putative TIM-barrel protein, nifR3 family	12.96	12.95	12.8	12.9	0.16	0.05	0.01	-0.1	-0.56	-0.51	-0.17	0.11	-0.58	-0.7	2.1
Cthe_02574	binding-protein-dependent transport systems	2	1	3.58	2	-1.58	-1	1	1.58	-2.34	-2.06	1.06	2.65	-0.58	-0.7	0.61
Cthe_02678	hypothetical protein	11.39	11.22	10.99	11.25	0.4	-0.03	0.17	-0.26	-0.32	-0.63	0.03	-0.14	-0.58	-0.7	2.77
Cthe_02468	hypothetical protein	2.32	1.58	2	2	0.32	-0.42	0.74	0	-0.4	-1.21	0.74	0.26	-0.58	-0.7	0.91
Cthe_01099	hypothetical protein	11.71	12.91	12.84	13.13	-1.13	-0.22	-1.2	-0.29	-1.88	-0.91	-1.69	-0.18	-0.58	-0.7	0.69
Cthe_00165	hypothetical protein	12.02	11.13	11.48	11.08	0.54	0.05	0.89	0.4	-0.17	-0.51	0.92	0.86	-0.58	-0.7	0.24
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_02574	binding-protein-dependent transport systems	2	1	3.58	2	-1.58	-1	1	1.58	-2.34	-2.06	1.06	2.65	-0.58	-0.7	0.61
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_01256	glycoside hydrolase, family 3-like protein	9.66	8.75	10.21	9.46	-0.55	-0.71	0.91	0.75	-1.29	-1.63	0.95	1.39	-0.58	-0.7	0.69
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_01256	glycoside hydrolase, family 3-like protein	9.66	8.75	10.21	9.46	-0.55	-0.71	0.91	0.75	-1.29	-1.63	0.95	1.39	-0.58	-0.7	0.69
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_02705	Transketolase, central region	12.27	13.33	12.19	12.6	0.08	0.73	-1.06	-0.41	-0.64	0.49	-1.51	-0.36	-0.58	-0.7	0.29
Cthe_01256	glycoside hydrolase, family 3-like protein	9.66	8.75	10.21	9.46	-0.55	-0.71	0.91	0.75	-1.29	-1.63	0.95	1.39	-0.58	-0.7	0.69
Cthe_01256	glycoside hydrolase, family 3-like protein	9.66	8.75	10.21	9.46	-0.55	-0.71	0.91	0.75	-1.29	-1.63	0.95	1.39	-0.58	-0.7	0.69
Cthe_01256	glycoside hydrolase, family 3-like protein	9.66	8.75	10.21	9.46	-0.55	-0.71	0.91	0.75	-1.29	-1.63	0.95	1.39	-0.58	-	



Cthe_01294	Recombinase	8.24	6.97	7.52	7.14	0.72	-0.17	1.27	0.38	0.01	-0.84	1.4	0.83	-0.61	-0.73	0.29
Cthe_01530	transposase, IS204/IS1001/IS1096/IS1165	10.44	9.35	12.14	10.46	-1.7	-1.11	1.09	1.68	-2.46	-2.22	1.18	2.8	-0.61	-0.73	0.61
Cthe_00044	cellulosome enzyme, dockerin type I	9.95	8.3	8.59	8.5	1.36	-0.2	1.65	0.09	0.66	-0.88	1.88	0.39	-0.61	-0.73	0.32
Cthe_02093	hypothetical protein	10.28	11.2	10.29	11.03	-0.01	0.17	-0.92	-0.74	-0.73	-0.34	-1.34	-0.86	-0.61	-0.73	0.28
Cthe_01835	Viral A-type inclusion protein repeat containing	10.14	9.71	9.62	9.99	0.52	-0.28	0.43	-0.37	-0.19	-1	0.35	-0.3	-0.61	-0.73	1.24
Cthe_03043	hypothetical protein	8.72	8.25	8.57	8.49	0.15	-0.24	0.47	0.08	-0.57	-0.94	0.4	0.38	-0.61	-0.73	1.12
Cthe_00535	hypothetical protein	11.74	10.47	11.96	11.41	-0.22	-0.94	1.27	0.55	-0.95	-1.97	1.4	1.09	-0.61	-0.73	0.69
Cthe_02572	hypothetical protein	10.64	10.01	10.07	10.42	0.57	-0.41	0.63	-0.35	-0.14	-1.19	0.6	-0.27	-0.61	-0.73	1.02
Cthe_02565	hypothetical protein	5.32	3.58	4.81	4.17	0.51	-0.59	1.74	0.64	-0.2	-1.46	1.99	1.23	-0.61	-0.73	0.35
Cthe_01281	hypothetical protein	8.09	7.85	8.62	8.08	-0.53	-0.23	0.24	0.54	-1.27	-0.93	0.11	1.08	-0.61	-0.73	0.81
Cthe_01727	hypothetical protein	5.52	4.17	4.58	4.32	0.94	-0.15	1.35	0.26	0.23	-0.81	1.5	0.65	-0.61	-0.73	0.29
Cthe_02398	putative spore coat protein	7.21	6.54	8.16	6.58	-0.95	-0.04	0.67	1.58	-1.69	-0.65	0.65	2.65	-0.62	-0.75	0.37
Cthe_00286	response regulator receiver sensor signal	10.06	10.88	9.76	10.25	0.3	0.63	-0.82	-0.49	-0.42	0.34	-1.21	-0.48	-0.62	-0.75	0.23
Cthe_00889	putative transmembrane anti-sigma factor	8.92	8.47	8.77	8.7	0.15	-0.23	0.45	0.07	-0.57	-0.93	0.38	0.36	-0.62	-0.75	1.17
Cthe_01050	recA protein	12.63	12.89	13.16	12.87	-0.53	0.02	-0.26	0.29	-1.27	-0.56	-0.51	0.7	-0.62	-0.75	0.9
Cthe_02952	IstB-like ATP-binding protein	7.76	6.81	7.03	6.73	0.73	0.08	0.95	0.3	0.02	-0.47	1	0.71	-0.62	-0.75	0.22
Cthe_01360	polysaccharide biosynthesis protein CpsF	10.7	11.64	10.55	11.02	0.15	0.62	-0.94	-0.47	-0.57	0.32	-1.36	-0.45	-0.62	-0.75	0.26
Cthe_01366	dTDP-4-dehydroharmose 3,5-epimerase	12.21	12.07	12.28	12.13	-0.07	-0.06	0.14	0.15	-0.8	-0.68	-0.01	0.48	-0.62	-0.75	1.23
Cthe_00286	response regulator receiver sensor signal	10.06	10.88	9.76	10.25	0.3	0.63	-0.82	-0.49	-0.42	0.34	-1.21	-0.48	-0.62	-0.75	0.23
Cthe_00302	hypothetical protein	6.27	5.7	7.33	5.67	-1.06	0.03	0.57	1.66	-1.81	-0.54	0.52	2.77	-0.62	-0.75	0.38
Cthe_01463	protein of unknown function DUF891	8.22	7.92	9.38	8.34	-1.16	-0.42	0.3	1.04	-1.91	-1.21	0.19	1.83	-0.62	-0.75	0.69
Cthe_01370	hypothetical protein	6.61	7.35	7.22	7.58	-0.61	-0.23	-0.74	-0.36	-1.35	-0.93	-1.11	-0.29	-0.62	-0.75	0.8
Cthe_00888	type IV pilus assembly PilZ	9.34	8.55	9.07	9.04	0.27	-0.49	0.79	0.03	-0.45	-1.31	0.8	0.3	-0.62	-0.75	0.91
Cthe_00043	glycoside hydrolase, family 9	12.17	12.56	12.42	12.68	-0.25	-0.12	-0.39	-0.26	-0.98	-0.76	-0.68	-0.14	-0.62	-0.75	1
Cthe_02161	hypothetical protein	15.06	15.93	14.97	15.53	0.09	0.4	-0.87	-0.56	-0.63	0	-1.27	-0.59	-0.62	-0.75	0.25
Cthe_00286	response regulator receiver sensor signal	10.06	10.88	9.76	10.25	0.3	0.63	-0.82	-0.49	-0.42	0.34	-1.21	-0.48	-0.62	-0.75	0.23
Cthe_01366	dTDP-4-dehydroharmose 3,5-epimerase	12.21	12.07	12.28	12.13	-0.07	-0.06	0.14	0.15	-0.8	-0.68	-0.01	0.48	-0.62	-0.75	1.23
Cthe_01366	dTDP-4-dehydroharmose 3,5-epimerase	12.21	12.07	12.28	12.13	-0.07	-0.06	0.14	0.15	-0.8	-0.68	-0.01	0.48	-0.62	-0.75	1.23
Cthe_02762	transcriptional regulator-like protein	9.13	9.32	9.26	9.31	-0.13	0.01	-0.19	-0.05	-0.86	-0.57	-0.42	0.18	-0.63	-0.76	1.27
Cthe_02756	transposase	3.7	3.58	4.52	3.81	-0.82	-0.23	0.12	0.71	-1.56	-0.93	-0.04	1.33	-0.63	-0.76	0.77
Cthe_02734	VanW	6.63	5.86	6.74	6.39	-0.11	-0.53	0.77	0.35	-0.84	-1.37	0.77	0.79	-0.63	-0.76	0.82
Cthe_02768	metallophosphoesterase	8.11	8.68	8.9	8.65	-0.79	0.03	-0.57	0.25	-1.53	-0.54	-0.9	0.64	-0.64	-0.77	0.83
Cthe_02784	cobalamin B12-binding protein	0	0	0	0	0	0	0	0	-0.72	-0.59	-0.19	0.26	-0.64	-0.77	1.62
Cthe_01018	binding-protein-dependent transport systems	15.56	16.01	15.05	15.6	0.51	0.41	-0.45	-0.55	-0.2	0.01	-0.75	-0.58	-0.64	-0.77	0.12
Cthe_00848	peptidase M24	7.87	9.14	7.98	8.41	-0.11	0.73	-1.27	-0.43	-0.84	0.49	-1.77	-0.39	-0.64	-0.77	0.3
Cthe_02977	MAEBL, putative	4.95	3.58	4.58	3.91	0.37	-0.33	1.37	0.67	-0.35	-1.07	1.53	1.27	-0.64	-0.77	0.32
Cthe_00336	DRTGG domain containing protein	8.37	8.22	8.02	8.36	0.35	-0.14	0.15	-0.34	-0.37	-0.79	0	-0.26	-0.64	-0.77	1.88
Cthe_01043	hypothetical protein	8.39	6.49	7.45	7.06	0.94	-0.57	1.9	0.39	0.23	-1.43	2.19	0.85	-0.64	-0.77	0.35
Cthe_02871	TipAS antibiotic-recognition	7.59	6.49	7.28	7.24	0.31	-0.75	1.1	0.04	-0.41	-1.69	1.19	0.32	-0.64	-0.77	0.79
Cthe_03058	hypothetical protein	10.51	9.04	9.54	9.26	0.97	-0.22	1.47	0.28	0.27	-0.91	1.65	0.68	-0.64	-0.77	0.3
Cthe_02867	hypothetical protein	0	0	0	0	0	0	0	0	-0.72	-0.59	-0.19	0.26	-0.64	-0.77	1.62
Cthe_01018	binding-protein-dependent transport systems	15.56	16.01	15.05	15.6	0.51	0.41	-0.45	-0.55	-0.2	0.01	-0.75	-0.58	-0.64	-0.77	0.12
Cthe_00848	peptidase M24	7.87	9.14	7.98	8.41	-0.11	0.73	-1.27	-0.43	-0.84	0.49	-1.77	-0.39	-0.64	-0.77	0.3
Cthe_02768	metallophosphoesterase	8.11	8.68	8.9	8.65	-0.79	0.03	-0.57	0.25	-1.53	-0.54	-0.9	0.64	-0.64	-0.77	0.83
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_03089	UspA	11.07	10.55	10.75	10.2	0.32	0.35	0.52	0.55	-0.4	-0.07	0.46	1.09	-0.65	-0.78	0.19
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_02766	hypothetical protein	4.58	4.58	5.7	4.81	-1.12	-0.23	0	0.89	-1.87	-0.93	-0.19	1.61	-0.65	-0.78	0.72
Cthe_00956	hypothetical protein	10.63	10.18	10.24	9.72	0.39	0.46	0.45	0.52	-0.33	0.09	0.38	1.05	-0.65	-0.78	0.17
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	10.33	12.2	11.28	12.05	-0.95	0.15	-1.87	-0.77	-1.69	-0.37	-2.52	-0.91	-0.65	-0.78	0.36
Cthe_01506	metal dependent phosphohydrolase	10.46	10.1	10.03	10.3	0.43	-0.2	0.36	-0.27	-0.29	-0.88	0.26	-0.15	-0.66	-0.8	1.73
Cthe_01734	phage / plasmid primase, P4 family	7.77	7.29	7.25	6.83	0.52	0.46	0.48	0.42	-0.19	0.09	0.41	0.89	-0.66	-0.8	0.12
Cthe_01506	metal dependent phosphohydrolase	10.46	10.1	10.03	10.3	0.43	-0.2	0.36	-0.27	-0.29	-0.88	0.26	-0.15	-0.66	-0.8	1.73
Cthe_02759	transcriptional regulator, AraC family	9.89	10.19	9.24	9.87	0.65	0.32	-0.3	-0.63	-0.06	-0.12	-0.56	-0.7	-0.66	-0.8	0.08
Cthe_00075	hypothetical protein	4.81	4.32	6.64	5.04	-1.83	-0.72	0.49	1.6	-2.59	-1.65	0.42	2.68	-0.66	-0.8	0.64
Cthe_01830	hypothetical protein	9.74	10.38	9.44	10.18	0.3	0.2	-0.64	-0.74	-0.42	-0.29	-0.99	-0.86	-0.66	-0.8	0.22
Cthe_03234	hypothetical protein	13.45	12.1	12.8	12.33	0.65	-0.23	1.35	0.47	-0.06	-0.93	1.5	0.97	-0.66	-0.8	0.29
Cthe_01929	hypothetical protein	10.95	9.23	10.19	9.71	0.76	-0.48	1.72	0.48	0.05	-1.29	1.96	0.98	-0.66	-0.8	0.33
Cthe_02679	Tettricropeptide TPR_2	13.33	12.96	12.94	13.13	0.39	-0.17	0.37	-0.19	-0.33	-0.84	0.27	-0.03	-0.66	-0.8	1.87
Cthe_00608	peptidase M42	6.89	7.79	6.66	7.17	0.23	0.62	-0.9	-0.51	-0.49	0.32	-1.31	-0.52	-0.67	-0.81	0.23
Cthe_02147	glycoside hydrolase, family 5	10.82	10.7	10.53	10.69	0.29	0.01	0.12	-0.16	-0.43	-0.57	-0.04	0.02	-0.67	-0.81	8.97
Cthe_01822	inner-membrane translocator	3.17	2.81	3.17	2.32	0	0.49	0.36	0.85	-0.72	0.13	0.26	1.55	-0.67	-0.81	0.26
Cthe_03131	von Willebrand factor, type A	11.68	11.85	11.74	11.89	-0.06	-0.04	-0.17	-0.15	-0.79	-0.65	-0.4	0.03	-0.67	-0.81	1.43
Cthe_02606	ATP synthase F1, alpha subunit	9.59	10.62	9.63	10.25	-0.04	0.37	-1.03	-0.62	-0.77	-0.04	-1.47	-0.68	-0.67	-0.81	0.27
Cthe_03121	hypothetical protein	5.39	4.7	5.98	5.29	-0.59	-0.59	0.69	0.69	-1.33	-1.46					



Cthe_01136	serine/threonine protein kinase with TPR repeats	7.2	8.09	8.14	8.22	-0.94	-0.13	-0.89	-0.08	-1.68	-0.78	-1.3	0.14	-0.69	-0.84	0.8
Cthe_02120	RNA polymerase sigma factor	9.65	9.55	10.16	9.73	-0.51	-0.18	0.1	0.43	-1.24	-0.85	-0.06	0.91	-0.69	-0.84	0.93
Cthe_00206	UvrD/REP helicase	9.63	10.62	9.54	10.07	0.09	0.55	-0.99	-0.53	-0.63	0.22	-1.42	-0.55	-0.69	-0.84	0.25
Cthe_01136	serine/threonine protein kinase with TPR repeats	7.2	8.09	8.14	8.22	-0.94	-0.13	-0.89	-0.08	-1.68	-0.78	-1.3	0.14	-0.69	-0.84	0.8
Cthe_01136	serine/threonine protein kinase with TPR repeats	7.2	8.09	8.14	8.22	-0.94	-0.13	-0.89	-0.08	-1.68	-0.78	-1.3	0.14	-0.69	-0.84	0.8
Cthe_02834	intein	9.9	8.71	9.21	8.79	0.69	-0.08	1.19	0.42	-0.02	-0.71	1.3	0.89	-0.69	-0.84	0.25
Cthe_00131	hypothetical protein	7.52	7.81	8.09	7.83	-0.57	-0.02	-0.29	0.26	-1.31	-0.62	-0.55	0.65	-0.69	-0.84	0.96
Cthe_00303	hypothetical protein	11.14	9.71	10.76	10.06	0.38	-0.35	1.43	0.7	-0.34	-1.1	1.6	1.32	-0.69	-0.84	0.31
Cthe_01440	hypothetical protein	0	1		1.58	0	-0.58	-1	-1.58	-0.72	-1.44	-1.44	-2.14	-0.69	-0.84	0.35
Cthe_02097	hypothetical protein	7.48	7.06	8.65	6.88	-1.17	0.18	0.42	1.77	-1.92	-0.32	0.34	2.94	-0.69	-0.84	0.37
Cthe_00437	hypothetical protein	10.06	10.47	10.46	10.54	-0.4	-0.07	-0.41	-0.08	-1.13	-0.69	-0.7	0.14	-0.69	-0.84	1.04
Cthe_00206	UvrD/REP helicase	9.63	10.62	9.54	10.07	0.09	0.55	-0.99	-0.53	-0.63	0.22	-1.42	-0.55	-0.69	-0.84	0.25
Cthe_01136	serine/threonine protein kinase with TPR repeats	7.2	8.09	8.14	8.22	-0.94	-0.13	-0.89	-0.08	-1.68	-0.78	-1.3	0.14	-0.69	-0.84	0.8
Cthe_02174	transcription termination factor Rho	13.71	13.59	13.62	13.64	0.09	-0.05	0.12	-0.02	-0.63	-0.66	-0.04	0.23	-0.7	-0.85	2.2
Cthe_01527	periplasmic sensor signal transduction histidine	7.46	6.21	7.82	6.58	-0.36	-0.37	1.25	1.24	-1.09	-1.13	1.38	2.14	-0.7	-0.85	0.35
Cthe_02917	ribosomal protein S8	10.25	10.85	9.88	10.74	0.37	0.11	-0.6	-0.86	-0.35	-0.43	-0.94	-1.05	-0.7	-0.85	0.22
Cthe_00997	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate	9.16	9.7	8.73	9.52	0.43	0.18	-0.54	-0.79	-0.29	-0.32	-0.86	-0.94	-0.7	-0.85	0.19
Cthe_02571	RNA related	8.2	7.71	7.71	8.09	0.49	-0.38	0.49	-0.38	-0.22	-1.15	0.42	-0.32	-0.7	-0.85	1.25
Cthe_02812	glycoside hydrolase, family 9	13.21	13.31	13.12	13.65	0.09	-0.34	-0.1	-0.53	-0.63	-1.09	-0.31	-0.55	-0.7	-0.85	1.12
Cthe_02917	ribosomal protein S8	10.25	10.85	9.88	10.74	0.37	0.11	-0.6	-0.86	-0.35	-0.43	-0.94	-1.05	-0.7	-0.85	0.22
Cthe_02917	ribosomal protein S8	10.25	10.85	9.88	10.74	0.37	0.11	-0.6	-0.86	-0.35	-0.43	-0.94	-1.05	-0.7	-0.85	0.22
Cthe_00997	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate	9.16	9.7	8.73	9.52	0.43	0.18	-0.54	-0.79	-0.29	-0.32	-0.86	-0.94	-0.7	-0.85	0.19
Cthe_00997	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate	9.16	9.7	8.73	9.52	0.43	0.18	-0.54	-0.79	-0.29	-0.32	-0.86	-0.94	-0.7	-0.85	0.19
Cthe_00997	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate	9.16	9.7	8.73	9.52	0.43	0.18	-0.54	-0.79	-0.29	-0.32	-0.86	-0.94	-0.7	-0.85	0.19
Cthe_00834	NusB antitermination factor	9.29	9.56	9.64	9.6	-0.35	-0.04	-0.27	0.04	-1.08	-0.65	-0.53	0.32	-0.71	-0.86	1.14
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.48	9.43	9.5	9.57	-1.02	-0.14	-0.95	-0.07	-1.77	-0.79	-1.37	0.15	-0.71	-0.86	0.79
Cthe_00836	hypothetical protein	12.69	12.43	12.74	12.6	-0.05	-0.17	0.26	0.14	-0.78	-0.84	0.14	0.47	-0.71	-0.86	1.31
Cthe_01648	hypothetical protein	1.58	2.58	1.58	3	0	-0.42	-1	-1.42	-0.72	-1.21	-1.44	-1.89	-0.71	-0.86	0.33
Cthe_00578	glycoside hydrolase, family 9	13.21	13.66	12.69	13.37	0.52	0.29	-0.45	-0.68	-0.19	-0.16	-0.75	-0.77	-0.71	-0.86	0.13
Cthe_00326	hypothetical protein	10.91	9.8	11.27	10.05	-0.36	-0.25	1.11	1.22	-1.09	-0.96	1.2	2.11	-0.71	-0.86	0.34
Cthe_03223	hypothetical protein	7.21	6.23	7.55	7.01	-0.34	-0.78	0.98	0.54	-1.07	-1.74	1.04	1.08	-0.71	-0.86	0.77
Cthe_00733	type IV pilus assembly PilZ	11.3	9.98	11.43	10.35	-0.13	-0.37	1.32	1.08	-0.86	-1.13	1.46	1.89	-0.71	-0.86	0.33
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.48	9.43	9.5	9.57	-1.02	-0.14	-0.95	-0.07	-1.77	-0.79	-1.37	0.15	-0.71	-0.86	0.79
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.48	9.43	9.5	9.57	-1.02	-0.14	-0.95	-0.07	-1.77	-0.79	-1.37	0.15	-0.71	-0.86	0.79
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.48	9.43	9.5	9.57	-1.02	-0.14	-0.95	-0.07	-1.77	-0.79	-1.37	0.15	-0.71	-0.86	0.79
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.48	9.43	9.5	9.57	-1.02	-0.14	-0.95	-0.07	-1.77	-0.79	-1.37	0.15	-0.71	-0.86	0.79
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.48	9.43	9.5	9.57	-1.02	-0.14	-0.95	-0.07	-1.77	-0.79	-1.37	0.15	-0.71	-0.86	0.79
Cthe_00654	biotin and thiamin synthesis associated protein	12.03	12.3	12.67	12.35	-0.64	-0.05	-0.27	0.32	-1.38	-0.66	-0.53	0.74	-0.72	-0.87	0.94
Cthe_00654	biotin and thiamin synthesis associated protein	12.03	12.3	12.67	12.35	-0.64	-0.05	-0.27	0.32	-1.38	-0.66	-0.53	0.74	-0.72	-0.87	0.94
Cthe_00983	cell cycle protein	9.94	10.19	10.27	10.23	-0.33	-0.04	-0.25	0.04	-1.06	-0.65	-0.5	0.32	-0.72	-0.87	1.18
Cthe_03214	hypothetical protein	6.04	6.3	6.6	6.34	-0.56	-0.04	-0.26	0.26	-1.3	-0.65	-0.51	0.65	-0.72	-0.87	0.99
Cthe_00835	hypothetical protein	9.66	9.79	9.88	9.83	-0.22	-0.04	-0.13	0.05	-0.95	-0.65	-0.35	0.33	-0.72	-0.87	1.34
Cthe_02132	abortive infection protein, putative	9.64	9.36	10.5	9.75	-0.86	-0.39	0.28	0.75	-1.6	-1.16	0.16	1.39	-0.73	-0.89	0.79
Cthe_01761	protein of unknown function DUF214	9.66	10.57	9.51	10.1	0.15	0.47	-0.91	-0.59	-0.57	0.1	-1.32	-0.64	-0.73	-0.89	0.22
Cthe_00898	metal dependent phosphohydrolase	8.59	7.29	7.59	7.31	1	-0.02	1.3	0.28	0.3	-0.62	1.44	0.68	-0.73	-0.89	0.24
Cthe_01174	protein of unknown function DUF155	9.71	8.83	9.72	8.82	-0.01	0.01	0.88	0.9	-0.73	-0.57	0.91	1.62	-0.73	-0.89	0.28
Cthe_01388	TrpR like protein, YecC/YecD	9.91	9.66	9.71	9.77	0.2	-0.11	0.25	-0.06	-0.52	-0.75	0.12	0.17	-0.73	-0.89	2.46
Cthe_01507	protein of unknown function UPF0131	4.17	4.58	5.25	4.64	-1.08	-0.06	-0.41	0.61	-1.83	-0.68	-0.7	1.18	-0.73	-0.89	0.8
Cthe_03175	protein of unknown function DUF421	6.29	5.52	7.38	5.61	-1.09	-0.09	0.77	1.77	-1.84	-0.72	0.77	2.94	-0.73	-0.89	0.37
Cthe_02290	ABC transporter related protein	3.46	2.58	2.58	2.32	0.88	0.26	0.88	0.26	0.17	-0.21	0.91	0.65	-0.73	-0.89	0.14
Cthe_00224	RNA related	5.98	6.09	6.94	6.27	-0.96	-0.18	-0.11	0.67	-1.7	-0.85	-0.33	1.27	-0.73	-0.89	0.81
Cthe_00010	hypothetical protein	7.38	7.09	7.41	7.28	-0.03	-0.19	0.29	0.13	-0.76	-0.87	0.17	0.45	-0.73	-0.89	1.35
Cthe_00049	transcriptional regulator, XRE family	9.17	8.11	10.41	9.15	-1.24	-1.04	1.06	1.26	-1.99	-2.12	1.14	2.17	-0.73	-0.89	0.67
Cthe_02995	hypothetical protein	8.95	8.39	9.52	8.19	-0.57	0.2	0.56	1.33	-1.31	-0.29	0.51	2.27	-0.73	-0.89	0.32
Cthe_01982	hypothetical protein	6.87	6.46	6.61	6.7	0.26	-0.24	0.41	-0.09	-0.46	-0.94	0.33	0.12	-0.73	-0.89	1.67
Cthe_02591	hypothetical protein	13.21	13.39	13.58	13.44	-0.37	-0.05	-0.18	0.14	-1.1	-0.66	-0.41	0.47	-0.73	-0.89	1.16
Cthe_01737	phage NTP-binding protein	5.58	4.46	4.86	4.46	0.72	0	1.12	0.4	0.01	-0.59	1.21	0.86	-0.73	-0.89	0.22
Cthe_00225	RNA related	6.15	5.32	6.94	6.09	-0.79	-0.77	0.83	0.85	-1.53	-1.72	0.85	1.55	-0.73	-0.89	0.73
Cthe_01761	protein of unknown function DUF214	9.66	10.57	9.51	10.1	0.15	0.47	-0.91	-0.59	-0.57	0.1	-1.32	-0.64	-0.73	-0.89	0.22
Cthe_02290	ABC transporter related protein	3.46	2.58	2.58	2.32	0.88	0.26	0.88	0.26	0.17	-0.21	0.91	0.65	-0.73	-0.89	0.14
Cthe_01722	phage Terminase	5.32	3.7	4.64	4.09	0.68	-0.39	1.62	0.55	-0.03	-1.16	1.84	1.09	-0.74	-0.9	0.3
Cthe_02918	ribosomal protein L6	10.25	11.25	10.27	11.18	-0.02	0.07	-1	-0.91	-0.74	-0.49	-1.44	-1.12	-0.74	-0.9	0.27
Cthe_00935	malonyl CoA-acyl carrier protein transacylase	10.14	12.09	11.1	11.82	-0.96	0.27	-1.95	-0.72	-1.7	-0.19	-2.62	-0.83	-0.74	-0.9	0.35
Cthe_02918	ribosomal protein L6	10.25	11.25	10.27	11.18	-0.02	0.07	-1	-0.91	-0.74	-0.49	-1.44	-1.12	-0.74	-0.9	0.27
Cthe_00935	malonyl CoA-acyl carrier protein transacylase	10.14	12.09	11.1	11.82	-0.96	0.27	-1.95	-0.72	-1.7	-0.19	-2.62	-0.83	-0.74	-0.9	0.35
Cthe_02918	ribosomal protein L6	10.25	11.25	10.27	11.18	-0.02	0.07	-1	-0.91	-0.74	-0.49	-1.44	-1.12	-0.74	-0.9	0.27
Cthe_00935	malonyl CoA-acyl carrier protein transacylase	10.14	12.09	11.1	11.82	-0.96	0.27	-1.95	-0.72	-1.7	-0.19	-2.62	-0.83	-0.74	-0.9	0.35
Cthe_00935	malonyl CoA-acyl carrier protein transacylase	10.14	12.09	11.1	11.82	-0.96	0.27	-1.95	-0.72	-1.7	-0.19	-2.62	-0.83	-0.74	-0.9	0.35
Cthe_02844	intein	10.12	8.9	9.37	8.96	0.75	-0.06	1.22	0.41	0.04	-0.68	1.34	0.88	-0.75	-0.91	0.24
Cthe_01450	hypothetical protein	7.27	6.07	6.94	6.23	0.33	-0.16	1.2	0.71	-0.39	-0.82	1.31	1.33	-0.75	-0.91	0.27
Cthe_03145	transcriptional repressor, CopY family	7.67	7.07	7.67	6.79	0	0.28	0.6	0.88	-0.72	-1.18	0.56	1.59	-0.76	-0.92	0.25
Cthe_00991	bacterial translation initiation factor 2	9.9	11.58	10.43	10.92	-0.53	0.66	-1.68	-0.49	-1.27	0.38	-2.29	-0.48	-0.76	-0.92	0.32
Cthe_03032	hypothetical protein	10.47	10.99	11.81	11.06	-1.34	-0.07	-0.52	0.75	-2.09	-0.69	-0.84	1.39	-0.76	-0.92	0.76
Cthe_03079	cellulosome anchoring protein, cohesion region	13.85	14.39	14.42	14.53	-0.57	-0.14	-0.54	-0.11	-1.31	-0.79	-0.86	0.09	-0.76	-0.92	0.99
Cthe_02864	hypothetical protein	4.95	3.46	6.02	4.81	-1.07	-1.35	1.49	1.21	-1.82	-2.57	1.68	2.09	-0.76	-0.92	0.66
Cthe_02471																



Cthe_00406	hypothetical protein	10.47	10.18	10.32	10.36	0.15	-0.18	0.29	-0.04	-0.57	-0.85	0.17	0.2	-0.79	-0.96	2.19
Cthe_01831	hypothetical protein	9.68	10.08	8.97	10.19	0.71	-0.11	-0.4	-1.22	0	-0.75	-0.69	-1.59	-0.79	-0.96	0.24
Cthe_01400	glycosyl hydrolase 53	10.01	9.9	9.8	9.96	0.21	-0.06	0.11	-0.16	-0.51	-0.68	-0.05	0.02	-0.8	-0.97	8.87
Cthe_00773	SOS-response transcriptional repressor, LexA	12.88	12.4	12.77	12.74	0.11	-0.34	0.48	0.03	-0.61	-1.09	0.41	0.3	-0.8	-0.97	1.38
Cthe_00874	glutamine amidotransferase of anthranilate	8.34	9.93	8.91	10.38	-0.57	-0.45	-1.59	-1.47	-1.31	-1.25	-2.17	-1.97	-0.8	-0.97	0.35
Cthe_00874	glutamine amidotransferase of anthranilate	8.34	9.93	8.91	10.38	-0.57	-0.45	-1.59	-1.47	-1.31	-1.25	-2.17	-1.97	-0.8	-0.97	0.35
Cthe_00773	SOS-response transcriptional repressor, LexA	12.88	12.4	12.77	12.74	0.11	-0.34	0.48	0.03	-0.61	-1.09	0.41	0.3	-0.8	-0.97	1.38
Cthe_00881	diguanylate cyclase	11.74	11.79	11.72	11.9	0.02	-0.11	-0.05	-0.18	-0.7	-0.75	-0.25	-0.02	-0.8	-0.97	2.3
Cthe_00988	tRNA pseudouridine synthase B	8.99	10.21	9.13	9.8	-0.14	0.41	-1.22	-0.67	-0.87	0.01	-1.71	-0.76	-0.8	-0.97	0.26
Cthe_01685	ABC transporter related protein	7.67	7.01	7.02	6.67	0.65	0.34	0.66	0.35	-0.06	-0.09	0.64	0.79	-0.8	-0.97	0.06
Cthe_02337	hypothetical protein	8.24	9.54	8.43	9.06	-0.19	0.48	-1.3	-0.63	-0.92	0.12	-1.81	-0.7	-0.8	-0.97	0.27
Cthe_00955	hypothetical protein	6.58	6.71	7.28	5.46	-0.7	1.25	-0.13	1.82	-1.44	1.25	-0.35	3.02	-0.8	-0.97	0.35
Cthe_01711	hypothetical protein	8.62	7.48	8.07	7.52	0.55	-0.04	1.14	0.55	-0.16	-0.65	1.24	1.09	-0.8	-0.97	0.23
Cthe_01126	hypothetical protein	7.58	5.93	6.43	6.13	1.15	-0.2	1.65	0.3	0.45	-0.88	1.88	0.71	-0.8	-0.97	0.28
Cthe_00874	glutamine amidotransferase of anthranilate	8.34	9.93	8.91	10.38	-0.57	-0.45	-1.59	-1.47	-1.31	-1.25	-2.17	-1.97	-0.8	-0.97	0.35
Cthe_01685	ABC transporter related protein	7.67	7.01	7.02	6.67	0.65	0.34	0.66	0.35	-0.06	-0.09	0.64	0.79	-0.8	-0.97	0.06
Cthe_01400	glycosyl hydrolase 53	10.01	9.9	9.8	9.96	0.21	-0.06	0.11	-0.16	-0.51	-0.68	-0.05	0.02	-0.8	-0.97	8.87
Cthe_00988	tRNA pseudouridine synthase B	8.99	10.21	9.13	9.8	-0.14	0.41	-1.22	-0.67	-0.87	0.01	-1.71	-0.76	-0.8	-0.97	0.26
Cthe_00874	glutamine amidotransferase of anthranilate	8.34	9.93	8.91	10.38	-0.57	-0.45	-1.59	-1.47	-1.31	-1.25	-2.17	-1.97	-0.8	-0.97	0.35
Cthe_00773	SOS-response transcriptional repressor, LexA	12.88	12.4	12.77	12.74	0.11	-0.34	0.48	0.03	-0.61	-1.09	0.41	0.3	-0.8	-0.97	1.38
Cthe_00874	glutamine amidotransferase of anthranilate	8.34	9.93	8.91	10.38	-0.57	-0.45	-1.59	-1.47	-1.31	-1.25	-2.17	-1.97	-0.8	-0.97	0.35
Cthe_00874	glutamine amidotransferase of anthranilate	8.34	9.93	8.91	10.38	-0.57	-0.45	-1.59	-1.47	-1.31	-1.25	-2.17	-1.97	-0.8	-0.97	0.35
Cthe_01685	ABC transporter related protein	7.67	7.01	7.02	6.67	0.65	0.34	0.66	0.35	-0.06	-0.09	0.64	0.79	-0.8	-0.97	0.06
Cthe_01685	ABC transporter related protein	7.67	7.01	7.02	6.67	0.65	0.34	0.66	0.35	-0.06	-0.09	0.64	0.79	-0.8	-0.97	0.06
Cthe_01685	ABC transporter related protein	7.67	7.01	7.02	6.67	0.65	0.34	0.66	0.35	-0.06	-0.09	0.64	0.79	-0.8	-0.97	0.06
Cthe_01685	ABC transporter related protein	7.67	7.01	7.02	6.67	0.65	0.34	0.66	0.35	-0.06	-0.09	0.64	0.79	-0.8	-0.97	0.06
Cthe_01685	ABC transporter related protein	7.67	7.01	7.02	6.67	0.65	0.34	0.66	0.35	-0.06	-0.09	0.64	0.79	-0.8	-0.97	0.06
Cthe_01049	regulatory protein RecX	9.74	9.76	9.84	9.85	-0.1	-0.09	-0.02	-0.01	-0.83	-0.72	-0.21	0.24	-0.81	-0.99	1.94
Cthe_00912	glycoside hydrolase, family 10	10.54	10.39	10.28	10.57	0.26	-0.18	0.15	-0.29	-0.46	-0.85	0	-0.18	-0.81	-0.99	3.02
Cthe_02813	two component transcriptional regulator, winged	6.04	6	5.88	6.32	0.16	-0.32	0.04	-0.44	-0.56	-1.06	-0.14	-0.41	-0.81	-0.99	1.55
Cthe_02813	two component transcriptional regulator, winged	6.04	6	5.88	6.32	0.16	-0.32	0.04	-0.44	-0.56	-1.06	-0.14	-0.41	-0.81	-0.99	1.55
Cthe_02927	bacterial translation initiation factor 1	8.26	9.38	8.26	8.89	0	0.49	-1.12	-0.63	-0.72	0.13	-1.59	-0.7	-0.81	-0.99	0.24
Cthe_02608	ATP synthase F1, beta subunit	10.39	11.2	10.17	11.16	0.22	0.04	-0.81	-0.99	-0.5	-0.53	-1.2	-1.24	-0.81	-0.99	0.24
Cthe_02826	hypothetical protein	11.5	9.95	11.96	11.25	-0.46	-1.3	1.55	0.71	-1.19	-2.5	1.75	1.33	-0.81	-0.99	0.71
Cthe_00252	hypothetical protein	9.43	10.13	8.98	9.61	0.45	0.52	-0.7	-0.63	-0.27	0.18	-1.06	-0.7	-0.81	-0.99	0.14
Cthe_01534	hypothetical protein	7.94	6.27	7.18	6.64	0.76	-0.37	1.67	0.54	0.05	-1.13	1.9	1.08	-0.81	-0.99	0.29
Cthe_00096	protein of unknown function UPF0180	9.78	9.32	10.3	8.96	-0.52	0.36	0.46	1.34	-1.26	-0.06	0.39	2.29	-0.81	-0.99	0.31
Cthe_00820	hypothetical protein	10.1	9.08	9.72	9.87	0.38	-0.79	1.02	-0.15	-0.34	-1.75	1.09	0.03	-0.81	-0.99	0.92
Cthe_02608	ATP synthase F1, beta subunit	10.39	11.2	10.17	11.16	0.22	0.04	-0.81	-0.99	-0.5	-0.53	-1.2	-1.24	-0.81	-0.99	0.24
Cthe_02608	ATP synthase F1, beta subunit	10.39	11.2	10.17	11.16	0.22	0.04	-0.81	-0.99	-0.5	-0.53	-1.2	-1.24	-0.81	-0.99	0.24
Cthe_02608	ATP synthase F1, beta subunit	10.39	11.2	10.17	11.16	0.22	0.04	-0.81	-0.99	-0.5	-0.53	-1.2	-1.24	-0.81	-0.99	0.24
Cthe_02608	ATP synthase F1, beta subunit	10.39	11.2	10.17	11.16	0.22	0.04	-0.81	-0.99	-0.5	-0.53	-1.2	-1.24	-0.81	-0.99	0.24
Cthe_02024	transposase (S116/S110/S902	6.61	6.02	6.15	5.61	0.46	0.41	0.59	0.54	-0.26	0.01	0.55	1.08	-0.82	-1	0.12
Cthe_00310	hypothetical protein	13.42	12.86	13.51	13.31	-0.09	-0.45	0.56	0.2	-0.82	-1.25	0.51	0.56	-0.82	-1	1.11
Cthe_00739	hypothetical protein	13.65	13.04	13.01	12.64	0.64	0.4	0.61	0.37	-0.07	0	0.57	0.82	-0.82	-1	0.04
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_01123	hypothetical protein	7.38	7.28	8.29	7.61	-0.91	-0.33	0.1	0.68	-1.65	-1.07	-0.06	1.29	-0.82	-1	0.86
Cthe_01399	C_GCAxxG_C_C family protein	8.76	8.79	8.68	9.01	0.08	-0.22	-0.03	-0.33	-0.64	-0.91	-0.22	-0.24	-0.82	-1	1.92
Cthe_03033	hypothetical protein	9.41	10.15	10.87	10.21	-1.46	-0.06	-0.74	0.66	-2.21	-0.68	-1.11	1.26	-0.82	-1	0.77
Cthe_00604	hypothetical protein	8.87	7.52	8.29	8.59	0.58	-1.07	1.35	-0.3	-0.13	-2.16	1.5	-0.2	-0.82	-1	0.8
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.57	-0.76	0.43	-1.8	-0.61	-0.82	-1	0.26
Cthe_00394	iron-containing alcohol dehydrogenase	16.54	17.83	16.57	17.14	-0.03	0.69	-1.29	-0.5							



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Cthe_00135	beta-ketoacyl synthase	8.68	10.4	9.29	10.4	-0.61	0	-1.72	-1.11	-1.35	-0.59	-2.34	-1.42	-0.96	-1.18	0.3
Cthe_00932	beta-ketoacyl synthase	12.33	13.2	11.92	12.64	0.41	0.56	-0.87	-0.72	-0.31	0.24	-1.27	-0.83	-0.96	-1.18	0.15
Cthe_00875	anthranilate synthase component I	11.85	12.28	11.03	12.44	0.82	-0.16	-0.43	-1.41	0.11	-0.82	-0.72	-1.88	-0.96	-1.18	0.23
Cthe_00932	beta-ketoacyl synthase	12.33	13.2	11.92	12.64	0.41	0.56	-0.87	-0.72	-0.31	0.24	-1.27	-0.83	-0.96	-1.18	0.15
Cthe_01148	hypothetical protein	7.75	8.28	8.62	8.47	-0.87	-0.19	-0.53	0.15	-1.61	-0.87	-0.85	0.48	-0.96	-1.18	1.05
Cthe_00932	beta-ketoacyl synthase	12.33	13.2	11.92	12.64	0.41	0.56	-0.87	-0.72	-0.31	0.24	-1.27	-0.83	-0.96	-1.18	0.15
Cthe_00932	beta-ketoacyl synthase	12.33	13.2	11.92	12.64	0.41	0.56	-0.87	-0.72	-0.31	0.24	-1.27	-0.83	-0.96	-1.18	0.15
Cthe_00875	anthranilate synthase component I	11.85	12.28	11.03	12.44	0.82	-0.16	-0.43	-1.41	0.11	-0.82	-0.72	-1.88	-0.96	-1.18	0.23
Cthe_00932	beta-ketoacyl synthase	12.33	13.2	11.92	12.64	0.41	0.56	-0.87	-0.72	-0.31	0.24	-1.27	-0.83	-0.96	-1.18	0.15
Cthe_00875	anthranilate synthase component I	11.85	12.28	11.03	12.44	0.82	-0.16	-0.43	-1.41	0.11	-0.82	-0.72	-1.88	-0.96	-1.18	0.23
Cthe_00875	anthranilate synthase component I	11.85	12.28	11.03	12.44	0.82	-0.16	-0.43	-1.41	0.11	-0.82	-0.72	-1.88	-0.96	-1.18	0.23
Cthe_00875	anthranilate synthase component I	11.85	12.28	11.03	12.44	0.82	-0.16	-0.43	-1.41	0.11	-0.82	-0.72	-1.88	-0.96	-1.18	0.23
Cthe_00932	beta-ketoacyl synthase	12.33	13.2	11.92	12.64	0.41	0.56	-0.87	-0.72	-0.31	0.24	-1.27	-0.83	-0.96	-1.18	0.15
Cthe_00932	beta-ketoacyl synthase	12.33	13.2	11.92	12.64	0.41	0.56	-0.87	-0.72	-0.31	0.24	-1.27	-0.83	-0.96	-1.18	0.15
Cthe_01191	HAD-superfamily hydrolase, subfamily IA, variant	7.97	7.18	7.34	6.87	0.63	0.31	0.79	0.47	-0.08	-0.13	0.8	0.97	-0.97	-1.19	0.07
Cthe_01369	histidine triad (HIT) protein	10.74	10.53	10.99	10.83	-0.25	-0.3	0.21	0.16	-0.98	-1.03	0.07	0.5	-0.97	-1.19	1.58
Cthe_01369	histidine triad (HIT) protein	10.74	10.53	10.99	10.83	-0.25	-0.3	0.21	0.16	-0.98	-1.03	0.07	0.5	-0.97	-1.19	1.58
Cthe_01369	histidine triad (HIT) protein	10.74	10.53	10.99	10.83	-0.25	-0.3	0.21	0.16	-0.98	-1.03	0.07	0.5	-0.97	-1.19	1.58
Cthe_02929	ribosomal protein S13	8.86	9.74	8.49	9.21	0.37	0.53	-0.88	-0.72	-0.35	0.19	-1.29	-0.83	-0.97	-1.19	0.15
Cthe_00915	hypothetical protein	10.75	12.47	11.17	11.82	-0.42	0.65	-1.72	-0.65	-1.15	0.37	-2.34	-0.73	-0.97	-1.19	0.28
Cthe_00011	hypothetical protein	6.54	6.39	6.7	6.63	-0.16	-0.24	0.15	0.07	-0.89	-0.94	0	0.36	-0.97	-1.19	2.02
Cthe_02855	hypothetical protein	11.37	10.2	11.52	11.22	-0.15	-1.02	1.17	0.3	-0.88	-2.09	1.27	0.71	-0.97	-1.19	0.88
Cthe_02929	ribosomal protein S13	8.86	9.74	8.49	9.21	0.37	0.53	-0.88	-0.72	-0.35	0.19	-1.29	-0.83	-0.97	-1.19	0.15
Cthe_02929	ribosomal protein S13	8.86	9.74	8.49	9.21	0.37	0.53	-0.88	-0.72	-0.35	0.19	-1.29	-0.83	-0.97	-1.19	0.15
Cthe_01191	HAD-superfamily hydrolase, subfamily IA, variant	7.97	7.18	7.34	6.87	0.63	0.31	0.79	0.47	-0.08	-0.13	0.8	0.97	-0.97	-1.19	0.07
Cthe_01191	HAD-superfamily hydrolase, subfamily IA, variant	7.97	7.18	7.34	6.87	0.63	0.31	0.79	0.47	-0.08	-0.13	0.8	0.97	-0.97	-1.19	0.07
Cthe_00393	sugar ABC transporter (sugar-binding protein)	16.31	17.48	16.12	16.82	0.19	0.66	-1.17	-0.7	-0.53	0.38	-1.65	-0.8	-0.98	-1.2	0.2
Cthe_01788	glycosyl transferase, family 2	8.26	7.06	9.33	7.38	-1.07	-0.32	1.2	1.95	-1.82	-1.06	1.31	3.21	-0.98	-1.2	0.34
Cthe_01343	D-tyrosyl-tRNA[Tyr] deacylase	7.92	8.52	7.39	8.28	0.53	0.24	-0.6	-0.89	-0.18	-0.24	-0.94	-1.09	-0.98	-1.2	0.12
Cthe_02913	ribosomal protein L14	9.48	10.8	9.68	10.81	-0.2	-0.01	-1.32	-1.13	-0.93	-0.6	-1.84	-1.45	-0.98	-1.2	0.27
Cthe_00246	Carbohydrate binding family 6	9.27	8.23	9.12	9.13	0.15	-0.9	1.04	-0.01	-0.57	-1.91	1.11	0.24	-0.98	-1.2	0.99
Cthe_02913	ribosomal protein L14	9.48	10.8	9.68	10.81	-0.2	-0.01	-1.32	-1.13	-0.93	-0.6	-1.84	-1.45	-0.98	-1.2	0.27
Cthe_00393	sugar ABC transporter (sugar-binding protein)	16.31	17.48	16.12	16.82	0.19	0.66	-1.17	-0.7	-0.53	0.38	-1.65	-0.8	-0.98	-1.2	0.2
Cthe_00393	sugar ABC transporter (sugar-binding protein)	16.31	17.48	16.12	16.82	0.19	0.66	-1.17	-0.7	-0.53	0.38	-1.65	-0.8	-0.98	-1.2	0.2
Cthe_02913	ribosomal protein L14	9.48	10.8	9.68	10.81	-0.2	-0.01	-1.32	-1.13	-0.93	-0.6	-1.84	-1.45	-0.98	-1.2	0.27
Cthe_01343	D-tyrosyl-tRNA[Tyr] deacylase	7.92	8.52	7.39	8.28	0.53	0.24	-0.6	-0.89	-0.18	-0.24	-0.94	-1.09	-0.98	-1.2	0.12
Cthe_02526	precorrin-2 oxidase / ferrochelatase	2.81	4.64	3.46	4.32	-0.65	0.32	-1.83	-0.86	-1.39	-0.12	-2.47	-1.05	-0.99	-1.22	0.29
Cthe_02851	hypothetical protein	8.32	7.33	7.66	7.15	0.66	0.18	0.99	0.51	-0.05	-0.32	1.05	1.03	-0.99	-1.22	0.12
Cthe_03061	transcriptional repressor, CopY family	6.97	6.13	6.52	5.88	0.45	0.25	0.84	0.64	-0.27	-0.22	0.86	1.23	-0.99	-1.22	0.13
Cthe_02526	precorrin-2 oxidase / ferrochelatase	2.81	4.64	3.46	4.32	-0.65	0.32	-1.83	-0.86	-1.39	-0.12	-2.47	-1.05	-0.99	-1.22	0.29
Cthe_02526	precorrin-2 oxidase / ferrochelatase	2.81	4.64	3.46	4.32	-0.65	0.32	-1.83	-0.86	-1.39	-0.12	-2.47	-1.05	-0.99	-1.22	0.29
Cthe_02526	precorrin-2 oxidase / ferrochelatase	2.81	4.64	3.46	4.32	-0.65	0.32	-1.83	-0.86	-1.39	-0.12	-2.47	-1.05	-0.99	-1.22	0.29
Cthe_00240	hypothetical protein	10.43	10.59	11.08	10.82	-0.65	-0.23	-0.16	0.26	-1.39	-0.93	-0.39	0.65	-1	-1.23	1.24
Cthe_00254	protein of unknown function DUF58	8.92	10.18	8.85	9.57	0.07	0.61	-1.26	-0.72	-0.65	0.31	-1.76	-0.83	-1.01	-1.24	0.21
Cthe_00805	response regulator receiver protein	8.06	6.27	6.95	6.49	1.11	-0.22	1.79	0.46	0.41	-0.91	2.05	0.95	-1.01	-1.24	0.25
Cthe_00805	response regulator receiver protein	8.06	6.27	6.95	6.49	1.11	-0.22	1.79	0.46	0.41	-0.91	2.05	0.95	-1.01	-1.24	0.25
Cthe_03201	CRISPR-associated protein, Csh1 family	13.25	14.22	14.5	14.55	-1.25	-0.33	-0.97	-0.05	-2	-1.07	-1.4	0.18	-1.01	-1.24	0.9
Cthe_02869	hypothetical protein	4.7	4	4.17	3.58	0.53	0.42	0.7	0.59	-0.18	0.03	0.69	1.15	-1.01	-1.24	0.08
Cthe_02358	Accessory gene regulator B	12.06	12.27	12.78	12.51	-0.72	-0.24	-0.21	0.27	-1.46	-0.94	-0.45	0.67	-1.02	-1.25	1.21
Cthe_02358	Accessory gene regulator B	12.06	12.27	12.78	12.51	-0.72	-0.24	-0.21	0.27	-1.46	-0.94	-0.45	0.67	-1.02	-1.25	1.21
Cthe_01526	ABC transporter related protein	6.77	5.98	6.29	5.67	0.48	0.31	0.79	0.62	-0.23	-0.13	0.8	1.2	-1.02	-1.25	0.1
Cthe_02358	Accessory gene regulator B	12.06	12.27	12.78	12.51	-0.72	-0.24	-0.21	0.27	-1.46	-0.94	-0.45	0.67	-1.02	-1.25	1.21
Cthe_00050	hypothetical protein	6.21	5.78	7.41	6.48	-1.2	-0.7	0.43	0.93	-1.95	-1.62	0.35	1.67	-1.02	-1.25	0.83
Cthe_01526	ABC transporter related protein	6.77	5.98	6.29	5.67	0.48	0.31	0.79	0.62	-0.23	-0.13	0.8	1.2	-1.02	-1.25	0.1
Cthe_01585	signal transduction histidine kinase, LysT	6.46	5.55	6.15	5.36	0.31	0.19	0.91	0.79	-0.41	-0.31	0.95	1.45	-1.03	-1.27	0.17
Cthe_01730	hypothetical protein	2.81	1	2.81	1.58	0	-0.58	1.81	1.23	-0.72	-1.44	2.08	2.12	-1.03	-1.27	0.3
Cthe_00085	Negative regulator of genetic competence	13.92	13.3	14.5	14	-0.58	-0.7	0.62	0.5	-1.32	-1.62	0.59	1.02	-1.04	-1.28	1
Cthe_00085	Negative regulator of genetic competence	13.92	13.3	14.5	14	-0.58	-0.7	0.62	0.5	-1.32	-1.62	0.59	1.02	-1.04	-1.28	1
Cthe_00085	Negative regulator of genetic competence	13.92	13.3	14.5	14	-0.58	-0.7	0.62	0.5	-1.32	-1.62	0.59	1.02	-1.04	-1.28	1
Cthe_02159	hypothetical protein	8.21	7.79	8.35	8.24	-0.14	-0.45	0.42	0.11	-0.87	-1.25	0.34	0.42	-1.04	-1.28	1.58
Cthe_00701	conserved carboxylase region containing protein	14.07	15	13.71	14.48	0.36	0.52	-0.93	-0.77	-0.36	0.18	-1.35	-0.91	-1.05	-1.29	0.14
Cthe_02522	membrane associated protein	10.8	12.06	10.68	11.42	0.12	0.64	-1.26	-0.74	-0.6	0.35	-1.76	-0.86	-1.05	-1.29	0.2
Cthe_00701	conserved carboxylase region containing protein	14.07	15	13.71	14.48	0.36	0.52	-0.93	-0.77	-0.36	0.18	-1.35	-0.91	-1.05	-1.29	0.14
Cthe_00701	conserved carboxylase region containing protein	14.07	15	13.71	14.48	0.36	0.52	-0.93	-0.77	-0.36	0.18	-1.35	-0.91	-1.05	-1.29	0.14
Cthe_00701	conserved carboxylase region containing protein	14.07	15	13.71	14.48	0.36	0.52	-0.93	-0.77	-0.36	0.18	-1.35	-0.91	-1.05	-1.29	0.14
Cthe_02503	Cupin 2, conserved barrel	7.9	6.57	8.46	6.87	-0.56	-0.3	1.33	1.59	-1.3	-1.03	1.48	2.67	-1.06	-1.3	0.31
Cthe_01012	RNA polymerase, sigma 28 subunit	8.28	7.17	8.94	7.3	-0.66	-0.13	1.11	1.64	-1.4	-0.78	1.2	2.74	-1.06	-1.3	0.3
Cthe_00009	YD repeat containing protein	9.45	9.38	9.73	9.65	-0.28	-0.27	0.07	0.08	-1.01	-0.99	-0.1	0.38	-1.06	-1.3	2.02
Cthe_02421	hypothetical protein	11.46	10.02	10.46	9.99	1	0.03	1.44	0.47	0.3	-0.54	1.61	0.97	-1.06	-1.3	0.18
Cthe_00108	type IV pilus assembly PilZ	11.85	11.07	11.14	10.69	0.71	0.38	0.78	0.45	0	-0.03	0.79	0.94	-1.06	-1.3	0.01
Cthe_01981	hypothetical protein	6.6	5.83	8.67	6.99	-2.07	-1.16	0.77	1.68	-2.84	-2.29	0.77	2.8	-1.06	-1.3	0.71
Cthe_01978	hypothetical protein	7.92	6.94	7.29	6.73	0.63	0.21	0.98	0.56	-0.08	-0.28	1.04	1.11	-1.06	-1.3	0.11
Cthe_01102	fimbrial assembly protein	11.12	11.55	11.95	11.8	-0.83	-0.25	-0.43	0.15	-1.57	-0.96	-0.72	0.48	-1.07	-1.32	1.19
Cthe_01102	fimbrial assembly protein	11.12	11.55	11.95	11.8	-0.83	-0.25	-0.43	0.15	-1.57	-0.96	-0.72	0.48	-1.07	-1.32	1.19
Cthe_02912	ribosomal protein S17	9.59	10.65	9.47	10.61	0.12	0.04	-1.06	-1.14	-0.6	-0.53	-1.51	-1.47	-1.07	-1.32	0.21
Cthe_02915	ribosomal protein L5	11.01	11.98	10.8	11.89</											



Cthe_00021	dethiobiotin synthase	4.32	4.95	3.7	4.91	0.62	0.04	-0.63	-1.21	-0.09	-0.53	-0.97	-1.58	-1.11	-1.37	0.16
Cthe_01915	periplasmic sensor signal transduction histidine	9.13	9.18	9.39	9.44	-0.26	-0.26	-0.05	-0.05	-0.99	-0.97	-0.25	0.18	-1.11	-1.37	2.53
Cthe_03225	hypothetical protein	5.73	5.52	7.06	6.15	-1.33	-0.63	0.21	0.91	-2.08	-1.51	0.07	1.64	-1.11	-1.37	0.88
Cthe_00021	dethiobiotin synthase	4.32	4.95	3.7	4.91	0.62	0.04	-0.63	-1.21	-0.09	-0.53	-0.97	-1.58	-1.11	-1.37	0.16
Cthe_00021	dethiobiotin synthase	4.32	4.95	3.7	4.91	0.62	0.04	-0.63	-1.21	-0.09	-0.53	-0.97	-1.58	-1.11	-1.37	0.16
Cthe_00021	dethiobiotin synthase	4.32	4.95	3.7	4.91	0.62	0.04	-0.63	-1.21	-0.09	-0.53	-0.97	-1.58	-1.11	-1.37	0.16
Cthe_02055	hypothetical protein	10.65	11.2	11.58	11.51	-0.93	-0.31	-0.55	0.07	-1.67	-1.04	-0.88	0.36	-1.12	-1.38	1.16
Cthe_02150	integral membrane protein-like protein	12.36	13.08	11.8	12.61	0.56	0.47	-0.72	-0.81	-0.15	0.1	-1.09	-0.97	-1.12	-1.38	0.07
Cthe_01925	hypothetical protein	7.66	5.83	6.63	6.07	1.03	-0.24	1.83	0.56	0.33	-0.94	2.1	1.11	-1.12	-1.38	0.24
Cthe_00274	glycoside hydrolase, family 9	11.63	11.32	11.81	11.73	-0.18	-0.41	0.31	0.08	-0.91	-1.19	0.2	0.38	-1.12	-1.38	1.96
Cthe_02160	hypothetical protein	11.75	11.57	12.3	11.99	-0.55	-0.42	0.18	0.31	-1.29	-1.21	0.04	0.73	-1.12	-1.38	1.36
Cthe_01834	hypothetical protein	8.67	8.24	8.47	8.79	0.2	-0.55	0.43	-0.32	-0.52	-1.4	0.35	-0.23	-1.12	-1.38	2
Cthe_02783	hypothetical protein	1		1		0		1	1	-0.72		1.06	1.77	-1.12	-1.38	0.2
Cthe_02919	ribosomal protein L18	9.38	10.57	9.35	10.42	0.03	0.15	-1.19	-1.07	-0.69	-0.37	-1.67	-1.36	-1.13	-1.39	0.2
Cthe_00736	cellulosome anchoring protein, cohesion region	11.56	13.28	11.93	12.74	-0.37	0.54	-1.72	-0.81	-1.1	0.21	-2.34	-0.97	-1.13	-1.39	0.25
Cthe_00528	hypothetical protein	0	0	0	2	0	-2	0	-2	-0.72	-3.53	-0.19	-2.77	-1.13	-1.39	0.73
Cthe_02919	ribosomal protein L18	9.38	10.57	9.35	10.42	0.03	0.15	-1.19	-1.07	-0.69	-0.37	-1.67	-1.36	-1.13	-1.39	0.2
Cthe_02919	ribosomal protein L18	9.38	10.57	9.35	10.42	0.03	0.15	-1.19	-1.07	-0.69	-0.37	-1.67	-1.36	-1.13	-1.39	0.2
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01497	hypothetical protein	6.64	5.21	7.61	6.66	-0.97	-1.45	1.43	0.95	-1.71	-2.72	1.6	1.7	-1.14	-1.41	0.77
Cthe_00413	glycoside hydrolase, family 9	13.04	13.01	13.07	13.81	-0.03	-0.8	0.03	-0.74	-0.76	-1.76	-0.15	-0.86	-1.14	-1.41	1.23
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_01079	Nucleotidyl transferase	9.06	7.52	8.44	7.69	0.62	-0.17	1.54	0.75	-0.09	-0.84	1.74	1.39	-1.14	-1.41	0.21
Cthe_02128	extracellular solute-binding protein, family 1	7.38	6.57	7.31	6.25	0.07	0.32	0.81	1.06	-0.65	-0.12	0.82	1.86	-1.15	-1.42	0.18
Cthe_00141	Integrase, catalytic region	6.67	5.32	6.99	6.6	-0.32	-1.28	1.35	0.39	-1.05	-2.47	1.5	0.85	-1.15	-1.42	0.87
Cthe_01322	chaperone protein DnaK	11.83	11.57	12.52	10.62	-0.69	0.95	0.26	1.9	-1.43	0.81	0.14	3.14	-1.15	-1.42	0.29
Cthe_01180	uncharacterized predicted metal-binding protein	7.68	8.61	8.95	9.03	-1.27	-0.42	-0.93	-0.08	-2.02	-1.21	-1.35	0.14	-1.15	-1.42	0.97
Cthe_00625	glycoside hydrolase, family 9	12.58	14.02	12.75	13.69	-0.17	0.33	-1.44	-0.94	-0.9	-0.1	-1.99	-1.17	-1.15	-1.42	0.22
Cthe_02051	CRISPR-associated RAMP protein, SSO1426 family	6.54	7.55	7.69	8.39	-1.15	-0.84	-1.01	-0.7	-1.9	-1.82	-1.45	-0.8	-1.16	-1.43	0.89
Cthe_01988	hypothetical protein	10.76	8.96	9.79	9.18	0.97	-0.22	1.8	0.61	0.27	-0.91	2.06	1.18	-1.16	-1.43	0.22
Cthe_01133	hypothetical protein	9.85	10.34	10.83	10.65	-0.98	-0.31	-0.49	0.18	-1.72	-1.04	-0.8	0.53	-1.16	-1.43	1.18
Cthe_02087	metalloenzyme	9.7	9.5	9.65	9.8	0.05	-0.3	0.2	-0.15	-0.67	-1.03	0.06	0.03	-1.17	-1.44	10.29
Cthe_02911	ribosomal protein L29	8.57	9.74	8.51	9.69	0.06	0.05	-1.17	-1.18	-0.66	-0.51	-1.65	-1.53	-1.17	-1.44	0.21
Cthe_03123	von Willebrand factor, type A	9.46	11.2	9.94	10.99	-0.48	0.21	-1.74	-1.05	-1.21	-0.28	-2.36	-1.33	-1.17	-1.44	0.26
Cthe_02911	ribosomal protein L29	8.57	9.74	8.51	9.69	0.06	0.05	-1.17	-1.18	-0.66	-0.51	-1.65	-1.53	-1.17	-1.44	0.21
Cthe_02911	ribosomal protein L29	8.57	9.74	8.51	9.69	0.06	0.05	-1.17	-1.18	-0.66	-0.51	-1.65	-1.53	-1.17	-1.44	0.21
Cthe_02962	oligopeptide/dipeptide ABC transporter, ATPase	9.47	9.73	8.12	10.12	1.35	-0.39	-0.26	-2	0.65	-1.16	-0.51	-2.77	-1.18	-1.46	0.27
Cthe_01131	hypothetical protein	5.58	6.57	7.1	6.92	-1.52	-0.35	-0.99	0.18	-2.28	-1.1	-1.42	0.53	-1.18	-1.46	0.94
Cthe_02003	RNA related	3.46	3.17	3.32	3.81	0.14	-0.64	0.29	-0.49	-0.58	-1.53	0.17	-0.48	-1.18	-1.46	1.81
Cthe_02962	oligopeptide/dipeptide ABC transporter, ATPase	9.47	9.73	8.12	10.12	1.35	-0.39	-0.26	-2	0.65	-1.16	-0.51	-2.77	-1.18	-1.46	0.27
Cthe_02461	transcriptional regulator, XRE family	4.17	2.58	3.7	2.81	0.47	-0.23	1.59	0.89	-0.24	-0.93	1.8	1.61	-1.19	-1.47	0.22
Cthe_01924		7.01	5.83	7.55	5.93	-0.54	-0.1	1.18	1.62	-1.28	-0.74	1.29	2.71	-1.19	-1.47	0.28
Cthe_02501	hypothetical protein	11.3	10.98	11.4	11.41	-0.1	-0.43	0.32	-0.01	-0.83	-1.22	0.21	0.24	-1.19	-1.47	2.6
Cthe_00012	YD repeat protein	5.46	5.32	5.43	6.07	0.03	-0.75	0.14	-0.64	-0.69	-1.69	-0.01	-0.71	-1.19	-1.47	1.44
Cthe_01214	hypothetical protein	5	3.32	5.43	3.81	-0.43	-0.49	1.68	1.62	-1.16	-1.31	1.91	2.71	-1.2	-1.48	0.3
Cthe_00798	lipolytic enzyme, G-D-S-L	10.27	10.39	10.49	10.9	-0.22	-0.51	-0.12	-0.41	-0.95	-1.34	-0.34	-0.36	-1.2	-1.48	1.86
Cthe_01747	DNA mismatch endonuclease vsr	6.25	5.64	6	6.46	0.25	-0.82	0.61	-0.46	-0.47	-1.79	0.57	-0.44	-1.21	-1.49	1.44
Cthe_00227	hypothetical protein	7.17	7.07	7.31	7.38	-0.14	-0.31	0.1	-0.07	-0.87	-1.04	-0.06	0.15	-1.21	-1.49	4.72
Cthe_01746	hypothetical protein	6.49	4.7	6.09	5.09	0.4	-0.39	1.79	1	-0.32	-1.16	2.05	1.77	-1.21	-1.49	0.25
Cthe_01747	DNA mismatch endonuclease vsr	6.25	5.64	6	6.46	0.25	-0.82	0.61	-0.46	-0.47	-1.79	0.57	-0.44	-1.21	-1.49	1.44
Cthe_01103	prepilin-type cleavage/methylation	10.64	10.93	11.39	11.27	-0.75	-0.34	-0.29	0.12	-1.49	-1.09	-0.55	0.44	-1.22	-1.51	1.47
Cthe_01103	prepilin-type cleavage/methylation	10.64	10.93	11.39	11.27	-0.75	-0.34	-0.29	0.12	-1.49	-1.09	-0.55	0.44	-1.22	-1.51	1.47
Cthe_02926	hypothetical protein	7.33	8.97	7.67	8.69	-0.34	0.28	-1.64	-1.02	-1.07	-1.08	-2.24	-1.29	-1.22	-1.51	0.24
Cthe_01970	hypothetical protein	8.84	8.23	9.76	9.08	-0.92	-0.85	0.61	0.68	-1.66	-1.84	0.57	1.29	-1.22	-1.51	0.99
Cthe_02960	hypothetical protein	7.77	6.88	8.49	6.73	-0.72	0.15	0.89	1.76	-1.46	-0.37	0.92	2.92	-1.22	-1.51	0.28
Cthe_00434	ATPase	4.17	4.86	6.6	5.29	-2.43	-0.43	-0.69	1.31	-3.2	-1.22	-1.05	2.24	-1.22	-1.51	0.78
Cthe_00184	type IV pilus assembly protein PilM	14.33	14.97	15.67	15.32	-1.34	-0.35	-0.64	0.35	-2.09	-1.1	-0.99	0.79	-1.23	-1.52	1.05
Cthe_03212	protein of unknown function DUF324	5.78	5.58	5.91	5.95	-0.13	-0.37	0.2	-0.04	-0.86	-1.13	0.06	0.2	-1.23	-1.52	3.82
Cthe_00184	type IV pilus assembly protein PilM	14.33	14.97	15.67	15.32	-1.34	-0.35	-0.64	0.35	-2.09	-1.1	-0.99	0.79	-1.23	-1.52	1.05
Cthe_01968	cell divisionFtsK/SpoIIe	10.48	10.71	11.44	11.09	-0.96	-0.38	-0.23	0.35	-1.7	-1.15	-0.47	0.79	-1.23	-1.52	1.25
Cthe_00785	hypothetical protein	11.41	10.54	13.31	11.81	-1.9	-1.27	0.87	1.5	-2.66	-2.46	0.9	2.53	-1.23	-1.52	0.76
Cthe_00624	glycoside hydrolase, family 9-like Ig-like	12.6	13.76	12.49	13.7	0.11	0.06	-1.16	-1.21	-0.61	-0.5	-1.64	-1.58	-1.24	-1.53	0.19
Cthe_00989	phosphoesterase, RecJ-like protein	9.18	10.9	9.31	10.13	-0.13	0.77	-1.72	-0.82	-0.86	0.54	-2.34	-0.98	-1.24	-1.53	0.22
Cthe_02567	hypothetical protein	2	1.58	4.09	2.58	-2.09	-1	0.42	1.51	-2.86	-2.06	0.34	2.55	-1.24	-1.53	0.77
Cthe_																



Cthe_03008	Superoxide dismutase	4.7	3.17	5	3.46	-0.3	-0.29	1.53	1.54	-1.03	-1.01	1.73	2.59	-1.33	-1.65	0.26
Cthe_03008	Superoxide dismutase	4.7	3.17	5	3.46	-0.3	-0.29	1.53	1.54	-1.03	-1.01	1.73	2.59	-1.33	-1.65	0.26
Cthe_03008	Superoxide dismutase	4.7	3.17	5	3.46	-0.3	-0.29	1.53	1.54	-1.03	-1.01	1.73	2.59	-1.33	-1.65	0.26
Cthe_01934	Abortive infection protein	11.19	10.88	11.28	11.38	-0.09	-0.5	0.31	-0.1	-0.82	-1.32	0.2	0.11	-1.35	-1.67	3.82
Cthe_01101	hypothetical protein	12.11	12.46	13.07	12.88	-0.96	-0.42	-0.35	0.19	-1.7	-1.21	-0.62	0.55	-1.35	-1.67	1.41
Cthe_00334	putative anti-sigma regulatory factor,	8.31	9	7.63	8.58	0.68	0.42	-0.69	-0.95	-0.03	0.03	-1.05	-1.18	-1.36	-1.68	0.02
Cthe_01971	hypothetical protein	9.07	8.42	10.1	9.38	-1.03	-0.96	0.65	0.72	-1.78	-2	0.62	1.35	-1.36	-1.68	1.01
Cthe_01135	SEFIR domain containing protein	6.87	7.09	7.44	7.52	-0.57	-0.43	-0.22	-0.08	-1.31	-1.22	-0.46	0.14	-1.36	-1.68	2.09
Cthe_00670	spore germination protein	6.23	4.91	7.02	5.09	-0.79	-0.18	1.32	1.93	-1.53	-0.85	1.46	3.18	-1.36	-1.68	0.28
Cthe_00818	hypothetical protein	8.75	8.46	8.72	9.19	0.03	-0.73	0.29	-0.47	-0.69	-1.66	0.17	-0.45	-1.37	-1.7	2.1
Cthe_01916	two component transcriptional regulator, winged	8.59	8.41	9.09	8.93	-0.5	-0.52	0.18	0.16	-1.23	-1.35	0.04	0.5	-1.38	-1.71	2.05
Cthe_01916	two component transcriptional regulator, winged	8.59	8.41	9.09	8.93	-0.5	-0.52	0.18	0.16	-1.23	-1.35	0.04	0.5	-1.38	-1.71	2.05
Cthe_00035	4Fe-4S ferredoxin, iron-sulfur binding	5.67	6.43	7.68	6.87	-2.01	-0.44	-0.76	0.81	-2.78	-1.24	-1.14	1.48	-1.38	-1.71	0.92
Cthe_01372	hypothetical protein	10.47	10	10.65	10.66	-0.18	-0.66	0.47	-0.01	-0.91	-1.56	0.4	0.24	-1.39	-1.72	2.18
Cthe_02881	ATP phosphoribosyltransferase	3.46	5.32	5.73	6.38	-2.27	-1.06	-1.86	-0.65	-3.04	-2.15	-2.51	-0.73	-1.4	-1.73	0.8
Cthe_02042	RNA related	6.41	6.23	6.71	6.7	-0.3	-0.47	0.18	0.01	-1.03	-1.28	0.04	0.27	-1.4	-1.73	3.38
Cthe_02089	glycoside hydrolase, family 48	14.99	15.99	16.3	16.87	-1.31	-0.88	-1	-0.57	-2.06	-1.88	-1.44	-0.61	-1.4	-1.73	1
Cthe_00008	hypothetical protein	6.43	5.58	6.48	6.57	-0.05	-0.99	0.85	-0.09	-0.78	-2.04	0.87	0.12	-1.4	-1.73	1.4
Cthe_03070	protein of unknown function DUF1256	11.25	10.76	11.49	11.45	-0.24	-0.69	0.49	0.04	-0.97	-1.6	0.42	0.32	-1.4	-1.73	1.99
Cthe_00821	coagulation factor 5/8 type-like protein	14.73	13.24	14.71	14.76	0.02	-1.52	1.49	-0.05	-0.7	-2.82	1.68	0.18	-1.4	-1.73	0.97
Cthe_02881	ATP phosphoribosyltransferase	3.46	5.32	5.73	6.38	-2.27	-1.06	-1.86	-0.65	-3.04	-2.15	-2.51	-0.73	-1.4	-1.73	0.8
Cthe_02881	ATP phosphoribosyltransferase	3.46	5.32	5.73	6.38	-2.27	-1.06	-1.86	-0.65	-3.04	-2.15	-2.51	-0.73	-1.4	-1.73	0.8
Cthe_02881	ATP phosphoribosyltransferase	3.46	5.32	5.73	6.38	-2.27	-1.06	-1.86	-0.65	-3.04	-2.15	-2.51	-0.73	-1.4	-1.73	0.8
Cthe_01744	hypothetical protein	4.95	3.7	6.11	5.17	-1.16	-1.47	1.25	0.94	-1.91	-2.75	1.38	1.68	-1.41	-1.75	0.87
Cthe_01883	SMC protein-like protein	6.82	5.13	7.57	6.88	-0.75	-1.75	1.69	0.69	-1.49	-3.16	1.93	1.3	-1.42	-1.76	0.84
Cthe_02921	ribosomal protein L30	8.49	9.82	8.33	9.34	0.16	0.48	-1.33	-1.01	-0.56	0.12	-1.85	-1.27	-1.42	-1.76	0.14
Cthe_01603	phosphate ABC transporter, inner membrane	5.64	6.93	5.55	6.95	0.09	-0.02	-1.29	-1.4	-0.63	-0.62	-1.8	-1.86	-1.42	-1.76	0.19
Cthe_02921	ribosomal protein L30	8.49	9.82	8.33	9.34	0.16	0.48	-1.33	-1.01	-0.56	0.12	-1.85	-1.27	-1.42	-1.76	0.14
Cthe_01603	phosphate ABC transporter, inner membrane	5.64	6.93	5.55	6.95	0.09	-0.02	-1.29	-1.4	-0.63	-0.62	-1.8	-1.86	-1.42	-1.76	0.19
Cthe_02921	ribosomal protein L30	8.49	9.82	8.33	9.34	0.16	0.48	-1.33	-1.01	-0.56	0.12	-1.85	-1.27	-1.42	-1.76	0.14
Cthe_02149	amine oxidase	11.37	12.79	11.11	12.1	0.26	0.69	-1.42	-0.99	-0.46	0.43	-1.96	-1.24	-1.43	-1.77	0.15
Cthe_02542	SirA-like protein	4.17	3.91	4.52	4.46	-0.35	-0.55	0.26	0.06	-1.08	-1.4	0.14	0.35	-1.43	-1.77	2.64
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_02088	protein of unknown function DUF710	10.13	9.68	10.65	10.41	-0.52	-0.73	0.45	0.24	-1.26	-1.66	0.38	0.62	-1.44	-1.78	1.61
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_02049	protein of unknown function DUF324	7.75	8.61	8.93	9.46	-1.18	-0.85	-0.86	-0.53	-1.93	-1.84	-1.26	-0.55	-1.44	-1.78	1.09
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type IV	9.16	8.68	9.18	9.41	-0.02	-0.73	0.48	-0.23	-0.74	-1.66	0.41	-0.09	-1.44	-1.78	2.43
Cthe_01335	peptidase A24A, prelin type															



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Cthe_02910	ribosomal protein L16	10.34	11.57	9.98	11.24	0.36	0.33	-1.23	-1.26	-0.36	-0.1	-1.72	-1.65	-1.75	-2.18	0.09
Cthe_02129	RNA related	1	0	2.81	1.58	-1.81	-1.58	1	1.23	-2.57	-2.91	1.06	2.12	-1.77	-2.2	0.92
Cthe_02400	peptidase U57, YabG	3.17	1.58	2.81	1.58	0.36	0	1.59	1.23	-0.36	-0.59	1.8	2.12	-1.78	-2.22	0.14
Cthe_01373	YD repeat protein	9.15	9.09	10.01	9.81	-0.86	-0.72	0.06	0.2	-1.6	-1.65	-0.11	0.56	-1.79	-2.23	2.26
Cthe_02909	ribosomal protein S3	11.33	12.37	10.78	12.06	0.55	0.31	-1.04	-1.28	-0.16	-0.13	-1.49	-1.68	-1.79	-2.23	0.05
Cthe_02909	ribosomal protein S3	11.33	12.37	10.78	12.06	0.55	0.31	-1.04	-1.28	-0.16	-0.13	-1.49	-1.68	-1.79	-2.23	0.05
Cthe_02909	ribosomal protein S3	11.33	12.37	10.78	12.06	0.55	0.31	-1.04	-1.28	-0.16	-0.13	-1.49	-1.68	-1.79	-2.23	0.05
Cthe_00245	transcriptional regulator, ArsR family	12.36	13.11	13.92	13.84	-1.56	-0.73	-0.75	0.08	-2.32	-1.66	-1.12	0.38	-1.8	-2.24	1.36
Cthe_02880	histidyl-tRNA synthetase	6.99	7.89	8.39	9.1	-1.4	-1.21	-0.9	-0.71	-2.15	-2.37	-1.31	-0.82	-1.82	-2.27	1.16
Cthe_02880	histidyl-tRNA synthetase	6.99	7.89	8.39	9.1	-1.4	-1.21	-0.9	-0.71	-2.15	-2.37	-1.31	-0.82	-1.82	-2.27	1.16
Cthe_03094	glycosyl transferase, family 2	11	12.88	11.02	12.23	-0.02	0.65	-1.88	-1.21	-0.74	0.37	-2.54	-1.58	-1.83	-2.28	0.16
Cthe_01699	RNA related	1.58		3.17	2	-1.59	-2	1.58	1.17	-2.35	-3.53	1.79	2.03	-1.83	-2.28	0.88
Cthe_03094	glycosyl transferase, family 2	11	12.88	11.02	12.23	-0.02	0.65	-1.88	-1.21	-0.74	0.37	-2.54	-1.58	-1.83	-2.28	0.16
Cthe_03094	glycosyl transferase, family 2	11	12.88	11.02	12.23	-0.02	0.65	-1.88	-1.21	-0.74	0.37	-2.54	-1.58	-1.83	-2.28	0.16
Cthe_02805	Carbohydrate-binding, CnC-like protein	11.42	10.88	12.56	12	-1.14	-1.12	0.54	0.56	-1.89	-2.24	0.49	1.11	-1.85	-2.3	1.36
Cthe_00004	YD repeat containing protein	7.07	6.78	8.21	7.74	-1.14	-0.96	0.29	0.47	-1.89	-2	0.17	0.97	-1.88	-2.34	1.57
Cthe_01170	Dihydrodipicolinate reductase	9.79	8.59	11.35	10.31	-1.56	-1.72	1.2	1.04	-2.32	-3.12	1.31	1.83	-1.89	-2.35	0.97
Cthe_02057	CRISPR-associated protein, TM1812 family	9.41	9.02	10.47	10.03	-1.06	-1.01	0.39	0.44	-1.81	-2.07	0.3	0.92	-1.89	-2.35	1.6
Cthe_01170	Dihydrodipicolinate reductase	9.79	8.59	11.35	10.31	-1.56	-1.72	1.2	1.04	-2.32	-3.12	1.31	1.83	-1.89	-2.35	0.97
Cthe_01170	Dihydrodipicolinate reductase	9.79	8.59	11.35	10.31	-1.56	-1.72	1.2	1.04	-2.32	-3.12	1.31	1.83	-1.89	-2.35	0.97
Cthe_01170	Dihydrodipicolinate reductase	9.79	8.59	11.35	10.31	-1.56	-1.72	1.2	1.04	-2.32	-3.12	1.31	1.83	-1.89	-2.35	0.97
Cthe_01170	Dihydrodipicolinate reductase	9.79	8.59	11.35	10.31	-1.56	-1.72	1.2	1.04	-2.32	-3.12	1.31	1.83	-1.89	-2.35	0.97
Cthe_01170	Dihydrodipicolinate reductase	9.79	8.59	11.35	10.31	-1.56	-1.72	1.2	1.04	-2.32	-3.12	1.31	1.83	-1.89	-2.35	0.97
Cthe_01170	Dihydrodipicolinate reductase	9.79	8.59	11.35	10.31	-1.56	-1.72	1.2	1.04	-2.32	-3.12	1.31	1.83	-1.89	-2.35	0.97
Cthe_01967	DNA segregation ATPase FtsK/SpoIIIE and related	10.13	10.08	10.64	10.77	-0.51	-0.69	0.05	-0.13	-1.24	-1.6	-0.12	0.06	-1.9	-2.37	8.48
Cthe_01625	phage protein, HK97 gp10 family	1		1	1.58	0	-1.58	1	-0.58	-0.72	-2.91	1.06	-0.62	-1.9	-2.37	1.37
Cthe_02806	hypothetical protein	10.71	10.1	12.12	11.36	-1.41	-1.26	0.61	0.76	-2.16	-2.44	0.57	1.41	-1.91	-2.38	1.2
Cthe_01340	hypothetical protein	8.16	8.55	10.14	9.39	-1.98	-0.84	-0.39	0.75	-2.74	-1.82	-0.68	1.39	-1.91	-2.38	1.19
Cthe_00844	stage III sporulation protein spoIIAB	3.7	3.17	6.46	4.7	-2.76	-1.53	0.53	1.76	-3.54	-2.84	0.47	2.92	-1.91	-2.38	0.86
Cthe_01122	hypothetical protein	2.81	2.81	3.32	4.17	-0.51	-1.36	0	-0.85	-1.24	-2.59	-0.19	-1.03	-1.94	-2.42	1.54
Cthe_02993	hypothetical protein	11.03	9.99	11.62	11.45	-0.59	-1.46	1.04	0.17	-1.33	-2.74	1.11	0.52	-1.95	-2.43	1.4
Cthe_01694	hypothetical protein	5.67	4.52	6	4.09	-0.33	0.43	1.15	1.91	-1.06	0.04	1.25	3.15	-1.96	-2.44	0.18
Cthe_02301	CRISPR-associated autoregulator, DevR family	8.97	9.69	10.45	10.6	-1.48	-0.91	-0.72	-0.15	-2.23	-1.93	-1.09	0.03	-1.98	-2.47	1.52
Cthe_01742	Helix-turn-helix, type 11 containing protein	3.17	1.58	3	3.7	0.17	-2.12	1.59	-0.7	-0.55	-3.71	1.8	-0.8	-2	-2.49	1.07
Cthe_01230	competence protein ComEA helix-hairpin-helix	5.09	5.39	6.93	6.29	-1.84	-0.9	-0.3	0.64	-2.6	-1.91	-0.56	1.23	-2.02	-2.52	1.34
Cthe_01645	conserved hypothetical phage-associated protein	3.17	2	3.32	3.7	-0.15	-1.7	1.17	-0.38	-0.88	-3.09	1.27	-0.32	-2.05	-2.56	1.38
Cthe_00190	proteinase inhibitor I4, serpin	9.79	10.11	11.25	10.97	-1.46	-0.86	-0.32	0.28	-2.21	-1.85	-0.59	0.68	-2.08	-2.59	1.8
Cthe_00048	copper amine oxidase-like protein	3.7	3.46	6.13	4.81	-2.43	-1.35	0.24	1.32	-3.2	-2.57	0.11	2.26	-2.09	-2.61	1.02
Cthe_02564	hypothetical protein	10.3	10.08	11.22	11.03	-0.92	-0.95	0.22	0.19	-1.66	-1.99	0.09	0.55	-2.1	-2.62	2.61
Cthe_02300	CRISPR-associated protein Cas5	9.32	9.88	10.62	10.89	-1.3	-1.01	-0.56	-0.27	-2.05	-2.07	-0.89	-0.15	-2.11	-2.63	1.81
Cthe_02052	hypothetical protein	3.91	4.58	5.55	5.49	-1.64	-0.91	-0.67	0.06	-2.4	-1.93	-1.02	0.35	-2.12	-2.65	1.6
Cthe_01045	hypothetical protein	7.77	6	6.88	5.78	0.89	0.22	1.77	1.1	0.18	-0.26	2.02	1.92	-2.16	-2.7	0.06
Cthe_02303	CRISPR-associated protein Cas6	9.33	9.01	11.14	10.29	-1.81	-1.28	0.32	0.85	-2.57	-2.47	0.21	1.55	-2.17	-2.71	1.28
Cthe_02122	hypothetical protein	5.73	4.39	5.88	6.32	-0.15	-1.93	1.34	-0.44	-0.88	-3.43	1.49	-0.41	-2.17	-2.71	1.29
Cthe_03221	hypothetical protein	5.73	5.55	7.96	6.87	-2.23	-1.32	0.18	1.09	-3	-2.53	0.04	1.91	-2.22	-2.77	1.15
Cthe_00045	copper amine oxidase-like protein	6.48	6.21	7.67	7.35	-1.19	-1.14	0.27	0.32	-1.94	-2.26	0.15	0.74	-2.31	-2.89	2.22
Cthe_02302	hypothetical protein	9.61	9.86	11.15	10.86	-1.54	-1	-0.25	0.29	-2.3	-2.06	-0.5	0.7	-2.32	-2.9	2.02
Cthe_02396	hypothetical protein	7.13	6.64	9.18	8.15	-2.05	-1.51	0.49	1.03	-2.82	-2.81	0.42	1.82	-2.32	-2.9	1.2
Cthe_00415	spore coat protein CotUB		2	0	1.58	0	0.42	-2	-1.58	-0.72	0.03	-2.69	-2.14	-2.34	-2.92	0.12
Cthe_01338	Flp pilus assembly protein TadB-like protein	7.04	7.61	8.72	8.64	-1.68	-1.03	-0.57	0.08	-2.44	-2.1	-0.9	0.38	-2.35	-2.94	1.85
Cthe_02387	peptidase M14, carboxypeptidase A	7.73	6.17	7.49	5.86	0.24	0.31	1.56	1.63	-0.48	-0.13	1.76	2.73	-2.39	-2.99	0.09
Cthe_02387	peptidase M14, carboxypeptidase A	7.73	6.17	7.49	5.86	0.24	0.31	1.56	1.63	-0.48	-0.13	1.76	2.73	-2.39	-2.99	0.09
Cthe_00591	Integrase, catalytic region	6.83	5.73	7.83	7.52	-1	-1.79	1.1	0.31	-1.74	-3.22	1.19	0.73	-2.42	-3.03	1.47
Cthe_03215	CRISPR-associated protein, TM1812 family	5.83	5.64	6.73	6.7	-0.9	-1.06	0.19	0.03	-1.64	-2.15	0.05	0.3	-2.43	-3.04	4.99
Cthe_01974	hypothetical protein	8.12	7.89	9.84	9.21	-1.72	-1.32	0.23	0.63	-2.48	-2.53	0.1	1.21	-2.46	-3.08	1.64
Cthe_00534	ABC-type bacteriocin transporter	9.36	8.77	10.3	10.16	-0.94	-1.39	0.59	0.14	-1.68	-2.63	0.55	0.47	-2.48	-3.1	2.42
Cthe_02569	hypothetical protein	4.91	4.09	6.79	5.86	-1.88	-1.77	0.82	0.93	-2.64	-3.19	0.84	1.67	-2.48	-3.1	1.24
Cthe_02127	ATPase associated with various cellular	10.35	9.82	12.16	11.4	-1.81	-1.58	0.53	0.76	-2.57	-2.91	0.47	1.41	-2.56	-3.2	1.47
Cthe_00929	Stage V sporulation protein S	10.92	9.74	12.54	11.77	-1.62	-2.03	1.18	0.77	-2.38	-3.57	1.29	1.42	-2.58	-3.23	1.26
Cthe_01966	hypothetical protein	6.88	6.67	7.58	8.07	-0.7	-1.4	0.21	-0.49	-1.44	-2.65	0.07	-0.48	-2.58	-3.23	3.49
Cthe_02048	hypothetical protein	5.93	5.93	6.86	7.22	-0.93	-1.29	0	-0.36	-1.67	-2.49	-0.19	-0.29	-2.69	-3.37	4.86
Cthe_00211	glycoside hydrolase, family 16	9.78	8.01	9.55	7.69	0.23	0.32	1.77	1.86	-0.49	-0.12	2.02	3.08	-2.77	-3.47	0.08
Cthe_02310	hypothetical protein	7.89	7.01	9.2	8.84	-1.31	-1.83	0.88	0.36	-2.06	-3.28	0.91	0.8	-2.79	-3.49	1.8
Cthe_01336	hypothetical protein	8.25	7.71	9.07	9.24	-0.82	-1.53	0.54	-0.17	-1.56	-2.84	0.49	0	-2.8	-3.51	3.72
Cthe_01243	GCN5-related N-acetyltransferase	6.51	6.04	8.36	7.7	-1.85	-1.66	0.47	0.66	-2.61	-3.03	0.4	1.26	-2.82	-3.53	1.7
Cthe_01337	type II secretion system protein	6.86	6.99	8.06	8.28	-1.2	-1.29	-0.13	-0.22	-1.95	-2.49	-0.35	-0.08	-2.84	-3.56	4.95
Cthe_02123	hypothetical protein	6.86	6.36	7.6	8.13	-0.74	-1.77	0.5	-0.53	-1.48	-3.19	0.44	-0.55	-2.89	-3.62	2.8
Cthe_02774	hypothetical protein	6.98	6.38	9.11	8.23	-2.13	-1.85	0.6	0.88	-2.9	-3.31	0.56	1.59	-2.9	-3.63	1.47
Cthe_02296	CRISPR-associated protein Cas2	6.15	5.17	7.17	7.13	-1.02	-1.96	0.98	0.04	-1.77	-3.47	1.04	0.32	-2.93	-3.67	2.01
Cthe_02195	Carbohydrate binding family 6	4.81	3	4.25	2.58	0.56	0.42	1.81	1.67	-0.15	0.03	2.08	2.79	-2.94	-3.68	0.02
Cthe_02299	CRISPR-associated helicase Cas3	8.24	8.65	9.78	10.35	-1.54	-1.7	-0.41	-0.57	-2.3	-3.09	-0.7	-0.61	-3.03	-3.8	2.33
Cthe_00191	proteinase inhibitor I4, serpin	9.94	9.51	11.44	11.17	-1.5	-1.66	0.43	0.27	-2.26	-3.03	0.35	0.67	-3.11	-3.9	2.81
Cthe_02297	CRISPR-associated protein Cas1	7.18	7.02	8.25	8.83	-1.07	-1.81	0.16	-0.58	-1.82	-3.25	0.01	-0.62	-3.17	-3.97	3.37
Cthe_00449	hypothetical protein	1	0	4.46	2.58	-3.46	-2.58	1	1.88	-4.26	-4.38	1.06	3.11	-3.19	-4	1.04
Cthe_02126	binding-protein-dependent transport systems	8.14	8.33	9.99	9.92	-1.85	-1.59	-0.19	0.07	-2.61	-2.93	-0.42	0.36	-3.43	-4.3	3.99
Cthe_02126	binding-protein-dependent transport systems	8.14	8.33	9.99	9.92	-1.85	-1.59	-0.19	0.07	-2.61	-2.93	-0.42	0.36	-3.43	-4.3	3.99
Cthe_01437																







locus	locus-description	log2 100-mer reads			Intersample				Intersample				Wnet	Wstats		
		Cellobiose	$\alpha$ -cellulose	CB vs $\alpha$ C (Z)	Cellobiose	$\alpha$ -cellulose	CB vs $\alpha$ C (Znet)	Cellobiose	$\alpha$ -cellulose	W						
Cthe_02881	ATP phosphoribosyltransferase	6.19	6.49	3.7	3.32	2.49	3.17	-0.3	0.38	4.19	3.65	-0.9	-0.64	5.07	5.01	5.72
Cthe_02881	ATP phosphoribosyltransferase	6.19	6.49	3.7	3.32	2.49	3.17	-0.3	0.38	4.19	3.65	-0.9	-0.64	5.07	5.01	5.72
Cthe_02881	ATP phosphoribosyltransferase	6.19	6.49	3.7	3.32	2.49	3.17	-0.3	0.38	4.19	3.65	-0.9	-0.64	5.07	5.01	5.72
Cthe_02881	ATP phosphoribosyltransferase	6.19	6.49	3.7	3.32	2.49	3.17	-0.3	0.38	4.19	3.65	-0.9	-0.64	5.07	5.01	5.72
Cthe_02880	histidyl-tRNA synthetase	8.1	8.37	6.11	5.04	1.99	3.33	-0.27	1.07	3.51	3.85	-0.8	0.83	4.7	4.64	5.14
Cthe_02880	histidyl-tRNA synthetase	8.1	8.37	6.11	5.04	1.99	3.33	-0.27	1.07	3.51	3.85	-0.8	0.83	4.7	4.64	5.14
Cthe_02882	Histidinol dehydrogenase	8.46	9.19	6.54	5.21	1.92	3.98	-0.73	1.33	3.42	4.62	-2.33	1.38	4.56	4.5	2.41
Cthe_02882	Histidinol dehydrogenase	8.46	9.19	6.54	5.21	1.92	3.98	-0.73	1.33	3.42	4.62	-2.33	1.38	4.56	4.5	2.41
Cthe_02882	Histidinol dehydrogenase	8.46	9.19	6.54	5.21	1.92	3.98	-0.73	1.33	3.42	4.62	-2.33	1.38	4.56	4.5	2.41
Cthe_02882	Histidinol dehydrogenase	8.46	9.19	6.54	5.21	1.92	3.98	-0.73	1.33	3.42	4.62	-2.33	1.38	4.56	4.5	2.41
Cthe_01433	short-chain dehydrogenase/reductase SD	14.58	14.67	12.51	12.05	2.07	2.62	-0.09	0.46	3.62	3	-0.2	-0.47	4.48	4.43	10.46
Cthe_01433	short-chain dehydrogenase/reductase SD	14.58	14.67	12.51	12.05	2.07	2.62	-0.09	0.46	3.62	3	-0.2	-0.47	4.48	4.43	10.46
Cthe_01433	short-chain dehydrogenase/reductase SD	14.58	14.67	12.51	12.05	2.07	2.62	-0.09	0.46	3.62	3	-0.2	-0.47	4.48	4.43	10.46
Cthe_01433	short-chain dehydrogenase/reductase SD	14.58	14.67	12.51	12.05	2.07	2.62	-0.09	0.46	3.62	3	-0.2	-0.47	4.48	4.43	10.46
Cthe_01433	short-chain dehydrogenase/reductase SD	14.58	14.67	12.51	12.05	2.07	2.62	-0.09	0.46	3.62	3	-0.2	-0.47	4.48	4.43	10.46
Cthe_02883	histidinol-phosphate aminotransferase	9.6	10.19	7.83	6.73	1.77	3.46	-0.59	1.1	3.22	4	-1.87	0.89	4.22	4.17	2.82
Cthe_02883	histidinol-phosphate aminotransferase	9.6	10.19	7.83	6.73	1.77	3.46	-0.59	1.1	3.22	4	-1.87	0.89	4.22	4.17	2.82
Cthe_02883	histidinol-phosphate aminotransferase	9.6	10.19	7.83	6.73	1.77	3.46	-0.59	1.1	3.22	4	-1.87	0.89	4.22	4.17	2.82
Cthe_02883	histidinol-phosphate aminotransferase	9.6	10.19	7.83	6.73	1.77	3.46	-0.59	1.1	3.22	4	-1.87	0.89	4.22	4.17	2.82
Cthe_02883	histidinol-phosphate aminotransferase	9.6	10.19	7.83	6.73	1.77	3.46	-0.59	1.1	3.22	4	-1.87	0.89	4.22	4.17	2.82
Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
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Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
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Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
Cthe_02797	thiamine pyrophosphate enzyme-like TPP	7.86	7.64	5.86	5.09	2	2.55	0.22	0.77	3.53	2.92	0.83	0.19	4.21	4.16	6.11
Cthe_02797																







[illegible]



[illegible]



Cthe_00856	branched-chain amino acid aminotransfer	14.35	14.29	13.79	12.91	0.56	1.38	0.06	0.88	1.58	1.52	0.3	0.43	1.96	1.93	4.75
Cthe_00856	branched-chain amino acid aminotransfer	14.35	14.29	13.79	12.91	0.56	1.38	0.06	0.88	1.58	1.52	0.3	0.43	1.96	1.93	4.75
Cthe_00856	branched-chain amino acid aminotransfer	14.35	14.29	13.79	12.91	0.56	1.38	0.06	0.88	1.58	1.52	0.3	0.43	1.96	1.93	4.75
Cthe_00856	branched-chain amino acid aminotransfer	14.35	14.29	13.79	12.91	0.56	1.38	0.06	0.88	1.58	1.52	0.3	0.43	1.96	1.93	4.75
Cthe_01563	ABC transporter related protein	10.27	10.58	9.92	8.2	0.35	2.38	-0.31	1.72	1.3	2.71	-0.93	2.21	1.95	1.92	1.42
Cthe_01563	ABC transporter related protein	10.27	10.58	9.92	8.2	0.35	2.38	-0.31	1.72	1.3	2.71	-0.93	2.21	1.95	1.92	1.42
Cthe_01948	cytochrome c biogenesis protein, transme	10.43	10.29	9.77	9.07	0.66	2.22	0.14	0.7	1.72	1.33	0.57	0.04	1.92	1.89	4.32
Cthe_02256	replicative DNA helicase	13.69	13.76	13.24	12.25	0.45	1.51	-0.07	0.99	1.43	1.68	-0.13	0.66	1.91	1.88	3.73
Cthe_02256	replicative DNA helicase	13.69	13.76	13.24	12.25	0.45	1.51	-0.07	0.99	1.43	1.68	-0.13	0.66	1.91	1.88	3.73
Cthe_00891	response regulator receiver protein	10.66	10.85	10.22	9.33	0.44	1.52	-0.19	0.89	1.42	1.69	-0.53	0.45	1.9	1.87	3.61
Cthe_00328	peptide chain release factor 3	13.16	13.32	12.58	12.04	0.58	1.28	-0.16	0.54	1.61	1.4	-0.43	-0.3	1.9	1.87	4.62
Cthe_02573	ABC transporter related protein	4.39	4.09	3.7	2	0.69	2.09	0.3	1.7	1.76	2.37	1.1	2.17	1.88	1.85	1.38
Cthe_02573	ABC transporter related protein	4.39	4.09	3.7	2	0.69	2.09	0.3	1.7	1.76	2.37	1.1	2.17	1.88	1.85	1.38
Cthe_01464	Endoribonuclease L-PSP	7.21	6.97	6.44	5.78	0.77	1.19	0.24	0.66	1.86	1.3	0.9	-0.04	1.87	1.84	2.86
Cthe_00505	formate acetyltransferase	14.32	14.28	13.75	13.16	0.57	1.12	0.04	0.59	1.59	1.21	0.23	-0.19	1.87	1.84	7.61
Cthe_00505	formate acetyltransferase	14.32	14.28	13.75	13.16	0.57	1.12	0.04	0.59	1.59	1.21	0.23	-0.19	1.87	1.84	7.61
Cthe_00505	formate acetyltransferase	14.32	14.28	13.75	13.16	0.57	1.12	0.04	0.59	1.59	1.21	0.23	-0.19	1.87	1.84	7.61
Cthe_00505	formate acetyltransferase	14.32	14.28	13.75	13.16	0.57	1.12	0.04	0.59	1.59	1.21	0.23	-0.19	1.87	1.84	7.61
Cthe_00505	formate acetyltransferase	14.32	14.28	13.75	13.16	0.57	1.12	0.04	0.59	1.59	1.21	0.23	-0.19	1.87	1.84	7.61
Cthe_00505	formate acetyltransferase	14.32	14.28	13.75	13.16	0.57	1.12	0.04	0.59	1.59	1.21	0.23	-0.19	1.87	1.84	7.61
Cthe_00505	formate acetyltransferase	14.32	14.28	13.75	13.16	0.57	1.12	0.04	0.59	1.59	1.21	0.23	-0.19	1.87	1.84	7.61
Cthe_02889	phosphoribosyl-AMP cyclohydrolase	8.25	8.49	7.86	6.78	0.39	1.71	-0.24	1.08	1.35	1.92	-0.7	0.85	1.86	1.83	2.42
Cthe_02434	electron transport complex, RnfABCDGE t	10.84	10.98	10.35	9.72	0.49	1.26	-0.14	0.63	1.49	1.38	-0.37	-0.11	1.86	1.83	5.98
Cthe_02889	phosphoribosyl-AMP cyclohydrolase	8.25	8.49	7.86	6.78	0.39	1.71	-0.24	1.08	1.35	1.92	-0.7	0.85	1.86	1.83	2.42
Cthe_02889	phosphoribosyl-AMP cyclohydrolase	8.25	8.49	7.86	6.78	0.39	1.71	-0.24	1.08	1.35	1.92	-0.7	0.85	1.86	1.83	2.42
Cthe_02889	phosphoribosyl-AMP cyclohydrolase	8.25	8.49	7.86	6.78	0.39	1.71	-0.24	1.08	1.35	1.92	-0.7	0.85	1.86	1.83	2.42
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00235	Glutaredoxin-like protein, YruB-family	10.69	10.73	10.11	9.61	0.58	1.12	-0.04	0.5	1.61	1.21	-0.03	-0.38	1.85	1.82	6
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_00053	ribonucleoside-diphosphate reductase,	14.09	14.06	13.62	12.79	0.47	1.27	0.03	0.83	1.46	1.39	0.2	0.32	1.85	1.82	6.07
Cthe_01848	copper-translocating P-type ATPase	10.88	10.95	10.49	9.34	0.39	1.61	-0.07	1.15	1.35	1.8	-0.13	1	1.81	1.78	2.54
Cthe_03008	Superoxide dismutase	5	4.46	4.09	2.58	0.91	1.88	0.54	1.51	2.05	2.12	1.9	1.77	1.81	1.78	1.29
Cthe_03008	Superoxide dismutase	5	4.46	4.09	2.58	0.91	1.88	0.54	1.51	2.05	2.12	1.9	1.77	1.81	1.78	1.29
Cthe_01848	copper-translocating P-type ATPase	10.88	10.95	10.49	9.34	0.39	1.61	-0.07	1.15	1.35	1.8	-0.13	1	1.81	1.78	2.54
Cthe_01848	copper-translocating P-type ATPase	10.88	10.95	10.49	9.34	0.39	1.61	-0.07	1.15	1.35	1.8	-0.13	1	1.81	1.78	2.54
Cthe_03008	Superoxide dismutase	5	4.46	4.09	2.58	0.91	1.88	0.54	1.51	2.05	2.12	1.9	1.77	1.81	1.78	1.29
Cthe_00567	peptide deformylase	10.13	10.09	9.68	8.67	0.45	1.42	0.04	1.01	1.43	1.57	0.23	0.7	1.8	1.77	3.28
Cthe_02878	peptidase C39, bacteriocin processing	10.41	10.58	9.97	9.29	0.44	1.29	-0.17	0.68	1.42	1.42	-0.47	0	1.8	1.77	4.86
Cthe_00567	peptide deformylase	10.13	10.09	9.68	8.67	0.45	1.42	0.04	1.01	1.43	1.57	0.23	0.7	1.8	1.77	3.28
Cthe_01472	Carbohydrate binding family 11	10.89	10.79	10.27	9.72	0.62	1.07	0.1	0.55	1.66	1.15	0.43	-0.28	1.79	1.76	4.47
Cthe_02448	inner-membrane translocator	6.67	6.81	6.27	5.52	0.4	1.29	-0.14	0.75	1.36	1.42	-0.37	0.15	1.79	1.76	5.6
Cthe_01184	hypothetical protein	10.55	10.65	10.14	9.47	0.41	1.18	-0.1	0.67	1.38	1.29	-0.23	-0.02	1.79	1.76	9.3
Cthe_02448	inner-membrane translocator	6.67	6.81	6.27	5.52	0.4	1.29	-0.14	0.75	1.36	1.42	-0.37	0.15	1.79	1.76	5.6
Cthe_01472	Carbohydrate binding family 11	10.89	10.79	10.27	9.72	0.62	1.07	0.1	0.55	1.66	1.15	0.43	-0.28	1.79	1.76	4.47
Cthe_01472	Carbohydrate binding family 11	10.89	10.79	10.27	9.72	0.62	1.07	0.1	0.55	1.66	1.15	0.43	-0.28	1.79	1.76	4.47
Cthe_00454	hypothetical protein	4.46	4.39	3.91	3.32	0.55	1.07	0.07	0.59	1.57	1.15	0.33	-0.19	1.78	1.75	5.81
Cthe_00341	NADH dehydrogenase (quinone)	14.36	14.56	14.01	13.04	0.35	1.52	-0.2	0.97	1.3	1.69	-0.57	0.62	1.76	1.73	2.88
Cthe_00341	NADH dehydrogenase (quinone)	14.36	14.56	14.01	13.04	0.35	1.52	-0.2	0.97	1.3	1.69	-0.57	0.62	1.76	1.73	2.88
Cthe_00341	NADH dehydrogenase (quinone)	14.36	14.56	14.01	13.04	0.35	1.52	-0.2	0.97	1.3	1.69	-0.57	0.62	1.76	1.73	2.88
Cthe_00341	NADH dehydrogenase (quinone)	14.36	14.56	14.01	13.04	0.35	1.52	-0.2	0.97	1.3	1.69	-0.57	0.62	1.76	1.73	2.88
Cthe_00341	NADH dehydrogenase (quinone)	14.36	14.56	14.01	13.04	0.35	1.52	-0.2	0.97	1.3	1.69	-0.57	0.62	1.76	1.73	2.88
Cthe_00341	NADH dehydrogenase (quinone)	14.36	14.56	14.01	13.04	0.35	1.52	-0.2	0.97	1.3	1.69	-0.57	0.62	1.76	1.73	2.88
Cthe_00341	NADH dehydrogenase (quinone)	14.36	14.56	14.01	13.04	0.35	1.52	-0.2	0.97	1.3	1.69	-0.57	0.62	1.76	1.73	2.88
Cthe_01187	protein of unknown function DUF990	10.93	11.15	10.24	9.94	0.69	1.21	-0.22	0.3	1.76	1.32	-0.63	-0.81	1.75	1.72	2.44
Cthe_01094	Radical SAM-like protein	11.75	11.96	11.43	10.29	0.32	1.67	-0.21	1.14	1.26	1.87	-0.6	0.98	1.75	1.72	2.23
Cthe_00655	cysteine desulfurase family protein	13.52	13.05	12.64	11.7	0.88	1.35	0.47	0.94	2.01	1.49	1.67	0.55	1.73	1.7	1.62
Cthe_01458	extracellular solute-binding protein, famil	10.19	10.15	9.78	8.89	0.41	1.26	0.04	0.89	1.38	1.38	0.23	0.45	1.73	1.7	4.39
Cthe_01458	extracellular solute-binding protein, famil	10.19	10.15	9.78	8.89	0.41	1.26	0.04	0.89	1.38	1.38	0.23	0.45	1.73	1.7	4.39
Cthe_01995	hypothetical protein	1	2			1	2	-1		2.18	2.26	-3.23		1.72	1.69	1.1
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32	1.51	-0.14	1.05	1.26	1.68	-0.37	0.79	1.72	1.69	2.74
Cthe_00064	Na/PI-cotransporter II-related protein	15.29	15.3	14.46	14.31	0.83	0.99	-0.01	0.15	1.95	1.06	0.07	-1.13	1.72	1.69	2.23
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32	1.51	-0.14	1.05	1.26	1.68	-0.37	0.79	1.72	1.69	2.74
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32	1.51	-0.14	1.05	1.26	1.68	-0.37	0.79	1.72	1.69	2.74
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32	1.51	-0.14	1.05	1.26	1.68	-0.37	0.79	1.72	1.69	2.74
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32	1.51	-0.14	1.05	1.26	1.68	-0.37	0.79	1.72	1.69	2.74
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32	1.51	-0.14	1.05	1.26	1.68	-0.37	0.79	1.72	1.69	2.74
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32	1.51	-0.14	1.05	1.26	1.68	-0.37	0.79	1.72	1.69	2.74
Cthe_02393	thiamine pyrophosphate enzyme-like TPP	14.56	14.7	14.24	13.19	0.32										



Cthe_02269	V-type ATPase, D subunit	9.91	9.68	9.04	8.77	0.87	0.91	0.23	0.27	2	0.96	0.87	-0.87	1.68	1.65	2.05
Cthe_02082	hypothetical protein	1.58	0	1.58	0	0	0	1.58	1.58	0.82	-0.12	5.37	1.91	1.68	1.65	0.17
Cthe_02269	V-type ATPase, D subunit	9.91	9.68	9.04	8.77	0.87	0.91	0.23	0.27	2	0.96	0.87	-0.87	1.68	1.65	2.05
Cthe_02269	V-type ATPase, D subunit	9.91	9.68	9.04	8.77	0.87	0.91	0.23	0.27	2	0.96	0.87	-0.87	1.68	1.65	2.05
Cthe_02269	V-type ATPase, D subunit	9.91	9.68	9.04	8.77	0.87	0.91	0.23	0.27	2	0.96	0.87	-0.87	1.68	1.65	2.05
Cthe_01562	protein of unknown function DUF214	12.14	12.39	11.94	10.22	0.2	2.17	-0.25	1.72	1.09	2.46	-0.73	2.21	1.67	1.64	1.31
Cthe_01561	hypothetical protein	10.37	10.68	10.17	8.61	0.2	2.07	-0.31	1.56	1.09	2.35	-0.93	1.87	1.67	1.64	1.41
Cthe_01562	protein of unknown function DUF214	12.14	12.39	11.94	10.22	0.2	2.17	-0.25	1.72	1.09	2.46	-0.73	2.21	1.67	1.64	1.31
Cthe_00143	Phosphopyruvate hydratase	14.58	14.73	14.31	13.08	0.27	1.65	-0.15	1.23	1.19	1.85	-0.4	1.17	1.66	1.63	2.02
Cthe_00600	thiamine biosynthesis protein ThiF	9.51	9.42	9.1	8.08	0.41	1.34	0.09	1.02	1.38	1.48	0.4	0.72	1.66	1.63	2.79
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_00143	Phosphopyruvate hydratase	14.58	14.73	14.31	13.08	0.27	1.65	-0.15	1.23	1.19	1.85	-0.4	1.17	1.66	1.63	2.02
Cthe_00143	Phosphopyruvate hydratase	14.58	14.73	14.31	13.08	0.27	1.65	-0.15	1.23	1.19	1.85	-0.4	1.17	1.66	1.63	2.02
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_00600	thiamine biosynthesis protein ThiF	9.51	9.42	9.1	8.08	0.41	1.34	0.09	1.02	1.38	1.48	0.4	0.72	1.66	1.63	2.79
Cthe_00143	Phosphopyruvate hydratase	14.58	14.73	14.31	13.08	0.27	1.65	-0.15	1.23	1.19	1.85	-0.4	1.17	1.66	1.63	2.02
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_00143	Phosphopyruvate hydratase	14.58	14.73	14.31	13.08	0.27	1.65	-0.15	1.23	1.19	1.85	-0.4	1.17	1.66	1.63	2.02
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_00600	thiamine biosynthesis protein ThiF	9.51	9.42	9.1	8.08	0.41	1.34	0.09	1.02	1.38	1.48	0.4	0.72	1.66	1.63	2.79
Cthe_00143	Phosphopyruvate hydratase	14.58	14.73	14.31	13.08	0.27	1.65	-0.15	1.23	1.19	1.85	-0.4	1.17	1.66	1.63	2.02
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35	-0.08	0.96	1.24	1.49	-0.17	0.6	1.66	1.63	3.53
Cthe_02392	pyruvate flavodoxin/ferredoxin	14.19	14.27	13.88	12.92	0.31	1.35									







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Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_01028	acetate kinase	11.58	11.64	11.52	10.84	0.06	0.8	-0.06	0.68	0.91	0.83	-0.1	0	1.19	1.17	14
Cthe_02186	single-strand binding protein	14.02	14.05	13.86	13.3	0.16	0.75	-0.03	0.56	1.04	0.77	0	-0.26	1.18	1.16	5.66
Cthe_00420	dipicolinate synthase	7.97	7.91	7.55	7.24	0.42	0.67	0.06	0.31	1.39	0.68	0.3	-0.79	1.18	1.16	2.08
Cthe_02885	phosphoribosylaminoimidazole-succinoc	11.79	12.08	11.49	11.07	0.3	1.01	-0.29	0.42	1.23	1.08	-0.87	-0.55	1.18	1.16	1.81
Cthe_02885	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02885	phosphoribosylaminoimidazole-succinoc	11.79	12.08	11.49	11.07	0.3	1.01	-0.29	0.42	1.23	1.08	-0.87	-0.55	1.18	1.16	1.81
Cthe_02885	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02885	phosphoribosylaminoimidazole-succinoc	11.79	12.08	11.49	11.07	0.3	1.01	-0.29	0.42	1.23	1.08	-0.87	-0.55	1.18	1.16	1.81
Cthe_02885	phosphoribosylaminoimidazole-succinoc	11.79	12.08	11.49	11.07	0.3	1.01	-0.29	0.42	1.23	1.08	-0.87	-0.55	1.18	1.16	1.81
Cthe_02885	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18	1.16	8.68
Cthe_02390	pyruvate/ketoisovalerate oxidoreductase,	12.93	12.93	12.86	12.12	0.07	0.81	0	0.74	0.92	0.85	0.1	0.13	1.18		



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Cthe_00699	carboxyl transferase	14.6	14.77	14.57	13.94	0.03	0.83	-0.17	0.63	0.86	0.87	-0.47	-0.11	1.01	0.99	2.88
Cthe_02603	ATP synthase F0, C subunit	9.62	9.5	9.32	8.92	0.3	0.58	0.12	0.4	1.23	0.57	0.5	-0.6	1.01	0.99	1.97
Cthe_00699	carboxyl transferase	14.6	14.77	14.57	13.94	0.03	0.83	-0.17	0.63	0.86	0.87	-0.47	-0.11	1.01	0.99	2.88
Cthe_00622	methylthioadenosine phosphorylase	12.04	12.09	11.8	11.45	0.24	0.64	-0.05	0.35	1.15	0.64	-0.07	-0.7	1.01	0.99	2.13
Cthe_00699	carboxyl transferase	14.6	14.77	14.57	13.94	0.03	0.83	-0.17	0.63	0.86	0.87	-0.47	-0.11	1.01	0.99	2.88
Cthe_00699	carboxyl transferase	14.6	14.77	14.57	13.94	0.03	0.83	-0.17	0.63	0.86	0.87	-0.47	-0.11	1.01	0.99	2.88
Cthe_00699	carboxyl transferase	14.6	14.77	14.57	13.94	0.03	0.83	-0.17	0.63	0.86	0.87	-0.47	-0.11	1.01	0.99	2.88
Cthe_02603	ATP synthase F0, C subunit	9.62	9.5	9.32	8.92	0.3	0.58	0.12	0.4	1.23	0.57	0.5	-0.6	1.01	0.99	1.97
Cthe_00284	protein of unknown function DUF815	10.58	10.66	10.64	9.85	-0.06	0.81	-0.08	0.79	0.74	0.85	-0.17	0.23	1	0.98	4.48
Cthe_01838	glycoside hydrolase, family 10	14.17	14.31	14.18	13.51	-0.01	0.8	-0.14	0.67	0.81	0.83	-0.37	-0.02	1	0.98	3.56
Cthe_00373	oxidoreductase FAD/NAD(P)-binding	10.72	10.85	10.71	10.09	0.01	0.76	-0.13	0.62	0.84	0.79	-0.33	-0.13	1	0.98	3.69
Cthe_01004	uridylyate kinase	9.39	9.38	9.41	8.44	-0.02	0.94	0.01	0.97	0.8	1	0.13	0.62	1	0.98	2.3
Cthe_00373	oxidoreductase FAD/NAD(P)-binding	10.72	10.85	10.71	10.09	0.01	0.76	-0.13	0.62	0.84	0.79	-0.33	-0.13	1	0.98	3.69
Cthe_01452	KWG repeat containing protein	11.45	11.66	11.44	10.76	0.01	0.9	-0.21	0.68	0.84	0.95	-0.6	0	1	0.98	2.4
Cthe_01386	hypothetical protein	11.06	11.17	10.97	10.46	0.09	0.71	-0.11	0.51	0.95	0.73	-0.27	-0.36	1	0.98	3.03
Cthe_01912	copper amine oxidase-like protein	15.14	15.12	15.13	14.46	0.01	0.66	0.02	0.67	0.84	0.67	0.17	-0.02	1	0.98	7.13
Cthe_01838	glycoside hydrolase, family 10	14.17	14.31	14.18	13.51	-0.01	0.8	-0.14	0.67	0.81	0.83	-0.37	-0.02	1	0.98	3.56
Cthe_01004	uridylyate kinase	9.39	9.38	9.41	8.44	-0.02	0.94	0.01	0.97	0.8	1	0.13	0.62	1	0.98	2.3
Cthe_00373	oxidoreductase FAD/NAD(P)-binding	10.72	10.85	10.71	10.09	0.01	0.76	-0.13	0.62	0.84	0.79	-0.33	-0.13	1	0.98	3.69
Cthe_00373	oxidoreductase FAD/NAD(P)-binding	10.72	10.85	10.71	10.09	0.01	0.76	-0.13	0.62	0.84	0.79	-0.33	-0.13	1	0.98	3.69
Cthe_01004	uridylyate kinase	9.39	9.38	9.41	8.44	-0.02	0.94	0.01	0.97	0.8	1	0.13	0.62	1	0.98	2.3
Cthe_01004	uridylyate kinase	9.39	9.38	9.41	8.44	-0.02	0.94	0.01	0.97	0.8	1	0.13	0.62	1	0.98	2.3
Cthe_00609	peptidase M42	8.14	8.17	7.94	7.54	0.2	0.63	-0.03	0.4	1.09	0.63	0	-0.6	0.99	0.97	2.38
Cthe_02626	UDP-N-acetylmuramate--alanine ligase	11.57	11.94	11.81	10.25	-0.24	1.69	-0.37	1.56	0.5	1.89	-1.13	1.87	0.99	0.97	1.02
Cthe_03006	ErkK/YbiS/YcfS/YnhG	2.58	2	2	1	0.58	1	0.58	1	1.61	1.07	2.03	0.68	0.99	0.97	1.03
Cthe_00730	hypothetical protein	10.66	10.78	10.68	10.02	-0.02	0.76	-0.12	0.66	0.8	0.79	-0.3	-0.04	0.99	0.97	4.22
Cthe_02626	UDP-N-acetylmuramate--alanine ligase	11.57	11.94	11.81	10.25	-0.24	1.69	-0.37	1.56	0.5	1.89	-1.13	1.87	0.99	0.97	1.02
Cthe_00609	peptidase M42	8.14	8.17	7.94	7.54	0.2	0.63	-0.03	0.4	1.09	0.63	0	-0.6	0.99	0.97	2.38
Cthe_02626	UDP-N-acetylmuramate--alanine ligase	11.57	11.94	11.81	10.25	-0.24	1.69	-0.37	1.56	0.5	1.89	-1.13	1.87	0.99	0.97	1.02
Cthe_00609	peptidase M42	8.14	8.17	7.94	7.54	0.2	0.63	-0.03	0.4	1.09	0.63	0	-0.6	0.99	0.97	2.38
Cthe_02626	UDP-N-acetylmuramate--alanine ligase	11.57	11.94	11.81	10.25	-0.24	1.69	-0.37	1.56	0.5	1.89	-1.13	1.87	0.99	0.97	1.02
Cthe_02626	UDP-N-acetylmuramate--alanine ligase	11.57	11.94	11.81	10.25	-0.24	1.69	-0.37	1.56	0.5	1.89	-1.13	1.87	0.99	0.97	1.02
Cthe_00609	peptidase M42	8.14	8.17	7.94	7.54	0.2	0.63	-0.03	0.4	1.09	0.63	0	-0.6	0.99	0.97	2.38
Cthe_02626	UDP-N-acetylmuramate--alanine ligase	11.57	11.94	11.81	10.25	-0.24	1.69	-0.37	1.56	0.5	1.89	-1.13	1.87	0.99	0.97	1.02
Cthe_02626	UDP-N-acetylmuramate--alanine ligase	11.57	11.94	11.81	10.25	-0.24	1.69	-0.37	1.56	0.5	1.89	-1.13	1.87	0.99	0.97	1.02
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_00719	transcriptional regulator, BadM/Rrf2 fami	9.57	9.48	9.47	8.83	0.1	0.65	0.09	0.64	0.96	0.65	0.4	-0.09	0.98	0.96	3.21
Cthe_02212	transcriptional regulator, AraC family	10.03	10.03	9.91	9.42	0.12	0.61	0	0.49	0.99	0.61	0.1	-0.4	0.98	0.96	3.2
Cthe_00644	Vitamin B12 dependent methionine synth	9.67	9.67	9.43	9.08	0.24	0.59	0	0.35	1.15	0.58	0.1	-0.7	0.98	0.96	2.07
Cthe_01852	Hsp33 protein	10.64	10.79	10.66	9.99	-0.02	0.8	-0.15	0.67	0.8	0.83	-0.4	-0.02	0.98	0.96	3.27
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.34	0.98	0.96	2.62
Cthe_02704	Transketolase-like protein	13.49	13.4	13.32	12.8	0.17	0.6	0.09	0.52	1.05	0.6	0.4	-0.			



Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.07	8.85	8.91	7.93	0.16	0.92	0.22	0.98	1.04	0.98	0.83	0.64	0.97	0.95	1.55
Cthe_00112	UDP-N-acetylenolpyruvoylglucosamine re	9.63	9.69	9.7	8.97	-0.07	0.72	-0.06	0.73	0.73	0.74	-0.1	0.11	0.97	0.95	7.95
Cthe_02625	beta-hydroxyacyl-(acyl-carrier-protein)	9.07	8.85	8.91	7.93	0.16	0.92	0.22	0.98	1.04	0.98	0.83	0.64	0.97	0.95	1.55
Cthe_00422	CoA-binding protein	14.46	14.43	14.42	13.82	0.04	0.61	0.03	0.6	0.88	0.61	0.2	-0.17	0.96	0.94	4.64
Cthe_02876	ATP-dependent DNA helicase PcrA	12.13	12.23	12.17	11.52	-0.04	0.71	-0.1	0.65	0.77	0.73	-0.23	-0.06	0.96	0.94	5.07
Cthe_02875	sigma 54 modulation protein/ribosomal p	14.3	14.19	14.25	13.38	0.05	0.81	0.11	0.87	0.89	0.85	0.47	0.4	0.96	0.94	2.27
Cthe_02876	ATP-dependent DNA helicase PcrA	12.13	12.23	12.17	11.52	-0.04	0.71	-0.1	0.65	0.77	0.73	-0.23	-0.06	0.96	0.94	5.07
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00975	stage V sporulation protein E	10.26	10.51	10.43	9.21	-0.17	1.3	-0.25	1.22	0.59	1.43	-0.73	1.15	0.95	0.93	1.29
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_00099	5,10-methylenetetrahydrofolate reductas	10.67	10.88	10.83	9.62	-0.16	1.26	-0.21	1.21	0.61	1.38	-0.6	1.13	0.95	0.93	1.34
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36	-2.67	1.89	0.95	0.93	0.83
Cthe_01869	ornithine carbamoyltransferase	11.93	12.76	12.25	10.68	-0.32	2.08	-0.83	1.57	0.39	2.36					



Cthe_01766	glutamate 5-kinase	11.63	11.57	11.54	10.99	0.09	0.58	0.06	0.55	0.95	0.57	0.3	-0.28	0.93	0.91	3.07
Cthe_00206	UvrD/REP helicase	10.57	10.77	10.71	9.66	-0.14	1.11	-0.2	1.05	0.64	1.2	-0.57	0.79	0.93	0.91	1.59
Cthe_00810	CheA signal transduction histidine kinases	7.68	7.81	7.85	6.41	-0.17	1.4	-0.13	1.44	0.59	1.55	-0.33	1.62	0.93	0.91	1.14
Cthe_00810	CheA signal transduction histidine kinases	7.68	7.81	7.85	6.41	-0.17	1.4	-0.13	1.44	0.59	1.55	-0.33	1.62	0.93	0.91	1.14
Cthe_01543	aspartyl-tRNA synthetase	10.76	11.21	10.73	10.03	0.03	1.18	-0.45	0.7	0.86	1.29	-1.4	0.04	0.93	0.91	1.26
Cthe_00445	cell division protein FtsZ	11.64	11.57	11.63	10.9	0.01	0.67	0.07	0.73	0.84	0.68	0.33	0.11	0.93	0.91	3.53
Cthe_01766	glutamate 5-kinase	11.63	11.57	11.54	10.99	0.09	0.58	0.06	0.55	0.95	0.57	0.3	-0.28	0.93	0.91	3.07
Cthe_01543	aspartyl-tRNA synthetase	10.76	11.21	10.73	10.03	0.03	1.18	-0.45	0.7	0.86	1.29	-1.4	0.04	0.93	0.91	1.26
Cthe_01543	aspartyl-tRNA synthetase	10.76	11.21	10.73	10.03	0.03	1.18	-0.45	0.7	0.86	1.29	-1.4	0.04	0.93	0.91	1.26
Cthe_01862	ABC transporter related protein	14.65	15	14.82	13.67	-0.17	1.33	-0.35	1.15	0.59	1.46	-1.07	1	0.93	0.91	1.22
Cthe_01862	ABC transporter related protein	14.65	15	14.82	13.67	-0.17	1.33	-0.35	1.15	0.59	1.46	-1.07	1	0.93	0.91	1.22
Cthe_01543	aspartyl-tRNA synthetase	10.76	11.21	10.73	10.03	0.03	1.18	-0.45	0.7	0.86	1.29	-1.4	0.04	0.93	0.91	1.26
Cthe_01766	glutamate 5-kinase	11.63	11.57	11.54	10.99	0.09	0.58	0.06	0.55	0.95	0.57	0.3	-0.28	0.93	0.91	3.07
Cthe_00206	UvrD/REP helicase	10.57	10.77	10.71	9.66	-0.14	1.11	-0.2	1.05	0.64	1.2	-0.57	0.79	0.93	0.91	1.59
Cthe_00810	CheA signal transduction histidine kinases	7.68	7.81	7.85	6.41	-0.17	1.4	-0.13	1.44	0.59	1.55	-0.33	1.62	0.93	0.91	1.14
Cthe_01766	glutamate 5-kinase	11.63	11.57	11.54	10.99	0.09	0.58	0.06	0.55	0.95	0.57	0.3	-0.28	0.93	0.91	3.07
Cthe_01766	glutamate 5-kinase	11.63	11.57	11.54	10.99	0.09	0.58	0.06	0.55	0.95	0.57	0.3	-0.28	0.93	0.91	3.07
Cthe_01543	aspartyl-tRNA synthetase	10.76	11.21	10.73	10.03	0.03	1.18	-0.45	0.7	0.86	1.29	-1.4	0.04	0.93	0.91	1.26
Cthe_01385	preprotein translocase, SecA subunit	12.74	12.89	12.74	12.15	0	0.74	-0.15	0.59	0.82	0.76	-0.4	-0.19	0.92	0.9	2.87
Cthe_01211	pyridoxal-phosphate dependent TrpB-like	15.24	15.23	15.06	14.67	0.18	0.56	0.01	0.39	1.07	0.55	0.13	-0.62	0.92	0.9	2.16
Cthe_00731	Shikimate kinase	9.93	10.02	9.97	9.35	-0.04	0.67	-0.09	0.62	0.77	0.68	-0.2	-0.13	0.92	0.9	4.89
Cthe_00309	excinuclease ABC, B subunit	12.32	12.48	12.32	11.73	0	0.75	-0.16	0.59	0.82	0.77	-0.43	-0.19	0.92	0.9	2.72
Cthe_00334	putative anti-sigma regulatory factor,	8.76	8.91	8.85	8.09	-0.09	0.82	-0.15	0.76	0.7	0.86	-0.4	0.17	0.92	0.9	2.9
Cthe_02116	binding-protein-dependent transport syst	9.07	8.99	8.69	8.51	0.38	0.48	0.08	0.18	1.34	0.45	0.37	-1.06	0.92	0.9	1.43
Cthe_00731	Shikimate kinase	9.93	10.02	9.97	9.35	-0.04	0.67	-0.09	0.62	0.77	0.68	-0.2	-0.13	0.92	0.9	4.89
Cthe_02116	binding-protein-dependent transport syst	9.07	8.99	8.69	8.51	0.38	0.48	0.08	0.18	1.34	0.45	0.37	-1.06	0.92	0.9	1.43
Cthe_01385	preprotein translocase, SecA subunit	12.74	12.89	12.74	12.15	0	0.74	-0.15	0.59	0.82	0.76	-0.4	-0.19	0.92	0.9	2.87
Cthe_01211	pyridoxal-phosphate dependent TrpB-like	15.24	15.23	15.06	14.67	0.18	0.56	0.01	0.39	1.07	0.55	0.13	-0.62	0.92	0.9	2.16
Cthe_00731	Shikimate kinase	9.93	10.02	9.97	9.35	-0.04	0.67	-0.09	0.62	0.77	0.68	-0.2	-0.13	0.92	0.9	4.89
Cthe_01211	pyridoxal-phosphate dependent TrpB-like	15.24	15.23	15.06	14.67	0.18	0.56	0.01	0.39	1.07	0.55	0.13	-0.62	0.92	0.9	2.16
Cthe_00731	Shikimate kinase	9.93	10.02	9.97	9.35	-0.04	0.67	-0.09	0.62	0.77	0.68	-0.2	-0.13	0.92	0.9	4.89
Cthe_00731	Shikimate kinase	9.93	10.02	9.97	9.35	-0.04	0.67	-0.09	0.62	0.77	0.68	-0.2	-0.13	0.92	0.9	4.89
Cthe_01842	O-acetylhomoserine/O-acetylserine sulphy	10.26	10.47	10.07	9.73	0.19	0.74	-0.21	0.34	1.08	0.76	-0.6	-0.72	0.91	0.89	1.6
Cthe_02628	SpoVG	14.64	14.89	14.8	13.74	-0.16	1.15	-0.25	1.06	0.61	1.25	-0.73	0.81	0.91	0.89	1.45
Cthe_01842	O-acetylhomoserine/O-acetylserine sulphy	10.26	10.47	10.07	9.73	0.19	0.74	-0.21	0.34	1.08	0.76	-0.6	-0.72	0.91	0.89	1.6
Cthe_01842	O-acetylhomoserine/O-acetylserine sulphy	10.26	10.47	10.07	9.73	0.19	0.74	-0.21	0.34	1.08	0.76	-0.6	-0.72	0.91	0.89	1.6
Cthe_01811	transcriptional repressor, CopY family	4.75	3.7	4.91	3.91	-0.16	-0.21	1.05	1	0.61	-0.37	3.6	0.68	0.9	0.88	0.22
Cthe_02066	serine O-acetyltransferase	10.51	10.53	10.46	9.95	0.05	0.58	-0.02	0.51	0.89	0.57	0.03	-0.36	0.9	0.88	3.32
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_00110	HPr kinase	8.89	8.92	8.44	8.41	0.45	0.51	-0.03	0.03	1.43	0.49	0	-1.38	0.9	0.88	1.24
Cthe_02103	4Fe-4S ferredoxin, iron-sulfur binding	14.83	14.7	14.67	14.14	0.16	0.56	0.13	0.53	1.04	0.55	0.53	-0.32	0.9	0.88	2.16
Cthe_00057	hypothetical protein	6.95	6.93	7.09	5.25	-0.14	1.68	0.02	1.84	0.64	1.88	0.17	2.47	0.9	0.88	0.91
Cthe_00018	hypothetical protein	9.39	9.35	9.3	8.8	0.09	0.55	0.04	0.5	0.95	0.54	0.23	-0.38	0.9	0.88	2.8
Cthe_00066	hypothetical protein	9.2	9.17	9.26	8.32	-0.06	0.85	0.03	0.94	0.74	0.89	0.2	0.55	0.9	0.88	2.25
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_02066	serine O-acetyltransferase	10.51	10.53	10.46	9.95	0.05	0.58	-0.02	0.51	0.89	0.57	0.03	-0.36	0.9	0.88	3.32
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_02066	serine O-acetyltransferase	10.51	10.53	10.46	9.95	0.05	0.58	-0.02	0.51	0.89	0.57	0.03	-0.36	0.9	0.88	3.32
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_00110	HPr kinase	8.89	8.92	8.44	8.41	0.45	0.51	-0.03	0.03	1.43	0.49	0	-1.38	0.9	0.88	1.24
Cthe_00110	HPr kinase	8.89	8.92	8.44	8.41	0.45	0.51	-0.03	0.03	1.43	0.49	0	-1.38	0.9	0.88	1.24
Cthe_00110	HPr kinase	8.89	8.92	8.44	8.41	0.45	0.51	-0.03	0.03	1.43	0.49	0	-1.38	0.9	0.88	1.24
Cthe_00110	HPr kinase	8.89	8.92	8.44	8.41	0.45	0.51	-0.03	0.03	1.43	0.49	0	-1.38	0.9	0.88	1.24
Cthe_00110	HPr kinase	8.89	8.92	8.44	8.41	0.45	0.51	-0.03	0.03	1.43	0.49	0	-1.38	0.9	0.88	1.24
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_02066	serine O-acetyltransferase	10.51	10.53	10.46	9.95	0.05	0.58	-0.02	0.51	0.89	0.57	0.03	-0.36	0.9	0.88	3.32
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_00186	UDP-glucose 4-epimerase	11.21	11.18	11.27	10.38	-0.06	0.8	0.03	0.89	0.74	0.83	0.2	0.45	0.9	0.88	2.57
Cthe_03088		12.87	12.66	12.36	12.27	0.51	0.39	0.21	0.09	1.51	0.35	0.8	-1.26	0.89	0.87	1.18
Cthe_01052	competence/damage-inducible protein Ci	9.87	10.11	9.7	9.35	0.17	0.76	-0.24	0.35	1.05	0.79	-0.7	-0.7	0.88	0.86	1.51
Cthe_02252	thioesterase family protein	8.64	8.6	8.43	8.09	0.21	0.51	0.04	0.34	1.11	0.49	0.23	-0.72	0.88	0.86	1.82
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.36	11.54	11.53	10.46	-0.17	1.08	-0.18	1.07	0.59	1.17	-0.5	0.83	0.88	0.86	1.54
Cthe_01012	RNA polymerase, sigma 28 subunit	8.09	7.35	8.49	6.82	-0.4	0.53	0.74	1.67	0.28	0.51	2.57	2.11	0.88	0.86	0.2
Cthe_01035	DNA ligase, NAD-dependent	10.77	10.92	10.98	9.58	-0.21	1.34	-0.15	1.4	0.54	1.48	-0.4	1.53	0.88	0.86	1.13
Cthe_00877	GTP-binding protein YchF	12.76	12.73	12.52	12.22	0.24	0.51	0.03	0.3	1.15	0.49	0.2	-0.81	0.88	0.86	1.7
Cthe_02531	sulfate ABC transporter, periplasmic	3.32	3.91	2.81	2.81	0.51	1.1	-0.59	0	1.51	1.19	-1.87	-1.45	0.88	0.86	0.92
Cthe_01484	transcriptional regulator	10.43	10.47	10.28	9.91	0.15	0.56	-0.04	0.37	1.03	0.55	-0.03	-0.66	0.88	0.86	2.01
Cthe_02531	sulfate ABC transporter, periplasmic	3.32	3.91	2.81	2.81	0.51	1.1	-0.59	0	1.51	1.19	-1.87	-1.45	0.88	0.86	0.92
Cthe_01035	DNA ligase, NAD-dependent	10.77	10.92	10.98	9.58	-0.21	1.34	-0.15	1.4	0.54	1.48	-0.4	1.53	0.88	0.86	1.13
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.36	11.54	11.53	10.46	-0.17	1.08	-0.18	1.07	0.59	1.17	-0.5	0.83	0.88	0.86	1.54
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.36	11.54	11.53	10.46	-0.17	1.08	-0.18	1.07	0.59	1.17	-0.5	0.83	0.88	0.86	1.54
Cthe_03166	glucose-1-phosphate adenyllyltransferase	11.36	11.54	11.53	10.46	-0.17	1.08	-0.18	1.07	0.59	1.17	-0.5	0.83	0.88	0.86	1.54
Cthe_02301	CRISPR-associated autoregulator, DevR fa	9.56	9.63	9.77	8.03	-0.21	1.6	-0.07	1.74	0.54	1.79	-0.13	2.26	0.87	0.85	0.94
Cthe_02583																







Cthe_02582	dihydroneopterin aldolase	8.08	8.04	8.19	7.14	-0.11	0.9	0.04	1.05	0.68	0.95	0.23	0.79	0.81	0.79	1.61
Cthe_00138	Phosphoglycerate kinase	15.02	15.01	14.99	14.5	0.03	0.51	0.01	0.49	0.86	0.49	0.13	-0.4	0.8	0.78	2.67
Cthe_01527	periplasmic sensor signal transduction his	6.93	6.49	7.53	6.38	-0.6	0.11	0.44	1.15	0.01	0.01	1.57	1	0.8	0.78	0.01
Cthe_01213	hypothetical protein	7.71	7.64	7.52	7.19	0.19	0.45	0.07	0.33	1.08	0.42	0.33	-0.74	0.8	0.78	1.63
Cthe_00138	Phosphoglycerate kinase	15.02	15.01	14.99	14.5	0.03	0.51	0.01	0.49	0.86	0.49	0.13	-0.4	0.8	0.78	2.67
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Cthe_00138	Phosphoglycerate kinase	15.02	15.01	14.99	14.5	0.03	0.51	0.01	0.49	0.86	0.49	0.13	-0.4	0.8	0.78	2.67
Cthe_00138	Phosphoglycerate kinase	15.02	15.01	14.99	14.5	0.03	0.51	0.01	0.49	0.86	0.49	0.13	-0.4	0.8	0.78	2.67



Cthe_01292	proposed homoserine kinase	12.87	13.11	12.91	12.35	-0.04	0.76	-0.24	0.56	0.77	0.79	-0.7	-0.26	0.77	0.75	1.68
Cthe_01292	proposed homoserine kinase	12.87	13.11	12.91	12.35	-0.04	0.76	-0.24	0.56	0.77	0.79	-0.7	-0.26	0.77	0.75	1.68
Cthe_01292	proposed homoserine kinase	12.87	13.11	12.91	12.35	-0.04	0.76	-0.24	0.56	0.77	0.79	-0.7	-0.26	0.77	0.75	1.68
Cthe_01292	proposed homoserine kinase	12.87	13.11	12.91	12.35	-0.04	0.76	-0.24	0.56	0.77	0.79	-0.7	-0.26	0.77	0.75	1.68
Cthe_01292	proposed homoserine kinase	12.87	13.11	12.91	12.35	-0.04	0.76	-0.24	0.56	0.77	0.79	-0.7	-0.26	0.77	0.75	1.68
Cthe_01236	Fibronectin, type III	10.65	10.67	10.83	9.75	-0.18	0.92	-0.02	1.08	0.58	0.98	0.03	0.85	0.76	0.74	1.52
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate al	13.43	13.52	13.58	12.93	-0.15	0.59	-0.09	0.65	0.62	0.58	-0.2	-0.06	0.76	0.74	4.62
Cthe_00673	ribonuclease H	8.76	8.41	8.49	7.82	0.27	0.59	0.35	0.67	1.19	0.58	1.27	-0.02	0.76	0.74	1.18
Cthe_00977	UDP-N-acetylmuramoylalanyl-D-glutamyl-	9.62	9.65	9.9	7.98	-0.28	1.67	-0.03	1.92	0.45	1.87	0	2.64	0.76	0.74	0.83
Cthe_00687	chromosome segregation and condensati	12.32	12.52	12.31	11.85	0.01	0.67	-0.2	0.46	0.84	0.68	-0.57	-0.47	0.76	0.74	1.66
Cthe_02115	protein of unknown function DUF77	8.63	8.38	8.44	7.88	0.19	0.5	0.25	0.56	1.08	0.48	0.93	-0.26	0.76	0.74	1.39
Cthe_02185	ribosomal protein S18	13.22	13.26	13.15	12.76	0.07	0.5	-0.04	0.39	0.92	0.48	-0.03	-0.62	0.76	0.74	1.9
Cthe_00195	RNA polymerase, sigma-24 subunit, ECF su	8.48	8.47	8.18	8.06	0.3	0.41	0.01	0.12	1.23	0.37	0.13	-1.19	0.76	0.74	1.22
Cthe_01755	hypothetical protein	14.95	14.74	14.76	14.28	0.19	0.46	0.21	0.48	1.08	0.43	0.8	-0.43	0.76	0.74	1.45
Cthe_01929	hypothetical protein	9	8.75	8.89	8.07	0.11	0.68	0.25	0.82	0.97	0.69	0.93	0.3	0.76	0.74	1.38
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate al	13.43	13.52	13.58	12.93	-0.15	0.59	-0.09	0.65	0.62	0.58	-0.2	-0.06	0.76	0.74	4.62
Cthe_02185	ribosomal protein S18	13.22	13.26	13.15	12.76	0.07	0.5	-0.04	0.39	0.92	0.48	-0.03	-0.62	0.76	0.74	1.9
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate al	13.43	13.52	13.58	12.93	-0.15	0.59	-0.09	0.65	0.62	0.58	-0.2	-0.06	0.76	0.74	4.62
Cthe_00673	ribonuclease H	8.76	8.41	8.49	7.82	0.27	0.59	0.35	0.67	1.19	0.58	1.27	-0.02	0.76	0.74	1.18
Cthe_00977	UDP-N-acetylmuramoylalanyl-D-glutamyl-	9.62	9.65	9.9	7.98	-0.28	1.67	-0.03	1.92	0.45	1.87	0	2.64	0.76	0.74	0.83
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate al	13.43	13.52	13.58	12.93	-0.15	0.59	-0.09	0.65	0.62	0.58	-0.2	-0.06	0.76	0.74	4.62
Cthe_00977	UDP-N-acetylmuramoylalanyl-D-glutamyl-	9.62	9.65	9.9	7.98	-0.28	1.67	-0.03	1.92	0.45	1.87	0	2.64	0.76	0.74	0.83
Cthe_01795	phospho-2-dehydro-3-deoxyheptonate al	13.43	13.52	13.58	12.93	-0.15	0.59	-0.09	0.65	0.62	0.58	-0.2	-0.06	0.76	0.74	4.62
Cthe_00977	UDP-N-acetylmuramoylalanyl-D-glutamyl-	9.62	9.65	9.9	7.98	-0.28	1.67	-0.03	1.92	0.45	1.87	0	2.64	0.76	0.74	0.83
Cthe_00977	UDP-N-acetylmuramoylalanyl-D-glutamyl-	9.62	9.65	9.9	7.98	-0.28	1.67	-0.03	1.92	0.45	1.87	0	2.64	0.76	0.74	0.83
Cthe_01083	Putative homoserine kinase type II (protei	5.93	5.49	5.7	4.32	0.23	1.17	0.44	1.38	1.14	1.27	1.57	1.49	0.75	0.73	0.9
Cthe_01188	protein of unknown function DUF990	9.58	9.94	9.43	9.12	0.15	0.82	-0.36	0.31	1.03	0.86	-1.1	-0.79	0.75	0.73	1.13
Cthe_03155	beta-lactamase-like protein	9.09	9.15	9.14	8.63	-0.05	0.52	-0.06	0.51	0.76	0.5	-0.1	-0.36	0.75	0.73	2.77
Cthe_00726	peptidase M18, aminopeptidase I	12.34	12.36	12.52	11.64	-0.18	0.72	-0.02	0.88	0.58	0.74	0.03	0.43	0.75	0.73	2.48
Cthe_01771	Rubryerythrin	12.36	12.38	12.51	11.87	-0.15	0.51	-0.02	0.64	0.62	0.49	0.03	-0.09	0.75	0.73	9.47
Cthe_02693	hypothetical protein	11.45	11.5	11.62	10.96	-0.17	0.54	-0.05	0.66	0.59	0.52	-0.07	-0.04	0.75	0.73	11.08
Cthe_02193	Carbohydrate binding family 6	10.81	10.87	11	10.28	-0.19	0.59	-0.06	0.72	0.57	0.58	-0.1	0.09	0.75	0.73	6.87
Cthe_01188	protein of unknown function DUF990	9.58	9.94	9.43	9.12	0.15	0.82	-0.36	0.31	1.03	0.86	-1.1	-0.79	0.75	0.73	1.13
Cthe_00726	peptidase M18, aminopeptidase I	12.34	12.36	12.52	11.64	-0.18	0.72	-0.02	0.88	0.58	0.74	0.03	0.43	0.75	0.73	2.48
Cthe_02079	signal peptidase I	12.46	12.36	12.37	11.92	0.09	0.44	0.1	0.45	0.95	0.4	0.43	-0.49	0.74	0.72	1.8
Cthe_03045	FHA domain containing protein	9.56	9.65	9.83	8.42	-0.27	1.23	-0.09	1.41	0.46	1.35	-0.2	1.55	0.74	0.72	1.04
Cthe_02187	ribosomal protein S6	13.33	13.45	13.3	12.89	0.03	0.56	-0.12	0.41	0.86	0.55	-0.3	-0.57	0.74	0.72	1.8
Cthe_02079	signal peptidase I	12.46	12.36	12.37	11.92	0.09	0.44	0.1	0.45	0.95	0.4	0.43	-0.49	0.74	0.72	1.8
Cthe_00194	hypothetical protein	9.43	9.26	8.92	9.01	0.51	0.25	0.17	-0.09	1.51	0.18	0.67	-1.64	0.74	0.72	0.98
Cthe_02187	ribosomal protein S6	13.33	13.45	13.3	12.89	0.03	0.56	-0.12	0.41	0.86	0.55	-0.3	-0.57	0.74	0.72	1.8
Cthe_02079	signal peptidase I	12.46	12.36	12.37	11.92	0.09	0.44	0.1	0.45	0.95	0.4	0.43	-0.49	0.74	0.72	1.8
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_02667	transcriptional regulator, TetR family	5.46	5.49	5.49	5	-0.03	0.49	-0.03	0.49	0.78	0.46	0	-0.4	0.73	0.71	2.57
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_00105	riboflavin synthase, alpha subunit	10.2	10.1	10.18	9.63	0.02	0.47	0.1	0.55	0.85	0.44	0.43	-0.28	0.73	0.71	2.12
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_01244	glycosyl transferase, family 2	11.22	11.6	11.67	10.03	-0.45	1.57	-0.38	1.64	0.22	1.75	-1.17	2.04	0.73	0.71	0.85
Cthe_00398	protein of unknown function DUF74	8.15	8.27	8.37	7.52	-0.22	0.75	-0.12	0.85	0.53	0.77	-0.3	0.36	0.73	0.71	2.27
Cthe_00665	HRK protein	7.99	8.29	8.36	6.93	-0.37	1.36	-0.3	1.43	0.32	1.5	-0.9	1.6	0.73	0.71	0.95
Cthe_02695	hypothetical protein	10.81	10.76	10.92	10.23	-0.11	0.53	0.05	0.69	0.68	0.51	0.27	0.02	0.73	0.71	3.57
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_00105	riboflavin synthase, alpha subunit	10.2	10.1	10.18	9.63	0.02	0.47	0.1	0.55	0.85	0.44	0.43	-0.28	0.73	0.71	2.12
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_00105	riboflavin synthase, alpha subunit	10.2	10.1	10.18	9.63	0.02	0.47	0.1	0.55	0.85	0.44	0.43	-0.28	0.73	0.71	2.12
Cthe_00071	Cellulose 1,4-beta-cellobiosidase	11.49	11.95	11.86	10.52	-0.37	1.43	-0.46	1.34	0.32	1.58	-1.43	1.4	0.73	0.71	0.92
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_00665	HRK protein	7.99	8.29	8.36	6.93	-0.37	1.36	-0.3	1.43	0.32	1.5	-0.9	1.6	0.73	0.71	0.95
Cthe_00105	riboflavin synthase, alpha subunit	10.2	10.1	10.18	9.63	0.02	0.47	0.1	0.55	0.85	0.44	0.43	-0.28	0.73	0.71	2.12
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_00105	riboflavin synthase, alpha subunit	10.2	10.1	10.18	9.63	0.02	0.47	0.1	0.55	0.85	0.44	0.43	-0.28	0.73	0.71	2.12
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_02516	acetolactate synthase, large subunit,	12.78	13.03	12.81	12.29	-0.03	0.74	-0.25	0.52	0.78	0.76	-0.73	-0.34	0.73	0.71	1.54
Cthe_01253	phosphoenolpyruvate synthase	10.4	10.39	10.57	9.81	-0.17	0.58	0.01	0.76	0.59	0.57	0.13	0.17	0.73	0.71	4.36
Cthe_00105	riboflavin synthase, alpha subunit	10.2	10.1	10.18	9.63	0.02	0.47	0.1	0.55	0.85	0.44	0.43	-0.28	0.73		



Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00389	PfkB	15.41	15.58	15.55	14.91	-0.14	0.67	-0.17	0.64	0.64	0.68	-0.47	-0.09	0.72	0.7	2.22
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_02403	4-diphosphocytidyl-2C-methyl-D-erythritol	10.9	10.67	10.71	10.23	0.19	0.44	0.23	0.48	1.08	0.4	0.87	-0.43	0.72	0.7	1.35
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00389	PfkB	15.41	15.58	15.55	14.91	-0.14	0.67	-0.17	0.64	0.64	0.68	-0.47	-0.09	0.72	0.7	2.22
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00389	PfkB	15.41	15.58	15.55	14.91	-0.14	0.67	-0.17	0.64	0.64	0.68	-0.47	-0.09	0.72	0.7	2.22
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00389	PfkB	15.41	15.58	15.55	14.91	-0.14	0.67	-0.17	0.64	0.64	0.68	-0.47	-0.09	0.72	0.7	2.22
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00816	NAD(+) kinase	11.56	11.54	11.72	11.01	-0.16	0.53	0.02	0.71	0.61	0.51	0.17	0.06	0.72	0.7	5.01
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_01923	CTP synthase	12.49	12.54	12.7	11.92	-0.21	0.62	-0.05	0.78	0.54	0.62	-0.07	0.21	0.72	0.7	4.22
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00389	PfkB	15.41	15.58	15.55	14.91	-0.14	0.67	-0.17	0.64	0.64	0.68	-0.47	-0.09	0.72	0.7	2.22
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00139	Triose-phosphate isomerase	14.21	14.22	14.18	13.76	0.03	0.46	-0.01	0.42	0.86	0.43	0.07	-0.55	0.72	0.7	1.97
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00423	iron-containing alcohol dehydrogenase	16.66	16.95	16.58	16.21	0.08	0.74	-0.29	0.37	0.93	0.76	-0.87	-0.66	0.72	0.7	1.25
Cthe_00816	NAD(+) kinase	11.56	11.54	11.72	11.01	-0.16	0.53	0.02	0.71	0.61	0.51	0.17	0.06	0.72	0.7	5.01
Cthe_01030	TPR repeat domain containing protein	9.42	9.32	9.35	8.9	0.07	0.42	0.1	0.45	0.92	0.38	0.43	-0.49	0.71	0.69	1.74
Cthe_01473	NADPH-dependent FMN reductase	11.91	11.81	11.97	11.27	-0.06	0.54	0.1	0.7	0.74	0.52	0.43	0.04	0.71	0.69	2.38
Cthe_03003	hydrogenase, Fe-only	13.3	13.77	13.02	12.87	0.28	0.9	-0.47	0.15	1.2	0.95	-1.47	-1.13	0.71	0.69	0.94
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_02736	phosphoenolpyruvate-protein phosphotransferase	11.9	11.93	12.11	11.22	-0.21	0.71	-0.03	0.89	0.54	0.73	0	0.45	0.71	0.69	2.29
Cthe_00458	exodeoxyribonuclease III Xth	11.82	11.76	11.59	11.4	0.23	0.36	0.06	0.19	1.14	0.31	0.3	-1.04	0.71	0.69	1.24
Cthe_00823	hypothetical protein	5.04	4.86	5.09	3.91	-0.05	0.95	0.18	1.18	0.76	1.01	0.7	1.06	0.71	0.69	1.13
Cthe_01455	hypothetical protein	8.02	8	8.18	7.49	-0.12	0.51	0.02	0.69	0.61	0.49	0.17	0.02	0.71	0.69	5.19
Cthe_02419	primosome, DnaD subunit	12.35	12.31	12.33	11.87	-0.06	0.44	0.04	0.46	0.85	0.4	0.23	-0.47	0.71	0.69	2.04
Cthe_00678	pyrimidine-nucleoside phosphorylase	10.29	10.57	10.67	9.23	-0.38	1.34	-0.28	1.44	0.31	1.48	-0.83	1.62	0.71	0.69	0.94
Cthe_00509	sodium ion-translocating decarboxylase, b	12.11	12.08	12.21	11.6	-0.1	0.48	0.03	0.61	0.69	0.45	0.2	-0.15	0.71	0.69	3.74
Cthe_02606	ATP synthase F1, alpha subunit	11.27	11.19	11.24	10.75	0.03	0.44	0.08	0.49	0.86	0.4	0.37	-0.4	0.71	0.69	1.98
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_03003	hydrogenase, Fe-only	13.3	13.77	13.02	12.87	0.28	0.9	-0.47	0.15	1.2	0.95	-1.47	-1.13	0.71	0.69	0.94
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_02225	Glyoxalase/bleomycin resistance	5.83	6.23	6.19	4.91	-0.36	1.32	-0.4	1.28	0.34	1.45	-1.23	1.28	0.71	0.69	0.95
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_02606	ATP synthase F1, alpha subunit	11.27	11.19	11.24	10.75	0.03	0.44	0.08	0.49	0.86	0.4	0.37	-0.4	0.71	0.69	1.98
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_02606	ATP synthase F1, alpha subunit	11.27	11.19	11.24	10.75	0.03	0.44	0.08	0.49	0.86	0.4	0.37	-0.4	0.71	0.69	1.98
Cthe_02225	Glyoxalase/bleomycin resistance	5.83	6.23	6.19	4.91	-0.36	1.32	-0.4	1.28	0.34	1.45	-1.23	1.28	0.71	0.69	0.95
Cthe_02225	Glyoxalase/bleomycin resistance	5.83	6.23	6.19	4.91	-0.36	1.32	-0.4	1.28	0.34	1.45	-1.23	1.28	0.71	0.69	0.95
Cthe_02606	ATP synthase F1, alpha subunit	11.27	11.19	11.24	10.75	0.03	0.44	0.08	0.49	0.86	0.4	0.37	-0.4	0.71	0.69	1.98
Cthe_00509	sodium ion-translocating decarboxylase, b	12.11	12.08	12.21	11.6	-0.1	0.48	0.03	0.61	0.69	0.45	0.2	-0.15	0.71	0.69	3.74
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00678	pyrimidine-nucleoside phosphorylase	10.29	10.57	10.67	9.23	-0.38	1.34	-0.28	1.44	0.31	1.48	-0.83	1.62	0.71	0.69	0.94
Cthe_00458	exodeoxyribonuclease III Xth	11.82	11.76	11.59	11.4	0.23	0.36	0.06	0.19	1.14	0.31	0.3	-1.04	0.71	0.69	1.24
Cthe_03003	hydrogenase, Fe-only	13.3	13.77	13.02	12.87	0.28	0.9	-0.47	0.15	1.2	0.95	-1.47	-1.13	0.71	0.69	0.94
Cthe_00509	sodium ion-translocating decarboxylase, b	12.11	12.08	12.21	11.6	-0.1	0.48	0.03	0.61	0.69	0.45	0.2	-0.15	0.71	0.69	3.74
Cthe_00678																



Cthe_03003	hydrogenase, Fe-only	13.3	13.77	13.02	12.87	0.28	0.9	-0.47	0.15	1.2	0.95	-1.47	-1.13	0.71	0.69	0.94
Cthe_00678	pyrimidine-nucleoside phosphorylase	10.29	10.57	10.67	9.23	-0.38	1.34	-0.28	1.44	0.31	1.48	-0.83	1.62	0.71	0.69	0.94
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00509	sodium ion-translocating decarboxylase, b	12.11	12.08	12.21	11.6	-0.1	0.48	0.03	0.61	0.69	0.45	0.2	-0.15	0.71	0.69	3.74
Cthe_03003	hydrogenase, Fe-only	13.3	13.77	13.02	12.87	0.28	0.9	-0.47	0.15	1.2	0.95	-1.47	-1.13	0.71	0.69	0.94
Cthe_00509	sodium ion-translocating decarboxylase, b	12.11	12.08	12.21	11.6	-0.1	0.48	0.03	0.61	0.69	0.45	0.2	-0.15	0.71	0.69	3.74
Cthe_00678	pyrimidine-nucleoside phosphorylase	10.29	10.57	10.67	9.23	-0.38	1.34	-0.28	1.44	0.31	1.48	-0.83	1.62	0.71	0.69	0.94
Cthe_00509	sodium ion-translocating decarboxylase, b	12.11	12.08	12.21	11.6	-0.1	0.48	0.03	0.61	0.69	0.45	0.2	-0.15	0.71	0.69	3.74
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_00217	Glucose-6-phosphate isomerase	12.63	12.68	12.75	12.18	-0.12	0.5	-0.05	0.57	0.66	0.48	-0.07	-0.23	0.71	0.69	3.86
Cthe_03003	hydrogenase, Fe-only	13.3	13.77	13.02	12.87	0.28	0.9	-0.47	0.15	1.2	0.95	-1.47	-1.13	0.71	0.69	0.94
Cthe_02225	Glyoxalase/bleomycin resistance	5.83	6.23	6.19	4.91	-0.36	1.32	-0.4	1.28	0.34	1.45	-1.23	1.28	0.71	0.69	0.95
Cthe_02606	ATP synthase F1, alpha subunit	11.27	11.19	11.24	10.75	0.03	0.44	0.08	0.49	0.86	0.4	0.37	-0.4	0.71	0.69	1.98
Cthe_03003	hydrogenase, Fe-only	13.3	13.77	13.02	12.87	0.28	0.9	-0.47	0.15	1.2	0.95	-1.47	-1.13	0.71	0.69	0.94
Cthe_01421	signal peptide peptidase SppA, 36K type	12.5	12.5	12.54	12.05	-0.04	0.45	0	0.49	0.77	0.42	0.1	-0.4	0.7	0.68	2.42
Cthe_02963	oligopeptide/dipeptide ABC transporter, A	8.06	7.88	7.73	7.59	0.33	0.29	0.18	0.14	1.27	0.23	0.7	-1.15	0.7	0.68	1.09
Cthe_00135	beta-ketoacyl synthase	9.75	9.73	9.42	9.38	0.33	0.35	0.02	0.04	1.27	0.3	0.17	-1.36	0.7	0.68	1.08
Cthe_02237	flagellin-like protein	7.48	7.58	7.72	6.87	-0.24	0.71	-0.1	0.85	0.5	0.73	-0.23	0.36	0.7	0.68	2.35
Cthe_02694	O-antigen polymerase	12.39	12.55	12.52	11.92	-0.13	0.63	-0.16	0.6	0.65	0.73	-0.43	-0.17	0.7	0.68	2.22
Cthe_02228	MaoC-like dehydratase	6.69	7.01	7.1	5.61	-0.41	1.4	-0.32	1.49	0.27	1.55	-0.97	1.72	0.7	0.68	0.91
Cthe_02595	translation factor SUAS	11.63	11.59	11.6	11.16	0.03	0.43	0.04	0.44	0.86	0.39	0.23	-0.51	0.7	0.68	1.92
Cthe_02963	oligopeptide/dipeptide ABC transporter, A	8.06	7.88	7.73	7.59	0.33	0.29	0.18	0.14	1.27	0.23	0.7	-1.15	0.7	0.68	1.09
Cthe_03169	short-chain dehydrogenase/reductase SD	12.94	12.98	13.17	12.06	-0.23	0.92	-0.04	1.11	0.51	0.98	-0.03	0.91	0.7	0.68	1.38
Cthe_01421	signal peptide peptidase SppA, 36K type	12.5	12.5	12.54	12.05	-0.04	0.45	0	0.49	0.77	0.42	0.1	-0.4	0.7	0.68	2.42
Cthe_02584	hypothetical protein	10.12	10.1	10.3	9.35	-0.18	0.75	0.02	0.95	0.58	0.77	0.17	0.57	0.7	0.68	1.84
Cthe_01524	hypothetical protein	6.98	7.04	7.08	6.54	-0.11	0.5	-0.06	0.54	0.69	0.48	-0.1	-0.3	0.7	0.68	3.02
Cthe_00246	Carbohydrate binding family 6	7.98	7.94	8.14	7.3	-0.16	0.64	0.04	0.84	0.61	0.64	0.23	0.34	0.7	0.68	2.45
Cthe_02707	ABC-type transport system involved in	9.71	9.63	9.65	9.22	0.06	0.41	0.08	0.43	0.91	0.37	0.37	-0.53	0.7	0.68	1.73
Cthe_02963	oligopeptide/dipeptide ABC transporter, A	8.06	7.88	7.73	7.59	0.33	0.29	0.18	0.14	1.27	0.23	0.7	-1.15	0.7	0.68	1.09
Cthe_03169	short-chain dehydrogenase/reductase SD	12.94	12.98	13.17	12.06	-0.23	0.92	-0.04	1.11	0.51	0.98	-0.03	0.91	0.7	0.68	1.38
Cthe_03169	short-chain dehydrogenase/reductase SD	12.94	12.98	13.17	12.06	-0.23	0.92	-0.04	1.11	0.51	0.98	-0.03	0.91	0.7	0.68	1.38
Cthe_03169	short-chain dehydrogenase/reductase SD	12.94	12.98	13.17	12.06	-0.23	0.92	-0.04	1.11	0.51	0.98	-0.03	0.91	0.7	0.68	1.38
Cthe_03169	short-chain dehydrogenase/reductase SD	12.94	12.98	13.17	12.06	-0.23	0.92	-0.04	1.11	0.51	0.98	-0.03	0.91	0.7	0.68	1.38
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00504	Putative enzyme of poly-gamma-glutamyl	11.25	11.28	11.49	10.26	-0.24	1.02	-0.03	1.23	0.5	1.1	0	1.17	0.69	0.67	1.17
Cthe_02598	uracil phosphoribosyltransferase	11.86	11.97	12.01	11.41	-0.15	0.56	-0.11	0.6	0.62	0.55	-0.27	-0.17	0.69	0.67	2.95
Cthe_00250	protein of unknown function UPF0027	10.11	10	10.2	9.38	-0.09	0.62	0.11	0.82	0.7	0.62	0.47	0.3	0.69	0.67	1.91
Cthe_01207	membrane protein-like protein	11.89	12.25	12.09	11.26	-0.2	0.99	-0.36	0.83	0.55	1.06	-1.1	0.32	0.69	0.67	1.18
Cthe_02619	cell shape determining protein, MreB/Mrl	12.39	12.25	12.38	11.78	0.01	0.47	0.14	0.6	0.84	0.44	0.57	-0.17	0.69	0.67	1.81
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.82	11.79	11.93	11.33	-0.11	0.46	0.03	0.6	0.68	0.43	0.2	-0.17	0.69	0.67	3.48
Cthe_01410	cation diffusion facilitator family transpor	9.94	9.81	9.96	9.32	-0.02	0.49	0.13	0.64	0.8	0.46	0.53	-0.09	0.69	0.67	1.95
Cthe_01801	ABC transporter related protein	10.9	10.98	11	10.47	-0.1	0.51	-0.08	0.53	0.69	0.49	-0.17	-0.32	0.69	0.67	2.65
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00937	fatty acid/phospholipid synthesis protein	14.01	14.04	14.23	13.56	-0.22	0.48	-0.03	0.67	0.53	0.45	0	-0.02	0.69	0.67	39.5
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.82	11.79	11.93	11.33	-0.11	0.46	0.03	0.6	0.68	0.43	0.2	-0.17	0.69	0.67	3.48
Cthe_01801	ABC transporter related protein	10.9	10.98	11	10.47	-0.1	0.51	-0.08	0.53	0.69	0.49	-0.17	-0.32	0.69	0.67	2.65
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.82	11.79	11.93	11.33	-0.11	0.46	0.03	0.6	0.68	0.43	0.2	-0.17	0.69	0.67	3.48
Cthe_01801	ABC transporter related protein	10.9	10.98	11	10.47	-0.1	0.51	-0.08	0.53	0.69	0.49	-0.17	-0.32	0.69	0.67	2.65
Cthe_00937	fatty acid/phospholipid synthesis protein	14.01	14.04	14.23	13.56	-0.22	0.48	-0.03	0.67	0.53	0.45	0	-0.02	0.69	0.67	39.5
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.82	11.79	11.93	11.33	-0.11	0.46	0.03	0.6	0.68	0.43	0.2	-0.17	0.69	0.67	3.48
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.82	11.79	11.93	11.33	-0.11	0.46	0.03	0.6	0.68	0.43	0.2	-0.17	0.69	0.67	3.48
Cthe_02598	uracil phosphoribosyltransferase	11.86	11.97	12.01	11.41	-0.15	0.56	-0.11	0.6	0.62	0.55	-0.27	-0.17	0.69	0.67	2.95
Cthe_00937	fatty acid/phospholipid synthesis protein	14.01	14.04	14.23	13.56	-0.22	0.48	-0.03	0.67	0.53	0.45	0	-0.02	0.69	0.67	39.5
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00937	fatty acid/phospholipid synthesis protein	14.01	14.04	14.23	13.56	-0.22	0.48	-0.03	0.67	0.53	0.45	0	-0.02	0.69	0.67	39.5
Cthe_02598	uracil phosphoribosyltransferase	11.86	11.97	12.01	11.41	-0.15	0.56	-0.11	0.6	0.62	0.55	-0.27	-0.17	0.69	0.67	2.95
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00937	fatty acid/phospholipid synthesis protein	14.01	14.04	14.23	13.56	-0.22	0.48	-0.03	0.67	0.53	0.45	0	-0.02	0.69	0.67	39.5
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_02598	uracil phosphoribosyltransferase	11.86	11.97	12.01	11.41	-0.15	0.56	-0.11	0.6	0.62	0.55	-0.27	-0.17	0.69	0.67	2.95
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.82	11.79	11.93	11.33	-0.11	0.46	0.03	0.6	0.68	0.43	0.2	-0.17	0.69	0.67	3.48
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00866	pyruvate flavodoxin/ferredoxin	11.82	11.79	11.93	11.33	-0.11	0.46	0.03	0.6	0.68	0.43	0.2	-0.17	0.69	0.67	3.48
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00934	3-oxoacyl-(acyl-carrier-protein) reductase	13.87	14.11	14.06	13.32	-0.19	0.79	-0.24	0.74	0.57	0.82	-0.7	0.13	0.69	0.67	1.59
Cthe_00937	fatty acid/phospholipid synthesis protein	14.01	14.04	14.23	13											



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Cthe_01590	peptidase M56, BlaR1	8.93	8.78	8.86	8.42	0.07	0.36	0.15	0.44	0.92	0.31	0.6	-0.51	0.62	0.6	1.4
Cthe_00674	NUDIX hydrolase	9.97	10.04	9.93	9.61	0.04	0.43	-0.07	0.32	0.88	0.39	-0.13	-0.77	0.62	0.6	1.4
Cthe_01590	peptidase M56, BlaR1	8.93	8.78	8.86	8.42	0.07	0.36	0.15	0.44	0.92	0.31	0.6	-0.51	0.62	0.6	1.4
Cthe_03185	tRNA-guanine transglycosylases, various	9.43	9.31	9.44	8.92	-0.01	0.39	0.12	0.52	0.81	0.35	0.5	-0.34	0.62	0.6	1.66
Cthe_02942	ABC transporter related protein	8.69	8.71	8.76	8.29	-0.07	0.42	-0.02	0.47	0.73	0.38	0.03	-0.45	0.62	0.6	2.07
Cthe_02942	ABC transporter related protein	8.69	8.71	8.76	8.29	-0.07	0.42	-0.02	0.47	0.73	0.38	0.03	-0.45	0.62	0.6	2.07
Cthe_00400	hypothetical protein	10.36	10.47	10.65	9.75	-0.29	0.72	-0.11	0.9	0.43	0.74	-0.27	0.47	0.62	0.6	1.79
Cthe_02942	ABC transporter related protein	8.69	8.71	8.76	8.29	-0.07	0.42	-0.02	0.47	0.73	0.38	0.03	-0.45	0.62	0.6	2.07
Cthe_00674	NUDIX hydrolase	9.97	10.04	9.93	9.61	0.04	0.43	-0.07	0.32	0.88	0.39	-0.13	-0.77	0.62	0.6	1.4
Cthe_01408	two component transcriptional regulator,	6.97	7.33	6.97	6.55	0	0.78	-0.36	0.42	0.82	0.81	-1.1	-0.55	0.61	0.59	1.07
Cthe_01408	two component transcriptional regulator,	6.97	7.33	6.97	6.55	0	0.78	-0.36	0.42	0.82	0.81	-1.1	-0.55	0.61	0.59	1.07
Cthe_01521	hypothetical protein	7.46	6.95	7.94	6.97	-0.48	-0.02	0.51	0.97	0.18	-0.14	1.8	0.62	0.61	0.59	0.14
Cthe_02101	Protein of unknown function UPF0011	9.65	9.54	9.77	9.04	-0.12	0.5	0.11	0.73	0.66	0.48	0.47	0.11	0.6	0.58	1.92
Cthe_02427	protein of unknown function DUF1385	12.07	12.02	12.08	11.66	-0.01	0.36	0.05	0.42	0.81	0.31	0.27	-0.55	0.6	0.58	1.61
Cthe_00747	extracellular solute-binding protein, famil	10.54	10.29	10.42	9.92	0.12	0.37	0.25	0.5	0.99	0.32	0.93	-0.38	0.6	0.58	1.18
Cthe_00247	DNA mismatch repair protein MutS-like pr	11.73	11.71	12.04	10.41	-0.31	1.3	0.02	1.63	0.41	1.43	0.17	2.02	0.6	0.58	0.83
Cthe_01530	transposase, IS204/IS1001/IS1096/IS1165	10.6	10.41	10.68	9.7	-0.08	0.71	0.19	0.98	0.72	0.73	0.73	0.64	0.6	0.58	1.2
Cthe_02236	flagellin-like protein	7.62	7.46	7.71	6.86	-0.09	0.6	0.16	0.85	0.7	0.6	0.63	0.36	0.6	0.58	1.44
Cthe_01758	protein of unknown function DUF583	10.52	10.42	10.52	10.06	0	0.36	0.1	0.46	0.82	0.31	0.43	-0.47	0.6	0.58	1.56
Cthe_00339	histidine kinase	13.33	13.56	13.5	12.89	-0.17	0.67	-0.23	0.61	0.59	0.68	-0.67	-0.15	0.6	0.58	1.49
Cthe_00060	SEC-C motif containing protein	10.08	10.05	10.29	9.58	-0.21	0.47	0.03	0.71	0.54	0.44	0.2	0.06	0.6	0.58	3.79
Cthe_02925	methionine aminopeptidase, type I	13.13	13.61	13.55	13.47	-0.42	0.14	-0.48	0.08	0.26	0.05	-1.5	-1.28	0.6	0.58	0.15
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_02612	Fibronectin, type III	7.29	7.39	7.73	5.88	-0.44	1.51	-0.1	1.85	0.23	1.68	-0.23	2.49	0.6	0.58	0.77
Cthe_02879	cellulosome enzyme, dockerin type I	9.69	9.91	9.66	9.33	0.03	0.58	-0.22	0.33	0.86	0.57	-0.63	-0.74	0.6	0.58	1.21
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_00747	extracellular solute-binding protein, famil	10.54	10.29	10.42	9.92	0.12	0.37	0.25	0.5	0.99	0.32	0.93	-0.38	0.6	0.58	1.18
Cthe_02925	methionine aminopeptidase, type I	13.13	13.61	13.55	13.47	-0.42	0.14	-0.48	0.08	0.26	0.05	-1.5	-1.28	0.6	0.58	0.15
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_00338	NADH-quinone oxidoreductase, E subunit	12.76	12.92	12.96	12.33	-0.2	0.59	-0.16	0.63	0.55	0.58	-0.43	-0.11	0.6	0.58	2.05
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00388	Alcohol dehydrogenase GroES-like protein	17.17	17.12	17.36	16.66	-0.19	0.46	0.05	0.7	0.57	0.43	0.27	0.04	0.59	0.57	2.97
Cthe_03167	glucose-1-phosphate adenyllyltransferase,	10.2	10.43	10.54	9.52	-0.34	0.91	-0.23	1.02	0.36	0.96	-0.67	0.72	0.59	0.57	1.18
Cthe_01843	transcriptional regulator, BadM/Rrf2 fami	9.22	9.34	9.28	8.86	-0.06	0.48	-0.12	0.42	0.74	0.45	-0.3	-0.55	0.59	0.57	1.57
Cthe_02969	transcriptional regulator, GntR family	6.21	5.91	6.07	5.49	0.14	0.42	0.3	0.58	1.01	0.38	1.1	-0.21	0.59	0.57	1.1
Cthe_00388	Alcohol dehydrogenase GroES-like protein	17.17	17.12	17.36	16.66	-0.19	0.46	0.05	0.7	0.57	0.43	0.27	0.04	0.59	0.57	2.97
Cthe_00106	GTP cyclohydrolase II	10.27	10.12	10.31	9.7	-0.04	0.42	0.15	0.61	0.77	0.38	0.6	-0.15	0.59	0.57	1.58
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_02637	glycosyl transferase, group 1	4.17	3	3.91	2.32	0.26	0.68	1.17	1.59	1.18	0.69	4	1.94	0.59	0.57	0.35
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.2	12.15	12.39	11.7	-0.19	0.45	0.05	0.69	0.57	0.42	0.27	0.02	0.59	0.57	2.97
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.2	12.15	12.39	11.7	-0.19	0.45	0.05	0.69	0.57	0.42	0.27	0.02	0.59	0.57	2.97
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.2	12.15	12.39	11.7	-0.19	0.45	0.05	0.69	0.57	0.42	0.27	0.02	0.59	0.57	2.97
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.2	12.15	12.39	11.7	-0.19	0.45	0.05	0.69	0.57	0.42	0.27	0.02	0.59	0.57	2.97
Cthe_00106	GTP cyclohydrolase II	10.27	10.12	10.31	9.7	-0.04	0.42	0.15	0.61	0.77	0.38	0.6	-0.15	0.59	0.57	1.58
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.2	12.15	12.39	11.7	-0.19	0.45	0.05	0.69	0.57	0.42	0.27	0.02	0.59	0.57	2.97
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00106	GTP cyclohydrolase II	10.27	10.12	10.31	9.7	-0.04	0.42	0.15	0.61	0.77	0.38	0.6	-0.15	0.59	0.57	1.58
Cthe_00388	Alcohol dehydrogenase GroES-like protein	17.17	17.12	17.36	16.66	-0.19	0.46	0.05	0.7	0.57	0.43	0.27	0.04	0.59	0.57	2.97
Cthe_03167	glucose-1-phosphate adenyllyltransferase,	10.2	10.43	10.54	9.52	-0.34	0.91	-0.23	1.02	0.36	0.96	-0.67	0.72	0.59	0.57	1.18
Cthe_00106	GTP cyclohydrolase II	10.27	10.12	10.31	9.7	-0.04	0.42	0.15	0.61	0.77	0.38	0.6	-0.15	0.59	0.57	1.58
Cthe_00388	Alcohol dehydrogenase GroES-like protein	17.17	17.12	17.36	16.66	-0.19	0.46	0.05	0.7	0.57	0.43	0.27	0.04	0.59	0.57	2.97
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
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Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
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Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02								



Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
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Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.2	12.15	12.39	11.7	-0.19	0.45	0.05	0.69	0.57	0.42	0.27	0.02	0.59	0.57	2.97
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00388	Alcohol dehydrogenase GroES-like protein	17.17	17.12	17.36	16.66	-0.19	0.46	0.05	0.7	0.57	0.43	0.27	0.04	0.59	0.57	2.97
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00865	3-methyl-2-oxobutanoate dehydrogenase	12.2	12.15	12.39	11.7	-0.19	0.45	0.05	0.69	0.57	0.42	0.27	0.02	0.59	0.57	2.97
Cthe_00388	Alcohol dehydrogenase GroES-like protein	17.17	17.12	17.36	16.66	-0.19	0.46	0.05	0.7	0.57	0.43	0.27	0.04	0.59	0.57	2.97
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_00106	GTP cyclohydrolase II	10.27	10.12	10.31	9.7	-0.04	0.42	0.15	0.61	0.77	0.38	0.6	-0.15	0.59	0.57	1.58
Cthe_00852	peptidase A24A-like protein	11.48	11.46	11.72	10.89	-0.24	0.57	0.02	0.83	0.5	0.56	0.17	0.32	0.59	0.57	2.35
Cthe_02696	carbohydrate kinase, YjeF related protein	10.08	10.16	10.3	9.7	-0.22	0.46	-0.08	0.6	0.53	0.43	-0.17	-0.17	0.58	0.56	3.23
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_01538	transcriptional regulator, XRE family	8.52	8.21	8.33	7.87	0.19	0.34	0.31	0.46	1.08	0.29	1.13	-0.47	0.58	0.56	1.04
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_02525	glutamyl-tRNA reductase	7.8	7.8	7.86	7.42	-0.06	0.38	0	0.44	0.74	0.33	0.1	-0.51	0.58	0.56	1.77
Cthe_01858	peptidase M23B	12.39	12.37	12.47	12	-0.08	0.37	0.02	0.47	0.72	0.32	0.17	-0.45	0.58	0.56	1.86
Cthe_02696	carbohydrate kinase, YjeF related protein	10.08	10.16	10.3	9.7	-0.22	0.46	-0.08	0.6	0.53	0.43	-0.17	-0.17	0.58	0.56	3.23
Cthe_01031	glutamyl-tRNA(Gln) amidotransferase, B s	9.17	9.28	9.47	8.67	-0.3	0.61	-0.11	0.8	0.42	0.61	-0.27	0.26	0.58	0.56	2.25
Cthe_01032	glutamyl-tRNA(Gln) amidotransferase, A s	9.42	9.45	9.7	9.03	-0.28	0.42	-0.03	0.67	0.45	0.38	0	-0.02	0.58	0.56	33.46
Cthe_00036	hybrid cluster protein	7.88	8.26	8.29	7.11	-0.41	1.15	-0.38	1.18	0.27	1.25	-1.17	1.06	0.58	0.56	0.92
Cthe_00819	ABC transporter related protein	8.5	8.14	8.4	7.39	0.1	0.75	0.36	1.01	0.96	0.77	1.3	0.7	0.58	0.56	0.95
Cthe_02525	glutamyl-tRNA reductase	7.8	7.8	7.86	7.42	-0.06	0.38	0	0.44	0.74	0.33	0.1	-0.51	0.58	0.56	1.77
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_01031	glutamyl-tRNA(Gln) amidotransferase, B s	9.17	9.28	9.47	8.67	-0.3	0.61	-0.11	0.8	0.42	0.61	-0.27	0.26	0.58	0.56	2.25
Cthe_01032	glutamyl-tRNA(Gln) amidotransferase, A s	9.42	9.45	9.7	9.03	-0.28	0.42	-0.03	0.67	0.45	0.38	0	-0.02	0.58	0.56	33.46
Cthe_00036	hybrid cluster protein	7.88	8.26	8.29	7.11	-0.41	1.15	-0.38	1.18	0.27	1.25	-1.17	1.06	0.58	0.56	0.92
Cthe_02525	glutamyl-tRNA reductase	7.8	7.8	7.86	7.42	-0.06	0.38	0	0.44	0.74	0.33	0.1	-0.51	0.58	0.56	1.77
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_01031	glutamyl-tRNA(Gln) amidotransferase, B s	9.17	9.28	9.47	8.67	-0.3	0.61	-0.11	0.8	0.42	0.61	-0.27	0.26	0.58	0.56	2.25
Cthe_01032	glutamyl-tRNA(Gln) amidotransferase, A s	9.42	9.45	9.7	9.03	-0.28	0.42	-0.03	0.67	0.45	0.38	0	-0.02	0.58	0.56	33.46
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_01031	glutamyl-tRNA(Gln) amidotransferase, B s	9.17	9.28	9.47	8.67	-0.3	0.61	-0.11	0.8	0.42	0.61	-0.27	0.26	0.58	0.56	2.25
Cthe_01032	glutamyl-tRNA(Gln) amidotransferase, A s	9.42	9.45	9.7	9.03	-0.28	0.42	-0.03	0.67	0.45	0.38	0	-0.02	0.58	0.56	33.46
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_01031	glutamyl-tRNA(Gln) amidotransferase, B s	9.17	9.28	9.47	8.67	-0.3	0.61	-0.11	0.8	0.42	0.61	-0.27	0.26	0.58	0.56	2.25
Cthe_01032	glutamyl-tRNA(Gln) amidotransferase, A s	9.42	9.45	9.7	9.03	-0.28	0.42	-0.03	0.67	0.45	0.38	0	-0.02	0.58	0.56	33.46
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_01031	glutamyl-tRNA(Gln) amidotransferase, B s	9.17	9.28	9.47	8.67	-0.3	0.61	-0.11	0.8	0.42	0.61	-0.27	0.26	0.58	0.56	2.25
Cthe_01032	glutamyl-tRNA(Gln) amidotransferase, A s	9.42	9.45	9.7	9.03	-0.28	0.42	-0.03	0.67	0.45	0.38	0	-0.02	0.58	0.56	33.46
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_01031	glutamyl-tRNA(Gln) amidotransferase, B s	9.17	9.28	9.47	8.67	-0.3	0.61	-0.11	0.8	0.42	0.61	-0.27	0.26	0.58	0.56	2.25
Cthe_01032	glutamyl-tRNA(Gln) amidotransferase, A s	9.42	9.45	9.7	9.03	-0.28	0.42	-0.03	0.67	0.45	0.38	0	-0.02	0.58	0.56	33.46
Cthe_02713	dihydroxy-acid dehydratase	11.86	12.17	12.02	11.41	-0.16	0.76	-0.31	0.61	0.61	0.79	-0.93	-0.15	0.58	0.56	1.2
Cthe_02525	glutamyl-tRNA reductase	7.8	7.8	7.86	7.42	-0.06	0.38	0	0.44	0.74	0.33	0.1	-0.51	0.58	0.56	1.77
Cthe_00607	peptidase M42	8.46	8.63	8.44	8.13	0.02	0.5	-0.17	0.31	0.85	0.48	-0.47	-0.79	0.57	0.55	1.21
Cthe_00608	peptidase M42	7.52	7.83	7.36	7.21	0.16	0.62	-0.31	0.15	1.04	0.62	-0.93	-1.13	0.57	0.55	0.94
Cthe_00566	primosomal protein N'	10.24	10.19	10.11	9.9	0.14	0.29	0.05	0.2	1.01	0.23	0.27	-1.02	0.57	0.55	1.12
Cthe_02657	histone-like DNA-binding protein	12.18	12.07	12.27	11.67	-0.09	0.4	0.11	0.6	0.7	0.36	0.47	-0.17	0.57	0.55	1.79
Cthe_02737	exinuclease ABC, C subunit	10.14	10.02	10.3	9.39	-0.16	0.63	0.12	0.91	0.61	0.63	0.5	0.49	0.57	0.55	1.42
Cthe_01767	hypothetical protein	12.02	12.07	11.57	11.82	0.45	0.25	-0.05	-0.25	1.43	0.18	-0.07	-1.98	0.57	0.55	0.83
Cthe_00607	peptidase M42	8.46	8.63	8.44	8.13	0.02	0.5	-0.17	0.31	0.85	0.48	-0.47	-0.79	0.57	0.55	1.21
Cthe_00608	peptidase M42	7.52	7.83	7.36	7.21	0.16	0.62	-0.31	0.15	1.04	0.62	-0.93	-1.13	0.57	0.55	0.94
Cthe_00566	primosomal protein N'	10.24	10.19	10.11	9.9	0.14	0.29	0.05	0.2	1.01	0.23	0.27	-1.02	0.57	0.55	1.12
Cthe_00607	peptidase M42	8.46	8.63	8.44	8.13	0.02	0.5	-0.17	0.31	0.85	0.48	-0.47	-0.79	0.57	0.55	1.21
Cthe_00608	peptidase M42	7.52	7.83	7.36	7.21	0.16	0.62	-0.31	0.15	1.04	0.62	-0.93	-1.13	0.57	0.55	0.94
Cthe_00616	amino acid-binding ACT	10.84	11.25	11.47	11.1	-0.63	0.15	-0.41	0.37	-0.03	0.06	-1.27	-0.66	0.56	0.54	0.05
Cthe_01183	ATPase associated with various cellular	11.37	11.29	11.58	10.63	-0.21	0.66	0.08	0.95	0.54	0.67	0.37	0.57	0.56	0.54	1.44
Cthe_00815	arginine repressor, ArgR	9.54	9.53	9.61	9.17	-0.07	0.36	0.01	0.44	0.73	0.31	0.13	-0.51	0.56	0.54	1.71
Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.47	12.42	12.65	12.01	-0.18	0.41	0.05	0.64	0.58	0.37	0.27	-0.09	0.56	0.54	2.75
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.51	9.5	9.78	8.93	-0.27	0.57	0.01	0.85	0.46	0.56	0.13	0.36	0.56	0.54	2.15
Cthe_02615	UDP-N-acetylglucosamine	10.74	10.89	11.15	9.81	-0.41	1.08	-0.15	1.34	0.27	1.17	-0.4	1.4	0.56	0.54	0.94
Cthe_01235	Cellulose 1,4-beta-cellobiosidase	11.95	12.16													



Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.47	12.42	12.65	12.01	-0.18	0.41	0.05	0.64	0.58	0.37	0.27	-0.09	0.56	0.54	2.75	
Cthe_02615	UDP-N-acetylglucosamine	10.74	10.89	11.15	9.81	-0.41	1.08	-0.15	1.34	0.27	1.17	-0.4	1.4	0.56	0.54	0.94	
Cthe_01183	ATPase associated with various cellular	11.37	11.29	11.58	10.63	-0.21	0.66	0.08	0.95	0.54	0.67	0.37	0.57	0.56	0.54	1.44	
Cthe_02615	UDP-N-acetylglucosamine	10.74	10.89	11.15	9.81	-0.41	1.08	-0.15	1.34	0.27	1.17	-0.4	1.4	0.56	0.54	0.94	
Cthe_01241	nicotinate (nicotinamide) nucleotide	9.51	9.5	9.78	8.93	-0.27	0.57	0.01	0.85	0.46	0.56	0.13	0.36	0.56	0.54	2.15	
Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.47	12.42	12.65	12.01	-0.18	0.41	0.05	0.64	0.58	0.37	0.27	-0.09	0.56	0.54	2.75	
Cthe_01183	ATPase associated with various cellular	11.37	11.29	11.58	10.63	-0.21	0.66	0.08	0.95	0.54	0.67	0.37	0.57	0.56	0.54	1.44	
Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.47	12.42	12.65	12.01	-0.18	0.41	0.05	0.64	0.58	0.37	0.27	-0.09	0.56	0.54	2.75	
Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.47	12.42	12.65	12.01	-0.18	0.41	0.05	0.64	0.58	0.37	0.27	-0.09	0.56	0.54	2.75	
Cthe_01918	Orn/Lys/Arg decarboxylase, major region	12.47	12.42	12.65	12.01	-0.18	0.41	0.05	0.64	0.58	0.37	0.27	-0.09	0.56	0.54	2.75	
Cthe_03178	protein of unknown function DUF342	10.68	10.81	11.17	9.33	-0.49	1.48	-0.13	1.84	0.16	1.64	-0.33	2.47	0.55	0.53	0.75	
Cthe_02709	hypothetical protein	11.06	10.96	11.2	10.55	-0.14	0.41	0.1	0.65	0.64	0.37	0.43	-0.06	0.55	0.53	1.93	
Cthe_01546	4Fe-4S ferredoxin, iron-sulfur binding	9.16	9.41	9.54	8.51	-0.38	0.9	-0.25	1.03	0.31	0.95	-0.73	0.74	0.54	0.52	1.09	
Cthe_03168	hypothetical protein	10.11	10.14	10.42	9.47	-0.31	0.67	-0.03	0.95	0.41	0.68	0	0.57	0.54	0.52	1.58	
Cthe_00115	glycogen debranching enzyme, putative	10.41	10.41	10.65	10.02	-0.24	0.39	0	0.63	0.5	0.35	0.1	-0.11	0.54	0.52	4.67	
Cthe_00305	DNA topoisomerase (ATP-hydrolyzing)	9.68	9.77	9.99	9.25	-0.31	0.52	-0.09	0.74	0.41	0.5	-0.2	0.13	0.54	0.52	3.08	
Cthe_03202	CRISPR-associated protein, Csh2 family	1		0			1		1	0		3.43	-1.45	0.54	0.52	0.67	
Cthe_00160	ribosomal protein L21	13.53	13.42	13.52	13.12	0.01	0.3	0.11	0.4	0.84	0.24	0.47	-0.6	0.54	0.52	1.3	
Cthe_00093	septum site-determining protein MinD	12.67	12.52	12.77	12.07	-0.1	0.45	0.15	0.7	0.69	0.42	0.6	0.04	0.54	0.52	1.53	
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_00016	Ferritin and Dps	15.67	15.33	15.55	14.86	0.12	0.47	0.34	0.69	0.99	0.44	1.23	0.02	0.54	0.52	1	
Cthe_03168	hypothetical protein	10.11	10.14	10.42	9.47	-0.31	0.67	-0.03	0.95	0.41	0.68	0	0.57	0.54	0.52	1.58	
Cthe_01439	hypothetical protein	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_00317	hypothetical protein	11.31	11.31	11.55	10.92	-0.24	0.39	0	0.63	0.5	0.35	0.1	-0.11	0.54	0.52	4.67	
Cthe_02500	hypothetical protein	1		0			1	1	0	2.18		3.43	-1.45	0.54	0.52	0.67	
Cthe_03205	hypothetical protein	1		0			1	1	0	2.18		3.43	-1.45	0.54	0.52	0.67	
Cthe_03055	hypothetical protein	1		0			1	1	0	2.18		3.43	-1.45	0.54	0.52	0.67	
Cthe_03203	CRISPR-associated protein Cas5, Hmari su	1	0				1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_00160	ribosomal protein L21	13.53	13.42	13.52	13.12	0.01	0.3	0.11	0.4	0.84	0.24	0.47	-0.6	0.54	0.52	1.3	
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_00305	DNA topoisomerase (ATP-hydrolyzing)	9.68	9.77	9.99	9.25	-0.31	0.52	-0.09	0.74	0.41	0.5	-0.2	0.13	0.54	0.52	3.08	
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_00016	Ferritin and Dps	15.67	15.33	15.55	14.86	0.12	0.47	0.34	0.69	0.99	0.44	1.23	0.02	0.54	0.52	1	
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45	0.54	0.52	0.67
Cthe_02795	pyruvate ferredoxin/flavodoxin oxidoredu	1		0			1	0	1	0	2.18	-0.12	3.43	-1.45			



Cthe_02137	cellulosome enzyme, dockerin type I	7.48	7.75	7.86	6.88	-0.38	0.87	-0.27	0.98	0.31	0.92	-0.8	0.64	0.52	0.5	1.08
Cthe_00249	peptidase C11, clostripain	11.1	11.45	11.43	10.54	-0.33	0.91	-0.35	0.89	0.38	0.96	-1.07	0.45	0.52	0.5	1.01
Cthe_02302	hypothetical protein	10.37	10.49	10.77	9.59	-0.4	0.9	-0.12	1.18	0.28	0.95	-0.3	1.06	0.51	0.5	1.02
Cthe_00078	hypothetical protein	14.99	14.91	15.2	14.45	-0.21	0.46	0.08	0.75	0.54	0.43	0.37	0.15	0.51	0.5	1.96
Cthe_02984		8.04	8.01	8.17	7.67	-0.13	0.34	0.03	0.5	0.65	0.29	0.2	-0.38	0.52	0.5	1.88
Cthe_02533	sulfate ABC transporter, inner membrane	3.17	1.58	1.58	1.58	1.59	0	1.59	0	2.97	-0.12	5.4	-1.45	0.51	0.5	0.6
Cthe_00428	NADH dehydrogenase (ubiquinone), 24 kD	12.98	13.33	12.92	12.66	0.06	0.67	-0.35	0.26	0.91	0.68	-1.07	-0.89	0.52	0.5	0.93
Cthe_01040	DNA polymerase III, delta subunit	10.39	10.3	10.58	9.88	-0.19	0.42	0.09	0.7	0.57	0.38	0.4	0.04	0.51	0.5	1.94
Cthe_02107	thymidylate kinase	9.47	9.49	9.55	9.15	-0.08	0.34	-0.02	0.4	0.72	0.29	0.03	-0.6	0.51	0.5	1.47
Cthe_02107	thymidylate kinase	9.47	9.49	9.55	9.15	-0.08	0.34	-0.02	0.4	0.72	0.29	0.03	-0.6	0.51	0.5	1.47
Cthe_01040	DNA polymerase III, delta subunit	10.39	10.3	10.58	9.88	-0.19	0.42	0.09	0.7	0.57	0.38	0.4	0.04	0.51	0.5	1.94
Cthe_00976	phospho-N-acetylmuramoyl-pentapeptide	10.55	10.61	10.95	9.44	-0.4	1.17	-0.06	1.51	0.28	1.27	-0.1	1.77	0.52	0.5	0.83
Cthe_00428	NADH dehydrogenase (ubiquinone), 24 kD	12.98	13.33	12.92	12.66	0.06	0.67	-0.35	0.26	0.91	0.68	-1.07	-0.89	0.52	0.5	0.93
Cthe_00428	NADH dehydrogenase (ubiquinone), 24 kD	12.98	13.33	12.92	12.66	0.06	0.67	-0.35	0.26	0.91	0.68	-1.07	-0.89	0.52	0.5	0.93
Cthe_00428	NADH dehydrogenase (ubiquinone), 24 kD	12.98	13.33	12.92	12.66	0.06	0.67	-0.35	0.26	0.91	0.68	-1.07	-0.89	0.52	0.5	0.93
Cthe_00976	phospho-N-acetylmuramoyl-pentapeptide	10.55	10.61	10.95	9.44	-0.4	1.17	-0.06	1.51	0.28	1.27	-0.1	1.77	0.52	0.5	0.83
Cthe_00428	NADH dehydrogenase (ubiquinone), 24 kD	12.98	13.33	12.92	12.66	0.06	0.67	-0.35	0.26	0.91	0.68	-1.07	-0.89	0.52	0.5	0.93
Cthe_02107	thymidylate kinase	9.47	9.49	9.55	9.15	-0.08	0.34	-0.02	0.4	0.72	0.29	0.03	-0.6	0.51	0.5	1.47
Cthe_00428	NADH dehydrogenase (ubiquinone), 24 kD	12.98	13.33	12.92	12.66	0.06	0.67	-0.35	0.26	0.91	0.68	-1.07	-0.89	0.52	0.5	0.93
Cthe_02107	thymidylate kinase	9.47	9.49	9.55	9.15	-0.08	0.34	-0.02	0.4	0.72	0.29	0.03	-0.6	0.51	0.5	1.47
Cthe_00976	phospho-N-acetylmuramoyl-pentapeptide	10.55	10.61	10.95	9.44	-0.4	1.17	-0.06	1.51	0.28	1.27	-0.1	1.77	0.52	0.5	0.83
Cthe_02107	thymidylate kinase	9.47	9.49	9.55	9.15	-0.08	0.34	-0.02	0.4	0.72	0.29	0.03	-0.6	0.51	0.5	1.47
Cthe_00976	phospho-N-acetylmuramoyl-pentapeptide	10.55	10.61	10.95	9.44	-0.4	1.17	-0.06	1.51	0.28	1.27	-0.1	1.77	0.52	0.5	0.83
Cthe_00976	phospho-N-acetylmuramoyl-pentapeptide	10.55	10.61	10.95	9.44	-0.4	1.17	-0.06	1.51	0.28	1.27	-0.1	1.77	0.52	0.5	0.83
Cthe_00428	NADH dehydrogenase (ubiquinone), 24 kD	12.98	13.33	12.92	12.66	0.06	0.67	-0.35	0.26	0.91	0.68	-1.07	-0.89	0.52	0.5	0.93
Cthe_00904	protein-export membrane protein SecD	13.53	13.56	13.58	13.23	-0.05	0.33	-0.03	0.35	0.76	0.27	0	-0.7	0.5	0.49	1.31
Cthe_00399	protein of unknown function DUF477	9.92	10.26	10.31	9.33	-0.39	0.93	-0.34	0.98	0.3	0.99	-1.03	0.64	0.5	0.49	0.97
Cthe_01426	AzC-like protein	9.11	9.17	9.16	8.82	-0.05	0.35	-0.06	0.34	0.76	0.3	-0.1	-0.72	0.5	0.49	1.28
Cthe_00807	response regulator receiver modulated Ch	6.51	7.02	7.17	5.55	-0.66	1.47	-0.51	1.62	-0.07	1.63	-1.6	2	0.5	0.49	0.72
Cthe_01326	small GTP-binding protein	11.17	11.2	11.5	10.71	-0.33	0.49	-0.03	0.79	0.38	0.46	0	0.23	0.5	0.49	2.95
Cthe_00807	response regulator receiver modulated Ch	6.51	7.02	7.17	5.55	-0.66	1.47	-0.51	1.62	-0.07	1.63	-1.6	2	0.5	0.49	0.72
Cthe_00158	ribonuclease, Rne/Rng family	10.02	10.07	10.35	9.63	-0.33	0.44	-0.05	0.72	0.38	0.4	-0.07	0.09	0.5	0.49	5.5
Cthe_02523	hypothetical protein	10.68	10.48	10.43	10.35	0.25	0.13	0.2	0.08	1.16	0.04	0.77	-1.28	0.5	0.49	0.88
Cthe_00904	protein-export membrane protein SecD	13.53	13.56	13.58	13.23	-0.05	0.33	-0.03	0.35	0.76	0.27	0	-0.7	0.5	0.49	1.31
Cthe_00158	ribonuclease, Rne/Rng family	10.02	10.07	10.35	9.63	-0.33	0.44	-0.05	0.72	0.38	0.4	-0.07	0.09	0.5	0.49	5.5
Cthe_00807	response regulator receiver modulated Ch	6.51	7.02	7.17	5.55	-0.66	1.47	-0.51	1.62	-0.07	1.63	-1.6	2	0.5	0.49	0.72
Cthe_00212	Beta-glucosidase	11.82	11.99	11.9	11.52	-0.08	0.47	-0.17	0.38	0.72	0.44	-0.47	-0.64	0.49	0.48	1.21
Cthe_00677	phosphopentomutase	11.08	11.15	11.47	10.24	-0.39	0.91	-0.07	1.23	0.3	0.96	-0.13	1.17	0.49	0.48	0.97
Cthe_01777	amidohydrolase	11.25	11.17	11.33	10.88	-0.08	0.29	0.08	0.45	0.72	0.23	0.37	-0.49	0.49	0.48	1.4
Cthe_01757	peptidase M23B	12.54	12.48	12.57	12.2	-0.03	0.28	0.06	0.37	0.78	0.21	0.3	-0.66	0.49	0.48	1.27
Cthe_00461	gid protein	10.99	10.9	11.03	10.62	-0.04	0.28	0.09	0.41	0.77	0.21	0.4	-0.57	0.49	0.48	1.3
Cthe_01860	cell division ATP-binding protein FtsE	11.46	11.49	11.61	11.14	-0.15	0.35	-0.03	0.47	0.62	0.3	0	-0.45	0.49	0.48	1.74
Cthe_01053	L-lactate dehydrogenase	12.32	12.24	12.56	11.68	-0.24	0.56	0.08	0.88	0.5	0.55	0.37	0.43	0.49	0.48	1.49
Cthe_02594	zinc/iron permease	11.13	11.22	11.08	10.87	0.05	0.35	-0.09	0.21	0.89	0.3	-0.2	-1	0.49	0.48	1.05
Cthe_02614	hypothetical protein	11.25	11.25	11.6	10.29	-0.35	0.96	0	1.31	0.35	1.02	0.1	1.34	0.49	0.48	0.91
Cthe_01547	hypothetical protein	10.56	10.46	10.82	9.56	-0.26	0.9	0.1	1.26	0.47	0.95	0.43	1.23	0.49	0.48	0.92
Cthe_00165	hypothetical protein	11.66	11.73	12.04	10.9	-0.38	0.83	-0.07	1.14	0.31	0.87	-0.13	0.98	0.49	0.48	1.06
Cthe_01860	cell division ATP-binding protein FtsE	11.46	11.49	11.61	11.14	-0.15	0.35	-0.03	0.47	0.62	0.3	0	-0.45	0.49	0.48	1.74
Cthe_00212	Beta-glucosidase	11.82	11.99	11.9	11.52	-0.08	0.47	-0.17	0.38	0.72	0.44	-0.47	-0.64	0.49	0.48	1.21
Cthe_01053	L-lactate dehydrogenase	12.32	12.24	12.56	11.68	-0.24	0.56	0.08	0.88	0.5	0.55	0.37	0.43	0.49	0.48	1.49
Cthe_00677	phosphopentomutase	11.08	11.15	11.47	10.24	-0.39	0.91	-0.07	1.23	0.3	0.96	-0.13	1.17	0.49	0.48	0.97
Cthe_00677	phosphopentomutase	11.08	11.15	11.47	10.24	-0.39	0.91	-0.07	1.23	0.3	0.96	-0.13	1.17	0.49	0.48	0.97
Cthe_00212	Beta-glucosidase	11.82	11.99	11.9	11.52	-0.08	0.47	-0.17	0.38	0.72	0.44	-0.47	-0.64	0.49	0.48	1.21
Cthe_01053	L-lactate dehydrogenase	12.32	12.24	12.56	11.68	-0.24	0.56	0.08	0.88	0.5	0.55	0.37	0.43	0.49	0.48	1.49
Cthe_01053	L-lactate dehydrogenase	12.32	12.24	12.56	11.68	-0.24	0.56	0.08	0.88	0.5	0.55	0.37	0.43	0.49	0.48	1.49
Cthe_01053	L-lactate dehydrogenase	12.32	12.24	12.56	11.68	-0.24	0.56	0.08	0.88	0.5	0.55	0.37	0.43	0.49	0.48	1.49
Cthe_00677	phosphopentomutase	11.08	11.15	11.47	10.24	-0.39	0.91	-0.07	1.23	0.3	0.96	-0.13	1.17	0.49	0.48	0.97
Cthe_00212	Beta-glucosidase	11.82	11.99	11.9	11.52	-0.08	0.47	-0.17	0.38	0.72	0.44	-0.47	-0.64	0.49	0.48	1.21
Cthe_00677	phosphopentomutase	11.08	11.15	11.47	10.24	-0.39	0.91	-0.07	1.23	0.3	0.96	-0.13	1.17	0.49	0.48	0.97
Cthe_00677	phosphopentomutase	11.08	11.15	11.47	10.24	-0.39	0.91	-0.07	1.23	0.3	0.96	-0.13	1.17	0.49	0.48	0.97
Cthe_00231	Radical SAM	11.1	11.37	11.22	10.77	-0.12	0.6	-0.27	0.45	0.66	0.6	-0.8	-0.49	0.48	0.47	1.08
Cthe_02754	beta-lactamase-like protein	7.45	7.5	7.85	6.49	-0.4	1.01	-0.05	1.36	0.28	1.08	-0.07	1.45	0.48	0.47	0.87
Cthe_00137	glyceraldehyde-3-phosphate dehydrogenase	16.89	17.04	16.97	16.6	-0.08	0.44	-0.15	0.37	0.72	0.4	-0.4	-0.66	0.48	0.47	1.21
Cthe_01019	binding-protein-dependent transport syst	14.76	14.93	15.05	14.38	-0.29	0.55	-0.17	0.67	0.43	0.54	-0.47	-0.02	0.48	0.47	1.67
Cthe_01491	transcriptional regulator, PadR-like family	4.39	4.75	4.81	4.86	-0.42	-0.11	-0.36	-0.05	0.26	-0.25	-1.1	-1.55	0.48	0.47	0.22
Cthe_00488	type IV pilus assembly PilZ	5.29	4.75	5.7	4.86	-0.41	-0.11	0.54	0.84	0.27	-0.25	1.9	0.34	0.48	0.47	0.22
Cthe_00771	putative helix-turn-helix protein, YlxM/p1	11.37	11.7	11.75	10.83	-0.38	0.87	-0.33	0.92	0.31	0.92	-1	0.51	0.48	0.47	0.98
Cthe_01793	protein of unknown function DUF1624	8.71	8.84	8.77	8.43	-0.06	0.41	-0.13	0.34	0.74	0.37	-0.33	-0.72	0.48	0.47	1.19
Cthe_02631	Aminoacyl-tRNA hydrolase	9.31	9.35	9.66	8.79	-0.35	0.56	-0.04	0.87	0.35	0.55	-0.03	0.4	0.48	0.47	1.85
Cthe_02727	ribosomal protein S12	12.94	13.16	12.95	12.66	-0.01	0.5	-0.22	0.29	0.81	0.48	-0.63	-0.83	0.48	0.47	1.03
Cthe_02605	ATP synthase F1, delta subunit	9.58	9.58	9.75	9.25	-0.17	0.33	0	0.5	0.59	0.27	0.1	-0.38	0.48	0.47	1.88
Cthe_02727	ribosomal protein S12	12.94	13.16	12.95	12.66	-0.01	0.5	-0.22	0.29	0.81	0.48	-0.63	-0.83	0.48	0.47	1.03
Cthe_00137	glyceraldehyde-3-phosphate dehydrogenase	16.89	17.04	16.97	16.6	-0.08	0.44	-0.15	0.37	0.72	0.4	-0.4	-0.66	0.48	0.47	1.21
Cthe_01019	binding-protein-dependent transport syst	14.76	14.93	15.05	14.38	-0.29	0.55	-0.17	0.67	0.43	0.54	-0.47	-0.02	0.48	0.47	1.67
Cthe_02605	ATP synthase F1, delta subunit	9.58	9.58	9.75	9.25	-0.17	0.33	0	0.5</							



Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_01054	ATPase associated with various cellular	12.25	12.33	12.44	11.95	-0.19	0.38	-0.08	0.49	0.57	0.33	-0.17	-0.4	0.47	0.46	1.72
Cthe_00639	glycoside hydrolase, family 13-like protein	11.06	11.19	11.44	10.57	-0.38	0.62	-0.13	0.87	0.31	0.62	-0.33	0.4	0.47	0.46	1.52
Cthe_01305	Cupin 2, conserved barrel	10.01	9.92	10.25	9.39	-0.24	0.53	0.09	0.86	0.5	0.51	0.4	0.38	0.47	0.46	1.47
Cthe_02208	LexA DNA-binding region containing prote	13.9	13.82	13.55	13.74	0.35	0.08	0.08	-0.19	1.3	-0.02	0.37	-1.85	0.47	0.46	0.78
Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_02968	4Fe-4S ferredoxin, iron-sulfur binding	8.34	8.26	8.14	8.1	0.2	0.16	0.08	0.04	1.09	0.07	0.37	-1.36	0.47	0.46	0.88
Cthe_02599	CMP/dCMP deaminase, zinc-binding	11.9	12.09	12.1	11.57	-0.2	0.52	-0.19	0.53	0.55	0.5	-0.53	-0.32	0.47	0.46	1.36
Cthe_02208	LexA DNA-binding region containing prote	13.9	13.82	13.55	13.74	0.35	0.08	0.08	-0.19	1.3	-0.02	0.37	-1.85	0.47	0.46	0.78
Cthe_03154	hypothetical protein	6.6	6.54	6.54	6.32	0.06	0.22	0.06	0.22	0.91	0.14	0.3	-0.98	0.47	0.46	1.02
Cthe_02968	4Fe-4S ferredoxin, iron-sulfur binding	8.34	8.26	8.14	8.1	0.2	0.16	0.08	0.04	1.09	0.07	0.37	-1.36	0.47	0.46	0.88
Cthe_02936	ABC transporter related protein	7.29	7.23	7.29	6.98	0	0.25	0.06	0.31	0.82	0.18	0.3	-0.79	0.47	0.46	1.13
Cthe_01775	peptidase M22, glycoprotease	9.82	9.85	9.96	9.52	-0.14	0.33	-0.03	0.44	0.64	0.27	0	-0.51	0.47	0.46	1.55
Cthe_03115	hypothetical protein	8.77	8.79	9.11	8.21	-0.34	0.58	-0.02	0.9	0.36	0.57	0.03	0.47	0.47	0.46	1.63
Cthe_02936	ABC transporter related protein	7.29	7.23	7.29	6.98	0	0.25	0.06	0.31	0.82	0.18	0.3	-0.79	0.47	0.46	1.13
Cthe_02936	ABC transporter related protein	7.29	7.23	7.29	6.98	0	0.25	0.06	0.31	0.82	0.18	0.3	-0.79	0.47	0.46	1.13
Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_01054	ATPase associated with various cellular	12.25	12.33	12.44	11.95	-0.19	0.38	-0.08	0.49	0.57	0.33	-0.17	-0.4	0.47	0.46	1.72
Cthe_02599	CMP/dCMP deaminase, zinc-binding	11.9	12.09	12.1	11.57	-0.2	0.52	-0.19	0.53	0.55	0.5	-0.53	-0.32	0.47	0.46	1.36
Cthe_02208	LexA DNA-binding region containing prote	13.9	13.82	13.55	13.74	0.35	0.08	0.08	-0.19	1.3	-0.02	0.37	-1.85	0.47	0.46	0.78
Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_01054	ATPase associated with various cellular	12.25	12.33	12.44	11.95	-0.19	0.38	-0.08	0.49	0.57	0.33	-0.17	-0.4	0.47	0.46	1.72
Cthe_01054	ATPase associated with various cellular	12.25	12.33	12.44	11.95	-0.19	0.38	-0.08	0.49	0.57	0.33	-0.17	-0.4	0.47	0.46	1.72
Cthe_01054	ATPase associated with various cellular	12.25	12.33	12.44	11.95	-0.19	0.38	-0.08	0.49	0.57	0.33	-0.17	-0.4	0.47	0.46	1.72
Cthe_01054	ATPase associated with various cellular	12.25	12.33	12.44	11.95	-0.19	0.38	-0.08	0.49	0.57	0.33	-0.17	-0.4	0.47	0.46	1.72
Cthe_00325	NAD+ synthetase	10.57	10.61	10.9	10.24	-0.33	0.37	-0.04	0.66	0.38	0.32	-0.03	-0.04	0.47	0.46	11.29
Cthe_01054	ATPase associated with various cellular	12.25	12.33	12.44	11.95	-0.19	0.38	-0.08	0.49	0.57	0.33	-0.17	-0.4	0.47	0.46	1.72
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00161	protein of unknown function DUF464	13.11	12.96	13.13	12.71	-0.02	0.25	0.15	0.42	0.8	0.18	0.6	-0.55	0.46	0.45	1.14
Cthe_02604	ATP synthase F0, B subunit	11.22	11.11	11.29	10.84	-0.07	0.27	0.11	0.45	0.73	0.2	0.47	-0.49	0.46	0.45	1.27
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_01010	peptidase U32	11.73	11.95	11.75	11.46	-0.02	0.49	-0.22	0.29	0.8	0.46	-0.63	-0.83	0.46	0.45	1.01
Cthe_01060	Alr synthase related protein-like protein	11.21	11.1	11.44	10.51	-0.23	0.59	0.11	0.93	0.51	0.58	0.47	0.53	0.46	0.45	1.24
Cthe_02052	hypothetical protein	6.09	5.75	6.43	5.29	-0.64	0.46	0.34	1.44	-0.04	0.43	1.23	1.62	0.46	0.45	0.24
Cthe_02604	ATP synthase F0, B subunit	11.22	11.11	11.29	10.84	-0.07	0.27	0.11	0.45	0.73	0.2	0.47	-0.49	0.46	0.45	1.27
Cthe_02604	ATP synthase F0, B subunit	11.22	11.11	11.29	10.84	-0.07	0.27	0.11	0.45	0.73	0.2	0.47	-0.49	0.46	0.45	1.27
Cthe_02604	ATP synthase F0, B subunit	11.22	11.11	11.29	10.84	-0.07	0.27	0.11	0.45	0.73	0.2	0.47	-0.49	0.46	0.45	1.27
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_01010	peptidase U32	11.73	11.95	11.75	11.46	-0.02	0.49	-0.22	0.29	0.8	0.46	-0.63	-0.83	0.46	0.45	1.01
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_02604	ATP synthase F0, B subunit	11.22	11.11	11.29	10.84	-0.07	0.27	0.11	0.45	0.73	0.2	0.47	-0.49	0.46	0.45	1.27
Cthe_00234	AMP-dependent synthetase and ligase	12.78	13.28	12.9	12.37	-0.12	0.91	-0.5	0.53	0.66	0.96	-1.57	-0.32	0.46	0.45	0.83
Cthe_00350	signal peptidase I	11.73	11.5	11.7	11.23	0.03	0.27	0.23	0.47	0.86	0.2	0.87	-0.45	0.45	0.44	1.02
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_01844	transcriptional regulator, BadM/Rrf2 fami	9.99	10.03	10.35	9.67	-0.36	0.36	-0.04	0.68	0.34	0.31	-0.03	0	0.45	0.44	17.43
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_00638	FHA domain containing protein	10.73	10.95	11	10.37	-0.27	0.58	-0.22	0.63	0.46	0.57	-0.63	-0.11	0.45	0.44	1.3
Cthe_01289	hypothetical protein	9.86	9.58	9.82	9.27	0.04	0.31	0.28	0.55	0.88	0.25	1.03	-0.28	0.45	0.44	0.97
Cthe_00238	hypothetical protein	7.73	7.75	8.08	7.36	-0.35	0.39	-0.02	0.72	0.35	0.35	0.03	0.09	0.45	0.44	5.93
Cthe_02587	hypothetical protein	7.91	7.8	8.14	7.26	-0.23	0.54	0.11	0.88	0.51	0.52	0.47	0.43	0.45	0.44	1.3
Cthe_01837	hypothetical protein	11.19	11.06	11.41	10.49	-0.22	0.57	0.13	0.92	0.53	0.56	0.53	0.51	0.45	0.44	1.19
Cthe_00002	hypothetical protein	8.38	8.46	8.79	7.65	-0.41	0.81	-0.08	1.14	0.27	0.85	-0.17	0.98	0.45	0.44	1.02
Cthe_01036	hypothetical protein	9.33	9.36	9.8	8.06	-0.47	1.3	-0.03	1.74	0.19	1.43	0	2.26	0.45	0.44	0.73
Cthe_00350	signal peptidase I	11.73	11.5	11.7	11.23	0.03	0.27	0.23	0.47	0.86	0.2	0.87	-0.45	0.45	0.44	1.02
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_00372	glutamate synthase (NADPH), homotetra	10.89	11	10.84	10.66	0.05	0.34	-0.11	0.18	0.89	0.29	-0.27	-1.06	0.45	0.44	0.97
Cthe_01330	signal peptidase I	10.96	10.75	11.01	10.42	-0.05	0.33	0.21	0.59	0.76	0.27	0.8	-0.19	0.44	0.43	1.11
Cthe_00277	hypothetical protein	9.12	9.06	9.37	8.71	-0.25	0.35	0.06	0.66	0.49	0.3	0.3	-0.04	0.44	0.43	2.16
Cthe_00507	Exonuclease, RNase T and DNA polymeras	11	11.16	11.05	10.75	-0.05	0.41	-0.16	0.3	0.76	0.37	-0.43	-0.81	0.44	0.43	1.05
Cthe_01027	protein of unknown function DUF177	14.75	14.59	14.79	14.34	-0.04	0.25	0.16	0.45	0.77	0.18	0.63	-0.49	0.44	0.43	1.13
Cthe_03017	hydrogenase accessory protein HypB	10.38	10.44	10.16												



[illegible]



Cthe_00605	NLP/P60	14.3	14.42	14.49	14.03	-0.19	0.39	-0.12	0.46	0.57	0.35	-0.3	-0.47	0.42	0.41	1.36
Cthe_00583	response regulator receiver protein	11.64	11.56	11.78	11.3	-0.14	0.26	0.08	0.48	0.64	0.19	0.37	-0.43	0.42	0.41	1.34
Cthe_00621	putative translation initiation factor, aIF-2	12.38	12.49	12.44	12.14	-0.06	0.35	-0.11	0.3	0.74	0.3	-0.27	-0.81	0.42	0.41	1.06
Cthe_02947	prolyl-tRNA synthetase	10.03	10.01	10.29	9.7	-0.26	0.31	0.02	0.59	0.47	0.25	0.17	-0.19	0.42	0.41	2.37
Cthe_02955	hypothetical protein	0	1.58	0	0	1.58	-1.58	0	0.82	1.76	-5.17	-1.45	0.42	0.41	0.41	
Cthe_01192	hypothetical protein	8.6	8.61	8.98	7.86	-0.38	0.75	-0.01	1.12	0.31	0.77	0.07	0.94	0.42	0.41	1
Cthe_02947	prolyl-tRNA synthetase	10.03	10.01	10.29	9.7	-0.26	0.31	0.02	0.59	0.47	0.25	0.17	-0.19	0.42	0.41	2.37
Cthe_00621	putative translation initiation factor, aIF-2	12.38	12.49	12.44	12.14	-0.06	0.35	-0.11	0.3	0.74	0.3	-0.27	-0.81	0.42	0.41	1.06
Cthe_02947	prolyl-tRNA synthetase	10.03	10.01	10.29	9.7	-0.26	0.31	0.02	0.59	0.47	0.25	0.17	-0.19	0.42	0.41	2.37
Cthe_00621	putative translation initiation factor, aIF-2	12.38	12.49	12.44	12.14	-0.06	0.35	-0.11	0.3	0.74	0.3	-0.27	-0.81	0.42	0.41	1.06
Cthe_02947	prolyl-tRNA synthetase	10.03	10.01	10.29	9.7	-0.26	0.31	0.02	0.59	0.47	0.25	0.17	-0.19	0.42	0.41	2.37
Cthe_00605	NLP/P60	14.3	14.42	14.49	14.03	-0.19	0.39	-0.12	0.46	0.57	0.35	-0.3	-0.47	0.42	0.41	1.36
Cthe_02947	prolyl-tRNA synthetase	10.03	10.01	10.29	9.7	-0.26	0.31	0.02	0.59	0.47	0.25	0.17	-0.19	0.42	0.41	2.37
Cthe_00621	putative translation initiation factor, aIF-2	12.38	12.49	12.44	12.14	-0.06	0.35	-0.11	0.3	0.74	0.3	-0.27	-0.81	0.42	0.41	1.06
Cthe_02691	galactoside O-acetyltransferase	7.89	8.02	8.26	7.53	-0.37	0.49	-0.13	0.73	0.32	0.46	-0.33	0.11	0.41	0.4	1.83
Cthe_02232	polysaccharide biosynthesis protein CapD	4.7	4.39	5.29	4	-0.59	0.39	0.31	1.29	0.03	0.35	1.13	1.3	0.41	0.4	0.23
Cthe_00749	binding-protein-dependent transport syst	8.56	8.42	8.61	8.21	-0.05	0.21	0.14	0.4	0.76	0.13	0.57	-0.6	0.41	0.4	1.06
Cthe_02232	polysaccharide biosynthesis protein CapD	4.7	4.39	5.29	4	-0.59	0.39	0.31	1.29	0.03	0.35	1.13	1.3	0.41	0.4	0.23
Cthe_01477	deoxycytidine triphosphate deaminase	11.42	11.36	11.74	10.73	-0.32	0.63	0.06	1.01	0.39	0.63	0.3	0.7	0.41	0.4	1.11
Cthe_00157	hypothetical protein	8.95	9.19	9.2	8.63	-0.25	0.56	-0.24	0.57	0.49	0.55	-0.7	-0.23	0.41	0.4	1.14
Cthe_00563	Heptaprenyl diphosphate synthase compo	8.78	8.89	9.07	8.49	-0.29	0.4	-0.11	0.58	0.43	0.36	-0.27	-0.21	0.41	0.4	1.86
Cthe_00791	protein of unknown function DUF552	13.13	13.07	13.44	12.53	-0.31	0.54	0.06	0.91	0.41	0.52	0.3	0.49	0.41	0.4	1.31
Cthe_01481	membrane protein-like protein	6.81	6.75	6.98	6.48	-0.17	0.27	0.06	0.5	0.59	0.2	0.3	-0.38	0.41	0.4	1.46
Cthe_03019	4Fe-4S ferredoxin, iron-sulfur binding	9.17	9.34	8.95	9.03	0.22	0.31	-0.17	-0.08	1.12	0.25	-0.47	-1.62	0.41	0.4	0.77
Cthe_02007	RNA related	5	4.52	4.75	4.25	0.25	0.27	0.48	0.5	1.16	0.2	1.7	-0.38	0.41	0.4	0.77
Cthe_02170	hypothetical protein	9.96	10.17	10.38	9.49	-0.42	0.68	-0.21	0.89	0.26	0.69	-0.6	0.45	0.41	0.4	1.12
Cthe_00749	binding-protein-dependent transport syst	8.56	8.42	8.61	8.21	-0.05	0.21	0.14	0.4	0.76	0.13	0.57	-0.6	0.41	0.4	1.06
Cthe_01477	deoxycytidine triphosphate deaminase	11.42	11.36	11.74	10.73	-0.32	0.63	0.06	1.01	0.39	0.63	0.3	0.7	0.41	0.4	1.11
Cthe_01477	deoxycytidine triphosphate deaminase	11.42	11.36	11.74	10.73	-0.32	0.63	0.06	1.01	0.39	0.63	0.3	0.7	0.41	0.4	1.11
Cthe_00563	Heptaprenyl diphosphate synthase compo	8.78	8.89	9.07	8.49	-0.29	0.4	-0.11	0.58	0.43	0.36	-0.27	-0.21	0.41	0.4	1.86
Cthe_01477	deoxycytidine triphosphate deaminase	11.42	11.36	11.74	10.73	-0.32	0.63	0.06	1.01	0.39	0.63	0.3	0.7	0.41	0.4	1.11
Cthe_01477	deoxycytidine triphosphate deaminase	11.42	11.36	11.74	10.73	-0.32	0.63	0.06	1.01	0.39	0.63	0.3	0.7	0.41	0.4	1.11
Cthe_00563	Heptaprenyl diphosphate synthase compo	8.78	8.89	9.07	8.49	-0.29	0.4	-0.11	0.58	0.43	0.36	-0.27	-0.21	0.41	0.4	1.86
Cthe_02248	phosphoribosyltransferase	6.02	6.23	6.41	5.61	-0.39	0.62	-0.21	0.8	0.3	0.62	-0.6	0.26	0.4	0.39	1.2
Cthe_00289	DEAD_2	9.54	9.41	9.67	9.15	-0.13	0.26	0.13	0.52	0.65	0.19	0.53	-0.34	0.4	0.39	1.22
Cthe_01411	tryptophan synthase, alpha subunit	10.39	10.31	10.5	10.09	-0.11	0.22	0.08	0.41	0.68	0.14	0.37	-0.57	0.4	0.39	1.16
Cthe_00289	DEAD_2	9.54	9.41	9.67	9.15	-0.13	0.26	0.13	0.52	0.65	0.19	0.53	-0.34	0.4	0.39	1.22
Cthe_00809	CheW protein	6.02	6.04	6.51	4.81	-0.49	1.23	-0.02	1.7	0.16	1.35	0.03	2.17	0.4	0.39	0.71
Cthe_01250	phosphoribosylaminoimidazole carboxyla	9.94	10.1	10.08	9.7	-0.14	0.4	-0.16	0.38	0.64	0.36	-0.43	-0.64	0.4	0.39	1.08
Cthe_00809	CheW protein	6.02	6.04	6.51	4.81	-0.49	1.23	-0.02	1.7	0.16	1.35	0.03	2.17	0.4	0.39	0.71
Cthe_01076	protein of unknown function DUF881	9.65	9.36	10.21	9.07	-0.56	0.29	0.29	1.14	0.07	0.23	1.07	0.98	0.4	0.39	0.19
Cthe_03013	hydrogenase expression/formation protei	8.61	9.11	8.96	8.79	-0.35	0.32	-0.5	0.17	0.35	0.26	-1.57	-1.09	0.4	0.39	0.26
Cthe_01988	hypothetical protein	12.66	12.51	12.89	11.91	-0.23	0.6	0.15	0.98	0.51	0.6	0.6	0.64	0.4	0.39	1.02
Cthe_02454	Fibronectin, type III	4.64	4.95	5.09	4.95	-0.45	0	-0.31	0.14	0.22	-0.12	-0.93	-1.15	0.4	0.39	0.19
Cthe_00851	hypothetical protein	10.1	10.04	10.39	9.66	-0.29	0.38	0.06	0.73	0.43	0.33	0.3	0.11	0.4	0.39	1.93
Cthe_02417	Abortive infection protein	11.44	11.67	11.82	11.03	-0.38	0.64	-0.23	0.79	0.31	0.64	-0.67	0.23	0.4	0.39	1.14
Cthe_01941	putative regulatory protein, FmdB family	7.95	8.07	8.35	7.56	-0.4	0.51	-0.12	0.79	0.28	0.49	-0.3	0.23	0.4	0.39	1.7
Cthe_01250	phosphoribosylaminoimidazole carboxyla	9.94	10.1	10.08	9.7	-0.14	0.4	-0.16	0.38	0.64	0.36	-0.43	-0.64	0.4	0.39	1.08
Cthe_00289	DEAD_2	9.54	9.41	9.67	9.15	-0.13	0.26	0.13	0.52	0.65	0.19	0.53	-0.34	0.4	0.39	1.22
Cthe_01411	tryptophan synthase, alpha subunit	10.39	10.31	10.5	10.09	-0.11	0.22	0.08	0.41	0.68	0.14	0.37	-0.57	0.4	0.39	1.16
Cthe_01250	phosphoribosylaminoimidazole carboxyla	9.94	10.1	10.08	9.7	-0.14	0.4	-0.16	0.38	0.64	0.36	-0.43	-0.64	0.4	0.39	1.08
Cthe_00289	DEAD_2	9.54	9.41	9.67	9.15	-0.13	0.26	0.13	0.52	0.65	0.19	0.53	-0.34	0.4	0.39	1.22
Cthe_01411	tryptophan synthase, alpha subunit	10.39	10.31	10.5	10.09	-0.11	0.22	0.08	0.41	0.68	0.14	0.37	-0.57	0.4	0.39	1.16
Cthe_01250	phosphoribosylaminoimidazole carboxyla	9.94	10.1	10.08	9.7	-0.14	0.4	-0.16	0.38	0.64	0.36	-0.43	-0.64	0.4	0.39	1.08
Cthe_02740	ATP-dependent Clp protease, proteolytic s	13.46	13.46	13.81	13.14	-0.35	0.32	0	0.67	0.35	0.26	0.1	-0.02	0.39	0.38	4.86
Cthe_02055	hypothetical protein	11.9	12.04	12.34	11.39	-0.44	0.65	-0.14	0.95	0.23	0.65	-0.37	0.57	0.39	0.38	1.15
Cthe_02147	glycoside hydrolase, family 5	9.79	9.85	10.21	9.24	-0.42	0.61	-0.06	0.97	0.26	0.61	-0.1	0.62	0.39	0.38	1.2
Cthe_00553	transcriptional regulator, LysR family	8.58	8.69	8.77	8.33	-0.19	0.36	-0.11	0.44	0.57	0.31	-0.27	-0.51	0.39	0.38	1.28
Cthe_02517	acetolactate synthase, small subunit	10.98	11.28	11.58	11.13	-0.6	0.15	-0.3	0.45	0.01	0.06	-0.9	-0.49	0.39	0.38	0.07
Cthe_02131	hypothetical protein	9.34	8.84	9.7	8.91	-0.36	-0.07	0.5	0.79	0.34	-0.2	1.77	0.23	0.39	0.38	0.25
Cthe_01006	ribosomal protein S2	13.8	13.96	13.73	13.63	0.07	0.33	-0.16	0.1	0.92	0.27	-0.43	-1.23	0.39	0.38	0.84
Cthe_01026	ribosomal protein L32	12.76	12.68	12.99	12.38	-0.23	0.3	0.08	0.61	0.51	0.24	0.37	-0.15	0.39	0.38	1.6
Cthe_02740	ATP-dependent Clp protease, proteolytic s	13.46	13.46	13.81	13.14	-0.35	0.32	0	0.67	0.35	0.26	0.1	-0.02	0.39	0.38	4.86
Cthe_01239	hypothetical protein	8.7	8.75	9.09	8.4	-0.39	0.35	-0.05	0.69	0.3	0.3	-0.07	0.02	0.39	0.38	6.62
Cthe_00894	hypothetical protein	5.21	4.91	5.98	4.25	-0.77	0.66	0.3	1.73	-0.22	0.67	1.1	2.23	0.39	0.38	0.32
Cthe_01006	ribosomal protein S2	13.8	13.96	13.73	13.63	0.07	0.33	-0.16	0.1	0.92	0.27	-0.43	-1.23	0.39	0.38	0.84
Cthe_02517	acetolactate synthase, small subunit	10.98	11.28	11.58	11.13	-0.6	0.15	-0.3	0.45	0.01	0.06	-0.9	-0.49	0.39	0.38	0.07
Cthe_01006	ribosomal protein S2	13.8	13.96	13.73	13.63	0.07	0.33	-0.16	0.1	0.92	0.27	-0.43	-1.23	0.39	0.38	0.84
Cthe_01026	ribosomal protein L32	12.76	12.68	12.99	12.38	-0.23	0.3	0.08	0.61	0.51	0.24	0.37	-0.15	0.39	0.38	1.6
Cthe_02740	ATP-dependent Clp protease, proteolytic s	13.46	13.46	13.81	13.14	-0.35	0.32	0	0.67	0.35	0.26	0.1	-0.02	0.39	0.38	4.86
Cthe_02517	acetolactate synthase, small subunit	10.98	11.28	11.58	11.13	-0.6	0.15	-0.3	0.45	0.01	0.06	-0.9	-0.49	0.39	0.38	0.07
Cthe_02517	acetolactate synthase, small subunit	10.98	11.28	11.58	11.13	-0.6	0.15	-0.3	0.45	0.01	0.06	-0.9	-0.49	0.39	0.38	0.07
Cthe_02517	acetolactate synthase, small subunit	10.98	11.28	11.58	11.13	-0.6	0.15	-0.3	0.45	0.01	0.06	-0.9	-0.49	0.39	0.38	0.07
Cthe_02517	acetolactate synthase, small subunit	10.98	11.28	11.58	11.13	-0.6	0.15	-0.3	0.45	0.01	0.06	-0.9	-0.49	0.39	0.38	0.07
Cthe_02517	acetolactate synthase, small subunit	10.98	11.28	11.58	11.13	-0.6	0.15	-0.3	0.45	0.01	0.06	-0.9	-0.49	0.39	0.38	0.07
Cthe_02517	acetolactate synthase, small subunit															



Cthe_02941	2-C-methyl-D-erythritol 4-phosphate	8.08	7.91	8.22	7.62	-0.14	0.29	0.17	0.6	0.64	0.23	0.67	-0.17	0.38	0.37	1.12
Cthe_02209	3-isopropylmalate dehydrogenase	12.11	12.77	12.48	11.59	-0.37	1.18	-0.66	0.89	0.32	1.29	-2.1	0.45	0.38	0.37	0.7
Cthe_01542	glutamyl-tRNA(Gln) amidotransferase, C s	6.78	7.26	6.98	6.41	-0.2	0.85	-0.48	0.57	0.55	0.89	-1.5	-0.23	0.38	0.37	0.78
Cthe_00188	ribonuclease PH	9.31	9.46	9.99	8.01	-0.68	1.45	-0.15	1.98	-0.09	1.61	-0.4	2.77	0.38	0.37	0.65
Cthe_02941	2-C-methyl-D-erythritol 4-phosphate	8.08	7.91	8.22	7.62	-0.14	0.29	0.17	0.6	0.64	0.23	0.67	-0.17	0.38	0.37	1.12
Cthe_01542	glutamyl-tRNA(Gln) amidotransferase, C s	6.78	7.26	6.98	6.41	-0.2	0.85	-0.48	0.57	0.55	0.89	-1.5	-0.23	0.38	0.37	0.78
Cthe_00950	carbamoyl-phosphate synthase, small sub	8.93	8.95	9.01	8.71	-0.08	0.24	-0.02	0.3	0.72	0.17	0.03	-0.81	0.38	0.37	1.04
Cthe_02578	Ppx/GppA phosphatase	12.35	12.47	12.9	11.4	-0.55	1.07	-0.12	1.5	0.08	1.15	-0.3	1.74	0.38	0.37	0.74
Cthe_00950	carbamoyl-phosphate synthase, small sub	8.93	8.95	9.01	8.71	-0.08	0.24	-0.02	0.3	0.72	0.17	0.03	-0.81	0.38	0.37	1.04
Cthe_02941	2-C-methyl-D-erythritol 4-phosphate	8.08	7.91	8.22	7.62	-0.14	0.29	0.17	0.6	0.64	0.23	0.67	-0.17	0.38	0.37	1.12
Cthe_00950	carbamoyl-phosphate synthase, small sub	8.93	8.95	9.01	8.71	-0.08	0.24	-0.02	0.3	0.72	0.17	0.03	-0.81	0.38	0.37	1.04
Cthe_00188	ribonuclease PH	9.31	9.46	9.99	8.01	-0.68	1.45	-0.15	1.98	-0.09	1.61	-0.4	2.77	0.38	0.37	0.65
Cthe_00950	carbamoyl-phosphate synthase, small sub	8.93	8.95	9.01	8.71	-0.08	0.24	-0.02	0.3	0.72	0.17	0.03	-0.81	0.38	0.37	1.04
Cthe_00950	carbamoyl-phosphate synthase, small sub	8.93	8.95	9.01	8.71	-0.08	0.24	-0.02	0.3	0.72	0.17	0.03	-0.81	0.38	0.37	1.04
Cthe_01542	glutamyl-tRNA(Gln) amidotransferase, C s	6.78	7.26	6.98	6.41	-0.2	0.85	-0.48	0.57	0.55	0.89	-1.5	-0.23	0.38	0.37	0.78
Cthe_02209	3-isopropylmalate dehydrogenase	12.11	12.77	12.48	11.59	-0.37	1.18	-0.66	0.89	0.32	1.29	-2.1	0.45	0.38	0.37	0.7
Cthe_01542	glutamyl-tRNA(Gln) amidotransferase, C s	6.78	7.26	6.98	6.41	-0.2	0.85	-0.48	0.57	0.55	0.89	-1.5	-0.23	0.38	0.37	0.78
Cthe_02822	oxidoreductase-like protein	11.36	11.31	11.67	10.99	-0.31	0.32	0.05	0.68	0.41	0.26	0.27	0	0.37	0.36	2.04
Cthe_03018	hydrogenase expression/synthesis, HypA	9.05	9.12	8.78	8.98	0.27	0.14	-0.07	-0.2	1.19	0.05	-0.13	-1.87	0.37	0.36	0.72
Cthe_01867	carbamoyl-phosphate synthase, small sub	10.88	11.76	11.74	10.06	-0.86	1.7	-0.88	1.68	-0.34	1.9	-2.83	2.13	0.37	0.36	0.62
Cthe_00587	transposase, mutator type	6.48	5.58	6.34	5.32	0.14	0.26	0.9	1.02	1.01	0.19	3.1	0.72	0.37	0.36	0.37
Cthe_02832	transposase, mutator type	1	0		1	1	-1	1	-1	2.18	-1.31	3.43	-3.57	0.37	0.36	0.58
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimid	6.48	6.13	6.92	6.02	-0.44	0.11	0.35	0.9	0.23	0.01	1.27	0.47	0.37	0.36	0.19
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01938	D-alanine-D-alanine ligase	10.5	10.57	10.81	10.24	-0.31	0.33	-0.07	0.57	0.41	0.27	-0.13	-0.23	0.37	0.36	2.11
Cthe_01953	cell wall hydrolase, SleB	7.89	8.01	8.33	7.44	-0.44	0.57	-0.12	0.89	0.23	0.56	-0.3	0.45	0.37	0.36	1.27
Cthe_01867	carbamoyl-phosphate synthase, small sub	10.88	11.76	11.74	10.06	-0.86	1.7	-0.88	1.68	-0.34	1.9	-2.83	2.13	0.37	0.36	0.62
Cthe_03085	response regulator receiver protein	10.76	11.01	11.06	10.44	-0.3	0.57	-0.25	0.62	0.42	0.56	-0.73	-0.13	0.37	0.36	1.07
Cthe_00917	glutaminyl-tRNA synthetase	12.86	12.94	13.04	12.63	-0.18	0.31	-0.08	0.41	0.58	0.25	-0.17	-0.57	0.37	0.36	1.21
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01802	cobalt ABC transporter, inner membrane s	11.69	11.86	11.84	11.46	-0.15	0.4	-0.17	0.38	0.62	0.36	-0.47	-0.64	0.37	0.36	1.03
Cthe_01928	intein	1	0	0	1	1	-1	1	-1	2.18	-1.31	3.43	-3.57	0.37	0.36	0.58
Cthe_00264	hypothetical protein	4.25	3.91	3.81	4.17	0.44	-0.26	0.34	-0.36	1.42	-0.43	1.23	-2.21	0.37	0.36	0.67
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_00917	glutaminyl-tRNA synthetase	12.86	12.94	13.04	12.63	-0.18	0.31	-0.08	0.41	0.58	0.25	-0.17	-0.57	0.37	0.36	1.21
Cthe_01802	cobalt ABC transporter, inner membrane s	11.69	11.86	11.84	11.46	-0.15	0.4	-0.17	0.38	0.62	0.36	-0.47	-0.64	0.37	0.36	1.03
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01867	carbamoyl-phosphate synthase, small sub	10.88	11.76	11.74	10.06	-0.86	1.7	-0.88	1.68	-0.34	1.9	-2.83	2.13	0.37	0.36	0.62
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimid	6.48	6.13	6.92	6.02	-0.44	0.11	0.35	0.9	0.23	0.01	1.27	0.47	0.37	0.36	0.19
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimid	6.48	6.13	6.92	6.02	-0.44	0.11	0.35	0.9	0.23	0.01	1.27	0.47	0.37	0.36	0.19
Cthe_00917	glutaminyl-tRNA synthetase	12.86	12.94	13.04	12.63	-0.18	0.31	-0.08	0.41	0.58	0.25	-0.17	-0.57	0.37	0.36	1.21
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01867	carbamoyl-phosphate synthase, small sub	10.88	11.76	11.74	10.06	-0.86	1.7	-0.88	1.68	-0.34	1.9	-2.83	2.13	0.37	0.36	0.62
Cthe_01938	D-alanine-D-alanine ligase	10.5	10.57	10.81	10.24	-0.31	0.33	-0.07	0.57	0.41	0.27	-0.13	-0.23	0.37	0.36	2.11
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01953	cell wall hydrolase, SleB	7.89	8.01	8.33	7.44	-0.44	0.57	-0.12	0.89	0.23	0.56	-0.3	0.45	0.37	0.36	1.27
Cthe_01867	carbamoyl-phosphate synthase, small sub	10.88	11.76	11.74	10.06	-0.86	1.7	-0.88	1.68	-0.34	1.9	-2.83	2.13	0.37	0.36	0.62
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01867	carbamoyl-phosphate synthase, small sub	10.88	11.76	11.74	10.06	-0.86	1.7	-0.88	1.68	-0.34	1.9	-2.83	2.13	0.37	0.36	0.62
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01867	carbamoyl-phosphate synthase, small sub	10.88	11.76	11.74	10.06	-0.86	1.7	-0.88	1.68	-0.34	1.9	-2.83	2.13	0.37	0.36	0.62
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01297	Nicotinate-nucleotide--dimethylbenzimid	6.48	6.13	6.92	6.02	-0.44	0.11	0.35	0.9	0.23	0.01	1.27	0.47	0.37	0.36	0.19
Cthe_00917	glutaminyl-tRNA synthetase	12.86	12.94	13.04	12.63	-0.18	0.31	-0.08	0.41	0.58	0.25	-0.17	-0.57	0.37	0.36	1.21
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01938	D-alanine-D-alanine ligase	10.5	10.57	10.81	10.24	-0.31	0.33	-0.07	0.57	0.41	0.27	-0.13	-0.23	0.37	0.36	2.11
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01938	D-alanine-D-alanine ligase	10.5	10.57	10.81	10.24	-0.31	0.33	-0.07	0.57	0.41	0.27	-0.13	-0.23	0.37	0.36	2.11
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_02238	aldehyde dehydrogenase	7.41	7.2	7.55	6.81	-0.14	0.39	0.21	0.74	0.64	0.35	0.8	0.13	0.37	0.36	1.02
Cthe_01352	UDP-glucose 6-dehydrogenase	12.28	12.18	12.53	11.86	-0.25	0.32	0.1	0.67	0.49	0.26	0.43	-0.02	0.37	0.36	1.46
Cthe_01765	hypothetical protein	10.87	10.9	11.16	10.61	-0.29	0.29	-0.03	0.55	0.43	0.23	0	-0.28	0.36	0.35	1.98
Cthe_00335	hydrogenase large subunit-like protein	10.15	10.44	10.49	9.79	-0.34	0.65	-0.29	0.7	0.36	0.65	-0.87	0.04	0.36	0.35	0.97
Cthe_02073	amidohydrolase	8.99	9.24	9.5	8.45	-0.51	0.79	-0.25	1.05	0.14	0.82	-0.				



Cthe_01765	hypothetical protein	10.87	10.9	11.16	10.61	-0.29	0.29	-0.03	0.55	0.43	0.23	0	-0.28	0.36	0.35	1.98
Cthe_02075	protein of unknown function DUF28	11.67	11.37	11.66	11.12	0.01	0.25	0.3	0.54	0.84	0.18	1.1	-0.3	0.36	0.35	0.86
Cthe_02780	hypothetical protein	6.67	6.75	7.11	6.17	-0.44	0.58	-0.08	0.94	0.23	0.57	-0.17	0.55	0.36	0.35	1.21
Cthe_00769	ribosomal protein S16	9.36	9.98	9.94	9.44	-0.58	0.54	-0.62	0.5	0.04	0.52	-1.97	-0.38	0.36	0.35	0.3
Cthe_00435	cellulosome enzyme, dockerin type I	11.97	12.02	12.41	11.34	-0.44	0.68	-0.05	1.07	0.23	0.69	-0.07	0.83	0.36	0.35	0.99
Cthe_00818	hypothetical protein	8.29	8.06	8.43	7.61	-0.14	0.45	0.23	0.82	0.64	0.42	0.87	0.3	0.36	0.35	0.95
Cthe_02073	amidohydrolase	8.99	9.24	9.5	8.45	-0.51	0.79	-0.25	1.05	0.14	0.82	-0.73	0.79	0.36	0.35	0.88
Cthe_00769	ribosomal protein S16	9.36	9.98	9.94	9.44	-0.58	0.54	-0.62	0.5	0.04	0.52	-1.97	-0.38	0.36	0.35	0.3
Cthe_00107	Riboflavin synthase	9.73	9.78	9.81	9.54	-0.08	0.24	-0.05	0.27	0.72	0.17	-0.07	-0.87	0.36	0.35	0.96
Cthe_00107	Riboflavin synthase	9.73	9.78	9.81	9.54	-0.08	0.24	-0.05	0.27	0.72	0.17	-0.07	-0.87	0.36	0.35	0.96
Cthe_01817	urease, beta subunit	1	0	0	1.58	1	-1.58	1	-1.58	2.18	-2	3.43	-4.81	0.36	0.35	0.57
Cthe_02073	amidohydrolase	8.99	9.24	9.5	8.45	-0.51	0.79	-0.25	1.05	0.14	0.82	-0.73	0.79	0.36	0.35	0.88
Cthe_00107	Riboflavin synthase	9.73	9.78	9.81	9.54	-0.08	0.24	-0.05	0.27	0.72	0.17	-0.07	-0.87	0.36	0.35	0.96
Cthe_00107	Riboflavin synthase	9.73	9.78	9.81	9.54	-0.08	0.24	-0.05	0.27	0.72	0.17	-0.07	-0.87	0.36	0.35	0.96
Cthe_00107	Riboflavin synthase	9.73	9.78	9.81	9.54	-0.08	0.24	-0.05	0.27	0.72	0.17	-0.07	-0.87	0.36	0.35	0.96
Cthe_00107	Riboflavin synthase	9.73	9.78	9.81	9.54	-0.08	0.24	-0.05	0.27	0.72	0.17	-0.07	-0.87	0.36	0.35	0.96
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Cthe_00107	Riboflavin synthase	9.73	9.78	9.81	9.54	-0.08	0.24	-0.05	0.2							



Cthe_00723	tyrosyl-tRNA synthetase	12.53	12.59	12.83	12.3	-0.3	0.29	-0.06	0.53	0.42	0.23	-0.1	-0.32	0.33	0.32	1.62
Cthe_01556	binding-protein-dependent transport syst	13.45	13.73	13.83	13.11	-0.38	0.62	-0.28	0.72	0.31	0.62	-0.83	0.09	0.33	0.32	0.94
Cthe_00980	hypothetical protein	12.79	12.75	13.3	11.49	-0.51	1.26	0.04	1.81	0.14	1.38	0.23	2.4	0.33	0.32	0.65
Cthe_00497	RNA related	2.32	1.58	1.58	2.32	0.74	-0.74	0.74	-0.74	1.82	-1	2.57	-3.02	0.33	0.32	0.6
Cthe_00723	tyrosyl-tRNA synthetase	12.53	12.59	12.83	12.3	-0.3	0.29	-0.06	0.53	0.42	0.23	-0.1	-0.32	0.33	0.32	1.62
Cthe_00681	IMP dehydrogenase/GMP reductase	14.8	14.64	14.92	14.45	-0.12	0.19	0.16	0.47	0.66	0.11	0.63	-0.45	0.33	0.32	0.98
Cthe_00723	tyrosyl-tRNA synthetase	12.53	12.59	12.83	12.3	-0.3	0.29	-0.06	0.53	0.42	0.23	-0.1	-0.32	0.33	0.32	1.62
Cthe_01345	adenine phosphoribosyltransferase	11.1	11.19	11.59	10.49	-0.49	0.7	-0.09	1.1	0.16	0.71	-0.2	0.89	0.33	0.32	0.91
Cthe_01345	adenine phosphoribosyltransferase	11.1	11.19	11.59	10.49	-0.49	0.7	-0.09	1.1	0.16	0.71	-0.2	0.89	0.33	0.32	0.91
Cthe_02328	UDP-N-acetylglucosamine	11.75	11.74	11.98	11.51	-0.23	0.23	0.01	0.47	0.51	0.15	0.13	-0.45	0.33	0.32	1.29
Cthe_01345	adenine phosphoribosyltransferase	11.1	11.19	11.59	10.49	-0.49	0.7	-0.09	1.1	0.16	0.71	-0.2	0.89	0.33	0.32	0.91
Cthe_00723	tyrosyl-tRNA synthetase	12.53	12.59	12.83	12.3	-0.3	0.29	-0.06	0.53	0.42	0.23	-0.1	-0.32	0.33	0.32	1.62
Cthe_00681	IMP dehydrogenase/GMP reductase	14.8	14.64	14.92	14.45	-0.12	0.19	0.16	0.47	0.66	0.11	0.63	-0.45	0.33	0.32	0.98
Cthe_01345	adenine phosphoribosyltransferase	11.1	11.19	11.59	10.49	-0.49	0.7	-0.09	1.1	0.16	0.71	-0.2	0.89	0.33	0.32	0.91
Cthe_00681	IMP dehydrogenase/GMP reductase	14.8	14.64	14.92	14.45	-0.12	0.19	0.16	0.47	0.66	0.11	0.63	-0.45	0.33	0.32	0.98
Cthe_02328	UDP-N-acetylglucosamine	11.75	11.74	11.98	11.51	-0.23	0.23	0.01	0.47	0.51	0.15	0.13	-0.45	0.33	0.32	1.29
Cthe_00681	IMP dehydrogenase/GMP reductase	14.8	14.64	14.92	14.45	-0.12	0.19	0.16	0.47	0.66	0.11	0.63	-0.45	0.33	0.32	0.98
Cthe_00681	IMP dehydrogenase/GMP reductase	14.8	14.64	14.92	14.45	-0.12	0.19	0.16	0.47	0.66	0.11	0.63	-0.45	0.33	0.32	0.98
Cthe_02328	UDP-N-acetylglucosamine	11.75	11.74	11.98	11.51	-0.23	0.23	0.01	0.47	0.51	0.15	0.13	-0.45	0.33	0.32	1.29
Cthe_01345	adenine phosphoribosyltransferase	11.1	11.19	11.59	10.49	-0.49	0.7	-0.09	1.1	0.16	0.71	-0.2	0.89	0.33	0.32	0.91
Cthe_01480	hypothetical protein	3.91	3.91	4.09	3.7	-0.18	0.21	0	0.39	0.58	0.13	0.1	-0.62	0.32	0.31	1.08
Cthe_01202	major facilitator superfamily MFS_1	9.56	9.57	9.7	9.37	-0.14	0.2	-0.01	0.33	0.64	0.12	0.07	-0.74	0.32	0.31	1
Cthe_00786	3-dehydroquinate synthase	11.35	11.3	11.33	11.2	0.02	0.1	0.05	0.13	0.85	0	0.27	-1.17	0.32	0.31	0.8
Cthe_02350	cell wall hydrolase, SleB	6.52	6.44	6.82	6.15	-0.3	0.29	0.08	0.67	0.42	0.23	0.37	-0.02	0.32	0.31	1.47
Cthe_01383	Tetratricopeptide TPR_2	11.61	11.58	11.99	11.21	-0.38	0.37	0.03	0.78	0.31	0.32	0.2	0.21	0.32	0.31	1.75
Cthe_01850	hypothetical protein	5.25	5.29	5.73	4.52	-0.48	0.77	-0.04	1.21	0.18	0.8	-0.03	1.13	0.32	0.31	0.82
Cthe_00215	phenylalanyl-tRNA synthetase, beta subun	10.92	11.12	10.96	10.76	-0.04	0.36	-0.2	0.2	0.77	0.31	-0.57	-1.02	0.32	0.31	0.81
Cthe_01859	protein of unknown function DUF214	11.37	11.35	11.62	11.13	-0.25	0.22	0.02	0.49	0.49	0.14	0.17	-0.4	0.32	0.31	1.33
Cthe_01786	DNA repair protein Rada	10.78	10.96	11.27	10.34	-0.49	0.62	-0.18	0.93	0.16	0.62	-0.5	0.53	0.32	0.31	1
Cthe_03165	PpiC-type peptidyl-prolyl cis-trans isomera	11.21	11.18	11.63	10.47	-0.42	0.71	0.03	1.16	0.26	0.73	0.2	1.02	0.32	0.31	0.85
Cthe_00786	3-dehydroquinate synthase	11.35	11.3	11.33	11.2	0.02	0.1	0.05	0.13	0.85	0	0.27	-1.17	0.32	0.31	0.8
Cthe_01859	protein of unknown function DUF214	11.37	11.35	11.62	11.13	-0.25	0.22	0.02	0.49	0.49	0.14	0.17	-0.4	0.32	0.31	1.33
Cthe_00215	phenylalanyl-tRNA synthetase, beta subun	10.92	11.12	10.96	10.76	-0.04	0.36	-0.2	0.2	0.77	0.31	-0.57	-1.02	0.32	0.31	0.81
Cthe_00215	phenylalanyl-tRNA synthetase, beta subun	10.92	11.12	10.96	10.76	-0.04	0.36	-0.2	0.2	0.77	0.31	-0.57	-1.02	0.32	0.31	0.81
Cthe_00215	phenylalanyl-tRNA synthetase, beta subun	10.92	11.12	10.96	10.76	-0.04	0.36	-0.2	0.2	0.77	0.31	-0.57	-1.02	0.32	0.31	0.81
Cthe_00786	3-dehydroquinate synthase	11.35	11.3	11.33	11.2	0.02	0.1	0.05	0.13	0.85	0	0.27	-1.17	0.32	0.31	0.8
Cthe_00786	3-dehydroquinate synthase	11.35	11.3	11.33	11.2	0.02	0.1	0.05	0.13	0.85	0	0.27	-1.17	0.32	0.31	0.8
Cthe_00786	3-dehydroquinate synthase	11.35	11.3	11.33	11.2	0.02	0.1	0.05	0.13	0.85	0	0.27	-1.17	0.32	0.31	0.8
Cthe_00215	phenylalanyl-tRNA synthetase, beta subun	10.92	11.12	10.96	10.76	-0.04	0.36	-0.2	0.2	0.77	0.31	-0.57	-1.02	0.32	0.31	0.81
Cthe_02299	CRISPR-associated helicase Cas3	8.95	8.91	9.38	8.08	-0.43	0.83	0.04	1.3	0.24	0.87	0.23	1.32	0.31	0.3	0.77
Cthe_00450	Ribonucleotide reductase regulator NrdR-	9.36	9.15	9.91	9.01	-0.55	0.14	0.21	0.9	0.08	0.05	0.8	0.47	0.31	0.3	1.12
Cthe_02897	transcription elongation factor GreA	15.46	15.19	15.48	15.03	-0.02	0.16	0.27	0.45	0.8	0.07	1	-0.49	0.31	0.3	0.82
Cthe_01845	Homoserine O-succinyltransferase	12.15	12.06	12.42	11.8	-0.27	0.26	0.09	0.62	0.46	0.19	0.4	-0.13	0.31	0.3	1.34
Cthe_00022	8-amino-7-oxononanoate synthase	5.55	4.95	5.32	4.39	0.23	0.56	0.6	0.93	1.14	0.55	2.1	0.53	0.31	0.3	0.66
Cthe_01756	Putative virion core protein (lumpy skin di	13.42	13.5	13.87	13.11	-0.45	0.39	-0.08	0.76	0.22	0.35	-0.17	0.17	0.31	0.3	1.95
Cthe_02513	peptidase S1 and S6, chymotrypsin/Hap	8.6	8.75	8.84	8.39	-0.24	0.36	-0.15	0.45	0.5	0.31	-0.4	-0.49	0.31	0.3	1.06
Cthe_01989	RNA related	12.04	11.84	12.29	11.14	-0.25	0.7	0.2	1.15	0.49	0.71	0.77	1	0.31	0.3	0.78
Cthe_03226	copper amine oxidase-like protein	5.81	5.93	6.49	4.7	-0.68	1.23	-0.12	1.79	-0.09	1.35	-0.3	2.36	0.31	0.3	0.65
Cthe_01845	Homoserine O-succinyltransferase	12.15	12.06	12.42	11.8	-0.27	0.26	0.09	0.62	0.46	0.19	0.4	-0.13	0.31	0.3	1.34
Cthe_01845	Homoserine O-succinyltransferase	12.15	12.06	12.42	11.8	-0.27	0.26	0.09	0.62	0.46	0.19	0.4	-0.13	0.31	0.3	1.34
Cthe_00022	8-amino-7-oxononanoate synthase	5.55	4.95	5.32	4.39	0.23	0.56	0.6	0.93	1.14	0.55	2.1	0.53	0.31	0.3	0.66
Cthe_01845	Homoserine O-succinyltransferase	12.15	12.06	12.42	11.8	-0.27	0.26	0.09	0.62	0.46	0.19	0.4	-0.13	0.31	0.3	1.34
Cthe_00022	8-amino-7-oxononanoate synthase	5.55	4.95	5.32	4.39	0.23	0.56	0.6	0.93	1.14	0.55	2.1	0.53	0.31	0.3	0.66
Cthe_02126	binding-protein-dependent transport syst	10.54	10.67	11.28	9.31	-0.74	1.36	-0.13	1.97	-0.18	1.5	-0.33	2.74	0.3	0.29	0.62
Cthe_00181	Holliday junction DNA helicase RuvA	8.49	8.54	8.94	8.18	-0.45	0.36	-0.05	0.76	0.22	0.31	-0.07	0.17	0.3	0.29	2.35
Cthe_02418	ATPase	11.02	11.14	11.26	10.82	-0.24	0.32	-0.12	0.44	0.5	0.26	-0.3	-0.51	0.3	0.29	1.08
Cthe_00850		9.01	8.89	9.21	8.69	-0.2	0.2	0.12	0.52	0.55	0.12	0.5	-0.34	0.3	0.29	1.06
Cthe_01178	isochorismatase hydrolase	6.95	6.92	7.46	5.83	-0.51	1.09	0.03	1.63	0.14	1.18	0.2	2.02	0.3	0.29	0.67
Cthe_01380	response regulator receiver protein	10.88	10.77	11.18	10.42	-0.3	0.35	0.11	0.76	0.42	0.3	0.47	0.17	0.3	0.29	1.17
Cthe_02284	CheA signal transduction histidine kinases	7.6	7.59	7.89	7.36	-0.29	0.23	0.01	0.53	0.43	0.15	0.13	-0.32	0.3	0.29	1.5
Cthe_02589	hypothetical protein	10.75	10.83	10.9	10.58	-0.15	0.25	-0.08	0.32	0.62	0.18	-0.17	-0.77	0.3	0.29	0.93
Cthe_00203	response regulator receiver and ANTAR d	7.74	8.13	8.31	7.82	-0.57	0.31	-0.39	0.49	0.05	0.25	-1.2	-0.4	0.3	0.29	0.23
Cthe_01380	response regulator receiver protein	10.88	10.77	11.18	10.42	-0.3	0.35	0.11	0.76	0.42	0.3	0.47	0.17	0.3	0.29	1.17
Cthe_02284	CheA signal transduction histidine kinases	7.6	7.59	7.89	7.36	-0.29	0.23	0.01	0.53	0.43	0.15	0.13	-0.32	0.3	0.29	1.5
Cthe_01514	protein of unknown function DUF125,	9	9.11	9.21	8.81	-0.21	0.3	-0.11	0.4	0.54	0.24	-0.27	-0.6	0.3	0.29	1.02
Cthe_00094	Septum formation topological specificity f	11.1	11.06	11.45	10.79	-0.35	0.27	0.04	0.66	0.35	0.2	0.23	-0.04	0.3	0.29	1.96
Cthe_00101	iron-containing alcohol dehydrogenase	12.04	12.03	12.45	11.67	-0.41	0.36	0.01	0.78	0.27	0.31	0.13	0.21	0.3	0.29	1.89
Cthe_01763	ABC transporter related protein	9.84	9.83	10.07	9.62	-0.23	0.21	0.01	0.45	0.51	0.13	0.13	-0.49	0.3	0.29	1.18
Cthe_02734	VanW	5.58	5.36	6.23	4.95	-0.65	0.41	0.22	1.28	-0.05	0.37	0.83	1.28	0.3	0.29	0.28
Cthe_01322	chaperone protein DnaK	10.61	10.35	11.29	9.7	-0.68	0.65	0.26	1.59	-0.09	0.65	0.97	1.94	0.3	0.29	0.34
Cthe_03188	copper amine oxidase-like protein	13.47	13.51	13.74	13.26	-0.27	0.25	-0.04	0.48	0.46	0.18	-0.03	-0.43	0.3	0.29	1.3
Cthe_01763	ABC transporter related protein	9.84	9.83	10.07	9.62	-0.23	0.21	0.01	0.45	0.51	0.13	0.13	-0.49	0.3	0.29	1.18
Cthe_02126	binding-protein-dependent transport syst	10.54	10.67	11.28	9.31	-0.74	1.36	-0.13	1.97	-0.18	1.5	-0.33	2.74	0.3	0.29	0.62
Cthe_02284	CheA signal transduction histidine kinases	7.6	7.59	7.89	7.36	-0.29	0.23	0.01	0.53	0.43	0.15	0.13	-0.32	0.3	0.29	1.5
Cthe_00850		9.01	8.89	9.21	8.69	-0.2	0.2	0.12	0.52	0.55	0.12	0.5	-0.34	0.3	0.29	



Cthe_01541	glutamyl-tRNA(Gln) amidotransferase, A s	7.71	8.41	8.01	7.76	-0.3	0.65	-0.7	0.25	0.42	0.65	-2.23	-0.91	0.29	0.28	0.37
Cthe_01182	protein of unknown function DUF58	10.64	10.68	11.1	10.22	-0.46	0.46	-0.04	0.88	0.2	0.43	-0.03	0.43	0.28	0.27	1.25
Cthe_02524	transcriptional regulator, BadM/Rrf2 fami	8.42	8.21	8.5	8.1	-0.08	0.11	0.21	0.4	0.72	0.01	0.8	-0.6	0.28	0.27	0.82
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransf	13.51	13.77	14.15	13.61	-0.64	0.16	-0.26	0.54	-0.04	0.07	-0.77	-0.3	0.28	0.27	0.11
Cthe_01346	single-stranded-DNA-specific exonuclease	12.52	12.55	12.98	12.06	-0.46	0.49	-0.03	0.92	0.2	0.46	0	0.51	0.28	0.27	1.12
Cthe_02983	methyl-accepting chemotaxis sensory tran	7.39	7.17	7.4	7.13	-0.01	0.04	0.22	0.27	0.81	-0.07	0.83	-0.87	0.28	0.27	0.77
Cthe_00189	non-canonical purine NTP pyrophosphata	10.76	10.77	11.26	9.95	-0.5	0.82	-0.01	1.31	0.15	0.86	0.07	1.34	0.28	0.27	0.74
Cthe_00375	GMP synthase, large subunit	13.49	13.32	13.44	13.34	0.05	-0.02	0.17	0.1	0.89	-0.14	0.67	-1.23	0.28	0.27	0.73
Cthe_02983	methyl-accepting chemotaxis sensory tran	7.39	7.17	7.4	7.13	-0.01	0.04	0.22	0.27	0.81	-0.07	0.83	-0.87	0.28	0.27	0.77
Cthe_00847	translation elongation factor P (EF-P)	13.01	12.96	13.29	12.76	-0.28	0.2	0.05	0.53	0.45	0.12	0.27	-0.32	0.28	0.27	1.26
Cthe_02264	H+-transporting two-sector ATPase, E sub	9.86	9.92	10.33	9.49	-0.47	0.43	-0.06	0.84	0.19	0.39	-0.1	0.34	0.28	0.27	1.39
Cthe_03170	ABC transporter related protein	5.98	5.75	6.67	5.17	-0.69	0.58	0.23	1.5	-0.11	0.57	0.87	1.74	0.28	0.27	0.34
Cthe_00857	protein of unknown function DUF107	10.74	10.77	11.14	10.52	-0.4	0.25	-0.03	0.62	0.28	0.18	0	-0.13	0.28	0.27	2.91
Cthe_02276	AAA ATPase, central region	12.58	12.68	12.68	12.44	-0.1	0.24	-0.1	0.24	0.69	0.17	-0.23	-0.94	0.28	0.27	0.83
Cthe_01002	hypothetical protein	9.31	9.33	9.6	9.11	-0.29	0.22	-0.02	0.49	0.43	0.14	0.03	-0.4	0.28	0.27	1.28
Cthe_00361	hypothetical protein	12.22	12.11	12.55	11.62	-0.33	0.49	0.11	0.93	0.38	0.46	0.47	0.53	0.28	0.27	0.96
Cthe_01407	hypothetical protein	4.09	4.25	3.81	4.09	0.28	0.16	-0.16	-0.28	1.2	0.07	-0.43	-2.04	0.28	0.27	0.66
Cthe_00938	regulatory protein, DeoR	14.16	14.02	14.41	13.75	-0.25	0.27	0.14	0.66	0.49	0.2	0.57	-0.04	0.28	0.27	1.05
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransf	13.51	13.77	14.15	13.61	-0.64	0.16	-0.26	0.54	-0.04	0.07	-0.77	-0.3	0.28	0.27	0.11
Cthe_03170	ABC transporter related protein	5.98	5.75	6.67	5.17	-0.69	0.58	0.23	1.5	-0.11	0.57	0.87	1.74	0.28	0.27	0.34
Cthe_02264	H+-transporting two-sector ATPase, E sub	9.86	9.92	10.33	9.49	-0.47	0.43	-0.06	0.84	0.19	0.39	-0.1	0.34	0.28	0.27	1.39
Cthe_00375	GMP synthase, large subunit	13.49	13.32	13.44	13.34	0.05	-0.02	0.17	0.1	0.89	-0.14	0.67	-1.23	0.28	0.27	0.73
Cthe_02264	H+-transporting two-sector ATPase, E sub	9.86	9.92	10.33	9.49	-0.47	0.43	-0.06	0.84	0.19	0.39	-0.1	0.34	0.28	0.27	1.39
Cthe_00189	non-canonical purine NTP pyrophosphata	10.76	10.77	11.26	9.95	-0.5	0.82	-0.01	1.31	0.15	0.86	0.07	1.34	0.28	0.27	0.74
Cthe_01346	single-stranded-DNA-specific exonuclease	12.52	12.55	12.98	12.06	-0.46	0.49	-0.03	0.92	0.2	0.46	0	0.51	0.28	0.27	1.12
Cthe_00375	GMP synthase, large subunit	13.49	13.32	13.44	13.34	0.05	-0.02	0.17	0.1	0.89	-0.14	0.67	-1.23	0.28	0.27	0.73
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransf	13.51	13.77	14.15	13.61	-0.64	0.16	-0.26	0.54	-0.04	0.07	-0.77	-0.3	0.28	0.27	0.11
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransf	13.51	13.77	14.15	13.61	-0.64	0.16	-0.26	0.54	-0.04	0.07	-0.77	-0.3	0.28	0.27	0.11
Cthe_01797	3-phosphoshikimate 1-carboxyvinyltransf	13.51	13.77	14.15	13.61	-0.64	0.16	-0.26	0.54	-0.04	0.07	-0.77	-0.3	0.28	0.27	0.11
Cthe_00375	GMP synthase, large subunit	13.49	13.32	13.44	13.34	0.05	-0.02	0.17	0.1	0.89	-0.14	0.67	-1.23	0.28	0.27	0.73
Cthe_00375	GMP synthase, large subunit	13.49	13.32	13.44	13.34	0.05	-0.02	0.17	0.1	0.89	-0.14	0.67	-1.23	0.28	0.27	0.73
Cthe_02264	H+-transporting two-sector ATPase, E sub	9.86	9.92	10.33	9.49	-0.47	0.43	-0.06	0.84	0.19	0.39	-0.1	0.34	0.28	0.27	1.39
Cthe_01008	aminodeoxychorismate lyase	12.43	12.58	12.71	12.24	-0.28	0.34	-0.15	0.47	0.45	0.29	-0.4	-0.45	0.27	0.26	1.01
Cthe_01018	binding-protein-dependent transport syst	15.18	15.38	15.53	14.94	-0.35	0.44	-0.2	0.59	0.35	0.4	-0.57	-0.19	0.27	0.26	1.01
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_00814	DNA repair protein RecN	10.2	10.23	10.66	9.88	-0.46	0.35	-0.03	0.78	0.2	0.3	0	0.21	0.27	0.26	1.95
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01937	glutamate racemase	10.44	10.58	10.69	10.26	-0.25	0.32	-0.14	0.43	0.49	0.26	-0.37	-0.53	0.27	0.26	0.98
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B s	8.08	8.32	8.58	7.71	-0.5	0.61	-0.24	0.87	0.15	0.61	-0.7	0.4	0.27	0.26	0.89
Cthe_00613	thiamine pyrophosphate enzyme-like TPP	13	13.12	13.27	12.82	-0.27	0.3	-0.12	0.45	0.46	0.24	-0.3	-0.49	0.27	0.26	1.03
Cthe_01979	intein	10.79	10.75	11.23	10.08	-0.44	0.67	0.04	1.15	0.23	0.68	0.23	1	0.27	0.26	0.79
Cthe_01645	conserved hypothetical phage-associated	3.7	4.75	4.64	3	-0.94	1.75	-1.05	1.64	-0.45	1.96	-3.4	2.04	0.27	0.26	0.58
Cthe_00271	type 3a, cellulose-binding	11.86	12.18	12.39	11.45	-0.53	0.73	-0.32	0.94	0.11	0.75	-0.97	0.55	0.27	0.26	0.77
Cthe_00613	thiamine pyrophosphate enzyme-like TPP	13	13.12	13.27	12.82	-0.27	0.3	-0.12	0.45	0.46	0.24	-0.3	-0.49	0.27	0.26	1.03
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01018	binding-protein-dependent transport syst	15.18	15.38	15.53	14.94	-0.35	0.44	-0.2	0.59	0.35	0.4	-0.57	-0.19	0.27	0.26	1.01
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B s	8.08	8.32	8.58	7.71	-0.5	0.61	-0.24	0.87	0.15	0.61	-0.7	0.4	0.27	0.26	0.89
Cthe_00613	thiamine pyrophosphate enzyme-like TPP	13	13.12	13.27	12.82	-0.27	0.3	-0.12	0.45	0.46	0.24	-0.3	-0.49	0.27	0.26	1.03
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B s	8.08	8.32	8.58	7.71	-0.5	0.61	-0.24	0.87	0.15	0.61	-0.7	0.4	0.27	0.26	0.89
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_01937	glutamate racemase	10.44	10.58	10.69	10.26	-0.25	0.32	-0.14	0.43	0.49	0.26	-0.37	-0.53	0.27	0.26	0.98
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01937	glutamate racemase	10.44	10.58	10.69	10.26	-0.25	0.32	-0.14	0.43	0.49	0.26	-0.37	-0.53	0.27	0.26	0.98
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01937	glutamate racemase	10.44	10.58	10.69	10.26	-0.25	0.32	-0.14	0.43	0.49	0.26	-0.37	-0.53	0.27	0.26	0.98
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B s	8.08	8.32	8.58	7.71	-0.5	0.61	-0.24	0.87	0.15	0.61	-0.7	0.4	0.27	0.26	0.89
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01540	glutamyl-tRNA(Gln) amidotransferase, B s	8.08	8.32	8.58	7.71	-0.5	0.61	-0.24	0.87	0.15	0.61	-0.7	0.4	0.27	0.26	0.89
Cthe_01937	glutamate racemase	10.44	10.58	10.69	10.26	-0.25	0.32	-0.14	0.43	0.49	0.26	-0.37	-0.53	0.27	0.26	0.98
Cthe_02714	acetolactate synthase, large subunit,	12.22	12.7	12.81	12.26	-0.59	0.44	-0.48	0.55	0.03	0.4	-1.5	-0.28	0.27	0.26	0.3
Cthe_01937	glutamate racemase	10.44	10.58	10.69	10.26	-0.25	0.32	-0.14	0.43	0.49	0.26	-0.37	-0.53	0.27	0.26	0.98
Cthe_01866	acetylornithine and succinylornithine	10.85	11.56	11.75	10.18	-0.9	1.38	-0.71	1.57	-0.39	1.52	-2.27	1.89	0.27	0.26	0.6
Cthe_00564	Trans-hexaprenyltranstransferase	10.33	10.39	10.44	10.21	-0.11	0.18	-0.06	0.23	0.68	0.1	-0.1	-0.96	0.26	0.25	0.81
Cthe_01536	ABC transporter related protein	6.23	6.55	6.75	6.3	-0.52	0.25	-0.32	0.45	0.12	0.18	-0.97	-0.49	0.2		



Cthe_02791	binding-protein-dependent transport syst	2	1.58	2.32	1.58	-0.32	0	0.42	0.74	0.39	-0.12	1.5	0.13	0.25	0.24	0.31
Cthe_02964	binding-protein-dependent transport syst	7.85	7.73	7.69	7.85	0.16	-0.12	0.12	-0.16	1.04	-0.26	0.5	-1.79	0.25	0.24	0.66
Cthe_02675	hypothetical protein	11.65	11.7	12.21	10.85	-0.56	0.85	-0.05	1.36	0.07	0.89	-0.07	1.45	0.25	0.24	0.7
Cthe_00653	putative transcriptional regulator, CopG fa	13.39	13.34	13.77	13.06	-0.38	0.28	0.05	0.71	0.31	0.21	0.27	0.06	0.25	0.24	1.54
Cthe_02791	binding-protein-dependent transport syst	2	1.58	2.32	1.58	-0.32	0	0.42	0.74	0.39	-0.12	1.5	0.13	0.25	0.24	0.31
Cthe_00646	anaerobic ribonucleoside-triphosphate re	12.74	12.49	13.21	12.35	-0.47	0.14	0.25	0.86	0.19	0.05	0.93	0.38	0.25	0.24	0.22
Cthe_01384	FoIC bifunctional protein	10.39	10.53	10.76	10.18	-0.37	0.35	-0.14	0.58	0.32	0.3	-0.37	-0.21	0.25	0.24	1.17
Cthe_00646	anaerobic ribonucleoside-triphosphate re	12.74	12.49	13.21	12.35	-0.47	0.14	0.25	0.86	0.19	0.05	0.93	0.38	0.25	0.24	0.22
Cthe_01513	DNA adenine methylase	8.65	8.65	9.1	8.32	-0.45	0.33	0	0.78	0.22	0.27	0.1	0.21	0.25	0.24	1.7
Cthe_02363	methyltransferase GidB	10.36	10.28	10.38	10.27	-0.02	0.01	0.08	0.11	0.8	-0.11	0.37	-1.21	0.25	0.24	0.73
Cthe_01384	FoIC bifunctional protein	10.39	10.53	10.76	10.18	-0.37	0.35	-0.14	0.58	0.32	0.3	-0.37	-0.21	0.25	0.24	1.17
Cthe_01384	FoIC bifunctional protein	10.39	10.53	10.76	10.18	-0.37	0.35	-0.14	0.58	0.32	0.3	-0.37	-0.21	0.25	0.24	1.17
Cthe_01268	histidine kinase	4.25	3.81	4.25	3.17	0	0.64	0.44	1.08	0.82	0.64	1.57	0.85	0.25	0.24	0.66
Cthe_00646	anaerobic ribonucleoside-triphosphate re	12.74	12.49	13.21	12.35	-0.47	0.14	0.25	0.86	0.19	0.05	0.93	0.38	0.25	0.24	0.22
Cthe_00261	HAD-superfamily hydrolase, subfamily IA,	8.67	8.41	8.75	8.29	-0.08	0.12	0.26	0.46	0.72	0.02	0.97	-0.47	0.25	0.24	0.76
Cthe_00261	HAD-superfamily hydrolase, subfamily IA,	8.67	8.41	8.75	8.29	-0.08	0.12	0.26	0.46	0.72	0.02	0.97	-0.47	0.25	0.24	0.76
Cthe_01384	FoIC bifunctional protein	10.39	10.53	10.76	10.18	-0.37	0.35	-0.14	0.58	0.32	0.3	-0.37	-0.21	0.25	0.24	1.17
Cthe_01384	FoIC bifunctional protein	10.39	10.53	10.76	10.18	-0.37	0.35	-0.14	0.58	0.32	0.3	-0.37	-0.21	0.25	0.24	1.17
Cthe_01384	FoIC bifunctional protein	10.39	10.53	10.76	10.18	-0.37	0.35	-0.14	0.58	0.32	0.3	-0.37	-0.21	0.25	0.24	1.17
Cthe_02270	ABC transporter related protein	9.79	9.79	9.82	9.72	-0.03	0.07	0	0.1	0.78	-0.04	0.1	-1.23	0.24	0.23	0.72
Cthe_01963	glycoside hydrolase, family 10	13.45	13.56	14.05	12.78	-0.6	0.78	-0.11	1.27	0.01	0.81	-0.27	1.26	0.24	0.23	0.71
Cthe_01092	hypothetical protein	9.86	9.96	10.35	9.58	-0.49	0.38	-0.1	0.77	0.16	0.33	-0.23	0.19	0.24	0.23	1.4
Cthe_02792	Phenylacetate-CoA ligase	2.32	2.58	2.58	2.58	-0.26	0	-0.26	0	0.47	-0.12	-0.77	-1.45	0.24	0.23	0.34
Cthe_00039	methyl-accepting chemotaxis sensory tran	6.75	6.61	7.39	6.38	-0.64	0.23	0.14	1.01	-0.04	0.15	0.57	0.7	0.24	0.23	0.2
Cthe_00039	methyl-accepting chemotaxis sensory tran	6.75	6.61	7.39	6.38	-0.64	0.23	0.14	1.01	-0.04	0.15	0.57	0.7	0.24	0.23	0.2
Cthe_03118	hemerythrin-like metal-binding protein	11.55	11.72	11.95	11.32	-0.4	0.4	-0.17	0.63	0.28	0.36	-0.47	-0.11	0.24	0.23	1.07
Cthe_01762	efflux transporter, RND family, MFP subun	10.36	10.41	10.67	10.19	-0.31	0.22	-0.05	0.48	0.41	0.14	-0.07	0.43	0.24	0.23	1.13
Cthe_01963	glycoside hydrolase, family 10	13.45	13.56	14.05	12.78	-0.6	0.78	-0.11	1.27	0.01	0.81	-0.27	1.26	0.24	0.23	0.71
Cthe_02792	Phenylacetate-CoA ligase	2.32	2.58	2.58	2.58	-0.26	0	-0.26	0	0.47	-0.12	-0.77	-1.45	0.24	0.23	0.34
Cthe_02792	Phenylacetate-CoA ligase	2.32	2.58	2.58	2.58	-0.26	0	-0.26	0	0.47	-0.12	-0.77	-1.45	0.24	0.23	0.34
Cthe_02792	Phenylacetate-CoA ligase	2.32	2.58	2.58	2.58	-0.26	0	-0.26	0	0.47	-0.12	-0.77	-1.45	0.24	0.23	0.34
Cthe_01024	small GTP-binding protein	10.93	10.93	11.3	10.73	-0.37	0.2	0	0.57	0.32	0.12	0.1	-0.23	0.23	0.22	1.55
Cthe_02109	copper amine oxidase-like protein	11.73	11.79	12.16	11.54	-0.43	0.25	-0.06	0.62	0.24	0.18	-0.1	-0.13	0.23	0.22	2.08
Cthe_01810	peptidase M56, BlaR1	5.88	5.73	6.13	5.52	-0.25	0.21	0.15	0.61	0.49	0.13	0.6	-0.15	0.23	0.22	0.93
Cthe_02404	transcriptional regulator, GntR family	10.65	10.64	10.91	10.49	-0.26	0.15	0.01	0.42	0.47	0.06	0.13	-0.55	0.23	0.22	0.95
Cthe_01316	4'-phosphopantetheinyl transferase	8.85	8.8	8.77	8.84	0.08	-0.04	0.05	-0.07	0.93	-0.17	0.27	-1.66	0.23	0.22	0.66
Cthe_00266	methyl-accepting chemotaxis sensory tran	9.66	9.74	10.05	9.48	-0.39	0.26	-0.08	0.57	0.3	0.19	-0.17	-0.23	0.23	0.22	1.41
Cthe_00266	methyl-accepting chemotaxis sensory tran	9.66	9.74	10.05	9.48	-0.39	0.26	-0.08	0.57	0.3	0.19	-0.17	-0.23	0.23	0.22	1.41
Cthe_01293	metal dependent phosphohydrolase	10.73	10.99	11.05	10.51	-0.32	0.48	-0.26	0.54	0.39	0.45	-0.77	-0.3	0.23	0.22	0.82
Cthe_01810	peptidase M56, BlaR1	5.88	5.73	6.13	5.52	-0.25	0.21	0.15	0.61	0.49	0.13	0.6	-0.15	0.23	0.22	0.93
Cthe_02722	ribosomal protein L10	13.15	13.41	13.34	13.47	-0.19	-0.06	-0.26	-0.13	0.57	-0.19	-0.77	-1.72	0.23	0.22	0.36
Cthe_03196	Uncharacterized conserved protein UCP03	11.87	11.64	11.92	11.66	-0.05	-0.02	0.23	0.26	0.76	-0.14	0.87	-0.89	0.23	0.22	0.71
Cthe_01173	type IV pilus assembly PilZ	10.83	11.09	11.41	10.43	-0.58	0.66	-0.26	0.98	0.04	0.67	-0.77	0.64	0.23	0.22	0.76
Cthe_02722	ribosomal protein L10	13.15	13.41	13.34	13.47	-0.19	-0.06	-0.26	-0.13	0.57	-0.19	-0.77	-1.72	0.23	0.22	0.36
Cthe_02722	ribosomal protein L10	13.15	13.41	13.34	13.47	-0.19	-0.06	-0.26	-0.13	0.57	-0.19	-0.77	-1.72	0.23	0.22	0.36
Cthe_01581	inner-membrane translocator	3.17	4	4.09	2.58	-0.92	1.42	-0.83	1.51	-0.42	1.57	-2.67	1.77	0.22	0.21	0.58
Cthe_01288	two component transcriptional regulator,	11.08	11.01	11.34	10.88	-0.26	0.13	0.07	0.46	0.47	0.04	0.33	-0.47	0.22	0.21	0.93
Cthe_02095	hydrolase, TatD family	10.38	10.35	10.67	10.2	-0.29	0.15	0.03	0.47	0.43	0.06	0.2	-0.45	0.22	0.21	1
Cthe_00615	Phenylacetate-CoA ligase	12.01	12.27	12.55	12.06	-0.54	0.21	-0.26	0.49	0.09	0.13	-0.77	-0.4	0.22	0.21	0.21
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_02585	biotin--acetyl-CoA-carboxylase ligase	10.11	10.12	10.6	9.62	-0.49	0.5	-0.01	0.98	0.16	0.48	0.07	0.64	0.22	0.21	0.89
Cthe_01162	glucosamine--fructose-6-phosphate	11.49	11.63	11.88	11.3	-0.39	0.33	-0.14	0.58	0.3	0.27	-0.37	-0.21	0.22	0.21	1.08
Cthe_01288	two component transcriptional regulator,	11.08	11.01	11.34	10.88	-0.26	0.13	0.07	0.46	0.47	0.04	0.33	-0.47	0.22	0.21	0.93
Cthe_01279	ribosomal protein L28	13.69	13.61	13.91	13.51	-0.22	0.1	0.08	0.4	0.53	0	0.37	-0.6	0.22	0.21	0.85
Cthe_02860	RNA related	5.04	5.09	5.55	4.64	-0.51	0.45	-0.05	0.91	0.14	0.42	-0.07	0.49	0.22	0.21	1.02
Cthe_01475	hypothetical protein	11.07	11.18	11.64	10.61	-0.57	0.57	-0.11	1.03	0.05	0.56	-0.27	0.74	0.22	0.21	0.81
Cthe_01368	S-layer-like domain containing protein	14.84	15.06	15.36	14.52	-0.52	0.54	-0.22	0.84	0.12	0.52	-0.63	0.34	0.22	0.21	0.85
Cthe_01431	hypothetical protein	11.76	11.98	12.12	11.98	-0.36	0	-0.22	0.14	0.34	-0.12	-0.63	-1.15	0.22	0.21	0.31
Cthe_01581	inner-membrane translocator	3.17	4	4.09	2.58	-0.92	1.42	-0.83	1.51	-0.42	1.57	-2.67	1.77	0.22	0.21	0.58
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_01279	ribosomal protein L28	13.69	13.61	13.91	13.51	-0.22	0.1	0.08	0.4	0.53	0	0.37	-0.6	0.22	0.21	0.85
Cthe_02585	biotin--acetyl-CoA-carboxylase ligase	10.11	10.12	10.6	9.62	-0.49	0.5	-0.01	0.98	0.16	0.48	0.07	0.64	0.22	0.21	0.89
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_01162	glucosamine--fructose-6-phosphate	11.49	11.63	11.88	11.3	-0.39	0.33	-0.14	0.58	0.3	0.27	-0.37	-0.21	0.22	0.21	1.08
Cthe_00615	Phenylacetate-CoA ligase	12.01	12.27	12.55	12.06	-0.54	0.21	-0.26	0.49	0.09	0.13	-0.77	-0.4	0.22	0.21	0.21
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_02095	hydrolase, TatD family	10.38	10.35	10.67	10.2	-0.29	0.15	0.03	0.47	0.43	0.06	0.2	-0.45	0.22	0.21	1
Cthe_00615	Phenylacetate-CoA ligase	12.01	12.27	12.55	12.06	-0.54	0.21	-0.26	0.49	0.09	0.13	-0.77	-0.4	0.22	0.21	0.21
Cthe_01162	glucosamine--fructose-6-phosphate	11.49	11.63	11.88	11.3	-0.39	0.33	-0.14	0.58	0.3	0.27	-0.37	-0.21	0.22	0.21	1.08
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_00615	Phenylacetate-CoA ligase	12.01	12.27	12.55	12.06	-0.54	0.21	-0.26	0.49	0.09	0.13	-0.77	-0.4	0.22	0.21	0.21
Cthe_02528	uroporphyrin-III C-methyltransferase	6.81	6.39	6.78	6.13	0.03	0.26	0.42	0.65	0.86	0.19	1.5	-0.06	0.22	0.21	0.67
Cthe_02585	biotin--acetyl-CoA-carboxylase ligase	10.11	10.12	10.6	9.62	-0.49	0.5	-0.01	0.							



Cthe_01097	peptidase S14, ClpP	7.85	8.17	8.63	7.27	-0.78	0.9	-0.32	1.36	-0.23	0.95	-0.97	1.45	0.21	0.2	0.64
Cthe_02519	2-isopropylmalate synthase/homocitrate	13.09	13.44	13.65	13.11	-0.56	0.33	-0.35	0.54	0.07	0.27	-1.07	-0.3	0.21	0.2	0.29
Cthe_02536	phosphoadenosine phosphosulfate reduct	3.46	2.32	3	1.58	0.46	0.74	1.14	1.42	1.45	0.76	3.9	1.57	0.21	0.2	0.44
Cthe_01557	ABC transporter related protein	14.38	14.39	14.73	14.21	-0.35	0.18	-0.01	0.52	0.35	0.1	0.07	-0.34	0.21	0.2	1.19
Cthe_02519	2-isopropylmalate synthase/homocitrate	13.09	13.44	13.65	13.11	-0.56	0.33	-0.35	0.54	0.07	0.27	-1.07	-0.3	0.21	0.2	0.29
Cthe_00040	Cellulase., Cellulose 1,4-beta-cellobiosidas	9.47	9.41	9.67	9.32	-0.2	0.09	0.06	0.35	0.55	-0.01	0.3	-0.7	0.21	0.2	0.82
Cthe_00968	UvrD/REP helicase	8.08	8.02	8.41	7.85	-0.33	0.17	0.06	0.56	0.38	0.08	0.3	-0.26	0.21	0.2	1.11
Cthe_00574	serine/threonine protein kinase	12.48	12.56	12.84	12.32	-0.36	0.24	-0.08	0.52	0.34	0.17	-0.17	-0.34	0.21	0.2	1.14
Cthe_00040	Cellulase., Cellulose 1,4-beta-cellobiosidas	9.47	9.41	9.67	9.32	-0.2	0.09	0.06	0.35	0.55	-0.01	0.3	-0.7	0.21	0.2	0.82
Cthe_02536	phosphoadenosine phosphosulfate reduct	3.46	2.32	3	1.58	0.46	0.74	1.14	1.42	1.45	0.76	3.9	1.57	0.21	0.2	0.44
Cthe_00040	Cellulase., Cellulose 1,4-beta-cellobiosidas	9.47	9.41	9.67	9.32	-0.2	0.09	0.06	0.35	0.55	-0.01	0.3	-0.7	0.21	0.2	0.82
Cthe_02536	phosphoadenosine phosphosulfate reduct	3.46	2.32	3	1.58	0.46	0.74	1.14	1.42	1.45	0.76	3.9	1.57	0.21	0.2	0.44
Cthe_02519	2-isopropylmalate synthase/homocitrate	13.09	13.44	13.65	13.11	-0.56	0.33	-0.35	0.54	0.07	0.27	-1.07	-0.3	0.21	0.2	0.29
Cthe_02536	phosphoadenosine phosphosulfate reduct	3.46	2.32	3	1.58	0.46	0.74	1.14	1.42	1.45	0.76	3.9	1.57	0.21	0.2	0.44
Cthe_02536	phosphoadenosine phosphosulfate reduct	3.46	2.32	3	1.58	0.46	0.74	1.14	1.42	1.45	0.76	3.9	1.57	0.21	0.2	0.44
Cthe_02536	phosphoadenosine phosphosulfate reduct	3.46	2.32	3	1.58	0.46	0.74	1.14	1.42	1.45	0.76	3.9	1.57	0.21	0.2	0.44
Cthe_00895	RNA polymerase, sigma 38 subunit, RpoS	11.68	11.92	12.29	11.72	-0.61	0.2	-0.24	0.57	0	0.12	-0.7	-0.23	0.2	0.19	0.19
Cthe_01792	Firmicute transcriptional repressor of clas	10.08	9.85	10.73	9.1	-0.65	0.75	0.23	1.63	-0.05	0.77	0.87	2.02	0.2	0.19	0.4
Cthe_00554	phosphoribosylformylglycinamidine synth	12.82	12.82	13.02	12.71	-0.2	0.11	0	0.31	0.55	0.01	0.1	-0.79	0.2	0.19	0.79
Cthe_02596	protein tyrosine phosphatase	9.94	10.08	10.2	9.8	-0.26	0.28	-0.14	0.4	0.47	0.21	-0.37	-0.6	0.2	0.19	0.83
Cthe_01090	hypothetical protein	11.65	11.84	12.16	11.75	-0.51	0.09	-0.19	0.41	0.14	-0.01	-0.53	-0.57	0.2	0.19	0.2
Cthe_03200	alanyl-tRNA synthetase	10.47	10.54	10.96	10.26	-0.49	0.28	-0.07	0.7	0.16	0.21	-0.13	0.04	0.2	0.19	2.21
Cthe_02779	hypothetical protein	5.7	5.58	6.52	5.09	-0.82	0.49	0.12	1.43	-0.28	0.46	0.5	1.6	0.2	0.19	0.37
Cthe_01299	hypothetical protein	5.09	4.75	5	5	0.09	-0.25	0.34	0	0.95	-0.42	1.23	-1.45	0.2	0.19	0.62
Cthe_03200	alanyl-tRNA synthetase	10.47	10.54	10.96	10.26	-0.49	0.28	-0.07	0.7	0.16	0.21	-0.13	0.04	0.2	0.19	2.21
Cthe_03200	alanyl-tRNA synthetase	10.47	10.54	10.96	10.26	-0.49	0.28	-0.07	0.7	0.16	0.21	-0.13	0.04	0.2	0.19	2.21
Cthe_00554	phosphoribosylformylglycinamidine synth	12.82	12.82	13.02	12.71	-0.2	0.11	0	0.31	0.55	0.01	0.1	-0.79	0.2	0.19	0.79
Cthe_03200	alanyl-tRNA synthetase	10.47	10.54	10.96	10.26	-0.49	0.28	-0.07	0.7	0.16	0.21	-0.13	0.04	0.2	0.19	2.21
Cthe_02596	protein tyrosine phosphatase	9.94	10.08	10.2	9.8	-0.26	0.28	-0.14	0.4	0.47	0.21	-0.37	-0.6	0.2	0.19	0.83
Cthe_00554	phosphoribosylformylglycinamidine synth	12.82	12.82	13.02	12.71	-0.2	0.11	0	0.31	0.55	0.01	0.1	-0.79	0.2	0.19	0.79
Cthe_00554	phosphoribosylformylglycinamidine synth	12.82	12.82	13.02	12.71	-0.2	0.11	0	0.31	0.55	0.01	0.1	-0.79	0.2	0.19	0.79
Cthe_03200	alanyl-tRNA synthetase	10.47	10.54	10.96	10.26	-0.49	0.28	-0.07	0.7	0.16	0.21	-0.13	0.04	0.2	0.19	2.21
Cthe_00554	phosphoribosylformylglycinamidine synth	12.82	12.82	13.02	12.71	-0.2	0.11	0	0.31	0.55	0.01	0.1	-0.79	0.2	0.19	0.79
Cthe_00554	phosphoribosylformylglycinamidine synth	12.82	12.82	13.02	12.71	-0.2	0.11	0	0.31	0.55	0.01	0.1	-0.79	0.2	0.19	0.79
Cthe_00459	DNA protecting protein DprA	10.39	10.46	10.54	10.32	-0.15	0.14	-0.07	0.22	0.62	0.05	-0.13	-0.98	0.19	0.18	0.71
Cthe_02752	beta-lactamase-like protein	7.29	7.62	7.72	7.03	-0.43	0.59	-0.33	0.69	0.24	0.58	-1	0.02	0.19	0.18	0.71
Cthe_02784	cobalamin B12-binding protein	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02847	phage / plasmid primase, P4 family	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_03076	Radical SAM	10.79	10.66	11.36	10.48	-0.57	0.18	0.13	0.88	0.05	0.1	0.53	0.43	0.19	0.18	0.19
Cthe_01453		5.73	5.95	6.21	5.49	-0.48	0.46	-0.22	0.72	0.18	0.43	-0.63	0.09	0.19	0.18	0.83
Cthe_01261	6-phosphofructokinase	11.61	11.42	11.79	11.35	-0.18	0.07	0.19	0.44	0.58	-0.04	0.73	-0.51	0.19	0.18	0.74
Cthe_00521	helicase-like protein	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_01467	hypothetical protein	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02452	oligoendopeptidase F	10.33	10.47	10.89	10	-0.56	0.47	-0.14	0.89	0.07	0.44	-0.37	0.45	0.19	0.18	0.87
Cthe_00459	DNA protecting protein DprA	10.39	10.46	10.54	10.32	-0.15	0.14	-0.07	0.22	0.62	0.05	-0.13	-0.98	0.19	0.18	0.71
Cthe_00521	helicase-like protein	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_01264	DNA polymerase III, alpha subunit	10.74	10.93	11.25	10.48	-0.51	0.45	-0.19	0.77	0.14	0.42	-0.53	0.19	0.19	0.18	0.89
Cthe_01901	transposase, mutator type	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02325	Recombinase	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02671	transposase, mutator type	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_01529		9.64	9.48	10	8.89	-0.36	0.59	0.16	1.11	0.34	0.58	0.63	0.91	0.19	0.18	0.69
Cthe_00885	dephosho-CoA kinase	8.97	8.84	9.63	8.52	-0.66	0.32	0.13	1.11	-0.07	0.26	0.53	0.91	0.19	0.18	0.29
Cthe_01177	putative nicotinate phosphoribosyltransfe	8.2	7.99	8.78	7.48	-0.58	0.51	0.21	1.3	0.04	0.49	0.8	1.32	0.19	0.18	0.36
Cthe_02786	methyltransferase MtaA/CmuA family	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02242	flagellar hook-associated protein 3	7.02	6.71	7.44	6.75	-0.42	-0.04	0.31	0.69	0.26	-0.17	1.13	0.02	0.19	0.18	0.31
Cthe_00998	putative membrane-associated zinc	10.93	11.14	11.44	10.99	-0.51	0.15	-0.21	0.45	0.14	0.06	-0.6	-0.49	0.19	0.18	0.22
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_01696	hypothetical protein	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02312	hypothetical protein	9.47	9.24	10.04	8.69	-0.57	0.55	0.23	1.35	0.05	0.54	0.87	1.43	0.19	0.18	0.37
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_02937	cobalt transport protein	6.97	7.01	7.18	6.87	-0.21	0.14	-0.04	0.31	0.54	0.05	-0.03	-0.79	0.19	0.18	0.78
Cthe_00518	type III restriction enzyme, res subunit	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_03136	peptidase S8 and S53, subtilisin, kexin,	11.14	11.15	11.33	11.06	-0.19	0.09	-0.01	0.27	0.57	-0.01	0.07	-0.87	0.19	0.18	0.74
Cthe_03211	protein of unknown function DUF324	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02006	RNA related	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02611	Fibronectin, type III	8.16	8.29	8.86	7.43	-0.7	0.86	-0.13	1.43	-0.12	0.9	-0.33	1.6	0.19	0.18	0.63
Cthe_02175	hypothetical protein	10.41	10.39	10.93	9.72	-0.52	0.67	0.02	1.21	0.12	0.68	0.17	1.13	0.19	0.18	0.69
Cthe_01098	hypothetical protein	14	13.92	14.42	13.44	-0.42	0.48	0.08	0.98	0.26	0.45	0.37	0.64	0.19	0.18	0.8
Cthe_00385	hypothetical protein	1	1	1	1	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02472	hypothetical protein	0	0	0	0	0	0	0	0	0.82	-0.12	0.1	-1.45	0.19	0.18	0.65
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_02937	cobalt transport protein	6.97	7.01	7.18	6.87	-0.21	0.14	-0.04	0.31	0.54	0.05	-0.03	-0.79	0.19	0.18	0.78
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_02937	cobalt transport protein	6.97	7.01	7.18	6.87	-0.21	0.14	-0.04	0.31	0.54	0.05	-0.03	-0.79	0.19	0.18	0.78
Cthe_01261	6-phosphofructokinase	11.61	11.42	11.79	11.35	-0.18	0.07	0.19	0.44	0.58	-0.04	0.73	-0.51	0.19	0.18	0.74
Cthe_01264	DNA polymerase III, alpha subunit	10.74	10.93	11.25	10.48	-0.51	0.45	-0.19	0.77	0.14	0.42	-0.53	0.19	0.19	0.18	0.89
Cthe_01261																



Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_01177	putative nicotinate phosphoribosyltransfe	8.2	7.99	8.78	7.48	-0.58	0.51	0.21	1.3	0.04	0.49	0.8	1.32	0.19	0.18	0.36
Cthe_00885	dephospho-CoA kinase	8.97	8.84	9.63	8.52	-0.66	0.32	0.13	1.11	-0.07	0.26	0.53	0.91	0.19	0.18	0.29
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_01261	6-phosphofructokinase	11.61	11.42	11.79	11.35	-0.18	0.07	0.19	0.44	0.58	-0.04	0.73	-0.51	0.19	0.18	0.74
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_01261	6-phosphofructokinase	11.61	11.42	11.79	11.35	-0.18	0.07	0.19	0.44	0.58	-0.04	0.73	-0.51	0.19	0.18	0.74
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_01261	6-phosphofructokinase	11.61	11.42	11.79	11.35	-0.18	0.07	0.19	0.44	0.58	-0.04	0.73	-0.51	0.19	0.18	0.74
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_01261	6-phosphofructokinase	11.61	11.42	11.79	11.35	-0.18	0.07	0.19	0.44	0.58	-0.04	0.73	-0.51	0.19	0.18	0.74
Cthe_01261	6-phosphofructokinase	11.61	11.42	11.79	11.35	-0.18	0.07	0.19	0.44	0.58	-0.04	0.73	-0.51	0.19	0.18	0.74
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_00684	Polynucleotide adenyllyltransferase region	10.63	10.87	11.25	10.66	-0.62	0.21	-0.24	0.59	-0.01	0.13	-0.7	-0.19	0.19	0.18	0.2
Cthe_02183	UTP-glucose-1-phosphate uridylyltransfer	12.19	12.03	12.48	11.77	-0.29	0.26	0.16	0.71	0.43	0.19	0.63	0.06	0.19	0.18	0.84
Cthe_01688	Radical SAM			0					0	0.82			-1.45	0.18	0.17	0.64
Cthe_01957	extracellular solute-binding protein, famil	9.12	9.36	9.76	8.73	-0.64	0.63	-0.24	1.03	-0.04	0.63	-0.7	0.74	0.18	0.17	0.7
Cthe_00688	putative transcriptional regulator	10.97	11.21	11.27	10.81	-0.3	0.4	-0.24	0.46	0.42	0.36	-0.7	-0.47	0.18	0.17	0.75
Cthe_01886	Integrase, catalytic region			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02749	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02770	transposase IS116/IS110/IS902			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02850	transposase IS116/IS110/IS902			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_03210	protein of unknown function DUF324			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_01606				0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02426	OmpA/MotB	6.09	5	5.7	5.49	0.39	-0.49	1.09	0.21	1.35	-0.7	3.73	-1	0.18	0.17	0.45
Cthe_02600	glycosyl transferase, family 4	11.79	11.91	12.08	11.67	-0.29	0.24	-0.12	0.41	0.43	0.17	-0.3	-0.57	0.18	0.17	0.82
Cthe_03232	YD repeat protein	8.48	8.28	9.03	7.87	-0.55	0.41	0.2	1.16	0.08	0.37	0.77	1.02	0.18	0.17	0.34
Cthe_01393	multi-sensor signal transduction histidine	9.03	9.18	9.58	9.14	-0.55	0.04	-0.15	0.44	0.08	-0.07	-0.4	-0.51	0.18	0.17	0.19
Cthe_01463	protein of unknown function DUF891	9.1	8.88	9.83	7.96	-0.73	0.92	0.22	1.87	-0.16	0.98	0.83	2.53	0.18	0.17	0.42
Cthe_01630	phage portal protein, HK97 family			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02492	Baseplate J-like protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02676	GumN	12.3	12.42	12.87	11.95	-0.57	0.47	-0.12	0.92	0.05	0.44	-0.3	0.51	0.18	0.17	0.85
Cthe_00942	MiaB-like tRNA modifying enzyme YliG	11.46	11.46	11.84	11.3	-0.38	0.16	0	0.54	0.31	0.07	0.1	-0.3	0.18	0.17	1.14
Cthe_01389	metal dependent phosphohydrolase	10.63	10.54	10.63	10.65	0	-0.11	0.09	-0.02	0.82	-0.25	0.4	-1.49	0.18	0.17	0.63
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	7.43	7.1	7.45	7.19	-0.02	-0.09	0.33	0.26	0.8	-0.23	1.2	-0.89	0.18	0.17	0.63
Cthe_01659	TrkA-N			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_01873	HMG-I and HMG-Y, DNA-binding			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_01370	hypothetical protein	7.8	7.78	8.34	7.04	-0.54	0.74	0.02	1.3	0.09	0.76	0.17	1.32	0.18	0.17	0.65
Cthe_00520	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02457	hypothetical protein	0		0		0		0	0	0.82		0.1	-1.45	0.18	0.17	0.64
Cthe_00590	transposase IS3/IS911	0		0		0		0	0	0.82		0.1	-1.45	0.18	0.17	0.64
Cthe_01662	transposase IS3/IS911			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02851	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02976	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_01622	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_03209	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02485	hypothetical protein	0		0		0		0	0	0.82		0.1	-1.45	0.18	0.17	0.64
Cthe_02501	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_00155	hypothetical protein	9.14	9.41	9.63	8.87	-0.49	0.54	-0.27	0.76	0.16	0.52	-0.8	0.17	0.18	0.17	0.76
Cthe_01748	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02246	anti-sigma-28 factor, FlgM	7.66	7.52	8.27	7.2	-0.61	0.32	0.14	1.07	0	0.26	0.57	0.83	0.18	0.17	0.29
Cthe_01143	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_00793	hypothetical protein	10.19	10.42	10.65	10.25	-0.46	0.17	-0.23	0.4	0.2	0.08	-0.67	-0.6	0.18	0.17	0.27
Cthe_02835	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02159	hypothetical protein	6.98	6.78	7.48	6.74	-0.5	0.04	0.2	0.74	0.15	-0.07	0.77	0.13	0.18	0.17	0.24
Cthe_01872	Tn7-like transposition protein C			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02853	prophage Lp4 protein 7, DNA replication			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_02316	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_01727	hypothetical protein			0		0			0	0.82			-1.45	0.18	0.17	0.64
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	7.43	7.1	7.45	7.19	-0.02	-0.09	0.33	0.26	0.8	-0.23	1.2	-0.89	0.18	0.17	0.63
Cthe_01957	extracellular solute-binding protein, famil	9.12	9.36	9.76	8.73	-0.64	0.63	-0.24	1.03	-0.04	0.63	-0.7	0.74	0.18	0.17	0.7
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	7.43	7.1	7.45	7.19	-0.02	-0.09	0.33	0.26	0.8	-0.23	1.2	-0.89	0.18	0.17	0.63
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	7.43	7.1	7.45	7.19	-0.02	-0.09	0.33	0.26	0.8	-0.23	1.2	-0.89	0.18	0.17	0.63
Cthe_00867	4Fe-4S ferredoxin, iron-sulfur binding	7.43	7.1	7.45	7.19	-0.02	-0.09	0.33	0.26	0.8	-0.23	1.2	-0.89	0.18	0.17	0.63
Cthe_01393	multi-sensor signal transduction histidine	9.03	9.18	9.58	9.14	-0.55	0.04	-0.15	0.44	0.08	-0.07	-0.4	-0.51	0.18	0.17	0.19
Cthe_01389	metal dependent phosphohydrolase	10.63	10.54	10.63	10.65	0	-0.11	0.09	-0.02	0.82	-0.25	0.4	-1.49	0.18	0.17	0.63
Cthe_01389	metal dependent phosphohydrolase	10.63	10.54	10.63	10.65	0	-0.11	0.09	-0.02	0.82	-0.25	0.4	-1.49	0.18	0.17	0.63
Cthe_01389	metal dependent phosphohydrolase	10.63	10.54	10.63	10.65	0	-0.11	0.09	-0.02	0.82	-0.25	0.4	-1.49	0.18	0.17	0.63
Cthe_02600	glycosyl transferase, family 4	11.79	11.91	12.08	11.67	-0.29	0.24	-0.12	0.41	0.43	0.17	-0.3	-0.57	0.18	0.17	0.82
Cthe_02600	glycosyl transferase, family 4	11.79	11.91	12.08	11.67	-0.29	0.24	-0.12	0.41	0.43	0.17	-0.3	-0.57	0.18	0.17	0.82
Cthe_01389	metal dependent phosphohydrolase	10.63	10.54	10.63	10.65	0	-0.11	0.09	-0.02	0.82	-0.25	0.4	-1.			



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Cthe_03094	glycosyl transferase, family 2	11.84	12.02	12.12	12.13	-0.28	-0.11	-0.18	-0.01	0.45	-0.25	-0.5	-1.47	0.17	0.16	0.38
Cthe_00571	sun protein	11.5	11.6	11.94	11.34	-0.44	0.26	-0.1	0.6	0.23	0.19	-0.23	-0.17	0.17	0.16	1.19
Cthe_00571	sun protein	11.5	11.6	11.94	11.34	-0.44	0.26	-0.1	0.6	0.23	0.19	-0.23	-0.17	0.17	0.16	1.19
Cthe_00571	sun protein	11.5	11.6	11.94	11.34	-0.44	0.26	-0.1	0.6	0.23	0.19	-0.23	-0.17	0.17	0.16	1.19
Cthe_00571	sun protein	11.5	11.6	11.94	11.34	-0.44	0.26	-0.1	0.6	0.23	0.19	-0.23	-0.17	0.17	0.16	1.19
Cthe_00571	sun protein	11.5	11.6	11.94	11.34	-0.44	0.26	-0.1	0.6	0.23	0.19	-0.23	-0.17	0.17	0.16	1.19
Cthe_00571	sun protein	11.5	11.6	11.94	11.34	-0.44	0.26	-0.1	0.6	0.23	0.19	-0.23	-0.17	0.17	0.16	1.19
Cthe_00319	class II aldolase/adducin-like protein	8.57	8.71	8.94	8.43	-0.37	0.28	-0.14	0.51	0.32	0.21	-0.37	-0.36	0.16	0.15	0.84
Cthe_00727	cell envelope-related transcriptional atten	10.82	10.81	10.88	10.83	-0.06	-0.02	0.01	0.05	0.74	-0.14	0.13	-1.34	0.16	0.15	0.64
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00020	biotin synthase	5.98	6	6.49	5.81	-0.51	0.19	-0.02	0.68	0.14	0.11	0.03	0	0.16	0.15	6.74
Cthe_01249	amidophosphoribosyltransferase	10.97	11.27	11.36	10.77	-0.39	0.5	-0.3	0.59	0.3	0.48	-0.9	-0.19	0.16	0.15	0.7
Cthe_02901	putative anti-sigma regulatory factor,	11.65	11.34	11.77	11.19	-0.12	0.15	0.31	0.58	0.66	0.06	1.13	-0.21	0.16	0.15	0.66
Cthe_00892	protein of unknown function DUF34	9.03	8.91	9.36	8.74	-0.33	0.17	0.12	0.62	0.38	0.08	0.5	-0.13	0.16	0.15	0.85
Cthe_01494	protein of unknown function DUF6, trans	8.04	7.66	8.09	7.47	-0.05	0.19	0.38	0.62	0.76	0.11	1.37	-0.13	0.16	0.15	0.63
Cthe_01270	proteinase inhibitor I4, serpin	10.84	10.87	11.13	10.74	-0.29	0.13	-0.03	0.39	0.43	0.04	0	-0.62	0.16	0.15	0.79
Cthe_01462	transcriptional regulator, XRE family	9.32	9.16	9.75	8.31	-0.43	0.85	0.16	1.44	0.24	0.89	0.63	1.62	0.16	0.15	0.6
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_01348	ribosomal protein S21	13.33	13.06	13.75	12.7	-0.42	0.36	0.27	1.05	0.26	0.31	1	0.79	0.16	0.15	0.36
Cthe_00020	biotin synthase	5.98	6	6.49	5.81	-0.51	0.19	-0.02	0.68	0.14	0.11	0.03	0	0.16	0.15	6.74
Cthe_01249	amidophosphoribosyltransferase	10.97	11.27	11.36	10.77	-0.39	0.5	-0.3	0.59	0.3	0.48	-0.9	-0.19	0.16	0.15	0.7
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_01249	amidophosphoribosyltransferase	10.97	11.27	11.36	10.77	-0.39	0.5	-0.3	0.59	0.3	0.48	-0.9	-0.19	0.16	0.15	0.7
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00319	class II aldolase/adducin-like protein	8.57	8.71	8.94	8.43	-0.37	0.28	-0.14	0.51	0.32	0.21	-0.37	-0.36	0.16	0.15	0.84
Cthe_02901	putative anti-sigma regulatory factor,	11.65	11.34	11.77	11.19	-0.12	0.15	0.31	0.58	0.66	0.06	1.13	-0.21	0.16	0.15	0.66
Cthe_00020	biotin synthase	5.98	6	6.49	5.81	-0.51	0.19	-0.02	0.68	0.14	0.11	0.03	0	0.16	0.15	6.74
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00020	biotin synthase	5.98	6	6.49	5.81	-0.51	0.19	-0.02	0.68	0.14	0.11	0.03	0	0.16	0.15	6.74
Cthe_00319	class II aldolase/adducin-like protein	8.57	8.71	8.94	8.43	-0.37	0.28	-0.14	0.51	0.32	0.21	-0.37	-0.36	0.16	0.15	0.84
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_01249	amidophosphoribosyltransferase	10.97	11.27	11.36	10.77	-0.39	0.5	-0.3	0.59	0.3	0.48	-0.9	-0.19	0.16	0.15	0.7
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_01249	amidophosphoribosyltransferase	10.97	11.27	11.36	10.77	-0.39	0.5	-0.3	0.59	0.3	0.48	-0.9	-0.19	0.16	0.15	0.7
Cthe_00319	class II aldolase/adducin-like protein	8.57	8.71	8.94	8.43	-0.37	0.28	-0.14	0.51	0.32	0.21	-0.37	-0.36	0.16	0.15	0.84
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_01249	amidophosphoribosyltransferase	10.97	11.27	11.36	10.77	-0.39	0.5	-0.3	0.59	0.3	0.48	-0.9	-0.19	0.16	0.15	0.7
Cthe_00580	aminotransferase, class I and II	10.47	10.63	11.01	10.51	-0.54	0.12	-0.16	0.5	0.09	0.02	-0.43	-0.38	0.16	0.15	0.18
Cthe_00237	response regulator receiver protein	10.83	10.99	10.67	10.92	0.16	0.07	-0.16	-0.25	1.04	-0.04	-0.43	-1.98	0.15	0.14	0.58
Cthe_02544	RNA polymerase, sigma-24 subunit, ECF su	10.78	11.43	11.48	10.37	-0.7	1.06	-0.65	1.11	-0.12	1.14	-2.07	0.91	0.15	0.14	0.58
Cthe_00069	Aspartate-ammonia ligase	11.11	11.15	11.47	11	-0.36	0.15	-0.04	0.47	0.34	0.06	-0.03	-0.45	0.15	0.14	0.87
Cthe_00290	Homoserine dehydrogenase	10.46	10.36	10.7	10.35	-0.24	0.01	0.1	0.35	0.5	-0.11	0.43	-0.7	0.15	0.14	0.71
Cthe_00748	binding-protein-dependent transport syst	8.61	8.69	8.86	8.54	-0.25	0.15	-0.08	0.32	0.49	0.06	-0.17	-0.77	0.15	0.14	0.71
Cthe_01554	methylated-DNA--protein-cysteine	12.87	13.02	13.49	12.89	-0.62	0.13	-0.15	0.6	-0.01	0.04	-0.4	-0.17	0.15	0.14	0.11
Cthe_00602	thiamine biosynthesis protein ThiC	10.57	10.44	10.65	10.59	-0.08	-0.15	0.13	0.06	0.72	-0.3	0.53	-1.32	0.15	0.14	0.62
Cthe_02230	acyneuraminat cytidylyltransferase	6.43	6	6.82	5	-0.39	1	0.43	1.82	0.3	1.07	1.53	2.43	0.15	0.14	0.44
Cthe_00237	response regulator receiver protein	10.83	10.99	10.67	10.92	0.16	0.07	-0.16	-0.25	1.04	-0.04	-0.43	-1.98	0.15	0.14	0.58
Cthe_00958	queuine tRNA-ribosyltransferase	9.89	10.08	10.41	9.92	-0.52	0.16	-0.19	0.49	0.12	0.07	-0.53	-0.4	0.15	0.14	0.24
Cthe_01390	alpha/beta hydrolase fold	10.13	10.48	10.62	10.12	-0.49	0.36	-0.35	0.5	0.16	0.31	-1.07	-0.38	0.15	0.14	0.35
Cthe_00187	hypothetical protein	10.23	10.27	10.99	9.14	-0.76	1.13	-0.04	1.85	-0.2	1.23	-0.03	2.49	0.15	0.14	0.57
Cthe_02988	hypothetical protein	5.25	5.52	5.98	4.86	-0.73	0.66	-0.27	1.12	-0.16	0.67	-0.8	0.94	0.15	0.14	0.63
Cthe_00649	hypothetical protein	8.13	7.97	8.62	6.91	-0.49	1.06	0.16	1.71	-0.16	1.14	-0.63	2.19	0.15	0.14	0.57
Cthe_00735	cellulosome anchoring protein, cohesion re	10.67	10.69	11.1	10.53	-0.43	0.16	-0.02	0.57	0.24	0.07	0.03	-0.23	0.15	0.14	1.22
Cthe_00602	thiamine biosynthesis protein ThiC	10.57	10.44	10.65	10.59	-0.08	-0.15	0.13	0.06	0.72	-0.3	0.53	-1.32	0.15	0.14	0.62
Cthe_00748	binding-protein-dependent transport syst	8.61	8.69	8.86	8.54	-0.25	0.15	-0.08	0.32	0.49	0.06	-0.17	-0.77	0.15	0.14	0.71
Cthe_00290	Homoserine dehydrogenase	10.46	10.36	10.7	10.35	-0.24	0.01	0.1	0.35	0.5	-0.11	0.43	-0.7	0.15	0.14	0.71
Cthe_00290	Homoserine dehydrogenase	10.46	10.36	10.7	10.35	-0.24	0.01	0.1	0.35	0.5	-0.11	0.43	-0.7	0.15	0.14	0.71
Cthe_01554	methylated-DNA--protein-cysteine	12.87	13.02	13.49	12.89	-0.62	0.13	-0.15	0.6	-0.01	0.04	-0.4	-0.17	0.15	0.14	0.11
Cthe_00290	Homoserine dehydrogenase	10.46	10.36	10.7	10.35	-0.24	0.01	0.1	0.35	0.5	-0.11	0.43	-0.7	0.15	0.14	0.71
Cthe_00958	queuine tRNA-ribosyltransferase	9.89	10.08	10.41	9.92	-0.52	0.16	-0.19	0.49	0.12	0.07	-0.53	-0.4	0.15	0.14	0.24
Cthe_00069	Aspartate-ammonia ligase	11.11	11.15	11.47	11	-0.36	0.15	-0.04	0.47	0.34	0.06	-0.03	-0.45	0.15	0.14	0.87
Cthe_00290	Homoserine dehydrogenase	10.46	10.36	10.7	10.35	-0.24	0.01	0.1	0.35	0.5	-0.11	0.43	-0.7	0.15	0.14	0.71
Cthe_00069	Aspartate-ammonia ligase	11.11	11.15	11.47	11	-0.36	0.15	-0.04	0.47	0.34	0.06	-0.03	-0.45	0.15	0.14	0.87
Cthe_02586	amidohydrolase 2	10.76	10.94	11.33	10.5	-0.57	0.44	-0.18	0.83	0.05	0.4	-0.5	0.32	0.14	0.13	0.77
Cthe_02768	metallophosphoesterase	9.06	8.92	9.67	8.49	-0.61	0.43	0.14	1.18	0	0.39	0.57	1.06	0.14	0.13	0.37
Cthe_03007	ErkK/YbiS/YcfS/YnhG	2.58	3.91	3.17	2.32	-0.59	1.59	-1.33	0.85	0.03	1.77	-4.33	0.36	0.14	0.13	0.46
Cthe_01449	transcriptional regulator, MarR family	6.27	6.04	6.39	6.15	-0.12	-0.11	0.23	0.24	0.66	-0.25	0.87	-0.94	0.14	0.13	0.63
Cthe_01796	Prephenate dehydrogenase	13.33	13.58	13.74	13.15	-0.41	0.43	-0.25	0.59	0.27	0.39	-0.73	-0.19	0.14	0.13	0.71
Cthe_02356	quinolinate synthetase complex, A subuni	13.1	12.91	13.25	13.02	-0.15	-0.11	0.19	0.23	0.62	-0.25	0.73	-0.96	0.14	0.13	0.61
Cthe_01919	MgtC/SapB transporter	8.09	8.04	8.68												



Cthe_01228	threonyl-tRNA synthetase	14.26	14.24	14.74	14.05	-0.48	0.19	0.02	0.69	0.18	0.11	0.17	0.02	0.14	0.13	1.4
Cthe_02356	quinolinate synthetase complex, A subuni	13.1	12.91	13.25	13.02	-0.15	-0.11	0.19	0.23	0.62	-0.25	0.73	-0.96	0.14	0.13	0.63
Cthe_01796	Prephenate dehydrogenase	13.33	13.58	13.74	13.15	-0.41	0.43	-0.25	0.59	0.27	0.39	-0.73	-0.19	0.14	0.13	0.71
Cthe_01228	threonyl-tRNA synthetase	14.26	14.24	14.74	14.05	-0.48	0.19	0.02	0.69	0.18	0.11	0.17	0.02	0.14	0.13	1.4
Cthe_01935	arginyl-tRNA synthetase	12.56	12.78	12.97	12.62	-0.41	0.16	-0.22	0.35	0.27	0.07	-0.63	-0.7	0.14	0.13	0.34
Cthe_01580	inner-membrane translocator	2.81	3.17	3.91	2.32	-1.1	0.85	-0.36	1.59	-0.66	0.89	-1.1	1.94	0.13	0.12	0.56
Cthe_02127	ATPase associated with various cellular	12.57	12.66	13.41	11.58	-0.84	1.08	-0.09	1.83	-0.31	1.17	-0.2	2.45	0.13	0.12	0.56
Cthe_00971		7.76	7.76	8.31	7.3	-0.55	0.46	0	1.01	0.08	0.43	0.1	0.7	0.13	0.12	0.7
Cthe_00661	Ricin B lectin	10.38	10.71	10.99	10.1	-0.61	0.61	-0.33	0.89	0	0.61	-1	0.45	0.13	0.12	0.63
Cthe_00795	alpha amylase, catalytic region	8.58	8.6	9.16	8.1	-0.58	0.5	-0.02	1.06	0.04	0.48	0.03	0.81	0.13	0.12	0.68
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_01861	transcriptional regulator, CdaR	12.22	12.41	12.7	12.26	-0.48	0.15	-0.19	0.44	0.18	0.06	-0.53	-0.51	0.13	0.12	0.29
Cthe_00873	anthranilate phosphoribosyltransferase	7.66	7.68	8.24	7.17	-0.58	0.51	-0.02	1.07	0.04	0.49	0.03	0.83	0.13	0.12	0.67
Cthe_00498	protein of unknown function DUF342	12.24	12.06	12.71	11.9	-0.47	0.16	0.18	0.81	0.19	0.07	0.7	0.28	0.13	0.12	0.31
Cthe_02509	DNA topoisomerase	7.82	8.09	8.17	7.88	-0.35	0.21	-0.27	0.29	0.35	0.13	-0.8	-0.83	0.13	0.12	0.37
Cthe_02355	L-aspartate oxidase	11.5	11.38	11.75	11.4	-0.25	-0.02	0.12	0.35	0.49	-0.14	0.5	-0.7	0.13	0.12	0.67
Cthe_00085	Negative regulator of genetic competence	14.2	14.1	14.65	13.6	-0.45	0.5	0.1	1.05	0.22	0.48	0.43	0.79	0.13	0.12	0.67
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_00085	Negative regulator of genetic competence	14.2	14.1	14.65	13.6	-0.45	0.5	0.1	1.05	0.22	0.48	0.43	0.79	0.13	0.12	0.67
Cthe_00811	response regulator receiver protein	3.91	4.25	4.86	3.46	-0.95	0.79	-0.34	1.4	-0.46	0.82	-1.03	1.53	0.13	0.12	0.58
Cthe_01861	transcriptional regulator, CdaR	12.22	12.41	12.7	12.26	-0.48	0.15	-0.19	0.44	0.18	0.06	-0.53	-0.51	0.13	0.12	0.29
Cthe_02978	transcriptional regulator, Crp/Fnr family	7.52	7.3	7.71	7.34	-0.19	-0.04	0.22	0.37	0.57	-0.17	0.83	-0.66	0.13	0.12	0.64
Cthe_00643	hypothetical protein	5.46	4.32	4.91	3.91	0.55	0.41	1.14	1	1.57	0.37	3.9	0.68	0.13	0.12	0.46
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_02720	ribosomal protein L11	13.39	13.54	13.81	13.54	-0.42	0	-0.15	0.27	0.26	-0.12	-0.4	-0.87	0.13	0.12	0.34
Cthe_00092	septum site-determining protein MinC	9.15	8.95	9.39	8.88	-0.24	0.07	0.2	0.51	0.5	-0.04	0.77	-0.36	0.13	0.12	0.67
Cthe_00085	Negative regulator of genetic competence	14.2	14.1	14.65	13.6	-0.45	0.5	0.1	1.05	0.22	0.48	0.43	0.79	0.13	0.12	0.67
Cthe_01387	hypothetical protein	10.87	10.81	11.28	10.66	-0.41	0.15	0.06	0.62	0.27	0.06	0.3	-0.13	0.13	0.12	0.96
Cthe_02176	Abortive infection protein	9.54	9.66	10.08	9.61	-0.54	0.05	-0.12	0.47	0.09	-0.06	-0.3	-0.45	0.13	0.12	0.23
Cthe_02720	ribosomal protein L11	13.39	13.54	13.81	13.54	-0.42	0	-0.15	0.27	0.26	-0.12	-0.4	-0.87	0.13	0.12	0.34
Cthe_01580	inner-membrane translocator	2.81	3.17	3.91	2.32	-1.1	0.85	-0.36	1.59	-0.66	0.89	-1.1	1.94	0.13	0.12	0.56
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_02720	ribosomal protein L11	13.39	13.54	13.81	13.54	-0.42	0	-0.15	0.27	0.26	-0.12	-0.4	-0.87	0.13	0.12	0.34
Cthe_02355	L-aspartate oxidase	11.5	11.38	11.75	11.4	-0.25	-0.02	0.12	0.35	0.49	-0.14	0.5	-0.7	0.13	0.12	0.67
Cthe_00873	anthranilate phosphoribosyltransferase	7.66	7.68	8.24	7.17	-0.58	0.51	-0.02	1.07	0.04	0.49	0.03	0.83	0.13	0.12	0.67
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_02355	L-aspartate oxidase	11.5	11.38	11.75	11.4	-0.25	-0.02	0.12	0.35	0.49	-0.14	0.5	-0.7	0.13	0.12	0.67
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_00922	diaminopimelate dehydrogenase	10.1	9.97	10.42	9.86	-0.32	0.11	0.13	0.56	0.39	0.01	0.53	-0.26	0.13	0.12	0.75
Cthe_00873	anthranilate phosphoribosyltransferase	7.66	7.68	8.24	7.17	-0.58	0.51	-0.02	1.07	0.04	0.49	0.03	0.83	0.13	0.12	0.67
Cthe_00873	anthranilate phosphoribosyltransferase	7.66	7.68	8.24	7.17	-0.58	0.51	-0.02	1.07	0.04	0.49	0.03	0.83	0.13	0.12	0.67
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_02355	L-aspartate oxidase	11.5	11.38	11.75	11.4	-0.25	-0.02	0.12	0.35	0.49	-0.14	0.5	-0.7	0.13	0.12	0.67
Cthe_00922	diaminopimelate dehydrogenase	10.1	9.97	10.42	9.86	-0.32	0.11	0.13	0.56	0.39	0.01	0.53	-0.26	0.13	0.12	0.75
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_01079	Nucleotidyl transferase	8.39	8.37	8.99	7.61	-0.6	0.76	0.02	1.38	0.01	0.79	0.17	1.49	0.13	0.12	0.6
Cthe_00023	pimeloyl-CoA synthesis (biotin biosynthes	4.32	3.81	4.25	3.7	0.07	0.11	0.51	0.55	0.92	0.01	1.8	-0.28	0.12	0.11	0.57
Cthe_01382	Patatin	10.38	10.39	11.01	9.65	-0.63	0.74	-0.01	1.36	-0.03	0.76	0.07	1.45	0.12	0.11	0.6
Cthe_01522	NADPH-dependent FMN reductase	5.04	5.25	5.39	5.13	-0.35	0.12	-0.21	0.26	0.35	0.02	-0.6	-0.89	0.12	0.11	0.37
Cthe_01620	Protein of unknown function DUF132	1.58	1	1.58	0	1	0.58	1.58	0.82	1.07	2.03	1.91	1.91	0.12	0.11	0.55
Cthe_02132	abortive infection protein, putative	10.49	10.48	10.84	10.4	-0.35	0.08	0.01	0.44	0.35	-0.02	0.13	-0.51	0.12	0.11	0.76
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_01904	amino acid adenylation domain	4.39	4.17	5	3.32	-0.61	0.85	0.22	1.68	0	0.89	0.83	2.13	0.12	0.11	0.44
Cthe_00009	YD repeat containing protein	8.79	8.7	9.51	8.21	-0.72	0.49	0.09	1.3	-0.15	0.46	0.4	1.32	0.12	0.11	0.4
Cthe_00442	Polypeptide-transport-associated, FtsQ-ty	11.5	11.56	12.13	11.01	-0.63	0.55	-0.06	1.12	-0.03	0.54	-0.1	0.94	0.12	0.11	0.65
Cthe_01555	NLPA lipoprotein	14.36	14.62	14.88	14.14	-0.52	0.48	-0.26	0.74	0.12	0.45	-0.77	0.13	0.12	0.11	0.68
Cthe_00455	Mg chelatase, subunit Chll	7.82	7.61	8.03	7.64	-0.21	-0.03	0.21	0.39	0.54	-0.15	0.8	-0.62	0.12	0.11	0.63
Cthe_01578	Radical SAM	4.75	4.95	5.61	4.17	-0.86	0.78	-0.2	1.44	-0.34	0.81	-0.57	1.62	0.12	0.11	0.58
Cthe_02111	protein of unknown function DUF214	7.67	7.64	8.16	7.4	-0.49	0.24	0.03	0.76	0.16	0.17	0.2	0.17	0.12	0.11	1.01
Cthe_00336	DRTGG domain containing protein	8.12	8.34	8.79	7.82	-0.67	0.52	-0.22	0.97	-0.08	0.5	-0.63	0.62	0.12	0.11	0.65
Cthe_01219	hypothetical protein	10.98	11.22	11.81	10.55	-0.83	0.67	-0.24	1.26	-0.3	0.68	-0.7	1.23	0.12	0.11	0.6
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_01555	NLPA lipoprotein	14.36	14.62	14.88	14.14	-0.52	0.48	-0.26	0.74	0.12	0.45	-0.77	0.13	0.12	0.11	0.68
Cthe_01578	Radical SAM	4.75	4.95	5.61	4.17	-0.86	0.78	-0.2	1.44	-0.34	0.81	-0.57	1.62	0.12	0.11	0.58
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10.34	-0.25	-0.04	0.09	0.3	0.49	-0.17	0.4	-0.81	0.12	0.11	0.65
Cthe_00576	Ribulose-phosphate 3-epimerase	10.39	10.3	10.64	10											



Cthe_00836	hypothetical protein	12.86	12.87	13.39	12.68	-0.53	0.19	-0.01	0.71	0.11	0.11	0.07	0.06	0.11	0.1	1.92
Cthe_02118	ABC transporter related protein	9.7	9.87	10	9.85	-0.3	0.02	-0.17	0.15	0.42	-0.1	-0.47	-1.13	0.11	0.1	0.4
Cthe_02172	ribosomal protein L31	13.3	13.08	13.39	13.5	-0.09	-0.42	0.22	-0.11	0.7	-0.62	0.83	-1.68	0.11	0.1	0.57
Cthe_00999	1-deoxy-D-xylulose 5-phosphate reductois	11.41	11.68	11.77	11.27	-0.36	0.41	-0.27	0.5	0.34	0.37	-0.8	-0.38	0.11	0.1	0.64
Cthe_02946	2C-methyl-D-erythritol 2,4-cyclodiphosph	8.41	8.55	8.96	8.41	-0.55	0.14	-0.14	0.55	0.08	0.05	-0.37	-0.28	0.11	0.1	0.23
Cthe_02946	2C-methyl-D-erythritol 2,4-cyclodiphosph	8.41	8.55	8.96	8.41	-0.55	0.14	-0.14	0.55	0.08	0.05	-0.37	-0.28	0.11	0.1	0.23
Cthe_00418	Polyribonucleotide nucleotidyltransferase	13.42	13.46	13.76	13.35	-0.34	0.11	-0.04	0.41	0.36	0.01	-0.03	-0.57	0.11	0.1	0.72
Cthe_00068	Peptidylprolyl isomerase	11.43	11.49	11.54	11.47	-0.11	0.02	-0.06	0.07	0.68	-0.1	-0.1	-1.3	0.11	0.1	0.6
Cthe_01295	5-formyltetrahydrofolate cyclo-ligase	9.01	9.05	9.56	8.82	-0.55	0.23	-0.04	0.74	0.08	0.15	-0.03	0.13	0.11	0.1	1.45
Cthe_00999	1-deoxy-D-xylulose 5-phosphate reductois	11.41	11.68	11.77	11.27	-0.36	0.41	-0.27	0.5	0.34	0.37	-0.8	-0.38	0.11	0.1	0.64
Cthe_00185	cell wall hydrolase/autolysin	9.97	10.06	10.42	9.86	-0.45	0.2	-0.09	0.56	0.22	0.12	-0.2	-0.26	0.11	0.1	0.87
Cthe_00999	1-deoxy-D-xylulose 5-phosphate reductois	11.41	11.68	11.77	11.27	-0.36	0.41	-0.27	0.5	0.34	0.37	-0.8	-0.38	0.11	0.1	0.64
Cthe_02946	2C-methyl-D-erythritol 2,4-cyclodiphosph	8.41	8.55	8.96	8.41	-0.55	0.14	-0.14	0.55	0.08	0.05	-0.37	-0.28	0.11	0.1	0.23
Cthe_01295	5-formyltetrahydrofolate cyclo-ligase	9.01	9.05	9.56	8.82	-0.55	0.23	-0.04	0.74	0.08	0.15	-0.03	0.13	0.11	0.1	1.45
Cthe_01295	5-formyltetrahydrofolate cyclo-ligase	9.01	9.05	9.56	8.82	-0.55	0.23	-0.04	0.74	0.08	0.15	-0.03	0.13	0.11	0.1	1.45
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_02327	beta-lactamase-like protein	9.67	9.63	10.05	9.57	-0.38	0.06	0.04	0.48	0.31	-0.05	0.23	-0.43	0.1	0.09	0.73
Cthe_02895	glycoside hydrolase, family 18	11.17	10.99	11.25	11.49	-0.08	0.5	0.18	-0.24	0.72	-0.71	0.7	-1.96	0.1	0.09	0.55
Cthe_02100	transcriptional regulator, AbrB family	11.46	10.94	11.38	11.29	0.08	-0.35	0.52	0.09	0.93	-0.54	1.83	-1.26	0.1	0.09	0.55
Cthe_02112	two component transcriptional regulator,	8.88	8.73	9.41	8.38	-0.53	0.35	0.15	1.03	0.11	0.3	0.6	0.74	0.1	0.09	0.38
Cthe_02437	shikimate kinase	12.28	12.07	12.57	11.85	-0.29	0.22	0.21	0.72	0.43	0.14	0.8	0.09	0.1	0.09	0.64
Cthe_02962	oligopeptide/dipeptide ABC transporter, A	7.75	7.91	8.04	7.91	-0.29	0	-0.16	0.13	0.43	-0.12	-0.43	-1.17	0.1	0.09	0.41
Cthe_00180	crossover junction endodeoxyribonucleas	8.6	8.67	9.11	8.48	-0.51	0.19	-0.07	0.63	0.14	0.11	-0.13	-0.11	0.1	0.09	1.19
Cthe_02663	methyl-accepting chemotaxis sensory tran	8.42	8.69	9.49	8.06	-1.07	0.63	-0.27	1.43	-0.62	0.63	-0.8	1.6	0.1	0.09	0.56
Cthe_02680	peptidase S41	10.31	10.58	10.66	10.18	-0.35	0.4	-0.27	0.48	0.35	0.36	-0.8	-0.43	0.1	0.09	0.63
Cthe_02112	two component transcriptional regulator,	8.88	8.73	9.41	8.38	-0.53	0.35	0.15	1.03	0.11	0.3	0.6	0.74	0.1	0.09	0.38
Cthe_02663	methyl-accepting chemotaxis sensory tran	8.42	8.69	9.49	8.06	-1.07	0.63	-0.27	1.43	-0.62	0.63	-0.8	1.6	0.1	0.09	0.56
Cthe_00103	protein of unknown function UPF0047	7.64	7.09	7.58	6.71	0.06	0.38	0.55	0.87	0.91	0.33	1.93	0.4	0.1	0.09	0.56
Cthe_00151	protein of unknown function DUF965	11.11	11.09	11.55	10.98	-0.44	0.11	0.02	0.57	0.23	0.01	0.17	-0.23	0.1	0.09	0.91
Cthe_01168	Extradial ring-cleavage dioxygenase, class	9.56	9.42	10.01	8.78	-0.45	0.64	0.14	1.23	0.22	0.64	0.57	1.17	0.1	0.09	0.59
Cthe_00765	ribosomal protein L19	13.33	13.48	13.81	13.36	-0.48	0.12	-0.15	0.45	0.18	0.02	-0.4	-0.49	0.1	0.09	0.33
Cthe_00344	Malate dehydrogenase	15.18	15.35	15.38	15.39	-0.2	-0.04	-0.17	-0.01	0.55	-0.17	-0.47	-1.47	0.1	0.09	0.42
Cthe_03107	Radical SAM	9.76	9.88	10.15	9.93	-0.39	-0.05	-0.12	0.22	0.3	-0.18	-0.3	-0.98	0.1	0.09	0.39
Cthe_00333	hypothetical protein	8.93	8.87	9.41	8.55	-0.48	0.32	0.06	0.86	0.18	0.26	0.3	0.38	0.1	0.09	0.74
Cthe_02072	hypothetical protein	6.38	6.34	7.26	5.88	-0.88	0.46	0.04	1.38	-0.36	0.43	0.23	1.49	0.1	0.09	0.42
Cthe_01015	hypothetical protein	7.4	7.31	7.9	6.74	-0.5	0.57	0.09	1.16	0.15	0.56	0.4	1.02	0.1	0.09	0.6
Cthe_01198	hypothetical protein	7.93	7.95	8.6	7.22	-0.67	0.73	-0.02	1.38	-0.08	0.75	0.03	1.49	0.1	0.09	0.58
Cthe_01460	hypothetical protein	8.16	7.99	8.87	7.07	-0.71	0.92	0.17	1.8	-0.14	0.98	0.67	2.38	0.1	0.09	0.45
Cthe_02437	shikimate kinase	12.28	12.07	12.57	11.85	-0.29	0.22	0.21	0.72	0.43	0.14	0.8	0.09	0.1	0.09	0.64
Cthe_02962	oligopeptide/dipeptide ABC transporter, A	7.75	7.91	8.04	7.91	-0.29	0	-0.16	0.13	0.43	-0.12	-0.43	-1.17	0.1	0.09	0.41
Cthe_00765	ribosomal protein L19	13.33	13.48	13.81	13.36	-0.48	0.12	-0.15	0.45	0.18	0.02	-0.4	-0.49	0.1	0.09	0.33
Cthe_00180	crossover junction endodeoxyribonucleas	8.6	8.67	9.11	8.48	-0.51	0.19	-0.07	0.63	0.14	0.11	-0.13	-0.11	0.1	0.09	1.19
Cthe_00344	Malate dehydrogenase	15.18	15.35	15.38	15.39	-0.2	-0.04	-0.17	-0.01	0.55	-0.17	-0.47	-1.47	0.1	0.09	0.42
Cthe_02437	shikimate kinase	12.28	12.07	12.57	11.85	-0.29	0.22	0.21	0.72	0.43	0.14	0.8	0.09	0.1	0.09	0.64
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42	11.86	11.21	-0.52	0.21	-0.08	0.65	0.12	0.13	-0.17	-0.06	0.1	0.09	1.12
Cthe_00572	radical SAM enzyme, Cfr family	11.34	11.42													



Cthe_00102	tRNA (guanine-N(7))-methyltransferase	8.92	9.22	9.36	8.89	-0.44	0.33	-0.3	0.47	0.23	0.27	-0.9	-0.45	0.09	0.08	0.4
Cthe_02309	Nitrilase/cyanide hydratase and apolipop	5.73	5.36	5.98	5.09	-0.25	0.27	0.37	0.89	0.49	0.2	1.33	0.45	0.09	0.08	0.43
Cthe_02334	polysaccharide biosynthesis protein CapD	11.97	11.85	12.17	12.05	-0.2	0.12	0.12	0.12	0.55	-0.36	0.5	-1.19	0.09	0.08	0.58
Cthe_00834	NusB antitermination factor	10.02	10.04	10.59	9.73	-0.57	0.31	-0.02	0.86	0.05	0.25	0.03	0.38	0.09	0.08	0.76
Cthe_02451	SNF2-related protein	9.64	9.8	10.11	9.66	-0.47	0.14	-0.16	0.45	0.19	0.05	-0.43	-0.49	0.09	0.08	0.34
Cthe_02451	SNF2-related protein	9.64	9.8	10.11	9.66	-0.47	0.14	-0.16	0.45	0.19	0.05	-0.43	-0.49	0.09	0.08	0.34
Cthe_02203	GTP cyclohydrolase I	10.91	10.63	11.12	10.48	-0.21	0.15	0.28	0.64	0.54	0.06	1.03	-0.09	0.09	0.08	0.6
Cthe_02334	polysaccharide biosynthesis protein CapD	11.97	11.85	12.17	12.05	-0.2	0.12	0.12	0.12	0.55	-0.36	0.5	-1.19	0.09	0.08	0.58
Cthe_00070	asparaginyl-tRNA synthetase	12.09	11.99	12.44	11.98	-0.35	0.01	0.1	0.46	0.35	-0.11	0.43	-0.47	0.09	0.08	0.65
Cthe_00611	RNA-metabolising metallo-beta-lactamase	11.28	11.41	11.99	10.96	-0.71	0.45	-0.13	1.03	-0.14	0.42	-0.33	0.74	0.09	0.08	0.62
Cthe_02730	translation elongation factor 1A (EF-1A)/EF	16.65	17.02	16.95	16.66	-0.3	0.36	-0.37	0.29	0.42	0.31	-1.13	-0.83	0.09	0.08	0.42
Cthe_00626	hypothetical protein	11.7	11.69	11.87	11.76	-0.17	-0.07	0.01	0.11	0.59	-0.2	0.13	-1.21	0.09	0.08	0.58
Cthe_02607	ATP synthase F1, gamma subunit	11.11	10.87	11.32	10.92	-0.21	-0.05	0.24	0.4	0.54	-0.18	0.9	-0.6	0.09	0.08	0.6
Cthe_02110	ABC transporter related protein	8.46	8.46	8.93	8.35	-0.47	0.11	0	0.58	0.19	0.01	0.1	-0.21	0.09	0.08	0.93
Cthe_01321	chaperone protein DnaJ	8.85	8.66	9.13	8.66	-0.28	0	0.19	0.47	0.45	-0.12	0.73	-0.45	0.09	0.08	0.62
Cthe_02739	trigger factor	13.11	13.36	13.72	12.89	-0.61	0.47	-0.25	0.83	0	0.44	-0.73	0.32	0.09	0.08	0.63
Cthe_01296	hypothetical protein	9.58	9.72	9.97	9.49	-0.39	0.23	-0.14	0.48	0.3	0.15	-0.37	-0.43	0.09	0.08	0.67
Cthe_02110	ABC transporter related protein	8.46	8.46	8.93	8.35	-0.47	0.11	0	0.58	0.19	0.01	0.1	-0.21	0.09	0.08	0.93
Cthe_02203	GTP cyclohydrolase I	10.91	10.63	11.12	10.48	-0.21	0.15	0.28	0.64	0.54	0.06	1.03	-0.09	0.09	0.08	0.6
Cthe_00070	asparaginyl-tRNA synthetase	12.09	11.99	12.44	11.98	-0.35	0.01	0.1	0.46	0.35	-0.11	0.43	-0.47	0.09	0.08	0.65
Cthe_00070	asparaginyl-tRNA synthetase	12.09	11.99	12.44	11.98	-0.35	0.01	0.1	0.46	0.35	-0.11	0.43	-0.47	0.09	0.08	0.65
Cthe_02607	ATP synthase F1, gamma subunit	11.11	10.87	11.32	10.92	-0.21	-0.05	0.24	0.4	0.54	-0.18	0.9	-0.6	0.09	0.08	0.6
Cthe_02607	ATP synthase F1, gamma subunit	11.11	10.87	11.32	10.92	-0.21	-0.05	0.24	0.4	0.54	-0.18	0.9	-0.6	0.09	0.08	0.6
Cthe_02607	ATP synthase F1, gamma subunit	11.11	10.87	11.32	10.92	-0.21	-0.05	0.24	0.4	0.54	-0.18	0.9	-0.6	0.09	0.08	0.6
Cthe_02730	translation elongation factor 1A (EF-1A)/EF	16.65	17.02	16.95	16.66	-0.3	0.36	-0.37	0.29	0.42	0.31	-1.13	-0.83	0.09	0.08	0.42
Cthe_02203	GTP cyclohydrolase I	10.91	10.63	11.12	10.48	-0.21	0.15	0.28	0.64	0.54	0.06	1.03	-0.09	0.09	0.08	0.6
Cthe_00070	asparaginyl-tRNA synthetase	12.09	11.99	12.44	11.98	-0.35	0.01	0.1	0.46	0.35	-0.11	0.43	-0.47	0.09	0.08	0.65
Cthe_01012	tRNA (guanine-N(7))-methyltransferase	8.92	9.22	9.36	8.89	-0.44	0.33	-0.3	0.47	0.23	0.27	-0.9	-0.45	0.09	0.08	0.4
Cthe_02203	GTP cyclohydrolase I	10.91	10.63	11.12	10.48	-0.21	0.15	0.28	0.64	0.54	0.06	1.03	-0.09	0.09	0.08	0.6
Cthe_02203	GTP cyclohydrolase I	10.91	10.63	11.12	10.48	-0.21	0.15	0.28	0.64	0.54	0.06	1.03	-0.09	0.09	0.08	0.6
Cthe_00070	asparaginyl-tRNA synthetase	12.09	11.99	12.44	11.98	-0.35	0.01	0.1	0.46	0.35	-0.11	0.43	-0.47	0.09	0.08	0.65
Cthe_02203	GTP cyclohydrolase I	10.91	10.63	11.12	10.48	-0.21	0.15	0.28	0.64	0.54	0.06	1.03	-0.09	0.09	0.08	0.6
Cthe_02607	ATP synthase F1, gamma subunit	11.11	10.87	11.32	10.92	-0.21	-0.05	0.24	0.4	0.54	-0.18	0.9	-0.6	0.09	0.08	0.6
Cthe_01191	HAD-superfamily hydrolase, subfamily IA,	8.18	8.22	8.99	7.24	-0.81	0.98	-0.04	1.75	-0.27	1.05	-0.03	2.28	0.08	0.07	0.54
Cthe_02365	tRNA modification GTPase TrmE	9.43	9.35	9.6	9.52	-0.17	-0.17	0.08	0.08	0.59	-0.32	0.37	-1.28	0.08	0.07	0.57
Cthe_03112	glycosidase, PH1107-related	7.33	7.33	7.89	7.02	-0.56	0.31	0	0.87	0.07	0.25	0.1	0.4	0.08	0.07	0.72
Cthe_02083	DNA-directed DNA polymerase	7.71	7.72	7.96	7.73	-0.25	-0.01	-0.01	0.23	0.49	-0.13	0.07	-0.96	0.08	0.07	0.6
Cthe_01266	methyl-accepting chemotaxis sensory tran	6.43	6.17	6.79	5.95	-0.36	0.22	0.26	0.84	0.34	0.14	0.97	0.34	0.08	0.07	0.41
Cthe_01041	UDP-N-acetylmuramoylalanine--D-glutam	12.36	12.52	12.92	12.2	-0.56	0.32	-0.16	0.72	0.07	0.26	-0.43	0.09	0.08	0.07	0.7
Cthe_01266	methyl-accepting chemotaxis sensory tran	6.43	6.17	6.79	5.95	-0.36	0.22	0.26	0.84	0.34	0.14	0.97	0.34	0.08	0.07	0.41
Cthe_01422	RDD domain containing protein	12.29	12.35	12.79	12.19	-0.5	0.16	-0.06	0.6	0.15	0.07	-0.1	-0.17	0.08	0.07	0.95
Cthe_02746	protein of unknown function DUF402	9.65	9.44	9.88	9.6	-0.23	-0.16	0.21	0.28	0.51	-0.31	0.8	-0.85	0.08	0.07	0.58
Cthe_02726	ribosomal protein L7Ae/L30e/S12e/Gadd4	11.37	11.39	11.57	11.41	-0.2	-0.02	-0.02	0.16	0.55	-0.14	0.03	-1.11	0.08	0.07	0.58
Cthe_02728	ribosomal protein S7	12.86	13.06	13.24	12.89	-0.38	0.17	-0.2	0.35	0.31	0.08	-0.57	-0.7	0.08	0.07	0.4
Cthe_00088	cell shape determining protein, MreB/Mrl	9.64	9.5	9.96	9.51	-0.32	-0.01	0.14	0.45	0.39	-0.13	0.57	-0.49	0.08	0.07	0.62
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_01448	MATE efflux family protein	7.36	7.48	7.69	7.52	-0.33	-0.04	-0.12	0.17	0.38	-0.17	-0.3	-1.09	0.08	0.07	0.42
Cthe_00647	anaerobic ribonucleoside-triphosphate re	11.98	11.63	12.15	11.27	-0.17	0.36	0.35	0.88	0.59	0.31	1.27	0.43	0.08	0.07	0.56
Cthe_03230	hypothetical protein	11.89	11.82	12.35	11.63	-0.46	0.19	0.07	0.72	0.2	0.11	0.33	0.09	0.08	0.07	0.76
Cthe_01179	hypothetical protein	6.15	5.75	6.55	4.64	-0.4	1.11	0.4	1.91	0.28	1.2	1.43	2.62	0.08	0.07	0.47
Cthe_03228	copper amine oxidase-like protein	8.26	8.23	8.94	7.97	-0.68	0.26	0.03	0.97	-0.09	0.19	0.2	0.62	0.08	0.07	0.37
Cthe_01307	cellulosome anchoring protein, cohesion re	11.85	12.09	12.43	11.65	-0.58	0.44	-0.24	0.78	0.04	0.4	-0.7	0.21	0.08	0.07	0.63
Cthe_00047	copper amine oxidase-like protein	6.43	6.64	7.37	6.09	-0.94	0.55	-0.21	1.28	-0.45	0.54	-0.6	1.28	0.08	0.07	0.57
Cthe_02728	ribosomal protein S7	12.86	13.06	13.24	12.89	-0.38	0.17	-0.2	0.35	0.31	0.08	-0.57	-0.7	0.08	0.07	0.4
Cthe_02726	ribosomal protein L7Ae/L30e/S12e/Gadd4	11.37	11.39	11.57	11.41	-0.2	-0.02	-0.02	0.16	0.55	-0.14	0.03	-1.11	0.08	0.07	0.58
Cthe_02728	ribosomal protein S7	12.86	13.06	13.24	12.89	-0.38	0.17	-0.2	0.35	0.31	0.08	-0.57	-0.7	0.08	0.07	0.4
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_00647	anaerobic ribonucleoside-triphosphate re	11.98	11.63	12.15	11.27	-0.17	0.36	0.35	0.88	0.59	0.31	1.27	0.43	0.08	0.07	0.56
Cthe_02083	DNA-directed DNA polymerase	7.71	7.72	7.96	7.73	-0.25	-0.01	-0.01	0.23	0.49	-0.13	0.07	-0.96	0.08	0.07	0.6
Cthe_01041	UDP-N-acetylmuramoylalanine--D-glutam	12.36	12.52	12.92	12.2	-0.56	0.32	-0.16	0.72	0.07	0.26	-0.43	0.09	0.08	0.07	0.7
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_01191	HAD-superfamily hydrolase, subfamily IA,	8.18	8.22	8.99	7.24	-0.81	0.98	-0.04	1.75	-0.27	1.05	-0.03	2.28	0.08	0.07	0.54
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_01191	HAD-superfamily hydrolase, subfamily IA,	8.18	8.22	8.99	7.24	-0.81	0.98	-0.04	1.75	-0.27	1.05	-0.03	2.28	0.08	0.07	0.54
Cthe_01041	UDP-N-acetylmuramoylalanine--D-glutam	12.36	12.52	12.92	12.2	-0.56	0.32	-0.16	0.72	0.07	0.26	-0.43	0.09	0.08	0.07	0.7
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_01041	UDP-N-acetylmuramoylalanine--D-glutam	12.36	12.52	12.92	12.2	-0.56	0.32	-0.16	0.72	0.07	0.26	-0.43	0.09	0.08	0.07	0.7
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_01041	UDP-N-acetylmuramoylalanine--D-glutam	12.36	12.52	12.92	12.2	-0.56	0.32	-0.16	0.72	0.07	0.26	-0.43	0.09	0.08	0.07	0.7
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_01041	UDP-N-acetylmuramoylalanine--D-glutam	12.36	12.52	12.92	12.2	-0.56	0.32	-0.16	0.72	0.07	0.26	-0.43	0.09	0.08	0.07	0.7
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_02537	sulfate adenylyltransferase, large subunit	3.58	3.17	3.81	3.32	-0.23	-0.15	0.41	0.49	0.51	-0.3	1.47	-0.4	0.08	0.07	0.44
Cthe_003																







[illegible]



