

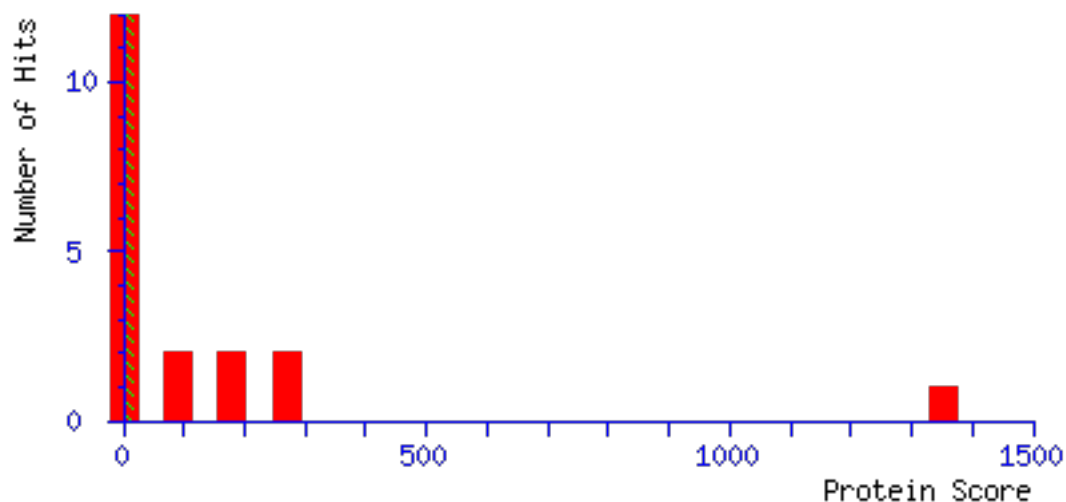
Cambridge Centre for Proteomics Mascot Search Results

User : anja
 Email : aa2030@cam.ac.uk
 Search title : P378 (\\prot-filesvr1\data\CORE\PARAMETERS\Mascot_search_parameters\Yagnesh\M291_Ben_Luisi_tolc_arca_velos_xlink_ox_chymo_041218.par), submitted from Daemon on CCP-PC158
 MS data file : \\prot-filesvr1\data\CORE\RAW_DATA_2018_Velos\P378_Ben_Luisi\P378_Band_5.mgf
 Database 1 : cRAP_20181217 (120 sequences; 39582 residues)
 Database 2 : M291_ARCA ARCA_20181203 (1 sequences; 238 residues)
 Database 3 : M291_TOLC TOLC_20181203 (1 sequences; 493 residues)
 Timestamp : 19 Dec 2018 at 10:00:05 GMT

| | |
|-----------------------|--|
| Protein hits : | 1::sp cRAP087 P02769 ALBU BOVIN Serum albumin OS=Bos taurus GN=ALB PE=1 1::sp cRAP022 P00766 CTRA BOVIN Chymotrypsinogen A OS=Bos taurus PE=1 S 3::sp P02930 TOLC ECOLI Outer membrane protein TolC OS=Escheric 1::sp cRAP008 P00722 BGAL ECOLI Beta-galactosidase OS=Escherichia coli 1::sp cRAP002 P02768 ALBU HUMAN Serum albumin OS=Homo sapiens GN=ALB PE 1::sp cRAP112 P00761 TRYP PIG Trypsin OS=Sus scrofa PE=1 SV=1 1::sp cRAP030 P32503 GAG SCVLA Major capsid protein OS=Saccharomyces c 1::sp cRAP115 P63279 UBC9 HUMAN SUMO-conjugating enzyme UBC9 OS=Homo sa 1::sp cRAP034 P09211 GSTP1 HUMAN Glutathione S-transferase P OS=Homo sap 1::sp cRAP015 P02666 CASB BOVIN Beta-casein OS=Bos taurus GN=CSN2 PE=1 1::sp cRAP020 P01031 CO5 HUMAN Complement C5 OS=Homo sapiens GN=C5 PE= 1::sp cRAP089 P00792 PEPA BOVIN Pepsin A OS=Bos taurus GN=PGA PE=1 SV=2 1::sp cRAP104 P12081 SYHC HUMAN Histidine--tRNA ligase, cytoplasmic OS= 1::sp cRAP054 P04264 K2C1 HUMAN Keratin, type II cytoskeletal 1 OS=Homo 1::sp cRAP004 P04745 AMY1 HUMAN Alpha-amylase 1 OS=Homo sapiens GN=AMY1 1::sp cRAP084 P15559 NQO1 HUMAN NAD(P)H dehydrogenase [quinone] 1 OS=Ho 1::sp cRAP077 P41159 LEP HUMAN Leptin OS=Homo sapiens GN=LEP PE=1 SV=1 1::sp cRAP086 P01012 OVAL CHICK Ovalbumin OS=Gallus gallus GN=SERPINB14 1::sp cRAP114 O00762 UBE2C HUMAN Ubiquitin-conjugating enzyme E2 C OS=Ho |
|-----------------------|--|

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Individual ions scores > 15 indicate identity or extensive homology ($p < 0.05$).
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

| | | | | |
|--|-----------------|-------------------------------|-----------------------------|-----|
| Protein Family Summary | Peptide Summary | Select Summary (protein hits) | Select Summary (unassigned) | Exp |
| Significance threshold p< | | | | |
| Standard scoring MudPIT scoring | | | | |
| Show pop-ups Suppress pop-ups | | | | |
| Preferred taxonomy All entries . . Archaea (Archaeobacteria) . . Eukaryota (eucaryotes) Alveolata (alveolates and relatives) bony vertebrates lobe-finned fish and tetrapod clade Mammalia (mammals) Mus Mus musculus (house mouse) Rattus Other mammals (rodents, primates, etc.) fishes) Takifugu rubripes (Japanese Pufferfish) Danio rerio (zebra fish) Schizosaccharomyces pombe (fission yeast) Pneumocystis carinii Other Fungi Viridiplantae (green plants) Mycobacterium tuberculosis complex Other Actinobacteria (class) Firmicutes (gram-positive bacteria) Agrobacterium tumefaciens Campylobacter jejuni Escherichia coli Neisseria meningitidis Species information unavailable | | | | |

