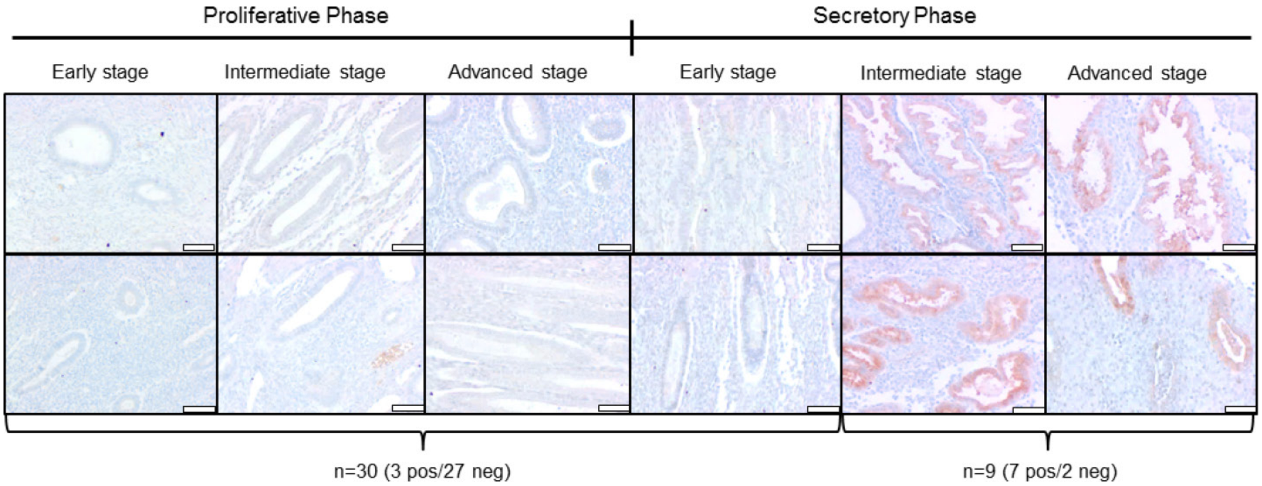
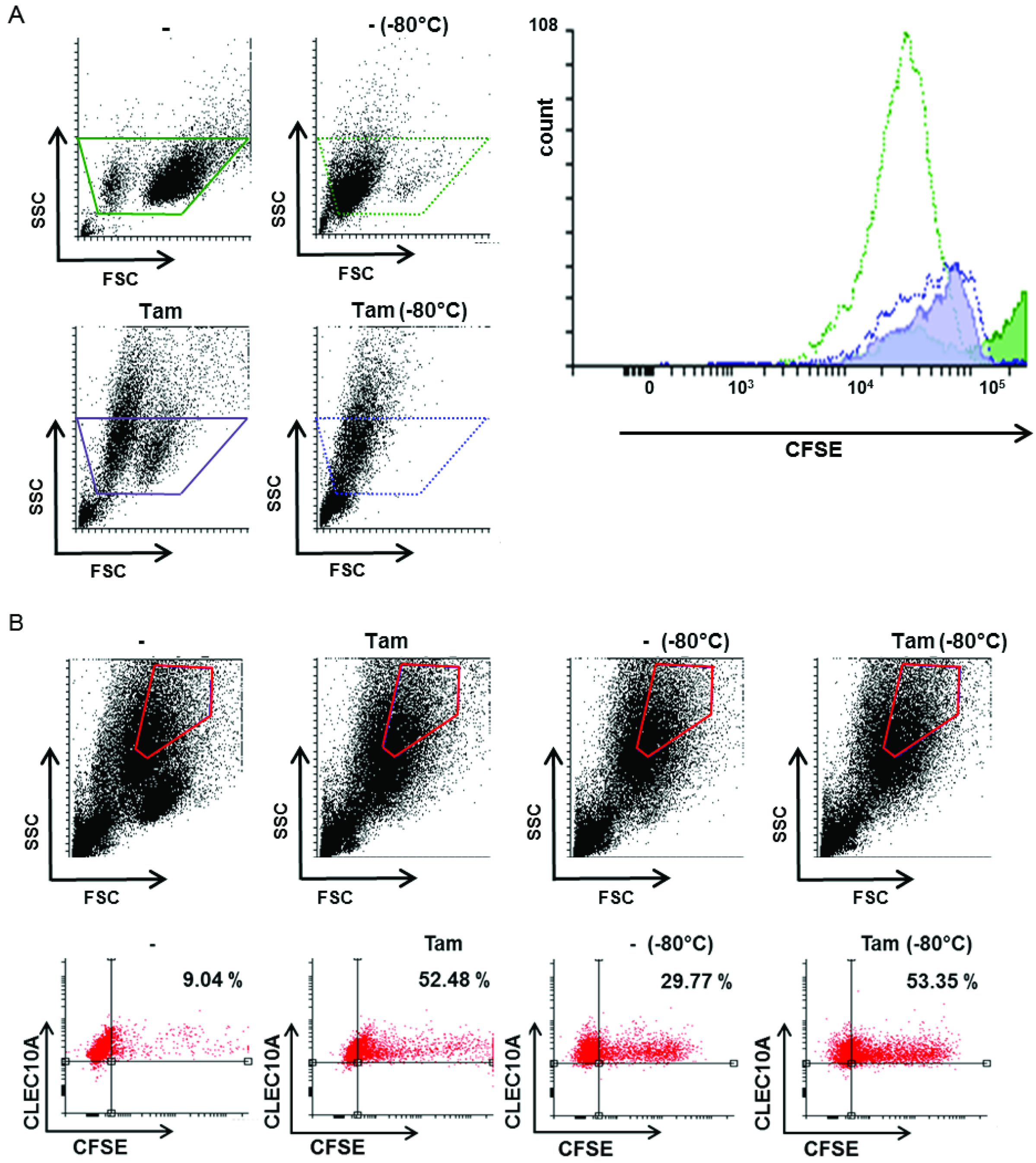
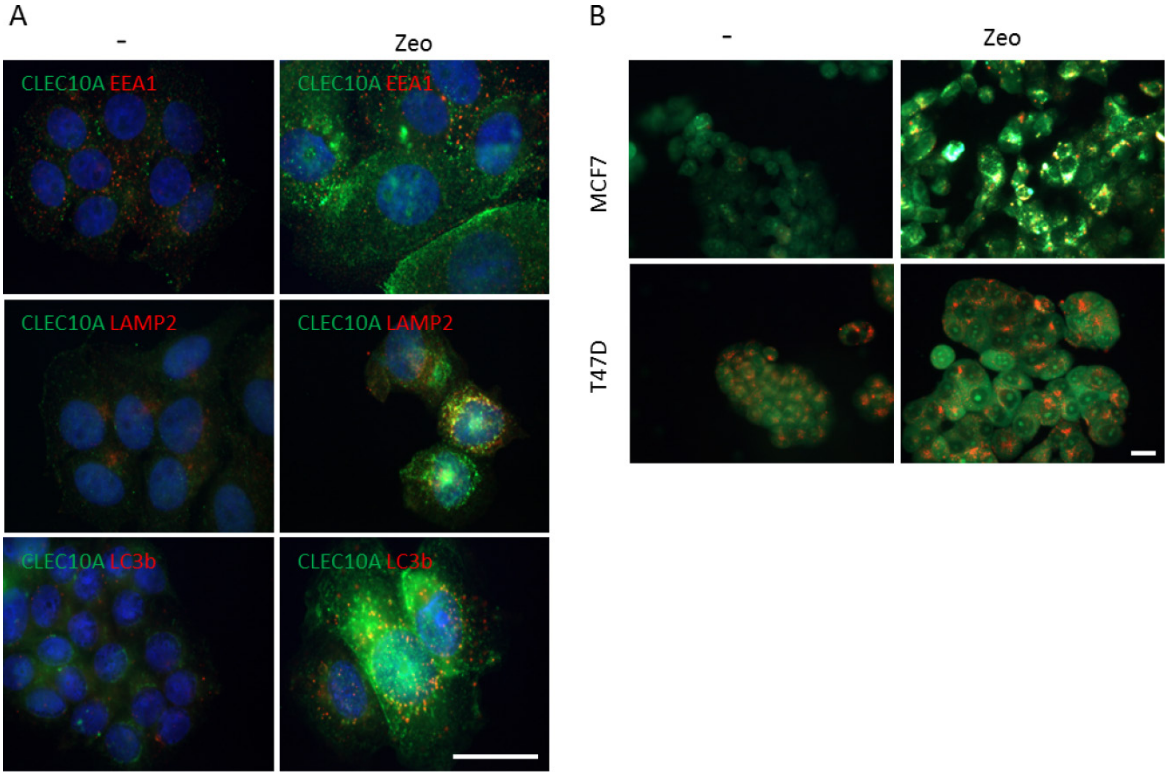


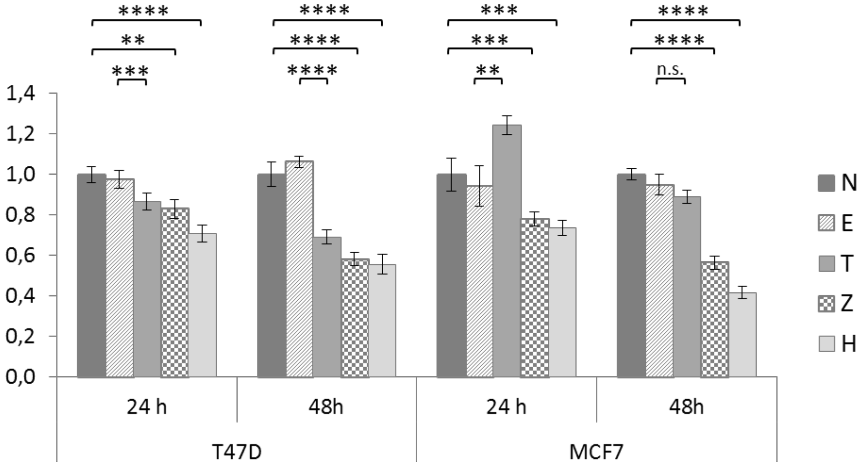
Suppl. Fig. 1: Positivity for CLEC10A ligands correlates with the secretory phase of the female hormonal cycle. 39 premenopausal human endometrium samples were stained by recombinant CLEC10A. 12 representative cases are shown. DAB was used for detection and sections were counterstained by hematoxylin. Scale bar: 100 µm.



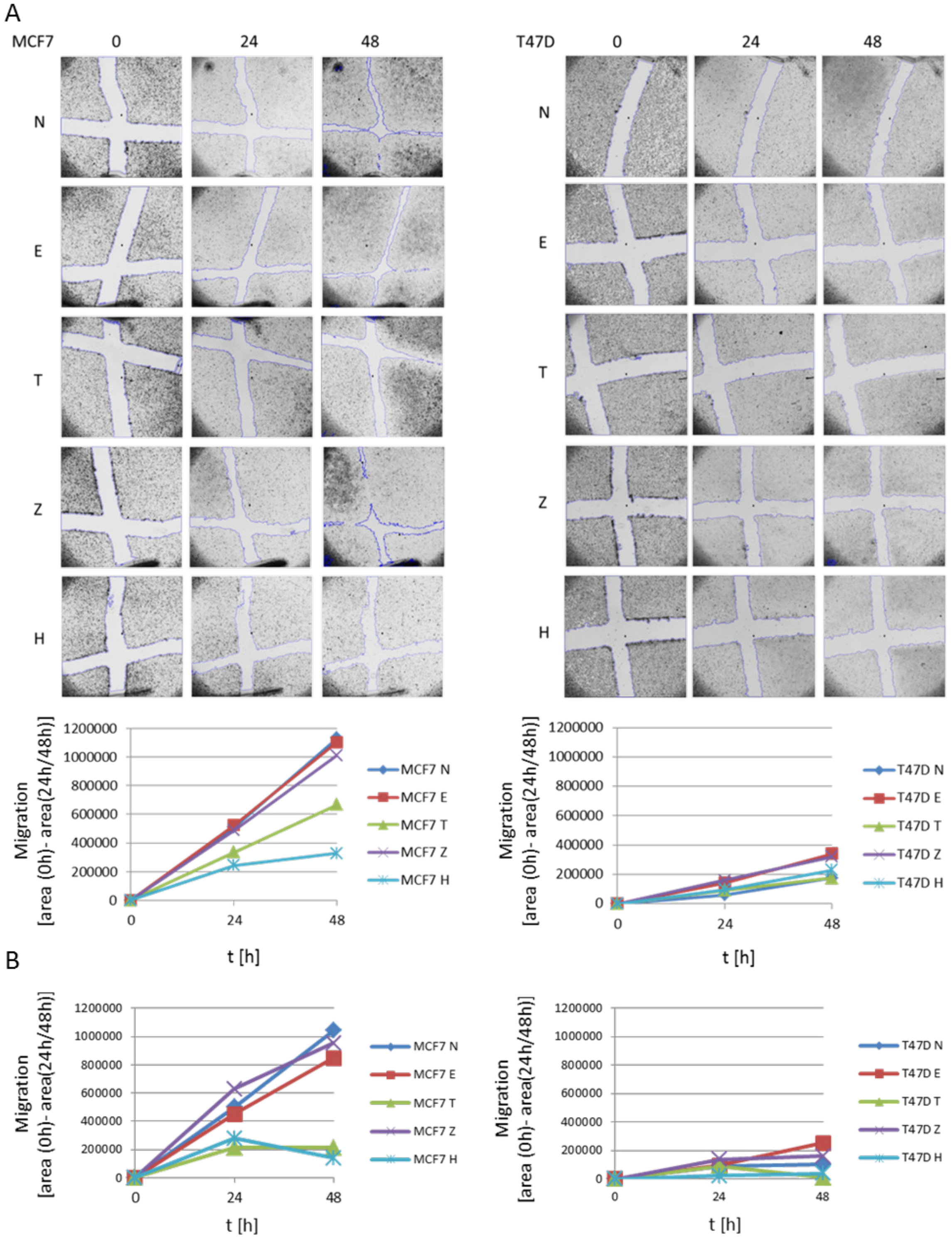
Suppl. Figure 2: Phagocytosis of CFSE-labelled MCF7cells. A) MCF7 cells were treated with tamoxifen (Tam, blue solid line) or ethanol as solvent control (green, solid line). Subsequnetly, cells were labeled with CFSE. Aliquots were killed by freeze and thaw cycles (-80°C). The fluorescence intensity of CFSE labelled cells is shown in the overlay-histogram (-: green filled histogram; Tam: blue filled histogram; -(-80°C): green dotted line; Tam (-80°C): blue dotted line). B) Examples of four representative measurements. Macrophages were incubated for 2 h with CFSE labelled MCF7 cells. CFSE-positive macrophages in the red gate were detected using anti CLEC10A antibody and double positive cells were counted.



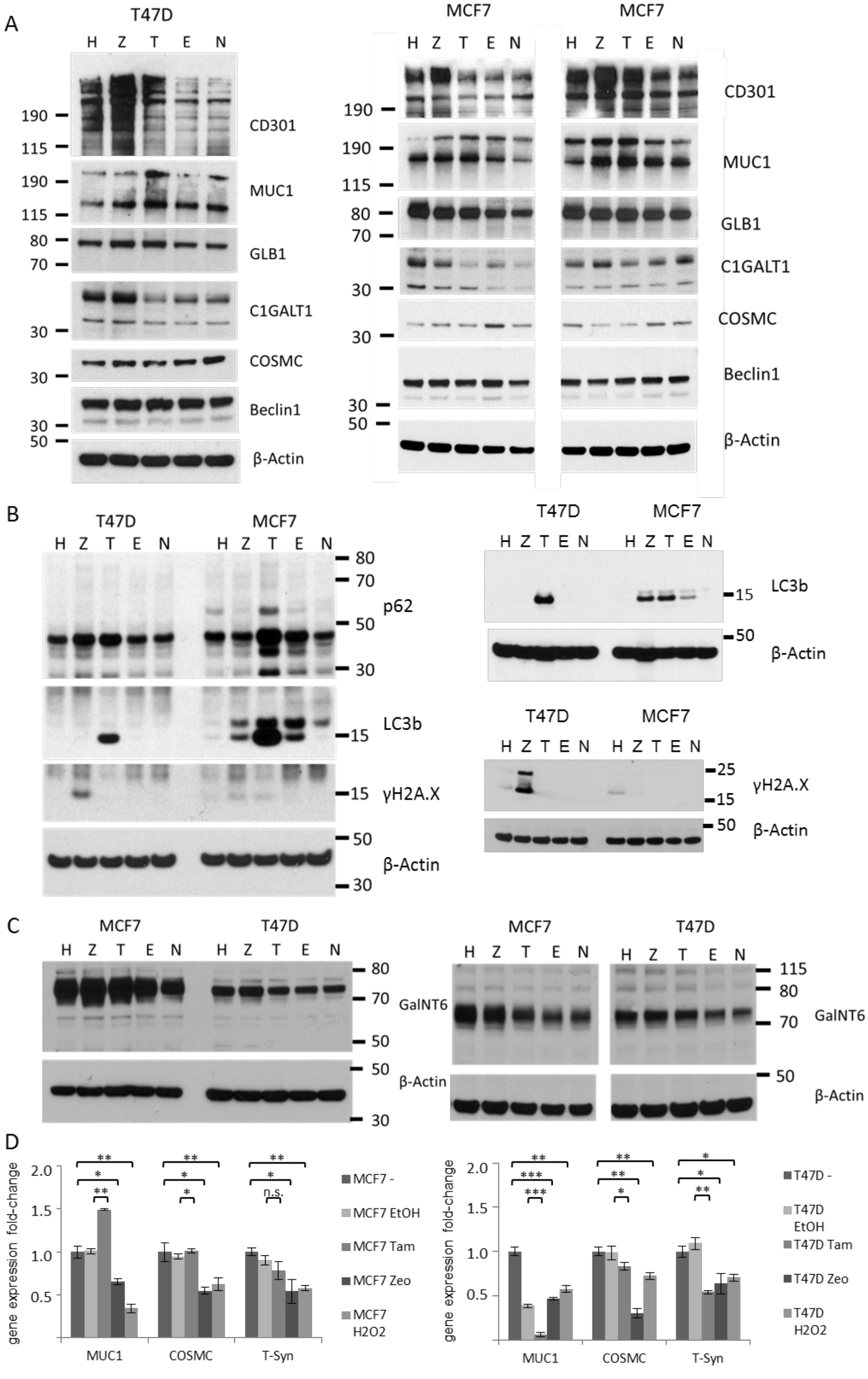
Suppl. Figure 3: Zeocin leads to accumulation of CLEC10A ligands in the endosomal/lysosomal pathway and in autophagosomes. (A) Immunofluorescence staining of CLEC10A ligands (Alexa 488, green), endosomes (early endosomal antigen, EEA1; Alexa 555, red), lysosomes (LAMP2; Alexa 555, red) and autophagosomes (LC3b; Alexa 555, red) in MCF7 cells after 48 h Zeocin treatment. Untreated cells(-) served as control (B) Acridine orange staining of MCF7 and T47D cells treated with Zeocin for 48h showed enlargement of intracellular vesicles. Alkalization of acidic organelles was observed predominantly in MCF7 cells. Sale bar: 20 µm



Suppl. Figure 4: Effects of tamoxifen, zeocin and hydrogen peroxide on cell viability. Cells were seeded in sextuplicates and treated with 4 µM tamoxifen (T), 250 µg/ml zeocin (Z) or 30 µM hydrogen peroxide (H) for indicated time periods. Non-treated cells (N) and ethanol treated cells (E) served as controls. Columns show the averages of the replicates normalized to non-treated cells and error bars depict the standard deviation. **:*P* <0.01, *** *P* <0.001, **** *P* <0.0001

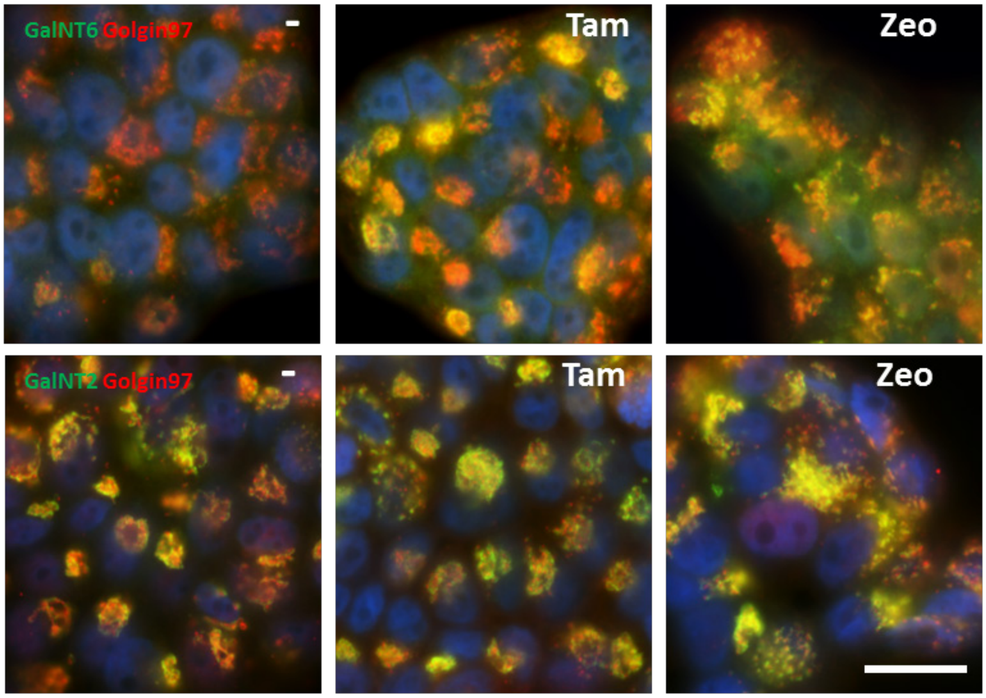


Suppl. Figure 5: Scratch assay: (A) Cells were incubated for 24 h and scratches were created *in vitro* by scraping the cell monolayer with a sterile pipette. Cells were treated with 4 µM tamoxifen (T), 250 µg/ml zeocin (Z) or 30 µM hydrogen peroxide (H) and photographs were taken at the time points indicated. Non-treated cells (N) and ethanol treated cells (E) served as controls. Diagrams show the differences of the scratch areas after 24 h and 48h, respectively. (B) Diagrams show the results of an independent experiment.