Cthe_00893	protein of unknown function DUF633	8.79	8.57	9.16	8.41	-0.37	0.16	0.22	0.75	0.32	0.07	0.83	0.15	0.04	0.03	0.44
Cthe_00095	methylglyoxal synthase	11.44	11.42	11.84	11.44	-0.4	-0.02	0.02	0.4	0.28	-0.14	0.17	-0.6	0.04	0.03	0.57
Cthe_02210	3-isopropylmalate dehydratase, small sub	10.38	11.08	11.09	10.17	-0.71	0.91	-0.7	0.92	-0.14	0.96	-2.23	0.51	0.04	0.03	0.48
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_02105	DNA-directed DNA polymerase	9.6	9.31	9.84	9.09	-0.24	0.22	0.29	0.75	0.5	0.14	1.07	0.15	0.04	0.03	0.55
Cthe_02144	DNA polymerase III, subunits gamma and	10.09	10.35	10.71	10	-0.62	0.35	-0.26	0.71	-0.01	0.3	-0.77	0.06	0.04	0.03	0.44
Cthe_00021	dethiobiotin synthase	5.49	5.49	5.81	5.55	-0.32	-0.06	0	0.26	0.39	-0.19	0.1	-0.89	0.04	0.03	0.55
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_01488	methyl-accepting chemotaxis sensory tran	6.74	6.74	7.46	6.44	-0.72	0.3	0	1.02	-0.15	0.24	0.1	0.72	0.04	0.03	0.44
Cthe_02638	O-antigen polymerase	5.04	4.95	5.64	4.46	-0.6	0.49	0.09	1.18	0.01	0.46	0.4	1.06	0.04	0.03	0.46
Cthe_01488	methyl-accepting chemotaxis sensory tran	6.74	6.74	7.46	6.44	-0.72	0.3	0	1.02	-0.15	0.24	0.1	0.72	0.04	0.03	0.44
Cthe_01238	iojap-like protein	9.02	8.95	9.52	8.69	-0.5	0.26	0.07	0.83	0.15	0.19	0.33	0.32	0.04	0.03	0.6
Cthe_02065	cysteinyI-tRNA synthetase	11.79	11.75	12.19	11.85	-0.4	-0.1	0.04	0.34	0.28	-0.24	0.23	-0.72	0.04	0.03	0.55
Cthe_02685	putative TIM-barrel protein, nifR3 family	13.09	12.87	13.47	12.89	-0.38	-0.02	0.22	0.58	0.31	-0.14	0.83	-0.21	0.04	0.03	0.45
Cthe_03000	phosphate transporter	10.75	10.78	11.22	10.7	-0.47	0.08	-0.03	0.52	0.19	-0.02	0	-0.34	0.04	0.03	0.64
Cthe_02873	hypothetical protein	9.45	9.52	9.66	9.52	-0.21	0	-0.07	0.14	0.54	-0.12	-0.13	-1.15	0.04	0.03	0.54
Cthe_03134	hypothetical protein	2.81	2.81	3.46	2.58	-0.65	0.23	0	0.88	-0.05	0.15	0.1	0.43	0.04	0.03	0.41
Cthe_00308	hypothetical protein	11.75	11.8	12.09	11.96	-0.34	-0.16	-0.05	0.13	0.36	-0.31	-0.07	-1.17	0.04	0.03	0.46
Cthe_02310	hypothetical protein	8.33	8.46	9.41	7.58	-1.08	0.88	-0.13	1.83	-0.64	0.93	-0.33	2.45	0.04	0.03	0.52
Cthe_02065	cysteinyI-tRNA synthetase	11.79	11.75	12.19	11.85	-0.4	-0.1	0.04	0.34	0.28	-0.24	0.23	-0.72	0.04	0.03	0.55
Cthe_02210	3-isopropylmalate dehydratase, small sub	10.38	11.08	11.09	10.17	-0.71	0.91	-0.7	0.92	-0.14	0.96	-2.23	0.51	0.04	0.03	0.48
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_02065	cysteinyI-tRNA synthetase	11.79	11.75	12.19	11.85	-0.4	-0.1	0.04	0.34	0.28	-0.24	0.23	-0.72	0.04	0.03	0.55
Cthe_02105	DNA-directed DNA polymerase	9.6	9.31	9.84	9.09	-0.24	0.22	0.29	0.75	0.5	0.14	1.07	0.15	0.04	0.03	0.55
Cthe_02144	DNA polymerase III, subunits gamma and	10.09	10.35	10.71	10	-0.62	0.35	-0.26	0.71	-0.01	0.3	-0.77	0.06	0.04	0.03	0.44
Cthe_00021	dethiobiotin synthase	5.49	5.49	5.81	5.55	-0.32	-0.06	0	0.26	0.39	-0.19	0.1	-0.89	0.04	0.03	0.55
Cthe_00144	preprotein translocase, SecG subunit	14.32	14.25	14.85	14.16	-0.53	0.09	0.07	0.69	0.11	-0.01	0.33	0.02	0.04	0.03	0.38
Cthe_00095	methylglyoxal synthase	11.44	11.42	11.84	11.44	-0.4	-0.02	0.02	0.4	0.28	-0.14	0.17	-0.6	0.04	0.03	0.57
Cthe_00021	dethiobiotin synthase	5.49	5.49	5.81	5.55	-0.32	-0.06	0	0.26	0.39	-0.19	0.1	-0.89	0.04	0.03	0.55
Cthe_02210	3-isopropylmalate dehydratase, small sub	10.38	11.08	11.09	10.17	-0.71	0.91	-0.7	0.92	-0.14	0.96	-2.23	0.51	0.04	0.03	0.48
Cthe_02065	cysteinyI-tRNA synthetase	11.79	11.75	12.19	11.85	-0.4	-0.1	0.04	0.34	0.28	-0.24	0.23	-0.72	0.04	0.03	0.55
Cthe_02210	3-isopropylmalate dehydratase, small sub	10.38	11.08	11.09	10.17	-0.71	0.91	-0.7	0.92	-0.14	0.96	-2.23	0.51	0.04	0.03	0.48
Cthe_02105	DNA-directed DNA polymerase	9.6	9.31	9.84	9.09	-0.24	0.22	0.29	0.75	0.5	0.14	1.07	0.15	0.04	0.03	0.55
Cthe_02144	DNA polymerase III, subunits gamma and	10.09	10.35	10.71	10	-0.62	0.35	-0.26	0.71	-0.01	0.3	-0.77	0.06	0.04	0.03	0.44
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_00021	dethiobiotin synthase	5.49	5.49	5.81	5.55	-0.32	-0.06	0	0.26	0.39	-0.19	0.1	-0.89	0.04	0.03	0.55
Cthe_02210	3-isopropylmalate dehydratase, small sub	10.38	11.08	11.09	10.17	-0.71	0.91	-0.7	0.92	-0.14	0.96	-2.23	0.51	0.04	0.03	0.48
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_02065	cysteinyI-tRNA synthetase	11.79	11.75	12.19	11.85	-0.4	-0.1	0.04	0.34	0.28	-0.24	0.23	-0.72	0.04	0.03	0.55
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_02210	3-isopropylmalate dehydratase, small sub	10.38	11.08	11.09	10.17	-0.71	0.91	-0.7	0.92	-0.14	0.96	-2.23	0.51	0.04	0.03	0.48
Cthe_02518	ketol-acid reductoisomerase	13.31	13.6	13.81	13.23	-0.5	0.37	-0.29	0.58	0.15	0.32	-0.87	-0.21	0.04	0.03	0.45
Cthe_00483	type III secretion system inner membrane	8.64	8.75	9.05	8.66	-0.41	0.09	-0.11	0.39	0.27	-0.01	-0.27	-0.62	0.03	0.02	0.45
Cthe_00685	peptidase M50	10.49	10.54	11.19	10.1	-0.7	0.44	-0.05	1.09	-0.12	0.4	-0.07	0.87	0.03	0.02	0.54
Cthe_01051	integral membrane protein MviN	8.8	8.92	9.1	8.88	-0.3	0.04	-0.12	0.22	0.42	-0.07	-0.3	-0.98	0.03	0.02	0.47
Cthe_03075	von Willebrand factor, type A	9.76	9.66	10.26	9.63	-0.5	0.03	0.1	0.63	0.15	-0.08	0.43	-0.11	0.03	0.02	0.44
Cthe_00149	HPNtr domain containing protein	13.07	13.02	13.63	12.83	-0.56	0.19	0.05	0.8	0.07	0.11	0.27	0.26	0.03	0.02	0.4
Cthe_00391	ABC transporter related protein	16.54	16.58	17.14	16.43	-0.6	0.15	-0.04	0.71	0.01	0.06	-0.03	0.06	0.03	0.02	1.03
Cthe_00806	PAS/PAC sensor hybrid histidine kinase	6.63	6.64	7.48	6.02	-0.85	0.62	-0.01	1.46	-0.32	0.62	0.07	1.66	0.03	0.02	0.48
Cthe_01825	multi-sensor hybrid histidine kinase	6	6.02	6.82	5.55	-0.82	0.47	-0.02	1.27	-0.28	0.44	0.03	1.26	0.03	0.02	0.47
Cthe_02632	transcription-repair coupling factor	9.98	10.02	10.36	10	-0.38	0.02	-0.04	0.36	0.31	-0.1	-0.03	-0.68	0.03	0.02	0.54
Cthe_03146	peptidase M56, BlaR1	8.02	7.81	8.41	7.83	-0.39	-0.02	0.21	0.58	0.3	-0.14	0.8	-0.21	0.03	0.02	0.45
Cthe_01181	transglutaminase-like protein	10.31	10.29	10.85	10.15	-0.54	0.14	0.02	0.7	0.09	0.05	0.17	0.04	0.03	0.02	0.67
Cthe_02211	3-isopropylmalate dehydratase, large sub	11.27	11.65	11.93	11.14	-0.66	0.51	-0.38	0.79	-0.07	0.49	-1.17	0.23	0.03	0.02	0.47
Cthe_02632	transcription-repair coupling factor	9.98	10.02	10.36	10	-0.38	0.02	-0.04	0.36	0.31	-0.1	-0.03	-0.68	0.03	0.02	0.54
Cthe_03108	phage SPO1 DNA polymerase-related prot	8.93	8.82	9.36	8.89	-0.43	-0.07	0.11	0.47	0.24	-0.2	0.47	-0.45	0.03	0.02	0.55
Cthe_02226	FkbH like protein	8.38	8.24	9.01	7.42	-0.63	0.82	0.14	1.59	-0.03	0.86	0.57	1.94	0.03	0.02	0.48
Cthe_00483	type III secretion system inner membrane	8.64	8.75	9.05	8.66	-0.41	0.09	-0.11	0.39	0.27	-0.01	-0.27	-0.62	0.03	0.02	0.45
Cthe_00243	copper amine oxidase-like protein	12	11.91	12.45	11.87	-0.45	0.04	0.09	0.58	0.22	-0.07	0.4	-0.21	0.03	0.02	0.58
Cthe_01857	carboxyl-terminal protease	11.55	11.42	11.99	11.14	-0.44	0.28	0.13	0.85	0.23	0.21	0.53	0.36	0.03	0.02	0.55
Cthe_00142	metal dependent phosphohydrolase	10.5	10.55	11.64	9.74	-1.14	0.81	-0.05	1.9	-0.72	0.85	-0.07	2.6	0.03	0.02	0.49
Cthe_00409	ACT domain-containing protein	8.18	8.23	8.61	8.26	-0.43	-0.03	-0.05	0.35	0.24	-0.15	-0.07	-0.7	0.03	0.02	0.46
Cthe_00806	PAS/PAC sensor hybrid histidine kinase	6.63	6.64	7.48	6.02	-0.85	0.62	-0.01	1.46	-0.32	0.62	0.07	1.66	0.03	0.02	0.48
Cthe_01825	multi-sensor hybrid histidine kinase	6	6.02	6.82	5.55	-0.82	0.47	-0.02	1.27	-0.28	0.44	0.03	1.26	0.03	0.02	0.47
Cthe_03146	peptidase M56, BlaR1	8.02	7.81	8.41	7.83	-0.39	-0.02	0.21	0.58	0.3	-0.14	0.8	-0.21	0.03	0.02	0.45
Cthe_00858	protein of unknown function DUF1432	12.11	12.38	12.74	11.94	-0.63	0.44	-0.27	0.8	-0.03	0.4	-0.8	0.26	0.03	0.02	0.54
Cthe_00152	aldo/keto reductase	11.04	10.97	11.51	11	-0.47	-0.03	0.07	0.51	0.19	-0.15	0.33	-0.36	0.03	0.02	0.56
Cthe_02405	Heavy metal transport/detoxification prot	9.14	9.01	9.56	9.09	-0.42	-0.08	0.13	0.47	0.26	-0.21	0.53	-0.45	0.03	0.02	0.55
Cthe_00232	hypothetical protein	10.42	10.54	10.97	10.32	-0.55	0.22	-0.12	0.65	0.08	0.14	-0.3	-0.06	0.03	0.02	0.6
Cthe_00307	hypothetical protein	12.84	12.82	13.12	13	-0.28	-0.18	0.02	0.12	0.45	-0.33	0.17	-1.19	0.03	0.02	0.53
Cthe_03189	hypothetical protein	10.13	10.06	10.59	10.06	-0.46	0	0.07	0.53	0.2	-0.12	0.33	-0.32	0.03	0.02	0.58
Cthe_00259	Rhomboid-like protein	9.22	9.33	9.94	9.08	-0.72	0.25	-0.11	0.86	-0.15	0.18	-0.27	0.38	0.03	0.02	0.57
Cthe_01966	hypothetical protein	7.88	7.53	8.18	6.71	-0.3	0.82	0.35	1.47	0.42	0.86	1.27	1.68	0.03	0.02	



Cthe_02629	UDP-N-acetylglucosamine pyrophosphory	11.02	11.09	11.51	11.02	-0.49	0.07	-0.07	0.49	0.16	-0.04	-0.13	-0.4	0.02	0.01	0.45
Cthe_03114	glycosyl transferase, group 1	9.15	9.06	9.67	8.78	-0.52	0.28	0.09	0.89	0.12	0.21	0.4	0.45	0.02	0.01	0.46
Cthe_02113	periplasmic sensor signal transduction his	7.88	7.89	8.55	7.64	-0.67	0.25	-0.01	0.91	-0.08	0.18	0.07	0.49	0.02	0.01	0.45
Cthe_00369	protein of unknown function DUF111	9.81	9.84	10.24	9.81	-0.43	0.03	-0.03	0.43	0.24	-0.08	0	-0.53	0.02	0.01	0.54
Cthe_00233	GCN5-related N-acetyltransferase	9.78	9.77	10.3	9.73	-0.52	0.04	0.01	0.57	0.12	-0.07	0.13	-0.23	0.02	0.01	0.6
Cthe_00278	pseudouridine synthase	9.42	9.5	9.87	9.39	-0.45	0.11	-0.08	0.48	0.22	0.01	-0.17	-0.43	0.02	0.01	0.54
Cthe_01320	ribosomal protein L11 methyltransferase	8.02	8.19	8.35	8	-0.33	0.19	-0.17	0.35	0.38	0.11	-0.47	-0.7	0.02	0.01	0.53
Cthe_01331	aspartyl-tRNA synthetase	13.05	13.18	13.65	12.94	-0.6	0.24	-0.13	0.71	0.01	0.17	-0.33	0.06	0.02	0.01	0.58
Cthe_02743	putative metalloendopeptidase, glycoprot	9.69	9.66	10.22	9.59	-0.53	0.07	0.03	0.63	0.11	-0.04	0.2	-0.11	0.02	0.01	0.58
Cthe_01072	putative stage IV sporulation YqfD	11.2	11.14	11.74	10.81	-0.54	0.33	0.06	0.93	0.09	0.27	0.3	0.53	0.02	0.01	0.53
Cthe_01932	S-layer-like domain containing protein	6.34	6.64	7.08	6.23	-0.74	0.41	-0.3	0.85	-0.18	0.37	-0.9	0.36	0.02	0.01	0.48
Cthe_01971	hypothetical protein	9.84	9.82	10.68	8.96	-0.84	0.86	0.02	1.72	-0.31	0.9	0.17	2.21	0.02	0.01	0.49
Cthe_02838	intein	6.13	4.25	4.75	3.32	1.38	0.93	1.88	1.43	2.69	0.99	6.37	1.6	0.02	0.01	0.5
Cthe_00320	hypothetical protein	9.83	9.91	10.46	9.72	-0.63	0.19	-0.08	0.74	-0.03	0.11	-0.17	0.13	0.02	0.01	0.61
Cthe_02834	intein	8.58	8.16	8.78	7.55	-0.2	0.61	0.42	1.23	0.55	0.61	1.5	1.17	0.02	0.01	0.49
Cthe_00100	hypothetical protein	11.81	11.77	12.37	11.7	-0.56	0.07	0.04	0.67	0.07	-0.04	0.23	-0.02	0.02	0.01	0.4
Cthe_00796	hypothetical protein	6.15	6.36	6.77	6.02	-0.62	0.34	-0.21	0.75	-0.01	0.29	-0.6	0.15	0.02	0.01	0.53
Cthe_01331	aspartyl-tRNA synthetase	13.05	13.18	13.65	12.94	-0.6	0.24	-0.13	0.71	0.01	0.17	-0.33	0.06	0.02	0.01	0.58
Cthe_02629	UDP-N-acetylglucosamine pyrophosphory	11.02	11.09	11.51	11.02	-0.49	0.07	-0.07	0.49	0.16	-0.04	-0.13	-0.4	0.02	0.01	0.45
Cthe_01331	aspartyl-tRNA synthetase	13.05	13.18	13.65	12.94	-0.6	0.24	-0.13	0.71	0.01	0.17	-0.33	0.06	0.02	0.01	0.58
Cthe_01331	aspartyl-tRNA synthetase	13.05	13.18	13.65	12.94	-0.6	0.24	-0.13	0.71	0.01	0.17	-0.33	0.06	0.02	0.01	0.58
Cthe_02629	UDP-N-acetylglucosamine pyrophosphory	11.02	11.09	11.51	11.02	-0.49	0.07	-0.07	0.49	0.16	-0.04	-0.13	-0.4	0.02	0.01	0.45
Cthe_02333	GCN5-related N-acetyltransferase	9.78	9.77	10.3	9.73	-0.52	0.04	0.01	0.57	0.12	-0.07	0.13	-0.23	0.02	0.01	0.6
Cthe_00848	peptidase M24	9.66	9.71	10.29	9.49	-0.63	0.22	-0.05	0.8	-0.03	0.14	-0.07	0.26	0.02	0.01	0.6
Cthe_00278	pseudouridine synthase	9.42	9.5	9.87	9.39	-0.45	0.11	-0.08	0.48	0.22	0.01	-0.17	-0.43	0.02	0.01	0.54
Cthe_02743	putative metalloendopeptidase, glycoprot	9.69	9.66	10.22	9.59	-0.53	0.07	0.03	0.63	0.11	-0.04	0.2	-0.11	0.02	0.01	0.58
Cthe_01320	ribosomal protein L11 methyltransferase	8.02	8.19	8.35	8	-0.33	0.19	-0.17	0.35	0.38	0.11	-0.47	-0.7	0.02	0.01	0.53
Cthe_02629	UDP-N-acetylglucosamine pyrophosphory	11.02	11.09	11.51	11.02	-0.49	0.07	-0.07	0.49	0.16	-0.04	-0.13	-0.4	0.02	0.01	0.45
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Cthe_01320	ribosomal protein L11 methyltransferase	8.02	8.19	8.35	8	-0.33	0.19	-0.17	0.35	0.38	0.11	-0.47				



Cthe_02848	phage major capsid protein, HK97																
Cthe_02865	phage / plasmid primase, P4 family																
Cthe_02866	phage major capsid protein, HK97																
Cthe_01136	serine/threonine protein kinase with TPR repeats																
Cthe_01478	transcriptional regulator, TetR family	9.24	9.4	9.86	9.12	-0.62	0.28	-0.16	0.74	-0.01	0.21	-0.43	0.13	0.01	0	0.53	
Cthe_01596	transcriptional regulator, MarR family																
Cthe_01600	two component transcriptional regulator, winged																
Cthe_01649	BRO-like protein																
Cthe_01653	SNF2-related protein																
Cthe_01655	hypothetical protein																
Cthe_01664	transcriptional regulator, MerR family																
Cthe_01729	DNA methylase N-4/N-6																
Cthe_01739	SNF2-related protein																
Cthe_01740	BRO-like protein																
Cthe_01742	Helix-turn-helix, type 11 containing protein																
Cthe_02461	transcriptional regulator, XRE family																
Cthe_02462	BRO-like protein																
Cthe_02459	protein of unknown function DUF955																
Cthe_00001	Recombinase																
Cthe_00141	Integrase, catalytic region																
Cthe_00159	Integrase, catalytic region																
Cthe_00348	Integrase, catalytic region																
Cthe_00496	Integrase, catalytic region																
Cthe_00510	Integrase, catalytic region																
Cthe_00512	phage integrase																
Cthe_00514	DNA methylase N-4/N-6																
Cthe_00516	IS66 Orf2 like																
Cthe_00523	Resolvase-like protein																
Cthe_00588	Integrase, catalytic region																
Cthe_00692	Integrase, catalytic region																
Cthe_00698	Integrase, catalytic region																
Cthe_00879	Integrase, catalytic region																
Cthe_01127	phage integrase																
Cthe_01136	serine/threonine protein kinase with TPR repeats																
Cthe_01156	zinc finger, CHC2-type																
Cthe_01193	transposase, mutator type																
Cthe_01206	Integrase, catalytic region																
Cthe_01242	Integrase, catalytic region																
Cthe_01392	Integrase, catalytic region																
Cthe_01469	Integrase, catalytic region																
Cthe_01496	Integrase, catalytic region																
Cthe_01609	Recombinase																
Cthe_01650	DNA-directed DNA polymerase																
Cthe_01653	SNF2-related protein																
Cthe_01656	Integrase, catalytic region																
Cthe_01661	Integrase, catalytic region																
Cthe_01671	Recombinase																
Cthe_01674	Integrase, catalytic region																
Cthe_01676	Integrase, catalytic region																
Cthe_01683	Integrase, catalytic region																
Cthe_01684	transposase IS3/IS911																
Cthe_01687	Integrase, catalytic region																
Cthe_01691	Integrase, catalytic region																
Cthe_01700	Recombinase																
Cthe_01701	Recombinase																
Cthe_01712	Integrase, catalytic region																
Cthe_01723	phage terminase, small subunit, putative, P27																
Cthe_01728	DNA-cytosine methyltransferase																
Cthe_01729	DNA methylase N-4/N-6																
Cthe_01735	phage DNA polymerase																
Cthe_01739	SNF2-related protein																
Cthe_01747	DNA mismatch endonuclease vsr																
Cthe_01749	DNA-cytosine methyltransferase																
Cthe_01881	Integrase, catalytic region																
Cthe_01883	SMC protein-like protein																
Cthe_01885	phage integrase-like SAM-like																
Cthe_01889	transposase, mutator type																
Cthe_01976	Integrase, catalytic region																
Cthe_01983	transposase IS116/IS110/IS902																
Cthe_01993	Integrase, catalytic region																
Cthe_01996	IstB-like ATP-binding protein																
Cthe_01999	Integrase, catalytic region																
Cthe_02000	Integrase, catalytic region																
Cthe_02004	transposase																
Cthe_02005	IstB-like ATP-binding protein																
Cthe_02012	Integrase, catalytic region																
Cthe_02017	transposase, mutator type																
Cthe_02114	Integrase, catalytic region																
Cthe_02135	Integrase, catalytic region																
Cthe_02153	Integrase, catalytic region																
Cthe_02173	Integrase, catalytic region																
Cthe_02188	Integrase, catalytic region																
Cthe_02198	transposase																
Cthe_02199	IstB-like ATP-binding protein																
Cthe_02201	transposase, mutator type																
Cthe_02294	transposase																
Cthe_02295	IstB-like ATP-binding protein																
Cthe_02315	DNA mismatch endonuclease vsr																
Cthe_02322	DNA recombinase																
Cthe_02324	Resolvase-like protein																
Cthe_02455	phage integrase																
Cthe_02467	replicative DNA helicase																
Cthe_02484	transposase IS116/IS110/IS902																
Cthe_02508	TOPRIM domain containing protein	8.39	8.62	8.89	8.3	-0.5	0.32	-0.23	0.59	0.15	0.26	-0.67	-0.19	0.01	0	0.49	
Cthe_02672	transposase, mutator type																
Cthe_02715	Integrase, catalytic region																



Cthe_02716	Integrase, catalytic region Ist8-																
Cthe_02750	like ATP-binding protein Integrase,																
Cthe_02773	catalytic region transposase,																
Cthe_02816	mutator type ISDet4,																
Cthe_02829	transposase																
Cthe_02830	Ist8-like ATP-binding protein																
Cthe_02831	transposase																
Cthe_02868	transposase IS116/IS110/IS902																
Cthe_02958	transposase, mutator type																
Cthe_03051	transposase, mutator type																
Cthe_03181	Integrase, catalytic region																
Cthe_03182	Integrase, catalytic region																
Cthe_03207	transposase, mutator type																
Cthe_03208	Integrase, catalytic region																
Cthe_03216	transposase, mutator type																
Cthe_03219	CRISPR-associated protein Cas2																
Cthe_01681																	
Cthe_02158																	
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_01679	Methyltransferase type 11																
Cthe_02538	thiamine biosynthesis protein ThiS																
Cthe_01702	cell wall hydrolase/autolysin N-																
Cthe_02498	acetylmuramoyl-L-alanine amidase																
Cthe_02085	deoxyuridine 5'-triphosphate nucleotidoh	8.35	7.96	8.55	8.18	-0.2	-0.22	0.39	0.37	0.55	-0.38	1.4	-0.66	0.01	0	0.49	
Cthe_00273	metal dependent phosphohydrolase	11.02	11.19	11.66	10.9	-0.64	0.29	-0.17	0.76	-0.04	0.23	-0.47	0.17	0.01	0	0.53	
Cthe_01136	serine/threonine protein kinase with TPR repeats																
Cthe_01304	PhoH-like protein	9.46	9.49	10.22	9.02	-0.76	0.47	-0.03	1.2	-0.2	0.44	0	1.11	0.01	0	0.49	
Cthe_01599	multi-sensor signal transduction histidine																
Cthe_01600	two component transcriptional regulator, winged																
Cthe_02476	phage putative head morphogenesis protein, SPP1																
Cthe_00451	protein of unknown function DUF115	9.61	9.76	10.26	9.52	-0.65	0.24	-0.15	0.74	-0.05	0.17	-0.4	0.13	0.01	0	0.48	
Cthe_01113	SEC-C motif containing protein																
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01616	phage minor structural protein																
Cthe_01707	phage minor structural protein																
Cthe_01708	phage putative tail component																
Cthe_01709	Phage-related protein-like protein																
Cthe_01721	phage portal protein, HK97 family																
Cthe_01849	Heavy metal transport/detoxification prot	6.78	6.82	6.99	6.93	-0.21	-0.11	-0.04	0.06	0.54	-0.25	-0.03	-1.32	0.01	0	0.51	
Cthe_02106	protein of unknown function DUF327	9.05	9.08	9.38	9.14	-0.33	-0.06	-0.03	0.24	0.38	-0.19	0	-0.94	0.01	0	0.51	
Cthe_02489	Peptidoglycan-binding LysM																
Cthe_02495	hypothetical protein																
Cthe_00033	small GTP-binding protein	8.14	8.21	8.63	8.12	-0.49	0.09	-0.07	0.51	0.16	-0.01	-0.13	-0.36	0.01	0	0.48	
Cthe_00214	phenylalanyl-tRNA synthetase, alpha subu	9.87	9.9	10.25	9.99	-0.38	-0.09	-0.03	0.26	0.31	-0.23	0	-0.89	0.01	0	0.49	
Cthe_01663	Endoribonuclease L-PSP																
Cthe_02939	tRNA pseudouridine synthase A	8.41	8.1	8.64	7.98	-0.23	0.12	0.31	0.66	0.51	0.02	1.13	-0.04	0.01	0	0.51	
Cthe_01597	flavodoxin																
Cthe_02266	Vacuolar H+-transporting two-sector ATPase, F																
Cthe_00031	putative membrane transporter																
Cthe_01601	phosphate uptake regulator, PhoU																
Cthe_01602	phosphate ABC transporter, ATPase subunit																
Cthe_01603	phosphate ABC transporter, inner membrane																
Cthe_01604	phosphate ABC transporter, inner membrane																
Cthe_01605	phosphate ABC transporter (binding protein)-like																
Cthe_01849	Heavy metal transport/detoxification prot	6.78	6.82	6.99	6.93	-0.21	-0.11	-0.04	0.06	0.54	-0.25	-0.03	-1.32	0.01	0	0.51	
Cthe_01917	ATPase, P-type (transporting), HAD superfamily	10.98	11.05	11.9	10.43	-0.92	0.62	-0.07	1.47	-0.42	0.62	-0.13	1.68	0.01	0	0.51	
Cthe_00030	phosphatidate cytidylyltransferase																
Cthe_01144	restriction modification system DNA specificity N-																
Cthe_01145	6 DNA methylase																
Cthe_01668	ABC transporter related protein																
Cthe_01685	ABC transporter related protein																
Cthe_00351	PpiC-type peptidyl-prolyl cis-trans isomera	10.99	10.82	11.39	10.83	-0.4	-0.01	0.17	0.56	0.28	-0.13	0.67	-0.26	0.01	0	0.49	
Cthe_01167	Radical SAM	8.97	9.03	9.72	8.7	-0.75	0.33	-0.06	1.02	-0.19	0.27	-0.1	0.72	0.01	0	0.52	
Cthe_01629	peptidase S14, ClpP																
Cthe_01665	Hsp33 protein																
Cthe_01720	peptidase S14, ClpP																
Cthe_01115	Tn7-like transposition protein C																
Cthe_03032	hypothetical protein	11.06	11.08	11.49	11.09	-0.43	-0.01	-0.02	0.4	0.24	-0.13	0.03	-0.6	0.01	0	0.52	
Cthe_01518	hypothetical protein																
Cthe_01648	hypothetical protein																
Cthe_01131	hypothetical protein																
Cthe_02497	hypothetical protein																
Cthe_01730	hypothetical protein																
Cthe_01750	hypothetical protein																
Cthe_02859	hypothetical protein																
Cthe_01719	phage major capsid protein, HK97 family																
Cthe_02480	hypothetical protein																
Cthe_01875	HMG-I and HMG-Y, DNA-binding																
Cthe_01636	hypothetical protein																
Cthe_01610	hypothetical protein																
Cthe_01733	hypothetical protein																
Cthe_01699	RNA related																
Cthe_01706	hypothetical protein																
Cthe_01614	hypothetical protein																
Cthe_02837	prophage Lp4 protein 7, DNA replication																
Cthe_01876	Tn7-like transposition protein A																
Cthe_01119	hypothetical protein																
Cthe_01744	hypothetical protein																
Cthe_01146	hypothetical protein																
Cthe_01715	phage protein, HK97 gp10 family																
Cthe_01134	hypothetical protein																
Cthe_00921	hypothetical protein																
Cthe_02845	hypothetical protein																
Cthe_00525	hypothetical protein																
Cthe_01738	hypothetical protein																
Cthe_02493	phage-like element PB5X protein																



Cthe_01594	hypothetical protein																
Cthe_01994	hypothetical protein																
Cthe_02015	hypothetical protein																
Cthe_00526	hypothetical protein																
Cthe_01725	hypothetical protein																
Cthe_01139	hypothetical protein																
Cthe_02861	hypothetical protein																
Cthe_02321	hypothetical protein																
Cthe_01731	HNH endonuclease																
Cthe_01158	hypothetical protein																
Cthe_01157	hypothetical protein																
Cthe_01987	hypothetical protein																
Cthe_01142	hypothetical protein																
Cthe_01114	Tn7-like transposition protein D																
Cthe_01152	hypothetical protein																
Cthe_02028	hypothetical protein																
Cthe_03236	hypothetical protein																
Cthe_02478	phage minor structural GP20																
Cthe_01654	hypothetical protein																
Cthe_01635	hypothetical protein																
Cthe_02468	hypothetical protein																
Cthe_01129	hypothetical protein																
Cthe_01128	hypothetical protein																
Cthe_01135	SEFIR domain containing protein																
Cthe_00010	hypothetical protein	6.07	6.34	6.75	5.95	-0.68	0.39	-0.27	0.8	-0.09	0.35	-0.8	0.26	0.01	0	0.49	
Cthe_02758	hypothetical protein																
Cthe_01710	hypothetical protein																
Cthe_01147	hypothetical protein																
Cthe_01669	DNA recombinase, putative																
Cthe_01652	hypothetical protein																
Cthe_01877	hypothetical protein																
Cthe_01680	DNA polymerase, beta-like region																
Cthe_00522	hypothetical protein																
Cthe_01698	hypothetical protein																
Cthe_02008	conserved hypothetical protein, CF-22 family																
Cthe_01118	hypothetical protein																
Cthe_01615	hypothetical protein																
Cthe_02852	hypothetical protein																
Cthe_01672	hypothetical protein																
Cthe_01724	hypothetical protein																
Cthe_01984	hypothetical protein																
Cthe_02466	hypothetical protein																
Cthe_01154	transcriptional regulator, XRE family																
Cthe_02016	RNA related																
Cthe_02846	hypothetical protein																
Cthe_02864	hypothetical protein																
Cthe_02469	phage transcriptional regulator, RinA family																
Cthe_02318	hypothetical protein																
Cthe_01871	Tn7-like transposition protein D																
Cthe_01741	hypothetical protein																
Cthe_01626	phage head-tail adaptor, putative																
Cthe_01608	Recombinase																
Cthe_01713	phage major tail protein, phi13 family																
Cthe_02317	response regulator receiver protein																
Cthe_01694	hypothetical protein																
Cthe_02479	lJ928 prophage protein																
Cthe_02494	hypothetical protein																
Cthe_01670	Recombinase																
Cthe_01623	phage major tail protein, phi13 family																
Cthe_01634	hypothetical protein																
Cthe_01745	transcriptional regulator, XRE family																
Cthe_01726	hypothetical protein																
Cthe_02464	hypothetical protein																
Cthe_02490	hypothetical protein																
Cthe_01651	hypothetical protein																
Cthe_01159	hypothetical protein																
Cthe_01641	HNH endonuclease																
Cthe_01689	hypothetical protein																
Cthe_01121	hypothetical protein																
Cthe_02499	hypothetical protein																
Cthe_01717	hypothetical protein																
Cthe_02482	hypothetical protein																
Cthe_02471	hypothetical protein																
Cthe_01120	hypothetical protein																
Cthe_01888	hypothetical protein																
Cthe_03080	cellulosome anchoring protein, cohesion re	13.42	13.78	14.16	13.26	-0.74	0.52	-0.36	0.9	-0.18	0.5	-1.1	0.47	0.01	0	0.5	
Cthe_02849	hypothetical protein																
Cthe_02465	hypothetical protein																
Cthe_01882	hypothetical protein																
Cthe_01155	hypothetical protein																
Cthe_01878	hypothetical protein																
Cthe_02014	hypothetical protein																
Cthe_01197	intein	8.22	8.28	9.15	7.74	-0.93	0.54	-0.06	1.41	-0.43	0.52	-0.1	1.55	0.01	0	0.49	
Cthe_01598	nitroreductase																
Cthe_01627	uncharacterized phage protein																
Cthe_01117	Tn7-like transposition protein A																
Cthe_00527	hypothetical protein																
Cthe_02009	intein																
Cthe_02486	hypothetical protein																
Cthe_01150	hypothetical protein																
Cthe_01125	hypothetical protein																
Cthe_02487	hypothetical protein																
Cthe_02463	DNA binding domain, excisionase family																
Cthe_01595	hypothetical protein																
Cthe_02314	hypothetical protein																
Cthe_01637	virulence-related protein																



Cthe_01633	hypothetical protein																
Cthe_00918	cellulosome enzyme, dockerin type I	7.31	7.29	7.95	6.82	-0.64	0.47	0.02	1.13	-0.04	0.44	0.17	0.96	0.01	0	0.51	
Cthe_02491	hypothetical protein																
Cthe_01122	hypothetical protein																
Cthe_02496	hypothetical protein																
Cthe_01982	hypothetical protein																
Cthe_02483	hypothetical protein																
Cthe_01140	hypothetical protein																
Cthe_01130	hypothetical protein																
Cthe_01137	hypothetical protein																
Cthe_01736	hypothetical protein																
Cthe_01714	hypothetical protein																
Cthe_01746	hypothetical protein																
Cthe_01677	Abortive infection protein																
Cthe_00513	DNA binding domain, excisionase family																
Cthe_02824	hypothetical protein																
Cthe_02836	hypothetical protein																
Cthe_01640	hypothetical protein																
Cthe_01927	hypothetical protein																
Cthe_01703	HNH endonuclease																
Cthe_02843	hypothetical protein																
Cthe_03238	hypothetical protein																
Cthe_02458	hypothetical protein																
Cthe_01718	hypothetical protein																
Cthe_01621	hypothetical protein																
Cthe_01160	S23 ribosomal protein																
Cthe_02867	hypothetical protein																
Cthe_02477	hypothetical protein																
Cthe_00517	hypothetical protein																
Cthe_01737	phage NTP-binding protein																
Cthe_00524	hypothetical protein																
Cthe_02488	phage tape measure protein																
Cthe_01732	hypothetical protein																
Cthe_01151	hypothetical protein																
Cthe_01646	hypothetical protein																
Cthe_01133	hypothetical protein																
Cthe_01149	hypothetical protein																
Cthe_01126	hypothetical protein																
Cthe_01116	HMG-I and HMG-Y, DNA-binding																
Cthe_01879	hypothetical protein																
Cthe_01668	ABC transporter related protein																
Cthe_02266	Vacuolar H <sup>+</sup> -transporting two-sector ATPase, F																
Cthe_01667	ABC-2 type transporter																
Cthe_01668	ABC transporter related protein																
Cthe_00214	phenylalanyl-tRNA synthetase, alpha subu	9.87	9.9	10.25	9.99	-0.38	-0.09	-0.03	0.26	0.31	-0.23	0	-0.89	0.01	0	0.49	
Cthe_00214	phenylalanyl-tRNA synthetase, alpha subu	9.87	9.9	10.25	9.99	-0.38	-0.09	-0.03	0.26	0.31	-0.23	0	-0.89	0.01	0	0.49	
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_01602	phosphate ABC transporter, ATPase subunit																
Cthe_01603	phosphate ABC transporter, inner membrane																
Cthe_01604	phosphate ABC transporter, inner membrane																
Cthe_01605	phosphate ABC transporter (binding protein)-like																
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_02085	deoxyuridine 5'-triphosphate nucleotidoh	8.35	7.96	8.55	8.18	-0.2	-0.22	0.39	0.37	0.55	-0.38	1.4	-0.66	0.01	0	0.49	
Cthe_00903	protein-export membrane protein SecF	14.01	14.1	14.26	14.09	-0.25	0.01	-0.09	0.17	0.49	-0.11	-0.2	-1.09	0.01	0	0.51	
Cthe_01728	DNA-cytosine methyltransferase																
Cthe_01749	DNA-cytosine methyltransferase																
Cthe_02266	Vacuolar H <sup>+</sup> -transporting two-sector ATPase, F																
Cthe_02085	deoxyuridine 5'-triphosphate nucleotidoh	8.35	7.96	8.55	8.18	-0.2	-0.22	0.39	0.37	0.55	-0.38	1.4	-0.66	0.01	0	0.49	
Cthe_01144	restriction modification system DNA specificity																
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_01747	DNA mismatch endonuclease vsr																
Cthe_02315	DNA mismatch endonuclease vsr																
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_01685	ABC transporter related protein																
Cthe_01917	ATPase, P-type (transporting), HAD superf	10.98	11.05	11.9	10.43	-0.92	0.62	-0.07	1.47	-0.42	0.62	-0.13	1.68	0.01	0	0.51	
Cthe_01602	phosphate ABC transporter, ATPase subunit																
Cthe_00214	phenylalanyl-tRNA synthetase, alpha subu	9.87	9.9	10.25	9.99	-0.38	-0.09	-0.03	0.26	0.31	-0.23	0	-0.89	0.01	0	0.49	
Cthe_02939	tRNA pseudouridine synthase A	8.41	8.1	8.64	7.98	-0.23	0.12	0.31	0.66	0.51	0.02	1.13	-0.04	0.01	0	0.51	
Cthe_01136	serine/threonine protein kinase with TPR repeats																
Cthe_01629	peptidase S14, ClpP																
Cthe_01720	peptidase S14, ClpP																
Cthe_01167	Radical SAM	8.97	9.03	9.72	8.7	-0.75	0.33	-0.06	1.02	-0.19	0.27	-0.1	0.72	0.01	0	0.52	
Cthe_01650	DNA-directed DNA polymerase																
Cthe_01735	phage DNA polymerase																
Cthe_01728	DNA-cytosine methyltransferase																
Cthe_01749	DNA-cytosine methyltransferase																
Cthe_01599	multi-sensor signal transduction histidine																
Cthe_01702	cell wall hydrolase/autolysin																
Cthe_02498	N-acetylmuramoyl-L-alanine amidase																
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_00831	Polyprenyl synthetase	9.61	9.63	10.32	9.33	-0.71	0.3	-0.02	0.99	-0.14	0.24	0.03	0.66	0.01	0	0.48	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	
Cthe_01319	protein of unknown function DUF558	8.97	8.86	9.44	8.9	-0.47	-0.04	0.11	0.54	0.19	-0.17	0.47	-0.3	0.01	0	0.52	



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Cthe_01262	hypothetical protein	10.26	9.9	10.71	10.28	-0.45	-0.38	0.36	0.43	0.22	-0.57	1.3	-0.53	-0.01	-0.02	0.49
Cthe_02994	hypothetical protein	9.51	9.29	10.1	9.52	-0.59	-0.23	0.22	0.58	0.03	-0.39	0.83	-0.21	-0.01	-0.02	0.52
Cthe_02857	hypothetical protein	5.58	6	6.58	6.17	-1	-0.17	-0.42	0.41	-0.53	-0.32	-1.3	-0.57	-0.01	-0.02	0.5
Cthe_00007	hypothetical protein	7.61	7.57	8.71	7.29	-1.1	0.28	0.04	1.42	-0.66	0.21	0.23	1.57	-0.01	-0.02	0.5
Cthe_03225	hypothetical protein	6.91	6.99	7.98	6.44	-1.07	0.55	-0.08	1.54	-0.62	0.54	-0.17	1.83	-0.01	-0.02	0.51
Cthe_00050	hypothetical protein	7.49	7.15	9	7.16	-1.51	-0.01	0.34	1.84	-1.22	-0.13	1.23	2.47	-0.01	-0.02	0.51
Cthe_00225	RNA related	5	4.25	6.27	4.95	-1.27	-0.7	0.75	1.32	-0.89	-0.95	2.6	1.36	-0.01	-0.02	0.5
Cthe_01290	hypothetical protein	10.18	10.29	10.84	10.35	-0.66	-0.06	-0.11	0.49	-0.07	-0.19	-0.27	-0.4	-0.01	-0.02	0.48
Cthe_02280	ABC transporter related protein	10.02	10.05	10.3	10.83	-0.28	-0.78	-0.03	-0.53	0.45	-1.05	0	-2.57	-0.01	-0.02	0.51
Cthe_02721	ribosomal protein L1	13.88	14.12	14.58	14.71	-0.7	-0.59	-0.24	-0.13	-0.12	-0.82	-0.7	-1.72	-0.01	-0.02	0.51
Cthe_01312	glycyl-tRNA synthetase	13.06	13.07	13.65	13.03	-0.59	0.04	-0.01	0.62	0.03	-0.07	0.07	-0.13	-0.01	-0.02	0.59
Cthe_02965	binding-protein-dependent transport syst	8.59	8.58	8.89	9.01	-0.3	-0.43	0.01	-0.12	0.42	-0.63	0.13	-1.7	-0.01	-0.02	0.5
Cthe_01312	glycyl-tRNA synthetase	13.06	13.07	13.65	13.03	-0.59	0.04	-0.01	0.62	0.03	-0.07	0.07	-0.13	-0.01	-0.02	0.59
Cthe_02721	ribosomal protein L1	13.88	14.12	14.58	14.71	-0.7	-0.59	-0.24	-0.13	-0.12	-0.82	-0.7	-1.72	-0.01	-0.02	0.51
Cthe_02280	ABC transporter related protein	10.02	10.05	10.3	10.83	-0.28	-0.78	-0.03	-0.53	0.45	-1.05	0	-2.57	-0.01	-0.02	0.51
Cthe_01312	glycyl-tRNA synthetase	13.06	13.07	13.65	13.03	-0.59	0.04	-0.01	0.62	0.03	-0.07	0.07	-0.13	-0.01	-0.02	0.59
Cthe_02998	ABC transporter related protein	10.92	10.92	11.51	10.89	-0.59	0.03	0	0.62	0.03	-0.08	0.1	-0.13	-0.01	-0.02	0.59
Cthe_02998	ABC transporter related protein	10.92	10.92	11.51	10.89	-0.59	0.03	0	0.62	0.03	-0.08	0.1	-0.13	-0.01	-0.02	0.59
Cthe_01312	glycyl-tRNA synthetase	13.06	13.07	13.65	13.03	-0.59	0.04	-0.01	0.62	0.03	-0.07	0.07	-0.13	-0.01	-0.02	0.59
Cthe_02998	ABC transporter related protein	10.92	10.92	11.51	10.89	-0.59	0.03	0	0.62	0.03	-0.08	0.1	-0.13	-0.01	-0.02	0.59
Cthe_02998	ABC transporter related protein	10.92	10.92	11.51	10.89	-0.59	0.03	0	0.62	0.03	-0.08	0.1	-0.13	-0.01	-0.02	0.59
Cthe_02998	ABC transporter related protein	10.92	10.92	11.51	10.89	-0.59	0.03	0	0.62	0.03	-0.08	0.1	-0.13	-0.01	-0.02	0.59
Cthe_03105	exsB protein	10.85	10.86	11.31	11.17	-0.46	-0.31	-0.01	0.14	0.2	-0.49	0.07	-1.15	-0.02	-0.03	0.52
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_00889	putative transmembrane anti-sigma facto	8.8	8.98	9.56	9.07	-0.76	-0.09	-0.18	0.49	-0.2	-0.23	-0.5	-0.4	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00849	3-dehydroquinase dehydratase, type II	7.58	7.47	8.06	7.55	-0.48	-0.08	0.11	0.51	0.18	-0.21	0.47	-0.36	-0.02	-0.03	0.53
Cthe_01381	threonine synthase	14.05	14.07	14.77	13.84	-0.72	0.23	-0.02	0.93	-0.15	0.15	0.03	0.53	-0.02	-0.03	0.45
Cthe_02786	extracellular solute-binding protein, famil	12.56	12.51	12.63	13.33	-0.07	-0.82	0.05	-0.7	0.73	-1.1	0.27	-2.94	-0.02	-0.03	0.51
Cthe_02630	ribose-phosphate pyrophosphokinase	11.38	11.41	11.74	11.6	-0.36	-0.19	-0.03	0.14	0.34	-0.35	0	-1.15	-0.02	-0.03	0.48
Cthe_00559	single-strand binding protein/Primosomal	7.68	7.32	9.1	7.38	-1.42	-0.06	0.36	1.72	-1.09	-0.19	1.3	2.21	-0.02	-0.03	0.49
Cthe_02297	CRISPR-associated protein Cas1	7.12	7.1	8.36	6.73	-1.24	0.37	0.02	1.63	-0.85	0.32	0.17	2.02	-0.02	-0.03	0.51
Cthe_01313	phosphopantothenoicysteine	10.93	11.11	11.68	11.09	-0.75	0.02	-0.18	0.59	-0.19	-0.1	-0.5	-0.19	-0.02	-0.03	0.46
Cthe_02149	amine oxidase	11.6	11.65	12.1	11.8	-0.5	-0.15	-0.05	0.3	0.15	-0.3	-0.07	-0.81	-0.02	-0.03	0.47
Cthe_03106	6-pyruvoyl tetrahydropterin synthase and CheW protein	10.45	10.43	10.83	10.77	-0.38	-0.34	0.02	0.06	0.31	-0.52	0.17	-1.32	-0.02	-0.03	0.52
Cthe_00491	CheW protein	5.75	5.81	6.46	5.61	-0.71	0.2	-0.06	0.85	-0.14	0.12	-0.1	0.36	-0.02	-0.03	0.56
Cthe_02345	DegT/DnrI/ErpC1/StrS aminotransferase	9.61	9.49	10.12	9.59	-0.51	-0.1	0.12	0.53	0.14	-0.24	0.5	-0.32	-0.02	-0.03	0.53
Cthe_02414	Monogalactosyldiacylglycerol synthase	7.67	7.73	9	7.14	-1.33	0.59	-0.06	1.86	-0.97	0.58	-0.1	2.51	-0.02	-0.03	0.51
Cthe_03050	Fibronectin, type III	5.75	5.86	6.91	5.21	-1.16	0.65	-0.11	1.7	-0.74	0.65	-0.27	2.17	-0.02	-0.03	0.51
Cthe_01246	phosphoribosylaminoimidazolecarboxami	10.46	10.86	11.4	11.17	-0.94	-0.31	-0.4	0.23	-0.45	-0.49	-1.23	-0.96	-0.02	-0.03	0.48
Cthe_02630	ribose-phosphate pyrophosphokinase	11.38	11.41	11.74	11.6	-0.36	-0.19	-0.03	0.14	0.34	-0.35	0	-1.15	-0.02	-0.03	0.48
Cthe_00479	response regulator receiver protein	4.75	4.17	5.39	4.81	-0.64	-0.64	0.58	0.58	-0.04	-0.88	2.03	-0.21	-0.02	-0.03	0.49
Cthe_00491	CheW protein	5.75	5.81	6.46	5.61	-0.71	0.2	-0.06	0.85	-0.14	0.12	-0.1	0.36	-0.02	-0.03	0.56
Cthe_00573	protein serine/threonine phosphatases	11.37	11.38	11.92	11.42	-0.55	-0.04	-0.01	0.5	0.08	-0.17	0.07	-0.38	-0.02	-0.03	0.55
Cthe_02278	extracellular solute-binding protein, famil	12.56	12.51	12.63	13.33	-0.07	-0.82	0.05	-0.7	0.73	-1.1	0.27	-2.94	-0.02	-0.03	0.51
Cthe_00324	valyl-tRNA synthetase	11.11	11.32	11.89	11.48	-0.78	-0.16	-0.21	0.41	-0.23	-0.31	-0.6	-0.57	-0.02	-0.03	0.53
Cthe_02906	ribosomal protein L2	12.11	12.47	13.01	12.89	-0.9	-0.42	-0.36	0.12	-0.39	-0.62	-1.1	-1.19	-0.02	-0.03	0.51
Cthe_02916	ribosomal protein S14	10.58	10.97	11.5	11.47	-0.92	-0.5	-0.39	0.03	-0.42	-0.71	-1.2	-1.38	-0.02	-0.03	0.51
Cthe_00614	pyruvate ferredoxin/flavodoxin oxidoredu	10.73	10.78	11.29	10.76	-0.56	0.02	-0.05	0.53	0.07	-0.1	-0.07	-0.32	-0.02	-0.03	0.42
Cthe_01190	hypothetical protein	7.31	7.7	8.29	7.26	-0.98	0.44	-0.39	1.03	-0.5	0.4	-1.2	0.74	-0.02	-0.03	0.52
Cthe_01537	hypothetical protein	4.17	4.17	4.75	4.17	-0.58	0	0	0.58	0.04	-0.12	0.1	-0.21	-0.02	-0.03	0.62
Cthe_02711	hypothetical protein	11.66	11.54	12.24	11.65	-0.58	-0.11	0.12	0.59	0.04	-0.25	0.5	-0.19	-0.02	-0.03	0.54
Cthe_01454	hypothetical protein	7.73	7.79	8.36	7.71	-0.63	0.08	-0.06	0.65	-0.03	-0.02	-0.1	-0.06	-0.02	-0.03	0.35
Cthe_00835	hypothetical protein	10.13	10.05	10.76	10.07	-0.63	-0.02	0.08	0.69	-0.03	-0.14	0.37	0.02	-0.02	-0.03	0.44
Cthe_00586	transposase IS3/IS911	12.75	12.61	13.24	12.68	-0.49	-0.07	0.14	0.56	0.16	-0.2	0.57	-0.26	-0.02	-0.03	0.46
Cthe_00096	protein of unknown function UPF0180	9.34	8.92	10.29	9.27	-0.95	-0.35	0.42	1.02	-0.46	-0.54	1.5	0.72	-0.02	-0.03	0.48
Cthe_01914	TPR repeat domain containing protein	9.94	9.85	10.69	9.84	-0.75	0.01	0.09	0.85	-0.19	-0.11	0.4	0.36	-0.02	-0.03	0.46
Cthe_00614	pyruvate ferredoxin/flavodoxin oxidoredu	10.73	10.78	11.29	10.76	-0.56	0.02	-0.05	0.53	0.07	-0.1	-0.07	-0.32	-0.02	-0.03	0.42
Cthe_00849	3-dehydroquinase dehydratase, type II	7.58	7.47	8.06	7.55	-0.48	-0.08	0.11	0.51	0.18	-0.21	0.47	-0.36	-0.02	-0.03	0.53
Cthe_02906	ribosomal protein L2	12.11	12.47	13.01	12.89	-0.9	-0.42	-0.36	0.12	-0.39	-0.62	-1.1	-1.19	-0.02	-0.03	0.51
Cthe_02916	ribosomal protein S14	10.58	10.97	11.5	11.47	-0.92	-0.5	-0.39	0.03	-0.42	-0.71	-1.2	-1.38	-0.02	-0.03	0.51
Cthe_00324	valyl-tRNA synthetase	11.11	11.32	11.89	11.48	-0.78	-0.16	-0.21	0.41	-0.23	-0.31	-0.6	-0.57	-0.02	-0.03	0.53
Cthe_02630	ribose-phosphate pyrophosphokinase	11.38	11.41	11.74	11.6	-0.36	-0.19	-0.03	0.14	0.34	-0.35	0	-1.15	-0.02	-0.03	0.48
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_00324	valyl-tRNA synthetase	11.11	11.32	11.89	11.48	-0.78	-0.16	-0.21	0.41	-0.23	-0.31	-0.6	-0.57	-0.02	-0.03	0.53
Cthe_02906	ribosomal protein L2	12.11	12.47	13.01	12.89	-0.9	-0.42	-0.36	0.12	-0.39	-0.62	-1.1	-1.19	-0.02	-0.03	0.51
Cthe_02916	ribosomal protein S14	10.58	10.97	11.5	11.47	-0.92	-0.5	-0.39	0.03	-0.42	-0.71	-1.2	-1.38	-0.02	-0.03	0.51
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_01246	phosphoribosylaminoimidazolecarboxami	10.46	10.86	11.4	11.17	-0.94	-0.31	-0.4	0.23	-0.45	-0.49	-1.23	-0.96	-0.02	-0.03	0.48
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_01313	phosphopantothenoicysteine	10.93	11.11	11.68	11.09	-0.75	0.02	-0.18	0.59	-0.19	-0.1	-0.5	-0.19	-0.02	-0.03	0.46
Cthe_01381	threonine synthase	14.05	14.07	14.77	13.84	-0.72	0.23	-0.02	0.93	-0.15	0.15	0.03	0.53	-0.02	-0.03	0.45
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_02414	Monogalactosyldiacylglycerol synthase	7.67	7.73	9	7.14	-1.33	0.59	-0.06	1.86	-0.97	0.58	-0.1	2.51	-0.02	-0.03	0.51
Cthe_00849	3-dehydroquinase dehydratase, type II	7.58	7.47	8.06	7.55	-0.48	-0.08	0.11	0.51	0.18	-0.21	0.47	-0.36	-0.02	-0.03	0.53
Cthe_02630																



Cthe_00849	3-dehydroquinate dehydratase, type II	7.58	7.47	8.06	7.55	-0.48	-0.08	0.11	0.51	0.18	-0.21	0.47	-0.36	-0.02	-0.03	0.53
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_01313	phosphopantothenoylcysteine	10.93	11.11	11.68	11.09	-0.75	0.02	-0.18	0.59	-0.19	-0.1	-0.5	-0.19	-0.02	-0.03	0.46
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00849	3-dehydroquinate dehydratase, type II	7.58	7.47	8.06	7.55	-0.48	-0.08	0.11	0.51	0.18	-0.21	0.47	-0.36	-0.02	-0.03	0.53
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_03106	6-pyruvoyl tetrahydropterin synthase and	10.45	10.43	10.83	10.77	-0.38	-0.34	0.02	0.06	0.31	-0.52	0.17	-1.32	-0.02	-0.03	0.52
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_01381	threonine synthase	14.05	14.07	14.77	13.84	-0.72	0.23	-0.02	0.93	-0.15	0.15	0.03	0.53	-0.02	-0.03	0.45
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_02414	Mongalactosyldiacylglycerol synthase	7.67	7.73	9	7.14	-1.33	0.59	-0.06	1.86	-0.97	0.58	-0.1	2.51	-0.02	-0.03	0.51
Cthe_00324	valyl-tRNA synthetase	11.11	11.32	11.89	11.48	-0.78	-0.16	-0.21	0.41	-0.23	-0.31	-0.6	-0.57	-0.02	-0.03	0.53
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_01246	phosphoribosylaminoimidazolecarboxami	10.46	10.86	11.4	11.17	-0.94	-0.31	-0.4	0.23	-0.45	-0.49	-1.23	-0.96	-0.02	-0.03	0.48
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_00849	3-dehydroquinate dehydratase, type II	7.58	7.47	8.06	7.55	-0.48	-0.08	0.11	0.51	0.18	-0.21	0.47	-0.36	-0.02	-0.03	0.53
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_00849	3-dehydroquinate dehydratase, type II	7.58	7.47	8.06	7.55	-0.48	-0.08	0.11	0.51	0.18	-0.21	0.47	-0.36	-0.02	-0.03	0.53
Cthe_03106	6-pyruvoyl tetrahydropterin synthase and	10.45	10.43	10.83	10.77	-0.38	-0.34	0.02	0.06	0.31	-0.52	0.17	-1.32	-0.02	-0.03	0.52
Cthe_00363	aminotransferase, class I and II	13.14	13.27	13.86	13.07	-0.72	0.2	-0.13	0.79	-0.15	0.12	-0.33	0.23	-0.02	-0.03	0.54
Cthe_01435	Phosphoglycerate mutase	8.04	7.95	8.6	8.03	-0.56	-0.08	0.09	0.57	0.07	-0.21	0.4	-0.23	-0.02	-0.03	0.55
Cthe_00596	GTP-binding protein	8	8.1	8.7	8.06	-0.7	0.04	-0.1	0.64	-0.12	-0.07	-0.23	-0.09	-0.03	-0.04	0.64
Cthe_00774	RNA chaperone Hfq	10.71	10.8	11.68	10.37	-0.97	0.43	-0.09	1.31	-0.49	0.39	-0.2	1.34	-0.03	-0.04	0.53
Cthe_01055	protein of unknown function DUF58	10.79	11	11.56	11.02	-0.77	-0.02	-0.21	0.54	-0.22	-0.14	-0.6	-0.3	-0.03	-0.04	0.44
Cthe_01069	protein of unknown function UPF0054	9.71	9.8	10.43	9.64	-0.72	0.16	-0.09	0.79	-0.15	0.07	-0.2	0.23	-0.03	-0.04	0.62
Cthe_01301	protein of unknown function DUF795	7.61	7.94	8.57	7.87	-0.96	0.07	-0.33	0.7	-0.47	-0.04	-1	0.04	-0.03	-0.04	0.54
Cthe_00175	polysaccharide deacetylase	11.67	11.64	12.22	11.71	-0.55	-0.07	0.03	0.51	0.08	-0.2	0.2	-0.36	-0.03	-0.04	0.59
Cthe_00910	extracellular solute-binding protein, famil	9.74	9.72	10.66	9.57	-0.92	0.15	0.02	1.09	-0.42	0.06	0.17	0.87	-0.03	-0.04	0.54
Cthe_00153	Holliday junction resolvase YagG	6.77	6.88	7.43	6.87	-0.66	0.01	-0.11	0.56	-0.07	-0.11	-0.27	-0.26	-0.03	-0.04	0.4
Cthe_01014	MutS2 family protein	11.19	11.12	11.65	11.2	-0.46	-0.08	0.07	0.45	0.2	-0.21	0.33	-0.49	-0.03	-0.04	0.56
Cthe_03172	protein of unknown function DUF214	6.36	6.15	7.07	6.3	-0.71	-0.15	0.21	0.77	-0.14	-0.3	0.8	0.19	-0.03	-0.04	0.46
Cthe_00779	copper amine oxidase-like protein	8.47	8.54	9.12	8.59	-0.65	-0.05	-0.07	0.53	-0.05	-0.18	-0.13	-0.32	-0.03	-0.04	0.61
Cthe_02759	transcriptional regulator, AraC family	8.46	8.31	9.03	8.47	-0.57	-0.16	0.15	0.56	0.05	-0.31	0.6	-0.26	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00766	tRNA (guanine-N1)-methyltransferase	10.68	11.12	11.7	11.22	-1.02	-0.1	-0.44	0.48	-0.55	-0.24	-1.37	-0.43	-0.03	-0.04	0.47
Cthe_01005	translation elongation factor Ts (EF-Ts)	12.87	12.99	13.49	13.14	-0.62	-0.15	-0.12	0.35	-0.01	-0.3	-0.3	-0.7	-0.03	-0.04	0.45
Cthe_02910	ribosomal protein L16	11.82	12.18	12.75	12.48	-0.93	-0.3	-0.36	0.27	-0.43	-0.48	-1.1	-0.87	-0.03	-0.04	0.52
Cthe_01232	AMP-dependent synthetase and ligase	11.82	11.85	12.16	12.14	-0.34	-0.29	-0.03	0.02	0.36	-0.46	0	-1.4	-0.03	-0.04	0.47
Cthe_02610	hypothetical protein	9.8	9.88	11.02	9.33	-1.22	0.55	-0.08	1.69	-0.82	0.54	-0.17	2.15	-0.03	-0.04	0.52
Cthe_00279	hypothetical protein	7.06	6.97	7.86	6.98	-0.8	-0.01	0.09	0.88	-0.26	-0.13	0.4	0.43	-0.03	-0.04	0.56
Cthe_00500	hypothetical protein	8.2	8.1	8.8	8.19	-0.6	-0.09	0.1	0.61	0.01	-0.23	0.43	-0.15	-0.03	-0.04	0.57
Cthe_02438	hypothetical protein	9.19	8.92	10.07	9.14	-0.88	-0.22	0.27	0.93	-0.36	-0.38	1	0.53	-0.03	-0.04	0.53
Cthe_01232	AMP-dependent synthetase and ligase	11.82	11.85	12.16	12.14	-0.34	-0.29	-0.03	0.02	0.36	-0.46	0	-1.4	-0.03	-0.04	0.47
Cthe_00910	extracellular solute-binding protein, famil	9.74	9.72	10.66	9.57	-0.92	0.15	0.02	1.09	-0.42	0.06	0.17	0.87	-0.03	-0.04	0.54
Cthe_02910	ribosomal protein L16	11.82	12.18	12.75	12.48	-0.93	-0.3	-0.36	0.27	-0.43	-0.48	-1.1	-0.87	-0.03	-0.04	0.52
Cthe_00153	Holliday junction resolvase YagG	6.77	6.88	7.43	6.87	-0.66	0.01	-0.11	0.56	-0.07	-0.11	-0.27	-0.26	-0.03	-0.04	0.4
Cthe_01232	AMP-dependent synthetase and ligase	11.82	11.85	12.16	12.14	-0.34	-0.29	-0.03	0.02	0.36	-0.46	0	-1.4	-0.03	-0.04	0.47
Cthe_00766	tRNA (guanine-N1)-methyltransferase	10.68	11.12	11.7	11.22	-1.02	-0.1	-0.44	0.48	-0.55	-0.24	-1.37	-0.43	-0.03	-0.04	0.47
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_01232	AMP-dependent synthetase and ligase	11.82	11.85	12.16	12.14	-0.34	-0.29	-0.03	0.02	0.36	-0.46	0	-1.4	-0.03	-0.04	0.47
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09	0.03	0.4	0.2	-0.23	0.2	-0.6	-0.03	-0.04	0.55
Cthe_00127	RNA methyltransferase, TrmH family, grou	7.88	7.85	8.34	7.94	-0.46	-0.09									







Cthe_01533	transposase, mutator type			0	1.58	0	-1.58		-1.58	0.82	-2		-4.81	-0.05	-0.06	0.51
Cthe_02035		7.69	7.77	9.06	7.16	-1.37	0.61	-0.08	1.9	-1.03	0.61	-0.17	2.6	-0.05	-0.06	0.52
Cthe_01176	CheC-like protein	9.98	10.14	11.17	9.41	-1.19	0.73	-0.16	1.76	-0.78	0.75	-0.43	2.3	-0.05	-0.06	0.53
Cthe_00089	rod shape-determining protein MreC	9.72	9.61	10.35	9.74	-0.63	-0.13	0.11	0.61	-0.03	-0.27	0.47	-0.15	-0.05	-0.06	0.63
Cthe_00097	peptidase M23B	9.73	9.36	11.22	9.37	-1.49	-0.01	0.37	1.85	-1.19	-0.13	1.33	2.49	-0.05	-0.06	0.48
Cthe_00909	lipoprotein signal peptidase	9.13	9.02	9.58	9.17	-0.45	-0.15	0.11	0.41	0.22	-0.3	0.47	-0.57	-0.05	-0.06	0.57
Cthe_02562	glucose-1-phosphate cytidylyltransferase	6.78	6.71	7.2	6.92	-0.42	-0.21	0.07	0.28	0.26	-0.37	0.33	-0.85	-0.05	-0.06	0.56
Cthe_03093	Adenylosuccinate synthase	11.51	11.54	12.23	11.44	-0.72	0.1	-0.03	0.79	-0.15	0	0	0.23	-0.05	-0.06	0.74
Cthe_00799	two component transcriptional regulator,	9.56	9.34	10.3	9.48	-0.74	-0.14	0.22	0.82	-0.18	-0.29	0.83	0.3	-0.05	-0.06	0.44
Cthe_01318	response regulator receiver protein	7.53	7.58	8.18	7.61	-0.65	-0.03	-0.05	0.57	-0.05	-0.15	-0.07	-0.23	-0.05	-0.06	0.75
Cthe_00310	hypothetical protein	13	13.09	13.72	13	-0.72	0.09	-0.09	0.72	-0.15	-0.01	-0.2	0.09	-0.05	-0.06	0.78
Cthe_01165	YbbR-like protein	11.38	11.52	12.13	11.51	-0.75	0.01	-0.14	0.62	-0.19	-0.11	-0.37	-0.13	-0.05	-0.06	0.64
Cthe_02562	glucose-1-phosphate cytidylyltransferase	6.78	6.71	7.2	6.92	-0.42	-0.21	0.07	0.28	0.26	-0.37	0.33	-0.85	-0.05	-0.06	0.56
Cthe_02815	lysyl-tRNA synthetase	14.18	14.12	14.67	14.3	-0.49	-0.18	0.06	0.37	0.16	-0.33	0.3	-0.66	-0.05	-0.06	0.57
Cthe_00314	glycosyltransferase 28-like protein	6.98	7.38	7.91	7.02	-0.93	0.36	-0.4	0.89	-0.43	0.31	-1.23	0.45	-0.05	-0.06	0.46
Cthe_01001	undecaprenyl diphosphate synthase	11.93	12	12.49	11.96	-0.56	0.04	-0.07	0.53	0.07	-0.07	-0.13	-0.32	-0.05	-0.06	0.33
Cthe_00710	hypothetical protein	11.82	11.7	12.35	11.88	-0.53	-0.18	0.12	0.47	0.11	-0.33	0.5	-0.45	-0.05	-0.06	0.59
Cthe_00627	hypothetical protein	10.91	10.78	11.34	10.99	-0.43	-0.21	0.13	0.35	0.24	-0.37	0.53	-0.7	-0.05	-0.06	0.57
Cthe_01974	hypothetical protein	10.07	10	11.28	9.63	-1.21	0.37	0.07	1.65	-0.81	0.32	0.33	2.06	-0.05	-0.06	0.47
Cthe_03227	copper amine oxidase-like protein	6.82	7.03	7.69	6.73	-0.87	0.3	-0.21	0.96	-0.35	0.24	-0.6	0.6	-0.05	-0.06	0.57
Cthe_03034	hypothetical protein	9.74	10.01	10.6	10.23	-0.86	-0.22	-0.27	0.37	-0.34	-0.38	-0.8	-0.66	-0.05	-0.06	0.56
Cthe_02279	polar amino acid ABC transporter, inner m	10.64	10.69	10.78	11.47	-0.14	-0.78	-0.05	-0.69	0.64	-1.05	-0.07	-2.91	-0.05	-0.06	0.48
Cthe_03093	Adenylosuccinate synthase	11.51	11.54	12.23	11.44	-0.72	0.1	-0.03	0.79	-0.15	0	0	0.23	-0.05	-0.06	0.74
Cthe_02815	lysyl-tRNA synthetase	14.18	14.12	14.67	14.3	-0.49	-0.18	0.06	0.37	0.16	-0.33	0.3	-0.66	-0.05	-0.06	0.57
Cthe_02932	DNA-directed RNA polymerase, alpha sub	13.9	14.51	15.1	14.98	-1.2	-0.47	-0.61	0.12	-0.8	-0.68	-1.93	-1.19	-0.05	-0.06	0.53
Cthe_03092	inner-membrane translocator	14.89	15.04	15.58	15.06	-0.69	-0.02	-0.15	0.52	-0.11	-0.14	-0.4	-0.34	-0.05	-0.06	0.39
Cthe_02562	glucose-1-phosphate cytidylyltransferase	6.78	6.71	7.2	6.92	-0.42	-0.21	0.07	0.28	0.26	-0.37	0.33	-0.85	-0.05	-0.06	0.56
Cthe_01001	undecaprenyl diphosphate synthase	11.93	12	12.49	11.96	-0.56	0.04	-0.07	0.53	0.07	-0.07	-0.13	-0.32	-0.05	-0.06	0.33
Cthe_02562	glucose-1-phosphate cytidylyltransferase	6.78	6.71	7.2	6.92	-0.42	-0.21	0.07	0.28	0.26	-0.37	0.33	-0.85	-0.05	-0.06	0.56
Cthe_02815	lysyl-tRNA synthetase	14.18	14.12	14.67	14.3	-0.49	-0.18	0.06	0.37	0.16	-0.33	0.3	-0.66	-0.05	-0.06	0.57
Cthe_00764	signal peptidase I	11.56	11.44	12.09	11.6	-0.53	-0.16	0.12	0.49	0.11	-0.31	0.5	-0.4	-0.05	-0.06	0.58
Cthe_00909	lipoprotein signal peptidase	9.13	9.02	9.58	9.17	-0.45	-0.15	0.11	0.41	0.22	-0.3	0.47	-0.57	-0.05	-0.06	0.57
Cthe_03093	Adenylosuccinate synthase	11.51	11.54	12.23	11.44	-0.72	0.1	-0.03	0.79	-0.15	0	0	0.23	-0.05	-0.06	0.74
Cthe_02932	DNA-directed RNA polymerase, alpha sub	13.9	14.51	15.1	14.98	-1.2	-0.47	-0.61	0.12	-0.8	-0.68	-1.93	-1.19	-0.05	-0.06	0.53
Cthe_02562	glucose-1-phosphate cytidylyltransferase	6.78	6.71	7.2	6.92	-0.42	-0.21	0.07	0.28	0.26	-0.37	0.33	-0.85	-0.05	-0.06	0.56
Cthe_02562	glucose-1-phosphate cytidylyltransferase	6.78	6.71	7.2	6.92	-0.42	-0.21	0.07	0.28	0.26	-0.37	0.33	-0.85	-0.05	-0.06	0.56
Cthe_02815	lysyl-tRNA synthetase	14.18	14.12	14.67	14.3	-0.49	-0.18	0.06	0.37	0.16	-0.33	0.3	-0.66	-0.05	-0.06	0.57
Cthe_03093	Adenylosuccinate synthase	11.51	11.54	12.23	11.44	-0.72	0.1	-0.03	0.79	-0.15	0	0	0.23	-0.05	-0.06	0.74
Cthe_03093	Adenylosuccinate synthase	11.51	11.54	12.23	11.44	-0.72	0.1	-0.03	0.79	-0.15	0	0	0.23	-0.05	-0.06	0.74
Cthe_01001	undecaprenyl diphosphate synthase	11.93	12	12.49	11.96	-0.56	0.04	-0.07	0.53	0.07	-0.07	-0.13	-0.32	-0.05	-0.06	0.33
Cthe_00370	conserved hypothetical radical SAM prote	9.72	9.59	10.11	9.82	-0.39	-0.23	0.13	0.29	0.3	-0.39	0.53	-0.83	-0.06	-0.07	0.57
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.95	10.08	10.65	10.29	-0.7	-0.21	-0.13	0.36	-0.12	-0.37	-0.33	-0.68	-0.06	-0.07	0.58
Cthe_01163	phosphoglucosamine mutase	9.86	10.05	10.72	9.84	-0.86	0.21	-0.19	0.88	-0.34	0.13	-0.53	0.43	-0.06	-0.07	0.61
Cthe_02967	major facilitator superfamily MFS_1	7.4	7.33	7.62	8.01	-0.22	-0.68	0.07	-0.39	0.53	-0.93	0.33	-2.28	-0.06	-0.07	0.53
Cthe_00930	Radical SAM	10.7	10.92	11.46	10.98	-0.76	-0.06	-0.22	0.48	-0.2	-0.19	-0.63	-0.43	-0.06	-0.07	0.41
Cthe_02634	transcriptional regulator, AraC family	8.45	8.43	8.99	8.67	-0.54	-0.24	0.02	0.32	0.09	-0.4	0.17	-0.77	-0.06	-0.07	0.59
Cthe_02361	DNA gyrase, A subunit	11.92	11.95	12.54	12.08	-0.62	-0.13	-0.03	0.46	-0.01	-0.27	0	-0.47	-0.06	-0.07	0.65
Cthe_01234	methyl-accepting chemotaxis sensory tran	7.76	8.21	8.78	8.19	-1.02	0.02	-0.45	0.59	-0.55	-0.1	-1.4	-0.19	-0.06	-0.07	0.45
Cthe_01011	Peptidoglycan glycosyltransferase	8.72	8.81	9.78	8.43	-1.06	0.38	-0.09	1.35	-0.61	0.33	-0.2	1.43	-0.06	-0.07	0.55
Cthe_00582	PAS/PAC sensor signal transduction histidi	9.16	9.41	10.02	9.51	-0.86	-0.1	-0.25	0.51	-0.34	-0.24	-0.73	-0.36	-0.06	-0.07	0.58
Cthe_01234	methyl-accepting chemotaxis sensory tran	7.76	8.21	8.78	8.19	-1.02	0.02	-0.45	0.59	-0.55	-0.1	-1.4	-0.19	-0.06	-0.07	0.45
Cthe_00116	protein of unknown function DUF199	10.39	10.32	10.84	10.6	-0.45	-0.28	0.07	0.24	0.22	-0.45	0.33	-0.94	-0.06	-0.07	0.57
Cthe_00213	protein of unknown function DUF975	11.19	11.19	11.7	11.5	-0.51	-0.31	0	0.2	0.14	-0.49	0.1	-1.02	-0.06	-0.07	0.57
Cthe_00457	protein of unknown function DUF307	6.23	6.07	6.66	6.32	-0.43	-0.25	0.16	0.34	0.24	-0.42	0.63	-0.72	-0.06	-0.07	0.57
Cthe_02510	protein of unknown function DUF368	12.58	12.68	13.18	13.18	-0.6	-0.5	-0.1	0	0.01	-0.71	-0.23	-1.45	-0.06	-0.07	0.55
Cthe_01033	glutamyl-tRNA(Gln) amidotransferase, C s	7.77	7.69	8.39	7.79	-0.62	-0.1	0.08	0.6	-0.01	-0.24	0.37	-0.17	-0.06	-0.07	0.67
Cthe_01451	GCNS-related N-acetyltransferase	5.29	5.17	5.67	5.36	-0.38	-0.19	0.12	0.31	0.31	-0.35	0.5	-0.79	-0.06	-0.07	0.57
Cthe_02092	dimethyladenosine transferase	9.89	9.96	10.57	9.97	-0.68	-0.01	-0.07	0.6	-0.09	-0.13	-0.13	-0.17	-0.06	-0.07	0.84
Cthe_02911	ribosomal protein L29	10.26	10.75	11.35	11.12	-1.09	-0.37	-0.49	0.23	-0.65	-0.56	-1.53	-0.96	-0.06	-0.07	0.54
Cthe_00762	protein of unknown function DUF1121	9.48	9.53	10.1	9.71	-0.62	-0.18	-0.05	0.39	-0.01	-0.33	-0.07	-0.62	-0.06	-0.07	0.6
Cthe_00930	Radical SAM	10.7	10.92	11.46	10.98	-0.76	-0.06	-0.22	0.48	-0.2	-0.19	-0.63	-0.43	-0.06	-0.07	0.41
Cthe_02823	hypothetical protein	7.64	7.41	8.43	7.64	-0.79	-0.23	0.23	0.79	-0.24	-0.39	0.87	0.23	-0.06	-0.07	0.58
Cthe_00499	hypothetical protein	6.43	6.69	7.35	6.44	-0.92	0.25	-0.26	0.91	-0.42	0.18	-0.77	0.49	-0.06	-0.07	0.57
Cthe_02129	RNA related	2.58	2.58	3	3.17	-0.42	-0.59	0	-0.17	0.26	-0.82	0.1	-1.81	-0.06	-0.07	0.54
Cthe_02192	hypothetical protein	11.31	11.28	12.57	10.72	-1.26	0.56	0.03	1.85	-0.88	0.55	0.2	2.49	-0.06	-0.07	0.47
Cthe_02854	intein	5.17	5.32	6.52	4.58	-1.35	0.74	-0.15	1.94	-1	0.76	-0.4	2.68	-0.06	-0.07	0.53
Cthe_02033	hypothetical protein	4.09	3	5.36	4.09	-1.27	-1.09	1.09	1.27	-0.89	-1.42	3.73	1.26	-0.06	-0.07	0.48
Cthe_02911	ribosomal protein L29	10.26	10.75	11.35	11.12	-1.09	-0.37	-0.49	0.23	-0.65	-0.56	-1.53	-0.96	-0.06	-0.07	0.54
Cthe_02911	ribosomal protein L29	10.26	10.75	11.35	11.12	-1.09	-0.37	-0.49	0.23	-0.65	-0.56	-1.53	-0.96	-0.06	-0.07	0.54
Cthe_02092	dimethyladenosine transferase	9.89	9.96	10.57	9.97	-0.68	-0.01	-0.07	0.6	-0.09	-0.13	-0.13	-0.17	-0.06	-0.07	0.84
Cthe_02361	DNA gyrase, A subunit	11.92	11.95	12.54	12.08	-0.62	-0.13	-0.03	0.46	-0.01	-0.27	0	-0.47	-0.06	-0.07	0.65
Cthe_01033	glutamyl-tRNA(Gln) amidotransferase, C s	7.77	7.69	8.39	7.79	-0.62	-0.1	0.08	0.6	-0.01	-0.24	0.37	-0.17	-0.06	-0.07	0.67
Cthe_01011	Peptidoglycan glycosyltransferase	8.72	8.81	9.78	8.43	-1.06	0.38	-0.09	1.35	-0.61	0.33	-0.2	1.43	-0.06	-0.07	0.55
Cthe_01033	glutamyl-tRNA(Gln) amidotransferase, C s	7.77	7.69	8.39	7.79	-0.62	-0.1	0.08	0.6	-0.01	-0.24	0.37	-0.17	-0.06	-0.07	0.67
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.95	10.08	10.65	10.29	-0.7	-0.21	-0.13	0.36	-0.12	-0.37	-0.33	-0.68	-0.06	-0.07	0.58
Cthe_01163	phosphoglucosamine mutase	9.86														



Cthe_01423	protein of unknown function UPF0118	9.96	9.79	10.66	9.87	-0.7	-0.08	0.17	0.79	-0.12	-0.21	0.67	0.23	-0.07	-0.08	0.39
Cthe_01579	ABC transporter related protein	4.09	5.13	5.81	4.25	-1.72	0.88	-1.04	1.56	-1.5	0.93	-3.37	1.87	-0.07	-0.08	0.52
Cthe_00275	glycosyltransferase 36	12.81	12.91	13.29	13.17	-0.48	-0.26	-0.1	0.12	0.18	-0.43	-0.23	-1.19	-0.07	-0.08	0.44
Cthe_00773	SOS-response transcriptional repressor, Le	11.71	11.81	12.39	12.03	-0.68	-0.22	-0.1	0.36	-0.09	-0.38	-0.23	-0.68	-0.07	-0.08	0.62
Cthe_00724	histidinol phosphate phosphatase HisJ fam	9.87	9.97	10.38	10.13	-0.51	-0.16	-0.1	0.25	0.14	-0.31	-0.23	-0.91	-0.07	-0.08	0.41
Cthe_01277	putative methyltransferase	9.37	9.22	9.82	9.49	-0.45	-0.27	0.15	0.33	0.22	-0.44	0.6	-0.74	-0.07	-0.08	0.59
Cthe_01350	single-strand binding protein	11.63	11.6	12.37	11.41	-0.74	0.19	0.03	0.96	-0.18	0.11	0.2	0.6	-0.07	-0.08	0.38
Cthe_02767	Methyltransferase type 12	8.54	8.58	9.45	8.4	-0.91	0.18	-0.04	1.05	-0.41	0.1	-0.03	0.79	-0.07	-0.08	0.61
Cthe_00257	twitching motility protein	5.46	5.39	6.02	5.55	-0.56	-0.16	0.07	0.47	0.07	-0.31	0.33	-0.45	-0.07	-0.08	0.65
Cthe_00436	Tetratricopeptide TPR_2	11.67	11.79	12.61	11.48	-0.94	0.31	-0.12	1.13	-0.45	0.25	-0.3	0.96	-0.07	-0.08	0.58
Cthe_01366	dTDP-4-dehydrohamnose 3,5-epimerase	11.76	11.67	12.5	11.73	-0.74	-0.06	0.09	0.77	-0.18	-0.19	0.4	0.19	-0.07	-0.08	0.67
Cthe_00951	orotidine 5'-phosphate decarboxylase	7.72	7.46	8.11	7.83	-0.39	-0.37	0.26	0.28	0.3	-0.56	0.97	-0.85	-0.07	-0.08	0.56
Cthe_00773	SOS-response transcriptional repressor, Le	11.71	11.81	12.39	12.03	-0.68	-0.22	-0.1	0.36	-0.09	-0.38	-0.23	-0.68	-0.07	-0.08	0.62
Cthe_01585	signal transduction histidine kinase, LytS	5.13	4.91	6.63	4.81	-1.5	0.1	0.22	1.82	-1.2	0	0.83	2.43	-0.07	-0.08	0.53
Cthe_02699	transcriptional modulator of MazE/toxin,	9.96	9.67	10.91	9.92	-0.95	-0.25	0.29	0.99	-0.46	-0.42	1.07	0.66	-0.07	-0.08	0.56
Cthe_02898	anti-sigma-factor antagonist	11.37	11.29	11.88	11.48	-0.51	-0.19	0.08	0.4	0.14	-0.35	0.37	-0.6	-0.07	-0.08	0.61
Cthe_02233	protein of unknown function DUF115	6.36	6.3	7.29	6.07	-0.93	0.23	0.06	1.22	-0.43	0.15	0.3	1.15	-0.07	-0.08	0.44
Cthe_00628	hypothetical protein	10.93	10.82	11.29	11.14	-0.36	-0.32	0.11	0.15	0.34	-0.5	0.47	-1.13	-0.07	-0.08	0.56
Cthe_02943	ABC-2 type transporter	9.39	9.29	9.92	9.48	-0.53	-0.19	0.1	0.44	0.11	-0.35	0.43	-0.51	-0.07	-0.08	0.62
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_02943	ABC-2 type transporter	9.39	9.29	9.92	9.48	-0.53	-0.19	0.1	0.44	0.11	-0.35	0.43	-0.51	-0.07	-0.08	0.62
Cthe_02305	putative undecaprenol kinase	10.2	10.3	10.64	10.67	-0.44	-0.37	-0.1	-0.03	0.23	-0.56	-0.23	-1.51	-0.07	-0.08	0.45
Cthe_00313	hypothetical protein	7.26	7.23	8.26	7.1	-1	0.13	0.03	1.16	-0.53	0.04	0.2	1.02	-0.07	-0.08	0.58
Cthe_02841	hypothetical protein	4.75	4.39	5.81	4.58	-1.06	-0.19	0.36	1.23	-0.61	-0.35	1.3	1.17	-0.07	-0.08	0.46
Cthe_00252	hypothetical protein	9.62	9.79	10.33	9.71	-0.71	0.08	-0.17	0.62	-0.14	-0.02	-0.47	-0.13	-0.07	-0.08	0.33
Cthe_01990	hypothetical protein	5.46	5.25	6.81	5.04	-1.35	0.21	0.21	1.77	-1	0.13	0.8	2.32	-0.07	-0.08	0.47
Cthe_02152	hypothetical protein	12.72	12.69	13.25	12.92	-0.53	-0.23	0.03	0.33	0.11	-0.39	0.2	-0.74	-0.07	-0.08	0.6
Cthe_02409	hypothetical protein	11.1	11.16	11.73	11.39	-0.63	-0.23	-0.06	0.34	-0.03	-0.39	-0.1	-0.72	-0.07	-0.08	0.61
Cthe_00943	hypothetical protein	6.19	6.25	6.71	6.81	-0.52	-0.56	-0.06	-0.1	0.12	-0.79	-0.1	-1.66	-0.07	-0.08	0.55
Cthe_00330	hypothetical protein	7.22	7.1	7.99	7.08	-0.77	0.02	0.12	0.91	-0.22	-0.1	0.5	0.49	-0.07	-0.08	0.39
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_00724	histidinol phosphate phosphatase HisJ fam	9.87	9.97	10.38	10.13	-0.51	-0.16	-0.1	0.25	0.14	-0.31	-0.23	-0.91	-0.07	-0.08	0.41
Cthe_01579	ABC transporter related protein	4.09	5.13	5.81	4.25	-1.72	0.88	-1.04	1.56	-1.5	0.93	-3.37	1.87	-0.07	-0.08	0.52
Cthe_02943	ABC-2 type transporter	9.39	9.29	9.92	9.48	-0.53	-0.19	0.1	0.44	0.11	-0.35	0.43	-0.51	-0.07	-0.08	0.62
Cthe_00951	orotidine 5'-phosphate decarboxylase	7.72	7.46	8.11	7.83	-0.39	-0.37	0.26	0.28	0.3	-0.56	0.97	-0.85	-0.07	-0.08	0.56
Cthe_01579	ABC transporter related protein	4.09	5.13	5.81	4.25	-1.72	0.88	-1.04	1.56	-1.5	0.93	-3.37	1.87	-0.07	-0.08	0.52
Cthe_00275	glycosyltransferase 36	12.81	12.91	13.29	13.17	-0.48	-0.26	-0.1	0.12	0.18	-0.43	-0.23	-1.19	-0.07	-0.08	0.44
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_00951	orotidine 5'-phosphate decarboxylase	7.72	7.46	8.11	7.83	-0.39	-0.37	0.26	0.28	0.3	-0.56	0.97	-0.85	-0.07	-0.08	0.56
Cthe_00724	histidinol phosphate phosphatase HisJ fam	9.87	9.97	10.38	10.13	-0.51	-0.16	-0.1	0.25	0.14	-0.31	-0.23	-0.91	-0.07	-0.08	0.41
Cthe_01366	dTDP-4-dehydrohamnose 3,5-epimerase	11.76	11.67	12.5	11.73	-0.74	-0.06	0.09	0.77	-0.18	-0.19	0.4	0.19	-0.07	-0.08	0.67
Cthe_00773	SOS-response transcriptional repressor, Le	11.71	11.81	12.39	12.03	-0.68	-0.22	-0.1	0.36	-0.09	-0.38	-0.23	-0.68	-0.07	-0.08	0.62
Cthe_02305	putative undecaprenol kinase	10.2	10.3	10.64	10.67	-0.44	-0.37	-0.1	-0.03	0.23	-0.56	-0.23	-1.51	-0.07	-0.08	0.45
Cthe_00724	histidinol phosphate phosphatase HisJ fam	9.87	9.97	10.38	10.13	-0.51	-0.16	-0.1	0.25	0.14	-0.31	-0.23	-0.91	-0.07	-0.08	0.41
Cthe_00951	orotidine 5'-phosphate decarboxylase	7.72	7.46	8.11	7.83	-0.39	-0.37	0.26	0.28	0.3	-0.56	0.97	-0.85	-0.07	-0.08	0.56
Cthe_01366	dTDP-4-dehydrohamnose 3,5-epimerase	11.76	11.67	12.5	11.73	-0.74	-0.06	0.09	0.77	-0.18	-0.19	0.4	0.19	-0.07	-0.08	0.67
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_00548	ABC transporter related protein	9.37	9.41	10.22	9.27	-0.85	0.14	-0.04	0.95	-0.32	0.05	-0.03	0.57	-0.07	-0.08	0.64
Cthe_01124	phenazine biosynthesis protein PhzF family	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_01379	oxidoreductase-like protein	8.72	8.69	9.53	8.36	-0.81	0.33	0.03	1.17	-0.27	0.27	0.2	1.04	-0.08	-0.09	0.41
Cthe_01704	toxin secretion/phage lysis holin	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_01985	phage major capsid protein, HK97	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00376	transcriptional repressor, CopY family	5.39	5.43	5.93	5.91	-0.54	-0.48	-0.04	0.02	0.09	-0.69	-0.03	-1.4	-0.08	-0.09	0.56
Cthe_00861	cell envelope-related transcriptional atten	12.29	12.17	12.72	12.5	-0.43	-0.33	0.12	0.22	0.24	-0.51	0.5	-0.98	-0.08	-0.09	0.58
Cthe_01697	transcriptional regulator, ArsR family	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_02460	transcriptional regulator, XRE family	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_01064	aminotransferase, class V	11.34	11.21	12.1	11.33	-0.76	-0.12	0.13	0.77	-0.2	-0.26	0.53	0.19	-0.08	-0.09	0.66
Cthe_00515	transposase IS66	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_01884	transposase IS116/IS110/IS902	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_02473	Terminase small subunit	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_00489	response regulator receiver modulated Ch	6.58	6.36	7.34	6.6	-0.76	-0.24	0.22	0.74	-0.2	-0.4	0.83	0.13	-0.08	-0.09	0.6
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_03097	glycosyl transferase, family 2	12.64	12.66	13.21	12.97	-0.57	-0.31	-0.02	0.24	0.05	-0.49	0.03	-0.94	-0.08	-0.09	0.6
Cthe_00489	response regulator receiver modulated Ch	6.58	6.36	7.34	6.6	-0.76	-0.24	0.22	0.74	-0.2	-0.4	0.83	0.13	-0.08	-0.09	0.6
Cthe_01153	diguanylate cyclase	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_01617	phage putative tail component	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_02915	ribosomal protein L5	12.79	13.32	13.81	13.79	-1.02	-0.47	-0.53	0.02	-0.55	-0.68	-1.67	-1.4	-0.08	-0.09	0.46
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02774	hypothetical protein	6.98	6.6	7.63	6.94	-0.65	-0.34	0.38	0.69	-0.05	-0.52	1.37	0.02	-0.08	-0.09	0.43
Cthe_03024	NADH dehydrogenase (quinone)	11.05	11.14	11.52	12.02	-0.47	-0.88	-0.09	-0.5	0.19	-1.17	-0.2	-2.51	-0.08	-0.09	0.53
Cthe_03024	NADH dehydrogenase (quinone)	11.05	11.14	11.52	12.02	-0.47	-0.88	-0.09	-0.5	0.19	-1.17	-0.2	-2.51	-0.08	-0.09	0.53
Cthe_01693	hypothetical protein	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_03206	hypothetical protein	0	0	0	0	0	0	0	0	-0.12	0.1	0	-0.08	-0.09	1.36	0.41
Cthe_01625	phage protein, HK97 gp10 family															



Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_01064	aminotransferase, class V	11.34	11.21	12.1	11.33	-0.76	-0.12	0.13	0.77	-0.2	-0.26	0.53	0.19	-0.08	-0.09	0.66
Cthe_03024	NADH dehydrogenase (quinone)	11.05	11.14	11.52	12.02	-0.47	-0.88	-0.09	-0.5	0.19	-1.17	-0.2	-2.51	-0.08	-0.09	0.53
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_00489	response regulator receiver modulated Ch	6.58	6.36	7.34	6.6	-0.76	-0.24	0.22	0.74	-0.2	-0.4	0.83	0.13	-0.08	-0.09	0.6
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_01064	aminotransferase, class V	11.34	11.21	12.1	11.33	-0.76	-0.12	0.13	0.77	-0.2	-0.26	0.53	0.19	-0.08	-0.09	0.66
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00884	Lytic transglycosylase, catalytic	8.7	8.85	9.52	8.73	-0.82	0.12	-0.15	0.79	-0.28	0.02	-0.4	0.23	-0.08	-0.09	0.69
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_00345	L-lactate dehydrogenase	14.62	14.78	15.12	15.25	-0.5	-0.47	-0.16	-0.13	0.15	-0.68	-0.43	-1.72	-0.08	-0.09	0.45
Cthe_02449	Phosphoglycerate mutase	6.15	6.29	6.98	6.13	-0.83	0.16	-0.14	0.85	-0.3	0.07	-0.37	0.36	-0.08	-0.09	0.68
Cthe_03049	TPR repeat domain containing protein	10.1	10.29	10.82	10.26	-0.72	0.03	-0.19	0.56	-0.15	-0.08	-0.53	-0.26	-0.09	-0.1	0.33
Cthe_00652	4-oxalocrotonate tautomerase	5.91	5.43	6.86	5.81	-0.95	-0.38	0.48	1.05	-0.46	-0.57	1.7	0.79	-0.09	-0.1	0.44
Cthe_01855	Methyltransferase type 11	8.69	8.58	9.09	9.02	-0.4	-0.44	0.11	0.07	0.28	-0.64	0.47	-1.3	-0.09	-0.1	0.57
Cthe_01367	PHP-like protein	10.9	10.87	11.83	10.44	-0.93	0.43	0.03	1.39	-0.43	0.39	0.2	1.51	-0.09	-0.1	0.43
Cthe_02689	transcriptional regulator, GntR family	10.77	10.98	11.9	10.36	-1.13	0.62	-0.21	1.54	-0.7	0.62	-0.6	1.83	-0.09	-0.1	0.55
Cthe_02689	transcriptional regulator, GntR family	10.77	10.98	11.9	10.36	-1.13	0.62	-0.21	1.54	-0.7	0.62	-0.6	1.83	-0.09	-0.1	0.55
Cthe_00292	transposase, mutator type	9.5	9.43	10.38	9.22	-0.88	0.21	0.07	1.16	-0.36	0.13	0.33	1.02	-0.09	-0.1	0.41
Cthe_00298	methyl-accepting chemotaxis sensory tran	7.95	8.24	8.89	8.27	-0.94	-0.03	-0.29	0.62	-0.45	-0.15	-0.87	-0.13	-0.09	-0.1	0.61
Cthe_01037	cell wall hydrolase/autolysin	11.22	11.02	11.47	11.43	-0.25	-0.41	0.2	0.04	0.49	-0.61	0.77	-1.36	-0.09	-0.1	0.57
Cthe_01367	PHP-like protein	10.9	10.87	11.83	10.44	-0.93	0.43	0.03	1.39	-0.43	0.39	0.2	1.51	-0.09	-0.1	0.43
Cthe_00298	methyl-accepting chemotaxis sensory tran	7.95	8.24	8.89	8.27	-0.94	-0.03	-0.29	0.62	-0.45	-0.15	-0.87	-0.13	-0.09	-0.1	0.61
Cthe_01824	two component transcriptional regulator,	4.52	4.39	5.58	4.17	-1.06	0.22	0.13	1.41	-0.61	0.14	0.53	1.55	-0.09	-0.1	0.43
Cthe_01166	protein of unknown function DUF147	11.66	11.58	12.23	11.53	-0.57	0.05	0.08	0.7	0.05	-0.06	0.37	0.04	-0.09	-0.1	0.24
Cthe_00941	CDP-diacylglycerol--glycerol-3-phosphate	10.6	10.59	11.13	10.94	-0.53	-0.35	0.01	0.19	0.11	-0.54	0.13	-1.04	-0.09	-0.1	0.6
Cthe_00299	MATE efflux family protein	9.08	8.88	9.3	9.33	-0.22	-0.45	0.2	-0.03	0.53	-0.65	0.77	-1.51	-0.09	-0.1	0.56
Cthe_02030	intein	8.17	8.27	8.9	8.29	-0.73	-0.02	-0.1	0.61	-0.16	-0.14	-0.23	-0.15	-0.09	-0.1	0.88
Cthe_02133	hypothetical protein	8.43	8.66	9.27	8.85	-0.84	-0.19	-0.23	0.42	-0.31	-0.35	-0.67	-0.55	-0.09	-0.1	0.61
Cthe_00869	hypothetical protein	11.38	11.26	11.88	11.55	-0.5	-0.29	0.12	0.33	0.15	-0.46	0.5	-0.74	-0.09	-0.1	0.62
Cthe_01972	hypothetical protein	8.32	8.46	9.38	8.06	-1.06	0.4	-0.14	1.32	-0.61	0.36	-0.37	1.36	-0.09	-0.1	0.57</







Cthe_02917	ribosomal protein S8	11.89	12.3	12.77	12.63	-0.88	-0.33	-0.41	0.14	-0.36	-0.51	-1.27	-1.15	-0.13	-0.14	0.41
Cthe_00130	3-oxoacyl-(acyl-carrier-protein) synthase	11.16	11.01	11.64	11.41	-0.48	-0.4	0.15	0.23	0.18	-0.6	0.6	-0.96	-0.13	-0.14	0.63
Cthe_01276	panthetheine-phosphate adenyllyltransferase	8.99	8.99	9.55	9.49	-0.56	-0.5	0	0.06	0.07	-0.71	0.1	-1.32	-0.13	-0.14	0.61
Cthe_00833	exodeoxyribonuclease VII, large subunit	10.37	10.55	11.21	10.61	-0.84	-0.06	-0.18	0.6	-0.31	-0.19	-0.5	-0.17	-0.13	-0.14	0.78
Cthe_00130	3-oxoacyl-(acyl-carrier-protein) synthase	11.16	11.01	11.64	11.41	-0.48	-0.4	0.15	0.23	0.18	-0.6	0.6	-0.96	-0.13	-0.14	0.63
Cthe_01276	panthetheine-phosphate adenyllyltransferase	8.99	8.99	9.55	9.49	-0.56	-0.5	0	0.06	0.07	-0.71	0.1	-1.32	-0.13	-0.14	0.61
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_00648	glutamyl-tRNA synthetase	11.75	11.85	12.47	12.05	-0.72	-0.2	-0.1	0.42	-0.15	-0.36	-0.23	-0.55	-0.13	-0.14	0.74
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01276	panthetheine-phosphate adenyllyltransferase	8.99	8.99	9.55	9.49	-0.56	-0.5	0	0.06	0.07	-0.71	0.1	-1.32	-0.13	-0.14	0.61
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_00130	3-oxoacyl-(acyl-carrier-protein) synthase	11.16	11.01	11.64	11.41	-0.48	-0.4	0.15	0.23	0.18	-0.6	0.6	-0.96	-0.13	-0.14	0.63
Cthe_00130	3-oxoacyl-(acyl-carrier-protein) synthase	11.16	11.01	11.64	11.41	-0.48	-0.4	0.15	0.23	0.18	-0.6	0.6	-0.96	-0.13	-0.14	0.63
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_00130	3-oxoacyl-(acyl-carrier-protein) synthase	11.16	11.01	11.64	11.41	-0.48	-0.4	0.15	0.23	0.18	-0.6	0.6	-0.96	-0.13	-0.14	0.63
Cthe_00130	3-oxoacyl-(acyl-carrier-protein) synthase	11.16	11.01	11.64	11.41	-0.48	-0.4	0.15	0.23	0.18	-0.6	0.6	-0.96	-0.13	-0.14	0.63
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01548	Enoyl-CoA hydratase/isomerase	10.29	10.38	11.3	10.18	-1.01	0.2	-0.09	1.12	-0.54	0.12	-0.2	0.94	-0.13	-0.14	0.65
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_01428	glycoside hydrolase, family 1	5.52	6.07	6.64	6.85	-1.12	-0.78	-0.55	-0.21	-0.69	-1.05	-1.73	-1.89	-0.13	-0.14	0.56
Cthe_00408	diguanylate cyclase/phosphodiesterase w	10.82	10.98	11.43	11.06	-0.61	-0.08	-0.16	0.37	0	-0.21	-0.43	-0.66	-0.14	-0.15	0.3
Cthe_00231	Methyltransferase type 11	4	3.91	4.91	3.58	-0.91	0.33	0.09	1.33	-0.41	0.27	0.4	1.38	-0.14	-0.15	0.39
Cthe_01102	fimbrial assembly protein	11.65	11.81	12.51	11.76	-0.86	0.05	-0.16	0.75	-0.34	-0.06	-0.43	0.15	-0.14	-0.15	0.86
Cthe_03030	methyl-accepting chemotaxis sensory tran	3.91	3.58	4.7	4	-0.79	-0.42	0.33	0.7	-0.24	-0.62	1.2	0.04	-0.14	-0.15	0.63
Cthe_01355	glycosyl transferase, family 2	11.84	11.74	12.36	12.14	-0.52	-0.4	0.1	0.22	0.12	-0.6	0.43	-0.98	-0.14	-0.15	0.65
Cthe_00408	diguanylate cyclase/phosphodiesterase w	10.82	10.98	11.43	11.06	-0.61	-0.08	-0.16	0.37	0	-0.21	-0.43	-0.66	-0.14	-0.15	0.3
Cthe_03030	methyl-accepting chemotaxis sensory tran	3.91	3.58	4.7	4	-0.79	-0.42	0.33	0.7	-0.24	-0.62	1.2	0.04	-0.14	-0.15	0.63
Cthe_00150	RNA modification enzyme, MiaB family	8.53	8.76	9.26	8.64	-0.73	0.12	-0.23	0.62	-0.16	0.02	-0.67	-0.13	-0.14	-0.15	0.27
Cthe_00959	S-adenosylmethionine--tRNA-ribosyltrans	10.61	10.52	11.21	10.79	-0.6	-0.27	0.09	0.42	0.01	-0.44	0.4	-0.55	-0.14	-0.15	0.74
Cthe_01815	UreE urease accessory-like protein	2.81	3.46	4.25	3	-1.44	0.46	-0.65	1.25	-1.12	0.43	-2.07	1.21	-0.14	-0.15	0.57
Cthe_01441	hypothetical protein	1.58	1	2.81	1.58	-1.23	-0.58	0.58	1.23	-0.84	-0.81	2.03	1.17	-0.14	-0.15	0.57
Cthe_00346	hypothetical protein	8.86	8.81	9.43	9.17	-0.57	-0.36	0.05	0.26	0.05	-0.55	0.27	-0.89	-0.14	-0.15	0.67
Cthe_02245	hypothetical protein	5.43	5.36	6.15	5.46	-0.72	-0.1	0.07	0.69	-0.15	-0.24	0.33	0.02	-0.14	-0.15	0.97
Cthe_03111	hypothetical protein	8.3	8.04	8.75	8.55	-0.45	-0.51	0.26	0.2	0.22	-0.73	0.97	-1.02	-0.14	-0.15	0.62
Cthe_00820	hypothetical protein	7.39	7.04	8.36	7.42	-0.97	-0.38	0.35	0.94	-0.49	-0.57	1.27	0.55	-0.14	-0.15	0.62
Cthe_00150	RNA modification enzyme, MiaB family	8.53	8.76	9.26	8.64	-0.73	0.12	-0.23	0.62	-0.16	0.02	-0.67	-0.13	-0.14	-0.15	0.27
Cthe_00959	S-adenosylmethionine--tRNA-ribosyltrans	10.61	10.52	11.21	10.79	-0.6	-0.27	0.09	0.42	0.01	-0.44	0.4	-0.55	-0.14	-0.15	0.74
Cthe_02664	ABC-1	8.77	8.93	9.79	8.71	-1.02	0.22	-0.16	1.08	-0.55	0.14	-0.43	0.85	-0.15	-0.16	0.68
Cthe_01592	Glycerate kinase	8.47	8.45	9.11	8.67	-0.64	-0.22	0.02	0.44	-0.04	-0.38	0.17	-0.51	-0.15	-0.16	0.81
Cthe_00146	ribonuclease R	10.02	10.2	10.95	10.08	-0.93	0.12	-0.18	0.87	-0.43	0.02	-0.5	0.4	-0.15	-0.16	0.76
Cthe_01085	glycosyl transferase, group 1	5.55	5.46	6.46	5.09	-0.91	0.37	0.09	1.37	-0.41	0.32	0.4	1.47	-0.15	-0.16	0.39
Cthe_00034	cyclic nucleotide-binding protein	7.37	7.71	8.16	7.45	-0.79	0.26	-0.34	0.71	-0.24	0.19	-1.03	0.06	-0.15	-0.16	0.34
Cthe_02899	putative anti-sigma regulatory factor,	11.49	11.45	12.08	11.8	-0.59	-0.35	0.04	0.28	0.03	-0.54	0.23	-0.85	-0.15	-0.16	0.7
Cthe_00775	tRNA delta(2)-isopentenylpyrophosphate	11.93	11.85	12.77	11.5	-0.84	0.35	0.08	1.27	-0.31	0.3	0.37	1.26	-0.15	-0.16	0.37
Cthe_02658	RNA-binding S4	8.48	8.2	9.03	8.34	-0.55	-0.14	0.28	0.69	0.08	-0.29	1.03	0.02	-0.15	-0.16	0.33
Cthe_03037	nitroreductase	8.65	8.41	9.23	8.84	-0.58	-0.43	0.24	0.39	0.04	-0.63	0.9	-0.62	-0.15	-0.16	0.66
Cthe_01508	hypothetical protein	7.04	7.44	8.34	6.69	-1.3	0.75	-0.4	1.65	-0.93	0.77	-1.23	2.06	-0.15	-0.16	0.57
Cthe_00743	MATE efflux family protein	11.18	10.98	11.53	11.61	-0.35	-0.63	0.2	-0.08	0.35	-0.87	0.77	-1.62	-0.15	-0.16	0.59
Cthe_02547	hypothetical protein	9.95	9.67	10.59	10.11	-0.64	-0.44	0.28	0.48	-0.04	-0.64	1.03	-0.43	-0.15	-0.16	0.65
Cthe_02130	hypothetical protein	12.21	11.86	13.18	12.25	-0.97	-0.39	0.35	0.93	-0.49	-0.58	1.27	0.53	-0.15	-0.16	0.63
Cthe_03058	hypothetical protein	7.77	7.73	8.35	8.08	-0.58	-0.35	0.04	0.27	0.04	-0.54	0.23	-0.87	-0.15	-0.16	0.68
Cthe_03040	hypothetical protein	7.15	7.09	7.85	7.21	-0.7	-0.12	0.06	0.64	-0.12	-0.26	0.3	-0.09	-0.15	-0.16	1.04
Cthe_00883	flagellar protein	8.16	8.1	8.96	8.16	-0.8	-0.06	0.06	0.8	-0.26	-0.19	0.3	0.26	-0.15	-0.16	0.92
Cthe_02664	ABC-1	8.77	8.93	9.79	8.71	-1.02	0.22	-0.16	1.08	-0.55	0.14	-0.43	0.85	-0.15	-0.16	0.68
Cthe_01592	Glycerate kinase	8.47	8.45	9.11	8.67	-0.64	-0.22	0.02	0.44	-0.04	-0.38	0.17	-0.51	-0.15	-0.16	0.81
Cthe_00146	ribonuclease R	10.02	10.2	10.95	10.08	-0.93	0.12	-0.18	0.87	-0.43	0.02	-0.5	0.4	-0.15	-0.16	0.76
Cthe_01508	hypothetical protein	7.04	7.44	8.34	6.69	-1.3	0.75	-0.4	1.65	-0.93	0.77	-1.23	2.06	-0.15	-0.16	0.57
Cthe_02899	putative anti-sigma regulatory factor,	11.49	11.45	12.08	11.8	-0.59	-0.35	0.04	0.28	0.03	-0.54	0.23	-0.85	-0.15	-0.16	0.7
Cthe_01592	Glycerate kinase	8.47	8.45	9.11	8.67	-0.64	-0.22	0.02	0.44	-0.04	-0.38	0.17	-0.51	-0.15	-0.16	0.81
Cthe_00775	tRNA delta(2)-isopentenylpyrophosphate	11.93	11.85	12.77	11.5	-0.84	0.35	0.08	1.27	-0.31	0.3	0.37	1.26	-0.15	-0.16	0.37
Cthe_01592	Glycerate kinase	8.47	8.45	9.11	8.67	-0.64	-0.22	0.02	0.44	-0.04	-0.38	0.17	-0.51	-0.15	-0.16	0.81
Cthe_01508	hypothetical protein	7.04	7.44	8.34	6.69	-1.3	0.75	-0.4	1.65	-0.93	0.77	-1.23	2.06	-0.15	-0.16	0.57
Cthe_01508	hypothetical protein	7.04	7.44	8.34	6.69	-1.3	0.75	-0.4	1.65	-0.93	0.77	-1.23	2.06			



Cthe_01839	Radical SAM	12.67	12.84	13.45	13.28	-0.78	-0.44	-0.17	0.17	-0.23	-0.64	-0.47	-1.09	-0.16	-0.17	0.65
Cthe_00163	GTP1/OBG subdomain containing protein	12.02	12.18	12.52	12.27	-0.5	-0.09	-0.16	0.25	0.15	-0.23	-0.43	-0.91	-0.17	-0.18	0.31
Cthe_02556	Radical SAM	5.64	5.46	6.27	5.49	-0.63	-0.03	0.18	0.78	-0.03	-0.15	0.7	0.21	-0.17	-0.18	0.24
Cthe_02119	glycoside hydrolase, family 10	10.85	11.12	11.59	10.97	-0.74	0.15	-0.27	0.62	-0.18	0.06	-0.8	-0.13	-0.17	-0.18	0.27
Cthe_00872	Indole-3-glycerol-phosphate synthase	7.33	7.3	8.28	7.29	-0.95	0.01	0.03	0.99	-0.46	-0.11	0.2	0.66	-0.17	-0.18	0.78
Cthe_01511	DNA methylase N-4/N-6	7.06	7.55	8.04	7.65	-0.98	-0.1	-0.49	0.39	-0.5	-0.24	-1.53	-0.62	-0.17	-0.18	0.38
Cthe_02339	glycosyl transferase, group 1	9.3	9.19	9.86	9.62	-0.56	-0.43	0.11	0.24	0.07	-0.63	0.47	-0.94	-0.17	-0.18	0.69
Cthe_02177	hypothetical protein	6.44	6.27	7.03	6.66	-0.59	-0.39	0.17	0.37	0.03	-0.58	0.67	-0.66	-0.17	-0.18	0.7
Cthe_01365	hypothetical protein	10.62	10.54	11.43	10.64	-0.81	-0.1	0.08	0.79	-0.27	-0.24	0.37	0.23	-0.17	-0.18	0.94
Cthe_02966	hypothetical protein	5.04	4.75	5.67	4.91	-0.63	-0.16	0.29	0.76	-0.03	-0.31	1.07	0.17	-0.17	-0.18	0.33
Cthe_00651	hypothetical protein	6.95	6.81	7.94	6.55	-0.99	0.26	0.14	1.39	-0.51	0.19	0.57	1.51	-0.17	-0.18	0.38
Cthe_02684	hypothetical protein	12.92	12.64	13.53	13.12	-0.61	-0.48	0.28	0.41	0	-0.69	1.03	-0.57	-0.17	-0.18	0.67
Cthe_00872	Indole-3-glycerol-phosphate synthase	7.33	7.3	8.28	7.29	-0.95	0.01	0.03	0.99	-0.46	-0.11	0.2	0.66	-0.17	-0.18	0.78
Cthe_00872	Indole-3-glycerol-phosphate synthase	7.33	7.3	8.28	7.29	-0.95	0.01	0.03	0.99	-0.46	-0.11	0.2	0.66	-0.17	-0.18	0.78
Cthe_00763	GTP-binding protein	10.68	10.68	11.35	10.95	-0.67	-0.27	0	0.4	-0.08	-0.44	0.1	-0.6	-0.18	-0.19	0.84
Cthe_01896	metallophosphoesterase	10.23	10.1	10.98	10.31	-0.75	-0.21	0.13	0.67	-0.19	-0.37	0.53	-0.02	-0.18	-0.19	0.89
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	12.02	12.23	12.98	12.16	-0.96	0.07	-0.21	0.82	-0.47	-0.04	-0.6	0.3	-0.18	-0.19	0.8
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	12.02	12.23	12.98	12.16	-0.96	0.07	-0.21	0.82	-0.47	-0.04	-0.6	0.3	-0.18	-0.19	0.8
Cthe_02332	multi-sensor signal transduction histidine	10.27	10.22	10.88	10.6	-0.61	-0.38	0.05	0.28	0	-0.57	0.27	-0.85	-0.18	-0.19	0.73
Cthe_01772	protein of unknown function DUF218	9.69	9.86	10.48	10.33	-0.79	-0.47	-0.17	0.15	-0.24	-0.68	-0.47	-1.13	-0.18	-0.19	0.67
Cthe_02093	hypothetical protein	11.66	11.35	12.32	11.85	-0.66	-0.5	0.31	0.47	-0.07	-0.71	1.13	-0.45	-0.18	-0.19	0.67
Cthe_02577	adenylate cyclase	7.92	8.2	8.94	8.17	-1.02	0.03	-0.28	0.77	-0.55	-0.08	-0.83	0.19	-0.18	-0.19	0.74
Cthe_00992	ribosomal protein L7Ae/L30e/S12e/Gadd4	8.14	7.92	8.84	7.98	-0.7	-0.06	0.22	0.86	-0.12	-0.19	0.83	0.38	-0.18	-0.19	0.28
Cthe_00579	nitroreductase	7.45	7.26	8.39	7.13	-0.94	0.13	0.19	1.26	-0.45	0.04	0.73	1.23	-0.18	-0.19	0.36
Cthe_03001	protein of unknown function DUF47	10.08	10.03	10.78	10.18	-0.7	-0.15	0.05	0.6	-0.12	-0.3	0.27	-0.17	-0.18	-0.19	1.15
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_02086	peptidase U32	9.26	9.12	9.72	9.76	-0.46	-0.64	0.14	-0.04	0.2	-0.88	0.57	-1.53	-0.18	-0.19	0.63
Cthe_01545	hypothetical protein	4.86	4.52	5.64	5	-0.78	-0.48	0.34	0.64	-0.23	-0.69	1.23	-0.09	-0.18	-0.19	0.67
Cthe_02384	S-layer-like domain containing protein	12.62	12.56	13.25	12.87	-0.63	-0.31	0.06	0.38	-0.03	-0.49	0.3	-0.64	-0.18	-0.19	0.79
Cthe_02569	hypothetical protein	5.46	5.73	6.99	5.04	-1.53	0.69	-0.27	1.95	-1.24	0.7	-0.8	2.7	-0.18	-0.19	0.57
Cthe_00008	hypothetical protein	5.49	5.32	6.3	5.25	-0.81	0.07	0.17	1.05	-0.27	-0.04	0.67	0.79	-0.18	-0.19	0.3
Cthe_00824	copper amine oxidase-like protein	10.62	10.88	11.68	10.71	-1.06	-0.17	-0.26	0.97	-0.61	0.08	-0.77	0.62	-0.18	-0.19	0.71
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	12.02	12.23	12.98	12.16	-0.96	0.07	-0.21	0.82	-0.47	-0.04	-0.6	0.3	-0.18	-0.19	0.8
Cthe_02332	multi-sensor signal transduction histidine	10.27	10.22	10.88	10.6	-0.61	-0.38	0.05	0.28	0	-0.57	0.27	-0.85	-0.18	-0.19	0.73
Cthe_02086	peptidase U32	9.26	9.12	9.72	9.76	-0.46	-0.64	0.14	-0.04	0.2	-0.88	0.57	-1.53	-0.18	-0.19	0.63
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	12.02	12.23	12.98	12.16	-0.96	0.07	-0.21	0.82	-0.47	-0.04	-0.6	0.3	-0.18	-0.19	0.8
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01344	(p)ppGpp synthetase I, SpoT/RelA	12.02	12.23	12.98	12.16	-0.96	0.07	-0.21	0.82	-0.47	-0.04	-0.6	0.3	-0.18	-0.19	0.8
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01396	phospholipase D/Transphosphatidylase	7.5	7.58	8.24	7.78	-0.74	-0.2	-0.08	0.46	-0.18	-0.36	-0.17	-0.47	-0.18	-0.19	0.92
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_01058	Glycine hydroxymethyltransferase	13.15	13.26	13.94	13.33	-0.79	-0.07	-0.11	0.61	-0.24	-0.2	-0.27	-0.15	-0.18	-0.19	1.15
Cthe_00484	flagellar biosynthetic protein FlhB	8.47	8.31	9.06	8.72	-0.59	-0.41	0.16	0.34	0.03	-0.61	0.63	-0.72	-0.19	-0.2	0.73
Cthe_00780	HAD-superfamily hydrolase, subfamily IA,	7.34	7.3	7.98	7.62	-0.64	-0.32	0.04	0.36	-0.04	-0.5	0.23	-0.68	-0.19	-0.2	0.79
Cthe_02552	Radical SAM	3.32	4	4.86	3.17	-1.54	0.83	-0.68	1.69	-1.26	0.87	-2.17	2.15	-0.19	-0.2	0.57
Cthe_01864	acetylglutamate kinase	9.03	10.17	11.04	9.44	-2.01	0.73	-1.14	1.6	-1.89	0.75	-3.7	1.96	-0.19	-0.2	0.55
Cthe_00484	flagellar biosynthetic protein FlhB	8.47	8.31	9.06	8.72	-0.59	-0.41	0.16	0.34	0.03	-0.61	0.63	-0.72	-0.19	-0.2	0.73
Cthe_00486	GTP-binding signal recognition particle SR	8.48	8.19	9.09	8.7	-0.61	-0.51	0.29	0.39	0	-0.73	1.07	-0.62	-0.19	-0.2	0.67
Cthe_02406	hypothetical protein	9.82	9.8	10.48	10.1	-0.66	-0.3	0.02	0.38	-0.07	-0.48	0.17	-0.64	-0.19	-0.2	0.83
Cthe_00876	glycosyl transferase, family 39	10.12	10.3	10.96	10.59	-0.84	-0.29	-0.18	0.37	-0.31	-0.46	-0.5	-0.66	-0.19	-0.2	0.76
Cthe_02338	glycosyl transferase, group 1	8.96	9.07	9.71	9.44	-0.75	-0.37	-0.11	0.27	-0.19	-0.56	-0.27	-0.87	-0.19	-0.2	0.74
Cthe_00741	adenylosuccinate lyase	12.11	12.07	12.66	12.7	-0.55	-0.63	0.04	-0.04	0.08	-0.87	0.23	-1.53	-0.19	-0.2	0.64
Cthe_02944	periplasmic sensor signal transduction his	9.14	9.28	10.13	9.15	-0.99	0.13	-0.14	0.98	-0.51	0.04	-0.37	0.64	-0.19	-0.2	0.79
Cthe_00915	hypothetical protein	10.78	11.26	11.68	10.93	-0.9	0.33	-0.48	0.75	-0.39	0.27	-1.5	0.15	-0.19	-0.2	0.36
Cthe_01535	hypothetical protein	5.29	5.46	6.13	5.7											



Cthe_02717	ribosomal protein L33	8.2	7.85	8.97	8.36	-0.77	-0.51	0.35	0.61	-0.22	-0.73	1.27	-0.15	-0.2	-0.21	0.68
Cthe_00960	SpolID/LytB domain containing protein	9.64	9.58	10.29	9.89	-0.65	-0.31	0.06	0.4	-0.05	-0.49	0.3	-0.6	-0.2	-0.21	0.83
Cthe_03011	hypothetical protein	4.7	5.13	5.95	4.91	-1.25	0.22	-0.43	1.04	-0.86	0.14	-1.33	0.77	-0.2	-0.21	0.64
Cthe_01894	hypothetical protein	11.36	11.31	12.35	11.34	-0.99	-0.03	0.05	1.01	-0.51	-0.15	0.27	0.7	-0.2	-0.21	0.81
Cthe_00316	PA14	6.7	6.91	7.64	6.92	-0.94	-0.01	-0.21	0.72	-0.45	-0.13	-0.6	0.09	-0.2	-0.21	0.88
Cthe_02717	ribosomal protein L33	8.2	7.85	8.97	8.36	-0.77	-0.51	0.35	0.61	-0.22	-0.73	1.27	-0.15	-0.2	-0.21	0.68
Cthe_00871	Phosphoribosylanthranilate isomerase	6.64	6.36	7.33	6.48	-0.69	-0.12	0.28	0.85	-0.11	-0.26	1.03	0.36	-0.2	-0.21	0.29
Cthe_03149	aminoacyl-histidine dipeptidase	10.12	10.14	10.82	10.41	-0.7	-0.27	-0.02	0.41	-0.12	-0.44	0.03	-0.57	-0.2	-0.21	0.91
Cthe_00871	Phosphoribosylanthranilate isomerase	6.64	6.36	7.33	6.48	-0.69	-0.12	0.28	0.85	-0.11	-0.26	1.03	0.36	-0.2	-0.21	0.29
Cthe_00871	Phosphoribosylanthranilate isomerase	6.64	6.36	7.33	6.48	-0.69	-0.12	0.28	0.85	-0.11	-0.26	1.03	0.36	-0.2	-0.21	0.29
Cthe_02304	hypothetical protein	8.87	9.06	9.27	9.33	-0.4	-0.27	-0.19	-0.06	0.28	-0.44	-0.53	-1.57	-0.21	-0.22	0.36
Cthe_02818	CheA signal transduction histidine kinases	5.83	6.25	6.7	6.39	-0.87	-0.14	-0.42	0.31	-0.35	-0.29	-1.3	-0.79	-0.21	-0.22	0.34
Cthe_02818	CheA signal transduction histidine kinases	5.83	6.25	6.7	6.39	-0.87	-0.14	-0.42	0.31	-0.35	-0.29	-1.3	-0.79	-0.21	-0.22	0.34
Cthe_00487	Cobyrinic acid a,c-diamide synthase	6.87	6.63	7.44	7.16	-0.57	-0.53	0.24	0.28	0.05	-0.75	0.9	-0.85	-0.21	-0.22	0.69
Cthe_01812	Urease accessory protein UreD	3.46	3.7	4.75	3.32	-1.29	0.38	-0.24	1.43	-0.92	0.33	-0.7	1.6	-0.21	-0.22	0.64
Cthe_02712	hypothetical protein	9.92	9.74	10.55	10.16	-0.63	-0.42	0.18	0.39	-0.03	-0.62	0.7	-0.62	-0.21	-0.22	0.75
Cthe_01445	uncharacterized Zn-finger protein	9.39	9.27	10.13	9.05	-0.74	0.22	0.12	1.08	-0.18	0.14	0.5	0.85	-0.21	-0.22	0.26
Cthe_02896	hypothetical protein	9.13	9.06	9.68	9.67	-0.55	-0.61	0.07	0.01	0.08	-0.85	0.33	-1.43	-0.21	-0.22	0.66
Cthe_00957	preprotein translocase, YajC subunit	9.98	9.84	10.63	10.22	-0.65	-0.38	0.14	0.41	-0.05	-0.57	0.57	-0.57	-0.22	-0.23	0.81
Cthe_00612	SSS sodium solute transporter superfamily	11.95	12.05	12.73	12.29	-0.78	-0.24	-0.1	0.44	-0.23	-0.4	-0.23	-0.51	-0.22	-0.23	0.94
Cthe_00634	serine/threonine protein kinase	10.74	11.04	11.5	11	-0.76	0.04	-0.3	0.5	-0.2	-0.07	-0.9	-0.38	-0.22	-0.23	0.25
Cthe_01510	short-chain dehydrogenase/reductase SD	5.75	5.93	6.6	6.25	-0.85	-0.32	-0.18	0.35	-0.32	-0.5	-0.5	-0.7	-0.22	-0.23	0.78
Cthe_00634	serine/threonine protein kinase	10.74	11.04	11.5	11	-0.76	0.04	-0.3	0.5	-0.2	-0.07	-0.9	-0.38	-0.22	-0.23	0.25
Cthe_00612	SSS sodium solute transporter superfamily	11.95	12.05	12.73	12.29	-0.78	-0.24	-0.1	0.44	-0.23	-0.4	-0.23	-0.51	-0.22	-0.23	0.94
Cthe_00634	serine/threonine protein kinase	10.74	11.04	11.5	11	-0.76	0.04	-0.3	0.5	-0.2	-0.07	-0.9	-0.38	-0.22	-0.23	0.25
Cthe_00728	phage integrase	6.39	6.75	7.52	6.75	-1.13	0	-0.36	0.77	-0.7	-0.12	-1.1	0.19	-0.22	-0.23	0.72
Cthe_02031	transposase IS200-like protein	10.12	10.08	10.95	10.16	-0.83	-0.08	0.04	0.79	-0.3	-0.21	0.23	0.23	-0.22	-0.23	1.28
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_01510	short-chain dehydrogenase/reductase SD	5.75	5.93	6.6	6.25	-0.85	-0.32	-0.18	0.35	-0.32	-0.5	-0.5	-0.7	-0.22	-0.23	0.78
Cthe_00294		7.48	7.85	8.85	7.35	-1.37	0.5	-0.37	1.5	-1.03	0.48	-1.13	1.74	-0.22	-0.23	0.62
Cthe_00952	dihydroorotase, multifunctional complex t	8.58	8.81	9.46	9.28	-0.88	-0.47	-0.23	0.18	-0.36	-0.68	-0.67	-1.06	-0.22	-0.23	0.7
Cthe_00634	serine/threonine protein kinase	10.74	11.04	11.5	11	-0.76	0.04	-0.3	0.5	-0.2	-0.07	-0.9	-0.38	-0.22	-0.23	0.25
Cthe_00302	hypothetical protein	5.95	5.52	6.63	5.81	-0.68	-0.29	0.43	0.82	-0.09	-0.46	1.53	0.3	-0.22	-0.23	0.34
Cthe_02771	beta-lactamase-like protein	10.09	9.73	10.94	9.89	-0.85	-0.16	0.36	1.05	-0.32	-0.31	1.3	0.79	-0.22	-0.23	0.33
Cthe_01510	short-chain dehydrogenase/reductase SD	5.75	5.93	6.6	6.25	-0.85	-0.32	-0.18	0.35	-0.32	-0.5	-0.5	-0.7	-0.22	-0.23	0.78
Cthe_00006	hypothetical protein	2.58	2.32	3.7	2.58	-1.12	-0.26	0.26	1.12	-0.69	-0.43	0.97	0.94	-0.22	-0.23	0.68
Cthe_02042	RNA related	4.95	4.58	6.32	4.46	-1.37	0.12	0.37	1.86	-1.03	0.02	1.33	2.51	-0.22	-0.23	0.41
Cthe_00956	hypothetical protein	10.04	9.74	10.65	9.87	-0.61	-0.13	0.3	0.78	0	-0.27	1.1	0.21	-0.22	-0.23	0.27
Cthe_00411	hypothetical protein	13.36	13.4	14.1	13.52	-0.74	-0.12	-0.04	0.58	-0.18	-0.26	-0.03	-0.21	-0.22	-0.23	1.69
Cthe_01770	hypothetical protein	9.78	9.53	10.58	9.91	-0.8	-0.38	0.25	0.67	-0.26	-0.57	0.93	-0.02	-0.22	-0.23	0.77
Cthe_00297	hypothetical protein	5.75	6.41	6.87	6.64	-1.12	-0.23	-0.66	0.23	-0.69	-0.39	-2.1	-0.96	-0.22	-0.23	0.39
Cthe_00940	hypothetical protein	6.3	6.04	7.03	6.49	-0.73	-0.45	0.26	0.54	-0.16	-0.65	0.97	-0.3	-0.22	-0.23	0.75
Cthe_01490	RNA related	6.25	5.86	6.81	6.09	-0.56	-0.23	0.39	0.72	0.07	-0.39	1.4	0.09	-0.22	-0.23	0.32
Cthe_00059	type 3a, cellulose-binding	8.31	8.34	9.08	8.36	-0.77	-0.02	-0.03	0.72	-0.22	-0.14	0	0.09	-0.22	-0.23	3.29
Cthe_00501	hypothetical protein	8.75	8.67	9.61	8.79	-0.68	-0.12	0.08	0.82	-0.34	-0.26	0.37	0.3	-0.22	-0.23	1.02
Cthe_00957	preprotein translocase, YajC subunit	9.98	9.84	10.63	10.22	-0.65	-0.38	0.14	0.41	-0.05	-0.57	0.57	-0.57	-0.22	-0.23	0.81
Cthe_00952	dihydroorotase, multifunctional complex t	8.58	8.81	9.46	9.28	-0.88	-0.47	-0.23	0.18	-0.36	-0.68	-0.67	-1.06	-0.22	-0.23	0.7
Cthe_00952	dihydroorotase, multifunctional complex t	8.58	8.81	9.46	9.28	-0.88	-0.47	-0.23	0.18	-0.36	-0.68	-0.67	-1.06	-0.22	-0.23	0.7
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75							



Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_03084	putative RNA methylase	9.18	9.28	10.03	9.28	-0.85	0	-0.1	0.75	-0.32	-0.12	-0.23	0.15	-0.22	-0.23	1.41
Cthe_02335	polysaccharide biosynthesis protein	8.88	9.01	9.57	9.91	-0.69	-0.9	-0.13	-0.34	-0.11	-1.19	-0.33	-2.17	-0.23	-0.24	0.62
Cthe_00015	alpha-L-arabinofuranosidase B	7.24	7.43	8.21	7.39	-0.97	0.04	-0.19	0.82	-0.49	-0.07	-0.53	0.3	-0.23	-0.24	0.92
Cthe_01638	ParB-like nuclease	0		1		-1		0	1	-0.53		0.1	0.68	-0.23	-0.24	0.88
Cthe_01638	ParB-like nuclease	0		1		-1		0	1	-0.53		0.1	0.68	-0.23	-0.24	0.88
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.52	10.4	11.35	10.59	-0.83	-0.19	0.12	0.76	-0.3	-0.35	0.5	0.17	-0.23	-0.24	0.99
Cthe_00744	copper amine oxidase-like protein	9.88	9.91	10.59	10.28	-0.71	-0.37	-0.03	0.31	-0.14	-0.56	0	-0.79	-0.23	-0.24	0.83
Cthe_01287	periplasmic sensor signal transduction his	10.44	10.38	11.09	10.78	-0.65	-0.4	0.06	0.31	-0.05	-0.6	0.3	-0.79	-0.23	-0.24	0.81
Cthe_03187	putative anti-sigma regulatory factor,	9.32	9.27	10.07	9.42	-0.75	-0.15	0.05	0.65	-0.19	-0.3	0.27	-0.06	-0.23	-0.24	1.46
Cthe_00204	protein of unknown function DUF1294	9.14	8.88	9.71	9.48	-0.57	-0.6	0.26	0.23	0.05	-0.83	0.97	-0.96	-0.23	-0.24	0.69
Cthe_00367	NADP oxidoreductase, coenzyme F420-de	9.44	9.43	10.1	9.92	-0.66	-0.49	0.01	0.18	-0.07	-0.7	0.13	-1.06	-0.23	-0.24	0.75
Cthe_01611	Peptidoglycan-binding LysM			1		-1			1	-0.53			0.68	-0.23	-0.24	0.89
Cthe_03060	hypothetical protein	5.13	4.81	5.73	4.95	-0.6	-0.14	0.32	0.78	0.01	-0.29	1.17	0.21	-0.23	-0.24	0.28
Cthe_02029	hypothetical protein			1		-1			1	-0.53			0.68	-0.23	-0.24	0.89
Cthe_02520	hypothetical protein	10.45	10.83	11.28	10.9	-0.83	-0.07	-0.38	0.38	-0.3	-0.2	-1.17	-0.64	-0.23	-0.24	0.31
Cthe_02783	hypothetical protein			1		-1			1	-0.53			0.68	-0.23	-0.24	0.89
Cthe_01450	hypothetical protein	6.67	6.39	7.41	6.86	-0.74	-0.47	0.28	0.55	-0.18	-0.68	1.03	-0.28	-0.23	-0.24	0.75
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.52	10.4	11.35	10.59	-0.83	-0.19	0.12	0.76	-0.3	-0.35	0.5	0.17	-0.23	-0.24	0.99
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.52	10.4	11.35	10.59	-0.83	-0.19	0.12	0.76	-0.3	-0.35	0.5	0.17	-0.23	-0.24	0.99
Cthe_01611	Peptidoglycan-binding LysM			1		-1			1	-0.53			0.68	-0.23	-0.24	0.89
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.52	10.4	11.35	10.59	-0.83	-0.19	0.12	0.76	-0.3	-0.35	0.5	0.17	-0.23	-0.24	0.99
Cthe_02354	nicotinate-nucleotide pyrophosphorylase	10.52	10.4	11.35	10.59	-0.83	-0.19	0.12	0.76	-0.3	-0.35	0.5	0.17	-0.23	-0.24	0.99
Cthe_01103	prepilin-type cleavage/methylation	0	0	1		-1	0	0	1	-0.53	-0.12	0.1	0.68	-0.24	-0.25	0.9
Cthe_02718	preprotein translocase, SecE subunit	10.54	10.51	11.2	10.98	-0.66	-0.47	0.03	0.22	-0.07	-0.68	0.2	-0.98	-0.24	-0.25	0.78
Cthe_01070	metal dependent phosphohydrolase	11.02	11.33	12.08	11.42	-1.06	-0.09	-0.31	0.66	-0.61	-0.23	-0.93	-0.04	-0.24	-0.25	0.8
Cthe_01324	heat-inducible transcription repressor Hrc	10.08	9.89	11.39	10	-1.31	-0.11	0.19	1.39	-0.95	-0.25	0.73	1.51	-0.24	-0.25	0.67
Cthe_00996	DNA polymerase III, alpha subunit	10.66	10.79	11.44	11.3	-0.78	-0.51	-0.13	0.14	-0.23	-0.73	-0.33	-1.15	-0.24	-0.25	0.73
Cthe_02410	protein of unknown function DUF342	10.35	10.31	11.07	10.53	-0.72	-0.22	0.04	0.54	-0.15	-0.38	0.23	-0.3	-0.24	-0.25	1.23
Cthe_02858	transposase, mutator type		0	1	0	-1	0	0	1	-0.53	-0.12	0.1	0.68	-0.24	-0.25	0.9
Cthe_02122	protein of unknown function DUF324	0	0	1		-1	0	0	1	-0.53	-0.12	0.1	0.68	-0.24	-0.25	0.9
Cthe_01959	Methyltransferase type 11	7.35	7.67	8.46	7.64	-1.11	0.03	-0.32	0.82	-0.68	-0.08	-0.97	0.3	-0.24	-0.25	0.77
Cthe_01103	prepilin-type cleavage/methylation	0	0	1		-1	0	0	1	-0.53	-0.12	0.1	0.68	-0.24	-0.25	0.9
Cthe_01643	Uncharacterized phage-associated protein-like		0	1		-1	0	0	1	-0.53	-0.12	0.1	0.68	-0.24	-0.25	0.9
Cthe_03160	putative RNA methylase, NOL1/NOP2/sun	8.34	8.63	9.29	9.18	-0.95	-0.55	-0.29	0.11	-0.46	-0.77	-0.87	-1.21	-0.24	-0.25	0.68
Cthe_02874	Phosphoenolpyruvate carboxykinase (GTP	15.25	15.69	16.4	16.04	-1.15	-0.35	-0.44	0.36	-0.73	-0.54	-1.37	-0.68	-0.24	-0.25	0.67
Cthe_02893	response regulator receiver protein	10.27	10.17	10.96	10.51	-0.69	-0.34	0.1	0.45	-0.11	-0.52	0.43	-0.49	-0.24	-0.25	0.93
Cthe_02121	hypothetical protein	10.06	9.97	10.94	10.11	-0.88	-0.14	0.09	0.83	-0.36	-0.29	0.4	0.32	-0.24	-0.25	1.03
Cthe_01619	transcriptional regulator, AbrB family	0	0	1		-1	0	0	1	-0.53	-0.12	0.1	0.68	-0.24	-0.25	0.9
Cthe_02570	hypothetical protein	6.69	6.29	7.43	6.52	-0.74	-0.23	0.4	0.91	-0.18	-0.39	1.43	0.49	-0.24	-0.25	0.32
Cthe_01372	hypothetical protein	11.1	10.97	11.78	10.85	-0.68	0.12	0.13	0.93	-0.09	0.02	0.53	0.53	-0.24	-0.25	0.14
Cthe_02027	hypothetical protein		0	1		-1	0	0	1	-0.53	-0.12	0.1	0.68	-0.24	-0.25	0.9
Cthe_00041	hypothetical protein	6.29	6.49	7.16	6.92	-0.87	-0.43	-0.2	0.24	-0.35	-0.63	-0.57	-0.94	-0.24	-0.25	0.74
Cthe_02041	hypothetical protein	2.32	2.58	3.91	2	-1.59	0.58	-0.26	1.91	-1.32	0.57	-0.77	2.62	-0.24	-0.25	0.6
Cthe_02160	hypothetical protein	10.19	10.39	11.09	10.65	-0.9	-0.26	-0.2	0.44	-0.39	-0.43	-0.57	-0.51	-0.24	-0.25	0.86
Cthe_00996	DNA polymerase III, alpha subunit	10.66	10.79	11.44	11.3	-0.78	-0.51	-0.13	0.14	-0.23	-0.73	-0.33	-1.15	-0.24	-0.25	0.73
Cthe_02718	preprotein translocase, SecE subunit	10.54	10.51	11.2	10.98	-0.66	-0.47	0.03	0.22	-0.07	-0.68	0.2	-0.98	-0.24	-0.25	0.78
Cthe_02874	Phosphoenolpyruvate carboxykinase (GTP	15.25	15.69	16.4	16.04	-1.15	-0.35	-0.44	0.36	-0.73	-0.54	-1.37	-0.68	-0.24	-0.25	0.67
Cthe_02874	Phosphoenolpyruvate carboxykinase (GTP	15.25	15.69	16.4	16.04	-1.15	-0.35	-0.44	0.36	-0.73	-0.54	-1.37	-0.68	-0.24	-0.25	0.67
Cthe_00996	DNA polymerase III, alpha subunit	10.66	10.79	11.44	11.3	-0.78	-0.51	-0.13	0.14	-0.23	-0.73	-0.33	-1.15	-0.24	-0.25	0.73
Cthe_00042	small GTP-binding protein	10.73	10.95	11.64	11.27	-0.91	-0.32	-0.22	0.37	-0.41	-0.5	-0.63	-0.66	-0.25	-0.26	0.81
Cthe_00098	peptidase M50	7.27	7.23	8.92	7	-1.65	0.23	0.04	1.92	-1.41	0.15	0.23	2.64	-0.25	-0.26	0.61
Cthe_01895	transcriptional regulator, PadR-like family	11	10.85	11.76	10.65	-0.76	0.2	0.15	1.11	-0.2	0.12	0.6	0.91	-0.25	-0.26	0.24
Cthe_01056	transglutaminase-like protein	9.82	10.11	10.88	10.16	-1.06	-0.05	-0.29	0.72	-0.61	-0.18	-0.87	0.09	-0.25	-0.26	0.83
Cthe_01930	carboxyl-terminal protease	9.06	9.21	10.02	9.18	-0.96	0.03	-0.15	0.84	-0.47	-0.08	-0.4	0.34	-0.25	-0.26	1.03
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02235	protein of unknown function DUF115	6.25	6.23	7.55	6.15	-1.3	0.08	0.02	1.4	-0.93	-0.02	0.17	1.53	-0.25	-0.26	0.69
Cthe_01223	ribosomal protein L20	12.85	12.95	13.6	13.52	-0.75	-0.57	-0.1	0.08	-0.19	-0.8	-0.23	-1.28	-0.25	-0.26	0.72
Cthe_00631	hypothetical protein	11.15	11.02	11.69	11.7	-0.54	-0.68	0.13	-0.01	0.09	-0.93	0.53	-1.47	-0.25	-0.26	0.68
Cthe_01223	ribosomal protein L20	12.85	12.95	13.6	13.52	-0.75	-0.57	-0.1	0.08	-0.19	-0.8	-0.23	-1.28	-0.25	-0.26	0.72
Cthe_01930	carboxyl-terminal protease	9.06	9.21	10.02	9.18	-0.96	0.03	-0.15	0.84	-0.47	-0.08	-0.4	0.34	-0.25	-0.26	1.03
Cthe_00098	peptidase M50	7.27	7.23	8.92	7	-1.65	0.23	0.04	1.92	-1.41	0.15	0.23	2.64	-0.25	-0.26	0.61
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2							



Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_02340	UDP-glucose/GDP-mannose dehydrogena	9.22	9.02	9.8	9.6	-0.58	-0.58	0.2	0.2	0.04	-0.81	0.77	-1.02	-0.25	-0.26	0.72
Cthe_00926	signal recognition particle-docking protein	9.92	9.77	10.61	10.17	-0.69	-0.4	0.15	0.44	-0.11	-0.6	0.6	-0.51	-0.26	-0.27	0.88
Cthe_01049	regulatory protein ReX	10.53	10.45	11.31	10.65	-0.78	-0.2	0.08	0.66	-0.23	-0.36	0.37	-0.04	-0.26	-0.27	1.3
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_01528	two component transcriptional regulator,	6.94	6.79	7.64	6.61	-0.7	0.18	0.15	1.03	-0.12	0.1	0.6	0.74	-0.26	-0.27	0.19
Cthe_00492	CheC, inhibitor of MCP methylation	5.36	5.81	6.49	6.43	-1.13	-0.62	-0.45	0.06	-0.7	-0.86	-1.4	-1.32	-0.26	-0.27	0.65
Cthe_00492	CheC, inhibitor of MCP methylation	5.36	5.81	6.49	6.43	-1.13	-0.62	-0.45	0.06	-0.7	-0.86	-1.4	-1.32	-0.26	-0.27	0.65
Cthe_01528	two component transcriptional regulator,	6.94	6.79	7.64	6.61	-0.7	0.18	0.15	1.03	-0.12	0.1	0.6	0.74	-0.26	-0.27	0.19
Cthe_03068	periplasmic sensor signal transduction his	10.19	10.24	10.92	10.73	-0.73	-0.49	-0.05	0.19	-0.16	-0.7	-0.07	-1.04	-0.26	-0.27	0.78
Cthe_02624		5.29	5.75	6.52	5.91	-1.23	-0.16	-0.46	0.61	-0.84	-0.31	-1.43	-0.15	-0.26	-0.27	0.71
Cthe_00778	hypothetical protein	10.78	10.55	11.52	11	-0.74	-0.45	0.23	0.52	-0.18	-0.65	0.87	-0.34	-0.26	-0.27	0.82
Cthe_00671	hypothetical protein	5.21	4.86	6.78	5.09	-1.57	-0.23	0.35	1.69	-1.3	-0.39	1.27	2.15	-0.26	-0.27	0.62
Cthe_03195	hypothetical protein	5.17	5.04	5.81	4.91	-0.64	0.13	0.13	0.9	-0.04	0.04	0.53	0.47	-0.26	-0.27	0.09
Cthe_01440	hypothetical protein				1		-1		-1		-1.31		-3.57	-0.26	-0.27	0.42
Cthe_02010	hypothetical protein				1		-1		-1		-1.31		-3.57	-0.26	-0.27	0.42
Cthe_01831	hypothetical protein	10.94	10.91	11.69	11.08	-0.75	-0.17	0.03	0.61	-0.19	-0.32	0.2	-0.15	-0.26	-0.27	1.69
Cthe_02624		5.29	5.75	6.52	5.91	-1.23	-0.16	-0.46	0.61	-0.84	-0.31	-1.43	-0.15	-0.26	-0.27	0.71
Cthe_00926	signal recognition particle-docking protein	9.92	9.77	10.61	10.17	-0.69	-0.4	0.15	0.44	-0.11	-0.6	0.6	-0.51	-0.26	-0.27	0.88
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_02359	metal dependent phosphohydrolase	9.79	9.71	10.41	10.29	-0.62	-0.58	0.08	0.12	-0.01	-0.81	0.37	-1.19	-0.26	-0.27	0.74
Cthe_01353	polysaccharide biosynthesis protein	11.8	11.78	12.48	12.29	-0.68	-0.51	0.02	0.19	-0.09	-0.73	0.17	-1.04	-0.27	-0.28	0.79
Cthe_00362	transcriptional regulator, AsnC family	12.07	12.06	12.83	12.19	-0.76	-0.13	0.01	0.64	-0.2	-0.27	0.13	-0.09	-0.27	-0.28	2.41
Cthe_01363	lipopolysaccharide biosynthesis	12.33	12.22	12.96	12.76	-0.63	-0.54	0.11	0.2	-0.03	-0.76	0.47	-1.02	-0.27	-0.28	0.77
Cthe_01245	phosphoribosylamine-glycine ligase	10.92	11.27	11.69	11.33	-0.77	-0.06	-0.35	0.36	-0.22	-0.19	-1.07	-0.68	-0.27	-0.28	0.26
Cthe_01247	phosphoribosylglycinamide formyltransfe	9.13	9.45	10.19	9.68	-1.06	-0.23	-0.32	0.51	-0.61	-0.39	-0.97	-0.36	-0.27	-0.28	0.8
Cthe_02912	ribosomal protein S17	11.28	11.68	12.36	12.26	-1.08	-0.58	-0.4	0.1	-0.64	-0.81	-1.23	-1.23	-0.27	-0.28	0.67
Cthe_01363	lipopolysaccharide biosynthesis	12.33	12.22	12.96	12.76	-0.63	-0.54	0.11	0.2	-0.03	-0.76	0.47	-1.02	-0.27	-0.28	0.77
Cthe_00549	ABC-3	9.62	9.79	10.53	9.92	-0.91	-0.13	-0.17	0.61	-0.41	-0.27	-0.47	-0.15	-0.27	-0.28	1.13
Cthe_00551	AMP-dependent synthetase and ligase	12.11	12.3	12.71	12.22	-0.6	0.08	-0.19	0.49	0.01	-0.02	-0.53	-0.4	-0.27	-0.28	0.04
Cthe_02782	N-acetylmuramyl-L-alanine amidase, nega	6.11	6.36	7.23	6.27	-1.12	0.09	-0.25	0.96	-0.69	-0.01	-0.73	0.6	-0.27	-0.28	0.83
Cthe_02764	TROVE domain containing protein	9.33	9.16	10.08	9.01	-0.75	0.15	0.17	1.07	-0.19	0.06	0.67	0.83	-0.27	-0.28	0.21
Cthe_00086	hypothetical protein	3.46	3.7	4.39	4.17	-0.93	-0.47	-0.24	0.22	-0.43	-0.68	-0.7	-0.98	-0.27	-0.28	0.76
Cthe_02912	ribosomal protein S17	11.28	11.68	12.36	12.26	-1.08	-0.58	-0.4	0.1	-0.64	-0.81	-1.23	-1.23	-0.27	-0.28	0.67
Cthe_00549	ABC-3	9.62	9.79	10.53	9.92	-0.91	-0.13	-0.17	0.61	-0.41	-0.27	-0.47	-0.15	-0.27	-0.28	1.13
Cthe_02912	ribosomal protein S17	11.28	11.68	12.36	12.26	-1.08	-0.58	-0.4	0.1	-0.64	-0.81	-1.23	-1.23	-0.27	-0.28	0.67
Cthe_01245	phosphoribosylamine-glycine ligase	10.92	11.27	11.69	11.33	-0.77	-0.06	-0.35	0.36	-0.22	-0.19	-1.07	-0.68	-0.27	-0.28	0.26
Cthe_01247	phosphoribosylglycinamide formyltransfe	9.13	9.45	10.19	9.68	-1.06	-0.23	-0.32	0.51	-0.61	-0.39	-0.97	-0.36	-0.27	-0.28	0.8
Cthe_01245	phosphoribosylamine-glycine ligase	10.92	11.27	11.69	11.33	-0.77	-0.06	-0.35	0.36	-0.22	-0.19	-1.07	-0.68	-0.27	-0.28	0.26
Cthe_00551	AMP-dependent synthetase and ligase	12.11	12.3	12.71	12.22	-0.6	0.08	-0.19	0.49	0.01	-0.02	-0.53	-0.4	-0.27	-0.28	0.04
Cthe_01247	phosphoribosylglycinamide formyltransfe	9.13	9.45	10.19	9.68	-1.06	-0.23	-0.32	0.51	-0.61	-0.39	-0.97	-0.36	-0.27	-0.28	0.8
Cthe_01363	lipopolysaccharide biosynthesis	12.33	12.22	12.96	12.76	-0.63	-0.54	0.11	0.2	-0.03	-0.76	0.47	-1.02	-0.27	-0.28	0.77
Cthe_00551	AMP-dependent synthetase and ligase	12.11	12.3	12.71	12.22	-0.6	0.08	-0.19	0.49	0.01	-0.02	-0.53	-0.4	-0.27	-0.28	0.04
Cthe_01245	phosphoribosylamine-glycine ligase	10.92	11.27	11.69	11.33	-0.77	-0.06	-0.35	0.36	-0.22	-0.19	-1.07	-0.68	-0.27	-0.28	0.26
Cthe_00551	AMP-dependent synthetase and ligase	12.11	12.3	12.71	12.22	-0.6	0.08	-0.19	0.49	0.01	-0.02	-0.53	-0.4	-0.27	-0.28	0.04
Cthe_00551	AMP-dependent synthetase and ligase	12.11	12.3	12.71	12.22	-0.6	0.08	-0.19	0.49	0.01	-0.02	-0.53	-0.4	-0.27	-0.28	0.04
Cthe_01247	phosphoribosylglycinamide formyltransfe	9.13	9.45	10.19	9.68	-1.06	-0.23	-0.32	0.51	-0.61	-0.39	-0.97	-0.36	-0.27	-0.28	0.8
Cthe_01245	phosphoribosylamine-glycine ligase	10.92	11.27	11.69	11.33	-0.77	-0.06	-0.35	0.36	-0.22	-0.19	-1.07	-0.68	-0.27	-0.28	0.26
Cthe_00551	AMP-dependent synthetase and ligase	12.11	12.3	12.71	12.22	-0.6	0.08	-0.19	0.49	0.01	-0.02	-0.53	-0.4	-0.27	-0.28	0.04
Cthe_00551	AMP-dependent synthetase and ligase	12.11	12.3	12.71	12.22	-0.6	0.08	-0.19	0.49	0.01	-0.02	-0.53	-0.4	-0.27	-0.28	0.04
Cthe_01245	phosphoribosylamine-glycine ligase	10.92	11.27	11.69	11.33	-0.77	-0.06	-0.35	0.36	-0.22	-0.19	-1.07	-0.68	-0.27	-0.28	0.26
Cthe_01247	phosphoribosylglycinamide formyltransfe	9.13	9.45	10.19	9.68	-1.06	-0.23	-0.32	0.51	-0.61	-0.39	-0.97	-0.36	-0.27	-0.28	0.8
Cthe_01100	prepilin-type cleavage/methylation	10.04	10.08	10.81	10.15	-0.77	-0.07	-0.04	0.66	-0.22	-0.2	-0.03	-0.04	-0.28	-0.29	6.76
Cthe_01100	prepilin-type cleavage/methylation	10.04	10.08	10.81	10.15	-0.77	-0.07	-0.04	0.66	-0.22	-0.2	-0.03	-0.04	-0.28	-0.29	6.76
Cthe_02282	MCP methyltransferase, CheR-type	5.13	4.64	5.81	5.46	-0.68	-0.82	0.49	0.35	-0.09	-1.1	1.73	-0.7	-0.28	-0.29	0.67
Cthe_02511	MscS Mechanosensitive ion channel	7.61	7.48	8.19	8.19	-0.58	-0.71	0.13	0	0.04	-0.96	0.53	-1.45	-0.28	-0.29	0.71
Cthe_02189	diguanylate cyclase with GAF sensor	11.73	11.86	12.61	11.95	-0.88	-0.09	-0.13	0.66	-0.36	-0.23	-0.33	-0.04	-0.28	-0.29	1.46
Cthe_02282	MCP methyltransferase, CheR-type	5.13	4.64	5.81	5.46	-0.68	-0.82	0.49	0.35	-0.09	-1.1	1.73	-0.7	-0.28	-0.29	0.67
Cthe_01851	protein of unknown function DUF1113	9.9	9.66	11	9.95	-1.1	-0.29	0.24	1.05	-0.66	-0.46	0.9	0.79	-0.28	-0.29	0.76
Cthe_00365	peptide chain release factor 2	12.7	12.57	13.43	12.92	-0.73	-0.35	0.13	0.51	-0.16	-0.54	0.53	-0.36	-0.28	-0.29	1
Cthe_00990	ribosome-binding factor A	8.71	8.95	9.34	8.97	-0.63	-0.02	-0.24	0.37	-0.03	-0.14	-0.7	-0.66	-0.28	-0.29	0.17
Cthe_02592	hypothetical protein	9.23	9.21	10	9.35	-0.77	-0.14	0.02	0.65	-0.22	-0.29	0.17	-0.06	-0.28	-0.29	2.29
Cthe_02178	hypothetical protein	7.52	7.61	8.33	7.86	-0.81	-0.25	-0.09	0.47	-0.27	-0.42	-0.2	-0.45	-0.28	-0.29	1.15
Cthe_00321	TPR repeat domain containing protein	9.1	9.22	10.17	9.15	-1.07	0.07	-0.12	1.02	-0.62	-0.04	-0.3	0.72	-0.28	-0.29	0.91
Cthe_02568	hypothetical protein	6.93	7.19	8.4	6.79	-1.47	0.4	-0.26	1.61	-1.16	0.36	-0.77	1.98	-0.28	-0.29	0.65
Cthe_02282	MCP methyltransferase, CheR-type	5.13	4.64	5.81	5.46	-0.68	-0.82	0.49	0.35	-0.09	-1.1	1.73	-0.7	-0.28	-0.29	0.67
Cthe_01764	Outer membrane protein-like protein	10.64	10.68	11.49	10.73	-0.85	-0.05	-0.04	0.76	-0.32	-0.18	-0.03	0.17	-0.29	-0.3	2.42
Cthe_00269	glycoside hydrolase, family 8	13.82	14.02	14.96	13.91	-1.14	0.11	-0.2	1.05	-0.72	0.01	-0.57	0.79	-0.29	-0.3	0.84
Cthe_00585	Integrase, catalytic region	13.16	13.16	13.91												



Cthe_01000	phosphatidate cytidyltransferase	11.68	11.89	12.27	11.83	-0.59	0.06	-0.21	0.44	0.03	-0.05	-0.6	-0.51	-0.29	-0.3	0.08
Cthe_01000	phosphatidate cytidyltransferase	11.68	11.89	12.27	11.83	-0.59	0.06	-0.21	0.44	0.03	-0.05	-0.6	-0.51	-0.29	-0.3	0.08
Cthe_01226	dihydrofolate reductase region	10.15	10.18	10.9	10.6	-0.75	-0.42	-0.03	0.3	-0.19	-0.62	0	-0.81	-0.29	-0.3	0.91
Cthe_01226	dihydrofolate reductase region	10.15	10.18	10.9	10.6	-0.75	-0.42	-0.03	0.3	-0.19	-0.62	0	-0.81	-0.29	-0.3	0.91
Cthe_01000	phosphatidate cytidyltransferase	11.68	11.89	12.27	11.83	-0.59	0.06	-0.21	0.44	0.03	-0.05	-0.6	-0.51	-0.29	-0.3	0.08
Cthe_01226	dihydrofolate reductase region	10.15	10.18	10.9	10.6	-0.75	-0.42	-0.03	0.3	-0.19	-0.62	0	-0.81	-0.29	-0.3	0.91
Cthe_01164	FAD dependent oxidoreductase	10.56	10.65	11.49	10.68	-0.93	-0.03	-0.09	0.81	-0.43	-0.15	-0.2	0.28	-0.3	-0.31	1.5
Cthe_00874	glutamine amidotransferase of anthranila	7.61	7.98	8.37	8.08	-0.76	-0.1	-0.37	0.29	-0.2	-0.24	-1.13	-0.83	-0.3	-0.31	0.25
Cthe_03109	Uracil-DNA glycosylase superfamily	8.54	8.64	9.33	9.24	-0.79	-0.6	-0.1	0.09	-0.24	-0.83	-0.23	-1.26	-0.3	-0.31	0.77
Cthe_00874	glutamine amidotransferase of anthranila	7.61	7.98	8.37	8.08	-0.76	-0.1	-0.37	0.29	-0.2	-0.24	-1.13	-0.83	-0.3	-0.31	0.25
Cthe_01325	putative oxygen-independent coproporph	9.39	9.37	10.17	9.53	-0.78	-0.16	0.02	0.64	-0.23	-0.31	0.17	-0.09	-0.3	-0.31	2.28
Cthe_00080	CheW protein	9.64	9.67	10.41	10	-0.77	-0.33	-0.03	0.41	-0.22	-0.51	0	-0.57	-0.3	-0.31	1.11
Cthe_00080	CheW protein	9.64	9.67	10.41	10	-0.77	-0.33	-0.03	0.41	-0.22	-0.51	0	-0.57	-0.3	-0.31	1.11
Cthe_00331	hypothetical protein	7.71	7.83	8.57	7.97	-0.86	-0.14	-0.12	0.6	-0.34	-0.29	-0.3	-0.17	-0.3	-0.31	1.47
Cthe_00803	pseudouridine synthase, RluA family	8.34	8.35	9.11	8.52	-0.77	-0.17	-0.01	0.59	-0.22	-0.32	0.07	-0.19	-0.3	-0.31	2.18
Cthe_01259	CDP-alcohol phosphatidyltransferase	9.64	9.78	10.45	10.48	-0.81	-0.7	-0.14	-0.03	-0.27	-0.95	-0.37	-1.51	-0.3	-0.31	0.72
Cthe_02576	hypothetical protein	11.2	11.21	12.1	11.28	-0.9	-0.07	-0.01	0.82	-0.39	-0.2	0.07	0.3	-0.3	-0.31	1.62
Cthe_00049	transcriptional regulator, XRE family	9.61	9.33	10.84	9	-1.23	0.33	0.28	1.84	-0.84	0.27	1.03	2.47	-0.3	-0.31	0.37
Cthe_01981	hypothetical protein	3.91	3	4.7	4.32	-0.79	-1.32	0.91	0.38	-0.24	-1.69	3.13	-0.64	-0.3	-0.31	0.61
Cthe_00630	hypothetical protein	11.15	11.02	11.74	11.74	-0.59	-0.72	0.13	0	0.03	-0.98	0.53	-1.45	-0.3	-0.31	0.72
Cthe_02261	hypothetical protein	10.64	10.68	11.41	11	-0.77	-0.32	-0.04	0.41	-0.22	-0.5	-0.03	-0.57	-0.3	-0.31	1.09
Cthe_01325	putative oxygen-independent coproporph	9.39	9.37	10.17	9.53	-0.78	-0.16	0.02	0.64	-0.23	-0.31	0.17	-0.09	-0.3	-0.31	2.28
Cthe_00874	glutamine amidotransferase of anthranila	7.61	7.98	8.37	8.08	-0.76	-0.1	-0.37	0.29	-0.2	-0.24	-1.13	-0.83	-0.3	-0.31	0.25
Cthe_02261	hypothetical protein	10.64	10.68	11.41	11	-0.77	-0.32	-0.04	0.41	-0.22	-0.5	-0.03	-0.57	-0.3	-0.31	1.09
Cthe_01259	CDP-alcohol phosphatidyltransferase	9.64	9.78	10.45	10.48	-0.81	-0.7	-0.14	-0.03	-0.27	-0.95	-0.37	-1.51	-0.3	-0.31	0.72
Cthe_01325	putative oxygen-independent coproporph	9.39	9.37	10.17	9.53	-0.78	-0.16	0.02	0.64	-0.23	-0.31	0.17	-0.09	-0.3	-0.31	2.28
Cthe_00803	pseudouridine synthase, RluA family	8.34	8.35	9.11	8.52	-0.77	-0.17	-0.01	0.59	-0.22	-0.32	0.07	-0.19	-0.3	-0.31	2.18
Cthe_00874	glutamine amidotransferase of anthranila	7.61	7.98	8.37	8.08	-0.76	-0.1	-0.37	0.29	-0.2	-0.24	-1.13	-0.83	-0.3	-0.31	0.25
Cthe_03109	Uracil-DNA glycosylase superfamily	8.54	8.64	9.33	9.24	-0.79	-0.6	-0.1	0.09	-0.24	-0.83	-0.23	-1.26	-0.3	-0.31	0.77
Cthe_00874	glutamine amidotransferase of anthranila	7.61	7.98	8.37	8.08	-0.76	-0.1	-0.37	0.29	-0.2	-0.24	-1.13	-0.83	-0.3	-0.31	0.25
Cthe_00874	glutamine amidotransferase of anthranila	7.61	7.98	8.37	8.08	-0.76	-0.1	-0.37	0.29	-0.2	-0.24	-1.13	-0.83	-0.3	-0.31	0.25
Cthe_01259	CDP-alcohol phosphatidyltransferase	9.64	9.78	10.45	10.48	-0.81	-0.7	-0.14	-0.03	-0.27	-0.95	-0.37	-1.51	-0.3	-0.31	0.72
Cthe_01259	CDP-alcohol phosphatidyltransferase	9.64	9.78	10.45	10.48	-0.81	-0.7	-0.14	-0.03	-0.27	-0.95	-0.37	-1.51	-0.3	-0.31	0.72
Cthe_01259	CDP-alcohol phosphatidyltransferase	9.64	9.78	10.45	10.48	-0.81	-0.7	-0.14	-0.03	-0.27	-0.95	-0.37	-1.51	-0.3	-0.31	0.72
Cthe_01325	putative oxygen-independent coproporph	9.39	9.37	10.17	9.53	-0.78	-0.16	0.02	0.64	-0.23	-0.31	0.17	-0.09	-0.3	-0.31	2.28
Cthe_02261	hypothetical protein	10.64	10.68	11.41	11	-0.77	-0.32	-0.04	0.41	-0.22	-0.5	-0.03	-0.57	-0.3	-0.31	1.09
Cthe_01259	CDP-alcohol phosphatidyltransferase	9.64	9.78	10.45	10.48	-0.81	-0.7	-0.14	-0.03	-0.27	-0.95	-0.37	-1.51	-0.3	-0.31	0.72
Cthe_01774	ribosomal-protein-alanine acetyltransfera	8.29	8.36	9.07	8.9	-0.78	-0.54	-0.07	0.17	-0.23	-0.76	-0.13	-1.09	-0.31	-0.32	0.82
Cthe_02058	Appr-1-p processing protein	7.66	7.59	8.38	8.01	-0.72	-0.42	0.07	0.37	-0.15	-0.62	0.33	-0.66	-0.31	-0.32	0.98
Cthe_03074	Cof-like hydrolase	8.24	8.2	8.97	8.61	-0.73	-0.41	0.04	0.36	-0.16	-0.61	0.23	-0.68	-0.31	-0.32	1
Cthe_00715	Adenosylmethionine decarboxylase	11.01	10.95	11.7	11.47	-0.69	-0.52	0.06	0.23	-0.11	-0.74	0.3	-0.96	-0.31	-0.32	0.85
Cthe_00029	hypothetical protein	6.82	6.52	7.82	6.41	-1	0.11	0.3	1.41	-0.53	0.01	1.1	1.55	-0.31	-0.32	0.32
Cthe_02913	ribosomal protein L14	11.41	11.78	12.48	12.4	-1.07	-0.62	-0.37	0.08	-0.62	-0.86	-1.13	-1.28	-0.31	-0.32	0.71
Cthe_02991	NADH:flavin oxidoreductase/NADH oxidas	8.96	8.75	9.8	8.55	-0.84	0.2	0.21	1.25	-0.31	0.12	0.8	1.21	-0.31	-0.32	0.26
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_02991	NADH:flavin oxidoreductase/NADH oxidas	8.96	8.75	9.8	8.55	-0.84	0.2	0.21	1.25	-0.31	0.12	0.8	1.21	-0.31	-0.32	0.26
Cthe_01827	copper amine oxidase-like protein	10.63	10.84	11.75	10.78	-1.12	0.06	-0.21	0.97	-0.69	-0.05	-0.6	0.62	-0.31	-0.32	0.91
Cthe_00131	hypothetical protein	7.44	7.5	8.2	8.1	-0.76	-0.6	-0.06	0.1	-0.2	-0.83	-0.1	-1.23	-0.31	-0.32	0.79
Cthe_00829	hypothetical protein	10.95	10.91	11.72	11.14	-0.77	-0.23	0.04	0.58	-0.22	-0.39	0.23	-0.21	-0.31	-0.32	1.63
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_02913	ribosomal protein L14	11.41	11.78	12.48	12.4	-1.07	-0.62	-0.37	0.08	-0.62	-0.86	-1.13	-1.28	-0.31	-0.32	0.71
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_00715	Adenosylmethionine decarboxylase	11.01	10.95	11.7	11.47	-0.69	-0.52	0.06	0.23	-0.11	-0.74	0.3	-0.96	-0.31	-0.32	0.85
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_00715	Adenosylmethionine decarboxylase	11.01	10.95	11.7	11.47	-0.69	-0.52	0.06	0.23	-0.11	-0.74	0.3	-0.96	-0.31	-0.32	0.85
Cthe_02913	ribosomal protein L14	11.41	11.78	12.48	12.4	-1.07	-0.62	-0.37	0.08	-0.62	-0.86	-1.13	-1.28	-0.31	-0.32	0.71
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_01774	ribosomal-protein-alanine acetyltransfera	8.29	8.36	9.07	8.9	-0.78	-0.54	-0.07	0.17	-0.23	-0.76	-0.13	-1.09	-0.31	-0.32	0.82
Cthe_00715	Adenosylmethionine decarboxylase	11.01	10.95	11.7	11.47	-0.69	-0.52	0.06	0.23	-0.11	-0.74	0.3	-0.96	-0.31	-0.32	0.85
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69
Cthe_03158	putative aconitate hydratase	11.02	11.2	11.86	12.01	-0.84	-0.81	-0.18	-0.15	-0.31	-1.08	-0.5	-1.77	-0.31	-0.32	0.69



Cthe_02344	Undecaprenyl-phosphate galactose	8.57	8.58	9.33	9	-0.76	-0.42	-0.01	0.33	-0.2	-0.62	0.07	-0.74	-0.32	-0.33	1
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_00610	histidinol-phosphate aminotransferase	8.58	8.64	9.35	9.2	-0.77	-0.56	-0.06	0.15	-0.22	-0.79	-0.1	-1.13	-0.32	-0.33	0.82
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_00610	histidinol-phosphate aminotransferase	8.58	8.64	9.35	9.2	-0.77	-0.56	-0.06	0.15	-0.22	-0.79	-0.1	-1.13	-0.32	-0.33	0.82
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01863	N-acetyl-gamma-glutamyl-phosphate redu	9.33	9.99	11.05	9.42	-1.72	0.57	-0.66	1.63	-1.5	0.56	-2.1	2.02	-0.32	-0.33	0.62
Cthe_01251	Xanthine/uracil/vitamin C permease	13.19	13.54	13.92	13.61	-0.73	-0.07	-0.35	0.31	-0.16	-0.2	-1.07	-0.79	-0.33	-0.34	0.22
Cthe_02548	Alpha-N-arabinofuranosidase	9.41	9.45	10.14	10.19	-0.73	-0.74	-0.04	-0.05	-0.16	-1	-0.03	-1.55	-0.33	-0.34	0.74
Cthe_02918	ribosomal protein L6	12.06	12.53	12.93	12.54	-0.87	-0.01	-0.47	0.39	-0.35	-0.13	-1.47	-0.62	-0.33	-0.34	0.27
Cthe_00384	ABC transporter related protein	3.17	3	3.46	4.58	-0.29	-1.58	0.17	-1.12	0.43	-2	0.67	-3.83	-0.33	-0.34	0.6
Cthe_00359	hypothetical protein	5.17	4.46	6.39	4.86	-1.22	-0.4	0.71	1.53	-0.82	-0.6	2.47	1.81	-0.33	-0.34	0.38
Cthe_00494	hypothetical protein	5.52	5.39	6.23	5.88	-0.71	-0.49	0.13	0.35	-0.14	-0.7	0.53	-0.7	-0.33	-0.34	0.92
Cthe_02277	hypothetical protein	8.59	8.49	9.17	9.37	-0.58	-0.88	0.1	-0.2	0.04	-1.17	0.43	-1.87	-0.33	-0.34	0.69
Cthe_02331	hypothetical protein	13.57	13.19	14.23	13.96	-0.66	-0.77	0.38	0.27	-0.07	-1.04	1.37	-0.87	-0.33	-0.34	0.73
Cthe_02918	ribosomal protein L6	12.06	12.53	12.93	12.54	-0.87	-0.01	-0.47	0.39	-0.35	-0.13	-1.47	-0.62	-0.33	-0.34	0.27
Cthe_00384	ABC transporter related protein	3.17	3	3.46	4.58	-0.29	-1.58	0.17	-1.12	0.43	-2	0.67	-3.83	-0.33	-0.34	0.6
Cthe_02918	ribosomal protein L6	12.06	12.53	12.93	12.54	-0.87	-0.01	-0.47	0.39	-0.35	-0.13	-1.47	-0.62	-0.33	-0.34	0.27
Cthe_02548	Alpha-N-arabinofuranosidase	9.41	9.45	10.14	10.19	-0.73	-0.74	-0.04	-0.05	-0.16	-1	-0.03	-1.55	-0.33	-0.34	0.74
Cthe_01799	ABC transporter related protein	10.62	10.68	11.43	11.12	-0.81	-0.44	-0.06	0.31	-0.27	-0.64	-0.1	-0.79	-0.34	-0.35	0.99
Cthe_03064	polysaccharide biosynthesis protein	10.25	10.55	10.92	10.58	-0.67	-0.03	-0.3	0.34	-0.08	-0.15	-0.9	-0.72	-0.34	-0.35	0.17
Cthe_00886	DNA polymerase I	10.3	10.37	11.18	10.45	-0.88	-0.08	-0.07	0.73	-0.36	-0.21	-0.13	0.11	-0.34	-0.35	2.78
Cthe_02285	CheW protein	4.75	5.49	5.88	5.32	-1.13	0.17	-0.74	0.56	-0.7	0.08	-2.37	-0.26	-0.34	-0.35	0.34
Cthe_02285	CheW protein	4.75	5.49	5.88	5.32	-1.13	0.17	-0.74	0.56	-0.7	0.08	-2.37	-0.26	-0.34	-0.35	0.34
Cthe_01222	RNA methyltransferase, TrmH family, grou	7.79	8.04	8.73	8.8	-0.94	-0.76	-0.25	-0.07	-0.45	-1.02	-0.73	-1.6	-0.34	-0.35	0.72
Cthe_02907	ribosomal protein S19	10.86	11.19	11.92	11.72	-1.06	-0.53	-0.33	0.2	-0.61	-0.75	-1	-1.02	-0.34	-0.35	0.77
Cthe_01403	FeoA	1.58	2.58	3.32	3.58	-1.74	-1	-1	-0.26	-1.53	-1.31	-3.23	-2	-0.34	-0.35	0.6
Cthe_00397	ABC transporter related protein	9.45	9.83	10.18	9.98	-0.73	-0.15	-0.38	0.2	-0.16	-0.3	-1.17	-1.02	-0.34	-0.35	0.25
Cthe_02862	hypothetical protein	5.09	4.58	5.88	4.86	-0.79	-0.28	0.51	1.02	-0.24	-0.45	1.8	0.72	-0.34	-0.35	0.3
Cthe_00380	hypothetical protein	5.09	4.09	5.39	4.91	-0.3	-0.82	1	0.48	0.42	-1.1	3.43	-0.43	-0.34	-0.35	0.39
Cthe_02436	hypothetical protein	7.65	7.42	8.63	6.97	-0.98	0.45	0.23	1.66	-0.5	0.42	0.87	2.09	-0.34	-0.35	0.33
Cthe_01978	hypothetical protein	6.38	6.09	7.34	6.55	-0.96	-0.46	0.29	0.79	-0.47	-0.67	1.07	0.23	-0.34	-0.35	0.85
Cthe_02439	GCN5-related N-acetyltransferase	9.94	9.76	10.99	10.04	-1.05	-0.28	0.18	0.95	-0.59	-0.45	0.7	0.57	-0.34	-0.35	0.93
Cthe_02765	hypothetical protein	8.89	8.89	9.75	9	-0.86	-0.11	0	0.75	-0.34	-0.25	0.1	0.15	-0.34	-0.35	2.66
Cthe_02907	ribosomal protein S19	10.86	11.19	11.92	11.72	-1.06	-0.53	-0.33	0.2	-0.61	-0.75	-1	-1.02	-0.34	-0.35	0.77
Cthe_02907	ribosomal protein S19	10.86	11.19	11.92	11.72	-1.06	-0.53	-0.33	0.2	-0.61	-0.75	-1	-1.02	-0.34	-0.35	0.77
Cthe_00886	DNA polymerase I	10.3	10.37	11.18	10.45	-0.88	-0.08	-0.07	0.73	-0.36	-0.21	-0.13	0.11	-0.34	-0.35	2.78
Cthe_01471	glycoside hydrolase, family 5	9.29	9.46	10.19	9.99	-0.9	-0.53	-0.17	0.2	-0.39	-0.75	-0.47	-1.02	-0.35	-0.36	0.86
Cthe_00620	iron (metal) dependent repressor, DtxR fa	12.28	12.08	12.92	12.01	-0.64	0.07	0.2	0.91	-0.04	-0.04	0.77	0.49	-0.35	-0.36	0.07
Cthe_02900	RNA polymerase, sigma 28 subunit	11.8	11.81	12.57	12.28	-0.77	-0.47	-0.01	0.29	-0.22	-0.68	0.07	-0.83	-0.35	-0.36	0.98
Cthe_00355	hypothetical protein	8.9	8.5	9.42	8.62	-0.52	-0.12	0.4	0.8	0.12	-0.26	1.43	0.26	-0.35	-0.36	0.22
Cthe_03069	two component transcriptional regulator,	8.04	7.79	8.74	8.44	-0.7	-0.65	0.25	0.3	-0.12	-0.89	0.93	-0.81	-0.36	-0.37	0.83
Cthe_00617	AAA ATPase, central region	12.41	12.7	13.07	12.65	-0.66	0.05	-0.29	0.42	-0.07	-0.06	-0.87	-0.55	-0.36	-0.37	0.1
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	10.92	10.94	11.73	11.09	-0.81	-0.15	-0.02	0.64	-0.27	-0.3	0.03	-0.09	-0.36	-0.37	4.83
Cthe_01227	Thymidylate synthase	11.5	11.47	12.24	12.03	-0.74	-0.56	0.03	0.21	-0.18	-0.79	0.2	-1	-0.36	-0.37	0.9
Cthe_01584	two component transcriptional regulator,	5.39	4.95	6.46	5	-1.07	-0.05	0.44	1.46	-0.62	-0.18	1.57	1.66	-0.36	-0.37	0.32
Cthe_03069	two component transcriptional regulator,	8.04	7.79	8.74	8.44	-0.7	-0.65	0.25	0.3	-0.12	-0.89	0.93	-0.81	-0.36	-0.37	0.83
Cthe_01466	protein of unknown function DUF1706	5.81	6.09	6.27	6.17	-0.46	-0.08	-0.28	0.1	0.2	-0.21	-0.83	-1.23	-0.36	-0.37	0.22
Cthe_02150	integral membrane protein-like protein	11.79	11.82	12.59	12.22	-0.8	-0.4	-0.03	0.37	-0.26	-0.6	0	-0.66	-0.36	-0.37	1.13
Cthe_02504	hypothetical protein	8.23	8.49	9.24	8.95	-1.01	-0.46	-0.26	0.29	-0.54	-0.67	-0.77	-0.83	-0.36	-0.37	0.86
Cthe_02914	ribosomal protein L24	11.46	11.86	12.6	12.45	-1.14	-0.59	-0.4	0.15	-0.72	-0.82	-1.23	-1.13	-0.36	-0.37	0.74
Cthe_02971	hypothetical protein	6.87	7.08	7.88	7.25	-1.01	-0.17	-0.21	0.63	-0.54	-0.32	-0.6	-0.11	-0.36	-0.37	1.17
Cthe_01828	hypothetical protein	9.85	9.96	10.98	9.95	-1.13	0.01	-0.11	1.03	-0.7	-0.11	-0.27	0.74	-0.36	-0.37	1.02
Cthe_02914	ribosomal protein L24	11.46	11.86	12.6	12.45	-1.14	-0.59	-0.4	0.15	-0.72	-0.82	-1.23	-1.13	-0.36	-0.37	0.74
Cthe_02914	ribosomal protein L24	11.46	11.86	12.6	12.45	-1.14	-0.59	-0.4	0.15	-0.72	-0.82	-1.23	-1.13	-0.36	-0.37	0.74
Cthe_01227	Thymidylate synthase	11.5	11.47	12.24	12.03	-0.74	-0.56	0.03	0.21	-0.18	-0.79	0.2	-1	-0.36	-0.37	0.9
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	10.92	10.94	11.73	11.09	-0.81	-0.15	-0.02	0.64	-0.27	-0.3	0.03	-0.09	-0.36	-0.37	4.83
Cthe_01227	Thymidylate synthase	11.5	11.47	12.24	12.03	-0.74	-0.56	0.03	0.21	-0.18	-0.79	0.2	-1	-0.36	-0.37	0.9
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	10.92	10.94	11.73	11.09	-0.81	-0.15	-0.02	0.64	-0.27	-0.3	0.03	-0.09	-0.36	-0.37	4.83
Cthe_01227	Thymidylate synthase	11.5	11.47	12.24	12.03	-0.74	-0.56	0.03	0.21	-0.18	-0.79	0.2	-1	-0.36	-0.37	0.9
Cthe_01171	Serine-type D-Ala-D-Ala carboxypeptidase	10.92	10.94	11.73	11.09	-0.81	-0.15	-0.02	0.64	-0.27	-0.3	0.03	-0.09	-0.36	-0.37	4.83
Cthe_01227	Thymidylate synthase	11.5	11.47	12.24	12.03	-0.74	-0.56	0.03	0.21	-0.18	-0.79	0.2	-1	-0.36	-0.37	0.9
Cthe_01189	ABC transporter related protein	9.06	9.51	9.82	9.27	-0.76	0.24	-0.45	0.55	-0.2	0.17	-1.4	-0.28	-0.37	-0.38	0.21
Cthe_01517	type I phosphodiesterase/nucleotide	6.61	7.03	8.29	6.54	-1.68	0.49	-0.42	1.75	-1.45	0.46	-1.3	2.28	-0.37	-0.38	0.66
Cthe_02169	metallophosphoesterase	7.99	7.75	8.8	8.28	-0.81	-0.53	0.24	0.52	-0.27	-0.75	0.9	-0.34	-0.37	-0.38	0.94
Cthe_00395	RbsD or FucU transport	15.77	16.07	16.44	15.99	-0.67	0.08	-0.3	0.45	-0.08	-0.02	-0.9	-0.49	-0.37	-0.38	0.09
Cthe_00581	Fibronectin-binding A-like protein	10.24	10.4	11.15	10.82	-0.91	-0.42	-0.								



