**Mascot Search Results**

**User : LabKey User** **Email : markeys@mail.nih.gov** **Search title : Conversion of E:\Sandy\Dhaval\Controls\@files\Control\mascot\remainingS2\_filesDec21\_Copy6\09MAR16\_OT\_03.work\09MAR16\_OT\_03.mzXML to mascot generic** **MS data file : 09MAR16\_OT\_03.mgf** **Database : sprot\_mammal\_rev mammal\_rev\_122010 (130376 sequences; 63679660 residues)** **Timestamp : 21 Dec 2010 at 21:06:54 GMT** **Warning : No taxonomy indexes for sprot\_mammal\_rev, taxonomy 'Mammalia (mammals)' ignored. Searching all entries in sprot\_mammal\_rev** **Enzyme : Trypsin** **Fixed modifications : [Carbamidomethyl (C)](http://biospec.nih.gov/cgi/client.pl?modification&mod_name=Carbamidomethyl+%28C%29&file=../data/20101221/F593086.dat" \t "_blank)** **Variable modifications : [Acetyl (Protein N-term)](http://biospec.nih.gov/cgi/client.pl?modification&mod_name=Acetyl+%28Protein+N%2dterm%29&file=../data/20101221/F593086.dat" \t "_blank),[Oxidation (M)](http://biospec.nih.gov/cgi/client.pl?modification&mod_name=Oxidation+%28M%29&file=../data/20101221/F593086.dat" \t "_blank)** **Mass values : Monoisotopic** **Protein Mass : Unrestricted** **Peptide Mass Tolerance : ± 50 ppm** **Fragment Mass Tolerance: ± 0.8 Da** **Max Missed Cleavages : 1** **Instrument type : Default** **Number of queries : 1055**

|  |  |  |
| --- | --- | --- |
| **Protein hits           :** | [**sp|Q4R5B3|TBB2A\_MACFA|Tubulin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit1) | beta-2A chain OS=Macaca fascicularis GN=TUBB2A PE=2 SV=1 |
|  | [**sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit2) | anion-selective channel protein 1 OS=Sus scrofa GN=VDAC1 PE=2 SV=3 |
|  | [**sp|Q2HJ86|TBA1D\_BOVIN|Tubulin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit3) | alpha-1D chain OS=Bos taurus GN=TUBA1D PE=1 SV=1 |
|  | [**sp|Q3MHM5|TBB2C\_BOVIN|Tubulin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit4) | beta-2C chain OS=Bos taurus GN=TUBB2C PE=2 SV=1 |
|  | [**sp|Q0PGG4|ACTB\_BOSMU|Actin,**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit5) | cytoplasmic 1 OS=Bos mutus grunniens GN=ACTB PE=2 SV=1 |
|  | [**sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit6) | OS=Mus musculus GN=Ank2 PE=1 SV=2 |
|  | [**sp|P02686|MBP\_HUMAN|Myelin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit7) | basic protein OS=Homo sapiens GN=MBP PE=1 SV=3 |
|  | [**sp|P23565|AINX\_RAT|Alpha-internexin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit8) | OS=Rattus norvegicus GN=Ina PE=1 SV=2 |
|  | [**sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit9) | 3'-phosphodiesterase OS=Rattus norvegicus GN=Cnp PE=1 SV=2 |
|  | [**sp|Q3KR86|IMMT\_RAT|Mitochondrial**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit10) | inner membrane protein (Fragment) OS=Rattus norvegicus GN=Immt PE=1 SV=1 |
|  | [**sp|P02769|ALBU\_BOVIN|Serum**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit11) | albumin OS=Bos taurus GN=ALB PE=1 SV=4 |
|  | [**sp|P16086|SPTA2\_RAT|Spectrin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit12) | alpha chain, brain OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 |
|  | [**sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit13) | anion-selective channel protein 2 OS=Sus scrofa GN=VDAC2 PE=2 SV=1 |
|  | [**sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit14) | anion-selective channel protein 3 OS=Rattus norvegicus GN=Vdac3 PE=1 SV=2 |
|  | [**sp|P15205|MAP1B\_RAT|Microtubule-associated**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit15) | protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=2 |
|  | [**sp|Q3ZBU7|TBB4\_BOVIN|Tubulin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit16) | beta-4 chain OS=Bos taurus GN=TUBB4 PE=2 SV=1 |
|  | [**sp|P09951|SYN1\_RAT|Synapsin-1**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit17) | OS=Rattus norvegicus GN=Syn1 PE=1 SV=3 |
|  | [**sp|Q08DH7|AINX\_BOVIN|Alpha-internexin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit18) | OS=Bos taurus GN=INA PE=2 SV=1 |
|  | [**sp|Q2T9S0|TBB3\_BOVIN|Tubulin**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit19) | beta-3 chain OS=Bos taurus GN=TUBB3 PE=1 SV=1 |
|  | [**sp|Q9Z214|HOME1\_RAT|Homer**](http://biospec.nih.gov/cgi/master_results.pl?file=..%2Fdata%2F20101221%2FF593086.dat#Hit20) | protein homolog 1 OS=Rattus norvegicus GN=Homer1 PE=1 SV=2 |

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**Select Summary Report**

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|  |  |  | [Help](http://biospec.nih.gov/help/msms_summaries_help.html" \t "_blank) |
|  | Significance threshold p< | Max. number of hits |  |
|  | Standard scoring   MudPIT scoring | Ions score or expect cut-off | Show sub-sets |
|  | Show pop-ups   Suppress pop-ups |  | Require bold red |

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      All queries      Unassigned      Below homology threshold      Below identity threshold

|  |  |
| --- | --- |
| **1.** | [sp|Q4R5B3|TBB2A\_MACFA|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50274    **Score:** 899    **Matches:** 38(37)  **Sequences:** 5(5)  **emPAI:** 1.54 |
|  | beta-2A chain OS=Macaca fascicularis GN=TUBB2A PE=2 SV=1 |

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [181](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=181&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **420.2395** | **1257.6966** | **1257.6830** | **10.8** | **1** | **44** | **0.0062** | **1** |  | **R.FPGQLNADLRK.L** [182](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=182&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [860](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=860&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **911.9750** | **1821.9355** | **1821.9156** | **11.0** | **0** | **68** | **2.3e-05** | **1** |  | **R.EIVHIQAGQCGNQIGAK.F** [859](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=859&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [861](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=861&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [862](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=862&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **608.3197** | **1821.9373** | **1821.9156** | **11.9** | **0** | **(60)** | **0.00014** | **1** |  | **R.EIVHIQAGQCGNQIGAK.F** [863](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=863&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [864](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=864&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [889](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=889&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **935.9870** | **1869.9594** | **1869.9373** | **11.8** | **1** | **106** | **3.5e-09** | **1** | **U** | **R.INVYYNEAAGNKYVPR.A** [887](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=887&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [893](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=893&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [890](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=890&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **624.3271** | **1869.9596** | **1869.9373** | **11.9** | **1** | **(49)** | **0.0018** | **1** | **U** | **R.INVYYNEAAGNKYVPR.A** [886](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=886&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [888](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=888&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [891](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=891&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [892](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=892&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [909](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=909&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **641.9778** | **1922.9115** | **1922.8900** | **11.2** | **1** | **(51)** | **0.0011** | **1** |  | **R.MSMKEVDEQMLNVQNK.N** [911](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=911&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [912](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=912&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [913](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=913&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **962.4642** | **1922.9138** | **1922.8900** | **12.4** | **1** | **103** | **7.2e-09** | **1** |  | **R.MSMKEVDEQMLNVQNK.N** [908](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=908&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [910](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=910&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [921](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=921&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **647.3096** | **1938.9069** | **1938.8849** | **11.3** | **1** | **(45)** | **0.0037** | **1** |  | **R.MSMKEVDEQMLNVQNK.N** [922](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=922&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [923](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=923&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **647.3099** | **1938.9078** | **1938.8849** | **11.8** | **1** | **(53)** | **0.00057** | **1** |  | **R.MSMKEVDEQMLNVQNK.N** [919](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=919&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [920](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=920&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [928](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=928&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **652.6414** | **1954.9024** | **1954.8798** | **11.6** | **1** | **(51)** | **0.00079** | **1** |  | **R.MSMKEVDEQMLNVQNK.N** [927](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=927&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [929](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=929&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **657.9724** | **1970.8954** | **1970.8747** | **10.5** | **1** | **(54)** | **0.00046** | **1** |  | **R.MSMKEVDEQMLNVQNK.N** |
|  | [944](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=944&hit=2&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **672.0272** | **2013.0597** | **2013.0353** | **12.1** | **1** | **(53)** | **0.00061** | **2** |  | **K.MSATFIGNSTAIQELFKR.I** [942](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=942&hit=2&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [943](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=943&hit=2&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [945](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=945&hit=2&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1007.5408** | **2013.0671** | **2013.0353** | **15.8** | **1** | **57** | **0.00026** | **1** |  | **K.MSATFIGNSTAIQELFKR.I** |
|  | [952](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=952&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **677.3583** | **2029.0532** | **2029.0302** | **11.3** | **1** | **(38)** | **0.022** | **1** |  | **K.MSATFIGNSTAIQELFKR.I** [950](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=950&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [951](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=951&hit=3&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [953](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=953&hit=1&index=sp%7cQ4R5B3%7cTBB2A_MACFA%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|Q7TMM9|TBB2A\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ7TMM9%7cTBB2A_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50274    **Score:** 899    **Matches:** 38(37)  **Sequences:** 5(5) |
|  | beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1 |

|  |  |
| --- | --- |
|  | [sp|P02554|TBB\_PIG|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP02554%7cTBB_PIG%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50285    **Score:** 899    **Matches:** 38(37)  **Sequences:** 5(5) |
|  | beta chain OS=Sus scrofa PE=1 SV=1 |

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|  | [sp|Q13885|TBB2A\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ13885%7cTBB2A_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50274    **Score:** 899    **Matches:** 38(37)  **Sequences:** 5(5) |
|  | beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 |

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|  | [sp|P85108|TBB2A\_RAT|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP85108%7cTBB2A_RAT%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50274    **Score:** 899    **Matches:** 38(37)  **Sequences:** 5(5) |
|  | beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 |

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| **2.** | [sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 30822    **Score:** 790    **Matches:** 28(17)  **Sequences:** 3(3)  **emPAI:** 1.00 |
|  | anion-selective channel protein 1 OS=Sus scrofa GN=VDAC1 PE=2 SV=3 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [542](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=542&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **764.8943** | **1527.7740** | **1527.7569** | **11.2** | **1** | **75** | **5.2e-06** | **1** | **U** | **K.LTFDSSFSPNTGKK.N** [541](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=541&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [545](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=545&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [544](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=544&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **510.2654** | **1527.7742** | **1527.7569** | **11.3** | **1** | **(44)** | **0.0067** | **1** | **U** | **K.LTFDSSFSPNTGKK.N** [543](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=543&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [546](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=546&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [547](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=547&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [548](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=548&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [549](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=549&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [980](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=980&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1052.1049** | **2102.1952** | **2102.1735** | **10.3** | **0** | **91** | **3.8e-08** | **1** | **U** | **K.VNNSSLIGLGYTQTLKPGIK.L** [974](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=974&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [975](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=975&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [976](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=976&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [981](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=981&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [982](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=982&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [984](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=984&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **701.7397** | **2102.1974** | **2102.1735** | **11.4** | **0** | **(50)** | **0.00046** | **1** | **U** | **K.VNNSSLIGLGYTQTLKPGIK.L** [972](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=972&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [973](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=973&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [977](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=977&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [978](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=978&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [979](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=979&hit=2&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [983](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=983&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [985](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=985&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [999](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=999&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1095.0249** | **2188.0353** | **2188.0131** | **10.1** | **1** | **137** | **2.6e-12** | **1** | **U** | **K.TKSENGLEFTSSGSANTETTK.V** [1000](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1000&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [1001](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1001&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **730.3528** | **2188.0365** | **2188.0131** | **10.7** | **1** | **(86)** | **2.7e-07** | **1** | **U** | **K.TKSENGLEFTSSGSANTETTK.V** [1002](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1002&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [1003](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1003&hit=1&index=sp%7cQ9MZ16%7cVDAC1_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|Q9TT15|VDAC1\_RABIT|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9TT15%7cVDAC1_RABIT%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 30836    **Score:** 790    **Matches:** 28(17)  **Sequences:** 3(3) |
|  | anion-selective channel protein 1 OS=Oryctolagus cuniculus GN=VDAC1 PE=2 SV=3 |

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|  | [sp|Q9Z2L0|VDAC1\_RAT|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9Z2L0%7cVDAC1_RAT%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 30851    **Score:** 790    **Matches:** 28(17)  **Sequences:** 3(3) |
|  | anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 |

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|  | [sp|P21796|VDAC1\_HUMAN|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP21796%7cVDAC1_HUMAN%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 30868    **Score:** 790    **Matches:** 28(17)  **Sequences:** 3(3) |
|  | anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 |

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|  | [sp|P45879|VDAC1\_BOVIN|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP45879%7cVDAC1_BOVIN%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 30836    **Score:** 790    **Matches:** 28(17)  **Sequences:** 3(3) |
|  | anion-selective channel protein 1 OS=Bos taurus GN=VDAC1 PE=1 SV=3 |

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|  | [sp|Q60932|VDAC1\_MOUSE|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ60932%7cVDAC1_MOUSE%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 32502    **Score:** 790    **Matches:** 28(17)  **Sequences:** 3(3) |
|  | anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3 |

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| **3.** | [sp|Q2HJ86|TBA1D\_BOVIN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50935    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4)  **emPAI:** 0.89 |
|  | alpha-1D chain OS=Bos taurus GN=TUBA1D PE=1 SV=1 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [368](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=368&hit=2&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **705.8989** | **1409.7832** | **1409.7667** | **11.7** | **0** | **54** | **0.00043** | **1** | **U** | **R.QLFHPEQLITGK.E** |
|  | [369](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=369&hit=2&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **470.9350** | **1409.7833** | **1409.7667** | **11.7** | **0** | **(36)** | **0.026** | **1** | **U** | **R.QLFHPEQLITGK.E** [370](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=370&hit=2&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [371](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=371&hit=2&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [735](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=735&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **859.9542** | **1717.8938** | **1717.8747** | **11.1** | **0** | **61** | **0.00012** | **1** | **U** | **R.NLDIERPTYTNLNR.L** [741](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=741&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [742](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=742&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [739](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=739&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **573.6387** | **1717.8944** | **1717.8747** | **11.4** | **0** | **(49)** | **0.0018** | **1** | **U** | **R.NLDIERPTYTNLNR.L** [727](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=727&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [728](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=728&hit=3&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [729](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=729&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [730](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=730&hit=6&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [731](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=731&hit=3&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [733](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=733&hit=2&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [734](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=734&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [736](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=736&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [737](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=737&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [738](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=738&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [740](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=740&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [743](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=743&hit=3&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [744](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=744&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [745](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=745&hit=6&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [746](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=746&hit=5&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [747](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=747&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [748](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=748&hit=4&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [750](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=750&hit=2&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [751](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=751&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [752](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=752&hit=3&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [753](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=753&hit=3&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [807](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=807&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **586.3331** | **1755.9774** | **1755.9559** | **12.2** | **0** | **(50)** | **0.00087** | **1** | **U** | **R.IHFPLATYAPVISAEK.A** [793](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=793&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [794](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=794&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [797](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=797&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [798](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=798&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [800](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=800&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [802](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=802&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [803](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=803&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [805](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=805&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [806](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=806&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [809](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=809&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [811](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=811&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [814](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=814&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [815](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=815&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [816](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=816&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [817](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=817&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [818](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=818&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [808](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=808&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **878.9960** | **1755.9775** | **1755.9559** | **12.3** | **0** | **85** | **3.2e-07** | **1** | **U** | **R.IHFPLATYAPVISAEK.A** [795](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=795&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [796](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=796&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [799](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=799&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [801](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=801&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [804](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=804&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [810](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=810&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [812](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=812&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [813](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=813&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [874](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=874&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **922.9566** | **1843.8987** | **1843.8783** | **11.0** | **1** | **48** | **0.0027** | **1** | **U** | **K.YMACCLLYRGDVVPK.D** |
|  | [877](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=877&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **615.6409** | **1843.9008** | **1843.8783** | **12.2** | **1** | **(29)** | **0.19** | **1** | **U** | **K.YMACCLLYRGDVVPK.D** [875](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=875&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [876](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=876&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [879](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=879&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **620.9722** | **1859.8947** | **1859.8732** | **11.5** | **1** | **(23)** | **0.76** | **1** | **U** | **K.YMACCLLYRGDVVPK.D** [878](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=878&hit=1&index=sp%7cQ2HJ86%7cTBA1D_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|Q2XVP4|TBA1B\_PIG|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ2XVP4%7cTBA1B_PIG%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Sus scrofa GN=TUBA1B PE=2 SV=1 |

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|  | [sp|Q4R538|TBA1B\_MACFA|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ4R538%7cTBA1B_MACFA%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Macaca fascicularis GN=TUBA1B PE=2 SV=1 |

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|  | [sp|A5A6J1|TBA1A\_PANTR|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cA5A6J1%7cTBA1A_PANTR%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50788    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1A chain OS=Pan troglodytes GN=TUBA1A PE=2 SV=1 |

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|  | [sp|Q5R1W4|TBA1B\_PANTR|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ5R1W4%7cTBA1B_PANTR%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50788    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Pan troglodytes GN=TUBA1B PE=2 SV=1 |

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|  | [sp|Q5XIF6|TBA4A\_RAT|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ5XIF6%7cTBA4A_RAT%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50634    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-4A chain OS=Rattus norvegicus GN=Tuba4a PE=2 SV=1 |

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|  | [sp|Q6AYZ1|TBA1C\_RAT|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ6AYZ1%7cTBA1C_RAT%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50590    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1C chain OS=Rattus norvegicus GN=Tuba1c PE=1 SV=1 |

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|  | [sp|Q6P9V9|TBA1B\_RAT|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ6P9V9%7cTBA1B_RAT%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Rattus norvegicus GN=Tuba1b PE=1 SV=1 |

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|  | [sp|Q9BQE3|TBA1C\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9BQE3%7cTBA1C_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50548    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 |

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|  | [sp|Q71U36|TBA1A\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ71U36%7cTBA1A_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50788    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 |

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|  | [sp|P05213|TBA1B\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP05213%7cTBA1B_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2 |

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|  | [sp|P68360|TBA1B\_MERUN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68360%7cTBA1B_MERUN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Meriones unguiculatus GN=TUBA1B PE=2 SV=1 |

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|  | [sp|P68361|TBA1B\_CRIGR|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68361%7cTBA1B_CRIGR%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Cricetulus griseus GN=TUBA1B PE=2 SV=1 |

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|  | [sp|P68362|TBA1A\_CRIGR|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68362%7cTBA1A_CRIGR%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50788    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1A chain OS=Cricetulus griseus GN=TUBA1A PE=2 SV=1 |

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|  | [sp|P68363|TBA1B\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68363%7cTBA1B_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 |

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|  | [sp|P68365|TBA1C\_CRIGR|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68365%7cTBA1C_CRIGR%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50562    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1C chain OS=Cricetulus griseus GN=TUBA1C PE=2 SV=1 |

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|  | [sp|P68366|TBA4A\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68366%7cTBA4A_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50634    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 |

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|  | [sp|P68367|TBA4A\_MACFA|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68367%7cTBA4A_MACFA%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50634    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-4A chain OS=Macaca fascicularis GN=TUBA4A PE=2 SV=1 |

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|  | [sp|P68368|TBA4A\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68368%7cTBA4A_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50634    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1 |

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|  | [sp|P68369|TBA1A\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68369%7cTBA1A_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50788    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1 |

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|  | [sp|P68370|TBA1A\_RAT|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68370%7cTBA1A_RAT%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50788    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1A chain OS=Rattus norvegicus GN=Tuba1a PE=1 SV=1 |

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|  | [sp|P68373|TBA1C\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68373%7cTBA1C_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50562    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1 |

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|  | [sp|P81947|TBA1B\_BOVIN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP81947%7cTBA1B_BOVIN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50804    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-1B chain OS=Bos taurus PE=1 SV=2 |

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|  | [sp|P81948|TBA4A\_BOVIN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP81948%7cTBA4A_BOVIN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50634    **Score:** 716    **Matches:** 61(31)  **Sequences:** 4(4) |
|  | alpha-4A chain OS=Bos taurus GN=TUBA4A PE=1 SV=2 |

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| **4.** | [sp|Q3MHM5|TBB2C\_BOVIN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50255    **Score:** 631    **Matches:** 30(29)  **Sequences:** 4(4)  **emPAI:** 1.20 |
|  | beta-2C chain OS=Bos taurus GN=TUBB2C PE=2 SV=1 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [181](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=181&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 420.2395 | 1257.6966 | 1257.6830 | 10.8 | 1 | 44 | 0.0062 | 1 |  | R.FPGQLNADLRK.L [182](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=182&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [860](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=860&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 911.9750 | 1821.9355 | 1821.9156 | 11.0 | 0 | 68 | 2.3e-05 | 1 |  | R.EIVHLQAGQCGNQIGAK.F [859](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=859&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [861](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=861&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [862](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=862&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 608.3197 | 1821.9373 | 1821.9156 | 11.9 | 0 | (60) | 0.00014 | 1 |  | R.EIVHLQAGQCGNQIGAK.F [863](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=863&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [864](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=864&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [909](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=909&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 641.9778 | 1922.9115 | 1922.8900 | 11.2 | 1 | (51) | 0.0011 | 1 |  | R.MSMKEVDEQMLNVQNK.N [911](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=911&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [912](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=912&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [913](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=913&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 962.4642 | 1922.9138 | 1922.8900 | 12.4 | 1 | 103 | 7.2e-09 | 1 |  | R.MSMKEVDEQMLNVQNK.N [908](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=908&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [910](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=910&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [921](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=921&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 647.3096 | 1938.9069 | 1938.8849 | 11.3 | 1 | (45) | 0.0037 | 1 |  | R.MSMKEVDEQMLNVQNK.N [922](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=922&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [923](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=923&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 647.3099 | 1938.9078 | 1938.8849 | 11.8 | 1 | (53) | 0.00057 | 1 |  | R.MSMKEVDEQMLNVQNK.N [919](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=919&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [920](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=920&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [928](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=928&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 652.6414 | 1954.9024 | 1954.8798 | 11.6 | 1 | (51) | 0.00079 | 1 |  | R.MSMKEVDEQMLNVQNK.N [927](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=927&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [929](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=929&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 657.9724 | 1970.8954 | 1970.8747 | 10.5 | 1 | (54) | 0.00046 | 1 |  | R.MSMKEVDEQMLNVQNK.N |
|  | [944](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=944&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 672.0272 | 2013.0597 | 2013.0353 | 12.1 | 1 | (53) | 0.00061 | 2 |  | K.MSATFIGNSTAIQELFKR.I [942](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=942&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [943](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=943&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [945](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=945&hit=2&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 1007.5408 | 2013.0671 | 2013.0353 | 15.8 | 1 | 57 | 0.00026 | 1 |  | K.MSATFIGNSTAIQELFKR.I |
|  | [952](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=952&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 677.3583 | 2029.0532 | 2029.0302 | 11.3 | 1 | (38) | 0.022 | 1 |  | K.MSATFIGNSTAIQELFKR.I [950](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=950&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [951](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=951&hit=3&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [953](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=953&hit=1&index=sp%7cQ3MHM5%7cTBB2C_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|Q6P9T8|TBB2C\_RAT|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ6P9T8%7cTBB2C_RAT%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50225    **Score:** 631    **Matches:** 30(29)  **Sequences:** 4(4) |
|  | beta-2C chain OS=Rattus norvegicus GN=Tubb2c PE=1 SV=1 |

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|  | [sp|P68371|TBB2C\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68371%7cTBB2C_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50255    **Score:** 631    **Matches:** 30(29)  **Sequences:** 4(4) |
|  | beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1 |

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|  | [sp|P68372|TBB2C\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68372%7cTBB2C_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50255    **Score:** 631    **Matches:** 30(29)  **Sequences:** 4(4) |
|  | beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1 |

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| **5.** | [sp|Q0PGG4|ACTB\_BOSMU|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42064    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3)  **emPAI:** 1.56 |
|  | cytoplasmic 1 OS=Bos mutus grunniens GN=ACTB PE=2 SV=1 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [562](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=562&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **774.9182** | **1547.8219** | **1547.8051** | **10.8** | **1** | **(68)** | **2.2e-05** | **1** | **U** | **R.MQKEITALAPSTMK.I** [560](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=560&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [564](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=564&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [566](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=566&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **516.9489** | **1547.8249** | **1547.8051** | **12.8** | **1** | **(36)** | **0.04** | **1** | **U** | **R.MQKEITALAPSTMK.I** [563](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=563&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [565](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=565&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [587](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=587&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **782.9150** | **1563.8154** | **1563.8000** | **9.84** | **1** | **(74)** | **6.2e-06** | **1** | **U** | **R.MQKEITALAPSTMK.I** [588](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=588&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [590](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=590&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **782.9160** | **1563.8174** | **1563.8000** | **11.1** | **1** | **93** | **7.8e-08** | **1** | **U** | **R.MQKEITALAPSTMK.I** [589](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=589&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [592](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=592&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **522.2801** | **1563.8184** | **1563.8000** | **11.8** | **1** | **(38)** | **0.026** | **1** | **U** | **R.MQKEITALAPSTMK.I** [591](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=591&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [593](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=593&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [596](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=596&hit=5&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **522.2940** | **1563.8602** | **1563.8000** | **38.5** | **1** | **(7)** | **23** | **5** | **U** | **R.MQKEITALAPSTMK.I** |
|  | [612](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=612&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **527.6114** | **1579.8123** | **1579.7949** | **11.0** | **1** | **(28)** | **0.24** | **1** | **U** | **R.MQKEITALAPSTMK.I** [613](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=613&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [648](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=648&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **543.9515** | **1628.8326** | **1628.8158** | **10.3** | **1** | **(36)** | **0.045** | **1** | **U** | **R.GYSFTTTAEREIVR.D** [649](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=649&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [651](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=651&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [652](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=652&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **815.4245** | **1628.8344** | **1628.8158** | **11.4** | **1** | **37** | **0.033** | **1** | **U** | **R.GYSFTTTAEREIVR.D** [650](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=650&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [1035](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1035&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **796.6679** | **3182.6425** | **3182.6071** | **11.1** | **0** | **(45)** | **0.0026** | **1** | **U** | **R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L** [1034](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1034&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [1036](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1036&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [1037](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1037&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1061.8895** | **3182.6467** | **3182.6071** | **12.5** | **0** | **71** | **5.5e-06** | **1** | **U** | **R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L** [1033](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1033&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [1038](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1038&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1067.2194** | **3198.6363** | **3198.6020** | **10.7** | **0** | **(57)** | **0.00014** | **1** | **U** | **R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L** [1039](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1039&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [1040](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1040&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [1043](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1043&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **800.6679** | **3198.6425** | **3198.6020** | **12.7** | **0** | **(45)** | **0.0026** | **1** | **U** | **R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L** [1041](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1041&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [1042](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1042&hit=1&index=sp%7cQ0PGG4%7cACTB_BOSMU%7cActin%2c&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|Q4L0Y2|ACTB\_SPECI|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ4L0Y2%7cACTB_SPECI%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Spermophilus citellus GN=ACTB PE=2 SV=1 |

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|  | [sp|Q4R561|ACTB\_MACFA|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ4R561%7cACTB_MACFA%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Macaca fascicularis GN=ACTB PE=2 SV=1 |

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|  | [sp|Q5R1X3|ACTB\_PANTR|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ5R1X3%7cACTB_PANTR%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Pan troglodytes GN=ACTB PE=2 SV=1 |

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|  | [sp|Q5R6G0|ACTB\_PONAB|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ5R6G0%7cACTB_PONAB%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Pongo abelii GN=ACTB PE=2 SV=1 |

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|  | [sp|Q6QAQ1|ACTB\_PIG|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ6QAQ1%7cACTB_PIG%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Sus scrofa GN=ACTB PE=2 SV=2 |

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|  | [sp|Q71FK5|ACTB\_CAVPO|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ71FK5%7cACTB_CAVPO%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Cavia porcellus GN=ACTB PE=2 SV=1 |

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|  | [sp|Q76N69|ACTB\_CERAE|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ76N69%7cACTB_CERAE%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Cercopithecus aethiops GN=ACTB PE=2 SV=1 |

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|  | [sp|Q91ZK5|ACTB\_SIGHI|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ91ZK5%7cACTB_SIGHI%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42034    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Sigmodon hispidus GN=ACTB PE=2 SV=1 |

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|  | [sp|Q711N9|ACTB\_MESAU|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ711N9%7cACTB_MESAU%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Mesocricetus auratus GN=ACTB PE=1 SV=1 |

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|  | [sp|O18840|ACTB\_CANFA|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cO18840%7cACTB_CANFA%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Canis familiaris GN=ACTB PE=2 SV=3 |

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|  | [sp|P29751|ACTB\_RABIT|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP29751%7cACTB_RABIT%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42071    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Oryctolagus cuniculus GN=ACTB PE=2 SV=1 |

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|  | [sp|P48975|ACTB\_CRIGR|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP48975%7cACTB_CRIGR%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42053    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Cricetulus griseus GN=ACTB PE=3 SV=1 |

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|  | [sp|P60707|ACTB\_TRIVU|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP60707%7cACTB_TRIVU%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Trichosurus vulpecula GN=ACTB PE=1 SV=1 |

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|  | [sp|P60708|ACTB\_HORSE|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP60708%7cACTB_HORSE%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Equus caballus GN=ACTB PE=2 SV=1 |

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|  | [sp|P60709|ACTB\_HUMAN|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP60709%7cACTB_HUMAN%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 |

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|  | [sp|P60710|ACTB\_MOUSE|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP60710%7cACTB_MOUSE%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 |

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|  | [sp|P60711|ACTB\_RAT|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP60711%7cACTB_RAT%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV=1 |

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|  | [sp|P60712|ACTB\_BOVIN|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP60712%7cACTB_BOVIN%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Bos taurus GN=ACTB PE=1 SV=1 |

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|  | [sp|P60713|ACTB\_SHEEP|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP60713%7cACTB_SHEEP%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42052    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Ovis aries GN=ACTB PE=2 SV=1 |

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|  | [sp|P63257|ACTG\_TRIVU|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP63257%7cACTG_TRIVU%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42108    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=1 SV=1 |

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|  | [sp|P63258|ACTG\_BOVIN|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP63258%7cACTG_BOVIN%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42108    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 2 OS=Bos taurus GN=ACTG1 PE=1 SV=1 |

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|  | [sp|P63259|ACTG\_RAT|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP63259%7cACTG_RAT%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42108    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 2 OS=Rattus norvegicus GN=Actg1 PE=1 SV=1 |

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|  | [sp|P63260|ACTG\_MOUSE|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP63260%7cACTG_MOUSE%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42108    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 |

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|  | [sp|P63261|ACTG\_HUMAN|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP63261%7cACTG_HUMAN%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42108    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 |

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|  | [sp|P84336|ACTB\_CAMDR|Actin,](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP84336%7cACTB_CAMDR%7cActin%2c&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 42174    **Score:** 608    **Matches:** 32(21)  **Sequences:** 3(3) |
|  | cytoplasmic 1 OS=Camelus dromedarius GN=ACTB PE=1 SV=1 |

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| **6.** | [sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 428451   **Score:** 586    **Matches:** 31(24)  **Sequences:** 7(7)  **emPAI:** 0.11 |
|  | OS=Mus musculus GN=Ank2 PE=1 SV=2 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [295](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=295&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **674.8845** | **1347.7544** | **1347.7398** | **10.8** | **1** | **73** | **6.6e-06** | **1** | **U** | **R.AGNLDKVVEYLK.G** [298](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=298&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [296](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=296&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **450.2590** | **1347.7551** | **1347.7398** | **11.3** | **1** | **(54)** | **0.00052** | **1** | **U** | **R.AGNLDKVVEYLK.G** [297](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=297&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [299](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=299&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [350](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=350&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **703.8987** | **1405.7828** | **1405.7678** | **10.7** | **0** | **61** | **0.0001** | **1** | **U** | **K.EGHVGLVQELLGR.G** [351](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=351&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [353](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=353&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [352](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=352&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **469.6018** | **1405.7836** | **1405.7678** | **11.3** | **0** | **(36)** | **0.03** | **1** | **U** | **K.EGHVGLVQELLGR.G** [354](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=354&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [355](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=355&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [397](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=397&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **725.8823** | **1449.7500** | **1449.7351** | **10.3** | **1** | **57** | **0.00037** | **1** | **U** | **K.IKTFDELEQEAK.Q** [398](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=398&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [399](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=399&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **484.2576** | **1449.7509** | **1449.7351** | **10.9** | **1** | **(45)** | **0.005** | **1** | **U** | **K.IKTFDELEQEAK.Q** [400](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=400&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [503](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=503&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **498.9413** | **1493.8019** | **1493.7838** | **12.1** | **0** | **(44)** | **0.006** | **1** | **U** | **R.SGHDQVVELLLER.K** [501](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=501&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [504](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=504&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [505](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=505&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **747.9085** | **1493.8025** | **1493.7838** | **12.5** | **0** | **71** | **1.2e-05** | **1** | **U** | **R.SGHDQVVELLLER.K** [502](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=502&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [506](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=506&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [555](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=555&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **768.9220** | **1535.8294** | **1535.8130** | **10.7** | **0** | **61** | **0.00011** | **1** | **U** | **R.VGLQAQPMHSELVK.K** [556](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=556&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [557](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=557&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **512.9507** | **1535.8302** | **1535.8130** | **11.2** | **0** | **(28)** | **0.24** | **1** | **U** | **R.VGLQAQPMHSELVK.K** [558](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=558&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [559](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=559&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [567](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=567&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **518.2825** | **1551.8258** | **1551.8079** | **11.5** | **0** | **(32)** | **0.079** | **1** | **U** | **R.VGLQAQPMHSELVK.K** |
|  | [828](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=828&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **593.6703** | **1777.9890** | **1777.9686** | **11.5** | **0** | **57** | **0.00015** | **1** |  | **K.GNTALHIASLAGQAEVVK.V** |
|  | [850](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=850&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **602.3256** | **1803.9550** | **1803.9342** | **11.6** | **0** | **52** | **0.00092** | **1** | **U** | **K.LGYTPLIVACHYGNVK.M** [849](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=849&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [851](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=851&hit=1&index=sp%7cQ8C8R3%7cANK2_MOUSE%7cAnkyrin%2d2&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

|  |  |
| --- | --- |
| **7.** | [sp|P02686|MBP\_HUMAN|Myelin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP02686%7cMBP_HUMAN%7cMyelin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 33097    **Score:** 524    **Matches:** 62(19)  **Sequences:** 2(2)  **emPAI:** 0.72 |
|  | basic protein OS=Homo sapiens GN=MBP PE=1 SV=3 |

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [275](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=275&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **668.8254** | **1335.6363** | **1335.6241** | **9.14** | **0** | **(50)** | **0.0017** | **1** | **U** | **K.YLATASTMDHAR.H** |
|  | [277](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=277&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **446.2205** | **1335.6396** | **1335.6241** | **11.6** | **0** | **(36)** | **0.041** | **1** | **U** | **K.YLATASTMDHAR.H** [276](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=276&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [305](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=305&hit=2&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **451.5524** | **1351.6354** | **1351.6190** | **12.1** | **0** | **(29)** | **0.23** | **2** | **U** | **K.YLATASTMDHAR.H** [300](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=300&hit=2&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [301](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=301&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [302](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=302&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [303](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=303&hit=4&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [304](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=304&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [306](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=306&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [307](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=307&hit=10&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [308](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=308&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [309](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=309&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [310](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=310&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [311](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=311&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **676.8259** | **1351.6372** | **1351.6190** | **13.4** | **0** | **65** | **5.1e-05** | **1** | **U** | **K.YLATASTMDHAR.H** |
|  | [434](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=434&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **730.8702** | **1459.7258** | **1459.7096** | **11.1** | **0** | **63** | **9.2e-05** | **1** | **U** | **R.TQDENPVVHFFK.N** [419](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=419&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [423](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=423&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [429](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=429&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [430](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=430&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [431](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=431&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [435](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=435&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [436](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=436&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [444](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=444&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [449](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=449&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **487.5829** | **1459.7270** | **1459.7096** | **11.9** | **0** | **(44)** | **0.0068** | **1** | **U** | **R.TQDENPVVHFFK.N** [412](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=412&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [413](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=413&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [414](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=414&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [415](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=415&hit=2&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [416](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=416&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [417](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=417&hit=3&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [418](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=418&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [420](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=420&hit=2&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [421](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=421&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [422](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=422&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [424](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=424&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [425](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=425&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [426](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=426&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [427](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=427&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [428](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=428&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [432](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=432&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [433](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=433&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [437](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=437&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [438](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=438&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [439](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=439&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [440](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=440&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [441](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=441&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [442](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=442&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [443](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=443&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [445](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=445&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [446](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=446&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [447](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=447&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [448](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=448&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [450](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=450&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [451](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=451&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [452](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=452&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [453](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=453&hit=9&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [454](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=454&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [455](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=455&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [456](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=456&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [457](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=457&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [458](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=458&hit=1&index=sp%7cP02686%7cMBP_HUMAN%7cMyelin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|P02688|MBP\_RAT|Myelin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP02688%7cMBP_RAT%7cMyelin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 21546    **Score:** 524    **Matches:** 62(19)  **Sequences:** 2(2) |
|  | basic protein S OS=Rattus norvegicus GN=Mbp PE=1 SV=3 |

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|  | [sp|P04370|MBP\_MOUSE|Myelin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP04370%7cMBP_MOUSE%7cMyelin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 27151    **Score:** 524    **Matches:** 62(19)  **Sequences:** 2(2) |
|  | basic protein OS=Mus musculus GN=Mbp PE=1 SV=2 |

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|  | [sp|P06906|MBP\_PANTR|Myelin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP06906%7cMBP_PANTR%7cMyelin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 18548    **Score:** 524    **Matches:** 62(19)  **Sequences:** 2(2) |
|  | basic protein OS=Pan troglodytes GN=MBP PE=1 SV=1 |

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| **8.** | [sp|P23565|AINX\_RAT|Alpha-internexin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 56253    **Score:** 484    **Matches:** 15(15)  **Sequences:** 3(3)  **emPAI:** 0.38 |
|  | OS=Rattus norvegicus GN=Ina PE=1 SV=2 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [531](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=531&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **506.9619** | **1517.8637** | **1517.8453** | **12.1** | **1** | **(39)** | **0.01** | **1** |  | **K.KVESLLDELAFVR.Q** [528](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=528&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [530](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=530&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [533](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=533&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **759.9394** | **1517.8642** | **1517.8453** | **12.5** | **1** | **97** | **1.7e-08** | **1** |  | **K.KVESLLDELAFVR.Q** [529](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=529&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [532](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=532&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [662](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=662&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **820.9487** | **1639.8828** | **1639.8642** | **11.4** | **1** | **86** | **3.3e-07** | **1** | **U** | **R.RLPASDGLDLSQAAAR.T** [661](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=661&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [663](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=663&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [665](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=665&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **547.6355** | **1639.8847** | **1639.8642** | **12.5** | **1** | **(51)** | **0.001** | **1** | **U** | **R.RLPASDGLDLSQAAAR.T** [664](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=664&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [666](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=666&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [907](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=907&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **640.9637** | **1919.8692** | **1919.8472** | **11.5** | **1** | **49** | **0.0013** | **1** | **U** | **M.SFGSEHYLCSASSYRK.V** [905](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=905&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [906](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=906&hit=1&index=sp%7cP23565%7cAINX_RAT%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|P46660|AINX\_MOUSE|Alpha-internexin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP46660%7cAINX_MOUSE%7cAlpha%2dinternexin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 55879    **Score:** 484    **Matches:** 15(15)  **Sequences:** 3(3) |
|  | OS=Mus musculus GN=Ina PE=1 SV=2 |

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| --- | --- |
| **9.** | [sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 47638    **Score:** 446    **Matches:** 19(15)  **Sequences:** 3(3)  **emPAI:** 0.46 |
|  | 3'-phosphodiesterase OS=Rattus norvegicus GN=Cnp PE=1 SV=2 |

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [221](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=221&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **649.8608** | **1297.7071** | **1297.6918** | **11.8** | **1** | **49** | **0.0018** | **1** | **U** | **K.EKLDLVSYFGK.R** [224](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=224&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [225](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=225&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [222](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=222&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **433.5763** | **1297.7071** | **1297.6918** | **11.8** | **1** | **(14)** | **5.5** | **1** | **U** | **K.EKLDLVSYFGK.R** [220](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=220&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [223](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=223&hit=4&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [392](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=392&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **721.3836** | **1440.7527** | **1440.7361** | **11.5** | **0** | **91** | **1.5e-07** | **1** | **U** | **K.AGQVFLEELGNHK.A** [391](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=391&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [393](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=393&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [396](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=396&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **481.2584** | **1440.7533** | **1440.7361** | **11.9** | **0** | **(56)** | **0.00046** | **1** | **U** | **K.AGQVFLEELGNHK.A** [394](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=394&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [395](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=395&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [490](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=490&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **744.4044** | **1486.7942** | **1486.7780** | **10.9** | **1** | **54** | **0.00061** | **1** | **U** | **K.NQWQLSLDDLKK.L** [491](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=491&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [493](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=493&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [495](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=495&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **496.6056** | **1486.7950** | **1486.7780** | **11.5** | **1** | **(44)** | **0.007** | **1** | **U** | **K.NQWQLSLDDLKK.L** [492](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=492&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [494](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=494&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [496](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=496&hit=1&index=sp%7cP13233%7cCN37_RAT%7c2%27%2c3%27%2dcyclic%2dnucleotide&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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| **10.** | [sp|Q3KR86|IMMT\_RAT|Mitochondrial](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 67477    **Score:** 404    **Matches:** 16(12)  **Sequences:** 4(3)  **emPAI:** 0.31 |
|  | inner membrane protein (Fragment) OS=Rattus norvegicus GN=Immt PE=1 SV=1 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [174](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=174&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **622.3557** | **1242.6968** | **1242.6819** | **11.9** | **1** | **85** | **4.2e-07** | **1** | **U** | **R.KAVDEAADALLK.A** [173](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=173&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [175](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=175&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [261](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=261&hit=3&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **440.5567** | **1318.6484** | **1318.6915** | **-32.68** | **1** | **9** | **23** | **3** | **U** | **K.LAGRVAMIDETK.N** |
|  | [408](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=408&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **485.9400** | **1454.7983** | **1454.7803** | **12.4** | **0** | **(30)** | **0.14** | **1** | **U** | **K.LHSMIVDLDSVVK.K** [407](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=407&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [410](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=410&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [409](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=409&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **728.4064** | **1454.7983** | **1454.7803** | **12.4** | **0** | **53** | **0.00059** | **1** | **U** | **K.LHSMIVDLDSVVK.K** [405](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=405&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [406](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=406&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [537](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=537&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **764.4265** | **1526.8384** | **1526.8205** | **11.7** | **0** | **94** | **4.8e-08** | **1** | **U** | **K.VVSQYHELVVQAR.D** [535](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=535&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [536](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=536&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [539](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=539&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **509.9536** | **1526.8389** | **1526.8205** | **12.0** | **0** | **(42)** | **0.0069** | **1** | **U** | **K.VVSQYHELVVQAR.D** [538](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=538&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [540](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=540&hit=1&index=sp%7cQ3KR86%7cIMMT_RAT%7cMitochondrial&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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| **11.** | [sp|P02769|ALBU\_BOVIN|Serum](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP02769%7cALBU_BOVIN%7cSerum&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 71244    **Score:** 357    **Matches:** 8(8)  **Sequences:** 2(2)  **emPAI:** 0.16 |
|  | albumin OS=Bos taurus GN=ALB PE=1 SV=4 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [604](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=604&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **784.3851** | **1566.7556** | **1566.7354** | **12.9** | **0** | **78** | **2.8e-06** | **1** | **U** | **K.DAFLGSFLYEYSR.R** [603](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=603&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [605](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=605&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [657](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=657&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **820.4819** | **1638.9492** | **1638.9305** | **11.4** | **1** | **97** | **1.2e-08** | **1** | **U** | **R.KVPQVSTPTLVEVSR.S** [659](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=659&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [660](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=660&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **547.3240** | **1638.9501** | **1638.9305** | **12.0** | **1** | **(55)** | **0.00019** | **1** | **U** | **R.KVPQVSTPTLVEVSR.S** [656](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=656&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [658](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=658&hit=1&index=sp%7cP02769%7cALBU_BOVIN%7cSerum&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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| **12.** | [sp|P16086|SPTA2\_RAT|Spectrin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 285261   **Score:** 345    **Matches:** 19(15)  **Sequences:** 4(4)  **emPAI:** 0.11 |
|  | alpha chain, brain OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [138](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=138&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **400.9156** | **1199.7251** | **1199.7125** | **10.5** | **1** | **(39)** | **0.0097** | **1** | **U** | **K.LLEATELKGVK.L** [139](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=139&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [140](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=140&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **600.8705** | **1199.7265** | **1199.7125** | **11.7** | **1** | **52** | **0.00043** | **1** | **U** | **K.LLEATELKGVK.L** |
|  | [238](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=238&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **653.8518** | **1305.6891** | **1305.6751** | **10.7** | **1** | **(43)** | **0.0089** | **1** | **U** | **R.YEALKEPMVAR.K** [240](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=240&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [241](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=241&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [242](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=242&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **436.2372** | **1305.6899** | **1305.6751** | **11.4** | **1** | **48** | **0.0029** | **1** | **U** | **R.YEALKEPMVAR.K** [239](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=239&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [243](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=243&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [250](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=250&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **437.5889** | **1309.7450** | **1309.7282** | **12.8** | **1** | **(31)** | **0.078** | **1** | **U** | **R.KVEDLFLTFAK.K** [252](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=252&hit=6&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [253](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=253&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **655.8811** | **1309.7477** | **1309.7282** | **14.9** | **1** | **76** | **2e-06** | **1** | **U** | **R.KVEDLFLTFAK.K** [249](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=249&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [251](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=251&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [265](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=265&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **441.5692** | **1321.6857** | **1321.6700** | **11.9** | **1** | **(34)** | **0.069** | **1** | **U** | **R.YEALKEPMVAR.K** [264](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=264&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [844](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=844&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **600.9756** | **1799.9049** | **1799.8842** | **11.5** | **1** | **54** | **0.00061** | **1** | **U** | **K.GRELPTAFDYVEFTR.S** [843](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=843&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [845](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=845&hit=1&index=sp%7cP16086%7cSPTA2_RAT%7cSpectrin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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| **13.** | [sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 32086    **Score:** 332    **Matches:** 20(13)  **Sequences:** 2(2)  **emPAI:** 0.56 |
|  | anion-selective channel protein 2 OS=Sus scrofa GN=VDAC2 PE=2 SV=1 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [577](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=577&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **778.9103** | **1555.8061** | **1555.7882** | **11.5** | **1** | **59** | **0.00023** | **1** | **U** | **K.LTFDTTFSPNTGKK.S** [575](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=575&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [576](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=576&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [578](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=578&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **519.6095** | **1555.8067** | **1555.7882** | **11.8** | **1** | **(31)** | **0.15** | **1** | **U** | **K.LTFDTTFSPNTGKK.S** [579](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=579&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [580](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=580&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [973](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=973&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 701.7312 | 2102.1718 | 2102.1484 | 11.1 | 0 | (41) | 0.0051 | 1 | U | K.VNNSSLIGVGYTQTLRPGVK.L [972](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=972&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [977](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=977&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [978](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=978&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [979](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=979&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [983](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=983&hit=2&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [984](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=984&hit=2&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [985](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=985&hit=2&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [976](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=976&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 1052.0935 | 2102.1725 | 2102.1484 | 11.4 | 0 | 87 | 1.2e-07 | 1 | U | K.VNNSSLIGVGYTQTLRPGVK.L [974](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=974&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [975](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=975&hit=1&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [980](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=980&hit=2&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [981](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=981&hit=2&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [982](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=982&hit=2&index=sp%7cQ9MZ15%7cVDAC2_PIG%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|P45880|VDAC2\_HUMAN|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP45880%7cVDAC2_HUMAN%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 32060    **Score:** 332    **Matches:** 20(13)  **Sequences:** 2(2) |
|  | anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 |

