```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P20.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

TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo s     2e-014  20.7     250.2    0.0        0
  17.35 - 17.4K.LAGESESNLR.K                         1075.5378 2  3e-007  0.95    2.869  0.636    978.3  1    16/18
  19.26        R.ESIESEIR.R                          962.4789  2  0.001   0.73    1.674  0.302    509.4  1    11/14
  19.45        R.ESIESEIR.R                          962.4789  2  0.0003  0.29    1.666  0.317    250.6  1    7/14
  20.04        R.KYEM*FAQTLQQSR.G                    1645.8003 3  0.0004  0.73    2.396  0.789    261.9  1    14/48
  20.25        R.VINQILTEM*DGM*STK.K                 1711.8241 2  1e-012  0.98    3.611  0.883    1688.3 1    22/28
  20.27        R.VINQILTEM*DGM*STK.K                 1711.8241 3  0.001   0.87    3.043  0.931    260.0  1    18/56
  20.38        K.YEM*FAQTLQQSR.G                     1517.7053 2  3e-008  0.95    2.879  0.914    937.4  1    13/22
  21.24        R.QTNPSAM*EVEEDDPVPEIR.R              2171.9761 2  2e-013  0.91    3.003  0.816    553.5  1    16/36
  21.25        R.QTNPSAM*EVEEDDPVPEIR.R              2171.9761 3  4e-009  0.93    2.811  0.885    875.4  1    30/72
  21.37        R.QTNPSAM*EVEEDDPVPEIR.R              2171.9761 2  7e-009  0.90    2.878  0.837    491.9  1    15/36
  21.42        R.EDEEESLNEVGYDDIGGCR.K               2185.8826 2  1e-011  0.58    2.342  -        716.5  1    19/36
  21.44        R.WALSQSNPSALR.E                      1329.6910 2  4e-007  0.94    3.253  0.691    832.2  1    14/22
  21.45        R.QTNPSAM*EVEEDDPVPEIR.R              2171.9761 3  9e-006  0.23    0.991  0.745    91.5   1    11/72
  21.53        R.EVDIGIPDATGR.L                      1242.6325 2  0.0005  0.91    2.625  0.708    543.6  1    15/22
  21.69        K.GDDLSTAILK.Q                        1032.5572 2  3e-005  0.95    2.861  0.641    933.2  1    15/18
  21.81        R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG. 3220.3210 3  3e-005  0.03    1.163  -        38.1   1    9/132
  21.87        K.GDDLSTAILK.Q                        1032.5572 2  2e-005  0.93    2.282  0.621    916.4  1    15/18
  21.95        R.FPSGNQGGAGPSQGSGGGTGGSVYTEDNDDDLYG. 3220.3210 3  0.0008  0.02    0.652  -        10.1   1    5/132
  22.02        K.AIANECQANFISIK.G                    1578.7944 2  8e-007  0.93    2.902  0.727    888.0  1    15/26
  22.17        R.LGDVISIQPCPDVK.Y                    1540.8040 2  4e-008  0.96    4.080  0.702    855.5  1    17/26
  22.36        K.GVLFYGPPGCGK.T                      1251.6191 2  1e-005  0.87    2.430  0.784    498.1  1    12/22
  22.41        R.LGDVISIQPCPDVK.Y                    1540.8040 2  4e-006  0.91    3.037  0.775    547.0  1    14/26
  22.48        R.GILLYGPPGTGK.T                      1172.6674 2  6e-008  0.96    3.738  0.000    924.6  1    16/22
  22.66        R.GILLYGPPGTGK.T                      1172.6674 2  7e-007  0.96    3.114  0.000    1205.0 1    18/22
  22.97        K.GDIFLVR.G                           819.4723  2  0.003   0.76    2.120  0.149    630.8  1    10/12
  23.28        K.M*DELQLFR.G                         1067.5190 2  0.0001  0.97    2.953  0.686    1523.3 1    13/14
  23.31        R.LIVDEAINEDNSVVSLSQPK.M              2170.1238 3  2e-006  0.96    4.573  0.896    811.8  1    25/76
  23.45        R.LIVDEAINEDNSVVSLSQPK.M              2170.1238 2  2e-014  0.98    4.785  0.949    2007.3 1    25/38
  23.47        K.M*DELQLFR.G                         1067.5190 2  0.0002  0.97    2.834  0.687    1487.9 1    13/14
  23.52        R.LIVDEAINEDNSVVSLSQPK.M              2170.1238 3  7e-007  0.93    3.354  0.927    753.6  1    25/76
  23.63        R.LIVDEAINEDNSVVSLSQPK.M              2170.1238 2  1e-013  0.98    3.711  0.953    1950.6 1    26/38