Suppl. Figure 6: (A-C) Independent reproduction of western blots shown in Figure 5 and 6.(D) mRNA expression analysis of mucin 1 (MUC1), COSMC and T-synthase (T-Syn) in MCF7 and T47D cells**.** RT-PCR was performed with cDNA generated from mRNA of untreated (-) cells and cells treated by ethanol (EtOH), Tam, Zeocin (Zeo) or hydrogen peroxide under conditions described above. Mean values were calculated by the $2^{-\Delta\Delta CT}$ method and f*old changes* in gene expression *relative* to the *untreated* control are given. Error bars depict the standard deviations of three technical replicates.

A



B

GalNTs-Golgin97	M1	M2
T47D - GalNT6	0.36 ± 0.09	0.36 ± 0.09
T47D T GalNT6	0.73 ± 0.09	0.73 ± 0.08
T47D Z GalNT6	0.70 ± 0.05	0.71 ± 0.06
T47D - GalNT2	0.81 ± 0.07	0.81 ± 0.06
T47D T GalNT2	0.80 ± 0.05	0.81 ± 0.06
T47D Z GalNT2	0.77 ± 0.07	0.77 ± 0.06

****

****

n.s.

n.s.

Suppl. Figure 7: Immunofluorescence of GalNT2 and GalNT6 in T47D. (A) Co-localization of GalNT2 and GalNT6 (Alexa 488, green) in the trans-Golgi (Golgin97; Alexa 555, red) in T47D cells after treatment by Tam and Zeocin for 48h, respectively. Predominantly, GalNT6 showed increased expression and shifted towards the trans-Golgi compartment after treatment. Scale bar: 20 µm. (B) Determination of Mander's coefficient for quantification of co-localization from ten images applying JACOP. Averages and standard deviations are given. P-values were calculated with Student's t-test. **** *P*<0.0001.

Material and methods

Suppl. Table 1. Clinico-pathological characteristics of the 146 invasive ductal breast carcinomas. Age is given in years, survival time in month. (ER = estrogen receptor status, PR = progesterone receptor status, neg = negative, pos = positive).

	median	**range**
age	60	30-88
survival	65.5	1.6-102
stage	**n**	**%**
IA	39	26.7
IIA	52	35.6
IIB	46	31.5
IIIA-C	9	6.2
grade	**n**	**%**
1	17	11.6
2	69	47.3
3	60	41.1

ER	**n**	**%**
neg	26	17.8
pos	120	82.2
PR	**n**	**%**
neg	38	26.0
pos	108	74.0
Her2/neu	**n**	**%**
neg	121	82.9
pos	25	17.1

Suppl. Table 2 Antibodies and the corresponding dilutions used for western blot (WB) and immunofluorescence (IF). Methanol [M] or formaldehyde [FA] were used for fixation of cells for immunofluorescence.

Antibody	Source	Dilution WB/ FACS	Dilution IF [Fixation]
Beclin 1	Cell Signaling	1:1000	
COSMC (C1GALT1C1) antibody [N3C3],	Biozol	1:500/-	-
c-Myc Antibody [9E10]	Santa Cruz	1:1000/-	1:100 [FA/M]
c-Myc Antibody [9E10] biotin conjugated	Santa Cruz	1:500/-	1:100[FA/M]
E-Cadherin (24E10)	Cell Signaling	1:1000/-	-
EEA1 [C45B10]	New England BioLabs	-/-	1:200 [FA]
GALNT2 Antibody	Novus Biotech.	1:1000/-	1:250 [FA]
GALNT6 Polyclonal Antibody	Thermo Fisher	1:1000/-	1:250 [FA]
Golgin-97 Monoclonal Antibody [CDF4]	Thermo Fisher Scientific	-	1:200 [FA]
γH2A.X [Phospho-Histone H2A.X (Ser139)] (D7T2V)	Cell Signaling	1:1000	
Her2/ErbB2 [29D8]	Cell Signaling	1:1000/-	-
LAMP2 [2D5]	provided by Prof. Thomas Braulke (University of Hamburg, Germany)	1:1000/-	1:250 [FA]
LC3B [D11] XP®	Cell Signaling	-/-	1:200 [M]
T-Synthase (C1GALT1) antibody	abcam	1:500/-	-
Mucin 1 Antikörper [VU4H5]	Santa Cruz Biotechnologie	1:1000/-	-
APC anti-human CD301 (CLEC10A)	Biolegend	-/ 5µl per 10^6 cells	-
mouse IgG2a, κ APC isotype control	Biolegend	according to manufacturer	
PerCP anti-human CD16 (3G8)	Biolegend	-/ 5µl per 10^6 cells	
PerCP Mouse IgG1, κ isotype control	Biolegend	according to manufacturer	
Goat anti mouse-HRP	Dako	1:25.000/-	-
Goat anti rabbit-HRP	Dako	1:50.000/-	-
Anti-rabbit IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 488 Conjugate)	Cell Signaling	-/-	1:1000
Anti-mouse IgG (H+L), F(ab')2 Fragment (Alexa Fluor® 555 Conjugate)	Cell Signaling	-/-	1:1000

Quantitative real time PCR

Total RNA was extracted from cells of untreated (-) cells and cells treated by ethanol (EtOH), Tam, Zeocin (Zeo) or hydrogen peroxide under conditions described above using phenol/chlorform followed by purification with RNeasy Mini Kit (Quiagen). 1 µg of RNA was reverse transcribed to cDNA using iScript™ Advanced cDNA Synthesis Kit (Biorad). qPCR was performed using LightCycler® 480 Probes Master (Roche) on a Light Cycler 480 II Real-Time PCR System (Roche) under standard conditions. The fold change of mean values was calculated by the $2^{-\Delta\Delta CT}$ method relative to the untreated samples. Target gene levels of three technical replicates were normalized to the housekeeping gene β2-microglobulin (B2M). The following intron-spanning Universal Probe assay primers (P) and probes were used: MUC1 (P1 5'-tcgtagcccctatgagaagg-3'; P2 5'-ccactgctgggtttgtgtaa-3'; Probe 66), T-Synthase (C1GALT1) (P1 5'-ccgcagctgatgtcagaa-3'; P2 5'-gaacataaaagaaatcctattgctgat-3'; Probe 6), COSMC (C1GALT1C) (P1 5'-ttagcgagaccaacgagagaa-3'; P2 5'-accactccgttacgctcct-3'; Probe 65), B2M (P1 5′-ttctggcctggaggctatc-3′; P2 5′-tcaggaaatttgactttccattc-3′; Probe 42)

MTT assay

Viability was determined by a cell titer 96 non-radioactive cell proliferation assay kit (MTT assays) according to the manufacturer's instructions (Promega). Cells (0.5×10^5) were plated in sextuplicate in 96-well plates for 24 h and afterwards incubated with media containing ethanol (E), Tamoxifen (T), zeocin (Z) or hydrogen peroxide (H), respectively. After 24 h or 48h, dye solution was added for 4 h, followed by incubation with lysis buffer at 37 °C overnight. Absorbance was recorded at 570 nm using a Tecan 96-well plate reader with a reference wavelength of 650 nm. Average values and standard deviations were calculated and levels of significance were determined by Student's t-test.

Scratch assay

The migration capabilities of MCF7 and T47D cells were assessed using a scratch wound assay. Cells were seeded into 6-well tissue culture dishes. Scratches were generated in the cell monolayer with a sterile 100 µl plastic pipette tip and cellular debris was removed by washing with phosphate buffer saline (PBS). Cells were treated with 4 µM tamoxifen (T), 250 µg/ml zeocin (Z) or 30 µM hydrogen peroxide (H), respectively. Non-treated (N) and ethanol (E) treated cells served as controls. During treatment DMEM containing 1% FCS was used to inhibit cell proliferation. Photographs were taken at 0 h, 24 h and 48 h. The migration was calculated from the difference of the areas between 0 h and 24 h or 48 h, respectively.

nanoHPLC-ESI-MS/MS

Protein identification was performed by Proteome Factory (Proteome Factory AG, Berlin, Germany). The LCMS system consisted of an Agilent 1100 nanoHPLC system (Agilent, Waldbronn, Germany), PicoTip electrospray emitter (New Objective, Woburn, MA) and an Orbitrap XL or LTQ-FT Ultra mass spectrometer (ThermoFisher Scientific, Bremen, Germany). Protein spots were in-gel digested by trypsin (Promega, Mannheim, Germany) and analysed by nanoHPLC-ESI-MS/MS. Peptides were first trapped and desalted on the enrichment column (Zorbax 300SB-C18, 0.3 x 5 mm, Agilent) for five minutes (solvent: 2.5% acetonitrile/0.5% formic acid), then separated on a Zorbax 300SB-C18, 75 µm x 150 mm column (Agilent) using a linear gradient from 10% to 32% B (solvent A: 5% acetonitrile in water, solvent B: acetonitrile, both with 0.1% formic acid). Ions of interest were data-dependently subjected to MS/MS according to the expected charge state distribution of peptide ions. Proteins were identified by database search against the NCBInr protein database (National Center for Biotechnology Information,

Sample T12 blue box

```
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Fixed modifications : Carbamidomethyl (C)
Variable modifications : Deamidated (NQ),Oxidation (M)
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Fragment Mass Tolerance: ± 0.6 Da
Max Missed Cleavages : 1
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                    P35908 Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1
                    SV=2
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                    A7Y9J9 Mucin 5AC, oligomeric mucus/gel-forming OS=Homo sapiens GN=MUC5AC PE=4
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Significance threshold p< Max. number of hits
Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

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Thrombospondin 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1
P07996 Mass: 133291 Score: 113 Queries matched: 3
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2
9. Q6MZM7 Mass: 242944 Score: 47 Queries matched: 1 emPAI: 0.01
Putative uncharacterized protein DKFZp686O12165 (Fragment) OS=Homo sapiens GN=DKFZp686O12165 PE=1
SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1356 866.9787 1731.9428 1731.9407 1.22 0 47 0.00021 1 R.NLQPASEYTVSLVAIK.G
Proteins matching the same set of peptides:
B7ZLE5 Mass:250136 Score:47 Queries matched:1                                  FN1 protein
OS=Homo sapiens GN=FN1 PE=2 SV=1
F8W7G7 Mass: 246447 Score: 47 Queries matched: 1
Ugl-Y3 OS=Homo sapiens GN=FN1 PE=2 SV=1
P02751 Mass: 266052 Score: 47 Queries matched: 1
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4
10. H7C4T5 Mass: 36596 Score: 47 Queries matched: 2 emPAI: 0.18
Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
991 434.7661 867.5176 867.5178 -0.29 0 25 0.021 1 -.PVSVTPIR.D
994 435.7734 869.5323 869.5335 -1.38 0 22 0.055 1 -.VVSVTPIR.D
11. A0N4V7 Mass: 2269 Score: 44 Queries matched: 14 emPAI: 1.75
HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
939 421.7581 841.5016 841.5022 -0.64 1 44 0.0008 1 K.GITLSVRP.- 938 940 941 942 944 945 946 947
948 949 950 951 952
12. L0R5A1 Mass: 11752 Score: 31 Queries matched: 1 emPAI: 0.28
Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
978 428.7653 855.5160 855.5178 -2.07 0 31 0.013 1 R.LASIVTPR.N
```

13. I3L4V6 **Mass:** 26188 **Score:** 26 **Queries matched:** 2 **emPAI:** 0.12
Nucleoredoxin (Fragment) OS=Homo sapiens GN=NXN PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1376 **913.8992 1825.7838 1825.7854 -0.86 0 26 0.015 1 R.LYGIQDSEDDGESEAAK.Q** 1375
Proteins matching the same set of peptides:
B4DNN6 **Mass:** 14224 **Score:** 26 **Queries matched:** 2
Nucleoredoxin OS=Homo sapiens GN=NXN PE=2 SV=1
14. Q8WWR7 **Score:** 24 **Queries matched:** 1
Desmoglein 2 (Fragment) OS=Homo sapiens GN=DSG2 PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
500 **584.4383 583.4310 583.4309 0.19 0 24 0.0044 1 R.LLLLL.-**
15. Q1RMC9 **Mass:** 154105 **Score:** 23 **Queries matched:** 2
ERBB2IP protein OS=Homo sapiens GN=ERBB2IP PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1138 **533.2573 1064.5000 1064.5026 -2.42 0 23 0.077 1 K.YPNLESVNK.V** 1139

Proteins matching the same set of peptides:
Q96RT1 **Mass:** 158941 **Score:** 23 **Queries matched:** 2
Protein LAP2 OS=Homo sapiens GN=ERBB2IP PE=1 SV=2

Sample: T12 red box

Database : HumanUniprot uniprot140506 (136615 sequences; 43285968 residues)
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Deamidated (NQ),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 3 ppm
Fragment Mass Tolerance: ± 0.6 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 2296
Protein hits : **H6VRF8** Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG2 Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
P13645 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
P35527 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 **P35908**
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
B4DVE1 cDNA FLJ53478, highly similar to Galectin-3-binding protein OS=Homo
sapiens PE=2 SV=1
P08779 Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4
P02533 Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
P04259 Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5
A8K477 Sulfhydryl oxidase OS=Homo sapiens PE=2 SV=1
P13647 Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 **F5H1F3**
Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=2 SV=1
P23142 Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4
G3XAP6 Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=4 SV=1
B1AVQ5 Mucin-1 subunit alpha OS=Homo sapiens GN=MUC1 PE=2 SV=1
H7C4T5 Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=4 SV=1
A0N4V7 HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1 **Q2VPJ6**
HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=1 SV=1 **L0R5A1**
Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1 **Q8WWR7** Desmoglein
2 (Fragment) OS=Homo sapiens GN=DSG2 PE=4 SV=1
Q86TT1 Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens
(human) OS=Homo sapiens PE=2 SV=1
B7Z945 Protein LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1