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|  | [sp|Q60930|VDAC2\_MOUSE|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ60930%7cVDAC2_MOUSE%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 32340    **Score:** 332    **Matches:** 20(13)  **Sequences:** 2(2) |
|  | anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2 |

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|  | [sp|P68002|VDAC2\_BOVIN|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68002%7cVDAC2_BOVIN%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 32113    **Score:** 332    **Matches:** 20(13)  **Sequences:** 2(2) |
|  | anion-selective channel protein 2 OS=Bos taurus GN=VDAC2 PE=2 SV=2 |

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|  | [sp|P68003|VDAC2\_RABIT|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP68003%7cVDAC2_RABIT%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 32074    **Score:** 332    **Matches:** 20(13)  **Sequences:** 2(2) |
|  | anion-selective channel protein 2 OS=Oryctolagus cuniculus GN=VDAC2 PE=2 SV=1 |

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|  | [sp|P81155|VDAC2\_RAT|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP81155%7cVDAC2_RAT%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 32353    **Score:** 332    **Matches:** 20(13)  **Sequences:** 2(2) |
|  | anion-selective channel protein 2 OS=Rattus norvegicus GN=Vdac2 PE=1 SV=2 |

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|  | [sp|P86223|VDAC2\_MESAU|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP86223%7cVDAC2_MESAU%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 13583    **Score:** 332    **Matches:** 20(13)  **Sequences:** 2(2) |
|  | anion-selective channel protein 2 (Fragments) OS=Mesocricetus auratus GN=VDAC2 PE=1 SV=1 |

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| **14.** | [sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 31178    **Score:** 306    **Matches:** 9(9)  **Sequences:** 2(2)  **emPAI:** 0.41 |
|  | anion-selective channel protein 3 OS=Rattus norvegicus GN=Vdac3 PE=1 SV=2 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [554](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=554&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **511.6339** | **1531.8798** | **1531.8610** | **12.3** | **1** | **42** | **0.0045** | **1** | **U** | **K.LTVDTIFVPNTGKK.S** |
|  | [965](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=965&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **1044.0958** | **2086.1771** | **2086.1535** | **11.3** | **0** | **98** | **8.8e-09** | **1** | **U** | **K.VNNASLIGLGYTQSLRPGVK.L** [964](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=964&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [966](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=966&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [967](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=967&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **696.3998** | **2086.1775** | **2086.1535** | **11.5** | **0** | **(57)** | **0.00011** | **1** | **U** | **K.VNNASLIGLGYTQSLRPGVK.L** [963](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=963&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [968](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=968&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [969](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=969&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [970](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=970&hit=1&index=sp%7cQ9R1Z0%7cVDAC3_RAT%7cVoltage%2ddependent&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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| **15.** | [sp|P15205|MAP1B\_RAT|Microtubule-associated](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 270532   **Score:** 305    **Matches:** 19(10)  **Sequences:** 5(4)  **emPAI:** 0.07 |
|  | protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=2 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [341](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=341&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **464.5500** | **1390.6283** | **1390.6122** | **11.6** | **0** | **49** | **0.0017** | **1** | **U** | **K.HMDPPPAPMQDR.S** [339](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=339&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [340](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=340&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [356](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=356&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **469.8811** | **1406.6214** | **1406.6071** | **10.2** | **0** | **(22)** | **0.65** | **1** | **U** | **K.HMDPPPAPMQDR.S** [358](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=358&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [357](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=357&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **704.3185** | **1406.6224** | **1406.6071** | **10.9** | **0** | **(14)** | **4.3** | **1** | **U** | **K.HMDPPPAPMQDR.S** [361](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=361&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [360](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=360&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **469.8817** | **1406.6232** | **1406.6071** | **11.5** | **0** | **(26)** | **0.25** | **1** | **U** | **K.HMDPPPAPMQDR.S** [359](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=359&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [362](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=362&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **704.3208** | **1406.6271** | **1406.6071** | **14.2** | **0** | **(12)** | **6.8** | **1** | **U** | **K.HMDPPPAPMQDR.S** |
|  | [668](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=668&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **822.3976** | **1642.7806** | **1642.7627** | **10.9** | **0** | **70** | **1.3e-05** | **1** | **U** | **K.TIQAHDVGGYYYEK.T** |
|  | [669](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=669&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **548.6009** | **1642.7808** | **1642.7627** | **11.0** | **0** | **(69)** | **2e-05** | **1** | **U** | **K.TIQAHDVGGYYYEK.T** [667](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=667&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [670](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=670&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [683](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=683&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **553.9400** | **1658.7982** | **1658.7788** | **11.7** | **1** | **46** | **0.004** | **1** | **U** | **R.TPEVSGYTYEKTER.S** [682](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=682&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [926](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=926&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **649.9888** | **1946.9447** | **1946.9221** | **11.6** | **1** | **79** | **2e-06** | **1** | **U** | **K.ITKTPQASTYSYETSDR.C** [925](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=925&hit=1&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [957](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=957&hit=8&index=sp%7cP15205%7cMAP1B_RAT%7cMicrotubule%2dassociated&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **678.9664** | **2033.8775** | **2033.8975** | **-9.86** | **1** | **1** | **48** | **8** | **U** | **K.EMQYFMQQWTGTNKDK.A** |

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| **16.** | [sp|Q3ZBU7|TBB4\_BOVIN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50010    **Score:** 299    **Matches:** 12(12)  **Sequences:** 3(3)  **emPAI:** 0.43 |
|  | beta-4 chain OS=Bos taurus GN=TUBB4 PE=2 SV=1 |

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [181](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=181&hit=1&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 420.2395 | 1257.6966 | 1257.6830 | 10.8 | 1 | 44 | 0.0062 | 1 |  | R.FPGQLNADLRK.L [182](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=182&hit=1&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [860](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=860&hit=2&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 911.9750 | 1821.9355 | 1821.9156 | 11.0 | 0 | 68 | 2.3e-05 | 1 |  | R.EIVHLQAGQCGNQIGAK.F [859](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=859&hit=2&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [861](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=861&hit=2&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [862](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=862&hit=2&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 608.3197 | 1821.9373 | 1821.9156 | 11.9 | 0 | (60) | 0.00014 | 1 |  | R.EIVHLQAGQCGNQIGAK.F [863](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=863&hit=2&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [864](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=864&hit=2&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [944](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=944&hit=1&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 672.0272 | 2013.0597 | 2013.0353 | 12.1 | 1 | 54 | 0.00057 | 1 | U | K.MAATFIGNSTAIQELFKR.I [942](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=942&hit=1&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [943](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=943&hit=1&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [945](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=945&hit=3&index=sp%7cQ3ZBU7%7cTBB4_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 1007.5408 | 2013.0671 | 2013.0353 | 15.8 | 1 | (47) | 0.0022 | 3 | U | K.MAATFIGNSTAIQELFKR.I |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|Q4R4X8|TBB4\_MACFA|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ4R4X8%7cTBB4_MACFA%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50010    **Score:** 299    **Matches:** 12(12)  **Sequences:** 3(3) |
|  | beta-4 chain OS=Macaca fascicularis GN=TUBB4 PE=2 SV=1 |

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|  | [sp|Q9D6F9|TBB4\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9D6F9%7cTBB4_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50010    **Score:** 299    **Matches:** 12(12)  **Sequences:** 3(3) |
|  | beta-4 chain OS=Mus musculus GN=Tubb4 PE=1 SV=3 |

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|  | [sp|P04350|TBB4\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP04350%7cTBB4_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50010    **Score:** 299    **Matches:** 12(12)  **Sequences:** 3(3) |
|  | beta-4 chain OS=Homo sapiens GN=TUBB4 PE=1 SV=2 |

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| **17.** | [sp|P09951|SYN1\_RAT|Synapsin-1](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 74114    **Score:** 297    **Matches:** 17(8)  **Sequences:** 4(3)  **emPAI:** 0.28 |
|  | OS=Rattus norvegicus GN=Syn1 PE=1 SV=3 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [512](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=512&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **748.9293** | **1495.8441** | **1495.8259** | **12.1** | **0** | **(38)** | **0.014** | **1** | **U** | **R.QGPPQKPPGPAGPIR.Q** [508](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=508&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [509](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=509&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [513](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=513&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **499.6220** | **1495.8441** | **1495.8259** | **12.1** | **0** | **55** | **0.00028** | **1** | **U** | **R.QGPPQKPPGPAGPIR.Q** [510](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=510&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [511](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=511&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [514](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=514&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [515](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=515&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [516](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=516&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [517](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=517&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [947](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=947&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **672.6633** | **2014.9680** | **2014.9452** | **11.3** | **1** | **34** | **0.053** | **1** | **U** | **K.TNTGSAMLEQIAMSDRYK.L** [946](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=946&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [961](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=961&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **693.0388** | **2076.0944** | **2076.0712** | **11.2** | **1** | **75** | **3.7e-06** | **1** | **U** | **R.QASISGPAPPKVSGASPGGQQR.Q** [960](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=960&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [1052](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1052&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **848.9500** | **3391.7707** | **3391.7372** | **9.89** | **1** | **28** | **0.073** | **1** | **U** | **K.SQSLTNAFNLPEPAPPRPSLSQDEVKAETIR.S** [1053](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1053&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [1054](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=1054&hit=1&index=sp%7cP09951%7cSYN1_RAT%7cSynapsin%2d1&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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| **18.** | [sp|Q08DH7|AINX\_BOVIN|Alpha-internexin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 55533    **Score:** 256    **Matches:** 9(9)  **Sequences:** 2(2)  **emPAI:** 0.22 |
|  | OS=Bos taurus GN=INA PE=2 SV=1 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [531](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=531&hit=1&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 506.9619 | 1517.8637 | 1517.8453 | 12.1 | 1 | (39) | 0.01 | 1 |  | K.KVESLLDELAFVR.Q [528](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=528&hit=1&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [530](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=530&hit=1&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [533](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=533&hit=1&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 759.9394 | 1517.8642 | 1517.8453 | 12.5 | 1 | 97 | 1.7e-08 | 1 |  | K.KVESLLDELAFVR.Q [529](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=529&hit=1&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [532](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=532&hit=1&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [907](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=907&hit=2&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 640.9637 | 1919.8692 | 1919.8472 | 11.5 | 1 | 40 | 0.011 | 2 | U | M.SFGSEHYLCASSSYRK.V [905](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=905&hit=2&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [906](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=906&hit=2&index=sp%7cQ08DH7%7cAINX_BOVIN%7cAlpha%2dinternexin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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| **19.** | [sp|Q2T9S0|TBB3\_BOVIN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50856    **Score:** 252    **Matches:** 15(9)  **Sequences:** 3(3)  **emPAI:** 0.33 |
|  | beta-3 chain OS=Bos taurus GN=TUBB3 PE=1 SV=1 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [181](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=181&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 420.2395 | 1257.6966 | 1257.6830 | 10.8 | 1 | 44 | 0.0062 | 1 |  | R.FPGQLNADLRK.L [182](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=182&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [860](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=860&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 911.9750 | 1821.9355 | 1821.9156 | 11.0 | 0 | 68 | 2.3e-05 | 1 |  | R.EIVHIQAGQCGNQIGAK.F [859](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=859&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [861](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=861&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [862](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=862&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 608.3197 | 1821.9373 | 1821.9156 | 11.9 | 0 | (60) | 0.00014 | 1 |  | R.EIVHIQAGQCGNQIGAK.F [863](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=863&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [864](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=864&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [951](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=951&hit=2&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | 677.3583 | 2029.0532 | 2029.0302 | 11.3 | 1 | 41 | 0.011 | 2 | U | K.MSSTFIGNSTAIQELFKR.I [949](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=949&hit=2&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [950](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=950&hit=3&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [952](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=952&hit=3&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [953](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=953&hit=3&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [958](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=958&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **682.6904** | **2045.0493** | **2045.0252** | **11.8** | **1** | **(19)** | **1.6** | **1** | **U** | **K.MSSTFIGNSTAIQELFKR.I** [959](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=959&hit=1&index=sp%7cQ2T9S0%7cTBB3_BOVIN%7cTubulin&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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|  | **Proteins matching the same set of peptides:** |

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|  | [sp|Q4QRB4|TBB3\_RAT|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ4QRB4%7cTBB3_RAT%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50842    **Score:** 252    **Matches:** 15(9)  **Sequences:** 3(3) |
|  | beta-3 chain OS=Rattus norvegicus GN=Tubb3 PE=1 SV=1 |

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|  | [sp|Q9ERD7|TBB3\_MOUSE|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9ERD7%7cTBB3_MOUSE%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50842    **Score:** 252    **Matches:** 15(9)  **Sequences:** 3(3) |
|  | beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1 |

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|  | [sp|Q60HC2|TBB3\_MACFA|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ60HC2%7cTBB3_MACFA%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50856    **Score:** 252    **Matches:** 15(9)  **Sequences:** 3(3) |
|  | beta-3 chain OS=Macaca fascicularis GN=TUBB3 PE=2 SV=1 |

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|  | [sp|Q13509|TBB3\_HUMAN|Tubulin](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ13509%7cTBB3_HUMAN%7cTubulin&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 50856    **Score:** 252    **Matches:** 15(9)  **Sequences:** 3(3) |
|  | beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 |

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| **20.** | [sp|Q9Z214|HOME1\_RAT|Homer](http://biospec.nih.gov/cgi/protein_view.pl?file=../data/20101221/F593086.dat&hit=sp%7cQ9Z214%7cHOME1_RAT%7cHomer&db_idx=1&px=1&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank)    **Mass:** 41394    **Score:** 249    **Matches:** 5(5)  **Sequences:** 1(1)  **emPAI:** 0.19 |
|  | protein homolog 1 OS=Rattus norvegicus GN=Homer1 PE=1 SV=2 |

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|  | **Query** | **Observed** | **Mr(expt)** | **Mr(calc)** | **ppm** | **Miss** | **Score** | **Expect** | **Rank** | **Unique** | **Peptide** |
|  | [679](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=679&hit=1&index=sp%7cQ9Z214%7cHOME1_RAT%7cHomer&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **829.9299** | **1657.8453** | **1657.8271** | **11.0** | **1** | **115** | **4.5e-10** | **1** | **U** | **R.NKDLEGQLSELEQR.L** [677](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=677&hit=1&index=sp%7cQ9Z214%7cHOME1_RAT%7cHomer&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |
|  | [680](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=680&hit=1&index=sp%7cQ9Z214%7cHOME1_RAT%7cHomer&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) | **553.6226** | **1657.8460** | **1657.8271** | **11.4** | **1** | **(58)** | **0.00027** | **1** | **U** | **R.NKDLEGQLSELEQR.L** [678](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=678&hit=1&index=sp%7cQ9Z214%7cHOME1_RAT%7cHomer&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) [681](http://biospec.nih.gov/cgi/peptide_view.pl?file=../data/20101221/F593086.dat&query=681&hit=1&index=sp%7cQ9Z214%7cHOME1_RAT%7cHomer&px=1&section=5&ave_thresh=33&_ignoreionsscorebelow=0&report=20&_sigthreshold=0.05&_msresflags=1089&_msresflags2=2&percolate=-1&percolate_rt=0" \t "_blank) |

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

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| |  | | --- | | Top scoring peptide matches to query 138 09MAR16\_OT\_03.01822.01822.3 Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.7 0.0097 10.5 12 sp|P16086|SPTA2\_RAT|Spectrin K.LLEATELKGVK.L  21.5 0.5 46.3 R.NCXVGANLLVK.I  21.5 0.5 46.3 R.NCLVGANLLVK.I  21.5 0.5 46.3 R.NCXVGANLLVK.I  17.9 1.2 36.9 R.MNLKGIQLQR.A  17.6 1.2 10.5 K.LLKEAEVSLAK.E  16.0 1.8 10.5 R.LIESSTKPVVK.L  16.0 1.8 30.4 R.LLLHQNHVAR.V  15.9 1.8 46.3 -.KPTVAGLQQMK.E  15.1 2.2 10.5 K.QLLTSLLSTPK.M | | | |
| |  | | --- | | Top scoring peptide matches to query 139 09MAR16\_OT\_03.01827.01827.3 Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.9 0.012 10.9 12 sp|P16086|SPTA2\_RAT|Spectrin K.LLEATELKGVK.L  21.4 0.52 46.6 R.NCXVGANLLVK.I  21.4 0.52 46.6 R.NCLVGANLLVK.I  21.4 0.52 46.6 R.NCXVGANLLVK.I  17.7 1.2 37.3 R.MNLKGIQLQR.A  17.5 1.3 10.9 K.LLKEAEVSLAK.E  15.9 1.8 10.9 R.LIESSTKPVVK.L  15.9 1.8 30.7 R.LLLHQNHVAR.V  14.1 2.7 46.6 K.ILCKTQNVPK.D  13.5 3.2 -4.64 K.LNMILVQILK.Q | |

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| |  | | --- | | Top scoring peptide matches to query 140 09MAR16\_OT\_03.01830.01830.2 Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  51.6 0.00043 11.7 12 sp|P16086|SPTA2\_RAT|Spectrin K.LLEATELKGVK.L  18.8 0.84 19.9 K.IISTLPSWRK.L  15.6 1.8 11.7 R.LIESSTKPVVK.L  14.3 2.3 42.0 R.LIELIQEQSK.G  13.0 3.2 38.1 R.LLEQVMGVRR.H  12.8 3.3 11.7 K.ILIEKQESIK.L  10.9 5.2 47.5 R.LQNNQLMLVK.L  9.6 6.9 32.7 K.LITEEAIRQK.L  9.6 7 47.5 R.LLEQMGALAVR.G  9.0 8 11.7 K.IILKGSEVDVK.L | |
| |  | | --- | | Top scoring peptide matches to query 173 09MAR16\_OT\_03.01880.01880.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  82.5 8e-07 11.3 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial R.KAVDEAADALLK.A  25.1 0.44 2.28 K.KAVDQVALGQSK.I  24.1 0.56 -32.94 K.KAVILNVDMLK.L  21.3 1.1 11.3 R.ETKASPSVPSLK.E  15.5 4.1 19.3 K.QVTLEAWLQR.E  13.2 7 -17.93 R.SNLEVEIAKLK.K  13.0 7.2 -26.98 K.KVNAASQTLAIK.L  12.6 8 -17.93 R.NELSEKLGILK.G  10.7 12 -0.94 K.IGSNWLEAILK.L  10.3 13 11.3 K.QVAESLLDAGLK.C | |

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| |  | | --- | | Top scoring peptide matches to query 174 09MAR16\_OT\_03.01890.01890.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  85.3 4.2e-07 11.9 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial R.KAVDEAADALLK.A  21.3 1.1 11.9 R.ETKASPSVPSLK.E  21.1 1.1 -17.35 R.NELSEKLGILK.G  19.0 1.8 -32.35 K.KAVILNVDMLK.L  17.7 2.4 2.86 K.KAVDQVALGQSK.I  15.4 4.1 28.9 K.QDEKISIWPK.T  14.5 5.1 -17.35 R.SNLEVEIAKLK.K  14.2 5.5 -26.39 K.KVNAASQTLAIK.L  13.1 7 -26.39 R.LERGSSIQIIK.S  12.4 8.2 -17.35 K.ESNIKLLDAIK.N | |
| |  | | --- | | Top scoring peptide matches to query 175 09MAR16\_OT\_03.01876.01876.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  66.9 2.9e-05 11.9 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial R.KAVDEAADALLK.A  21.9 0.92 11.9 R.ETKASPSVPSLK.E  20.7 1.2 2.86 K.KAVDQVALGQSK.I  14.8 4.7 -32.35 K.KAVILNVDMLK.L  14.3 5.3 -17.35 R.NELSEKLGILK.G  13.7 6.1 -17.35 R.SNLEVEIAKLK.K  11.0 11 -18.06 K.GLKPMTMKPLK.F  10.9 12 -46.64 K.KSDIVLLLSQK.Q  9.9 15 11.9 R.LNSSDPSLIGLK.Q  9.4 16 -26.39 R.LERGSSIQIIK.S | |

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| |  | | --- | | Top scoring peptide matches to query 181 09MAR16\_OT\_03.01811.01811.3 Score greater than 33 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.1 0.0062 10.8 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.FPGQLNADLRK.L  18.6 2.2 31.9 K.STNPGISIGDVAK.K  17.6 2.8 46.0 M.MQSAAVPAEGAVK.G  15.0 5.1 -18.08 K.SRAHYITVIAK.D  14.7 5.4 31.2 R.LEKCAPGMKPK.C  13.5 7.1 19.8 K.FPEKGGAQIPSK.G  13.5 7.1 46.0 -.MALTPTNLNNK.M  12.7 8.6 26.0 K.MPTVSLPSVSPK.T  12.5 8.9 -23.97 K.WGATVKPLMKK.K  12.4 9.1 19.8 R.TWSLLAPSQGAK.R | |
| |  | | --- | | Top scoring peptide matches to query 182 09MAR16\_OT\_03.01806.01806.3 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.8 0.017 10.8 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.FPGQLNADLRK.L  16.8 3.3 23.0 K.QNSAKEASAKPK.E  15.8 4.2 31.2 R.LEKCAPGMKPK.C  15.8 4.2 17.1 K.EQVAAMQAGLLK.V  15.3 4.7 46.0 -.MALTPTNLNNK.M  13.1 7.8 37.1 -.MAEAALEAVRR.A  13.0 7.9 26.0 K.MPTVSLPSVSPK.T  13.0 8 -23.97 K.WGATVKPLMKK.K  12.9 8.2 -29.17 K.IVVSIIDSWVK.K  12.9 8.2 -17.00 R.LKEIEEALSVK.D | |

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| |  | | --- | | Top scoring peptide matches to query 220 09MAR16\_OT\_03.02301.02301.3 Score greater than 20 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  12.8 7.9 11.7 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.EKLDLVSYFGK.R  6.5 33 -21.88 K.NKVNEIAELIR.E  6.5 34 -2.54 R.IRQTVVSGDPAR.T  6.3 35 11.7 K.EALISSFYAGIK.S  5.2 45 -2.51 R.LRVEAQGGELAR.C  4.7 50 6.14 K.EKAVSNNVNPVK.T  4.3 56 -21.91 R.QGIVVGSGLLEAR.S  3.8 62 -21.88 K.ELRAQQILEAK.K  3.8 63 -32.62 K.IALTDSLPLEVK.A  3.8 63 42.9 K.TEGAAEAKAEPPK.A | |
| |  | | --- | | Top scoring peptide matches to query 221 09MAR16\_OT\_03.02300.02300.2 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  49.3 0.0018 11.8 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.EKLDLVSYFGK.R  12.1 9.2 14.9 R.GLSLDQPKEPSK.G  12.0 9.3 6.28 R.QELPGASARLEK.V  11.9 9.7 -21.77 K.ADIQGGRDLLLK.V  11.8 9.8 3.16 K.DLIYVGGLPHSK.A  10.3 14 23.6 R.EQDVEVLEPLK.C  9.0 19 -13.12 R.EAGLILGVSPSAGK.A  8.4 21 -21.77 -.AGQTQLVELIAR.F  7.9 24 -2.55 R.FMVQIVLFSSK.L  7.2 28 48.0 K.CKNIADPVEPR.V | |

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| |  | | --- | | Top scoring peptide matches to query 222 09MAR16\_OT\_03.02296.02296.3 Score greater than 21 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  14.4 5.5 11.8 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.EKLDLVSYFGK.R  7.4 27 16.9 M.ATMVPSVLWPR.A  6.8 31 -2.39 R.IRQTVVSGDPAR.T  6.5 33 11.8 K.EALISSFYAGIK.S  5.0 47 -21.76 K.AVADAIRTSLGPK.G  4.9 48 -13.09 R.EVKASEKPVSPK.S  3.4 68 19.9 R.VLECQAVLGGPR.G  3.4 69 43.0 K.TEGAAEAKAEPPK.A  2.9 77 25.7 R.NNAQAEKNGKPK.E  2.8 79 6.30 R.EAALGGAQEALLR.S | |
| |  | | --- | | Top scoring peptide matches to query 223 09MAR16\_OT\_03.02307.02307.3 Score greater than 22 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  12.4 8.5 -21.59 K.NKVNEIAELIR.E  9.1 18 -2.22 R.LLENRALGDAAR.Y  8.9 19 17.0 M.ATMVPSVLWPR.A  8.4 22 12.0 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.EKLDLVSYFGK.R  8.2 23 25.8 R.NNAQAEKNGKPK.E  8.0 24 43.1 K.TEGAAEAKAEPPK.A  7.8 25 -46.68 R.LMDKVELLLPK.K  6.7 32 15.1 K.GANIIDPDVEKK.L  5.7 40 12.0 K.EALISSFYAGIK.S  5.4 43 6.42 K.VTREDSLLTHK.N | |

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| |  | | --- | | Top scoring peptide matches to query 224 09MAR16\_OT\_03.02294.02294.2 Score greater than 27 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  48.1 0.0023 12.6 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.EKLDLVSYFGK.R  11.2 11 24.3 R.EQDVEVLEPLK.C  8.9 19 -21.02 K.ADIQGGRDLLLK.V  8.4 22 -21.02 -.AGQTQLVELIAR.F  8.4 22 15.7 R.GLSLDQPKEPSK.G  8.0 24 -1.80 R.FMVQIVLFSSK.L  8.0 24 7.03 R.QELPGASARLEK.V  7.8 25 3.91 K.DLIYVGGLPHSK.A  6.9 30 -12.37 R.EAGLILGVSPSAGK.A  6.6 33 -21.01 K.QELQLLQKNGK.S | |
| |  | | --- | | Top scoring peptide matches to query 225 09MAR16\_OT\_03.02306.02306.2 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  43.6 0.0065 12.9 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.EKLDLVSYFGK.R  17.0 3 24.6 R.EQDVEVLEPLK.C  10.6 13 -12.06 K.KELIPTEEALR.L  9.6 17 7.31 K.RTEALEQGGLPK.K  8.5 21 -12.08 R.EAGLILGVSPSAGK.A  8.5 21 -20.74 -.AGQTQLVELIAR.F  8.2 23 16.0 R.GLSLDQPKEPSK.G  7.3 28 -20.74 QTQKLQNLTPK  7.2 28 -40.11 K.NEIQTLLVQLK.Q  7.2 28 35.3 R.GDVQLKGDTHTK.K | |

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| |  | | --- | | Top scoring peptide matches to query 238 09MAR16\_OT\_03.01757.01757.2 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  42.7 0.0089 10.7 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  11.8 11 16.4 R.EYLAQLSNNVR.-  10.9 14 22.4 R.DTLMKEIVEGR.T  10.7 14 25.0 K.YEVNQDGAVIAK.F  9.4 19 10.7 R.FDMVQLIDVAR.Q  8.8 22 12.7 K.CTHHQLVAGRK.I  8.6 23 25.0 K.FSLEQEVDALR.D  8.3 25 19.3 R.LDALSLFVAPNM.-  8.3 25 31.0 R.MILQDEDITTK.I  8.2 25 30.0 R.CEWSTLRNLK.E | |
| |  | | --- | | Top scoring peptide matches to query 239 09MAR16\_OT\_03.01742.01742.3 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  42.5 0.0094 10.9 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  12.4 9.7 49.8 R.CLAPMMSEVIR.I  12.4 9.7 49.8 R.CLAPMMSEVLR.I  12.1 10 38.8 K.GQITMWDLASGK.L  11.8 11 -2.70 R.FKASGVEGADVVK.L  11.0 13 -42.23 K.FESPLFLKGLR.L  10.7 14 44.5 K.YLSLSGNHSSNK.R  10.7 15 7.97 R.HRPVDVEDLAR.T  10.1 17 -2.68 K.QGYTIEAVQAVK.E  10.0 17 38.8 R.CNFELVKPGDK.T | |

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| |  | | --- | | Top scoring peptide matches to query 240 09MAR16\_OT\_03.01745.01745.2 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.9 0.022 11.2 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  11.1 13 22.9 R.DTLMKEIVEGR.T  10.7 14 25.4 K.YEVNQDGAVIAK.F  9.8 18 16.8 R.EYLAQLSNNVR.-  8.5 24 31.5 R.MILQDEDITTK.I  8.4 24 36.1 K.FSENGNQKNLR.I  8.4 24 19.8 R.LDALSLFVAPNM.-  7.9 27 2.56 K.TRIAMEVPSFR.R  7.7 28 11.2 R.LFQVLEELCR.G  7.2 32 11.2 R.FDMVQLIDVAR.Q | |
| |  | | --- | | Top scoring peptide matches to query 241 09MAR16\_OT\_03.01750.01750.2 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.1 0.051 11.2 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  10.4 15 22.9 R.DTLMKEIVEGR.T  8.6 23 16.8 R.EYLAQLSNNVR.-  7.6 29 19.8 R.LDALSLFVAPNM.-  6.4 38 -32.89 R.TKTSSLLACVVK.K  6.3 39 31.5 R.MILQDEDITTK.I  6.0 42 44.7 K.YLSLSGNHSSNK.R  5.0 54 18.9 K.HGQSPAAQAQRR.G  4.7 57 25.4 K.YEVNQDGAVIAK.F  4.0 67 11.2 R.FDMVQLIDVAR.Q | |

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| |  | | --- | | Top scoring peptide matches to query 242 09MAR16\_OT\_03.01740.01740.3 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  47.6 0.0029 11.4 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  16.1 4.1 -41.81 K.FESPLFLKGLR.L  15.8 4.4 17.0 R.EYLAQLSNNVR.-  13.3 7.8 34.2 K.YEKVLVDEGSAP.-  12.9 8.7 44.9 K.YLSLSGNHSSNK.R  11.4 12 -2.24 K.EYLEKIQGAQK.E  10.3 16 36.3 K.FSENGNQKNLR.I  10.3 16 19.9 R.LDALSLFVAPNM.-  10.2 16 -2.24 K.EYDILRIEQK.L  9.9 17 23.0 R.KIDDNTMQVVK.E | |
| |  | | --- | | Top scoring peptide matches to query 243 09MAR16\_OT\_03.01748.01748.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  40.0 0.017 11.4 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  11.6 12 8.40 R.HRPVDVEDLAR.T  11.1 13 -35.78 -.LAMTFIIQLAK.T  10.0 17 17.0 R.EYLAQLSNNVR.-  10.0 17 17.0 K.SDEIDRFVVAR.L  9.8 18 25.6 R.TYVVTDQPGAQK.A  9.5 19 28.0 K.CLVNKQSCVAK.V  9.0 21 44.9 K.YLSLSGNHSSNK.R  8.8 22 -4.85 K.TQTIKSVPTGMK.T  8.1 26 25.6 K.YEVNQDGAVIAK.F | |

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| |  | | --- | | Top scoring peptide matches to query 249 09MAR16\_OT\_03.02444.02444.2 Score greater than 31 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  66.9 2e-05 11.4 12 sp|P16086|SPTA2\_RAT|Spectrin KVEDLFLTFAK  14.7 3.3 5.92 R.LSRPGSQLDPIK.Q  11.5 7 30.6 R.QYATDFLLLAR.H  9.9 9.9 47.3 K.VQQYRVAMTAK.D  7.7 17 -21.86 -.XVGDLKTPAILR.V  7.3 18 -13.27 K.GAVELENLPLKK.D  6.9 20 25.1 R.KVDIENRPSPR.L  5.9 25 38.2 R.GNWPQHLLFAK.L  4.2 37 36.7 K.EVKIEMAYLAK.R  3.9 40 -32.48 R.LLDPSAEIIVLK.E | |
| |  | | --- | | Top scoring peptide matches to query 250 09MAR16\_OT\_03.02450.02450.3 Score greater than 26 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  30.8 0.078 12.8 12 sp|P16086|SPTA2\_RAT|Spectrin KVEDLFLTFAK  11.3 6.9 32.0 R.QYATDFLLLAR.H  6.3 22 48.7 -.MSVRYTLNLR.V  4.6 32 23.4 R.QVSITGFFQRK.-  4.6 33 40.1 K.THINLLCGGVAR.A  4.1 36 23.4 K.HITIEDLWKR.W  3.9 38 7.31 R.LSRPGSQLDPIK.Q  3.1 46 1.67 R.IRMIIAVTSYK.R  3.1 46 1.67 R.IRMILAVTSYK.R  3.0 47 43.7 R.ADSTVQLAPSPPK.S | |

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| |  | | --- | | Top scoring peptide matches to query 251 09MAR16\_OT\_03.02455.02455.2 Score greater than 28 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  58.2 0.00014 12.8 12 sp|P16086|SPTA2\_RAT|Spectrin KVEDLFLTFAK  11.7 6.4 7.32 R.LSRPGSQLDPIK.Q  11.5 6.6 32.0 R.QYATDFLLLAR.H  8.1 15 15.9 R.VEKQSGDPLPLK.L  7.7 16 -20.46 -.XVGDLKTPAILR.V  7.0 19 26.5 R.KVDIENRPSPR.L  6.8 20 -11.87 K.GAVELENLPLKK.D  5.9 24 10.2 R.LDKMTFSVLLK.N  5.7 25 48.7 K.VQQYRVAMTAK.D  4.5 34 42.6 R.KVHGPQQVDFR.S | |
| |  | | --- | | Top scoring peptide matches to query 252 09MAR16\_OT\_03.02446.02446.3 Score greater than 21 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  8.9 12 -28.01 R.LPRGALTGVTAVR.L  8.4 14 33.1 R.QYATDFLLLAR.H  8.1 15 -39.64 R.AVVYRHLLLAR.F  7.2 18 43.7 R.HYPPLGSGARGAK.D  6.5 21 33.1 K.AEFTEFVKLAR.S  6.2 23 13.9 12 sp|P16086|SPTA2\_RAT|Spectrin KVEDLFLTFAK  5.1 29 41.1 K.THINLLCGGVAR.A  4.7 32 39.1 R.LQEMEILYKK.E  3.7 40 46.8 M.AAAPVAAGSGAGRGR.R  3.6 41 -0.23 R.VRLPQSAGDLVR.A | |

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| |  | | --- | | Top scoring peptide matches to query 253 09MAR16\_OT\_03.02449.02449.2 Score greater than 29 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  76.4 2e-06 14.9 12 sp|P16086|SPTA2\_RAT|Spectrin KVEDLFLTFAK  12.1 5.4 34.1 R.QYATDFLLLAR.H  9.8 9.2 9.37 R.LSRPGSQLDPIK.Q  5.9 23 -49.25 K.KLPQLNFLIPK.E  5.6 24 -18.42 -.XVGDLKTPAILR.V  5.4 25 44.7 R.KVHGPQQVDFR.S  4.2 34 -9.82 K.GAVELENLPLKK.D  3.7 38 42.1 R.MQPARSAPPTVR.S  3.3 42 17.9 R.VEKQSGDPLPLK.L  2.7 47 45.7 R.LPEDDAAKVAPGK.K | |
| |  | | --- | | Top scoring peptide matches to query 261 09MAR16\_OT\_03.01793.01793.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  11.7 13 -14.63 K.SPMITHQRGHR.A  9.9 19 -22.14 R.ALMAGVGTGSGARR.Q  9.2 23 -32.68 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial K.LAGRVAMIDETK.N  8.2 29 10.9 K.AIADNVKDWCK.V  7.3 35 -38.64 K.ANFQTIGLSAAAR.F  7.2 36 -16.66 SPAMAGGLFAIER  6.8 40 4.95 K.GPAVSPQDFHHK.Q  5.2 58 -13.59 R.IAEMERSLSQR.T  5.0 60 -19.57 K.ASAKTHSLDPHR.T  4.5 67 47.0 K.GKFYTCTDEAK.H | |

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| |  | | --- | | Top scoring peptide matches to query 264 09MAR16\_OT\_03.01653.01653.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.0 0.14 11.6 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  11.3 14 -1.90 K.ASQLQTVETAFK.R  11.1 14 -4.43 R.NESALKTTLAMK.E  10.3 17 27.5 R.FESIXLPGCPR.G  10.3 17 24.6 K.YKGIHFGNSSGR.Q  10.0 18 -7.50 K.GLFISTDLLVNM.-  9.9 19 -20.92 K.LYSLIGATVIEGS.-  9.7 20 22.6 K.FESLWEEVVGK.E  9.6 20 -13.43 R.YPKQSGIAPSFK.S  9.5 21 -10.38 K.AYGALTENVTRK.Y | |
| |  | | --- | | Top scoring peptide matches to query 265 09MAR16\_OT\_03.01660.01660.3 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.2 0.069 11.9 12 sp|P16086|SPTA2\_RAT|Spectrin R.YEALKEPMVAR.K  13.7 7.8 -1.55 K.ASQLQTVETAFK.R  12.1 11 -7.13 K.FKTPLMIAEEK.Y  11.9 12 -4.08 R.NESALKTTLAMK.E  11.3 14 -1.53 R.YKGELDESLLR.G  11.2 14 25.0 K.YKGIHFGNSSGR.Q  11.1 14 -10.04 K.AYGALTENVTRK.Y  9.9 19 27.9 R.FESIXLPGCPR.G  9.6 20 5.93 K.SSGGLLGFWKDR.Y  9.5 20 -20.58 K.LYSLIGATVIEGS.- | |

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| |  | | --- | | Top scoring peptide matches to query 275 09MAR16\_OT\_03.01566.01566.2 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  50.0 0.0017 9.14 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  13.3 8.1 -36.92 K.IYPANAKGMVEK.W  10.7 15 29.0 -.MEAAGSPAATETGK.Y  9.9 18 -31.38 K.YLTESLQAANAR.A  7.4 32 -19.98 R.SGDISAASTLSATR.S  7.3 32 9.14 R.VMAEAQGFQEAR.A  7.3 32 29.0 -.METAIEDAGLDR.G  7.2 33 -42.82 R.EFRGYPGLNGVK.F  7.0 35 47.8 R.EMAQKEGNEER.L  7.0 35 -18.10 K.FEACLAKQVDR.T | |
| |  | | --- | | Top scoring peptide matches to query 276 09MAR16\_OT\_03.01564.01564.3 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.5 0.064 10.9 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  13.4 8.3 22.4 R.ETSMDPELRSR.L  10.5 16 -29.58 K.YLTESLQAANAR.A  10.5 16 -0.01 -.MQSARMTPSVGR.Q  9.0 23 8.41 K.QMAQMTKEPTR.N  8.8 24 21.9 R.YISDWDLDPGR.C  8.8 24 -48.43 K.YITTPISVNNSK.I  8.5 25 -35.12 K.IYPANAKGMVEK.W  7.6 31 30.8 -.MEAAGSPAATETGK.Y  7.4 33 -32.62 R.YLFPVPKDDSR.R | |

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| |  | | --- | | Top scoring peptide matches to query 277 09MAR16\_OT\_03.01569.01569.3 Score greater than 32 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  36.4 0.041 11.6 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  17.5 3.2 14.0 K.CCQAGMVLGGRK.F  9.9 18 5.73 R.NWKAGFGGNGSNK.N  9.8 19 -15.63 K.DPGVSGYQRVMK.E  9.6 20 9.10 K.QMAQMTKEPTR.N  8.8 23 -47.75 K.YITTPISVNNSK.I  8.8 24 22.5 R.YISDWDLDPGR.C  8.4 26 -1.31 K.EMAMLLEEVQK.E  8.1 28 41.4 R.YGGGSRYEEYR.G  8.0 28 -28.91 R.HKAPPTQETAEK.D | |
| |  | | --- | | Top scoring peptide matches to query 295 09MAR16\_OT\_03.02172.02172.2 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  72.5 6.6e-06 10.8 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.AGNLDKVVEYLK.G  24.0 0.47 2.48 K.QLQTRADYLIK.L  24.0 0.47 2.48 K.QLQTRADYLLK.L  17.7 2 -29.99 R.LKLAMIQQYLK.V  17.6 2 -14.18 K.QLNNRVNHIIK.K  16.8 2.5 37.8 K.NAGNIEVYLDIK.V  12.7 6.3 -7.84 K.EILIKELDTFK.S  12.2 7.1 10.8 K.IKIGVVGGSDFEK.V  10.7 10 35.3 R.EDILAGMSGKAIK.G  10.5 10 10.8 K.GAVTPKPVPEPEK.Q | |

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| |  | | --- | | Top scoring peptide matches to query 296 09MAR16\_OT\_03.02171.02171.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.5 0.00052 11.3 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.AGNLDKVVEYLK.G  27.3 0.22 38.4 K.NAGNIEVYLDIK.V  22.1 0.73 -5.34 K.KGGPTQVVAHLNK.E  16.7 2.5 46.7 K.QIEDLVFEVEK.S  16.5 2.6 11.3 K.GAVTPKPVPEPEK.Q  14.9 3.8 30.4 R.KMEMVLPIIDK.S  13.1 5.8 -26.98 K.FGPHLVPILVEK.C  12.9 6 24.5 R.ALRVLFEPMEK.T  12.1 7.3 3.02 K.QLQTRADYLIK.L  12.1 7.3 3.02 K.QLQTRADYLLK.L | |
| |  | | --- | | Top scoring peptide matches to query 297 09MAR16\_OT\_03.02176.02176.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  46.9 0.0024 11.3 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.AGNLDKVVEYLK.G  20.8 0.99 38.4 K.NAGNIEVYLDIK.V  13.6 5.2 48.5 R.IYSLFNLYMGK.L  12.6 6.4 11.3 K.GAVTPKPVPEPEK.Q  11.3 8.8 46.7 K.QIEDLVFEVEK.S  10.0 12 30.0 R.AGKPPGAEPPSAAAK.G  9.0 15 3.02 K.QLQTRADYLIK.L  9.0 15 3.02 K.QLQTRADYLLK.L  8.9 15 -26.98 K.FGPHLVPILVEK.C  8.5 17 -7.31 K.EILIKELDTFK.S | |

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| |  | | --- | | Top scoring peptide matches to query 298 09MAR16\_OT\_03.02177.02177.2 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  72.2 7.1e-06 11.5 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.AGNLDKVVEYLK.G  18.5 1.7 3.21 K.QLQTRADYLIK.L  18.5 1.7 3.21 K.QLQTRADYLLK.L  16.5 2.6 38.5 K.NAGNIEVYLDIK.V  14.9 3.8 -5.15 K.KGGPTQVVAHLNK.E  13.7 5 -13.46 K.QLNNRVNHIIK.K  12.6 6.4 -7.12 K.EILIKELDTFK.S  10.2 11 -29.26 R.LKLAMIQQYLK.V  10.1 12 -15.45 K.ASNTPKLLTIYK.E  10.1 12 -15.45 K.ASNTPKLLTLYK.E | |
| |  | | --- | | Top scoring peptide matches to query 299 09MAR16\_OT\_03.02166.02166.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  52.0 0.00073 11.8 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.AGNLDKVVEYLK.G  25.0 0.37 38.8 K.NAGNIEVYLDIK.V  16.9 2.4 47.1 K.QIEDLVFEVEK.S  16.8 2.4 11.7 K.GAVTPKPVPEPEK.Q  15.3 3.4 3.42 K.QLQTRADYLIK.L  15.3 3.4 3.42 K.QLQTRADYLLK.L  15.3 3.4 30.8 R.KMEMVLPIIDK.S  11.7 7.9 43.6 R.QPPSCKPVNPPK.W  11.5 8.2 24.9 R.MPQEITNKFLK.E  10.7 9.8 30.4 R.AGKPPGAEPPSAAAK.G | |

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| |  | | --- | | Top scoring peptide matches to query 300 09MAR16\_OT\_03.01459.01459.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  13.4 7.6 -27.47 R.NRPEGRPGAADGR.S  11.7 11 10.6 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  9.0 21 8.11 R.RNQMAVETMEK.E  8.2 25 -29.46 R.YLAAQNLSTTDR.L  8.1 26 -46.21 R.YLYKLCDLHK.E  7.8 27 9.93 K.VVMWVCNLCR.K  7.0 33 -43.24 K.AMHTPKPAVSGEK.N  6.9 34 8.11 R.RNQMAVETMEK.E  6.7 35 14.1 R.ATPEPEPEPEEK.E  6.3 39 -0.22 -.MQSARMTPSVGR.Q | |
| |  | | --- | | Top scoring peptide matches to query 301 09MAR16\_OT\_03.01472.01472.3 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  18.9 2.2 11.5 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  15.9 4.3 -44.22 R.ASLTGTSSTASLTR.T  12.6 9.2 -28.58 R.YLAAQNLSTTDR.L  12.2 10 -39.88 R.YLGERTTFHTK.I  12.1 10 15.0 R.ATPEPEPEPEEK.E  11.9 11 -8.13 R.FGATARYGCPPR.N  10.4 15 -42.36 K.AMHTPKPAVSGEK.N  9.8 17 -28.59 R.YLRDVSEVDTR.T  9.3 20 -26.59 R.NRPEGRPGAADGR.S  9.1 21 -15.46 K.DPGVSGYQRVMK.E | |

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| |  | | --- | | Top scoring peptide matches to query 302 09MAR16\_OT\_03.01427.01427.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  21.1 1.3 11.7 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  9.4 19 9.20 R.RNQMAVETMEK.E  8.2 25 -28.37 R.YLAAQNLSTTDR.L  7.9 27 -46.95 R.AKEPKPEPEAEK.S  6.7 36 15.2 R.ATPEPEPEPEEK.E  6.2 41 -26.39 R.NRPEGRPGAADGR.S  5.9 43 9.84 R.SESESEGSGLSKR.H  5.8 44 -7.93 R.FGATARYGCPPR.N  5.7 45 -45.00 R.GAAQGSDPLPQRR.I  5.4 48 -9.77 K.GDSHAAHEVKSSK.Q | |
| |  | | --- | | Top scoring peptide matches to query 303 09MAR16\_OT\_03.01432.01432.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.6 2.9 -45.06 R.YLYKLCDLHK.E  13.0 8.4 -46.89 R.AKEPKPEPEAEK.S  12.6 9.2 9.24 K.GIMEGNCVSLTR.I  12.6 9.3 11.7 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  12.4 9.6 -36.28 R.QMVTGLMTKAEK.S  12.4 9.6 -36.28 R.QMVTGLMTKAEK.S  9.8 17 -39.60 K.YLNFDPRTAQK.I  9.0 21 -9.70 K.GDSHAAHEVKSSK.Q  8.8 22 -28.31 R.YLAAQNLSTTDR.L  7.6 29 11.7 R.SFCKQGAPSGGEK.M | |

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| |  | | --- | | Top scoring peptide matches to query 304 09MAR16\_OT\_03.01373.01373.3 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  18.5 2.4 12.0 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  14.6 5.8 -26.05 R.NRPEGRPGAADGR.S  10.8 14 -28.04 R.YLAAQNLSTTDR.L  10.7 14 -14.92 K.DPGVSGYQRVMK.E  8.4 24 -44.79 R.YLYKLCDLHK.E  7.4 31 -36.01 R.MSVDLDMLLRK.Q  7.2 32 15.5 R.ATPEPEPEPEEK.E  4.6 58 -46.62 R.AKEPKPEPEAEK.S  4.3 62 -31.52 R.SPQPQRHIMSR.S  4.3 62 22.8 K.GSAFPEWSGDATK.K | |
| |  | | --- | | Top scoring peptide matches to query 305 09MAR16\_OT\_03.01395.01395.3 Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.8 0.022 -27.97 R.YLAAQNLSTTDR.L  28.6 0.23 12.1 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  12.4 9.7 9.60 R.QMKMLDSENTR.L  11.1 13 -4.04 K.QFAAQAEPTFDK.G  10.2 16 -44.72 R.YLYKLCDLHK.E  9.9 17 -27.98 R.YLRDVSEVDTR.T  9.4 19 -27.96 R.YNANTAVEQSKK.A  9.1 21 -0.69 K.EMAMLLEEVQK.E  9.0 21 -23.16 R.SYRISPGCGVTR.N  8.7 23 -25.13 K.SIVMIPGFSEEK.A | |