Cthe_02701	glycosyl transferase, WecB/TagA/CpsF fam	8.15	8.43	8.77	8.41	-0.62	0.02	-0.28	0.36	-0.01	-0.1	-0.83	-0.68	-0.37	-0.38	0.11
Cthe_02701	glycosyl transferase, WecB/TagA/CpsF fam	8.15	8.43	8.77	8.41	-0.62	0.02	-0.28	0.36	-0.01	-0.1	-0.83	-0.68	-0.37	-0.38	0.11
Cthe_02190	N-acetylglucosamine-6-phosphate deacet	7.14	7.44	8.35	7.46	-1.21	-0.02	-0.3	0.89	-0.81	-0.14	-0.9	0.45	-0.38	-0.39	0.93
Cthe_02050	CRISPR-associated RAMP protein, SSO142	9.82	9.85	10.98	9.89	-1.16	-0.04	-0.03	1.09	-0.74	-0.17	0	0.87	-0.38	-0.39	0.99
Cthe_00767	16S rRNA processing protein RimM	10.03	10.7	11.07	10.61	-1.04	0.09	-0.67	0.46	-0.58	-0.01	-2.13	-0.47	-0.38	-0.39	0.3
Cthe_03148	ABC transporter related protein	9.84	9.94	10.68	10.59	-0.84	-0.65	-0.1	0.09	-0.31	-0.89	-0.23	-1.26	-0.38	-0.39	0.84
Cthe_02407	AAA ATPase, central region	11.36	11.3	12.15	11.69	-0.79	-0.39	0.06	0.46	-0.24	-0.58	0.3	-0.47	-0.38	-0.39	1.28
Cthe_02422	hypothetical protein	13.07	12.96	13.75	13.69	-0.68	-0.73	0.11	0.06	-0.09	-0.99	0.47	-1.32	-0.38	-0.39	0.81
Cthe_02827	hypothetical protein	3	4.25	5.21	4.39	-2.21	-0.14	-1.25	0.82	-2.16	-0.29	-4.07	0.3	-0.38	-0.39	0.61
Cthe_03067	membrane spanning protein	12.63	12.67	13.38	13.5	-0.75	-0.83	-0.04	-0.12	-0.19	-1.11	-0.03	-1.7	-0.38	-0.39	0.75
Cthe_02190	N-acetylglucosamine-6-phosphate deacet	7.14	7.44	8.35	7.46	-1.21	-0.02	-0.3	0.89	-0.81	-0.14	-0.9	0.45	-0.38	-0.39	0.93
Cthe_02190	N-acetylglucosamine-6-phosphate deacet	7.14	7.44	8.35	7.46	-1.21	-0.02	-0.3	0.89	-0.81	-0.14	-0.9	0.45	-0.38	-0.39	0.93
Cthe_02190	N-acetylglucosamine-6-phosphate deacet	7.14	7.44	8.35	7.46	-1.21	-0.02	-0.3	0.89	-0.81	-0.14	-0.9	0.45	-0.38	-0.39	0.93
Cthe_03073	HAD-superfamily hydrolase, subfamily IA,	6.55	6.41	7.27	7.02	-0.72	-0.61	0.14	0.25	-0.15	-0.85	0.57	-0.91	-0.39	-0.4	0.91
Cthe_00414	manganese containing catalase	3.17	4.39	4.75	4	-1.58	0.39	-1.22	0.75	-1.31	0.35	-3.97	0.15	-0.39	-0.4	0.39
Cthe_00291	protein of unknown function DUF255	6.3	6.04	7.23	5.67	-0.93	0.37	0.26	1.56	-0.43	0.32	0.97	1.87	-0.39	-0.4	0.29
Cthe_00226	hypothetical protein	7.07	7.29	8.12	7.46	-1.05	-0.17	-0.22	0.66	-0.59	-0.32	-0.63	-0.04	-0.39	-0.4	1.21
Cthe_02551	Radical SAM	4.17	4.17	5.36	4.25	-1.19	-0.08	0	1.11	-0.78	-0.21	0.1	0.91	-0.4	-0.41	1
Cthe_00880	phospho-2-dehydro-3-deoxyheptonate al	10.54	10.55	11.36	10.91	-0.82	-0.36	-0.01	0.45	-0.28	-0.55	0.07	-0.49	-0.4	-0.41	1.42
Cthe_01373	YD repeat protein	10.12	10.29	11.22	10.33	-1.1	-0.04	-0.17	0.89	-0.66	-0.17	-0.47	0.45	-0.4	-0.41	1.19
Cthe_01899	Serine-type D-Ala-D-Ala carboxypeptidase	10.5	10.32	11.25	10.9	-0.75	-0.58	0.18	0.35	-0.19	-0.81	0.7	-0.7	-0.4	-0.41	0.96
Cthe_00712	cytidylate kinase	12.43	12.47	13.26	12.94	-0.83	-0.47	-0.04	0.32	-0.3	-0.68	-0.03	-0.77	-0.4	-0.41	1.1
Cthe_00759	flagellar biosynthesis	6.73	6.92	7.69	7.38	-0.96	-0.46	-0.19	0.31	-0.47	-0.67	-0.53	-0.79	-0.4	-0.41	0.98
Cthe_01224	ribosomal protein L35	11.16	11.28	12.05	11.77	-0.89	-0.49	-0.12	0.28	-0.38	-0.7	-0.3	-0.85	-0.4	-0.41	1
Cthe_02927	bacterial translation initiation factor 1	10.01	10.43	10.75	10.57	-0.74	-0.14	-0.42	0.18	-0.18	-0.29	-1.3	-1.06	-0.4	-0.41	0.23
Cthe_01977	hypothetical protein	7.41	7.47	8.54	7.52	-1.13	-0.05	-0.06	1.02	-0.7	-0.18	-0.1	0.72	-0.4	-0.41	1.13
Cthe_02049	protein of unknown function DUF324	8.96	8.94	10.06	9.06	-1.1	-0.12	0.02	1	-0.66	-0.26	0.17	0.68	-0.4	-0.41	1.15
Cthe_00880	phospho-2-dehydro-3-deoxyheptonate al	10.54	10.55	11.36	10.91	-0.82	-0.36	-0.01	0.45	-0.28	-0.55	0.07	-0.49	-0.4	-0.41	1.42
Cthe_00712	cytidylate kinase	12.43	12.47	13.26	12.94	-0.83	-0.47	-0.04	0.32	-0.3	-0.68	-0.03	-0.77	-0.4	-0.41	1.1
Cthe_01224	ribosomal protein L35	11.16	11.28	12.05	11.77	-0.89	-0.49	-0.12	0.28	-0.38	-0.7	-0.3	-0.85	-0.4	-0.41	1
Cthe_00712	cytidylate kinase	12.43	12.47	13.26	12.94	-0.83	-0.47	-0.04	0.32	-0.3	-0.68	-0.03	-0.77	-0.4	-0.41	1.1
Cthe_01899	Serine-type D-Ala-D-Ala carboxypeptidase	10.5	10.32	11.25	10.9	-0.75	-0.58	0.18	0.35	-0.19	-0.81	0.7	-0.7	-0.4	-0.41	0.96
Cthe_00880	phospho-2-dehydro-3-deoxyheptonate al	10.54	10.55	11.36	10.91	-0.82	-0.36	-0.01	0.45	-0.28	-0.55	0.07	-0.49	-0.4	-0.41	1.42
Cthe_00880	phospho-2-dehydro-3-deoxyheptonate al	10.54	10.55	11.36	10.91	-0.82	-0.36	-0.01	0.45	-0.28	-0.55	0.07	-0.49	-0.4	-0.41	1.42
Cthe_01899	Serine-type D-Ala-D-Ala carboxypeptidase	10.5	10.32	11.25	10.9	-0.75	-0.58	0.18	0.35	-0.19	-0.81	0.7	-0.7	-0.4	-0.41	0.96
Cthe_01899	Serine-type D-Ala-D-Ala carboxypeptidase	10.5	10.32	11.25	10.9	-0.75	-0.58	0.18	0.35	-0.19	-0.81	0.7	-0.7	-0.4	-0.41	0.96
Cthe_00855	HAD superfamily (subfamily IIA) phospho	10.35	10.18	11.16	10.67	-0.81	-0.49	0.17	0.49	-0.27	-0.7	0.67	-0.4	-0.41	-0.42	1.09
Cthe_01826	response regulator receiver sensor signal	9.48	9.6	10.89	9.51	-1.41	0.09	-0.12	1.38	-1.08	-0.01	-0.3	1.49	-0.41	-0.42	0.81
Cthe_01498	methyl-accepting chemotaxis sensory tran	5.52	5.25	6.11	5.21	-0.59	0.04	0.27	0.9	0.03	-0.07	1	0.47	-0.41	-0.42	0.08
Cthe_01498	methyl-accepting chemotaxis sensory tran	5.52	5.25	6.11	5.21	-0.59	0.04	0.27	0.9	0.03	-0.07	1	0.47	-0.41	-0.42	0.08
Cthe_01826	response regulator receiver sensor signal	9.48	9.6	10.89	9.51	-1.41	0.09	-0.12	1.38	-1.08	-0.01	-0.3	1.49	-0.41	-0.42	0.81
Cthe_00837	protein of unknown function DUF322	9.28	9.03	10.04	8.85	-0.76	0.18	0.25	1.19	-0.2	0.1	0.93	1.09	-0.41	-0.42	0.18
Cthe_02766	hypothetical protein	3	2.81	3.81	3.32	-0.81	-0.51	0.19	0.49	-0.27	-0.73	0.73	-0.4	-0.41	-0.42	1.06
Cthe_00079	hypothetical protein	6.61	7	7.8	7.47	-1.19	-0.47	-0.39	0.33	-0.78	-0.68	-1.2	-0.74	-0.41	-0.42	0.83
Cthe_01048	Rhomboid-like protein	11.28	11.27	12.13	11.46	-0.85	-0.19	0.01	0.67	-0.32	-0.35	0.13	-0.02	-0.42	-0.43	4.1
Cthe_02453	hypothetical protein	9.2	9.27	10.08	9.48	-0.88	-0.21	-0.07	0.6	-0.36	-0.37	-0.13	-0.17	-0.42	-0.43	2.74
Cthe_01902	Pyridoxal-5'-phosphate-dependent enzym	4.81	5.32	6.17	5.67	-1.36	-0.35	-0.51	0.5	-1.01	-0.54	-1.6	-0.38	-0.42	-0.43	0.79
Cthe_02381	seryl-tRNA synthetase	11.26	11.16	12.13	11.48	-0.87	-0.32	0.1	0.65	-0.35	-0.5	0.43	-0.06	-0.42	-0.43	1.6
Cthe_02931	ribosomal protein S4	12.79	13.47	13.8	13.73	-1.01	-0.26	-0.68	0.07	-0.54	-0.43	-2.17	-1.3	-0.42	-0.43	0.31
Cthe_00134	hypothetical protein	8.26	8.31	9.04	9.21	-0.78	-0.9	-0.05	-0.17	-0.23	-1.19	-0.07	-1.81	-0.42	-0.43	0.76
Cthe_00224	RNA related	5.49	5.39	6.86	5.52	-1.37	-0.13	0.1	1.34	-1.03	-0.27	0.43	1.4	-0.42	-0.43	0.83
Cthe_01591	hypothetical protein	6.43	6.66	7.56	6.75	-1.13	-0.09	-0.23	0.81	-0.7	-0.23	-0.67	0.28	-0.42	-0.43	1.15
Cthe_00589	RNA related	6.36	6.41	7.2	6.92	-0.84	-0.51	-0.05	0.28	-0.31	-0.73	-0.07	-0.85	-0.42	-0.43	1.06
Cthe_02931	ribosomal protein S4	12.79	13.47	13.8	13.73	-1.01	-0.26	-0.68	0.07	-0.54	-0.43	-2.17	-1.3	-0.42	-0.43	0.31
Cthe_02381	seryl-tRNA synthetase	11.26	11.16	12.13	11.48	-0.87	-0.32	0.1	0.65	-0.35	-0.5	0.43	-0.06	-0.42	-0.43	1.6
Cthe_02381	seryl-tRNA synthetase	11.26	11.16	12.13	11.48	-0.87	-0.32	0.1	0.65	-0.35	-0.5	0.43	-0.06	-0.42	-0.43	1.6
Cthe_02931	ribosomal protein S4	12.79	13.47	13.8	13.73	-1.01	-0.26	-0.68	0.07	-0.54	-0.43	-2.17	-1.3	-0.42	-0.43	0.31
Cthe_02381	seryl-tRNA synthetase	11.26	11.16	12.13	11.48	-0.87	-0.32	0.1	0.65	-0.35	-0.5	0.43	-0.06	-0.42	-0.43	1.6
Cthe_02381	seryl-tRNA synthetase	11.26	11.16	12.13	11.48	-0.87	-0.32	0.1	0.65	-0.35	-0.5	0.43	-0.06	-0.42	-0.43	1.6
Cthe_02381	seryl-tRNA synthetase	11.26	11.16	12.13	11.48	-0.87	-0.32	0.1	0.65	-0.35	-0.5	0.43	-0.06	-0.42	-0.43	1.6
Cthe_00145	metal dependent phosphohydrolase	12.57	12.45	13.4	12.87	-0.83	-0.42	0.12	0.53	-0.3	-0.62	0.5	-0.32	-0.43	-0.44	1.32
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrog	9.05	8.85	9.77	9.58	-0.72	-0.73	0.2	0.19	-0.15	-0.99	0.77	-1.04	-0.43	-0.44	0.88
Cthe_02120	RNA polymerase sigma factor	9.56	9.64	10.59	9.73	-1.03	-0.09	-0.08	0.86	-0.57	-0.23	-0.17	0.38	-0.43	-0.44	1.68
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrog	9.05	8.85	9.77	9.58	-0.72	-0.73	0.2	0.19	-0.15	-0.99	0.77	-1.04	-0.43	-0.44	0.88
Cthe_01063	thiamine biosynthesis/rRNA modification	10.81	10.82	11.66	11.05	-0.85	-0.23	-0.01	0.61	-0.32	-0.39	0.07	-0.15	-0.43	-0.44	3.46
Cthe_00800	periplasmic sensor signal transduction his	9.51	9.7	10.52	9.95	-1.01	-0.25	-0.19	0.57	-0.54	-0.42	-0.53	-0.23	-0.43	-0.44	1.35
Cthe_02060	RNA methyltransferase, TrmH family, grou	9.6	9.5	10.45	9.86	-0.85	-0.36	0.1	0.59	-0.32	-0.55	0.43	-0.19	-0.43	-0.44	1.54
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrog	9.05	8.85	9.77	9.58	-0.72	-0.73	0.2	0.19	-0.15	-0.99	0.77	-1.04	-0.43	-0.44	0.88
Cthe_02934	ABC transporter related protein	8.9	9.53	10.38	9.97	-1.48	-0.44	-0.63	0.41	-1.18	-0.64	-2	-0.57	-0.43	-0.44	0.73
Cthe_00046	hypothetical protein	11	11.16	12.07	11.25	-1.07	-0.09	-0.16	0.82	-0.62	-0.23	-0.43	0.3	-0.43	-0.44	1.43
Cthe_00887	hypothetical protein	5.83	5.32	6.36	5.52	-0.53	-0.2	0.51	0.84	0.11	-0.36	1.8	0.34	-0.43	-0.44	0.23
Cthe_03130	hypothetical protein	10.63	10.6	11.61	10.78	-0.98	-0.18	0.03	0.83	-0.5	-0.33	0.2	0.32	-0.43	-0.44	1.8
Cthe_03217	hypothetical protein	7.81	7.71	8.81	7.96	-1	-0.25	0.1	0.85	-0.53	-0.42	0.43	0.36	-0.43	-0.44	1.37
Cthe_00276	D-isomer specific 2-hydroxyacid dehydrog	9.05	8.85	9.77	9.58	-0.72	-0.73	0.2	0.19	-0.15	-0.99	0.77	-1.04	-0.43	-0.44	0.88
Cthe_02934	ABC transporter related protein	8.9	9.53	10.38	9.97	-1.48	-0.44	-0.63	0.41	-1.18	-0.64	-2	-0.57	-0.43	-0.44	0.73
Cthe_02934	ABC transporter related protein	8.9	9.5													



[illegible]



Cthe_00133	AMP-dependent synthetase and ligase	8.58	8.71	9.48	9.6	-0.9	-0.89	-0.13	-0.12	-0.39	-1.18	-0.33	-1.7	-0.48	-0.49	0.82
Cthe_00133	AMP-dependent synthetase and ligase	8.58	8.71	9.48	9.6	-0.9	-0.89	-0.13	-0.12	-0.39	-1.18	-0.33	-1.7	-0.48	-0.49	0.82
Cthe_00133	AMP-dependent synthetase and ligase	8.58	8.71	9.48	9.6	-0.9	-0.89	-0.13	-0.12	-0.39	-1.18	-0.33	-1.7	-0.48	-0.49	0.82
Cthe_01105	type II secretion system protein	13.02	13.07	14.12	13.21	-1.1	-0.14	-0.05	0.91	-0.66	-0.29	-0.07	0.49	-0.5	-0.5	1.66
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01256	glycoside hydrolase, family 3-like protein	8.37	8.28	9.25	8.69	-0.88	-0.41	0.09	0.56	-0.36	-0.61	0.4	-0.26	-0.5	-0.5	1.69
Cthe_01265	phosphoglucumutase/phosphomannomut	13.06	13.02	13.91	13.49	-0.85	-0.47	0.04	0.42	-0.32	-0.68	0.23	-0.55	-0.49	-0.5	1.43
Cthe_00377	peptidase M56, BlaR1	5.75	5.58	6.44	6.57	-0.69	-0.99	0.17	-0.13	-0.11	-1.3	0.67	-1.72	-0.49	-0.5	0.8
Cthe_00756	Membrane dipeptidase	9.38	9.42	10.86	9.44	-1.48	-0.02	-0.04	1.42	-1.18	-0.14	-0.03	1.57	-0.5	-0.5	0.86
Cthe_01549	Methyltransferase type 12	9.24	9.09	10.2	9.49	-0.96	-0.4	0.15	0.71	-0.47	-0.6	0.6	0.06	-0.5	-0.5	1.44
Cthe_01105	type II secretion system protein	13.02	13.07	14.12	13.21	-1.1	-0.14	-0.05	0.91	-0.66	-0.29	-0.07	0.49	-0.5	-0.5	1.66
Cthe_00377	peptidase M56, BlaR1	5.75	5.58	6.44	6.57	-0.69	-0.99	0.17	-0.13	-0.11	-1.3	0.67	-1.72	-0.49	-0.5	0.8
Cthe_00983	cell cycle protein	10.51	10.33	11.35	10.91	-0.84	-0.58	0.18	0.44	-0.31	-0.81	0.7	-0.51	-0.49	-0.5	1.14
Cthe_02541	nitrite and sulphite reductase 4Fe-4S regio	4.32	4.7	5.67	4.81	-1.35	-0.11	-0.38	0.86	-1	-0.25	-1.17	0.38	-0.49	-0.5	0.95
Cthe_01323	GrpE protein	7.89	7.86	9.34	7.95	-1.45	-0.09	0.03	1.39	-1.14	-0.23	0.2	1.51	-0.49	-0.5	0.87
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_00255	hypothetical protein	7.15	7.31	8.12	7.87	-0.97	-0.56	-0.16	0.25	-0.49	-0.79	-0.43	-0.91	-0.49	-0.5	1.0
Cthe_00222	hypothetical protein	2.81	3	3.81	3.58	-1	-0.58	-0.19	0.23	-0.53	-0.81	-0.53	-0.96	-0.49	-0.5	1
Cthe_03053	hypothetical protein	8.3	8.23	9.15	8.73	-0.85	-0.5	0.07	0.42	-0.32	-0.71	0.33	-0.55	-0.5	-0.5	1.38
Cthe_00263	hypothetical protein	2.81	1	3.46	3.7	-0.65	-2.7	1.81	-0.24	-0.05	-3.33	6.13	-1.96	-0.5	-0.5	0.59
Cthe_01265	phosphoglucumutase/phosphomannomut	13.06	13.02	13.91	13.49	-0.85	-0.47	0.04	0.42	-0.32	-0.68	0.23	-0.55	-0.49	-0.5	1.43
Cthe_01265	phosphoglucumutase/phosphomannomut	13.06	13.02	13.91	13.49	-0.85	-0.47	0.04	0.42	-0.32	-0.68	0.23	-0.55	-0.49	-0.5	1.43
Cthe_00756	Membrane dipeptidase	9.38	9.42	10.86	9.44	-1.48	-0.02	-0.04	1.42	-1.18	-0.14	-0.03	1.57	-0.5	-0.5	0.86
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01265	phosphoglucumutase/phosphomannomut	13.06	13.02	13.91	13.49	-0.85	-0.47	0.04	0.42	-0.32	-0.68	0.23	-0.55	-0.49	-0.5	1.43
Cthe_01256	glycoside hydrolase, family 3-like protein	8.37	8.28	9.25	8.69	-0.88	-0.41	0.09	0.56	-0.36	-0.61	0.4	-0.26	-0.5	-0.5	1.69
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4	-0.76	-1.03	0.03	-0.24	-0.2	-1.35	0.2	-1.96	-0.5	-0.5	0.79
Cthe_01335	peptidase A24A, prelin type IV	9.4	9.37	10.16	10.4											



Cthe_00012	YD repeat protein	4.95	4.17	5.83	4.64	-0.88	-0.47	0.78	1.19	-0.36	-0.68	2.7	1.09	-0.51	-0.51	0.3
Cthe_01314	DNA-directed RNA polymerase, omega su	8.82	9.05	9.94	9.31	-1.12	-0.26	-0.23	0.63	-0.69	-0.43	-0.67	-0.11	-0.51	-0.51	1.36
Cthe_01314	DNA-directed RNA polymerase, omega su	8.82	9.05	9.94	9.31	-1.12	-0.26	-0.23	0.63	-0.69	-0.43	-0.67	-0.11	-0.51	-0.51	1.36
Cthe_00223	hypothetical protein	4.46	4.86	5.75	5.25	-1.29	-0.39	-0.4	0.5	-0.92	-0.58	-1.23	-0.38	-0.52	-0.52	0.96
Cthe_01639	DNA methylase N-4/N-6				0		0		0		-0.12		-1.45	-0.52	-0.52	0.09
Cthe_00164	protein of unknown function UPF0044	9.66	9.55	10.69	9.88	-1.03	-0.33	0.11	0.81	-0.57	-0.51	0.47	0.28	-0.52	-0.52	1.59
Cthe_02905	Ribosomal protein L25/L23	11.44	11.79	12.61	12.52	-1.17	-0.73	-0.35	0.09	-0.76	-0.99	-1.07	-1.26	-0.52	-0.52	0.86
Cthe_01939	magnesium transporter	10.84	10.97	11.81	11.49	-0.97	-0.52	-0.13	0.32	-0.49	-0.74	-0.33	-0.77	-0.52	-0.52	1.2
Cthe_00274	glycoside hydrolase, family 9	9.8	9.95	11.08	10.01	-1.28	-0.06	-0.15	1.07	-0.91	-0.19	-0.4	0.83	-0.52	-0.52	1.15
Cthe_00090	hypothetical protein	8.09	8.18	9.02	8.84	-0.93	-0.66	-0.09	0.18	-0.43	-0.9	-0.2	-1.06	-0.52	-0.52	1.05
Cthe_00473	flagellar operon protein	5.7	6.21	7.18	6.41	-1.48	-0.2	-0.51	0.77	-1.18	-0.36	-1.6	0.19	-0.52	-0.52	0.87
Cthe_02905	Ribosomal protein L25/L23	11.44	11.79	12.61	12.52	-1.17	-0.73	-0.35	0.09	-0.76	-0.99	-1.07	-1.26	-0.52	-0.52	0.86
Cthe_02905	Ribosomal protein L25/L23	11.44	11.79	12.61	12.52	-1.17	-0.73	-0.35	0.09	-0.76	-0.99	-1.07	-1.26	-0.52	-0.52	0.86
Cthe_02949	Pectinesterase	4.32	3.91	5.25	4.75	-0.93	-0.84	0.41	0.5	-0.43	-1.12	1.47	-0.38	-0.53	-0.53	0.9
Cthe_02566	Radical SAM	6.04	6.51	7.84	6.21	-1.8	0.3	-0.47	1.63	-1.61	0.24	-1.47	2.02	-0.53	-0.53	0.74
Cthe_00742	hypothetical protein	8.81	8.82	9.64	9.77	-0.83	-0.95	-0.01	-0.13	-0.3	-1.25	0.07	-1.72	-0.53	-0.53	0.85
Cthe_01934	Abortive infection protein	10.7	10.78	11.65	11.07	-0.95	-0.29	-0.08	0.58	-0.46	-0.46	-0.17	-0.21	-0.53	-0.53	2.74
Cthe_03231	hypothetical protein	4.17	4.52	5.46	4.75	-1.29	-0.23	-0.35	0.71	-0.92	-0.39	-1.07	0.06	-0.53	-0.53	1.06
Cthe_02346	O-antigen polymerase	10.26	10.26	11.12	10.99	-0.86	-0.73	0	0.13	-0.34	-0.99	0.1	-1.17	-0.53	-0.53	1.01
Cthe_02949	Pectinesterase	4.32	3.91	5.25	4.75	-0.93	-0.84	0.41	0.5	-0.43	-1.12	1.47	-0.38	-0.53	-0.53	0.9
Cthe_02370	ribosomal protein L34	8.55	8.27	9.53	8.88	-0.98	-0.61	0.28	0.65	-0.5	-0.85	1.03	-0.06	-0.53	-0.53	1.09
Cthe_02949	Pectinesterase	4.32	3.91	5.25	4.75	-0.93	-0.84	0.41	0.5	-0.43	-1.12	1.47	-0.38	-0.53	-0.53	0.9
Cthe_02949	Pectinesterase	4.32	3.91	5.25	4.75	-0.93	-0.84	0.41	0.5	-0.43	-1.12	1.47	-0.38	-0.53	-0.53	0.9
Cthe_02553	Radical SAM	3.17	3.81	5.09	3.46	-1.92	0.35	-0.64	1.63	-1.77	0.3	-2.03	2.02	-0.54	-0.54	0.71
Cthe_02154	Methyltransferase type 11	9.95	9.92	11.04	10.15	-1.09	-0.23	0.03	0.89	-0.65	-0.39	0.2	0.45	-0.54	-0.54	1.75
Cthe_02620	protein of unknown function DUF1078-lik	7.27	7.5	8.36	7.97	-1.09	-0.47	-0.23	0.39	-0.65	-0.68	-0.67	-0.62	-0.54	-0.54	1.17
Cthe_02622	hypothetical protein	11.6	11.39	12.55	11.94	-0.95	-0.55	0.21	0.61	-0.46	-0.77	0.8	-0.15	-0.54	-0.54	1.25
Cthe_02622	hypothetical protein	11.6	11.39	12.55	11.94	-0.95	-0.55	0.21	0.61	-0.46	-0.77	0.8	-0.15	-0.54	-0.54	1.25
Cthe_02622	hypothetical protein	11.6	11.39	12.55	11.94	-0.95	-0.55	0.21	0.61	-0.46	-0.77	0.8	-0.15	-0.54	-0.54	1.25
Cthe_02440	hypothetical protein	10.29	10.28	11.25	10.52	-0.96	-0.24	0.01	0.73	-0.47	-0.4	0.13	0.11	-0.54	-0.54	4.12
Cthe_01865	type IV pilus assembly PilZ	10.78	10.99	11.86	11.36	-1.08	-0.37	-0.21	0.5	-0.64	-0.56	-0.6	-0.38	-0.54	-0.54	1.36
Cthe_01106	twitching motility protein	11.51	11.87	12.9	11.99	-1.39	-0.12	-0.36	0.91	-1.05	-0.26	-1.1	0.49	-0.55	-0.55	1.02
Cthe_00407	Radical SAM	8.82	9.02	9.87	9.63	-1.05	-0.61	-0.2	0.24	-0.59	-0.85	-0.57	-0.94	-0.55	-0.55	1.07
Cthe_00882	protein of unknown function DUF6, trans	7.72	7.62	8.57	8.29	-0.85	-0.67	0.1	0.28	-0.32	-0.92	0.43	-0.85	-0.55	-0.55	1.16
Cthe_02762	transcriptional regulator-like protein	8.27	8.17	9.47	8.45	-1.2	-0.28	0.1	1.02	-0.8	-0.45	0.43	0.72	-0.55	-0.55	1.24
Cthe_00777	DNA mismatch repair protein MutS	11.07	11.22	12.07	11.8	-1	-0.58	-0.15	0.27	-0.53	-0.81	-0.4	-0.87	-0.55	-0.55	1.15
Cthe_03041	UbiA prenyltransferase	9.11	8.94	9.91	9.77	-0.8	-0.83	0.17	0.14	-0.26	-1.11	0.67	-1.15	-0.55	-0.55	0.97
Cthe_01106	twitching motility protein	11.51	11.87	12.9	11.99	-1.39	-0.12	-0.36	0.91	-1.05	-0.26	-1.1	0.49	-0.55	-0.55	1.02
Cthe_02341	glycosyl transferase, family 2	8.45	8.33	9.31	8.94	-0.86	-0.61	0.12	0.37	-0.34	-0.85	0.5	-0.66	-0.55	-0.55	1.26
Cthe_02522	membrane associated protein	10.74	11.08	11.93	11.73	-1.19	-0.65	-0.34	0.2	-0.78	-0.89	-1.03	-1.02	-0.55	-0.55	0.93
Cthe_00216	small acid-soluble spore protein, alpha/be	8.2	7.61	8.69	7.8	-0.49	-0.19	0.59	0.89	0.16	-0.35	2.07	0.45	-0.55	-0.55	0.21
Cthe_00697	type IV pilus assembly PilZ	8.89	8.99	9.87	9.26	-0.98	-0.27	-0.1	0.61	-0.5	-0.44	-0.23	-0.15	-0.55	-0.55	2.76
Cthe_02045	intein	4.86	5.75	6.83	5.81	-1.97	-0.06	-0.89	1.02	-1.84	-0.19	-2.87	0.72	-0.55	-0.55	0.71
Cthe_03043	hypothetical protein	9.33	9.37	10.26	9.65	-0.93	-0.28	-0.04	0.61	-0.43	-0.45	-0.03	-0.15	-0.56	-0.56	4.62
Cthe_02046	hypothetical protein	8.58	8.67	9.55	9.06	-0.97	-0.39	-0.09	0.49	-0.49	-0.58	-0.2	-0.4	-0.56	-0.56	1.93
Cthe_01336	hypothetical protein	10.74	10.66	11.63	11.2	-0.89	-0.54	0.08	0.43	-0.38	-0.76	0.37	-0.53	-0.57	-0.57	1.49
Cthe_02558	NAD-dependent epimerase/dehydratase	2.58	2.32	3.81	2.81	-1.23	-0.49	0.26	1	-0.84	-0.7	0.97	0.68	-0.57	-0.57	1.05
Cthe_02558	NAD-dependent epimerase/dehydratase	2.58	2.32	3.81	2.81	-1.23	-0.49	0.26	1	-0.84	-0.7	0.97	0.68	-0.57	-0.57	1.05
Cthe_01427	branched-chain amino acid transport	6.21	6.44	7.32	6.91	-1.11	-0.47	-0.23	0.41	-0.68	-0.68	-0.67	-0.57	-0.57	-0.57	1.24
Cthe_00550	heat shock protein Hsp90	8.82	8.73	9.8	9.09	-0.98	-0.36	0.09	0.71	-0.5	-0.55	0.4	0.06	-0.57	-0.57	2.09
Cthe_01196	hypothetical protein	7.48	7.3	8.53	7.76	-1.05	-0.46	0.18	0.77	-0.59	-0.67	0.7	0.19	-0.57	-0.57	1.4
Cthe_02928	ribosomal protein L36	7.35	7.77	7.79	7.92	-0.44	-0.15	-0.42	-0.13	0.23	-0.3	-1.3	-1.72	-0.57	-0.57	0.2
Cthe_00471	flagellar hook-length control protein	8.76	8.89	9.78	9.27	-1.02	-0.38	-0.13	0.51	-0.55	-0.57	-0.33	-0.36	-0.58	-0.58	1.84
Cthe_02313	protein of unknown function DUF218	9.46	9.42	10.33	10.21	-0.87	-0.79	0.04	0.12	-0.35	-1.06	0.23	-1.19	-0.58	-0.58	1.05
Cthe_02904	ribosomal protein L4/L1e	11.56	11.82	12.67	12.54	-1.11	-0.72	-0.26	0.13	-0.68	-0.98	-0.77	-1.17	-0.58	-0.58	0.97
Cthe_02921	ribosomal protein L30	10.59	11.1	11.35	11.07	-0.76	0.03	-0.51	0.28	-0.2	-0.08	-1.6	-0.85	-0.58	-0.58	0.14
Cthe_01829	Chromosome segregation ATPases-like pr	9.38	9.58	10.71	9.67	-1.33	-0.09	-0.2	1.04	-0.97	-0.23	-0.57	0.77	-0.58	-0.58	1.18
Cthe_02262	V-type ATPase, 116 kDa subunit	12.19	12.38	13.27	12.77	-1.08	-0.39	-0.19	0.5	-0.64	-0.58	-0.53	-0.38	-0.58	-0.58	1.51
Cthe_01769	hypothetical protein	8.38	8.16	9.2	9.01	-0.82	-0.85	0.22	0.19	-0.28	-1.13	0.83	-1.04	-0.58	-0.58	0.99
Cthe_02678	hypothetical protein	9.82	9.95	10.84	10.31	-1.02	-0.36	-0.13	0.53	-0.55	-0.55	-0.33	-0.32	-0.58	-0.58	1.92
Cthe_02330	hypothetical protein	12.16	11.98	12.95	12.92	-0.79	-0.94	0.18	0.03	-0.24	-1.24	0.7	-1.38	-0.58	-0.58	0.93
Cthe_02921	ribosomal protein L30	10.59	11.1	11.35	11.07	-0.76	0.03	-0.51	0.28	-0.2	-0.08	-1.6	-0.85	-0.58	-0.58	0.14
Cthe_02262	V-type ATPase, 116 kDa subunit	12.19	12.38	13.27	12.77	-1.08	-0.39	-0.19	0.5	-0.64	-0.58	-0.53	-0.38	-0.58	-0.58	1.51
Cthe_02904	ribosomal protein L4/L1e	11.56	11.82	12.67	12.54	-1.11	-0.72	-0.26	0.13	-0.68	-0.98	-0.77	-1.17	-0.58	-0.58	0.97
Cthe_02921	ribosomal protein L30	10.59	11.1	11.35	11.07	-0.76	0.03	-0.51	0.28	-0.2	-0.08	-1.6	-0.85	-0.58	-0.58	0.14
Cthe_02262	V-type ATPase, 116 kDa subunit	12.19	12.38	13.27	12.77	-1.08	-0.39	-0.19	0.5	-0.64	-0.58	-0.53	-0.38	-0.58	-0.58	1.51
Cthe_02262	V-type ATPase, 116 kDa subunit	12.19	12.38	13.27	12.77	-1.08	-0.39	-0.19	0.5	-0.64	-0.58	-0.53	-0.38	-0.58	-0.58	1.51
Cthe_00229	NAD-dependent epimerase/dehydratase	9.5	9.51	10.43	10.02	-0.93	-0.51	-0.01	0.41	-0.43	-0.73	0.07	-0.57	-0.59	-0.59	1.68
Cthe_02378	parB-like partition protein	9.06	9.11	10.02	9.56	-0.96	-0.45	-0.05	0.46	-0.47	-0.65	-0.07	-0.47	-0.59	-0.59	1.92
Cthe_01854	methylated-DNA-protein-cysteine	6.87	6.71	7.75	7.38	-0.88	-0.67	0.16	0.37	-0.36	-0.92	0.63	-0.66	-0.59	-0.59	1.23
Cthe_00493	CheD, stimulates methylation of MCP prot	5.46	5.46	6.41	5.73	-0.95	-0.27	0	0.68	-0.46	-0.44	0.1	0	-0.59	-0.59	7.23
Cthe_00229	NAD-dependent epimerase/dehydratase	9.5	9.51	10.43	10.02	-0.93	-0.51	-0.01	0.41	-0.43	-0.73	0.07	-0.57	-0.59	-0.59	1.68
Cthe_01349	Undecaprenyl-phosphate galactose	10.69	10.74	11.66	10.97	-0.97	-0.23	-0.05	0.69	-0.49	-0.39	-0.07	0.02	-0.59	-0.59	9.78
Cthe_01357	glycosyl transferase, group 1	11.41	11.33	12.3	11.99	-0.89	-0.66	0.08	0.31	-0.38	-0.9	0.37	-0.79	-0.59	-0.59	1.27
Cthe_00493	CheD, stimulates methylation of MCP prot	5.46	5.46	6.41	5.73	-0.95	-0.27	0	0.68	-0.46	-0.44	0.1	0	-0.59	-0.59	7.23
Cthe_00925	protein of unknown function DUF218	7.24	7.16	8.13	7.8	-0.89	-0.64	0.08	0.33	-0.38	-0.88	0.				



Cthe_03152	cobalamin 5'-phosphate synthase	6.36	6.11	7.24	6.89	-0.88	-0.78	0.25	0.35	-0.36	-1.05	0.93	-0.7	-0.6	-0.6	1.08
Cthe_03152	cobalamin 5'-phosphate synthase	6.36	6.11	7.24	6.89	-0.88	-0.78	0.25	0.35	-0.36	-1.05	0.93	-0.7	-0.6	-0.6	1.08
Cthe_03152	cobalamin 5'-phosphate synthase	6.36	6.11	7.24	6.89	-0.88	-0.78	0.25	0.35	-0.36	-1.05	0.93	-0.7	-0.6	-0.6	1.08
Cthe_03152	cobalamin 5'-phosphate synthase	6.36	6.11	7.24	6.89	-0.88	-0.78	0.25	0.35	-0.36	-1.05	0.93	-0.7	-0.6	-0.6	1.08
Cthe_03152	cobalamin 5'-phosphate synthase	6.36	6.11	7.24	6.89	-0.88	-0.78	0.25	0.35	-0.36	-1.05	0.93	-0.7	-0.6	-0.6	1.08
Cthe_01107	type II secretion system protein E	12.55	12.75	13.98	12.82	-1.43	-0.07	-0.2	1.16	-1.11	-0.2	-0.57	1.02	-0.61	-0.61	1.1
Cthe_02561	CDP-glucose 4,6-dehydratase	6.27	6.23	7.18	6.86	-0.91	-0.63	0.04	0.32	-0.41	-0.87	0.23	-0.77	-0.61	-0.61	1.36
Cthe_00591	Integrase, catalytic region	7.9	7.04	8.79	7.54	-0.89	-0.5	0.86	1.25	-0.38	-0.71	2.97	1.21	-0.61	-0.61	0.29
Cthe_02411	metallophosphoesterase	9.81	9.71	10.79	10.14	-0.98	-0.43	0.1	0.65	-0.5	-0.63	0.43	-0.06	-0.61	-0.61	2.11
Cthe_01107	type II secretion system protein E	12.55	12.75	13.98	12.82	-1.43	-0.07	-0.2	1.16	-1.11	-0.2	-0.57	1.02	-0.61	-0.61	1.1
Cthe_02561	CDP-glucose 4,6-dehydratase	6.27	6.23	7.18	6.86	-0.91	-0.63	0.04	0.32	-0.41	-0.87	0.23	-0.77	-0.61	-0.61	1.36
Cthe_02924	adenylate kinases	12.99	13.59	13.82	13.63	-0.83	-0.04	-0.6	0.19	-0.3	-0.17	-1.9	-1.04	-0.61	-0.61	0.18
Cthe_02368	protein of unknown function DUF37	9.69	9.68	10.63	10.12	-0.94	-0.44	0.01	0.51	-0.45	-0.64	0.13	-0.36	-0.61	-0.61	2.32
Cthe_02450	hypothetical protein	6.23	5.88	7.7	6.43	-1.47	-0.55	0.35	1.27	-1.16	-0.77	1.27	1.26	-0.61	-0.61	0.88
Cthe_01416	hypothetical protein	5.46	5.04	6.04	6.54	-0.58	-1.5	0.42	-0.5	0.04	-1.9	1.5	-2.51	-0.61	-0.61	0.74
Cthe_01544	hypothetical protein	6.07	6.04	7.23	6.3	-1.16	-0.26	0.03	0.93	-0.74	-0.43	0.2	0.53	-0.61	-0.61	1.72
Cthe_02924	adenylate kinases	12.99	13.59	13.82	13.63	-0.83	-0.04	-0.6	0.19	-0.3	-0.17	-1.9	-1.04	-0.61	-0.61	0.18
Cthe_02924	adenylate kinases	12.99	13.59	13.82	13.63	-0.83	-0.04	-0.6	0.19	-0.3	-0.17	-1.9	-1.04	-0.61	-0.61	0.18
Cthe_02561	CDP-glucose 4,6-dehydratase	6.27	6.23	7.18	6.86	-0.91	-0.63	0.04	0.32	-0.41	-0.87	0.23	-0.77	-0.61	-0.61	1.36
Cthe_02924	adenylate kinases	12.99	13.59	13.82	13.63	-0.83	-0.04	-0.6	0.19	-0.3	-0.17	-1.9	-1.04	-0.61	-0.61	0.18
Cthe_02561	CDP-glucose 4,6-dehydratase	6.27	6.23	7.18	6.86	-0.91	-0.63	0.04	0.32	-0.41	-0.87	0.23	-0.77	-0.61	-0.61	1.36
Cthe_02561	CDP-glucose 4,6-dehydratase	6.27	6.23	7.18	6.86	-0.91	-0.63	0.04	0.32	-0.41	-0.87	0.23	-0.77	-0.61	-0.61	1.36
Cthe_02924	adenylate kinases	12.99	13.59	13.82	13.63	-0.83	-0.04	-0.6	0.19	-0.3	-0.17	-1.9	-1.04	-0.61	-0.61	0.18
Cthe_01587	ABC transporter related protein	5	5.43	6.86	5.21	-1.86	0.22	-0.43	1.65	-1.69	0.14	-1.33	2.06	-0.62	-0.62	0.79
Cthe_03063	Acetyl xylan esterase	8.88	9.04	10.06	9.24	-1.18	-0.2	-0.16	0.82	-0.77	-0.36	-0.43	0.3	-0.62	-0.62	1.84
Cthe_01316	protein of unknown function DUF370	9.67	9.66	10.62	10.01	-0.95	-0.35	0.01	0.61	-0.46	-0.54	0.13	-0.15	-0.62	-0.62	4.06
Cthe_02930	ribosomal protein S11	10.68	11.33	11.55	11.47	-0.87	-0.14	-0.65	0.08	-0.35	-0.29	-2.07	-1.28	-0.62	-0.62	0.21
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.95	8.82	9.8	9.71	-0.85	-0.89	0.13	0.09	-0.32	-1.18	0.53	-1.26	-0.62	-0.62	1.02
Cthe_02342	hypothetical protein	8.41	8.29	9.32	8.9	-0.91	-0.61	0.12	0.42	-0.41	-0.85	0.5	-0.55	-0.62	-0.62	1.44
Cthe_00154	protein of unknown function DUF1292	7.86	7.83	8.8	8.27	-0.94	-0.44	0.03	0.53	-0.45	-0.64	0.2	-0.32	-0.62	-0.62	2.36
Cthe_02018	hypothetical protein	2	3.46	4.7	3.32	-2.7	0.14	-1.46	1.38	-2.82	0.05	-4.77	1.49	-0.62	-0.62	0.64
Cthe_01836	hypothetical protein	5.46	5.75	6.74	6	-1.28	-0.25	-0.29	0.74	-0.91	-0.42	-0.87	0.13	-0.62	-0.62	1.29
Cthe_02930	ribosomal protein S11	10.68	11.33	11.55	11.47	-0.87	-0.14	-0.65	0.08	-0.35	-0.29	-2.07	-1.28	-0.62	-0.62	0.21
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.95	8.82	9.8	9.71	-0.85	-0.89	0.13	0.09	-0.32	-1.18	0.53	-1.26	-0.62	-0.62	1.02
Cthe_01587	ABC transporter related protein	5	5.43	6.86	5.21	-1.86	0.22	-0.43	1.65	-1.69	0.14	-1.33	2.06	-0.62	-0.62	0.79
Cthe_02930	ribosomal protein S11	10.68	11.33	11.55	11.47	-0.87	-0.14	-0.65	0.08	-0.35	-0.29	-2.07	-1.28	-0.62	-0.62	0.21
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.95	8.82	9.8	9.71	-0.85	-0.89	0.13	0.09	-0.32	-1.18	0.53	-1.26	-0.62	-0.62	1.02
Cthe_03063	Acetyl xylan esterase	8.88	9.04	10.06	9.24	-1.18	-0.2	-0.16	0.82	-0.77	-0.36	-0.43	0.3	-0.62	-0.62	1.84
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.95	8.82	9.8	9.71	-0.85	-0.89	0.13	0.09	-0.32	-1.18	0.53	-1.26	-0.62	-0.62	1.02
Cthe_01587	ABC transporter related protein	5	5.43	6.86	5.21	-1.86	0.22	-0.43	1.65	-1.69	0.14	-1.33	2.06	-0.62	-0.62	0.79
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.95	8.82	9.8	9.71	-0.85	-0.89	0.13	0.09	-0.32	-1.18	0.53	-1.26	-0.62	-0.62	1.02
Cthe_00132	3-oxoacyl-(acyl-carrier-protein) synthase	8.95	8.82	9.8	9.71	-0.85	-0.89	0.13	0.09	-0.32	-1.18	0.53	-1.26	-0.62	-0.62	1.02
Cthe_02367	60 kDa inner membrane insertion protein	12.07	12.07	13.02	12.59	-0.95	-0.52	0	0.43	-0.46	-0.74	0.1	-0.53	-0.63	-0.63	1.84
Cthe_02763	hypothetical protein	7.88	8.08	9.04	8.38	-1.16	-0.3	-0.2	0.66	-0.74	-0.48	-0.57	-0.04	-0.63	-0.63	1.75
Cthe_02554	glycosyl transferase, group 1	4.46	4.64	5.55	5.13	-1.09	-0.49	-0.18	0.42	-0.65	-0.7	-0.5	-0.55	-0.63	-0.63	1.46
Cthe_01315	Guanylate kinase	10.23	10.22	11.24	10.51	-1.01	-0.29	0.01	0.73	-0.54	-0.46	0.13	0.11	-0.63	-0.63	4.73
Cthe_02903	ribosomal protein L3	11.62	11.79	12.7	12.28	-1.08	-0.49	-0.17	0.42	-0.64	-0.7	-0.47	-0.55	-0.63	-0.63	1.49
Cthe_02424	copper amine oxidase-like protein	12.33	12.39	13.47	12.6	-1.14	-0.21	-0.06	0.87	-0.72	-0.37	-0.1	0.4	-0.63	-0.63	2.23
Cthe_02064	spore germination B3 GerAC like	6.69	6.79	7.71	7.24	-1.02	-0.45	-0.1	0.47	-0.55	-0.65	-0.23	-0.45	-0.63	-0.63	1.91
Cthe_00434	ATPase	6.81	6.21	8.07	7.2	-1.26	-0.99	0.6	0.87	-0.88	-1.3	2.1	0.4	-0.63	-0.63	0.83
Cthe_02999	hypothetical protein	7.53	7.92	8.91	8.26	-1.38	-0.34	-0.39	0.65	-1.04	-0.52	-1.2	-0.06	-0.63	-0.63	1.1
Cthe_02903	ribosomal protein L3	11.62	11.79	12.7	12.28	-1.08	-0.49	-0.17	0.42	-0.64	-0.7	-0.47	-0.55	-0.63	-0.63	1.49
Cthe_01315	Guanylate kinase	10.23	10.22	11.24	10.51	-1.01	-0.29	0.01	0.73	-0.54	-0.46	0.13	0.11	-0.63	-0.63	4.73
Cthe_02903	ribosomal protein L3	11.62	11.79	12.7	12.28	-1.08	-0.49	-0.17	0.42	-0.64	-0.7	-0.47	-0.55	-0.63	-0.63	1.49
Cthe_02367	60 kDa inner membrane insertion protein	12.07	12.07	13.02	12.59	-0.95	-0.52	0	0.43	-0.46	-0.74	0.1	-0.53	-0.63	-0.63	1.84
Cthe_01315	Guanylate kinase	10.23	10.22	11.24	10.51	-1.01	-0.29	0.01	0.73	-0.54	-0.46	0.13	0.11	-0.63	-0.63	4.73
Cthe_01315	Guanylate kinase	10.23	10.22	11.24	10.51	-1.01	-0.29	0.01	0.73	-0.54	-0.46	0.13	0.11	-0.63	-0.63	4.73
Cthe_01315	Guanylate kinase	10.23	10.22	11.24	10.51	-1.01	-0.29	0.01	0.73	-0.54	-0.46	0.13	0.11	-0.63	-0.63	4.73
Cthe_00986	peptidase M16-like protein	11.44	11.54	12.47	11.85	-1.03	-0.31	-0.1	0.62	-0.57	-0.49	-0.23	-0.13	-0.64	-0.64	3.23
Cthe_02636	integral membrane protein MvIN	4.39	3.7	5.43	4.95	-1.04	-1.25	0.69	0.48	-0.58	-1.61	2.4	-0.43	-0.64	-0.64	0.8
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.48	11.48	12.44	11.91	-0.96	-0.43	0	0.53	-0.47	-0.63	0.1	-0.32	-0.64	-0.64	2.66
Cthe_00463	flagellar basal-body rod protein FlgC	11.3	11.17	12.39	11.59	-1.09	-0.42	0.13	0.8	-0.65	-0.62	0.53	0.26	-0.64	-0.64	1.73
Cthe_00272	Serine-type D-Ala-D-Ala carboxypeptidase	9.97	10.17	11.13	10.48	-1.16	-0.31	-0.2	0.65	-0.74	-0.49	-0.57	-0.06	-0.64	-0.64	1.76
Cthe_01575	purine nucleoside phosphorylase	4.17	4.7	4.91	4.64	-0.74	0.06	-0.53	0.27	-0.18	-0.05	-1.67	-0.87	-0.64	-0.64	0.11
Cthe_00051	hypothetical protein	5.52	5.09	6.49	4.7	-0.97	0.39	0.43	1.79	-0.49	0.35	1.53	2.36	-0.64	-0.64	0.24
Cthe_02729	translation elongation factor 2 (EF-2/EF-G	15.56	16.04	16.22	16.1	-0.66	-0.06	-0.48	0.12	-0.07	-0.19	-1.5	-1.19	-0.64	-0.64	0.12
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.48	11.48	12.44	11.91	-0.96	-0.43	0	0.53	-0.47	-0.63	0.1	-0.32	-0.64	-0.64	2.66
Cthe_00228	hypothetical protein	8.46	8.54	9.46	9.06	-1	-0.52	-0.08	0.4	-0.53	-0.74	-0.17	-0.6	-0.64	-0.64	1.66
Cthe_01489	hypothetical protein	3.32	3.58	4.52	4	-1.2	-0.42	-0.26	0.52	-0.8	-0.62	-0.77	-0.34	-0.64	-0.64	1.37
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.48	11.48	12.44	11.91	-0.96	-0.43	0	0.53	-0.47	-0.63	0.1	-0.32	-0.64	-0.64	2.66
Cthe_00272	Serine-type D-Ala-D-Ala carboxypeptidase	9.97	10.17	11.13	10.48	-1.16	-0.31	-0.2	0.65	-0.74	-0.49	-0.57	-0.06	-0.64	-0.64	1.76
Cthe_00828	deoxyxylulose-5-phosphate synthase	11.48	11.48	12.44	11.91	-0.96	-0.43	0	0.53	-0.47	-0.63	0.1	-0.32	-0.64	-0.64	2.66
Cthe_02633	hypothetical protein	12.64	12.42	13.52	13.25	-0.88	-0.83	0.22	0.27	-0.36	-1.11	0.83	-0.87	-0.64	-0.64	1.1
Cthe_02729	translation elongation factor 2 (EF-2/EF-G	15.56	16.04	16.22	16.1	-0.66	-0.06	-0.48	0.12	-0.07	-0.19	-1.5	-1.19	-0.64	-0.64	0.12
Cthe_01575	purine nucleoside phosphorylase	4.17	4.7	4.91	4.64	-0.74	0.06	-0.53	0.27	-0.18	-0.05	-1.67	-0.87	-0.64	-0.64	0.11



Cthe_00401	methyl-accepting chemotaxis sensory tran	11	10.93	11.99	11.34	-0.99	-0.41	0.07	0.65	-0.51	-0.61	0.33	-0.06	-0.65	-0.65	2.69
Cthe_01317	hypothetical protein	10.55	10.4	11.59	10.9	-1.04	-0.5	0.15	0.69	-0.58	-0.71	0.6	0.02	-0.65	-0.65	1.74
Cthe_03010	hypothetical protein	5.46	5.55	6.57	5.78	-1.11	-0.23	-0.09	0.79	-0.68	-0.39	-0.2	0.23	-0.65	-0.65	2.92
Cthe_00438	cellulosome enzyme, dockerin type I	4.32	3.81	5.39	4.81	-1.07	-1	0.51	0.58	-0.62	-1.31	1.8	-0.21	-0.65	-0.65	0.91
Cthe_02337	hypothetical protein	7.71	7.72	8.63	8.72	-0.92	-1	-0.01	-0.09	-0.42	-1.31	0.07	-1.64	-0.65	-0.65	0.95
Cthe_02555	methyltransferase FkbM family	4.91	4.86	5.88	5.29	-0.97	-0.43	0.05	0.59	-0.49	-0.63	0.27	-0.19	-0.65	-0.65	2.75
Cthe_02828	hypothetical protein	4.81	4	6.36	5.17	-1.55	-1.17	0.81	1.19	-1.27	-1.51	2.8	1.09	-0.65	-0.65	0.75
Cthe_02869	hypothetical protein	5.32	5.04	6.49	5.64	-1.17	-0.6	0.28	0.85	-0.76	-0.83	1.03	0.36	-0.65	-0.65	1.17
Cthe_02993	hypothetical protein	8.73	8.79	10.13	8.95	-1.4	-0.16	-0.06	1.18	-1.07	-0.31	-0.1	1.06	-0.65	-0.65	1.19
Cthe_01360	polysaccharide biosynthesis protein CpsF	10.82	10.85	11.79	11.56	-0.97	-0.71	-0.03	0.23	-0.49	-0.96	0	-0.96	-0.66	-0.66	1.28
Cthe_03061	transcriptional repressor, CopY family	6.02	6.09	7.02	6.75	-1	-0.66	-0.07	0.27	-0.53	-0.9	-0.13	-0.87	-0.66	-0.66	1.35
Cthe_01447	hypothetical protein	8.16	8.31	9.26	8.66	-1.1	-0.35	-0.15	0.6	-0.66	-0.54	-0.4	-0.17	-0.66	-0.66	2.23
Cthe_00108	type IV pilus assembly PilZ	10.84	10.76	11.77	11.43	-0.93	-0.67	0.08	0.34	-0.43	-0.92	0.37	-0.72	-0.66	-0.66	1.43
Cthe_02156	hypothetical protein	3	2.58	4.32	3.32	-1.32	-0.74	0.42	1	-0.96	-1	1.5	0.68	-0.66	-0.66	0.96
Cthe_02151	hypothetical protein	11.19	11.23	12.16	12.01	-0.97	-0.78	-0.04	0.15	-0.49	-1.05	-0.03	-1.13	-0.66	-0.66	1.16
Cthe_02366	single-stranded nucleic acid binding R3H	10.72	10.66	11.72	11.07	-1	-0.41	0.06	0.65	-0.53	-0.61	0.3	-0.06	-0.67	-0.67	3
Cthe_00472	flagellar hook capping protein	7.44	7.67	8.65	8.02	-1.21	-0.35	-0.23	0.63	-0.81	-0.54	-0.67	-0.11	-0.67	-0.67	1.63
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00693	Pseudouridine synthase, Rsu	9.45	9.49	10.44	9.85	-0.99	-0.36	-0.04	0.59	-0.51	-0.55	-0.03	-0.19	-0.67	-0.67	4.43
Cthe_03083	hypothetical protein	7.11	7.22	8.79	7.28	-1.68	-0.06	-0.11	1.51	-1.45	-0.19	-0.27	1.77	-0.67	-0.67	0.93
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00693	Pseudouridine synthase, Rsu	9.45	9.49	10.44	9.85	-0.99	-0.36	-0.04	0.59	-0.51	-0.55	-0.03	-0.19	-0.67	-0.67	4.43
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
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Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
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Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67	3.25
Cthe_00716	Nucleoside-diphosphate kinase	10.57	10.57	11.55	10.99	-0.98	-0.42	0	0.56	-0.5	-0.62	0.1	-0.26	-0.67	-0.67</	



Cthe_02163	anti-sigma-factor antagonist	8.63	8.23	9.57	9.31	-0.94	-1.08	0.4	0.26	-0.45	-1.4	1.43	-0.89	-0.73	-0.73	0.99
Cthe_00888	type IV pilus assembly PilZ	9.07	9.19	10.15	9.82	-1.08	-0.63	-0.12	0.33	-0.64	-0.87	-0.3	-0.74	-0.73	-0.73	1.54
Cthe_00657	hypothetical protein	10.92	11.01	11.98	11.59	-1.06	-0.58	-0.09	0.39	-0.61	-0.81	-0.2	-0.62	-0.73	-0.73	1.77
Cthe_02048	hypothetical protein	5.91	5.61	7.2	6.25	-1.29	-0.64	0.3	0.95	-0.92	-0.88	1.1	0.57	-0.73	-0.73	1.17
Cthe_02560	dTDP-4-dehydrohamnose 3,5-epimerase	5.17	6.09	7.17	6.69	-2	-0.6	-0.92	0.48	-1.88	-0.83	-2.97	-0.43	-0.73	-0.73	0.78
Cthe_02560	dTDP-4-dehydrohamnose 3,5-epimerase	5.17	6.09	7.17	6.69	-2	-0.6	-0.92	0.48	-1.88	-0.83	-2.97	-0.43	-0.73	-0.73	0.78
Cthe_01531	hypothetical protein	2	1.58	3.46	2.32	-1.46	-0.74	0.42	1.14	-1.15	-1	1.5	0.98	-0.74	-0.74	0.97
Cthe_01267	two component transcriptional regulator,	3.17	1.58	3.46	2.81	-0.29	-1.23	1.59	0.65	0.43	-1.58	5.4	-0.06	-0.74	-0.74	0.34
Cthe_02702	polysaccharide pyruvyl transferase	9.55	9.69	10.68	10.13	-1.13	-0.44	-0.14	0.55	-0.7	-0.64	-0.37	-0.28	-0.74	-0.74	2.32
Cthe_01267	two component transcriptional regulator,	3.17	1.58	3.46	2.81	-0.29	-1.23	1.59	0.65	0.43	-1.58	5.4	-0.06	-0.74	-0.74	0.34
Cthe_03031	protein of unknown function DUF1212	4.17	4	5.52	4.46	-1.35	-0.46	0.17	1.06	-1	-0.67	0.67	0.81	-0.74	-0.74	1.3
Cthe_02702	polysaccharide pyruvyl transferase	9.55	9.69	10.68	10.13	-1.13	-0.44	-0.14	0.55	-0.7	-0.64	-0.37	-0.28	-0.74	-0.74	2.32
Cthe_00827	hemolysin A	9.55	9.3	10.6	10.04	-1.05	-0.74	0.25	0.56	-0.59	-1	0.93	-0.26	-0.74	-0.74	1.37
Cthe_01225	bacterial translation initiation factor 3	12.29	12.33	13.29	13.34	-1	-1.01	-0.04	-0.05	-0.53	-1.32	-0.03	-1.55	-0.74	-0.74	1.04
Cthe_02377	Cobyrinic acid a,c-diamide synthase	10.18	10.01	11.15	10.8	-0.97	-0.79	0.17	0.35	-0.49	-1.06	0.67	-0.7	-0.74	-0.74	1.37
Cthe_01108	hypothetical protein	3.17	3.46	4.95	3.46	-1.78	0	-0.29	1.49	-1.58	-0.12	-0.87	1.72	-0.74	-0.74	0.93
Cthe_00760	hypothetical protein	10.83	10.91	11.89	11.5	-1.06	-0.59	-0.08	0.39	-0.61	-0.82	-0.17	-0.62	-0.74	-0.74	1.81
Cthe_02032	hypothetical protein	8.21	8.03	9.38	8.57	-1.17	-0.54	0.18	0.81	-0.76	-0.76	0.7	0.28	-0.74	-0.74	1.62
Cthe_00464	flagellar hook-basal body complex subunit	9.96	9.8	10.98	10.47	-1.02	-0.67	0.16	0.51	-0.55	-0.92	0.63	-0.36	-0.75	-0.75	1.68
Cthe_00464	flagellar hook-basal body complex subunit	9.96	9.8	10.98	10.47	-1.02	-0.67	0.16	0.51	-0.55	-0.92	0.63	-0.36	-0.75	-0.75	1.68
Cthe_03052	YD repeat protein	7.91	8.19	9.17	8.77	-1.26	-0.58	-0.28	0.4	-0.88	-0.81	-0.83	-0.6	-0.75	-0.75	1.33
Cthe_01805	diguanylate cyclase	10.03	9.86	11.01	10.65	-0.98	-0.79	0.17	0.36	-0.5	-1.06	0.67	-0.68	-0.75	-0.75	1.4
Cthe_02935	methyltransferase small	8.48	9.28	10.32	10.01	-1.84	-0.73	-0.8	0.31	-1.66	-0.99	-2.57	-0.79	-0.75	-0.75	0.82
Cthe_00733	type IV pilus assembly PilZ	10.54	10.37	11.65	10.94	-1.11	-0.57	0.17	0.71	-0.68	-0.8	0.67	0.06	-0.75	-0.75	1.77
Cthe_00545	prepilin peptidase CpaA	6.36	6.41	7.41	6.82	-1.05	-0.41	-0.05	0.59	-0.59	-0.61	-0.07	-0.19	-0.76	-0.76	4.76
Cthe_00268	hypothetical protein	9.49	9.55	10.76	9.83	-1.27	-0.28	-0.06	0.93	-0.89	-0.45	-0.1	0.53	-0.76	-0.76	2.1
Cthe_02940	transcriptional regulator, CarD family	11.29	11.16	12.65	11.59	-1.36	-0.43	0.13	1.06	-1.01	-0.63	0.53	0.81	-0.76	-0.76	1.4
Cthe_00545	prepilin peptidase CpaA	6.36	6.41	7.41	6.82	-1.05	-0.41	-0.05	0.59	-0.59	-0.61	-0.07	-0.19	-0.76	-0.76	4.76
Cthe_00432	hypothetical protein	11.53	11.8	12.78	12.44	-1.25	-0.64	-0.27	0.34	-0.86	-0.88	-0.8	-0.72	-0.76	-0.76	1.3
Cthe_01552	MAEBL putative	8.93	8.92	9.97	9.3	-1.04	-0.38	0.01	0.67	-0.58	-0.57	0.13	-0.02	-0.76	-0.76	7.03
Cthe_00545	prepilin peptidase CpaA	6.36	6.41	7.41	6.82	-1.05	-0.41	-0.05	0.59	-0.59	-0.61	-0.07	-0.19	-0.76	-0.76	4.76
Cthe_00465	flagellar M-ring protein Flif	11.3	11.39	12.38	12.04	-1.08	-0.65	-0.09	0.34	-0.64	-0.89	-0.2	-0.72	-0.77	-0.77	1.67
Cthe_01342	beta-lactamase-like protein	8.75	8.91	9.93	9.3	-1.18	-0.39	-0.16	0.63	-0.77	-0.58	-0.43	-0.11	-0.77	-0.77	2.47
Cthe_02034	serine/threonine protein kinase	8.09	8.26	9.53	8.47	-1.44	-0.21	-0.17	1.06	-1.12	-0.37	-0.47	0.81	-0.77	-0.77	1.43
Cthe_00058	RNA polymerase sigma factor	7.73	7.43	8.82	8.24	-1.09	-0.81	0.3	0.58	-0.65	-1.08	1.1	-0.21	-0.77	-0.77	1.28
Cthe_00993	protein of unknown function DUF448	8.54	8.57	9.59	9.07	-1.05	-0.5	-0.03	0.52	-0.59	-0.71	0	-0.34	-0.77	-0.77	3.09
Cthe_02034	serine/threonine protein kinase	8.09	8.26	9.53	8.47	-1.44	-0.21	-0.17	1.06	-1.12	-0.37	-0.47	0.81	-0.77	-0.77	1.43
Cthe_02034	serine/threonine protein kinase	8.09	8.26	9.53	8.47	-1.44	-0.21	-0.17	1.06	-1.12	-0.37	-0.47	0.81	-0.77	-0.77	1.43
Cthe_00465	flagellar M-ring protein Flif	11.3	11.39	12.38	12.04	-1.08	-0.65	-0.09	0.34	-0.64	-0.89	-0.2	-0.72	-0.77	-0.77	1.67
Cthe_02141	metal-dependent phosphohydrolase, HD s	8.37	8.53	9.56	8.89	-1.19	-0.36	-0.16	0.67	-0.78	-0.55	-0.43	-0.02	-0.77	-0.77	2.52
Cthe_02034	serine/threonine protein kinase	8.09	8.26	9.53	8.47	-1.44	-0.21	-0.17	1.06	-1.12	-0.37	-0.47	0.81	-0.77	-0.77	1.43
Cthe_01420	protein of unknown function DUF204	10.48	10.43	11.48	11.2	-1	-0.77	0.05	0.28	-0.53	-1.04	0.27	-0.85	-0.77	-0.77	1.49
Cthe_02635	pyridoxamine 5'-phosphate oxidase-relate	6.19	6.48	7.48	7.04	-1.29	-0.56	-0.29	0.44	-0.92	-0.79	-0.87	-0.51	-0.77	-0.77	1.37
Cthe_00923	hypothetical protein	6.64	6.69	7.67	7.65	-1.03	-0.96	-0.05	0.02	-0.57	-1.26	-0.07	-1.4	-0.77	-0.77	1.12
Cthe_01194	hypothetical protein	8.65	8.63	10.1	8.93	-1.45	-0.3	0.02	1.17	-1.14	-0.48	0.17	1.04	-0.77	-0.77	1.33
Cthe_02141	metal-dependent phosphohydrolase, HD s	8.37	8.53	9.56	8.89	-1.19	-0.36	-0.16	0.67	-0.78	-0.55	-0.43	-0.02	-0.77	-0.77	2.52
Cthe_00481	flagellar biosynthetic protein Flif	6.07	5.81	6.98	6.92	-0.91	-1.11	0.26	0.06	-0.41	-1.44	0.97	-1.32	-0.78	-0.78	1.04
Cthe_02809	glycoside hydrolase, family 16	8.3	8.16	9.54	8.65	-1.24	-0.49	0.14	0.89	-0.85	-0.7	0.57	0.45	-0.78	-0.78	1.72
Cthe_03141	lipolytic enzyme, G-D-S-L	5.55	5.93	7.3	6	-1.75	-0.07	-0.38	1.3	-1.54	-0.2	-1.17	1.32	-0.78	-0.78	1
Cthe_00758	protein of unknown function UPF0102	7.86	7.71	9.11	8.21	-1.25	-0.5	0.15	0.9	-0.86	-0.71	0.6	0.47	-0.78	-0.78	1.66
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00481	flagellar biosynthetic protein Flif	6.07	5.81	6.98	6.92	-0.91	-1.11	0.26	0.06	-0.41	-1.44	0.97	-1.32	-0.78	-0.78	1.04
Cthe_02922	ribosomal protein L15	12.5	13.06	13.19	13.04	-0.69	0.02	-0.56	0.15	-0.11	-0.1	-1.77	-1.13	-0.78	-0.78	0.08
Cthe_02140	hypothetical protein	9.19	9.17	10.37	9.53	-1.18	-0.36	0.02	0.84	-0.77	-0.55	0.17	0.34	-0.78	-0.78	2.83
Cthe_02922	ribosomal protein L15	12.5	13.06	13.19	13.04	-0.69	0.02	-0.56	0.15	-0.11	-0.1	-1.77	-1.13	-0.78	-0.78	0.08
Cthe_02922	ribosomal protein L15	12.5	13.06	13.19	13.04	-0.69	0.02	-0.56	0.15	-0.11	-0.1	-1.77	-1.13	-0.78	-0.78	0.08
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00987	riboflavin biosynthesis protein RibF	10.9	11.01	11.99	11.91	-1.09	-0.9	-0.11	0.08	-0.65	-1.19	-0.27	-1.28	-0.78	-0.78	1.18
Cthe_00267	type 3a, cellulose-binding	8.64	8.9	10.12	9.12	-1.48	-0.22	-0.26	1	-1.18	-0.38	-0.77	0.68	-0.79	-0.79	1.37
Cthe_02347	lipopolysaccharide biosynthesis	10.49	10.56	11.57	11.14	-1.08	-0.58	-0.07	0.43	-0.64	-0.81	-0.13	-0.53	-0.79	-0.79	2.15
Cthe_00014	hypothetical protein	6.21	5.98	7.17	6.97	-0.96	-0.99	0.23	0.2	-0.47	-1.3	0.87	-1.02	-0.79	-0.79	1.17
Cthe_01338	Flp pilus assembly protein TadB-like prote	10.12	10.14	11.17	10.88	-1.05	-0.74	-0.02	0.29	-0.59	-1	0.03	-0.83	-0.8	-0.8	1.59
Cthe_00024	biotin biosynthesis protein BioC	5.04	5.09	6.11	5.49	-1.07	-0.4	-0.05	0.62	-0.62	-0.6	-0.07	-0.13	-0.8	-0.8	6.64
Cthe_01364	hypothetical protein	9.54	9.45	10.5	10.58	-0.96	-1.13	0.09	-0.08	-0.47	-1.46	0.4	-1.62	-0.8	-0.8	1.04
Cthe_03131	von Willebrand factor, type A	10.79	10.83	12.02	11.15	-1.23	-0.32	-0.04	0.87	-0.84	-0.5	-0.03	0.4	-0.8	-0.8	2.77
Cthe_02423	hypothetical protein	11.06	11.37	12.54	11.64	-1.48	-0.27	-0.31	0.9	-1.18	-0.44	-0.93	0.47	-0.8	-0.8	1.37
Cthe_01470	RNA polymerase, sigma-24 subunit, ECF su	9.6	9.58	10.65	10.21	-1.05	-0.63	0.02	0.44	-0.59	-0.87	0.17	-0.51	-0.81	-0.81	2.22
Cthe_03159	transcriptional regulator, GntR family	10.54	10.64	11.63	11.65	-1.09	-1.01	-0.1	-0.02	-0.65	-1.32	-0.23	-1.49	-0.81	-0.81	1.11
Cthe_00713	1-acyl-sn-glycerol-3-phosphate acyltransfe	11.79	11.97	12.98	12.58	-1.19	-0.61	-0.18	0.4	-0.78	-0.85	-0.5	-0.6	-0.81	-0.81	1.68
Cthe_00713	1-acyl-sn															



Cthe_02945	histidine kinase	8.4	8.46	9.5	9.11	-1.1	-0.65	-0.06	0.39	-0.66	-0.89	-0.1	-0.62	-0.83	-0.83	2
Cthe_03147	ABC transporter related protein	9.32	9.42	10.42	10.46	-1.1	-1.04	-0.1	-0.04	-0.66	-1.36	-0.23	-1.53	-0.83	-0.83	1.11
Cthe_01773	peptidase S16, Ion-like protein	9.06	8.92	10.07	9.84	-1.01	-0.92	0.14	0.23	-0.54	-1.21	0.57	-0.96	-0.83	-0.83	1.35
Cthe_02047	intein	7.7	7.43	8.78	8.28	-1.08	-0.85	0.27	0.5	-0.64	-1.13	1	-0.38	-0.83	-0.83	1.38
Cthe_03224	hypothetical protein	7.66	7.66	8.93	8.02	-1.27	-0.36	0	0.91	-0.89	-0.55	0.1	0.49	-0.83	-0.83	2.38
Cthe_00939	hypothetical protein	6.48	6.44	7.51	7.35	-1.03	-0.91	0.04	0.16	-0.57	-1.2	0.23	-1.11	-0.83	-0.83	1.33
Cthe_01781	hypothetical protein	8.25	8.09	9.29	8.88	-1.04	-0.79	0.16	0.41	-0.58	-1.06	0.63	-0.57	-0.83	-0.83	1.62
Cthe_01252	Auxin Efflux Carrier	10.06	10.15	11.12	11.51	-1.06	-1.36	-0.09	-0.39	-0.61	-1.74	-0.2	-2.28	-0.84	-0.84	0.92
Cthe_01359	glycosyltransferase 28-like protein	10.36	10.32	11.41	11.1	-1.05	-0.78	0.04	0.31	-0.59	-1.05	0.23	-0.79	-0.84	-0.84	1.66
Cthe_00535	hypothetical protein	10.03	9.85	11.37	10.4	-1.34	-0.55	0.18	0.97	-0.99	-0.77	0.7	0.62	-0.84	-0.84	1.52
Cthe_01212	hypothetical protein	13.61	13.34	15.1	13.95	-1.49	-0.61	0.27	1.15	-1.19	-0.85	1	1	-0.84	-0.84	1.18
Cthe_00729	cellulosome enzyme, dockerin type I	8.26	8.37	9.6	8.67	-1.34	-0.3	-0.11	0.93	-0.99	-0.48	-0.27	0.53	-0.84	-0.84	2.1
Cthe_00075	hypothetical protein	4.52	4.95	6.55	4.91	-2.03	0.04	-0.43	1.64	-1.92	-0.07	-1.33	2.04	-0.85	-0.85	0.9
Cthe_03139	hypothetical protein	4.25	5.13	6.67	4.91	-2.42	0.22	-0.88	1.76	-2.45	0.14	-2.83	2.3	-0.85	-0.85	0.76
Cthe_02731	RNA polymerase, sigma-24 subunit, ECF su	10.14	10.3	11.46	10.64	-1.32	-0.34	-0.16	0.82	-0.96	-0.52	-0.43	0.3	-0.86	-0.86	2.37
Cthe_00462	flagellar basal-body rod protein FlgB	10.85	10.75	11.99	11.3	-1.14	-0.55	0.1	0.69	-0.72	-0.77	0.43	0.02	-0.86	-0.86	2.78
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.43	6.46	7.52	6.92	-1.09	-0.46	-0.03	0.6	-0.65	-0.67	0	-0.17	-0.86	-0.86	6.24
Cthe_02380	TPR repeat domain containing protein	9.88	9.92	10.97	10.82	-1.09	-0.9	-0.04	0.15	-0.65	-1.19	-0.03	-1.13	-0.86	-0.86	1.36
Cthe_02956	hypothetical protein	5.58	5.61	6.67	6.43	-1.09	-0.82	-0.03	0.24	-0.65	-1.1	0	-0.94	-0.86	-0.86	1.54
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.43	6.46	7.52	6.92	-1.09	-0.46	-0.03	0.6	-0.65	-0.67	0	-0.17	-0.86	-0.86	6.24
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.43	6.46	7.52	6.92	-1.09	-0.46	-0.03	0.6	-0.65	-0.67	0	-0.17	-0.86	-0.86	6.24
Cthe_01086	dTDP-glucose 4,6-dehydratase	6.43	6.46	7.52	6.92	-1.09	-0.46	-0.03	0.6	-0.65	-0.67	0	-0.17	-0.86	-0.86	6.24
Cthe_02174	transcription termination factor Rho	13.82	13.84	14.92	14.5	-1.1	-0.66	-0.02	0.42	-0.66	-0.9	0.03	-0.55	-0.87	-0.87	2.3
Cthe_02757	sodium/hydrogen exchanger	8.75	8.96	10.04	9.42	-1.29	-0.46	-0.21	0.62	-0.92	-0.67	-0.6	-0.13	-0.87	-0.87	2.11
Cthe_00260	peptidase S1 and S6, chymotrypsin/Hap	6.32	6.04	7.46	6.88	-1.14	-0.84	0.28	0.58	-0.72	-1.12	1.03	-0.21	-0.87	-0.87	1.44
Cthe_00578	glycoside hydrolase, family 9	12.06	12.16	13.25	12.55	-1.19	-0.39	-0.1	0.7	-0.78	-0.58	-0.23	0.04	-0.87	-0.87	4.73
Cthe_00323	hypothetical protein	7.19	7.14	8.27	7.77	-1.08	-0.63	0.05	0.5	-0.64	-0.87	0.27	-0.38	-0.87	-0.87	2.63
Cthe_01334	FHA domain containing protein	9.27	9.42	10.45	10.24	-1.18	-0.82	-0.15	0.21	-0.77	-1.1	-0.4	-1	-0.87	-0.87	1.42
Cthe_03153	Phosphoglycerate mutase	6.89	6.83	8.06	7.31	-1.17	-0.48	0.06	0.75	-0.76	-0.69	0.3	0.15	-0.88	-0.88	3.48
Cthe_03153	Phosphoglycerate mutase	6.89	6.83	8.06	7.31	-1.17	-0.48	0.06	0.75	-0.76	-0.69	0.3	0.15	-0.88	-0.88	3.48
Cthe_03153	Phosphoglycerate mutase	6.89	6.83	8.06	7.31	-1.17	-0.48	0.06	0.75	-0.76	-0.69	0.3	0.15	-0.88	-0.88	3.48
Cthe_03153	Phosphoglycerate mutase	6.89	6.83	8.06	7.31	-1.17	-0.48	0.06	0.75	-0.76	-0.69	0.3	0.15	-0.88	-0.88	3.48
Cthe_03153	Phosphoglycerate mutase	6.89	6.83	8.06	7.31	-1.17	-0.48	0.06	0.75	-0.76	-0.69	0.3	0.15	-0.88	-0.88	3.48
Cthe_00985	peptidase M16-like protein	11.01	11.13	12.19	11.71	-1.18	-0.58	-0.12	0.48	-0.77	-0.81	-0.3	-0.43	-0.89	-0.89	2.42
Cthe_02250	hypothetical protein	3.81	2.81	4.17	3.17	-0.36	-0.36	1	1	0.34	-0.55	3.43	0.68	-0.89	-0.89	0.21
Cthe_01784	hypothetical protein	13.23	13.17	14.33	13.76	-1.1	-0.59	0.06	0.57	-0.66	-0.82	0.3	-0.23	-0.89	-0.89	3.16
Cthe_02382	major facilitator superfamily MFS_1	9.71	10.03	11.16	10.49	-1.45	-0.46	-0.32	0.67	-1.14	-0.67	-0.97	-0.02	-0.9	-0.9	1.55
Cthe_00495	RNA polymerase, sigma 28 subunit	6.49	6.63	7.7	7.19	-1.21	-0.56	-0.14	0.51	-0.81	-0.79	-0.37	-0.36	-0.9	-0.9	2.49
Cthe_00878	CheW protein	10.31	9.94	11.25	11.33	-0.94	-1.39	0.37	-0.08	-0.45	-1.77	1.33	-1.62	-0.9	-0.9	0.99
Cthe_00878	CheW protein	10.31	9.94	11.25	11.33	-0.94	-1.39	0.37	-0.08	-0.45	-1.77	1.33	-1.62	-0.9	-0.9	0.99
Cthe_00783	RNA modification enzyme, MiaB family	9.51	9.38	10.58	10.23	-1.07	-0.85	0.13	0.35	-0.62	-1.13	0.53	-0.7	-0.9	-0.9	1.67
Cthe_00862	hypothetical protein	9.38	9.22	10.41	10.23	-1.03	-1.01	0.16	0.18	-0.57	-1.32	0.63	-1.06	-0.9	-0.9	1.33
Cthe_02155	S-layer-like domain containing protein	5.95	6.11	7.18	6.66	-1.23	-0.55	-0.16	0.52	-0.84	-0.77	-0.43	-0.34	-0.9	-0.9	2.36
Cthe_01534	hypothetical protein	5.25	4.32	6.58	5.98	-1.33	-1.66	0.93	0.6	-0.97	-2.1	3.2	-0.17	-0.9	-0.9	0.82
Cthe_02817	CheW protein	4.95	5.46	6.58	6.11	-1.63	-0.65	-0.51	0.47	-1.38	-0.89	-1.6	-0.45	-0.91	-0.91	1.12
Cthe_02817	CheW protein	4.95	5.46	6.58	6.11	-1.63	-0.65	-0.51	0.47	-1.38	-0.89	-1.6	-0.45	-0.91	-0.91	1.12
Cthe_00636	hypothetical protein	9.11	9.1	10.22	9.65	-1.11	-0.55	0.01	0.57	-0.68	-0.77	0.13	-0.23	-0.91	-0.91	4.42
Cthe_00528	hypothetical protein	7.11	7.1	8.2	8.11	-1.09	-1.01	0.01	0.09	-0.65	-1.32	0.13	-1.26	-0.91	-0.91	1.32
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_03157	pyruvate carboxyltransferase	10.05	10.43	11.46	11.53	-1.41	-1.1	-0.38	-0.07	-1.08	-1.43	-1.17	-1.6	-0.92	-0.92	1.03
Cthe_02669	hypothetical protein	8.12	8.06	9.58	8.5	-1.46	-0.44	0.06	1.08	-1.15	-0.64	0.3	0.85	-0.92	-0.92	1.66
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00707	Phosphoglycerate mutase	9.92	9.91	11.03	10.58	-1.11	-0.67	0.01	0.45	-0.68	-0.92	0.13	-0.49	-0.92	-0.92	2.56
Cthe_00011	hypothetical protein	5.88	4.95	6.67	5.32	-0.79	-0.37	0.93	1.35	-0.24	-0.56	3.2	1.43	-0.93	-0.93	0.2
Cthe_02379	hypothetical protein	8.75	8.87	9.95	9.58	-1.2	-0.71	-0.12	0.37	-0.8	-0.96	-0.3	-0.66	-0.93	-0.93	1.96
Cthe_03135	hypothetical protein	4	4	5.09	5.17	-1.09	-1.17	0	-0.08	-0.65	-1.51	0.1	-1.62	-0.93	-0.93	1.15
Cthe_01516	ribosome small subunit-dependent GTPas	2.81	3.7	5.29	3.58	-2.48	0.12	-0.89	1.71	-2.53	0.02	-2.87	2.19	-0.94	-0.94	0.8
Cthe_00083	serine phosphatase	11.1	11.24	12.33	11.8	-1.23	-0.56	-0.14	0.53	-0.84	-0.79	-0.37	-0.32	-0.94	-0.94	2.68
Cthe_00540	protein of unknown function DUF214	11.87	12.41	13.49	13.36	-1.62	-0.95	-0.54	0.13	-1.36	-1.25	-1.7	-1.17	-0.94	-0.94	1.02
Cthe_00083	serine phosphatase	11.1	11.24	12.33	11.8	-1.23	-0.56	-0.14	0.53	-0.84	-0.79	-0.37	-0.32	-0.94	-0.94	2.68
Cthe_00955	hypothetical protein	6.71	6.93	8.62	7.09	-1.91	-0.16	-0.22	1.53	-1.76	-0.31	-0.63	1.81	-0.94	-0.94	1.06
Cthe_01419	hypothetical protein	7.54	7.72	8.75	9.03	-1.21	-1.31	-0.18	-0.28	-0.81	-1.68	-0.5	-2.04	-0.94	-0.94	1.01
Cthe_00540	protein of unknown function DUF214	11.87	12.41	13.49	13.36	-1.62	-0.95	-0.54	0.13	-1.36	-1.25	-1.7	-1.17	-0.94	-0.94	1.02
Cthe_01516	ribosome small subunit-dependent GTPas	2.81	3.7	5.29	3.58	-2.48	0.12	-0.89	1.71	-2.53	0.02	-2.87	2.19	-0.94	-0.94	0.8
Cthe_01516	ribosome small subunit-dependent GTPas	2.81	3.7	5.29	3.58	-2.48	0.12	-0.89	1.71	-2.53	0.02	-2.87	2.19	-0.94	-0.94	0.8
Cthe_01516	ribosome small subunit-dependent GTPas	2.81	3.7	5.29	3.58	-2.48	0.12	-0.89	1.71	-2.53	0.02	-2.87				



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Cthe_00366	hypothetical protein	9.54	9.43	10.67	10.8	-1.13	-1.37	0.11	-0.13	-0.7	-1.75	0.47	-1.72	-1.1	-1.1	1.2
Cthe_00924	hypothetical protein	7.15	7.14	8.36	8.04	-1.21	-0.9	0.01	0.32	-0.81	-1.19	0.13	-0.77	-1.1	-1.1	2.09
Cthe_01281	hypothetical protein	8.34	8.45	9.89	8.89	-1.55	-0.44	-0.11	1	-1.27	-0.64	-0.27	0.68	-1.1	-1.1	2.21
Cthe_02670	hypothetical protein	7.4	7.77	9.27	8.1	-1.87	-0.33	-0.37	1.17	-1.7	-0.51	-1.13	1.04	-1.1	-1.1	1.31
Cthe_00928	4-hydroxythreonine-4-phosphate dehydro	7.18	7.46	8.63	8.25	-1.45	-0.79	-0.28	0.38	-1.14	-1.06	-0.83	-0.64	-1.1	-1.1	1.69
Cthe_00928	4-hydroxythreonine-4-phosphate dehydro	7.18	7.46	8.63	8.25	-1.45	-0.79	-0.28	0.38	-1.14	-1.06	-0.83	-0.64	-1.1	-1.1	1.69
Cthe_00737	Phosphopantetheine-protein transferase	10.42	10.31	11.69	11.02	-1.27	-0.71	0.11	0.67	-0.89	-0.96	0.47	-0.02	-1.1	-1.1	3.16
Cthe_00737	Phosphopantetheine-protein transferase	10.42	10.31	11.69	11.02	-1.27	-0.71	0.11	0.67	-0.89	-0.96	0.47	-0.02	-1.1	-1.1	3.16
Cthe_00737	Phosphopantetheine-protein transferase	10.42	10.31	11.69	11.02	-1.27	-0.71	0.11	0.67	-0.89	-0.96	0.47	-0.02	-1.1	-1.1	3.16
Cthe_00737	Phosphopantetheine-protein transferase	10.42	10.31	11.69	11.02	-1.27	-0.71	0.11	0.67	-0.89	-0.96	0.47	-0.02	-1.1	-1.1	3.16
Cthe_00737	Phosphopantetheine-protein transferase	10.42	10.31	11.69	11.02	-1.27	-0.71	0.11	0.67	-0.89	-0.96	0.47	-0.02	-1.1	-1.1	3.16
Cthe_00928	4-hydroxythreonine-4-phosphate dehydro	7.18	7.46	8.63	8.25	-1.45	-0.79	-0.28	0.38	-1.14	-1.06	-0.83	-0.64	-1.1	-1.1	1.69
Cthe_00737	Phosphopantetheine-protein transferase	10.42	10.31	11.69	11.02	-1.27	-0.71	0.11	0.67	-0.89	-0.96	0.47	-0.02	-1.1	-1.1	3.16
Cthe_00737	Phosphopantetheine-protein transferase	10.42	10.31	11.69	11.02	-1.27	-0.71	0.11	0.67	-0.89	-0.96	0.47	-0.02	-1.1	-1.1	3.16
Cthe_00282	glycogen/starch synthases, ADP-glucose t	8.04	8.11	9.53	8.58	-1.49	-0.47	-0.07	0.95	-1.19	-0.68	-0.13	0.57	-1.11	-1.11	2.66
Cthe_00282	glycogen/starch synthases, ADP-glucose t	8.04	8.11	9.53	8.58	-1.49	-0.47	-0.07	0.95	-1.19	-0.68	-0.13	0.57	-1.11	-1.11	2.66
Cthe_00282	glycogen/starch synthases, ADP-glucose t	8.04	8.11	9.53	8.58	-1.49	-0.47	-0.07	0.95	-1.19	-0.68	-0.13	0.57	-1.11	-1.11	2.66
Cthe_00282	glycogen/starch synthases, ADP-glucose t	8.04	8.11	9.53	8.58	-1.49	-0.47	-0.07	0.95	-1.19	-0.68	-0.13	0.57	-1.11	-1.11	2.66
Cthe_00475	flagellar protein	8.52	8.19	9.65	9.58	-1.13	-1.39	0.33	0.07	-0.7	-1.77	1.2	-1.3	-1.12	-1.12	1.22
Cthe_02373	RNA-binding S4	6.93	6.95	8.17	7.67	-1.24	-0.72	-0.02	0.5	-0.85	-0.98	0.03	-0.38	-1.13	-1.13	3.87
Cthe_00383	protein of unknown function DUF214	3.58	2.32	4.86	4.7	-1.28	-2.38	1.26	0.16	-0.91	-2.95	4.3	-1.11	-1.13	-1.13	0.79
Cthe_02957	hypothetical protein	6.99	7.24	8.5	7.84	-1.51	-0.6	-0.25	0.66	-1.22	-0.83	-0.73	-0.04	-1.15	-1.15	2.29
Cthe_01337	type II secretion system protein	8.81	8.98	10.17	10.04	-1.36	-1.06	-0.17	0.13	-1.01	-1.38	-0.47	-1.17	-1.16	-1.16	1.54
Cthe_02343	GCN5-related N-acetyltransferase	7.5	7.45	8.74	8.32	-1.24	-0.87	0.05	0.42	-0.85	-1.15	0.27	-0.55	-1.16	-1.16	2.65
Cthe_00265	aminotransferase, class V	6.04	5.25	6.88	5.25	-0.84	0	0.79	1.63	-0.31	-0.12	2.73	2.02	-1.16	-1.16	0.11
Cthe_01835	Viral A-type inclusion protein repeat conta	9.83	10.11	11.45	10.63	-1.62	-0.52	-0.28	0.82	-1.36	-0.74	-0.83	0.3	-1.16	-1.16	1.99
Cthe_02571	RNA related	6.99	6.91	8.28	7.61	-1.29	-0.7	0.08	0.67	-0.92	-0.95	0.37	-0.02	-1.16	-1.16	4.06
Cthe_00530	hypothetical protein	7.2	7.19	8.44	8.29	-1.24	-1.1	0.01	0.15	-0.85	-1.43	0.13	-1.13	-1.16	-1.16	1.66
Cthe_03123	von Willebrand factor, type A	11.66	11.65	12.91	12.55	-1.25	-0.9	0.01	0.36	-0.86	-1.19	0.13	-0.68	-1.16	-1.16	2.41
Cthe_02732	hypothetical protein	9.94	9.97	11.2	10.59	-1.26	-0.62	-0.03	0.61	-0.88	-0.86	0	-0.15	-1.16	-1.16	9.32
Cthe_00853	type II secretion system protein E	9.96	10.02	11.25	10.83	-1.29	-0.81	-0.06	0.42	-0.92	-1.08	-0.1	-0.55	-1.17	-1.17	2.88
Cthe_00853	type II secretion system protein E	9.96	10.02	11.25	10.83	-1.29	-0.81	-0.06	0.42	-0.92	-1.08	-0.1	-0.55	-1.17	-1.17	2.88
Cthe_01065	type IV pilus assembly PilZ	9.91	9.73	11.32	10.51	-1.41	-0.78	0.18	0.81	-1.08	-1.05	0.7	0.28	-1.17	-1.17	2.27
Cthe_02813	two component transcriptional regulator,	5.49	5.49	6.75	6.38	-1.26	-0.89	0	0.37	-0.88	-1.18	0.1	-0.66	-1.18	-1.18	2.51
Cthe_01874	transposase, mutator type	3.58	3	4.64	4.86	-1.06	-1.86	0.58	-0.22	-0.61	-2.33	2.03	-1.91	-1.18	-1.18	0.98
Cthe_02813	two component transcriptional regulator,	5.49	5.49	6.75	6.38	-1.26	-0.89	0	0.37	-0.88	-1.18	0.1	-0.66	-1.18	-1.18	2.51
Cthe_02289	hypothetical protein	2.81	2.32	4.39	3.46	-1.58	-1.14	0.49	0.93	-1.31	-1.48	1.73	0.53	-1.18	-1.18	1.24
Cthe_01043	hypothetical protein	6.17	6.17	7.62	6.73	-1.45	-0.56	0	0.89	-1.14	-0.79	0.1	0.45	-1.18	-1.18	3.42
Cthe_00270	glycoside hydrolase, family 18	9.92	10.13	11.43	10.7	-1.51	-0.57	-0.21	0.73	-1.22	-0.8	-0.6	0.11	-1.19	-1.19	2.72
Cthe_02810	Na/Pi-cotransporter II-related protein	7.95	8.07	9.29	9.2	-1.34	-1.13	-0.12	0.09	-0.99	-1.46	-0.3	-1.26	-1.19	-1.19	1.55
Cthe_02674	hypothetical protein	6.02	5.81	7.38	6.69	-1.36	-0.88	0.21	0.69	-1.01	-1.17	0.8	0.02	-1.19	-1.19	2.19
Cthe_00240	hypothetical protein	8.64	8.65	10.05	9.21	-1.41	-0.56	-0.01	0.84	-1.08	-0.79	0.07	0.34	-1.19	-1.19	4.38
Cthe_00543	glycoside hydrolase, family 9	11.41	11.61	12.9	12.19	-1.49	-0.58	-0.2	0.71	-1.19	-0.81	-0.57	0.06	-1.19	-1.19	2.85
Cthe_00270	glycoside hydrolase, family 18	9.92	10.13	11.43	10.7	-1.51	-0.57	-0.21	0.73	-1.22	-0.8	-0.6	0.11	-1.19	-1.19	2.72
Cthe_00555	PpiC-type peptidyl-prolyl cis-trans isomera	13.17	13.08	14.43	13.95	-1.26	-0.87	0.09	0.48	-0.88	-1.15	0.4	-0.43	-1.19	-1.19	2.8
Cthe_02372	DNA polymerase III, beta subunit	9.06	9.45	10.7	10.3	-1.64	-0.85	-0.39	0.4	-1.39	-1.13	-1.2	-0.6	-1.2	-1.2	1.52
Cthe_00902	3-methyl-2-oxobutanoate hydroxymethylt	10.92	10.75	12.24	11.62	-1.32	-0.87	0.17	0.62	-0.96	-1.15	0.67	-0.13	-1.2	-1.2	2.49
Cthe_00288	MCP methyltransferase, CheR-type	9.45	9.39	10.7	10.37	-1.25	-0.98	0.06	0.33	-0.86	-1.29	0.3	-0.74	-1.2	-1.2	2.21
Cthe_00288	MCP methyltransferase, CheR-type	9.45	9.39	10.7	10.37	-1.25	-0.98	0.06	0.33	-0.86	-1.29	0.3	-0.74	-1.2	-1.2	2.21
Cthe_00663	hypothetical protein	9.23	9.07	10.77	9.79	-1.54	-0.72	0.16	0.98	-1.26	-0.98	0.63	0.64	-1.2	-1.2	2.02
Cthe_01909	copper amine oxidase-like protein	9.11	9.24	10.47	10.03	-1.36	-0.79	-0.13	0.44	-1.01	-1.06	-0.33	-0.51	-1.2	-1.2	2.74
Cthe_01414	hypothetical protein	7.28	7.11	8.44	8.65	-1.16	-1.54	0.17	-0.21	-0.74	-1.95	0.67	-1.89	-1.2	-1.2	1.18
Cthe_00902	3-methyl-2-oxobutanoate hydroxymethylt	10.92	10.75	12.24	11.62	-1.32	-0.87	0.17	0.62	-0.96	-1.15	0.67	-0.13	-1.2	-1.2	2.49
Cthe_02372	DNA polymerase III, beta subunit	9.06	9.45	10.7	10.3	-1.64	-0.85	-0.39	0.4	-1.39	-1.13	-1.2	-0.6	-1.2	-1.2	1.52
Cthe_00288	MCP methyltransferase, CheR-type	9.45	9.39	10.7	10.37	-1.25	-0.98	0.06	0.33	-0.86	-1.29	0.3	-0.74	-1.2	-1.2	2.21
Cthe_02372	DNA polymerase III, beta subunit	9.06	9.45	10.7	10.3	-1.64	-0.85	-0.39	0.4	-1.39	-1.13	-1.2	-0.6	-1.2	-1.2	1.52
Cthe_00902	3-methyl-2-oxobutanoate hydroxymethylt	10.92	10.75	12.24	11.62	-1.32	-0.87	0.17	0.62	-0.96	-1.15	0.67	-0.13	-1.2	-1.2	2.49
Cthe_00902	3-methyl-2-oxobutanoate hydroxymethylt	10.92	10.75	12.24	11.62	-1.32	-0.87	0.17	0.62	-0.96	-1.15	0.67	-0.13	-1.2	-1.2	2.49
Cthe_00902	3-methyl-2-oxobutanoate hydroxymethylt	10.92	10.75	12.24	11.62	-1.32	-0.87	0.17	0.62	-0.96	-1.15	0.67	-0.13	-1.2	-1.2	2.49
Cthe_02987	hypothetical protein	2.58	2.81	4.09	3.46	-1.51	-0.65	-0.23	0.63	-1.22	-0.89	-0.67	-0.11	-1.21	-1.21	2.53
Cthe_03180	hypothetical protein	7.68	7.38	8.98	8.51	-1.3	-1.13	0.3	0.47	-0.93	-1.46	1.1	-0.45	-1.21	-1.21	1.66
Cthe_00303	hypothetical protein	9.28	8.91	10.46	10.37	-1.18	-1.46	0.37	0.09	-0.77	-1.86	1.33	-1.26	-1.21	-1.21	1.25
Cthe_03150	cobalamin biosynthesis protein CobD	10.94	10.96	12.23	11.74	-1.29	-0.78	-0.02	0.49	-0.92	-1.05	0.03	-0.4	-1.22	-1.22	3.95
Cthe_01111	Bile acid:sodium symporter	6.39	6.46	7.75	7.03	-1.36	-0.57	-0.07	0.72	-1.01	-0.8	-0.13	0.09	-1.22	-1.22	9.26
Cthe_00785	hypothetical protein	11.52	11.48	13.63	11.97	-2.11	-0.49	0.04	1.66	-2.03	-0.7	0.23	2.09	-1.22	-1.22	1.16
Cthe_03150	cobalamin biosynthesis protein CobD	10.94	10.96	12.23	11.74	-1.29	-0.78	-0.02	0.49	-0.92	-1.05	0.03	-0.4	-1.22	-1.22	3.95
Cthe_03150	cobalamin biosynthesis protein CobD	10.94	10.96	12.23	11.74	-1.29	-0.78	-0.02	0.49	-0.92	-1.05	0.03	-0.4	-1.22	-1.22	3.95
Cthe_03150	cobalamin biosynthesis protein CobD	10.94	10.96	12.23	11.74	-1.29	-0.78	-0.02	0.49	-0.92	-1.05	0.03	-0.4	-1.22	-1.22	3.95
Cthe_03150	cobalamin biosynthesis protein CobD	10.94	10.96	12.23	11.74	-1.29	-0.78	-0.02	0.49	-0.92	-1.05	0.03	-0.4	-1.22	-1.22	3.95
Cthe_02139	alpha-L-arabinofuranosidase B	7.02	7.43	9.03	7.82	-2.01	-0.39	-0.41	1.21	-1.89	-0.58	-1.27	1.13	-1.23	-1.23	1.32
Cthe_00190	proteinase inhibitor I4, serpin	10.04	10.01	11.83	10.57	-1.79	-0.56	0.03	1.26	-1.59	-0.79	0.2	1.23	-1.23	-1.23	1.62
Cthe_01780	hypothetical protein	7.92	7.93	9.22	8.9	-1.3	-0.97	-0.01	0.32	-0.93	-1.27	0.07	-0.77	-1.23	-1.23	2.31
Cthe_00315	DNA-directed RNA polymerase sigma fact	6.41	6.43	7.96	7	-1.55	-0.57	-0.02	0.96	-1.27	-0.8	0.03	0.6	-1.24	-1.24	2.84
Cthe_01274	nucleoside recognition	9.76	9.85	11.12	10.53	-1.36	-0.68	-0.09	0.59	-1.01	-0.93	-0.2	-0.19	-1.25	-1.25	5.66
Cthe_00027	hypothetical protein	7.11	6.85	8.43	7.96	-1.32	-1.11	0.26	0.47	-0.96	-1.44	0.97	-0.45	-1.26	-1.26	1.84
Cthe_00027																



Cthe_02990	peptide methionine sulfoxide reductase	7.64	7.8	9.11	8.59	-1.47	-0.79	-0.16	0.52	-1.16	-1.06	-0.43	-0.34	-1.33	-1.33	3.26
Cthe_01903	polysaccharide deacetylase	3.81	2.32	4.25	3	-0.44	-0.68	1.49	1.25	0.23	-0.93	5.07	1.21	-1.34	-1.34	0.21
Cthe_02088	protein of unknown function DUF710	9.6	8.96	11.05	10.57	-1.45	-1.61	0.64	0.48	-1.14	-2.04	2.23	-0.43	-1.34	-1.34	1.17
Cthe_02564	hypothetical protein	6.75	6.82	8.14	7.61	-1.39	-0.79	-0.07	0.53	-1.05	-1.06	-0.13	-0.32	-1.34	-1.34	4.91
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_02623	Exopolysaccharide biosynthesis protein	8.04	8.07	9.41	8.85	-1.37	-0.78	-0.03	0.56	-1.03	-1.05	0	-0.26	-1.36	-1.36	6.43
Cthe_00433	glycoside hydrolase, family 9	11.85	11.94	13.27	12.74	-1.42	-0.8	-0.09	0.53	-1.09	-1.07	-0.2	-0.32	-1.36	-1.36	4.6
Cthe_03162	SAM dependent methyltransferase	8.04	8.01	9.38	9.25	-1.44	-1.24	0.03	0.13	-0.99	-1.6	0.2	-1.17	-1.36	-1.36	1.8
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_01377	amino acid-binding ACT	9.21	9.08	10.71	9.9	-1.5	-0.82	0.13	0.81	-1.2	-1.1	0.53	0.28	-1.36	-1.36	3.09
Cthe_00898	metal dependent phosphohydrolase	7.11	6.83	8.35	8.49	-1.24	-1.66	0.28	-0.14	-0.85	-2.1	1.03	-1.74	-1.38	-1.38	1.27
Cthe_01087	hypothetical protein	7.23	7	8.53	8.43	-1.3	-1.43	0.23	0.1	-0.93	-1.82	0.87	-1.23	-1.38	-1.38	1.54
Cthe_00084	hypothetical protein	10.8	10.87	12.33	11.52	-1.53	-0.65	-0.07	0.81	-1.24	-0.89	-0.13	0.28	-1.39	-1.39	5.62
Cthe_01779	hypothetical protein	7.41	7.55	8.9	8.36	-1.49	-0.81	-0.14	0.54	-1.19	-1.08	-0.37	-0.3	-1.4	-1.4	3.83
Cthe_00482	flagellar biosynthetic protein FltQ	3.46	3.32	4.86	4.32	-1.4	-1	0.14	0.54	-1.07	-1.31	0.57	-0.3	-1.41	-1.41	2.98
Cthe_02197	Carbohydrate binding family 6	3	3.58	5.04	4.39	-2.04	-0.81	-0.58	0.65	-1.93	-1.08	-1.83	-0.06	-1.41	-1.41	1.37
Cthe_00482	flagellar biosynthetic protein FltQ	3.46	3.32	4.86	4.32	-1.4	-1	0.14	0.54	-1.07	-1.31	0.57	-0.3	-1.41	-1.41	2.98
Cthe_02197	Carbohydrate binding family 6	3	3.58	5.04	4.39	-2.04	-0.81	-0.58	0.65	-1.93	-1.08	-1.83	-0.06	-1.41	-1.41	1.37
Cthe_02197	Carbohydrate binding family 6	3	3.58	5.04	4.39	-2.04	-0.81	-0.58	0.65	-1.93	-1.08	-1.83	-0.06	-1.41	-1.41	1.37
Cthe_00706	transcriptional regulator, RpiR family	10.29	10.38	11.74	11.45	-1.45	-1.07	-0.09	0.29	-1.14	-1.39	-0.2	-0.83	-1.42	-1.42	2.39
Cthe_02002	hypothetical protein	6.58	6.6	8.09	7.29	-1.51	-0.69	-0.02	0.8	-1.22	-0.94	0.03	0.26	-1.42	-1.42	6.69
Cthe_01915	periplasmic sensor signal transduction his	9.66	9.53	11.14	10.42	-1.48	-0.89	0.13	0.72	-1.18	-1.18	0.53	0.09	-1.43	-1.43	3.53
Cthe_02057	CRISPR-associated protein, TM1812 family	9.87	9.7	11.46	10.59	-1.59	-0.89	0.17	0.87	-1.32	-1.18	0.67	0.4	-1.43	-1.43	2.58
Cthe_00167	response regulator receiver protein	7.22	7.18	8.61	8.41	-1.39	-1.23	0.04	0.2	-1.05	-1.58	0.23	-1.02	-1.44	-1.44	2.06
Cthe_03164	two component transcriptional regulator,	10.62	10.54	12.06	11.41	-1.44	-0.87	0.08	0.65	-1.12	-1.15	0.37	-0.06	-1.44	-1.44	4.87
Cthe_01341	Radical SAM	9.72	9.85	11.23	10.65	-1.51	-0.8	-0.13	0.58	-1.22	-1.07	-0.33	-0.21	-1.45	-1.45	4.71
Cthe_00413	glycoside hydrolase, family 9	11.33	11.49	13.07	12.12	-1.74	-0.63	-0.16	0.95	-1.53	-0.87	-0.43	0.57	-1.45	-1.45	2.8
Cthe_03025	hypothetical protein	3	3.7	5.09	4.91	-2.09	-1.21	-0.7	0.18	-2	-1.56	-2.23	-1.06	-1.45	-1.45	1.17
Cthe_01341	Radical SAM	9.72	9.85	11.23	10.65	-1.51	-0.8	-0.13	0.58	-1.22	-1.07	-0.33	-0.21	-1.45	-1.45	4.71
Cthe_01341	Radical SAM	9.72	9.85	11.23	10.65	-1.51	-0.8	-0.13	0.58	-1.22	-1.07	-0.33	-0.21	-1.45	-1.45	4.71
Cthe_01341	Radical SAM	9.72	9.85	11.23	10.65	-1.51	-0.8	-0.13	0.58	-1.22	-1.07	-0.33	-0.21	-1.45	-1.45	4.71
Cthe_03103	2-hydroxyglutaryl-CoA dehydratase, D-co	8.84	8.77	10.23	10.07	-1.39	-1.3	0.07	0.16	-1.05	-1.67	0.33	-1.11	-1.46	-1.46	1.94
Cthe_00702	hypothetical protein	8.94	9	10.57	9.68	-1.63	-0.68	-0.06	0.89	-1.38	-0.93	-0.1	0.45	-1.46	-1.46	4.1
Cthe_01926	intein	5.64	5.86	7.29	6.61	-1.65	-0.75	-0.22	0.68	-1.41	-1.01	-0.63	0	-1.46	-1.46	3.13
Cthe_02286	phage integrase	6.21	6.02	7.59	7.3	-1.38	-1.28	0.19	0.29	-1.04	-1.64	0.73	-0.83	-1.46	-1.46	2
Cthe_00708	FAD dependent oxidoreductase	8.78	8.92	10.29	10.06	-1.51	-1.14	-0.14	0.23	-1.22	-1.48	-0.37	-0.96	-1.47	-1.47	2.12
Cthe_01013	protein of unknown function UPF0118	8.81	8.85	10.46	9.54	-1.65	-0.69	-0.04	0.92	-1.41	-0.94	-0.03	0.51	-1.47	-1.47	3.77
Cthe_00087	maf protein	8.45	8.29	9.82	9.65	-1.37	-1.36	0.16	0.17	-1.03	-1.74	0.63	-1.09	-1.47	-1.47	1.83
Cthe_01830	hypothetical protein	9.46	9.27	10.98	10.26	-1.52	-0.99	0.19	0.72	-1.23	-1.3	0.73	0.09	-1.47	-1.47	2.76
Cthe_03143	hypothetical protein	6.89	7.19	8.6	8.09	-1.71	-0.9	-0.3	0.51	-1.49	-1.19	-0.9	-0.36	-1.48	-1.48	2.24
Cthe_01258	copper amine oxidase-like protein	9.33	9.13	10.75	10.35	-1.42	-1.22	0.2	0.4	-1.09	-1.57	0.77	-0.6	-1.48	-1.48	2.22
Cthe_02975	DNA-directed RNA polymerase sigma fact	4.32	5.13	6.95	5.58	-2.63	-0.45	-0.81	1.37	-2.73	-0.65	-2.6	1.47	-1.49	-1.49	1.07
Cthe_01280	hypothetical protein	2	3	5.04	3.17	-3.04	-0.17	-1	1.87	-3.28	-0.32	-3.23	2.53	-1.49	-1.49	0.91
Cthe_01417	hypothetical protein	7.06	7.18	8.54	9	-1.48	-1.82	-0.12	-0.46	-1.18	-2.29	-0.3	-2.43	-1.5	-1.5	1.2
Cthe_02665	Zn-finger containing protein	6.19	6.77	8.24	7.82	-2.05	-1.05	-0.58	0.42	-1.95	-1.37	-1.83	-0.55	-1.54	-1.53	1.42
Cthe_00403	DNA-directed RNA polymerase sigma fact	9.94	10.05	11.6	10.78	-1.66	-0.73	-0.11	0.82	-1.42	-0.99	-0.27	0.3	-1.55	-1.54	4.87
Cthe_03218	CRISPR-associated protein Cas1	8.58	8.5	10.04	9.54	-1.46	-1.04	0.08	0.5	-1.15	-1.36	0.37	-0.38	-1.55	-1.54	3.82
Cthe_03098	hypothetical protein	2.32	2.81	4.7	3.32	-2.38	-0.51	-0.49	1.38	-2.39	-0.73	-1.53	1.49	-1.56	-1.55	1.33
Cthe_00256	histidine kinase	7.14	7.16	8.63	8.38	-1.49	-1.22	-0.02	0.25	-1.19	-1.57	0.03	-0.91	-1.57	-1.56	2.46
Cthe_00256	histidine kinase	7.14	7.16	8.63	8.38	-1.49	-1.22	-0.02	0.25	-1.19	-1.57	0.03	-0.91	-1.57	-1.56	2.46
Cthe_01395		2.32	2.32	3.81	3.17	-1.49	-0.85	0	0.64	-1.19	-1.13	0.1	-0.09	-1.58	-1.57	13.86
Cthe_03082	hypothetical protein	4.95	4.81	6.44	5.93	-1.49	-1.12	0.14	0.51	-1.19	-1.45	0.57	-0.36	-1.58	-1.57	3.16
Cthe_01233	hypothetical protein	5	5.32	6.75	6.49	-1.75	-1.17	-0.32	0.26	-1.54	-1.51	-0.97	-0.89	-1.58	-1.57	1.86
Cthe_00467	Flagellar biosynthesis/type III secretory	9.01	9.03	10.58	9.81	-1.57	-0.78	-0.02	0.77	-1.3	-1.05	0.03	0.19	-1.59	-1.58	9.87
Cthe_00028	uncharacterized protein, YcgT-like protein	7.97	7.92	9.48	8.83	-1.51	-0.91	0.05	0.65	-1.22	-1.2	0.27	-0.06	-1.59	-1.58	7.03
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_00467	Flagellar biosynthesis/type III secretory	9.01	9.03	10.58	9.81	-1.57	-0.78	-0.02	0.77	-1.3	-1.05	0.03	0.19	-1.59	-1.58	9.87
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_03116	mannose-6-phosphate isomerase, class I	5.09	5.36	7.4	5.91	-2.31	-0.55	-0.27	1.49	-2.3	-0.77	-0.8	1.72	-1.59	-1.58	1.45
Cthe_02371	chromosomal replication initiator protein	10.28	10.43	11.88	11.57	-1.6	-1.14	-0.15	0.31	-1.34	-1.48	-0.4	-0.79	-1.61	-1.6	2.56
Cthe_03062	signal transduction histidine kinase regula	9.86	9.91	11.38	10.81	-1.52	-0.9	-0.05	0.57	-1.23	-1.19	-0.07	-0.23	-1.61	-1.6	8.09
Cthe_02134	RNA related	5.78	6.11	7.64	7	-1.86	-0.89	-0.33	0.64	-1.69	-1.18	-1	-0.09	-1.62	-1.61	2.33
Cthe_02751	hypothetical protein	7.84	7.92	9.4	9.23	-1.56	-1.31	-0.08	0.17	-1.28	-1.68	-0.17	-1.09	-1.63	-1.62	2.18
Cthe_00964	amino acid-binding ACT	10.85	11.24	12.74	12.31	-1.89	-1.07	-0.39	0.43	-1.73	-1.39	-1.2	-0.53	-1.64	-1.63	1.92
Cthe_00477	flagellar motor switch protein FltM	7.69	7.5	9.1	9.42	-1.41	-1.92	0.19	-0.32	-1.08	-2.4	0.73	-2.13	-1.64	-1.63	1.33
Cthe_03089	UspA	9.71	9.66	11.26	10											



Cthe_00962	dihydrodipicolinate synthase	12.19	12.49	13.99	13.54	-1.8	-1.05	-0.3	0.45	-1.61	-1.37	-0.9	-0.49	-1.66	-1.65	2.34
Cthe_01916	two component transcriptional regulator,	9.78	9.59	11.5	10.63	-1.72	-1.04	0.19	0.87	-1.5	-1.36	0.73	0.4	-1.66	-1.65	2.76
Cthe_00962	dihydrodipicolinate synthase	12.19	12.49	13.99	13.54	-1.8	-1.05	-0.3	0.45	-1.61	-1.37	-0.9	-0.49	-1.66	-1.65	2.34
Cthe_00962	dihydrodipicolinate synthase	12.19	12.49	13.99	13.54	-1.8	-1.05	-0.3	0.45	-1.61	-1.37	-0.9	-0.49	-1.66	-1.65	2.34
Cthe_00825	glycoside hydrolase, family 9	10.42	10.52	12.02	11.41	-1.6	-0.89	-0.1	0.61	-1.34	-1.18	-0.23	-0.15	-1.66	-1.65	7.39
Cthe_00962	dihydrodipicolinate synthase	12.19	12.49	13.99	13.54	-1.8	-1.05	-0.3	0.45	-1.61	-1.37	-0.9	-0.49	-1.66	-1.65	2.34
Cthe_00962	dihydrodipicolinate synthase	12.19	12.49	13.99	13.54	-1.8	-1.05	-0.3	0.45	-1.61	-1.37	-0.9	-0.49	-1.66	-1.65	2.34
Cthe_00825	glycoside hydrolase, family 9	10.42	10.52	12.02	11.41	-1.6	-0.89	-0.1	0.61	-1.34	-1.18	-0.23	-0.15	-1.66	-1.65	7.39
Cthe_00962	dihydrodipicolinate synthase	12.19	12.49	13.99	13.54	-1.8	-1.05	-0.3	0.45	-1.61	-1.37	-0.9	-0.49	-1.66	-1.65	2.34
Cthe_00962	dihydrodipicolinate synthase	12.19	12.49	13.99	13.54	-1.8	-1.05	-0.3	0.45	-1.61	-1.37	-0.9	-0.49	-1.66	-1.65	2.34
Cthe_01892	RNA related	6.63	6.48	8.35	7.48	-1.72	-1	0.15	0.87	-1.5	-1.31	0.6	0.4	-1.67	-1.66	3.14
Cthe_00241	hypothetical protein	8.29	8.48	10	9.43	-1.71	-0.95	-0.19	0.57	-1.49	-1.25	-0.53	-0.23	-1.69	-1.68	3.83
Cthe_02550	glycosyltransferase sugar-binding region	4.09	3.46	5.58	5.52	-1.49	-2.06	0.63	0.06	-1.19	-2.57	2.2	-1.32	-1.7	-1.69	1.25
Cthe_01897	hypothetical protein	6.44	6.48	8.01	7.58	-1.57	-1.1	-0.04	0.43	-1.3	-1.43	-0.03	-0.53	-1.7	-1.69	4.14
Cthe_00963	Dihydrodipicolinate reductase	11.49	11.9	13.46	12.94	-1.97	-1.04	-0.41	0.52	-1.84	-1.36	-1.27	-0.34	-1.71	-1.7	1.98
Cthe_00963	Dihydrodipicolinate reductase	11.49	11.9	13.46	12.94	-1.97	-1.04	-0.41	0.52	-1.84	-1.36	-1.27	-0.34	-1.71	-1.7	1.98
Cthe_00963	Dihydrodipicolinate reductase	11.49	11.9	13.46	12.94	-1.97	-1.04	-0.41	0.52	-1.84	-1.36	-1.27	-0.34	-1.71	-1.7	1.98
Cthe_00963	Dihydrodipicolinate reductase	11.49	11.9	13.46	12.94	-1.97	-1.04	-0.41	0.52	-1.84	-1.36	-1.27	-0.34	-1.71	-1.7	1.98
Cthe_00963	Dihydrodipicolinate reductase	11.49	11.9	13.46	12.94	-1.97	-1.04	-0.41	0.52	-1.84	-1.36	-1.27	-0.34	-1.71	-1.7	1.98
Cthe_00963	Dihydrodipicolinate reductase	11.49	11.9	13.46	12.94	-1.97	-1.04	-0.41	0.52	-1.84	-1.36	-1.27	-0.34	-1.71	-1.7	1.98
Cthe_00963	Dihydrodipicolinate reductase	11.49	11.9	13.46	12.94	-1.97	-1.04	-0.41	0.52	-1.84	-1.36	-1.27	-0.34	-1.71	-1.7	1.98
Cthe_01169	Beta-lactamase class A-like protein	8.08	7.77	10.15	8.9	-2.07	-1.13	0.31	1.25	-1.97	-1.46	1.13	1.21	-1.72	-1.71	1.68
Cthe_00404	type 3a, cellulose-binding	10.14	10.22	11.77	11.09	-1.63	-0.87	-0.08	0.68	-1.38	-1.15	-0.17	0	-1.72	-1.71	12.01
Cthe_00480	hypothetical protein	5.29	5.36	6.89	6.38	-1.6	-1.02	-0.07	0.51	-1.34	-1.33	-0.13	-0.36	-1.72	-1.71	5.61
Cthe_01169	Beta-lactamase class A-like protein	8.08	7.77	10.15	8.9	-2.07	-1.13	0.31	1.25	-1.97	-1.46	1.13	1.21	-1.72	-1.71	1.68
Cthe_00043	glycoside hydrolase, family 9	10.74	10.89	12.5	11.75	-1.76	-0.86	-0.15	0.75	-1.55	-1.14	-0.4	0.15	-1.74	-1.73	5.12
Cthe_00703	hypothetical protein	10.46	10.57	12.11	11.74	-1.65	-1.17	-0.11	0.37	-1.41	-1.51	-0.27	-0.66	-1.75	-1.74	3.29
Cthe_00286	response regulator receiver sensor signal	8.72	8.89	10.47	9.82	-1.75	-0.93	-0.17	0.65	-1.54	-1.23	-0.47	-0.06	-1.76	-1.75	4.73
Cthe_00286	response regulator receiver sensor signal	8.72	8.89	10.47	9.82	-1.75	-0.93	-0.17	0.65	-1.54	-1.23	-0.47	-0.06	-1.76	-1.75	4.73
Cthe_00286	response regulator receiver sensor signal	8.72	8.89	10.47	9.82	-1.75	-0.93	-0.17	0.65	-1.54	-1.23	-0.47	-0.06	-1.76	-1.75	4.73
Cthe_02863	intein	4.46	4.86	6.66	5.64	-2.2	-0.78	-0.4	1.02	-2.15	-1.05	-1.23	0.72	-1.77	-1.76	1.91
Cthe_01175	hypothetical protein	6.49	6.66	8.58	7.45	-2.09	-0.79	-0.17	1.13	-2	-1.06	-0.47	0.96	-1.79	-1.78	2.41
Cthe_00281	hypothetical protein	2	2.81	4.81	3.46	-2.81	-0.65	-0.81	1.35	-2.97	-0.89	-2.6	1.43	-1.79	-1.78	1.19
Cthe_01044	hypothetical protein	5.17	5.32	6.99	6.19	-1.82	-0.87	-0.15	0.8	-1.64	-1.15	-0.4	0.26	-1.79	-1.78	4.77
Cthe_00405	glycoside hydrolase, family 5	10.38	10.52	12.23	11.38	-1.85	-0.86	-0.14	0.85	-1.68	-1.14	-0.37	0.36	-1.8	-1.79	4.47
Cthe_00044	cellulosome enzyme, dockerin type I	5.83	6.04	8.36	6.71	-2.53	-0.67	-0.21	1.65	-2.59	-0.92	-0.6	2.06	-1.8	-1.79	1.46
Cthe_00405	glycoside hydrolase, family 5	10.38	10.52	12.23	11.38	-1.85	-0.86	-0.14	0.85	-1.68	-1.14	-0.37	0.36	-1.8	-1.79	4.47
Cthe_00405	glycoside hydrolase, family 5	10.38	10.52	12.23	11.38	-1.85	-0.86	-0.14	0.85	-1.68	-1.14	-0.37	0.36	-1.8	-1.79	4.47
Cthe_03220	CRISPR-associated protein Cas4	7.13	7.01	8.76	8.22	-1.63	-1.21	0.12	0.54	-1.38	-1.56	0.5	-0.3	-1.83	-1.82	4.06
Cthe_02559	DegT/DnrI/EryC1/StrS aminotransferase	7.99	7.97	9.62	9.03	-1.63	-1.06	0.02	0.59	-1.38	-1.38	0.17	-0.19	-1.84	-1.83	8.7
Cthe_02146	copper amine oxidase-like protein	3.46	3.81	6.25	4.39	-2.79	-0.58	-0.35	1.86	-2.95	-0.81	-1.07	2.51	-1.86	-1.85	1.27
Cthe_01272	DNA-directed RNA polymerase sigma fact	4.95	5.17	6.77	6.48	-1.82	-1.31	-0.22	0.29	-1.64	-1.68	-0.63	-0.83	-1.89	-1.88	2.56
Cthe_02761	glycoside hydrolase, family 9	9.14	9.33	10.99	10.34	-1.85	-1.01	-0.19	0.65	-1.68	-1.32	-0.53	-0.06	-1.9	-1.89	4.55
Cthe_01401	hypothetical protein	8.97	9.05	10.69	10.44	-1.72	-1.39	-0.08	0.25	-1.5	-1.77	-0.17	-0.91	-1.91	-1.9	2.85
Cthe_00704	hypothetical protein	10.08	10.23	11.86	11.63	-1.78	-1.4	-0.15	0.23	-1.58	-1.79	-0.4	-0.96	-1.93	-1.92	6.61
Cthe_02808	transcriptional regulator, LacI family	7.34	7.02	9.37	8.34	-2.03	-1.32	0.32	1.03	-1.92	-1.69	1.17	0.74	-1.95	-1.94	2.1
Cthe_01231	Serine-type D-Ala-D-Ala carboxypeptidase	9.49	9.57	11.23	11.05	-1.74	-1.48	-0.08	0.18	-1.53	-1.88	-0.17	-1.06	-1.95	-1.94	2.57
Cthe_01231	Serine-type D-Ala-D-Ala carboxypeptidase	9.49	9.57	11.23	11.05	-1.74	-1.48	-0.08	0.18	-1.53	-1.88	-0.17	-1.06	-1.95	-1.94	2.57
Cthe_01231	Serine-type D-Ala-D-Ala carboxypeptidase	9.49	9.57	11.23	11.05	-1.74	-1.48	-0.08	0.18	-1.53	-1.88	-0.17	-1.06	-1.95	-1.94	2.57
Cthe_01231	Serine-type D-Ala-D-Ala carboxypeptidase	9.49	9.57	11.23	11.05	-1.74	-1.48	-0.08	0.18	-1.53	-1.88	-0.17	-1.06	-1.95	-1.94	2.57
Cthe_01231	Serine-type D-Ala-D-Ala carboxypeptidase	9.49	9.57	11.23	11.05	-1.74	-1.48	-0.08	0.18	-1.53	-1.88	-0.17	-1.06	-1.95	-1.94	2.57
Cthe_01506	metal dependent phosphohydrolase	8.7	8.86	10.68	9.8	-1.98	-0.94	-0.16	0.88	-1.85	-1.24	-0.43	0.43	-1.96	-1.95	4.16
Cthe_01506	metal dependent phosphohydrolase	8.7	8.86	10.68	9.8	-1.98	-0.94	-0.16	0.88	-1.85	-1.24	-0.43	0.43	-1.96	-1.95	4.16
Cthe_01418	hypothetical protein	6.78	6.89	8.53	8.87	-1.75	-1.98	-0.11	-0.34	-1.54	-2.48	-0.27	-2.17	-1.96	-1.95	1.52
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/C	7.86	8	9.67	9.43	-1.81	-1.43	-0.14	0.24	-1.62	-1.82	-0.37	-0.94	-1.99	-1.98	2.74
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/C	7.86	8	9.67	9.43	-1.81	-1.43	-0.14	0.24	-1.62	-1.82	-0.37	-0.94	-1.99	-1.98	2.74
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/C	7.86	8	9.67	9.43	-1.81	-1.43	-0.14	0.24	-1.62	-1.82	-0.37	-0.94	-1.99	-1.98	2.74
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/C	7.86	8	9.67	9.43	-1.81	-1.43	-0.14	0.24	-1.62	-1.82	-0.37	-0.94	-1.99	-1.98	2.74
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/C	7.86	8	9.67	9.43	-1.81	-1.43	-0.14	0.24	-1.62	-1.82	-0.37	-0.94	-1.99	-1.98	2.74
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/C	7.86	8	9.67	9.43	-1.81	-1.43	-0.14	0.24	-1.62	-1.82	-0.37	-0.94	-1.99	-1.98	2.74
Cthe_00965	ATP:corrinoid adenosyltransferase BtuR/C	7.86	8	9.67	9.43	-1.81	-1.43	-0.14	0.24	-1.62	-1.82	-0.37	-0.94	-1.99	-1.98	2.74
Cthe_00556	asparagine synthase [glutamine-hydrolyzi	9.58	9.62	11.31	10.67	-1.73	-1.05	-0.04	0.64	-1.51	-1.37	-0.03	-0.09	-2	-1.99	24.42
Cthe_00191	proteinase inhibitor 14, serpin	9.9	9.91	12.25	10.86	-2.35	-0.95	-0.01	1.39	-2.35	-1.25	0.07	1.51	-2	-1.99	2
Cthe_00556	asparagine synthase [glutamine-hydrolyzi	9.58	9.62	11.31	10.67	-1.73	-1.05	-0.04	0.64	-1.51	-1.37	-0.03	-0.09	-2	-1.99	24.42
Cthe_00556	asparagine synthase [glutamine-hydrolyzi	9.58	9.62	11.31	10.67	-1.73	-1.05	-0.04	0.64	-1.51	-1.37	-0.03	-0.09	-2	-1.99	24.42
Cthe_00623	transcriptional regulators, TraR/DksA fami	7.33	7.48	9.19	8.6	-1.86	-1.12	-0.15	0.59	-1.69	-1.45	-0.4	-0.19	-2.03	-2.02	5.71
Cthe_01045	hypothetical protein	4.64	5	6.71	6.29	-2.07	-1.29	-0.36	0.42	-1.97	-1.65	-1.1	-0.55	-2.03	-2.02	2.37
Cthe_02549	cellulosome enzyme, dockerin type I	7.14	7.01	8.8	9.15	-1.66	-2.14	0.13	-0.35	-1.42	-2.67	0.53	-2.19	-2.03	-2.02	1.53
Cthe_02360	glycoside hydrolase, family 9	10.68	10.76	12.47	11.92	-1.79	-1.16	-0.08	0.55	-1.59	-1.5	-0.17	-0.28	-2.04	-2.03	7.58
Cthe_01438	RNA polymerase, sigma-24 subunit, ECF su	7.48	7.64	9.69	8.58	-2.21	-0.94	-0.16	1.11	-2.16	-1.24	-0.43	0.91	-2.05	-2.04	2.81
Cthe_01170	Dihydrodipicolinate reductase	9.74	9.63	11.86	10.75	-2.12	-1.12	0.11	1.11	-2.04	-1.45	0.47	0.91	-2.05	-2.04	2.78
Cthe_02673	hypothetical protein	5.17	5.04	7.73	6.09	-2.56	-1.05	0.13	1.64	-2.64	-1.37	0.53	2.04	-2.05	-2.04	1.6
Cthe_01170	Dihydrodipicolinate reductase	9.74	9.63	11.86	10.75	-2.12	-1.12	0.11	1.11	-2.04	-1.45	0.47	0.91	-2.05	-2.04	2.78
Cthe_01170	Dihydrodipicolinate reductase	9.74	9.63	11.86	10.75	-2.12	-1.12	0.11	1.11	-2.04	-1.45	0.47	0.91	-2.05	-2.04	2.78
Cthe_01170	Dihydrodipicolinate reductase	9.74	9.63	11.86	10.75	-2.12										



Cthe_00196	glutamine synthetase, catalytic region	10.58	10.85	12.58	12.27	-2	-1.42	-0.27	0.31	-1.88	-1.81	-0.8	-0.79	-2.11	-2.1	2.64
Cthe_00196	glutamine synthetase, catalytic region	10.58	10.85	12.58	12.27	-2	-1.42	-0.27	0.31	-1.88	-1.81	-0.8	-0.79	-2.11	-2.1	2.64
Cthe_00196	glutamine synthetase, catalytic region	10.58	10.85	12.58	12.27	-2	-1.42	-0.27	0.31	-1.88	-1.81	-0.8	-0.79	-2.11	-2.1	2.64
Cthe_00196	glutamine synthetase, catalytic region	10.58	10.85	12.58	12.27	-2	-1.42	-0.27	0.31	-1.88	-1.81	-0.8	-0.79	-2.11	-2.1	2.64
Cthe_00196	glutamine synthetase, catalytic region	10.58	10.85	12.58	12.27	-2	-1.42	-0.27	0.31	-1.88	-1.81	-0.8	-0.79	-2.11	-2.1	2.64
Cthe_00196	glutamine synthetase, catalytic region	10.58	10.85	12.58	12.27	-2	-1.42	-0.27	0.31	-1.88	-1.81	-0.8	-0.79	-2.11	-2.1	2.64
Cthe_00074	RNA polymerase, sigma-24 subunit, ECF su	0	0	2.58	1	-2.58	-1	0	1.58	-2.66	-1.31	0.1	1.91	-2.12	-2.11	1.76
Cthe_00038	chemotaxis protein cheW	3	3.32	5.09	4.64	-2.09	-1.32	-0.32	0.45	-2	-1.69	-0.97	-0.49	-2.14	-2.13	2.74
Cthe_00038	chemotaxis protein cheW	3	3.32	5.09	4.64	-2.09	-1.32	-0.32	0.45	-2	-1.69	-0.97	-0.49	-2.14	-2.13	2.74
Cthe_00705	hypothetical protein	7.61	7.61	9.41	8.79	-1.8	-1.18	0	0.62	-1.61	-1.52	0.1	-0.13	-2.14	-2.13	15.34
Cthe_00406	hypothetical protein	9.38	9.56	11.33	10.75	-1.95	-1.19	-0.18	0.58	-1.81	-1.54	-0.5	-0.21	-2.14	-2.13	4.98
Cthe_00782	putative methyl-accepting chemotaxis sen	2.81	2.58	4.64	4.17	-1.83	-1.59	0.23	0.47	-1.65	-2.01	0.87	-0.45	-2.17	-2.16	3.02
Cthe_02290	ABC transporter related protein	1	2.81	2.81	2.81	-1.81	-2.81	1	0	-1.62	-3.46	3.43	-1.45	-2.18	-2.17	1.17
Cthe_02290	ABC transporter related protein	1	2.81	2.81	2.81	-1.81	-2.81	1	0	-1.62	-3.46	3.43	-1.45	-2.18	-2.17	1.17
Cthe_01922	hypothetical protein	8.59	8.64	10.57	9.74	-1.98	-1.1	-0.05	0.83	-1.85	-1.43	-0.07	0.32	-2.19	-2.18	8.11
Cthe_00168	hypothetical protein	6.46	6.38	8.28	7.95	-1.82	-1.57	0.08	0.33	-1.64	-1.99	0.37	-0.74	-2.21	-2.2	3.54
Cthe_01890	cellulosome enzyme, dockerin type I	10.9	10.58	13.47	11.94	-2.57	-1.36	0.32	1.53	-2.65	-1.74	1.17	1.81	-2.22	-2.21	1.67
Cthe_01820	ABC transporter related protein	2.32	2	4.17	3.81	-1.85	-1.81	0.32	0.36	-1.68	-2.27	1.17	-0.68	-2.23	-2.22	2.37
Cthe_01820	ABC transporter related protein	2.32	2	4.17	3.81	-1.85	-1.81	0.32	0.36	-1.68	-2.27	1.17	-0.68	-2.23	-2.22	2.37
Cthe_01046	extracellular solute-binding protein, fami	7.06	6.95	8.97	8.29	-1.91	-1.34	0.11	0.68	-1.76	-1.71	0.47	0	-2.25	-2.24	5.93
Cthe_01174	protein of unknown function DUF155	8.02	8.01	10.13	9.17	-2.11	-1.16	0.01	0.96	-2.03	-1.5	0.13	0.6	-2.25	-2.24	4.67
Cthe_00682	hypothetical protein	9.6	9.8	11.71	10.94	-2.11	-1.14	-0.2	0.77	-2.03	-1.48	-0.57	0.19	-2.25	-2.24	4.75
Cthe_03144	transcriptional regulator, AraC family	6.34	6.51	8.35	7.75	-2.01	-1.24	-0.17	0.6	-1.89	-1.6	-0.47	-0.17	-2.26	-2.25	5.63
Cthe_00953	aspartate carbamoyltransferase	8.48	8.52	10.39	10.22	-1.91	-1.7	-0.04	0.17	-1.76	-2.14	-0.03	-1.09	-2.29	-2.28	2.89
Cthe_02145	RNA related	6.13	6.19	8.55	7.29	-2.42	-1.1	-0.06	1.26	-2.45	-1.43	-0.1	1.23	-2.29	-2.28	2.61
Cthe_01891	hypothetical protein	6.15	6.09	8.18	7.33	-2.03	-1.24	0.06	0.85	-1.92	-1.6	0.3	0.36	-2.29	-2.28	6.06
Cthe_00953	aspartate carbamoyltransferase	8.48	8.52	10.39	10.22	-1.91	-1.7	-0.04	0.17	-1.76	-2.14	-0.03	-1.09	-2.29	-2.28	2.89
Cthe_00953	aspartate carbamoyltransferase	8.48	8.52	10.39	10.22	-1.91	-1.7	-0.04	0.17	-1.76	-2.14	-0.03	-1.09	-2.29	-2.28	2.89
Cthe_00953	aspartate carbamoyltransferase	8.48	8.52	10.39	10.22	-1.91	-1.7	-0.04	0.17	-1.76	-2.14	-0.03	-1.09	-2.29	-2.28	2.89
Cthe_02138	glycoside hydrolase, family 43	5.43	5.67	8.2	6.64	-2.77	-0.97	-0.24	1.56	-2.92	-1.27	-0.7	1.87	-2.31	-2.3	1.81
Cthe_00954	Uracil phosphoribosyltransferase	10.38	10.06	12.28	11.9	-1.9	-1.84	0.32	0.38	-1.74	-2.31	1.17	-0.64	-2.31	-2.3	2.46
Cthe_00476	hypothetical protein	8.33	8.07	10.15	10.18	-1.82	-2.11	0.26	-0.03	-1.64	-2.63	0.97	-1.51	-2.31	-2.3	1.96
Cthe_00954	Uracil phosphoribosyltransferase	10.38	10.06	12.28	11.9	-1.9	-1.84	0.32	0.38	-1.74	-2.31	1.17	-0.64	-2.31	-2.3	2.46
Cthe_00954	Uracil phosphoribosyltransferase	10.38	10.06	12.28	11.9	-1.9	-1.84	0.32	0.38	-1.74	-2.31	1.17	-0.64	-2.31	-2.3	2.46
Cthe_00954	Uracil phosphoribosyltransferase	10.38	10.06	12.28	11.9	-1.9	-1.84	0.32	0.38	-1.74	-2.31	1.17	-0.64	-2.31	-2.3	2.46
Cthe_00244	heavy metal translocating P-type ATPase	11.09	11.02	13.28	12.26	-2.19	-1.24	0.07	1.02	-2.14	-1.6	0.33	0.72	-2.32	-2.31	3.83
Cthe_00244	heavy metal translocating P-type ATPase	11.09	11.02	13.28	12.26	-2.19	-1.24	0.07	1.02	-2.14	-1.6	0.33	0.72	-2.32	-2.31	3.83
Cthe_00244	heavy metal translocating P-type ATPase	11.09	11.02	13.28	12.26	-2.19	-1.24	0.07	1.02	-2.14	-1.6	0.33	0.72	-2.32	-2.31	3.83
Cthe_00244	heavy metal translocating P-type ATPase	11.09	11.02	13.28	12.26	-2.19	-1.24	0.07	1.02	-2.14	-1.6	0.33	0.72	-2.32	-2.31	3.83
Cthe_02760	glycoside hydrolase, family 9	9.12	9.22	11.15	10.45	-2.03	-1.23	-0.1	0.7	-1.92	-1.58	-0.23	0.04	-2.38	-2.37	12.1
Cthe_02972	glycoside hydrolase, family 11	11.81	12.11	14.53	13.18	-2.72	-1.07	-0.3	1.35	-2.85	-1.39	-0.9	1.43	-2.43	-2.42	2.13
Cthe_00736	cellulosome anchoring protein, cohesin re	10.44	10.67	12.57	12.63	-2.13	-1.96	-0.23	-0.06	-2.05	-2.45	-0.67	-1.57	-2.44	-2.43	2.13
Cthe_00533	Radical SAM	7.91	7.91	10.32	9.16	-2.41	-1.25	0	1.16	-2.43	-1.61	0.1	1.02	-2.46	-2.45	3.23
Cthe_00533	Radical SAM	7.91	7.91	10.32	9.16	-2.41	-1.25	0	1.16	-2.43	-1.61	0.1	1.02	-2.46	-2.45	3.23
Cthe_00533	Radical SAM	7.91	7.91	10.32	9.16	-2.41	-1.25	0	1.16	-2.43	-1.61	0.1	1.02	-2.46	-2.45	3.23
Cthe_00245	transcriptional regulator, ArsR family	10.49	10.15	12.71	11.83	-2.22	-1.68	0.34	0.88	-2.18	-2.12	1.23	0.43	-2.47	-2.46	2.65
Cthe_02395	transcriptional regulator, XRE family	4	4.46	6.73	5.61	-2.73	-1.15	-0.46	1.12	-2.86	-1.49	-1.43	0.94	-2.47	-2.46	2.14
Cthe_02200	hypothetical protein	1	1	3	2.58	-2	-1.58	0	0.42	-1.88	-2	0.1	-0.55	-2.5	-2.49	5.58
Cthe_00219	5-nitroimidazole antibiotic resistance prot	6	6.11	8.08	8	-2.08	-1.89	-0.11	0.08	-1.99	-2.37	-0.27	-1.28	-2.52	-2.5	2.69
Cthe_02590	glycoside hydrolase, family 10	9.71	9.79	11.92	11.05	-2.21	-1.26	-0.08	0.87	-2.16	-1.62	-0.17	0.4	-2.51	-2.5	7.06
Cthe_00147	protein of unknown function DUF523	6.94	7.17	9.17	8.57	-2.23	-1.4	-0.23	0.6	-2.19	-1.79	-0.67	-0.17	-2.52	-2.5	4.65
Cthe_00966	hypothetical protein	5	4.75	7.12	6.44	-2.12	-1.69	0.25	0.68	-2.04	-2.13	0.93	0	-2.54	-2.52	3.6
Cthe_01834	hypothetical protein	8.1	8.03	10.13	9.58	-2.03	-1.55	0.07	0.55	-1.92	-1.96	0.33	-0.28	-2.55	-2.53	7.2
Cthe_03029	CheW protein	1.58	2.58	4.7	4.25	-3.12	-1.67	-1	0.45	-3.39	-2.11	-3.23	-0.49	-2.56	-2.54	1.39
Cthe_03029	CheW protein	1.58	2.58	4.7	4.25	-3.12	-1.67	-1	0.45	-3.39	-2.11	-3.23	-0.49	-2.56	-2.54	1.39
Cthe_01273	alpha-L-arabinofuranosidase B	7.74	7.84	10.22	9.11	-2.48	-1.27	-0.1	1.11	-2.53	-1.63	-0.23	0.91	-2.6	-2.58	3.64
Cthe_02812	glycoside hydrolase, family 9	10.81	11.08	13.13	12.57	-2.32	-1.49	-0.27	0.56	-2.31	-1.89	-0.8	-0.26	-2.61	-2.59	4.03
Cthe_01832	hypothetical protein	10.22	10.22	12.28	11.78	-2.06	-1.56	0	0.5	-1.96	-1.98	0.1	-0.38	-2.61	-2.59	8.06
Cthe_01833	copper amine oxidase-like protein	7.52	7.83	10.11	9.1	-2.59	-1.27	-0.31	1.01	-2.68	-1.63	-0.93	0.7	-2.62	-2.6	3.06
Cthe_02807	glycoside hydrolase, family 5	7.76	7.39	10.35	9.09	-2.59	-1.7	0.37	1.26	-2.68	-2.14	1.33	1.23	-2.63	-2.61	2.15
Cthe_02807	glycoside hydrolase, family 5	7.76	7.39	10.35	9.09	-2.59	-1.7	0.37	1.26	-2.68	-2.14	1.33	1.23	-2.63	-2.61	2.15
Cthe_02807	glycoside hydrolase, family 5	7.76	7.39	10.35	9.09	-2.59	-1.7	0.37	1.26	-2.68	-2.14	1.33	1.23	-2.63	-2.61	2.15
Cthe_00625	glycoside hydrolase, family 9	12.46	12.63	14.79	14.02	-2.33	-1.39	-0.17	0.77	-2.32	-1.77	-0.47	0.19	-2.7	-2.68	6.54
Cthe_01921	transcriptional regulator, PadR-like family	7.97	7.92	10.54	9.34	-2.57	-1.42	0.05	1.2	-2.65	-1.81	0.27	1.11	-2.71	-2.69	3.19
Cthe_00753	hypothetical protein	6.55	6.49	8.67	8.12	-2.12	-1.63	0.06	0.55	-2.04	-2.06	0.3	-0.28	-2.72	-2.7	8.03
Cthe_03077	cellulosome anchoring protein, cohesin re	15.15	15.3	17.44	16.75	-2.29	-1.45	-0.15	0.69	-2.27	-1.85	-0.4	0.02	-2.75	-2.73	8.31
Cthe_00469	flagellar export protein FljI	5.78	5.61	8.09	7.26	-2.31	-1.65	0.17	0.83	-2.3	-2.08	0.67	0.32	-2.77	-2.75	4.75
Cthe_00469	flagellar export protein FljI	5.78	5.61	8.09	7.26	-2.31	-1.65	0.17	0.83	-2.3	-2.08	0.67	0.32	-2.77	-2.75	4.75
Cthe_00469	flagellar export protein FljI	5.78	5.61	8.09	7.26	-2.31	-1.65	0.17	0.83	-2.3	-2.08	0.67	0.32	-2.77	-2.75	4.75
Cthe_03229	transposase, IS4	6.07	6.39	8.52	8.07	-2.45	-1.68	-0.32	0.45	-2.49	-2.12	-0.97	-0.49	-2.79	-2.77	3.42
Cthe_00169	dehydrogenase (flavoproteins)	6.86	6.87	9.03	8.48	-2.17	-1.61	-0.01	0.55	-2.11	-2.04	0.07	-0.28	-2.81	-2.79	11.56
Cthe_01821	inner-membrane translocator	2	3	5.46	4.46	-3.46	-1.46	-1	1	-3.85	-1.86	-3.23	0.68	-2.82	-2.8	1.47
Cthe_01821	inner-membrane translocator	2	3	5.46	4.46	-3.46	-1.46	-1	1	-3.85	-1.86	-3.23	0.68	-2.82	-2.8	1.47
Cthe_00412	glycoside hydrolase, family 9	13.42	13.55	15.72	15.21	-2.3	-1.66	-0.13	0.51	-2.28	-2.1	-0.33	-0.36	-2.88	-2.86	7.21
Cthe_01402	iron (metal) dependent repressor, DtxR fa	6.98	7.09	9.27	8.85	-2.29	-1.76	-0.11	0.42	-2.27	-2.21	-0.27	-0.55	-2.9	-2.88	5.88
Cthe_00752	hypothetical protein	4.32	4.81	7.03	6.67	-2.71	-1.86	-0.49	0.36	-2.84	-2.33	-1.53	-0.68	-2.9		



Cthe_00683	diaminopimelate decarboxylase	11.09	11.01	13.79	13.49	-2.7	-2.48	0.08	0.3	-2.82	-3.07	0.37	-0.81	-3.78	-3.75	5.32
Cthe_00683	diaminopimelate decarboxylase	11.09	11.01	13.79	13.49	-2.7	-2.48	0.08	0.3	-2.82	-3.07	0.37	-0.81	-3.78	-3.75	5.32
Cthe_00683	diaminopimelate decarboxylase	11.09	11.01	13.79	13.49	-2.7	-2.48	0.08	0.3	-2.82	-3.07	0.37	-0.81	-3.78	-3.75	5.32
Cthe_01823	Extracellular ligand-binding receptor	4.46	5.17	8.08	7.39	-3.62	-2.22	-0.71	0.69	-4.07	-2.76	-2.27	0.02	-3.92	-3.89	2.46
Cthe_01823	Extracellular ligand-binding receptor	4.46	5.17	8.08	7.39	-3.62	-2.22	-0.71	0.69	-4.07	-2.76	-2.27	0.02	-3.92	-3.89	2.46
Cthe_00797	glycoside hydrolase, family 5	7.08	7.47	10.24	9.82	-3.16	-2.35	-0.39	0.42	-3.45	-2.92	-1.2	-0.55	-3.94	-3.91	3.89
Cthe_00754	hypothetical protein	7.41	7.32	10.35	10	-2.94	-2.68	0.09	0.35	-3.15	-3.31	0.4	-0.7	-4.21	-4.18	6.44
Cthe_00624	glycoside hydrolase, family 9-like Ig-like	10.65	10.72	13.66	12.99	-3.01	-2.27	-0.07	0.67	-3.24	-2.82	-0.13	-0.02	-4.24	-4.21	37.11
Cthe_01822	inner-membrane translocator	3	1.58	6.43	6.07	-3.43	-4.49	1.42	0.36	-3.81	-5.46	4.83	-0.68	-4.51	-4.48	1.55
Cthe_01822	inner-membrane translocator	3	1.58	6.43	6.07	-3.43	-4.49	1.42	0.36	-3.81	-5.46	4.83	-0.68	-4.51	-4.48	1.55
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00755	aminotransferase, class I and II	12.15	12.3	15.38	15.18	-3.23	-2.88	-0.15	0.2	-3.54	-3.55	-0.4	-1.02	-4.53	-4.5	5.2
Cthe_00199	4Fe-4S ferredoxin, iron-sulfur binding	3.91	3.17	7.28	6.7	-3.37	-3.53	0.74	0.58	-3.73	-4.32	2.57	-0.21	-4.57	-4.53	2.52
Cthe_02089	glycoside hydrolase, family 48	13.28	13.45	16.91	15.84	-3.63	-2.39	-0.17	1.07	-4.08	-2.96	-0.47	0.83	-4.62	-4.58	6.01
Cthe_03100	Diaminopimelate epimerase	7.79	7.43	11.11	10.59	-3.32	-3.16	0.36	0.52	-3.66	-3.88	1.3	-0.34	-4.74	-4.7	4.51
Cthe_03100	Diaminopimelate epimerase	7.79	7.43	11.11	10.59	-3.32	-3.16	0.36	0.52	-3.66	-3.88	1.3	-0.34	-4.74	-4.7	4.51
Cthe_03100	Diaminopimelate epimerase	7.79	7.43	11.11	10.59	-3.32	-3.16	0.36	0.52	-3.66	-3.88	1.3	-0.34	-4.74	-4.7	4.51
Cthe_03100	Diaminopimelate epimerase	7.79	7.43	11.11	10.59	-3.32	-3.16	0.36	0.52	-3.66	-3.88	1.3	-0.34	-4.74	-4.7	4.51
Cthe_03100	Diaminopimelate epimerase	7.79	7.43	11.11	10.59	-3.32	-3.16	0.36	0.52	-3.66	-3.88	1.3	-0.34	-4.74	-4.7	4.51
Cthe_03100	Diaminopimelate epimerase	7.79	7.43	11.11	10.59	-3.32	-3.16	0.36	0.52	-3.66	-3.88	1.3	-0.34	-4.74	-4.7	4.51
Cthe_00197	glutamine amidotransferase, class-II	7.64	7.61	11.27	10.74	-3.63	-3.13	0.03	0.53	-4.08	-3.85	0.2	-0.32	-5.44	-5.4	16.89
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_00198	Glutamate synthase (NADPH)	6.02	6.32	10.05	9.63	-4.03	-3.31	-0.3	0.42	-4.62	-4.06	-0.9	-0.55	-5.69	-5.64	6.63
Cthe_02811	glycoside hydrolase, family 26	9.05	8.9	13.03	12.41	-3.98	-3.51	0.15	0.62	-4.55	-4.3	0.6	-0.13	-5.99	-5.94	11.59
Cthe_03102	cell envelope-related transcriptional atten	7.9	7.97	11.96	11.72	-4.06	-3.75	-0.07	0.24	-4.66	-4.58	-0.13	-0.94	-6.12	-6.07	7.82
Cthe_03101	aminotransferase, class I and II	7.92	8.05	12.22	11.98	-4.3	-3.93	-0.13	0.24	-4.99	-4.8	-0.33	-0.94	-6.49	-6.44	7.9
Cthe_03101	aminotransferase, class I and II	7.92	8.05	12.22	11.98	-4.3	-3.93	-0.13	0.24	-4.99	-4.8	-0.33	-0.94	-6.49	-6.44	7.9
Cthe_03101	aminotransferase, class I and II	7.92	8.05	12.22	11.98	-4.3	-3.93	-0.13	0.24	-4.99	-4.8	-0.33	-0.94	-6.49	-6.44	7.9
Cthe_00821	coagulation factor 5/8 type-like protein	4.7	4.64	11.11	10.44	-6.41	-5.8	0.06	0.67	-7.84	-7.02	0.3	-0.02	-10.39	-10.3	39.77











Cthe_00229 NAD-dependent epimerase/dehydr	11.22	11.88	9.7	9.77	1.52	2.11	-0.66	-0.07	1.77	1.81	-0.13	-0.31	2.44	2.1	13.45
Cthe_00229 NAD-dependent epimerase/dehydr	11.22	11.88	9.7	9.77	1.52	2.11	-0.66	-0.07	1.77	1.81	-0.13	-0.31	2.44	2.1	13.45
Cthe_00229 NAD-dependent epimerase/dehydr	11.22	11.88	9.7	9.77	1.52	2.11	-0.66	-0.07	1.77	1.81	-0.13	-0.31	2.44	2.1	13.45
Cthe_00229 NAD-dependent epimerase/dehydr	11.22	11.88	9.7	9.77	1.52	2.11	-0.66	-0.07	1.77	1.81	-0.13	-0.31	2.44	2.1	13.45
Cthe_00951 orotidine 5'-phosphate decarboxyla	9.37	10.03	7.03	7.94	2.34	2.09	-0.66	-0.91	2.42	1.79	-0.13	-2.06	2.43	2.09	2.6
Cthe_00951 orotidine 5'-phosphate decarboxyla	9.37	10.03	7.03	7.94	2.34	2.09	-0.66	-0.91	2.42	1.79	-0.13	-2.06	2.43	2.09	2.6
Cthe_00951 orotidine 5'-phosphate decarboxyla	9.37	10.03	7.03	7.94	2.34	2.09	-0.66	-0.91	2.42	1.79	-0.13	-2.06	2.43	2.09	2.6
Cthe_00951 orotidine 5'-phosphate decarboxyla	9.37	10.03	7.03	7.94	2.34	2.09	-0.66	-0.91	2.42	1.79	-0.13	-2.06	2.43	2.09	2.6
Cthe_02798 putative endoribonuclease L-PSP	9.63	10.23	8.31	7.92	1.32	2.31	-0.6	0.39	1.61	1.97	0.07	0.65	2.36	2.03	6.95
Cthe_00228 hypothetical protein	10.51	11.1	9.22	9.11	1.29	1.99	-0.59	0.11	1.59	1.7	0.1	0.06	2.3	1.98	35.64
Cthe_01482 Cof-like hydrolase	11.05	11.78	9.78	9.67	1.27	2.11	-0.73	0.11	1.57	1.81	-0.37	0.06	2.29	1.97	11.41
Cthe_00786 3-dehydroquininate synthase	12.71	13.4	11.5	11.09	1.21	2.31	-0.69	0.41	1.52	1.97	-0.23	0.69	2.28	1.97	6.11
Cthe_00786 3-dehydroquininate synthase	12.71	13.4	11.5	11.09	1.21	2.31	-0.69	0.41	1.52	1.97	-0.23	0.69	2.28	1.97	6.11
Cthe_00786 3-dehydroquininate synthase	12.71	13.4	11.5	11.09	1.21	2.31	-0.69	0.41	1.52	1.97	-0.23	0.69	2.28	1.97	6.11
Cthe_00786 3-dehydroquininate synthase	12.71	13.4	11.5	11.09	1.21	2.31	-0.69	0.41	1.52	1.97	-0.23	0.69	2.28	1.97	6.11
Cthe_00786 3-dehydroquininate synthase	12.71	13.4	11.5	11.09	1.21	2.31	-0.69	0.41	1.52	1.97	-0.23	0.69	2.28	1.97	6.11
Cthe_00947 dihydroorotate dehydrogenase fam	8.79	9.53	7.32	7.53	1.47	2	-0.74	-0.21	1.73	1.71	-0.4	-0.6	2.23	1.92	6.02
Cthe_00947 dihydroorotate dehydrogenase fam	8.79	9.53	7.32	7.53	1.47	2	-0.74	-0.21	1.73	1.71	-0.4	-0.6	2.23	1.92	6.02
Cthe_00947 dihydroorotate dehydrogenase fam	8.79	9.53	7.32	7.53	1.47	2	-0.74	-0.21	1.73	1.71	-0.4	-0.6	2.23	1.92	6.02
Cthe_00947 dihydroorotate dehydrogenase fam	8.79	9.53	7.32	7.53	1.47	2	-0.74	-0.21	1.73	1.71	-0.4	-0.6	2.23	1.92	6.02
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00946 Phosphoglycerate mutase	9.75	10.65	8.26	8.5	1.49	2.15	-0.9	-0.24	1.75	1.84	-0.93	-0.67	2.22	1.91	3.96
Cthe_00617 AAA ATPase, central region	13.34	13.74	11.77	11.85	1.57	1.89	-0.4	-0.08	1.81	1.62	0.73	-0.33	2.2	1.9	5.41
Cthe_00954 Uracil phosphoribosyltransferase	10.48	10.67	8.32	8.9	2.16	1.77	-0.19	-0.58	2.28	1.52	1.43	-1.37	2.19	1.89	2.47
Cthe_00954 Uracil phosphoribosyltransferase	10.48	10.67	8.32	8.9	2.16	1.77	-0.19	-0.58	2.28	1.52	1.43	-1.37	2.19	1.89	2.47
Cthe_00954 Uracil phosphoribosyltransferase	10.48	10.67	8.32	8.9	2.16	1.77	-0.19	-0.58	2.28	1.52	1.43	-1.37	2.19	1.89	2.47
Cthe_00954 Uracil phosphoribosyltransferase	10.48	10.67	8.32	8.9	2.16	1.77	-0.19	-0.58	2.28	1.52	1.43	-1.37	2.19	1.89	2.47
Cthe_00948 oxidoreductase FAD/NAD(P)-bindin	9.81	10.66	8.3	8.62	1.51	2.04	-0.85	-0.32	1.76	1.75	-0.77	-0.83	2.16	1.86	3.91
Cthe_00948 oxidoreductase FAD/NAD(P)-bindin	9.81	10.66	8.3	8.62	1.51	2.04	-0.85	-0.32	1.76	1.75	-0.77	-0.83	2.16	1.86	3.91
Cthe_00324 valyl-tRNA synthetase	11.98	12.53	10.7	10.71	1.28	1.82	-0.55	-0.01	1.58	1.56	0.23	-0.19	2.14	1.84	13.29
Cthe_00324 valyl-tRNA synthetase	11.98	12.53	10.7	10.71	1.28	1.82	-0.55	-0.01	1.58	1.56	0.23	-0.19	2.14	1.84	13.29
Cthe_00324 valyl-tRNA synthetase	11.98	12.53	10.7	10.71	1.28	1.82	-0.55	-0.01	1.58	1.56	0.23	-0.19	2.14	1.84	13.29
Cthe_00324 valyl-tRNA synthetase	11.98	12.53	10.7	10.71	1.28	1.82	-0.55	-0.01	1.58	1.56	0.23	-0.19	2.14	1.84	13.29
Cthe_00324 valyl-tRNA synthetase	11.98	12.53	10.7	10.71	1.28	1.82	-0.55	-0.01	1.58	1.56	0.23	-0.19	2.14	1.84	13.29
Cthe_00619 FeoA	12.43	13.18	11.45	10.6	0.98	2.58	-0.75	0.85	1.34	2.2	-0.43	1.6	2.11	1.82	2.78
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00138 Phosphoglycerate kinase	15.87	16.43	14.73	14.57	1.14	1.86	-0.56	0.16	1.47	1.59	0.2	0.17	2.09	1.8	14.73
Cthe_00945 metallophosphoesterase	10.14	10.82	8.34	9.01	1.8	1.81	-0.68	-0.67	1.99	1.55	-0.2	-1.56	2.08	1.79	2.86
Cthe_02008 conserved hypothetical protein, CF	3.7	5.13	2.58	2.32	1.12	2.81	-1.43	0.26	1.45	2.4	-2.7	0.38	2.04	1.76	1.84
Cthe_01302 hypothetical protein	12.92	13.48	11.68	11.76	1.24	1.72	-0.56	-0.08	1.55	1.47	0.2	-0.33	2.03	1.75	9.89
Cthe_00952 dihydroorotase, multifunctional co	10.42	11	8.89	9.29	1.53	1.71	-0.58	-0.4	1.78	1.47	0.13	-1	2.03	1.75	4.09
Cthe_00952 dihydroorotase, multifunctional co	10.42	11	8.89	9.29	1.53	1.71	-0.58	-0.4	1.78	1.47	0.13	-1	2.03	1.75	4.09
Cthe_00952 dihydroorotase, multifunctional co	10.42	11	8.89	9.29	1.53	1.71	-0.58	-0.4	1.78	1.47	0.13	-1	2.03	1.75	4.09
Cthe_01302 hypothetical protein	12.92	13.48	11.68	11.76	1.24	1.72	-0.56	-0.08	1.55	1.47	0.2	-0.33	2.03	1.75	9.89
Cthe_00952 dihydroorotase, multifunctional co	10.42	11	8.89	9.29	1.53	1.71	-0.58	-0.4	1.78	1.47	0.13	-1	2.03	1.75	4.09
Cthe_00944 SMC protein-like protein	10.07	10.6	8.34	8.94	1.73	1.66	-0.53	-0.6	1.94	1.42	0.3	-1.42	2	1.72	2.96
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03												



Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_02579 iron-containing alcohol dehydrogen	11.11	11.72	10.03	10.04	1.08	1.68	-0.61	-0.01	1.42	1.44	0.03	-0.19	1.97	1.7	18.77
Cthe_00860 Rubrerythrin	12.72	13.34	11.66	11.67	1.06	1.67	-0.62	-0.01	1.4	1.43	0	-0.19	1.95	1.68	18.81
Cthe_01243 GCN5-related N-acetyltransferase	9.81	10.16	8.31	8.52	1.5	1.64	-0.35	-0.21	1.75	1.41	0.9	-0.6	1.94	1.67	3.71
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02801 carbon-monoxide dehydrogenase,	7.89	8.79	6.88	6.78	1.01	2.01	-0.9	0.1	1.37	1.72	-0.93	0.04	1.94	1.67	4.22
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49	1.29	1.75	-0.07	0.85	1.94	1.67	4.55
Cthe_02797 thiamine pyrophosphate enzyme-li	11.04	11.68	10.12	9.63	0.92	2.05	-0.64	0.49							



Cthe_00290 Homoserine dehydrogenase	12.36	13.1	11.65	11.46	0.71	1.64	-0.74	0.19	1.13	1.41	-0.4	0.23	1.68	1.45	6.99
Cthe_01308 pyruvate, phosphate dikinase	14.85	15.51	14.15	13.77	0.7	1.74	-0.66	0.38	1.12	1.49	-0.13	0.63	1.68	1.45	5.17
Cthe_01308 pyruvate, phosphate dikinase	14.85	15.51	14.15	13.77	0.7	1.74	-0.66	0.38	1.12	1.49	-0.13	0.63	1.68	1.45	5.17
Cthe_01308 pyruvate, phosphate dikinase	14.85	15.51	14.15	13.77	0.7	1.74	-0.66	0.38	1.12	1.49	-0.13	0.63	1.68	1.45	5.17
Cthe_00290 Homoserine dehydrogenase	12.36	13.1	11.65	11.46	0.71	1.64	-0.74	0.19	1.13	1.41	-0.4	0.23	1.68	1.45	6.99
Cthe_01439 hypothetical protein	1.58	0	1.58	0	0	0	1.58	1.58	0.56	0.02	7.33	3.13	1.67	1.44	0.13
Cthe_03156 methyl-accepting chemotaxis senso	10.24	10.71	9.41	9.05	0.83	1.66	-0.47	0.36	1.22	1.42	0.5	0.58	1.66	1.43	4.37
Cthe_03156 methyl-accepting chemotaxis senso	10.24	10.71	9.41	9.05	0.83	1.66	-0.47	0.36	1.22	1.42	0.5	0.58	1.66	1.43	4.37
Cthe_00943 hypothetical protein	6.89	7.38	5.55	6.02	1.34	1.36	-0.49	-0.47	1.63	1.17	0.43	-1.15	1.66	1.43	2.92
Cthe_01491 transcriptional regulator, PadR-like	4.52	5.39	3.7	3.7	0.82	1.69	-0.87	0	1.21	1.45	-0.83	-0.17	1.65	1.42	3.98
Cthe_02525 glutamyl-tRNA reductase	10.72	11.22	9.15	9.89	1.57	1.33	-0.5	-0.74	1.81	1.14	0.4	-1.71	1.65	1.42	2.18
Cthe_00013 hypothetical protein	7.48	8.1	6.29	6.69	1.19	1.41	-0.62	-0.4	1.51	1.21	0	-1	1.65	1.42	3.46
Cthe_02471 hypothetical protein	1	0	1.58	0	-0.58	0	1	1.58	0.1	0.02	5.4	3.13	1.65	1.42	0.03
Cthe_02525 glutamyl-tRNA reductase	10.72	11.22	9.15	9.89	1.57	1.33	-0.5	-0.74	1.81	1.14	0.4	-1.71	1.65	1.42	2.18
Cthe_02525 glutamyl-tRNA reductase	10.72	11.22	9.15	9.89	1.57	1.33	-0.5	-0.74	1.81	1.14	0.4	-1.71	1.65	1.42	2.18
Cthe_02525 glutamyl-tRNA reductase	10.72	11.22	9.15	9.89	1.57	1.33	-0.5	-0.74	1.81	1.14	0.4	-1.71	1.65	1.42	2.18
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00673 ribonuclease H	9.52	10.16	8.83	8.68	0.69	1.48	-0.64	0.15	1.11	1.27	-0.07	0.15	1.64	1.41	18.2
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00673 ribonuclease H	9.52	10.16	8.83	8.68	0.69	1.48	-0.64	0.15	1.11	1.27	-0.07	0.15	1.64	1.41	18.2
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_00137 glyceraldehyde-3-phosphate dehyd	17.64	18.21	16.94	16.46	0.7	1.75	-0.57	0.48	1.12	1.5	0.17	0.83	1.63	1.41	3.95
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_01028 acetate kinase	11.24	11.82	10.38	10.43	0.86	1.39	-0.58	-0.05	1.25	1.19	0.13	-0.27	1.64	1.41	10.28
Cthe_00561 ApbE-like lipoprotein	10.55	10.95	9.33	9.61	1.22	1.34	-0.4	-0.28	1.53	1.15	0.73	-0.75	1.62	1.4	3.27
Cthe_03118 hemerythrin-like metal-binding pro	11.74	12.35	10.81	10.97	0.93	1.38	-0.61	-0.16	1.3	1.19	0.03	-0.5	1.62	1.4	6.28
Cthe_03119 flavin reductase-like, FMN-binding	11.8	12.51	11.12	11.01	0.68	1.5	-0.71	0.11	1.1	1.29	-0.3	0.06	1.61	1.39	9.9
Cthe_03109 Uracil-DNA glycosylase superfamily	9.48	10.02	8.73	8.56	0.75	1.46	-0.54	0.17	1.16	1.25	0.27	0.19	1.61	1.39	9.22
Cthe_03119 flavin reductase-like, FMN-binding	11.8	12.51	11.12	11.01	0.68	1.5	-0.71	0.11	1.1	1.29	-0.3	0.06	1.61	1.39	9.9
Cthe_03109 Uracil-DNA glycosylase superfamily	9.48	10.02	8.73	8.56	0.75	1.46	-0.54	0.17	1.16	1.25	0.27	0.19	1.61	1.39	9.22
Cthe_00562 protein of unknown function DUF1	8.44	8.97	7.45	7.65	0.99	1.32	-0.53	-0.2	1.35	1.14	0.3	-0.58	1.58	1.36	4.83
Cthe_01098 hypothetical protein	14.81	15.36	14.13	13.84	0.68	1.52	-0.55	0.29	1.1	1.31	0.23	0.44	1.57	1.35	6.15
Cthe_01112 transcriptional regulator, ArsR fami	4.46	5.17	3.91	3.46	0.55	1.71	-0.71	0.45	1	1.47	-0.3	0.77	1.55	1.34	3.84
Cthe_03017 hydrogenase accessory protein Hyp	10.87	11.62	10.31	9.94	0.56	1.68	-0.75	0.37	1.01	1.44	-0.43	0.6	1.55	1.34	4.25
Cthe_00106 GTP cyclohydrolase II	12.44	13.37	11.82	11.58	0.62	1.79	-0.93	0.24	1.06	1.53	-1.03	0.33	1.56	1.34	3.07
Cthe_00331 hypothetical protein	7.55	8.12	6.89	6.66	0.66	1.46	-0.57	0.23	1.09	1.25	0.17	0.31	1.56	1.34	8.38
Cthe_01946 FAD-dependent pyridine nucleotid	12.7	13.43	12.12	11.81	0.58	1.62	-0.73	0.31	1.02	1.39	-0.37	0.48	1.55	1.34	5.08
Cthe_03017 hydrogenase accessory protein Hyp	10.87	11.62	10.31	9.94	0.56	1.68	-0.75	0.37	1.01	1.44	-0.43	0.6	1.55	1.34	4.25
Cthe_00106 GTP cyclohydrolase II	12.44	13.37	11.82	11.58	0.62	1.79	-0.93	0.24	1.06	1.53	-1.03	0.33	1.56	1.34	3.07
Cthe_01946 FAD-dependent pyridine nucleotid	12.7	13.43	12.12	11.81	0.58	1.62	-0.73	0.31	1.02	1.39	-0.37	0.48	1.55	1.34	5.08
Cthe_00106 GTP cyclohydrolase II	12.44	13.37	11.82	11.58	0.62	1.79	-0.93	0.24	1.06	1.53	-1.03	0.33	1.56	1.34	3.07
Cthe_00106 GTP cyclohydrolase II	12.44	13.37	11.82	11.58	0.62	1.79	-0.93	0.24	1.06	1.53	-1.03	0.33	1.56	1.34	3.07
Cthe_00106 GTP cyclohydrolase II	12.44	13.37	11.82	11.58	0.62	1.79	-0.93	0.24	1.06	1.53	-1.03	0.33	1.56	1.34	3.07
Cthe_01946 FAD-dependent pyridine nucleotid	12.7	13.43	12.12	11.81	0.58	1.62	-0.73	0.31	1.02	1.39	-0.37	0.48	1.55	1.34	5.08
Cthe_00106 GTP cyclohydrolase II	12.44	13.37	11.82	11.58	0.62	1.79	-0.93	0.24	1.06	1.53	-1.03	0.33	1.56	1.34	3.07
Cthe_02580 phosphodiesterase, MJ0936 family	9.33	9.88	8.46	8.58	0.87	1.3	-0.55	-0.12	1.25	1.12	0.23	-0.42	1.54	1.33	6.26
Cthe_03107 Radical SAM	10.56	11.22	9.98	9.7	0.58	1.52	-0.66	0.28	1.02	1.31	-0.13	0.42	1.54	1.33	6.74
Cthe_03155 beta-lactamase-like protein	10.26	10.81	9.63	9.19	0.63	1.62	-0.55	0.44	1.06	1.39	0.23	0.75	1.53	1.32	3.98
Cthe_00245 transcriptional regulator, ArsR fami	13.07	13.84	12.6	11.83	0.47	2.01	-0.77	0.77	0.94	1.72	-0.5	1.44	1.53	1.32	2.3
Cthe_00694 spermidine synthase	12.73	13.31	12.09	12	0.64	1.31	-0.58	0.09	1.07	1.13	0.13	0.02	1.52	1.31	21.13
Cthe_02792 Phenylacetate--CoA ligase	3.91	4.81	3.46	2.81	0.45	2	-0.9	0.65	0.92	1.71	-0.93	1.19	1.52	1.31	2.3
Cthe_00552 transcriptional regulator, XRE fami	10.59	11.25	9.86	9.93	0.73	1.32	-0.66	-0.07	1.14	1.14	-0.13	-0.31	1.52	1.31	8.56
Cthe_00908 pseudouridine synthase, RluA fami	10.11	10.65	9.3	9.37	0.81	1.28	-0.54	-0.07	1.21	1.1	0.27	-0.31	1.52	1.31	7.1
Cthe_00694 spermidine synthase	12.73	13.31	12.09	12	0.64	1.31	-0.58	0.09	1.07	1.13	0.13	0.02	1.52	1.31	21.13
Cthe_00694 spermidine synthase															



Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_01093 Methenyltetrahydrofolate cyclohyd	12.49	13.28	11.83	11.8	0.66	1.48	-0.79	0.03	1.09	1.27	-0.57	-0.1	1.51	1.3	5.16
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00143 Phosphopyruvate hydratase	16.24	16.99	15.71	15.35	0.53	1.64	-0.75	0.36	0.98	1.41	-0.43	0.58	1.51	1.3	4.25
Cthe_00774 RNA chaperone Hfq	11.48	12.23	10.97	10.56	0.51	1.67	-0.75	0.41	0.97	1.43	-0.43	0.69	1.5	1.29	3.8
Cthe_01202 major facilitator superfamily MFS_	10.44	11.11	9.59	9.82	0.85	1.29	-0.67	-0.23	1.24	1.11	-0.17	-0.65	1.48	1.28	4.42
Cthe_03152 cobalamin 5'-phosphate synthase	8.57	9.27	7.99	7.89	0.58	1.38	-0.7	0.1	1.02	1.19	-0.27	0.04	1.49	1.28	10.25
Cthe_00674 NUDIX hydrolase	10.93	11.6	10.39	10.11	0.54	1.49	-0.67	0.28	0.99	1.28	-0.17	0.42	1.49	1.28	6.38
Cthe_01238 iojap-like protein	10.07	10.54	8.98	9.32	1.09	1.22	-0.47	-0.34	1.43	1.05	0.5	-0.88	1.49	1.28	3.13
Cthe_03152 cobalamin 5'-phosphate synthase	8.57	9.27	7.99	7.89	0.58	1.38	-0.7	0.1	1.02	1.19	-0.27	0.04	1.49	1.28	10.25
Cthe_00674 NUDIX hydrolase	10.93	11.6	10.39	10.11	0.54	1.49	-0.67	0.28	0.99	1.28	-0.17	0.42	1.49	1.28	6.38
Cthe_03152 cobalamin 5'-phosphate synthase	8.57	9.27	7.99	7.89	0.58	1.38	-0.7	0.1	1.02	1.19	-0.27	0.04	1.49	1.28	10.25
Cthe_03152 cobalamin 5'-phosphate synthase	8.57	9.27	7.99	7.89	0.58	1.38	-0.7	0.1	1.02	1.19	-0.27	0.04	1.49	1.28	10.25
Cthe_03152 cobalamin 5'-phosphate synthase	8.57	9.27	7.99	7.89	0.58	1.38	-0.7	0.1	1.02	1.19	-0.27	0.04	1.49	1.28	10.25
Cthe_03152 cobalamin 5'-phosphate synthase	8.57	9.27	7.99	7.89	0.58	1.38	-0.7	0.1	1.02	1.19	-0.27	0.04	1.49	1.28	10.25
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01241 nicotinate (nicotinamide) nucleotid	10.36	10.9	9.6	9.66	0.76	1.24	-0.54	-0.06	1.17	1.07	0.27	-0.29	1.47	1.27	7.15
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01241 nicotinate (nicotinamide) nucleotid	10.36	10.9	9.6	9.66	0.76	1.24	-0.54	-0.06	1.17	1.07	0.27	-0.29	1.47	1.27	7.15
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01241 nicotinate (nicotinamide) nucleotid	10.36	10.9	9.6	9.66	0.76	1.24	-0.54	-0.06	1.17	1.07	0.27	-0.29	1.47	1.27	7.15
Cthe_01241 nicotinate (nicotinamide) nucleotid	10.36	10.9	9.6	9.66	0.76	1.24	-0.54	-0.06	1.17	1.07	0.27	-0.29	1.47	1.27	7.15
Cthe_01241 nicotinate (nicotinamide) nucleotid	10.36	10.9	9.6	9.66	0.76	1.24	-0.54	-0.06	1.17	1.07	0.27	-0.29	1.47	1.27	7.15
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01241 nicotinate (nicotinamide) nucleotid	10.36	10.9	9.6	9.66	0.76	1.24	-0.54	-0.06	1.17	1.07	0.27	-0.29	1.47	1.27	7.15
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_01058 Glycine hydroxymethyltransferase	13.04	13.58	12.38	12.31	0.66	1.27	-0.54	0.07	1.09	1.09	0.27	-0.02	1.47	1.27	10.17
Cthe_00117 HPrNtr domain containing protein	9.46	10.13	8.95	8.7	0.51	1.43	-0.67	0.25	0.97	1.23	-0.17	0.35	1.46	1.26	7.19
Cthe_00150 RNA modification enzyme, MiaB fa	10.4	11.16	9.59	9.81	0.81	1.35	-0.76	-0.22	1.21	1.16	-0.47	-0.63	1.46	1.26	3.81
Cthe_00150 RNA modification enzyme, MiaB fa	10.4	11.16	9.59	9.81	0.81	1.35	-0.76	-0.22	1.21	1.16	-0.47	-0.63	1.46	1.26	3.81
Cthe_02024 transposase IS116/IS110/IS902	7.96	8.71	7.51	7.03	0.45	1.68	-0.75	0.48	0.92	1.44	-0.43	0.83	1.45	1.25	3.26
Cthe_01003 ribosome recycling factor	11.01	11.57	10.33	10.34	0.68	1.23	-0.56	-0.01	1.1	1.06	0.2	-0.19	1.45	1.25	9.89
Cthe_00550 heat shock protein Hsp90	9.97	10.38	9.18	9.05	0.79	1.33	-0.41	0.13	1.19	1.14	0.7	0.1	1.45	1.25	4.16
Cthe_00012 YD repeat protein	6.44	7.11	4.58	5.93	1.86	1.18	-0.67	-1.35	2.04	1.02	-0.17	-2.98	1.45	1.25	1.36
Cthe_00460 DNA topoisomerase I	12.07	12.8	11.46	11.47	0.61	1.33	-0.73	-0.01	1.05	1.14	-0.37	-0.19	1.43	1.23	6.65
Cthe_00886 DNA polymerase I	10.74	11.34	9.96	10.13	0.78	1.21	-0.6	-0.17	1.18	1.04	0.07	-0.52	1.43	1.23	5.35
Cthe_01004 uridylylate kinase	9.45	10.11	8.9	8.86	0.55	1.25	-0.66	0.04	1	1.08	-0.13	-0.08	1.43	1.23	17.22
Cthe_00460 DNA topoisomerase I	12.07	12.8	11.46	11.47	0.61	1.33	-0.73	-0.01	1.05	1.14	-0.37	-0.19	1.43	1.23	6.65
Cthe_01004 uridylylate kinase	9.45	10.11	8.9	8.86	0.55	1.25	-0.66	0.04	1	1.08	-0.13	-0.08	1.43	1.23	17.22
Cthe_00886 DNA polymerase I	10.74	11.34	9.96	10.13	0.78	1.21	-0.6	-0.17	1.18	1.04	0.07	-0.52	1.43	1.23	5.35
Cthe_01004 uridylylate kinase	9.45	10.11	8.9	8.86	0.55	1.25	-0.66	0.04	1	1.08	-0.13	-0.08	1.43	1.23	17.22
Cthe_01004 uridylylate kinase	9.45	10.11	8.9	8.86	0.55	1.25	-0.66	0.04	1	1.08	-0.13	-0.08	1.43	1.23	17.22
Cthe_02429 protein of unknown function UPF0	10.85	11.66	9.91	10.32	0.94	1.34	-0.81	-0.41	1.31	1.15	-0.63	-1.02	1.41	1.22	2.6
Cthe_00564 Trans-hexaprenyltranstransferase	10.2	10.86	9.55	9.63	0.65	1.23	-0.66	-0.08	1.08	1.06	-0.13	-0.33	1.41	1.22	7.62
Cthe_00186 UDP-glucose 4-epimerase	11.88	12.55	11.4	11.15	0.48	1.4	-0.67	0.25	0.94	1.2	-0.17	0.35	1.42	1.22	7
Cthe_00186 UDP-glucose 4-epimerase	1														



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Cthe_03153 Phosphoglycerate mutase	8.82	9.65	8.53	8.19	0.29	1.46	-0.83	0.34	0.79	1.25	-0.7	0.54	1.23	1.06	2.99
Cthe_00750 spermidine/putrescine ABC transpo	10.01	10.57	9.57	9.53	0.44	1.04	-0.56	0.04	0.91	0.9	0.2	-0.08	1.22	1.05	10.61
Cthe_02585 biotin--acetyl-CoA-carboxylase liga	10.81	11.44	10.46	10.4	0.35	1.04	-0.63	0.06	0.84	0.9	-0.03	-0.04	1.22	1.05	43.97
Cthe_00868 type IV pilus assembly PilZ	9.53	10.07	8.89	9.06	0.64	1.01	-0.54	-0.17	1.07	0.87	0.27	-0.52	1.22	1.05	4.2
Cthe_00750 spermidine/putrescine ABC transpo	10.01	10.57	9.57	9.53	0.44	1.04	-0.56	0.04	0.91	0.9	0.2	-0.08	1.22	1.05	10.61
Cthe_02585 biotin--acetyl-CoA-carboxylase liga	10.81	11.44	10.46	10.4	0.35	1.04	-0.63	0.06	0.84	0.9	-0.03	-0.04	1.22	1.05	43.97
Cthe_00750 spermidine/putrescine ABC transpo	10.01	10.57	9.57	9.53	0.44	1.04	-0.56	0.04	0.91	0.9	0.2	-0.08	1.22	1.05	10.61
Cthe_02585 biotin--acetyl-CoA-carboxylase liga	10.81	11.44	10.46	10.4	0.35	1.04	-0.63	0.06	0.84	0.9	-0.03	-0.04	1.22	1.05	43.97
Cthe_01030 TPR repeat domain containing prot	8.71	9.16	7.87	8.19	0.84	0.97	-0.45	-0.32	1.23	0.84	0.57	-0.83	1.21	1.04	2.64
Cthe_02208 LexA DNA-binding region containin	13.76	14.47	13.47	13.2	0.29	1.27	-0.71	0.27	0.79	1.09	-0.3	0.4	1.21	1.04	4.81
Cthe_02208 LexA DNA-binding region containin	13.76	14.47	13.47	13.2	0.29	1.27	-0.71	0.27	0.79	1.09	-0.3	0.4	1.21	1.04	4.81
Cthe_01505 S-layer-like domain containing prot	10.52	11.09	9.66	10.1	0.86	0.99	-0.57	-0.44	1.25	0.86	0.17	-1.08	1.21	1.04	2.81
Cthe_02208 LexA DNA-binding region containin	13.76	14.47	13.47	13.2	0.29	1.27	-0.71	0.27	0.79	1.09	-0.3	0.4	1.21	1.04	4.81
Cthe_01100 prepilin-type cleavage/methylation	10.77	11.68	10.49	10.19	0.28	1.49	-0.91	0.3	0.79	1.28	-0.97	0.46	1.2	1.03	2.5
Cthe_00574 serine/threonine protein kinase	12.47	13.03	11.83	12.04	0.64	0.99	-0.56	-0.21	1.07	0.86	0.2	-0.6	1.2	1.03	3.88
Cthe_00751 transcriptional regulator, XRE famil	8.97	9.65	8.6	8.58	0.37	1.07	-0.68	0.02	0.86	0.92	-0.2	-0.13	1.19	1.03	9.43
Cthe_00574 serine/threonine protein kinase	12.47	13.03	11.83	12.04	0.64	0.99	-0.56	-0.21	1.07	0.86	0.2	-0.6	1.2	1.03	3.88
Cthe_00574 serine/threonine protein kinase	12.47	13.03	11.83	12.04	0.64	0.99	-0.56	-0.21	1.07	0.86	0.2	-0.6	1.2	1.03	3.88
Cthe_02361 DNA gyrase, A subunit	11.79	12.38	11.09	11.38	0.7	1	-0.59	-0.29	1.12	0.86	0.1	-0.77	1.19	1.03	3.25
Cthe_01240 metal dependent phosphohydrolas	10.26	10.84	9.73	9.84	0.53	1	-0.58	-0.11	0.98	0.86	0.13	-0.4	1.19	1.03	5.54
Cthe_03151 Adenosylcobinamide-phosphate gu	9.33	10.07	9.08	8.68	0.25	1.39	-0.74	0.4	0.76	1.19	-0.4	0.67	1.19	1.03	3.23
Cthe_01100 prepilin-type cleavage/methylation	10.77	11.68	10.49	10.19	0.28	1.49	-0.91	0.3	0.79	1.28	-0.97	0.46	1.2	1.03	2.5
Cthe_00696 putative rRNA methylase	12.06	12.59	11.64	11.54	0.42	1.05	-0.53	0.1	0.9	0.91	0.3	0.04	1.2	1.03	7.55
Cthe_00953 aspartate carbamoyltransferase	9.22	9.57	8.01	8.68	1.21	0.89	-0.35	-0.67	1.52	0.77	0.9	-1.56	1.2	1.03	1.69
Cthe_00574 serine/threonine protein kinase	12.47	13.03	11.83	12.04	0.64	0.99	-0.56	-0.21	1.07	0.86	0.2	-0.6	1.2	1.03	3.88
Cthe_00574 serine/threonine protein kinase	12.47	13.03	11.83	12.04	0.64	0.99	-0.56	-0.21	1.07	0.86	0.2	-0.6	1.2	1.03	3.88
Cthe_02403 4-diphosphocytidyl-2C-methyl-D-er	9.5	10.01	8.93	9.01	0.57	1	-0.51	-0.08	1.02	0.86	0.37	-0.33	1.2	1.03	4.81
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02046 hypothetical protein	9.31	9.72	8.73	8.63	0.58	1.09	-0.41	0.1	1.02	0.94	0.7	0.04	1.19	1.03	3.53
Cthe_01386 hypothetical protein	10.81	11.27	10.2	10.25	0.61	1.02	-0.46	-0.05	1.05	0.88	0.53	-0.27	1.2	1.03	4.11
Cthe_03227 copper amine oxidase-like protein	7.51	8.27	7.27	6.89	0.24	1.38	-0.76	0.38	0.75	1.19	-0.47	0.63	1.19	1.03	3.2
Cthe_00649 hypothetical protein	8.46	9.31	7.68	8.11	0.78	1.2	-0.85	-0.43	1.18	1.03	-0.77	-1.06	1.2	1.03	2.13
Cthe_00230 hypothetical protein	11.65	12.2	11.04	11.2	0.61	1	-0.55	-0.16	1.05	0.86	0.23	-0.5	1.2	1.03	4.4
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_00953 aspartate carbamoyltransferase	9.22	9.57	8.01	8.68	1.21	0.89	-0.35	-0.67	1.52	0.77	0.9	-1.56	1.2	1.03	1.69
Cthe_02403 4-diphosphocytidyl-2C-methyl-D-er	9.5	10.01	8.93	9.01	0.57	1	-0.51	-0.08	1.02	0.86	0.37	-0.33	1.2	1.03	4.81
Cthe_03151 Adenosylcobinamide-phosphate gu	9.33	10.07	9.08	8.68	0.25	1.39	-0.74	0.4	0.76	1.19	-0.4	0.67	1.19	1.03	3.23
Cthe_02361 DNA gyrase, A subunit	11.79	12.38	11.09	11.38	0.7	1	-0.59	-0.29	1.12	0.86	0.1	-0.77	1.19	1.03	3.25
Cthe_03151 Adenosylcobinamide-phosphate gu	9.33	10.07	9.08	8.68	0.25	1.39	-0.74	0.4	0.76	1.19	-0.4	0.67	1.19	1.03	3.23
Cthe_03151 Adenosylcobinamide-phosphate gu	9.33	10.07	9.08	8.68	0.25	1.39	-0.74	0.4	0.76	1.19	-0.4	0.67	1.19	1.03	3.23
Cthe_00574 serine/threonine protein kinase	12.47	13.03	11.83	12.04	0.64	0.99	-0.56	-0.21	1.07	0.86	0.2	-0.6	1.2	1.03	3.88
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02403 4-diphosphocytidyl-2C-methyl-D-er	9.5	10.01	8.93	9.01	0.57	1	-0.51	-0.08	1.02	0.86	0.37	-0.33	1.2	1.03	4.81
Cthe_00953 aspartate carbamoyltransferase	9.22	9.57	8.01	8.68	1.21	0.89	-0.35	-0.67	1.52	0.77	0.9	-1.56	1.2	1.03	1.69
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02403 4-diphosphocytidyl-2C-methyl-D-er	9.5	10.01	8.93	9.01	0.57	1	-0.51	-0.08	1.02	0.86	0.37	-0.33	1.2	1.03	4.81
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_00953 aspartate carbamoyltransferase	9.22	9.57	8.01	8.68	1.21	0.89	-0.35	-0.67	1.52	0.77	0.9	-1.56	1.2	1.03	1.69
Cthe_03151 Adenosylcobinamide-phosphate gu	9.33	10.07	9.08	8.68	0.25	1.39	-0.74	0.4	0.76	1.19	-0.4	0.67	1.19	1.03	3.23
Cthe_03151 Adenosylcobinamide-phosphate gu	9.33	10.07	9.08	8.68	0.25	1.39	-0.74	0.4	0.76	1.19	-0.4	0.67	1.19	1.03	3.23
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_03151 Adenosylcobinamide-phosphate gu	9.33	10.07	9.08	8.68	0.25	1.39	-0.74	0.4	0.76	1.19	-0.4	0.67	1.19	1.03	3.23
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_02625 beta-hydroxyacyl-(acyl-carrier-prot	9.93	10.45	9.54	9.28	0.39	1.17	-0.52	0.26	0.87	1.01	0.33	0.38	1.19	1.03	4.73
Cthe_00572 radical SAM enzyme, Cfr family	11.75	12.4	11.15	11.38	0.6	1.02	-0.65	-0.23	1.04	0.88	-0.1	-0.65	1.18	1.02	3.7
Cthe_00146 ribonuclease R	13.4	14.04	12.91	13.02	0.49	1.02	-0.64	-0.11	0.95	0.88	-0.07	-0.4	1.18	1.02	5.69
Cthe_01031 glutamyl-tRNA(Gln) amidotransfera	8.88	9.39	7.95	8.45	0.93	0.94	-0.51	-0.5	1.3	0.81	0.37	-1.21	1.18	1.02	2.16
Cthe_02658 RNA-binding S4	8.86	9.18	8.06	8.17	0.8	1.01	-0.32	-0.11	1.2	0.87	1	-0.4	1.18	1.02	2.46
Cthe_00014 hypothetical protein	6.54	7.3	5.46	6.23	1.08	1.07	-0.76	-0.77	1.42	0.92	-0.47	-1.77	1.18	1.02	1.65
Cthe_00047 copper amine oxidase-like protein	8.09	8.66	7.01	7.71	1.08	0.95	-0.57	-0.7	1.42	0.82	0.17	-1.62	1.18	1.02	1.8
Cthe_01031 glutamyl-tRNA(Gln) amidotransfera	8.88	9.39	7.95	8.45	0.93	0.94	-0.51	-0.5	1.3	0.81	0.37	-1.21	1.18	1.02	2.16
Cthe_00146 ribonuclease R	13.4	14.04	12.91	13.02	0.49	1.02	-0.64	-0.11	0.95	0.88	-0.07	-0.4	1.18	1.02	5.69
Cthe_01031 glutamyl-tRNA(Gln) amidotransfera	8.88	9.39	7.95	8.45	0.93	0.94									







Cthe_01332 histidyl-tRNA synthetase	11.49	12.24	10.45	11.22	1.04	1.02	-0.75	-0.77	1.39	0.88	-0.43	-1.77	1.14	0.98	1.61
Cthe_01332 histidyl-tRNA synthetase	11.49	12.24	10.45	11.22	1.04	1.02	-0.75	-0.77	1.39	0.88	-0.43	-1.77	1.14	0.98	1.61
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_01332 histidyl-tRNA synthetase	11.49	12.24	10.45	11.22	1.04	1.02	-0.75	-0.77	1.39	0.88	-0.43	-1.77	1.14	0.98	1.61
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_01332 histidyl-tRNA synthetase	11.49	12.24	10.45	11.22	1.04	1.02	-0.75	-0.77	1.39	0.88	-0.43	-1.77	1.14	0.98	1.61
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_00347 phosphofructokinase	15.61	16.24	15.36	15.09	0.25	1.15	-0.63	0.27	0.76	0.99	-0.03	0.4	1.14	0.98	5.56
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_02226 FkbH like protein	10.88	11.53	10.65	10.38	0.23	1.15	-0.65	0.27	0.75	0.99	-0.1	0.4	1.13	0.97	5.38
Cthe_01063 thiamine biosynthesis/tRNA modifi	11.6	12.2	11.08	11.25	0.52	0.95	-0.6	-0.17	0.98	0.82	0.07	-0.52	1.13	0.97	4.35
Cthe_00288 MCP methyltransferase, CheR-type	9.91	10.55	9.25	9.59	0.66	0.96	-0.64	-0.34	1.09	0.83	-0.07	-0.88	1.12	0.97	2.77
Cthe_00288 MCP methyltransferase, CheR-type	9.91	10.55	9.25	9.59	0.66	0.96	-0.64	-0.34	1.09	0.83	-0.07	-0.88	1.12	0.97	2.77
Cthe_00369 protein of unknown function DUF1	10.37	10.92	10.08	9.71	0.29	1.21	-0.55	0.37	0.79	1.04	0.23	0.6	1.13	0.97	3.63
Cthe_01203 SpoVR	13.52	14.38	13.21	13.14	0.31	1.24	-0.86	0.07	0.81	1.07	-0.8	-0.02	1.12	0.97	2.99
Cthe_00626 hypothetical protein	10.64	11.38	10.04	10.34	0.6	1.04	-0.74	-0.3	1.04	0.9	-0.4	-0.79	1.13	0.97	2.77
Cthe_01939 magnesium transporter	11.68	12.43	11.4	11.33	0.28	1.1	-0.75	0.07	0.79	0.95	-0.43	-0.02	1.12	0.97	5.13
Cthe_02789 NLPA lipoprotein	4.25	4.91	4.09	3.32	0.16	1.59	-0.66	0.77	0.69	1.36	-0.13	1.44	1.12	0.97	1.88
Cthe_01945 Thioredoxin-disulfide reductase	12.67	13.43	12.48	12.1	0.19	1.33	-0.76	0.38	0.71	1.14	-0.47	0.63	1.12	0.97	3.05
Cthe_00187 hypothetical protein	10.3	10.86	9.68	9.94	0.62	0.92	-0.56	-0.26	1.06	0.8	0.2	-0.71	1.12	0.97	3.21
Cthe_00381 hypothetical protein	7.81	8.33	7.5	7.15	0.31	1.18	-0.52	0.35	0.81	1.02	0.33	0.56	1.12	0.97	3.58
Cthe_01925 hypothetical protein	6.92	7.16	6.23	6.02	0.69	1.14	-0.24	0.21	1.11	0.98	1.27	0.27	1.12	0.97	2.04
Cthe_01911 Carbohydrate binding family 6	12.37	13.32	12.08	11.94	0.29	1.38	-0.95	0.14	0.79	1.19	-1.1	0.13	1.12	0.97	2.3
Cthe_02396 hypothetical protein	10.28	10.76	9.3	9.9	0.98	0.86	-0.48	-0.6	1.34	0.75	0.47	-1.42	1.12	0.97	1.83
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_02789 NLPA lipoprotein	4.25	4.91	4.09	3.32	0.16	1.59	-0.66	0.77	0.69	1.36	-0.13	1.44	1.12	0.97	1.88
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.55	0.46	0.79	1.11	0.23	0.79	1.13	0.97	2.96
Cthe_00349 fructose-1,6-bisphosphate aldolase	16.28	16.83	16	15.54	0.28	1.29	-0.								