  24.54        R.IVSQLLTLM*DGLK.Q                    1446.8236 2  6e-009  0.98    4.335  0.793    1417.4 1    18/24
  24.57        K.DVDLEFLAK.M                         1049.5514 2  3e-005  0.91    1.928  0.747    580.2  1    13/16
  24.69        R.IVSQLLTLM*DGLK.Q                    1446.8236 2  3e-008  0.97    4.021  0.836    1375.3 1    18/24
  24.74        K.DVDLEFLAK.M                         1049.5514 2  2e-007  0.90    1.862  0.726    546.3  1    13/16
  25.99        R.LDQLIYIPLPDEK.S                     1556.8570 2  2e-008  0.96    3.862  0.707    1069.4 1    17/24
  26.14        R.LDQLIYIPLPDEK.S                     1556.8570 2  2e-007  0.95    3.226  0.746    914.1  1    16/24
  27.98        R.AVANETGAFFFLINGPEIM*SK.L            2272.1318 3  8e-007  0.75    2.780  0.826    224.2  1    13/80
  28.85        K.M*DLIDLEDETIDAEVM*NSLAVTM*DDFR.W    3149.3847 3  2e-009  0.89    3.396  0.879    278.6  1    21/104
  28.89 - 28.9R.QAAPCVLFFDELDSIAK.A                  1923.9521 2  1e-011  0.70    1.400  0.748    422.0  1    14/32
  28.94        K.M*DLIDLEDETIDAEVM*NSLAVTM*DDFR.W    3149.3847 3  0.0005  0.35    1.242  0.724    38.6   1    8/104
  28.98        R.QAAPCVLFFDELDSIAK.A                 1923.9521 3  2e-005  0.52    2.199  0.563    340.2  1    14/64
  29.20 - 29.2K.NAPAIIFIDELDAIAPK.R                  1810.9949 2  2e-011  0.94    2.283  0.729    1206.1 1    22/32
  29.38 - 29.4K.NAPAIIFIDELDAIAPK.R                  1810.9949 3  3e-009  0.84    2.642  0.798    494.9  1    20/64

  44 of 55 peptide matches reported, 11 removed due to filtering


TBA1A_HUMAN Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A P     6e-007  3.7        40.2     0.0        0
  20.76        K.DVNAAIATIK.T                        1015.5782 2  0.0006  0.93    2.883  0.566    939.3  1    14/18
  25.25        K.EIIDLVLDR.I                         1085.6201 2  5e-006  0.91    2.013  0.619    758.5  1    13/16
  25.65        R.AVFVDLEPTVIDEVR.T                   1701.9058 2  6e-007  0.97     4.075  0.806    987.1  1    21/28
  25.89        R.AVFVDLEPTVIDEVR.T                   1701.9058 2  0.0003  0.55    1.924  0.817    138.1  1    8/28
  28.11 - 28.1R.LIGQIVSSITASLR.F                     1457.8686 2  1e-007  0.89    2.528  0.843    581.9  1    13/26

  5 of 9 peptide matches reported, 4 removed due to filtering


TBA1B_HUMAN Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B P     6e-007  3.8       40.2     0.0        0
  20.76        K.DVNAAIATIK.T                        1015.5782 2  0.0006  0.93    2.883  0.566    939.3  1    14/18
  25.25        K.EIIDLVLDR.I                         1085.6201 2  5e-006  0.91    2.013  0.619    758.5  1    13/16
  25.65        R.AVFVDLEPTVIDEVR.T                   1701.9058 2  6e-007  0.97     4.075  0.806    987.1  1    21/28
  25.89        R.AVFVDLEPTVIDEVR.T                   1701.9058 2  0.0003  0.55    1.924  0.817    138.1  1    8/28
  28.31 - 28.3R.LISQIVSSITASLR.F                     1487.8792 2  4e-006  0.96     3.441  0.916    1001.0 1    17/26

  5 of 9 peptide matches reported, 4 removed due to filtering


TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C P     6e-007  3.8       40.2     0.0        0
  20.76        K.DVNAAIATIK.T                        1015.5782 2  0.0006  0.93    2.883  0.566    939.3  1    14/18
  25.25        K.EIIDLVLDR.I                         1085.6201 2  5e-006  0.91    2.013  0.619    758.5  1    13/16
  25.65        R.AVFVDLEPTVIDEVR.T                   1701.9058 2  6e-007  0.97     4.075  0.806    987.1  1    21/28
  25.89        R.AVFVDLEPTVIDEVR.T                   1701.9058 2  0.0003  0.55    1.924  0.817    138.1  1    8/28
  28.31 - 28.3R.LISQIVSSITASLR.F                     1487.8792 2  4e-006  0.96     3.441  0.916    1001.0 1    17/26

  5 of 9 peptide matches reported, 4 removed due to filtering
```