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| |  | | --- | | Top scoring peptide matches to query 306 09MAR16\_OT\_03.01401.01401.3 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.2 0.41 12.2 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  17.4 3.1 -27.83 R.YLAAQNLSTTDR.L  12.8 8.8 -44.58 R.YLYKLCDLHK.E  12.3 9.8 -14.71 K.DPGVSGYQRVMK.E  12.2 10 15.7 R.ATPEPEPEPEEK.E  9.6 18 -3.90 K.QFAAQAEPTFDK.G  8.8 22 -33.27 K.NYNKALELMEK.V  8.0 27 -27.83 R.LGEQPGPEDALAR.H  7.9 28 -23.02 R.SYRISPGCGVTR.N  7.5 30 -33.28 K.NSFLNEKIEMK.K | |
| |  | | --- | | Top scoring peptide matches to query 307 09MAR16\_OT\_03.01360.01360.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  13.5 7.5 -27.62 R.YNANTAVEQSKK.A  12.7 9 -38.92 K.YLNFDPRTAQK.I  10.1 16 -25.64 R.NRPEGRPGAADGR.S  10.1 17 -46.21 R.AKEPKPEPEAEK.S  9.8 17 -14.48 K.TMEHHEIEAKK.M  8.5 24 -46.23 R.YDLDSALTQAKK.A  8.3 25 -27.64 R.YLRDVSEVDTR.T  8.2 25 9.94 R.MEKMAEQQAVR.E  8.1 26 -19.99 K.MSTVFLHCLTK.L  7.7 29 12.4 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H | |

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| |  | | --- | | Top scoring peptide matches to query 308 09MAR16\_OT\_03.01398.01398.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  23.8 0.7 12.6 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  12.4 9.6 -14.38 K.DPGVSGYQRVMK.E  12.2 10 16.1 R.ATPEPEPEPEEK.E  11.4 12 -27.49 R.YLAAQNLSTTDR.L  9.6 18 26.7 R.EEVAADSMIMEK.K  8.8 22 -32.94 K.NYNKALELMEK.V  8.2 26 5.25 R.MENPKESSSSLK.T  8.1 26 -16.86 R.VTGSMNMLNLTR.G  7.7 28 -27.49 R.LGEQPGPEDALAR.H  7.3 31 -25.51 R.NRPEGRPGAADGR.S | |
| |  | | --- | | Top scoring peptide matches to query 309 09MAR16\_OT\_03.01370.01370.3 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  20.6 1.5 12.8 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  17.0 3.3 -25.24 R.NRPEGRPGAADGR.S  14.0 6.8 16.3 R.ATPEPEPEPEEK.E  12.1 11 -27.21 R.YNANTAVEQSKK.A  12.0 11 -6.78 R.FGATARYGCPPR.N  8.6 23 -45.80 R.AKEPKPEPEAEK.S  7.4 30 21.1 K.AFQDLVNCEEK.V  7.4 31 -27.22 R.LGEQPGPEDALAR.H  7.2 32 -11.61 K.QFVRDWSETGK.A  6.9 34 -32.68 K.NSFLNEKIEMK.K | |

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| |  | | --- | | Top scoring peptide matches to query 310 09MAR16\_OT\_03.01425.01425.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.9 2.7 13.0 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  9.7 18 -43.84 R.YLYKLCDLHK.E  9.6 19 10.5 R.RNQMAVETMEK.E  9.2 20 -42.73 R.ASLTGTSSTASLTR.T  9.1 21 44.7 K.GCSASCSKWPGR.Y  6.8 35 16.5 R.ATPEPEPEPEEK.E  6.5 37 18.8 R.EMVQADVELMR.T  6.1 41 -35.06 R.MSVDLDMLLRK.Q  5.2 51 -46.68 K.RWALLHGDQEK.Q  4.9 54 10.5 K.GIMEGNCVSLTR.I | |
| |  | | --- | | Top scoring peptide matches to query 311 09MAR16\_OT\_03.01412.01412.2 Score greater than 33 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  65.2 5.1e-05 13.4 7 sp|P02686|MBP\_HUMAN|Myelin K.YLATASTMDHAR.H  16.4 3.9 -26.63 R.YLAAQNLSTTDR.L  12.4 9.6 0.65 K.EMAMLLEEVQK.E  10.2 16 -20.80 K.EMKSLEQSGSLK.G  9.3 20 -7.67 -.TLGMMAQLEQAK.D  9.2 20 -37.93 R.FRDQQVPYATK.G  8.9 22 -26.28 -.MSLLMITENVK.L  8.7 23 46.2 K.LSMTANEPCDAK.R  8.6 23 43.2 R.IYASCYMTTDK.N  8.0 27 46.8 K.GTDEQSAATTDEK.G | |

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| |  | | --- | | Top scoring peptide matches to query 339 09MAR16\_OT\_03.01572.01572.3 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.8 0.034 11.3 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  14.2 4.9 -45.76 K.FPKGTDTTMLHK.L  12.7 7 -45.62 R.TSTTAAAAASGRGGGR.T  11.4 9.4 -14.90 K.FGGNAPMALTPCR.K  11.4 9.4 -42.84 K.ETLMRVDLENR.C  10.2 12 -22.96 R.VAMAMGSHPRYR.A  8.9 17 -33.32 R.TWQFSPRGDAAR.Q  8.9 17 -22.01 K.VLDGEMVAMSAPR.K  8.9 17 -43.32 K.HFFNVTDEAALK.D  8.8 17 -40.42 R.VANQAFDKNAGEK.S | |
| |  | | --- | | Top scoring peptide matches to query 340 09MAR16\_OT\_03.01583.01583.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.1 0.01 11.4 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  21.1 1 -14.76 K.FGGNAPMALTPCR.K  19.3 1.5 -45.49 R.TSTTAAAAASGRGGGR.T  19.2 1.6 -47.41 K.TIEESDALLTGSR.D  15.9 3.4 -42.71 K.ETLMRVDLENR.C  15.6 3.6 -40.91 R.LGNAVHAMIMYR.R  14.0 5.1 -47.39 R.NSEENTAISSIVK.K  13.9 5.3 -21.87 R.EELCLTCLPTR.C  13.7 5.6 -27.52 -.VHSEYIICTNR.D  12.7 6.9 8.62 R.KNWMSGGGGGGGGGGR.S | |

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| |  | | --- | | Top scoring peptide matches to query 341 09MAR16\_OT\_03.01576.01576.3 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  48.9 0.0017 11.6 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  16.3 3 -21.68 K.VLDGEMVAMSAPR.K  11.9 8.3 -1.17 K.AYPGQETPGMQGR.Y  10.9 11 -45.29 R.TSTTAAAAASGRGGGR.T  10.9 11 23.2 K.VSSEANGESPGSDR.A  10.5 12 -24.46 R.CDVVSGGTGIRDR.T  10.3 12 15.0 K.DLEMFSVESYR.W  10.1 13 -42.99 K.HFFNVTDEAALK.D  10.1 13 -3.62 R.CTLGVDPSCQVR.Q  9.9 13 -14.57 K.FGGNAPMALTPCR.K | |
| |  | | --- | | Top scoring peptide matches to query 350 09MAR16\_OT\_03.02397.02397.2 Score greater than 32 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  60.7 0.0001 10.7 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.EGHVGLVQELLGR.G  15.3 3.6 -28.40 R.RKPPLLPEMLGR.E  15.2 3.6 13.5 K.QMLELVNLYVGK.A  11.6 8.5 36.6 K.QGAPGPIGDQGPKGK.E  9.3 14 -43.91 M.QGPWVLLLLGLR.L  9.1 15 31.3 R.FSSTGRPLLLNAM.-  8.5 17 -18.04 R.QGALAPWPIVGLGK.F  8.3 18 28.6 R.AQQDILQHQLGR.I  7.4 22 -5.25 R.HREARPALLTSR.L  6.3 28 15.4 K.SPMKPPGPNRIGR.R | |

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| |  | | --- | | Top scoring peptide matches to query 351 09MAR16\_OT\_03.02402.02402.2 Score greater than 25 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  47.3 0.0023 10.7 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.EGHVGLVQELLGR.G  9.4 14 24.3 R.AGESLMKLVSDLK.Q  6.8 26 13.5 K.QMLELVNLYVGK.A  6.3 29 -28.40 R.RKPPLLPEMLGR.E  3.9 50 31.3 R.FSSTGRPLLLNAM.-  3.1 59 28.6 R.AQQDILQHQLGR.I  2.1 75 2.73 R.ATHPRPALTSISR.K  2.0 77 10.7 K.ASTLRVVVFGSDR.I | |
| |  | | --- | | Top scoring peptide matches to query 352 09MAR16\_OT\_03.02395.02395.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  36.1 0.03 11.3 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.EGHVGLVQELLGR.G  19.7 1.3 -1.98 -.MLATRVFNLIGR.R  15.2 3.6 19.3 R.QELSREFSLIGK.R  12.1 7.5 -19.87 K.KPQAPGLQKLVPM.-  11.7 8.3 24.9 R.AGESLMKLVSDLK.Q  11.4 8.8 34.8 -.MLTLQSSGTGQRK.V  9.6 13 8.40 K.LTTFVWDKALGR.A  9.3 14 3.28 R.GSLPHISSPRISR.S  9.2 15 19.3 K.KAGSLYLSGAPGTGK.T  8.8 16 -27.85 R.RKPPLLPEMLGR.E | |

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| |  | | --- | | Top scoring peptide matches to query 353 09MAR16\_OT\_03.02408.02408.2 Score greater than 23 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  43.4 0.0056 11.4 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.EGHVGLVQELLGR.G  7.6 21 14.1 K.QMLELVNLYVGK.A  6.4 28 16.1 K.SPMKPPGPNRIGR.R  5.3 36 -25.32 K.SGFAVLRPRYIK.T  1.7 82 -17.33 K.IYGPKGVGAIYIR.R  1.7 82 -17.33 K.LYGPKGVGAIYIR.R  1.5 87 3.42 R.GSLPHISSPRISR.S | | | |
| |  | | --- | | Top scoring peptide matches to query 354 09MAR16\_OT\_03.02401.02401.3 Score greater than 29 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.2 0.091 11.8 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.EGHVGLVQELLGR.G  14.9 3.8 19.8 K.KAGSLYLSGAPGTGK.T  13.4 5.4 19.8 R.QELSREFSLIGK.R  12.8 6.2 -19.35 K.KPQAPGLQKLVPM.-  11.2 9 -1.46 -.MLATRVFNLIGR.R  11.1 9.3 25.4 R.AGESLMKLVSDLK.Q  10.1 12 11.8 R.YSLETRVVLNGR.E  9.2 15 35.3 K.TTLLDAMSGRLGR.A  7.6 21 47.9 K.NMKLVMVQGSQR.H  7.6 21 3.81 R.GSLPHISSPRISR.S | |

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| |  | | --- | | Top scoring peptide matches to query 355 09MAR16\_OT\_03.02406.02406.3 Score greater than 32 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.6 0.081 12.2 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.EGHVGLVQELLGR.G  17.3 2.2 -18.89 K.KPQAPGLQKLVPM.-  14.7 4 -1.01 -.MLATRVFNLIGR.R  13.1 5.9 20.2 R.QELSREFSLIGK.R  12.4 6.7 20.2 K.KAGSLYLSGAPGTGK.T  12.2 7.1 35.7 K.TTLLDAMSGRLGR.A  12.0 7.4 6.99 R.KSLAGMLTPYVAR.K  11.8 7.8 12.2 R.YSLETRVVLNGR.E  10.8 9.7 20.2 VTYQAQQDKVVK  9.8 13 12.2 R.NLDLHILLQGDR.A | |
| |  | | --- | | Top scoring peptide matches to query 356 09MAR16\_OT\_03.01423.01423.3 Score greater than 31 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  22.0 0.65 10.2 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  17.1 2 -20.37 K.DTGFAAVVQDCPK.Q  16.5 2.3 10.2 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  16.5 2.3 -5.32 R.GYLYFTNMQDR.A  15.3 3.1 -30.72 R.MQGQEAVLAMSSR.S  14.3 3.8 8.39 M.AAAVAMETDDAGNR.L  13.9 4.2 -41.56 K.ALKMHMFGQNSK.L  12.3 6.1 -17.46 K.LEALMASNDSANR.T  11.8 6.9 -48.58 K.LAMNEAEMLLTR.I  10.9 8.4 -32.93 K.YLNEAAGAAAEEAK.N | |

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| |  | | --- | | Top scoring peptide matches to query 357 09MAR16\_OT\_03.01436.01436.2 Score greater than 21 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  13.8 4.3 10.9 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  11.3 7.7 10.9 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  7.4 19 -27.60 K.AEAGSMVPHEVHK.L  5.5 29 21.7 K.EQPGMVSCNVDR.Q  5.2 31 -4.13 -.MPLNDTTMDRR.G  5.1 32 -48.21 K.YRSSNVQGSGPQK.Q  4.9 34 -30.00 K.VMLMDAGERVDR.D  4.6 36 -45.49 R.KFNDPVVQADMK.L  4.6 36 -45.49 R.KFNDPVVQSDMK.L  4.5 37 -48.20 R.APESQQQPAAPAGR.R | |
| |  | | --- | | Top scoring peptide matches to query 358 09MAR16\_OT\_03.01460.01460.3 Score greater than 31 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.1 1.3 11.1 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  17.6 1.8 -25.50 -.MAAHHRQNTAGR.R  17.5 1.9 -40.67 K.LTMFHVCSQIR.R  14.6 3.6 16.6 K.DSVLSVCNMVHM.-  14.0 4.2 -1.56 K.AYPGQETPGMQGR.Y  13.0 5.2 16.6 K.DSVLSVCNMVHM.-  13.0 5.3 -17.05 R.FDDGVLDPNYPR.E  12.6 5.7 4.67 K.DTNESESAIEGQK.I  12.2 6.4 -45.29 DVMYHTEKISGK  12.1 6.5 -16.56 K.DELMEESQVRR.A | |

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| |  | | --- | | Top scoring peptide matches to query 359 09MAR16\_OT\_03.01431.01431.3 Score greater than 26 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  20.2 1 11.1 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  19.2 1.3 -19.46 K.DTGFAAVVQDCPK.Q  16.6 2.3 11.1 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  12.7 5.6 -27.43 R.DTNKWDVQMVR.V  11.1 8.1 -1.56 K.DTNQWDKDMVR.R  10.9 8.6 -4.41 R.GYLYFTNMQDR.A  9.4 12 -40.67 K.LTMFHVCSQIR.R  9.2 12 -47.67 K.LAMNEAEMLLTR.I  8.9 14 -12.39 K.SDYFMAFSAGRR.A  8.8 14 30.5 R.NDEGEESKDEAGK.L | |
| |  | | --- | | Top scoring peptide matches to query 360 09MAR16\_OT\_03.01428.01428.3 Score greater than 28 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.3 0.25 11.5 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  20.7 0.9 11.5 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  14.5 3.7 -28.80 R.DSSAQRADLESTK.A  14.4 3.8 -4.02 R.GYLYFTNMQDR.A  13.0 5.3 -16.16 K.LEALMASNDSANR.T  12.7 5.6 -16.18 K.QAESVMQDLGSSR.A  12.6 5.8 -27.04 R.DTNKWDVQMVR.V  11.9 6.7 -40.28 K.LTMFHVCSQIR.R  11.9 6.8 8.70 R.KNWMSGGGGGGGGGGR.S  11.7 7.2 -8.19 K.CEILETAEEGTR.V | |

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| |  | | --- | | Top scoring peptide matches to query 361 09MAR16\_OT\_03.01448.01448.2 Score greater than 19 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  13.4 5 13.1 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  7.0 22 13.1 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  5.2 33 -32.45 K.AVEEMNGKEISGK.I  4.6 38 -38.07 R.VEGNGGFDLDRTK.F  3.4 50 -33.88 K.WTNYLSGWQPR.W  3.2 53 -30.07 -.LEDHGASPEVSPK.I  3.1 54 10.8 R.GQQSYDYGAYQK.S  2.8 57 -14.58 K.LENKDIMGSNDR.D  2.6 60 -32.45 K.MRDLETELEQK.S  1.3 81 -6.60 R.VQEGASEGQMEVK.K | |
| |  | | --- | | Top scoring peptide matches to query 362 09MAR16\_OT\_03.01440.01440.2 Score greater than 22 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  12.1 6.8 14.2 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  11.6 7.7 14.2 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.HMDPPPAPMQDR.S  9.1 14 -1.18 R.RADGPPASHDGGDR.S  7.9 18 -0.83 -.MPLNDTTMDRR.G  6.7 24 4.44 R.NREEIDMAGSNR.K  5.6 30 -13.45 K.LENKDIMGSNDR.D  5.1 35 11.4 R.GGGGGGGGGGSMWNKR.W  4.4 40 -24.29 R.SIQEYNLCPQR.A  3.2 53 -44.90 R.NRETATFINDAR.A  2.7 60 -44.89 K.APREAGPAEEQPR.K | |

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| |  | | --- | | Top scoring peptide matches to query 368 09MAR16\_OT\_03.02165.02165.2 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  54.0 0.00043 11.7 R.QIFHPEQLITGK.E  54.0 0.00043 11.7 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.QLFHPEQLITGK.E  17.5 1.9 -3.29 K.DPLAQINVAALTGK.K  14.3 4 40.7 R.KIMSTLADMQLK.I  10.1 11 9.31 R.VADLLQHINLMK.T  9.4 12 4.06 R.LKMLQMVQLFK.C  9.4 12 11.7 RKPEPPEPIGYK  8.8 14 22.5 R.KLEGAEAEHLVSK.R  8.5 15 -3.28 K.EGAIIVDPARELK.V  8.4 15 11.7 R.GKWEQPAVPGTLK.R | |
| |  | | --- | | Top scoring peptide matches to query 369 09MAR16\_OT\_03.02170.02170.3 Score greater than 31 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  36.1 0.026 11.7 R.QIFHPEQLITGK.E  36.1 0.026 11.7 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.QLFHPEQLITGK.E  16.0 2.7 9.37 R.VADLLQHINLMK.T  11.5 7.5 -3.23 K.DPLAQINVAALTGK.K  8.7 14 9.37 K.LPGKIDPSMLPAR.W  5.8 28 -6.09 R.FLTASQDKILFK.D  2.4 61 -14.05 R.GFHLPPSKLSSLK.F  2.4 62 6.50 K.LIFMVIQDLFR.N  2.4 62 22.0 K.LAGPPSCIVPLMR.Q  2.2 65 17.3 R.KQLLEYQTMLK.G | |

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| |  | | --- | | Top scoring peptide matches to query 370 09MAR16\_OT\_03.02159.02159.3 Score greater than 32 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.4 0.031 12.0 R.QIFHPEQLITGK.E  35.4 0.031 12.0 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.QLFHPEQLITGK.E  17.1 2.1 9.63 R.VADLLQHINLMK.T  13.6 4.7 40.7 K.YGTDLSRGLTTAR.A  9.4 12 -2.97 K.DPLAQINVAALTGK.K  6.9 22 4.04 K.HLVAQLAQDIFR.S  6.7 23 27.5 R.KVAMIQESPVHR.M  6.5 24 47.7 R.KHGQLTSEHAFR.K  4.5 38 9.63 K.LPGKIDPSMLPAR.W  4.0 42 6.88 R.GLGGALGGLLGGGGQAR.A | |
| |  | | --- | | Top scoring peptide matches to query 371 09MAR16\_OT\_03.02163.02163.3 Score greater than 31 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  20.9 0.87 12.1 R.QIFHPEQLITGK.E  20.9 0.87 12.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.QLFHPEQLITGK.E  16.8 2.2 9.69 R.VADLLQHINLMK.T  11.5 7.6 -2.91 K.DPLAQINVAALTGK.K  8.5 15 26.6 K.QRCAPLWRPAR.Q  7.5 19 47.8 R.KHGQLTSEHAFR.K  7.0 22 9.69 K.LPGKIDPSMLPAR.W  6.8 23 17.7 K.QTLEILKYMQK.K  4.5 38 43.5 K.SLLEEMVSSIFR.R  4.4 39 43.5 K.SSDLPLLLYSMR.N | |

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| |  | | --- | | Top scoring peptide matches to query 391 09MAR16\_OT\_03.02109.02109.2 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  90.5 1.5e-07 11.4 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.AGQVFLEELGNHK.A  9.5 19 -33.64 DLEKQVILQPMK  9.2 20 6.27 K.LVGKDLAEFYMR.K  8.9 21 -11.03 R.RLAAAEENIEVAR.A  8.9 21 -11.03 R.RLAAAEENLEVAR.A  7.0 33 -6.99 K.IFHKFSNLNGHK.V  6.6 36 -28.51 R.QQVGRLLEEIEK.Q  5.7 45 -11.04 K.QQEQLAQALERK.G  5.4 48 11.4 K.GQVINTVDPFSHK.S  4.7 57 -45.95 R.LEINVLEKINEK.D | |
| |  | | --- | | Top scoring peptide matches to query 392 09MAR16\_OT\_03.02124.02124.2 Score greater than 32 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  90.5 1.5e-07 11.5 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.AGQVFLEELGNHK.A  13.5 7.5 -10.97 R.QQLNDGRQLLEK.V  12.2 10 11.5 R.EQRPAYEPVQPK.S  11.0 13 6.36 K.LVGKDLAEFYMR.K  10.9 14 -33.56 DLEKQVILQPMK  8.5 24 -28.42 R.QQVGRLLEEIEK.Q  7.8 28 3.68 K.ENKVQIGGQFHGK.S  7.4 30 -45.87 K.QIELDLDNKILK.L  6.6 37 16.9 R.IELVCPEEPLSR.K  6.5 37 -28.42 K.QNLGELIGTLNAAK.V | |

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| |  | | --- | | Top scoring peptide matches to query 393 09MAR16\_OT\_03.02115.02115.2 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  90.5 1.5e-07 11.5 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.AGQVFLEELGNHK.A  9.3 19 -33.56 DLEKQVILQPMK  9.1 21 6.36 K.LVGKDLAEFYMR.K  7.4 30 -6.90 K.IFHKFSNLNGHK.V  7.2 32 -28.42 R.QQVGRLLEEIEK.Q  6.6 36 44.5 K.QQFYDIPTSSQK.A  6.0 42 11.5 K.GQVINTVDPFSHK.S  5.6 46 -10.96 K.QQEQLAQALERK.G  5.0 53 -10.97 R.QQLNDGRQLLEK.V  4.8 55 4.62 K.EPGDTTPKENLIK.N | |
| |  | | --- | | Top scoring peptide matches to query 394 09MAR16\_OT\_03.02114.02114.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  42.9 0.0085 11.8 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.AGQVFLEELGNHK.A  9.2 20 -41.00 R.EKALMALQVSPVR.I  8.3 24 11.8 R.EQRPAYEPVQPK.S  7.4 30 44.9 K.QQFYDIPTSSQK.A  7.3 31 -0.94 R.AANVARAAASNQAAR.A  6.7 36 -13.41 R.EKIYTDLAPHVR.R  6.4 38 -2.81 R.EKAAAASVPNADGLK.D  6.3 39 -10.62 R.QQLNDGRQLLEK.V  5.9 43 47.7 R.EQPLRSDQDPEK.E  5.8 44 -18.42 R.EVQARLSGGVGAAAR.Q | |

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| |  | | --- | | Top scoring peptide matches to query 395 09MAR16\_OT\_03.02103.02103.3 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  52.0 0.0011 11.8 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.AGQVFLEELGNHK.A  13.0 8.3 11.8 R.EQRPAYEPVQPK.S  9.3 19 -41.00 R.EKALMALQVSPVR.I  9.0 21 -10.61 K.QQEQLAQALERK.G  8.7 22 -28.09 R.EQVLSVLTSNPVR.K  7.6 29 -0.94 R.AANVARAAASNQAAR.A  7.1 33 27.0 K.AGPKPSSLSMAHSR.V  7.0 33 14.6 K.QEVLDQALQQNR.E  6.9 34 6.84 EKRPAGGQGGSAAAGK  6.4 38 -28.07 K.QNLGELIGTLNAAK.V | |
| |  | | --- | | Top scoring peptide matches to query 396 09MAR16\_OT\_03.02108.02108.3 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  55.6 0.00046 11.9 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.AGQVFLEELGNHK.A  10.7 14 -40.94 R.EKALMALQVSPVR.I  10.6 14 -10.55 R.QQLNDGRQLLEK.V  10.5 15 44.5 M.QQEGGPVRSAPCR.T  10.3 15 11.9 R.EQRPAYEPVQPK.S  10.3 15 -10.54 K.QQEQLAQALERK.G  8.5 23 -35.81 K.QQLQRVEAQLTK.T  8.3 24 -28.01 R.QQVGRLLEEIEK.Q  7.6 29 -3.70 R.GAQVIHTQEFRR.W  7.5 30 -13.35 R.EKIYTDLAPHVR.R | |

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| |  | | --- | | Top scoring peptide matches to query 397 09MAR16\_OT\_03.01943.01943.2 Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  56.7 0.00037 10.3 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.IKTFDELEQEAK.Q  19.4 1.9 -39.94 K.KLYSLIGATVIEGS.-  14.8 5.6 -20.74 R.LQTLQPSAHGSRR.V  14.6 5.9 33.0 R.QTIMDDPLTTATK.I  14.0 6.7 10.3 K.QIYKPSETLEDK.V  13.3 8 -15.44 K.LKIFAMPMQDIK.M  12.9 8.7 -30.33 R.LQHEVGAKELQAK.F  12.4 9.7 -33.13 K.KITDPDVVHIWK.T  12.0 11 -12.97 K.NLHRASAPEQSLK.E  11.6 12 -10.36 K.LQTTGPMFIIGTR.M | |
| |  | | --- | | Top scoring peptide matches to query 398 09MAR16\_OT\_03.01948.01948.2 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.8 0.018 10.5 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.IKTFDELEQEAK.Q  16.3 4 -30.08 R.LQHEVGAKELQAK.F  15.1 5.2 -15.18 K.LKIFAMPMQDIK.M  14.9 5.4 -39.69 K.KLYSLIGATVIEGS.-  11.1 13 -20.49 R.LQTLQPSAHGSRR.V  9.3 20 45.5 R.DLNMDCIIAEIK.A  9.1 21 25.5 K.DNIMVANTTVTQK.M  8.6 23 45.1 R.KMSEEEFYLFK.N  8.1 26 17.3 R.TKEVFHFSQAEK.V  8.1 26 -10.11 K.LQTTGPMFIIGTR.M | |

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| |  | | --- | | Top scoring peptide matches to query 399 09MAR16\_OT\_03.01941.01941.3 Score greater than 30 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  45.3 0.005 10.9 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.IKTFDELEQEAK.Q  14.8 5.6 25.9 R.SENKEQNILTMK.R  13.8 7.1 45.5 R.KMSEEEFYLFK.N  13.7 7.2 -29.71 R.LQHEVGAKELQAK.F  13.2 8.1 -1.97 R.MFVLNELVQTEK.D  12.7 9.1 27.3 K.HHSGGEKPFQAQK.Q  11.5 12 -42.56 M.LHSKPKGCLQLK.K  9.9 17 -39.31 R.YTELLLLDNTKK.E  9.7 18 -12.35 K.NLHRASAPEQSLK.E  9.4 19 -4.29 K.LMDEVIKSMKPK.- | |
| |  | | --- | | Top scoring peptide matches to query 400 09MAR16\_OT\_03.01946.01946.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.7 0.091 11.1 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.IKTFDELEQEAK.Q  11.8 11 27.5 K.HHSGGEKPFQAQK.Q  10.8 14 26.1 R.SENKEQNILTMK.R  9.6 18 7.82 R.GLCSGELHLSHLK.G  9.6 18 -42.37 M.LHSKPKGCLQLK.K  9.4 19 0.99 -.MAVEGSTITSRIK.N  8.6 23 -1.78 R.MFVLNELVQTEK.D  8.4 24 21.0 K.LLMEEVLQSMNK.L  8.3 25 38.3 K.LINCCTLISNDK.K  8.0 27 -21.77 K.LLFSSPASGAKSSAK.G | |

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| |  | | --- | | Top scoring peptide matches to query 405 09MAR16\_OT\_03.02325.02325.2 Score greater than 30 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.2 0.0099 11.5 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial K.LHSMIVDLDSVVK.K  15.1 4 23.8 K.LHMLSEMPSIAVK.I  10.4 12 -8.38 R.HLSLTSTSVPSAKK.A  9.7 14 36.6 K.MIYSSSNLKTPSK.L  8.5 18 -8.36 K.ARLQLEVEEQLK.R  7.1 25 -8.37 R.LLQNIDEVVEKR.Y  6.2 31 -0.64 R.LLIEIEETPDRK.S  5.4 37 -18.86 K.HIQDVLQFSKLK.A  4.7 44 16.6 R.HISTLNIQLSDSK.K  3.9 52 -1.57 R.LHAFESIVQQRK.T | |
| |  | | --- | | Top scoring peptide matches to query 406 09MAR16\_OT\_03.02320.02320.2 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  40.1 0.013 12.0 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial K.LHSMIVDLDSVVK.K  14.4 4.6 24.3 K.LHMLSEMPSIAVK.I  8.6 18 -1.07 R.LHAFESIVQQRK.T  8.4 19 37.1 K.MIYSSSNLKTPSK.L  7.3 24 -7.85 K.ARLQLEVEEQLK.R  6.5 29 -7.86 R.LLQNIDEVVEKR.Y  6.5 29 17.1 R.HISTLNIQLSDSK.K  5.6 35 -0.13 R.LLIEIEETPDRK.S  4.6 45 4.34 K.LTSKQLMSVHSPK.G  4.5 45 16.5 -.MMTEVIIHTPKR.L | |

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| |  | | --- | | Top scoring peptide matches to query 407 09MAR16\_OT\_03.02332.02332.3 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  27.4 0.24 12.1 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial K.LHSMIVDLDSVVK.K  10.8 11 9.47 R.VKKPQTDLGGDAAR.R  9.7 14 14.4 K.LYSAPQLEPVPNK.R  9.4 15 21.2 R.LNRYINTTFWK.A  8.4 19 -35.60 R.FVVNTLTIPLPNK.F  8.4 19 -31.10 R.FPMQRNLIVIPK.S  7.9 21 6.70 K.LGWVRPDLGDLSK.V  6.6 28 6.70 R.FPSPPRDQLTGIK.N  6.3 30 17.2 QQLQQAEEALVAK  5.9 33 -7.80 K.ARLQLEVEEQLK.R | |
| |  | | --- | | Top scoring peptide matches to query 408 09MAR16\_OT\_03.02324.02324.3 Score greater than 27 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.7 0.14 12.4 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial K.LHSMIVDLDSVVK.K  12.4 7.4 9.72 R.VKKPQTDLGGDAAR.R  11.0 10 -30.85 R.FPMQRNLIVIPK.S  11.0 10 29.7 K.KSKPSMVGEHDLK.V  9.1 16 -7.55 K.ARLQLEVEEQLK.R  7.6 22 -49.86 R.LLEVLISKQDVAK.T  7.4 24 6.95 R.FPSPPRDQLTGIK.N  7.0 26 21.5 R.LNRYINTTFWK.A  6.6 29 34.6 K.FAVLAFMIEVGDK.V  6.5 29 12.4 -.MPTAAAPIISSVQK.L | |

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| |  | | --- | | Top scoring peptide matches to query 409 09MAR16\_OT\_03.02333.02333.2 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.4 0.00059 12.4 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial K.LHSMIVDLDSVVK.K  12.5 7.3 42.5 K.QGPGEINVVEGQTK.V  10.5 11 24.6 K.LHMLSEMPSIAVK.I  10.3 12 37.4 K.MIYSSSNLKTPSK.L  8.3 19 49.3 K.IHAELSPDRFDR.T  7.8 22 -3.50 K.VERPTKFFIYR.R  6.5 29 -15.24 K.QNIINQAITAKNK.K  5.6 36 -7.52 K.ARLQLEVEEQLK.R  5.4 37 -24.81 R.QVILQELLDKEK.V  5.4 38 9.75 R.VKKPQTDLGGDAAR.R | |
| |  | | --- | | Top scoring peptide matches to query 410 09MAR16\_OT\_03.02319.02319.3 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  20.3 1.2 12.7 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial K.LHSMIVDLDSVVK.K  11.1 10 -30.54 R.FPMQRNLIVIPK.S  8.7 18 47.2 R.GSVPTRALGMEGHK.T  8.7 18 -7.24 M.NKVNILPSDTNIK.I  8.7 18 15.0 K.FVVGYSGEGTKALK.E  8.4 19 7.26 R.FPSPPRDQLTGIK.N  8.0 21 -14.97 R.NGGRLDALSVNVIK.N  7.8 21 10.0 R.VKKPQTDLGGDAAR.R  7.5 23 -17.76 R.VFVGDHVGKVSAIK.L  6.5 29 36.8 R.VCLHERNFVPGK.S | |

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| |  | | --- | | Top scoring peptide matches to query 412 09MAR16\_OT\_03.02676.02676.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  22.7 1 8.11 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.6 26 -21.75 R.EVRELVGPGHPDR.Q  3.6 82 38.4 R.EPAMYANTGVYTK.A  3.5 84 -9.10 R.DLAALFSYAFNTK.V  3.1 93 -38.98 R.DIGLSVTHRFSTK.S  2.8 1e+02 -19.10 R.LLAATMEKGFHLN.-  1.9 1.2e+02 18.0 K.TEFFIEMMRTR.K  1.4 1.4e+02 -29.43 R.NDGLGERPPPRPR.R  1.4 1.4e+02 -19.10 K.DLEYGCLKIPPR.C  1.3 1.4e+02 -7.28 K.AGRLVFGFGEHDR.K | |
| |  | | --- | | Top scoring peptide matches to query 413 09MAR16\_OT\_03.02588.02588.3 Score greater than 22 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  16.5 4.3 8.80 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.8 25 -32.87 K.DIKMIIAANNTEK.R  7.7 32 -47.81 K.DLPFNLITEALSK.L  7.5 33 -3.50 K.NINLCCDLAIVR.K  5.5 53 -7.95 R.DIGMAVLAEKEER.L  5.4 54 -0.29 K.VEGDMKVPDVDIK.G  4.4 69 -30.58 R.EALGEGFALLADVR.E  4.2 72 -30.59 R.DLDEVLQKFTPR.Q  4.1 74 -33.35 R.IDFLPHYDTLVK.S  4.0 76 -6.59 K.AGRLVFGFGEHDR.K | |

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| |  | | --- | | Top scoring peptide matches to query 414 09MAR16\_OT\_03.02880.02880.3 Score greater than 19 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  14.8 6.3 9.36 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  5.9 49 -32.30 K.NQAMALVEEALKK.D  5.5 53 -30.02 R.ENPERTFDLVLK.V  5.5 54 -24.62 K.QDLLEMKELVDK.R  2.7 1e+02 -32.34 R.TMPGETAVSISVLR.R  1.9 1.2e+02 -22.78 R.TELCLSRSNRPK.Q  1.8 1.3e+02 -37.70 K.NNGAYLQLVEIAR.A  1.8 1.3e+02 -30.03 R.DLDEVLQKFTPR.Q  1.7 1.3e+02 -2.46 R.TELLLDFMYTSK.V  1.6 1.3e+02 -42.77 R.VEMKIRPEAFKP.- | |
| |  | | --- | | Top scoring peptide matches to query 415 09MAR16\_OT\_03.02540.02540.3 Score greater than 20 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  8.2 29 -2.14 K.KATDAEADVASLNR.R  7.8 32 9.55 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  6.9 39 -2.15 K.QTTASEQQQAAVAK.L  6.3 44 -32.12 K.NQAMALVEEALKK.D  6.2 46 -4.90 K.ITANSTWEPDKAK.Y  5.7 51 21.8 R.QTSDGQVHHQAPR.K  4.2 72 -33.05 M.WALCSLLRSAAGR.T  3.6 84 29.9 K.HEMAEQMIKAEK.K  3.4 87 -32.60 R.IDFLPHYDTLVK.S  3.0 95 -14.91 R.NDGMQLSQLAVLR.L | |

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| |  | | --- | | Top scoring peptide matches to query 416 09MAR16\_OT\_03.02637.02637.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.9 3.1 9.86 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  9.1 23 -6.88 R.DIGMAVLAEKEER.L  8.9 25 -44.60 K.QTLPVMVLSGKCK.A  7.7 32 2.63 -.MSSPAVARTSPGGSR.E  6.6 41 -31.81 -.MAVAAALTGLQAEAK.C  6.1 47 -1.82 K.KATDAEADVASLNR.R  6.1 47 23.1 R.LNVNATDSSTSSHK.Q  5.9 49 -25.04 -.MAAATLGQVWARK.L  5.9 49 35.3 R.DSKGAGQEQGMPAGK.K  5.7 52 -42.27 -.WSCLLLEKLTR.R | |
| |  | | --- | | Top scoring peptide matches to query 417 09MAR16\_OT\_03.03037.03037.3 Score greater than 21 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  9.1 24 -5.52 K.AGRLVFGFGEHDR.K  7.9 31 23.1 R.LNVNATDSSTSSHK.Q  6.3 44 9.86 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  5.8 51 37.9 K.TLEEPAMEMLHK.V  4.8 64 -17.35 R.LLAATMEKGFHLN.-  2.9 97 -6.91 K.GLMGSVGEPGLKGDK.G  2.5 1.1e+02 -19.66 R.SEMHKLVLQTMK.V  2.2 1.2e+02 -14.60 R.LVALQSLQMGDNR.L  1.6 1.3e+02 -31.81 K.LSEKISMTASLHK.S  1.5 1.3e+02 -12.29 R.GGAEGSPKPAVYATR.K | |

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| |  | | --- | | Top scoring peptide matches to query 418 09MAR16\_OT\_03.02415.02415.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.0 0.03 9.99 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.6 27 -6.76 R.DIGMAVLAEKEER.L  8.1 30 -19.87 R.DPHGPGVLERVER.L  8.0 30 -36.17 K.AIIDSSIGDLTIDK.G  7.5 34 -19.54 -.MVMEVGILDAGGLR.A  7.4 35 22.3 R.QTSDGQVHHQAPR.K  7.2 36 40.5 K.NSASGAGAGAGAGAGAGEK.H  6.8 40 -6.77 R.NLMEGVEQNLSVK.N  6.8 40 -31.69 -.MAVAAALTGLQAEAK.C  6.3 44 2.74 R.DGGIRVMQLQGDR.D | |
| |  | | --- | | Top scoring peptide matches to query 419 09MAR16\_OT\_03.02274.02274.2 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  63.1 9.4e-05 10.1 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  14.5 6.8 -9.42 R.EMVPPFGVELQAK.L  13.8 7.9 27.3 R.HDNLHSTQSFFK.G  12.6 10 5.15 R.GGGGPDGYGRGQGVVK.L  10.4 17 43.2 R.GTADVTHDLQEMK.E  10.1 19 18.3 K.KMNEPVSGQEPTK.V  9.5 21 7.82 K.DMNLNEHSLLFK.S  7.8 32 35.5 EQDTSAHLERMK  7.2 36 3.35 K.YETIHLTEEPTK.L  6.5 43 2.86 R.DGGIRVMQLQGDR.D | |

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| |  | | --- | | Top scoring peptide matches to query 420 09MAR16\_OT\_03.02659.02659.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  11.8 13 -6.14 R.NNQLGSLMPTIEK.H  10.8 16 10.6 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  7.5 33 -31.08 R.APGSGTVSKPLMTSK.A  7.4 35 -31.05 K.NQAMALVEEALKK.D  6.2 46 -38.76 R.VIAGRDMLAEITR.K  5.8 50 -23.37 K.QSEILSMLPESVK.S  5.8 50 -13.84 R.NDGMQLSQLAVLR.L  4.9 61 -31.53 R.IDFLPHYDTLVK.S  4.8 63 -13.84 R.LVALQSLQMGDNR.L  3.8 79 41.1 K.VEGNEERSAGGAER.A | |
| |  | | --- | | Top scoring peptide matches to query 421 09MAR16\_OT\_03.02599.02599.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  12.5 11 10.7 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.2 18 -6.02 R.TKQMNPTAPSIEK.Q  7.5 33 31.7 K.LDQEPNSNESSIK.L  7.3 35 -19.70 K.VMFRNLLQMHR.L  4.4 69 11.2 K.QLTDPAMDLRER.Y  3.6 83 -41.42 R.TVHGLDGIKFMVK.N  3.4 86 -0.96 K.QTTASEQQQAAVAK.L  3.0 96 -11.41 R.GGAEGSPKPAVYATR.K  2.9 98 -6.61 -.MACAAVMIPGLLR.C  2.6 1e+02 -30.96 R.RDSVPVTLAMVEK.W | |

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| |  | | --- | | Top scoring peptide matches to query 422 09MAR16\_OT\_03.02503.02503.3 Score greater than 21 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.3 2.2 10.7 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  7.0 38 -31.41 R.IDFLPHYDTLVK.S  5.9 49 31.7 K.LDQEPNSNESSIK.L  5.6 53 -30.92 K.NQAMALVEEALKK.D  5.5 54 -19.70 K.VMFRNLLQMHR.L  4.8 63 -13.72 R.NDGMQLSQLAVLR.L  4.6 66 -18.16 K.KEVELSSEIAEAR.K  3.4 86 -0.96 K.QTTASEQQQAAVAK.L  3.3 89 31.7 -.VNSTTLPAEDEER.S  3.2 91 6.75 R.LSQAAGASPLSESDK.E | |
| |  | | --- | | Top scoring peptide matches to query 423 09MAR16\_OT\_03.02181.02181.2 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  54.8 0.00063 10.9 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.1 19 5.90 R.GGGGPDGYGRGQGVVK.L  9.8 20 -36.22 R.QTLNKAPFSGAQAK.V  9.4 22 -5.91 K.AVGTEECQLNVLK.H  8.4 27 43.9 R.GTADVTHDLQEMK.E  8.1 30 19.0 K.KMNEPVSGQEPTK.V  6.4 43 -24.06 R.HRMLGPESVPPPK.R  5.8 50 19.0 K.DNLECELEALVR.R  5.7 51 36.3 EQDTSAHLERMK  5.4 54 -8.67 R.EMVPPFGVELQAK.L | |

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| |  | | --- | | Top scoring peptide matches to query 424 09MAR16\_OT\_03.02665.02665.3 Score greater than 19 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  10.6 17 10.9 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  5.6 52 -30.80 K.NQAMALVEEALKK.D  1.9 1.2e+02 3.62 R.DGGIRVMQLQGDR.D  1.9 1.2e+02 -48.99 R.TTCHPLALPVVPR.L  1.7 1.3e+02 -36.22 R.DIGLSVTHRFSTK.S  1.4 1.4e+02 37.5 K.NFHFVEPPCWK.V  1.4 1.4e+02 -45.74 K.DLPFNLITEALSK.L  1.2 1.4e+02 -4.51 K.ARDFVNEAVFHR.E  1.0 1.5e+02 -5.91 K.GLMGSVGEPGLKGDK.G  0.9 1.5e+02 -16.34 R.KPTMTLEEGLWR.A | |
| |  | | --- | | Top scoring peptide matches to query 425 09MAR16\_OT\_03.02289.02289.3 Score greater than 21 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  22.7 1 10.9 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  6.7 41 3.69 -.MSSPAVARTSPGGSR.E  5.8 50 19.1 K.DNLECELEALVR.R  5.4 55 -43.53 K.QTLPVMVLSGKCK.A  4.5 68 -0.77 K.QTTASEQQQAAVAK.L  4.2 72 -13.52 K.RVMALLQENQDK.I  4.0 75 -0.76 K.KATDAEADVASLNR.R  3.8 79 -5.83 R.NLMEGVEQNLSVK.N  3.6 83 -0.77 K.DLPQGSGNSSAATKK.K  3.4 87 31.9 K.LDQEPNSNESSIK.L | |

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| |  | | --- | | Top scoring peptide matches to query 426 09MAR16\_OT\_03.02605.02605.3 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.3 3.5 11.0 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  13.3 8.7 -13.47 R.NDGMQLSQLAVLR.L  8.1 30 33.6 R.GATENSVYLGMYR.G  6.6 42 -13.47 R.STTHSNMQVIKAK.N  5.3 56 36.4 R.DSKGAGQEQGMPAGK.K  5.2 57 -8.54 R.EMVPPFGVELQAK.L  4.8 63 3.76 -.MSSPAVARTSPGGSR.E  4.7 64 -13.47 R.IDQTLAAMGASGAVR.E  4.2 71 -0.73 R.GGDLKLDGVQTSDR.Y  4.2 71 -36.07 K.NNGAYLQLVEIAR.A | |
| |  | | --- | | Top scoring peptide matches to query 427 09MAR16\_OT\_03.02510.02510.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.3 0.14 11.0 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.3 18 -30.67 K.NQAMALVEEALKK.D  7.4 35 -5.75 R.DIGMAVLAEKEER.L  7.1 37 -18.53 R.SEMHKLVLQTMK.V  6.3 44 -0.71 K.QTTASEQQQAAVAK.L  6.0 47 -16.22 R.LLAATMEKGFHLN.-  5.5 53 49.2 K.VQDEAASADGEAAAR.Y  5.5 54 -16.24 -.MPTNFTVVPVEAR.A  5.2 57 -3.45 K.SPQDPNYSIQIAK.V  4.8 62 -13.47 R.NDGMQLSQLAVLR.L | |

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| |  | | --- | | Top scoring peptide matches to query 428 09MAR16\_OT\_03.02517.02517.3 Score greater than 22 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  15.4 5.5 11.0 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.9 24 -30.67 K.NQAMALVEEALKK.D  8.7 25 -5.75 R.DIGMAVLAEKEER.L  7.2 36 1.91 K.VEGDMKVPDVDIK.G  7.0 38 -0.71 K.QTTASEQQQAAVAK.L  6.4 43 -13.47 R.NDGMQLSQLAVLR.L  5.6 52 -45.63 R.KTFVSDLLPPTDK.E  5.4 54 24.2 R.INSTATPDQDRDK.I  5.2 57 4.23 K.GVAYPSTLTYSSSK.T  4.4 69 -45.61 K.DLPFNLITEALSK.L | |
| |  | | --- | | Top scoring peptide matches to query 429 09MAR16\_OT\_03.02267.02267.2 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  63.0 9.5e-05 11.0 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  14.8 6.3 8.74 K.DMNLNEHSLLFK.S  10.0 19 44.1 R.GTADVTHDLQEMK.E  9.7 20 6.07 R.GGGGPDGYGRGQGVVK.L  9.6 21 4.27 K.YETIHLTEEPTK.L  8.8 25 26.0 K.NMPEVEGTFHKR.D  7.8 32 36.4 EQDTSAHLERMK  7.3 35 19.2 K.KMNEPVSGQEPTK.V  7.2 36 28.3 R.HDNLHSTQSFFK.G  6.8 40 -22.96 K.QSEILSMLPESVK.S | |

