

## Supplementary information

### Identification of potential novel interacting partners for coagulation Factor XIII B (FXIII-B) subunit, a protein associated with a rare bleeding disorder

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**Supplementary Table:**

**Table S1:** Table depicting the FXIII Generation assay parameters obtained at different spiking conditions.

|  | <b>AUC</b> | <b>t<sub>max</sub> (min)</b> | <b>t<sub>lag</sub> (min)</b> | <b>K<sub>a</sub></b> | <b>K<sub>b</sub></b> |
|--|------------|------------------------------|------------------------------|----------------------|----------------------|
| <b>Standard plasma (SP)</b>            | 925,5      | 15,1                         | 9,9                          | 0,69                 | 0,02                 |
| <b>FXIII A (2U/mL)</b>                 | 671,2      | 29,5                         | 13,1                         | 0,06                 | 0,06                 |
| <b>FXIII A (1U/mL)</b>                 | 476,7      | 28,9                         | 12                           | 0,06                 | 0,06                 |
| <b>FXIII A (2U/mL) + FXIII B</b>       | 1047,3     | 18                           | 10,2                         | 0,43                 | 0,02                 |
| <b>FXIII A (1U/mL) + FXIII B</b>       | 586,3      | 16,3                         | 9,9                          | 0,53                 | 0,02                 |
| <b>FXIII A (2U/mL) + CFH</b>           | 1005,2     | 28,2                         | 11,8                         | 0,10                 | 0,04                 |
| <b>FXIII A (1U/mL) + CFH</b>           | 414        | 26,4                         | 9,9                          | 0,06                 | 0,06                 |
| <b>FXIII A (2U/mL) + FXIII B + CFH</b> | 1192,1     | 17,6                         | 9,1                          | 0,37                 | 0,02                 |
| <b>FXIII A (1U/mL) + FXIII B + CFH</b> | 580,4      | 17,5                         | 9,6                          | 0,37                 | 0,02                 |

## Supplementary figures

**Figure S1:** Peak table from SEC of Fibrogammin P. Highlighted Peak correspond to Proteomic constituents in the sample at specific retention time (in minutes), and Area under peak (mAU\*min).

### Peak table: Fibrogammin P Large Scale Purification

140616 Fibrogammin Prep Sup200:10\_UV1\_280nm@01, PEAK

| No | Ret<br>min | Area<br>mAU*min | Area/Peak area<br>(time) % | Height<br>mAU |
|----|------------|-----------------|----------------------------|---------------|
| 1  | 0.07       | 0.3012          | 0.00                       | 1.688         |
| 2  | 0.35       | 0.2807          | 0.00                       | 1.578         |
| 3  | 19.47      | 253.5121        | 3.88                       | 140.487       |
| 4  | 23.31      | 1177.3246       | 18.01                      | 299.231       |
| 5  | 29.33      | 148.7012        | 2.27                       | 79.121        |
| 6  | 34.51      | 1598.5213       | 24.45                      | 1638.463      |
| 7  | 34.67      | 1456.2326       | 22.27                      | 1663.050      |
| 8  | 45.32      | 3.0772          | 0.05                       | 6.396         |
| 9  | 45.68      | 4.8692          | 0.07                       | 9.008         |
| 10 | 47.36      | 19.3370         | 0.30                       | 33.259        |
| 11 | 48.65      | 0.2840          | 0.00                       | 1.252         |
| 12 | 49.13      | 0.3210          | 0.00                       | 1.257         |
| 13 | 53.02      | 1867.6034       | 28.56                      | 1408.756      |
| 14 | 55.10      | 1.0523          | 0.02                       | 7.242         |
| 15 | 55.29      | 1.2979          | 0.02                       | 6.757         |
| 16 | 55.54      | 1.3947          | 0.02                       | 6.941         |
| 17 | 55.69      | 3.1471          | 0.05                       | 6.650         |
| 18 | 56.33      | 0.7146          | 0.01                       | 2.661         |
| 19 | 67.13      | 0.3679          | 0.01                       | 1.021         |
| 20 | 68.11      | 0.2931          | 0.00                       | 1.340         |

Total number of detected peaks = 141

Total area = 6550.5640 mAU\*min

Area in evaluated peaks = 6538.6329 mAU\*min

Ratio peak area / total area = 0.998179

Total peak width = 29.50 min

Column height = 30.00 cm

Calculated from : 140616 Fibrogammin Prep Sup200:10\_UV1\_280nm

Baseline : 140616 Fibrogammin Prep Sup200:10\_UV1\_280nm@01, BASEM

Peak rejection on:

Maximum number of peaks: 20

Current peak filter settings:

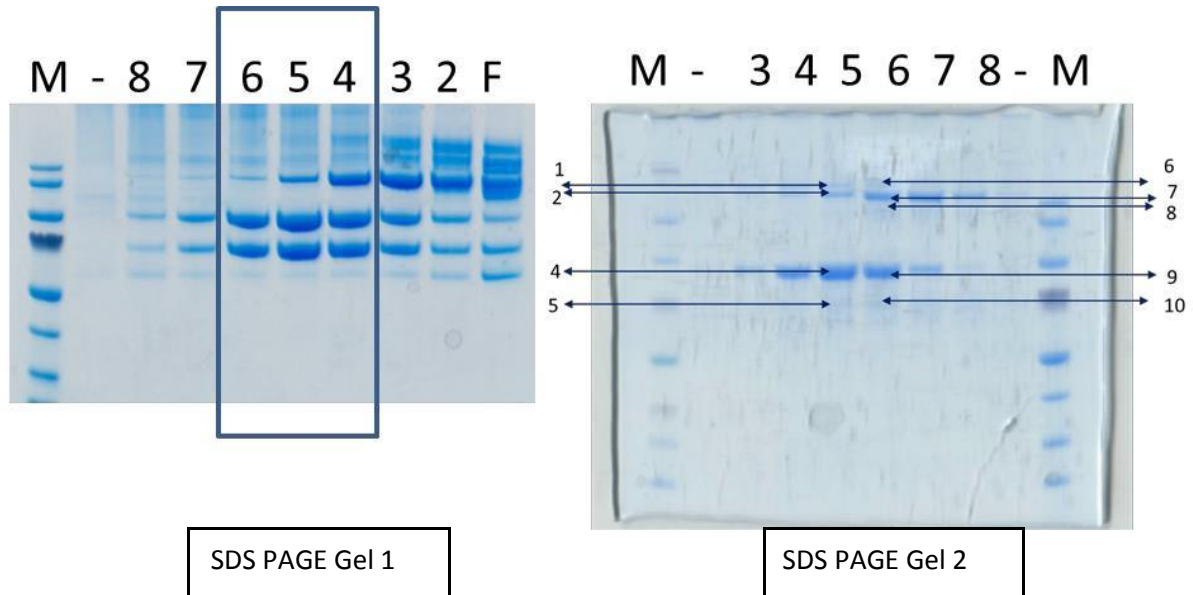
Maximum number of peaks: 20

**Figure S2:** MS result showing the protein hits corresponding to the bands on SDS PAGE for interactome analyses of FXIIIB (Figure 4, main manuscript).

| Band | A      | Description  | S      | SC   | E    | P  | M |
|------|--------|--|--------|------|------|----|---|
| A1   | P02675 | Fibrinogen beta chain Homo sapiens                         | 1324,4 | 26,1 | 3,8  | 9  | 1 |
|      | P02679 | Fibrinogen gamma chain Homo sapiens                        | 804,6  | 30,5 | 4,9  | 13 | 3 |
|      | P02671 | Fibrinogen alpha chain Homo sapiens                        | 570,3  | 16,9 | 5,0  | 13 | 5 |
|      | P01023 | Alpha 2 macroglobulin Homo sapiens                         | 76,6   | 5,6  | 3,2  | 7  | 1 |
| A2   |        | negative   |        |      |      |    |   |
| A3   | P01857 | Ig gamma 1 chain C region Homo sapiens                     | 1353,4 | 26,1 | 4,2  | 8  | 0 |
|      | P01834 | Ig kappa chain C region Homo sapiens                       | 129,8  | 31,1 | 6,7  | 2  | 0 |
| A4   | P02768 | Serum albumin Homo sapiens                                 | 456,8  | 8,0  | 3,9  | 9  | 2 |
| A5   | P02747 | Complement C1q subcomponent subunit C Homo sapiens         | 2224,5 | 21,2 | 5,2  | 6  | 2 |
| C1   |        | negative   |        |      |      |    |   |
| D1   | P02747 | Complement C1q subcomponent subunit C Homo sapiens         | 926,2  | 16,3 | 17,7 | 4  | 0 |
| D2   | P02675 | Fibrinogen beta chain Homo sapiens                         | 1667,0 | 31,0 | 4,8  | 16 | 2 |
|      | P02679 | Fibrinogen gamma chain Homo sapiens                        | 766,4  | 32,2 | 5,5  | 15 | 3 |
|      | P02671 | Fibrinogen alpha chain Homo sapiens                        | 551,2  | 16,9 | 5,5  | 15 | 5 |
| D3   | P01876 | Ig alpha 1 chain C region Homo sapiens                     | 267,5  | 5,9  | 2,1  | 3  | 0 |
|      | P01024 | Complement C3 Homo sapiens                                 | 129,2  | 11,7 | 3,9  | 16 | 3 |
|      | P01857 | Ig gamma 1 chain C region Homo sapiens                     | 121,8  | 7,9  | 2,6  | 2  | 0 |
| D4   | P01857 | Ig gamma 1 chain C region Homo sapiens                     | 1449,9 | 26,7 | 4,5  | 8  | 0 |
|      | P01834 | Ig kappa chain C region Homo sapiens                       | 1048,4 | 32,1 | 3,1  | 3  | 0 |
| D5   | P05160 | Coagulation factor XIII B chain Homo sapiens               | 32,8   | 4,4  | 15,7 | 5  | 0 |
| D6   | P05160 | Coagulation factor XIII B chain Homo sapiens               | 1016,9 | 31,5 | 3,9  | 17 | 4 |
| D7   | P02787 | Serotransferrin Homo sapiens                               | 64,8   | 5,4  | 2,7  | 3  | 0 |
| D8   | P02768 | Serum albumin Homo sapiens                                 | 3085,6 | 45,3 | 6,0  | 28 | 5 |
| E1   | P02768 | Serum albumin Homo sapiens                                 | 143,5  | 4,6  | 5,3  | 3  | 1 |
| E2   | P02768 | Serum albumin Homo sapiens                                 | 1165,9 | 12,5 | 7,1  | 8  | 1 |
| E3   | P02768 | Serum albumin Homo sapiens                                 | 161,7  | 5,9  | 3,2  | 3  | 1 |
| E4   | P02768 | Serum albumin Homo sapiens                                 | 540,4  | 2,3  | 1,8  | 1  | 0 |
| F1   | Q86VM9 | Zinc finger CCCH domain containing protein 18 Homo sapiens | 26,3   | 0,8  | 8,9  | 1  | 0 |
| F2   | P02768 | Serum albumin Homo sapiens                                 | 281,2  | 2,0  | 6,5  | 8  | 1 |

**A: UniProt Accession number; S: PLGS Protein Score; SC: Sequence coverage in %, E Mean mass error in ppm; P: number of identified peptides; M; number of modified peptides**

**Figure S3:** SDS-PAGE analysis of Fibrogammin P. Gel 1 depicts fraction of eluates obtained after Gel filtration of FibrogamminP, when resuspended in 20mM tris 120mM NaCl, pH 7.4 (Column: Superdex200 100/300 GL (GE healthcare)). The numbers on top represent the fraction number when ran at a constant flow rate of 400uL/min. (F is crude fraction). The marked box for fraction 4-6, was re-ran on GFC, with fractions separated on SDS-PAGE (gel 2 here). The marked bands on gel were cut ant analyzed by Mass spectrometry.



**Supplementary Results:** The following supplementary attached files are corresponding to the raw data obtained from MS analyses of bands on gel 2 in figure S3. MS analyses were performed based on MASCOT probability based scoring.

#### Supplementary references

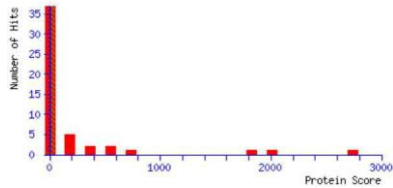
R1. Albrecht M, Alessandri S, Conti A, Reuter A, Lauer I, Vieths S, et al. High level expression, purification and physico- and immunochemical characterization of recombinant Pen a 1: a major allergen of shrimp. *Mol. Nutr. Food Res.* 2008;52 Suppl 2: S186-S195.

**MASCOT** (SCIENCE) Mascot Search Results

User : Julian  
 Email : julian.langer@mpibp-frankfurt.mpg.de  
 Search title : Submitted from 140318 842 ChKretzler 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
 MS data file : D:\Data\140318\140318\_842\_ChReinhard\_1\_Tray01-C6\_01\_17682.d\140314 842 ChReinhard 1\_Tray01-C6\_01\_17682.mgf  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Timestamp : 19 Mar 2014 at 09:48:02 GMT  
 Protein hits : **A2MG HUMAN** Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2  
**CH60 EC024** 60 kDa chaperonin OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=groL PE=3 SV=1  
**CH60 ENTIT** 60 kDa chaperonin (Fragment) OS=Enterobacter intermedium GN=groL PE=3 SV=1  
**TRYP PIG** Trypsin OS=Sus scrofa PE=1 SV=1  
**K2C1 HUMAN** Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
**K1C9 HUMAN** Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
**CPAH HUMAN** Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
**K1C10 HUMAN** Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
**K22E HUMAN** Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
**ALBU HUMAN** Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
**K2C6B HUMAN** Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5  
**F13B HUMAN** Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
**K1C14 HUMAN** Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4  
**F13A HUMAN** Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
**CH602 BURKL** 60 kDa chaperonin 2 OS=Burkholderia xenovorans (strain LB400) GN=groL2 PE=3 SV=1

**Mascot Score Histogram**

Ions score is  $-10 * \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 38 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



**Peptide Summary Report**

Format As **Peptide Summary** [Help](#)

Significance threshold p<0.05 Max. number of hits AUTO

Standard scoring  MudPIT scoring  Ions score or expect cut-off  Show sub-sets 0

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

Select All  Select None  Search Selected  Error tolerant  Archive Report

1. **A2MG HUMAN** Mass: 164614 Score: 2744 Matches: 130 (82) Sequences: 56 (41) eMPAI: 2.30  
 Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide                         |
|-------|----------|-----------|-----------|---------|------|-------|----------|------|--------|---------------------------------|
| 68    | 593.3666 | 592.3593  | 592.3584  | 0.0009  | 0    | 34    | 0.19     | 1    | U      | K.LSFVK.V                       |
| 69    | 593.3673 | 592.3601  | 592.3584  | 0.0016  | 0    | (30)  | 0.44     | 1    | U      | K.LSFVK.V                       |
| 82    | 634.3942 | 633.3869  | 633.3850  | 0.0019  | 0    | 13    | 44       | 1    | U      | K.VFQLK.R                       |
| 93    | 724.4370 | 723.4297  | 723.4279  | 0.0018  | 0    | 18    | 5.2      | 1    | U      | K.GVPIFNK.V                     |
| 96    | 765.4163 | 764.4090  | 764.4068  | 0.0022  | 0    | 25    | 3        | 1    | U      | R.GEAFPLK.A                     |
| 101   | 414.7336 | 827.4527  | 827.4501  | 0.0026  | 0    | 63    | 0.00035  | 1    | U      | K.SDIAPVAR.L                    |
| 102   | 414.7337 | 827.4528  | 827.4501  | 0.0027  | 0    | (63)  | 0.00039  | 1    | U      | K.SDIAPVAR.L                    |
| 103   | 414.7337 | 827.4529  | 827.4501  | 0.0028  | 0    | (48)  | 0.011    | 1    | U      | K.SDIAPVAR.L                    |
| 112   | 432.2723 | 862.5301  | 862.5276  | 0.0025  | 1    | 24    | 1.5      | 1    | U      | K.TKVFQLK.R                     |
| 116   | 442.2850 | 882.5554  | 882.5538  | 0.0015  | 0    | (37)  | 0.055    | 1    | U      | R.DLKPATVK.V                    |
| 117   | 442.2855 | 882.5564  | 882.5538  | 0.0026  | 0    | (32)  | 0.19     | 1    | U      | R.DLKPATVK.V                    |
| 118   | 442.2856 | 882.5566  | 882.5538  | 0.0028  | 0    | 39    | 0.035    | 1    | U      | R.DLKPATVK.V                    |
| 119   | 442.2862 | 882.5578  | 882.5538  | 0.0040  | 0    | (33)  | 0.13     | 1    | U      | R.DLKPATVK.V                    |
| 127   | 463.2787 | 924.5428  | 924.5393  | 0.0036  | 0    | 39    | 0.047    | 1    | U      | R.TGTHGLLVK.Q                   |
| 128   | 463.2789 | 924.5432  | 924.5393  | 0.0039  | 0    | (18)  | 5.1      | 2    | U      | R.TGTHGLLVK.Q                   |
| 129   | 463.2789 | 924.5433  | 924.5393  | 0.0040  | 0    | (28)  | 0.55     | 2    | U      | R.TGTHGLLVK.Q                   |
| 134   | 509.8020 | 1017.5894 | 1017.5859 | 0.0035  | 0    | (46)  | 0.016    | 1    | U      | K.ATVLYLTK.C                    |
| 135   | 509.8023 | 1017.5901 | 1017.5859 | 0.0042  | 0    | (31)  | 0.53     | 1    | U      | K.ATVLYLTK.C                    |
| 136   | 509.8024 | 1017.5902 | 1017.5859 | 0.0043  | 0    | 48    | 0.0092   | 1    | U      | K.ATVLYLTK.C                    |
| 137   | 509.8027 | 1017.5908 | 1017.5859 | 0.0049  | 0    | (31)  | 0.55     | 1    | U      | K.ATVLYLTK.C                    |
| 145   | 523.7997 | 1045.5848 | 1045.5808 | 0.0040  | 0    | 36    | 0.18     | 1    | U      | K.FEYQVTVK.I                    |
| 147   | 523.8002 | 1045.5859 | 1045.5808 | 0.0051  | 0    | (35)  | 0.25     | 1    | U      | K.FEYQVTVK.I                    |
| 158   | 542.8125 | 1083.6105 | 1083.6077 | 0.0028  | 0    | 46    | 0.016    | 1    | U      | K.GHFSISIPVK.S                  |
| 159   | 542.8133 | 1083.6119 | 1083.6077 | 0.0043  | 0    | (39)  | 0.065    | 1    | U      | K.GHFSISIPVK.S                  |
| 164   | 552.3077 | 1102.6008 | 1102.5982 | 0.0026  | 0    | (55)  | 0.0025   | 1    | U      | R.SSGSLNNAIK.G                  |
| 165   | 552.3080 | 1102.6015 | 1102.5982 | 0.0033  | 0    | (51)  | 0.0067   | 1    | U      | R.SSGSLNNAIK.G                  |
| 166   | 552.3083 | 1102.6020 | 1102.5982 | 0.0038  | 0    | 59    | 0.0011   | 1    | U      | R.SSGSLNNAIK.G                  |
| 170   | 558.8074 | 1115.6003 | 1115.5975 | 0.0027  | 0    | (77)  | 1.6e-005 | 1    | U      | R.QTVSWAVTFK.S                  |
| 171   | 558.8079 | 1115.6012 | 1115.5975 | 0.0036  | 0    | (77)  | 1.6e-005 | 1    | U      | R.QTVSWAVTFK.S                  |
| 172   | 558.8082 | 1115.6019 | 1115.5975 | 0.0044  | 0    | 77    | 1.6e-005 | 1    | U      | R.QTVSWAVTFK.S                  |
| 173   | 560.8235 | 1119.6324 | 1119.6288 | 0.0036  | 0    | (39)  | 0.074    | 1    | U      | K.SIKYKQVTK.F                   |
| 174   | 560.8236 | 1119.6327 | 1119.6288 | 0.0039  | 0    | (32)  | 0.36     | 1    | U      | K.SIKYKQVTK.F                   |
| 175   | 560.8237 | 1119.6329 | 1119.6288 | 0.0041  | 0    | (34)  | 0.22     | 1    | U      | K.SIKYKQVTK.F                   |
| 176   | 560.8239 | 1119.6332 | 1119.6288 | 0.0044  | 0    | 42    | 0.038    | 1    | U      | K.SIKYKQVTK.F                   |
| 179   | 567.7944 | 1133.5742 | 1133.5750 | -0.0008 | 0    | 84    | 2.9e-006 | 1    | U      | R.SASNMAIVDVK.M                 |
| 181   | 574.8164 | 1147.6183 | 1147.6138 | 0.0044  | 0    | 46    | 0.021    | 1    | U      | R.QGIPFFQVLR.L                  |
| 182   | 574.8166 | 1147.6186 | 1147.6138 | 0.0048  | 0    | (41)  | 0.067    | 1    | U      | R.QGIPFFQVLR.L                  |
| 185   | 575.7933 | 1149.5720 | 1149.5700 | 0.0020  | 0    | (56)  | 0.0015   | 1    | U      | R.SASNMAIVDVK.M + Oxidation (M) |
| 186   | 575.7935 | 1149.5725 | 1149.5700 | 0.0026  | 0    | (80)  | 7.4e-006 | 1    | U      | R.SASNMAIVDVK.M + Oxidation (M) |
| 187   | 575.7936 | 1149.5726 | 1149.5700 | 0.0026  | 0    | (74)  | 3e-005   | 1    | U      | R.SASNMAIVDVK.M + Oxidation (M) |
| 202   | 605.8264 | 1209.6383 | 1209.6353 | 0.0030  | 0    | (50)  | 0.0053   | 1    | U      | K.LPPNVVEESAR.A                 |
| 203   | 605.8270 | 1209.6395 | 1209.6353 | 0.0041  | 0    | (50)  | 0.0052   | 1    | U      | K.LPPNVVEESAR.A                 |
| 204   | 605.8271 | 1209.6396 | 1209.6353 | 0.0043  | 0    | 67    | 0.00011  | 1    | U      | K.LPPNVVEESAR.A                 |
| 207   | 613.2816 | 1224.5487 | 1224.5445 | 0.0043  | 0    | 50    | 0.0024   | 1    | U      | K.YDVENCLANK.V                  |
| 208   | 613.2820 | 1224.5494 | 1224.5445 | 0.0049  | 0    | (39)  | 0.028    | 1    | U      | K.YDVENCLANK.V                  |
| 220   | 628.3273 | 1254.6400 | 1254.6357 | 0.0043  | 0    | (63)  | 0.00026  | 1    | U      | K.AIGYLYNGYQK.R                 |
| 221   | 628.3279 | 1254.6412 | 1254.6357 | 0.0056  | 0    | 79    | 7.5e-006 | 1    | U      | K.AIGYLYNGYQK.R                 |
| 226   | 630.2920 | 1258.5694 | 1258.5652 | 0.0042  | 0    | (74)  | 9.2e-006 | 1    | U      | R.VGFYSDVMGR.G                  |
| 223   | 630.2921 | 1258.5695 | 1258.5652 | 0.0043  | 0    | 92    | 1.4e-007 | 1    | U      | R.VGFYSDVMGR.G                  |
| 224   | 630.2924 | 1258.5702 | 1258.5652 | 0.0049  | 0    | (83)  | 1.1e-006 | 1    | U      | R.VGFYSDVMGR.G                  |
| 227   | 636.8415 | 1271.6685 | 1271.6656 | 0.0029  | 0    | (70)  | 6.9e-005 | 1    | U      | R.VTAAPQSCALR.A                 |
| 228   | 636.8421 | 1271.6696 | 1271.6656 | 0.0040  | 0    | 74    | 2.5e-005 | 1    | U      | R.VTAAPQSCALR.A                 |
| 229   | 638.2889 | 1274.5633 | 1274.5602 | 0.0032  | 0    | (48)  | 0.0028   | 1    | U      | R.VGFYSDVMGR.G + Oxidation (M)  |
| 230   | 638.2890 | 1274.5633 | 1274.5602 | 0.0032  | 0    | (54)  | 0.00072  | 1    | U      | R.VGFYSDVMGR.G + Oxidation (M)  |
| 242   | 669.8319 | 1337.6492 | 1337.6438 | 0.0054  | 0    | (63)  | 0.00028  | 1    | U      | R.NALFCLSAWK.T                  |
| 243   | 669.8323 | 1337.6500 | 1337.6438 | 0.0062  | 0    | (68)  | 8.7e-005 | 1    | U      | R.NALFCLSAWK.T                  |
| 244   | 669.8325 | 1337.6504 | 1337.6438 | 0.0066  | 0    | 82    | 3.3e-006 | 1    | U      | R.NALFCLSAWK.T                  |
| 255   | 697.8458 | 1393.6771 | 1393.6725 | 0.0046  | 0    | 72    | 3.1e-005 | 1    | U      | K.NEDSLVFGYQDK.S                |
| 260   | 471.5446 | 1411.6119 | 1411.6085 | 0.0035  | 0    | (57)  | 0.00031  | 1    | U      | K.EQAPHCICANGR.Q                |
| 261   | 706.8135 | 1411.6125 | 1411.6085 | 0.0040  | 0    | (32)  | 0.11     | 1    | U      | K.EQAPHCICANGR.Q                |
| 262   | 471.5448 | 1411.6125 | 1411.6085 | 0.0040  | 0    | 62    | 0.00011  | 1    | U      | K.EQAPHCICANGR.Q                |
| 263   | 709.8044 | 1417.5943 | 1417.5899 | 0.0044  | 0    | (23)  | 0.35     | 1    | U      | K.HYDGSYTFEGR.V                 |
| 264   | 709.8046 | 1417.5947 | 1417.5899 | 0.0048  | 0    | 48    | 0.0012   | 1    | U      | K.HYDGSYTFEGR.V                 |
| 265   | 724.8277 | 1447.6409 | 1447.6363 | 0.0046  | 0    | 61    | 0.00014  | 1    | U      | K.DMYSFLEDMLK.A                 |
| 267   | 724.8280 | 1447.6415 | 1447.6363 | 0.0052  | 0    | (45)  | 0.0056   | 1    | U      | K.DMYSFLEDMLK.A                 |
| 275   | 756.3885 | 1510.7625 | 1510.7627 | -0.0002 | 0    | 46    | 0.011    | 1    | U      | K.AAQTIVISQSTFSSK.F             |
| 277   | 515.9404 | 1544.7993 | 1544.7947 | 0.0046  | 0    | (37)  | 0.12     | 1    | U      | R.LVHVEEHPHTVTR.K               |
| 278   | 515.9409 | 1544.8008 | 1544.7947 | 0.0061  | 0    | 52    | 0.0042   | 1    | U      | R.LVHVEEHPHTVTR.K               |

Table with columns: Index, Score, Mr (exp/alc), Delta Miss Score, Expect Rank, Unique, Peptide, and Protein Name. Contains a list of protein identifications with their respective scores and peptide sequences.

2. CH60 ECO24 Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11) emPAI: 2.84

60 kDa chaperonin OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=groL PE=3 SV=1

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

Table with columns: Query, Observed, Mr (exp/alc), Delta Miss Score, Expect Rank, Unique, Peptide. Lists query peptides and their matches to the protein sequence.

Proteins matching the same set of peptides:

CH60 ECO27 Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)

60 kDa chaperonin OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=groL PE=3 SV=1

CH60 ECO45 Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)

60 kDa chaperonin OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=grgL PE=3 SV=1  
**CH60 EC055** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain 55989 / EABC) GN=grgL PE=3 SV=1  
**CH60 EC057** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O157:H7 GN=grL PE=3 SV=2  
**CH60 EC05E** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=grL PE=3 SV=1  
**CH60 EC07I** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=grL PE=3 SV=1  
**CH60 EC08I** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O8I (strain ED1a) GN=grL PE=3 SV=1  
**CH60 EC08A** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O8 (strain IAI1) GN=grL PE=3 SV=1  
**CH60 EC08W** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain K12 / BW2952) GN=grL PE=3 SV=1  
**CH60 EC0DH** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain K12 / DH10B) GN=grL PE=3 SV=1  
**CH60 EC0HS** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O9:H4 (strain HS) GN=grL PE=3 SV=1  
**CH60 EC0LS** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=grL PE=3 SV=1  
**CH60 EC0L6** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O6 GN=grL PE=3 SV=2  
**CH60 EC0LC** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=grL PE=3 SV=1  
**CH60 EC0LI** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain K12) GN=grL PE=1 SV=2  
**CH60 EC0LU** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=grL PE=3 SV=1  
**CH60 EC0SE** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain SE11) GN=grL PE=3 SV=1  
**CH60 EC0SM** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=grL PE=3 SV=1  
**CH60 EC0UT** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Escherichia coli (strain UTI89 / UPEC) GN=grL PE=1 SV=1  
**CH60 SH1B3** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=grL PE=3 SV=1  
**CH60 SH1B5** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Shigella boydii serotype 4 (strain Sb227) GN=grL PE=3 SV=1  
**CH60 SH1DS** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=grL PE=3 SV=1  
**CH60 SH1F8** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Shigella flexneri serotype 5b (strain 8401) GN=grL PE=3 SV=1  
**CH60 SH1FL** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Shigella flexneri GN=grL PE=3 SV=2  
**CH60 SH1SS** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin OS=Shigella sonnei (strain Ss046) GN=grL PE=3 SV=1  
**CH601 EC0K1** Mass: 57464 Score: 2070 Matches: 59(45) Sequences: 11(11)  
60 kDa chaperonin 1 OS=Escherichia coli O1:K1 / APEC GN=grL1 PE=3 SV=1

3. **CH60 ENTIT** Mass: 56741 Score: 1801 Matches: 51(39) Sequences: 10(10) emPAI: 2.09

60 kDa chaperonin (Fragment) OS=Enterobacter intermedium GN=grL PE=3 SV=1

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

| Query | Observed  | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide   |
|-------|-----------|-----------|-----------|--------|------|-------|----------|------|--------|---|
| 287   | 784.4470  | 1566.8793 | 1566.8730 | 0.0064 | 0    | (70)  | 3.5e-005 | 1    |        | R.AAVEEGVAGGVALIR.V                             |
| 288   | 784.4470  | 1566.8795 | 1566.8730 | 0.0065 | 0    | 85    | 1.2e-006 | 1    |        | R.AAVEEGVAGGVALIR.V                             |
| 318   | 880.9573  | 1759.9001 | 1759.8952 | 0.0049 | 0    | (69)  | 7.1e-005 | 1    |        | K.AIAQVGTISANSDETGVK.L                          |
| 319   | 880.9587  | 1759.9028 | 1759.8952 | 0.0076 | 0    | 85    | 1.9e-006 | 1    |        | K.AIAQVGTISANSDETGVK.L                          |
| 342   | 670.9913  | 2009.9522 | 2009.9438 | 0.0084 | 1    | (28)  | 0.49     | 1    |        | R.EIELEDFKFNMGQVMK.E                            |
| 343   | 670.9920  | 2009.9543 | 2009.9438 | 0.0105 | 1    | 47    | 0.006    | 1    |        | R.EIELEDFKFNMGQVMK.E                            |
| 345   | 681.6552  | 2041.9436 | 2041.9336 | 0.0100 | 1    | (34)  | 0.093    | 1    |        | R.EIELEDFKFNMGQVMK.E + 2 Oxidation (M)          |
| 346   | 681.6552  | 2041.9439 | 2041.9336 | 0.0103 | 1    | (35)  | 0.072    | 1    |        | R.EIELEDFKFNMGQVMK.E + 2 Oxidation (M)          |
| 398   | 800.4345  | 2398.2818 | 2398.2704 | 0.0114 | 1    | (85)  | 8.5e-007 | 1    |        | R.VVINKDTTIDVGEAAIQGR.V                         |
| 399   | 800.4349  | 2398.2830 | 2398.2704 | 0.0126 | 1    | 105   | 1e-008   | 1    |        | R.VVINKDTTIDVGEAAIQGR.V                         |
| 418   | 1325.1766 | 2648.3387 | 2648.3288 | 0.0098 | 0    | (64)  | 0.00013  | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A                    |
| 419   | 883.7868  | 2648.3387 | 2648.3288 | 0.0098 | 0    | (76)  | 7.8e-006 | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A                    |
| 420   | 883.7870  | 2648.3393 | 2648.3288 | 0.0104 | 0    | (60)  | 0.0003   | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A                    |
| 421   | 1325.1769 | 2648.3393 | 2648.3288 | 0.0104 | 0    | (73)  | 1.5e-005 | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A                    |
| 422   | 889.1178  | 2664.3315 | 2664.3238 | 0.0078 | 0    | (34)  | 0.12     | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 423   | 1333.1731 | 2664.3315 | 2664.3238 | 0.0078 | 0    | (23)  | 1.5      | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 424   | 1333.1737 | 2664.3328 | 2664.3238 | 0.0090 | 0    | (45)  | 0.0098   | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 425   | 889.1185  | 2664.3336 | 2664.3238 | 0.0099 | 0    | (91)  | 2.4e-007 | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 426   | 1333.1741 | 2664.3336 | 2664.3238 | 0.0099 | 0    | (55)  | 0.00098  | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 427   | 889.1187  | 2664.3342 | 2664.3238 | 0.0104 | 0    | (35)  | 0.096    | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 428   | 889.1187  | 2664.3342 | 2664.3238 | 0.0105 | 0    | (81)  | 2.5e-006 | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 430   | 889.1191  | 2664.3354 | 2664.3238 | 0.0117 | 0    | (42)  | 0.02     | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 431   | 889.1192  | 2664.3359 | 2664.3238 | 0.0121 | 0    | (36)  | 0.084    | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 432   | 1333.1752 | 2664.3359 | 2664.3238 | 0.0121 | 0    | (77)  | 5.6e-006 | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 433   | 1333.1753 | 2664.3359 | 2664.3238 | 0.0122 | 0    | (39)  | 0.04     | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 434   | 889.1193  | 2664.3360 | 2664.3238 | 0.0122 | 0    | 109   | 3.6e-009 | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)    |
| 435   | 1341.1713 | 2680.3281 | 2680.3187 | 0.0094 | 0    | (26)  | 0.76     | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + 2 Oxidation (M)  |
| 436   | 894.4507  | 2680.3303 | 2680.3187 | 0.0117 | 0    | (61)  | 0.00025  | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + 2 Oxidation (M)  |
| 437   | 894.4508  | 2680.3307 | 2680.3187 | 0.0120 | 0    | (82)  | 2.2e-006 | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + 2 Oxidation (M)  |
| 438   | 1341.1730 | 2680.3315 | 2680.3187 | 0.0128 | 0    | (30)  | 0.3      | 1    |        | K.AMLQDIATLTGGTVISEIGMELEK.A + 2 Oxidation (M)  |
| 447   | 908.5087  | 2722.5042 | 2722.4939 | 0.0103 | 0    | (90)  | 1.3e-007 | 1    |        | K.AGKPLLIADVEGALATLVNTMR.G                      |
| 448   | 908.5089  | 2722.5047 | 2722.4939 | 0.0109 | 0    | 109   | 1.5e-009 | 1    |        | K.AGKPLLIADVEGALATLVNTMR.G                      |
| 449   | 908.5092  | 2722.5057 | 2722.4939 | 0.0118 | 0    | (61)  | 0.0001   | 1    |        | K.AGKPLLIADVEGALATLVNTMR.G                      |
| 450   | 908.5093  | 2722.5060 | 2722.4939 | 0.0121 | 0    | (93)  | 5.5e-008 | 1    |        | K.AGKPLLIADVEGALATLVNTMR.G                      |
| 453   | 913.8394  | 2738.4963 | 2738.4888 | 0.0075 | 0    | (67)  | 2.8e-005 | 1    |        | K.AGKPLLIADVEGALATLVNTMR.G + Oxidation (M)      |
| 454   | 685.6324  | 2738.5005 | 2738.4888 | 0.0117 | 0    | (72)  | 8.4e-006 | 1    |        | K.AGKPLLIADVEGALATLVNTMR.G + Oxidation (M)      |
| 479   | 931.8177  | 2792.4313 | 2792.4187 | 0.0126 | 1    | (105) | 8.8e-009 | 1    |        | R.KAMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)   |
| 480   | 931.8181  | 2792.4324 | 2792.4187 | 0.0137 | 1    | (84)  | 1.1e-006 | 1    |        | R.KAMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)   |
| 481   | 931.8181  | 2792.4326 | 2792.4187 | 0.0138 | 1    | (84)  | 1.1e-006 | 1    |        | R.KAMLQDIATLTGGTVISEIGMELEK.A + Oxidation (M)   |
| 482   | 937.1476  | 2808.4209 | 2808.4136 | 0.0073 | 1    | 111   | 2.4e-009 | 1    |        | R.KAMLQDIATLTGGTVISEIGMELEK.A + 2 Oxidation (M) |
| 483   | 937.1488  | 2808.4246 | 2808.4136 | 0.0109 | 1    | (96)  | 7.4e-008 | 1    |        | R.KAMLQDIATLTGGTVISEIGMELEK.A + 2 Oxidation (M) |
| 484   | 937.1491  | 2808.4254 | 2808.4136 | 0.0118 | 1    | (94)  | 1.2e-007 | 1    |        | R.KAMLQDIATLTGGTVISEIGMELEK.A + 2 Oxidation (M) |
| 501   | 956.7828  | 2867.3267 | 2867.3019 | 0.0248 | 0    | 88    | 2.1e-007 | 1    |        | K.EGVITVEDGEGLEDELVDVGMQFDR.G + Oxidation (M)   |
| 502   | 1434.6706 | 2867.3267 | 2867.3019 | 0.0248 | 0    | (12)  | 7.7      | 1    |        | K.EGVITVEDGEGLEDELVDVGMQFDR.G + Oxidation (M)   |
| 515   | 1037.8861 | 3110.6365 | 3110.6216 | 0.0149 | 0    | (71)  | 1.5e-005 | 1    |        | R.GYLSPFYFNKPETGAVELESFPILLADK.K                |
| 516   | 1037.8866 | 3110.6379 | 3110.6216 | 0.0163 | 0    | 81    | 1.6e-006 | 1    |        | R.GYLSPFYFNKPETGAVELESFPILLADK.K                |
| 517   | 1037.8868 | 3110.6385 | 3110.6216 | 0.0169 | 0    | (60)  | 0.00019  | 1    |        | R.GYLSPFYFNKPETGAVELESFPILLADK.K                |
| 530   | 810.6904  | 3238.7324 | 3238.7165 | 0.0159 | 1    | (41)  | 0.012    | 1    |        | R.GYLSPFYFNKPETGAVELESFPILLADK.K                |
| 531   | 1080.5847 | 3238.7324 | 3238.7165 | 0.0159 | 1    | (13)  | 6.3      | 1    |        | R.GYLSPFYFNKPETGAVELESFPILLADK.K                |
| 532   | 810.6910  | 3238.7350 | 3238.7165 | 0.0185 | 1    | (23)  | 0.65     | 1    |        | R.GYLSPFYFNKPETGAVELESFPILLADK.K                |
| 534   | 810.6915  | 3238.7368 | 3238.7165 | 0.0203 | 1    | 50    | 0.0015   | 1    |        | R.GYLSPFYFNKPETGAVELESFPILLADK.K                |





|     |          |           |           |         |   |      |         |   |                          |
|-----|----------|-----------|-----------|---------|---|------|---------|---|--------------------------|
| 162 | 545.7707 | 1089.5268 | 1089.5237 | 0.0031  | 0 | (54) | 0.0022  | 1 | K.VTMQNLNDR.L            |
| 168 | 555.2483 | 1108.4821 | 1108.4825 | -0.0004 | 0 | 47   | 0.0039  | 1 | K.DAEAWFNK.S             |
| 169 | 555.2509 | 1108.4872 | 1108.4825 | 0.0047  | 0 | (39) | 0.028   | 1 | K.DAEAWFNK.S             |
| 211 | 617.8466 | 1233.6786 | 1233.6717 | 0.0069  | 1 | 40   | 0.068   | 1 | R.LKYENEVALR.Q           |
| 212 | 617.8467 | 1233.6788 | 1233.6717 | 0.0071  | 1 | (25) | 1.9     | 1 | R.LKYENEVALR.Q           |
| 213 | 617.8470 | 1233.6794 | 1233.6717 | 0.0077  | 1 | (8)  | 98      | 1 | R.LKYENEVALR.Q           |
| 247 | 679.3649 | 1356.7151 | 1356.7110 | 0.0042  | 1 | 14   | 27      | 1 | R.QSVEADINGLR.V          |
| 249 | 691.3300 | 1380.6455 | 1380.6408 | 0.0047  | 0 | 58   | 0.00055 | 1 | R.ALEENVELEK.I           |
| 272 | 747.3735 | 1492.7324 | 1492.7270 | 0.0054  | 1 | (28) | 0.85    | 1 | U.R.SQYEQLAENRK.D        |
| 273 | 747.3736 | 1492.7327 | 1492.7270 | 0.0057  | 1 | 42   | 0.031   | 1 | U.R.SQYEQLAENRK.D        |
| 274 | 747.3742 | 1492.7339 | 1492.7270 | 0.0069  | 1 | (37) | 0.11    | 1 | U.R.SQYEQLAENRK.D        |
| 312 | 854.3928 | 1706.7711 | 1706.7649 | 0.0062  | 0 | (48) | 0.0031  | 1 | U.K.GSLGGGFSGGFSGGFSR.G  |
| 313 | 854.3929 | 1706.7712 | 1706.7649 | 0.0063  | 0 | 86   | 5e-007  | 1 | U.K.GSLGGGFSGGFSGGFSR.G  |
| 325 | 899.0123 | 1796.0101 | 1796.0043 | 0.0058  | 0 | 58   | 0.00042 | 1 | U.R.NVQALETELQSQALK.Q    |
| 374 | 738.0407 | 2211.1001 | 2211.0906 | 0.0095  | 1 | 30   | 0.35    | 1 | U.K.SKELTEIDNNIEQISSYK.S |

9. **K22E HUMAN** Mass: 65678 Score: 255 Matches: 10(6) Sequences: 7(4) emPAI: 0.29

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

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

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss Score | Expect Rank Unique | Peptide            |
|-------|----------|-----------|-----------|------------------|--------------------|--------------------|
| 104   | 416.2465 | 830.4784  | 830.4862  | -0.0078          | 0 27 2.1 1 U       | R.SLVGLGGTK.S      |
| 132   | 487.2707 | 972.5268  | 972.5240  | 0.0029           | 0 32 0.6 1 U       | K.IEISELNR.V       |
| 167   | 554.2769 | 1106.5392 | 1106.5356 | 0.0036           | 0 38 0.095 1 U     | K.AQYEEIAQR.S      |
| 219   | 627.8086 | 1253.6027 | 1253.6001 | 0.0027           | 0 45 0.014 1 U     | R.GFSSGSAVVSQVSR.R |
| 240   | 665.3693 | 1328.7241 | 1328.7187 | 0.0054           | 0 (46) 0.015 1 U   | R.NLDDLSIAAEVK.A   |
| 241   | 665.3699 | 1328.7252 | 1328.7187 | 0.0065           | 0 73 3.3e-005 1 U  | R.NLDDLSIAAEVK.A   |
| 268   | 730.9056 | 1459.7966 | 1459.7922 | 0.0044           | 0 86 1.7e-006 1 U  | K.VDLLNQETFLK.V    |
| 269   | 730.9060 | 1459.7974 | 1459.7922 | 0.0052           | 0 (63) 0.00033 1 U | K.VDLLNQETFLK.V    |
| 270   | 738.3928 | 1474.7710 | 1474.7780 | -0.0070          | 0 (26) 1.8 1 U     | R.FLEQQNQVLQTK.W   |
| 271   | 738.3986 | 1474.7826 | 1474.7780 | 0.0046           | 0 91 5e-007 1 U    | R.FLEQQNQVLQTK.W   |

10. **ALBU HUMAN** Mass: 71317 Score: 147 Matches: 6(5) Sequences: 3(2) emPAI: 0.15

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) | Delta Miss Score | Expect Rank Unique | Peptide             |
|-------|----------|-----------|-----------|------------------|--------------------|---------------------|
| 183   | 575.3129 | 1148.6112 | 1148.6077 | 0.0035           | 0 64 0.00031 1 U   | K.LVNEVTEFAK.T      |
| 184   | 575.3133 | 1148.6121 | 1148.6077 | 0.0043           | 0 (42) 0.05 1 U    | K.LVNEVTEFAK.T      |
| 265   | 722.3264 | 1442.6383 | 1442.6347 | 0.0036           | 0 28 0.29 1 U      | K.YICENQDSISSK.L    |
| 296   | 547.3193 | 1638.9362 | 1638.9305 | 0.0057           | 1 (48) 0.0045 1 U  | K.KVPQVSTPTLVEVSR.N |
| 297   | 547.3194 | 1638.9363 | 1638.9305 | 0.0059           | 1 54 0.001 1 U     | K.KVPQVSTPTLVEVSR.N |
| 298   | 547.3198 | 1638.9375 | 1638.9305 | 0.0070           | 1 (44) 0.011 1 U   | K.KVPQVSTPTLVEVSR.N |

Proteins matching the same set of peptides:

**ALBU PONAB** Mass: 71317 Score: 147 Matches: 6(5) Sequences: 3(2)

Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=1

11. **K2C6B HUMAN** Mass: 60315 Score: 140 Matches: 5(4) Sequences: 4(3) emPAI: 0.25

Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5

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

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss Score | Expect Rank Unique | Peptide           |
|-------|----------|-----------|-----------|------------------|--------------------|-------------------|
| 167   | 554.2769 | 1106.5392 | 1106.5356 | 0.0036           | 0 38 0.095 1 U     | K.AQYEEIAQR.S     |
| 192   | 590.3040 | 1178.5935 | 1178.5931 | 0.0004           | 0 54 0.0029 1 U    | K.YEELQITAGR.H    |
| 240   | 665.3693 | 1328.7241 | 1328.7187 | 0.0054           | 0 (46) 0.015 1 U   | R.NLDDLSIAAEVK.A  |
| 241   | 665.3699 | 1328.7252 | 1328.7187 | 0.0065           | 0 73 3.3e-005 1 U  | R.NLDDLSIAAEVK.A  |
| 259   | 704.3626 | 1406.7106 | 1406.7041 | 0.0065           | 0 75 1.9e-005 1 U  | K.ADTLTDIEINFLR.A |

12. **F13B HUMAN** Mass: 77742 Score: 113 Matches: 5(3) Sequences: 3(2) emPAI: 0.14

Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3

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

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss Score | Expect Rank Unique | Peptide                    |
|-------|----------|-----------|-----------|------------------|--------------------|----------------------------|
| 177   | 565.7718 | 1129.5291 | 1129.5226 | 0.0065           | 0 30 0.36 1 U      | R.CNEYEYLLR.G              |
| 353   | 695.0044 | 2081.9914 | 2081.9840 | 0.0074           | 0 (37) 0.061 1 U   | K.VACEEPPPIEINGAANLHRS.I   |
| 354   | 695.0047 | 2081.9943 | 2081.9840 | 0.0083           | 0 (51) 0.023 1 U   | K.VACEEPPPIEINGAANLHRS.I   |
| 355   | 695.0059 | 2081.9959 | 2081.9840 | 0.0119           | 0 55 0.00097 1 U   | K.VACEEPPPIEINGAANLHRS.I   |
| 441   | 899.7396 | 2696.1969 | 2696.1807 | 0.0162           | 1 38 0.01 1 U      | K.TYQKDEEVVQCLSDGHSQPTCR.K |

13. **K1C14 HUMAN** Mass: 51872 Score: 95 Matches: 7(4) Sequences: 3(2) emPAI: 0.14

Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4

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

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss Score | Expect Rank Unique | Peptide       |
|-------|----------|-----------|-----------|------------------|--------------------|---------------|
| 98    | 404.2046 | 806.3947  | 806.3923  | 0.0024           | 0 (38) 0.15 1 U    | R.LAADDFR.T   |
| 99    | 404.2048 | 806.3950  | 806.3923  | 0.0027           | 0 (47) 0.016 1 U   | R.LAADDFR.T   |
| 100   | 404.2050 | 806.3954  | 806.3923  | 0.0032           | 0 62 0.00056 1 U   | R.LAADDFR.T   |
| 138   | 515.3023 | 1028.5901 | 1028.5866 | 0.0035           | 0 42 0.06 1 U      | R.VLDELTLAR.A |
| 160   | 545.7700 | 1089.5254 | 1089.5237 | 0.0017           | 0 (34) 0.27 1 U    | K.VTMQNLNDR.L |
| 161   | 545.7705 | 1089.5265 | 1089.5237 | 0.0029           | 0 54 0.0022 1 U    | K.VTMQNLNDR.L |
| 162   | 545.7707 | 1089.5268 | 1089.5237 | 0.0031           | 0 (54) 0.0022 1 U  | K.VTMQNLNDR.L |

Proteins matching the same set of peptides:

**K1C14 MOUSE** Mass: 53176 Score: 95 Matches: 7(4) Sequences: 3(2)

Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2

**K1C14 RAT** Mass: 52936 Score: 95 Matches: 7(4) Sequences: 3(2)

Keratin, type I cytoskeletal 14 OS=Rattus norvegicus GN=Krt14 PE=2 SV=1

**K1C15 MOUSE** Mass: 49278 Score: 95 Matches: 7(4) Sequences: 3(2)

Keratin, type I cytoskeletal 15 OS=Mus musculus GN=Krt15 PE=1 SV=2

**K1C15 RAT** Mass: 49011 Score: 95 Matches: 7(4) Sequences: 3(2)

Keratin, type I cytoskeletal 15 OS=Rattus norvegicus GN=Krt15 PE=1 SV=1

**K1C16 HUMAN** Mass: 51578 Score: 95 Matches: 7(4) Sequences: 3(2)

Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4

14. **F13A HUMAN** Mass: 83728 Score: 72 Matches: 5(2) Sequences: 4(2) emPAI: 0.13

Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

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

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss Score | Expect Rank Unique | Peptide              |
|-------|----------|-----------|-----------|------------------|--------------------|----------------------|
| 234   | 640.8520 | 1279.6895 | 1279.6846 | 0.0050           | 0 58 0.00088 1 U   | R.LALETAIMYGAK.K     |
| 239   | 663.9182 | 1325.8219 | 1325.8170 | 0.0049           | 0 29 0.18 1 U      | K.STVLTIPRIILK.V     |
| 300   | 827.4443 | 1652.8740 | 1652.8661 | 0.0078           | 1 49 0.0056 1 U    | K.ETFDVLEPLSFKK.E    |
| 308   | 844.4697 | 1686.9249 | 1686.9192 | 0.0056           | 0 30 0.48 1 U      | K.GTYIPVPIVSELQSGK.W |
| 309   | 844.4699 | 1686.9252 | 1686.9192 | 0.0060           | 0 (25) 1.5 1 U     | K.GTYIPVPIVSELQSGK.W |

15. **CH602 BURXL** Mass: 56983 Score: 21 Matches: 6(0) Sequences: 1(0) emPAI: 0.06

60 kDa chaperonin 2 OS=Burkholderia xenovorans (strain LB400) GN=groL2 PE=3 SV=1

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

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



|                     |           |           |
|---------------------|-----------|-----------|
| <a href="#">53</a>  | 551.5046  | 550.4973  |
| <a href="#">54</a>  | 551.5046  | 550.4973  |
| <a href="#">55</a>  | 551.5047  | 550.4974  |
| <a href="#">56</a>  | 551.5047  | 550.4974  |
| <a href="#">57</a>  | 551.5048  | 550.4975  |
| <a href="#">58</a>  | 551.5051  | 550.4978  |
| <a href="#">59</a>  | 551.5051  | 550.4979  |
| <a href="#">60</a>  | 564.3607  | 563.3535  |
| <a href="#">61</a>  | 564.3610  | 563.3537  |
| <a href="#">62</a>  | 579.5360  | 578.5287  |
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| <a href="#">66</a>  | 591.3591  | 590.3518  |
| <a href="#">67</a>  | 591.5721  | 590.5649  |
| <a href="#">70</a>  | 608.3872  | 607.3799  |
| <a href="#">71</a>  | 608.3875  | 607.3802  |
| <a href="#">72</a>  | 614.5658  | 613.5586  |
| <a href="#">73</a>  | 615.4045  | 614.3972  |
| <a href="#">74</a>  | 615.4049  | 614.3976  |
| <a href="#">75</a>  | 615.4052  | 614.3979  |
| <a href="#">76</a>  | 615.4052  | 614.3979  |
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| <a href="#">81</a>  | 630.4436  | 629.4363  |
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| <a href="#">92</a>  | 718.4972  | 717.4899  |
| <a href="#">94</a>  | 752.5480  | 751.5408  |
| <a href="#">95</a>  | 752.5483  | 751.5410  |
| <a href="#">106</a> | 832.4908  | 831.4835  |
| <a href="#">120</a> | 444.1146  | 886.2147  |
| <a href="#">121</a> | 444.1148  | 886.2150  |
| <a href="#">122</a> | 447.1334  | 892.2522  |
| <a href="#">123</a> | 918.6715  | 917.6643  |
| <a href="#">124</a> | 461.3302  | 920.6458  |
| <a href="#">131</a> | 969.9088  | 968.9015  |
| <a href="#">140</a> | 1037.2643 | 1036.2570 |
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| <a href="#">146</a> | 1046.5932 | 1045.5859 |
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| <a href="#">148</a> | 578.7679  | 1155.5212 |
| <a href="#">149</a> | 582.8355  | 1163.6563 |
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| <a href="#">163</a> | 574.8157  | 1721.4252 |
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| <a href="#">166</a> | 647.4261  | 1939.2564 |
| <a href="#">167</a> | 415.3390  | 2071.6587 |
| <a href="#">168</a> | 728.6481  | 2182.9225 |
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| <a href="#">170</a> | 558.9748  | 2231.8699 |
| <a href="#">171</a> | 755.3486  | 2263.0239 |
| <a href="#">380</a> | 1142.0996 | 2282.1847 |
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| <a href="#">384</a> | 779.3736  | 2335.0991 |
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| <a href="#">386</a> | 610.7860  | 2439.1147 |
| <a href="#">387</a> | 818.0726  | 2451.1961 |
| <a href="#">388</a> | 503.3067  | 2511.4970 |
| <a href="#">389</a> | 632.3882  | 2525.5236 |
| <a href="#">390</a> | 858.9123  | 2573.7152 |
| <a href="#">391</a> | 647.4276  | 2585.6815 |
| <a href="#">392</a> | 652.4100  | 2605.6108 |
| <a href="#">429</a> | 1333.1750 | 2664.3354 |
| <a href="#">439</a> | 1343.1719 | 2684.3292 |
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| <a href="#">444</a> | 914.7524  | 2741.2353 |
| <a href="#">445</a> | 691.1200  | 2760.4511 |
| <a href="#">446</a> | 922.8448  | 2765.5125 |
| <a href="#">447</a> | 926.1470  | 2775.4191 |
| <a href="#">448</a> | 926.1476  | 2775.4210 |
| <a href="#">449</a> | 931.4791  | 2791.4155 |
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| <a href="#">451</a> | 698.8613  | 2791.4159 |
| <a href="#">452</a> | 931.4797  | 2791.4174 |
| <a href="#">453</a> | 949.4558  | 2845.3457 |
| <a href="#">454</a> | 712.3437  | 2845.3457 |
| <a href="#">497</a> | 408.7863  | 2854.4534 |

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| 499 | 1434.1728 | 2866.3311 |
| 504 | 412.1694  | 2878.1349 |
| 505 | 1442.1693 | 2882.3240 |
| 506 | 968.7578  | 2903.2517 |
| 507 | 968.7580  | 2903.2521 |
| 508 | 974.0881  | 2919.2425 |
| 509 | 974.0893  | 2919.2461 |
| 510 | 730.8188  | 2919.2461 |
| 511 | 974.0895  | 2919.2466 |
| 514 | 1037.2703 | 3108.7889 |
| 518 | 520.3340  | 3115.9602 |
| 519 | 1054.5086 | 3160.5039 |
| 522 | 1055.5244 | 3163.5513 |
| 523 | 791.8951  | 3163.5513 |
| 526 | 1079.8515 | 3236.5328 |
| 527 | 1079.8532 | 3236.5378 |
| 528 | 1079.8542 | 3236.5407 |
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| 533 | 1080.5862 | 3238.7368 |
| 535 | 652.4031  | 3256.9789 |
| 540 | 823.9199  | 3291.6503 |
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| 544 | 1103.9201 | 3308.7384 |
| 547 | 830.1166  | 3316.4373 |
| 550 | 673.3377  | 3361.6523 |
| 551 | 841.4209  | 3361.6543 |
| 552 | 842.1644  | 3364.6285 |
| 553 | 842.1646  | 3364.6294 |
| 554 | 484.9330  | 3387.4799 |
| 557 | 447.2910  | 3570.2699 |
| 558 | 1192.3861 | 3574.1366 |
| 560 | 904.1412  | 3612.5357 |
| 561 | 607.9010  | 3641.3625 |
| 562 | 523.8003  | 3659.5515 |
| 563 | 528.3601  | 3691.4700 |
| 564 | 934.8793  | 3735.4879 |
| 565 | 551.5029  | 3853.4692 |
| 567 | 500.3081  | 3994.4068 |
| 568 | 802.9248  | 4009.5876 |
| 571 | 4117.4670 | 4116.4597 |
| 573 | 608.3862  | 4251.6526 |
| 574 | 551.5055  | 4403.9862 |
| 575 | 630.4464  | 4406.0739 |
| 576 | 651.8589  | 4555.9613 |
| 577 | 652.4142  | 4559.8487 |
| 579 | 4628.6665 | 4627.6592 |
| 580 | 582.8301  | 4654.5824 |
| 581 | 594.3630  | 4746.8456 |
| 582 | 800.4289  | 4796.5296 |
| 583 | 4859.4724 | 4858.4651 |
| 585 | 4970.9711 | 4969.9638 |
| 587 | 5018.5784 | 5017.5711 |
| 588 | 5230.6058 | 5229.5985 |
| 589 | 5318.0365 | 5317.0292 |
| 591 | 5345.0781 | 5344.0708 |
| 592 | 5399.4136 | 5398.4063 |
| 593 | 1100.9730 | 5499.8288 |
| 594 | 5567.0896 | 5566.0823 |
| 595 | 697.8462  | 5574.7116 |
| 596 | 5693.8017 | 5692.7944 |
| 597 | 5724.3392 | 5723.3319 |
| 598 | 716.9174  | 5727.2812 |
| 599 | 718.4972  | 5739.9193 |
| 601 | 5966.2178 | 5965.2105 |
| 602 | 5993.2904 | 5992.2831 |
| 603 | 1011.0022 | 6059.9694 |
| 604 | 6439.5208 | 6438.5135 |
| 605 | 6464.1858 | 6463.1785 |
| 606 | 924.9322  | 6467.4747 |
| 607 | 6492.0414 | 6491.0341 |
| 608 | 942.5341  | 6590.6878 |
| 609 | 6734.6303 | 6733.6230 |
| 610 | 857.4237  | 6851.3311 |
| 611 | 6919.3963 | 6918.3890 |
| 612 | 6954.3064 | 6953.2991 |
| 613 | 7010.1415 | 7009.1342 |
| 614 | 883.8968  | 7063.1158 |
| 615 | 914.0821  | 7304.5987 |
| 617 | 7790.3373 | 7789.3300 |
| 618 | 7951.0228 | 7950.0155 |
| 619 | 1326.1777 | 7951.0228 |
| 620 | 8232.6010 | 8231.5937 |
| 621 | 8391.5766 | 8390.5693 |
| 622 | 9756.3243 | 9755.3170 |

## Search Parameters

Type of search :MS/MS Ion Search  
 Enzyme :Trypsin  
 Fixed modifications :[Carbamidomethyl \(C\)](#)  
 Variable modifications :[Oxidation \(M\)](#)  
 Mass values :Monoisotopic  
 Protein Mass :Unrestricted  
 Peptide Mass Tolerance : ± 0.05 Da  
 Fragment Mass Tolerance: ± 0.05 Da  
 Max Missed Cleavages :2  
 Instrument type :Default  
 Number of queries :622

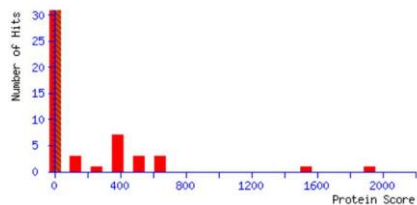
Mascot: <http://www.matrixscience.com/>

**MASCOT** SCIENCE Mascot Search Results

User : Julian  
 Email : julian.langer@mpibp-frankfurt.mpg.de  
 Search title : Submitted from 140318 842 ChKrettler 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
 MS data file : D:\Data\140318\140318\140314 842 ChReinhard 2\_Tray01-C7\_01\_17683.d\140314 842 ChReinhard 2\_Tray01-C7\_01\_17683.mgf  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Timestamp : 19 Mar 2014 at 09:48:48 GMT  
 Protein hits : **CFAH HUMAN** Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
**K2C1 HUMAN** Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
**K1C9 HUMAN** Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
**TRYP PIC** Trypsin OS=Sus scrofa PE=1 SV=1  
**K1C16 HUMAN** Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4  
**K2C1 RAT** Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1  
**K1C10 HUMAN** Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
**K1C14 HUMAN** Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4  
**CH60 CITKS** 60 kDa chaperonin OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=groL PE=3 SV=1  
**K2C6B HUMAN** Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5  
**K2C5 RAT** Keratin, type II cytoskeletal 5 OS=Rattus norvegicus GN=Krt5 PE=1 SV=1  
**K2C6C HUMAN** Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3  
**K2C5 HUMAN** Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3  
**K2C6A HUMAN** Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3  
**K22E HUMAN** Keratin, type II cytoskeletal 22 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
**K1C17 HUMAN** Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2  
**HORN HUMAN** Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2  
**ALBU HUMAN** Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
**K2C4 HUMAN** Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4  
**ALM RAT** Alpha-1-macroglobulin OS=Rattus norvegicus GN=Alm PE=1 SV=1  
**AZMG HUMAN** Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2

**Mascot Score Histogram**

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 38 indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



**Peptide Summary Report**

Format As  Peptide Summary  [Help](#)

Significance threshold  $p < 0.05$  Max. number of hits AUTO

Standard scoring  MudPIT scoring  Ions score or expect cut-off 0 Show sub-sets 0

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

Select All  Select None  Search Selected  Error tolerant  Archive Report

emPAI: 1.  
 1. **CFAH HUMAN** Mass: 143680 Score: 1917 Matches: 84(58) Sequences: 42(34) 89  
 Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

| Query                                   | Observed | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide                        |
|---|----------|-----------|-----------|--------|------|-------|----------|------|--------|--------------------------------|
| <input checked="" type="checkbox"/> 97  | 463.2317 | 924.4488  | 924.4454  | 0.0034 | 0    | 55    | 0.0015   | 1    | U      | R.NGFYPATR.G                   |
| <input checked="" type="checkbox"/> 98  | 463.2319 | 924.4493  | 924.4454  | 0.0040 | 0    | (52)  | 0.0033   | 1    | U      | R.NGFYPATR.G                   |
| <input checked="" type="checkbox"/> 99  | 463.2320 | 924.4494  | 924.4454  | 0.0040 | 0    | (43)  | 0.022    | 1    | U      | R.NGFYPATR.G                   |
| <input checked="" type="checkbox"/> 100 | 463.2324 | 924.4502  | 924.4454  | 0.0049 | 0    | (44)  | 0.02     | 1    | U      | R.NGFYPATR.G                   |
| <input checked="" type="checkbox"/> 109 | 487.7253 | 973.4360  | 973.4328  | 0.0033 | 0    | (30)  | 0.32     | 1    | U      | R.FVCNSGYK.I                   |
| <input checked="" type="checkbox"/> 110 | 487.7253 | 973.4360  | 973.4328  | 0.0033 | 0    | 60    | 0.00032  | 1    | U      | R.FVCNSGYK.I                   |
| <input checked="" type="checkbox"/> 111 | 487.7253 | 973.4360  | 973.4328  | 0.0033 | 0    | (45)  | 0.0084   | 1    | U      | R.FVCNSGYK.I                   |
| <input checked="" type="checkbox"/> 132 | 521.7529 | 1041.4912 | 1041.4879 | 0.0033 | 0    | (24)  | 1.3      | 1    | U      | R.NGWSEPPK.C                   |
| <input checked="" type="checkbox"/> 133 | 521.7535 | 1041.4924 | 1041.4879 | 0.0044 | 0    | 31    | 0.25     | 1    | U      | R.NGWSEPPK.C                   |
| <input checked="" type="checkbox"/> 134 | 521.7536 | 1041.4925 | 1041.4879 | 0.0046 | 0    | (27)  | 0.64     | 1    | U      | R.NGWSEPPK.C                   |
| <input checked="" type="checkbox"/> 143 | 532.3006 | 1062.5867 | 1062.5822 | 0.0045 | 0    | (57)  | 0.0013   | 1    | U      | K.IDVHLVDR.K                   |
| <input checked="" type="checkbox"/> 144 | 532.3009 | 1062.5873 | 1062.5822 | 0.0051 | 0    | 61    | 0.00062  | 1    | U      | K.IDVHLVDR.K                   |
| <input checked="" type="checkbox"/> 145 | 532.7920 | 1063.5694 | 1063.5662 | 0.0032 | 1    | (42)  | 0.042    | 1    | U      | K.IIYKENER.F                   |
| <input checked="" type="checkbox"/> 146 | 532.7921 | 1063.5696 | 1063.5662 | 0.0035 | 1    | 43    | 0.039    | 1    | U      | K.IIYKENER.F                   |
| <input checked="" type="checkbox"/> 165 | 552.7755 | 1103.5364 | 1103.5281 | 0.0084 | 0    | 50    | 0.0055   | 1    | U      | K.IVVSAMEPDR.E                 |
| <input checked="" type="checkbox"/> 166 | 552.7755 | 1103.5365 | 1103.5281 | 0.0085 | 0    | (43)  | 0.027    | 1    | U      | K.IVVSAMEPDR.E                 |
| <input checked="" type="checkbox"/> 171 | 556.2729 | 1110.5313 | 1110.5280 | 0.0032 | 0    | 18    | 6.3      | 1    | U      | K.WSHPPSCIK.T                  |
| <input checked="" type="checkbox"/> 176 | 560.7701 | 1119.5257 | 1119.5230 | 0.0027 | 0    | (17)  | 11       | 1    | U      | K.IVVSAMEPDR.E + Oxidation (M) |
| <input checked="" type="checkbox"/> 181 | 566.2641 | 1130.5135 | 1130.5105 | 0.0031 | 0    | (29)  | 0.36     | 1    | U      | K.EFDHNSNIR.Y                  |
| <input checked="" type="checkbox"/> 182 | 566.2641 | 1130.5136 | 1130.5105 | 0.0032 | 0    | (44)  | 0.011    | 1    | U      | K.EFDHNSNIR.Y                  |
| <input checked="" type="checkbox"/> 183 | 566.2647 | 1130.5148 | 1130.5105 | 0.0043 | 0    | 53    | 0.0014   | 1    | U      | K.EFDHNSNIR.Y                  |
| <input checked="" type="checkbox"/> 184 | 567.3294 | 1132.6443 | 1132.6393 | 0.0050 | 0    | 55    | 0.002    | 1    | U      | R.RPYFPVAVGK.Y                 |
| <input checked="" type="checkbox"/> 187 | 571.2852 | 1140.5558 | 1140.5532 | 0.0026 | 0    | 38    | 0.071    | 1    | U      | K.CLHPCVISR.E                  |
| <input checked="" type="checkbox"/> 188 | 574.8016 | 1147.5885 | 1147.5842 | 0.0044 | 0    | 45    | 0.028    | 1    | U      | R.SLGNVIMVCR.K                 |
| <input checked="" type="checkbox"/> 198 | 593.3027 | 1184.5908 | 1184.5860 | 0.0048 | 0    | (58)  | 0.00085  | 1    | U      | K.CLFPVAPENGI.I                |
| <input checked="" type="checkbox"/> 199 | 593.3028 | 1184.5911 | 1184.5860 | 0.0052 | 0    | 71    | 4.1e-005 | 1    | U      | K.CLFPVAPENGI.I                |
| <input checked="" type="checkbox"/> 200 | 593.8014 | 1185.5883 | 1185.5819 | 0.0064 | 1    | 59    | 0.00062  | 1    | U      | R.TKNDFTWFK.L                  |
| <input checked="" type="checkbox"/> 201 | 595.2712 | 1188.5278 | 1188.5234 | 0.0045 | 0    | (46)  | 0.0055   | 1    | U      | K.LSYTCGGFR.I                  |
| <input checked="" type="checkbox"/> 202 | 595.2716 | 1188.5287 | 1188.5234 | 0.0054 | 0    | 47    | 0.0047   | 1    | U      | K.LSYTCGGFR.I                  |
| <input checked="" type="checkbox"/> 215 | 405.1903 | 1212.5490 | 1212.5458 | 0.0032 | 0    | 47    | 0.0047   | 1    | U      | K.HGGLYHENMR.R                 |
| <input checked="" type="checkbox"/> 216 | 405.1903 | 1212.5492 | 1212.5458 | 0.0034 | 0    | (40)  | 0.025    | 1    | U      | K.HGGLYHENMR.R                 |
| <input checked="" type="checkbox"/> 224 | 621.7758 | 1241.5370 | 1241.5347 | 0.0024 | 0    | 73    | 8e-006   | 1    | U      | R.TGDEITYQCR.N                 |
| <input checked="" type="checkbox"/> 225 | 621.7767 | 1241.5387 | 1241.5347 | 0.0041 | 0    | (55)  | 0.00054  | 1    | U      | R.TGDEITYQCR.N                 |
| <input checked="" type="checkbox"/> 227 | 623.3083 | 1244.6021 | 1244.5972 | 0.0049 | 0    | 70    | 5.5e-005 | 1    | U      | K.CTSTGWIAPR.C                 |
| <input checked="" type="checkbox"/> 229 | 630.3285 | 1258.6424 | 1258.6380 | 0.0044 | 0    | 37    | 0.14     | 1    | U      | R.WQSIPLCVEK.I                 |
| <input checked="" type="checkbox"/> 230 | 630.3295 | 1258.6444 | 1258.6380 | 0.0064 | 0    | (27)  | 1.5      | 1    | U      | R.WQSIPLCVEK.I                 |
| <input checked="" type="checkbox"/> 234 | 631.7976 | 1261.5806 | 1261.5761 | 0.0045 | 0    | (37)  | 0.064    | 1    | U      | K.DGWSAQPTCIK.S                |
| <input checked="" type="checkbox"/> 235 | 631.7978 | 1261.5810 | 1261.5761 | 0.0049 | 0    | 60    | 0.0003   | 1    | U      | K.DGWSAQPTCIK.S                |
| <input checked="" type="checkbox"/> 243 | 641.8699 | 1281.7252 | 1281.7193 | 0.0058 | 1    | 50    | 0.0036   | 1    | U      | R.KGNVALNPLR.K                 |
| <input checked="" type="checkbox"/> 257 | 655.3072 | 1308.5999 | 1308.5955 | 0.0044 | 0    | (34)  | 0.13     | 1    | U      | K.SCDIPVFNMR.T                 |
| <input checked="" type="checkbox"/> 258 | 655.3079 | 1308.6013 | 1308.5955 | 0.0058 | 0    | (36)  | 0.087    | 1    | U      | K.SCDIPVFNMR.T                 |
| <input checked="" type="checkbox"/> 260 | 663.3035 | 1324.5924 | 1324.5904 | 0.0020 | 0    | (28)  | 0.39     | 1    | U      | K.SCDIPVFNMR.T + Oxidation (M) |
| <input checked="" type="checkbox"/> 261 | 663.3044 | 1324.5942 | 1324.5904 | 0.0038 | 0    | 37    | 0.045    | 1    | U      | K.SCDIPVFNMR.T + Oxidation (M) |
| <input checked="" type="checkbox"/> 272 | 671.3542 | 1340.6939 | 1340.6936 | 0.0003 | 0    | 53    | 0.0025   | 1    | U      | K.SPDVINGSPTISQK.I             |
| <input checked="" type="checkbox"/> 284 | 683.3478 | 1364.6811 | 1364.6758 | 0.0053 | 0    | (59)  | 0.00068  | 1    | U      | R.EIMENYIALR.W                 |
| <input checked="" type="checkbox"/> 285 | 683.3479 | 1364.6813 | 1364.6758 | 0.0055 | 0    | (63)  | 0.0003   | 1    | U      | R.EIMENYIALR.W                 |
| <input checked="" type="checkbox"/> 286 | 683.3485 | 1364.6825 | 1364.6758 | 0.0067 | 0    | (63)  | 0.00029  | 1    | U      | R.EIMENYIALR.W                 |
| <input checked="" type="checkbox"/> 288 | 691.3457 | 1380.6768 | 1380.6707 | 0.0061 | 0    | 68    | 7.5e-005 | 1    | U      | R.EIMENYIALR.W + Oxidation (M) |
| <input checked="" type="checkbox"/> 297 | 465.9347 | 1394.7823 | 1394.7769 | 0.0054 | 0    | (29)  | 0.5      | 1    | U      | K.SSNLILLEHLK.N                |
| <input checked="" type="checkbox"/> 298 | 698.3985 | 1394.7823 | 1394.7769 | 0.0055 | 0    | (45)  | 0.014    | 1    | U      | K.SSNLILLEHLK.N                |
| <input checked="" type="checkbox"/> 299 | 698.3999 | 1394.7852 | 1394.7769 | 0.0083 | 0    | 59    | 0.00044  | 1    | U      | K.SSNLILLEHLK.N                |

Table with 15 columns: Accession, Score, Mass, Score, Matches, Sequences, emPAI, and Peptide. Rows include protein sequences such as K.EGWHTVCINGR.W, K.CFEGFGIDGPAIAK.C, etc.

2. K2C1 HUMAN Mass: 66170 Score: 1587 Matches: 54(42) Sequences: 26(21) emPAI: 2.57

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

Table with 15 columns: Query, Observed, Mr (expt), Mr (calc), Delta, Miss, Score, Expect, Rank, Unique, Peptide. Contains detailed search results for K2C1 HUMAN, including various peptide sequences and their scores.

3. K1C9 HUMAN Mass: 62255 Score: 655 Matches: 35(24) Sequences: 22(17) emPAI: 1.95

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

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

Table with 15 columns: Query, Observed, Mr (expt), Mr (calc), Delta, Miss, Score, Expect, Rank, Unique, Peptide. Contains detailed search results for K1C9 HUMAN, including various peptide sequences and their scores.





|     |          |           |           |         |   |      |          |   |                        |
|-----|----------|-----------|-----------|---------|---|------|----------|---|------------------------|
| 147 | 532.8106 | 1063.6066 | 1063.6026 | 0.0041  | 1 | (51) | 0.0038   | 1 | R.LASYLDKVR.A          |
| 148 | 532.8110 | 1063.6074 | 1063.6026 | 0.0049  | 1 | 56   | 0.0012   | 1 | R.LASYLDKVR.A          |
| 159 | 545.7705 | 1089.5264 | 1089.5237 | 0.0027  | 0 | 56   | 0.0015   | 1 | K.VTMQNLNDR.L          |
| 169 | 555.2506 | 1108.4867 | 1108.4825 | 0.0042  | 0 | (41) | 0.016    | 1 | K.DAEAWFNEK.S          |
| 170 | 555.2512 | 1108.4877 | 1108.4825 | 0.0052  | 0 | 64   | 9.8e-005 | 1 | K.DAEAWFNEK.S          |
| 236 | 631.8045 | 1261.5944 | 1261.5899 | 0.0046  | 0 | 60   | 0.00044  | 1 | U R.SLLEGGSSGGGGGR.G   |
| 277 | 679.3650 | 1356.7155 | 1356.7110 | 0.0046  | 1 | (47) | 0.014    | 1 | R.QSVEADINLRR.V        |
| 281 | 679.3655 | 1356.7164 | 1356.7110 | 0.0055  | 1 | 67   | 0.00014  | 1 | R.QSVEADINLRR.V        |
| 282 | 453.2461 | 1356.7164 | 1356.7110 | 0.0055  | 1 | (23) | 3.1      | 1 | R.QSVEADINLRR.V        |
| 291 | 695.8428 | 1389.6711 | 1389.6736 | -0.0024 | 0 | 63   | 0.00023  | 1 | U K.QSLEASLAETGR.Y     |
| 320 | 747.3738 | 1492.7330 | 1492.7270 | 0.0061  | 1 | (56) | 0.0013   | 1 | U R.SQYQLAEQNRK.D      |
| 321 | 498.5852 | 1492.7337 | 1492.7270 | 0.0067  | 1 | (46) | 0.014    | 1 | U R.SQYQLAEQNRK.D      |
| 322 | 747.3741 | 1492.7337 | 1492.7270 | 0.0067  | 1 | 57   | 0.001    | 1 | U R.SQYQLAEQNRK.D      |
| 344 | 854.3934 | 1706.7723 | 1706.7649 | 0.0074  | 0 | 128  | 3.1e-011 | 1 | U K.GSLGGGSSGGSSGSSR.G |
| 357 | 899.0140 | 1796.0135 | 1796.0043 | 0.0092  | 0 | 90   | 2.7e-007 | 1 | U R.NVQALEIELQSLALK.Q  |
| 380 | 998.9932 | 1995.9719 | 1995.9636 | 0.0083  | 0 | (28) | 0.58     | 1 | U K.ELTTEIDNNEIQSSYK.S |
| 381 | 998.9932 | 1995.9719 | 1995.9636 | 0.0083  | 0 | 42   | 0.024    | 1 | U K.ELTTEIDNNEIQSSYK.S |

8. **KIC14 HUMAN** Mass: 51872 Score: 492 Matches: 26(15) Sequences: 16(10) emPAI: 1.82

Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

| Query | Observed  | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide                   |
|-------|-----------|-----------|-----------|--------|------|-------|----------|------|--------|---------------------------|
| 71    | 404.2052  | 806.3958  | 806.3923  | 0.0036 | 0    | 56    | 0.0021   | 1    |        | R.LAADDFR.T               |
| 72    | 404.2052  | 806.3959  | 806.3923  | 0.0036 | 0    | (51)  | 0.0076   | 1    |        | R.LAADDFR.T               |
| 73    | 809.4437  | 808.4364  | 808.4330  | 0.0033 | 0    | (32)  | 0.46     | 1    |        | R.LASYLDK.V               |
| 74    | 405.2255  | 808.4364  | 808.4330  | 0.0033 | 0    | 41    | 0.053    | 1    |        | R.LASYLDK.V               |
| 112   | 495.2739  | 988.5332  | 988.5301  | 0.0030 | 1    | (13)  | 48       | 7    |        | K.SEISELRR.T              |
| 113   | 495.2739  | 988.5332  | 988.5301  | 0.0030 | 1    | 22    | 6.4      | 5    |        | K.SEISELRR.T              |
| 114   | 495.2740  | 988.5334  | 988.5301  | 0.0033 | 1    | (11)  | 81       | 9    |        | K.SEISELRR.T              |
| 124   | 515.3031  | 1028.5916 | 1028.5866 | 0.0050 | 0    | (43)  | 0.046    | 1    |        | R.VLDELTLAR.A             |
| 125   | 515.3033  | 1028.5921 | 1028.5866 | 0.0055 | 0    | 43    | 0.046    | 1    |        | R.VLDELTLAR.A             |
| 130   | 518.7721  | 1035.5295 | 1035.5250 | 0.0046 | 1    | 35    | 0.24     | 1    |        | K.IRDYQQR.Q               |
| 147   | 532.8106  | 1063.6066 | 1063.6026 | 0.0041 | 1    | (51)  | 0.0038   | 1    |        | R.LASYLDKVR.A             |
| 148   | 532.8110  | 1063.6074 | 1063.6026 | 0.0049 | 1    | 56    | 0.0012   | 1    |        | R.LASYLDKVR.A             |
| 159   | 545.7705  | 1089.5264 | 1089.5237 | 0.0027 | 0    | 56    | 0.0015   | 1    |        | K.VTMQNLNDR.L             |
| 226   | 621.7820  | 1241.5495 | 1241.5458 | 0.0037 | 0    | 23    | 1.1      | 1    |        | K.NHEEEMNALR.G            |
| 240   | 633.8407  | 1265.6669 | 1265.6615 | 0.0053 | 1    | 27    | 1.3      | 1    |        | R.TKYETELNLR.M            |
| 247   | 651.3356  | 1300.6567 | 1300.6510 | 0.0057 | 0    | 119   | 8.2e-010 | 1    |        | R.ALEEANADLEVK.I          |
| 248   | 651.3360  | 1300.6575 | 1300.6510 | 0.0065 | 0    | (118) | 8.5e-010 | 1    |        | R.ALEEANADLEVK.I          |
| 283   | 681.3514  | 1360.6882 | 1360.6834 | 0.0048 | 0    | 70    | 7.1e-005 | 1    |        | R.EVATNSELVQSGK.S         |
| 304   | 713.3553  | 1424.6961 | 1424.6896 | 0.0066 | 0    | 99    | 6.8e-008 | 1    |        | U R.APSTYGGSLVSSSR.F      |
| 306   | 719.8567  | 1437.6988 | 1437.6922 | 0.0066 | 1    | 58    | 0.00074  | 1    |        | R.ILNEMRDQYEK.M           |
| 307   | 480.2402  | 1437.6988 | 1437.6922 | 0.0066 | 1    | (39)  | 0.065    | 1    |        | R.ILNEMRDQYEK.M           |
| 308   | 719.8571  | 1437.6996 | 1437.6922 | 0.0074 | 1    | (56)  | 0.0014   | 1    |        | R.ILNEMRDQYEK.M           |
| 309   | 480.2405  | 1437.6996 | 1437.6922 | 0.0074 | 1    | (9)   | 69       | 1    |        | R.ILNEMRDQYEK.M           |
| 396   | 1043.5028 | 2084.9909 | 2084.9797 | 0.0112 | 0    | 70    | 2.6e-005 | 1    |        | R.GQVGDVNVEMDAPGVDLR.I    |
| 440   | 770.3644  | 2308.0713 | 2308.0567 | 0.0146 | 0    | 28    | 0.31     | 1    |        | U R.LLEGDAHLSSQSSGSSR.D   |
| 442   | 778.0790  | 2331.2151 | 2331.2030 | 0.0121 | 2    | 31    | 0.28     | 1    |        | R.EVATNSELVQSGKSEISELRR.T |

9. **CH60 CITR8** Mass: 57543 Score: 418 Matches: 16(15) Sequences: 5(5) emPAI: 0.42

kDa chaperonin OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=groL PE=3 SV=1  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide  |
|-------|----------|-----------|-----------|---------|------|-------|----------|------|--------|--|
| 476   | 889.1182 | 2664.3327 | 2664.3238 | 0.0089  | 0    | (42)  | 0.017    | 1    | U      | K.AMLQDIATLTGGTVISEEIGMELEK.S + Oxidation (M)  |
| 477   | 889.1188 | 2664.3346 | 2664.3238 | 0.0109  | 0    | 53    | 0.0015   | 1    | U      | K.AMLQDIATLTGGTVISEEIGMELEK.S + Oxidation (M)  |
| 478   | 889.1189 | 2664.3350 | 2664.3238 | 0.0112  | 0    | (44)  | 0.014    | 1    | U      | K.AMLQDIATLTGGTVISEEIGMELEK.S + Oxidation (M)  |
| 480   | 908.5092 | 2722.5057 | 2722.4939 | 0.0118  | 0    | (63)  | 5.5e-005 | 1    |        | K.AGKPLLIIAEDVEGEALATLVVNTMR.G                 |
| 481   | 908.5117 | 2722.5134 | 2722.4939 | 0.0195  | 0    | (39)  | 0.012    | 1    |        | K.AGKPLLIIAEDVEGEALATLVVNTMR.G                 |
| 483   | 913.8386 | 2738.4941 | 2738.4888 | 0.0053  | 0    | (75)  | 5.3e-006 | 1    |        | K.AGKPLLIIAEDVEGEALATLVVNTMR.G + Oxidation (M) |
| 484   | 913.8389 | 2738.4948 | 2738.4888 | 0.0060  | 0    | 81    | 1.2e-006 | 1    |        | K.AGKPLLIIAEDVEGEALATLVVNTMR.G + Oxidation (M) |
| 485   | 913.8390 | 2738.4953 | 2738.4888 | 0.0065  | 0    | (55)  | 0.00047  | 1    |        | K.AGKPLLIIAEDVEGEALATLVVNTMR.G + Oxidation (M) |
| 486   | 913.8400 | 2738.4982 | 2738.4888 | 0.0094  | 0    | (61)  | 0.00013  | 1    |        | K.AGKPLLIIAEDVEGEALATLVVNTMR.G + Oxidation (M) |
| 487   | 913.8411 | 2738.5015 | 2738.4888 | 0.0127  | 0    | (76)  | 3.9e-006 | 1    |        | K.AGKPLLIIAEDVEGEALATLVVNTMR.G + Oxidation (M) |
| 492   | 931.8190 | 2792.4352 | 2792.4187 | 0.0165  | 1    | (49)  | 0.0035   | 1    | U      | R.KAMLQDIATLTGGTVISEEIGMELEK.S + Oxidation (M) |
| 493   | 931.8222 | 2792.4448 | 2792.4187 | 0.0261  | 1    | 75    | 8.9e-006 | 1    | U      | R.KAMLQDIATLTGGTVISEEIGMELEK.S + Oxidation (M) |
| 500   | 956.4513 | 2866.3321 | 2866.3179 | 0.0142  | 0    | 78    | 2.6e-006 | 1    | U      | K.EGVITVEDGTGLQDELVVEGMDQFDR.G + Oxidation (M) |
| 501   | 956.4526 | 2866.3361 | 2866.3179 | 0.0182  | 0    | (63)  | 7.3e-005 | 1    | U      | K.EGVITVEDGTGLQDELVVEGMDQFDR.G + Oxidation (M) |
| 524   | 810.6849 | 3238.7107 | 3238.7165 | -0.0058 | 1    | 39    | 0.02     | 1    | U      | R.GYLSYPYFINKPETGAVELESPTLLADKK.I              |
| 525   | 810.6931 | 3238.7432 | 3238.7165 | 0.0267  | 1    | (31)  | 0.095    | 1    | U      | R.GYLSYPYFINKPETGAVELESPTLLADKK.I              |

Proteins matching the same set of peptides:

- [CH60 ECO24](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=groL PE=3 SV=1
- [CH60 ECO27](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=groL PE=3 SV=1
- [CH60 ECO45](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=groL PE=3 SV=1
- [CH60 ECO55](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli (strain 55989 / EAEC) GN=groL PE=3 SV=1
- [CH60 ECO57](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O157:H7 GN=groL PE=3 SV=2
- [CH60 ECO5E](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=groL PE=3 SV=1
- [CH60 ECO7I](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=groL PE=3 SV=1
- [CH60 ECO81](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O81 (strain ED1a) GN=groL PE=3 SV=1
- [CH60 ECO8A](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O8 (strain IAI1) GN=groL PE=3 SV=1
- [CH60 ECOBW](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli (strain K12 / BW2952) GN=groL PE=3 SV=1
- [CH60 ECODH](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli (strain K12 / DH10B) GN=groL PE=3 SV=1
- [CH60 ECOHS](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O9:H4 (strain HS) GN=groL PE=3 SV=1
- [CH60 ECOL5](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=groL PE=3 SV=1
- [CH60 ECOL6](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli O6 GN=groL PE=3 SV=2
- [CH60 ECOLC](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=groL PE=3 SV=1
- [CH60 ECOLI](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
60 kDa chaperonin OS=Escherichia coli (strain K12) GN=groL PE=1 SV=2

[CH60\\_ECOLU](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=groL PE=3 SV=1

[CH60\\_ECOSE](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Escherichia coli (strain SE11) GN=groL PE=3 SV=1

[CH60\\_ECOSM](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=groL PE=3 SV=1

[CH60\\_ECOUT](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Escherichia coli (strain UTI89 / UPEC) GN=groL PE=1 SV=1

[CH60\\_ESCF3](#) Mass: 57522 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=groL PE=3 SV=1

[CH60\\_KLEPL](#) Mass: 56791 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin (Fragment) OS=Klebsiella planticola GN=groL PE=3 SV=1

[CH60\\_SALA4](#) Mass: 57176 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella agona (strain SL483) GN=groL PE=3 SV=1

[CH60\\_SALAR](#) Mass: 57434 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=groL PE=3 SV=1

[CH60\\_SALCH](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella choleraesuis GN=groL PE=3 SV=1

[CH60\\_SALDC](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella dublin (strain CT\_02021853) GN=groL PE=3 SV=1

[CH60\\_SALPE](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella enteritidis PT4 (strain P125109) GN=groL PE=3 SV=1

[CH60\\_SALG2](#) Mass: 57349 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=groL PE=3 SV=1

[CH60\\_SALHS](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella heidelberg (strain SL476) GN=groL PE=3 SV=1

[CH60\\_SALPA](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella paratyphi A GN=groL PE=3 SV=1

[CH60\\_SALPB](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella paratyphi B (strain ATCC BAA-1250 / SPB7) GN=groL PE=3 SV=1

[CH60\\_SALPC](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella paratyphi C (strain RKS4594) GN=groL PE=3 SV=1

[CH60\\_SALPK](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella paratyphi A (strain AKU\_12601) GN=groL PE=3 SV=1

[CH60\\_SALSV](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella schwarzengrund (strain CVM19633) GN=groL PE=3 SV=1

[CH60\\_SALTI](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella typhi GN=groL PE=3 SV=2

[CH60\\_SALTY](#) Mass: 57421 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Salmonella typhimurium GN=groL PE=3 SV=2

[CH60\\_SHIB3](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=groL PE=3 SV=1

[CH60\\_SHIB5](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Shigella boydii serotype 4 (strain Sb227) GN=groL PE=3 SV=1

[CH60\\_SHIDS](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=groL PE=3 SV=1

[CH60\\_SHIF8](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Shigella flexneri serotype 5b (strain 8401) GN=groL PE=3 SV=1

[CH60\\_SHIFL](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Shigella flexneri GN=groL PE=3 SV=2

[CH60\\_SHISS](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Shigella sonnei (strain Ss046) GN=groL PE=3 SV=1

[CH60\\_STEMA](#) Mass: 57766 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin OS=Stenotrophomonas maltophilia GN=groL PE=3 SV=1

[CH601\\_ECOK1](#) Mass: 57464 Score: 418 Matches: 16(15) Sequences: 5(5)  
 60 kDa chaperonin 1 OS=Escherichia coli O1:K1 / APEC GN=groL1 PE=3 SV=1

10. [K2C6B\\_HUMAN](#) Mass: 60315 Score: 406 Matches: 21(17) Sequences: 12(10) emPAI: 0.75  
 Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5  
 Check to include this hit in error tolerant search or archive report

| Query   | Observed | Mr(expt)  | Mr(calc)  | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide             |
|---|----------|-----------|-----------|---------|------|-------|----------|------|--------|---------------------|
| <a href="#">76</a>                                      | 827.4315 | 826.4242  | 826.4225  | 0.0017  | 0    | 27    | 0.97     | 1    | 1      | K.FASFDK.V          |
| <a href="#">77</a>                                      | 414.2201 | 826.4256  | 826.4225  | 0.0031  | 0    | (10)  | 50       | 1    | 1      | K.FASFDK.V          |
| <input checked="" type="checkbox"/> <a href="#">105</a> | 473.2607 | 944.5069  | 944.5039  | 0.0030  | 1    | (36)  | 0.26     | 1    | 1      | R.GRLDSELR.N        |
| <input checked="" type="checkbox"/> <a href="#">106</a> | 473.2612 | 944.5078  | 944.5039  | 0.0038  | 1    | 42    | 0.072    | 1    | 1      | R.GRLDSELR.N        |
| <a href="#">157</a>                                     | 541.8055 | 1081.5965 | 1081.5920 | 0.0044  | 1    | (51)  | 0.0039   | 1    | 1      | K.FASFDKVR.F        |
| <a href="#">158</a>                                     | 541.8060 | 1081.5973 | 1081.5920 | 0.0053  | 1    | 61    | 0.00043  | 1    | 1      | K.FASFDKVR.F        |
| <input checked="" type="checkbox"/> <a href="#">167</a> | 554.2748 | 1106.5350 | 1106.5356 | -0.0006 | 0    | (43)  | 0.032    | 1    | 1      | K.AQYEEIAQR.S       |
| <input checked="" type="checkbox"/> <a href="#">168</a> | 554.2763 | 1106.5381 | 1106.5356 | 0.0025  | 0    | 55    | 0.0021   | 1    | 1      | K.AQYEEIAQR.S       |
| <a href="#">196</a>                                     | 590.3059 | 1178.5972 | 1178.5931 | 0.0041  | 0    | 63    | 0.00031  | 1    | 1      | K.YEELQITAGR.H      |
| <input checked="" type="checkbox"/> <a href="#">209</a> | 602.3239 | 1202.6333 | 1202.6295 | 0.0038  | 0    | (49)  | 0.011    | 1    | 1      | K.WTLLEQGTK.T       |
| <input checked="" type="checkbox"/> <a href="#">210</a> | 602.3245 | 1202.6344 | 1202.6295 | 0.0048  | 0    | 49    | 0.011    | 1    | 1      | K.WTLLEQGTK.T       |
| <input checked="" type="checkbox"/> <a href="#">214</a> | 606.7828 | 1211.5511 | 1211.5458 | 0.0052  | 0    | 49    | 0.0034   | 1    | 1      | R.AEASWYQTK.Y       |
| <a href="#">254</a>                                     | 436.8911 | 1307.6515 | 1307.6469 | 0.0045  | 2    | 63    | 0.00031  | 1    | 1      | K.NKYEDENKR.T       |
| <a href="#">255</a>                                     | 436.8913 | 1307.6522 | 1307.6469 | 0.0053  | 2    | (56)  | 0.0014   | 1    | 1      | K.NKYEDENKR.T       |
| <a href="#">256</a>                                     | 436.8917 | 1307.6532 | 1307.6469 | 0.0063  | 2    | (60)  | 0.0006   | 1    | 1      | K.NKYEDENKR.T       |
| <input checked="" type="checkbox"/> <a href="#">262</a> | 665.3687 | 1328.7228 | 1328.7187 | 0.0041  | 0    | 75    | 2.2e-005 | 1    | 1      | R.NLDDLIIAEVK.A     |
| <input checked="" type="checkbox"/> <a href="#">273</a> | 675.8695 | 1349.7244 | 1349.7191 | 0.0054  | 1    | 46    | 0.017    | 1    | 1      | R.TAAENEFVTLK.D     |
| <input checked="" type="checkbox"/> <a href="#">302</a> | 704.3618 | 1406.7090 | 1406.7041 | 0.0048  | 0    | 59    | 0.00082  | 1    | 1      | K.ADTLTDEINFLR.A    |
| <input checked="" type="checkbox"/> <a href="#">303</a> | 704.3620 | 1406.7094 | 1406.7041 | 0.0053  | 0    | (51)  | 0.005    | 1    | 1      | K.ADTLTDEINFLR.A    |
| <input checked="" type="checkbox"/> <a href="#">347</a> | 587.3274 | 1758.9604 | 1758.9516 | 0.0088  | 1    | 57    | 0.00092  | 1    | 1      | K.VLDTKWTLLQEQGTK.T |
| <input checked="" type="checkbox"/> <a href="#">348</a> | 587.3281 | 1758.9625 | 1758.9516 | 0.0109  | 1    | (55)  | 0.0014   | 1    | 1      | K.VLDTKWTLLQEQGTK.T |

11. [K2C5\\_RAT](#) Mass: 61959 Score: 406 Matches: 21(14) Sequences: 11(7) emPAI: 0.46  
 Keratin, type II cytoskeletal 5 OS=Rattus norvegicus GN=Krt5 PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

| Query   | Observed | Mr(expt)  | Mr(calc)  | Delta  | Miss | Score | Expect  | Rank | Unique | Peptide       |
|---|----------|-----------|-----------|--------|------|-------|---------|------|--------|---------------|
| <a href="#">76</a>                                      | 827.4315 | 826.4242  | 826.4225  | 0.0017 | 0    | 27    | 0.97    | 1    | 1      | K.FASFDK.V    |
| <a href="#">77</a>                                      | 414.2201 | 826.4256  | 826.4225  | 0.0031 | 0    | (10)  | 50      | 1    | 1      | K.FASFDK.V    |
| <a href="#">105</a>                                     | 473.2607 | 944.5069  | 944.5039  | 0.0030 | 1    | (36)  | 0.26    | 1    | 1      | R.GRLDSELR.N  |
| <a href="#">106</a>                                     | 473.2612 | 944.5078  | 944.5039  | 0.0038 | 1    | 42    | 0.072   | 1    | 1      | R.GRLDSELR.N  |
| <a href="#">154</a>                                     | 537.3022 | 1072.5899 | 1072.5876 | 0.0022 | 1    | 35    | 0.31    | 1    | 1      | R.LRSEIDNVK.K |
| <a href="#">155</a>                                     | 537.3026 | 1072.5907 | 1072.5876 | 0.0031 | 1    | (27)  | 2       | 1    | 1      | R.LRSEIDNVK.K |
| <a href="#">157</a>                                     | 541.8055 | 1081.5965 | 1081.5920 | 0.0044 | 1    | (51)  | 0.0039  | 1    | 1      | K.FASFDKVR.F  |
| <a href="#">158</a>                                     | 541.8060 | 1081.5973 | 1081.5920 | 0.0053 | 1    | 61    | 0.00043 | 1    | 1      | K.FASFDKVR.F  |
| <input checked="" type="checkbox"/> <a href="#">206</a> | 597.7933 | 1193.5720 | 1193.5676 | 0.0043 | 0    | (39)  | 0.06    | 1    | 1      | K.YEELQTAGR.H |
| <input checked="" type="checkbox"/> <a href="#">207</a> | 597.7937 | 1193.5728 | 1193.5676 | 0.0052 | 0    | 54    | 0.0022  | 1    | 1      | K.YEELQTAGR.H |
| <a href="#">208</a>                                     | 401.2361 | 1200.6866 | 1200.6826 | 0.0040 | 2    | 21    | 5.2     | 1    | 1      | R.LRSEIDNVK.K |
| <a href="#">209</a>                                     | 602.3239 | 1202.6333 | 1202.6295 | 0.0038 | 0    | (49)  | 0.011   | 1    | 1      | K.WTLLEQGTK.T |

|   |                 |                  |                  |               |          |           |                |          |                                 |
|---|-----------------|------------------|------------------|---------------|----------|-----------|----------------|----------|---------------------------------|
| <a href="#">210</a>                                     | 602.3245        | 1202.6344        | 1202.6295        | 0.0048        | 0        | 49        | 0.011          | 1        | K.WTLLQEQTG.T                   |
| <a href="#">249</a>                                     | 651.8633        | 1301.7120        | 1301.7078        | 0.0042        | 0        | (77)      | 1.2e-005       | 1        | R.SLDLDSIIAEVK.A                |
| <a href="#">250</a>                                     | 651.8635        | 1301.7125        | 1301.7078        | 0.0047        | 0        | 97        | 1.3e-007       | 1        | R.SLDLDSIIAEVK.A                |
| <a href="#">254</a>                                     | 436.8911        | 1307.6515        | 1307.6469        | 0.0045        | 2        | 63        | 0.00031        | 1        | K.NKYEDEINKR.T                  |
| <a href="#">255</a>                                     | 436.8913        | 1307.6522        | 1307.6469        | 0.0053        | 2        | (56)      | 0.0014         | 1        | K.NKYEDEINKR.T                  |
| <a href="#">256</a>                                     | 436.8917        | 1307.6532        | 1307.6469        | 0.0063        | 2        | (60)      | 0.0006         | 1        | K.NKYEDEINKR.T                  |
| <a href="#">347</a>                                     | 587.3274        | 1758.9604        | 1758.9516        | 0.0088        | 1        | 57        | 0.00092        | 1        | K.VLDTKWTLLQEQTG.T              |
| <a href="#">348</a>                                     | 587.3281        | 1758.9625        | 1758.9516        | 0.0109        | 1        | (55)      | 0.0014         | 1        | K.VLDTKWTLLQEQTG.T              |
| <input checked="" type="checkbox"/> <a href="#">454</a> | <b>806.7160</b> | <b>2417.1261</b> | <b>2417.1135</b> | <b>0.0126</b> | <b>1</b> | <b>58</b> | <b>0.00031</b> | <b>1</b> | <b>R.TEAESWYQTKYEELQQTAGR.H</b> |

