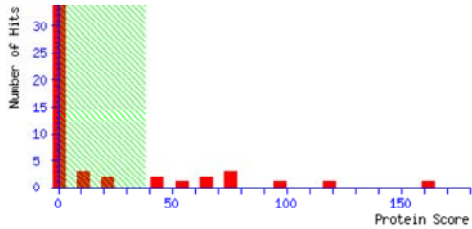


MASCOT SCIENCE **Mascot Search Results**

User : JPROS
 Email : pro@jbios.co.jp
 Search title : D:\JPROS\L046\2_4micro-2.wiff (sample number 1)
 MS data file : mas141.tmp
 Database : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)
 Taxonomy : Homo sapiens (human) (327411 sequences)
 Timestamp : 23 Apr 2019 at 10:02:33 GMT
 Protein hits : [NP_006588.1](#) heat shock cognate 71 kDa protein isoform 1 [Homo sapiens]
[NP_006112.3](#) keratin, type II cytoskeletal 1 [Homo sapiens]
[AFA52006.1](#) keratin 1 [Homo sapiens]
[BAG58351.1](#) unnamed protein product [Homo sapiens]
[NP_005337.2](#) heat shock 70 kDa protein 1B [Homo sapiens]
[NP_002941.1](#) dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Homo sapiens]
[NP_002146.2](#) heat shock 70 kDa protein 6 [Homo sapiens]
[BAX03527.1](#) heat shock 70kDa protein 1-like [Homo sapiens]
[NP_000412.3](#) keratin, type I cytoskeletal 10 [Homo sapiens]
[BAB40929.2](#) alpha 1,6-fucosyltransferase [Homo sapiens]
[SJM28204.1](#) chaperone Hsp70, co-chaperone with DnaJ [Homo sapiens]
[BAA19418.1](#) mutant keratin 9, partial [Homo sapiens]
[NP_000217.2](#) keratin, type I cytoskeletal 9 [Homo sapiens]
[EAW66317.1](#) hCG2039691, partial [Homo sapiens]
[AAF03489.1](#) monocarboxylate transporter MCT3 [Homo sapiens]
[AAM28904.1](#) HUS1B [Homo sapiens]

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 38 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: Peptide Summary [Help](#)

Significance threshold p<: Max. number of hits:

Standard scoring: MudPIT scoring Display non-significant matches Show sub-sets:

Show pop-ups: Suppress pop-ups Sort unassigned: Require bold red:

Preferred taxonomy:

Error tolerant

1. [NP_006588.1](#) Mass: 70854 Score: 162 Matches: 13(5) Sequences: 12(5) emPAI: 0.28
 heat shock cognate 71 kDa protein isoform 1 [Homo sapiens]
 Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 155	429.7633	857.5121	857.4494	0.0627	0	20	7.9	1	U	R.GTLDPVEK.A
<input checked="" type="checkbox"/> 218	472.8165	943.6184	943.5161	0.1024	0	9	82	8	U	K.VCNPIITK.L + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 271	541.3396	1080.6647	1080.5604	0.1044	0	44	0.023	1	U	K.LLQDFPFGK.E
<input checked="" type="checkbox"/> 285	600.3997	1198.7848	1198.6670	0.1179	0	43	0.022	1	U	K.DAGTIAGLVLR.I
<input checked="" type="checkbox"/> 294	614.8673	1227.7200	1227.6207	0.0993	0	36	0.15	1	U	K.VEIIANDQGNR.T
<input checked="" type="checkbox"/> 334	652.3899	1302.7652	1302.5914	0.1738	0	25	1.9	1	U	K.NSLESYAFNMK.A
<input checked="" type="checkbox"/> 366	494.6632	1480.9677	1480.7998	0.1679	0	24	0.76	1	U	K.SQIHDIIVLVGGSTR.I
<input checked="" type="checkbox"/> 396	825.4657	1648.9169	1648.7879	0.1290	0	(10)	59	1	U	K.NQVAMNPTNTVFDK.R
<input checked="" type="checkbox"/> 401	833.4889	1664.9633	1664.7828	0.1805	0	50	0.0049	1	U	K.NQVAMNPTNTVFDK.R + Oxidation (M)
<input checked="" type="checkbox"/> 407	564.6413	1690.9020	1690.7183	0.1837	0	34	0.23	1	U	K.STAGDTHLGGEDFDNR.M
<input checked="" type="checkbox"/> 416	596.7300	1787.1680	1786.9828	0.1852	1	46	0.0014	1	U	R.IINPEPTAALAYLQDK.V
<input checked="" type="checkbox"/> 420	613.3992	1837.1757	1837.0058	0.1699	1	36	0.033	1	U	K.LDKSQIHDIIVLVGGSTR.I
<input checked="" type="checkbox"/> 436	661.4005	1981.1795	1980.9905	0.1890	0	11	17	1	U	K.TVTNAVVTVPAYFNDSQR.Q

2. [NP_006112.3](#) Mass: 65999 Score: 120 Matches: 6(3) Sequences: 6(3) emPAI: 0.17
 keratin, type II cytoskeletal 1 [Homo sapiens]
 Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 176	437.7925	873.5705	873.4920	0.0785	0	26	2.1	1	U	R.SLVNLGGSK.S
<input checked="" type="checkbox"/> 230	487.3099	972.6053	972.5240	0.0813	0	17	13	1	U	K.IEISELNR.V
<input checked="" type="checkbox"/> 265	533.2834	1064.5523	1064.5138	0.0385	0	40	0.071	1	U	K.AQYEDIAQK.S
<input checked="" type="checkbox"/> 281	590.3493	1178.6841	1178.5931	0.0910	0	49	0.0075	1	U	K.YEELQITAGR.H
<input checked="" type="checkbox"/> 333	651.9133	1301.8120	1301.7078	0.1042	0	71	3.9e-05	1	U	R.SLDDLSIIAEVK.A
<input checked="" type="checkbox"/> 364	738.4733	1474.9321	1474.7780	0.1541	0	60	0.00033	1	U	R.FLEQNVQLQTK.W

