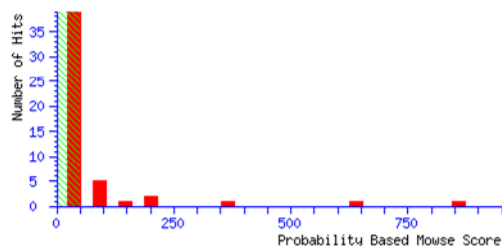


Mascot Search Results

Search title :
MS data file : L:\Client Info\Kitching\Data\20061017-PK-GP\20061101-02 20061017-PK-GP band A.mgf
Database : MSDB 20060831 (3239079 sequences; 1079594700 residues)
Timestamp : 22 Nov 2006 at 14:51:53 GMT
Significant hits: [Q8JTS2 LSDV](#) Putative virion core protein.- Lumpy skin disease virus (LSDV).
[Q77GJ8 LSDV](#) Putative virion core protein.- Lumpy skin disease virus NW-LW.
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cytokeratin) (Hair
[KRHU2](#) keratin 1, type II, cytoskeletal - human
[TRPGTR](#) trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
[Q8JTT4 LSDV](#) Putative early transcription factor small subunit.- Lumpy skin disease virus (LSDV).
[Q4VAQ2 HUMAN](#) Keratin 2A (Epidermal ichthyosis bullosa of Siemens).- Homo sapiens (Human).
[Q6IG03 RAT](#) Type II keratin Kb36.- Rattus norvegicus (Rat).
[Q77GM4 LSDV](#) Putative DNA-binding virion core protein.- Lumpy skin disease virus NW-LW.
[KRBOVI](#) keratin, 54K type I cytoskeletal - bovine
[Q9DHL2 YLDV](#) 101L protein.- Yaba-like disease virus (YLDV).
[Q6PVZ3 CHICK](#) Type II alpha-keratin IIC.- Gallus gallus (Chicken).
[Q90ZF7 RANCA](#) Keratin 8.- Rana catesbeiana (Bull frog).
[K2C8 MOUSE](#) Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Cytokeratin endo A).- Mus
[T08212](#) RNA-directed RNA polymerase (EC 2.7.7.48) - Hendra virus

Probability Based Mowse Score

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Individual ions scores > 48 indicate identity or extensive homology ($p < 0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold p< Max. number of hits

Standard scoring ☒ MudPIT scoring ☐ Ions score cut-off Show sub-sets ☐

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☐ Require bold red ☐

☐ Error tolerant

1. [Q8JTS2 LSDV](#) Mass: 104651 Score: 859 Queries matched: 51
Putative virion core protein.- Lumpy skin disease virus (LSDV).
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Score	Expect	Rank	Peptide
9	387.2242	772.4338	772.4330	0.0008	0	24	31	3	K.SPELSIK.E
16	405.2216	808.4286	808.4079	0.0207	0	10	4.8e+02	5	K.YVDISGR.D
☒ 29	412.7236	823.4327	823.4262	0.0065	0	27	8.5	1	R.ELLMYR.L
☒ 31	414.7536	827.4926	827.4865	0.0062	0	34	2	1	R.LNNLNK.Y
43	438.2365	874.4585	874.4548	0.0036	0	36	1.7	3	R.FQDQIPK.L
☒ 75	531.7860	1061.5574	1061.5505	0.0069	0	(28)	8.4	1	R.DFENLLGVR.R
☒ 76	531.7903	1061.5660	1061.5505	0.0155	0	28	7.9	1	R.DFENLLGVR.R
☒ 77	531.7946	1061.5747	1061.5505	0.0242	0	(18)	97	1	R.DFENLLGVR.R
☒ 99	568.8259	1135.6372	1135.6311	0.0062	0	(40)	0.44	1	K.EVLMYAGLK.I
100	568.8304	1135.6462	1135.6311	0.0151	0	(11)	3.4e+02	2	K.EVLMYAGLK.I
☒ 104	576.8200	1151.6254	1151.6260	-0.0006	0	44	0.17	1	K.EVLMYAGLK.I + Oxidation (M)
113	585.2987	1168.5828	1168.5876	-0.0048	1	(29)	6.6	4	R.LKYPEYNSR.F
☒ 114	585.3055	1168.5964	1168.5876	0.0088	1	40	0.64	1	R.LKYPEYNSR.F
☒ 131	403.5504	1207.6293	1207.6197	0.0097	0	41	0.39	1	K.IDDNGSPHLIK.K
☒ 140	611.8180	1221.6214	1221.6353	-0.0139	0	(33)	2.5	1	K.DVLSTSIQGFR.V
☒ 141	611.8226	1221.6307	1221.6353	-0.0046	0	(21)	37	1	K.DVLSTSIQGFR.V
☒ 142	611.8250	1221.6354	1221.6353	0.0000	0	37	0.92	1	K.DVLSTSIQGFR.V
☒ 143	611.8250	1221.6354	1221.6353	0.0000	0	(24)	20	1	K.DVLSTSIQGFR.V
144	611.8296	1221.6446	1221.6353	0.0093	0	(13)	2.4e+02	2	K.DVLSTSIQGFR.V
☒ 145	611.8319	1221.6493	1221.6353	0.0140	0	(16)	1.2e+02	1	K.DVLSTSIQGFR.V