12. [K2C6C HUMAN](#) Mass: 60273 Score: 395 Matches: 21(16) Sequences: 12(9) emPAI: 0.75

Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3

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

| Query   | Observed        | Mr (expt)        | Mr (calc)        | Delta         | Miss     | Score     | Expect       | Rank     | Unique   | Peptide               |
|---|-----------------|------------------|------------------|---------------|----------|-----------|--------------|----------|----------|-----------------------|
| <a href="#">76</a>                                      | 827.4315        | 826.4242         | 826.4225         | 0.0017        | 0        | 27        | 0.97         | 1        | 1        | K.FASPIDK.V           |
| <a href="#">77</a>                                      | 414.2201        | 826.4256         | 826.4225         | 0.0031        | 0        | (10)      | 50           | 1        | 1        | K.FASPIDK.V           |
| <a href="#">105</a>                                     | 473.2607        | 944.5069         | 944.5039         | 0.0030        | 1        | (36)      | 0.26         | 1        | 1        | R.GRLDSELR.N          |
| <a href="#">106</a>                                     | 473.2612        | 944.5078         | 944.5039         | 0.0038        | 1        | 42        | 0.072        | 1        | 1        | R.GRLDSELR.N          |
| <a href="#">157</a>                                     | 541.8055        | 1081.5965        | 1081.5920        | 0.0044        | 1        | (51)      | 0.0039       | 1        | 1        | K.FASPIDKVR.F         |
| <a href="#">158</a>                                     | 541.8060        | 1081.5973        | 1081.5920        | 0.0053        | 1        | 61        | 0.00043      | 1        | 1        | K.FASPIDKVR.F         |
| <a href="#">167</a>                                     | 554.2748        | 1106.5350        | 1106.5356        | -0.0006       | 0        | (43)      | 0.032        | 1        | 1        | K.AQYEEIAQR.S         |
| <a href="#">168</a>                                     | 554.2763        | 1106.5381        | 1106.5356        | 0.0025        | 0        | 55        | 0.0021       | 1        | 1        | K.AQYEEIAQR.S         |
| <input checked="" type="checkbox"/> <a href="#">194</a> | <b>583.2980</b> | <b>1164.5815</b> | <b>1164.5775</b> | <b>0.0040</b> | <b>0</b> | <b>39</b> | <b>0.091</b> | <b>1</b> | <b>1</b> | <b>K.YEELQVTAGR.H</b> |
| <a href="#">209</a>                                     | 602.3239        | 1202.6333        | 1202.6295        | 0.0038        | 0        | (49)      | 0.011        | 1        | 1        | K.WTLLQEQTG.T         |
| <a href="#">210</a>                                     | 602.3245        | 1202.6344        | 1202.6295        | 0.0048        | 0        | 49        | 0.011        | 1        | 1        | K.WTLLQEQTG.T         |
| <a href="#">214</a>                                     | 606.7828        | 1211.5511        | 1211.5458        | 0.0052        | 0        | 49        | 0.0034       | 1        | 1        | R.AEAEWSYQTK.Y        |
| <a href="#">254</a>                                     | 436.8911        | 1307.6515        | 1307.6469        | 0.0045        | 2        | 63        | 0.00031      | 1        | 1        | K.NKYEDEINKR.T        |
| <a href="#">255</a>                                     | 436.8913        | 1307.6522        | 1307.6469        | 0.0053        | 2        | (56)      | 0.0014       | 1        | 1        | K.NKYEDEINKR.T        |
| <a href="#">256</a>                                     | 436.8917        | 1307.6532        | 1307.6469        | 0.0063        | 2        | (60)      | 0.0006       | 1        | 1        | K.NKYEDEINKR.T        |
| <a href="#">262</a>                                     | 665.3687        | 1328.7228        | 1328.7187        | 0.0041        | 0        | 75        | 2.2e-005     | 1        | 1        | R.NLDLDSIIAEVK.A      |
| <a href="#">273</a>                                     | 675.8695        | 1349.7244        | 1349.7191        | 0.0054        | 1        | 46        | 0.017        | 1        | 1        | R.TAENEFVTLKK.D       |
| <a href="#">302</a>                                     | 704.3618        | 1406.7090        | 1406.7041        | 0.0048        | 0        | 59        | 0.00082      | 1        | 1        | K.ADTLTDEINFLR.A      |
| <a href="#">303</a>                                     | 704.3620        | 1406.7094        | 1406.7041        | 0.0053        | 0        | (51)      | 0.005        | 1        | 1        | K.ADTLTDEINFLR.A      |
| <a href="#">347</a>                                     | 587.3274        | 1758.9604        | 1758.9516        | 0.0088        | 1        | 57        | 0.00092      | 1        | 1        | K.VLDTKWTLLQEQTG.T    |
| <a href="#">348</a>                                     | 587.3281        | 1758.9625        | 1758.9516        | 0.0109        | 1        | (55)      | 0.0014       | 1        | 1        | K.VLDTKWTLLQEQTG.T    |

13. [K2C5 HUMAN](#) Mass: 62568 Score: 365 Matches: 21(14) Sequences: 12(8) emPAI: 0.62

Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3

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

| Query   | Observed        | Mr (expt)        | Mr (calc)        | Delta         | Miss     | Score       | Expect       | Rank     | Unique   | Peptide                  |
|---|-----------------|------------------|------------------|---------------|----------|-------------|--------------|----------|----------|--------------------------|
| <a href="#">76</a>                                      | 827.4315        | 826.4242         | 826.4225         | 0.0017        | 0        | 27          | 0.97         | 1        | 1        | K.FASPIDK.V              |
| <a href="#">77</a>                                      | 414.2201        | 826.4256         | 826.4225         | 0.0031        | 0        | (10)        | 50           | 1        | 1        | K.FASPIDK.V              |
| <input checked="" type="checkbox"/> <a href="#">104</a> | <b>469.7528</b> | <b>937.4911</b>  | <b>937.4869</b>  | <b>0.0043</b> | <b>0</b> | <b>18</b>   | <b>9.1</b>   | <b>1</b> | <b>1</b> | <b>R.SLYNLGGSK.R</b>     |
| <a href="#">105</a>                                     | 473.2607        | 944.5069         | 944.5039         | 0.0030        | 1        | (36)        | 0.26         | 1        | 1        | R.GRLDSELR.N             |
| <a href="#">106</a>                                     | 473.2612        | 944.5078         | 944.5039         | 0.0038        | 1        | 42          | 0.072        | 1        | 1        | R.GRLDSELR.N             |
| <a href="#">157</a>                                     | 541.8055        | 1081.5965        | 1081.5920        | 0.0044        | 1        | (51)        | 0.0039       | 1        | 1        | K.FASPIDKVR.F            |
| <a href="#">158</a>                                     | 541.8060        | 1081.5973        | 1081.5920        | 0.0053        | 1        | 61          | 0.00043      | 1        | 1        | K.FASPIDKVR.F            |
| <input checked="" type="checkbox"/> <a href="#">160</a> | <b>547.2687</b> | <b>1092.5228</b> | <b>1092.5199</b> | <b>0.0028</b> | <b>0</b> | <b>36</b>   | <b>0.14</b>  | <b>1</b> | <b>1</b> | <b>K.AQYEEIANR.S</b>     |
| <input checked="" type="checkbox"/> <a href="#">161</a> | <b>547.2693</b> | <b>1092.5240</b> | <b>1092.5199</b> | <b>0.0041</b> | <b>0</b> | <b>(29)</b> | <b>0.76</b>  | <b>1</b> | <b>1</b> | <b>K.AQYEEIANR.S</b>     |
| <input checked="" type="checkbox"/> <a href="#">172</a> | <b>556.2934</b> | <b>1110.5722</b> | <b>1110.5669</b> | <b>0.0052</b> | <b>0</b> | <b>57</b>   | <b>0.001</b> | <b>1</b> | <b>1</b> | <b>R.ISISTSGGSR.N</b>    |
| <a href="#">206</a>                                     | 597.7933        | 1193.5720        | 1193.5676        | 0.0043        | 0        | (39)        | 0.06         | 1        | 1        | K.YEELQQTAGR.H           |
| <a href="#">207</a>                                     | 597.7937        | 1193.5728        | 1193.5676        | 0.0052        | 0        | 54          | 0.0022       | 1        | 1        | K.YEELQQTAGR.H           |
| <a href="#">209</a>                                     | 602.3239        | 1202.6333        | 1202.6295        | 0.0038        | 0        | (49)        | 0.011        | 1        | 1        | K.WTLLQEQTG.T            |
| <a href="#">210</a>                                     | 602.3245        | 1202.6344        | 1202.6295        | 0.0048        | 0        | 49          | 0.011        | 1        | 1        | K.WTLLQEQTG.T            |
| <a href="#">254</a>                                     | 436.8911        | 1307.6515        | 1307.6469        | 0.0045        | 2        | 63          | 0.00031      | 1        | 1        | K.NKYEDEINKR.T           |
| <a href="#">255</a>                                     | 436.8913        | 1307.6522        | 1307.6469        | 0.0053        | 2        | (56)        | 0.0014       | 1        | 1        | K.NKYEDEINKR.T           |
| <a href="#">256</a>                                     | 436.8917        | 1307.6532        | 1307.6469        | 0.0063        | 2        | (60)        | 0.0006       | 1        | 1        | K.NKYEDEINKR.T           |
| <a href="#">262</a>                                     | 665.3687        | 1328.7228        | 1328.7187        | 0.0041        | 0        | 75          | 2.2e-005     | 1        | 1        | R.NLDLDSIIAEVK.A         |
| <a href="#">347</a>                                     | 587.3274        | 1758.9604        | 1758.9516        | 0.0088        | 1        | 57          | 0.00092      | 1        | 1        | K.VLDTKWTLLQEQTG.T       |
| <a href="#">348</a>                                     | 587.3281        | 1758.9625        | 1758.9516        | 0.0109        | 1        | (55)        | 0.0014       | 1        | 1        | K.VLDTKWTLLQEQTG.T       |
| <a href="#">454</a>                                     | 806.7160        | 2417.1261        | 2417.1135        | 0.0126        | 1        | 58          | 0.00031      | 1        | 1        | R.TEAESWYQTKYEELQQTAGR.H |

14. [K2C6A HUMAN](#) Mass: 60293 Score: 359 Matches: 20(15) Sequences: 12(9) emPAI: 0.75

Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3

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

| Query   | Observed        | Mr (expt)        | Mr (calc)        | Delta         | Miss     | Score     | Expect         | Rank     | Unique   | Peptide              |
|---|-----------------|------------------|------------------|---------------|----------|-----------|----------------|----------|----------|----------------------|
| <a href="#">76</a>                                      | 827.4315        | 826.4242         | 826.4225         | 0.0017        | 0        | 27        | 0.97           | 1        | 1        | K.FASPIDK.V          |
| <a href="#">77</a>                                      | 414.2201        | 826.4256         | 826.4225         | 0.0031        | 0        | (10)      | 50             | 1        | 1        | K.FASPIDK.V          |
| <a href="#">105</a>                                     | 473.2607        | 944.5069         | 944.5039         | 0.0030        | 1        | (36)      | 0.26           | 1        | 1        | R.GRLDSELR.G         |
| <a href="#">106</a>                                     | 473.2612        | 944.5078         | 944.5039         | 0.0038        | 1        | 42        | 0.072          | 1        | 1        | R.GRLDSELR.G         |
| <input checked="" type="checkbox"/> <a href="#">122</a> | <b>506.7589</b> | <b>1011.5031</b> | <b>1011.4985</b> | <b>0.0046</b> | <b>0</b> | <b>66</b> | <b>0.00012</b> | <b>1</b> | <b>1</b> | <b>R.SGFSVSVSR.S</b> |
| <a href="#">157</a>                                     | 541.8055        | 1081.5965        | 1081.5920        | 0.0044        | 1        | (51)      | 0.0039         | 1        | 1        | K.FASPIDKVR.F        |
| <a href="#">158</a>                                     | 541.8060        | 1081.5973        | 1081.5920        | 0.0053        | 1        | 61        | 0.00043        | 1        | 1        | K.FASPIDKVR.F        |
| <a href="#">167</a>                                     | 554.2748        | 1106.5350        | 1106.5356        | -0.0006       | 0        | (43)      | 0.032          | 1        | 1        | K.AQYEEIAQR.S        |
| <a href="#">168</a>                                     | 554.2763        | 1106.5381        | 1106.5356        | 0.0025        | 0        | 55        | 0.0021         | 1        | 1        | K.AQYEEIAQR.S        |
| <a href="#">194</a>                                     | 583.2980        | 1164.5815        | 1164.5775        | 0.0040        | 0        | 39        | 0.091          | 1        | 1        | K.YEELQVTAGR.H       |
| <a href="#">209</a>                                     | 602.3239        | 1202.6333        | 1202.6295        | 0.0038        | 0        | (49)      | 0.011          | 1        | 1        | K.WTLLQEQTG.T        |
| <a href="#">210</a>                                     | 602.3245        | 1202.6344        | 1202.6295        | 0.0048        | 0        | 49        | 0.011          | 1        | 1        | K.WTLLQEQTG.T        |
| <a href="#">214</a>                                     | 606.7828        | 1211.5511        | 1211.5458        | 0.0052        | 0        | 49        | 0.0034         | 1        | 1        | R.AEAEWSYQTK.Y       |
| <a href="#">254</a>                                     | 436.8911        | 1307.6515        | 1307.6469        | 0.0045        | 2        | 63        | 0.00031        | 1        | 1        | K.NKYEDEINKR.T       |
| <a href="#">255</a>                                     | 436.8913        | 1307.6522        | 1307.6469        | 0.0053        | 2        | (56)      | 0.0014         | 1        | 1        | K.NKYEDEINKR.T       |
| <a href="#">256</a>                                     | 436.8917        | 1307.6532        | 1307.6469        | 0.0063        | 2        | (60)      | 0.0006         | 1        | 1        | K.NKYEDEINKR.T       |
| <a href="#">262</a>                                     | 665.3687        | 1328.7228        | 1328.7187        | 0.0041        | 0        | 75        | 2.2e-005       | 1        | 1        | R.NLDLDSIIAEVK.A     |
| <a href="#">273</a>                                     | 675.8695        | 1349.7244        | 1349.7191        | 0.0054        | 1        | 46        | 0.017          | 1        | 1        | R.TAENEFVTLKK.D      |
| <a href="#">302</a>                                     | 704.3618        | 1406.7090        | 1406.7041        | 0.0048        | 0        | 59        | 0.00082        | 1        | 1        | K.ADTLTDEINFLR.A     |
| <a href="#">303</a>                                     | 704.3620        | 1406.7094        | 1406.7041        | 0.0053        | 0        | (51)      | 0.005          | 1        | 1        | K.ADTLTDEINFLR.A     |

15. [K22E HUMAN](#) Mass: 65678 Score: 351 Matches: 13(9) Sequences: 8(5) emPAI: 0.36

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

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

| Query              | Observed | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect | Rank | Unique | Peptide     |
|--------------------|----------|-----------|-----------|--------|------|-------|--------|------|--------|-------------|
| <a href="#">76</a> | 827.4315 | 826.4242  | 826.4225  | 0.0017 | 0    | 27    | 0.97   | 1    | 1      | K.FASPIDK.V |

|     |                 |                  |                  |                |          |             |                 |          |          |                 |
|-----|-----------------|------------------|------------------|----------------|----------|-------------|-----------------|----------|----------|-----------------|
| 77  | 414.2201        | 826.4256         | 826.4225         | 0.0031         | 0        | (10)        | 50              | 1        |          | K.FASFDK.V      |
| 79  | <b>416.2428</b> | <b>830.4711</b>  | <b>830.4862</b>  | <b>-0.0150</b> | <b>0</b> | <b>7</b>    | <b>2.4e+002</b> | <b>1</b> | <b>U</b> | R.SLVGLGGTK.S   |
| 108 | 487.2717        | 972.5288         | 972.5240         | 0.0049         | 0        | 41          | 0.08            | 1        |          | K.IEISELNR.V    |
| 157 | 541.8055        | 1081.5965        | 1081.5920        | 0.0044         | 1        | (51)        | 0.0039          | 1        |          | K.FASFDKVR.F    |
| 158 | 541.8060        | 1081.5973        | 1081.5920        | 0.0053         | 1        | 61          | 0.00043         | 1        |          | K.FASFDKVR.F    |
| 167 | 554.2748        | 1106.5350        | 1106.5356        | -0.0006        | 0        | (43)        | 0.032           | 1        |          | K.AQYEEIAQR.S   |
| 168 | 554.2763        | 1106.5381        | 1106.5356        | 0.0025         | 0        | 55          | 0.0021          | 1        |          | K.AQYEEIAQR.S   |
| 262 | 665.3687        | 1328.7228        | 1328.7187        | 0.0041         | 0        | 75          | 2.2e-005        | 1        |          | R.NLDDSIIEVK.A  |
| 313 | <b>730.9065</b> | <b>1459.7984</b> | <b>1459.7922</b> | <b>0.0062</b>  | <b>0</b> | <b>(42)</b> | <b>0.041</b>    | <b>1</b> | <b>U</b> | K.VDLLNQIEFLK.V |
| 314 | <b>730.9071</b> | <b>1459.7997</b> | <b>1459.7922</b> | <b>0.0075</b>  | <b>0</b> | <b>92</b>   | <b>3.9e-007</b> | <b>1</b> | <b>U</b> | K.VDLLNQIEFLK.V |
| 316 | 738.3987        | 1474.7829        | 1474.7780        | 0.0049         | 0        | 113         | 3.1e-009        | 1        |          | R.FLEQQNQLQTK.W |
| 317 | 738.3998        | 1474.7850        | 1474.7780        | 0.0070         | 0        | (112)       | 4.1e-009        | 1        |          | R.FLEQQNQLQTK.W |

16. **K1C17 HUMAN** Mass: 48361 Score: 198 Matches: 20(10) Sequences: 11(6) emPAI: 1.15  
Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2

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

| Query | Observed        | Mr(expt)         | Mr(calc)         | Delta         | Miss     | Score     | Expect       | Rank     | Unique | Peptide                  |
|-------|-----------------|------------------|------------------|---------------|----------|-----------|--------------|----------|--------|--------------------------|
| 71    | 404.2052        | 806.3958         | 806.3923         | 0.0036        | 0        | 56        | 0.0021       | 1        |        | R.LAADDPR.T              |
| 72    | 404.2052        | 806.3959         | 806.3923         | 0.0036        | 0        | (51)      | 0.0076       | 1        |        | R.LAADDPR.T              |
| 73    | 809.4437        | 808.4364         | 808.4330         | 0.0033        | 0        | (32)      | 0.46         | 1        |        | R.LASYLDK.V              |
| 74    | 405.2255        | 808.4364         | 808.4330         | 0.0033        | 0        | 41        | 0.053        | 1        |        | R.LASYLDK.V              |
| 112   | 495.2739        | 988.5332         | 988.5301         | 0.0030        | 1        | (13)      | 48           | 7        |        | K.SEISELRR.T             |
| 113   | 495.2739        | 988.5332         | 988.5301         | 0.0030        | 1        | 22        | 6.4          | 5        |        | K.SEISELRR.T             |
| 114   | 495.2740        | 988.5334         | 988.5301         | 0.0033        | 1        | (11)      | 81           | 9        |        | K.SEISELRR.T             |
| 124   | 515.3031        | 1028.5916        | 1028.5866        | 0.0050        | 0        | (43)      | 0.046        | 1        |        | R.VLDELTLAR.A            |
| 125   | 515.3033        | 1028.5921        | 1028.5866        | 0.0055        | 0        | 43        | 0.046        | 1        |        | R.VLDELTLAR.A            |
| 130   | 518.7721        | 1035.5295        | 1035.5250        | 0.0046        | 1        | 35        | 0.24         | 1        |        | K.IRDWYQR.Q              |
| 140   | <b>531.7561</b> | <b>1061.4977</b> | <b>1061.4924</b> | <b>0.0053</b> | <b>0</b> | <b>38</b> | <b>0.084</b> | <b>1</b> |        | K.ATMQLNDR.L             |
| 147   | 532.8106        | 1063.6066        | 1063.6026        | 0.0041        | 1        | (51)      | 0.0038       | 1        |        | R.LASYLDKVR.A            |
| 148   | 532.8110        | 1063.6074        | 1063.6026        | 0.0049        | 1        | 56        | 0.0012       | 1        |        | R.LASYLDKVR.A            |
| 226   | 621.7820        | 1241.5495        | 1241.5458        | 0.0037        | 0        | 23        | 1.1          | 1        |        | K.NHEEEMNALR.G           |
| 283   | 681.3514        | 1360.6882        | 1360.6834        | 0.0048        | 0        | 70        | 7.1e-005     | 1        |        | R.EVATNSLVQSGK.S         |
| 306   | 719.8567        | 1437.6988        | 1437.6922        | 0.0066        | 1        | 58        | 0.00074      | 1        |        | R.ILNEMRDQYEK.M          |
| 307   | 480.2402        | 1437.6988        | 1437.6922        | 0.0066        | 1        | (39)      | 0.065        | 1        |        | R.ILNEMRDQYEK.M          |
| 308   | 719.8571        | 1437.6996        | 1437.6922        | 0.0074        | 1        | (56)      | 0.0014       | 1        |        | R.ILNEMRDQYEK.M          |
| 309   | 480.2405        | 1437.6996        | 1437.6922        | 0.0074        | 1        | (9)       | 69           | 1        |        | R.ILNEMRDQYEK.M          |
| 442   | 778.0790        | 2331.2151        | 2331.2030        | 0.0121        | 2        | 31        | 0.28         | 1        |        | R.EVATNSLVQSGKSEISELRR.T |

17. **HORN HUMAN** Mass: 283140 Score: 140 Matches: 4(4) Sequences: 2(2) emPAI: 0.02  
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2

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

| Query | Observed | Mr(expt)  | Mr(calc)  | Delta  | Miss | Score | Expect  | Rank | Unique | Peptide               |
|-------|----------|-----------|-----------|--------|------|-------|---------|------|--------|-----------------------|
| 331   | 528.9113 | 1583.7121 | 1583.7077 | 0.0044 | 0    | (47)  | 0.0044  | 1    | U      | R.GPYESGSHSSGLGHR.E   |
| 332   | 528.9117 | 1583.7132 | 1583.7077 | 0.0055 | 0    | 73    | 1e-005  | 1    | U      | R.GPYESGSHSSGLGHR.E   |
| 333   | 528.9122 | 1583.7148 | 1583.7077 | 0.0071 | 0    | (56)  | 0.00055 | 1    | U      | R.GPYESGSHSSGLGHR.E   |
| 376   | 649.9751 | 1946.9035 | 1946.8943 | 0.0091 | 0    | 48    | 0.0036  | 1    | U      | R.QLGHGQHGSGGQSPSPR.G |

18. **ALBU HUMAN** Mass: 71317 Score: 97 Matches: 6(3) Sequences: 6(3) emPAI: 0.15  
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)  | Delta   | Miss | Score | Expect  | Rank | Unique | Peptide            |
|-------|----------|-----------|-----------|---------|------|-------|---------|------|--------|--------------------|
| 107   | 480.7738 | 959.5330  | 959.5552  | -0.0222 | 0    | 15    | 30      | 1    | U      | K.FQNALVLR.Y       |
| 119   | 500.8072 | 999.5998  | 999.5964  | 0.0034  | 0    | 52    | 0.0041  | 1    | U      | K.QTALVELVK.H      |
| 190   | 575.3137 | 1148.6128 | 1148.6077 | 0.0051  | 0    | 42    | 0.055   | 1    | U      | K.LVNEVEFAK.T      |
| 312   | 722.3262 | 1442.6379 | 1442.6347 | 0.0032  | 0    | 11    | 14      | 1    | U      | K.YICENQDSISSK.L   |
| 329   | 516.2728 | 1545.7966 | 1545.7894 | 0.0071  | 1    | 12    | 36      | 1    | U      | K.LKECEKPLEK.S     |
| 338   | 547.3201 | 1638.9385 | 1638.9305 | 0.0080  | 1    | 57    | 0.00055 | 1    | U      | K.KVPQVSTPLVEVSR.N |

Proteins matching the same set of peptides:

**ALBU PONAB** Mass: 71317 Score: 97 Matches: 6(3) Sequences: 6(3)  
Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=1

19. **K2C4 HUMAN** Mass: 57649 Score: 91 Matches: 6(3) Sequences: 4(2) emPAI: 0.12  
Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4

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

| Query | Observed        | Mr(expt)         | Mr(calc)         | Delta         | Miss     | Score    | Expect          | Rank     | Unique   | Peptide            |
|-------|-----------------|------------------|------------------|---------------|----------|----------|-----------------|----------|----------|--------------------|
| 76    | 827.4315        | 826.4242         | 826.4225         | 0.0017        | 0        | 27       | 0.97            | 1        |          | K.FASFDK.V         |
| 77    | 414.2201        | 826.4256         | 826.4225         | 0.0031        | 0        | (10)     | 50              | 1        |          | K.FASFDK.V         |
| 167   | 554.2748        | 1106.5350        | 1106.5356        | -0.0006       | 0        | (43)     | 0.032           | 1        |          | R.AQYEEIAQR.S      |
| 168   | 554.2763        | 1106.5381        | 1106.5356        | 0.0025        | 0        | 55       | 0.0021          | 1        |          | R.AQYEEIAQR.S      |
| 242   | 639.3594        | 1276.7043        | 1276.7027        | 0.0016        | 0        | 61       | 0.00046         | 1        |          | K.LALDIETATYR.K    |
| 375   | <b>648.0098</b> | <b>1941.0075</b> | <b>1940.9996</b> | <b>0.0079</b> | <b>1</b> | <b>5</b> | <b>1.3e+002</b> | <b>1</b> | <b>U</b> | K.FASFDKVFLEQQNK.V |

20. **A1M RAT** Mass: 168388 Score: 63 Matches: 1(1) Sequences: 1(1) emPAI: 0.02  
Alpha-1-macroglobulin OS=Rattus norvegicus GN=A1m PE=1 SV=1

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

| Query | Observed        | Mr(expt)         | Mr(calc)         | Delta          | Miss     | Score     | Expect         | Rank     | Unique   | Peptide        |
|-------|-----------------|------------------|------------------|----------------|----------|-----------|----------------|----------|----------|----------------|
| 173   | <b>558.8049</b> | <b>1115.5953</b> | <b>1115.6339</b> | <b>-0.0386</b> | <b>1</b> | <b>63</b> | <b>0.00047</b> | <b>1</b> | <b>U</b> | R.KTVSWAVTPK.S |

Proteins matching the same set of peptides:

**A2M MOUSE** Mass: 167144 Score: 63 Matches: 1(1) Sequences: 1(1)  
Alpha-2-macroglobulin OS=Mus musculus GN=A2m PE=1 SV=2

21. **A2MG HUMAN** Mass: 164614 Score: 58 Matches: 5(1) Sequences: 5(1) emPAI: 0.06  
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2

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

| Query | Observed        | Mr(expt)         | Mr(calc)         | Delta         | Miss     | Score     | Expect     | Rank     | Unique   | Peptide                   |
|-------|-----------------|------------------|------------------|---------------|----------|-----------|------------|----------|----------|---------------------------|
| 173   | 558.8049        | 1115.5953        | 1115.5975        | -0.0022       | 0        | 63        | 0.00047    | 1        | U        | R.QTVSWAVTPK.S            |
| 189   | <b>574.8189</b> | <b>1147.6233</b> | <b>1147.6138</b> | <b>0.0094</b> | <b>0</b> | <b>27</b> | <b>1.5</b> | <b>1</b> | <b>U</b> | R.QGIPFFGQVR.L            |
| 328   | 515.9413        | 1544.8020        | 1544.7947        | 0.0073        | 0        | 21        | 4.8        | 1        | U        | R.LVHVEPHETVTR.K          |
| 362   | 923.0254        | 1844.0361        | 1844.0295        | 0.0066        | 0        | 27        | 0.54       | 1        | U        | R.LLIYAVLPTGDVIGDSAK.Y    |
| 395   | 1042.0145       | 2082.0145        | 2082.0052        | 0.0093        | 0        | 13        | 16         | 1        | U        | K.AGAFCLSEADAGLISSTASLR.A |



|                                     |                     |           |           |
|-------------------------------------|---------------------|-----------|-----------|
| <input checked="" type="checkbox"/> | <a href="#">30</a>  | 545.7710  | 544.7637  |
| <input checked="" type="checkbox"/> | <a href="#">31</a>  | 547.3329  | 546.3257  |
| <input checked="" type="checkbox"/> | <a href="#">32</a>  | 550.6289  | 549.6216  |
| <input checked="" type="checkbox"/> | <a href="#">33</a>  | 564.3608  | 563.3535  |
| <input checked="" type="checkbox"/> | <a href="#">34</a>  | 564.3611  | 563.3538  |
| <input checked="" type="checkbox"/> | <a href="#">35</a>  | 579.3376  | 578.3303  |
| <input checked="" type="checkbox"/> | <a href="#">36</a>  | 579.5349  | 578.5276  |
| <input checked="" type="checkbox"/> | <a href="#">37</a>  | 579.5349  | 578.5276  |
| <input checked="" type="checkbox"/> | <a href="#">38</a>  | 579.5350  | 578.5277  |
| <input checked="" type="checkbox"/> | <a href="#">39</a>  | 579.5356  | 578.5283  |
| <input checked="" type="checkbox"/> | <a href="#">40</a>  | 586.4168  | 585.4095  |
| <input checked="" type="checkbox"/> | <a href="#">41</a>  | 594.3677  | 593.3604  |
| <input checked="" type="checkbox"/> | <a href="#">42</a>  | 608.3875  | 607.3802  |
| <input checked="" type="checkbox"/> | <a href="#">43</a>  | 610.3919  | 609.3846  |
| <input checked="" type="checkbox"/> | <a href="#">44</a>  | 613.3543  | 612.3470  |
| <input checked="" type="checkbox"/> | <a href="#">45</a>  | 614.5715  | 613.5642  |
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| <input checked="" type="checkbox"/> | <a href="#">131</a> | 1038.2681 | 1037.2609 |
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| <input checked="" type="checkbox"/> | <a href="#">607</a> | 6267.8791 | 6266.8718 |
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| <input checked="" type="checkbox"/> | <a href="#">618</a> | 7753.5011 | 7752.4938 |
| <input checked="" type="checkbox"/> | <a href="#">619</a> | 1005.4948 | 8035.9001 |
| <input checked="" type="checkbox"/> | <a href="#">620</a> | 8131.2861 | 8130.2788 |
| <input checked="" type="checkbox"/> | <a href="#">621</a> | 8440.3326 | 8439.3253 |
| <input checked="" type="checkbox"/> | <a href="#">622</a> | 9496.9094 | 9495.9021 |

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## Search Parameters

Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Fixed modifications : [Carbamidomethyl \(C\)](#)  
Variable modifications : [Oxidation \(M\)](#)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 0.05$  Da  
Fragment Mass Tolerance :  $\pm 0.05$  Da  
Max Missed Cleavages : 2  
Instrument type : Default  
Number of queries : 622

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

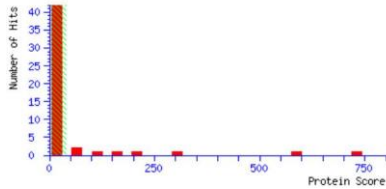


# MASCOT Search Results

User : Julian  
Email : julian.langer@mpibp-frankfurt.mpg.de  
Search title : Submitted from 140318 842 ChKrettler 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
MS data file : D:\Data\140318\140314 842 ChReinhard 3\_Tray01-C8\_01\_17684.d\140314 842 ChReinhard 3\_Tray01-C8\_01\_17684.mgf  
Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
Timestamp : 19 Mar 2014 at 09:49:22 GMT  
Protein hits : [TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[CFAB HUMAN](#) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
[K22B HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[K1C10 HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
[ALBU HUMAN](#) Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
[CH60 ACTP2](#) 60 kDa chaperonin OS=Actinobacillus pleuropneumoniae serotype 5b (strain L20) GN=groL PE=3 SV=1

## Mascot Score Histogram

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
Individual ions scores > 38 indicate identity or extensive homology ( $p < 0.05$ ).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



## Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold  $p < 0.05$  Max. number of hits AUTO

Standard scoring  MudPIT scoring  Ions score or expect cut-off 0 Show sub-sets 0

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

Select All Select None Search Selected  Error tolerant Archive Report

1. [TRYP PIG](#) Mass: 25078 Score: 732 Matches: 33 (30) Sequences: 9 (9) emPAI: 3.90  
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) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide   |
|---|----------|-----------|-----------|---------|------|-------|----------|------|--------|---|
| <input checked="" type="checkbox"/> 88  | 421.7594 | 841.5042  | 841.5022  | 0.0020  | 0    | 54    | 0.0029   | 1    | U      | R.VATVSLPR.S                                      |
| <input checked="" type="checkbox"/> 90  | 421.7595 | 841.5045  | 841.5022  | 0.0024  | 0    | (49)  | 0.0096   | 1    | U      | R.VATVSLPR.S                                      |
| <input checked="" type="checkbox"/> 91  | 842.5118 | 841.5046  | 841.5022  | 0.0024  | 0    | (15)  | 20       | 1    | U      | R.VATVSLPR.S                                      |
| <input checked="" type="checkbox"/> 92  | 421.7596 | 841.5047  | 841.5022  | 0.0025  | 0    | (54)  | 0.003    | 1    | U      | R.VATVSLPR.S                                      |
| <input checked="" type="checkbox"/> 93  | 523.2865 | 1044.5585 | 1044.5564 | 0.0021  | 0    | 65    | 0.00035  | 1    | U      | K.LSSPATLNSR.V                                    |
| <input checked="" type="checkbox"/> 108 | 523.2866 | 1044.5587 | 1044.5564 | 0.0024  | 0    | (55)  | 0.003    | 1    | U      | K.LSSPATLNSR.V                                    |
| <input checked="" type="checkbox"/> 110 | 523.2870 | 1044.5595 | 1044.5564 | 0.0031  | 0    | (45)  | 0.034    | 1    | U      | K.LSSPATLNSR.V                                    |
| <input checked="" type="checkbox"/> 111 | 523.2871 | 1044.5597 | 1044.5564 | 0.0034  | 0    | (56)  | 0.0024   | 1    | U      | K.LSSPATLNSR.V                                    |
| <input checked="" type="checkbox"/> 112 | 523.2875 | 1044.5604 | 1044.5564 | 0.0040  | 0    | (55)  | 0.003    | 1    | U      | K.LSSPATLNSR.V                                    |
| <input checked="" type="checkbox"/> 113 | 523.2875 | 1044.5604 | 1044.5564 | 0.0041  | 0    | (53)  | 0.0044   | 1    | U      | K.LSSPATLNSR.V                                    |
| <input checked="" type="checkbox"/> 114 | 523.2876 | 1044.5606 | 1044.5564 | 0.0043  | 0    | (50)  | 0.01     | 1    | U      | K.LSSPATLNSR.V                                    |
| <input checked="" type="checkbox"/> 116 | 532.2567 | 1062.4988 | 1062.5016 | -0.0027 | 0    | 94    | 2.2e-007 | 1    | U      | K.APVLSDSCK.S                                     |
| <input checked="" type="checkbox"/> 136 | 763.8822 | 1525.7499 | 1525.7446 | 0.0053  | 0    | 65    | 0.00013  | 1    | U      | K.SSGSSYPSLLQCLK.A                                |
| <input checked="" type="checkbox"/> 174 | 941.9272 | 1881.8399 | 1881.8349 | 0.0050  | 0    | (84)  | 5.8e-007 | 1    | U      | R.SCAAAGTECLISGWGNTK.S                            |
| <input checked="" type="checkbox"/> 175 | 941.9279 | 1881.8412 | 1881.8349 | 0.0063  | 0    | 116   | 4e-010   | 1    | U      | R.SCAAAGTECLISGWGNTK.S                            |
| <input checked="" type="checkbox"/> 190 | 737.7085 | 2210.1036 | 2210.0967 | 0.0069  | 0    | (82)  | 2.7e-006 | 1    | U      | R.LGEHNDVLEGNQFVNAK.I                             |
| <input checked="" type="checkbox"/> 192 | 737.7093 | 2210.1060 | 2210.0967 | 0.0092  | 0    | (106) | 9.3e-009 | 1    | U      | R.LGEHNDVLEGNQFVNAK.I                             |
| <input checked="" type="checkbox"/> 193 | 737.7094 | 2210.1064 | 2210.0967 | 0.0097  | 0    | 119   | 4.5e-010 | 1    | U      | R.LGEHNDVLEGNQFVNAK.I                             |
| <input checked="" type="checkbox"/> 198 | 761.7347 | 2282.1822 | 2282.1729 | 0.0094  | 0    | (52)  | 0.0021   | 1    | U      | K.IITHPNFNGNTLNDIIMLIK.L                          |
| <input checked="" type="checkbox"/> 200 | 761.7351 | 2282.1835 | 2282.1729 | 0.0107  | 0    | (63)  | 0.00019  | 1    | U      | K.IITHPNFNGNTLNDIIMLIK.L                          |
| <input checked="" type="checkbox"/> 201 | 761.7354 | 2282.1845 | 2282.1729 | 0.0116  | 0    | (48)  | 0.0054   | 1    | U      | K.IITHPNFNGNTLNDIIMLIK.L                          |
| <input checked="" type="checkbox"/> 206 | 767.0663 | 2298.1772 | 2298.1678 | 0.0094  | 0    | (27)  | 0.71     | 1    | U      | K.IITHPNFNGNTLNDIIMLIK.L + Oxidation (M)          |
| <input checked="" type="checkbox"/> 207 | 767.0669 | 2298.1788 | 2298.1678 | 0.0110  | 0    | (41)  | 0.027    | 1    | U      | K.IITHPNFNGNTLNDIIMLIK.L + Oxidation (M)          |
| <input checked="" type="checkbox"/> 208 | 767.0675 | 2298.1806 | 2298.1678 | 0.0128  | 0    | 67    | 7.9e-005 | 1    | U      | K.IITHPNFNGNTLNDIIMLIK.L + Oxidation (M)          |
| <input checked="" type="checkbox"/> 226 | 903.1476 | 2706.4211 | 2706.4089 | 0.0122  | 1    | (44)  | 0.0095   | 1    | U      | R.IQVRLGEHNDVLEGNQFVNAK.I                         |
| <input checked="" type="checkbox"/> 227 | 677.6126 | 2706.4211 | 2706.4089 | 0.0122  | 1    | (57)  | 0.0005   | 1    | U      | R.IQVRLGEHNDVLEGNQFVNAK.I                         |
| <input checked="" type="checkbox"/> 228 | 677.6129 | 2706.4224 | 2706.4089 | 0.0135  | 1    | 60    | 0.00023  | 1    | U      | R.IQVRLGEHNDVLEGNQFVNAK.I                         |
| <input checked="" type="checkbox"/> 229 | 903.1481 | 2706.4224 | 2706.4089 | 0.0135  | 1    | (31)  | 0.2      | 1    | U      | R.IQVRLGEHNDVLEGNQFVNAK.I                         |
| <input checked="" type="checkbox"/> 246 | 828.1906 | 3308.7334 | 3308.7187 | 0.0147  | 1    | 92    | 1.1e-007 | 1    | U      | K.IITHPNFNGNTLNDIIMLIKSSPATLNSR.V                 |
| <input checked="" type="checkbox"/> 248 | 828.1913 | 3308.7334 | 3308.7187 | 0.0175  | 1    | (69)  | 2.1e-005 | 1    | U      | K.IITHPNFNGNTLNDIIMLIKSSPATLNSR.V                 |
| <input checked="" type="checkbox"/> 249 | 828.1914 | 3308.7366 | 3308.7187 | 0.0179  | 1    | (64)  | 7.2e-005 | 1    | U      | K.IITHPNFNGNTLNDIIMLIKSSPATLNSR.V                 |
| <input checked="" type="checkbox"/> 251 | 832.1900 | 3324.7310 | 3324.7136 | 0.0174  | 1    | (41)  | 0.016    | 1    | U      | K.IITHPNFNGNTLNDIIMLIKSSPATLNSR.V + Oxidation (M) |
| <input checked="" type="checkbox"/> 253 | 832.1901 | 3324.7313 | 3324.7136 | 0.0177  | 1    | (52)  | 0.0011   | 1    | U      | K.IITHPNFNGNTLNDIIMLIKSSPATLNSR.V + Oxidation (M) |

2. [K2C1 HUMAN](#) Mass: 66170 Score: 590 Matches: 18 (17) Sequences: 9 (9) emPAI: 0.58

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) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide                  |
|---|----------|-----------|-----------|--------|------|-------|----------|------|--------|--------------------------|
| <input checked="" type="checkbox"/> 102 | 487.2703 | 972.5261  | 972.5240  | 0.0022 | 0    | 44    | 0.043    | 1    | U      | K.IEISELNR.V             |
| <input checked="" type="checkbox"/> 103 | 487.2707 | 972.5269  | 972.5240  | 0.0030 | 0    | (43)  | 0.047    | 1    | U      | K.IEISELNR.V             |
| <input checked="" type="checkbox"/> 104 | 487.2709 | 972.5273  | 972.5240  | 0.0033 | 0    | (32)  | 0.66     | 1    | U      | K.IEISELNR.V             |
| <input checked="" type="checkbox"/> 134 | 639.3607 | 1276.7069 | 1276.7027 | 0.0042 | 0    | 77    | 1e-005   | 1    | U      | K.LALDLEIATYR.T          |
| <input checked="" type="checkbox"/> 135 | 639.3609 | 1276.7071 | 1276.7027 | 0.0045 | 0    | (65)  | 0.00018  | 1    | U      | K.LALDLEIATYR.T          |
| <input checked="" type="checkbox"/> 136 | 651.8636 | 1301.7126 | 1301.7078 | 0.0048 | 0    | 60    | 0.00065  | 1    | U      | R.SLDLSDIIEVKA.A         |
| <input checked="" type="checkbox"/> 137 | 651.8638 | 1301.7130 | 1301.7078 | 0.0052 | 0    | (49)  | 0.0093   | 1    | U      | R.SLDLSDIIEVKA.A         |
| <input checked="" type="checkbox"/> 149 | 738.3968 | 1474.7791 | 1474.7780 | 0.0011 | 0    | (70)  | 6.6e-005 | 1    | U      | R.FLEQQNQVLQTK.W         |
| <input checked="" type="checkbox"/> 150 | 738.3976 | 1474.7807 | 1474.7780 | 0.0027 | 0    | 82    | 4.2e-006 | 1    | U      | R.FLEQQNQVLQTK.W         |
| <input checked="" type="checkbox"/> 151 | 738.3981 | 1474.7816 | 1474.7780 | 0.0037 | 0    | (78)  | 1.1e-005 | 1    | U      | R.FLEQQNQVLQTK.W         |
| <input checked="" type="checkbox"/> 159 | 800.4229 | 1598.8313 | 1598.8264 | 0.0049 | 1    | 63    | 0.00025  | 1    | U      | K.NKLNLEDAALQQAEDLAR.L   |
| <input checked="" type="checkbox"/> 166 | 858.9337 | 1715.8528 | 1715.8438 | 0.0090 | 0    | 95    | 1.6e-007 | 1    | U      | K.QISNLLQSSIDAEQGENALK.D |
| <input checked="" type="checkbox"/> 176 | 648.0037 | 1940.9892 | 1940.9803 | 0.0089 | 1    | 42    | 0.028    | 1    | U      | K.NLNLEDAALQQAEDLAR.L    |
| <input checked="" type="checkbox"/> 186 | 728.7162 | 2183.1257 | 2183.1182 | 0.0085 | 2    | (56)  | 0.001    | 1    | U      | K.NKLNLEDAALQQAEDLAR.L   |
| <input checked="" type="checkbox"/> 187 | 728.7164 | 2183.1273 | 2183.1182 | 0.0091 | 2    | 78    | 6.9e-006 | 1    | U      | K.NKLNLEDAALQQAEDLAR.L   |
| <input checked="" type="checkbox"/> 188 | 728.7173 | 2183.1302 | 2183.1182 | 0.0120 | 2    | (46)  | 0.0094   | 1    | U      | K.NKLNLEDAALQQAEDLAR.L   |
| <input checked="" type="checkbox"/> 196 | 777.0661 | 2328.1764 | 2328.1669 | 0.0095 | 1    | (48)  | 0.0065   | 1    | U      | K.QISNLLQSSIDAEQGENALK.D |
| <input checked="" type="checkbox"/> 210 | 777.0665 | 2328.1778 | 2328.1669 | 0.0108 | 1    | 51    | 0.0033   | 1    | U      | K.QISNLLQSSIDAEQGENALK.D |

### Proteins matching the same set of peptides:

[K2C1 PANTR](#) Mass: 65621 Score: 590 Matches: 18 (17) Sequences: 9 (9)  
Keratin, type II cytoskeletal 1 OS=Pan troglodytes GN=KRT1 PE=2 SV=1

3. [CFAB HUMAN](#) Mass: 143680 Score: 323 Matches: 15 (9) Sequences: 7 (4) emPAI: 0.18

Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

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

|     |           |           |           |         |   |      |          |   |   |                                |
|-----|-----------|-----------|-----------|---------|---|------|----------|---|---|--------------------------------|
| 117 | 532.2997  | 1062.5848 | 1062.5822 | 0.0026  | 0 | 60   | 0.00081  | 1 | U | K.IDVHLPVDR.K                  |
| 118 | 532.2997  | 1062.5849 | 1062.5822 | 0.0027  | 0 | (59) | 0.00088  | 1 | U | K.IDVHLPVDR.K                  |
| 119 | 532.3001  | 1062.5856 | 1062.5822 | 0.0034  | 0 | (59) | 0.00081  | 1 | U | K.IDVHLPVDR.K                  |
| 120 | 532.3002  | 1062.5859 | 1062.5822 | 0.0037  | 0 | (48) | 0.013    | 1 | U | K.IDVHLPVDR.K                  |
| 130 | 593.8002  | 1185.5858 | 1185.5819 | 0.0039  | 1 | 19   | 7        | 1 | U | R.TKNDFTWFK.L                  |
| 133 | 631.7948  | 1261.5750 | 1261.5761 | -0.0011 | 0 | 21   | 2.7      | 1 | U | K.DGWSAQPTCIK.S                |
| 138 | 655.3071  | 1308.5996 | 1308.5955 | 0.0041  | 0 | 38   | 0.053    | 1 | U | K.SCDIIVFMAR.T                 |
| 139 | 663.3093  | 1324.5921 | 1324.5904 | 0.0017  | 0 | (18) | 3.8      | 1 | U | K.SCDIIVFMAR.T + Oxidation (M) |
| 143 | 698.3978  | 1394.7811 | 1394.7769 | 0.0042  | 0 | 51   | 0.003    | 1 | U | R.SNNLILEHLK.N                 |
| 144 | 465.9343  | 1394.7811 | 1394.7769 | 0.0042  | 0 | (20) | 4.5      | 1 | U | K.SNNLILEHLK.N                 |
| 145 | 698.3983  | 1394.7821 | 1394.7769 | 0.0052  | 0 | (47) | 0.0077   | 1 | U | K.SNNLILEHLK.N                 |
| 146 | 698.3988  | 1394.7831 | 1394.7769 | 0.0062  | 0 | (50) | 0.0044   | 1 | U | K.SNNLILEHLK.N                 |
| 153 | 741.3607  | 1480.7069 | 1480.7021 | 0.0049  | 0 | 85   | 1.6e-006 | 1 | U | K.CFEGFGIDGPAIK.C              |
| 177 | 1010.9948 | 2019.9750 | 2019.9684 | 0.0066  | 0 | (37) | 0.069    | 1 | U | R.DTSCVNPPTVQNAVIVSR.Q         |
| 178 | 1010.9961 | 2019.9777 | 2019.9684 | 0.0093  | 0 | 51   | 0.0029   | 1 | U | R.DTSCVNPPTVQNAVIVSR.Q         |

4. **K22E HUMAN** Mass: 65678 Score: 187 Matches: 8(7) Sequences: 3(3) emPAI: 0.17  
 Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt)  | Mr(calc)  | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide         |
|-------|----------|-----------|-----------|--------|------|-------|----------|------|--------|-----------------|
| 102   | 487.2703 | 972.5261  | 972.5240  | 0.0022 | 0    | 44    | 0.043    | 1    | U      | K.IEISELNR.V    |
| 103   | 487.2707 | 972.5269  | 972.5240  | 0.0030 | 0    | (43)  | 0.047    | 1    | U      | K.IEISELNR.V    |
| 104   | 487.2709 | 972.5273  | 972.5240  | 0.0033 | 0    | (32)  | 0.66     | 1    | U      | K.IEISELNR.V    |
| 140   | 665.3682 | 1328.7219 | 1328.7187 | 0.0031 | 0    | 61    | 0.00053  | 1    | U      | R.NLDDLSIAEVK.A |
| 141   | 665.3694 | 1328.7241 | 1328.7187 | 0.0054 | 0    | (49)  | 0.0085   | 1    | U      | R.NLDDLSIAEVK.A |
| 149   | 738.3968 | 1474.7791 | 1474.7780 | 0.0011 | 0    | (70)  | 6.6e-005 | 1    | U      | R.FLEQQNVLQTK.W |
| 150   | 738.3976 | 1474.7807 | 1474.7780 | 0.0027 | 0    | 82    | 4.2e-006 | 1    | U      | R.FLEQQNVLQTK.W |
| 151   | 738.3981 | 1474.7816 | 1474.7780 | 0.0037 | 0    | (78)  | 1.1e-005 | 1    | U      | R.FLEQQNVLQTK.W |