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| |  | | --- | | Top scoring peptide matches to query 430 09MAR16\_OT\_03.02192.02192.2 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.5 0.00084 11.0 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.5 27 44.1 R.GTADVTHDLQEMK.E  8.1 29 6.07 R.GGGGPDGYGRGQGVVK.L  7.0 38 -36.05 R.QTLNKAPFSGAQAK.V  6.4 43 36.4 EQDTSAHLERMK  6.0 47 19.2 K.KMNEPVSGQEPTK.V  5.7 51 4.27 K.YETIHLTEEPTK.L  5.2 57 26.0 K.NMPEVEGTFHKR.D  5.0 60 -13.88 K.SPQKEWNPSLFK.V  4.7 65 8.74 K.DMNLNEHSLLFK.S | |
| |  | | --- | | Top scoring peptide matches to query 431 09MAR16\_OT\_03.02234.02234.2 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  58.8 0.00025 11.0 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.2 15 6.07 R.GGGGPDGYGRGQGVVK.L  9.6 21 44.1 R.GTADVTHDLQEMK.E  8.4 27 19.2 K.KMNEPVSGQEPTK.V  6.9 39 36.4 EQDTSAHLERMK  6.3 44 -36.05 R.QTLNKAPFSGAQAK.V  5.7 51 19.2 -.ICDVKEETPQNK.E  5.5 54 28.3 R.HDNLHSTQSFFK.G  5.4 55 -43.44 K.QTLPVMVLSGKCK.A  5.2 57 7.03 R.SLGSKDASSPPSAEK.E | |

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| |  | | --- | | Top scoring peptide matches to query 432 09MAR16\_OT\_03.02398.02398.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.2 0.23 11.1 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.9 12 -5.69 R.DIGMAVLAEKEER.L  11.2 14 3.82 -.MSSPAVARTSPGGSR.E  10.4 17 -0.64 K.QTTASEQQQAAVAK.L  9.0 24 11.5 R.TGAKCVPGETGDLR.E  8.9 24 -35.11 K.AIIDSSIGDLTIDK.G  8.0 30 -13.40 K.RVMALLQENQDK.I  7.3 35 -3.39 M.VRYSLDPENPTK.S  5.9 48 1.97 K.VEGDMKVPDVDIK.G  5.7 51 -30.64 K.LTCDSKVVINSPK.L | |
| |  | | --- | | Top scoring peptide matches to query 433 09MAR16\_OT\_03.02560.02560.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  27.8 0.32 11.1 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.7 13 -13.41 R.NDGMQLSQLAVLR.L  11.5 13 1.97 K.VEGDMKVPDVDIK.G  9.2 23 -5.70 R.NNQLGSLMPTIEK.H  7.9 31 -30.61 K.NQAMALVEEALKK.D  6.9 38 -0.63 K.KATDAEADVASLNR.R  6.1 46 20.9 K.TEFFIEMMRTR.K  6.0 47 39.1 K.TLEEPAMEMLHK.V  5.6 52 -30.62 -.MAVAAALTGLQAEAK.C  5.0 60 -36.01 K.NNGAYLQLVEIAR.A | |

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| |  | | --- | | Top scoring peptide matches to query 434 09MAR16\_OT\_03.02187.02187.2 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  63.1 9.2e-05 11.1 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  12.5 11 6.15 R.GGGGPDGYGRGQGVVK.L  11.6 13 19.3 K.KMNEPVSGQEPTK.V  9.3 22 44.2 R.GTADVTHDLQEMK.E  6.5 42 28.3 R.HDNLHSTQSFFK.G  6.4 44 36.5 EQDTSAHLERMK  6.2 45 19.3 -.ICDVKEETPQNK.E  5.8 50 -5.65 R.NLMEGVEQNLSVK.N  5.8 50 -35.97 R.QTLNKAPFSGAQAK.V  5.5 54 4.35 K.YETIHLTEEPTK.L | |
| |  | | --- | | Top scoring peptide matches to query 435 09MAR16\_OT\_03.02223.02223.2 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  58.1 0.00029 11.3 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.4 27 44.3 R.GTADVTHDLQEMK.E  8.3 28 6.32 R.GGGGPDGYGRGQGVVK.L  7.3 35 -23.64 R.HRMLGPESVPPPK.R  7.3 35 4.52 K.YETIHLTEEPTK.L  6.4 44 36.7 EQDTSAHLERMK  5.4 54 -35.80 R.QTLNKAPFSGAQAK.V  5.3 56 -13.19 R.IDQTLAAMGASGAVR.E  5.2 57 26.2 K.NMPEVEGTFHKR.D  4.6 65 28.5 R.HDNLHSTQSFFK.G | |

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| |  | | --- | | Top scoring peptide matches to query 436 09MAR16\_OT\_03.02229.02229.2 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  58.1 0.0003 11.3 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.7 13 28.5 R.HDNLHSTQSFFK.G  10.7 16 6.32 R.GGGGPDGYGRGQGVVK.L  9.1 23 44.3 R.GTADVTHDLQEMK.E  8.7 26 -35.80 R.QTLNKAPFSGAQAK.V  7.5 33 -23.64 R.HRMLGPESVPPPK.R  7.0 38 4.52 K.YETIHLTEEPTK.L  6.7 41 -13.63 K.SPQKEWNPSLFK.V  6.2 45 36.7 EQDTSAHLERMK  6.0 47 19.4 K.KMNEPVSGQEPTK.V | |
| |  | | --- | | Top scoring peptide matches to query 437 09MAR16\_OT\_03.02469.02469.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  21.7 1.3 11.3 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.1 19 -13.15 R.NDGMQLSQLAVLR.L  9.3 22 -0.39 K.QTTASEQQQAAVAK.L  9.1 23 -0.99 K.NINLCCDLAIVR.K  7.9 30 -19.13 K.VMFRNLLQMHR.L  7.3 35 -4.07 K.ARDFVNEAVFHR.E  7.1 37 -30.84 R.IDFLPHYDTLVK.S  6.5 42 -30.36 K.NQAMALVEEALKK.D  5.3 56 -5.44 R.DIGMAVLAEKEER.L  5.2 57 14.1 R.REWGALASEXSANL.- | |

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| |  | | --- | | Top scoring peptide matches to query 438 09MAR16\_OT\_03.02178.02178.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.4 0.055 11.3 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.6 13 -5.45 R.NLMEGVEQNLSVK.N  10.9 15 -30.39 K.LTCDSKVVINSPK.L  7.7 32 -30.37 -.MAVAAALTGLQAEAK.C  7.5 33 -5.44 R.DIGMAVLAEKEER.L  6.8 39 -45.30 K.DLPFNLITEALSK.L  6.3 45 -5.45 K.AADSGAIGMAIGIDAK.K  6.1 47 -30.84 R.IDFLPHYDTLVK.S  5.7 51 46.1 K.DLLDEVWMHMR.L  5.2 56 -42.57 K.ETGVISVLTTGLDR.E | |
| |  | | --- | | Top scoring peptide matches to query 439 09MAR16\_OT\_03.02265.02265.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.8 0.13 11.4 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.9 15 4.20 -.MSSPAVARTSPGGSR.E  9.9 19 -13.02 K.RVMALLQENQDK.I  8.2 29 -5.33 R.NLMEGVEQNLSVK.N  7.1 37 -0.27 K.QTTASEQQQAAVAK.L  6.7 40 -30.25 -.MAVAAALTGLQAEAK.C  6.0 48 -43.03 K.CKGSLVMVPLTQK.D  4.8 63 -5.35 K.GLMGSVGEPGLKGDK.G  4.6 65 -45.17 K.DLPFNLITEALSK.L  4.6 65 -5.33 K.AADSGAIGMAIGIDAK.K | |

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| |  | | --- | | Top scoring peptide matches to query 440 09MAR16\_OT\_03.02340.02340.3 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.0 0.015 11.5 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  12.8 9.9 -30.20 K.LTCDSKVVINSPK.L  9.6 21 -5.26 R.TKQMNPTAPSIEK.Q  8.3 28 -5.25 R.DIGMAVLAEKEER.L  7.4 34 32.4 K.LDQEPNSNESSIK.L  7.2 36 -30.17 R.DIENLKALLMER.K  6.8 39 -30.17 K.DIKMIIAANNTEK.R  6.4 44 -0.19 K.KATDAEADVASLNR.R  5.9 49 44.6 K.TQSSMYGTTDLTR.N  5.4 55 28.7 K.SNGSNQGFFIFSR.L | |
| |  | | --- | | Top scoring peptide matches to query 441 09MAR16\_OT\_03.02650.02650.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  21.2 1.4 11.5 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.7 13 -0.20 K.QTTASEQQQAAVAK.L  8.6 26 -0.19 K.KATDAEADVASLNR.R  7.7 32 -42.97 K.CKGSLVMVPLTQK.D  7.4 34 -5.25 R.DIGMAVLAEKEER.L  7.4 35 -30.18 K.GLSMAKEGVVAAAEK.T  6.8 39 -30.20 K.LTCDSKVVINSPK.L  6.7 40 -27.89 R.DLDEVLQKFTPR.Q  6.5 43 46.3 K.DLLDEVWMHMR.L  5.0 60 -30.65 R.IDFLPHYDTLVK.S | |

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| |  | | --- | | Top scoring peptide matches to query 442 09MAR16\_OT\_03.02474.02474.3 Score greater than 20 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.0 3.8 11.5 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  6.9 39 -5.25 R.DIGMAVLAEKEER.L  6.0 47 4.26 -.MSSPAVARTSPGGSR.E  6.0 48 -12.97 R.NDGMQLSQLAVLR.L  5.9 49 -30.17 K.NQAMALVEEALKK.D  5.5 53 19.7 K.DNLECELEALVR.R  5.0 59 -10.66 R.QGNDSSVRYLPPK.K  4.0 74 14.3 R.REWGALASEXSANL.-  4.0 75 23.8 R.QTSDGQVHHQAPR.K  3.3 89 36.9 R.DSKGAGQEQGMPAGK.K | |
| |  | | --- | | Top scoring peptide matches to query 443 09MAR16\_OT\_03.02254.02254.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  28.9 0.25 11.5 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.0 19 -5.26 R.NLMEGVEQNLSVK.N  5.7 51 4.26 -.MSSPAVARTSPGGSR.E  5.1 58 -30.65 R.IDFLPHYDTLVK.S  5.1 59 -3.88 K.ARDFVNEAVFHR.E  5.0 60 -30.20 K.LTCDSKVVINSPK.L  4.9 61 34.1 K.AASYFVKDQEMR.S  4.9 61 -42.97 K.QTLPVMVLSGKCK.A  4.8 62 24.7 R.INSTATPDQDRDK.I  4.7 64 -5.27 K.AVGTEECQLNVLK.H | |

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| |  | | --- | | Top scoring peptide matches to query 444 09MAR16\_OT\_03.02279.02279.2 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  62.9 9.7e-05 11.5 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.5 17 44.6 R.GTADVTHDLQEMK.E  9.6 21 4.77 K.YETIHLTEEPTK.L  9.1 23 -13.38 K.SPQKEWNPSLFK.V  9.0 24 -12.94 R.IDQTLAAMGASGAVR.E  8.4 27 6.57 R.GGGGPDGYGRGQGVVK.L  7.2 36 19.7 K.KMNEPVSGQEPTK.V  7.0 38 28.8 R.HDNLHSTQSFFK.G  6.2 45 9.24 K.DMNLNEHSLLFK.S  6.2 46 7.53 R.SLGSKDASSPPSAEK.E | |
| |  | | --- | | Top scoring peptide matches to query 445 09MAR16\_OT\_03.02180.02180.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  33.4 0.087 11.6 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.3 18 -30.12 -.MAVAAALTGLQAEAK.C  10.2 18 -5.20 R.NLMEGVEQNLSVK.N  9.7 20 -0.14 K.QTTASEQQQAAVAK.L  8.5 27 -30.14 K.LTCDSKVVINSPK.L  8.0 30 -5.20 K.AADSGAIGMAIGIDAK.K  7.2 36 19.7 K.KMNEPVSGQEPTK.V  6.0 48 22.1 K.SAEWLQEELEAR.G  5.8 50 -45.05 K.DLPFNLITEALSK.L  5.5 54 46.5 M.CSRGDANAAGAAAAR.R | |

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| |  | | --- | | Top scoring peptide matches to query 446 09MAR16\_OT\_03.02346.02346.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.6 0.021 11.6 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.8 16 -30.08 K.LTCDSKVVINSPK.L  10.6 17 -0.07 K.KATDAEADVASLNR.R  10.0 19 -0.08 K.QTTASEQQQAAVAK.L  8.1 29 4.38 -.MSSPAVARTSPGGSR.E  8.0 30 17.0 K.MDEPLVTYDHLK.K  7.8 32 -30.06 K.GLSMAKEGVVAAAEK.T  7.5 34 -5.13 R.DIGMAVLAEKEER.L  6.1 46 -18.82 K.VMFRNLLQMHR.L  4.8 63 24.8 R.INSTATPDQDRDK.I | |
| |  | | --- | | Top scoring peptide matches to query 447 09MAR16\_OT\_03.02476.02476.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  15.3 5.6 11.8 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.7 13 -4.94 R.DIGMAVLAEKEER.L  11.1 15 0.11 K.QTTASEQQQAAVAK.L  10.3 18 -49.74 R.TLSQGEKTGLLSAR.Y  7.5 34 -30.34 R.IDFLPHYDTLVK.S  6.9 38 -15.40 R.LLAATMEKGFHLN.-  6.9 39 25.0 R.STGQELEEAVQNR.F  6.7 41 -15.42 -.MPTNFTVVPVEAR.A  6.2 46 42.3 K.EGAGAGAGAGAGAGSASNK.D  5.7 51 -12.65 R.NDGMQLSQLAVLR.L | |

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| |  | | --- | | Top scoring peptide matches to query 448 09MAR16\_OT\_03.02186.02186.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  30.9 0.15 11.9 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  10.1 18 -4.89 R.NLMEGVEQNLSVK.N  7.4 34 -29.83 K.LTCDSKVVINSPK.L  6.8 40 -4.91 K.GLMGSVGEPGLKGDK.G  6.5 43 -37.51 K.KVDLTLLNMQNR.I  5.2 57 -30.28 R.IDFLPHYDTLVK.S  5.2 57 -3.51 K.ARDFVNEAVFHR.E  5.0 60 -29.80 R.DIENLKALLMER.K  4.8 62 -44.73 K.DLPFNLITEALSK.L  4.6 66 0.17 K.QTTASEQQQAAVAK.L | |
| |  | | --- | | Top scoring peptide matches to query 449 09MAR16\_OT\_03.02261.02261.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.4 0.0068 11.9 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  9.5 21 -41.94 K.ETGVISVLTTGLDR.E  7.7 32 -4.81 R.DIGMAVLAEKEER.L  6.9 39 -29.76 K.LTCDSKVVINSPK.L  6.0 47 0.25 K.KATDAEADVASLNR.R  5.3 55 -12.52 K.RVMALLQENQDK.I  5.2 57 -4.82 R.NNQLGSLMPTIEK.H  5.2 58 -18.51 K.VMFRNLLQMHR.L  5.1 58 -4.82 R.NLMEGVEQNLSVK.N  4.7 64 32.9 K.LDQEPNSNESSIK.L | |

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| |  | | --- | | Top scoring peptide matches to query 450 09MAR16\_OT\_03.02304.02304.3 Score greater than 34 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.2 0.028 12.0 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  19.4 2.2 -4.76 R.NLMEGVEQNLSVK.N  9.9 19 20.2 K.DNLECELEALVR.R  7.8 31 -30.15 R.IDFLPHYDTLVK.S  7.4 34 -4.75 R.DIGMAVLAEKEER.L  7.3 35 -49.55 R.TLSQGEKTGLLSAR.Y  6.7 40 -44.61 K.DLPFNLITEALSK.L  6.6 41 -29.68 -.MAVAAALTGLQAEAK.C  6.5 42 -29.70 K.LTCDSKVVINSPK.L  5.8 49 -40.13 -.WSCLLLEKLTR.R | |
| |  | | --- | | Top scoring peptide matches to query 451 09MAR16\_OT\_03.02902.02902.3 Score greater than 22 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  14.9 6.1 12.2 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.9 25 -37.20 R.ITMVKLQAEQQR.I  3.8 79 -19.96 K.TRLQMQGEAALAR.L  3.6 82 -21.80 K.QSEILSMLPESVK.S  3.0 96 9.90 K.LGYETRYINGMK.G  2.6 1e+02 -9.97 R.LLPSQSPDQHPNK.T  2.6 1e+02 0.50 K.KATDAEADVASLNR.R  1.6 1.3e+02 -3.19 K.ARDFVNEAVFHR.E  0.9 1.5e+02 7.59 K.ALNHMEVDKIMK.A  0.9 1.5e+02 -15.03 R.LLAATMEKGFHLN.- | |

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| |  | | --- | | Top scoring peptide matches to query 452 09MAR16\_OT\_03.02297.02297.3 Score greater than 21 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.3 0.44 12.2 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  6.4 43 -4.57 R.NLMEGVEQNLSVK.N  5.7 51 0.49 K.QTTASEQQQAAVAK.L  5.1 58 47.0 K.DLLDEVWMHMR.L  5.1 58 -41.69 K.ETGVISVLTTGLDR.E  4.6 66 -4.56 R.DIGMAVLAEKEER.L  4.2 71 -29.49 R.SVSENVAIAMAGIAK.V  2.6 1e+02 0.50 K.KATDAEADVASLNR.R  2.5 1.1e+02 12.6 R.TGAKCVPGETGDLR.E  2.2 1.1e+02 -27.21 K.TQPQGQVVIFSEK.G | |
| |  | | --- | | Top scoring peptide matches to query 453 09MAR16\_OT\_03.02542.02542.3 Score greater than 21 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  8.5 27 30.1 -.MSTGPTAAPGSNRR.L  7.6 33 0.08 K.NINLCCDLAIVR.K  5.4 54 -12.09 -.MLLSSPTTPSRGR.T  5.2 57 -12.08 R.AIVSADEPRMSIR.A  4.8 63 35.0 K.MYLVYAREEDR.D  3.8 79 32.7 K.HEMAEQMIKAEK.K  3.8 79 -3.01 K.ARDFVNEAVFHR.E  3.6 83 24.5 K.KTHMFNFTSGFK.V  3.5 85 12.4 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  3.2 90 42.2 R.GRMLSMAPGHTDR.I | |

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| |  | | --- | | Top scoring peptide matches to query 454 09MAR16\_OT\_03.02228.02228.3 Score greater than 21 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.3 0.14 12.6 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  7.0 38 5.33 -.MSSPAVARTSPGGSR.E  4.8 63 25.8 R.INSTATPDQDRDK.I  4.8 64 -44.04 K.DLPFNLITEALSK.L  4.5 67 20.7 K.DNLECELEALVR.R  4.5 68 0.86 K.QTTASEQQQAAVAK.L  4.1 74 -4.20 R.NLMEGVEQNLSVK.N  3.7 81 33.5 K.LDQEPNSNESSIK.L  3.1 93 -29.11 K.DIKMIIAANNTEK.R  3.0 95 -2.82 K.ARDFVNEAVFHR.E | |
| |  | | --- | | Top scoring peptide matches to query 455 09MAR16\_OT\_03.02222.02222.3 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.1 0.058 12.7 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  13.3 8.8 -28.95 K.LTCDSKVVINSPK.L  10.1 18 -4.01 R.NLMEGVEQNLSVK.N  10.0 19 1.05 K.QTTASEQQQAAVAK.L  6.7 40 -4.03 K.GLMGSVGEPGLKGDK.G  5.2 57 -29.40 R.IDFLPHYDTLVK.S  5.2 58 -2.63 K.ARDFVNEAVFHR.E  4.9 62 -43.85 K.DLPFNLITEALSK.L  4.5 68 -4.01 K.AADSGAIGMAIGIDAK.K  4.4 69 -41.71 K.CKGSLVMVPLTQK.D | |

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| |  | | --- | | Top scoring peptide matches to query 456 09MAR16\_OT\_03.02351.02351.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.6 0.41 12.8 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.1 15 -3.95 R.NLMEGVEQNLSVK.N  9.1 23 -3.94 R.DIGMAVLAEKEER.L  9.0 24 3.73 K.VEGDMKVPDVDIK.G  7.9 31 -43.81 R.KTFVSDLLPPTDK.E  6.8 40 -28.87 -.MAVAAALTGLQAEAK.C  6.5 42 5.58 -.MSSPAVARTSPGGSR.E  5.5 54 -2.57 K.ARDFVNEAVFHR.E  5.0 60 35.5 K.AASYFVKDQEMR.S  4.9 61 5.57 R.DGGIRVMQLQGDR.D | |
| |  | | --- | | Top scoring peptide matches to query 457 09MAR16\_OT\_03.02216.02216.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  33.6 0.082 12.9 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  11.1 15 -3.88 R.NLMEGVEQNLSVK.N  9.5 21 3.79 K.VEGDMKVPDVDIK.G  8.7 25 -16.65 R.SEMHKLVLQTMK.V  8.6 26 -3.87 R.DIGMAVLAEKEER.L  6.0 48 -2.50 K.ARDFVNEAVFHR.E  5.7 51 -29.27 R.IDFLPHYDTLVK.S  5.4 54 -43.73 K.DLPFNLITEALSK.L  5.3 56 -28.83 R.TMPGETAVSISVLR.R  5.2 57 5.63 R.DGGIRVMQLQGDR.D | |

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| |  | | --- | | Top scoring peptide matches to query 458 09MAR16\_OT\_03.02721.02721.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.7 2.1 14.3 7 sp|P02686|MBP\_HUMAN|Myelin R.TQDENPVVHFFK.N  8.9 25 -19.67 K.VEEVDLKPMKEK.N  8.9 25 -47.23 R.TLSQGEKTGLLSAR.Y  5.8 51 -2.44 R.NNQLGSLMPTIEK.H  5.8 51 -12.89 R.LLAATMEKGFHLN.-  5.6 53 -27.35 K.KLAEEVLAMAQNK.H  4.9 63 -17.36 R.INEVLDPEYQLK.K  4.9 63 -32.78 R.DIGLSVTHRFSTK.S  4.6 67 -23.22 R.NDGLGERPPPRPR.R  4.2 74 49.1 K.DLLDEVWMHMR.L | |
| |  | | --- | | Top scoring peptide matches to query 490 09MAR16\_OT\_03.02219.02219.2 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  54.3 0.00061 10.9 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.NQWQLSLDDLKK.L  12.3 9.6 -15.85 R.MAGAIPLVTAGSQKK.L  10.7 14 10.9 -.AQEFVNSKIQPGK.V  8.8 21 -28.68 K.ASNIHRLHLIGEK.E  8.5 23 -6.03 R.VLDISTLNWAVEK.S  8.4 24 -15.83 K.EMENLLLTRIQK.S  8.1 25 27.8 K.GTAINQLGGQPEFR.R  7.3 30 -21.12 -.SLHLHLIEEARK.L  7.2 31 -20.22 R.LELTKQEELVASK.E  6.6 36 4.24 K.QLISNVVELSEEK.V | |

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| |  | | --- | | Top scoring peptide matches to query 491 09MAR16\_OT\_03.02225.02225.2 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  52.6 0.0009 10.9 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.NQWQLSLDDLKK.L  10.1 16 8.64 K.ELMILKEQNNQK.K  8.5 23 27.8 K.GTAINQLGGQPEFR.R  8.3 24 10.9 -.AQEFVNSKIQPGK.V  8.2 25 -15.85 R.MAGAIPLVTAGSQKK.L  8.1 26 -6.03 R.VLDISTLNWAVEK.S  8.0 26 -15.83 K.EMENLLLTRIQK.S  7.5 29 -8.28 R.MLAQIGEELDKLK.E  6.7 35 38.1 K.ELEGGQLRTAEER.Q  6.6 36 -21.12 -.SLHLHLIEEARK.L | |
| |  | | --- | | Top scoring peptide matches to query 492 09MAR16\_OT\_03.02256.02256.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.7 0.35 11.1 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.NQWQLSLDDLKK.L  11.7 11 -20.03 K.GGKDVTLLELSVEK.R  10.1 16 -8.06 K.LEELMKPSVADKK.A  8.8 21 16.4 R.LELAGQIMNLEEK.V  8.1 25 8.85 K.LEQMEVIAAIQSR.L  7.6 28 -4.00 R.NQRGALPQATIYR.G  6.6 36 28.9 K.LEKPTEGLTEDQK.D  6.3 38 8.86 K.ELMILKEQNNQK.K  6.1 40 47.5 K.QGQFGPVGPLGMDGK.S  5.9 41 8.86 K.QNNQEKLIMLEK.H | |

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| |  | | --- | | Top scoring peptide matches to query 493 09MAR16\_OT\_03.02230.02230.2 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.7 0.0055 11.1 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.NQWQLSLDDLKK.L  10.4 15 -8.03 R.MLAQIGEELDKLK.E  8.2 25 47.6 R.IECGPWIEQLSR.V  7.9 26 11.1 -.AQEFVNSKIQPGK.V  5.8 43 28.0 K.GTAINQLGGQPEFR.R  5.3 48 -20.87 -.SLHLHLIEEARK.L  5.2 49 -15.61 R.MAGAIPLVTAGSQKK.L  5.0 51 8.89 K.ELMILKEQNNQK.K  4.9 53 21.4 K.QLEEGLKDTDLAR.V  3.6 71 21.4 R.QIEQNITGESAGLK.K | |
| |  | | --- | | Top scoring peptide matches to query 494 09MAR16\_OT\_03.02218.02218.3 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.8 0.027 11.4 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.NQWQLSLDDLKK.L  14.2 6.2 -10.41 R.TQARTLSQENLVK.L  13.5 7.2 11.4 -.AQEFVNSKIQPGK.V  11.6 11 -5.56 K.KLFQVEIQPEEK.H  10.1 16 9.11 K.QNNQEKLIMLEK.H  9.4 18 -2.85 K.IKSQLEGLEESVR.D  9.1 20 -20.69 R.ELRFLVTGSPNVR.T  8.6 22 -32.28 K.LKLNSIEAMLDLK.Q  8.6 23 -13.13 R.KLEDPSLVGFQVR.K  8.4 23 41.1 K.IECEPTQLLAEGK.L | |

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| |  | | --- | | Top scoring peptide matches to query 495 09MAR16\_OT\_03.02213.02213.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  43.6 0.007 11.5 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.NQWQLSLDDLKK.L  9.0 20 9.22 K.LEQMEVIAAIQSR.L  8.3 24 -7.69 R.MLAQIGEELDKLK.E  7.8 27 -20.56 R.ELRFLVTGSPNVR.T  6.8 34 16.8 R.LELAGQIMNLEEK.V  6.6 35 -2.75 GVSIRSDIAIDDVK  6.3 38 9.23 K.QNNQEKLIMLEK.H  6.1 40 -20.57 K.AGPSRTVGLFLQGGK.D  5.9 42 9.23 K.ELMILKEQNNQK.K  5.7 44 3.91 -.LEPTHTPALPAQGR.S | |
| |  | | --- | | Top scoring peptide matches to query 496 09MAR16\_OT\_03.02224.02224.3 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.9 0.016 11.9 9 sp|P13233|CN37\_RAT|2',3'-cyclic-nucleotide K.NQWQLSLDDLKK.L  16.5 3.6 22.2 K.QLEEGLKDTDLAR.V  11.7 11 -9.86 R.TQARTLSQENLVK.L  11.6 11 11.9 K.DRDDFPIVLVGNK.A  11.2 12 38.5 LQLAEHMMQRAK  11.1 13 -5.00 K.KLFQVEIQPEEK.H  10.1 16 41.7 K.IECEPTQLLAEGK.L  9.8 17 11.9 -.AQEFVNSKIQPGK.V  9.6 18 -20.13 R.ELRFLVTGSPNVR.T  9.4 19 -31.73 K.LKLNSIEAMLDLK.Q | |

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| |  | | --- | | Top scoring peptide matches to query 501 09MAR16\_OT\_03.02330.02330.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  42.2 0.0087 11.2 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 SGHDQVVELLLER  35.0 0.045 -30.04 R.VPPSVASDQLLLQK.N  25.6 0.4 -6.25 K.ITAMKCFLLELR.V  24.1 0.56 11.2 K.EATDLLHDALQIR.E  23.1 0.71 3.65 R.SQSIVEQILANHR.L  22.6 0.79 -14.08 R.HAHLHALGQLIER.C  19.3 1.7 35.5 R.TTFNSSQLQALER.V  19.0 1.8 -13.19 K.QAADVGLVPLLNER.C  18.3 2.1 -13.18 K.VQDHIASELLKNK.D  17.9 2.3 3.65 K.RDLNHTAQGILEK.D | |
| |  | | --- | | Top scoring peptide matches to query 502 09MAR16\_OT\_03.02331.02331.2 Score greater than 22 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  57.8 0.00023 11.7 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 SGHDQVVELLLER  6.1 34 11.7 K.EATDLLHDALQIR.E  5.7 37 -5.73 K.ITAMKCFLLELR.V  2.0 88 45.7 K.MNSRVVGGIMTGEK.K  1.3 1e+02 48.8 K.LETTMDLATLNEK.V  1.2 1.1e+02 6.74 K.AIMEGISSVFGKAGK.D  1.0 1.1e+02 31.1 R.SHSVFTLVMTQTK.T  0.5 1.3e+02 -6.04 K.HLGRVLSIWEER.S  0.5 1.3e+02 -5.13 K.YALRLSSVISEEK.S  0.3 1.3e+02 45.2 -.MLWFSGVGALAER.Y | |

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| |  | | --- | | Top scoring peptide matches to query 503 09MAR16\_OT\_03.02336.02336.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  43.6 0.006 12.1 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 SGHDQVVELLLER  27.6 0.24 12.2 K.EATDLLHDALQIR.E  26.3 0.32 -29.05 R.VPPSVASDQLLLQK.N  23.8 0.58 -5.27 K.ITAMKCFLLELR.V  20.9 1.1 -13.10 R.HAHLHALGQLIER.C  18.4 2 4.63 R.SQSIVEQILANHR.L  18.1 2.1 36.5 R.TTFNSSQLQALER.V  18.0 2.2 33.3 K.HTCLTGAHSLNKR.C  17.8 2.3 -12.21 K.QAADVGLVPLLNER.C  17.5 2.5 4.63 K.RDLNHTAQGILEK.D | |
| |  | | --- | | Top scoring peptide matches to query 504 09MAR16\_OT\_03.02326.02326.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  36.3 0.033 12.2 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 SGHDQVVELLLER  28.8 0.19 -28.99 R.VPPSVASDQLLLQK.N  25.7 0.37 -5.20 K.ITAMKCFLLELR.V  25.7 0.38 12.2 K.EATDLLHDALQIR.E  22.7 0.74 -13.04 R.HAHLHALGQLIER.C  19.4 1.6 36.6 R.TTFNSSQLQALER.V  19.0 1.8 -12.14 K.VQDHIASELLKNK.D  18.4 2 4.69 K.RDLNHTAQGILEK.D  17.2 2.6 -12.15 K.QAADVGLVPLLNER.C  15.8 3.7 29.1 K.ISKSNNQNVEPHK.R | |

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| |  | | --- | | Top scoring peptide matches to query 505 09MAR16\_OT\_03.02327.02327.2 Score greater than 24 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  70.8 1.2e-05 12.5 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 SGHDQVVELLLER  7.0 28 12.5 K.EATDLLHDALQIR.E  6.8 29 -4.91 K.ITAMKCFLLELR.V  6.0 35 -12.75 R.HAHLHALGQLIER.C  3.6 61 33.7 K.HTCLTGAHSLNKR.C  2.7 74 -14.54 K.NYFNILDKIVQK.V  2.2 83 46.5 K.MNSRVVGGIMTGEK.K  2.0 88 12.5 K.SSIHISNLEPELR.A  1.5 99 31.9 R.SHSVFTLVMTQTK.T  1.5 1e+02 49.6 K.LETTMDLATLNEK.V | |
| |  | | --- | | Top scoring peptide matches to query 506 09MAR16\_OT\_03.02337.02337.2 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  66.9 2.8e-05 13.0 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 SGHDQVVELLLER  8.0 22 13.0 K.EATDLLHDALQIR.E  5.8 37 -4.42 K.ITAMKCFLLELR.V  2.6 76 -12.25 R.HAHLHALGQLIER.C  1.9 90 47.0 K.MNSRVVGGIMTGEK.K  1.1 1.1e+02 8.04 K.AIMEGISSVFGKAGK.D  0.8 1.2e+02 32.4 R.SHSVFTLVMTQTK.T  0.7 1.2e+02 -14.05 K.NYFNILDKIVQK.V  0.4 1.3e+02 -4.74 K.HLGRVLSIWEER.S  0.4 1.3e+02 -3.83 K.YALRLSSVISEEK.S | |

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| |  | | --- | | Top scoring peptide matches to query 508 09MAR16\_OT\_03.01558.01558.2 Score greater than 21 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  22.8 0.48 12.1 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  7.2 17 49.2 K.ITGDSKMEIFALR.C  6.4 21 48.7 K.VWVIFNFLSEDK.Y  4.6 32 27.1 -.PSPVEFPVNLELR.D  3.1 45 10.3 K.ILYELLGSFKDAK.L  2.9 47 1.86 R.RPHPSFLAIPPXK.D  2.2 56 41.6 K.SQMTAATVVAKFSR.K  1.8 61 34.1 R.VRELLETCHALR.E  1.7 62 49.2 K.TMAGNLEKLFQTK.L  1.3 68 43.9 K.KGGLTLGNTFFGER.D | |
| |  | | --- | | Top scoring peptide matches to query 509 09MAR16\_OT\_03.01545.01545.2 Score greater than 24 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.9 0.19 12.1 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  9.8 9.7 27.1 -.PSPVEFPVNLELR.D  6.3 22 22.3 R.QEQLQLINNQLR.E  5.6 25 10.3 K.ILYELLGSFKDAK.L  5.3 27 17.3 R.CQLPALGLLQDIR.D  3.1 45 19.6 K.KPPFSDKPSIPAGR.S  3.0 47 31.0 K.FFAWSVLNFLPR.A  2.5 52 46.6 K.SSSSSLFGSKTRPR.Y  2.1 57 41.6 K.SQMTAATVVAKFSR.K  2.0 58 43.9 K.KGGLTLGNTFFGER.D | |

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| |  | | --- | | Top scoring peptide matches to query 510 09MAR16\_OT\_03.01520.01520.3 Score greater than 29 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  30.7 0.078 12.1 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  14.6 3.2 37.3 -.LAPGQGVDGLVDDLK.L  3.9 38 46.6 R.VPSGPGLSGAGQVAGSR.S  3.2 44 34.6 R.VQFFVDSVSLIDK.T  2.6 51 7.13 R.VPVLGGLFHRAALM.-  1.9 59 27.1 R.FVFKVGTAAAAETGK.E  1.8 62 49.2 R.SKDEAFVVMIVSR.V  1.6 63 36.4 K.HTAGRELAGPGFVGK.A  1.2 69 41.7 K.QVNRAMETLPPPK.Q  0.9 74 46.6 K.VLDANKEAAPGQQR.L | |
| |  | | --- | | Top scoring peptide matches to query 511 09MAR16\_OT\_03.01562.01562.3 Score greater than 24 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  52.0 0.00058 12.1 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  8.7 12 37.3 -.LAPGQGVDGLVDDLK.L  7.9 15 46.6 R.SPPAQSPVQSASGKR.G  7.8 15 9.83 R.AVTSPAVGRILPCR.T  3.6 40 36.7 K.GEFMMVLKLVASR.K  1.5 66 36.4 K.HTAGRELAGPGFVGK.A  1.4 67 7.13 R.VPVLGGLFHRAALM.-  1.3 69 27.1 -.PSPVEFPVNLELR.D  1.2 70 46.6 K.VLDANKEAAPGQQR.L  1.0 73 22.3 K.RSPTSSAIPLQSPR.N | |

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| |  | | --- | | Top scoring peptide matches to query 512 09MAR16\_OT\_03.01551.01551.2 Score greater than 23 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.2 0.014 12.1 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  8.3 14 24.3 R.MRGMVAILIAFMK.Q  5.1 29 27.2 -.PSPVEFPVNLELR.D  3.1 45 1.94 R.RPHPSFLAIPPXK.D  2.5 52 41.7 K.SQMTAATVVAKFSR.K  2.3 54 10.4 K.ILYELLGSFKDAK.L  2.0 58 49.2 K.TMAGNLEKLFQTK.L  1.7 62 37.3 -.LAPGQGVDGLVDDLK.L  1.4 67 12.2 R.RLVYHSKPPSANK.Q  1.3 68 -26.29 GEGSQIRLIAALIR | |
| |  | | --- | | Top scoring peptide matches to query 513 09MAR16\_OT\_03.01529.01529.3 Score greater than 24 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  55.1 0.00028 12.1 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  8.0 14 27.2 -.PSPVEFPVNLELR.D  4.7 32 44.0 R.LAQSLAAANXGYVR.U  4.5 33 37.4 -.LAPGQGVDGLVDDLK.L  4.4 33 41.7 K.TLELYQMAISRR.L  3.7 39 34.2 R.IDPGNLGRSPMLAR.T  2.7 49 7.20 R.VPVLGGLFHRAALM.-  2.2 55 44.0 R.FEVAQVESLRYR.Q  1.4 68 46.7 K.VLDANKEAAPGQQR.L  0.7 78 9.90 R.EGPCAVNLVLRLR.N | |

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| |  | | --- | | Top scoring peptide matches to query 514 09MAR16\_OT\_03.01517.01517.3 Score greater than 22 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.8 0.061 12.3 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  7.8 15 27.3 -.PSPVEFPVNLELR.D  5.9 24 37.5 -.LAPGQGVDGLVDDLK.L  5.8 24 44.1 R.LAQSLAAANXGYVR.U  4.3 34 -6.79 K.GLIEPISMIVPRR.S  2.4 53 4.77 K.LDRHIIGASHLHK.I  1.9 60 7.32 R.VPVLGGLFHRAALM.-  1.7 62 26.7 R.MVRVAWLFMLSK.V  1.4 67 -35.47 K.AIVPIINVKSDLSK.M  1.3 69 -12.05 K.LFLHIRQDIVSR.V | |
| |  | | --- | | Top scoring peptide matches to query 515 09MAR16\_OT\_03.01587.01587.3 Score greater than 27 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.6 0.1 12.3 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  12.9 4.7 37.5 -.LAPGQGVDGLVDDLK.L  8.8 12 46.8 K.VLDANKEAAPGQQR.L  4.5 33 34.4 R.IDPGNLGRSPMLAR.T  3.5 42 17.5 -.TLPPVPAGNVTMKR.G  3.4 42 26.8 K.RPPADRTALALCR.L  2.8 48 12.3 R.HRPDLIDYAKLR.K  2.2 55 7.32 R.VPVLGGLFHRAALM.- | |

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| |  | | --- | | Top scoring peptide matches to query 516 09MAR16\_OT\_03.01556.01556.3 Score greater than 21 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.6 0.00038 13.5 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  4.7 30 38.7 -.LAPGQGVDGLVDDLK.L  3.5 39 48.0 R.SPPAQSPVQSASGKR.G  2.3 51 38.1 K.GEFMMVLKLVASR.K  2.3 51 38.1 K.GEFMMVLKLVASR.K  1.6 60 37.8 K.HTAGRELAGPGFVGK.A  0.8 73 8.54 R.VPVLGGLFHRAALM.-  0.5 77 48.0 K.VLDANKEAAPGQQR.L  0.3 81 48.0 K.SPPASQEQLQQKR.Q  0.1 85 11.2 R.AVTSPAVGRILPCR.T | |
| |  | | --- | | Top scoring peptide matches to query 517 09MAR16\_OT\_03.01550.01550.3 Score greater than 23 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  54.5 0.00031 13.9 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QGPPQKPPGPAGPIR.Q  7.6 15 48.4 R.SPPAQSPVQSASGKR.G  5.5 25 48.4 K.VLDANKEAAPGQQR.L  5.1 27 39.1 -.LAPGQGVDGLVDDLK.L  4.0 34 38.5 K.GEFMMVLKLVASR.K  1.9 56 38.2 K.HTAGRELAGPGFVGK.A  1.3 64 8.91 R.VPVLGGLFHRAALM.-  0.7 73 6.36 K.LDRHIIGASHLHK.I  0.5 77 28.9 -.PSPVEFPVNLELR.D  0.3 82 48.3 R.GNMGFVIELPYLK.G | |

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| |  | | --- | | Top scoring peptide matches to query 528 09MAR16\_OT\_03.02639.02639.3 Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  33.2 0.04 11.9 8+ sp|P23565|AINX\_RAT|Alpha-internexin K.KVESLLDELAFVR.Q  28.0 0.13 32.7 K.GMIFVGENGRVIAR.G  10.5 7.4 45.9 R.SIGEIVQSKSDVEK.E  9.5 9.4 45.3 -.MTVKSLHVTAMVK.Y  9.3 9.8 26.2 R.LSKVVASTQAICNK.I  8.5 12 40.2 K.TFNPIRAIVDNMK.V  8.3 12 26.2 K.LQLTAQSQVQMKK.Q  8.1 13 33.6 K.ELIQTDNKMLGLK.V  8.1 13 45.0 R.GLQAASLSQNAGFVR.L  7.5 15 -10.32 K.VHAIEGQLRQIVR.N | |
| |  | | --- | | Top scoring peptide matches to query 529 09MAR16\_OT\_03.02640.02640.2 Score greater than 26 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  92.1 5.2e-08 11.9 8+ sp|P23565|AINX\_RAT|Alpha-internexin K.KVESLLDELAFVR.Q  7.3 15 11.9 R.IIELSATGEVFAIR.Y  6.1 20 11.9 K.QLPIAEQPLAPDVK.G  4.7 28 -12.08 K.KPEVTPVKVPEAPK.E  3.6 36 21.1 -.VQSISNALRFSVR.K  2.4 48 42.8 R.VRTPLMTGATTGSAR.R  2.3 49 -43.45 R.LLIHQSLAGGIIGVK.G  2.1 52 45.9 K.KDITTSADQIAEVK.T  0.6 73 40.2 R.QHMSLTSKQIFAK.G  0.5 74 13.7 R.LAGRVAHDGLLPSGR.E | |

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| |  | | --- | | Top scoring peptide matches to query 530 09MAR16\_OT\_03.02642.02642.3 Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.0 0.034 11.9 8+ sp|P23565|AINX\_RAT|Alpha-internexin K.KVESLLDELAFVR.Q  29.8 0.087 32.8 K.GMIFVGENGRVIAR.G  9.6 9.2 45.1 K.FEKQSLSDRPGVR.V  9.0 10 -10.26 K.VHAIEGQLRQIVR.N  7.1 16 45.4 -.MTVKSLHVTAMVK.Y  6.8 18 28.5 M.ANSLRGEVLNLYK.N  6.0 21 -7.73 K.TVVKPMTLKQFAR.Q  6.0 21 26.3 K.LQLTAQSQVQMKK.Q  5.9 22 28.5 R.YQELVVVGQLGASR.R  4.9 27 26.3 K.AKTQSNLQIAMSVK.S | |
| |  | | --- | | Top scoring peptide matches to query 531 09MAR16\_OT\_03.02634.02634.3 Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.1 0.01 12.1 8+ sp|P23565|AINX\_RAT|Alpha-internexin K.KVESLLDELAFVR.Q  18.2 1.2 33.0 K.GMIFVGENGRVIAR.G  12.6 4.5 33.9 K.ELIQTDNKMLGLK.V  10.4 7.5 45.6 -.MTVKSLHVTAMVK.Y  9.3 9.7 -10.08 K.VHAIEGQLRQIVR.N  8.7 11 26.5 R.LSKVVASTQAICNK.I  8.4 12 40.4 K.TFNPIRAIVDNMK.V  7.9 13 21.3 K.TLLGSQVDQRVFR.D  6.3 19 33.0 R.LLEQMRKPNAFR.K  6.0 21 40.4 R.EPELALLRQFMR.L | |

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| |  | | --- | | Top scoring peptide matches to query 532 09MAR16\_OT\_03.02636.02636.2 Score greater than 25 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  87.4 1.5e-07 12.3 8+ sp|P23565|AINX\_RAT|Alpha-internexin K.KVESLLDELAFVR.Q  7.0 17 12.3 R.IIELSATGEVFAIR.Y  4.4 30 21.5 -.VQSISNALRFSVR.K | | | |
| |  | | --- | | Top scoring peptide matches to query 533 09MAR16\_OT\_03.02643.02643.2 Score greater than 27 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  96.9 1.7e-08 12.5 8+ sp|P23565|AINX\_RAT|Alpha-internexin K.KVESLLDELAFVR.Q  8.4 12 12.5 R.IIELSATGEVFAIR.Y  2.7 44 9.80 K.KPEIPTFEVLAFK.N  2.2 49 40.7 K.DVNPMINGIVKYR.F  1.2 62 21.6 -.VQSISNALRFSVR.K  1.0 65 -42.89 R.LLIHQSLAGGIIGVK.G  0.6 72 33.3 K.GMIFVGENGRVIAR.G | |

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| |  | | --- | | Top scoring peptide matches to query 535 09MAR16\_OT\_03.01788.01788.2 Score greater than 25 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  62.9 6.3e-05 10.7 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial VVSQYHELVVQAR  8.5 17 -3.09 K.NISEIKELINQAR.K  5.9 31 1.17 R.LCALLLRGGAAADAR.D  4.0 49 27.2 R.RGWGEQELQGVLR.G  3.8 51 22.3 R.VVQMQTWPLAQAR.R  3.7 52 28.1 K.VVGEEAQEVLEGLR.S  3.6 53 -19.57 R.IEVDNSGQILLAKK.L  3.3 57 37.2 K.LENDQIENLRQR.F  3.2 58 -19.60 M.DGVVTDLITVGLKR.G  2.8 65 -19.58 K.KSGGLISATLEPQVK.K | |
| |  | | --- | | Top scoring peptide matches to query 536 09MAR16\_OT\_03.01774.01774.2 Score greater than 29 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  81.1 9.5e-07 11.5 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial VVSQYHELVVQAR  11.6 8.3 28.9 K.VVGEEAQEVLEGLR.S  11.0 9.6 -2.29 K.NISEIKELINQAR.K  7.7 21 23.1 R.VVQMQTWPLAQAR.R  4.0 49 -33.50 R.ILGLRSSVGTAVQAR.G  3.9 50 45.3 K.ESASPSVRHTDLTK.I  3.0 61 38.0 K.LENDQIENLRQR.F  2.9 62 11.5 R.SSNLGLPFAGAVAPAR.D  2.7 64 -36.14 R.VLFIVATDLGRPAR.S  2.7 65 38.0 R.VPRSQGTEAELNAR.L | |

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| |  | | --- | | Top scoring peptide matches to query 537 09MAR16\_OT\_03.01779.01779.2 Score greater than 28 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  94.1 4.8e-08 11.7 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial VVSQYHELVVQAR  10.0 12 23.3 R.VVQMQTWPLAQAR.R  9.9 12 40.2 K.VLFLFEFEEQAR.E  9.5 14 -12.16 R.VVLYRGXPGAGTPVK.G  7.3 22 29.0 K.VVGEEAQEVLEGLR.S  7.3 23 -35.98 R.VLFIVATDLGRPAR.S  6.2 29 38.2 R.VPRSQGTEAELNAR.L  4.4 44 -33.34 R.ILGLRSSVGTAVQAR.G  4.1 47 -2.13 K.NISEIKELINQAR.K  4.1 48 -18.62 K.KSGGLISATLEPQVK.K | |
| |  | | --- | | Top scoring peptide matches to query 538 09MAR16\_OT\_03.01778.01778.3 Score greater than 26 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.9 0.02 11.7 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial VVSQYHELVVQAR  11.6 8.4 -2.05 K.NISEIKELINQAR.K  8.5 17 29.1 K.VVGEEAQEVLEGLR.S  8.0 19 -12.09 R.VVLYRGXPGAGTPVK.G  3.8 51 23.4 R.VVQMQTWPLAQAR.R  3.7 52 -33.27 R.AQVATGVSSRLGLIR.F  3.6 53 30.7 R.FQNMERVFSLIK.D  3.1 59 39.9 -.MAPGWAGVGAAVRAR.L  2.7 66 38.2 R.VPRSQGTEAELNAR.L  2.6 66 45.0 R.DRHTPLLLMMER.A | |