☒	146	611.8342	1221.6539	1221.6353	0.0186	0	(25)	15	1	K.DVLSTSIQGFR.V
☒	147	611.8389	1221.6632	1221.6353	0.0279	0	(23)	21	1	K.DVLSTSIQGFR.V
☒	167	636.2887	1270.5629	1270.5506	0.0124	0	(18)	1e+02	1	R.NYQEYYTYK.N
☒	168	636.2911	1270.5677	1270.5506	0.0171	0	18	93	1	R.NYQEYYTYK.N
☒	209	678.8099	1355.6052	1355.6135	-0.0083	0	73	0.00023	1	R.AMDTDILTMSMK.H
☒	220	686.8148	1371.6150	1371.6084	0.0066	0	(40)	0.51	1	R.AMDTDILTMSMK.H + Oxidation (M)
☒	223	694.8146	1387.6147	1387.6033	0.0114	0	(38)	0.74	1	R.AMDTDILTMSMK.H + 2 Oxidation (M)
☒	320	795.4419	1588.8693	1588.8613	0.0080	0	70	0.00036	1	R.DHYINLLNLLAK.E
☒	321	530.6315	1588.8728	1588.8613	0.0115	0	(52)	0.025	1	R.DHYINLLNLLAK.E
☒	322	530.6315	1588.8728	1588.8613	0.0115	0	(49)	0.052	1	R.DHYINLLNLLAK.E
☒	323	530.6380	1588.8923	1588.8613	0.0310	0	(50)	0.035	1	R.DHYINLLNLLAK.E
☒	331	799.9269	1597.8393	1597.8351	0.0042	0	58	0.0065	1	K.LGINYLLDVYSSNK.L
☒	334	804.4405	1606.8664	1606.8640	0.0024	0	20	42	2	K.VISSILPSLCLDYK.V
☒	395	588.6642	1762.9709	1762.9802	-0.0093	0	43	0.17	1	K.SIIGSNNHTIISVRPR.V
☒	396	888.9325	1775.8505	1775.8406	0.0099	0	27	7.5	1	K.LSLFWDGIDYQEK.S
☒	435	663.3000	1986.8782	1986.9839	-0.1057	0	(13)	2.1e+02	2	K.TSYVHPFDVLLHPDYGK.I
☒	436	663.3273	1986.9601	1986.9839	-0.0238	0	62	0.0028	1	K.TSYVHPFDVLLHPDYGK.I
☒	437	663.3418	1987.0036	1986.9839	0.0197	0	(19)	51	1	K.TSYVHPFDVLLHPDYGK.I
☒	438	663.3442	1987.0108	1986.9839	0.0269	0	(16)	1.2e+02	1	K.TSYVHPFDVLLHPDYGK.I
☒	439	663.3539	1987.0398	1986.9839	0.0559	0	(33)	2.3	1	K.TSYVHPFDVLLHPDYGK.I
☒	461	713.0257	2136.0553	2136.1367	-0.0814	0	(26)	7.5	1	K.LFHNVINPGYITPNDVVPK.F
☒	462	713.0432	2136.1079	2136.1367	-0.0288	0	(7)	6.1e+02	1	K.LFHNVINPGYITPNDVVPK.F
☒	463	713.0508	2136.1305	2136.1367	-0.0062	0	51	0.022	1	K.LFHNVINPGYITPNDVVPK.F
☒	464	713.0533	2136.1380	2136.1367	0.0013	0	(33)	1.5	1	K.LFHNVINPGYITPNDVVPK.F
☒	465	713.0558	2136.1455	2136.1367	0.0088	0	(22)	15	1	K.LFHNVINPGYITPNDVVPK.F
☒	466	713.0583	2136.1530	2136.1367	0.0163	0	(36)	0.71	1	K.LFHNVINPGYITPNDVVPK.F
☒	475	720.0307	2157.0704	2157.0564	0.0140	0	34	1.2	1	K.LISASYDLLHPMVSAGDYR.N
☒	481	733.0410	2196.1011	2196.1102	-0.0091	0	48	0.047	1	R.FVGGYVQKPVGEGFDIQVEEK.I
☒	525	1229.6131	2457.2116	2457.1807	0.0309	0	36	0.65	1	-.MMPINAVTTLDQLEDSEYLFK.V
☒	529	1237.6021	2473.1896	2473.1756	0.0139	0	(21)	20	1	-.MMPINAVTTLDQLEDSEYLFK.V + Oxidation (M)
☒	530	1245.5970	2489.1795	2489.1705	0.0089	0	(29)	3.1	1	-.MMPINAVTTLDQLEDSEYLFK.V + 2 Oxidation (M)