Proteins matching the same set of peptides:

AAG41947.1	Mass: 66027	Score: 120	Matches: 6(3)	Sequences: 6(3)
keratin 1 [Homo sapiens]				
AFA52002.1	Mass: 66013	Score: 120	Matches: 6(3)	Sequences: 6(3)
keratin 1 [Homo sapiens]				
AFA52004.1	Mass: 65930	Score: 120	Matches: 6(3)	Sequences: 6(3)
keratin 1 [Homo sapiens]				
AFA52005.1	Mass: 66086	Score: 120	Matches: 6(3)	Sequences: 6(3)
keratin 1 [Homo sapiens]				
AFA52007.1	Mass: 66071	Score: 120	Matches: 6(3)	Sequences: 6(3)
keratin 1 [Homo sapiens]				

3. [AFA52006.1](#) Mass: 66026 Score: 101 Matches: 6(3) Sequences: 6(3) emPAI: 0.17
keratin 1 [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
176	437.7925	873.5705	873.4920	0.0785	0	26	2.1	1		R.SLVNLGGSK.S
230	487.3099	972.6053	972.5240	0.0813	0	17	13	1		K.IEISELNR.V
265	533.2834	1064.5523	1064.5138	0.0385	0	40	0.071	1		K.AQVEDIAQK.S
281	590.3493	1178.6841	1178.5931	0.0910	0	49	0.0075	1		K.YEELQITAGR.H
<input checked="" type="checkbox"/> 345	665.4255	1328.8364	1328.7187	0.1177	0	40	0.039	1	U	R.NLDDLSIAEVK.A
364	738.4733	1474.9321	1474.7780	0.1541	0	60	0.00033	1		R.FLEQQNQVLQTK.W

4. [BAG58351.1](#) Mass: 67490 Score: 78 Matches: 7(1) Sequences: 7(1) emPAI: 0.05
unnamed protein product [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 276	555.3490	1108.6835	1108.5665	0.1170	0	37	0.094	1		K.LLQDFFNGR.D
<input checked="" type="checkbox"/> 283	599.4135	1196.8125	1196.6877	0.1248	0	10	24	1		K.DAGVIAGLNVLR.I
<input checked="" type="checkbox"/> 287	602.8486	1203.6827	1203.5255	0.1572	0	6	1.7e+02	1		K.GSGSGPTIEEVD.-
294	614.8673	1227.7200	1227.6207	0.0993	0	36	0.15	1		K.VEIIANDQGNR.T
<input checked="" type="checkbox"/> 363	489.3196	1464.9369	1464.8049	0.1320	0	44	0.0099	1		K.AQIHDLVLVGGSTR.I
<input checked="" type="checkbox"/> 403	559.3032	1674.8877	1674.7234	0.1643	0	26	1.4	1		K.ATAGDTHLGGEDFDNR.L
<input checked="" type="checkbox"/> 406	844.5275	1687.0405	1686.8940	0.1464	0	33	0.13	1		R.IINEPTAAAIAYGLDR.T

Proteins matching the same set of peptides:

BAG62811.1	Mass: 59097	Score: 78	Matches: 7(1)	Sequences: 7(1)
unnamed protein product [Homo sapiens]				
BAG63067.1	Mass: 67952	Score: 78	Matches: 7(1)	Sequences: 7(1)
unnamed protein product [Homo sapiens]				

5. [NP_005337.2](#) Mass: 70009 Score: 77 Matches: 8(1) Sequences: 8(1) emPAI: 0.05
heat shock 70 kDa protein 1B [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
276	555.3490	1108.6835	1108.5665	0.1170	0	37	0.094	1		K.LLQDFFNGR.D
283	599.4135	1196.8125	1196.6877	0.1248	0	10	24	1		K.DAGVIAGLNVLR.I
287	602.8486	1203.6827	1203.5255	0.1572	0	6	1.7e+02	1		K.GSGSGPTIEEVD.-
294	614.8673	1227.7200	1227.6207	0.0993	0	36	0.15	1		K.VEIIANDQGNR.T
363	489.3196	1464.9369	1464.8049	0.1320	0	44	0.0099	1		K.AQIHDLVLVGGSTR.I
<input checked="" type="checkbox"/> 398	830.0154	1658.0162	1657.8424	0.1739	0	14	12	1	U	K.NQVALNPQTVFDAK.R
403	559.3032	1674.8877	1674.7234	0.1643	0	26	1.4	1		K.ATAGDTHLGGEDFDNR.L
406	844.5275	1687.0405	1686.8940	0.1464	0	33	0.13	1		R.IINEPTAAAIAYGLDR.T

Proteins matching the same set of peptides:

AAD21815.1	Mass: 69982	Score: 77	Matches: 8(1)	Sequences: 8(1)
HSP70-2 [Homo sapiens]				
AAD21816.1	Mass: 69995	Score: 77	Matches: 8(1)	Sequences: 8(1)
HSP70-1 [Homo sapiens]				
AAA52697.1	Mass: 69825	Score: 77	Matches: 8(1)	Sequences: 8(1)
heat shock protein [Homo sapiens]				
BAD93055.1	Mass: 77448	Score: 77	Matches: 8(1)	Sequences: 8(1)
heat shock 70kDa protein 1A variant, partial [Homo sapiens]				