Error tolerant

1. [1::sp|cRAP087|P02769|ALBU_BOVIN](#) **Mass:** 71244 **Score:** 1352 **Matches:** 154 (154) **S**
Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | ppm | Miss | Score | Expect | Rank | Unique | Pepti |
|----------------------|----------|-----------|-----------|-------|------|-------|---------|------|--------|-------|
| 300 | 392.7144 | 783.4142 | 783.4127 | 2.00 | 0 | 20 | 0.0099 | 1 | U | L.KPD |
| 399 | 396.6891 | 791.3636 | 791.3636 | -0.06 | 1 | (20) | 0.0092 | 1 | | Y.LQQ |
| 400 | 396.6891 | 791.3637 | 791.3636 | 0.09 | 1 | 23 | 0.0046 | 1 | | Y.LQQ |
| 888 | 415.2610 | 828.5075 | 828.5069 | 0.75 | 2 | 22 | 0.0056 | 1 | U | L.SLI |
| 1154 | 426.2107 | 850.4068 | 850.4072 | -0.56 | 1 | (23) | 0.0059 | 1 | U | L.VNE |
| 1155 | 426.2108 | 850.4070 | 850.4072 | -0.28 | 1 | 36 | 0.00027 | 1 | U | L.VNE |
| 1157 | 426.2111 | 850.4076 | 850.4072 | 0.38 | 1 | (35) | 0.00035 | 1 | U | L.VNE |

| | | | | | | | | | | |
|-------------|----------|-----------|-----------|--------|---|------|---------|---|---|-------|
| <u>1347</u> | 434.7153 | 867.4161 | 867.4160 | 0.09 | 0 | 34 | 0.00042 | 1 | U | L.KTV |
| <u>1348</u> | 434.7159 | 867.4173 | 867.4160 | 1.50 | 0 | (33) | 0.00045 | 1 | U | L.KTV |
| <u>1795</u> | 457.2243 | 912.4341 | 912.4341 | -0.01 | 1 | (27) | 0.0025 | 1 | U | Y.ANK |
| <u>1796</u> | 457.2244 | 912.4342 | 912.4341 | 0.15 | 1 | 31 | 0.00091 | 1 | U | Y.ANK |
| <u>1904</u> | 461.2377 | 920.4608 | 920.4603 | 0.50 | 1 | (21) | 0.0074 | 1 | U | Y.QEA |
| <u>1906</u> | 461.2380 | 920.4613 | 920.4603 | 1.11 | 1 | 23 | 0.0047 | 1 | U | Y.QEA |
| <u>2600</u> | 487.7263 | 973.4380 | 973.4505 | -12.79 | 1 | (24) | 0.0041 | 1 | U | F.KDL |
| <u>2604</u> | 487.7319 | 973.4492 | 973.4505 | -1.29 | 1 | (33) | 0.00052 | 1 | U | F.KDL |
| <u>2605</u> | 487.7321 | 973.4496 | 973.4505 | -0.96 | 1 | (22) | 0.0061 | 1 | U | F.KDL |
| <u>2606</u> | 487.7322 | 973.4498 | 973.4505 | -0.71 | 1 | (33) | 0.00052 | 1 | U | F.KDL |
| <u>2607</u> | 487.7322 | 973.4498 | 973.4505 | -0.71 | 1 | (34) | 0.0004 | 1 | U | F.KDL |
| <u>2608</u> | 487.7323 | 973.4501 | 973.4505 | -0.40 | 1 | (49) | 1.4e-05 | 1 | U | F.KDL |
| <u>2609</u> | 487.7323 | 973.4501 | 973.4505 | -0.40 | 1 | 52 | 6.1e-06 | 1 | U | F.KDL |
| <u>2610</u> | 487.7323 | 973.4501 | 973.4505 | -0.40 | 1 | (23) | 0.0055 | 1 | U | F.KDL |
| <u>2611</u> | 487.7324 | 973.4502 | 973.4505 | -0.34 | 1 | (31) | 0.00078 | 1 | U | F.KDL |
| <u>2612</u> | 487.7324 | 973.4503 | 973.4505 | -0.16 | 1 | (21) | 0.0089 | 1 | U | F.KDL |
| <u>2613</u> | 487.7325 | 973.4504 | 973.4505 | -0.09 | 1 | (32) | 0.00073 | 1 | U | F.KDL |
| <u>2614</u> | 487.7326 | 973.4507 | 973.4505 | 0.23 | 1 | (22) | 0.0059 | 1 | U | F.KDL |
| <u>2615</u> | 487.7327 | 973.4508 | 973.4505 | 0.30 | 1 | (49) | 1.4e-05 | 1 | U | F.KDL |
| <u>2616</u> | 487.7327 | 973.4508 | 973.4505 | 0.36 | 1 | (28) | 0.0017 | 1 | U | F.KDL |
| <u>2617</u> | 487.7329 | 973.4512 | 973.4505 | 0.73 | 1 | (29) | 0.0012 | 1 | U | F.KDL |
| <u>2619</u> | 487.7329 | 973.4513 | 973.4505 | 0.79 | 1 | (25) | 0.003 | 1 | U | F.KDL |
| <u>2620</u> | 487.7330 | 973.4514 | 973.4505 | 0.91 | 1 | (25) | 0.0031 | 1 | U | F.KDL |