Proteins matching the same set of peptides:

[Q91MR2_LSDV](#) Mass: 104665 Score: 859 Queries matched: 51
LSDV101 putative virion core protein.- Lumpy skin disease virus NI-2490.

2. [Q77GJ8_LSDV](#) Mass: 76229 Score: 660 Queries matched: 26
Putative virion core protein.- Lumpy skin disease virus NW-LW.
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒	52	464.2518	926.4890	926.5007	-0.0118	0	32	3	1 R.ANIHTMIK.K
☒	68	521.7648	1041.5151	1041.5130	0.0020	0	52	0.032	1 K.GEGASFFLSK.Q
☒	69	521.7648	1041.5151	1041.5130	0.0020	0	(9)	6.8e+02	2 K.GEGASFFLSK.Q
☒	72	530.8087	1059.6029	1059.5924	0.0105	0	49	0.068	1 K.QEILLSTTR.F
☒	101	570.7783	1139.5420	1139.5492	-0.0072	0	32	3	1 K.SSLTNSSMSVK.S
☒	112	583.7816	1165.5486	1165.5471	0.0015	0	45	0.13	1 K.MEEAMSLISR.Q
☒	119	591.7884	1181.5623	1181.5420	0.0203	0	(27)	9.5	1 K.MEEAMSLISR.Q + Oxidation (M)
☒	187	656.8641	1311.7136	1311.7186	-0.0051	0	(44)	0.2	1 R.NELFELLAHVK.S
☒	188	656.8713	1311.7280	1311.7186	0.0094	0	(38)	0.8	1 R.NELFELLAHVK.S
☒	189	656.8761	1311.7376	1311.7186	0.0190	0	44	0.19	1 R.NELFELLAHVK.S
☒	244	724.3739	1446.7332	1446.7289	0.0044	0	51	0.034	1 K.VNPDNYMLLVNR.L
☒	245	724.3890	1446.7635	1446.7289	0.0347	0	(16)	1e+02	1 K.VNPDNYMLLVNR.L
☒	253	732.3732	1462.7319	1462.7238	0.0081	0	(40)	0.42	1 K.VNPDNYMLLVNR.L + Oxidation (M)
☒	316	525.9468	1574.8186	1574.8238	-0.0052	1	41	0.3	1 K.KVNPDNYMLLVNR.L
☒	325	531.2821	1590.8245	1590.8188	0.0057	1	(32)	2.3	1 K.KVNPDNYMLLVNR.L + Oxidation (M)
☒	367	557.3079	1668.9020	1668.8947	0.0073	1	31	2.9	1 R.SNRNELFELLAHVK.S
☒	369	558.6573	1672.9500	1672.9161	0.0338	0	(24)	15	1 K.STHPLVLIHSHAHPK.I
☒	370	558.6595	1672.9566	1672.9161	0.0405	0	32	2.5	1 K.STHPLVLIHSHAHPK.I
☒	455	698.3349	2091.9829	2091.9791	0.0037	0	30	2.8	1 K.QQMLMNHITMFDDLLK.M
☒	456	1051.9661	2101.9177	2101.9228	-0.0052	0	61	0.002	1 K.TSNNQLDESDFYEWLK.G
☒	457	703.6693	2107.9860	2107.9740	0.0119	0	(18)	44	1 K.QQMLMNHITMFDDLLK.M + Oxidation (M)
☒	459	709.0040	2123.9901	2123.9690	0.0211	0	(24)	11	1 K.QQMLMNHITMFDDLLK.M + 2 Oxidation (M)
☒	491	744.3471	2230.0194	2230.0178	0.0016	1	45	0.087	1 R.KTSNNQLDESDFYEWLK.G
☒	513	594.2805	2373.0928	2373.0848	0.0080	0	62	0.0014	1 R.FQSIHFVDMSSSSDLAFHYR.D
☒	515	598.2795	2389.0891	2389.0797	0.0094	0	(61)	0.0019	1 R.FQSIHFVDMSSSSDLAFHYR.D + Oxidation (M)
☒	518	1209.6478	2417.2811	2417.2689	0.0122	0	54	0.0087	1 R.LTEEAPIVFTGISDVISTEIQR.A

