```
Database... 070909ipiHUMANv361Processed.fasta
Filter(s)... None
Mods:  (M* +15.99492) C=161.01468

Reference                                                           P     Score   Coverage   Accession
  Scan(s)       Sequence                                MH+    z    P       XC  DeltaCn   Sp   RSp  Ions

IPI:IPI00022463.1|SWISS-PROT:P02787|TREMBL:A0PJA6;B4DEX9;B4DHZ    1e-007  22.2     0.0       0
  19287468 - 1R.WCAVSEHEATK.C                        1318.57   2  1e-007  4.487  0.529   1202.0 1   20/30
  19287468 - 1K.SKEFQLFSSPHGK.D                      1491.76   3  8e-007  4.643  0.609   849.7  1   27/72
  19287468 - 1K.KASYLDCIR.A                          1126.56   2  0.06    1.175  0.496   163.9  4   10/24

  3 of 3 peptide matches reported, 0 removed due to filtering


IPI:IPI00877763.1|VEGA:OTTHUMP0000                                1e-007  12.2     0.0       0
  19287468 - 1R.WCAVSEHEATK.C                        1318.57   2  1e-007  4.487  0.529   1202.0 1   20/30
  19287468 - 1K.KASYLDCIR.A                          1126.56   2  0.06    1.175  -       163.9  4   10/24

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


IPI:IPI00879916.1|VEGA:OTTHUMP0000                                1e-007  10.2     0.0       0
  19287468 - 1R.WCAVSEHEATK.C                        1318.57   2  1e-007  4.487  0.529   1202.0 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00791330.1|VEGA:OTTHUMP0000                                8e-007  10.2     0.0       0
  19287468 - 1K.SKEFQLFSSPHGK.D                      1491.76   3  8e-007  4.643  0.609   849.7  1   27/72

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00792626.1|VEGA:OTTHUMP0000                                8e-007  10.2     0.0       0
  19287468 - 1K.SKEFQLFSSPHGK.D                      1491.76   3  8e-007  4.643  0.609   849.7  1   27/72

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00798430.2|VEGA:OTTHUMP0000                                8e-007  10.2     0.0       0
  19287468 - 1K.SKEFQLFSSPHGK.D                      1491.76   3  8e-007  4.643  0.609   849.7  1   27/72

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00305461.3|SWISS-PROT:P19823|TREMBL:A2RTY6|ENSEMBL:ENSP    1e-006  10.2     0.0       0
  2118291816 -R.LSNENHGIAQR.I                        1238.62   2  1e-006  4.292  0.485   789.7  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00645038.1|TREMBL:Q5T985|EN                                1e-006  10.2     0.0       0
  2118291816 -R.LSNENHGIAQR.I                        1238.62   2  1e-006  4.292  0.485   789.7  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00910636.1|TREMBL:B4DM79 Ta                                1e-006  10.2     0.0       0
  2118291816 -R.LSNENHGIAQR.I                        1238.62   2  1e-006  4.292  0.485   789.7  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00017601.1|SWISS-PROT:P00450|TREMBL:A5PL27;A8K5A4;B7Z5Q    1e-006  20.2     0.0       0
  19287468 - 1K.ALYLQYTDETFR.T                       1519.74   2  1e-006  4.725  0.473   1101.8 1   20/33
  2118291816 -K.VNKDDEEFIESNK.M                      1566.73   3  3e-005  3.718  0.554   800.2  1   25/72

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


IPI:IPI00879084.1|VEGA:OTTHUMP0000                                1e-006  10.2     0.0       0
  19287468 - 1K.ALYLQYTDETFR.T                       1519.74   2  1e-006  4.725  0.473   1101.8 1   20/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00916434.1|TREMBL:A2KBB9;A2                                1e-006  20.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  2 of 2 peptide matches reported, 0 removed due to filtering
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IPI:IPI00929201.1|TREMBL:A2KBC2;A2                                 1e-006  20.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

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


IPI:IPI00784985.1|TREMBL:Q6PJF2 Ta                                 1e-006  20.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45
  19287468 - 1K.SGTASVVCLLNNFYPR.E                   1798.88   2  5e-005  3.485  0.433   766.8  1   17/45

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


IPI:IPI00889156.1|TREMBL:Q15537;Q6                                 1e-006  20.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45
  19287468 - 1K.SGTASVVCLLNNFYPR.E                   1798.88   2  5e-005  3.485  0.433   766.8  1   17/45

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


IPI:IPI00030205.3|SWISS-PROT:P18135|ENSEMBL:ENSP00000374790|VE     1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384576.1|SWISS-PROT:P1813                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00385252.1|SWISS-PROT:P0420                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00387115.1|SWISS-PROT:P0162                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00387117.5|SWISS-PROT:P0162                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00387118.1|SWISS-PROT:P0162                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827510.1|TREMBL:A2IPI5 Ta                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827560.1|TREMBL:A2IPI2;A2                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827637.1|TREMBL:A2NXP9 Ta                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00854644.2|TREMBL:A6NLY3|EN                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00885193.1|TREMBL:Q9UL78 Ta                                 1e-006  10.2     0.0       0
  19287468 - 1R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45
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  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022426.1|SWISS-PROT:P02760|TREMBL:P78492|ENSEMBL:ENSP    1e-006  10.2     0.0       0
  19287468 - 1R.AFIQLWAFDAVK.G                       1408.76   2  1e-006  3.585  0.380   1474.7 1   21/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022371.1|SWISS-PROT:P04196|TREMBL:B2R8I2;B9EK35;Q68DR    2e-006  10.1     0.0       0
  19287468 - 1R.ADLFYDVEALDLESPK.N                   1824.89   2  2e-006  2.497  0.458   790.6  1   18/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828156.1|TREMBL:A2NKM6 Ta                                3e-006  20.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30
  2118291816 -R.LSCAASGFTFR.S                        1217.56   2  6e-006  3.492  0.654   1231.4 1   20/30

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


IPI:IPI00383887.1|TREMBL:Q9UGP3 Tax_Id=9606 Gene_Symbol=- Immu    3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384392.1|TREMBL:Q9UL72 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00413194.1|TREMBL:Q9UL93 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00736507.2|TREMBL:Q0ZCG7;Q0                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00748665.3|TREMBL:A2J1N3;Q0                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00748998.1|TREMBL:Q65ZC9 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00760721.3|ENSEMBL:ENSP0000                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783094.1|TREMBL:Q0ZCG4;Q0                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783116.1|TREMBL:Q0ZCI5 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783244.1|TREMBL:Q0ZCH1;Q0                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00783393.1|TREMBL:Q0ZCI2 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783818.1|TREMBL:Q0ZCJ1 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783909.1|TREMBL:Q0ZCH0 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00784513.1|TREMBL:Q0ZCI3 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827581.1|TREMBL:A2NZ55 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827589.1|TREMBL:A2NXP8 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827678.1|TREMBL:A2NWX5 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827814.1|TREMBL:A2NWX1 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827929.1|TREMBL:A2NWW9 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827938.1|TREMBL:A2NWW5 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827940.1|SWISS-PROT:P0176                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827989.1|TREMBL:A2NWW6 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828022.1|TREMBL:A2NWW7 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828061.1|TREMBL:A2JA14 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                    1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00828085.1|TREMBL:A2NWW4 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828099.1|TREMBL:A2KUC3 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828105.1|TREMBL:A2J423 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828153.1|TREMBL:A2NWW1 Ta                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829724.1|TREMBL:A6NFJ8|EN                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829747.2|ENSEMBL:ENSP0000                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829806.1|TREMBL:Q0ZCH8;Q0                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829976.1|TREMBL:A2N192|EN                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00830088.1|ENSEMBL:ENSP0000                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00854707.1|TREMBL:A2J1M5;Q0                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00873155.2|TREMBL:A6NG04|EN                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00888191.1|REFSEQ:XP_001714                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00888954.1|REFSEQ:XP_001717                                3e-006  10.2     0.0       0
  19287468 - 1K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022432.1|SWISS-PROT:P02766|TREMBL:A6XMH1;Q53WY6;Q549C    3e-006  10.3     0.0       0
  19287468 - 1K.TSESGELHGLTTEEEFVEGIYK.V             2455.15   3  3e-006  5.015  0.570    946.8  1   30/126

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00646384.1|VEGA:OTTHUMP0000                                 3e-006  10.3     0.0       0
  19287468 - 1K.TSESGELHGLTTEEEFVEGIYK.V              2455.15   3  3e-006  5.015  0.570   946.8  1    30/126

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00855916.1|TREMBL:A6XGL1 Ta                                 3e-006  10.3     0.0       0
  19287468 - 1K.TSESGELHGLTTEEEFVEGIYK.V              2455.15   3  3e-006  5.015  0.570   946.8  1    30/126

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00423463.1|TREMBL:Q6N094 Ta                                 6e-006  20.2     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                        1186.65   2  0.02    2.948  0.348   465.0  1    15/33
  2118291816 -R.LSCAASGFTFR.S                         1217.56   2  6e-006  3.492  0.654   1231.4 1    20/30

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


IPI:IPI00784842.1|TREMBL:Q6MZQ6 Ta                                 6e-006  20.2     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                        1186.65   2  0.02    2.948  0.348   465.0  1    15/33
  2118291816 -R.LSCAASGFTFR.S                         1217.56   2  6e-006  3.492  0.654   1231.4 1    20/30

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


IPI:IPI00783023.1|TREMBL:Q0ZCI6 Ta                                 6e-006  10.2     0.0       0
  2118291816 -R.LSCAASGFTFR.S                         1217.56   2  6e-006  3.492  0.654   1231.4 1    20/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022391.1|SWISS-PROT:P02743|ENSEMBL:ENSP00000255040|RE    6e-006  10.2     0.0       0
  19287468 - 1R.VGEYSLYIGR.H                          1156.60   2  6e-006  3.220  0.492   1273.1 1    18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00166729.4|SWISS-PROT:P25311|ENSEMBL:ENSP00000292401|RE    8e-006  10.1     0.0       0
  2118291816 -R.YSLTYIYTGLSK.H                        1408.74   2  8e-006  2.703  0.530   554.0  1    14/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00816309.1|TREMBL:A0JLQ0 Ta                                 8e-006  10.1     0.0       0
  2118291816 -R.YSLTYIYTGLSK.H                        1408.74   2  8e-006  2.703  0.530   554.0  1    14/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00924948.1|VEGA:OTTHUMP0000                                 8e-006  10.1     0.0       0
  2118291816 -R.YSLTYIYTGLSK.H                        1408.74   2  8e-006  2.703  0.530   554.0  1    14/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00292530.1|SWISS-PROT:P19827|TREMBL:A8K9N5;B7Z539;B7Z54     1e-005  10.2     0.0       0
  19682592 - 21R.GHMLENHVER.L                         1221.58   2  1e-005  3.514  0.577   794.8  1    19/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00383338.1|TREMBL:Q9P1C5|VE                                 1e-005  10.2     0.0       0
  19682592 - 21R.GHMLENHVER.L                         1221.58   2  1e-005  3.514  0.577   794.8  1    19/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00877852.1|VEGA:OTTHUMP0000                                 1e-005  10.2     0.0       0
  19682592 - 21R.GHMLENHVER.L                         1221.58   2  1e-005  3.514  0.577   794.8  1    19/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022434.4|TREMBL:A6NBZ8;B2RBS8;B4DPP6;Q56G89|ENSEMBL:E     2e-005  20.2     0.0       0
  19287468 - 1K.CCTESLVNR.R                           1140.47   2  0.0001  3.308  0.574   935.4  1    15/24
  19287468 - 1K.LVNEVTEFAK.T                          1149.62   2  2e-005  4.222  0.525   792.1  1    18/27

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


IPI:IPI00216773.4|TREMBL:Q8IUK7|EN                                 2e-005  20.2     0.0       0
  19287468 - 1K.CCTESLVNR.R                           1140.47   2  0.0001  3.308  0.574   935.4  1    15/24
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  19287468 - 1K.LVNEVTEFAK.T                        1149.62   2  2e-005  4.222  0.525   792.1  1   18/27

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


IPI:IPI00745872.2|SWISS-PROT:P0276                                2e-005  20.2     0.0       0
  19287468 - 1K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24
  19287468 - 1K.LVNEVTEFAK.T                        1149.62   2  2e-005  4.222  0.525   792.1  1   18/27

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


gi|113576|sp|P02768|ALBU_HUMAN SER                                2e-005  20.2     0.0       113576
  19287468 - 1K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24
  19287468 - 1K.LVNEVTEFAK.T                        1149.62   2  2e-005  4.222  0.525   792.1  1   18/27

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


IPI:IPI00878282.1|VEGA:OTTHUMP0000                                2e-005  10.2     0.0       0
  19287468 - 1K.LVNEVTEFAK.T                        1149.62   2  2e-005  4.222  0.525   792.1  1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00418163.3|TREMBL:B4E344;Q6                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00643525.1|TREMBL:A7E2V2;B4                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00843913.3|TREMBL:B0V2C8;B2                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00887154.2|TREMBL:B0UZ85;Q6                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00889723.1|TREMBL:B0QZR6;B4                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00892547.1|TREMBL:B0UZ83|RE                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00892604.1|TREMBL:A2BHY4;Q6                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00937598.1|TREMBL:A6H8M8|RE                                2e-005  20.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
  2118291816 -K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

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


IPI:IPI00922744.1|TREMBL:Q9UNU2 Ta                                2e-005  10.2     0.0       0
  19287468 - 1K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126
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  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00793108.1|VEGA:OTTHUMP0000                                3e-005  10.2     0.0       0
  2118291816 -K.VNKDDEEFIESNK.M                     1566.73    3  3e-005  3.718  0.554   800.2  1   25/72

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00794184.1|TREMBL:B3KTA8|VE                                3e-005  10.2     0.0       0
  2118291816 -K.VNKDDEEFIESNK.M                     1566.73    3  3e-005  3.718  0.554   800.2  1   25/72

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00021857.1|SWISS-PROT:P02656|TREMBL:A3KPE2|ENSEMBL:ENSP    4e-005  10.2     0.0       0
  19287468 - 1R.GWVTDGFSSLK.D                       1196.59    2  4e-005  3.932  0.552   725.3  1   17/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00657670.1|TREMBL:B0YIW2|EN                                4e-005  10.2     0.0       0
  19287468 - 1R.GWVTDGFSSLK.D                       1196.59    2  4e-005  3.932  0.552   725.3  1   17/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00550731.2|SWISS-PROT:P06310|TREMBL:Q8TCD0|ENSEMBL:ENSP    5e-005  10.2     0.0       0
  19287468 - 1K.SGTASVVCLLNNFYPR.E                  1798.88    2  5e-005  3.485  0.433   766.8  1   17/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00556287.1|TREMBL:Q569I7 Ta                                5e-005  10.2     0.0       0
  19287468 - 1K.SGTASVVCLLNNFYPR.E                  1798.88    2  5e-005  3.485  0.433   766.8  1   17/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00784773.7|TREMBL:Q7Z3Y4|EN                                5e-005  10.2     0.0       0
  19287468 - 1K.SGTASVVCLLNNFYPR.E                  1798.88    2  5e-005  3.485  0.433   766.8  1   17/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00784865.1|TREMBL:Q6P5S8 Ta                                5e-005  10.2     0.0       0
  19287468 - 1K.SGTASVVCLLNNFYPR.E                  1798.88    2  5e-005  3.485  0.433   766.8  1   17/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00853045.1|TREMBL:Q5EFE6 Ta                                5e-005  10.2     0.0       0
  19287468 - 1K.SGTASVVCLLNNFYPR.E                  1798.88    2  5e-005  3.485  0.433   766.8  1   17/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00909649.2|SWISS-PROT:P0183                                5e-005  10.2     0.0       0
  19287468 - 1K.SGTASVVCLLNNFYPR.E                  1798.88    2  5e-005  3.485  0.433   766.8  1   17/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00658130.1|TREMBL:Q5NV84;Q6                                5e-005  20.2     0.0       0
              K.RPSGVPDR.F                          883.47     2  0.1     2.914  0.384   612.6  1   14/21
  19287468 - 1K.YAASSYLSLTPEQWK.S                   1743.86    2  5e-005  3.671  0.433   421.7  1   16/42

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


IPI:IPI00807428.1|TREMBL:A0A5E4 Ta                                5e-005  20.2     0.0       0
  19287468 - 1R.FSGSILGNK.A                         922.50     2  0.004   2.914  0.340   661.6  1   16/24
  19287468 - 1K.YAASSYLSLTPEQWK.S                   1743.86    2  5e-005  3.671  0.433   421.7  1   16/42

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


IPI:IPI00154742.6|SWISS-PROT:P01842|TREMBL:Q6PJR7;Q8N355;Q8TCJ    5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                   1743.86    2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00450309.1|TREMBL:Q6IN99 Ta                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00642632.1|TREMBL:A0M8Q6|EN                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00719373.2|TREMBL:Q6NS95|EN                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00719452.1|TREMBL:Q5NV69;Q6                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00744476.6|TREMBL:A2MYD6;Q6                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00784935.1|TREMBL:Q6GMW3 Ta                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00788824.3|TREMBL:Q567P1;Q5                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827875.1|TREMBL:A2MYD2;A2                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829640.1|TREMBL:Q6GMW4 Ta                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00830047.1|TREMBL:A6NKU1|EN                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00852577.2|TREMBL:A0M8Q9|EN                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00887169.2|TREMBL:A2MYD0;A2                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00893178.1|ENSEMBL:ENSP0000                                 5e-005  10.2     0.0       0
  19287468 - 1K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00026197.7|SWISS-PROT:P06312|ENSEMBL:ENSP00000374778|H-     5e-005  10.2     0.0       0
  2118291816 -K.LLIYWASTR.E                          1122.63   2  5e-005  3.929  0.542  1464.4 1   19/24

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00385143.1|TREMBL:Q9NP29 Ta                         5e-005  10.2     0.0       0
  2118291816 -K.LLIYWASTR.E                      1122.63   2  5e-005  3.929  0.542   1464.4 1   19/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00386132.1|SWISS-PROT:P0631                         5e-005  10.2     0.0       0
  2118291816 -K.LLIYWASTR.E                      1122.63   2  5e-005  3.929  0.542   1464.4 1   19/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00386133.1|SWISS-PROT:P0631                         5e-005  10.2     0.0       0
  2118291816 -K.LLIYWASTR.E                      1122.63   2  5e-005  3.929  0.542   1464.4 1   19/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00387120.1|SWISS-PROT:P0162                         5e-005  10.2     0.0       0
  2118291816 -K.LLIYWASTR.E                      1122.63   2  5e-005  3.929  0.542   1464.4 1   19/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00029739.5|SWISS-PROT:P0860                         5e-005  20.2     0.0       0
  19287468 - 1R.RPYFPVAVGK.Y                     1133.65   2  0.02    3.852  0.322   1065.5 1   18/27
  19287468 - 1R.EIMENYNIALR.W                    1365.68   2  5e-005  3.298  0.403   992.9  1   18/30

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


IPI:IPI00011264.2|SWISS-PROT:Q03591|ENSEMBL:ENSP00000314299|RE    5e-005  10.2     0.0       0
  19287468 - 1R.EIMENYNIALR.W                    1365.68   2  5e-005  3.298  0.403   992.9  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00513925.1|ENSEMBL:ENSP0000                         5e-005  10.2     0.0       0
  19287468 - 1R.EIMENYNIALR.W                    1365.68   2  5e-005  3.298  0.403   992.9  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00883722.1|TREMBL:B1AKG0;Q6                         5e-005  10.2     0.0       0
  19287468 - 1R.EIMENYNIALR.W                    1365.68   2  5e-005  3.298  0.403   992.9  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00654755.3|SWISS-PROT:P6887                         6e-005  20.1     0.0       0
  19287468 - 1K.LHVDPENFR.L                      1126.56   2  0.06    2.171  0.417   654.7  1   14/24
  19287468 - 1R.LLGNVLVCVLAHHFGK.E               1777.98   3  6e-005  2.552  0.484   158.2  1   22/90

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


IPI:IPI00884107.1|TREMBL:Q14473 Ta                         6e-005  20.1     0.0       0
  19287468 - 1K.LHVDPENFR.L                      1126.56   2  0.06    2.171  0.417   654.7  1   14/24
  19287468 - 1R.LLGNVLVCVLAHHFGK.E               1777.98   3  6e-005  2.552  0.484   158.2  1   22/90

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


IPI:IPI00816644.1|TREMBL:Q5GMQ1;Q9                         6e-005  10.1     0.0       0
  19287468 - 1R.LLGNVLVCVLAHHFGK.E               1777.98   3  6e-005  2.552  0.484   158.2  1   22/90

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384697.2|SWISS-PROT:P0276                         0.0001  10.2     0.0       0
  19287468 - 1K.CCTESLVNR.R                      1140.47   2  0.0001  3.308  0.574   935.4  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00878517.1|TREMBL:B7WNR0|EN                         0.0001  10.2     0.0       0
  19287468 - 1K.CCTESLVNR.R                      1140.47   2  0.0001  3.308  0.574   935.4  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00908876.1|TREMBL:B4DPR2 Ta                         0.0001  10.2     0.0       0
  19287468 - 1K.CCTESLVNR.R                      1140.47   2  0.0001  3.308  0.574   935.4  1   15/24
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  1 of 1 peptide matches reported, 0 removed due to filtering


gi|229552|prf||754920A albumin [Bo                                0.0001  10.2     0.0       229552
  19287468 - 1K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


gi|113574|sp|P02769|ALBU_BOVIN SER                                0.0001  10.2     0.0       113574
  19287468 - 1K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00386879.1|TREMBL:Q96K68 Ta                                0.0001  18.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

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


IPI:IPI00784950.1|TREMBL:Q6MZV6 Ta                                0.0001  18.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

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


IPI:IPI00383164.1|TREMBL:Q8WY24 Tax_Id=9606 Gene_Symbol=IGHA1     0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384952.1|TREMBL:Q7Z379 Ta                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00386524.3|TREMBL:Q96DK0 Ta                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00423460.3|TREMBL:Q6N090 Ta                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00423461.3|TREMBL:Q6N091 Ta                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00423462.5|TREMBL:Q6N092 Ta                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00426060.3|TREMBL:Q6MZW0 Ta                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00449920.1|SWISS-PROT:P0187                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00641229.4|SWISS-PROT:P0187                                0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering
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```
IPI:IPI00642017.1|TREMBL:Q7Z374|VE                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00644497.4|H-INV:HIT0002157                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00647704.1|TREMBL:Q6ZW64 Ta                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00784758.1|TREMBL:Q6MZX9 Ta                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00784830.1|TREMBL:Q6ZVX0 Ta                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00785067.1|TREMBL:Q6P089 Ta                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829711.1|TREMBL:A6NE94|EN                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00893853.1|VEGA:OTTHUMP0000                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00894384.1|TREMBL:Q6N041;Q9                                  0.0001  10.2     0.0       0
  19287468 - 1R.WLQGSQELPR.E                        1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00032258.4|SWISS-PROT:P0C0L4 Tax_Id=9606 Gene_Symbol=C4      0.0002  10.2     0.0       0
  2118291816 -K.ITQVLHFTK.D                         1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00654875.1|SWISS-PROT:P0C0L                                  0.0002  10.2     0.0       0
  2118291816 -K.ITQVLHFTK.D                         1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00935601.1|TREMBL:Q9UM89|EN                                  0.0002  10.2     0.0       0
  2118291816 -K.ITQVLHFTK.D                         1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00032328.2|SWISS-PROT:P01042-1|TREMBL:B4E1C2|ENSEMBL:EN      0.0003  10.2     0.0       0
  2118291816 -K.TVGSDTFYSFK.Y                       1251.59   2  0.0003  3.649  0.643   417.3  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00215894.1|SWISS-PROT:P0104                                  0.0003  10.2     0.0       0
  2118291816 -K.TVGSDTFYSFK.Y                       1251.59   2  0.0003  3.649  0.643   417.3  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00797097.1|VEGA:OTTHUMP0000                                 0.0003  10.2     0.0       0
  2118291816 -K.TVGSDTFYSFK.Y                         1251.59   2  0.0003  3.649  0.643   417.3  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00797833.4|VEGA:OTTHUMP0000                                 0.0003  10.2     0.0       0
  2118291816 -K.TVGSDTFYSFK.Y                         1251.59   2  0.0003  3.649  0.643   417.3  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00924859.1|VEGA:OTTHUMP0000                                 0.0003  10.2     0.0       0
  2118291816 -K.TVGSDTFYSFK.Y                         1251.59   2  0.0003  3.649  0.643   417.3  1   18/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022420.3|SWISS-PROT:P02753|ENSEMBL:ENSP00000360519;EN    0.0003  10.2     0.0       0
  19287468 - 1K.YWGVASFLQK.G                          1198.63   2  0.0003  3.463  0.383   766.9  1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00480192.1|TREMBL:Q5VY30|EN                                 0.0003  10.2     0.0       0
  19287468 - 1K.YWGVASFLQK.G                          1198.63   2  0.0003  3.463  0.383   766.9  1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00844536.2|TREMBL:A6NCP9|EN                                 0.0003  10.2     0.0       0
  19287468 - 1K.YWGVASFLQK.G                          1198.63   2  0.0003  3.463  0.383   766.9  1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00426051.3|TREMBL:Q6MZU6 Ta                                 0.0004  18.2     0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                        1354.68   2  0.002   2.168  0.118   607.2  1   14/30
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

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


IPI:IPI00168728.1|TREMBL:Q8NF17|ENSEMBL:ENSP00000374992 Tax_Id    0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00383957.1|TREMBL:O95978 Ta                                 0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00399007.7|SWISS-PROT:P0185                                 0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00418153.1|TREMBL:Q6N030 Ta                                 0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827754.3|SWISS-PROT:P0186                                 0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829716.2|TREMBL:A6NJI8|EN                                 0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829814.1|SWISS-PROT:P0186                                 0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00829940.1|TREMBL:A6NGU3|EN                                0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00830132.1|TREMBL:A6NNZ4|EN                                0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00930072.1|TREMBL:Q68CN4 Ta                                0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00930442.1|TREMBL:Q6MZX7 Ta                                0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00930684.1|TREMBL:Q5EBM2 Ta                                0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00936490.1|REFSEQ:XP_002348                                0.0004  10.2     0.0       0
  19287468 - 1K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600   416.0  1   16/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00218732.3|SWISS-PROT:P27169|TREMBL:B4DX19;Q96P89;Q96P9    0.0005  24.2     0.0       0
  19287468 - 1R.IQNILTEEPK.V                        1184.65   2  0.001   3.049  0.518   731.0  1   15/27
  19287468 - 1K.LLIGTVFHK.A                         1027.63   2  0.0005  2.467  0.391   636.3  1   16/24
  19287468 - 1K.LLIGTVFHKALYCEL.-                   1777.96   3  0.02    1.300  0.501   63.0   3   14/84

  3 of 3 peptide matches reported, 0 removed due to filtering


IPI:IPI00299778.2|SWISS-PROT:Q15166|TREMBL:A4D1H8|ENSEMBL:ENSP    0.0005  10.1     0.0       0
  19287468 - 1K.ILIGTVFHK.T                         1027.63   2  0.0005  2.467  0.000   636.3  1   16/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00925751.1|VEGA:OTTHUMP0000                                0.0005  10.1     0.0       0
  19287468 - 1K.ILIGTVFHK.T                         1027.63   2  0.0005  2.467  0.000   636.3  1   16/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00645363.2|TREMBL:Q6N089 Ta                                0.1     18.1     0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30
  2118291816 -K.GPSVFPLAPSSK.S                      1186.65   2  0.02    2.948  0.348   465.0  1   15/33

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


IPI:IPI00930124.1|TREMBL:Q6MZV7 Ta                                0.1     18.1     0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30
  2118291816 -K.GPSVFPLAPSSK.S                      1186.65   2  0.02    2.948  0.348   465.0  1   15/33

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


IPI:IPI00007899.4|TREMBL:Q9HCC1 Tax_Id=9606 Gene_Symbol=- Sing    0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382500.1|SWISS-PROT:P0178                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384391.1|TREMBL:Q9UL71 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30
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  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00555872.5|TREMBL:Q9UL91 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00782983.2|TREMBL:Q0ZCH4;Q0                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783287.1|TREMBL:Q0ZCH9 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783451.1|TREMBL:Q0ZCJ5 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783689.1|TREMBL:Q0ZCF9;Q0                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827690.1|TREMBL:A2NWX2 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827733.1|TREMBL:A2NWX3 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829752.1|TREMBL:A6NK61|EN                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829812.2|TREMBL:A6NHF5|EN                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00854667.1|TREMBL:A6NKU8|EN                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00854841.1|TREMBL:A6NL39|EN                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00884078.2|TREMBL:A2J1N2|EN                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00884183.1|TREMBL:Q9ULB6 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00894177.2|TREMBL:Q9UL87|VE                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30
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  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00914985.1|TREMBL:B6EDE2 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00915820.1|TREMBL:A2NYQ9 Ta                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00936563.1|ENSEMBL:ENSP0000                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00936661.1|REFSEQ:XP_001718                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00937119.1|REFSEQ:XP_002344                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00937583.1|TREMBL:A0N5G2|EN                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00937669.1|REFSEQ:XP_002343                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00937796.1|TREMBL:A2J1N1;Q0                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00937964.1|REFSEQ:XP_002346                                0.1     8.1      0.0       0
  19287468 - 1K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00550991.3|SWISS-PROT:P01011-2|TREMBL:B3KS79|ENSEMBL:EN    0.3     10.1     0.0       0
  19287468 - 1K.KLINDYVK.N                          992.58    2  0.004   2.401  0.272   505.2  1   12/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00847635.1|SWISS-PROT:P0101                                0.3     10.1     0.0       0
  19287468 - 1K.KLINDYVK.N                          992.58    2  0.004   2.401  0.272   505.2  1   12/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00935915.1|ENSEMBL:ENSP0000                                0.3     10.1     0.0       0
  19287468 - 1K.KLINDYVK.N                          992.58    2  0.004   2.401  0.272   505.2  1   12/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00019568.1|SWISS-PROT:P00734|TREMBL:B4DDT3;Q15253;Q69EZ    0.3     10.2     0.0       0
  19287468 - 1R.SGIECQLWR.S                         1149.54   2  0.004   3.490  0.339   1292.4 1   17/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00877967.1|VEGA:OTTHUMP0000                                0.3     10.2     0.0       0
  19287468 - 1R.SGIECQLWR.S                         1149.54   2  0.004   3.490  0.339   1292.4 1   17/24
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  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00006662.1|SWISS-PROT:P05090|TREMBL:B2R579|ENSEMBL:ENSP    0.3     10.1     0.0       0
  19287468 - 1K.VLNQELR.A                            871.50    2  0.004   2.210  0.309   564.0  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00910432.1|TREMBL:B4DGC3 Ta                                0.3     10.1     0.0       0
  19287468 - 1K.VLNQELR.A                            871.50    2  0.004   2.210  0.309   564.0  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00924574.1|VEGA:OTTHUMP0000                                0.3     10.1     0.0       0
  19287468 - 1K.VLNQELR.A                            871.50    2  0.004   2.210  0.309   564.0  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00927914.1|VEGA:OTTHUMP0000                                0.3     10.1     0.0       0
  19287468 - 1K.VLNQELR.A                            871.50    2  0.004   2.210  0.309   564.0  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00019580.1|SWISS-PROT:P00747|TREMBL:B2R7F8;B4DPH4;Q68DS    0.3     10.1     0.0       0
  19287468 - 1K.LSSPAVITDK.V                        1030.58    2  0.004   2.679  0.346   201.9  1   13/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00477714.5|TREMBL:Q5NV62|ENSEMBL:ENSP00000374818|VEGA:O    0.3     10.1     0.0       0
  19287468 - 1R.FSGSILGNK.A                          922.50    2  0.004   2.914  0.340   661.6  1   16/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00873719.1|TREMBL:A8MXK2|EN                                0.3     10.1     0.0       0
  19287468 - 1R.FSGSILGNK.A                          922.50    2  0.004   2.914  0.340   661.6  1   16/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00218192.3|SWISS-PROT:Q14624-2|TREMBL:B7Z544|ENSEMBL:EN    0.3     10.1     0.0       0
  19287468 - 1K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00791097.2|TREMBL:B7Z8Q7|VE                                0.3     10.1     0.0       0
  19287468 - 1K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00798006.1|VEGA:OTTHUMP0000                                0.3     10.1     0.0       0
  19287468 - 1K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00896413.1|ENSEMBL:ENSP0000                                0.3     10.1     0.0       0
  19287468 - 1K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00896419.2|SWISS-PROT:Q1462                                0.3     10.1     0.0       0
  19287468 - 1K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00922043.1|VEGA:OTTHUMP0000                                0.3     10.1     0.0       0
  19287468 - 1K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022295.1|SWISS-PROT:P10720|TREMBL:A1L4S0|ENSEMBL:ENSP    0.5     10.1     0.0       0
  2118291816 -R.HITSLEVIK.A                         1039.61    2  0.01    2.472  0.301   457.5  1   14/24
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  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022446.1|SWISS-PROT:P0277                                0.5     10.1     0.0       0
  2118291816 -R.HITSLEVIK.A                          1039.61   2  0.01    2.472  0.301   457.5  1   14/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384401.1|TREMBL:Q9UL85 Tax_Id=9606 Gene_Symbol=- Myos    0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00385253.1|SWISS-PROT:P0420                                0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00387097.1|SWISS-PROT:P0160                                0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00387119.1|SWISS-PROT:P0162                                0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00549330.4|TREMBL:Q9UL83|EN                                0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829834.1|SWISS-PROT:P0443                                0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00892594.1|TREMBL:A6NGI0|EN                                0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00936553.1|REFSEQ:XP_002345                                0.5     10.1     0.0       0
  19287468 - 1R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00387116.1|SWISS-PROT:P01621 Tax_Id=9606 Gene_Symbol=-     0.5     8.1      0.0       0
  19287468 - 1R.LLIYGATSR.A                          993.57    2  0.01    2.784  0.369   580.4  2   14/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022488.1|SWISS-PROT:P02790|TREMBL:Q9BS19|ENSEMBL:ENSP    0.6     18.1     0.0       0
  19287468 - 1R.LHIMAGR.R                            797.45    2  0.07    2.141  0.129   350.3  1   10/18
  19287468 - 1K.NFPSPVDAAFR.Q                        1220.61   2  0.01    2.871  0.432   324.9  1   16/30

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


IPI:IPI00922564.1|TREMBL:B7Z8Q4 Ta                                0.6     10.1     0.0       0
  19287468 - 1K.NFPSPVDAAFR.Q                        1220.61   2  0.01    2.871  0.432   324.9  1   16/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00027507.1|SWISS-PROT:Q02985|ENSEMBL:ENSP00000356395|RE    0.8     10.2     0.0       0
  19287468 - 1R.RPYFPVAVGK.Y                         1133.65   2  0.02    3.852  0.322   1065.5 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00218999.2|SWISS-PROT:P0860                           0.8     10.2     0.0       0
  19287468 - 1R.RPYFPVAVGK.Y                      1133.65   2  0.02    3.852  0.322   1065.5 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00515041.5|TREMBL:A8MPQ4;Q5                           0.8     10.2     0.0       0
  19287468 - 1R.RPYFPVAVGK.Y                      1133.65   2  0.02    3.852  0.322   1065.5 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00654723.1|TREMBL:B1AKF8;Q8                           0.8     10.2     0.0       0
  19287468 - 1R.RPYFPVAVGK.Y                      1133.65   2  0.02    3.852  0.322   1065.5 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00844262.1|TREMBL:Q6NSD3|EN                           0.8     10.2     0.0       0
  19287468 - 1R.RPYFPVAVGK.Y                      1133.65   2  0.02    3.852  0.322   1065.5 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00908535.1|TREMBL:B4DPR0 Ta                           0.8     10.2     0.0       0
  19287468 - 1R.RPYFPVAVGK.Y                      1133.65   2  0.02    3.852  0.322   1065.5 1   18/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00876888.1|TREMBL:A8K008 Ta                           0.8     20.1     0.0       0
  19287468 - 1K.GLEWVGR.I                         816.44    2  0.4     2.817  0.203   839.1  1   13/18
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

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


IPI:IPI00383732.1|TREMBL:Q9Y509 Tax_Id=9606 Gene_Symbol=- VH3    0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384938.1|TREMBL:Q7Z351 Ta                           0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00423464.1|TREMBL:Q6N095 Ta                           0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00423466.1|TREMBL:Q6N097 Ta                           0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00442911.1|TREMBL:Q6ZP87 Ta                           0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00784817.1|TREMBL:Q5EFE5 Ta                           0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00785084.2|SWISS-PROT:P0185                           0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00816314.1|TREMBL:Q6N096 Ta                           0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                    1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00844239.1|TREMBL:A4F255 Ta                                0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                       1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00892671.1|VEGA:OTTHUMP0000                                0.8     10.1     0.0       0
  2118291816 -K.GPSVFPLAPSSK.S                       1186.65   2  0.02    2.948  0.348   465.0  1   15/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00030229.4|TREMBL:Q5QPP4|ENSEMBL:ENSP00000363622|VEGA:O    0.9     10.1     0.0       0
  19287468 - 1K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00553131.2|SWISS-PROT:Q1437                                0.9     10.1     0.0       0
  19287468 - 1K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00641123.1|TREMBL:Q5QPP1|VE                                0.9     10.1     0.0       0
  19287468 - 1K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00644339.1|TREMBL:Q5QPP3|VE                                0.9     10.1     0.0       0
  19287468 - 1K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00644364.1|TREMBL:Q5QPP2|VE                                0.9     10.1     0.0       0
  19287468 - 1K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00414914.3|SWISS-PROT:P61580 Tax_Id=9606 Gene_Symbol=-     0.9     8.1      0.0       0
  19287468 - 1R.WCLQVYPTAPKR.Q                       1519.77   2  0.04    2.492  0.609   380.1  2   13/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00414915.1|SWISS-PROT:P6158                                0.9     8.1      0.0       0
  19287468 - 1R.WCLQVYPTAPKR.Q                       1519.77   2  0.04    2.492  0.609   380.1  2   13/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00414916.3|SWISS-PROT:P6158                                0.9     8.1      0.0       0
  19287468 - 1R.WCLQVYPTAPKR.Q                       1519.77   2  0.04    2.492  0.609   380.1  2   13/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00414917.1|SWISS-PROT:P6158                                0.9     8.1      0.0       0
  19287468 - 1R.WCLQVYPTAPKR.Q                       1519.77   2  0.04    2.492  0.609   380.1  2   13/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00021727.1|SWISS-PROT:P04003|TREMBL:B4E1D8;B4E1E1;Q5VVQ    1       10.1     0.0       0
  19287468 - 1K.YTCLPGYVR.S                          1129.53   2  0.05    2.580  0.512   346.1  1   12/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00855766.1|VEGA:OTTHUMP0000                                1       10.1     0.0       0
  19287468 - 1K.YTCLPGYVR.S                          1129.53   2  0.05    2.580  0.512   346.1  1   12/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00872510.1|TREMBL:A8MVU6|EN                                1       10.1     0.0       0
  19287468 - 1K.YTCLPGYVR.S                          1129.53   2  0.05    2.580  0.512   346.1  1   12/24

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00880200.1|TREMBL:A6PVY5|VE                                1       10.1     0.0       0
  19287468 - 1K.YTCLPGYVR.S                          1129.53   2  0.05    2.580  0.512   346.1  1   12/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00473011.3|SWISS-PROT:P02042|TREMBL:A0N071|ENSEMBL:ENSP    1       10.1     0.0       0
  19287468 - 1K.LHVDPENFR.L                          1126.56   2  0.06    2.171  0.417   654.7  1   14/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00657660.1|ENSEMBL:ENSP0000                                1       10.1     0.0       0
  19287468 - 1K.LHVDPENFR.L                          1126.56   2  0.06    2.171  0.417   654.7  1   14/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00796636.14|TREMBL:A9YUX2;B                                1       10.1     0.0       0
  19287468 - 1K.LHVDPENFR.L                          1126.56   2  0.06    2.171  0.417   654.7  1   14/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829896.1|TREMBL:Q670S4 Ta                                1       10.1     0.0       0
  19287468 - 1K.LHVDPENFR.L                          1126.56   2  0.06    2.171  0.417   654.7  1   14/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00871791.2|SWISS-PROT:Q96NG8|TREMBL:B4DQZ9;B7Z9R3|ENSEM    1       8.1      0.0       0
  19287468 - 1R.VSHLTVHYRIHTGEKPYECK.E               2455.22   3  1       2.157  0.637   199.9  2   17/114

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00888034.1|REFSEQ:XP_001732886 Tax_Id=9606 Gene_Symbol=    1       8.1      0.0       0
  19287468 - 1K.VXXPCXR.R                            871.51    2  0.06    1.526  0.312   361.0  2   11/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00021274.2|SWISS-PROT:P29322|ENSEMBL:ENSP00000166244|RE    1       8.1      0.0       0
  19287468 - 1R.ALGITLM*GHQK.K                       1184.65   2  1       1.470  0.526   80.2   12  6/30

  1 of 1 peptide matches reported, 0 removed due to filtering


gi|113580|sp|P02770|ALBU_RAT SERUM ALBUMIN PRECURSOR. [MASS=68    1       8.1      0.0       113580
  19287468 - 1K.LVQEVTDFAK.T                         1149.62   2  1       2.007  0.529   95.0   6   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382748.2|SWISS-PROT:Q5T013-3|TREMBL:A8MSM3|ENSEMBL:EN    1       10.1     0.0       0
  19287468 - 1R.IHLMAGR.V                            797.45    2  0.07    2.141  0.000   350.3  1   10/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00465271.2|SWISS-PROT:Q5T01                                1       10.1     0.0       0
  19287468 - 1R.IHLMAGR.V                            797.45    2  0.07    2.141  0.000   350.3  1   10/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00514542.1|TREMBL:Q5T017|EN                                1       10.1     0.0       0
  19287468 - 1R.IHLMAGR.V                            797.45    2  0.07    2.141  0.000   350.3  1   10/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00647220.1|TREMBL:Q5T014|EN                                1       10.1     0.0       0
  19287468 - 1R.IHLMAGR.V                            797.45    2  0.07    2.141  0.000   350.3  1   10/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00743712.1|ENSEMBL:ENSP0000                                1       10.1     0.0       0
  19287468 - 1R.IHLMAGR.V                            797.45    2  0.07    2.141  0.000   350.3  1   10/18

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00847938.1|SWISS-PROT:Q5T01                               1       10.1     0.0       0
  19287468 - 1R.IHLMAGR.V                          797.45    2  0.07    2.141  0.000   350.3  1   10/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00848045.1|SWISS-PROT:Q5T01                               1       10.1     0.0       0
  19287468 - 1R.IHLMAGR.V                          797.45    2  0.07    2.141  0.000   350.3  1   10/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00655605.1|TREMBL:Q3C2D8|ENSEMBL:ENSP00000356952|REFSEQ    1       8.1      0.0       0
  19287468 - 1R.GTGIALSADVGPR.K                    1213.65   2  1       2.499  0.397   295.1  4   13/36

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00655889.1|TREMBL:Q3C259|RE                               1       8.1      0.0       0
  19287468 - 1R.GTGIALSADVGPR.K                    1213.65   2  1       2.499  0.397   295.1  4   13/36

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00740527.3|SWISS-PROT:A8MUQ0|REFSEQ:XP_001717830 Tax_Id    1       8.1      0.0       0
  19287468 - 1R.NQDTRM*TSRLK.F                     1365.69   2  1       1.969  0.491   279.0  2   12/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00888926.1|REFSEQ:XP_943402                               1       8.1      0.0       0
  19287468 - 1R.NQDTRM*TSRLK.F                     1365.69   2  1       1.969  0.491   279.0  2   12/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00103871.3|SWISS-PROT:Q8WZ75-1|ENSEMBL:ENSP00000304945|    1       8.1      0.0       0
  19287468 - 1R.ARGPDSNVLLLRLPEK.V                 1778.03   3  1       1.316  0.491   55.0   6   14/90

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00179778.1|TREMBL:B4DNB7;B5                               1       8.1      0.0       0
  19287468 - 1R.ARGPDSNVLLLRLPEK.V                 1778.03   3  1       1.316  0.491   55.0   6   14/90

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00418144.1|SWISS-PROT:Q8WZ7                               1       8.1      0.0       0
  19287468 - 1R.ARGPDSNVLLLRLPEK.V                 1778.03   3  1       1.316  0.491   55.0   6   14/90

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00418145.4|SWISS-PROT:Q8WZ7                               1       8.1      0.0       0
  19287468 - 1R.ARGPDSNVLLLRLPEK.V                 1778.03   3  1       1.316  0.491   55.0   6   14/90

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00782966.1|SWISS-PROT:Q9H2Y7|TREMBL:B4DGC7;B4DZ40;Q05C4    1       4.1      0.0       0
  19287468 - 1K.SLSQKQDPK.N                        1030.55   2  1       1.289  0.531   59.0   19  7/24
  19287468 - 1K.LIKGGKVTTSTWEDSR.T                 1777.94   3  1       1.235  -       42.4   23  12/90

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


IPI:IPI00166518.6|SWISS-PROT:Q6WCQ1-3|TREMBL:Q5ZEZ6;Q96EE5|ENS    1       8.1      0.0       0
  19287468 - 1K.EEESAMSSDR.M                       1140.45   2  1       1.408  0.594   105.5  5   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00295457.6|SWISS-PROT:Q6WCQ                               1       8.1      0.0       0
  19287468 - 1K.EEESAMSSDR.M                       1140.45   2  1       1.408  0.594   105.5  5   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00305344.7|SWISS-PROT:Q6WCQ                               1       8.1      0.0       0
  19287468 - 1K.EEESAMSSDR.M                       1140.45   2  1       1.408  0.594   105.5  5   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00796460.1|TREMBL:A8MTJ7|VE                                1       8.1     0.0       0
  19287468 - 1K.EEESAMSSDR.M                     1140.45   2  1       1.408  0.594   105.5  5   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00797228.1|VEGA:OTTHUMP0000                                1       8.1     0.0       0
  19287468 - 1K.EEESAMSSDR.M                     1140.45   2  1       1.408  0.594   105.5  5   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382420.1|SWISS-PROT:P01700 Tax_Id=9606 Gene_Symbol=-     1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382426.1|SWISS-PROT:P0170                                1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382427.1|SWISS-PROT:P0170                                1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382434.1|SWISS-PROT:P0171                                1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00383016.1|TREMBL:Q8TE63 Ta                                1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827815.1|TREMBL:A2NYV4 Ta                                1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828048.1|TREMBL:A2KUC4 Ta                                1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00828149.1|TREMBL:A2NYQ8 Ta                                1       10.1    0.0       0
              K.RPSGVPDR.F                       883.47    2  0.1     2.914  0.384   612.6  1   14/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00890754.1|TREMBL:B1N7B6 Tax_Id=9606 Gene_Symbol=- Cryo    1       10.1    0.0       0
  19287468 - 1K.NTVYLQM*NSLR.A                   1354.68   2  0.1     2.168  0.000   607.2  1   14/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022438.1|SWISS-PROT:O75444-1|TREMBL:Q8IX32|ENSEMBL:EN    1       8.1     0.0       0
  19287468 - 1R.VQQRHVLESEK.N                    1352.73   2  1       1.436  0.647   201.9  2   10/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00219060.1|SWISS-PROT:O7544                                1       8.1     0.0       0
  19287468 - 1R.VQQRHVLESEK.N                    1352.73   2  1       1.436  0.647   201.9  2   10/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00445079.1|TREMBL:Q6ZTG6|REFSEQ:XP_001714376;XP_0017207    1       8.1     0.0       0
  19287468 - 1R.LYLNAHVVPGPPQSSRPRP.-            2085.14   3  0.1     1.550  0.564   118.3  8   13/108

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00935923.1|REFSEQ:XP_002342                                 1       8.1      0.0       0
  19287468 - 1R.LYLNAHVVPGPPQSSRPRP.-                 2085.14   3  0.1     1.550  0.564   118.3  8   13/108

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00418845.1|TREMBL:Q6ZS85|H-INV:HIT000047515 Tax_Id=9606    1       8.1      0.0       0
  19287468 - 1R.GPASRTPSR.A                           928.50    2  1       1.431  0.467   166.7  10  10/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00069817.2|SWISS-PROT:Q9UIG0-1|ENSEMBL:ENSP00000342434;     1       8.1      0.0       0
  2118291816 -R.WASMSEEQRK.E                          1251.58   2  1       1.301  0.654   32.9   10  7/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00216695.1|SWISS-PROT:Q9UIG                                 1       8.1      0.0       0
  2118291816 -R.WASMSEEQRK.E                          1251.58   2  1       1.301  0.654   32.9   10  7/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00411614.1|SWISS-PROT:O75717|TREMBL:A8KAE0;Q05DR3|ENSEM     1       8.1      0.0       0
  19287468 - 1K.GETASEGTEAKKRK.R                      1491.78   3  1       1.815  0.629   168.0  2   16/78

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00513835.1|TREMBL:A8MRA5;B3                                 1       8.1      0.0       0
  19287468 - 1K.GETASEGTEAKKRK.R                      1491.78   3  1       1.815  0.629   168.0  2   16/78

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00418991.5|SWISS-PROT:Q2KHR3-1|TREMBL:B3KWV1|ENSEMBL:EN     1       10.1     0.0       0
  19287468 - 1K.GKGQVKEEDNSNQK.Q                      1560.76   2  0.2     2.747  0.382   212.8  1   11/39

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00745241.1|TREMBL:Q9H6S7 Ta                                 1       10.1     0.0       0
  19287468 - 1K.GKGQVKEEDNSNQK.Q                      1560.76   2  0.2     2.747  0.382   212.8  1   11/39

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00847870.1|SWISS-PROT:Q2KHR                                 1       10.1     0.0       0
  19287468 - 1K.GKGQVKEEDNSNQK.Q                      1560.76   2  0.2     2.747  0.382   212.8  1   11/39

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00003330.4|SWISS-PROT:Q9NTU4|ENSEMBL:ENSP00000330877|RE     1       8.1      0.0       0
  19287468 - 1K.SSSM*SSLNIAKHMPHR.A                   1798.87   2  0.2     1.976  0.523   81.9   6   7/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00477176.1|SWISS-PROT:Q96LC9-1|ENSEMBL:ENSP00000346697;     1       8.1      0.0       0
  19287468 - 1K.LQCIADQFHR.L                          1288.61   2  1       1.350  0.621   61.6   3   6/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783294.1|SWISS-PROT:Q9P267-1|TREMBL:B4E2U1|ENSEMBL:EN     1       8.1      0.0       0
  19287468 - 1K.SVNGCVPSPSDAK.S                       1318.59   2  0.2     2.111  0.618   149.8  3   10/36

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00879134.1|TREMBL:B3KQW0|EN                                 1       8.1      0.0       0
  19287468 - 1K.SVNGCVPSPSDAK.S                       1318.59   2  0.2     2.111  0.618   149.8  3   10/36

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00936423.1|REFSEQ:XP_002343325 Tax_Id=9606 Gene_Symbol=     1       8.1      0.0       0
  19287468 - 1K.FLGLIM*GR.G                           922.52    2  0.3     1.924  0.405   193.5  3   10/21

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00937991.1|REFSEQ:XP_002347                                 1       8.1      0.0       0
  19287468 - 1K.FLGLIM*GR.G                          922.52    2  0.3     1.924  0.405   193.5  3   10/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00893555.1|VEGA:OTTHUMP00000201682 Tax_Id=9606 Gene_Sym     1       8.1      0.0       0
  19287468 - 1R.MFVSTVWTR.M                          1126.57   2  1       1.265  0.427   69.9   27  5/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00328929.3|SWISS-PROT:Q86VM9-1|ENSEMBL:ENSP00000301011|     1       8.1      0.0       0
  2118291816 -K.LTLLNKAADK.G                         1086.65   2  0.4     2.083  0.466   185.2  3   10/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00642285.1|TREMBL:B3KRL4|VE                                 1       8.1      0.0       0
  2118291816 -K.LTLLNKAADK.G                         1086.65   2  0.4     2.083  0.466   185.2  3   10/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00908725.1|TREMBL:B4DTK7 Ta                                 1       8.1      0.0       0
  2118291816 -K.LTLLNKAADK.G                         1086.65   2  0.4     2.083  0.466   185.2  3   10/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00065529.1|TREMBL:Q96MJ9|H-INV:HIT000013428 Tax_Id=9606     1       8.1      0.0       0
  2118291816 -R.GDLSGASGPAETR.G                      1217.58   2  1       1.209  0.711   107.4  3   8/36

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00384404.4|TREMBL:A2J1N6 Tax_Id=9606 Gene_Symbol=- Rheu     1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783024.1|TREMBL:Q9UL88 Ta                                 1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00783184.1|TREMBL:Q0ZCI0 Ta                                 1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00827892.1|TREMBL:A2N2G5 Ta                                 1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829590.1|TREMBL:A6NNW3|EN                                 1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00829841.1|ENSEMBL:ENSP0000                                 1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00921238.1|H-INV:HIT0003928                                 1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00936370.1|TREMBL:Q0ZCJ6|EN                                 1       10.1     0.0       0
  19287468 - 1K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00021856.3|SWISS-PROT:P02655|TREMBL:C0JYY4;Q6P163|ENSEM     1       10.1     0.0       0
  19287468 - 1K.LRDLYSK.S                             894.50    2  0.6     2.716  0.205   1098.8 1   15/18

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00555595.1|TREMBL:Q59GS1 Tax_Id=9606 Gene_Symbol=UCHL1      1       8.1      0.0       0
  19287468 - 1R.RGRPPVPAAGR.D                         1133.67   2  1       2.610  0.428    386.9  2   13/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00937422.1|REFSEQ:XP_002346542 Tax_Id=9606 Gene_Symbol=     1       8.1      0.0       0
  19287468 - 1R.KGSNIGQLR.P                           972.56    2  0.4     2.427  0.100    721.2  2   13/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00168913.1|SWISS-PROT:Q86UK5-2|TREMBL:Q4W5A4;Q4W5B1|ENS     1       8.1      0.0       0
  19287468 - 1R.SAVECSNLLR.T                          1149.56   2  0.4     2.306  0.370    355.1  4   12/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382523.1|SWISS-PROT:Q86UK                                 1       8.1      0.0       0
  19287468 - 1R.SAVECSNLLR.T                          1149.56   2  0.4     2.306  0.370    355.1  4   12/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00382525.1|SWISS-PROT:Q86UK                                 1       8.1      0.0       0
  19287468 - 1R.SAVECSNLLR.T                          1149.56   2  0.4     2.306  0.370    355.1  4   12/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00375358.2|SWISS-PROT:P35251-1|TREMBL:A8K6E7|ENSEMBL:EN     1       8.1      0.0       0
  19287468 - 1K.IGEVSSPK.A                            816.45    2  0.6     2.245  0.317    420.5  3   11/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00375359.2|SWISS-PROT:P3525                                 1       8.1      0.0       0
  19287468 - 1K.IGEVSSPK.A                            816.45    2  0.6     2.245  0.317    420.5  3   11/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00065348.2|TREMBL:B1AL16;Q05BG6;Q96LW0|ENSEMBL:ENSP0000     1       8.1      0.0       0
  19287468 - 1R.LSITGTEQFERK.L                        1408.74   2  0.7     2.224  0.498    271.7  3   11/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00293188.5|SWISS-PROT:Q8IX2                                 1       8.1      0.0       0
  19287468 - 1R.LSITGTEQFERK.L                        1408.74   2  0.7     2.224  0.498    271.7  3   11/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00640126.1|TREMBL:B1AL17|EN                                 1       8.1      0.0       0
  19287468 - 1R.LSITGTEQFERK.L                        1408.74   2  0.7     2.224  0.498    271.7  3   11/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00217895.4|SWISS-PROT:Q6S5L8-1|TREMBL:B3KWT2|ENSEMBL:EN     1       8.1      0.0       0
  2118291816 -K.SNLQFSGMNIK.L                         1238.62   2  0.8     2.210  0.498    104.6  16  8/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00043430.5|SWISS-PROT:Q8IUR5-2|TREMBL:B3KVW1|ENSEMBL:EN     1       8.1      0.0       0
  19287468 - 1R.LLSAIYSK.Q                            894.53    2  0.8     2.159  0.253    634.7  2   13/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00216822.3|SWISS-PROT:Q8IUR                                 1       8.1      0.0       0
  19287468 - 1R.LLSAIYSK.Q                            894.53    2  0.8     2.159  0.253    634.7  2   13/21

  1 of 1 peptide matches reported, 0 removed due to filtering
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IPI:IPI00795924.2|SWISS-PROT:Q8IUR                                1       8.1      0.0       0
  19287468 - 1R.LLSAIYSK.Q                           894.53    2  0.8     2.159  0.253   634.7  2   13/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00433499.6|SWISS-PROT:Q6PJF5-1|ENSEMBL:ENSP00000322775|    1       8.1      0.0       0
  19287468 - 1K.EYGRAPVPGPR.R                        1198.63   2  0.8     2.135  0.461   245.0  3   11/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00446876.3|TREMBL:Q6ZWP8|EN                                1       8.1      0.0       0
  19287468 - 1K.EYGRAPVPGPR.R                        1198.63   2  0.8     2.135  0.461   245.0  3   11/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00470604.2|SWISS-PROT:Q6PJF                                1       8.1      0.0       0
  19287468 - 1K.EYGRAPVPGPR.R                        1198.63   2  0.8     2.135  0.461   245.0  3   11/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00922473.1|TREMBL:B7Z8H4 Ta                                1       8.1      0.0       0
  19287468 - 1K.EYGRAPVPGPR.R                        1198.63   2  0.8     2.135  0.461   245.0  3   11/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00023129.1|SWISS-PROT:O95813|TREMBL:Q3SY34|ENSEMBL:ENSP    1       8.1      0.0       0
  19287468 - 1R.FWKKPEREM*HPSR.D                     1743.87   2  1       2.081  0.445   89.0   4   8/36

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00009771.6|H-INV:HIT000278695|VEGA:OTTHUMP00000077225 T    1       8.1      0.0       0
  2118291816 -K.LRAELDEVNK.S                         1186.64   2  1       1.923  0.445   146.4  3   9/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00879819.1|SWISS-PROT:Q0325                                1       8.1      0.0       0
  2118291816 -K.LRAELDEVNK.S                         1186.64   2  1       1.923  0.445   146.4  3   9/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00032087.4|SWISS-PROT:Q9Y2E4|TREMBL:Q86XV3|ENSEMBL:ENSP    1       8.1      0.0       0
  2118291816 -K.LLWFVTESK.H                          1122.62   2  1       1.798  0.549   133.1  18  8/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00643330.5|TREMBL:B3KWX2;Q5                                1       8.1      0.0       0
  2118291816 -K.LLWFVTESK.H                          1122.62   2  1       1.798  0.549   133.1  18  8/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00018279.7|SWISS-PROT:P25940|TREMBL:Q59GD4|ENSEMBL:ENSP    1       8.1      0.0       0
            R.RPPGTAER.P                             883.47    2  1       1.794  0.387   146.8  6   7/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00021304.1|SWISS-PROT:P35908|ENSEMBL:ENSP00000310861|RE    1       8.1      0.0       0
  19287468 - 1K.KDVDNAYMIK.V                         1196.60   2  1       1.761  0.589   130.6  4   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering


gi|254622|bbs|112352 (S43646) cyto                                1       8.1      0.0       254622
  19287468 - 1K.KDVDNAYMIK.V                         1196.60   2  1       1.761  0.589   130.6  4   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering


gi|547754|sp|P35908|K22E_HUMAN KER                                1       8.1      0.0       547754
  19287468 - 1K.KDVDNAYMIK.V                         1196.60   2  1       1.761  0.589   130.6  4   8/27

  1 of 1 peptide matches reported, 0 removed due to filtering
```

```
IPI:IPI00418876.3|SWISS-PROT:Q70Z35-1|TREMBL:B4DFX0|ENSEMBL:EN    1       8.1      0.0       0
  19287468 - 1K.LSCPKRLR.L                           1030.58   2  0.9     1.753  0.426   105.7  3    9/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00845229.1|SWISS-PROT:Q70Z3                                1       8.1      0.0       0
  19287468 - 1K.LSCPKRLR.L                           1030.58   2  0.9     1.753  0.426   105.7  3    9/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00294519.2|SWISS-PROT:Q99973-1|ENSEMBL:ENSP00000262715|    1       8.1      0.0       0
  19287468 - 1R.QLLTRPHK.A                           992.60    2  0.8     1.747  0.306   184.8  5    8/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00413874.2|SWISS-PROT:Q9997                                1       8.1      0.0       0
  19287468 - 1R.QLLTRPHK.A                           992.60    2  0.8     1.747  0.306   184.8  5    8/21

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00448364.1|TREMBL:Q6IEV0|H-INV:HIT000391565 Tax_Id=9606    1       8.1      0.0       0
  2118291816 -R.IHSTQGRIK.V                          1039.60   2  0.4     1.729  0.349   149.9  3    9/24

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00307200.9|SWISS-PROT:Q9UH65|TREMBL:B4E245|ENSEMBL:ENSP    1       8.1      0.0       0
  19287468 - 1K.KLEEAASRAAEEEK.K                     1560.79   2  1       1.699  0.383   106.1  4    9/39

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00903155.1|TREMBL:B3KUB9 Ta                                1       8.1      0.0       0
  19287468 - 1K.KLEEAASRAAEEEK.K                     1560.79   2  1       1.699  0.383   106.1  4    9/39

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00022963.3|SWISS-PROT:O95926|TREMBL:B2RBX8;B4E0Y8|ENSEM    1       8.1      0.0       0
  2118291816 -K.PDMETYERLREK.H                       1566.76   3  0.5     1.657  0.583   147.7  12  14/66

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00410388.1|ENSEMBL:ENSP0000                                1       8.1      0.0       0
  2118291816 -K.PDMETYERLREK.H                       1566.76   3  0.5     1.657  0.583   147.7  12  14/66

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00929282.1|H-INV:HIT000046184 Tax_Id=9606 Gene_Symbol=N    1       8.1      0.0       0
  19287468 - 1R.HLLATCDLGR.S                         1156.58   2  0.6     1.635  0.619   232.9  3    11/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00937649.1|REFSEQ:XP_002343712 Tax_Id=9606 Gene_Symbol=    1       8.1      0.0       0
  19287468 - 1R.GSQTARSSSPSR.A                       1220.60   2  0.6     1.630  0.445   83.5   9    8/33

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00016604.1|SWISS-PROT:Q07343-1|TREMBL:Q5TEK6|ENSEMBL:EN    1       8.1      0.0       0
  19682592 - 21R.VNPQEESYQK.L                        1221.57   2  0.8     1.486  0.615   103.8  3    9/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00220621.1|SWISS-PROT:Q0734                                1       8.1      0.0       0
  19682592 - 21R.VNPQEESYQK.L                        1221.57   2  0.8     1.486  0.615   103.8  3    9/27

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00329088.4|SWISS-PROT:Q86WJ1-1|ENSEMBL:ENSP00000358262|    1       8.1      0.0       0
  19287468 - 1K.AILM*KDLDAFENETAK.K                  1824.90   2  0.6     1.353  0.548   73.7   15  7/45

  1 of 1 peptide matches reported, 0 removed due to filtering
```

```
IPI:IPI00400835.6|TREMBL:B5MDZ7|EN                                1       8.1      0.0       0
  19287468 - 1K.AILM*KDLDAFENETAK.K                 1824.90   2  0.6     1.353  0.548   73.7   15  7/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00854584.1|SWISS-PROT:Q86WJ                                1       8.1      0.0       0
  19287468 - 1K.AILM*KDLDAFENETAK.K                 1824.90   2  0.6     1.353  0.548   73.7   15  7/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00890729.1|SWISS-PROT:Q86WJ                                1       8.1      0.0       0
  19287468 - 1K.AILM*KDLDAFENETAK.K                 1824.90   2  0.6     1.353  0.548   73.7   15  7/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00890749.1|SWISS-PROT:Q86WJ                                1       8.1      0.0       0
  19287468 - 1K.AILM*KDLDAFENETAK.K                 1824.90   2  0.6     1.353  0.548   73.7   15  7/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00909123.1|TREMBL:B4DPN5 Ta                                1       8.1      0.0       0
  19287468 - 1K.AILM*KDLDAFENETAK.K                 1824.90   2  0.6     1.353  0.548   73.7   15  7/45

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00007775.1|SWISS-PROT:Q9UKT6|TREMBL:Q3KPF8|ENSEMBL:ENSP    1       8.1      0.0       0
  19287468 - 1K.CEVSCSAFIRFVR.L                     1632.75   2  1       1.324  0.637   67.0   3   6/36

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00003519.1|SWISS-PROT:Q15029|TREMBL:A8KAP3;B3KX19;B4DMC    1       8.1      0.0       0
  2118291816 -K.RLWGDIYFNPK.T                       1408.74   2  0.6     1.270  0.699   132.3  2   8/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00903143.1|TREMBL:B3KWY2 Ta                                1       8.1      0.0       0
  2118291816 -K.RLWGDIYFNPK.T                       1408.74   2  0.6     1.270  0.699   132.3  2   8/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00917777.1|TREMBL:B4DK30;B4                                1       8.1      0.0       0
  2118291816 -K.RLWGDIYFNPK.T                       1408.74   2  0.6     1.270  0.699   132.3  2   8/30

  1 of 1 peptide matches reported, 0 removed due to filtering


IPI:IPI00028954.1|SWISS-PROT:O60318|TREMBL:B3KT88;B3KWZ4;B3KXE    1       8.1      0.0       0
  19287468 - 1R.TYCRWKSK.S                          1129.55   2  0.9     1.258  0.606   56.9   5   5/21

  1 of 1 peptide matches reported, 0 removed due to filtering
```

```
Database... 070909ipiHUMANv361Processed.fasta
Filter(s)... None
Mods:  (M* +15.99492) C=161.01468

Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

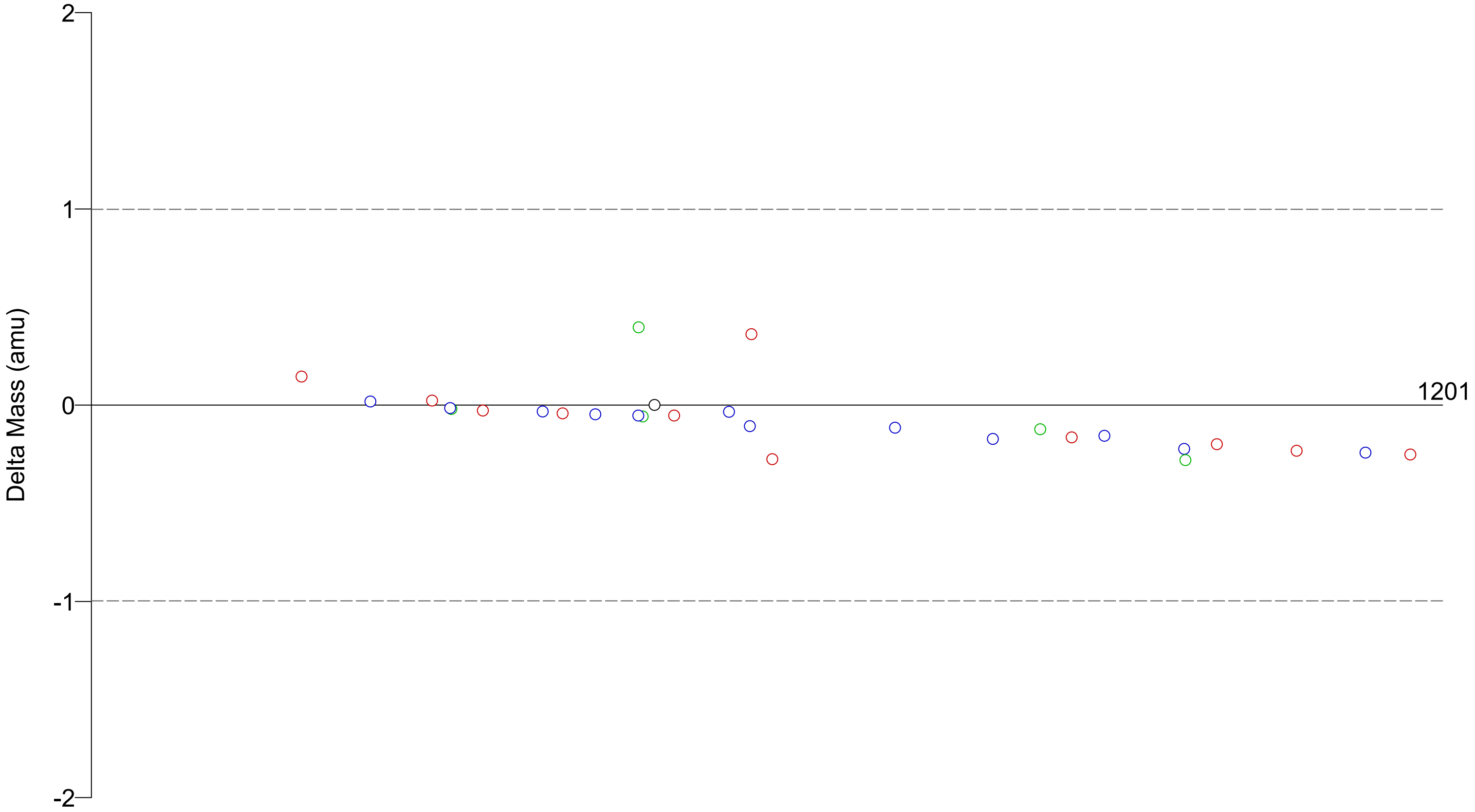
IPI:IPI00022463.1|SWISS-PROT:P02787|TREMBL:A0PJA6;B4DEX9;B4DHZ    1e-007  22.2     0.0       0
19287468 - 1  R.WCAVSEHEATK.C                        1318.57   2  1e-007  4.487  0.529   1202.0 1   20/30   2
19287468 - 1  K.SKEFQLFSSPHGK.D                      1491.76   3  8e-007  4.643  0.609   849.7  1   27/72   3
19287468 - 1  K.KASYLDCIR.A                          1126.56   2  0.06    1.175  0.496   163.9  4   10/24   1

3 of 3 peptide matches reported, 0 removed due to filtering
```

