Table 3a. Proteins identified from gel-based separation of RelA-TA affinity pull-down in three cell types

Same as Table 1, but includes number of peptides and percentages of sequence recovery

Band	Acc no#	MW	Abbr	THP1 score	pep	%cov	JURKAT score	pep	%cov	HeLa score	pep	% cov	Description
1	no id	-	- -	-	-	-	-	-	-	-	-	-	-
2	P78527	473	DNA-PKcs	175	5	1	137	5	1	1126	36	8	DNA-dependent protein kinase catalytic subunit
3+4	Q92793	268	CBP	137	3	1	675	16	7	245	8	4	CREB-binding protein
3+4	Q09472	265	p300	229	5	2	594	15	7	212	7	2	E1A-associated protein p300
3+4	O75691	318	DRIM	-			747	18	6	-	-	-	DRIM protein
5	Q92616	293	hGCN1	-	-	-	403	15	7	-	-	-	KIAA0219 protein. Human GCN1-like-1
6	no id	-	-	-	-	-	-	-	-	-	-	-	-
7	Q09472	265	p300	-	-	-	-	-	-	111	3	1	E1A-associated protein p300
8	Q86VI3	185	IQGAP3	69	4	2	-	-	-	67*	3	1	Ras GTPase-activating-like protein IQGAP3
	P46940	189	IQGAP1	-	-	-	-	-	-	67*	3	1	Ras GTPase-activating-like protein IQGAP1
9a	P53621	139	COPA	305	8	5	-	-	-	736	22	18	Coatomer alpha subunit
9b	Q9P0V5	148	MYBBP1A	187	5	4	773	21	17	351	12	9	MYB-binding protein 1A

all database accession number are according to UNIPROT (SWISSPROT+TrEMBL)

* only peptides in common to the sequences of IQGAP1, IQGAP3 were matched, therefore it is impossible to discriminate between the two proteins"

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Table 3b. Proteins identified from gel-based separation of RelA-TA affinity pull-down in three cell types
Raw mascot outputs

job#

Band 2 - THP1 - 8302

Search title : 220604_QT_MOH_cty3_b52.wiff : Owen celltype3 manual cut

Significant hits: PRKD_HUMAN (P78527) DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37) (DNA-PKcs) (DNPK1) (p460)

1 PRKD_HUMAN Mass: 473749 Score: 175 Queries matched: 6

(P78527) DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37) (DNA-PKcs) (DNPK1) (p460)

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
129	394.8	787.58	787.43	0.14	0	30	0.2	1	APGLGAFR
240	442.84	883.66	883.55	0.11	0	28	0.21	1	LLQIIER
252	447.85	893.68	893.5	0.18	0	15	4.3	2	LLNFLMK + Oxidation (M)
300	473.37	944.73	944.57	0.16	0	29	0.2	1	MAVLALLAK + Oxidation (M)
305	478.88	955.74	955.57	0.17	0	59	0.00014	1	LLEEALLR
405	552.37	1102.72	1102.56	0.16	0	17	2.7	1	LQETLSAADR

seq. coverage =1%

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Band 2 - Jurkat - 8298

Search title : 220604_QT_MOH_cty3_b23_24.wiff : Owen celltype3 manual cut

Significant hits: PRKD_HUMAN (P78527) DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37) (DNA-PKcs) (DNPK1) (p460)

1 PRKD_HUMAN Mass: 473749 Score: 137 Queries matched: 6

(P78527) DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37) (DNA-PKcs) (DNPK1) (p460)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
48	394.8	787.59	787.43	0.16	0	32	0.25	1	APGLGAFR
110	447.83	893.66	893.5	0.15	0	15	9.4	2	LLNFLMK + Oxidation (M)
143	478.87	955.72	955.57	0.15	0	30	0.29	1	LLEEALLR
205	575.42	1148.82	1148.64	0.18	0	14	9.8	1	AALSALESFLK
212	588.4	1174.79	1174.62	0.17	0	17	6.4	1	VTELALTASDR
262	670.45	1338.89	1338.75	0.13	0	34	0.087	1	QLFSSLFSGILK

seq. coverage =1%

==========

Band 2 - HeLa - 8299

Search title : 220604_QT_MOH_cty3_b3.wiff : Owen celltype3 manual cut

Significant hits: PRKD_HUMAN (P78527) DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37) (DNA-PKcs) (DNPK1) (p460)

1 PRKD_HUMAN Mass: 473749 Score: 1126 Queries matched: 36

(P78527) DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37) (DNA-PKcs) (DNPK1) (p460)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
81	378.29	754.57	754.46	0.11	0	23	0.54	1	VPADLLK
103	389.29	776.57	776.44	0.13	0	21	1.3	1	AFLGELK
129	394.82	787.63	787.43	0.2	0	34	0.066	1	APGLGAFR
140	397.3	792.58	792.44	0.14	0	26	0.35	1	IGELFSK
187	416.84	831.66	831.52	0.14	0	22	1	1	VFLALAAK
199	423.37	844.73	844.52	0.22	0	21	1.2	1	TFPVLLR
254	442.85	883.69	883.55	0.14	0	36	0.037	1	LLQIIER
265	447.85	893.68	893.5	0.17	0	33	0.058	1	LLNFLMK + Oxidation (M)

277 453.33 904.65 904.48 0.17 0 30 0.15 1
LLQDFNR
280 458.32 914.62 914.48 0.14 0 33 0.076 1
LPSNTLDR
281 460.33 918.65 918.53 0.12 0 22 0.96 1
VIAGLYQR
297 467.33 932.64 932.51 0.13 0 29 0.18 1
YAVPSAGLR
301 470.83 939.64 939.47 0.18 0 16 2.5 1
TETVTSFR
303 473.38 944.74 944.57 0.17 0 42 0.0095 1
MAVLALLAK + Oxidation (M)
308 478.86 955.71 955.57 0.14 0 64 4.10E-05 1
LLEEALLR
310 483.31 964.62 964.5 0.12 0 15 5.1 1 SLNSIEFR
311 485.87 969.73 969.57 0.16 0 28 0.17 1
LPVLAGCLK
316 491.3 980.59 980.46 0.12 0 15 3.3 1
MYAALGDPK + Oxidation (M)
321 505.35 1008.69 1008.56 0.12 0 28 0.19 1
EIFNFVLK
324 510.35 1018.68 1018.57 0.11 0 25 0.42 1
IAPYSVEIK
330 519.4 1036.79 1036.6 0.19 0 32 0.066 1
LPLISGFYK
343 526.35 1050.69 1050.53 0.15 0 34 0.046 1
SIGEYDVLR
344 526.85 1051.69 1051.55 0.13 0 31 0.074 1
GIFTSEIGTK
402 552.38 1102.75 1102.56 0.19 0 47 0.0028 1
LQETLSAADR
443 575.37 1148.73 1148.64 0.08 0 34 0.042 1
AALSALESFLK
449 578.87 1155.72 1155.58 0.15 0 16 2.7 1
LGLPGDEVDNK
467 588.4 1174.78 1174.62 0.16 0 65 4.20E-05 1
VTELALTASDR
502 603.47 1204.92 1204.73 0.19 0 23 0.55 1
LGNPIVPLNIR
511 609.91 1217.82 1217.7 0.11 0 48 0.002 1
LLALNSLYSPK
533 627.93 1253.84 1253.65 0.19 0 25 0.33 1
AYVPALQMAFK + Oxidation (M)
575 650.94 1299.87 1299.71 0.16 0 41 0.0077 1
QITQSALLAEAR
589 442.99 1325.96 1325.74 0.22 1 28 0.15 1
QGNLSSQVPLKR
598 669.93 1337.84 1337.71 0.13 0 65 3.30E-05 1
LGASLAFNNIYR
600 671.93 1341.84 1341.72 0.12 0 25 0.3 1
FMNAVFFLLPK + Oxidation (M)
643 730.51 1459.01 1458.79 0.23 0 36 0.027 1
VVQMLGSLGGQINK + Oxidation (M)
678 574.01 1719.01 1718.94 0.07 0 35 0.025 1
EMKPVIFLDVFLPR + Oxidation (M)

seq. coverage =8%

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Band 3+4 - THP1 - 11861

Search title : 250105_QS_MQ_MOH_Ct4_T5_6_include_OWEN- with inclusion list CBP

"Significant hits: K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
" K1CI_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"
P300_HUMAN (Q09472) E1A-associated protein p300 (EC 2.3.1.48)

" K22E_HUMAN (P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)"
" K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"
CBP_HUMAN (Q92793) CREB-binding protein (EC 2.3.1.48)

" K1CN_HUMAN (P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)"
" K2C4_HUMAN (P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)"
Q96RF1 (Q96RF1) HEJ1

1 K2C1_HUMAN Mass: 66018 Score: 1322 Queries matched: 48

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
2	401.7	801.39	801.43	-0.05	1	21	1.4	8	EREQIK
43	473.2	944.39	944.49	-0.11	1	42	0.0081		1 GENALKDAK
46	487.2	972.39	972.52	-0.14	0	-52	0.00088		1 IEISELNR
47	487.24	972.47	972.52	-0.05	0	53	0.00071		1 IEISELNR
50	500.2	998.39	998.44	-0.05	0	-39	0.016		1 DVDGAYMTK
51	500.21	998.4	998.44	-0.04	0	42	0.0073		1 DVDGAYMTK
54	503.69	1005.36	1005.42	-0.06	0	19	1.9		1 GGSGGGGGGSSGGR
61	517.2	1032.39	1032.51	-0.12	0	29	0.2		1 TLLEGEESR
62	517.24	1032.46	1032.51	-0.05	0	-20	1.1		1 TLLEGEESR
82	546.7	1091.39	1091.5	-0.11	0	46	0.0033		1 GSGGGSSGGSIGGR
91	563.2	1124.39	1124.53	-0.15	0	55	0.00045		1 AEAESLYQSK

96 571.2 1140.39 1140.51 -0.13 0 54 0.00059 1
DYQELMNTK
98 571.23 1140.45 1140.51 -0.06 0 -43 0.0057 1
DYQELMNTK
99 579.2 1156.39 1156.51 -0.12 0 -29 0.21 1
DYQELMNTK + Oxidation (M)
106 590.3 1178.59 1178.59 -0.01 0 65 3.30E-05 1
YEELQITAGR
136 633.29 1264.56 1264.63 -0.07 0 -27 0.21 1
TNAENEFVTIK
137 633.3 1264.59 1264.63 -0.04 0 52 0.00059 1
TNAENEFVTIK
138 639.3 1276.59 1276.7 -0.12 0 54 0.00035 1
LALDLEIATYR
139 639.32 1276.63 1276.7 -0.07 0 -53 0.00055 1
LALDLEIATYR
144 650.7 1299.39 1299.52 -0.14 0 54 0.00067 1
NMQDMVEDYR
145 651.8 1301.59 1301.71 -0.12 0 61 7.50E-05 1
SLDLDSIIAEVK
146 651.82 1301.63 1301.71 -0.08 0 -45 0.0035 1
SLDLDSIIAEVK
152 658.7 1315.39 1315.52 -0.13 0 -44 0.0092 1
NMQDMVEDYR + Oxidation (M)
153 658.73 1315.45 1315.52 -0.07 0 -41 0.013 1
NMQDMVEDYR + Oxidation (M)
161 447.5 1339.48 1339.66 -0.18 1 30 0.12 1
SKAEAESLYQSK
162 670.8 1339.59 1339.66 -0.08 1 -29 0.14 1
SKAEAESLYQSK
164 670.81 1339.61 1339.66 -0.06 1 -14 3.9 2
SKAEAESLYQSK
167 679.3 1356.59 1356.69 -0.1 0 78 1.60E-06 1
LNDLEDALQQAK
170 692.3 1382.59 1382.68 -0.1 0 74 4.30E-06 1
SLNNQFASFIDK
175 465.2 1392.58 1392.72 -0.15 1 54 0.00039 1
TNAENEFVTIKK
176 697.3 1392.59 1392.72 -0.14 1 -24 0.46 1
TNAENEFVTIKK
177 465.22 1392.65 1392.72 -0.07 1 -28 0.16 1
TNAENEFVTIKK
178 697.34 1392.66 1392.72 -0.06 1 -21 0.78 1
TNAENEFVTIKK
190 738.3 1474.59 1474.74 -0.16 0 42 0.0074 1
WELLQQVDTSTR
191 738.36 1474.71 1474.78 -0.07 0 -64 4.00E-05 1
FLEQQNQVLQTK
192 738.4 1474.79 1474.78 0.01 0 68 1.50E-05 1
FLEQQNQVLQTK
220 533.9 1598.68 1598.83 -0.15 1 51 0.00077 1
NKLNDLEDALQQAK
221 800.39 1598.76 1598.83 -0.07 1 -17 1.9 2
NKLNDLEDALQQAK
239 546.9 1637.68 1637.85 -0.17 1 35 0.034 1
SLNNQFASFIDKVR

240 546.93 1637.76 1637.85 -0.1 1 -24 0.35 1
SLNNQFASFIDKVR
248 829.4 1656.79 1656.79 0 0 79 9.70E-07 1
SGGGFSSGSAGIINYQR
265 858.89 1715.76 1715.84 -0.09 0 -19 1.1 1
QISNLQQSISDAEQR
266 858.9 1715.79 1715.84 -0.06 0 52 0.00046 1
QISNLQQSISDAEQR
314 648 1940.98 1940.98 0 1 36 0.016 1
LNDLEDALQQAKEDLAR
323 665.29 1992.85 1992.97 -0.12 0 -18 1.1 1
THNLEPYFESFINNLR
324 665.3 1992.88 1992.97 -0.09 0 54 0.0003 1
THNLEPYFESFINNLR
396 795.28 2382.83 2382.94 -0.12 0 28 0.17 1
GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR
397 795.3 2382.88 2382.94 -0.07 0 -14 4 1
GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR

2 K1CI_HUMAN Mass: 62178 Score: 763 Queries matched: 31

"(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
6 405.2 808.39 808.43 -0.05 0 42 0.0067 1
LASYLDK
7 405.2 808.39 808.43 -0.04 0 -25 0.33 1 LASYLDK
33 449.18 896.35 896.41 -0.05 0 -31 0.087 1
MTLDDFR
34 449.2 896.39 896.41 -0.02 0 40 0.01 1 MTLDDFR
37 457.18 912.35 912.4 -0.05 0 -18 1.8 1 MTLDDFR
+ Oxidation (M)
38 457.2 912.39 912.4 -0.02 0 -39 0.014 1 MTLDDFR +
Oxidation (M)
67 530.76 1059.5 1059.56 -0.05 0 42 0.0084 1
TLLDIDNTR
68 530.8 1059.59 1059.56 0.03 0 -41 0.0095 1
TLLDIDNTR
70 533.2 1064.39 1064.49 -0.11 0 42 0.0089 1
STMQELNSR
71 533.22 1064.43 1064.49 -0.06 0 -34 0.047 1
STMQELNSR

78 541.2 1080.39 1080.49 -0.1 0 -29 0.15 1
STMQELNSR + Oxidation (M)
88 561.27 1120.52 1120.58 -0.05 0 -54 0.0005 1
QEYEQLIAK
89 561.3 1120.59 1120.58 0.01 0 57 0.00022 1
QEYEQLIAK
100 579.27 1156.53 1156.58 -0.06 0 -51 0.00089 1
QGVDADINGLR
101 579.3 1156.59 1156.58 0 0 74 4.30E-06 1
QGVDADINGLR

114 603.78 1205.54 1205.6 -0.05 0 23 0.54 1
QVLDNLTMEK + Oxidation (M)
115 603.8 1205.59 1205.6 -0.01 0 -22 0.63 1
QVLDNLTMEK + Oxidation (M)
126 618.2 1234.39 1234.52 -0.14 0 66 4.40E-05 1
FSSSSGYGGGSSR
127 618.24 1234.46 1234.52 -0.06 0 -60 0.00013 1
FSSSSGYGGGSSR
148 654.3 1306.59 1306.67 -0.08 1 24 0.4 1
IKFEMEQNLR
285 896.3 1790.59 1790.72 -0.13 0 99 2.00E-08 1
GGSGGSYGGGGSGGGYGGGSGSR
294 613.29 1836.85 1836.96 -0.11 0 -53 0.00039 1
HGVQELEIELQSQLSK
295 613.3 1836.88 1836.96 -0.08 0 64 3.20E-05 1
HGVQELEIELQSQLSK
384 767 2297.98 2298.11 -0.13 1 35 0.021 1
SDLEMQYETLQEELMALKK
390 777.7 2330.08 2330.1 -0.02 1 -16 1.3 1
SDLEMQYETLQEELMALKK + 2 Oxidation (M)
394 793 2375.98 2376.18 -0.2 1 18 1.3 1
LASYLDKVQALEEANNDLENK
413 837.3 2508.88 2509.12 -0.25 0 44 0.0038 1
EIETYHNLLEGGQEDFESSGAGK
414 837.34 2508.99 2509.12 -0.13 0 -21 0.66 1
EIETYHNLLEGGQEDFESSGAGK
430 902.36 2704.05 2704.15 -0.11 0 -22 0.54 1
GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR
431 902.4 2704.18 2704.15 0.02 0 77 1.30E-06 1
GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR
461 1088.8 3263.38 3263.51 -0.13 0 18 0.78 1
DIENQYETQITQIEHEVSSSGQEVQSSAK

3 P300_HUMAN Mass: 266881 Score: 229 Queries matched: 8

(Q09472) E1A-associated protein p300 (EC 2.3.1.48)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
44 475.2 948.39 948.5 -0.12 0 43 0.0058 1 LGTFLENR
45 475.23 948.45 948.5 -0.05 0 -30 0.13 1 LGTFLENR
52 502.2 1002.39 1002.53 -0.14 0 22 0.91 1 LQQAQMLR
+ Oxidation (M)
79 541.69 1081.36 1081.52 -0.17 0 49 0.0019 1
MENLVAYAR + Oxidation (M)
81 544.68 1087.35 1087.53 -0.18 0 44 0.0092 1
QDPESLPFR
214 790.9 1579.79 1579.9 -0.11 0 15 2.5 1
LVQAIFPTPDPAALK
299 617.98 1850.93 1851.03 -0.1 1 -38 0.012 1
LVQAIFPTPDPAALKDR
300 618 1850.98 1851.03 -0.05 1 56 0.00018 1
LVQAIFPTPDPAALKDR

seq. coverage =2%

4 K22E_HUMAN Mass: 66110 Score: 189 Queries matched: 7

"(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
46	487.2	972.39	972.52	-0.14	0	-52	0.00088	1	IEISELNR
47	487.24	972.47	972.52	-0.05	0	53	0.00071	1	IEISELNR
108	597.28	1192.54	1192.61	-0.07	0	43	0.0051	1	YEELQVTVGR
109	597.3	1192.59	1192.61	-0.02	0	-16	2.4	1	YEELQVTVGR
186	730.9	1459.79	1459.79	-0.01	0	27	0.18	1	VDLLNQEIEFLK
191	738.36	1474.71	1474.78	-0.07	0	-64	4.00E-05	1	FLEQQNQVLQTK
192	738.4	1474.79	1474.78	0.01	0	68	1.50E-05	1	FLEQQNQVLQTK

5 K1CJ_HUMAN Mass: 59711 Score: 169 Queries matched: 8

"(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4	404.18	806.35	806.39	-0.04	0	-42	0.0071	1	LAADDFR
5	404.2	806.39	806.39	-0.01	0	45	0.0039	1	LAADDFR
6	405.2	808.39	808.43	-0.05	0	42	0.0067	1	LASYLDK
7	405.2	808.39	808.43	-0.04	0	-25	0.33	1	LASYLDK
87	555.2	1108.39	1108.48	-0.1	0	17	2.9	1	DAEAWFNEK
174	695.8	1389.59	1389.67	-0.09	0	45	0.0029	1	QSLEASLAETEGR
195	498.56	1492.65	1492.73	-0.08	1	20	1.1	1	SQYEQLAEQNRK
196	498.6	1492.78	1492.73	0.05	1	-17	1.8	1	SQYEQLAEQNRK

Proteins matching the same set of peptides:

Q8N175 Mass: 59020 Score: 169 Queries matched: 8

(Q8N175) Keratin 10

6 CBP_HUMAN Mass: 268019 Score: 137 Queries matched: 5

(Q92793) CREB-binding protein (EC 2.3.1.48)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
52 502.2 1002.39 1002.53 -0.14 0 22 0.91 1 LQQAQLMR
+ Oxidation (M)
81 544.68 1087.35 1087.53 -0.18 0 44 0.0092 1
QDPESLPFR
214 790.9 1579.79 1579.9 -0.11 0 15 2.5 1
LVQAIFPTPDPAALK
299 617.98 1850.93 1851.03 -0.1 1 -38 0.012 1
LVQAIFPTPDPAALKDR
300 618 1850.98 1851.03 -0.05 1 56 0.00018 1
LVQAIFPTPDPAALKDR

seq. coverage =1%

7 K1CN_HUMAN Mass: 51744 Score: 111 Queries matched: 6

"(P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
4 404.18 806.35 806.39 -0.04 0 -42 0.0071 1
LAADDFR
5 404.2 806.39 806.39 -0.01 0 45 0.0039 1
LAADDFR
6 405.2 808.39 808.43 -0.05 0 42 0.0067 1
LASYLDK
7 405.2 808.39 808.43 -0.04 0 -25 0.33 1 LASYLDK
57 515.27 1028.53 1028.59 -0.05 0 23 0.56 1
VLDELTLAR
58 515.3 1028.59 1028.59 0 0 -19 1.4 1
VLDELTLAR

Proteins matching the same set of peptides:

K1CO_HUMAN Mass: 49365 Score: 111 Queries matched: 6

"(P19012) Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15)"

K1CP_HUMAN Mass: 51447 Score: 111 Queries matched: 6

"(P08779) Keratin, type I cytoskeletal 16 (Cytokeratin 16) (K16) (CK 16)"

K1CQ_HUMAN Mass: 48230 Score: 111 Queries matched: 6

"(Q04695) Keratin, type I cytoskeletal 17 (Cytokeratin 17) (K17) (CK 17) (39.1)"

K1CS_HUMAN Mass: 44079 Score: 111 Queries matched: 6

"(P08727) Keratin, type I cytoskeletal 19 (Cytokeratin 19) (K19) (CK 19)"

Q6NW33 Mass: 46179 Score: 111 Queries matched: 6

(Q6NW33) KRT19 protein (Fragment)

Q7L5M9 Mass: 45587 Score: 111 Queries matched: 6

(Q7L5M9) Keratin 19 (Fragment)

Q8N1P6 Mass: 47859 Score: 111 Queries matched: 6

(Q8N1P6) Hypothetical protein FLJ38023

Q96A53 Mass: 44065 Score: 111 Queries matched: 6

(Q96A53) Keratin 19

Q96FV1 Mass: 45870 Score: 111 Queries matched: 6

(Q96FV1) KRT19 protein (Fragment)

8 K2C4_HUMAN Mass: 57602 Score: 71 Queries matched: 3

"(P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
138	639.3	1276.59	1276.7	-0.12	0	54	0.00035	1	LALDIEIATYR
139	639.32	1276.63	1276.7	-0.07	0	-53	0.00055	1	LALDIEIATYR
167	679.3	1356.59	1356.72	-0.14	0	17	2.6	2	NLDLDSIIAEVR

Proteins matching the same set of peptides:

Q9BTL1 Mass: 35750 Score: 71 Queries matched: 3

(Q9BTL1) KRT4 protein (Fragment)

9 Q96RF1 Score: 47 Queries matched: 2

(Q96RF1) HEJ1

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide

88 561.27 1120.52 1120.61 -0.09 0 -43 0.0054 2
EQYSAVIIAK
89 561.3 1120.59 1120.61 -0.03 0 47 0.0026 2
EQYSAVIIAK

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Band 3+4 - Jurkat - 11289

Search title : OWEN LAST CHANCE - 271104_QS_MOH_Ct4_J5_6

Significant hits: O75691 (O75691) DRIM protein
CBP_HUMAN (Q92793) CREB-binding protein (EC 2.3.1.48)
P300_HUMAN (Q09472) E1A-associated protein p300 (EC 2.3.1.48)
" K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1
(Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
" K1CI_HUMAN (P35527) Keratin, type I cytoskeletal 9
(Cytokeratin 9) (K9) (CK 9)"
" K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10
(Cytokeratin 10) (K10) (CK 10)"
" K2C4_HUMAN (P19013) Keratin, type II cytoskeletal 4
(Cytokeratin 4) (K4) (CK4)"
" K22E_HUMAN (P35908) Keratin, type II cytoskeletal 2
epidermal (Cytokeratin 2e) (K2e) (CK 2e)"
Q96S69 (Q96S69) Pex1pQ261Ter
Q8NFL1 (Q8NFL1) Cdc42-interaction protein 4 long isoform
Q6ZMZ3 (Q6ZMZ3) Hypothetical protein FLJ16564
ACIN_HUMAN (Q9UKV3) Apoptotic chromatin condensation inducer
in the nucleus (Acinus)

1 O75691 Mass: 320846 Score: 747 Queries matched: 26

(O75691) DRIM protein
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
24 419.3 836.59 836.46 0.12 0 15 3.8 1 YITDVVK
29 426.3 850.59 850.5 0.09 0 17 2.3 1 YFPLLAK
33 432.2 862.39 862.43 -0.04 0 47 0.0023 1
LNAFDQR
34 432.24 862.46 862.43 0.03 0 -36 0.033 1
LNAFDQR
45 442.3 882.59 882.46 0.13 0 30 0.13 1 FLTFAER
52 453.8 905.59 905.46 0.12 0 38 0.021 1 LEAAYSPR
58 467.3 932.59 932.54 0.04 0 60 0.00014 1
QSVFAILR
64 487.8 973.59 973.56 0.03 0 34 0.048 1 ELSPLFLR
65 487.81 973.6 973.56 0.04 0 -34 0.056 1 ELSPLFLR
66 496.3 990.59 990.56 0.03 0 20 1.2 1
VPLAFAMVK + Oxidation (M)
67 496.3 990.59 990.56 0.03 0 -17 2.5 1
VPLAFAMVK + Oxidation (M)

88 529.8 1057.59 1057.54 0.05 0 68 2.30E-05 1
VVNDEEVVR
94 534.86 1067.7 1067.66 0.04 0 40 0.0091 1
LGTVLPVIEK
95 534.9 1067.79 1067.66 0.13 0 -32 0.062 1
LGTVLPVIEK
110 564.8 1127.59 1127.59 -0.01 0 58 0.00017 1
LAVSAQSEPAR
111 564.83 1127.64 1127.59 0.05 0 -41 0.0087 1
LAVSAQSEPAR
112 570.3 1138.59 1138.47 0.12 0 28 0.16 1
DIMEETEEK + Oxidation (M)
129 602.9 1203.79 1203.75 0.04 0 47 0.0023 1
LLETYLILVK
130 602.9 1203.79 1203.75 0.05 0 -32 0.074 1
LLETYLILVK
167 650.4 1298.79 1298.74 0.04 0 47 0.002 1
NLSQEIIELLK
190 681.89 1361.76 1361.72 0.04 0 -21 0.72 1
FLDQSLGEQVVK
191 681.9 1361.79 1361.72 0.07 0 62 5.60E-05 1
FLDQSLGEQVVK
208 739.4 1476.79 1476.75 0.04 0 42 0.0065 1
FETFQTITSYIK
209 739.41 1476.8 1476.75 0.05 0 -19 1.3 1
FETFQTITSYIK
234 788.4 1574.79 1574.8 -0.02 0 62 5.70E-05 1
GPLSQEALMELFPK + Oxidation (M)
259 818.9 1635.79 1635.8 -0.01 0 38 0.013 1
ELNSTYSEQDPLLK

seq. coverage =6%

2 CBP_HUMAN Mass: 268019 Score: 675 Queries matched: 23

(Q92793) CREB-binding protein (EC 2.3.1.48)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
31 429.77 857.53 857.5 0.03 0 -22 0.98 2 QLSELLR
32 429.8 857.59 857.5 0.09 0 29 0.18 1 QLSELLR
37 436.3 870.59 870.42 0.17 0 15 3.8 1 LYATMEK
+ Oxidation (M)
51 453.77 905.53 905.5 0.04 0 -25 0.36 1 DAFLTLAR
53 453.8 905.59 905.5 0.09 0 34 0.055 1 DAFLTLAR
69 502.3 1002.59 1002.53 0.06 0 14 4.5 2 LQQAQLMR
+ Oxidation (M)
71 502.8 1003.59 1003.54 0.05 0 32 0.089 1
TVEVKPGMK + Oxidation (M)
76 516.3 1030.59 1030.58 0 0 26 0.28 1 IFKPEELR
78 516.32 1030.62 1030.58 0.04 0 -21 0.94 1
IFKPEELR
103 544.79 1087.56 1087.53 0.03 0 -26 0.34 1
QDPESLPFR