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| |  | | --- | | Top scoring peptide matches to query 539 09MAR16\_OT\_03.01772.01772.3 Score greater than 26 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  42.4 0.0069 12.0 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial VVSQYHELVVQAR  11.0 9.5 29.4 K.VVGEEAQEVLEGLR.S  8.0 19 12.1 R.SSNLGLPFAGAVAPAR.D  6.7 25 23.7 R.VVQMQTWPLAQAR.R  6.5 26 29.4 R.ELEEKTIAAEAPAR.M  6.1 29 9.85 R.VVSEVPAECLIRR.V  5.8 31 -1.75 K.NISEIKELINQAR.K  5.2 36 -11.79 R.VVLYRGXPGAGTPVK.G  4.4 43 -14.43 R.VVTLLEHPFVFAR.D  4.4 43 29.4 R.VPEERLQDSVDLK.R | |
| |  | | --- | | Top scoring peptide matches to query 540 09MAR16\_OT\_03.01768.01768.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.1 0.018 12.4 10 sp|Q3KR86|IMMT\_RAT|Mitochondrial VVSQYHELVVQAR  18.5 1.7 29.8 K.VVGEEAQEVLEGLR.S  12.3 6.9 -11.43 R.VVLYRGXPGAGTPVK.G  10.7 10 24.0 R.VVQMQTWPLAQAR.R  8.6 17 29.8 R.ELEEKTIAAEAPAR.M  8.5 17 -1.39 K.NISEIKELINQAR.K  7.8 20 38.9 R.VPRSQGTEAELNAR.L  7.0 24 43.6 R.EPQELPHTSPPPAK.E  6.2 29 34.0 K.VDTLPGKCTGGPLGR.V  6.1 29 -17.91 M.DGVVTDLITVGLKR.G | |

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| |  | | --- | | Top scoring peptide matches to query 541 09MAR16\_OT\_03.01923.01923.2 Score greater than 21 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  60.9 0.00014 10.7 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  4.8 59 -20.43 K.LHLLSREEEQFK.F  4.2 66 -20.45 R.LSYLSRSSFGGGLGK.G  3.6 76 -10.46 K.VIQEQLQVNDNTK.G  1.7 1.2e+02 19.8 R.HVLQQFADNDVSR.F  1.4 1.3e+02 20.7 R.NDEEGPAGIAVDTLK.D  0.1 1.7e+02 48.8 K.AANLTYMPSSSGSAR.S  0.1 1.7e+02 10.7 K.KGTNPSFSSDFTLK.L  0.1 1.7e+02 8.08 K.LESFADIFFTPNK.T | |
| |  | | --- | | Top scoring peptide matches to query 542 09MAR16\_OT\_03.01934.01934.2 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  75.2 5.2e-06 11.2 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  8.0 28 49.3 K.AANLTYMPSSSGSAR.S  4.9 57 -22.60 R.ESLWQKVIPDWK.E  4.8 57 22.8 NFVNKEFVMQEK  4.6 61 -19.95 K.LHLLSREEEQFK.F  4.2 66 -9.97 R.NVENLVQQELQSK.R  4.2 67 35.0 K.GFLDYILGDSSDAR.L  3.5 78 -19.97 R.LSYLSRSSFGGGLGK.G  3.1 86 -3.51 -.LFRLTAAGXGGHEGK.A  2.2 1.1e+02 21.2 R.NDEEGPAGIAVDTLK.D | |

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| |  | | --- | | Top scoring peptide matches to query 543 09MAR16\_OT\_03.01919.01919.3 Score greater than 30 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.3 0.032 11.2 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  15.5 4.9 -46.41 EPIVFAFLLHTNK  13.7 7.5 -43.78 K.TGLLSLTAQAPPFGR.K  12.3 10 -38.62 K.LTPKPEVISECKK.R  11.9 11 -9.98 K.TLNLSDIPVQDTGR.V  9.5 20 -13.05 R.VSAIARSHVNTMAR.S  8.5 25 -17.32 K.DVVANLTQREIDR.Q  8.4 25 -33.79 R.LTVSGKSGPLDELGR.D  7.9 29 -43.76 R.NHSKQYLPLSTLK.R  7.8 29 -33.78 K.DVLNEDVRNLTLK.I | |
| |  | | --- | | Top scoring peptide matches to query 544 09MAR16\_OT\_03.01960.01960.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.2 0.0067 11.3 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  10.0 18 -43.64 R.NHSKQYLPLSTLK.R  9.9 18 -22.47 K.WIFNPNEAVPITK.N  9.7 19 -9.85 K.VIQEQLQVNDNTK.G  9.0 22 -9.86 K.TLNLSDIPVQDTGR.V  8.3 26 -17.20 K.DVVANLTQREIDR.Q  5.3 52 -43.65 R.TNFLIDTIAKQHK.A  5.0 55 -5.14 K.SKFDSLDFDTLLK.Q  4.9 56 -46.29 EPIVFAFLLHTNK  4.9 57 -38.50 K.LTPKPEVISECKK.R | |

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| |  | | --- | | Top scoring peptide matches to query 545 09MAR16\_OT\_03.01929.01929.2 Score greater than 22 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  61.2 0.00013 11.4 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  5.8 46 -19.73 R.ITFTEPNIQNVPR.D  4.4 64 -19.71 K.LHLLSREEEQFK.F  4.2 67 -19.73 R.LSYLSRSSFGGGLGK.G  4.0 70 -45.74 R.ALDLSMRQQILPK.E  3.5 78 30.4 -.MTADELVFFVNGK.K  3.3 82 -43.53 K.LHKVVEPEEIHAK.C  3.2 85 9.23 R.TMQLDELSDHVLK.V  2.5 99 1.00 R.LTSFRPVACANHR.D  2.2 1.1e+02 -38.39 K.LTPKPEVISECKK.R | |
| |  | | --- | | Top scoring peptide matches to query 546 09MAR16\_OT\_03.01972.01972.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.9 0.058 11.6 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  8.1 28 34.9 K.KAPGDGMIAAPPAWM.-  7.8 30 -9.56 K.TLNLSDIPVQDTGR.V  6.3 42 -2.77 K.TLSKVMGMVSFNAK.T  4.3 66 -45.99 EPIVFAFLLHTNK  3.0 89 28.1 K.NVYRFELDTSER.K  2.9 92 4.27 R.TLNEIIDFHDVGR.L  2.5 99 -43.35 R.TNFLIDTIAKQHK.A  2.1 1.1e+02 -34.25 R.LERPDGQVVRFGR.E  2.0 1.1e+02 -2.77 K.TLSKVMGMVSFNAK.T | |

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| |  | | --- | | Top scoring peptide matches to query 547 09MAR16\_OT\_03.01965.01965.3 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  42.1 0.011 11.6 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  8.2 27 -9.56 K.TLNLSDIPVQDTGR.V  7.4 32 -38.20 K.LTPKPEVISECKK.R  5.6 49 -21.75 K.DQGAGKELMLVVPR.L  5.1 54 -2.77 K.TLSKVMGMVSFNAK.T  5.1 55 -45.56 R.IVAAPSLASGGMLVAR.R  4.8 59 28.1 K.NVYRFELDTSER.K  4.8 60 -22.20 R.GFPTPVSPVVSQWK.D  3.3 83 -43.35 R.TNFLIDTIAKQHK.A  3.2 85 -31.71 R.TLKPNQLWMELR.Q | |
| |  | | --- | | Top scoring peptide matches to query 548 09MAR16\_OT\_03.01922.01922.3 Score greater than 30 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.3 0.1 12.0 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  15.3 5.2 -9.20 K.TLNLSDIPVQDTGR.V  14.8 5.9 -12.27 R.VSAIARSHVNTMAR.S  12.0 11 -43.00 K.TGLLSLTAQAPPFGR.K  10.6 15 -33.00 K.DVLNEDVRNLTLK.I  10.4 16 -42.98 R.NHSKQYLPLSTLK.R  10.1 17 -21.39 K.DQGAGKELMLVVPR.L  8.6 24 4.63 R.TLNEIIDFHDVGR.L  8.5 25 -37.84 K.LTPKPEVISECKK.R  8.0 28 -16.54 K.DVVANLTQREIDR.Q | |

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| |  | | --- | | Top scoring peptide matches to query 549 09MAR16\_OT\_03.01928.01928.3 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.8 0.093 12.9 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.LTFDSSFSPNTGKK.N  14.1 6.9 -8.30 K.TLNLSDIPVQDTGR.V  11.1 14 -15.65 R.TNKPRTSVNADPTK.G  11.0 14 -32.11 R.LTVSGKSGPLDELGR.D  10.1 17 -20.49 K.DQGAGKELMLVVPR.L  8.9 23 -11.37 R.VSAIARSHVNTMAR.S  7.9 28 -15.65 K.DVVANLTQREIDR.Q  7.3 32 -1.51 K.TLSKVMGMVSFNAK.T  7.2 33 -32.10 K.DVLNEDVRNLTLK.I  6.8 37 -25.62 K.QSAGNLLGRDWLAK.N | |
| |  | | --- | | Top scoring peptide matches to query 554 09MAR16\_OT\_03.02160.02160.3 Score greater than 26 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.9 0.0045 12.3 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.LTVDTIFVPNTGKK.S  11.4 5 21.4 R.LAHQPVDLREGVAK.A  9.5 7.8 -13.65 K.VTSMIKIVSNILAK.L  8.1 11 37.8 K.LVVHVDQSSHQRK.E  7.5 12 45.1 K.VNVPFSKSGAVNSAR.L  5.9 18 33.9 K.NCIDKIETIISVK.L  5.4 20 45.1 M.AAARPDPPIPSSPTR.E  5.2 21 45.1 R.GGQAFTQQIEGLKR.Q  5.1 22 21.4 R.FSSNLAGGRKPLSAK.S  4.5 25 28.7 R.TLEVSFRGTAQPVK.L | |

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| |  | | --- | | Top scoring peptide matches to query 555 09MAR16\_OT\_03.01824.01824.2 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  61.1 0.00011 10.7 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.VGLQAQPMHSELVK.K  16.0 3.5 -48.23 R.SNKPLGPGISVQLVK.N  10.7 12 39.5 K.QLQEIMSATCIVK.T  8.9 18 -17.22 K.LVATDPDLLLNQPK.I  7.0 28 -31.84 R.INARLGKPPENTVK.V  6.7 30 -5.66 R.VCEPPKGEPLIGIK.R  6.2 33 29.3 K.EHLSWLNADRPAK.N  4.1 54 -48.21 R.LELQLPVSNLALAR.A  3.3 65 -12.96 K.KIPLMHIEQSNVK.K  3.3 65 34.4 R.QCAPATYIGSSIIR.Q | |
| |  | | --- | | Top scoring peptide matches to query 556 09MAR16\_OT\_03.01828.01828.2 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  51.7 0.00093 10.9 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.VGLQAQPMHSELVK.K  8.9 18 -48.07 R.SNKPLGPGISVQLVK.N  8.7 19 -17.07 K.LVATDPDLLLNQPK.I  6.5 31 -31.68 R.INARLGKPPENTVK.V  4.9 45 39.7 K.QLQEIMSATCIVK.T  3.4 63 -48.05 R.LELQLPVSNLALAR.A  2.4 80 29.4 R.FYSVGQSTNRLHK.C  1.8 92 29.4 K.DPPTWTSRVPGPAR.R  0.3 1.3e+02 6.64 K.EEIPKNDVSAPLPK.E  0.2 1.3e+02 33.7 K.FHIPLNGCGTRHK.F | |

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| |  | | --- | | Top scoring peptide matches to query 557 09MAR16\_OT\_03.01826.01826.3 Score greater than 23 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  27.6 0.24 11.2 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.VGLQAQPMHSELVK.K  8.5 20 17.7 R.MHLSLISNFRFR.K  6.3 33 -31.33 R.KLLDTAALLATNHR.Q  6.1 34 -0.36 K.GVLVQTKGTGASGSFK.L  4.8 46 39.7 R.DTQAQAKYIQTNR.D  4.5 50 -19.78 R.VLGRPITAHLCTAK.S  4.4 50 46.5 K.VVCSSPLCPAYRK.E  3.6 60 16.3 R.IATVVMMTRLEEK.S  2.9 70 37.1 K.QIDAPGDPFPLNPR.G  2.5 78 -7.64 R.ALLAGLHARSEGDVK.Q | |
| |  | | --- | | Top scoring peptide matches to query 558 09MAR16\_OT\_03.01833.01833.3 Score greater than 19 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  21.6 0.96 11.3 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.VGLQAQPMHSELVK.K  5.3 41 17.8 R.MHLSLISNFRFR.K  4.6 48 30.2 R.QLMDMISQIWKK.Q  4.6 48 -0.24 K.GVLVQTKGTGASGSFK.L  2.8 72 39.8 R.VDVQEHGLDVAAGAR.H  2.5 78 29.3 K.VLWVRACIFGCR.S  1.8 92 37.7 R.RILSQSTDSLNMR.N  1.5 98 20.4 R.RLPNDHTALALCR.L  0.7 1.2e+02 32.5 K.VGGAIASGSSFGRSAGR.V  0.5 1.2e+02 18.7 R.VIGEELAYLCKNK.G | |

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| |  | | --- | | Top scoring peptide matches to query 560 09MAR16\_OT\_03.01857.01857.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  62.1 9.4e-05 10.8 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  22.0 0.97 22.2 R.MQKEIAALAPSMMK.I  19.4 1.7 -5.79 K.QQEIYQELTRLK.A  19.4 1.7 -5.79 K.QQEIYXELTRLK.A  18.8 2 1.47 R.LAQLEADYQEKLK.D  17.0 3.1 34.8 K.AETETVQDGTEKLK.N  16.2 3.7 1.47 R.EQLEEYKIQLQK.L  16.1 3.7 11.3 K.SKEEETATAITQLK.L  15.8 4 17.7 R.YGAPSSADLGLGKAGGK.S  15.6 4.2 36.4 R.EVAAQFKEEIPCK.E | |

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| |  | | --- | | Top scoring peptide matches to query 562 09MAR16\_OT\_03.01862.01862.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  68.5 2.2e-05 10.8 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  25.6 0.42 17.8 R.YGAPSSADLGLGKAGGK.S  24.4 0.55 22.3 R.MQKEIAALAPSMMK.I  24.1 0.6 -5.71 K.QQEIYQELTRLK.A  24.1 0.6 -5.71 K.QQEIYXELTRLK.A  16.9 3.1 1.55 R.EQLEEYKIQLQK.L  15.9 3.9 34.9 K.AETETVQDGTEKLK.N  15.9 3.9 1.55 R.LAQLEADYQEKLK.D  14.9 4.9 1.55 K.NSALEYQLLEIQK.S  14.1 5.9 -21.99 K.TIDGSAVQFIISGIK.M | |
| |  | | --- | | Top scoring peptide matches to query 563 09MAR16\_OT\_03.01845.01845.3 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.3 0.18 11.4 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  13.3 7.2 46.9 -.MAATASAGVPATVSEK.Q  11.3 11 -0.96 -.MEALGARGALAGFLR.A  10.5 14 -3.56 K.GAILHAFEMFRLK.S  9.5 17 37.0 R.LTADMISPPLGDFR.H  9.2 18 34.6 R.LAPSHQPSSPPSSTR.R  8.8 20 -21.42 K.AAYLQSLNSXDLLK.A  8.8 20 -21.42 K.AAYLQSLNSXDLLK.A  8.2 23 3.81 R.FSSAPRRPSTSSLR.H  7.9 25 8.89 -.MSSNTRVALVTGANK.G | |

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| |  | | --- | | Top scoring peptide matches to query 564 09MAR16\_OT\_03.01851.01851.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  67.6 2.7e-05 11.4 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  23.3 0.72 -5.16 K.QQEIYQELTRLK.A  23.3 0.72 -5.16 K.QQEIYXELTRLK.A  18.8 2 2.10 R.EQLEEYKIQLQK.L  17.5 2.7 37.1 R.EVAAQFKEEIPCK.E  15.8 4.1 22.9 R.MQKEIAALAPSMMK.I  15.7 4.1 12.0 K.SKEEETATAITQLK.L  15.3 4.5 18.3 R.YGAPSSADLGLGKAGGK.S  14.7 5.2 23.4 R.LQEKMTASLGDIDK.G  14.6 5.3 2.10 R.LAQLEADYQEKLK.D | |
| |  | | --- | | Top scoring peptide matches to query 565 09MAR16\_OT\_03.01856.01856.3 Score greater than 27 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.3 0.36 12.0 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  12.8 8.1 35.2 R.LAPSHQPSSPPSSTR.R  11.8 10 47.5 -.MAATASAGVPATVSEK.Q  10.6 13 -0.37 -.MEALGARGALAGFLR.A  8.3 23 11.7 R.EYNNLLALGTERR.L  7.8 25 -2.97 K.GAILHAFEMFRLK.S  6.8 32 4.40 R.FSSAPRRPSTSSLR.H  6.7 33 26.2 R.AEAQYAEVQELIGK.V  6.5 34 32.6 K.KAIGAFAAADSFDHK.K  6.1 38 -46.51 R.IASISKSLTMVAIAK.L | |

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| |  | | --- | | Top scoring peptide matches to query 566 09MAR16\_OT\_03.01850.01850.3 Score greater than 34 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.8 0.04 12.8 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  19.3 1.8 0.46 -.MEALGARGALAGFLR.A  14.4 5.5 48.3 -.MAATASAGVPATVSEK.Q  12.4 8.7 36.0 R.LAPSHQPSSPPSSTR.R  11.3 11 38.5 R.EQFGEATVPAMAAVK.R  10.0 15 -2.14 K.GAILHAFEMFRLK.S  9.4 18 -6.35 K.LYEPGQLNLLFNK.R  9.3 18 -20.01 R.NALLVYQIVESTAK.K  9.1 19 12.5 R.EYNNLLALGTERR.L  8.8 20 36.8 R.TADVAESLQTAVTDK.A | |
| |  | | --- | | Top scoring peptide matches to query 567 09MAR16\_OT\_03.01656.01656.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.5 0.079 11.5 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 R.VGLQAQPMHSELVK.K  20.9 1.1 -30.61 R.VQLGAQELQLQGLR.G  10.2 13 16.3 K.GGPGEAEGKKPELGAR.A  6.8 29 32.8 K.VLQKSISSLDMCR.N  5.2 42 0.06 R.DQGPGAAEVLLDVIR.Y  5.0 44 -14.42 R.LVSPGSSVVSTHRAR.V  4.8 47 -26.40 K.LRQASLSVLHCLR.C  2.8 73 39.7 K.STLNIPTEEQGHAR.K  2.7 75 32.5 K.VGLHQENEDSRLR.W  2.5 78 3.86 K.KVANEGLVYFWAR.N | |

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| |  | | --- | | Top scoring peptide matches to query 575 09MAR16\_OT\_03.02013.02013.2 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  51.3 0.0013 10.7 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent K.LTFDTTFSPNTGKK.S  7.1 35 17.5 R.APQLDMSLRPAGER.R  4.8 59 -38.22 R.LGQPKMEPVTTLVK.V  4.4 65 10.7 KGTNPSFTTDFTLK  4.3 66 31.1 K.HPGNFAAEAQGAMKK.A  3.4 83 -40.67 K.RPTSLPLNTKNSTK.E  3.2 87 -19.86 R.GLYLRSAYLASGASK.I  3.0 91 38.3 K.KDSVFTSMFHSVR.R  2.9 92 -33.45 K.GQLNIILDQNSTLK.S  2.9 92 40.9 K.DGTHIAMHTTLTSR.V | |
| |  | | --- | | Top scoring peptide matches to query 576 09MAR16\_OT\_03.02020.02020.2 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  57.9 0.00029 10.9 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent K.LTFDTTFSPNTGKK.S  6.9 37 17.8 R.APQLDMSLRPAGER.R  6.6 39 31.3 K.HPGNFAAEAQGAMKK.A  6.4 41 -3.17 -.MTTLPPLPMTRPK.L  5.6 50 43.6 K.MCLEQYTGEIGKK.Q  4.6 63 3.74 K.LVFGDEGVQHEAKK.Q  2.2 1.1e+02 41.1 R.ISNCRYTQTTANK.Y  2.2 1.1e+02 40.7 K.AFGYSSDLIQHYR.T  2.1 1.1e+02 4.06 K.LYSLVSMIDKEMK.C  2.1 1.1e+02 -33.21 K.GQLNIILDQNSTLK.S | |

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| |  | | --- | | Top scoring peptide matches to query 577 09MAR16\_OT\_03.02010.02010.2 Score greater than 23 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  58.9 0.00023 11.5 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent K.LTFDTTFSPNTGKK.S  7.3 34 18.3 R.APQLDMSLRPAGER.R  6.5 40 -2.63 -.MTTLPPLPMTRPK.L  4.5 64 41.7 K.DGTHIAMHTTLTSR.V  4.1 70 32.8 R.TMLSRFESELSEK.G  3.9 74 -16.49 K.SENARLVVQIDNAK.L  3.8 75 8.06 R.LWLSVQWPWEGR.G  3.5 80 41.7 R.ISNCRYTQTTANK.Y  3.4 82 39.1 K.KDSVFTSMFHSVR.R  2.9 92 -7.66 K.RLYQYMLNAGLAK.V | |
| |  | | --- | | Top scoring peptide matches to query 578 09MAR16\_OT\_03.02008.02008.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  30.9 0.15 11.8 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent K.LTFDTTFSPNTGKK.S  9.5 20 -2.58 R.APPYLGRVGVADEGR.T  6.5 40 46.7 K.TQMSEQYFPAVQK.F  5.1 56 -16.15 K.SENARLVVQIDNAK.L  4.9 58 33.1 IEHTMATPLEDVGK  4.2 68 9.70 R.LDNMLLAEGVAGPEK.G  4.0 73 -25.10 K.LVSIGAEEIVDGNLK.M  4.0 73 -44.29 K.LVPLGKAAAVEMSVR.H  3.9 73 9.69 K.TLLDTTYNKSLCK.S  3.9 74 7.23 K.TLPANSVKQGEEQR.K | |

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| |  | | --- | | Top scoring peptide matches to query 579 09MAR16\_OT\_03.02012.02012.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  23.5 0.8 12.0 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent K.LTFDTTFSPNTGKK.S  11.1 14 35.4 R.NTEYLFELADSVR.K  8.3 27 46.8 K.TQMSEQYFPAVQK.F  7.0 36 -2.47 R.APPYLGRVGVADEGR.T  6.8 38 -18.64 R.QPPGPVPVPSLPSER.A  6.2 43 -24.98 K.LVSIGAEEIVDGNLK.M  5.7 49 -11.83 R.TNRPPLSLSRMXR.K  5.4 52 4.75 K.LVFGDEGVQHEAKK.Q  5.0 57 -16.03 K.SENARLVVQIDNAK.L  4.5 64 6.79 R.LRCLQMLSPPGER.E | |
| |  | | --- | | Top scoring peptide matches to query 580 09MAR16\_OT\_03.02018.02018.3 Score greater than 22 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.2 0.22 12.3 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent K.LTFDTTFSPNTGKK.S  7.9 29 -4.27 K.VLDANKMVAPSQQR.L  7.2 35 47.1 K.TQMSEQYFPAVQK.F  6.2 43 -24.63 K.LVSIGAEEIVDGNLK.M  6.2 44 -2.11 R.APPYLGRVGVADEGR.T  4.2 68 -43.82 K.LVPLGKAAAVEMSVR.H  4.2 69 10.2 K.TLLDTTYNKSLCK.S  3.8 75 7.70 K.TLPANSVKQGEEQR.K  3.7 77 -15.69 K.LTEQAQTLQQQLR.Q  3.5 81 9.30 K.TIIMETQHRHFK.L | |

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| |  | | --- | | Top scoring peptide matches to query 587 09MAR16\_OT\_03.01780.01780.2 Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  74.1 6.2e-06 9.84 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  25.7 0.43 21.2 R.MQKEIAALAPSMMK.I  18.9 2.1 23.9 K.TNSNIEFLLEQEK.M  18.0 2.5 32.2 R.QFMQRVIQNPCK.I  10.8 13 -6.24 K.EILLAMLMVDKEK.K  10.1 16 16.7 K.AVAASYQAQAEAKEK.I  10.1 16 16.7 R.AVAASYQEQAAAKEK.I  9.4 18 -45.90 R.LVPEPLVGNLSGIEK.E  8.3 23 23.9 K.LFSKSSTQTSTYSK.Y  8.0 25 21.7 R.LQEKMTASLGDIDK.G | |
| |  | | --- | | Top scoring peptide matches to query 588 09MAR16\_OT\_03.01785.01785.2 Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  69.2 1.9e-05 10.5 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  21.0 1.3 21.8 R.MQKEIAALAPSMMK.I  15.8 4.2 24.5 K.TNSNIEFLLEQEK.M  13.3 7.4 32.9 R.QFMQRVIQNPCK.I  11.1 12 30.7 R.ILCQMMQQVNKR.Y  10.4 15 -17.83 R.NLFMKALEITTQR.E  10.3 15 22.4 R.LQEKMTASLGDIDK.G  8.7 21 38.5 K.MKAGKPEETSLDSR.E  8.2 24 -13.11 K.HGISRLTGPLGAEEK.N  8.2 24 35.9 R.EQFGEATVPAMSAVK.R | |

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| |  | | --- | | Top scoring peptide matches to query 589 09MAR16\_OT\_03.01710.01710.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  91.2 1.2e-07 10.9 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  20.8 1.3 22.2 R.MQKEIAALAPSMMK.I  14.4 5.7 -12.72 R.ALGRHDLDGLGALEK.L  13.5 7 22.2 R.MQKEIAALAPSMMK.I  12.7 8.5 -24.63 K.KGTHIIQHMSLTAK.Q  11.3 12 -1.78 K.RHNELPFTFYIK.E  10.9 13 -5.53 R.TQIGRYSELEQLK.S  9.0 20 -10.28 K.MQVYKDDQVVVIK.D  8.6 22 -10.70 R.QLPLPTFDVPYFK.Y  8.1 24 -3.09 R.ETMSPPLTIVGYLK.E | |
| |  | | --- | | Top scoring peptide matches to query 590 09MAR16\_OT\_03.01703.01703.2 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  93.0 7.8e-08 11.1 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  23.4 0.72 22.5 R.MQKEIAALAPSMMK.I  19.8 1.7 22.5 R.MQKEIAALAPSMMK.I  16.1 3.9 -12.49 R.ALGRHDLDGLGALEK.L  14.6 5.5 15.4 R.YNVPATPDGVQYLK.N  14.0 6.3 -5.29 R.TQIGRYSELEQLK.S  12.9 8 -2.86 R.ETMSPPLTIVGYLK.E  12.6 8.6 -14.75 K.ELKLSVPMPYMLK.V  11.7 11 13.2 K.NALDLKFDMEQLK.D  11.3 12 1.90 R.LAQSYKDLEEQLK.S | |

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| |  | | --- | | Top scoring peptide matches to query 591 09MAR16\_OT\_03.01714.01714.3 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.6 0.086 11.5 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  14.8 5.1 -17.18 M.GAPTLPPAWQPFLK.D  12.0 9.8 15.8 R.YVDSDPPVLFGSIR.A  11.2 12 11.5 K.QLQIMKDLSNLVM.-  10.9 13 29.8 K.GQGLAEMDALFEKR.E  10.8 13 -2.40 R.ETMSPPLTIVGYLK.E  9.4 18 18.4 R.EVYSNGLPGSGTQKK.E  9.3 18 -23.08 K.VLTAENTMLTSKLK.E  8.5 22 48.9 K.TAPSQSFVPSGTEEK.M  7.3 29 13.7 R.KEWLLGMLGAESSK.L | |
| |  | | --- | | Top scoring peptide matches to query 592 09MAR16\_OT\_03.01707.01707.3 Score greater than 33 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.7 0.026 11.8 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  18.6 2.1 11.8 K.QLQIMKDLSNLVM.-  15.2 4.8 16.1 R.YVDSDPPVLFGSIR.A  10.5 14 -16.94 M.GAPTLPPAWQPFLK.D  10.5 14 -22.85 K.VLTAENTMLTSKLK.E  10.1 15 20.7 R.EMQSQSVMLALRR.G  9.7 17 18.7 R.EVYSNGLPGSGTQKK.E  9.4 18 30.0 K.GQGLAEMDALFEKR.E  9.4 18 20.7 R.EMQSQSVMLALRR.G  9.3 18 20.2 K.LHFFQEVLGTSMR.A | |

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| |  | | --- | | Top scoring peptide matches to query 593 09MAR16\_OT\_03.01700.01700.3 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.3 0.093 12.0 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  13.8 6.5 16.3 R.YVDSDPPVLFGSIR.A  10.4 14 14.2 R.KEWLLGMLGAESSK.L  10.3 15 18.9 R.EVYSNGLPGSGTQKK.E  10.0 16 6.56 K.ELYNSPVWGKFPK.V  9.8 16 -14.13 K.ANDHKPLPIIDFGK.I  9.8 16 12.0 K.QLQIMKDLSNLVM.-  9.7 17 -22.61 K.VLTAENTMLTSKLK.E  9.5 17 -1.93 R.ETMSPPLTIVGYLK.E  8.2 23 20.5 K.LHFFQEVLGTSMR.A | |
| |  | | --- | | Top scoring peptide matches to query 596 09MAR16\_OT\_03.01773.01773.3 Score greater than 29 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  27.4 0.2 14.9 K.ILSASTIGPEGVHQR.G  14.9 3.6 14.9 K.VQGRTIIFSSATER.I  9.0 14 -36.77 R.EPLLLFFAAKLFR.G  7.2 21 30.9 K.LSPYSKAAWMAPVK.G  7.0 23 38.5 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  6.4 26 -20.29 K.VVPSAQVTLVMHKR.A  6.1 28 45.4 K.LENSKLGLGAEYDR.L  6.0 28 22.1 ILVDQGHGALDAEVK  5.6 31 19.1 K.SHPIAGILEVRGCR.L  4.2 42 10.2 R.ALQQAYDVLIKMR.K | |

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| |  | | --- | | Top scoring peptide matches to query 603 09MAR16\_OT\_03.02684.02684.2 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  59.8 0.00016 10.4 11 sp|P02769|ALBU\_BOVIN|Serum K.DAFLGSFLYEYSR.R  8.8 21 -49.99 -.MDAPRALAAKPPTGR.K  7.8 26 17.5 R.ENFSIYIFEYDK.R  6.8 33 -2.70 M.MSSSSSEIDVVKTR.I  5.7 42 -3.55 -.MSSRPPASPPAQGSR.L  5.3 47 31.9 R.KCELSTACDGGELK.D  5.1 49 -45.28 R.QASTPRPQGQLAASR.S  4.9 50 40.3 R.GFGGRHCELEYDK.C  4.9 51 -13.30 R.MRHIPLSPGSDWR.D  3.2 75 -22.17 K.WFIDSNILMEKR.D | |
| |  | | --- | | Top scoring peptide matches to query 604 09MAR16\_OT\_03.02687.02687.2 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  77.6 2.8e-06 12.9 11 sp|P02769|ALBU\_BOVIN|Serum K.DAFLGSFLYEYSR.R  14.4 5.8 42.8 R.GFGGRHCELEYDK.C  12.1 9.7 20.0 R.ENFSIYIFEYDK.R  9.1 20 -42.79 R.QASTPRPQGQLAASR.S  8.3 23 21.8 R.RLEWENWEYSR.V  7.4 29 -31.03 -.FDALIFDTIDKGGR.I  7.4 29 -1.06 -.MSSRPPASPPAQGSR.L  6.0 39 -19.68 K.WFIDSNILMEKR.D  5.7 43 -0.21 M.MSSSSSEIDVVKTR.I  4.9 51 -12.39 HGNLEEQLLTNGSR | |

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| |  | | --- | | Top scoring peptide matches to query 605 09MAR16\_OT\_03.02680.02680.2 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  68.3 2.4e-05 15.0 11 sp|P02769|ALBU\_BOVIN|Serum K.DAFLGSFLYEYSR.R  9.6 18 29.3 K.SSLCSDSNVLAVCR.L  9.6 18 45.0 R.GFGGRHCELEYDK.C  9.1 20 22.2 R.ENFSIYIFEYDK.R  8.0 25 -17.50 K.WFIDSNILMEKR.D  7.2 31 -28.85 -.FDALIFDTIDKGGR.I  6.3 37 23.9 R.RLEWENWEYSR.V  6.0 41 1.12 -.MSSRPPASPPAQGSR.L  5.2 49 -7.78 K.ECGKAFTQSTPLTK.H  5.0 51 8.27 R.SPSGFSAGMVSVQASR.E | |
| |  | | --- | | Top scoring peptide matches to query 612 09MAR16\_OT\_03.01630.01630.3 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  28.4 0.24 11.0 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  14.3 6.1 -21.14 K.TDTLVQSTIKEAFK.S  13.3 7.8 19.4 K.MFVGQIPRSWSEK.E  11.9 11 1.37 K.EIRYPVMLTAMEK.L  11.8 11 22.0 R.GGKDMAQNIYRPSK.N  11.3 12 19.4 K.MFVGQVPRTWSEK.D  10.9 13 29.1 K.GQGLAEMDALFEKR.E  10.8 14 -42.58 R.IKMNFALGPVISFK.Y  10.7 14 -16.98 R.IRQSIQYLEMTAK.A  10.4 15 11.0 K.VDEAMRTLLLMEK.T | |

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| |  | | --- | | Top scoring peptide matches to query 613 09MAR16\_OT\_03.01638.01638.3 Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  25.5 0.47 11.1 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.MQKEITALAPSTMK.I  21.6 1.1 29.2 K.GQGLAEMDALFEKR.E  17.0 3.3 -22.71 R.HLVHQHHIYALGR.L  16.2 4 22.1 R.LHAEQAECKEPIR.Q  14.2 6.3 19.5 R.FNELMVDHYLKR.Q  13.8 6.9 -44.89 K.EHKGQAVPLLYLGR.V  13.7 7 18.0 K.EGLSESSLQAEFRK.L  13.1 8.1 19.5 K.MFVGQVPRTWSEK.D  12.3 9.7 48.1 K.SGEEDEEILFKER.A  10.0 17 -42.45 K.LNLMALGGFLYQLK.K | |
| |  | | --- | | Top scoring peptide matches to query 648 09MAR16\_OT\_03.02056.02056.3 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.8 0.045 10.3 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.GYSFTTTAEREIVR.D  13.5 7.6 36.6 K.TFSQELTLTCHHR.L  9.9 18 41.2 R.TFSGAAGGNGAGSTRYR.Y  6.8 36 21.2 R.LADGQLQQAQIWGAM.-  6.4 39 -5.12 R.SFEKQIEEEILHK.K  6.3 39 -47.87 K.RGLKPSCTIIPLMK.K  5.1 53 26.0 -.MAVFNQKSVSDMIK.E  5.0 54 -5.13 R.AGAQLLSSLSGYAYTK.R  4.8 56 19.1 R.HGLELKVQVACSSAM.-  4.7 57 -18.09 R.EKLDQDQALISELK.K | |

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| |  | | --- | | Top scoring peptide matches to query 649 09MAR16\_OT\_03.02048.02048.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  24.3 0.64 11.0 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.GYSFTTTAEREIVR.D  10.5 15 45.9 K.CFSHSRSLSQHQR.A  9.1 21 10.1 R.HQNLPVWTDNHLR.E  8.0 27 41.9 R.TFSGAAGGNGAGSTRYR.Y  8.0 27 1.61 R.KTFSLEQHFVEHK.K  7.9 28 8.89 R.LIQGGGEMIGGDVEVR.Q  7.8 28 15.0 R.FCPSTQGAKIIHDR.H  7.8 28 19.8 R.HGLELKVQVACSSAM.-  7.3 31 28.8 K.GYSIPFMGSDVSVVR.R  7.1 33 -39.76 R.LTVIEEEVKTLEAR.L | |
| |  | | --- | | Top scoring peptide matches to query 650 09MAR16\_OT\_03.02046.02046.2 Score greater than 32 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  36.1 0.042 11.4 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.GYSFTTTAEREIVR.D  17.1 3.3 -42.27 R.VSSLLSSCARPLLAR.L  15.3 5 38.5 R.TNDEITCQDPIPVK.K  11.1 13 -23.97 K.TGEVNVTLTQNGGLVK.H  11.1 13 -28.48 K.KEAMPSLQALDALVK.E  9.3 20 -4.06 K.DEWLVKEEELLAR.E  9.1 21 35.2 K.GYNYTFSHLCVLR.N  9.1 21 -26.43 R.IDTTILGFGHESLVK.Q  8.6 23 29.1 K.GYSIPFMGSDVSVVR.R  8.2 26 2.39 R.QPSAQLACSATQLVR.G | |

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| |  | | --- | | Top scoring peptide matches to query 651 09MAR16\_OT\_03.02042.02042.3 Score greater than 25 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.9 2.8 11.4 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.GYSFTTTAEREIVR.D  11.7 12 37.8 K.TFSQELTLTCHHR.L  10.6 15 29.2 K.GYSIPFMGSDVSVVR.R  8.8 22 20.3 R.HGLELKVQVACSSAM.-  8.4 24 -40.13 K.GYDLRPDAIAIKAAR.A  7.5 30 -17.79 K.NELEWSLILRSNR.I  7.2 32 -30.77 R.TEAVRSLISGGEALAR.Q  6.3 40 -30.79 R.GKANSTGTLVITNPTR.I  5.8 44 42.3 R.TFSGAAGGNGAGSTRYR.Y  5.6 46 6.88 -.PVMQLDLPDYPSVR.M | |
| |  | | --- | | Top scoring peptide matches to query 652 09MAR16\_OT\_03.02051.02051.2 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.1 0.033 11.4 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.GYSFTTTAEREIVR.D  14.2 6.3 47.1 K.SDSTRNYCTTLVGR.D  13.3 7.8 -42.20 R.VSSLLSSCARPLLAR.L  12.2 10 2.47 R.QPSAQLACSATQLVR.G  10.1 16 -33.23 K.LAEGTYHLETKLVR.S  10.0 17 4.57 R.REEEPQKPNYALR.L  8.7 23 42.6 R.MGPLGLDHMASSIER.M  8.2 26 13.9 K.ERTGETQPESLGGLR.S  7.7 29 -20.27 R.GSLFYHPLAGAELVR.S  7.5 30 -3.99 K.DEWLVKEEELLAR.E | |

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| |  | | --- | | Top scoring peptide matches to query 656 09MAR16\_OT\_03.01964.01964.3 Score greater than 28 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  45.6 0.0015 11.3 11 sp|P02769|ALBU\_BOVIN|Serum KVPQVSTPTLVEVSR  12.5 3.2 -4.04 R.VIQEGLEGLVLKDVK.G  12.1 3.5 24.2 K.LAGWSGPKQVGLIDAK.V  11.5 4 15.3 -.MATGAVLPRLLGAGVR.A  8.9 7.1 26.7 K.LGSSQTPLVPAKQSAR.K  7.2 11 22.1 R.QPILMTQSTAVVPVR.T  7.1 11 11.3 K.SGVKVITQIPGATSPGK.V  6.5 12 24.2 R.EDLLVVAHYAGALLR.G  6.4 13 -4.03 K.IDLINNLLPVSSTLK.G  5.3 16 48.9 R.VPLDEALQRGTVDAR.T | |
| |  | | --- | | Top scoring peptide matches to query 657 09MAR16\_OT\_03.01977.01977.2 Score greater than 27 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  96.7 1.2e-08 11.4 11 sp|P02769|ALBU\_BOVIN|Serum KVPQVSTPTLVEVSR  8.9 7.2 -15.27 R.LLPLDMILISLGVSR.F  5.2 17 -4.74 R.KVIVVVSQHFIQSR.W  4.3 21 41.2 R.QVPCFLWPRLPAR.V  3.4 26 44.5 R.LLHVKEIMQIDER.K  2.9 29 24.3 K.KVSIIQLFTNASYR.Q  2.6 30 2.12 K.KVSLPTPQPLFGLSR.K  2.5 31 19.9 R.VKPTGRIGADSASRPK.L  2.0 35 35.2 K.LLHVVMGQNPKEFK.S  1.5 39 17.5 R.ILQEQARLVWVER.G | |

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| |  | | --- | | Top scoring peptide matches to query 658 09MAR16\_OT\_03.01970.01970.3 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.4 0.00026 11.6 11 sp|P02769|ALBU\_BOVIN|Serum KVPQVSTPTLVEVSR  20.5 0.5 22.5 R.QPILMTQSTAVVPVR.T  14.1 2.2 15.6 -.MATGAVLPRLLGAGVR.A  14.0 2.2 24.5 R.EDLLVVAHYAGALLR.G  13.5 2.5 41.8 R.LLSRVAPCRPARPM.-  7.6 9.7 24.5 K.LAGWSGPKQVGLIDAK.V  6.8 12 43.9 R.LMRWGGGIGLLHSSR.W  6.5 13 44.7 K.ELLQSCAVLGIPPSR.V  5.6 15 27.0 K.LGSSQTPLVPAKQSAR.K  5.5 16 -3.70 R.VIQEGLEGLVLKDVK.G | |
| |  | | --- | | Top scoring peptide matches to query 659 09MAR16\_OT\_03.01971.01971.2 Score greater than 24 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  94.9 1.8e-08 11.6 11 sp|P02769|ALBU\_BOVIN|Serum KVPQVSTPTLVEVSR  5.2 17 -4.52 R.KVIVVVSQHFIQSR.W  3.5 25 44.7 R.LLHVKEIMQIDER.K  2.4 32 2.34 K.KVSLPTPQPLFGLSR.K  2.2 34 35.4 K.LLHVVMGQNPKEFK.S  1.8 37 24.6 K.KVSIIQLFTNASYR.Q  1.4 40 41.4 R.QVPCFLWPRLPAR.V  1.3 41 43.9 R.QVRIPQMPAPPHPR.T  1.2 42 27.0 K.KVNIENVALIQDGAR.L  1.2 42 49.2 K.KVQDLSTGTDHAIVR.L | |

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| |  | | --- | | Top scoring peptide matches to query 660 09MAR16\_OT\_03.01976.01976.3 Score greater than 30 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  54.6 0.00019 12.0 11 sp|P02769|ALBU\_BOVIN|Serum KVPQVSTPTLVEVSR  13.8 2.3 24.9 R.EDLLVVAHYAGALLR.G  9.7 6 22.8 R.QPILMTQSTAVVPVR.T  9.4 6.4 27.3 K.LGSSQTPLVPAKQSAR.K  8.2 8.4 18.0 R.RPAVYHTNLVQTLK.C  7.3 10 -3.36 R.VIQEGLEGLVLKDVK.G  7.1 11 -15.54 K.VRPLPHSLMHLLVK.Q  5.7 15 45.0 K.ELLQSCAVLGIPPSR.V  4.8 18 34.2 K.VQLQTQELQPQSLK.Q  3.1 27 44.2 R.LMRWGGGIGLLHSSR.W | |
| |  | | --- | | Top scoring peptide matches to query 661 09MAR16\_OT\_03.01902.01902.2 Score greater than 30 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  83.2 6e-07 11.3 8 sp|P23565|AINX\_RAT|Alpha-internexin R.RLPASDGLDLSQAAAR.T  12.2 7.5 -4.04 K.NLNAVRGDLDLLAEK.K  10.7 11 10.8 K.MGGHLRLLNIACAAK.A  9.7 14 15.7 R.TPAQIEPEPVQLYR.A  7.6 22 -4.04 R.IRELQQQIEDLQK.S  7.5 22 12.8 R.SWNKSLLHLICNR.N  7.3 23 -10.91 -.ELKPRVSNDVTGGIR.E  5.8 33 -26.24 R.RNLASPEGTLATLGLK.T  5.7 34 33.5 R.ELRAGIPVTDENGNR.L  5.4 36 1.98 R.HTPETSYGKLRPVR.A | |

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| |  | | --- | | Top scoring peptide matches to query 662 09MAR16\_OT\_03.01907.01907.2 Score greater than 25 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  85.8 3.3e-07 11.4 8 sp|P23565|AINX\_RAT|Alpha-internexin R.RLPASDGLDLSQAAAR.T  7.6 22 12.9 R.SWNKSLLHLICNR.N  6.9 26 -17.69 R.LQQQVLSQGSGRALR.A  6.8 26 -3.99 R.GVKLVEVDDAQVAAAR.K  6.8 26 -10.84 -.ELKPRVSNDVTGGIR.E  6.7 27 12.9 K.GMGGWEGGIRVPGIVR.W  6.3 30 -3.97 R.IRELQQQIEDLQK.S  5.9 33 39.6 R.GNVFAGGLQNLGGHGSR.I  5.7 34 33.6 R.AGRPGASAEEEALGGIR.G  5.2 38 -26.16 R.RNLASPEGTLATLGLK.T | |
| |  | | --- | | Top scoring peptide matches to query 663 09MAR16\_OT\_03.01893.01893.2 Score greater than 29 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  66.3 3e-05 11.4 8 sp|P23565|AINX\_RAT|Alpha-internexin R.RLPASDGLDLSQAAAR.T  12.0 7.9 -3.97 R.IRELQQQIEDLQK.S  11.3 9.3 -3.97 K.NLNAVRGDLDLLAEK.K  9.5 14 12.9 R.SWNKSLLHLICNR.N  8.9 16 15.8 R.TPAQIEPEPVQLYR.A  7.5 22 -26.16 R.RNLASPEGTLATLGLK.T  4.5 45 -17.69 R.LQQQVLSQGSGRALR.A  3.1 62 29.0 R.RPPDMNTLQSIGSPK.L  2.5 71 39.6 R.GNVFAGGLQNLGGHGSR.I  1.8 83 -8.50 R.LEVSMVKPTPGLTPR.F | |

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| |  | | --- | | Top scoring peptide matches to query 664 09MAR16\_OT\_03.01888.01888.3 Score greater than 30 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  47.8 0.0021 12.1 8 sp|P23565|AINX\_RAT|Alpha-internexin R.RLPASDGLDLSQAAAR.T  14.4 4.5 3.56 R.EAPTKAQIDVTPVGSK.L  11.3 9.2 13.6 R.SWNKSLLHLICNR.N  11.1 9.8 -25.47 K.SSVLESLVGRDLLPR.G  10.3 12 40.3 R.GNVFAGGLQNLGGHGSR.I  9.8 13 -7.78 K.DLLDQILMLDPAKR.I  9.7 13 25.2 R.CVTCTYILAAKAAAK.Q  9.7 14 16.5 K.IYGESFTRIDAAVAK.V  9.5 14 12.1 K.DLEQLQNLLGADRR.R  8.8 16 35.8 K.DRWQHLLDLMAAR.V | |
| |  | | --- | | Top scoring peptide matches to query 665 09MAR16\_OT\_03.01900.01900.3 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  50.9 0.001 12.5 8 sp|P23565|AINX\_RAT|Alpha-internexin R.RLPASDGLDLSQAAAR.T  16.6 2.8 41.6 K.QLKEAENTPPEASAR.F  16.5 2.8 10.0 K.LTDGSAHRFEVPIAK.F  14.8 4.2 -2.84 R.GVKLVEVDDAQVAAAR.K  13.3 5.9 37.0 K.EEPVAADVINPMALR.Q  12.8 6.6 4.01 R.EAPTKAQIDVTPVGSK.L  12.7 6.8 14.0 R.SWNKSLLHLICNR.N  12.5 7.1 12.5 K.DLEQLQNLLGADRR.R  12.1 7.8 -25.02 K.SSVLESLVGRDLLPR.G  11.9 8.1 16.9 K.AYTADISAVFDKLAR.Q | |