6. [NP_002941.1](#) Mass: 68527 Score: 73 Matches: 7(1) Sequences: 7(1) emPAI: 0.05
dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 208	455.2878	908.5610	908.4967	0.0643	0	16	17	1	U	K.IDHILDAL.-
<input checked="" type="checkbox"/> 313	635.8744	1269.7341	1269.5877	0.1464	0	18	10	1	U	R.DVPAYSQDTFK.V
<input checked="" type="checkbox"/> 332	651.4265	1300.8385	1300.7350	0.1035	0	32	0.24	1	U	K.ALTSETALLQSR.L
<input checked="" type="checkbox"/> 340	656.3974	1310.7803	1310.6143	0.1660	0	12	34	1	U	R.SEDLLDYGFR.D
<input checked="" type="checkbox"/> 360	718.4240	1434.8334	1434.6990	0.1343	0	20	5	1	U	K.NIEIDSPYEISR.A
<input checked="" type="checkbox"/> 397	552.0287	1653.0642	1652.8846	0.1796	0	52	0.00068	1	U	K.VTAEVVLAHLGGGSTR.A
<input checked="" type="checkbox"/> 399	830.5377	1659.0608	1658.8879	0.1729	0	26	0.43	1	U	R.ATSFLLALEPELEAR.L

Proteins matching the same set of peptides:

AAH07995.1	Mass: 64542	Score: 73	Matches: 7(1)	Sequences: 7(1)
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Similar to ribophorin I, partial [Homo sapiens]

[CAG33023.1](#) Mass: 68564 Score: 73 Matches: 7(1) Sequences: 7(1)
RPN1 [Homo sapiens]
[BAD97315.1](#) Mass: 68537 Score: 73 Matches: 7(1) Sequences: 7(1)
ribophorin I variant, partial [Homo sapiens]

7. [NP_002146.2](#) Mass: 70984 Score: 69 Matches: 4(1) Sequences: 4(1) emPAI: 0.05
heat shock 70 kDa protein 6 [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
271	541.3396	1080.6647	1080.5604	0.1044	0	44	0.023	1		K.LLQDFFNKG.E
294	614.8673	1227.7200	1227.6207	0.0993	0	36	0.15	1	U	R.VEILANDQGNR.T
403	559.3032	1674.8877	1674.7234	0.1643	0	26	1.4	1		K.ATAGDTHLGGEDFDNR.L
406	844.5275	1687.0405	1686.8940	0.1464	0	33	0.13	1		R.IINEPTAAAIAYGLDR.R

Proteins matching the same set of peptides:

[BAG35622.1](#) Mass: 70914 Score: 69 Matches: 4(1) Sequences: 4(1)
unnamed protein product [Homo sapiens]
[CAA36061.1](#) Mass: 70810 Score: 69 Matches: 4(1) Sequences: 4(1)
unnamed protein product [Homo sapiens]
[BAG52788.1](#) Mass: 70928 Score: 69 Matches: 4(1) Sequences: 4(1)
unnamed protein product [Homo sapiens]
[BAD97082.1](#) Mass: 70960 Score: 69 Matches: 4(1) Sequences: 4(1)
heat shock 70kDa protein 6 (HSP70B') variant, partial [Homo sapiens]

8. [EAX03527.1](#) Mass: 77514 Score: 61 Matches: 4(1) Sequences: 4(1) emPAI: 0.05
heat shock 70kDa protein 1-like [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
283	599.4135	1196.8125	1196.6877	0.1248	0	10	24	1		K.DAGVIAGLNVL.R
294	614.8673	1227.7200	1227.6207	0.0993	0	36	0.15	1		K.VEILANDQGNR.T
363	489.3196	1464.9369	1464.8413	0.0956	1	44	0.0099	1	U	K.AKIHIDIVLGGSTR.I
403	559.3032	1674.8877	1674.7234	0.1643	0	26	1.4	1		K.ATAGDTHLGGEDFDNR.L

Proteins matching the same set of peptides:

[NP_005518.3](#) Mass: 70331 Score: 61 Matches: 4(1) Sequences: 4(1)
heat shock 70 kDa protein 1-like [Homo sapiens]
[AAD21817.1](#) Mass: 70361 Score: 61 Matches: 4(1) Sequences: 4(1)
HSP70-HOM [Homo sapiens]
[BAA32521.1](#) Mass: 70393 Score: 61 Matches: 4(1) Sequences: 4(1)
heat shock protein 70 testis variant [Homo sapiens]
[AAH34483.1](#) Mass: 70349 Score: 61 Matches: 4(1) Sequences: 4(1)
Heat shock 70kDa protein 1-like [Homo sapiens]
[BAG37656.1](#) Mass: 70332 Score: 61 Matches: 4(1) Sequences: 4(1)
unnamed protein product [Homo sapiens]
[BAG58366.1](#) Mass: 77513 Score: 61 Matches: 4(1) Sequences: 4(1)
unnamed protein product [Homo sapiens]
[AAA63228.1](#) Mass: 70355 Score: 61 Matches: 4(1) Sequences: 4(1)
heat shock-induced protein [Homo sapiens]
[BAG63545.1](#) Mass: 58296 Score: 61 Matches: 4(1) Sequences: 4(1)
unnamed protein product [Homo sapiens]
[AQY76891.1](#) Mass: 70303 Score: 61 Matches: 4(1) Sequences: 4(1)
HSPAL [Homo sapiens]
[BAD97106.1](#) Mass: 70360 Score: 61 Matches: 4(1) Sequences: 4(1)
heat shock 70kDa protein 1-like variant, partial [Homo sapiens]