Select Summary Report

Significance threshold p< Max. number of hits
Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets
Show pop-ups Suppress pop-ups Sort unassigned Decreasing Score Require bold red
1. H6VRF8 **Mass:** 66184 **Score:** 1598 **Queries matched:** 66 **emPAI:** 2.65
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
999 **437.7531 873.4917 873.4920 -0.30 0 49 0.00057 1 R.SLVNLGGSK.S** 1000 1001
1117 **487.2697 972.5248 972.5240 0.86 0 62 2.7e-005 1 K.IEISELNR.V** 1116 1118
1149 **500.2269 998.4392 998.4379 1.33 0 58 2.2e-005 1 K.DVDGAYMTK.V** 1148 1150
1190 **517.2629 1032.5113 1032.5087 2.51 0 57 8.3e-005 1 R.TLLEGEESR.M** 1191
1227 **533.2651 1064.5157 1064.5138 1.74 0 47 0.00047 1 K.AQYEDIAQK.S** 1225 1226
1283 **563.2755 1124.5364 1124.5349 1.28 0 80 1.7e-007 1 K.AEAESLYQSK.Y** 1284

```
1308 571.2647 1140.5149 1140.5121 2.47 0 54 5.7e-005 1 R.DYQELMNTK.L 1309 1310
1353 590.3044 1178.5942 1178.5931 0.91 0 82 1.7e-007 1 K.YEELQITAGR.H 1351 1352
1409 633.3224 1264.6303 1264.6299 0.30 0 69 2.9e-006 1 R.TNAENEFVTIK.K 1408 1410
1419 639.3590 1276.7035 1276.7027 0.62 0 79 1.6e-007 1 K.LALDLEIATYR.T 1418 1420
1430 651.8619 1301.7092 1301.7078 1.03 0 106 4.3e-010 1 R.SLDLDSIIAEVK.A 1431
1463 670.8391 1339.6637 1339.6619 1.33 1 81 1.8e-007 1 K.SKAEAESLYQSK.Y 1459 1460 1461 1462
1501 692.3487 1382.6829 1382.6830 -0.08 0 86 5.2e-008 1 K.SLNNQFASFIDK.V 1500 1502
1507 697.3693 1392.7241 1392.7249 -0.53 1 67 2.7e-006 1 R.TNAENEFVTIKK.D 1508 1509 1510 1511
1554 738.3784 1474.7423 1474.7416 0.49 0 75 5.7e-007 1 K.WELLQQVDTSTR.T 1555 1556
1557 738.3983 1474.7820 1474.7780 2.71 0 93 9e-009 1 R.FLEQQNQVLQTK.W 1558
1608 508.6007 1522.7804 1522.7813 -0.63 1 41 0.001 1 R.LLRDYQELMNTK.L 1609
1668 546.9582 1637.8528 1637.8525 0.16 1 49 0.00015 1 K.SLNNQFASFIDKVR.F 1667 1669
1673 829.4014 1656.7883 1656.7856 1.61 0 91 1.8e-008 1 R.SGGGFSSGSAGIINYQR.R
1799 648.0022 1940.9846 1940.9803 2.24 1 51 0.00011 1 K.LNDLEDALQQAKEDLAR.L 1798
1821 662.6357 1984.8852 1984.8870 -0.93 1 45 0.00047 1 R.LDSELKNMQDMVEDYR.N
1858 538.2763 2149.0760 2149.0705 2.59 1 40 0.0023 1 R.THNLEPYFESFINNLRR.R 1854 1857
1930 777.0620 2328.1642 2328.1669 -1.17 1 40 0.0019 1 K.QISNLQQSISDAEQRGENALK.D
1978 855.7286 2564.1641 2564.1595 1.78 0 41 0.00085 1 R.MSGECAPNVSVSVSTSHTTISGGGSR.G 1977
2072 978.1786 2931.5138 2931.5090 1.64 1 54 6.2e-005 1 R.FLEQQNQVLQTKWELLQQVDTSTR.T 2070 2071
Proteins matching the same set of peptides:
H6VRG0 Mass: 66101 Score: 1598 Queries matched: 66
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG1 Mass: 66257 Score: 1598 Queries matched: 66
Keratin 1 OS=Homo sapiens GN=KRT1 PE=2 SV=1
H6VRG3 Mass: 66242 Score: 1598 Queries matched: 66
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
P04264 Mass: 66170 Score: 1598 Queries matched: 66
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
2. H6VRG2 Mass: 66197 Score: 1574 Queries matched: 66 emPAI: 2.65
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
999 437.7531 873.4917 873.4920 -0.30 0 49 0.00057 1 R.SLVNLGGSK.S 1000 1001
1117 487.2697 972.5248 972.5240 0.86 0 62 2.7e-005 1 K.IEISELNR.V 1116 1118
1149 500.2269 998.4392 998.4379 1.33 0 58 2.2e-005 1 K.DVDGAYMTK.V 1148 1150
1190 517.2629 1032.5113 1032.5087 2.51 0 57 8.3e-005 1 R.TLLEGEESR.M 1191
1227 533.2651 1064.5157 1064.5138 1.74 0 47 0.00047 1 K.AQYEDIAQK.S 1225 1226
1283 563.2755 1124.5364 1124.5349 1.28 0 80 1.7e-007 1 K.AEAESLYQSK.Y 1284
1308 571.2647 1140.5149 1140.5121 2.47 0 54 5.7e-005 1 R.DYQELMNTK.L 1309 1310
1353 590.3044 1178.5942 1178.5931 0.91 0 82 1.7e-007 1 K.YEELQITAGR.H 1351 1352
1409 633.3224 1264.6303 1264.6299 0.30 0 69 2.9e-006 1 R.TNAENEFVTIK.K 1408 1410
1419 639.3590 1276.7035 1276.7027 0.62 0 79 1.6e-007 1 K.LALDLEIATYR.T 1418 1420
1453 665.3673 1328.7201 1328.7187 1.06 0 83 9.6e-008 1 R.NLDLDSIIAEVK.A 1454
1463 670.8391 1339.6637 1339.6619 1.33 1 81 1.8e-007 1 K.SKAEAESLYQSK.Y 1459 1460 1461 1462
1501 692.3487 1382.6829 1382.6830 -0.08 0 86 5.2e-008 1 K.SLNNQFASFIDK.V 1500 1502
1507 697.3693 1392.7241 1392.7249 -0.53 1 67 2.7e-006 1 R.TNAENEFVTIKK.D 1508 1509 1510 1511
1554 738.3784 1474.7423 1474.7416 0.49 0 75 5.7e-007 1 K.WELLQQVDTSTR.T 1555 1556
1557 738.3983 1474.7820 1474.7780 2.71 0 93 9e-009 1 R.FLEQQNQVLQTK.W 1558
1608 508.6007 1522.7804 1522.7813 -0.63 1 41 0.001 1 R.LLRDYQELMNTK.L 1609
1668 546.9582 1637.8528 1637.8525 0.16 1 49 0.00015 1 K.SLNNQFASFIDKVR.F 1667 1669
1673 829.4014 1656.7883 1656.7856 1.61 0 91 1.8e-008 1 R.SGGGFSSGSAGIINYQR.R
1799 648.0022 1940.9846 1940.9803 2.24 1 51 0.00011 1 K.LNDLEDALQQAKEDLAR.L 1798
1821 662.6357 1984.8852 1984.8870 -0.93 1 45 0.00047 1 R.LDSELKNMQDMVEDYR.N
1858 538.2763 2149.0760 2149.0705 2.59 1 40 0.0023 1 R.THNLEPYFESFINNLRR.R 1854 1857
1930 777.0620 2328.1642 2328.1669 -1.17 1 40 0.0019 1 K.QISNLQQSISDAEQRGENALK.D
1978 855.7286 2564.1641 2564.1595 1.78 0 41 0.00085 1 R.MSGECAPNVSVSVSTSHTTISGGGSR.G 1977
2072 978.1786 2931.5138 2931.5090 1.64 1 54 6.2e-005 1 R.FLEQQNQVLQTKWELLQQVDTSTR.T 2070 2071
3. P13645 Mass: 59020 Score: 1214 Queries matched: 50 emPAI: 1.96
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
841 404.2035 806.3924 806.3923 0.12 0 58 2.5e-005 1 R.LAADDFR.L 842 843
852 405.2239 808.4332 808.4330 0.17 0 51 0.00013 1 R.LASYLDK.V 853
1135 497.2542 992.4939 992.4927 1.28 0 57 5.3e-005 1 K.YENEVALR.Q 1133 1134
1139 332.5112 994.5118 994.5123 -0.51 1 32 0.0034 1 K.IKEWYEK.H
1157 502.2809 1002.5472 1002.5458 1.45 1 24 0.098 1 K.SEITELRR.N 1155 1156
1186 516.3024 1030.5902 1030.5910 -0.77 0 66 2e-006 1 R.VLDELTLTK.A 1187 1188
1221 532.8085 1063.6024 1063.6026 -0.17 1 63 5.5e-006 1 R.LASYLDKVR.A 1220 1222 1224
1250 545.7702 1089.5259 1089.5237 2.07 0 74 7.9e-007 1 K.VTMQNLNDR.L 1249 1251
1265 555.2493 1108.4840 1108.4825 1.37 0 64 4e-006 1 K.DAEAWFNEK.S 1263 1264
1341 583.2965 1164.5784 1164.5775 0.84 0 56 7.6e-005 1 R.LENEIQTYR.S 1340
1375 601.3118 1200.6091 1200.6098 -0.59 0 55 7.9e-005 1 R.QSVEADINGLR.R
1396 617.8427 1233.6708 1233.6717 -0.75 1 64 5.2e-006 1 R.LKYENEVALR.Q
1406 631.8035 1261.5924 1261.5899 2.04 0 97 2.3e-009 1 R.SLLEGEGSSGGGGR.G 1405 1407
1478 453.2443 1356.7110 1356.7110 0.05 1 (38) 0.0034 1 R.QSVEADINGLRR.V 1479
```

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1482 453.5725 1357.6958 1357.6950 0.61 1 66 5.3e-006 1 R.QSVEADINGLRR.V 1483
1487 683.3245 1364.6345 1364.6320 1.81 0 69 1.8e-006 1 R.SQYEQLAEQNR.K
1498 691.3282 1380.6419 1380.6408 0.79 0 80 1.4e-007 1 R.ALEESNYELEGK.I 1496 1497
1530 478.9291 1433.7654 1433.7626 1.96 1 35 0.0052 1 K.IRLENEIQTYR.S 1528 1529
1593 498.5828 1492.7267 1492.7270 -0.20 1 40 0.0019 1 R.SQYEQLAEQNRK.D 1594
1694 854.3899 1706.7653 1706.7649 0.21 0 121 1e-011 1 K.GSLGGGFSSGGFSGGSFSR.G 1695
1892 738.0382 2211.0926 2211.0906 0.92 1 43 0.00059 1 K.SKELTTEIDNNIEQISSYK.S 1891 1893
4. P35527 Mass: 62255 Score: 892 Queries matched: 47 emPAI: 1.42
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
852 405.2239 808.4332 808.4330 0.17 0 51 0.00013 1 R.LASYLDK.V 853
1033 449.2099 896.4052 896.4062 -1.14 0 44 0.0006 1 R.MTLDDFR.I 1032
1218 530.7855 1059.5564 1059.5560 0.39 0 71 2.3e-006 1 K.TLLDIDNTR.M 1216 1217
1331 579.2995 1156.5845 1156.5836 0.72 0 (76) 4.3e-007 1 1332
1334 579.7911 1157.5677 1157.5677 0.05 0 97 2.6e-009 1 R.QGVDADINGLR.Q 1333 1335
1364 595.8081 1189.6016 1189.6013 0.27 0 54 7.8e-005 1 R.QVLDNLTMEK.S 1363 1365
1392 616.8011 1231.5877 1231.5906 -2.33 0 124 4.8e-012 1 R.SGGGGGGGLGSGGSIR.S 1393 1394
1436 654.3436 1306.6727 1306.6703 1.85 1 (40) 0.001 1 R.IKFEMEQNLR.Q 1433 1434 1435 1437
1444 441.8963 1322.6671 1322.6652 1.40 1 50 0.00013 1 R.IKFEMEQNLR.Q 1443 1445
1746 919.4888 1836.9631 1836.9581 2.70 0 123 6.3e-012 1 R.HGVQELEIELQSQLSK.K 1742 1743 1744 1745
1758 617.9810 1850.9213 1850.9196 0.92 1 50 0.00019 1 K.TLNDMRQEYEQLIAK.N 1759 1760 1761 1762
1809 656.0253 1965.0541 1965.0531 0.52 1 73 2.8e-007 1 R.HGVQELEIELQSQLSKK.A 1808 1810
1921 767.0453 2298.1141 2298.1123 0.81 1 27 0.035 1 K.SDLEMQYETLQEELMALKK.N
1959 837.3819 2509.1239 2509.1245 -0.23 0 61 7.3e-006 1 K.EIETYHNLLEGGQEDFESSGAGK.I 1958 1960
2109 1088.8426 3263.5060 3263.5066 -0.18 0 67 1.8e-006 1 K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E 2108
2110 2111
5. P35908 Mass: 65678 Score: 713 Queries matched: 27 emPAI: 0.75
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
909 416.2511 830.4877 830.4862 1.83 0 50 0.00029 1 R.SLVGLGGTK.S
1117 487.2697 972.5248 972.5240 0.86 0 62 2.7e-005 1 K.IEISELNR.V 1116 1118
1193 519.2667 1036.5188 1036.5189 -0.14 0 62 1.5e-005 1 R.YLDGLTAER.T 1192 1194
1241 541.8034 1081.5923 1081.5920 0.29 1 65 3.5e-006 1 K.FASFIDKVR.F 1239 1240 1242 1243 1244
1261 554.2759 1106.5372 1106.5356 1.46 0 61 2.3e-005 1 K.AQYEEIAQR.S 1260 1262
1401 627.8083 1253.6021 1253.6001 1.65 0 110 1.7e-010 1 R.GFSSGSAVVSGGSR.R 1400
1441 440.8661 1319.5765 1319.5756 0.66 0 60 7.7e-006 1 R.HGGGGGGFGGGGFGSR.S 1440
1453 665.3673 1328.7201 1328.7187 1.06 0 83 9.6e-008 1 R.NLDLDSIIAEVK.A 1454
1542 730.9045 1459.7945 1459.7922 1.58 0 68 1.1e-006 1 K.VDLLNQEIEFLK.V 1543 1544
1557 738.3983 1474.7820 1474.7780 2.71 0 93 9e-009 1 R.FLEQQNQVLQTK.W 1558
6. B4DVE1 Mass: 64911 Score: 526 Queries matched: 23 emPAI: 0.68
cDNA FLJ53478, highly similar to Galectin-3-binding protein OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
705 368.1773 734.3401 734.3388 1.79 0 31 0.017 1 R.YFYSR.R 703 704
896 413.7272 825.4398 825.4385 1.61 0 30 0.01 1 R.VEIFYR.G 894 895
1178 343.8490 1028.5251 1028.5251 0.07 0 43 0.00077 1 R.STHTLDLSR.E 1179
1302 566.3411 1130.6677 1130.6659 1.58 1 49 5.2e-005 1 R.RIDITLSSVK.C 1301
1379 603.7814 1205.5483 1205.5465 1.50 0 51 9.5e-005 1 K.AVDTWSWGER.A
1451 663.8321 1325.6496 1325.6463 2.47 0 53 9.8e-005 1 R.ASHEEVEGLVEK.I 1447 1448 1449 1450
1468 678.3938 1354.7730 1354.7708 1.65 0 71 4.9e-007 1 R.SDLAVPSELALLK.A 1467
1645 796.8997 1591.7849 1591.7842 0.45 0 67 4.1e-006 1 R.ELSEALGQIFDSQR.G
1817 662.0402 1983.0988 1983.0942 2.31 0 69 5.9e-007 1 K.TLQALEFHTVPFQLLAR.Y 1815 1816
1861 1081.5122 2161.0099 2161.0116 -0.82 0 62 1e-005 1 R.IYTSPTWSAFVTDSSWSAR.K
Proteins matching the same set of peptides:
Q08380 Mass: 66202 Score: 526 Queries matched: 23
Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1
7. P08779 Mass: 51578 Score: 443 Queries matched: 17 emPAI: 0.60
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
841 404.2035 806.3924 806.3923 0.12 0 58 2.5e-005 1 R.LAADDFR.T 842 843
852 405.2239 808.4332 808.4330 0.17 0 51 0.00013 1 R.LASYLDK.V 853
1182 515.3016 1028.5886 1028.5866 1.91 0 62 1.8e-005 1 R.VLDELTLAR.T 1181
1221 532.8085 1063.6024 1063.6026 -0.17 1 63 5.5e-006 1 R.LASYLDKVR.A 1220 1222 1224
1250 545.7702 1089.5259 1089.5237 2.07 0 74 7.9e-007 1 K.VTMQNLNDR.L 1249 1251
1427 651.3332 1300.6519 1300.6510 0.69 0 64 1.2e-005 1 R.ALEEANADLEVK.I 1428
1457 669.8362 1337.6579 1337.6575 0.30 0 70 1.2e-006 1 R.APSTYGGGLSVSSR.F
8. P02533 Mass: 51872 Score: 433 Queries matched: 18 emPAI: 0.60
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
841 404.2035 806.3924 806.3923 0.12 0 58 2.5e-005 1 R.LAADDFR.T 842 843
852 405.2239 808.4332 808.4330 0.17 0 51 0.00013 1 R.LASYLDK.V 853
1182 515.3016 1028.5886 1028.5866 1.91 0 62 1.8e-005 1 R.VLDELTLAR.A 1181
1221 532.8085 1063.6024 1063.6026 -0.17 1 63 5.5e-006 1 R.LASYLDKVR.A 1220 1222 1224
1250 545.7702 1089.5259 1089.5237 2.07 0 74 7.9e-007 1 K.VTMQNLNDR.L 1249 1251
```

```
1427 651.3332 1300.6519 1300.6510 0.69 0 64 1.2e-005 1 R.ALEEANADLEVK.I 1428
1524 713.3537 1424.6928 1424.6896 2.24 0 61 2e-005 1 R.APSTYGGGLSVSSSR.F 1523
9. P04259 Mass: 60315 Score: 390 Queries matched: 17 emPAI: 0.43
Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1084 473.2590 944.5034 944.5039 -0.52 1 36 0.015 1 R.GRLDSELR.N
1241 541.8034 1081.5923 1081.5920 0.29 1 65 3.5e-006 1 K.FASFIDKVR.F 1239 1240 1242 1243 1244
1261 554.2759 1106.5372 1106.5356 1.46 0 61 2.3e-005 1 K.AQYEEIAQR.S 1260 1262
1353 590.3044 1178.5942 1178.5931 0.91 0 82 1.7e-007 1 K.YEELQITAGR.H 1351 1352
1377 602.3231 1202.6317 1202.6295 1.77 0 64 8e-006 1 K.WTLLQEQGTK.T 1376
1453 665.3673 1328.7201 1328.7187 1.06 0 83 9.6e-008 1 R.NLDLDSIIAEVK.A 1454
10. A8K477 Mass: 67567 Score: 389 Queries matched: 14 emPAI: 0.31
Sulfhydryl oxidase OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1073 465.7577 929.5009 929.5004 0.47 0 46 0.00013 1 R.VPVLMESR.S 1072 1074
1273 557.8134 1113.6123 1113.6142 -1.69 0 68 3.2e-006 1 R.VLNTEANVVR.K 1274 1275
1469 678.8437 1355.6729 1355.6721 0.61 0 77 3.1e-007 1 R.LAGAPSEDPQFPK.V 1470 1471
1564 741.8782 1481.7418 1481.7402 1.11 0 63 9.1e-006 1 R.NNEEYLALIFEK.G 1563
1780 631.9962 1892.9668 1892.9646 1.16 0 25 0.049 1 R.VGSPNAAVLWLWSSHNR.V
1836 1024.0394 2046.0642 2046.0633 0.41 0 109 1.4e-010 1 R.SALYSPSDPLTLLQADTVR.G 1835
Proteins matching the same set of peptides:
A8K4C2 Mass: 67521 Score: 389 Queries matched: 14
Sulfhydryl oxidase OS=Homo sapiens PE=2 SV=1
O00391 Mass: 83324 Score: 389 Queries matched: 14
Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3
11. P13647 Mass: 62568 Score: 386 Queries matched: 16 emPAI: 0.41
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1084 473.2590 944.5034 944.5039 -0.52 1 36 0.015 1 R.GRLDSELR.N
1241 541.8034 1081.5923 1081.5920 0.29 1 65 3.5e-006 1 K.FASFIDKVR.F 1239 1240 1242 1243 1244
1255 547.2669 1092.5192 1092.5199 -0.69 0 61 1.2e-005 1 K.AQYEEIANR.S 1256
1269 556.2909 1110.5672 1110.5669 0.27 0 77 2.9e-007 1 R.ISISTSGGSFR.N 1268 1270
1377 602.3231 1202.6317 1202.6295 1.77 0 64 8e-006 1 K.WTLLQEQGTK.T 1376
1453 665.3673 1328.7201 1328.7187 1.06 0 83 9.6e-008 1 R.NLDLDSIIAEVK.A 1454
12. F5H1F3 Mass: 135130 Score: 329 Queries matched: 11 emPAI: 0.17
Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
945 422.2289 842.4433 842.4432 0.06 0 29 0.0054 1 R.NPLICAR.G 946
1210 526.2931 1050.5717 1050.5710 0.66 0 48 0.00018 1 R.QGSVTTFLAK.M 1211
1290 565.2484 1128.4822 1128.4836 -1.23 0 58 8.5e-006 1 K.GNEEGYFGTR.R
1388 614.3169 1226.6193 1226.6158 2.80 0 26 0.036 1 K.MHIFFTTFAL.-
1513 698.8848 1395.7551 1395.7510 2.89 0 80 1e-007 1 R.LNAYTGVVYLQR.A
1550 734.3514 1466.6883 1466.6864 1.30 0 25 0.05 1 R.FECPPNYVQVSK.T
1726 906.5167 1811.0189 1811.0193 -0.20 0 64 1.2e-006 1 R.IGPAPAFTGDTIALNIIK.G 1727 1728
Proteins matching the same set of peptides:
B7Z6T9 Mass: 60778 Score: 329 Queries matched: 11
cDNA FLJ50237, highly similar to Homo sapiens fibulin 2 (FBLN2), transcript variant 1, mRNA
OS=Homo sapiens PE=2 SV=1
B7Z9B8 Mass: 135058 Score: 329 Queries matched: 11
cDNA FLJ56912, highly similar to Fibulin-2 OS=Homo sapiens PE=2 SV=1
Q9Y3V7 Mass: 66767 Score: 329 Queries matched: 11
Putative uncharacterized protein DKFZp586A1519 (Fragment) OS=Homo sapiens GN=DKFZp586A1519 PE=2
SV=1
P98095 Mass: 132248 Score: 329 Queries matched: 11
Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=1 SV=2
13. P23142 Mass: 81268 Score: 249 Queries matched: 10 emPAI: 0.35
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1137 497.2719 992.5292 992.5291 0.14 1 33 0.012 1 R.DSFDIIKR.Y
1387 614.2972 1226.5798 1226.5788 0.82 0 78 2.5e-007 1 R.YMDGMTVGVVR.Q 1385 1386
1397 622.2946 1242.5747 1242.5737 0.80 0 (58) 2.1e-005 1 R.YMDGMTVGVVR.Q
1416 635.7854 1269.5562 1269.5547 1.21 0 33 0.0054 1 K.DCSLPYATESK.E
1620 775.4236 1548.8326 1548.8300 1.66 1 25 0.029 1 R.EFTRPEEIIFLR.A 1619
1627 520.6062 1558.7969 1558.7926 2.77 0 33 0.01 1 K.LEMNYVVGGVVSHR.N
1951 825.7732 2474.2977 2474.2917 2.41 0 47 0.00016 1 R.AITPPHPASQANIIFDITEGNLR.D
14. G3XAP6 Mass: 82212 Score: 171 Queries matched: 8 emPAI: 0.12
Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1174 513.3044 1024.5943 1024.5917 2.55 0 50 9.2e-005 1 R.AVAEPGIQLK.A 1172 1173
1575 743.8788 1485.7430 1485.7423 0.47 0 82 1.4e-007 1 R.ELQETNAALQDVR.E 1576 1577
1654 538.5930 1612.7571 1612.7594 -1.39 0 40 0.0011 1 R.NALWHTGDTESQVR.L 1655
Proteins matching the same set of peptides:
B4DKJ3 Mass: 79446 Score: 171 Queries matched: 8
```