5. **K1C9 HUMAN** Mass: 62255 Score: 138 Matches: 6(4) Sequences: 3(2) emPAI: 0.18  
 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
 Check to include this hit in error tolerant search or archive report

| Query | Observed  | Mr(expt)  | Mr(calc)  | Delta  | Miss | Score | Expect  | Rank | Unique | Peptide                         |
|-------|-----------|-----------|-----------|--------|------|-------|---------|------|--------|---------------------------------|
| 115   | 530.7871  | 1059.5597 | 1059.5560 | 0.0037 | 0    | 46    | 0.021   | 1    | U      | K.IILDINDTR.M                   |
| 127   | 579.3006  | 1156.5867 | 1156.5836 | 0.0030 | 0    | (55)  | 0.0019  | 1    | U      | R.QGVDDADINGLR.Q                |
| 128   | 579.3007  | 1156.5868 | 1156.5836 | 0.0031 | 0    | (54)  | 0.0021  | 1    | U      | R.QGVDDADINGLR.Q                |
| 129   | 579.3010  | 1156.5874 | 1156.5836 | 0.0038 | 0    | 60    | 0.00054 | 1    | U      | R.QGVDDADINGLR.Q                |
| 243   | 1088.8476 | 3263.5210 | 3263.5066 | 0.0145 | 0    | 31    | 0.094   | 1    | U      | K.DIENQYETIQIEHEVSSSGQEVQSSAK.E |
| 244   | 1088.8488 | 3263.5244 | 3263.5066 | 0.0179 | 0    | (22)  | 0.83    | 1    | U      | K.DIENQYETIQIEHEVSSSGQEVQSSAK.E |

6. **K1C10 HUMAN** Mass: 59020 Score: 112 Matches: 3(2) Sequences: 2(1) emPAI: 0.12  
 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt)  | Mr(calc)  | Delta  | Miss | Score | Expect | Rank | Unique | Peptide             |
|-------|----------|-----------|-----------|--------|------|-------|--------|------|--------|---------------------|
| 106   | 516.3041 | 1030.5936 | 1030.5910 | 0.0026 | 0    | 35    | 0.23   | 1    | U      | R.VLDELTLTK.A       |
| 171   | 899.0122 | 1796.0098 | 1796.0043 | 0.0055 | 0    | (39)  | 0.034  | 1    | U      | R.NVQALETELQSLALK.Q |
| 172   | 899.0135 | 1796.0124 | 1796.0043 | 0.0081 | 0    | 77    | 5e-006 | 1    | U      | R.NVQALETELQSLALK.Q |

7. **ALBU HUMAN** Mass: 71317 Score: 74 Matches: 4(1) Sequences: 3(1) emPAI: 0.10  
 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)  | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide              |
|-------|----------|-----------|-----------|---------|------|-------|----------|------|--------|----------------------|
| 105   | 500.8024 | 999.5903  | 999.5964  | -0.0061 | 0    | 6     | 1.9e+002 | 1    | U      | K.QTALVELVK.H        |
| 123   | 575.3114 | 1148.6082 | 1148.6077 | 0.0005  | 0    | 47    | 0.014    | 1    | U      | K.LVNEVTEFAK.T       |
| 179   | 682.3727 | 2044.0963 | 2044.0881 | 0.0082  | 0    | (15)  | 11       | 1    | U      | K.VFDEFKPLVEEPQNLK.Q |
| 180   | 682.3728 | 2044.0967 | 2044.0881 | 0.0086  | 0    | 21    | 2.8      | 1    | U      | K.VFDEFKPLVEEPQNLK.Q |

Proteins matching the same set of peptides:

**ALBU PONAB** Mass: 71317 Score: 74 Matches: 4(1) Sequences: 3(1)  
 Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=1

8. **CH60 ACTP2** Mass: 57781 Score: 63 Matches: 2(2) Sequences: 1(1) emPAI: 0.06  
 60 kDa chaperonin OS=Actinobacillus pleuropneumoniae serotype 5b (strain AP76) GN=grOL PE=3 SV=1  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr(expt)  | Mr(calc)  | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide                                      |
|-------|----------|-----------|-----------|--------|------|-------|----------|------|--------|--|
| 230   | 913.8403 | 2738.4991 | 2738.4888 | 0.0103 | 0    | 63    | 7.6e-005 | 1    | U      | K.AGKPLLVAEDIEGALATLVVNTMR.G + Oxidation (M) |
| 231   | 913.8411 | 2738.5016 | 2738.4888 | 0.0128 | 0    | (52)  | 0.00093  | 1    | U      | K.AGKPLLVAEDIEGALATLVVNTMR.G + Oxidation (M) |

Proteins matching the same set of peptides:

**CH60 ACTP7** Mass: 57726 Score: 63 Matches: 2(2) Sequences: 1(1)  
 60 kDa chaperonin OS=Actinobacillus pleuropneumoniae serotype 7 (strain AP76) GN=grOL PE=3 SV=1  
**CH60 ACTPJ** Mass: 57726 Score: 63 Matches: 2(2) Sequences: 1(1)  
 60 kDa chaperonin OS=Actinobacillus pleuropneumoniae serotype 3 (strain JL03) GN=grOL PE=3 SV=1  
**CH60 ACTPL** Mass: 57722 Score: 63 Matches: 2(2) Sequences: 1(1)  
 60 kDa chaperonin OS=Actinobacillus pleuropneumoniae GN=grOL PE=3 SV=3

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

| Query | Observed  | Mr(expt)  | Mr(calc)  | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide  |
|-------|-----------|-----------|-----------|---------|------|-------|----------|------|--------|--|
| 122   | 558.8063  | 1115.5981 | 1115.6339 | -0.0358 | 1    | 35    | 0.26     | 1    | U      | KTVSNVATPK   |
| 127   | 581.3180  | 1160.6215 | 1160.6223 | -0.0008 | 0    | 33    | 0.47     | 1    | U      | NOVSLTCLVK   |
| 128   | 581.3200  | 1160.6254 | 1160.6401 | -0.0147 | 2    | 22    | 5        | 1    | U      | NKVSLSKEEK   |
| 132   | 613.8008  | 1225.5871 | 1225.6134 | -0.0263 | 1    | 22    | 2.9      | 1    | U      | FICRMMLAGK   |
| 170   | 887.9561  | 1773.8976 | 1773.8857 | 0.0120  | 2    | 15    | 18       | 1    | U      | GRVELGEIGRESSK   |
| 36    | 802.4329  | 801.4256  | 801.4093  | 0.0163  | 0    | 15    | 48       | 1    | U      | EASSRPR  |
| 95    | 846.4454  | 845.4381  | 845.4607  | -0.0226 | 0    | 12    | 75       | 1    | U      | LTTVAADR   |
| 241   | 532.2578  | 3187.5034 | 3187.5109 | -0.0075 | 0    | 10    | 14       | 1    | U      | TTDYAMLVTMGFTMVISYVVVYR + 2 Oxidation (M)  |
| 97    | 432.2389  | 862.4632  | 862.4331  | 0.0302  | 0    | 10    | 94       | 1    | U      | NMAGSLVR + Oxidation (M)   |
| 147   | 702.3095  | 1402.6045 | 1402.6212 | -0.0167 | 0    | 8     | 17       | 1    | U      | SESTWEIEHEK  |
| 37    | 802.4327  | 801.4254  | 801.4345  | -0.0091 | 0    | 8     | 2.2e+002 | 1    | U      | TSVPTAR  |
| 199   | 540.2999  | 539.2926  | 539.3067  | -0.0141 | 0    | 8     | 74       | 1    | U      | EQAPK  |
| 240   | 593.8207  | 4742.5072 | 4742.5550 | -0.0478 | 2    | 7     | 6.4      | 1    | U      | AVKPYPFYVKKASGATLVVDGVELIDVVLGYPLLIHGHMK + Oxidation (M)                             |
| 183   | 826.8315  | 1651.6484 | 1651.6645 | -0.0161 | 0    | 6     | 3.5      | 1    | U      | ACSSHSGEEGFGSAGR   |
| 188   | 883.8985  | 1765.7824 | 1765.8318 | -0.0494 | 1    | 6     | 34       | 1    | U      | SNDPKSNHFGWLMR   |
| 38    | 846.4454  | 845.4381  | 845.4130  | 0.0251  | 1    | 6     | 2.8e+002 | 1    | U      | EPSEKKK  |
| 41    | 534.3148  | 533.3075  | 533.3173  | -0.0098 | 2    | 6     | 2.1e+002 | 1    | U      | KKTTG  |
| 238   | 530.7833  | 3178.6613 | 3178.6339 | 0.0223  | 1    | 6     | 52       | 1    | U      | GFFGEGGLVSETLIPALQELADAYKAAK   |
| 185   | 555.2480  | 1662.7223 | 1662.7640 | -0.0417 | 2    | 6     | 27       | 1    | U      | VGMVGTSTRYSR + 2 Oxidation (M)   |
| 204   | 762.0633  | 2283.1682 | 2283.1470 | 0.0212  | 0    | 5     | 1.1e+002 | 1    | U      | LQATEPNSGHILHAYCGIK  |
| 182   | 826.8306  | 1651.6466 | 1651.6645 | -0.0179 | 0    | 5     | 4.1      | 1    | U      | ACSSHSGEEGFGSAGR   |
| 189   | 883.8989  | 1765.7832 | 1765.7723 | 0.0109  | 1    | 5     | 51       | 1    | U      | DAVQNCCKISKTEER  |
| 269   | 655.3027  | 3925.7725 | 3925.7299 | 0.0427  | 2    | 4     | 15       | 1    | U      | EQGYDVIQFMKRWDDTENGVCATEDYKDVAK  |
| 187   | 883.8983  | 1765.7820 | 1765.8226 | -0.0406 | 1    | 4     | 54       | 1    | U      | KMQESIDQLCEK + Oxidation (M)   |
| 259   | 914.1791  | 3652.6875 | 3652.7072 | -0.0198 | 1    | 4     | 30       | 1    | U      | TMTYQAIACQCKAGGTCAFIDAEHALDPQYAR + Oxidation (M)                                     |
| 321   | 7706.7262 | 7705.7189 | 7705.7641 | -0.0451 | 0    | 4     | 4        | 1    | U      | GMVTVDYAYLFCFCILAITATTITIIYGSYYPVLTSGFISCIITYTWSIDNANQIMFYGLIPVWKG + 2 Oxidation (M) |
| 213   | 575.3127  | 2871.5273 | 2871.4899 | 0.0373  | 2    | 4     | 81       | 1    | U      | GVNPKVVELLSDLSNKRKSVEDCTK  |
| 237   | 802.4317  | 2404.2732 | 2404.3226 | -0.0494 | 2    | 3     | 1.4e+002 | 1    | U      | LLQATEAVFRERVDEALAHK   |
| 236   | 575.3221  | 3445.8898 | 3445.8470 | 0.0418  | 2    | 3     | 27       | 1    | U      | ALLEPLGADGVRVDFLEVAPEINWIGIGRGLR   |
| 268   | 651.8617  | 3905.1267 | 3905.1313 | -0.0046 | 1    | 3     | 22       | 1    | U      | EACVPLLAGSFTIIVLILFLAIFIPMVKGMNK + 2 Oxidation (M)                                   |
| 298   | 665.3631  | 5314.8468 | 5314.8248 | 0.0220  | 1    | 3     | 11       | 1    | U      | RGLFPFTSLHQLLELTIPPPSEEDLLALSGCRASVHLQLGSRPR   |
| 297   | 500.8073  | 3498.6004 | 3498.6449 | -0.0445 | 1    | 3     | 36       | 1    | U      | DLIARHEVDCNLVNTGWTGAYGTHRMPIK + Oxidation (M)  |

|     |           |           |           |         |   |   |          |   |   |
|-----|-----------|-----------|-----------|---------|---|---|----------|---|---|
| 316 | 6328.0751 | 6327.0678 | 6327.0804 | -0.0126 | 2 | 3 | 17       | 1 | GIIGNLDHAFILINVSYYDCSPNAPNIPAAAYAFFMFMFANITPLMLTGAFARVFKF + 2 Oxidation (M) |
| 315 | 430.2417  | 2146.1720 | 2146.2011 | -0.0291 | 2 | 3 | 1.5e+002 | 1 | QSGIKPKVPAIPRHSNFTGLK   |
| 313 | 762.0632  | 2283.1679 | 2283.1706 | -0.0027 | 1 | 2 | 2.2e+002 | 1 | EALRDSAI PADAIQLLEDTSR  |
| 314 | 846.4451  | 845.4378  | 845.4494  | -0.0116 | 1 | 2 | 7e+002   | 1 | AIEEEKK   |
| 319 | 692.3365  | 4147.9751 | 4147.9931 | -0.0180 | 1 | 2 | 57       | 1 | ILACKGMDISDYSEFISILSALFFASEELTSMCLK + Oxidation (M)                         |
| 318 | 738.3927  | 4424.3126 | 4424.2979 | 0.0147  | 2 | 2 | 45       | 1 | LMQKMTIMAFIGNFAESIQLMLTPQLHAIIAASVSIKSSQK + 3 Oxidation (M)                 |
| 317 | 515.9397  | 1544.7972 | 1544.8021 | -0.0048 | 2 | 2 | 4e+002   | 1 | KMWDELPEVVRK + Oxidation (M)  |
| 315 | 639.3576  | 5106.8025 | 5106.7540 | 0.0486  | 2 | 2 | 6.8      | 1 | LDGEIRISGAKNSALPTLAATLLADGPFVTVQNLPHLHDITMIELFGR + Oxidation (M)            |
| 314 | 824.6312  | 4118.1198 | 4118.1562 | -0.0364 | 0 | 1 | 72       | 1 | LLLGSLVVASVSSDAGETENSILDQIPVASPFSIK   |
| 317 | 655.3088  | 4580.1103 | 4580.1536 | -0.0433 | 2 | 1 | 33       | 1 | LPHCSAAPSHQDHSAMQFGPELWCPKGTHELLRLQDSELR + Oxidation (M)                    |
| 311 | 4746.4014 | 4745.3941 | 4745.3793 | 0.0149  | 2 | 1 | 65       | 1 | AVAVAVVVDATDAFLDRIVSAMQPDMLQLHGSEHPERVAELKAR + Oxidation (M)                |
| 313 | 5738.0792 | 5737.0719 | 5737.0694 | 0.0025  | 2 | 0 | 16       | 1 | ISMMSIPITIASGVLIGADVAVTSDQAARDGAIIAAFAFVSAALLSLMMLLR + 4 Oxidation (M)      |
| 312 | 692.3424  | 4839.3455 | 4839.3095 | 0.0360  | 2 | 0 | 71       | 1 | MDMSRVKIVSSPADIPVYTVGVSVVWIDGYDEENQMATVHLR                                  |
| 311 | 402.3574  | 401.3501  |           |         |   |   |          |   |   |
| 310 | 413.2665  | 412.2592  |           |         |   |   |          |   |   |
| 309 | 413.2669  | 412.2596  |           |         |   |   |          |   |   |
| 308 | 415.2128  | 414.2055  |           |         |   |   |          |   |   |
| 307 | 415.2131  | 414.2058  |           |         |   |   |          |   |   |
| 306 | 415.2132  | 414.2059  |           |         |   |   |          |   |   |
| 305 | 415.2545  | 414.2472  |           |         |   |   |          |   |   |
| 304 | 415.3424  | 414.3351  |           |         |   |   |          |   |   |
| 303 | 415.3425  | 414.3352  |           |         |   |   |          |   |   |
| 302 | 430.2446  | 429.2373  |           |         |   |   |          |   |   |
| 301 | 430.2449  | 429.2376  |           |         |   |   |          |   |   |
| 300 | 430.3888  | 429.3815  |           |         |   |   |          |   |   |
| 299 | 432.2394  | 431.2321  |           |         |   |   |          |   |   |
| 298 | 432.2395  | 431.2322  |           |         |   |   |          |   |   |
| 297 | 432.2810  | 431.2737  |           |         |   |   |          |   |   |
| 296 | 432.2812  | 431.2740  |           |         |   |   |          |   |   |
| 295 | 432.2819  | 431.2747  |           |         |   |   |          |   |   |
| 294 | 442.3314  | 441.3242  |           |         |   |   |          |   |   |
| 293 | 444.1172  | 443.1099  |           |         |   |   |          |   |   |
| 292 | 444.1180  | 443.1107  |           |         |   |   |          |   |   |
| 291 | 446.2611  | 445.2538  |           |         |   |   |          |   |   |
| 290 | 447.2916  | 446.2843  |           |         |   |   |          |   |   |
| 289 | 453.3446  | 452.3373  |           |         |   |   |          |   |   |
| 288 | 456.2808  | 455.2736  |           |         |   |   |          |   |   |
| 287 | 459.2810  | 458.2737  |           |         |   |   |          |   |   |
| 286 | 467.0942  | 466.0870  |           |         |   |   |          |   |   |
| 285 | 475.2310  | 474.2237  |           |         |   |   |          |   |   |
| 284 | 476.3073  | 475.3001  |           |         |   |   |          |   |   |
| 283 | 476.3081  | 475.3008  |           |         |   |   |          |   |   |
| 282 | 476.3083  | 475.3010  |           |         |   |   |          |   |   |
| 281 | 500.3072  | 499.2999  |           |         |   |   |          |   |   |
| 280 | 500.3076  | 499.3003  |           |         |   |   |          |   |   |
| 279 | 500.3078  | 499.3005  |           |         |   |   |          |   |   |
| 278 | 500.8047  | 499.7975  |           |         |   |   |          |   |   |
| 277 | 506.3167  | 505.3095  |           |         |   |   |          |   |   |
| 276 | 520.3341  | 519.3268  |           |         |   |   |          |   |   |
| 275 | 520.3341  | 519.3268  |           |         |   |   |          |   |   |
| 274 | 520.3343  | 519.3270  |           |         |   |   |          |   |   |
| 273 | 520.3347  | 519.3274  |           |         |   |   |          |   |   |
| 272 | 528.3660  | 527.3588  |           |         |   |   |          |   |   |
| 271 | 544.3343  | 543.3270  |           |         |   |   |          |   |   |
| 270 | 547.3335  | 546.3262  |           |         |   |   |          |   |   |
| 269 | 550.6299  | 549.6226  |           |         |   |   |          |   |   |
| 268 | 564.3606  | 563.3533  |           |         |   |   |          |   |   |
| 267 | 564.3607  | 563.3534  |           |         |   |   |          |   |   |
| 266 | 564.3609  | 563.3536  |           |         |   |   |          |   |   |
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| 260 | 586.4176  | 585.4103  |           |         |   |   |          |   |   |
| 259 | 591.3608  | 590.3536  |           |         |   |   |          |   |   |
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| 257 | 594.3689  | 593.3617  |           |         |   |   |          |   |   |
| 256 | 608.3862  | 607.3789  |           |         |   |   |          |   |   |
| 255 | 608.3866  | 607.3793  |           |         |   |   |          |   |   |
| 254 | 608.3871  | 607.3798  |           |         |   |   |          |   |   |
| 253 | 614.5703  | 613.5631  |           |         |   |   |          |   |   |
| 252 | 614.5713  | 613.5640  |           |         |   |   |          |   |   |
| 251 | 615.4044  | 614.3971  |           |         |   |   |          |   |   |
| 250 | 615.4051  | 614.3978  |           |         |   |   |          |   |   |
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| 248 | 617.4080  | 616.4007  |           |         |   |   |          |   |   |
| 247 | 622.3662  | 621.3590  |           |         |   |   |          |   |   |
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| 242 | 674.4690  | 673.4617  |           |         |   |   |          |   |   |
| 241 | 674.4702  | 673.4630  |           |         |   |   |          |   |   |
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| 234 | 677.6846  | 676.6774  |           |         |   |   |          |   |   |
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| 220 | 591.3499  | 1180.6853 |           |         |   |   |          |   |   |
| 219 | 1216.0437 | 1215.0364 |           |         |   |   |          |   |   |
| 218 | 678.3208  | 1354.6270 |           |         |   |   |          |   |   |

|                     |            |            |
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| <a href="#">326</a> | 11476.0369 | 11475.0296 |

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## Search Parameters

Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Fixed modifications : [Carbamidomethyl \(C\)](#)  
Variable modifications : [Oxidation \(M\)](#)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 0.05$  Da  
Fragment Mass Tolerance :  $\pm 0.05$  Da  
Max Missed Cleavages : 2  
Instrument type : Default  
Number of queries : 326

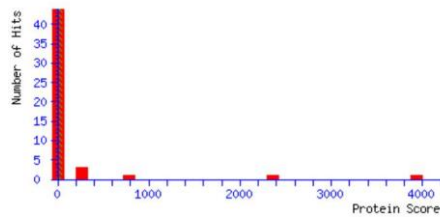
Mascot: <http://www.matrixscience.com/>

**MASCOT** (SCIENCE) **Mascot Search Results**

User : Julian  
 Email : julian.langer@mpibp-frankfurt.mpg.de  
 Search title : Submitted from 140318 842 ChKrettler 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
 MS data file : D:\Data\1403\140318\140314 842 ChReinhard 4\_Tray01-C9\_01\_17685.d\140314 842 ChReinhard 4\_Tray01-C9\_01\_17685.mgf  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Timestamp : 19 Mar 2014 at 09:49:55 GMT  
 Protein hits : [F13A HUMAN](#) Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
[F13B HUMAN](#) Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
[F13A RAT](#) Coagulation factor XIII A chain OS=Rattus norvegicus GN=F13a1 PE=2 SV=3  
[TRYF PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[F13A BOVIN](#) Coagulation factor XIII A chain (Fragment) OS=Bos taurus GN=F13A1 PE=1 SV=2  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[TSPH SYNS3](#) 4-hydroxy-3-methylbut-2-enyl diphosphate reductase OS=Synecococcus sp. (strain CC9311) GN=ispH PE=3 SV=1

**Mascot Score Histogram**

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 38 indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



**Peptide Summary Report**

Format As  Peptide Summary [Help](#)

Significance threshold  $p < 0.05$  Max. number of hits AUTO

Standard scoring  MudPIT scoring  Ions score or expect cut-off 0 Show sub-sets 0

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

Select All  Select None  Search Selected  Error tolerant  Archive Report

1. [F13A HUMAN](#) Mass: 83728 Score: 3932 Matches: 117(91) Sequences: 36(29) emPAI: 5.15  
 Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

| Query                                   | Observed | Mr (expt) | Mr (calc) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide                             |
|---|----------|-----------|-----------|---------|------|-------|----------|------|--------|-------------------------------------|
| <input type="checkbox"/> 119            | 418.2390 | 834.4634  | 834.4599  | 0.0034  | 0    | (11)  | 63       | 3    |        | R.VEYVIGR.Y                         |
| <input checked="" type="checkbox"/> 120 | 418.2390 | 834.4635  | 834.4599  | 0.0036  | 0    | 32    | 0.56     | 1    |        | R.VEYVIGR.Y                         |
| <input checked="" type="checkbox"/> 125 | 430.2476 | 858.4806  | 858.4811  | -0.0004 | 0    | (58)  | 0.002    | 1    | U      | R.LSIQSSPK.C                        |
| <input checked="" type="checkbox"/> 126 | 430.2493 | 858.4841  | 858.4811  | 0.0030  | 0    | 63    | 0.00066  | 1    | U      | R.LSIQSSPK.C                        |
| <input checked="" type="checkbox"/> 127 | 430.2493 | 858.4841  | 858.4811  | 0.0030  | 0    | (49)  | 0.016    | 1    | U      | R.LSIQSSPK.C                        |
| <input checked="" type="checkbox"/> 128 | 430.2494 | 858.4843  | 858.4811  | 0.0033  | 0    | (61)  | 0.001    | 1    | U      | R.LSIQSSPK.C                        |
| <input checked="" type="checkbox"/> 129 | 430.2513 | 858.4879  | 858.4811  | 0.0069  | 0    | (54)  | 0.0048   | 1    | U      | R.LSIQSSPK.C                        |
| <input checked="" type="checkbox"/> 131 | 438.7282 | 875.4419  | 875.4535  | -0.0116 | 0    | (35)  | 0.3      | 1    |        | R.VGSAMVNAK.D                       |
| <input checked="" type="checkbox"/> 132 | 438.7342 | 875.4539  | 875.4535  | 0.0004  | 0    | (36)  | 0.24     | 1    |        | R.VGSAMVNAK.D                       |
| <input checked="" type="checkbox"/> 133 | 438.7346 | 875.4546  | 875.4535  | 0.0011  | 0    | (54)  | 0.004    | 1    |        | R.VGSAMVNAK.D                       |
| <input checked="" type="checkbox"/> 134 | 438.7347 | 875.4549  | 875.4535  | 0.0015  | 0    | 60    | 0.001    | 1    |        | R.VGSAMVNAK.D                       |
| <input checked="" type="checkbox"/> 135 | 438.7348 | 875.4550  | 875.4535  | 0.0016  | 0    | (56)  | 0.0023   | 1    |        | R.VGSAMVNAK.D                       |
| <input checked="" type="checkbox"/> 136 | 439.2146 | 876.4147  | 876.4123  | 0.0024  | 0    | (37)  | 0.14     | 1    | U      | R.AQMDLSGR.G                        |
| <input checked="" type="checkbox"/> 137 | 439.2148 | 876.4150  | 876.4123  | 0.0027  | 0    | (38)  | 0.1      | 1    | U      | R.AQMDLSGR.G                        |
| <input checked="" type="checkbox"/> 138 | 439.2151 | 876.4157  | 876.4123  | 0.0034  | 0    | 39    | 0.084    | 1    | U      | R.AQMDLSGR.G                        |
| <input checked="" type="checkbox"/> 151 | 515.7723 | 1029.5301 | 1029.5277 | 0.0024  | 0    | (66)  | 0.0002   | 1    | U      | R.CGPAVSQAIAK.H                     |
| <input checked="" type="checkbox"/> 152 | 515.7725 | 1029.5305 | 1029.5277 | 0.0028  | 0    | 66    | 0.00018  | 1    | U      | R.CGPAVSQAIAK.H                     |
| <input checked="" type="checkbox"/> 153 | 515.7726 | 1029.5307 | 1029.5277 | 0.0030  | 0    | (63)  | 0.00041  | 1    | U      | R.CGPAVSQAIAK.H                     |
| <input checked="" type="checkbox"/> 154 | 515.7727 | 1029.5309 | 1029.5277 | 0.0032  | 0    | (63)  | 0.00042  | 1    | U      | R.CGPAVSQAIAK.H                     |
| <input checked="" type="checkbox"/> 162 | 558.8085 | 1115.6024 | 1115.6009 | 0.0016  | 0    | (44)  | 0.038    | 1    | U      | K.KPLNTEGVMK.S                      |
| <input checked="" type="checkbox"/> 163 | 558.8088 | 1115.6029 | 1115.6009 | 0.0021  | 0    | (62)  | 0.00059  | 1    | U      | K.KPLNTEGVMK.S                      |
| <input checked="" type="checkbox"/> 164 | 558.8088 | 1115.6030 | 1115.6009 | 0.0022  | 0    | 67    | 0.00016  | 1    | U      | K.KPLNTEGVMK.S                      |
| <input checked="" type="checkbox"/> 165 | 558.8092 | 1115.6038 | 1115.6009 | 0.0029  | 0    | (53)  | 0.004    | 1    | U      | K.KPLNTEGVMK.S                      |
| <input checked="" type="checkbox"/> 177 | 566.8062 | 1131.5979 | 1131.5958 | 0.0021  | 0    | (25)  | 2.6      | 1    | U      | K.KPLNTEGVMK.S + Oxidation (M)      |
| <input checked="" type="checkbox"/> 178 | 566.8070 | 1131.5995 | 1131.5958 | 0.0037  | 0    | (57)  | 0.0018   | 1    | U      | K.KPLNTEGVMK.S + Oxidation (M)      |
| <input checked="" type="checkbox"/> 182 | 590.3076 | 1178.6006 | 1178.5965 | 0.0041  | 0    | (70)  | 6.3e-005 | 1    | U      | K.LIASMSDSL.R.H                     |
| <input checked="" type="checkbox"/> 183 | 590.3080 | 1178.6014 | 1178.5965 | 0.0049  | 0    | 81    | 5.5e-006 | 1    | U      | K.LIASMSDSL.R.H                     |
| <input checked="" type="checkbox"/> 184 | 598.3049 | 1194.5952 | 1194.5914 | 0.0038  | 0    | (75)  | 1.9e-005 | 1    | U      | K.LIASMSDSL.R.H + Oxidation (M)     |
| <input checked="" type="checkbox"/> 185 | 598.3049 | 1194.5952 | 1194.5914 | 0.0038  | 0    | (75)  | 1.8e-005 | 1    | U      | K.LIASMSDSL.R.H + Oxidation (M)     |
| <input checked="" type="checkbox"/> 186 | 598.3049 | 1194.5953 | 1194.5914 | 0.0039  | 0    | (78)  | 9.3e-006 | 1    | U      | K.LIASMSDSL.R.H + Oxidation (M)     |
| <input checked="" type="checkbox"/> 187 | 598.3051 | 1194.5956 | 1194.5914 | 0.0042  | 0    | (70)  | 6.3e-005 | 1    | U      | K.LIASMSDSL.R.H + Oxidation (M)     |
| <input checked="" type="checkbox"/> 213 | 640.8524 | 1279.6903 | 1279.6846 | 0.0058  | 0    | (78)  | 9.2e-006 | 1    |        | R.LALETALMYGAK.K                    |
| <input checked="" type="checkbox"/> 215 | 648.8493 | 1295.6840 | 1295.6795 | 0.0045  | 0    | 101   | 4e-008   | 1    |        | R.LALETALMYGAK.K + Oxidation (M)    |
| <input checked="" type="checkbox"/> 216 | 648.8498 | 1295.6851 | 1295.6795 | 0.0056  | 0    | (96)  | 1.3e-007 | 1    |        | R.LALETALMYGAK.K + Oxidation (M)    |
| <input checked="" type="checkbox"/> 217 | 648.8502 | 1295.6859 | 1295.6795 | 0.0064  | 0    | (77)  | 1.1e-005 | 1    |        | R.LALETALMYGAK.K + Oxidation (M)    |
| <input checked="" type="checkbox"/> 229 | 441.9041 | 1322.6904 | 1322.6864 | 0.0040  | 1    | (21)  | 4.7      | 1    | U      | R.KLIASMSDSL.R.H + Oxidation (M)    |
| <input checked="" type="checkbox"/> 230 | 441.9045 | 1322.6915 | 1322.6864 | 0.0052  | 1    | 38    | 0.096    | 1    | U      | R.KLIASMSDSL.R.H + Oxidation (M)    |
| <input checked="" type="checkbox"/> 231 | 663.9189 | 1325.8232 | 1325.8170 | 0.0062  | 0    | (44)  | 0.0059   | 1    | U      | K.STVLTPEIILK.V                     |
| <input checked="" type="checkbox"/> 232 | 663.9190 | 1325.8234 | 1325.8170 | 0.0065  | 0    | 50    | 0.0017   | 1    | U      | K.STVLTPEIILK.V                     |
| <input checked="" type="checkbox"/> 245 | 683.8809 | 1365.7472 | 1365.7405 | 0.0067  | 1    | (8)   | 67       | 1    |        | R.DLFVVEYVIGR.Y                     |
| <input checked="" type="checkbox"/> 246 | 683.8814 | 1365.7482 | 1365.7405 | 0.0078  | 1    | 29    | 0.57     | 1    |        | R.DLFVVEYVIGR.Y                     |
| <input checked="" type="checkbox"/> 268 | 486.2581 | 1455.7524 | 1455.7470 | 0.0054  | 0    | (68)  | 9.3e-005 | 1    | U      | R.HVYGELDVQIQR.R                    |
| <input checked="" type="checkbox"/> 269 | 728.8835 | 1455.7524 | 1455.7470 | 0.0054  | 0    | 79    | 6.7e-006 | 1    | U      | R.HVYGELDVQIQR.R                    |
| <input checked="" type="checkbox"/> 270 | 728.8841 | 1455.7537 | 1455.7470 | 0.0067  | 0    | (58)  | 0.00076  | 1    | U      | R.HVYGELDVQIQR.R                    |
| <input checked="" type="checkbox"/> 271 | 486.2585 | 1455.7537 | 1455.7470 | 0.0067  | 0    | (69)  | 6.3e-005 | 1    | U      | R.HVYGELDVQIQR.R                    |
| <input checked="" type="checkbox"/> 280 | 763.3956 | 1524.7767 | 1524.7712 | 0.0055  | 0    | 82    | 3.3e-006 | 1    | U      | K.ETFDVTEPLSFK.K                    |
| <input checked="" type="checkbox"/> 281 | 763.3957 | 1524.7769 | 1524.7712 | 0.0057  | 0    | (65)  | 0.00017  | 1    | U      | K.ETFDVTEPLSFK.K                    |
| <input checked="" type="checkbox"/> 287 | 785.9112 | 1569.8079 | 1569.8014 | 0.0065  | 0    | 64    | 0.0002   | 1    | U      | R.MYVAWVTPEYVLR.T + Oxidation (M)   |
| <input checked="" type="checkbox"/> 294 | 532.2811 | 1593.8216 | 1593.8151 | 0.0065  | 1    | 29    | 0.66     | 1    |        | R.VEYVIGRYPQENK.G                   |
| <input checked="" type="checkbox"/> 295 | 532.2815 | 1593.8226 | 1593.8151 | 0.0075  | 1    | (25)  | 1.6      | 1    |        | R.VEYVIGRYPQENK.G                   |
| <input checked="" type="checkbox"/> 296 | 822.8686 | 1643.7227 | 1643.7171 | 0.0056  | 0    | (125) | 4e-011   | 1    | U      | K.QIGGDGMDITDITYK.F                 |
| <input checked="" type="checkbox"/> 301 | 551.9656 | 1652.8750 | 1652.8661 | 0.0089  | 1    | 40    | 0.049    | 1    | U      | K.ETFDVTEPLSFK.E                    |
| <input checked="" type="checkbox"/> 307 | 830.8668 | 1659.7191 | 1659.7120 | 0.0070  | 0    | (123) | 5.1e-011 | 1    | U      | K.QIGGDGMDITDITYK.F + Oxidation (M) |
| <input checked="" type="checkbox"/> 308 | 830.8671 | 1659.7196 | 1659.7120 | 0.0076  | 0    | (115) | 3.5e-010 | 1    | U      | K.QIGGDGMDITDITYK.F + Oxidation (M) |
| <input checked="" type="checkbox"/> 309 | 830.8675 | 1659.7205 | 1659.7120 | 0.0085  | 0    | 142   | 6.7e-013 | 1    | U      | K.QIGGDGMDITDITYK.F + Oxidation (M) |



|     |           |           |           |         |   |       |          |   |   |   |
|-----|-----------|-----------|-----------|---------|---|-------|----------|---|---|---|
| 311 | 838.8643  | 1675.7141 | 1675.7446 | -0.0306 | 1 | 2     | 54       | 2 | U | K.IQENMRYGCASGYK.T                              |
| 321 | 848.9166  | 1695.8187 | 1695.8138 | 0.0049  | 0 | (86)  | 1e-006   | 1 | U | K.CTKFDLSNGYISDVK.L                             |
| 322 | 566.2805  | 1695.8198 | 1695.8138 | 0.0060  | 0 | (66)  | 0.00011  | 1 | U | K.CTKFDLSNGYISDVK.L                             |
| 323 | 848.9172  | 1695.8198 | 1695.8138 | 0.0060  | 0 | (75)  | 1.2e-005 | 1 | U | K.CTKFDLSNGYISDVK.L                             |
| 324 | 566.2806  | 1695.8201 | 1695.8138 | 0.0063  | 0 | (81)  | 3.2e-006 | 1 | U | K.CTKFDLSNGYISDVK.L                             |
| 325 | 848.9173  | 1695.8201 | 1695.8138 | 0.0063  | 0 | 98    | 6.5e-008 | 1 | U | K.CTKFDLSNGYISDVK.L                             |
| 326 | 566.2809  | 1695.8209 | 1695.8138 | 0.0072  | 0 | (65)  | 0.00014  | 1 | U | K.CTKFDLSNGYISDVK.L                             |
| 334 | 574.2763  | 1719.8071 | 1719.7999 | 0.0073  | 0 | 62    | 0.00018  | 1 | U | K.SGYLLHGSNEITCNR.G                             |
| 341 | 884.9630  | 1767.9115 | 1767.9043 | 0.0072  | 0 | 78    | 8.2e-006 | 1 | U | R.GDTPYPAELYITGSILR.M                           |
| 382 | 637.6272  | 1909.8598 | 1909.8524 | 0.0082  | 1 | 60    | 0.00017  | 1 | U | K.DKVQYECATGYITAGGK.K                           |
| 383 | 956.9567  | 1911.8989 | 1911.8916 | 0.0065  | 0 | 95    | 9.2e-008 | 1 | U | K.TEEVECLTYGWSLTPK.C                            |
| 396 | 1018.4400 | 2034.8654 | 2034.8589 | 0.0065  | 0 | 114   | 2.4e-010 | 1 | U | R.QEEQTTCTTEGWSPEPR.C                           |
| 397 | 1018.4414 | 2034.8682 | 2034.8589 | 0.0093  | 0 | (108) | 8.5e-010 | 1 | U | R.QEEQTTCTTEGWSPEPR.C                           |
| 398 | 681.0058  | 2039.9956 | 2039.9874 | 0.0082  | 1 | 60    | 0.00038  | 1 | U | K.TEEVECLTYGWSLTPK.C                            |
| 399 | 681.0068  | 2039.9985 | 2039.9874 | 0.0112  | 1 | (58)  | 0.00052  | 1 | U | K.TEEVECLTYGWSLTPK.C                            |
| 402 | 692.3182  | 2073.9328 | 2073.9248 | 0.0080  | 1 | (50)  | 0.0013   | 1 | U | R.GKWTLPPECVENNENCK.H                           |
| 403 | 692.3185  | 2073.9336 | 2073.9248 | 0.0088  | 1 | (51)  | 0.001    | 1 | U | R.GKWTLPPECVENNENCK.H                           |
| 404 | 692.3187  | 2073.9341 | 2073.9248 | 0.0093  | 1 | 62    | 7.8e-005 | 1 | U | R.GKWTLPPECVENNENCK.H                           |
| 406 | 695.0050  | 2081.9932 | 2081.9840 | 0.0092  | 0 | (70)  | 2.8e-005 | 1 | U | K.VACEEPPFIENGAANLHSK.I                         |
| 407 | 695.0056  | 2081.9949 | 2081.9840 | 0.0109  | 0 | 73    | 1.6e-005 | 1 | U | K.VACEEPPFIENGAANLHSK.I                         |
| 408 | 695.0059  | 2081.9957 | 2081.9840 | 0.0117  | 0 | (66)  | 7.5e-005 | 1 | U | K.VACEEPPFIENGAANLHSK.I                         |
| 418 | 713.3482  | 2137.0227 | 2137.0150 | 0.0077  | 2 | 51    | 0.0023   | 1 | U | K.VKDKVQYECATGYITAGGK.K                         |
| 419 | 713.3489  | 2137.0249 | 2137.0150 | 0.0099  | 2 | (40)  | 0.036    | 1 | U | K.VKDKVQYECATGYITAGGK.K                         |
| 431 | 1139.0669 | 2276.1193 | 2276.1107 | 0.0087  | 0 | (28)  | 0.61     | 1 | U | K.QGYDLSPLTPLSELSVQCNR.G                        |
| 432 | 1139.0684 | 2276.1223 | 2276.1107 | 0.0116  | 0 | 88    | 5.2e-007 | 1 | U | K.QGYDLSPLTPLSELSVQCNR.G                        |
| 433 | 759.7147  | 2276.1223 | 2276.1107 | 0.0116  | 0 | (29)  | 0.46     | 1 | U | K.QGYDLSPLTPLSELSVQCNR.G                        |
| 509 | 899.7385  | 2696.1936 | 2696.1807 | 0.0129  | 1 | (67)  | 1.4e-005 | 1 | U | K.TTGGKDEEVVQCLSDGWSQPTCR.K                     |
| 510 | 899.7391  | 2696.1956 | 2696.1807 | 0.0149  | 1 | 105   | 2.1e-009 | 1 | U | K.TTGGKDEEVVQCLSDGWSQPTCR.K                     |
| 511 | 899.7393  | 2696.1961 | 2696.1807 | 0.0154  | 1 | (99)  | 7.8e-009 | 1 | U | K.TTGGKDEEVVQCLSDGWSQPTCR.K                     |
| 512 | 899.7396  | 2696.1970 | 2696.1807 | 0.0164  | 1 | (87)  | 1.5e-007 | 1 | U | K.TTGGKDEEVVQCLSDGWSQPTCR.K                     |
| 527 | 926.4617  | 2776.3632 | 2776.3490 | 0.0142  | 0 | 87    | 5.5e-007 | 1 | U | K.HPPVVMNGAVADGILASYATGSSVEYR.C + Oxidation (M) |
| 528 | 926.4618  | 2776.3635 | 2776.3490 | 0.0145  | 0 | (35)  | 0.084    | 1 | U | K.HPPVVMNGAVADGILASYATGSSVEYR.C + Oxidation (M) |

3. [F13A RAT](#) Mass: 83120 Score: 789 Matches: 30(21) Sequences: 9(6) emPAI: 0.44

Coagulation factor XIII A chain OS=Rattus norvegicus GN=F13a1 PE=2 SV=3

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

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank     | Unique | Peptide                                   |
|-------|----------|-----------|-----------|------------|-------|--------|----------|--------|---|
| 119   | 418.2390 | 834.4634  | 834.4599  | 0.0034     | 0     | (11)   | 63       | 3      | R.VEYVIGR.Y                               |
| 120   | 418.2390 | 834.4635  | 834.4599  | 0.0036     | 0     | 32     | 0.56     | 1      | R.VEYVIGR.Y                               |
| 131   | 438.7282 | 875.4419  | 875.4535  | -0.0116    | 0     | (35)   | 0.3      | 1      | R.VGSAMVNAK.D                             |
| 132   | 438.7342 | 875.4539  | 875.4535  | 0.0004     | 0     | (36)   | 0.24     | 1      | R.VGSAMVNAK.D                             |
| 133   | 438.7346 | 875.4546  | 875.4535  | 0.0011     | 0     | (54)   | 0.004    | 1      | R.VGSAMVNAK.D                             |
| 134   | 438.7347 | 875.4549  | 875.4535  | 0.0015     | 0     | 60     | 0.001    | 1      | R.VGSAMVNAK.D                             |
| 135   | 438.7348 | 875.4550  | 875.4535  | 0.0016     | 0     | (56)   | 0.0023   | 1      | R.VGSAMVNAK.D                             |
| 213   | 640.8524 | 1279.6903 | 1279.6846 | 0.0058     | 0     | (78)   | 9.2e-006 | 1      | R.LALETALMYGAK.K                          |
| 215   | 648.8493 | 1295.6840 | 1295.6795 | 0.0045     | 0     | 101    | 4e-008   | 1      | R.LALETALMYGAK.K + Oxidation (M)          |
| 216   | 648.8498 | 1295.6851 | 1295.6795 | 0.0056     | 0     | (96)   | 1.3e-007 | 1      | R.LALETALMYGAK.K + Oxidation (M)          |
| 217   | 648.8502 | 1295.6859 | 1295.6795 | 0.0064     | 0     | (77)   | 1.1e-005 | 1      | R.LALETALMYGAK.K + Oxidation (M)          |
| 245   | 683.8809 | 1365.7472 | 1365.7405 | 0.0067     | 1     | (8)    | 67       | 1      | K.DLFRVEYVIGR.Y                           |
| 246   | 683.8814 | 1365.7482 | 1365.7405 | 0.0078     | 1     | 29     | 0.57     | 1      | K.DLFRVEYVIGR.Y                           |
| 294   | 532.2811 | 1593.8216 | 1593.8151 | 0.0065     | 1     | 29     | 0.66     | 1      | R.VEYVIGRYPQENK.G                         |
| 295   | 532.2815 | 1593.8226 | 1593.8151 | 0.0075     | 1     | (25)   | 1.6      | 1      | R.VEYVIGRYPQENK.G                         |
| 313   | 844.4696 | 1686.9247 | 1686.9192 | 0.0055     | 0     | (33)   | 0.21     | 3      | U K.GTYIPVVPVTELQSGK.W                    |
| 314   | 844.4700 | 1686.9255 | 1686.9192 | 0.0062     | 0     | (40)   | 0.042    | 3      | U K.GTYIPVVPVTELQSGK.W                    |
| 315   | 844.4708 | 1686.9270 | 1686.9192 | 0.0077     | 0     | 46     | 0.011    | 3      | U K.GTYIPVVPVTELQSGK.W                    |
| 316   | 564.6187 | 1690.8343 | 1690.8275 | 0.0068     | 0     | (66)   | 0.00012  | 1      | K.DGTHVVENVVDATHIGK.L                     |
| 317   | 564.6188 | 1690.8346 | 1690.8275 | 0.0071     | 0     | 95     | 1.8e-007 | 1      | K.DGTHVVENVVDATHIGK.L                     |
| 318   | 564.6188 | 1690.8347 | 1690.8275 | 0.0072     | 0     | (70)   | 5.3e-005 | 1      | K.DGTHVVENVVDATHIGK.L                     |
| 319   | 564.6196 | 1690.8369 | 1690.8275 | 0.0094     | 0     | (53)   | 0.0026   | 1      | K.DGTHVVENVVDATHIGK.L                     |
| 363   | 607.3167 | 1818.9282 | 1818.9224 | 0.0058     | 1     | (69)   | 7.6e-005 | 1      | K.KDGTHVVENVVDATHIGK.L                    |
| 364   | 607.3170 | 1818.9293 | 1818.9224 | 0.0068     | 1     | (64)   | 0.00022  | 1      | K.KDGTHVVENVVDATHIGK.L                    |
| 365   | 607.3177 | 1818.9314 | 1818.9224 | 0.0089     | 1     | 87     | 1e-006   | 1      | K.KDGTHVVENVVDATHIGK.L                    |
| 455   | 805.0649 | 2412.1730 | 2412.1631 | 0.0099     | 1     | (53)   | 0.0016   | 1      | K.FQEGQEEERLALETALMYGAK.K                 |
| 456   | 805.0663 | 2412.1772 | 2412.1631 | 0.0141     | 1     | 79     | 3.9e-006 | 1      | K.FQEGQEEERLALETALMYGAK.K                 |
| 458   | 810.3970 | 2428.1691 | 2428.1580 | 0.0111     | 1     | (54)   | 0.001    | 1      | K.FQEGQEEERLALETALMYGAK.K + Oxidation (M) |
| 459   | 810.3978 | 2428.1715 | 2428.1580 | 0.0136     | 1     | (37)   | 0.055    | 1      | K.FQEGQEEERLALETALMYGAK.K + Oxidation (M) |
| 460   | 810.3984 | 2428.1732 | 2428.1580 | 0.0152     | 1     | (48)   | 0.0041   | 1      | K.FQEGQEEERLALETALMYGAK.K + Oxidation (M) |

4. [TRYP PIG](#) Mass: 25078 Score: 377 Matches: 13(10) Sequences: 5(4) emPAI: 1.21

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) | Delta Miss | Score | Expect | Rank     | Unique | Peptide                                    |
|-------|----------|-----------|-----------|------------|-------|--------|----------|--------|--|
| 121   | 421.7596 | 841.5047  | 841.5022  | 0.0025     | 0     | 54     | 0.0027   | 1      | U R.VATVSLPR.S                             |
| 122   | 421.7600 | 841.5054  | 841.5022  | 0.0032     | 0     | (54)   | 0.0029   | 1      | U R.VATVSLPR.S                             |
| 155   | 523.2863 | 1044.5580 | 1044.5564 | 0.0016     | 0     | (49)   | 0.012    | 1      | U K.LSSPATLNSR.V                           |
| 156   | 523.2868 | 1044.5591 | 1044.5564 | 0.0028     | 0     | (41)   | 0.083    | 1      | U K.LSSPATLNSR.V                           |
| 157   | 523.2869 | 1044.5592 | 1044.5564 | 0.0028     | 0     | 56     | 0.0025   | 1      | U K.LSSPATLNSR.V                           |
| 426   | 737.7100 | 2210.1081 | 2210.0967 | 0.0114     | 0     | (76)   | 9.5e-006 | 1      | U R.LGEHNDIVLEGNEQFINAAK.I                 |
| 427   | 737.7101 | 2210.1084 | 2210.0967 | 0.0117     | 0     | 108    | 6.6e-009 | 1      | U R.LGEHNDIVLEGNEQFINAAK.I                 |
| 428   | 737.7106 | 2210.1101 | 2210.0967 | 0.0134     | 0     | (91)   | 3.3e-007 | 1      | U R.LGEHNDIVLEGNEQFINAAK.I                 |
| 434   | 761.7352 | 2282.1838 | 2282.1729 | 0.0109     | 0     | (58)   | 0.0006   | 1      | U K.IITHPNFNGNTLDNDIMLIK.L                 |
| 436   | 761.7359 | 2282.1860 | 2282.1729 | 0.0131     | 0     | 60     | 0.00035  | 1      | U K.IITHPNFNGNTLDNDIMLIK.L                 |
| 437   | 767.0674 | 2298.1804 | 2298.1678 | 0.0126     | 0     | (31)   | 0.3      | 1      | U K.IITHPNFNGNTLDNDIMLIK.L + Oxidation (M) |
| 438   | 767.0684 | 2298.1834 | 2298.1678 | 0.0156     | 0     | (45)   | 0.012    | 1      | U K.IITHPNFNGNTLDNDIMLIK.L + Oxidation (M) |
| 544   | 828.1912 | 3308.7359 | 3308.7187 | 0.0172     | 1     | 35     | 0.054    | 1      | U K.IITHPNFNGNTLDNDIMLIK.LSLSPATLNSR.V     |