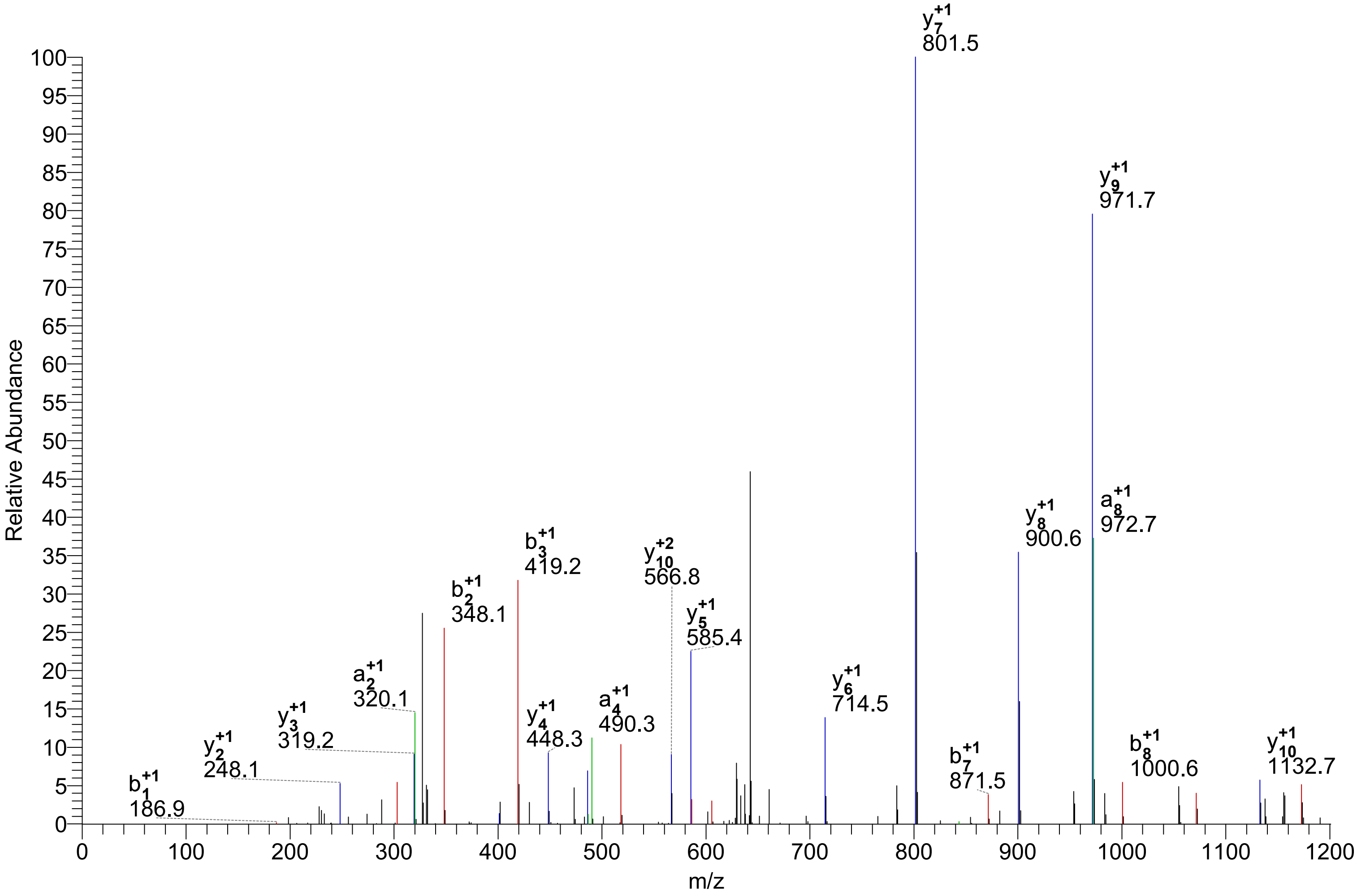
```
DTA for scans: 19287468-1
Precursor ion: 659.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 C    320.11     348.10                                     1132.49
 A    391.14     419.14                                      971.48
 V    490.21     518.21                                      900.44
 S    577.24     605.24                                      801.37
 E    706.29     734.28                                      714.34
 H    843.35     871.34                                      585.30
 E    972.39    1000.38                                      448.24
 A   1043.43    1071.42                                      319.20
 T   1144.47    1172.47                                      248.16
 K                                                           147.11
```