| <u>2621</u> | 487.7331 | 973.4517 | 973.4505 | 1.22 | 1 | (31) | 0.00087 | 1 | U | F.KDL |
| <u>2623</u> | 487.7332 | 973.4518 | 973.4505 | 1.34 | 1 | (40) | 0.00011 | 1 | U | F.KDL |
| <u>2625</u> | 487.7335 | 973.4524 | 973.4505 | 1.92 | 1 | (33) | 0.00054 | 1 | U | F.KDL |
| <u>2915</u> | 498.7297 | 995.4449 | 995.4447 | 0.12 | 1 | 45 | 3.1e-05 | 1 | U | F.SAL |
| <u>2916</u> | 498.7301 | 995.4456 | 995.4447 | 0.84 | 1 | (43) | 4.6e-05 | 1 | U | F.SAL |
| <u>3639</u> | 525.2418 | 1048.4691 | 1048.4681 | 0.90 | 0 | (26) | 0.0025 | 1 | U | L.KEC |
| <u>3640</u> | 525.2425 | 1048.4704 | 1048.4681 | 2.18 | 0 | 32 | 0.00063 | 1 | U | L.KEC |
| <u>3664</u> | 526.2816 | 1050.5486 | 1050.5498 | -1.18 | 1 | 46 | 2.5e-05 | 1 | U | F.KAD |
| <u>3665</u> | 526.2823 | 1050.5500 | 1050.5498 | 0.21 | 1 | (36) | 0.00024 | 1 | U | F.KAD |
| <u>3667</u> | 526.7447 | 1051.4748 | 1051.4757 | -0.81 | 0 | (21) | 0.014 | 1 | U | L.IKQ |
| <u>3670</u> | 526.7458 | 1051.4770 | 1051.4757 | 1.28 | 0 | 48 | 2.7e-05 | 1 | U | L.IKQ |
| <u>3671</u> | 526.7462 | 1051.4779 | 1051.4757 | 2.10 | 0 | (42) | 0.00011 | 1 | U | L.IKQ |
| <u>3681</u> | 527.2366 | 1052.4586 | 1052.4597 | -1.04 | 0 | (35) | 0.00048 | 1 | U | L.IKQ |
| <u>3682</u> | 527.2368 | 1052.4591 | 1052.4597 | -0.57 | 0 | (39) | 0.00021 | 1 | U | L.IKQ |
| <u>3826</u> | 532.7194 | 1063.4242 | 1063.4240 | 0.13 | 0 | (33) | 0.00053 | 1 | | L.ECA |
| <u>3827</u> | 532.7194 | 1063.4242 | 1063.4240 | 0.13 | 0 | (26) | 0.0023 | 1 | | L.ECA |
| <u>3828</u> | 532.7201 | 1063.4257 | 1063.4240 | 1.62 | 0 | 38 | 0.00015 | 1 | | L.ECA |
| <u>4098</u> | 541.2878 | 1080.5610 | 1080.5604 | 0.58 | 0 | 38 | 0.00015 | 1 | U | L.SQK |
| <u>4099</u> | 541.2881 | 1080.5617 | 1080.5604 | 1.27 | 0 | (22) | 0.0064 | 1 | U | L.SQK |
| <u>4100</u> | 541.2886 | 1080.5626 | 1080.5604 | 2.04 | 0 | (32) | 0.00067 | 1 | U | L.SQK |
| <u>4110</u> | 541.7769 | 1081.5393 | 1081.5444 | -4.72 | 0 | (30) | 0.00091 | 1 | U | L.SQK |
| <u>5225</u> | 589.2618 | 1176.5090 | 1176.5081 | 0.78 | 1 | (37) | 0.0002 | 1 | | L.LEC |
| <u>5226</u> | 589.2618 | 1176.5090 | 1176.5081 | 0.78 | 1 | 41 | 8.4e-05 | 1 | | L.LEC |
| <u>5267</u> | 590.8275 | 1179.6405 | 1179.6400 | 0.37 | 2 | (35) | 0.00028 | 1 | U | Y.GFQ |
| <u>5268</u> | 590.8289 | 1179.6433 | 1179.6400 | 2.76 | 2 | 42 | 6e-05 | 1 | U | Y.GFQ |
| <u>5446</u> | 596.8188 | 1191.6231 | 1191.6248 | -1.36 | 1 | (38) | 0.00016 | 1 | U | L.KHL |
| <u>5447</u> | 596.8189 | 1191.6233 | 1191.6248 | -1.26 | 1 | 48 | 1.5e-05 | 1 | U | L.KHL |
| <u>5466</u> | 597.3115 | 1192.6085 | 1192.6088 | -0.24 | 1 | (40) | 0.00011 | 1 | U | L.KHL |
| <u>5467</u> | 597.3123 | 1192.6101 | 1192.6088 | 1.10 | 1 | (45) | 3.3e-05 | 1 | U | L.KHL |
| <u>5469</u> | 398.5569 | 1192.6489 | 1192.6492 | -0.22 | 2 | (21) | 0.0071 | 1 | U | Y.VPK |
| <u>5471</u> | 398.5572 | 1192.6498 | 1192.6492 | 0.53 | 2 | (23) | 0.0055 | 1 | U | Y.VPK |
| <u>5472</u> | 398.5573 | 1192.6502 | 1192.6492 | 0.83 | 2 | 30 | 0.0011 | 1 | U | Y.VPK |
| <u>5892</u> | 613.8142 | 1225.6139 | 1225.6125 | 1.13 | 1 | 22 | 0.0068 | 1 | U | L.CKV |
| <u>6102</u> | 621.2696 | 1240.5246 | 1240.5394 | -11.88 | 0 | (23) | 0.0052 | 1 | U | F.AED |