5. [K2C1 HUMAN](#) Mass: 66170 Score: 150 Matches: 4(4) Sequences: 3(3) emPAI: 0.17

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) | Delta Miss | Score | Expect | Rank     | Unique | Peptide               |
|-------|----------|-----------|-----------|------------|-------|--------|----------|--------|-----------------------|
| 149   | 487.2714 | 972.5282  | 972.5240  | 0.0042     | 0     | 43     | 0.047    | 1      | K.IEISELNR.V          |
| 218   | 651.8635 | 1301.7124 | 1301.7078 | 0.0046     | 0     | (64)   | 0.00028  | 1      | U R.SLDLDSIIAEVK.A    |
| 219   | 651.8639 | 1301.7133 | 1301.7078 | 0.0055     | 0     | 64     | 0.00025  | 1      | U R.SLDLDSIIAEVK.A    |
| 330   | 858.9317 | 1715.8489 | 1715.8438 | 0.0051     | 0     | 84     | 2.2e-006 | 1      | U K.QISNLQSSISDAEQR.G |

Proteins matching the same set of peptides:

[K2C1 PANTR](#) Mass: 65621 Score: 150 Matches: 4(4) Sequences: 3(3)





|                                     |                     |           |           |           |         |   |   |          |   |                                     |
|-------------------------------------|---------------------|-----------|-----------|-----------|---------|---|---|----------|---|-------------------------------------|
| <input checked="" type="checkbox"/> | <a href="#">299</a> | 827.4443  | 1652.8739 | 1652.8352 | 0.0388  | 2 | 0 | 4.6e+002 | 1 | MVHGRMVHGRSVSGK + Oxidation (M)     |
| <input checked="" type="checkbox"/> | <a href="#">516</a> | 904.4122  | 2710.2148 | 2710.2479 | -0.0331 | 2 | 0 | 75       | 1 | RYINDLEMQIDREISMPWR + Oxidation (M) |
| <input checked="" type="checkbox"/> | <a href="#">449</a> | 1185.5327 | 2369.0507 | 2369.0747 | -0.0239 | 1 | 0 | 92       | 1 | SGFKSTHEFVTCFGDSIDAHK               |
| <input checked="" type="checkbox"/> | <a href="#">448</a> | 1185.5316 | 2369.0487 | 2369.0747 | -0.0260 | 1 | 0 | 87       | 1 | SGFKSTHEFVTCFGDSIDAHK               |
| <input checked="" type="checkbox"/> | <a href="#">303</a> | 552.5936  | 1654.7589 | 1654.7872 | -0.0284 | 1 | 0 | 2.3e+002 | 1 | GITDDMKSFQSAIDK                     |
| <input checked="" type="checkbox"/> | <a href="#">1</a>   | 402.3583  | 401.3510  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">2</a>   | 413.2507  | 412.2434  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">3</a>   | 415.2121  | 414.2048  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">4</a>   | 415.2126  | 414.2053  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">5</a>   | 415.2127  | 414.2054  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">6</a>   | 415.3426  | 414.3353  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">7</a>   | 425.3091  | 424.3019  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">8</a>   | 432.2391  | 431.2318  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">9</a>   | 432.2392  | 431.2319  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">10</a>  | 432.2393  | 431.2320  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">11</a>  | 432.2819  | 431.2746  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">12</a>  | 433.3534  | 432.3461  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">13</a>  | 443.2693  | 442.2620  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">14</a>  | 444.1173  | 443.1100  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">15</a>  | 444.1206  | 443.1133  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">16</a>  | 444.3516  | 443.3443  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">17</a>  | 446.2614  | 445.2541  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">18</a>  | 447.2924  | 446.2852  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">19</a>  | 456.2815  | 455.2742  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">20</a>  | 500.3068  | 499.2995  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">21</a>  | 500.3074  | 499.3001  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">22</a>  | 507.9564  | 506.9491  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">23</a>  | 520.3339  | 519.3266  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">24</a>  | 528.3597  | 527.3525  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">25</a>  | 531.2753  | 530.2681  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">26</a>  | 539.3347  | 538.3274  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">27</a>  | 547.3350  | 546.3277  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">28</a>  | 548.9835  | 547.9762  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">32</a>  | 551.5020  | 550.4948  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">33</a>  | 551.5045  | 550.4972  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">34</a>  | 552.3064  | 551.2991  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">35</a>  | 564.3606  | 563.3533  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">36</a>  | 564.3616  | 563.3543  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">37</a>  | 566.9574  | 565.9502  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">38</a>  | 579.5336  | 578.5263  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">39</a>  | 579.5337  | 578.5265  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">40</a>  | 579.5340  | 578.5267  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">41</a>  | 579.5341  | 578.5269  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">42</a>  | 579.5345  | 578.5273  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">43</a>  | 579.5348  | 578.5275  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">44</a>  | 579.5352  | 578.5279  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">45</a>  | 579.5354  | 578.5281  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">46</a>  | 579.5359  | 578.5286  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">47</a>  | 579.5360  | 578.5287  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">48</a>  | 579.5360  | 578.5287  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">49</a>  | 579.5361  | 578.5288  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">50</a>  | 579.5362  | 578.5289  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">51</a>  | 579.5362  | 578.5289  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">52</a>  | 579.5362  | 578.5289  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">53</a>  | 579.5363  | 578.5290  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">54</a>  | 579.5363  | 578.5290  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">55</a>  | 579.5365  | 578.5292  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">56</a>  | 579.5365  | 578.5292  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">57</a>  | 579.5372  | 578.5299  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">58</a>  | 586.4172  | 585.4099  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">60</a>  | 597.5438  | 596.5365  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">61</a>  | 597.5444  | 596.5372  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">62</a>  | 597.5451  | 596.5379  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">63</a>  | 614.5705  | 613.5632  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">64</a>  | 614.5705  | 613.5632  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">65</a>  | 614.5708  | 613.5635  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">66</a>  | 614.5711  | 613.5638  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">67</a>  | 614.5711  | 613.5638  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">68</a>  | 614.5712  | 613.5639  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">69</a>  | 615.4045  | 614.3972  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">70</a>  | 615.4051  | 614.3979  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">71</a>  | 615.4058  | 614.3985  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">72</a>  | 617.4077  | 616.4004  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">73</a>  | 619.5271  | 618.5199  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">74</a>  | 619.5297  | 618.5224  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">75</a>  | 622.3659  | 621.3587  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">77</a>  | 630.4437  | 629.4365  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">78</a>  | 630.4445  | 629.4372  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">79</a>  | 650.2052  | 649.1979  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">80</a>  | 650.2061  | 649.1988  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">81</a>  | 652.4138  | 651.4065  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">82</a>  | 661.5631  | 660.5559  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">83</a>  | 661.5633  | 660.5561  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">84</a>  | 661.5663  | 660.5590  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">85</a>  | 661.5681  | 660.5608  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">86</a>  | 662.2433  | 661.2360  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">87</a>  | 674.4704  | 673.4631  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">88</a>  | 674.4710  | 673.4637  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">89</a>  | 675.6770  | 674.6697  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">90</a>  | 675.6774  | 674.6701  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">91</a>  | 675.6795  | 674.6722  |           |         |   |   |          |   |                                     |
| <input checked="" type="checkbox"/> | <a href="#">92</a>  | 677.6837  | 676.6764  |           |         |   |   |          |   |                                     |

|   |           |           |
|---|-----------|-----------|
| <a href="#">93</a>                                      | 693.5644  | 692.5572  |
| <input checked="" type="checkbox"/> <a href="#">95</a>  | 717.6259  | 716.6186  |
| <input checked="" type="checkbox"/> <a href="#">96</a>  | 717.6259  | 716.6187  |
| <input checked="" type="checkbox"/> <a href="#">97</a>  | 717.6264  | 716.6191  |
| <input checked="" type="checkbox"/> <a href="#">98</a>  | 718.4973  | 717.4900  |
| <input checked="" type="checkbox"/> <a href="#">100</a> | 734.6498  | 733.6425  |
| <input checked="" type="checkbox"/> <a href="#">101</a> | 739.6073  | 738.6000  |
| <input checked="" type="checkbox"/> <a href="#">102</a> | 739.6074  | 738.6001  |
| <input checked="" type="checkbox"/> <a href="#">103</a> | 739.6076  | 738.6003  |
| <input checked="" type="checkbox"/> <a href="#">104</a> | 752.5467  | 751.5394  |
| <input checked="" type="checkbox"/> <a href="#">105</a> | 752.5477  | 751.5404  |
| <input checked="" type="checkbox"/> <a href="#">106</a> | 786.4310  | 785.4237  |
| <input checked="" type="checkbox"/> <a href="#">107</a> | 786.4314  | 785.4242  |
| <input checked="" type="checkbox"/> <a href="#">108</a> | 786.4325  | 785.4252  |
| <input checked="" type="checkbox"/> <a href="#">109</a> | 788.1409  | 787.1336  |
| <input checked="" type="checkbox"/> <a href="#">110</a> | 788.1410  | 787.1338  |
| <input checked="" type="checkbox"/> <a href="#">112</a> | 412.1703  | 822.3260  |
| <input checked="" type="checkbox"/> <a href="#">118</a> | 835.4707  | 834.4634  |
| <input checked="" type="checkbox"/> <a href="#">130</a> | 433.3528  | 864.6911  |
| <input checked="" type="checkbox"/> <a href="#">139</a> | 901.8107  | 900.8035  |
| <input checked="" type="checkbox"/> <a href="#">141</a> | 934.8787  | 933.8715  |
| <input checked="" type="checkbox"/> <a href="#">142</a> | 934.8794  | 933.8721  |
| <input checked="" type="checkbox"/> <a href="#">143</a> | 934.8820  | 933.8747  |
| <input checked="" type="checkbox"/> <a href="#">144</a> | 468.1520  | 934.2895  |
| <input checked="" type="checkbox"/> <a href="#">146</a> | 481.1877  | 960.3607  |
| <input checked="" type="checkbox"/> <a href="#">147</a> | 481.1879  | 960.3612  |
| <input checked="" type="checkbox"/> <a href="#">148</a> | 481.1879  | 960.3613  |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 544.1362  | 1086.2579 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 544.1366  | 1086.2587 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 579.2432  | 1156.4719 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 583.2926  | 1164.5707 |
| <input checked="" type="checkbox"/> <a href="#">195</a> | 1216.0683 | 1215.0610 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 610.2518  | 1218.4889 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 610.2519  | 1218.4893 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 625.5586  | 1249.1026 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 625.5590  | 1249.1035 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 628.2837  | 1254.5528 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 628.7195  | 1255.4245 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 640.7225  | 1279.4304 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 641.7692  | 1281.5238 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 661.7541  | 1321.4936 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 674.7664  | 1347.5182 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 674.7674  | 1347.5202 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 680.7450  | 1359.4755 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 680.7455  | 1359.4765 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 680.7456  | 1359.4766 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 680.7458  | 1359.4770 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 682.8925  | 1363.7705 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 694.2993  | 1386.5841 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 703.8006  | 1405.5866 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 721.8052  | 1441.5959 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 721.8055  | 1441.5964 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 722.2978  | 1442.5810 |
| <input checked="" type="checkbox"/> <a href="#">---</a> | 481.8676  | 1442.5810 |
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## Search Parameters

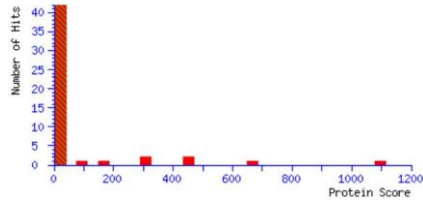
Type of search : MS/MS Ion Search  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance : ± 0.05 Da  
 Fragment Mass Tolerance : ± 0.05 Da  
 Max Missed Cleavages : 2  
 Instrument type : Default  
 Number of queries : 632

# Mascot Search Results

User : Julian  
 Email : julian.langer@mpibp-frankfurt.mpg.de  
 Search title : Submitted from 140318 842 ChKrettlner 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
 MS data file : f:\MAD\140318\140318\140318 842 ChReinhard 5\_Tray01-D1\_01\_17686.d\140314 842 ChReinhard 5\_Tray01-D1\_01\_17686.mgf  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Timestamp : 19 Mar 2014 at 09:50:30 GMT  
 Protein hits : [ALBU HUMAN](#) Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[K1C10 CANFA](#) Keratin, type I cytoskeletal 10 OS=Canis familiaris GN=KRT10 PE=2 SV=1  
[F13A HUMAN](#) Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
[F13B HUMAN](#) Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
[ALBG HUMAN](#) Alpha-1B-glycoprotein OS=Homo sapiens GN=ALBG PE=1 SV=3

## 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 > 39 indicate identity or extensive homology ( $p < 0.05$ ).  
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



## Peptide Summary Report

Format As  Peptide Summary  [Help](#)

Significance threshold  $p < 0.05$  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

Select All  Select None  Search Selected  Error tolerant  Archive Report

1. [ALBU HUMAN](#) Mass: 71317 Score: 1094 Matches: 49 (25) Sequences: 25 (13) emPAI: 1.34  
 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) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide                                       |
|---|-----------|-----------|-----------|--------|------|-------|----------|------|--------|---|
| <input checked="" type="checkbox"/> 73  | 673.3795  | 672.3722  | 672.3707  | 0.0015 | 0    | 33    | 0.79     | 1    | U      | K.AWAVAR.L                                    |
| <input checked="" type="checkbox"/> 86  | 772.4411  | 771.4338  | 771.4313  | 0.0025 | 0    | 18    | 20       | 1    | U      | K.AACLLEK.L                                   |
| <input checked="" type="checkbox"/> 87  | 789.4739  | 788.4667  | 788.4644  | 0.0023 | 0    | (14)  | 35       | 8    |        | K.LVTDLTK.V                                   |
| <input checked="" type="checkbox"/> 88  | 789.4741  | 788.4668  | 788.4644  | 0.0025 | 0    | 33    | 0.49     | 1    |        | K.LVTDLTK.V                                   |
| <input checked="" type="checkbox"/> 105 | 438.2597  | 874.5048  | 874.5025  | 0.0023 | 1    | 23    | 5.4      | 1    |        | R.LSQRFPK.A                                   |
| <input checked="" type="checkbox"/> 106 | 440.7258  | 879.4370  | 879.4338  | 0.0033 | 0    | 33    | 0.35     | 1    | U      | K.AEFAEVSK.L                                  |
| <input checked="" type="checkbox"/> 112 | 927.4963  | 926.4890  | 926.4861  | 0.0029 | 0    | (20)  | 5.3      | 1    |        | K.YLYEYAR.R                                   |
| <input checked="" type="checkbox"/> 113 | 464.2518  | 926.4890  | 926.4861  | 0.0029 | 0    | 35    | 0.15     | 1    |        | K.YLYEYAR.R                                   |
| <input checked="" type="checkbox"/> 115 | 464.2521  | 926.4897  | 926.4861  | 0.0035 | 0    | (35)  | 0.15     | 1    |        | K.YLYEYAR.R                                   |
| <input checked="" type="checkbox"/> 119 | 480.7858  | 959.5570  | 959.5552  | 0.0017 | 0    | 43    | 0.044    | 1    | U      | K.FQNALLVR.Y                                  |
| <input checked="" type="checkbox"/> 122 | 492.7505  | 983.4865  | 983.4811  | 0.0054 | 0    | 25    | 1.4      | 1    | U      | K.TYETLEK.C                                   |
| <input checked="" type="checkbox"/> 124 | 500.8071  | 999.5997  | 999.5964  | 0.0033 | 0    | (43)  | 0.038    | 1    |        | K.QTALVELVK.H                                 |
| <input checked="" type="checkbox"/> 125 | 500.8071  | 999.5997  | 999.5964  | 0.0033 | 0    | 53    | 0.0036   | 1    |        | K.QTALVELVK.H                                 |
| <input checked="" type="checkbox"/> 126 | 500.8072  | 999.5998  | 999.5964  | 0.0034 | 0    | (51)  | 0.0054   | 1    |        | K.QTALVELVK.H                                 |
| <input checked="" type="checkbox"/> 127 | 507.3040  | 1012.5934 | 1012.5917 | 0.0017 | 0    | (14)  | 22       | 1    | U      | K.LVAASQAALGL.-                               |
| <input checked="" type="checkbox"/> 128 | 1013.6017 | 1012.5945 | 1012.5917 | 0.0028 | 0    | 49    | 0.0068   | 1    | U      | K.LVAASQAALGL.-                               |
| <input checked="" type="checkbox"/> 129 | 1013.6021 | 1012.5948 | 1012.5917 | 0.0031 | 0    | (29)  | 0.71     | 1    | U      | K.LVAASQAALGL.-                               |
| <input checked="" type="checkbox"/> 139 | 528.2997  | 1054.5848 | 1054.5811 | 0.0037 | 1    | 18    | 7.1      | 1    | U      | K.KYLYEYAR.R                                  |
| <input checked="" type="checkbox"/> 154 | 564.8546  | 1127.6947 | 1127.6914 | 0.0033 | 1    | (58)  | 0.00064  | 1    |        | K.KQTALVELVK.H                                |
| <input checked="" type="checkbox"/> 155 | 564.8553  | 1127.6961 | 1127.6914 | 0.0047 | 1    | 72    | 2.2e-005 | 1    |        | K.KQTALVELVK.H                                |
| <input checked="" type="checkbox"/> 157 | 569.7540  | 1137.4935 | 1137.4907 | 0.0028 | 0    | (49)  | 0.0026   | 1    |        | K.CCTESLVNR.R                                 |
| <input checked="" type="checkbox"/> 158 | 569.7547  | 1137.4949 | 1137.4907 | 0.0042 | 0    | 53    | 0.0011   | 1    |        | K.CCTESLVNR.R                                 |
| <input checked="" type="checkbox"/> 160 | 575.3122  | 1148.6098 | 1148.6077 | 0.0021 | 0    | 48    | 0.013    | 1    |        | K.LVNEVTEFAK.T                                |
| <input checked="" type="checkbox"/> 173 | 613.8087  | 1225.6028 | 1225.5979 | 0.0050 | 1    | 63    | 0.00025  | 1    | U      | R.FKDLGEEFK.A                                 |
| <input checked="" type="checkbox"/> 174 | 409.5416  | 1225.6029 | 1225.5979 | 0.0050 | 1    | (28)  | 0.8      | 1    | U      | R.FKDLGEEFK.A                                 |
| <input checked="" type="checkbox"/> 175 | 613.8090  | 1225.6035 | 1225.5979 | 0.0056 | 1    | (39)  | 0.064    | 1    | U      | R.FKDLGEEFK.A                                 |
| <input checked="" type="checkbox"/> 197 | 679.8210  | 1357.6273 | 1357.6224 | 0.0049 | 0    | 99    | 3.7e-008 | 1    | U      | K.AVMDDFAAFVEK.C + Oxidation (M)              |
| <input checked="" type="checkbox"/> 197 | 722.3270  | 1442.6395 | 1442.6347 | 0.0047 | 0    | (67)  | 3.5e-005 | 1    | U      | K.YICENQDSISSK.L                              |
| <input checked="" type="checkbox"/> 198 | 722.3273  | 1442.6400 | 1442.6347 | 0.0053 | 0    | 78    | 2.6e-006 | 1    | U      | K.YICENQDSISSK.L                              |
| <input checked="" type="checkbox"/> 199 | 722.3284  | 1442.6423 | 1442.6347 | 0.0076 | 0    | (56)  | 0.0004   | 1    | U      | K.YICENQDSISSK.L                              |
| <input checked="" type="checkbox"/> 202 | 516.2719  | 1545.7940 | 1545.7894 | 0.0045 | 1    | (48)  | 0.011    | 1    | U      | K.LKECEKPLLEK.S                               |
| <input checked="" type="checkbox"/> 203 | 516.2724  | 1545.7954 | 1545.7894 | 0.0060 | 1    | (55)  | 0.0022   | 1    | U      | K.LKECEKPLLEK.S                               |
| <input checked="" type="checkbox"/> 204 | 516.2725  | 1545.7956 | 1545.7894 | 0.0061 | 1    | 62    | 0.00041  | 1    | U      | K.LKECEKPLLEK.S                               |
| <input checked="" type="checkbox"/> 205 | 516.2726  | 1545.7960 | 1545.7894 | 0.0066 | 1    | (56)  | 0.0018   | 1    | U      | K.LKECEKPLLEK.S                               |
| <input checked="" type="checkbox"/> 209 | 547.3191  | 1638.9355 | 1638.9305 | 0.0051 | 1    | (65)  | 9.2e-005 | 1    | U      | K.KVPQVSTPLVEVSR.N                            |
| <input checked="" type="checkbox"/> 210 | 547.3196  | 1638.9370 | 1638.9305 | 0.0065 | 1    | 68    | 4.1e-005 | 1    | U      | K.KVPQVSTPLVEVSR.N                            |
| <input checked="" type="checkbox"/> 225 | 637.6510  | 1909.9311 | 1909.9244 | 0.0067 | 0    | (46)  | 0.0084   | 1    | U      | R.RPCFSALEVDETYVPK.E                          |
| <input checked="" type="checkbox"/> 227 | 637.6513  | 1909.9321 | 1909.9244 | 0.0077 | 0    | 54    | 0.0014   | 1    | U      | R.RPCFSALEVDETYVPK.E                          |
| <input checked="" type="checkbox"/> 233 | 682.3719  | 2044.0940 | 2044.0881 | 0.0059 | 0    | (44)  | 0.016    | 1    | U      | K.VFDFKPLVEEPQNLK.Q                           |
| <input checked="" type="checkbox"/> 235 | 682.3723  | 2044.0951 | 2044.0881 | 0.0070 | 0    | 52    | 0.0026   | 1    | U      | K.VFDFKPLVEEPQNLK.Q                           |
| <input checked="" type="checkbox"/> 266 | 647.0378  | 2584.1221 | 2584.1105 | 0.0116 | 1    | (4)   | 20       | 1    | U      | K.VHTECCHGDLLECADDRADLAK.Y                    |
| <input checked="" type="checkbox"/> 267 | 647.0379  | 2584.1225 | 2584.1105 | 0.0120 | 1    | 10    | 5.6      | 1    | U      | K.VHTECCHGDLLECADDRADLAK.Y                    |
| <input checked="" type="checkbox"/> 270 | 659.8151  | 2635.2315 | 2635.2197 | 0.0117 | 2    | (21)  | 1.3      | 1    | U      | K.QEPRNECFLQKDDNPFLR.L                        |
| <input checked="" type="checkbox"/> 271 | 659.8154  | 2635.2323 | 2635.2197 | 0.0126 | 2    | (16)  | 4.6      | 1    | U      | K.QEPRNECFLQKDDNPFLR.L                        |
| <input checked="" type="checkbox"/> 272 | 659.8156  | 2635.2333 | 2635.2197 | 0.0135 | 2    | 29    | 0.2      | 1    | U      | K.QEPRNECFLQKDDNPFLR.L                        |
| <input checked="" type="checkbox"/> 273 | 659.8157  | 2635.2335 | 2635.2197 | 0.0138 | 2    | (20)  | 1.6      | 1    | U      | K.QEPRNECFLQKDDNPFLR.L                        |
| <input checked="" type="checkbox"/> 280 | 699.3466  | 2793.3572 | 2793.3466 | 0.0106 | 1    | (22)  | 1.6      | 1    | U      | R.LVRPEVDVMCTAFHDNEETFLK.Y + Oxidation (M)    |
| <input checked="" type="checkbox"/> 282 | 699.3466  | 2793.3573 | 2793.3466 | 0.0107 | 1    | 27    | 0.6      | 1    | U      | R.LVRPEVDVMCTAFHDNEETFLK.Y + Oxidation (M)    |
| <input checked="" type="checkbox"/> 286 | 997.4552  | 2989.3436 | 2989.3321 | 0.0115 | 0    | 20    | 0.75     | 1    | U      | K.SHCIAEVNDEMPADLPSLAADFVSK.D + Oxidation (M) |

Proteins matching the same set of peptides:  
[ALBU PONAB](#) Mass: 71317 Score: 1094 Matches: 49 (25) Sequences: 25 (13)  
 Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=1

2. [K2C1 HUMAN](#) Mass: 66170 Score: 679 Matches: 22 (16) Sequences: 14 (11) emPAI: 0.94  
 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) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide       |
|---|----------|-----------|-----------|---------|------|-------|----------|------|--------|---------------|
| <input checked="" type="checkbox"/> 93  | 832.4852 | 831.4779  | 831.4814  | -0.0035 | 0    | 8     | 1.6e+002 | 5    | U      | K.SISISVAR.G  |
| <input checked="" type="checkbox"/> 103 | 437.7539 | 873.4933  | 873.4920  | 0.0014  | 0    | (23)  | 6.1      | 1    | U      | R.SLVNLGGSK.S |



Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3

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

Table with 10 columns: Query, Observed, Mr(expt), Mr(calc), Delta Miss Score, Expect Rank, Unique, Peptide. Rows 169-240.

8. A1BG HUMAN Mass: 54809 Score: 59 Matches: 2(2) Sequences: 1(1) emPAI: 0.06

Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=3

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

Table with 10 columns: Query, Observed, Mr(expt), Mr(calc), Delta Miss Score, Expect Rank, Unique, Peptide. Rows 101-102.

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

Large table with 10 columns: Query, Observed, Mr(expt), Mr(calc), Delta Miss Score, Expect Rank, Unique, Peptide. Rows 177-41.



|                                     |                     |           |           |
|-------------------------------------|---------------------|-----------|-----------|
| <input checked="" type="checkbox"/> | <a href="#">42</a>  | 578.3392  | 577.3320  |
| <input checked="" type="checkbox"/> | <a href="#">43</a>  | 579.5353  | 578.5281  |
| <input checked="" type="checkbox"/> | <a href="#">44</a>  | 579.5361  | 578.5288  |
| <input checked="" type="checkbox"/> | <a href="#">45</a>  | 579.5362  | 578.5290  |
| <input checked="" type="checkbox"/> | <a href="#">46</a>  | 579.5364  | 578.5291  |
| <input checked="" type="checkbox"/> | <a href="#">47</a>  | 579.5371  | 578.5298  |
| <input checked="" type="checkbox"/> | <a href="#">48</a>  | 586.4171  | 585.4099  |
| <input checked="" type="checkbox"/> | <a href="#">49</a>  | 594.3709  | 593.3636  |
| <input checked="" type="checkbox"/> | <a href="#">50</a>  | 595.3703  | 594.3630  |
| <input checked="" type="checkbox"/> | <a href="#">51</a>  | 597.5448  | 596.5375  |
| <input checked="" type="checkbox"/> | <a href="#">52</a>  | 608.3862  | 607.3789  |
| <input checked="" type="checkbox"/> | <a href="#">53</a>  | 608.3864  | 607.3791  |
| <input checked="" type="checkbox"/> | <a href="#">54</a>  | 608.3864  | 607.3791  |
| <input checked="" type="checkbox"/> | <a href="#">55</a>  | 608.3871  | 607.3798  |
| <input checked="" type="checkbox"/> | <a href="#">56</a>  | 614.5713  | 613.5641  |
| <input checked="" type="checkbox"/> | <a href="#">58</a>  | 615.4045  | 614.3972  |
| <input checked="" type="checkbox"/> | <a href="#">59</a>  | 615.4048  | 614.3976  |
| <input checked="" type="checkbox"/> | <a href="#">60</a>  | 617.4081  | 616.4008  |
| <input checked="" type="checkbox"/> | <a href="#">62</a>  | 619.5272  | 618.5199  |
| <input checked="" type="checkbox"/> | <a href="#">63</a>  | 619.5275  | 618.5202  |
| <input checked="" type="checkbox"/> | <a href="#">64</a>  | 619.5275  | 618.5202  |
| <input checked="" type="checkbox"/> | <a href="#">65</a>  | 630.4399  | 629.4327  |
| <input checked="" type="checkbox"/> | <a href="#">66</a>  | 630.4446  | 629.4373  |
| <input checked="" type="checkbox"/> | <a href="#">67</a>  | 640.5862  | 639.5789  |
| <input checked="" type="checkbox"/> | <a href="#">68</a>  | 650.2048  | 649.1976  |
| <input checked="" type="checkbox"/> | <a href="#">69</a>  | 652.4126  | 651.4053  |
| <input checked="" type="checkbox"/> | <a href="#">70</a>  | 652.4138  | 651.4065  |
| <input checked="" type="checkbox"/> | <a href="#">72</a>  | 668.6227  | 667.6154  |
| <input checked="" type="checkbox"/> | <a href="#">74</a>  | 674.4697  | 673.4624  |
| <input checked="" type="checkbox"/> | <a href="#">75</a>  | 675.6768  | 674.6695  |
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| <input checked="" type="checkbox"/> | <a href="#">77</a>  | 675.6787  | 674.6714  |
| <input checked="" type="checkbox"/> | <a href="#">78</a>  | 675.6794  | 674.6721  |
| <input checked="" type="checkbox"/> | <a href="#">79</a>  | 696.4390  | 695.4317  |
| <input checked="" type="checkbox"/> | <a href="#">80</a>  | 696.4390  | 695.4317  |
| <input checked="" type="checkbox"/> | <a href="#">81</a>  | 718.4947  | 717.4874  |
| <input checked="" type="checkbox"/> | <a href="#">82</a>  | 752.5469  | 751.5396  |
| <input checked="" type="checkbox"/> | <a href="#">83</a>  | 752.5478  | 751.5405  |
| <input checked="" type="checkbox"/> | <a href="#">84</a>  | 762.5228  | 761.5155  |
| <input checked="" type="checkbox"/> | <a href="#">85</a>  | 765.4677  | 764.4605  |
| <input checked="" type="checkbox"/> | <a href="#">90</a>  | 412.7547  | 823.4948  |
| <input checked="" type="checkbox"/> | <a href="#">92</a>  | 415.2535  | 828.4925  |
| <input checked="" type="checkbox"/> | <a href="#">107</a> | 444.3481  | 886.6817  |
| <input checked="" type="checkbox"/> | <a href="#">110</a> | 456.2779  | 910.5412  |
| <input checked="" type="checkbox"/> | <a href="#">111</a> | 457.2620  | 912.5094  |
| <input checked="" type="checkbox"/> | <a href="#">114</a> | 927.4969  | 926.4897  |
| <input checked="" type="checkbox"/> | <a href="#">116</a> | 934.8788  | 933.8715  |
| <input checked="" type="checkbox"/> | <a href="#">117</a> | 474.8311  | 947.6476  |
| <input checked="" type="checkbox"/> | <a href="#">118</a> | 476.3093  | 950.6041  |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 534.2642  | 1066.5139 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 549.7446  | 1097.4746 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 1104.2522 | 1103.2449 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 1111.2840 | 1110.2767 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 608.2578  | 1214.5011 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 608.2578  | 1214.5011 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 608.2581  | 1214.5016 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 613.3599  | 1224.7052 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 613.3612  | 1224.7079 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 444.1164  | 1329.3273 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 739.2770  | 1476.5394 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 540.3380  | 1617.9921 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 545.7281  | 1634.1626 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 564.3524  | 1690.0353 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 591.3599  | 1771.0578 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 607.2404  | 1818.6992 |
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| <input checked="" type="checkbox"/> | <a href="#">---</a> | 651.1993  | 1950.5760 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 666.3927  | 1996.1563 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 402.3567  | 2006.7473 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 679.8196  | 2036.4369 |
| <input checked="" type="checkbox"/> | <a href="#">234</a> | 1023.0548 | 2044.0951 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 686.3129  | 2055.9168 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 520.3305  | 2077.2930 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 528.9691  | 2111.8475 |
| <input checked="" type="checkbox"/> | <a href="#">248</a> | 1106.0602 | 2210.1059 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 755.3479  | 2263.0219 |
| <input checked="" type="checkbox"/> | <a href="#">252</a> | 1142.0971 | 2282.1796 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 762.0616  | 2283.1629 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 779.3719  | 2335.0938 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 779.3723  | 2335.0952 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 614.5705  | 2454.2529 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 415.2487  | 2485.4485 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 432.2587  | 2587.5084 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 432.2832  | 2587.6553 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 883.8915  | 2648.6527 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 459.2864  | 2749.6747 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 695.8552  | 2779.3916 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 466.2883  | 2791.6862 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 559.6787  | 2793.3573 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 412.1669  | 2878.1172 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 550.3366  | 3295.9759 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 671.8101  | 3354.0141 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 570.7426  | 3418.4121 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 490.2867  | 3424.9563 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 579.5246  | 3471.1041 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 613.3506  | 3674.0601 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 921.1313  | 3680.4960 |
| <input checked="" type="checkbox"/> | <a href="#">---</a> | 3700.5419 | 3699.5346 |

|   |           |           |           |         |   |     |   |  |  |  |
|---|-----------|-----------|-----------|---------|---|-----|---|--|--|--|
| <a href="#">307</a>                                     | 533.7458  | 3729.1697 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">308</a> | 934.8803  | 3735.4922 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">309</a> | 476.2974  | 3802.3212 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">310</a> | 544.8278  | 3806.7439 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">311</a> | 3863.1885 | 3862.1812 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">312</a> | 3881.0809 | 3880.0736 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">313</a> | 650.2066  | 3895.1959 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">316</a> | 561.3165  | 3922.1648 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">317</a> | 564.8592  | 3946.9636 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">318</a> | 666.6047  | 3993.5847 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">319</a> | 500.3184  | 3994.4894 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">320</a> | 4007.2522 | 4006.2449 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">321</a> | 671.8196  | 4024.8742 | 4024.9206 | -0.0465 | 2 | --- | 1 |  |  | EKFPDQWLAYNLSPSFNPKAMSVDEQHTFIQR + Oxidation (M) |
| <input checked="" type="checkbox"/> <a href="#">322</a> | 579.5374  | 4049.7108 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">323</a> | 4117.4703 | 4116.4630 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">324</a> | 4143.1475 | 4142.1402 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">325</a> | 594.3717  | 4153.5512 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">326</a> | 696.4206  | 4172.4801 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">327</a> | 525.2883  | 4194.2482 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">328</a> | 527.1981  | 4209.5266 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">329</a> | 608.3702  | 4251.5405 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">330</a> | 534.9907  | 4271.8673 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">331</a> | 614.5584  | 4294.8580 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">332</a> | 539.3160  | 4306.4700 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">333</a> | 619.5404  | 4329.7317 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">334</a> | 622.3605  | 4349.4722 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">335</a> | 4385.5684 | 4384.5611 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">336</a> | 632.4063  | 4419.7928 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">338</a> | 555.2476  | 4433.9224 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">339</a> | 640.8509  | 4478.9053 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">340</a> | 4520.6378 | 4519.6305 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">341</a> | 566.7990  | 4526.3340 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">342</a> | 569.7537  | 4549.9712 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">343</a> | 651.8542  | 4555.9287 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">344</a> | 763.9217  | 4577.4868 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">345</a> | 4751.3792 | 4750.3719 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">346</a> | 679.7935  | 4751.5033 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">349</a> | 4964.4531 | 4963.4458 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">351</a> | 5193.2507 | 5192.2434 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">352</a> | 650.2043  | 5193.5758 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">353</a> | 5196.0230 | 5195.0157 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">354</a> | 5240.5009 | 5239.4936 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">355</a> | 5246.9749 | 5245.9676 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">357</a> | 5280.1156 | 5279.1083 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">358</a> | 883.8831  | 5297.2547 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">359</a> | 5313.2883 | 5312.2810 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">360</a> | 763.8495  | 5339.8952 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">361</a> | 5343.0446 | 5342.0373 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">363</a> | 5428.0298 | 5427.0225 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">364</a> | 5487.3537 | 5486.3464 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">365</a> | 1101.1728 | 5500.8276 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">366</a> | 1101.1738 | 5500.8325 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">368</a> | 696.4286  | 5563.3705 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">369</a> | 5592.2301 | 5591.2228 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">370</a> | 802.4295  | 5609.9558 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">371</a> | 5758.4364 | 5757.4291 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">373</a> | 5827.5714 | 5826.5641 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">376</a> | 741.4618  | 5923.6364 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">377</a> | 6038.4185 | 6037.4112 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">378</a> | 6061.1975 | 6060.1902 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">379</a> | 763.8837  | 6103.0116 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">381</a> | 6202.3284 | 6201.3211 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">382</a> | 6328.3006 | 6327.2933 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">384</a> | 6399.7439 | 6398.7366 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">385</a> | 6533.2925 | 6532.2852 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">386</a> | 6650.8648 | 6649.8575 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">387</a> | 6655.1091 | 6654.1018 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">388</a> | 6749.2971 | 6748.2898 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">389</a> | 6840.4088 | 6839.4015 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">390</a> | 7002.9920 | 7001.9847 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">391</a> | 7816.7668 | 7815.7595 |           |         |   |     |   |  |  |  |
| <input checked="" type="checkbox"/> <a href="#">392</a> | 9045.7312 | 9044.7239 |           |         |   |     |   |  |  |  |

## Search Parameters

Type of search : MS/MS Ion Search  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance : ± 0.05 Da  
 Fragment Mass Tolerance : ± 0.05 Da  
 Max Missed Cleavages : 2  
 Instrument type : Default  
 Number of queries : 392

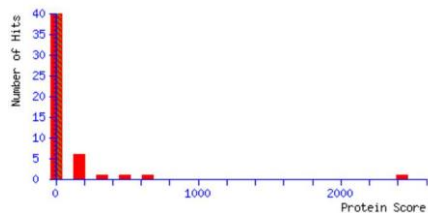
Mascot: <http://www.matrixscience.com/>

# MASCOT Search Results

**User** : Julian  
**Email** : julian.langer@mpibp-frankfurt.mpg.de  
**Search title** : Submitted from 140318 842 ChKrettl 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
**MS data file** : D:\Data\140318\140318 842 ChReinhard 6\_Tray01-D2\_01\_17687.d\140314 842 ChReinhard 6\_Tray01-D2\_01\_17687.mgf  
**Database** : SwissProt 57.15 (515203 sequences; 181334896 residues)  
**Timestamp** : 19 Mar 2014 at 09:51:01 GMT  
**Protein hits** : [A2MG HUMAN](#) Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2  
[TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[CFAH HUMAN](#) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
[K1C10 HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
[K1C14 HUMAN](#) Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4  
[K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[F13B HUMAN](#) Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[ALBU FELCA](#) Serum albumin OS=Felis catus GN=ALB PE=1 SV=1  
[F13A HUMAN](#) Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4

## Mascot Score Histogram

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
 Individual ions scores > 38 indicate identity or extensive homology ( $p < 0.05$ ).  
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



## Peptide Summary Report

Format As  Peptide Summary [Help](#)  
 Significance threshold  $p < 0.05$  Max. number of hits AUTO  
 Standard scoring  MudPIT scoring  Ions score or expect cut-off 0 Show sub-sets 0  
 Show pop-ups  Suppress pop-ups  Sort unassigned Decreasing Score Require bold red   
    Error tolerant

1. [A2MG HUMAN](#) Mass: 164614 Score: 2428 Matches: 108(78) Sequences: 50(37) emPAI: 1.98  
 Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

| Query                                   | Observed | Mr (expt) | Mr (calc) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide                           |
|---|----------|-----------|-----------|---------|------|-------|----------|------|--------|-----------------------------------|
| <input checked="" type="checkbox"/> 86  | 593.3675 | 592.3602  | 592.3584  | 0.0018  | 0    | 33    | 0.21     | 1    | U      | K.LSFVK.V                         |
| <input checked="" type="checkbox"/> 87  | 593.3682 | 592.3609  | 592.3584  | 0.0024  | 0    | (32)  | 0.26     | 1    | U      | K.LSFVK.V                         |
| <input checked="" type="checkbox"/> 100 | 634.3947 | 633.3875  | 633.3850  | 0.0025  | 0    | 23    | 4.1      | 4    | U      | K.VFQLK.R                         |
| <input checked="" type="checkbox"/> 102 | 647.4263 | 646.4190  | 646.4166  | 0.0024  | 0    | 30    | 0.36     | 1    | U      | K.VIFIR.G                         |
| <input checked="" type="checkbox"/> 120 | 724.4377 | 723.4304  | 723.4279  | 0.0025  | 0    | 23    | 1.3      | 1    | U      | K.GVPIPNK.V                       |
| <input checked="" type="checkbox"/> 145 | 414.7332 | 827.4518  | 827.4501  | 0.0017  | 0    | (62)  | 0.00039  | 1    | U      | K.SDIAPVAR.L                      |
| <input checked="" type="checkbox"/> 146 | 414.7337 | 827.4528  | 827.4501  | 0.0027  | 0    | (62)  | 0.0004   | 1    | U      | K.SDIAPVAR.L                      |
| <input checked="" type="checkbox"/> 147 | 414.7337 | 827.4529  | 827.4501  | 0.0028  | 0    | 63    | 0.00038  | 1    | U      | K.SDIAPVAR.L                      |
| <input checked="" type="checkbox"/> 148 | 414.7339 | 827.4533  | 827.4501  | 0.0032  | 0    | (50)  | 0.0064   | 1    | U      | K.SDIAPVAR.L                      |
| <input checked="" type="checkbox"/> 149 | 414.7340 | 827.4534  | 827.4501  | 0.0033  | 0    | (62)  | 0.00039  | 1    | U      | K.SDIAPVAR.L                      |
| <input checked="" type="checkbox"/> 156 | 438.7471 | 875.4795  | 875.4752  | 0.0043  | 0    | 18    | 15       | 1    | U      | K.YNLLPEK.E                       |
| <input checked="" type="checkbox"/> 157 | 442.2855 | 882.5565  | 882.5538  | 0.0027  | 0    | (31)  | 0.21     | 1    | U      | R.DLKPAAVK.V                      |
| <input checked="" type="checkbox"/> 158 | 442.2860 | 882.5575  | 882.5538  | 0.0036  | 0    | 42    | 0.018    | 1    | U      | R.DLKPAAVK.V                      |
| <input checked="" type="checkbox"/> 168 | 463.2781 | 924.5417  | 924.5393  | 0.0025  | 0    | 33    | 0.18     | 1    | U      | R.TGTHGLLVK.Q                     |
| <input checked="" type="checkbox"/> 174 | 509.8019 | 1017.5892 | 1017.5859 | 0.0034  | 0    | (46)  | 0.014    | 1    | U      | K.ATVNLNLPK.C                     |
| <input checked="" type="checkbox"/> 175 | 509.8023 | 1017.5901 | 1017.5859 | 0.0043  | 0    | (43)  | 0.033    | 1    | U      | K.ATVNLNLPK.C                     |
| <input checked="" type="checkbox"/> 176 | 509.8027 | 1017.5909 | 1017.5859 | 0.0050  | 0    | 51    | 0.0051   | 1    | U      | K.ATVNLNLPK.C                     |
| <input checked="" type="checkbox"/> 184 | 523.7994 | 1045.5843 | 1045.5808 | 0.0035  | 0    | (46)  | 0.021    | 1    | U      | K.FEVQVTPK.I                      |
| <input checked="" type="checkbox"/> 185 | 523.7998 | 1045.5851 | 1045.5808 | 0.0043  | 0    | 46    | 0.02     | 1    | U      | K.FEVQVTPK.I                      |
| <input checked="" type="checkbox"/> 191 | 542.8138 | 1083.6131 | 1083.6077 | 0.0054  | 0    | 35    | 0.16     | 1    | U      | K.GHFSISIPVK.S                    |
| <input checked="" type="checkbox"/> 192 | 542.8139 | 1083.6132 | 1083.6077 | 0.0055  | 0    | (35)  | 0.16     | 1    | U      | K.GHFSISIPVK.S                    |
| <input checked="" type="checkbox"/> 199 | 552.3076 | 1102.6006 | 1102.5982 | 0.0024  | 0    | (61)  | 0.00064  | 1    | U      | R.SSGSLLNNAIK.G                   |
| <input checked="" type="checkbox"/> 200 | 552.3081 | 1102.6016 | 1102.5982 | 0.0034  | 0    | 63    | 0.00041  | 1    | U      | R.SSGSLLNNAIK.G                   |
| <input checked="" type="checkbox"/> 203 | 558.8072 | 1115.5999 | 1115.5975 | 0.0024  | 0    | 77    | 1.6e-005 | 1    | U      | R.QTVSWAVTEK.S                    |
| <input checked="" type="checkbox"/> 204 | 558.8081 | 1115.6016 | 1115.5975 | 0.0040  | 0    | (64)  | 0.00032  | 1    | U      | R.QTVSWAVTEK.S                    |
| <input checked="" type="checkbox"/> 207 | 560.8234 | 1119.6323 | 1119.6288 | 0.0035  | 0    | 18    | 11       | 1    | U      | K.SIYKPGQTVK.F                    |
| <input checked="" type="checkbox"/> 211 | 567.7968 | 1133.5790 | 1133.5750 | 0.0040  | 0    | (56)  | 0.002    | 1    | U      | R.SASNMAIVDVK.M                   |
| <input checked="" type="checkbox"/> 212 | 567.8010 | 1133.5874 | 1133.5750 | 0.0123  | 0    | (23)  | 4.3      | 1    | U      | R.SASNMAIVDVK.M                   |
| <input checked="" type="checkbox"/> 213 | 574.8164 | 1147.6183 | 1147.6138 | 0.0044  | 0    | (34)  | 0.3      | 1    | U      | R.QGIPFFGQVR.L                    |
| <input checked="" type="checkbox"/> 214 | 574.8166 | 1147.6187 | 1147.6138 | 0.0049  | 0    | 48    | 0.014    | 1    | U      | R.QGIPFFGQVR.L                    |
| <input checked="" type="checkbox"/> 217 | 575.7932 | 1149.5719 | 1149.5700 | 0.0019  | 0    | (66)  | 0.00016  | 1    | U      | R.SASNMAIVDVK.M + Oxidation (M)   |
| <input checked="" type="checkbox"/> 218 | 575.7933 | 1149.5720 | 1149.5700 | 0.0020  | 0    | (64)  | 0.0003   | 1    | U      | R.SASNMAIVDVK.M + Oxidation (M)   |
| <input checked="" type="checkbox"/> 219 | 575.7940 | 1149.5734 | 1149.5700 | 0.0035  | 0    | 80    | 6.3e-006 | 1    | U      | R.SASNMAIVDVK.M + Oxidation (M)   |
| <input checked="" type="checkbox"/> 229 | 605.8271 | 1209.6396 | 1209.6353 | 0.0043  | 0    | (44)  | 0.022    | 1    | U      | K.LPPNVVEESAR.A                   |
| <input checked="" type="checkbox"/> 230 | 605.8280 | 1209.6414 | 1209.6353 | 0.0061  | 0    | 67    | 0.00012  | 1    | U      | K.LPPNVVEESAR.A                   |
| <input checked="" type="checkbox"/> 232 | 613.2820 | 1224.5494 | 1224.5445 | 0.0049  | 0    | 50    | 0.022    | 1    | U      | K.YDVNCLANK.V                     |
| <input checked="" type="checkbox"/> 241 | 628.3274 | 1254.6403 | 1254.6357 | 0.0046  | 0    | 65    | 0.00015  | 1    | U      | K.AIGYLNITGVR.Q                   |
| <input checked="" type="checkbox"/> 242 | 630.2919 | 1258.5693 | 1258.5652 | 0.0040  | 0    | 79    | 3.1e-006 | 1    | U      | R.VGFYSDVMGR.G                    |
| <input checked="" type="checkbox"/> 243 | 630.2923 | 1258.5701 | 1258.5652 | 0.0049  | 0    | (79)  | 3.3e-006 | 1    | U      | R.VGFYSDVMGR.G                    |
| <input checked="" type="checkbox"/> 247 | 636.8419 | 1271.6692 | 1271.6656 | 0.0036  | 0    | 67    | 0.00014  | 1    | U      | R.VTAAPQSVCAALR.A                 |
| <input checked="" type="checkbox"/> 248 | 636.8429 | 1271.6711 | 1271.6656 | 0.0055  | 0    | (65)  | 0.00022  | 1    | U      | R.VTAAPQSVCAALR.A                 |
| <input checked="" type="checkbox"/> 249 | 638.2889 | 1274.5632 | 1274.5602 | 0.0031  | 0    | (55)  | 0.00058  | 1    | U      | R.VGFYSDVMGR.G + Oxidation (M)    |
| <input checked="" type="checkbox"/> 250 | 638.2891 | 1274.5636 | 1274.5602 | 0.0035  | 0    | (75)  | 5.4e-006 | 1    | U      | R.VGFYSDVMGR.G + Oxidation (M)    |
| <input checked="" type="checkbox"/> 251 | 638.2893 | 1274.5641 | 1274.5602 | 0.0040  | 0    | (56)  | 0.00049  | 1    | U      | R.VGFYSDVMGR.G + Oxidation (M)    |
| <input checked="" type="checkbox"/> 261 | 669.8318 | 1337.6490 | 1337.6438 | 0.0053  | 0    | 56    | 0.0013   | 1    | U      | R.NALFCLSAWK.T                    |
| <input checked="" type="checkbox"/> 272 | 697.8468 | 1393.6791 | 1393.6725 | 0.0066  | 0    | 61    | 0.00042  | 1    | U      | K.NEDSLVVFQTDK.S                  |
| <input checked="" type="checkbox"/> 276 | 708.9170 | 1415.8195 | 1415.8210 | -0.0016 | 0    | (48)  | 0.0062   | 1    | U      | K.MVSGFIPLKPTVK.M                 |
| <input checked="" type="checkbox"/> 277 | 472.9471 | 1415.8195 | 1415.8210 | -0.0015 | 0    | (41)  | 0.029    | 1    | U      | K.MVSGFIPLKPTVK.M                 |
| <input checked="" type="checkbox"/> 278 | 709.8035 | 1417.5924 | 1417.5899 | 0.0026  | 0    | 36    | 0.018    | 1    | U      | K.HYDGSYSTFGR.Y                   |
| <input checked="" type="checkbox"/> 279 | 716.9181 | 1431.8216 | 1431.8160 | 0.0056  | 0    | 68    | 6.8e-005 | 1    | U      | K.MVSGFIPLKPTVK.M + Oxidation (M) |
| <input checked="" type="checkbox"/> 280 | 478.2812 | 1431.8216 | 1431.8160 | 0.0057  | 0    | (48)  | 0.0065   | 1    | U      | K.MVSGFIPLKPTVK.M + Oxidation (M) |
| <input checked="" type="checkbox"/> 284 | 724.8219 | 1447.6293 | 1447.6363 | -0.0070 | 0    | (45)  | 0.0039   | 1    | U      | K.DMYSFLEDMLK.A                   |
| <input checked="" type="checkbox"/> 285 | 724.8264 | 1447.6383 | 1447.6363 | 0.0020  | 0    | (48)  | 0.0028   | 1    | U      | K.DMYSFLEDMLK.A                   |
| <input checked="" type="checkbox"/> 286 | 724.8271 | 1447.6397 | 1447.6363 | 0.0034  | 0    | 66    | 3.8e-005 | 1    | U      | K.DMYSFLEDMLK.A                   |
| <input checked="" type="checkbox"/> 289 | 746.4066 | 1490.7987 | 1490.7882 | 0.0105  | 0    | 62    | 0.00043  | 1    | U      | R.NQGNITWLTAFVLLK.T               |
| <input checked="" type="checkbox"/> 291 | 756.3924 | 1510.7702 | 1510.7627 | 0.0075  | 0    | 45    | 0.015    | 1    | U      | K.AAQVTIQSSGFSSK.F                |
| <input checked="" type="checkbox"/> 293 | 515.9406 | 1544.7999 | 1544.7947 | 0.0052  | 0    | (41)  | 0.051    | 1    | U      | R.LVHVEEHTETVR.K                  |



|     |           |           |           |        |   |      |          |   |   |   |
|-----|-----------|-----------|-----------|--------|---|------|----------|---|---|---|
| 225 | 595.2715  | 1188.5285 | 1188.5234 | 0.0051 | 0 | 49   | 0.003    | 1 | U | K.LSYTCEGGFR.I                          |
| 239 | 621.7767  | 1241.5388 | 1241.5347 | 0.0041 | 0 | 28   | 0.25     | 1 | U | R.TGDEITYQCR.N                          |
| 240 | 623.3078  | 1244.6010 | 1244.5972 | 0.0038 | 0 | 64   | 0.00018  | 1 | U | K.CTSTGWIPAPR.C                         |
| 244 | 630.3283  | 1258.6421 | 1258.6380 | 0.0041 | 0 | 47   | 0.015    | 1 | U | R.WQSIPLCVK.I                           |
| 254 | 655.3075  | 1308.6004 | 1308.5955 | 0.0050 | 0 | 38   | 0.057    | 1 | U | K.SCDIPVFMNAR.T                         |
| 262 | 671.3550  | 1340.6954 | 1340.6936 | 0.0018 | 0 | (48) | 0.0091   | 1 | U | K.SPDVINGSPISQK.I                       |
| 263 | 671.3568  | 1340.6991 | 1340.6936 | 0.0055 | 0 | 56   | 0.0013   | 1 | U | K.SPDVINGSPISQK.I                       |
| 265 | 691.3430  | 1380.6715 | 1380.6707 | 0.0008 | 0 | 17   | 0.10     | 1 | U | R.EIMENYNIALR.W + Oxidation (M)         |
| 273 | 698.3990  | 1394.7834 | 1394.7769 | 0.0066 | 0 | 72   | 2.4e-005 | 1 | U | K.SSNLIIEHLK.N                          |
| 363 | 1010.9986 | 2019.9826 | 2019.9684 | 0.0142 | 0 | 51   | 0.003    | 1 | U | R.DTSCVNPPTVQNAIVSR.Q                   |
| 386 | 552.7683  | 2207.0440 | 2207.0429 | 0.0011 | 1 | (0)  | 2.5e+002 | 1 | U | K.IVSSAMEPDREYHFGQAVR.F + Oxidation (M) |
| 387 | 552.7707  | 2207.0538 | 2207.0429 | 0.0108 | 1 | 31   | 0.22     | 1 | U | K.IVSSAMEPDREYHFGQAVR.F + Oxidation (M) |