```
Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=2 SV=1
B4DN90 Mass: 83983 Score: 171 Queries matched: 8
cDNA FLJ53494, highly similar to Cartilage oligomeric matrix protein OS=Homo sapiens PE=2 SV=1
A8K3I0 Mass: 85457 Score: 171 Queries matched: 8
cDNA FLJ78437, highly similar to Homo sapiens cartilage oligomeric matrix protein (COMP), mRNA
OS=Homo sapiens PE=2 SV=1
Q53FR6 Mass: 85345 Score: 171 Queries matched: 8
Cartilage oligomeric matrix protein variant (Fragment) OS=Homo sapiens PE=2 SV=1
P49747 Mass: 85431 Score: 171 Queries matched: 8
Cartilage oligomeric matrix protein OS=Homo sapiens GN=COMP PE=1 SV=2
15. B1AVQ5 Mass: 49365 Score: 73 Queries matched: 2 emPAI: 0.06
Mucin-1 subunit alpha OS=Homo sapiens GN=MUC1 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1504 693.8528 1385.6910 1385.6901 0.65 0 73 9.8e-007 1 R.DISEMFLQIYK.Q 1503
Proteins matching the same set of peptides:
B4DWK6 Mass: 57362 Score: 73 Queries matched: 2
cDNA FLJ60927, highly similar to Mucin-1 OS=Homo sapiens PE=2 SV=1
A5YRU5 Mass: 30583 Score: 73 Queries matched: 2
MUC1 isoform Z-LSP OS=Homo sapiens GN=MUC1 PE=2 SV=1
A5YRU7 Mass: 23793 Score: 73 Queries matched: 2
MUC1 isoform T7 OS=Homo sapiens GN=MUC1 PE=2 SV=1
A5YRU8 Mass: 26639 Score: 73 Queries matched: 2
MUC1 isoform T8 OS=Homo sapiens GN=MUC1 PE=2 SV=1
A5YRU9 Mass: 12249 Score: 73 Queries matched: 2
MUC1 isoform T9 OS=Homo sapiens GN=MUC1 PE=4 SV=1
A6ZID5 Mass: 29402 Score: 73 Queries matched: 2
MUC1 isoform M2 OS=Homo sapiens GN=MUC1 PE=2 SV=1
A6ZIE1 Mass: 11261 Score: 73 Queries matched: 2
MUC1 isoform SV4-LSP OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6EC96 Mass: 11260 Score: 73 Queries matched: 2
MUC1 isoform J8 OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6ECA3 Mass: 29700 Score: 73 Queries matched: 2
MUC1 isoform J14 OS=Homo sapiens GN=MUC1 PE=2 SV=1
B6ECA9 Mass: 13226 Score: 73 Queries matched: 2
MUC1 isoform J20 OS=Homo sapiens GN=MUC1 PE=2 SV=1
B6ECB0 Mass: 12447 Score: 73 Queries matched: 2
MUC1 isoform J21 OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6ECB1 Mass: 11249 Score: 73 Queries matched: 2
MUC1 isoform J22 OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6ECB2 Mass: 19749 Score: 73 Queries matched: 2
MUC1 isoform J23 OS=Homo sapiens GN=MUC1 PE=2 SV=1
Q7Z536 Mass: 16424 Score: 73 Queries matched: 2
Mucin short variant SV10 OS=Homo sapiens GN=MUC1 PE=2 SV=1
P15941 Mass: 122200 Score: 73 Queries matched: 2
Mucin-1 OS=Homo sapiens GN=MUC1 PE=1 SV=3
16. H7C4T5 Mass: 36596 Score: 53 Queries matched: 3 emPAI: 0.09
Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
987 435.7737 869.5329 869.5335 -0.70 0 29 0.012 1 -.VVSVTPIR.D 993
1038 450.2695 898.5244 898.5236 0.84 0 24 0.082 1 -.QVSVTPIR.D
17. A0N4V7 Mass: 2269 Score: 42 Queries matched: 17 emPAI: 6.57
HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
941 421.7592 841.5039 841.5022 2.08 1 42 0.0014 1 K.GITLSVRP.- 926 927 928 929 930 932 933 934
935 936 937 938 939 940 942 943
18. Q2VPJ6 Mass: 68614 Score: 38 Queries matched: 1 emPAI: 0.05
HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1319 576.2839 1150.5532 1150.5506 2.31 0 38 0.0038 1 K.YIDQEELNK.T
Proteins matching the same set of peptides:
B4DGL0 Mass: 82518 Score: 38 Queries matched: 1
cDNA FLJ53619, highly similar to Heat shock protein HSP 90-beta OS=Homo sapiens PE=2 SV=1
B4DMA2 Mass: 79487 Score: 38 Queries matched: 1
cDNA FLJ54023, highly similar to Heat shock protein HSP 90-beta OS=Homo sapiens PE=2 SV=1
Q6PK50 Mass: 40270 Score: 38 Queries matched: 1
HSP90AB1 protein (Fragment) OS=Homo sapiens GN=HSP90AB1 PE=2 SV=1
Q8TBA7 Mass: 74179 Score: 38 Queries matched: 1
HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=2
K9JA46 Mass: 85006 Score: 38 Queries matched: 1
Epididymis luminal secretory protein 52 OS=Homo sapiens GN=EL52 PE=2 SV=1
Q58FF8 Mass: 44492 Score: 38 Queries matched: 1
Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2
Q86U12 Mass: 49669 Score: 38 Queries matched: 1
```

Full-length cDNA clone CS0CAP007YF18 of Thymus of Homo sapiens (human) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=1

P07900 **Mass:** 85006 **Score:** 38 **Queries matched:** 1

Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5

P08238 **Mass:** 83554 **Score:** 38 **Queries matched:** 1

Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4

Q14568 **Mass:** 39454 **Score:** 38 **Queries matched:** 1

Putative heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2

O75322 **Mass:** 63839 **Score:** 38 **Queries matched:** 1

Hsp89-alpha-delta-N OS=Homo sapiens PE=2 SV=1

19. L0R5A1 **Mass:** 11752 **Score:** 34 **Queries matched:** 6 **emPAI:** 0.63

Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1

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

965 **428.7660 855.5174 855.5178 -0.40 0 34 0.0055 1 R.LASIVTPR.N** 962 963 967 968 969

20. Q8WWR7 **Score:** 26 **Queries matched:** 2

Desmoglein 2 (Fragment) OS=Homo sapiens GN=DSG2 PE=4 SV=1

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

428 **584.4394 583.4321 583.4309 2.09 0 26 0.0023 1 R.LLLLL.-** 427

21. Q86TT1 **Mass:** 41817 **Score:** 23 **Queries matched:** 1 **emPAI:** 0.08

Full-length cDNA clone CS0DD006YL02 of Neuroblastoma of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1

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

1665 **819.4687 1636.9228 1636.9229 -0.05 0 23 0.016 1 R.VFAIPPSFASIFLTK.S**

Proteins matching the same set of peptides:

P01871 **Mass:** 49960 **Score:** 23 **Queries matched:** 1

Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3

P04220 **Mass:** 43543 **Score:** 23 **Queries matched:** 1

Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1

22. B7Z945 **Mass:** 20378 **Score:** 23 **Queries matched:** 3 **emPAI:** 0.16

Protein LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1

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

1425 **648.3393 1294.6641 1294.6629 0.88 1 23 0.057 1 R.VGAQVQNPRAPR.K** 1423 1424

Sample T12 green box

```
Database : HumanUniprot uniprot140506 (136615 sequences; 43285968 residues)
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Deamidated (NQ),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 3 ppm
Fragment Mass Tolerance: ± 0.6 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 2179
Protein hits :     H6VRF8 Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
                   Q1KLZ0 HCG15971, isoform CRA_a OS=Homo sapiens GN=PS1TP5BP1 PE=2 SV=1 P13645
                   Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
                   P35527 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 D2JYH4
                   Actin, alpha 2, smooth muscle, aorta OS=Homo sapiens GN=ACTA2 PE=2 SV=1
                   Q2TSD0 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens PE=2 SV=1
                   J3KR22 C-type lectin domain family 10 member A OS=Homo sapiens GN=CLEC10A PE=2
                   SV=1
                   P35908 Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1
                   SV=2
                   P04259 Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5
                   B4DE59 cDNA FLJ60424, highly similar to Junction plakoglobin OS=Homo sapiens
                   PE=2 SV=1
                   P02533 Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
                   P08779 Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4
                   Q1KSF8 XTP3TPA-transactivated protein 1 OS=Homo sapiens GN=XTP3TPATP1 PE=2 SV=1
                   B4DNE0 cDNA FLJ52573, highly similar to Elongation factor 1-alpha 1 OS=Homo
                   sapiens PE=2 SV=1
                   Q7L4M3 KRT8 protein OS=Homo sapiens PE=2 SV=1
                   H0YAS8 Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1 H0YKS4
                   Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=3 SV=1
                   A6NE09 40S ribosomal protein SA OS=Homo sapiens GN=RPSAP58 PE=3 SV=1 F8VV57
                   Keratin, type II cytoskeletal 5 (Fragment) OS=Homo sapiens GN=KRT5 PE=2 SV=1
                   Q0Z944 Beta globin (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
                   H7C4T5 Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=4 SV=1
                   A0N4V7 HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1 Q9NSB2
                   Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=2 SV=2
                   Q1ZYQ1 Tubulin, alpha 2 OS=Homo sapiens GN=TUBA2 PE=2 SV=1
                   L0R5A1 Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1 B7Z945
                   Protein LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1 Q59E90
                   Mannosidase, alpha, class 2B, member 1 variant (Fragment) OS=Homo sapiens PE=2
                   SV=1
```

Select Summary Report

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

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