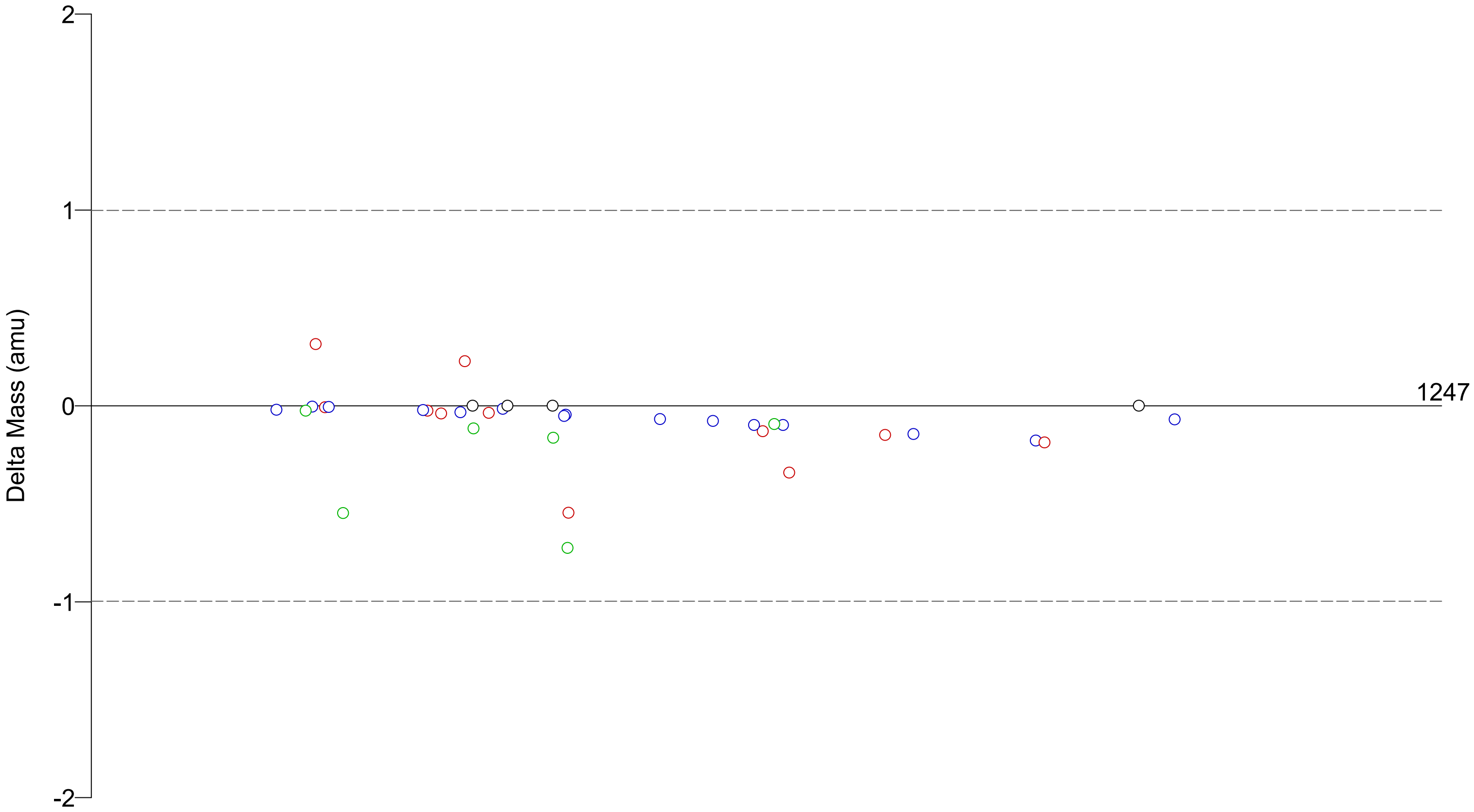
#19287468-1 NL: 2.05E5



```
DTA for scans: 19287468-1
Precursor ion: 497.93
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 K    188.14     216.13                                    1404.73
 E    317.18     345.18                                    1276.63
 F    464.25     492.25                                    1147.59
 Q    592.31     620.30                                    1000.52
 L    705.39     733.39                                     872.46
 F    852.46     880.46                                     759.38
 S    939.49     967.49                                     612.31
 S   1026.53    1054.52                                     525.28
 P   1123.58    1151.57                                     438.25
 H   1260.64    1288.63                                     341.19
 G   1317.66    1345.65                                     204.13
 K                                                          147.11
```



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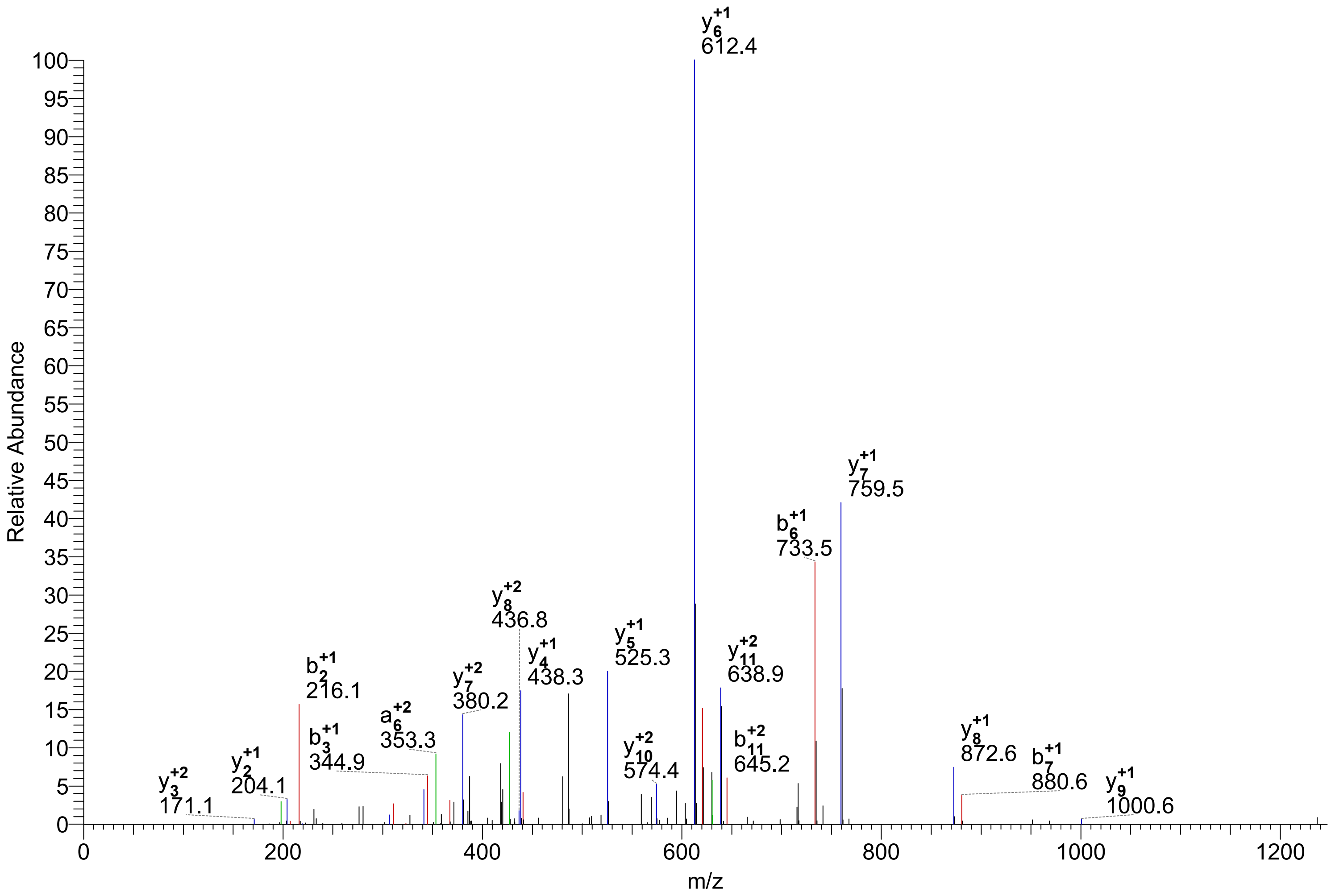
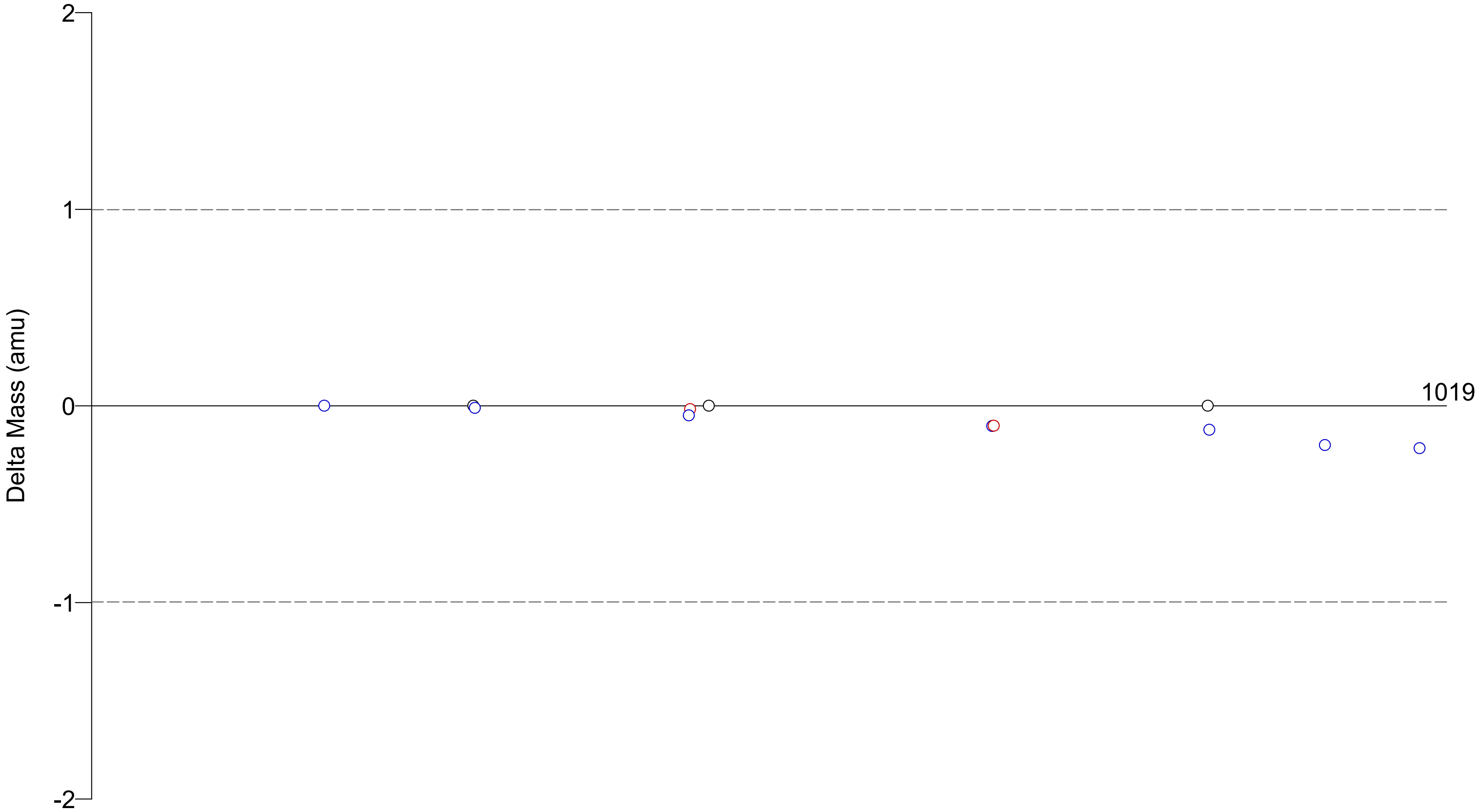


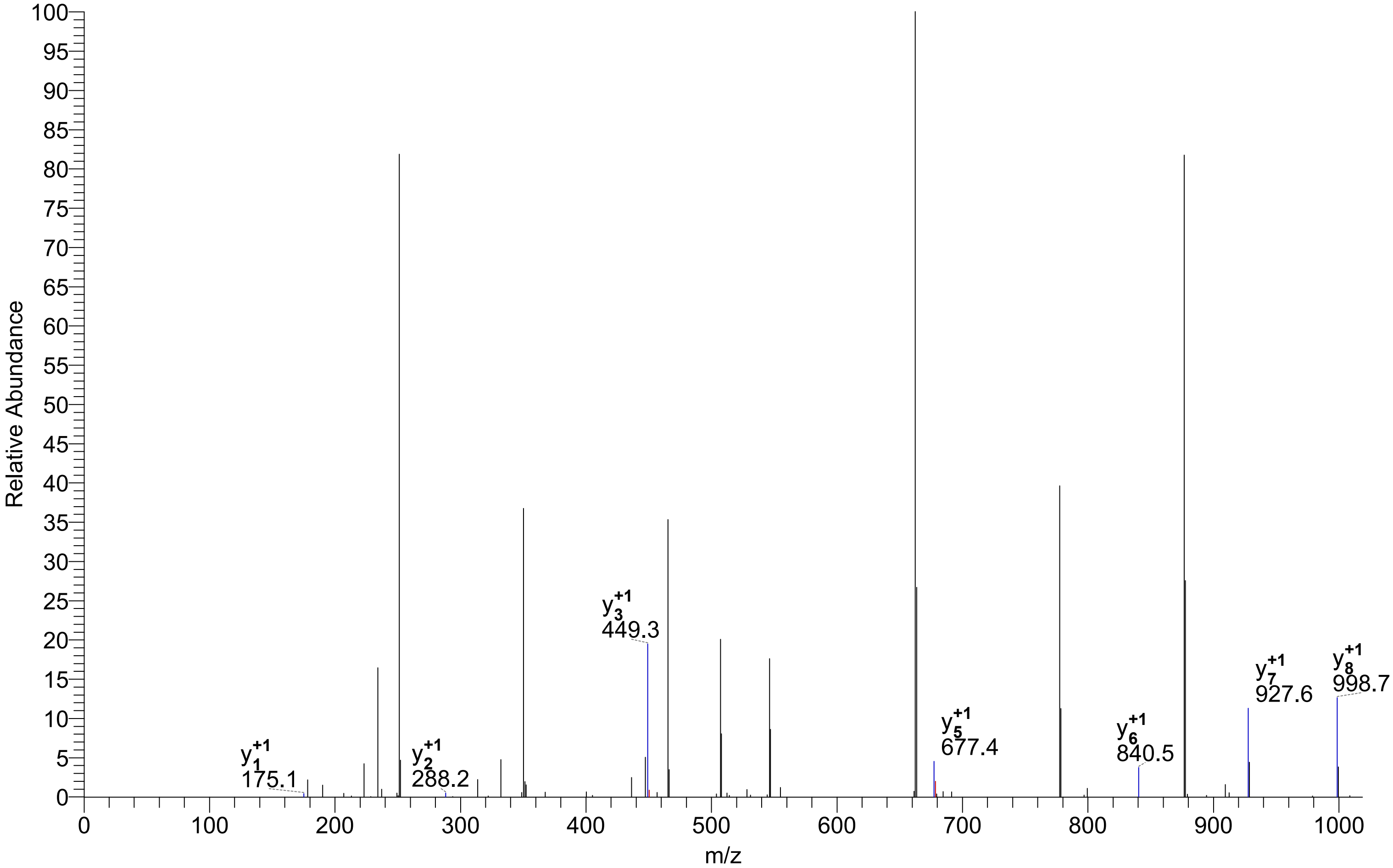
```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 K    101.11     129.10
 A    172.14     200.14                                      998.46
 S    259.18     287.17                                      927.42
 Y    422.24     450.23                                      840.39
 L    535.32     563.32                                      677.33
 D    650.35     678.35                                      564.24
 C    811.37     839.36                                      449.22
 I    924.45     952.44                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 7.10E5



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Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00877763.1|VEGA:OTTHUMP0000                               1e-007  12.2     0.0       0
19287468 - 1  R.WCAVSEHEATK.C                        1318.57   2  1e-007  4.487  0.529   1202.0 1   20/30   2
19287468 - 1  K.KASYLDCIR.A                          1126.56   2  0.06    1.175  -       163.9  4   10/24   1

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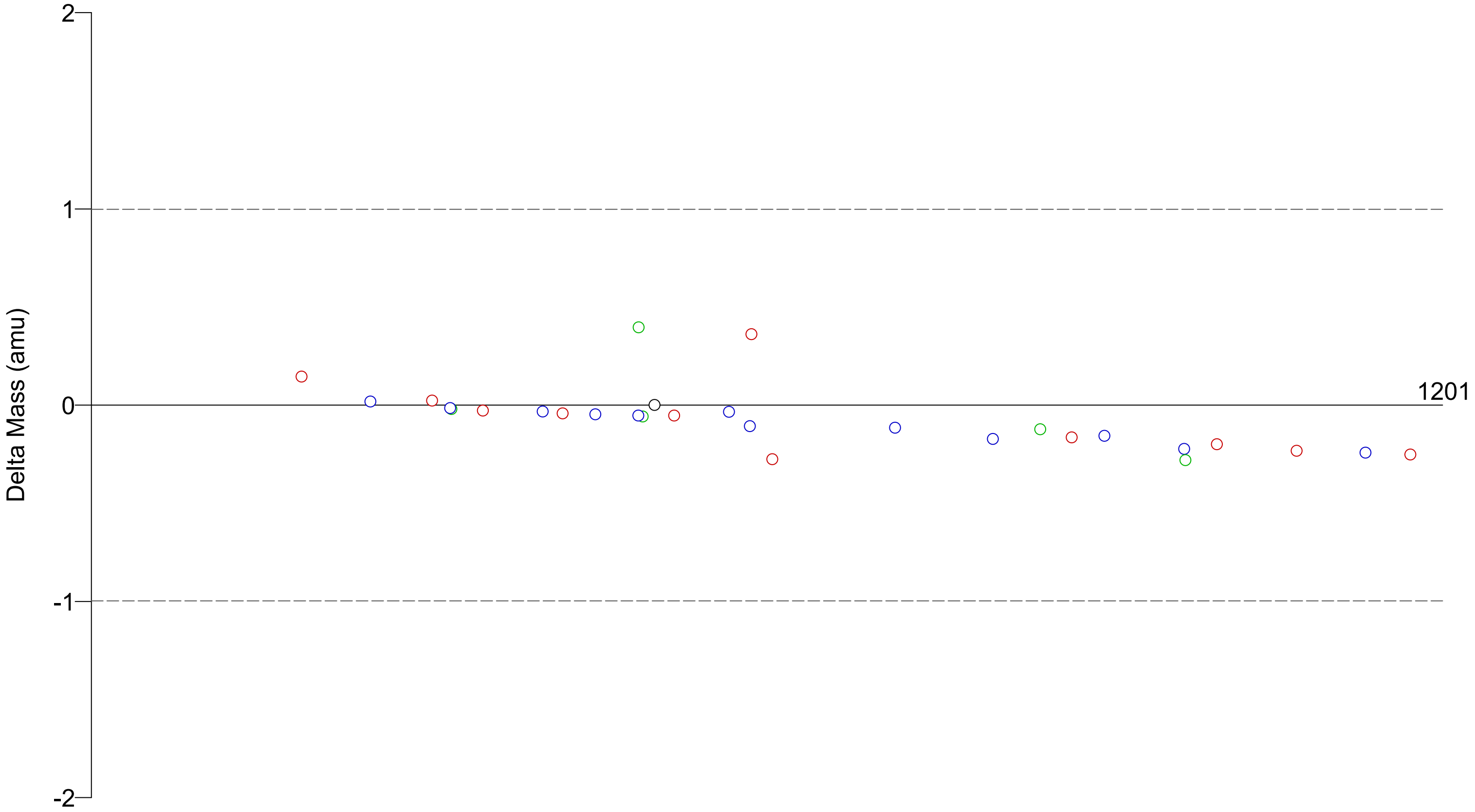