3. [K2C1_HUMAN](#) Mass: 66018 Score: 365 Queries matched: 8
Keratin, type II cytoskeletal 1 (Cytokeratin-1) (CK-1) (Keratin-1) (K1) (67 kDa cyto keratin) (Hair)
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
179	650.7722	1299.5298	1299.5223	0.0075	0	14	1.6e+02	2	K.NMQDMVEDYR.N
☒ 181	651.8637	1301.7129	1301.7078	0.0051	0	69	0.00065	1	R.SLDLDSIAAEVK.A
☒ 210	679.3525	1356.6904	1356.6885	0.0020	0	62	0.0029	1	K.LNDLEDALQQAQ.E
☒ 222	692.3469	1382.6792	1382.6830	-0.0038	0	56	0.01	1	K.SLNNQFASFDK.V
☒ 260	738.3990	1474.7834	1474.7780	0.0055	0	41	0.33	1	R.FLEQQNQVLQTK.W
☒ 356	546.9624	1637.8655	1637.8525	0.0130	1	35	1.1	1	K.SLNNQFASFDKVR.F
☒ 386	858.9312	1715.8478	1715.8438	0.0040	0	54	0.015	1	K.QISNLQQSISDAEQR.G
☒ 554	1104.8028	3311.3865	3311.3006	0.0859	0	36	0.16	1	R.GSYSGGSSYSGGGGSGGGGGGHHGSYSGSSSGGYR.G

Proteins matching the same set of peptides:

[AAG41947](#) Mass: 66198 Score: 365 Queries matched: 8
 AF304164 NID: - Homo sapiens
[AAF60327](#) Mass: 66149 Score: 365 Queries matched: 8
 AF237621 NID: - Homo sapiens

4. [KRHU2](#) Mass: 65569 Score: 205 Queries matched: 5
 keratin 1, type II, cytoskeletal - human
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
179	650.7722	1299.5298	1299.5223	0.0075	0	14	1.6e+02	2	K.NMQDMVEDYR.N
210	679.3525	1356.6904	1356.6885	0.0020	0	62	0.0029	1	K.LNDLEDALQQAQ.E
260	738.3990	1474.7834	1474.7780	0.0055	0	41	0.33	1	R.FLEQQNQVLQTK.W
386	858.9312	1715.8478	1715.8438	0.0040	0	54	0.015	1	K.QISNLQQSISDAEQR.G
554	1104.8028	3311.3865	3311.3006	0.0859	0	35	0.2	2	R.GSYSGGSSYSGGGGSGGGGGGHHGSYSGSSSGGYR.G

5. [TRPGTR](#) Mass: 25078 Score: 185 Queries matched: 3
 trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 36	421.7629	841.5113	841.5021	0.0092	0	55	0.017	1	R.VATVSLPR.S
☒ 70	523.2807	1044.5468	1044.5564	-0.0095	0	42	0.36	1	K.LSSPATLNSR.V
☒ 487	737.7059	2210.0958	2210.0967	-0.0009	0	88	4.6e-06	1	R.LGEHNIDVLEGNQFINAAK.I

Proteins matching the same set of peptides:

