

MASCOT Search Results

User : keding
 E-mail : chengkening@yahoo.com
 Search title : flagellin
 MS data file : C:\Xcalibur\data\20120119-001-0023-00866-prp\20120119-007-20120118-18.RAW
 Database : NCBI nr 20120121 (17,072,391 sequences; 5,860,213,228 residues)
 Taxonomy : Mammalia (mammals) (1,041,094 sequences)
 Timestamp : 24 Jan 2012 at 15:40:48 GMT

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- ▶ Search parameters
- ▶ Score distribution
- ▶ Legend

Protein Family Summary

Significance threshold p< Max. number of families
 Ions score or expect cut-off Dendrograms cut at
 Preferred taxonomy

Protein families 1-10 (out of 42)

10 per page 1

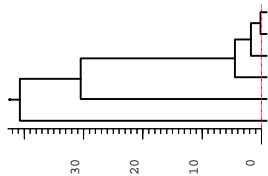
▼1 **gi|359545611** 4987 Chain A, Structure Of The Chr Of The Prion Protein In Dpc Micelles

	Score	Mass	Matches	Sequences	emPAI
1.1 gi 359545611	4987	2490	103 (100)	1 (1)	39009.33
Chain A, Structure Of The Chr Of The Prion Protein In Dpc Micelles					

▼**103 peptide matches (21 non-duplicate, 82 duplicate)**

Query	Dupes	Observed	Mr (expt)	Mr (calc)	ppm	M	Score	Expect	Rank	U	Peptide
2054		591.5416	2362.1373	2362.1344	1.22	0	64	3.4e-05	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.-
2059	▶ <u>16</u>	788.3868	2362.1386	2362.1344	1.76	0	108	3.5e-10	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.-
2062	▶ <u>1</u>	1182.0770	2362.1394	2362.1344	2.13	0	154	2.7e-14	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.-
2090	▶ <u>17</u>	793.7181	2378.1325	2378.1293	1.32	0	83	1.2e-07	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2097		595.5406	2378.1333	2378.1293	1.67	0	47	0.0014	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2099	▶ <u>4</u>	793.7184	2378.1334	2378.1293	1.70	0	97	4.3e-09	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2100	▶ <u>2</u>	1190.0740	2378.1334	2378.1293	1.73	0	132	4.7e-11	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2101		1190.0740	2378.1334	2378.1293	1.73	0	123	2.7e-11	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2111		595.5412	2378.1357	2378.1293	2.68	0	18	0.11	▶ <u>2</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2112	▶ <u>2</u>	793.7194	2378.1364	2378.1293	2.96	0	89	4.2e-08	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2113		1190.0760	2378.1374	2378.1293	3.41	0	129	3.5e-12	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + Oxidation (M)
2132	▶ <u>1</u>	799.0500	2394.1282	2394.1243	1.64	0	126	2.1e-11	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2137		599.5395	2394.1289	2394.1243	1.94	0	63	4.1e-05	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2140		1198.0720	2394.1294	2394.1243	2.17	0	117	6.1e-11	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2143	▶ <u>1</u>	799.0507	2394.1303	2394.1243	2.51	0	111	4.1e-10	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2144		599.5399	2394.1305	2394.1243	2.61	0	31	0.019	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2147		1198.0730	2394.1314	2394.1243	3.01	0	132	7.3e-12	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2148		1198.0730	2394.1314	2394.1243	3.01	0	138	1.7e-12	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2149	▶ <u>20</u>	799.0511	2394.1315	2394.1243	3.02	0	110	4.8e-10	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 2 Oxidation (M)
2184		1206.0690	2410.1234	2410.1192	1.77	0	86	4.2e-08	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 3 Oxidation (M)
2186	▶ <u>18</u>	804.3820	2410.1242	2410.1192	2.08	0	126	2.4e-11	▶ <u>1</u>	U	K.HMAGAAAAGAVVGGGLGGYMLGSAMSR.- + 3 Oxidation (M)