```
1. H6VRF8 Mass: 66184 Score: 932 Queries matched: 34 emPAI: 1.19
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
754 416.7487 831.4829 831.4814 1.80 0 41 0.0015 1 K.SISISVAR.G
960 487.2694 972.5242 972.5240 0.28 0 59 5.3e-005 1 K.IEISELNR.V 959
992 500.2267 998.4388 998.4379 0.90 0 50 0.00015 1 K.DVDGAYMTK.V 991 993
1015 517.2624 1032.5102 1032.5087 1.38 0 60 3.6e-005 1 R.TLLEGEESR.M 1017
1144 590.3038 1178.5931 1178.5931 -0.02 0 84 8.4e-008 1 K.YEELQITAGR.H 1145 1146
1208 633.3213 1264.6281 1264.6299 -1.43 0 69 2.3e-006 1 R.TNAENEFVTIK.K 1209 1210
1215 639.3587 1276.7027 1276.7027 0.06 0 74 5e-007 1 K.LALDLEIATYR.T
1229 651.8602 1301.7059 1301.7078 -1.45 0 108 2.4e-010 1 R.SLDLDSIIAEVK.A 1228 1230
1267 692.3483 1382.6821 1382.6830 -0.68 0 80 1.6e-007 1 K.SLNNQFASFIDK.V 1266 1268
1273 465.2482 1392.7228 1392.7249 -1.46 1 45 0.00045 1 R.TNAENEFVTIKK.D
1308 738.3981 1474.7816 1474.7780 2.48 0 71 1.2e-006 1 R.FLEQQNQVLQTK.W 1306 1307
1407 546.9581 1637.8525 1637.8525 -0.01 1 43 0.00057 1 K.SLNNQFASFIDKVR.F 1408
1666 538.2752 2149.0717 2149.0705 0.56 1 32 0.013 1 R.THNLEPYFESFINNLRR.R 1667 1668
1736 762.7132 2285.1178 2285.1175 0.13 1 59 1.7e-005 1 K.AEAESLYQSKYEELQITAGR.H 1735
1811 855.7277 2564.1612 2564.1595 0.64 0 23 0.06 1 R.MSGECAPNVSVSVSTSHTTISGGGSR.G
1916 978.1779 2931.5119 2931.5090 0.99 1 32 0.0089 1 R.FLEQQNQVLQTKWELLQQVDTSTR.T
Proteins matching the same set of peptides:
H6VRF9 Mass: 66200 Score: 932 Queries matched: 34
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG0 Mass: 66101 Score: 932 Queries matched: 34
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG1 Mass: 66257 Score: 932 Queries matched: 34
Keratin 1 OS=Homo sapiens GN=KRT1 PE=2 SV=1
H6VRG3 Mass: 66242 Score: 932 Queries matched: 34
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
P04264 Mass: 66170 Score: 932 Queries matched: 34
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
2. Q1KLZ0 Mass: 42052 Score: 861 Queries matched: 47 emPAI: 4.65
HCG15971, isoform CRA_a OS=Homo sapiens GN=PS1TP5BP1 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
434 322.6899 643.3653 643.3653 0.03 0 39 0.012 1 R.LDLAGR.D
438 322.7208 643.4270 643.4268 0.29 0 27 0.017 1 R.GILTLK.Y 437 439 440
695 398.2404 794.4663 794.4650 1.57 0 27 0.017 1 K.IIAPPER.K 693
696 400.7714 799.5282 799.5280 0.32 1 24 0.031 1 K.RGILTLK.Y 697
964 488.7276 975.4406 975.4410 -0.41 0 64 4.6e-006 1 K.AGFAGDDAPR.A
988 499.7467 997.4788 997.4790 -0.26 0 28 0.021 1 R.DLTDYLMK.I 987
1102 566.7671 1131.5196 1131.5197 -0.03 0 74 4.6e-007 1 R.GYSFTTTAER.E 1101 1103
1122 581.3137 1160.6128 1160.6111 1.48 0 61 1.3e-005 1 K.EITALAPSTMK.I 1121
1133 586.2881 1170.5617 1170.5638 -1.83 0 60 1.4e-005 1 R.HQGVMVGMGQK.D 1135
1141 589.3107 1176.6069 1176.6060 0.80 0 (34) 0.0057 1 K.EITALAPSTMK.I 1142 1143
1161 599.8567 1197.6989 1197.6982 0.54 1 41 0.00071 1 R.AVFPSIVGRPR.H
1397 541.9517 1622.8332 1622.8338 -0.35 1 45 0.00055 1 R.LDLAGRDLTDYLMK.I 1395 1396 1398 1399
1402 543.9470 1628.8193 1628.8158 2.14 1 25 1.4 1 R.GYSFTTTAEREIVR.D 1401
1411 547.2833 1638.8279 1638.8287 -0.46 1 (36) 0.0038 1 R.LDLAGRDLTDYLMK.I
1469 895.9509 1789.8873 1789.8846 1.49 0 74 7.9e-007 1 K.SYELPDGQVITIGNER.F 1468
1576 977.5376 1953.0607 1953.0571 1.84 0 64 2.5e-006 2 R.VAPEEHPVLLTEAPLNPK.A 1574 1575 1577 1578
1579
1705 1108.0398 2214.0651 2214.0627 1.09 0 68 2.6e-006 1 K.DLYANTVLSGGTTMYPGIADR.M 1704 1706
1802 850.7299 2549.1678 2549.1665 0.51 0 99 2.1e-009 1 K.LCYVALDFEQEMATAASSSSLEK.S
1959 1061.8781 3182.6125 3182.6071 1.71 0 41 0.00091 1 R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1957
1960 1961
Proteins matching the same set of peptides:
Q8WVW5 Mass: 40819 Score: 861 Queries matched: 47
Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1
Q53G76 Mass: 42036 Score: 861 Queries matched: 47
Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1
Q53G99 Mass: 42080 Score: 861 Queries matched: 47
Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1
Q53GK6 Mass: 42038 Score: 861 Queries matched: 47
Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1
P60709 Mass: 42052 Score: 861 Queries matched: 47
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
P63261 Mass: 42108 Score: 861 Queries matched: 47
Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
3. P13645 Mass: 59020 Score: 559 Queries matched: 22 emPAI: 0.59
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
705 404.2036 806.3926 806.3923 0.38 0 45 0.00048 1 R.LAADDFR.L 704 706
979 497.2539 992.4933 992.4927 0.65 0 37 0.0051 1 K.YENEVALR.Q 977 978
1011 516.3031 1030.5917 1030.5910 0.62 0 63 2.8e-006 1 R.VLDELTLTK.A 1012
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1206 631.8033 1261.5921 1261.5899 1.74 0 88 1.9e-008 1 R.SLLEGEGSSGGGGR.G 1207
1253 453.2445 1356.7116 1356.7110 0.44 1 (35) 0.0047 1 R.QSVEADINGLRR.V 1252
1255 453.5723 1357.6952 1357.6950 0.17 1 40 0.0026 1 R.QSVEADINGLRR.V 1256
1265 691.3281 1380.6416 1380.6408 0.55 0 87 3.8e-008 1 R.ALEESNYELEGK.I 1263 1264
1288 478.9292 1433.7658 1433.7626 2.21 1 23 0.092 1 K.IRLENEIQTYR.S
1434 854.3906 1706.7667 1706.7649 1.07 0 134 5e-013 1 K.GSLGGGFSSGGFSGGSFSR.G 1432 1433
1703 738.0382 2211.0928 2211.0906 0.99 1 43 0.00099 1 K.SKELTTEIDNNIEQISSYK.S
4. P35527 Mass: 62255 Score: 525 Queries matched: 29 emPAI: 0.89
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
871 449.2103 896.4060 896.4062 -0.22 0 38 0.002 1 R.MTLDDFR.I 872
1038 530.7850 1059.5555 1059.5560 -0.49 0 52 0.00018 1 K.TLLDIDNTR.M 1039 1040
1118 579.2991 1156.5836 1156.5836 -0.06 0 77 1.8e-007 1 R.QGVDADINGLR.Q 1117
1119 579.7917 1157.5689 1157.5677 1.08 0 (22) 0.089 1 R.QGVDADINGLR.Q
1233 436.5640 1306.6701 1306.6703 -0.17 1 39 0.002 1 R.IKFEMEQNLR.Q 1231 1232 1234 1235
1503 613.3266 1836.9581 1836.9581 -0.02 0 62 6.8e-006 1 R.HGVQELEIELQSQLSK.K 1501 1502 1504
1521 617.9814 1850.9224 1850.9196 1.53 1 36 0.0045 1 K.TLNDMRQEYEQLIAK.N 1519 1520
1529 623.3133 1866.9182 1866.9145 1.97 1 (29) 0.022 1 K.TLNDMRQEYEQLIAK.N 1528
1585 656.0253 1965.0541 1965.0531 0.52 1 74 2e-007 1 R.HGVQELEIELQSQLSKK.A 1584
1793 837.3826 2509.1261 2509.1245 0.63 0 65 2.8e-006 1 K.EIETYHNLLEGGQEDFESSGAGK.I 1792
1970 1075.0994 3222.2764 3222.2744 0.63 0 29 0.0012 1
R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S
1979 1088.8423 3263.5050 3263.5066 -0.46 0 52 5.8e-005 1 K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E 1978
5. D2JYH4 Mass: 42381 Score: 511 Queries matched: 29 emPAI: 2.15
Actin, alpha 2, smooth muscle, aorta OS=Homo sapiens GN=ACTA2 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
434 322.6899 643.3653 643.3653 0.03 0 39 0.012 1 R.LDLAGR.D
438 322.7208 643.4270 643.4268 0.29 0 27 0.017 1 R.GILTLK.Y 437 439 440
695 398.2404 794.4663 794.4650 1.57 0 27 0.017 1 K.IIAPPER.K 693
696 400.7714 799.5282 799.5280 0.32 1 24 0.031 1 K.RGILTLK.Y 697
964 488.7276 975.4406 975.4410 -0.41 0 64 4.6e-006 1 K.AGFAGDDAPR.A
988 499.7467 997.4788 997.4790 -0.26 0 28 0.021 1 R.DLTDYLMK.I 987
1122 581.3137 1160.6128 1160.6111 1.48 0 61 1.3e-005 1 K.EITALAPSTMK.I 1121
1133 586.2881 1170.5617 1170.5638 -1.83 0 60 1.4e-005 1 R.HQGVMVGMGQK.D 1135
1141 589.3107 1176.6069 1176.6060 0.80 0 (34) 0.0057 1 K.EITALAPSTMK.I 1142 1143
1161 599.8567 1197.6989 1197.6982 0.54 1 41 0.00071 1 R.AVFPSIVGRPR.H
1397 541.9517 1622.8332 1622.8338 -0.35 1 45 0.00055 1 R.LDLAGRDLTDYLMK.I 1395 1396 1398 1399
1411 547.2833 1638.8279 1638.8287 -0.46 1 (36) 0.0038 1 R.LDLAGRDLTDYLMK.I
1469 895.9509 1789.8873 1789.8846 1.49 0 74 7.9e-007 1 K.SYELPDGQVITIGNER.F 1468
1582 652.6871 1955.0396 1955.0364 1.65 0 20 0.093 1 R.VAPEEHPTLLTEAPLNPK.A
Proteins matching the same set of peptides:
A8K3K1 Mass: 42362 Score: 511 Queries matched: 29
cDNA FLJ78096, highly similar to Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA OS=Homo
sapiens PE=2 SV=1
P62736 Mass: 42381 Score: 511 Queries matched: 29
Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
P63267 Mass: 42249 Score: 511 Queries matched: 29
Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
P68032 Mass: 42334 Score: 511 Queries matched: 29
Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
P68133 Mass: 42366 Score: 511 Queries matched: 29
Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1
6. Q2TSD0 Mass: 36197 Score: 408 Queries matched: 11 emPAI: 0.80
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
692 398.2132 794.4119 794.4109 1.25 0 31 0.007 1 K.LTGMAFR.V
703 403.7110 805.4074 805.4083 -1.06 0 34 0.0036 1 K.VGVNGFGR.I
1241 444.2216 1329.6430 1329.6421 0.69 1 23 0.29 1 R.VVDLMAHMASKE.-
1277 706.3995 1410.7845 1410.7831 1.05 0 66 1.9e-006 1 R.GALQNIIPASTGAAK.A 1278
1340 765.9007 1529.7868 1529.7872 -0.23 0 89 3.9e-008 1 R.VPTANVSVVDLTCR.L
1458 882.4067 1762.7989 1762.7951 2.16 0 85 4.3e-008 1 K.LISWYDNEFGYSNR.V 1457
1500 917.4656 1832.9166 1832.9124 2.29 0 42 0.0011 1 K.IISNASCTTNCLAPLAK.V
1815 649.5958 2594.3540 2594.3527 0.51 0 37 0.0014 1 K.VIHDNFGIVEGLMTTVHAITATQK.T 1816
Proteins matching the same set of peptides:
V9HVZ4 Mass: 36201 Score: 408 Queries matched: 11
Epididymis secretory sperm binding protein Li 162eP OS=Homo sapiens GN=HEL-S-162eP PE=2 SV=1
P04406 Mass: 36201 Score: 408 Queries matched: 11
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
7. J3KR22 Mass: 33175 Score: 406 Queries matched: 30 emPAI: 1.98
C-type lectin domain family 10 member A OS=Homo sapiens GN=CLEC10A PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1005 511.2508 1020.4871 1020.4876 -0.49 0 30 0.017 1 R.EEQNFVQK.Y
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1045 535.8146 1069.6147 1069.6132 1.41 0 70 1.9e-006 1 R.VQQLVQDLK.K 1046
1082 561.8242 1121.6338 1121.6305 2.94 0 50 0.0001 1 K.NAHLVVINSR.E 1078 1079 1080 1081
1152 592.3168 1182.6190 1182.6179 0.89 0 51 5.1e-005 1 R.QAVHSEMLLR.V 1148 1149 1150 1151
1167 599.8619 1197.7092 1197.7081 0.89 1 71 6.6e-007 1 R.VQQLVQDLKK.L 1165 1166 1168 1169 1170
1172 400.5456 1198.6151 1198.6128 1.86 0 (29) 0.013 1 R.QAVHSEMLLR.V 1171
1649 709.0426 2124.1060 2124.1076 -0.74 1 37 0.0024 1 K.NAHLVVINSREEQNFVQK.Y 1650 1652 1653 1654
1661 1066.4959 2130.9772 2130.9721 2.40 0 97 3.2e-009 1 K.YLGSAYTWMGLSDPEGAWK.W 1658 1659 1660
8. P35908 Mass: 65678 Score: 351 Queries matched: 10 emPAI: 0.26
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
751 416.2512 830.4879 830.4862 2.12 0 20 0.25 1 R.SLVGLGGTK.S
960 487.2694 972.5242 972.5240 0.28 0 59 5.3e-005 1 K.IEISELNR.V 959
1020 519.2677 1036.5209 1036.5189 1.90 0 65 9.2e-006 1 R.YLDGLTAER.T
1066 554.2765 1106.5384 1106.5356 2.57 0 46 0.00067 1 K.AQYEEIAQR.S
1197 627.8084 1253.6023 1253.6001 1.79 0 90 1.8e-008 1 R.GFSSGSAVVSGGSR.R 1196
1308 738.3981 1474.7816 1474.7780 2.48 0 71 1.2e-006 1 R.FLEQQNQVLQTK.W 1306 1307
9. P04259 Mass: 60315 Score: 259 Queries matched: 6 emPAI: 0.22
Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1066 554.2765 1106.5384 1106.5356 2.57 0 46 0.00067 1 K.AQYEEIAQR.S
1144 590.3038 1178.5931 1178.5931 -0.02 0 84 8.4e-008 1 K.YEELQITAGR.H 1145 1146
1376 799.8839 1597.7533 1597.7519 0.90 0 83 5.7e-008 1 R.ISIGGGSCAISGGYGSR.A
1420 556.5945 1666.7616 1666.7594 1.30 0 45 0.0016 1 R.SRGSGGLGGACGGAGFGSR.S
10. B4DE59 Mass: 62862 Score: 239 Queries matched: 8 emPAI: 0.21
cDNA FLJ60424, highly similar to Junction plakoglobin OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
705 404.2036 806.3926 806.3923 0.38 0 45 0.00048 1 R.LAADDFR.T 704 706
1010 515.3009 1028.5873 1028.5866 0.67 0 49 0.00034 1 R.VLDELTLAR.T
1026 521.3071 1040.5996 1040.5978 1.68 0 63 5.7e-006 1 R.IVLQIDNAR.L 1024 1025
1272 695.3479 1388.6812 1388.6783 2.06 0 82 9.3e-008 1 K.AALEDTLAETEAR.F
Proteins matching the same set of peptides:
P08727 Mass: 44079 Score: 239 Queries matched: 8
Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4
11. P02533 Mass: 51872 Score: 223 Queries matched: 8 emPAI: 0.27
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
705 404.2036 806.3926 806.3923 0.38 0 45 0.00048 1 R.LAADDFR.T 704 706
1010 515.3009 1028.5873 1028.5866 0.67 0 49 0.00034 1 R.VLDELTLAR.A
1064 553.7847 1105.5549 1105.5550 -0.04 0 62 1.1e-005 1 R.ISSVLAGGSCR.A 1065
1280 713.3518 1424.6890 1424.6896 -0.41 0 68 2.6e-006 1 R.APSTYGGGLSVSSSR.F 1281
12. P08779 Mass: 51578 Score: 214 Queries matched: 7 emPAI: 0.27
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
705 404.2036 806.3926 806.3923 0.38 0 45 0.00048 1 R.LAADDFR.T 704 706
1010 515.3009 1028.5873 1028.5866 0.67 0 49 0.00034 1 R.VLDELTLAR.T
1064 553.7847 1105.5549 1105.5550 -0.04 0 62 1.1e-005 1 R.ISSVLAGGSCR.A 1065
1243 669.8368 1337.6590 1337.6575 1.10 0 58 2.1e-005 1 R.APSTYGGGLSVSSR.F
13. Q1KSF8 Mass: 23896 Score: 151 Queries matched: 4 emPAI: 0.46
XTP3TPA-transactivated protein 1 OS=Homo sapiens GN=XTP3TPATP1 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1109 572.3206 1142.6266 1142.6270 -0.41 0 53 0.00016 1 K.LAVNMVPFPR.L 1110
1238 660.3553 1318.6960 1318.6955 0.37 0 43 0.00065 1 R.IMNTFSVVPSPK.V
1388 540.9493 1619.8261 1619.8283 -1.31 0 55 6.4e-005 1 R.LHFFMPGFAPLTSR.G
Proteins matching the same set of peptides:
B3KML9 Mass: 44916 Score: 151 Queries matched: 4
cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain OS=Homo sapiens
PE=2 SV=1
B4DE77 Mass: 46211 Score: 151 Queries matched: 4
cDNA FLJ55189, highly similar to Tubulin beta-4 chain OS=Homo sapiens PE=2 SV=1
B4DQN9 Mass: 42096 Score: 151 Queries matched: 4
cDNA FLJ50617, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B4DY90 Mass: 52414 Score: 151 Queries matched: 4
cDNA FLJ56903, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B4E052 Mass: 40000 Score: 151 Queries matched: 4
cDNA FLJ52378, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
Q5JP53 Mass: 48135 Score: 151 Queries matched: 4
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=4 SV=1
Q5ST81 Mass: 42114 Score: 151 Queries matched: 4
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=3 SV=1
Q5SU16 Mass: 50095 Score: 151 Queries matched: 4
Beta 5-tubulin OS=Homo sapiens GN=TUBB PE=2 SV=1
Q6LC01 Mass: 49362 Score: 151 Queries matched: 4
MRNA encoding beta-tubulin. (from clone D-beta-1) (Fragment) OS=Homo sapiens PE=2 SV=1
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B7ZAF0 Mass: 46936 Score: 151 Queries matched: 4
cDNA, FLJ79164, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
Q8IWP6 Mass: 50177 Score: 151 Queries matched: 4
Class IVb beta tubulin OS=Homo sapiens PE=2 SV=1
Q8IZ29 Mass: 50264 Score: 151 Queries matched: 4
Tubulin, beta 2C OS=Homo sapiens GN=TUBB2C PE=2 SV=1
Q8N6N5 Mass: 50232 Score: 151 Queries matched: 4
Tubulin, beta 2C OS=Homo sapiens GN=TUBB2C PE=2 SV=1
Q9BUU9 Mass: 38690 Score: 151 Queries matched: 4
TUBB protein (Fragment) OS=Homo sapiens GN=TUBB PE=2 SV=1
P04350 Mass: 50010 Score: 151 Queries matched: 4
Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2
P07437 Mass: 50095 Score: 151 Queries matched: 4
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2
P68371 Mass: 50255 Score: 151 Queries matched: 4
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1
14. B4DNE0 Mass: 42911 Score: 128 Queries matched: 2 emPAI: 0.15
cDNA FLJ52573, highly similar to Elongation factor 1-alpha 1 OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1009 513.3086 1024.6026 1024.6030 -0.37 0 98 1e-009 1 K.IGGIGTVPVGR.V
1369 530.2985 1587.8737 1587.8733 0.25 0 30 0.0068 1 K.THINIVVIGHVDSGK.S
Proteins matching the same set of peptides:
Q5VTE0 Mass: 50495 Score: 128 Queries matched: 2
Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1
Q6IPN6 Mass: 50433 Score: 128 Queries matched: 2
Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1
Q6IPS9 Mass: 50451 Score: 128 Queries matched: 2
Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1
Q6IPT9 Mass: 50438 Score: 128 Queries matched: 2
Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1
Q6IQ15 Mass: 48181 Score: 128 Queries matched: 2
EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1
A8K9C4 Mass: 50511 Score: 128 Queries matched: 2
Elongation factor 1-alpha OS=Homo sapiens PE=2 SV=1
Q53G85 Mass: 50423 Score: 128 Queries matched: 2
Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1
Q53GA1 Mass: 50421 Score: 128 Queries matched: 2
Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1
Q53GE9 Mass: 50421 Score: 128 Queries matched: 2
Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1
Q53HM9 Mass: 50452 Score: 128 Queries matched: 2
Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1
Q53HQ7 Mass: 50509 Score: 128 Queries matched: 2
Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1
Q53HR5 Mass: 50435 Score: 128 Queries matched: 2
Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1
Q05639 Mass: 50780 Score: 128 Queries matched: 2
Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1
P68104 Mass: 50451 Score: 128 Queries matched: 2
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1
15. Q7L4M3 Mass: 30802 Score: 98 Queries matched: 2 emPAI: 0.22
KRT8 protein OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1215 639.3587 1276.7027 1276.7027 0.06 0 74 5e-007 1 K.LALDIEIATYR.K
1245 447.9210 1340.7410 1340.7412 -0.12 1 24 0.12 1 R.LQAEIEGLKGQR.A
Proteins matching the same set of peptides:
Q969I0 Mass: 41083 Score: 98 Queries matched: 2
KRT8 protein (Fragment) OS=Homo sapiens GN=KRT8 PE=2 SV=2
P05787 Mass: 53671 Score: 98 Queries matched: 2
Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7
16. H0YAS8 Mass: 16224 Score: 92 Queries matched: 3 emPAI: 0.44
Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1221 644.8236 1287.6327 1287.6306 1.64 0 59 2.5e-005 1 R.ELDESLQVAER.L 1220
1747 772.0651 2313.1736 2313.1700 1.52 0 33 0.028 1 R.VTTVASHTSDSDVPSGVTEVVVK.L
Proteins matching the same set of peptides:
H0YC35 Mass: 33794 Score: 92 Queries matched: 3
Clusterin (Fragment) OS=Homo sapiens GN=CLU PE=3 SV=1
B4DW11 Mass: 25952 Score: 92 Queries matched: 3
cDNA FLJ57622, highly similar to Clusterin OS=Homo sapiens PE=2 SV=1
P10909 Mass: 53031 Score: 92 Queries matched: 3
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1
17. H0YKS4 Mass: 19632 Score: 67 Queries matched: 2 emPAI: 0.35
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Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1179 611.8025 1221.5904 1221.5877 2.17 0 30 0.48 1 K.TPAQYDASELK.A
1195 622.8156 1243.6167 1243.6156 0.85 0 37 0.0035 1 R.TNQELQEINR.V
Proteins matching the same set of peptides:
H0YM50 Mass: 28582 Score: 67 Queries matched: 2
Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=3 SV=1
H0YMD0 Mass: 25440 Score: 67 Queries matched: 2
Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1
H0YMM1 Mass: 16563 Score: 67 Queries matched: 2
Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1
H0YMU9 Mass: 25667 Score: 67 Queries matched: 2
Annexin OS=Homo sapiens GN=ANXA2 PE=2 SV=1
H0YN42 Mass: 28921 Score: 67 Queries matched: 2
Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1
H0YNP5 Mass: 19829 Score: 67 Queries matched: 2
Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1
B4DNH8 Mass: 21827 Score: 67 Queries matched: 2
Annexin OS=Homo sapiens PE=2 SV=1
A6NMY6 Mass: 38806 Score: 67 Queries matched: 2
Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2P2 PE=5 SV=2
V9HW65 Mass: 38780 Score: 67 Queries matched: 2
Annexin OS=Homo sapiens GN=HEL-S-270 PE=2 SV=1
P07355 Mass: 38808 Score: 67 Queries matched: 2

Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2
18. A6NE09 Mass: 33002 Score: 65 Queries matched: 1 emPAI: 0.10
40S ribosomal protein SA OS=Homo sapiens GN=RPSAP58 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1174 602.3288 1202.6430 1202.6408 1.86 0 65 7.8e-006 1 K.FAAATGATPIAGR.F
Proteins matching the same set of peptides:
C9J9K3 Mass: 29601 Score: 65 Queries matched: 1
40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=3 SV=1
Q96RS2 Mass: 33089 Score: 65 Queries matched: 1
40S ribosomal protein SA OS=Homo sapiens GN=LAMR1P15 PE=2 SV=1
P08865 Mass: 32947 Score: 65 Queries matched: 1
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4
19. F8VV57 Mass: 12207 Score: 58 Queries matched: 2 emPAI: 0.27
Keratin, type II cytoskeletal 5 (Fragment) OS=Homo sapiens GN=KRT5 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1068 556.2908 1110.5670 1110.5669 0.01 0 58 2.8e-005 1 R.ISISTSGGSFR.N 1069
Proteins matching the same set of peptides:
P13647 Mass: 62568 Score: 58 Queries matched: 2
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3
20. Q0Z944 Mass: 11554 Score: 55 Queries matched: 1 emPAI: 0.28
Beta globin (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1237 657.8374 1313.6603 1313.6575 2.11 0 55 5.4e-005 1 K.VNVDEVGGEALGR.L
Proteins matching the same set of peptides:
B3VL05 Mass: 11536 Score: 55 Queries matched: 1
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1
B3VL12 Mass: 4263 Score: 55 Queries matched: 1
Truncated beta globin OS=Homo sapiens PE=2 SV=1
B3VL17 Mass: 11534 Score: 55 Queries matched: 1
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1
B3VL31 Mass: 11550 Score: 55 Queries matched: 1
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1
B3VL86 Mass: 15175 Score: 55 Queries matched: 1
Mutant beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1
Q3LR79 Mass: 11532 Score: 55 Queries matched: 1
Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q3Y9I8 Mass: 11013 Score: 55 Queries matched: 1
Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q4TWB7 Mass: 11537 Score: 55 Queries matched: 1
Beta globin (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q4TZM4 Mass: 11073 Score: 55 Queries matched: 1
Hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
B5ANL9 Mass: 9464 Score: 55 Queries matched: 1
Beta globin chain (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
D5FZW3 Mass: 4547 Score: 55 Queries matched: 1
Beta globin (Fragment) OS=Homo sapiens PE=2 SV=1
Q6V0K9 Mass: 11524 Score: 55 Queries matched: 1
Mutant hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
```