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Cthe_00871	Phosphoribosylanthranilate isomer	9.18	9.66	8.89	8.54	0.29	1.12	-0.48	0.35	0.79	0.97	0.47	0.56	1.05	0.91	3.06
Cthe_01211	pyridoxal-phosphate dependent Tr	14	14.55	13.7	13.64	0.3	0.91	-0.55	0.06	0.8	0.79	0.23	-0.04	1.06	0.91	8.6
Cthe_01032	glutamyl-tRNA(Gln) amidotransfera	9.03	9.66	8.54	8.76	0.49	0.9	-0.63	-0.22	0.95	0.78	-0.03	-0.63	1.05	0.91	3.48
Cthe_00551	AMP-dependent synthetase and lig	12.45	13.17	12.18	12.18	0.27	0.99	-0.72	0	0.78	0.86	-0.33	-0.17	1.06	0.91	5.59
Cthe_00871	Phosphoribosylanthranilate isomer	9.18	9.66	8.89	8.54	0.29	1.12	-0.48	0.35	0.79	0.97	0.47	0.56	1.05	0.91	3.06
Cthe_01032	glutamyl-tRNA(Gln) amidotransfera	9.03	9.66	8.54	8.76	0.49	0.9	-0.63	-0.22	0.95	0.78	-0.03	-0.63	1.05	0.91	3.48
Cthe_00850		8.01	8.56	7.35	7.71	0.66	0.85	-0.55	-0.36	1.09	0.74	0.23	-0.92	1.05	0.91	2.48
Cthe_01211	pyridoxal-phosphate dependent Tr	14	14.55	13.7	13.64	0.3	0.91	-0.55	0.06	0.8	0.79	0.23	-0.04	1.06	0.91	8.6
Cthe_00871	Phosphoribosylanthranilate isomer	9.18	9.66	8.89	8.54	0.29	1.12	-0.48	0.35	0.79	0.97	0.47	0.56	1.05	0.91	3.06
Cthe_00551	AMP-dependent synthetase and lig	12.45	13.17	12.18	12.18	0.27	0.99	-0.72	0	0.78	0.86	-0.33	-0.17	1.06	0.91	5.59
Cthe_00551	AMP-dependent synthetase and lig	12.45	13.17	12.18	12.18	0.27	0.99	-0.72	0	0.78	0.86	-0.33	-0.17	1.06	0.91	5.59
Cthe_01032	glutamyl-tRNA(Gln) amidotransfera	9.03	9.66	8.54	8.76	0.49	0.9	-0.63	-0.22	0.95	0.78	-0.03	-0.63	1.05	0.91	3.48
Cthe_00551	AMP-dependent synthetase and lig	12.45	13.17	12.18	12.18	0.27	0.99	-0.72	0	0.78	0.86	-0.33	-0.17	1.06	0.91	5.59
Cthe_01032	glutamyl-tRNA(Gln) amidotransfera	9.03	9.66	8.54	8.76	0.49	0.9	-0.63	-0.22	0.95	0.78	-0.03	-0.63	1.05	0.91	3.48
Cthe_00551	AMP-dependent synthetase and lig	12.45	13.17	12.18	12.18	0.27	0.99	-0.72	0	0.78	0.86	-0.33	-0.17	1.06	0.91	5.59
Cthe_00551	AMP-dependent synthetase and lig	12.45	13.17	12.18	12.18	0.27	0.99	-0.72	0	0.78	0.86	-0.33	-0.17	1.06	0.91	5.59
Cthe_00596	GTP-binding protein	8.47	8.89	8.1	7.84	0.37	1.05	-0.42	0.26	0.86	0.91	0.67	0.38	1.04	0.9	2.9
Cthe_01191	HAD-superfamily hydrolase, subfam	7.69	8.16	7.35	7.17	0.34	0.99	-0.47	0.18	0.83	0.86	0.5	0.21	1.04	0.9	3.94
Cthe_02227	phosphopantetheine-binding	7.87	8.28	7.29	7.41	0.58	0.87	-0.41	-0.12	1.02	0.75	0.7	-0.42	1.04	0.9	2.77
Cthe_00421	flavoprotein	8.69	9.3	8.46	8.42	0.23	0.88	-0.61	0.04	0.75	0.76	0.03	-0.08	1.04	0.9	22.32
Cthe_01384	FoC bifunctional protein	10.05	10.77	9.58	9.82	0.47	0.95	-0.72	-0.24	0.94	0.82	-0.33	-0.67	1.04	0.9	2.98
Cthe_00573	protein serine/threonine phosphat	11.34	11.91	10.62	11.06	0.72	0.85	-0.57	-0.44	1.13	0.74	0.17	-1.08	1.04	0.9	2.21
Cthe_01504	Linocin_M18 bacteriocin protein	15.71	16.31	15.51	15.41	0.2	0.9	-0.6	0.1	0.72	0.78	0.07	0.04	1.04	0.9	23.51
Cthe_02227	phosphopantetheine-binding	7.87	8.28	7.29	7.41	0.58	0.87	-0.41	-0.12	1.02	0.75	0.7	-0.42	1.04	0.9	2.77
Cthe_02337	hypothetical protein	8.75	9.28	8.4	8.4	0.35	0.88	-0.53	0	0.84	0.76	0.3	-0.17	1.04	0.9	5.87
Cthe_00829	hypothetical protein	10.47	10.94	9.69	10.13	0.78	0.81	-0.47	-0.44	1.18	0.7	0.5	-1.08	1.04	0.9	2.06
Cthe_02263	H+-transporting two-sector ATPase	10.49	11.04	10.13	10.17	0.36	0.87	-0.55	-0.04	0.85	0.75	0.23	-0.25	1.04	0.9	5.96
Cthe_01384	FoC bifunctional protein	10.05	10.77	9.58	9.82	0.47	0.95	-0.72	-0.24	0.94	0.82	-0.33	-0.67	1.04	0.9	2.98
Cthe_02263	H+-transporting two-sector ATPase	10.49	11.04	10.13	10.17	0.36	0.87	-0.55	-0.04	0.85	0.75	0.23	-0.25	1.04	0.9	5.96
Cthe_01384	FoC bifunctional protein	10.05	10.77	9.58	9.82	0.47	0.95	-0.72	-0.24	0.94	0.82	-0.33	-0.67	1.04	0.9	2.98
Cthe_01384	FoC bifunctional protein	10.05	10.77	9.58	9.82	0.47	0.95	-0.72	-0.24	0.94	0.82	-0.33	-0.67	1.04	0.9	2.98
Cthe_00573	protein serine/threonine phosphat	11.34	11.91	10.62	11.06	0.72	0.85	-0.57	-0.44	1.13	0.74	0.17	-1.08	1.04	0.9	2.21
Cthe_01191	HAD-superfamily hydrolase, subfam	7.69	8.16	7.35	7.17	0.34	0.99	-0.47	0.18	0.83	0.86	0.5	0.21	1.04	0.9	3.94
Cthe_01191	HAD-superfamily hydrolase, subfam	7.69	8.16	7.35	7.17	0.34	0.99	-0.47	0.18	0.83	0.86	0.5	0.21	1.04	0.9	3.94
Cthe_01384	FoC bifunctional protein	10.05	10.77	9.58	9.82	0.47	0.95	-0.72	-0.24	0.94	0.82	-0.33	-0.67	1.04	0.9	2.98
Cthe_01384	FoC bifunctional protein	10.05	10.77	9.58	9.82	0.47	0.95	-0.72	-0.24	0.94	0.82	-0.33	-0.67	1.04	0.9	2.98
Cthe_02263	H+-transporting two-sector ATPase	10.49	11.04	10.13	10.17	0.36	0.87	-0.55	-0.04	0.85	0.75	0.23	-0.25	1.04	0.9	5.96
Cthe_01384	FoC bifunctional protein	10.05	10.77	9.58	9.82	0.47	0.95	-0.72	-0.24	0.94	0.82	-0.33	-0.67	1.04	0.9	2.98
Cthe_01102	fimbrial assembly protein	10.64	11.22	10.37	10.35	0.27	0.87	-0.58	0.02	0.78	0.75	0.13	-0.13	1.03	0.89	10.51
Cthe_02179	Pectate lyase/Amb allergen	14.29	14.99	14.08	14.03	0.21	0.96	-0.7	0.05	0.73	0.83	-0.27	-0.06	1.03	0.89	7.14
Cthe_01314	DNA-directed RNA polymerase, om	9.08	9.81	8.9	8.78	0.18	1.03	-0.73	0.12	0.71	0.89	-0.37	0.08	1.03	0.89	5.37
Cthe_00577	thiamine pyrophosphokinase	12.9	13.4	12.49	12.54	0.41	0.86	-0.5	-0.05	0.89	0.75	0.4	-0.27	1.03	0.89	4.31
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_01102	fimbrial assembly protein	10.64	11.22	10.37	10.35	0.27	0.87	-0.58	0.02	0.78	0.75	0.13	-0.13	1.03	0.89	10.51
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_01314	DNA-directed RNA polymerase, om	9.08	9.81	8.9	8.78	0.18	1.03	-0.73	0.12	0.71	0.89	-0.37	0.08	1.03	0.89	5.37
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_00577	thiamine pyrophosphokinase	12.9	13.4	12.49	12.54	0.41	0.86	-0.5	-0.05	0.89	0.75	0.4	-0.27	1.03	0.89	4.31
Cthe_01314	DNA-directed RNA polymerase, om	9.08	9.81	8.9	8.78	0.18	1.03	-0.73	0.12	0.71	0.89	-0.37	0.08	1.03	0.89	5.37
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_00987	riboflavin biosynthesis protein RibF	11.05	11.71	10.67	10.81	0.38	0.9	-0.66	-0.14	0.87	0.78	-0.13	-0.46	1.03	0.89	4.36
Cthe_00577	thiamine pyrophosphokinase	12.9	13.4	12.49	12.54	0.41	0.86	-0.5	-0.05	0.89	0.75	0.4	-0.27	1.03	0.89	4.31
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0	1	1	0	0	1.36	0.86	2.07	-0.17	1.03	0.89	1.38
Cthe_02795	pyruvate ferredoxin/flavodoxin oxi	1	1		0											



Cthe_00112	UDP-N-acetylenolpyruvoylglucosam	8.42	8.98	8.15	8.12	0.27	0.86	-0.56	0.03	0.78	0.75	0.2	-0.1	1.02	0.88	8.64
Cthe_01053	L-lactate dehydrogenase	11.05	11.61	10.84	10.68	0.21	0.93	-0.56	0.16	0.73	0.81	0.2	0.17	1.02	0.88	7.42
Cthe_00996	DNA polymerase III, alpha subunit	10.67	11.44	10.26	10.46	0.41	0.98	-0.77	-0.2	0.89	0.85	-0.5	-0.58	1.02	0.88	2.87
Cthe_01053	L-lactate dehydrogenase	11.05	11.61	10.84	10.68	0.21	0.93	-0.56	0.16	0.73	0.81	0.2	0.17	1.02	0.88	7.42
Cthe_01053	L-lactate dehydrogenase	11.05	11.61	10.84	10.68	0.21	0.93	-0.56	0.16	0.73	0.81	0.2	0.17	1.02	0.88	7.42
Cthe_00112	UDP-N-acetylenolpyruvoylglucosam	8.42	8.98	8.15	8.12	0.27	0.86	-0.56	0.03	0.78	0.75	0.2	-0.1	1.02	0.88	8.64
Cthe_01053	L-lactate dehydrogenase	11.05	11.61	10.84	10.68	0.21	0.93	-0.56	0.16	0.73	0.81	0.2	0.17	1.02	0.88	7.42
Cthe_01053	L-lactate dehydrogenase	11.05	11.61	10.84	10.68	0.21	0.93	-0.56	0.16	0.73	0.81	0.2	0.17	1.02	0.88	7.42
Cthe_00112	UDP-N-acetylenolpyruvoylglucosam	8.42	8.98	8.15	8.12	0.27	0.86	-0.56	0.03	0.78	0.75	0.2	-0.1	1.02	0.88	8.64
Cthe_00112	UDP-N-acetylenolpyruvoylglucosam	8.42	8.98	8.15	8.12	0.27	0.86	-0.56	0.03	0.78	0.75	0.2	-0.1	1.02	0.88	8.64
Cthe_00111	PHP-like protein	7.82	8.23	7.41	7.29	0.41	0.94	-0.41	0.12	0.89	0.81	0.7	0.08	1.01	0.87	3.05
Cthe_00111	PHP-like protein	7.82	8.23	7.41	7.29	0.41	0.94	-0.41	0.12	0.89	0.81	0.7	0.08	1.01	0.87	3.05
Cthe_00655	cysteine desulfurase family protein	13.42	14.19	13.33	13	0.09	1.19	-0.77	0.33	0.63	1.03	-0.5	0.52	1.01	0.87	2.99
Cthe_02583	2-amino-4-hydroxy-6-	9.48	10.1	9.09	9.24	0.39	0.86	-0.62	-0.15	0.87	0.75	0	-0.48	1.01	0.87	4.27
Cthe_00009	YD repeat containing protein	9.32	10	8.75	9.11	0.57	0.89	-0.68	-0.36	1.02	0.77	-0.2	-0.92	1.01	0.87	2.42
Cthe_03154	hypothetical protein	7.34	8.11	7.22	6.99	0.12	1.12	-0.77	0.23	0.66	0.97	-0.5	0.31	1.01	0.87	3.56
Cthe_02185	ribosomal protein S18	12.92	13.37	12.66	12.12	0.26	1.25	-0.45	0.54	0.77	1.08	0.57	0.96	1.01	0.87	2.12
Cthe_01095	cell divisionFtsK/SpolIE	12.5	13.3	12.36	12.15	0.14	1.15	-0.8	0.21	0.67	0.99	-0.6	0.27	1.01	0.87	3.24
Cthe_01814	Urease accessory protein UreF	4.58	5.25	4.46	4.17	0.12	1.08	-0.67	0.29	0.66	0.93	-0.17	0.44	1.01	0.87	4.32
Cthe_01413	hypothetical protein	8.17	8.76	7.89	7.92	0.28	0.84	-0.59	-0.03	0.79	0.73	0.1	-0.23	1.01	0.87	7.66
Cthe_02583	2-amino-4-hydroxy-6-	9.48	10.1	9.09	9.24	0.39	0.86	-0.62	-0.15	0.87	0.75	0	-0.48	1.01	0.87	4.27
Cthe_02185	ribosomal protein S18	12.92	13.37	12.66	12.12	0.26	1.25	-0.45	0.54	0.77	1.08	0.57	0.96	1.01	0.87	2.12
Cthe_02583	2-amino-4-hydroxy-6-	9.48	10.1	9.09	9.24	0.39	0.86	-0.62	-0.15	0.87	0.75	0	-0.48	1.01	0.87	4.27
Cthe_02583	2-amino-4-hydroxy-6-	9.48	10.1	9.09	9.24	0.39	0.86	-0.62	-0.15	0.87	0.75	0	-0.48	1.01	0.87	4.27
Cthe_02217	flagellar protein FljS	11.12	11.87	10.96	10.84	0.16	1.03	-0.75	0.12	0.69	0.89	-0.43	0.08	1	0.86	4.6
Cthe_01265	phosphoglucomutase/phosphoman	11.97	12.49	11.68	11.63	0.29	0.86	-0.52	0.05	0.79	0.75	0.33	-0.06	1	0.86	5.8
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02217	flagellar protein FljS	11.12	11.87	10.96	10.84	0.16	1.03	-0.75	0.12	0.69	0.89	-0.43	0.08	1	0.86	4.6
Cthe_02434	electron transport complex, RnfAB	11.76	12.59	11.71	11.26	0.05	1.33	-0.83	0.45	0.6	1.14	-0.7	0.77	1	0.86	2.21
Cthe_02217	flagellar protein FljS	11.12	11.87	10.96	10.84	0.16	1.03	-0.75	0.12	0.69	0.89	-0.43	0.08	1	0.86	4.6
Cthe_01265	phosphoglucomutase/phosphoman	11.97	12.49	11.68	11.63	0.29	0.86	-0.52	0.05	0.79	0.75	0.33	-0.06	1	0.86	5.8
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_01265	phosphoglucomutase/phosphoman	11.97	12.49	11.68	11.63	0.29	0.86	-0.52	0.05	0.79	0.75	0.33	-0.06	1	0.86	5.8
Cthe_01265	phosphoglucomutase/phosphoman	11.97	12.49	11.68	11.63	0.29	0.86	-0.52	0.05	0.79	0.75	0.33	-0.06	1	0.86	5.8
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_01265	phosphoglucomutase/phosphoman	11.97	12.49	11.68	11.63	0.29	0.86	-0.52	0.05	0.79	0.75	0.33	-0.06	1	0.86	5.8
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
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Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokinase, ROK family	10.24	10.92	10.09	9.99	0.15	0.93	-0.68	0.1	0.68	0.81	-0.2	0.04	1	0.86	9.26
Cthe_02938	putative glucokin															



Cthe_00070 asparaginyl-tRNA synthetase	11.91	12.5	11.65	11.69	0.26	0.81	-0.59	-0.04	0.77	0.7	0.1	-0.25	0.97	0.84	6.9
Cthe_00156 Radical SAM	11.28	11.83	11.02	11	0.26	0.83	-0.55	0.02	0.77	0.72	0.23	-0.13	0.98	0.84	7.13
Cthe_02269 V-type ATPase, D subunit	11.26	12.11	11.16	10.94	0.1	1.17	-0.85	0.22	0.64	1.01	-0.77	0.29	0.97	0.84	2.6
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_01849 Heavy metal transport/detoxificati	7.93	8.75	7.74	7.7	0.19	1.05	-0.82	0.04	0.71	0.91	-0.67	-0.08	0.97	0.84	3.05
Cthe_02375 hypothetical protein	8.07	8.4	7.43	7.58	0.64	0.82	-0.33	-0.15	1.07	0.71	0.97	-0.48	0.98	0.84	2.12
Cthe_03231 hypothetical protein	3.7	4.25	2.32	3.58	1.38	0.67	-0.55	-1.26	1.66	0.58	0.23	-2.79	0.97	0.84	1.12
Cthe_00327 S-layer-like domain containing prot	10.75	11.71	10.43	10.54	0.32	1.17	-0.96	-0.11	0.82	1.01	-1.13	-0.4	0.97	0.84	1.94
Cthe_03025 hypothetical protein	4.17	4.91	4.09	3.81	0.08	1.1	-0.74	0.28	0.63	0.95	-0.4	0.42	0.98	0.84	3.51
Cthe_00918 cellulosome enzyme, dockerin type	10.63	11.2	10.44	10.36	0.19	0.84	-0.57	0.08	0.71	0.73	0.17	0	0.97	0.84	10.7
Cthe_01101 hypothetical protein	13.35	14.14	13.2	13.07	0.15	1.07	-0.79	0.13	0.68	0.92	-0.57	0.1	0.98	0.84	3.53
Cthe_02439 GCN5-related N-acetyltransferase	10.28	10.62	9.56	9.85	0.72	0.77	-0.34	-0.29	1.13	0.67	0.93	-0.77	0.98	0.84	1.94
Cthe_02269 V-type ATPase, D subunit	11.26	12.11	11.16	10.94	0.1	1.17	-0.85	0.22	0.64	1.01	-0.77	0.29	0.97	0.84	2.6
Cthe_00715 Adenosylmethionine decarboxylase	13.04	13.43	12.7	12.34	0.34	1.09	-0.39	0.36	0.83	0.94	0.77	0.58	0.98	0.84	2.32
Cthe_00070 asparaginyl-tRNA synthetase	11.91	12.5	11.65	11.69	0.26	0.81	-0.59	-0.04	0.77	0.7	0.1	-0.25	0.97	0.84	6.9
Cthe_00715 Adenosylmethionine decarboxylase	13.04	13.43	12.7	12.34	0.34	1.09	-0.39	0.36	0.83	0.94	0.77	0.58	0.98	0.84	2.32
Cthe_00070 asparaginyl-tRNA synthetase	11.91	12.5	11.65	11.69	0.26	0.81	-0.59	-0.04	0.77	0.7	0.1	-0.25	0.97	0.84	6.9
Cthe_01040 DNA polymerase III, delta subunit	9.41	9.92	9.14	9.07	0.27	0.85	-0.51	0.07	0.78	0.74	0.37	-0.02	0.97	0.84	5.18
Cthe_01200 adenosylhomocysteinase	11.3	11.84	10.77	11.04	0.53	0.8	-0.54	-0.27	0.98	0.69	0.27	-0.73	0.98	0.84	2.75
Cthe_02269 V-type ATPase, D subunit	11.26	12.11	11.16	10.94	0.1	1.17	-0.85	0.22	0.64	1.01	-0.77	0.29	0.97	0.84	2.6
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_00350 signal peptidase I	10.11	10.72	9.87	9.89	0.24	0.83	-0.61	-0.02	0.75	0.72	0.03	-0.21	0.98	0.84	8.75
Cthe_00110 HPr kinase	8.32	9.23	8.15	8.04	0.17	1.19	-0.91	0.11	0.7	1.03	-0.97	0.06	0.97	0.84	2.29
Cthe_00715 Adenosylmethionine decarboxylase	13.04	13.43	12.7	12.34	0.34	1.09	-0.39	0.36	0.83	0.94	0.77	0.58	0.98	0.84	2.32
Cthe_01040 DNA polymerase III, delta subunit	9.41	9.92	9.14	9.07	0.27	0.85	-0.51	0.07	0.78	0.74	0.37	-0.02	0.97	0.84	5.18
Cthe_00110 HPr kinase	8.32	9.23	8.15	8.04	0.17	1.19	-0.91	0.11	0.7	1.03	-0.97	0.06	0.97	0.84	2.29
Cthe_01200 adenosylhomocysteinase	11.3	11.84	10.77	11.04	0.53	0.8	-0.54	-0.27	0.98	0.69	0.27	-0.73	0.98	0.84	2.75
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_00070 asparaginyl-tRNA synthetase	11.91	12.5	11.65	11.69	0.26	0.81	-0.59	-0.04	0.77	0.7	0.1	-0.25	0.97	0.84	6.9
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_00110 HPr kinase	8.32	9.23	8.15	8.04	0.17	1.19	-0.91	0.11	0.7	1.03	-0.97	0.06	0.97	0.84	2.29
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_01200 adenosylhomocysteinase	11.3	11.84	10.77	11.04	0.53	0.8	-0.54	-0.27	0.98	0.69	0.27	-0.73	0.98	0.84	2.75
Cthe_00715 Adenosylmethionine decarboxylase	13.04	13.43	12.7	12.34	0.34	1.09	-0.39	0.36	0.83	0.94	0.77	0.58	0.98	0.84	2.32
Cthe_00110 HPr kinase	8.32	9.23	8.15	8.04	0.17	1.19	-0.91	0.11	0.7	1.03	-0.97	0.06	0.97	0.84	2.29
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_00110 HPr kinase	8.32	9.23	8.15	8.04	0.17	1.19	-0.91	0.11	0.7	1.03	-0.97	0.06	0.97	0.84	2.29
Cthe_00110 HPr kinase	8.32	9.23	8.15	8.04	0.17	1.19	-0.91	0.11	0.7	1.03	-0.97	0.06	0.97	0.84	2.29
Cthe_01200 adenosylhomocysteinase	11.3	11.84	10.77	11.04	0.53	0.8	-0.54	-0.27	0.98	0.69	0.27	-0.73	0.98	0.84	2.75
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_00070 asparaginyl-tRNA synthetase	11.91	12.5	11.65	11.69	0.26	0.81	-0.59	-0.04	0.77	0.7	0.1	-0.25	0.97	0.84	6.9
Cthe_02269 V-type ATPase, D subunit	11.26	12.11	11.16	10.94	0.1	1.17	-0.85	0.22	0.64	1.01	-0.77	0.29	0.97	0.84	2.6
Cthe_03020 NADH dehydrogenase (ubiquinone	12.6	13.23	12.49	12.24	0.11	0.99	-0.63	0.25	0.65	0.86	-0.03	0.35	0.98	0.84	5.48
Cthe_00715 Adenosylmethionine decarboxylase	13.04	13.43	12.7	12.34	0.34	1.09	-0.39	0.36	0.83	0.94	0.77	0.58	0.98	0.84	2.32
Cthe_00909 lipoprotein signal peptidase	8.41	8.97	8.23	8.13	0.18	0.84	-0.56	0.1	0.71	0.73	0.2	0.04	0.96	0.83	8.92
Cthe_00236 aldo/keto reductase	13.22	13.93	12.79	13.05	0.43	0.88	-0.71	-0.26	0.9	0.76	-0.3	-0.71	0.96	0.83	2.73
Cthe_00606 DNA internalization-related compe	11.15	11.82	10.53	10.99	0.62	0.83	-0.67	-0.46	1.06	0.72	-0.17	-1.13	0.96	0.83	2
Cthe_02897 transcription elongation factor Gre	13.83	14.25	13.09	13.52	0.74	0.73	-0.42	-0.43	1.15	0.64	0.67	-1.06	0.96	0.83	1.87
Cthe_01412 tryptophan synthase, beta subunit	11.05	11.7	10.38	10.89	0.67	0.81	-0.65	-0.51	1.1	0.7	-0.1	-1.23	0.96	0.83	1.89
Cthe_00909 lipoprotein signal peptidase	8.41	8.97	8.23	8.13	0.18	0.84	-0.56	0.1	0.71	0.73	0.2	0.04	0.96	0.83	8.92
Cthe_00584 protein of unknown function DUF5	7.29	7.98	7.04	7.11	0.25	0.87	-0.69	-0.07	0.76	0.75	-0.23	-0.31	0.96	0.83	4.94
Cthe_03183 TrkA-N	10	10.51	9.73	9.67	0.27	0.84	-0.51	0.06	0.78	0.73	0.37	-0.04	0.96	0.83	5.13
Cthe_00125 stage V sporulation AE	8.14	8.7	7.98	7.79	0.16	0.91	-0.56	0.19	0.69	0.79	0.2	0.23	0.96	0.83	6.15
Cthe_01412 tryptophan synthase, beta subunit	11.05	11.7	10.38	10.89	0.67	0.81	-0.65	-0.51	1.1	0.7	-0.1	-1.23	0.96	0.83	1.89
Cthe_00909 lipoprotein signal peptidase	8.41	8.97	8.23	8.13	0.18	0.84	-0.56	0.1	0.71	0.73	0.2	0.04	0.96	0.83	8.92
Cthe_01412 tryptophan synthase, beta subunit	11.05	11.7	10.38	10.89	0.67	0.81	-0.65	-0.51	1.1	0.7	-0.1	-1.23	0.96	0.83	1.89
Cthe_00436 Tetratricopeptide TPR_2	12.41	12.95	12.13	12.16	0.28	0.79	-0.54	-0.03	0.79	0.69	0.27	-0.23	0.95	0.82	5.28
Cthe_00370 conserved hypothetical radical SAM	10.01	10.72	9.78	9.84	0.23	0.88	-0.71	-0.06	0.75	0.76	-0.3	-0.29	0.95	0.82	4.57
Cthe_01813 urease accessory protein UreG	4.7	5.29	4.58	4.39	0.12	0.9	-0.59	0.19	0.66	0.78	0.1	0.23	0.95	0.82	7.28
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00436 Tetratricopeptide TPR_2	12.41	12.95	12.13	12.16	0.28	0.79	-0.54	-0.03	0.79	0.69	0.27	-0.23	0.95	0.82	5.28
Cthe_00332 phosphoribulokinase/uridine kinas	10.93	11.6	10.66	10.76	0.27	0.84	-0.67	-0.1	0.78	0.73	-0.17	-0.38	0.95	0.82	4.58
Cthe_00158 ribonuclease, Rne/Rng family	10	10.52	9.76	9.69	0.24	0.83	-0.52	0.07	0.75	0.72	0.33	-0.02	0.95	0.82	5.62
Cthe_01813 urease accessory protein UreG	4.7	5.29	4.58	4.39	0.12	0.9	-0.59	0.19	0.66	0.78	0.1	0.23	0.95	0.82	7.28
Cthe_02841 hypothetical protein	6.11	6.75	6.04	5.67	0.07	1.08	-0.64	0.37	0.62	0.93	-0.07	0.6	0.95	0.82	3.3
Cthe_00124 SpoVA protein	4.7	5.36	4.58	4.52	0.12	0.84	-0.66	0.06	0.66	0.73	-0.13	-0.04	0.95	0.82	12.92
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00158 ribonuclease, Rne/Rng family	10	10.52	9.76	9.69	0.24	0.83	-0.52	0.07	0.75	0.72	0.33	-0.02	0.95	0.82	5.62
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00332 phosphoribulokinase/uridine kinas	10.93	11.6	10.66	10.76	0.27	0.84	-0.67	-0.1	0.78	0.73	-0.17	-0.38	0.95	0.82	4.58
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00332 phosphoribulokinase/uridine kinas	10.93	11.6	10.66	10.76	0.27	0.84	-0.67	-0.1	0.78	0.73	-0.17	-0.38	0.95	0.82	4.58
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0.82	4.44
Cthe_00856 branched-chain amino acid aminot	13.73	14.29	13.59	13.33	0.14	0.96	-0.56	0.26	0.67	0.83	0.2	0.38	0.95	0	



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Cthe_00215 phenylalanyl-tRNA synthetase, bet	10.8	11.35	10.53	10.6	0.27	0.75	-0.55	-0.07	0.78	0.65	0.23	-0.31	0.91	0.78	4.7
Cthe_03200 alanyl-tRNA synthetase	10.41	11.04	10.16	10.26	0.25	0.78	-0.63	-0.1	0.76	0.68	-0.03	-0.38	0.91	0.78	4.78
Cthe_00215 phenylalanyl-tRNA synthetase, bet	10.8	11.35	10.53	10.6	0.27	0.75	-0.55	-0.07	0.78	0.65	0.23	-0.31	0.91	0.78	4.7
Cthe_03200 alanyl-tRNA synthetase	10.41	11.04	10.16	10.26	0.25	0.78	-0.63	-0.1	0.76	0.68	-0.03	-0.38	0.91	0.78	4.78
Cthe_01264 DNA polymerase III, alpha subunit	12.83	13.59	12.81	12.55	0.02	1.04	-0.76	0.26	0.58	0.9	-0.47	0.38	0.9	0.78	3.16
Cthe_03200 alanyl-tRNA synthetase	10.41	11.04	10.16	10.26	0.25	0.78	-0.63	-0.1	0.76	0.68	-0.03	-0.38	0.91	0.78	4.78
Cthe_00215 phenylalanyl-tRNA synthetase, bet	10.8	11.35	10.53	10.6	0.27	0.75	-0.55	-0.07	0.78	0.65	0.23	-0.31	0.91	0.78	4.7
Cthe_00988 tRNA pseudouridine synthase B	10.37	11.05	10.03	10.24	0.34	0.81	-0.68	-0.21	0.83	0.7	-0.2	-0.6	0.91	0.78	3.07
Cthe_01264 DNA polymerase III, alpha subunit	12.83	13.59	12.81	12.55	0.02	1.04	-0.76	0.26	0.58	0.9	-0.47	0.38	0.9	0.78	3.16
Cthe_00215 phenylalanyl-tRNA synthetase, bet	10.8	11.35	10.53	10.6	0.27	0.75	-0.55	-0.07	0.78	0.65	0.23	-0.31	0.91	0.78	4.7
Cthe_03200 alanyl-tRNA synthetase	10.41	11.04	10.16	10.26	0.25	0.78	-0.63	-0.1	0.76	0.68	-0.03	-0.38	0.91	0.78	4.78
Cthe_01103 prepilin-type cleavage/methylation	10.89	11.38	10.44	10.67	0.45	0.71	-0.49	-0.23	0.92	0.62	0.43	-0.65	0.89	0.77	2.54
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_02437 shikimate kinase	15.12	15.72	15.06	14.84	0.06	0.88	-0.6	0.22	0.61	0.76	0.07	0.29	0.89	0.77	5.83
Cthe_01749 DNA-cytosine methyltransferase	1.58	1			1.58	1	0.58		1.82	0.86	4		0.89	0.77	0.9
Cthe_01103 prepilin-type cleavage/methylation	10.89	11.38	10.44	10.67	0.45	0.71	-0.49	-0.23	0.92	0.62	0.43	-0.65	0.89	0.77	2.54
Cthe_01326 small GTP-binding protein	10.89	11.53	10.66	10.77	0.23	0.76	-0.64	-0.11	0.75	0.66	-0.07	-0.4	0.89	0.77	4.39
Cthe_02363 methyltransferase GidB	10.03	10.75	9.81	9.92	0.22	0.83	-0.72	-0.11	0.74	0.72	-0.33	-0.4	0.89	0.77	3.56
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_02739 trigger factor	12.36	12.98	11.8	12.24	0.56	0.74	-0.62	-0.44	1.01	0.64	0	-1.08	0.89	0.77	1.98
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_02437 shikimate kinase	15.12	15.72	15.06	14.84	0.06	0.88	-0.6	0.22	0.61	0.76	0.07	0.29	0.89	0.77	5.83
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_01749 DNA-cytosine methyltransferase	1.58	1			1.58	1	0.58		1.82	0.86	4		0.89	0.77	0.9
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_02363 methyltransferase GidB	10.03	10.75	9.81	9.92	0.22	0.83	-0.72	-0.11	0.74	0.72	-0.33	-0.4	0.89	0.77	3.56
Cthe_02437 shikimate kinase	15.12	15.72	15.06	14.84	0.06	0.88	-0.6	0.22	0.61	0.76	0.07	0.29	0.89	0.77	5.83
Cthe_01749 DNA-cytosine methyltransferase	1.58	1			1.58	1	0.58		1.82	0.86	4		0.89	0.77	0.9
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_02437 shikimate kinase	15.12	15.72	15.06	14.84	0.06	0.88	-0.6	0.22	0.61	0.76	0.07	0.29	0.89	0.77	5.83
Cthe_02437 shikimate kinase	15.12	15.72	15.06	14.84	0.06	0.88	-0.6	0.22	0.61	0.76	0.07	0.29	0.89	0.77	5.83
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_00372 glutamate synthase (NADPH), hom	10.64	11.25	10.32	10.5	0.32	0.75	-0.61	-0.18	0.82	0.65	0.03	-0.54	0.89	0.77	3.45
Cthe_00866 pyruvate flavodoxin/ferredoxin	11.3	11.89	10.9	11.15	0.4	0.74	-0.59	-0.25	0.88	0.64	0.1	-0.69	0.89	0.77	2.79
Cthe_03049 TPR repeat domain containing prot	10.6	11.37	10.55	10.41	0.05	0.96	-0.77	0.14	0.6	0.83	-0.5	0.13	0.88	0.76	3.54
Cthe_02102 methyltransferase small	10.87	11.59	10.89	10.55	-0.02	1.04	-0.72	0.34	0.55	0.9	-0.33	0.54	0.88	0.76	2.98
Cthe_02427 protein of unknown function DUF1	13.64	14.36	13.68	13.21	-0.04	1.15	-0.72	0.47	0.53	0.99	-0.33	0.81	0.88	0.76	2.29
Cthe_02447 ABC transporter related protein	7.93	8.52	7.89	7.55	0.04	0.97	-0.59	0.34	0.6	0.84	0.1	0.54	0.88	0.76	3.36
Cthe_00201 glutamate synthase, alpha subunit	11.6	12.35	11.45	11.48	0.15	0.87	-0.75	-0.03	0.68	0.75	-0.43	-0.23	0.88	0.76	3.71
Cthe_00781 GCN5-related N-acetyltransferase	6.67	7.44	6.39	6.58	0.28	0.86	-0.77	-0.19	0.79	0.75	-0.5	-0.56	0.88	0.76	2.59
Cthe_02239 carbon storage regulator, CsrA	7.24	7.93	7.21	7.08	0.03	0.85	-0.69	0.13	0.59	0.74	-0.23	0.1	0.88	0.76	6.74
Cthe_01090 hypothetical protein	10.38	11.06	10	10.29	0.38	0.77	-0.68	-0.29	0.87	0.67	-0.2	-0.77	0.88	0.76	2.46
Cthe_00188 ribonuclease PH	9.7	10.22	9.11	9.54	0.59	0.68	-0.52	-0.43	1.03	0.59	0.33	-1.06	0.88	0.76	1.91
Cthe_02267 Sodium-transporting two-sector AT	11.54	12.44	11.41	11.38	0.13	1.06	-0.9	0.03	0.67	0.92	-0.93	-0.1	0.88	0.76	2.17
Cthe_00048 copper amine oxidase-like protein	6.04	6.51	5.32	5.86	0.72	0.65	-0.47	-0.54	1.13	0.57	0.5	-1.29	0.88	0.76	1.63
Cthe_01462 transcriptional regulator, XRE family	11.49	12	11.4	10.85	0.09	1.15	-0.51	0.55	0.63	0.99	0.37	0.98	0.88	0.76	2
Cthe_00790 conserved hythetical protein	10.38	10.8	9.88	10.1	0.5	0.7	-0.42	-0.22	0.96	0.61	0.67	-0.63	0.88	0.76	2.21
Cthe_02267 Sodium-transporting two-sector AT	11.54	12.44	11.41	11.38	0.13	1.06	-0.9	0.03	0.67	0.92	-0.93	-0.1	0.88	0.76	2.17
Cthe_02447 ABC transporter related protein	7.93	8.52	7.89	7.55	0.04	0.97	-0.59	0.34	0.6	0.84	0.1	0.54	0.88	0.76	3.36
Cthe_02267 Sodium-transporting two-sector AT	11.54	12.44	11.41	11.38	0.13	1.06	-0.9	0.03	0.67	0.92	-0.93	-0.1	0.88	0.76	2.17
Cthe_00188 ribonuclease PH	9.7	10.22	9.11	9.54	0.59	0.68	-0.52	-0.43	1.03	0.59	0.33	-1.06	0.88	0.76	1.91
Cthe_02447 ABC transporter related protein	7.93	8.52	7.89	7.55	0.04	0.97	-0.59	0.34	0.6	0.84	0.1	0.54	0.88	0.76	3.36
Cthe_00188 ribonuclease PH	9.7	10.22	9.11	9.54	0.59	0.68	-0.52	-0.43	1.03	0.59	0.33	-1.06	0.88	0.76	1.91
Cthe_02267 Sodium-transporting two-sector AT	11.54	12.44	11.41	11.38	0.13	1.06	-0.9	0.03	0.67	0.92	-0.93	-0.1	0.88	0.76	2.17
Cthe_00656 type IV pilus assembly protein PilM	14.32	15.07	14.34	14.03	-0.02	1.04	-0.75	0.31	0.55	0.9	-0.43	0.48	0.87	0.75	2.92
Cthe_00610 histidinol-phosphate aminotransfer	9.08	9.73	9.06	8.94	0.02	0.79	-0.65	0.12	0.58	0.69	-0.1	0.08	0.87	0.75	12.57
Cthe_00656 type IV pilus assembly protein PilM	14.32	15.07	14.34	14.03	-0.02	1.04	-0.75	0.31	0.55	0.9	-0.43	0.48	0.87	0.75	2.92
Cthe_01037 cell wall hydrolase/autolysin	9.49	10.02	9.05	9.32	0.44	0.7	-0.53	-0.27	0.91	0.61	0.3	-0.73	0.87	0.75	2.48
Cthe_02589 hypothetical protein	9.27	9.97	9.15	9.16	0.12	0.81	-0.7	-0.01	0.66	0.7	-0.27	-0.19	0.87	0.75	5.2
Cthe_02596 protein tyrosine phosphatase	10.81	11.59	10.77	10.64	0.04	0.95	-0.78	0.13	0.6	0.82	-0.53	0.1	0.87	0.75	3.36
Cthe_00837 protein of unknown function DUF3	7.58	8.11	7.22	7.41	0.36	0.7	-0.53	-0.19	0.85	0.61	0.3	-0.56	0.87	0.75	2.94
Cthe_01793 protein of unknown function DUF1	12.55	13.14	12.53	12	0.02	1.14	-0.59	0.53	0.58	0.98	0.1	0.94	0.87	0.75	2.15
Cthe_02228 MaoC-like dehydratase	9.78	10.08	9.11	9.41	0.67	0.67	-0.3	-0.3	1.1	0.58	1.07	-0.79	0.87	0.75	1.67
Cthe_02432 electron transport complex, RnfAB	12.26	13.11	12.32	11.9	-0.06	1.21	-0.85	0.42	0.52	1.04	-0.77	0.71	0.87	0.75	1.98
Cthe_02757 sodium/hydrogen exchanger	9.18	9.54	8.77	8.76	0.41	0.78	-0.36	0.01	0.89	0.68	0.87	-0.15	0.87	0.75	2.27
Cthe_01465 Redoxin	10.64	11.23	10.62	10.12	0.02	1.11	-0.59	0.5	0.58	0.96	0.1	0.88	0.87	0.75	2.26
Cthe_01940 RDD domain containing protein	9.1	9.86	8.83	9.01	0.27	0.85	-0.76	-0.18	0.78	0.74	-0.47	-0.54	0.87	0.75	2.68
Cthe_00011 hypothetical protein	7.19	7.83	6.46	7.12	0.73	0.71	-0.64	-0.66	1.14	0.62	-0.07	-1.54	0.87	0.75	1.5
Cthe_00194 hypothetical protein	6.7	7.13	6.41	6.34	0.29	0.79	-0.43	0.07	0.79	0.69	0.63	-0.02	0.87	0.75	2.97
Cthe_00610 histidinol-phosphate aminotransfer	9.08	9.73	9.06	8.94	0.02	0.79	-0.65	0.12	0.58						



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Cthe_01372 hypothetical protein	11.51	11.88	11.18	11.08	0.33	0.8	-0.37	0.1	0.83	0.69	0.83	0.04	0.85	0.73	2.32
Cthe_00548 ABC transporter related protein	9.72	10.27	9.47	9.57	0.25	0.7	-0.55	-0.1	0.76	0.61	0.23	-0.38	0.85	0.73	3.92
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_00548 ABC transporter related protein	9.72	10.27	9.47	9.57	0.25	0.7	-0.55	-0.1	0.76	0.61	0.23	-0.38	0.85	0.73	3.92
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_00373 oxidoreductase FAD/NAD(P)-bindin	10.27	10.91	9.7	10.2	0.57	0.71	-0.64	-0.5	1.02	0.62	-0.07	-1.21	0.85	0.73	1.76
Cthe_00998 putative membrane-associated zinc	10.87	11.51	10.4	10.8	0.47	0.71	-0.64	-0.4	0.94	0.62	-0.07	-1	0.85	0.73	2.01
Cthe_00373 oxidoreductase FAD/NAD(P)-bindin	10.27	10.91	9.7	10.2	0.57	0.71	-0.64	-0.5	1.02	0.62	-0.07	-1.21	0.85	0.73	1.76
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_00548 ABC transporter related protein	9.72	10.27	9.47	9.57	0.25	0.7	-0.55	-0.1	0.76	0.61	0.23	-0.38	0.85	0.73	3.92
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_00548 ABC transporter related protein	9.72	10.27	9.47	9.57	0.25	0.7	-0.55	-0.1	0.76	0.61	0.23	-0.38	0.85	0.73	3.92
Cthe_00548 ABC transporter related protein	9.72	10.27	9.47	9.57	0.25	0.7	-0.55	-0.1	0.76	0.61	0.23	-0.38	0.85	0.73	3.92
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_00645 homocysteine S-methyltransferase	11.4	12.03	11.39	11.28	0.01	0.75	-0.63	0.11	0.57	0.65	-0.03	0.06	0.85	0.73	23.01
Cthe_01067 GTP-binding protein Era	11.18	11.87	11.11	11.11	0.07	0.76	-0.69	0	0.62	0.66	-0.23	-0.17	0.83	0.72	5.65
Cthe_01955 RNA binding S1	9.81	10.57	9.74	9.72	0.07	0.85	-0.76	0.02	0.62	0.74	-0.47	-0.13	0.83	0.72	3.54
Cthe_00748 binding-protein-dependent transpo	9.44	10.06	9.34	9.36	0.1	0.7	-0.62	-0.02	0.64	0.61	0	-0.21	0.83	0.72	7.52
Cthe_02095 hydrolase, TatD family	10.03	10.8	9.95	9.94	0.08	0.86	-0.77	0.01	0.63	0.75	-0.5	-0.15	0.83	0.72	3.35
Cthe_00885 dephospho-CoA kinase	8.97	9.45	8.49	8.8	0.48	0.65	-0.48	-0.31	0.94	0.57	0.47	-0.81	0.84	0.72	2.1
Cthe_01380 response regulator receiver protein	13.01	13.66	13.08	12.54	-0.07	1.12	-0.65	0.54	0.51	0.97	-0.1	0.96	0.83	0.72	2.03
Cthe_00504 Putative enzyme of poly-gamma-gl	9.76	10.36	9.74	9.59	0.02	0.77	-0.6	0.15	0.58	0.67	0.07	0.15	0.84	0.72	9.56
Cthe_01380 response regulator receiver protein	13.01	13.66	13.08	12.54	-0.07	1.12	-0.65	0.54	0.51	0.97	-0.1	0.96	0.83	0.72	2.03
Cthe_00791 protein of unknown function DUF5	12.3	12.86	12.13	12.16	0.17	0.7	-0.56	-0.03	0.7	0.61	0.2	-0.23	0.84	0.72	5.44
Cthe_01859 protein of unknown function DUF2	10.6	11.26	10.24	10.54	0.36	0.72	-0.66	-0.3	0.85	0.63	-0.13	-0.79	0.83	0.72	2.36
Cthe_02430 electron transport complex, RnfAB	13.83	14.69	13.98	13.38	-0.15	1.31	-0.86	0.6	0.44	1.13	-0.8	1.08	0.84	0.72	1.61
Cthe_02253 ATP-dependent metalloprotease Ft	14.31	14.93	14.24	14.23	0.07	0.7	-0.62	0.01	0.62	0.61	0	-0.15	0.83	0.72	10.35
Cthe_02408 phage shock protein A, PspA	13.11	13.64	12.98	12.9	0.13	0.74	-0.53	0.08	0.67	0.64	0.3	0	0.84	0.72	5.52
Cthe_00452 cellulosome anchoring protein, coh	10.18	10.74	10.13	9.96	0.05	0.78	-0.56	0.17	0.6	0.68	0.2	0.19	0.83	0.72	5.87
Cthe_02438 hypothetical protein	9.17	9.61	8.74	8.94	0.43	0.67	-0.44	-0.2	0.9	0.58	0.6	-0.58	0.84	0.72	2.29
Cthe_01859 protein of unknown function DUF2	10.6	11.26	10.24	10.54	0.36	0.72	-0.66	-0.3	0.85	0.63	-0.13	-0.79	0.83	0.72	2.36
Cthe_00748 binding-protein-dependent transpo	9.44	10.06	9.34	9.36	0.1	0.7	-0.62	-0.02	0.64	0.61	0	-0.21	0.83	0.72	7.52
Cthe_00885 dephospho-CoA kinase	8.97	9.45	8.49	8.8	0.48	0.65	-0.48	-0.31	0.94	0.57	0.47	-0.81	0.84	0.72	2.1
Cthe_00885 dephospho-CoA kinase	8.97	9.45	8.49	8.8	0.48	0.65	-0.48	-0.31	0.94	0.57	0.47	-0.81	0.84	0.72	2.1
Cthe_02253 ATP-dependent metalloprotease Ft	14.31	14.93	14.24	14.23	0.07	0.7	-0.62	0.01	0.62	0.61	0	-0.15	0.83	0.72	10.35
Cthe_02095 hydrolase, TatD family	10.03	10.8	9.95	9.94	0.08	0.86	-0.77	0.01	0.63	0.75	-0.5	-0.15	0.83	0.72	3.35
Cthe_00885 dephospho-CoA kinase	8.97	9.45	8.49	8.8	0.48	0.65	-0.48	-0.31	0.94	0.57	0.47	-0.81	0.84	0.72	2.1
Cthe_00926 signal recognition particle-docking	10.5	11.16	10.3	10.44	0.2	0.72	-0.66	-0.14	0.72	0.63	-0.13	-0.46	0.82	0.71	3.57
Cthe_00024 biotin biosynthesis protein BioC	6.43	7.04	6.44	6.32	-0.01	0.72	-0.61	0.12	0.56	0.63	0.03	0.08	0.82	0.71	17.62
Cthe_02096 methionyl-tRNA synthetase	10.62	11.12	10.41	10.43	0.21	0.69	-0.5	-0.02	0.73	0.6	0.4	-0.21	0.82	0.71	3.74
Cthe_01163 phosphoglucosamine mutase	9.31	10.11	9.13	9.26	0.18	0.85	-0.8	-0.13	0.71	0.74	-0.6	-0.44	0.82	0.71	2.46
Cthe_02222 glycosyltransferase 28-like protein	8.98	9.78	9.06	8.72	-0.08	1.06	-0.8	0.34	0.5	0.92	-0.6	0.54	0.82	0.71	2.32
Cthe_00103 protein of unknown function UPF0	7.94	8.41	7.79	7.61	0.15	0.8	-0.47	0.18	0.68	0.69	0.5	0.21	0.82	0.71	3.19
Cthe_01479 hypothetical protein	2	2.32	1.58	1.58	0.42	0.74	-0.32	0	0.9	0.64	1	-0.17	0.82	0.71	1.94
Cthe_00278 pseudouridine synthase	9.95	10.67	9.93	9.86	0.02	0.81	-0.72	0.07	0.58	0.7	-0.33	-0.02	0.82	0.71	4.91
Cthe_02096 methionyl-tRNA synthetase	10.62	11.12	10.41	10.43	0.21	0.69	-0.5	-0.02	0.73	0.6	0.4	-0.21	0.82	0.71	3.74
Cthe_02939 tRNA pseudouridine synthase A	7.06	7.7	7.08	6.94	-0.02	0.76	-0.64	0.14	0.55	0.66	-0.07	0.13	0.82	0.71	10.39
Cthe_02433 electron transport complex, RnfAB	12.12	13.06	12.26	11.75	-0.14	1.31	-0.94	0.51	0.45	1.13	-1.07	0.9	0.82	0.71	1.55
Cthe_01010 peptidase U32	11.52	12.24	11.45	11.45	0.07	0.79	-0.72	0	0.62	0.69	-0.33	-0.17	0.82	0.71	4.46
Cthe_00454 hypothetical protein	3.91	4.64	4	3.58	-0.09	1.06	-0.73	0.42	0.49	0.92	-0.37	0.71	0.82	0.71	2.32
Cthe_00248 transposase, IS4	7.04	7.22	6.78	5.64	0.26	1.58	-0.18	1.14	0.77	1.36	1.47	2.21	0.82	0.71	1.05
Cthe_01966 hypothetical protein	8.38	8.72	8.07	7.89	0.31	0.83	-0.34	0.18	0.81	0.72	0.93	0.21	0.82	0.71	2.03
Cthe_00100 hypothetical protein	10.27	10.91	9.71	10.23	0.56	0.68	-0.64	-0.52	1.01	0.59	-0.07	-1.25	0.82	0.71	1.67
Cthe_03234 hypothetical protein	1	1.58	0	1	1	0.58	-0.58	-1	1.36	0.51	0.13	-2.25	0.82	0.71	1.15
Cthe_01941 putative regulatory protein, FmdB f	9.36	10.29	9.12	9.3	0.24	0.99	-0.93	-0.18	0.75	0.86	-1.03	-0.54	0.82	0.71	1.75
Cthe_01450 hypothetical protein	8.54	9.16	8.41	8.47	0.13	0.69	-0.62	-0.06	0.67	0.6	0	-0.29	0.82	0.71	5.54
Cthe_02096 methionyl-tRNA synthetase	10.62	11.12	10.41	10.43	0.21	0.69	-0.5	-0.02	0.73	0.6	0.4	-0.21	0.82	0.71	3.74
Cthe_02096 methionyl-tRNA synthetase	10.62	11.12	10.41	10.43	0.21	0.69	-0.5	-0.02	0.73	0.6	0.4	-0.21	0.82	0.71	3.74
Cthe_00926 signal recognition particle-docking	10.5	11.16	10.3	10.44	0.2	0.72	-0.66	-0.14	0.72	0.63	-0.13	-0.46	0.82	0.71	3.57
Cthe_00278 pseudouridine synthase	9.95	10.67	9.93	9.86	0.02	0.81	-0.72	0.07	0.58	0.7	-0.33	-0.02	0.82	0.71	4.91
Cthe_02939 tRNA pseudouridine synthase A	7.06	7.7	7.08	6.94	-0.02	0.76	-0.64	0.14	0.55	0.66	-0.07	0.13	0.82	0.71	10.39
Cthe_02096 methionyl-tRNA synthetase	10.62	11.12	10.41	10.43	0.21	0.69	-0.5	-0.02	0.73	0.6	0.4	-0.21	0.82	0.71	3.74
Cthe_01010 peptidase U32	11.52	12.24	11.45	11.45	0.07	0.79	-0.72	0	0.62	0.69	-0.33	-0.17	0.82	0.71	4.46
Cthe_01163 phosphoglucosamine mutase	9.31	10.11	9.13	9.26	0.18	0.85	-0.8	-0.13	0.71	0.74	-0.6	-0.44	0.82	0.71	2.46
Cthe_02096 methionyl-tRNA synthetase	10.62	11.12	10.41	10.43	0.21	0.69	-0.5	-0.02	0.73	0.6	0.4	-0.21	0.82	0.71	3.74
Cthe_01163 phosphoglucosamine mutase	9.31	10.11	9.13	9.26	0.18	0.85	-0.8	-0.13	0.71	0.74	-0.6	-0.44	0.82	0.71	2.46
Cthe_02524 transcriptional regulator, BadM/Rrf	10.6	11.25	10.05	10.57	0.55	0.68	-0.65	-0.52	1	0.59	-0.1	-1.25	0.81	0.7	1.65
Cthe_00251 transglutaminase-like protein	10.67	11.42	10.53	10.62	0.14	0.8	-0.75	-0.09	0.67	0.69	-0.43	-0.35	0.81	0.7	3.1
Cthe_00104 riboflavin biosynthesis protein RibD	12.67	13.47	12.76	12.42	-0.09	1.05	-0.8	0.34	0.49	0.91	-0.6	0.54	0.81	0.7	2.29
Cthe_00681 IMP dehydrogenase/GMP reductas	12.93	13.63	12.6	12.9	0.33	0.73	-0.7	-0.3	0.83	0.64	-0.27	-0.79	0.81	0.7	2.24
Cthe_01235 Cellulose 1,4-beta-cellobiosidase	12.1	12.74	12.13	12.01	-0.03	0.73	-0.64	0.12	0.54	0.64	-0.07	0.08	0.81	0.7	14.07
Cthe_02947 prolyl-tRNA synthetase	10.19	10.72	10.1	10	0.09	0.72	-0.53	0.1	0.63	0.63	0.3	0.04	0.81	0.7	5.26
Cthe_01448 MATE efflux family protein	8.02	8.59	8	7.83	0.02	0.76	-0.57	0.17	0.58	0.66	0.17	0.19	0.81	0.7	6.15
Cthe_01306 hypothetical protein	11.82	12.49	11.87	11.63	-0.05	0.86	-0.67	0.24	0.52	0.75	-0.17	0.33	0.81	0.7	4.39
Cthe_00018 hypothetical protein	8.34	8.95	7.99	8.28	0.35	0.67	-0.61	-0.29	0.84	0.58	0.03	-0.77	0.81	0.7	2.37
Cthe_02947 prolyl-tRNA synthetase	10.19	10.72	10.1	10	0.09	0.72	-0.53	0.1	0.63	0.63	0.3	0.04	0.81	0.7	5.26



Cthe_00681 IMP dehydrogenase/GMP reductas	12.93	13.63	12.6	12.9	0.33	0.73	-0.7	-0.3	0.83	0.64	-0.27	-0.79	0.81	0.7	2.24
Cthe_00681 IMP dehydrogenase/GMP reductas	12.93	13.63	12.6	12.9	0.33	0.73	-0.7	-0.3	0.83	0.64	-0.27	-0.79	0.81	0.7	2.24
Cthe_00104 riboflavin biosynthesis protein RibD	12.67	13.47	12.76	12.42	-0.09	1.05	-0.8	0.34	0.49	0.91	-0.6	0.54	0.81	0.7	2.29
Cthe_00027 hypothetical protein	6.19	7.1	5.61	6.21	0.58	0.89	-0.91	-0.6	1.02	0.77	-0.97	-1.42	0.8	0.69	1.33
Cthe_02025 Resolvase helix-turn-helix region co	9.01	9.92	9.17	8.65	-0.16	1.27	-0.91	0.52	0.44	1.09	-0.97	0.92	0.8	0.69	1.57
Cthe_00027 hypothetical protein	6.19	7.1	5.61	6.21	0.58	0.89	-0.91	-0.6	1.02	0.77	-0.97	-1.42	0.8	0.69	1.33
Cthe_00105 riboflavin synthase, alpha subunit	11.96	12.85	12.05	11.73	-0.09	1.12	-0.89	0.32	0.49	0.97	-0.9	0.5	0.8	0.69	1.88
Cthe_00622 methylthioadenosine phosphorylas	11.84	12.52	11.9	11.68	-0.06	0.84	-0.68	0.22	0.52	0.73	-0.2	0.29	0.8	0.69	4.54
Cthe_00712 cytidylate kinase	12.05	12.58	11.5	11.97	0.55	0.61	-0.53	-0.47	1	0.53	0.3	-1.15	0.8	0.69	1.7
Cthe_01315 Guanylate kinase	9.54	10.01	9.27	9.35	0.27	0.66	-0.47	-0.08	0.78	0.58	0.5	-0.33	0.8	0.69	2.9
Cthe_00214 phenylalanyl-tRNA synthetase, alph	9.5	10.12	9.21	9.44	0.29	0.68	-0.62	-0.23	0.79	0.59	0	-0.65	0.8	0.69	2.71
Cthe_02266 Vacuolar H+-transporting two-sect	9.28	10.3	9.07	9.21	0.21	1.09	-1.02	-0.14	0.73	0.94	-1.33	-0.46	0.8	0.69	1.51
Cthe_00941 CDP-diacylglycerol-glycerol-3-phos	10.99	11.47	10.81	10.78	0.18	0.69	-0.48	0.03	0.71	0.6	0.47	-0.1	0.8	0.69	3.45
Cthe_02342 hypothetical protein	8.76	9.46	8.56	8.73	0.2	0.73	-0.7	-0.17	0.72	0.64	-0.27	-0.52	0.8	0.69	2.94
Cthe_02159 hypothetical protein	8.64	9.15	8.54	8.41	0.1	0.74	-0.51	0.13	0.64	0.64	0.37	0.1	0.8	0.69	4.22
Cthe_02148 Carbohydrate-binding, CenC-like pr	10.47	10.8	9.9	10.19	0.57	0.61	-0.33	-0.29	1.02	0.53	0.97	-0.77	0.8	0.69	1.66
Cthe_02266 Vacuolar H+-transporting two-sect	9.28	10.3	9.07	9.21	0.21	1.09	-1.02	-0.14	0.73	0.94	-1.33	-0.46	0.8	0.69	1.51
Cthe_00712 cytidylate kinase	12.05	12.58	11.5	11.97	0.55	0.61	-0.53	-0.47	1	0.53	0.3	-1.15	0.8	0.69	1.7
Cthe_00214 phenylalanyl-tRNA synthetase, alph	9.5	10.12	9.21	9.44	0.29	0.68	-0.62	-0.23	0.79	0.59	0	-0.65	0.8	0.69	2.71
Cthe_00622 methylthioadenosine phosphorylas	11.84	12.52	11.9	11.68	-0.06	0.84	-0.68	0.22	0.52	0.73	-0.2	0.29	0.8	0.69	4.54
Cthe_01315 Guanylate kinase	9.54	10.01	9.27	9.35	0.27	0.66	-0.47	-0.08	0.78	0.58	0.5	-0.33	0.8	0.69	2.9
Cthe_00214 phenylalanyl-tRNA synthetase, alph	9.5	10.12	9.21	9.44	0.29	0.68	-0.62	-0.23	0.79	0.59	0	-0.65	0.8	0.69	2.71
Cthe_00105 riboflavin synthase, alpha subunit	11.96	12.85	12.05	11.73	-0.09	1.12	-0.89	0.32	0.49	0.97	-0.9	0.5	0.8	0.69	1.88
Cthe_02266 Vacuolar H+-transporting two-sect	9.28	10.3	9.07	9.21	0.21	1.09	-1.02	-0.14	0.73	0.94	-1.33	-0.46	0.8	0.69	1.51
Cthe_00712 cytidylate kinase	12.05	12.58	11.5	11.97	0.55	0.61	-0.53	-0.47	1	0.53	0.3	-1.15	0.8	0.69	1.7
Cthe_01315 Guanylate kinase	9.54	10.01	9.27	9.35	0.27	0.66	-0.47	-0.08	0.78	0.58	0.5	-0.33	0.8	0.69	2.9
Cthe_00941 CDP-diacylglycerol-glycerol-3-phos	10.99	11.47	10.81	10.78	0.18	0.69	-0.48	0.03	0.71	0.6	0.47	-0.1	0.8	0.69	3.45
Cthe_00214 phenylalanyl-tRNA synthetase, alph	9.5	10.12	9.21	9.44	0.29	0.68	-0.62	-0.23	0.79	0.59	0	-0.65	0.8	0.69	2.71
Cthe_00105 riboflavin synthase, alpha subunit	11.96	12.85	12.05	11.73	-0.09	1.12	-0.89	0.32	0.49	0.97	-0.9	0.5	0.8	0.69	1.88
Cthe_00622 methylthioadenosine phosphorylas	11.84	12.52	11.9	11.68	-0.06	0.84	-0.68	0.22	0.52	0.73	-0.2	0.29	0.8	0.69	4.54
Cthe_00105 riboflavin synthase, alpha subunit	11.96	12.85	12.05	11.73	-0.09	1.12	-0.89	0.32	0.49	0.97	-0.9	0.5	0.8	0.69	1.88
Cthe_01315 Guanylate kinase	9.54	10.01	9.27	9.35	0.27	0.66	-0.47	-0.08	0.78	0.58	0.5	-0.33	0.8	0.69	2.9
Cthe_00105 riboflavin synthase, alpha subunit	11.96	12.85	12.05	11.73	-0.09	1.12	-0.89	0.32	0.49	0.97	-0.9	0.5	0.8	0.69	1.88
Cthe_00941 CDP-diacylglycerol-glycerol-3-phos	10.99	11.47	10.81	10.78	0.18	0.69	-0.48	0.03	0.71	0.6	0.47	-0.1	0.8	0.69	3.45
Cthe_00941 CDP-diacylglycerol-glycerol-3-phos	10.99	11.47	10.81	10.78	0.18	0.69	-0.48	0.03	0.71	0.6	0.47	-0.1	0.8	0.69	3.45
Cthe_00214 phenylalanyl-tRNA synthetase, alph	9.5	10.12	9.21	9.44	0.29	0.68	-0.62	-0.23	0.79	0.59	0	-0.65	0.8	0.69	2.71
Cthe_01315 Guanylate kinase	9.54	10.01	9.27	9.35	0.27	0.66	-0.47	-0.08	0.78	0.58	0.5	-0.33	0.8	0.69	2.9
Cthe_02266 Vacuolar H+-transporting two-sect	9.28	10.3	9.07	9.21	0.21	1.09	-1.02	-0.14	0.73	0.94	-1.33	-0.46	0.8	0.69	1.51
Cthe_00941 CDP-diacylglycerol-glycerol-3-phos	10.99	11.47	10.81	10.78	0.18	0.69	-0.48	0.03	0.71	0.6	0.47	-0.1	0.8	0.69	3.45
Cthe_00105 riboflavin synthase, alpha subunit	11.96	12.85	12.05	11.73	-0.09	1.12	-0.89	0.32	0.49	0.97	-0.9	0.5	0.8	0.69	1.88
Cthe_03166 glucose-1-phosphate adenylyltrans	9.93	10.49	9.4	9.87	0.53	0.62	-0.56	-0.47	0.98	0.54	0.2	-1.15	0.79	0.68	1.71
Cthe_00362 transcriptional regulator, AsnC fam	11.04	11.42	10.29	10.9	0.75	0.52	-0.38	-0.61	1.16	0.46	0.8	-1.44	0.79	0.68	1.35
Cthe_01014 MutS2 family protein	10.97	11.54	10.54	10.91	0.43	0.63	-0.57	-0.37	0.9	0.55	0.17	-0.94	0.79	0.68	1.97
Cthe_03124 AMP-dependent synthetase and lig	12.72	13.34	12.76	12.68	-0.04	0.66	-0.62	0.08	0.53	0.58	0	0	0.79	0.68	30
Cthe_01960 Peptidoglycan-binding domain 1	13.6	14.2	13.63	13.39	-0.03	0.81	-0.6	0.24	0.54	0.7	0.07	0.33	0.79	0.68	4.68
Cthe_02898 anti-sigma-factor antagonist	9.74	10.35	9.44	9.69	0.3	0.66	-0.61	-0.25	0.8	0.58	0.03	-0.69	0.79	0.68	2.55
Cthe_03044 protein of unknown function DUF9	10.73	11.34	10.77	10.56	-0.04	0.78	-0.61	0.21	0.53	0.68	0.03	0.27	0.79	0.68	5.67
Cthe_00064 Na/PI-cotransporter II-related prot	15.9	16.57	15.99	15.59	-0.09	0.98	-0.67	0.4	0.49	0.85	-0.17	0.67	0.79	0.68	2.53
Cthe_02687 thioesterase superfamily	8.04	8.42	7.77	7.67	0.27	0.75	-0.38	0.1	0.78	0.65	0.8	0.04	0.79	0.68	2.26
Cthe_03124 AMP-dependent synthetase and lig	12.72	13.34	12.76	12.68	-0.04	0.66	-0.62	0.08	0.53	0.58	0	0	0.79	0.68	30
Cthe_03166 glucose-1-phosphate adenylyltrans	9.93	10.49	9.4	9.87	0.53	0.62	-0.56	-0.47	0.98	0.54	0.2	-1.15	0.79	0.68	1.71
Cthe_03166 glucose-1-phosphate adenylyltrans	9.93	10.49	9.4	9.87	0.53	0.62	-0.56	-0.47	0.98	0.54	0.2	-1.15	0.79	0.68	1.71
Cthe_03166 glucose-1-phosphate adenylyltrans	9.93	10.49	9.4	9.87	0.53	0.62	-0.56	-0.47	0.98	0.54	0.2	-1.15	0.79	0.68	1.71
Cthe_00576 Ribulose-phosphate 3-epimerase	13.03	13.61	13.05	12.88	-0.02	0.73	-0.58	0.17	0.55	0.64	0.13	0.19	0.78	0.67	6.55
Cthe_01261 6-phosphofructokinase	11.09	11.75	11.08	11.06	0.01	0.69	-0.66	0.02	0.57	0.6	-0.13	-0.13	0.78	0.67	8.04
Cthe_00206 UvrD/REP helicase	11.23	12.19	11.18	11.12	0.05	1.07	-0.96	0.06	0.6	0.92	-1.13	-0.04	0.78	0.67	1.73
Cthe_00784 hypothetical protein	8.29	8.72	7.88	8.11	0.41	0.61	-0.43	-0.23	0.89	0.53	0.63	-0.65	0.78	0.67	2.04
Cthe_02627 purine operon repressor, PurR	10.46	11	10.39	10.32	0.07	0.68	-0.54	0.07	0.62	0.59	0.27	-0.02	0.78	0.67	5.64
Cthe_02899 putative anti-sigma regulatory fact	9.92	10.57	9.62	9.9	0.3	0.67	-0.65	-0.28	0.8	0.58	-0.1	-0.75	0.78	0.67	2.33
Cthe_00569 protein of unknown function DUF1	11.01	11.65	11.07	10.93	-0.06	0.72	-0.64	0.14	0.52	0.63	-0.07	0.13	0.78	0.67	9.88
Cthe_01481 membrane protein-like protein	6.94	7.62	7.03	6.67	-0.09	0.95	-0.68	0.36	0.49	0.82	-0.2	0.58	0.78	0.67	2.78
Cthe_00917 glutaminyl-tRNA synthetase	12.82	13.27	12.31	12.69	0.51	0.58	-0.45	-0.38	0.97	0.51	0.57	-0.96	0.78	0.67	1.75
Cthe_00713 1-acyl-sn-glycerol-3-phosphate acyl	11.71	12.18	11.14	11.61	0.57	0.57	-0.47	-0.47	1.02	0.5	0.5	-1.15	0.78	0.67	1.62
Cthe_00361 hypothetical protein	12.32	12.49	11.85	11.61	0.47	0.88	-0.17	0.24	0.94	0.76	1.5	0.33	0.78	0.67	1.41
Cthe_00249 peptidase C11, clostripain	11.05	11.81	10.98	11.02	0.07	0.79	-0.76	-0.04	0.62	0.69	-0.47	-0.25	0.78	0.67	3.11
Cthe_00917 glutaminyl-tRNA synthetase	12.82	13.27	12.31	12.69	0.51	0.58	-0.45	-0.38	0.97	0.51	0.57	-0.96	0.78	0.67	1.75
Cthe_00576 Ribulose-phosphate 3-epimerase	13.03	13.61	13.05	12.88	-0.02	0.73	-0.58	0.17	0.55	0.64	0.13	0.19	0.78	0.67	6.55
Cthe_00917 glutaminyl-tRNA synthetase	12.82	13.27	12.31	12.69	0.51	0.58	-0.45	-0.38	0.97	0.51	0.57	-0.96	0.78	0.67	1.75
Cthe_01261 6-phosphofructokinase	11.09	11.75	11.08	11.06	0.01	0.69	-0.66	0.02	0.57	0.6	-0.13	-0.13	0.78	0.67	8.04
Cthe_00713 1-acyl-sn-glycerol-3-phosphate acyl	11.71	12.18	11.14	11.61	0.57	0.57	-0.47	-0.47	1.02	0.5	0.5	-1.15	0.78	0.67	1.62
Cthe_00576 Ribulose-phosphate 3-epimerase	13.03	13.61	13.05	12.88	-0.02	0.73	-0.58	0.17	0.55	0.64	0.13	0.19	0.78	0.67	6.55
Cthe_01261 6-phosphofructokinase	11.09	11.75	11.08	11.06	0.01	0.69	-0.66	0.02	0.57	0.6	-0.13	-0.13	0.78	0.67	8.04
Cthe_00917 glutaminyl-tRNA synthetase	12.82	13.27	12.31	12.69	0.51	0.58	-0.45	-0.38	0.97	0.51	0.57	-0.96	0.78	0.67	1.75
Cthe_01261 6-phosphofructokinase	11.09	11.75	11.08	11.06	0.01	0.69	-0.66	0.02	0.57	0.6	-0.13	-0.13	0.78	0.67	8.04
Cthe_00206 UvrD/REP helicase	11.23	12.19	11.18	11.12	0.05	1.07	-0.96	0.06	0.6	0.92	-1.13	-0.04	0.78	0.67	1.73
Cthe_02899 putative anti-sigma regulatory fact	9.92	10.57	9.62	9.9	0.3	0.67	-0.65	-0.28	0.8	0.58	-0.1	-0.75	0.78	0.67	2.33
Cthe_00576 Ribulose-phosphate 3-epimerase	13.03	13.61	13.05	12.88	-0.02	0.73	-0.58	0.17	0.55	0.64	0.13	0.19	0.78	0.67	



Cthe_00576 Ribulose-phosphate 3-epimerase	13.03	13.61	13.05	12.88	-0.02	0.73	-0.58	0.17	0.55	0.64	0.13	0.19	0.78	0.67	6.55
Cthe_00917 glutaminyl-tRNA synthetase	12.82	13.27	12.31	12.69	0.51	0.58	-0.45	-0.38	0.97	0.51	0.57	-0.96	0.78	0.67	1.75
Cthe_01261 6-phosphofructokinase	11.09	11.75	11.08	11.06	0.01	0.69	-0.66	0.02	0.57	0.6	-0.13	-0.13	0.78	0.67	8.04
Cthe_00713 1-acyl-sn-glycerol-3-phosphate acyl	11.71	12.18	11.14	11.61	0.57	0.57	-0.47	-0.47	1.02	0.5	0.5	-1.15	0.78	0.67	1.62
Cthe_01261 6-phosphofructokinase	11.09	11.75	11.08	11.06	0.01	0.69	-0.66	0.02	0.57	0.6	-0.13	-0.13	0.78	0.67	8.04
Cthe_01261 6-phosphofructokinase	11.09	11.75	11.08	11.06	0.01	0.69	-0.66	0.02	0.57	0.6	-0.13	-0.13	0.78	0.67	8.04
Cthe_00576 Ribulose-phosphate 3-epimerase	13.03	13.61	13.05	12.88	-0.02	0.73	-0.58	0.17	0.55	0.64	0.13	0.19	0.78	0.67	6.55
Cthe_00713 1-acyl-sn-glycerol-3-phosphate acyl	11.71	12.18	11.14	11.61	0.57	0.57	-0.47	-0.47	1.02	0.5	0.5	-1.15	0.78	0.67	1.62
Cthe_00576 Ribulose-phosphate 3-epimerase	13.03	13.61	13.05	12.88	-0.02	0.73	-0.58	0.17	0.55	0.64	0.13	0.19	0.78	0.67	6.55
Cthe_01097 peptidase S14, ClpP	8.96	9.75	9.09	8.74	-0.13	1.01	-0.79	0.35	0.46	0.87	-0.57	0.56	0.76	0.66	2.2
Cthe_00261 HAD-superfamily hydrolase, subfam	7.48	8.49	7.17	7.48	0.31	1.01	-1.01	-0.31	0.81	0.87	-1.3	-0.81	0.76	0.66	1.39
Cthe_00724 histidinol phosphate phosphatase	10.5	11	10.19	10.4	0.31	0.6	-0.5	-0.21	0.81	0.53	0.4	-0.6	0.77	0.66	2.4
Cthe_00906 Radical SAM	9.97	10.56	9.55	9.96	0.42	0.6	-0.59	-0.41	0.9	0.53	0.1	-1.02	0.76	0.66	1.82
Cthe_01091 metal dependent phosphohydrolas	13.49	14.27	13.28	13.5	0.21	0.77	-0.78	-0.22	0.73	0.67	-0.53	-0.63	0.76	0.66	2.15
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_00724 histidinol phosphate phosphatase	10.5	11	10.19	10.4	0.31	0.6	-0.5	-0.21	0.81	0.53	0.4	-0.6	0.77	0.66	2.4
Cthe_01796 Prephenate dehydrogenase	13.02	13.8	12.99	12.98	0.03	0.82	-0.78	0.01	0.59	0.71	-0.53	-0.15	0.77	0.66	2.99
Cthe_02630 ribose-phosphate pyrophosphokina	11.12	11.63	11.04	10.93	0.08	0.7	-0.51	0.11	0.63	0.61	0.37	0.06	0.77	0.66	4.18
Cthe_02968 4Fe-4S ferredoxin, iron-sulfur bindi	7.44	8.19	7.25	7.44	0.19	0.75	-0.75	-0.19	0.71	0.65	-0.43	-0.56	0.76	0.66	2.43
Cthe_02218 flagellar hook-associated 2-like pro	13.11	13.94	13.17	12.99	-0.06	0.95	-0.83	0.18	0.52	0.82	-0.7	0.21	0.77	0.66	2.37
Cthe_02344 Undecaprenyl-phosphate galactose	9.38	9.78	8.85	9.22	0.53	0.56	-0.4	-0.37	0.98	0.49	0.73	-0.94	0.76	0.66	1.64
Cthe_02630 ribose-phosphate pyrophosphokina	11.12	11.63	11.04	10.93	0.08	0.7	-0.51	0.11	0.63	0.61	0.37	0.06	0.77	0.66	4.18
Cthe_00203 response regulator receiver and AN	11.4	12.36	11.5	11.2	-0.1	1.16	-0.96	0.3	0.48	1	-1.13	0.46	0.77	0.66	1.62
Cthe_01783 ribosomal protein L13	11.68	12.22	11.56	11.58	0.12	0.64	-0.54	-0.02	0.66	0.56	0.27	-0.21	0.77	0.66	4.52
Cthe_02968 4Fe-4S ferredoxin, iron-sulfur bindi	7.44	8.19	7.25	7.44	0.19	0.75	-0.75	-0.19	0.71	0.65	-0.43	-0.56	0.76	0.66	2.43
Cthe_00455 Mg chelatase, subunit ChlI	9.91	10.6	9.71	9.91	0.2	0.69	-0.69	-0.2	0.72	0.6	-0.23	-0.58	0.76	0.66	2.68
Cthe_00666 HflC protein	8.2	8.61	7.77	8.01	0.43	0.6	-0.41	-0.24	0.9	0.53	0.7	-0.67	0.77	0.66	1.92
Cthe_01097 peptidase S14, ClpP	8.96	9.75	9.09	8.74	-0.13	1.01	-0.79	0.35	0.46	0.87	-0.57	0.56	0.76	0.66	2.2
Cthe_01947 Redoxin	12.24	13.03	12.41	11.92	-0.17	1.11	-0.79	0.49	0.43	0.96	-0.57	0.85	0.77	0.66	1.84
Cthe_02741 ATP-dependent Clp protease, ATP-	15.75	16.32	15.76	15.61	-0.01	0.71	-0.57	0.15	0.56	0.62	0.17	0.15	0.77	0.66	6.58
Cthe_03016 (NifE) hydrogenase maturation pro	10.08	11.12	10.31	9.71	-0.23	1.41	-1.04	0.6	0.38	1.21	-1.4	1.08	0.77	0.66	1.28
Cthe_00313 hypothetical protein	8.44	8.92	7.92	8.37	0.52	0.55	-0.48	-0.45	0.98	0.48	0.47	-1.1	0.76	0.66	1.63
Cthe_00005 hypothetical protein	8.74	9.17	8.37	8.58	0.37	0.59	-0.43	-0.21	0.86	0.52	0.63	-0.6	0.76	0.66	2.06
Cthe_02026 hypothetical protein	5.93	6.75	6.15	5.52	-0.22	1.23	-0.82	0.63	0.39	1.06	-0.67	1.15	0.76	0.66	1.52
Cthe_00820 hypothetical protein	13.58	14	13.45	13.17	0.13	0.83	-0.42	0.28	0.67	0.72	0.67	0.42	0.76	0.66	2.22
Cthe_01783 ribosomal protein L13	11.68	12.22	11.56	11.58	0.12	0.64	-0.54	-0.02	0.66	0.56	0.27	-0.21	0.77	0.66	4.52
Cthe_00724 histidinol phosphate phosphatase	10.5	11	10.19	10.4	0.31	0.6	-0.5	-0.21	0.81	0.53	0.4	-0.6	0.77	0.66	2.4
Cthe_02630 ribose-phosphate pyrophosphokina	11.12	11.63	11.04	10.93	0.08	0.7	-0.51	0.11	0.63	0.61	0.37	0.06	0.77	0.66	4.18
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01783 ribosomal protein L13	11.68	12.22	11.56	11.58	0.12	0.64	-0.54	-0.02	0.66	0.56	0.27	-0.21	0.77	0.66	4.52
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01796 Prephenate dehydrogenase	13.02	13.8	12.99	12.98	0.03	0.82	-0.78	0.01	0.59	0.71	-0.53	-0.15	0.77	0.66	2.99
Cthe_01796 Prephenate dehydrogenase	13.02	13.8	12.99	12.98	0.03	0.82	-0.78	0.01	0.59	0.71	-0.53	-0.15	0.77	0.66	2.99
Cthe_02630 ribose-phosphate pyrophosphokina	11.12	11.63	11.04	10.93	0.08	0.7	-0.51	0.11	0.63	0.61	0.37	0.06	0.77	0.66	4.18
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_02344 Undecaprenyl-phosphate galactose	9.38	9.78	8.85	9.22	0.53	0.56	-0.4	-0.37	0.98	0.49	0.73	-0.94	0.76	0.66	1.64
Cthe_00724 histidinol phosphate phosphatase	10.5	11	10.19	10.4	0.31	0.6	-0.5	-0.21	0.81	0.53	0.4	-0.6	0.77	0.66	2.4
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_00261 HAD-superfamily hydrolase, subfam	7.48	8.49	7.17	7.48	0.31	1.01	-1.01	-0.31	0.81	0.87	-1.3	-0.81	0.76	0.66	1.39
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_00666 HflC protein	8.2	8.61	7.77	8.01	0.43	0.6	-0.41	-0.24	0.9	0.53	0.7	-0.67	0.77	0.66	1.92
Cthe_00261 HAD-superfamily hydrolase, subfam	7.48	8.49	7.17	7.48	0.31	1.01	-1.01	-0.31	0.81	0.87	-1.3	-0.81	0.76	0.66	1.39
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_00724 histidinol phosphate phosphatase	10.5	11	10.19	10.4	0.31	0.6	-0.5	-0.21	0.81	0.53	0.4	-0.6	0.77	0.66	2.4
Cthe_02630 ribose-phosphate pyrophosphokina	11.12	11.63	11.04	10.93	0.08	0.7	-0.51	0.11	0.63	0.61	0.37	0.06	0.77	0.66	4.18
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01796 Prephenate dehydrogenase	13.02	13.8	12.99	12.98	0.03	0.82	-0.78	0.01	0.59	0.71	-0.53	-0.15	0.77	0.66	2.99
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_03003 hydrogenase, Fe-only	13.43	14.32	13.42	13.35	0.01	0.97	-0.89	0.07	0.57	0.84	-0.9	-0.02	0.76	0.66	2.01
Cthe_01292 proposed homoserine kinase	12.46	13.13	12.52	12.38	-0.06	0.75	-0.67	0.14	0.52	0.65	-0.17	0.13	0.77	0.66	6.95
Cthe_01009 O-methyltransferase, family 3	10.1	10.93	9.91	10.11	0.19	0.82	-0.83	-0.2	0.71	0.71	-0.7	-0.58	0.75	0.65	1.97
Cthe_00607 peptidase M42	10.67	11.55	10.9	10.32	-0.23	1.23	-0.88	0.58	0.38	1.06	-0.87	1.04	0.75	0.65	1.48
Cthe_01367 PHP-like protein	10.45	10.95	9.94	10.4	0.51	0.55	-0.5	-0.46	0.97	0.48	0.4	-1.13	0.75	0.65	1.61
Cthe_00727 cell envelope-related transcription	9.93	10.38	9.63	9.77	0.3	0.61	-0.45	-0.14	0.8	0.53	0.57	-0.46	0.75	0.65	2.34
Cthe_02212 transcriptional regulator, AraC fam	13.16	13.9	13.26	13.04	-0.1	0.86	-0.74	0.22	0.48	0.75	-0.4	0.29	0.75	0.65	3.22
Cthe_02333 two component transcriptional reg	8.74	9.38	8.3	8.75	0.44	0.63	-0.64	-0.45	0.91	0.55	-0.07	-1.1	0.75	0.65	1.72
Cthe_00174 sulfatase	11.17	11.7	11.02	11.08	0.15	0.62	-0.53	-0.06	0.68	0.54	0.3	-0.29	0.75	0.65	3.72



Cthe_00607 peptidase M42	10.67	11.55	10.9	10.32	-0.23	1.23	-0.88	0.58	0.38	1.06	-0.87	1.04	0.75	0.65	1.48
Cthe_01423 protein of unknown function UPF0	9.18	9.64	9	9.01	0.18	0.63	-0.46	-0.01	0.71	0.55	0.53	-0.19	0.74	0.64	2.85
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00749 binding-protein-dependent transpo	9.45	9.85	9.22	9.18	0.23	0.67	-0.4	0.04	0.75	0.58	0.73	-0.08	0.74	0.64	2.31
Cthe_02595 translation factor SUA5	12.12	12.71	12.19	11.91	-0.07	0.8	-0.59	0.28	0.51	0.69	0.1	0.42	0.74	0.64	3.55
Cthe_00063 Rubredoxin-type Fe(Cys)4 protein	15.61	16.22	15.7	15.34	-0.09	0.88	-0.61	0.36	0.49	0.76	0.03	0.58	0.74	0.64	2.78
Cthe_00549 ABC-3	10.27	10.73	10.16	10.03	0.11	0.7	-0.46	0.13	0.65	0.61	0.53	0.1	0.74	0.64	2.95
Cthe_01210 hypothetical protein	6.13	6.61	5.61	6.07	0.52	0.54	-0.48	-0.46	0.98	0.47	0.47	-1.13	0.74	0.64	1.59
Cthe_01459 hypothetical protein	8	8.57	8.03	7.9	-0.03	0.67	-0.57	0.13	0.54	0.58	0.17	0.1	0.74	0.64	7.17
Cthe_02192 hypothetical protein	11.73	12.41	11.73	11.73	0	0.68	-0.68	0	0.56	0.59	-0.2	-0.17	0.74	0.64	5.53
Cthe_02853 prophage Lp4 protein 7, DNA replic	5.49	5.86	5.32	5.04	0.17	0.82	-0.37	0.28	0.7	0.71	0.83	0.42	0.74	0.64	1.91
Cthe_01047 hypothetical protein	12.25	12.78	12.26	11.98	-0.01	0.8	-0.53	0.28	0.56	0.69	0.3	0.42	0.74	0.64	3.07
Cthe_01194 hypothetical protein	10.6	11.02	10.26	10.43	0.34	0.59	-0.42	-0.17	0.83	0.52	0.67	-0.52	0.74	0.64	2.06
Cthe_01290 hypothetical protein	9.69	10.38	9.74	9.68	-0.05	0.7	-0.69	0.06	0.52	0.61	-0.23	-0.04	0.74	0.64	6.13
Cthe_00002 hypothetical protein	8.05	8.52	7.77	7.94	0.28	0.58	-0.47	-0.17	0.79	0.51	0.5	-0.52	0.74	0.64	2.33
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00549 ABC-3	10.27	10.73	10.16	10.03	0.11	0.7	-0.46	0.13	0.65	0.61	0.53	0.1	0.74	0.64	2.95
Cthe_00749 binding-protein-dependent transpo	9.45	9.85	9.22	9.18	0.23	0.67	-0.4	0.04	0.75	0.58	0.73	-0.08	0.74	0.64	2.31
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00922 diaminopimelate dehydrogenase	10.44	11.04	10.49	10.41	-0.05	0.63	-0.6	0.08	0.52	0.55	0.07	0	0.74	0.64	19.31
Cthe_00922 diaminopimelate dehydrogenase	10.44	11.04	10.49	10.41	-0.05	0.63	-0.6	0.08	0.52	0.55	0.07	0	0.74	0.64	19.31
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_00711 chorismate mutase	11.09	11.58	10.5	11.06	0.59	0.52	-0.49	-0.56	1.03	0.46	0.43	-1.33	0.74	0.64	1.44
Cthe_03168 hypothetical protein	11.83	12.35	11.82	11.64	0.01	0.71	-0.52	0.18	0.57	0.62	0.33	0.21	0.73	0.63	3.84
Cthe_00069 Aspartate--ammonia ligase	9.98	10.7	9.64	10.02	0.34	0.68	-0.72	-0.38	0.83	0.59	-0.33	-0.96	0.73	0.63	1.79
Cthe_03045 FHA domain containing protein	8.41	9.21	7.79	8.51	0.62	0.7	-0.8	-0.72	1.06	0.61	-0.6	-1.67	0.73	0.63	1.23
Cthe_01420 protein of unknown function DUF2	7.83	8.58	7.35	7.89	0.48	0.69	-0.75	-0.54	0.94	0.6	-0.43	-1.29	0.73	0.63	1.46
Cthe_02240 protein of unknown function DUF1	10.81	11.26	10.67	10.6	0.14	0.66	-0.45	0.07	0.67	0.58	0.57	-0.02	0.73	0.63	2.77
Cthe_02412 SMC protein-like protein	8.03	8.62	8.01	8.01	0.02	0.61	-0.59	0	0.58	0.53	0.1	-0.17	0.73	0.63	7.11
Cthe_01228 threonyl-tRNA synthetase	12.91	13.38	12.18	12.9	0.73	0.48	-0.47	-0.72	1.14	0.42	0.5	-1.67	0.73	0.63	1.24
Cthe_02262 V-type ATPase, 116 kDa subunit	12.72	13.36	12.77	12.73	-0.05	0.63	-0.64	0.04	0.52	0.55	-0.07	-0.08	0.73	0.63	12.71
Cthe_03168 hypothetical protein	11.83	12.35	11.82	11.64	0.01	0.71	-0.52	0.18	0.57	0.62	0.33	0.21	0.73	0.63	3.84
Cthe_00851 hypothetical protein	9.46	9.94	9.19	9.37	0.27	0.57	-0.48	-0.18	0.78	0.5	0.47	-0.54	0.73	0.63	2.31
Cthe_01213 hypothetical protein	9.67	10.2	9.73	9.21	-0.06	0.99	-0.53	0.52	0.52	0.86	0.3	0.92	0.73	0.63	1.85
Cthe_02262 V-type ATPase, 116 kDa subunit	12.72	13.36	12.77	12.73	-0.05	0.63	-0.64	0.04	0.52	0.55	-0.07	-0.08	0.73	0.63	12.71
Cthe_01228 threonyl-tRNA synthetase	12.91	13.38	12.18	12.9	0.73	0.48	-0.47	-0.72	1.14	0.42	0.5	-1.67	0.73	0.63	1.24
Cthe_01228 threonyl-tRNA synthetase	12.91	13.38	12.18	12.9	0.73	0.48	-0.47	-0.72	1.14	0.42	0.5	-1.67	0.73	0.63	1.24
Cthe_02262 V-type ATPase, 116 kDa subunit	12.72	13.36	12.77	12.73	-0.05	0.63	-0.64	0.04	0.52	0.55	-0.07	-0.08	0.73	0.63	12.71
Cthe_00069 Aspartate--ammonia ligase	9.98	10.7	9.64	10.02	0.34	0.68	-0.72	-0.38	0.83	0.59	-0.33	-0.96	0.73	0.63	1.79
Cthe_01228 threonyl-tRNA synthetase	12.91	13.38	12.18	12.9	0.73	0.48	-0.47	-0.72	1.14	0.42	0.5	-1.67	0.73	0.63	1.24
Cthe_01228 threonyl-tRNA synthetase	12.91	13.38	12.18	12.9	0.73	0.48	-0.47	-0.72	1.14	0.42	0.5	-1.67	0.73	0.63	1.24
Cthe_02262 V-type ATPase, 116 kDa subunit	12.72	13.36	12.77	12.73	-0.05	0.63	-0.64	0.04	0.52	0.55	-0.07	-0.08	0.73	0.63	12.71
Cthe_00069 Aspartate--ammonia ligase	9.98	10.7	9.64	10.02	0.34	0.68	-0.72	-0.38	0.83	0.59	-0.33	-0.96	0.73	0.63	1.79
Cthe_01052 competence/damage-inducible pro	8	8.85	7.94	8.01	0.06	0.84	-0.85	-0.07	0.61	0.73	-0.77	-0.31	0.72	0.62	2.05
Cthe_01199 amidohydrolase	11.39	12	11.3	11.4	0.09	0.6	-0.61	-0.1	0.63	0.53	0.03	-0.38	0.72	0.62	3.86
Cthe_01841 hypothetical protein	10.57	11.37	10.63	10.54	-0.06	0.83	-0.8	0.09	0.52	0.72	-0.6	0.02	0.72	0.62	2.64
Cthe_02691 galactoside O-acetyltransferase	7.97	8.69	7.89	8	0.08	0.69	-0.72	-0.11	0.63	0.6	-0.33	-0.4	0.72	0.62	3
Cthe_02890 putative transcriptional regulator	10.07	10.73	10.01	10.1	0.06	0.63	-0.66	-0.09	0.61	0.55	-0.13	-0.35	0.72	0.62	3.93
Cthe_00849 3-dehydroquininate dehydratase, typ	6.55	6.97	6.15	6.43	0.4	0.54	-0.42	-0.28	0.88	0.47	0.67	-0.75	0.72	0.62	1.77
Cthe_00910 extracellular solute-binding protein	9.1	9.66	8.55	9.13	0.55	0.53	-0.56	-0.58	1	0.47	0.2	-1.37	0.72	0.62	1.43
Cthe_01426 AzIC-like protein	8.12	8.82	8.2	8.11	-0.08	0.71	-0.7	0.09	0.5	0.62	-0.27	0.02	0.72	0.62	5.25
Cthe_02211 3-isopropylmalate dehydratase, lar	12.51	13.28	12.48	12.53	0.03	0.75	-0.77	-0.05	0.59	0.65	-0.5	-0.27	0.72	0.62	2.76
Cthe_02031 transposase IS200-like protein	8.71	9.46	8.84	8.61	-0.13	0.85	-0.75	0.23	0.46	0.74	-0.43	0.31	0.72	0.62	2.94
Cthe_01363 lipopolysaccharide biosynthesis	11.72	12.29	11.25	11.74	0.47	0.55	-0.57	-0.49	0.94	0.48	0.17	-1.19	0.72	0.62	1.57
Cthe_01199 amidohydrolase	11.39	12	11.3	11.4	0.09	0.6	-0.61	-0.1	0.63	0.53	0.03	-0.38	0.72	0.62	3.86
Cthe_02502 CMP/dCMP deaminase, zinc-bindin	10.08	10.53	9.96	9.85	0.12	0.68	-0.45	0.11	0.66	0.59	0.57	0.06	0.72	0.62	2.76
Cthe_00635 protein serine/threonine phosphat	9.31	10.01	9.01	9.36	0.3	0.65	-0.7	-0.35	0.8	0.57	-0.27	-0.9	0.72	0.62	1.87
Cthe_02502 CMP/dCMP deaminase, zinc-bindin	10.08	10.53	9.96	9.85	0.12	0.68	-0.45	0.11	0.66	0.59	0.57	0.06	0.72	0.62	2.76
Cthe_01363 lipopolysaccharide biosynthesis	11.72	12.29	11.25	11.74	0.47	0.55	-0.57	-0.49	0.94	0.48	0.17	-1.19	0.72	0.62	1.57
Cthe_01111 Bile acid:sodium symporter	6.93	7.28	6.83	6.21	0.1	1.07	-0.35	0.62	0.64	0.92	0.9	1.13	0.72	0.62	1.39
Cthe_01259 CDP-alcohol phosphatidyltransfera	9.49	10.14	9.62	9.3	-0.13	0.84	-0.65	0.32	0.46	0.73	-0.1	0.5	0.72	0.62	3.02
Cthe_02048 hypothetical protein	6.36	7.26	6.38	6.32	-0.02	0.94	-0.9	0.06	0.55	0.81	-0.93	-0.04	0.72	0.62	1.88
Cthe_03228 copper amine oxidase-like protein	7.73	8.85	7.77	7.61	-0.04	1.24	-1.12	0.16	0.53	1.07	-1.67	0.17	0.72	0.62	1.27
Cthe_01220 hypothetical protein	12.12	12.57	11.69	12.03	0.43	0.54	-0.45	-0.34	0.9	0.47	0.57	-0.88	0.72	0.62	1.73
Cthe_01197 intein	9.33	9.73	8.89	9.2	0.44	0.53	-0.4	-0.31	0.91	0.47	0.73	-0.81	0.72	0.62	1.68
Cthe_00849 3-dehydroquininate dehydratase, typ	6.55	6.97	6.15	6.43	0.4	0.54	-0.42	-0.28	0.88	0.47	0.67	-0.75	0.72	0.62	1.77
Cthe_02211 3-isopropylmalate dehydratase, lar	12.51	13.28	12.48	12.53	0.03	0.75	-0.77	-0.05	0.59	0.65	-0.5	-0.27	0.72	0.62	2.76
Cthe_00910 extracellular solute-binding protein	9.1	9.66	8.55	9.13	0.55	0.53	-0.56	-0.58	1	0.47	0.2	-1.37	0.72	0.62	1.43
Cthe_00849 3-dehydroquininate dehydratase, typ	6.55	6.97	6.15	6.43	0.4	0.54	-0.42	-0.28	0.88	0.47	0.67	-0.75	0.72	0.62	1.77
Cthe_01259 CDP-alcohol phosphatidyltransfera	9.49	10.14	9.62	9.3	-0.13	0.84	-0.65	0.32	0.46	0.73	-0.1	0.5	0.72	0.62	3.02
Cthe_02211 3-isopropylmalate dehydratase, lar	12.51	13.28	12.48	12.53	0.03	0.75	-0.77	-0.05	0.59	0.65	-0.5	-0.27	0.72	0.62	2.76
Cthe_02211 3-isopropylmalate dehydratase, lar	12.51	13.28	12.48	12.53	0.03	0.75	-0.77	-0.05	0.59	0.65	-0.5	-0.27	0.72	0.62	2.76
Cthe_01363 lipopolysaccharide biosynthesis	11.72	12.29	11.25	11.74	0.										



Cthe_02211 3-isopropylmalate dehydratase, lar	12.51	13.28	12.48	12.53	0.03	0.75	-0.77	-0.05	0.59	0.65	-0.5	-0.27	0.72	0.62	2.76
Cthe_00849 3-dehydroquinatate dehydratase, typ	6.55	6.97	6.15	6.43	0.4	0.54	-0.42	-0.28	0.88	0.47	0.67	-0.75	0.72	0.62	1.77
Cthe_00849 3-dehydroquinatate dehydratase, typ	6.55	6.97	6.15	6.43	0.4	0.54	-0.42	-0.28	0.88	0.47	0.67	-0.75	0.72	0.62	1.77
Cthe_01259 CDP-alcohol phosphatidyltransferase	9.49	10.14	9.62	9.3	-0.13	0.84	-0.65	0.32	0.46	0.73	-0.1	0.5	0.72	0.62	3.02
Cthe_01480 hypothetical protein	4.52	4.17	4.95	4.32	-0.43	-0.15	0.35	0.63	0.22	-0.11	3.23	1.15	0.71	0.61	0.13
Cthe_01510 short-chain dehydrogenase/reduct	7.97	8.4	7.52	7.89	0.45	0.51	-0.43	-0.37	0.92	0.45	0.63	-0.94	0.71	0.61	1.62
Cthe_00812 response regulator receiver protein	11.7	12.39	11.94	11.16	-0.24	1.23	-0.69	0.78	0.37	1.06	-0.23	1.46	0.71	0.61	1.36
Cthe_02876 ATP-dependent DNA helicase PcrA	12.95	13.65	12.55	13.02	0.4	0.63	-0.7	-0.47	0.88	0.55	-0.27	-1.15	0.71	0.61	1.57
Cthe_01510 short-chain dehydrogenase/reduct	7.97	8.4	7.52	7.89	0.45	0.51	-0.43	-0.37	0.92	0.45	0.63	-0.94	0.71	0.61	1.62
Cthe_00812 response regulator receiver protein	11.7	12.39	11.94	11.16	-0.24	1.23	-0.69	0.78	0.37	1.06	-0.23	1.46	0.71	0.61	1.36
Cthe_00686 tryptophanyl-tRNA synthetase	11.82	12.47	11.59	11.87	0.23	0.6	-0.65	-0.28	0.75	0.53	-0.1	-0.75	0.71	0.61	2.17
Cthe_00638 FHA domain containing protein	11.2	11.86	11.37	10.89	-0.17	0.97	-0.66	0.48	0.43	0.84	-0.13	0.83	0.71	0.61	2.01
Cthe_02431 electron transport complex, RnfAB	12.93	13.83	13.19	12.65	-0.26	1.18	-0.9	0.54	0.36	1.02	-0.93	0.96	0.71	0.61	1.45
Cthe_01510 short-chain dehydrogenase/reduct	7.97	8.4	7.52	7.89	0.45	0.51	-0.43	-0.37	0.92	0.45	0.63	-0.94	0.71	0.61	1.62
Cthe_03222 hypothetical protein	9.17	9.35	8.53	8.81	0.64	0.54	-0.18	-0.28	1.07	0.47	1.47	-0.75	0.71	0.61	1.26
Cthe_00686 tryptophanyl-tRNA synthetase	11.82	12.47	11.59	11.87	0.23	0.6	-0.65	-0.28	0.75	0.53	-0.1	-0.75	0.71	0.61	2.17
Cthe_00686 tryptophanyl-tRNA synthetase	11.82	12.47	11.59	11.87	0.23	0.6	-0.65	-0.28	0.75	0.53	-0.1	-0.75	0.71	0.61	2.17
Cthe_00686 tryptophanyl-tRNA synthetase	11.82	12.47	11.59	11.87	0.23	0.6	-0.65	-0.28	0.75	0.53	-0.1	-0.75	0.71	0.61	2.17
Cthe_02876 ATP-dependent DNA helicase PcrA	12.95	13.65	12.55	13.02	0.4	0.63	-0.7	-0.47	0.88	0.55	-0.27	-1.15	0.71	0.61	1.57
Cthe_00686 tryptophanyl-tRNA synthetase	11.82	12.47	11.59	11.87	0.23	0.6	-0.65	-0.28	0.75	0.53	-0.1	-0.75	0.71	0.61	2.17
Cthe_01221 glycosyltransferase 36	8.84	9.52	8.69	8.89	0.15	0.63	-0.68	-0.2	0.68	0.55	-0.2	-0.58	0.7	0.6	2.55
Cthe_01844 transcriptional regulator, BadM/Rrf	9.75	10.42	9.84	9.77	-0.09	0.65	-0.67	0.07	0.49	0.57	-0.17	-0.02	0.7	0.6	7.84
Cthe_03035 D-isomer specific 2-hydroxyacid de	14.07	14.73	14.23	13.86	-0.16	0.87	-0.66	0.37	0.44	0.75	-0.13	0.6	0.7	0.6	2.53
Cthe_03035 D-isomer specific 2-hydroxyacid de	14.07	14.73	14.23	13.86	-0.16	0.87	-0.66	0.37	0.44	0.75	-0.13	0.6	0.7	0.6	2.53
Cthe_00258 cellulosome enzyme, dockerin type	9.23	9.87	9.34	9.26	-0.11	0.61	-0.64	0.08	0.48	0.53	-0.07	0	0.7	0.6	18.24
Cthe_00741 adenylsuccinate lyase	12.12	12.63	11.93	12.07	0.19	0.56	-0.51	-0.14	0.71	0.49	0.37	-0.46	0.7	0.6	2.61
Cthe_00213 protein of unknown function DUF9	9.47	10.04	9.26	9.48	0.21	0.56	-0.57	-0.22	0.73	0.49	0.17	-0.63	0.7	0.6	2.41
Cthe_00398 protein of unknown function DUF7	7.98	8.86	8.03	7.95	-0.05	0.91	-0.88	0.08	0.52	0.79	-0.87	0	0.7	0.6	1.94
Cthe_00827 hemolysin A	8.86	9.53	8.45	8.93	0.41	0.6	-0.67	-0.48	0.89	0.53	-0.17	-1.17	0.7	0.6	1.56
Cthe_00877 GTP-binding protein YchF	12.45	13.01	12.31	12.44	0.14	0.57	-0.56	-0.13	0.67	0.5	0.2	-0.44	0.7	0.6	3.09
Cthe_00258 cellulosome enzyme, dockerin type	9.23	9.87	9.34	9.26	-0.11	0.61	-0.64	0.08	0.48	0.53	-0.07	0	0.7	0.6	18.24
Cthe_00006 hypothetical protein	7.29	7.44	6.82	6.69	0.47	0.75	-0.15	0.13	0.94	0.65	1.57	0.1	0.7	0.6	1.3
Cthe_00252 hypothetical protein	9.96	10.74	9.84	10.02	0.12	0.72	-0.78	-0.18	0.66	0.63	-0.53	-0.54	0.7	0.6	2.15
Cthe_00940 hypothetical protein	5.78	6.63	5.61	5.83	0.17	0.8	-0.85	-0.22	0.7	0.69	-0.77	-0.63	0.7	0.6	1.76
Cthe_00741 adenylsuccinate lyase	12.12	12.63	11.93	12.07	0.19	0.56	-0.51	-0.14	0.71	0.49	0.37	-0.46	0.7	0.6	2.61
Cthe_03035 D-isomer specific 2-hydroxyacid de	14.07	14.73	14.23	13.86	-0.16	0.87	-0.66	0.37	0.44	0.75	-0.13	0.6	0.7	0.6	2.53
Cthe_00741 adenylsuccinate lyase	12.12	12.63	11.93	12.07	0.19	0.56	-0.51	-0.14	0.71	0.49	0.37	-0.46	0.7	0.6	2.61
Cthe_03035 D-isomer specific 2-hydroxyacid de	14.07	14.73	14.23	13.86	-0.16	0.87	-0.66	0.37	0.44	0.75	-0.13	0.6	0.7	0.6	2.53
Cthe_00741 adenylsuccinate lyase	12.12	12.63	11.93	12.07	0.19	0.56	-0.51	-0.14	0.71	0.49	0.37	-0.46	0.7	0.6	2.61
Cthe_00741 adenylsuccinate lyase	12.12	12.63	11.93	12.07	0.19	0.56	-0.51	-0.14	0.71	0.49	0.37	-0.46	0.7	0.6	2.61
Cthe_00741 adenylsuccinate lyase	12.12	12.63	11.93	12.07	0.19	0.56	-0.51	-0.14	0.71	0.49	0.37	-0.46	0.7	0.6	2.61
Cthe_00741 adenylsuccinate lyase	12.12	12.63	11.93	12.07	0.19	0.56	-0.51	-0.14	0.71	0.49	0.37	-0.46	0.7	0.6	2.61
Cthe_00419 peptidase M16-like protein	10.03	10.24	9.12	9.93	0.91	0.31	-0.21	-0.81	1.29	0.28	1.37	-1.85	0.68	0.59	1.02
Cthe_00570 peptidase, membrane zinc metallo	11.45	12.05	11.57	11.35	-0.12	0.7	-0.6	0.22	0.47	0.61	0.07	0.29	0.69	0.59	4.61
Cthe_00986 peptidase M16-like protein	11.25	11.85	10.82	11.3	0.43	0.55	-0.6	-0.48	0.9	0.48	0.07	-1.17	0.69	0.59	1.55
Cthe_01008 aminodeoxychorismate lyase	12.07	12.73	12.22	11.93	-0.15	0.8	-0.66	0.29	0.44	0.69	-0.13	0.44	0.69	0.59	3.19
Cthe_01027 protein of unknown function DUF1	13.68	14.12	13.36	13.6	0.32	0.52	-0.44	-0.24	0.82	0.46	0.6	-0.67	0.69	0.59	1.87
Cthe_00289 DEAD_2	11.98	12.78	12.06	11.99	-0.08	0.79	-0.8	0.07	0.5	0.69	-0.6	-0.02	0.68	0.59	2.53
Cthe_02632 transcription-repair coupling factor	8.92	9.65	8.82	8.98	0.1	0.67	-0.73	-0.16	0.64	0.58	-0.37	-0.5	0.69	0.59	2.48
Cthe_02719 NusG antitermination factor	11.99	12.54	11.69	12.01	0.3	0.53	-0.55	-0.32	0.8	0.47	0.23	-0.83	0.69	0.59	1.92
Cthe_01411 tryptophan synthase, alpha subunit	9.92	10.59	10.01	9.97	-0.09	0.62	-0.67	0.04	0.49	0.54	-0.17	-0.08	0.68	0.59	6.93
Cthe_01842 O-acetylhomoserine/O-acetylerin	11.93	12.7	12.12	11.78	-0.19	0.92	-0.77	0.34	0.41	0.8	-0.5	0.54	0.69	0.59	2.18
Cthe_00289 DEAD_2	11.98	12.78	12.06	11.99	-0.08	0.79	-0.8	0.07	0.5	0.69	-0.6	-0.02	0.68	0.59	2.53
Cthe_02632 transcription-repair coupling factor	8.92	9.65	8.82	8.98	0.1	0.67	-0.73	-0.16	0.64	0.58	-0.37	-0.5	0.69	0.59	2.48
Cthe_02356 quinolinate synthetase complex, A	12.21	12.65	12.09	12.04	0.12	0.61	-0.44	0.05	0.66	0.53	0.6	-0.06	0.68	0.59	2.51
Cthe_00441 UDP-N-acetylglucosamine	9.38	10.08	9.05	9.47	0.33	0.61	-0.7	-0.42	0.83	0.53	-0.27	-1.04	0.68	0.59	1.64
Cthe_02221 DegT/DnrI/EryC1/StrS aminotransf	8.71	9.73	8.81	8.64	-0.1	1.09	-1.02	0.17	0.48	0.94	-1.33	0.19	0.68	0.59	1.4
Cthe_02692 glycosyl transferase, group 1	9.74	10.5	9.76	9.79	-0.02	0.71	-0.76	-0.03	0.55	0.62	-0.47	-0.23	0.68	0.59	2.83
Cthe_02697 alanine racemase	10.03	10.54	9.99	9.96	0.04	0.58	-0.51	0.03	0.6	0.51	0.37	-0.1	0.68	0.59	3.67
Cthe_01110 protein tyrosine phosphatase	4.25	4.86	4.46	3.7	-0.21	1.16	-0.61	0.76	0.4	1	0.03	1.42	0.68	0.59	1.35
Cthe_00162 ribosomal protein L27	12.49	13.07	12.49	12.5	0	0.57	-0.58	-0.01	0.56	0.5	0.13	-0.19	0.69	0.59	5.82
Cthe_02815 lysyl-tRNA synthetase	13.62	14.14	13.23	13.62	0.39	0.52	-0.52	-0.39	0.87	0.46	0.33	-0.98	0.69	0.59	1.7
Cthe_02875 sigma 54 modulation protein/ribos	16.4	16.95	16.55	15.86	-0.15	1.09	-0.55	0.69	0.44	0.94	0.23	1.27	0.68	0.59	1.44
Cthe_02268 Sodium-transporting two-sector AT	11.71	12.58	11.87	11.62	-0.16	0.96	-0.87	0.25	0.44	0.83	-0.83	0.35	0.69	0.59	1.86
Cthe_02802 NLPA lipoprotein	6.49	7.13	6.7	6.09	-0.21	1.04	-0.64	0.61	0.4	0.9	-0.07	1.1	0.68	0.59	1.6
Cthe_00997 1-hydroxy-2-methyl-2-(E)-butenyl 4	9.49	10.05	9.03	9.54	0.46	0.51	-0.56	-0.51	0.93	0.45	0.2	-1.23	0.68	0.59	1.48
Cthe_01965 alkyl hydroperoxide reductase/ Thi	17.62	18.3	17.83	17.29	-0.21	1.01	-0.68	0.54	0.4	0.87	-0.2	0.96	0.68	0.59	1.74
Cthe_02693 hypothetical protein	10.46	11.04	10.56	10.4	-0.1	0.64	-0.58	0.16	0.48	0.56	0.13	0.17	0.68	0.59	6.15
Cthe_02348 Ig-related protein	18.67	19.42	18.87	18.51	-0.2	0.91	-0.75	0.36	0.4	0.79	-0.43	0.58	0.68	0.59	2.19
Cthe_00689 RDD domain containing protein	9.84	10.45	9.57	9.9	0.27	0.55	-0.61	-0.33	0.78	0.48	0.03	-0.85	0.68	0.59	1.92
Cthe_00008 hypothetical protein	6.36	6.58	5.32	6.3	1.04	0.28	-0.22	-0.98	1.39	0.25	1.33	-2.21	0.69	0.59	0.98
Cthe_00818 hypothetical protein	11.88	12.55	12.03	11.84	-0.15	0.71	-0.67	0.19	0.44	0.62	-0.17	0.23	0.68	0.59	4.75
Cthe_01830 hypothetical protein	13.39	13.77	13.14	13.17	0.25	0.6	-0.38	-0.03	0.76	0.53	0.8	-0.23	0.69	0.59	1.99
Cthe_03165 PpiC-type peptidyl-prolyl cis-trans i	10.37	10.84	9.89	10.36	0.48	0.48	-0.47	-0.47	0.94	0.42	0.5	-1.15	0.68	0.59	1.47
Cthe_01982 hypothetical protein	7.27	7.55	6.92	6.91	0.35	0.64	-0.28	0.01	0.84	0.56	1.13	-0.15	0.69	0.59	1.58
Cthe_02802 NLPA lipoprotein	6.49	7.13	6.7	6.09	-0.21	1.04	-0.64	0.61	0.4	0.9	-0.07	1.1	0.68	0.59	1.6
Cthe_02268 Sodium-transporting two-sector AT	11.71	12.58	11.87	11.62	-0.16	0.96	-0.87	0.25	0.44	0.83	-0.83	0.35	0.69	0.59	1.86
Cthe_02815 lysyl-tRNA synthetase	13.62	14.14	13.23	13.62	0.39										



Cthe_00997 1-hydroxy-2-methyl-2-(E)-butenyl 4	9.49	10.05	9.03	9.54	0.46	0.51	-0.56	-0.51	0.93	0.45	0.2	-1.23	0.68	0.59	1.48
Cthe_02356 quinolinate synthetase complex, A	12.21	12.65	12.09	12.04	0.12	0.61	-0.44	0.05	0.66	0.53	0.6	-0.06	0.68	0.59	2.51
Cthe_02697 alanine racemase	10.03	10.54	9.99	9.96	0.04	0.58	-0.51	0.03	0.6	0.51	0.37	-0.1	0.68	0.59	3.67
Cthe_01411 tryptophan synthase, alpha subunit	9.92	10.59	10.01	9.97	-0.09	0.62	-0.67	0.04	0.49	0.54	-0.17	-0.08	0.68	0.59	6.93
Cthe_02632 transcription-repair coupling factor	8.92	9.65	8.82	8.98	0.1	0.67	-0.73	-0.16	0.64	0.58	-0.37	-0.5	0.69	0.59	2.48
Cthe_01842 O-acetylhomoserine/O-acetylserin	11.93	12.7	12.12	11.78	-0.19	0.92	-0.77	0.34	0.41	0.8	-0.5	0.54	0.69	0.59	2.18
Cthe_00997 1-hydroxy-2-methyl-2-(E)-butenyl 4	9.49	10.05	9.03	9.54	0.46	0.51	-0.56	-0.51	0.93	0.45	0.2	-1.23	0.68	0.59	1.48
Cthe_01842 O-acetylhomoserine/O-acetylserin	11.93	12.7	12.12	11.78	-0.19	0.92	-0.77	0.34	0.41	0.8	-0.5	0.54	0.69	0.59	2.18
Cthe_01110 protein tyrosine phosphatase	4.25	4.86	4.46	3.7	-0.21	1.16	-0.61	0.76	0.4	1	0.03	1.42	0.68	0.59	1.35
Cthe_00441 UDP-N-acetylglucosamine	9.38	10.08	9.05	9.47	0.33	0.61	-0.7	-0.42	0.83	0.53	-0.27	-1.04	0.68	0.59	1.64
Cthe_02697 alanine racemase	10.03	10.54	9.99	9.96	0.04	0.58	-0.51	0.03	0.6	0.51	0.37	-0.1	0.68	0.59	3.67
Cthe_02356 quinolinate synthetase complex, A	12.21	12.65	12.09	12.04	0.12	0.61	-0.44	0.05	0.66	0.53	0.6	-0.06	0.68	0.59	2.51
Cthe_02815 lysyl-tRNA synthetase	13.62	14.14	13.23	13.62	0.39	0.52	-0.52	-0.39	0.87	0.46	0.33	-0.98	0.69	0.59	1.7
Cthe_01110 protein tyrosine phosphatase	4.25	4.86	4.46	3.7	-0.21	1.16	-0.61	0.76	0.4	1	0.03	1.42	0.68	0.59	1.35
Cthe_00441 UDP-N-acetylglucosamine	9.38	10.08	9.05	9.47	0.33	0.61	-0.7	-0.42	0.83	0.53	-0.27	-1.04	0.68	0.59	1.64
Cthe_00441 UDP-N-acetylglucosamine	9.38	10.08	9.05	9.47	0.33	0.61	-0.7	-0.42	0.83	0.53	-0.27	-1.04	0.68	0.59	1.64
Cthe_02697 alanine racemase	10.03	10.54	9.99	9.96	0.04	0.58	-0.51	0.03	0.6	0.51	0.37	-0.1	0.68	0.59	3.67
Cthe_02268 Sodium-transporting two-sector AT	11.71	12.58	11.87	11.62	-0.16	0.96	-0.87	0.25	0.44	0.83	-0.83	0.35	0.69	0.59	1.86
Cthe_01069 protein of unknown function UPF0	10.22	10.71	10.19	10.11	0.03	0.6	-0.49	0.08	0.59	0.53	0.43	0	0.67	0.58	3.29
Cthe_02586 amidohydrolase 2	11.18	11.95	11.45	10.86	-0.27	1.09	-0.77	0.59	0.35	0.94	-0.5	1.06	0.67	0.58	1.53
Cthe_00609 peptidase M42	9.47	10.34	9.74	9.24	-0.27	1.1	-0.87	0.5	0.35	0.95	-0.83	0.88	0.67	0.58	1.49
Cthe_01697 transcriptional regulator, ArsR fami	0	1	0	0	0	1	-1	0	0.56	0.86	-1.27	-0.17	0.67	0.58	1.43
Cthe_00848 peptidase M24	9.18	9.56	8.82	9.05	0.36	0.51	-0.38	-0.23	0.85	0.45	0.8	-0.65	0.67	0.58	1.67
Cthe_00208 single-stranded-DNA-specific exonu	10.48	11.27	10.59	10.49	-0.11	0.78	-0.79	0.1	0.48	0.68	-0.57	0.04	0.67	0.58	2.6
Cthe_01297 Nicotinate-nucleotide-dimethylbe	6.25	6.78	5.95	6.27	0.3	0.51	-0.53	-0.32	0.8	0.45	0.3	-0.83	0.67	0.58	1.86
Cthe_01162 glucosamine-fructose-6-phosphat	10.82	11.45	10.57	10.89	0.25	0.56	-0.63	-0.32	0.76	0.49	-0.03	-0.83	0.67	0.58	1.94
Cthe_01643 Uncharacterized phage-associated	0	1	0	0	0	1	-1	0	0.56	0.86	-1.27	-0.17	0.67	0.58	1.44
Cthe_00445 cell division protein FtsZ	11.57	12.18	11.71	11.5	-0.14	0.68	-0.61	0.21	0.45	0.59	0.03	0.27	0.67	0.58	4.88
Cthe_01771 Rubrerythrin	11.99	12.66	12.2	11.69	-0.21	0.97	-0.67	0.51	0.4	0.84	-0.17	0.9	0.67	0.58	1.81
Cthe_00397 ABC transporter related protein	9.45	10.14	9.29	9.54	0.16	0.6	-0.69	-0.25	0.69	0.53	-0.23	-0.69	0.67	0.58	2.14
Cthe_01060 AIR synthase related protein-like pr	9.87	10.55	9.65	9.96	0.22	0.59	-0.68	-0.31	0.74	0.52	-0.2	-0.81	0.67	0.58	1.94
Cthe_02849 hypothetical protein	0	1	0	0	0	1	-1	0	0.56	0.86	-1.27	-0.17	0.67	0.58	1.43
Cthe_00017 protein of unknown function DUF1	11.87	12.37	11.93	11.58	-0.06	0.79	-0.5	0.35	0.52	0.69	0.4	0.56	0.67	0.58	2.24
Cthe_02843 hypothetical protein	0	1	0	0	0	1	-1	0	0.56	0.86	-1.27	-0.17	0.67	0.58	1.43
Cthe_01297 Nicotinate-nucleotide-dimethylbe	6.25	6.78	5.95	6.27	0.3	0.51	-0.53	-0.32	0.8	0.45	0.3	-0.83	0.67	0.58	1.86
Cthe_01297 Nicotinate-nucleotide-dimethylbe	6.25	6.78	5.95	6.27	0.3	0.51	-0.53	-0.32	0.8	0.45	0.3	-0.83	0.67	0.58	1.86
Cthe_00208 single-stranded-DNA-specific exonu	10.48	11.27	10.59	10.49	-0.11	0.78	-0.79	0.1	0.48	0.68	-0.57	0.04	0.67	0.58	2.6
Cthe_01162 glucosamine-fructose-6-phosphat	10.82	11.45	10.57	10.89	0.25	0.56	-0.63	-0.32	0.76	0.49	-0.03	-0.83	0.67	0.58	1.94
Cthe_00848 peptidase M24	9.18	9.56	8.82	9.05	0.36	0.51	-0.38	-0.23	0.85	0.45	0.8	-0.65	0.67	0.58	1.67
Cthe_00040 Cellulase., Cellulose 1,4-beta-cellob	9.12	9.78	9.01	9.2	0.11	0.58	-0.66	-0.19	0.65	0.51	-0.13	-0.56	0.67	0.58	2.57
Cthe_00609 peptidase M42	9.47	10.34	9.74	9.24	-0.27	1.1	-0.87	0.5	0.35	0.95	-0.83	0.88	0.67	0.58	1.49
Cthe_00040 Cellulase., Cellulose 1,4-beta-cellob	9.12	9.78	9.01	9.2	0.11	0.58	-0.66	-0.19	0.65	0.51	-0.13	-0.56	0.67	0.58	2.57
Cthe_01162 glucosamine-fructose-6-phosphat	10.82	11.45	10.57	10.89	0.25	0.56	-0.63	-0.32	0.76	0.49	-0.03	-0.83	0.67	0.58	1.94
Cthe_01297 Nicotinate-nucleotide-dimethylbe	6.25	6.78	5.95	6.27	0.3	0.51	-0.53	-0.32	0.8	0.45	0.3	-0.83	0.67	0.58	1.86
Cthe_01297 Nicotinate-nucleotide-dimethylbe	6.25	6.78	5.95	6.27	0.3	0.51	-0.53	-0.32	0.8	0.45	0.3	-0.83	0.67	0.58	1.86
Cthe_01297 Nicotinate-nucleotide-dimethylbe	6.25	6.78	5.95	6.27	0.3	0.51	-0.53	-0.32	0.8	0.45	0.3	-0.83	0.67	0.58	1.86
Cthe_00040 Cellulase., Cellulose 1,4-beta-cellob	9.12	9.78	9.01	9.2	0.11	0.58	-0.66	-0.19	0.65	0.51	-0.13	-0.56	0.67	0.58	2.57
Cthe_00609 peptidase M42	9.47	10.34	9.74	9.24	-0.27	1.1	-0.87	0.5	0.35	0.95	-0.83	0.88	0.67	0.58	1.49
Cthe_01297 Nicotinate-nucleotide-dimethylbe	6.25	6.78	5.95	6.27	0.3	0.51	-0.53	-0.32	0.8	0.45	0.3	-0.83	0.67	0.58	1.86
Cthe_01162 glucosamine-fructose-6-phosphat	10.82	11.45	10.57	10.89	0.25	0.56	-0.63	-0.32	0.76	0.49	-0.03	-0.83	0.67	0.58	1.94
Cthe_00253 ATPase associated with various cell	9.88	10.72	9.76	9.97	0.12	0.75	-0.84	-0.21	0.66	0.65	-0.73	-0.6	0.66	0.57	1.75
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00129 metal dependent phosphohydrolas	10.4	11	10.31	10.45	0.09	0.55	-0.6	-0.14	0.63	0.48	0.07	-0.46	0.66	0.57	3.04
Cthe_00457 protein of unknown function DUF3	7.62	8.12	7.25	7.64	0.37	0.48	-0.5	-0.39	0.86	0.42	0.4	-0.98	0.66	0.57	1.61
Cthe_01005 translation elongation factor Ts (EF	12.2	12.6	11.86	12.1	0.34	0.5	-0.4	-0.24	0.83	0.44	0.73	-0.67	0.66	0.57	1.69
Cthe_01860 cell division ATP-binding protein Ft	10.22	10.84	10.1	10.29	0.12	0.55	-0.62	-0.19	0.66	0.48	0	-0.56	0.66	0.57	2.6
Cthe_03046 cell cycle protein	8.69	9.48	8.73	8.75	-0.04	0.73	-0.79	-0.02	0.53	0.64	-0.57	-0.21	0.66	0.57	2.44
Cthe_01167 Radical SAM	9.48	10.22	9.48	9.56	0	0.66	-0.74	-0.08	0.56	0.58	-0.4	-0.33	0.66	0.57	2.78
Cthe_00531 hypothetical protein	7.65	8.12	6.94	7.73	0.71	0.39	-0.47	-0.79	1.13	0.35	0.5	-1.81	0.66	0.57	1.12
Cthe_00041 hypothetical protein	6.04	6.58	5.64	6.09	0.4	0.49	-0.54	-0.45	0.88	0.43	0.27	-1.1	0.66	0.57	1.54
Cthe_01860 cell division ATP-binding protein Ft	10.22	10.84	10.1	10.29	0.12	0.55	-0.62	-0.19	0.66	0.48	0	-0.56	0.66	0.57	2.6
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00253 ATPase associated with various cell	9.88	10.72	9.76	9.97	0.12	0.75	-0.84	-0.21	0.66	0.65	-0.73	-0.6	0.66	0.57	1.75
Cthe_01167 Radical SAM	9.48	10.22	9.48	9.56	0	0.66	-0.74	-0.08	0.56	0.58	-0.4	-0.33	0.66	0.57	2.78
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00253 ATPase associated with various cell	9.88	10.72	9.76	9.97	0.12	0.75	-0.84	-0.21	0.66	0.65	-0.73	-0.6	0.66	0.57	1.75
Cthe_00965 ATP:corrinoid adenosyltransferase	8.98	9.61	8.51	9.09	0.47	0.52	-0.63	-0.58	0.94	0.46	-0.03	-1.37	0.66	0.57	1.36
Cthe_00253 ATPase associated with various cell	9.88	10.72	9.76	9.97	0.12	0.75	-0.84	-0.21	0.66	0.65	-0.73	-0.6	0.66	0.57	1.75
Cthe_00253 ATPase associated with various cell	9.88	10.72	9.76	9.97	0.12	0.75	-0.84	-0.21	0.66	0.65	-0.73	-0.6	0.66	0.57	1.75
Cthe_00253 ATPase associated with various cell	9.88	10.72	9.76	9.97	0.12	0.75	-0.84	-0.21	0.66	0.65	-0.73	-0.6	0.66	0.57	1.75
Cthe_01855 Methyltransferase type 11	7.83	8.5	7.84	7.92	-0.01	0.58	-0.67	-0.08	0.56	0.51	-0.17	-0.33	0.65	0.56	3.64
Cthe_02979 4Fe-4S ferredoxin, iron-sulfur bindi	9.45	10.12	9.66	9.29	-0.21	0.83	-0.67	0.37	0.4	0.72	-0.17	0.6	0.65	0.56	2.36
Cthe_00620 iron (metal) dependent repressor,	11.43	11.98	11.43	11.44	0	0.54	-0.55	-0.01	0.56	0.47	0.23	-0.19	0.65	0.56	4.38
Cthe_01478 transcriptional regulator, TetR fami	8.24	8.64	8.14	7.99	0.1	0.65	-0.4	0.15	0.64	0.57	0.73	0.15	0.65	0	



Cthe_00959	S-adenosylmethionine--tRNA-ribos	8.89	9.29	8.34	8.88	0.55	0.41	-0.4	-0.54	1	0.36	0.73	-1.29	0.65	0.56	1.28
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_00458	exodeoxyribonuclease III Xth	12.3	12.83	12.43	11.92	-0.13	0.91	-0.53	0.51	0.46	0.79	0.3	0.9	0.65	0.56	1.72
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_01375	aspartate kinase	11.13	11.71	11.21	11.16	-0.08	0.55	-0.58	0.05	0.5	0.48	0.13	-0.06	0.65	0.56	8.64
Cthe_00780	HAD-superfamily hydrolase, subfam	6.43	6.99	6.3	6.49	0.13	0.5	-0.56	-0.19	0.67	0.44	0.2	-0.56	0.64	0.55	2.41
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_02848	phage major capsid protein, HK97	2.58	3.91	3.17	3.81	-0.59	0.1	-1.33	-0.64	0.1	0.1	-2.37	-1.5	0.64	0.55	0.09
Cthe_03074	Cof-like hydrolase	8.57	8.98	8.38	8.45	0.19	0.53	-0.41	-0.07	0.71	0.47	0.7	-0.31	0.64	0.55	1.99
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_01041	UDP-N-acetylmuramoylalanine--D-	10.96	11.43	10.87	10.88	0.09	0.55	-0.47	-0.01	0.63	0.48	0.5	-0.19	0.64	0.55	2.64
Cthe_01858	peptidase M23B	11.56	12.22	11.62	11.66	-0.06	0.56	-0.66	-0.04	0.52	0.49	-0.13	-0.25	0.64	0.55	4.53
Cthe_00567	peptide deformylase	9.06	9.42	8.64	8.97	0.42	0.45	-0.36	-0.33	0.9	0.4	0.87	-0.85	0.64	0.55	1.45
Cthe_01006	ribosomal protein S2	13	13.51	12.95	12.97	0.05	0.54	-0.51	-0.02	0.6	0.47	0.37	-0.21	0.64	0.55	3.2
Cthe_00613	thiamine pyrophosphate enzyme-li	12.06	12.76	11.94	12.17	0.12	0.59	-0.7	-0.23	0.66	0.52	-0.27	-0.65	0.64	0.55	2.13
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_01025	protein of unknown function DUF5	10.29	10.72	9.58	10.37	0.71	0.35	-0.43	-0.79	1.13	0.31	0.63	-1.81	0.64	0.55	1.09
Cthe_01387	hypothetical protein	9.79	10.24	9.65	9.71	0.14	0.53	-0.45	-0.06	0.67	0.47	0.57	-0.29	0.64	0.55	2.29
Cthe_01296	hypothetical protein	9.08	9.39	8.95	8.57	0.13	0.82	-0.31	0.38	0.67	0.71	1.03	0.63	0.64	0.55	1.44
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_00613	thiamine pyrophosphate enzyme-li	12.06	12.76	11.94	12.17	0.12	0.59	-0.7	-0.23	0.66	0.52	-0.27	-0.65	0.64	0.55	2.13
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_01006	ribosomal protein S2	13	13.51	12.95	12.97	0.05	0.54	-0.51	-0.02	0.6	0.47	0.37	-0.21	0.64	0.55	3.2
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_01006	ribosomal protein S2	13	13.51	12.95	12.97	0.05	0.54	-0.51	-0.02	0.6	0.47	0.37	-0.21	0.64	0.55	3.2
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_00613	thiamine pyrophosphate enzyme-li	12.06	12.76	11.94	12.17	0.12	0.59	-0.7	-0.23	0.66	0.52	-0.27	-0.65	0.64	0.55	2.13
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_01041	UDP-N-acetylmuramoylalanine--D-	10.96	11.43	10.87	10.88	0.09	0.55	-0.47	-0.01	0.63	0.48	0.5	-0.19	0.64	0.55	2.64
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_00567	peptide deformylase	9.06	9.42	8.64	8.97	0.42	0.45	-0.36	-0.33	0.9	0.4	0.87	-0.85	0.64	0.55	1.45
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_01041	UDP-N-acetylmuramoylalanine--D-	10.96	11.43	10.87	10.88	0.09	0.55	-0.47	-0.01	0.63	0.48	0.5	-0.19	0.64	0.55	2.64
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_01041	UDP-N-acetylmuramoylalanine--D-	10.96	11.43	10.87	10.88	0.09	0.55	-0.47	-0.01	0.63	0.48	0.5	-0.19	0.64	0.55	2.64
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_01041	UDP-N-acetylmuramoylalanine--D-	10.96	11.43	10.87	10.88	0.09	0.55	-0.47	-0.01	0.63	0.48	0.5	-0.19	0.64	0.55	2.64
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_01041	UDP-N-acetylmuramoylalanine--D-	10.96	11.43	10.87	10.88	0.09	0.55	-0.47	-0.01	0.63	0.48	0.5	-0.19	0.64	0.55	2.64
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_01041	UDP-N-acetylmuramoylalanine--D-	10.96	11.43	10.87	10.88	0.09	0.55	-0.47	-0.01	0.63	0.48	0.5	-0.19	0.64	0.55	2.64
Cthe_00865	3-methyl-2-oxobutanoate dehydro	11.51	12.15	11.58	11.6	-0.07	0.55	-0.64	-0.02	0.51	0.48	-0.07	-0.21	0.64	0.55	5.65
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_01260	4-hydroxybenzoyl-CoA thioesterase	9.42	10.31	9.44	9.49	-0.02	0.82	-0.89	-0.05	0.55	0.71	-0.9	-0.27	0.64	0.55	1.71
Cthe_02597	sugar-phosphate isomerases, RpiB/	11.41	12.13	11.54	11.48	-0.13	0.65	-0.72	0.06	0.46	0.57	-0.33	-0.04	0.64	0.55	3.93
Cthe_01051	integral membrane protein MviN	8.33	8.86	8.39	8.3	-0.06	0.56	-0.53	0.09	0.52	0.49	0.3	0.02	0.63	0.54	4.24
Cthe_01070	metal dependent phosphohydrolas	11.4	11.99	11.49	11.47	-0.09	0.52	-0.59	0.02	0.49	0.46	0.1	-0.13	0.63	0.54	7.32
Cthe_01376	Homoserine dehydrogenase	9.58	9.99	9.29	9.52	0.29	0.47	-0.41	-0.23	0.79	0.42	0.7	-0.65	0.63	0.54	1.67
Cthe_01066	DNA repair protein RecO	9.71	10.47	9.81	9.78	-0.1	0.69	-0.76	0.03	0.48	0.6	-0.47	-0.1	0.63	0.54	2.86
Cthe_02372	DNA polymerase III, beta subunit	10.27	10.92	10.13	10.37	0.14	0.55	-0.65	-0.24	0.67	0.48	-0.1	-0.67	0.63	0.54	2.17
Cthe_02406	hypothetical protein	8.88	9.46	8.51	8.99	0.37	0.47	-0.58	-0.48	0.86	0.42	0.13	-1.17	0.63	0.54	1.45
Cthe_00114	hypothetical protein	9.63	10.47	9.67	9.71	-0.04	0.76	-0.84	-0.04	0.53	0.66	-0.73	-0.25	0.63	0.54	1.96
Cthe_00461	gid protein	11.31	12.15	11.4	11.37	-0.09	0.78	-0.84	0.03	0.49	0.68	-0.73	-0.1	0.63	0.54	2.03
Cthe_00958	queuine tRNA-ribosyltransferase	8.82	9.49	8.59	8.94	0.23	0.55	-0.67	-0.35	0.75	0.48	-0.17	-0.9	0.63	0.54	1.74
Cthe_00360	thioredoxin	13.12	13.62	13.31	12.41	-0.19	1.21	-0.5	0.9	0.41	1.04	0.4	1.71	0.63	0.54	1.14
Cthe_02842	hypothetical protein	6.21	6.95	6.46	6.09	-0.25	0.86	-0.74	0.37	0.37	0.75	-0.4	0.6	0.63	0.54	2.07
Cthe_01971	hypothetical protein	10.88	11.44	11.02	10.7	-0.14	0.74	-0.56	0.32	0.45	0.64	0.2	0.5	0.63	0.54	2.59
Cthe_01980	hypothetical protein	5.43	6.04	5.61	5.29	-0.18	0.75	-0.61	0.32	0.42	0.					



Cthe_02508 TOPRIM domain containing protein	9.12	9.71	9.33	8.81	-0.21	0.9	-0.59	0.52	0.4	0.78	0.1	0.92	0.62	0.53	1.69
Cthe_01325 putative oxygen-independent copr	8.78	9.25	8.33	8.85	0.45	0.4	-0.47	-0.52	0.92	0.36	0.5	-1.25	0.61	0.53	1.31
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_00004 YD repeat containing protein	8.23	8.72	8.3	8.04	-0.07	0.68	-0.49	0.26	0.51	0.59	0.43	0.38	0.62	0.53	2.43
Cthe_00744 copper amine oxidase-like protein	9.39	9.91	9.2	9.43	0.19	0.48	-0.52	-0.23	0.71	0.42	0.33	-0.65	0.62	0.53	2.02
Cthe_00876 glycosyl transferase, family 39	9.96	10.49	9.92	9.99	0.04	0.5	-0.53	-0.07	0.6	0.44	0.3	-0.31	0.62	0.53	3.08
Cthe_02702 polysaccharide pyruvyl transferase	9.54	10.34	9.67	9.61	-0.13	0.73	-0.8	0.06	0.46	0.64	-0.6	-0.04	0.62	0.53	2.34
Cthe_00334 putative anti-sigma regulatory fact	8.35	8.84	8.01	8.41	0.34	0.43	-0.49	-0.4	0.83	0.38	0.43	-1	0.61	0.53	1.5
Cthe_01458 extracellular solute-binding protein	8.24	8.91	8.2	8.37	0.04	0.54	-0.67	-0.17	0.6	0.47	-0.17	-0.52	0.61	0.53	2.49
Cthe_01076 protein of unknown function DUF8	9.04	9.68	8.75	9.18	0.29	0.5	-0.64	-0.43	0.79	0.44	-0.07	-1.06	0.61	0.53	1.52
Cthe_01168 Extradiol ring-cleavage dioxygenase	9.86	10.63	9.83	9.99	0.03	0.64	-0.77	-0.16	0.59	0.56	-0.5	-0.5	0.62	0.53	2.05
Cthe_01204 protein of unknown function DUF4	13.2	13.96	13.37	13.25	-0.17	0.71	-0.76	0.12	0.43	0.62	-0.47	0.08	0.62	0.53	2.83
Cthe_01317 hypothetical protein	9.77	10.09	9.49	9.58	0.28	0.51	-0.32	-0.09	0.79	0.45	1	-0.35	0.61	0.53	1.53
Cthe_02510 protein of unknown function DUF3	11.87	12.35	11.81	11.83	0.06	0.52	-0.48	-0.02	0.61	0.46	0.47	-0.21	0.62	0.53	2.65
Cthe_02702 polysaccharide pyruvyl transferase	9.54	10.34	9.67	9.61	-0.13	0.73	-0.8	0.06	0.46	0.64	-0.6	-0.04	0.62	0.53	2.34
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00200 FAD-dependent pyridine nucleotid	11.92	12.57	12.14	11.89	-0.22	0.68	-0.65	0.25	0.39	0.59	-0.1	0.35	0.61	0.53	3.47
Cthe_02942 ABC transporter related protein	7.99	8.57	7.92	8.08	0.07	0.49	-0.58	-0.16	0.62	0.43	0.13	-0.5	0.61	0.53	2.61
Cthe_00794 aluminium resistance protein	9.74	10.15	9.61	9.61	0.13	0.54	-0.41	0	0.67	0.47	0.7	-0.17	0.62	0.53	2.03
Cthe_02942 ABC transporter related protein	7.99	8.57	7.92	8.08	0.07	0.49	-0.58	-0.16	0.62	0.43	0.13	-0.5	0.61	0.53	2.61
Cthe_01001 undecaprenyl diphosphate synthas	10.87	11.33	10.45	10.93	0.42	0.4	-0.46	-0.48	0.9	0.36	0.53	-1.17	0.61	0.53	1.35
Cthe_01763 ABC transporter related protein	8.66	9.3	8.73	8.78	-0.07	0.52	-0.64	-0.05	0.51	0.46	-0.07	-0.27	0.61	0.53	4.4
Cthe_02306 MATE efflux family protein	9.38	10.11	9.63	9.29	-0.25	0.82	-0.73	0.34	0.37	0.71	-0.37	0.54	0.62	0.53	2.18
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_00205 hypothetical protein	12.2	13.05	12.47	12.13	-0.27	0.92	-0.85	0.34	0.35	0.8	-0.77	0.54	0.61	0.53	1.66
Cthe_00923 hypothetical protein	6.09	6.55	5.7	6.13	0.39	0.42	-0.46	-0.43	0.87	0.37	0.53	-1.06	0.61	0.53	1.42
Cthe_00220 transposase, IS4	11.55	12.2	11.74	11.62	-0.19	0.58	-0.65	0.12	0.41	0.51	-0.1	0.08	0.62	0.53	9.12
Cthe_00007 hypothetical protein	8.35	8.59	7.93	8.1	0.42	0.49	-0.24	-0.17	0.9	0.43	1.27	-0.52	0.61	0.53	1.3
Cthe_00379 hypothetical protein	5.36	5.78	5.13	5.32	0.23	0.46	-0.42	-0.19	0.75	0.41	0.67	-0.56	0.61	0.53	1.75
Cthe_03111 hypothetical protein	8.55	9.1	8.51	8.61	0.04	0.49	-0.55	-0.1	0.6	0.43	0.23	-0.38	0.61	0.53	2.97
Cthe_01377 amino acid-binding ACT	8.64	9.19	8.4	8.72	0.24	0.47	-0.55	-0.32	0.75	0.42	0.23	-0.83	0.62	0.53	1.78
Cthe_01763 ABC transporter related protein	8.66	9.3	8.73	8.78	-0.07	0.52	-0.64	-0.05	0.51	0.46	-0.07	-0.27	0.61	0.53	4.4
Cthe_01325 putative oxygen-independent copr	8.78	9.25	8.33	8.85	0.45	0.4	-0.47	-0.52	0.92	0.36	0.5	-1.25	0.61	0.53	1.31
Cthe_02942 ABC transporter related protein	7.99	8.57	7.92	8.08	0.07	0.49	-0.58	-0.16	0.62	0.43	0.13	-0.5	0.61	0.53	2.61
Cthe_02724 DNA-directed RNA polymerase, bet	12.7	13.32	12.37	12.84	0.33	0.48	-0.62	-0.47	0.83	0.42	0	-1.15	0.61	0.53	1.44
Cthe_02446 ABC-type sugar transport system p	8.02	8.68	8.26	7.81	-0.24	0.87	-0.66	0.45	0.37	0.75	-0.13	0.77	0.62	0.53	1.91
Cthe_02105 DNA-directed DNA polymerase	11.24	11.77	11.4	10.93	-0.16	0.84	-0.53	0.47	0.44	0.73	0.3	0.81	0.61	0.53	1.76
Cthe_01377 amino acid-binding ACT	8.64	9.19	8.4	8.72	0.24	0.47	-0.55	-0.32	0.75	0.42	0.23	-0.83	0.62	0.53	1.78
Cthe_01377 amino acid-binding ACT	8.64	9.19	8.4	8.72	0.24	0.47	-0.55	-0.32	0.75	0.42	0.23	-0.83	0.62	0.53	1.78
Cthe_01001 undecaprenyl diphosphate synthas	10.87	11.33	10.45	10.93	0.42	0.4	-0.46	-0.48	0.9	0.36	0.53	-1.17	0.61	0.53	1.35
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01325 putative oxygen-independent copr	8.78	9.25	8.33	8.85	0.45	0.4	-0.47	-0.52	0.92	0.36	0.5	-1.25	0.61	0.53	1.31
Cthe_02105 DNA-directed DNA polymerase	11.24	11.77	11.4	10.93	-0.16	0.84	-0.53	0.47	0.44	0.73	0.3	0.81	0.61	0.53	1.76
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_02724 DNA-directed RNA polymerase, bet	12.7	13.32	12.37	12.84	0.33	0.48	-0.62	-0.47	0.83	0.42	0	-1.15	0.61	0.53	1.44
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74	-0.05	0.52	0.55	-0.4	-0.27	0.62	0.53	2.8
Cthe_00852 peptidase A24A-like protein	11.12	11.64	10.83	11.18	0.29	0.46	-0.52	-0.35	0.79	0.41	0.33	-0.9	0.62	0.53	1.66
Cthe_01320 ribosomal protein L11 methyltransf	7.9	8.64	7.96	8.01	-0.06	0.63	-0.74								



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Cthe_00039 methyl-accepting chemotaxis senso	5.17	5.67	5.17	5.17	0	0.5	-0.5	0	0.56	0.44	0.4	-0.17	0.59	0.51	2.93
Cthe_00443 protein of unknown function DUF1	8.48	9	8.41	8.54	0.07	0.46	-0.52	-0.13	0.62	0.41	0.33	-0.44	0.59	0.51	2.41
Cthe_01023 protein of unknown function DUF2	9.14	9.71	8.92	9.26	0.22	0.45	-0.57	-0.34	0.74	0.4	0.17	-0.88	0.59	0.51	1.68
Cthe_00621 putative translation initiation facto	12.28	12.98	12.51	12.32	-0.23	0.66	-0.7	0.19	0.38	0.58	-0.27	0.23	0.59	0.51	3.49
Cthe_01190 hypothetical protein	7.07	7.61	6.82	7.17	0.25	0.44	-0.54	-0.35	0.76	0.39	0.27	-0.9	0.59	0.51	1.62
Cthe_00380 hypothetical protein	4.17	5	4.32	4.25	-0.15	0.75	-0.83	0.07	0.44	0.65	-0.7	-0.02	0.59	0.51	2
Cthe_00710 hypothetical protein	11.09	11.58	10.66	11.19	0.43	0.39	-0.49	-0.53	0.9	0.35	0.43	-1.27	0.59	0.51	1.29
Cthe_01831 hypothetical protein	12.05	12.57	11.99	12.11	0.06	0.46	-0.52	-0.12	0.61	0.41	0.33	-0.42	0.59	0.51	2.46
Cthe_00621 putative translation initiation facto	12.28	12.98	12.51	12.32	-0.23	0.66	-0.7	0.19	0.38	0.58	-0.27	0.23	0.59	0.51	3.49
Cthe_01023 protein of unknown function DUF2	9.14	9.71	8.92	9.26	0.22	0.45	-0.57	-0.34	0.74	0.4	0.17	-0.88	0.59	0.51	1.68
Cthe_00872 Indole-3-glycerol-phosphate syntha	9.5	9.67	9.15	9.02	0.35	0.65	-0.17	0.13	0.84	0.57	1.5	0.1	0.59	0.51	1.21
Cthe_00720 aminotransferase, class V	17.06	17.82	17.41	16.81	-0.35	1.01	-0.76	0.6	0.29	0.87	-0.47	1.08	0.59	0.51	1.39
Cthe_01023 protein of unknown function DUF2	9.14	9.71	8.92	9.26	0.22	0.45	-0.57	-0.34	0.74	0.4	0.17	-0.88	0.59	0.51	1.68
Cthe_00621 putative translation initiation facto	12.28	12.98	12.51	12.32	-0.23	0.66	-0.7	0.19	0.38	0.58	-0.27	0.23	0.59	0.51	3.49
Cthe_00872 Indole-3-glycerol-phosphate syntha	9.5	9.67	9.15	9.02	0.35	0.65	-0.17	0.13	0.84	0.57	1.5	0.1	0.59	0.51	1.21
Cthe_00872 Indole-3-glycerol-phosphate syntha	9.5	9.67	9.15	9.02	0.35	0.65	-0.17	0.13	0.84	0.57	1.5	0.1	0.59	0.51	1.21
Cthe_01023 protein of unknown function DUF2	9.14	9.71	8.92	9.26	0.22	0.45	-0.57	-0.34	0.74	0.4	0.17	-0.88	0.59	0.51	1.68
Cthe_01023 protein of unknown function DUF2	9.14	9.71	8.92	9.26	0.22	0.45	-0.57	-0.34	0.74	0.4	0.17	-0.88	0.59	0.51	1.68
Cthe_00720 aminotransferase, class V	17.06	17.82	17.41	16.81	-0.35	1.01	-0.76	0.6	0.29	0.87	-0.47	1.08	0.59	0.51	1.39
Cthe_01023 protein of unknown function DUF2	9.14	9.71	8.92	9.26	0.22	0.45	-0.57	-0.34	0.74	0.4	0.17	-0.88	0.59	0.51	1.68
Cthe_00621 putative translation initiation facto	12.28	12.98	12.51	12.32	-0.23	0.66	-0.7	0.19	0.38	0.58	-0.27	0.23	0.59	0.51	3.49
Cthe_01421 signal peptide peptidase SppA, 36K	11.92	12.56	12.14	12	-0.22	0.56	-0.64	0.14	0.39	0.49	-0.07	0.13	0.58	0.5	7.57
Cthe_01024 small GTP-binding protein	10.12	10.84	9.68	10.33	0.44	0.51	-0.72	-0.65	0.91	0.45	-0.33	-1.52	0.58	0.5	1.17
Cthe_01342 beta-lactamase-like protein	8.46	8.95	8.12	8.55	0.34	0.4	-0.49	-0.43	0.83	0.36	0.43	-1.06	0.58	0.5	1.41
Cthe_00202 glutamine synthetase, type I	12.62	13.54	12.85	12.64	-0.23	0.9	-0.92	0.21	0.38	0.78	-1	0.27	0.58	0.5	1.5
Cthe_02144 DNA polymerase III, subunits gamm	9.55	10.22	9.42	9.72	0.13	0.5	-0.67	-0.3	0.67	0.44	-0.17	-0.79	0.58	0.5	1.77
Cthe_02284 CheA signal transduction histidine k	5.43	5.67	4.75	5.39	0.68	0.28	-0.24	-0.64	1.1	0.25	1.27	-1.5	0.58	0.5	1.02
Cthe_01303 glycosyl transferase, group 1	10.64	11.12	10.54	10.66	0.1	0.46	-0.48	-0.12	0.64	0.41	0.47	-0.42	0.58	0.5	2.15
Cthe_02284 CheA signal transduction histidine k	5.43	5.67	4.75	5.39	0.68	0.28	-0.24	-0.64	1.1	0.25	1.27	-1.5	0.58	0.5	1.02
Cthe_00183 protein of unknown function DUF2	7.95	8.69	7.85	8.12	0.1	0.57	-0.74	-0.27	0.64	0.5	-0.4	-0.73	0.58	0.5	1.74
Cthe_01410 cation diffusion facilitator family tr	10.05	10.74	9.99	10.21	0.06	0.53	-0.69	-0.22	0.61	0.47	-0.23	-0.63	0.58	0.5	2.05
Cthe_01421 signal peptide peptidase SppA, 36K	11.92	12.56	12.14	12	-0.22	0.56	-0.64	0.14	0.39	0.49	-0.07	0.13	0.58	0.5	7.57
Cthe_02712 hypothetical protein	10.04	10.55	10.02	10.09	0.02	0.46	-0.51	-0.07	0.58	0.41	0.37	-0.31	0.58	0.5	2.63
Cthe_02144 DNA polymerase III, subunits gamm	9.55	10.22	9.42	9.72	0.13	0.5	-0.67	-0.3	0.67	0.44	-0.17	-0.79	0.58	0.5	1.77
Cthe_00202 glutamine synthetase, type I	12.62	13.54	12.85	12.64	-0.23	0.9	-0.92	0.21	0.38	0.78	-1	0.27	0.58	0.5	1.5
Cthe_02144 DNA polymerase III, subunits gamm	9.55	10.22	9.42	9.72	0.13	0.5	-0.67	-0.3	0.67	0.44	-0.17	-0.79	0.58	0.5	1.77
Cthe_01421 signal peptide peptidase SppA, 36K	11.92	12.56	12.14	12	-0.22	0.56	-0.64	0.14	0.39	0.49	-0.07	0.13	0.58	0.5	7.57
Cthe_02284 CheA signal transduction histidine k	5.43	5.67	4.75	5.39	0.68	0.28	-0.24	-0.64	1.1	0.25	1.27	-1.5	0.58	0.5	1.02
Cthe_00202 glutamine synthetase, type I	12.62	13.54	12.85	12.64	-0.23	0.9	-0.92	0.21	0.38	0.78	-1	0.27	0.58	0.5	1.5
Cthe_00202 glutamine synthetase, type I	12.62	13.54	12.85	12.64	-0.23	0.9	-0.92	0.21	0.38	0.78	-1	0.27	0.58	0.5	1.5
Cthe_00202 glutamine synthetase, type I	12.62	13.54	12.85	12.64	-0.23	0.9	-0.92	0.21	0.38	0.78	-1	0.27	0.58	0.5	1.5
Cthe_00202 glutamine synthetase, type I	12.62	13.54	12.85	12.64	-0.23	0.9	-0.92	0.21	0.38	0.78	-1	0.27	0.58	0.5	1.5
Cthe_00853 type II secretion system protein E	10.13	10.69	9.85	10.28	0.28	0.41	-0.56	-0.43	0.79	0.36	0.2	-1.06	0.57	0.49	1.44
Cthe_02747 PHP-like protein	11.3	11.66	11.28	10.95	0.02	0.71	-0.36	0.33	0.58	0.62	0.87	0.52	0.57	0.49	1.5
Cthe_02895 glycoside hydrolase, family 18	10.77	11.39	10.95	10.91	-0.18	0.48	-0.62	0.04	0.42	0.42	0	-0.08	0.57	0.49	13.26
Cthe_00853 type II secretion system protein E	10.13	10.69	9.85	10.28	0.28	0.41	-0.56	-0.43	0.79	0.36	0.2	-1.06	0.57	0.49	1.44
Cthe_00974 UDP-N-acetylglucosamine--N-acety	10.04	10.74	10.11	10.2	-0.07	0.54	-0.7	-0.09	0.51	0.47	-0.27	-0.35	0.57	0.49	2.8
Cthe_01857 carboxyl-terminal protease	10.73	11.18	10.65	10.72	0.08	0.46	-0.45	-0.07	0.63	0.41	0.57	-0.31	0.57	0.49	2.07
Cthe_02601 UDP-N-acetylglucosamine 2-epime	11.78	12.47	11.96	11.92	-0.18	0.55	-0.69	0.04	0.42	0.48	-0.23	-0.08	0.57	0.49	4.68
Cthe_01039 ribosomal protein S20	14.44	15.1	14.59	14.59	-0.15	0.51	-0.66	0	0.44	0.45	-0.13	-0.17	0.57	0.49	5.25
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_00819 ABC transporter related protein	12.1	12.65	12.19	12.18	-0.09	0.47	-0.55	0.01	0.49	0.42	0.23	-0.15	0.57	0.49	4.2
Cthe_02305 putative undecaprenol kinase	9.57	10.15	9.78	9.48	-0.21	0.67	-0.58	0.3	0.4	0.58	0.13	0.46	0.57	0.49	2.63
Cthe_02706 ABC transporter related protein	10.37	11.05	10.52	10.51	-0.15	0.54	-0.68	0.01	0.44	0.47	-0.2	-0.15	0.57	0.49	4.6
Cthe_03225 hypothetical protein	6.6	6.77	6.13	6.32	0.47	0.45	-0.17	-0.19	0.94	0.4	1.5	-0.56	0.57	0.49	1.14
Cthe_00632 hypothetical protein	11.63	12.27	11.88	11.63	-0.25	0.64	-0.64	0.25	0.37	0.56	-0.07	0.35	0.57	0.49	3.36
Cthe_02706 ABC transporter related protein	10.37	11.05	10.52	10.51	-0.15	0.54	-0.68	0.01	0.44	0.47	-0.2	-0.15	0.57	0.49	4.6
Cthe_02601 UDP-N-acetylglucosamine 2-epime	11.78	12.47	11.96	11.92	-0.18	0.55	-0.69	0.04	0.42	0.48	-0.23	-0.08	0.57	0.49	4.68
Cthe_01039 ribosomal protein S20	14.44	15.1	14.59	14.59	-0.15	0.51	-0.66	0	0.44	0.45	-0.13	-0.17	0.57	0.49	5.25
Cthe_02601 UDP-N-acetylglucosamine 2-epime	11.78	12.47	11.96	11.92	-0.18	0.55	-0.69	0.04	0.42	0.48	-0.23	-0.08	0.57	0.49	4.68
Cthe_01857 carboxyl-terminal protease	10.73	11.18	10.65	10.72	0.08	0.46	-0.45	-0.07	0.63	0.41	0.57	-0.31	0.57	0.49	2.07
Cthe_00974 UDP-N-acetylglucosamine--N-acety	10.04	10.74	10.11	10.2	-0.07	0.54	-0.7	-0.09	0.51	0.47	-0.27	-0.35	0.57	0.49	2.8
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_02305 putative undecaprenol kinase	9.57	10.15	9.78	9.48	-0.21	0.67	-0.58	0.3	0.4	0.58	0.13	0.46	0.57	0.49	2.63
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_00974 UDP-N-acetylglucosamine--N-acety	10.04	10.74	10.11	10.2	-0.07	0.54	-0.7	-0.09	0.51	0.47	-0.27	-0.35	0.57	0.49	2.8
Cthe_02601 UDP-N-acetylglucosamine 2-epime	11.78	12.47	11.96	11.92	-0.18	0.55	-0.69	0.04	0.42	0.48	-0.23	-0.08	0.57	0.49	4.68
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_02601 UDP-N-acetylglucosamine 2-epime	11.78	12.47	11.96	11.92	-0.18	0.55	-0.69	0.04	0.42	0.48	-0.23	-0.08	0.57	0.49	4.68
Cthe_02601 UDP-N-acetylglucosamine 2-epime	11.78	12.47	11.96	11.92	-0.18	0.55	-0.69	0.04	0.42	0.48	-0.23	-0.08	0.57	0.49	4.68
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.51	9.18	-0.18	0.69	-0.54	0.33	0.42	0.6	0.27	0.52	0.57	0.49	2.23
Cthe_00974 UDP-N-acetylglucosamine--N-acety	10.04	10.74	10.11	10.2	-0.07	0.54	-0.7	-0.09	0.51	0.47	-0.27	-0.35	0.57	0.49	2.8
Cthe_00974 UDP-N-acetylglucosamine--N-acety	10.04	10.74	10.11	10.2	-0.07	0.54	-0.7	-0.09	0.51	0.47	-0.27	-0.35	0.57	0.49	2.8
Cthe_03072 acyl-ACP thioesterase	9.33	9.87	9.												