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| |  | | --- | | Top scoring peptide matches to query 666 09MAR16\_OT\_03.01892.01892.3 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  49.0 0.0016 12.5 8 sp|P23565|AINX\_RAT|Alpha-internexin R.RLPASDGLDLSQAAAR.T  15.4 3.6 14.0 R.SWNKSLLHLICNR.N  14.6 4.4 -25.02 K.SSVLESLVGRDLLPR.G  13.1 6.2 4.01 R.EAPTKAQIDVTPVGSK.L  12.8 6.7 41.6 K.QLKEAENTPPEASAR.F  11.6 8.7 16.9 K.AYTADISAVFDKLAR.Q  11.0 10 -2.84 R.GVKLVEVDDAQVAAAR.K  10.6 11 49.5 -.CNNQHAIQCRLVK.L  9.6 14 41.6 R.AELEPEQEAERLAR.A  8.8 17 16.9 K.IYGESFTRIDAAVAK.V | |
| |  | | --- | | Top scoring peptide matches to query 667 09MAR16\_OT\_03.01730.01730.3 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  49.4 0.0016 10.7 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.TIQAHDVGGYYYEK.T  12.6 7.8 -42.49 R.LFSNKVGCAAAPLQPA.-  12.4 8.2 -17.90 R.DVKVHTISLNCSDR.A  11.7 9.6 3.72 R.LVQLPDRCAMCHK.E  10.7 12 -37.18 K.DDLETAVITEATPIR.E  8.0 23 -28.81 K.LYNMQVFEETILK.R  7.9 23 -7.08 R.LTQHLAAASMCTPSR.A  7.5 25 -9.01 K.NTEVGKHNLQFDIE.-  7.3 27 8.63 R.FTLGMVDIDEQGYR.F  7.0 28 7.82 K.WTQFTTYTRHMR.F | |

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| |  | | --- | | Top scoring peptide matches to query 668 09MAR16\_OT\_03.01727.01727.2 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  70.4 1.3e-05 10.9 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.TIQAHDVGGYYYEK.T  8.4 21 -30.15 R.DVPTILSSDTPIEEK.V  4.5 50 -46.27 K.GQDILIDLQPGPYSK.V  4.2 53 -30.96 K.LTVGGPWGQSQEKEK.G  3.0 71 15.8 R.GAAESQAGSGSAHEKEK.K  2.7 77 6.77 K.NVSGGSMTEMFVQLK.L  2.6 78 -36.96 R.LDLKESDLESPAAQK.E  1.9 91 24.2 K.DDLPPNMRFHEEK.R  1.6 98 -39.42 K.LPEVIYLDNPDVEK.G  1.2 1.1e+02 -13.33 R.KMFLGDAVDVFETR.R | |
| |  | | --- | | Top scoring peptide matches to query 669 09MAR16\_OT\_03.01721.01721.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  68.6 2e-05 11.0 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.TIQAHDVGGYYYEK.T  21.8 0.93 -17.57 R.DVKVHTISLNCSDR.A  11.9 9.2 -8.67 K.NTEVGKHNLQFDIE.-  11.3 10 -42.15 R.LFSNKVGCAAAPLQPA.-  8.4 20 -17.96 K.WKGASVNWNGSDPIL.-  7.7 24 -28.47 K.LYNMQVFEETILK.R  7.3 26 -39.69 K.SQLCAALQQIENLR.K  6.9 29 -28.35 R.NLDSLDNRINEVNK.T  6.2 34 4.05 R.LVQLPDRCAMCHK.E  5.3 42 -48.99 K.NVEFIHSLLQRCK.V | |

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| |  | | --- | | Top scoring peptide matches to query 670 09MAR16\_OT\_03.01726.01726.3 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  59.8 0.00015 11.3 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.TIQAHDVGGYYYEK.T  12.5 8 -41.93 R.LFSNKVGCAAAPLQPA.-  12.3 8.3 -17.35 R.DVKVHTISLNCSDR.A  11.7 9.6 4.28 R.LVQLPDRCAMCHK.E  10.7 12 -36.62 K.DDLETAVITEATPIR.E  8.1 22 -8.45 K.NTEVGKHNLQFDIE.-  7.8 23 -37.44 K.IDNRTGHIFTNVEK.C  7.3 26 -6.53 R.LTQHLAAASMCTPSR.A  6.8 30 -28.25 K.LYNMQVFEETILK.R  6.1 35 37.8 K.DSDSTCVFCRIAGR.Q | |
| |  | | --- | | Top scoring peptide matches to query 677 09MAR16\_OT\_03.02050.02050.2 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide** 100.5 1.4e-08 10.8 20 sp|Q9Z214|HOME1\_RAT|Homer R.NKDLEGQLSELEQR.L  10.2 15 12.3 R.CSGPVFHISLEKER.G  9.5 18 -35.49 R.TEVWGLVLLSEEKR.L  9.5 18 -11.11 R.ELDESLQVAERLTR.K  7.6 27 10.8 R.QNDIKLEALTENDR.L  7.6 27 -0.40 R.LQDPSMLSVKAGEQR.Q  7.6 28 16.8 R.NQYGEPANQPKGSLR.L  7.5 28 -22.35 K.QNVENVTVDMLLRK.F  6.5 36 -0.39 R.GLCIERLSASPAQEK.E  5.1 49 -33.07 K.LTDTLVSKQQLEQR.L | |

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| |  | | --- | | Top scoring peptide matches to query 678 09MAR16\_OT\_03.02057.02057.3 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  46.1 0.0039 10.9 20 sp|Q9Z214|HOME1\_RAT|Homer R.NKDLEGQLSELEQR.L  16.0 3.9 32.8 K.LSSVEEDPGANQERK.V  15.0 4.9 -35.46 R.TEVWGLVLLSEEKR.L  13.7 6.8 -20.30 K.AGGVFANSGPKQILGDK.S  12.7 8.4 -33.04 K.LTDTLVSKQQLEQR.L  10.2 15 12.4 R.CSGPVFHISLEKER.G  9.1 19 16.8 R.NQYGEPANQPKGSLR.L  8.0 25 -7.15 R.RQEMVTQLQQELR.N  8.0 25 -15.55 R.SIVMETQDLASPVLR.T  7.9 26 21.2 R.HFQGTLELEVGDWK.D | | | |
| |  | | --- | | Top scoring peptide matches to query 679 09MAR16\_OT\_03.02045.02045.2 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide** 115.5 4.5e-10 11.0 20 sp|Q9Z214|HOME1\_RAT|Homer R.NKDLEGQLSELEQR.L  12.2 9.4 -35.34 R.TEVWGLVLLSEEKR.L  10.6 14 17.0 R.NQYGEPANQPKGSLR.L  10.4 15 -10.96 R.ELDESLQVAERLTR.K  10.3 15 -0.25 R.LQDPSMLSVKAGEQR.Q  9.6 17 11.0 R.QNDIKLEALTENDR.L  9.6 17 12.5 R.CSGPVFHISLEKER.G  8.2 24 -20.18 K.AGGVFANSGPKQILGDK.S  8.0 25 -0.24 R.GLCIERLSASPAQEK.E  7.7 27 -22.21 K.QNVENVTVDMLLRK.F | |

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| |  | | --- | | Top scoring peptide matches to query 680 09MAR16\_OT\_03.02049.02049.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  57.7 0.00027 11.4 20 sp|Q9Z214|HOME1\_RAT|Homer R.NKDLEGQLSELEQR.L  23.1 0.76 -19.75 K.AGGVFANSGPKQILGDK.S  23.0 0.79 12.9 R.CSGPVFHISLEKER.G  20.9 1.3 -34.90 R.TEVWGLVLLSEEKR.L  19.7 1.7 -32.48 K.LTDTLVSKQQLEQR.L  14.3 5.9 -25.70 K.VEDEQTLSLQLQKK.I  14.0 6.2 -36.96 -.MDGVVTDLITVGLKR.G  13.0 7.9 -30.97 -.MFQLPVNNLGSLRK.A  12.7 8.3 33.4 K.LSSVEEDPGANQERK.V  11.8 10 -10.52 R.QSSLLQNLDEVEKR.A | | | |
| |  | | --- | | Top scoring peptide matches to query 681 09MAR16\_OT\_03.02043.02043.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  57.4 0.00029 11.9 20 sp|Q9Z214|HOME1\_RAT|Homer R.NKDLEGQLSELEQR.L  29.6 0.17 13.4 R.CSGPVFHISLEKER.G  16.9 3.2 -34.46 R.TEVWGLVLLSEEKR.L  16.6 3.4 -19.30 K.AGGVFANSGPKQILGDK.S  16.1 3.9 -30.52 -.MFQLPVNNLGSLRK.A  14.8 5.2 -32.04 K.LTDTLVSKQQLEQR.L  14.2 5.9 31.4 R.WDGILTDPEAEKER.I  12.2 9.5 -10.10 R.SVLKIEDAQVQDTGR.Y  11.9 10 17.8 R.NQYGEPANQPKGSLR.L  11.7 11 13.4 ANGGAWGGAVCLIADVK | |

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| |  | | --- | | Top scoring peptide matches to query 682 09MAR16\_OT\_03.01606.01606.3 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.7 0.1 11.7 15 sp|P15205|MAP1B\_RAT|Microtubule-associated R.TPEVSGYTYEKTER.S  17.2 2.9 -34.20 K.TPEVSTVDAMLDLIR.N  11.7 11 -32.57 R.QQAVMAISQELNRR.A  8.3 23 -21.46 K.TPNEPQLEFILACK.D  8.0 24 -45.72 R.TLLVATDHHIGGPSNK.S  7.8 25 15.6 R.RTQEFMAELDFTR.A  7.2 29 -3.87 R.TPAARPCSSLDELSR.S  6.5 34 18.1 K.QSPGDHGKMETLSTR.A  5.3 46 46.8 K.ESSMGSGQAEFSALSR.L  5.0 49 -32.68 K.VPMHKLFSEMLEAK.V | |
| |  | | --- | | Top scoring peptide matches to query 683 09MAR16\_OT\_03.01599.01599.3 Score greater than 30 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  45.9 0.004 11.7 15 sp|P15205|MAP1B\_RAT|Microtubule-associated R.TPEVSGYTYEKTER.S  14.2 5.9 -34.20 K.TPEVSTVDAMLDLIR.N  8.4 22 -45.72 R.TLLVATDHHIGGPSNK.S  6.2 37 -32.57 R.QQAVMAISQELNRR.A  5.0 49 7.25 R.LLASYFSPTEMGAEK.M  4.8 51 18.1 R.RIAAELNCDPTDER.V  4.5 54 -38.95 K.LLEGLPFGTDGTGNIR.T  3.9 64 -13.59 K.MLMKPFMHPRSPR.R  3.9 64 -13.59 K.MLMKPFMHPRSPR.R  3.1 76 -35.02 R.IGQQLGMTFISVGHR.Q | |

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| |  | | --- | | Top scoring peptide matches to query 727 09MAR16\_OT\_03.02724.02724.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.4 1.9 8.78 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  10.9 14 4.47 K.VKNGYVNPELAMQGAK.N  10.2 16 49.2 K.THTMGGDLSGKAQNASK.G  9.9 17 -37.89 K.LDLIHESILHKCIK.T  7.6 29 30.2 R.NLDLDKQPMMQLEK.W  7.3 31 2.22 K.ARILPTSDSGPPSQHR.S  7.2 32 8.76 K.RVSLEPHQGPGTPESK.K  6.8 35 -18.67 K.LNTKMLQQQINMLK.F  6.7 36 0.67 K.NLDNLFEQVLEVASK.A  6.6 36 -25.49 M.ARARPSVAGGGVAAPPER.A | |
| |  | | --- | | Top scoring peptide matches to query 728 09MAR16\_OT\_03.02689.02689.3 Score greater than 32 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  20.5 1.5 -37.35 K.LDLIHESILHKCIK.T  18.5 2.3 5.00 K.VKNGYVNPELAMQGAK.N  14.4 6 9.31 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  13.0 8.4 -9.54 K.NLSSASQSARGTTGLLR.R  12.3 9.8 -27.31 R.WRPTGPPAKGGGTIAPR.L  11.7 11 30.8 R.NLDLDKQPMMQLEK.W  11.7 11 30.8 R.NLDLDKQPMMQLEK.W  11.0 13 -11.86 K.INESILASVNYPRSR.L  9.6 18 -11.11 K.LDDLVSKSEVLGTQSK.A  9.4 19 -24.95 M.ARARPSVAGGGVAAPPER.A | |

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| |  | | --- | | Top scoring peptide matches to query 729 09MAR16\_OT\_03.02682.02682.3 Score greater than 27 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  15.3 4.9 9.42 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  14.2 6.4 -37.25 K.LDLIHESILHKCIK.T  11.6 11 -3.39 R.VRISADAMMQALLGAR.A  10.5 15 -30.70 K.LNIKYDGVELAMKPK.L  10.4 15 -24.85 M.ARARPSVAGGGVAAPPER.A  10.4 15 -26.40 R.QPSSLPEGLPAPLEKR.V  10.4 15 -11.00 K.LDDLVSKSEVLGTQSK.A  9.7 18 -3.76 K.LNLNNYQIMWKGPK.F  8.3 24 30.9 R.NLDLDKQPMMQLEK.W  8.3 24 30.9 R.NLDLDKQPMMQLEK.W | |
| |  | | --- | | Top scoring peptide matches to query 730 09MAR16\_OT\_03.02530.02530.3 Score greater than 30 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  24.2 0.61 -4.60 R.EDDKVPLGTNGHLVPK.E  15.7 4.3 -36.61 K.LDLIHESILHKCIK.T  12.7 8.7 1.95 K.NLDNLFEQVLEVASK.A  11.1 13 5.75 K.VKNGYVNPELAMQGAK.N  9.0 21 -24.21 M.ARARPSVAGGGVAAPPER.A  8.9 21 10.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  6.9 33 -25.76 R.LNGATLQKFLNAATEK.N  6.2 39 -3.12 K.LNLNNYQIMWKGPK.F  6.2 39 -17.39 K.LNTKMLQQQINMLK.F  6.2 39 3.40 -.SPNIFMQVIHIFSK.L | |

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| |  | | --- | | Top scoring peptide matches to query 731 09MAR16\_OT\_03.02521.02521.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  15.9 4.2 2.16 K.NLDNLFEQVLEVASK.A  10.8 13 -29.85 K.LNIKYDGVELAMKPK.L  10.3 15 10.3 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  10.1 16 -23.99 M.ARARPSVAGGGVAAPPER.A  9.7 17 -36.39 K.LDLIHESILHKCIK.T  8.4 23 5.96 K.VKNGYVNPELAMQGAK.N  7.3 30 0.21 QLEMTLIKLQDENK  6.9 33 -34.44 R.QPLPPPPPPSSIPAPAR.E  6.8 34 -4.39 R.EDDKVPLGTNGHLVPK.E  6.4 37 31.7 R.NLDLDKQPMMQLEK.W | |
| |  | | --- | | Top scoring peptide matches to query 733 09MAR16\_OT\_03.03026.03026.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  14.9 5.3 -23.57 M.ARARPSVAGGGVAAPPER.A  14.5 5.8 10.7 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  13.0 8.1 6.39 K.VKNGYVNPELAMQGAK.N  10.6 14 -48.66 K.DLILRTSFVDLWLK.R  10.3 15 32.2 R.NLDLDKQPMMQLEK.W  10.3 15 32.2 R.NLDLDKQPMMQLEK.W  8.8 21 -35.97 K.LDLIHESILHKCIK.T  7.8 27 -3.97 R.EDDKVPLGTNGHLVPK.E  7.3 30 10.7 K.EPPSEGRLDALQGPPR.T  6.5 36 28.4 M.MAVEEEEVKEVLQK.L | |

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| |  | | --- | | Top scoring peptide matches to query 734 09MAR16\_OT\_03.02616.02616.3 Score greater than 24 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  11.7 11 10.8 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  10.7 14 15.4 R.RAVEVLQLAMEGDGSK.A  9.2 19 32.3 R.NLDLDKQPMMQLEK.W  8.2 24 -12.36 R.TGIDLGTTGRLQLMAR.L  8.1 25 6.50 K.VKNGYVNPELAMQGAK.N  7.7 28 30.0 R.SAKGGAPMPVSNSVSASR.D  7.1 31 6.51 -.MPPRELSEAEPPPLR.A  6.6 35 -35.86 K.LDLIHESILHKCIK.T  6.6 35 32.3 R.NLDLDKQPMMQLEK.W  6.3 38 -2.38 K.LNLNNYQIMWKGPK.F | |
| |  | | --- | | Top scoring peptide matches to query 735 09MAR16\_OT\_03.01899.01899.2 Score greater than 28 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  61.3 0.00012 11.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  11.3 12 -7.75 K.NLSSASQSARGTTGLLR.R  10.2 16 4.53 R.SPTGRQGQSPGPSPPLR.R  9.6 18 38.8 K.DDQPLHSDASGPGVVPK.S  9.4 19 -5.50 LQSTEMENLAIAVKR  7.9 26 36.8 R.AGTLSMKPDLSNEPSR.S  6.9 33 -9.81 -.MVLNSLDKMIQLQK.N  6.8 34 -29.03 K.ASLSLIKDLFDMLPR.L  6.8 34 43.4 -.MAEDKTKPSELDQGK.Y  6.1 39 29.9 R.AAPTPGIFSFQPESNR.T | |

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| |  | | --- | | Top scoring peptide matches to query 736 09MAR16\_OT\_03.01947.01947.3 Score greater than 29 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  38.1 0.025 11.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  14.2 6.2 -35.54 K.LDLIHESILHKCIK.T  12.3 9.5 -3.54 R.EDDKVPLGTNGHLVPK.E  9.9 17 32.6 R.NLDLDKQPMMQLEK.W  9.8 17 -9.30 K.LDDLVSKSEVLGTQSK.A  9.3 19 -7.72 K.NLSSASQSARGTTGLLR.R  9.3 19 1.06 QLEMTLIKLQDENK  9.1 20 21.5 K.KQSLCEVLQAWNSR.L  7.8 27 -16.32 K.LNTKMLQQQINMLK.F  7.3 30 -29.00 K.LNIKYDGVELAMKPK.L | |
| |  | | --- | | Top scoring peptide matches to query 737 09MAR16\_OT\_03.02660.02660.3 Score greater than 33 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.7 0.17 11.2 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  18.4 2.3 -35.43 K.LDLIHESILHKCIK.T  12.4 9.2 11.2 R.NLNTYTPREIDLNR.R  12.2 9.8 -28.89 K.LNIKYDGVELAMKPK.L  10.3 15 32.7 R.NLDLDKQPMMQLEK.W  10.3 15 32.7 R.NLDLDKQPMMQLEK.W  9.7 17 -23.04 M.ARARPSVAGGGVAAPPER.A  9.1 20 -7.72 K.QVDPETMLLPYLRK.K  7.8 27 15.8 R.RAVEVLQLAMEGDGSK.A  6.7 34 -25.39 R.WRPTGPPAKGGGTIAPR.L | |

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| |  | | --- | | Top scoring peptide matches to query 738 09MAR16\_OT\_03.01940.01940.3 Score greater than 30 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.0 0.0064 11.3 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  14.8 5.3 -35.33 K.LDLIHESILHKCIK.T  13.7 6.8 28.2 R.QMEQQLFHLSSNLK.E  13.4 7.3 11.3 R.NLNTYTPREIDLNR.R  12.3 9.4 32.8 R.NLDLDKQPMMQLEK.W  11.6 11 -3.33 R.EDDKVPLGTNGHLVPK.E  11.1 12 11.3 K.NNQYNISVVAVDAVGR.S  10.8 14 -16.11 K.LNTKMLQQQINMLK.F  10.8 14 -15.61 R.LTKETSAAVSDQSLLR.A  9.5 18 32.8 R.NLDLDKQPMMQLEK.W | |
| |  | | --- | | Top scoring peptide matches to query 739 09MAR16\_OT\_03.01895.01895.3 Score greater than 31 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  49.4 0.0018 11.4 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  15.7 4.4 -35.22 K.LDLIHESILHKCIK.T  15.1 5 11.4 K.RVSLEPHQGPGTPESK.K  14.2 6.1 32.9 R.NLDLDKQPMMQLEK.W  13.3 7.5 11.4 R.NLNTYTPREIDLNR.R  12.2 9.7 -16.00 K.LNTKMLQQQINMLK.F  11.9 10 -7.40 K.NLSSASQSARGTTGLLR.R  11.5 11 -16.29 K.LPSRPGAQGVEPQNLR.T  11.2 12 32.9 R.NLDLDKQPMMQLEK.W  10.5 14 11.4 K.NNQYNISVVAVDAVGR.S | |

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| |  | | --- | | Top scoring peptide matches to query 740 09MAR16\_OT\_03.01935.01935.3 Score greater than 33 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.0 0.13 11.8 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  18.4 2.4 -34.90 K.LDLIHESILHKCIK.T  18.0 2.5 33.2 R.NLDLDKQPMMQLEK.W  13.2 7.7 33.2 R.NLDLDKQPMMQLEK.W  12.1 9.9 16.3 R.RAVEVLQLAMEGDGSK.A  10.6 14 -22.50 M.ARARPSVAGGGVAAPPER.A  10.4 15 3.66 K.NLDNLFEQVLEVASK.A  10.4 15 22.1 K.KQSLCEVLQAWNSR.L  10.1 16 -2.90 R.EDDKVPLGTNGHLVPK.E  9.7 17 -28.36 K.LNIKYDGVELAMKPK.L | |
| |  | | --- | | Top scoring peptide matches to query 741 09MAR16\_OT\_03.01905.01905.2 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.0 0.0063 11.9 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  10.8 13 -15.85 K.VQIQNASLPHSQQLR.D  10.7 14 33.8 K.DILDQKINEVSSDDK.D  10.2 16 44.2 -.MAEDKTKPSELDQGK.Y  9.6 18 33.8 R.STGPLESSAAEEATQLK.E  8.5 23 -34.79 K.LDLIHESILHKCIK.T  7.4 29 -38.59 K.IQTFLLSSEVNLLNK.I  6.3 38 -17.42 K.EPIVEKPEEPVTVPR.V  6.1 40 37.6 R.AGTLSMKPDLSNEPSR.S  5.8 43 34.5 K.QLTNPYGSWRMHTK.I | |

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| |  | | --- | | Top scoring peptide matches to query 742 09MAR16\_OT\_03.01910.01910.2 Score greater than 32 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.3 0.00076 11.9 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  16.0 4 5.31 R.SPTGRQGQSPGPSPPLR.R  15.4 4.6 -34.79 K.LDLIHESILHKCIK.T  13.8 6.7 -19.37 R.LKTEMTLLQELDLR.T  13.1 7.9 -15.60 R.ATGLSCVTCLVGVLLR.L  12.2 9.7 -2.77 R.VLENNSANYVVDIIR.T  11.6 11 -23.94 K.SLADLQKQFSEILAR.S  10.0 16 37.6 R.AGTLSMKPDLSNEPSR.S  8.9 21 37.6 R.ELDRMLDEVEGQLR.Q  8.5 23 5.23 DFISEPAMWKLPLR | |
| |  | | --- | | Top scoring peptide matches to query 743 09MAR16\_OT\_03.02644.02644.3 Score greater than 26 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.5 1.8 -34.58 K.LDLIHESILHKCIK.T  12.8 8.3 -2.56 K.EVIIVEEQSFQKNR.Y  12.6 8.8 12.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  10.9 13 -22.18 M.ARARPSVAGGGVAAPPER.A  10.8 13 -47.27 K.DLILRTSFVDLWLK.R  10.3 15 -9.11 K.LNKVQYSTRPGVNDK.I  9.2 19 -6.87 K.LLIPVADGMNEVYLR.C  8.8 21 33.5 R.NLDLDKQPMMQLEK.W  8.3 23 28.9 R.NVQLMHASSVLDNFK.E  8.1 25 34.0 K.DILDQKINEVSSDDK.D | |

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| |  | | --- | | Top scoring peptide matches to query 744 09MAR16\_OT\_03.02526.02526.3 Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.9 0.33 12.2 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  23.1 0.78 -34.48 K.LDLIHESILHKCIK.T  15.3 4.7 4.08 K.NLDNLFEQVLEVASK.A  12.3 9.4 -22.08 M.ARARPSVAGGGVAAPPER.A  11.8 11 12.4 K.VKSCSMAPPVDLLTGK.V  11.4 11 16.8 R.RAVEVLQLAMEGDGSK.A  11.3 12 31.0 DLLNHAFFAEDTGLR  10.7 13 -2.47 R.EDDKVPLGTNGHLVPK.E  10.4 15 34.1 K.DILDQKINEVSSDDK.D  9.0 20 12.2 R.NLNTYTPREIDLNR.R | |
| |  | | --- | | Top scoring peptide matches to query 745 09MAR16\_OT\_03.03048.03048.3 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  20.0 1.6 -34.16 K.LDLIHESILHKCIK.T  18.2 2.4 -7.91 K.LDDLVSKSEVLGTQSK.A  14.5 5.6 -2.15 R.EDDKVPLGTNGHLVPK.E  13.4 7.2 -31.43 K.LLLDKGLEDIDTVFK.E  12.6 8.6 -2.63 R.LILLAACTSAAARWAM.-  12.6 8.8 12.5 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  9.0 20 -14.94 K.LNTKMLQQQINMLK.F  8.2 24 -27.61 K.LNIKYDGVELAMKPK.L  8.1 24 -4.10 K.LAIENTMALLGTDGKR.V  7.9 25 19.0 K.INEKPQVIADYESGR.A | |

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| |  | | --- | | Top scoring peptide matches to query 746 09MAR16\_OT\_03.02727.02727.3 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.7 2.7 17.2 R.RAVEVLQLAMEGDGSK.A  14.2 6 -34.05 K.LDLIHESILHKCIK.T  13.8 6.6 34.1 R.NLDLDKQPMMQLEK.W  12.8 8.2 34.1 R.NLDLDKQPMMQLEK.W  10.9 13 12.6 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  9.8 17 -6.34 K.QVDPETMLLPYLRK.K  8.4 23 2.55 QLEMTLIKLQDENK  7.6 28 44.9 R.NDMLQNELIDEQIK.E  7.0 31 17.2 K.LNTQINVKMSPTNDK.Y  7.0 32 -21.65 M.ARARPSVAGGGVAAPPER.A | |
| |  | | --- | | Top scoring peptide matches to query 747 09MAR16\_OT\_03.01898.01898.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  40.4 0.014 12.7 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  20.2 1.5 -33.94 K.LDLIHESILHKCIK.T  17.3 2.9 -1.94 R.EDDKVPLGTNGHLVPK.E  13.6 6.9 34.2 R.NLDLDKQPMMQLEK.W  9.9 16 3.33 R.ARPMMKHPEHIFPK.Q  9.5 18 2.66 QLEMTLIKLQDENK  9.3 19 12.7 R.NLNTYTPREIDLNR.R  9.1 19 6.17 K.ARILPTSDSGPPSQHR.S  8.9 21 34.2 R.NLDLDKQPMMQLEK.W  8.5 22 -6.12 K.NLSSASQSARGTTGLLR.R | |

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| |  | | --- | | Top scoring peptide matches to query 748 09MAR16\_OT\_03.02478.02478.3 Score greater than 22 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  12.3 9.3 -33.84 K.LDLIHESILHKCIK.T  12.0 10 8.52 K.INDAIADQMALFIQR.M  9.2 19 34.3 K.QLAEEKAAMSDAMVPK.A  8.4 23 12.8 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  7.2 30 -1.83 R.EDDKVPLGTNGHLVPK.E  7.0 31 -8.36 K.LNKVQYSTRPGVNDK.I  6.0 40 -21.44 M.ARARPSVAGGGVAAPPER.A  5.3 46 2.77 QLEMTLIKLQDENK  4.8 52 -22.99 R.LNGATLQKFLNAATEK.N  4.5 55 34.3 R.NLDLDKQPMMQLEK.W | | | |
| |  | | --- | | Top scoring peptide matches to query 750 09MAR16\_OT\_03.02594.02594.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.0 0.1 5.25 K.NLDNLFEQVLEVASK.A  22.6 0.87 13.4 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  19.5 1.8 -33.30 K.LDLIHESILHKCIK.T  16.5 3.5 -14.08 K.LNTKMLQQQINMLK.F  16.4 3.6 -45.99 K.DLILRTSFVDLWLK.R  14.9 5.1 32.2 DLLNHAFFAEDTGLR  14.4 5.7 35.3 K.DILDQKINEVSSDDK.D  13.3 7.3 34.8 R.NLDLDKQPMMQLEK.W  13.3 7.3 34.8 R.NLDLDKQPMMQLEK.W  13.3 7.4 23.7 K.KQSLCEVLQAWNSR.L | |

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| |  | | --- | | Top scoring peptide matches to query 751 09MAR16\_OT\_03.01904.01904.3 Score greater than 33 indicates homology Score greater than 35 indicates identity  **Score Expect ppm Hit Protein Peptide**  40.7 0.014 13.7 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  18.3 2.3 -32.98 K.LDLIHESILHKCIK.T  14.5 5.6 -20.58 M.ARARPSVAGGGVAAPPER.A  13.7 6.7 -0.98 R.EDDKVPLGTNGHLVPK.E  13.6 6.9 35.1 R.NLDLDKQPMMQLEK.W  11.9 10 -13.76 K.LNTKMLQQQINMLK.F  10.9 13 -35.22 R.GGIRADLEAGQLILHR.A  9.6 17 -5.16 K.NLSSASQSARGTTGLLR.R  9.2 19 35.1 R.NLDLDKQPMMQLEK.W  9.2 19 13.7 R.NLNTYTPREIDLNR.R | |
| |  | | --- | | Top scoring peptide matches to query 752 09MAR16\_OT\_03.02737.02737.3 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  16.7 3.4 -32.24 K.LDLIHESILHKCIK.T  16.2 3.8 -44.93 K.DLILRTSFVDLWLK.R  11.9 10 14.4 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  10.5 14 -4.53 R.LEPTAPPTMAPGLAQPK.A  9.6 17 10.1 K.INDAIADQMALFIQR.M  9.1 19 -4.42 K.NLSSASQSARGTTGLLR.R  8.1 24 14.7 K.VKDEMLIDLNLQCK.I  8.0 25 21.0 K.INEKPQVIADYESGR.A  7.7 27 10.1 K.VKNGYVNPELAMQGAK.N  7.6 27 25.6 R.LEELKADMEELVQR.E | |

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| |  | | --- | | Top scoring peptide matches to query 753 09MAR16\_OT\_03.02973.02973.3 Score greater than 22 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  9.4 18 -12.48 K.LNTKMLQQQINMLK.F  8.6 21 -31.70 K.LDLIHESILHKCIK.T  7.6 27 15.0 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin NLDIERPTYTNLNR  7.2 30 -5.46 K.LDDLVSKSEVLGTQSK.A  6.8 33 25.3 K.KQSLCEVLQAWNSR.L  5.9 40 4.90 QLEMTLIKLQDENK  5.6 43 36.4 R.NLDLDKQPMMQLEK.W  5.5 44 -44.40 K.DLILRTSFVDLWLK.R  5.5 44 -12.48 K.LNTKMLQQQINMLK.F  5.4 45 8.30 -.SPNIFMQVIHIFSK.L | |
| |  | | --- | | Top scoring peptide matches to query 793 09MAR16\_OT\_03.02516.02516.3 Score greater than 27 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  26.1 0.24 9.81 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  13.0 4.9 10.2 K.SGLDVMPNISDVLLRK.L  12.6 5.4 40.8 K.QNFQKPGNVKNSPGNK.-  12.1 6 5.72 R.GGFALSLLANAEAARAPK.G  8.0 15 18.5 K.IAEWIENASQELLLK.K  5.7 26 48.9 R.QAACCVARPGTPSLLR.F  5.5 28 28.6 K.LFNMDKASAQLLVYK.E  5.0 31 42.9 R.QYPSAVVPATDMRPPK.L  4.7 33 30.9 R.DMVSSAVPLAAVNQNIK.K  4.5 35 27.2 K.NEILDEVISLSQATPK.H | |

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| |  | | --- | | Top scoring peptide matches to query 794 09MAR16\_OT\_03.02569.02569.3 Score greater than 29 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.7 1 10.8 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  18.8 1.2 11.1 K.SGLDVMPNISDVLLRK.L  15.1 2.9 19.5 K.IAEWIENASQELLLK.K  11.8 6.2 19.5 K.ISEWIENAAQELLLK.K  10.9 7.6 28.1 K.NEILDEVISLSQATPK.H  9.2 11 41.7 K.QNFQKPGNVKNSPGNK.-  8.5 13 43.9 R.QYPSAVVPATDMRPPK.L  8.4 14 28.1 K.LLDDNGNIAEELSILK.W  8.4 14 21.7 R.VAELNDVTAKIAAGQEK.H  8.3 14 4.72 R.DLATRNCXVGANLLVK.I | |
| |  | | --- | | Top scoring peptide matches to query 795 09MAR16\_OT\_03.02391.02391.2 Score greater than 25 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  63.0 4.7e-05 11.0 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  8.5 13 32.1 K.LHMSLKVQNDLEVSK.T  3.0 47 -28.13 K.QVLGPLSTPIPVHTAVK.S  1.6 64 42.0 M.DPGVGNALGEGPPAPRPR.R  1.4 68 -13.80 K.NVANTVTISHILPHIK.I  1.1 73 -10.09 R.SNPVPILIPCHRVVR.S  1.0 74 -7.38 K.LLGAERIAAPGYEVGLK.K  0.3 87 -7.38 K.INGIYLTESKAIGHLK.R  0.1 92 48.4 K.IHNDVNSFTINLGQGK.E  0.1 92 23.4 K.KPGDKIYSGPVMSLHK.G | |

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| |  | | --- | | Top scoring peptide matches to query 796 09MAR16\_OT\_03.02394.02394.2 Score greater than 18 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  59.5 0.0001 11.0 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  2.3 56 32.1 K.LHMSLKVQNDLEVSK.T  1.7 63 -7.38 K.INGIYLTESKAIGHLK.R  0.8 77 -13.80 K.NVANTVTISHILPHIK.I | |
| |  | | --- | | Top scoring peptide matches to query 797 09MAR16\_OT\_03.02344.02344.3 Score greater than 28 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.8 0.031 11.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  13.4 4.3 42.0 K.QNFQKPGNVKNSPGNK.-  11.5 6.7 11.4 K.SGLDVMPNISDVLLRK.L  10.2 8.9 21.3 K.LSPHKAPPGEGQGNVIR.N  9.7 10 19.8 K.IAEWIENASQELLLK.K  7.5 17 30.0 R.TLATRSASLLNHNSSGK.E  6.6 20 32.1 K.DCVEVKGLLPTSVSPR.V  6.0 23 -16.05 K.TFRPAIQPLKPPTYK.L  5.5 26 32.2 K.EADALMQQQLLLQQK.Q  4.6 33 46.5 K.QSRTCVGPQLGLTPDK.R | |

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| |  | | --- | | Top scoring peptide matches to query 798 09MAR16\_OT\_03.02354.02354.3 Score greater than 28 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  43.9 0.0038 11.2 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  12.9 4.8 42.1 K.QNFQKPGNVKNSPGNK.-  10.2 8.9 11.5 K.SGLDVMPNISDVLLRK.L  10.2 9 19.9 K.IAEWIENASQELLLK.K  5.8 24 35.6 -.MALTVNVVGPAPWGFR.I  5.3 28 30.0 R.VALCNWAELTPELLK.I  5.0 30 32.3 R.DMVSSAVPLAAVNQNIK.K  4.7 31 46.6 K.QSRTCVGPQLGLTPDK.R  4.7 32 19.5 -.MVAAAAVAVAAVGARSAGR.W  4.6 32 -17.87 R.KGSFLLVLRPSAGLPAM.- | |
| |  | | --- | | Top scoring peptide matches to query 799 09MAR16\_OT\_03.02361.02361.2 Score greater than 27 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  76.9 1.9e-06 11.2 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  9.7 9.9 32.3 K.LHMSLKVQNDLEVSK.T  4.5 33 4.77 K.VKGLIHYINGSFPSPK.I  1.5 66 -27.99 K.QVLGPLSTPIPVHTAVK.S  1.3 69 -19.27 K.QDNLALIKSLNLSLSK.D  1.1 73 17.2 R.QMHHTVVQVEVPKPK.I  1.0 75 -20.04 M.VHLLASEVRQLLHNK.F  0.6 82 42.1 M.DPGVGNALGEGPPAPRPR.R  0.3 86 -7.24 K.INGIYLTESKAIGHLK.R  0.3 88 27.8 K.QLDLQREVLHYSQK.A | |

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| |  | | --- | | Top scoring peptide matches to query 800 09MAR16\_OT\_03.02425.02425.3 Score greater than 28 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  42.6 0.0051 11.6 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  13.0 4.7 42.5 K.QNFQKPGNVKNSPGNK.-  12.5 5.3 20.3 K.IAEWIENASQELLLK.K  10.7 8 12.0 K.SGLDVMPNISDVLLRK.L  9.6 10 32.7 K.DCVEVKGLLPTSVSPR.V  8.8 12 44.7 R.QYPSAVVPATDMRPPK.L  7.9 15 30.4 R.VALCNWAELTPELLK.I  7.6 16 36.9 R.AGVLGETAGGTVGLGPSGTR.G  5.9 24 13.9 R.VPSSTRSVALPPPSSFK.R  5.5 26 29.0 K.NEILDEVISLSQATPK.H | | | |
| |  | | --- | | Top scoring peptide matches to query 801 09MAR16\_OT\_03.02400.02400.2 Score greater than 26 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  68.7 1.3e-05 11.6 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  8.9 12 -13.24 K.NVANTVTISHILPHIK.I  8.7 13 32.7 K.LHMSLKVQNDLEVSK.T  4.7 32 -18.85 K.QDNLALIKSLNLSLSK.D  2.4 54 -6.83 K.INGIYLTESKAIGHLK.R  1.9 60 42.5 K.LALQLHPDRNPDDPR.A  1.6 64 -27.58 K.QVLGPLSTPIPVHTAVK.S  1.0 73 -6.83 K.LLGAERIAAPGYEVGLK.K  0.4 85 10.8 R.GQVLLRFFWNNHLL.-  0.2 88 24.0 K.KPGDKIYSGPVMSLHK.G | |

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| |  | | --- | | Top scoring peptide matches to query 802 09MAR16\_OT\_03.02349.02349.3 Score greater than 29 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.5 0.033 11.7 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  14.0 3.7 12.1 K.SGLDVMPNISDVLLRK.L  13.2 4.5 20.4 K.IAEWIENASQELLLK.K  12.6 5.2 42.6 K.QNFQKPGNVKNSPGNK.-  8.3 14 37.0 R.AGVLGETAGGTVGLGPSGTR.G  7.8 15 48.5 K.FMNGIIIHMPQGVQR.S  7.5 17 32.8 K.DCVEVKGLLPTSVSPR.V  6.4 21 7.60 R.GGFALSLLANAEAARAPK.G  6.2 22 -17.35 R.KGSFLLVLRPSAGLPAM.-  5.6 26 37.0 IERDIDNNLITSTPR | |
| |  | | --- | | Top scoring peptide matches to query 803 09MAR16\_OT\_03.02467.02467.3 Score greater than 26 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  16.5 2.1 11.9 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  12.0 5.8 20.6 K.IAEWIENASQELLLK.K  9.9 9.4 33.0 K.DCVEVKGLLPTSVSPR.V  9.9 9.6 12.3 K.SGLDVMPNISDVLLRK.L  9.1 12 20.6 K.ISEWIENAAQELLLK.K  6.5 21 50.0 R.QLNEADEITEPLTVGK.T  6.4 21 47.3 K.QSRTCVGPQLGLTPDK.R  6.4 21 26.6 K.TKGMSLSEHALSAAVVR.N  5.0 29 43.1 K.CPSGLIMANVETLPVR.A  4.9 30 42.8 K.QNFQKPGNVKNSPGNK.- | |

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| |  | | --- | | Top scoring peptide matches to query 804 09MAR16\_OT\_03.02428.02428.2 Score greater than 29 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  66.7 2e-05 12.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  11.9 6 -12.75 K.NVANTVTISHILPHIK.I  10.3 8.6 33.2 K.LHMSLKVQNDLEVSK.T  2.6 51 3.76 R.LMPHLATALALTFVSR.Y  2.0 58 12.4 K.SGLDVMPNISDVLLRK.L  1.9 60 -27.09 K.QVLGPLSTPIPVHTAVK.S  1.2 70 -6.34 K.LLGAERIAAPGYEVGLK.K  0.8 78 38.8 R.FIHVSHLNASMKSSAK.S  0.7 79 20.8 R.HIEEATELKFLIADK.G  0.6 81 24.5 K.KPGDKIYSGPVMSLHK.G | |
| |  | | --- | | Top scoring peptide matches to query 805 09MAR16\_OT\_03.02390.02390.3 Score greater than 28 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  46.4 0.0021 12.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  13.1 4.6 43.0 K.QNFQKPGNVKNSPGNK.-  11.8 6.1 45.2 R.QYPSAVVPATDMRPPK.L  10.9 7.5 20.8 K.IAEWIENASQELLLK.K  10.4 8.5 12.5 K.SGLDVMPNISDVLLRK.L  7.5 17 -16.93 R.KGSFLLVLRPSAGLPAM.-  6.0 24 33.2 R.DMVSSAVPLAAVNQNIK.K  5.8 24 2.36 R.TSNGGEVGILSAIALIGGK.R  5.3 27 29.5 K.NEILDEVISLSQATPK.H  4.8 31 8.02 R.GGFALSLLANAEAARAPK.G | |

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| |  | | --- | | Top scoring peptide matches to query 806 09MAR16\_OT\_03.02432.02432.3 Score greater than 27 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.0 0.018 12.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  12.5 5.2 43.0 K.QNFQKPGNVKNSPGNK.-  12.1 5.7 12.5 K.SGLDVMPNISDVLLRK.L  6.6 20 24.5 R.LLAIPGGYPAAAVLCDR.L  5.4 27 22.3 K.LSPHKAPPGEGQGNVIR.N  4.6 32 20.8 K.IAEWIENASQELLLK.K  4.0 36 -16.93 R.KGSFLLVLRPSAGLPAM.-  3.6 40 33.2 R.DMVSSAVPLAAVNQNIK.K  3.5 41 33.2 K.DCVEVKGLLPTSVSPR.V  2.9 47 20.8 K.ISEWIENAAQELLLK.K | |
| |  | | --- | | Top scoring peptide matches to query 807 09MAR16\_OT\_03.02418.02418.3 Score greater than 29 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  50.3 0.00087 12.2 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  13.2 4.5 20.9 K.IAEWIENASQELLLK.K  13.1 4.5 43.2 K.QNFQKPGNVKNSPGNK.-  11.5 6.6 12.6 K.SGLDVMPNISDVLLRK.L  8.1 14 33.3 K.DCVEVKGLLPTSVSPR.V  8.0 15 45.3 R.QYPSAVVPATDMRPPK.L  5.8 24 -16.83 R.KGSFLLVLRPSAGLPAM.-  5.0 29 33.3 R.DMVSSAVPLAAVNQNIK.K  4.8 31 29.6 K.NEILDEVISLSQATPK.H  4.1 36 -14.91 K.TFRPAIQPLKPPTYK.L | |

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| |  | | --- | | Top scoring peptide matches to query 808 09MAR16\_OT\_03.02357.02357.2 Score greater than 27 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  84.6 3.2e-07 12.3 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  9.1 11 33.4 K.LHMSLKVQNDLEVSK.T  5.4 27 -6.13 K.LLGAERIAAPGYEVGLK.K  1.8 61 -26.88 K.QVLGPLSTPIPVHTAVK.S  1.6 63 26.6 K.LQNIERGNLYFVYK.F  1.0 74 33.0 R.HLVTLSNTVFTFSYK.K  0.7 78 49.6 K.IHNDVNSFTINLGQGK.E  0.7 78 -6.13 K.LHGIAKSETLYIGNIK.V  0.5 82 -6.13 K.INGIYLTESKAIGHLK.R  0.3 86 26.6 K.RFLGSGGFIGYAPSLSK.L | |
| |  | | --- | | Top scoring peptide matches to query 809 09MAR16\_OT\_03.02378.02378.3 Score greater than 28 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.8 0.049 12.3 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  13.2 4.5 43.3 K.QNFQKPGNVKNSPGNK.-  10.4 8.5 12.7 K.SGLDVMPNISDVLLRK.L  8.8 12 21.0 K.IAEWIENASQELLLK.K  5.6 25 29.7 K.NEILDEVISLSQATPK.H  5.0 29 33.4 R.DMVSSAVPLAAVNQNIK.K  4.8 30 -16.72 R.KGSFLLVLRPSAGLPAM.-  4.7 31 22.5 K.LSPHKAPPGEGQGNVIR.N  4.5 33 8.22 K.RPAGFLEGSEPSKLLR.L  3.7 40 21.0 K.ISEWIENAAQELLLK.K | |

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| |  | | --- | | Top scoring peptide matches to query 810 09MAR16\_OT\_03.02367.02367.2 Score greater than 24 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  57.9 0.00015 12.4 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  8.0 15 33.5 K.LHMSLKVQNDLEVSK.T  6.1 23 -12.47 K.NVANTVTISHILPHIK.I  3.2 45 -26.81 K.QVLGPLSTPIPVHTAVK.S  0.9 76 -8.76 R.SNPVPILIPCHRVVR.S  0.7 78 -6.06 K.INGIYLTESKAIGHLK.R  0.2 89 24.8 K.KPGDKIYSGPVMSLHK.G | |
| |  | | --- | | Top scoring peptide matches to query 811 09MAR16\_OT\_03.02384.02384.3 Score greater than 31 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  35.5 0.025 12.8 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  15.8 2.4 43.8 K.QNFQKPGNVKNSPGNK.-  9.9 9.1 21.5 K.IAEWIENASQELLLK.K  9.8 9.4 13.2 K.SGLDVMPNISDVLLRK.L  5.7 24 33.9 K.DCVEVKGLLPTSVSPR.V  5.3 27 -16.20 R.KGSFLLVLRPSAGLPAM.-  4.9 29 46.0 R.QYPSAVVPATDMRPPK.L  4.8 30 33.9 R.DMVSSAVPLAAVNQNIK.K  4.2 34 8.75 R.GGFALSLLANAEAARAPK.G  4.2 35 23.0 K.LSPHKAPPGEGQGNVIR.N | |