```
J7LKS8 Mass: 3518 Score: 55 Queries matched: 1
Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
C8C504 Mass: 16101 Score: 55 Queries matched: 1
Beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1
F8W6P5 Mass: 9664 Score: 55 Queries matched: 1
LVV-hemorphin-7 (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
Q8IUL9 Mass: 11598 Score: 55 Queries matched: 1
Hemoglobin beta chain variant Hb.Sinai-Bel Air (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q8IZI0 Mass: 11555 Score: 55 Queries matched: 1
Hemoglobin beta chain variant Hb-I_Toulouse (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
A9YUX2 Mass: 7051 Score: 55 Queries matched: 1
Truncated beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1
D9YZU5 Mass: 16102 Score: 55 Queries matched: 1
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=2 SV=1
E9M263 Mass: 6248 Score: 55 Queries matched: 1
Hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
E9NGZ5 Mass: 11544 Score: 55 Queries matched: 1
Hemoglobin beta globin chain (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q9BWU5 Mass: 11551 Score: 55 Queries matched: 1
Mutant hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q9BWV6 Mass: 12283 Score: 55 Queries matched: 1
Mutant beta globin OS=Homo sapiens GN=HBB PE=3 SV=1
Q9BXA2 Mass: 6459 Score: 55 Queries matched: 1
Beta-globin (Fragment) OS=Homo sapiens PE=2 SV=1
Q9GZL9 Mass: 12635 Score: 55 Queries matched: 1
Beta-globin (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
Q9H1I6 Mass: 3292 Score: 55 Queries matched: 1
Mutant beta-globin (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
Q9UBV6 Mass: 6656 Score: 55 Queries matched: 1
Beta-globin (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q9UP81 Mass: 9740 Score: 55 Queries matched: 1
Mutant beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1
Q52MT0 Mass: 11526 Score: 55 Queries matched: 1
Beta globin (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
Q14473 Mass: 19204 Score: 55 Queries matched: 1
Beta-globin gene from a thalassemia patient, OS=Homo sapiens PE=3 SV=1
Q14484 Mass: 6686 Score: 55 Queries matched: 1
Beta-globin (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1
P68871 Mass: 16102 Score: 55 Queries matched: 1
Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2
O95408 Mass: 6262 Score: 55 Queries matched: 1
Beta globin (Fragment) OS=Homo sapiens GN=HBB PE=3 SV=1
21. H7C4T5 Mass: 36596 Score: 48 Queries matched: 3 emPAI: 0.09
Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
828 434.7670 867.5195 867.5178 1.97 0 21 0.088 1 -.PVSVTPIR.D
832 435.7737 869.5328 869.5335 -0.74 0 27 0.019 1 -.VVSVTPIR.D 841
22. A0N4V7 Mass: 2269 Score: 44 Queries matched: 17 emPAI: 6.57
HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
774 421.7588 841.5030 841.5022 1.01 1 44 0.00078 1 K.GITLSVRP.- 766 767 768 769 770 771 775 776
777 779 780 781 782 783 784 785
23. Q9NSB2 Mass: 65942 Score: 41 Queries matched: 1 emPAI: 0.05
Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=2 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1257 679.8672 1357.7199 1357.7202 -0.15 0 41 0.0013 1 R.VAPATGDLLSTGTR.S
24. Q1ZYQ1 Mass: 50612 Score: 39 Queries matched: 2 emPAI: 0.06
Tubulin, alpha 2 OS=Homo sapiens GN=TUBA2 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1775 604.5575 2414.2011 2414.1978 1.34 1 39 0.0019 1 R.QLFHPEQLITGKEDAANNYAR.G 1774
Proteins matching the same set of peptides:
B3KPS3 Mass: 46725 Score: 39 Queries matched: 2
cDNA FLJ32131 fis, clone PEBLM2000267, highly similar to Tubulin alpha-ubiquitous chain OS=Homo
sapiens PE=2 SV=1
B3KT06 Mass: 46825 Score: 39 Queries matched: 2
cDNA FLJ37398 fis, clone BRAMY2027467, highly similar to Tubulin alpha-ubiquitous chain OS=Homo
sapiens PE=2 SV=1
F5H5D3 Mass: 58606 Score: 39 Queries matched: 2
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1
Q6QMJ5 Mass: 10870 Score: 39 Queries matched: 2
Tubulin alpha-1 (Fragment) OS=Homo sapiens GN=TUBA1 PE=2 SV=1
B7Z1K5 Mass: 58636 Score: 39 Queries matched: 2
cDNA FLJ55956, highly similar to Tubulin alpha-6 chain OS=Homo sapiens PE=2 SV=1
```

Q7Z3M3 **Mass:** 54619 **Score:** 39 **Queries matched:** 2
Putative uncharacterized protein DKFZp686L04275 (Fragment) OS=Homo sapiens GN=DKFZp686L04275 PE=2 SV=1

A8JZY9 **Mass:** 50788 **Score:** 39 **Queries matched:** 2
cDNA FLJ78587 OS=Homo sapiens PE=2 SV=1

A8MUB1 **Mass:** 48982 **Score:** 39 **Queries matched:** 2
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1

F8VQQ4 **Mass:** 24377 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1A chain (Fragment) OS=Homo sapiens GN=TUBA1A PE=2 SV=1

F8VRZ4 **Mass:** 12269 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1A chain (Fragment) OS=Homo sapiens GN=TUBA1A PE=2 SV=1

F8VS66 **Mass:** 14563 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1

F8VVB9 **Mass:** 27877 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1B chain (Fragment) OS=Homo sapiens GN=TUBA1B PE=2 SV=1

F8VWV9 **Mass:** 8938 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1B chain (Fragment) OS=Homo sapiens GN=TUBA1B PE=2 SV=1

F8VX09 **Mass:** 8283 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1B chain (Fragment) OS=Homo sapiens GN=TUBA1B PE=2 SV=1

Q8N532 **Mass:** 37309 **Score:** 39 **Queries matched:** 2
TUBA1C protein OS=Homo sapiens GN=TUBA1C PE=2 SV=1

Q8WU19 **Mass:** 37707 **Score:** 39 **Queries matched:** 2
TUBA1B protein OS=Homo sapiens GN=TUBA1B PE=2 SV=1

C9J2C0 **Mass:** 52750 **Score:** 39 **Queries matched:** 2
Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=3 SV=1

C9JDL2 **Mass:** 13455 **Score:** 39 **Queries matched:** 2
Tubulin alpha-4A chain (Fragment) OS=Homo sapiens GN=TUBA4A PE=2 SV=1

C9JEV8 **Mass:** 17093 **Score:** 39 **Queries matched:** 2
Tubulin alpha-4A chain (Fragment) OS=Homo sapiens GN=TUBA4A PE=2 SV=1

C9JJQ8 **Mass:** 21949 **Score:** 39 **Queries matched:** 2
Tubulin alpha-4A chain (Fragment) OS=Homo sapiens GN=TUBA4A PE=2 SV=1

C9JQ00 **Mass:** 20024 **Score:** 39 **Queries matched:** 2
Tubulin alpha-4A chain (Fragment) OS=Homo sapiens GN=TUBA4A PE=2 SV=1

C9K0S6 **Mass:** 5331 **Score:** 39 **Queries matched:** 2
Tubulin alpha-8 chain (Fragment) OS=Homo sapiens GN=TUBA8 PE=4 SV=1

Q9BQE3 **Mass:** 50548 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1

Q9NY65 **Mass:** 50746 **Score:** 39 **Queries matched:** 2
Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8 PE=1 SV=1

Q53GA7 **Mass:** 50476 **Score:** 39 **Queries matched:** 2
Tubulin alpha 6 variant (Fragment) OS=Homo sapiens PE=2 SV=1

Q71U36 **Mass:** 50788 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1

Q13748 **Mass:** 50612 **Score:** 39 **Queries matched:** 2
Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3

P68363 **Mass:** 50804 **Score:** 39 **Queries matched:** 2
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1

P68366 **Mass:** 50634 **Score:** 39 **Queries matched:** 2
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1

25. L0R5A1 **Mass:** 11752 **Score:** 39 **Queries matched:** 5 **emPAI:** 0.28
Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
810 **428.7663 855.5180 855.5178 0.27 0 39 0.0021 1 R.LASIVTPR.N** 805 806 808 809

26. B7Z945 **Mass:** 20378 **Score:** 33 **Queries matched:** 3 **emPAI:** 0.16
Protein LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1224 **648.3391 1294.6637 1294.6629 0.56 1 33 0.0066 1 R.VGAQVQNPRAPR.K** 1223 1225

27. Q59E90 **Mass:** 113918 **Score:** 25 **Queries matched:** 2 **emPAI:** 0.03
Mannosidase, alpha, class 2B, member 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1184 **613.8599 1225.7052 1225.7030 1.77 0 25 0.021 1 K.LIQLVNAQQAK.G** 1185

Sample T9 blue box

Database : HumanUniprot uniprot140506 (136615 sequences; 43285968 residues)
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Deamidated (NQ),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 3 ppm
Fragment Mass Tolerance: ± 0.6 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 1647

Protein hits : P49327 Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 **H6VRF8** Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 **A7Y9J9** Mucin 5AC, oligomeric mucus/gel-forming OS=Homo sapiens GN=MUC5AC PE=4 SV=1 **P13645** Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 **B1AVQ5** Mucin-1 subunit alpha OS=Homo sapiens GN=MUC1 PE=2 SV=1 **P35527** Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 **H0Y4K8** Ugl-Y3 (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1 **A0N4V7** HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1 **L0R5A1** Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1 **H7C4T5** Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=4 SV=1

Select Summary Report

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

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

1. P49327 **Mass:** 275877 **Score:** 395 **Queries matched:** 13 **emPAI:** 0.11
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
705 **481.2706 960.5267 960.5240 2.84 0 44 0.0011 1 K.TGTVSLEVR.L**
951 **704.8665 1407.7184 1407.7180 0.24 0 41 0.0013 1 R.LSIPTYGLQCTR.A**
953 **713.8916 1425.7686 1425.7650 2.56 0 65 4.1e-006 1 R.SLLVNPEGPTLMR.L** 952
1065 **889.5010 1776.9874 1776.9873 0.07 0 82 2e-008 1 K.LPEDPLLSGLLDSPALK.A**
1111 **630.0052 1886.9938 1886.9963 -1.32 0 50 0.00013 1 R.VTVAGGVHISGLHTESAPR.R**
1195 **731.4058 2191.1954 2191.2001 -2.12 0 22 0.022 1 R.IPGLLSPHPLLQLSYTATDR.H**
1259 **824.7715 2471.2926 2471.2961 -1.44 0 29 0.0089 1 R.LHLSGIDANPNALFPPVEFPAPR.G**
1274 **848.0757 2541.2054 2541.2023 1.19 0 32 0.012 1 R.SLYQSAGVAPESFEYIEAHGTGTK.V** 1275
1276
1301 **667.5919 2666.3384 2666.3340 1.66 1 30 0.0092 1 R.HFLLEEDKPEEPTAHAFVSTLTR.G** 1300

2. H6VRF8 **Mass:** 66184 **Score:** 376 **Queries matched:** 10 **emPAI:** 0.38
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
637 **437.7531 873.4917 873.4920 -0.36 0 39 0.0053 1 R.SLVNLGGSK.S**
774 **517.2608 1032.5071 1032.5087 -1.55 0 27 0.051 1 R.TLLEGEESR.M**
799 **533.2653 1064.5161 1064.5138 2.13 0 56 5.5e-005 1 K.AQYEDIAQK.S** 798

```
880 633.3235 1264.6324 1264.6299 1.93 0 57 4.4e-005 1 R.TNAENEFVTIK.K
903 651.8626 1301.7106 1301.7078 2.15 0 108 3e-010 1 R.SLDLDSIIAEVK.A 901 902
974 738.3951 1474.7757 1474.7780 -1.56 0 60 1.3e-005 1 R.FLEQQNQVLQTK.W
1180 717.3628 2149.0666 2149.0705 -1.80 1 28 0.035 1 R.THNLEPYFESFINNLRR.R
Proteins matching the same set of peptides:
H6VRG0 Mass: 66101 Score: 376 Queries matched: 10
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG1 Mass: 66257 Score: 376 Queries matched: 10
Keratin 1 OS=Homo sapiens GN=KRT1 PE=2 SV=1
H6VRG3 Mass: 66242 Score: 376 Queries matched: 10
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
P04264 Mass: 66170 Score: 376 Queries matched: 10
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
3. A7Y9J9 Mass: 666520 Score: 215 Queries matched: 6 emPAI: 0.01
Mucin 5AC, oligomeric mucus/gel-forming OS=Homo sapiens GN=MUC5AC PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
777 518.7977 1035.5809 1035.5825 -1.53 0 37 0.0033 1 R.AQAQPGVPLR.E
995 754.8740 1507.7334 1507.7307 1.77 0 105 5.7e-010 1 R.SVVGDALEFGNSWK.L 993 994
1040 844.3973 1686.7800 1686.7818 -1.05 0 80 1.1e-007 1 R.AAGGAVCEQPLGLECR.A 1041
Proteins matching the same set of peptides:
E9PBJ0 Mass: 611987 Score: 215 Queries matched: 6
Mucin-5B OS=Homo sapiens GN=MUC5B PE=2 SV=1
Q9HC84 Mass: 611584 Score: 215 Queries matched: 6
Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3
4. P13645 Mass: 59020 Score: 172 Queries matched: 4 emPAI: 0.17
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide          771
516.3036 1030.5927 1030.5910 1.60 0 56 2.3e-005 1 R.VLDELTLTK.A 770
928 453.2444 1356.7114 1356.7110 0.30 1 30 0.016 1 R.QSVEADINGLRR.V
1045 854.3906 1706.7667 1706.7649 1.05 0 86 2.9e-008 1 K.GSLGGGFSSGGFSGGSFSR.G
5. B1AVQ5 Mass: 49365 Score: 125 Queries matched: 4 emPAI: 0.13
Mucin-1 subunit alpha OS=Homo sapiens GN=MUC1 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
837 567.3196 1132.6246 1132.6241 0.52 0 48 0.00027 1 K.QGGFLGLSNIK.F 838
941 693.8518 1385.6890 1385.6901 -0.78 0 77 3.6e-007 1 R.DISEMFLQIYK.Q 942
Proteins matching the same set of peptides:
B4DWK6 Mass: 57362 Score: 125 Queries matched: 4
cDNA FLJ60927, highly similar to Mucin-1 OS=Homo sapiens PE=2 SV=1
A5YRU5 Mass: 30583 Score: 125 Queries matched: 4
MUC1 isoform Z-LSP OS=Homo sapiens GN=MUC1 PE=2 SV=1
A5YRU7 Mass: 23793 Score: 125 Queries matched: 4
MUC1 isoform T7 OS=Homo sapiens GN=MUC1 PE=2 SV=1
A5YRU8 Mass: 26639 Score: 125 Queries matched: 4
MUC1 isoform T8 OS=Homo sapiens GN=MUC1 PE=2 SV=1
A5YRU9 Mass: 12249 Score: 125 Queries matched: 4
MUC1 isoform T9 OS=Homo sapiens GN=MUC1 PE=4 SV=1
A6ZID5 Mass: 29402 Score: 125 Queries matched: 4
MUC1 isoform M2 OS=Homo sapiens GN=MUC1 PE=2 SV=1
A6ZIE1 Mass: 11261 Score: 125 Queries matched: 4
MUC1 isoform SV4-LSP OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6EC96 Mass: 11260 Score: 125 Queries matched: 4
MUC1 isoform J8 OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6ECA3 Mass: 29700 Score: 125 Queries matched: 4
MUC1 isoform J14 OS=Homo sapiens GN=MUC1 PE=2 SV=1
B6ECB0 Mass: 12447 Score: 125 Queries matched: 4
MUC1 isoform J21 OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6ECB1 Mass: 11249 Score: 125 Queries matched: 4
MUC1 isoform J22 OS=Homo sapiens GN=MUC1 PE=4 SV=1
B6ECB2 Mass: 19749 Score: 125 Queries matched: 4
MUC1 isoform J23 OS=Homo sapiens GN=MUC1 PE=2 SV=1
Q7Z536 Mass: 16424 Score: 125 Queries matched: 4
Mucin short variant SV10 OS=Homo sapiens GN=MUC1 PE=2 SV=1
P15941 Mass: 122200 Score: 125 Queries matched: 4
Mucin-1 OS=Homo sapiens GN=MUC1 PE=1 SV=3
6. P35527 Mass: 62255 Score: 90 Queries matched: 2 emPAI: 0.10
```

```
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide         792
530.7853 1059.5561 1059.5560 0.02 0 38 0.0053 1 K.TLLDIDNTR.M
1091 613.3273 1836.9600 1836.9581 1.04 0 53 7.1e-005 1 R.HGVQELEIELQSQLSK.K
7. H0Y4K8 Mass: 26596 Score: 45 Queries matched: 1 emPAI: 0.12
Ugl-Y3 (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1120 957.0023 1911.9900 1911.9902 -0.10 0 45 0.00046 1 R.SSPVVIDASTAIDAPSNLR.F
Proteins matching the same set of peptides:
H0Y7Z1 Mass: 121669 Score: 45 Queries matched: 1
Ugl-Y3 (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1
B4DTK1 Mass: 112204 Score: 45 Queries matched: 1
cDNA FLJ53292, highly similar to Homo sapiens fibronectin 1 (FN1), transcript variant
5, mRNA OS=Homo sapiens PE=2 SV=1
B4DU16 Mass: 99064 Score: 45 Queries matched: 1
cDNA FLJ54550, highly similar to Homo sapiens fibronectin 1 (FN1), transcript variant
6, mRNA OS=Homo sapiens PE=2 SV=1
Q5CZ99 Mass: 85628 Score: 45 Queries matched: 1
Putative uncharacterized protein DKFZp686I1370 (Fragment) OS=Homo sapiens
GN=DKFZp686I1370 PE=2 SV=1
A6YID2 Mass: 66823 Score: 45 Queries matched: 1
Fibronectin splice variant A (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1
A6YID3 Mass: 64111 Score: 45 Queries matched: 1
Fibronectin splice variant B (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1
A6YID4 Mass: 57016 Score: 45 Queries matched: 1
Fibronectin splice variant C (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1
A6YID5 Mass: 57053 Score: 45 Queries matched: 1
Fibronectin splice variant D (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1
A6YID6 Mass: 70230 Score: 45 Queries matched: 1
Fibronectin splice variant E (Fragment) OS=Homo sapiens GN=FN1 PE=2 SV=1
Q6MZM7 Mass: 242944 Score: 45 Queries matched: 1
Putative uncharacterized protein DKFZp686O12165 (Fragment) OS=Homo sapiens
GN=DKFZp686O12165 PE=1 SV=1
Q6N084 Mass: 114328 Score: 45 Queries matched: 1
Putative uncharacterized protein DKFZp686L11144 (Fragment) OS=Homo sapiens
GN=DKFZp686L11144 PE=2 SV=1
B7ZLE5 Mass: 250136 Score: 45 Queries matched: 1
FN1 protein OS=Homo sapiens GN=FN1 PE=2 SV=1
F8W7G7 Mass: 246447 Score: 45 Queries matched: 1
Ugl-Y3 OS=Homo sapiens GN=FN1 PE=2 SV=1
Q9UQS6 Mass: 38632 Score: 45 Queries matched: 1
Fibronectin (Fragment) OS=Homo sapiens PE=2 SV=1
Q59G22 Mass: 111785 Score: 45 Queries matched: 1
Fibronectin 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1
P02751 Mass: 266052 Score: 45 Queries matched: 1
Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4
O95617 Mass: 41345 Score: 45 Queries matched: 1
Fibronectin (Fragment) OS=Homo sapiens PE=2 SV=1
Q68CX6 Mass: 237220 Score: 43 Queries matched: 1
Putative uncharacterized protein DKFZp686O13149 OS=Homo sapiens GN=DKFZp686O13149 PE=2
SV=1
8. A0N4V7 Mass: 2269 Score: 42 Queries matched: 9 emPAI: 1.75
HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
576 421.7577 841.5009 841.5022 -1.44 1 42 0.0013 1 K.GITLSVRP.- 577 578 579 580 582 583
584 585
9. L0R5A1 Mass: 11752 Score: 38 Queries matched: 4 emPAI: 0.63
Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
608 428.7661 855.5176 855.5178 -0.26 0 38 0.0025 1 R.LASIVTPR.N 607 609 611
10. H7C4T5 Mass: 36596 Score: 26 Queries matched: 2 emPAI: 0.09
Muscleblind-like protein 1 (Fragment) OS=Homo sapiens GN=MBNL1 PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
632 435.7742 869.5338 869.5335 0.39 0 26 0.021 1 -.VVSVTPIR.D 630
```

Sample T9 red box

