

# Mascot Search Results

User : processingkernel  
 Email :  
 Search title : Amazon\_human CID\_PE  
 MS data file : 56294995342131482.mgf  
 Database : SwissProt 2011\_08 (531473 sequences; 188463640 residues)  
 Taxonomy : Homo sapiens (human) (20319 sequences)  
 Timestamp :  
 Enzyme : Trypsin/P  
 Fixed modifications : Carbamidomethyl (C)  
 Variable modifications : Oxidation (M)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance :  $\pm 0.35$  Da (#  $^{13}\text{C} = 1$ )  
 Fragment Mass Tolerance:  $\pm 0.35$  Da  
 Max Missed Cleavages : 1  
 Instrument type : ESI-TRAP  
 Number of queries : 4954  
 Protein hits :

- [K2C1\\_HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
- [K1C9\\_HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
- [K1C10\\_HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
- [K2C4\\_HUMAN](#) Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4
- [CLUS\\_HUMAN](#) Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1
- [K22E\\_HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
- [AKAP4\\_HUMAN](#) A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1
- [SACA4\\_HUMAN](#) Sperm acrosome membrane-associated protein 4 OS=Homo sapiens GN=SPACA4 PE=1 SV=1
- [FL2D\\_HUMAN](#) Pre-mRNA-splicing regulator WTAP OS=Homo sapiens GN=WTAP PE=1 SV=2

## SwissProt [Decoy](#) False discovery rate

Peptide matches above identity threshold	39	5	12.82 %
Peptide matches above homology or identity threshold	91	27	29.67 %

## Select Summary Report

Format As

Select Summary (protein hits)

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Significance threshold p &lt; 0.05

Max. number of hits AUTO

Standard scoring MudPIT scoring 

Ions score or expect cut-off 34

Show sub-sets 0

Show pop-ups Suppress pop-ups 

Sort unassigned Decreasing Score

Require bold red 1. [K2C1\\_HUMAN](#) Mass: 66170 Score: 549 Queries matched: 17 emPAI: 0.45

Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">533</a>	437.8000	873.5854	873.4920	0.0935	0	53	0.0014	1	R.SLVNLGGSK.S
<a href="#">1214</a>	517.3000	1032.5854	1032.5087	0.0767	0	61	0.00018	1	R.TLLEGEESR.M <a href="#">1213</a>
<a href="#">2620</a>	633.3000	1264.5854	1264.6299	-0.0445	0	49	0.0023	1	R.TNAENEFVTIK.K
<a href="#">2705</a>	639.4000	1276.7855	1276.7027	0.0828	0	66	4.1e-005	1	K.LALDLEIATYR.T <a href="#">2706</a> <a href="#">2707</a>
<a href="#">2848</a>	651.8000	1301.5854	1301.7078	-0.1224	0	78	1.8e-006	1	R.SLDLDSIIAEVK.A <a href="#">2850</a> <a href="#">2853</a>
<a href="#">3411</a>	697.4000	1392.7855	1392.7249	0.0606	1	51	0.0013	1	R.TNAENEFVTIKK.D <a href="#">3412</a> <a href="#">3413</a>
<a href="#">4683</a>	883.3000	1764.5854	1764.7275	-0.1421	0	78	1.3e-006	1	R.FSSCGGGGSGFGAGGGFGR.S <a href="#">4684</a> <a href="#">4685</a>
<a href="#">4623</a>	856.0000	2564.9782	2564.1595	0.8186	0	43	0.0051	1	R.MSGECAPNVSVSVSTSHTTISGGGR.G