9. [NP_000412.3](#) Mass: 58766 Score: 49 Matches: 3(1) Sequences: 3(1) emPAI: 0.06
keratin, type I cytoskeletal 10 [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 273	545.8498	1089.6851	1089.5237	0.1614	0	26	1.7	1	U	K.VTMQNLNDR.L
<input checked="" type="checkbox"/> 354	691.3655	1380.7164	1380.6408	0.0756	0	49	0.0088	1	U	R.ALEESNYLEGGK.I
<input checked="" type="checkbox"/> 368	498.6191	1492.8354	1492.7270	0.1084	1	13	32	1	U	R.SQYQLAEQNRK.D

Proteins matching the same set of peptides:

[P13645.6](#) Mass: 58792 Score: 49 Matches: 3(1) Sequences: 3(1)
RecName: Full=Keratin, type I cytoskeletal 10; AltName: Full=Cytokeratin-10; Short=CK-10; AltName: Full=Keratin-10; Short=K10
[CAA32649.1](#) Mass: 59492 Score: 49 Matches: 3(1) Sequences: 3(1)
unnamed protein product [Homo sapiens]
[AAH34697.1](#) Mass: 58792 Score: 49 Matches: 3(1) Sequences: 3(1)
Keratin 10 [Homo sapiens]
[EAW60681.1](#) Mass: 63308 Score: 49 Matches: 3(1) Sequences: 3(1)
keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens]
[XP_005257400.1](#) Mass: 63308 Score: 49 Matches: 3(1) Sequences: 3(1)
keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]

10. [BAB40929.2](#) Mass: 35772 Score: 46 Matches: 4(1) Sequences: 4(1) emPAI: 0.10
alpha 1,6-fucosyltransferase [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
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<input checked="" type="checkbox"/>	223	479.3236	956.6327	956.5542	0.0785	0	16	16	1	U	R.VLEEQLVK.A
<input checked="" type="checkbox"/>	231	487.3183	972.6220	972.5240	0.0980	0	31	0.55	1	U	K.DLTELVQR.R
	268	536.8229	1071.6313	1071.5309	0.1004	0	8	1.2e+02	3	U	K.NLEGNELQR.H
<input checked="" type="checkbox"/>	359	710.4528	1418.8911	1418.7518	0.1393	0	46	0.009	1	U	R.IPEGPIDQQAIGR.V

Proteins matching the same set of peptides:

AAI42959.1	Mass: 35798	Score: 46	Matches: 4(1)	Sequences: 4(1)
FUT8 protein [Homo sapiens]				
EAW80914.1	Mass: 51782	Score: 46	Matches: 4(1)	Sequences: 4(1)
fucosyltransferase 8 (alpha (1,6) fucosyltransferase), isoform CRA_d [Homo sapiens]				
BAF85102.1	Mass: 66474	Score: 46	Matches: 4(1)	Sequences: 4(1)
unnamed protein product [Homo sapiens]				
BAA92858.1	Mass: 32161	Score: 46	Matches: 4(1)	Sequences: 4(1)
alpha1,6 fucosyltransferase, partial [Homo sapiens]				
NP_835368.1	Mass: 66474	Score: 46	Matches: 4(1)	Sequences: 4(1)
alpha-(1,6)-fucosyltransferase isoform a [Homo sapiens]				
XP_016876625.1	Mass: 70347	Score: 46	Matches: 4(1)	Sequences: 4(1)
alpha-(1,6)-fucosyltransferase isoform X1 [Homo sapiens]				
XP_016876629.1	Mass: 62866	Score: 46	Matches: 4(1)	Sequences: 4(1)
alpha-(1,6)-fucosyltransferase isoform X2 [Homo sapiens]				

11. [SJM28204.1](#) Mass: 74896 Score: 46 Matches: 1(1) Sequences: 1(1) empAI: 0.05
chaperone Hsp70, co-chaperone with DnaJ [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
416	596.7300	1787.1680	1786.9828	0.1852	1	46	0.0014	1	U	R.IINEPTAAALAYGLDKK.E

12. [BAA19418.1](#) Mass: 25913 Score: 26 Matches: 1(0) Sequences: 1(0)
mutant keratin 9, partial [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 280	579.3766	1156.7386	1156.5836	0.1550	0	26	1.4	1	U	R.QGVDADINGLR.Q

13. [NP_000217.2](#) Mass: 62027 Score: 24 Matches: 3(0) Sequences: 3(0)
keratin, type I cytoskeletal 9 [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
265	533.2834	1064.5523	1064.4920	0.0603	0	12	47	3	U	K.STMQELNSR.L
280	579.3766	1156.7386	1156.5836	0.1550	0	26	1.4	1	U	R.QGVDADINGLR.Q
<input checked="" type="checkbox"/> 419	613.3798	1837.1175	1836.9581	0.1594	0	15	7.5	1	U	R.HGVQLELELQSQLSK.K

Proteins matching the same set of peptides:

CAA52924.1	Mass: 61950	Score: 24	Matches: 3(0)	Sequences: 3(0)
keratin 9 [Homo sapiens]				
EAW60744.1	Mass: 57526	Score: 24	Matches: 3(0)	Sequences: 3(0)
keratin 9 (epidermolytic palmoplantar keratoderma) [Homo sapiens]				
CAA82315.1	Mass: 62092	Score: 24	Matches: 3(0)	Sequences: 3(0)
cytokeratin 9 [Homo sapiens]				

14. [EAW66317.1](#) Mass: 1934 Score: 16 Matches: 1(0) Sequences: 1(0)
hCG2039691, partial [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 130	422.2864	842.5582	842.3995	0.1587	1	16	17	1	U	K.GNTTHRGT.-