104 544.8 1087.59 1087.53 0.06 0 48 0.0021 1
QDPESLPFR
121 595.78 1189.55 1189.51 0.04 0 -43 0.0055 1
ELEQEEEER
122 595.8 1189.59 1189.51 0.08 0 55 0.00039 1
ELEQEEEER
134 607.8 1213.59 1213.59 0 0 37 0.019 1
VNINNSMPPGR + Oxidation (M)
135 607.83 1213.64 1213.59 0.05 0 -20 1.1 1
VNINNSMPPGR + Oxidation (M)
144 618.28 1234.54 1234.64 -0.09 0 21 0.87 1
SNPQLMAAFIK + Oxidation (M)
198 711.4 1420.79 1420.74 0.05 0 40 0.0078 1
QALMPTLEALYR + Oxidation (M)
204 735.9 1469.78 1469.74 0.05 0 -28 0.14 1
SPLSQGDSSAPSLPK
205 735.9 1469.79 1469.74 0.05 0 74 3.90E-06 1
SPLSQGDSSAPSLPK
236 791 1579.99 1579.9 0.09 0 43 0.0043 1
LVQAIFPTPDPAALK
266 825.9 1649.79 1649.7 0.08 0 53 0.00036 2
FVDSGEMSESFPYR
303 898 1793.99 1793.96 0.02 0 59 8.80E-05 1
SPSSPQQQQQVLNILK
347 1012 2021.99 2022 -0.01 0 94 2.30E-08 1
SALSSELSLVGDTTGDTLEK

seq. coverage =7%

3 P300_HUMAN Mass: 266881 Score: 594 Queries matched: 24

(Q09472) E1A-associated protein p300 (EC 2.3.1.48)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
31 429.77 857.53 857.5 0.03 0 -22 0.98 2 QLSELLR
32 429.8 857.59 857.5 0.09 0 29 0.18 1 QLSELLR
37 436.3 870.59 870.42 0.17 0 15 3.8 1 LYATMEK
+ Oxidation (M)
51 453.77 905.53 905.5 0.04 0 -25 0.36 1 DAFLTLAR
53 453.8 905.59 905.5 0.09 0 34 0.055 1 DAFLTLAR
60 475.28 948.54 948.5 0.04 0 57 0.00028 1
LGTFLENR
61 475.3 948.59 948.5 0.08 0 -49 0.0017 1 LGTFLENR
69 502.3 1002.59 1002.53 0.06 0 18 2 1 LQQAQMLR
+ Oxidation (M)
71 502.8 1003.59 1003.54 0.05 0 32 0.089 1
TVEVKPGMK + Oxidation (M)
76 516.3 1030.59 1030.58 0 0 26 0.28 1 IFKPEELR
78 516.32 1030.62 1030.58 0.04 0 -21 0.94 1
IFKPEELR
101 541.79 1081.57 1081.52 0.04 0 -26 0.29 1
MENLVAYAR + Oxidation (M)

102 541.8 1081.59 1081.52 0.06 0 58 0.00016 1
MENLVAYAR + Oxidation (M)
103 544.79 1087.56 1087.53 0.03 0 -26 0.34 1
QDPESLPFR
104 544.8 1087.59 1087.53 0.06 0 48 0.0021 1
QDPESLPFR
121 595.78 1189.55 1189.51 0.04 0 -43 0.0055 1
ELEQEEEER
122 595.8 1189.59 1189.51 0.08 0 55 0.00039 1
ELEQEEEER
198 711.4 1420.79 1420.74 0.05 0 40 0.0078 1
QALMPTLEALYR + Oxidation (M)
236 791 1579.99 1579.9 0.09 0 43 0.0043 1
LVQAIFPTPDPAALK
265 825.89 1649.76 1649.7 0.05 0 -21 0.71 1
FVDSGEMAESFPYR + Oxidation (M)
266 825.9 1649.79 1649.7 0.08 0 66 1.90E-05 1
FVDSGEMAESFPYR + Oxidation (M)
425 843.79 2528.34 2528.25 0.09 0 -23 0.24 1
ITPQSGLNQFGQMSMAQPPIVPR + 2 Oxidation (M)
426 843.8 2528.38 2528.25 0.13 0 51 0.00043 1
ITPQSGLNQFGQMSMAQPPIVPR + 2 Oxidation (M)
498 1054.3 4213.17 4213.16 0.01 0 22 0.12 1
NQQPILTGAPVGLGNPSSLGVGQQSAPNLSTVSQIDPSSIER

seq. coverage =7%

4 K2C1_HUMAN Mass: 66018 Score: 533 Queries matched: 22

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
40 437.8 873.59 873.49 0.09 0 31 0.12 1
SLVNLGGSK
62 487.29 972.56 972.52 0.04 0 -31 0.11 1
IEISELNR
63 487.3 972.59 972.52 0.06 0 50 0.0015 1
IEISELNR
73 508.2 1014.39 1014.43 -0.05 0 18 1.9 1
DVDGAYMTK + Oxidation (M)
81 517.28 1032.55 1032.51 0.04 0 -20 1.1 1
TLLEGEESR
82 517.3 1032.59 1032.51 0.08 0 28 0.21 1
TLLEGEESR
107 546.78 1091.55 1091.5 0.05 0 -19 1.6 1
GSGGGSSGGSIGGR
108 546.8 1091.59 1091.5 0.09 0 51 0.0009 1
GSGGGSSGGSIGGR
158 633.3 1264.59 1264.63 -0.04 0 -50 0.0011 1
TNAENEFVTIK
159 633.34 1264.67 1264.63 0.04 0 54 0.00036 1
TNAENEFVTIK

162 639.39 1276.76 1276.7 0.05 0 -59 0.00011 1
LALDLEIATYR
163 639.4 1276.79 1276.7 0.08 0 68 1.70E-05 1
LALDLEIATYR
168 651.89 1301.76 1301.71 0.05 0 56 0.00027 1
SLDLDSIIAEVK
169 651.9 1301.79 1301.71 0.08 0 -55 0.00028 1
SLDLDSIIAEVK
186 679.38 1356.75 1356.69 0.06 0 -32 0.073 1
LNDLEDALQQAK
187 679.4 1356.79 1356.69 0.1 0 53 0.00059 1
LNDLEDALQQAK
193 465.27 1392.78 1392.72 0.05 1 21 0.74 1
TNAENEFVTIKK
194 465.3 1392.88 1392.72 0.15 1 -20 0.89 1
TNAENEFVTIKK
206 738.4 1474.79 1474.74 0.04 0 47 0.0017 1
WELLQQVDTSTR
207 738.41 1474.8 1474.74 0.05 0 -34 0.035 1
WELLQQVDTSTR
341 665.36 1993.06 1992.97 0.09 0 -41 0.0048 1
THNLEPYFESFINNLR
342 665.4 1993.18 1992.97 0.21 0 61 5.90E-05 1
THNLEPYFESFINNLR

5 K1CI_HUMAN Mass: 62178 Score: 444 Queries matched: 16

"(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
7 405.2 808.39 808.43 -0.05 0 41 0.0099 1
LASYLDK
8 405.24 808.46 808.43 0.03 0 -33 0.057 1
LASYLDK
54 457.2 912.39 912.4 -0.02 0 -32 0.068 1 MTLDDFR +
Oxidation (M)
55 457.22 912.43 912.4 0.03 0 48 0.0017 1
MTLDDFR + Oxidation (M)
89 530.8 1059.59 1059.56 0.03 0 -42 0.0084 1
TLLDIDNTR
90 530.81 1059.6 1059.56 0.04 0 65 4.40E-05 1
TLLDIDNTR
99 541.28 1080.54 1080.49 0.05 0 -23 0.53 1
STMQELNSR + Oxidation (M)
100 541.3 1080.59 1080.49 0.1 0 40 0.0088 1
STMQELNSR + Oxidation (M)
117 579.3 1156.59 1156.58 0 0 70 1.10E-05 1
QGVDADINGLR
118 579.32 1156.62 1156.58 0.04 0 -20 1.1 1
QGVDADINGLR
145 618.29 1234.56 1234.52 0.04 0 -39 0.014 1
FSSSSGYGGGSSR

146 618.3 1234.59 1234.52 0.06 0 62 7.70E-05 1
FSSSSGYGGGSSR
177 441.92 1322.72 1322.67 0.06 1 17 2 1
IKFEMEQNLR + Oxidation (M)
315 613.3 1836.88 1836.96 -0.08 0 68 1.00E-05 1
HGVQELEIELQSQLSK
316 613.35 1837.04 1836.96 0.08 0 -18 1.2 1
HGVQELEIELQSQLSK
422 837.4 2509.18 2509.12 0.05 0 35 0.017 1
EIETYHNLLEGGQEDFESSGAGK

6 K1CJ_HUMAN Mass: 59711 Score: 235 Queries matched: 7

"(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
5 404.2 806.39 806.39 -0.01 0 47 0.0026 1
LAADDFR
6 404.22 806.42 806.39 0.03 0 -46 0.003 1
LAADDFR
7 405.2 808.39 808.43 -0.05 0 41 0.0099 1
LASYLDK
8 405.24 808.46 808.43 0.03 0 -33 0.057 1
LASYLDK
77 516.3 1030.59 1030.59 -0.01 0 50 0.0012 1
VLDELTLTK
109 553.8 1105.59 1105.52 0.07 0 55 0.0004 1
VTMQNLNDR + Oxidation (M)
452 968.8 2903.38 2903.38 0 0 43 0.0022 1
NVSTGDVNVEMNAAPGVDLTQLLNNMR + 2 Oxidation (M)

Proteins matching the same set of peptides:

Q8N175 Mass: 59020 Score: 235 Queries matched: 7

(Q8N175) Keratin 10

7 K2C4_HUMAN Mass: 57602 Score: 90 Queries matched: 4

"(P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
162 639.39 1276.76 1276.7 0.05 0 -59 0.00011 1
LALDIEIATYR
163 639.4 1276.79 1276.7 0.08 0 68 1.70E-05 1
LALDIEIATYR
186 679.38 1356.75 1356.72 0.02 0 -19 1.3 2
NLDLDSIIAEVR

187 679.4 1356.79 1356.72 0.06 0 22 0.67 2
NLDLDSIIAEVR

Proteins matching the same set of peptides:

Q9BTL1 Mass: 35750 Score: 90 Queries matched: 4

(Q9BTL1) KRT4 protein (Fragment)

8 K22E_HUMAN Mass: 66110 Score: 76 Queries matched: 3

"(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)"
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
62 487.29 972.56 972.52 0.04 0 -31 0.11 1
IEISELNR
63 487.3 972.59 972.52 0.06 0 50 0.0015 1
IEISELNR
202 730.9 1459.79 1459.79 -0.01 0 26 0.22 1
VDLLNQEIEFLK

9 Q96S69 Mass: 29213 Score: 40 Queries matched: 2

(Q96S69) Pex1pQ261Ter
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
99 541.28 1080.54 1080.53 0.01 1 -22 0.58 2
GMMKELQTK + Oxidation (M)
100 541.3 1080.59 1080.53 0.05 1 40 0.0088 1
GMMKELQTK + Oxidation (M)

Proteins matching the same set of peptides:

PEX1_HUMAN Mass: 143804 Score: 39 Queries matched: 2

(O43933) Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)
Q96S70 Mass: 71632 Score: 39 Queries matched: 2

(Q96S70) Pex1pR633Ter
10 Q8NFL1 Score: 40 Queries matched: 3

(Q8NFL1) Cdc42-interaction protein 4 long isoform

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
46 442.9 883.79 883.48 0.31 0 18 1.5 4
VAANAVDPK
60 475.28 948.54 948.55 -0.01 1 22 0.83 2
LASFRSLR
61 475.3 948.59 948.55 0.04 1 -21 0.92 3 LASFRSLR

11 Q6ZMZ3 Score: 38 Queries matched: 2

(Q6ZMZ3) Hypothetical protein FLJ16564

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
121 595.78 1189.55 1189.53 0.03 0 -26 0.31 2
ALWEEEEER
122 595.8 1189.59 1189.53 0.06 0 38 0.019 2
ALWEEEEER

Proteins matching the same set of peptides:

Q86SX5 Score: 38 Queries matched: 2

12 ACIN_HUMAN Score: 34 Queries matched: 1

(Q9UKV3) Apoptotic chromatin condensation inducer in the nucleus (Acinus)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
122 595.8 1189.59 1189.55 0.04 0 34 0.048 3
TTSPLEEEER

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Band 3+4 - HeLA - 11853

Search title : 250105_QS_MQ_MOH_Ct4_H5_6_Owen repeat celltype 4 - Heather sypro bands_1_01.tmp

Significant hits: CBP_HUMAN (Q92793) CREB-binding protein (EC 2.3.1.48)

P300_HUMAN (Q09472) E1A-associated protein p300 (EC 2.3.1.48)

" K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"

KCH1_HUMAN (O95259) Potassium voltage-gated channel subfamily H member 1 (Voltage-gated potassium channel subu

Q8TBA7 (Q8TBA7) HSPCA protein

1 CBP_HUMAN Mass: 268019 Score: 245 Queries matched: 8

(Q92793) CREB-binding protein (EC 2.3.1.48)

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
429.7	857.39	857.5	-0.11	0	0	37	0.033	1	QLSELLR
453.7	905.39	905.5	-0.11	0	0	31	0.096	1	DAFLTLAR
544.7	1087.39	1087.53	-0.14	0	0	37	0.034	1	QDPESLPFR
618.3	1234.59	1234.64	-0.05	0	0	15	3.6	1	SNPQLMAAFIK + Oxidation (M)
735.8	1469.59	1469.74	-0.15	0	0	59	0.00016	1	SPLSQGDSSAPSLPK
790.9	1579.79	1579.9	-0.11	0	0	17	1.5	1	LVQAIFPTPDPAALK
637.6	1909.78	1910.02	-0.24	0	0	20	1.1	1	TAVYHEILIGYLEYVK
1012	2021.99	2022	-0.01	0	0	29	0.082	1	SALSSELSLVGDTTGDTLEK

seq. coverage = 4%

2 P300_HUMAN Mass: 266881 Score: 212 Queries matched: 7

(Q09472) E1A-associated protein p300 (EC 2.3.1.48)