```
Database : HumanUniprot uniprot140506 (136615 sequences; 43285968 residues)
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Deamidated (NQ),Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 3 ppm
Fragment Mass Tolerance: ± 0.6 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 1748
Protein hits :      H6VRF8 Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
                    P13645 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
                    H6VRG2 Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
                    P35908 Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1
                    SV=2
                    P35527 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
                    A0N4V7 HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1 L0R5A1
                    Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1 B7Z945 Protein
                    LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1 Q8NBH6 cDNA PSEC0266
                    fis, clone NT2RP3003649, highly similar to Homo sapiens fibulin-1D mRNA
                    OS=Homo sapiens PE=2 SV=1
```

Select Summary Report

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

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

```
1. H6VRF8 Mass: 66184 Score: 1463 Queries matched: 53 emPAI: 2.48
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
508 416.7476 831.4806 831.4814 -0.95 0 31 0.015 1 K.SISISVAR.G 509
588 437.7532 873.4919 873.4920 -0.05 0 37 0.0081 1 R.SLVNLGGSK.S
698 487.2692 972.5239 972.5240 -0.12 0 62 2.6e-005 1 K.IEISELNR.V 699 700
722 500.2269 998.4392 998.4379 1.32 0 49 0.00016 1 K.DVDGAYMTK.V 721
750 517.2613 1032.5081 1032.5087 -0.62 0 64 1.1e-005 1 R.TLLEGEESR.M 749 751
776 533.2632 1064.5118 1064.5138 -1.85 0 60 1.8e-005 1 K.AQYEDIAQK.S 777
846 590.3044 1178.5942 1178.5931 0.89 0 85 8.4e-008 1 K.YEELQITAGR.H 845 847
894 633.3220 1264.6295 1264.6299 -0.31 0 75 7.2e-007 1 R.TNAENEFVTIK.K 893
901 639.3587 1276.7029 1276.7027 0.17 0 75 3.9e-007 1 K.LALDLEIATYR.T 900
909 650.7684 1299.5222 1299.5224 -0.09 0 68 5.9e-007 1 K.NMQDMVEDYR.N
911 651.8613 1301.7081 1301.7078 0.18 0 121 1.1e-011 1 R.SLDLDSIIAEVK.A 910 912
934 670.8388 1339.6631 1339.6619 0.92 1 76 5e-007 1 K.SKAEAESLYQSK.Y 935
962 692.3487 1382.6829 1382.6830 -0.09 0 74 8e-007 1 K.SLNNQFASFIDK.V 963
971 465.2486 1392.7240 1392.7249 -0.61 1 49 0.00015 1 R.TNAENEFVTIKK.D 969 970
1008 738.3782 1474.7419 1474.7416 0.18 0 78 3.5e-007 1 K.WELLQQVDTSTR.T 1007 1009
1012 738.3970 1474.7795 1474.7780 1.01 0 84 5.9e-008 1 R.FLEQQNQVLQTK.W 1010 1011
1038 508.6014 1522.7823 1522.7813 0.65 1 31 0.012 1 R.LLRDYQELMNTK.L
1067 546.9574 1637.8504 1637.8525 -1.31 1 33 0.0052 1 K.SLNNQFASFIDKVR.F 1068 1069
1090 858.9311 1715.8476 1715.8438 2.18 0 83 1.1e-007 1 K.QISNLQQSISDAEQR.G
```

```
1100 883.3710 1764.7275 1764.7275 0.01 0 40 0.00036 1 R.FSSCGGGGGSFGAGGGFGSR.S
1183 662.6355 1984.8848 1984.8870 -1.10 1 46 0.00032 1 R.LDSELKNMQDMVEDYR.N 1184
1222 538.2751 2149.0714 2149.0705 0.45 1 32 0.014 1 R.THNLEPYFESFINNLRR.R 1221 1223
1280 762.7125 2285.1156 2285.1175 -0.83 1 33 0.0078 1 K.AEAESLYQSKYEELQITAGR.H
1354 861.0599 2580.1580 2580.1545 1.36 0 32 0.0063 1 R.MSGECAPNVSVSVSTSHTTISGGGSR.G
1447 978.1792 2931.5159 2931.5090 2.35 1 43 0.00066 1 R.FLEQQNQVLQTKWELLQQVDTSTR.T 1445 1446
Proteins matching the same set of peptides:
H6VRG0 Mass: 66101 Score: 1463 Queries matched: 53
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG1 Mass: 66257 Score: 1463 Queries matched: 53
Keratin 1 OS=Homo sapiens GN=KRT1 PE=2 SV=1
H6VRG3 Mass: 66242 Score: 1463 Queries matched: 53
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
P04264 Mass: 66170 Score: 1463 Queries matched: 53
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
2. P13645 Mass: 59020 Score: 1456 Queries matched: 64 emPAI: 2.64
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
464 404.2034 806.3922 806.3923 -0.04 0 47 0.00029 1 R.LAADDFR.L 463
471 405.2236 808.4327 808.4330 -0.47 0 45 0.00066 1 R.LASYLDK.V 472 473
713 497.2540 992.4935 992.4927 0.85 0 57 5.1e-005 1 K.YENEVALR.Q 711 712
725 502.2802 1002.5458 1002.5458 0.03 1 24 0.053 1 K.SEITELRR.N
747 516.3025 1030.5905 1030.5910 -0.54 0 66 1.9e-006 1 R.VLDELTLTK.A 748
775 532.8094 1063.6043 1063.6026 1.67 1 47 0.00024 1 R.LASYLDKVR.A 772 773 774
791 545.7700 1089.5254 1089.5237 1.55 0 66 4.1e-006 1 K.VTMQNLNDR.L 790
805 555.2489 1108.4832 1108.4825 0.64 0 64 4e-006 1 K.DAEAWFNEK.S 804 806
841 583.2966 1164.5786 1164.5775 0.98 0 59 3.5e-005 1 R.LENEIQTYR.S 839 840
859 601.3117 1200.6088 1200.6098 -0.83 0 71 2.1e-006 1 R.QSVEADINGLR.R
872 617.8442 1233.6738 1233.6717 1.69 1 49 0.00019 1 R.LKYENEVALR.Q 871
889 631.8022 1261.5899 1261.5899 0.00 0 89 1.1e-008 1 R.SLLEGEGSSGGGGR.G 890 891
939 453.2440 1356.7102 1356.7110 -0.53 1 (40) 0.0018 1 R.QSVEADINGLRR.V 940
943 453.5714 1357.6924 1357.6950 -1.92 1 43 0.001 1 R.QSVEADINGLRR.V
946 683.3250 1364.6354 1364.6320 2.45 0 77 3.6e-007 1 R.SQYEQLAEQNR.K 945 947
959 691.3279 1380.6413 1380.6408 0.36 0 87 2.9e-008 1 R.ALEESNYELEGK.I 960 961
965 695.8443 1389.6741 1389.6736 0.40 0 88 2.8e-008 1 K.QSLEASLAETEGR.Y
987 717.8894 1433.7643 1433.7626 1.17 1 44 0.00061 1 K.IRLENEIQTYR.S 984 985 986 988
1030 498.5833 1492.7282 1492.7270 0.80 1 45 0.00051 1 R.SQYEQLAEQNRK.D 1028 1029
1086 854.3900 1706.7655 1706.7649 0.37 0 139 1.3e-013 1 K.GSLGGGFSSGGFSGGSFSR.G 1082 1083 1084
1085
1191 998.9910 1995.9674 1995.9636 1.86 0 92 1.1e-008 1 K.ELTTEIDNNIEQISSYK.S 1189 1190
1253 738.0368 2211.0887 2211.0906 -0.87 1 75 5.6e-007 1 K.SKELTTEIDNNIEQISSYK.S 1254 1255
1437 968.8001 2903.3784 2903.3753 1.06 0 32 0.012 1 R.NVSTGDVNVEMNAAPGVDLTQLLNNMR.S 1435 1436
1477 1018.2140 3051.6201 3051.6200 0.03 1 49 8.3e-005 1 K.TIDDLKNQILNLTTDNANILLQIDNAR.L 1478 1480
3. H6VRG2 Mass: 66197 Score: 1442 Queries matched: 52 emPAI: 2.48
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
508 416.7476 831.4806 831.4814 -0.95 0 31 0.015 1 K.SISISVAR.G 509
588 437.7532 873.4919 873.4920 -0.05 0 37 0.0081 1 R.SLVNLGGSK.S
698 487.2692 972.5239 972.5240 -0.12 0 62 2.6e-005 1 K.IEISELNR.V 699 700
722 500.2269 998.4392 998.4379 1.32 0 49 0.00016 1 K.DVDGAYMTK.V 721
750 517.2613 1032.5081 1032.5087 -0.62 0 64 1.1e-005 1 R.TLLEGEESR.M 749 751
776 533.2632 1064.5118 1064.5138 -1.85 0 60 1.8e-005 1 K.AQYEDIAQK.S 777
846 590.3044 1178.5942 1178.5931 0.89 0 85 8.4e-008 1 K.YEELQITAGR.H 845 847
894 633.3220 1264.6295 1264.6299 -0.31 0 75 7.2e-007 1 R.TNAENEFVTIK.K 893
901 639.3587 1276.7029 1276.7027 0.17 0 75 3.9e-007 1 K.LALDLEIATYR.T 900
909 650.7684 1299.5222 1299.5224 -0.09 0 68 5.9e-007 1 K.NMQDMVEDYR.N
931 665.3685 1328.7225 1328.7187 2.87 0 100 1.6e-009 1 R.NLDLDSIIAEVK.A 930
934 670.8388 1339.6631 1339.6619 0.92 1 76 5e-007 1 K.SKAEAESLYQSK.Y 935
962 692.3487 1382.6829 1382.6830 -0.09 0 74 8e-007 1 K.SLNNQFASFIDK.V 963
971 465.2486 1392.7240 1392.7249 -0.61 1 49 0.00015 1 R.TNAENEFVTIKK.D 969 970
1008 738.3782 1474.7419 1474.7416 0.18 0 78 3.5e-007 1 K.WELLQQVDTSTR.T 1007 1009
1012 738.3970 1474.7795 1474.7780 1.01 0 84 5.9e-008 1 R.FLEQQNQVLQTK.W 1010 1011
1038 508.6014 1522.7823 1522.7813 0.65 1 31 0.012 1 R.LLRDYQELMNTK.L
1067 546.9574 1637.8504 1637.8525 -1.31 1 33 0.0052 1 K.SLNNQFASFIDKVR.F 1068 1069
1090 858.9311 1715.8476 1715.8438 2.18 0 83 1.1e-007 1 K.QISNLQQSISDAEQR.G
1100 883.3710 1764.7275 1764.7275 0.01 0 40 0.00036 1 R.FSSCGGGGGSFGAGGGFGSR.S
1183 662.6355 1984.8848 1984.8870 -1.10 1 46 0.00032 1 R.LDSELKNMQDMVEDYR.N 1184
1222 538.2751 2149.0714 2149.0705 0.45 1 32 0.014 1 R.THNLEPYFESFINNLRR.R 1221 1223
1280 762.7125 2285.1156 2285.1175 -0.83 1 33 0.0078 1 K.AEAESLYQSKYEELQITAGR.H
1354 861.0599 2580.1580 2580.1545 1.36 0 32 0.0063 1 R.MSGECAPNVSVSVSTSHTTISGGGSR.G
1447 978.1792 2931.5159 2931.5090 2.35 1 43 0.00066 1 R.FLEQQNQVLQTKWELLQQVDTSTR.T 1445 1446
4. P35908 Mass: 65678 Score: 981 Queries matched: 31 emPAI: 0.92
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
```

```
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
698 487.2692 972.5239 972.5240 -0.12 0 62 2.6e-005 1 K.IEISELNR.V 699 700
755 519.2667 1036.5189 1036.5189 -0.03 0 68 3.6e-006 1 R.YLDGLTAER.T 754 756
802 554.2760 1106.5375 1106.5356 1.69 0 61 2.3e-005 1 K.AQYEEIAQR.S 801
857 597.3123 1192.6101 1192.6088 1.08 0 81 2.2e-007 1 K.YEELQVTVGR.H 856 858
862 604.8112 1207.6078 1207.6085 -0.55 0 84 8.6e-008 1 R.TAAENDFVTLK.K 863
880 627.8076 1253.6006 1253.6001 0.42 0 110 1.9e-010 1 R.GFSSGSAVVSGGSR.R 881 882
923 440.8664 1319.5773 1319.5756 1.27 0 76 1.6e-007 1 R.HGGGGGGFGGGGFGSR.S 921 922
929 665.3236 1328.6327 1328.6320 0.52 0 93 6.2e-009 1 K.NVQDAIADAEQR.G 927 928
931 665.3685 1328.7225 1328.7187 2.87 0 100 1.6e-009 1 R.NLDLDSIIAEVK.A 930
933 446.2421 1335.7044 1335.7034 0.72 1 40 0.0018 1 R.TAAENDFVTLKK.D
950 686.3606 1370.7066 1370.7041 1.80 0 62 1.5e-005 1 K.LNDLEEALQQAK.E
1012 738.3970 1474.7795 1474.7780 1.01 0 84 5.9e-008 1 R.FLEQQNQVLQTK.W 1010 1011
1271 752.6859 2255.0359 2255.0376 -0.74 1 24 0.052 1 R.TSQNSELNNMQDLVEDYKK.K
1482 1022.1699 3063.4878 3063.4819 1.93 0 35 0.0029 1 K.VLYDAEISQIHQSVTDTNVILSMDNSR.N
5. P35527 Mass: 62255 Score: 669 Queries matched: 37 emPAI: 1.19
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
471 405.2236 808.4327 808.4330 -0.47 0 45 0.00066 1 R.LASYLDK.V 472 473
618 449.2101 896.4056 896.4062 -0.62 0 34 0.0052 1 R.MTLDDFR.I
771 530.7853 1059.5560 1059.5560 -0.07 0 52 0.00018 1 K.TLLDIDNTR.M 769 770
834 579.2993 1156.5841 1156.5836 0.40 0 89 1e-008 1 R.QGVDADINGLR.Q 832 833
835 579.7915 1157.5684 1157.5677 0.68 0 (64) 6.8e-006 1 R.QGVDADINGLR.Q
852 595.8072 1189.5998 1189.6013 -1.26 0 56 5.2e-005 1 R.QVLDNLTMEK.S 853 854
917 436.5648 1306.6727 1306.6703 1.79 1 51 8.1e-005 1 R.IKFEMEQNLR.Q 914 915 916 918
1135 919.4882 1836.9617 1836.9581 1.98 0 77 2.1e-007 1 R.HGVQELEIELQSQLSK.K 1133 1134
1145 617.9805 1850.9198 1850.9196 0.10 1 46 0.00042 1 K.TLNDMRQEYEQLIAK.N 1144 1146 1147
1154 623.3138 1866.9195 1866.9145 2.69 1 (36) 0.005 1 K.TLNDMRQEYEQLIAK.N 1152 1153
1180 656.0262 1965.0569 1965.0531 1.95 1 49 6.4e-005 1 R.HGVQELEIELQSQLSKK.A
1331 837.3821 2509.1246 2509.1245 0.04 0 78 1.5e-007 1 K.EIETYHNLLEGGQEDFESSGAGK.I 1330 1332
1387 902.3914 2704.1525 2704.1539 -0.52 0 34 0.0019 1 R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G
1503 1088.8429 3263.5069 3263.5066 0.10 0 55 2.5e-005 1 K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E 1501
1502
6. A0N4V7 Mass: 2269 Score: 47 Queries matched: 13 emPAI: 6.57
HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
539 421.7589 841.5033 841.5022 1.32 1 47 0.00048 1 K.GITLSVRP.- 527 528 529 530 531 532 533 534
535 536 537 538
7. L0R5A1 Mass: 11752 Score: 34 Queries matched: 3 emPAI: 0.28
Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
555 428.7658 855.5170 855.5178 -0.87 0 34 0.0059 1 R.LASIVTPR.N 556 557
8. B7Z945 Mass: 20378 Score: 32 Queries matched: 2 emPAI: 0.16
Protein LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
908 648.3389 1294.6633 1294.6629 0.31 1 32 0.0073 1 R.VGAQVQNPRAPR.K 907
9. Q8NBH6 Mass: 74066 Score: 27 Queries matched: 2 emPAI: 0.04
cDNA PSEC0266 fis, clone NT2RP3003649, highly similar to Homo sapiens fibulin-1D mRNA OS=Homo
sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1050 517.2836 1548.8290 1548.8300 -0.62 1 27 0.028 1 R.EFTRPEEIIFLR.A 1051
Proteins matching the same set of peptides:
P23142 Mass: 81268 Score: 27 Queries matched: 2
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4
```

Sample T9 green box

Database : HumanUniprot uniprot140506 (136615 sequences; 43285968 residues)

Enzyme : Trypsin

Fixed modifications : Carbamidomethyl (C)

Variable modifications : Deamidated (NQ),Oxidation (M)

Mass values : Monoisotopic

Protein Mass : Unrestricted

Peptide Mass Tolerance : ± 3 ppm

Fragment Mass Tolerance: ± 0.6 Da

Max Missed Cleavages : 1

Instrument type : ESI-TRAP

Number of queries : 1700

Protein hits : Q1KLZ0 HCG15971, isoform CRA_a OS=Homo sapiens GN=PS1TP5BP1 PE=2 SV=1

D2JYH4 Actin, alpha 2, smooth muscle, aorta OS=Homo sapiens GN=ACTA2 PE=2 SV=1

J3KR22 C-type lectin domain family 10 member A OS=Homo sapiens GN=CLEC10A PE=2 SV=1

B4DE59 cDNA FLJ60424, highly similar to Junction plakoglobin OS=Homo sapiens PE=2 SV=1

P13645 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6

Q562R1 Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2

Q0QET7 Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens GN=GAPDH PE=2 SV=1

H6VRF8 Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1

P35908 Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2

B0YJC4 Vimentin OS=Homo sapiens GN=VIM PE=3 SV=1

E2DH89 MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1

I0CMK4 Beta-tubulin 4Q isoform 1 (Fragment) OS=Homo sapiens GN=TUBB4Q PE=3 SV=1

A0N4V7 HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1 **L0R5A1** Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1

B7Z945 Protein LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1

I3L4V6 Nucleoredoxin (Fragment) OS=Homo sapiens GN=NXN PE=4 SV=1 **Q59E90** Mannosidase, alpha, class 2B, member 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1

Select Summary Report

Significance threshold p< Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

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

1. Q1KLZ0 **Mass:** 42052 **Score:** 646 **Queries matched:** 34 **emPAI:** 2.17

HCG15971, isoform CRA_a OS=Homo sapiens GN=PS1TP5BP1 PE=2 SV=1

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

658 **488.7273 975.4401 975.4410 -0.98 0 82 9.1e-008 1 K.AGFAGDDAPR.A** 659 660

801 **566.7668 1131.5191 1131.5197 -0.49 0 79 6.1e-008 1 R.GYSFTTTAER.E** 802

819 **581.3135 1160.6124 1160.6111 1.09 0 59 1.8e-005 1 K.EITALAPSTMK.I** 818 820

830 **391.1947 1170.5623 1170.5638 -1.29 0 36 0.0035 1 R.HQGVMVGMGQK.D**

835 **589.3102 1176.6059 1176.6060 -0.05 0 (53) 0.00011 1 K.EITALAPSTMK.I** 834 836

854 **599.8574 1197.7002 1197.6982 1.66 1 49 0.00012 1 R.AVFPSIVGRPR.H** 851

999 **541.9516 1622.8329 1622.8338 -0.53 1 42 0.00088 1 R.LDLAGRDLTDYLMK.I** 1000