▼2



1	gi 4406457	913	prion protein [Addax nasomaculatus]
5	gi 115361493	444	prion protein [Ovis aries]
6	gi 163954796	359	prion protein [Ovis aries]
4	gi 63253843	452	prion protein [Ovis aries]
2	gi 27733816	820	prion protein [Galeopterus variegatus]
3	gi 191432	459	PrP 27-30 protein [Mesocricetus auratus]

Threshold (0):

	Score	Mass	Matches	Sequences	emPAI
✓ 2.1 gi 4406457	913	21308	78 (60)	7 (6)	2.73
prion protein [Addax nasomaculatus]					
✓ 2.2 gi 27733816	820	26720	59 (50)	6 (5)	1.28
prion protein [Galeopterus variegatus]					
✓ 2.3 gi 191432	459	16490	37 (29)	6 (5)	4.35
PrP 27-30 protein [Mesocricetus auratus]					
▶ 1 same set of gi 191432					
✓ 2.4 gi 63253843	452	13298	64 (38)	6 (5)	5.22
prion protein [Ovis aries]					
✓ 2.5 gi 115361493	444	27883	55 (34)	9 (5)	1.21

	Score	Mass	Matches	Sequences	emPAI
prion protein [Ovis aries]					
2.6 gi 163954796	359	15203	31 (24)	5 (4)	1.74
prion protein [Ovis aries]					
▶ 1 sameset of gi 163954796					

▼ 107 peptide matches (29 non-duplicate, 78 duplicate)

