Mascot Search Results

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SwissProt       Decoy     False discovery rate
Peptide matches above identity threshold    66       5        7.58 %
Peptide matches above homology or identity threshold  77       5        6.49 %

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 > 30 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

1. **K2C1_HUMAN**
   - **Mass:** 65999
   - **Score:** 401
   - **Matches:** 17(10)
   - **Sequences:** 16(9)
   - **emPAI:** 0.93

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### Peptide Summary Report

#### K1C9_HUMAN

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Peptide Summary Report (Submitted from PROJ13988 by Mascot Daemon on APAF-WS-08)

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- **Sequences:** 9(6)
- **emPAI:** 0.14

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- **emPAI:** 0.17

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- **Sequences:** 5(5)
- **emPAI:** 0.35

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   **Sequences:** 6(2)  
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   Spectrin alpha chain, brain OS=Homo sapiens GN=SPTAN1 PE=1 SV=3

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     - 293 495.7772 989.5398 989.5294 10.5 0 43 1 U K.LPGAAEVQR.F
     - 382 540.3046 1078.5947 1078.5811 12.6 0 15 2.1 1 U R.QSFVPAAYVK.K
     - 450 631.8101 1261.6057 1261.5799 20.5 0 5 19 7 U R.EANQQQPFQR.N
     - 490 651.8390 1301.6635 1301.6463 13.3 0 75 1.8e-006 1 U K.VLETAEDIQER.R
     - 567 579.9626 1736.8660 1736.8217 25.5 1 10 4.4 1 U K.TATDEAYKDFSNLQQK.V

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   **Score:** 80  
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   **Sequences:** 4(3)  
   **emPAI:** 0.19
   
   Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3

   - **Query  Observed  Mr(expt)  Mr(calc)  ppm  Miss Score Expect Rank Unique  Peptide**
     - 318 508.7782 1015.5418 1015.5298 11.8 0 13 3.8 1 U R.QLDSIVGER.G
     - 360 547.2715 1092.5284 1092.5199 7.76 0 46 0.0014 1 U K.AQYEEIAN.R
     - 406 602.3331 1202.6516 1202.6295 18.3 0 33 0.033 1 U K.WTLLQEQGTK.T
     - 516 665.3767 1328.7388 1328.7187 15.1 0 58 0.00011 1 U K.NLDDSITAIKV.A

13. **K1H2_HUMAN**  
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   **Matches:** 3(1)  
   **Sequences:** 3(1)  
   **emPAI:** 0.07
   
   Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 PE=1 SV=3

   - **Query  Observed  Mr(expt)  Mr(calc)  ppm  Miss Score Expect Rank Unique  Peptide**
     - 19 404.2074 806.4002 806.3923 9.91 0 41 0.0055 1 U K.LAADDFOR.A
     - 486 649.2909 1296.5673 1296.6422 -57.77 1 9 6.8 1 U K.KNHEEVEGSLR.C
     - 533 450.1000 1347.2782 1347.5734 -219.07 0 31 8 U R.TVGMPCSPCPGQR.Y + Oxidation (M)

14. **K1C24_HUMAN**  
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   **Sequences:** 2(1)  
   **emPAI:** 0.07
   
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     - 392 586.3228 1170.6310 1170.5921 33.2 0 7 12 1 U K.YSIIIEDLR.N

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   **Sequences:** 2(1)  
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   - **Peptide Summary Report (Submitted from PROJ13988 by Mascot Daemon on APAF-WS-08)**
### Peptide Summary Report

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Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2

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Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1

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**Sequences:** 2(0)  
**emPAI:** 0.03  

1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Homo sapiens GN=PLCB1 PE=1 SV=1

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**Notes:**
- Peptide Summary Report (Submitted from PROJ13988 by Mascot Daemon on APAF-WS-08)
- Mascot Daemon results include oxidations and propionamidations.
Peptide Summary Report (Submitted from PROJ13988 by Mascot Daemon on APAF-WS-08)

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Peptide Summary Report (Submitted from PROJ13988 by Mascot Daemon on APAF-WS-08)

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Peptide Summary Report

Search Parameters

Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Variable modifications : Oxidation (M), Propionamide (C)
Mass values            : Monoisotopic
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