[1AKSA](#) Mass: 13569 Score: 185 Queries matched: 3
 alpha trypsin (EC 3.4.21.4), chain A - pig
[1AN1E](#) Mass: 24142 Score: 185 Queries matched: 3
 trypsin inhibitor, chain E - medicinal leech (fragments)
[1AVWA](#) Mass: 24145 Score: 185 Queries matched: 3
 trypsin (EC 3.4.21.4), chain A - pig
[1D3OA](#) Mass: 24143 Score: 185 Queries matched: 3
 trypsin (EC 3.4.21.4), chain A - pig
[1EPTB](#) Mass: 8928 Score: 185 Queries matched: 3
 Porcine e-trypsin (EC 3.4.21.4), chain B - pig

6. [Q8JTT4 LSDV](#) Mass: 73485 Score: 137 Queries matched: 3
 Putative early transcription factor small subunit.- Lumpy skin disease virus (LSDV).
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 203	669.8513	1337.6881	1337.6867	0.0015	0	61	0.0038	1	R.YNDEIITVPFK.L
☒ 227	699.9470	1397.8794	1397.8646	0.0148	0	28	5.2	1	K.VYILVPNINILK.I
☒ 364	830.4257	1658.8369	1658.8403	-0.0034	0	48	0.08	1	R.IYSILESISENYTK.E

Proteins matching the same set of peptides:

[Q91MS8 LSDV](#) Mass: 73500 Score: 137 Queries matched: 3
 LSDV084 putative early transcription factor small subunit.- Lumpy skin disease virus NI-2490.

7. [Q4VAQ2 HUMAN](#) Mass: 65678 Score: 102 Queries matched: 2
 Keratin 2A (Epidermal ichthyosis bullosa of Siemens).- Homo sapiens (Human).
☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 196	665.3678	1328.7210	1328.7187	0.0023	0	62	0.0032	1	R.NLDLDSIAAEVK.A
260	738.3990	1474.7834	1474.7780	0.0055	0	41	0.33	1	R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:

[A44861](#) Mass: 66110 Score: 102 Queries matched: 2

keratin, 67K type II epidermal - human

8. [Q6IG03_RAT](#) Mass: 60977 Score: 76 Queries matched: 2
Type II keratin Kb36.- Rattus norvegicus (Rat).

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
210	679.3525	1356.6904	1356.7249	-0.0344	0	35	1.4	3	R.NLDLDSIIAEVR.A
220	738.3990	1474.7834	1474.7780	0.0055	0	41	0.33	1	R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:

[Q6NXH9_MOUSE](#) Mass: 59502 Score: 76 Queries matched: 2
Type II keratin Kb36.- Mus musculus (Mouse).

9. [Q77GM4_LSDV](#) Mass: 29074 Score: 76 Queries matched: 2
Putative DNA-binding virion core protein.- Lumpy skin disease virus NW-LW.

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 183	653.8817	1305.7489	1305.7445	0.0044	0	45	0.16	1	R.SFLSIFNIIPR.N
☒ 406	606.3156	1815.9250	1815.9002	0.0248	0	31	2.8	1	K.EIDEYSNKPLQEPVR.L

10. [KRBOVI](#) Mass: 54986 Score: 66 Queries matched: 2
keratin, 54K type I cytoskeletal - bovine

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
211	679.3672	1356.7198	1356.7109	0.0089	1	12	2.9e+02	3	R.QSVEADINGLRR.V
☒ 224	695.8337	1389.6528	1389.6735	-0.0208	0	54	0.021	1	K.QSLEASLAETEGR.Y

Proteins matching the same set of peptides:

[KRHU0](#) Mass: 59720 Score: 66 Queries matched: 2
keratin 10, type I, cytoskeletal - human

[K1C10_HUMAN](#) Mass: 59711 Score: 66 Queries matched: 2
Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10).- Homo sapiens (Human).

[KRMSE1](#) Mass: 57847 Score: 66 Queries matched: 2
keratin, 59K type I cytoskeletal - mouse

[Q2ENC7_RABIT](#) Mass: 31541 Score: 66 Queries matched: 2
Keratin 10 (Fragment).- Oryctolagus cuniculus (Rabbit).

[Q6IFW6_RAT](#) Mass: 56699 Score: 66 Queries matched: 2
Type I keratin KA10.- Rattus norvegicus (Rat).