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
429.7	857.39	857.5	-0.11	0	0	37	0.033	1	QLSELLR
453.7	905.39	905.5	-0.11	0	0	31	0.096	1	DAFLTLAR
475.2	948.39	948.5	-0.12	0	0	56	0.00033	1	LGTFLENR
504.2	1006.39	1006.5	-0.12	0	0	14	5.1	1	SPMDLSTIK + Oxidation (M)
544.7	1087.39	1087.53	-0.14	0	0	37	0.034	1	QDPESLPFR
790.9	1579.79	1579.9	-0.11	0	0	17	1.5	1	LVQAIFPTPDPAALK
637.6	1909.78	1910.02	-0.24	0	0	20	1.1	1	TAVYHEILIGYLEYVK

seq. coverage = 2%

3 K2C1_HUMAN Mass: 66018 Score: 49 Queries matched: 1

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
68	651.8	1301.59	1301.71	-0.12	0	51	0.00087	1	SLDLDSIIAEVK

4 KCH1_HUMAN Mass: 112435 Score: 37 Queries matched: 1

(O95259) Potassium voltage-gated channel subfamily H member 1 (Voltage-gated potassium channel subu
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
14	429.7	857.39	857.5	-0.11	0	37	0.033	1	QLSEILR

5 Q8TBA7 Mass: 73952 Score: 37 Queries matched: 1

(Q8TBA7) HSPCA protein
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
14	429.7	857.39	857.53	-0.15	1	37	0.033	1	KLSELLR

Proteins matching the same set of peptides:

HS9A_HUMAN Mass: 84889 Score: 37 Queries matched: 1

(P07900) Heat shock protein HSP 90-alpha (HSP 86)

Q86U12 Mass: 49669 Score: 37 Queries matched: 1

(Q86U12) Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human)

Q96HX7 Mass: 49561 Score: 37 Queries matched: 1

(Q96HX7) HSPCA protein (Fragment)

O75322 Mass: 63839 Score: 37 Queries matched: 1

(O75322) Hsp89-alpha-delta-N

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Band 5 - HeLa - - 11876

Search title : 270105_QS_MQ_MOH_Ct4_H7_Heather band sypro Ct4

Significant hits: Q92616 (Q92616) KIAA0219 protein (Fragment)

" K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"

1 Q92616 Mass: 295351 Score: 403 Queries matched: 16

(Q92616) KIAA0219 protein (Fragment)

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
29	445.7	889.39	889.5	-0.12	0	14	5.2	1	FVIQGAGAK
36	456.3	910.59	910.56	0.03	0	16	2.3	1	IPIAVSGVR
61	521.8	1041.59	1041.62	-0.03	0	18	2	1	AIITALGVER
76	573.8	1145.59	1145.61	-0.03	0	28	0.17	1	LMDEAVLALR + Oxidation (M)
77	582.2	1162.39	1162.56	-0.18	0	42	0.011	1	ALADENEFVR
78	588.3	1174.59	1174.63	-0.04	0	21	0.87	1	LMPEIVATASK + Oxidation (M)
80	598.3	1194.59	1194.66	-0.08	0	35	0.028	1	ASLLDPVPEVR
88	619.8	1237.59	1237.63	-0.04	0	15	3	2	VDENGPELLPR
100	643.3	1284.59	1284.73	-0.14	0	69	1.20E-05	1	IIIEDLLEATR
101	643.34	1284.66	1284.73	-0.07	0	-24	0.43	1	IIIEDLLEATR
109	659.3	1316.59	1316.69	-0.11	0	16	2.4	5	SIIQSAQQDSIK
114	667.8	1333.59	1333.72	-0.14	0	39	0.012	1	AYSDQAIVNLLK
147	760.4	1518.79	1518.84	-0.06	0	22	0.69	1	VLAFLSSVAGDALTR
227	638	1910.98	1911.02	-0.04	0	34	0.03	1	VLPLEALVTDAGEVTEAGK
244	508.85	2031.38	2031.2	0.18	1	17	2.6	2	LGEKILPEIIPILEEGLR
249	689.42	2065.24	2065.19	0.05	0	32	0.065	1	LTSADALRPSVVSITGPLIR

seq. coverage =7 %

2 K2C1_HUMAN Mass: 66018 Score: 108 Queries matched: 5

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
59 517.2 1032.39 1032.51 -0.12 0 20 1.3 1
TLLEGEESR
72 546.7 1091.39 1091.5 -0.11 0 15 4.7 1
GSGGGSSGGSIGGR
79 590.3 1178.59 1178.59 -0.01 0 21 0.83 1
YEELQITAGR
105 651.8 1301.59 1301.71 -0.12 0 53 0.00051 1
SLDLDSIIAEVK
106 651.82 1301.63 1301.71 -0.08 0 -17 1.8 2
SLDLDSIIAEVK
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Band 7 - HeLa - 11876

Search title : OWEN LAST CHANCE - 271104_QS_MOH_Ct4_H8

"Significant hits: K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"

" K1CI_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

" K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"

P300_HUMAN (Q09472) E1A-associated protein p300 (EC 2.3.1.48)

Q92616 (Q92616) KIAA0219 protein (Fragment)

DDF2_HUMAN (O43150) Development and differentiation-enhancing factor 2 (Pyk2 C-terminus associated protein) (P

Q96RF1 (Q96RF1) HEJ1

1 K2C1_HUMAN Mass: 66018 Score: 713 Queries matched: 21

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
51 437.8 873.59 873.49 0.09 0 16 3.6 1
SLVNLGGSK
70 487.29 972.56 972.52 0.03 0 -35 0.039 1
IEISELNR
71 487.3 972.59 972.52 0.06 0 42 0.0085 1
IEISELNR
75 517.3 1032.59 1032.51 0.08 0 17 2.3 1
TLLEGEESR

90 546.77 1091.53 1091.5 0.04 0 -43 0.0051 1
GSGGGSSGGSIGGR
91 546.8 1091.59 1091.5 0.09 0 67 2.20E-05 1
GSGGGSSGGSIGGR
95 571.28 1140.55 1140.51 0.04 0 -17 2.2 1
DYQELMNTK
96 571.3 1140.59 1140.51 0.07 0 30 0.11 1
DYQELMNTK
101 590.3 1178.59 1178.59 -0.01 0 54 0.00046 1
YEELQITAGR
102 590.32 1178.63 1178.59 0.04 0 -43 0.0056 1
YEELQITAGR
140 633.3 1264.59 1264.63 -0.04 0 59 0.00011 1
TNAENEFVTIK
141 633.34 1264.67 1264.63 0.04 0 -52 0.00056 1
TNAENEFVTIK
149 651.9 1301.79 1301.71 0.08 0 67 1.90E-05 1
SLDLDSIIAEVK
155 658.8 1315.59 1315.52 0.07 0 46 0.003 1
NMQDMVEDYR + Oxidation (M)
162 679.4 1356.79 1356.69 0.1 0 63 5.70E-05 1
LNDLEDALQQAK
175 738.4 1474.79 1474.78 0.01 0 64 4.00E-05 1
FLEQQNQVLQTK
176 738.4 1474.79 1474.74 0.04 0 38 0.015 1
WELLQQVDTSTR
177 738.42 1474.83 1474.78 0.05 0 -25 0.3 1
FLEQQNQVLQTK
219 829.4 1656.79 1656.79 0 0 40 0.0084 1
SGGGFSSGSAGIINYQR
244 859 1715.99 1715.84 0.14 0 70 7.90E-06 1
QISNLQQSISDAEQR
284 665.4 1993.18 1992.97 0.21 0 45 0.0022 1
THNLEPYFESFINNLR

2 K1CI_HUMAN Mass: 62178 Score: 332 Queries matched: 15

"(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
57 449.2 896.39 896.41 -0.02 0 -26 0.23 1 MTLDDFR
58 449.23 896.44 896.41 0.03 0 -20 1 1
MTLDDFR
61 457.2 912.39 912.4 -0.02 0 47 0.0023 1 MTLDDFR
+ Oxidation (M)
62 457.22 912.43 912.4 0.03 0 -18 1.6 1 MTLDDFR
+ Oxidation (M)
79 530.8 1059.59 1059.56 0.03 0 59 0.00017 1
TLLDIDNTR
80 530.8 1059.59 1059.56 0.03 0 -39 0.016 1
TLLDIDNTR
82 533.3 1064.59 1064.49 0.09 0 23 0.53 1
STMQELNSR

87 541.3 1080.59 1080.49 0.1 0 -18 1.5 1
STMQELNSR + Oxidation (M)
93 561.3 1120.59 1120.58 0.01 0 47 0.0026 1
QEYEQLIAK
94 561.32 1120.62 1120.58 0.04 0 -46 0.0029 1
QEYEQLIAK
99 579.3 1156.59 1156.58 0 0 47 0.0023 1
QGVDADINGLR
121 618.28 1234.56 1234.52 0.03 0 -23 0.51 1
FSSSSGYGGGSSR
122 618.3 1234.59 1234.52 0.06 0 41 0.0081 1
FSSSSGYGGGSSR
191 793.9 1585.79 1585.76 0.03 0 28 0.12 1
VQALEEANNDLENK
333 837.4 2509.18 2509.12 0.05 0 41 0.0043 1
EIETYHNLLEGGQEDFESSGAGK

3 K1CJ_HUMAN Mass: 59711 Score: 125 Queries matched: 5

"(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
8 404.2 806.39 806.39 -0.01 0 42 0.0082 1
LAADDFR
10 404.22 806.42 806.39 0.03 0 -34 0.047 1
LAADDFR
73 516.3 1030.59 1030.59 -0.01 0 21 0.93 1
VLDELTLTK
92 553.8 1105.59 1105.52 0.07 0 20 1.4 1
VTMQNLNDR + Oxidation (M)
100 583.3 1164.59 1164.58 0.01 0 43 0.0055 1
LENEIQTYR

Proteins matching the same set of peptides:

Q8N175 Mass: 59020 Score: 125 Queries matched: 5

(Q8N175) Keratin 10

4 P300_HUMAN Mass: 266881 Score: 111 Queries matched: 4

(Q09472) E1A-associated protein p300 (EC 2.3.1.48)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
59 453.77 905.53 905.5 0.03 0 -24 0.56 1 DAFLTLAR
60 453.8 905.59 905.5 0.09 0 42 0.0081 1 DAFLTLAR
69 475.3 948.59 948.5 0.08 0 47 0.0025 1 LGTFLENR
89 544.8 1087.59 1087.53 0.06 0 22 0.83 1
QDPESLPFR

seq. coverage = 1 %

5 Q92616 Mass: 295351 Score: 43 Queries matched: 2

(Q92616) KIAA0219 protein (Fragment)

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
97	573.8	1145.59	1145.61	-0.03	0	27	0.2	1	LMDEAVLALR + Oxidation (M)
198	803	1603.99	1603.95	0.03	0	16	2.6	1	ILPEIIPILEEGLR

Proteins matching the same set of peptides:

O95001 Mass: 264181 Score: 43 Queries matched: 2

(O95001) WUGSC:H_267D11.3 protein (Fragment)

6 DDF2_HUMAN Mass: 112835 Score: 35 Queries matched: 2

(O43150) Development and differentiation-enhancing factor 2 (Pyk2 C-terminus associated protein) (P

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
70	487.29	972.56	972.52	0.03	0	35	0.039	1	EIISEVQR
71	487.3	972.59	972.52	0.06	0	-28	0.22	2	EIISEVQR

7 Q96RF1 Mass: 7522 Score: 35 Queries matched: 2

(Q96RF1) HEJ1

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
93	561.3	1120.59	1120.61	-0.03	0	35	0.036	2	EQYSAVIIAK
94	561.32	1120.62	1120.61	0	0	-20	1.1	2	EQYSAVIIAK

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Band 8 - THP1 - 11291

Search title : OWEN LAST CHANCE - 271104_QS_MOH_Ct4_T_11

"Significant hits: K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
" K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"
" K1CI_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"
" K22E_HUMAN (P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)"
" K2CF_HUMAN (P48669) Keratin, type II cytoskeletal 6F (Cytokeratin 6F) (CK 6F) (K6f keratin)"
" K1CN_HUMAN (P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)"
Q86Y46 (Q86Y46) Keratin 6 irs3
" K2C4_HUMAN (P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)"
" K1CL_HUMAN (Q99456) Keratin, type I cytoskeletal 12 (Cytokeratin 12) (K12) (CK 12)"
" K2C5_HUMAN (P13647) Keratin, type II cytoskeletal 5 (Cytokeratin 5) (K5) (CK 5) (58 kDa cytokeratin)"
IQG3_HUMAN (Q86VI3) Ras GTPase-activating-like protein IQGAP3

" K2C8_HUMAN (P05787) Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)"
Q96RF1 (Q96RF1) HEJ1

PEX1_HUMAN (O43933) Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)

NUMA_HUMAN (Q14980) Nuclear mitotic apparatus protein 1 (NuMA protein) (SP-H antigen)

1 K2C1_HUMAN Mass: 66018 Score: 907 Queries matched: 27

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
58	466.8	931.59	931.5	0.09	1	21	1	1	SEIDNVKK
61	487.29	972.56	972.52	0.04	0	-33	0.063	1	IEISELNR
62	487.3	972.59	972.52	0.06	0	39	0.016	1	IEISELNR
65	500.2	998.39	998.44	-0.05	0	26	0.32	1	DVDGAYMTK
74	517.28	1032.55	1032.51	0.04	0	-38	0.02	1	TLLEGEESR
75	517.3	1032.59	1032.51	0.08	0	45	0.0042	1	TLLEGEESR
92	546.78	1091.54	1091.5	0.04	0	-44	0.0049	1	GSGGGSSGGSIGGR
93	546.8	1091.59	1091.5	0.09	0	84	4.70E-07	1	GSGGGSSGGSIGGR
104	571.28	1140.55	1140.51	0.04	0	48	0.0016	1	DYQELMNTK