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|----------------------|----------|-----------|-----------|-------|---|------|---------|---|---|-------|
| 6105 | 414.5203 | 1240.5391 | 1240.5394 | -0.20 | 0 | (20) | 0.011 | 1 | U | F.AED |
| 6106 | 414.5208 | 1240.5404 | 1240.5394 | 0.84 | 0 | (21) | 0.0087 | 1 | U | F.AED |
| 6107 | 621.2783 | 1240.5420 | 1240.5394 | 2.08 | 0 | 37 | 0.00022 | 1 | U | F.AED |
| 6108 | 621.2792 | 1240.5439 | 1240.5394 | 3.66 | 0 | (30) | 0.001 | 1 | U | F.AED |
| 7015 | 654.8673 | 1307.7201 | 1307.7197 | 0.27 | 0 | (41) | 8.9e-05 | 1 | U | L.KHK |
| 7019 | 654.8676 | 1307.7207 | 1307.7197 | 0.73 | 0 | (25) | 0.0031 | 1 | U | L.KHK |
| 7020 | 654.8677 | 1307.7208 | 1307.7197 | 0.84 | 0 | (30) | 0.00096 | 1 | U | L.KHK |
| 7024 | 654.8693 | 1307.7241 | 1307.7197 | 3.35 | 0 | 41 | 7.1e-05 | 1 | U | L.KHK |
| 7240 | 663.8904 | 1325.7662 | 1325.7667 | -0.38 | 0 | (34) | 0.00037 | 1 | U | Y.TRK |
| 7241 | 663.8917 | 1325.7688 | 1325.7667 | 1.55 | 0 | 41 | 8.3e-05 | 1 | U | Y.TRK |
| 7486 | 451.2334 | 1350.6784 | 1350.6779 | 0.33 | 0 | 36 | 0.00033 | 1 | U | L.SHK |
| 7487 | 451.2335 | 1350.6786 | 1350.6779 | 0.46 | 0 | (35) | 0.00036 | 1 | U | L.SHK |
| 7876 | 697.3342 | 1392.6539 | 1392.6555 | -1.13 | 0 | (25) | 0.0038 | 1 | U | Y.ICD |
| 7877 | 697.3344 | 1392.6543 | 1392.6555 | -0.88 | 0 | (50) | 1.3e-05 | 1 | U | Y.ICD |
| 7878 | 697.3346 | 1392.6546 | 1392.6555 | -0.62 | 0 | (33) | 0.00057 | 1 | U | Y.ICD |
| 7879 | 697.3350 | 1392.6554 | 1392.6555 | -0.09 | 0 | (37) | 0.00022 | 1 | U | Y.ICD |
| 7880 | 697.3350 | 1392.6554 | 1392.6555 | -0.09 | 0 | (45) | 3.7e-05 | 1 | U | Y.ICD |
| 7881 | 697.3353 | 1392.6561 | 1392.6555 | 0.45 | 0 | (55) | 3.9e-06 | 1 | U | Y.ICD |
| 7882 | 697.3357 | 1392.6568 | 1392.6555 | 0.96 | 0 | (37) | 0.00022 | 1 | U | Y.ICD |
| 7883 | 697.3357 | 1392.6568 | 1392.6555 | 0.96 | 0 | (59) | 1.5e-06 | 1 | U | Y.ICD |
| 7884 | 697.3358 | 1392.6571 | 1392.6555 | 1.15 | 0 | (66) | 3.1e-07 | 1 | U | Y.ICD |
| 7885 | 697.3359 | 1392.6572 | 1392.6555 | 1.24 | 0 | (33) | 0.00058 | 1 | U | Y.ICD |
| 7886 | 697.3360 | 1392.6574 | 1392.6555 | 1.41 | 0 | (68) | 2.1e-07 | 1 | U | Y.ICD |
| 7887 | 697.3361 | 1392.6577 | 1392.6555 | 1.58 | 0 | (25) | 0.0035 | 1 | U | Y.ICD |
| 7888 | 697.3362 | 1392.6578 | 1392.6555 | 1.67 | 0 | (56) | 2.8e-06 | 1 | U | Y.ICD |
| 7889 | 697.3363 | 1392.6580 | 1392.6555 | 1.84 | 0 | (49) | 1.2e-05 | 1 | U | Y.ICD |
| 7890 | 697.3364 | 1392.6583 | 1392.6555 | 2.03 | 0 | (53) | 5.1e-06 | 1 | U | Y.ICD |
| 7891 | 697.3365 | 1392.6584 | 1392.6555 | 2.11 | 0 | (31) | 0.00086 | 1 | U | Y.ICD |
| 7892 | 697.3366 | 1392.6587 | 1392.6555 | 2.28 | 0 | (48) | 1.6e-05 | 1 | U | Y.ICD |
| 7893 | 697.3367 | 1392.6588 | 1392.6555 | 2.37 | 0 | (70) | 1.1e-07 | 1 | U | Y.ICD |
| 7894 | 697.3367 | 1392.6588 | 1392.6555 | 2.37 | 0 | (60) | 1e-06 | 1 | U | Y.ICD |
| 7895 | 697.3368 | 1392.6590 | 1392.6555 | 2.54 | 0 | (71) | 8.4e-08 | 1 | U | Y.ICD |
| 7896 | 697.3369 | 1392.6591 | 1392.6555 | 2.63 | 0 | (46) | 2.6e-05 | 1 | U | Y.ICD |
| 7897 | 697.3369 | 1392.6593 | 1392.6555 | 2.71 | 0 | (40) | 0.00011 | 1 | U | Y.ICD |
| 7898 | 697.3370 | 1392.6594 | 1392.6555 | 2.82 | 0 | (53) | 5.4e-06 | 1 | U | Y.ICD |
| 7899 | 697.3371 | 1392.6596 | 1392.6555 | 2.99 | 0 | (43) | 5e-05 | 1 | U | Y.ICD |
| 7900 | 697.3372 | 1392.6599 | 1392.6555 | 3.16 | 0 | (22) | 0.0061 | 1 | U | Y.ICD |
| 7901 | 697.3372 | 1392.6599 | 1392.6555 | 3.16 | 0 | (64) | 4e-07 | 1 | U | Y.ICD |
| 7902 | 697.3373 | 1392.6600 | 1392.6555 | 3.25 | 0 | (57) | 2.2e-06 | 1 | U | Y.ICD |
| 7903 | 697.3373 | 1392.6600 | 1392.6555 | 3.25 | 0 | (50) | 1.1e-05 | 1 | U | Y.ICD |
| 7904 | 697.3375 | 1392.6604 | 1392.6555 | 3.50 | 0 | (60) | 9.6e-07 | 1 | U | Y.ICD |
| 7905 | 697.3377 | 1392.6609 | 1392.6555 | 3.86 | 0 | (40) | 9.7e-05 | 1 | U | Y.ICD |
| 7917 | 697.8267 | 1393.6389 | 1393.6395 | -0.44 | 0 | 72 | 1.2e-07 | 1 | U | Y.ICD |
| 7918 | 697.8386 | 1393.6627 | 1393.6395 | 16.6 | 0 | (21) | 0.013 | 1 | U | Y.ICD |
| 8142 | 711.4101 | 1420.8056 | 1420.8038 | 1.32 | 1 | (27) | 0.0021 | 1 | U | L.LKH |
| 8143 | 711.4114 | 1420.8082 | 1420.8038 | 3.12 | 1 | 31 | 0.00083 | 1 | U | L.LKH |
| 9210 | 784.8124 | 1567.6102 | 1567.6065 | 2.36 | 0 | (31) | 0.00073 | 1 | U | F.QEC |
| 9211 | 784.8126 | 1567.6106 | 1567.6065 | 2.59 | 0 | (27) | 0.002 | 1 | U | F.QEC |
| 9212 | 784.8128 | 1567.6111 | 1567.6065 | 2.91 | 0 | (38) | 0.00017 | 1 | U | F.QEC |
| 9213 | 784.8144 | 1567.6142 | 1567.6065 | 4.93 | 0 | (31) | 0.00087 | 1 | U | F.QEC |
| 9229 | 785.3032 | 1568.5919 | 1568.5905 | 0.88 | 0 | (40) | 9.4e-05 | 1 | U | F.QEC |
| 9230 | 785.3054 | 1568.5963 | 1568.5905 | 3.68 | 0 | 44 | 4e-05 | 1 | U | F.QEC |
| 9267 | 787.3892 | 1572.7638 | 1572.7671 | -2.14 | 2 | (39) | 0.00013 | 1 | U | F.DEH |
| 9269 | 787.3913 | 1572.7680 | 1572.7671 | 0.58 | 2 | 46 | 2.5e-05 | 1 | U | F.DEH |
| 9328 | 792.4545 | 1582.8945 | 1582.8930 | 0.94 | 2 | (21) | 0.0074 | 1 | U | F.AVE |
| 9335 | 792.9462 | 1583.8778 | 1583.8770 | 0.48 | 2 | 23 | 0.005 | 1 | U | F.AVE |
| 9336 | 792.9481 | 1583.8816 | 1583.8770 | 2.87 | 2 | (22) | 0.0066 | 1 | U | F.AVE |