```
DTA for scans: 19287468-1
Precursor ion: 659.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 C    320.11     348.10                                      1132.49
 A    391.14     419.14                                       971.48
 V    490.21     518.21                                       900.44
 S    577.24     605.24                                       801.37
 E    706.29     734.28                                       714.34
 H    843.35     871.34                                       585.30
 E    972.39    1000.38                                       448.24
 A   1043.43    1071.42                                       319.20
 T   1144.47    1172.47                                       248.16
 K                                                            147.11
```



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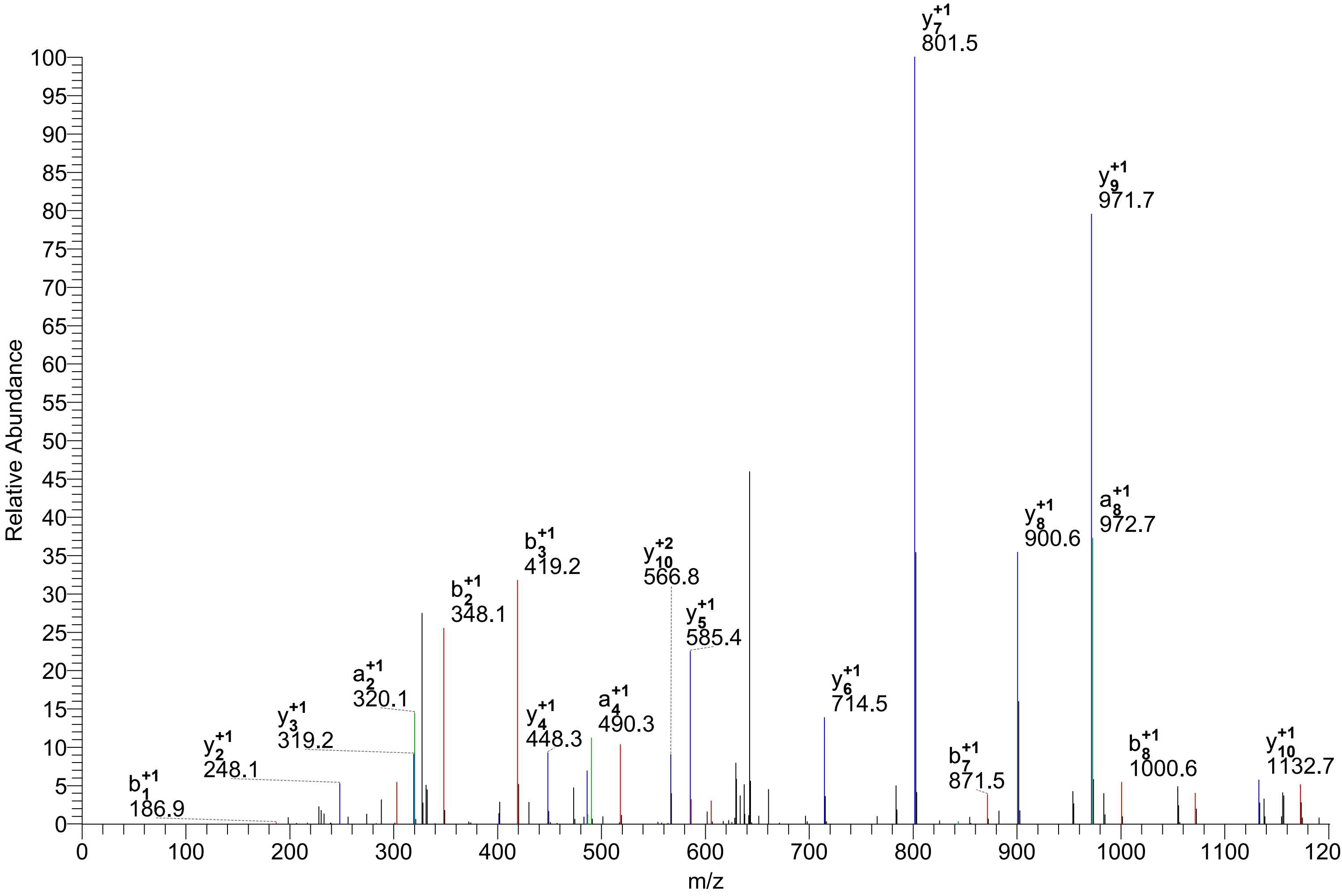
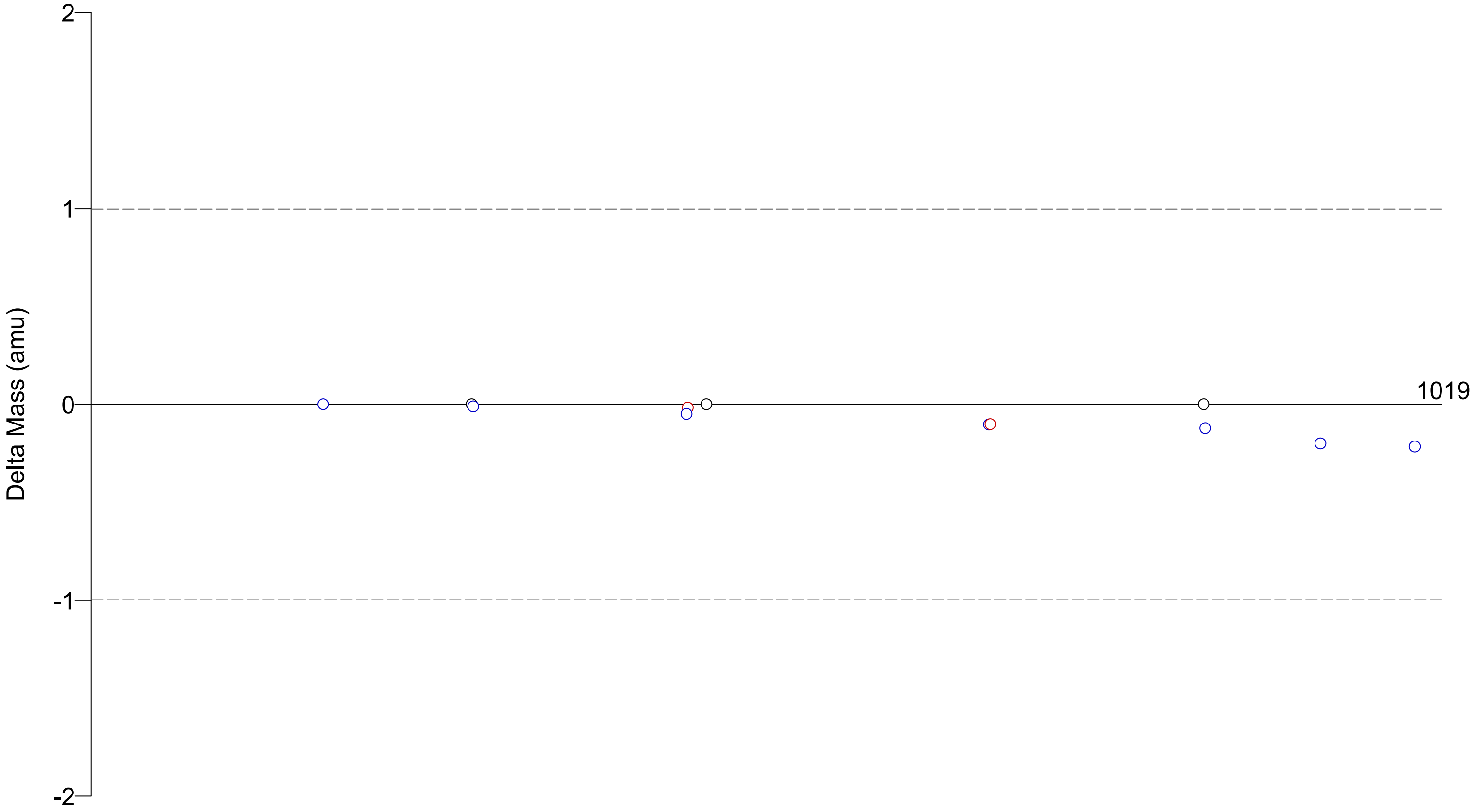


```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 K    101.11     129.10
 A    172.14     200.14                                      998.46
 S    259.18     287.17                                      927.42
 Y    422.24     450.23                                      840.39
 L    535.32     563.32                                      677.33
 D    650.35     678.35                                      564.24
 C    811.37     839.36                                      449.22
 I    924.45     952.44                                      288.20
 R                                                           175.12
```



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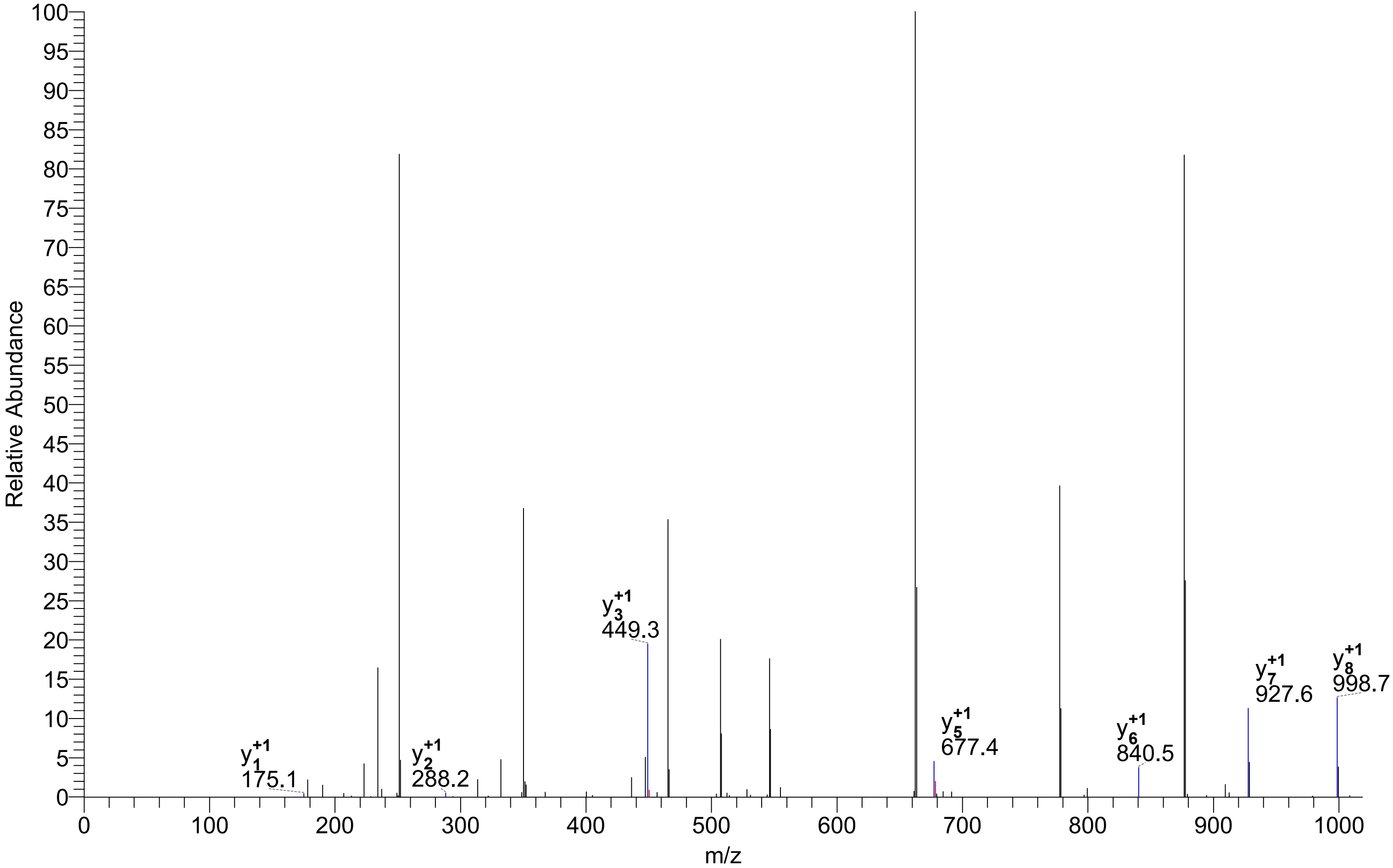

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Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

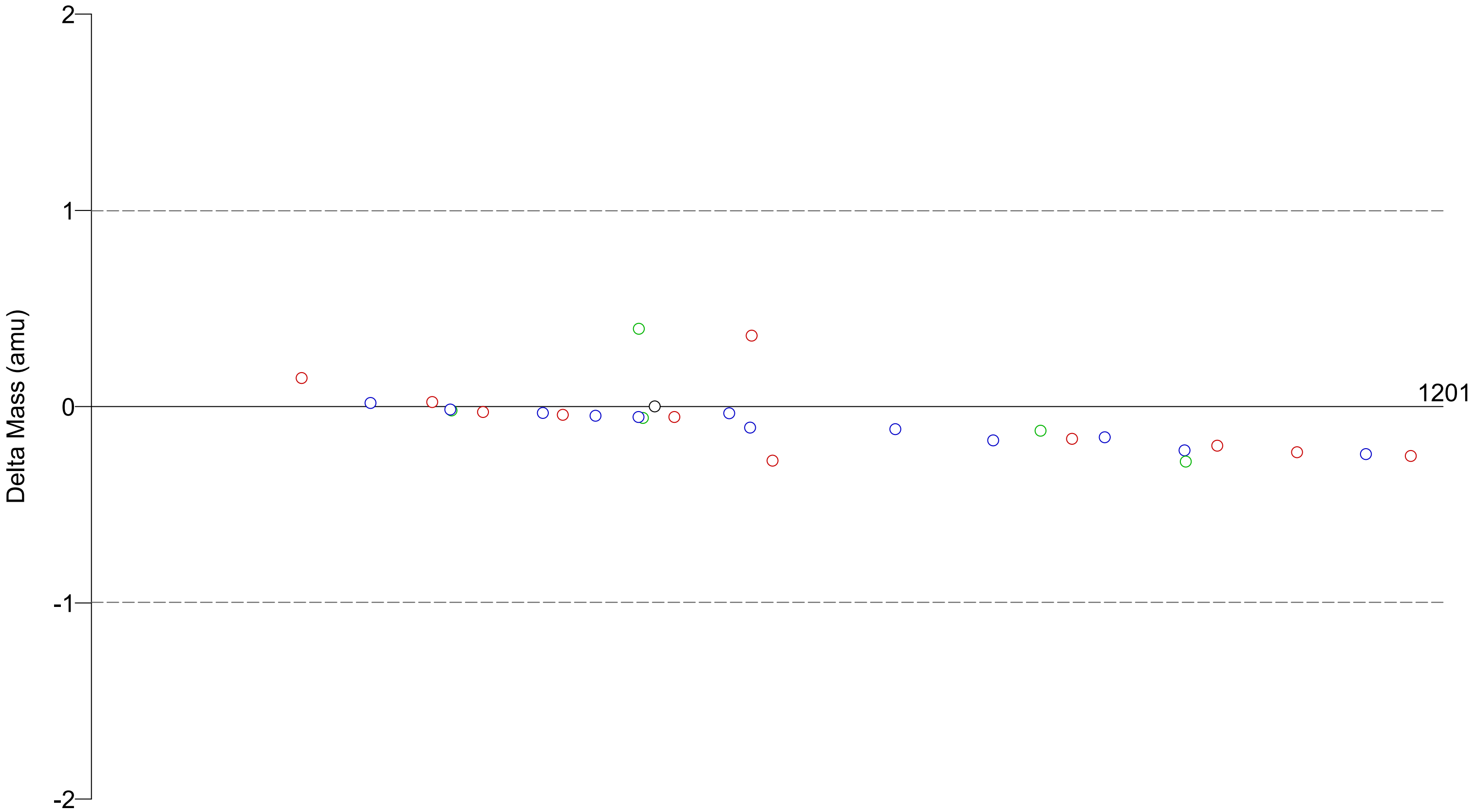
IPI:IPI00879916.1|VEGA:OTTHUMP0000                                    1e-007  10.2     0.0       0
19287468 - 1  R.WCAVSEHEATK.C                           1318.57   2  1e-007  4.487  0.529   1202.0 1   20/30   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 659.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 C    320.11     348.10                                     1132.49
 A    391.14     419.14                                      971.48
 V    490.21     518.21                                      900.44
 S    577.24     605.24                                      801.37
 E    706.29     734.28                                      714.34
 H    843.35     871.34                                      585.30
 E    972.39    1000.38                                      448.24
 A   1043.43    1071.42                                      319.20
 T   1144.47    1172.47                                      248.16
 K                                                           147.11
```



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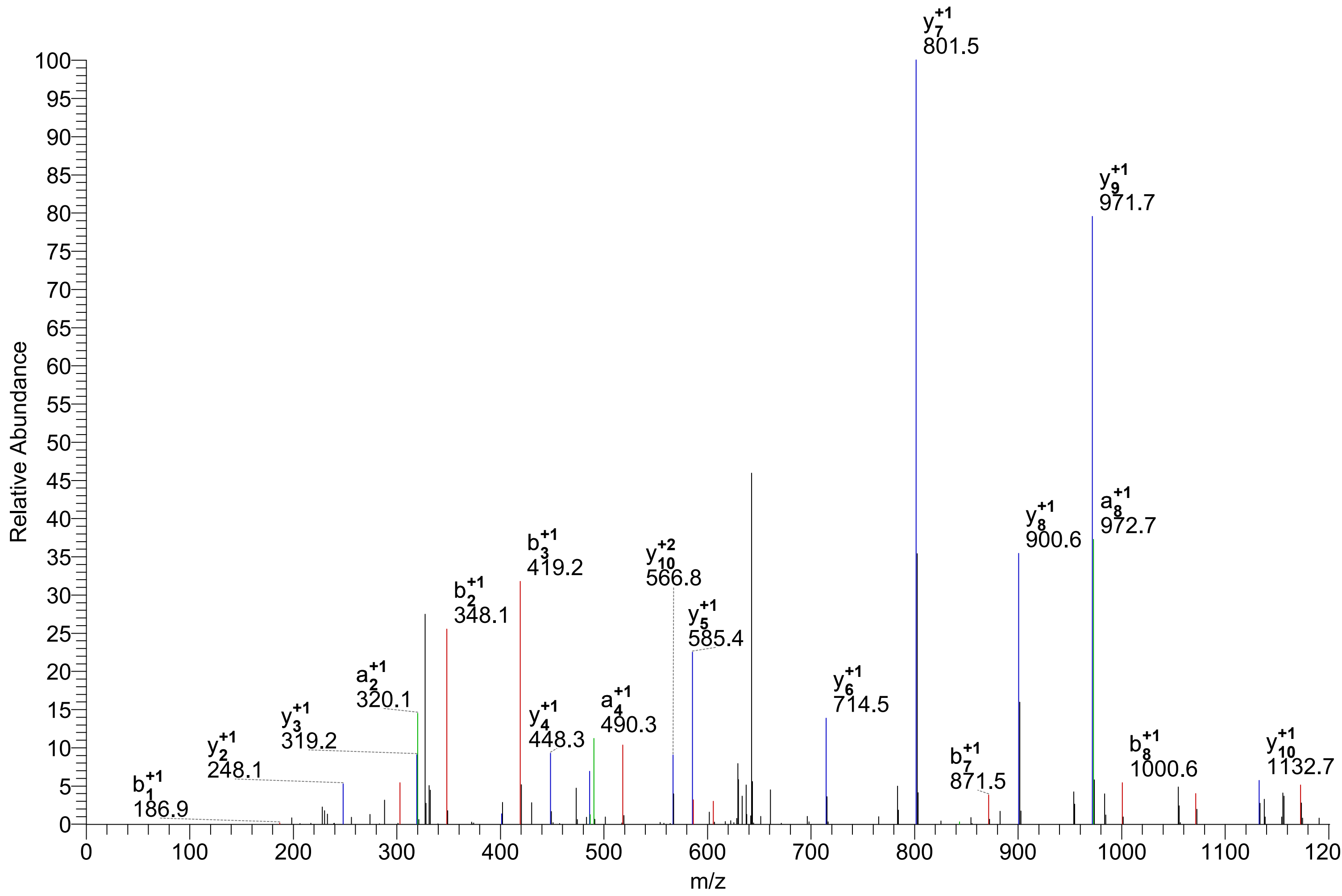

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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn    Sp  RSp  Ions  Count

IPI:IPI00791330.1|VEGA:OTTHUMP0000                                8e-007  10.2     0.0       0
19287468 - 1  K.SKEFQLFSSPHGK.D                     1491.76   3  8e-007  4.643  0.609   849.7   1   27/72   3

1 of 1 peptide matches reported, 0 removed due to filtering
```
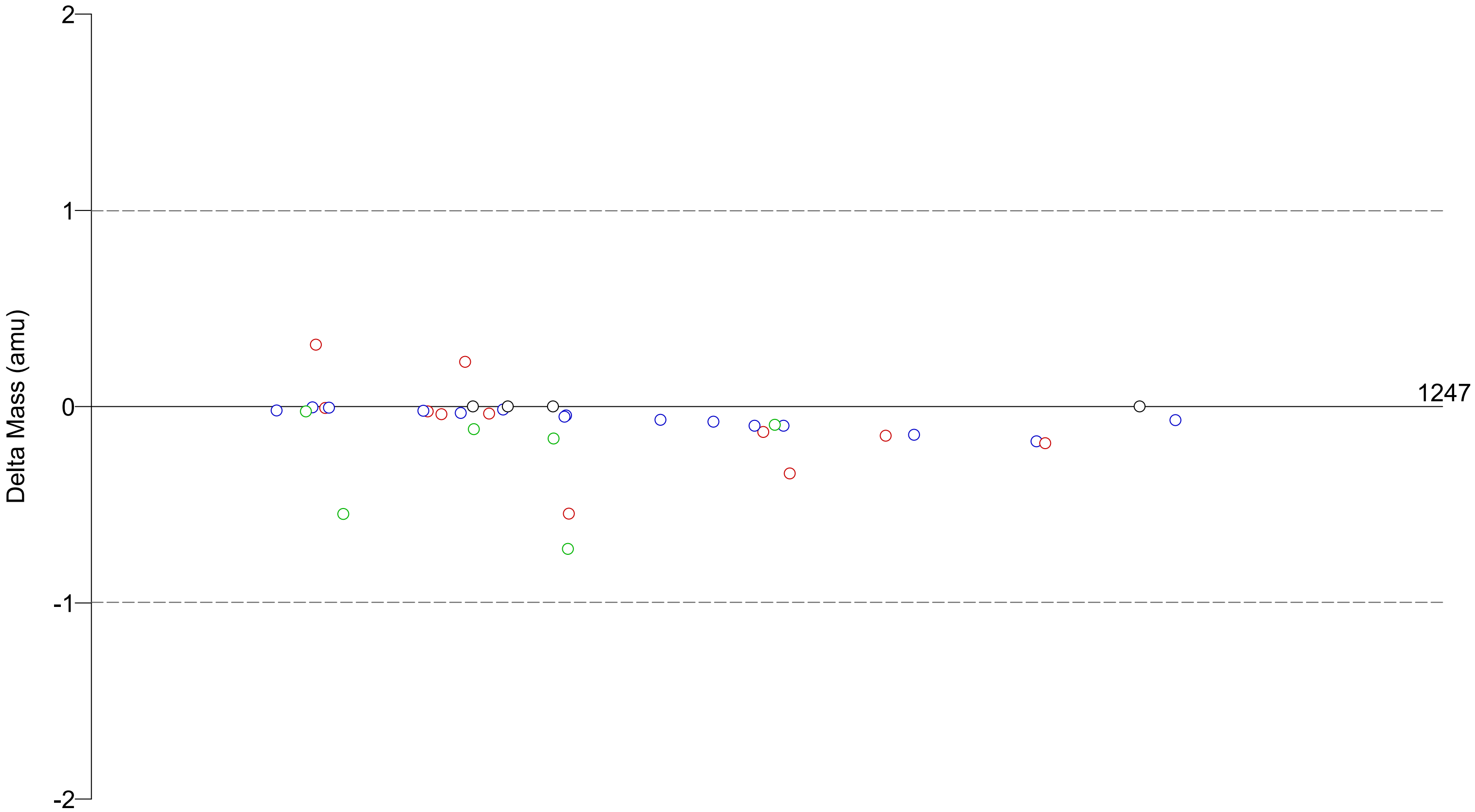

