```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P24.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

G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sap    3e-012  5.0      70.2     0.0       0
  18.12       K.LTGM*AFR.V                           811.4131  2  0.0008  0.84   1.927  0.524   362.7  1   10/12
  18.24       K.LTGM*AFR.V                           811.4131  2  0.0009  0.88   1.937  0.667   360.0  1   10/12
  21.64       R.VIISAPSADAPM*FVM*GVNHEK.Y            2245.0992 3  0.0008  0.57   2.168  0.839   65.8   1   11/80
  21.67       R.GALQNIIPASTGAAK.A                    1411.7904 2  1e-006  0.90   2.616  0.794   471.1  1   16/28
  21.78       R.GALQNIIPASTGAAK.A                    1411.7904 2  6e-006  0.90   2.957  0.795   392.9  1   15/28
  21.97       R.VPTANVSVVDLTCR.L                     1530.7944 2  5e-011  0.95   3.186  0.870   854.8  1   17/26
  22.10       R.VPTANVSVVDLTCR.L                     1530.7944 2  4e-012  0.95   2.734  0.866   928.7  1   18/26
  22.98       R.GALQNIIPASTGAAK.A                    1411.7904 2  1e-005  0.28   1.502  0.689   128.8  1   8/28
  24.43       K.LISWYDNEFGYSNR.V                     1763.8024 2  3e-012  0.98   3.588  0.890   1554.8 1   19/26
  24.56       K.LISWYDNEFGYSNR.V                     1763.8024 2  1e-010  0.97   3.188  0.870   1387.4 1   18/26
  25.75       K.LVINGNPITIFQER.D                     1613.9010 2  7e-012  0.71   2.261  0.734   255.2  1   10/26
  28.38       K.VDIVAINDPFIDLNYM*VYM*FQYDSTHGK.F     3340.5541 3  4e-005  0.04   1.385  -       64.3   1   9/108

  12 of 15 peptide matches reported, 3 removed due to filtering

ALBU_HUMAN Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2           0.0002  1.8      20.2     0.0       0
  20.90       K.YLYEIAR.R                            927.4934  2  0.0002  0.89   2.166  0.495   444.3  1   11/12
  21.01       K.KVPQVSTPTLVEVSR.N                    1639.9377 3  0.0003  0.96   3.778  0.938   1030.5 1   26/56

  2 of 4 peptide matches reported, 2 removed due to filtering
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