```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P01.srf
Database... 100211_uniprot_sprot_human.fasta
Filter(s)... peptide probability<=5e-003 ; # distinct peptides>=2 ; protein probability<=1e-003
Mods: (M* +15.99492) C=160.03064

Reference                                                      P       Sf     Score   Coverage   Accession
  Time(s)       Sequence                              MH+    z    P       Sf       XC  DeltaCn   Sp   RSp  Ions

NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protei     2e-011  2.7      30.2     0.0       0
  23.72       K.SLVDLTAVDVPTR.Q                    1385.7635 2  2e-007  0.85   2.032  0.982   168.8  1   13/24
  24.05       R.VVAEPVELAQEFR.K                    1486.7900 2  2e-011  0.97   3.912  0.834   1004.4 1   19/24
  27.20 - 27.24K.TYTDELTPIESAVSVFK.A               1899.9586 2  3e-010  0.91   3.171  0.785   408.1  1   16/32

  3 of 3 peptide matches reported, 0 removed due to filtering


GSTM3_HUMAN Glutathione S-transferase Mu 3 OS=Homo sapiens GN=     8e-007  4.6         60.2     0.0       0
  20.92       K.IAAYLQSDQFCK.M                     1443.6937 2  8e-007  0.98      4.147  0.889   1711.6 1   18/22
  21.17       K.IAAYLQSDQFCK.M                     1443.6937 2  6e-007  0.90   2.563  0.915   538.1  1   11/22
  21.59       K.QFSM*FLGK.F                        973.4812  2  0.002   0.52   1.265  0.808   69.2   1   7/14
  21.80       K.QFSM*FLGK.F                        973.4812  2  0.0006  0.08   0.817  0.703   30.3   1   4/14
  22.40       K.LKPQYLEELPGQLK.Q                   1655.9367 3  3e-006  0.74   2.527  0.744   251.2  1   16/52
  22.53       R.VDIIENQVM*DFR.T                    1494.7257 2  5e-003  0.97    3.683  0.800   1426.9 1   17/22
  22.71       R.VDIIENQVM*DFR.T                    1494.7257 2  6e-006  0.96    3.395  0.796   1101.3 1   16/22
  24.48       R.LLLEFTDTSYEEK.R                    1587.7788 2  2e-006  0.97    3.725  0.754   1557.5 1   19/24
  28.63 - 28.66K.LDLDFPNLPYLLDGK.N                 1732.9156 2  3e-006  0.88     2.387  0.889   386.7  1   14/28

  9 of 12 peptide matches reported, 3 removed due to filtering


ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 S     4e-005  3.9        50.2     0.0       0
  19.45       R.GYSFTTTAER.E                       1132.5269 2  3e-005  0.84   2.009  0.704   499.4  1   11/18
  19.67       R.GYSFTTTAER.E                       1132.5269 2  2e-005  0.69   1.771  0.704   351.8  1   9/18
  22.05       R.DLTDYLM*K.I                        1014.4812 2  0.0008  0.85   1.457  0.734   336.1  1   11/14
  22.21       R.DLTDYLM*K.I                        1014.4812 2  0.0006  0.86   1.575  0.744   317.2  1   11/14
  22.73       R.AVFPSIVGR.P                        945.5516  2  0.0007  0.72   1.453  0.593   314.4  1   11/16
  23.44       K.DLYANTVLSGGTTM*YPGIADR.M           2231.0649 2  4e-009  0.94   3.150  0.878   830.7  1   19/40
  27.03       K.LCYVALDFEQEMATAASSSSLEK.S          2550.1738 2  6e-008  0.73   1.423  -       353.3  1   12/44

  7 of 10 peptide matches reported, 3 removed due to filtering


ACTG_HUMAN Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1      4e-005  3.9        50.2     0.0       0
  19.45       R.GYSFTTTAER.E                       1132.5269 2  3e-005  0.84   2.009  0.704   499.4  1   11/18
  19.67       R.GYSFTTTAER.E                       1132.5269 2  2e-005  0.69   1.771  0.704   351.8  1   9/18
  22.05       R.DLTDYLM*K.I                        1014.4812 2  0.0008  0.85   1.457  0.734   336.1  1   11/14
  22.21       R.DLTDYLM*K.I                        1014.4812 2  0.0006  0.86   1.575  0.744   317.2  1   11/14
  22.73       R.AVFPSIVGR.P                        945.5516  2  0.0007  0.72   1.453  0.593   314.4  1   11/16
  23.44       K.DLYANTVLSGGTTM*YPGIADR.M           2231.0649 2  4e-009  0.94   3.150  0.878   830.7  1   19/40
  27.03       K.LCYVALDFEQEMATAASSSSLEK.S          2550.1738 2  6e-008  0.73   1.423  -       353.3  1   12/44

  7 of 10 peptide matches reported, 3 removed due to filtering


GFAP_HUMAN Glial fibrillary acidic protein OS=Homo sapiens GN=     6e-004  1.9        20.2     0.0       0
  20.81       K.LADVYQAELR.E                       1177.6212 2  6e-004  0.94     2.206  0.725   1013.2 1   15/18
  21.75       K.ALAAELNQLR.A                       1098.6266 2  1e-004  0.97    3.327  0.462   1805.0 1   16/18

  2 of 2 peptide matches reported, 0 removed due to filtering
```