```
DTA for scans: 19287468-1
Precursor ion: 497.93
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 K    188.14     216.13                                      1404.73
 E    317.18     345.18                                      1276.63
 F    464.25     492.25                                      1147.59
 Q    592.31     620.30                                      1000.52
 L    705.39     733.39                                       872.46
 F    852.46     880.46                                       759.38
 S    939.49     967.49                                       612.31
 S   1026.53    1054.52                                       525.28
 P   1123.58    1151.57                                       438.25
 H   1260.64    1288.63                                       341.19
 G   1317.66    1345.65                                       204.13
 K                                                            147.11
```



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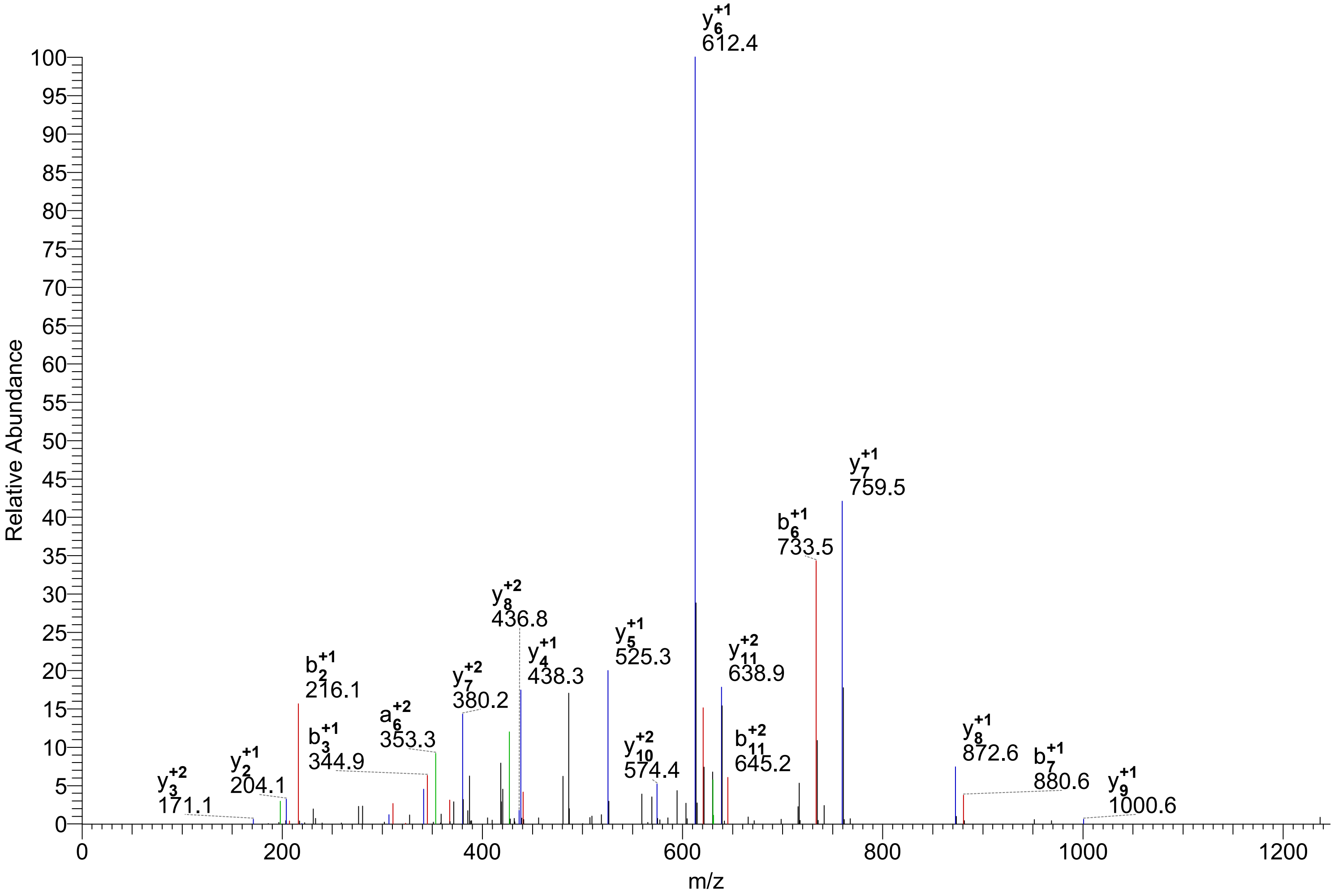

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Reference                                                                P      Score   Coverage   Accession
Scan(s)        Sequence                                      MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

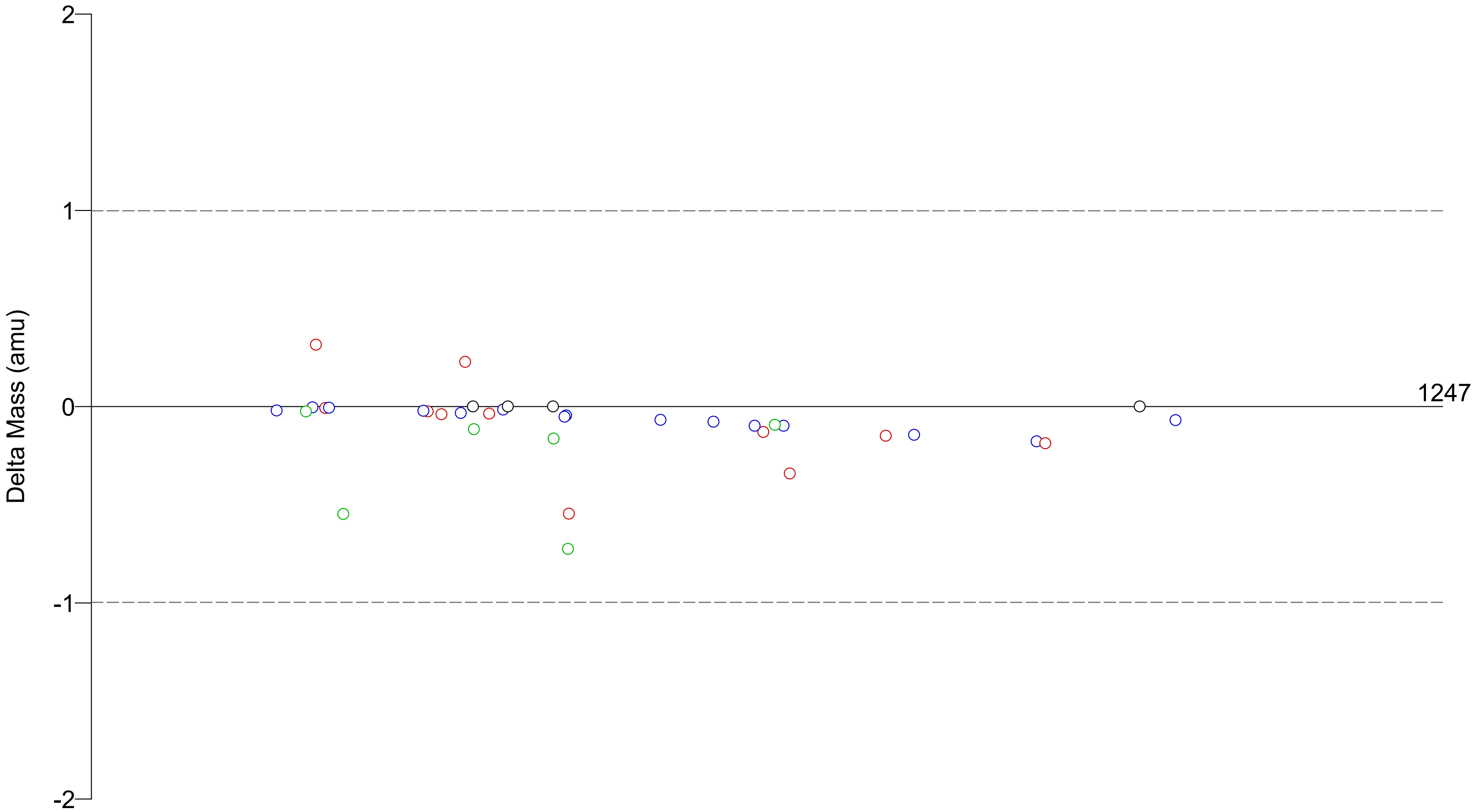
IPI:IPI00792626.1|VEGA:OTTHUMP0000                                      8e-007  10.2     0.0        0
19287468 - 1  K.SKEFQLFSSPHGK.D                           1491.76   3  8e-007  4.643  0.609   849.7  1   27/72   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

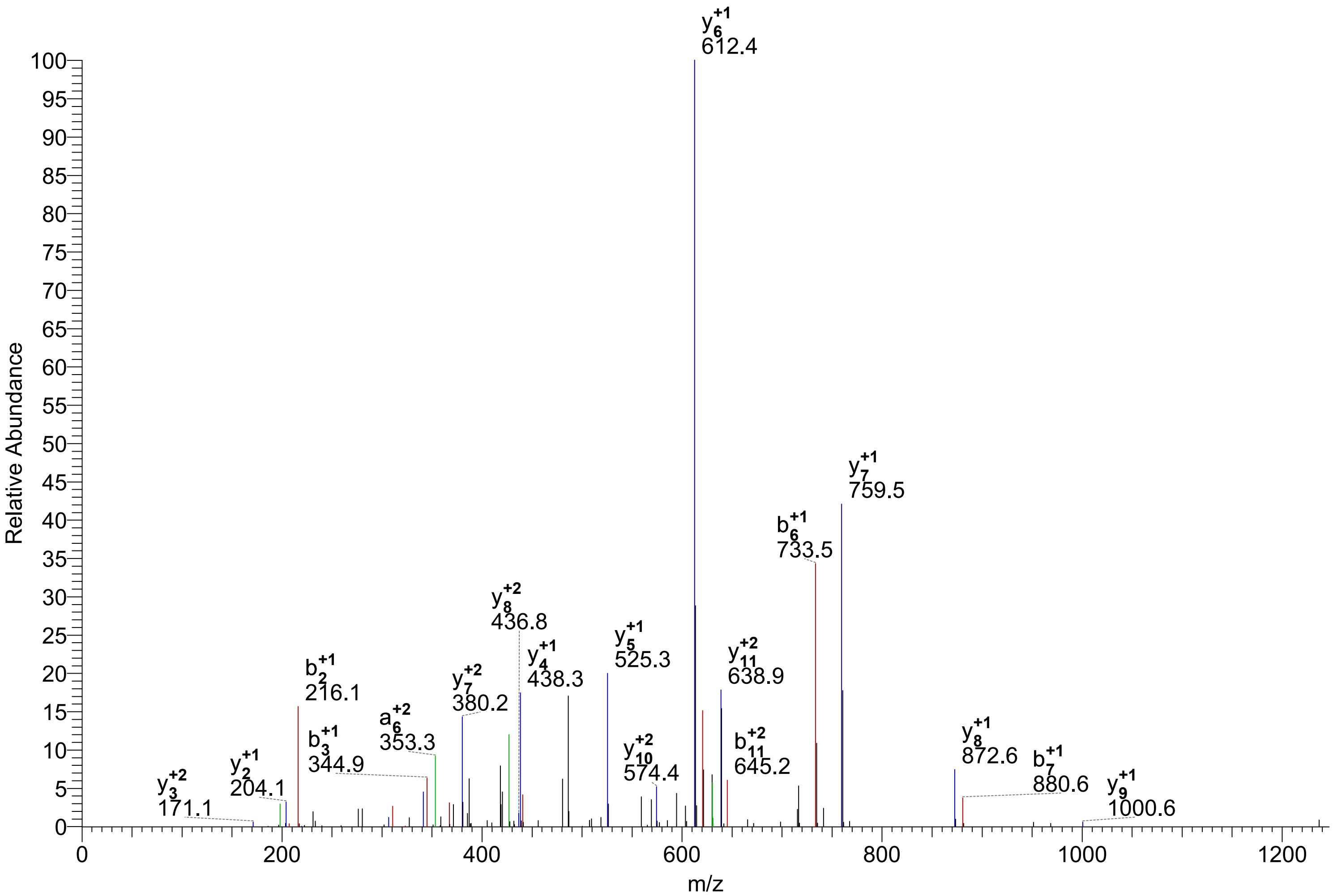
```
DTA for scans: 19287468-1
Precursor ion: 497.93
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 K    188.14     216.13                                    1404.73
 E    317.18     345.18                                    1276.63
 F    464.25     492.25                                    1147.59
 Q    592.31     620.30                                    1000.52
 L    705.39     733.39                                     872.46
 F    852.46     880.46                                     759.38
 S    939.49     967.49                                     612.31
 S   1026.53    1054.52                                     525.28
 P   1123.58    1151.57                                     438.25
 H   1260.64    1288.63                                     341.19
 G   1317.66    1345.65                                     204.13
 K                                                          147.11
```



#19287468-1 NL: 3.10E6



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

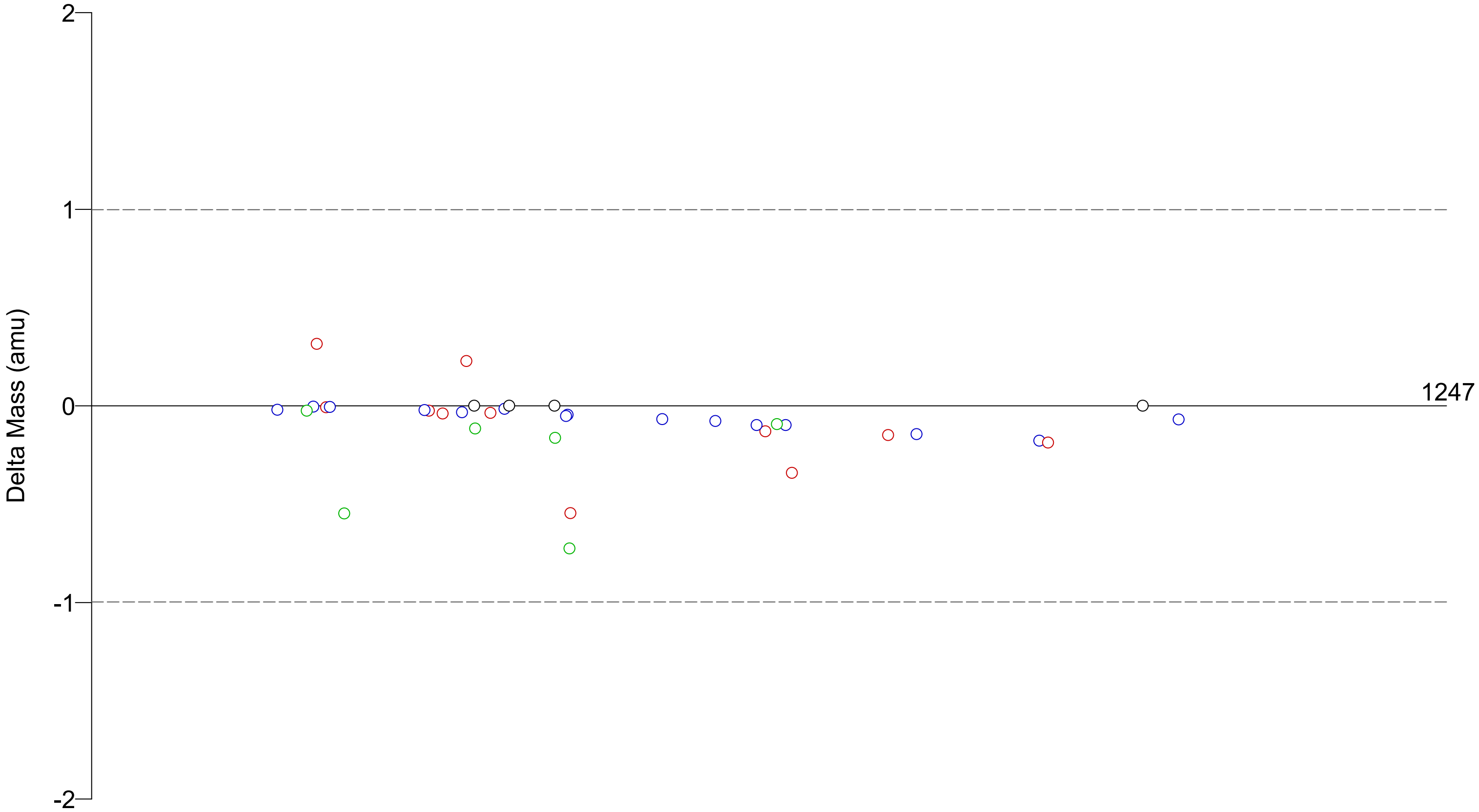
IPI:IPI00798430.2|VEGA:OTTHUMP0000                                8e-007  10.2     0.0       0
19287468 - 1  K.SKEFQLFSSPHGK.D                      1491.76   3  8e-007  4.643  0.609   849.7  1   27/72   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

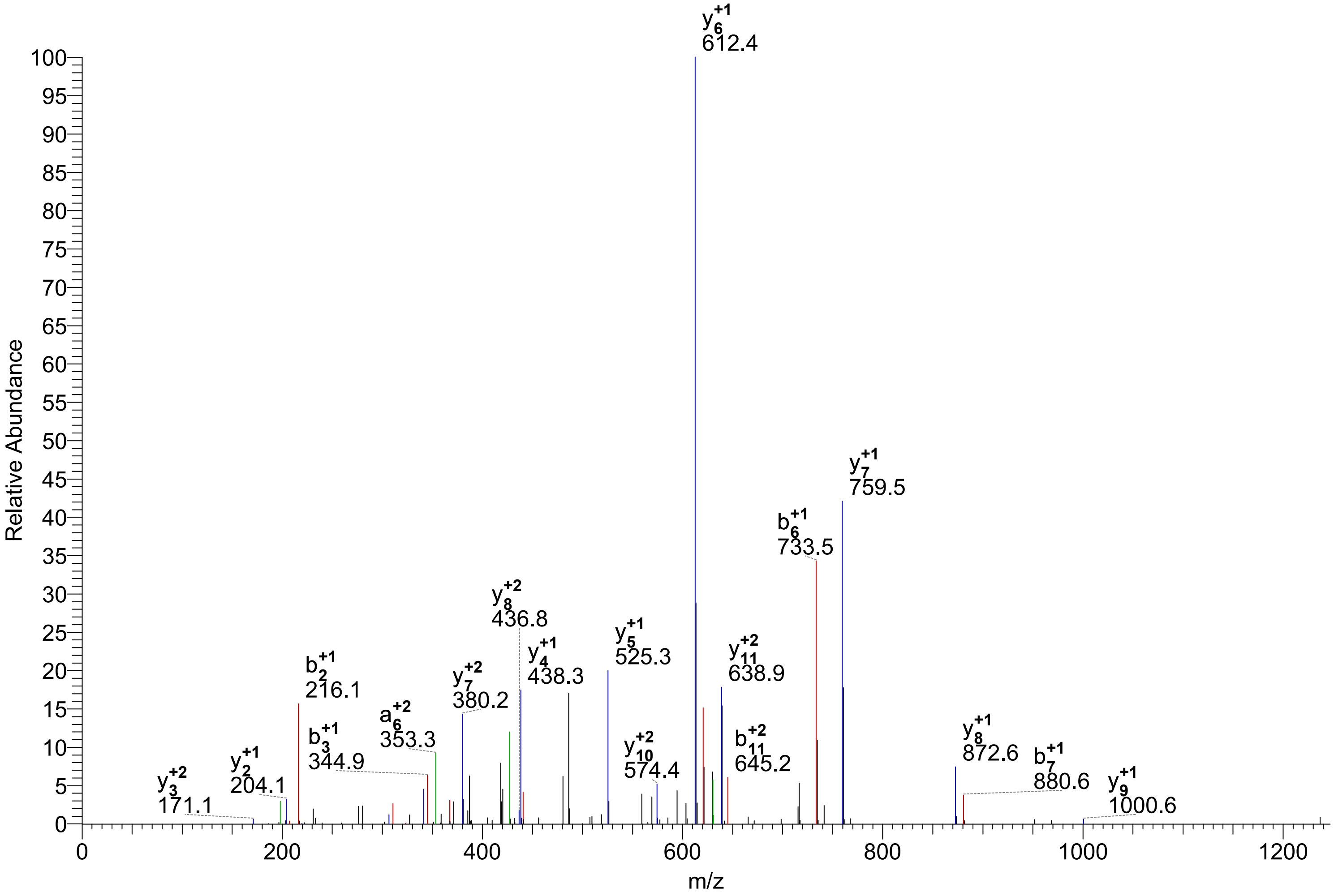
```
DTA for scans: 19287468-1
Precursor ion: 497.93
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 K    188.14     216.13                                     1404.73
 E    317.18     345.18                                     1276.63
 F    464.25     492.25                                     1147.59
 Q    592.31     620.30                                     1000.52
 L    705.39     733.39                                      872.46
 F    852.46     880.46                                      759.38
 S    939.49     967.49                                      612.31
 S   1026.53    1054.52                                      525.28
 P   1123.58    1151.57                                      438.25
 H   1260.64    1288.63                                      341.19
 G   1317.66    1345.65                                      204.13
 K                                                           147.11
```



#19287468-1 NL: 3.10E6



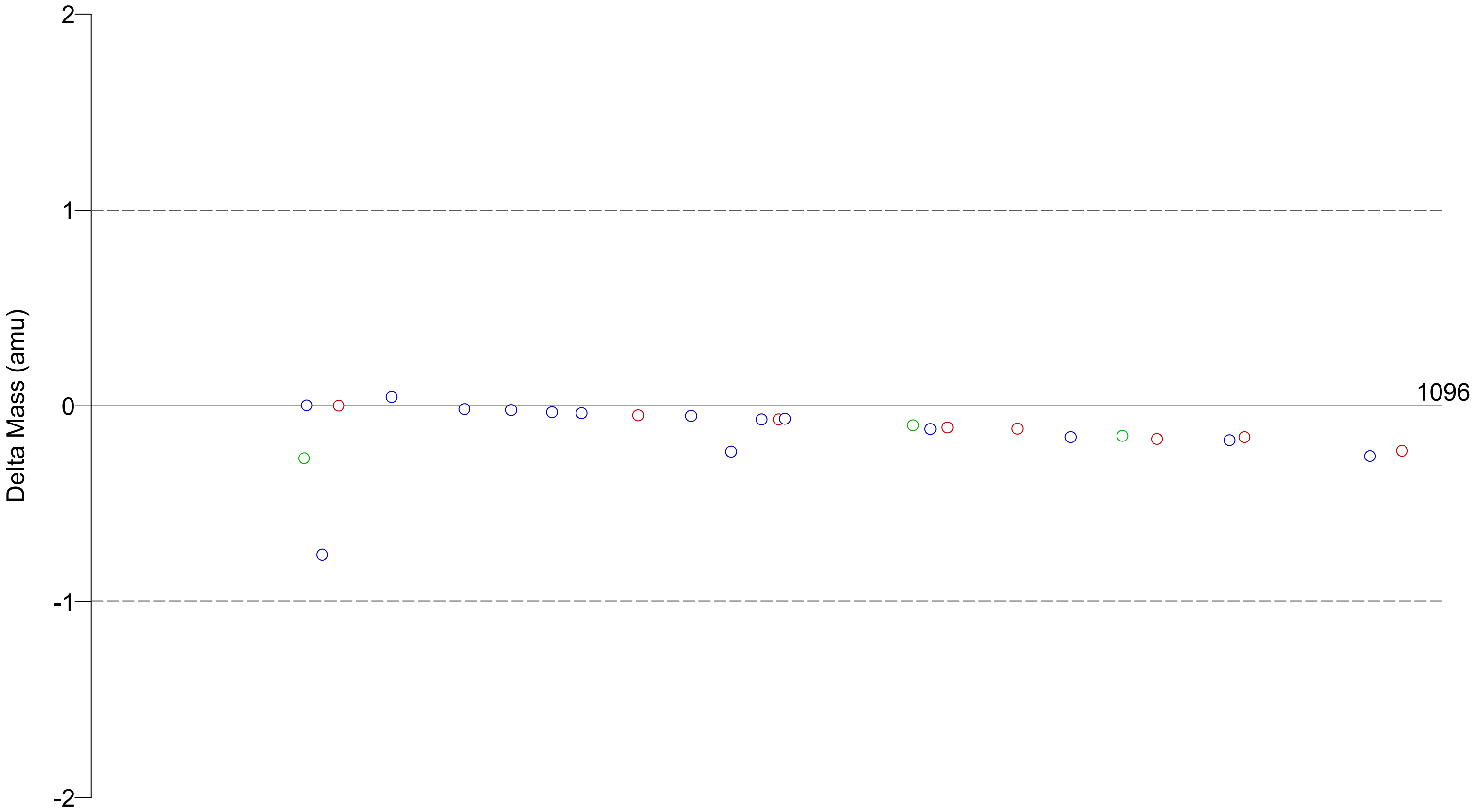
```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00305461.3|SWISS-PROT:P19823|TREMBL:A2RTY6|ENSEMBL:ENSP     1e-006  10.2     0.0        0
2118291816 -  R.LSNENHGIAQR.I                              1238.62   2  1e-006  4.292  0.485   789.7  1   18/30   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

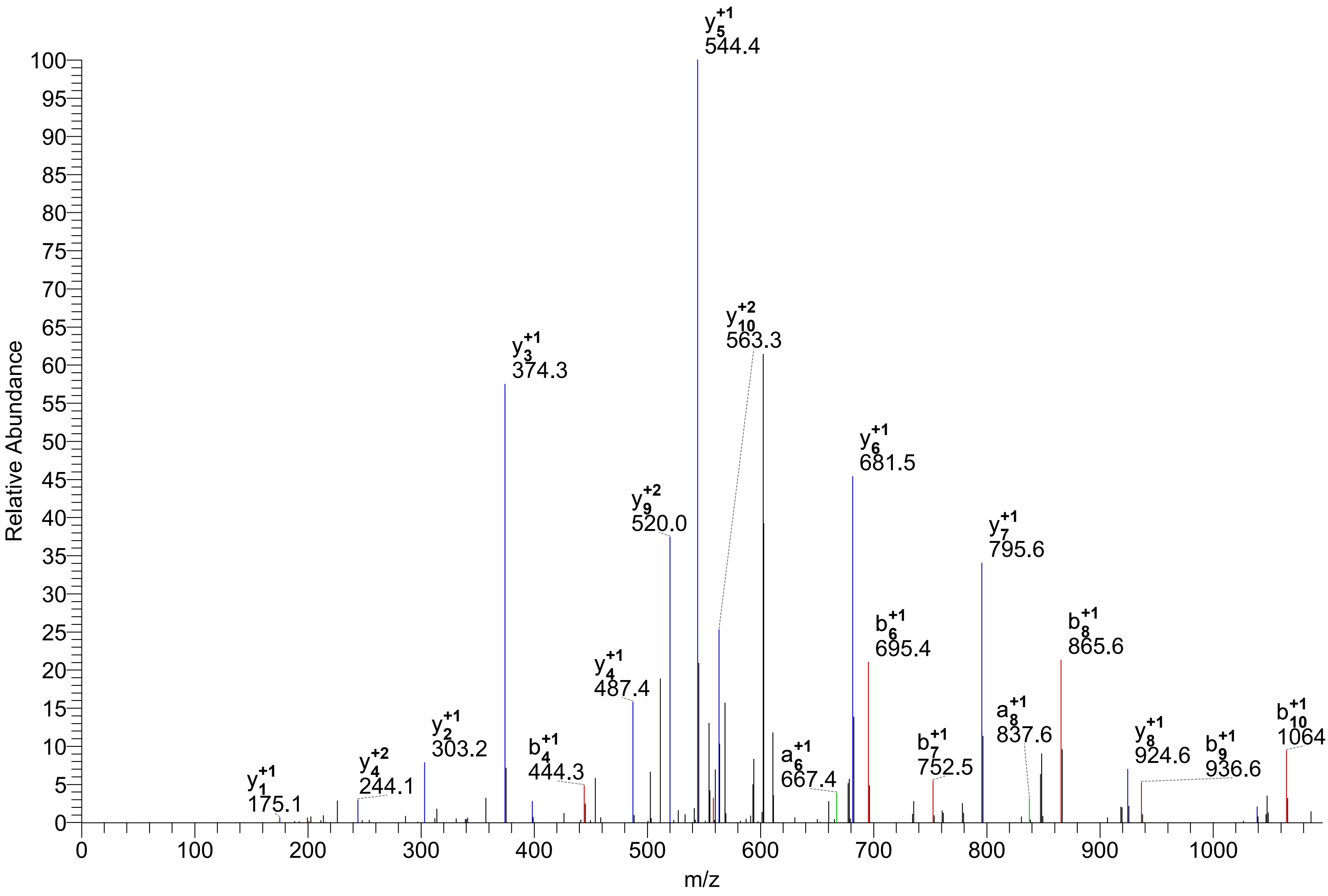
```
DTA for scans: 2118291816-26226248
Precursor ion: 619.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                    1125.54
 N    287.17     315.17                                    1038.51
 E    416.21     444.21                                     924.46
 N    530.26     558.25                                     795.42
 H    667.32     695.31                                     681.38
 G    724.34     752.33                                     544.32
 I    837.42     865.42                                     487.30
 A    908.46     936.45                                     374.21
 Q   1036.52    1064.51                                     303.18
 R                                                          175.12
```



#2118291816-26226248 NL: 2.79E5



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count

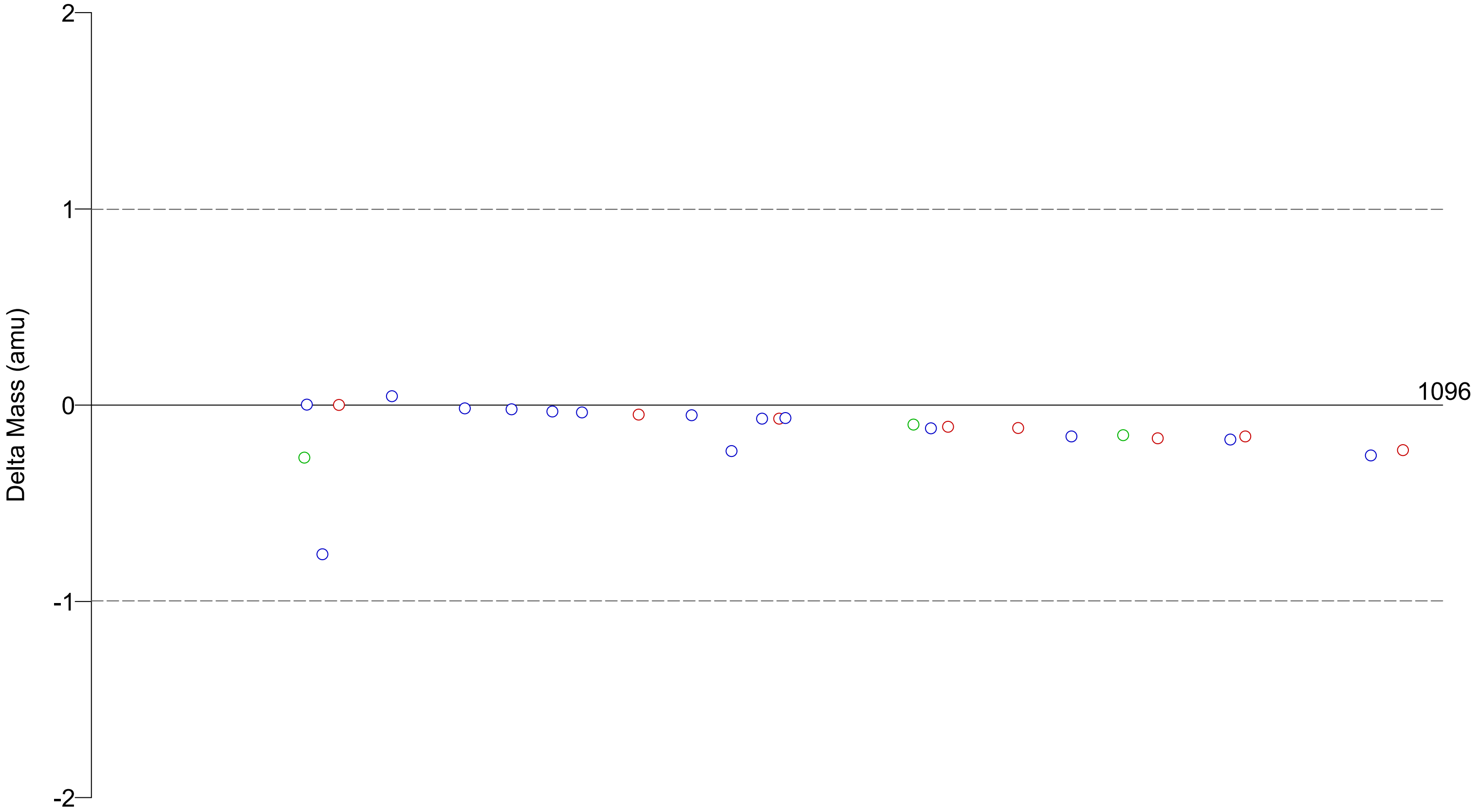
IPI:IPI00645038.1|TREMBL:Q5T985|EN                                 1e-006  10.2      0.0        0
2118291816 -  R.LSNENHGIAQR.I                            1238.62   2  1e-006  4.292  0.485   789.7  1   18/30   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