15. [AAF03489.1](#) Mass: 52287 Score: 15 Matches: 1(0) Sequences: 1(0)
monocarboxylate transporter MCT3 [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 98	409.2796	816.5446	816.4025	0.1421	1	15	18	1	U	--MGAGGPRR.G + Oxidation (M)

Proteins matching the same set of peptides:

NP_037488.2	Mass: 52285	Score: 15	Matches: 1(0)	Sequences: 1(0)
monocarboxylate transporter 3 [Homo sapiens]				
EAW60214.1	Mass: 52257	Score: 15	Matches: 1(0)	Sequences: 1(0)
solute carrier 16 (monocarboxylic acid transporters), member 8, isoform CRA_a [Homo sapiens]				

16. [AAM28904.1](#) Mass: 31010 Score: 14 Matches: 1(0) Sequences: 1(0)
HUS1B [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 405	421.7930	1683.1429	1682.9679	0.1749	0	14	1.5	1	U	R.RPPLTVAVELVSSLGR.A

Proteins matching the same set of peptides:

NP_683762.2	Mass: 30962	Score: 14	Matches: 1(0)	Sequences: 1(0)
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checkpoint protein HUS1B [Homo sapiens]

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
218	472.8165	943.6184	943.6066	0.0118	1	25	2.1	1	1	SSVKAVILK
128	421.7940	841.5734	841.5022	0.0712	0	23	2.4	1	1	GITLSVRP
150	428.8073	855.6000	855.5178	0.0823	0	22	3	1	1	LASIVTPR
417	897.9971	1793.9796	1793.9321	0.0475	0	20	4.4	1	1	CLGLHFLSLGMVYLR + Carbamidomethyl (C); Oxidation
129	421.7990	841.5834	841.5022	0.0813	0	18	6.3	1	1	GITLSVRP
251	523.3513	1044.6881	1044.6583	0.0298	0	16	13	1	1	LLTTFLLPIK
248	523.3378	1044.6610	1044.6179	0.0432	0	16	17	1	1	ILAINSSSLK
250	523.3413	1044.6680	1044.6583	0.0097	0	16	17	1	1	LLTTFLLPIK
97	409.2698	816.5251	816.4566	0.0685	1	15	21	1	1	TASGRGLR
127	421.2634	840.5123	840.5797	-0.0674	1	15	15	1	1	AAKVILK
247	523.3351	1044.6557	1044.6179	0.0378	0	14	25	1	1	ILAINSSSLK
190	445.1618	888.3091	888.4739	-0.1648	1	14	29	1	1	QLLGKADL + Carbamidomethyl (C)
246	523.3291	1044.6436	1044.5564	0.0872	0	14	27	1	1	LSSDGLQVAR
102	412.7892	823.5639	823.5392	0.0247	0	14	17	1	1	VRPLALR
326	428.8075	1283.4008	1283.6002	-0.1995	1	13	7.4	1	1	LEAMCFDGVKR + Oxidation (M)
118	418.2603	834.5061	834.5327	-0.0266	1	13	29	1	1	KVPVPPAK
149	428.8057	855.5968	855.5290	0.0678	1	13	25	1	1	IALKQQR
243	518.3139	1034.6133	1034.4927	0.1206	1	12	37	1	1	MGIGRSEGGK + Oxidation (M)
148	428.7974	855.5802	855.5429	0.0373	0	12	28	1	1	LVLSSLPK
193	446.2846	890.5546	890.4532	0.1015	0	12	50	1	1	MITTQGPK + Oxidation (M)
211	462.2237	922.4328	922.5124	-0.0795	0	12	40	1	1	AISSSAIFK
233	493.3341	984.6537	984.4586	0.1951	0	12	34	1	1	MVPSDPPDK
178	439.3211	876.6276	876.5181	0.1095	1	11	35	1	1	KQLVSFR
240	513.3287	1024.6428	1024.6030	0.0398	0	11	45	1	1	IGGIGTVPVGR
346	445.1624	1332.4654	1332.6285	-0.1631	1	11	27	1	1	RTTSTCGFFWK
169	435.8103	869.6060	869.4607	0.1453	0	11	39	1	1	VAEAVPER
73	402.2701	802.5256	802.4912	0.0343	1	10	51	1	1	IATKAATK
219	474.2802	946.5459	946.4616	0.0843	0	10	72	1	1	MNPLCLLQ + Oxidation (M)
147	428.7953	855.5761	855.5178	0.0583	0	10	48	1	1	LSIIPASR
393	536.2000	1605.5782	1605.6152	-0.0370	0	10	29	1	1	MGGMGIMGMPPGMGK + 4 Oxidation (M)
268	536.8229	1071.6313	1071.5672	0.0641	1	10	88	1	1	NLEANVEKR
133	423.2588	844.5031	844.5018	0.0013	0	9	99	1	1	LSTLGINK
367	744.4580	1486.9015	1486.7674	0.1340	1	9	53	1	1	NANSQKLLGCLR + Carbamidomethyl (C)
249	523.3385	1044.6624	1044.5564	0.1061	0	9	75	1	1	LSSDGLQVAR