105 571.3 1140.59 1140.51 0.07 0 -33 0.059 1
DYQELMNTK
111 590.3 1178.59 1178.59 -0.01 0 -63 5.20E-05 1
YEELQITAGR
112 590.33 1178.64 1178.59 0.05 0 79 1.40E-06 1
YEELQITAGR
148 633.3 1264.59 1264.63 -0.04 0 55 0.00033 1
TNAENEFVTIK
149 633.34 1264.67 1264.63 0.04 0 -18 1.4 1
TNAENEFVTIK
155 651.9 1301.79 1301.71 0.08 0 66 2.30E-05 1
SLDLDSIIAEVK
170 679.38 1356.74 1356.69 0.05 0 -37 0.021 1
LNDLEDALQQAK
171 679.4 1356.79 1356.69 0.1 0 72 6.30E-06 1
LNDLEDALQQAK
175 692.38 1382.74 1382.68 0.05 0 -32 0.058 1
SLNNQFASFIDK
176 692.4 1382.79 1382.68 0.1 0 105 2.90E-09 1
SLNNQFASFIDK
183 465.3 1392.88 1392.72 0.15 1 23 0.46 1
TNAENEFVTIKK
191 738.4 1474.79 1474.78 0.01 0 76 2.20E-06 1
FLEQQNQVLQTK
192 738.4 1474.79 1474.74 0.04 0 -51 0.00077 1
WELLQQVDTSTR
193 738.41 1474.8 1474.74 0.06 0 60 8.40E-05 1
WELLQQVDTSTR
194 738.43 1474.84 1474.78 0.06 0 -65 2.80E-05 1
FLEQQNQVLQTK
271 858.96 1715.9 1715.84 0.06 0 -26 0.21 1
QISNLQQSISDAEQR
272 859 1715.99 1715.84 0.14 0 74 3.20E-06 1
QISNLQQSISDAEQR
319 665.3 1992.88 1992.97 -0.09 0 39 0.0084 1
THNLEPYFESFINNLR

2 K1CJ_HUMAN Mass: 59711 Score: 548 Queries matched: 18

"(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
8 404.2 806.39 806.39 -0.01 0 -46 0.0034 1
LAADDFR
9 404.22 806.43 806.39 0.03 0 47 0.0023 1
LAADDFR
10 405.2 808.39 808.43 -0.05 0 46 0.0031 1
LASYLDK
72 516.3 1030.59 1030.59 -0.01 0 50 0.0012 1
VLDELTLTK
73 516.32 1030.63 1030.59 0.04 0 -31 0.095 1
VLDELTLTK

94 553.8 1105.59 1105.52 0.07 0 22 0.88 1
VTMQNLNDR + Oxidation (M)
97 555.27 1108.53 1108.48 0.05 0 -27 0.18 1
DAEAWFNEK
98 555.3 1108.59 1108.48 0.1 0 28 0.17 1
DAEAWFNEK
108 583.3 1164.59 1164.58 0.01 0 62 5.80E-05 1
LENEIQTYR
109 583.32 1164.62 1164.58 0.04 0 -30 0.1 1
LENEIQTYR
132 412.2 1233.58 1233.67 -0.09 1 -19 1.4 1
LKYENEVALR
133 412.25 1233.72 1233.67 0.05 1 21 0.89 1
LKYENEVALR
146 631.8 1261.59 1261.59 0 0 -48 0.0015 1
SLLEGEGSSGGGGR
147 631.82 1261.63 1261.59 0.05 0 72 6.00E-06 1
SLLEGEGSSGGGGR
174 691.4 1380.79 1380.64 0.14 0 50 0.00092 1
ALEESNYELEGK
181 695.9 1389.79 1389.67 0.11 0 51 0.00081 1
QSLEASLAETEGR
198 498.6 1492.78 1492.73 0.05 1 32 0.063 1
SQYEQLAEQNRK
266 854.4 1706.79 1706.76 0.02 0 67 1.70E-05 1
GSLGGGFSSGGFSGGSFSR

Proteins matching the same set of peptides:

Q8N175 Mass: 59020 Score: 548 Queries matched: 18

(Q8N175) Keratin 10
3 K1CI_HUMAN Mass: 62178 Score: 314 Queries matched: 10

"(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
10 405.2 808.39 808.43 -0.05 0 46 0.0031 1
LASYLDK
52 457.2 912.39 912.4 -0.02 0 33 0.053 1 MTLDDFR +
Oxidation (M)
53 457.22 912.43 912.4 0.03 0 -32 0.062 1 MTLDDFR
+ Oxidation (M)
79 530.8 1059.59 1059.56 0.03 0 54 0.00051 1
TLLDIDNTR
80 530.81 1059.6 1059.56 0.04 0 -52 0.00088 1
TLLDIDNTR
81 533.28 1064.54 1064.49 0.05 0 -29 0.13 1
STMQELNSR
82 533.3 1064.59 1064.49 0.09 0 40 0.01 1
STMQELNSR

100 561.3 1120.59 1120.58 0.01 0 48 0.0018 1
QEYEQLIAK
134 618.3 1234.59 1234.52 0.06 0 28 0.16 1
FSSSSGYGGGSSR
393 837.4 2509.18 2509.12 0.05 0 65 1.70E-05 1
EIETYHNLLEGGQEDFESSGAGK

4 K22E_HUMAN Mass: 66110 Score: 245 Queries matched: 10

"(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)"
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
17 414.2 826.39 826.42 -0.04 0 38 0.016 1 FASFIDK
18 414.23 826.45 826.42 0.03 0 -18 1.6 1
FASFIDK
61 487.29 972.56 972.52 0.04 0 -33 0.063 1
IEISELNR
62 487.3 972.59 972.52 0.06 0 39 0.016 1 IEISELNR
95 554.3 1106.58 1106.54 0.04 0 -24 0.5 2
AQYEEIAQR
96 554.3 1106.59 1106.54 0.05 0 37 0.025 1
AQYEEIAQR
115 597.3 1192.59 1192.61 -0.02 0 29 0.12 1
YEELQVTVGR
188 730.9 1459.79 1459.79 -0.01 0 27 0.19 1
VDLLNQEIEFLK
191 738.4 1474.79 1474.78 0.01 0 76 2.20E-06 1
FLEQQNQVLQTK
194 738.43 1474.84 1474.78 0.06 0 -65 2.80E-05 1
FLEQQNQVLQTK

5 K2CF_HUMAN Mass: 60184 Score: 172 Queries matched: 7

"(P48669) Keratin, type II cytoskeletal 6F (Cytokeratin 6F) (CK 6F) (K6f keratin)"
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
17 414.2 826.39 826.42 -0.04 0 38 0.016 1 FASFIDK
18 414.23 826.45 826.42 0.03 0 -18 1.6 1
FASFIDK
95 554.3 1106.58 1106.54 0.04 0 -24 0.5 2
AQYEEIAQR
96 554.3 1106.59 1106.54 0.05 0 37 0.025 1
AQYEEIAQR
111 590.3 1178.59 1178.59 -0.01 0 -63 5.20E-05 1
YEELQITAGR
112 590.33 1178.64 1178.59 0.05 0 79 1.40E-06 1
YEELQITAGR
118 602.3 1202.59 1202.63 -0.04 0 19 1.3 1
WTLLQEQGTK

6 K1CN_HUMAN Mass: 51744 Score: 153 Queries matched: 5

"(P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
8	404.2	806.39	806.39	-0.01	0	-46	0.0034	1	LAADDFR
9	404.22	806.43	806.39	0.03	0	47	0.0023	1	LAADDFR
10	405.2	808.39	808.43	-0.05	0	46	0.0031	1	LASYLDK
71	515.3	1028.59	1028.59	0	0	40	0.011	1	VLDELTLAR
94	553.8	1105.59	1105.52	0.07	0	22	0.88	1	VTMQNLNDR + Oxidation (M)

Proteins matching the same set of peptides:

K1CP_HUMAN Mass: 51447 Score: 153 Queries matched: 5

"(P08779) Keratin, type I cytoskeletal 16 (Cytokeratin 16) (K16) (CK 16)"

7 Q86Y46 Mass: 59457 Score: 109 Queries matched: 6

(Q86Y46) Keratin 6 irs3
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
17	414.2	826.39	826.42	-0.04	0	38	0.016	1	FASFIDK
18	414.23	826.45	826.42	0.03	0	-18	1.6	1	FASFIDK
95	554.3	1106.58	1106.57	0.01	1	38	0.018	1	AQYEEIARK
96	554.3	1106.59	1106.57	0.01	1	-37	0.025	1	AQYEEIARK
170	679.38	1356.74	1356.72	0.02	0	32	0.069	2	NLDLDSIIAEVR
171	679.4	1356.79	1356.72	0.06	0	-21	0.88	2	NLDLDSIIAEVR

8 K2C4_HUMAN Mass: 57602 Score: 107 Queries matched: 6

"(P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide

17 414.2 826.39 826.42 -0.04 0 38 0.016 1 FASFIDK
18 414.23 826.45 826.42 0.03 0 -18 1.6 1
FASFIDK
95 554.3 1106.58 1106.54 0.04 0 -24 0.5 2
AQYEEIAQR
96 554.3 1106.59 1106.54 0.05 0 37 0.025 1
AQYEEIAQR
170 679.38 1356.74 1356.72 0.02 0 32 0.069 2
NLDLDSIIAEVR
171 679.4 1356.79 1356.72 0.06 0 -21 0.88 2
NLDLDSIIAEVR

9 K1CL_HUMAN Mass: 53592 Score: 90 Queries matched: 2

"(Q99456) Keratin, type I cytoskeletal 12 (Cytokeratin 12) (K12) (CK 12)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
10 405.2 808.39 808.43 -0.05 0 46 0.0031 1
LASYLDK
108 583.3 1164.59 1164.6 -0.02 0 44 0.0037 2
LELEIETYR

10 K2C5_HUMAN Mass: 62651 Score: 75 Queries matched: 4

"(P13647) Keratin, type II cytoskeletal 5 (Cytokeratin 5) (K5) (CK 5) (58 kDa cytokeratin)"
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
17 414.2 826.39 826.42 -0.04 0 38 0.016 1 FASFIDK
18 414.23 826.45 826.42 0.03 0 -18 1.6 1
FASFIDK
118 602.3 1202.59 1202.63 -0.04 0 19 1.3 1
WTLLQEQGTK
154 649.8 1297.59 1297.62 -0.04 0 17 1.8 1
TTAENEFVMLK + Oxidation (M)

Proteins matching the same set of peptides:

Q6PI71 Mass: 62568 Score: 75 Queries matched: 4

(Q6PI71) Keratin 5
11 IQG3_HUMAN Mass: 185173 Score: 69 Queries matched: 4

(Q86VI3) Ras GTPase-activating-like protein IQGAP3

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
36 436.8 871.59 871.48 0.11 0 15 4 2 LQEEVVR
106 572.3 1142.59 1142.63 -0.04 0 23 0.63 1
GQSALQEILGK
177 692.9 1383.79 1383.8 -0.01 0 19 1.1 1
VLAVSLINEALDK
182 465.27 1392.77 1392.63 0.14 1 14 3.6 1
LTAEEMDEQRR + Oxidation (M)

seq.coverage=2%

12 K2C8_HUMAN Mass: 53510 Score: 53 Queries matched: 3

"(P05787) Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
17 414.2 826.39 826.42 -0.04 0 38 0.016 1 FASFIDK
18 414.23 826.45 826.42 0.03 0 -18 1.6 1
FASFIDK
191 738.4 1474.79 1474.69 0.09 0 14 3.5 2
LESGMQNMSIHTK

Proteins matching the same set of peptides:

Q6GMY0 Mass: 53774 Score: 53 Queries matched: 3

(Q6GMY0) Keratin 8
Q6P4C7 Mass: 55874 Score: 53 Queries matched: 3

(Q6P4C7) KRT8 protein (Fragment)

13 Q96RF1 Score: 45 Queries matched: 1

(Q96RF1) HEJ1
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
100 561.3 1120.59 1120.61 -0.03 0 45 0.0033 2
EQYSAVIIAK

14 PEX1_HUMAN Score: 40 Queries matched: 2

(O43933) Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide

81 533.28 1064.54 1064.54 0 1 -29 0.13 1
GMMKELQTK
82 533.3 1064.59 1064.54 0.05 1 40 0.01 1
GMMKELQTK

Proteins matching the same set of peptides:

Q96S69 Score: 40 Queries matched: 2

Q96S70 Score: 40 Queries matched: 2

15 NUMA_HUMAN Score: 39 Queries matched: 2

(Q14980) Nuclear mitotic apparatus protein 1 (NuMA protein) (SP-H antigen)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
3 401.74 801.47 801.43 0.04 1 19 2.1 2
ERDAALK
155 651.9 1301.79 1301.64 0.15 1 20 0.96 2
AEDEWKAQVAR

Proteins matching the same set of peptides:

Q14981 Score: 39 Queries matched: 2

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Band 8 - HeLa - 11971

Search title : 100205_QS_MOH_ct4_H9_b.wiff : OWEN ct4 last bands conc

Significant hits: IQG1_HUMAN (P46940) Ras GTPase-activating-like protein IQGAP1 (p195)

1 IQG1_HUMAN Mass: 189761 Score: 67 Queries matched: 4

(P46940) Ras GTPase-activating-like protein IQGAP1 (p195)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
20 466.19 930.36 930.5 -0.14 0 46 0.0033 1
TALQEEIK
21 466.2 930.39 930.5 -0.12 0 -32 0.08 1 TALQEEIK
32 567.7 1133.39 1133.59 -0.2 0 20 1.6 1
LIFQMPQNK + Oxidation (M)

33 567.71 1133.41 1133.59 -0.18 0 -17 2.7 1
LIFQMPQNK + Oxidation (M)

seq. coverage=1%

Proteins matching the same set of peptides:

IQG3_HUMAN Mass: 185173 Score: 67 Queries matched: 4

(Q86VI3) Ras GTPase-activating-like protein IQGAP3

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Band 9 - THP1 - 11290

Search title : OWEN LAST CHANCE - 271104_QS_MOH_Ct4_T_12_14

"Significant hits: K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
" K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"
" K1CI_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"
COPA_HUMAN (P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
" K1CN_HUMAN (P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)"
Q9BQG0 (Q9BQG0) Hypothetical protein DKFZp761F0324 (Fragment)
" K22E_HUMAN (P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)"
" K2CF_HUMAN (P48669) Keratin, type II cytoskeletal 6F (Cytokeratin 6F) (CK 6F) (K6f keratin)"
" K2C5_HUMAN (P13647) Keratin, type II cytoskeletal 5 (Cytokeratin 5) (K5) (CK 5) (58 kDa cytokeratin)"
" K2C4_HUMAN (P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)"
" K2C8_HUMAN (P05787) Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)"
O6T1_HUMAN (Q8NGN1) Olfactory receptor 6T1
PEX1_HUMAN (O43933) Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)

1 K2C1_HUMAN Mass: 66018 Score: 775 Queries matched: 24

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss Score Expect Rank Peptide
40 437.77 873.53 873.49 0.04 0 31 0.13 1
SLVNLGGSK

41 437.8 873.59 873.49 0.09 0 -29 0.2 1
SLVNLGGSK
63 517.28 1032.55 1032.51 0.04 0 43 0.0066 1
TLLEGEESR
64 517.3 1032.59 1032.51 0.08 0 -32 0.083 1
TLLEGEESR
78 546.8 1091.59 1091.5 0.09 0 67 2.30E-05 1
GSGGGSSGGSIGGR
81 563.3 1124.58 1124.53 0.04 0 -38 0.017 1
AEAESLYQSK
82 563.3 1124.59 1124.53 0.05 0 49 0.0012 1
AEAESLYQSK
83 571.28 1140.55 1140.51 0.04 0 -22 0.72 1
DYQELMNTK
84 571.3 1140.59 1140.51 0.07 0 30 0.1 1
DYQELMNTK
90 590.3 1178.59 1178.59 -0.01 0 59 0.00015 1
YEELQITAGR
91 590.33 1178.64 1178.59 0.05 0 -45 0.0033 1
YEELQITAGR
124 633.3 1264.59 1264.63 -0.04 0 51 0.00082 1
TNAENEFVTIK
125 633.34 1264.67 1264.63 0.04 0 -20 0.91 2
TNAENEFVTIK
135 651.9 1301.79 1301.71 0.08 0 69 1.30E-05 1
SLDLDSIIAEVK
149 679.4 1356.79 1356.69 0.1 0 58 0.00016 1
LNDLEDALQQAK
152 692.4 1382.79 1382.68 0.1 0 77 1.90E-06 1
SLNNQFASFIDK
154 465.27 1392.78 1392.72 0.05 1 -15 3.1 1
TNAENEFVTIKK
155 465.3 1392.88 1392.72 0.15 1 22 0.66 1
TNAENEFVTIKK
160 738.4 1474.79 1474.78 0.01 0 72 6.30E-06 1
FLEQQNQVLQTK
161 738.4 1474.79 1474.74 0.04 0 41 0.0074 1
WELLQQVDTSTR
162 738.41 1474.8 1474.74 0.06 0 -35 0.03 1
WELLQQVDTSTR
163 738.42 1474.83 1474.78 0.05 0 -24 0.4 1
FLEQQNQVLQTK
224 859 1715.99 1715.84 0.14 0 64 3.30E-05 1
QISNLQQSISDAEQR
268 665.4 1993.18 1992.97 0.21 0 47 0.0013 1
THNLEPYFESFINNLR

2 K1CJ_HUMAN Mass: 59711 Score: 346 Queries matched: 11

"(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
4 404.2 806.39 806.39 -0.01 0 -48 0.002 1 LAADDFR

5 404.22 806.43 806.39 0.03 0 54 0.00043 1
LAADDFR
7 405.2 808.39 808.43 -0.05 0 48 0.0019 1
LASYLDK
61 516.3 1030.59 1030.59 -0.01 0 -25 0.43 1
VLDELTLTK
62 516.32 1030.63 1030.59 0.04 0 31 0.097 1
VLDELTLTK
74 545.79 1089.57 1089.52 0.05 0 60 0.00012 1
VTMQNLNDR
75 545.8 1089.59 1089.52 0.06 0 -54 0.00047 1
VTMQNLNDR
79 555.3 1108.59 1108.48 0.1 0 51 0.00083 1
DAEAWFNEK
153 695.9 1389.79 1389.67 0.11 0 29 0.12 1
QSLEASLAETEGR
167 498.6 1492.78 1492.73 0.05 1 18 1.7 1
SQYEQLAEQNRK
219 854.4 1706.79 1706.76 0.02 0 54 0.0003 1
GSLGGGFSSGGFSGGSFSR

Proteins matching the same set of peptides:

Q8N175 Mass: 59020 Score: 346 Queries matched: 11

(Q8N175) Keratin 10
3 K1CI_HUMAN Mass: 62178 Score: 327 Queries matched: 11

"(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
7 405.2 808.39 808.43 -0.05 0 48 0.0019 1
LASYLDK
47 449.2 896.39 896.41 -0.02 0 -31 0.073 1 MTLDDFR
50 457.2 912.39 912.4 -0.02 0 -24 0.44 1 MTLDDFR +
Oxidation (M)
51 457.23 912.44 912.4 0.03 0 43 0.005 1 MTLDDFR
+ Oxidation (M)
69 530.8 1059.59 1059.56 0.03 0 45 0.0041 1
TLLDIDNTR
70 530.8 1059.59 1059.56 0.04 0 -39 0.015 1
TLLDIDNTR
71 533.3 1064.59 1064.49 0.09 0 40 0.011 1
STMQELNSR
86 579.3 1156.59 1156.58 0 0 59 0.00013 1
QGVDADINGLR
87 579.32 1156.63 1156.58 0.05 0 -28 0.16 1
QGVDADINGLR
114 618.3 1234.59 1234.52 0.06 0 47 0.002 1
FSSSSGYGGGSSR
327 837.4 2509.18 2509.12 0.05 0 45 0.0016 1
EIETYHNLLEGGQEDFESSGAGK

4 COPA_HUMAN Mass: 139783 Score: 305 Queries matched: 8

(P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
6	404.7	807.39	807.42	-0.04	0	55	0.00042	1	TGVQTFR
31	430.8	859.59	859.49	0.09	0	20	1.7	1	ISPLQFR
53	474.3	946.59	946.49	0.09	0	42	0.0084	1	DVAVMQLR + Oxidation (M)
54	477.3	952.59	952.54	0.05	0	43	0.0045	1	TALNLFFK
68	528.8	1055.59	1055.53	0.06	0	36	0.03	1	GFFEGTIASK
88	581.8	1161.59	1161.63	-0.04	0	36	0.024	1	VLTIDPTEFK
92	595.9	1189.79	1189.67	0.11	0	18	1.6	1	TLDLPIYVTR
142	666.9	1331.79	1331.78	0	0	56	0.00025	1	LVGQSIIAYLQK

seq.coverage=5%

Proteins matching the same set of peptides:

Q8IXZ9 Mass: 140832 Score: 305 Queries matched: 8

(Q8IXZ9) COPA protein

5 K1CN_HUMAN Mass: 51744 Score: 214 Queries matched: 6

"(P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
4	404.2	806.39	806.39	-0.01	0	-48	0.002	1	LAADDFR
5	404.22	806.43	806.39	0.03	0	54	0.00043	1	LAADDFR
7	405.2	808.39	808.43	-0.05	0	48	0.0019	1	LASYLDK
60	515.3	1028.59	1028.59	0	0	51	0.00096	1	VLDELTLAR
74	545.79	1089.57	1089.52	0.05	0	60	0.00012	1	VTMQNLNDR
75	545.8	1089.59	1089.52	0.06	0	-54	0.00047	1	VTMQNLNDR

Proteins matching the same set of peptides:

K1CP_HUMAN Mass: 51447 Score: 214 Queries matched: 6

"(P08779) Keratin, type I cytoskeletal 16 (Cytokeratin 16) (K16) (CK 16)"

6 Q9BQG0 Mass: 141383 Score: 187 Queries matched: 6

(Q9BQG0) Hypothetical protein DKFZp761F0324 (Fragment)

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
56	494.3	986.59	986.54	0.05	0	45	0.0041	1	SPSLLQSGAK
89	587.4	1172.79	1172.67	0.12	0	38	0.019	1	ALVDILSEVSK
106	614.4	1226.79	1226.75	0.04	0	47	0.0018	1	VLDLVEVLVTK
110	617.35	1232.69	1232.64	0.04	0	-35	0.037	1	EQLMTVLQAGK + Oxidation (M)
111	617.4	1232.79	1232.64	0.14	0	38	0.018	1	EQLMTVLQAGK + Oxidation (M)
148	677.4	1352.79	1352.79	-0.01	0	21	0.77	1	ATLQEILPEVLK

Proteins matching the same set of peptides:

Q9P0V5 Mass: 149727 Score: 187 Queries matched: 6

(Q9P0V5) MYB-binding protein 1A

Q86VM3 Mass: 149750 Score: 187 Queries matched: 6

(Q86VM3) MYB binding protein 1a

seq.coverage=4%

7 K22E_HUMAN Mass: 66110 Score: 163 Queries matched: 4

"(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
15	414.2	826.39	826.42	-0.04	0	29	0.13	1	FASFIDK
96	604.8	1207.59	1207.61	-0.02	0	62	6.70E-05	1	TAAENDFVTLK
160	738.4	1474.79	1474.78	0.01	0	72	6.30E-06	1	FLEQQNQVLQTK
163	738.42	1474.83	1474.78	0.05	0	-24	0.4	1	FLEQQNQVLQTK

8 K2CF_HUMAN Mass: 60184 Score: 87 Queries matched: 3

"(P48669) Keratin, type II cytoskeletal 6F (Cytokeratin 6F) (CK 6F) (K6f keratin)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
15	414.2 826.39	826.42	-0.04	0	29	0.13	1	FASFIDK	
90	590.3 1178.59	1178.59	-0.01	0	59	0.00015	1	YEELQITAGR	
91	590.33 1178.64	1178.59	0.05	0	-45	0.0033	1	YEELQITAGR	

9 K2C5_HUMAN Mass: 62651 Score: 75 Queries matched: 2

"(P13647) Keratin, type II cytoskeletal 5 (Cytokeratin 5) (K5) (CK 5) (58 kDa cytokeratin)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
15	414.2 826.39	826.42	-0.04	0	29	0.13	1	FASFIDK	
93	597.8 1193.59	1193.57	0.02	0	46	0.0027	1	YEELQQTAGR	

Proteins matching the same set of peptides:

Q6PI71 Mass: 62568 Score: 75 Queries matched: 2

(Q6PI71) Keratin 5

10 K2C4_HUMAN Mass: 57602 Score: 63 Queries matched: 2

"(P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
15	414.2 826.39	826.42	-0.04	0	29	0.13	1	FASFIDK	
149	679.4 1356.79	1356.72	0.06	0	34	0.042	2	NLDLDSIIAEVR	

Proteins matching the same set of peptides:

Q86Y46 Mass: 59457 Score: 63 Queries matched: 2

(Q86Y46) Keratin 6 irs3

11 K2C8_HUMAN Mass: 53510 Score: 46 Queries matched: 2

"(P05787) Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
15 414.2 826.39 826.42 -0.04 0 29 0.13 1 FASFIDK
160 738.4 1474.79 1474.69 0.09 0 16 2.2 2
LESGMQNMSIHTK

Proteins matching the same set of peptides:

Q6GMY0 Mass: 53774 Score: 46 Queries matched: 2

(Q6GMY0) Keratin 8
Q6P4C7 Mass: 55874 Score: 46 Queries matched: 2

(Q6P4C7) KRT8 protein (Fragment)

12 O6T1_HUMAN Score: 42 Queries matched: 1

(Q8NGN1) Olfactory receptor 6T1

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
53 474.3 946.59 946.56 0.02 1 42 0.0084 1
LTAVMKLR + Oxidation (M)

13 PEX1_HUMAN Mass: 143804 Score: 40 Queries matched: 1

(O43933) Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
71 533.3 1064.59 1064.54 0.05 1 40 0.011 1
GMMKELQTK

Proteins matching the same set of peptides:

Q96S69 Mass: 29213 Score: 40 Queries matched: 1

(Q96S69) Pex1pQ261Ter
Q96S70 Mass: 71632 Score: 40 Queries matched: 1

(Q96S70) Pex1pR633Ter
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Band 9 - Jurkat - 8282

Search title : 220604_QT_MOH_cty3_m30.wiff : Owen celltype3 manual cut

Significant hits: Q86VM3 (Q86VM3) MYBBP1A protein

NPH4_HUMAN (O75161) Nephrocystin 4 (Nephroretinin)

1 Q86VM3 Mass: 149750 Score: 773 Queries matched: 21

(Q86VM3) MYBBP1A protein

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1	350.8	699.58	699.46	0.12	0	42	0.0074	1	LSLVIR
82	396.27	790.52	790.42	0.1	0	21	1.1	1	GFLPETK
90	403.8	805.58	805.47	0.11	0	42	0.01	1	LLEYLR
114	427.28	852.55	852.45	0.11	0	40	0.011	1	SPAPGAPTR
126	443.34	884.67	884.54	0.12	0	21	0.92	1	LITGLGVGR
131	502.31	1002.61	1002.55	0.05	0	50	0.0012	1	QLMGQVLAK + Oxidation (M)
133	507.82	1013.63	1013.58	0.05	0	34	0.045	1	EVVEQGLLK
172	555.43	1108.84	1108.72	0.12	0	41	0.0094	1	LLGAALPLLTK
199	587.37	1172.72	1172.67	0.06	0	63	5.90E-05	1	ALVDILSEVSK
204	592.87	1183.72	1183.62	0.1	0	31	0.099	1	VPAQANGTPTTK
206	397.61	1189.81	1189.64	0.17	1	14	4.3	1	LVKDQEALMK + Oxidation (M)
216	611.97	1221.93	1221.78	0.15	1	27	0.23	1	KLPAIALDLLR
221	614.43	1226.85	1226.75	0.1	0	72	6.30E-06	1	VLDLVEVLVTK
225	617.41	1232.8	1232.64	0.16	0	50	0.0013	1	EQLMTVLQAGK + Oxidation (M)
233	629.36	1256.71	1256.66	0.05	0	49	0.0013	1	EIPSATQSPISK
244	658.95	1315.89	1315.7	0.19	0	37	0.023	1	VYSTALSSFLTK
248	677.46	1352.91	1352.79	0.12	0	30	0.094	1	ATLQEILPEVLK
250	481.64	1441.9	1441.71	0.18	0	27	0.2	1	HPFSFPLENQAR
255	592.06	1773.16	1772.94	0.22	1	41	0.0071	1	KLVGSVNLFSDENVPR
256	684.15	2049.42	2049.08	0.35	0	26	0.13	1	LLQALAQYQNHLQEQPR