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| |  | | --- | | Top scoring peptide matches to query 812 09MAR16\_OT\_03.02434.02434.2 Score greater than 24 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  79.3 1.1e-06 12.8 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  6.1 22 29.4 K.AGLAEAPLVTGQPGPGHGK.K  4.0 36 25.2 K.KPGDKIYSGPVMSLHK.G  2.9 46 33.9 K.LHMSLKVQNDLEVSK.T  1.8 60 -26.33 K.QVLGPLSTPIPVHTAVK.S  1.6 63 -17.60 K.QDNLALIKSLNLSLSK.D  1.4 65 4.52 R.LMPHLATALALTFVSR.Y  0.9 74 0.05 R.LHQIFALFNRVAEAK.S  0.8 74 -5.58 K.LLGAERIAAPGYEVGLK.K  0.8 76 -5.58 K.INGIYLTESKAIGHLK.R | |
| |  | | --- | | Top scoring peptide matches to query 813 09MAR16\_OT\_03.02439.02439.2 Score greater than 27 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  60.4 8.3e-05 13.1 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  10.6 7.9 46.2 R.QYPSAVVPATDMRPPK.L  10.5 8 34.2 K.LHMSLKVQNDLEVSK.T  5.3 27 25.5 K.KPGDKIYSGPVMSLHK.G  5.2 27 44.1 K.QNFQKPGNVKNSPGNK.-  3.6 40 4.80 R.LMPHLATALALTFVSR.Y  2.2 54 -17.32 K.QDNLALIKSLNLSLSK.D  1.6 63 29.7 K.AGLAEAPLVTGQPGPGHGK.K  1.4 65 42.1 R.AGDGLRALAAEGQMQLR.T  0.6 78 44.8 R.DPGQGPTAVVTTVKSGDK.D | |

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| |  | | --- | | Top scoring peptide matches to query 814 09MAR16\_OT\_03.02566.02566.3 Score greater than 24 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  21.6 0.62 13.9 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  10.5 8.1 44.8 K.QNFQKPGNVKNSPGNK.-  6.6 20 47.0 R.QYPSAVVPATDMRPPK.L  5.5 25 22.6 K.IAEWIENASQELLLK.K  4.6 31 32.7 K.LFNMDKASAQLLVYK.E  4.6 31 22.6 K.ISEWIENAAQELLLK.K  3.8 38 16.2 R.ELDQQKLWLQQSIK.N  3.5 40 15.4 K.GNVAHKHWLGPSNLVK.C  3.5 40 14.2 K.SGLDVMPNISDVLLRK.L  3.5 41 -15.16 R.KGSFLLVLRPSAGLPAM.- | |
| |  | | --- | | Top scoring peptide matches to query 815 09MAR16\_OT\_03.02459.02459.3 Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.7 0.048 14.4 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  17.8 1.5 14.8 K.SGLDVMPNISDVLLRK.L  8.9 12 23.1 K.IAEWIENASQELLLK.K  7.4 16 31.8 K.NEILDEVISLSQATPK.H  4.9 29 45.3 K.QNFQKPGNVKNSPGNK.-  4.3 33 24.9 K.LRLSVHMLILDDGMK.N  4.3 33 -14.64 R.KGSFLLVLRPSAGLPAM.-  3.6 39 23.1 K.ISEWIENAAQELLLK.K  3.6 39 20.4 R.QMHHTVVQVEVPKPK.I  3.1 43 39.2 R.EALRICSMPPGVISAR.L | |

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| |  | | --- | | Top scoring peptide matches to query 816 09MAR16\_OT\_03.02465.02465.3 Score greater than 26 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  22.3 0.53 14.5 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  12.0 5.6 45.4 K.QNFQKPGNVKNSPGNK.-  11.1 7 23.2 K.IAEWIENASQELLLK.K  11.0 7.1 35.6 K.DCVEVKGLLPTSVSPR.V  10.8 7.4 47.6 R.QYPSAVVPATDMRPPK.L  10.4 8.1 14.9 K.SGLDVMPNISDVLLRK.L  8.4 13 33.4 K.EGLSNQLRVQTEINR.E  6.2 21 -14.53 R.KGSFLLVLRPSAGLPAM.-  5.8 24 23.2 K.ISEWIENAAQELLLK.K  5.2 27 33.4 R.TLATRSASLLNHNSSGK.E | |
| |  | | --- | | Top scoring peptide matches to query 817 09MAR16\_OT\_03.02500.02500.3 Score greater than 26 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  16.3 2 14.6 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  12.2 5.3 23.3 K.IAEWIENASQELLLK.K  7.8 14 23.3 K.ISEWIENAAQELLLK.K  7.3 16 45.5 K.QNFQKPGNVKNSPGNK.-  6.8 18 15.0 K.SGLDVMPNISDVLLRK.L  5.1 27 10.5 R.GGFALSLLANAEAARAPK.G  4.3 32 -14.43 R.KGSFLLVLRPSAGLPAM.-  4.2 33 49.7 K.DRPKDWSEVTIWPK.A  4.1 34 4.09 R.RPITPPTHGTSLVQPR.Q  3.5 39 -0.10 R.ILGALPSMNAAIPHVPR.Y | |

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| |  | | --- | | Top scoring peptide matches to query 818 09MAR16\_OT\_03.02504.02504.3 Score greater than 26 indicates homology Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  18.0 1.3 17.7 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin R.IHFPLATYAPVISAEK.A  12.0 5.2 26.0 -.MVAAAAVAVAAVGARSAGR.W  11.0 6.6 38.8 K.DCVEVKGLLPTSVSPR.V  10.2 7.9 18.1 K.SGLDVMPNISDVLLRK.L  5.8 22 26.4 K.IAEWIENASQELLLK.K  5.7 22 48.7 K.QNFQKPGNVKNSPGNK.-  5.1 26 -11.30 R.KGSFLLVLRPSAGLPAM.-  3.9 33 49.4 R.QSAPTAQAASTGLSPELK.E  3.9 34 26.4 K.ISEWIENAAQELLLK.K  3.8 34 42.6 R.EALRICSMPPGVISAR.L | |
| |  | | --- | | Top scoring peptide matches to query 828 09MAR16\_OT\_03.02105.02105.3 Score greater than 32 indicates identity  **Score Expect ppm Hit Protein Peptide**  57.3 0.00015 11.5 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.GNTALHIASLAGQAEVVK.V  17.2 1.6 38.2 R.DTYLDTQIVGQTGVIR.S  11.7 5.5 46.4 K.DGSTMLIMLEQQLRK.G  8.9 10 7.59 R.TILKIPMTEMMTILK.T  8.9 10 7.59 R.TILKIPMTEMMTILK.T  8.0 13 35.2 R.GALIHNVSKEPGGWWK.G  7.6 14 36.0 FVWLIGDQEDTTVKK  7.2 16 25.6 R.RPTLPGGSEGPGVDGRVK.K  6.2 20 37.5 K.SWAQLSGKPVGHEGGLR.G  5.6 22 17.3 R.MVMLGTQLTGRLPFSK.V | |

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| |  | | --- | | Top scoring peptide matches to query 843 09MAR16\_OT\_03.02364.02364.3 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  47.8 0.0025 11.0 12 sp|P16086|SPTA2\_RAT|Spectrin K.GRELPTAFDYVEFTR.S  15.4 4.5 -41.18 K.IPNVVQTTNKPGLYEK.L  9.6 17 -20.99 R.GLDHLNVTVGVDGTLYK.L  9.4 18 1.40 K.LDGSYEMELLNLYLK.T  9.0 20 -2.63 R.QLLQEEVGPVGVETMR.Q  8.4 22 33.4 R.LHADGKAEEEGGSPFTR.T  8.2 23 25.7 K.GEADALSLDGGYIYTAGK.C  8.2 24 47.3 R.MFEAGDYDSPNWKLK.Y  7.4 28 -47.43 K.GPGVLQNLFQLNGSTKK.L  7.2 29 17.6 K.LLAEAAGDGPPASRVTEM.- | |
| |  | | --- | | Top scoring peptide matches to query 844 09MAR16\_OT\_03.02373.02373.3 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  54.0 0.00061 11.5 12 sp|P16086|SPTA2\_RAT|Spectrin K.GRELPTAFDYVEFTR.S  11.8 10 -2.12 R.QLLQEEVGPVGVETMR.Q  9.3 18 25.7 K.EMFPIIGQYGDMLVR.N  9.2 18 33.9 R.LHADGKAEEEGGSPFTR.T  9.0 19 -0.97 K.YNHHTAKNSIFELAR.G  8.3 23 -40.67 K.IPNVVQTTNKPGLYEK.L  8.1 24 46.0 K.ECYVFKPKNPDMEK.D  8.1 24 11.5 K.EDLRFNDFIVYDVR.L  7.6 27 -2.85 K.ERHAGTPLYLGATAGMR.L  7.5 28 26.2 K.GEADALSLDGGYIYTAGK.C | |

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| |  | | --- | | Top scoring peptide matches to query 845 09MAR16\_OT\_03.02366.02366.3 Score greater than 26 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  50.0 0.0015 11.9 12 sp|P16086|SPTA2\_RAT|Spectrin K.GRELPTAFDYVEFTR.S  10.5 14 34.4 R.LHADGKAEEEGGSPFTR.T  9.7 16 42.0 R.FKCEDHFSPTTYLR.G  9.2 19 -44.28 R.GIASIQEGGVTVSARTVR.Q  8.8 20 -34.77 K.GYRVQLGVIYYTNVR.V  8.8 20 -7.96 K.GMINDLLGQGAVDQLTR.L  8.6 21 -1.72 R.QLLQEEVGPVGVETMR.Q  8.5 22 11.9 K.EDLRFNDFIVYDVR.L  8.0 24 46.4 K.ECYVFKPKNPDMEK.D  8.0 24 -26.28 R.SYVNRSPSPNVKPVEK.F | |
| |  | | --- | | Top scoring peptide matches to query 849 09MAR16\_OT\_03.02208.02208.3 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  47.1 0.0026 11.1 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.LGYTPLIVACHYGNVK.M  9.6 15 23.1 R.AHILYEMLAGCVQRK.D  7.8 22 -15.97 R.ALSDATEELTVIKSSLK.D  7.7 23 17.7 R.NRVSEELIMVVQEMK.K  5.2 40 27.2 R.RPRPALPGGGAADGPGLDM.-  5.1 41 15.9 K.VVYVVIGDGVEEEQAAK.K  4.5 47 38.3 K.QLQESQTSGDVKVEEK.L  4.3 50 23.9 K.IEEISCNKLVDPLMK.Q  3.0 66 32.1 R.SNDQLDDSSNILKSIR.K  2.5 74 35.7 R.RSQLMQNEGQLSELR.T | |

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| |  | | --- | | Top scoring peptide matches to query 850 09MAR16\_OT\_03.02201.02201.3 Score greater than 26 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  51.5 0.00092 11.6 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.LGYTPLIVACHYGNVK.M  10.7 11 32.6 R.SNDQLDDSSNILKSIR.K  8.7 18 23.7 R.AHILYEMLAGCVQRK.D  5.7 36 -21.68 R.LLSATSALETNQSKLTK.V  4.5 47 4.23 R.VMAGKVEMTLEILNEK.E  3.2 64 -15.46 R.ALSDATEELTVIKSSLK.D  2.8 69 -9.98 K.LPFSLKSQSNTDQLVK.D  2.4 75 28.5 K.LVNTQDMSASQVDVAVK.I  2.3 77 26.3 R.ADYIIELPEAEIICR.Q  2.3 77 18.2 R.LINEMGGMQQVTDLKK.W | |
| |  | | --- | | Top scoring peptide matches to query 851 09MAR16\_OT\_03.02194.02194.3 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.0 0.017 11.9 6 sp|Q8C8R3|ANK2\_MOUSE|Ankyrin-2 K.LGYTPLIVACHYGNVK.M  9.7 14 32.9 R.SNDQLDDSSNILKSIR.K  8.7 18 24.0 R.AHILYEMLAGCVQRK.D  7.9 21 22.6 K.ERLTAMTIDLEAQAAR.L  6.1 32 10.0 R.FINMLLGHMSIEVLR.E  6.0 33 24.7 R.HEMLSMEISILQTLK.F  4.1 50 4.54 R.VMAGKVEMTLEILNEK.E  4.0 52 -6.05 FLELMKPIDRGISNR  3.5 59 -15.90 K.IYGNNTALTTLNQLIR.G  3.0 65 24.7 K.IEEISCNKLVDPLMK.Q | |

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| |  | | --- | | Top scoring peptide matches to query 859 09MAR16\_OT\_03.01713.01713.2 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  65.6 4e-05 10.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.EIVHIQAGQCGNQIGAK.F  65.6 4e-05 10.6 4+ sp|Q3MHM5|TBB2C\_BOVIN|Tubulin R.EIVHLQAGQCGNQIGAK.F  12.6 7.8 44.7 K.VMMETQQQEMANVRK.S  10.1 14 44.7 K.KVMMETQQQEMANVR.K  7.3 27 2.98 R.IFTVAQVDDNSVQMKK.D  7.0 29 -20.57 R.GSESGLFLDVSTIEIKK.G  6.7 31 -1.32 K.QFNRNLSEFGLIQEK.F  4.7 49 -9.34 R.KMQVSHLPQSAVNVER.L  4.1 57 36.4 R.YEHTFLKSEFEHQK.E  3.5 65 32.7 K.KLEEMSCQVLQWQK.Q | |
| |  | | --- | | Top scoring peptide matches to query 860 09MAR16\_OT\_03.01724.01724.2 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  68.0 2.3e-05 11.0 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.EIVHIQAGQCGNQIGAK.F  68.0 2.3e-05 11.0 4+ sp|Q3MHM5|TBB2C\_BOVIN|Tubulin R.EIVHLQAGQCGNQIGAK.F  12.0 9 45.0 K.VMMETQQQEMANVRK.S  9.3 17 45.0 K.KVMMETQQQEMANVR.K  7.6 25 -5.06 K.DWRYVAMLLLQGDVK.R  6.4 33 -20.23 R.GSESGLFLDVSTIEIKK.G  5.0 46 3.31 R.IFTVAQVDDNSVQMKK.D  4.4 52 33.0 K.KLEEMSCQVLQWQK.Q  3.5 64 -10.48 M.SLTKTEGTIIVSMWAK.I  2.3 84 36.7 R.YEHTFLKSEFEHQK.E | |

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| |  | | --- | | Top scoring peptide matches to query 861 09MAR16\_OT\_03.01719.01719.2 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  64.7 4.9e-05 11.2 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.EIVHIQAGQCGNQIGAK.F  64.7 4.9e-05 11.2 4+ sp|Q3MHM5|TBB2C\_BOVIN|Tubulin R.EIVHLQAGQCGNQIGAK.F  12.6 7.9 45.3 K.VMMETQQQEMANVRK.S  10.4 13 45.3 K.KVMMETQQQEMANVR.K  7.6 25 -19.96 R.GSESGLFLDVSTIEIKK.G  6.4 33 -4.79 K.DWRYVAMLLLQGDVK.R  5.9 37 -0.72 K.QFNRNLSEFGLIQEK.F  5.3 43 3.58 R.IFTVAQVDDNSVQMKK.D  1.9 93 7.65 K.NLDVDKGQEHAEVLQK.I  1.9 93 13.8 K.FSGTILNVPDTSDNSKK.Q | |
| |  | | --- | | Top scoring peptide matches to query 862 09MAR16\_OT\_03.01706.01706.3 Score greater than 33 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  60.0 0.00014 11.9 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.EIVHIQAGQCGNQIGAK.F  60.0 0.00014 11.9 4+ sp|Q3MHM5|TBB2C\_BOVIN|Tubulin R.EIVHLQAGQCGNQIGAK.F  16.6 3.2 -0.02 K.QFNRNLSEFGLIQEK.F  11.8 9.4 23.5 R.FRLQNGSSSGWPIMAR.E  9.2 17 4.28 K.VETIGDAYMVASGLPKR.N  9.2 17 24.3 K.VETIGDAYMVASGLPQR.N  9.2 17 18.1 R.IELQRSPPPNADPNMK.L  7.5 26 46.0 K.KVMMETQQQEMANVR.K  7.4 26 -23.23 R.KLSSTGISTSSLQLSGTR.V  7.1 28 2.43 R.AAVQTTCDLMSLVAKAK.E | |

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| |  | | --- | | Top scoring peptide matches to query 863 09MAR16\_OT\_03.01712.01712.3 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  59.3 0.00017 12.8 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.EIVHIQAGQCGNQIGAK.F  59.3 0.00017 12.8 4+ sp|Q3MHM5|TBB2C\_BOVIN|Tubulin R.EIVHLQAGQCGNQIGAK.F  14.3 5.3 0.88 K.QFNRNLSEFGLIQEK.F  12.6 7.8 24.4 R.FRLQNGSSSGWPIMAR.E  10.9 12 -22.32 R.KLSSTGISTSSLQLSGTR.V  9.6 16 -6.75 R.SWELFLSNVTKEIEK.A  8.1 22 3.00 EIYELARIMEPSPFK  6.0 36 46.9 K.KVMMETQQQEMANVR.K  5.8 38 20.9 K.SHLHPFKEAAQEVDSK.L  5.1 44 32.8 R.AGSGVCVNGAVFGTGGGSLR.G | |
| |  | | --- | | Top scoring peptide matches to query 864 09MAR16\_OT\_03.01718.01718.3 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  58.4 0.00021 13.0 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.EIVHIQAGQCGNQIGAK.F  58.4 0.00021 13.0 4+ sp|Q3MHM5|TBB2C\_BOVIN|Tubulin R.EIVHLQAGQCGNQIGAK.F  14.7 4.9 1.08 K.QFNRNLSEFGLIQEK.F  11.5 10 24.6 R.FRLQNGSSSGWPIMAR.E  11.4 10 47.1 K.KVMMETQQQEMANVR.K  10.6 12 -22.12 R.KLSSTGISTSSLQLSGTR.V  9.7 15 -18.16 R.GSESGLFLDVSTIEIKK.G  9.5 16 -6.55 R.SWELFLSNVTKEIEK.A  7.5 25 -4.35 K.NIQSIFQSSSVDLEKK.D  6.8 30 3.20 EIYELARIMEPSPFK | |

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| |  | | --- | | Top scoring peptide matches to query 874 09MAR16\_OT\_03.02154.02154.2 Score greater than 26 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  47.7 0.0027 11.0 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin YMACCLLYRGDVVPK  11.0 12 -16.13 R.IGSALMIETARNPACPK.V  6.8 33 -40.50 K.FRTSLEHGFWGVLAPK.I  6.7 34 -20.42 R.EGQSRPAVCRVFDVPK.R  6.7 34 -21.86 R.ELKDQGPPPSFLELMK.V  4.6 54 -16.14 K.QNEAMDTGLLLCRPVK.S  4.4 57 -10.30 R.EGGENKALLSYVGQHSR.Q  2.8 82 -6.39 K.QALEEQFNEWVLNPK.G  2.6 86 -4.59 K.RSVSGNNRPMVQPSSGR.N  2.6 87 -6.05 K.ENVGKATATPVTPEMQR.V | |
| |  | | --- | | Top scoring peptide matches to query 875 09MAR16\_OT\_03.02150.02150.3 Score greater than 22 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  23.1 0.77 11.6 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin YMACCLLYRGDVVPK  8.6 22 -19.48 R.FFIGGSLELEDLSYVR.I  7.2 30 4.14 R.GHKAEAQVVMMGLDSAGK.T  5.6 43 49.7 R.LAEQAERYDDMASAMK.A  5.5 44 27.8 K.MVEVDIYESGKHFMK.G  4.8 52 29.2 R.YMDGHHVKDISCLNR.D  4.8 52 49.7 -.MSSLEISNSCFSPETR.S  4.4 56 10.2 R.GNVMTKCVYTNSDLVK.A  4.4 57 -9.74 R.HRTETPYEAVQSSALR.I  4.2 59 29.6 R.FFEHFGDLSTADAIMK.N | |

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| |  | | --- | | Top scoring peptide matches to query 876 09MAR16\_OT\_03.02144.02144.3 Score greater than 21 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  22.5 0.88 11.6 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin YMACCLLYRGDVVPK  6.8 32 26.0 R.EYVMSMGVCPVSSSALK.Y  6.2 37 4.14 R.GHKAEAQVVMMGLDSAGK.T  5.7 42 16.1 YDGAETPEVTHVGDAKR  5.3 46 49.7 -.MSSLEISNSCFSPETR.S  4.4 57 29.2 R.YMDGHHVKDISCLNR.D  4.0 62 30.0 R.SQAEARQLMEYDLMK.K  3.8 65 -11.93 R.AEQDAFIHGPQLSYLR.L  3.4 71 -23.87 K.VGKLQLHQGMFPQAMK.N  3.3 74 -19.48 R.FFIGGSLELEDLSYVR.I | |
| |  | | --- | | Top scoring peptide matches to query 877 09MAR16\_OT\_03.02156.02156.3 Score greater than 20 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.0 0.19 12.2 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin YMACCLLYRGDVVPK  6.0 38 28.4 K.MVEVDIYESGKHFMK.G  6.0 39 4.74 R.GHKAEAQVVMMGLDSAGK.T  4.9 50 29.8 R.YMDGHHVKDISCLNR.D  4.8 51 30.6 R.SQAEARQLMEYDLMK.K  4.3 58 -11.33 R.AEQDAFIHGPQLSYLR.L  3.8 64 -23.27 K.VGKLQLHQGMFPQAMK.N  3.5 68 44.2 R.NDANCIHMVDNGIVEK.L  3.5 69 -18.89 R.FFIGGSLELEDLSYVR.I  3.2 74 26.6 R.EYVMSMGVCPVSSSALK.Y | |

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| |  | | --- | | Top scoring peptide matches to query 878 09MAR16\_OT\_03.02067.02067.3 Score greater than 20 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  17.1 2.9 11.2 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin YMACCLLYRGDVVPK  6.2 36 -25.23 -.MELQSRSEALAVELAR.H  5.9 38 -43.83 K.WAFIGVPYVSLLCAHK.K  4.9 48 1.68 K.VIPACLPSQDFMVPDR.T  4.1 57 25.5 R.SGTFCLADTCLLLMDK.R  2.5 84 -23.90 R.VMLACALYLSHKPDAR.L  2.1 91 19.4 K.KLLMMAGIDDCYTSAR.G  1.9 95 -49.03 K.RPGASVELVEYLESRR.R  1.9 95 23.3 R.YPEPMTPDTMMKLYK.E  1.6 1e+02 -49.51 R.VMAVPFNRRPEILMR.I | |
| |  | | --- | | Top scoring peptide matches to query 879 09MAR16\_OT\_03.02062.02062.3 Score greater than 18 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  22.9 0.76 11.5 3 sp|Q2HJ86|TBA1D\_BOVIN|Tubulin YMACCLLYRGDVVPK  3.7 63 25.8 R.SGTFCLADTCLLLMDK.R  2.5 83 -23.61 R.VMLACALYLSHKPDAR.L  2.3 87 1.97 K.VIPACLPSQDFMVPDR.T  2.1 90 -48.73 K.RPGASVELVEYLESRR.R  2.1 91 2.08 K.MSGNRVASQGSGLHQSTK.V  2.0 94 -32.43 R.IMEVNELTDAELKNLI.-  1.9 96 -0.06 R.NEPPLAPRMEAPGHNSK.R  1.9 96 19.7 K.KLLMMAGIDDCYTSAR.G  1.8 99 -15.41 K.KGPIMQSGLGGAGCAELAK.Q | |

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| |  | | --- | | Top scoring peptide matches to query 886 09MAR16\_OT\_03.01944.01944.3 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.7 0.0094 11.2 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  14.4 5 -0.18 K.IIVYGTNTHPDTDVGLR.G  11.3 10 -25.73 R.LLVESAKFFAVMFPQK.S  11.2 10 -13.62 R.LLVEGNKELTVEHFDK.N  9.0 18 -21.75 K.ARKPLEALYGYDYLAK.T  7.8 23 43.6 K.LGGHWKPSDCMPRWK.V  7.5 25 15.4 -.MAPSVPAAEPEYPKGIR.A  7.2 26 -16.14 K.NLVKIFEPCGRPAVDR.L  7.2 26 -44.37 R.NLVTEVLGALEAKTGVEK.R  7.0 27 -47.23 R.LLVARAAGPEAAWLTFGK.D | |
| |  | | --- | | Top scoring peptide matches to query 887 09MAR16\_OT\_03.01917.01917.2 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  91.4 1e-07 11.3 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  14.2 5.3 25.0 K.NPFTTMLVFSTAAMAPR.A  7.6 24 36.7 R.MVWEQRSATIVMMTR.L  6.5 31 36.7 R.MVWEQRSATIVMMTR.L  6.1 34 20.8 K.WIVGQPLHAFANNMEK.F  5.5 39 45.9 R.DYSLTCRNHALHMPR.G  4.6 48 27.2 R.IYAVATSGMRLSDMSPR.S  4.3 51 -47.08 K.ALPVPHFLQGAVPKGDPK.H  3.7 59 -44.92 R.QGTLLPHNAPLKETVPR.V  3.2 67 20.8 K.LWLQAQAHIENCYPK.V | |

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| |  | | --- | | Top scoring peptide matches to query 888 09MAR16\_OT\_03.01906.01906.3 Score greater than 32 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.3 0.026 11.8 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  17.5 2.5 0.50 K.IIVYGTNTHPDTDVGLR.G  10.9 11 23.4 K.DMGLLVGRGGNFSQTFR.I  9.6 15 -25.05 R.LLVESAKFFAVMFPQK.S  8.1 21 -28.90 R.IDVIVQNLKQMWLDR.E  8.1 21 -28.90 R.IDVLVQNLKQMWLDR.E  7.4 25 -21.07 K.ARKPLEALYGYDYLAK.T  6.7 30 9.55 K.MPVCIMNNFLPLHIR.R  6.4 32 -43.68 R.NLVTEVLGALEAKTGVEK.R  6.3 33 2.57 K.ITNSSFVLIPFKDMDK.Q | |
| |  | | --- | | Top scoring peptide matches to query 889 09MAR16\_OT\_03.01908.01908.2 Score greater than 27 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide** 106.0 3.5e-09 11.8 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  8.4 20 25.5 K.NPFTTMLVFSTAAMAPR.A  6.2 33 -1.29 R.ILEVPGTGEVQLTCQAR.G  5.6 38 -46.56 K.ALPVPHFLQGAVPKGDPK.H  5.5 39 14.0 R.FLGENTNRATLNYTTR.E  5.2 42 37.2 R.MVWEQRSATIVMMTR.L  4.9 45 46.4 R.DYSLTCRNHALHMPR.G  4.9 45 -44.39 R.QGTLLPHNAPLKETVPR.V  4.7 47 35.5 K.YESGHVPMPPNTVLSDK.D  4.7 48 -19.65 R.GGRAAPGPPPPPPPPGQAPR.W | |

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| |  | | --- | | Top scoring peptide matches to query 890 09MAR16\_OT\_03.01901.01901.3 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  48.8 0.0018 11.9 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  15.6 3.8 0.60 K.IIVYGTNTHPDTDVGLR.G  11.4 10 -24.95 R.LLVESAKFFAVMFPQK.S  11.3 10 -12.83 R.LLVEGNKELTVEHFDK.N  10.6 12 -14.99 R.NLISTFVLDFEFNLAK.L  9.0 17 -20.97 K.ARKPLEALYGYDYLAK.T  8.3 20 18.3 K.QVASSYSRMASILASGDK.I  8.0 22 12.3 M.NTELVAMEPGVSRNGVR.T  7.8 23 44.4 K.LGGHWKPSDCMPRWK.V  7.3 26 -15.35 K.NLVKIFEPCGRPAVDR.L | |
| |  | | --- | | Top scoring peptide matches to query 891 09MAR16\_OT\_03.01894.01894.3 Score greater than 25 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.7 0.015 11.9 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  10.4 13 -24.95 R.LLVESAKFFAVMFPQK.S  8.8 18 -28.80 R.IDVIVQNLKQMWLDR.E  8.8 18 -28.80 R.IDVLVQNLKQMWLDR.E  8.5 20 9.65 K.MPVCIMNNFLPLHIR.R  8.1 22 -20.97 K.ARKPLEALYGYDYLAK.T  7.0 28 -1.20 R.ILEVPGTGEVQLTCQAR.G  7.0 28 -43.59 R.NLVTEVLGALEAKTGVEK.R  6.7 29 43.8 K.VLLEMEDQRSSYEQK.A  5.9 36 0.60 K.IIVYGTNTHPDTDVGLR.G | |

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| |  | | --- | | Top scoring peptide matches to query 892 09MAR16\_OT\_03.01938.01938.3 Score greater than 24 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  43.9 0.0057 11.9 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  8.7 19 0.60 K.IIVYGTNTHPDTDVGLR.G  5.1 43 8.33 R.LNANVMLLLHNSEQMK.A  4.9 45 -43.59 R.NLVTEVLGALEAKTGVEK.R  4.6 48 -28.80 R.IDVIVQNLKQMWLDR.E  4.6 48 -28.80 R.IDVLVQNLKQMWLDR.E  4.5 49 14.0 K.VFDKYMLIGHVEEFK.E  4.2 53 -15.35 K.LIIQWNXPESNRMVR.L  4.0 55 -24.95 R.LLVESAKFFAVMFPQK.S  4.0 56 -15.35 K.NLVKIFEPCGRPAVDR.L | |
| |  | | --- | | Top scoring peptide matches to query 893 09MAR16\_OT\_03.01911.01911.2 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  91.5 9.9e-08 12.4 1 sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.INVYYNEAAGNKYVPR.A  12.4 8 -43.81 R.QGTLLPHNAPLKETVPR.V  7.8 23 37.8 R.MVWEQRSATIVMMTR.L  6.8 29 26.1 K.NPFTTMLVFSTAAMAPR.A  6.6 30 -0.70 R.ILEVPGTGEVQLTCQAR.G  6.6 31 37.8 R.MVWEQRSATIVMMTR.L  5.0 44 47.0 R.DYSLTCRNHALHMPR.G  4.9 45 -28.31 K.LGHTQVLKESMIFVPR.Q  4.5 49 14.6 R.FLGENTNRATLNYTTR.E  4.5 50 16.6 K.LLDCSTEIKGFHEPPK.L | |

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| |  | | --- | | Top scoring peptide matches to query 905 09MAR16\_OT\_03.01936.01936.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.1 0.0041 10.7 8 sp|P23565|AINX\_RAT|Alpha-internexin M.SFGSEHYLCSASSYRK.V  37.9 0.017 10.7 18 sp|Q08DH7|AINX\_BOVIN|Alpha-internexin M.SFGSEHYLCASSSYRK.V  6.3 25 -13.84 K.EMSEMLQLCSYVRFK.V  4.0 42 2.77 K.EGFSFINDWNNMYRK.W  4.0 42 23.7 R.CLMNECHRELCNLR.S  2.5 59 -49.21 K.MAGLGTGVGTTKGDLQAAEK.E  2.4 61 -36.44 K.EFGNTLEDKAWEVINR.I  1.7 72 28.3 K.SEGHEGQGQLFSTDDGEK.A  1.6 74 5.11 K.CEECVKAFNSFSALMK.H  1.4 78 16.4 R.SDMICGYACLKGTAAMR.N | |
| |  | | --- | | Top scoring peptide matches to query 906 09MAR16\_OT\_03.01930.01930.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  45.1 0.0033 11.2 8 sp|P23565|AINX\_RAT|Alpha-internexin M.SFGSEHYLCSASSYRK.V  37.7 0.018 11.2 18 sp|Q08DH7|AINX\_BOVIN|Alpha-internexin M.SFGSEHYLCASSSYRK.V  5.2 32 3.25 K.EGFSFINDWNNMYRK.W  5.1 33 -38.06 K.FSHVQASSYIYDFKTK.S  4.9 34 -48.74 K.MAGLGTGVGTTKGDLQAAEK.E  4.1 41 -11.61 R.RYILEMYCEEPFVR.E  3.0 53 28.8 K.SEGHEGQGQLFSTDDGEK.A  2.8 56 2.19 R.YETLCNELSFLSDAMK.S  1.8 70 -35.96 K.EFGNTLEDKAWEVINR.I  1.4 77 -20.88 K.GMFTDDLHKLVDDWTK.E | |

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| |  | | --- | | Top scoring peptide matches to query 907 09MAR16\_OT\_03.01926.01926.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  49.3 0.0013 11.5 8 sp|P23565|AINX\_RAT|Alpha-internexin M.SFGSEHYLCSASSYRK.V  39.9 0.011 11.5 18 sp|Q08DH7|AINX\_BOVIN|Alpha-internexin M.SFGSEHYLCASSSYRK.V  6.5 24 -13.08 K.EMSEMLQLCSYVRFK.V  5.8 28 -48.45 K.MAGLGTGVGTTKGDLQAAEK.E  4.8 35 42.0 R.RLEMMDCSPCDLSFK.S  3.1 52 29.1 K.SEGHEGQGQLFSTDDGEK.A  3.0 53 -35.67 K.EFGNTLEDKAWEVINR.I  2.9 55 -4.07 R.SSYHNHKMIHFMSSSK.S  2.8 56 3.53 K.EGFSFINDWNNMYRK.W  2.7 57 -11.32 R.RYILEMYCEEPFVR.E | |
| |  | | --- | | Top scoring peptide matches to query 908 09MAR16\_OT\_03.02093.02093.2 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  92.0 8.2e-08 11.2 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  13.1 6.4 -16.97 K.LQMLQETIKAQMSENK.G  12.2 7.8 -19.53 K.AFCPDKMIVMIVPMQK.D  10.3 12 11.2 R.IGKCGCEQLLSVEAAAAM.-  8.9 16 -42.08 R.FNIINMTFPTESQIIR.I  8.9 17 -11.15 R.ELTMNDMLTQVQVLEK.K  8.4 19 -4.35 K.EVGRCMMLTNVQMLNK.E  7.9 21 -11.13 R.TMQELEIELQSQLSMK.A  6.3 30 -47.24 K.INFKVLDSEMVAVVTDK.W  5.5 37 1.60 R.VNAESEGFWMTLLEPGK.I | |

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| |  | | --- | | Top scoring peptide matches to query 909 09MAR16\_OT\_03.02086.02086.3 Score greater than 31 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  50.7 0.0011 11.2 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  15.8 3.4 -11.12 R.ELTMNDMLTQVQVLEK.K  15.2 4 -4.33 K.EVGRCMMLTNVQMLNK.E  12.8 6.7 -19.51 K.AFCPDKMIVMIVPMQK.D  11.8 8.6 39.8 R.QQLLGAEEQMQDMQDK.C  11.3 9.6 -42.06 R.FNIINMTFPTESQIIR.I  10.7 11 28.5 R.LYEDSTSDYCTVTKNK.R  10.1 13 -19.51 K.AFCPDKMIVMIVPMQK.D  9.6 14 -30.74 K.MPQDHHITSLLMVNKK.Y  9.4 15 1.98 R.IGDMRIMENNLESELK.S | |
| |  | | --- | | Top scoring peptide matches to query 910 09MAR16\_OT\_03.02098.02098.2 Score greater than 28 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  64.0 5.2e-05 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  11.3 9.5 0.43 K.DENEFLTEQLSETQIK.F  7.8 22 11.3 R.IGKCGCEQLLSVEAAAAM.-  4.5 46 -19.41 K.AFCPDKMIVMIVPMQK.D  4.3 48 7.22 K.AGYPSTEEARPCCGKLK.V  3.3 60 17.1 R.CIVDEAMLTGESVPQMK.E  3.0 66 18.5 K.KMLTQNYIFSECMMK.L  1.3 95 -11.02 R.ELTMNDMLTQVQVLEK.K  0.1 1.3e+02 21.4 K.TVLESGGETGDGDNDTTKK.K | |

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| |  | | --- | | Top scoring peptide matches to query 911 09MAR16\_OT\_03.02096.02096.3 Score greater than 34 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.5 0.0091 11.5 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  18.8 1.7 -10.84 R.ELTMNDMLTQVQVLEK.K  18.0 2.1 -19.22 K.AFCPDKMIVMIVPMQK.D  17.6 2.2 -30.45 K.MPQDHHITSLLMVNKK.Y  11.9 8.4 1.55 K.ICQSNLQLAQAQFCSR.I  10.8 11 18.4 R.DCIPFFRSAPSCPQNK.N  10.5 12 2.26 K.EMMEQIRQQTDILEK.E  10.4 12 -4.04 K.EVGRCMMLTNVQMLNK.E  10.2 12 0.61 K.DENEFLTEQLSETQIK.F  9.3 15 -30.00 R.TDALSGTVTLYEGQARNK.I | |
| |  | | --- | | Top scoring peptide matches to query 912 09MAR16\_OT\_03.02091.02091.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.6 0.0089 11.7 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  24.7 0.44 -10.65 R.ELTMNDMLTQVQVLEK.K  21.1 1 0.80 K.DENEFLTEQLSETQIK.F  16.2 3.1 -19.03 K.AFCPDKMIVMIVPMQK.D  15.4 3.7 -30.26 K.MPQDHHITSLLMVNKK.Y  13.2 6.2 -19.03 K.AFCPDKMIVMIVPMQK.D  11.0 10 -41.58 R.FNIINMTFPTESQIIR.I  10.9 10 18.6 R.DCIPFFRSAPSCPQNK.N  10.6 11 -5.50 -.FLMETVVQASAKDMHGK.V  10.5 11 -3.85 K.EVGRCMMLTNVQMLNK.E | |

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| |  | | --- | | Top scoring peptide matches to query 913 09MAR16\_OT\_03.02088.02088.2 Score greater than 30 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide** 102.5 7.2e-09 12.4 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  11.2 9.9 -18.33 K.AFCPDKMIVMIVPMQK.D  8.6 18 12.4 R.IGKCGCEQLLSVEAAAAM.-  8.5 18 -33.39 R.VMTPMMNPLIYSLRNK.D  8.5 18 -33.39 R.VMTPMMNPLIYSLRNK.D  6.3 30 -3.15 K.EVGRCMMLTNVQMLNK.E  5.6 36 -29.10 R.TDALSGTVTLYEGQARNK.I  4.8 43 18.2 R.CIVDEAMLTGESVPQMK.E  4.0 52 -9.94 R.ELTMNDMLTQVQVLEK.K  4.0 52 22.5 K.TVLESGGETGDGDNDTTKK.K | |
| |  | | --- | | Top scoring peptide matches to query 919 09MAR16\_OT\_03.01846.01846.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  36.0 0.031 11.1 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  35.0 0.038 11.1 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  23.1 0.59 -23.36 R.RICGTGGCLASAPLHQNK.S  22.3 0.71 11.1 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  14.9 3.9 -4.35 K.EVGRCMMLTNVQMLNK.E  13.4 5.5 -45.12 K.IYENVNEILSLFDKDK.Y  12.8 6.3 -4.35 K.EVGRCMMLTNVQMLNK.E  11.7 8.1 -33.90 R.LGHGSSEDEAIPMLVAGLK.G  10.0 12 -32.15 R.YLIPDSAFSETAERVNK.I  8.9 15 30.3 K.SEDCRESEIETNTELK.E | |

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| |  | | --- | | Top scoring peptide matches to query 920 09MAR16\_OT\_03.01841.01841.3 Score greater than 32 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  47.3 0.0022 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  46.1 0.0029 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  25.8 0.31 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  16.2 2.9 -31.87 R.YLIPDSAFSETAERVNK.I  14.4 4.3 -4.07 K.EVGRCMMLTNVQMLNK.E  12.4 6.8 -19.12 K.AFCPDKMIVMIVPMQK.D  10.1 12 -4.07 K.EVGRCMMLTNVQMLNK.E  8.9 15 -23.08 R.RICGTGGCLASAPLHQNK.S  8.8 16 -46.58 K.DFILLTMRVSTEEELK.F  7.8 20 26.5 K.EANELSDSAGEDHPAELR.K | |
| |  | | --- | | Top scoring peptide matches to query 921 09MAR16\_OT\_03.01798.01798.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  45.1 0.0037 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  30.5 0.11 -23.08 R.RICGTGGCLASAPLHQNK.S  22.0 0.76 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  22.0 0.76 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  17.2 2.3 -44.84 K.IYENVNEILSLFDKDK.Y  11.5 8.4 -31.87 R.YLIPDSAFSETAERVNK.I  9.9 12 -45.29 R.AGPMGEMPYKLFITQLK.G  9.8 13 -24.45 -.MDSRNMLVVYSVNLEK.K  9.5 14 30.6 K.SEDCRESEIETNTELK.E  9.2 14 19.3 R.FEDLVTDEETASDALER.N | |

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| |  | | --- | | Top scoring peptide matches to query 922 09MAR16\_OT\_03.01791.01791.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  41.9 0.0078 11.5 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  22.2 0.72 11.5 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  22.2 0.72 11.5 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  21.6 0.84 -22.89 R.RICGTGGCLASAPLHQNK.S  17.6 2.1 -45.10 R.AGPMGEMPYKLFITQLK.G  14.7 4 -31.68 R.YLIPDSAFSETAERVNK.I  13.8 4.9 -45.10 R.AGPMGEMPYKLFITQLK.G  13.6 5.2 -44.65 K.IYENVNEILSLFDKDK.Y  11.3 8.8 -29.60 R.LEIDTIKHQNQETENK.Y  11.2 9 -26.24 R.CLNSAVGEHEKVINNQK.E | |
| |  | | --- | | Top scoring peptide matches to query 923 09MAR16\_OT\_03.01853.01853.3 Score greater than 32 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.2 0.00057 11.8 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  51.0 0.00094 11.8 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  22.2 0.72 11.8 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  16.5 2.7 -3.59 K.EVGRCMMLTNVQMLNK.E  13.4 5.4 -3.59 K.EVGRCMMLTNVQMLNK.E  13.2 5.8 -41.01 R.FNIINMTFPTESQIIR.I  11.8 7.9 -28.05 R.FPIAQLGTFKQDSAGMGR.I  11.7 8.1 -22.61 R.RICGTGGCLASAPLHQNK.S  11.1 9.3 -18.65 K.AFCPDKMIVMIVPMQK.D  10.1 12 -44.36 K.IYENVNEILSLFDKDK.Y | |

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| |  | | --- | | Top scoring peptide matches to query 925 09MAR16\_OT\_03.01571.01571.3 Score greater than 22 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  63.6 6.6e-05 11.3 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.ITKTPQASTYSYETSDR.C  5.4 44 35.8 K.NESEDPDTVPEEKPFSK.K  4.8 50 -26.78 R.WRLSDQASPDGVLHAAPK.L  4.5 54 18.7 K.MDKSESAYMLSSLGQLR.D  4.2 58 -37.62 K.TIGAQGNKYVLDQLNSAR.V  4.2 58 14.6 K.SDMEQYQVQHILVEGR.S  3.6 66 -26.11 R.TSIGLGEFLVGSDPPTTTR.R  3.4 70 -14.90 R.VTDLVNQQQTLEEKMR.E  3.4 70 -4.05 R.NMRSQHPYVLTEDTLK.V  2.1 94 32.0 K.DEDALEPQVKGSSNTSDR.D | |
| |  | | --- | | Top scoring peptide matches to query 926 09MAR16\_OT\_03.01577.01577.3 Score greater than 23 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  78.9 2e-06 11.6 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.ITKTPQASTYSYETSDR.C  5.6 42 -25.83 R.TSIGLGEFLVGSDPPTTTR.R  4.2 58 31.9 R.DSSMTAITTQASMEFRR.K  4.0 61 19.0 K.MDKSESAYMLSSLGQLR.D  3.6 67 -0.07 K.LTYAVGMAFGDDTFAAGLK.N  3.2 72 14.9 K.SDMEQYQVQHILVEGR.S  2.7 82 -41.12 -.MKPSPAGTAKELEPPAPAR.G  1.7 1e+02 36.0 K.NESEDPDTVPEEKPFSK.K  1.3 1.1e+02 -9.54 K.ENNVVEPAMYGVTGVRGR.V  1.2 1.1e+02 -7.56 R.TQFEMMYLTLTELRR.V | |

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| |  | | --- | | Top scoring peptide matches to query 927 09MAR16\_OT\_03.01601.01601.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  48.3 0.0016 11.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  45.7 0.0029 11.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  23.8 0.45 -44.60 R.AGPMGEMPYKLFITQLK.G  19.4 1.2 11.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  12.8 5.6 -46.56 K.AHFQKLHQEMTEIISK.Q  10.4 9.7 -18.18 K.NMLELLEEMPNGVPPEK.V  9.0 13 -3.71 K.EVGRCMMLTNVQMLNK.E  8.7 14 -4.06 K.MFQVEKVNCICVDWK.R  8.7 15 -1.53 K.EVYEEVLGRESGSMQSR.L  8.4 16 -25.97 K.NYMWLKMQLELETEK.E | |
| |  | | --- | | Top scoring peptide matches to query 928 09MAR16\_OT\_03.01596.01596.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  51.4 0.00079 11.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  44.5 0.0038 11.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  20.9 0.87 -44.60 R.AGPMGEMPYKLFITQLK.G  19.9 1.1 11.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  14.3 4 -46.56 K.AHFQKLHQEMTEIISK.Q  12.3 6.3 -5.33 R.VAVTDMKSDFQACLNEK.V  12.1 6.7 19.0 R.MEEPTGSFENIADQMIK.T  11.0 8.5 11.3 R.CQGEQAVSDHAAQIAENK.E  10.0 11 -3.71 K.EVGRCMMLTNVQMLNK.E  7.6 19 -9.11 K.KCVIFIDDMNMPSLEK.Y | |

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| |  | | --- | | Top scoring peptide matches to query 929 09MAR16\_OT\_03.01535.01535.3 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.6 0.00046 10.5 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin R.MSMKEVDEQMLNVQNK.N  17.5 1.9 -26.74 K.ETELELQMKLWMYNK.K  13.9 4.4 -37.48 K.MIKTCISEETQIDIFK.F  12.8 5.6 8.01 R.EMQYSCMPVMGLAMVPK.I  12.8 5.7 -26.74 K.ETELELQMKLWMYNK.K  12.4 6.1 2.41 K.FLEECPSGTLFMHEFK.R  12.3 6.3 39.3 K.QCQIAGGKCTCSQTCGR.N  9.9 11 -23.01 -.MFSPGQEEPSAPNKEPVK.Y  9.2 13 0.46 R.FNWFVCKTEGGSPSNNK.F  8.8 14 19.5 K.CLTMLQDPTMCQSINK.S | |
| |  | | --- | | Top scoring peptide matches to query 942 09MAR16\_OT\_03.02576.02576.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  52.6 0.00074 9.90 16 sp|Q3ZBU7|TBB4\_BOVIN|Tubulin K.MAATFIGNSTAIQELFKR.I  52.2 0.00081 9.90 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  42.1 0.0084 9.90 K.MASTFIGNSTAIQELFKR.I  6.8 28 49.7 R.ASGVPDRFSGSGSGTDFTLR.I  6.1 33 36.9 K.QHSIGGGGVANRSSMLDVGR.R  4.5 48 35.5 K.NTVTDDILCTSPGHLDKK.E  4.4 49 49.7 LTFDTGSGSGSFRDPVGSAR  4.1 53 -8.19 R.EGPGPTPVAMGPGPPLAVTIR.L  4.0 54 40.5 R.HTLAPEARDWVSLMSER.G  3.7 57 35.6 M.NATSVPPAEGSCPSNALITK.Q | |

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| |  | | --- | | Top scoring peptide matches to query 943 09MAR16\_OT\_03.02573.02573.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.5 0.047 11.3 16 sp|Q3ZBU7|TBB4\_BOVIN|Tubulin K.MAATFIGNSTAIQELFKR.I  34.3 0.049 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  26.6 0.29 11.3 K.MASTFIGNSTAIQELFKR.I  8.6 18 41.8 R.HTLAPEARDWVSLMSER.G  6.0 33 -2.47 K.ESGVSSLPVSLTNIKEEPK.E  5.4 38 34.9 K.FELEMGTVHEGPEVQALK.Q  3.5 59 -4.81 R.NTSSMAGELRPASLVVLPR.S  3.2 64 47.4 K.NCNTPLLRAYYGSLEDK.R  2.8 70 5.36 R.EYVWAPFIPLHQGSNKK.N  2.6 73 25.7 R.FVAICNPLLYTVNMSQK.L | | | |
| |  | | --- | | Top scoring peptide matches to query 944 09MAR16\_OT\_03.02578.02578.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.6 0.00057 12.1 16 sp|Q3ZBU7|TBB4\_BOVIN|Tubulin K.MAATFIGNSTAIQELFKR.I  53.3 0.00061 12.1 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  46.2 0.0031 12.1 K.MASTFIGNSTAIQELFKR.I  10.8 11 42.7 R.HTLAPEARDWVSLMSER.G  5.7 36 39.0 K.KAPSPGYPLVCVTPCDPR.Y  4.6 46 40.7 K.GEMFTVFNANYKNTHLK.E  3.4 60 -0.41 NLIPMDPNGLSDPYVKLK  3.3 61 39.6 R.SMVAFIAADTMVTTEIGEK.S  2.6 72 35.7 M.SSDTEMEVFGIAAPFLRK.S  2.4 75 37.4 R.NYIFEIEGGAFDGLAELR.H | |

