```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P12.srf
Database... 100211_uniprot_sprot_human.fasta
Filter(s)... peptide probability<=5e-003 ; # distinct peptides>=2 ; protein probability<=1e-011
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


GFAP_HUMAN Glial fibrillary acidic protein OS=Homo sapiens GN=    1e-011  12.2    128.2    0.0       0
  18.87       R.EAASYQEALAR.L                        1208.5906 2  4e-007  0.97   3.434  0.725   1221.9 1   16/20
  19.07       R.EAASYQEALAR.L                        1208.5906 2  5e-006  0.81   2.447  0.779   400.9  1   9/20
  19.71       R.LEAENNLAAYR.Q                        1263.6328 2  5e-008  0.96   3.069  0.664   1336.1 1   17/20
  19.87       R.LEAENNLAAYR.Q                        1263.6328 2  4e-005  0.88   2.386  0.513   837.8  1   13/20
  19.97       K.FADLTDAAAR.N                         1050.5214 2  2e-007  0.97   3.234  0.736   1385.2 1   17/18
  19.99       R.SYVSSGEM*M*VGGLAPGR.R                1729.7884 2  1e-011  0.93   2.125  0.753   956.6  1   21/32
  20.11       R.KIESLEEEIR.F                         1245.6685 2  4e-006  0.94   3.002  0.392   1123.6 1   15/18
  20.15       K.FADLTDAAAR.N                         1050.5214 2  1e-007  0.97   2.830  0.812   1290.5 1   16/18
  20.18       R.SYVSSGEM*M*VGGLAPGR.R                1729.7884 2  1e-010  0.79   1.320  -       412.9  1   14/32
  20.33       R.KIESLEEEIR.F                         1245.6685 2  3e-005  0.85   2.234  0.608   591.5  1   11/18
  20.60       R.LRLDQLTANSAR.L                       1357.7546 3  0.0001  0.87   2.732  0.695   749.5  1   18/44
  21.73       K.ALAAELNQLR.A                         1098.6266 2  7e-006  0.97   3.429  0.489   1867.5 1   16/18
  21.89       K.ALAAELNQLR.A                         1098.6266 2  1e-005  0.97   3.302  0.467   1857.8 1   16/18
  21.90       R.HLQEYQDLLNVK.L                       1499.7853 2  7e-008  0.98   3.672  0.872   1871.5 1   19/22
  21.94       R.HLQEYQDLLNVK.L                       1499.7853 3  0.0003  0.94   3.526  0.854   778.4  1   18/44
  22.11       R.HLQEYQDLLNVK.L                       1499.7853 2  4e-006  0.92   2.756  0.862   556.9  1   12/22
  22.41       R.LEVERDNLAQDLATVR.Q                   1841.9716 3  0.0002  0.85   2.449  0.767   710.7  1   19/60
  22.69       R.DNLAQDLATVR.Q                        1215.6328 2  1e-007  0.98   3.773  0.732   1921.7 1   18/20
  22.85       R.DNLAQDLATVR.Q                        1215.6328 2  3e-007  0.96   3.045  0.683   986.0  1   18/20
  24.54       K.LALDIEIATYR.K                        1277.7100 2  1e-006  0.96   3.160  0.891   1159.6 1   14/20
  24.79       K.LALDIEIATYR.K                        1277.7100 2  4e-009  0.98   3.328  0.883   1851.2 1   17/20
  25.08       R.ITIPVQTFSNLQIR.E                     1629.9323 2  1e-011  0.92   2.670  0.618   718.9  1   18/26
  25.31       R.ITIPVQTFSNLQIR.E                     1629.9323 2  7e-010  0.64   1.721  0.574   286.5  1   13/26
  26.22       R.VDFSLAGALNAGFK.E                     1409.7423 2  1e-009  0.94   2.137  0.621   1445.0 1   20/26
  26.41       R.VDFSLAGALNAGFK.E                     1409.7423 2  8e-007  0.80   1.948  0.716   553.5  1   13/26
  27.78       K.LALDIEIATYR.K                        1277.7100 2  5e-005  0.87   1.855  0.819   733.5  1   11/20
  28.26       K.LALDIEIATYR.K                        1277.7100 2  1e-005  0.73   1.787  0.815   377.0  1   9/20

  27 of 37 peptide matches reported, 10 removed due to filtering
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