244	520.3591	1038.7036	1038.5399	0.1637	1	9	49	1	1	FGRWAGFAK
309	421.2366	1260.6879	1260.6462	0.0417	0	9	1.3e+02	1	1	GLEWVSAISGSR
194	447.2000	892.3854	892.4072	-0.0218	1	9	93	1	1	MGREEQK + Oxidation (M)
210	460.3097	918.6048	918.4957	0.1091	1	8	1e+02	1	1	VGLARMEK + Oxidation (M)
177	439.2336	876.4526	876.4301	0.0225	0	8	1.1e+02	1	1	NASSLSGDK
185	441.3460	880.6775	880.5130	0.1645	0	8	20	1	1	ELITLHR
391	401.1995	1600.7687	1600.8097	-0.0409	0	8	98	1	1	GQDEVSLANSPLPFK
343	441.2122	1320.6149	1320.6166	-0.0017	0	7	1.2e+02	1	1	SGVGVAVTMEPCR + Oxidation (M)
260	530.3199	1058.6252	1058.5468	0.0784	1	7	1.2e+02	1	1	QKAENNSLR
143	427.2860	852.5574	852.4164	0.1410	0	7	83	1	1	LAAFMER + Oxidation (M)
107	414.2741	826.5337	826.4409	0.0928	1	7	82	1	1	SPRAGPSR
109	415.1855	828.3564	828.4705	-0.1141	0	7	1.1e+02	1	1	DQVVGLAK
72	402.2342	802.4538	802.3834	0.0704	1	7	1.1e+02	1	1	RWGGGDR
267	536.2000	1070.3854	1070.5244	-0.1389	0	7	1.1e+02	1	1	NPDVQEEIK
371	509.3356	1524.9850	1524.8511	0.1338	1	7	39	1	1	SQPDKQLTSLPALK
259	530.3176	1058.6206	1058.5906	0.0299	1	7	1.4e+02	1	1	GMIVQVKER
209	455.3000	908.5854	908.4320	0.1534	1	7	1.2e+02	1	1	RVGGMSMR + Oxidation (M)
266	536.1861	1070.3577	1070.4121	-0.0544	0	7	92	1	1	MDMGTQSGSR + 2 Oxidation (M)
132	423.2542	844.4939	844.4403	0.0536	1	7	1.9e+02	1	1	EEARGQVK
168	435.8088	869.6031	869.4429	0.1602	0	7	97	1	1	TPCPSLPR
154	429.6771	857.3396	857.4719	-0.1323	1	7	1.6e+02	1	1	GGAELRGAK
282	599.3774	1196.7402	1196.5608	0.1794	1	6	1.1e+02	1	1	IEMGRSFADR + Oxidation (M)
388	401.1883	1600.7242	1600.7708	-0.0466	0	6	1.3e+02	1	1	EYHIPCPYQAVPK + Carbamidomethyl (C)
463	898.6625	3590.6207	3590.6951	-0.0744	1	6	39	1	1	TISFTRCVIQMSVSYTMGSTECLLVAVMAYDR + Oxidation (M)
389	401.1949	1600.7507	1600.7708	-0.0201	0	6	1.4e+02	1	1	EYHIPCPYQAVPK + Carbamidomethyl (C)
350	446.8870	1337.6391	1337.6550	-0.0160	0	6	2.1e+02	1	1	TDFHIPHACLK + Carbamidomethyl (C)
93	409.1998	816.3851	816.4341	-0.0491	1	6	1.6e+02	1	1	QPESKTK
357	463.1675	1386.4807	1386.6206	-0.1399	1	6	66	1	1	MNARTYMDVMR
108	414.7982	827.5818	827.4865	0.0954	1	6	1.4e+02	1	1	VPDTLRK
356	462.1885	1383.5438	1383.7068	-0.1630	0	5	1.3e+02	1	1	LGADAPLANTAEPK
96	409.2624	816.5103	816.3912	0.1191	0	5	1.9e+02	1	1	ISCQGPGR + Carbamidomethyl (C)
172	437.2764	872.5383	872.5079	0.0303	1	5	2.5e+02	1	1	EATSKLGR
84	406.3155	810.6164	810.4599	0.1564	0	5	45	1	1	GPGLKPK
375	518.9977	1553.9712	1553.7726	0.1987	0	5	80	1	1	IYTPGSTNYNPSLK
86	407.2391	812.4636	812.4756	-0.0120	0	5	1.1e+02	1	1	LVTQAPGK
145	428.2942	854.5738	854.4208	0.1530	1	5	1.3e+02	1	1	KDTLYIC
142	427.2000	852.3854	852.4229	-0.0374	0	5	1.5e+02	1	1	LTLEFSSG
131	423.2000	844.3854	844.4290	-0.0436	0	5	2.8e+02	1	1	AVAAEQK
424	925.5415	1849.0684	1848.9729	0.0955	0	5	1.1e+02	1	1	MEMNFNILEEILIK
207	455.2728	908.5310	908.4617	0.0693	1	5	2e+02	1	1	RGWFTSR
365	738.9566	1475.8986	1475.7959	0.1028	0	5	1.4e+02	1	1	LVMNPYFFINIR
348	445.3000	1332.8782	1332.6894	0.1888	0	5	90	1	1	MASVPSIGCLLAR + Oxidation (M)
351	447.2000	1338.5782	1338.6754	-0.0973	1	5	2e+02	1	1	APKSGFEGMFIK
395	808.9783	1615.9420	1615.7631	0.1789	0	4	1.6e+02	1	1	YTFSPDTPHISHSK
136	425.2355	848.4565	848.4215	0.0350	1	4	2.3e+02	1	1	GFKMHLT + Oxidation (M)
361	480.1962	1437.5667	1437.7584	-0.1918	1	4	1.6e+02	1	1	APRCLLDPIGPMR
191	445.3000	888.5854	888.4553	0.1302	0	4	3e+02	1	1	DGGVIDSVK