[Q8BUX3_MOUSE](#) Mass: 49642 Score: 66 Queries matched: 2
16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130087C14 product:EPIDERMAL KE

[Q8BV09_MOUSE](#) Mass: 52824 Score: 66 Queries matched: 2
16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130014E24 product:KERATIN, TYP

[Q8BVU3_MOUSE](#) Mass: 57178 Score: 66 Queries matched: 2
0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833432L21 product:KERATIN, TYPE

[Q8N175_HUMAN](#) Mass: 59020 Score: 66 Queries matched: 2
Keratin 10.- Homo sapiens (Human).

[Q9CXH6_MOUSE](#) Mass: 58758 Score: 66 Queries matched: 2
17 days embryo head cDNA, RIKEN full-length enriched library, clone:3300001N19 product:inferred: pu

[A31994](#) Mass: 57384 Score: 66 Queries matched: 2
keratin 10, type I, epidermal - human

[AAA39391](#) Mass: 57978 Score: 66 Queries matched: 2
MUSKTEPI2 NID: - Mus musculus

[AAA59199](#) Mass: 39832 Score: 66 Queries matched: 2
HUMK10A NID: - Homo sapiens

[AAA59468](#) Mass: 46473 Score: 66 Queries matched: 2
HUMKRT10A NID: - Homo sapiens

11. [Q9DHL2_YLDV](#) Mass: 103662 Score: 64 Queries matched: 4
101L protein.- Yaba-like disease virus (YLDV).

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
75	531.7860	1061.5574	1061.5505	0.0069	0	(28)	8.4	1	R.DFENLLGVR.S
76	531.7903	1061.5660	1061.5505	0.0155	0	28	7.9	1	R.DFENLLGVR.S
77	531.7946	1061.5747	1061.5505	0.0242	0	(18)	97	1	R.DFENLLGVR.S
131	403.5504	1207.6293	1207.6197	0.0097	0	36	1.1	2	K.LNDDGSPHLIK.K

12. [Q6PVZ3_CHICK](#) Mass: 57268 Score: 62 Queries matched: 1
Type II alpha-keratin IIC.- Gallus gallus (Chicken).

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
196	665.3678	1328.7210	1328.7187	0.0023	0	62	0.0032	1	R.NLGLDSTIADLK.A

13. [Q90ZF7_RANCA](#) Score: 62 Queries matched: 1

Keratin 8.- Rana catesbeiana (Bull frog).

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
196	665.3678	1328.7210	1328.7187	0.0023	0	62	0.0032	1	R.NLGLDSILAELVK.A

14. [K2C8_MOUSE](#) Mass: 54400 Score: 56 Queries matched: 1

Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (K8) (Cytokeratin endo A).- Mus

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
222	692.3469	1382.6792	1382.7194	-0.0402	1	56	0.01	1	K.SLNKFFASFDK.V

Proteins matching the same set of peptides:

[JT0407](#) Mass: 54277 Score: 56 Queries matched: 1

keratin 8, type II cytoskeletal, embryonic - mouse

[JS0658](#) Mass: 54531 Score: 56 Queries matched: 1

cytokeratin EndoA - mouse

[S05474](#) Mass: 54415 Score: 56 Queries matched: 1

keratin 8, type II, cytoskeletal - mouse

[AAI06155](#) Mass: 54514 Score: 56 Queries matched: 1

BC106154 NID: - Mus musculus

[AAA37551](#) Mass: 53210 Score: 56 Queries matched: 1

MUSENDOAA NID: - Mus musculus

[BAE38980](#) Mass: 54546 Score: 56 Queries matched: 1

AK166737 NID: - Mus musculus

[BAE40567](#) Mass: 54459 Score: 56 Queries matched: 1

AK168726 NID: - Mus musculus

15. [T08212](#) Score: 54 Queries matched: 3

RNA-directed RNA polymerase (EC 2.7.7.48) - Hendra virus

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
36	421.7629	841.5113	841.4810	0.0303	0	33	2.8	7	R.LGTWLPR.G
132	403.8745	1208.6018	1208.5673	0.0345	0	14	1.7e+02	10	R.VPYVGSSTDER.S
439	663.3539	1987.0398	1986.9356	0.1042	1	7	8.8e+02	9	K.SFEEDLELATFLMDRR.I + Oxidation (M)

Proteins matching the same set of peptides:

[AAC83194](#) Score: 54 Queries matched: 3

16. [Q7RG06_PLAYO](#) Mass: 128859 Score: 48 Queries matched: 2

Mitochondrial carrier protein, putative.- Plasmodium yoelii yoelii.

