```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P11.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

ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2        5e-010  2.6      40.1     0.0       0
  23.26 - 23.30R.GNPTVEVDLFTSK.G                          1406.7162 2  6e-008  0.29    2.266  0.240   178.1  1   10/24
  23.66 - 23.72K.FTASAGIQVVGDDLTVTNPK.R                   2033.0550 2  5e-007  0.73    2.149  0.843   244.7  1   12/38
  24.59 - 24.63K.VVIGM*DVAASEFFR.S                        1556.7777 2  3e-009  0.91    2.390  0.885   659.6  1   14/26
  24.80 - 24.84R.AAVPSGASTGIYEALELR.D                     1804.9440 2  5e-010  0.71    1.701  0.808   178.3  1   15/34

  4 of 4 peptide matches reported, 0 removed due to filtering


ENOG_HUMAN Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3        5e-010  0.7      18.1     0.0       0
  23.26 - 23.30R.GNPTVEVDLYTAK.G                          1406.7162 2  4e-005  0.03    1.721  0.903   104.1  2   8/24
  24.80 - 24.84R.AAVPSGASTGIYEALELR.D                     1804.9440 2  5e-010  0.71    1.701  0.808   178.3  1   15/34

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