5. [K1C10 HUMAN](#) Mass: 59020 Score: 214 Matches: 16(11) Sequences: 8(4) emPAI: 0.26  
 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide          |
|-------|----------|-----------|-----------|--------|------|-------|----------|------|--------|------------------|
| 133   | 404.2046 | 806.3947  | 806.3923  | 0.0024 | 0    | (47)  | 0.018    | 1    |        | R.LAADDFR.L      |
| 134   | 404.2046 | 806.3947  | 806.3923  | 0.0024 | 0    | (50)  | 0.0081   | 1    |        | R.LAADDFR.L      |
| 135   | 404.2047 | 806.3948  | 806.3923  | 0.0026 | 0    | 53    | 0.0047   | 1    |        | R.LAADDFR.L      |
| 136   | 405.2248 | 808.4350  | 808.4330  | 0.0020 | 0    | (12)  | 0.47     | 2    |        | R.LASYLDK.V      |
| 137   | 405.2250 | 808.4354  | 808.4330  | 0.0023 | 0    | 35    | 0.22     | 1    |        | R.LASYLDK.V      |
| 177   | 516.3039 | 1030.5932 | 1030.5910 | 0.0022 | 0    | 19    | 7.9      | 1    |        | R.VLDELTLTK.A    |
| 193   | 545.7700 | 1089.5254 | 1089.5237 | 0.0017 | 0    | (55)  | 0.0021   | 1    |        | K.VTMQNLDNR.L    |
| 194   | 545.7701 | 1089.5256 | 1089.5237 | 0.0019 | 0    | (54)  | 0.0024   | 1    |        | K.VTMQNLDNR.L    |
| 195   | 545.7705 | 1089.5265 | 1089.5237 | 0.0028 | 0    | 71    | 4.8e-005 | 1    |        | K.VTMQNLDNR.L    |
| 196   | 545.7707 | 1089.5268 | 1089.5237 | 0.0031 | 0    | (55)  | 0.0021   | 1    |        | K.VTMQNLDNR.L    |
| 202   | 555.2499 | 1108.4852 | 1108.4825 | 0.0027 | 0    | 20    | 2        | 1    | U      | K.DAEAWFNEK.S    |
| 236   | 617.8460 | 1233.6775 | 1233.6717 | 0.0058 | 1    | (62)  | 0.00039  | 1    |        | R.LKYENEVALR.Q   |
| 237   | 617.8461 | 1233.6777 | 1233.6717 | 0.0060 | 1    | (44)  | 0.025    | 1    |        | R.LKYENEVALR.Q   |
| 238   | 617.8475 | 1233.6804 | 1233.6717 | 0.0087 | 1    | 77    | 1.2e-005 | 1    |        | R.LKYENEVALR.Q   |
| 246   | 631.8044 | 1261.5942 | 1261.5899 | 0.0043 | 0    | 50    | 0.0039   | 1    |        | R.SLLEGGSSGGGR.G |
| 281   | 478.9294 | 1433.7663 | 1433.7626 | 0.0036 | 1    | 13    | 32       | 1    | U      | K.IRLNEIQYTR.S   |

6. [K1C14 HUMAN](#) Mass: 51872 Score: 167 Matches: 10(8) Sequences: 4(3) emPAI: 0.21  
 Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide         |
|-------|----------|-----------|-----------|--------|------|-------|----------|------|--------|-----------------|
| 133   | 404.2046 | 806.3947  | 806.3923  | 0.0024 | 0    | (47)  | 0.018    | 1    |        | R.LAADDFR.T     |
| 134   | 404.2046 | 806.3947  | 806.3923  | 0.0024 | 0    | (50)  | 0.0081   | 1    |        | R.LAADDFR.T     |
| 135   | 404.2047 | 806.3948  | 806.3923  | 0.0026 | 0    | 53    | 0.0047   | 1    |        | R.LAADDFR.T     |
| 136   | 405.2248 | 808.4350  | 808.4330  | 0.0020 | 0    | (12)  | 0.47     | 2    |        | R.LASYLDK.V     |
| 137   | 405.2250 | 808.4354  | 808.4330  | 0.0023 | 0    | 35    | 0.22     | 1    |        | R.LASYLDK.V     |
| 193   | 545.7700 | 1089.5254 | 1089.5237 | 0.0017 | 0    | (55)  | 0.0021   | 1    |        | K.VTMQNLDNR.L   |
| 194   | 545.7701 | 1089.5256 | 1089.5237 | 0.0019 | 0    | (54)  | 0.0024   | 1    |        | K.VTMQNLDNR.L   |
| 195   | 545.7705 | 1089.5265 | 1089.5237 | 0.0028 | 0    | 71    | 4.8e-005 | 1    |        | K.VTMQNLDNR.L   |
| 196   | 545.7707 | 1089.5268 | 1089.5237 | 0.0031 | 0    | (55)  | 0.0021   | 1    |        | K.VTMQNLDNR.L   |
| 252   | 651.3353 | 1300.6560 | 1300.6510 | 0.0050 | 0    | 68    | 9.2e-005 | 1    |        | R.ALEENADLEVK.I |

Proteins matching the same set of peptides:

[K1C16 HUMAN](#) Mass: 51578 Score: 167 Matches: 10(8) Sequences: 4(3)  
 Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4

7. [K22E HUMAN](#) Mass: 65678 Score: 162 Matches: 6(5) Sequences: 4(3) emPAI: 0.17  
 Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide           |
|-------|----------|-----------|-----------|---------|------|-------|----------|------|--------|-------------------|
| 144   | 414.2184 | 826.4222  | 826.4225  | -0.0003 | 0    | 14    | 21       | 3    |        | K.FASFIDK.V       |
| 201   | 554.2762 | 1106.5379 | 1106.5356 | 0.0023  | 0    | 45    | 0.023    | 1    |        | R.AQYEIQAQR.S     |
| 258   | 665.3691 | 1328.7237 | 1328.7187 | 0.0050  | 0    | (44)  | 0.029    | 1    |        | R.NLGLDLSIIAEVK.A |
| 259   | 665.3692 | 1328.7238 | 1328.7187 | 0.0050  | 0    | 64    | 0.00026  | 1    |        | R.NLGLDLSIIAEVK.A |
| 287   | 738.3929 | 1474.7712 | 1474.7780 | -0.0067 | 0    | (72)  | 4.4e-005 | 1    |        | R.FLEQQNQLVQTK.W  |
| 288   | 738.3988 | 1474.7831 | 1474.7780 | 0.0051  | 0    | 92    | 4.2e-007 | 1    |        | R.FLEQQNQLVQTK.W  |

8. [F13B HUMAN](#) Mass: 77742 Score: 140 Matches: 8(4) Sequences: 6(2) emPAI: 0.19  
 Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide                    |
|-------|----------|-----------|-----------|--------|------|-------|----------|------|--------|----------------------------|
| 226   | 598.8054 | 1195.5963 | 1195.5913 | 0.0049 | 0    | 63    | 0.00027  | 1    | U      | R.IAQYIYFFK.S              |
| 274   | 468.8771 | 1403.6096 | 1403.6041 | 0.0055 | 0    | 28    | 0.18     | 1    | U      | R.CFDHFFLEGR.E             |
| 275   | 708.3753 | 1414.7360 | 1414.7279 | 0.0081 | 0    | 29    | 0.87     | 1    | U      | K.VLHGDLIDFVCK.Q           |
| 319   | 848.9168 | 1695.8190 | 1695.8138 | 0.0052 | 0    | 4     | 1.6e+002 | 1    | U      | K.CTKPDLNNGYISDVK.L        |
| 367   | 695.0040 | 2081.9903 | 2081.9840 | 0.0063 | 0    | (50)  | 0.0033   | 1    | U      | K.VACEEPPFIENGAANLHSK.I    |
| 368   | 695.0051 | 2081.9934 | 2081.9840 | 0.0094 | 0    | (40)  | 0.028    | 1    | U      | K.VACEEPPFIENGAANLHSK.I    |
| 369   | 695.0051 | 2081.9935 | 2081.9840 | 0.0095 | 0    | 57    | 0.00066  | 1    | U      | K.VACEEPPFIENGAANLHSK.I    |
| 438   | 899.7417 | 2696.2034 | 2696.1807 | 0.0227 | 1    | 20    | 0.77     | 1    | U      | K.TTGGKDEEVVQLSDGWSQPTCR.K |

9. [K1C9 HUMAN](#) Mass: 62255 Score: 136 Matches: 9(4) Sequences: 6(4) emPAI: 0.31  
 Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
 Check to include this hit in error tolerant search or archive report

| Query | Observed  | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect  | Rank | Unique | Peptide                           |
|-------|-----------|-----------|-----------|--------|------|-------|---------|------|--------|-----------------------------------|
| 136   | 405.2248  | 808.4350  | 808.4330  | 0.0020 | 0    | (12)  | 0.47    | 2    |        | R.LASYLDK.V                       |
| 137   | 405.2250  | 808.4354  | 808.4330  | 0.0023 | 0    | 35    | 0.22    | 1    |        | R.LASYLDK.V                       |
| 186   | 530.7868  | 1059.5590 | 1059.5560 | 0.0030 | 0    | 68    | 0.00013 | 1    | U      | K.TLLDIDNTR.M                     |
| 208   | 561.2975  | 1120.5805 | 1120.5764 | 0.0041 | 0    | (12)  | 0.47    | 1    | U      | R.QEYEQLIAR.N                     |
| 209   | 561.2977  | 1120.5808 | 1120.5764 | 0.0044 | 0    | 42    | 0.048   | 1    | U      | R.QEYEQLIAR.N                     |
| 342   | 613.3300  | 1836.9682 | 1836.9581 | 0.0101 | 0    | 32    | 0.27    | 1    | U      | R.HGVQLEIIEIQLSK.K                |
| 430   | 837.3877  | 2509.1413 | 2509.1245 | 0.0168 | 0    | 49    | 0.0014  | 1    | U      | K.EIETYNHLEGGQEDFESSGAGK.I        |
| 463   | 1088.8475 | 3263.5206 | 3263.5066 | 0.0141 | 0    | 43    | 0.0068  | 1    | U      | K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E |
| 464   | 1088.8481 | 3263.5224 | 3263.5066 | 0.0158 | 0    | (31)  | 0.092   | 1    | U      | K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E |

10. [ALBU FELCA](#) Mass: 70611 Score: 117 Matches: 3(3) Sequences: 2(2) emPAI: 0.10  
 Serum albumin OS=Felis catus GN=ALB PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect  | Rank | Unique | Peptide        |
|-------|----------|-----------|-----------|--------|------|-------|---------|------|--------|----------------|
| 215   | 575.3127 | 1148.6108 | 1148.6077 | 0.0031 | 0    | 64    | 0.00028 | 1    | U      | K.LVNEVTEFAK.G |



|                                     |                     |          |          |
|-------------------------------------|---------------------|----------|----------|
| <input checked="" type="checkbox"/> | <a href="#">17</a>  | 433.3536 | 432.3463 |
| <input checked="" type="checkbox"/> | <a href="#">18</a>  | 433.3537 | 432.3464 |
| <input checked="" type="checkbox"/> | <a href="#">19</a>  | 435.2728 | 434.2655 |
| <input checked="" type="checkbox"/> | <a href="#">20</a>  | 442.3377 | 441.3304 |
| <input checked="" type="checkbox"/> | <a href="#">21</a>  | 444.1167 | 443.1094 |
| <input checked="" type="checkbox"/> | <a href="#">22</a>  | 444.1176 | 443.1103 |
| <input checked="" type="checkbox"/> | <a href="#">23</a>  | 444.1191 | 443.1119 |
| <input checked="" type="checkbox"/> | <a href="#">24</a>  | 456.2813 | 455.2741 |
| <input checked="" type="checkbox"/> | <a href="#">25</a>  | 458.9448 | 457.9376 |
| <input checked="" type="checkbox"/> | <a href="#">26</a>  | 458.9449 | 457.9376 |
| <input checked="" type="checkbox"/> | <a href="#">27</a>  | 459.2812 | 458.2739 |
| <input checked="" type="checkbox"/> | <a href="#">28</a>  | 459.2820 | 458.2748 |
| <input checked="" type="checkbox"/> | <a href="#">29</a>  | 476.3074 | 475.3002 |
| <input checked="" type="checkbox"/> | <a href="#">30</a>  | 476.3082 | 475.3009 |
| <input checked="" type="checkbox"/> | <a href="#">31</a>  | 476.3084 | 475.3011 |
| <input checked="" type="checkbox"/> | <a href="#">32</a>  | 476.3087 | 475.3014 |
| <input checked="" type="checkbox"/> | <a href="#">33</a>  | 478.3145 | 477.3073 |
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| <input checked="" type="checkbox"/> | <a href="#">35</a>  | 500.3075 | 499.3002 |
| <input checked="" type="checkbox"/> | <a href="#">36</a>  | 500.3725 | 499.3652 |
| <input checked="" type="checkbox"/> | <a href="#">37</a>  | 504.3030 | 503.2957 |
| <input checked="" type="checkbox"/> | <a href="#">38</a>  | 518.2830 | 517.2757 |
| <input checked="" type="checkbox"/> | <a href="#">39</a>  | 520.3342 | 519.3270 |
| <input checked="" type="checkbox"/> | <a href="#">40</a>  | 520.3347 | 519.3275 |
| <input checked="" type="checkbox"/> | <a href="#">41</a>  | 520.3348 | 519.3275 |
| <input checked="" type="checkbox"/> | <a href="#">42</a>  | 525.3216 | 524.3143 |
| <input checked="" type="checkbox"/> | <a href="#">43</a>  | 528.3648 | 527.3576 |
| <input checked="" type="checkbox"/> | <a href="#">44</a>  | 531.2788 | 530.2715 |
| <input checked="" type="checkbox"/> | <a href="#">45</a>  | 534.9819 | 533.9746 |
| <input checked="" type="checkbox"/> | <a href="#">46</a>  | 539.3373 | 538.3301 |
| <input checked="" type="checkbox"/> | <a href="#">47</a>  | 539.8208 | 538.8136 |
| <input checked="" type="checkbox"/> | <a href="#">49</a>  | 548.3295 | 547.3222 |
| <input checked="" type="checkbox"/> | <a href="#">50</a>  | 549.9541 | 548.9468 |
| <input checked="" type="checkbox"/> | <a href="#">51</a>  | 549.9555 | 548.9482 |
| <input checked="" type="checkbox"/> | <a href="#">52</a>  | 550.3436 | 549.3363 |
| <input checked="" type="checkbox"/> | <a href="#">53</a>  | 554.5514 | 553.5441 |
| <input checked="" type="checkbox"/> | <a href="#">54</a>  | 564.3609 | 563.3536 |
| <input checked="" type="checkbox"/> | <a href="#">55</a>  | 568.3423 | 567.3350 |
| <input checked="" type="checkbox"/> | <a href="#">56</a>  | 578.3406 | 577.3333 |
| <input checked="" type="checkbox"/> | <a href="#">57</a>  | 579.5336 | 578.5264 |
| <input checked="" type="checkbox"/> | <a href="#">58</a>  | 579.5345 | 578.5272 |
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| <input checked="" type="checkbox"/> | <a href="#">60</a>  | 579.5352 | 578.5280 |
| <input checked="" type="checkbox"/> | <a href="#">61</a>  | 579.5360 | 578.5287 |
| <input checked="" type="checkbox"/> | <a href="#">62</a>  | 579.5361 | 578.5288 |
| <input checked="" type="checkbox"/> | <a href="#">63</a>  | 579.5362 | 578.5289 |
| <input checked="" type="checkbox"/> | <a href="#">64</a>  | 579.5363 | 578.5290 |
| <input checked="" type="checkbox"/> | <a href="#">65</a>  | 579.5363 | 578.5290 |
| <input checked="" type="checkbox"/> | <a href="#">66</a>  | 579.5363 | 578.5290 |
| <input checked="" type="checkbox"/> | <a href="#">67</a>  | 579.5363 | 578.5290 |
| <input checked="" type="checkbox"/> | <a href="#">68</a>  | 579.5363 | 578.5290 |
| <input checked="" type="checkbox"/> | <a href="#">69</a>  | 579.5363 | 578.5291 |
| <input checked="" type="checkbox"/> | <a href="#">70</a>  | 579.5364 | 578.5291 |
| <input checked="" type="checkbox"/> | <a href="#">71</a>  | 579.5364 | 578.5292 |
| <input checked="" type="checkbox"/> | <a href="#">72</a>  | 579.5365 | 578.5292 |
| <input checked="" type="checkbox"/> | <a href="#">73</a>  | 579.5366 | 578.5293 |
| <input checked="" type="checkbox"/> | <a href="#">74</a>  | 579.5366 | 578.5293 |
| <input checked="" type="checkbox"/> | <a href="#">75</a>  | 579.5366 | 578.5294 |
| <input checked="" type="checkbox"/> | <a href="#">76</a>  | 579.5367 | 578.5294 |
| <input checked="" type="checkbox"/> | <a href="#">77</a>  | 579.5367 | 578.5294 |
| <input checked="" type="checkbox"/> | <a href="#">78</a>  | 579.5368 | 578.5295 |
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| <input checked="" type="checkbox"/> | <a href="#">80</a>  | 579.5370 | 578.5297 |
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| <input checked="" type="checkbox"/> | <a href="#">82</a>  | 579.5372 | 578.5299 |
| <input checked="" type="checkbox"/> | <a href="#">83</a>  | 579.5375 | 578.5302 |
| <input checked="" type="checkbox"/> | <a href="#">84</a>  | 580.5383 | 579.5310 |
| <input checked="" type="checkbox"/> | <a href="#">85</a>  | 586.4179 | 585.4106 |
| <input checked="" type="checkbox"/> | <a href="#">88</a>  | 594.3716 | 593.3643 |
| <input checked="" type="checkbox"/> | <a href="#">89</a>  | 608.3876 | 607.3803 |
| <input checked="" type="checkbox"/> | <a href="#">90</a>  | 608.3881 | 607.3809 |
| <input checked="" type="checkbox"/> | <a href="#">91</a>  | 614.5718 | 613.5646 |
| <input checked="" type="checkbox"/> | <a href="#">92</a>  | 615.4046 | 614.3973 |
| <input checked="" type="checkbox"/> | <a href="#">93</a>  | 615.4049 | 614.3977 |
| <input checked="" type="checkbox"/> | <a href="#">94</a>  | 615.4050 | 614.3977 |
| <input checked="" type="checkbox"/> | <a href="#">95</a>  | 617.4078 | 616.4005 |
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| <input checked="" type="checkbox"/> | <a href="#">98</a>  | 630.4424 | 629.4352 |
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| <input checked="" type="checkbox"/> | <a href="#">106</a> | 674.4692 | 673.4619 |
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| <input checked="" type="checkbox"/> | <a href="#">111</a> | 675.6782 | 674.6709 |
| <input checked="" type="checkbox"/> | <a href="#">112</a> | 676.4079 | 675.4007 |
| <input checked="" type="checkbox"/> | <a href="#">113</a> | 677.6846 | 676.6773 |
| <input checked="" type="checkbox"/> | <a href="#">114</a> | 691.3203 | 690.3130 |
| <input checked="" type="checkbox"/> | <a href="#">116</a> | 709.6426 | 708.6353 |

|                                     |                     |           |           |
|-------------------------------------|---------------------|-----------|-----------|
| <input checked="" type="checkbox"/> | <a href="#">117</a> | 717.6259  | 716.6186  |
| <input checked="" type="checkbox"/> | <a href="#">118</a> | 717.6270  | 716.6197  |
| <input checked="" type="checkbox"/> | <a href="#">121</a> | 739.6037  | 738.5965  |
| <input checked="" type="checkbox"/> | <a href="#">122</a> | 739.6040  | 738.5968  |
| <input checked="" type="checkbox"/> | <a href="#">123</a> | 739.6060  | 738.5987  |
| <input checked="" type="checkbox"/> | <a href="#">124</a> | 739.6078  | 738.6006  |
| <input checked="" type="checkbox"/> | <a href="#">125</a> | 739.6119  | 738.6046  |
| <input checked="" type="checkbox"/> | <a href="#">126</a> | 739.6159  | 738.6086  |
| <input checked="" type="checkbox"/> | <a href="#">127</a> | 740.4663  | 739.4590  |
| <input checked="" type="checkbox"/> | <a href="#">128</a> | 752.5484  | 751.5411  |
| <input checked="" type="checkbox"/> | <a href="#">129</a> | 752.5484  | 751.5412  |
| <input checked="" type="checkbox"/> | <a href="#">130</a> | 762.5230  | 761.5158  |
| <input checked="" type="checkbox"/> | <a href="#">131</a> | 402.3619  | 802.7093  |
| <input checked="" type="checkbox"/> | <a href="#">132</a> | 806.5498  | 805.5425  |
| <input checked="" type="checkbox"/> | <a href="#">138</a> | 407.7941  | 813.5737  |
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| <input checked="" type="checkbox"/> | <a href="#">141</a> | 408.7904  | 815.5663  |
| <input checked="" type="checkbox"/> | <a href="#">142</a> | 412.7550  | 823.4954  |
| <input checked="" type="checkbox"/> | <a href="#">143</a> | 412.7550  | 823.4955  |
| <input checked="" type="checkbox"/> | <a href="#">159</a> | 884.9651  | 883.9578  |
| <input checked="" type="checkbox"/> | <a href="#">160</a> | 444.1150  | 886.2154  |
| <input checked="" type="checkbox"/> | <a href="#">161</a> | 444.1153  | 886.2160  |
| <input checked="" type="checkbox"/> | <a href="#">162</a> | 450.3816  | 898.7487  |
| <input checked="" type="checkbox"/> | <a href="#">163</a> | 459.2792  | 916.5438  |
| <input checked="" type="checkbox"/> | <a href="#">164</a> | 463.1566  | 924.2987  |
| <input checked="" type="checkbox"/> | <a href="#">165</a> | 463.1575  | 924.3004  |
| <input checked="" type="checkbox"/> | <a href="#">169</a> | 467.1945  | 932.3744  |
| <input checked="" type="checkbox"/> | <a href="#">170</a> | 934.8824  | 933.8751  |
| <input checked="" type="checkbox"/> | <a href="#">171</a> | 934.8826  | 933.8753  |
| <input checked="" type="checkbox"/> | <a href="#">172</a> | 934.8829  | 933.8757  |
| <input checked="" type="checkbox"/> | <a href="#">179</a> | 523.7459  | 1045.4773 |
| <input checked="" type="checkbox"/> | <a href="#">180</a> | 523.7460  | 1045.4774 |
| <input checked="" type="checkbox"/> | <a href="#">181</a> | 523.7463  | 1045.4780 |
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| <input checked="" type="checkbox"/> | <a href="#">197</a> | 550.2262  | 1098.4378 |
| <input checked="" type="checkbox"/> | <a href="#">198</a> | 550.2577  | 1098.5009 |
| <input checked="" type="checkbox"/> | <a href="#">205</a> | 560.6762  | 1119.3379 |
| <input checked="" type="checkbox"/> | <a href="#">206</a> | 560.6774  | 1119.3402 |
| <input checked="" type="checkbox"/> | <a href="#">210</a> | 563.7871  | 1125.5597 |
| <input checked="" type="checkbox"/> | <a href="#">220</a> | 585.2675  | 1168.5205 |
| <input checked="" type="checkbox"/> | <a href="#">227</a> | 601.2743  | 1200.5339 |
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## Search Parameters

Type of search : MS/MS Ion Search  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance :  $\pm 0.05$  Da  
 Fragment Mass Tolerance :  $\pm 0.05$  Da  
 Max Missed Cleavages : 2  
 Instrument type : Default  
 Number of queries : 603

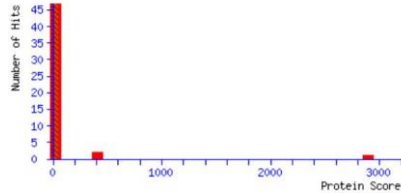
Mascot: <http://www.matrixscience.com/>

**(MATRIX) Mascot Search Results**  
**(SCIENCE)**

User : Julian  
 Email : julian.langer@mpibp-frankfurt.mpg.de  
 Search title : Submitted from 140318 842 ChKrettler 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
 MS data file : D:\Data\1403\140318\140314 842 ChReinhard 7\_Tray01-D3\_01\_17688.d\140314 842 ChReinhard 7\_Tray01-D3\_01\_17688.mgf  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Timestamp : 19 Mar 2014 at 09:51:38 GMT  
 Protein hits : [CFAH HUMAN](#) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
[TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[ALBU EQUAS](#) Serum albumin OS=Equus asinus GN=ALB PE=1 SV=1  
[IGHG1 HUMAN](#) Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1  
[A2MG HUMAN](#) Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2  
[RPNP HALMA](#) DNA-directed RNA polymerase subunit N OS=Haloarcula marismortui GN=rpoN PE=3 SV=1

**Mascot Score Histogram**

Ions score is  $-10 * \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 38 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



**Peptide Summary Report**

Format As Peptide Summary [Help](#)

Significance threshold p< 0.05 Max. number of hits AUTO

Standard scoring  MudPIT scoring  Ions score or expect cut-off 0 Show sub-sets 0

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

Select All Select None Search Selected Error tolerant Archive Report

1. [CFAH HUMAN](#) Mass: 143680 Score: 2892 Matches: 121 (92) Sequences: 47 (40) empAI: 2.75  
 Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

| Query                        | Observed | Mr(expt)  | Mr(calc)  | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide                         |
|------------------------------|----------|-----------|-----------|---------|------|-------|----------|------|--------|---------------------------------|
| <input type="checkbox"/> 112 | 463.2312 | 924.4479  | 924.4454  | 0.0025  | 0    | (37)  | 0.088    | 1    | U      | R.NGFYPATR.G                    |
| <input type="checkbox"/> 113 | 463.2312 | 924.4479  | 924.4454  | 0.0026  | 0    | 45    | 0.015    | 1    | U      | R.NGFYPATR.G                    |
| <input type="checkbox"/> 114 | 463.2314 | 924.4482  | 924.4454  | 0.0029  | 0    | (40)  | 0.045    | 1    | U      | R.NGFYPATR.G                    |
| <input type="checkbox"/> 115 | 463.2322 | 924.4498  | 924.4454  | 0.0045  | 0    | (43)  | 0.023    | 1    | U      | R.NGFYPATR.G                    |
| <input type="checkbox"/> 122 | 479.2287 | 956.4429  | 956.4392  | 0.0037  | 0    | 11    | 23       | 1    | U      | K.NDFYTFWK.L                    |
| <input type="checkbox"/> 134 | 532.3004 | 1062.5862 | 1062.5822 | 0.0040  | 0    | (56)  | 0.002    | 1    | U      | K.IDVHLVPR.K                    |
| <input type="checkbox"/> 135 | 532.3005 | 1062.5865 | 1062.5822 | 0.0043  | 0    | (53)  | 0.0036   | 1    | U      | K.IDVHLVPR.K                    |
| <input type="checkbox"/> 136 | 532.3009 | 1062.5872 | 1062.5822 | 0.0050  | 0    | 64    | 0.0003   | 1    | U      | K.IDVHLVPR.K                    |
| <input type="checkbox"/> 138 | 567.3293 | 1132.6440 | 1132.6393 | 0.0047  | 0    | 75    | 2.2e-005 | 1    | U      | R.RPYFFVAVGK.Y                  |
| <input type="checkbox"/> 139 | 567.3293 | 1132.6441 | 1132.6393 | 0.0048  | 0    | (71)  | 4.7e-005 | 1    | U      | R.RPYFFVAVGK.Y                  |
| <input type="checkbox"/> 140 | 567.3293 | 1132.6441 | 1132.6393 | 0.0048  | 0    | (69)  | 7.4e-005 | 1    | U      | R.RPYFFVAVGK.Y                  |
| <input type="checkbox"/> 141 | 574.8011 | 1147.5877 | 1147.5842 | 0.0035  | 0    | (47)  | 0.017    | 1    | U      | R.SLGNVIMVCR.K                  |
| <input type="checkbox"/> 142 | 574.8019 | 1147.5892 | 1147.5842 | 0.0039  | 0    | 64    | 0.00031  | 1    | U      | R.SLGNVIMVCR.K                  |
| <input type="checkbox"/> 144 | 578.2731 | 1154.5317 | 1154.5278 | 0.0039  | 0    | 73    | 1.6e-005 | 1    | U      | R.TGESVDFVCK.R                  |
| <input type="checkbox"/> 148 | 582.7984 | 1163.5893 | 1163.5791 | 0.0032  | 0    | (52)  | 0.0043   | 1    | U      | R.SLGNVIMVCR.K + Oxidation (M)  |
| <input type="checkbox"/> 149 | 582.7991 | 1163.5836 | 1163.5791 | 0.0045  | 0    | (50)  | 0.008    | 1    | U      | R.SLGNVIMVCR.K + Oxidation (M)  |
| <input type="checkbox"/> 150 | 593.3017 | 1184.5889 | 1184.5860 | 0.0029  | 0    | (38)  | 0.077    | 1    | U      | K.CLFVTPAPENCK.I                |
| <input type="checkbox"/> 151 | 593.3020 | 1184.5894 | 1184.5860 | 0.0034  | 0    | 42    | 0.032    | 1    | U      | K.CLFVTPAPENCK.I                |
| <input type="checkbox"/> 152 | 593.8008 | 1185.5870 | 1185.5819 | 0.0051  | 1    | 60    | 0.0006   | 1    | U      | R.TNDFYTFWK.L                   |
| <input type="checkbox"/> 153 | 593.8009 | 1185.5872 | 1185.5819 | 0.0053  | 1    | (57)  | 0.0011   | 1    | U      | R.TNDFYTFWK.L                   |
| <input type="checkbox"/> 154 | 595.2676 | 1188.5205 | 1188.5234 | -0.0028 | 0    | (40)  | 0.017    | 1    | U      | K.LSYTCGGFR.I                   |
| <input type="checkbox"/> 155 | 595.2711 | 1188.5276 | 1188.5234 | 0.0043  | 0    | 49    | 0.0027   | 1    | U      | K.LSYTCGGFR.I                   |
| <input type="checkbox"/> 156 | 595.2716 | 1188.5286 | 1188.5234 | 0.0052  | 0    | (47)  | 0.0045   | 1    | U      | K.LSYTCGGFR.I                   |
| <input type="checkbox"/> 157 | 595.2718 | 1188.5290 | 1188.5234 | 0.0057  | 0    | (43)  | 0.011    | 1    | U      | K.LSYTCGGFR.I                   |
| <input type="checkbox"/> 158 | 405.1907 | 1212.5503 | 1212.5458 | 0.0045  | 0    | 38    | 0.045    | 1    | U      | K.HGGLYHENMR.R                  |
| <input type="checkbox"/> 162 | 621.7763 | 1241.5381 | 1241.5347 | 0.0035  | 0    | (50)  | 0.0018   | 1    | U      | R.TGDEITYQCR.N                  |
| <input type="checkbox"/> 163 | 621.7764 | 1241.5383 | 1241.5347 | 0.0037  | 0    | 59    | 0.0002   | 1    | U      | R.TGDEITYQCR.N                  |
| <input type="checkbox"/> 164 | 621.7768 | 1241.5391 | 1241.5347 | 0.0044  | 0    | (52)  | 0.0011   | 1    | U      | R.TGDEITYQCR.N                  |
| <input type="checkbox"/> 165 | 623.3082 | 1244.6019 | 1244.5972 | 0.0047  | 0    | 65    | 0.00016  | 1    | U      | K.CTSTGWIAPR.C                  |
| <input type="checkbox"/> 166 | 623.3084 | 1244.6022 | 1244.5972 | 0.0050  | 0    | (64)  | 0.00018  | 1    | U      | K.CTSTGWIAPR.C                  |
| <input type="checkbox"/> 169 | 630.3288 | 1258.6430 | 1258.6380 | 0.0050  | 0    | 50    | 0.0071   | 1    | U      | R.WQSIFLPCVEK.I                 |
| <input type="checkbox"/> 170 | 630.3291 | 1258.6436 | 1258.6380 | 0.0056  | 0    | (42)  | 0.044    | 1    | U      | R.WQSIFLPCVEK.I                 |
| <input type="checkbox"/> 171 | 631.7977 | 1261.5808 | 1261.5761 | 0.0047  | 0    | (41)  | 0.027    | 1    | U      | K.DGWSAQPTCIK.S                 |
| <input type="checkbox"/> 172 | 631.7977 | 1261.5809 | 1261.5761 | 0.0048  | 0    | 46    | 0.0081   | 1    | U      | K.DGWSAQPTCIK.S                 |
| <input type="checkbox"/> 173 | 428.2491 | 1281.7254 | 1281.7193 | 0.0061  | 1    | (51)  | 0.0027   | 1    | U      | R.KGEWVALNPLR.K                 |
| <input type="checkbox"/> 174 | 641.8700 | 1281.7254 | 1281.7193 | 0.0061  | 1    | 80    | 3.3e-006 | 1    | U      | R.KGEWVALNPLR.K                 |
| <input type="checkbox"/> 175 | 428.2492 | 1281.7258 | 1281.7193 | 0.0064  | 1    | (50)  | 0.0038   | 1    | U      | R.KGEWVALNPLR.K                 |
| <input type="checkbox"/> 179 | 655.3067 | 1308.5988 | 1308.5955 | 0.0034  | 0    | 53    | 0.0014   | 1    | U      | K.SCDIPVFMNAR.T                 |
| <input type="checkbox"/> 185 | 663.3003 | 1324.5861 | 1324.5904 | -0.0042 | 0    | (22)  | 1.4      | 1    | U      | K.SCDIPVFMNAR.T + Oxidation (M) |
| <input type="checkbox"/> 186 | 663.3050 | 1324.5955 | 1324.5904 | 0.0051  | 0    | (39)  | 0.033    | 1    | U      | K.SCDIPVFMNAR.T + Oxidation (M) |
| <input type="checkbox"/> 188 | 671.3554 | 1340.6963 | 1340.6936 | 0.0027  | 0    | (76)  | 1.5e-005 | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 190 | 671.3558 | 1340.6971 | 1340.6936 | 0.0035  | 0    | (72)  | 3.5e-005 | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 191 | 671.3559 | 1340.6973 | 1340.6936 | 0.0037  | 0    | (75)  | 1.7e-005 | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 192 | 671.3562 | 1340.6979 | 1340.6936 | 0.0043  | 0    | (50)  | 0.0059   | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 193 | 671.3565 | 1340.6984 | 1340.6936 | 0.0049  | 0    | (55)  | 0.0018   | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 194 | 671.3567 | 1340.6988 | 1340.6936 | 0.0052  | 0    | (60)  | 0.00051  | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 195 | 671.3569 | 1340.6992 | 1340.6936 | 0.0056  | 0    | (58)  | 0.00087  | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 196 | 671.3569 | 1340.6993 | 1340.6936 | 0.0057  | 0    | 81    | 4e-006   | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 197 | 671.3572 | 1340.6999 | 1340.6936 | 0.0063  | 0    | (73)  | 3e-005   | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 198 | 671.3573 | 1340.6999 | 1340.6936 | 0.0064  | 0    | (57)  | 0.00096  | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 199 | 671.3574 | 1340.7003 | 1340.6936 | 0.0067  | 0    | (57)  | 0.001    | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 200 | 671.3577 | 1340.7009 | 1340.6936 | 0.0073  | 0    | (73)  | 2.9e-005 | 1    | U      | K.SPDVINGSPIQK.I                |
| <input type="checkbox"/> 205 | 683.3477 | 1364.6809 | 1364.6758 | 0.0051  | 0    | 76    | 1.4e-005 | 1    | U      | R.EIMENYNIALR.W                 |
| <input type="checkbox"/> 206 | 683.3482 | 1364.6818 | 1364.6758 | 0.0060  | 0    | (61)  | 0.00051  | 1    | U      | R.EIMENYNIALR.W                 |
| <input type="checkbox"/> 207 | 691.3453 | 1380.6760 | 1380.6707 | 0.0053  | 0    | (38)  | 0.082    | 1    | U      | R.EIMENYNIALR.W + Oxidation (M) |
| <input type="checkbox"/> 208 | 690.3904 | 1394.7822 | 1394.7769 | 0.0053  | 0    | 60    | 0.00045  | 1    | U      | K.SSNLILLEHLK.N                 |
| <input type="checkbox"/> 210 | 465.9347 | 1394.7836 | 1394.7769 | 0.0053  | 0    | (51)  | 0.0032   | 1    | U      | K.SSNLILLEHLK.N                 |
| <input type="checkbox"/> 211 | 698.3991 | 1394.7836 | 1394.7769 | 0.0068  | 0    | (60)  | 0.00045  | 1    | U      | K.SSNLILLEHLK.N                 |
| <input type="checkbox"/> 212 | 465.9352 | 1394.7837 | 1394.7769 | 0.0068  | 0    | (22)  | 2.4      | 1    | U      | K.SSNLILLEHLK.N                 |
| <input type="checkbox"/> 213 | 698.3992 | 1394.7838 | 1394.7769 | 0.0069  | 0    | (55)  | 0.0013   | 1    | U      | K.SSNLILLEHLK.N                 |
| <input type="checkbox"/> 215 | 470.9475 | 1409.8206 | 1409.8143 | 0.0063  | 2    | (35)  | 0.076    | 1    | U      | R.KGEWVALNPLR.C                 |
| <input type="checkbox"/> 216 | 470.9475 | 1409.8208 | 1409.8143 | 0.0065  | 2    | 36    | 0.061    | 1    | U      | R.KGEWVALNPLR.C                 |
| <input type="checkbox"/> 220 | 721.3568 | 1440.6990 | 1440.6932 | 0.0058  | 0    | (13)  | 19       | 1    | U      | K.EGWIHVPCINR.W                 |
| <input type="checkbox"/> 221 | 481.2403 | 1440.6990 | 1440.6932 | 0.0058  | 0    | (31)  | 0.36     | 1    | U      | K.EGWIHVPCINR.W                 |
| <input type="checkbox"/> 222 | 481.2406 | 1440.7000 | 1440.6932 | 0.0068  | 0    | 42    | 0.023    | 1    | U      | K.EGWIHVPCINR.W                 |
| <input type="checkbox"/> 223 | 721.3573 | 1440.7000 | 1440.6932 | 0.0068  | 0    | (36)  | 0.098    | 1    | U      | K.EGWIHVPCINR.W                 |
| <input type="checkbox"/> 228 | 741.3621 | 1480.7096 | 1480.7021 | 0.0075  | 0    | 93    | 2.5e-007 | 1    | U      | K.CPEGFIDGPAIAK.C               |



379 1088.8494 3263.5263 3263.5066 0.0198 0 1 96 1 U K.DIENQYETQITQIEHEVSSGGQEVQSSAK.E

6. ALBU EQUAS Mass: 70490 Score: 64 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Serum albumin OS=Equus asinus GN=ALB PE=1 SV=1

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

Query 143 Observed 575.3137 Mr(expt) 1148.6128 Mr(calc) 1148.6077 Delta Miss Score 0.0051 0 64 Expect Rank Unique 0.00029 1 U Peptide K.LVNEVTEFAK.K

Proteins matching the same set of peptides:

ALBU FELCA Mass: 70611 Score: 64 Matches: 1(1) Sequences: 1(1)
Serum albumin OS=Felis catus GN=ALB PE=1 SV=1
ALBU HORSE Mass: 70550 Score: 64 Matches: 1(1) Sequences: 1(1)
Serum albumin OS=Equus caballus GN=ALB PE=1 SV=1
ALBU MACFA Mass: 70825 Score: 64 Matches: 1(1) Sequences: 1(1)
Serum albumin OS=Macaca fascicularis GN=ALB PE=2 SV=1
ALBU MACMU Mass: 69832 Score: 64 Matches: 1(1) Sequences: 1(1)
Serum albumin (Fragment) OS=Macaca mulatta GN=ALB PE=2 SV=1
ALBU HUMAN Mass: 71317 Score: 64 Matches: 1(1) Sequences: 1(1)
Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2
ALBU PONAB Mass: 71317 Score: 64 Matches: 1(1) Sequences: 1(1)
Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=1

7. IGHG1 HUMAN Mass: 36596 Score: 46 Matches: 2(0) Sequences: 2(0)

Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1

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

Query 146 Observed 581.3185 Mr(expt) 1160.6225 Mr(calc) 1160.6223 Delta Miss Score 0.0002 0 39 Expect Rank Unique 0.11 1 U Peptide K.NQVSLTCLVK.G
266 937.4697 1872.9249 1872.9146 0.0104 0 7 87 1 U Peptide K.TTPPVLSDSGFFLYSK.L

8. A2MG HUMAN Mass: 164614 Score: 44 Matches: 2(1) Sequences: 2(1) emPAI: 0.02

Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2

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

Query 168 Observed 630.2925 Mr(expt) 1258.5705 Mr(calc) 1258.5652 Delta Miss Score 0.0053 0 3 Expect Rank Unique 1.2e+002 7 U Peptide R.VGFYSDVMGR.G
261 923.0259 1844.0373 1844.0295 0.0078 0 41 Expect Rank Unique 0.024 1 U Peptide R.LLIYALVPLTGVIGDSAK.Y

Proteins matching the same set of peptides:

A2MG PONAB Mass: 164585 Score: 44 Matches: 2(1) Sequences: 2(1)
Alpha-2-macroglobulin OS=Pongo abelii GN=A2M PE=2 SV=1

9. RPON HALMA Mass: 7954 Score: 42 Matches: 1(0) Sequences: 1(0)

DNA-directed RNA polymerase subunit N OS=Haloarcula marismortui GN=rpoN PE=3 SV=1

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

Query 125 Observed 515.3025 Mr(expt) 1028.5905 Mr(calc) 1028.5502 Delta Miss Score 0.0403 0 42 Expect Rank Unique 0.057 1 U Peptide K.VLDELGVRR.H

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

Table with 10 columns: Query, Observed, Mr(expt), Mr(calc), Delta Miss Score, Expect Rank Unique, Peptide. Lists various peptide sequences and their associated scores and ranks.