257 698.11 2091.32 2091.03 0.29 0 18 1.1 1
NQKPSQVNGAPGSPTEPAGQK

seq.coverage=17%

2 NPH4_HUMAN Mass: 158754 Score: 42 Queries matched: 1

(O75161) Nephrocystin 4 (Nephroretinin)

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
1 350.8 699.58 699.46 0.12 0 42 0.0074 1
LSLVLR

Proteins matching the same set of peptides:

BAC86471 Mass: 15245 Score: 42 Queries matched: 1

"(BAC86471) CDNA FLJ44184 fis, clone THYMU2038739"

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Band 9 - HeLa - 11877

Search title : 270105_QS_MQ_MOH_Ct4_H10_11_Heather band sypro Ct4

Significant hits: COPA_HUMAN (P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni

Q9P0V5 (Q9P0V5) MYB-binding protein 1A

" K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"

" K1CI_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

1 COPA_HUMAN Mass: 139783 Score: 736 Queries matched: 28

(P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
5 404.7 807.39 807.42 -0.04 0 43 0.0055 1
TGVQTFR
19 426.2 850.39 850.41 -0.02 0 22 0.71 1 FEEAVEK

22	430.7	859.39	859.49	-0.11	0	20	1.6	1	ISPLQFR
51	469.7	937.39	937.45	-0.07	0	25	0.35	1	QLDFNSSK
52	469.7	937.39	937.45	-0.06	0	-19	1.4	1	QLDFNSSK
53	477.2	952.39	952.54	-0.15	0	28	0.19	1	TALNLFFK
56	481.7	961.39	961.47	-0.09	0	14	4.8	1	HVLEGHDR
64	516.2	1030.39	1030.54	-0.16	1	21	1	3	ETLEQQKR
70	528.7	1055.39	1055.53	-0.14	0	39	0.016	1	GFFEGTIASK
85	570.3	1138.59	1138.61	-0.03	0	28	0.15	1	QLFLQTYAR
88	581.8	1161.59	1161.63	-0.04	0	34	0.042	1	VLTIDPTEFK
92	595.8	1189.59	1189.67	-0.09	0	55	0.00037	1	TLDLPIYVTR
93	595.8	1189.59	1189.67	-0.08	0	-30	0.12	1	TLDLPIYVTR
112	622.3	1242.59	1242.62	-0.03	0	48	0.0015	1	NLSPGAVESDVR
122	638.3	1274.59	1274.64	-0.05	0	28	0.16	1	QELILSNSEDK
128	434.87	1301.58	1301.67	-0.1	0	-19	1.1	1	YAVTTGDHGIIR
130	434.9	1301.68	1301.67	0.01	0	28	0.16	1	YAVTTGDHGIIR
138	666.85	1331.69	1331.78	-0.09	0	-40	0.012	1	LVGQSIIAYLQK
139	666.9	1331.79	1331.78	0	0	55	0.00043	1	LVGQSIIAYLQK
158	697.8	1393.59	1393.71	-0.12	0	44	0.0038	1	EYIVGLSVETER
169	740.3	1478.59	1478.73	-0.14	0	55	0.00032	1	DADSITLFDVQQK
170	740.31	1478.62	1478.73	-0.11	0	-36	0.022	1	DADSITLFDVQQK
175	755.4	1508.79	1508.92	-0.13	0	28	0.16	1	SILLSVPLLVVDNK
190	796.9	1591.79	1591.85	-0.06	0	48	0.0013	1	GITGVDLFGTTDAVVK
193	534.27	1599.79	1599.92	-0.13	1	28	0.13	2	VTTVTEIGKDVIGLR
194	534.3	1599.88	1599.92	-0.04	1	-25	0.28	1	VTTVTEIGKDVIGLR
217	560.28	1677.83	1677.94	-0.11	0	-26	0.2	1	LLELGPKPEVAQQTR
218	560.3	1677.88	1677.94	-0.06	0	46	0.0018	1	LLELGPKPEVAQQTR

Proteins matching the same set of peptides:

Q8IXZ9 Mass: 140832 Score: 736 Queries matched: 28

(Q8IXZ9) COPA protein

seq.coverage=12%

2 Q9P0V5 Mass: 149727 Score: 351 Queries matched: 14

(Q9P0V5) MYB-binding protein 1A

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
8	407.7	813.39	813.47	-0.09	0	31	0.11	1	SPLSALAR
32	443.2	884.39	884.54	-0.16	0	19	1.4	1	LITGLGVGR
58	494.2	986.39	986.54	-0.15	0	16	3.6	1	SPSLLQSGAK
59	502.2	1002.39	1002.55	-0.17	0	23	0.7	1	QLMGQVLAK + Oxidation (M)
81	556.7	1111.39	1111.53	-0.14	0	46	0.0035	1	ELEAHSAEAR
89	587.3	1172.59	1172.67	-0.08	0	44	0.0048	1	ALVDILSEVSK
104	614.3	1226.59	1226.75	-0.16	0	-29	0.13	1	VLDLVEVLVTK
105	614.34	1226.66	1226.75	-0.09	0	31	0.07	1	VLDLVEVLVTK
106	617.3	1232.59	1232.64	-0.06	0	36	0.029	1	EQLMTVLQAGK + Oxidation (M)
115	629.3	1256.59	1256.66	-0.08	0	45	0.0036	1	EIPSATQSPISK
149	677.4	1352.79	1352.79	-0.01	0	27	0.18	1	ATLQEILPEVLK
185	518.6	1552.78	1552.8	-0.02	0	14	3.5	1	EQLHLVMQGDVIR + Oxidation (M)
206	823.37	1644.73	1644.85	-0.12	0	23	0.54	1	LVGSVNLFSDENVPR
207	823.4	1644.79	1644.85	-0.06	0	-17	1.8	1	LVGSVNLFSDENVPR

Proteins matching the same set of peptides:

Q86VM3 Mass: 149750 Score: 351 Queries matched: 14

(Q86VM3) MYB binding protein 1a

seq.coverage=9%

3 K2C1_HUMAN Mass: 66018 Score: 72 Queries matched: 3

"(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp"

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

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide

65 517.2 1032.39 1032.51 -0.12 0 26 0.34 1
TLLEGEESR
118 633.3 1264.59 1264.63 -0.04 0 14 3.6 3
TNAENEFVTIK
129 651.8 1301.59 1301.71 -0.12 0 33 0.05 1
SLDLDSIIAEVK

4 K1CI_HUMAN Mass: 62178 Score: 43 Queries matched: 1

"(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)"

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

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
71 533.2 1064.39 1064.49 -0.11 0 43 0.0058 1
STMQELNSR

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Band GT THP-1 negative control (GST only) GT band (same migration as band 9b)

Significant hits: K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp
K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)
K1C9_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)
K22E_HUMAN (P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)
COPA_HUMAN (P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
K1CN_HUMAN (P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)
K2C4_HUMAN (P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)
Q86Y46_HUMAN (Q86Y46) Keratin 6 irs3
PEX1_HUMAN (O43933) Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)
EHD1_HUMAN (Q9H4M9) EH-domain containing protein 1 (Testilin) (hPAST1)
PPRB_HUMAN (Q15648) Peroxisome proliferator-activated receptor binding protein (PBP) (PPAR binding protein) (T

1. K2C1_HUMAN Mass: 66018 Score: 769 Queries matched: 17
(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
53 517.30 1032.59 1032.51 0.08 0 36 0.035 1
TLLEGEESR
71 546.80 1091.59 1091.50 0.09 0 58 0.0002 1
GSGGGSSGGSIGGR
80 563.30 1124.59 1124.53 0.05 0 36 0.03 1
AEAESLYQSK

84 571.30 1140.59 1140.51 0.07 0 27 0.26 1
DYQELMNTK
92 590.30 1178.59 1178.59 -0.01 0 41 0.0094
1 YEELQITAGR
125 633.40 1264.79 1264.63 0.16 0 44 0.0053 1
TNAENEFVTIK
127 639.40 1276.79 1276.70 0.08 0 33 0.064 1
LALDLEIATYR
132 650.80 1299.59 1299.52 0.06 0 56 0.00025 1
NMQDMVEDYR
134 651.90 1301.79 1301.71 0.08 0 56 0.00032 1
SLDLDSIIAEVK
148 679.40 1356.79 1356.69 0.10 0 58 0.0002 1
LNDLEDALQQAK
156 692.40 1382.79 1382.68 0.10 0 44 0.0049 1
SLNNQFASFIDK
163 465.30 1392.88 1392.72 0.15 1 43 0.0077 1
TNAENEFVTIKK
175 738.40 1474.79 1474.78 0.01 0 52 0.0007 1
FLEQQNQVLQTK
176 738.40 1474.79 1474.74 0.04 0 55 0.0003 1
WELLQQVDTSTR
209 534.00 1598.98 1598.83 0.15 1 46 0.003 1
NKLNDLEDALQQAK
243 573.00 1715.98 1715.84 0.13 0 45 0.0032 1
QISNLQQSISDAEQR
311 665.40 1993.18 1992.97 0.21 0 47 0.0023 1
THNLEPYFESFINNLR

2. K1CJ_HUMAN Mass: 59711 Score: 432 Queries matched: 11
(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
4 404.20 806.39 806.39 -0.01 0 42 0.0084
1 LAADDFR
6 405.34 808.67 808.43 0.24 0 41 0.017 1
LASYLDK
52 516.30 1030.59 1030.59 -0.01 0 16 3.5 1
VLDELTLTK
69 545.80 1089.59 1089.52 0.06 0 55 0.00041 1
VTMQNLNDR
75 555.30 1108.59 1108.48 0.10 0 44 0.005 1
DAEAWFNEK
91 583.30 1164.59 1164.58 0.01 0 30 0.11 1
LENEIQTYR
123 631.90 1261.79 1261.59 0.20 0 51 0.0011 1
SLLEGEGSSGGGGR
149 453.30 1356.88 1356.71 0.17 1 32 0.11 1
QSVEADINGLRR
154 691.40 1380.79 1380.64 0.14 0 62 7.2e-05 1
ALEESNYELEGK
160 695.90 1389.79 1389.67 0.11 0 27 0.19 1
QSLEASLAETEGR
238 854.40 1706.79 1706.76 0.02 0 30 0.088 1
GSLGGGFSSGGFSGGSFSR

Proteins matching the same set of peptides:
Q8N175_HUMAN Mass: 59020 Score: 432 Queries matched:
(Q8N175) Keratin 10

3. K1C9_HUMAN Mass: 62178 Score: 360 Queries matched: 10
(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
6	405.34	808.67	808.43	0.24	0	41	0.017		1	LASYLDK
25	449.20	896.39	896.41	-0.02		0	42	0.0074	1	MTLDDFR
60	530.80	1059.59	1059.56	0.03	0	42	0.0091		1	TLLDIDNTR
62	533.30	1064.59	1064.49	0.09	0	52	0.00084		1	STMQELNSR
77	561.28	1120.54	1120.58	-0.04		0	21	1.1	1	QEYEQLIAK
116	618.30	1234.59	1234.52	0.06	0	17	2.7	1		FSSSSGYGGGSSR
138	436.60	1306.78	1306.67	0.11	1	25	0.39	1		IKFEMEQNLR
276	613.40	1837.18	1836.96	0.22	0	68	2.4e-05		1	HGVQELEIELQSQLSK
283	618.00	1850.98	1850.92	0.06	1	24	0.3	1		TLNDMRQEYEQLIAK
408	837.40	2509.18	2509.12	0.05	0	29	0.074		1	EIETYHNLLEGGQEDFESSGAGK

4. K22E_HUMAN Mass: 66110 Score: 248 Queries matched: 8
(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
10	414.20	826.39	826.42	-0.04		0	32	0.084	1	FASFIDK
12	416.30	830.59	830.49	0.10	0	18	3.2	1		SLVGLGGTK
65	534.80	1067.59	1067.50	0.09	0	14	4.1	1		DVDNAYMIK
73	554.30	1106.59	1106.54	0.05	0	32	0.078		1	AQYEEIAQR
95	597.30	1192.59	1192.61	-0.02		0	43	0.0055	1	YEELQVTVGR
122	627.90	1253.79	1253.60	0.19	0	24	0.48	1		GFSSGSAVVSGGSR
172	730.90	1459.79	1459.79	-0.01		0	34	0.04	1	VDLLNQEIEFLK
175	738.40	1474.79	1474.78	0.01	0	52	0.0007		1	FLEQQNQVLQTK

5. COPA_HUMAN Mass: 139783 Score: 244 Queries matched: 9
(P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
18	436.30	870.59	870.49	0.09	0	44	0.0064		1	LNDLIQR
41	477.30	952.59	952.54	0.05	0	24	0.41		1	TALNLFFK
58	528.80	1055.59	1055.53	0.06	0	34	0.047		1	GFFEGTIASK
90	581.90	1161.79	1161.63	0.16	0	19	2.5		1	VLTIDPTEFK
94	595.90	1189.79	1189.67	0.11	0	30	0.18		1	TLDLPIYVTR
119	622.40	1242.79	1242.62	0.17	0	30	0.15		1	NLSPGAVESDVR
126	638.40	1274.79	1274.64	0.15	0	26	0.33		1	QELILSNSEDK
187	755.50	1508.99	1508.92	0.07	0	20	1.9		1	SILLSVPLLVVDNK
231	560.40	1678.18	1677.94	0.24	0	18	2.8		2	LLELGPKPEVAQQTR

Proteins matching the same set of peptides:
Q5T201_HUMAN Mass: 139797 Score: 244 Queries matched: 9
(Q5T201) Coatomer protein complex, subunit alpha
Q8IXZ9_HUMAN Mass: 140832 Score: 244 Queries matched: 9
(Q8IXZ9) COPA protein (Coatomer protein complex, subunit alpha)

seq.coverage=7%

6. K1CN_HUMAN Mass: 51744 Score: 171 Queries matched: 4
(P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
4	404.20	806.39	806.39	-0.01		0	42	0.0084		1 LAADDFR
6	405.34	808.67	808.43	0.24	0	41	0.017		1	LASYLDK
51	515.30	1028.59	1028.59	-0.00		0	32	0.09	1	VLDELTLAR
69	545.80	1089.59	1089.52	0.06	0	55	0.00041		1	VTMQNLNDR