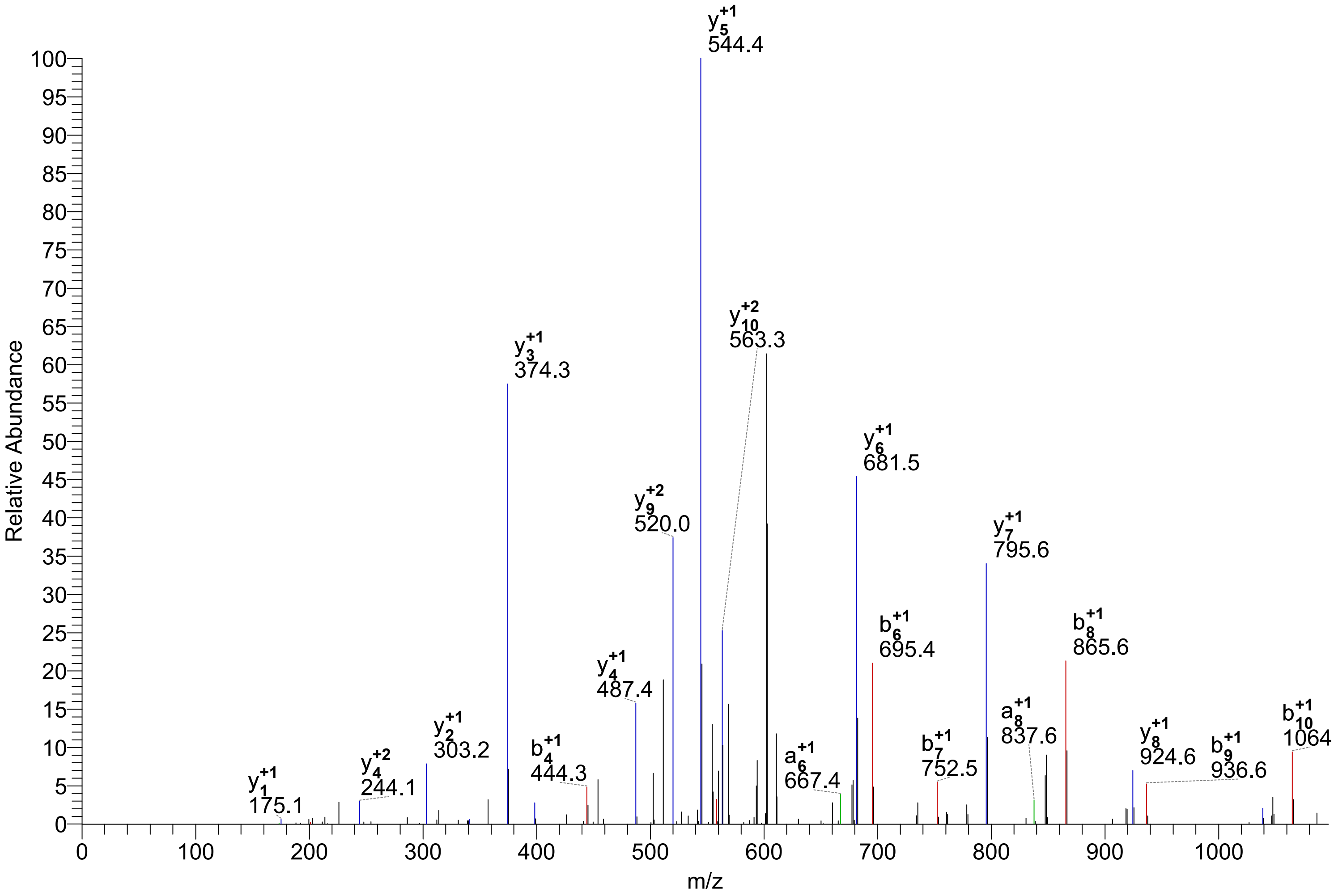
```
DTA for scans: 2118291816-26226248
Precursor ion: 619.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13    201.12                                     1125.54
 N    287.17    315.17                                     1038.51
 E    416.21    444.21                                      924.46
 N    530.26    558.25                                      795.42
 H    667.32    695.31                                      681.38
 G    724.34    752.33                                      544.32
 I    837.42    865.42                                      487.30
 A    908.46    936.45                                      374.21
 Q   1036.52   1064.51                                      303.18
 R                                                          175.12
```



#2118291816-26226248 NL: 2.79E5



```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

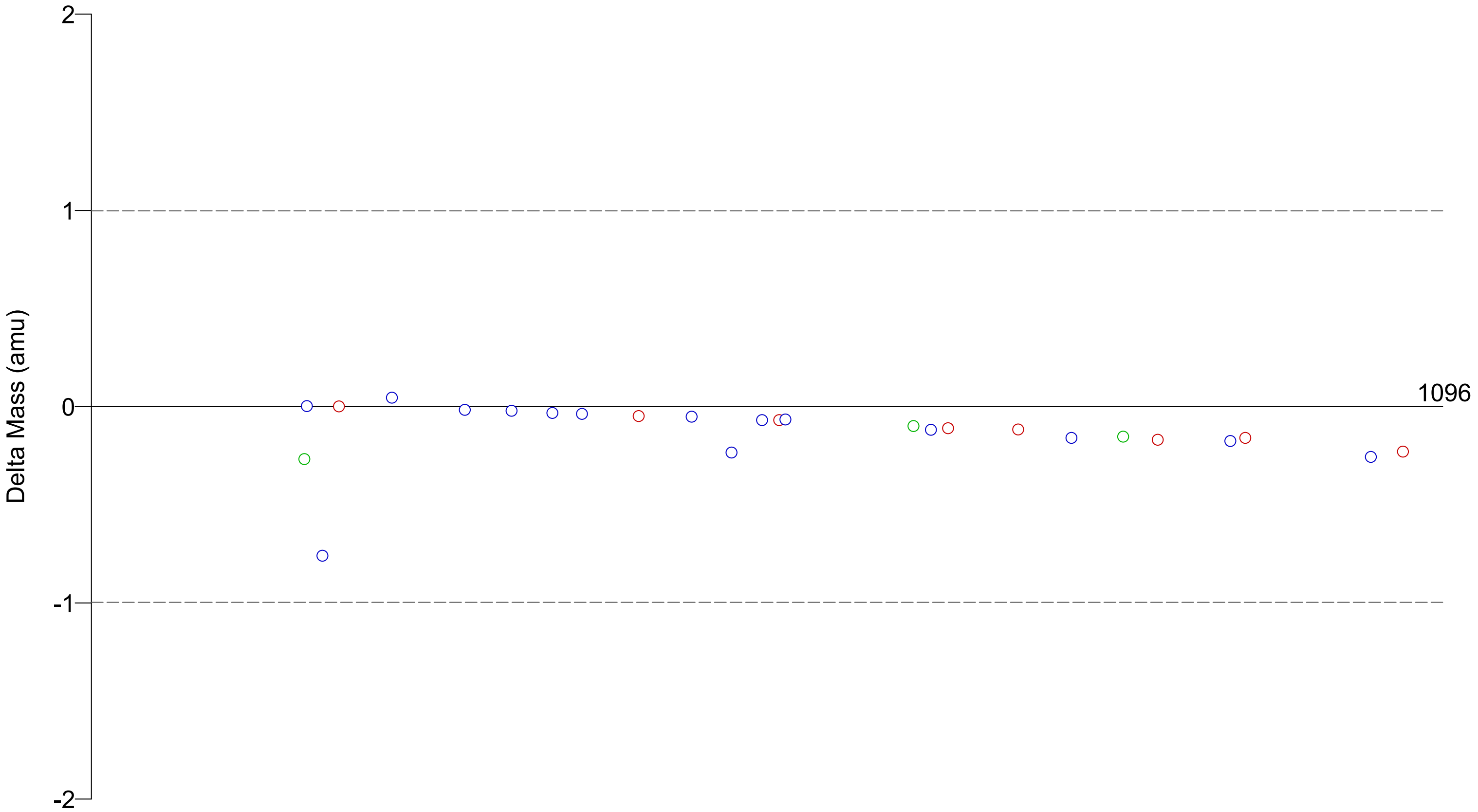
IPI:IPI00910636.1|TREMBL:B4DM79 Ta                                   1e-006  10.2     0.0        0
2118291816 -  R.LSNENHGIAQR.I                             1238.62   2  1e-006  4.292  0.485   789.7  1   18/30   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

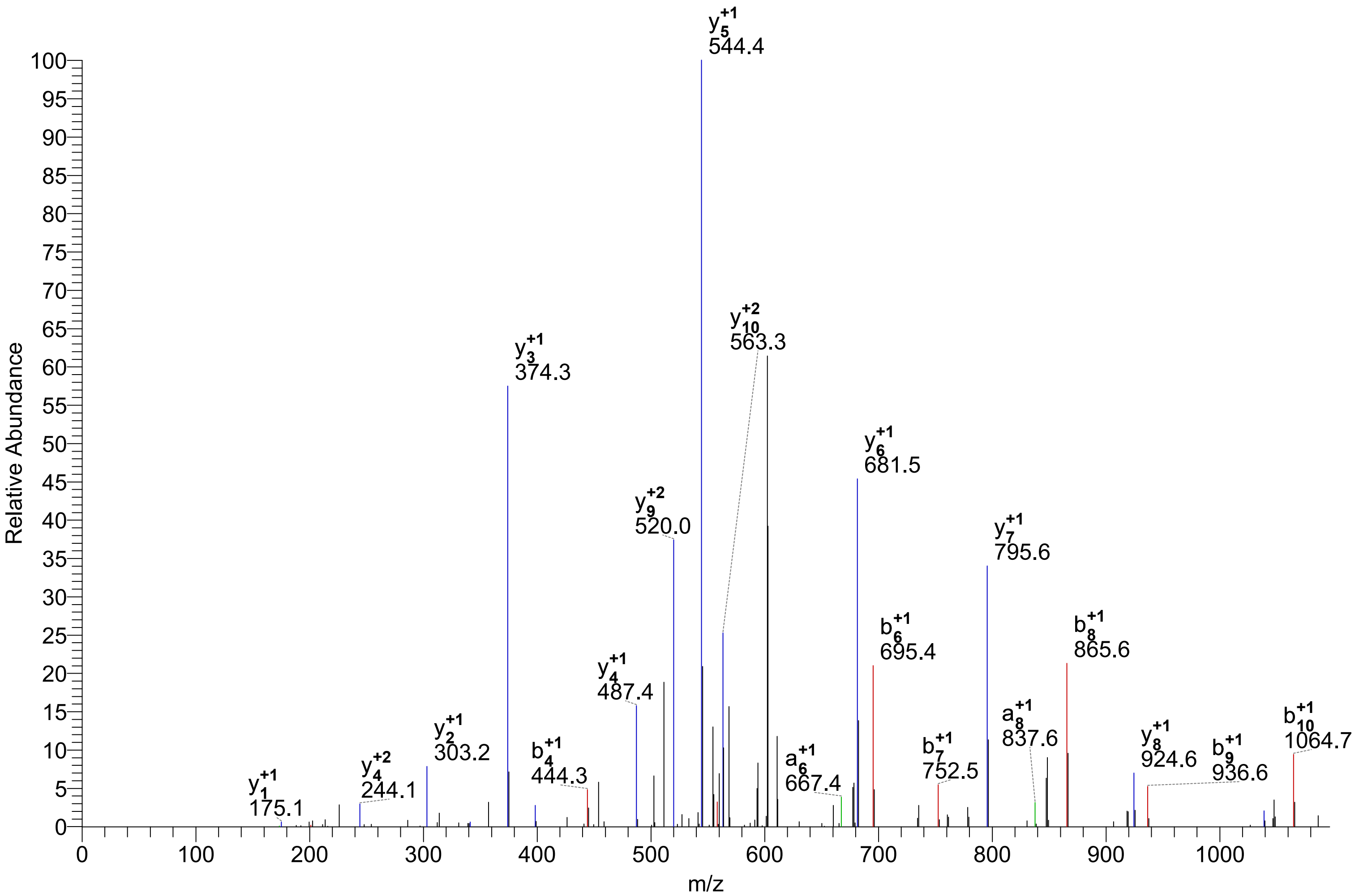
```
DTA for scans: 2118291816-26226248
Precursor ion: 619.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                     1125.54
 N    287.17     315.17                                     1038.51
 E    416.21     444.21                                      924.46
 N    530.26     558.25                                      795.42
 H    667.32     695.31                                      681.38
 G    724.34     752.33                                      544.32
 I    837.42     865.42                                      487.30
 A    908.46     936.45                                      374.21
 Q   1036.52    1064.51                                      303.18
 R                                                           175.12
```



#2118291816-26226248 NL: 2.79E5



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

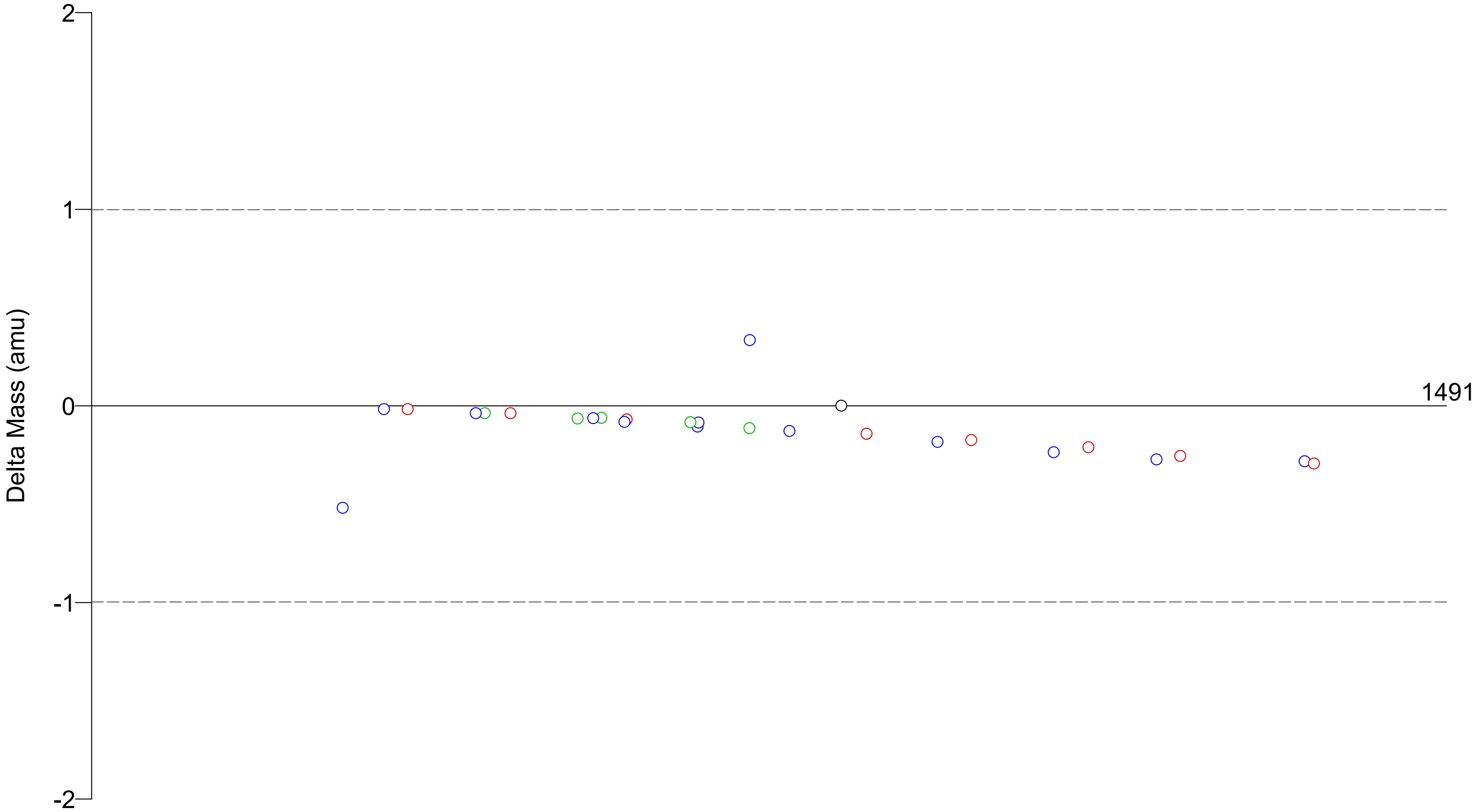
IPI:IPI00017601.1|SWISS-PROT:P00450|TREMBL:A5PL27;A8K5A4;B7Z5Q     1e-006  20.2     0.0       0
19287468 - 1  K.ALYLQYTDETFR.T                         1519.74   2  1e-006  4.725  0.473   1101.8 1   20/33   1
2118291816 -  K.VNKDDEEFIESNK.M                        1566.73   3  3e-005  3.718  0.554   800.2  1   25/72   2

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

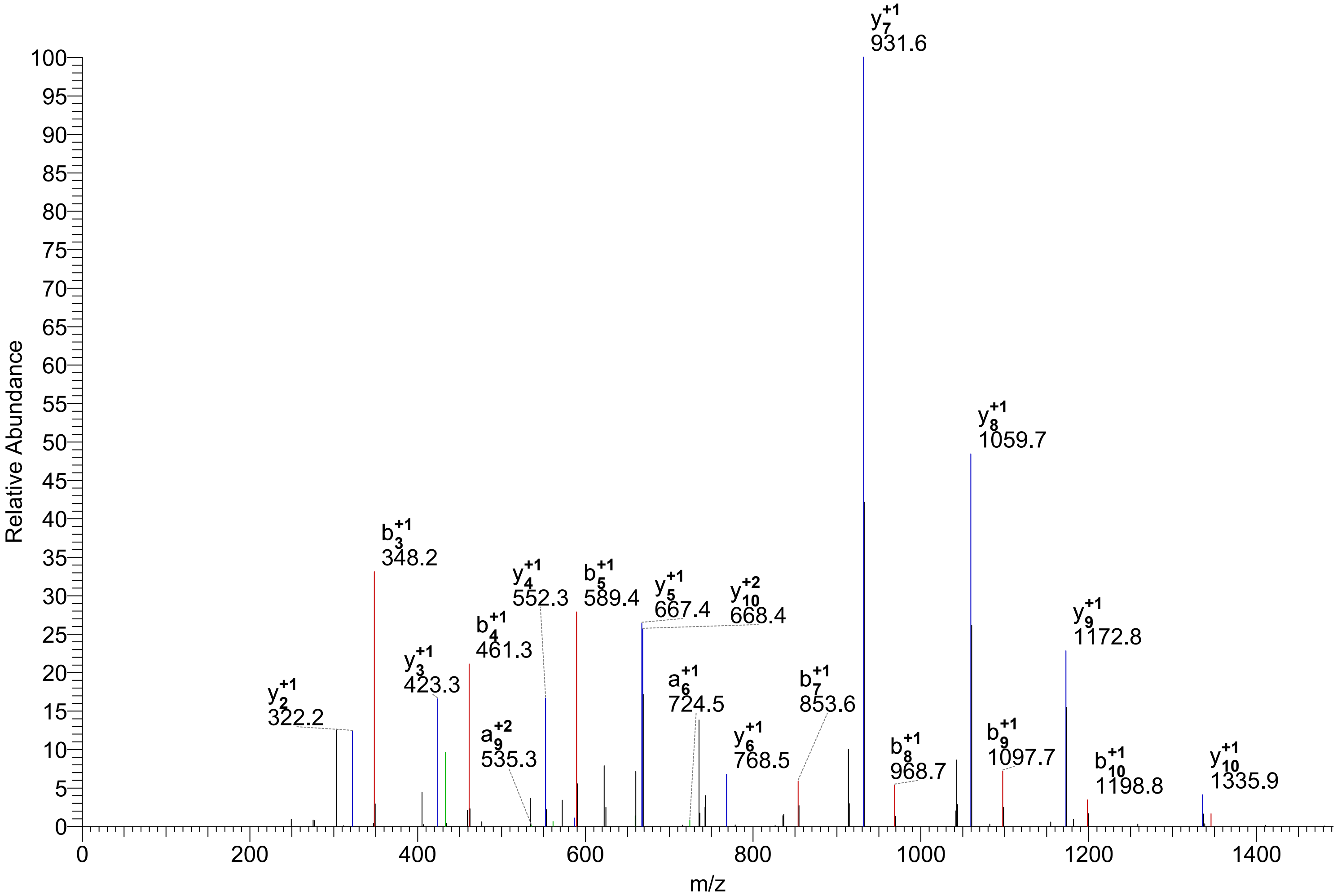
```
DTA for scans: 19287468-1
Precursor ion: 760.38
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 L    157.13     185.13                                      1448.71
 Y    320.20     348.19                                      1335.62
 L    433.28     461.28                                      1172.56
 Q    561.34     589.33                                      1059.47
 Y    724.40     752.40                                       931.42
 T    825.45     853.45                                       768.35
 D    940.48     968.47                                       667.30
 E   1069.52    1097.51                                       552.28
 T   1170.57    1198.56                                       423.24
 F   1317.64    1345.63                                       322.19
 R                                                            175.12
```



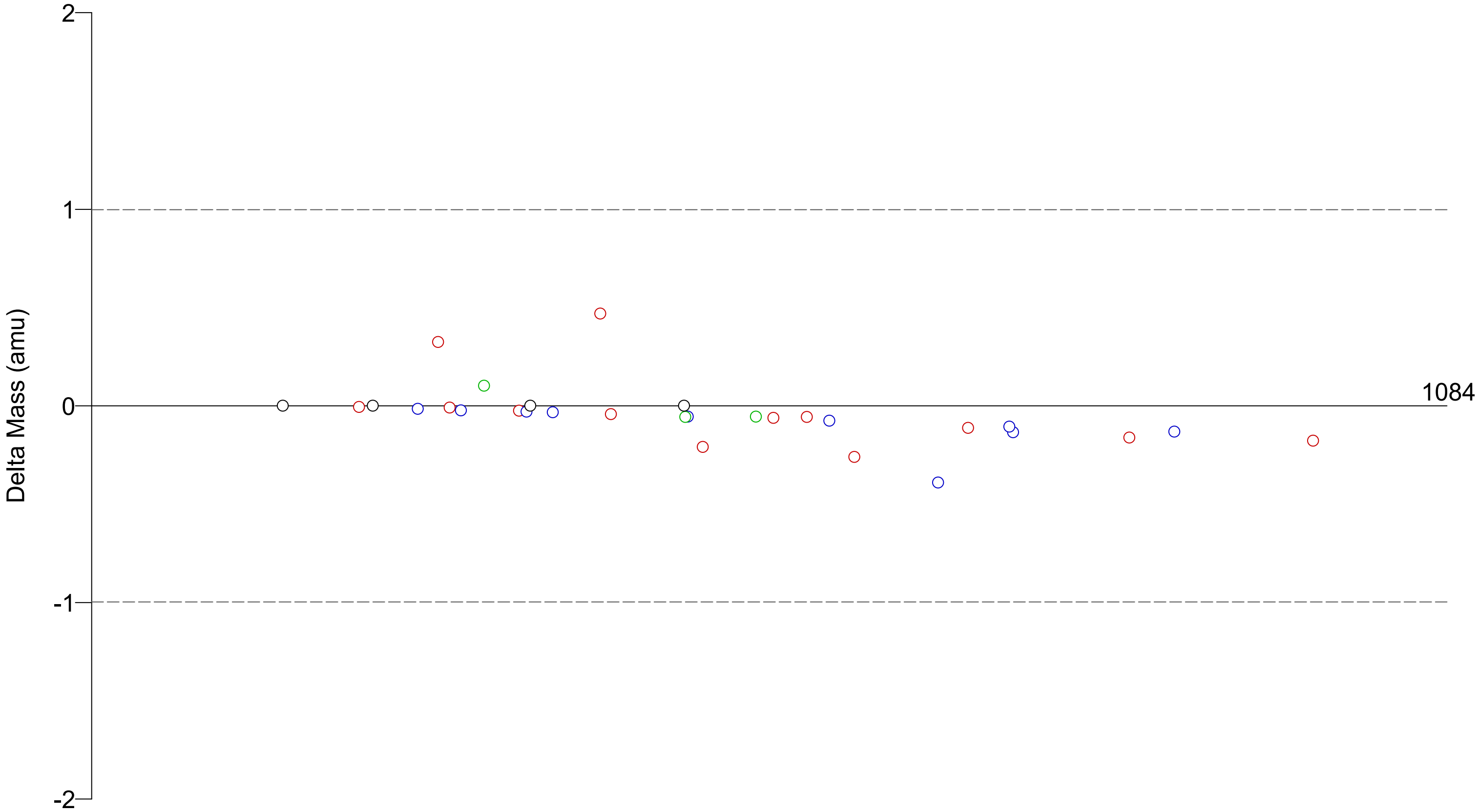
#19287468-1 NL: 6.47E4



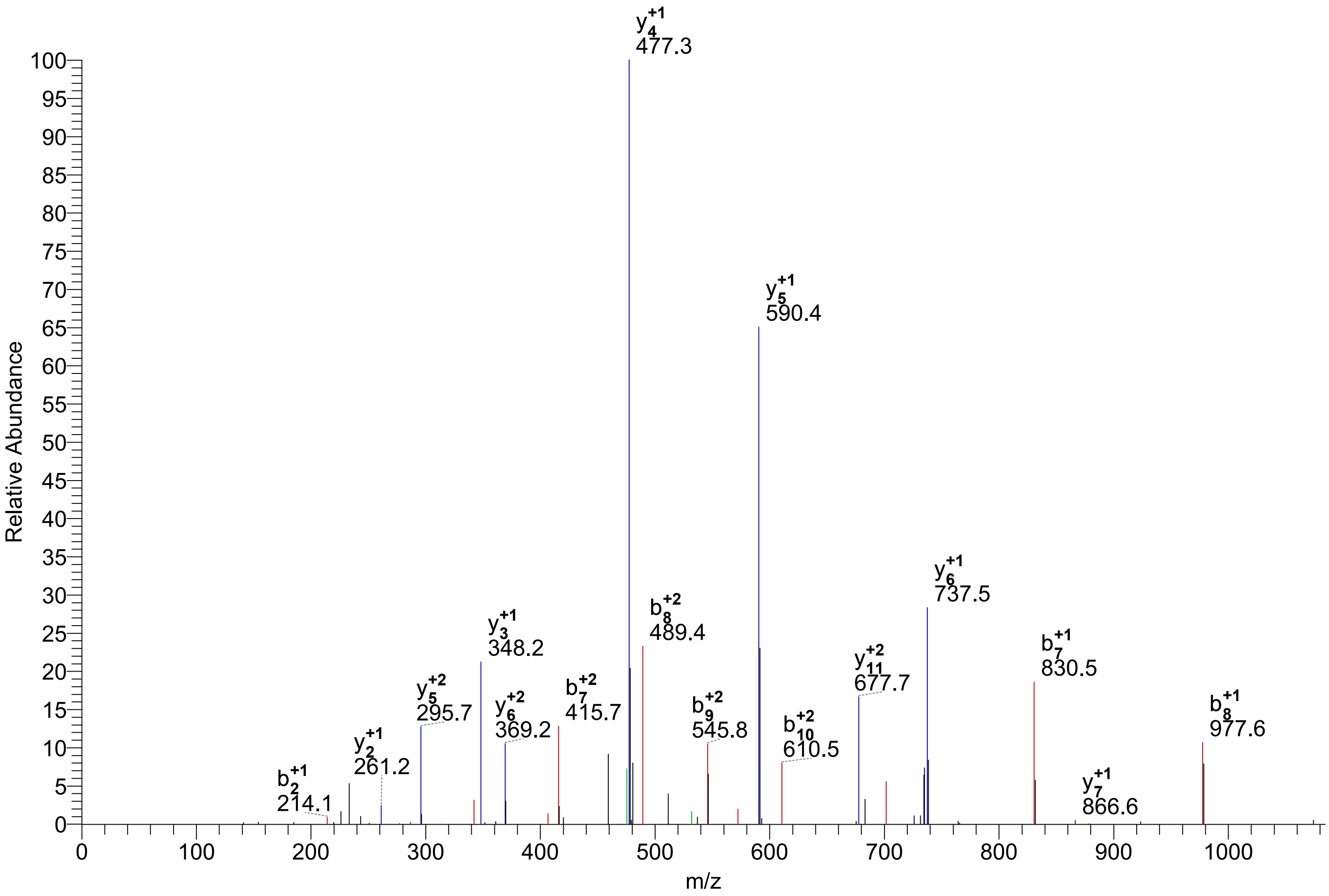
```
DTA for scans: 2118291816-26226248
Precursor ion: 522.91
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 N    186.12     214.12                                    1467.66
 K    314.22     342.21                                    1353.62
 D    429.25     457.24                                    1225.52
 D    544.27     572.27                                    1110.49
 E    673.32     701.31                                     995.47
 E    802.36     830.35                                     866.43
 F    949.43     977.42                                     737.38
 I   1062.51    1090.51                                     590.31
 E   1191.55    1219.55                                     477.23
 S   1278.58    1306.58                                     348.19
 N   1392.63    1420.62                                     261.16
 K                                                          147.11
```



#2118291816-26226248 NL: 8.32E4



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z  P        XC  DeltaCn   Sp   RSp  Ions  Count

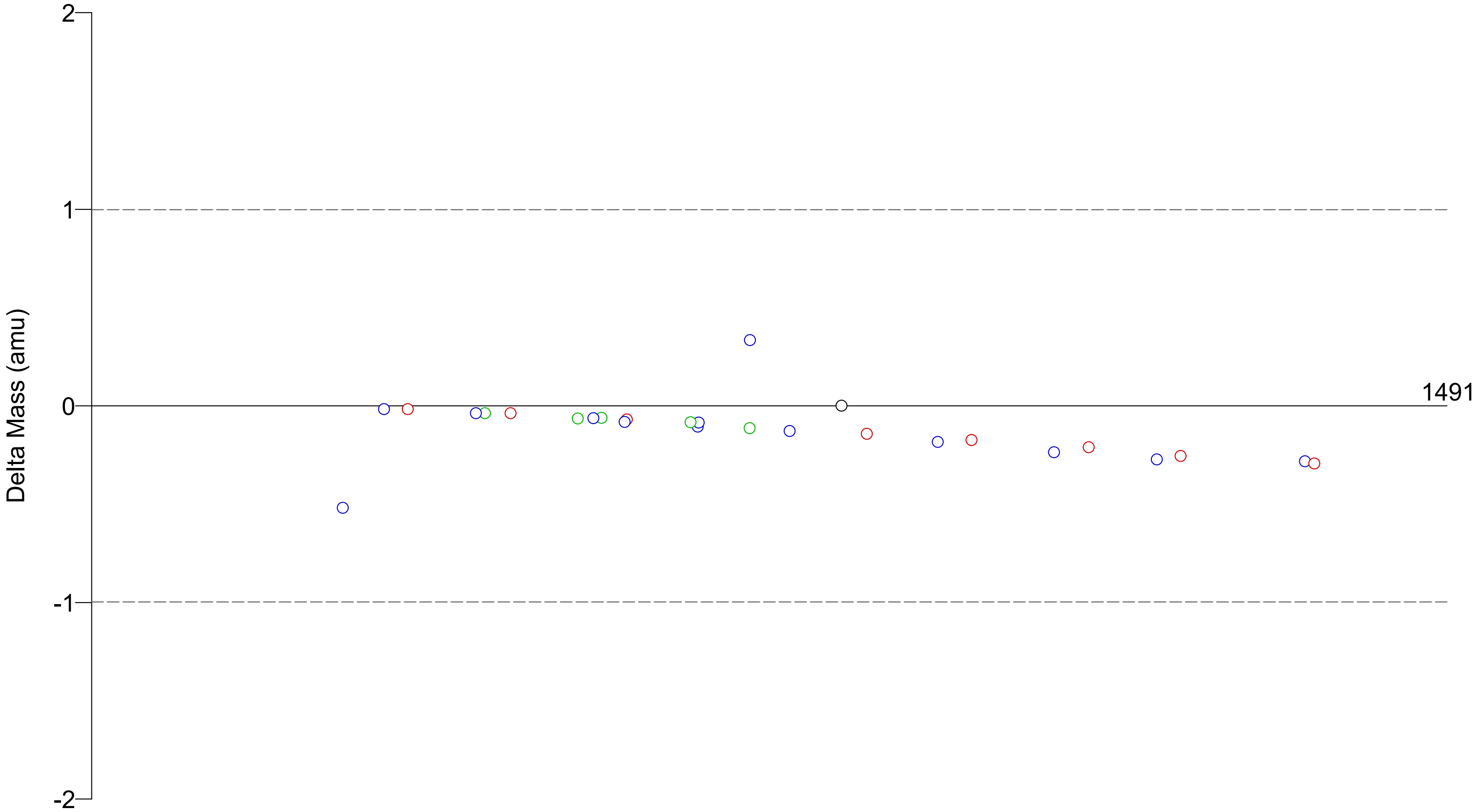
IPI:IPI00879084.1|VEGA:OTTHUMP0000                                 1e-006  10.2     0.0       0
19287468 - 1  K.ALYLQYTDETFR.T                       1519.74   2  1e-006  4.725  0.473   1101.8 1   20/33   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

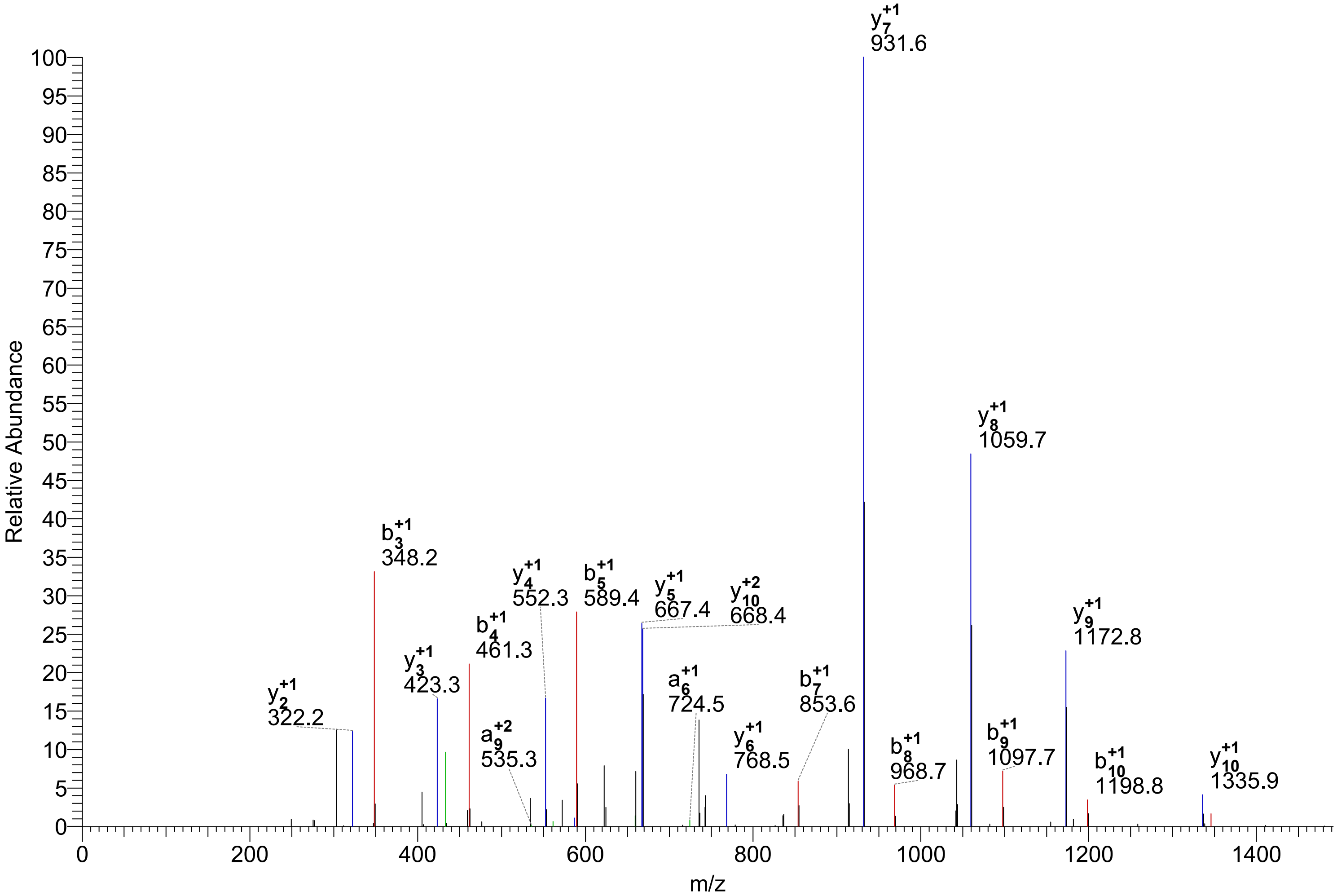
```
DTA for scans: 19287468-1
Precursor ion: 760.38
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 L    157.13     185.13                                     1448.71
 Y    320.20     348.19                                     1335.62
 L    433.28     461.28                                     1172.56
 Q    561.34     589.33                                     1059.47
 Y    724.40     752.40                                      931.42
 T    825.45     853.45                                      768.35
 D    940.48     968.47                                      667.30
 E   1069.52    1097.51                                      552.28
 T   1170.57    1198.56                                      423.24
 F   1317.64    1345.63                                      322.19
 R                                                           175.12
```



#19287468-1 NL: 6.47E4