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|-----------------------|-----------|-----------|-----------|-------|---|------|---------|---|---|-------|
| 9705 | 827.8019 | 1653.5892 | 1653.5858 | 2.08 | 0 | 38 | 0.00015 | 1 | U | L.EEC |
| 9707 | 827.8025 | 1653.5904 | 1653.5858 | 2.82 | 0 | (27) | 0.0018 | 1 | U | L.EEC |
| 9912 | 844.8381 | 1687.6616 | 1687.6640 | -1.45 | 0 | (29) | 0.0012 | 1 | U | F.VDK |
| 9913 | 563.5617 | 1687.6633 | 1687.6640 | -0.43 | 0 | (28) | 0.0016 | 1 | U | F.VDK |
| 9914 | 844.8394 | 1687.6643 | 1687.6640 | 0.15 | 0 | (41) | 8.1e-05 | 1 | U | F.VDK |
| 9916 | 844.8400 | 1687.6654 | 1687.6640 | 0.80 | 0 | (61) | 8.2e-07 | 1 | U | F.VDK |
| 9919 | 844.8417 | 1687.6688 | 1687.6640 | 2.82 | 0 | 62 | 6.2e-07 | 1 | U | F.VDK |
| 9920 | 844.8445 | 1687.6744 | 1687.6640 | 6.15 | 0 | (38) | 0.00021 | 1 | U | F.VDK |
| 10325 | 591.2817 | 1770.8234 | 1770.8247 | -0.72 | 2 | 29 | 0.0022 | 1 | U | L.IKQ |
| 11147 | 1034.9087 | 2067.8028 | 2067.7972 | 2.72 | 1 | 52 | 5.9e-06 | 1 | U | Y.EAT |
| 11148 | 690.2750 | 2067.8031 | 2067.7972 | 2.82 | 1 | (28) | 0.0015 | 1 | U | Y.EAT |
| 11150 | 1034.9093 | 2067.8040 | 2067.7972 | 3.31 | 1 | (51) | 7.8e-06 | 1 | U | Y.EAT |
| 11271 | 530.0267 | 2116.0778 | 2116.0800 | -1.05 | 1 | (23) | 0.0052 | 1 | U | L.SHK |
| 11272 | 706.3679 | 2116.0819 | 2116.0800 | 0.90 | 1 | (33) | 0.00061 | 1 | U | L.SHK |
| 11273 | 1059.0488 | 2116.0831 | 2116.0800 | 1.45 | 1 | 53 | 6.4e-06 | 1 | U | L.SHK |
| 11274 | 530.0281 | 2116.0835 | 2116.0800 | 1.62 | 1 | (27) | 0.0022 | 1 | U | L.SHK |
| 11275 | 706.3689 | 2116.0849 | 2116.0800 | 2.29 | 1 | (35) | 0.0004 | 1 | U | L.SHK |
| 11276 | 530.0286 | 2116.0851 | 2116.0800 | 2.41 | 1 | (28) | 0.0019 | 1 | U | L.SHK |
| 11279 | 1059.0516 | 2116.0887 | 2116.0800 | 4.11 | 1 | (44) | 3.9e-05 | 1 | U | L.SHK |
| 11404 | 744.0605 | 2229.1596 | 2229.1641 | -2.00 | 2 | (35) | 0.00029 | 1 | U | F.LSH |
| 11406 | 1115.5895 | 2229.1644 | 2229.1641 | 0.14 | 2 | (32) | 0.00062 | 1 | U | F.LSH |
| 11408 | 744.0624 | 2229.1653 | 2229.1641 | 0.55 | 2 | 37 | 0.00019 | 1 | U | F.LSH |
| 11410 | 558.2993 | 2229.1679 | 2229.1641 | 1.72 | 2 | (23) | 0.0052 | 1 | U | F.LSH |
| 11412 | 558.2996 | 2229.1691 | 2229.1641 | 2.26 | 2 | (21) | 0.0074 | 1 | U | F.LSH |
| 11413 | 1115.5930 | 2229.1715 | 2229.1641 | 3.32 | 2 | (29) | 0.0014 | 1 | U | F.LSH |
| 11472 | 758.9560 | 2273.8461 | 2273.8446 | 0.69 | 0 | (35) | 0.00029 | 1 | U | Y.GDM |
| 11473 | 1137.9316 | 2273.8487 | 2273.8446 | 1.83 | 0 | 48 | 1.4e-05 | 1 | U | Y.GDM |
| 11474 | 1137.9341 | 2273.8536 | 2273.8446 | 3.97 | 0 | (37) | 0.00018 | 1 | U | Y.GDM |
| 11475 | 758.9586 | 2273.8539 | 2273.8446 | 4.08 | 0 | (47) | 2.1e-05 | 1 | U | Y.GDM |
| 11476 | 759.2891 | 2274.8454 | 2274.8286 | 7.37 | 0 | (33) | 0.00056 | 1 | U | Y.GDM |
| 11492 | 764.2882 | 2289.8428 | 2289.8395 | 1.45 | 0 | (40) | 0.00011 | 1 | U | Y.GDM |
| 11493 | 1145.9294 | 2289.8443 | 2289.8395 | 2.11 | 0 | (27) | 0.0018 | 1 | U | Y.GDM |
| 11494 | 764.2891 | 2289.8454 | 2289.8395 | 2.56 | 0 | (31) | 0.0008 | 1 | U | Y.GDM |