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
131	403.5504	1207.6293	1207.7441	-0.1147	1	22	26	3	K.KVNLFPPIIK.N
☒ 133	605.3136	1208.6127	1208.6917	-0.0790	0	27	8.2	1	K.EVNLFPPIIK.N

17. [Q6BL61_DEBHA](#) Score: 46 Queries matched: 1

Similar to CA4877|IPF1667 Candida albicans IPF1667.- Debaryomyces hansenii (Yeast) (Torulaspora hansenii).

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
210	679.3525	1356.6904	1356.7864	-0.0959	1	46	0.1	2	K.KTLLEEGIVDIK.D

18. [Q2ADE5_9FIRM](#) Mass: 54626 Score: 44 Queries matched: 1

Outer membrane efflux protein precursor.- Halothermothrix orenii H 168.

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒ 113	585.2987	1168.5828	1168.5798	0.0030	0	44	0.24	1	K.QLYVMSGLDK.S + Oxidation (M)

19. [Q1UAH7_LACRE](#) Mass: 28733 Score: 44 Queries matched: 3

Peptidase S14, ClpP.- Lactobacillus reuteri 100-23.

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒	44	438.2405	874.4664	874.4396	0.0268	1	44	0.29	1	K.AGDKLDEK.T
☒	45	438.2424	874.4703	874.4396	0.0307	1	(41)	0.53	1	K.AGDKLDEK.T
☒	46	438.2522	874.4899	874.4396	0.0503	1	(29)	8.7	1	K.AGDKLDEK.T

20. [Q24EG4_TETTH](#) Score: 44 Queries matched: 3
Hypothetical protein.- Tetrahymena thermophila SB210.

☐ Check to include this hit in error tolerant search or archive report

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
	44	438.2405	874.4664	874.4396	0.0268	1	44	0.29	1	K.QDKIDEK.N
	45	438.2424	874.4703	874.4396	0.0307	1	(41)	0.53	1	K.QDKIDEK.N
	46	438.2522	874.4899	874.4396	0.0503	1	(29)	8.7	1	K.QDKIDEK.N

Peptide matches not assigned to protein hits: (no details means no match)