```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                        MH+      z    P        XC  DeltaCn   Sp    RSp  Ions   Count

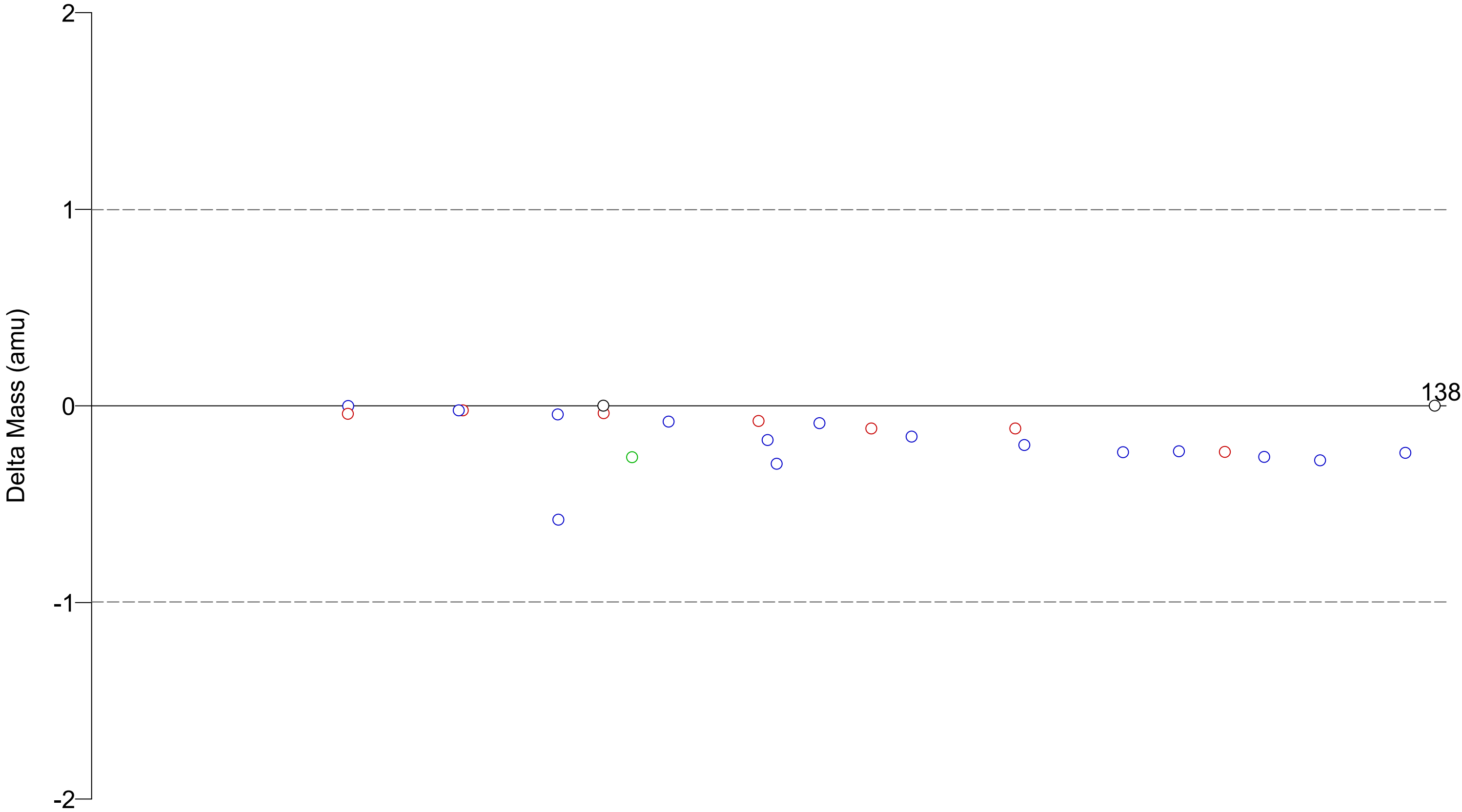
IPI:IPI00916434.1|TREMBL:A2KBB9;A2                                       1e-006  20.2     0.0       0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                          1632.79    2  1e-006  3.219  0.589   674.9  1   19/45   14
19287468 - 1  K.NTLYLQMNSLR.A                                1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

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

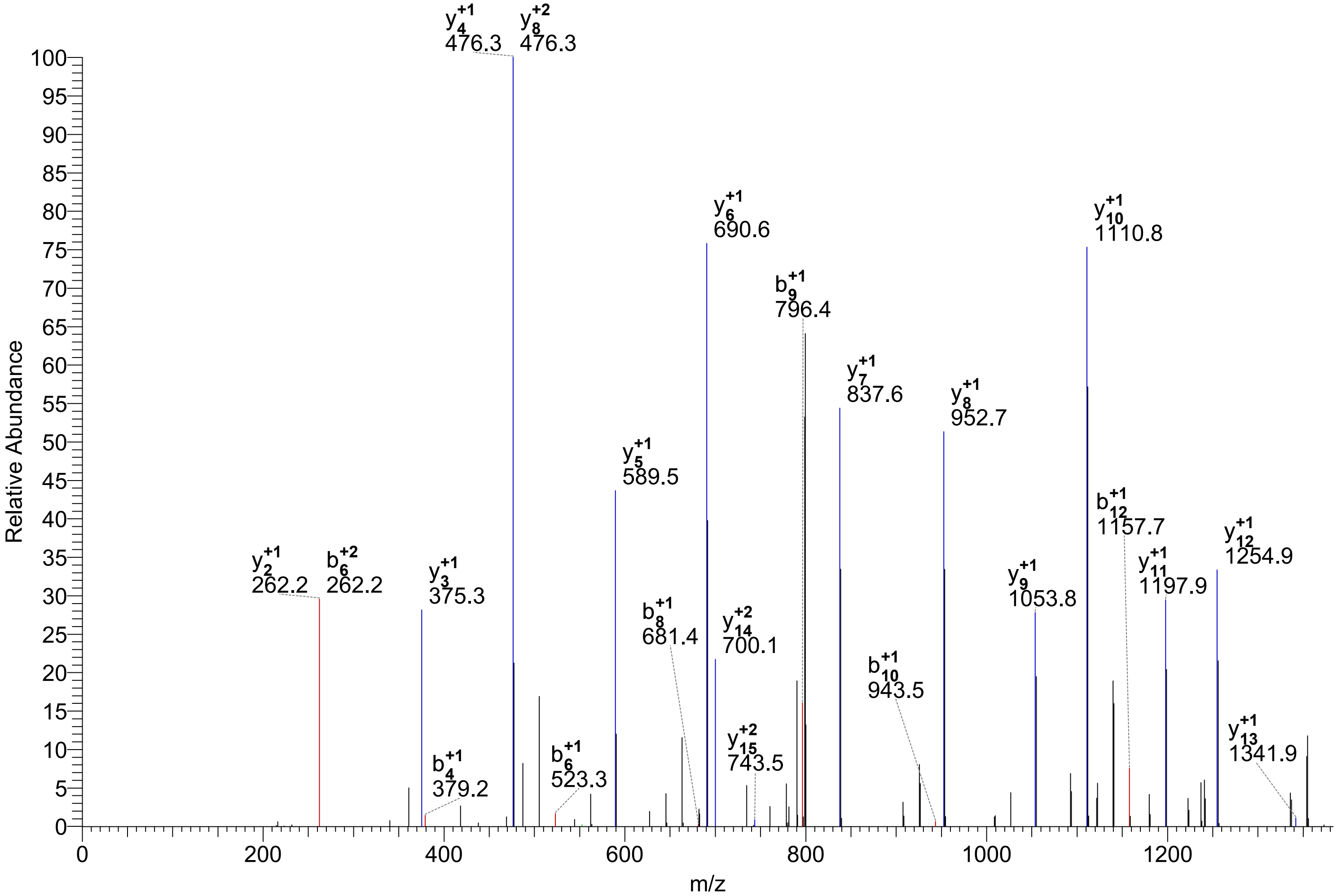
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



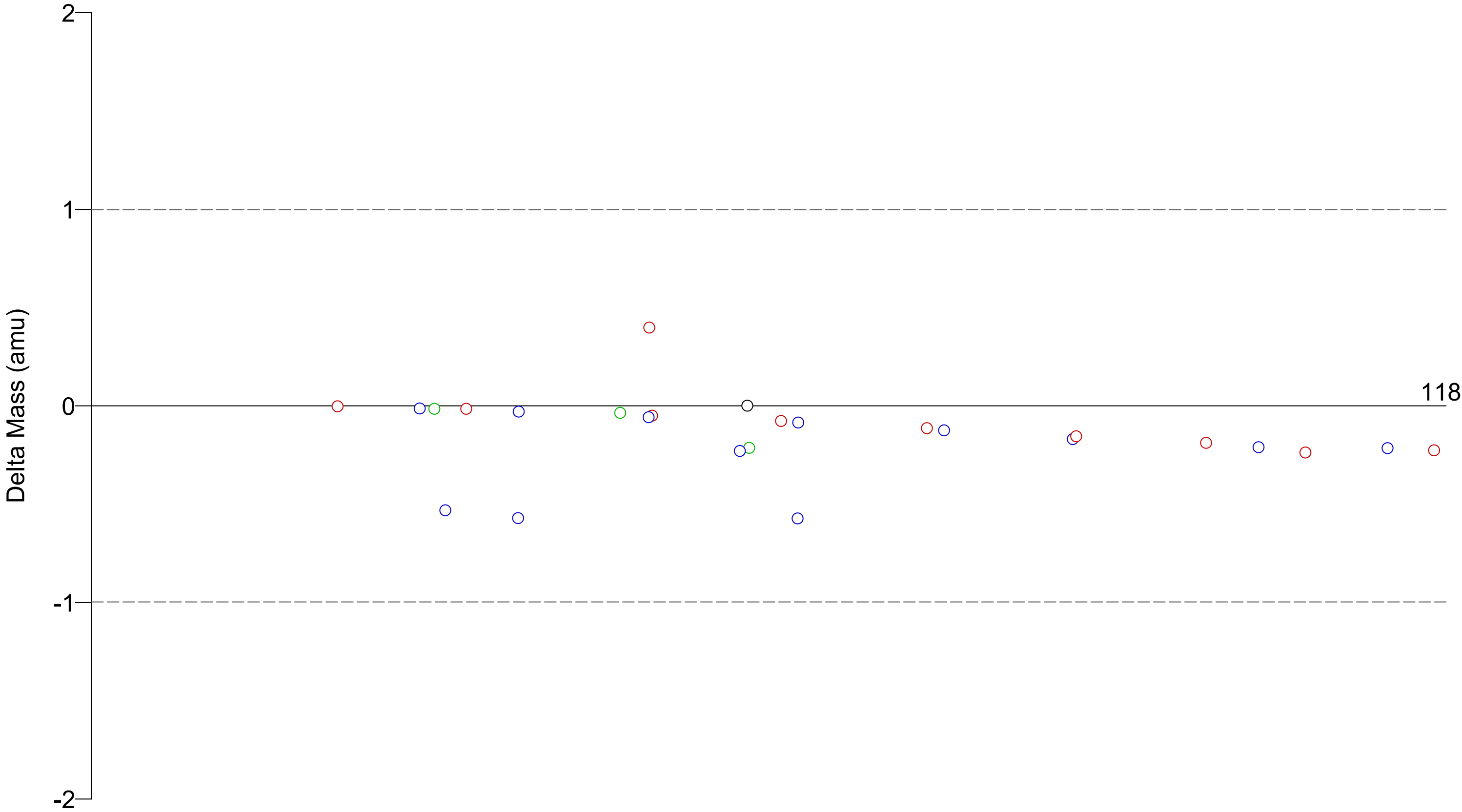
#19287468-1 NL: 6.55E4



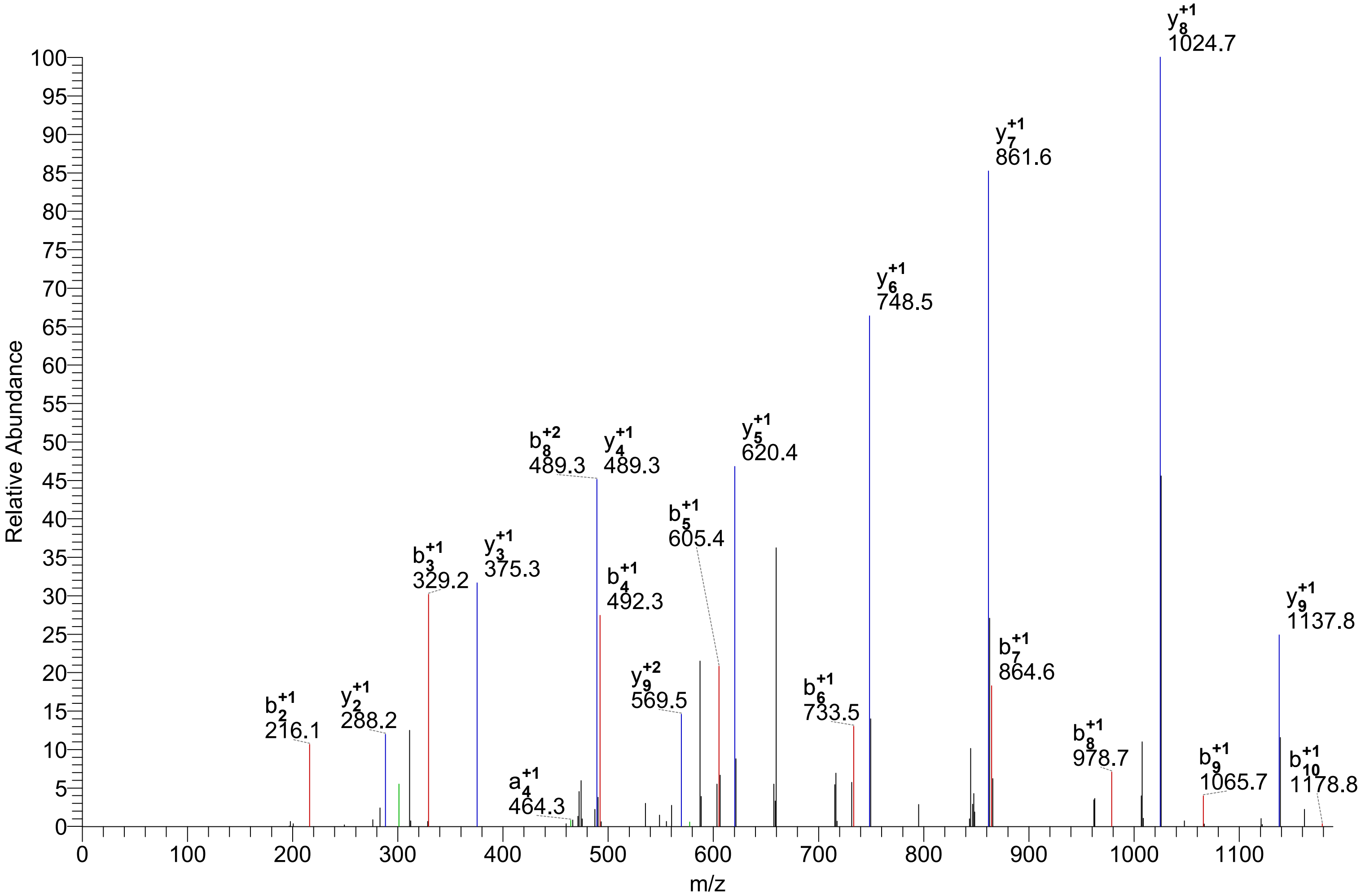
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

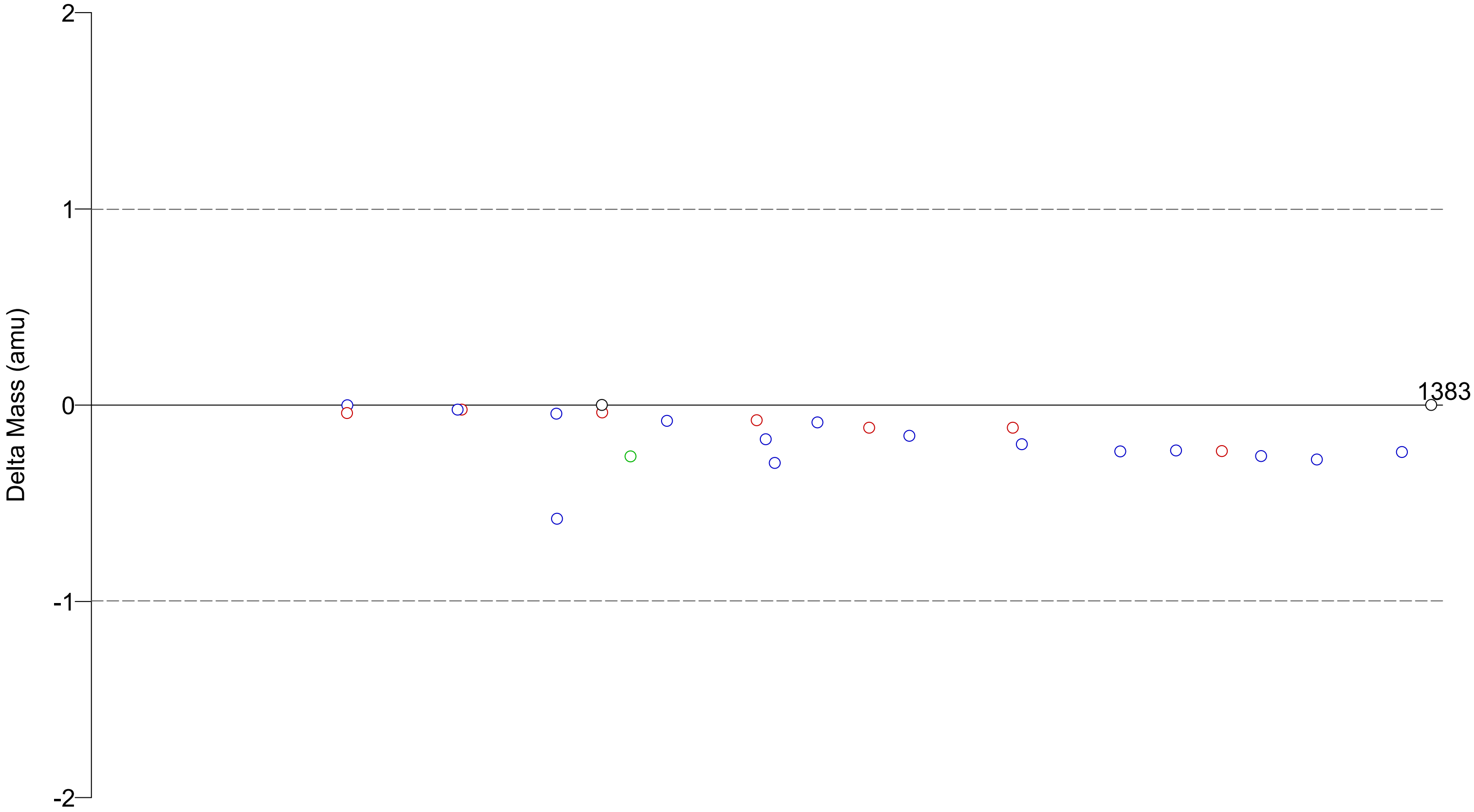
IPI:IPI00929201.1|TREMBL:A2KBC2;A2                                1e-006  20.2     0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                     1632.79   2  1e-006  3.219  0.589    674.9  1    19/45   14
19287468 - 1  K.NTLYLQMNSLR.A                          1352.70   2  3e-006  4.027  0.643   1526.5  1    20/30   39

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

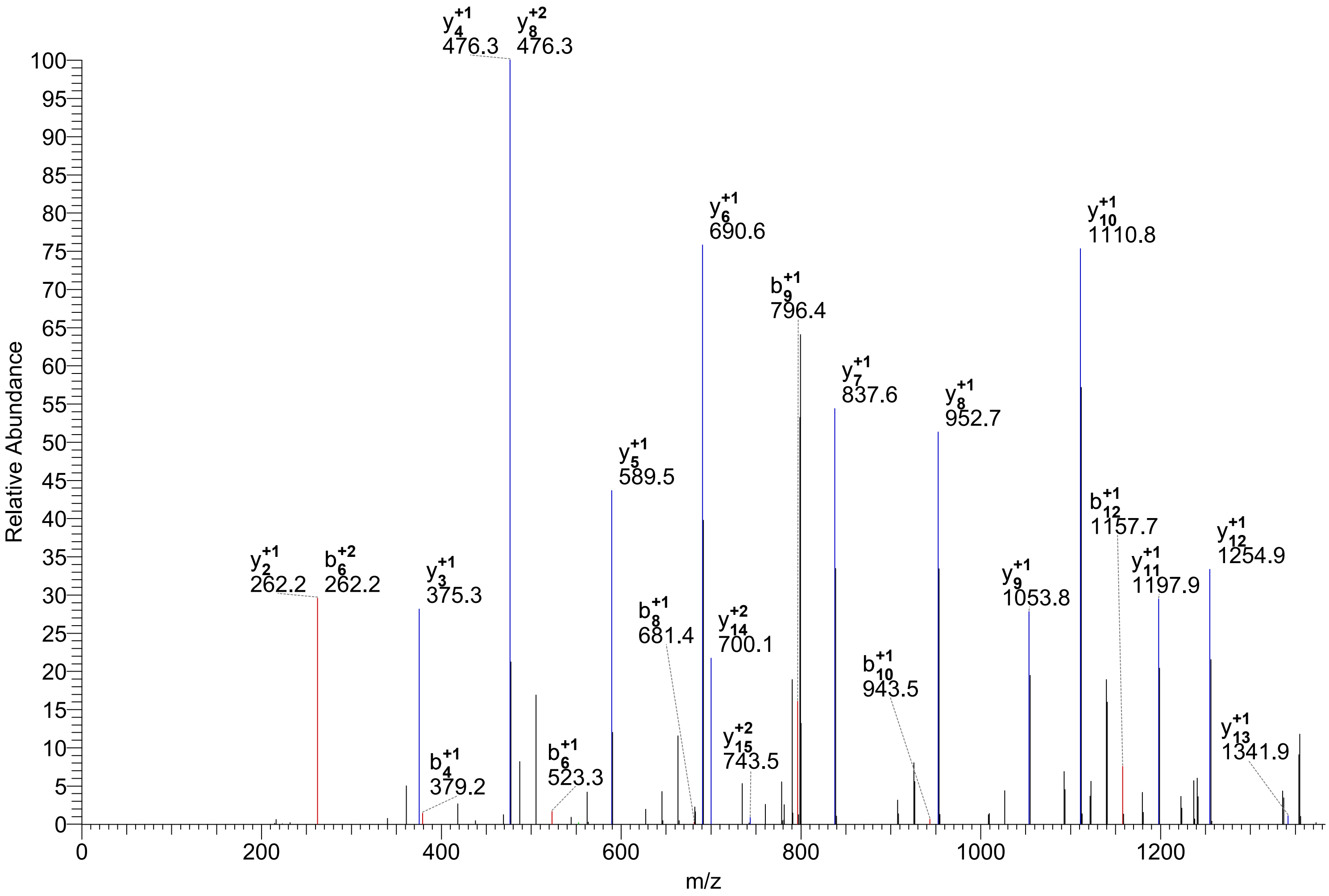
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
--------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