Cthe_02969	transcriptional regulator, GntR fam	6.32	6.54	6.32	5.25	0	1.29	-0.22	1.07	0.56	1.11	1.33	2.06	0.56	0.48	0.91
Cthe_00880	phospho-2-dehydro-3-deoxyhepto	10.12	10.87	10.02	10.31	0.1	0.56	-0.75	-0.29	0.64	0.49	-0.43	-0.77	0.56	0.48	1.63
Cthe_01766	glutamate 5-kinase	9.94	10.54	10.08	10.08	-0.14	0.46	-0.6	0	0.45	0.41	0.07	-0.17	0.56	0.48	5.91
Cthe_01840	cysteine synthase A	12.12	12.83	12.46	11.92	-0.34	0.91	-0.71	0.54	0.29	0.79	-0.3	0.96	0.56	0.48	1.49
Cthe_00919	Integrase, catalytic region		0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_03190	helicase, RecD/TraA family	10.64	11.28	10.5	10.81	0.14	0.47	-0.64	-0.31	0.67	0.42	-0.07	-0.81	0.56	0.48	1.74
Cthe_01681			0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01761	protein of unknown function DUF2	9.6	10.06	9.57	9.6	0.03	0.46	-0.46	-0.03	0.59	0.41	0.53	-0.23	0.56	0.48	2.22
Cthe_02694	O-antigen polymerase	11.62	12.26	11.87	11.68	-0.25	0.58	-0.64	0.19	0.37	0.51	-0.07	0.23	0.56	0.48	4.68
Cthe_00286	response regulator receiver sensor	9.5	10.34	9.11	9.73	0.39	0.61	-0.84	-0.62	0.87	0.53	-0.73	-1.46	0.56	0.48	1.11
Cthe_01311	signal transduction histidine kinase	8.38	8.99	8.6	8.53	-0.22	0.46	-0.61	0.07	0.39	0.41	0.03	-0.02	0.56	0.48	28.03
Cthe_02332	multi-sensor signal transduction his	9.19	9.89	8.93	9.39	0.26	0.5	-0.7	-0.46	0.77	0.44	-0.27	-1.13	0.56	0.48	1.36
Cthe_01696	hypothetical protein		0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_00942	MiaB-like tRNA modifying enzyme	10.88	11.43	10.59	11.03	0.29	0.4	-0.55	-0.44	0.79	0.36	0.23	-1.08	0.56	0.48	1.4
Cthe_00087	maf protein	8.12	8.88	7.77	8.35	0.35	0.53	-0.76	-0.58	0.84	0.47	-0.47	-1.37	0.56	0.48	1.19
Cthe_01605	phosphate ABC transporter (binding protein)-I		0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_01289	hypothetical protein	8.29	8.55	7.91	8.15	0.38	0.4	-0.26	-0.24	0.87	0.36	1.2	-0.67	0.56	0.48	1.22
Cthe_00525	hypothetical protein		0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_00076	hypothetical protein	12.22	12.75	12.45	11.81	-0.23	0.94	-0.53	0.64	0.38	0.81	0.3	1.17	0.56	0.48	1.32
Cthe_01263	tryptophan RNA-binding attenuato	10.68	11.25	10.75	10.8	-0.07	0.45	-0.57	-0.05	0.51	0.4	0.17	-0.27	0.56	0.48	3.63
Cthe_01440	hypothetical protein		0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_02491	hypothetical protein		0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_02310	hypothetical protein	10.3	10.96	10.53	10.44	-0.23	0.52	-0.66	0.09	0.38	0.46	-0.13	0.02	0.56	0.48	8.1
Cthe_00880	phospho-2-dehydro-3-deoxyhepto	10.12	10.87	10.02	10.31	0.1	0.56	-0.75	-0.29	0.64	0.49	-0.43	-0.77	0.56	0.48	1.63
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01766	glutamate 5-kinase	9.94	10.54	10.08	10.08	-0.14	0.46	-0.6	0	0.45	0.41	0.07	-0.17	0.56	0.48	5.91
Cthe_01761	protein of unknown function DUF2	9.6	10.06	9.57	9.6	0.03	0.46	-0.46	-0.03	0.59	0.41	0.53	-0.23	0.56	0.48	2.22
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01840	cysteine synthase A	12.12	12.83	12.46	11.92	-0.34	0.91	-0.71	0.54	0.29	0.79	-0.3	0.96	0.56	0.48	1.49
Cthe_01605	phosphate ABC transporter (binding protein)-I		0				0	0			0.02	2.07		0.56	0.48	0.02
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_02718	preprotein translocase, SecE subun	10.02	10.38	9.45	10.1	0.57	0.28	-0.36	-0.65	1.02	0.25	0.87	-1.52	0.56	0.48	1.07
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01311	signal transduction histidine kinase	8.38	8.99	8.6	8.53	-0.22	0.46	-0.61	0.07	0.39	0.41	0.03	-0.02	0.56	0.48	28.03
Cthe_00880	phospho-2-dehydro-3-deoxyhepto	10.12	10.87	10.02	10.31	0.1	0.56	-0.75	-0.29	0.64	0.49	-0.43	-0.77	0.56	0.48	1.63
Cthe_01766	glutamate 5-kinase	9.94	10.54	10.08	10.08	-0.14	0.46	-0.6	0	0.45	0.41	0.07	-0.17	0.56	0.48	5.91
Cthe_03190	helicase, RecD/TraA family	10.64	11.28	10.5	10.81	0.14	0.47	-0.64	-0.31	0.67	0.42	-0.07	-0.81	0.56	0.48	1.74
Cthe_00286	response regulator receiver sensor	9.5	10.34	9.11	9.73	0.39	0.61	-0.84	-0.62	0.87	0.53	-0.73	-1.46	0.56	0.48	1.11
Cthe_02332	multi-sensor signal transduction his	9.19	9.89	8.93	9.39	0.26	0.5	-0.7	-0.46	0.77	0.44	-0.27	-1.13	0.56	0.48	1.36
Cthe_01840	cysteine synthase A	12.12	12.83	12.46	11.92	-0.34	0.91	-0.71	0.54	0.29	0.79	-0.3	0.96	0.56	0.48	1.49
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_00880	phospho-2-dehydro-3-deoxyhepto	10.12	10.87	10.02	10.31	0.1	0.56	-0.75	-0.29	0.64	0.49	-0.43	-0.77	0.56	0.48	1.63
Cthe_01766	glutamate 5-kinase	9.94	10.54	10.08	10.08	-0.14	0.46	-0.6	0	0.45	0.41	0.07	-0.17	0.56	0.48	5.91
Cthe_01766	glutamate 5-kinase	9.94	10.54	10.08	10.08	-0.14	0.46	-0.6	0	0.45	0.41	0.07	-0.17	0.56	0.48	5.91
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_00880	phospho-2-dehydro-3-deoxyhepto	10.12	10.87	10.02	10.31	0.1	0.56	-0.75	-0.29	0.64	0.49	-0.43	-0.77	0.56	0.48	1.63
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01840	cysteine synthase A	12.12	12.83	12.46	11.92	-0.34	0.91	-0.71	0.54	0.29	0.79	-0.3	0.96	0.56	0.48	1.49
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_01352	UDP-glucose 6-dehydrogenase	9.73	10.43	9.53	9.92	0.2	0.51	-0.7	-0.39	0.72	0.45	-0.27	-0.98	0.56	0.48	1.49
Cthe_00102	tRNA (guanine-N(7)-)-methyltransf	9.39	9.92	9.58	9.29	-0.19	0.63	-0.53	0.29	0.41	0.55	0.3	0.44	0.54	0.47	2.3
Cthe_01291	amidohydrolase 2	9.66	10.27	9.73	9.83	-0.07	0.44	-0.61	-0.1	0.51	0.39	0.03	-0.38	0.54	0.47	3.01
Cthe_01942	hypothetical protein	13.52	14.26	13.83	13.54	-0.31	0.72	-0.74	0.29	0.32	0.63	-0.4	0.44	0.54	0.47	2.12
Cthe_03073	HAD-superfamily hydrolase, subfam	7.52	7.76	7.34	7.1	0.18	0.66	-0.24	0.24	0.71	0.58	1.27	0.33	0.55	0.47	1.25
Cthe_02704	Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_00993	protein of unknown function DUF4	7.51	8.28	7.2	7.74	0.31	0.54	-0.77	-0.54	0.81	0.47	-0.5	-1.29	0.55	0.47	1.21
Cthe_00994	NusA antitermination factor	11.46	11.92	10.95	11.61	0.51	0.31	-0.46	-0.66	0.97	0.28	0.53	-1.54	0.55	0.47	1.11
Cthe_02210	3-isopropylmalate dehydratase, sm	11.23	12.17	11.46	11.3	-0.23	0.87	-0.94	0.16	0.38	0.75	-1.07	0.17	0.54	0.47	1.39
Cthe_00676	tyrosine recombinase XerD	13.2	13.7	13.42	12.81	-0.22	0.89	-0.5	0.61	0.39	0.77	0.4	1.1	0.54	0.47	1.32
Cthe_01455	hypothetical protein	6.88	7.4	6.98	6.93	-0.1	0.47	-0.52	0.05	0.48	0.42	0.33	-0.06	0.54	0.47	3.4
Cthe_02376	DNA gyrase, B subunit	13.31	13.83	13.46	13.25	-0.15	0.58	-0.52	0.21	0.44	0.51	0.33	0.27	0.55	0.47	2.82
Cthe_02419	primosome, DnaD subunit	10.27	10.89	10.37	10.44	-0.1	0.45	-0.62	-0.07	0.48	0.4	0	-0.31	0.54	0.47	3.6
Cthe_02770	transposase IS116/IS110/IS902	6.04	5.98	6.64	5.73	-0.6	0.25	0.06	0.91	0.09	0.23	2.27	1.73	0.55	0.47	0.15
Cthe_02820	MCP methyltransferase, CheR-type	5.13	6.11	4.52	5.43	0.61	0.68	-0.98	-0.91	1.05	0.59	-1.2	-2.06	0.54	0.47	0.9
Cthe_03114	glycosyl transferase, group 1	10.02	10.73	10.29	10.09	-0.27	0.64	-0.71	0.2	0.35	0.56	-0.3	0.25	0.55	0.47	3.02
Cthe_01068	cytidine deaminase	9.68	10.27	9.92	9.68	-0.24	0.59	-0.59	0.24	0.37	0.52	0.1	0.33	0.54	0.47	3.31
Cthe_02578	Ppx/GppA phosphatase	12.37	13.12	12.73	12.22	-0.36	0.9	-0.75	0.51	0.28	0.78	-0.43	0.9	0.55	0.47	1.48
Cthe_00142	metal dependent phosphohydrolas	11.66	12.19	11.4	11.81	0.26	0.38	-0.53	-0.41	0.77	0.34	0.3	-1.02	0.54	0.47	1.41
Cthe_00511	histidine kinase	13.17	13.83	13.42	13.33	-0.25	0.5	-0.66	0.09	0.37	0.44	-0.13	0.02	0.54	0.47	7.81
Cthe_02820	MCP methyltransferase, CheR-type	5.13	6.11	4.52	5.43	0.61	0.68	-0.98	-0.91	1.05	0.59	-1.2	-2.06	0.54	0.47	0.9
Cthe_00892	protein of unknown function DUF3	8.9	9.4	8.73	9.02	0.17	0.38	-0.5	-0.29	0.7	0.34	0.4	-0.77	0.54	0.47	1.6
Cthe_02759	transcriptional regulator, AraC fam	9.77	10.15	9.77	9.52	0	0.63	-0.38	0.25	0.56	0.55	0.8	0.35	0.54	0.47	1.61
Cthe_01026	ribosomal protein L32	11.73	12.39	11.72	11.92	0.01	0.47	-0.66	-0.2	0.57	0.42	-0.13	-0.58	0.54	0.47	2.13
Cthe_00864	pyruvate ferredoxin/flavodoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe																



Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_02210 3-isopropylmalate dehydratase, sm	11.23	12.17	11.46	11.3	-0.23	0.87	-0.94	0.16	0.38	0.75	-1.07	0.17	0.54	0.47	1.39
Cthe_00864 pyruvate ferredoxin/ferredoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_00864 pyruvate ferredoxin/ferredoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe_01026 ribosomal protein L32	11.73	12.39	11.72	11.92	0.01	0.47	-0.66	-0.2	0.57	0.42	-0.13	-0.58	0.54	0.47	2.13
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_00864 pyruvate ferredoxin/ferredoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe_01425 Inorganic diphosphatase	12.84	13.35	13.05	12.48	-0.21	0.87	-0.51	0.57	0.4	0.75	0.37	1.02	0.55	0.47	1.4
Cthe_02376 DNA gyrase, B subunit	13.31	13.83	13.46	13.25	-0.15	0.58	-0.52	0.21	0.44	0.51	0.33	0.27	0.55	0.47	2.82
Cthe_02820 MCP methyltransferase, CheR-type	5.13	6.11	4.52	5.43	0.61	0.68	-0.98	-0.91	1.05	0.59	-1.2	-2.06	0.54	0.47	0.9
Cthe_02210 3-isopropylmalate dehydratase, sm	11.23	12.17	11.46	11.3	-0.23	0.87	-0.94	0.16	0.38	0.75	-1.07	0.17	0.54	0.47	1.39
Cthe_01068 cytidine deaminase	9.68	10.27	9.92	9.68	-0.24	0.59	-0.59	0.24	0.37	0.52	0.1	0.33	0.54	0.47	3.31
Cthe_02210 3-isopropylmalate dehydratase, sm	11.23	12.17	11.46	11.3	-0.23	0.87	-0.94	0.16	0.38	0.75	-1.07	0.17	0.54	0.47	1.39
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_00102 tRNA (guanine-N(7))-methyltransf	9.39	9.92	9.58	9.29	-0.19	0.63	-0.53	0.29	0.41	0.55	0.3	0.44	0.54	0.47	2.3
Cthe_02578 Ppx/GppA phosphatase	12.37	13.12	12.73	12.22	-0.36	0.9	-0.75	0.51	0.28	0.78	-0.43	0.9	0.55	0.47	1.48
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_01068 cytidine deaminase	9.68	10.27	9.92	9.68	-0.24	0.59	-0.59	0.24	0.37	0.52	0.1	0.33	0.54	0.47	3.31
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_02210 3-isopropylmalate dehydratase, sm	11.23	12.17	11.46	11.3	-0.23	0.87	-0.94	0.16	0.38	0.75	-1.07	0.17	0.54	0.47	1.39
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_01068 cytidine deaminase	9.68	10.27	9.92	9.68	-0.24	0.59	-0.59	0.24	0.37	0.52	0.1	0.33	0.54	0.47	3.31
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_01068 cytidine deaminase	9.68	10.27	9.92	9.68	-0.24	0.59	-0.59	0.24	0.37	0.52	0.1	0.33	0.54	0.47	3.31
Cthe_00864 pyruvate ferredoxin/ferredoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_00864 pyruvate ferredoxin/ferredoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe_02210 3-isopropylmalate dehydratase, sm	11.23	12.17	11.46	11.3	-0.23	0.87	-0.94	0.16	0.38	0.75	-1.07	0.17	0.54	0.47	1.39
Cthe_00864 pyruvate ferredoxin/ferredoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe_00864 pyruvate ferredoxin/ferredoxin oxi	11.66	12.33	11.91	11.81	-0.25	0.52	-0.67	0.1	0.37	0.46	-0.17	0.04	0.54	0.47	6.04
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_01068 cytidine deaminase	9.68	10.27	9.92	9.68	-0.24	0.59	-0.59	0.24	0.37	0.52	0.1	0.33	0.54	0.47	3.31
Cthe_02704 Transketolase-like protein	13.24	14.02	13.5	13.32	-0.26	0.7	-0.78	0.18	0.36	0.61	-0.53	0.21	0.55	0.47	2.22
Cthe_00747 extracellular solute-binding protein	10.95	11.56	11.22	10.98	-0.27	0.58	-0.61	0.24	0.35	0.51	0.03	0.33	0.53	0.46	3.33
Cthe_00587 transposase, mutator type	6.29	7.37	6.61	6.29	-0.32	1.08	-1.08	0.32	0.31	0.93	-1.53	0.5	0.53	0.46	1.09
Cthe_00777 DNA mismatch repair protein MutS	10.17	10.67	9.89	10.33	0.28	0.34	-0.5	-0.44	0.79	0.31	0.4	-1.08	0.53	0.46	1.32
Cthe_02737 excinuclease ABC, C subunit	12.38	13.19	12.57	12.53	-0.19	0.66	-0.81	0.04	0.41	0.58	-0.63	-0.08	0.53	0.46	2
Cthe_01967 DNA segregation ATPase FtsK/SpoII	11.69	12.3	11.96	11.66	-0.27	0.64	-0.61	0.3	0.35	0.56	0.03	0.46	0.53	0.46	2.56
Cthe_01022 Glycerol-3-phosphate dehydrogena	10.35	11.09	10.1	10.59	0.25	0.5	-0.74	-0.49	0.76	0.44	-0.4	-1.19	0.53	0.46	1.25
Cthe_02605 ATP synthase F1, delta subunit	8.19	8.7	7.82	8.37	0.37	0.33	-0.51	-0.55	0.86	0.3	0.37	-1.31	0.53	0.46	1.19
Cthe_01812 Urease accessory protein UreD	4.64	5.55	5.04	4.58	-0.4	0.97	-0.91	0.46	0.25	0.84	-0.97	0.79	0.53	0.46	1.25
Cthe_02610 hypothetical protein	11.83	12.59	12.25	11.59	-0.42	1	-0.76	0.66	0.23	0.86	-0.47	1.21	0.53	0.46	1.22
Cthe_03137 hypothetical protein	8.5	9.02	8.61	8.57	-0.11	0.45	-0.52	0.04	0.48	0.4	0.33	-0.08	0.53	0.46	3.29
Cthe_02994 hypothetical protein	8.32	8.95	8.12	8.52	0.2	0.43	-0.63	-0.4	0.72	0.38	-0.03	-1	0.53	0.46	1.45
Cthe_02160 hypothetical protein	11.45	12.2	11.7	11.6	-0.25	0.6	-0.75	0.1	0.37	0.53	-0.43	0.04	0.53	0.46	2.67
Cthe_02605 ATP synthase F1, delta subunit	8.19	8.7	7.82	8.37	0.37	0.33	-0.51	-0.55	0.86	0.3	0.37	-1.31	0.53	0.46	1.19
Cthe_00747 extracellular solute-binding protein	10.95	11.56	11.22	10.98	-0.27	0.58	-0.61	0.24	0.35	0.51	0.03	0.33	0.53	0.46	3.33
Cthe_02605 ATP synthase F1, delta subunit	8.19	8.7	7.82	8.37	0.37	0.33	-0.51	-0.55	0.86	0.3	0.37	-1.31	0.53	0.46	1.19
Cthe_02605 ATP synthase F1, delta subunit	8.19	8.7	7.82	8.37	0.37	0.33	-0.51	-0.55	0.86	0.3	0.37	-1.31	0.53	0.46	1.19
Cthe_01022 Glycerol-3-phosphate dehydrogena	10.35	11.09	10.1	10.59	0.25	0.5	-0.74	-0.49	0.76	0.44	-0.4	-1.19	0.53	0.46	1.25
Cthe_01022 Glycerol-3-phosphate dehydrogena	10.35	11.09	10.1	10.59	0.25	0.5	-0.74	-0.49	0.76	0.44	-0.4	-1.19	0.53	0.46	1.25
Cthe_01022 Glycerol-3-phosphate dehydrogena	10.35	11.09	10.1	10.59	0.25	0.5	-0.74	-0.49	0.76	0.44	-0.4	-1.19	0.53	0.46	1.25
Cthe_02605 ATP synthase F1, delta subunit	8.19	8.7	7.82	8.37	0.37	0.33	-0.51	-0.55	0.86	0.3	0.37	-1.31	0.53	0.46	1.19
Cthe_01022 Glycerol-3-phosphate dehydrogena	10.35	11.09	10.1	10.59	0.25	0.5	-0.74	-0.49	0.76	0.44	-0.4	-1.19	0.53	0.46	1.25
Cthe_00218 metallophosphoesterase	11.03	11.5	11.1	11.03	-0.07	0.47	-0.47	0.07	0.51	0.42	0.5	-0.02	0.52	0.45	2.36
Cthe_00989 phosphoesterase, RecJ-like protein	11.12	11.97	11.36	11.23	-0.24	0.74	-0.85	0.13	0.37	0.64	-0.77	0.1	0.52	0.45	1.7
Cthe_01382 Patatin	9.98	10.61	10.26	10.14	-0.28	0.47	-0.63	0.12	0.34	0.42	-0.03	0.08	0.52	0.45	11.29
Cthe_01019 binding-protein-dependent transpo	14.59	15.21	14.87	14.62	-0.28	0.59	-0.62	0.25	0.34	0.52	0	0.35	0.52	0.45	3.17
Cthe_01278 ATP-dependent DNA helicase RecG	8.17	9.01	8.27	8.36	-0.1	0.65	-0.84	-0.09	0.48	0.57	-0.73	-0.35	0.52	0.45	1.64
Cthe_00363 aminotransferase, class I and II	12.14	12.61	11.77	12.3	0.37	0.31	-0.47	-0.53	0.86	0.28	0.5	-1.27	0.52	0.45	1.18
Cthe_01278 ATP-dependent DNA helicase RecG	8.17	9.01	8.27	8.36	-0.1	0.65	-0.84	-0.09	0.48	0.57	-0.73	-0.35	0.52	0.45	1.64
Cthe_02050 CRISPR-associated RAMP protein, S	9.47	10.2	9.34	9.7	0.13	0.5	-0.73	-0.36	0.67	0.44	-0.37	-0.92	0.52	0.45	1.44
Cthe_02203 GTP cyclohydrolase I	10	10.73	10.1	10.2	-0.1	0.53	-0.73	-0.1	0.48	0.47	-0.37	-0.38	0.52	0.45	2.26
Cthe_02818 CheA signal transduction histidine k	6.41	7.04	6.39	6.61	0.02	0.43	-0.63	-0.22	0.58	0.38	-0.03	-0.63	0.52	0.45	1.96
Cthe_01757 peptidase M23B	11.38	11.93	11.38	11.53	0	0.4	-0.55	-0.15	0.56	0.36	0.23	-0.48	0.52	0.45	2.23
Cthe_02336 glycosyl transferase, group 1	8.63	9.41	8.56	8.86	0.07	0.55	-0.78	-0.3	0.62	0.48	-0.53	-0.79	0.52	0.45	1.47
Cthe_01071 PhoH-like protein	10.33	10.88	10.33	10.48	0	0.4	-0.55	-0.15	0.56	0.36	0.23	-0.48	0.52	0.45	2.23
Cthe_02775 transcriptional regulator, Crp/Fnr f	8.15	8.64	8.37	7.75	-0.22	0.89	-0.49	0.62	0.39	0.77	0.43	1.13	0.52	0.45	1.27
Cthe_02818 CheA signal transduction histidine k	6.41	7.04	6.39	6.61	0.02	0.43	-0.63	-0.22	0.58	0.38	-0.03	-0.63	0.52	0.45	1.96
Cthe_02978 transcriptional regulator, Crp/Fnr f	6.6	7.19	6.87	6.49	-0.27	0.7	-0.59	0.38	0.35	0.61	0.1	0.63	0.52	0.45	1.97
Cthe_01351 acetobutylicum phosphotransbutyr	8.16	8.44	7.89	8.02	0.27	0.42	-0.28	-0.13	0.78	0.37	1.13	-0.44	0.52	0.45	1.27
Cthe_00233 GCN5-related N-acetyltransferase	10.92	11.61	11.24	10.92	-0.32	0.69	-0.69	0.32	0.31	0.6	-0.23	0.5	0.52	0.45	2.19
Cthe_00990 ribosome-binding factor A	9.74	10.38	9.75	9.94	-0.01	0.44	-0.64	-0.19	0.56	0.39	-0.07	-0.56	0.52	0.45	2.16
Cthe_00992 ribosomal protein L7Ae/L30e/S12e	8.14	8.54	7.81	8.23	0.33	0.31	-0.4	-0.42	0.83	0.28	0.73	-1.04	0.52	0.45	1.23
Cthe_03120 pyruvate flavodoxin/ferredoxin	14.55	15.46	14.97	14.47	-0.42	0.99	-0.91	0.5	0.23						



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Cthe_02629 UDP-N-acetylglucosamine pyropho	10.41	11.02	10.07	10.66	0.34	0.36	-0.61	-0.59	0.83	0.32	0.03	-1.4	0.5	0.43	1.13
Cthe_02629 UDP-N-acetylglucosamine pyropho	10.41	11.02	10.07	10.66	0.34	0.36	-0.61	-0.59	0.83	0.32	0.03	-1.4	0.5	0.43	1.13
Cthe_00542 protein of unknown function DUF4	6.78	7.31	6.38	7.02	0.4	0.29	-0.53	-0.64	0.88	0.26	0.3	-1.5	0.49	0.42	1.07
Cthe_02967 major facilitator superfamily MFS_	6.09	6.41	5.61	6.19	0.48	0.22	-0.32	-0.58	0.94	0.2	1	-1.37	0.49	0.42	1.01
Cthe_00890 RNA polymerase, sigma-24 subunit	7.07	7.74	7.08	7.31	-0.01	0.43	-0.67	-0.23	0.56	0.38	-0.17	-0.65	0.49	0.42	1.8
Cthe_01449 transcriptional regulator, MarR fam	6.69	6.87	6.38	6.41	0.31	0.46	-0.18	-0.03	0.81	0.41	1.47	-0.23	0.49	0.42	1.09
Cthe_02690 UbiA prenyltransferase	8.37	9.07	8.63	8.57	-0.26	0.5	-0.7	0.06	0.36	0.44	-0.27	-0.04	0.49	0.42	3.72
Cthe_00442 Polypeptide-transport-associated,	9.99	10.57	10.02	10.19	-0.03	0.38	-0.58	-0.17	0.54	0.34	0.13	-0.52	0.49	0.42	2.13
Cthe_00605 NLP/P60	12.86	13.49	13.1	13.07	-0.24	0.42	-0.63	0.03	0.37	0.37	-0.03	-0.1	0.49	0.42	8.95
Cthe_00365 peptide chain release factor 2	11.71	12.25	11.61	11.89	0.1	0.36	-0.54	-0.28	0.64	0.32	0.27	-0.75	0.49	0.42	1.6
Cthe_00503 2'-5' RNA ligase	8.16	8.83	8.52	8.09	-0.36	0.74	-0.67	0.43	0.28	0.64	-0.17	0.73	0.49	0.42	1.66
Cthe_01751 RNA methyltransferase, TrmA fami	7.79	8.29	7.97	7.77	-0.18	0.52	-0.5	0.2	0.42	0.46	0.4	0.25	0.49	0.42	2.36
Cthe_01782 ribosomal protein S9	12.96	13.52	13.22	12.99	-0.26	0.53	-0.56	0.23	0.36	0.47	0.2	0.31	0.49	0.42	2.87
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00742 hypothetical protein	6.99	7.55	6.81	7.2	0.18	0.35	-0.56	-0.39	0.71	0.31	0.2	-0.98	0.49	0.42	1.38
Cthe_01418 hypothetical protein	5.61	5.98	5.36	5.67	0.25	0.31	-0.37	-0.31	0.76	0.28	0.83	-0.81	0.49	0.42	1.25
Cthe_02869 hypothetical protein	8.21	8.48	8.09	7.93	0.12	0.55	-0.27	0.16	0.66	0.48	1.17	0.17	0.49	0.42	1.23
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_01782 ribosomal protein S9	12.96	13.52	13.22	12.99	-0.26	0.53	-0.56	0.23	0.36	0.47	0.2	0.31	0.49	0.42	2.87
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_01782 ribosomal protein S9	12.96	13.52	13.22	12.99	-0.26	0.53	-0.56	0.23	0.36	0.47	0.2	0.31	0.49	0.42	2.87
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00605 NLP/P60	12.86	13.49	13.1	13.07	-0.24	0.42	-0.63	0.03	0.37	0.37	-0.03	-0.1	0.49	0.42	8.95
Cthe_00503 2'-5' RNA ligase	8.16	8.83	8.52	8.09	-0.36	0.74	-0.67	0.43	0.28	0.64	-0.17	0.73	0.49	0.42	1.66
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00345 L-lactate dehydrogenase	12.9	13.47	13.07	13.07	-0.17	0.4	-0.57	0	0.43	0.36	0.17	-0.17	0.49	0.42	4.17
Cthe_00855 HAD superfamily (subfamily IIA) ph	9.12	9.77	9.46	9.19	-0.34	0.58	-0.65	0.27	0.29	0.51	-0.1	0.4	0.47	0.41	2.54
Cthe_01048 Rhomboid-like protein	10.39	10.95	10.27	10.62	0.12	0.33	-0.56	-0.35	0.66	0.3	0.2	-0.9	0.47	0.41	1.4
Cthe_00608 peptidase M42	9.66	10.7	10.22	9.54	-0.56	1.16	-1.04	0.68	0.12	1	-1.4	1.25	0.48	0.41	0.96
Cthe_01847 two component transcriptional reg	10.62	11.59	10.98	10.7	-0.36	0.89	-0.97	0.28	0.28	0.77	-1.17	0.42	0.47	0.41	1.18
Cthe_02900 RNA polymerase, sigma 28 subunit	10.55	11.15	10.38	10.79	0.17	0.36	-0.6	-0.41	0.7	0.32	0.07	-1.02	0.48	0.41	1.34
Cthe_01790 ATP:guanine phosphotransferase	12.3	13.14	12.8	12.16	-0.5	0.98	-0.84	0.64	0.17	0.85	-0.73	1.17	0.48	0.41	1.12
Cthe_02884 Imidazoleglycerol-phosphate dehyd	9.69	10.39	9.92	9.93	-0.23	0.46	-0.7	-0.01	0.38	0.41	-0.27	-0.19	0.47	0.41	3.02
Cthe_00247 DNA mismatch repair protein MutS	9.31	10.05	9.1	9.61	0.21	0.44	-0.74	-0.51	0.73	0.39	-0.4	-1.23	0.47	0.41	1.14
Cthe_02256 replicative DNA helicase	12.47	13.39	12.67	12.64	-0.2	0.75	-0.92	0.03	0.4	0.65	-1	-0.1	0.48	0.41	1.36
Cthe_02374 DNA replication and repair protein	9.21	9.57	9.01	9.24	0.2	0.33	-0.36	-0.23	0.72	0.3	0.87	-0.65	0.48	0.41	1.28
Cthe_00020 biotin synthase	4.75	5.81	4.91	4.91	-0.16	0.9	-1.06	0	0.44	0.78	-1.47	-0.17	0.48	0.41	1.08
Cthe_00420 dipicolinate synthase	8.2	8.58	8.06	8.22	0.14	0.36	-0.38	-0.16	0.67	0.32	0.8	-0.5	0.48	0.41	1.41
Cthe_00601 thiamine-phosphate pyrophosphor	8.58	9.25	8.83	8.82	-0.25	0.43	-0.67	0.01	0.37	0.38	-0.17	-0.15	0.47	0.41	4.18
Cthe_02819 methyl-accepting chemotaxis senso	6.19	7.21	6.07	6.44	0.12	0.77	-1.02	-0.37	0.66	0.67	-1.33	-0.94	0.48	0.41	1.03
Cthe_02821 response regulator receiver modul	5.67	6.29	5.78	5.91	-0.11	0.38	-0.62	-0.13	0.48	0.34	0	-0.44	0.47	0.41	2.39
Cthe_00714 hydroxymethylbutenyl pyrophosph	14.02	14.5	14.01	14.13	0.01	0.37	-0.48	-0.12	0.57	0.33	0.47	-0.42	0.48	0.41	1.87
Cthe_01847 two component transcriptional reg	10.62	11.59	10.98	10.7	-0.36	0.89	-0.97	0.28	0.28	0.77	-1.17	0.42	0.47	0.41	1.18
Cthe_02819 methyl-accepting chemotaxis senso	6.19	7.21	6.07	6.44	0.12	0.77	-1.02	-0.37	0.66	0.67	-1.33	-0.94	0.48	0.41	1.03
Cthe_02821 response regulator receiver modul	5.67	6.29	5.78	5.91	-0.11	0.38	-0.62	-0.13	0.48	0.34	0	-0.44	0.47	0.41	2.39
Cthe_03068 periplasmic sensor signal transduct	8.91	9.6	9.07	9.16	-0.16	0.44	-0.69	-0.09	0.44	0.39	-0.23	-0.35	0.47	0.41	2.51
Cthe_01165 YbbR-like protein	10.85	11.4	10.77	11.07	0.08	0.33	-0.55	-0.3	0.63	0.3	0.23	-0.79	0.47	0.41	1.51
Cthe_00161 protein of unknown function DUF4	11.71	12.28	11.68	11.93	0.03	0.35	-0.57	-0.25	0.59	0.31	0.17	-0.69	0.47	0.41	1.67
Cthe_00714 hydroxymethylbutenyl pyrophosph	14.02	14.5	14.01	14.13	0.01	0.37	-0.48	-0.12	0.57	0.33	0.47	-0.42	0.48	0.41	1.87
Cthe_00444 cell division protein FtsA	9.32	9.89	9.17	9.55	0.15	0.34	-0.57	-0.38	0.68	0.31	0.17	-0.96	0.47	0.41	1.37
Cthe_00960 SpoIID/LytB domain containing pro	10.34	10.81	10.52	10.23	-0.18	0.58	-0.47	0.29	0.42	0.51	0.5	0.44	0.47	0.41	1.77
Cthe_02377 Cobyrinic acid a,c-diamide synthase	9.79	10.37	9.63	10.03	0.16	0.34	-0.58	-0.4	0.69	0.31	0.13	-1	0.47	0.41	1.34
Cthe_00560 FAD-dependent pyridine nucleotid	16.52	17.18	16.94	16.23	-0.42	0.95	-0.66	0.71	0.23	0.82	-0.13	1.31	0.48	0.41	1.16
Cthe_02238 aldehyde dehydrogenase	7.84	8.56	8.25	7.78	-0.41	0.78	-0.72	0.47	0.24	0.68	-0.33	0.81	0.48	0.41	1.47
Cthe_02604 ATP synthase F0, B subunit	9.55	10.12	9.39	9.77	0.16	0.35	-0.57	-0.38	0.69	0.31	0.17	-0.96	0.48	0.41	1.39
Cthe_00714 hydroxymethylbutenyl pyrophosph	14.02	14.5	14.01	14.13	0.01	0.37	-0.48	-0.12	0.57	0.33	0.47	-0.42	0.48	0.41	1.87
Cthe_02955 hypothetical protein	2.58	3.58	2.58	2.81	0	0.77	-1	-0.23	0.56	0.67	-1.27	-0.65	0.47	0.41	1.09
Cthe_01988 hypothetical protein	11.28	11.83	11.4	11.46	-0.12	0.37	-0.55	-0.06	0.47	0.33	0.23	-0.29	0.47	0.41	2.77
Cthe_00050 hypothetical protein	6.88	7.34	6.04	7.23	0.84	0.11	-0.46	-1.19	1.23	0.11	0.53	-2.65	0.48	0.41	0.82
Cthe_00593 copper amine oxidase-like protein	9.42	9.83	9.63	8.92	-0.21	0.91	-0.41	0.71	0.4	0.79	0.7				







Cthe_02886 imidazole glycerol phosphate synth	9.27	9.81	9.53	9.35	-0.26	0.46	-0.54	0.18	0.36	0.41	0.27	0.21	0.45	0.39	2.85
Cthe_02442 carbohydrate kinase, FGGY	7.74	8.22	8.03	7.33	-0.29	0.89	-0.48	0.7	0.33	0.77	0.47	1.29	0.45	0.39	1.09
Cthe_01818 urease, gamma subunit	3.7	3.58	4.25	3	-0.55	0.58	0.12	1.25	0.13	0.51	2.47	2.44	0.45	0.39	0.27
Cthe_02886 imidazole glycerol phosphate synth	9.27	9.81	9.53	9.35	-0.26	0.46	-0.54	0.18	0.36	0.41	0.27	0.21	0.45	0.39	2.85
Cthe_02442 carbohydrate kinase, FGGY	7.74	8.22	8.03	7.33	-0.29	0.89	-0.48	0.7	0.33	0.77	0.47	1.29	0.45	0.39	1.09
Cthe_00654 biotin and thiamin synthesis associ	13.89	14.71	14.32	13.98	-0.43	0.73	-0.82	0.34	0.22	0.64	-0.67	0.54	0.44	0.38	1.4
Cthe_02989 glycosyltransferase 36	13.64	14.38	13.9	13.89	-0.26	0.49	-0.74	0.01	0.36	0.43	-0.4	-0.15	0.44	0.38	2.34
Cthe_02378 parB-like partition protein	9.03	9.58	8.97	9.27	0.06	0.31	-0.55	-0.3	0.61	0.28	0.23	-0.79	0.44	0.38	1.46
Cthe_00262 gamma-glutamyl phosphate reduct	12.6	13.18	12.91	12.78	-0.31	0.4	-0.58	0.13	0.32	0.36	0.13	0.1	0.44	0.38	5.24
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_01777 amidohydrolase	10.16	10.74	10.19	10.41	-0.03	0.33	-0.58	-0.22	0.54	0.3	0.13	-0.63	0.44	0.38	1.71
Cthe_00654 biotin and thiamin synthesis associ	13.89	14.71	14.32	13.98	-0.43	0.73	-0.82	0.34	0.22	0.64	-0.67	0.54	0.44	0.38	1.4
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_01371 YD repeat protein	9.86	10.56	9.84	10.15	0.02	0.41	-0.7	-0.31	0.58	0.36	-0.27	-0.81	0.44	0.38	1.43
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_00189 non-canonical purine NTP pyropho	10.35	10.94	10.68	10.38	-0.33	0.56	-0.59	0.3	0.3	0.49	0.1	0.46	0.44	0.38	2.18
Cthe_01255 hypothetical protein	9.25	9.56	9.34	8.78	-0.09	0.78	-0.31	0.56	0.49	0.68	1.03	1	0.44	0.38	1.04
Cthe_02479 U928 prophage protein	4.25	3.81	3.17	3.46	1.08	0.35	0.44	-0.29	1.42	0.31	3.53	-0.77	0.44	0.38	0.72
Cthe_01358 glycosyltransferase	2.58	1.58	2	2	0.58	-0.42	1	0	1.02	-0.34	5.4	-0.17	0.44	0.38	0.36
Cthe_00264 hypothetical protein	3.17	3.17	4	2.58	-0.83	0.59	0	1.42	-0.1	0.52	2.07	2.79	0.44	0.38	0.27
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_00262 gamma-glutamyl phosphate reduct	12.6	13.18	12.91	12.78	-0.31	0.4	-0.58	0.13	0.32	0.36	0.13	0.1	0.44	0.38	5.24
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_00189 non-canonical purine NTP pyropho	10.35	10.94	10.68	10.38	-0.33	0.56	-0.59	0.3	0.3	0.49	0.1	0.46	0.44	0.38	2.18
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_00262 gamma-glutamyl phosphate reduct	12.6	13.18	12.91	12.78	-0.31	0.4	-0.58	0.13	0.32	0.36	0.13	0.1	0.44	0.38	5.24
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_00262 gamma-glutamyl phosphate reduct	12.6	13.18	12.91	12.78	-0.31	0.4	-0.58	0.13	0.32	0.36	0.13	0.1	0.44	0.38	5.24
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_02183 UTP-glucose-1-phosphate uridylyl	11.43	12.12	11.76	11.66	-0.33	0.46	-0.69	0.1	0.3	0.41	-0.23	0.04	0.44	0.38	3.89
Cthe_02536 phosphoadenosine phosphosulfate	4.17	5.32	4.81	4.09	-0.64	1.23	-1.15	0.72	0.06	1.06	-1.77	1.33	0.44	0.38	0.86
Cthe_01516 ribosome small subunit-dependent	4.25	5.13	4.09	4.58	0.16	0.55	-0.88	-0.49	0.69	0.48	-0.87	-1.19	0.43	0.37	1.02
Cthe_01896 metallophosphoesterase	9.18	9.44	8.75	9.26	0.43	0.18	-0.26	-0.51	0.9	0.17	1.2	-1.23	0.43	0.37	0.95
Cthe_02451 SNF2-related protein	9.71	10.42	9.9	9.99	-0.19	0.43	-0.71	-0.09	0.41	0.38	-0.3	-0.35	0.43	0.37	2.17
Cthe_02888 imidazoleglycerol phosphate synth	7.82	8.57	8.06	8.08	-0.24	0.49	-0.75	-0.02	0.37	0.43	-0.43	-0.21	0.43	0.37	2.12
Cthe_00728 phage integrase	7.12	7.95	7.6	7.14	-0.48	0.81	-0.83	0.46	0.18	0.7	-0.7	0.79	0.43	0.37	1.22
Cthe_02451 SNF2-related protein	9.71	10.42	9.9	9.99	-0.19	0.43	-0.71	-0.09	0.41	0.38	-0.3	-0.35	0.43	0.37	2.17
Cthe_02527 porphobilinogen deaminase	7.64	8.18	7.42	7.92	0.22	0.26	-0.54	-0.5	0.74	0.24	0.27	-1.21	0.43	0.37	1.12
Cthe_01227 Thymidylate synthase	9.02	9.64	8.81	9.33	0.21	0.31	-0.62	-0.52	0.73	0.28	0	-1.25	0.43	0.37	1.12
Cthe_02885 phosphoribosylaminoimidazole-suc	11.36	11.92	11.69	11.34	-0.33	0.58	-0.56	0.35	0.3	0.51	0.2	0.56	0.43	0.37	1.78
Cthe_03093 Adenylosuccinate synthase	11.66	12.21	11.52	11.92	0.14	0.29	-0.55	-0.4	0.67	0.26	0.23	-1	0.43	0.37	1.25
Cthe_00911 protein of unknown function DUF1	8.78	9.37	8.68	9.06	0.1	0.31	-0.59	-0.38	0.64	0.28	0.1	-0.96	0.43	0.37	1.29
Cthe_01936 hypothetical protein	7.95	8.48	7.9	8.18	0.05	0.3	-0.53	-0.28	0.6	0.27	0.3	-0.75	0.43	0.37	1.45
Cthe_02213 hypothetical protein	11.24	11.99	11.63	11.39	-0.39	0.6	-0.75	0.24	0.25	0.53	-0.43	0.33	0.43	0.37	1.93
Cthe_01780 hypothetical protein	7.93	8.37	7.64	8.15	0.29	0.22	-0.44	-0.51	0.79	0.2	0.6	-1.23	0.43	0.37	1.06
Cthe_03162 SAM dependent methyltransferase	8.25	8.85	8.31	8.52	-0.06	0.33	-0.6	-0.21	0.52	0.3	0.07	-0.6	0.43	0.37	1.77
Cthe_01969 hypothetical protein	12.75	13.35	13.08	12.93	-0.33	0.42	-0.6	0.15	0.3	0.37	0.07	0.15	0.43	0.37	5.14
Cthe_02888 imidazoleglycerol phosphate synth	7.82	8.57	8.06	8.08	-0.24	0.49	-0.75	-0.02	0.37	0.43	-0.43	-0.21	0.43	0.37	2.12
Cthe_03093 Adenylosuccinate synthase	11.66	12.21	11.52	11.92	0.14	0.29	-0.55	-0.4	0.67	0.26	0.23	-1	0.43	0.37	1.25
Cthe_02527 porphobilinogen deaminase	7.64	8.18	7.42	7.92	0.22	0.26	-0.54	-0.5	0.74	0.24	0.27	-1.21	0.43	0.37	1.12
Cthe_01227 Thymidylate synthase	9.02	9.64	8.81	9.33	0.21	0.31	-0.62	-0.52	0.73	0.28	0	-1.25	0.43	0.37	1.12
Cthe_02885 phosphoribosylaminoimidazole-suc	11.36	11.92	11.69	11.34	-0.33	0.58	-0.56	0.35	0.3	0.51	0.2	0.56	0.43	0.37	1.78
Cthe_01516 ribosome small subunit-dependent	4.25	5.13	4.09	4.58	0.16	0.55	-0.88	-0.49	0.69	0.48	-0.87	-1.19	0.43	0.37	1.02
Cthe_02527 porphobilinogen deaminase	7.64	8.18	7.42	7.92	0.22	0.26	-0.54	-0.5	0.74	0.24	0.27	-1.21	0.43	0.37	1.12
Cthe_02888 imidazoleglycerol phosphate synth	7.82	8.57	8.06	8.08	-0.24	0.49	-0.75	-0.02	0.37	0.43	-0.43	-0.21	0.43	0.37	2.12
Cthe_03093 Adenylosuccinate synthase	11.66	12.21	11.52	11.92	0.14	0.29	-0.55	-0.4	0.67	0.26	0.23	-1	0.43	0.37	1.25
Cthe_01227 Thymidylate synthase	9.02	9.64	8.81	9.33	0.21	0.31	-0.62	-0.52	0.73	0.28	0	-1.25	0.43	0.37	1.12
Cthe_02885 phosphoribosylaminoimidazole-suc	11.36	11.92	11.69	11.34	-0.33	0.58	-0.56	0.35	0.3	0.51	0.2	0.56	0.43	0.37	1.78
Cthe_02885 phosphoribosylaminoimidazole-suc	11.36	11.92	11.69	11.34	-0.33	0.58	-0.56	0.35	0.3	0.51	0.2	0.56	0.43	0.37	1.78
Cthe_01516 ribosome small subunit-dependent	4.25	5.13	4.09	4.58	0.16	0.55	-0.88	-0.49	0.69	0.48	-0.87	-1.19	0.43	0.37	1.02
Cthe_02527 porphobilinogen deaminase	7.64	8.18	7.42	7.92	0.22	0.26	-0.54	-0.5	0.74	0.24	0.27	-1.21	0.43	0.37	1.12
Cthe_02888 imidazoleglycerol phosphate synth	7.82	8.57	8.06	8.08	-0.24	0.49	-0.75	-0.02	0.37	0.43	-0.43	-0.21	0.43	0.37	2.12
Cthe_01516 ribosome small subunit-dependent	4.25	5.13	4.09	4.58	0.16	0.55	-0.88	-0.49	0.69	0.48	-0.87	-1.19	0.43	0.37	1.02
Cthe_01516 ribosome small subunit-dependent	4.25	5.13	4.09	4.58	0.16	0.55	-0.88	-0.49	0.69	0.48	-0.87	-1.19	0.43	0.37	1.02
Cthe_02888 imidazoleglycerol phosphate synth	7.82	8.57	8.06	8.08	-0.24	0.49	-0.75	-0.02	0.37	0.43	-0.43	-0.21	0.43	0.37	2.12
Cthe_01227 Thymidylate synthase	9.02	9.64	8.81	9.33	0.21	0.									



Cthe_00854 shikimate 5-dehydrogenase	10.09	10.57	10.19	10.22	-0.1	0.35	-0.48	-0.03	0.48	0.31	0.47	-0.23	0.42	0.36	1.95
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_03057 transposase	5.09	5.43	5.09	5	0	0.43	-0.34	0.09	0.56	0.38	0.93	0.02	0.42	0.36	1.3
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_00978 UDP-N-acetylmuramyl-tripeptide s	9.88	10.49	9.96	10.16	-0.08	0.33	-0.61	-0.2	0.5	0.3	0.03	-0.58	0.42	0.36	1.79
Cthe_00678 pyrimidine-nucleoside phosphoryla	9.77	10.42	9.88	10.06	-0.11	0.36	-0.65	-0.18	0.48	0.32	-0.1	-0.54	0.42	0.36	1.88
Cthe_00237 response regulator receiver protein	11.46	12.05	11.81	11.56	-0.35	0.49	-0.59	0.25	0.29	0.43	0.1	0.35	0.42	0.36	2.54
Cthe_01422 RDD domain containing protein	12.33	12.84	12.58	12.4	-0.25	0.44	-0.51	0.18	0.37	0.39	0.37	0.21	0.42	0.36	2.26
Cthe_01829 Chromosome segregation ATPase-	10.07	10.32	9.75	10.09	0.32	0.23	-0.25	-0.34	0.82	0.21	1.23	-0.88	0.42	0.36	1
Cthe_02255 tRNA(Ile)-lysine synthetase	12.52	13.38	12.89	12.7	-0.37	0.68	-0.86	0.19	0.27	0.59	-0.8	0.23	0.42	0.36	1.39
Cthe_03191 ATPase involved in chromosome pa	12.92	13.54	13.29	13.05	-0.37	0.49	-0.62	0.24	0.27	0.43	0	0.33	0.42	0.36	2.75
Cthe_01852 Hsp33 protein	9.38	9.9	9.25	9.64	0.13	0.26	-0.52	-0.39	0.67	0.24	0.33	-0.98	0.42	0.36	1.23
Cthe_01173 type IV pilus assembly PilZ	10.4	10.95	10.65	10.59	-0.25	0.36	-0.55	0.06	0.37	0.32	0.23	-0.04	0.42	0.36	3.74
Cthe_02011 RNA related	5.29	6.07	5.58	5.55	-0.29	0.52	-0.78	0.03	0.33	0.46	-0.53	-0.1	0.42	0.36	1.87
Cthe_02957 hypothetical protein	7.77	8.1	7.71	7.73	0.06	0.37	-0.33	-0.02	0.61	0.33	0.97	-0.21	0.42	0.36	1.25
Cthe_00854 shikimate 5-dehydrogenase	10.09	10.57	10.19	10.22	-0.1	0.35	-0.48	-0.03	0.48	0.31	0.47	-0.23	0.42	0.36	1.95
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_00854 shikimate 5-dehydrogenase	10.09	10.57	10.19	10.22	-0.1	0.35	-0.48	-0.03	0.48	0.31	0.47	-0.23	0.42	0.36	1.95
Cthe_00678 pyrimidine-nucleoside phosphoryla	9.77	10.42	9.88	10.06	-0.11	0.36	-0.65	-0.18	0.48	0.32	-0.1	-0.54	0.42	0.36	1.88
Cthe_02255 tRNA(Ile)-lysine synthetase	12.52	13.38	12.89	12.7	-0.37	0.68	-0.86	0.19	0.27	0.59	-0.8	0.23	0.42	0.36	1.39
Cthe_00678 pyrimidine-nucleoside phosphoryla	9.77	10.42	9.88	10.06	-0.11	0.36	-0.65	-0.18	0.48	0.32	-0.1	-0.54	0.42	0.36	1.88
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_00978 UDP-N-acetylmuramyl-tripeptide s	9.88	10.49	9.96	10.16	-0.08	0.33	-0.61	-0.2	0.5	0.3	0.03	-0.58	0.42	0.36	1.79
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_00678 pyrimidine-nucleoside phosphoryla	9.77	10.42	9.88	10.06	-0.11	0.36	-0.65	-0.18	0.48	0.32	-0.1	-0.54	0.42	0.36	1.88
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_00854 shikimate 5-dehydrogenase	10.09	10.57	10.19	10.22	-0.1	0.35	-0.48	-0.03	0.48	0.31	0.47	-0.23	0.42	0.36	1.95
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_00854 shikimate 5-dehydrogenase	10.09	10.57	10.19	10.22	-0.1	0.35	-0.48	-0.03	0.48	0.31	0.47	-0.23	0.42	0.36	1.95
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_00678 pyrimidine-nucleoside phosphoryla	9.77	10.42	9.88	10.06	-0.11	0.36	-0.65	-0.18	0.48	0.32	-0.1	-0.54	0.42	0.36	1.88
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_00978 UDP-N-acetylmuramyl-tripeptide s	9.88	10.49	9.96	10.16	-0.08	0.33	-0.61	-0.2	0.5	0.3	0.03	-0.58	0.42	0.36	1.79
Cthe_02518 ketol-acid reductoisomerase	12.64	13.2	12.89	12.86	-0.25	0.34	-0.56	0.03	0.37	0.31	0.2	-0.1	0.42	0.36	3.85
Cthe_00978 UDP-N-acetylmuramyl-tripeptide s	9.88	10.49	9.96	10.16	-0.08	0.33	-0.61	-0.2	0.5	0.3	0.03	-0.58	0.42	0.36	1.79
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_02705 Transketolase, central region	13.27	14.13	13.63	13.47	-0.36	0.66	-0.86	0.16	0.28	0.58	-0.8	0.17	0.42	0.36	1.41
Cthe_00335 hydrogenase large subunit-like pro	9.43	10	9.45	9.7	-0.02	0.3	-0.57	-0.25	0.55	0.27	0.17	-0.69	0.41	0.35	1.54
Cthe_02334 polysaccharide biosynthesis protei	10.27	10.83	10.29	10.54	-0.02	0.29	-0.56	-0.25	0.55	0.26	0.2	-0.69	0.41	0.35	1.51
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_01341 Radical SAM	9.59	10.18	9.29	9.93	0.3	0.25	-0.59	-0.64	0.8	0.23	0.1	-1.5	0.41	0.35	0.99
Cthe_02334 polysaccharide biosynthesis protei	10.27	10.83	10.29	10.54	-0.02	0.29	-0.56	-0.25	0.55	0.26	0.2	-0.69	0.41	0.35	1.51
Cthe_01205 putative serine protein kinase, PrkA	15.5	16.22	15.91	15.65	-0.41	0.57	-0.72	0.26	0.24	0.5	-0.33	0.38	0.41	0.35	1.97
Cthe_00789 RNA-binding S4	11.69	12.15	11.67	11.87	0.02	0.28	-0.46	-0.2	0.58	0.25	0.53	-0.58	0.41	0.35	1.44
Cthe_02075 protein of unknown function DUF2	11.66	12.35	12.07	11.8	-0.41	0.55	-0.69	0.27	0.24	0.48	-0.23	0.4	0.41	0.35	2.08
Cthe_02380 TPR repeat domain containing prot	10.05	10.33	9.67	10.19	0.38	0.14	-0.28	-0.52	0.87	0.14	1.13	-1.25	0.41	0.35	0.93
Cthe_00775 tRNA delta(2)-isopentenylpyrophos	10.69	11.09	10.61	10.82	0.08	0.27	-0.4	-0.21	0.63	0.25	0.73	-0.6	0.41	0.35	1.28
Cthe_01768 NifU-related domain containing pro	9.86	10.4	10.15	9.97	-0.29	0.43	-0.54	-0.18	0.33	0.38	0.27	0.21	0.41	0.35	2.63
Cthe_02804 ABC transporter related protein	7.14	8.01	7.3	7.43	-0.16	0.58	-0.87	-0.13	0.44	0.51	-0.83	-0.44	0.41	0.35	1.28
Cthe_00506 pyruvate formate-lyase activating e	13.04	13.87	13.53	13.1	-0.49	0.77	-0.83	0.43	0.17	0.67	-0.7	0.73	0.41	0.35	1.22
Cthe_02157 hypothetical protein	0	2	0	1	0	1	-2	-1	0.56	0.86	-4.6	-2.25	0.41	0.35	0.36
Cthe_02331 hypothetical protein	13	13.57	13.36	12.97	-0.36	0.6	-0.57	0.39	0.28	0.53	0.17	0.65	0.41	0.35	1.59
Cthe_02804 ABC transporter related protein	7.14	8.01	7.3	7.43	-0.16	0.58	-0.87	-0.13	0.44	0.51	-0.83	-0.44	0.41	0.35	1.28
Cthe_01341 Radical SAM	9.59	10.18	9.29	9.93	0.3	0.25	-0.59	-0.64	0.8	0.23	0.1	-1.5	0.41	0.35	0.99
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_01341 Radical SAM	9.59	10.18	9.29	9.93	0.3	0.25	-0.59	-0.64	0.8	0.23	0.1	-1.5	0.41	0.35	0.99
Cthe_00506 pyruvate formate-lyase activating e	13.04	13.87	13.53	13.1	-0.49	0.77	-0.83	0.43	0.17	0.67	-0.7	0.73	0.41	0.35	1.22
Cthe_00775 tRNA delta(2)-isopentenylpyrophos	10.69	11.09	10.61	10.82	0.08	0.27	-0.4	-0.21	0.63	0.25	0.73	-0.6	0.41	0.35	1.28
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41	0.35	1.46
Cthe_00775 tRNA delta(2)-isopentenylpyrophos	10.69	11.09	10.61	10.82	0.08	0.27	-0.4	-0.21	0.63	0.25	0.73	-0.6	0.41	0.35	1.28
Cthe_00580 aminotransferase, class I and II	10.11	10.91	10.55	10.25	-0.44	0.66	-0.8	0.3	0.21	0.58	-0.6	0.46	0.41		



Cthe_01181 transglutaminase-like protein	10.47	11.13	10.63	10.78	-0.16	0.35	-0.66	-0.15	0.44	0.31	-0.13	-0.48	0.4	0.34	1.93
Cthe_01845 Homoserine O-succinyltransferase	11.91	12.76	12.44	11.94	-0.53	0.82	-0.85	0.5	0.14	0.71	-0.77	0.88	0.4	0.34	1.11
Cthe_02209 3-isopropylmalate dehydrogenase	12.44	13.34	12.82	12.63	-0.38	0.71	-0.9	0.19	0.26	0.62	-0.93	0.23	0.4	0.34	1.25
Cthe_02260 Prephenate dehydratase	9.51	10.25	9.59	9.83	-0.08	0.42	-0.74	-0.24	0.5	0.37	-0.4	-0.67	0.4	0.34	1.42
Cthe_00634 serine/threonine protein kinase	11.22	11.89	11.39	11.53	-0.17	0.36	-0.67	-0.14	0.43	0.32	-0.17	-0.46	0.4	0.34	1.95
Cthe_02249 helicase, RecD/TraA family	9.08	9.82	9.27	9.39	-0.19	0.43	-0.74	-0.12	0.41	0.38	-0.4	-0.42	0.4	0.34	1.72
Cthe_02868 transposase IS116/IS110/IS902	3.7	4.39	4.17	3.7	-0.47	0.69	-0.69	0.47	0.19	0.6	-0.23	0.81	0.39	0.34	1.33
Cthe_00875 anthranilate synthase component I	10.02	10.5	10.12	10.2	-0.1	0.3	-0.48	-0.08	0.48	0.27	0.47	-0.33	0.39	0.34	1.71
Cthe_01226 dihydrofolate reductase region	8.74	9.16	8.81	8.82	-0.07	0.34	-0.42	-0.01	0.51	0.31	0.67	-0.19	0.4	0.34	1.53
Cthe_02622 hypothetical protein	11.49	12.05	11.65	11.75	-0.16	0.3	-0.56	-0.1	0.44	0.27	0.2	-0.38	0.4	0.34	2.15
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_02622 hypothetical protein	11.49	12.05	11.65	11.75	-0.16	0.3	-0.56	-0.1	0.44	0.27	0.2	-0.38	0.4	0.34	2.15
Cthe_02254 hypoxanthine phosphoribosyltrans	12.33	13	12.73	12.55	-0.4	0.45	-0.67	0.18	0.25	0.4	-0.17	0.21	0.4	0.34	3.12
Cthe_00634 serine/threonine protein kinase	11.22	11.89	11.39	11.53	-0.17	0.36	-0.67	-0.14	0.43	0.32	-0.17	-0.46	0.4	0.34	1.95
Cthe_01824 two component transcriptional reg	5.58	5.39	5.88	5.61	-0.3	-0.22	0.19	0.27	0.33	-0.17	2.7	0.4	0.39	0.34	0.24
Cthe_01861 transcriptional regulator, CdaR	11.47	11.94	11.63	11.61	-0.16	0.33	-0.47	0.02	0.44	0.3	0.5	-0.13	0.39	0.34	1.84
Cthe_01507 protein of unknown function UPFO	7.11	7.79	6.46	7.58	0.65	0.21	-0.68	-1.12	1.08	0.19	-0.2	-2.5	0.39	0.34	0.78
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_00505 formate acetyltransferase	15.53	16.25	16.04	15.46	-0.51	0.79	-0.72	0.58	0.16	0.69	-0.33	1.04	0.4	0.34	1.16
Cthe_02103 4Fe-4S ferredoxin, iron-sulfur bindi	14.92	15.66	15.41	14.91	-0.49	0.75	-0.74	0.5	0.17	0.65	-0.4	0.88	0.4	0.34	1.24
Cthe_02209 3-isopropylmalate dehydrogenase	12.44	13.34	12.82	12.63	-0.38	0.71	-0.9	0.19	0.26	0.62	-0.93	0.23	0.4	0.34	1.25
Cthe_02622 hypothetical protein	11.49	12.05	11.65	11.75	-0.16	0.3	-0.56	-0.1	0.44	0.27	0.2	-0.38	0.4	0.34	2.15
Cthe_02740 ATP-dependent Clp protease, prote	14.98	15.59	15.4	14.96	-0.42	0.63	-0.61	0.44	0.23	0.55	0.03	0.75	0.39	0.34	1.42
Cthe_00238 hypothetical protein	7.77	8.82	7.8	8.08	-0.03	0.74	-1.05	-0.28	0.54	0.64	-1.43	-0.75	0.39	0.34	0.93
Cthe_02851 hypothetical protein	9.61	10.04	9.89	9.24	-0.28	0.8	-0.43	0.65	0.34	0.69	0.63	1.19	0.39	0.34	1.02
Cthe_02751 hypothetical protein	6.48	7.1	6.88	6.55	-0.4	0.55	-0.62	0.33	0.25	0.48	0	0.52	0.4	0.34	1.86
Cthe_00633 hypothetical protein	11.7	12.34	12.12	11.76	-0.42	0.58	-0.64	0.36	0.23	0.51	-0.07	0.58	0.4	0.34	1.71
Cthe_01827 copper amine oxidase-like protein	11.33	11.72	11.06	11.56	0.27	0.16	-0.39	-0.5	0.78	0.15	0.77	-1.21	0.39	0.34	0.99
Cthe_02695 hypothetical protein	9.18	9.79	9.12	9.5	0.06	0.29	-0.61	-0.38	0.61	0.26	0.03	-0.96	0.39	0.34	1.23
Cthe_01419 hypothetical protein	7.35	8.08	7.38	7.69	-0.03	0.39	-0.73	-0.31	0.54	0.35	-0.37	-0.81	0.39	0.34	1.29
Cthe_00086 hypothetical protein	4.81	5.67	5.29	4.91	-0.48	0.76	-0.86	0.38	0.18	0.66	-0.8	0.63	0.4	0.34	1.2
Cthe_01908 copper amine oxidase-like protein	9.51	10.07	9.55	9.78	-0.04	0.29	-0.56	-0.23	0.53	0.26	0.2	-0.65	0.4	0.34	1.55
Cthe_02045 intein	6.3	7.26	6.15	6.66	0.15	0.6	-0.96	-0.51	0.68	0.53	-1.13	-1.23	0.39	0.34	0.92
Cthe_03067 membrane spanning protein	11.14	11.84	11.47	11.42	-0.33	0.42	-0.7	0.05	0.3	0.37	-0.27	-0.06	0.4	0.34	3.08
Cthe_02260 Prephenate dehydratase	9.51	10.25	9.59	9.83	-0.08	0.42	-0.74	-0.24	0.5	0.37	-0.4	-0.67	0.4	0.34	1.42
Cthe_01226 dihydrofolate reductase region	8.74	9.16	8.81	8.82	-0.07	0.34	-0.42	-0.01	0.51	0.31	0.67	-0.19	0.4	0.34	1.53
Cthe_02209 3-isopropylmalate dehydrogenase	12.44	13.34	12.82	12.63	-0.38	0.71	-0.9	0.19	0.26	0.62	-0.93	0.23	0.4	0.34	1.25
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_00875 anthranilate synthase component I	10.02	10.5	10.12	10.2	-0.1	0.3	-0.48	-0.08	0.48	0.27	0.47	-0.33	0.39	0.34	1.71
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_01845 Homoserine O-succinyltransferase	11.91	12.76	12.44	11.94	-0.53	0.82	-0.85	0.5	0.14	0.71	-0.77	0.88	0.4	0.34	1.11
Cthe_02209 3-isopropylmalate dehydrogenase	12.44	13.34	12.82	12.63	-0.38	0.71	-0.9	0.19	0.26	0.62	-0.93	0.23	0.4	0.34	1.25
Cthe_01845 Homoserine O-succinyltransferase	11.91	12.76	12.44	11.94	-0.53	0.82	-0.85	0.5	0.14	0.71	-0.77	0.88	0.4	0.34	1.11
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_00505 formate acetyltransferase	15.53	16.25	16.04	15.46	-0.51	0.79	-0.72	0.58	0.16	0.69	-0.33	1.04	0.4	0.34	1.16
Cthe_01226 dihydrofolate reductase region	8.74	9.16	8.81	8.82	-0.07	0.34	-0.42	-0.01	0.51	0.31	0.67	-0.19	0.4	0.34	1.53
Cthe_00357 alpha-glucan phosphorylases	16.39	17.28	16.76	16.59	-0.37	0.69	-0.89	0.17	0.27	0.6	-0.9	0.19	0.4	0.34	1.28
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_02740 ATP-dependent Clp protease, prote	14.98	15.59	15.4	14.96	-0.42	0.63	-0.61	0.44	0.23	0.55	0.03	0.75	0.39	0.34	1.42
Cthe_00875 anthranilate synthase component I	10.02	10.5	10.12	10.2	-0.1	0.3	-0.48	-0.08	0.48	0.27	0.47	-0.33	0.39	0.34	1.71
Cthe_02249 helicase, RecD/TraA family	9.08	9.82	9.27	9.39	-0.19	0.43	-0.74	-0.12	0.41	0.38	-0.4	-0.42	0.4	0.34	1.72
Cthe_02260 Prephenate dehydratase	9.51	10.25	9.59	9.83	-0.08	0.42	-0.74	-0.24	0.5	0.37	-0.4	-0.67	0.4	0.34	1.42
Cthe_02254 hypoxanthine phosphoribosyltrans	12.33	13	12.73	12.55	-0.4	0.45	-0.67	0.18	0.25	0.4	-0.17	0.21	0.4	0.34	3.12
Cthe_00875 anthranilate synthase component I	10.02	10.5	10.12	10.2	-0.1	0.3	-0.48	-0.08	0.48	0.27	0.47	-0.33	0.39	0.34	1.71
Cthe_00505 formate acetyltransferase	15.53	16.25	16.04	15.46	-0.51	0.79	-0.72	0.58	0.16	0.69	-0.33	1.04	0.4	0.34	1.16
Cthe_00875 anthranilate synthase component I	10.02	10.5	10.12	10.2	-0.1	0.3	-0.48	-0.08	0.48	0.27	0.47	-0.33	0.39	0.34	1.71
Cthe_00505 formate acetyltransferase	15.53	16.25	16.04	15.46	-0.51	0.79	-0.72	0.58	0.16	0.69	-0.33	1.04	0.4	0.34	1.16
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_02254 hypoxanthine phosphoribosyltrans	12.33	13	12.73	12.55	-0.4	0.45	-0.67	0.18	0.25	0.4	-0.17	0.21	0.4	0.34	3.12
Cthe_01845 Homoserine O-succinyltransferase	11.91	12.76	12.44	11.94	-0.53	0.82	-0.85	0.5	0.14	0.71	-0.77	0.88	0.4	0.34	1.11
Cthe_02254 hypoxanthine phosphoribosyltrans	12.33	13	12.73	12.55	-0.4	0.45	-0.67	0.18	0.25	0.4	-0.17	0.21	0.4	0.34	3.12
Cthe_02254 hypoxanthine phosphoribosyltrans	12.33	13	12.73	12.55	-0.4	0.45	-0.67	0.18	0.25	0.4	-0.17	0.21	0.4	0.34	3.12
Cthe_00505 formate acetyltransferase	15.53	16.25	16.04	15.46	-0.51	0.79	-0.72	0.58	0.16	0.69	-0.33	1.04	0.4	0.34	1.16
Cthe_00357 alpha-glucan phosphorylases	16.39	17.28	16.76	16.59	-0.37	0.69	-0.89	0.17	0.27	0.6	-0.9	0.19	0.4	0.34	1.28
Cthe_01226 dihydrofolate reductase region	8.74	9.16	8.81	8.82	-0.07	0.34	-0.42	-0.01	0.51	0.31	0.67	-0.19	0.4	0.34	1.53
Cthe_02254 hypoxanthine phosphoribosyltrans	12.33	13	12.73	12.55	-0.4	0.45	-0.67	0.18	0.25	0.4	-0.17	0.21	0.4	0.34	3.12
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_02254 hypoxanthine phosphoribosyltrans	12.33	13	12.73	12.55	-0.4	0.45	-0.67	0.18	0.25	0.4	-0.17	0.21	0.4	0.34	3.12
Cthe_02209 3-isopropylmalate dehydrogenase	12.44	13.34	12.82	12.63	-0.38	0.71	-0.9	0.19	0.26	0.62	-0.93	0.23	0.4	0.34	1.25
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_01961 Nucleotidyl transferase	13.86	14.73	14.49	13.77	-0.63	0.96	-0.87	0.72	0.06	0.83	-0.83	1.33	0.39	0.34	0.95
Cthe_00505 formate acetyltransferase	15.53	16.25	16.04	15.46	-0.51	0.79	-0.72	0.58	0.16	0.69	-0.33	1.04	0.4	0.34	1.16
Cthe_00357 alpha-glucan phosphorylases	16.39	17.28	16.76	16.59	-0.37	0.69	-0.89	0.17	0.27	0.6	-0.9	0.19	0.4	0.34	1.28
Cthe_01226 dihydrofolate reductase region	8.74	9.16	8.81	8.82	-0.07	0.34	-0.42	-0.01	0.51	0.31	0.67	-0.19	0.4	0.34	1.53
Cthe_00357 alpha-glucan phosphorylases	16.39	17.28	16.76	16.59	-0.37	0.69	-0.89	0.17	0.27	0.6	-0.9	0.19	0.4	0.34	1.28
Cthe_00505 formate acetyltransferase	15.53	16.25	16.04	15.46	-0.51	0.79	-0.72	0.58	0.16	0.69	-0.33	1.04	0.4	0.34	1.16
Cthe_01226 dihydrofolate reductase region	8.74														







Cthe_02863 intein	5.93	6.73	6.43	6.07	-0.5	0.66	-0.8	0.36	0.17	0.58	-0.6	0.58	0.37	0.32	1.29
Cthe_03002 hypothetical protein	11.03	11.63	11.06	11.36	-0.03	0.27	-0.6	-0.3	0.54	0.25	0.07	-0.79	0.37	0.32	1.34
Cthe_02286 phage integrase	7.12	7.69	7.54	6.99	-0.42	0.7	-0.57	0.55	0.23	0.61	0.17	0.98	0.37	0.32	1.17
Cthe_01417 hypothetical protein	6.52	6.93	6.69	6.49	-0.17	0.44	-0.41	0.2	0.43	0.39	0.7	0.25	0.37	0.32	1.39
Cthe_02675 hypothetical protein	11.3	11.97	11.6	11.63	-0.3	0.34	-0.67	-0.03	0.33	0.31	-0.17	-0.23	0.37	0.32	2.83
Cthe_00735 cellulosome anchoring protein, coh	9.61	10.09	9.53	9.88	0.08	0.21	-0.48	-0.35	0.63	0.19	0.47	-0.9	0.37	0.32	1.16
Cthe_01000 phosphatidate cytidylyltransferase	10.69	11.23	10.67	11	0.02	0.23	-0.54	-0.33	0.58	0.21	0.27	-0.85	0.37	0.32	1.24
Cthe_02717 ribosomal protein L33	7.32	8.01	7.2	7.7	0.12	0.31	-0.69	-0.5	0.66	0.28	-0.23	-1.21	0.37	0.32	1.04
Cthe_02229 N-acetylneuraminate synthase	11.38	11.94	11.78	11.27	-0.4	0.67	-0.56	0.51	0.25	0.58	0.2	0.9	0.37	0.32	1.22
Cthe_01000 phosphatidate cytidylyltransferase	10.69	11.23	10.67	11	0.02	0.23	-0.54	-0.33	0.58	0.21	0.27	-0.85	0.37	0.32	1.24
Cthe_01000 phosphatidate cytidylyltransferase	10.69	11.23	10.67	11	0.02	0.23	-0.54	-0.33	0.58	0.21	0.27	-0.85	0.37	0.32	1.24
Cthe_01000 phosphatidate cytidylyltransferase	10.69	11.23	10.67	11	0.02	0.23	-0.54	-0.33	0.58	0.21	0.27	-0.85	0.37	0.32	1.24
Cthe_02229 N-acetylneuraminate synthase	11.38	11.94	11.78	11.27	-0.4	0.67	-0.56	0.51	0.25	0.58	0.2	0.9	0.37	0.32	1.22
Cthe_01000 phosphatidate cytidylyltransferase	10.69	11.23	10.67	11	0.02	0.23	-0.54	-0.33	0.58	0.21	0.27	-0.85	0.37	0.32	1.24
Cthe_02420 HD superfamily phosphohydrolases	11.76	12.32	11.98	12.04	-0.22	0.28	-0.56	-0.06	0.39	0.25	0.2	-0.29	0.36	0.31	2.35
Cthe_01177 putative nicotinate phosphoribosyl	9.43	9.99	9.86	9.25	-0.43	0.74	-0.56	0.61	0.22	0.64	0.2	1.1	0.36	0.31	1.08
Cthe_00089 rod shape-determining protein Mre	8.78	9.58	8.85	9.15	-0.07	0.43	-0.8	-0.3	0.51	0.38	-0.6	-0.79	0.36	0.31	1.14
Cthe_02644 DegT/DnrI/EryC1/StrS aminotransf	2.58	4.25	4.25	2.32	-1.67	1.93	-1.67	1.93	-0.76	1.65	-3.5	3.85	0.36	0.31	0.62
Cthe_00643 hypothetical protein	6.58	7.5	7.11	6.7	-0.53	0.8	-0.92	0.41	0.14	0.69	-1	0.69	0.36	0.31	1.03
Cthe_03184 cation transporter	9.01	9.74	9.27	9.35	-0.26	0.39	-0.73	-0.08	0.36	0.35	-0.37	-0.33	0.36	0.31	1.81
Cthe_01322 chaperone protein DnaK	11.78	12.29	12.13	11.72	-0.35	0.57	-0.51	0.41	0.29	0.5	0.37	0.69	0.36	0.31	1.32
Cthe_00529 RNA related	4.17	4.39	3.7	4.39	0.47	0	-0.22	-0.69	0.94	0.02	1.33	-1.6	0.36	0.31	0.81
Cthe_01365 hypothetical protein	10.13	10.52	10.08	10.29	0.05	0.23	-0.39	-0.21	0.6	0.21	0.77	-0.6	0.36	0.31	1.16
Cthe_01954 hypothetical protein	9.1	9.44	9.15	9.06	-0.05	0.38	-0.34	0.09	0.52	0.34	0.93	0.02	0.36	0.31	1.19
Cthe_01832 hypothetical protein	11.71	12.14	11.34	12.06	0.37	0.08	-0.43	-0.72	0.86	0.08	0.63	-1.67	0.36	0.31	0.86
Cthe_02514 hypothetical protein	6.51	7	6.79	6.57	-0.28	0.43	-0.49	0.22	0.34	0.38	0.43	0.29	0.36	0.31	1.76
Cthe_02016 RNA related	10.21	10.73	10.41	10.44	-0.2	0.29	-0.52	-0.03	0.4	0.26	0.33	-0.23	0.36	0.31	2.12
Cthe_01926 intein	7.2	7.59	7.29	7.25	-0.09	0.34	-0.39	0.04	0.49	0.31	0.77	-0.08	0.36	0.31	1.34
Cthe_02956 hypothetical protein	5.86	6.49	6.15	6.19	-0.29	0.3	-0.63	-0.04	0.33	0.27	-0.03	-0.25	0.36	0.31	3.02
Cthe_01177 putative nicotinate phosphoribosyl	9.43	9.99	9.86	9.25	-0.43	0.74	-0.56	0.61	0.22	0.64	0.2	1.1	0.36	0.31	1.08
Cthe_01177 putative nicotinate phosphoribosyl	9.43	9.99	9.86	9.25	-0.43	0.74	-0.56	0.61	0.22	0.64	0.2	1.1	0.36	0.31	1.08
Cthe_01177 putative nicotinate phosphoribosyl	9.43	9.99	9.86	9.25	-0.43	0.74	-0.56	0.61	0.22	0.64	0.2	1.1	0.36	0.31	1.08
Cthe_00685 peptidase M50	8.96	9.29	8.88	9.06	0.08	0.23	-0.33	-0.18	0.63	0.21	0.97	-0.54	0.35	0.3	1.07
Cthe_02288 PEBP	6.11	6.51	6.21	6.19	-0.1	0.32	-0.4	0.02	0.48	0.29	0.73	-0.13	0.35	0.3	1.35
Cthe_01381 threonine synthase	13.04	13.54	13.25	13.26	-0.21	0.28	-0.5	-0.01	0.4	0.25	0.4	-0.19	0.35	0.3	1.9
Cthe_02040 ATP-dependent exonuclease synth	8.98	9.54	9.37	9.05	-0.39	0.49	-0.56	0.32	0.25	0.43	0.2	0.5	0.35	0.3	1.65
Cthe_02350 cell wall hydrolase, SleB	6.32	7	6.75	6.6	-0.43	0.4	-0.68	0.15	0.22	0.36	-0.2	0.15	0.35	0.3	3.01
Cthe_00897 putative deoxyguanosinetriphosph	7.91	8.23	7.99	7.79	-0.08	0.44	-0.32	0.2	0.5	0.39	1	0.25	0.35	0.3	1.1
Cthe_00151 protein of unknown function DUF9	9.95	10.62	10.42	10.11	-0.47	0.51	-0.67	0.31	0.19	0.45	-0.17	0.48	0.35	0.3	1.71
Cthe_02401 protein of unknown function DUF1	14.99	15.55	15.39	15.01	-0.4	0.54	-0.56	0.38	0.25	0.47	0.2	0.63	0.35	0.3	1.44
Cthe_02172 ribosomal protein L31	13.24	13.74	13.6	13.14	-0.36	0.6	-0.5	0.46	0.28	0.53	0.4	0.79	0.35	0.3	1.21
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_01508 hypothetical protein	10.25	10.84	10.64	10.49	-0.39	0.35	-0.59	0.15	0.25	0.31	0.1	0.15	0.35	0.3	3.94
Cthe_02941 2-C-methyl-D-erythritol 4-phospha	7	7.59	7	7.35	0	0.24	-0.59	-0.35	0.56	0.22	0.1	-0.9	0.35	0.3	1.19
Cthe_02892 chaperonin GroEL	13.26	13.88	13.76	13.14	-0.5	0.74	-0.62	0.62	0.17	0.64	0	1.13	0.35	0.3	1.05
Cthe_02003 RNA related	6.73	6.95	6.46	6.79	0.27	0.16	-0.22	-0.33	0.78	0.15	1.33	-0.85	0.35	0.3	0.9
Cthe_02409 hypothetical protein	10.39	10.93	10.26	10.75	0.13	0.18	-0.54	-0.49	0.67	0.17	0.27	-1.19	0.35	0.3	1.01
Cthe_00589 RNA related	6.54	6.75	7.35	6.51	-0.81	0.24	-0.21	0.84	-0.08	0.22	1.37	1.58	0.35	0.3	0.2
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_02172 ribosomal protein L31	13.24	13.74	13.6	13.14	-0.36	0.6	-0.5	0.46	0.28	0.53	0.4	0.79	0.35	0.3	1.21
Cthe_02941 2-C-methyl-D-erythritol 4-phospha	7	7.59	7	7.35	0	0.24	-0.59	-0.35	0.56	0.22	0.1	-0.9	0.35	0.3	1.19
Cthe_01381 threonine synthase	13.04	13.54	13.25	13.26	-0.21	0.28	-0.5	-0.01	0.4	0.25	0.4	-0.19	0.35	0.3	1.9
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_02941 2-C-methyl-D-erythritol 4-phospha	7	7.59	7	7.35	0	0.24	-0.59	-0.35	0.56	0.22	0.1	-0.9	0.35	0.3	1.19
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_01508 hypothetical protein	10.25	10.84	10.64	10.49	-0.39	0.35	-0.59	0.15	0.25	0.31	0.1	0.15	0.35	0.3	3.94
Cthe_00897 putative deoxyguanosinetriphosph	7.91	8.23	7.99	7.79	-0.08	0.44	-0.32	0.2	0.5	0.39	1	0.25	0.35	0.3	1.1
Cthe_01381 threonine synthase	13.04	13.54	13.25	13.26	-0.21	0.28	-0.5	-0.01	0.4	0.25	0.4	-0.19	0.35	0.3	1.9
Cthe_02040 ATP-dependent exonuclease synth	8.98	9.54	9.37	9.05	-0.39	0.49	-0.56	0.32	0.25	0.43	0.2	0.5	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_02941 2-C-methyl-D-erythritol 4-phospha	7	7.59	7	7.35	0	0.24	-0.59	-0.35	0.56	0.22	0.1	-0.9	0.35	0.3	1.19
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_01508 hypothetical protein	10.25	10.84	10.64	10.49	-0.39	0.35	-0.59	0.15	0.25	0.31	0.1	0.15	0.35	0.3	3.94
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_01381 threonine synthase	13.04	13.54	13.25	13.26	-0.21	0.28	-0.5	-0.01	0.4	0.25	0.4	-0.19	0.35	0.3	1.9
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_03027 Citrate (Si)-synthase	13.85	14.42	14.25	13.92	-0.4	0.5	-0.57	0.33	0.25	0.44	0.17	0.52	0.35	0.3	1.65
Cthe_00033 small GTP-binding protein	7.58	8.11	7.68	7.88	-0.1	0.23	-0.53	-0.2	0.48	0.21	0.3	-0.58	0.34	0.29	1.43
Cthe_01369 histidine triad (HIT) protein	11.23	11.87	11.75	11.15	-0.52	0.72	-0.64	0.6	0.15	0.63	-0.07	1.08	0.34	0.29	1.07
Cthe_01369 histidine triad (HIT) protein	11.23	11.87	11.75	11.15	-0.52	0.72	-0.64	0.6	0.15	0.63	-0.07	1.08	0.34	0.29	1.07
Cthe_01787 glycoside hydrolase 15-related	10.68	11.34	10.81	11.05	-0.13	0.29	-0.66	-0.24	0.46	0.26	-0.13	-0.67	0.34	0.29	1.38
Cthe_00581 Fibronectin-binding A-like protein	9.83	1													



Cthe_03037 nitroreductase	8.43	8.85	8.61	8.49	-0.18	0.36	-0.42	0.12	0.42	0.32	0.67	0.08	0.34	0.29	1.4
Cthe_01186 Alpha/beta hydrolase fold-3	9.66	10.76	10.28	9.78	-0.62	0.98	-1.1	0.5	0.07	0.85	-1.6	0.88	0.34	0.29	0.83
Cthe_03169 short-chain dehydrogenase/reduct	11.57	12.14	11.87	11.88	-0.3	0.26	-0.57	-0.01	0.33	0.24	0.17	-0.19	0.34	0.29	2.86
Cthe_02998 ABC transporter related protein	9.91	10.64	10.08	10.28	-0.17	0.36	-0.73	-0.2	0.43	0.32	-0.37	-0.58	0.34	0.29	1.39
Cthe_01015 hypothetical protein	8.24	8.94	8.68	8.52	-0.44	0.42	-0.7	0.16	0.21	0.37	-0.27	0.17	0.34	0.29	2.38
Cthe_00019 regulatory protein, P-II family	10.37	11.2	10.91	10.51	-0.54	0.69	-0.83	0.4	0.13	0.6	-0.7	0.67	0.34	0.29	1.13
Cthe_00303 hypothetical protein	9.13	9.76	9.35	9.48	-0.22	0.28	-0.63	-0.13	0.39	0.25	-0.03	-0.44	0.34	0.29	1.88
Cthe_03169 short-chain dehydrogenase/reduct	11.57	12.14	11.87	11.88	-0.3	0.26	-0.57	-0.01	0.33	0.24	0.17	-0.19	0.34	0.29	2.86
Cthe_03169 short-chain dehydrogenase/reduct	11.57	12.14	11.87	11.88	-0.3	0.26	-0.57	-0.01	0.33	0.24	0.17	-0.19	0.34	0.29	2.86
Cthe_00180 crossover junction endodeoxyribon	7.34	7.95	7.22	7.74	0.12	0.21	-0.61	-0.52	0.66	0.19	0.03	-1.25	0.34	0.29	0.98
Cthe_02998 ABC transporter related protein	9.91	10.64	10.08	10.28	-0.17	0.36	-0.73	-0.2	0.43	0.32	-0.37	-0.58	0.34	0.29	1.39
Cthe_00761 Ribonuclease H	9.05	9.66	8.8	9.47	0.25	0.19	-0.61	-0.67	0.76	0.18	0.03	-1.56	0.34	0.29	0.89
Cthe_02281 response regulator receiver modul	7.29	7.92	7.77	7.3	-0.48	0.62	-0.63	0.47	0.18	0.54	-0.03	0.81	0.34	0.29	1.25
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_02998 ABC transporter related protein	9.91	10.64	10.08	10.28	-0.17	0.36	-0.73	-0.2	0.43	0.32	-0.37	-0.58	0.34	0.29	1.39
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_03169 short-chain dehydrogenase/reduct	11.57	12.14	11.87	11.88	-0.3	0.26	-0.57	-0.01	0.33	0.24	0.17	-0.19	0.34	0.29	2.86
Cthe_02998 ABC transporter related protein	9.91	10.64	10.08	10.28	-0.17	0.36	-0.73	-0.2	0.43	0.32	-0.37	-0.58	0.34	0.29	1.39
Cthe_02998 ABC transporter related protein	9.91	10.64	10.08	10.28	-0.17	0.36	-0.73	-0.2	0.43	0.32	-0.37	-0.58	0.34	0.29	1.39
Cthe_03169 short-chain dehydrogenase/reduct	11.57	12.14	11.87	11.88	-0.3	0.26	-0.57	-0.01	0.33	0.24	0.17	-0.19	0.34	0.29	2.86
Cthe_02998 ABC transporter related protein	9.91	10.64	10.08	10.28	-0.17	0.36	-0.73	-0.2	0.43	0.32	-0.37	-0.58	0.34	0.29	1.39
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_02998 ABC transporter related protein	9.91	10.64	10.08	10.28	-0.17	0.36	-0.73	-0.2	0.43	0.32	-0.37	-0.58	0.34	0.29	1.39
Cthe_03169 short-chain dehydrogenase/reduct	11.57	12.14	11.87	11.88	-0.3	0.26	-0.57	-0.01	0.33	0.24	0.17	-0.19	0.34	0.29	2.86
Cthe_02600 glycosyl transferase, family 4	12.18	12.85	12.66	12.3	-0.48	0.55	-0.67	0.36	0.18	0.48	-0.17	0.58	0.34	0.29	1.51
Cthe_00764 signal peptidase I	9.61	10.1	9.3	10.02	0.31	0.08	-0.49	-0.72	0.81	0.08	0.43	-1.67	0.33	0.28	0.84
Cthe_00893 protein of unknown function DUF6	7.81	8.3	7.64	8.2	0.17	0.1	-0.49	-0.56	0.7	0.1	0.43	-1.33	0.32	0.28	0.9
Cthe_01083 Putative homoserine kinase type II	2.81	4.17	4.25	2.58	-1.44	1.59	-1.36	1.67	-0.58	1.36	-2.47	3.31	0.32	0.28	0.64
Cthe_01185 hypothetical protein	10.59	11.48	10.97	10.9	-0.38	0.58	-0.89	0.07	0.26	0.51	-0.9	-0.02	0.32	0.28	1.14
Cthe_02171 type III restriction enzyme, res subu	10.56	11.38	10.86	10.92	-0.3	0.46	-0.82	-0.06	0.33	0.41	-0.67	-0.29	0.32	0.28	1.29
Cthe_01511 DNA methylase N-4/N-6	7.99	8.48	8.06	8.28	-0.07	0.2	-0.49	-0.22	0.51	0.19	0.43	-0.63	0.33	0.28	1.27
Cthe_02171 type III restriction enzyme, res subu	10.56	11.38	10.86	10.92	-0.3	0.46	-0.82	-0.06	0.33	0.41	-0.67	-0.29	0.32	0.28	1.29
Cthe_03056 transposase, IS204/IS1001/IS1096/	8.89	9.03	9.01	7.97	-0.12	1.06	-0.14	1.04	0.47	0.92	1.6	2	0.32	0.28	0.72
Cthe_02708 hypothetical protein	11.01	11.84	11.47	11.28	-0.46	0.56	-0.83	0.19	0.2	0.49	-0.7	0.23	0.32	0.28	1.28
Cthe_01360 polysaccharide biosynthesis protei	1.58	1.58	1	1.58	0.58	0	0	-0.58	1.02	0.02	2.07	-1.37	0.33	0.28	0.73
Cthe_00544 protein serine/threonine phosphat	8.15	8.96	8.26	8.55	-0.11	0.41	-0.81	-0.29	0.48	0.36	-0.63	-0.77	0.32	0.28	1.08
Cthe_00905 metal dependent phosphohydrolas	8.86	9.5	8.72	9.29	0.14	0.21	-0.64	-0.57	0.67	0.19	-0.07	-1.35	0.32	0.28	0.92
Cthe_02143 hypothetical protein	9.81	10.36	9.94	10.14	-0.13	0.22	-0.55	-0.2	0.46	0.2	0.23	-0.58	0.33	0.28	1.44
Cthe_00160 ribosomal protein L21	11.96	12.57	12.08	12.33	-0.12	0.24	-0.61	-0.25	0.47	0.22	0.03	-0.69	0.33	0.28	1.34
Cthe_01962 pseudouridine synthase, RluA famil	11.5	12.25	12	11.72	-0.5	0.53	-0.75	0.28	0.17	0.47	-0.43	0.42	0.33	0.28	1.48
Cthe_02609 ATP synthase F1, epsilon subunit	9	9.65	9.21	9.38	-0.21	0.27	-0.65	-0.17	0.4	0.25	-0.1	-0.52	0.32	0.28	1.59
Cthe_02991 NADH:flavin oxidoreductase/NADH	10.3	11.18	10.72	10.57	-0.42	0.61	-0.88	0.15	0.23	0.53	-0.87	0.15	0.33	0.28	1.17
Cthe_02116 binding-protein-dependent transpo	10.52	11.25	10.94	10.86	-0.42	0.39	-0.73	0.08	0.23	0.35	-0.37	0	0.32	0.28	2.02
Cthe_01501 ABC transporter, transmembrane r	7.81	8.57	8.41	7.84	-0.6	0.73	-0.76	0.57	0.09	0.64	-0.47	1.02	0.33	0.28	1.03
Cthe_01789 ATPase AAA-2	14.26	15.05	14.89	14.25	-0.63	0.8	-0.79	0.64	0.06	0.69	-0.57	1.17	0.33	0.28	0.95
Cthe_02991 NADH:flavin oxidoreductase/NADH	10.3	11.18	10.72	10.57	-0.42	0.61	-0.88	0.15	0.23	0.53	-0.87	0.15	0.33	0.28	1.17
Cthe_03010 hypothetical protein	4.95	5.39	5.21	5	-0.26	0.39	-0.44	0.21	0.36	0.35	0.6	0.27	0.32	0.28	1.36
Cthe_00077 hypothetical protein	10.67	11.28	11.16	10.63	-0.49	0.65	-0.61	0.53	0.17	0.57	0.03	0.94	0.33	0.28	1.13
Cthe_02091 hypothetical protein	5.64	5.78	6.21	5.91	-0.57	-0.13	-0.14	0.3	0.11	-0.09	1.6	0.46	0.32	0.28	0.15
Cthe_00336 DRTGG domain containing protein	7.49	8.17	7.91	7.83	-0.42	0.34	-0.68	0.08	0.23	0.31	-0.2	0	0.33	0.28	3.45
Cthe_02155 S-layer-like domain containing prot	6.66	7.19	6.97	6.91	-0.31	0.28	-0.53	0.06	0.32	0.25	0.3	-0.04	0.32	0.28	2.4
Cthe_02116 binding-protein-dependent transpo	10.52	11.25	10.94	10.86	-0.42	0.39	-0.73	0.08	0.23	0.35	-0.37	0	0.32	0.28	2.02
Cthe_02609 ATP synthase F1, epsilon subunit	9	9.65	9.21	9.38	-0.21	0.27	-0.65	-0.17	0.4	0.25	-0.1	-0.52	0.32	0.28	1.59
Cthe_00160 ribosomal protein L21	11.96	12.57	12.08	12.33	-0.12	0.24	-0.61	-0.25	0.47	0.22	0.03	-0.69	0.33	0.28	1.34
Cthe_02609 ATP synthase F1, epsilon subunit	9	9.65	9.21	9.38	-0.21	0.27	-0.65	-0.17	0.4	0.25	-0.1	-0.52	0.32	0.28	1.59
Cthe_02609 ATP synthase F1, epsilon subunit	9	9.65	9.21	9.38	-0.21	0.27	-0.65	-0.17	0.4	0.25	-0.1	-0.52	0.32	0.28	1.59
Cthe_00764 signal peptidase I	9.61	10.1	9.3	10.02	0.31	0.08	-0.49	-0.72	0.81	0.08	0.43	-1.67	0.33	0.28	0.84
Cthe_01962 pseudouridine synthase, RluA famil	11.5	12.25	12	11.72	-0.5	0.53	-0.75	0.28	0.17	0.47	-0.43	0.42	0.33	0.28	1.48
Cthe_00544 protein serine/threonine phosphat	8.15	8.96	8.26	8.55	-0.11	0.41	-0.81	-0.29	0.48	0.36	-0.63	-0.77	0.32	0.28	1.08
Cthe_02609 ATP synthase F1, epsilon subunit	9	9.65	9.21	9.38	-0.21	0.27	-0.65	-0.17	0.4	0.25	-0.1	-0.52	0.32	0.28	1.59
Cthe_01394 two component transcriptional reg	6.81	7.22	6.89	7.01	-0.08	0.21	-0.41	-0.12	0.5	0.19	0.7	-0.42	0.31	0.27	1.17
Cthe_01816 urease, alpha subunit	5.64	6.82	6.13	5.86	-0.49	0.96	-1.18	0.27	0.17	0.83	-1.87	0.4	0.31	0.27	0.79
Cthe_02887 phosphoribosylformimino-5-amino	8.33	9.24	8.59	8.69	-0.26	0.55	-0.91	-0.1	0.36	0.48	-0.97	-0.38	0.31	0.27	1.03
Cthe_02051 CRISPR-associated RAMP protein, S	7.6	8.43	7.58	8.04	0.02	0.39	-0.83	-0.46	0.58	0.35	-0.7	-1.13	0.31	0.27	0.91
Cthe_02850 transposase IS116/IS110/IS902	3.81	4.91	4.81	3.7	-1	1.21	-1.1	1.11	-0.23	1.04	-1.6	2.15	0.31	0.27	0.71
Cthe_01394 two component transcriptional reg	6.81	7.22	6.89	7.01	-0.08	0.21	-0.41	-0.12	0.5	0.19	0.7	-0.42	0.31	0.27	1.17
Cthe_00355 hypothetical protein	8.9	9.57	9.19	9.28	-0.29	0.29	-0.67	-0.09	0.33	0.26	-0.17	-0.35	0.31	0.27	1.93
Cthe_01316 protein of unknown function DUF3	9.2	9.83	9.7	9.3	-0.5	0.53	-0.63	0.4	0.17	0.47	-0.03	0.67	0.31	0.27	1.33
Cthe_01406 hypothetical protein	4.09	4.75	3.58	4.64	0.51	0.11	-0.66	-1.06	0.97	0.11	-0.13	-2.38	0.31	0.27	0.73
Cthe_00783 RNA modification enzyme, MiaB fa	8.99	9.59	9.01	9.39	-0.02	0.2	-0.6	-0.38	0.55	0.19	0.07	-0.96	0.31	0.27	1.08
Cthe_01968 cell divisionFtsK/SpolIIE	11.98	12.55	12.24	12.32	-0.26	0.23	-0.57	-0.08	0.36	0.21	0.17	-0.33	0.31	0.27	2
Cthe_02541 nitrite and sulphite reductase 4Fe-4	4.64	5.7	4.95	4.95	-0.31	0.75	-1.06	0	0.32	0.65	-1.47	-0.17	0.31	0.27	0.87
Cthe_02407 AAA ATPase, central region	10.46	11.11	10.33	10.91	0.13	0.2	-0.65	-0.58	0.67						



Cthe_03171 S-layer domain-like protein	7.83	8.69	8.73	7.59	-0.9	1.1	-0.86	1.14	-0.15	0.95	-0.8	2.21	0.3	0.26	0.73
Cthe_00925 protein of unknown function DUF2	7.71	8.54	7.79	8.13	-0.08	0.41	-0.83	-0.34	0.5	0.36	-0.7	-0.88	0.3	0.26	0.98
Cthe_00082 ATP-dependent protease La	14.43	14.96	14.91	14.22	-0.48	0.74	-0.53	0.69	0.18	0.64	0.3	1.27	0.3	0.26	0.91
Cthe_00351 PpiC-type peptidyl-prolyl cis-trans i	10.15	10.54	10.37	10.13	-0.22	0.41	-0.39	0.24	0.39	0.36	0.77	0.33	0.3	0.26	1.13
Cthe_00123 Stage V sporulation AD	7.23	7.61	7.5	7.04	-0.27	0.57	-0.38	0.46	0.35	0.5	0.8	0.79	0.3	0.26	0.97
Cthe_01088 hypothetical protein	7.46	8.21	8.02	7.65	-0.56	0.56	-0.75	0.37	0.12	0.49	-0.43	0.6	0.3	0.26	1.22
Cthe_00320 hypothetical protein	9.71	10.19	9.75	10.03	-0.04	0.16	-0.48	-0.28	0.53	0.15	0.47	-0.75	0.3	0.26	1.11
Cthe_02032 hypothetical protein	9.2	9.96	9.61	9.56	-0.41	0.4	-0.76	0.05	0.24	0.36	-0.47	-0.06	0.3	0.26	1.63
Cthe_02713 dihydroxy-acid dehydratase	12.3	13.24	12.88	12.51	-0.58	0.73	-0.94	0.37	0.1	0.64	-1.07	0.6	0.3	0.26	0.94
Cthe_02328 UDP-N-acetylglucosamine	10.4	11.2	10.87	10.71	-0.47	0.49	-0.8	0.16	0.19	0.43	-0.6	0.17	0.3	0.26	1.35
Cthe_02713 dihydroxy-acid dehydratase	12.3	13.24	12.88	12.51	-0.58	0.73	-0.94	0.37	0.1	0.64	-1.07	0.6	0.3	0.26	0.94
Cthe_00082 ATP-dependent protease La	14.43	14.96	14.91	14.22	-0.48	0.74	-0.53	0.69	0.18	0.64	0.3	1.27	0.3	0.26	0.91
Cthe_00026	9.13	9.86	9.55	9.49	-0.42	0.37	-0.73	0.06	0.23	0.33	-0.37	-0.04	0.3	0.26	1.93
Cthe_02713 dihydroxy-acid dehydratase	12.3	13.24	12.88	12.51	-0.58	0.73	-0.94	0.37	0.1	0.64	-1.07	0.6	0.3	0.26	0.94
Cthe_02328 UDP-N-acetylglucosamine	10.4	11.2	10.87	10.71	-0.47	0.49	-0.8	0.16	0.19	0.43	-0.6	0.17	0.3	0.26	1.35
Cthe_02713 dihydroxy-acid dehydratase	12.3	13.24	12.88	12.51	-0.58	0.73	-0.94	0.37	0.1	0.64	-1.07	0.6	0.3	0.26	0.94
Cthe_02713 dihydroxy-acid dehydratase	12.3	13.24	12.88	12.51	-0.58	0.73	-0.94	0.37	0.1	0.64	-1.07	0.6	0.3	0.26	0.94
Cthe_02713 dihydroxy-acid dehydratase	12.3	13.24	12.88	12.51	-0.58	0.73	-0.94	0.37	0.1	0.64	-1.07	0.6	0.3	0.26	0.94
Cthe_02328 UDP-N-acetylglucosamine	10.4	11.2	10.87	10.71	-0.47	0.49	-0.8	0.16	0.19	0.43	-0.6	0.17	0.3	0.26	1.35
Cthe_02713 dihydroxy-acid dehydratase	12.3	13.24	12.88	12.51	-0.58	0.73	-0.94	0.37	0.1	0.64	-1.07	0.6	0.3	0.26	0.94
Cthe_02328 UDP-N-acetylglucosamine	10.4	11.2	10.87	10.71	-0.47	0.49	-0.8	0.16	0.19	0.43	-0.6	0.17	0.3	0.26	1.35
Cthe_00026	9.13	9.86	9.55	9.49	-0.42	0.37	-0.73	0.06	0.23	0.33	-0.37	-0.04	0.3	0.26	1.93
Cthe_01765 hypothetical protein	9.66	10.37	9.8	10.08	-0.14	0.29	-0.71	-0.28	0.45	0.26	-0.3	-0.75	0.29	0.25	1.15
Cthe_01765 hypothetical protein	9.66	10.37	9.8	10.08	-0.14	0.29	-0.71	-0.28	0.45	0.26	-0.3	-0.75	0.29	0.25	1.15
Cthe_00060 SEC-C motif containing protein	9.91	10.47	10.21	10.26	-0.3	0.21	-0.56	-0.05	0.33	0.19	0.2	-0.27	0.29	0.25	2.02
Cthe_02115 protein of unknown function DUF7	9.76	10.7	10.13	10.09	-0.37	0.61	-0.94	0.04	0.27	0.53	-1.07	-0.08	0.29	0.25	0.99
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00093 septum site-determining protein M	11.18	11.74	11.33	11.55	-0.15	0.19	-0.56	-0.22	0.44	0.18	0.2	-0.63	0.29	0.25	1.28
Cthe_03039 cell divisionFtsK/SpolIIE	8.17	8.77	8.67	8.23	-0.5	0.54	-0.6	0.44	0.17	0.47	0.07	0.75	0.29	0.25	1.18
Cthe_00344 Malate dehydrogenase	13.46	14.14	13.93	13.82	-0.47	0.32	-0.68	0.11	0.19	0.29	-0.2	0.06	0.29	0.25	2.96
Cthe_03186 Radical SAM	9.46	10.06	9.9	9.81	-0.44	0.25	-0.6	0.09	0.21	0.23	0.07	0.02	0.29	0.25	7.64
Cthe_01910 hypothetical protein	8.68	9.02	8.66	8.86	0.02	0.16	-0.34	-0.2	0.58	0.15	0.93	-0.58	0.29	0.25	0.98
Cthe_00065 hypothetical protein	9.78	10.52	9.86	10.22	-0.08	0.3	-0.74	-0.36	0.5	0.27	-0.4	-0.92	0.29	0.25	1.01
Cthe_01368 S-layer-like domain containing prot	14.06	14.72	14.56	14.34	-0.5	0.38	-0.66	0.22	0.17	0.34	-0.13	0.29	0.29	0.25	2.14
Cthe_00344 Malate dehydrogenase	13.46	14.14	13.93	13.82	-0.47	0.32	-0.68	0.11	0.19	0.29	-0.2	0.06	0.29	0.25	2.96
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami	6.66	7.21	6.75	7.04	-0.09	0.17	-0.55	-0.29	0.49	0.16	0.23	-0.77	0.29	0.25	1.15
Cthe_00127 RNA methyltransferase, TrmH fami															



Cthe_00293 hypothetical protein	7.64	8.3	7.85	8.06	-0.21	0.24	-0.66	-0.21	0.4	0.22	-0.13	-0.6	0.28	0.24	1.33
Cthe_02781 hypothetical protein	9.16	9.78	9.56	9.55	-0.4	0.23	-0.62	0.01	0.25	0.21	0	-0.15	0.28	0.24	3.89
Cthe_02758 hypothetical protein	3	3.17	2.81	3	0.19	0.17	-0.17	-0.19	0.71	0.16	1.5	-0.56	0.28	0.24	0.81
Cthe_01219 hypothetical protein	10.56	11.21	10.43	11.04	0.13	0.17	-0.65	-0.61	0.67	0.16	-0.1	-1.44	0.28	0.24	0.85
Cthe_00938 regulatory protein, DeoR	11.75	12.27	12.01	12.07	-0.26	0.2	-0.52	-0.06	0.36	0.19	0.33	-0.29	0.28	0.24	1.65
Cthe_02946 2C-methyl-D-erythritol 2,4-cyclodip	8.55	9.03	8.88	8.68	-0.33	0.35	-0.48	0.2	0.3	0.31	0.47	0.25	0.28	0.24	1.45
Cthe_02946 2C-methyl-D-erythritol 2,4-cyclodip	8.55	9.03	8.88	8.68	-0.33	0.35	-0.48	0.2	0.3	0.31	0.47	0.25	0.28	0.24	1.45
Cthe_01346 single-stranded-DNA-specific exonu	10.92	11.52	10.5	11.49	0.42	0.03	-0.6	-0.99	0.9	0.04	0.07	-2.23	0.28	0.24	0.72
Cthe_02599 CMP/dCMP deaminase, zinc-bindin	11.29	12.02	11.77	11.64	-0.48	0.38	-0.73	0.13	0.18	0.34	-0.37	0.1	0.28	0.24	1.79
Cthe_02946 2C-methyl-D-erythritol 2,4-cyclodip	8.55	9.03	8.88	8.68	-0.33	0.35	-0.48	0.2	0.3	0.31	0.47	0.25	0.28	0.24	1.45
Cthe_01506 metal dependent phosphohydrolas	9.53	10.06	9.65	9.91	-0.12	0.15	-0.53	-0.26	0.47	0.14	0.3	-0.71	0.27	0.23	1.14
Cthe_02866 phage major capsid protein, HK97	3.17	3.46	3.46	2.58	-0.29	0.88	-0.29	0.88	0.33	0.76	1.1	1.67	0.27	0.23	0.74
Cthe_01408 two component transcriptional reg	6.07	7	6.74	6.27	-0.67	0.73	-0.93	0.47	0.03	0.64	-1.03	0.81	0.27	0.23	0.87
Cthe_01826 response regulator receiver sensor	10.36	10.87	10.41	10.75	-0.05	0.12	-0.51	-0.34	0.52	0.12	0.37	-0.88	0.27	0.23	1
Cthe_00776 DNA mismatch repair protein MutL	10.48	10.98	10.5	10.88	-0.02	0.1	-0.5	-0.38	0.55	0.1	0.4	-0.96	0.27	0.23	0.96
Cthe_00902 3-methyl-2-oxobutanoate hydroxy	9.61	10.43	9.96	10.01	-0.35	0.42	-0.82	-0.05	0.29	0.37	-0.67	-0.27	0.27	0.23	1.16
Cthe_02817 CheW protein	4.75	5.13	4.32	5.25	0.43	-0.12	-0.38	-0.93	0.9	-0.08	0.8	-2.1	0.27	0.23	0.72
Cthe_01943 deoxyribose-phosphate aldolase	13.63	14.33	14.24	13.74	-0.61	0.59	-0.7	0.5	0.08	0.52	-0.27	0.88	0.27	0.23	1.02
Cthe_01408 two component transcriptional reg	6.07	7	6.74	6.27	-0.67	0.73	-0.93	0.47	0.03	0.64	-1.03	0.81	0.27	0.23	0.87
Cthe_01826 response regulator receiver sensor	10.36	10.87	10.41	10.75	-0.05	0.12	-0.51	-0.34	0.52	0.12	0.37	-0.88	0.27	0.23	1
Cthe_02817 CheW protein	4.75	5.13	4.32	5.25	0.43	-0.12	-0.38	-0.93	0.9	-0.08	0.8	-2.1	0.27	0.23	0.72
Cthe_01506 metal dependent phosphohydrolas	9.53	10.06	9.65	9.91	-0.12	0.15	-0.53	-0.26	0.47	0.14	0.3	-0.71	0.27	0.23	1.14
Cthe_02313 protein of unknown function DUF2	7.75	8.41	7.61	8.24	0.14	0.17	-0.66	-0.63	0.67	0.16	-0.13	-1.48	0.27	0.23	0.83
Cthe_02619 cell shape determining protein, Mr	11.26	11.73	11.35	11.6	-0.09	0.13	-0.47	-0.25	0.49	0.13	0.5	-0.69	0.27	0.23	1.06
Cthe_02164 Rubredoxin-type Fe(Cys)4 protein	12.15	12.64	12.64	11.88	-0.49	0.76	-0.49	0.76	0.17	0.66	0.43	1.42	0.27	0.23	0.82
Cthe_00508 hypothetical protein	7.72	8.89	8.14	8.61	-0.42	0.28	-1.17	-0.47	0.23	0.25	-1.83	-1.15	0.27	0.23	0.28
Cthe_03189 hypothetical protein	9.88	10.41	10.09	10.24	-0.21	0.17	-0.53	-0.15	0.4	0.16	0.3	-0.48	0.27	0.23	1.36
Cthe_00296 hypothetical protein	8.14	9	8.49	8.54	-0.35	0.46	-0.86	-0.05	0.29	0.41	-0.8	-0.27	0.27	0.23	1.06
Cthe_01108 hypothetical protein		1.58	1.58	0	-1.58	1.58	-1.58	1.58	-0.69	1.36	-3.2	3.13	0.27	0.23	0.61
Cthe_02501 hypothetical protein	0	1.58	1.58		-1.58	1.58	-1.58	1.58	-0.69	1.36	-3.2	3.13	0.27	0.23	0.61
Cthe_00902 3-methyl-2-oxobutanoate hydroxy	9.61	10.43	9.96	10.01	-0.35	0.42	-0.82	-0.05	0.29	0.37	-0.67	-0.27	0.27	0.23	1.16
Cthe_01943 deoxyribose-phosphate aldolase	13.63	14.33	14.24	13.74	-0.61	0.59	-0.7	0.5	0.08	0.52	-0.27	0.88	0.27	0.23	1.02
Cthe_00902 3-methyl-2-oxobutanoate hydroxy	9.61	10.43	9.96	10.01	-0.35	0.42	-0.82	-0.05	0.29	0.37	-0.67	-0.27	0.27	0.23	1.16
Cthe_01943 deoxyribose-phosphate aldolase	13.63	14.33	14.24	13.74	-0.61	0.59	-0.7	0.5	0.08	0.52	-0.27	0.88	0.27	0.23	1.02
Cthe_00902 3-methyl-2-oxobutanoate hydroxy	9.61	10.43	9.96	10.01	-0.35	0.42	-0.82	-0.05	0.29	0.37	-0.67	-0.27	0.27	0.23	1.16
Cthe_01943 deoxyribose-phosphate aldolase	13.63	14.33	14.24	13.74	-0.61	0.59	-0.7	0.5	0.08	0.52	-0.27	0.88	0.27	0.23	1.02
Cthe_00902 3-methyl-2-oxobutanoate hydroxy	9.61	10.43	9.96	10.01	-0.35	0.42	-0.82	-0.05	0.29	0.37	-0.67	-0.27	0.27	0.23	1.16
Cthe_01973 Tetra(ri)copeptide TPR_2	12.35	12.88	12.76	12.59	-0.41	0.29	-0.53	0.17	0.24	0.26	0.3	0.19	0.25	0.22	1.78
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_01054 ATPase associated with various cell	10.21	10.82	10.69	10.6	-0.48	0.22	-0.61	0.09	0.18	0.2	0.03	0.02	0.26	0.22	13.33
Cthe_00806 PAS/PAC sensor hybrid histidine kin	8.1	8.62	8.13	8.52	-0.03	0.1	-0.52	-0.39	0.54	0.1	0.33	-0.98	0.26	0.22	0.95
Cthe_01442 ATP-dependent transcriptional reg	4.09	4.86	4.75	4.25	-0.66	0.61	-0.77	0.5	0.04	0.53	-0.5	0.88	0.25	0.22	0.94
Cthe_00295 phosphoserine aminotransferase	13.05	13.78	13.73	13.08	-0.68	0.7	-0.73	0.65	0.02	0.61	-0.37	1.19	0.26	0.22	0.87
Cthe_02066 serine O-acetyltransferase	12.04	12.85	12.79	12.13	-0.75	0.72	-0.81	0.66	-0.03	0.63	-0.63	1.21	0.25	0.22	0.83
Cthe_00566 primosomal protein N'	9.78	10.48	10.38	9.94	-0.6	0.54	-0.7	0.44	0.09	0.47	-0.27	0.75	0.26	0.22	1.07
Cthe_00295 phosphoserine aminotransferase	13.05	13.78	13.73	13.08	-0.68	0.7	-0.73	0.65	0.02	0.61	-0.37	1.19	0.26	0.22	0.87
Cthe_02149 amine oxidase	11.56	12.12	11.82	11.95	-0.26	0.17	-0.56	-0.13	0.36	0.16	0.2	-0.44	0.26	0.22	1.46
Cthe_03150 cobalamin biosynthesis protein Cob	10.31	10.69	10.41	10.53	-0.1	0.16	-0.38	-0.12	0.48	0.15	0.8	-0.42	0.25	0.22	0.99
Cthe_00734 peptidase M23B	9.78	10.17	9.76	10.09	0.02	0.08	-0.39	-0.33	0.58	0.08	0.77	-0.85	0.26	0.22	0.91
Cthe_00977 UDP-N-acetylmuramoylalanyl-D-glu	8.8	9.28	8.73	9.25	0.07	0.03	-0.48	-0.52	0.62	0.04	0.47	-1.25	0.25	0.22	0.83
Cthe_00806 PAS/PAC sensor hybrid histidine kin	8.1	8.62	8.13	8.52	-0.03	0.1	-0.52	-0.39	0.54	0.1	0.33	-0.98	0.26	0.22	0.95
Cthe_00242 hypothetical protein	9.74	10.27	9.75	10.19	-0.01	0.08	-0.53	-0.44	0.56	0.08	0.3	-1.08	0.25	0.22	0.9
Cthe_02746 protein of unknown function DUF4	9.65	10.24	10.16	9.85	-0.51	0.39	-0.59	0.31	0.16	0.35	0.1	0.48	0.25	0.22	1.4
Cthe_00762 protein of unknown function DUF1	8.61	9.03	8.37	9.09	0.24	-0.06	-0.42	-0.72	0.75	-0.03	0.67	-1.67	0.25	0.22	0.74
Cthe_00546 ferric uptake regulator, Fur family	8.35	8.95	8.68	8.76	-0.33	0.19	-0.6	-0.08	0.3	0.18	0.07	-0.33	0.26	0.22	1.85
Cthe_02117 putative sulfonate transport system	10.86	11.73	11.44	11.16	-0.58	0.57	-0.87	0.28	0.1	0.5	-0.83	0.42	0.25	0.22	0.98
Cthe_02215 Mg2+ transporter protein, CorA-lik	9.61	10.39	9.98	10.03	-0.37	0.36	-0.78	-0.05	0.27	0.32	-0.53	-0.27	0.25	0.22	1.26
Cthe_00999 1-deoxy-D-xylulose 5-phosphate re	11.14	11.8	11.46	11.58	-0.32	0.22	-0.66	-0.12	0.31	0.2	-0.13	-0.42	0.25	0.22	1.5
Cthe_02878 peptidase C39, bacteriocin processi	9.19	9.82	9.59	9.61	-0.4	0.21	-0.63	-0.02	0.25	0.19	-0.03	-0.21	0.25	0.22	2.64
Cthe_02002 hypothetical protein	7.5	7.69	7.25	7.69	0.25	0	-0.19	-0.44	0.76	0.02	1.43	-1.08	0.26	0.22	0.76
Cthe_00435 cellulosome enzyme, dockerin type	11.76	12.35	12.25	11.98	-0.49	0.37	-0.59	0.27	0.17	0.33	0.1	0.4	0.26	0.22	1.61
Cthe_02614 hypothetical protein	11	11.62	11.28	11.43	-0.28	0.19	-0.62	-0.15	0.34	0.18	0	-0.48	0.25	0.22	1.43
Cthe_02523 hypothetical protein	13.8	14.21	14.18	13.57	-0.38	0.64	-0.41	0.61	0.26	0.56	0.7	1.1	0.25	0.22	0.85
Cthe_00316 PA14	7.2	7.97	7.72	7.54	-0.52	0.43	-0.77	0.18	0.15	0.38	-0.5	0.21	0.26	0.22	1.35
Cthe_03180 hypothetical protein	9.02	9.43	9.15	9.29	-0.13	0.14	-0.41	-0.14	0.46	0.14	0.7	-0.46	0.25	0.22	1.03
Cthe_02764 TROVE domain containing protein	10.28	10.96	10.89	10.41	-0.61	0.55	-0.68	0.48	0.08	0.48	-0.2	0.83	0.25	0.22	1.02
Cthe_01828 hypothetical protein	10.08	10.26	9.68	10.45	0.4	-0.19	-0.18	-0.77	0.88	-0.14	1.47	-1.77	0.25	0.22	0.69
Cthe_01059 hypothetical protein	11.97	12.34	12.68	12.33	-0.71	0.01	-0.37	0.35	0	0.03	0.83	0.56	0.25	0.22	0.05
Cthe_00939 hypothetical protein	7.64	7.67	7.43	7.31	0.21	0.36	-0.03	0.12	0.73	0.32	1.97	0.08	0.25	0.22	0.72
Cthe_00066 hypothetical protein	9.7	10.62	9.58	10.21	0.12	0.41	-0.92	-0.63	0.66	0.36	-1	-1.48	0.25	0.22	0.75
Cthe_00295 phosphoserine aminotransferase	13.05	13.78	13.73	13.08	-0.68	0.7	-0.73	0.65	0.02	0.61	-0.37	1.19	0.26	0.22	0.87
Cthe_02117 putative sulfonate transport system	10.86	11.73	11.44	11.16	-0.58	0.57	-0.87	0.28	0.1	0.5	-0.83	0.42	0.25	0.22	0.98
Cthe_02066 serine O-acetyltransferase	12.04	12.85	12.79	12.13	-0.75	0.72	-0.81	0.66	-0.03	0.63	-0.63	1.21	0.25	0.22	0.83
Cthe_00295 phosphoserine aminotransferase	13.05	13.78	13.73	13.08	-0.68	0.7	-0.73	0.65	0.02	0.61	-0.37	1.19	0.26	0.22	0.87
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00999 1-deoxy-D-xylulose 5-phosphate re	11.14	11.8	11.46	11.58	-0.32	0.22	-0.66	-0.12	0.31	0.2	-0.13	-0.42	0.25	0.22	1.5
Cthe_03150 cobalamin biosynthesis protein Cob	10.31	10.69	10.41	10.53	-0.1	0.16	-0.38	-0.12	0.48	0.15	0.8	-0.42	0.25	0.22	0.99
Cthe_03150 cobalamin biosynthesis protein Cob	10.31	10.69	10.41	10.53	-0.1	0.16	-0.38	-0.12	0.48	0.15					



Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00999 1-deoxy-D-xylulose 5-phosphate re	11.14	11.8	11.46	11.58	-0.32	0.22	-0.66	-0.12	0.31	0.2	-0.13	-0.42	0.25	0.22	1.5
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00977 UDP-N-acetylmuramoylalanyl-D-glu	8.8	9.28	8.73	9.25	0.07	0.03	-0.48	-0.52	0.62	0.04	0.47	-1.25	0.25	0.22	0.83
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_03150 cobalamin biosynthesis protein Cob	10.31	10.69	10.41	10.53	-0.1	0.16	-0.38	-0.12	0.48	0.15	0.8	-0.42	0.25	0.22	0.99
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
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Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_03150 cobalamin biosynthesis protein Cob	10.31	10.69	10.41	10.53	-0.1	0.16	-0.38	-0.12	0.48	0.15	0.8	-0.42	0.25	0.22	0.99
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_01054 ATPase associated with various cell	10.21	10.82	10.69	10.6	-0.48	0.22	-0.61	0.09	0.18	0.2	0.03	0.02	0.26	0.22	13.33
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_03150 cobalamin biosynthesis protein Cob	10.31	10.69	10.41	10.53	-0.1	0.16	-0.38	-0.12	0.48	0.15	0.8	-0.42	0.25	0.22	0.99
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00295 phosphoserine aminotransferase	13.05	13.78	13.73	13.08	-0.68	0.7	-0.73	0.65	0.02	0.61	-0.37	1.19	0.26	0.22	0.87
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_02066 serine O-acetyltransferase	12.04	12.85	12.79	12.13	-0.75	0.72	-0.81	0.66	-0.03	0.63	-0.63	1.21	0.25	0.22	0.83
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_01054 ATPase associated with various cell	10.21	10.82	10.69	10.6	-0.48	0.22	-0.61	0.09	0.18	0.2	0.03	0.02	0.26	0.22	13.33
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_01054 ATPase associated with various cell	10.21	10.82	10.69	10.6	-0.48	0.22	-0.61	0.09	0.18	0.2	0.03	0.02	0.26	0.22	13.33
Cthe_00295 phosphoserine aminotransferase	13.05	13.78	13.73	13.08	-0.68	0.7	-0.73	0.65	0.02	0.61	-0.37	1.19	0.26	0.22	0.87
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00977 UDP-N-acetylmuramoylalanyl-D-glu	8.8	9.28	8.73	9.25	0.07	0.03	-0.48	-0.52	0.62	0.04	0.47	-1.25	0.25	0.22	0.83
Cthe_01054 ATPase associated with various cell	10.21	10.82	10.69	10.6	-0.48	0.22	-0.61	0.09	0.18	0.2	0.03	0.02	0.26	0.22	13.33
Cthe_00977 UDP-N-acetylmuramoylalanyl-D-glu	8.8	9.28	8.73	9.25	0.07	0.03	-0.48	-0.52	0.62	0.04	0.47	-1.25	0.25	0.22	0.83
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_01054 ATPase associated with various cell	10.21	10.82	10.69	10.6	-0.48	0.22	-0.61	0.09	0.18	0.2	0.03	0.02	0.26	0.22	13.33
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00277 hypothetical protein	9.42	9.88	9.81	9.4	-0.39	0.48	-0.46	0.41	0.25	0.42	0.53	0.69	0.25	0.22	1
Cthe_00763 GTP-binding protein	9.21	9.57	8.83	9.77	0.38	-0.2	-0.36	-0.94	0.87	-0.15	0.87	-2.13	0.24	0.21	0.69
Cthe_03064 polysaccharide biosynthesis protei	9.48	10.22	9.74	9.95	-0.26	0.27	-0.74	-0.21	0.36	0.25	-0.4	-0.6	0.24	0.21	1.09
Cthe_01432 transposase IS200-like protein	12.6	13.38	13.11	12.97	-0.51	0.41	-0.78	0.14	0.16	0.36	-0.53	0.13	0.24	0.21	1.29
Cthe_01313 phosphopantothenoylecysteine	10.23	10.9	10.4	10.7	-0.17	0.2	-0.67	-0.3	0.43	0.19	-0.17	-0.79	0.24	0.21	1.04
Cthe_01923 CTP synthase	11.77	12.33	11.81	12.23	-0.04	0.1	-0.56	-0.42	0.53	0.1	0.2	-1.04	0.24	0.21	0.91
Cthe_00817 diguanylate cyclase	11.15	11.55	11.29	11.4	-0.14	0.15	-0.4	-0.11	0.45	0.14	0.73	-0.4	0.24	0.21	1.01
Cthe_00052 hypothetical protein	11.42	11.99	11.87	11.78	-0.45	0.21	-0.57	0.09	0.21	0.19	0.17	0.02	0.24	0.21	2.95
Cthe_01509 protein of unknown function DUF4	14.67	15.35	15.38	14.59	-0.71	0.76	-0.68	0.79	0	0.66	-0.2	1.48	0.24	0.21	0.79
Cthe_03014 hydrogenase formation HypD prote	8.58	9.67	9.17	8.87	-0.59	0.8	-1.09	0.3	0.1	0.69	-1.57	0.46	0.24	0.21	0.76
Cthe_01970 hypothetical protein	10.42	10.98	10.94	10.48	-0.52	0.5	-0.56	0.46	0.15	0.44	0.2	0.79	0.24	0.21	1.02
Cthe_01096 hypothetical protein	5.61	6.46	6.11	5.98	-0.5	0.48	-0.85	0.13	0.17	0.42	-0.77	0.1	0.24	0.21	1.04
Cthe_02564 hypothetical protein	9.1	9.82	9.15	9.59	-0.05	0.23	-0.72	-0.44	0.52	0.21	-0.33	-1.08	0.24	0.21	0.89
Cthe_02053 hypothetical protein	8.05	8.97	8.46	9.05	-0.41	-0.08	-0.92	-0.59	0.24	-0.05	-1	-1.4	0.24	0.21	0.25
Cthe_01923 CTP synthase	11.77	12.33	11.81	12.23	-0.04	0.1	-0.56	-0.42	0.53	0.1	0.2	-1.04	0.24	0.21	0.91
Cthe_01313 phosphopantothenoylecysteine	10.23	10.9	10.4	10.7	-0.17	0.2	-0.67	-0.3	0.43	0.19	-0.17	-0.79	0.24	0.21	1.04
Cthe_01313 phosphopantothenoylecysteine	10.23	10.9	10.4	10.7	-0.17	0.2	-0.67	-0.3	0.43	0.19	-0.17	-0.79	0.24	0.21	1.04
Cthe_01313 phosphopantothenoylecysteine	10.23	10.9	10.4	10.7	-0.17	0.2	-0.67	-0.3	0.43	0.19	-0.17	-0.79	0.24	0.21	1.04
Cthe_01923 CTP synthase	11.77	12.33	11.81	12.23	-0.04	0.1	-0.56	-0.42	0.53	0.1	0.2	-1.04	0.24	0.21	0.91
Cthe_01313 phosphopantothenoylecysteine	10.23	10.9	10.4	10.7	-0.17	0.2	-0.67	-0.3	0.43	0.19	-0.17	-0.79	0.24	0.21	1.04
Cthe_01923 CTP synthase	11.77	12.33	11.81	12.23	-0.04	0.1	-0.56	-0.42	0.53	0.1	0.2	-1.04	0.24	0.21	0.91
Cthe_00515 transposase IS66	1.58		0	1.58		1.58	0	1.82		7.33	-0.17	0.23	0.2	0.44	
Cthe_02515 Guanine deaminase	9.04	9.69	9.61	9.27	-0.57	0.42	-0.65	0.34	0.11	0.37	-0.1	0.54	0.23	0.2	1.26
Cthe_01427 branched-chain amino acid transpo	5.61	6.46	6.11	6	-0.5	0.46	-0.85	0.11	0.17	0.41	-0.77	0.06	0.23	0.2	1.03
Cthe_02257 ribosomal protein L9	10.98	11.76	11.5	11.37	-0.52	0.39	-0.78	0.13	0.15	0.35	-0.53	0.1	0.23	0.2	1.26
Cthe_02515 Guanine deaminase															



Cthe_01087 hypothetical protein	4.58	5.39	5.13	4.95	-0.55	0.44	-0.81	0.18	0.13	0.39	-0.63	0.21	0.23	0.2	1.11
Cthe_00010 hypothetical protein	7.39	7.82	7.69	7.55	-0.3	0.27	-0.43	0.14	0.33	0.25	0.63	0.13	0.23	0.2	1.15
Cthe_02999 hypothetical protein	6.3	7.16	6.88	7.28	-0.58	-0.12	-0.86	-0.4	0.1	-0.08	-0.8	-1	0.23	0.2	0.18
Cthe_03066 ABC transporter related protein	11.27	11.77	11.62	11.56	-0.35	0.21	-0.5	0.06	0.29	0.19	0.4	-0.04	0.23	0.2	1.54
Cthe_02791 binding-protein-dependent transpo	3.32	4.75	4	3.58	-0.68	1.17	-1.43	0.42	0.02	1.01	-2.7	0.71	0.23	0.2	0.65
Cthe_03066 ABC transporter related protein	11.27	11.77	11.62	11.56	-0.35	0.21	-0.5	0.06	0.29	0.19	0.4	-0.04	0.23	0.2	1.54
Cthe_02257 ribosomal protein L9	10.98	11.76	11.5	11.37	-0.52	0.39	-0.78	0.13	0.15	0.35	-0.53	0.1	0.23	0.2	1.26
Cthe_02726 ribosomal protein L7Ae/L30e/S12e	10.54	11	10.65	10.93	-0.11	0.07	-0.46	-0.28	0.48	0.08	0.53	-0.75	0.23	0.2	0.95
Cthe_01218 Leucyltransferase	9.07	9.86	8.99	9.61	0.08	0.25	-0.79	-0.62	0.63	0.23	-0.57	-1.46	0.23	0.2	0.76
Cthe_02515 Guanine deaminase	9.04	9.69	9.61	9.27	-0.57	0.42	-0.65	0.34	0.11	0.37	-0.1	0.54	0.23	0.2	1.26
Cthe_02515 Guanine deaminase	9.04	9.69	9.61	9.27	-0.57	0.42	-0.65	0.34	0.11	0.37	-0.1	0.54	0.23	0.2	1.26
Cthe_02515 Guanine deaminase	9.04	9.69	9.61	9.27	-0.57	0.42	-0.65	0.34	0.11	0.37	-0.1	0.54	0.23	0.2	1.26
Cthe_02515 Guanine deaminase	9.04	9.69	9.61	9.27	-0.57	0.42	-0.65	0.34	0.11	0.37	-0.1	0.54	0.23	0.2	1.26
Cthe_02515 Guanine deaminase	9.04	9.69	9.61	9.27	-0.57	0.42	-0.65	0.34	0.11	0.37	-0.1	0.54	0.23	0.2	1.26
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_00740 transcriptional regulator, GntR fam	10.56	11.14	10.72	11.03	-0.16	0.11	-0.58	-0.31	0.44	0.11	0.13	-0.81	0.22	0.19	0.99
Cthe_01499 ammonium transporter	6.41	7.13	7.13	6.46	-0.72	0.67	-0.72	0.67	-0.01	0.58	-0.33	1.23	0.22	0.19	0.81
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_00598 thiazole biosynthesis	8.52	9.3	9.15	8.81	-0.63	0.49	-0.78	0.34	0.06	0.43	-0.53	0.54	0.22	0.19	1.02
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_00640 cellulosome enzyme, dockerin type	9.57	10.43	10.34	9.77	-0.77	0.66	-0.86	0.57	-0.05	0.58	-0.8	1.02	0.22	0.19	0.8
Cthe_02974 hypothetical protein	10.32	10.96	10.92	10.47	-0.6	0.49	-0.64	0.45	0.09	0.43	-0.07	0.77	0.22	0.19	1.01
Cthe_00164 protein of unknown function UPF0	9.16	9.73	9.42	9.6	-0.26	0.13	-0.57	-0.18	0.36	0.13	0.17	-0.54	0.22	0.19	1.21
Cthe_02930 ribosomal protein S11	9.83	10.46	10.06	10.3	-0.23	0.16	-0.63	-0.24	0.38	0.15	-0.03	-0.67	0.22	0.19	1.09
Cthe_02607 ATP synthase F1, gamma subunit	9.2	10.06	9.3	9.7	-0.1	0.36	-0.86	-0.4	0.48	0.32	-0.8	-1	0.22	0.19	0.8
Cthe_01499 ammonium transporter	6.41	7.13	7.13	6.46	-0.72	0.67	-0.72	0.67	-0.01	0.58	-0.33	1.23	0.22	0.19	0.81
Cthe_02542 SirA-like protein	4.7	5.64	5.36	5	-0.66	0.64	-0.94	0.36	0.04	0.56	-1.07	0.58	0.22	0.19	0.82
Cthe_00378 hypothetical protein	4.25	4.91	4.7	4.7	-0.45	0.21	-0.66	0	0.21	0.19	-0.13	-0.17	0.22	0.19	2.36
Cthe_02951 hypothetical protein	7.47	7.79	7.64	7.51	-0.17	0.28	-0.32	0.13	0.43	0.25	1	0.1	0.22	0.19	0.88
Cthe_01990 hypothetical protein	4.95	5.78	5.64	5.81	-0.69	-0.03	-0.83	-0.17	0.02	-0.01	-0.7	-0.52	0.22	0.19	0.05
Cthe_03224 hypothetical protein	6.86	7.38	6.91	7.33	-0.05	0.05	-0.52	-0.42	0.52	0.06	0.33	-1.04	0.22	0.19	0.86
Cthe_00165 hypothetical protein	9.82	10.34	10.18	10.17	-0.36	0.17	-0.52	0.01	0.28	0.16	0.33	-0.15	0.22	0.19	1.59
Cthe_02010 hypothetical protein	7.72	7.95	7.83	7.55	-0.11	0.4	-0.23	0.28	0.48	0.36	1.3	0.42	0.22	0.19	0.78
Cthe_02930 ribosomal protein S11	9.83	10.46	10.06	10.3	-0.23	0.16	-0.63	-0.24	0.38	0.15	-0.03	-0.67	0.22	0.19	1.09
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02607 ATP synthase F1, gamma subunit	9.2	10.06	9.3	9.7	-0.1	0.36	-0.86	-0.4	0.48	0.32	-0.8	-1	0.22	0.19	0.8
Cthe_02930 ribosomal protein S11	9.83	10.46	10.06	10.3	-0.23	0.16	-0.63	-0.24	0.38	0.15	-0.03	-0.67	0.22	0.19	1.09
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02607 ATP synthase F1, gamma subunit	9.2	10.06	9.3	9.7	-0.1	0.36	-0.86	-0.4	0.48	0.32	-0.8	-1	0.22	0.19	0.8
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02607 ATP synthase F1, gamma subunit	9.2	10.06	9.3	9.7	-0.1	0.36	-0.86	-0.4	0.48	0.32	-0.8	-1	0.22	0.19	0.8
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43	0.29	0.22	0.19	1.24
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_02516 acetolactate synthase, large subuni	11.03	11.92	11.57	11.91	-0.54	0.01	-0.89	-0.34	0.13	0.03	-0.9	-0.88	0.22	0.19	0.19
Cthe_01435 Phosphoglycerate mutase	6.51	7	6.92	6.7	-0.41	0.3	-0.49	0.22	0.24	0.27	0.43				



Cthe_00660 glycoside hydrolase, family 81	9.62	10.43	10.18	10.02	-0.56	0.41	-0.81	0.16	0.12	0.36	-0.63	0.17	0.2	0.17	1.04
Cthe_01764 Outer membrane protein-like prote	9.92	10.3	10.06	10.2	-0.14	0.1	-0.38	-0.14	0.45	0.1	0.8	-0.46	0.2	0.17	0.89
Cthe_01937 glutamate racemase	9.55	10.25	9.98	10.02	-0.43	0.23	-0.7	-0.04	0.22	0.21	-0.27	-0.25	0.2	0.17	1.48
Cthe_02647 protein of unknown function DUF2	3.58	4.81	4	4.39	-0.42	0.42	-1.23	-0.39	0.23	0.37	-2.03	-0.98	0.2	0.17	0.35
Cthe_03172 protein of unknown function DUF2	9.08	9.82	9.89	9.08	-0.81	0.74	-0.74	0.81	-0.08	0.64	-0.4	1.52	0.2	0.17	0.73
Cthe_01345 adenine phosphoribosyltransferase	9.57	10.14	9.35	10.2	0.22	-0.06	-0.57	-0.85	0.74	-0.03	0.17	-1.94	0.2	0.17	0.68
Cthe_01944 protein of unknown function DUF4	11.42	12.14	12.02	11.79	-0.6	0.35	-0.72	0.23	0.09	0.31	-0.33	0.31	0.2	0.17	1.27
Cthe_01446 peptidase S1 and S6, chymotrypsin	9.93	10.82	10.61	10.74	-0.68	0.08	-0.89	-0.13	0.02	0.08	-0.9	-0.44	0.2	0.17	0.15
Cthe_02806 hypothetical protein	12.34	12.91	12.86	12.62	-0.52	0.29	-0.57	0.24	0.15	0.26	0.17	0.33	0.2	0.17	1.44
Cthe_03143 hypothetical protein	6.61	6.79	6.51	6.73	0.1	0.06	-0.18	-0.22	0.64	0.07	1.47	-0.63	0.2	0.17	0.72
Cthe_00057 hypothetical protein	6.02	6.95	6.43	6.46	-0.41	0.49	-0.93	-0.03	0.24	0.43	-1.03	-0.23	0.2	0.17	0.83
Cthe_02379 hypothetical protein	8.73	9.12	8.64	9.21	0.09	-0.09	-0.39	-0.57	0.63	-0.06	0.77	-1.35	0.2	0.17	0.73
Cthe_00081 arginine biosynthesis bifunctional p	11.19	11.75	11.72	11.38	-0.53	0.37	-0.56	0.34	0.14	0.33	0.2	0.54	0.2	0.17	1.11
Cthe_00021 dethiobiotin synthase	4.64	5.81	4.86	5.09	-0.22	0.72	-1.17	-0.23	0.39	0.63	-1.83	-0.65	0.2	0.17	0.68
Cthe_00873 anthranilate phosphoribosyltransfe	8.63	9.12	9.06	8.81	-0.43	0.31	-0.49	0.25	0.22	0.28	0.43	0.35	0.2	0.17	1.15
Cthe_00021 dethiobiotin synthase	4.64	5.81	4.86	5.09	-0.22	0.72	-1.17	-0.23	0.39	0.63	-1.83	-0.65	0.2	0.17	0.68
Cthe_02207 isoaaspartyl dipeptidase	6.17	7.27	6.78	6.51	-0.61	0.76	-1.1	0.27	0.08	0.66	-1.6	0.4	0.2	0.17	0.72
Cthe_00212 Beta-glucosidase	10.06	10.75	10.75	10.2	-0.69	0.55	-0.69	0.55	0.02	0.48	-0.23	0.98	0.2	0.17	0.85
Cthe_00615 Phenylacetate--CoA ligase	11.13	11.75	11.31	11.64	-0.18	0.11	-0.62	-0.33	0.42	0.11	0	-0.85	0.2	0.17	0.91
Cthe_01345 adenine phosphoribosyltransferase	9.57	10.14	9.35	10.2	0.22	-0.06	-0.57	-0.85	0.74	-0.03	0.17	-1.94	0.2	0.17	0.68
Cthe_00081 arginine biosynthesis bifunctional p	11.19	11.75	11.72	11.38	-0.53	0.37	-0.56	0.34	0.14	0.33	0.2	0.54	0.2	0.17	1.11
Cthe_01937 glutamate racemase	9.55	10.25	9.98	10.02	-0.43	0.23	-0.7	-0.04	0.22	0.21	-0.27	-0.25	0.2	0.17	1.48
Cthe_00081 arginine biosynthesis bifunctional p	11.19	11.75	11.72	11.38	-0.53	0.37	-0.56	0.34	0.14	0.33	0.2	0.54	0.2	0.17	1.11
Cthe_00873 anthranilate phosphoribosyltransfe	8.63	9.12	9.06	8.81	-0.43	0.31	-0.49	0.25	0.22	0.28	0.43	0.35	0.2	0.17	1.15
Cthe_01345 adenine phosphoribosyltransferase	9.57	10.14	9.35	10.2	0.22	-0.06	-0.57	-0.85	0.74	-0.03	0.17	-1.94	0.2	0.17	0.68
Cthe_00615 Phenylacetate--CoA ligase	11.13	11.75	11.31	11.64	-0.18	0.11	-0.62	-0.33	0.42	0.11	0	-0.85	0.2	0.17	0.91
Cthe_00873 anthranilate phosphoribosyltransfe	8.63	9.12	9.06	8.81	-0.43	0.31	-0.49	0.25	0.22	0.28	0.43	0.35	0.2	0.17	1.15
Cthe_00212 Beta-glucosidase	10.06	10.75	10.75	10.2	-0.69	0.55	-0.69	0.55	0.02	0.48	-0.23	0.98	0.2	0.17	0.85
Cthe_00081 arginine biosynthesis bifunctional p	11.19	11.75	11.72	11.38	-0.53	0.37	-0.56	0.34	0.14	0.33	0.2	0.54	0.2	0.17	1.11
Cthe_00021 dethiobiotin synthase	4.64	5.81	4.86	5.09	-0.22	0.72	-1.17	-0.23	0.39	0.63	-1.83	-0.65	0.2	0.17	0.68
Cthe_01937 glutamate racemase	9.55	10.25	9.98	10.02	-0.43	0.23	-0.7	-0.04	0.22	0.21	-0.27	-0.25	0.2	0.17	1.48
Cthe_00081 arginine biosynthesis bifunctional p	11.19	11.75	11.72	11.38	-0.53	0.37	-0.56	0.34	0.14	0.33	0.2	0.54	0.2	0.17	1.11
Cthe_00081 arginine biosynthesis bifunctional p	11.19	11.75	11.72	11.38	-0.53	0.37	-0.56	0.34	0.14	0.33	0.2	0.54	0.2	0.17	1.11
Cthe_00212 Beta-glucosidase	10.06	10.75	10.75	10.2	-0.69	0.55	-0.69	0.55	0.02	0.48	-0.23	0.98	0.2	0.17	0.85
Cthe_00212 Beta-glucosidase	10.06	10.75	10.75	10.2	-0.69	0.55	-0.69	0.55	0.02	0.48	-0.23	0.98	0.2	0.17	0.85
Cthe_00615 Phenylacetate--CoA ligase	11.13	11.75	11.31	11.64	-0.18	0.11	-0.62	-0.33	0.42	0.11	0	-0.85	0.2	0.17	0.91
Cthe_01345 adenine phosphoribosyltransferase	9.57	10.14	9.35	10.2	0.22	-0.06	-0.57	-0.85	0.74	-0.03	0.17	-1.94	0.2	0.17	0.68
Cthe_00212 Beta-glucosidase	10.06	10.75	10.75	10.2	-0.69	0.55	-0.69	0.55	0.02	0.48	-0.23	0.98	0.2	0.17	0.85
Cthe_01345 adenine phosphoribosyltransferase	9.57	10.14	9.35	10.2	0.22	-0.06	-0.57	-0.85	0.74	-0.03	0.17	-1.94	0.2	0.17	0.68
Cthe_01937 glutamate racemase	9.55	10.25	9.98	10.02	-0.43	0.23	-0.7	-0.04	0.22	0.21	-0.27	-0.25	0.2	0.17	1.48
Cthe_01937 glutamate racemase	9.55	10.25	9.98	10.02	-0.43	0.23	-0.7	-0.04	0.22	0.21	-0.27	-0.25	0.2	0.17	1.48
Cthe_01345 adenine phosphoribosyltransferase	9.57	10.14	9.35	10.2	0.22	-0.06	-0.57	-0.85	0.74	-0.03	0.17	-1.94	0.2	0.17	0.68
Cthe_00904 protein-export membrane protein	12.05	12.68	12.52	12.54	-0.47	0.14	-0.63	-0.02	0.19	0.14	-0.03	-0.21	0.18	0.16	1.99
Cthe_00957 preprotein translocase, YajC subun	8.13	8.85	8.49	8.64	-0.36	0.21	-0.72	-0.15	0.28	0.19	-0.33	-0.48	0.18	0.16	1.04
Cthe_00276 D-isomer specific 2-hydroxyacid de	8.23	8.79	8.39	8.73	-0.16	0.06	-0.56	-0.34	0.44	0.07	0.2	-0.88	0.19	0.16	0.88
Cthe_00599 thiazole biosynthesis protein ThiH	9.2	10.21	9.58	9.65	-0.38	0.56	-1.01	-0.07	0.26	0.49	-1.3	-0.31	0.18	0.16	0.74
Cthe_01187 protein of unknown function DUF9	9.17	9.92	9.76	9.6	-0.59	0.32	-0.75	0.16	0.1	0.29	-0.43	0.17	0.18	0.16	1.18
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_02822 oxidoreductase-like protein	11.03	11.5	11.27	11.42	-0.24	0.08	-0.47	-0.15	0.37	0.08	0.5	-0.48	0.18	0.16	0.98
Cthe_02870 protein of unknown function DUF2	8.36	9.03	8.74	8.85	-0.38	0.18	-0.67	-0.11	0.26	0.17	-0.17	-0.4	0.19	0.16	1.28
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.07	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_02059 RNA polymerase, sigma-24 subunit	10.63	11.28	11.2	11.06	-0.57	0.22	-0.65	0.14	0.11	0.2	-0.1	0.13	0.18	0.16	2.49
Cthe_02932 DNA-directed RNA polymerase, alp	13.4	14	13.78	13.88	-0.38	0.12	-0.6	-0.1	0.26	0.12	0.07	-0.38	0.18	0.16	1.32
Cthe_00197 glutamine amidotransferase, class-	6.04	6.41	6.07	6.43	-0.03	-0.02	-0.37	-0.36	0.54	0	0.83	-0.92	0.19	0.16	0.78
Cthe_01170 Dihydrodipicolinate reductase	8.97	9.3	9.18	9.06	-0.21	0.24	-0.33	0.12	0.4	0.22	0.97	0.08	0.18	0.16	0.84
Cthe_02889 phosphoribosyl-AMP cyclohydrolas	7.92	8.64	8.22	8.43	-0.3	0.21	-0.72	-0.21	0.33	0.19	-0.33	-0.6	0.19	0.16	0.99
Cthe_02982 hypothetical protein	7.88	8.61	8.44	8.3	-0.56	0.31	-0.73	0.14	0.12	0.28	-0.37	0.13	0.19	0.16	1.39
Cthe_00913 transposase IS116/IS110/IS902	14.32	15.21	14.9	14.72	-0.58	0.49	-0.89	0.18	0.1	0.43	-0.9	0.21	0.18	0.16	0.85
Cthe_01294 Recombinase	7.36	8.08	7.31	7.95	0.05	0.13	-0.72	-0.64	0.6	0.13	-0.33	-1.5	0.18	0.16	0.71
Cthe_00276 D-isomer specific 2-hydroxyacid de	8.23	8.79	8.39	8.73	-0.16	0.06	-0.56	-0.34	0.44	0.07	0.2	-0.88	0.19	0.16	0.88
Cthe_00599 thiazole biosynthesis protein ThiH	9.2	10.21	9.58	9.65	-0.38	0.56	-1.01	-0.07	0.26	0.49	-1.3	-0.31	0.18	0.16	0.74
Cthe_02035	6.52	7.01	6.57	7.01	-0.05	0	-0.49	-0.44	0.52	0.02	0.43	-1.08	0.19	0.16	0.8
Cthe_01085 glycosyl transferase, group 1	4.09	5	4.64	4.91	-0.55	0.09	-0.91	-0.27	0.13	0.09	-0.97	-0.73	0.18	0.16	0.23
Cthe_02982 hypothetical protein	7.88	8.61	8.44	8.3	-0.56	0.31	-0.73	0.14	0.12	0.28	-0.37	0.13	0.19	0.16	1.39
Cthe_01347 GatB/YqeY	13.86	14.3	14.04	14.26	-0.18	0.04	-0.44	-0.22	0.42	0.05	0.6	-0.63	0.18	0.16	0.87
Cthe_01494 protein of unknown function DUF6	4.86	5.25	4.95	5.25	-0.09	0	-0.39	-0.3	0.49	0.02	0.77	-0.79	0.18	0.16	0.79
Cthe_02312 hypothetical protein	12.7	13.4	13.45	12.79	-0.75	0.61	-0.7	0.66	-0.03	0.53	-0.27	1.21	0.18	0.16	0.76
Cthe_00765 ribosomal protein L19	12.58	13.19	13.1	13.05	-0.52	0.14	-0.61	0.05	0.15	0.14	0.03	-0.06	0.19	0.16	5.46
Cthe_00769 ribosomal protein S16	8.18	8.89	8.69	8.64	-0.51	0.25	-0.71	0.05	0.16	0.23	-0.3	-0.06	0.19	0.16	1.64
Cthe_01312 glycyl-tRNA synthetase	12.13	12.78	12.64	12.61	-0.51	0.17	-0.65	0.03	0.16	0.16	-0.1	-0.1	0.19	0.16	2.86
Cthe_01343 D-tyrosyl-tRNA(Tyr) deacylase	7.5	7.84	7.57	7.83	-0.07	0.01	-0.34	-0.26	0.51	0.03	0.93	-0.71	0.18	0.16	0.78
Cthe_02721 ribosomal protein L1	13.38	13.96	13.69	13.85	-0.31	0.11	-0.58	-0.16	0.32	0.11	0.13	-0.5	0.19	0.16	1.17
Cthe_02931 ribosomal protein S4	12.41	13.09	12.77	12.91	-0.36	0.18	-0.68	-0.14	0.28	0.17	-0.2	-0.46	0.19	0.16	1.17
Cthe_00088 cell shape determining protein, Mr	8.89	9.51	9.13	9.4	-0.24	0.11	-0.62	-0.27	0.37	0.11	0	-0.73	0.18	0.16	0.94
Cthe_00276 D-isomer specific 2-hydroxyacid de	8.23	8.79	8.39	8.73	-0.16	0.06	-0.56	-0.34	0.44	0.07	0.2	-0.88	0.19	0.16	0.88
Cthe_02390 pyruvate/ketoisovalerate oxidore	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_03147 ABC transporter related protein	8.42	8.93	8.53	8.93	-0.11	0	-0.51	-0.4							



Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02721 ribosomal protein L1	13.38	13.96	13.69	13.85	-0.31	0.11	-0.58	-0.16	0.32	0.11	0.13	-0.5	0.19	0.16	1.17
Cthe_02931 ribosomal protein S4	12.41	13.09	12.77	12.91	-0.36	0.18	-0.68	-0.14	0.28	0.17	-0.2	-0.46	0.19	0.16	1.17
Cthe_01170 Dihydropicolinate reductase	8.97	9.3	9.18	9.06	-0.21	0.24	-0.33	0.12	0.4	0.22	0.97	0.08	0.18	0.16	0.84
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_02889 phosphoribosyl-AMP cyclohydrolas	7.92	8.64	8.22	8.43	-0.3	0.21	-0.72	-0.21	0.33	0.19	-0.33	-0.6	0.19	0.16	0.99
Cthe_01312 glycyl-tRNA synthetase	12.13	12.78	12.64	12.61	-0.51	0.17	-0.65	0.03	0.16	0.16	-0.1	-0.1	0.19	0.16	2.86
Cthe_02932 DNA-directed RNA polymerase, alp	13.4	14	13.78	13.88	-0.38	0.12	-0.6	-0.1	0.26	0.12	0.07	-0.38	0.18	0.16	1.32
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_01312 glycyl-tRNA synthetase	12.13	12.78	12.64	12.61	-0.51	0.17	-0.65	0.03	0.16	0.16	-0.1	-0.1	0.19	0.16	2.86
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_00765 ribosomal protein L19	12.58	13.19	13.1	13.05	-0.52	0.14	-0.61	0.05	0.15	0.14	0.03	-0.06	0.19	0.16	5.46
Cthe_00769 ribosomal protein S16	8.18	8.89	8.69	8.64	-0.51	0.25	-0.71	0.05	0.16	0.23	-0.3	-0.06	0.19	0.16	1.64
Cthe_02721 ribosomal protein L1	13.38	13.96	13.69	13.85	-0.31	0.11	-0.58	-0.16	0.32	0.11	0.13	-0.5	0.19	0.16	1.17
Cthe_02931 ribosomal protein S4	12.41	13.09	12.77	12.91	-0.36	0.18	-0.68	-0.14	0.28	0.17	-0.2	-0.46	0.19	0.16	1.17
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_00904 protein-export membrane protein	12.05	12.68	12.52	12.54	-0.47	0.14	-0.63	-0.02	0.19	0.14	-0.03	-0.21	0.18	0.16	1.99
Cthe_00957 preprotein translocase, YajC subun	8.13	8.85	8.49	8.64	-0.36	0.21	-0.72	-0.15	0.28	0.19	-0.33	-0.48	0.18	0.16	1.04
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_00276 D-isomer specific 2-hydroxyacid de	8.23	8.79	8.39	8.73	-0.16	0.06	-0.56	-0.34	0.44	0.07	0.2	-0.88	0.19	0.16	0.88
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_01170 Dihydropicolinate reductase	8.97	9.3	9.18	9.06	-0.21	0.24	-0.33	0.12	0.4	0.22	0.97	0.08	0.18	0.16	0.84
Cthe_01312 glycyl-tRNA synthetase	12.13	12.78	12.64	12.61	-0.51	0.17	-0.65	0.03	0.16	0.16	-0.1	-0.1	0.19	0.16	2.86
Cthe_00068 Peptidylprolyl isomerase	10.39	10.95	10.91	10.68	-0.52	0.27	-0.56	0.23	0.15	0.25	0.2	0.31	0.19	0.16	1.41
Cthe_01343 D-tyrosyl-tRNA(Tyr) deacylase	7.5	7.84	7.57	7.83	-0.07	0.01	-0.34	-0.26	0.51	0.03	0.93	-0.71	0.18	0.16	0.78
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_02889 phosphoribosyl-AMP cyclohydrolas	7.92	8.64	8.22	8.43	-0.3	0.21	-0.72	-0.21	0.33	0.19	-0.33	-0.6	0.19	0.16	0.99
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02889 phosphoribosyl-AMP cyclohydrolas	7.92	8.64	8.22	8.43	-0.3	0.21	-0.72	-0.21	0.33	0.19	-0.33	-0.6	0.19	0.16	0.99
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_02990 peptide methionine sulfoxide redu	9.93	10.62	10.63	10.15	-0.7	0.47	-0.69	0.48	0.01	0.42	-0.23	0.83	0.18	0.16	0.87
Cthe_02932 DNA-directed RNA polymerase, alp	13.4	14	13.78	13.88	-0.38	0.12	-0.6	-0.1	0.26	0.12	0.07	-0.38	0.18	0.16	1.32
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_02889 phosphoribosyl-AMP cyclohydrolas	7.92	8.64	8.22	8.43	-0.3	0.21	-0.72	-0.21	0.33	0.19	-0.33	-0.6	0.19	0.16	0.99
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_00276 D-isomer specific 2-hydroxyacid de	8.23	8.79	8.39	8.73	-0.16	0.06	-0.56	-0.34	0.44	0.07	0.2	-0.88	0.19	0.16	0.88
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_01170 Dihydropicolinate reductase	8.97	9.3	9.18	9.06	-0.21	0.24	-0.33	0.12	0.4	0.22	0.97	0.08	0.18	0.16	0.84
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_01170 Dihydropicolinate reductase	8.97	9.3	9.18	9.06	-0.21	0.24	-0.33	0.12	0.4	0.22	0.97	0.08	0.18	0.16	0.84
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38									



Cthe_01170 Dihydrodipicolinate reductase	8.97	9.3	9.18	9.06	-0.21	0.24	-0.33	0.12	0.4	0.22	0.97	0.08	0.18	0.16	0.84
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_02359 metal dependent phosphohydrolas	8.64	9.19	9.09	9.06	-0.45	0.13	-0.55	0.03	0.21	0.13	0.23	-0.1	0.18	0.16	1.76
Cthe_03090 hydro-lyases, Fe-S type, tartrate/fu	7.01	7.89	7.26	7.51	-0.25	0.38	-0.88	-0.25	0.37	0.34	-0.87	-0.69	0.19	0.16	0.81
Cthe_02390 pyruvate/ketoisovalerate oxidored	10.58	11.4	11.12	11.52	-0.54	-0.12	-0.82	-0.4	0.13	-0.08	-0.67	-1	0.18	0.16	0.23
Cthe_00140 phosphoglycerate mutase,	15.63	16.31	16.33	15.76	-0.7	0.55	-0.68	0.57	0.01	0.48	-0.2	1.02	0.19	0.16	0.82
Cthe_00319 class II aldolase/adducin-like protei	8.7	9.13	9.38	9.16	-0.68	-0.03	-0.43	0.22	0.02	-0.01	0.63	0.29	0.17	0.15	0.06
Cthe_02735 HPrNtr domain containing protein	6.09	6.75	6.67	6.54	-0.58	0.21	-0.66	0.13	0.1	0.19	-0.13	0.1	0.17	0.15	2.34
Cthe_01513 DNA adenine methylase	7.48	8.19	7.9	7.99	-0.42	0.2	-0.71	-0.09	0.23	0.19	-0.3	-0.35	0.17	0.15	1.16
Cthe_01295 5-formyltetrahydrofolate cyclo-liga	9.08	9.39	9.38	8.91	-0.3	0.48	-0.31	0.47	0.33	0.42	1.03	0.81	0.17	0.15	0.73
Cthe_02767 Methyltransferase type 12	9.02	9.69	9.68	9.27	-0.66	0.42	-0.67	0.41	0.04	0.37	-0.17	0.69	0.17	0.15	0.94
Cthe_03177 hypothetical protein	10.7	11.37	11.32	11.07	-0.62	0.3	-0.67	0.25	0.07	0.27	-0.17	0.35	0.17	0.15	1.28
Cthe_01304 PhoH-like protein	8.67	9.36	8.91	9.2	-0.24	0.16	-0.69	-0.29	0.37	0.15	-0.23	-0.77	0.17	0.15	0.89
Cthe_02061 hypothetical protein	10.29	10.77	10.77	10.38	-0.48	0.39	-0.48	0.39	0.18	0.35	0.47	0.65	0.17	0.15	0.88
Cthe_00701 conserved carboxylase region cont	16.07	16.85	16.76	16.42	-0.69	0.43	-0.78	0.34	0.02	0.38	-0.53	0.54	0.17	0.15	0.9
Cthe_01062 VanW	10.34	10.96	11.24	9.98	-0.9	0.98	-0.62	1.26	-0.15	0.85	0	2.46	0.17	0.15	0.63
Cthe_00154 protein of unknown function DUF1	6.93	7.58	7.55	7.27	-0.62	0.31	-0.65	0.28	0.07	0.28	-0.7	0.42	0.17	0.15	1.19
Cthe_01898 hypothetical protein	8.18	8.57	8.34	8.54	-0.16	0.03	-0.39	-0.2	0.44	0.04	0.77	-0.58	0.17	0.15	0.82
Cthe_02856 hypothetical protein	5.04	5.75	5.78	5.21	-0.74	0.54	-0.71	0.57	-0.02	0.47	-0.3	1.02	0.17	0.15	0.79
Cthe_00701 conserved carboxylase region cont	16.07	16.85	16.76	16.42	-0.69	0.43	-0.78	0.34	0.02	0.38	-0.53	0.54	0.17	0.15	0.9
Cthe_01513 DNA adenine methylase	7.48	8.19	7.9	7.99	-0.42	0.2	-0.71	-0.09	0.23	0.19	-0.3	-0.35	0.17	0.15	1.16
Cthe_00319 class II aldolase/adducin-like protei	8.7	9.13	9.38	9.16	-0.68	-0.03	-0.43	0.22	0.02	-0.01	0.63	0.29	0.17	0.15	0.06
Cthe_01295 5-formyltetrahydrofolate cyclo-liga	9.08	9.39	9.38	8.91	-0.3	0.48	-0.31	0.47	0.33	0.42	1.03	0.81	0.17	0.15	0.73
Cthe_00701 conserved carboxylase region cont	16.07	16.85	16.76	16.42	-0.69	0.43	-0.78	0.34	0.02	0.38	-0.53	0.54	0.17	0.15	0.9
Cthe_00319 class II aldolase/adducin-like protei	8.7	9.13	9.38	9.16	-0.68	-0.03	-0.43	0.22	0.02	-0.01	0.63	0.29	0.17	0.15	0.06
Cthe_00701 conserved carboxylase region cont	16.07	16.85	16.76	16.42	-0.69	0.43	-0.78	0.34	0.02	0.38	-0.53	0.54	0.17	0.15	0.9
Cthe_01295 5-formyltetrahydrofolate cyclo-liga	9.08	9.39	9.38	8.91	-0.3	0.48	-0.31	0.47	0.33	0.42	1.03	0.81	0.17	0.15	0.73
Cthe_00701 conserved carboxylase region cont	16.07	16.85	16.76	16.42	-0.69	0.43	-0.78	0.34	0.02	0.38	-0.53	0.54	0.17	0.15	0.9
Cthe_00319 class II aldolase/adducin-like protei	8.7	9.13	9.38	9.16	-0.68	-0.03	-0.43	0.22	0.02	-0.01	0.63	0.29	0.17	0.15	0.06
Cthe_01295 5-formyltetrahydrofolate cyclo-liga	9.08	9.39	9.38	8.91	-0.3	0.48	-0.31	0.47	0.33	0.42	1.03	0.81	0.17	0.15	0.73
Cthe_00708 FAD dependent oxidoreductase	9.87	10.38	10.11	10.35	-0.24	0.03	-0.51	-0.24	0.37	0.04	0.37	-0.67	0.16	0.14	0.87
Cthe_01400 glycosyl hydrolase 53	9.57	10.15	10.2	9.68	-0.63	0.47	-0.58	0.52	0.06	0.42	0.13	0.92	0.16	0.14	0.82
Cthe_00805 response regulator receiver protein	7.73	8.48	8.25	8.22	-0.52	0.26	-0.75	0.03	0.15	0.24	-0.43	-0.1	0.16	0.14	1.14
Cthe_01819 ABC transporter related protein	2	3.58	2.81	2.32	-0.81	1.26	-1.58	0.49	-0.08	1.08	-3.2	0.85	0.16	0.14	0.58
Cthe_02371 chromosomal replication initiator p	10.48	11.16	10.88	11	-0.4	0.16	-0.68	-0.12	0.25	0.15	-0.2	-0.42	0.16	0.14	1.12
Cthe_02410 protein of unknown function DUF3	9.64	10.03	9.47	10.29	0.17	-0.26	-0.39	-0.82	0.7	-0.2	0.77	-1.87	0.16	0.14	0.64
Cthe_00034 cyclic nucleotide-binding protein	7.79	8.36	8.41	7.89	-0.62	0.47	-0.57	0.52	0.07	0.42	0.17	0.92	0.16	0.14	0.81
Cthe_00805 response regulator receiver protein	7.73	8.48	8.25	8.22	-0.52	0.26	-0.75	0.03	0.15	0.24	-0.43	-0.1	0.16	0.14	1.14
Cthe_00991 bacterial translation initiation facto	12.11	13.1	12.45	12.6	-0.34	0.5	-0.99	-0.15	0.29	0.44	-1.23	-0.48	0.16	0.14	0.71
Cthe_02608 ATP synthase F1, beta subunit	10.47	11.27	10.78	11	-0.31	0.27	-0.8	-0.22	0.32	0.25	-0.6	-0.63	0.16	0.14	0.83
Cthe_02937 cobalt transport protein	7.52	7.94	7.71	7.92	-0.19	0.02	-0.42	-0.21	0.41	0.03	0.67	-0.6	0.16	0.14	0.82
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_03013 hydrogenase expression/formation	8.75	9.82	9.37	9.16	-0.62	0.66	-1.07	0.21	0.07	0.58	-1.5	0.27	0.16	0.14	0.68
Cthe_00778 hypothetical protein	9.56	9.97	9.86	9.83	-0.3	0.14	-0.41	0.03	0.33	0.14	0.7	-0.1	0.16	0.14	0.91
Cthe_01897 hypothetical protein	5.75	6.02	5.81	5.98	-0.06	0.04	-0.27	-0.17	0.52	0.05	1.17	-0.52	0.16	0.14	0.73
Cthe_00226 hypothetical protein	6.41	6.34	6.61	6.69	-0.2	-0.35	0.07	-0.08	0.4	-0.28	2.3	-0.33	0.16	0.14	0.38
Cthe_01819 ABC transporter related protein	2	3.58	2.81	2.32	-0.81	1.26	-1.58	0.49	-0.08	1.08	-3.2	0.85	0.16	0.14	0.58
Cthe_02937 cobalt transport protein	7.52	7.94	7.71	7.92	-0.19	0.02	-0.42	-0.21	0.41	0.03	0.67	-0.6	0.16	0.14	0.82
Cthe_02937 cobalt transport protein	7.52	7.94	7.71	7.92	-0.19	0.02	-0.42	-0.21	0.41	0.03	0.67	-0.6	0.16	0.14	0.82
Cthe_01819 ABC transporter related protein	2	3.58	2.81	2.32	-0.81	1.26	-1.58	0.49	-0.08	1.08	-3.2	0.85	0.16	0.14	0.58
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_02608 ATP synthase F1, beta subunit	10.47	11.27	10.78	11	-0.31	0.27	-0.8	-0.22	0.32	0.25	-0.6	-0.63	0.16	0.14	0.83
Cthe_02608 ATP synthase F1, beta subunit	10.47	11.27	10.78	11	-0.31	0.27	-0.8	-0.22	0.32	0.25	-0.6	-0.63	0.16	0.14	0.83
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_02608 ATP synthase F1, beta subunit	10.47	11.27	10.78	11	-0.31	0.27	-0.8	-0.22	0.32	0.25	-0.6	-0.63	0.16	0.14	0.83
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_00699 carboxyl transferase	13.37	14.22	14.05	13.76	-0.68	0.46	-0.85	0.29	0.02	0.41	-0.77	0.44	0.16	0.14	0.83
Cthe_02608 ATP synthase F1, beta subunit	10.47	11.27	10.78	11	-0.31	0.27	-0.8	-0.22	0.32	0.25	-0.6	-0.63	0.16	0.14	0.83
Cthe_01301 protein of unknown function DUF7	8.34	9.06	9.1	8.57	-0.76	0.49	-0.72	0.53	-0.04	0.43	-0.33	0.94	0.15	0.13	0.77
Cthe_01433 short-chain dehydrogenase/reduct	15.09	15.89	16.03	15.24	-0.94	0.65	-0.8	0.79	-0.18	0.57	-0.6	1.48	0.15	0.13	0.67
Cthe_00639 glycoside hydrolase, family 13-like	10.16	10.8	10.79	10.5	-0.63	0.3	-0.64	0.29	0.06	0.27	-0.07	0.44	0.15	0.13	1.11
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00706 transcriptional regulator, RpiR fami	10.81	11.21	10.99	11.22	-0.18	-0.01	-0.4	-0.23	0.42	0.01	0.73	-0.65	0.15	0.13	0.77
Cthe_02667 transcriptional regulator, TetR fami	4.75	5.83	4.75	5.32	0	0.51	-1.08	-0.57	0.56	0.45	-1.53	-1.35	0.15	0.13	0.63
Cthe_01817 urease, beta subunit	2.32	4.25	3.81	3.17	-1.49	1.08	-1.93	0.64	-0.62	0.93	-4.37	1.17	0.15	0.13	0.44
Cthe_00814 DNA repair protein RecN	9.2	9.87	9.2	9.82	0	0.05	-0.67	-0.62	0.56	0.06	-0.17	-1.46	0.15	0.13	0.68
Cthe_01433 short-chain dehydrogenase/reduct	15.09	15.89	16.03	15.24	-0.94	0.65	-0.8	0.79	-0.18	0.57	-0.6	1.48	0.15	0.13	0.67
Cthe_00025 adenosylmethionine-8-amino-7-ox	7.53	8.27	8.48	7.55	-0.95	0.72	-0.74	0.93	-0.19	0.63	-0.4	1.77	0.15	0.13	0.65
Cthe_01498 methyl-accepting chemotaxis senso	6.82	7.73	7.13	7.71	-0.31	0.02	-0.91	-0.58	0.32	0.03	-0.97	-1.37	0.15	0.13	0.34
Cthe_01247 phosphoribosylglycinamide formylt	8.27	9.06	8.78	9.26	-0.51	-0.2	-0.79	-0.48	0.16	-0.15	-0.57	-1.17	0.15	0.13	0.3
Cthe_00881 diguanylate cyclase	11.52	11.91	12.17	11.79	-0.65	0.12	-0.39	0.38	0.05	0.12	0.77	0.63	0.15	0.13	0.23
Cthe_01498 methyl-accepting chemotaxis senso	6.82	7.73	7.13	7.71	-0.31	0.02	-0.91	-0.58	0.32	0.03	-0.97	-1.37	0.15	0.13	0.34
Cthe_02150 integral membrane protein-like pro	11.56	12.23	11.94	12.09	-0.38	0.14	-0.67	-0.15	0.26	0.14	-0.17	-0.48	0.15	0.13	1.04
Cthe_01451 GCN5-related N-acetyltransferase	8.14	8.68	8.84	7.97	-0.7	0.71	-0.54	0.87	0.01	0.62					



Cthe_02936 ABC transporter related protein	7.36	8.02	7.74	7.89	-0.38	0.13	-0.66	-0.15	0.26	0.13	-0.13	-0.48	0.15	0.13	1.04
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_02065 cysteinyl-tRNA synthetase	13.37	14.25	14.13	13.73	-0.76	0.52	-0.88	0.4	-0.04	0.46	-0.87	0.67	0.15	0.13	0.75
Cthe_02936 ABC transporter related protein	7.36	8.02	7.74	7.89	-0.38	0.13	-0.66	-0.15	0.26	0.13	-0.13	-0.48	0.15	0.13	1.04
Cthe_02370 ribosomal protein L34	7.73	7.81	7.58	7.8	0.15	0.01	-0.08	-0.22	0.68	0.03	1.8	-0.63	0.15	0.13	0.64
Cthe_02728 ribosomal protein S7	11.98	12.52	12.06	12.56	-0.08	-0.04	-0.54	-0.5	0.5	-0.02	0.27	-1.21	0.15	0.13	0.72
Cthe_02928 ribosomal protein L36	6.64	7.25	7.2	7.14	-0.56	0.11	-0.61	0.06	0.12	0.11	0.03	-0.04	0.15	0.13	5.81
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00025 adenosylmethionine-8-amino-7-ox	7.53	8.27	8.48	7.55	-0.95	0.72	-0.74	0.93	-0.19	0.63	-0.4	1.77	0.15	0.13	0.65
Cthe_01247 phosphoribosylglycinamide formylt	8.27	9.06	8.78	9.26	-0.51	-0.2	-0.79	-0.48	0.16	-0.15	-0.57	-1.17	0.15	0.13	0.3
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_01433 short-chain dehydrogenase/reduct	15.09	15.89	16.03	15.24	-0.94	0.65	-0.8	0.79	-0.18	0.57	-0.6	1.48	0.15	0.13	0.67
Cthe_01512 Type II site-specific deoxyribonucle	7.08	7.9	7.61	7.56	-0.53	0.34	-0.82	0.05	0.14	0.31	-0.67	-0.06	0.15	0.13	0.9
Cthe_00036 hybrid cluster protein	7.75	8.53	8.52	8.08	-0.77	0.45	-0.78	0.44	-0.05	0.4	-0.53	0.75	0.15	0.13	0.78
Cthe_01817 urease, beta subunit	2.32	4.25	3.81	3.17	-1.49	1.08	-1.93	0.64	-0.62	0.93	-4.37	1.17	0.15	0.13	0.44
Cthe_00614 pyruvate ferredoxin/flavodoxin oxi	9.76	10.26	9.82	10.36	-0.06	-0.1	-0.5	-0.54	0.52	-0.07	0.4	-1.29	0.15	0.13	0.69
Cthe_00025 adenosylmethionine-8-amino-7-ox	7.53	8.27	8.48	7.55	-0.95	0.72	-0.74	0.93	-0.19	0.63	-0.4	1.77	0.15	0.13	0.65
Cthe_02065 cysteinyl-tRNA synthetase	13.37	14.25	14.13	13.73	-0.76	0.52	-0.88	0.4	-0.04	0.46	-0.87	0.67	0.15	0.13	0.75
Cthe_01247 phosphoribosylglycinamide formylt	8.27	9.06	8.78	9.26	-0.51	-0.2	-0.79	-0.48	0.16	-0.15	-0.57	-1.17	0.15	0.13	0.3
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00025 adenosylmethionine-8-amino-7-ox	7.53	8.27	8.48	7.55	-0.95	0.72	-0.74	0.93	-0.19	0.63	-0.4	1.77	0.15	0.13	0.65
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_01433 short-chain dehydrogenase/reduct	15.09	15.89	16.03	15.24	-0.94	0.65	-0.8	0.79	-0.18	0.57	-0.6	1.48	0.15	0.13	0.67
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_01817 urease, beta subunit	2.32	4.25	3.81	3.17	-1.49	1.08	-1.93	0.64	-0.62	0.93	-4.37	1.17	0.15	0.13	0.44
Cthe_02065 cysteinyl-tRNA synthetase	13.37	14.25	14.13	13.73	-0.76	0.52	-0.88	0.4	-0.04	0.46	-0.87	0.67	0.15	0.13	0.75
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_01247 phosphoribosylglycinamide formylt	8.27	9.06	8.78	9.26	-0.51	-0.2	-0.79	-0.48	0.16	-0.15	-0.57	-1.17	0.15	0.13	0.3
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_01247 phosphoribosylglycinamide formylt	8.27	9.06	8.78	9.26	-0.51	-0.2	-0.79	-0.48	0.16	-0.15	-0.57	-1.17	0.15	0.13	0.3
Cthe_00707 Phosphoglycerate mutase	10.26	10.71	10.35	10.79	-0.09	-0.08	-0.45	-0.44	0.49	-0.05	0.57	-1.08	0.15	0.13	0.72
Cthe_02220 NAD-dependent epimerase/dehydr	7.91	9.13	8.3	8.67	-0.39	0.46	-1.22	-0.37	0.25	0.41	-2	-0.94	0.14	0.12	0.39
Cthe_00933 acyl carrier protein	13.27	13.9	13.89	13.67	-0.62	0.23	-0.63	0.22	0.07	0.21	-0.03	0.29	0.14	0.12	1.36
Cthe_01959 Methyltransferase type 11	7.08	7.71	7.33	7.66	-0.25	0.05	-0.63	-0.33	0.37	0.06	-0.03	-0.85	0.14	0.12	0.79
Cthe_02220 NAD-dependent epimerase/dehydr	7.91	9.13	8.3	8.67	-0.39	0.46	-1.22	-0.37	0.25	0.41	-2	-0.94	0.14	0.12	0.39
Cthe_02187 ribosomal protein S6	11.33	11.81	11.62	11.79	-0.29	0.02	-0.48	-0.17	0.33	0.03	0.47	-0.52	0.14	0.12	0.84
Cthe_00283 aldo/keto reductase	14.75	15.62	15.63	15.06	-0.88	0.56	-0.87	0.57	-0.13	0.49	-0.83	1.02	0.14	0.12	0.69
Cthe_02790 ABC transporter related protein	2.58	4	3.81	3.46	-1.23	0.54	-1.42	0.35	-0.41	0.47	-2.67	0.56	0.14	0.12	0.41
Cthe_02803 binding-protein-dependent transpo	6.94	7.53	7.64	6.98	-0.7	0.55	-0.59	0.66	0.01	0.48	0.1	1.21	0.14	0.12	0.71
Cthe_00933 acyl carrier protein	13.27	13.9	13.89	13.67	-0.62	0.23	-0.63	0.22	0.07	0.21	-0.03	0.29	0.14	0.12	1.36
Cthe_03104 putative CoA-substrate-specific enz	10.2	10.85	10.96	10.31	-0.76	0.54	-0.65	0.65	-0.04	0.47	-0.1	1.19	0.14	0.12	0.71
Cthe_00333 hypothetical protein	8.47	8.95	8.92	8.73	-0.45	0.22	-0.48	0.19	0.21	0.2	0.47	0.23	0.14	0.12	0.99
Cthe_00972 hypothetical protein	6.15	6.54	6.27	6.63	-0.12	-0.09	-0.39	-0.36	0.47	-0.06	0.77	-0.92	0.14	0.12	0.71
Cthe_00705 hypothetical protein	7.86	8.2	7.83	8.42	0.03	-0.22	-0.34	-0.59	0.59	-0.17	0.93	-1.4	0.14	0.12	0.65
Cthe_02871 TipAS antibiotic-recognition	6.09	6.86	6.78	6.49	-0.69	0.37	-0.77	0.29	0.02	0.33	-0.5	0.44	0.14	0.12	0.89
Cthe_02311 hypothetical protein	14.99	15.85	15.95	15.25	-0.96	0.6	-0.86	0.7	-0.2	0.53	-0.8	1.29	0.14	0.12	0.67
Cthe_01017 hypothetical protein	6.23	6.89	6.82	6.74	-0.59	0.15	-0.66	0.08	0.1	0.14	-0.13	0	0.14	0.12	2.36
Cthe_01834 hypothetical protein	8.29	8.7	8.19	8.95	0.1	-0.25	-0.41	-0.76	0.64	-0.19	0.7	-1.75	0.14	0.12	0.63
Cthe_02790 ABC transporter related protein	2.58	4	3.81	3.46	-1.23	0.54	-1.42	0.35	-0.41	0.47	-2.67	0.56	0.14	0.12	0.41
Cthe_02803 binding-protein-dependent transpo	6.94	7.53	7.64	6.98	-0.7	0.55	-0.59	0.66	0.01	0.48	0.1	1.21	0.14	0.12	0.71
Cthe_02187 ribosomal protein S6	11.33	11.81	11.62	11.79	-0.29	0.02	-0.48	-0.17	0.33	0.03	0.47	-0.52	0.14	0.12	0.84
Cthe_01215 permease	5.13	6.25	6.09	5.95	-0.96	0.3	-1.12	0.14	-0.2	0.27	-1.67	0.13	0.13	0.11	0.36
Cthe_02768 metallophosphoesterase	9.67	9.99	10.23	9.8	-0.56	0.19	-0.32	0.43	0.12	0.18	1	0.73	0.13	0.11	0.31
Cthe_00067 Silent information regulator protei	11.18	12.01	12.01	11.55	-0.83	0.46	-0.83	0.46	-0.1	0.41	-0.7	0.79	0.13	0.11	0.71
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_02786 methyltransferase MtaA/CmuA fam	3.81	3.81	3.7	3.46	0.11	0.35	0	0.24	0.65	0.31	2.07	0.33	0.13	0.11	0.61
Cthe_00979 Peptidoglycan glycosyltransferase	10.3	10.79	10.47	10.86	-0.17	-0.07	-0.49	-0.39	0.43	-0.04	0.43	-0.98	0.13	0.11	0.72
Cthe_03005 Peptidoglycan-binding LysM	2.81	3	2.81	3	0	0	-0.19	-0.19	0.56	0.02	1.43	-0.56	0.13	0.11	0.65
Cthe_02076 periplasmic sensor signal transduct	11.65	12.3	12.3	12.05	-0.65	0.25	-0.65	0.25	0.05	0.23	-0.1	0.35	0.13	0.11	1.15
Cthe_02814 periplasmic sensor signal transduct	7.76	8.55	8.44	8.2	-0.68	0.35	-0.79	0.24	0.02	0.31	-0.57	0.33	0.13	0.11	0.84
Cthe_02070 hypothetical protein	9.44	9.95	9.87	9.86	-0.43	0.09	-0.51	0.01	0.22	0.09	0.37	-0.15	0.13	0.11	1.06
Cthe_00152 aldo/keto reductase	9.59	10.09	10.05	9.95	-0.46	0.14	-0.5	0.1	0.2	0.14	0.4	0.04	0.13	0.11	1.08
Cthe_01803 cobalamin (vitamin B12) biosynthe	11.16	11.85	11.62	11.7	-0.46	0.15	-0.69	-0.08	0.2	0.14	-0.23	-0.33	0.13	0.11	1.08
Cthe_02534 sulfate ABC transporter, ATPase su	3.32	4.17	4.75	3.17	-1.43	1	-0.85	1.58	-0.57	0.86	-0.77	3.13	0.13	0.11	0.57
Cthe_00384 ABC transporter related protein	8.04	8.7	8.38	8.6	-0.34	0.1	-0.66	-0.22	0.29	0.1	-0.13	-0.63	0.13	0.11	0.85
Cthe_03015 hydrogenase assembly chaperone	6.27	7.68	6.85	6.69	-0.58	0.99	-1.41	-0.16	0.1	0.86	-2.63	0.17	0.13	0.11	0.59
Cthe_01468 hypothetical protein	8.13	8.73	8.38	8.71	-0.25	0.02	-0.6	-0.33	0.37	0.03	0.07	-0.85	0.13	0.11	0.78
Cthe_02030 intein	7.81	8.26	8.66	8.08	-0.85	0.18	-0.45	0.58	-0.11	0.17	0.57	1.04	0.13	0.11	0.3
Cthe_02745 hypothetical protein	9.46	10.13	10.29	9.56	-0.83	0.57	-0.67	0.73	-0.1	0.5	-0.17	1.35	0.13	0.11	0.67
Cthe_00528 hypothetical protein	6.21	6.52	6.25	6.66	-0.04	-0.14	-0.31	-0.41	0.53	-0.1	1.03	-1.02	0.13	0.11	0.66
Cthe_00384 ABC transporter related protein	8.04	8.7	8.38	8.6	-0.34	0.1	-0.66	-0.22	0.29	0.1	-0.13	-0.63	0.13	0.11	0.85
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.				



Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_00067 Silent information regulator protei	11.18	12.01	12.01	11.55	-0.83	0.46	-0.83	0.46	-0.1	0.41	-0.7	0.79	0.13	0.11	0.71
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_01918 Orn/Lys/Arg decarboxylase, major	12.64	13.34	13.04	13.19	-0.4	0.15	-0.7	-0.15	0.25	0.14	-0.27	-0.48	0.13	0.11	0.93
Cthe_00067 Silent information regulator protei	11.18	12.01	12.01	11.55	-0.83	0.46	-0.83	0.46	-0.1	0.41	-0.7	0.79	0.13	0.11	0.71
Cthe_00067 Silent information regulator protei	11.18	12.01	12.01	11.55	-0.83	0.46	-0.83	0.46	-0.1	0.41	-0.7	0.79	0.13	0.11	0.71
Cthe_02073 amidohydrolase	8.55	9.01	9.21	8.99	-0.66	0.02	-0.46	0.22	0.04	0.03	0.53	0.29	0.12	0.1	0.15
Cthe_02681 serine phosphatase	8.6	9.09	9.27	8.43	-0.67	0.66	-0.49	0.84	0.03	0.58	0.43	1.58	0.12	0.1	0.63
Cthe_01884 transposase IS116/IS110/IS902	8.92	10.08	9.84	9.31	-0.92	0.77	-1.16	0.53	-0.17	0.67	-1.8	0.94	0.12	0.1	0.61
Cthe_02959	9.99	10.38	10.56	9.65	-0.57	0.73	-0.39	0.91	0.11	0.64	0.77	1.73	0.12	0.1	0.61
Cthe_02154 Methyltransferase type 11	8.65	9.44	9.15	9.49	-0.5	-0.05	-0.79	-0.34	0.17	-0.03	-0.57	-0.88	0.12	0.1	0.29
Cthe_01234 methyl-accepting chemotaxis senso	7.37	8.13	7.15	8.1	0.22	0.03	-0.76	-0.95	0.74	0.04	-0.47	-2.15	0.12	0.1	0.6
Cthe_02397 hypothetical protein	6.73	7.31	6.97	7.31	-0.24	0	-0.58	-0.34	0.37	0.02	0.13	-0.88	0.12	0.1	0.74
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00891 response regulator receiver protein	8.9	9.49	9.51	9.3	-0.61	0.19	-0.59	0.21	0.08	0.18	0.1	0.27	0.12	0.1	1.22
Cthe_01234 methyl-accepting chemotaxis senso	7.37	8.13	7.15	8.1	0.22	0.03	-0.76	-0.95	0.74	0.04	-0.47	-2.15	0.12	0.1	0.6
Cthe_02681 serine phosphatase	8.6	9.09	9.27	8.43	-0.67	0.66	-0.49	0.84	0.03	0.58	0.43	1.58	0.12	0.1	0.63
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_01208 GCN5-related N-acetyltransferase	4.75	4.91	4.64	5.29	0.11	-0.38	-0.16	-0.65	0.65	-0.31	1.53	-1.52	0.12	0.1	0.6
Cthe_02730 translation elongation factor 1A (EF	16.24	16.89	16.94	16.56	-0.7	0.33	-0.65	0.38	0.01	0.3	-0.1	0.63	0.12	0.1	0.84
Cthe_02006 RNA related	5.29	5.43	5.61	5.25	-0.32	0.18	-0.14	0.36	0.31	0.17	1.6	0.58	0.12	0.1	0.37
Cthe_00760 hypothetical protein	10.17	10.56	10.25	10.76	-0.08	-0.2	-0.39	-0.51	0.5	-0.15	0.77	-1.23	0.12	0.1	0.64
Cthe_00924 hypothetical protein	6.61	7.43	6.74	7.65	-0.13	-0.22	-0.82	-0.91	0.46	-0.17	-0.67	-2.06	0.12	0.1	0.4
Cthe_01042 hypothetical protein	9.18	9.73	9.38	9.77	-0.2	-0.04	-0.55	-0.39	0.4	-0.02	0.23	-0.98	0.12	0.1	0.71
Cthe_01833 copper amine oxidase-like protein	8.68	8.73	8.43	9.29	0.25	-0.56	-0.05	-0.86	0.76	-0.46	1.9	-1.96	0.12	0.1	0.58
Cthe_02073 amidohydrolase	8.55	9.01	9.21	8.99	-0.66	0.02	-0.46	0.22	0.04	0.03	0.53	0.29	0.12	0.1	0.15
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_02633 hypothetical protein	11.11	11.6	11.26	11.69	-0.15	-0.09	-0.49	-0.43	0.44	-0.06	0.43	-1.06	0.12	0.1	0.69
Cthe_02730 translation elongation factor 1A (EF	16.24	16.89	16.94	16.56	-0.7	0.33	-0.65	0.38	0.01	0.3	-0.1	0.63	0.12	0.1	0.84
Cthe_02073 amidohydrolase	8.55	9.01	9.21	8.99	-0.66	0.02	-0.46	0.22	0.04	0.03	0.53	0.29	0.12	0.1	0.15
Cthe_02681 serine phosphatase	8.6	9.09	9.27	8.43	-0.67	0.66	-0.49	0.84	0.03	0.58	0.43	1.58	0.12	0.1	0.63
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684 Polynucleotide adenyltransferase	9.22	9.9	9.54	9.8	-0.32	0.1	-0.68	-0.26	0.31	0.1	-0.2	-0.71	0.12	0.1	0.79
Cthe_00684															



Cthe_00366 hypothetical protein	9.17	9.94	9.92	9.59	-0.75	0.35	-0.77	0.33	-0.03	0.31	-0.5	0.52	0.11	0.09	0.77
Cthe_01770 hypothetical protein	9.26	9.94	10.09	9.49	-0.83	0.45	-0.68	0.6	-0.1	0.4	-0.2	1.08	0.1	0.09	0.67
Cthe_02152 hypothetical protein	11.61	12.23	12.23	12.12	-0.62	0.11	-0.62	0.11	0.07	0.11	0	0.06	0.11	0.09	3.88
Cthe_00782 putative methyl-accepting chemota	3.17	3.58	4	3.17	-0.83	0.41	-0.41	0.83	-0.1	0.36	0.7	1.56	0.11	0.09	0.39
Cthe_00802 hypothetical protein	5.78	6.04	6.21	5.91	-0.43	0.13	-0.26	0.3	0.22	0.13	1.2	0.46	0.1	0.09	0.36
Cthe_02216 hypothetical protein	11.3	12.22	11.92	11.79	-0.62	0.43	-0.92	0.13	0.07	0.38	-1	0.1	0.1	0.09	0.69
Cthe_00453 hypothetical protein	3.46	3.17	3.32	2	0.14	1.17	0.29	1.32	0.67	1.01	3.03	2.58	0.1	0.09	0.54
Cthe_00602 thiamine biosynthesis protein ThiC	9.36	10.17	10.12	10.11	-0.76	0.06	-0.81	0.01	-0.04	0.07	-0.63	-0.15	0.1	0.09	0.22
Cthe_00417 ribosomal protein S15	12.7	12.97	12.91	12.77	-0.21	0.2	-0.27	0.14	0.4	0.19	1.17	0.13	0.11	0.09	0.67
Cthe_00928 4-hydroxythreonine-4-phosphate d	9.38	10.26	10.1	9.86	-0.72	0.4	-0.88	0.24	-0.01	0.36	-0.87	0.33	0.1	0.09	0.69
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_01802 cobalt ABC transporter, inner mem	9.88	10.69	10.59	10.61	-0.71	0.08	-0.81	-0.02	0	0.08	-0.63	-0.21	0.11	0.09	0.22
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_01802 cobalt ABC transporter, inner mem	9.88	10.69	10.59	10.61	-0.71	0.08	-0.81	-0.02	0	0.08	-0.63	-0.21	0.11	0.09	0.22
Cthe_00417 ribosomal protein S15	12.7	12.97	12.91	12.77	-0.21	0.2	-0.27	0.14	0.4	0.19	1.17	0.13	0.11	0.09	0.67
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00874 glutamine amidotransferase of ant	7.88	8.04	8.3	8.32	-0.42	-0.28	-0.16	-0.02	0.23	-0.22	1.53	-0.21	0.11	0.09	0.37
Cthe_01086 dTDP-glucose 4,6-dehydratase	4.39	5.49	5.29	4.81	-0.9	0.68	-1.1	0.48	-0.15	0.59	-1.6	0.83	0.1	0.09	0.6
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00022 8-amino-7-oxononanoate synthase	4.46	5.32	4.39	5.52	0.07	-0.2	-0.86	-1.13	0.62	-0.15	-0.8	-2.52	0.1	0.09	0.43
Cthe_00928 4-hydroxythreonine-4-phosphate d	9.38	10.26	10.1	9.86	-0.72	0.4	-0.88	0.24	-0.01	0.36	-0.87	0.33	0.1	0.09	0.69
Cthe_00198 Glutamate synthase (NADPH)	6.93	7.8	7.73	7.7	-0.8	0.1	-0.87	0.03	-0.07	0.1	-0.83	-0.1	0.11	0.09	0.26
Cthe_00282 glycogen/starch synthases, ADP-glu	10.01	10.55	10.43	10.54	-0.42	0.01	-0.54	-0.11	0.23	0.03	0.27	-0.4	0.1	0.09	0.86
Cthe_00874 glutamine amidotransferase of ant	7.88	8.04	8.3	8.32	-0.42	-0.28	-0.16	-0.02	0.23	-0.22	1.53	-0.21	0.11	0.09	0.37
Cthe_01848 copper-translocating P-type ATPase	13.91	14.6	14.84	13.98	-0.93	0.62	-0.69	0.86	-0.17	0.54	-0.23	1.63	0.11	0.09	0.61
Cthe_00198 Glutamate synthase (NADPH)	6.93	7.8	7.73	7.7	-0.8	0.1	-0.87	0.03	-0.07	0.1	-0.83	-0.1	0.11	0.09	0.26
Cthe_00874 glutamine amidotransferase of ant	7.88	8.04	8.3	8.32	-0.42	-0.28	-0.16	-0.02	0.23	-0.22	1.53	-0.21	0.11	0.09	0.37
Cthe_00874 glutamine amidotransferase of ant	7.88	8.04	8.3	8.32	-0.42	-0.28	-0.16	-0.02	0.23	-0.22	1.53	-0.21	0.11	0.09	0.37
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_01086 dTDP-glucose 4,6-dehydratase	4.39	5.49	5.29	4.81	-0.9	0.68	-1.1	0.48	-0.15	0.59	-1.6	0.83	0.1	0.09	0.6
Cthe_01848 copper-translocating P-type ATPase	13.91	14.6	14.84	13.98	-0.93	0.62	-0.69	0.86	-0.17	0.54	-0.23	1.63	0.11	0.09	0.61
Cthe_00282 glycogen/starch synthases, ADP-glu	10.01	10.55	10.43	10.54	-0.42	0.01	-0.54	-0.11	0.23	0.03	0.27	-0.4	0.1	0.09	0.86
Cthe_00282 glycogen/starch synthases, ADP-glu	10.01	10.55	10.43	10.54	-0.42	0.01	-0.54	-0.11	0.23	0.03	0.27	-0.4	0.1	0.09	0.86
Cthe_01086 dTDP-glucose 4,6-dehydratase	4.39	5.49	5.29	4.81	-0.9	0.68	-1.1	0.48	-0.15	0.59	-1.6	0.83	0.1	0.09	0.6
Cthe_01086 dTDP-glucose 4,6-dehydratase	4.39	5.49	5.29	4.81	-0.9	0.68	-1.1	0.48	-0.15	0.59	-1.6	0.83	0.1	0.09	0.6
Cthe_00928 4-hydroxythreonine-4-phosphate d	9.38	10.26	10.1	9.86	-0.72	0.4	-0.88	0.24	-0.01	0.36	-0.87	0.33	0.1	0.09	0.69
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00198 Glutamate synthase (NADPH)	6.93	7.8	7.73	7.7	-0.8	0.1	-0.87	0.03	-0.07	0.1	-0.83	-0.1	0.11	0.09	0.26
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00198 Glutamate synthase (NADPH)	6.93	7.8	7.73	7.7	-0.8	0.1	-0.87	0.03	-0.07	0.1	-0.83	-0.1	0.11	0.09	0.26
Cthe_00198 Glutamate synthase (NADPH)	6.93	7.8	7.73	7.7	-0.8	0.1	-0.87	0.03	-0.07	0.1	-0.83	-0.1	0.11	0.09	0.26
Cthe_00198 Glutamate synthase (NADPH)	6.93	7.8	7.73	7.7	-0.8	0.1	-0.87	0.03	-0.07	0.1	-0.83	-0.1	0.11	0.09	0.26
Cthe_00716 Nucleoside-diphosphate kinase	9.7	10.45	9.91	10.32	-0.21	0.13	-0.75	-0.41	0.4	0.13	-0.43	-1.02	0.11	0.09	0.68
Cthe_00022 8-amino-7-oxononanoate synthase	4.46	5.32	4.39	5.52	0.07	-0.2	-0.86	-1.13	0.62	-0.15	-0.8	-2.52	0.1	0.09	0.43
Cthe_00770 signal recognition particle protein	10.01	10.6	10.26	10.67	-0.25	-0.07	-0.59	-0.41	0.37	-0.04	0.1	-1.02	0.09	0.08	0.65
Cthe_01055 protein of unknown function DUF5	9.58	10.26	10.25	10.09	-0.67	0.17	-0.68	0.16	0.03	0.16	-0.2	0.17	0.09	0.08	1.11
Cthe_01473 NADPH-dependent FMN reductase	14.24	14.93	15.18	14.37	-0.94	0.56	-0.69	0.81	-0.18	0.49	-0.23	1.52	0.09	0.08	0.61
Cthe_02688 polysaccharide biosynthesis protei	8.23	8.63	8.8	8.55	-0.57	0.08	-0.4	0.25	0.11	0.08	0.73	0.35	0.09	0.08	0.3
Cthe_00816 NAD(+) kinase	10.29	11	10.84	10.85	-0.55	0.15	-0.71	-0.01	0.13	0.14	-0.3	-0.19	0.09	0.08	0.96
Cthe_00376 transcriptional repressor, CopY fam	4.58	4.7	4.52	4.95	0.06	-0.25	-0.12	-0.43	0.61	-0.19	1.67	-1.06	0.09	0.08	0.58
Cthe_01283 endonuclease III	12.33	12.99	12.87	12.89	-0.54	0.1	-0.66	-0.02	0.13	0.1	-0.13	-0.21	0.09	0.08	1.19
Cthe_02142 recombination protein RecR	11.17	11.88	11.51	11.78	-0.34	0.1	-0.71	-0.27	0.29	0.1	-0.3	-0.73	0.09	0.08	0.69
Cthe_00600 thiamine biosynthesis protein ThiF	7.89	8.64	8.46	8.44	-0.57	0.2	-0.75	0.02	0.11	0.19	-0.43	-0.13	0.09	0.08	0.87
Cthe_01244 glycosyl transferase, family 2	10.68	11.31	11.04	11.29	-0.36	0.02	-0.63	-0.25	0.28	0.03	-0.03	-0.69	0.09	0.08	0.73
Cthe_02615 UDP-N-acetylglucosamine	10.49	11.05	10.78	11.1	-0.29	-0.05	-0.56	-0.32	0.33	-0.03	0.2	-0.83	0.09	0.08	0.69
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_00779 copper amine oxidase-like protein	8.13	8.59	8.47	8.61	-0.34	-0.02	-0.46	-0.14	0.29	0	0.53	-0.46	0.09	0.08	0.74
Cthe_01935 arginyl-tRNA synthetase	12.37	12.87	13.17	12.74	-0.8	0.13	-0.5	0.43	-0.07	0.13	0.4	0.73	0.09	0.08	0.32
Cthe_02933 ribosomal protein L17	13.04	13.6	13.64	13.46	-0.6	0.14	-0.56	0.18	0.09	0.14	0.2	0.21	0.09	0.08	1.02
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_02674 hypothetical protein	7.43	7.74	7.59	7.89	-0.16	-0.15	-0.31	-0.3	0.44	-0.11	1.03	-0.79	0.09	0.08	0.62
Cthe_00894 hypothetical protein	4.75	5.52	5.32	5.29	-0.57	0.23	-0.77	0.03	0.11	0.21	-0.5	-0.1	0.09	0.08	0.83
Cthe_03040 hypothetical protein	6.95	7.43	7.24	7.52	-0.29	-0.09	-0.48	-0.28	0.33	-0.06	0.47	-0.75	0.09	0.08	0.68
Cthe_00385 hypothetical protein	4.32	4.52	4.39	4.58	-0.07	-0.06	-0.2	-0.19	0.51	-0.03	1.4	-0.56	0.09	0.08	0.61
Cthe_02057 CRISPR-associated protein, TM1812	9.54	10.05	9.66	10.25	-0.12	-0.2	-0.51	-0.59	0.47	-0.15	0.37	-1.4	0.09	0.08	0.61
Cthe_01837 hypothetical protein	10.29	10.77	10.85	10.43	-0.56	0.34	-0.48	0.42	0.12	0.31	0.47	0.71	0.09	0.08	0.7
Cthe_01935 arginyl-tRNA synthetase	12.37	12.87	13.17	12.74	-0.8	0.13	-0.5	0.43	-0.07	0.13	0.4	0.73	0.09	0.08	0.32
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_01935 arginyl-tRNA synthetase	12.37	12.87	13.17	12.74	-0.8	0.13	-0.5	0.43	-0.07	0.13	0.4	0.73	0.09	0.08	0.32
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_02933 ribosomal protein L17	13.04	13.6	13.64	13.46	-0.6	0.14	-0.56	0.18	0.09	0.14	0.2	0.21	0.09	0.08	1.02
Cthe_00770 signal recognition particle protein	10.01	10.6	10.26	10.67	-0.25	-0.07	-0.59	-0.41	0.37	-0.04	0.1	-1.02	0.09	0.08	0.65
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_01283 endonuclease III	12.33	12.99	12.87	12.89	-0.54	0.1	-0.66	-0.02	0.13	0.1	-0.13	-0.21	0.09	0.08	1.19
Cthe_00816 NAD(+) kinase	10.29	11	10.84	10.85	-0.55	0.15	-0.71	-0.01	0.13	0.14	-0.3	-0.19	0.09		



Cthe_01935 arginyl-tRNA synthetase	12.37	12.87	13.17	12.74	-0.8	0.13	-0.5	0.43	-0.07	0.13	0.4	0.73	0.09	0.08	0.32
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_03113 Nucleotidyl transferase	8.62	9.4	9.12	9.18	-0.5	0.22	-0.78	-0.06	0.17	0.2	-0.53	-0.29	0.09	0.08	0.78
Cthe_02615 UDP-N-acetylglucosamine	10.49	11.05	10.78	11.1	-0.29	-0.05	-0.56	-0.32	0.33	-0.03	0.2	-0.83	0.09	0.08	0.69
Cthe_02615 UDP-N-acetylglucosamine	10.49	11.05	10.78	11.1	-0.29	-0.05	-0.56	-0.32	0.33	-0.03	0.2	-0.83	0.09	0.08	0.69
Cthe_00816 NAD(+) kinase	10.29	11	10.84	10.85	-0.55	0.15	-0.71	-0.01	0.13	0.14	-0.3	-0.19	0.09	0.08	0.96
Cthe_02162 peptidase C26	7.28	8.25	7.88	7.8	-0.6	0.45	-0.97	0.08	0.09	0.4	-1.17	0	0.08	0.07	0.63
Cthe_02445 Alcohol dehydrogenase GroES-like	4.64	5.49	5.78	5.04	-1.14	0.45	-0.85	0.74	-0.34	0.4	-0.77	1.38	0.08	0.07	0.59
Cthe_02182 Ig-like, group 2	10.14	10.95	10.83	10.65	-0.69	0.3	-0.81	0.18	0.02	0.27	-0.63	0.21	0.08	0.07	0.73
Cthe_03167 glucose-1-phosphate adenyllyltrans	12.03	12.66	12.79	12.33	-0.76	0.33	-0.63	0.46	-0.04	0.3	-0.03	0.79	0.08	0.07	0.68
Cthe_02445 Alcohol dehydrogenase GroES-like	4.64	5.49	5.78	5.04	-1.14	0.45	-0.85	0.74	-0.34	0.4	-0.77	1.38	0.08	0.07	0.59
Cthe_00896 DNA primase	10.75	11	10.89	11.05	-0.14	-0.05	-0.25	-0.16	0.45	-0.03	1.23	-0.5	0.08	0.07	0.61
Cthe_00830 acid phosphatase/vanadium-depen	7.83	8.22	8.04	8.47	-0.21	-0.25	-0.39	-0.43	0.4	-0.19	0.77	-1.06	0.08	0.07	0.6
Cthe_00328 peptide chain release factor 3	11.48	12.05	11.98	12.03	-0.5	0.02	-0.57	-0.05	0.17	0.03	0.17	-0.27	0.08	0.07	0.97
Cthe_00788 DivIVA	9.66	10.12	9.85	10.35	-0.19	-0.23	-0.46	-0.5	0.41	-0.18	0.53	-1.21	0.08	0.07	0.61
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02943 ABC-2 type transporter	8.87	9.45	9.29	9.46	-0.42	-0.01	-0.58	-0.17	0.23	0.01	0.13	-0.52	0.08	0.07	0.77
Cthe_02943 ABC-2 type transporter	8.87	9.45	9.29	9.46	-0.42	-0.01	-0.58	-0.17	0.23	0.01	0.13	-0.52	0.08	0.07	0.77
Cthe_00299 MATE efflux family protein	7.16	8.08	7.77	7.86	-0.61	0.22	-0.92	-0.09	0.08	0.2	-1	-0.35	0.08	0.07	0.36
Cthe_01500 ABC transporter related protein	7.23	8.4	8.39	7.81	-1.06	0.59	-1.07	0.58	-0.28	0.52	-1.5	1.04	0.08	0.07	0.58
Cthe_02513 peptidase S1 and S6, chymotrypsin	9.21	10.38	9.82	9.7	-0.61	0.68	-1.17	0.12	0.08	0.59	-1.83	0.08	0.08	0.07	0.58
Cthe_00690 hypothetical protein	6	6.49	6.29	6.6	-0.29	-0.11	-0.49	-0.31	0.33	-0.08	0.43	-0.81	0.08	0.07	0.66
Cthe_03195 hypothetical protein	3.91	4.64	4.25	4.52	-0.34	0.12	-0.73	-0.27	0.29	0.12	-0.37	-0.73	0.08	0.07	0.68
Cthe_02044 hypothetical protein	5.39	5.7	5.64	5.64	-0.25	0.06	-0.31	0	0.37	0.07	1.03	-0.17	0.08	0.07	0.64
Cthe_00702 hypothetical protein	9.33	9.85	9.52	10	-0.19	-0.15	-0.52	-0.48	0.41	-0.11	0.33	-1.17	0.08	0.07	0.62
Cthe_01856 small acid-soluble spore protein be	7.22	7.5	7.38	7.67	-0.16	-0.17	-0.28	-0.29	0.44	-0.13	1.13	-0.77	0.08	0.07	0.6
Cthe_00329 hypothetical protein	9.46	9.92	10.23	9.64	-0.77	0.28	-0.46	0.59	-0.05	0.25	0.53	1.06	0.08	0.07	0.38
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02943 ABC-2 type transporter	8.87	9.45	9.29	9.46	-0.42	-0.01	-0.58	-0.17	0.23	0.01	0.13	-0.52	0.08	0.07	0.77
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_00555 PpiC-type peptidyl-prolyl cis-trans i	12.75	13.27	13.23	13.24	-0.48	0.03	-0.52	-0.01	0.18	0.04	0.33	-0.19	0.08	0.07	0.86
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02445 Alcohol dehydrogenase GroES-like	4.64	5.49	5.78	5.04	-1.14	0.45	-0.85	0.74	-0.34	0.4	-0.77	1.38	0.08	0.07	0.59
Cthe_03167 glucose-1-phosphate adenyllyltrans	12.03	12.66	12.79	12.33	-0.76	0.33	-0.63	0.46	-0.04	0.3	-0.03	0.79	0.08	0.07	0.68
Cthe_00896 DNA primase	10.75	11	10.89	11.05	-0.14	-0.05	-0.25	-0.16	0.45	-0.03	1.23	-0.5	0.08	0.07	0.61
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_00896 DNA primase	10.75	11	10.89	11.05	-0.14	-0.05	-0.25	-0.16	0.45	-0.03	1.23	-0.5	0.08	0.07	0.61
Cthe_00896 DNA primase	10.75	11	10.89	11.05	-0.14	-0.05	-0.25	-0.16	0.45	-0.03	1.23	-0.5	0.08	0.07	0.61
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_03167 glucose-1-phosphate adenyllyltrans	12.03	12.66	12.79	12.33	-0.76	0.33	-0.63	0.46	-0.04	0.3	-0.03	0.79	0.08	0.07	0.68
Cthe_02445 Alcohol dehydrogenase GroES-like	4.64	5.49	5.78	5.04	-1.14	0.45	-0.85	0.74	-0.34	0.4	-0.77	1.38	0.08	0.07	0.59
Cthe_00896 DNA primase	10.75	11	10.89	11.05	-0.14	-0.05	-0.25	-0.16	0.45	-0.03	1.23	-0.5	0.08	0.07	0.61
Cthe_03167 glucose-1-phosphate adenyllyltrans	12.03	12.66	12.79	12.33	-0.76	0.33	-0.63	0.46	-0.04	0.3	-0.03	0.79	0.08	0.07	0.68
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_00896 DNA primase	10.75	11	10.89	11.05	-0.14	-0.05	-0.25	-0.16	0.45	-0.03	1.23	-0.5	0.08	0.07	0.61
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_00896 DNA primase	10.75	11	10.89	11.05	-0.14	-0.05	-0.25	-0.16	0.45	-0.03	1.23	-0.5	0.08	0.07	0.61
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_02796 pyruvate flavodoxin/ferredoxin	3.58	3.7	3.81	3.58	-0.23	0.12	-0.12	0.23	0.38	0.12	1.67	0.31	0.08	0.07	0.42
Cthe_00439 CobB/CobQ-like glutamine amidotr	8.94	9.73	9.73	9.67	-0.79	0.06	-0.79	0.06	-0.06	0.07	-0.57	-0.04	0.07	0.06	0.29
Cthe_00507 Exonuclease, RNase T and DNA pol	11.31	12.2	12.13	12.03	-0.82	0.17	-0.89	0.1	-0.09	0.16	-0.9	0.04	0.07	0.06	0.36
Cthe_02077 CoA-binding protein	11.64	12.4	12.41	12.12	-0.77	0.28	-0.76	0.29	-0.05	0.25	-0.47	0.44	0.07	0.06	0.71
Cthe_02453 hypothetical protein	8.16	8.94	8.67	8.75	-0.51	0.19	-0.78	-0.08	0.16	0.18	-0.53	-0.33	0.07	0.06	0.69
Cthe_01470 RNA polymerase, sigma-24 subunit	8.06	9.1	8.9	8.76	-0.84	0.34	-1.04	0.14	-0.1	0.31	-1.4	0.13	0.07	0.06	0.41
Cthe_02546	2	1.58	1.58	1.58	0.42	0	0.42	0	0.9	0.02	3.47	-0.17	0.07	0.06	0.46
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_02186 single-strand binding protein	11.96	12.29	12.18	12.45	-0.22	-0.16	-0.33	-0.27	0.39	-0.12	0.97	-0.73	0.07	0.06	0.6
Cthe_02756 transposase	2	1.58	1.58	1.58	0.42	0	0.42	0	0.9	0.02	3.47	-0.17	0.07	0.06	0.46
Cthe_01532 flagellin-like protein	4.25	4.75	4.64	4.81	-0.39	-0.06	-0.5	-0.17	0.25	-0.03	0.4	-0.52	0.07	0.06	0.69
Cthe_00209 glycosyltransferase	6.32	7.34	6.79	6.88	-0.47	0.46	-1.02	-0.09	0.19	0.41	-1.33	-0.35	0.07	0.06	0.59
Cthe_01397 glycosyl transferase, family 8	6.6	7.44	7.25	7.3	-0.65	0.14	-0.84	-0.05	0.05	0.14	-0.73	-0.27	0.07	0.06	0.34
Cthe_02652 lipopolysaccharide biosynthesis	5.13	5.91	6.19	5.49	-1.06	0.42	-0.78	0.7	-0.28	0.37	-0.53	1.29	0.07	0.06	0.59
Cthe_01245 phosphoribosylamine-glycine ligas	10.02	10.66	10.54	10.61	-0.52	0.05	-0.64	-0.07	0.15	0.06	-0.07	-0.31	0.07	0.06	0.91
Cthe_01477 deoxycytidine triphosphate deamin	7.18	7.68	7.55	7.77	-0.37	-0.09	-0.5	-0.22	0.27	-0					



Cthe_01477 deoxycytidine triphosphate deamin	7.18	7.68	7.55	7.77	-0.37	-0.09	-0.5	-0.22	0.27	-0.06	0.4	-0.63	0.07	0.06	0.66
Cthe_01245 phosphoribosylamine-glycine ligas	10.02	10.66	10.54	10.61	-0.52	0.05	-0.64	-0.07	0.15	0.06	-0.07	-0.31	0.07	0.06	0.91
Cthe_01477 deoxycytidine triphosphate deamin	7.18	7.68	7.55	7.77	-0.37	-0.09	-0.5	-0.22	0.27	-0.06	0.4	-0.63	0.07	0.06	0.66
Cthe_01245 phosphoribosylamine-glycine ligas	10.02	10.66	10.54	10.61	-0.52	0.05	-0.64	-0.07	0.15	0.06	-0.07	-0.31	0.07	0.06	0.91
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_01245 phosphoribosylamine-glycine ligas	10.02	10.66	10.54	10.61	-0.52	0.05	-0.64	-0.07	0.15	0.06	-0.07	-0.31	0.07	0.06	0.91
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_01477 deoxycytidine triphosphate deamin	7.18	7.68	7.55	7.77	-0.37	-0.09	-0.5	-0.22	0.27	-0.06	0.4	-0.63	0.07	0.06	0.66
Cthe_01477 deoxycytidine triphosphate deamin	7.18	7.68	7.55	7.77	-0.37	-0.09	-0.5	-0.22	0.27	-0.06	0.4	-0.63	0.07	0.06	0.66
Cthe_01245 phosphoribosylamine-glycine ligas	10.02	10.66	10.54	10.61	-0.52	0.05	-0.64	-0.07	0.15	0.06	-0.07	-0.31	0.07	0.06	0.91
Cthe_02517 acetolactate synthase, small subun	9.78	10.65	10.22	10.52	-0.44	0.13	-0.87	-0.3	0.21	0.13	-0.83	-0.79	0.07	0.06	0.38
Cthe_01245 phosphoribosylamine-glycine ligas	10.02	10.66	10.54	10.61	-0.52	0.05	-0.64	-0.07	0.15	0.06	-0.07	-0.31	0.07	0.06	0.91
Cthe_00163 GTP1/OBG subdomain containing p	11.07	11.78	11.52	11.92	-0.45	-0.14	-0.71	-0.4	0.21	-0.1	-0.3	-1	0.06	0.05	0.4
Cthe_00985 peptidase M16-like protein	10.33	10.99	10.5	11.06	-0.17	-0.07	-0.66	-0.56	0.43	-0.04	-0.13	-1.33	0.06	0.05	0.58
Cthe_01344 (p)ppGpp synthetase I, SpoT/RelA	10.69	11.5	10.74	11.41	-0.05	0.09	-0.81	-0.67	0.52	0.09	-0.63	-1.56	0.06	0.05	0.56
Cthe_01825 multi-sensor hybrid histidine kinase	5.39	6.29	6.02	6.07	-0.63	0.22	-0.9	-0.05	0.06	0.2	-0.93	-0.27	0.06	0.05	0.39
Cthe_01853 cold-shock DNA-binding domain pr	11.05	11.82	11.72	11.6	-0.67	0.22	-0.77	0.12	0.03	0.2	-0.5	0.08	0.06	0.05	0.71
Cthe_00153 Holliday junction resolvase YagF	5.55	5.83	5.75	5.91	-0.2	-0.08	-0.28	-0.16	0.4	-0.05	1.13	-0.5	0.06	0.05	0.58
Cthe_00309 excinuclease ABC, B subunit	12.91	13.79	13.59	13.45	-0.68	0.34	-0.88	0.14	0.02	0.31	-0.87	0.13	0.06	0.05	0.63
Cthe_00901 pantoate-beta-alanine ligase	9.27	9.59	9.52	9.72	-0.25	-0.13	-0.32	-0.2	0.37	-0.09	1	-0.58	0.06	0.05	0.59
Cthe_00717 MCP methyltransferase, CheR-type	10.08	10.82	10.3	10.76	-0.22	0.06	-0.74	-0.46	0.39	0.07	-0.4	-1.13	0.06	0.05	0.59
Cthe_00091 Peptidoglycan glycosyltransferase	9.73	10.46	9.99	10.41	-0.26	0.05	-0.73	-0.42	0.36	0.06	-0.37	-1.04	0.06	0.05	0.59
Cthe_01930 carboxyl-terminal protease	9.19	9.83	9.68	9.8	-0.49	0.03	-0.64	-0.12	0.17	0.04	-0.07	-0.42	0.06	0.05	0.73
Cthe_01246 phosphoribosylaminoimidazolecarb	9.8	10.52	10.3	10.59	-0.5	-0.07	-0.72	-0.29	0.17	-0.04	-0.33	-0.77	0.06	0.05	0.37
Cthe_01248 phosphoribosylformylglycinamidin	8.75	9.47	9.1	9.67	-0.35	-0.2	-0.72	-0.57	0.29	-0.15	-0.33	-1.35	0.06	0.05	0.42
Cthe_00717 MCP methyltransferase, CheR-type	10.08	10.82	10.3	10.76	-0.22	0.06	-0.74	-0.46	0.39	0.07	-0.4	-1.13	0.06	0.05	0.59
Cthe_01344 (p)ppGpp synthetase I, SpoT/RelA	10.69	11.5	10.74	11.41	-0.05	0.09	-0.81	-0.67	0.52	0.09	-0.63	-1.56	0.06	0.05	0.56
Cthe_01825 multi-sensor hybrid histidine kinase	5.39	6.29	6.02	6.07	-0.63	0.22	-0.9	-0.05	0.06	0.2	-0.93	-0.27	0.06	0.05	0.39
Cthe_00054 protein of unknown function DUF1	7.91	8.43	8.55	8.13	-0.64	0.3	-0.52	0.42	0.06	0.27	0.33	0.71	0.06	0.05	0.63
Cthe_02769 protein of unknown function DUF5	8.53	9.02	9.75	8.29	-1.22	0.73	-0.49	1.46	-0.4	0.64	0.43	2.88	0.06	0.05	0.46
Cthe_01286 peptidase S1 and S6, chymotrypsin	10.52	11.05	11.21	10.67	-0.69	0.38	-0.53	0.54	0.02	0.34	0.3	0.96	0.06	0.05	0.6
Cthe_01441 hypothetical protein	2.32	3	2.58	3	-0.26	0	-0.68	-0.42	0.36	0.02	-0.2	-1.04	0.06	0.05	0.61
Cthe_02015 hypothetical protein	4.32	5.61	5.36	4.81	-1.04	0.8	-1.29	0.55	-0.26	0.69	-2.23	0.98	0.06	0.05	0.54
Cthe_01767 hypothetical protein	10.63	11.31	11.39	11.11	-0.76	0.2	-0.68	0.28	-0.04	0.19	-0.2	0.42	0.06	0.05	0.75
Cthe_03122 S-layer-like domain containing prot	10.54	11.23	10.84	11.21	-0.3	0.02	-0.69	-0.37	0.33	0.03	-0.23	-0.94	0.06	0.05	0.61
Cthe_00907 hypothetical protein	9.48	9.99	10.08	9.75	-0.6	0.24	-0.51	0.33	0.09	0.22	0.37	0.52	0.06	0.05	0.67
Cthe_03058 hypothetical protein	6.66	6.93	7.12	6.61	-0.46	0.32	-0.27	0.51	0.2	0.29	1.17	0.9	0.06	0.05	0.43
Cthe_02953 hypothetical protein	3.46	4.17	4.32	3.91	-0.86	0.26	-0.71	0.41	-0.12	0.24	-0.3	0.69	0.06	0.05	0.64
Cthe_02670 hypothetical protein	8.48	8.85	8.75	9.04	-0.27	-0.19	-0.37	-0.29	0.35	-0.14	0.83	-0.77	0.06	0.05	0.59
Cthe_02357 hypothetical protein	12.18	12.69	12.81	12.38	-0.63	0.31	-0.51	0.43	0.06	0.28	0.37	0.73	0.06	0.05	0.62
Cthe_00901 pantoate-beta-alanine ligase	9.27	9.59	9.52	9.72	-0.25	-0.13	-0.32	-0.2	0.37	-0.09	1	-0.58	0.06	0.05	0.59
Cthe_01246 phosphoribosylaminoimidazolecarb	9.8	10.52	10.3	10.59	-0.5	-0.07	-0.72	-0.29	0.17	-0.04	-0.33	-0.77	0.06	0.05	0.37
Cthe_01248 phosphoribosylformylglycinamidin	8.75	9.47	9.1	9.67	-0.35	-0.2	-0.72	-0.57	0.29	-0.15	-0.33	-1.35	0.06	0.05	0.42
Cthe_01248 phosphoribosylformylglycinamidin	8.75	9.47	9.1	9.67	-0.35	-0.2	-0.72	-0.57	0.29	-0.15	-0.33	-1.35	0.06	0.05	0.42
Cthe_00901 pantoate-beta-alanine ligase	9.27	9.59	9.52	9.72	-0.25	-0.13	-0.32	-0.2	0.37	-0.09	1	-0.58	0.06	0.05	0.59
Cthe_01246 phosphoribosylaminoimidazolecarb	9.8	10.52	10.3	10.59	-0.5	-0.07	-0.72	-0.29	0.17	-0.04	-0.33	-0.77	0.06	0.05	0.37
Cthe_00717 MCP methyltransferase, CheR-type	10.08	10.82	10.3	10.76	-0.22	0.06	-0.74	-0.46	0.39	0.07	-0.4	-1.13	0.06	0.05	0.59
Cthe_01344 (p)ppGpp synthetase I, SpoT/RelA	10.69	11.5	10.74	11.41	-0.05	0.09	-0.81	-0.67	0.52	0.09	-0.63	-1.56	0.06	0.05	0.56
Cthe_00153 Holliday junction resolvase YagF	5.55	5.83	5.75	5.91	-0.2	-0.08	-0.28	-0.16	0.4	-0.05	1.13	-0.5	0.06	0.05	0.58
Cthe_01246 phosphoribosylaminoimidazolecarb	9.8	10.52	10.3	10.59	-0.5	-0.07	-0.72	-0.29	0.17	-0.04	-0.33	-0.77	0.06	0.05	0.37
Cthe_01930 carboxyl-terminal protease	9.19	9.83	9.68	9.8	-0.49	0.03	-0.64	-0.12	0.17	0.04	-0.07	-0.42	0.06	0.05	0.73
Cthe_01246 phosphoribosylaminoimidazolecarb	9.8	10.52	10.3	10.59	-0.5	-0.07	-0.72	-0.29	0.17	-0.04	-0.33	-0.77	0.06	0.05	0.37
Cthe_00901 pantoate-beta-alanine ligase	9.27	9.59	9.52	9.72	-0.25	-0.13	-0.32	-0.2	0.37	-0.09	1	-0.58	0.06	0.05	0.59
Cthe_01248 phosphoribosylformylglycinamidin	8.75	9.47	9.1	9.67	-0.35	-0.2	-0.72	-0.57	0.29	-0.15	-0.33	-1.35	0.06	0.05	0.42
Cthe_01344 (p)ppGpp synthetase I, SpoT/RelA	10.69	11.5	10.74	11.41	-0.05	0.09	-0.81	-0.67	0.52	0.09	-0.63	-1.56	0.06	0.05	0.56
Cthe_01246 phosphoribosylaminoimidazolecarb	9.8	10.52	10.3	10.59	-0.5	-0.07	-0.72	-0.29	0.17	-0.04	-0.33	-0.77	0.06	0.05	0.37
Cthe_01248 phosphoribosylformylglycinamidin	8.75	9.47	9.1	9.67	-0.35	-0.2	-0.72	-0.57	0.29	-0.15	-0.33	-1.35	0.06	0.05	0.42
Cthe_01248 phosphoribosylformylglycinamidin	8.75	9.47	9.1	9.67	-0.35	-0.2	-0.72	-0.57	0.29	-0.15	-0.33	-1.35	0.06	0.05	0.42
Cthe_00145 metal dependent phosphohydrolas	11.58	12.22	12.11	12.19	-0.53	0.03	-0.64	-0.08	0.14	0.04	-0.07	-0.33	0.05	0.04	0.77
Cthe_01799 ABC transporter related protein	11.03	11.63	11.34	11.73	-0.31	-0.1	-0.6	-0.39	0.32	-0.07	0.07	-0.98	0.05	0.04	0.6
Cthe_00314 glycosyltransferase 28-like protein	8	8.63	8.38	8.67	-0.38	-0.04	-0.63	-0.29	0.26	-0.02	-0.03	-0.77	0.05	0.04	0.6
Cthe_00292 transposase, mutator type	10.06	10.77	10.64	10.78	-0.58	-0.01	-0.71	-0.14	0.1	0.01	-0.3	-0.46	0.05	0.04	0.33
Cthe_02054 protein of unknown function DUF3	7.92	8.63	8.18	8.85	-0.26	-0.22	-0.71	-0.67	0.36	-0.17	-0.3	-1.56	0.05	0.04	0.45
Cthe_03041 UbiA prenyltransferase	8.58	8.99	8.97	8.98	-0.39	0.01	-0.41	-0.01	0.25	0.03	0.7	-0.19	0.05	0.04	0.62
Cthe_00298 methyl-accepting chemotaxis senso	8.11	8.67	8.28	8.9	-0.17	-0.23	-0.56	-0.62	0.43	-0.18	0.2	-1.46	0.05	0.04	0.56
Cthe_00679 Serine-type D-Ala-D-Ala carboxype	10.4	11.1	10.89	11.18	-0.49	-0.08	-0.7	-0.29	0.17	-0.05	-0.27	-0.77	0.05	0.04	0.39
Cthe_02640 UDP-N-acetylglucosamine 2-epime	3.7	3.81	4.25	2.81	-0.55	1	-0.11	1.44	0.13	0.86	1.7	2.83	0.05	0.04	0.47
Cthe_02399 Formate-tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_00298 methyl-accepting chemotaxis senso	8.11	8.67	8.28	8.9	-0.17	-0.23	-0.56	-0.62	0.43	-0.18	0.2	-1.46	0.05	0.04	0.56
Cthe_02577 adenylate cyclase	7.71	8.49	8.35	8.28	-0.64	0.21	-0.78	0.07	0.06	0.19	-0.53	-0.02	0.05	0.04	0.67
Cthe_03160 putative RNA methylase, NOL1/NO	8.53	8.95	8.88	9.23	-0.35	-0.28	-0.42	-0.35	0.29	-0.22	0.67	-0			



Cthe_02640 UDP-N-acetylglucosamine 2-epime	3.7	3.81	4.25	2.81	-0.55	1	-0.11	1.44	0.13	0.86	1.7	2.83	0.05	0.04	0.47
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_00341 NADH dehydrogenase (quinone)	12.86	13.57	13.4	13.59	-0.54	-0.02	-0.71	-0.19	0.13	0	-0.3	-0.56	0.05	0.04	0.37
Cthe_00341 NADH dehydrogenase (quinone)	12.86	13.57	13.4	13.59	-0.54	-0.02	-0.71	-0.19	0.13	0	-0.3	-0.56	0.05	0.04	0.37
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_00341 NADH dehydrogenase (quinone)	12.86	13.57	13.4	13.59	-0.54	-0.02	-0.71	-0.19	0.13	0	-0.3	-0.56	0.05	0.04	0.37
Cthe_00679 Serine-type D-Ala-D-Ala carboxype	10.4	11.1	10.89	11.18	-0.49	-0.08	-0.7	-0.29	0.17	-0.05	-0.27	-0.77	0.05	0.04	0.39
Cthe_02640 UDP-N-acetylglucosamine 2-epime	3.7	3.81	4.25	2.81	-0.55	1	-0.11	1.44	0.13	0.86	1.7	2.83	0.05	0.04	0.47
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_00341 NADH dehydrogenase (quinone)	12.86	13.57	13.4	13.59	-0.54	-0.02	-0.71	-0.19	0.13	0	-0.3	-0.56	0.05	0.04	0.37
Cthe_02640 UDP-N-acetylglucosamine 2-epime	3.7	3.81	4.25	2.81	-0.55	1	-0.11	1.44	0.13	0.86	1.7	2.83	0.05	0.04	0.47
Cthe_02640 UDP-N-acetylglucosamine 2-epime	3.7	3.81	4.25	2.81	-0.55	1	-0.11	1.44	0.13	0.86	1.7	2.83	0.05	0.04	0.47
Cthe_00341 NADH dehydrogenase (quinone)	12.86	13.57	13.4	13.59	-0.54	-0.02	-0.71	-0.19	0.13	0	-0.3	-0.56	0.05	0.04	0.37
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_00679 Serine-type D-Ala-D-Ala carboxype	10.4	11.1	10.89	11.18	-0.49	-0.08	-0.7	-0.29	0.17	-0.05	-0.27	-0.77	0.05	0.04	0.39
Cthe_00679 Serine-type D-Ala-D-Ala carboxype	10.4	11.1	10.89	11.18	-0.49	-0.08	-0.7	-0.29	0.17	-0.05	-0.27	-0.77	0.05	0.04	0.39
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_00341 NADH dehydrogenase (quinone)	12.86	13.57	13.4	13.59	-0.54	-0.02	-0.71	-0.19	0.13	0	-0.3	-0.56	0.05	0.04	0.37
Cthe_02640 UDP-N-acetylglucosamine 2-epime	3.7	3.81	4.25	2.81	-0.55	1	-0.11	1.44	0.13	0.86	1.7	2.83	0.05	0.04	0.47
Cthe_02399 Formate--tetrahydrofolate ligase	10.46	11.25	11.25	11	-0.79	0.25	-0.79	0.25	-0.06	0.23	-0.57	0.35	0.05	0.04	0.63
Cthe_01105 type II secretion system protein	13.66	14.1	14.31	13.82	-0.65	0.28	-0.44	0.49	0.05	0.25	0.6	0.85	0.04	0.03	0.44
Cthe_01106 twitching motility protein	12.44	13.05	13.17	12.93	-0.73	0.12	-0.61	0.24	-0.02	0.12	0.03	0.33	0.03	0.03	0.66
Cthe_00042 small GTP-binding protein	9.88	10.68	10.45	10.47	-0.57	0.21	-0.8	-0.02	0.11	0.19	-0.6	-0.21	0.04	0.03	0.62
Cthe_01124 phenazine biosynthesis proteinPhzF family				0		0			0	0.02	-0.17	0.03	0.03		0.21
Cthe_02109 copper amine oxidase-like protein	10.98	11.64	11.65	11.65	-0.67	-0.01	-0.66	0	0.03	0.01	-0.13	-0.17	0.03	0.03	0.26
Cthe_02252 thioesterase family protein	8.12	8.87	8.62	8.83	-0.5	0.04	-0.75	-0.21	0.17	0.05	-0.43	-0.6	0.03	0.03	0.43
Cthe_00149 HPrNtr domain containing protein	12.45	12.86	13.17	12.37	-0.72	0.49	-0.41	0.8	-0.01	0.43	0.7	1.5	0.03	0.03	0.46
Cthe_01428 glycoside hydrolase, family 1	5.52	6.19	6.38	5.95	-0.86	0.24	-0.67	0.43	-0.12	0.22	-0.17	0.73	0.04	0.03	0.6
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_00210 transcriptional regulator, LacI fami	9.43	10.07	10.23	9.87	-0.8	0.2	-0.64	0.36	-0.07	0.19	-0.07	0.58	0.04	0.03	0.62
Cthe_00799 two component transcriptional reg	7.95	8.46	8.66	8.28	-0.71	0.18	-0.51	0.38	0	0.17	0.37	0.63	0.03	0.03	0.42
Cthe_00815 arginine repressor, ArgR	8.43	9.12	8.98	9.06	-0.55	0.06	-0.69	-0.08	0.13	0.07	-0.23	-0.33	0.04	0.03	0.66
Cthe_02505 transcriptional regulator, LacI fami	9.89	10.64	10.5	10.57	-0.61	0.07	-0.75	-0.07	0.08	0.08	-0.43	-0.31	0.04	0.03	0.38
Cthe_02698 putative transcriptional regulator,	9.41	9.99	10.15	9.7	-0.74	0.29	-0.58	0.45	-0.02	0.26	0.13	0.77	0.04	0.03	0.6
Cthe_02452 oligodeoxydiphosphatase F	10.55	11.24	11.16	11.16	-0.61	0.08	-0.69	0	0.08	0.08	-0.23	-0.17	0.03	0.03	0.71
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_03028 Pyridoxal-dependent decarboxylas	11.78	12.3	12.5	12.13	-0.72	0.17	-0.52	0.37	-0.01	0.16	0.33	0.6	0.03	0.03	0.42
Cthe_00223 hypothetical protein	3.58	4.32	3.7	4.52	-0.12	-0.2	-0.74	-0.82	0.47	-0.15	-0.4	-1.87	0.04	0.03	0.46
Cthe_00305 DNA topoisomerase (ATP-hydrolyzi	9.15	9.85	9.35	9.87	-0.2	-0.02	-0.7	-0.52	0.4	0	-0.27	-1.25	0.04	0.03	0.56
Cthe_01350 single-strand binding protein	10.51	11.2	11.06	11.25	-0.55	-0.05	-0.69	-0.19	0.13	-0.03	-0.23	-0.56	0.04	0.03	0.39
Cthe_01808 transposase IS116/IS110/IS902	10.43	11.03	11.27	10.62	-0.84	0.41	-0.6	0.65	-0.1	0.36	0.07	1.19	0.04	0.03	0.56
Cthe_02455 phage integrase				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_01904 amino acid adenylation domain	5.95	6.49	6.77	6.27	-0.82	0.22	-0.54	0.5	-0.09	0.2	0.27	0.88	0.04	0.03	0.43
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54
Cthe_01105 type II secretion system protein	13.66	14.1	14.31	13.82	-0.65	0.28	-0.44	0.49	0.05	0.25	0.6	0.85	0.04	0.03	0.44
Cthe_01106 twitching motility protein	12.44	13.05	13.17	12.93	-0.73	0.12	-0.61	0.24	-0.02	0.12	0.03	0.33	0.03	0.03	0.66
Cthe_01899 Serine-type D-Ala-D-Ala carboxype	9.7	10.26	10.06	10.41	-0.36	-0.15	-0.56	-0.35	0.28	-0.11	0.2	-0.9	0.04	0.03	0.58
Cthe_00409 ACT domain-containing protein	6.64	7.51	7.01	7.27	-0.37	0.24	-0.87	-0.26	0.27	0.22	-0.83	-0.71	0.04	0.03	0.57
Cthe_00799 two component transcriptional reg	7.95	8.46	8.66	8.28	-0.71	0.18	-0.51	0.38	0	0.17	0.37	0.63	0.03	0.03	0.42
Cthe_01153 diguanylate cyclase				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_01282 diguanylate cyclase with GAF senso	11.37	12.06	11.89	12.11	-0.52	-0.05	-0.69	-0.22	0.15	-0.03	-0.23	-0.63	0.03	0.03	0.41
Cthe_02078 protein of unknown function UPF0	12.13	12.7	12.98	12.54	-0.85	0.16	-0.57	0.44	-0.11	0.15	0.17	0.75	0.03	0.03	0.43
Cthe_03042 hypothetical protein	10.91	11.48	11.57	11.33	-0.66	0.15	-0.57	0.24	0.04	0.14	0.17	0.33	0.04	0.03	0.7
Cthe_01225 bacterial translation initiation facto	11.12	11.29	11.26	11.69	-0.14	-0.4	-0.17	-0.43	0.45	-0.32	1.5	-1.06	0.04	0.03	0.54
Cthe_02593 peptide chain release factor 1	11.15	11.86	12.11	11.61	-0.96	0.25	-0.71	0.5	-0.2	0.23	-0.3	0.88	0.04	0.03	0.59
Cthe_02606 ATP synthase F1, alpha subunit	9.5	10.48	9.84	10.12	-0.34	0.36	-0.98	-0.28	0.29	0.32	-1.2	-0.75	0.04	0.03	0.54
Cthe_03024 NADH dehydrogenase (quinone)	10.16	10.76	10.61	10.85	-0.45	-0.09	-0.6	-0.24	0.21	-0.06	0.07	-0.67	0.03	0.03	0.58
Cthe_03024 NADH dehydrogenase (quinone)	10.16	10.76	10.61	10.85	-0.45	-0.09	-0.6	-0.24	0.21	-0.06	0.07	-0.67	0.03	0.03	0.58
Cthe_02971 hypothetical protein	6.67	7.11	7.29	6.88	-0.62	0.23	-0.44	0.41	0.07	0.21	0.6	0.69	0.03	0.03	0.43
Cthe_01521 hypothetical protein	6.83	7.28	7.43	7.12	-0.6	0.16	-0.45	0.31	0.09	0.15	0.57	0.48	0.03	0.03	0.42
Cthe_02571 RNA related	6.97	7.4	7.51	7.47	-0.54	-0.07	-0.43	0.04	0.13	-0.04	0.63	-0.08	0.04	0.03	0.38
Cthe_02300 CRISPR-associated protein Cas5	10.38	11.03	11.11	10.94	-0.73	0.09	-0.65	0.17	-0.02	0.09	-0.1	0.19	0.03	0.03	0.77
Cthe_01139 hypothetical protein				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_02436 hypothetical protein	7.25	7.67	7.8	7.55	-0.55	0.12	-0.42	0.25	0.13	0.12	0.67	0.35	0.03	0.03	0.42
Cthe_00530 hypothetical protein	6.64	7.32	6.46	7.57	0.18	-0.25	-0.68	-1.11	0.71	-0.19	-0.2	-2.48	0.04	0.03	0.53
Cthe_00259 Rhomboid-like protein	9.99	10.62	10.84	10.34	-0.85	0.28	-0.63	0.5	-0.11	0.25	-0.03	0.88	0.03	0.03	0.55
Cthe_01705 hypothetical protein				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_01698 hypothetical protein				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_01118 hypothetical protein				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_02351 hypothetical protein	6.69	7.67	7.38	7.32	-0.69	0.35	-0.98	0.06	0.02	0.31	-1.2	-0.04	0.03	0.03	0.46
Cthe_01627 uncharacterized phage protein				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_01078 hypothetical protein	13.04	13.66	13.92	13.26	-0.88	0.4	-0.62	0.66	-0.13	0.36	0	1.21	0.04	0.03	0.56
Cthe_01711 hypothetical protein				0		0		0		0.02	-0.17	0.03	0.03		0.21
Cthe_00653 putative transcriptional regulator,	12.84	13.52	13.78	13.26	-0.94	0.26	-0.68	0.52	-0.18	0.24	-0.2	0.92	0.04	0.03	0.57
Cthe_01781 hypothetical protein	6.97	6.89	6.85	6.64	0.12	0.25	0.08	0.21	0.66	0.23	2.33	0.27	0.04	0.03	0.53
Cthe_02765 hypothetical protein	9.73	10.17	10.35	9.78	-0.62	0.39	-0.44	0.57	0.07	0.35	0.6	1.02	0.03	0.03	0.54
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54



Cthe_03024 NADH dehydrogenase (quinone)	10.16	10.76	10.61	10.85	-0.45	-0.09	-0.6	-0.24	0.21	-0.06	0.07	-0.67	0.03	0.03	0.58
Cthe_01428 glycoside hydrolase, family 1	5.52	6.19	6.38	5.95	-0.86	0.24	-0.67	0.43	-0.12	0.22	-0.17	0.73	0.04	0.03	0.6
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54
Cthe_02452 oligoendopeptidase F	10.55	11.24	11.16	11.16	-0.61	0.08	-0.69	0	0.08	0.08	-0.23	-0.17	0.03	0.03	0.71
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_01428 glycoside hydrolase, family 1	5.52	6.19	6.38	5.95	-0.86	0.24	-0.67	0.43	-0.12	0.22	-0.17	0.73	0.04	0.03	0.6
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54
Cthe_01899 Serine-type D-Ala-D-Ala carboxype	9.7	10.26	10.06	10.41	-0.36	-0.15	-0.56	-0.35	0.28	-0.11	0.2	-0.9	0.04	0.03	0.58
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_01428 glycoside hydrolase, family 1	5.52	6.19	6.38	5.95	-0.86	0.24	-0.67	0.43	-0.12	0.22	-0.17	0.73	0.04	0.03	0.6
Cthe_01428 glycoside hydrolase, family 1	5.52	6.19	6.38	5.95	-0.86	0.24	-0.67	0.43	-0.12	0.22	-0.17	0.73	0.04	0.03	0.6
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_01428 glycoside hydrolase, family 1	5.52	6.19	6.38	5.95	-0.86	0.24	-0.67	0.43	-0.12	0.22	-0.17	0.73	0.04	0.03	0.6
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02785 methyltransferase MtaA/CmuA fam	3.17	4.32	4.09	3.7	-0.92	0.62	-1.15	0.39	-0.17	0.54	-1.77	0.65	0.04	0.03	0.54
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_03028 Pyridoxal-dependent decarboxylas	11.78	12.3	12.5	12.13	-0.72	0.17	-0.52	0.37	-0.01	0.16	0.33	0.6	0.03	0.03	0.42
Cthe_01899 Serine-type D-Ala-D-Ala carboxype	9.7	10.26	10.06	10.41	-0.36	-0.15	-0.56	-0.35	0.28	-0.11	0.2	-0.9	0.04	0.03	0.58
Cthe_02714 acetolactate synthase, large subuni	12.29	13.3	13.05	12.84	-0.76	0.46	-1.01	0.21	-0.04	0.41	-1.3	0.27	0.04	0.03	0.55
Cthe_01899 Serine-type D-Ala-D-Ala carboxype	9.7	10.26	10.06	10.41	-0.36	-0.15	-0.56	-0.35	0.28	-0.11	0.2	-0.9	0.04	0.03	0.58
Cthe_02606 ATP synthase F1, alpha subunit	9.5	10.48	9.84	10.12	-0.34	0.36	-0.98	-0.28	0.29	0.32	-1.2	-0.75	0.04	0.03	0.54
Cthe_02449 Phosphoglycerate mutase	6.57	7.07	7.2	6.82	-0.63	0.25	-0.5	0.38	0.06	0.23	0.4	0.63	0.03	0.03	0.57
Cthe_01107 type II secretion system protein E	12.79	13.26	13.38	13.17	-0.59	0.09	-0.47	0.21	0.1	0.09	0.5	0.27	0.02	0.02	0.42
Cthe_00231 Radical SAM	10.21	10.94	10.61	10.89	-0.4	0.05	-0.73	-0.28	0.25	0.06	-0.37	-0.75	0.02	0.02	0.55
Cthe_01688 Radical SAM	0	0			0	0	0		0.56	0.02	2.07		0.02	0.02	0.48
Cthe_02474 phage terminase, large subunit, PB	0			0	0	0	0		0.56	0.02	2.07	-0.17	0.02	0.02	0.48
Cthe_03128 iron-sulfur flavoprotein	6.77	7.49	7.33	7.4	-0.56	0.09	-0.72	-0.07	0.12	0.09	-0.33	-0.31	0.02	0.02	0.59
Cthe_00971	6.64	7.37	7.25	7.3	-0.61	0.07	-0.73	-0.05	0.08	0.08	-0.37	-0.27	0.02	0.02	0.44
Cthe_00095 methylglyoxal synthase	9.73	10.36	10.15	10.45	-0.42	-0.09	-0.63	-0.3	0.23	-0.06	-0.03	-0.79	0.02	0.02	0.54
Cthe_00521 helicase-like protein	0	0			0	0	0	0	0.56	0.02	2.07	-0.17	0.02	0.02	0.48
Cthe_01742 Helix-turn-helix, type 11 containing	0				0				0.56		2.07		0.02	0.02	0.48
Cthe_02460 transcriptional regulator, XRE fami	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_02762 transcriptional regulator-like protei	8.78	9.37	9.54	9.33	-0.76	0.04	-0.59	0.21	-0.04	0.05	0.1	0.27	0.02	0.02	0.4
Cthe_02883 histidinol-phosphate aminotransfer	8.47	9.13	9.21	9.08	-0.74	0.05	-0.66	0.13	-0.02	0.06	-0.13	0.1	0.02	0.02	0.69
Cthe_00306 DNA gyrase/topoisomerase IV, sub	9.23	9.97	9.41	9.99	-0.18	-0.02	-0.74	-0.58	0.42	0	-0.4	-1.37	0.02	0.02	0.53
Cthe_00521 helicase-like protein	0	0			0	0	0	0	0.56	0.02	2.07	-0.17	0.02	0.02	0.48
Cthe_00585 Integrase, catalytic region	12.36	13.02	12.97	12.99	-0.61	0.03	-0.66	-0.02	0.08	0.04	-0.13	-0.21	0.02	0.02	0.65
Cthe_00833 exodeoxyribonuclease VII, large su	8.86	9.57	9.2	9.65	-0.34	-0.08	-0.71	-0.45	0.29	-0.05	-0.3	-1.1	0.02	0.02	0.46
Cthe_01161 hypothetical protein	0	0			0	0	0		0.56	0.02	2.07		0.02	0.02	0.48
Cthe_01874 transposase, mutator type	0	0			0	0	0		0.56	0.02	2.07		0.02	0.02	0.48
Cthe_02750 IstB-like ATP-binding protein	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_01107 type II secretion system protein E	12.79	13.26	13.38	13.17	-0.59	0.09	-0.47	0.21	0.1	0.09	0.5	0.27	0.02	0.02	0.42
Cthe_00243 copper amine oxidase-like protein	11.8	12.3	12.31	12.43	-0.51	-0.13	-0.5	-0.12	0.16	-0.09	0.4	-0.42	0.02	0.02	0.57
Cthe_02139 alpha-L-arabinofuranosidase B	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_02626 UDP-N-acetylmuramate-alanine lig	11.2	11.87	11.92	11.81	-0.72	0.06	-0.67	0.11	-0.01	0.07	-0.17	0.06	0.02	0.02	0.7
Cthe_03047 Peptidoglycan glycosyltransferase	9.38	10.32	9.93	9.99	-0.55	0.33	-0.94	-0.06	0.13	0.3	-1.07	-0.29	0.02	0.02	0.53
Cthe_02326 protein of unknown function DUF1	7.73	8.45	8.06	8.43	-0.33	0.02	-0.72	-0.37	0.3	0.03	-0.33	-0.94	0.02	0.02	0.54
Cthe_00803 pseudouridine synthase, RluA fami	7.52	8.07	8.24	7.82	-0.72	0.25	-0.55	0.42	-0.01	0.23	0.23	0.71	0.02	0.02	0.55
Cthe_02720 ribosomal protein L11	12.1	12.78	12.54	12.86	-0.44	-0.08	-0.68	-0.32	0.21	-0.05	-0.2	-0.83	0.02	0.02	0.45
Cthe_01604 phosphate ABC transporter, inner	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_02118 ABC transporter related protein	10.13	11.03	11.1	10.78	-0.97	0.25	-0.9	0.32	-0.21	0.23	-0.93	0.5	0.02	0.02	0.53
Cthe_02110 ABC transporter related protein	7.32	8.03	7.98	7.98	-0.66	0.05	-0.71	0	0.04	0.06	-0.3	-0.17	0.02	0.02	0.37
Cthe_00857 protein of unknown function DUF1	9.49	10.03	10.02	10.2	-0.53	-0.17	-0.54	-0.18	0.14	-0.13	0.27	-0.54	0.02	0.02	0.57
Cthe_02547 hypothetical protein	9.35	9.54	9.58	9.95	-0.23	-0.41	-0.19	-0.37	0.38	-0.33	1.43	-0.94	0.02	0.02	0.53
Cthe_02457 hypothetical protein	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_02500 hypothetical protein	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_01141 hypothetical protein	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_01416 hypothetical protein	4.95	4.95	4.95	5	0	-0.05	0	-0.05	0.56	-0.03	2.07	-0.27	0.02	0.02	0.48
Cthe_02976 hypothetical protein	0				0		0		0.56		2.07		0.02	0.02	0.48
Cthe_03188 copper amine oxidase-like protein	11.55	12.32	11.99	12.2	-0.44	0.12	-0.77	-0.21	0.21	0.12	-0.5	-0.6	0.02	0.02	0.55
Cthe_00090 hypothetical protein	7.95	8.24	8.31	8.35	-0.36	-0.11	-0.29	-0.04	0.28	-0.08	1.1	-0.25	0.02	0.02	0.46
Cthe_02835 hypothetical protein	10.18	10.69	10.96	10.2	-0.78	0.49	-0.51	0.76	-0.06	0.43	0.37	1.42	0.02	0.02	0.53
Cthe_01299 hypothetical protein	4.09	4.46	4.52	4.52	-0.43	-0.0									



Cthe_01552 MAEBL, putative	0	0		0	0	0	0.56	0.02	2.07		0.02	0.02	0.48		
Cthe_02720 ribosomal protein L11	12.1	12.78	12.54	12.86	-0.44	-0.08	-0.68	-0.32	0.21	-0.05	-0.2	-0.83	0.02	0.02	0.45
Cthe_02110 ABC transporter related protein	7.32	8.03	7.98	7.98	-0.66	0.05	-0.71	0	0.04	0.06	-0.3	-0.17	0.02	0.02	0.37
Cthe_02118 ABC transporter related protein	10.13	11.03	11.1	10.78	-0.97	0.25	-0.9	0.32	-0.21	0.23	-0.93	0.5	0.02	0.02	0.53
Cthe_02883 histidinol-phosphate aminotransfer	8.47	9.13	9.21	9.08	-0.74	0.05	-0.66	0.13	-0.02	0.06	-0.13	0.1	0.02	0.02	0.69
Cthe_01604 phosphate ABC transporter, inner	0			0			0		0.56		2.07		0.02	0.02	0.48
Cthe_02603 ATP synthase F0, C subunit	7.26	7.93	8.03	7.86	-0.77	0.07	-0.67	0.17	-0.05	0.08	-0.17	0.19	0.02	0.02	0.66
Cthe_02720 ribosomal protein L11	12.1	12.78	12.54	12.86	-0.44	-0.08	-0.68	-0.32	0.21	-0.05	-0.2	-0.83	0.02	0.02	0.45
Cthe_02603 ATP synthase F0, C subunit	7.26	7.93	8.03	7.86	-0.77	0.07	-0.67	0.17	-0.05	0.08	-0.17	0.19	0.02	0.02	0.66
Cthe_02883 histidinol-phosphate aminotransfer	8.47	9.13	9.21	9.08	-0.74	0.05	-0.66	0.13	-0.02	0.06	-0.13	0.1	0.02	0.02	0.69
Cthe_02603 ATP synthase F0, C subunit	7.26	7.93	8.03	7.86	-0.77	0.07	-0.67	0.17	-0.05	0.08	-0.17	0.19	0.02	0.02	0.66
Cthe_00095 methylglyoxal synthase	9.73	10.36	10.15	10.45	-0.42	-0.09	-0.63	-0.3	0.23	-0.06	-0.03	-0.79	0.02	0.02	0.54
Cthe_02626 UDP-N-acetylmuramate-alanine lig	11.2	11.87	11.92	11.81	-0.72	0.06	-0.67	0.11	-0.01	0.07	-0.17	0.06	0.02	0.02	0.7
Cthe_00306 DNA gyrase/topoisomerase IV, sub	9.23	9.97	9.41	9.99	-0.18	-0.02	-0.74	-0.58	0.42	0	-0.4	-1.37	0.02	0.02	0.53
Cthe_00833 exodeoxyribonuclease VII, large su	8.86	9.57	9.2	9.65	-0.34	-0.08	-0.71	-0.45	0.29	-0.05	-0.3	-1.1	0.02	0.02	0.46
Cthe_00803 pseudouridine synthase, RluA famil	7.52	8.07	8.24	7.82	-0.72	0.25	-0.55	0.42	-0.01	0.23	0.23	0.71	0.02	0.02	0.55
Cthe_03047 Peptidoglycan glycosyltransferase	9.38	10.32	9.93	9.99	-0.55	0.33	-0.94	-0.06	0.13	0.3	-1.07	-0.29	0.02	0.02	0.53
Cthe_02883 histidinol-phosphate aminotransfer	8.47	9.13	9.21	9.08	-0.74	0.05	-0.66	0.13	-0.02	0.06	-0.13	0.1	0.02	0.02	0.69
Cthe_02883 histidinol-phosphate aminotransfer	8.47	9.13	9.21	9.08	-0.74	0.05	-0.66	0.13	-0.02	0.06	-0.13	0.1	0.02	0.02	0.69
Cthe_02626 UDP-N-acetylmuramate-alanine lig	11.2	11.87	11.92	11.81	-0.72	0.06	-0.67	0.11	-0.01	0.07	-0.17	0.06	0.02	0.02	0.7
Cthe_03047 Peptidoglycan glycosyltransferase	9.38	10.32	9.93	9.99	-0.55	0.33	-0.94	-0.06	0.13	0.3	-1.07	-0.29	0.02	0.02	0.53
Cthe_03047 Peptidoglycan glycosyltransferase	9.38	10.32	9.93	9.99	-0.55	0.33	-0.94	-0.06	0.13	0.3	-1.07	-0.29	0.02	0.02	0.53
Cthe_02626 UDP-N-acetylmuramate-alanine lig	11.2	11.87	11.92	11.81	-0.72	0.06	-0.67	0.11	-0.01	0.07	-0.17	0.06	0.02	0.02	0.7
Cthe_03047 Peptidoglycan glycosyltransferase	9.38	10.32	9.93	9.99	-0.55	0.33	-0.94	-0.06	0.13	0.3	-1.07	-0.29	0.02	0.02	0.53
Cthe_02603 ATP synthase F0, C subunit	7.26	7.93	8.03	7.86	-0.77	0.07	-0.67	0.17	-0.05	0.08	-0.17	0.19	0.02	0.02	0.66
Cthe_03047 Peptidoglycan glycosyltransferase	9.38	10.32	9.93	9.99	-0.55	0.33	-0.94	-0.06	0.13	0.3	-1.07	-0.29	0.02	0.02	0.53
Cthe_00612 SSS sodium solute transporter supe	12.77	13.39	13.63	13.17	-0.86	0.22	-0.62	0.46	-0.12	0.2	0	0.79	0.01	0.01	0.53
Cthe_02169 metallophosphoesterase	5.93	6.51	6.13	6.92	-0.2	-0.41	-0.58	-0.79	0.4	-0.33	0.13	-1.81	0.01	0.01	0.51
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00537 two component transcriptional reg	7.32	7.68	7.7	7.85	-0.38	-0.17	-0.36	-0.15	0.26	-0.13	0.87	-0.48	0.01	0.01	0.52
Cthe_00612 SSS sodium solute transporter supe	12.77	13.39	13.63	13.17	-0.86	0.22	-0.62	0.46	-0.12	0.2	0	0.79	0.01	0.01	0.53
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00080 CheW protein	8.92	9.51	10.14	8.98	-1.22	0.53	-0.59	1.16	-0.4	0.47	0.1	2.25	0.01	0.01	0.49
Cthe_00080 CheW protein	8.92	9.51	10.14	8.98	-1.22	0.53	-0.59	1.16	-0.4	0.47	0.1	2.25	0.01	0.01	0.49
Cthe_00537 two component transcriptional reg	7.32	7.68	7.7	7.85	-0.38	-0.17	-0.36	-0.15	0.26	-0.13	0.87	-0.48	0.01	0.01	0.52
Cthe_00199 4Fe-4S ferredoxin, iron-sulfur bindi	4.46	5.09	4.64	5.46	-0.18	-0.37	-0.63	-0.82	0.42	-0.3	-0.03	-1.87	0.01	0.01	0.49
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00354 putative CoA-substrate-specific enz	5.81	6.39	6.44	6.41	-0.63	-0.02	-0.58	0.03	0.06	0	0.13	-0.1	0.01	0.01	0.65
Cthe_00255 hypothetical protein	6.95	7.37	7.45	7.5	-0.5	-0.13	-0.42	-0.05	0.17	-0.09	0.67	-0.27	0.01	0.01	0.48
Cthe_00232 hypothetical protein	10.05	10.48	10.52	10.55	-0.47	-0.07	-0.43	-0.03	0.19	-0.04	0.63	-0.23	0.01	0.01	0.52
Cthe_03214 hypothetical protein	10.82	11.44	11.36	11.59	-0.54	-0.15	-0.62	-0.23	0.13	-0.11	0	-0.65	0.01	0.01	0.47
Cthe_02384 S-layer-like domain containing prot	12.08	12.72	12.97	12.56	-0.89	0.16	-0.64	0.41	-0.14	0.15	-0.07	0.69	0.01	0.01	0.53
Cthe_00826 hypothetical protein	8.85	9.66	9.39	9.5	-0.54	0.16	-0.81	-0.11	0.13	0.15	-0.63	-0.4	0.01	0.01	0.47
Cthe_02023 RNA related	7.72	9.27	8.54	8.27	-0.82	1	-1.55	0.27	-0.09	0.86	-3.1	0.4	0.01	0.01	0.49
Cthe_01280 hypothetical protein	3.7	4.09	4.17	4.32	-0.47	-0.23	-0.39	-0.15	0.19	-0.18	0.77	-0.48	0.01	0.01	0.52
Cthe_01184 hypothetical protein	9.69	10.53	10.36	10.32	-0.67	0.21	-0.84	0.04	0.03	0.19	-0.73	-0.08	0.01	0.01	0.47
Cthe_01354 O-antigen polymerase	2	2	2.32	1	-0.32	1	0	1.32	0.31	0.86	2.07	2.58	0.01	0.01	0.49
Cthe_02591 hypothetical protein	13.21	13.79	13.93	13.73	-0.72	0.06	-0.58	0.2	-0.01	0.07	0.13	0.25	0.01	0.01	0.45
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_00234 AMP-dependent synthetase and lig	11.72	12.62	12.1	12.38	-0.38	0.24	-0.9	-0.28	0.26	0.22	-0.93	-0.75	0.01	0.01	0.51
Cthe_01720 peptidase S14, ClpP															
Cthe_01612 toxin secretion/phage lysis holin															
Cthe_01678 hypothetical protein															
Cthe_01690 Radical SAM															
Cthe_01695 Radical SAM															
Cthe_01704 toxin secretion/phage lysis holin															
Cthe_01716 phage head-tail adaptor, putative															
Cthe_01722 phage Terminase															
Cthe_01734 phage / plasmid primase, P4 family															
Cthe_02138 glycoside hydrolase, family 43															
Cthe_02996 intracellular protease, Pfpl family	11.24	11.86	12.18	11.62	-0.94	0.24	-0.62	0.56	-0.18	0.22	0	1	0	0	0.51
Cthe_01551															
Cthe_00536 glycoside hydrolase, family 5	12.02	12.51	12.65	12.33	-0.63	0.18	-0.49	0.32	0.06	0.17	0.43	0.5	0	0	0.49
Cthe_02567 hypothetical protein															
Cthe_01551															
Cthe_00895 RNA polymerase, sigma 38 subunit,	12.54	13.09	13.3	12.84	-0.76	0.25	-0.55	0.46	-0.04	0.23	0.23	0.79	0	0	0.51
Cthe_01600 two component transcriptional regulator, winged Cthe_01649 BRO-like protein															
Cthe_01603 SNP2-related protein Cthe_01605 hypothetical protein															
Cthe_01664 transcriptional regulator, MerR family Cthe_01729 DNA methylase N-4/N-6															
Cthe_01739 SNP2-related protein Cthe_01740 BRO-like protein															
Cthe_02358 Accessory gene regulator B	14.17	14.71	15.52	14.54</											



Cthe_00514 DNA methylase N-4/N-6															
Cthe_00516 IS66 Orf2 like															
Cthe_00523 Resolvase-like protein															
Cthe_00588 Integrase, catalytic region															
Cthe_00692 Integrase, catalytic region															
Cthe_00698 Integrase, catalytic region															
Cthe_00879 Integrase, catalytic region															
Cthe_01127 phage integrase															
Cthe_01156 zinc finger, CHC2-type															
Cthe_01206 Integrase, catalytic region															
Cthe_01242 Integrase, catalytic region															
Cthe_01392 Integrase, catalytic region															
Cthe_01469 Integrase, catalytic region															
Cthe_01496 Integrase, catalytic region															
Cthe_01550 transposase IS116/IS110/IS902	12.74	13.29	13.65	13.32	-0.91	-0.03	-0.55	0.33	-0.16	-0.01	0.23	0.52	0	0	0.5
Cthe_01650 DNA-directed DNA polymerase															
Cthe_01653 SNF2-related protein															
Cthe_01656 Integrase, catalytic region															
Cthe_01661 Integrase, catalytic region															
Cthe_01671 Recombinase															
Cthe_01674 Integrase, catalytic region															
Cthe_01676 Integrase, catalytic region															
Cthe_01683 Integrase, catalytic region															
Cthe_01684 transposase IS3/IS911															
Cthe_01687 Integrase, catalytic region															
Cthe_01691 Integrase, catalytic region															
Cthe_01700 Recombinase															
Cthe_01701 Recombinase															
Cthe_01712 Integrase, catalytic region															
Cthe_01723 phage terminase, small subunit, putative, P27 Cthe_01729 DNA methylase N-4/N-6															
Cthe_01735 phage DNA polymerase Cthe_01739 SNF2-related protein Cthe_01747 DNA mismatch endonuclease vsr Cthe_01883 Integrase, catalytic region Cthe_01885 SAMC protein-like protein Cthe_01885 phage integrase-like SAM-like Cthe_01889 transposase, mutator type Cthe_01976 Integrase, catalytic region Cthe_01993 Integrase, catalytic region Cthe_01999 integrase, catalytic region Cthe_02000 integrase, catalytic region Cthe_02004 transposase															
Cthe_02005 Isth-like ATP-binding protein Cthe_02012 Integrase, catalytic region Cthe_02017 transposase, mutator type Cthe_02114 Integrase, catalytic region Cthe_02135 Integrase, catalytic region Cthe_02153 Integrase, catalytic region Cthe_02173 Integrase, catalytic region Cthe_02188 Integrase, catalytic region Cthe_02198 transposase															
Cthe_02199 Isth-like ATP-binding protein Cthe_02201 transposase, mutator type Cthe_02294 transposase															
Cthe_02295 Isth-like ATP-binding protein Cthe_02315 DNA mismatch endonuclease vsr Cthe_02322 DNA recombinase															
Cthe_02324 Resolvase-like protein															
Cthe_02411 metallophosphoesterase	8.71	9.43	9.13	9.41	-0.42	0.02	-0.72	-0.28	0.23	0.03	-0.33	-0.75	0	0	0.51
Cthe_02418 ATPase	9.27	9.94	9.95	10.18	-0.68	-0.24	-0.67	-0.23	0.02	-0.19	-0.17	-0.65	0	0	0.51
Cthe_02467 replicative DNA helicase															
Cthe_02473 Terminase small subunit															
Cthe_02715 Integrase, catalytic region															
Cthe_02716 Integrase, catalytic region															
Cthe_02773 Integrase, catalytic region															
Cthe_02816 transposase, mutator type															
Cthe_02829 ISDet4, transposase															
Cthe_02830 Isth-like ATP-binding protein															
Cthe_02831 transposase															
Cthe_02858 transposase, mutator type															
Cthe_02958 transposase, mutator type															
Cthe_03051 transposase, mutator type															
Cthe_03181 Integrase, catalytic region															
Cthe_03182 Integrase, catalytic region															
Cthe_02158															
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_00900 aspartate 1-decarboxylase	6.92	7.35	7.59	7.58	-0.67	-0.23	-0.43	0.01	0.03	-0.18	0.63	-0.15	0	0	0.5
Cthe_01679 Methyltransferase type 11															
Cthe_01702 cell wall hydrolase/autolysin															
Cthe_02498 N-acetylmuramoyl-L-alanine amidase															
Cthe_01600 two component transcriptional regulator, winged															
Cthe_02358 Accessory gene regulator B	14.17	14.71	15.52	14.54	-1.35	0.17	-0.54	0.98	-0.51	0.16	0.27	1.88	0	0	0.5
Cthe_01132 hypothetical protein															
Cthe_01616 phage minor structural protein															
Cthe_01647 hypothetical protein															
Cthe_01707 phage minor structural protein															
Cthe_01708 phage putative tail component															
Cthe_01709 Phage-related protein-like protein															
Cthe_01721 phage portal protein, HK97 family															
Cthe_02489 Peptidoglycan-binding LysM															



Cthe_02492	Baseplate J-like protein															
Cthe_02495	hypothetical protein															
Cthe_02512	protein of unknown function DUF9	4.64	5.09	5.21	5.29	-0.57	-0.2	-0.45	-0.08	0.11	-0.15	0.57	-0.33	0	0	0.5
Cthe_01663	Endoribonuclease L-PSP															
Cthe_03185	tRNA-guanine transglycosylases, va	8.74	9.5	9.27	9.39	-0.53	0.11	-0.76	-0.12	0.14	0.11	-0.47	-0.42	0	0	0.5
Cthe_01601	phosphate uptake regulator, PhoU															
Cthe_01602 phosphate ABC transporter, ATPase subunit Cthe_03503 phosphate ABC transporter, inner membrane																
Cthe_01658 potassium uptake protein, TrkH family																
Cthe_00937	fatty acid/phospholipid synthesis p	11.48	12.1	12.13	12.19	-0.65	-0.09	-0.62	-0.06	0.05	-0.06	0	-0.29	0	0	0.48
Cthe_01232	AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_01396	phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_01144 restriction modification system DNA specificity Cthe_01245 W & DNA methylase																
Cthe_01668 ABC transporter related protein Cthe_05685 ABC transporter related																
protein Cthe_01665 Hsp33protein																
Cthe_01720 peptidase S14, ClpP																
Cthe_02358	Accessory gene regulator B	14.17	14.71	15.52	14.54	-1.35	0.17	-0.54	0.98	-0.51	0.16	0.27	1.88	0	0	0.5
Cthe_02748	SsrA-binding protein	9.32	10.08	10.19	10.15	-0.87	-0.07	-0.76	0.04	-0.13	-0.04	-0.47	-0.08	0	0	0.51
Cthe_02293	hypothetical protein															
Cthe_01115	Tn7-like transposition protein C															
Cthe_01123	hypothetical protein															
Cthe_01648	hypothetical protein															
Cthe_01131	hypothetical protein															
Cthe_00520	hypothetical protein															
Cthe_02497	hypothetical protein															
Cthe_01730	hypothetical protein															
Cthe_01750	hypothetical protein															
Cthe_01719	phage major capsid protein, HK97 family															
Cthe_02480	hypothetical protein															
Cthe_01875	HMG-I and HMG-Y, DNA-binding															
Cthe_01636	hypothetical protein															
Cthe_01743	protein of unknown function DUF955															
Cthe_02007	RNA related															
Cthe_01610	hypothetical protein															
Cthe_01733	hypothetical protein															
Cthe_02178	hypothetical protein	7.21	7.86	7.61	7.97	-0.4	-0.11	-0.65	-0.36	0.25	-0.08	-0.1	-0.92	0	0	0.51
Cthe_01699	RNA related															
Cthe_01706	hypothetical protein															
Cthe_01614	hypothetical protein															
Cthe_01876	Tn7-like transposition protein A															
Cthe_01693	hypothetical protein															
Cthe_02137	cellulosome enzyme, dockerin type I															
Cthe_01744	hypothetical protein															
Cthe_01146	hypothetical protein															
Cthe_00590	transposase IS3/IS911															
Cthe_01715	phage protein, HK97 gp10 family															
Cthe_01134	hypothetical protein															
Cthe_01625	phage protein, HK97 gp10 family															
Cthe_01738	hypothetical protein															
Cthe_02493	phage-like element PBSX protein															
Cthe_00526	hypothetical protein															
Cthe_01725	hypothetical protein															
Cthe_02861	hypothetical protein															
Cthe_02321	hypothetical protein															
Cthe_01731	HNH endonuclease															
Cthe_01158	hypothetical protein															
Cthe_01157	hypothetical protein															
Cthe_01142	hypothetical protein															
Cthe_01114	Tn7-like transposition protein D															
Cthe_03236	hypothetical protein															
Cthe_01654	hypothetical protein															
Cthe_02134	RNA related															
Cthe_01635	hypothetical protein															
Cthe_02468	hypothetical protein															
Cthe_01129	hypothetical protein															
Cthe_01622	hypothetical protein															
Cthe_02485	hypothetical protein															
Cthe_01642	hypothetical protein															
Cthe_01128	hypothetical protein															
Cthe_01135	SEFIR domain containing protein															
Cthe_01710	hypothetical protein															
Cthe_01669	DNA recombinase, putative															
Cthe_01652	hypothetical protein															
Cthe_01877	hypothetical protein															
Cthe_01680	DNA polymerase, beta-like region															
Cthe_00522	hypothetical protein															
Cthe_02481	hypothetical protein															
Cthe_01615	hypothetical protein															
Cthe_02852	hypothetical protein															
Cthe_01672	hypothetical protein															
Cthe_01724	hypothetical protein															
Cthe_02466	hypothetical protein															
Cthe_02864	hypothetical protein															
Cthe_02469 phage transcriptional regulator, RtnA family Cthe_02318 hypothetical protein																
Cthe_01741 hypothetical protein																
Cthe_01626 phage head-tail adaptor, putative Cthe_01608 Recombinase																
Cthe_01713 phage major tail protein, phi13 family																



Cthe\_02317 response regulator receiver protein Cthe\_01694 hypothetical protein  
Cthe\_02494 hypothetical protein Cthe\_01670 Recombinase Cthe\_01143  
hypothetical protein Cthe\_01634 hypothetical protein  
Cthe\_01745 transcriptional regulator, XRE family Cthe\_01725 hypothetical protein  
Cthe\_01664 hypothetical protein Cthe\_02450 hypothetical protein Cthe\_01651  
hypothetical protein Cthe\_01159 hypothetical protein Cthe\_01641 HNH  
endonuclease Cthe\_01121 hypothetical protein Cthe\_02499 hypothetical protein  
Cthe\_01717 hypothetical protein Cthe\_02482 hypothetical protein  
Cthe\_02475 phage portal protein, SPP1 family Cthe\_01872 Tn7-like transposition protein C  
Cthe\_01120 hypothetical protein  
Cthe\_01645 conserved hypothetical phage-associated protein Cthe\_01888 hypothetical protein  
Cthe\_02465 hypothetical protein Cthe\_01882 hypothetical protein Cthe\_01155  
hypothetical protein Cthe\_01878 hypothetical protein Cthe\_01117 Tn7-like  
transposition protein A Cthe\_00527 hypothetical protein Cthe\_02486 hypothetical  
protein Cthe\_01130 hypothetical protein Cthe\_01148 hypothetical protein Cthe\_01125  
hypothetical protein Cthe\_02487 hypothetical protein  
Cthe\_02463 DNA binding domain, excisionase Family Cthe\_01633 hypothetical protein  
Cthe\_01122 hypothetical protein Cthe\_02496 hypothetical protein Cthe\_01140  
hypothetical protein Cthe\_01130 hypothetical protein Cthe\_01736 hypothetical  
protein Cthe\_02316 hypothetical protein Cthe\_01714 hypothetical protein  
Cthe\_01746 hypothetical protein Cthe\_01677 Abortive infection protein  
Cthe\_00513 DNA binding domain, excisionase Family

Cthe_01927 hypothetical protein	6.52	6.67	7.03	7.2	-0.51	-0.53	-0.15	-0.17	0.16	-0.43	1.57	-0.52	0	0	0.5
Cthe_01703 HNH endonuclease															
Cthe_03238 hypothetical protein															
Cthe_01718 hypothetical protein															
Cthe_01621 hypothetical protein															
Cthe_01727 hypothetical protein															
Cthe_01160 S23 ribosomal protein															
Cthe_00517 hypothetical protein															
Cthe_01737 phage NTP-binding protein															
Cthe_00524 hypothetical protein															
Cthe_02488 phage tape measure protein															
Cthe_01644 hypothetical protein															
Cthe_01732 hypothetical protein															
Cthe_01646 hypothetical protein															
Cthe_02805 Carbohydrate-binding, CenC-like pr	12.47	13.09	13.11	13.19	-0.64	-0.1	-0.62	-0.08	0.06	-0.07	0	-0.33	0	0	0.5
Cthe_01133 hypothetical protein															
Cthe_01149 hypothetical protein															
Cthe_03054 hypothetical protein	2.81	3.91	4.09	3.91	-1.28	0	-1.1	0.18	-0.45	0.02	-1.6	0.21	0	0	0.5
Cthe_01126 hypothetical protein															
Cthe_02783 hypothetical protein															
Cthe_01116 HMG-I and HMG-Y, DNA-binding															
Cthe_01879 hypothetical protein															
Cthe_01668 ABC transporter related protein															
Cthe_01667 ABC-2 type transporter															
Cthe_01668 ABC transporter related protein															
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01602 phosphate ABC transporter, ATPase subunit															
Cthe_01603 phosphate ABC transporter, inner membrane															
Cthe_00900 aspartate 1-decarboxylase	6.92	7.35	7.59	7.58	-0.67	-0.23	-0.43	0.01	0.03	-0.18	0.63	-0.15	0	0	0.5
Cthe_00937 fatty acid/phospholipid synthesis p	11.48	12.1	12.13	12.19	-0.65	-0.09	-0.62	-0.06	0.05	-0.06	0	-0.29	0	0	0.48
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01144 restriction modification system DNA specificity															
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01747 DNA mismatch endonuclease vsr															
Cthe_02315 DNA mismatch endonuclease vsr															
Cthe_00937 fatty acid/phospholipid synthesis p	11.48	12.1	12.13	12.19	-0.65	-0.09	-0.62	-0.06	0.05	-0.06	0	-0.29	0	0	0.48
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01685 ABC transporter related protein															
Cthe_01602 phosphate ABC transporter, ATPase subunit															
Cthe_02996 intracellular protease, Pfpl family	11.24	11.86	12.18	11.62	-0.94	0.24	-0.62	0.56	-0.18	0.22	0	1	0	0	0.51
Cthe_01720 peptidase S14, ClpP															
Cthe_01650 DNA-directed DNA polymerase															
Cthe_01735 phage DNA polymerase															
Cthe_00900 aspartate 1-decarboxylase	6.92	7.35	7.59	7.58	-0.67	-0.23	-0.43	0.01	0.03	-0.18	0.63	-0.15	0	0	0.5



Cthe_01702 cell wall hydrolase/autolysin															
Cthe_02498 N-acetylmuramoyl-L-alanine amidase															
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_00937 fatty acid/phospholipid synthesis p	11.48	12.1	12.13	12.19	-0.65	-0.09	-0.62	-0.06	0.05	-0.06	0	-0.29	0	0	0.48
Cthe_00937 fatty acid/phospholipid synthesis p	11.48	12.1	12.13	12.19	-0.65	-0.09	-0.62	-0.06	0.05	-0.06	0	-0.29	0	0	0.48
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01685 ABC transporter related protein															
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_00900 aspartate 1-decarboxylase	6.92	7.35	7.59	7.58	-0.67	-0.23	-0.43	0.01	0.03	-0.18	0.63	-0.15	0	0	0.5
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01685 ABC transporter related protein															
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_00937 fatty acid/phospholipid synthesis p	11.48	12.1	12.13	12.19	-0.65	-0.09	-0.62	-0.06	0.05	-0.06	0	-0.29	0	0	0.48
Cthe_01685 ABC transporter related protein															
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01685 ABC transporter related protein															
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_01685 ABC transporter related protein															
Cthe_00831 Polyprenyl synthetase	8.12	8.76	8.74	9.03	-0.62	-0.27	-0.64	-0.29	0.07	-0.21	-0.07	-0.77	0	0	0.51
Cthe_01396 phospholipase D/Transphosphatidy	6.91	6.88	6.85	6.85	0.06	0.03	0.03	0	0.61	0.04	2.17	-0.17	0	0	0.5
Cthe_01232 AMP-dependent synthetase and lig	9.92	10.54	10.51	10.63	-0.59	-0.09	-0.62	-0.12	0.1	-0.06	0	-0.42	0	0	0.5
Cthe_02079 signal peptidase I	10.65	11.27	11.67	11.11	-1.02	0.16	-0.62	0.56	-0.25	0.15	0	1	-0.01	-0.01	0.52
Cthe_01188 protein of unknown function DUF9	8.31	8.99	9.03	9.22	-0.72	-0.23	-0.68	-0.19	-0.01	-0.18	-0.2	-0.56	-0.01	-0.01	0.54
Cthe_00275 glycosyltransferase 36	12.68	13.31	13.57	13.18	-0.89	0.13	-0.63	0.39	-0.14	0.13	-0.03	0.65	-0.01	-0.01	0.52
Cthe_01862 ABC transporter related protein	13.6	14.19	14.65	13.93	-1.05	0.26	-0.59	0.72	-0.27	0.24	0.1	1.33	-0.01	-0.01	0.48
Cthe_01906 glycosyl transferase, family 28	6.43	6.87	7.52	7.01	-1.09	-0.14	-0.44	0.51	-0.3	-0.1	0.6	0.9	-0.01	-0.01	0.52
Cthe_01963 glycoside hydrolase, family 10	13.23	14.16	14.31	13.99	-1.08	0.17	-0.93	0.32	-0.29	0.16	-1.03	0.5	-0.01	-0.01	0.52
Cthe_01050 recA protein	12.4	13.02	13.07	13.09	-0.67	-0.07	-0.62	-0.02	0.03	-0.04	0	-0.21	-0.01	-0.01	0.43
Cthe_00462 flagellar basal-body rod protein Flg	9.37	10.13	10.1	10.57	-0.73	-0.44	-0.76	-0.47	-0.02	-0.36	-0.47	-1.15	-0.01	-0.01	0.52
Cthe_02285 CheW protein	1	2.81	2.81	4.09	-1.81	-1.28	-1.81	-1.28	-0.87	-1.07	-3.97	-2.83	-0.01	-0.01	0.51
Cthe_00984 prolipoprotein diacylglyceryl transf	9.52	10.17	10.14	10.49	-0.62	-0.32	-0.65	-0.35	0.07	-0.25	-0.1	-0.9	-0.01	-0.01	0.51
Cthe_00375 GMP synthase, large subunit	11.94	12.37	12.51	12.6	-0.57	-0.23	-0.43	-0.09	0.11	-0.18	0.63	-0.35	-0.01	-0.01	0.52
Cthe_02285 CheW protein	1	2.81	2.81	4.09	-1.81	-1.28	-1.81	-1.28	-0.87	-1.07	-3.97	-2.83	-0.01	-0.01	0.51
Cthe_00410 protein of unknown function DUF7	10.41	11.01	11.05	11.15	-0.64	-0.14	-0.6	-0.1	0.06	-0.1	0.07	-0.38	-0.01	-0.01	0.54
Cthe_01223 ribosomal protein L20	11.65	12.07	12.24	12.29	-0.59	-0.22	-0.42	-0.05	0.1	-0.17	0.67	-0.27	-0.01	-0.01	0.49
Cthe_01794 translation elongation factor 2 (EF-	10.87	11.45	11.8	11.45	-0.93	0	-0.58	0.35	-0.17	0.02	0.13	0.56	-0.01	-0.01	0.53
Cthe_02729 translation elongation factor 2 (EF-	14.49	15.17	15.22	15.31	-0.73	-0.14	-0.68	-0.09	-0.02	-0.1	-0.2	-0.35	-0.01	-0.01	0.45
Cthe_02905 Ribosomal protein L25/L23	9.21	9.83	9.58	10.36	-0.37	-0.53	-0.62	-0.78	0.27	-0.43	0	-1.79	-0.01	-0.01	0.51
Cthe_01906 glycosyl transferase, family 28	6.43	6.87	7.52	7.01	-1.09	-0.14	-0.44	0.51	-0.3	-0.1	0.6	0.9	-0.01	-0.01	0.52
Cthe_02079 signal peptidase I	10.65	11.27	11.67	11.11	-1.02	0.16	-0.62	0.56	-0.25	0.15	0	1	-0.01	-0.01	0.52
Cthe_03065 hypothetical protein	11.07	11.59	11.75	11.71	-0.68	-0.12	-0.52	0.04	0.02	-0.08	0.33	-0.08	-0.01	-0.01	0.43
Cthe_02329 hypothetical protein	8.71	9.38	9.44	9.54	-0.73	-0.16	-0.67	-0.1	-0.02	-0.12	-0.17	-0.38	-0.01	-0.01	0.52
Cthe_01894 hypothetical protein	11.02	11.47	11.91	11.65	-0.89	-0.18	-0.45	0.26	-0.14	-0.14	0.57	0.38	-0.01	-0.01	0.52
Cthe_00411 hypothetical protein	12.13	12.68	13.02	12.71	-0.89	-0.03	-0.55	0.31	-0.14	-0.01	0.23	0.48	-0.01	-0.01	0.47
Cthe_00383 protein of unknown function DUF2	4	4	4.32	4.64	-0.32	-0.64	0	-0.32	0.31	-0.53	2.07	-0.83	-0.01	-0.01	0.49
Cthe_00121 hypothetical protein	4.95	4.86	5.04	5.52	-0.09	-0.66	0.09	-0.48	0.49	-0.54	2.37	-1.17	-0.01	-0.01	0.49
Cthe_00753 hypothetical protein	6.48	7.09	7.04	7.38	-0.56	-0.29	-0.61	-0.34	0.12	-0.23	0.03	-0.88	-0.01	-0.01	0.53
Cthe_02836 hypothetical protein	4.91	4.91	5.83	5.58	-0.92	-0.67	0	0.25	-0.17	-0.55	2.07	0.35	-0.01	-0.01	0.49
Cthe_01188 protein of unknown function DUF9	8.31	8.99	9.03	9.22	-0.72	-0.23	-0.68	-0.19	-0.01	-0.18	-0.2	-0.56	-0.01	-0.01	0.54
Cthe_02905 Ribosomal protein L25/L23	9.21	9.83	9.58	10.36	-0.37	-0.53	-0.62	-0.78	0.27	-0.43	0	-1.79	-0.01	-0.01	0.51
Cthe_00375 GMP synthase, large subunit	11.94	12.37	12.51	12.6	-0.57	-0.23	-0.43	-0.09	0.11	-0.18	0.63	-0.35	-0.01	-0.01	0.52
Cthe_01862 ABC transporter related protein	13.6	14.19	14.65	13.93	-1.05	0.26	-0.59	0.72	-0.27	0.24	0.1	1.33	-0.01	-0.01	0.48
Cthe_01862 ABC transporter related protein	13.6	14.19	14.65	13.93	-1.05	0.26	-0.59	0.72	-0.27	0.24	0.1	1.33	-0.01	-0.01	0.48
Cthe_01223 ribosomal protein L20	11.65	12.07	12.24	12.29	-0.59	-0.22	-0.42	-0.05	0.1	-0.17	0.67	-0.27	-0.01	-0.01	0.49
Cthe_02905 Ribosomal protein L25/L23	9.21	9.83	9.58	10.36	-0.37	-0.53	-0.62	-0.78	0.27	-0.43	0	-1.79	-0.01	-0.01	0.51
Cthe_01963 glycoside hydrolase, family 10	13.23	14.16	14.31	13.99	-1.08	0.17	-0.93	0.32	-0.29	0.16	-1.03	0.5	-0.01	-0.01	0.52
Cthe_00375 GMP synthase, large subunit	11.94	12.37	12.51	12.6	-0.57	-0.23	-0.43	-0.09	0.11	-0.18	0.63	-0.35	-0.01	-0.01	0.52
Cthe_00275 glycosyltransferase 36	12.68	13.31	13.57	13.18	-0.89	0.13	-0.63	0.39	-0.14	0.13	-0.03	0.65	-0.01	-0.01	0.52
Cthe_00984 prolipoprotein diacylglyceryl transf	9.52	10.17	10.14	10.49	-0.62	-0.32	-0.65	-0.35	0.07	-0.25	-0.1	-0.9	-0.01	-0.01	0.51
Cthe_02079 signal peptidase I	10.65	11.27	11.67	11.11	-1.02	0									



Cthe_00858 protein of unknown function DUF1	11.46	12.17	12.3	12.2	-0.84	-0.03	-0.71	0.1	-0.1	-0.01	-0.3	0.04	-0.02	-0.02	0.59
Cthe_02722 ribosomal protein L10	11.72	12.37	12.61	12.31	-0.89	0.06	-0.65	0.3	-0.14	0.07	-0.1	0.46	-0.02	-0.02	0.59
Cthe_02723 ribosomal protein L7/L12	11.6	12.14	12.48	12.17	-0.88	-0.03	-0.54	0.31	-0.13	-0.01	0.27	0.48	-0.02	-0.02	0.42
Cthe_00094 Septum formation topological spec	9.41	9.97	9.94	10.23	-0.53	-0.26	-0.56	-0.29	0.14	-0.2	0.2	-0.77	-0.02	-0.02	0.55
Cthe_02616 SpoID/LytB domain containing pro	4.52	5.21	5.21	5.52	-0.69	-0.31	-0.69	-0.31	0.02	-0.25	-0.23	-0.81	-0.02	-0.02	0.53
Cthe_00340 ferredoxin	10.22	10.76	10.66	11.03	-0.44	-0.27	-0.54	-0.37	0.21	-0.21	0.27	-0.94	-0.02	-0.02	0.54
Cthe_02594 zinc/iron permease	9.56	10.13	10.37	10.13	-0.81	0	-0.57	0.24	-0.08	0.02	0.17	0.33	-0.02	-0.02	0.4
Cthe_02576 hypothetical protein	9.87	10.32	10.58	10.57	-0.71	-0.25	-0.45	0.01	0	-0.19	0.57	-0.15	-0.02	-0.02	0.58
Cthe_00241 hypothetical protein	9.45	10.09	10.12	10.18	-0.67	-0.09	-0.64	-0.06	0.03	-0.06	-0.07	-0.29	-0.02	-0.02	0.4
Cthe_00709 hypothetical protein	7.47	8.04	7.85	8.4	-0.38	-0.36	-0.57	-0.55	0.26	-0.29	0.17	-1.31	-0.02	-0.02	0.53
Cthe_00835 hypothetical protein	6.39	6.73	7.3	7.01	-0.91	-0.28	-0.34	0.29	-0.16	-0.22	0.93	0.44	-0.02	-0.02	0.47
Cthe_01474 hypothetical protein	2.81	2.32	3.7	3.58	-0.89	-1.26	0.49	0.12	-0.14	-1.05	3.7	0.08	-0.02	-0.02	0.51
Cthe_01891 hypothetical protein	7.75	8.09	8.31	8.37	-0.56	-0.28	-0.34	-0.06	0.12	-0.22	0.93	-0.29	-0.02	-0.02	0.46
Cthe_02683 hypothetical protein	8.67	9.46	9.61	9.34	-0.94	0.12	-0.79	0.27	-0.18	0.12	-0.57	0.4	-0.02	-0.02	0.55
Cthe_01189 ABC transporter related protein	7.67	8.46	8.44	8.95	-0.77	-0.49	-0.79	-0.51	-0.05	-0.4	-0.57	-1.23	-0.02	-0.02	0.53
Cthe_01253 phosphoenolpyruvate synthase	9.46	10.32	10.45	10.14	-0.99	0.18	-0.86	0.31	-0.22	0.17	-0.8	0.48	-0.02	-0.02	0.53
Cthe_02722 ribosomal protein L10	11.72	12.37	12.61	12.31	-0.89	0.06	-0.65	0.3	-0.14	0.07	-0.1	0.46	-0.02	-0.02	0.59
Cthe_01253 phosphoenolpyruvate synthase	9.46	10.32	10.45	10.14	-0.99	0.18	-0.86	0.31	-0.22	0.17	-0.8	0.48	-0.02	-0.02	0.53
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_02725 DNA-directed RNA polymerase, bet	12.52	13.23	13.24	13.58	-0.72	-0.35	-0.71	-0.34	-0.01	-0.28	-0.3	-0.88	-0.02	-0.02	0.54
Cthe_02722 ribosomal protein L10	11.72	12.37	12.61	12.31	-0.89	0.06	-0.65	0.3	-0.14	0.07	-0.1	0.46	-0.02	-0.02	0.59
Cthe_02723 ribosomal protein L7/L12	11.6	12.14	12.48	12.17	-0.88	-0.03	-0.54	0.31	-0.13	-0.01	0.27	0.48	-0.02	-0.02	0.42
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_01253 phosphoenolpyruvate synthase	9.46	10.32	10.45	10.14	-0.99	0.18	-0.86	0.31	-0.22	0.17	-0.8	0.48	-0.02	-0.02	0.53
Cthe_02204 cyanophycin synthetase	6.02	6.95	6.94	7.55	-0.92	-0.6	-0.93	-0.61	-0.17	-0.49	-1.03	-1.44	-0.02	-0.02	0.52
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_00773 SOS-response transcriptional repre	9.9	10.57	10.72	10.51	-0.82	0.06	-0.67	0.21	-0.09	0.07	-0.17	0.27	-0.02	-0.02	0.64
Cthe_02725 DNA-directed RNA polymerase, bet	12.52	13.23	13.24	13.58	-0.72	-0.35	-0.71	-0.34	-0.01	-0.28	-0.3	-0.88	-0.02	-0.02	0.54
Cthe_01253 phosphoenolpyruvate synthase	9.46	10.32	10.45	10.14	-0.99	0.18	-0.86	0.31	-0.22	0.17	-0.8	0.48	-0.02	-0.02	0.53
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_01253 phosphoenolpyruvate synthase	9.46	10.32	10.45	10.14	-0.99	0.18	-0.86	0.31	-0.22	0.17	-0.8	0.48	-0.02	-0.02	0.53
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_01253 phosphoenolpyruvate synthase	9.46	10.32	10.45	10.14	-0.99	0.18	-0.86	0.31	-0.22	0.17	-0.8	0.48	-0.02	-0.02	0.53
Cthe_01253 phosphoenolpyruvate synthase	9.46	10.32	10.45	10.14	-0.99	0.18	-0.86	0.31	-0.22	0.17	-0.8	0.48	-0.02	-0.02	0.53
Cthe_02251 Methionine adenosyltransferase	10.57	11.11	11.37	11.23	-0.8	-0.12	-0.54	0.14	-0.07	-0.08	0.27	0.13	-0.02	-0.02	0.63
Cthe_00903 protein-export membrane protein	12.5	13.12	13.31	13.16	-0.81	-0.04	-0.62	0.15	-0.08	-0.02	0	0.15	-0.04	-0.03	0.98
Cthe_00616 amino acid-binding ACT	9.4	9.91	9.8	10.23	-0.4	-0.32	-0.51	-0.43	0.25	-0.25	0.37	-1.06	-0.04	-0.03	0.56
Cthe_02081 small GTP-binding protein	8.33	9.02	9.26	8.97	-0.93	0.05	-0.69	0.29	-0.17	0.06	-0.23	0.44	-0.04	-0.03	0.65
Cthe_02335 polysaccharide biosynthesis protei	9.22	9.74	9.95	9.82	-0.73	-0.08	-0.52	0.13	-0.02	-0.05	0.33	0.1	-0.04	-0.03	0.28
Cthe_02736 phosphoenolpyruvate-protein phos	14.67	15.36	15.78	15.01	-1.11	0.35	-0.69	0.77	-0.32	0.31	-0.23	1.44	-0.04	-0.03	0.55
Cthe_00931 Ribonuclease III	8.27	8.89	8.75	9.43	-0.48	-0.54	-0.62	-0.68	0.18	-0.44	0	-1.58	-0.03	-0.03	0.54
Cthe_03144 transcriptional regulator, AraC fam	6.77	7.19	7.28	7.53	-0.51	-0.34	-0.42	-0.25	0.16	-0.27	0.67	-0.69	-0.04	-0.03	0.58
Cthe_00148 transposase, mutator type	11.45	12.34	12.43	12.37	-0.98	-0.03	-0.89	0.06	-0.21	-0.01	-0.9	-0.04	-0.04	-0.03	0.42
Cthe_00758 protein of unknown function UPFO	6.89	7.49	7.29	8.05	-0.4	-0.56	-0.6	-0.76	0.25	-0.46	0.07	-1.75	-0.03	-0.03	0.53
Cthe_02663 methyl-accepting chemotaxis senso	8.61	9.18	9.59	9.06	-0.98	0.12	-0.57	0.53	-0.21	0.12	0.17	0.94	-0.03	-0.03	0.45
Cthe_00981 S-adenosyl-methyltransferase Mr	12.23	12.52	12.7	12.98	-0.47	-0.46	-0.29	-0.28	0.19	-0.37	1.1	-0.75	-0.04	-0.03	0.56
Cthe_01349 Undecaprenyl-phosphate galactose	10.63	11.15	11.42	11.22	-0.79	-0.07	-0.52	0.2	-0.06	-0.04	0.33	0.25	-0.04	-0.03	0.31
Cthe_01249 amidophosphoribosyltransferase	9.1	10.02	9.97	10.51	-0.87	-0.49	-0.92	-0.54	-0.13	-0.4	-1	-1.29	-0.04	-0.03	0.46
Cthe_01293 metal dependent phosphohydrolas	8.27	8.98	8.81	9.43	-0.54	-0.45	-0.71	-0.62	0.13	-0.36	-0.3	-1.46	-0.03	-0.03	0.46
Cthe_02352 putative signal-transduction protei	10.62	11.26	11.95	10.99	-1.33	0.27	-0.64	0.96	-0.49	0.25	-0.07	1.83	-0.04	-0.03	0.54
Cthe_02663 methyl-accepting chemotaxis senso	8.61	9.18	9.59	9.06	-0.98	0.12	-0.57	0.53	-0.21	0.12	0.17	0.94	-0.03	-0.03	0.45
Cthe_02699 transcriptional modulator of MazE/	9.57	10.19	10.32	10.25	-0.75	-0.06	-0.62	0.07	-0.03	-0.03	0	-0.02	-0.04	-0.03	3.79
Cthe_00337 PHP-like protein	8.38	9.18	9.24	9.55	-0.86	-0.37	-0.8	-0.31	-0.12	-0.3	-0.6	-0.81	-0.04	-0.03	0.57
Cthe_00771 putative helix-turn-helix protein, YI	8.17	8.93	8.8	9.36	-0.63	-0.43	-0.76	-0.56	0.06	-0.35	-0.47	-1.33	-0.04	-0.03	0.45
Cthe_02662 RNA binding S1	12.14	12.74	12.78	13	-0.64	-0.26	-0.6	-0.22	0.06	-0.2	0.07	-0.63	-0.03	-0.03	0.59
Cthe_02925 methionine aminopeptidase, type I	12.23	12.87	13.02	13.06	-0.69	-0.19	-0.54	-0.04	0.02	-0.14	0.27	-0.25	-0.04	-0.03	0.69
Cthe_02927 bacterial translation initiation facto	8.79	9.39	9.42	9.71	-0.63	-0.32	-0.6	-0.29	0.06	-0.25	0.07	-0.77	-0.04	-0.03	0.59
Cthe_00166 4Fe-4S ferredoxin, iron-sulfur bindi	8.17	8.74	8.78	8.95	-0.61	-0.21	-0.57	-0.17	0.08	-0.16	0.17	-0.52	-0.03	-0.03	0.58
Cthe_03158 putative aconitate hydratase	11.26	12.04	12.17	11.9	-0.91	0.14	-0.78	0.27	-0.16	0.14	-0.53	0.4	-0.03	-0.03	0.57
Cthe_01917 ATPase, P-type (transporting), HAD	9.86	10.54	10.46	11.09	-0.6	-0.55	-0.68	-0.63	0.09	-0.45	-0.2	-1.48	-0.04	-0.03	0.55
Cthe_02575 hypothetical protein	3.17	4.39	4.64	4.09	-1.47	0.3	-1.22	0.55	-0.6	0.27	-2	0.98	-0.03	-0.03	0.53
Cthe_02934 ABC transporter related protein	8.94	9.51	9.37	9.93	-0.43	-0.42	-0.57	-0.56	0.22	-0.34	0.17	-1.33	-0.03	-0.03	0.54
Cthe_02742 Endopeptidase La	7.39	8.13	8.15	8.3	-0.76	-0.17	-0.74	-0.15	-0.04	-0.13	-0.4	-0.48	-0.04	-0.03	0.39
Cthe_02121 hypothetical protein	9.41	10.08	10.51	9.81	-1.1	0.27	-0.67	0.7	-0.31	0.25	-0.17	1.29	-0.03	-0.03	0.55
Cthe_02592 hypothetical protein	10.16	10.73	10.93	10.75	-0.77	-0.02	-0.57	0.18	-0.05	0	0.17	0.21	-0.03	-0.03	0.33
Cthe_02837 prophage Lp4 protein 7, DNA replic	2.32	1.58	2	3	0.32	-1.42	0.74	-1	0.82	-1.19	4.53	-2.25	-0.03	-0.03	0.51
Cthe_00346 hypothetical protein	7.55	8.07	8.69	8.1	-1.14	-0.03	-0.52	0.59	-0.34	-0.01	0.33	1.06	-0.03	-0.03	0.55
Cthe_02980 hypothetical protein	9.36	10.05	10.44	9.82	-1.08	0.23	-0.69	0.62	-0.29	0.21	-0.23	1.13	-0.04	-0.03	0.55
Cthe_02611 Fibronectin, type III	9.91	10.62	10.8	10.53	-0.89	0.09	-0.71	0.27	-0.14	0.09	-0.3	0.4	-0.03	-0.03	0.59
Cthe_02997 hypothetical protein	6.57	7.07	7	7.38	-0.43	-0.31	-0.5	-0.38	0.22	-0.25	0.4	-0.96	-0.04	-0.03	0.57
Cthe_01748 hypothetical protein		0		1	-1	0	-1	-1	-0.83	2.07	-2.25	-0.03	-0.03	-0.03	0.48
Cthe_00497 RNA related	2.58	3.58	3.58	4.25	-1	-0.67	-1	-0.67	-0.23	-0.55	-1.27	-1.56	-0.03	-0.03	0.53
Cthe_00321 TPR repeat domain containing prot	8.79	9.42	9.54	9.54	-0.75	-0.12	-0.63	0	-0.03	-0.08	-0.03	-0.17	-0.04	-0.03	0.88
Cthe_00955 hypothetical protein	4.09	5.25	5.17	6.25	-1.08	-1	-1.16	-1.08	-0.29	-0.83	-1.8	-2.42	-0.03	-0.03	0.52
Cthe_02669 hypothetical protein	8.4	8.87	8.99	9.12	-0.59	-0.25	-0.47	-0.13	0.1	-0.19	0.5	-0.44	-0.03	-0.03	0.58
Cthe_03158 putative aconitate hydratase	11.26	12.04	12.17	11.9	-0.91	0.14	-0.78	0.27	-0.16	0.14	-0.53	0.4	-0.03	-0.03	0.57
Cthe_03158 putative a															







Cthe_03088	12.8	13.33	13.84	13.07	-1.04	0.26	-0.53	0.77	-0.26	0.24	0.3	1.44	-0.06	-0.05	0.43
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_00973 UDP-N-acetylglucosamine	4.25	4.46	4.64	5.04	-0.39	-0.58	-0.21	-0.4	0.25	-0.47	1.37	-1	-0.06	-0.05	0.56
Cthe_02637 glycosyl transferase, group 1	3.58	3.17	3.7	4.17	-0.12	-1	0.41	-0.47	0.47	-0.83	3.43	-1.15	-0.06	-0.05	0.47
Cthe_00583 response regulator receiver protein	9.7	10.34	10.56	10.38	-0.86	-0.04	-0.64	0.18	-0.12	-0.02	-0.07	0.21	-0.06	-0.05	0.98
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_02533 sulfate ABC transporter, inner mem	2.32	2.81	3.58	2.58	-1.26	0.23	-0.49	1	-0.44	0.21	0.43	1.92	-0.06	-0.05	0.44
Cthe_02826 hypothetical protein	11.6	12.13	12.66	11.84	-1.06	0.29	-0.53	0.82	-0.28	0.26	0.3	1.54	-0.06	-0.05	0.43
Cthe_01977 hypothetical protein	6.89	7.52	8.01	7.46	-1.12	0.06	-0.63	0.55	-0.33	0.07	-0.03	0.98	-0.06	-0.05	0.61
Cthe_02478 phage minor structural GP20	2.58	3	3.32	3.17	-0.74	-0.17	-0.42	0.15	-0.02	-0.13	0.67	0.15	-0.06	-0.05	0.34
Cthe_01407 hypothetical protein	3.17	4.17	4.39	4.32	-1.22	-0.15	-1	0.07	-0.4	-0.11	-1.27	-0.02	-0.06	-0.05	0.58
Cthe_01065 type IV pilus assembly PilZ	10.76	11.41	12	11.26	-1.24	0.15	-0.65	0.74	-0.42	0.14	-0.1	1.38	-0.06	-0.05	0.57
Cthe_00772 Peptidoglycan-binding LysM	9.54	9.96	10.65	10.17	-1.11	-0.21	-0.42	0.48	-0.32	-0.16	0.67	0.83	-0.06	-0.05	0.6
Cthe_00631 hypothetical protein	10.53	11.08	11.16	11.39	-0.63	-0.31	-0.55	-0.23	0.06	-0.25	0.23	-0.65	-0.06	-0.05	0.67
Cthe_02533 sulfate ABC transporter, inner mem	2.32	2.81	3.58	2.58	-1.26	0.23	-0.49	1	-0.44	0.21	0.43	1.92	-0.06	-0.05	0.44
Cthe_02548 Alpha-N-arabinofuranosidase	8.17	8.87	8.53	9.27	-0.36	-0.4	-0.7	-0.74	0.28	-0.32	-0.27	-1.71	-0.06	-0.05	0.44
Cthe_00973 UDP-N-acetylglucosamine	4.25	4.46	4.64	5.04	-0.39	-0.58	-0.21	-0.4	0.25	-0.47	1.37	-1	-0.06	-0.05	0.56
Cthe_01956 Tagatose-6-phosphate kinase	8.92	9.77	9.77	9.66	-0.85	0.11	-0.85	0.11	-0.11	0.11	-0.77	0.06	-0.06	-0.05	0.36
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_00973 UDP-N-acetylglucosamine	4.25	4.46	4.64	5.04	-0.39	-0.58	-0.21	-0.4	0.25	-0.47	1.37	-1	-0.06	-0.05	0.56
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_01956 Tagatose-6-phosphate kinase	8.92	9.77	9.77	9.66	-0.85	0.11	-0.85	0.11	-0.11	0.11	-0.77	0.06	-0.06	-0.05	0.36
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_00973 UDP-N-acetylglucosamine	4.25	4.46	4.64	5.04	-0.39	-0.58	-0.21	-0.4	0.25	-0.47	1.37	-1	-0.06	-0.05	0.56
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_00973 UDP-N-acetylglucosamine	4.25	4.46	4.64	5.04	-0.39	-0.58	-0.21	-0.4	0.25	-0.47	1.37	-1	-0.06	-0.05	0.56
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_03059 phosphotransferase KptA/Tpt1	7.01	7.45	7.92	7.55	-0.91	-0.1	-0.44	0.37	-0.16	-0.07	0.6	0.6	-0.06	-0.05	0.37
Cthe_01956 Tagatose-6-phosphate kinase	8.92	9.77	9.77	9.66	-0.85	0.11	-0.85	0.11	-0.11	0.11	-0.77	0.06	-0.06	-0.05	0.36
Cthe_00737 Phosphopantethiene-protein trans	10.28	10.59	10.93	11.05	-0.65	-0.46	-0.31	-0.12	0.05	-0.37	1.03	-0.42	-0.06	-0.05	0.6
Cthe_00342 hydrogenase, Fe-only	13.66	14.27	14.46	14.35	-0.8	-0.08	-0.61	0.11	-0.07	-0.05	0.03	0.06	-0.07	-0.06	2.29
Cthe_00912 glycoside hydrolase, family 10	11.44	11.92	12.97	11.92	-1.53	0	-0.48	1.05	-0.65	0.02	0.47	2.02	-0.07	-0.06	0.56
Cthe_00403 DNA-directed RNA polymerase sigma	9.06	9.56	9.73	9.62	-0.67	-0.06	-0.5	0.11	0.03	-0.03	0.4	0.06	-0.07	-0.06	0.19
Cthe_03159 transcriptional regulator, GntR fam	10.75	11.52	11.77	11.5	-1.02	0.02	-0.77	0.27	-0.25	0.03	-0.5	0.4	-0.07	-0.06	0.7
Cthe_03212 protein of unknown function DUF3	10.65	11.22	11.23	11.66	-0.58	-0.44	-0.57	-0.43	0.1	-0.36	0.17	-1.06	-0.07	-0.06	0.62
Cthe_01938 D-alanine--D-alanine ligase	9.77	10.56	10.88	10.29	-1.11	0.27	-0.79	0.59	-0.32	0.25	-0.57	1.06	-0.07	-0.06	0.6
Cthe_02141 metal-dependent phosphohydrolas	7.23	7.65	7.79	8.03	-0.56	-0.38	-0.42	-0.24	0.12	-0.31	0.67	-0.67	-0.07	-0.06	0.63
Cthe_00273 metal dependent phosphohydrolas	10.91	11.5	12.17	11.45	-1.26	0.05	-0.59	0.72	-0.44	0.06	0.1	1.33	-0.07	-0.06	0.59
Cthe_00800 periplasmic sensor signal transduct	7.74	8.45	8.69	8.47	-0.95	-0.02	-0.71	0.22	-0.19	0	-0.3	0.29	-0.07	-0.06	0.81
Cthe_00318 ErfK/YbiS/Ycf5/YnhG	1	0	2.81	1.58	-1.81	-1.58	1	1.23	-0.87	-1.32	5.4	2.4	-0.07	-0.06	0.48
Cthe_02780 hypothetical protein	7.74	8.51	8.79	8.43	-1.05	0.08	-0.77	0.36	-0.27	0.08	-0.5	0.58	-0.07	-0.06	0.66
Cthe_01224 ribosomal protein L35	9.68	10.1	10.16	10.54	-0.48	-0.44	-0.42	-0.38	0.18	-0.36	0.67	-0.96	-0.07	-0.06	0.61
Cthe_03161 Pseudouridine synthase, Rsu	7.14	7.67	7.89	7.88	-0.75	-0.21	-0.53	0.01	-0.03	-0.16	0.3	-0.15	-0.07	-0.06	0.87
Cthe_00291 protein of unknown function DUF2	8.65	9.58	9.82	9.21	-1.17	0.37	-0.93	0.61	-0.37	0.33	-1.03	1.1	-0.07	-0.06	0.59
Cthe_01775 peptidase M22, glycoprotease	8.28	8.86	8.98	9.13	-0.7	-0.27	-0.58	-0.15	0.01	-0.21	0.13	-0.48	-0.07	-0.06	0.75
Cthe_00836 hypothetical protein	11.03	11.66	11.83	11.73	-0.8	-0.07	-0.63	0.1	-0.07	-0.04	-0.03	0.04	-0.07	-0.06	2.88
Cthe_03163 Carbohydrate binding family 25	12.15	12.66	13.05	12.59	-0.9	0.07	-0.51	0.46	-0.15	0.08	0.37	0.79	-0.07	-0.06	0.35
Cthe_00279 hypothetical protein	7	7.77	8.09	7.67	-1.09	0.1	-0.77	0.42	-0.3	0.1	-0.5	0.71	-0.07	-0.06	0.65
Cthe_02394 hypothetical protein	7.83	8.48	8.79	8.5	-0.96	-0.02	-0.65	0.29	-0.2	0	-0.1	0.44	-0.07	-0.06	0.79
Cthe_01454 hypothetical protein	7.29	7.63	8.44	7.76	-1.15	-0.13	-0.34	0.68	-0.35	-0.09	0.93	1.25	-0.07	-0.06	0.41
Cthe_01043 hypothetical protein	5.36	5.21	6.09	6	-0.73	-0.79	0.15	0.09	-0.02	-0.65	2.57	0.02	-0.07	-0.06	0.45
Cthe_00859 hypothetical protein	10.92	11.47	11.72	11.63	-0.8	-0.16	-0.55	0.09	-0.07	-0.12	0.23	0.02	-0.07	-0.06	1.07
Cthe_00342 hydrogenase, Fe-only	13.66	14.27	14.46	14.35	-0.8	-0.08	-0.61	0.11	-0.07	-0.05	0.03	0.06	-0.07	-0.06	2.29
Cthe_01224 ribosomal protein L35	9.68	10.1	10.16	10.54	-0.48	-0.44	-0.42	-0.38	0.18	-0.36	0.67	-0.96	-0.07	-0.06	0.61
Cthe_02141 metal-dependent phosphohydrolas	7.23	7.65	7.79	8.03	-0.56	-0.38	-0.42	-0.24	0.12	-0.31	0.67	-0.67	-0.07	-0.06	0.63
Cthe_03161 Pseudouridine synthase, Rsu	7.14	7.67	7.89	7.88	-0.75	-0.21	-0.53	0.01	-0.03	-0.16	0.3	-0.15	-0.07	-0.06	0.87
Cthe_01938 D-alanine--D-alanine ligase	9.77	10.56	10.88	10.29	-1.11	0.27	-0.79	0.59	-0.32	0.25	-0.57	1.06	-0.07	-0.06	0.6
Cthe_00342 hydrogenase, Fe-only	13.66	14.27	14.46	14.35	-0.8	-0.08	-0.61	0.11	-0.07	-0.05	0.03	0.06	-0.07	-0.06	2.29
Cthe_00342 hydrogenase, Fe-only	13.66	14.27	14.46	14.35	-0.8	-0.08	-0.61	0.11	-0.07	-0.05	0.03	0.06	-0.07	-0.06	2.29
Cthe_00342 hydrogenase, Fe-only	13.66	14.27	14.46	14.35	-0.8	-0.08	-0.61	0.11	-0.07	-0.05	0.03	0.06	-0.07	-0.06	2.29
Cthe_01938 D-alanine--D-alanine ligase	9.77	10.56	10.88	10.29	-1.11	0.27	-0.79	0.59	-0.32	0.25	-0.57	1.06	-0.07	-0.06	0.6
Cthe_01938 D-alanine--D-alanine ligase	9.77	10.56	10.88	10.29	-1.11	0.27	-0.79	0.59	-0.32	0.25	-0.57	1.06	-0.07	-0.06	0.6
Cthe_00342 hydrogenase, Fe-only	13.66	14.27	14.46	14.35	-0.8	-0.08	-0.61	0.11	-0.07	-0.05	0.03	0.06	-0.07	-0.06	2.29
Cthe_02280 ABC transporter related protein	5.04	5.52	5.78	5.81	-0.74	-0.29	-0.48	-0.03	-0.02	-0.23	0.47	-0.23	-0.08	-0.07	0.79
Cthe_02039 UvrD/REP helicase	7.16	8.18	8.49	7.92	-1.33	0.26	-1.02	0.57	-0.49	0.24	-1.33	1.02	-0.08	-0.07	0.58
Cthe_02954 hypothetical protein	3.7	4.39	4.7	4.39	-1	0	-0.69	0.31	-0.23	0.02	-0.23	0.48	-0.08	-0.07	0.77
Cthe_01172 protein of unknown function DUF3	9.97	10.67	10.68	10.71	-0.71	-0.04	-0.7	-0.03	0	-0.02	-0.27	-0.23	-0.08	-0.07	0.1
Cthe_02926 hypothetical protein	8.58	8.99	8.95	9.51	-0.37	-0.52	-0.41	-0.56	0.27	-0.42	0.7	-1.33	-0.08	-0.07	



Cthe_01785 protein of unknown function DUF1	9.91	10.47	10.58	10.84	-0.67	-0.37	-0.56	-0.26	0.03	-0.3	0.2	-0.71	-0.09	-0.08	0.73
Cthe_02656 MazG family protein	9.25	9.35	9.58	10.1	-0.33	-0.75	-0.1	-0.52	0.3	-0.62	1.73	-1.25	-0.09	-0.08	0.58
Cthe_00211 glycoside hydrolase, family 16	9.73	10.42	10.89	10.35	-1.16	0.07	-0.69	0.54	-0.36	0.08	-0.23	0.96	-0.09	-0.08	0.67
Cthe_00322 glycoside hydrolase, family 3-like p	8.54	9.26	9.41	9.48	-0.87	-0.22	-0.72	-0.07	-0.13	-0.17	-0.33	-0.31	-0.09	-0.08	0.84
Cthe_01957 extracellular solute-binding protein	9.16	9.92	10.1	10.12	-0.94	-0.2	-0.76	-0.02	-0.18	-0.15	-0.47	-0.21	-0.09	-0.08	0.81
Cthe_02120 RNA polymerase sigma factor	9.17	9.96	10.39	9.8	-1.22	0.16	-0.79	0.59	-0.4	0.15	-0.57	1.06	-0.09	-0.08	0.63
Cthe_02992 RNA polymerase, sigma-24 subunit	7.68	8.13	9.25	8.19	-1.57	-0.06	-0.45	1.06	-0.68	-0.03	0.57	2.04	-0.09	-0.08	0.57
Cthe_02274 hypothetical protein	5.61	6.07	6.46	6.34	-0.85	-0.27	-0.46	0.12	-0.11	-0.21	0.53	0.08	-0.09	-0.08	0.79
Cthe_02894 hypothetical protein	9.22	9.61	9.92	10.02	-0.7	-0.41	-0.39	-0.1	0.01	-0.33	0.77	-0.38	-0.09	-0.08	0.69
Cthe_01957 extracellular solute-binding protein	9.16	9.92	10.1	10.12	-0.94	-0.2	-0.76	-0.02	-0.18	-0.15	-0.47	-0.21	-0.09	-0.08	0.81
Cthe_00322 glycoside hydrolase, family 3-like p	8.54	9.26	9.41	9.48	-0.87	-0.22	-0.72	-0.07	-0.13	-0.17	-0.33	-0.31	-0.09	-0.08	0.84
Cthe_00322 glycoside hydrolase, family 3-like p	8.54	9.26	9.41	9.48	-0.87	-0.22	-0.72	-0.07	-0.13	-0.17	-0.33	-0.31	-0.09	-0.08	0.84
Cthe_00322 glycoside hydrolase, family 3-like p	8.54	9.26	9.41	9.48	-0.87	-0.22	-0.72	-0.07	-0.13	-0.17	-0.33	-0.31	-0.09	-0.08	0.84
Cthe_02664 ABC-1	9.17	9.71	10.02	9.89	-0.85	-0.18	-0.54	0.13	-0.11	-0.14	0.27	0.1	-0.1	-0.09	1.1
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_02623 Exopolysaccharide biosynthesis pro	7.55	8.23	8.26	8.81	-0.71	-0.58	-0.68	-0.55	0	-0.47	-0.2	-1.31	-0.1	-0.09	0.63
Cthe_00553 transcriptional regulator, LysR fami	6.07	7.09	7.38	7.13	-1.31	-0.04	-1.02	0.25	-0.48	-0.02	-1.33	0.35	-0.1	-0.09	0.62
Cthe_01057 phage shock protein C, PspC	8.29	8.68	9.42	8.68	-1.13	0	-0.39	0.74	-0.33	0.02	0.77	1.38	-0.11	-0.09	0.37
Cthe_03149 aminoacyl-histidine dipeptidase	9.04	9.55	9.67	9.97	-0.63	-0.42	-0.51	-0.3	0.06	-0.34	0.37	-0.79	-0.1	-0.09	0.71
Cthe_00311 excinuclease ABC, A subunit	11.51	12.26	12.8	12.12	-1.29	0.14	-0.75	0.68	-0.46	0.14	-0.43	1.25	-0.11	-0.09	0.65
Cthe_00356 transposase, mutator type	6.85	8.55	8.67	8.81	-1.82	-0.26	-1.7	-0.14	-0.88	-0.2	-3.6	-0.46	-0.11	-0.09	0.44
Cthe_02952 IstB-like ATP-binding protein	4.86	5.78	6	6	-1.14	-0.22	-0.92	0	-0.34	-0.17	-1	-0.17	-0.1	-0.09	0.67
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_01171 Serine-type D-Ala-D-Ala carboxype	10.46	10.94	11.51	10.71	-1.05	0.23	-0.48	0.8	-0.27	0.21	0.47	1.5	-0.1	-0.09	0.39
Cthe_00538 periplasmic sensor signal transduct	7.19	7.55	7.61	8.17	-0.42	-0.62	-0.36	-0.56	0.23	-0.51	0.87	-1.33	-0.11	-0.09	0.63
Cthe_01057 phage shock protein C, PspC	8.29	8.68	9.42	8.68	-1.13	0	-0.39	0.74	-0.33	0.02	0.77	1.38	-0.11	-0.09	0.37
Cthe_00759 flagellar biosynthesis	6.98	7.22	7.14	7.88	-0.16	-0.66	-0.24	-0.74	0.44	-0.54	1.27	-1.71	-0.1	-0.09	0.58
Cthe_01851 protein of unknown function DUF1	10.33	10.72	11.55	10.69	-1.22	0.03	-0.39	0.86	-0.4	0.04	0.77	1.63	-0.1	-0.09	0.4
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_01556 binding-protein-dependent transpo	2	2.81	3.32	2.58	-1.32	0.23	-0.81	0.74	-0.48	0.21	-0.63	1.38	-0.1	-0.09	0.62
Cthe_00539 ABC transporter related protein	6.75	7.66	7.29	8.42	-0.54	-0.76	-0.91	-1.13	0.13	-0.63	-0.97	-2.52	-0.11	-0.09	0.43
Cthe_02572 hypothetical protein	8.99	9.56	9.74	9.83	-0.75	-0.27	-0.57	-0.09	-0.03	-0.21	0.17	-0.35	-0.1	-0.09	0.97
Cthe_01998 intein	7.61	7.53	7.99	8.48	-0.38	-0.95	0.08	-0.49	0.26	-0.79	2.33	-1.19	-0.1	-0.09	0.57
Cthe_00427 serine phosphatase	13.4	14.29	14.44	14.75	-1.04	-0.46	-0.89	-0.31	-0.26	-0.37	-0.9	-0.81	-0.11	-0.09	0.67
Cthe_02834 intein	8.09	8.44	9.27	8.77	-1.18	-0.33	-0.35	0.5	-0.37	-0.26	0.9	0.88	-0.1	-0.09	0.64
Cthe_02018 hypothetical protein	9.17	9.6	10.28	9.48	-1.11	0.12	-0.43	0.8	-0.32	0.12	0.63	1.5	-0.11	-0.09	0.38
Cthe_01489 hypothetical protein	4.75	4.46	6.11	5.49	-1.36	-1.03	0.29	0.62	-0.52	-0.86	3.03	1.13	-0.1	-0.09	0.55
Cthe_02417 Abortive infection protein	10.72	11.43	11.64	11.54	-0.92	-0.11	-0.71	0.1	-0.17	-0.08	-0.3	0.04	-0.1	-0.09	1.11
Cthe_02753 hypothetical protein	0	1.58	2	1	-2	0.58	-1.58	1	-1.02	0.51	-3.2	1.92	-0.1	-0.09	0.55
Cthe_02302 hypothetical protein	10.07	10.8	11.04	10.89	-0.97	-0.09	-0.73	0.15	-0.21	-0.06	-0.37	0.15	-0.11	-0.09	0.98
Cthe_00271 type 3a, cellulose-binding	11.38	12.15	12.48	12.15	-1.1	0	-0.77	0.33	-0.31	0.02	-0.5	0.52	-0.11	-0.09	0.77
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_00539 ABC transporter related protein	6.75	7.66	7.29	8.42	-0.54	-0.76	-0.91	-1.13	0.13	-0.63	-0.97	-2.52	-0.11	-0.09	0.43
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_02664 ABC-1	9.17	9.71	10.02	9.89	-0.85	-0.18	-0.54	0.13	-0.11	-0.14	0.27	0.1	-0.1	-0.09	1.1
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_01556 binding-protein-dependent transpo	2	2.81	3.32	2.58	-1.32	0.23	-0.81	0.74	-0.48	0.21	-0.63	1.38	-0.1	-0.09	0.62
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_01171 Serine-type D-Ala-D-Ala carboxype	10.46	10.94	11.51	10.71	-1.05	0.23	-0.48	0.8	-0.27	0.21	0.47	1.5	-0.1	-0.09	0.39
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_03149 aminoacyl-histidine dipeptidase	9.04	9.55	9.67	9.97	-0.63	-0.42	-0.51	-0.3	0.06	-0.34	0.37	-0.79	-0.1	-0.09	0.71
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_01171 Serine-type D-Ala-D-Ala carboxype	10.46	10.94	11.51	10.71	-1.05	0.23	-0.48	0.8	-0.27	0.21	0.47	1.5	-0.1	-0.09	0.39
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_01079 Nucleotidyl transferase	10.74	11.54	11.95	11.43	-1.21	0.11	-0.8	0.52	-0.4	0.11	-0.6	0.92	-0.11	-0.09	0.67
Cthe_01171 Serine-type D-Ala-D-Ala carboxype	10.46	10.94	11.51	10.71	-1.05	0.23	-0.48	0.8	-0.27	0.21	0.47	1.5	-0.1	-0.09	0.39
Cthe_01171 Serine-type D-Ala-D-Ala carboxype	10.46	10.94	11.51	10.71	-1.05	0.23	-0.48	0.8	-0.27	0.21	0.47	1.5	-0.1	-0.09	0.39
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_02443 Transketolase-like protein	3.81	4.86	5.17	4.86	-1.36	0	-1.05	0.31	-0.52	0.02	-1.43	0.48	-0.1	-0.09	0.62
Cthe_01774 ribosomal-protein-alanine acetyltra	6.63	7.38	7.58	7.59	-0.95	-0.21	-0.75	-0.01	-0.19	-0.16	-0.43	-0.19	-0.12	-0.1	0.94
Cthe_00834 NusB antitermination factor	7.75	8.09	8.31	8.67	-0.56	-0.58	-0.34	-0.36	0.12	-0.47	0.93	-0.92	-0.12	-0.1	0.66
Cthe_02544 RNA polymerase, sigma-24 subunit	10.52	11.18	11.81	11.15	-1.29	0.03	-0.66	0.66	-0.46	0.04	-0.13	1.21	-0.12	-0.1	0.68
Cthe_01357 glycosyl transferase, group 1	1	0	2.58	1.58	-1.58	-1.58	1	1	-0.69	-1.32	5.4	1.92	-0.12	-0.1	0.46
Cthe_00646 anaerobic ribonucleoside-triphosph	11.82	12.6	13.04	12.53	-1.22	0.07	-0.78	0.51	-0.4	0.08	-0.53	0.9	-0.12	-0.1	0.7
Cthe_01393 multi-sensor signal transduction his	7.5	8.5	8.51	8.51	-1.01	-0.01	-1	0	-0.24	0.01	-1.27	-0.17	-0.12	-0.1	0.33
Cthe_02677 histidine kinase	7.48	8.23	8.97	7.98	-1.49	0.25	-0.75	0.99	-0.62	0.23	-0.43	1.9	-0.12	-0.1	0.61
Cthe_03164 two component transcriptional reg	9.81	10.25	10.23	10.92	-0.42	-0.67	-0.44	-0.69							



Cthe_00061 BioY protein	9.73	10.47	10.84	10.5	-1.11	-0.03	-0.74	0.34	-0.32	-0.01	-0.4	0.54	-0.13	-0.11	0.85
Cthe_02353 PGAP1-like protein	8.21	8.88	8.89	9.6	-0.68	-0.72	-0.67	-0.71	0.02	-0.59	-0.17	-1.65	-0.13	-0.11	0.64
Cthe_02784 cobalamin B12-binding protein		1	1	1	-1	0	-1	0	-0.23	0.02	-1.27	-0.17	-0.13	-0.11	0.32
Cthe_02634 transcriptional regulator, AraC fam	5.78	6.02	6.49	6.64	-0.71	-0.62	-0.24	-0.15	0	-0.51	1.27	-0.48	-0.13	-0.11	0.67
Cthe_00556 asparagine synthase (glutamine-hy	7.23	8.04	7.58	8.54	-0.35	-0.5	-0.81	-0.96	0.29	-0.41	-0.63	-2.17	-0.13	-0.11	0.4
Cthe_01461 FAD dependent oxidoreductase	7.61	8.21	8.56	8.34	-0.95	-0.13	-0.6	0.22	-0.19	-0.09	0.07	0.29	-0.13	-0.11	1.26
Cthe_02230 acylneuraminate cytidyltransfera	6.91	7.75	7.52	8.16	-0.61	-0.41	-0.84	-0.64	0.08	-0.33	-0.73	-1.5	-0.13	-0.11	0.36
Cthe_01089 Stage V sporulation protein S	10.59	11.23	11.76	11.27	-1.17	-0.04	-0.64	0.49	-0.37	-0.02	-0.07	0.85	-0.13	-0.11	0.78
Cthe_02904 ribosomal protein L4/L1e	9.6	10.01	10.04	10.72	-0.44	-0.71	-0.41	-0.68	0.21	-0.58	0.7	-1.58	-0.13	-0.11	0.64
Cthe_00338 NADH-quinone oxidoreductase, E s	10.46	11.28	11.25	11.38	-0.79	-0.1	-0.82	-0.13	-0.06	-0.07	-0.67	-0.44	-0.13	-0.11	0.21
Cthe_03043 hypothetical protein	7.08	7.92	7.46	8.56	-0.38	-0.64	-0.84	-1.1	0.26	-0.53	-0.73	-2.46	-0.13	-0.11	0.41
Cthe_02782 N-acetylmuramyl-L-alanine amidas	5.75	6.27	6.43	6.71	-0.68	-0.44	-0.52	-0.28	0.02	-0.36	0.33	-0.75	-0.13	-0.11	0.79
Cthe_01786 DNA repair protein RadA	9.72	10.25	10.34	10.81	-0.62	-0.56	-0.53	-0.47	0.07	-0.46	0.3	-1.15	-0.13	-0.11	0.7
Cthe_00224 RNA related	4.86	5.49	6.23	5.49	-1.37	0	-0.63	0.74	-0.52	0.02	-0.03	1.38	-0.13	-0.11	0.67
Cthe_02684 hypothetical protein	11.52	12.06	13.51	11.89	-1.99	0.17	-0.54	1.62	-1.02	0.16	0.27	3.21	-0.13	-0.11	0.57
Cthe_00670 spore germination protein	6.7	7.07	7.67	7.45	-0.97	-0.38	-0.37	0.22	-0.21	-0.31	0.83	0.29	-0.13	-0.11	0.76
Cthe_02195 Carbohydrate binding family 6	5.46	6.38	7	5.95	-1.54	0.43	-0.92	1.05	-0.66	0.38	-1	2.02	-0.13	-0.11	0.6
Cthe_00338 NADH-quinone oxidoreductase, E s	10.46	11.28	11.25	11.38	-0.79	-0.1	-0.82	-0.13	-0.06	-0.07	-0.67	-0.44	-0.13	-0.11	0.21
Cthe_02904 ribosomal protein L4/L1e	9.6	10.01	10.04	10.72	-0.44	-0.71	-0.41	-0.68	0.21	-0.58	0.7	-1.58	-0.13	-0.11	0.64
Cthe_00556 asparagine synthase (glutamine-hy	7.23	8.04	7.58	8.54	-0.35	-0.5	-0.81	-0.96	0.29	-0.41	-0.63	-2.17	-0.13	-0.11	0.4
Cthe_00338 NADH-quinone oxidoreductase, E s	10.46	11.28	11.25	11.38	-0.79	-0.1	-0.82	-0.13	-0.06	-0.07	-0.67	-0.44	-0.13	-0.11	0.21
Cthe_00338 NADH-quinone oxidoreductase, E s	10.46	11.28	11.25	11.38	-0.79	-0.1	-0.82	-0.13	-0.06	-0.07	-0.67	-0.44	-0.13	-0.11	0.21
Cthe_00338 NADH-quinone oxidoreductase, E s	10.46	11.28	11.25	11.38	-0.79	-0.1	-0.82	-0.13	-0.06	-0.07	-0.67	-0.44	-0.13	-0.11	0.21
Cthe_00338 NADH-quinone oxidoreductase, E s	10.46	11.28	11.25	11.38	-0.79	-0.1	-0.82	-0.13	-0.06	-0.07	-0.67	-0.44	-0.13	-0.11	0.21
Cthe_00338 NADH-quinone oxidoreductase, E s	10.46	11.28	11.25	11.38	-0.79	-0.1	-0.82	-0.13	-0.06	-0.07	-0.67	-0.44	-0.13	-0.11	0.21
Cthe_00184 type IV pilus assembly protein PilM	14.62	15.1	16.14	15.23	-1.52	-0.13	-0.48	0.91	-0.64	-0.09	0.47	1.73	-0.14	-0.12	0.64
Cthe_03007 ErfK/YbiS/YcfS/YnhG	3.46	4.86	5.29	4.91	-1.83	-0.05	-1.4	0.38	-0.89	-0.03	-2.6	0.63	-0.14	-0.12	0.59
Cthe_00015 alpha-L-arabinofuranosidase B	10.06	10.92	11.38	10.85	-1.32	0.07	-0.86	0.53	-0.48	0.08	-0.8	0.94	-0.14	-0.12	0.7
Cthe_01530 transposase, IS204/IS1001/IS1096/	10.62	11.02	11.98	10.63	-1.36	0.39	-0.4	1.35	-0.52	0.35	0.73	2.65	-0.14	-0.12	0.41
Cthe_03210 protein of unknown function DUF3	10.16	10.52	10.76	11.12	-0.6	-0.6	-0.36	-0.36	0.09	-0.49	0.87	-0.92	-0.14	-0.12	0.7
Cthe_00184 type IV pilus assembly protein PilM	14.62	15.1	16.14	15.23	-1.52	-0.13	-0.48	0.91	-0.64	-0.09	0.47	1.73	-0.14	-0.12	0.64
Cthe_01250 phosphoribosylaminoimidazole car	7.18	7.92	7.97	8.63	-0.79	-0.71	-0.74	-0.66	-0.06	-0.58	-0.4	-1.54	-0.14	-0.12	0.65
Cthe_00167 response regulator receiver protein	7	7.38	7.69	7.88	-0.69	-0.5	-0.38	-0.19	0.02	-0.41	0.8	-0.56	-0.14	-0.12	0.75
Cthe_01466 protein of unknown function DUF1	4.95	5.83	6.21	5.83	-1.26	0	-0.88	0.38	-0.44	0.02	-0.87	0.63	-0.14	-0.12	0.73
Cthe_00031 putative membrane transporter	5.25	5.78	6.39	5.95	-1.14	-0.17	-0.53	0.44	-0.34	-0.13	0.3	0.75	-0.14	-0.12	0.8
Cthe_03008 Superoxide dismutase	3.32	4.46	4.46	4.64	-1.14	-0.18	-1.14	-0.18	-0.34	-0.14	-1.73	-0.54	-0.14	-0.12	0.36
Cthe_02111 protein of unknown function DUF2	6.93	7.9	8.26	7.98	-1.33	-0.08	-0.97	0.28	-0.49	-0.05	-1.17	0.42	-0.14	-0.12	0.71
Cthe_00752 hypothetical protein	4.17	5.21	5.21	5.32	-1.04	-0.11	-1.04	-0.11	-0.26	-0.08	-1.4	-0.4	-0.14	-0.12	0.33
Cthe_02383 hypothetical protein	14.91	15.65	15.97	15.73	-1.06	-0.08	-0.74	0.24	-0.28	-0.05	-0.4	0.33	-0.14	-0.12	0.98
Cthe_03123 von Willebrand factor, type A	9.48	9.98	9.95	10.74	-0.47	-0.76	-0.5	-0.79	0.19	-0.63	0.4	-1.81	-0.14	-0.12	0.63
Cthe_01250 phosphoribosylaminoimidazole car	7.18	7.92	7.97	8.63	-0.79	-0.71	-0.74	-0.66	-0.06	-0.58	-0.4	-1.54	-0.14	-0.12	0.65
Cthe_03008 Superoxide dismutase	3.32	4.46	4.46	4.64	-1.14	-0.18	-1.14	-0.18	-0.34	-0.14	-1.73	-0.54	-0.14	-0.12	0.36
Cthe_01250 phosphoribosylaminoimidazole car	7.18	7.92	7.97	8.63	-0.79	-0.71	-0.74	-0.66	-0.06	-0.58	-0.4	-1.54	-0.14	-0.12	0.65
Cthe_01250 phosphoribosylaminoimidazole car	7.18	7.92	7.97	8.63	-0.79	-0.71	-0.74	-0.66	-0.06	-0.58	-0.4	-1.54	-0.14	-0.12	0.65
Cthe_03008 Superoxide dismutase	3.32	4.46	4.46	4.64	-1.14	-0.18	-1.14	-0.18	-0.34	-0.14	-1.73	-0.54	-0.14	-0.12	0.36
Cthe_00795 alpha amylase, catalytic region	7.69	8.2	9.33	8.25	-1.64	-0.05	-0.51	1.08	-0.74	-0.03	0.37	2.08	-0.15	-0.13	0.63
Cthe_02191 1,4-alpha-glucan branching enzyme	11.35	11.94	12.16	12.26	-0.81	-0.32	-0.59	-0.1	-0.08	-0.25	0.1	-0.38	-0.15	-0.13	1.19
Cthe_01810 peptidase M56, BlaR1	6.94	7.41	8.48	7.55	-1.54	-0.14	-0.47	0.93	-0.66	-0.1	0.5	1.77	-0.15	-0.13	0.65
Cthe_03127 peptidase M56, BlaR1	7.91	8.35	8.81	8.25	-0.9	0.1	-0.44	0.56	-0.15	0.1	0.6	1	-0.15	-0.13	0.28
Cthe_01056 transglutaminase-like protein	9.38	10.2	10.5	10.33	-1.12	-0.13	-0.82	0.17	-0.33	-0.09	-0.67	0.19	-0.15	-0.13	0.88
Cthe_02882 Histidinol dehydrogenase	7.67	8.36	8.68	8.46	-1.01	-0.1	-0.69	0.22	-0.24	-0.07	-0.23	0.29	-0.15	-0.13	1.21
Cthe_01409 periplasmic sensor signal transduct	7.75	8.56	8.44	8.72	-0.69	-0.16	-0.81	-0.28	0.02	-0.12	-0.63	-0.75	-0.15	-0.13	0.22
Cthe_01810 peptidase M56, BlaR1	6.94	7.41	8.48	7.55	-1.54	-0.14	-0.47	0.93	-0.66	-0.1	0.5	1.77	-0.15	-0.13	0.65
Cthe_03127 peptidase M56, BlaR1	7.91	8.35	8.81	8.25	-0.9	0.1	-0.44	0.56	-0.15	0.1	0.6	1	-0.15	-0.13	0.28
Cthe_01359 glycosyltransferase 28-like protein	0	0	0	1	0	-1	0	-1	0.56	-0.83	2.07	-2.25	-0.15	-0.13	0.58
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02755 ADP-ribosylation/Crystallin J1	8.62	9.21	9.95	9.28	-1.33	-0.07	-0.59	0.67	-0.49	-0.04	0.1	1.23	-0.15	-0.13	0.71
Cthe_01518 hypothetical protein	3.46	4.75	4.46	5.75	-1	-1	-1.29	-1.29	-0.23	-0.83	-2.23	-2.85	-0.15	-0.13	0.43
Cthe_00718 hypothetical protein	4.39	5.21	5.36	5.73	-0.97	-0.52	-0.82	-0.37	-0.21	-0.42	-0.67	-0.94	-0.15	-0.13	0.73
Cthe_03215 CRISPR-associated protein, TM1812	10.17	10.43	10.86	11.08	-0.69	-0.65	-0.26	-0.22	0.02	-0.53	1.2	-0.63	-0.15	-0.13	0.7
Cthe_03209 hypothetical protein	10.52	11.03	11.14	11.64	-0.62	-0.61	-0.51	-0.5	0.07	-0.5	0.37	-1.21	-0.15	-0.13	0.71
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02882 Histidinol dehydrogenase	7.67	8.36	8.68	8.46	-1.01	-0.1	-0.69	0.22	-0.24	-0.07	-0.23	0.29	-0.15	-0.13	1.21
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02882 Histidinol dehydrogenase	7.67	8.36	8.68	8.46	-1.01	-0.1	-0.69	0.22	-0.24	-0.07	-0.23	0.29	-0.15	-0.13	1.21
Cthe_02191 1,4-alpha-glucan branching enzyme	11.35	11.94	12.16	12.26	-0.81	-0.32	-0.59	-0.1	-0.08	-0.25	0.1	-0.38	-0.15	-0.13	1.19
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02755 ADP-ribosylation/Crystallin J1	8.62	9.21	9.95	9.28	-1.33	-0.07	-0.59	0.67	-0.49	-0.04	0.1	1.23	-0.15	-0.13	0.71
Cthe_01409 periplasmic sensor signal transduct	7.75	8.56	8.44	8.72	-0.69	-0.16	-0.81	-0.28	0.02	-0.12	-0.63	-0.75	-0.15	-0.13	0.22
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02882 Histidinol dehydrogenase	7.67	8.36	8.68	8.46	-1.01	-0.1	-0.69	0.22	-0.24	-0.07	-0.23	0.29	-0.15	-0.13	1.21
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02191 1,4-alpha-glucan branching enzyme	11.35	11.94	12.16	12.26	-0.81	-0.32	-0.59	-0.1	-0.08	-0.25	0.1	-0.38	-0.15	-0.13	1.19
Cthe_02191 1,4-alpha-glucan branching enzyme	11.35	11.94	12.16	12.26	-0.81	-0.32	-0.59	-0.1	-0.08	-0.25	0.1	-0.38	-0.15	-0.13	1.19
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65														



Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_02392 pyruvate flavodoxin/ferredoxin	11.65	12.45	12.62	12.88	-0.97	-0.43	-0.8	-0.26	-0.21	-0.35	-0.6	-0.71	-0.15	-0.13	0.78
Cthe_00377 peptidase M56, BlaR1	4.58	5.73	5.61	5.49	-1.03	0.24	-1.15	0.12	-0.25	0.22	-1.77	0.08	-0.16	-0.14	0.34
Cthe_02303 CRISPR-associated protein Cas6	9.44	10.15	10.71	10.17	-1.27	-0.02	-0.71	0.54	-0.44	0	-0.3	0.96	-0.16	-0.14	0.78
Cthe_03063 Acetyl xylan esterase	10	10.44	10.65	11	-0.65	-0.56	-0.44	-0.35	0.05	-0.46	0.6	-0.9	-0.16	-0.14	0.76
Cthe_02924 adenylate kinases	11.34	12.09	12.27	12.51	-0.93	-0.42	-0.75	-0.24	-0.17	-0.34	-0.43	-0.67	-0.16	-0.14	0.85
Cthe_00377 peptidase M56, BlaR1	4.58	5.73	5.61	5.49	-1.03	0.24	-1.15	0.12	-0.25	0.22	-1.77	0.08	-0.16	-0.14	0.34
Cthe_00449 hypothetical protein	0	2	2.32	3	-2.32	-1	-2	-0.68	-1.28	-0.83	-4.6	-1.58	-0.16	-0.14	0.56
Cthe_02651 hypothetical protein	4.25	5.21	6.19	4.32	-1.94	0.89	-0.96	1.87	-0.98	0.77	-1.13	3.73	-0.16	-0.14	0.57
Cthe_02924 adenylate kinases	11.34	12.09	12.27	12.51	-0.93	-0.42	-0.75	-0.24	-0.17	-0.34	-0.43	-0.67	-0.16	-0.14	0.85
Cthe_03063 Acetyl xylan esterase	10	10.44	10.65	11	-0.65	-0.56	-0.44	-0.35	0.05	-0.46	0.6	-0.9	-0.16	-0.14	0.76
Cthe_02924 adenylate kinases	11.34	12.09	12.27	12.51	-0.93	-0.42	-0.75	-0.24	-0.17	-0.34	-0.43	-0.67	-0.16	-0.14	0.85
Cthe_02924 adenylate kinases	11.34	12.09	12.27	12.51	-0.93	-0.42	-0.75	-0.24	-0.17	-0.34	-0.43	-0.67	-0.16	-0.14	0.85
Cthe_02924 adenylate kinases	11.34	12.09	12.27	12.51	-0.93	-0.42	-0.75	-0.24	-0.17	-0.34	-0.43	-0.67	-0.16	-0.14	0.85
Cthe_01515 GCN5-related N-acetyltransferase	4.86	4.81	5.32	5.86	-0.46	-1.05	0.05	-0.54	0.2	-0.87	2.23	-1.29	-0.17	-0.15	0.62
Cthe_03012 Carbohydrate binding family 6	9.25	10.06	10.73	9.93	-1.48	0.13	-0.81	0.8	-0.61	0.13	-0.63	1.5	-0.17	-0.15	0.68
Cthe_00982 MrzA protein	12.03	12.53	13.01	12.81	-0.98	-0.28	-0.5	0.2	-0.21	-0.22	0.4	0.25	-0.17	-0.15	1.15
Cthe_00983 cell cycle protein	9.76	10.16	10.26	10.91	-0.5	-0.75	-0.4	-0.65	0.17	-0.62	0.73	-1.52	-0.17	-0.15	0.68
Cthe_02250 hypothetical protein	1.58	3.17	3.17	3.58	-1.59	-0.41	-1.59	-0.41	-0.7	-0.33	-3.23	-1.02	-0.17	-0.15	0.41
Cthe_02019 intein	7.91	8.27	8.83	8.33	-0.92	-0.06	-0.36	0.5	-0.17	-0.03	0.87	0.88	-0.17	-0.15	0.25
Cthe_02151 hypothetical protein	10.34	11.13	11.31	11.61	-0.97	-0.48	-0.79	-0.3	-0.21	-0.39	-0.57	-0.79	-0.17	-0.15	0.81
Cthe_00028 uncharacterized protein, YcgI-like	7.19	7.79	8.09	7.97	-0.9	-0.18	-0.6	0.12	-0.15	-0.14	0.07	0.08	-0.18	-0.16	3.45
Cthe_00219 5-nitroimidazole antibiotic resistan	5.25	5.39	6.07	5.73	-0.82	-0.34	-0.14	0.34	-0.09	-0.27	1.6	0.54	-0.19	-0.16	0.3
Cthe_01985 phase major capsid protein, HK97	4.25	5.29	6.02	4.86	-1.77	0.43	-1.04	1.16	-0.84	0.38	-1.4	2.25	-0.18	-0.16	0.62
Cthe_01903 polysaccharide deacetylase	4.09	4.95	4.86	5.04	-0.77	-0.09	-0.86	-0.18	-0.05	-0.06	-0.8	-0.54	-0.19	-0.16	0.14
Cthe_01596 transcriptional regulator, MarR fam	5.67	6.54	7	6.58	-1.33	-0.04	-0.87	0.42	-0.49	-0.02	-0.83	0.71	-0.18	-0.16	0.8
Cthe_02940 transcriptional regulator, CarD fam	11.27	11.84	12.92	11.87	-1.65	-0.03	-0.57	1.05	-0.75	-0.01	0.17	2.02	-0.18	-0.16	0.66
Cthe_01902 Pyridoxal-5'-phosphate-dependent	5.43	5.55	6.25	5.91	-0.82	-0.36	-0.12	0.34	-0.09	-0.29	1.67	0.54	-0.19	-0.16	0.31
Cthe_02301 CRISPR-associated autoregulator, D	9.98	10.61	11.04	10.76	-1.06	-0.15	-0.63	0.28	-0.28	-0.11	-0.03	0.42	-0.18	-0.16	1.28
Cthe_01405 Spore coat assembly protein-like pr	8.14	8.87	9.84	8.69	-1.7	0.18	-0.73	1.15	-0.79	0.17	-0.37	2.23	-0.18	-0.16	0.64
Cthe_00092 septum site-determining protein M	8.04	8.88	8.65	9.13	-0.61	-0.25	-0.84	-0.48	0.08	-0.19	-0.73	-1.17	-0.18	-0.16	0.27
Cthe_02862 hypothetical protein	7.65	7.91	8.71	8.03	-1.06	-0.12	-0.26	0.68	-0.28	-0.08	1.2	1.25	-0.19	-0.16	0.3
Cthe_01370 hypothetical protein	7.38	8.28	8.2	8.41	-0.82	-0.13	-0.9	-0.21	-0.09	-0.09	-0.93	-0.6	-0.18	-0.16	0.21
Cthe_01424 hypothetical protein	8.81	9.41	9.6	9.89	-0.79	-0.48	-0.6	-0.29	-0.06	-0.39	0.07	-0.77	-0.18	-0.16	0.91
Cthe_00627 hypothetical protein	9.7	10.24	10.46	10.72	-0.76	-0.48	-0.54	-0.26	-0.04	-0.39	0.27	-0.71	-0.18	-0.16	0.92
Cthe_01623 phage major tail protein, phi13 family			1.58	0	-1.58	0		1.58	-0.69	0.02		3.13	-0.19	-0.16	0.39
Cthe_03235 hypothetical protein	1.58	0	1	2	0.58	-2	1.58	-1	1.02	-1.68	7.33	-2.25	-0.18	-0.16	0.46
Cthe_03070 protein of unknown function DUF1	11.39	11.93	12.56	12.14	-1.17	-0.21	-0.54	0.42	-0.37	-0.16	0.27	0.71	-0.19	-0.16	0.95
Cthe_00838 hypothetical protein	5.98	6.71	7.43	6.69	-1.45	0.02	-0.73	0.74	-0.59	0.03	-0.37	1.38	-0.19	-0.16	0.74
Cthe_01637 virulence-related protein			1.58	0	-1.58	0		1.58	-0.69	0.02		3.13	-0.19	-0.16	0.39
Cthe_02033 hypothetical protein	5.29	4.75	5.73	5.81	-0.44	-1.06	0.54	-0.08	0.21	-0.88	3.87	-0.33	-0.18	-0.16	0.42
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_02398 putative spore coat protein	6.79	7.26	7.4	8.02	-0.61	-0.76	-0.47	-0.62	0.08	-0.63	0.5	-1.46	-0.2	-0.17	0.73
Cthe_02147 glycoside hydrolase, family 5	10.41	11.13	11.97	11.1	-1.56	0.03	-0.72	0.87	-0.67	0.04	-0.33	1.65	-0.2	-0.17	0.71
Cthe_02441 transcriptional regulator, DeoR fam	9.84	10.29	11.29	10.54	-1.45	-0.25	-0.45	0.75	-0.59	-0.19	0.57	1.4	-0.2	-0.17	0.73
Cthe_02654 PHP-like protein	5.52	6.15	6.74	6.3	-1.22	-0.15	-0.63	0.44	-0.4	-0.11	-0.03	0.75	-0.2	-0.17	0.99
Cthe_00315 DNA-directed RNA polymerase sigm	5.55	6.04	6.17	6.79	-0.62	-0.75	-0.49	-0.62	0.07	-0.62	0.43	-1.46	-0.2	-0.17	0.73
Cthe_02441 transcriptional regulator, DeoR fam	9.84	10.29	11.29	10.54	-1.45	-0.25	-0.45	0.75	-0.59	-0.19	0.57	1.4	-0.2	-0.17	0.73
Cthe_02519 2-isopropylmalate synthase/homoc	11.11	11.94	12.09	12.63	-0.98	-0.69	-0.83	-0.54	-0.21	-0.57	-0.7	-1.29	-0.2	-0.17	0.74
Cthe_00001 Recombinase				1	-1		-1		-0.83			-2.25	-0.2	-0.17	0.66
Cthe_03048 DNA repair protein RadC	7.15	8.03	8.42	8.2	-1.27	-0.17	-0.88	0.22	-0.44	-0.13	-0.87	0.29	-0.2	-0.17	0.89
Cthe_00463 flagellar basal-body rod protein Flg	9.71	10.39	10.5	11.17	-0.79	-0.78	-0.68	-0.67	-0.06	-0.64	-0.2	-1.56	-0.2	-0.17	0.73
Cthe_02654 PHP-like protein	5.52	6.15	6.74	6.3	-1.22	-0.15	-0.63	0.44	-0.4	-0.11	-0.03	0.75	-0.2	-0.17	0.99
Cthe_03179 Serine-type D-Ala-D-Ala carboxype	5.36	5.67	6	5.78	-0.64	-0.11	-0.31	0.22	0.06	-0.08	1.03	0.29	-0.2	-0.17	0.17
Cthe_00811 response regulator receiver protein	3.91	3.58	4.46	4.95	-0.55	-1.37	0.33	-0.49	0.13	-1.14	3.17	-1.19	-0.2	-0.17	0.61
Cthe_02743 putative metalloendopeptidase, gly	9.34	9.98	10.47	10.13	-1.13	-0.15	-0.64	0.34	-0.33	-0.11	-0.07	0.54	-0.2	-0.17	1.14
Cthe_02857 hypothetical protein	5.09	5.88	6.32	5.98	-1.23	-0.1	-0.79	0.34	-0.41	-0.07	-0.57	0.54	-0.2	-0.17	0.95
Cthe_00096 protein of unknown function UPFO	7.33	7.94	8.08	8.61	-0.75	-0.67	-0.61	-0.53	-0.03	-0.55	0.03	-1.27	-0.2	-0.17	0.77
Cthe_02458 hypothetical protein				1	-1		-1		-0.83			-2.25	-0.2	-0.17	0.66
Cthe_02519 2-isopropylmalate synthase/homoc	11.11	11.94	12.09	12.63	-0.98	-0.69	-0.83	-0.54	-0.21	-0.57	-0.7	-1.29	-0.2	-0.17	0.74
Cthe_03179 Serine-type D-Ala-D-Ala carboxype	5.36	5.67	6	5.78	-0.64	-0.11	-0.31	0.22	0.06	-0.08	1.03	0.29	-0.2	-0.17	0.17
Cthe_02519 2-isopropylmalate synthase/homoc	11.11	11.94	12.09	12.63	-0.98	-0.69	-0.83	-0.54	-0.21	-0.57	-0.7	-1.29	-0.2	-0.17	0.74
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_02654 PHP-like protein	5.52	6.15	6.74	6.3	-1.22	-0.15	-0.63	0.44	-0.4	-0.11	-0.03	0.75	-0.2	-0.17	0.99
Cthe_02743 putative metalloendopeptidase, gly	9.34	9.98	10.47	10.13	-1.13	-0.15	-0.64	0.34	-0.33	-0.11	-0.07	0.54	-0.2	-0.17	1.14
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_03179 Serine-type D-Ala-D-Ala carboxype	5.36	5.67	6	5.78	-0.64	-0.11	-0.31	0.22	0.06	-0.08	1.03	0.29	-0.2	-0.17	0.17
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_02519 2-isopropylmalate synthase/homoc	11.11	11.94	12.09	12.63	-0.98	-0.69	-0.83	-0.54	-0.21	-0.57	-0.7	-1.29	-0.2	-0.17	0.74
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_03179 Serine-type D-Ala-D-Ala carboxype	5.36	5.67	6	5.78	-0.64	-0.11	-0.31	0.22	0.06	-0.08	1.03	0.29	-0.2	-0.17	0.17
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_03179 Serine-type D-Ala-D-Ala carboxype	5.36	5.67	6	5.78	-0.64	-0.11	-0.31	0.22	0.06	-0.08	1.03	0.29	-0.2	-0.17	0.17
Cthe_00863 glutamine synthetase, catalytic reg	11.3	12.15	12.03	12.26	-0.73	-0.11	-0.85	-0.23	-0.02	-0.08	-0.77	-0.65	-0.2	-0.17	0.15
Cthe_01609 Recombinase	0	1.58	1.58	1.58	-1.58	0	-1.58	0	-0.69	0.02	-3.2	-0.17	-0.21	-0.18	0.38
Cthe_02530 glutamate-1-semialdehyde-2,1-ami	4.95	5.29	5.7	5.93	-0.75	-0.64	-0.34	-0.23	-0.03	-0.53	0.93	-0.65	-0.21	-0.18	0.84
Cthe_01207 membrane protein-like protein	10.87	11.58	12.05	11.71	-1.18	-0.13	-0.71	0.34	-0.37	-0.09	-0.3	0.54			