|                          |     |           |           |           |         |   |   |          |   |   |
|--------------------------|-----|-----------|-----------|-----------|---------|---|---|----------|---|---|
| <input type="checkbox"/> | 160 | 614.7927  | 1227.5708 | 1227.6095 | -0.0387 | 0 | 1 | 2.7e+002 | 1 | SGPVVIDALEAR  |
| <input type="checkbox"/> | 469 | 6330.0739 | 6329.0666 | 6329.0727 | -0.0061 | 2 | 1 | 22       | 1 | GMPLYAHIAELNLTAGVYSMPLPMMNININGGEHADNNVDIQEFMFIQVPGAKLKEAVR + 4 Oxidation (M) |
| <input type="checkbox"/> | 360 | 699.0611  | 2792.2154 | 2792.2244 | -0.0090 | 2 | 1 | 36       | 1 | TGCGMFEKGPQFYDDTCVVEPK  |
| <input type="checkbox"/> | 357 | 918.7784  | 2753.3133 | 2753.3384 | -0.0251 | 1 | 1 | 2e+002   | 1 | ALLTCDVWEHAYYIDYRNARPK  |
| <input type="checkbox"/> | 368 | 728.6078  | 2910.4021 | 2910.4002 | 0.0019  | 1 | 1 | 2.1e+002 | 1 | ATRNSPMALGTAQGDPEAGTRPGSDAGLR   |
| <input type="checkbox"/> | 377 | 802.4330  | 3205.7030 | 3205.6659 | 0.0371  | 0 | 0 | 1.5e+002 | 1 | VDGSVLPFFIAGGAIYGHSGALGEDVNIPELAK   |
| <input type="checkbox"/> | 375 | 1054.5092 | 3160.5057 | 3160.5023 | 0.0034  | 2 | 0 | 1.6e+002 | 1 | LEFTELTEVMKDVDFKVFSGPANSNDNR + Oxidation (M)                                  |
| <input type="checkbox"/> | 415 | 638.3202  | 4461.1907 | 4461.1911 | -0.0004 | 1 | 0 | 94       | 1 | MSQVIAIDQGTSSRAIIFDHDGNIYSTGLEHEQIFPK + Oxidation (M)                         |
| <input type="checkbox"/> | 408 | 1409.2648 | 4224.7724 | 4224.8160 | -0.0435 | 1 | 0 | 7.5      | 1 | QMDAGDYVQESIDILSDSDSGSLFERMQLAYSCKR + Oxidation (M)                           |
| <input type="checkbox"/> | 1   | 402.3579  | 401.3507  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 2   | 402.3585  | 401.3512  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 3   | 415.2116  | 414.2043  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 4   | 415.2125  | 414.2052  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 5   | 415.2143  | 414.2070  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 6   | 415.3426  | 414.3353  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 7   | 415.3440  | 414.3367  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 8   | 430.2454  | 429.2381  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 9   | 432.2389  | 431.2316  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 10  | 432.2396  | 431.2324  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 11  | 433.1820  | 432.1748  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 12  | 444.1166  | 443.1093  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 13  | 444.1172  | 443.1099  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 14  | 444.1188  | 443.1115  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 18  | 444.3478  | 443.3405  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 16  | 447.2940  | 446.2867  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 17  | 453.3454  | 452.3381  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 18  | 459.2814  | 458.2741  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 19  | 476.3080  | 475.3008  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 20  | 490.2883  | 489.2810  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 21  | 500.3069  | 499.2996  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 22  | 500.3078  | 499.3005  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 23  | 514.2343  | 513.2270  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 24  | 520.3344  | 519.3271  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 25  | 520.3350  | 519.3277  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 26  | 520.3370  | 519.3298  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 27  | 525.2902  | 524.2829  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 28  | 528.3630  | 527.3558  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 29  | 528.3654  | 527.3581  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 30  | 531.2759  | 530.2686  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 31  | 534.3143  | 533.3071  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 32  | 534.9821  | 533.9748  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 33  | 539.3339  | 538.3266  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 34  | 539.3364  | 538.3292  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 35  | 539.3371  | 538.3298  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 36  | 550.3491  | 549.3418  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 37  | 554.3103  | 553.3030  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 38  | 554.5518  | 553.5446  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 39  | 564.3611  | 563.3538  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 40  | 564.3612  | 563.3539  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 41  | 579.5359  | 578.5286  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 42  | 586.4175  | 585.4103  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 43  | 594.3699  | 593.3626  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 44  | 605.8036  | 604.7964  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 45  | 608.3871  | 607.3798  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 46  | 608.3872  | 607.3799  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 47  | 615.4051  | 614.3978  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 48  | 615.4054  | 614.3981  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 49  | 615.4055  | 614.3982  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 50  | 617.4071  | 616.3999  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 51  | 617.4085  | 616.4013  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 52  | 622.3666  | 621.3594  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 53  | 630.4438  | 629.4365  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 54  | 630.4448  | 629.4376  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 55  | 635.3870  | 634.3797  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 56  | 638.3899  | 637.3826  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 57  | 650.2071  | 649.1998  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 58  | 652.4144  | 651.4072  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 59  | 657.4451  | 656.4378  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 60  | 661.5572  | 660.5500  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 61  | 661.5627  | 660.5554  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 62  | 661.5634  | 660.5561  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 63  | 661.5688  | 660.5615  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 65  | 667.3980  | 666.3907  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 66  | 674.4709  | 673.4637  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 67  | 675.6759  | 674.6686  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 68  | 675.6763  | 674.6691  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 69  | 675.6772  | 674.6699  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 70  | 675.6772  | 674.6699  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 71  | 675.6773  | 674.6700  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 72  | 675.6779  | 674.6707  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 73  | 675.6804  | 674.6731  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 75  | 677.6845  | 676.6773  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 76  | 682.4243  | 681.4170  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 77  | 691.3439  | 690.3367  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 78  | 696.4402  | 695.4329  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 79  | 696.4407  | 695.4334  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 80  | 717.6228  | 716.6155  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 81  | 717.6242  | 716.6169  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 82  | 717.6261  | 716.6189  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 83  | 717.6263  | 716.6191  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 84  | 734.6520  | 733.6447  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 85  | 739.6048  | 738.5975  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 86  | 739.6055  | 738.5982  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 87  | 739.6061  | 738.5988  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 88  | 739.6067  | 738.5994  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 89  | 739.6087  | 738.6015  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 90  | 740.4659  | 739.4586  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 91  | 741.4703  | 740.4630  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 92  | 752.5464  | 751.5391  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 93  | 752.5497  | 751.5424  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 94  | 760.0343  | 759.0270  |           |         |   |   |          |   |   |
| <input type="checkbox"/> | 95  | 762.5239  | 761.5166  |           |         |   |   |          |   |   |

|                                     |     |           |           |
|-------------------------------------|-----|-----------|-----------|
| <input checked="" type="checkbox"/> | 97  | 806.5526  | 805.5453  |
| <input checked="" type="checkbox"/> | 106 | 433.3516  | 864.6886  |
| <input checked="" type="checkbox"/> | 107 | 433.3530  | 864.6915  |
| <input checked="" type="checkbox"/> | 111 | 883.8970  | 882.8897  |
| <input checked="" type="checkbox"/> | 118 | 934.8828  | 933.8755  |
| <input checked="" type="checkbox"/> | 119 | 935.8857  | 934.8785  |
| <input checked="" type="checkbox"/> | 121 | 476.3086  | 950.6026  |
| <input checked="" type="checkbox"/> | 124 | 489.8182  | 977.6218  |
| <input checked="" type="checkbox"/> |     | 613.3621  | 1224.7097 |
| <input checked="" type="checkbox"/> |     | 655.7161  | 1309.4177 |
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| <input checked="" type="checkbox"/> |     | 658.2556  | 1314.4966 |
| <input checked="" type="checkbox"/> |     | 442.3420  | 1324.0042 |
| <input checked="" type="checkbox"/> |     | 445.8876  | 1334.6409 |
| <input checked="" type="checkbox"/> |     | 674.7033  | 1347.3921 |
| <input checked="" type="checkbox"/> |     | 678.3213  | 1354.6280 |
| <input checked="" type="checkbox"/> |     | 682.2656  | 1362.5166 |
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| <input checked="" type="checkbox"/> |     | 709.8056  | 1417.5966 |
| <input checked="" type="checkbox"/> |     | 478.7073  | 1433.1001 |
| <input checked="" type="checkbox"/> |     | 721.1686  | 1440.3226 |
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| <input checked="" type="checkbox"/> |     | 817.3597  | 1632.7048 |
| <input checked="" type="checkbox"/> |     | 545.8757  | 1634.6053 |
| <input checked="" type="checkbox"/> |     | 551.8934  | 1652.6583 |
| <input checked="" type="checkbox"/> |     | 560.5936  | 1678.7590 |
| <input checked="" type="checkbox"/> |     | 564.3572  | 1690.0497 |
| <input checked="" type="checkbox"/> |     | 582.7990  | 1745.3751 |
| <input checked="" type="checkbox"/> |     | 608.3957  | 1822.1652 |
| <input checked="" type="checkbox"/> |     | 474.8363  | 1895.3160 |
| <input checked="" type="checkbox"/> |     | 640.9231  | 1919.7475 |
| <input checked="" type="checkbox"/> |     | 971.3777  | 1940.7408 |
| <input checked="" type="checkbox"/> |     | 500.3089  | 1997.2067 |
| <input checked="" type="checkbox"/> |     | 504.3019  | 2013.1786 |
| <input checked="" type="checkbox"/> |     | 677.9677  | 2030.8814 |
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| <input checked="" type="checkbox"/> |     | 412.1706  | 2055.8164 |
| <input checked="" type="checkbox"/> |     | 686.9829  | 2057.9269 |
| <input checked="" type="checkbox"/> |     | 687.9579  | 2060.8518 |
| <input checked="" type="checkbox"/> |     | 687.9582  | 2060.8529 |
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| <input checked="" type="checkbox"/> |     | 691.9720  | 2072.8941 |
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| <input checked="" type="checkbox"/> |     | 693.2885  | 2076.8436 |
| <input checked="" type="checkbox"/> |     | 520.3342  | 2077.3077 |
| <input checked="" type="checkbox"/> |     | 695.0068  | 2081.9987 |
| <input checked="" type="checkbox"/> |     | 719.6879  | 2156.0420 |
| <input checked="" type="checkbox"/> |     | 550.3446  | 2197.3493 |
| <input checked="" type="checkbox"/> |     | 735.2932  | 2202.8578 |
| <input checked="" type="checkbox"/> |     | 735.9890  | 2204.9451 |
| <input checked="" type="checkbox"/> |     | 740.4635  | 2218.3686 |
| <input checked="" type="checkbox"/> |     | 755.3482  | 2263.0228 |
| <input checked="" type="checkbox"/> |     | 755.3484  | 2263.0233 |
| <input checked="" type="checkbox"/> | 332 | 1142.0994 | 2282.1843 |
| <input checked="" type="checkbox"/> | 333 | 1142.0997 | 2282.1848 |
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| <input checked="" type="checkbox"/> |     | 696.4422  | 2781.7396 |
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| <input checked="" type="checkbox"/> |     | 412.1810  | 2878.2159 |
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| <input checked="" type="checkbox"/> |     | 741.5703  | 2962.2523 |
| <input checked="" type="checkbox"/> |     | 1004.9767 | 3011.9082 |
| <input checked="" type="checkbox"/> |     | 1004.9795 | 3011.9167 |
| <input checked="" type="checkbox"/> |     | 1042.0025 | 3122.9858 |
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| <input checked="" type="checkbox"/> |     | 414.7504  | 3309.9453 |
| <input checked="" type="checkbox"/> |     | 666.3902  | 3326.9145 |
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| <input checked="" type="checkbox"/> |     | 4111.6179 | 4110.6106 |
| <input checked="" type="checkbox"/> |     | 4143.3320 | 4142.3247 |
| <input checked="" type="checkbox"/> | 410 | 1409.2663 | 4224.7770 |

|   |           |           |
|---|-----------|-----------|
| <a href="#">411</a>                                     | 718.4968  | 4304.9370 |
| <input checked="" type="checkbox"/> <a href="#">412</a> | 544.3281  | 4346.5668 |
| <input checked="" type="checkbox"/> <a href="#">413</a> | 732.8679  | 4391.1636 |
| <input checked="" type="checkbox"/> <a href="#">416</a> | 641.9061  | 4486.2918 |
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| <input checked="" type="checkbox"/> <a href="#">418</a> | 650.1907  | 4544.2840 |
| <input checked="" type="checkbox"/> <a href="#">419</a> | 4552.6804 | 4551.6731 |
| <input checked="" type="checkbox"/> <a href="#">420</a> | 4552.8576 | 4551.8503 |
| <input checked="" type="checkbox"/> <a href="#">423</a> | 763.8979  | 4577.3437 |
| <input checked="" type="checkbox"/> <a href="#">424</a> | 658.2142  | 4600.4483 |
| <input checked="" type="checkbox"/> <a href="#">425</a> | 578.3454  | 4618.7049 |
| <input checked="" type="checkbox"/> <a href="#">429</a> | 4718.6962 | 4717.6889 |
| <input checked="" type="checkbox"/> <a href="#">430</a> | 4747.6071 | 4746.5998 |
| <input checked="" type="checkbox"/> <a href="#">431</a> | 608.3615  | 4858.8336 |
| <input checked="" type="checkbox"/> <a href="#">432</a> | 696.4430  | 4868.0501 |
| <input checked="" type="checkbox"/> <a href="#">433</a> | 614.5874  | 4908.6413 |
| <input checked="" type="checkbox"/> <a href="#">434</a> | 827.8764  | 4961.2145 |
| <input checked="" type="checkbox"/> <a href="#">435</a> | 4989.1836 | 4988.1763 |
| <input checked="" type="checkbox"/> <a href="#">437</a> | 639.3512  | 5106.7512 |
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| <input checked="" type="checkbox"/> <a href="#">454</a> | 943.0356  | 5652.1702 |
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| <input checked="" type="checkbox"/> <a href="#">456</a> | 5690.8136 | 5689.8063 |
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| <input checked="" type="checkbox"/> <a href="#">458</a> | 5738.0775 | 5737.0702 |
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| <input checked="" type="checkbox"/> <a href="#">466</a> | 6137.7248 | 6136.7175 |
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| <input checked="" type="checkbox"/> <a href="#">472</a> | 6419.8620 | 6418.8547 |
| <input checked="" type="checkbox"/> <a href="#">473</a> | 6492.0167 | 6491.0094 |
| <input checked="" type="checkbox"/> <a href="#">474</a> | 6529.9144 | 6528.9071 |
| <input checked="" type="checkbox"/> <a href="#">475</a> | 817.3341  | 6530.6144 |
| <input checked="" type="checkbox"/> <a href="#">476</a> | 942.5169  | 6590.5676 |
| <input checked="" type="checkbox"/> <a href="#">477</a> | 827.3401  | 6610.6627 |
| <input checked="" type="checkbox"/> <a href="#">478</a> | 6614.4295 | 6613.4222 |
| <input checked="" type="checkbox"/> <a href="#">479</a> | 6668.8001 | 6667.7928 |
| <input checked="" type="checkbox"/> <a href="#">480</a> | 6855.7952 | 6854.7879 |
| <input checked="" type="checkbox"/> <a href="#">481</a> | 6891.6955 | 6890.6882 |
| <input checked="" type="checkbox"/> <a href="#">482</a> | 6900.3039 | 6899.2966 |
| <input checked="" type="checkbox"/> <a href="#">483</a> | 7036.0719 | 7035.0646 |
| <input checked="" type="checkbox"/> <a href="#">484</a> | 7089.7764 | 7088.7691 |
| <input checked="" type="checkbox"/> <a href="#">487</a> | 7284.5022 | 7283.4949 |
| <input checked="" type="checkbox"/> <a href="#">488</a> | 923.5312  | 7380.1915 |
| <input checked="" type="checkbox"/> <a href="#">489</a> | 7408.1019 | 7407.0946 |
| <input checked="" type="checkbox"/> <a href="#">490</a> | 9220.1483 | 9219.1410 |

## Search Parameters

Type of search : MS/MS Ion Search  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance : ± 0.05 Da  
 Fragment Mass Tolerance : ± 0.05 Da  
 Max Missed Cleavages : 2  
 Instrument type : Default  
 Number of queries : 490

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

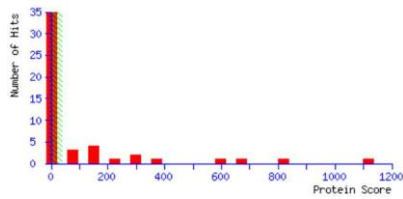


**(MATRIX) Mascot Search Results**  
**(SCIENCE)**

User : Julian  
 Email : julian.langer@mpibp-frankfurt.mpg.de  
 Search title : Submitted from 140318 842 ChKrettler 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
 MS data file : D:\Data\1403\140318\140314 842 ChReinhard 8\_Tray01-D4\_01\_17689.d\140314 842 ChReinhard 8\_Tray01-D4\_01\_17689.mgf  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Timestamp : 19 Mar 2014 at 09:52:08 GMT  
 Protein hits : [CFAH HUMAN](#) Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
               [TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1  
               [K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
               [K1C10 HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
               [K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
               [K2C1 RAT](#) Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1  
               [K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
               [ALBU HUMAN](#) Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
               [K2C6B HUMAN](#) Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5  
               [IGHG1 HUMAN](#) Ig gamma-1 chain C region OS=Homo sapiens GN=IGH1 PE=1 SV=1  
               [A2MG HUMAN](#) Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2  
               [K1C14 HUMAN](#) Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4  
               [F13B HUMAN](#) Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
               [F13A HUMAN](#) Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
               [CO4A HUMAN](#) Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1

**Mascot Score Histogram**

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 38 indicate identity or extensive homology (p<0.05). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



**Peptide Summary Report**

Format As  Peptide Summary  [Help](#)

Significance threshold p<0.05      Max. number of hits AUTO

Standard scoring  MudPIT scoring  Ions score or expect cut-off 0      Show sub-sets 0

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

Select All  Select None  Search Selected  Error tolerant  Archive Report

1. [CFAH HUMAN](#)    Mass: 143680    Score: 1117    Matches: 53(35)    Sequences: 32(24)    emPAI: 0.98  
 Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

| Query                        | Observed  | Mr (expt) | Mr (calc) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide                                     |
|------------------------------|-----------|-----------|-----------|---------|------|-------|----------|------|--------|---|
| <input type="checkbox"/> 132 | 463.2317  | 924.4488  | 924.4454  | 0.0035  | 0    | (33)  | 0.25     | 1    | U      | R.NGFYPATR.G                                |
| <input type="checkbox"/> 133 | 463.2319  | 924.4492  | 924.4454  | 0.0038  | 0    | (33)  | 0.26     | 1    | U      | R.NGFYPATR.G                                |
| <input type="checkbox"/> 134 | 463.2334  | 924.4522  | 924.4454  | 0.0069  | 0    | 41    | 0.039    | 1    | U      | R.NGFYPATR.G                                |
| <input type="checkbox"/> 160 | 532.3011  | 1062.5876 | 1062.5822 | 0.0054  | 0    | 63    | 0.00036  | 1    | U      | K.IDVHLPVDR.K                               |
| <input type="checkbox"/> 161 | 532.3013  | 1062.5880 | 1062.5822 | 0.0058  | 0    | (56)  | 0.0019   | 1    | U      | K.IDVHLPVDR.K                               |
| <input type="checkbox"/> 180 | 556.2727  | 1110.5308 | 1110.5280 | 0.0028  | 0    | (18)  | 6.8      | 1    | U      | K.WSHPPSCIK.T                               |
| <input type="checkbox"/> 181 | 556.2731  | 1110.5317 | 1110.5280 | 0.0036  | 0    | 32    | 0.26     | 1    | U      | K.WSHPPSCIK.T                               |
| <input type="checkbox"/> 187 | 566.2647  | 1130.5149 | 1130.5105 | 0.0044  | 0    | 52    | 0.002    | 1    | U      | K.EFDHNSNIR.Y                               |
| <input type="checkbox"/> 188 | 566.2648  | 1130.5151 | 1130.5105 | 0.0046  | 0    | (37)  | 0.064    | 1    | U      | K.EFDHNSNIR.Y                               |
| <input type="checkbox"/> 189 | 566.2655  | 1130.5165 | 1130.5105 | 0.0061  | 0    | (25)  | 0.9      | 1    | U      | K.EFDHNSNIR.Y                               |
| <input type="checkbox"/> 190 | 567.3293  | 1132.6440 | 1132.6393 | 0.0047  | 0    | 47    | 0.013    | 1    | U      | R.RYFPYVGVK.Y                               |
| <input type="checkbox"/> 192 | 578.2740  | 1154.5334 | 1154.5278 | 0.0056  | 0    | 65    | 0.00012  | 1    | U      | R.TGESVPEVCK.R                              |
| <input type="checkbox"/> 198 | 593.3025  | 1184.5905 | 1184.5860 | 0.0045  | 0    | 39    | 0.067    | 1    | U      | K.LPFTAPENK.I                               |
| <input type="checkbox"/> 199 | 593.8004  | 1185.5862 | 1185.5819 | 0.0044  | 1    | (46)  | 0.014    | 1    | U      | R.TKNDFTWFK.L                               |
| <input type="checkbox"/> 200 | 593.8014  | 1185.5883 | 1185.5819 | 0.0064  | 1    | 55    | 0.0016   | 1    | U      | R.TKNDFTWFK.L                               |
| <input type="checkbox"/> 202 | 595.2713  | 1188.5280 | 1188.5234 | 0.0046  | 0    | 47    | 0.0045   | 1    | U      | K.LSYTCGGFR.I                               |
| <input type="checkbox"/> 203 | 595.2718  | 1188.5291 | 1188.5234 | 0.0057  | 0    | (43)  | 0.011    | 1    | U      | K.LSYTCGGFR.I                               |
| <input type="checkbox"/> 211 | 405.1911  | 1212.5515 | 1212.5458 | 0.0057  | 0    | (24)  | 1.2      | 1    | U      | K.HGGLYHENMR.R                              |
| <input type="checkbox"/> 217 | 410.5183  | 1228.5331 | 1228.5407 | -0.0076 | 0    | 24    | 0.64     | 1    | U      | K.HGGLYHENMR.R + Oxidation (M)              |
| <input type="checkbox"/> 225 | 621.7764  | 1241.5382 | 1241.5347 | 0.0036  | 0    | 36    | 0.038    | 1    | U      | R.TGDEITYQCR.N                              |
| <input type="checkbox"/> 226 | 623.3088  | 1244.6030 | 1244.5972 | 0.0058  | 0    | (64)  | 0.00021  | 1    | U      | K.CTSTGNIAPR.C                              |
| <input type="checkbox"/> 227 | 623.3092  | 1244.6038 | 1244.5972 | 0.0066  | 0    | 65    | 0.00017  | 1    | U      | K.CTSTGNIAPR.C                              |
| <input type="checkbox"/> 230 | 630.3284  | 1258.6423 | 1258.6380 | 0.0044  | 0    | 29    | 0.81     | 1    | U      | R.WQSLPLVCK.I                               |
| <input type="checkbox"/> 241 | 655.3074  | 1308.6002 | 1308.5955 | 0.0047  | 0    | (41)  | 0.025    | 1    | U      | K.SCDIPVFMNAR.T                             |
| <input type="checkbox"/> 242 | 655.3074  | 1308.6002 | 1308.5955 | 0.0048  | 0    | 49    | 0.0042   | 1    | U      | K.SCDIPVFMNAR.T                             |
| <input type="checkbox"/> 249 | 663.3043  | 1324.5940 | 1324.5904 | 0.0037  | 0    | (42)  | 0.016    | 1    | U      | K.SCDIPVFMNAR.T + Oxidation (M)             |
| <input type="checkbox"/> 259 | 671.3577  | 1340.7008 | 1340.6936 | 0.0072  | 0    | 62    | 0.00037  | 1    | U      | K.SPDVINGSPISQK.I                           |
| <input type="checkbox"/> 265 | 691.3452  | 1380.6758 | 1380.6707 | 0.0051  | 0    | 61    | 0.00043  | 1    | U      | R.EIMENYNIALR.W + Oxidation (M)             |
| <input type="checkbox"/> 271 | 465.9346  | 1394.7819 | 1394.7769 | 0.0050  | 0    | (17)  | 8.5      | 1    | U      | K.SSNLILLEHLK.N                             |
| <input type="checkbox"/> 272 | 698.3982  | 1394.7819 | 1394.7769 | 0.0050  | 0    | 60    | 0.00044  | 1    | U      | K.SSNLILLEHLK.N                             |
| <input type="checkbox"/> 273 | 481.2406  | 1440.7000 | 1440.6932 | 0.0068  | 0    | 33    | 0.22     | 1    | U      | K.EQWHLVFCINGR.W                            |
| <input type="checkbox"/> 278 | 741.3608  | 1480.7069 | 1480.7021 | 0.0049  | 0    | 79    | 5.9e-006 | 1    | U      | K.CPEFGIDGPAIAK.C                           |
| <input type="checkbox"/> 280 | 503.9099  | 1508.7080 | 1508.7003 | 0.0077  | 0    | 10    | 39       | 1    | U      | R.CTLKPCDYPDIK.H                            |
| <input type="checkbox"/> 289 | 827.8778  | 1653.7410 | 1653.7345 | 0.0066  | 0    | 59    | 0.00023  | 1    | U      | K.AGEQVYTCATYYK.M                           |
| <input type="checkbox"/> 290 | 827.8797  | 1653.7449 | 1653.7345 | 0.0105  | 0    | (17)  | 4.2      | 1    | U      | K.AGEQVYTCATYYK.M                           |
| <input type="checkbox"/> 302 | 908.4298  | 1814.8451 | 1814.8357 | 0.0095  | 0    | 87    | 4.8e-007 | 1    | U      | K.LGYVTADGETSGSITCGK.D                      |
| <input type="checkbox"/> 306 | 934.4218  | 1866.8290 | 1866.8206 | 0.0084  | 0    | 6     | 35       | 1    | U      | K.SCDNPNYPNGDYSPLR.I                        |
| <input type="checkbox"/> 311 | 983.4920  | 1964.9694 | 1964.9626 | 0.0069  | 0    | 78    | 6e-006   | 1    | U      | K.EQVQSCGPPPELLNGNVK.E                      |
| <input type="checkbox"/> 312 | 983.4923  | 1964.9699 | 1964.9626 | 0.0074  | 0    | (69)  | 5.5e-005 | 1    | U      | K.EQVQSCGPPPELLNGNVK.E                      |
| <input type="checkbox"/> 314 | 1004.9758 | 2007.9370 | 2007.9281 | 0.0089  | 0    | 53    | 0.0013   | 1    | U      | K.TDQLSLPFFENAIPEK.K                        |
| <input type="checkbox"/> 316 | 1010.9970 | 2019.9794 | 2019.9684 | 0.0110  | 0    | (58)  | 0.00066  | 1    | U      | R.DTSCVNPPTVQNAIVSR.Q                       |
| <input type="checkbox"/> 317 | 1010.9972 | 2019.9798 | 2019.9684 | 0.0114  | 0    | 86    | 8.9e-007 | 1    | U      | R.DTSCVNPPTVQNAIVSR.Q                       |
| <input type="checkbox"/> 329 | 552.7704  | 2207.0523 | 2207.0429 | 0.0094  | 1    | 42    | 0.02     | 1    | U      | K.IVSSAMEPDREYHFGQAVR.F + Oxidation (M)     |
| <input type="checkbox"/> 330 | 552.7708  | 2207.0542 | 2207.0429 | 0.0112  | 1    | (3)   | 1.3e+002 | 1    | U      | K.IVSSAMEPDREYHFGQAVR.F + Oxidation (M)     |
| <input type="checkbox"/> 342 | 754.0085  | 2259.0037 | 2258.9902 | 0.0135  | 1    | (44)  | 0.0035   | 1    | U      | K.TREYGHSEVVEYVCNPR.F                       |
| <input type="checkbox"/> 343 | 754.0086  | 2259.0038 | 2258.9902 | 0.0136  | 1    | 48    | 0.0014   | 1    | U      | K.TREYGHSEVVEYVCNPR.F                       |
| <input type="checkbox"/> 344 | 754.0093  | 2259.0062 | 2258.9902 | 0.0160  | 1    | (30)  | 0.093    | 1    | U      | K.TREYGHSEVVEYVCNPR.F                       |
| <input type="checkbox"/> 348 | 1133.0546 | 2264.0946 | 2264.0848 | 0.0098  | 0    | 102   | 1.9e-008 | 1    | U      | K.SSIDIENGFIQSEGYTALK.E                     |
| <input type="checkbox"/> 363 | 1206.5798 | 2411.1451 | 2411.1348 | 0.0103  | 0    | 31    | 0.21     | 1    | U      | K.VSVLQENYLIQEGEITCKD.W                     |
| <input type="checkbox"/> 378 | 914.1078  | 2739.3015 | 2739.2844 | 0.0171  | 1    | (43)  | 0.011    | 1    | U      | K.VSVLQENYLIQEGEITCKDGR.W                   |
| <input type="checkbox"/> 379 | 914.1078  | 2739.3017 | 2739.2844 | 0.0174  | 1    | 60    | 0.0002   | 1    | U      | K.VSVLQENYLIQEGEITCKDGR.W                   |
| <input type="checkbox"/> 380 | 914.1121  | 2739.3144 | 2739.2844 | 0.0301  | 1    | (38)  | 0.041    | 1    | U      | K.VSVLQENYLIQEGEITCKDGR.W                   |
| <input type="checkbox"/> 386 | 732.3400  | 2925.3307 | 2925.3127 | 0.0180  | 0    | 38    | 0.016    | 1    | U      | K.SPPEISHGVVAMSDSYQGEVYTK.C + Oxidation (M) |

2. [TRYP PIG](#)    Mass: 25078    Score: 845    Matches: 28(20)    Sequences: 9(7)    emPAI: 3.29  
 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) | Delta  | Miss | Score | Expect | Rank | Unique | Peptide      |
|------------------------------|----------|-----------|-----------|--------|------|-------|--------|------|--------|--------------|
| <input type="checkbox"/> 120 | 421.7603 | 841.5060  | 841.5022  | 0.0039 | 0    | (52)  | 0.0047 | 1    | U      | R.VATVSLPR.S |
| <input type="checkbox"/> 121 | 421.7605 | 841.5065  | 841.5022  | 0.0044 | 0    | (49)  | 0.0081 | 1    | U      | R.VATVSLPR.S |



|     |           |           |           |        |   |      |          |   |   |                                  |
|-----|-----------|-----------|-----------|--------|---|------|----------|---|---|----------------------------------|
| 369 | 837.3864  | 2509.1373 | 2509.1245 | 0.0128 | 0 | 35   | 0.038    | 1 | U | K.EIETYHNLLEGGQEDFESSGAGK.I      |
| 397 | 1088.8470 | 3263.5191 | 3263.5066 | 0.0125 | 0 | (65) | 4.3e-005 | 1 | U | K.DIENQYETQITQIEHVSSSGQEVQSSAK.E |
| 398 | 1088.8484 | 3263.5233 | 3263.5066 | 0.0168 | 0 | 69   | 1.7e-005 | 1 | U | K.DIENQYETQITQIEHVSSSGQEVQSSAK.E |

6. **K2C1 RAT** Mass: 65190 Score: 332 Matches: 9(7) Sequences: 5(4) emPAI: 0.30

Keratin, type II cytoskeletal 1 OS=Rattus norvegicus GN=Krt1 PE=2 SV=1  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect Rank | Unique   | Peptide |
|-------|----------|-----------|-----------|------------|-------|-------------|----------|---------|
| 169   | 541.8061 | 1081.5977 | 1081.5920 | 0.0057     | 1     | 38          | 0.084    | 1       |
| 231   | 633.3247 | 1264.6349 | 1264.6299 | 0.0050     | 0     | 90          | 6.3e-007 | 1       |
| 232   | 633.3252 | 1264.6358 | 1264.6299 | 0.0059     | 0     | (82)        | 4.3e-006 | 1       |
| 266   | 697.3725 | 1392.7305 | 1392.7249 | 0.0057     | 1     | (51)        | 0.0051   | 1       |
| 269   | 465.2508 | 1392.7305 | 1392.7249 | 0.0057     | 1     | (28)        | 0.93     | 1       |
| 270   | 697.3733 | 1392.7320 | 1392.7249 | 0.0072     | 1     | 71          | 4.3e-005 | 1       |
| 275   | 738.3811 | 1474.7477 | 1474.7416 | 0.0061     | 0     | 57          | 0.0012   | 1       |
| 276   | 738.3994 | 1474.7842 | 1474.7780 | 0.0062     | 0     | (91)        | 5.7e-007 | 1       |
| 277   | 738.3999 | 1474.7852 | 1474.7780 | 0.0073     | 0     | 91          | 4.9e-007 | 1       |

7. **K22E HUMAN** Mass: 65678 Score: 295 Matches: 13(9) Sequences: 9(6) emPAI: 0.43

Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect Rank | Unique   | Peptide |
|-------|----------|-----------|-----------|------------|-------|-------------|----------|---------|
| 139   | 487.2715 | 972.5285  | 972.5240  | 0.0045     | 0     | 44          | 0.04     | 1       |
| 140   | 487.2718 | 972.5290  | 972.5240  | 0.0050     | 0     | (44)        | 0.043    | 1       |
| 141   | 497.7895 | 993.5645  | 993.5607  | 0.0038     | 0     | 5           | 1.5e+002 | 3       |
| 153   | 521.2798 | 1040.5451 | 1040.5502 | -0.0051    | 0     | 7           | 98       | 3       |
| 169   | 541.8061 | 1081.5977 | 1081.5920 | 0.0057     | 1     | 38          | 0.084    | 1       |
| 176   | 554.2761 | 1106.5376 | 1106.5356 | 0.0020     | 0     | 43          | 0.035    | 1       |
| 177   | 554.2762 | 1106.5379 | 1106.5356 | 0.0023     | 0     | (26)        | 1.5      | 1       |
| 228   | 627.8098 | 1253.6051 | 1253.6001 | 0.0051     | 0     | 66          | 0.00012  | 1       |
| 250   | 665.3694 | 1328.7243 | 1328.7187 | 0.0056     | 0     | (57)        | 0.0014   | 1       |
| 251   | 665.3696 | 1328.7245 | 1328.7187 | 0.0058     | 0     | 82          | 4.2e-006 | 1       |
| 252   | 668.8613 | 1335.7080 | 1335.7034 | 0.0046     | 1     | 50          | 0.0054   | 1       |
| 276   | 738.3994 | 1474.7842 | 1474.7780 | 0.0062     | 0     | (91)        | 5.7e-007 | 1       |
| 277   | 738.3999 | 1474.7852 | 1474.7780 | 0.0073     | 0     | 91          | 4.9e-007 | 1       |

8. **ALBU HUMAN** Mass: 71317 Score: 188 Matches: 14(5) Sequences: 10(4) emPAI: 0.46

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) | Delta Miss | Score | Expect Rank | Unique  | Peptide |
|-------|-----------|-----------|-----------|------------|-------|-------------|---------|---------|
| 135   | 464.2527  | 926.4907  | 926.4861  | 0.0046     | 0     | 31          | 0.37    | 1       |
| 137   | 480.7870  | 959.5595  | 959.5552  | 0.0043     | 0     | 46          | 0.019   | 1       |
| 138   | 480.7876  | 959.5607  | 959.5552  | 0.0054     | 0     | (35)        | 0.25    | 1       |
| 147   | 1013.6035 | 1012.5962 | 1012.5917 | 0.0046     | 0     | 27          | 1.1     | 1       |
| 186   | 564.8554  | 1127.6962 | 1127.6914 | 0.0048     | 1     | 28          | 0.53    | 1       |
| 191   | 575.3143  | 1148.6140 | 1148.6077 | 0.0062     | 0     | 65          | 0.00027 | 1       |
| 215   | 613.8088  | 1225.6031 | 1225.5979 | 0.0052     | 1     | (34)        | 0.19    | 1       |
| 216   | 613.8090  | 1225.6034 | 1225.5979 | 0.0056     | 1     | 39          | 0.062   | 1       |
| 274   | 722.3282  | 1442.6419 | 1442.6347 | 0.0072     | 0     | 52          | 0.001   | 1       |
| 283   | 516.2724  | 1545.7955 | 1545.7894 | 0.0060     | 1     | 16          | 17      | 1       |
| 286   | 547.3207  | 1638.9404 | 1638.9305 | 0.0099     | 1     | 63          | 0.00013 | 1       |
| 287   | 547.3209  | 1638.9409 | 1638.9305 | 0.0104     | 1     | (54)        | 0.001   | 1       |
| 316   | 682.3738  | 2044.0995 | 2044.0881 | 0.0115     | 0     | 29          | 0.43    | 1       |
| 319   | 682.3739  | 2044.0999 | 2044.0881 | 0.0119     | 0     | (21)        | 2.7     | 1       |

Proteins matching the same set of peptides:

**ALBU PONAB** Mass: 71317 Score: 188 Matches: 14(5) Sequences: 10(4)  
 Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=1

9. **K2C6B HUMAN** Mass: 60315 Score: 172 Matches: 9(6) Sequences: 6(4) emPAI: 0.40

Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect Rank | Unique   | Peptide |
|-------|----------|-----------|-----------|------------|-------|-------------|----------|---------|
| 169   | 541.8061 | 1081.5977 | 1081.5920 | 0.0057     | 1     | 38          | 0.084    | 1       |
| 176   | 554.2761 | 1106.5376 | 1106.5356 | 0.0020     | 0     | 43          | 0.035    | 1       |
| 177   | 554.2762 | 1106.5379 | 1106.5356 | 0.0023     | 0     | (26)        | 1.5      | 1       |
| 197   | 590.3061 | 1178.5977 | 1178.5931 | 0.0046     | 0     | 53          | 0.0031   | 1       |
| 239   | 436.8920 | 1307.6541 | 1307.6469 | 0.0071     | 2     | (46)        | 0.016    | 1       |
| 240   | 436.8922 | 1307.6548 | 1307.6469 | 0.0079     | 2     | 56          | 0.0015   | 1       |
| 250   | 665.3694 | 1328.7243 | 1328.7187 | 0.0056     | 0     | (57)        | 0.0014   | 1       |
| 251   | 665.3696 | 1328.7245 | 1328.7187 | 0.0058     | 0     | 82          | 4.2e-006 | 1       |
| 260   | 679.3731 | 1356.7316 | 1356.7249 | 0.0067     | 1     | 38          | 0.12     | 1       |

10. **IGHG1 HUMAN** Mass: 36596 Score: 164 Matches: 8(5) Sequences: 6(4) emPAI: 0.58

Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect Rank | Unique  | Peptide |
|-------|----------|-----------|-----------|------------|-------|-------------|---------|---------|
| 119   | 419.7571 | 837.4996  | 837.4960  | 0.0036     | 0     | 43          | 0.018   | 1       |
| 194   | 581.3209 | 1160.6272 | 1160.6223 | 0.0049     | 0     | (37)        | 0.18    | 1       |
| 195   | 581.3210 | 1160.6275 | 1160.6223 | 0.0051     | 0     | 40          | 0.09    | 1       |
| 201   | 593.8296 | 1185.6445 | 1185.6394 | 0.0052     | 0     | 63          | 0.00035 | 1       |
| 244   | 661.3450 | 1320.6755 | 1320.6708 | 0.0047     | 0     | 63          | 0.00034 | 1       |
| 245   | 661.3453 | 1320.6760 | 1320.6708 | 0.0052     | 0     | (51)        | 0.0048  | 1       |
| 292   | 839.4093 | 1676.8041 | 1676.7947 | 0.0094     | 0     | 42          | 0.024   | 1       |
| 307   | 937.4683 | 1872.9221 | 1872.9146 | 0.0076     | 0     | 10          | 44      | 1       |

11. **A2MG HUMAN** Mass: 164614 Score: 141 Matches: 6(6) Sequences: 4(4) emPAI: 0.11

Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2  
 Check to include this hit in error tolerant search or archive report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect Rank | Unique  | Peptide |
|-------|----------|-----------|-----------|------------|-------|-------------|---------|---------|
| 209   | 605.8271 | 1209.6396 | 1209.6353 | 0.0043     | 0     | 49          | 0.0066  | 1       |
| 210   | 605.8271 | 1209.6397 | 1209.6353 | 0.0044     | 0     | (46)        | 0.014   | 1       |
| 229   | 630.2915 | 1258.5683 | 1258.5652 | 0.0031     | 0     | 60          | 0.00023 | 1       |
| 233   | 638.2900 | 1274.5655 | 1274.5602 | 0.0053     | 0     | (50)        | 0.0018  | 1       |
| 305   | 923.0198 | 1844.0251 | 1844.0235 | -0.0044    | 0     | 48          | 0.0054  | 1       |
| 308   | 942.5307 | 1883.0408 | 1883.0404 | 0.0064     | 0     | 61          | 0.00026 | 1       |

Proteins matching the same set of peptides:

**A2MG PONAB** Mass: 164585 Score: 141 Matches: 6(6) Sequences: 4(4)  
 Alpha-2-macroglobulin OS=Pongo abelii GN=A2M PE=2 SV=1

12. **K1C14 HUMAN** Mass: 51872 Score: 121 Matches: 9(6) Sequences: 5(3) emPAI: 0.21



|                                     |     |           |           |           |         |   |   |          |   |  |
|-------------------------------------|-----|-----------|-----------|-----------|---------|---|---|----------|---|--|
| <input checked="" type="checkbox"/> | 504 | 6169.9418 | 6168.9345 | 6168.9324 | 0.0021  | 0 | 0 | 24       | 1 | VSGILDFSDMSFGYYIFELAITIMYMMIESNDPLHAGGYVLGFQSVIPLTDEEK + 2 Oxidation (M) |
| <input checked="" type="checkbox"/> | 416 | 500.8060  | 3998.3896 | 3998.3442 | 0.0454  | 2 | 0 | 0.98     | 1 | TNITIPQSQRDILTALKATGKPLVLVLMNGRPLALVK + Oxidation (M)                    |
| <input checked="" type="checkbox"/> | 370 | 854.3721  | 2560.0946 | 2560.0889 | 0.0057  | 0 | 0 | 34       | 1 | SPLMPGCELPGVGTCPDMCPAAER + Oxidation (M)                                 |
| <input checked="" type="checkbox"/> | 387 | 970.7859  | 2909.3360 | 2909.3395 | -0.0035 | 0 | 0 | 1.2e+002 | 1 | EEPLYLYNEVEFGVPYATQGDYSAR  |
| <input checked="" type="checkbox"/> | 1   | 412.1689  | 411.1617  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 2   | 415.2123  | 414.2050  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 3   | 415.2127  | 414.2054  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 4   | 415.2127  | 414.2054  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 5   | 415.2552  | 414.2479  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 6   | 415.3425  | 414.3352  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 7   | 419.1679  | 418.1607  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 8   | 430.2449  | 429.2376  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 9   | 432.2390  | 431.2318  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 10  | 432.2392  | 431.2319  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 11  | 432.2393  | 431.2320  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 12  | 432.2822  | 431.2749  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 13  | 433.1282  | 432.1210  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 14  | 433.1818  | 432.1745  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 15  | 433.3529  | 432.3456  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 16  | 444.1174  | 443.1101  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 17  | 444.1175  | 443.1102  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 18  | 444.1177  | 443.1104  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 19  | 444.1205  | 443.1132  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 20  | 447.1354  | 446.1281  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 21  | 447.1383  | 446.1310  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 22  | 456.2811  | 455.2738  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 23  | 456.2812  | 455.2740  |           |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 24  | 459.2815  | 458.2743  |           |         |   |   |          |   |  |
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| <a href="#">522</a> | 6948.6049 | 6947.5976 |
| <a href="#">523</a> | 6994.2515 | 6993.2442 |
| <a href="#">524</a> | 887.9511  | 7095.5503 |
| <a href="#">525</a> | 950.6145  | 7596.8581 |
| <a href="#">526</a> | 7628.7256 | 7627.7183 |
| <a href="#">528</a> | 8080.1805 | 8079.1732 |
| <a href="#">529</a> | 8134.2703 | 8133.2630 |
| <a href="#">530</a> | 8180.7440 | 8179.7367 |
| <a href="#">531</a> | 8210.0502 | 8209.0429 |
| <a href="#">532</a> | 8724.9338 | 8723.9265 |

## Search Parameters

Type of search : MS/MS Ion Search  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance :  $\pm 0.05$  Da  
 Fragment Mass Tolerance :  $\pm 0.05$  Da  
 Max Missed Cleavages : 2  
 Instrument type : Default  
 Number of queries : 532

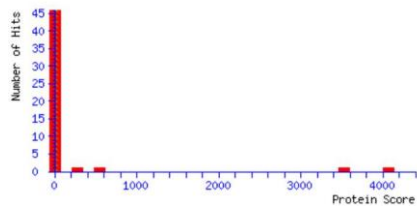
Mascot: <http://www.matrixscience.com/>

# MASCOT SCIENCE Mascot Search Results

User : Julian  
Email : julian.langer@mpibp-frankfurt.mpg.de  
Search title : Submitted from 140318 842 ChKrettler 1-10 swissprot\_full T 0.05Da by Mascot Daemon on CCSW010  
MS data file : D:\Data\140318\140318\_140314 842 ChReinhard 9\_Tray01-D5\_01\_17690.d\140314 842 ChReinhard 9\_Tray01-D5\_01\_17690.mgf  
Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
Timestamp : 19 Mar 2014 at 09:52:53 GMT  
Protein hits : [F13A HUMAN](#) Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
[F13B HUMAN](#) Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
[TRYP PIC](#) Trypsin OS=Sus scrofa PE=1 SV=1  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[K1C10 HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6

## 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 > 37 indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



## Peptide Summary Report

Format As Peptide Summary [Help](#)  
Significance threshold  $p < 0.05$  Max. number of hits AUTO  
Standard scoring  MudPIT scoring  Ions score or expect cut-off 0 Show sub-sets 0  
Show pop-ups  Suppress pop-ups  Sort unassigned Decreasing Score Require bold red

Select All Select None Search Selected Error tolerant Archive Report

1. [F13A HUMAN](#) Mass: 83728 Score: 4067 Matches: 114 (92) Sequences: 39 (35) emFAL: 8.97  
Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
 Check to include this hit in error tolerant search or archive report