2. [K1C9\\_HUMAN](#) Mass: 62255 Score: 289 Queries matched: 7 emPAI: 0.22

Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">601</a>	449.2000	896.3855	896.4062	-0.0207	0	38	0.035	1	R.MTLDDFR.I <a href="#">600</a>
<a href="#">2391</a>	616.8000	1231.5854	1231.5906	-0.0051	0	83	6.5e-007	1	R.SGGGGGGGLGSGGSIR.S
<a href="#">2416</a>	618.3000	1234.5854	1234.5215	0.0640	0	99	2.3e-008	1	R.FSSSSGYGGGSR.V <a href="#">2418</a> <a href="#">2419</a>
<a href="#">522</a>	436.6000	1306.7782	1306.6703	0.1079	1	37	0.045	1	R.IKFEMEQLR.Q

3. [K1C10\\_HUMAN](#) Mass: 59020 Score: 150 Queries matched: 5 emPAI: 0.11

Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">308</a>	404.2000	806.3855	806.3923	-0.0068	0	43	0.013	1	R.LAADDFR.L <a href="#">305</a>
<a href="#">2594</a>	631.8000	1261.5854	1261.5899	-0.0044	0	80	1.1e-006	1	R.SLLEGEESGGGR.G <a href="#">2598</a> <a href="#">2599</a>

4. [K2C4\\_HUMAN](#) Mass: 57649 Score: 130 Queries matched: 4 emPAI: 0.11

Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">1611</a>	554.3000	1106.5854	1106.5356	0.0498	0	37	0.04	1	R.AQYEEIAQR.S
<a href="#">2705</a>	639.4000	1276.7855	1276.7027	0.0828	0	66	4.1e-005	1	K.LALDIEIATYR.K <a href="#">2706</a> <a href="#">2707</a>

5. [CLUS\\_HUMAN](#) Mass: 53031 Score: 77 Queries matched: 2 emPAI: 0.06

Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">4679</a>	881.9000	1761.7855	1761.8203	-0.0348	0	56	0.00027	1	R.EILSVDCSTNNPSQAK.L <a href="#">4680</a>

6. [K22E\\_HUMAN](#) Mass: 65678 Score: 72 Queries matched: 4 emPAI: 0.15

Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">1611</a>	554.3000	1106.5854	1106.5356	0.0498	0	37	0.04	1	K.AQYEEIAQR.S
<a href="#">1758</a>	566.3000	1130.5854	1130.5026	0.0828	0	41	0.016	1	R.STSSFCLSR.H <a href="#">1759</a>
<a href="#">4663</a>	870.9000	1739.7855	1739.6983	0.0872	0	42	0.0054	1	R.GSSSGGGYSSGSSSYGSGGR.Q

7. [AKAP4\\_HUMAN](#) Mass: 95842 Score: 59 Queries matched: 3 emPAI: 0.07

A-kinase anchor protein 4 OS=Homo sapiens GN=AKAP4 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">1463</a>	542.3000	1082.5854	1082.5608	0.0247	0	39	0.026	1	K.SQSLSYASLK.A <a href="#">1464</a>
<a href="#">2114</a>	594.3000	1186.5854	1186.5870	-0.0016	0	41	0.014	1	K.SFLYSELSNK.S

8. [SACA4\\_HUMAN](#) Mass: 13622 Score: 58 Queries matched: 2 emPAI: 0.53

Sperm acrosome membrane-associated protein 4 OS=Homo sapiens GN=SPACA4 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">3774</a>	734.8000	1467.5854	1467.6664	-0.0810	0	38	0.022	1	R.ATSCGLEEPPVSYR.G
<a href="#">4238</a>	795.3000	1588.5854	1588.6974	-0.1120	0	39	0.017	1	R.GVTYSLTTNCTGR.L

9. [FL2D\\_HUMAN](#) Mass: 44388 Score: 36 Queries matched: 1 emPAI: 0.07

Pre-mRNA-splicing regulator WTAP OS=Homo sapiens GN=WTAP PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<a href="#">2276</a>	608.3000	1214.5854	1214.6805	-0.0951	1	36	0.045	1	K.VMARDELILR.W

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Mascot: <http://www.matrixscience.com/>