```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P02.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


ENOG_HUMAN Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3        1e-014  4.8      60.2     0.0       0
  18.49       R.IEEELGDEAR.F                          1160.5430 2  0.001   0.16   1.259  0.277   299.7  1   8/18
  21.33       R.GNPTVEVDLYTAK.G                       1406.7162 2  1e-008  0.81   3.124  0.140   515.5  1   17/24
  21.46       K.VNQIGSVTEAIQACK.L                     1617.8265 2  3e-013  0.98   4.238  0.866   1788.5 1   22/28
  22.43       K.LDNLM*LELDGTENK.S                     1620.7785 2  3e-011  0.97   3.369  0.799   1382.3 1   20/26
  24.84       R.AAVPSGASTGIYEALELR.D                  1804.9440 2  1e-014  0.92   2.538  0.691   594.2  1   24/34
  27.10       R.YITGDQLGALYQDFVR.D                    1858.9334 2  6e-012  0.97   3.463  0.912   1304.6 1   21/30

  6 of 7 peptide matches reported, 1 removed due to filtering


ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2        1e-012  1.4       18.1     0.0       0
  21.33       R.GNPTVEVDLFTSK.G                       1406.7162 2  0.0001  0.46   2.687  0.887   301.7  2   14/24
  24.84       R.AAVPSGASTGIYEALELR.D                  1804.9440 2  1e-012  0.92    2.538  0.691   594.2  1   24/34

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