Proteins matching the same set of peptides:
K1CP_HUMAN Mass: 51447 Score: 171 Queries matched: 4
(P08779) Keratin, type I cytoskeletal 16 (Cytokeratin 16) (K16) (CK 16)

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Band GJ Jurkat negative control (GST only) GJ band (same migration as band 9b)

Significant hits: K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp
K1C9_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)
K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)
K22E_HUMAN (P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)
K2C4_HUMAN (P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)
COPA_HUMAN (P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
EHD1_HUMAN (Q9H4M9) EH-domain containing protein 1 (Testilin) (hPAST1)
PEX1_HUMAN (O43933) Peroxisome biogenesis factor 1 (Peroxin-1) (Peroxisome biogenesis disorder protein 1)
Q86Y06_HUMAN (Q86Y06) Sister-of-mammalian grainyhead isoform 1
Q8IY17_HUMAN (Q8IY17) Neuropathy target esterase (Fragment)

1. K2C1_HUMAN Mass: 66018 Score: 657 Queries matched: 15
(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
45	487.29	972.57	972.52	0.05	0	42	0.01	1		IEISELNR
53	500.20	998.39	998.44	-0.05		0	42	0.0089	1	DVDGAYMTK
60	517.30	1032.59	1032.51	0.08	0	(38)	0.023		1	TLLEGEESR
73	546.80	1091.59	1091.50	0.09	0	46	0.0032		1	GSGGGSSGGSIGGR
82	571.30	1140.59	1140.51	0.07	0	31	0.11	1		DYQELMNTK
88	590.30	1178.59	1178.59	-0.01		0	75	4.2e-06	1	YEELQITAGR
110	633.30	1264.59	1264.63	-0.04		0	15	3.6	1	TNAENEFVTIK
113	639.40	1276.79	1276.70	0.08	0	62	8.6e-05		1	LALDLEIATYR
118	651.89	1301.77	1301.71	0.06	0	39	0.016		1	SLDLDSIIAEVK
137	679.40	1356.79	1356.69	0.10	0	75	3.6e-06		1	LNDLEDALQQAK
142	692.40	1382.79	1382.68	0.10	0	42	0.0069		1	SLNNQFASFIDK
147	465.30	1392.88	1392.72	0.15	1	33	0.069		1	TNAENEFVTIKK
162	738.40	1474.79	1474.78	0.01	0	66	2.6e-05		1	FLEQQNQVLQTK

164 738.42 1474.82 1474.74 0.08 0 29 0.13 1
WELLQQVDTSTR
283 665.40 1993.18 1992.97 0.21 0 31 0.1 1
THNLEPYFESFINNLR

2. K1C9_HUMAN Mass: 62178 Score: 282 Queries matched: 6
(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
27 449.20 896.39 896.41 -0.02 0 41 0.0096
1 MTLDDFR
65 530.80 1059.59 1059.56 0.03 0 42 0.0093 1
TLLDIDNTR
67 533.30 1064.59 1064.49 0.09 0 45 0.0036 1
STMQELNSR
85 579.30 1156.59 1156.58 0.00 0 61 8.5e-05 1
QGVDADINGLR
249 613.30 1836.88 1836.96 -0.08 0 43 0.0046
1 HGVQELEIELQSQLSK
349 837.40 2509.18 2509.12 0.05 0 50 0.00056 1
EIETYHNLLEGGQEDFESSGAGK

3. K1CJ_HUMAN Mass: 59711 Score: 186 Queries matched: 5
(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
72 545.80 1089.59 1089.52 0.06 0 46 0.0035 1
VTMQNLNDR
76 555.30 1108.59 1108.48 0.10 0 30 0.12 1
DAEAWFNEK
108 631.80 1261.59 1261.59 -0.00 0 28 0.2 1
SLLEGEGSSGGGGR
141 691.40 1380.79 1380.64 0.14 0 56 0.00028 1
ALEESNYELEGK
172 498.61 1492.81 1492.73 0.08 1 25 0.34 1
SQYEQLAEQNRK

Proteins matching the same set of peptides:
Q8N175_HUMAN Mass: 59020 Score: 186 Queries matched: 5
(Q8N175) Keratin 10

4. K22E_HUMAN Mass: 66110 Score: 130 Queries matched: 3
(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
7 414.20 826.39 826.42 -0.04 0 22 0.77 1
FASFIDK
45 487.29 972.57 972.52 0.05 0 42 0.01 1
IEISELNR

162 738.40 1474.79 1474.78 0.01 0 66 2.6e-05 1
FLEQQNQVLQTK

5. K2C4_HUMAN Mass: 57602 Score: 109 Queries matched: 3
(P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
7 414.20 826.39 826.42 -0.04 0 22 0.77 1
FASFIDK
113 639.40 1276.79 1276.70 0.08 0 62 8.6e-05 1
LALDIEIATYR
137 679.40 1356.79 1356.72 0.06 0 25 0.37 2
NLDLDSIIAEVR

6. COPA_HUMAN Mass: 139783 Score: 45 Queries matched: 1
(P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
17 436.30 870.59 870.49 0.09 0 45 0.0045 1
LNDLIQR

Proteins matching the same set of peptides:
Q5T201_HUMAN Mass: 139797 Score: 45 Queries matched: 1
(Q5T201) Coatomer protein complex, subunit alpha
Q8IXZ9_HUMAN Mass: 140832 Score: 45 Queries matched: 1
(Q8IXZ9) COPA protein (Coatomer protein complex, subunit alpha)

seq. coverage : <1%

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Band GH HeLa negative control (GST only) GH band (same migration as band 9b)

Significant hits: K2C1_HUMAN (P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp
K1CJ_HUMAN (P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)
K22E_HUMAN (P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)
K1C9_HUMAN (P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)
K2C4_HUMAN (P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)
K1CN_HUMAN (P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)
COPA_HUMAN (P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni
Q86Y46_HUMAN (Q86Y46) Keratin 6 irs3
Q96RF1_HUMAN (Q96RF1) HEJ1
K1CM_HUMAN (P13646) Keratin, type I cytoskeletal 13 (Cytokeratin 13) (K13) (CK 13)

1. K2C1_HUMAN Mass: 66018 Score: 680 Queries matched: 17
(P04264) Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67 kDa cytokeratin) (Hair alp
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
28	437.80	873.59	873.49	0.09	0	28	0.3	1	SLVNLGGSK
51	487.30	972.59	972.52	0.06	0	42	0.0098	1	IEISELNR
56	500.30	998.59	998.44	0.15	0	24	0.55	2	DVDGAYMTK
64	517.30	1032.59	1032.51	0.08	0	45	0.004	1	TLLEGEESR
81	546.80	1091.59	1091.50	0.09	0	63	6.6e-05	1	GSGGGSSGGSIGGR
86	563.30	1124.59	1124.53	0.05	0	32	0.069	1	AEAESLYQSK
89	571.30	1140.59	1140.51	0.07	0	17	2.5	1	DYQELMNTK
95	590.30	1178.59	1178.59	-0.01	0	45	0.0037	1	YEELQITAGR
124	633.40	1264.79	1264.63	0.16	0	21	1	1	TNAENEFVTIK
126	639.40	1276.79	1276.70	0.08	0	43	0.0062	1	LALDLEIATYR
133	651.90	1301.79	1301.71	0.08	0	63	6.9e-05	1	SLDLDSIIAEVK
151	679.40	1356.79	1356.69	0.10	0	31	0.092	1	LNDLEDALQQAK
160	692.40	1382.79	1382.68	0.10	0	55	0.00039	1	SLNNQFASFIDK
162	465.30	1392.88	1392.72	0.15	1	34	0.066	1	TNAENEFVTIKK
173	738.40	1474.79	1474.78	0.01	0	45	0.0033	1	FLEQQNQVLQTK
174	738.40	1474.79	1474.74	0.04	0	56	0.00026	1	WELLQQVDTSTR
291	665.40	1993.18	1992.97	0.21	0	46	0.003	1	THNLEPYFESFINNLR

2. K1CJ_HUMAN Mass: 59711 Score: 450 Queries matched: 13
(P13645) Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
3	404.20	806.39	806.39	-0.01	0	30	0.14	1	LAADDFR
7	405.20	808.39	808.43	-0.05	0	35	0.042	1	LASYLDK
62	516.27	1030.53	1030.59	-0.06	0	46	0.0032	1	VLDELTLTK

79 545.80 1089.59 1089.52 0.06 0 34 0.06 1
VTMQNLNDR
84 555.30 1108.59 1108.48 0.10 0 50 0.0013 1
DAEAWFNEK
93 583.30 1164.59 1164.58 0.01 0 36 0.03 1
LENEIQTYR
112 412.30 1233.88 1233.67 0.21 1 21 2 1
LKYENEVALR
152 453.30 1356.88 1356.71 0.17 1 22 1.1 1
QSVEADINGLRR
157 691.40 1380.79 1380.64 0.14 0 88 2.1e-07 1
ALEESNYELEGK
169 479.00 1433.98 1433.76 0.22 1 16 4.4 1
IRLENEIQTYR
180 498.60 1492.78 1492.73 0.05 1 22 0.79 1
SQYEQLAEQNRK
261 599.70 1796.08 1796.00 0.07 0 35 0.036 1
NVQALEIELQSQLALK
388 1018.29 3051.86 3051.62 0.24 1 17 1.8 1
TIDDLKNQILNLTTDNANILLQIDNAR

Proteins matching the same set of peptides:
Q8N175_HUMAN Mass: 59020 Score: 450 Queries matched: 16
(Q8N175) Keratin 10

3. K22E_HUMAN Mass: 66110 Score: 363 Queries matched: 10
(P35908) Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e) (CK 2e)
Check to include this hit in error tolerant search or archive report

Query Observed Mr(expt) Mr(calc) Delta Miss
Score Expect Rank Peptide
14 414.20 826.39 826.42 -0.04 0 32 0.075
1 FASFIDK
16 416.30 830.59 830.49 0.10 0 30 0.19 1
SLVGLGGTK
51 487.30 972.59 972.52 0.06 0 42 0.0098 1
IEISELNR
66 521.30 1040.59 1040.55 0.04 0 33 0.054 1
VDPEIQNVK
82 554.30 1106.59 1106.54 0.05 0 43 0.0074 1
AQYEEIAQR
98 597.40 1192.79 1192.61 0.18 0 35 0.051 1
YEELQVTVGR
120 627.80 1253.59 1253.60 -0.01 0 53 0.00058
1 GFSSGSAVVSGGSR
123 632.40 1262.79 1262.69 0.10 0 35 0.043 1
LALDVEIATYR
171 731.00 1459.99 1459.79 0.19 0 17 3.9 1
VDLLNQEIEFLK
173 738.40 1474.79 1474.78 0.01 0 45 0.0033 1
FLEQQNQVLQTK

4. K1C9_HUMAN Mass: 62178 Score: 308 Queries matched: 8
(P35527) Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)

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

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
7	405.20	808.39	808.43	-0.05	0	35	0.042	1		LASYLDK
39	449.20	896.39	896.41	-0.02	0	41	0.0081	1		MTLDDFR
70	530.80	1059.59	1059.56	0.03	0	47	0.0026	1		TLLDIDNTR
85	561.30	1120.59	1120.58	0.01	0	58	0.0002	1		QEYEQLIAK
91	579.34	1156.67	1156.58	0.09	0	29	0.17	1		QGVDADINGLR
135	436.60	1306.78	1306.67	0.11	1	14	4.7	3		IKFEMEQNLR
267	613.40	1837.18	1836.96	0.22	0	45	0.0049	1		HGVQELEIELQSQLSK
358	837.40	2509.18	2509.12	0.05	0	38	0.0091	1		EIETYHNLLEGGQEDFESSGAGK

5. K2C4_HUMAN Mass: 57602 Score: 118 Queries matched: 3
(P19013) Keratin, type II cytoskeletal 4 (Cytokeratin 4) (K4) (CK4)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
14	414.20	826.39	826.42	-0.04	0	32	0.075	1		FASFIDK
82	554.30	1106.59	1106.54	0.05	0	43	0.0074	1		AQYEEIAQR
126	639.40	1276.79	1276.70	0.08	0	43	0.0062	1		LALDIEIATYR

6. K1CN_HUMAN Mass: 51744 Score: 113 Queries matched: 4
(P02533) Keratin, type I cytoskeletal 14 (Cytokeratin 14) (K14) (CK 14)
Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
3	404.20	806.39	806.39	-0.01	0	30	0.14	1		LAADDFR
7	405.20	808.39	808.43	-0.05	0	35	0.042	1		LASYLDK
79	545.80	1089.59	1089.52	0.06	0	34	0.06	1		VTMQNLNDR
132	651.40	1300.79	1300.65	0.13	0	14	4.7	1		ALEEANADLEVK

Proteins matching the same set of peptides:
K1CP_HUMAN Mass: 51447 Score: 113 Queries matched: 4
(P08779) Keratin, type I cytoskeletal 16 (Cytokeratin 16) (K16) (CK 16)

7. COPA_HUMAN Mass: 139783 Score: 84 Queries matched: 4
(P53621) Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) [Contains: Xeni

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

Query	Observed	Mr(expt)	Mr(calc)	Delta		Miss	Score	Expect	Rank	Peptide
48	477.30	952.59	952.54	0.05	0	22	0.65	1		TALNLFFK
92	581.90	1161.79	1161.63	0.16	0	26	0.51	1		VLTIDPTEFK
96	595.90	1189.79	1189.67	0.11	0	18	2.9	1		TLDLPIYVTR
141	666.90	1331.79	1331.78	0.00	0	18	2	1		LVGQSIIAYLQK

Proteins matching the same set of peptides:
Q5T201_HUMAN Mass: 139797 Score: 84 Queries matched: 4
(Q5T201) Coatomer protein complex, subunit alpha
Q8IXZ9_HUMAN Mass: 140832 Score: 84 Queries matched: 4
(Q8IXZ9) COPA protein (Coatomer protein complex, subunit alpha)

seq.coverage=3%
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