<input checked="" type="checkbox"/>	85	407.2229	812.4313	812.4028	0.0285	0	4	1.4e+02	1	SITSSYR
<input checked="" type="checkbox"/>	65	400.2000	798.3854	798.3694	0.0160	0	4	1.3e+02	1	FVSVGMR + Oxidation (M)
<input checked="" type="checkbox"/>	121	419.3472	836.6799	836.4868	0.1931	0	4	16	1	APQPVVAR
<input checked="" type="checkbox"/>	241	513.3482	1024.6818	1024.5202	0.1616	1	4	1.9e+02	1	GFWRQPER
<input checked="" type="checkbox"/>	159	432.2817	862.5489	862.4185	0.1304	0	4	2.6e+02	1	TVAAPSGFN
<input checked="" type="checkbox"/>	122	419.3485	836.6825	836.4868	0.1957	0	4	17	1	APQPVVAR
<input checked="" type="checkbox"/>	234	494.3219	986.6293	986.6389	-0.0096	1	4	2.8e+02	1	RILLGIFR
<input checked="" type="checkbox"/>	151	429.1345	856.2544	856.3762	-0.1219	0	4	96	1	HACAGWR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	117	417.1000	832.1854	832.3675	-0.1820	0	4	35	1	ENAEQSR
<input checked="" type="checkbox"/>	324	428.7981	1283.3724	1283.5539	-0.1816	0	4	37	1	LSCPECWPHR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	327	428.8112	1283.4118	1283.5539	-0.1422	0	3	88	1	LSCPECWPHR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	220	475.6601	949.3057	949.4473	-0.1417	0	3	2.6e+02	1	CAALMASR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	339	656.3828	1310.7511	1310.6540	0.0971	0	3	2.8e+02	1	MEPAPGLVEQPK + Oxidation (M)
<input checked="" type="checkbox"/>	198	449.2908	896.5670	896.5304	0.0366	1	3	2.7e+02	1	NRPLKNR
<input checked="" type="checkbox"/>	222	477.3141	952.6136	952.4502	0.1635	0	3	2.5e+02	1	SEFNLESK
<input checked="" type="checkbox"/>	347	445.2000	1332.5782	1332.7415	-0.1633	1	3	3.1e+02	1	GHQVPPVWKQR
<input checked="" type="checkbox"/>	152	429.2617	856.5088	856.3241	0.1847	0	3	3.9e+02	1	MGLDMCR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	173	437.2805	872.5464	872.4790	0.0674	0	3	4.3e+02	1	KPPMATTK
<input checked="" type="checkbox"/>	64	400.0631	798.1116	798.3000	-0.1884	0	3	4.4	1	MGEMSGR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	423	925.4000	1848.7854	1848.7915	-0.0060	0	3	2.6e+02	1	YESNGEGWTTSAAGTYR
<input checked="" type="checkbox"/>	192	446.2639	890.5132	890.4531	0.0601	0	3	4.2e+02	1	LMQQIDK + Oxidation (M)
<input checked="" type="checkbox"/>	101	411.2326	820.4507	820.3450	0.1057	0	3	2.7e+02	1	EADEETK
<input checked="" type="checkbox"/>	170	436.2328	870.4511	870.5650	-0.1140	1	2	3.6e+02	1	KASLALIR
<input checked="" type="checkbox"/>	153	429.3477	856.6809	856.4879	0.1930	1	2	2.4e+02	1	ANAIGRGA
<input checked="" type="checkbox"/>	66	400.2025	798.3904	798.3396	0.0508	0	2	2e+02	1	YTVDNST
<input checked="" type="checkbox"/>	95	409.2406	816.4667	816.4276	0.0391	0	2	3.7e+02	1	CILNAAR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	120	419.3453	836.6761	836.4868	0.1892	0	2	26	1	APQPVVAR
<input checked="" type="checkbox"/>	312	423.5000	1267.4782	1267.5649	-0.0867	1	2	2.8e+02	1	CRCLGLNTSSTG + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	139	425.8035	849.5925	849.4014	0.1910	0	2	3.5e+02	1	TQMAEVR + Oxidation (M)
<input checked="" type="checkbox"/>	232	493.2691	984.5236	984.5175	0.0062	1	2	3.8e+02	1	VETICHRK
<input checked="" type="checkbox"/>	342	440.5601	1318.6585	1318.6135	0.0450	1	2	3.9e+02	1	CWAGTCRPRR + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	457	925.4000	2773.1782	2773.3421	-0.1640	1	2	1.6e+02	1	EAFFTLFDETQIWICKPTASNOGK
<input checked="" type="checkbox"/>	325	428.8023	1283.3852	1283.5782	-0.1931	0	2	68	1	EETQYFPGPTR
<input checked="" type="checkbox"/>	269	537.1996	1072.3846	1072.5699	-0.1853	1	2	3.4e+02	1	ENRLAMPVR + Oxidation (M)
<input checked="" type="checkbox"/>	438	509.3403	2033.3320	2033.2109	0.1211	1	2	13	1	AALGEGKLLVNVTVRPGLAR
<input checked="" type="checkbox"/>	434	487.3058	1945.1942	1945.0633	0.1309	0	2	1e+02	1	ALAILSQPTPSLVVDHER
<input checked="" type="checkbox"/>	212	925.4000	924.3927	924.4375	-0.0448	0	2	3.9e+02	1	DALMANFK + Oxidation (M)
<input checked="" type="checkbox"/>	296	411.2117	1230.6132	1230.5703	0.0429	0	2	4.6e+02	1	LSCGASGFTFNK
<input checked="" type="checkbox"/>	104	413.2788	824.5430	824.3520	0.1909	0	2	2.4e+02	1	MMEAATR + Oxidation (M)
<input checked="" type="checkbox"/>	189	443.2787	884.5429	884.6059	-0.0630	1	2	3.8e+02	1	KAILTLVK
<input checked="" type="checkbox"/>	174	437.2813	872.5480	872.4902	0.0578	1	2	5.7e+02	1	VTPCLGKR