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
☒	55	478.7857	955.5568	955.4909	0.0658	0	43	0.27	1	MELLAHAR + Oxidation (M)
☒	166	635.8416	1269.6687	1269.7292	-0.0605	0	42	0.27	1	QLIQSLQEIAR
☒	318	793.8898	1585.7651	1585.7583	0.0068	0	40	0.46	1	VQALEEANNNDLENK
☒	64	516.7633	1031.5121	1031.6491	-0.1370	1	38	0.83	1	ILNLYKLR
☒	96	564.7929	1127.5712	1127.6550	-0.0837	1	38	0.85	1	KIEDLGNLVK
☒	28	412.2569	822.4992	822.4276	0.0716	0	38	0.8	1	FFKPPST
☒	40	428.7728	855.5310	855.4814	0.0496	0	38	0.85	1	IATGELPR
☒	22	412.2378	822.4611	822.4276	0.0335	0	37	0.93	1	FFKPPST
☒	32	414.7536	827.4926	827.4977	-0.0051	1	37	1.2	1	INNIAR
☒	43	438.2365	874.4585	874.4508	0.0077	1	36	1.5	1	ENKIDTR
☒	21	412.2378	822.4611	822.4276	0.0335	0	33	2.2	1	FFKPPST
☒	24	412.2454	822.4763	822.4276	0.0488	0	33	2.5	1	FFKPPST
☒	90	552.7911	1103.5676	1103.5094	0.0582	0	33	3	1	EAVEQNESAK
☒	27	412.2493	822.4840	822.4276	0.0564	0	33	2.6	1	FFKPPST
☒	271	495.9762	1484.9069	1484.8463	0.0606	1	32	1.8	1	QFGVTLPEGIRLR
☒	34	415.2428	828.4710	828.4341	0.0368	0	32	3.8	1	IDIPDTR
☒	30	412.7636	823.5127	823.4916	0.0211	0	32	2.6	1	AALPSIPR
☒	234	709.8809	1417.7472	1417.6507	0.0965	0	31	3.1	1	TAMQDVEAVDSR
☒	19	412.2321	822.4497	822.4276	0.0221	0	31	3.6	1	FFKPPST
☒	26	412.2493	822.4840	822.4276	0.0564	0	30	4.5	1	FFKPPST
☒	25	412.2454	822.4763	822.4276	0.0488	0	30	4.7	1	FFKPPST
☒	23	412.2435	822.4725	822.4276	0.0450	0	30	4.8	1	FFKPPST
☒	190	658.8825	1315.7505	1315.7096	0.0409	1	30	4.8	1	TIQTDLINKDR
☒	239	723.4124	1444.8102	1444.7674	0.0428	0	30	4.5	1	TVPEVLLSGHHEK
☒	48	460.2246	918.4346	918.5650	-0.1304	0	30	7	1	LGGIPPIR
☒	237	716.3758	1430.7371	1430.7517	-0.0146	1	29	5	1	AEDASSWRIVLGK
☒	454	1042.0143	2082.0141	2082.0455	-0.0314	1	29	3.4	1	VMNKFVDIELVDGIGDPR + Oxidation (M)
☒	20	412.2321	822.4497	822.4276	0.0221	0	29	5.8	1	FFKPPST
☒	74	531.2951	1060.5756	1060.4019	0.1737	0	29	6.6	1	DTSSICYSE
☒	172	639.8427	1277.6709	1277.7455	-0.0746	1	29	6.7	1	RLDIHDILGVK
☒	98	566.3053	1130.5960	1130.6295	-0.0335	1	28	8.2	1	LLSAKDSLR
☒	297	766.4267	1530.8388	1530.7777	0.0611	0	27	9.9	1	VDLTPEESISQVSK
☒	58	487.7262	973.4378	973.5960	-0.1582	0	27	13	1	KPYLVNIK
☒	358	822.4415	1642.8685	1642.7872	0.0813	0	27	8	1	AEELGIPVLDEDGMR
☒	332	800.4204	1598.8263	1598.8701	-0.0438	1	26	9.9	1	LHSMIVDLDSVVK + Oxidation (M)
☒	7	386.2337	770.4528	770.4650	-0.0123	0	26	13	1	VSSILPR
☒	108	577.2909	1152.5673	1152.6502	-0.0830	0	26	11	1	IGLSEGHISIK
☒	82	535.3262	1068.6379	1068.5677	0.0701	0	26	11	1	LFEIICFK
☒	368	558.6351	1672.8834	1672.8018	0.0817	1	26	11	1	QFIDKLTEMYEEK
☒	157	622.7733	1243.5320	1243.5067	0.0253	0	25	13	1	MSPDDFEFEK
☒	9	387.2242	772.4338	772.4079	0.0259	0	25	21	1	SPEVSVR
☒	149	612.3076	1222.6007	1222.6339	-0.0332	1	25	14	1	QSLSTSVKAMR + Oxidation (M)
☒	315	787.4491	1572.8837	1572.7316	0.1521	0	25	11	1	EFMCLESPIYR + Oxidation (M)
☒	125	596.7892	1191.5639	1191.5917	-0.0279	0	25	16	1	EASQAMTSLVR
☒	298	766.9227	1531.8309	1531.7704	0.0605	0	25	15	1	ANQEVLEWLVGMK + Oxidation (M)
☒	221	686.8762	1371.7379	1371.6670	0.0709	0	25	16	1	TANEYINSLGKY
☒	175	645.8023	1289.5900	1289.5888	0.0013	0	24	18	1	ATTSAYSDAFTR
☒	158	623.3375	1244.6605	1244.7856	-0.1251	1	24	20	1	IVILKGQVTFK
☒	6	385.2297	768.4448	768.3701	0.0747	0	24	15	1	MVGPGRH + Oxidation (M)
☒	343	812.3504	1622.6863	1622.8337	-0.1474	0	24	14	1	GFTLNIMAGESGLGK + Oxidation (M)
☒	81	534.2590	1066.5034	1066.4791	0.0243	1	24	20	1	EYRDANSR
☒	204	669.8780	1337.7415	1337.8394	-0.0979	1	24	22	1	RIIAILQDIVGK
☒	171	638.8561	1275.6976	1275.6346	0.0630	0	24	21	1	DIAFLPAGTDEK