Query	Dupes	Observed	Mr (expt)	Mr (calc)	ppm	M	Score	Expect	Rank	U	1	2	3	4	5	6	Peptide
391		508.7719	1015.5292	1015.5298	-0.59	0	12	0.33	▶ 1		■	■	■	■	■	■	K.qHTVTTTTK.G
398		513.2664	1024.5182	1024.5302	-11.6	0	29	0.091	▶ 1	U							K.HHTVTTTTK.G
415	▶ 18	522.7407	1043.4668	1043.4672	-0.33	0	57	0.00014	▶ 1		■						R.ESQAYYQR
432		523.2330	1044.4514	1044.4512	0.24	0	35	0.031	▶ 1		■						R.ESQAYYQR + Deamidated (NQ)
518		543.2533	1084.4920	1084.4937	-1.56	0	23	0.025	▶ 1	U	■						K.EQQAYYQR.G
520		543.7463	1085.4780	1085.4778	0.27	0	37	0.083	▶ 1	U							K.EQQAYYQR.G + Deamidated (NQ)
523	▶ 24	545.2558	1088.4970	1088.4999	-2.64	0	58	0.00013	▶ 1		■	■					R.YPGQSPGGNR.Y
548	▶ 1	545.7485	1089.4824	1089.4839	-1.36	0	46	0.0013	▶ 1		■	■					R.YPGQSPGGNR.Y + Deamidated (NQ)
567	▶ 11	551.7697	1101.5248	1101.5243	0.48	0	46	0.02	▶ 1	U							R.YPNQVYYR.L
578	▶ 1	552.2625	1102.5104	1102.5083	1.92	0	38	0.029	▶ 1	U							R.YPNQVYYR.L + Deamidated (NQ)
671	▶ 23	577.2727	1152.5308	1152.5299	0.84	0	70	8.5e-05	▶ 1		■	■	■	■	■	■	K.GENFTETDIK.I
689		577.7654	1153.5162	1153.5139	2.05	0	48	0.0074	▶ 1		■	■	■	■	■	■	K.GENFTETDIK.I + Deamidated (NQ)
1149		723.8297	1445.6448	1445.6760	-21.5	1	33	0.0082	▶ 1	U	■						-.GGSRYPGGSPGGNR.Y
1239		761.8608	1521.7070	1521.7068	0.15	0	28	0.035	▶ 1	U							R.VVEQMCITHYQR.E + Oxidation (M)
1519		561.6074	1681.8004	1681.7981	1.34	1	9	0.52	▶ 1		■	■	■	■	■	■	K.GENFTETDIKIMER.V
1534		566.9387	1697.7943	1697.7930	0.73	1	6	1.2	▶ 2		■	■	■	■	■	■	K.GENFTETDIKIMER.V + Oxidation (M)
1535		849.9047	1697.7948	1697.7930	1.07	1	45	0.00034	▶ 1		■	■	■	■	■	■	K.GENFTETDIKIMER.V + Oxidation (M)
1655		607.6444	1819.9114	1819.9078	1.98	0	8	1.2	▶ 2	U							-.GQGGTHNQWPKPK.T
1658		607.9708	1820.8906	1820.8918	-0.67	0	31	0.0078	▶ 1	U							-.GQGGTHNQWPKPK.T + Deamidated (NQ)
1897		717.6898	2150.0476	2150.0492	-0.74	1	21	0.042	▶ 1		■	■	■	■	■	■	K.qHTVTTTTKGENFTETDIK.I
2435		879.1640	3512.6269	3512.6572	-8.62	0	16	0.094	▶ 1	U							R.YPNQVYYRVPDQYSNQNNFVHDCVNIIPVK.X
2439		888.1699	3548.6505	3548.6129	10.6	0	8	0.53	▶ 1	U							R.YPNQVYYRVPDQYSNQNNFVHDCVNIIMVK.X + 2 Deamidated (NQ)
2440		1189.2230	3564.6472	3564.6078	11.0	0	28	0.06	▶ 1	U							R.YPNQVYYRVPDQYSNQNNFVHDCVNIIMVK.X + 2 Deamidated (NQ)
2445		901.6812	3602.6957	3602.6677	7.76	0	9	0.46	▶ 1	U							R.YPNQVYYRVPDQYSNQNNFVHDCVNIIMVK.X + Deamidated (NQ)
2490		978.4406	3909.7333	3909.7266	1.71	0	66	3.5e-05	▶ 1	U							K.HMAGAAAAGAVVGGGLGGYMLGSAMSRPMMHFGNDWEDR.Y + 2 Ox
2492		982.4401	3925.7313	3925.7215	2.49	0	34	0.0039	▶ 1	U							K.HMAGAAAAGAVVGGGLGGYMLGSAMSRPMMHFGNDWEDR.Y + 3 Ox
2495		986.4385	3941.7249	3941.7164	2.14	0	39	0.0011	▶ 1	U							K.HMAGAAAAGAVVGGGLGGYMLGSAMSRPMMHFGNDWEDR.Y + 4 Ox
2496		986.4386	3941.7253	3941.7164	2.25	0	27	0.0054	▶ 1	U							K.HMAGAAAAGAVVGGGLGGYMLGSAMSRPMMHFGNDWEDR.Y + 4 Ox
2501		990.4383	3957.7241	3957.7114	3.22	0	48	0.00019	▶ 1	U							K.HMAGAAAAGAVVGGGLGGYMLGSAMSRPMMHFGNDWEDR.Y + 5 Ox

▶ 34 subsets and intersections (514 subset proteins in total)

▶ 3	gi 435476	340	cytokeratin 9 [Homo sapiens]
▶ 4	gi 136429	168	RecName: Full=Trypsin; Flags: Precursor
▶ 5	gi 11935049	167	keratin 1 [Homo sapiens]
▶ 6	gi 93279106	118	Chain E, Architecture Of Mammalian Fatty Acid Synthase
▶ 7	gi 125154	102	RecName: Full=Adenylate kinase 2, mitochondrial; Short=AK 2; AltName: Full=ATP-AMP transp...
▶ 8	gi 297303011	100	PREDICTED: NADH-quinone oxidoreductase subunit B-like, partial [Macaca mulatta]
▶ 9	gi 291410763	85	PREDICTED: histone cluster 1, H2ag-like [Oryctolagus cuniculus]
▶ 10	gi 49868	71	put. beta-actin (aa 27-375) [Mus musculus]

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