```
1002 543.9457 1628.8153 1628.8158 -0.29 1 36 0.12 1 R.GYSFTTTAEREIVR.D 1003 1004
1013 547.2833 1638.8281 1638.8287 -0.36 1 (29) 0.019 1 R.LDLAGRDLTDYLMK.I
1065 895.9501 1789.8857 1789.8846 0.60 0 62 1.2e-005 1 K.SYELPDGQVITIGNER.F 1064
1127 977.5377 1953.0609 1953.0571 1.93 0 51 5e-005 1 R.VAPEEHPVLLTEAPLNPK.A 1125 1126 1128
1220 1108.0414 2214.0683 2214.0627 2.53 0 99 2.1e-009 1 K.DLYANTVLSGGTTMYPGIADR.M 1219 1221
1484 1061.8782 3182.6128 3182.6071 1.81 0 50 0.0001 1 R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L 1482
1485 1486
1489 800.6573 3198.6000 3198.6020 -0.61 0 (37) 0.0026 1 R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
Proteins matching the same set of peptides:
Q8WVW5 Mass: 40819 Score: 646 Queries matched: 34
Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1
Q53G76 Mass: 42036 Score: 646 Queries matched: 34
Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1
Q53G99 Mass: 42080 Score: 646 Queries matched: 34
Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1
Q53GK6 Mass: 42038 Score: 646 Queries matched: 34
Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1
P60709 Mass: 42052 Score: 646 Queries matched: 34
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1
P63261 Mass: 42108 Score: 646 Queries matched: 34
Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1
2. D2JYH4 Mass: 42381 Score: 436 Queries matched: 22 emPAI: 1.05
Actin, alpha 2, smooth muscle, aorta OS=Homo sapiens GN=ACTA2 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
658 488.7273 975.4401 975.4410 -0.98 0 82 9.1e-008 1 K.AGFAGDDAPR.A 659 660
796 565.7784 1129.5422 1129.5404 1.64 0 64 6.1e-006 1 R.GYSFVTTAER.E 795
819 581.3135 1160.6124 1160.6111 1.09 0 59 1.8e-005 1 K.EITALAPSTMK.I 818 820
830 391.1947 1170.5623 1170.5638 -1.29 0 36 0.0035 1 R.HQGVMVGMGQK.D
835 589.3102 1176.6059 1176.6060 -0.05 0 (53) 0.00011 1 K.EITALAPSTMK.I 834 836
854 599.8574 1197.7002 1197.6982 1.66 1 49 0.00012 1 R.AVFPSIVGRPR.H 851
999 541.9516 1622.8329 1622.8338 -0.53 1 42 0.00088 1 R.LDLAGRDLTDYLMK.I 1000
1013 547.2833 1638.8281 1638.8287 -0.36 1 (29) 0.019 1 R.LDLAGRDLTDYLMK.I
1065 895.9501 1789.8857 1789.8846 0.60 0 62 1.2e-005 1 K.SYELPDGQVITIGNER.F 1064
1130 652.6877 1955.0413 1955.0364 2.50 0 42 0.00069 1 R.VAPEEHPTLLTEAPLNPK.A 1129 1131
Proteins matching the same set of peptides:
A8K3K1 Mass: 42362 Score: 436 Queries matched: 22
cDNA FLJ78096, highly similar to Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA OS=Homo
sapiens PE=2 SV=1
Q13707 Mass: 37125 Score: 436 Queries matched: 22
ACTA2 protein (Fragment) OS=Homo sapiens GN=ACTA2 PE=3 SV=1
P62736 Mass: 42381 Score: 436 Queries matched: 22
Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1
P63267 Mass: 42249 Score: 436 Queries matched: 22
Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1
P68032 Mass: 42334 Score: 436 Queries matched: 22
Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1
P68133 Mass: 42366 Score: 436 Queries matched: 22
Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1
3. J3KR22 Mass: 33175 Score: 411 Queries matched: 32 emPAI: 2.58
C-type lectin domain family 10 member A OS=Homo sapiens GN=CLEC10A PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
744 535.8144 1069.6143 1069.6132 1.10 0 74 7.4e-007 1 R.VQQLVQDLK.K 743 745
781 561.8234 1121.6323 1121.6305 1.57 0 46 0.00031 1 K.NAHLVVINSR.E 776 777 778 779 780
844 592.3169 1182.6192 1182.6179 1.13 0 43 0.00037 1 R.QAVHSEMLLR.V 838 839 840 841 842 843
849 398.2029 1191.5870 1191.5884 -1.18 1 28 0.025 1 K.AEVEGFKQER.Q
860 599.8617 1197.7089 1197.7081 0.61 1 67 1.7e-006 1 R.VQQLVQDLKK.L 855 856 857 858 859
1181 532.0347 2124.1097 2124.1076 0.99 1 37 0.0024 1 K.NAHLVVINSREEQNFVQK.Y 1177 1182
1184 709.3699 2125.0879 2125.0916 -1.74 1 (21) 0.1 1 K.NAHLVVINSREEQNFVQK.Y
1185 709.3730 2125.0972 2125.0916 2.64 1 (27) 0.03 1 K.NAHLVVINSREEQNFVQK.Y
1189 1066.4928 2130.9711 2130.9721 -0.47 0 (79) 1.9e-007 1 K.YLGSAYTWMGLSDPEGAWK.W
1191 1074.4879 2146.9612 2146.9670 -2.69 0 82 8.6e-008 1 K.YLGSAYTWMGLSDPEGAWK.W 1192
1466 1053.7857 3158.3352 3158.3359 -0.22 1 35 0.00074 1 R.WNDDVCQRPYHWVCEAGLGQTSQESH.-
4. B4DE59 Mass: 62862 Score: 256 Queries matched: 7 emPAI: 0.21
cDNA FLJ60424, highly similar to Junction plakoglobin OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
448 404.2034 806.3922 806.3923 -0.13 0 43 0.00068 1 R.LAADDFR.T
721 521.3067 1040.5989 1040.5978 1.00 0 48 0.0002 1 R.IVLQIDNAR.L 719 720
914 695.3457 1388.6769 1388.6783 -1.03 0 84 4.7e-008 1 K.AALEDTLAETEAR.F 915
1154 1007.5091 2013.0036 2013.0015 1.02 0 81 1.3e-007 1 R.GQVGGQVSVEVDSAPGTDLAK.I
Proteins matching the same set of peptides:
P08727 Mass: 44079 Score: 256 Queries matched: 7
Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4
5. P13645 Mass: 59020 Score: 207 Queries matched: 4 emPAI: 0.17
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Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
448 404.2034 806.3922 806.3923 -0.13 0 43 0.00068 1 R.LAADDFR.L
909 691.3278 1380.6411 1380.6408 0.16 0 65 4.3e-006 1 R.ALEESNYELEGK.I 910
1042 854.3896 1706.7647 1706.7649 -0.13 0 99 1.7e-009 1 K.GSLGGGFSSGGFSGGSFSR.G
6. Q562R1 Mass: 42318 Score: 173 Queries matched: 9 emPAI: 0.43
Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
830 391.1947 1170.5623 1170.5638 -1.29 0 36 0.0035 1 R.HQGVMVGMGQK.D
999 541.9516 1622.8329 1622.8338 -0.53 1 42 0.00088 1 R.LDLAGRDLTDYLMK.I 1000
1013 547.2833 1638.8281 1638.8287 -0.36 1 (29) 0.019 1 R.LDLAGRDLTDYLMK.I
1065 895.9501 1789.8857 1789.8846 0.60 0 62 1.2e-005 1 R.SYELPDGQVITIGNER.F 1064
1126 652.0274 1953.0603 1953.0571 1.64 0 32 0.0039 3 R.VAPDEHPILLTEAPLNPK.I 1124 1125
7. Q0QET7 Mass: 24776 Score: 153 Queries matched: 4 emPAI: 0.44
Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens GN=GAPDH PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
920 706.3995 1410.7845 1410.7831 1.03 0 52 5.6e-005 1 R.GALQNIIPASTGAAK.A 921
978 765.9027 1529.7908 1529.7872 2.38 0 40 0.0034 1 R.VPTANVSVVDLTCR.L
1088 917.4621 1832.9097 1832.9124 -1.52 0 61 1.6e-005 1 K.IISNASCTTNCLAPLAK.V
Proteins matching the same set of peptides:
Q2TSD0 Mass: 36197 Score: 153 Queries matched: 4
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens PE=2 SV=1
A4UCT1 Mass: 17463 Score: 153 Queries matched: 4
Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Homo sapiens PE=2 SV=1
E7EUT5 Mass: 28024 Score: 153 Queries matched: 4
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=2 SV=1
V9HVZ4 Mass: 36201 Score: 153 Queries matched: 4
Epididymis secretory sperm binding protein Li 162eP OS=Homo sapiens GN=HEL-S-162eP PE=2 SV=1
P04406 Mass: 36201 Score: 153 Queries matched: 4
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3
8. H6VRF8 Mass: 66184 Score: 142 Queries matched: 3 emPAI: 0.10
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
899 651.8615 1301.7085 1301.7078 0.50 0 108 2e-010 1 R.SLDLDSIIAEVK.A
947 738.3973 1474.7800 1474.7780 1.34 0 34 0.0057 1 R.FLEQQNQVLQTK.W 946
Proteins matching the same set of peptides:
H6VRF9 Mass: 66200 Score: 142 Queries matched: 3
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG0 Mass: 66101 Score: 142 Queries matched: 3
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
H6VRG1 Mass: 66257 Score: 142 Queries matched: 3
Keratin 1 OS=Homo sapiens GN=KRT1 PE=2 SV=1
H6VRG3 Mass: 66242 Score: 142 Queries matched: 3
Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1
P04264 Mass: 66170 Score: 142 Queries matched: 3
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
9. P35908 Mass: 65678 Score: 114 Queries matched: 3 emPAI: 0.10
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
877 627.8076 1253.6006 1253.6001 0.47 0 80 2e-007 1 R.GFSSGSAVVSGGSR.R
947 738.3973 1474.7800 1474.7780 1.34 0 34 0.0057 1 R.FLEQQNQVLQTK.W 946
10. B0YJC4 Mass: 49680 Score: 88 Queries matched: 2 emPAI: 0.13
Vimentin OS=Homo sapiens GN=VIM PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
761 547.2665 1092.5185 1092.5200 -1.31 0 56 3.6e-005 1 K.FADLSEAANR.N
1030 563.6142 1687.8208 1687.8199 0.52 1 32 0.014 1 R.VEVERDNLAEDIMR.L
Proteins matching the same set of peptides:
B3KRK8 Mass: 47062 Score: 88 Queries matched: 2
cDNA FLJ34494 fis, clone HLUNG2005030, highly similar to VIMENTIN OS=Homo sapiens PE=2 SV=1
V9HWE1 Mass: 53676 Score: 88 Queries matched: 2
Epididymis luminal protein 113 OS=Homo sapiens GN=HEL113 PE=2 SV=1
Q53HU8 Mass: 53708 Score: 88 Queries matched: 2
Vimentin variant (Fragment) OS=Homo sapiens PE=2 SV=1
P08670 Mass: 53676 Score: 88 Queries matched: 2
Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4
11. E2DH89 Mass: 21132 Score: 48 Queries matched: 1 emPAI: 0.15
MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1006 815.4178 1628.8211 1628.8199 0.76 0 48 0.0066 1 R.FIAVGYVDNTQFVR.F
Proteins matching the same set of peptides:
F2VNK8 Mass: 21213 Score: 48 Queries matched: 1
MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1
F2XI33 Mass: 31658 Score: 48 Queries matched: 1
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MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1
A3RKK0 **Mass:** 21071 **Score:** 48 **Queries matched:** 1
MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1
D5FHY9 **Mass:** 21213 **Score:** 48 **Queries matched:** 1
MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1
F6IR35 **Mass:** 38417 **Score:** 48 **Queries matched:** 1
MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1
12. I0CMK4 **Mass:** 24530 **Score:** 44 **Queries matched:** 1 **emPAI:** 0.13
Beta-tubulin 4Q isoform 1 (Fragment) OS=Homo sapiens GN=TUBB4Q PE=3 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
997 **540.9515 1619.8327 1619.8283 2.71 0 44 0.00061 1 R.LHFFMPGFAPLTSR.G**
Proteins matching the same set of peptides:
Q1KSF8 **Mass:** 23896 **Score:** 44 **Queries matched:** 1
XTP3TPA-transactivated protein 1 OS=Homo sapiens GN=XTP3TPATP1 PE=2 SV=1
B2R6L0 **Mass:** 50264 **Score:** 44 **Queries matched:** 1
cDNA, FLJ93005, highly similar to Homo sapiens tubulin, beta polypeptide (TUBB), mRNA OS=Homo sapiens PE=2 SV=1
B3KML9 **Mass:** 44916 **Score:** 44 **Queries matched:** 1
cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain OS=Homo sapiens PE=2 SV=1
B3KS31 **Mass:** 42324 **Score:** 44 **Queries matched:** 1
Tubulin, beta 6, isoform CRA_a OS=Homo sapiens GN=TUBB6 PE=2 SV=1
Q3ZCM7 **Mass:** 50257 **Score:** 44 **Queries matched:** 1
Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2
B4DE77 **Mass:** 46211 **Score:** 44 **Queries matched:** 1
cDNA FLJ55189, highly similar to Tubulin beta-4 chain OS=Homo sapiens PE=2 SV=1
B4DFH6 **Mass:** 27062 **Score:** 44 **Queries matched:** 1
cDNA FLJ52536, highly similar to Tubulin beta-4 chain OS=Homo sapiens PE=2 SV=1
B4DJ43 **Mass:** 40883 **Score:** 44 **Queries matched:** 1
cDNA FLJ53341, highly similar to Tubulin beta-4 chain OS=Homo sapiens PE=2 SV=1
B4DMU8 **Mass:** 36239 **Score:** 44 **Queries matched:** 1
cDNA FLJ53063, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B4DP54 **Mass:** 47014 **Score:** 44 **Queries matched:** 1
cDNA FLJ52712, highly similar to Tubulin beta-6 chain OS=Homo sapiens PE=2 SV=1
B4DQN9 **Mass:** 42096 **Score:** 44 **Queries matched:** 1
cDNA FLJ50617, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B4DXZ5 **Mass:** 30901 **Score:** 44 **Queries matched:** 1
cDNA FLJ52029, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B4DY90 **Mass:** 52414 **Score:** 44 **Queries matched:** 1
cDNA FLJ56903, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B4E052 **Mass:** 40000 **Score:** 44 **Queries matched:** 1
cDNA FLJ52378, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B4E386 **Mass:** 34289 **Score:** 44 **Queries matched:** 1
cDNA FLJ52847, highly similar to Tubulin beta-6 chain OS=Homo sapiens PE=2 SV=1
F5H0I4 **Mass:** 42233 **Score:** 44 **Queries matched:** 1
Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=3 SV=1
Q5JP53 **Mass:** 48135 **Score:** 44 **Queries matched:** 1
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=4 SV=1
Q5SQY0 **Mass:** 46033 **Score:** 44 **Queries matched:** 1
Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=3 SV=1
Q5ST81 **Mass:** 42114 **Score:** 44 **Queries matched:** 1
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=3 SV=1
Q5SU16 **Mass:** 50095 **Score:** 44 **Queries matched:** 1
Beta 5-tubulin OS=Homo sapiens GN=TUBB PE=2 SV=1
A6NKZ8 **Mass:** 42204 **Score:** 44 **Queries matched:** 1
Putative tubulin beta chain-like protein ENSP00000290377 OS=Homo sapiens PE=5 SV=2
Q6LC01 **Mass:** 49362 **Score:** 44 **Queries matched:** 1
MRNA encoding beta-tubulin. (from clone D-beta-1) (Fragment) OS=Homo sapiens PE=2 SV=1
B7Z4N1 **Mass:** 40211 **Score:** 44 **Queries matched:** 1
cDNA FLJ53906, highly similar to Tubulin beta chain OS=Homo sapiens PE=2 SV=1
B7ZAF0 **Mass:** 46936 **Score:** 44 **Queries matched:** 1
cDNA, FLJ79164, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
B7ZAK1 **Mass:** 42054 **Score:** 44 **Queries matched:** 1
cDNA, FLJ79215, highly similar to Tubulin beta-7 chain OS=Homo sapiens PE=2 SV=1
K7ESM5 **Mass:** 37870 **Score:** 44 **Queries matched:** 1
Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=2 SV=1
Q8IWP6 **Mass:** 50177 **Score:** 44 **Queries matched:** 1
Class IVb beta tubulin OS=Homo sapiens PE=2 SV=1
Q8IZ29 **Mass:** 50264 **Score:** 44 **Queries matched:** 1
Tubulin, beta 2C OS=Homo sapiens GN=TUBB2C PE=2 SV=1
Q8N6N5 **Mass:** 50232 **Score:** 44 **Queries matched:** 1
Tubulin, beta 2C OS=Homo sapiens GN=TUBB2C PE=2 SV=1
Q9BUF5 **Mass:** 50281 **Score:** 44 **Queries matched:** 1

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Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1
Q9BUU9 Mass: 38690 Score: 44 Queries matched: 1
TUBB protein (Fragment) OS=Homo sapiens GN=TUBB PE=2 SV=1
Q9BVA1 Mass: 50377 Score: 44 Queries matched: 1
Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1
Q9UGA2 Mass: 37191 Score: 44 Queries matched: 1
Putative uncharacterized protein DKFZp566F223 (Fragment) OS=Homo sapiens GN=DKFZp566F223 PE=2
SV=1
Q96B85 Mass: 30625 Score: 44 Queries matched: 1
TUBB protein (Fragment) OS=Homo sapiens GN=TUBB PE=2 SV=1
Q96HX0 Mass: 26029 Score: 44 Queries matched: 1
TUBB2C protein (Fragment) OS=Homo sapiens GN=TUBB2C PE=2 SV=1
P04350 Mass: 50010 Score: 44 Queries matched: 1
Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2
P07437 Mass: 50095 Score: 44 Queries matched: 1
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2
Q13885 Mass: 50274 Score: 44 Queries matched: 1
Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1
O43209 Mass: 38945 Score: 44 Queries matched: 1
Homo sapiens clone 23678 (Fragment) OS=Homo sapiens PE=2 SV=1
P68371 Mass: 50255 Score: 44 Queries matched: 1
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1
I3L2F9 Mass: 46054 Score: 42 Queries matched: 1
Uncharacterized protein OS=Homo sapiens PE=3 SV=1
A6NNZ2 Mass: 50168 Score: 42 Queries matched: 1
Tubulin beta-8 chain-like protein LOC260334 OS=Homo sapiens PE=1 SV=1
13. A0N4V7 Mass: 2269 Score: 42 Queries matched: 15 emPAI: 6.57
HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
496 421.7581 841.5016 841.5022 -0.63 1 42 0.0013 1 K.GITLSVRP.- 495 497 498 499 500 501 502 503
504 505 506 507 508 509
14. L0R5A1 Mass: 11752 Score: 37 Queries matched: 3 emPAI: 0.28
Alternative protein CSF2RB OS=Homo sapiens GN=CSF2RB PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
533 428.7661 855.5176 855.5178 -0.28 0 37 0.003 1 R.LASIVTPR.N 531 532
15. B7Z945 Mass: 20378 Score: 27 Queries matched: 3 emPAI: 0.16
Protein LOC100132891 OS=Homo sapiens GN=LOC100132891 PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
895 648.3401 1294.6656 1294.6629 2.06 1 27 0.024 1 R.VGAQVQNPRAPR.K 893 894
16. I3L4V6 Mass: 26188 Score: 27 Queries matched: 1 emPAI: 0.12
Nucleoredoxin (Fragment) OS=Homo sapiens GN=NXN PE=4 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
1083 913.8988 1825.7831 1825.7854 -1.25 0 27 0.014 1 R.LYGIQDSEDDGESEAAK.Q
Proteins matching the same set of peptides:
B4DNN6 Mass: 14224 Score: 27 Queries matched: 1
Nucleoredoxin OS=Homo sapiens GN=NXN PE=2 SV=1
17. Q59E90 Mass: 113918 Score: 25 Queries matched: 2 emPAI: 0.03
Mannosidase, alpha, class 2B, member 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
869 613.8600 1225.7054 1225.7030 1.95 0 25 0.021 1 K.LIQLVNAQQAK.G 868
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