| Query                                   | Observed | Mr (expt) | Mr (calc) | Delta  | Miss | Score | Expect   | Rank | Unique | Peptide                              |
|---|----------|-----------|-----------|--------|------|-------|----------|------|--------|--------------------------------------|
| <input checked="" type="checkbox"/> 124 | 430.2502 | 858.4858  | 858.4811  | 0.0047 | 0    | (61)  | 0.00097  | 1    | U      | R.LSIQSSPK.C                         |
| <input checked="" type="checkbox"/> 125 | 430.2505 | 858.4865  | 858.4811  | 0.0054 | 0    | 83    | 6.1e-006 | 1    | U      | R.LSIQSSPK.C                         |
| <input checked="" type="checkbox"/> 130 | 435.7630 | 869.5114  | 869.5083  | 0.0031 | 1    | 47    | 0.012    | 1    | U      | R.GNPIKIVSR.V                        |
| <input checked="" type="checkbox"/> 131 | 435.7636 | 869.5127  | 869.5083  | 0.0044 | 1    | (40)  | 0.056    | 1    | U      | R.GNPIKIVSR.V                        |
| <input checked="" type="checkbox"/> 132 | 438.7358 | 875.4570  | 875.4535  | 0.0036 | 0    | (70)  | 0.00011  | 1    | U      | R.VGSAMVNAK.D                        |
| <input checked="" type="checkbox"/> 133 | 438.7358 | 875.4571  | 875.4535  | 0.0037 | 0    | 70    | 0.00011  | 1    | U      | R.VGSAMVNAK.D                        |
| <input checked="" type="checkbox"/> 134 | 438.7363 | 875.4581  | 875.4535  | 0.0046 | 0    | (69)  | 0.00012  | 1    | U      | R.VGSAMVNAK.D                        |
| <input checked="" type="checkbox"/> 135 | 439.2154 | 876.4163  | 876.4123  | 0.0040 | 0    | (37)  | 0.13     | 1    | U      | R.AQMDLSGR.G                         |
| <input checked="" type="checkbox"/> 136 | 439.2155 | 876.4164  | 876.4123  | 0.0040 | 0    | 40    | 0.069    | 1    | U      | R.AQMDLSGR.G                         |
| <input checked="" type="checkbox"/> 137 | 439.2156 | 876.4167  | 876.4123  | 0.0043 | 0    | (37)  | 0.13     | 1    | U      | R.AQMDLSGR.G                         |
| <input checked="" type="checkbox"/> 157 | 515.7733 | 1029.5321 | 1029.5277 | 0.0044 | 0    | 72    | 6e-005   | 1    | U      | R.CGPASVQAIK.H                       |
| <input checked="" type="checkbox"/> 158 | 515.7736 | 1029.5326 | 1029.5277 | 0.0049 | 0    | (69)  | 0.00011  | 1    | U      | R.CGPASVQAIK.H                       |
| <input checked="" type="checkbox"/> 172 | 558.8105 | 1115.6065 | 1115.6009 | 0.0056 | 0    | (67)  | 0.00018  | 1    | U      | K.KPLNTEGVMSK.S                      |
| <input checked="" type="checkbox"/> 178 | 566.8073 | 1131.6001 | 1131.5958 | 0.0043 | 0    | (69)  | 0.00012  | 1    | U      | K.KPLNTEGVMSK.S + Oxidation (M)      |
| <input checked="" type="checkbox"/> 179 | 566.8078 | 1131.6009 | 1131.5958 | 0.0052 | 0    | 74    | 3.5e-005 | 1    | U      | K.KPLNTEGVMSK.S + Oxidation (M)      |
| <input checked="" type="checkbox"/> 180 | 566.8078 | 1131.6011 | 1131.5958 | 0.0053 | 0    | (68)  | 0.00012  | 1    | U      | K.KPLNTEGVMSK.S + Oxidation (M)      |
| <input checked="" type="checkbox"/> 183 | 576.2540 | 1150.4934 | 1150.4891 | 0.0044 | 0    | (43)  | 0.0079   | 1    | U      | K.FQEGQEEER.L                        |
| <input checked="" type="checkbox"/> 184 | 576.2543 | 1150.4941 | 1150.4891 | 0.0050 | 0    | 46    | 0.0039   | 1    | U      | K.FQEGQEEER.L                        |
| <input checked="" type="checkbox"/> 190 | 590.3072 | 1178.5999 | 1178.5965 | 0.0035 | 0    | (72)  | 4.3e-005 | 1    | U      | K.LIASMSSDSLR.H                      |
| <input checked="" type="checkbox"/> 191 | 590.3073 | 1178.6001 | 1178.5965 | 0.0036 | 0    | 83    | 3.4e-006 | 1    | U      | K.LIASMSSDSLR.H                      |
| <input checked="" type="checkbox"/> 194 | 598.3056 | 1194.5965 | 1194.5914 | 0.0051 | 0    | (75)  | 1.9e-005 | 1    | U      | K.LIASMSSDSLR.H + Oxidation (M)      |
| <input checked="" type="checkbox"/> 195 | 598.3056 | 1194.5966 | 1194.5914 | 0.0052 | 0    | (72)  | 3.2e-005 | 1    | U      | K.LIASMSSDSLR.H + Oxidation (M)      |
| <input checked="" type="checkbox"/> 223 | 648.8492 | 1295.6838 | 1295.6795 | 0.0043 | 0    | 84    | 2.3e-006 | 1    | U      | R.LALETALMYGAK.K + Oxidation (M)     |
| <input checked="" type="checkbox"/> 224 | 648.8494 | 1295.6843 | 1295.6795 | 0.0048 | 0    | (82)  | 3.2e-006 | 1    | U      | R.LALETALMYGAK.K + Oxidation (M)     |
| <input checked="" type="checkbox"/> 225 | 648.8496 | 1295.6846 | 1295.6795 | 0.0051 | 0    | (84)  | 2.3e-006 | 1    | U      | R.LALETALMYGAK.K + Oxidation (M)     |
| <input checked="" type="checkbox"/> 228 | 654.3554 | 1306.6962 | 1306.6915 | 0.0048 | 1    | 61    | 0.00049  | 1    | U      | R.KLIASMSSDSLR.H                     |
| <input checked="" type="checkbox"/> 239 | 441.9051 | 1322.6936 | 1322.6864 | 0.0072 | 1    | (57)  | 0.0012   | 1    | U      | R.KLIASMSSDSLR.H + Oxidation (M)     |
| <input checked="" type="checkbox"/> 240 | 663.9187 | 1325.8228 | 1325.8170 | 0.0058 | 0    | (43)  | 0.0077   | 1    | U      | K.STVLTPIEIIK.V                      |
| <input checked="" type="checkbox"/> 241 | 663.9191 | 1325.8237 | 1325.8170 | 0.0068 | 0    | 43    | 0.0072   | 1    | U      | K.STVLTPIEIIK.V                      |
| <input checked="" type="checkbox"/> 255 | 683.8797 | 1365.7449 | 1365.7405 | 0.0044 | 1    | 70    | 5.1e-005 | 1    | U      | R.DLREVEYVIGR.Y                      |
| <input checked="" type="checkbox"/> 256 | 456.2556 | 1365.7449 | 1365.7405 | 0.0044 | 1    | (45)  | 0.016    | 1    | U      | R.DLREVEYVIGR.Y                      |
| <input checked="" type="checkbox"/> 289 | 486.2583 | 1455.7530 | 1455.7470 | 0.0060 | 0    | (68)  | 8.7e-005 | 1    | U      | R.HVYGLDVIQQR.R                      |
| <input checked="" type="checkbox"/> 290 | 728.8838 | 1455.7530 | 1455.7470 | 0.0060 | 0    | (79)  | 6.7e-006 | 1    | U      | R.HVYGLDVIQQR.R                      |
| <input checked="" type="checkbox"/> 291 | 486.2586 | 1455.7539 | 1455.7470 | 0.0069 | 0    | (92)  | 3.3e-007 | 1    | U      | R.HVYGLDVIQQR.R                      |
| <input checked="" type="checkbox"/> 292 | 728.8842 | 1455.7539 | 1455.7470 | 0.0069 | 0    | 95    | 1.6e-007 | 1    | U      | R.HVYGLDVIQQR.R                      |
| <input checked="" type="checkbox"/> 305 | 763.3966 | 1524.7786 | 1524.7712 | 0.0074 | 0    | 82    | 3.2e-006 | 1    | U      | K.EFFDVTLEPLSFK.K                    |
| <input checked="" type="checkbox"/> 306 | 777.9139 | 1553.8133 | 1553.8065 | 0.0069 | 0    | (34)  | 0.2      | 1    | U      | R.MYAVWTPYGVLR.T                     |
| <input checked="" type="checkbox"/> 308 | 785.9111 | 1569.8077 | 1569.8014 | 0.0064 | 0    | (40)  | 0.051    | 1    | U      | R.MYAVWTPYGVLR.T + Oxidation (M)     |
| <input checked="" type="checkbox"/> 309 | 785.9114 | 1569.8082 | 1569.8014 | 0.0069 | 0    | 62    | 0.00034  | 1    | U      | R.MYAVWTPYGVLR.T + Oxidation (M)     |
| <input checked="" type="checkbox"/> 320 | 797.9184 | 1593.8221 | 1593.8151 | 0.0071 | 1    | 69    | 7.4e-005 | 1    | U      | R.VEYVIGRYQENK.G                     |
| <input checked="" type="checkbox"/> 321 | 532.2813 | 1593.8222 | 1593.8151 | 0.0071 | 1    | (45)  | 0.016    | 1    | U      | R.VEYVIGRYQENK.G                     |
| <input checked="" type="checkbox"/> 322 | 797.9187 | 1593.8228 | 1593.8151 | 0.0077 | 1    | (62)  | 0.00034  | 1    | U      | R.VEYVIGRYQENK.G                     |
| <input checked="" type="checkbox"/> 323 | 532.2816 | 1593.8228 | 1593.8151 | 0.0077 | 1    | (35)  | 0.18     | 1    | U      | R.VEYVIGRYQENK.G                     |
| <input checked="" type="checkbox"/> 325 | 822.8692 | 1643.7238 | 1643.7171 | 0.0067 | 0    | (101) | 1e-008   | 1    | U      | K.QIGSDGMDITDYYK.F                   |
| <input checked="" type="checkbox"/> 326 | 822.8697 | 1643.7249 | 1643.7171 | 0.0078 | 0    | 130   | 1.4e-011 | 1    | U      | K.QIGSDGMDITDYYK.F                   |
| <input checked="" type="checkbox"/> 345 | 830.8662 | 1659.7179 | 1659.7120 | 0.0059 | 0    | (86)  | 2.3e-007 | 1    | U      | K.QIGSDGMDITDYYK.F + Oxidation (M)   |
| <input checked="" type="checkbox"/> 346 | 830.8666 | 1659.7186 | 1659.7120 | 0.0066 | 0    | (101) | 7.5e-009 | 1    | U      | K.QIGSDGMDITDYYK.F + Oxidation (M)   |
| <input checked="" type="checkbox"/> 353 | 844.4707 | 1686.9268 | 1686.9192 | 0.0076 | 0    | (64)  | 0.00018  | 1    | U      | K.GTYIPVPIVSELQSGK.W                 |
| <input checked="" type="checkbox"/> 360 | 844.4710 | 1686.9274 | 1686.9192 | 0.0082 | 0    | (69)  | 6.3e-005 | 1    | U      | K.GTYIPVPIVSELQSGK.W                 |
| <input checked="" type="checkbox"/> 361 | 844.4710 | 1686.9274 | 1686.9192 | 0.0082 | 0    | 69    | 6.2e-005 | 1    | U      | K.GTYIPVPIVSELQSGK.W                 |
| <input checked="" type="checkbox"/> 362 | 564.6190 | 1690.8351 | 1690.8275 | 0.0077 | 0    | (86)  | 1.4e-006 | 1    | U      | K.DGTHVVENVDATHIGK.L                 |
| <input checked="" type="checkbox"/> 363 | 564.6195 | 1690.8367 | 1690.8275 | 0.0092 | 0    | 88    | 7.5e-007 | 1    | U      | K.DGTHVVENVDATHIGK.L                 |
| <input checked="" type="checkbox"/> 394 | 883.9197 | 1765.8248 | 1765.8193 | 0.0056 | 0    | (69)  | 4e-005   | 1    | U      | R.SNVDMDFEVENAVLGK.D                 |
| <input checked="" type="checkbox"/> 395 | 883.9199 | 1765.8253 | 1765.8193 | 0.0061 | 0    | (83)  | 1.7e-006 | 1    | U      | R.SNVDMDFEVENAVLGK.D                 |
| <input checked="" type="checkbox"/> 399 | 594.6645 | 1780.9717 | 1780.9611 | 0.0106 | 2    | 51    | 0.003    | 1    | U      | K.KETFVDTLEPLSFKK.E                  |
| <input checked="" type="checkbox"/> 401 | 891.9178 | 1781.8210 | 1781.8142 | 0.0069 | 0    | (97)  | 5.8e-008 | 1    | U      | R.SNVDMDFEVENAVLGK.D + Oxidation (M) |
| <input checked="" type="checkbox"/> 402 | 891.9185 | 1781.8224 | 1781.8142 | 0.0082 | 0    | 121   | 2.3e-010 | 1    | U      | R.SNVDMDFEVENAVLGK.D + Oxidation (M) |
| <input checked="" type="checkbox"/> 408 | 602.6567 | 1804.9484 | 1804.9407 | 0.0077 | 0    | 44    | 0.023    | 1    | U      | R.NVVHLDGPGVTRPMK.K                  |
| <input checked="" type="checkbox"/> 409 | 602.6571 | 1804.9495 | 1804.9407 | 0.0089 | 0    | (43)  | 0.027    | 1    | U      | R.NVVHLDGPGVTRPMK.K                  |
| <input checked="" type="checkbox"/> 412 | 607.3176 | 1818.9310 | 1818.9224 | 0.0085 | 1    | 62    | 0.00031  | 1    | U      | K.KDGTHTVVENVDATHIGK.L               |
| <input checked="" type="checkbox"/> 413 | 607.3180 | 1818.9321 | 1818.9224 | 0.0096 | 1    | (54)  | 0.00022  | 1    | U      | K.KDGTHTVVENVDATHIGK.L               |
| <input checked="" type="checkbox"/> 414 | 455.7403 | 1818.9321 | 1818.9224 | 0.0097 | 1    | (59)  | 0.00063  | 1    | U      | K.KDGTHTVVENVDATHIGK.L               |
| <input checked="" type="checkbox"/> 417 | 607.9882 | 1820.9427 | 1820.9356 | 0.0071 | 0    | (21)  | 3.9      | 1    | U      | R.NVVHLDGPGVTRPMK.K + Oxidation (M)  |
| <input checked="" type="checkbox"/> 418 | 607.9889 | 1820.9449 | 1820.9356 | 0.0093 | 0    | (24)  | 1.9      | 1    | U      | R.NVVHLDGPGVTRPMK.K + Oxidation (M)  |
| <input checked="" type="checkbox"/> 438 | 982.9804 | 1963.9462 | 1963.9404 | 0.0058 | 0    | 68    | 5.8e-005 | 1    | U      | R.YQCWVFGVFNTEL.R.C                  |





Table with columns: ID, Observed, Mr (expt), Mr (calc), Delta Miss Score, Expect, Rank Unique, Peptide. Contains protein entries for K.VQYECATGYTTAGGK.T, K.KCTKPDLSNGYISDVK.L, etc.

3. TRYP\_PIG Mass: 25078 Score: 492 Matches: 14 (12) Sequences: 6 (6) emPAI: 1.88

Trypsin OS=Sus scrofa PE=1 SV=1
Check to include this hit in error tolerant search or archive report

Table with columns: Query, Observed, Mr (expt), Mr (calc), Delta Miss Score, Expect, Rank Unique, Peptide. Lists peptides like R.VATVSLPR.S, R.VATVSLPR.S, etc.

4. K2C1\_HUMAN Mass: 66170 Score: 287 Matches: 8 (7) Sequences: 7 (6) emPAI: 0.43

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

Table with columns: Query, Observed, Mr (expt), Mr (calc), Delta Miss Score, Expect, Rank Unique, Peptide. Lists peptides like K.IEISELNR.V, R.SLDLSIIAEVK.A, etc.

Proteins matching the same set of peptides:
K2C1\_PANTR Mass: 65621 Score: 287 Matches: 8 (7) Sequences: 7 (6)
Keratin, type II cytoskeletal 1 OS=Pan troglodytes GN=KRT1 PE=2 SV=1

5. K1C9\_HUMAN Mass: 62255 Score: 54 Matches: 3 (1) Sequences: 3 (1) emPAI: 0.11

Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3
error tolerant search or archive report

Table with columns: Query, Observed, Mr (expt), Mr (calc), Delta Miss Score, Expect, Rank Unique, Peptide. Lists peptides like R.STMQELNSR.L, R.FSSSSGYGGSSR.V, etc.

6. K22E\_HUMAN Mass: 65678 Score: 41 Matches: 3 (1) Sequences: 3 (1) emPAI: 0.11

Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2
error tolerant search or archive report

Table with columns: Query, Observed, Mr (expt), Mr (calc), Delta Miss Score, Expect, Rank Unique, Peptide. Lists peptides like K.IEISELNR.V, R.SKEARALYHSK.Y, etc.

7. K1C10\_HUMAN Mass: 59020 Score: 26 Matches: 2 (0) Sequences: 2 (0) emPAI: 0.06

Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6
error tolerant search or archive report

Table with columns: Query, Observed, Mr (expt), Mr (calc), Delta Miss Score, Expect, Rank Unique, Peptide. Lists peptides like K.SEITELRR.N, R.NVALEIEIQSLALK.Q

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

Table with columns: Query, Observed, Mr (expt), Mr (calc), Delta Miss Score, Expect, Rank Unique, Peptide. Lists unassigned peptides like YTEEIGEIIILK, EPIISMVNLK, etc.



|                                     |     |           |           |           |         |   |   |          |   |  |
|-------------------------------------|-----|-----------|-----------|-----------|---------|---|---|----------|---|--|
| <input checked="" type="checkbox"/> | 729 | 662.2280  | 5289.7658 | 5289.7320 | 0.0338  | 2 | 0 | 35       | 1 | GAIENGNVIGLALMIITSLIAMFSLFRIFVVMYLGNNKGEAIVFNK + 3 Oxidation (M) |
| <input checked="" type="checkbox"/> | 757 | 5918.5668 | 5917.5595 | 5917.5816 | -0.0221 | 1 | 0 | 2.5      | 1 | VPPPPETPAQEEMETETASAPQKQDDTAAMLADFDICPPDDEKPPATEPDS              |
| <input checked="" type="checkbox"/> | 730 | 884.9725  | 5303.7912 | 5303.7773 | 0.0139  | 2 | 0 | 29       | 1 | VLALYNQHNPASAAAPCCVQVLEPLPIVYVGRKPKVEQLSNMIVR + Oxidation (M)    |
| <input checked="" type="checkbox"/> | 558 | 872.7859  | 2615.3358 | 2615.3853 | -0.0495 | 2 | 0 | 3.1e+002 | 1 | ENDLRLKILLLNQSCDFQQR   |
| <input checked="" type="checkbox"/> | 336 | 827.4440  | 1652.8735 | 1652.8352 | 0.0384  | 2 | 0 | 4.7e+002 | 1 | MVHGRMVHGRSVSGK + Oxidation (M)                                  |
| <input checked="" type="checkbox"/> | 510 | 794.7002  | 2381.0787 | 2381.0634 | 0.0153  | 2 | 0 | 1.2e+002 | 1 | EQMNHSMSSGSLRTNQKR + Oxidation (M)                               |
| <input checked="" type="checkbox"/> | 293 | 734.8316  | 1467.6486 | 1467.6594 | -0.0107 | 0 | 0 | 1.8e+002 | 1 | GEMCLDLMLMQK   |
| <input checked="" type="checkbox"/> | 1   | 415.1272  |           | 414.1200  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 2   | 415.2122  |           | 414.2049  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 3   | 415.2126  |           | 414.2054  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 4   | 415.2150  |           | 414.2077  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 5   | 415.3358  |           | 414.3285  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 6   | 415.3430  |           | 414.3357  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 7   | 419.1685  |           | 418.1612  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 8   | 419.1704  |           | 418.1631  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 9   | 432.2395  |           | 431.2322  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 10  | 432.2398  |           | 431.2326  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 11  | 432.2411  |           | 431.2338  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 12  | 433.1815  |           | 432.1742  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 13  | 441.9034  |           | 440.8961  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 14  | 444.1175  |           | 443.1102  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 15  | 444.1176  |           | 443.1103  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 16  | 444.1179  |           | 443.1106  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 17  | 444.1197  |           | 443.1125  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 18  | 447.1376  |           | 446.1303  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 19  | 453.7869  |           | 452.7796  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 20  | 455.3364  |           | 454.3291  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 21  | 474.8329  |           | 473.8257  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 22  | 500.3071  |           | 499.2999  |         |   |   |          |   |  |
| <input checked="" type="checkbox"/> | 23  | 500.3071  |           | 499.2999  |         |   |   |          |   |  |
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| <input checked="" type="checkbox"/> | <a href="#">611</a> | 594.3667  | 2966.7972 |
| <input checked="" type="checkbox"/> | <a href="#">613</a> | 433.1333  | 3024.8823 |
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| <input checked="" type="checkbox"/> | <a href="#">620</a> | 1532.6763 | 3063.3381 |
| <input checked="" type="checkbox"/> | <a href="#">622</a> | 622.3639  | 3106.7831 |
| <input checked="" type="checkbox"/> | <a href="#">623</a> | 1038.7616 | 3113.2630 |
| <input checked="" type="checkbox"/> | <a href="#">624</a> | 1038.7618 | 3113.2637 |
| <input checked="" type="checkbox"/> | <a href="#">625</a> | 1038.7622 | 3113.2649 |
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| <input checked="" type="checkbox"/> | <a href="#">628</a> | 639.8226  | 3194.0765 |
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|                                     |                     |           |           |
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| <input checked="" type="checkbox"/> | <a href="#">658</a> | 871.3766  | 3481.4773 |
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| <input checked="" type="checkbox"/> | <a href="#">660</a> | 602.2552  | 3607.4875 |
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| <input checked="" type="checkbox"/> | <a href="#">664</a> | 458.1804  | 3657.3852 |
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| <input checked="" type="checkbox"/> | <a href="#">719</a> | 5006.3432 | 5005.3359 |
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| <input checked="" type="checkbox"/> | <a href="#">721</a> | 5008.0722 | 5007.0649 |
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| <input checked="" type="checkbox"/> | <a href="#">728</a> | 5202.7784 | 5201.7711 |
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|                                     |                     |            |            |
|-------------------------------------|---------------------|------------|------------|
| <input checked="" type="checkbox"/> | <a href="#">763</a> | 777.9137   | 6215.2516  |
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| <input checked="" type="checkbox"/> | <a href="#">766</a> | 6423.0990  | 6422.0917  |
| <input checked="" type="checkbox"/> | <a href="#">768</a> | 6624.4769  | 6623.4696  |
| <input checked="" type="checkbox"/> | <a href="#">769</a> | 6682.9020  | 6681.8947  |
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| <input checked="" type="checkbox"/> | <a href="#">778</a> | 7127.8785  | 7126.8712  |
| <input checked="" type="checkbox"/> | <a href="#">779</a> | 1038.4815  | 7262.3197  |
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| <input checked="" type="checkbox"/> | <a href="#">781</a> | 7273.2353  | 7272.2280  |
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| <input checked="" type="checkbox"/> | <a href="#">783</a> | 1243.8963  | 7457.3343  |
| <input checked="" type="checkbox"/> | <a href="#">784</a> | 1248.5663  | 7485.3542  |
| <input checked="" type="checkbox"/> | <a href="#">785</a> | 1278.0685  | 7662.3675  |
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| <input checked="" type="checkbox"/> | <a href="#">787</a> | 8055.4159  | 8054.4086  |
| <input checked="" type="checkbox"/> | <a href="#">788</a> | 1155.0568  | 8078.3468  |
| <input checked="" type="checkbox"/> | <a href="#">789</a> | 8877.3495  | 8876.3422  |
| <input checked="" type="checkbox"/> | <a href="#">790</a> | 9132.7700  | 9131.7627  |
| <input checked="" type="checkbox"/> | <a href="#">791</a> | 9532.3817  | 9531.3744  |
| <input checked="" type="checkbox"/> | <a href="#">792</a> | 10909.9918 | 10908.9845 |
| <input checked="" type="checkbox"/> | <a href="#">793</a> | 11564.9140 | 11563.9067 |

## Search Parameters

Type of search :MS/MS Ion Search  
 Enzyme :Trypsin  
 Fixed modifications :Carbamidomethyl (C)  
 Variable modifications : Oxidation (M)  
 Mass values :Monoisotopic  
 Protein Mass :Unrestricted  
 Peptide Mass Tolerance : ± 0.05 Da  
 Fragment Mass Tolerance: ± 0.05 Da  
 Max Missed Cleavages :2  
 Instrument type :Default  
 Number of queries :793

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

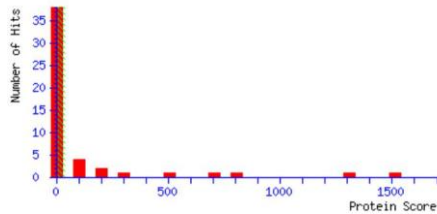


**MASCOT** SCIENCE **Mascot Search Results**

User : Julian  
 Email : julian.langer@mpibp-frankfurt.mpg.de  
 Search title : Submitted from 140318 842 ChKrettler 1-10 swissprot full T 0.05Da by Mascot Daemon on CCSW010  
 MS data file : D:\Data\1403\140318\140314 842 ChReinhard 10\_Tray01-D6\_01\_17691.d\140314 842 ChReinhard 10\_Tray01-D6\_01\_17691.mgf  
 Database : SwissProt 57.15 (515203 sequences; 181334896 residues)  
 Timestamp : 19 Mar 2014 at 09:53:27 GMT  
 Protein hits : [ALBU HUMAN](#) Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2  
[F13A HUMAN](#) Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4  
[K2C1 HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6  
[TRYP PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1  
[F13B HUMAN](#) Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3  
[K1C9 HUMAN](#) Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3  
[K1C10 HUMAN](#) Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6  
[K22E HUMAN](#) Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2  
[ALBG HUMAN](#) Alpha-1B-glycoprotein OS=Homo sapiens GN=ALBG PE=1 SV=3  
[K1C14 HUMAN](#) Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4  
[HEMO HUMAN](#) Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2  
[K1M1 SHEEP](#) Keratin, type I microfibrillar 48 kDa, component 8C-1 OS=Ovis aries PE=1 SV=2  
[K2M3 SHEEP](#) Keratin, type II microfibrillar, component 5 OS=Ovis aries PE=1 SV=1  
[C04A HUMAN](#) Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1

**Mascot Score Histogram**

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 38 indicate identity or extensive homology ( $p < 0.05$ ). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



**Peptide Summary Report**

Format As  [Help](#)

Significance threshold  $p < 0.05$  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  Require bold red

Select All  Select None  Search Selected   Error tolerant  Archive Report

1. [ALBU HUMAN](#) Mass: 71317 Score: 1513 Matches: 84(44) Sequences: 38(23) emPAI: 3.34  
 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) | Delta   | Miss | Score | Expect   | Rank | Unique | Peptide                          |
|---|----------|-----------|-----------|---------|------|-------|----------|------|--------|----------------------------------|
| <input checked="" type="checkbox"/> 127 | 772.4416 | 771.4344  | 771.4313  | 0.0031  | 0    | 27    | 2.7      | 1    |        | K.AACLLPK.L                      |
| <input checked="" type="checkbox"/> 128 | 772.4422 | 771.4349  | 771.4313  | 0.0036  | 0    | (21)  | 9.7      | 1    |        | K.AACLLPK.L                      |
| <input checked="" type="checkbox"/> 129 | 789.4750 | 788.4677  | 788.4644  | 0.0033  | 0    | (35)  | 0.29     | 1    |        | K.LVTDLTK.V                      |
| <input checked="" type="checkbox"/> 130 | 789.4750 | 788.4678  | 788.4644  | 0.0034  | 0    | 54    | 0.0035   | 1    |        | K.LVTDLTK.V                      |
| <input checked="" type="checkbox"/> 152 | 438.2495 | 874.4845  | 874.5025  | -0.0179 | 1    | (24)  | 4.4      | 1    |        | R.LSQRFPK.A                      |
| <input checked="" type="checkbox"/> 153 | 438.2498 | 874.4851  | 874.5025  | -0.0174 | 1    | (13)  | 53       | 3    |        | R.LSQRFPK.A                      |
| <input checked="" type="checkbox"/> 154 | 438.2518 | 874.4890  | 874.5025  | -0.0135 | 1    | (23)  | 6.3      | 1    |        | R.LSQRFPK.A                      |
| <input checked="" type="checkbox"/> 155 | 438.2586 | 874.5027  | 874.5025  | 0.0003  | 1    | 33    | 0.49     | 1    |        | R.LSQRFPK.A                      |
| <input checked="" type="checkbox"/> 159 | 440.7256 | 879.4367  | 879.4338  | 0.0029  | 0    | (29)  | 1        | 1    | U      | K.AEFAEVSK.L                     |
| <input checked="" type="checkbox"/> 160 | 440.7262 | 879.4379  | 879.4338  | 0.0041  | 0    | 63    | 0.00036  | 1    | U      | K.AEFAEVSK.L                     |
| <input checked="" type="checkbox"/> 161 | 880.4452 | 879.4379  | 879.4338  | 0.0041  | 0    | (19)  | 8.6      | 1    | U      | K.AEFAEVSK.L                     |
| <input checked="" type="checkbox"/> 162 | 440.7263 | 879.4380  | 879.4338  | 0.0042  | 0    | (40)  | 0.076    | 1    | U      | K.AEFAEVSK.L                     |
| <input checked="" type="checkbox"/> 166 | 464.2524 | 926.4902  | 926.4861  | 0.0041  | 0    | 35    | 0.15     | 1    |        | K.YLYEIAR.R                      |
| <input checked="" type="checkbox"/> 167 | 927.4981 | 926.4908  | 926.4861  | 0.0047  | 0    | (34)  | 0.18     | 1    |        | K.YLYEIAR.R                      |
| <input checked="" type="checkbox"/> 168 | 464.2527 | 926.4908  | 926.4861  | 0.0047  | 0    | (32)  | 0.29     | 1    |        | K.YLYEIAR.R                      |
| <input checked="" type="checkbox"/> 169 | 467.2652 | 932.5159  | 932.5113  | 0.0046  | 0    | 31    | 0.75     | 1    |        | K.LCTVATLR.E                     |
| <input checked="" type="checkbox"/> 172 | 470.7295 | 939.4444  | 939.4410  | 0.0035  | 0    | (30)  | 0.46     | 1    | U      | K.DDNPNLPR.L                     |
| <input checked="" type="checkbox"/> 173 | 470.7301 | 939.4456  | 939.4410  | 0.0047  | 0    | 33    | 0.19     | 1    | U      | K.DDNPNLPR.L                     |
| <input checked="" type="checkbox"/> 174 | 480.7870 | 959.5595  | 959.5552  | 0.0042  | 0    | 49    | 0.01     | 1    | U      | K.FQNALLVR.Y                     |
| <input checked="" type="checkbox"/> 178 | 492.7498 | 983.4850  | 983.4811  | 0.0039  | 0    | 38    | 0.061    | 1    | U      | K.TYETPLEK.C                     |
| <input checked="" type="checkbox"/> 183 | 500.8075 | 999.6004  | 999.5964  | 0.0039  | 0    | 55    | 0.0019   | 1    |        | K.QTALVELVK.H                    |
| <input checked="" type="checkbox"/> 185 | 500.8078 | 999.6011  | 999.5964  | 0.0047  | 0    | (46)  | 0.017    | 1    |        | K.QTALVELVK.H                    |
| <input checked="" type="checkbox"/> 189 | 507.3055 | 1012.5965 | 1012.5917 | 0.0049  | 0    | 14    | 23       | 2    | U      | K.LVAASQAALGL.-                  |
| <input checked="" type="checkbox"/> 190 | 509.2734 | 1016.5322 | 1016.5291 | 0.0031  | 0    | 32    | 0.61     | 1    |        | K.SLHTLFGDK.L                    |
| <input checked="" type="checkbox"/> 216 | 537.7763 | 1073.5380 | 1073.5353 | 0.0027  | 1    | (46)  | 0.021    | 1    | U      | K.LDELRLDEGK.A                   |
| <input checked="" type="checkbox"/> 217 | 537.7770 | 1073.5394 | 1073.5353 | 0.0042  | 1    | 47    | 0.014    | 1    | U      | K.LDELRLDEGK.A                   |
| <input checked="" type="checkbox"/> 218 | 537.7773 | 1073.5401 | 1073.5353 | 0.0048  | 1    | (40)  | 0.079    | 1    | U      | K.LDELRLDEGK.A                   |
| <input checked="" type="checkbox"/> 219 | 538.2543 | 1074.4941 | 1074.4917 | 0.0025  | 0    | 10    | 38       | 1    |        | R.NECLQHK.D                      |
| <input checked="" type="checkbox"/> 232 | 564.8553 | 1127.6961 | 1127.6914 | 0.0047  | 1    | (49)  | 0.0039   | 1    |        | K.QTALVELVK.H                    |
| <input checked="" type="checkbox"/> 233 | 564.8555 | 1127.6964 | 1127.6914 | 0.0050  | 1    | 73    | 1.9e-005 | 1    |        | K.QTALVELVK.H                    |
| <input checked="" type="checkbox"/> 238 | 569.7539 | 1137.4932 | 1137.4907 | 0.0026  | 0    | (44)  | 0.0073   | 1    |        | K.CCTESLVNR.R                    |
| <input checked="" type="checkbox"/> 239 | 569.7546 | 1137.4946 | 1137.4907 | 0.0039  | 0    | 53    | 0.001    | 1    |        | K.CCTESLVNR.R                    |
| <input checked="" type="checkbox"/> 241 | 571.3480 | 1140.6815 | 1140.6866 | -0.0051 | 1    | 28    | 0.78     | 1    | U      | K.KLVAASQAALGL.-                 |
| <input checked="" type="checkbox"/> 242 | 571.3521 | 1140.6896 | 1140.6866 | 0.0029  | 1    | (25)  | 1.2      | 1    | U      | K.KLVAASQAALGL.-                 |
| <input checked="" type="checkbox"/> 244 | 575.3136 | 1148.6127 | 1148.6077 | 0.0050  | 0    | (84)  | 3.4e-006 | 1    |        | K.LVNEVTEFAK.T                   |
| <input checked="" type="checkbox"/> 245 | 575.3137 | 1148.6129 | 1148.6077 | 0.0052  | 0    | 84    | 3.2e-006 | 1    |        | K.LVNEVTEFAK.T                   |
| <input checked="" type="checkbox"/> 264 | 613.8093 | 1225.6041 | 1225.5979 | 0.0063  | 1    | (39)  | 0.065    | 1    | U      | R.FKDLGGEENFK.A                  |
| <input checked="" type="checkbox"/> 265 | 613.8096 | 1225.6047 | 1225.5979 | 0.0068  | 1    | (76)  | 1.1e-005 | 1    | U      | R.FKDLGGEENFK.A                  |
| <input checked="" type="checkbox"/> 266 | 409.5422 | 1225.6047 | 1225.5979 | 0.0068  | 1    | (38)  | 0.081    | 1    | U      | R.FKDLGGEENFK.A                  |
| <input checked="" type="checkbox"/> 267 | 409.5423 | 1225.6049 | 1225.5979 | 0.0070  | 1    | (20)  | 5.2      | 1    | U      | R.FKDLGGEENFK.A                  |
| <input checked="" type="checkbox"/> 268 | 613.8097 | 1225.6049 | 1225.5979 | 0.0070  | 1    | 77    | 1e-005   | 1    | U      | R.FKDLGGEENFK.A                  |
| <input checked="" type="checkbox"/> 297 | 671.8237 | 1341.6327 | 1341.6275 | 0.0053  | 0    | 94    | 1.3e-007 | 1    | U      | K.AVMDDFAAFVEK.C                 |
| <input checked="" type="checkbox"/> 298 | 671.8244 | 1341.6342 | 1341.6275 | 0.0067  | 0    | (89)  | 4.2e-007 | 1    | U      | K.AVMDDFAAFVEK.C                 |
| <input checked="" type="checkbox"/> 302 | 679.8208 | 1357.6271 | 1357.6224 | 0.0047  | 0    | (86)  | 7.3e-007 | 1    | U      | K.AVMDDFAAFVEK.C + Oxidation (M) |
| <input checked="" type="checkbox"/> 303 | 679.8220 | 1357.6294 | 1357.6224 | 0.0070  | 0    | (87)  | 5.4e-007 | 1    | U      | K.AVMDDFAAFVEK.C + Oxidation (M) |
| <input checked="" type="checkbox"/> 304 | 686.2890 | 1370.5635 | 1370.5595 | 0.0040  | 0    | (59)  | 9.1e-005 | 1    | U      | K.AAFTECCQAADK.A                 |
| <input checked="" type="checkbox"/> 305 | 686.2894 | 1370.5643 | 1370.5595 | 0.0048  | 0    | 64    | 3.2e-005 | 1    | U      | K.AAFTECCQAADK.A                 |
| <input checked="" type="checkbox"/> 321 | 722.3276 | 1442.6407 | 1442.6347 | 0.0060  | 0    | 80    | 1.8e-006 | 1    | U      | K.YICENQDSISSK.L                 |
| <input checked="" type="checkbox"/> 324 | 489.9545 | 1466.8417 | 1466.8358 | 0.0060  | 1    | 43    | 0.015    | 1    |        | R.RHPDYSVLLLR.L                  |
| <input checked="" type="checkbox"/> 325 | 489.9547 | 1466.8422 | 1466.8358 | 0.0064  | 1    | (35)  | 0.093    | 1    |        | R.RHPDYSVLLLR.L                  |
| <input checked="" type="checkbox"/> 334 | 516.2718 | 1545.7937 | 1545.7894 | 0.0042  | 1    | (56)  | 0.0017   | 1    | U      | K.LKRCCEKPLLEK.S                 |





|   |     |          |           |           |         |   |      |          |   |   |                         |
|---|-----|----------|-----------|-----------|---------|---|------|----------|---|---|-------------------------|
| ✓ | 188 | 502.2844 | 1002.5542 | 1002.5458 | 0.0084  | 1 | (15) | 31       | 1 |   | K.SEITELRR.N            |
| ✓ | 271 | 617.8459 | 1233.6772 | 1233.6717 | 0.0055  | 1 | (49) | 0.0088   | 1 |   | R.LKYENEVALR.Q          |
| ✓ | 272 | 617.8461 | 1233.6776 | 1233.6717 | 0.0059  | 1 | 65   | 0.00021  | 1 |   | R.LKYENEVALR.Q          |
| ✓ | 301 | 679.3660 | 1356.7175 | 1356.7110 | 0.0066  | 1 | 7    | 1.3e+002 | 1 |   | R.QSVEADINGLRR.V        |
| ✓ | 307 | 691.3322 | 1380.6499 | 1380.6408 | 0.0090  | 0 | 75   | 1.3e-005 | 1 |   | R.ALEESNYLEGR.I         |
| ✓ | 308 | 695.8458 | 1389.6770 | 1389.6736 | 0.0035  | 0 | 55   | 0.0015   | 1 | U | K.QSLEASLAETGR.Y        |
| ✓ | 329 | 747.3725 | 1492.7305 | 1492.7270 | 0.0035  | 1 | 45   | 0.015    | 1 | U | R.SQYEQLAEQNRK.D        |
| ✓ | 330 | 498.5847 | 1492.7322 | 1492.7270 | 0.0053  | 1 | (13) | 26       | 1 | U | R.SQYEQLAEQNRK.D        |
| ✓ | 355 | 854.3927 | 1706.7708 | 1706.7649 | 0.0059  | 0 | 77   | 4.2e-006 | 1 | U | K.GSLGGFSGGFSR.G        |
| ✓ | 371 | 899.0132 | 1796.0119 | 1796.0043 | 0.0076  | 0 | 58   | 0.00043  | 1 | U | R.NVQALEIELQSLK.Q       |
| ✓ | 405 | 738.0352 | 2211.0838 | 2211.0906 | -0.0068 | 1 | 0    | 3.2e+002 | 1 | U | K.SKELTTEIDNNEIQISSYK.S |

8. [K22E HUMAN](#) Mass: 65678 Score: 234 Matches: 6(5) Sequences: 4(4) emPAI: 0.23

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

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

| Query | Observed | Mr(expt) | Mr(calc)  | Delta     | Miss   | Score | Expect | Rank     | Unique | Peptide          |                 |
|-------|----------|----------|-----------|-----------|--------|-------|--------|----------|--------|------------------|-----------------|
| ✓     | 175      | 487.2711 | 972.5276  | 972.5240  | 0.0036 | 0     | (38)   | 0.16     | 1      | K.IEISELNR.V     |                 |
| ✓     | 176      | 487.2713 | 972.5281  | 972.5240  | 0.0041 | 0     | 44     | 0.04     | 1      | K.IEISELNR.V     |                 |
| ✓     | 292      | 665.3692 | 1328.7239 | 1328.7187 | 0.0052 | 0     | 45     | 0.019    | 1      | R.NLDDLSTIAEVK.A |                 |
| ✓     | 323      | 730.9061 | 1459.7977 | 1459.7922 | 0.0054 | 0     | 69     | 8.5e-005 | 1      | U                | K.VDLLNQIEFLK.V |
| ✓     | 326      | 738.3997 | 1474.7848 | 1474.7780 | 0.0068 | 0     | 117    | 1.2e-009 | 1      | R.FLEQQNQVLTQK.W |                 |
| ✓     | 327      | 738.3999 | 1474.7851 | 1474.7780 | 0.0072 | 0     | (109)  | 7.8e-009 | 1      | R.FLEQQNQVLTQK.W |                 |

9. [A1BG HUMAN](#) Mass: 54809 Score: 82 Matches: 3(2) Sequences: 3(2) emPAI: 0.13

Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=3

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

| Query | Observed | Mr(expt) | Mr(calc)  | Delta     | Miss   | Score | Expect | Rank    | Unique | Peptide |                  |
|-------|----------|----------|-----------|-----------|--------|-------|--------|---------|--------|---------|------------------|
| ✓     | 149      | 435.7701 | 869.5256  | 869.5222  | 0.0034 | 0     | 61     | 0.00042 | 1      | U       | K.LLELTGPK.S     |
| ✓     | 276      | 619.3284 | 1236.6423 | 1236.6390 | 0.0033 | 0     | 9      | 88      | 1      | U       | R.LETDFQLFK.N    |
| ✓     | 306      | 686.8540 | 1371.6935 | 1371.6895 | 0.0040 | 0     | 57     | 0.0012  | 1      | U       | K.HQFLLTGDTQGR.Y |

10. [K1C14 HUMAN](#) Mass: 51872 Score: 67 Matches: 4(3) Sequences: 3(3) emPAI: 0.21

Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4

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

| Query | Observed | Mr(expt) | Mr(calc)  | Delta     | Miss    | Score | Expect | Rank   | Unique | Peptide          |
|-------|----------|----------|-----------|-----------|---------|-------|--------|--------|--------|------------------|
| ✓     | 132      | 404.2051 | 806.3957  | 806.3923  | 0.0034  | 0     | (29)   | 1.2    | 1      | R.LAADDFR.T      |
| ✓     | 133      | 404.2052 | 806.3959  | 806.3923  | 0.0037  | 0     | 50     | 0.0087 | 1      | R.LAADDFR.T      |
| ✓     | 191      | 515.3011 | 1028.5876 | 1028.5866 | 0.0010  | 0     | 53     | 0.0048 | 1      | R.VLDELTLAR.A    |
| ✓     | 284      | 651.3325 | 1300.6504 | 1300.6510 | -0.0006 | 0     | 41     | 0.049  | 1      | R.ALEEANADLEVK.I |

Proteins matching the same set of peptides:

- [K1C15 HUMAN](#) Mass: 49395 Score: 67 Matches: 4(3) Sequences: 3(3)  
Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=2
- [K1C16 HUMAN](#) Mass: 51578 Score: 67 Matches: 4(3) Sequences: 3(3)  
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4
- [K1C19 POTTR](#) Mass: 43860 Score: 67 Matches: 4(3) Sequences: 3(3)  
Keratin, type I cytoskeletal 19 OS=Potorous tridactylus GN=KRT19 PE=2 SV=1
- [K1C42 MOUSE](#) Mass: 50444 Score: 67 Matches: 4(3) Sequences: 3(3)  
Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1

11. [HEMO HUMAN](#) Mass: 52385 Score: 64 Matches: 3(1) Sequences: 3(1) emPAI: 0.14

Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2

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

| Query | Observed | Mr(expt) | Mr(calc)  | Delta     | Miss   | Score | Expect | Rank     | Unique | Peptide |                             |
|-------|----------|----------|-----------|-----------|--------|-------|--------|----------|--------|---------|-----------------------------|
| ✓     | 135      | 407.2244 | 812.4343  | 812.4327  | 0.0016 | 0     | 5      | 1.5e+002 | 1      | U       | R.LHIMAGR.R + Oxidation (M) |
| ✓     | 243      | 571.8226 | 1141.6307 | 1141.6244 | 0.0063 | 0     | 32     | 0.39     | 1      | U       | R.QGHNSVFLIK.G              |
| ✓     | 260      | 610.8088 | 1219.6030 | 1219.5986 | 0.0045 | 0     | 58     | 0.001    | 1      | U       | K.NFFSPVDAAFR.Q             |

Proteins matching the same set of peptides:

- [HEMO PONAB](#) Mass: 52323 Score: 64 Matches: 3(1) Sequences: 3(1)  
Hemopexin OS=Pongo abelii GN=HPX PE=2 SV=1

12. [K1M1 SHEEP](#) Mass: 48070 Score: 55 Matches: 6(3) Sequences: 5(3) emPAI: 0.23

Keratin, type I microfibrillar 48 kDa, component 8C-1 OS=Ovis aries PE=1 SV=2

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

| Query | Observed | Mr(expt) | Mr(calc)  | Delta     | Miss    | Score | Expect | Rank   | Unique | Peptide     |                      |
|-------|----------|----------|-----------|-----------|---------|-------|--------|--------|--------|-------------|----------------------|
| ✓     | 132      | 404.2051 | 806.3957  | 806.3923  | 0.0034  | 0     | (29)   | 1.2    | 1      | K.LAADDFR.T |                      |
| ✓     | 133      | 404.2052 | 806.3959  | 806.3923  | 0.0037  | 0     | 50     | 0.0087 | 1      | K.LAADDFR.T |                      |
| ✓     | 182      | 500.2943 | 998.5741  | 998.5760  | -0.0019 | 0     | 41     | 0.052  | 1      | U           | R.LVVQIDNAK.L        |
| ✓     | 223      | 555.2689 | 1108.5232 | 1108.5189 | 0.0043  | 0     | 24     | 1.9    | 2      | U           | R.DVEEWYIR.Q         |
| ✓     | 328      | 739.8556 | 1477.6966 | 1477.6896 | 0.0070  | 0     | 38     | 0.056  | 1      | U           | R.DSLENTLETPEAR.Y    |
| ✓     | 377      | 917.9986 | 1833.9827 | 1833.9697 | 0.0130  | 0     | 16     | 11     | 1      | U           | R.TVNALEVELQAQHNLR.D |

13. [K2M3 SHEEP](#) Mass: 56418 Score: 47 Matches: 2(0) Sequences: 2(0) emPAI: 0.13

Keratin, type II microfibrillar, component 5 OS=Ovis aries PE=1 SV=1

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

| Query | Observed | Mr(expt) | Mr(calc)  | Delta     | Miss   | Score | Expect | Rank  | Unique | Peptide |               |
|-------|----------|----------|-----------|-----------|--------|-------|--------|-------|--------|---------|---------------|
| ✓     | 177      | 490.2667 | 978.5188  | 978.5134  | 0.0053 | 0     | 39     | 0.099 | 1      | U       | R.ISPGYSVTR.T |
| ✓     | 197      | 519.7478 | 1037.4811 | 1037.4778 | 0.0033 | 0     | 32     | 0.3   | 1      | U       | K.AQYDDIASR.S |

14. [C04A HUMAN](#) Mass: 194247 Score: 39 Matches: 1(0) Sequences: 1(0) emPAI: 0.02

Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1

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

| Query | Observed | Mr(expt) | Mr(calc)  | Delta     | Miss   | Score | Expect | Rank  | Unique | Peptide |                     |
|-------|----------|----------|-----------|-----------|--------|-------|--------|-------|--------|---------|---------------------|
| ✓     | 333      | 771.4181 | 1540.8216 | 1540.8097 | 0.0119 | 0     | 39     | 0.067 | 1      | U       | K.VLSLAQEQVGGSPER.L |

Proteins matching the same set of peptides:



|                                     |                     |          |          |
|-------------------------------------|---------------------|----------|----------|
| <input type="checkbox"/>            | <a href="#">29</a>  | 444.1179 | 443.1107 |
| <input checked="" type="checkbox"/> | <a href="#">30</a>  | 447.1393 | 446.1320 |
| <input checked="" type="checkbox"/> | <a href="#">31</a>  | 456.2819 | 455.2746 |
| <input checked="" type="checkbox"/> | <a href="#">32</a>  | 476.3081 | 475.3009 |
| <input checked="" type="checkbox"/> | <a href="#">33</a>  | 484.3866 | 483.3793 |
| <input checked="" type="checkbox"/> | <a href="#">34</a>  | 500.3076 | 499.3003 |
| <input checked="" type="checkbox"/> | <a href="#">35</a>  | 500.3077 | 499.3005 |
| <input checked="" type="checkbox"/> | <a href="#">36</a>  | 500.3087 | 499.3014 |
| <input checked="" type="checkbox"/> | <a href="#">37</a>  | 500.3831 | 499.3759 |
| <input checked="" type="checkbox"/> | <a href="#">38</a>  | 502.3740 | 501.3667 |
| <input checked="" type="checkbox"/> | <a href="#">39</a>  | 503.3079 | 502.3006 |
| <input checked="" type="checkbox"/> | <a href="#">40</a>  | 504.3037 | 503.2964 |
| <input checked="" type="checkbox"/> | <a href="#">41</a>  | 520.3344 | 519.3272 |
| <input checked="" type="checkbox"/> | <a href="#">42</a>  | 520.3349 | 519.3276 |
| <input checked="" type="checkbox"/> | <a href="#">43</a>  | 525.3227 | 524.3155 |
| <input checked="" type="checkbox"/> | <a href="#">44</a>  | 528.3644 | 527.3571 |
| <input checked="" type="checkbox"/> | <a href="#">45</a>  | 528.3657 | 527.3584 |
| <input checked="" type="checkbox"/> | <a href="#">46</a>  | 539.3334 | 538.3261 |
| <input checked="" type="checkbox"/> | <a href="#">48</a>  | 544.3350 | 543.3278 |
| <input checked="" type="checkbox"/> | <a href="#">49</a>  | 546.3989 | 545.3917 |
| <input checked="" type="checkbox"/> | <a href="#">50</a>  | 546.4023 | 545.3951 |
| <input checked="" type="checkbox"/> | <a href="#">51</a>  | 548.3309 | 547.3236 |
| <input checked="" type="checkbox"/> | <a href="#">52</a>  | 578.3403 | 577.3331 |
| <input checked="" type="checkbox"/> | <a href="#">53</a>  | 579.2160 | 578.2088 |
| <input checked="" type="checkbox"/> | <a href="#">54</a>  | 579.5355 | 578.5282 |
| <input checked="" type="checkbox"/> | <a href="#">55</a>  | 579.5364 | 578.5291 |
| <input checked="" type="checkbox"/> | <a href="#">56</a>  | 579.5364 | 578.5291 |
| <input checked="" type="checkbox"/> | <a href="#">57</a>  | 579.5366 | 578.5294 |
| <input checked="" type="checkbox"/> | <a href="#">58</a>  | 586.4196 | 585.4124 |
| <input checked="" type="checkbox"/> | <a href="#">59</a>  | 590.4290 | 589.4217 |
| <input checked="" type="checkbox"/> | <a href="#">60</a>  | 606.3338 | 605.3265 |
| <input checked="" type="checkbox"/> | <a href="#">61</a>  | 607.5679 | 606.5606 |
| <input checked="" type="checkbox"/> | <a href="#">62</a>  | 608.3872 | 607.3799 |
| <input checked="" type="checkbox"/> | <a href="#">63</a>  | 614.5729 | 613.5656 |
| <input checked="" type="checkbox"/> | <a href="#">64</a>  | 615.4051 | 614.3978 |
| <input checked="" type="checkbox"/> | <a href="#">65</a>  | 615.4053 | 614.3980 |
| <input checked="" type="checkbox"/> | <a href="#">66</a>  | 615.4057 | 614.3984 |
| <input checked="" type="checkbox"/> | <a href="#">67</a>  | 617.4079 | 616.4007 |
| <input checked="" type="checkbox"/> | <a href="#">68</a>  | 617.4083 | 616.4010 |
| <input checked="" type="checkbox"/> | <a href="#">70</a>  | 625.9693 | 624.9620 |
| <input checked="" type="checkbox"/> | <a href="#">71</a>  | 630.4461 | 629.4389 |
| <input checked="" type="checkbox"/> | <a href="#">72</a>  | 630.4462 | 629.4389 |
| <input checked="" type="checkbox"/> | <a href="#">73</a>  | 638.1649 | 637.1576 |
| <input checked="" type="checkbox"/> | <a href="#">74</a>  | 638.3981 | 637.3908 |
| <input checked="" type="checkbox"/> | <a href="#">75</a>  | 638.4108 | 637.4036 |
| <input checked="" type="checkbox"/> | <a href="#">76</a>  | 650.2069 | 649.1996 |
| <input checked="" type="checkbox"/> | <a href="#">78</a>  | 661.5632 | 660.5559 |
| <input checked="" type="checkbox"/> | <a href="#">79</a>  | 661.5632 | 660.5559 |
| <input checked="" type="checkbox"/> | <a href="#">80</a>  | 661.5636 | 660.5564 |
| <input checked="" type="checkbox"/> | <a href="#">82</a>  | 675.3281 | 674.3208 |
| <input checked="" type="checkbox"/> | <a href="#">84</a>  | 675.6618 | 674.6545 |
| <input checked="" type="checkbox"/> | <a href="#">85</a>  | 675.6774 | 674.6701 |
| <input checked="" type="checkbox"/> | <a href="#">86</a>  | 675.6774 | 674.6701 |
| <input checked="" type="checkbox"/> | <a href="#">87</a>  | 675.6780 | 674.6707 |
| <input checked="" type="checkbox"/> | <a href="#">88</a>  | 675.6780 | 674.6707 |
| <input checked="" type="checkbox"/> | <a href="#">89</a>  | 675.6780 | 674.6708 |
| <input checked="" type="checkbox"/> | <a href="#">90</a>  | 675.6785 | 674.6713 |
| <input checked="" type="checkbox"/> | <a href="#">91</a>  | 675.6786 | 674.6714 |
| <input checked="" type="checkbox"/> | <a href="#">92</a>  | 675.6800 | 674.6727 |
| <input checked="" type="checkbox"/> | <a href="#">93</a>  | 675.6855 | 674.6782 |
| <input checked="" type="checkbox"/> | <a href="#">94</a>  | 677.6848 | 676.6776 |
| <input checked="" type="checkbox"/> | <a href="#">95</a>  | 677.6854 | 676.6781 |
| <input checked="" type="checkbox"/> | <a href="#">96</a>  | 678.4820 | 677.4747 |
| <input checked="" type="checkbox"/> | <a href="#">97</a>  | 678.5842 | 677.5769 |
| <input checked="" type="checkbox"/> | <a href="#">98</a>  | 678.5898 | 677.5825 |
| <input checked="" type="checkbox"/> | <a href="#">99</a>  | 678.5920 | 677.5847 |
| <input checked="" type="checkbox"/> | <a href="#">100</a> | 683.5453 | 682.5380 |
| <input checked="" type="checkbox"/> | <a href="#">101</a> | 683.5455 | 682.5383 |
| <input checked="" type="checkbox"/> | <a href="#">102</a> | 683.5456 | 682.5383 |
| <input checked="" type="checkbox"/> | <a href="#">103</a> | 696.4402 | 695.4329 |
| <input checked="" type="checkbox"/> | <a href="#">104</a> | 714.3241 | 713.3168 |
| <input checked="" type="checkbox"/> | <a href="#">105</a> | 717.5425 | 716.5352 |
| <input checked="" type="checkbox"/> | <a href="#">106</a> | 717.6301 | 716.6229 |
| <input checked="" type="checkbox"/> | <a href="#">107</a> | 717.6315 | 716.6243 |
| <input checked="" type="checkbox"/> | <a href="#">108</a> | 718.4981 | 717.4908 |
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Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Fixed modifications : [Carbamidomethyl \(C\)](#)  
Variable modifications : [Oxidation \(M\)](#)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm$  0.05 Da  
Fragment Mass Tolerance:  $\pm$  0.05 Da  
Max Missed Cleavages : 2  
Instrument type : Default  
Number of queries : 632

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