Cthe_00844 stage III sporulation protein spoIIIA	4.09	5.29	5.43	6.48	-1.34	-1.19	-1.2	-1.05	-0.5	-0.99	-1.93	-2.35	-0.26	-0.22	0.65
Cthe_02906 ribosomal protein L2	10.7	11.22	11.44	11.96	-0.74	-0.74	-0.52	-0.52	-0.02	-0.61	0.33	-1.25	-0.25	-0.22	0.84
Cthe_02908 ribosomal protein L22	9.21	9.86	9.97	10.82	-0.76	-0.96	-0.65	-0.85	-0.04	-0.8	-0.1	-1.94	-0.26	-0.22	0.74
Cthe_02909 ribosomal protein S3	10.55	11.37	11.53	12.22	-0.98	-0.85	-0.82	-0.69	-0.21	-0.7	-0.67	-1.6	-0.25	-0.22	0.75
Cthe_02916 ribosomal protein S14	8.63	9.36	9.57	10.09	-0.94	-0.73	-0.73	-0.52	-0.18	-0.6	-0.37	-1.25	-0.26	-0.22	0.86
Cthe_00962 dihydrodipicolinate synthase	11.2	11.98	12.32	12.27	-1.12	-0.29	-0.78	0.05	-0.33	-0.23	-0.53	-0.06	-0.25	-0.22	1.35
Cthe_01820 ABC transporter related protein	2	2.58	3.32	2.81	-1.32	-0.23	-0.58	0.51	-0.48	-0.18	0.13	0.9	-0.26	-0.22	1.01
Cthe_02906 ribosomal protein L2	10.7	11.22	11.44	11.96	-0.74	-0.74	-0.52	-0.52	-0.02	-0.61	0.33	-1.25	-0.25	-0.22	0.84
Cthe_02908 ribosomal protein L22	9.21	9.86	9.97	10.82	-0.76	-0.96	-0.65	-0.85	-0.04	-0.8	-0.1	-1.94	-0.26	-0.22	0.74
Cthe_02909 ribosomal protein S3	10.55	11.37	11.53	12.22	-0.98	-0.85	-0.82	-0.69	-0.21	-0.7	-0.67	-1.6	-0.25	-0.22	0.75
Cthe_02916 ribosomal protein S14	8.63	9.36	9.57	10.09	-0.94	-0.73	-0.73	-0.52	-0.18	-0.6	-0.37	-1.25	-0.26	-0.22	0.86
Cthe_01276 pantetheine-phosphate adenylyltra	7.48	8	8.36	8.46	-0.88	-0.46	-0.52	-0.1	-0.13	-0.37	0.33	-0.38	-0.25	-0.22	1.39
Cthe_01276 pantetheine-phosphate adenylyltra	7.48	8	8.36	8.46	-0.88	-0.46	-0.52	-0.1	-0.13	-0.37	0.33	-0.38	-0.25	-0.22	1.39
Cthe_00962 dihydrodipicolinate synthase	11.2	11.98	12.32	12.27	-1.12	-0.29	-0.78	0.05	-0.33	-0.23	-0.53	-0.06	-0.25	-0.22	1.35
Cthe_01276 pantetheine-phosphate adenylyltra	7.48	8	8.36	8.46	-0.88	-0.46	-0.52	-0.1	-0.13	-0.37	0.33	-0.38	-0.25	-0.22	1.39
Cthe_00962 dihydrodipicolinate synthase	11.2	11.98	12.32	12.27	-1.12	-0.29	-0.78	0.05	-0.33	-0.23	-0.53	-0.06	-0.25	-0.22	1.35
Cthe_00962 dihydrodipicolinate synthase	11.2	11.98	12.32	12.27	-1.12	-0.29	-0.78	0.05	-0.33	-0.23	-0.53	-0.06	-0.25	-0.22	1.35
Cthe_00962 dihydrodipicolinate synthase	11.2	11.98	12.32	12.27	-1.12	-0.29	-0.78	0.05	-0.33	-0.23	-0.53	-0.06	-0.25	-0.22	1.35
Cthe_00559 single-strand binding protein/Prim	6.51	7.22	7.55	7.52	-1.04	-0.3	-0.71	0.03	-0.26	-0.24	-0.3	-0.1	-0.27	-0.23	2
Cthe_02219 flagellar protein FlaG protein	7.19	7.85	8.14	8.29	-0.95	-0.44	-0.66	-0.15	-0.19	-0.36	-0.13	-0.48	-0.27	-0.23	1.46
Cthe_02944 periplasmic sensor signal transduct	8.18	8.65	8.85	9.57	-0.67	-0.92	-0.47	-0.72	0.03	-0.76	0.5	-1.67	-0.27	-0.23	0.78
Cthe_00628 hypothetical protein	9.84	10.32	10.64	10.96	-0.8	-0.64	-0.48	-0.32	-0.07	-0.53	0.47	-0.83	-0.27	-0.23	1
Cthe_01769 hypothetical protein	7.29	7.56	8.61	8.13	-1.32	-0.57	-0.27	0.48	-0.48	-0.47	1.17	0.83	-0.27	-0.23	0.84
Cthe_00177 hypothetical protein	5.43	5.83	6.43	6.34	-1	-0.51	-0.4	0.09	-0.23	-0.42	0.73	0.02	-0.27	-0.23	1.17
Cthe_01044 hypothetical protein	4.91	4.46	6	5.93	-1.09	-1.47	0.45	0.07	-0.3	-1.23	3.57	-0.02	-0.27	-0.23	0.63
Cthe_00407 Radical SAM	8.49	9.41	9.88	9.65	-1.39	-0.24	-0.92	0.23	-0.54	-0.19	-1	0.31	-0.28	-0.24	0.98
Cthe_03146 peptidase M56, BlaR1	8.21	8.8	9.29	9.08	-1.08	-0.28	-0.59	0.21	-0.29	-0.22	0.1	0.27	-0.28	-0.24	2.26
Cthe_00128 Integrase, catalytic region	0	1	1	1	-1	-1	0	0	-0.23	-0.83	2.07	-0.17	-0.28	-0.24	0.74
Cthe_01639 DNA methylase N-4/N-6	3.17	2.81	4.17	3.58	-1	-0.77	0.36	0.59	-0.23	-0.64	3.27	1.06	-0.28	-0.24	0.35
Cthe_02297 CRISPR-associated protein Cas1	8.04	8.59	9.22	8.89	-1.18	-0.3	-0.55	0.33	-0.37	-0.24	0.23	0.52	-0.28	-0.24	1.39
Cthe_03146 peptidase M56, BlaR1	8.21	8.8	9.29	9.08	-1.08	-0.28	-0.59	0.21	-0.29	-0.22	0.1	0.27	-0.28	-0.24	2.26
Cthe_02921 ribosomal protein L30	8.87	9.55	9.8	10.19	-0.93	-0.64	-0.68	-0.39	-0.17	-0.53	-0.2	-0.98	-0.28	-0.24	0.99
Cthe_01779 hypothetical protein	7.07	7.62	7.95	8.13	-0.88	-0.51	-0.55	-0.18	-0.13	-0.42	0.23	-0.54	-0.28	-0.24	1.34
Cthe_01045 hypothetical protein	4.64	4.86	5.98	5.49	-1.34	-0.63	-0.22	0.49	-0.5	-0.52	1.33	0.85	-0.28	-0.24	0.82
Cthe_01997 hypothetical protein	5.25	5.13	6.25	5.64	-1	-0.51	0.12	0.61	-0.23	-0.42	2.47	1.1	-0.28	-0.24	0.32
Cthe_02921 ribosomal protein L30	8.87	9.55	9.8	10.19	-0.93	-0.64	-0.68	-0.39	-0.17	-0.53	-0.2	-0.98	-0.28	-0.24	0.99
Cthe_02921 ribosomal protein L30	8.87	9.55	9.8	10.19	-0.93	-0.64	-0.68	-0.39	-0.17	-0.53	-0.2	-0.98	-0.28	-0.24	0.99
Cthe_01838 glycoside hydrolase, family 10	12.22	12.84	13.5	13.08	-1.28	-0.24	-0.62	0.42	-0.45	-0.19	0	0.71	-0.29	-0.25	1.23
Cthe_01821 inner-membrane translocator	3	4.25	4.91	4.32	-1.91	-0.07	-1.25	0.59	-0.95	-0.04	-2.1	1.06	-0.29	-0.25	0.72
Cthe_02414 Monogalactosyldiacetylglucosyl synth	7.9	8.33	8.72	9.01	-0.82	-0.68	-0.43	-0.29	-0.09	-0.56	0.63	-0.77	-0.29	-0.25	1.02
Cthe_02874 Phosphoenolpyruvate carboxykinas	14.9	15.57	16.26	15.76	-1.36	-0.19	-0.67	0.5	-0.52	-0.14	-0.17	0.88	-0.29	-0.25	1.07
Cthe_02450 hypothetical protein	6.02	6.58	7.23	6.87	-1.21	-0.29	-0.56	0.36	-0.4	-0.23	0.2	0.58	-0.29	-0.25	1.34
Cthe_02860 RNA related	6.3	6.78	7.59	7.14	-1.29	-0.36	-0.48	0.45	-0.46	-0.29	0.47	0.77	-0.29	-0.25	1.08
Cthe_01821 inner-membrane translocator	3	4.25	4.91	4.32	-1.91	-0.07	-1.25	0.59	-0.95	-0.04	-2.1	1.06	-0.29	-0.25	0.72
Cthe_02874 Phosphoenolpyruvate carboxykinas	14.9	15.57	16.26	15.76	-1.36	-0.19	-0.67	0.5	-0.52	-0.14	-0.17	0.88	-0.29	-0.25	1.07
Cthe_01838 glycoside hydrolase, family 10	12.22	12.84	13.5	13.08	-1.28	-0.24	-0.62	0.42	-0.45	-0.19	0	0.71	-0.29	-0.25	1.23
Cthe_02414 Monogalactosyldiacetylglucosyl synth	7.9	8.33	8.72	9.01	-0.82	-0.68	-0.43	-0.29	-0.09	-0.56	0.63	-0.77	-0.29	-0.25	1.02
Cthe_02874 Phosphoenolpyruvate carboxykinas	14.9	15.57	16.26	15.76	-1.36	-0.19	-0.67	0.5	-0.52	-0.14	-0.17	0.88	-0.29	-0.25	1.07
Cthe_02414 Monogalactosyldiacetylglucosyl synth	7.9	8.33	8.72	9.01	-0.82	-0.68	-0.43	-0.29	-0.09	-0.56	0.63	-0.77	-0.29	-0.25	1.02
Cthe_02132 abortive infection protein, putative	8.61	9.34	10.27	9.44	-1.66	-0.1	-0.73	0.83	-0.75	-0.07	-0.37	1.56	-0.3	-0.26	0.84
Cthe_02638 O-antigen polymerase	4	4.81	5.36	5	-1.36	-0.19	-0.81	0.36	-0.52	-0.14	-0.63	0.58	-0.3	-0.26	1.12
Cthe_01617 phage putative tail component	0	0	1.58	0	-1.58	0	-1.58	0.56	-1.32	2.07	-3.46	-0.3	-0.26	0.64	
Cthe_03006 ErfK/YbiS/YcfS/YnhG	1.58	2.32	1.58	2.32	-0.32	0	-1.58	0.74	-1.28	0.02	-3.2	1.38	-0.3	-0.26	0.66
Cthe_02700 hypothetical protein	9.42	9.86	10.39	10.37	-0.97	-0.51	-0.44	0.02	-0.21	-0.42	0.6	-0.13	-0.3	-0.26	1.37
Cthe_02682 hypothetical protein	7.13	8.23	8.77	8.49	-1.64	-0.26	-1.1	0.28	-0.74	-0.2	-1.6	0.42	-0.3	-0.26	0.83
Cthe_03217 hypothetical protein	10.87	11.21	11.64	12.03	-0.77	-0.82	-0.34	-0.39	-0.05	-0.68	0.93	-0.98	-0.3	-0.26	0.9
Cthe_02176 Abortive infection protein	7.68	8.22	8.61	8.7	-0.93	-0.48	-0.54	-0.09	-0.17	-0.39	0.27	-0.35	-0.3	-0.26	1.72
Cthe_00464 flagellar hook-basal body complex	7.47	8.02	8.16	9.14	-0.69	-1.12	-0.55	-0.98	0.02	-0.93	0.23	-2.21	-0.31	-0.27	0.75
Cthe_02128 extracellular solute-binding protein	6.77	7.43	8.09	7.66	-1.32	-0.23	-0.66	0.43	-0.48	-0.18	-0.13	0.73	-0.31	-0.27	1.23
Cthe_00058 RNA polymerase sigma factor	7.56	8.21	9.13	8.39	-1.57	-0.18	-0.65	0.74	-0.68	-0.14	-0.1	1.38	-0.31	-0.27	0.9
Cthe_00464 flagellar hook-basal body complex	7.47	8.02	8.16	9.14	-0.69	-1.12	-0.55	-0.98	0.02	-0.93	0.23	-2.21	-0.31	-0.27	0.75
Cthe_01011 Peptidoglycan glycosyltransferase	8.31	9.1	9.5	9.44	-1.19	-0.34	-0.79	0.06	-0.38	-0.27	-0.57	-0.04	-0.31	-0.27	1.46
Cthe_01599 multi-sensor signal transduction histidine	1	0	1	0	-1	0	1	-0.23	0.02	1.92	-0.31	-0.27	-0.27	0.21	
Cthe_02106 protein of unknown function DUF3	8.11	8.69	9.16	9.01	-1.05	-0.32	-0.58	0.15	-0.27	-0.25	0.13	0.15	-0.31	-0.27	3.31
Cthe_02917 ribosomal protein S8	9.84	10.53	10.76	11.39	-0.92	-0.86	-0.69	-0.63	-0.17	-0.71	-0.23	-1.48	-0.31	-0.27	0.87
Cthe_01662 transposase IS3/IS911	1	1	1	-1	-1	1	-0.23	1.92	-0.31	-0.27	0.21				
Cthe_02170 hypothetical protein	9.03	9.64	9.99	10.06	-0.96	-0.42	-0.61	-0.07	-0.2	-0.34	0.03	-0.31	-0.31	-0.27	2.26
Cthe_02028 hypothetical protein	1	0	1	-1	0	1	-0.23	1.92	-0.31	-0.27	0.21				
Cthe_02824 hypothetical protein	1	1	1	-1	0	1	-0.23	1.92	-0.31	-0.27	0.21				
Cthe_02917 ribosomal protein S8	9.84	10.53	10.76	11.39	-0.92	-0.86	-0.69	-0.63	-0.17	-0.71	-0.23	-1.48	-0.31	-0.27	0.87
Cthe_02917 ribosomal protein S8	9.84	10.53	10.76	11.39	-0.92	-0.86	-0.69	-0.63	-0.17	-0.71	-0.23	-1.48	-0.31	-0.27	0.87
Cthe_01011 Peptidoglycan glycosyltransferase	8.31	9.1	9.5	9.44	-1.19	-0.34	-0.79	0.06	-0.38	-0.27	-0.57	-0.04	-0.31	-0.27	1.46
Cthe_01599 multi-sensor signal transduction histidine	1	0	1	0	-1	0	1	-0.23	0.02	1.92	-0.31	-0.27	-0.27	0.21	
Cthe_01011 Peptidoglycan glycosyltransferase	8.31	9.1	9.5	9.44	-1.19	-0.34	-0.79	0.06	-0.38	-0.27	-0.57	-0.04	-0.31	-0.27	1.46
Cthe_01011 Peptidoglycan glycosyltransferase	8.31	9.1	9.5	9.44	-1.19	-0.34	-0.79	0.06	-0.38	-0.27	-0.57	-0.04	-0.31	-0.27	1.46
Cthe_01011 Peptidoglycan glycosyltransferase	8.31	9.1	9.5	9.44	-1.19	-0.34	-0.79	0.06	-0.38	-0.27	-0.57	-0.04	-0.31	-0.27	1.46
Cthe_01011 Peptidoglycan glycosyltransferase	8.31	9.1	9.5	9.44	-1.19	-0.34	-0.79	0.06	-0.38	-0.27	-0.57	-0.04	-0.31	-0.27	1.46
Cthe_01011 Peptidoglycan glycosyltransferase	8.31	9.1	9.5	9.44	-1.19	-0.34	-0.79	0.06	-0.38	-0.27	-0.57	-0.04	-0.31	-0.27	1.46
Cthe_00495 RNA polymerase, sigma 28 subunit	8.04	8.8	9.21	9.15	-1.17	-0.35	-0.76	0.06	-0.37	-0.28	-0.47	-0.04	-0.33	-0.28	1.76
Cthe_01895 transcriptional regulator, PadR-like	9.73	10.15	10.76	10.69	-1.03	-0.54	-0.42	0.07	-0.25	-0.44	0.67	-0.02</			



Cthe_00431 hypothetical protein	10.26	10.75	11.13	11.45	-0.87	-0.7	-0.49	-0.32	-0.13	-0.58	0.43	-0.83	-0.33	-0.28	1.14
Cthe_00085 Negative regulator of genetic comp	13.48	14.06	15.09	14.31	-1.61	-0.25	-0.58	0.78	-0.71	-0.19	0.13	1.46	-0.32	-0.28	0.9
Cthe_00647 anaerobic ribonucleoside-triphosph	10.73	11.44	12.34	11.6	-1.61	-0.16	-0.71	0.74	-0.71	-0.12	-0.3	1.38	-0.32	-0.28	0.91
Cthe_02520 hypothetical protein	8.5	9.39	9.71	10.1	-1.21	-0.71	-0.89	-0.39	-0.4	-0.58	-0.9	-0.98	-0.33	-0.28	0.95
Cthe_02279 polar amino acid ABC transporter, i	4.75	6.19	6.04	6.29	-1.29	-0.1	-1.44	-0.25	-0.46	-0.07	-2.73	-0.69	-0.32	-0.28	0.3
Cthe_03086 3-phosphoshikimate 1-carboxyviny	11.14	11.71	12.33	12.03	-1.19	-0.32	-0.57	0.3	-0.38	-0.25	0.17	0.46	-0.32	-0.28	1.66
Cthe_02902 ribosomal protein S10	9.37	9.7	9.99	10.79	-0.62	-1.09	-0.33	-0.8	0.07	-0.91	0.97	-1.83	-0.33	-0.28	0.79
Cthe_02922 ribosomal protein L15	10.9	11.63	11.95	12.18	-1.05	-0.55	-0.73	-0.23	-0.27	-0.45	-0.37	-0.65	-0.32	-0.28	1.25
Cthe_02880 histidyl-tRNA synthetase	6.69	7.18	7.74	7.63	-1.05	-0.45	-0.49	0.11	-0.27	-0.36	0.43	0.06	-0.33	-0.28	1.85
Cthe_00429 NADH dehydrogenase (quinone)	12.35	13.24	13.58	13.87	-1.23	-0.63	-0.89	-0.29	-0.41	-0.52	-0.9	-0.77	-0.33	-0.28	1
Cthe_02902 ribosomal protein S10	9.37	9.7	9.99	10.79	-0.62	-1.09	-0.33	-0.8	0.07	-0.91	0.97	-1.83	-0.33	-0.28	0.79
Cthe_02922 ribosomal protein L15	10.9	11.63	11.95	12.18	-1.05	-0.55	-0.73	-0.23	-0.27	-0.45	-0.37	-0.65	-0.32	-0.28	1.25
Cthe_00647 anaerobic ribonucleoside-triphosph	10.73	11.44	12.34	11.6	-1.61	-0.16	-0.71	0.74	-0.71	-0.12	-0.3	1.38	-0.32	-0.28	0.91
Cthe_00429 NADH dehydrogenase (quinone)	12.35	13.24	13.58	13.87	-1.23	-0.63	-0.89	-0.29	-0.41	-0.52	-0.9	-0.77	-0.33	-0.28	1
Cthe_03086 3-phosphoshikimate 1-carboxyviny	11.14	11.71	12.33	12.03	-1.19	-0.32	-0.57	0.3	-0.38	-0.25	0.17	0.46	-0.32	-0.28	1.66
Cthe_00429 NADH dehydrogenase (quinone)	12.35	13.24	13.58	13.87	-1.23	-0.63	-0.89	-0.29	-0.41	-0.52	-0.9	-0.77	-0.33	-0.28	1
Cthe_03086 3-phosphoshikimate 1-carboxyviny	11.14	11.71	12.33	12.03	-1.19	-0.32	-0.57	0.3	-0.38	-0.25	0.17	0.46	-0.32	-0.28	1.66
Cthe_00429 NADH dehydrogenase (quinone)	12.35	13.24	13.58	13.87	-1.23	-0.63	-0.89	-0.29	-0.41	-0.52	-0.9	-0.77	-0.33	-0.28	1
Cthe_00429 NADH dehydrogenase (quinone)	12.35	13.24	13.58	13.87	-1.23	-0.63	-0.89	-0.29	-0.41	-0.52	-0.9	-0.77	-0.33	-0.28	1
Cthe_00429 NADH dehydrogenase (quinone)	12.35	13.24	13.58	13.87	-1.23	-0.63	-0.89	-0.29	-0.41	-0.52	-0.9	-0.77	-0.33	-0.28	1
Cthe_03030 methyl-accepting chemotaxis senso	8.22	8.55	9.16	9.29	-0.94	-0.74	-0.33	-0.13	-0.18	-0.61	0.97	-0.44	-0.34	-0.29	1.07
Cthe_03030 methyl-accepting chemotaxis senso	8.22	8.55	9.16	9.29	-0.94	-0.74	-0.33	-0.13	-0.18	-0.61	0.97	-0.44	-0.34	-0.29	1.07
Cthe_02915 ribosomal protein L5	10.8	11.46	11.74	12.31	-0.94	-0.85	-0.66	-0.57	-0.18	-0.7	-0.13	-1.35	-0.34	-0.29	0.95
Cthe_02918 ribosomal protein L6	10.23	10.95	11.19	11.88	-0.96	-0.93	-0.72	-0.69	-0.2	-0.77	-0.33	-1.6	-0.34	-0.29	0.87
Cthe_02624	5.52	5.75	6.61	6.52	-1.09	-0.77	-0.23	0.09	-0.3	-0.64	1.3	0.02	-0.34	-0.29	0.97
Cthe_02038 cellulosome enzyme, dockerin type	11.51	12.06	12.99	12.38	-1.48	-0.32	-0.55	0.61	-0.61	-0.25	0.23	1.1	-0.34	-0.29	1.05
Cthe_00630 hypothetical protein	10.6	11.05	11.61	11.6	-1.01	-0.55	-0.45	0.01	-0.24	-0.45	0.57	-0.15	-0.34	-0.29	1.55
Cthe_02915 ribosomal protein L5	10.8	11.46	11.74	12.31	-0.94	-0.85	-0.66	-0.57	-0.18	-0.7	-0.13	-1.35	-0.34	-0.29	0.95
Cthe_02918 ribosomal protein L6	10.23	10.95	11.19	11.88	-0.96	-0.93	-0.72	-0.69	-0.2	-0.77	-0.33	-1.6	-0.34	-0.29	0.87
Cthe_02624	5.52	5.75	6.61	6.52	-1.09	-0.77	-0.23	0.09	-0.3	-0.64	1.3	0.02	-0.34	-0.29	0.97
Cthe_02915 ribosomal protein L5	10.8	11.46	11.74	12.31	-0.94	-0.85	-0.66	-0.57	-0.18	-0.7	-0.13	-1.35	-0.34	-0.29	0.95
Cthe_02918 ribosomal protein L6	10.23	10.95	11.19	11.88	-0.96	-0.93	-0.72	-0.69	-0.2	-0.77	-0.33	-1.6	-0.34	-0.29	0.87
Cthe_01251 Xanthine/uracil/vitamin C permeas	10.68	11.62	11.96	12.37	-1.28	-0.75	-0.94	-0.41	-0.45	-0.62	-1.07	-1.02	-0.35	-0.3	0.93
Cthe_02543 Spore germination protein-like pro	11.91	12.59	13.5	12.8	-1.59	-0.21	-0.68	0.7	-0.7	-0.16	-0.2	1.29	-0.35	-0.3	0.98
Cthe_00963 Dihydrodipicolinate reductase	11.19	12.01	12.45	12.4	-1.26	-0.39	-0.82	0.05	-0.44	-0.31	-0.67	-0.06	-0.35	-0.3	1.43
Cthe_03036 methyl-accepting chemotaxis senso	5.32	5.29	6.39	6.38	-1.07	-1.09	0.03	0.01	-0.29	-0.91	2.17	-0.15	-0.35	-0.3	0.78
Cthe_03036 methyl-accepting chemotaxis senso	5.32	5.29	6.39	6.38	-1.07	-1.09	0.03	0.01	-0.29	-0.91	2.17	-0.15	-0.35	-0.3	0.78
Cthe_03022 NADH ubiquinone oxidoreductase,	6.79	7.78	7.41	7.97	-0.62	-0.19	-0.99	-0.56	0.07	-0.14	-1.23	-1.33	-0.35	-0.3	0.15
Cthe_03032 hypothetical protein	9.58	10.08	10.79	10.49	-1.21	-0.41	-0.5	0.3	-0.4	-0.33	0.4	0.46	-0.35	-0.3	1.52
Cthe_00839 stage III sporulation protein AG	3.81	5.09	5.39	6.19	-1.58	-1.1	-1.28	-0.8	-0.69	-0.92	-2.2	-1.83	-0.35	-0.3	0.72
Cthe_00963 Dihydrodipicolinate reductase	11.19	12.01	12.45	12.4	-1.26	-0.39	-0.82	0.05	-0.44	-0.31	-0.67	-0.06	-0.35	-0.3	1.43
Cthe_00963 Dihydrodipicolinate reductase	11.19	12.01	12.45	12.4	-1.26	-0.39	-0.82	0.05	-0.44	-0.31	-0.67	-0.06	-0.35	-0.3	1.43
Cthe_00963 Dihydrodipicolinate reductase	11.19	12.01	12.45	12.4	-1.26	-0.39	-0.82	0.05	-0.44	-0.31	-0.67	-0.06	-0.35	-0.3	1.43
Cthe_00963 Dihydrodipicolinate reductase	11.19	12.01	12.45	12.4	-1.26	-0.39	-0.82	0.05	-0.44	-0.31	-0.67	-0.06	-0.35	-0.3	1.43
Cthe_00963 Dihydrodipicolinate reductase	11.19	12.01	12.45	12.4	-1.26	-0.39	-0.82	0.05	-0.44	-0.31	-0.67	-0.06	-0.35	-0.3	1.43
Cthe_01800 Peptidoglycan-binding LysM	8.78	9.37	9.75	10.02	-0.97	-0.65	-0.59	-0.27	-0.21	-0.53	0.1	-0.73	-0.36	-0.31	1.38
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_02920 ribosomal protein S5-like protein	10.56	11.23	11.53	12.05	-0.97	-0.82	-0.67	-0.52	-0.21	-0.68	-0.17	-1.25	-0.36	-0.31	1.01
Cthe_02920 ribosomal protein S5-like protein	10.56	11.23	11.53	12.05	-0.97	-0.82	-0.67	-0.52	-0.21	-0.68	-0.17	-1.25	-0.36	-0.31	1.01
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_02920 ribosomal protein S5-like protein	10.56	11.23	11.53	12.05	-0.97	-0.82	-0.67	-0.52	-0.21	-0.68	-0.17	-1.25	-0.36	-0.31	1.01
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00961 aspartate-semialdehyde dehydroge	11.32	12.02	12.45	12.37	-1.13	-0.35	-0.7	0.08	-0.33	-0.28	-0.27	0	-0.36	-0.31	2.86
Cthe_00629 type II secretion system protein E	11.21	11.83	12.23	12.33	-1.02	-0.5	-0.62	-0.1	-0.25	-0.41	0	-0.38	-0.37	-0.32	2.26
Cthe_00832 exodeoxyribonuclease VII, small su	5.04	6.25	5.98	6.57	-0.94	-0.32	-1.21	-0.59	-0.18	-0.25	-1.97	-1.4	-0.37	-0.32	0.23
Cthe_02531 sulfate ABC transporter, periplasm	2.81	3.58	4.09	3.91	-1.28	-0.33	-0.77	0.18	-0.45	-0.26	-0.5	0.21	-0.37	-0.32	1.71
Cthe_02247 regulatory protein, MerR	7.32	7.75	8.65	8.24	-1.33	-0.49	-0.43	0.41	-0.49	-0.4	0.63	0.69	-0.37	-0.32	1.21
Cthe_03009 hypothetical protein	3.91	4.09	4.81	4.17	-0.9	-0.08	-0.18	0.64	-0.15	-0.05	1.47	1.17	-0.37	-0.32	0.15
Cthe_02531 sulfate ABC transporter, periplasm	2.81	3.58	4.09	3.91	-1.28	-0.33	-0.77	0.18	-0.45	-0.26	-0.5	0.21	-0.37	-0.32	1.71
Cthe_00832 exodeoxyribonuclease VII, small su	5.04	6.25	5.98	6.57	-0.94	-0.32	-1.21	-0.59	-0.18	-0.25	-1.97	-1.4	-0.37	-0.32	0.23
Cthe_02299 CRISPR-associated helicase Cas3	9.16	9.63	10.41	10.1	-1.25	-0.47	-0.47	0.31	-0.43	-0.38	0.5	0.48	-0.38	-0.33	1.48
Cthe_02919 ribosomal protein L18	9.55	10.09	10.42	11.02	-0.87	-0.93	-0.54	-0.6	-0.13	-0.77	0.27	-1.42	-0.38	-0.33	0.96
Cthe_01555 NLPA lipoprotein	3.46	3.46	4.52	3.7	-1.06	-0.24	0	0.82	-0.28	-0.19	2.07	1.54	-0.38	-0.33	0.23
Cthe_03135 hypothetical protein	1	2.32	2.58	3.7	-1.58	-1.38	-1.32	-1.12	-0.69	-1.15	-2.33	-2.5	-0.38	-0.33	0.7
Cthe_02919 ribosomal protein L18	9.55	10.09	10.42	11.02	-0.87	-0.93	-0.54	-0.6	-0.13	-0.77	0.27	-1.42	-0.38	-0.33	0.96
Cthe_02919 ribosomal protein L18	9.55	10.09	10.42	11.02	-0.87	-0.93	-0.54	-0.6	-0.13	-0.77	0.27	-1.42	-0.38	-0.33	0.96
Cthe_01555 NLPA lipoprotein	3.46	3.46	4.52	3.7	-1.06	-0.24	0	0.82	-0.28	-0.19	2.07	1.54	-0.38	-0.33	0.23
Cthe_00430 hydrogenase, Fe-only	13.65	14.4	14.81	14.98	-1.16	-0.58	-0.75	-0.17	-0.36	-0.47	-0.43	-0.52	-0.4	-0.34	1.57
Cthe_00792 Protein of unknown function UPF0	8.77	9.24	9.91	9.76	-1.14	-0.52	-0.47	0.15	-0.34	-0.42	0.5	0.15	-0.39	-0.34	1.85
Cthe_03026 GreA/GreB family elongation factor	11.25	11.97	12.4	12.45	-1.15	-0.48	-0.72	-0.05	-0.35	-0.39	-0.33	-0.27	-0.4	-0.34	2.19
Cthe_02528 uroporphyrin-III C-methyltransfera	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02529 Porphobilinogen synthase	5.36	6.38	6.81												



Cthe_03206 hypothetical protein	7.99	8.41	8.87	9.29	-0.88	-0.88	-0.42	-0.42	-0.13	-0.73	0.67	-1.04	-0.4	-0.34	1.07
Cthe_02855 hypothetical protein	10.46	10.5	11.14	10.72	-0.68	-0.22	-0.04	0.42	0.02	-0.17	1.93	0.71	-0.4	-0.34	0.15
Cthe_01987 hypothetical protein	3.32	4.86	5.73	4.91	-2.41	-0.05	-1.54	0.82	-1.35	-0.03	-3.07	1.54	-0.39	-0.34	0.7
Cthe_02140 hypothetical protein	7.1	7.73	8.09	8.57	-0.99	-0.84	-0.63	-0.48	-0.22	-0.69	-0.03	-1.17	-0.4	-0.34	1.1
Cthe_00565 hypothetical protein	12.66	13.14	14.74	13.43	-2.08	-0.29	-0.48	1.31	-1.09	-0.23	0.47	2.56	-0.39	-0.34	0.76
Cthe_02903 ribosomal protein L3	9.49	9.67	10.06	11.01	-0.57	-1.34	-0.18	-0.95	0.11	-1.12	1.47	-2.15	-0.4	-0.34	0.77
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02529 Porphobilinogen synthase	5.36	6.38	6.81	7.04	-1.45	-0.66	-1.02	-0.23	-0.59	-0.54	-1.33	-0.65	-0.39	-0.34	0.96
Cthe_02903 ribosomal protein L3	9.49	9.67	10.06	11.01	-0.57	-1.34	-0.18	-0.95	0.11	-1.12	1.47	-2.15	-0.4	-0.34	0.77
Cthe_02085 deoxyuridine 5'-triphosphate nucle	7.66	8.5	8.93	9.09	-1.27	-0.59	-0.84	-0.16	-0.44	-0.48	-0.73	-0.5	-0.4	-0.34	1.31
Cthe_00554 phosphoribosylformylglycinamidine	8.58	9.21	9.49	10.29	-0.91	-1.08	-0.63	-0.8	-0.16	-0.9	-0.03	-1.83	-0.4	-0.34	0.89
Cthe_02085 deoxyuridine 5'-triphosphate nucle	7.66	8.5	8.93	9.09	-1.27	-0.59	-0.84	-0.16	-0.44	-0.48	-0.73	-0.5	-0.4	-0.34	1.31
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02529 Porphobilinogen synthase	5.36	6.38	6.81	7.04	-1.45	-0.66	-1.02	-0.23	-0.59	-0.54	-1.33	-0.65	-0.39	-0.34	0.96
Cthe_00554 phosphoribosylformylglycinamidine	8.58	9.21	9.49	10.29	-0.91	-1.08	-0.63	-0.8	-0.16	-0.9	-0.03	-1.83	-0.4	-0.34	0.89
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02529 Porphobilinogen synthase	5.36	6.38	6.81	7.04	-1.45	-0.66	-1.02	-0.23	-0.59	-0.54	-1.33	-0.65	-0.39	-0.34	0.96
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_00554 phosphoribosylformylglycinamidine	8.58	9.21	9.49	10.29	-0.91	-1.08	-0.63	-0.8	-0.16	-0.9	-0.03	-1.83	-0.4	-0.34	0.89
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02085 deoxyuridine 5'-triphosphate nucle	7.66	8.5	8.93	9.09	-1.27	-0.59	-0.84	-0.16	-0.44	-0.48	-0.73	-0.5	-0.4	-0.34	1.31
Cthe_02085 deoxyuridine 5'-triphosphate nucle	7.66	8.5	8.93	9.09	-1.27	-0.59	-0.84	-0.16	-0.44	-0.48	-0.73	-0.5	-0.4	-0.34	1.31
Cthe_00554 phosphoribosylformylglycinamidine	8.58	9.21	9.49	10.29	-0.91	-1.08	-0.63	-0.8	-0.16	-0.9	-0.03	-1.83	-0.4	-0.34	0.89
Cthe_00554 phosphoribosylformylglycinamidine	8.58	9.21	9.49	10.29	-0.91	-1.08	-0.63	-0.8	-0.16	-0.9	-0.03	-1.83	-0.4	-0.34	0.89
Cthe_02528 uroporphyrin-III C-methyltransferase	7.44	8.09	8.45	8.9	-1.01	-0.81	-0.65	-0.45	-0.24	-0.67	-0.1	-1.1	-0.4	-0.34	1.15
Cthe_02529 Porphobilinogen synthase	5.36	6.38	6.81	7.04	-1.45	-0.66	-1.02	-0.23	-0.59	-0.54	-1.33	-0.65	-0.39	-0.34	0.96
Cthe_02545 signal transduction histidine kinase	1.58	1.58	3	1.58	-1.42	0	0	1.42	-0.56	0.02	2.07	2.79	-0.41	-0.35	0.29
Cthe_01801 ABC transporter related protein	9.08	10.16	9.86	10.14	-0.78	0.02	-1.08	-0.28	-0.06	0.03	-1.53	-0.75	-0.41	-0.35	0.07
Cthe_00936 3-oxoacyl-(acyl-carrier-protein) syn	10.33	11.13	11.54	11.75	-1.21	-0.62	-0.8	-0.21	-0.4	-0.51	-0.6	-0.6	-0.41	-0.35	1.36
Cthe_02825 intein	9.06	9.61	10.68	9.98	-1.62	-0.37	-0.55	0.7	-0.72	-0.3	0.23	1.29	-0.41	-0.35	1.06
Cthe_03132 cellulosome enzyme, dockerin type	9.4	10.08	11.25	10.31	-1.85	-0.23	-0.68	0.94	-0.9	-0.18	-0.2	1.79	-0.41	-0.35	0.91
Cthe_03031 hypothetical protein	5.61	5.67	6.86	6.67	-1.25	-1	-0.06	0.19	-0.43	-0.83	1.87	0.23	-0.41	-0.35	0.89
Cthe_00936 3-oxoacyl-(acyl-carrier-protein) syn	10.33	11.13	11.54	11.75	-1.21	-0.62	-0.8	-0.21	-0.4	-0.51	-0.6	-0.6	-0.41	-0.35	1.36
Cthe_01801 ABC transporter related protein	9.08	10.16	9.86	10.14	-0.78	0.02	-1.08	-0.28	-0.06	0.03	-1.53	-0.75	-0.41	-0.35	0.07
Cthe_01801 ABC transporter related protein	9.08	10.16	9.86	10.14	-0.78	0.02	-1.08	-0.28	-0.06	0.03	-1.53	-0.75	-0.41	-0.35	0.07
Cthe_00936 3-oxoacyl-(acyl-carrier-protein) syn	10.33	11.13	11.54	11.75	-1.21	-0.62	-0.8	-0.21	-0.4	-0.51	-0.6	-0.6	-0.41	-0.35	1.36
Cthe_00936 3-oxoacyl-(acyl-carrier-protein) syn	10.33	11.13	11.54	11.75	-1.21	-0.62	-0.8	-0.21	-0.4	-0.51	-0.6	-0.6	-0.41	-0.35	1.36
Cthe_00936 3-oxoacyl-(acyl-carrier-protein) syn	10.33	11.13	11.54	11.75	-1.21	-0.62	-0.8	-0.21	-0.4	-0.51	-0.6	-0.6	-0.41	-0.35	1.36
Cthe_00936 3-oxoacyl-(acyl-carrier-protein) syn	10.33	11.13	11.54	11.75	-1.21	-0.62	-0.8	-0.21	-0.4	-0.51	-0.6	-0.6	-0.41	-0.35	1.36
Cthe_02813 two component transcriptional reg	5.04	5.58	6.07	6.19	-1.03	-0.61	-0.54	-0.12	-0.25	-0.5	0.27	-0.42	-0.42	-0.36	2
Cthe_02550 glycosyltransferase sugar-binding r	5.21	6.13	6.63	6.67	-1.42	-0.54	-0.92	-0.04	-0.56	-0.44	-1	-0.25	-0.42	-0.36	1.23
Cthe_02813 two component transcriptional reg	5.04	5.58	6.07	6.19	-1.03	-0.61	-0.54	-0.12	-0.25	-0.5	0.27	-0.42	-0.42	-0.36	2
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_03173 sodium/calcium exchanger membr	4.7	5.49	5.93	6.07	-1.23	-0.58	-0.79	-0.14	-0.41	-0.47	-0.57	-0.46	-0.42	-0.36	1.52
Cthe_01452 KWG repeat containing protein	9.38	10.04	10.49	10.49	-1.11	-0.45	-0.66	0	-0.32	-0.36	-0.13	-0.17	-0.42	-0.36	4.02
Cthe_01784 hypothetical protein	12.21	12.83	13.86	13.15	-1.65	-0.32	-0.62	0.71	-0.75	-0.25	0	1.31	-0.42	-0.36	1.08
Cthe_02167 glycoside hydrolase, family 8	5.64	6.54	7	7.13	-1.36	-0.59	-0.9	-0.13	-0.52	-0.48	-0.93	-0.44	-0.42	-0.36	1.23
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
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Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
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Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26</					



Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
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Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02060 RNA methyltransferase, TrmH fami	8.33	8.98	9.79	9.31	-1.46	-0.33	-0.65	0.48	-0.6	-0.26	-0.1	0.83	-0.42	-0.36	1.4
Cthe_02354 nicotinate-nucleotide pyrophospho	9.46	10.13	10.57	10.64	-1.11	-0.51	-0.67	-0.07	-0.32	-0.42	-0.17	-0.31	-0.43	-0.37	2.67
Cthe_01520 hypothetical protein	8.64	9.26	9.73	9.65	-1.09	-0.39	-0.62	0.08	-0.3	-0.31	0	0	-0.43	-0.37	30
Cthe_01430 hypothetical protein	2	3	3.7	3.32	-1.7	-0.32	-1	0.38	-0.79	-0.25	-1.27	0.63	-0.43	-0.37	1.04
Cthe_02354 nicotinate-nucleotide pyrophospho	9.46	10.13	10.57	10.64	-1.11	-0.51	-0.67	-0.07	-0.32	-0.42	-0.17	-0.31	-0.43	-0.37	2.67
Cthe_02354 nicotinate-nucleotide pyrophospho	9.46	10.13	10.57	10.64	-1.11	-0.51	-0.67	-0.07	-0.32	-0.42	-0.17	-0.31	-0.43	-0.37	2.67
Cthe_02354 nicotinate-nucleotide pyrophospho	9.46	10.13	10.57	10.64	-1.11	-0.51	-0.67	-0.07	-0.32	-0.42	-0.17	-0.31	-0.43	-0.37	2.67
Cthe_02354 nicotinate-nucleotide pyrophospho	9.46	10.13	10.57	10.64	-1.11	-0.51	-0.67	-0.07	-0.32	-0.42	-0.17	-0.31	-0.43	-0.37	2.67
Cthe_00469 flagellar export protein FljI	5.64	5.7	6.44	7	-0.8	-1.3	-0.06	-0.56	-0.07	-1.08	1.87	-1.33	-0.44	-0.38	0.84
Cthe_02923 preprotein translocase, SecY subun	12.6	13.35	13.8	13.93	-1.2	-0.58	-0.75	-0.13	-0.39	-0.47	-0.43	-0.44	-0.44	-0.38	1.77
Cthe_01391 2-isopropylmalate synthase	11.7	12.46	12.62	13.99	-0.92	-1.53	-0.76	-1.37	-0.17	-1.28	-0.47	-3.02	-0.44	-0.38	0.75
Cthe_00304 Integrase, catalytic region	6.66	7.79	7.44	7.99	-0.78	-0.2	-1.13	-0.55	-0.06	-0.15	-1.7	-1.31	-0.44	-0.38	0.13
Cthe_00469 flagellar export protein FljI	5.64	5.7	6.44	7	-0.8	-1.3	-0.06	-0.56	-0.07	-1.08	1.87	-1.33	-0.44	-0.38	0.84
Cthe_00469 flagellar export protein FljI	5.64	5.7	6.44	7	-0.8	-1.3	-0.06	-0.56	-0.07	-1.08	1.87	-1.33	-0.44	-0.38	0.84
Cthe_02532 sulfate ABC transporter, inner mem	2.81	3.58	4.95	3.7	-2.14	-0.12	-0.77	1.25	-1.13	-0.08	-0.5	2.44	-0.44	-0.38	0.81
Cthe_02122 hypothetical protein	2.58	3.46	4.32	3.7	-1.74	-0.24	-0.88	0.62	-0.82	-0.19	-0.87	1.13	-0.44	-0.38	1.05
Cthe_02846 hypothetical protein	6.51	7.32	8.11	7.61	-1.6	-0.29	-0.81	0.5	-0.71	-0.23	-0.63	0.88	-0.44	-0.38	1.23
Cthe_02549 cellulosome enzyme, dockerin type	5.32	5.78	5.98	7.29	-0.66	-1.51	-0.46	-1.31	0.04	-1.26	0.53	-2.9	-0.44	-0.38	0.76
Cthe_02532 sulfate ABC transporter, inner mem	2.81	3.58	4.95	3.7	-2.14	-0.12	-0.77	1.25	-1.13	-0.08	-0.5	2.44	-0.44	-0.38	0.81
Cthe_01391 2-isopropylmalate synthase	11.7	12.46	12.62	13.99	-0.92	-1.53	-0.76	-1.37	-0.17	-1.28	-0.47	-3.02	-0.44	-0.38	0.75
Cthe_02923 preprotein translocase, SecY subun	12.6	13.35	13.8	13.93	-1.2	-0.58	-0.75	-0.13	-0.39	-0.47	-0.43	-0.44	-0.44	-0.38	1.77
Cthe_01391 2-isopropylmalate synthase	11.7	12.46	12.62	13.99	-0.92	-1.53	-0.76	-1.37	-0.17	-1.28	-0.47	-3.02	-0.44	-0.38	0.75
Cthe_01391 2-isopropylmalate synthase	11.7	12.46	12.62	13.99	-0.92	-1.53	-0.76	-1.37	-0.17	-1.28	-0.47	-3.02	-0.44	-0.38	0.75
Cthe_01379 oxidoreductase-like protein	9.15	9.87	10.3	10.56	-1.15	-0.69	-0.72	-0.26	-0.35	-0.57	-0.33	-0.71	-0.45	-0.39	1.53
Cthe_03204 CRISPR-associated helicase Cas3	11.81	12.41	12.84	13.25	-1.03	-0.84	-0.6	-0.41	-0.25	-0.69	0.07	-1.02	-0.45	-0.39	1.28
Cthe_00889 putative transmembrane anti-sigm	7.91	8.18	9.84	8.8	-1.93	-0.62	-0.27	1.04	-0.97	-0.51	1.17	2	-0.45	-0.39	0.84
Cthe_02214 hypothetical protein	7.95	8.53	9.03	9.07	-1.08	-0.54	-0.58	-0.04	-0.29	-0.44	0.13	-0.25	-0.45	-0.39	3.34
Cthe_02984	6.15	6.64	7.17	7.38	-1.02	-0.74	-0.49	-0.21	-0.25	-0.61	0.43	-0.6	-0.45	-0.39	1.59
Cthe_00400 hypothetical protein	8.66	9.49	10.09	9.89	-1.43	-0.4	-0.83	0.2	-0.57	-0.32	-0.7	0.25	-0.45	-0.39	1.57
Cthe_00225 RNA related	4.75	5.46	6.02	5.86	-1.27	-0.4	-0.71	0.16	-0.44	-0.32	-0.3	0.17	-0.45	-0.39	2.82
Cthe_02668 hypothetical protein	6.86	7.48	7.96	7.93	-1.1	-0.45	-0.62	0.03	-0.31	-0.36	0	-0.1	-0.45	-0.39	8.48
Cthe_02984	6.15	6.64	7.17	7.38	-1.02	-0.74	-0.49	-0.21	-0.25	-0.61	0.43	-0.6	-0.45	-0.39	1.59
Cthe_00399 protein of unknown function DUF4	8.8	9.33	9.94	9.85	-1.14	-0.52	-0.53	0.09	-0.34	-0.42	0.3	0.02	-0.46	-0.4	3.21
Cthe_01752 ABC transporter related protein	12.82	13.5	14.73	13.77	-1.91	-0.27	-0.68	0.96	-0.95	-0.21	-0.2	1.83	-0.46	-0.4	0.94
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_01752 ABC transporter related protein	12.82	13.5	14.73	13.77	-1.91	-0.27	-0.68	0.96	-0.95	-0.21	-0.2	1.83	-0.46	-0.4	0.94
Cthe_03115 hypothetical protein	9.14	9.71	10.41	10.16	-1.27	-0.45	-0.57	0.25	-0.44	-0.36	0.17	0.35	-0.46	-0.4	2.61
Cthe_02612 Fibronectin, type III	8.69	9.55	10.12	10.02	-1.43	-0.47	-0.86	0.1	-0.57	-0.38	-0.8	0.04	-0.46	-0.4	1.53
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_01752 ABC transporter related protein	12.82	13.5	14.73	13.77	-1.91	-0.27	-0.68	0.96	-0.95	-0.21	-0.2	1.83	-0.46	-0.4	0.94
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_01752 ABC transporter related protein	12.82	13.5	14.73	13.77	-1.91	-0.27	-0.68	0.96	-0.95	-0.21	-0.2	1.83	-0.46	-0.4	0.94
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0.43	-0.38	-0.46	-0.4	1.92
Cthe_02393 thiamine pyrophosphate enzyme-li	12.03	12.78	13.25	13.35	-1.22	-0.57	-0.75	-0.1	-0.4	-0.47	-0				



Cthe_00582 PAS/PAC sensor signal transduction	8	8.7	9.17	9.41	-1.17	-0.71	-0.7	-0.24	-0.37	-0.58	-0.27	-0.67	-0.49	-0.42	1.7
Cthe_02881 ATP phosphoribosyltransferase	4.86	5.39	6.27	5.88	-1.41	-0.49	-0.53	0.39	-0.56	-0.4	0.3	0.65	-0.49	-0.42	1.72
Cthe_02881 ATP phosphoribosyltransferase	4.86	5.39	6.27	5.88	-1.41	-0.49	-0.53	0.39	-0.56	-0.4	0.3	0.65	-0.49	-0.42	1.72
Cthe_02881 ATP phosphoribosyltransferase	4.86	5.39	6.27	5.88	-1.41	-0.49	-0.53	0.39	-0.56	-0.4	0.3	0.65	-0.49	-0.42	1.72
Cthe_02636 integral membrane protein MvIN	3.46	4	4.39	5.25	-0.93	-1.25	-0.54	-0.86	-0.17	-1.04	0.27	-1.96	-0.5	-0.43	0.95
Cthe_00175 polysaccharide deacetylase	11.63	12.21	12.93	12.68	-1.3	-0.47	-0.58	0.25	-0.47	-0.38	0.13	0.35	-0.5	-0.43	2.89
Cthe_03145 transcriptional repressor, CopY fam	5.88	6.64	7.62	6.97	-1.74	-0.33	-0.76	0.65	-0.82	-0.26	-0.47	1.19	-0.5	-0.43	1.2
Cthe_02205 cyanophycinase	4.64	4.86	5.36	6.3	-0.72	-1.44	-0.22	-0.94	-0.01	-1.2	1.33	-2.13	-0.5	-0.43	0.85
Cthe_02092 dimethyladenosine transferase	8.26	8.72	9.28	9.6	-1.02	-0.88	-0.46	-0.32	-0.25	-0.73	0.53	-0.83	-0.5	-0.43	1.4
Cthe_01893 hypothetical protein	9.38	9.69	10.46	10.61	-1.08	-0.92	-0.31	-0.15	-0.29	-0.76	1.03	-0.48	-0.5	-0.43	1.28
Cthe_02205 cyanophycinase	4.64	4.86	5.36	6.3	-0.72	-1.44	-0.22	-0.94	-0.01	-1.2	1.33	-2.13	-0.5	-0.43	0.85
Cthe_00796 hypothetical protein	4.91	5.58	6.92	5.88	-2.01	-0.3	-0.67	1.04	-1.03	-0.24	-0.17	2	-0.5	-0.43	0.94
Cthe_02092 dimethyladenosine transferase	8.26	8.72	9.28	9.6	-1.02	-0.88	-0.46	-0.32	-0.25	-0.73	0.53	-0.83	-0.5	-0.43	1.4
Cthe_02205 cyanophycinase	4.64	4.86	5.36	6.3	-0.72	-1.44	-0.22	-0.94	-0.01	-1.2	1.33	-2.13	-0.5	-0.43	0.85
Cthe_01589 transcriptional repressor, CopY fam	6.27	6.97	7.45	7.73	-1.18	-0.76	-0.7	-0.28	-0.37	-0.63	-0.27	-0.75	-0.51	-0.44	1.64
Cthe_02069 hypothetical protein	10.73	11.39	12.36	11.79	-1.63	-0.4	-0.66	0.57	-0.73	-0.32	-0.13	1.02	-0.51	-0.44	1.38
Cthe_00216 small acid-soluble spore protein, al	7.22	7.85	8.7	8.29	-1.48	-0.44	-0.63	0.41	-0.61	-0.36	-0.03	0.69	-0.51	-0.44	1.83
Cthe_00822 IstB-like ATP-binding protein	9.22	9.82	10.41	10.3	-1.19	-0.48	-0.6	0.11	-0.38	-0.39	0.07	0.06	-0.52	-0.45	10.55
Cthe_00540 protein of unknown function DUF2	8.19	8.83	9.19	10.16	-1	-1.33	-0.64	-0.97	-0.23	-1.11	-0.07	-2.19	-0.52	-0.45	0.92
Cthe_02476 phage putative head morphogenes	4.52	5	6.49	5.49	-1.97	-0.49	-0.48	1	-1	-0.4	0.47	1.92	-0.52	-0.45	0.97
Cthe_02912 ribosomal protein S17	9.06	9.76	10.17	10.86	-1.11	-1.1	-0.7	-0.69	-0.32	-0.92	-0.27	-1.6	-0.52	-0.45	1.07
Cthe_00671 hypothetical protein	4.95	5.86	6.55	6.32	-1.6	-0.46	-0.91	0.23	-0.71	-0.37	-0.97	0.31	-0.52	-0.45	1.4
Cthe_03033 hypothetical protein	7.8	8.45	8.9	9.45	-1.1	-1	-0.65	-0.55	-0.31	-0.83	-0.1	-1.31	-0.52	-0.45	1.2
Cthe_01928 intein	5.46	5.91	6.58	6.66	-1.12	-0.75	-0.45	-0.08	-0.33	-0.62	0.57	-0.33	-0.52	-0.45	1.9
Cthe_01233 hypothetical protein	4.17	4.52	5.13	5.61	-0.96	-1.09	-0.35	-0.48	-0.2	-0.91	0.9	-1.17	-0.52	-0.45	1.13
Cthe_01640 hypothetical protein	0	2	1	-2	-1	0	1	-1.02	-0.83	2.07	1.92	-0.52	-0.45	0.83	
Cthe_02912 ribosomal protein S17	9.06	9.76	10.17	10.86	-1.11	-1.1	-0.7	-0.69	-0.32	-0.92	-0.27	-1.6	-0.52	-0.45	1.07
Cthe_00540 protein of unknown function DUF2	8.19	8.83	9.19	10.16	-1	-1.33	-0.64	-0.97	-0.23	-1.11	-0.07	-2.19	-0.52	-0.45	0.92
Cthe_02912 ribosomal protein S17	9.06	9.76	10.17	10.86	-1.11	-1.1	-0.7	-0.69	-0.32	-0.92	-0.27	-1.6	-0.52	-0.45	1.07
Cthe_00474 protein of unknown function DUF1	10.51	11.31	11.96	11.79	-1.45	-0.48	-0.8	0.17	-0.59	-0.39	-0.6	0.19	-0.53	-0.46	2.01
Cthe_00810 CheA signal transduction histidine k	7.9	8.56	9.05	9.42	-1.15	-0.86	-0.66	-0.37	-0.35	-0.71	-0.13	-0.94	-0.53	-0.46	1.49
Cthe_01807 hypothetical protein	6.69	7.47	8.12	7.95	-1.43	-0.48	-0.78	0.17	-0.57	-0.39	-0.53	0.19	-0.53	-0.46	2.19
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00810 CheA signal transduction histidine k	7.9	8.56	9.05	9.42	-1.15	-0.86	-0.66	-0.37	-0.35	-0.71	-0.13	-0.94	-0.53	-0.46	1.49
Cthe_02913 ribosomal protein L14	9.44	9.79	10.34	11.02	-0.9	-1.23	-0.35	-0.68	-0.15	-1.03	0.9	-1.58	-0.53	-0.46	1.02
Cthe_02914 ribosomal protein L24	9.35	9.82	10.26	11.13	-0.91	-1.31	-0.47	-0.87	-0.16	-1.09	0.5	-1.98	-0.53	-0.46	0.96
Cthe_02133 hypothetical protein	6.75	7.14	8.04	7.87	-1.29	-0.73	-0.39	0.17	-0.46	-0.6	0.77	0.19	-0.53	-0.46	1.7
Cthe_02156 hypothetical protein	2.81	3.46	4.32	3.91	-1.51	-0.45	-0.65	0.41	-0.63	-0.36	-0.1	0.69	-0.53	-0.46	1.86
Cthe_01431 hypothetical protein	9.83	10.64	11.13	11.45	-1.3	-0.81	-0.81	-0.32	-0.47	-0.67	-0.63	-0.83	-0.53	-0.46	1.4
Cthe_02477 hypothetical protein	2.32	3.46	4.64	3.58	-2.32	-0.12	-1.14	1.06	-1.28	-0.08	-1.73	2.04	-0.53	-0.46	0.86
Cthe_02913 ribosomal protein L14	9.44	9.79	10.34	11.02	-0.9	-1.23	-0.35	-0.68	-0.15	-1.03	0.9	-1.58	-0.53	-0.46	1.02
Cthe_02914 ribosomal protein L24	9.35	9.82	10.26	11.13	-0.91	-1.31	-0.47	-0.87	-0.16	-1.09	0.5	-1.98	-0.53	-0.46	0.96
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_02913 ribosomal protein L14	9.44	9.79	10.34	11.02	-0.9	-1.23	-0.35	-0.68	-0.15	-1.03	0.9	-1.58	-0.53	-0.46	1.02
Cthe_02914 ribosomal protein L24	9.35	9.82	10.26	11.13	-0.91	-1.31	-0.47	-0.87	-0.16	-1.09	0.5	-1.98	-0.53	-0.46	0.96
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00810 CheA signal transduction histidine k	7.9	8.56	9.05	9.42	-1.15	-0.86	-0.66	-0.37	-0.35	-0.71	-0.13	-0.94	-0.53	-0.46	1.49
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00053 ribonucleoside-diphosphate reduct	11.72	12.36	13.27	12.8	-1.55	-0.44	-0.64	0.47	-0.67	-0.36	-0.07	0.81	-0.53	-0.46	1.67
Cthe_00532 hydrolase (HAD superfamily)-like p	4.09	4	5.64	5.25	-1.55	-1.25	0.09	0.39	-0.67	-1.04	2.37	0.65	-0.55	-0.47	0.9
Cthe_00074 RNA polymerase, sigma-24 subunit	1	2.58	2.32	-1.58	-2.32	1	0.26	-0.69	-1.95	5.4	0.38	-0.55	-0.47	0.68	
Cthe_01809 RNA polymerase, sigma-24 subunit	6.54	7.04	8.09	7.6	-1.55	-0.56	-0.5	0.49	-0.67	-0.46	0.4	0.85	-0.55	-0.47	1.54
Cthe_02231 Methyltransferase type 11	6.27	6.99	7.52	7.71	-1.25	-0.72	-0.72	-0.19	-0.43	-0.59	-0.33	-0.56	-0.55	-0.47	2.01
Cthe_00294	6.57	7.3	7.96	7.78	-1.39	-0.48	-0.73	0.18	-0.54	-0.39	-0.37	0.21	-0.55	-0.47	2.8
Cthe_01953 cell wall hydrolase, SleB	8.41	9.28	10.43	9.55	-2.02	-0.27	-0.87	0.88	-1.04	-0.21	-0.83	1.67	-0.54	-0.47	1.02
Cthe_02901 putative anti-sigma regulatory fact	12.11	12.42	13.71	13.16	-1.6	-0.74	-0.31	0.55	-0.71	-0.61	1.03	0.98	-0.54	-0.47	1.18
Cthe_00845 stage III sporulation protein spoIIA	5.39	6	6.36	7.46	-0.97	-1.46	-0.61	-1.1	-0.21	-1.22	0.03	-2.46	-0.55	-0.47	0.9
Cthe_01630 phage portal protein, HK97 family	1	0	2.58	2.32	-1.58	-2.32	1	0.26	-0.69	-1.95	5.4	0.38	-0.55	-0.47	0.68
Cthe_00359 hypothetical protein	4.86	6.21	7.08	6.66	-2.22	-0.45	-1.35	0.42	-1.2	-0.36	-2.43	0.71	-0.54	-0.47	0.88
Cthe_00326 hypothetical protein	8.06	8.68	10.83	8.89	-2.77	-0.21	-0.62	1.94	-1.63	-0.16	0	3.88	-0.55	-0.47	0.75
Cthe_01979 intein	10.13	10.68	11.96	11.16	-1.83	-0.48	-0.55	0.8	-0.89	-0.39	0.23	1.5	-0.55	-0.47	1.14
Cthe_02854 intein	9.41	9.97	11.31	10.43	-1.9	-0.46	-0.56	0.88	-0.94	-0.37	0.2	1.67	-0.54	-0.47	1.07
Cthe_02901 putative anti-sigma regulatory fact	12.11	12.42	13.71	13.16	-1.6	-0.74	-0.31	0.55	-0.71	-0.61	1.03	0.98	-0.54	-0.47	1.18
Cthe_01953 cell wall hydrolase, SleB	8.41	9.28	10.43	9.55	-2.02	-0.27	-0.87	0.88	-1.04	-0.21	-0.83	1.67	-0.54	-0.47	1.02
Cthe_00257 twitching motility protein	4.25	5.29	5.93	5.98	-1.68	-0.69	-1.04	-0.05	-0.77	-0.57	-1.4	-0.27	-0.56	-0.48	1.2
Cthe_00270 glycoside hydrolase, family 18	9.01	9.68	10.62	10.14	-1.61	-0.46	-0.67	0.48	-0.71	-0.37	-0.17	0.83	-0.56	-0.48	1.69
Cthe_01533 transposase, mutator type	0	1	-1	0	0	0	1	-0.23	0.02	2.07	1.92	-0.56	-0.48	0.15	
Cthe_01886 Integrase, catalytic region	0	1	-1	0	0	0	1	-0.23	0.02	2.07	1.92	-0.56	-0.48	0.15	
Cthe_02325 Recombinase	0	1	0	-1	0	0	1	-0.23	0.02	2.07	1.92	-0.56	-0.48	0.15	
Cthe_00257 twitching motility protein	4.25	5.29	5.93	5.98	-1.68	-0.69	-1.04	-0.05	-0.77	-0.57	-1.4	-0.27	-0.56	-0.48	1.2
Cthe_00518 type III restriction enzyme, res subu	0	1	-1	0	0	0	1	-0.23	0.02	2.07	1.92	-0.56	-0.48	0.15	
Cthe_01892 RNA related	6.78	7.06	7.92	8.07	-1.14	-1.01	-0.28	-0.15	-0.34	-0.84	1.13	-0.48	-0.56	-0.48	1.32
Cthe_00270 glycoside hydrolase, family 18	9.01	9.68	10.62	10.14	-1.61	-0.46	-0.67	0.48	-0.71	-0.37	-0.17	0.83	-0.56	-0.48	1.69
Cthe_00518 type III restriction enzyme, res subu	0	1	-1	0	0	0	1	-0.23	0.02	2.07	1.92	-0.56	-0.48	0.15	
Cthe_02752 beta-lactamase-like protein	3	4.32	5	5.17	-2	-0.85	-1.32	-0.17	-1.02	-0.7	-2.33	-0.52	-0.57	-0.49	0.93
Cthe_02382 major facilitator superfamily MFS_	9.24	9.83	10.32	10.97	-1.08	-1.14	-0.59	-0.65	-0.29	-0.95					



Cthe_02734 VanW	5.78	6.41	7.22	6.91	-1.44	-0.5	-0.63	0.31	-0.58	-0.41	-0.03	0.48	-0.58	-0.5	2.64
Cthe_00697 type IV pilus assembly PilZ	8.43	9.08	9.84	9.58	-1.41	-0.5	-0.65	0.26	-0.56	-0.41	-0.1	0.38	-0.58	-0.5	3.15
Cthe_00364 transcriptional regulator, XRE family	6.17	7	7.69	7.55	-1.52	-0.55	-0.83	0.14	-0.64	-0.45	-0.7	0.13	-0.58	-0.5	1.96
Cthe_02763 hypothetical protein	6.98	7.63	8.5	8.13	-1.52	-0.5	-0.65	0.37	-0.64	-0.41	-0.1	0.6	-0.59	-0.51	2.23
Cthe_02296 CRISPR-associated protein Cas2	6.43	6.93	8.51	7.45	-2.08	-0.52	-0.5	1.06	-1.09	-0.42	0.4	2.04	-0.59	-0.51	1
Cthe_00310 hypothetical protein	11.91	12.55	13.55	13.04	-1.64	-0.49	-0.64	0.51	-0.74	-0.4	-0.07	0.9	-0.59	-0.51	1.66
Cthe_01175 hypothetical protein	7.93	8.24	9.36	9.09	-1.43	-0.85	-0.31	0.27	-0.57	-0.7	1.03	0.4	-0.59	-0.51	1.46
Cthe_01919 MgtC/SapB transporter	7.09	7.88	8.7	8.36	-1.61	-0.48	-0.79	0.34	-0.71	-0.39	-0.57	0.54	-0.59	-0.51	1.84
Cthe_00426 putative PAS/PAC sensor protein	13.43	14.21	14.75	15.16	-1.32	-0.95	-0.78	-0.41	-0.48	-0.79	-0.53	-1.02	-0.6	-0.52	1.44
Cthe_03133 alpha/beta hydrolase fold	8.04	8.64	9.8	9.16	-1.76	-0.52	-0.6	0.64	-0.83	-0.42	0.07	1.17	-0.6	-0.52	1.42
Cthe_02650 polysaccharide biosynthesis protei	1.58	2.81	4.32	2.81	-2.74	0	-1.23	1.51	-1.61	0.02	-2.03	2.98	-0.6	-0.52	0.8
Cthe_02809 glycoside hydrolase, family 16	9.27	10.21	11.23	10.61	-1.96	-0.4	-0.94	0.62	-0.99	-0.32	-1.07	1.13	-0.6	-0.52	1.19
Cthe_01811 transcriptional repressor, CopY fam	3.91	5.17	6.34	5.39	-2.43	-0.22	-1.26	0.95	-1.37	-0.17	-2.13	1.81	-0.6	-0.52	0.88
Cthe_01839 Radical SAM	11.2	11.81	12.4	12.6	-1.2	-0.79	-0.61	-0.2	-0.39	-0.65	0.03	-0.58	-0.6	-0.52	2.33
Cthe_00491 CheW protein	6.51	7.21	7.78	7.98	-1.27	-0.77	-0.7	-0.2	-0.44	-0.64	-0.27	-0.58	-0.6	-0.52	2.17
Cthe_01266 methyl-accepting chemotaxis senso	6.95	7.43	8.17	8.19	-1.22	-0.76	-0.48	-0.02	-0.4	-0.63	0.47	-0.21	-0.6	-0.52	2.59
Cthe_02650 polysaccharide biosynthesis protei	1.58	2.81	4.32	2.81	-2.74	0	-1.23	1.51	-1.61	0.02	-2.03	2.98	-0.6	-0.52	0.8
Cthe_02080 NUDIX hydrolase	7.07	7.88	8.51	8.53	-1.44	-0.65	-0.81	-0.02	-0.58	-0.53	-0.63	-0.21	-0.6	-0.52	2.11
Cthe_00491 CheW protein	6.51	7.21	7.78	7.98	-1.27	-0.77	-0.7	-0.2	-0.44	-0.64	-0.27	-0.58	-0.6	-0.52	2.17
Cthe_01266 methyl-accepting chemotaxis senso	6.95	7.43	8.17	8.19	-1.22	-0.76	-0.48	-0.02	-0.4	-0.63	0.47	-0.21	-0.6	-0.52	2.59
Cthe_03089 UspA	9.5	9.99	11.66	10.52	-2.16	-0.53	-0.49	1.14	-1.15	-0.43	0.43	2.21	-0.6	-0.52	0.97
Cthe_01753 transport system permease protein	11.82	12.33	13.9	12.86	-2.08	-0.53	-0.51	1.04	-1.09	-0.43	0.37	2	-0.6	-0.52	1.03
Cthe_02386 VanW	8.6	9.06	10.2	9.7	-1.6	-0.64	-0.46	0.5	-0.71	-0.53	0.53	0.88	-0.6	-0.52	1.54
Cthe_03134 hypothetical protein	0	2	1.58	2.58	-1.58	-0.58	-2	-1	-0.69	-0.47	-4.6	-2.25	-0.6	-0.52	0.29
Cthe_01753 transport system permease protein	11.82	12.33	13.9	12.86	-2.08	-0.53	-0.51	1.04	-1.09	-0.43	0.37	2	-0.6	-0.52	1.03
Cthe_01839 Radical SAM	11.2	11.81	12.4	12.6	-1.2	-0.79	-0.61	-0.2	-0.39	-0.65	0.03	-0.58	-0.6	-0.52	2.33
Cthe_01839 Radical SAM	11.2	11.81	12.4	12.6	-1.2	-0.79	-0.61	-0.2	-0.39	-0.65	0.03	-0.58	-0.6	-0.52	2.33
Cthe_01839 Radical SAM	11.2	11.81	12.4	12.6	-1.2	-0.79	-0.61	-0.2	-0.39	-0.65	0.03	-0.58	-0.6	-0.52	2.33
Cthe_01905 glycosyl transferase, family 28	6.3	6.85	7.77	7.45	-1.47	-0.6	-0.55	0.32	-0.6	-0.49	0.23	0.5	-0.62	-0.53	2.51
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02163 anti-sigma-factor antagonist	6.86	7.38	8.02	8.28	-1.16	-0.9	-0.52	-0.26	-0.36	-0.75	0.33	-0.71	-0.61	-0.53	1.9
Cthe_01174 protein of unknown function DUF1	8.42	9.04	10.07	9.56	-1.65	-0.52	-0.62	0.51	-0.75	-0.42	0	0.9	-0.61	-0.53	1.71
Cthe_02910 ribosomal protein L16	9.26	9.82	10.37	11.01	-1.11	-1.19	-0.56	-0.64	-0.32	-0.99	0.2	-1.5	-0.62	-0.53	1.23
Cthe_01905 glycosyl transferase, family 28	6.3	6.85	7.77	7.45	-1.47	-0.6	-0.55	0.32	-0.6	-0.49	0.23	0.5	-0.62	-0.53	2.51
Cthe_02566 Radical SAM	7.7	8.29	9.19	8.85	-1.49	-0.56	-0.59	0.34	-0.62	-0.46	0.1	0.54	-0.62	-0.53	2.51
Cthe_02146 copper amine oxidase-like protein	4.7	5.25	5.81	6.43	-1.11	-1.18	-0.55	-0.62	-0.32	-0.98	0.23	-1.46	-0.62	-0.53	1.25
Cthe_00084 hypothetical protein	10.22	10.76	11.75	11.35	-1.53	-0.59	-0.54	0.4	-0.65	-0.48	0.27	0.67	-0.61	-0.53	2
Cthe_00239 cellulosome enzyme, dockerin type	8.95	9.87	10.47	10.74	-1.52	-0.87	-0.92	-0.27	-0.64	-0.72	-1	-0.73	-0.62	-0.53	1.39
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02910 ribosomal protein L16	9.26	9.82	10.37	11.01	-1.11	-1.19	-0.56	-0.64	-0.32	-0.99	0.2	-1.5	-0.62	-0.53	1.23
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_02444 Transketolase-like protein	3.17	4.17	4.91	4.81	-1.74	-0.64	-1	0.1	-0.82	-0.53	-1.27	0.04	-0.62	-0.53	1.37
Cthe_00683 diaminopimelate decarboxylase	9.45	9.84	10.66	10.78	-1.21	-0.94	-0.39	-0.12	-0.4	-0.78	0.77	-0.42	-0.63	-0.54	1.78
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_03203 CRISPR-associated protein Cas5, H	11.3	11.81	12.43	12.93	-1.13	-1.12	-0.51	-0.5	-0.33	-0.93	0.37	-1.21	-0.63	-0.54	1.39
Cthe_00683 diaminopimelate decarboxylase	9.45	9.84	10.66	10.78	-1.21	-0.94	-0.39	-0.12	-0.4	-0.78	0.77	-0.42	-0.63	-0.54	1.78
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_00683 diaminopimelate decarboxylase	9.45	9.84	10.66	10.78	-1.21	-0.94	-0.39	-0.12	-0.4	-0.78	0.77	-0.42	-0.63	-0.54	1.78
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_00683 diaminopimelate decarboxylase	9.45	9.84	10.66	10.78	-1.21	-0.94	-0.39	-0.12	-0.4	-0.78	0.77	-0.42	-0.63	-0.54	1.78
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_00683 diaminopimelate decarboxylase	9.45	9.84	10.66	10.78	-1.21	-0.94	-0.39	-0.12	-0.4	-0.78	0.77	-0.42	-0.63	-0.54	1.78
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg decarboxylase, major	9.25	10.04	10.94	10.54	-1.69	-0.5	-0.79	0.4	-0.78	-0.41	-0.57	0.67	-0.63	-0.54	1.79
Cthe_02108 Orn/Lys/Arg dec															



Cthe_02082 hypothetical protein	0	2.58	1	-2.58	-1	0	1.58	-1.48	-0.83	2.07	3.13	-0.65	-0.56	0.81	
Cthe_02776 hypothetical protein	7.52	8.25	9.19	8.78	-1.67	-0.53	-0.73	0.41	-0.76	-0.43	-0.37	0.69	-0.65	-0.56	1.99
Cthe_02072 hypothetical protein	5.25	5.83	6.83	6.43	-1.58	-0.6	-0.58	0.4	-0.69	-0.49	0.13	0.67	-0.66	-0.57	2.21
Cthe_01434 hypothetical protein	5.39	6.21	7.45	6.64	-2.06	-0.43	-0.82	0.81	-1.07	-0.35	-0.67	1.52	-0.66	-0.57	1.21
Cthe_02680 peptidase S41	8.93	9.54	10.68	10.12	-1.75	-0.58	-0.61	0.56	-0.83	-0.47	0.03	1	-0.67	-0.58	1.7
Cthe_01285 metal dependent phosphohydrolas	6.73	7.09	8.1	7.99	-1.37	-0.9	-0.36	0.11	-0.52	-0.75	0.87	0.06	-0.67	-0.58	1.87
Cthe_00663 hypothetical protein	6.79	7.45	8.15	8.04	-1.36	-0.59	-0.66	0.11	-0.52	-0.48	-0.13	0.06	-0.67	-0.58	8.83
Cthe_02877 S-layer-like domain containing prot	10.39	10.96	11.82	11.59	-1.43	-0.63	-0.57	0.23	-0.57	-0.52	0.17	0.31	-0.67	-0.58	3.9
Cthe_00168 hypothetical protein	5.93	6.67	7.32	7.44	-1.39	-0.77	-0.74	-0.12	-0.54	-0.64	-0.4	-0.42	-0.67	-0.58	2.58
Cthe_00179 Argininosuccinate synthase	9.65	10.39	11.12	11.03	-1.47	-0.64	-0.74	0.09	-0.6	-0.53	-0.4	0.02	-0.69	-0.59	3.57
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_02484 transposase IS116/IS110/IS902	6.04	5.46	7.5	5.95	-1.46	-0.49	0.58	1.55	-0.6	-0.4	4	3.06	-0.69	-0.59	0.26
Cthe_02935 methyltransferase small	8.27	8.72	9.53	9.62	-1.26	-0.9	-0.45	-0.09	-0.44	-0.75	0.57	-0.35	-0.68	-0.59	2.32
Cthe_02405 Heavy metal transport/detoxificati	7.61	8.15	8.9	8.89	-1.29	-0.74	-0.54	0.01	-0.46	-0.61	0.27	-0.15	-0.68	-0.59	4.42
Cthe_00798 lipolytic enzyme, G-D-S-L	8.19	8.74	9.97	9.37	-1.78	-0.63	-0.55	0.6	-0.85	-0.52	0.23	1.08	-0.69	-0.59	1.61
Cthe_01994 hypothetical protein	4.86	5.86	6.74	6.48	-1.88	-0.62	-1	0.26	-0.93	-0.51	-1.27	0.38	-0.69	-0.59	1.43
Cthe_01073 protein of unknown function DUF1	2.58	4.25	5.09	5.32	-2.51	-1.07	-1.67	-0.23	-1.43	-0.89	-3.5	-0.65	-0.69	-0.59	0.84
Cthe_01307 cellulosome anchoring protein, coh	11.33	11.95	12.63	12.59	-1.3	-0.64	-0.62	0.04	-0.47	-0.53	0	-0.08	-0.69	-0.59	15.81
Cthe_00179 Argininosuccinate synthase	9.65	10.39	11.12	11.03	-1.47	-0.64	-0.74	0.09	-0.6	-0.53	-0.4	0.02	-0.69	-0.59	3.57
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00179 Argininosuccinate synthase	9.65	10.39	11.12	11.03	-1.47	-0.64	-0.74	0.09	-0.6	-0.53	-0.4	0.02	-0.69	-0.59	3.57
Cthe_00179 Argininosuccinate synthase	9.65	10.39	11.12	11.03	-1.47	-0.64	-0.74	0.09	-0.6	-0.53	-0.4	0.02	-0.69	-0.59	3.57
Cthe_00179 Argininosuccinate synthase	9.65	10.39	11.12	11.03	-1.47	-0.64	-0.74	0.09	-0.6	-0.53	-0.4	0.02	-0.69	-0.59	3.57
Cthe_00179 Argininosuccinate synthase	9.65	10.39	11.12	11.03	-1.47	-0.64	-0.74	0.09	-0.6	-0.53	-0.4	0.02	-0.69	-0.59	3.57
Cthe_00179 Argininosuccinate synthase	9.65	10.39	11.12	11.03	-1.47	-0.64	-0.74	0.09	-0.6	-0.53	-0.4	0.02	-0.69	-0.59	3.57
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00964 amino acid-binding ACT	10.29	10.9	11.61	11.51	-1.32	-0.61	-0.61	0.1	-0.48	-0.5	0.03	0.04	-0.68	-0.59	24.75
Cthe_00465 flagellar M-ring protein FlIF	9.67	10.25	10.86	11.55	-1.19	-1.3	-0.58	-0.69	-0.38	-1.08	0.13	-1.6	-0.7	-0.6	1.27
Cthe_02872 glycoside hydrolase, family 5	12.72	13.49	14.51	14.04	-1.79	-0.55	-0.77	0.47	-0.86	-0.45	-0.5	0.81	-0.7	-0.6	1.82
Cthe_01958 UV-endonuclease UvdE	7.73	8.51	9.25	9.19	-1.52	-0.68	-0.78	0.06	-0.64	-0.56	-0.53	-0.04	-0.7	-0.6	2.86
Cthe_00465 flagellar M-ring protein FlIF	9.67	10.25	10.86	11.55	-1.19	-1.3	-0.58	-0.69	-0.38	-1.08	0.13	-1.6	-0.7	-0.6	1.27
Cthe_00424 aminoglycoside phosphotransferas	13.45	14.29	14.93	15.26	-1.48	-0.97	-0.84	-0.33	-0.61	-0.81	-0.73	-0.85	-0.7	-0.6	1.62
Cthe_01497 hypothetical protein	5.49	6.66	7.77	7.14	-2.28	-0.48	-1.17	0.63	-1.25	-0.39	-1.83	1.15	-0.7	-0.6	1.08
Cthe_02289 hypothetical protein	2	2	3	3.7	-1	-1.7	0	-0.7	-0.23	-1.42	2.07	-1.62	-0.7	-0.6	0.98
Cthe_02161 hypothetical protein	9.38	9.91	10.87	10.6	-1.49	-0.69	-0.53	0.27	-0.62	-0.57	0.3	0.4	-0.7	-0.6	3.01
Cthe_00382 hypothetical protein	3.58	2.32	3.46	3.32	0.12	-1	1.26	0.14	0.66	-0.83	6.27	0.13	-0.7	-0.6	0.3
Cthe_00840 hypothetical protein	3.58	3.58	4.52	5.32	-0.94	-1.74	0	-0.8	-0.18	-1.46	2.07	-1.83	-0.7	-0.6	0.95
Cthe_01958 UV-endonuclease UvdE	7.73	8.51	9.25	9.19	-1.52	-0.68	-0.78	0.06	-0.64	-0.56	-0.53	-0.04	-0.7	-0.6	2.86
Cthe_00825 glycoside hydrolase, family 9	9.77	10.42	11.1	11.17	-1.33	-0.75	-0.65	-0.07	-0.49	-0.62	-0.1	-0.31	-0.7	-0.6	4.33
Cthe_00825 glycoside hydrolase, family 9	9.77	10.42	11.1	11.17	-1.33	-0.75	-0.65	-0.07	-0.49	-0.62	-0.1	-0.31	-0.7	-0.6	4.33
Cthe_00823 hypothetical protein	9.71	10.49	11.28	11.14	-1.57	-0.65	-0.78	0.14	-0.68	-0.53	-0.53	0.13	-0.71	-0.61	2.82
Cthe_00098 peptidase M50	5.83	6.46	7.17	7.14	-1.34	-0.68	-0.63	0.03	-0.5	-0.56	-0.03	-0.1	-0.72	-0.62	12.84
Cthe_00425 hypothetical protein	11.21	11.89	12.56	12.84	-1.35	-0.95	-0.68	-0.28	-0.51	-0.79	-0.2	-0.75	-0.72	-0.62	2.16
Cthe_02177 hypothetical protein	2.32	3.17	3.81	4.25	-1.49	-1.08	-0.85	-0.44	-0.62	-0.9	-0.77	-1.08	-0.72	-0.62	1.47
Cthe_01179 hypothetical protein	5.21	6.17	7.91	6.44	-2.7	-0.27	-0.96	1.47	-1.58	-0.21	-1.13	2.9	-0.72	-0.62	0.91
Cthe_03205 hypothetical protein	8.2	8.65	9.39	9.85	-1.19	-1.2	-0.45	-0.46	-0.38	-1	0.57	-1.13	-0.72	-0.62	1.51
Cthe_00098 peptidase M50	5.83	6.46	7.17	7.14	-1.34	-0.68	-0.63	0.03	-0.5	-0.56	-0.03	-0.1	-0.72	-0.62	12.84
Cthe_01252 Auxin Efflux Carrier	9.55	10.18	10.84	11.36	-1.29	-1.18	-0.63	-0.52	-0.46	-0.98	-0.03	-1.25	-0.73	-0.63	1.55
Cthe_01272 DNA-directed RNA polymerase sigma	4.39	5.25	5.98	6.07	-1.59	-0.82	-0.86	-0.09	-0.7	-0.68	-0.8	-0.35	-0.73	-0.63	2
Cthe_01932 S-layer-like domain containing prot	6.49	7.12	7.83	7.97	-1.34	-0.85	-0.63	-0.14	-0.5	-0.7	-0.03	-0.46	-0.73	-0.63	3.33
Cthe_02245 hypothetical protein	6.46	7.19	8.11	7.8	-1.65	-0.61	-0.73	0.31	-0.75	-0.5	-0.37	0.48	-0.73	-0.63	2.66
Cthe_01929 hypothetical protein	8.12	8.9	10.21	9.41	-2.09	-0.51	-0.78	0.8	-1.1	-0.42	-0.53	1.5	-0.73	-0.63	1.32
Cthe_03061 transcriptional repressor, CopY fam	4.32	4.7	5.67	5.7	-1.35	-1	-0.38	-0.03	-0.51	-0.83	0.8	-0.23	-0.74	-0.64	2.09
Cthe_01934 Abortive infection protein	10.5	11.16	12.01	11.81	-1.51	-0.65	-0.66	0.2	-0.63	-0.53	-0.13	0.25	-0.74	-0.64	5.22
Cthe_00071 Cellulose 1,4-beta-cellobiosidase	9.55	10.43	11.27	11.14	-1.72	-0.71	-0.88	0.13	-0.8	-0.58	-0.87	0.1	-0.74	-0.64	2.01
Cthe_02847 phage / plasmid primase, P4 family	5.04	4.75	5.86	5	-0.82	-0.25	0.29	0.86	-0.09	-0.19	3.03	1.63	-0.75	-0.65	0.11
Cthe_00185 cell wall hydrolase/autolysin	8.48	9.19	9.89	10.07	-1.41	-0.88	-0.71	-0.18	-0.56	-0.73	-0.3	-0.54	-0.75	-0.65	2.66
Cthe_01275 H <sup>+</sup> -ATPase subunit H	8.48	9.06	9.83	9.84	-1.35	-0.78	-0.58	-0.01	-0.51	-0.64	0.13	-0.19	-0.75	-0.65	6.35
Cthe_00185 cell wall hydrolase/autolysin	8.48	9.19	9.89	10.07	-1.41	-0.88	-0.71	-0.18	-0.56	-0.73	-0.3	-0.54	-0.75	-0.65	2.66
Cthe_01995 hypothetical protein	6.27	7.11	7.92	7.85	-1.65	-0.74	-0.84	0.07	-0.75	-0.61	-0.73	-0.02	-0.76	-0.66	2.36
Cthe_02554 glycosyl transferase, group 1	5.91	6.61	7.29	7.72	-1.38	-1.11	-0.7	-0.43	-0.53	-0.92	-0.27	-1.06	-0.76	-0.66	1.73
Cthe_01805 diguanylate cyclase	9	9.44	10.51	10.3	-1.51	-0.86	-0.44	0.21	-0.63	-0.71	0.6	0.27	-0.76	-0.66	2.58
Cthe_02273 hypothetical protein	7.71	8.4	9.1	9.42	-1.39	-1.02	-0.69	-0.32	-0.54	-0.85	-0.23	-0.83	-0.77	-0.66	2.09
Cthe_00173 dehydrogenase (flavoproteins)	5.04	5.21	6.58	6.41	-1.54	-1.2	-0.17	0.17	-0.66	-1	1.5	0.19	-0.77	-0.66	1.42
Cthe_00432 hypothetical protein	7.91	8.7	9.22	10.44	-1.31	-1.74	-0.79	-1.22	-0.48	-1.46	-0.57	-2.71	-0.76	-0.66	0.99
Cthe_01356 glycosyltransferase	1	1.58	2.32	2.58	-1.32	-1	-0.58	-0.26	-0.48	-0.83	0.13	-0.71	-0.76	-0.66	2.37
Cthe_02175 hypothetical protein	7.77	8.38	9.61	9.04	-1.84	-0.66	-0.61	0.57	-0.9	-0.54	0.03	1.02	-0.76	-0.66	1.84
Cthe_02424 copper amine oxidase-like protein	12.13	12.8	14	13.43	-1.87	-0.63	-0.67	0.57	-0.92	-0.52	-0.17	1.02	-0.77	-0.66	1.82
Cthe_00434 ATPase	4.46	5.75	6.82	6.43	-2.36	-0.68	-1.29	0.39	-1.31	-0.56	-2.23	0.65	-0.77	-0.66	1.1
Cthe_01822 inner-membrane translocator	3	3.58	4.39	4.32	-1.39	-0.74	-0.58	0.07	-0.54	-0.61	0.13	-0.02	-0.78	-0.67	11.06



Cthe_00841 mutants block sporulation after en	5.73	6.41	7.08	7.84	-1.35	-1.43	-0.68	-0.76	-0.51	-1.19	-0.2	-1.75	-0.8	-0.69	1.31
Cthe_00935 malonyl CoA-acyl carrier protein tr	10.72	11.38	12.13	12.31	-1.41	-0.93	-0.66	-0.18	-0.56	-0.77	-0.13	-0.54	-0.8	-0.69	3.06
Cthe_00935 malonyl CoA-acyl carrier protein tr	10.72	11.38	12.13	12.31	-1.41	-0.93	-0.66	-0.18	-0.56	-0.77	-0.13	-0.54	-0.8	-0.69	3.06
Cthe_02666 ATPase, P-type (transporting), HAD	8.09	8.82	10.16	9.43	-2.07	-0.61	-0.73	0.73	-1.08	-0.5	-0.37	1.35	-0.8	-0.69	1.52
Cthe_00935 malonyl CoA-acyl carrier protein tr	10.72	11.38	12.13	12.31	-1.41	-0.93	-0.66	-0.18	-0.56	-0.77	-0.13	-0.54	-0.8	-0.69	3.06
Cthe_01823 Extracellular ligand-binding recepto	3.46	4.81	5.75	5.78	-2.29	-0.97	-1.35	-0.03	-1.25	-0.81	-2.43	-0.23	-0.81	-0.7	1.09
Cthe_03202 CRISPR-associated protein, Csh2 fa	10.69	11.21	11.98	12.52	-1.29	-1.31	-0.52	-0.54	-0.46	-1.09	0.33	-1.29	-0.81	-0.7	1.59
Cthe_01900	2.81	3.32	4.17	4.32	-1.36	-1	-0.51	-0.15	-0.52	-0.83	0.37	-0.48	-0.81	-0.7	2.89
Cthe_00272 Serine-type D-Ala-D-Ala carboxype	9.01	9.78	10.7	10.49	-1.69	-0.71	-0.77	0.21	-0.78	-0.58	-0.5	0.27	-0.81	-0.7	3.05
Cthe_00729 cellulosome enzyme, dockerin type	8.57	9.17	10.37	9.88	-1.8	-0.71	-0.6	0.49	-0.87	-0.58	0.07	0.85	-0.81	-0.7	2.19
Cthe_01823 Extracellular ligand-binding recepto	3.46	4.81	5.75	5.78	-2.29	-0.97	-1.35	-0.03	-1.25	-0.81	-2.43	-0.23	-0.81	-0.7	1.09
Cthe_00272 Serine-type D-Ala-D-Ala carboxype	9.01	9.78	10.7	10.49	-1.69	-0.71	-0.77	0.21	-0.78	-0.58	-0.5	0.27	-0.81	-0.7	3.05
Cthe_00272 Serine-type D-Ala-D-Ala carboxype	9.01	9.78	10.7	10.49	-1.69	-0.71	-0.77	0.21	-0.78	-0.58	-0.5	0.27	-0.81	-0.7	3.05
Cthe_00272 Serine-type D-Ala-D-Ala carboxype	9.01	9.78	10.7	10.49	-1.69	-0.71	-0.77	0.21	-0.78	-0.58	-0.5	0.27	-0.81	-0.7	3.05
Cthe_00807 response regulator receiver modul	8.01	8.7	9.58	9.42	-1.57	-0.72	-0.69	0.16	-0.68	-0.59	-0.23	0.17	-0.82	-0.71	5.62
Cthe_01804 cell wall hydrolase/autolysin	7.69	7.81	9.1	9.21	-1.41	-1.4	-0.12	-0.11	-0.56	-1.17	1.67	-0.4	-0.82	-0.71	1.35
Cthe_00807 response regulator receiver modul	8.01	8.7	9.58	9.42	-1.57	-0.72	-0.69	0.16	-0.68	-0.59	-0.23	0.17	-0.82	-0.71	5.62
Cthe_01401 hypothetical protein	7.66	8.32	9.45	9.01	-1.79	-0.69	-0.66	0.44	-0.86	-0.57	-0.13	0.75	-0.82	-0.71	2.42
Cthe_00415 spore coat protein CotJB			2.58	1	-2.58	-1		1.58	-1.48	-0.83		3.13	-0.82	-0.71	0.97
Cthe_01436 RNA related	3	4	5.13	4.64	-2.13	-0.64	-1	0.49	-1.13	-0.53	-1.27	0.85	-0.82	-0.71	1.46
Cthe_01978 hypothetical protein	5	5.78	7.06	6.41	-2.06	-0.63	-0.78	0.65	-1.07	-0.52	-0.53	1.19	-0.82	-0.71	1.63
Cthe_00807 response regulator receiver modul	8.01	8.7	9.58	9.42	-1.57	-0.72	-0.69	0.16	-0.68	-0.59	-0.23	0.17	-0.82	-0.71	5.62
Cthe_01804 cell wall hydrolase/autolysin	7.69	7.81	9.1	9.21	-1.41	-1.4	-0.12	-0.11	-0.56	-1.17	1.67	-0.4	-0.82	-0.71	1.35
Cthe_00545 prepilin peptidase CpaA	6.17	6.89	7.83	7.61	-1.66	-0.72	-0.72	0.22	-0.75	-0.59	-0.33	0.29	-0.83	-0.72	3.88
Cthe_02127 ATPase associated with various cell	10.77	11.4	12.22	12.13	-1.45	-0.73	-0.63	0.09	-0.59	-0.6	-0.03	0.02	-0.83	-0.72	41.68
Cthe_01632		0	1	2	-1	-2	0	-1	-0.23	-1.68	2.07	-2.25	-0.84	-0.72	0.99
Cthe_01402 iron (metal) dependent repressor,	5.55	6.3	7.5	6.97	-1.95	-0.67	-0.75	0.53	-0.98	-0.55	-0.43	0.94	-0.83	-0.72	1.94
Cthe_00490 CheA signal transduction histidine k	9.11	9.72	10.54	10.51	-1.43	-0.79	-0.61	0.03	-0.57	-0.65	0.03	-0.1	-0.84	-0.72	14.79
Cthe_00490 CheA signal transduction histidine k	9.11	9.72	10.54	10.51	-1.43	-0.79	-0.61	0.03	-0.57	-0.65	0.03	-0.1	-0.84	-0.72	14.79
Cthe_02710 Uncharacterized membrane protei	4.95	5.7	6.48	6.7	-1.53	-1	-0.75	-0.22	-0.65	-0.83	-0.43	-0.63	-0.84	-0.72	2.47
Cthe_01754 periplasmic binding protein	11.7	12.21	13.91	12.97	-2.21	-0.76	-0.51	0.94	-1.19	-0.63	0.37	1.79	-0.83	-0.72	1.32
Cthe_01390 alpha/beta hydrolase fold	7.74	8.66	9.31	10.29	-1.57	-1.63	-0.92	-0.98	-0.68	-1.36	-1	-2.21	-0.84	-0.72	1.12
Cthe_00545 prepilin peptidase CpaA	6.17	6.89	7.83	7.61	-1.66	-0.72	-0.72	0.22	-0.75	-0.59	-0.33	0.29	-0.83	-0.72	3.88
Cthe_01323 GrpE protein	7.68	8.17	9.26	9.02	-1.58	-0.85	-0.49	0.24	-0.69	-0.7	0.43	0.33	-0.83	-0.72	3.24
Cthe_03201 CRISPR-associated protein, Csh1 fa	13.09	13.7	14.49	14.67	-1.4	-0.97	-0.61	-0.18	-0.55	-0.81	0.03	-0.54	-0.83	-0.72	3.23
Cthe_02844 intein	9.29	10.02	11.27	10.69	-1.98	-0.67	-0.73	0.58	-1.01	-0.55	-0.37	1.04	-0.84	-0.72	1.86
Cthe_02565 hypothetical protein	1.58	3.46	4.46	4.75	-2.88	-1.29	-1.88	-0.29	-1.72	-1.08	-4.2	-0.77	-0.84	-0.72	0.85
Cthe_02021 hypothetical protein	5.39	6.3	7.25	7.08	-1.86	-0.78	-0.91	0.17	-0.91	-0.64	-0.97	0.19	-0.84	-0.72	2.01
Cthe_02879 cellulosome enzyme, dockerin type	8.05	8.7	9.52	9.46	-1.47	-0.76	-0.65	0.06	-0.6	-0.63	-0.1	-0.04	-0.84	-0.72	14.42
Cthe_01077 hypothetical protein	5.49	5.75	7.22	6.83	-1.73	-1.08	-0.26	0.39	-0.81	-0.9	1.2	0.65	-0.83	-0.72	1.58
Cthe_01754 periplasmic binding protein	11.7	12.21	13.91	12.97	-2.21	-0.76	-0.51	0.94	-1.19	-0.63	0.37	1.79	-0.83	-0.72	1.32
Cthe_00545 prepilin peptidase CpaA	6.17	6.89	7.83	7.61	-1.66	-0.72	-0.72	0.22	-0.75	-0.59	-0.33	0.29	-0.83	-0.72	3.88
Cthe_00490 CheA signal transduction histidine k	9.11	9.72	10.54	10.51	-1.43	-0.79	-0.61	0.03	-0.57	-0.65	0.03	-0.1	-0.84	-0.72	14.79
Cthe_02126 binding-protein-dependent transpo	5.46	6.15	6.85	7.66	-1.39	-1.51	-0.69	-0.81	-0.54	-1.26	-0.23	-1.85	-0.85	-0.73	1.31
Cthe_00489 response regulator receiver modul	7.47	8.12	8.93	9.03	-1.46	-0.91	-0.65	-0.1	-0.6	-0.75	-0.1	-0.38	-0.85	-0.73	4.36
Cthe_00489 response regulator receiver modul	7.47	8.12	8.93	9.03	-1.46	-0.91	-0.65	-0.1	-0.6	-0.75	-0.1	-0.38	-0.85	-0.73	4.36
Cthe_01537 hypothetical protein	4	4.17	6	5.32	-2	-1.15	-0.17	0.68	-1.02	-0.96	1.5	1.25	-0.85	-0.73	1.28
Cthe_02123 hypothetical protein	4.25	4.7	5.67	5.75	-1.42	-1.05	-0.45	-0.08	-0.56	-0.87	0.57	-0.33	-0.85	-0.73	2.81
Cthe_02126 binding-protein-dependent transpo	5.46	6.15	6.85	7.66	-1.39	-1.51	-0.69	-0.81	-0.54	-1.26	-0.23	-1.85	-0.85	-0.73	1.31
Cthe_00489 response regulator receiver modul	7.47	8.12	8.93	9.03	-1.46	-0.91	-0.65	-0.1	-0.6	-0.75	-0.1	-0.38	-0.85	-0.73	4.36
Cthe_01638 ParB-like nuclease		2	3.46	2.58	-3.46	-0.58	-2	0.88	-2.18	-0.47	-4.6	1.67	-0.86	-0.74	0.81
Cthe_01638 ParB-like nuclease		2	3.46	2.58	-3.46	-0.58	-2	0.88	-2.18	-0.47	-4.6	1.67	-0.86	-0.74	0.81
Cthe_02685 putative TIM-barrel protein, nifR3 f	10.57	11.15	12.42	11.92	-1.85	-0.77	-0.58	0.5	-0.9	-0.64	0.13	0.88	-0.86	-0.74	2.22
Cthe_02423 hypothetical protein	12.06	12.83	14.37	13.45	-2.31	-0.62	-0.77	0.92	-1.27	-0.51	-0.5	1.75	-0.86	-0.74	1.34
Cthe_02034 serine/threonine protein kinase	7.9	8.57	9.89	9.29	-1.99	-0.72	-0.67	0.6	-1.02	-0.59	-0.17	1.08	-0.87	-0.75	1.92
Cthe_02034 serine/threonine protein kinase	7.9	8.57	9.89	9.29	-1.99	-0.72	-0.67	0.6	-1.02	-0.59	-0.17	1.08	-0.87	-0.75	1.92
Cthe_00408 diguanylate cyclase/phosphodieste	8.61	9.01	10.22	10.01	-1.61	-1	-0.4	0.21	-0.71	-0.83	0.73	0.27	-0.87	-0.75	2.51
Cthe_02034 serine/threonine protein kinase	7.9	8.57	9.89	9.29	-1.99	-0.72	-0.67	0.6	-1.02	-0.59	-0.17	1.08	-0.87	-0.75	1.92
Cthe_02244 flagellar hook-associated protein Fl	8.17	9.07	10.1	9.83	-1.93	-0.76	-0.9	0.27	-0.97	-0.63	-0.93	0.4	-0.87	-0.75	2.04
Cthe_00408 diguanylate cyclase/phosphodieste	8.61	9.01	10.22	10.01	-1.61	-1	-0.4	0.21	-0.71	-0.83	0.73	0.27	-0.87	-0.75	2.51
Cthe_02034 serine/threonine protein kinase	7.9	8.57	9.89	9.29	-1.99	-0.72	-0.67	0.6	-1.02	-0.59	-0.17	1.08	-0.87	-0.75	1.92
Cthe_03034 hypothetical protein	7.72	8.26	9.11	9.41	-1.39	-1.15	-0.54	-0.3	-0.54	-0.96	0.27	-0.79	-0.87	-0.75	2.36
Cthe_02507 peptidase U57, YabG	1	0	3	2.58	-2	-2.58	1	0.42	-1.02	-2.17	5.4	0.71	-0.87	-0.75	0.79
Cthe_02097 hypothetical protein	10.68	11.53	12.85	12.18	-2.17	-0.65	-0.85	0.67	-1.16	-0.53	-0.77	1.23	-0.87	-0.75	1.57
Cthe_00422 CoA-binding protein	11.98	12.63	13.42	13.9	-1.44	-1.27	-0.65	-0.48	-0.58	-1.06	-0.1	-1.17	-0.88	-0.76	1.84
Cthe_01013 protein of unknown function UPF0	9.11	9.65	10.55	10.64	-1.44	-0.99	-0.54	-0.09	-0.58	-0.82	0.27	-0.35	-0.88	-0.76	4.06
Cthe_01922 hypothetical protein	6.29	6.81	7.89	7.67	-1.6	-0.86	-0.52	0.22	-0.71	-0.71	0.33	0.29	-0.88	-0.76	4.08
Cthe_01949 hypothetical protein	2.32	2.81	4.91	3.58	-2.59	-0.77	-0.49	1.33	-1.49	-0.64	0.43	2.6	-0.88	-0.76	1.1
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00307 hypothetical protein	11.75	12.33	13.23	13.18	-1.48	-0.85	-0.58	0.05	-0.61	-0.7	0.13	-0.06	-0.89	-0.77	11.58
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.98	-0.8	-0.14	-0.74	-0.81	-0.6	-0.46	-0.89	-0.77	2.59
Cthe_00934 3-oxoacyl-(acyl-carrier-protein) red	11	11.8	12.64	12.78	-1.64	-0.9									



Cthe_03138 hypothetical protein	3.58	4.58	6.11	5.17	-2.53	-0.59	-1	0.94	-1.44	-0.48	-1.27	1.79	-0.9	-0.78	1.23
Cthe_00861 cell envelope-related transcription	10.04	10.58	11.51	11.64	-1.47	-1.06	-0.54	-0.13	-0.6	-0.88	0.27	-0.44	-0.92	-0.79	3.68
Cthe_02553 Radical SAM	5.43	6.34	7.14	7.75	-1.71	-1.41	-0.91	-0.61	-0.79	-1.18	-0.97	-1.44	-0.93	-0.8	1.46
Cthe_03116 mannose-6-phosphate isomerase,	5	5.39	6.51	6.57	-1.51	-1.18	-0.39	-0.06	-0.63	-0.98	0.77	-0.29	-0.93	-0.8	2.53
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_03116 mannose-6-phosphate isomerase,	5	5.39	6.51	6.57	-1.51	-1.18	-0.39	-0.06	-0.63	-0.98	0.77	-0.29	-0.93	-0.8	2.53
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_03116 mannose-6-phosphate isomerase,	5	5.39	6.51	6.57	-1.51	-1.18	-0.39	-0.06	-0.63	-0.98	0.77	-0.29	-0.93	-0.8	2.53
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_03116 mannose-6-phosphate isomerase,	5	5.39	6.51	6.57	-1.51	-1.18	-0.39	-0.06	-0.63	-0.98	0.77	-0.29	-0.93	-0.8	2.53
Cthe_00932 beta-ketoacyl synthase	11.94	12.74	13.68	13.62	-1.74	-0.88	-0.8	0.06	-0.82	-0.73	-0.6	-0.04	-0.93	-0.8	3.26
Cthe_03116 mannose-6-phosphate isomerase,	5	5.39	6.51	6.57	-1.51	-1.18	-0.39	-0.06	-0.63	-0.98	0.77	-0.29	-0.93	-0.8	2.53
Cthe_03116 mannose-6-phosphate isomerase,	5	5.39	6.51	6.57	-1.51	-1.18	-0.39	-0.06	-0.63	-0.98	0.77	-0.29	-0.93	-0.8	2.53
Cthe_03116 mannose-6-phosphate isomerase,	5	5.39	6.51	6.57	-1.51	-1.18	-0.39	-0.06	-0.63	-0.98	0.77	-0.29	-0.93	-0.8	2.53
Cthe_01471 glycoside hydrolase, family 5	8.02	8.63	9.82	9.45	-1.8	-0.82	-0.61	0.37	-0.87	-0.68	0.03	0.6	-0.94	-0.81	3.28
Cthe_02521 DNA-directed RNA polymerase sigm	8.01	8.62	9.42	10.22	-1.41	-1.6	-0.61	-0.8	-0.56	-1.34	0.03	-1.83	-0.94	-0.81	1.42
Cthe_00492 CheC, inhibitor of MCP methylation	6.87	7.49	8.4	8.4	-1.53	-0.91	-0.62	0	-0.65	-0.75	0	-0.17	-0.94	-0.81	10.43
Cthe_00492 CheC, inhibitor of MCP methylation	6.87	7.49	8.4	8.4	-1.53	-0.91	-0.62	0	-0.65	-0.75	0	-0.17	-0.94	-0.81	10.43
Cthe_01281 hypothetical protein	6.88	7.57	8.45	8.54	-1.57	-0.97	-0.69	-0.09	-0.68	-0.81	-0.23	-0.35	-0.94	-0.81	4.51
Cthe_01568 Radical SAM	2	2.32	4.58	3.32	-2.58	-1	-0.32	1.26	-1.48	-0.83	1	2.46	-0.95	-0.82	1.14
Cthe_01212 hypothetical protein	12.24	12.75	14.23	13.64	-1.99	-0.89	-0.51	0.59	-1.02	-0.74	0.37	1.06	-0.95	-0.82	2
Cthe_02574 binding-protein-dependent transpo	1.58	2.32	3.32	3.17	-1.74	-0.85	-0.74	0.15	-0.82	-0.7	-0.4	0.15	-0.96	-0.83	4.51
Cthe_00785 hypothetical protein	12.24	12.85	15	13.59	-2.76	-0.74	-0.61	1.41	-1.63	-0.61	0.03	2.77	-0.96	-0.83	1.12
Cthe_00703 hypothetical protein	8.51	9.24	10.14	10.25	-1.63	-1.01	-0.73	-0.11	-0.73	-0.84	-0.37	-0.4	-0.96	-0.83	3.65
Cthe_02555 methyltransferase FkbM family	6.17	6.25	7.47	8.09	-1.3	-1.84	-0.08	-0.62	-0.47	-1.54	1.8	-1.46	-0.96	-0.83	1.24
Cthe_01759 hypothetical protein	5	5.39	6.3	7.14	-1.3	-1.75	-0.39	-0.84	-0.47	-1.47	0.77	-1.92	-0.96	-0.83	1.33
Cthe_02574 binding-protein-dependent transpo	1.58	2.32	3.32	3.17	-1.74	-0.85	-0.74	0.15	-0.82	-0.7	-0.4	0.15	-0.96	-0.83	4.51
Cthe_00467 Flagellar biosynthesis/type III secre	7.61	8.11	8.92	10.02	-1.31	-1.91	-0.5	-1.1	-0.48	-1.6	0.4	-2.46	-0.97	-0.84	1.2
Cthe_00467 Flagellar biosynthesis/type III secre	7.61	8.11	8.92	10.02	-1.31	-1.91	-0.5	-1.1	-0.48	-1.6	0.4	-2.46	-0.97	-0.84	1.2
Cthe_02308 CheC-like protein	8.07	8.79	9.7	9.85	-1.63	-1.06	-0.72	-0.15	-0.73	-0.88	-0.33	-0.48	-0.98	-0.84	3.51
Cthe_01619 transcriptional regulator, AbrB fam	10.02	10.8	12.94	11.44	-2.92	-0.64	-0.78	1.5	-1.75	-0.53	-0.53	2.96	-0.99	-0.85	1.09
Cthe_01258 copper amine oxidase-like protein	8.32	8.76	10.54	9.73	-2.22	-0.97	-0.44	0.81	-1.2	-0.81	0.6	1.52	-0.99	-0.85	1.58
Cthe_00468 flagellar protein export ATPase FliI	7.61	8.23	9.09	9.87	-1.48	-1.64	-0.62	-0.78	-0.61	-1.37	0	-1.79	-1	-0.86	1.5
Cthe_02552 Radical SAM	4.75	5.93	6.83	7.41	-2.08	-1.48	-1.18	-0.58	-1.09	-1.24	-1.87	-1.37	-1	-0.86	1.27
Cthe_02100 transcriptional regulator, AbrB fam	9.88	10.07	11.78	11.38	-1.9	-1.31	-0.19	0.4	-0.94	-1.09	1.43	0.67	-1	-0.86	1.63
Cthe_00468 flagellar protein export ATPase FliI	7.61	8.23	9.09	9.87	-1.48	-1.64	-0.62	-0.78	-0.61	-1.37	0	-1.79	-1	-0.86	1.5
Cthe_02027 hypothetical protein	3.91	4.64	5.52	6.07	-1.61	-1.43	-0.73	-0.55	-0.71	-1.19	-0.37	-1.31	-1	-0.86	1.82
Cthe_00468 flagellar protein export ATPase FliI	7.61	8.23	9.09	9.87	-1.48	-1.64	-0.62	-0.78	-0.61	-1.37	0	-1.79	-1	-0.86	1.5
Cthe_00468 flagellar protein export ATPase FliI	7.61	8.23	9.09	9.87	-1.48	-1.64	-0.62	-0.78	-0.61	-1.37	0	-1.79	-1	-0.86	1.5
Cthe_02845 hypothetical protein	9.34	10.04	11.78	10.84	-2.44	-0.8	-0.7	0.94	-1.37	-0.66	-0.27	1.79	-1.01	-0.87	1.5
Cthe_01606	1.58	2.81	4	3.81	-2.42	-1	-1.23	0.19	-1.36	-0.83	-2.03	0.23	-1.02	-0.88	1.39
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_01773 peptidase S16, lon-like protein	7.15	7.67	8.67	8.95	-1.52	-1.28	-0.52	-0.28	-0.64	-1.07	0.33	-0.75	-1.02	-0.88	2.72
Cthe_03096 hypothetical protein	11.22	11.82	12.8	12.87	-1.58	-1.05	-0.6	-0.07	-0.69	-0.87	0.07	-0.31	-1.02	-0.88	6.24
Cthe_01544 hypothetical protein	7.26	7.75	8.9	8.8	-1.64	-1.05	-0.49	0.1	-0.74	-0.87	0.43	0.04	-1.02	-0.88	4.72
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0.66	-0.2	-0.71	-0.95	-0.13	-0.58	-1.02	-0.88	3.56
Cthe_00423 iron-containing alcohol dehydrogen	13.96	14.62	15.56	15.76	-1.6	-1.14	-0								



Cthe_00178 argininosuccinate lyase	10.19	10.85	11.92	11.75	-1.73	-0.9	-0.66	0.17	-0.81	-0.75	-0.13	0.19	-1.04	-0.9	8.56
Cthe_00178 argininosuccinate lyase	10.19	10.85	11.92	11.75	-1.73	-0.9	-0.66	0.17	-0.81	-0.75	-0.13	0.19	-1.04	-0.9	8.56
Cthe_00178 argininosuccinate lyase	10.19	10.85	11.92	11.75	-1.73	-0.9	-0.66	0.17	-0.81	-0.75	-0.13	0.19	-1.04	-0.9	8.56
Cthe_00178 argininosuccinate lyase	10.19	10.85	11.92	11.75	-1.73	-0.9	-0.66	0.17	-0.81	-0.75	-0.13	0.19	-1.04	-0.9	8.56
Cthe_02292 hypothetical protein	1	0	3	2.81	-2	-2.81	1	0.19	-1.02	-2.36	5.4	0.23	-1.06	-0.91	0.85
Cthe_02020 hypothetical protein	0		2	1.58	-2	-1.58	0	0.42	-1.02	-1.32	2.07	0.71	-1.06	-0.91	1.36
Cthe_01598 nitroreductase	7.71	8.33	9.53	9.25	-1.82	-0.92	-0.62	0.28	-0.88	-0.76	0	0.42	-1.05	-0.91	4.94
Cthe_00196 glutamine synthetase, catalytic reg	8.92	9.54	10.54	10.74	-1.62	-1.2	-0.62	-0.2	-0.72	-1	0	-0.58	-1.07	-0.92	3.79
Cthe_02649 HpcH/Hpal aldolase	2.58	3.46	5.46	4.17	-2.88	-0.71	-0.88	1.29	-1.72	-0.58	-0.87	2.52	-1.07	-0.92	1.22
Cthe_02950 Pectate lyase/Amb allergen	6.66	7.09	9.23	8.11	-2.57	-1.02	-0.43	1.12	-1.48	-0.85	0.63	2.17	-1.07	-0.92	1.35
Cthe_01590 peptidase M56, BlaR1	8.89	9.52	10.51	10.82	-1.62	-1.3	-0.63	-0.31	-0.72	-1.08	-0.03	-0.81	-1.07	-0.92	2.86
Cthe_01590 peptidase M56, BlaR1	8.89	9.52	10.51	10.82	-1.62	-1.3	-0.63	-0.31	-0.72	-1.08	-0.03	-0.81	-1.07	-0.92	2.86
Cthe_00682 hypothetical protein	6.71	7.64	8.66	8.84	-1.95	-1.2	-0.93	-0.18	-0.98	-1	-1.03	-0.54	-1.07	-0.92	2.15
Cthe_02733 hypothetical protein	3.91	4.09	5.61	5.58	-1.7	-1.49	-0.18	0.03	-0.79	-1.25	1.47	-0.1	-1.07	-0.92	1.79
Cthe_00473 flagellar operon protein	6.23	7.08	8.02	8.47	-1.79	-1.39	-0.85	-0.45	-0.86	-1.16	-0.77	-1.1	-1.07	-0.92	1.92
Cthe_00196 glutamine synthetase, catalytic reg	8.92	9.54	10.54	10.74	-1.62	-1.2	-0.62	-0.2	-0.72	-1	0	-0.58	-1.07	-0.92	3.79
Cthe_00196 glutamine synthetase, catalytic reg	8.92	9.54	10.54	10.74	-1.62	-1.2	-0.62	-0.2	-0.72	-1	0	-0.58	-1.07	-0.92	3.79
Cthe_00196 glutamine synthetase, catalytic reg	8.92	9.54	10.54	10.74	-1.62	-1.2	-0.62	-0.2	-0.72	-1	0	-0.58	-1.07	-0.92	3.79
Cthe_00196 glutamine synthetase, catalytic reg	8.92	9.54	10.54	10.74	-1.62	-1.2	-0.62	-0.2	-0.72	-1	0	-0.58	-1.07	-0.92	3.79
Cthe_00196 glutamine synthetase, catalytic reg	8.92	9.54	10.54	10.74	-1.62	-1.2	-0.62	-0.2	-0.72	-1	0	-0.58	-1.07	-0.92	3.79
Cthe_00196 glutamine synthetase, catalytic reg	8.92	9.54	10.54	10.74	-1.62	-1.2	-0.62	-0.2	-0.72	-1	0	-0.58	-1.07	-0.92	3.79
Cthe_00269 glycoside hydrolase, family 8	12	12.64	14.36	13.55	-2.36	-0.91	-0.64	0.81	-1.31	-0.75	-0.07	1.52	-1.08	-0.93	1.77
Cthe_02678 hypothetical protein	8.55	9.1	10.29	10.1	-1.74	-1	-0.55	0.19	-0.82	-0.83	0.23	0.23	-1.08	-0.93	6.41
Cthe_03098 hypothetical protein	3.81	3.91	5.49	5.55	-1.68	-1.64	-0.1	-0.06	-0.77	-1.37	1.73	-0.29	-1.08	-0.93	1.6
Cthe_00269 glycoside hydrolase, family 8	12	12.64	14.36	13.55	-2.36	-0.91	-0.64	0.81	-1.31	-0.75	-0.07	1.52	-1.08	-0.93	1.77
Cthe_03029 CheW protein	6.58	6.87	8.13	8.42	-1.55	-1.55	-0.29	-0.29	-0.67	-1.3	1.1	-0.77	-1.09	-0.94	1.95
Cthe_03029 CheW protein	6.58	6.87	8.13	8.42	-1.55	-1.55	-0.29	-0.29	-0.67	-1.3	1.1	-0.77	-1.09	-0.94	1.95
Cthe_00386 hypothetical protein	7.08	7.19	8.91	8.73	-1.83	-1.54	-0.11	0.18	-0.89	-1.29	1.7	0.21	-1.09	-0.94	1.63
Cthe_02679 Tetratricopeptide TPR_2	10.17	10.99	12.08	12.01	-1.91	-1.02	-0.82	0.07	-0.95	-0.85	-0.67	-0.02	-1.09	-0.94	3.4
Cthe_01986 phage / plasmid primase, P4 family	2	1.58	2.81	1.58	-0.81	0	0.42	1.23	-0.08	0.02	3.47	2.4	-1.1	-0.95	0.03
Cthe_02557 glycosyl transferase, family 2	7.71	8.45	9.47	9.59	-1.76	-1.14	-0.74	-0.12	-0.83	-0.95	-0.4	-0.42	-1.1	-0.95	3.88
Cthe_00604 hypothetical protein	6.19	6.54	8.67	7.68	-2.48	-1.14	-0.35	0.99	-1.4	-0.95	0.9	1.9	-1.1	-0.95	1.44
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01389 metal dependent phosphohydrolas	7.96	8.72	9.73	9.97	-1.77	-1.25	-0.76	-0.24	-0.84	-1.04	-0.47	-0.67	-1.11	-0.96	2.92
Cthe_01324 heat-inducible transcription repres	9.53	9.8	11.82	11.07	-2.29	-1.27	-0.27	0.75	-1.25	-1.06	1.17	1.4	-1.13	-0.97	1.6
Cthe_01528 two component transcriptional reg	7.81	8.34	10.02	9.38	-2.21	-1.04	-0.53	0.64	-1.19	-0.86	0.3	1.17	-1.13	-0.97	2.17
Cthe_01558 transcriptional regulator, BadM/Rrf	10.08	10.58	11.91	11.67	-1.83	-1.09	-0.5	0.24	-0.89	-0.91	0.4	0.33	-1.13	-0.97	4.38
Cthe_01528 two component transcriptional reg	7.81	8.34	10.02	9.38	-2.21	-1.04	-0.53	0.64	-1.19	-0.86	0.3	1.17	-1.13	-0.97	2.17
Cthe_00075 hypothetical protein	4.17	4.52	5.95	5.81	-1.78	-1.29	-0.35	0.14	-0.85	-1.08	0.9	0.13	-1.12	-0.97	2.7
Cthe_00406 hypothetical protein	8.19	8.87	9.98	9.85	-1.79	-0.98	-0.68	0.13	-0.86	-0.81	-0.2	0.1	-1.12	-0.97	9.43
Cthe_02422 hypothetical protein	11.85	12.46	13.79	13.45	-1.94	-0.99	-0.61	0.34	-0.98	-0.82	0.03	0.54	-1.13	-0.97	4.22
Cthe_01274 nucleoside recognition	8.47	9.17	10.32	10.17	-1.85	-1	-0.7	0.15	-0.9	-0.83	-0.27	0.15	-1.14	-0.98	7.08
Cthe_00268 hypothetical protein	8.04	8.84	10.52	9.74	-2.48	-0.9	-0.8	0.78	-1.4	-0.75	-0.6	1.46	-1.15	-0.99	1.8
Cthe_02184 putative ribonuclease BN	2.32	1.58	4.17	4.25	-1.85	-2.67	0.74	-0.08	-0.9	-2.25	4.53	-0.33	-1.15	-0.99	0.95
Cthe_00595 hypothetical protein	4.75	4.95	6.61	6.44	-1.86	-1.49	-0.2	0.17	-0.91	-1.25	1.4	0.19	-1.15	-0.99	1.95
Cthe_01517 type I phosphodiesterase/nucleotid	8.06	8.67	10.28	9.68	-2.22	-1.01	-0.61	0.6	-1.2	-0.84	0.03	1.08	-1.16	-1	2.42
Cthe_02808 transcriptional regulator, LacI famil	7.79	8.46	10.23	9.43	-2.44	-0.97	-0.67	0.8	-1.37	-0.81	-0.17	1.5	-1.17	-1.01	1.88
Cthe_02962 oligopeptide/dipeptide ABC transp	2.58	3.7	4.91	4.91	-2.33	-1.21	-1.12	0	-1.29	-1.01	-1.67	-0.17	-1.17	-1.01	1.74
Cthe_02962 oligopeptide/dipeptide ABC transp	2.58	3.7	4.91	4.91	-2.33	-1.21	-1.12	0	-1.29	-1.01	-1.67	-0.17	-1.17	-1.01	1.74
Cthe_00301 protein of unknown function DUF1	3.91	3.91	6.04	5.58	-2.13	-1.67	0	0.46	-1.13	-1.4	2.07	0.79	-1.18	-1.02	1.45
Cthe_01620 Protein of unknown function DUF1	10.77	11.49	14.11	12.31	-3.34	-0.82	-0.72	1.8	-2.09	-0.68	-0.33	3.58	-1.19	-1.03	1.09
Cthe_02503 Cupin 2, conserved barrel	4.75	5.43	6.49	6.93	-1.74	-1.5	-0.68	-0.44	-0.82	-1.25	-0.2	-1.08	-1.19	-1.03	2.43
Cthe_03112 glycosidase, PH1107-related	8.24	8.89	9.99	10.06	-1.75	-1.17	-0.65	-0.07	-0.83	-0.97	-0.1	-0.31	-1.19	-1.03	7
Cthe_00358 hypothetical protein	4.64	4.91	6.6	6.34	-1.96	-1.43	-0.27	0.26	-0.99	-1.19	1.17	0.38	-1.2	-1.03	2.25
Cthe_00843 Stage III sporulation AC	2	1.58	3.58	4.09	-1.58	-2.51	0.42	-0.51	-0.69	-2.11	3.47	-1.23	-1.19	-1.03	1.08
Cthe_01624 hypothetical protein	0	1.58	2.81	3.17	-2.81	-1.59	-1.58	-0.36	-1.67	-1.33	-3.2	-0.92	-1.2	-1.03	1.14
Cthe_00543 glycoside hydrolase, family 9	10.5	11.39	12.98	12.35	-2.48	-0.96	-0.89	0.63	-1.4	-0.8	-0.9	1.15	-1.2	-1.03	1.97
Cthe_02174 transcription termination factor Rh	11.38	11.88	13.13	13.13	-1.75	-1.25	-0.5	0	-0.83	-1.04	0.4	-0.17	-1.21	-1.04	5.47
Cthe_01569 O-acetylhomoserine aminocarboxy	4.39	5.32	6.88	6.29	-2.49	-0.97	-0.93	0.59	-1.41	-0.81	-1.03	1.06	-1.21	-1.04	1.96
Cthe_01061 hypothetical protein	5.78	6.04	8.24	7.37	-2.46	-1.33	-0.26	0.87	-1.39	-1.11	1.2	1.65	-1.21	-1.04	1.56
Cthe_01569 O-acetylhomoserine aminocarboxy	4.39	5.32	6.88	6.29	-2.49	-0.97	-0.93	0.59	-1.41	-0.81	-1.03	1.06	-1.21	-1.04	1.96
Cthe_01569 O-acetylhomoserine aminocarboxy	4.39	5.32	6.88	6.29	-2.49	-0.97	-0.93	0.59	-1.41	-0.81	-1.03	1.06	-1.21	-1.04	1.96
Cthe_00862 hypothetical protein	6.63	7.22	8.4	8.34	-1.77	-1.12	-0.59	0.06	-0.84	-0.93	0.1	-0.04	-1.22	-1.05	20.78
Cthe_00883 flagellar protein	7.73	8.46	10.53	9.42	-2.8	-0.96	-0.73	1.11	-1.66	-0.8	-0.37	2.15	-1.23	-1.06	1.51
Cthe_01519 putative RNA methylase	8.3	8.83	10.22	9.99	-1.92	-1.16	-0.53	0.23	-0.96	-0.97	0.3	0.31	-1.24	-1.07	5.65
Cthe_02083 DNA-directed DNA polymerase	6.27	7.11	8.53	8.16	-2.26	-1.05	-0.84	0.37	-1.23	-0.87	-0.73	0.6	-1.24	-1.07	2.85
Cthe_01772 protein of unknown function DUF2	7.23	7.84	8.99	9.2	-1.76	-1.36	-0.61	-0.21	-0.83	-1.14	0.03	-0.6	-1.24	-1.07	



[illegible]



Cthe_02551 Radical SAM	4.7	5.52	6.83	6.91	-2.13	-1.39	-0.82	-0.08	-1.13	-1.16	-0.67	-0.33	-1.41	-1.22	3.87
Cthe_02975 DNA-directed RNA polymerase sigma	5.7	6.41	8.67	7.55	-2.97	-1.14	-0.71	1.12	-1.79	-0.95	-0.3	2.17	-1.41	-1.22	1.65
Cthe_00374 Glutamate dehydrogenase (NADP(+))	11.24	11.71	13.2	13.15	-1.96	-1.44	-0.47	0.05	-0.99	-1.2	0.5	-0.06	-1.41	-1.22	5.52
Cthe_00691 hypothetical protein	6.86	7.58	8.92	8.85	-2.06	-1.27	-0.72	0.07	-1.07	-1.06	-0.33	-0.02	-1.41	-1.22	8.14
Cthe_00558 hypothetical protein	6.11	6.34	8.89	7.86	-2.78	-1.52	-0.23	1.03	-1.64	-1.27	1.3	1.98	-1.41	-1.22	1.56
Cthe_00374 Glutamate dehydrogenase (NADP(+))	11.24	11.71	13.2	13.15	-1.96	-1.44	-0.47	0.05	-0.99	-1.2	0.5	-0.06	-1.41	-1.22	5.52
Cthe_00374 Glutamate dehydrogenase (NADP(+))	11.24	11.71	13.2	13.15	-1.96	-1.44	-0.47	0.05	-0.99	-1.2	0.5	-0.06	-1.41	-1.22	5.52
Cthe_00374 Glutamate dehydrogenase (NADP(+))	11.24	11.71	13.2	13.15	-1.96	-1.44	-0.47	0.05	-0.99	-1.2	0.5	-0.06	-1.41	-1.22	5.52
Cthe_00374 Glutamate dehydrogenase (NADP(+))	11.24	11.71	13.2	13.15	-1.96	-1.44	-0.47	0.05	-0.99	-1.2	0.5	-0.06	-1.41	-1.22	5.52
Cthe_01907 amino acid adenylation domain	7.13	7.74	10.22	8.93	-3.09	-1.19	-0.61	1.29	-1.89	-0.99	0.03	2.52	-1.43	-1.23	1.51
Cthe_02235 protein of unknown function DUF1	7.55	8.07	9.43	9.73	-1.88	-1.66	-0.52	-0.3	-0.93	-1.39	0.33	-0.79	-1.43	-1.23	3.49
Cthe_03100 Diaminopimelate epimerase	4.25	5.36	6.66	7.13	-2.41	-1.77	-1.11	-0.47	-1.35	-1.48	-1.63	-1.15	-1.44	-1.24	1.79
Cthe_01298 ribosomal protein L25	5.64	6.19	7.58	7.58	-1.94	-1.39	-0.55	0	-0.98	-1.16	0.23	-0.17	-1.44	-1.24	9.48
Cthe_02168 Propeptide, PepSY amid peptidase	9.56	10.23	11.82	11.46	-2.26	-1.23	-0.67	0.36	-1.23	-1.03	-0.17	0.58	-1.44	-1.24	4.74
Cthe_01192 hypothetical protein	7.3	7.88	10.16	9.12	-2.86	-1.24	-0.58	1.04	-1.71	-1.03	0.13	2	-1.44	-1.24	1.78
Cthe_03100 Diaminopimelate epimerase	4.25	5.36	6.66	7.13	-2.41	-1.77	-1.11	-0.47	-1.35	-1.48	-1.63	-1.15	-1.44	-1.24	1.79
Cthe_01298 ribosomal protein L25	5.64	6.19	7.58	7.58	-1.94	-1.39	-0.55	0	-0.98	-1.16	0.23	-0.17	-1.44	-1.24	9.48
Cthe_03100 Diaminopimelate epimerase	4.25	5.36	6.66	7.13	-2.41	-1.77	-1.11	-0.47	-1.35	-1.48	-1.63	-1.15	-1.44	-1.24	1.79
Cthe_03100 Diaminopimelate epimerase	4.25	5.36	6.66	7.13	-2.41	-1.77	-1.11	-0.47	-1.35	-1.48	-1.63	-1.15	-1.44	-1.24	1.79
Cthe_03100 Diaminopimelate epimerase	4.25	5.36	6.66	7.13	-2.41	-1.77	-1.11	-0.47	-1.35	-1.48	-1.63	-1.15	-1.44	-1.24	1.79
Cthe_03100 Diaminopimelate epimerase	4.25	5.36	6.66	7.13	-2.41	-1.77	-1.11	-0.47	-1.35	-1.48	-1.63	-1.15	-1.44	-1.24	1.79
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01570 extracellular solute-binding protein	4.75	5.7	7.38	6.92	-2.63	-1.22	-0.95	0.46	-1.52	-1.02	-1.1	0.79	-1.45	-1.25	2.41
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01570 extracellular solute-binding protein	4.75	5.7	7.38	6.92	-2.63	-1.22	-0.95	0.46	-1.52	-1.02	-1.1	0.79	-1.45	-1.25	2.41
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01038 spore protease	6.51	7.39	9	8.63	-2.49	-1.24	-0.88	0.37	-1.41	-1.03	-0.87	0.6	-1.45	-1.25	2.95
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_01869 ornithine carbamoyltransferase	10.61	11.37	12.92	12.61	-2.31	-1.24	-0.76	0.31	-1.27	-1.03	-0.47	0.48	-1.45	-1.25	4.35
Cthe_00485 flagellar biosynthesis protein FlhA	8.14	8.57	10.2	10.05	-2.06	-1.48	-0.43	0.15	-1.07	-1.24	0.63	0.15	-1.46	-1.26	4.52
Cthe_00485 flagellar biosynthesis protein FlhA	8.14	8.57	10.2	10.05	-2.06	-1.48	-0.43	0.15	-1.07	-1.24	0.63	0.15	-1.46	-1.26	4.52
Cthe_00642 hypothetical protein	9.32	10.16	11.87	11.37	-2.55	-1.21	-0.84	0.5	-1.46	-1.01	-0.73	0.88	-1.46	-1.26	2.77
Cthe_03229 transposase, IS4	8.03	8.79	11.41	9.89	-3.38	-1.1	-0.76	1.52	-2.12	-0.92	-0.47	3	-1.46	-1.26	1.36
Cthe_01337 type II secretion system protein	7.84	8.54	9.83	10.38	-1.99	-1.84	-0.7	-0.55	-1.02	-1.54	-0.27	-1.31	-1.47	-1.27	2.47
Cthe_03220 CRISPR-associated protein Cas4	6.71	7.25	8.75	8.61	-2.04	-1.36	-0.54	0.14	-1.06	-1.14	0.27	0.13	-1.47	-1.27	9.28
Cthe_00032 glycoside hydrolase, family 26	9.44	10.09	12.16	11.34	-2.72	-1.25	-0.65	0.82	-1.6	-1.04	-0.1	1.54	-1.48	-1.28	2.21
Cthe_03218 CRISPR-associated protein Cas1	7.91	8.61	9.99	9.96	-2.08	-1.35	-0.7	0.03	-1.09	-1.13	-0.27	-0.1	-1.49	-1.28	9.74
Cthe_00472 flagellar hook capping protein	7.99	8.68	10.01	10.38	-2.02	-1.7	-0.69	-0.37	-1.04	-1.42	-0.23	-0.94	-1.49	-1.28	3.25
Cthe_02620 protein of unknown function DUF1	7.09	7.76	9.12	9.19	-2.03	-1.43	-0.67	-0.07	-1.05	-1.19	-0.17	-0.31	-1.49	-1.28	8.02
Cthe_02761 glycoside hydrolase, family 9	8.41	9.24	10.86	10.51	-2.45	-1.27	-0.83	0.35	-1.38	-1.06	-0.7	0.56	-1.49	-1.28	3.47
Cthe_00470 hypothetical protein	6.67	6.94	8.47	9.13	-1.8	-2.19	-0.27	-0.66	-0.87	-1.84	1.17	-1.54	-1.49	-1.28	1.88
Cthe_01567 Dinitrogenase iron-molybdenum cofactor		1.58	3.32	3	-3.32	-1.42	-1.58	0.32	-2.07	-1.19	-3.2	0.5	-1.48	-1.28	1.32
Cthe_00079 hypothetical protein	5.25	5.95	7.97	7.19	-2.72	-1.24	-0.7	0.78	-1.6	-1.03	-0.27	1.46	-1.49	-1.28	2.29
Cthe_01865 type IV pilus assembly PilZ	8.93	9.56	11.14	10.86	-2.21	-1.3	-0.63	0.28	-1.19	-1.08	-0.03	0.42	-1.49	-1.28	6.82
Cthe_01309 Radical SAM	12.51	13.16	15.17	14.44	-2.66	-1.28	-0.65	0.73	-1.55	-1.07	-0.1	1.35	-1.5	-1.29	2.48
Cthe_02561 CDP-glucose 4,6-dehydratase	6.27	7.29	8.59	9.21	-2.32	-1.92	-1.02	-0.62	-1.28	-1.61	-1.33	-1.46	-1.5	-1.29	1.86
Cthe_02561 CDP-glucose 4,6-dehydratase	6.27	7.29	8.59	9.21	-2.32	-1.92	-1.02	-0.62	-1.28	-1.61	-1.33	-1.46	-1.5	-1.29	1.86
Cthe_03085 response regulator receiver protein	10.03	10.68	12.52	11.97	-2.49	-1.29	-0.65	0.55	-1.41	-1.08	-0.1	0.98	-1.5	-1.29	3.22
Cthe_00480 hypothetical protein	6.74	7.37	8.74	8.92	-2	-1.55	-0.63	-0.18	-1.02	-1.3	-0.03	-0.54	-1.5	-1.29	5.46
Cthe_02561 CDP-glucose 4,6-dehydratase	6.27	7.29	8.59	9.21	-2.32	-1.92	-1.02	-0.62	-1.28	-1.61	-1.33	-1.46	-1.5	-1.29	1.86
Cthe_02561 CDP-glucose 4,6-dehydratase	6.27	7.29	8.59	9.21	-2.32	-1.92	-1.02	-0.62	-1.28	-1.61	-1.33	-1.46	-1.5	-1.29	1.86
Cthe_02963 oligopeptide/dipeptide ABC transp	2	2.32	4.09	4	-2.09	-1.68	-0.32	0.09	-1.1	-1.41	1	0.02	-1.51	-1.3	3.19
Cthe_02963 oligopeptide/dipeptide ABC transp	2	2.32	4.09	4	-2.09	-1.68	-0.32	0.09	-1.1	-1.41	1	0.02	-1.51	-1.3	3.19
Cthe_02963 oligopeptide/dipeptide ABC transp	2	2.32	4.09	4	-2.09	-1.68	-0.32	0.09	-1.1	-1.41	1	0.02	-1.51	-1.3	3.19
Cthe_01628 phage major capsid protein, HK97 family		0	2.32	2	-2.32	-2	0	0.32	-1.28	-1.68	2.07	0.5	-1.52	-1.31	1.77
Cthe_01046 extracellular solute-binding protein	6.29	7.14	8.59	8.58	-2.3	-1.44	-0.85	0.01	-1.26	-1.2	-0.77	-0.15	-1.52	-1.31	3.96
Cthe_01981 hypothetical protein	4.91	5.43	7.19	6.83	-2.28	-1.4	-0.52	0.36	-1.25	-1.17	0.33	0.58	-1.53	-1.32	4.58
Cthe_02556 Radical SAM	7.01	7.58	9.01	9.35	-2	-1.77	-0.57	-0.34	-1.02	-1.48	0.17	-0.88	-1.55	-1.34	3.58
Cthe_02560 dTDP-4-dehydrorhamnose 3,5-epim	6.81	7.64	9.22	8.99	-2.41	-1.35	-0.83	0.23	-1.35	-1.13	-0.7	0.31	-1.55	-1.34	4.11
Cthe_00956 hypothetical protein	7.31	8.3	10.13	9.61	-2.82	-1.31	-0.99	0.52	-1.67	-1.09	-1.23	0.92	-1.56	-1.34	2.32
Cthe_02071 hypothetical protein	7.81	8.2	10.12	9.76	-2.31	-1.56	-0.39	0.36	-1.27	-1.31	0.77	0.58	-1.55	-1.34	3.38
Cthe_02560 dTDP-4-dehydrorhamnose 3,5-epim	6.81	7.64	9.22	8.99	-2.41	-1.35	-0.83	0.23	-1.35	-1.13	-0.7	0.31	-1.55	-1.34	4.11
Cthe_02560 dTDP-4-dehydrorhamnose 3,5-epim	6.81	7.64	9.22	8.99	-2.41	-1.35	-0.83	0.23	-1.35	-1.13	-0.7	0.31	-1.55	-1.34	4.11
Cthe_02200 hypothetical protein		1	2.81	2.32	-2.81	-1.32	-1	0.49	-1.67	-1.1	-1.27	0.85	-1.57	-1.35	2.34
Cthe_00483 type III secretion system inner mem	7.3	8.07	9.62	9.46	-2.32	-1.39	-0.77	0.16	-1.28	-1.16	-0.5	0.17	-1.58	-1.36	5.84
Cthe_01924	4.32	5.13	6.49	7.15	-2.17	-2.02	-0.81	-0.66	-1.16	-1.69	-0.63	-1.54	-1.58	-1.36	2.2
Cthe_00483 type III secretion system inner mem	7.3	8.07	9.62	9.46	-2.32	-1.39	-0.77	0.16	-1.28	-1.16	-0.5	0.17	-1.58	-1.36	5.84
Cthe_00302 hypothetical protein	4.7	5.39	6.85	6.81	-2.15	-1.42	-0.69	0.04	-1.14	-1.19	-0.23	-0.08	-1.58	-1.36	12.08
Cthe_01526 ABC transporter related protein	5.25	5.88	7.55	7.26	-2.3	-1.38	-0.63	0.29	-1.26	-1.15	-0.03	0.44	-1.58	-1.36	6.91
Cthe_01334 FHA domain containing protein	8.86	9.37	10.91	11	-2.05	-1.63	-0.51	-0.09	-1.06	-1.36	0.37	-0.35	-1.58	-1.36	6.05
Cthe_01526 ABC transporter related protein	5.25	5.88	7.55	7.26	-2.3	-1.38	-0.63	0.29	-1.26	-1.15	-0.03	0.44	-1.58	-1.36	6.91
Cthe_01870 GCN5-related N-acetyltransferase	9.01	9.69	11.42	11.05	-2.41	-1.36	-0.68	0.37	-1.35	-1.14	-0.2	0.6	-1.59	-1.3	



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Cthe_01629 peptidase S14, ClpP	0	1	2.81	2.58	-2.81	-1.58	-1	0.23	-1.67	-1.32	-1.27	0.31	-1.76	-1.52	2.91
Cthe_01629 peptidase S14, ClpP	0	1	2.81	2.58	-2.81	-1.58	-1	0.23	-1.67	-1.32	-1.27	0.31	-1.76	-1.52	2.91
Cthe_02832 transposase, mutator type		0	3.58	2	-3.58	-2	0	1.58	-2.28	-1.68	2.07	3.13	-1.78	-1.53	1.35
Cthe_01572 ABC transporter related protein	8.14	9.14	10.98	10.72	-2.84	-1.58	-1	0.26	-1.69	-1.32	-1.27	0.38	-1.77	-1.53	2.89
Cthe_01572 ABC transporter related protein	8.14	9.14	10.98	10.72	-2.84	-1.58	-1	0.26	-1.69	-1.32	-1.27	0.38	-1.77	-1.53	2.89
Cthe_01538 transcriptional regulator, XRE famil	6.58	7.33	9.52	8.83	-2.94	-1.5	-0.75	0.69	-1.77	-1.25	-0.43	1.27	-1.79	-1.54	2.89
Cthe_01545 hypothetical protein	5.88	6.41	8.09	8.32	-2.21	-1.91	-0.53	-0.23	-1.19	-1.6	0.3	-0.65	-1.79	-1.54	4.97
Cthe_02732 hypothetical protein	9.23	9.74	11.88	11.38	-2.65	-1.64	-0.51	0.5	-1.54	-1.37	0.37	0.88	-1.79	-1.54	3.86
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_01591 hypothetical protein	4.64	5.29	6.82	7.83	-2.18	-2.54	-0.65	-1.01	-1.17	-2.14	-0.1	-2.27	-1.8	-1.55	1.92
Cthe_00669 spore germination B3 GerAC like	3	3	5.43	5.32	-2.43	-2.32	0	0.11	-1.37	-1.95	2.07	0.06	-1.8	-1.55	2.05
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_01867 carbamoyl-phosphate synthase, sm	9.01	9.89	11.77	11.44	-2.76	-1.55	-0.88	0.33	-1.63	-1.3	-0.87	0.52	-1.8	-1.55	3.67
Cthe_03081 transglutaminase-like protein	7.73	8.26	10.05	9.93	-2.32	-1.67	-0.53	0.12	-1.28	-1.4	0.3	0.08	-1.81	-1.56	10.91
Cthe_00898 metal dependent phosphohydrolas	6.82	7.4	9.24	9.01	-2.42	-1.61	-0.58	0.23	-1.36	-1.35	0.13	0.31	-1.82	-1.57	10.18
Cthe_02233 protein of unknown function DUF1	7.68	8.34	9.98	10.17	-2.3	-1.83	-0.66	-0.19	-1.26	-1.53	-0.13	-0.56	-1.82	-1.57	6.16
Cthe_03079 cellulosome anchoring protein, coh	11.35	12.15	14	13.72	-2.65	-1.57	-0.8	0.28	-1.54	-1.31	-0.6	0.42	-1.82	-1.57	4.93
Cthe_01566 Nitrogenase	3.32	4.25	6.15	5.88	-2.83	-1.63	-0.93	0.27	-1.68	-1.36	-1.03	0.4	-1.85	-1.59	3.49
Cthe_01566 Nitrogenase	3.32	4.25	6.15	5.88	-2.83	-1.63	-0.93	0.27	-1.68	-1.36	-1.03	0.4	-1.85	-1.59	3.49
Cthe_01566 Nitrogenase	3.32	4.25	6.15	5.88	-2.83	-1.63	-0.93	0.27	-1.68	-1.36	-1.03	0.4	-1.85	-1.59	3.49
Cthe_01566 Nitrogenase	3.32	4.25	6.15	5.88	-2.83	-1.63	-0.93	0.27	-1.68	-1.36	-1.03	0.4	-1.85	-1.59	3.49
Cthe_01310 Accessory gene regulator B	10.73	11.28	13.72	12.93	-2.99	-1.65	-0.55	0.79	-1.81	-1.38	0.23	1.48	-1.86	-1.6	2.71
Cthe_00401 methyl-accepting chemotaxis senso	9.34	9.87	12.82	11.5	-3.48	-1.63	-0.53	1.32	-2.2	-1.36	0.3	2.58	-1.86	-1.6	1.78
Cthe_00401 methyl-accepting chemotaxis senso	9.34	9.87	12.82	11.5	-3.48	-1.63	-0.53	1.32	-2.2	-1.36	0.3	2.58	-1.86	-1.6	1.78
Cthe_01310 Accessory gene regulator B	10.73	11.28	13.72	12.93	-2.99	-1.65	-0.55	0.79	-1.81	-1.38	0.23	1.48	-1.86	-1.6	2.71
Cthe_01310 Accessory gene regulator B	10.73	11.28	13.72	12.93	-2.99	-1.65	-0.55	0.79	-1.81	-1.38	0.23	1.48	-1.86	-1.6	2.71
Cthe_00641 Coat F	9.2	10.05	12.24	11.59	-3.04	-1.54	-0.85	0.65	-1.85	-1.29	-0.77	1.19	-1.86	-1.6	2.84
Cthe_01336 hypothetical protein	9.76	10.27	12.13	12.02	-2.37	-1.75	-0.51	0.11	-1.32	-1.47	0.37	0.06	-1.87	-1.61	9.41
Cthe_02232 polysaccharide biosynthesis protei	6.07	6.98	8.6	9.17	-2.53	-2.19	-0.91	-0.57	-1.44	-1.84	-0.97	-1.35	-1.87	-1.61	2.51
Cthe_02232 polysaccharide biosynthesis protei	6.07	6.98	8.6	9.17	-2.53	-2.19	-0.91	-0.57	-1.44	-1.84	-0.97	-1.35	-1.87	-1.61	2.51
Cthe_01557 ABC transporter related protein	5.7	6.81	8.96	8.39	-3.26	-1.58	-1.11	0.57	-2.02	-1.32	-1.63	1.02	-1.87	-1.61	2.24
Cthe_03121 hypothetical protein	3.32	4.09	6.38	5.64	-3.06	-1.55	-0.77	0.74	-1.87	-1.3	-0.5	1.38	-1.87	-1.61	2.77
Cthe_02062 GerA spore germination protein	6.29	7.34	9.15	9.12	-2.86	-1.78	-1.05	0.03	-1.71	-1.49	-1.43	-0.1	-1.87	-1.61	2.83
Cthe_01525 protein of unknown function DUF2	6.67	7.38	9.27	8.99	-2.6	-1.61	-0.71	0.28	-1.5	-1.35	-0.3	0.42	-1.87	-1.61	6.98
Cthe_01557 ABC transporter related protein	5.7	6.81	8.96	8.39	-3.26	-1.58	-1.11	0.57	-2.02	-1.32	-1.63	1.02	-1.87	-1.61	2.24
Cthe_02621 protein of unknown function DUF1	7.75	8.08	10.09	10.14	-2.34	-2.06	-0.33	-0.05	-1.29	-1.73	0.97	-0.27	-1.88	-1.62	3.83
Cthe_01573 nitrogenase iron protein	7.76	8.31	10.13	10.07	-2.37	-1.76	-0.55	0.06	-1.32	-1.47	0.23	-0.04	-1.91	-1.65	15.11
Cthe_01778 copper amine oxidase-like protein	10.39	10.88	12.77	12.72	-2.38	-1.84	-0.49	0.05	-1.33	-1.54	0.43	-0.06	-1.91	-1.65	8.37
Cthe_03080 cellulosome anchoring protein, coh	11.36	12.07	14.17	13.69	-2.81	-1.62	-0.71	0.48	-1.67	-1.36	-0.3	0.83	-1.91	-1.65	4.36
Cthe_01573 nitrogenase iron protein	7.76	8.31	10.13	10.07	-2.37	-1.76	-0.55	0.06	-1.32	-1.47	0.23	-0.04	-1.91	-1.65	15.11
Cthe_01573 nitrogenase iron protein	7.76	8.31	10.13	10.07	-2.37	-1.76	-0.55	0.06	-1.32	-1.47	0.23	-0.04	-1.91	-1.65	15.11
Cthe_01573 nitrogenase iron protein	7.76	8.31	10.13	10.07	-2.37	-1.76	-0.55	0.06	-1.32	-1.47	0.23	-0.04	-1.91	-1.65	15.11
Cthe_00267 type 3a, cellulose-binding	8.23	8.93	11.57	10.54	-3.34	-1.61	-0.7	1.03	-2.09	-1.35	-0.27	1.98	-1.93	-1.66	2.22
Cthe_01593 NUDIX hydrolase	7.67	8.54	10.25	10.57	-2.58	-2.03	-0.87	-0.32	-1.48	-1.7	-0.83	-0.83	-1.93	-1.66	3.43
Cthe_02063 spore germination protein	4.25	5.13	6.85	7.08	-2.6	-1.95	-0.88	-0.23	-1.5	-1.64	-0.87	-0.65	-1.92	-1.66	3.65
Cthe_00486 GTP-binding signal recognition part	7.73	8.41	10.18	10.15	-2.45	-1.74	-0.68	0.03	-1.38	-1.46	-0.2	-0.1	-1.95	-1.68	16.04
Cthe_00416 hypothetical protein			2	2.32	-2	-2.32		-0.32	-1.02	-1.95		-0.83	-1.97	-1.7	4.73
Cthe_01901 transposase, mutator type	0	1	2.81	3	-2.81	-2	-1	-0.19	-1.67	-1.68	-1.27	-0.56	-1.98	-1.71	3.05
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52						



Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98	-1.71	7.92
Cthe_03084 putative RNA methylase	8.47	9.23	11.1	10.98	-2.63	-1.75	-0.76	0.12	-1.52	-1.47	-0.47	0.08	-1.98		



Cthe_00755 aminotransferase, class I and II	9.38	9.77	11.96	12.2	-2.58	-2.43	-0.39	-0.24	-1.48	-2.04	0.77	-0.67	-2.23	-1.92	4.41
Cthe_00755 aminotransferase, class I and II	9.38	9.77	11.96	12.2	-2.58	-2.43	-0.39	-0.24	-1.48	-2.04	0.77	-0.67	-2.23	-1.92	4.41
Cthe_00755 aminotransferase, class I and II	9.38	9.77	11.96	12.2	-2.58	-2.43	-0.39	-0.24	-1.48	-2.04	0.77	-0.67	-2.23	-1.92	4.41
Cthe_00755 aminotransferase, class I and II	9.38	9.77	11.96	12.2	-2.58	-2.43	-0.39	-0.24	-1.48	-2.04	0.77	-0.67	-2.23	-1.92	4.41
Cthe_00755 aminotransferase, class I and II	9.38	9.77	11.96	12.2	-2.58	-2.43	-0.39	-0.24	-1.48	-2.04	0.77	-0.67	-2.23	-1.92	4.41
Cthe_02949 Pectinesterase	3.7	4.75	7.32	6.61	-3.62	-1.86	-1.05	0.71	-2.31	-1.56	-1.43	1.31	-2.24	-1.93	2.57
Cthe_02237 flagellin-like protein	11.07	11.79	13.8	13.89	-2.73	-2.1	-0.72	-0.09	-1.6	-1.76	-0.33	-0.35	-2.24	-1.93	8.83
Cthe_01523 glycosyl transferase, group 1	7.92	8.59	10.98	10.51	-3.06	-1.92	-0.67	0.47	-1.87	-1.61	-0.17	0.81	-2.24	-1.93	5.32
Cthe_01523 glycosyl transferase, group 1	7.92	8.59	10.98	10.51	-3.06	-1.92	-0.67	0.47	-1.87	-1.61	-0.17	0.81	-2.24	-1.93	5.32
Cthe_00745 glycoside hydrolase, family 9	8.85	9.45	12.22	11.4	-3.37	-1.95	-0.6	0.82	-2.11	-1.64	0.07	1.54	-2.24	-1.93	3.1
Cthe_01595 hypothetical protein	6.3	7.01	9.01	9.09	-2.71	-2.08	-0.71	-0.08	-1.59	-1.75	-0.3	-0.33	-2.24	-1.93	9.47
Cthe_02949 Pectinesterase	3.7	4.75	7.32	6.61	-3.62	-1.86	-1.05	0.71	-2.31	-1.56	-1.43	1.31	-2.24	-1.93	2.57
Cthe_02949 Pectinesterase	3.7	4.75	7.32	6.61	-3.62	-1.86	-1.05	0.71	-2.31	-1.56	-1.43	1.31	-2.24	-1.93	2.57
Cthe_02949 Pectinesterase	3.7	4.75	7.32	6.61	-3.62	-1.86	-1.05	0.71	-2.31	-1.56	-1.43	1.31	-2.24	-1.93	2.57
Cthe_00191 proteinase inhibitor I4, serpin	7.55	7.92	10.43	10.11	-2.88	-2.19	-0.37	0.32	-1.72	-1.84	0.83	0.5	-2.25	-1.94	4.64
Cthe_03101 aminotransferase, class I and II	6.21	6.57	8.73	9.28	-2.52	-2.71	-0.36	-0.55	-1.44	-2.28	0.87	-1.31	-2.26	-1.95	3.06
Cthe_03101 aminotransferase, class I and II	6.21	6.57	8.73	9.28	-2.52	-2.71	-0.36	-0.55	-1.44	-2.28	0.87	-1.31	-2.26	-1.95	3.06
Cthe_03101 aminotransferase, class I and II	6.21	6.57	8.73	9.28	-2.52	-2.71	-0.36	-0.55	-1.44	-2.28	0.87	-1.31	-2.26	-1.95	3.06
Cthe_00488 type IV pilus assembly PilZ	4.17	4.95	7.11	6.95	-2.94	-2	-0.78	0.16	-1.77	-1.68	-0.53	0.17	-2.28	-1.97	7.83
Cthe_01542 glutamyl-tRNA(Gln) amidotransfera	6.49	7.49	9.54	9.85	-3.05	-2.36	-1	-0.31	-1.86	-1.98	-1.27	-0.81	-2.29	-1.97	3.22
Cthe_01806 cellulosome enzyme, dockerin type	7.93	8.67	10.78	10.69	-2.85	-2.02	-0.74	0.09	-1.7	-1.69	-0.4	0.02	-2.28	-1.97	10.69
Cthe_02760 glycoside hydrolase, family 9	7.88	8.68	11.32	10.6	-3.44	-1.92	-0.8	0.72	-2.17	-1.61	-0.6	1.33	-2.29	-1.97	3.31
Cthe_01542 glutamyl-tRNA(Gln) amidotransfera	6.49	7.49	9.54	9.85	-3.05	-2.36	-1	-0.31	-1.86	-1.98	-1.27	-0.81	-2.29	-1.97	3.22
Cthe_01542 glutamyl-tRNA(Gln) amidotransfera	6.49	7.49	9.54	9.85	-3.05	-2.36	-1	-0.31	-1.86	-1.98	-1.27	-0.81	-2.29	-1.97	3.22
Cthe_01542 glutamyl-tRNA(Gln) amidotransfera	6.49	7.49	9.54	9.85	-3.05	-2.36	-1	-0.31	-1.86	-1.98	-1.27	-0.81	-2.29	-1.97	3.22
Cthe_01542 glutamyl-tRNA(Gln) amidotransfera	6.49	7.49	9.54	9.85	-3.05	-2.36	-1	-0.31	-1.86	-1.98	-1.27	-0.81	-2.29	-1.97	3.22
Cthe_02558 NAD-dependent epimerase/dehydr	4.86	5.49	7.55	7.72	-2.69	-2.23	-0.63	-0.17	-1.57	-1.87	-0.03	-0.52	-2.3	-1.98	8.37
Cthe_01562 protein of unknown function DUF2	5.7	6.36	9	8.34	-3.3	-1.98	-0.66	0.66	-2.06	-1.66	-0.13	1.21	-2.3	-1.98	3.88
Cthe_02558 NAD-dependent epimerase/dehydr	4.86	5.49	7.55	7.72	-2.69	-2.23	-0.63	-0.17	-1.57	-1.87	-0.03	-0.52	-2.3	-1.98	8.37
Cthe_01562 protein of unknown function DUF2	5.7	6.36	9	8.34	-3.3	-1.98	-0.66	0.66	-2.06	-1.66	-0.13	1.21	-2.3	-1.98	3.88
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_00801 transposase, mutator type	6.71	7	10.38	9.23	-3.67	-2.23	-0.29	1.15	-2.35	-1.87	1.1	2.23	-2.31	-1.99	2.16
Cthe_01594 hypothetical protein	6	6.52	8.66	8.8	-2.66	-2.28	-0.52	-0.14	-1.55	-1.92	0.33	-0.46	-2.31	-1.99	7.78
Cthe_01021 stage IV sporulation protein A	7	7.7	9.76	9.88	-2.76	-2.18	-0.7	-0.12	-1.63	-1.83	-0.27	-0.42	-2.31	-1.99	8.76
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_01864 acetylglutamate kinase	7.38	7.92	10.06	10.15	-2.68	-2.23	-0.54	-0.09	-1.56	-1.87	0.27	-0.35	-2.31	-1.99	9.84
Cthe_02671 transposase, mutator type	2.58	3.46	6.54	5.36	-3.96	-1.9	-0.88	1.18	-2.58	-1.59	-0.87	2.29	-2.34	-2.02	2.21
Cthe_01585 signal transduction histidine kinase	8.49	8.86	11.46	11.13	-2.97	-2.27	-0.37	0.33	-1.79	-1.91	0.83	0.52	-2.34	-2.02	4.77
Cthe_00535 hypothetical protein	9.61	10.26	13.19	12.26	-3.58	-2	-0.65	0.93	-2.28	-1.68	-0.1	1.77	-2.34	-2.02	2.85
Cthe_03077 cellulosome anchoring protein, coh	13.14	13.95	16.17	16.01	-3.03	-2.06	-0.81	0.16	-1.84	-1.73	-0.63	0.17	-2.34	-2.02	6.91
Cthe_01540 glutamyl-tRNA(Gln) amidotransfera	7.77	8.91	11.09	11.37	-3.32	-2.46	-1.14	-0.28	-2.07	-2.07	-1.73	-0.75	-2.4	-2.07	2.77
Cthe_01540 glutamyl-tRNA(Gln) amidotransfera	7.77	8.91	11.09	11.37	-3.32	-2.46	-1.14	-0.28	-2.07	-2.07	-1.73	-0.75	-2.4	-2.07	2.77
Cthe_01540 glutamyl-tRNA(Gln) amidotransfera	7.77	8.91	11.09	11.37	-3.32	-2.46	-1.14	-0.28	-2.07	-2.07	-1.73	-0.75	-2.4	-2.07	2.77
Cthe_01540 glutamyl-tRNA(Gln) amidotransfera	7.77	8.91	11.09	11.37	-3.32	-2.46	-1.14	-0.28	-2.07	-2.07	-1.73	-0.75	-2.4	-2.07	2.77
Cthe_01540 glutamyl-tRNA(Gln) amidotransfera	7.77	8.91	11.09	11.37	-3.32	-2.46	-1.14	-0.28	-2.07	-2.07	-1.73	-0.75	-2.4	-2.07	2.77
Cthe_02131 hypothetical protein	7.42	7.81	10.39	10.13	-2.97	-2.32	-0.39	0.26	-1.79	-1.95	0.77	0.38	-2.41	-2.08	5.5
Cthe_01080 carbohydrate binding family 25	3.81	4.17	7.38	6.44	-3.57	-2.27	-0.36	0.94	-2.27	-1.91	0.87	1.79	-2.41	-2.08	2.66
Cthe_01398 cellulosome enzyme, dockerin type	9.58	10.36	13.29	12.37	-3.71	-2.01	-0.78	0.92	-2.38	-1.69	-0.53	1.75	-2.41	-2.08	2.85
Cthe_02964 binding-protein-dependent transpo	1	1	3.58	4.32	-2.58	-3.32	0	-0.74	-1.48	-2.8	2.07	-1.71	-2.42	-2.09	2.11
Cthe_01541 glutamyl-tRNA(Gln) amidotransfera	7.87	8.99	11.24	11.39	-3.37	-2.4	-1.12	-0.15	-2.11	-2.02	-1.67	-0.48	-2.43	-2.09	3
Cthe_02964 binding-protein-dependent transpo	1	1	3.58	4.32	-2.58	-3.32	0	-0.74	-1.48	-2.8	2.07	-1.71	-2.42	-2.09	2.11
Cthe_01563 ABC transporter related protein	4.32	5.91	8.49	8.18	-4.17	-2.27	-1.59	0.31	-2.75	-1.91	-3.23	0.48	-2.43	-2.09	1.83
Cthe_02416 Propeptide, PepSY amd peptidase	5.86	6.64	8.79	9.02	-2.93	-2.38	-0.78	-0.23	-1.76	-2	-0.53	-0.65	-2.43	-2.09	5.67
Cthe_01563 ABC transporter related protein	4.32	5.91	8.49	8.18	-4.17	-2.27	-1.59	0.31	-2.75	-1.91	-3.23	0.48	-2.43	-2.09	1.83
Cthe_02964 binding-protein-dependent transpo	1	1	3.58	4.32	-2.58	-3.32	0	-0.74	-1.48	-2.8	2.07	-1.71	-2.42	-2.09	2.11
Cthe_01541 glutamyl-tRNA(Gln) amidotransfera	7.87	8.99	11.24	11.39	-3.37	-2.4	-1.12	-0.15	-2.11	-2.02	-1.67	-0.48	-2.43	-2.09	3
Cthe_01541 glutamyl-tRNA(Gln) amidotransfera	7.87	8.99	11.24	11.39	-3.37	-2.4	-1.12	-0.15	-2.11	-2.02	-1.67	-0.48	-2.43	-2.09	3
Cthe_01541 glutamyl-tRNA(Gln) amidotransfera	7.87	8.99	11.24	11.39	-3.37	-2.4	-1.12	-0.15	-2.11	-2.02	-1.67	-0.48	-2.43	-2.09	3
Cthe_01541 glutamyl-tRNA(Gln) amidotransfera	7.87	8.99	11.24	11.39	-3.37	-2.4	-1.12	-0.15	-2.11	-2.02	-1.67	-0.48	-2.43	-2.09	3
Cthe_01541 glutamyl-tRNA(Gln) amidotransfera	7.87	8.99	11.24	11.39	-3.37	-2.4	-1.12	-0.15	-2.11	-2.02	-1.67	-0.48	-2.43	-2.09	3
Cthe_00557 polysaccharide deacetylase	3	3	5.91	5.93	-2.91	-2.93	0	-0.02	-1.75	-2.47	2.07	-0.21	-2.44	-2.1	2.6
Cthe_00043 glycoside hydrolase, family 9	9.73	10.48	13.1	12.55	-3.37	-2.07	-0.75	0.55	-2.11	-1.74	-0.43	0.98	-2.44	-2.1	4.56
Cthe_02807 glycoside hydrolase, family 5	6.25	6.71	10.34	8.94	-4.09	-2.23	-0.46	1.4	-2.68	-1.87	0.53	2.75	-2.48	-2.14	2.08
Cthe_02807 glycoside hydrolase, family 5	6.25	6.71	10.34	8.94	-4.09	-2.23	-0.46	1.4	-2.68	-1.87	0.53	2.75	-2.48	-2.14	2.08
Cthe_02807 glycoside hydrolase, family 5	6.25	6.71	10.34	8.94	-4.09	-2.23	-0.46	1.4	-2.68	-1.87	0.53	2.75	-2.48	-2.14	2.08
Cthe_00265 aminotransferase, class V	4.52	5	7.65	7.27	-3.13	-2.27	-0.48	0.38	-1.92	-1.91	0.47	0.63	-2.49	-2.15	6.15
Cthe_00478 CheC, inhibitor of MCP methylation	7.97	8.61	10.98	10.78	-3.01	-2.17	-0.64	0.2	-1.83	-1.82	-0.07	0.25	-2.51	-2.16	17.75
Cthe_00478 CheC, inhibitor of MCP methylation	7.97	8.61	10.98	10.78	-3.01	-2.17	-0.64	0.2	-1.83	-1.82	-0.07	0.25	-2.51	-2.16	17.75
Cthe_00478 CheC, inhibitor of MCP methylation	7.97	8.61	10.98	10.78	-3.01	-2.17	-0.64	0.2	-1.83	-1.82	-0.07	0.25	-2.51	-2.16	17.75
Cthe_01534 hypothetical protein	5.17	6.04	8.36	8.3	-3.19	-2.26	-0.87	0.06	-1.97	-1.9	-0.83	-0.04	-2.5	-2.16	5.88
Cthe_01378 response regulator receiver modul	6.82	7.26	9.67	9.79	-2.85	-2.53	-0.44	-0.12	-1.7	-2.13	0.6	-0.42	-2.52	-2.17	6.64
Cthe_03141 lipolytic enzyme, G-D-S-L	3.7	4.64	7.09	6.86	-3.39	-2.22	-0.94	0.23	-2.13	-1.86	-1.07	0.31	-2.52	-2.17	4.53
Cthe_01378 response regulator receiver modul	6.82	7.26	9.67	9.79	-2.85	-2.53	-0.44	-0.12	-1.7	-					



Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_01575 purine nucleoside phosphorylase	5.04	5.93	8.65	8.25	-3.61	-2.32	-0.89	0.4	-2.3	-1.95	-0.9	0.67	-2.7	-2.33	4.8
Cthe_03175 protein of unknown function DUF4	3	4.25	6.93	6.74	-3.93	-2.49	-1.25	0.19	-2.56	-2.09	-2.1	0.23	-2.71	-2.34	2.79
Cthe_01256 glycoside hydrolase, family 3-like p	7.29	7.57	10.54	10.3	-3.25	-2.73	-0.28	0.24	-2.02	-2.3	1.13	0.33	-2.73	-2.35	4.64
Cthe_01256 glycoside hydrolase, family 3-like p	7.29	7.57	10.54	10.3	-3.25	-2.73	-0.28	0.24	-2.02	-2.3	1.13	0.33	-2.73	-2.35	4.64
Cthe_01256 glycoside hydrolase, family 3-like p	7.29	7.57	10.54	10.3	-3.25	-2.73	-0.28	0.24	-2.02	-2.3	1.13	0.33	-2.73	-2.35	4.64
Cthe_01256 glycoside hydrolase, family 3-like p	7.29	7.57	10.54	10.3	-3.25	-2.73	-0.28	0.24	-2.02	-2.3	1.13	0.33	-2.73	-2.35	4.64
Cthe_01256 glycoside hydrolase, family 3-like p	7.29	7.57	10.54	10.3	-3.25	-2.73	-0.28	0.24	-2.02	-2.3	1.13	0.33	-2.73	-2.35	4.64
Cthe_01256 glycoside hydrolase, family 3-like p	7.29	7.57	10.54	10.3	-3.25	-2.73	-0.28	0.24	-2.02	-2.3	1.13	0.33	-2.73	-2.35	4.64
Cthe_02272 hypothetical protein	5.73	6.38	8.8	9.36	-3.07	-2.98	-0.65	-0.56	-1.87	-2.51	-0.1	-1.33	-2.76	-2.38	4.19
Cthe_03199 protein of unknown function UPF0	3.32	3.32	6.48	6.58	-3.16	-3.26	0	-0.1	-1.94	-2.75	2.07	-0.38	-2.78	-2.4	2.86
Cthe_00675 hypothetical protein	4.09	4.91	7.41	7.47	-3.32	-2.56	-0.82	-0.06	-2.07	-2.15	-0.67	-0.29	-2.78	-2.4	7.3
Cthe_00448 RNA polymerase, sigma 28 subunit	6.54	7.13	9.65	9.78	-3.11	-2.65	-0.59	-0.13	-1.9	-2.23	0.1	-0.44	-2.8	-2.41	11.59
Cthe_00736 cellulosome anchoring protein, coh	9.41	10.16	12.71	12.66	-3.3	-2.5	-0.75	0.05	-2.06	-2.1	-0.43	-0.06	-2.82	-2.43	12.1
Cthe_02972 glycoside hydrolase, family 11	11.07	12	15.02	14.39	-3.95	-2.39	-0.93	0.63	-2.57	-2.01	-1.03	1.15	-2.83	-2.44	3.77
Cthe_02988 hypothetical protein	1	2	5.39	4.46	-4.39	-2.46	-1	0.93	-2.92	-2.07	-1.27	1.77	-2.97	-2.56	2.93
Cthe_01561 hypothetical protein	1	2.32	5.25	5.04	-4.25	-2.72	-1.32	0.21	-2.81	-2.29	-2.33	0.27	-2.97	-2.56	2.76
Cthe_00625 glycoside hydrolase, family 9	10.6	11.29	14.38	13.86	-3.78	-2.57	-0.69	0.52	-2.44	-2.16	-0.23	0.92	-2.99	-2.58	6.14
Cthe_00246 Carbohydrate binding family 6	5.52	6.3	9.88	8.83	-4.36	-2.53	-0.78	1.05	-2.9	-2.13	-0.53	2.02	-3.01	-2.59	3.08
Cthe_02590 glycoside hydrolase, family 10	7.66	8.38	11.34	10.97	-3.68	-2.59	-0.72	0.37	-2.36	-2.18	-0.33	0.6	-3.02	-2.6	8.38
Cthe_02659 YabP-like protein	2.58	3	5.78	6.41	-3.2	-3.41	-0.42	-0.63	-1.98	-2.87	0.67	-1.48	-3.03	-2.61	3.83
Cthe_02206 hypothetical protein	5.09	5.46	8.45	8.53	-3.36	-3.07	-0.37	-0.08	-2.1	-2.58	0.83	-0.33	-3.08	-2.66	6.65
Cthe_00433 glycoside hydrolase, family 9	9	9.73	12.77	12.4	-3.77	-2.67	-0.73	0.37	-2.43	-2.25	-0.37	0.6	-3.11	-2.68	8.39
Cthe_01437 hypothetical protein	6.74	7	11.67	9.92	-4.93	-2.92	-0.26	1.75	-3.35	-2.46	1.2	3.48	-3.13	-2.7	2.02
Cthe_02130 hypothetical protein	10.41	10.88	14.43	13.7	-4.02	-2.82	-0.47	0.73	-2.63	-2.37	0.5	1.35	-3.14	-2.71	4.39
Cthe_01547 hypothetical protein	12.33	12.9	16.35	15.66	-4.02	-2.76	-0.57	0.69	-2.63	-2.32	0.17	1.27	-3.15	-2.72	4.89
Cthe_03198 hypothetical protein	1.58	1	5.49	5.09	-3.91	-4.09	0.58	0.4	-2.54	-3.45	4	0.67	-3.15	-2.72	1.89
Cthe_02995 hypothetical protein	3.32	3.91	6.99	6.66	-3.67	-2.75	-0.59	0.33	-2.35	-2.31	0.1	0.52	-3.15	-2.72	11.11
Cthe_00274 glycoside hydrolase, family 9	8.55	9.21	13.13	11.96	-4.58	-2.75	-0.66	1.17	-3.07	-2.31	-0.13	2.27	-3.21	-2.77	3.02
Cthe_00109 cellulosome enzyme, dockerin type	4.52	4.7	8.72	7.86	-4.2	-3.16	-0.18	0.86	-2.77	-2.66	1.47	1.63	-3.23	-2.78	3.12
Cthe_02349 small, acid-soluble spore proteins,	6.49	7.01	10.68	9.88	-4.19	-2.87	-0.52	0.8	-2.76	-2.42	0.33	1.5	-3.24	-2.79	4.27
Cthe_02454 Fibronectin, type III	6.69	6.99	10.47	10.1	-3.78	-3.11	-0.3	0.37	-2.44	-2.62	1.07	0.6	-3.24	-2.79	5.21
Cthe_01257 Carbohydrate-binding, CenC-like pr	7.23	8.06	11.69	10.8	-4.46	-2.74	-0.83	0.89	-2.98	-2.31	-0.7	1.69	-3.26	-2.81	3.68
Cthe_02965 binding-protein-dependent transpo	2	3	6.07	5.95	-4.07	-2.95	-1	0.12	-2.67	-2.48	-1.27	0.08	-3.29	-2.84	5.11
Cthe_00135 beta-ketoacyl synthase	9.23	10.07	13.04	13.05	-3.81	-2.98	-0.84	-0.01	-2.46	-2.51	-0.73	-0.19	-3.3	-2.84	8.32
Cthe_02965 binding-protein-dependent transpo	2	3	6.07	5.95	-4.07	-2.95	-1	0.12	-2.67	-2.48	-1.27	0.08	-3.29	-2.84	5.11
Cthe_02246 anti-sigma-28 factor, FlgM	9	9.54	13.62	12.43	-4.62	-2.89	-0.54	1.19	-3.1	-2.43	0.27	2.31	-3.29	-2.84	3.02
Cthe_00055 hypothetical protein	4.58	5	8.39	8.03	-3.81	-3.03	-0.42	0.36	-2.46	-2.55	0.67	0.58	-3.3	-2.84	7.14
Cthe_02965 binding-protein-dependent transpo	2	3	6.07	5.95	-4.07	-2.95	-1	0.12	-2.67	-2.48	-1.27	0.08	-3.29	-2.84	5.11
Cthe_00534 ABC-type bacteriocin transporter	6.85	7.38	10.51	10.33	-3.66	-2.95	-0.53	0.18	-2.34	-2.48	0.3	0.21	-3.31	-2.85	16.63
Cthe_02165 protein of unknown function DUF1	4.25	5.13	8.32	8.03	-4.07	-2.9	-0.88	0.29	-2.67	-2.44	-0.87	0.44	-3.34	-2.88	6.62
Cthe_02360 glycoside hydrolase, family 9	8.9	9.58	12.89	12.47	-3.99	-2.89	-0.68	0.42	-2.6	-2.43	-0.2	0.71	-3.35	-2.89	8.62
Cthe_02415 cell wall hydrolase, SleB	3.7	4.58	7.52	7.99	-3.82	-3.41	-0.88	-0.47	-2.47	-2.87	-0.87	-1.15	-3.38	-2.91	4.69
Cthe_02415 cell wall hydrolase, SleB	3.7	4.58	7.52	7.99	-3.82	-3.41	-0.88	-0.47	-2.47	-2.87	-0.87	-1.15	-3.38	-2.91	4.69
Cthe_00073 hypothetical protein	7.41	8.16	12.14	11.04	-4.73	-2.88	-0.75	1.1	-3.19	-2.42	-0.43	2.13	-3.4	-2.93	3.29
Cthe_02811 glycoside hydrolase, family 26	8.55	9.55	13.17	12.5	-4.62	-2.95	-1	0.67	-3.1	-2.48	-1.27	1.23	-3.47	-2.99	4.01
Cthe_00072 phage shock protein C, PspC	5.98	6.79	10.57	9.72	-4.59	-2.93	-0.81	0.85	-3.08	-2.47	-0.63	1.6	-3.47	-2.99	4.1
Cthe_00072 phage shock protein C, PspC	5.98	6.79	10.57	9.72	-4.59	-2.93	-0.81	0.85	-3.08	-2.47	-0.63	1.6	-3.47	-2.99	4.1
Cthe_01524 hypothetical protein	6.25	6.94	10.01	10.27	-3.76	-3.33	-0.69	-0.26	-2.42	-2.81	-0.23	-0.71	-3.5	-3.02	8.87
Cthe_00136 4'-phosphopantetheinyl transferas	7.83	8.62	11.75	11.79	-3.92	-3.17	-0.79	-0.04	-2.55	-2.67	-0.57	-0.25	-3.52	-3.03	10.59
Cthe_02389 sigmaK-factor processing regulator	2.81	3.32	6.48	6.92	-3.67	-3.6	-0.51	-0.44	-2.35	-3.03	0.37	-1.08	-3.51	-3.03	6
Cthe_03078 cellulosome anchoring protein, coh	9.92	10.94	14.47	13.94	-4.55	-3	-1.02	0.53	-3.05	-2.53	-1.33	0.94	-3.51	-3.03	4.34
Cthe_00658 hypothetical protein	1.58	3.58	7.22	7.01	-5.64	-3.43	-2	0.21	-3.91	-2.89	-4.6	0.27	-3.57	-3.08	1.88
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_03176 small acid-soluble spore protein, al	7.46	8.11	11.67	11.21	-4.21	-3.1	-0.65	0.46	-2.78	-2.61	-0.1	0.79	-3.59	-3.09	8.55
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_01548 Enoyl-CoA hydratase/isomerase	11.65	12.34	15.88	15.43	-4.23	-3.09	-0.69	0.45	-2.79	-2.6	-0.23	0.77	-3.59	-3.09	8.47
Cthe_0154															



Cthe_01539 glutamine synthetase, catalytic reg	5.64	6.13	9.65	9.43	-4.01	-3.3	-0.49	0.22	-2.62	-2.78	0.43	0.29	-3.67	-3.16	13.15
Cthe_00172 hypothetical protein	2.58	1.58	7.27	6.55	-4.69	-4.97	1	0.72	-3.16	-4.19	5.4	1.33	-3.69	-3.18	1.69
Cthe_01564 GCN5-related N-acetyltransferase	5.46	6.34	10.41	9.46	-4.95	-3.12	-0.88	0.95	-3.37	-2.63	-0.87	1.81	-3.71	-3.2	3.8
Cthe_00664 hypothetical protein	7.43	7.86	11.7	11.23	-4.27	-3.37	-0.43	0.47	-2.83	-2.84	0.63	0.81	-3.72	-3.21	6.98
Cthe_01920 stage II sporulation protein R	5.98	6.51	9.9	9.88	-3.92	-3.37	-0.53	0.02	-2.55	-2.84	0.3	-0.13	-3.73	-3.22	20.85
Cthe_01581 inner-membrane translocator	4.75	5.17	8.99	8.6	-4.24	-3.43	-0.42	0.39	-2.8	-2.89	0.67	0.65	-3.76	-3.24	7.7
Cthe_01581 inner-membrane translocator	4.75	5.17	8.99	8.6	-4.24	-3.43	-0.42	0.39	-2.8	-2.89	0.67	0.65	-3.76	-3.24	7.7
Cthe_01300 hypothetical protein	2	3.17	7.72	6.23	-5.72	-3.06	-1.17	1.49	-3.98	-2.58	-1.83	2.94	-3.77	-3.25	2.45
Cthe_03083 hypothetical protein	4	5	8.55	8.33	-4.55	-3.33	-1	0.22	-3.05	-2.81	-1.27	0.29	-3.78	-3.26	5.68
Cthe_01579 ABC transporter related protein	4.39	5.81	9.52	9.24	-5.13	-3.43	-1.42	0.28	-3.51	-2.89	-2.67	0.42	-3.79	-3.27	3
Cthe_02067 hypothetical protein	6.25	7.11	10.63	10.41	-4.38	-3.3	-0.86	0.22	-2.91	-2.78	-0.8	0.29	-3.79	-3.27	8.45
Cthe_00413 glycoside hydrolase, family 9	9.5	10.24	14.31	13.48	-4.81	-3.24	-0.74	0.83	-3.25	-2.73	-0.4	1.56	-3.79	-3.27	4.71
Cthe_01579 ABC transporter related protein	4.39	5.81	9.52	9.24	-5.13	-3.43	-1.42	0.28	-3.51	-2.89	-2.67	0.42	-3.79	-3.27	3
Cthe_01579 ABC transporter related protein	4.39	5.81	9.52	9.24	-5.13	-3.43	-1.42	0.28	-3.51	-2.89	-2.67	0.42	-3.79	-3.27	3
Cthe_02812 glycoside hydrolase, family 9	8.36	9.13	12.91	12.42	-4.55	-3.29	-0.77	0.49	-3.05	-2.77	-0.5	0.85	-3.84	-3.31	7.46
Cthe_03194 hypothetical protein	4	4.52	9.11	7.92	-5.11	-3.4	-0.52	1.19	-3.49	-2.86	0.33	2.31	-3.86	-3.33	3.45
Cthe_00624 glycoside hydrolase, family 9-like Ig	9.83	10.57	14.45	13.89	-4.62	-3.32	-0.74	0.56	-3.1	-2.8	-0.4	1	-3.88	-3.34	6.93
Cthe_01580 inner-membrane translocator	3.58	4.75	8.46	8.19	-4.88	-3.44	-1.17	0.27	-3.31	-2.9	-1.83	0.4	-3.88	-3.34	4.2
Cthe_01580 inner-membrane translocator	3.58	4.75	8.46	8.19	-4.88	-3.44	-1.17	0.27	-3.31	-2.9	-1.83	0.4	-3.88	-3.34	4.2
Cthe_02948 Allergen V5/Tpx-1 related	7.15	7.74	11.3	11.13	-4.15	-3.39	-0.59	0.17	-2.73	-2.86	0.1	0.19	-3.89	-3.35	32.88
Cthe_00131 hypothetical protein	5.52	5.52	9.61	9.93	-4.09	-4.41	0	-0.32	-2.68	-3.72	2.07	-0.83	-3.96	-3.41	3.67
Cthe_01952 hypothetical protein	3	2	7.18	7.67	-4.18	-5.67	1	-0.49	-2.75	-4.79	5.4	-1.19	-3.97	-3.42	1.78
Cthe_00659 hypothetical protein	3.58	4.17	7.75	7.64	-4.17	-3.47	-0.59	0.11	-2.75	-2.92	0.1	0.06	-3.98	-3.43	61.42
Cthe_02617 peptidase M23B	10.33	10.95	15.07	14.41	-4.74	-3.46	-0.62	0.66	-3.2	-2.92	0	1.21	-3.99	-3.44	6.39
Cthe_02618 stage III sporulation protein D, Spol	1	1	5	5.67	-4	-4.67	0	-0.67	-2.61	-3.94	2.07	-1.56	-4	-3.45	3.26
Cthe_00170 hypothetical protein	3.46	3.81	7.87	7.55	-4.41	-3.74	-0.35	0.32	-2.94	-3.15	0.9	0.5	-4.02	-3.47	7.47
Cthe_00412 glycoside hydrolase, family 9	10.95	11.62	15.83	15.08	-4.88	-3.46	-0.67	0.75	-3.31	-2.92	-0.17	1.4	-4.02	-3.47	5.59
Cthe_01578 Radical SAM	4.39	5.55	9.54	9.1	-5.15	-3.55	-1.16	0.44	-3.52	-2.99	-1.8	0.75	-4.07	-3.51	4.23
Cthe_01578 Radical SAM	4.39	5.55	9.54	9.1	-5.15	-3.55	-1.16	0.44	-3.52	-2.99	-1.8	0.75	-4.07	-3.51	4.23
Cthe_00821 coagulation factor 5/8 type-like pro	7.41	8.14	12.21	11.68	-4.8	-3.54	-0.73	0.53	-3.25	-2.98	-0.37	0.94	-4.13	-3.56	7.79
Cthe_00132 3-oxoacyl-(acyl-carrier-protein) syn	7.91	8.57	12.22	12.59	-4.31	-4.02	-0.66	-0.37	-2.86	-3.39	-0.13	-0.94	-4.17	-3.59	8.35
Cthe_00132 3-oxoacyl-(acyl-carrier-protein) syn	7.91	8.57	12.22	12.59	-4.31	-4.02	-0.66	-0.37	-2.86	-3.39	-0.13	-0.94	-4.17	-3.59	8.35
Cthe_00132 3-oxoacyl-(acyl-carrier-protein) syn	7.91	8.57	12.22	12.59	-4.31	-4.02	-0.66	-0.37	-2.86	-3.39	-0.13	-0.94	-4.17	-3.59	8.35
Cthe_00132 3-oxoacyl-(acyl-carrier-protein) syn	7.91	8.57	12.22	12.59	-4.31	-4.02	-0.66	-0.37	-2.86	-3.39	-0.13	-0.94	-4.17	-3.59	8.35
Cthe_00132 3-oxoacyl-(acyl-carrier-protein) syn	7.91	8.57	12.22	12.59	-4.31	-4.02	-0.66	-0.37	-2.86	-3.39	-0.13	-0.94	-4.17	-3.59	8.35
Cthe_00132 3-oxoacyl-(acyl-carrier-protein) syn	7.91	8.57	12.22	12.59	-4.31	-4.02	-0.66	-0.37	-2.86	-3.39	-0.13	-0.94	-4.17	-3.59	8.35
Cthe_00970 transposase, mutator type	2	2	6.11	6.93	-4.11	-4.93	0	-0.82	-2.7	-4.16	2.07	-1.87	-4.18	-3.6	3.17
Cthe_02089 glycoside hydrolase, family 48	12.2	12.94	17.21	16.56	-5.01	-3.62	-0.74	0.65	-3.41	-3.05	-0.4	1.19	-4.22	-3.64	6.51
Cthe_03071 protein of unknown function DUF1	3.81	3.81	8.5	8.15	-4.69	-4.34	0	0.35	-3.16	-3.66	2.07	0.56	-4.23	-3.65	4.03
Cthe_02087 metalloenzyme	4.52	5.46	9.19	9.51	-4.67	-4.05	-0.94	-0.32	-3.14	-3.42	-1.07	-0.83	-4.26	-3.67	6.12
Cthe_03140 transcriptional regulator, TetR fami	4.58	4.95	10.52	8.79	-5.94	-3.84	-0.37	1.73	-4.15	-3.24	0.83	3.44	-4.27	-3.68	2.66
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_02088 protein of unknown function DUF7	5.86	6.57	10.31	10.64	-4.45	-4.07	-0.71	-0.33	-2.97	-3.43	-0.3	-0.85	-4.28	-3.69	8.99
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01	-4.38	-3.91	-0.58	-0.11	-2.91	-3.3	0.13	-0.4	-4.28	-3.69	18.68
Cthe_00133 AMP-dependent synthetase and lig	8.52	9.1	12.9	13.01											