```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P14.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
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GRHPR_HUMAN Glyoxylate reductase/hydroxypyruvate reductase OS=     1e-008  5.1      60.2     0.0        0
  19.48       R.ILDAAGANLK.V                         985.5677  2  2e-005  0.94    2.723  0.537   835.7  1   16/18
  19.60       R.ILDAAGANLK.V                         985.5677  2  0.0001  0.87    2.038  0.522   626.2  1   14/18
  19.97       R.RLPEAIEEVK.N                         1183.6681 2  6e-006  0.88    2.210  0.840   381.1  1   11/18
  20.04       R.RLPEAIEEVK.N                         1183.6681 2  0.001   0.67    1.778  0.719   252.1  1   9/18
  20.32 - 20.3R.LPEAIEEVK.N                          1027.5670 2  3e-006  0.92    2.709  0.681   465.5  1   13/16
  22.56       K.ETAVFINISR.G                         1149.6262 2  7e-005  0.83    2.174  0.543   499.1  1   12/18
  22.63       K.ETAVFINISR.G                         1149.6262 2  0.002   0.58    1.691  0.607   283.4  1   9/18
  24.28       K.IAAAGLDVTSPEPLPTNHPLLTLK.N           2468.3759 3  4e-005  0.56    2.090  0.759   135.5  1   13/92
  26.12 - 26.1R.NTM*SLLAANNLLAGLR.G                  1687.9160 2  1e-008  0.98    4.388  0.763   2144.4 1   22/30

  9 of 15 peptide matches reported, 6 removed due to filtering


RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=     4e-007  3.6      40.1     0.0        0
  22.21 - 22.2R.GNVGFVFTK.E                          968.5200  2  4e-005  0.91    1.607  0.794   700.2  1   13/16
  23.76       K.IIQLLDDYPK.C                         1217.6776 2  4e-007  0.96    2.391  0.819   1306.7 1   14/18
  25.58 - 25.6K.AFLADPSAFVAAAPVAAATTAAPAAAAAPAK.V    2752.4668 3  6e-005  0.82    2.561  0.971   209.6  1   20/120
  26.48 - 26.5K.TSFFQALGITTK.I                       1313.7100 2  5e-007  0.92    2.714  0.893   654.7  1   12/22

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


RLA0L_HUMAN 60S acidic ribosomal protein P0-like OS=Homo sapie     4e-007  1.9      20.1     0.0        0
  23.76       K.IIQLLDDYPK.C                         1217.6776 2  4e-007  0.96    2.391  0.819   1306.7 1   14/18
  26.48 - 26.5K.TSFFQALGITTK.I                       1313.7100 2  5e-007  0.92    2.714  0.893   654.7  1   12/22

  2 of 5 peptide matches reported, 3 removed due to filtering


GFAP_HUMAN Glial fibrillary acidic protein OS=Homo sapiens GN=     4e-007  1.4      18.1     0.0        0
  24.92       K.LALDIEIATYR.K                        1277.7100 2  2e-006  0.97    2.952  0.845   1488.8 1   15/20
  25.15       K.LALDIEIATYR.K                        1277.7100 2  4e-007  0.95    2.544  0.903   1090.7 1   13/20
  26.23       R.VDFSLAGALNAGFK.E                     1409.7423 2  0.0002  0.43    1.423  0.633   304.3  1   10/26

  3 of 4 peptide matches reported, 1 removed due to filtering


ALBU_HUMAN Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2          2e-006  2.2      30.2     0.0        0
  20.83       K.YLYEIAR.R                            927.4934  2  0.0003  0.89    2.102  0.523   442.8  1   11/12
  20.91       K.YLYEIAR.R                            927.4934  2  0.004   0.90    2.056  0.599   448.9  1   11/12
  20.93 - 20.9K.KVPQVSTPTLVEVSR.N                    1639.9377 3  2e-006  0.96    4.013  0.897   1131.8 1   25/56
  21.70       K.VPQVSTPTLVEVSR.N                     1511.8428 2  0.0002  0.35    1.892  0.478   246.3  1   9/26
  21.78       K.VPQVSTPTLVEVSR.N                     1511.8428 2  7e-005  0.37    2.174  0.346   263.6  1   10/26

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