2. [1::sp|cRAP022|P00766|CTRA_BOVIN](#) Mass: 26220 Score: 248 Matches: 16(16) Seq

Chymotrypsinogen A OS=Bos taurus PE=1 SV=1

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

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|-----------|-----------|-------|------|-------|---------|------|--------|---------|
| 838 | 412.7290 | 823.4434 | 823.4440 | -0.61 | 1 | (35) | 0.00032 | 1 | U | L.KLSTA |
| 840 | 412.7292 | 823.4439 | 823.4440 | -0.01 | 1 | 55 | 3e-06 | 1 | U | L.KLSTA |
| 1430 | 437.7557 | 873.4968 | 873.4960 | 0.91 | 1 | 23 | 0.005 | 1 | U | W.TLVGI |
| 1431 | 437.7557 | 873.4969 | 873.4960 | 0.97 | 1 | (23) | 0.0055 | 1 | U | W.TLVGI |
| 2995 | 501.2541 | 1000.4936 | 1000.4938 | -0.19 | 0 | (26) | 0.0027 | 1 | U | Y.TNANT |
| 2996 | 501.2541 | 1000.4937 | 1000.4938 | -0.07 | 0 | (25) | 0.0034 | 1 | U | Y.TNANT |
| 3001 | 501.7442 | 1001.4738 | 1001.4778 | -3.91 | 0 | (26) | 0.0025 | 1 | U | Y.TNANT |
| 3023 | 502.2356 | 1002.4567 | 1002.4618 | -5.06 | 0 | 32 | 0.00068 | 1 | U | Y.TNANT |
| 3024 | 502.2357 | 1002.4568 | 1002.4618 | -4.94 | 0 | (30) | 0.0011 | 1 | U | Y.TNANT |
| 3195 | 508.7852 | 1015.5559 | 1015.5550 | 0.91 | 1 | 56 | 2.4e-06 | 1 | U | L.TINND |
| 3196 | 508.7853 | 1015.5561 | 1015.5550 | 1.09 | 1 | (50) | 9.8e-06 | 1 | U | L.TINND |
| 3197 | 508.7860 | 1015.5574 | 1015.5550 | 2.41 | 1 | (28) | 0.0015 | 1 | U | L.TINND |
| 4559 | 561.7928 | 1121.5710 | 1121.5717 | -0.60 | 1 | 22 | 0.0069 | 1 | U | W.QVSLQ |

| | | | | | | | | | | |
|-----------------------|----------|-----------|-----------|-------|---|------|---------|---|---|---------|
| 10216 | 869.9562 | 1737.8978 | 1737.9009 | -1.80 | 1 | 39 | 0.00012 | 1 | U | Y.TNANT |
| 10217 | 869.9585 | 1737.9024 | 1737.9009 | 0.87 | 1 | (35) | 0.0003 | 1 | U | Y.TNANT |
| 10362 | 892.4424 | 1782.8703 | 1782.8689 | 0.79 | 0 | 21 | 0.018 | 1 | U | L.SRIVN |

3. [3::sp|P02930|TOLC_ECOLI](#) Mass: 53708 Score: 229 Matches: 11(11) Sequences: 11
Outer membrane protein TolC OS=Escherichia coli (strain K12) OX=83333 GN=tolC PE=1 SV=2
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|-----------------------|----------|-----------|-----------|-------|------|-------|---------|------|--------|---------|
| 1162 | 426.2224 | 850.4302 | 850.4297 | 0.59 | 0 | 23 | 0.0047 | 1 | U | L.RQITG |
| 1163 | 426.2226 | 850.4307 | 850.4297 | 1.18 | 0 | (22) | 0.0061 | 1 | U | L.RQITG |
| 2466 | 482.7404 | 963.4663 | 963.4662 | 0.14 | 1 | (31) | 0.00094 | 1 | U | Y.NFVGA |
| 2467 | 482.7406 | 963.4666 | 963.4662 | 0.51 | 1 | 38 | 0.00016 | 1 | U | Y.NFVGA |
| 3010 | 501.7584 | 1001.5023 | 1001.5029 | -0.58 | 2 | 35 | 0.00031 | 1 | U | L.GTLNE |
| 3604 | 523.7797 | 1045.5448 | 1045.5444 | 0.35 | 2 | 37 | 0.00018 | 1 | U | L.LPQLG |
| 3605 | 523.7800 | 1045.5454 | 1045.5444 | 0.94 | 2 | (33) | 0.00046 | 1 | U | L.LPQLG |
| 9452 | 804.9210 | 1607.8274 | 1607.8307 | -2.08 | 2 | 34 | 0.00049 | 1 | U | L.RQITG |
| 9453 | 804.9223 | 1607.8300 | 1607.8307 | -0.42 | 2 | (23) | 0.0061 | 1 | U | L.RQITG |
| 10698 | 936.4583 | 1870.9019 | 1870.9020 | -0.05 | 1 | 63 | 1.4e-06 | 1 | U | L.ANEVT |
| 10699 | 936.4597 | 1870.9049 | 1870.9020 | 1.52 | 1 | (47) | 6.2e-05 | 1 | U | L.ANEVT |

4. [1::sp|cRAP008|P00722|BGAL_ECOLI](#) Mass: 117321 Score: 197 Matches: 9(9) Sequences: 9
Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 SV=2
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|-----------|-----------|-------|------|-------|---------|------|--------|---------|
| 2292 | 477.2182 | 952.4218 | 952.4212 | 0.71 | 1 | 27 | 0.0022 | 1 | U | W.DLPLS |
| 3964 | 536.7924 | 1071.5703 | 1071.5461 | 22.5 | 0 | 24 | 0.0039 | 1 | U | L.AQVAE |
| 4113 | 541.8135 | 1081.6124 | 1081.6131 | -0.68 | 1 | (31) | 0.00086 | 1 | U | W.LSLPG |
| 4116 | 541.8146 | 1081.6147 | 1081.6131 | 1.46 | 1 | 38 | 0.00014 | 1 | U | W.LSLPG |
| 8576 | 736.3809 | 1470.7472 | 1470.7467 | 0.34 | 2 | (48) | 1.6e-05 | 1 | U | W.LGLGP |
| 8577 | 736.3816 | 1470.7486 | 1470.7467 | 1.33 | 2 | 80 | 1.1e-08 | 1 | U | W.LGLGP |
| 8594 | 736.8750 | 1471.7354 | 1471.7307 | 3.24 | 2 | (26) | 0.0027 | 1 | U | W.LGLGP |
| 8689 | 741.8747 | 1481.7348 | 1481.7362 | -0.91 | 1 | 33 | 0.00049 | 1 | U | F.RLSGQ |
| 8690 | 741.8773 | 1481.7401 | 1481.7362 | 2.64 | 1 | (32) | 0.00066 | 1 | U | F.RLSGQ |

5. [1::sp|cRAP002|P02768|ALBU_HUMAN](#) Mass: 71317 Score: 163 Matches: 32(32) Sequences: 32
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|-----------|-----------|-------|------|-------|---------|------|--------|---------|
| 204 | 387.2238 | 772.4330 | 772.4331 | -0.04 | 1 | 20 | 0.0095 | 1 | U | L.SVVLN |
| 399 | 396.6891 | 791.3636 | 791.3636 | -0.06 | 1 | (20) | 0.0092 | 1 | | Y.LQQCP |
| 400 | 396.6891 | 791.3637 | 791.3636 | 0.09 | 1 | 23 | 0.0046 | 1 | | Y.LQQCP |
| 3826 | 532.7194 | 1063.4242 | 1063.4240 | 0.13 | 0 | (33) | 0.00053 | 1 | | L.ECADD |
| 3827 | 532.7194 | 1063.4242 | 1063.4240 | 0.13 | 0 | (26) | 0.0023 | 1 | | L.ECADD |
| 3828 | 532.7201 | 1063.4257 | 1063.4240 | 1.62 | 0 | 38 | 0.00015 | 1 | | L.ECADD |
| 5225 | 589.2618 | 1176.5090 | 1176.5081 | 0.78 | 1 | (37) | 0.0002 | 1 | | L.LECAD |
| 5226 | 589.2618 | 1176.5090 | 1176.5081 | 0.78 | 1 | 41 | 8.4e-05 | 1 | | L.LECAD |

