```
SRF File: C:\Xcalibur\data\100730RS\100730RS-P03.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

GNAO_HUMAN Guanine nucleotide-binding protein G(o) subunit alp     6e-015  11.0     120.3    0.0       0
  18.57       K.IIHEDGFSGEDVK.Q                      1445.6907 3  0.002   0.88   2.796  0.693   748.8  1   20/48
  18.68       K.IIHEDGFSGEDVK.Q                      1445.6907 2  6e-010  0.94   2.801  0.730   822.5  1   18/24
  18.75       K.IIHEDGFSGEDVK.Q                      1445.6907 2  3e-011  0.95   2.916  0.696   964.8  1   19/24
  19.42       R.AM*DTLGIEYGDKER.K                    1613.7476 3  3e-006  0.85   3.049  0.825   258.2  1   18/52
  20.32       R.LFDVGGQR.S                           891.4683  2  0.0006  0.93   1.966  0.722   771.9  1   13/14
  20.35       R.AM*DTLGIEYGDK.E                      1328.6039 2  3e-008  0.98   4.064  0.862   1298.2 1   18/22
  20.47       R.LFDVGGQR.S                           891.4683  2  0.0003  0.94   2.003  0.727   752.2  1   13/14
  20.48       R.AM*DTLGIEYGDK.E                      1328.6039 2  5e-008  0.97   3.723  0.857   1271.9 1   18/22
  21.27       K.YYLDSLDR.I                           1044.4997 2  0.0004  0.88   2.506  0.199   690.1  1   13/14
  21.61       K.TTGIVETHFTFK.D                       1380.7158 2  6e-008  0.95   2.738  0.767   1002.5 1   17/22
  21.64       R.IGAADYQPTEQDILR.T                    1689.8442 2  9e-010  0.96   3.872  0.798   780.2  1   20/28
  21.72       R.IGAADYQPTEQDILR.T                    1689.8442 2  1e-009  0.96   3.958  0.757   689.8  1   19/28
  21.84       K.TTGIVETHFTFK.D                       1380.7158 2  7e-008  0.94   2.713  0.752   842.4  1   16/22
  22.67       K.LLLLGAGESGK.S                        1057.6252 2  1e-006  0.96   3.031  0.000   1101.7 1   16/20
  22.79       K.LLLLGAGESGK.S                        1057.6252 2  7e-007  0.97   3.390  0.000   1361.1 1   18/20
  23.42       R.M*EDTEPFSAELLSAM*M*R.L               2005.8551 2  6e-012  0.98   6.008  0.957   1422.1 1   22/32
  23.56       R.M*EDTEPFSAELLSAM*M*R.L               2005.8551 2  1e-012  0.98   4.799  0.927   1221.6 1   21/32
  23.63       R.M*EDTEPFSAELLSAM*M*R.L               2005.8551 3  4e-006  0.89   2.551  0.941   611.9  1   21/64
  25.62       K.QYKPVVYSNTIQSLAAIVR.A                2150.1968 3  4e-006  0.64   2.200  0.748   288.8  1   14/72
  26.49       K.PVVYSNTIQSLAAIVR.A                   1730.9799 2  8e-010  0.95   2.861  0.855   1126.2 1   16/30
  28.14       K.SPLTICFPEYTGPNTYEDAAAYIQAQFESK.N     3411.5726 3  6e-015  0.95   4.249  0.892   777.9  1   25/116
  28.24       K.SPLTICFPEYTGPNTYEDAAAYIQAQFESK.N     3411.5726 3  5e-011  0.93   3.953  0.840   608.1  1   24/116

  22 of 28 peptide matches reported, 6 removed due to filtering


IDH3A_HUMAN Isocitrate dehydrogenase [NAD] subunit alpha, mito     2e-008  4.7        50.3     0.0       0
  21.28       R.M*SDGLFLQK.C                         1054.5238 2  2e-005  0.92   2.188  0.783   564.3  1   13/16
  21.31       R.IEAACFATIK.D                         1123.5816 2  1e-006  0.84   2.301  0.570   461.0  1   12/18
  21.51       R.M*SDGLFLQK.C                         1054.5238 2  0.0005  0.77   1.302  0.697   376.5  1   11/16
  22.55       K.TPYTDVNIVTIR.E                       1391.7529 2  2e-008  0.95     3.026  0.760   1046.1 1   15/22
  23.44       R.IAEFAFEYAR.N                         1216.5997 2  4e-008  0.97   3.426  0.694   1602.8 1   17/18
  29.24       K.DM*ANPTALLLSAVM*M*LR.H               1894.9435 2  4e-008  0.97   4.570  0.846   1143.9 1   20/32

  6 of 6 peptide matches reported, 0 removed due to filtering
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