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| |  | | --- | | Top scoring peptide matches to query 945 09MAR16\_OT\_03.02584.02584.2 Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  56.8 0.00026 15.8 K.MASTFIGNSTAIQELFKR.I  56.8 0.00026 15.8 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  47.5 0.0022 15.8 16 sp|Q3ZBU7|TBB4\_BOVIN|Tubulin K.MAATFIGNSTAIQELFKR.I  6.2 30 27.0 K.TASFGGITVLTRGDSTSSTR.S  3.6 55 35.8 -.SRLMNETVTSGGGSIVFSR.S  2.6 68 26.6 K.MAKEMAVLADTAVQHGLGR.S  2.6 68 26.6 K.MAKEMAVLADTAVQHGLGR.S  2.4 72 -9.21 K.SEAVISFSIILAFVGVSKM.-  2.2 75 15.8 K.VPWVNVSKGNIEIGNMEK.V  2.0 78 25.1 R.RASYNETKPEVTYISQK.I | | | |
| |  | | --- | | Top scoring peptide matches to query 946 09MAR16\_OT\_03.02247.02247.3 Score greater than 20 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  21.0 1.1 10.7 17 sp|P09951|SYN1\_RAT|Synapsin-1 K.TNTGSAMLEQIAMSDRYK.L  5.8 35 -39.82 K.QRILGSGQSAEIMPSSINK.E  5.2 40 -23.77 R.TVMLRFAASPGPAADAAPEK.G  4.5 48 1.85 K.SEVDCPPGVTKEITAGAER.V  4.0 53 48.7 R.MMASLLEPSFPETDEMR.S  3.6 59 19.9 K.EYSQMQQQSTQKVEASK.V  3.5 59 16.3 K.GLMTIYEDEMKQEIGSR.S  3.4 61 37.2 K.DWVMYEMNAAPPYVSAR.I  3.1 66 -28.69 R.TLVGDILDPSLLNDIMDR.T  3.1 66 -7.64 R.FRQVGTVSSDIHDSPGASR.A | |

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| |  | | --- | | Top scoring peptide matches to query 947 09MAR16\_OT\_03.02240.02240.3 Score greater than 22 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.1 0.053 11.3 17 sp|P09951|SYN1\_RAT|Synapsin-1 K.TNTGSAMLEQIAMSDRYK.L  7.2 26 -41.17 -.SEISMANILHEVKYALR.Q  6.3 31 16.0 R.SQEWASGLHNRSASGSWR.E  6.1 33 -28.05 R.TLVGDILDPSLLNDIMDR.T  6.0 33 -41.21 R.GGVTSKYLPHIVGMDSVQK.F  5.0 43 20.5 M.AAATPTETPAPEGSGLGMDAR.L  4.7 46 -30.73 R.GGTIRFGWPAPGAVDVTLAM.-  4.5 47 11.3 R.GSATSTSPPCLSSFRMSVK.G  4.4 49 49.3 R.MMASLLEPSFPETDEMR.S  3.5 59 16.9 K.GLMTIYEDEMKQEIGSR.S | |
| |  | | --- | | Top scoring peptide matches to query 949 09MAR16\_OT\_03.02547.02547.3 Score greater than 29 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  16.1 3.3 8.24 K.MASTFIGNSTAIQELFKR.I  16.1 3.3 8.24 19 sp|Q2T9S0|TBB3\_BOVIN|Tubulin K.MSSTFIGNSTAIQELFKR.I  15.1 4.2 -15.25 R.GPPGPMGPQGLRGEVGLPGIK.G  12.3 8.1 26.2 R.VENFLGISSLEEMSFRR.-  11.3 10 0.39 K.KQGYPALHVFSTFFYPK.L  11.0 11 -9.71 R.EGPGPTPVAMGPGPPLAVTIR.L  11.0 11 24.9 K.DISSATSTSALSDRLYGSAK.E  8.6 19 15.0 K.KNYFXCVANVWDMLLK.I  8.6 19 15.0 K.KNYFXCVANVWDMLLK.I  7.9 22 31.7 K.ICDYLFNVSDSSALNLAK.N | |

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| |  | | --- | | Top scoring peptide matches to query 950 09MAR16\_OT\_03.02512.02512.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.1 0.082 11.1 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  22.4 0.75 11.1 K.MASTFIGNSTAIQELFKR.I  17.5 2.3 11.1 19 sp|Q2T9S0|TBB3\_BOVIN|Tubulin K.MSSTFIGNSTAIQELFKR.I  9.8 14 -8.04 K.LRAAVEEATETGESIIGVGK.A  8.7 18 3.27 K.KQGYPALHVFSTFFYPK.L  7.9 21 34.6 K.ICDYLFNVSDSSALNLAK.N  7.7 22 16.3 K.TTLSLHNCICRVGETIR.E  6.5 30 38.5 R.SMVAFIAADTMVTTEIGEK.S  6.2 31 43.8 R.LYLEKENESHIPADDEK.Y  4.5 46 -25.05 K.YAAWEKIILPSFEPPLR.N | |
| |  | | --- | | Top scoring peptide matches to query 951 09MAR16\_OT\_03.02550.02550.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  40.9 0.011 11.3 K.MASTFIGNSTAIQELFKR.I  40.6 0.011 11.3 19 sp|Q2T9S0|TBB3\_BOVIN|Tubulin K.MSSTFIGNSTAIQELFKR.I  34.1 0.051 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  14.8 4.3 29.2 R.VENFLGISSLEEMSFRR.-  9.7 14 18.1 K.KNYFXCVANVWDMLLK.I  9.7 14 18.1 K.KNYFXCVANVWDMLLK.I  9.1 16 38.6 R.SMVAFIAADTMVTTEIGEK.S  6.5 29 -10.28 R.TMLTYLVPPCLDPKPLR.D  5.8 34 -14.15 R.NTPIQVLGMWHYSKVLK.F  3.8 55 45.2 K.QGPDSPGQAPPPPFLMSYK.L | |

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| |  | | --- | | Top scoring peptide matches to query 952 09MAR16\_OT\_03.02509.02509.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.7 0.022 11.3 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  33.8 0.054 11.3 K.MASTFIGNSTAIQELFKR.I  31.9 0.084 11.3 19 sp|Q2T9S0|TBB3\_BOVIN|Tubulin K.MSSTFIGNSTAIQELFKR.I  16.7 2.8 -7.86 K.LRAAVEEATETGESIIGVGK.A  16.2 3.1 38.6 R.SMVAFIAADTMVTTEIGEK.S  8.5 19 -4.63 K.IQKPSLITSDINEMRER.E  7.5 23 0.89 R.LPKDVNTNQSGDQILIMK.V  7.1 26 31.2 R.RLLGAEEEAQCQQLQEK.Q  6.8 27 -12.18 R.GPPGPMGPQGLRGEVGLPGIK.G  6.7 28 7.43 K.SFLTLHERTHTGDKPYK.C | |
| |  | | --- | | Top scoring peptide matches to query 953 09MAR16\_OT\_03.02507.02507.3 Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.5 0.046 13.6 1+ sp|Q4R5B3|TBB2A\_MACFA|Tubulin K.MSATFIGNSTAIQELFKR.I  25.2 0.39 13.6 K.MASTFIGNSTAIQELFKR.I  18.7 1.7 13.6 19 sp|Q2T9S0|TBB3\_BOVIN|Tubulin K.MSSTFIGNSTAIQELFKR.I  10.5 12 13.5 K.VVPVSDPPVNSQQMVYVR.A  6.0 32 27.8 R.CTQYFIKLISDCSLPGK.C  4.6 44 -5.60 K.LRAAVEEATETGESIIGVGK.A  4.6 44 -22.61 K.YAAWEKIILPSFEPPLR.N  2.9 65 40.9 R.SMVAFIAADTMVTTEIGEK.S  1.1 1e+02 15.5 R.RVISDNGPPEATISMISSR.S  0.8 1.1e+02 40.0 R.NDHVSFPFQNNVAQKER.V | |

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| |  | | --- | | Top scoring peptide matches to query 957 09MAR16\_OT\_03.01840.01840.3 Score greater than 20 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.6 0.023 11.7 R.SGGRPEEYEGEYQCFAR.N  5.8 17 -45.64 R.MAAISMGGFIFLGAYDQAR.S  5.8 17 -45.64 R.MAAISMGGFIFLGAYDQAR.S  5.5 18 -34.52 R.GDVTIGVGSSCLGHFEASNK.A  1.6 45 28.1 R.LEGKLEEFCCEDCMSK.F  1.5 46 7.45 K.EDTTGPEEAGDVDDLLDMI.-  1.3 48 -23.88 R.LLPPMLDFMEPNDMEAR.Y  1.3 48 -9.86 15 sp|P15205|MAP1B\_RAT|Microtubule-associated K.EMQYFMQQWTGTNKDK.A  1.3 49 -43.67 K.ADAVVDQGGSWMATPVRMK.S  1.3 49 -18.27 K.AAKADVTQETDPLCAECR.V | |
| |  | | --- | | Top scoring peptide matches to query 958 09MAR16\_OT\_03.02494.02494.3 Score greater than 23 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.1 1.6 11.8 19 sp|Q2T9S0|TBB3\_BOVIN|Tubulin K.MSSTFIGNSTAIQELFKR.I  8.8 17 -1.72 R.IQINTTPESEDILISSSAK.A  4.3 47 43.8 K.ANASICFAVPDPLMPDPSK.Q  2.9 66 44.8 R.QSSPSLAPPGHQGHSHEHR.G  2.9 66 20.2 R.FMWIDKLNVSNEAGFFK.H  1.9 83 -4.35 K.HELLGGKWEAIYTLGGSSK.R  1.5 90 16.6 K.FDMIWDRGALVAINPGDR.K  1.5 91 -16.32 K.LNLAPTVTSELEQRMLSK.N  1.5 91 20.5 -.MSVSTPPDPLLHHTPAAMK.L  1.1 99 -0.50 K.KTETDMSLHPLLQEIYK.D | |

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| |  | | --- | | Top scoring peptide matches to query 959 09MAR16\_OT\_03.02497.02497.3 Score greater than 19 indicates homology Score greater than 34 indicates identity  **Score Expect ppm Hit Protein Peptide**  14.8 4.3 12.7 19 sp|Q2T9S0|TBB3\_BOVIN|Tubulin K.MSSTFIGNSTAIQELFKR.I  5.3 37 44.7 K.ANASICFAVPDPLMPDPSK.Q  2.4 73 24.3 R.AANGNRQHLFPTFATNMR.Q  1.1 98 0.40 K.KTETDMSLHPLLQEIYK.D  1.0 1e+02 -28.39 R.THPRPSISMPLPTVLLDR.K  0.7 1.1e+02 7.20 K.EALNLHGCSLNFLAKGSSK.Q  0.6 1.1e+02 20.1 R.VTGMENSSTLLVQSGEHLK.V  0.3 1.2e+02 -26.51 R.LAFLMINDSLVPTMVIPR.F  0.3 1.2e+02 5.21 K.HPPPSPSPVGPPCPTLPSPK.M  0.1 1.2e+02 21.4 -.MSVSTPPDPLLHHTPAAMK.L | |
| |  | | --- | | Top scoring peptide matches to query 960 09MAR16\_OT\_03.01625.01625.3 Score greater than 25 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  73.7 4.9e-06 10.6 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QASISGPAPPKVSGASPGGQQR.Q  8.2 17 49.4 R.SQANSIQSQMEIIQEQAR.N  6.8 24 38.2 R.FHMYEGYSLSKVTFPVR.V  6.2 27 -1.53 R.LESLQASDQARYLGVTGIR.Q  6.1 28 23.3 K.RVTLLTPAGATGSGGGTSGDSSK.G  5.1 35 38.3 K.EGTHTRGHIALSSSYSFAR.L  4.1 44 35.4 -.NTPPSADVKGMAEENFLLK.R  2.6 62 -17.62 -.MKLLILTCLVAAAFAMPR.L  2.4 66 13.7 R.VITSQGGKGLMHHLNNAQR.L  1.8 76 49.4 R.LMKELNQMQYEYTELK.K | |

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| |  | | --- | | Top scoring peptide matches to query 961 09MAR16\_OT\_03.01620.01620.3 Score greater than 27 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  74.9 3.7e-06 11.2 17 sp|P09951|SYN1\_RAT|Synapsin-1 R.QASISGPAPPKVSGASPGGQQR.Q  9.9 12 -0.92 R.LESLQASDQARYLGVTGIR.Q  6.5 26 -48.73 R.QATVANGTHPRLVALFLLR.M  3.9 46 49.4 R.QASIHSNHVARTDEAMPGR.F  3.5 51 32.4 K.MMIIEQQVVAFDEGPELK.I  2.4 66 50.0 R.LMKELNQMQYEYTELK.K  2.1 70 23.9 K.RVTLLTPAGATGSGGGTSGDSSK.G  1.6 80 -7.63 K.TLLLTSSATVYSIHISEGGK.L  1.6 80 -10.21 R.IARGFATFLPYRPIDDPK.K  1.5 80 14.3 R.VITSQGGKGLMHHLNNAQR.L | |
| |  | | --- | | Top scoring peptide matches to query 963 09MAR16\_OT\_03.02198.02198.3 Score greater than 25 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.1 0.0064 11.1 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.VNNASLIGLGYTQSLRPGVK.L  10.0 5.3 25.0 R.LKWAQIGADMEQTLLVVR.R  8.5 7.3 -39.40 R.VLVAMVVFIALSVSLSALVR.V  3.1 26 23.4 M.MLPLQGAQMLQVLEKSLR.R  1.6 36 47.8 K.LQNAVHEPLMAYLLTETK.K  1.4 37 49.7 R.ELRQALQDIETLEQCLK.E  1.3 39 -41.23 K.VLGQIVASAELNRHIIIIK.N  1.0 41 33.3 R.DPLQKTAKPGLHFVDQHR.A  0.4 47 30.4 R.VIDLYPTGPKVMLLDAGER.V  0.3 48 -19.05 K.VLSRWLAGLPLQLAHLGSR.N | |

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| |  | | --- | | Top scoring peptide matches to query 965 09MAR16\_OT\_03.02206.02206.2 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  97.7 8.8e-09 11.3 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.VNNASLIGLGYTQSLRPGVK.L | |

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| |  | | --- | | Top scoring peptide matches to query 966 09MAR16\_OT\_03.02199.02199.2 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  75.2 1.6e-06 11.4 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.VNNASLIGLGYTQSLRPGVK.L | | | |
| |  | | --- | | Top scoring peptide matches to query 967 09MAR16\_OT\_03.02195.02195.3 Score greater than 28 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  56.7 0.00011 11.5 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.VNNASLIGLGYTQSLRPGVK.L  11.8 3.4 -38.97 R.VLVAMVVFIALSVSLSALVR.V  8.9 6.6 35.6 K.LITSQAVHVTTHSKNASHR.V  5.3 15 49.9 R.DALWPEKGQELYSIVNPK.S  5.0 16 16.9 R.VLTRSLSDYTGPPQLQALK.A  2.6 28 23.8 M.MLPLQGAQMLQVLEKSLR.R  2.2 31 38.1 R.GIKTVVDLVCADLEEVAQK.C  1.2 38 34.4 R.TLSPVLESPRDLQFSEIR.E  0.8 43 30.8 R.VIDLYPTGPKVMLLDAGER.V  0.7 43 28.9 K.FMYTSVDALHPLLPIIEK.G | |

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| |  | | --- | | Top scoring peptide matches to query 968 09MAR16\_OT\_03.02204.02204.3 Score greater than 27 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  43.0 0.0026 11.6 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.VNNASLIGLGYTQSLRPGVK.L  11.4 3.7 -38.88 R.VLVAMVVFIALSVSLSALVR.V  5.0 16 11.6 R.VPEGTQLGRVSLEPVGPPVR.G  4.1 20 25.5 R.LKWAQIGADMEQTLLVVR.R  1.8 34 39.2 R.GHERLSSSIIPGYTGFIPR.A  1.2 39 33.8 R.DPLQKTAKPGLHFVDQHR.A  0.9 41 38.2 R.GIKTVVDLVCADLEEVAQK.C  0.9 41 44.5 R.GGPLAMMNIGIQLLAQKCR.D  0.9 41 44.5 R.GGPLAMMNIGIQLLAQKCR.D  0.2 48 -18.52 K.VLSRWLAGLPLQLAHLGSR.N | |
| |  | | --- | | Top scoring peptide matches to query 969 09MAR16\_OT\_03.02235.02235.3 Score greater than 22 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  33.1 0.024 12.1 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.VNNASLIGLGYTQSLRPGVK.L  7.0 10 -40.17 K.VLGQIVASAELNRHIIIIK.N  6.7 11 26.0 R.LKWAQIGADMEQTLLVVR.R  4.9 16 47.0 K.VIPRPPQNTSVTESPDPPR.N  3.6 22 -38.35 R.VLVAMVVFIALSVSLSALVR.V  1.1 39 29.6 K.LTRASQILNTILSNYDHK.L  0.1 49 15.9 K.GVGRVLICLTSSLDQLLDK.I  0.0 50 36.2 K.LITSQAVHVTTHSKNASHR.V | |

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| |  | | --- | | Top scoring peptide matches to query 970 09MAR16\_OT\_03.02243.02243.3 Score greater than 20 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  31.5 0.035 12.2 14 sp|Q9R1Z0|VDAC3\_RAT|Voltage-dependent K.VNNASLIGLGYTQSLRPGVK.L  5.1 15 -38.26 R.VLVAMVVFIALSVSLSALVR.V  4.8 16 47.1 K.VIPRPPQNTSVTESPDPPR.N  4.6 17 36.3 K.LITSQAVHVTTHSKNASHR.V  2.9 26 33.4 K.NLQEQVMAVTAQIQALTTK.V  0.9 41 26.1 R.LKWAQIGADMEQTLLVVR.R  0.4 46 31.5 R.VIDLYPTGPKVMLLDAGER.V  0.3 47 24.5 M.MLPLQGAQMLQVLEKSLR.R  0.1 50 33.4 K.QLEELNLQMGAKETVLVR.L | |
| |  | | --- | | Top scoring peptide matches to query 972 09MAR16\_OT\_03.02073.02073.3 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.5 0.022 10.8 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  28.7 0.083 -1.19 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  7.3 11 35.3 R.KTAAELLQSQGSQAGGSQTLK.R  7.0 12 -11.87 R.VLITLNQIRLNVDNNVHK.N  6.7 13 28.7 K.ESLATSLAAEKSNLLAELDK.L  5.8 16 -39.33 R.VLVAMVVFIALSVSLSALVR.V  2.6 34 43.8 R.ELNGSLAAQLSKMLDQQTR.E  2.1 38 1.60 K.ELLLDPHQTLVFKVWHK.G  1.9 39 21.5 K.VIGDKVLEEEISFPLTTGR.L  1.9 40 7.27 K.MLLSETQALPFKRPGAISK.R | |

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| |  | | --- | | Top scoring peptide matches to query 973 09MAR16\_OT\_03.02116.02116.3 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  40.7 0.0051 11.1 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  29.8 0.064 -0.84 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  10.0 6.1 35.7 R.KTAAELLQSQGSQAGGSQTLK.R  8.1 9.5 32.2 K.NLQEQVMAVTAQIQALTTK.V  6.8 13 47.6 K.QLPPGMSVDPKESSVLQFK.V  6.3 14 21.8 K.VIGDKVLEEEISFPLTTGR.L  6.1 15 -38.98 R.VLVAMVVFIALSVSLSALVR.V  5.3 18 43.7 -.MVRPLNCIVAVSQNMGIGK.N  5.0 19 42.2 K.VDISQWIGTGPSMDLKLSR.I  4.8 20 7.60 K.VNPGKLHLDVDPMSIKPVK.I | |
| |  | | --- | | Top scoring peptide matches to query 974 09MAR16\_OT\_03.02092.02092.2 Score greater than 27 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  72.3 3.6e-06 11.3 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  10.2 5.8 -0.63 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  1.8 41 46.2 R.KNMPPETPKPLSMTSTSLK.D  1.0 48 28.2 -.MLMLLVRGTHYENLRPK.V | |

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| |  | | --- | | Top scoring peptide matches to query 975 09MAR16\_OT\_03.02085.02085.2 Score greater than 25 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  76.1 1.5e-06 11.3 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  7.7 10 -0.63 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  1.9 40 46.2 R.KNMPPETPKPLSMTSTSLK.D | |
| |  | | --- | | Top scoring peptide matches to query 976 09MAR16\_OT\_03.02079.02079.2 Score greater than 30 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  87.2 1.2e-07 11.4 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  11.7 4.1 -0.51 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  2.7 33 6.11 R.QAPTSAPAAAPTRSPVSLKPR.K  1.9 40 46.3 R.KNMPPETPKPLSMTSTSLK.D  0.9 49 28.4 -.MLMLLVRGTHYENLRPK.V | |

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| |  | | --- | | Top scoring peptide matches to query 977 09MAR16\_OT\_03.02120.02120.3 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  34.0 0.024 11.8 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  23.8 0.25 -0.14 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  10.5 5.3 36.4 R.KTAAELLQSQGSQAGGSQTLK.R  8.1 9.2 8.30 K.VNPGKLHLDVDPMSIKPVK.I  8.0 9.6 34.5 R.KLFLDVNGSISDSLPSASPR.S  7.1 12 -38.28 R.VLVAMVVFIALSVSLSALVR.V  6.5 13 48.3 K.QLPPGMSVDPKESSVLQFK.V  5.3 18 32.9 K.NLQEQVMAVTAQIQALTTK.V  4.0 24 -10.83 R.VLITLNQIRLNVDNNVHK.N  3.5 27 49.9 R.VIEPTGQFYPEAPDLGTIR.G | |
| |  | | --- | | Top scoring peptide matches to query 978 09MAR16\_OT\_03.02078.02078.3 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.0 0.012 12.0 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  29.5 0.067 0.03 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  8.9 7.5 36.6 R.KTAAELLQSQGSQAGGSQTLK.R  8.6 8.1 -10.65 R.VLITLNQIRLNVDNNVHK.N  7.7 10 48.4 K.QLPPGMSVDPKESSVLQFK.V  6.5 13 -38.11 R.VLVAMVVFIALSVSLSALVR.V  6.0 15 34.7 R.KLFLDVNGSISDSLPSASPR.S  6.0 15 -5.32 K.VQVGINITLVTYGDRSIVR.V  4.5 21 40.0 K.STPTLILTSANEHDYLLSK.Q  3.5 27 -33.39 R.CHAVHVALVLFELKLLLK.S | |

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| |  | | --- | | Top scoring peptide matches to query 979 09MAR16\_OT\_03.02084.02084.3 Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  37.8 0.0097 12.5 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  28.6 0.082 0.56 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  6.3 14 49.0 K.QLPPGMSVDPKESSVLQFK.V  6.1 14 37.1 R.KTAAELLQSQGSQAGGSQTLK.R  5.5 17 -37.59 R.VLVAMVVFIALSVSLSALVR.V  3.9 24 43.6 K.VDISQWIGTGPSMDLKLSR.I  3.5 26 -10.13 R.VLITLNQIRLNVDNNVHK.N  3.5 26 40.5 K.STPTLILTSANEHDYLLSK.Q  2.1 36 31.7 R.VIDLYPTGPKVMLLDAGER.V  2.1 36 23.2 K.VIGDKVLEEEISFPLTTGR.L | |
| |  | | --- | | Top scoring peptide matches to query 980 09MAR16\_OT\_03.02207.02207.2 Score greater than 29 indicates identity  **Score Expect ppm Hit Protein Peptide**  90.6 3.8e-08 10.3 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  25.6 0.12 22.2 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  9.4 5 16.9 R.GTALLASLGLGRDLQPPGGPGR.E  1.0 34 37.9 K.SIVDAKLMPPEGEMVFVLK.V  0.2 42 43.3 R.NSQMSLVTLNTLADLNQLK.T | |

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| |  | | --- | | Top scoring peptide matches to query 981 09MAR16\_OT\_03.02212.02212.2 Score greater than 29 indicates identity  **Score Expect ppm Hit Protein Peptide**  83.9 1.8e-07 10.4 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  15.4 1.3 22.4 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  3.9 18 17.0 R.GTALLASLGLGRDLQPPGGPGR.E  0.4 40 38.0 K.SIVDAKLMPPEGEMVFVLK.V | | | |
| |  | | --- | | Top scoring peptide matches to query 982 09MAR16\_OT\_03.02220.02220.2 Score greater than 29 indicates identity  **Score Expect ppm Hit Protein Peptide**  85.9 1.1e-07 11.1 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  28.3 0.062 23.1 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  0.5 37 11.1 K.IGPKLTQTYGLGILSSNNVK.A | |

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| |  | | --- | | Top scoring peptide matches to query 983 09MAR16\_OT\_03.02210.02210.3 Score greater than 29 indicates identity  **Score Expect ppm Hit Protein Peptide**  39.5 0.0047 11.4 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  19.2 0.5 23.3 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  7.7 7.1 0.67 R.VLITLNQIRLNVDNNVHK.N  7.0 8.3 47.9 R.KTAAELLQSQGSQAGGSQTLK.R  6.7 8.9 40.6 R.AAAVTVNTSKNQYDVVIGPR.H  6.1 10 18.0 R.GTALLASLGLGRDLQPPGGPGR.E  3.5 19 44.4 K.NLQEQVMAVTAQIQALTTK.V  3.3 20 41.3 K.ESLATSLAAEKSNLLAELDK.L  1.4 30 42.5 R.VIDLYPTGPKVMLLDAGER.V  1.4 30 34.0 K.VIGDKVLEEEISFPLTTGR.L | |
| |  | | --- | | Top scoring peptide matches to query 984 09MAR16\_OT\_03.02205.02205.3 Score greater than 29 indicates identity  **Score Expect ppm Hit Protein Peptide**  49.5 0.00046 11.4 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  32.4 0.024 23.3 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  9.4 4.8 0.67 R.VLITLNQIRLNVDNNVHK.N  7.6 7.2 -26.79 R.VLVAMVVFIALSVSLSALVR.V  7.4 7.6 47.9 R.KTAAELLQSQGSQAGGSQTLK.R  6.0 10 18.0 R.GTALLASLGLGRDLQPPGGPGR.E  2.5 23 42.5 R.VIDLYPTGPKVMLLDAGER.V  2.3 25 41.3 K.ESLATSLAAEKSNLLAELDK.L  2.2 25 6.00 K.VQVGINITLVTYGDRSIVR.V  2.0 26 19.8 K.VNPGKLHLDVDPMSIKPVK.I | |

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| |  | | --- | | Top scoring peptide matches to query 985 09MAR16\_OT\_03.02217.02217.3 Score greater than 29 indicates identity  **Score Expect ppm Hit Protein Peptide**  49.4 0.00048 11.4 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.VNNSSLIGLGYTQTLKPGIK.L  30.2 0.04 23.4 13 sp|Q9MZ15|VDAC2\_PIG|Voltage-dependent VNNSSLIGVGYTQTLRPGVK  7.4 7.6 0.76 R.VLITLNQIRLNVDNNVHK.N  6.8 8.7 18.1 R.GTALLASLGLGRDLQPPGGPGR.E  6.4 9.5 -30.42 R.KLFLLLSLLLSHAAHLEGK.K  5.4 12 48.0 R.KTAAELLQSQGSQAGGSQTLK.R  5.0 13 42.5 R.VIDLYPTGPKVMLLDAGER.V  4.2 16 41.0 K.ILMPELASLRIAVMEEGSK.F  3.9 17 34.1 K.VPEAPQAAVVEEKTPEALPK.K  3.9 17 44.5 K.NLQEQVMAVTAQIQALTTK.V | | | |
| |  | | --- | | Top scoring peptide matches to query 999 09MAR16\_OT\_03.01644.01644.2 Score greater than 25 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide** 136.6 2.6e-12 10.1 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.TKSENGLEFTSSGSANTETTK.V  4.1 46 -15.66 K.GESGDLGPQGPRGPQGLMGPPGK.A  0.8 98 -10.51 K.QLHVTNENMEVTNQQFLK.T  0.2 1.1e+02 10.1 K.VGTSSSGHESPSSVLPDSETTK.A  0.0 1.2e+02 9.49 K.SGSSSTGEESHHFGSTTLPKR.E | |

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| |  | | --- | | Top scoring peptide matches to query 1000 09MAR16\_OT\_03.01647.01647.2 Score greater than 21 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide** 113.1 5.8e-10 10.6 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.TKSENGLEFTSSGSANTETTK.V  1.8 79 -10.07 K.QLHVTNENMEVTNQQFLK.T  1.0 94 -36.65 R.SIGDVWAVDKEGIPESLFAR.L | |
| |  | | --- | | Top scoring peptide matches to query 1001 09MAR16\_OT\_03.01640.01640.3 Score greater than 26 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  86.4 2.7e-07 10.7 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.TKSENGLEFTSSGSANTETTK.V  8.6 16 35.4 -.MDNNETSVDSKSINNFETK.T  4.2 46 -33.53 R.DYAMLDGGRPPPPPPLPLNR.A  3.5 53 -36.90 K.TASIYNPVIYIMMNKQFR.T  1.4 86 -34.67 R.YQNAHQQLLDLAKSETTTK.T | |

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| |  | | --- | | Top scoring peptide matches to query 1002 09MAR16\_OT\_03.01652.01652.3 Score greater than 20 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  72.6 6.6e-06 11.4 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.TKSENGLEFTSSGSANTETTK.V  2.8 62 -9.26 -.MGSGSSSYRPKAIYLDIDGR.I  2.7 64 7.58 K.TMKPGSMSVEAFLAEANVMK.T  0.9 98 -44.35 R.NAAWAPLDLPSIVSEHLPMK.Q  0.3 1.1e+02 -30.41 R.EQELVMKQNQDQLDTILK.E  0.2 1.1e+02 -34.00 R.YQNAHQQLLDLAKSETTTK.T  0.0 1.2e+02 -17.38 R.TGVSALYAATTTNATGRYGEGK.G  0.0 1.2e+02 17.3 R.SGADSSLKNCHNDTPLMVAR.S | |
| |  | | --- | | Top scoring peptide matches to query 1003 09MAR16\_OT\_03.01646.01646.3 Score greater than 21 indicates homology Score greater than 33 indicates identity  **Score Expect ppm Hit Protein Peptide**  50.5 0.0011 11.7 2 sp|Q9MZ16|VDAC1\_PIG|Voltage-dependent K.TKSENGLEFTSSGSANTETTK.V  5.3 35 -8.92 -.MGSGSSSYRPKAIYLDIDGR.I  3.7 51 -37.05 K.FNIVDEPGILMLSLGENTAR.A  1.4 86 -40.34 R.GLNVAATAAVMAASKGQGALSER.L  0.7 1e+02 -47.31 K.FNLMQILQDNGNLSKVQAR.L  0.6 1e+02 -44.01 R.NAAWAPLDLPSIVSEHLPMK.Q  0.6 1e+02 36.7 K.SDATEKDLSDLISEMEMMK.M  0.5 1.1e+02 -20.41 R.EXIRTYGQEIHMTELLDK.L  0.5 1.1e+02 36.7 K.SDATEKDLSDLISEMEMMK.M  0.2 1.1e+02 -32.82 R.DFQSRLPYQYLHYALFK.A | |

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| |  | | --- | | Top scoring peptide matches to query 1033 09MAR16\_OT\_03.02431.02431.3 Score greater than 19 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  63.7 3.1e-05 10.2 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  2.4 43 31.2 R.TIAETSIDPSITFQDPGSMSTGRSSIVETR.S  2.4 43 21.9 R.GAPMGMPPPGMRPPPPGMRGPPPPGMRPPRP.-  1.0 59 -34.34 -.MVMVLSPLLLVFILGLGLTPVAPAQDDYR.Y  0.8 62 37.6 K.IDAACDAFAAQLEPPHQDRAMLMLIEEK.L  0.7 63 46.9 R.LQQFDHAVEDFLKAMDMVTDTQDNLVK.Q | |
| |  | | --- | | Top scoring peptide matches to query 1034 09MAR16\_OT\_03.02427.02427.4 Score greater than 20 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  32.1 0.045 10.4 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  5.5 21 1.01 R.IIGNMALNEHLHPAIVHSGWVSLMAEALK.S  3.7 32 2.48 R.LVPITLVHDDEPVVYVSQMFNVPSDNKK.V  3.2 35 7.07 R.ASLPELPRMQRPSLPDLSRPNTTSSTGMK.H  3.0 37 -36.11 K.LETNITNALIIIENKIDIELQVYNLQR.N  2.7 40 -19.61 R.AFTMLGVVWLVAVIVGSPMWHVQQLEIK.Y  2.5 42 -29.50 R.SLPSPDDPRSSLSSWLVVLGLFSGVVLLSR.L  2.5 42 2.06 R.AYLHPTWPDVLNPFRIALDGTAVMLNSR.V  2.5 42 -3.53 K.IWSVFSLVRTFVQPASGDTQGYSVIGAAAR.K  2.5 42 -40.13 R.WPQPAGVTAGLQVALSLLLPWARVALVEPM.- | |

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| |  | | --- | | Top scoring peptide matches to query 1035 09MAR16\_OT\_03.02436.02436.4 Score greater than 23 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.5 0.0026 11.1 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  7.2 14 32.8 R.QLQLQGGSGLNTGSALSYVYANHFTEAGGSR.I  6.5 16 25.9 K.WMEELVLAVVEPSPVEGHFEIGMLNAMR.H  6.0 19 -2.60 K.LSSLCRAFVAEGILTVPMGYELASIATWK.G  5.1 23 -2.76 K.IWSVFSLVRTFVQPASGDTQGYSVIGAAAR.K  3.9 30 -6.54 -.MPAPALPTSAMAVQVPLWHHYLQAIRSR.E  2.8 39 16.5 R.HLLARVGGQAELSCQVIPPHSVMHMEVR.W  2.7 39 8.04 R.EGVDGNPPFIKLSDPGVSPTVLSLEMLTDR.I  2.7 40 1.77 K.LPLCLRMWYELVGLDEGGAGALTALGHVR.E  2.7 40 -45.58 K.VLGPGSEQLQVDSLIGPIATLLYLLSLVKM.- | |
| |  | | --- | | Top scoring peptide matches to query 1036 09MAR16\_OT\_03.02430.02430.4 Score greater than 24 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  29.1 0.09 11.6 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  9.2 8.8 -2.30 K.IWSVFSLVRTFVQPASGDTQGYSVIGAAAR.K  5.0 23 -14.36 K.LKVEXPQALSENVLFGMGNPLLDISAVVDK.D  4.5 26 17.0 R.HLLARVGGQAELSCQVIPPHSVMHMEVR.W  4.3 27 33.3 R.QLQLQGGSGLNTGSALSYVYANHFTEAGGSR.I  3.0 37 -18.38 R.AFTMLGVVWLVAVIVGSPMWHVQQLEIK.Y  2.2 44 -45.12 K.VLGPGSEQLQVDSLIGPIATLLYLLSLVKM.-  2.2 44 6.83 K.GWLAKLGPDGATFLQIPAEEIPAYMSVHR.L  1.9 48 2.24 R.IIGNMALNEHLHPAIVHSGWVSLMAEALK.S  1.7 50 36.9 K.CVTLSELYGQLDPNTMEWTDGLLSATIR.S | |

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| |  | | --- | | Top scoring peptide matches to query 1037 09MAR16\_OT\_03.02442.02442.3 Score greater than 28 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  71.3 5.5e-06 12.5 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  11.6 5.1 -9.89 K.TRAAAEVGINSETIVKPASVSEEELLNSIR.K  8.2 11 33.5 R.TIAETSIDPSITFQDPGSMSTGRSSIVETR.S  6.1 18 34.3 R.VIDSGPHCENSEIIVKLFNGNEVCLDPK.E  6.0 18 -1.27 K.LSSLCRAFVAEGILTVPMGYELASIATWK.G  4.2 28 18.0 K.KYIVVILFFMMCSLSFGSTYGLYGLNK.L  3.7 31 23.7 R.QFPSNTFLLDYLKDVSFNFVENVYQR.G  1.8 49 3.11 R.IIGNMALNEHLHPAIVHSGWVSLMAEALK.S  1.6 50 -13.90 R.MEPSLYLSPLPLSALIGGQRGWLGANSALR.V  0.5 65 24.2 R.GAPMGMPPPGMRPPPPGMRGPPPPGMRPPRP.- | |
| |  | | --- | | Top scoring peptide matches to query 1038 09MAR16\_OT\_03.02385.02385.3 Score greater than 25 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  57.3 0.00014 10.7 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  8.7 10 11.7 -.MATATGVAEERLLAALAYLQCAVGCAVFAR.N  8.0 12 -40.54 R.VSDGMQASGPATLKVVAVRPAIQILHNTGLR.L  6.9 15 -2.96 K.LSSLCRAFVAEGILTVPMGYELASIATWK.G  4.3 28 12.1 R.SPMPGVVVAVSVKPGDAVAEGQEICVIEAMK.M  2.5 43 -7.66 R.DELLNFTLVQLVYLQHAMENNIARQAR.I  1.4 55 7.22 R.GLHADTHSELEKPIQYVAYGISLMGQGIR.K  1.2 58 -43.85 K.VLGIVVQNTKVTNLSDPVVLTFQHQPQPK.N  1.0 60 8.27 R.VHITSRESLDSVEFDLHWAAVTLANNFK.C  0.8 63 38.0 K.EEILMLMARDQHPPELQAAFADCAADIK.S | |

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| |  | | --- | | Top scoring peptide matches to query 1039 09MAR16\_OT\_03.02380.02380.3 Score greater than 21 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  46.4 0.0018 10.7 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  5.3 22 24.1 R.GDVYQGHHLLPGAREAFLEQMMSLEGAVK.A  3.1 38 -2.96 K.LSSLCRAFVAEGILTVPMGYELASIATWK.G  2.8 40 -27.68 -.ISNGIPPALQPGTSAALTSLLSLPQLGSPNER.E  2.5 42 6.12 K.MEEMWDMLYLLDQFVKQLELNLLLR.E  0.5 67 -7.66 R.DELLNFTLVQLVYLQHAMENNIARQAR.I  0.4 69 12.1 R.SPMPGVVVAVSVKPGDAVAEGQEICVIEAMK.M  0.3 70 -4.94 R.EETGAALKPRLPAPPPVTTPPLAGGSSTEDSR.S  0.2 73 -3.11 R.LYPSGLGGAQYGTGKHGGLPQLPLAPSYSGQK.E | | | |
| |  | | --- | | Top scoring peptide matches to query 1040 09MAR16\_OT\_03.02374.02374.3 Score greater than 23 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  53.4 0.00035 11.3 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  6.7 16 24.7 R.GDVYQGHHLLPGAREAFLEQMMSLEGAVK.A  6.7 16 24.7 R.GDVYQGHHLLPGAREAFLEQMMSLEGAVK.A  4.0 30 -2.38 K.LSSLCRAFVAEGILTVPMGYELASIATWK.G  2.8 40 -2.54 R.LYPSGLGGAQYGTGKHGGLPQLPLAPSYSGQK.E  1.9 49 -7.09 R.DELLNFTLVQLVYLQHAMENNIARQAR.I  1.1 59 -16.35 K.LFLLIQMILNLVCGLVCLLACFVMWK.H  0.7 64 19.0 K.QAGFTTGMCVIILMGLLTLYCCYRVVK.S  0.7 65 48.9 K.CSEFPLTGEGARWSDEGIEDSLLFENLK.Q  0.5 67 -18.38 K.STAEVVFLMGLYMLPPICLGYLIGGLIMK.K | |

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| |  | | --- | | Top scoring peptide matches to query 1041 09MAR16\_OT\_03.02372.02372.4 Score greater than 20 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  36.7 0.016 11.4 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  4.8 25 -1.04 R.QKEGSLIGPTDIISISDLVPNPLQACMFR.N  4.3 28 -48.57 K.LAPALATGNTVVMKVAEQTPLSALYLASLIK.E  2.7 40 34.0 R.WMPLACCVITGLWGLVALATGTIELGMSM.-  2.5 43 31.4 K.SRELPPAWSSWMAHMAPFTVGEGLGELAR.L  1.9 49 -12.47 -.MPQLDTSTWFTTIVAMILSLFILMQLK.F  1.8 50 48.6 R.LYGWPTPEAGEGPGMAEQSLLSHQSAWAGR.R  1.7 51 -35.36 K.LLPEILQSASFLTANGALYITFFCILRK.I  1.3 56 26.0 K.WMEELVLAVVEPSPVEGHFEIGMLNAMR.H  1.1 59 6.04 K.VPEASEVALDTQCAVSRTLPGETGVSASVLR.R | | | |
| |  | | --- | | Top scoring peptide matches to query 1042 09MAR16\_OT\_03.02379.02379.4 Score greater than 24 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  27.3 0.14 11.8 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  9.4 8.6 17.9 R.EQMSGIEQLAPITEGTETGEPINQISRVR.Q  4.5 27 -34.90 K.RLICFFTIYLAGNATLFSASQLIEPLLK.Y  4.0 30 6.50 K.VPEASEVALDTQCAVSRTLPGETGVSASVLR.R  3.2 36 3.56 -.MEAGPWRVSAPPSGPPQFPAVVPGPSLEVAR.A  3.0 38 29.6 R.IHTGEKPFACNDCGKAFTQSANLIVHQR.S  2.8 40 49.1 R.LYGWPTPEAGEGPGMAEQSLLSHQSAWAGR.R  2.6 42 17.4 R.DRQMAAALLTAWSQMPVTFEDVALYLSR.E  2.2 45 -37.42 R.GIAAGYVFIPLFYGAPIPITTALILMWFK.M  1.5 53 43.4 K.TELSGPNSSSETVLSSSVTAQDNTVVNSSSSK.K | |

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| |  | | --- | | Top scoring peptide matches to query 1043 09MAR16\_OT\_03.02369.02369.4 Score greater than 22 indicates homology Score greater than 31 indicates identity  **Score Expect ppm Hit Protein Peptide**  44.6 0.0026 12.7 5 sp|Q0PGG4|ACTB\_BOSMU|Actin, R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L  6.7 16 14.4 M.PSSVPKTSIESLGSPSSLSSSQASEPLCPLK.H  6.5 17 49.9 R.GAWASQHSLLSQEAMGPGEGAEPTPWGYLR.A  2.8 39 -36.58 R.GIAAGYVFIPLFYGAPIPITTALILMWFK.M  2.2 45 17.3 R.LDNYDAPDIANIAISNELFEEAFAIFRK.F  2.2 46 0.28 K.KPPLPLPLNSSNRNIAAEIAIMEQEYMK.K  1.5 53 14.0 NSVLEVIAYSSSETPNRHDMLLVEPLNR  1.4 54 -5.72 K.DPNGLFVQRTVSPNMFDVLNVLARPVER.H  1.3 55 19.1 R.IEGLSFYHRPIQSDPYINELYWSFPK.C  1.1 58 35.3 R.WMPLACCVITGLWGLVALATGTIELGMSM.- | |
| |  | | --- | | Top scoring peptide matches to query 1052 09MAR16\_OT\_03.02268.02268.4 Score greater than 22 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  28.5 0.073 9.89 17 sp|P09951|SYN1\_RAT|Synapsin-1 K.SQSLTNAFNLPEPAPPRPSLSQDEVKAETIR.S  7.9 8.4 15.3 R.VIAPCCASSQVLYTAAAPSAMSVLLLLNEQAK.L  4.5 18 -21.17 K.LYIVGAQRVPLDLQESMTIQLLTSVFNLSK.H  3.0 26 14.3 R.KEPPPAVLEADLTEGDLANSHLPSEVLYMLK.N  2.8 27 50.0 R.HSQGRHFCYLGYTLAAATGLCGIPVMPNER.T  2.1 31 -45.99 M.PQLDTSMWLLTILSMLLTLFVLFQLKISK.H  1.6 35 38.8 R.SPEPALTPAAPSGGNGSGSGAREEAPGEAPPGPLPGR.A  1.6 35 47.2 -.MPADLSGTWTLLSSDNFEGYMLALGIDFATR.K  1.4 37 28.0 K.THYGLLFDEFQGLSHLEALEMLSRESEIK.V  1.4 37 22.5 K.LLSLASTASSQKFQSHMWSQMLVSTYGFLK.S | |

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| |  | | --- | | Top scoring peptide matches to query 1053 09MAR16\_OT\_03.02271.02271.4 Score greater than 16 indicates homology Score greater than 30 indicates identity  **Score Expect ppm Hit Protein Peptide**  12.5 2.9 10.1 17 sp|P09951|SYN1\_RAT|Synapsin-1 K.SQSLTNAFNLPEPAPPRPSLSQDEVKAETIR.S  2.9 26 -20.95 K.LYIVGAQRVPLDLQESMTIQLLTSVFNLSK.H  2.0 32 7.92 R.KLGVMFPSLDTLVLANNHLNAIEEPDDSLAR.L  1.8 34 12.4 R.SMANQIITFNISSKGQILANNVAVDETEVAAK.N  1.5 36 17.9 R.SIPELPGPGDSSKPLSAGQSVSGSLLIPGDEASSR.G  0.9 41 -13.93 K.GGQAGSHRPKPGPVSWKSLALTFAIGGSLLAGMK.Y  0.8 42 30.8 K.LFPRCAGGTDFSPVGHMIVFHLFLPSTNMK.M  0.8 43 47.5 -.MPADLSGTWTLLSSDNFEGYMLALGIDFATR.K  0.8 43 19.6 K.LIGIIEEEPTWIIMELYPYGELGHYLER.N  0.7 44 46.5 R.SMAQVHLDAMETGSDPRSEPVVASPALAGPSPR.G | |
| |  | | --- | | Top scoring peptide matches to query 1054 09MAR16\_OT\_03.02278.02278.4 Score greater than 24 indicates homology Score greater than 29 indicates identity  **Score Expect ppm Hit Protein Peptide**  19.6 0.52 13.9 17 sp|P09951|SYN1\_RAT|Synapsin-1 K.SQSLTNAFNLPEPAPPRPSLSQDEVKAETIR.S  10.4 4.3 32.0 K.THYGLLFDEFQGLSHLEALEMLSRESEIK.V  3.3 22 -10.12 K.GGQAGSHRPKPGPVSWKSLALTFAIGGSLLAGMK.Y  3.1 23 -41.96 M.PQLDTSMWLLTILSMLLTLFVLFQLKISK.H  2.9 24 -6.81 R.FLTLASHCTESTKPPVTLGWSAPVAISRPLR.A  2.8 25 34.6 K.LFPRCAGGTDFSPVGHMIVFHLFLPSTNMK.M  2.5 27 46.2 R.MVDVPVASTGVQTEAVCGDAAEEETPAVFIRK.S  1.7 32 -2.51 R.QLHISLQSEPVVTDAFLAVAGHIFSAGITWGK.V  1.3 35 23.4 K.LIGIIEEEPTWIIMELYPYGELGHYLER.N  1.1 37 44.6 K.LGISGHVHRLMAGSMAGMTAVICTYPLDMVR.V | |