| | | | | | | | | | | |
|----------------------|----------|-----------|-----------|-------|---|------|---------|---|---|---------|
| 7876 | 697.3342 | 1392.6539 | 1392.6555 | -1.12 | 0 | (21) | 0.0086 | 2 | U | Y.ICENQ |
| 7877 | 697.3344 | 1392.6543 | 1392.6555 | -0.86 | 0 | (27) | 0.0026 | 2 | U | Y.ICENQ |
| 7879 | 697.3350 | 1392.6554 | 1392.6555 | -0.07 | 0 | (27) | 0.0027 | 2 | U | Y.ICENQ |
| 7880 | 697.3350 | 1392.6554 | 1392.6555 | -0.07 | 0 | (22) | 0.0082 | 2 | U | Y.ICENQ |
| 7881 | 697.3353 | 1392.6561 | 1392.6555 | 0.46 | 0 | (24) | 0.0054 | 2 | U | Y.ICENQ |
| 7882 | 697.3357 | 1392.6568 | 1392.6555 | 0.97 | 0 | (23) | 0.0054 | 2 | U | Y.ICENQ |
| 7883 | 697.3357 | 1392.6568 | 1392.6555 | 0.97 | 0 | (22) | 0.007 | 2 | U | Y.ICENQ |
| 7884 | 697.3358 | 1392.6571 | 1392.6555 | 1.16 | 0 | (36) | 0.00033 | 2 | U | Y.ICENQ |
| 7886 | 697.3360 | 1392.6574 | 1392.6555 | 1.42 | 0 | (29) | 0.0014 | 2 | U | Y.ICENQ |
| 7888 | 697.3362 | 1392.6578 | 1392.6555 | 1.68 | 0 | (28) | 0.0021 | 2 | U | Y.ICENQ |
| 7889 | 697.3363 | 1392.6580 | 1392.6555 | 1.85 | 0 | (27) | 0.0023 | 2 | U | Y.ICENQ |
| 7890 | 697.3364 | 1392.6583 | 1392.6555 | 2.04 | 0 | (23) | 0.0049 | 2 | U | Y.ICENQ |
| 7892 | 697.3366 | 1392.6587 | 1392.6555 | 2.29 | 0 | (23) | 0.0049 | 2 | U | Y.ICENQ |
| 7893 | 697.3367 | 1392.6588 | 1392.6555 | 2.38 | 0 | (27) | 0.0021 | 2 | U | Y.ICENQ |
| 7894 | 697.3367 | 1392.6588 | 1392.6555 | 2.38 | 0 | (25) | 0.0032 | 2 | U | Y.ICENQ |
| 7895 | 697.3368 | 1392.6590 | 1392.6555 | 2.55 | 0 | 40 | 0.0001 | 2 | U | Y.ICENQ |
| 7897 | 697.3369 | 1392.6593 | 1392.6555 | 2.73 | 0 | (21) | 0.009 | 2 | U | Y.ICENQ |
| 7898 | 697.3370 | 1392.6594 | 1392.6555 | 2.83 | 0 | (21) | 0.008 | 2 | U | Y.ICENQ |
| 7901 | 697.3372 | 1392.6599 | 1392.6555 | 3.17 | 0 | (32) | 0.00062 | 2 | U | Y.ICENQ |
| 7902 | 697.3373 | 1392.6600 | 1392.6555 | 3.26 | 0 | (24) | 0.0041 | 2 | U | Y.ICENQ |
| 7903 | 697.3373 | 1392.6600 | 1392.6555 | 3.26 | 0 | (20) | 0.01 | 2 | U | Y.ICENQ |
| 7904 | 697.3375 | 1392.6604 | 1392.6555 | 3.52 | 0 | (25) | 0.0031 | 2 | U | Y.ICENQ |
| 7905 | 697.3377 | 1392.6609 | 1392.6555 | 3.87 | 0 | (21) | 0.0091 | 2 | U | Y.ICENQ |
| 7917 | 697.8267 | 1393.6389 | 1393.6395 | -0.43 | 0 | (33) | 0.00089 | 3 | U | Y.ICENQ |

6. [1::sp|cRAP112|P00761|TRYP_PIG](#) Mass: 25078 Score: 81 Matches: 4(4) Sequen
Trypsin OS=Sus scrofa PE=1 SV=1
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|-----------|-----------|-------|------|-------|---------|------|--------|---------|
| 4004 | 538.2632 | 1074.5118 | 1074.5094 | 2.21 | 1 | 36 | 0.00035 | 1 | U | Y.QVSLN |
| 4023 | 538.7634 | 1075.5123 | 1075.4934 | 17.5 | 1 | (22) | 0.0074 | 1 | U | Y.QVSLN |
| 6355 | 629.3325 | 1256.6505 | 1256.6513 | -0.66 | 1 | 46 | 2.8e-05 | 1 | U | Y.VNWIQ |
| 6356 | 629.3331 | 1256.6516 | 1256.6513 | 0.21 | 1 | (35) | 0.00031 | 1 | U | Y.VNWIQ |

7. [1::sp|cRAP030|P32503|GAG_SCVLA](#) Mass: 76402 Score: 48 Matches: 2(2) Sequen
Major capsid protein OS=Saccharomyces cerevisiae virus L-A GN=gag PE=1 SV=1
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|--------------------|----------|----------|----------|------|------|-------|---------|------|--------|-----------|
| 17 | 380.2215 | 758.4284 | 758.4174 | 14.5 | 2 | 48 | 1.6e-05 | 1 | U | F.LLSGDAA |
| 19 | 380.2217 | 758.4288 | 758.4174 | 15.0 | 2 | (35) | 0.0003 | 1 | U | F.LLSGDAA |

8. [1::sp|cRAP115|P63279|UBC9_HUMAN](#) Mass: 18223 Score: 31 Matches: 2(2) Sequen
SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|-----------------------|----------|-----------|-----------|------|------|-------|--------|------|--------|----------|
| 10206 | 579.3157 | 1734.9252 | 1734.9199 | 3.06 | 1 | 31 | 0.0011 | 1 | U | Y.EKRVRA |
| 10207 | 579.3174 | 1734.9305 | 1734.9199 | 6.12 | 1 | (27) | 0.0025 | 1 | U | Y.EKRVRA |