<input checked="" type="checkbox"/>	355	692.4032	1382.7919	1382.6686	0.1233	1	2	3.8e+02	1	RMGIGMAEFLDK + Oxidation (M)
<input checked="" type="checkbox"/>	100	411.2200	820.4255	820.4364	-0.0110	0	2	3.4e+02	1	DIVVTMK + Oxidation (M)
<input checked="" type="checkbox"/>	412	883.9793	1765.9440	1765.9098	0.0342	1	2	4.7e+02	1	FTNLLTSLDSEATKN
<input checked="" type="checkbox"/>	422	463.1732	1848.6636	1848.7982	-0.1346	0	2	1.4e+02	1	VIQCHGDVGEASGSSEMK + Oxidation (M)
<input checked="" type="checkbox"/>	125	419.3581	836.7016	836.5120	0.1896	0	1	11	1	APLQPLAK
<input checked="" type="checkbox"/>	126	420.2000	838.3854	838.3863	-0.0009	0	1	3.3e+02	1	CVMAMLR + Oxidation (M)
<input checked="" type="checkbox"/>	221	476.3035	950.5925	950.4379	0.1547	0	1	5e+02	1	SQELAMEK + Oxidation (M)
<input checked="" type="checkbox"/>	275	548.3887	1094.7628	1094.5682	0.1946	0	1	2.5e+02	1	MLPLSDIYK + Oxidation (M)
<input checked="" type="checkbox"/>	262	531.6891	1061.3636	1061.5479	-0.1843	1	1	4e+02	1	VHQETRRH
<input checked="" type="checkbox"/>	113	416.2668	830.5190	830.3923	0.1268	0	1	5.3e+02	1	FPEGPER
<input checked="" type="checkbox"/>	460	754.1373	3012.5199	3012.6623	-0.1424	0	1	2.4e+02	1	LSWGSTAVQLFILTIVTVFGLLAPLACHR
<input checked="" type="checkbox"/>	202	451.2749	900.5353	900.4818	0.0535	0	1	5.8e+02	1	VPPTGQFR
<input checked="" type="checkbox"/>	311	423.2000	1266.5782	1266.6204	-0.0422	1	1	5.2e+02	1	AVERSSTFENK
<input checked="" type="checkbox"/>	171	437.2645	872.5144	872.4789	0.0355	1	1	6.9e+02	1	EAMPKVK
<input checked="" type="checkbox"/>	394	537.2229	1608.6469	1608.8332	-0.1863	0	1	3.6e+02	1	TRPGAPAPGGGTSALGSR
<input checked="" type="checkbox"/>	105	413.2860	824.5575	824.3810	0.1765	1	1	3e+02	1	TCRSSGSK
<input checked="" type="checkbox"/>	254	527.6792	1053.3438	1053.4471	-0.1033	0	1	3.9e+02	1	GMGLDAMEK + Oxidation (M)
<input checked="" type="checkbox"/>	214	469.3588	936.7031	936.5392	0.1639	1	0	1.4e+02	1	SLLGKTYR
<input checked="" type="checkbox"/>	402	835.5263	1669.0381	1668.8981	0.1400	1	0	2.1e+02	1	LLLEKQAGGNPCLTGR
<input checked="" type="checkbox"/>	83	406.2795	810.5444	810.4058	0.1386	0	0	2.5e+02	1	MGIVYGR + Oxidation (M)
<input checked="" type="checkbox"/>	140	426.2981	850.5817	850.3967	0.1850	0	0	4.3e+02	1	LSSMQGGR + Oxidation (M)
<input checked="" type="checkbox"/>	92	408.3499	814.6853	814.5065	0.1788	0	0	1.1e+02	1	IPFLGIR
<input checked="" type="checkbox"/>	180	440.3000	878.5854	878.3891	0.1963	0	0	1e+03	1	MAHMAFR + Oxidation (M)
<input checked="" type="checkbox"/>	225	481.3179	960.6213	960.5756	0.0457	1	0	7.1e+02	1	ILQKQGFK
<input checked="" type="checkbox"/>	235	503.2000	1004.3854	1004.4828	-0.0974	0	0	6.6e+02	1	TYNAPHFR
<input checked="" type="checkbox"/>	1	400.3812	399.3740							
<input checked="" type="checkbox"/>	2	401.1915	400.1842							
<input checked="" type="checkbox"/>	3	402.2018	401.1945							
<input checked="" type="checkbox"/>	4	402.2026	401.1953							
<input checked="" type="checkbox"/>	5	402.2092	401.2019							
<input checked="" type="checkbox"/>	6	403.2072	402.1999							
<input checked="" type="checkbox"/>	7	403.2080	402.2007							
<input checked="" type="checkbox"/>	8	403.2433	402.2360							
<input checked="" type="checkbox"/>	9	403.4000	402.3927							
<input checked="" type="checkbox"/>	10	404.2328	403.2255							
<input checked="" type="checkbox"/>	11	405.4000	404.3927							
<input checked="" type="checkbox"/>	12	405.4000	404.3927							
<input checked="" type="checkbox"/>	13	405.4000	404.3927							
<input checked="" type="checkbox"/>	14	415.4000	414.3927							
<input checked="" type="checkbox"/>	15	415.4000	414.3927							
<input checked="" type="checkbox"/>	16	416.4000	415.3927							
<input checked="" type="checkbox"/>	17	416.4000	415.3927							
<input checked="" type="checkbox"/>	18	416.4000	415.3927							
<input checked="" type="checkbox"/>	19	417.1000	416.0927							
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Type of search : MS/MS Ion Search
Enzyme : Trypsin
Variable modifications : [Carbamidomethyl \(C\)](#), [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 0.2 Da
Fragment Mass Tolerance : ± 0.2 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 463

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