9. [1::sp|cRAP034|P09211|GSTP1 HUMAN](#) Mass: 23569 Score: 27 Matches: 2(2) Sequen
 Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|-----------|-----------|--------|------|-------|--------|------|--------|---------|
| 3689 | 527.2702 | 1052.5258 | 1052.5390 | -12.47 | 2 | 27 | 0.0021 | 1 | U | L.TLYQS |
| 3690 | 527.2707 | 1052.5268 | 1052.5390 | -11.54 | 2 | (22) | 0.0065 | 1 | U | L.TLYQS |

10. [1::sp|cRAP015|P02666|CASB BOVIN](#) Mass: 25148 Score: 24 Matches: 4(4) Sequen
 Beta-casein OS=Bos taurus GN=CSN2 PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|----------|----------|-------|------|-------|--------|------|--------|------------|
| 1177 | 426.7289 | 851.4432 | 851.4496 | -7.54 | 1 | (23) | 0.0048 | 1 | U | -.MKVLIL.A |
| 1178 | 426.7289 | 851.4433 | 851.4496 | -7.47 | 1 | (20) | 0.0097 | 1 | U | -.MKVLIL.A |
| 1179 | 426.7290 | 851.4435 | 851.4496 | -7.19 | 1 | 27 | 0.0021 | 1 | U | -.MKVLIL.A |
| 1180 | 426.7293 | 851.4441 | 851.4496 | -6.46 | 1 | (24) | 0.0037 | 1 | U | -.MKVLIL.A |

11. [1::sp|cRAP020|P01031|CO5 HUMAN](#) Mass: 189897 Score: 23 Matches: 1(1) Sequen
 Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|-----------------------|----------|-----------|-----------|-------|------|-------|--------|------|--------|----------|
| 10350 | 890.9603 | 1779.9061 | 1779.9189 | -7.20 | 1 | 23 | 0.0064 | 1 | U | Y.SVVRGE |

12. [1::sp|cRAP089|P00792|PEPA BOVIN](#) Mass: 40320 Score: 22 Matches: 1(1) Sequen
 Pepsin A OS=Bos taurus GN=PGA PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|---------------------|----------|----------|----------|--------|------|-------|--------|------|--------|-----------|
| 206 | 387.2243 | 772.4340 | 772.4443 | -13.24 | 0 | 22 | 0.0059 | 1 | U | Y.IREAATL |

13. [1::sp|cRAP104|P12081|SYHC HUMAN](#) Mass: 57944 Score: 22 Matches: 2(2) Sequen
 Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|-----------|-----------|--------|------|-------|--------|------|--------|---------|
| 4905 | 575.7841 | 1149.5536 | 1149.5773 | -20.67 | 1 | (21) | 0.0076 | 1 | U | L.VASAO |
| 4907 | 575.7863 | 1149.5581 | 1149.5773 | -16.74 | 1 | 22 | 0.0062 | 1 | U | L.VASAO |

14. [1::sp|cRAP054|P04264|K2C1 HUMAN](#) Mass: 66170 Score: 22 Matches: 1(1) Sequen
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|---------------------|----------|----------|----------|------|------|-------|--------|------|--------|------------|
| 415 | 397.6985 | 793.3824 | 793.3714 | 13.8 | 0 | 22 | 0.0067 | 1 | U | Y.MTKVDL.Q |

15. [1::sp|cRAP004|P04745|AMY1 HUMAN](#) Mass: 58415 Score: 22 Matches: 2(2) Sequen
Alpha-amylase 1 OS=Homo sapiens GN=AMY1A PE=1 SV=2
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|----------|----------|------|------|-------|--------|------|--------|------------|
| 1490 | 440.2264 | 878.4381 | 878.4246 | 15.4 | 0 | (21) | 0.0074 | 1 | U | F.GNGRVTEF |
| 1491 | 440.2269 | 878.4392 | 878.4246 | 16.6 | 0 | 22 | 0.007 | 1 | U | F.GNGRVTEF |

16. [1::sp|cRAP084|P15559|NQO1 HUMAN](#) Mass: 30905 Score: 21 Matches: 1(1) Sequen
NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|---------------------|----------|----------|----------|-------|------|-------|--------|------|--------|------------|
| 541 | 401.7374 | 801.4602 | 801.4643 | -5.14 | 0 | 21 | 0.0072 | 1 | U | -.MVGRRAL. |

17. [1::sp|cRAP077|P41159|LEP HUMAN](#) Mass: 18800 Score: 21 Matches: 2(2) Sequen
Leptin OS=Homo sapiens GN=LEP PE=1 SV=1
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|----------|----------|------|------|-------|--------|------|--------|------------|
| 1392 | 436.7490 | 871.4834 | 871.4763 | 8.11 | 2 | (20) | 0.01 | 1 | U | L.ENLRDLL. |
| 1395 | 436.7492 | 871.4839 | 871.4763 | 8.68 | 2 | 21 | 0.0086 | 1 | U | L.ENLRDLL. |

18. [1::sp|cRAP086|P01012|OVAL CHICK](#) Mass: 43196 Score: 21 Matches: 1(1) Sequen
Ovalbumin OS=Gallus gallus GN=SERPINB14 PE=1 SV=2
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|----------------------|----------|-----------|-----------|------|------|-------|--------|------|--------|----------|
| 4373 | 552.7748 | 1103.5351 | 1103.5094 | 23.3 | 0 | 21 | 0.0085 | 1 | U | F.QTAADQ |

19. [1::sp|cRAP114|O00762|UBE2C HUMAN](#) Mass: 19754 Score: 20 Matches: 1(1) Sequen
Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1
Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt) | Mr(calc) | ppm | Miss | Score | Expect | Rank | Unique | Peptide |
|---------------------|----------|----------|----------|------|------|-------|--------|------|--------|------------|
| 889 | 415.2612 | 828.5078 | 828.5069 | 1.15 | 1 | 20 | 0.0092 | 1 | U | Y.DVRTILL. |

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Chymotrypsin
Fixed modifications : [Carbamidomethyl \(C\)](#)
Variable modifications : [Deamidated \(NQ\)](#), [DTSSP Cross link \(K\)](#), [DTSSP Cross link di oxidation \(K\)](#), [DTSSP Cross link single oxidation \(K\)](#), [DTSSP Cross link tri oxidation \(K\)](#), [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 25 ppm
Fragment Mass Tolerance: ± 0.8 Da
Max Missed Cleavages : 2
Instrument type : ESI-TRAP
Number of queries : 11798

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| Mascot: http://www.matrixscience.com/ |
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