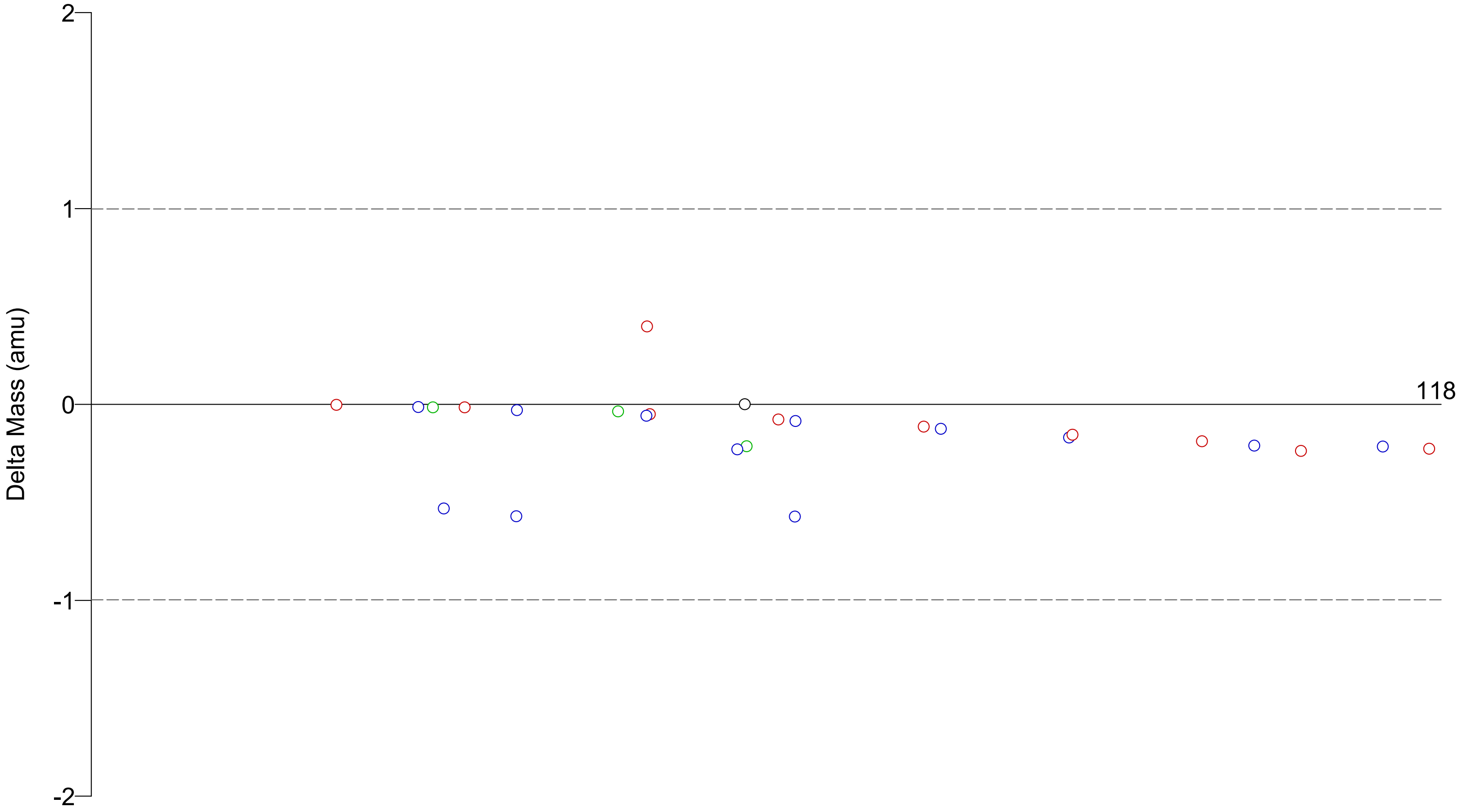
#19287468-1 NL: 6.55E4



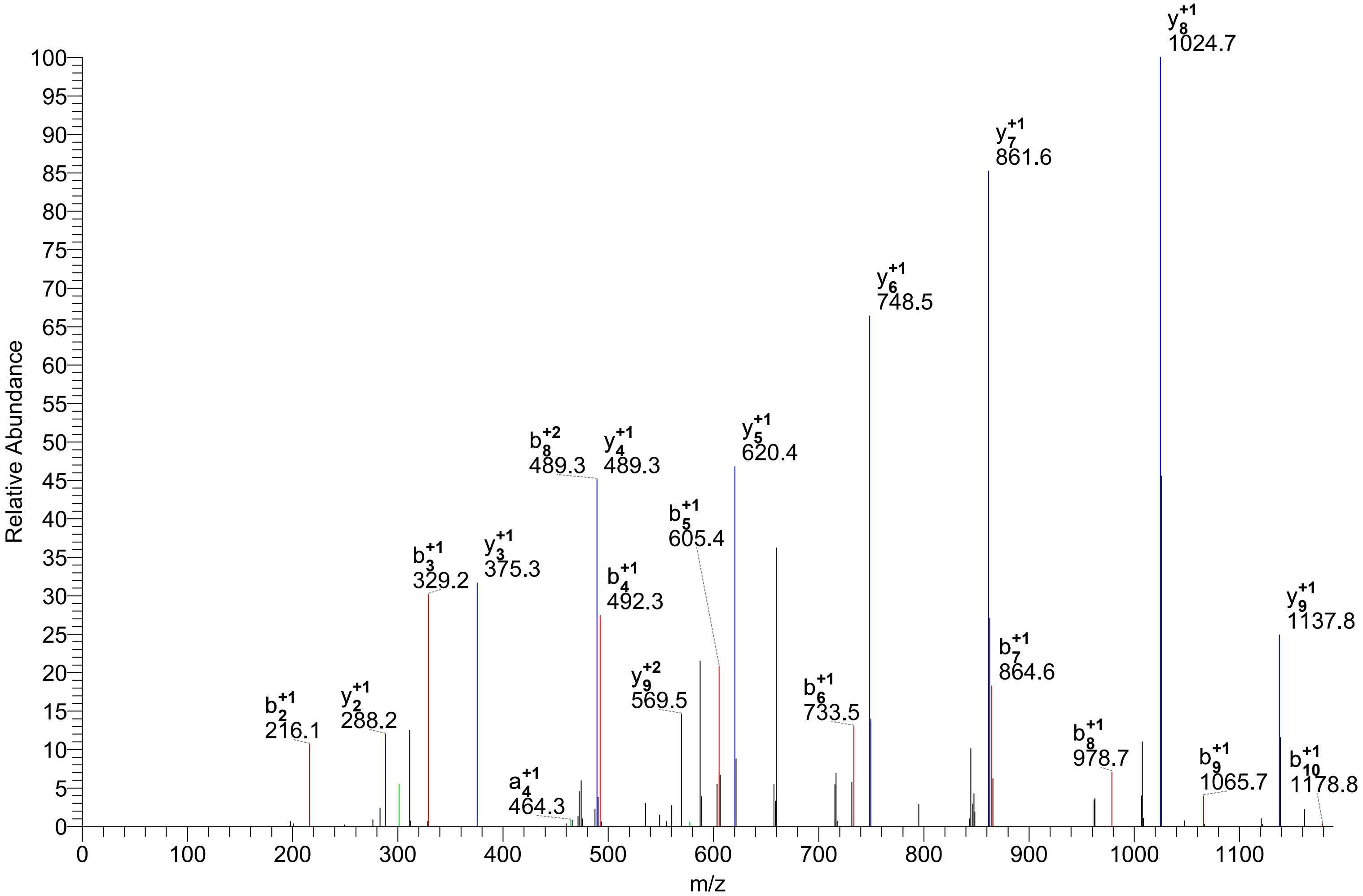
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

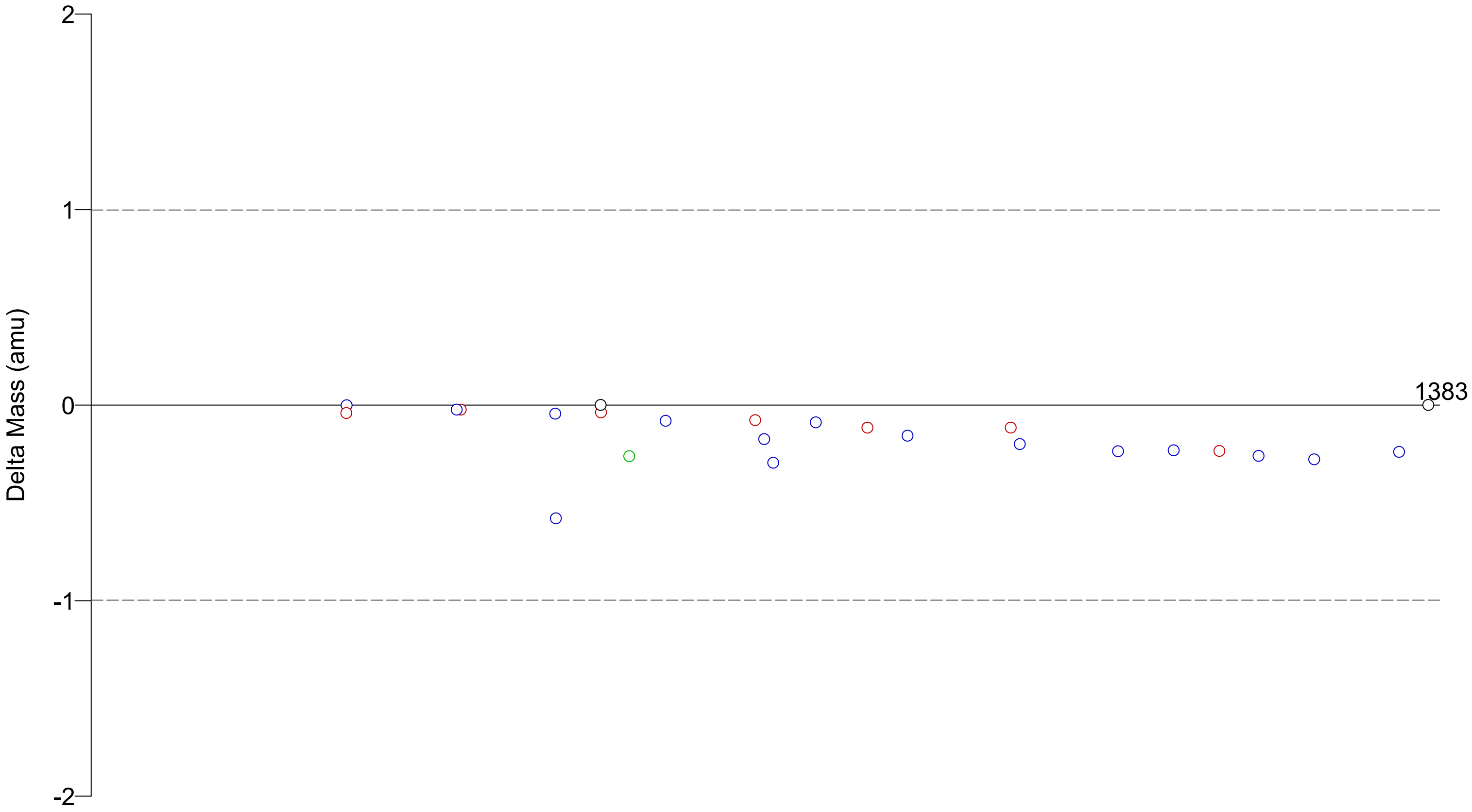
IPI:IPI00784985.1|TREMBL:Q6PJF2 Ta                                     1e-006  20.2     0.0       0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                       1632.79   2  1e-006  3.219  0.589   674.9  1   19/45   14
19287468 - 1  K.SGTASVVCLLNNFYPR.E                        1798.88   2  5e-005  3.485  0.433   766.8  1   17/45   7

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

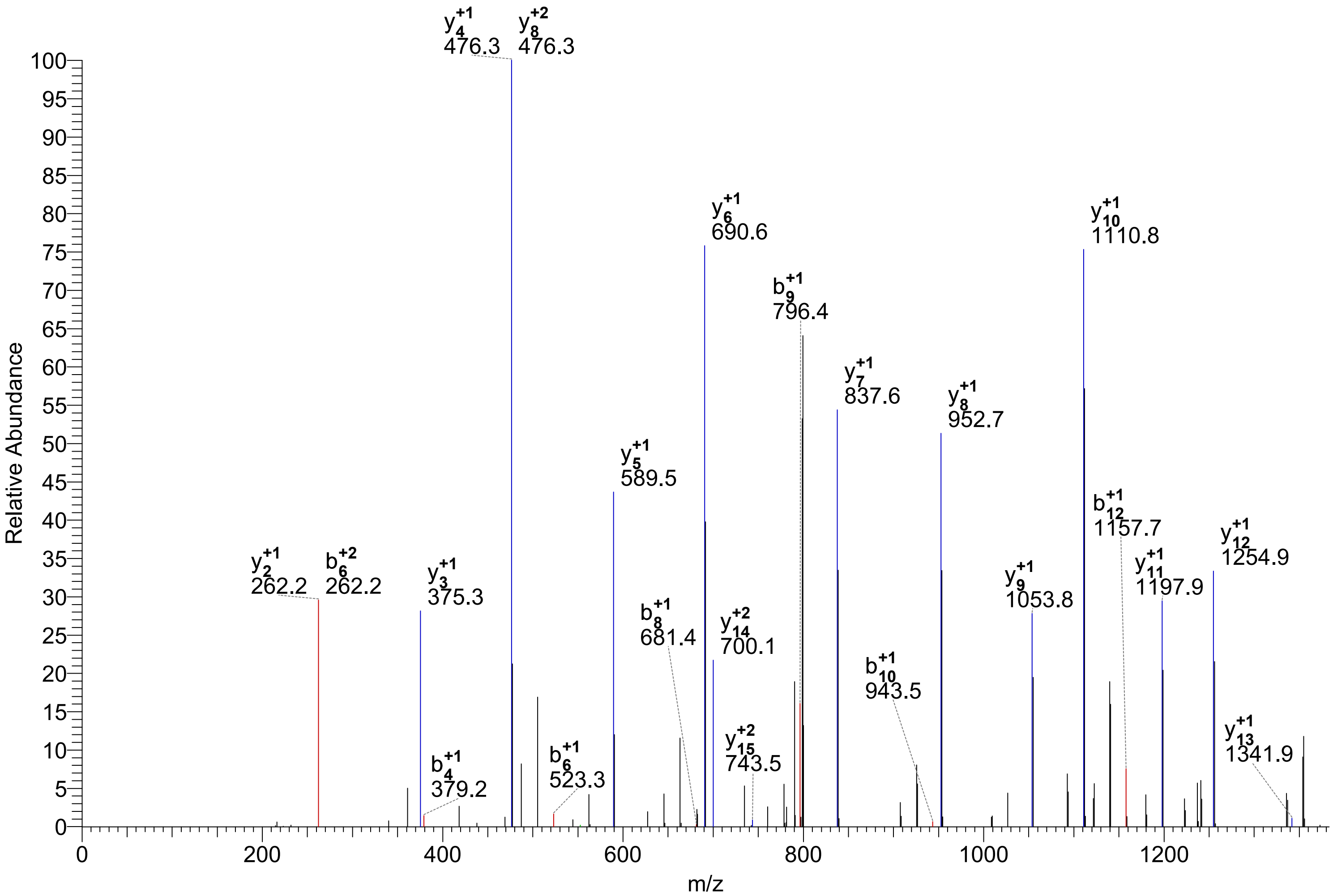
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



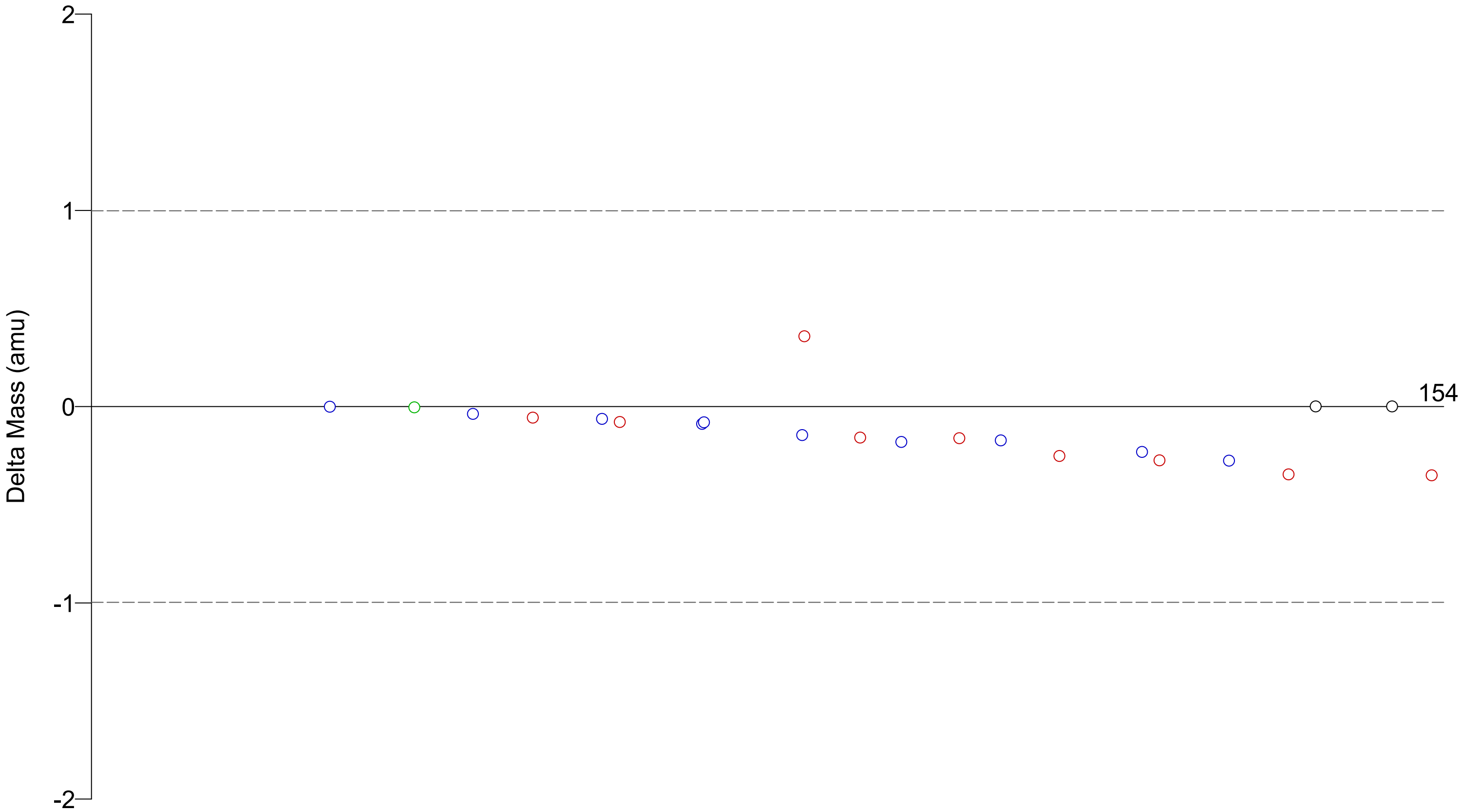
#19287468-1 NL: 6.55E4

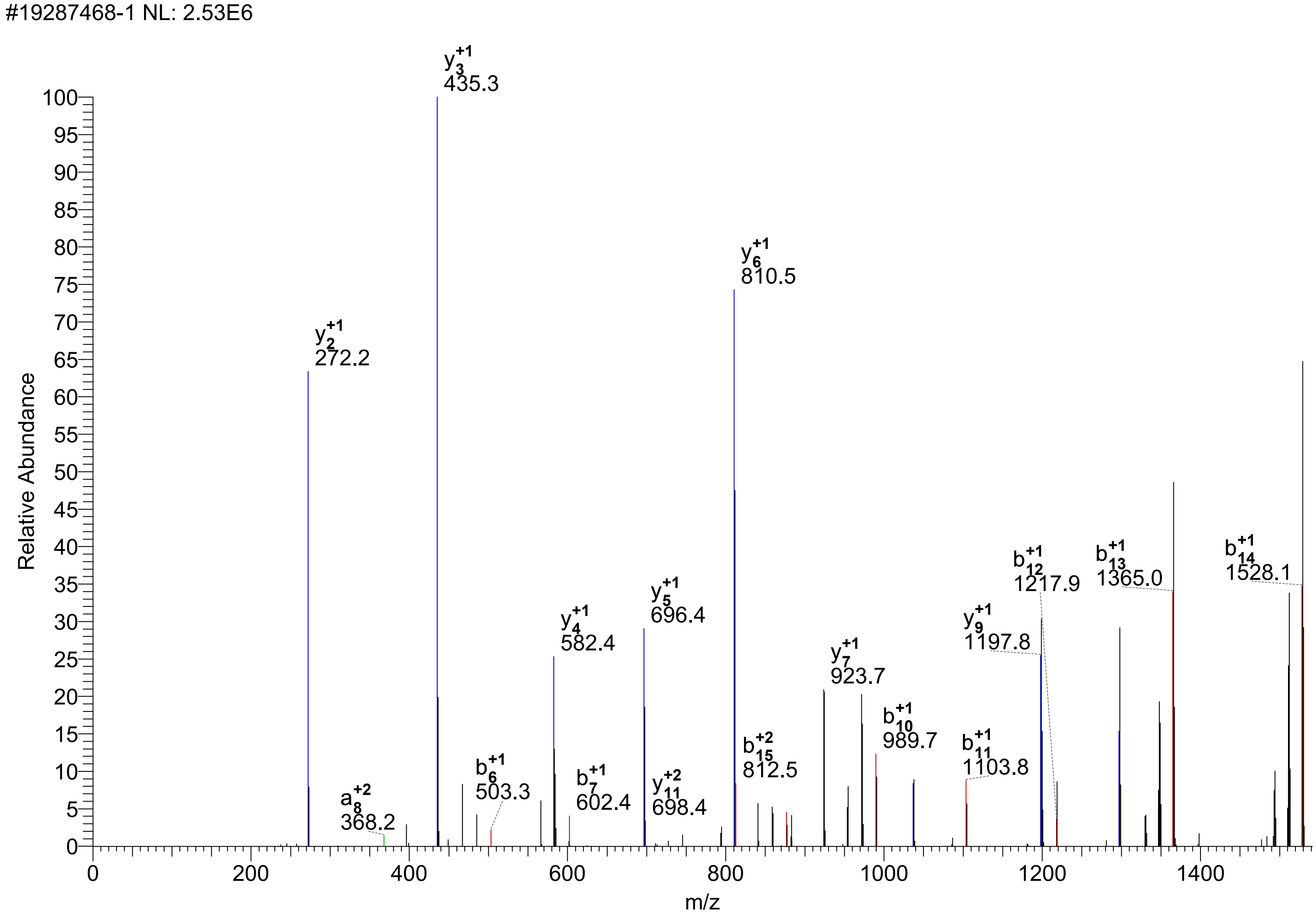


```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```


Delta Mass (amu)
2
1
0
-1
-2
1541


#19287468-1 NL: 2.53E6
Relative Abundance
m/z
y_3^{+1} 435.3
y_6^{+1} 810.5
y_2^{+1} 272.2
a_8^{+2} 368.2
b_6^{+1} 503.3
y_4^{+1} 582.4
b_7^{+1} 602.4
y_5^{+1} 696.4
y_{11}^{+2} 698.4
b_{15}^{+2} 812.5
y_7^{+1} 923.7
b_{10}^{+1} 989.7
b_{11}^{+1} 1103.8
y_9^{+1} 1197.8
b_{12}^{+1} 1217.9
b_{13}^{+1} 1365.0
b_{14}^{+1} 1528.1
0
200
400
600
800
1000
1200
1400
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100

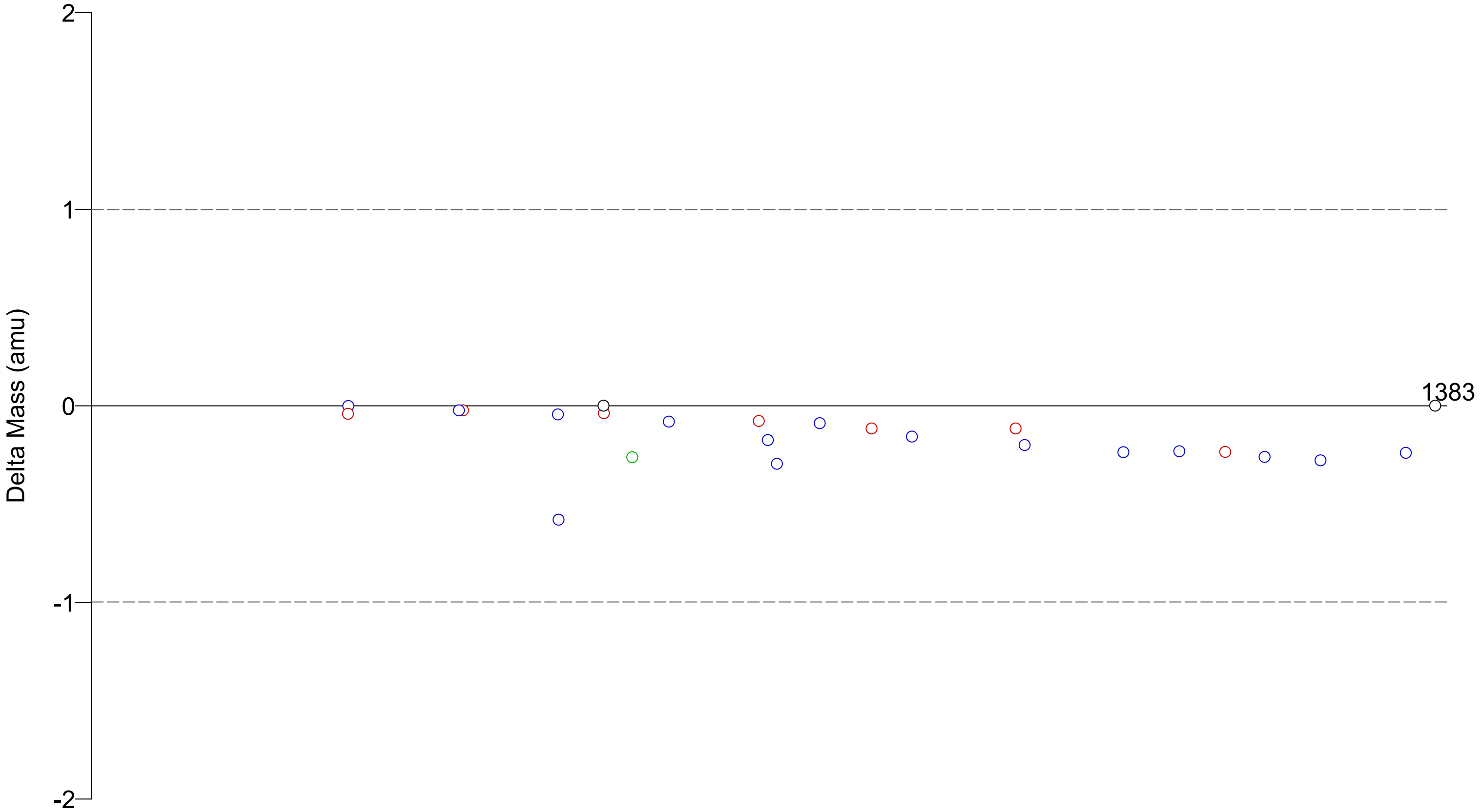
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)        Sequence                                    MH+      z   P        XC  DeltaCn    Sp   RSp  Ions   Count
IPI:IPI00889156.1|TREMBL:Q15537;Q6                                    1e-006  20.2     0.0       0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                       1632.79   2  1e-006  3.219  0.589   674.9  1   19/45   14
19287468 - 1  K.SGTASVVCLLNNFYPR.E                        1798.88   2  5e-005  3.485  0.433   766.8  1   17/45   7

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

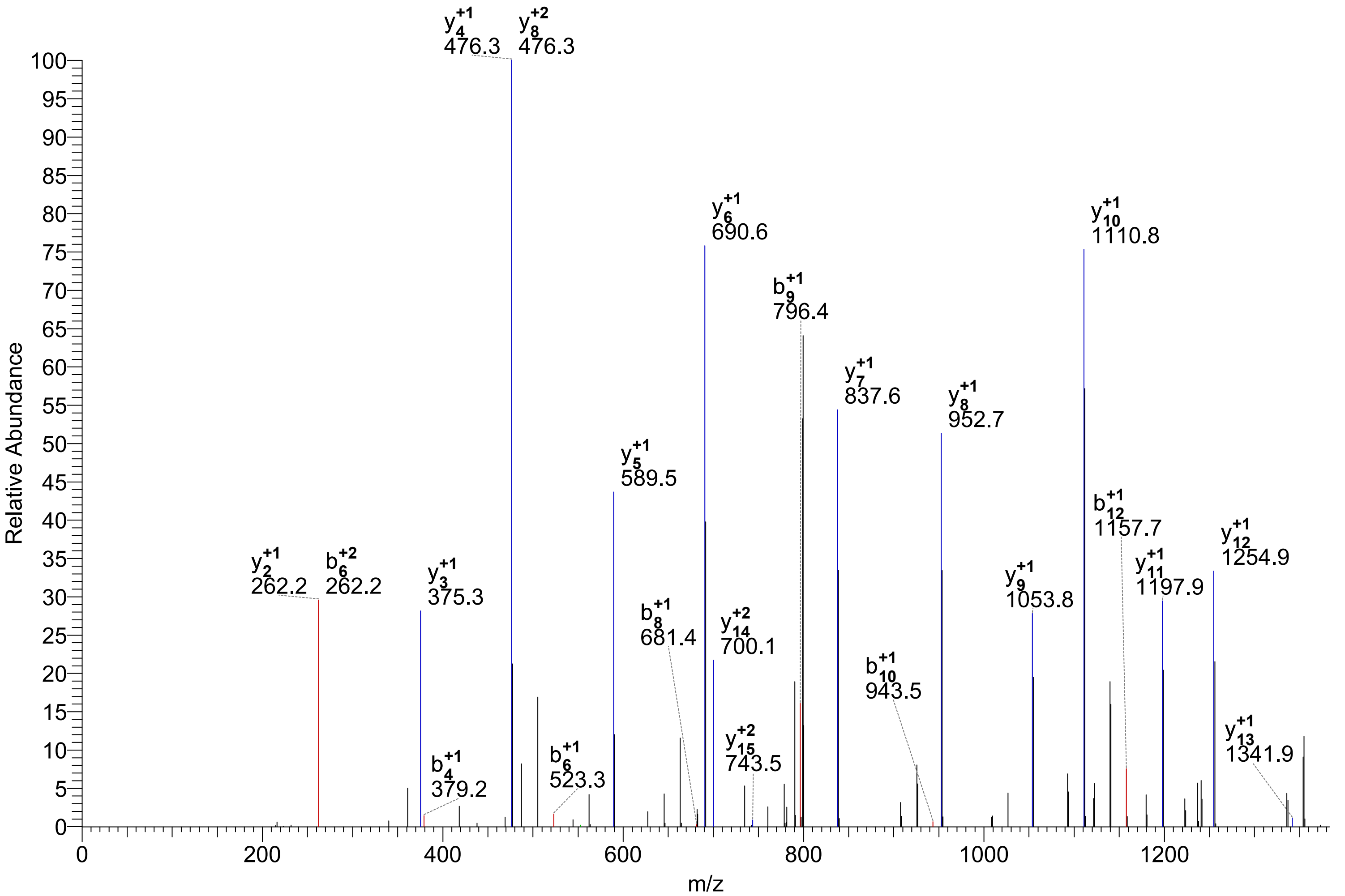
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



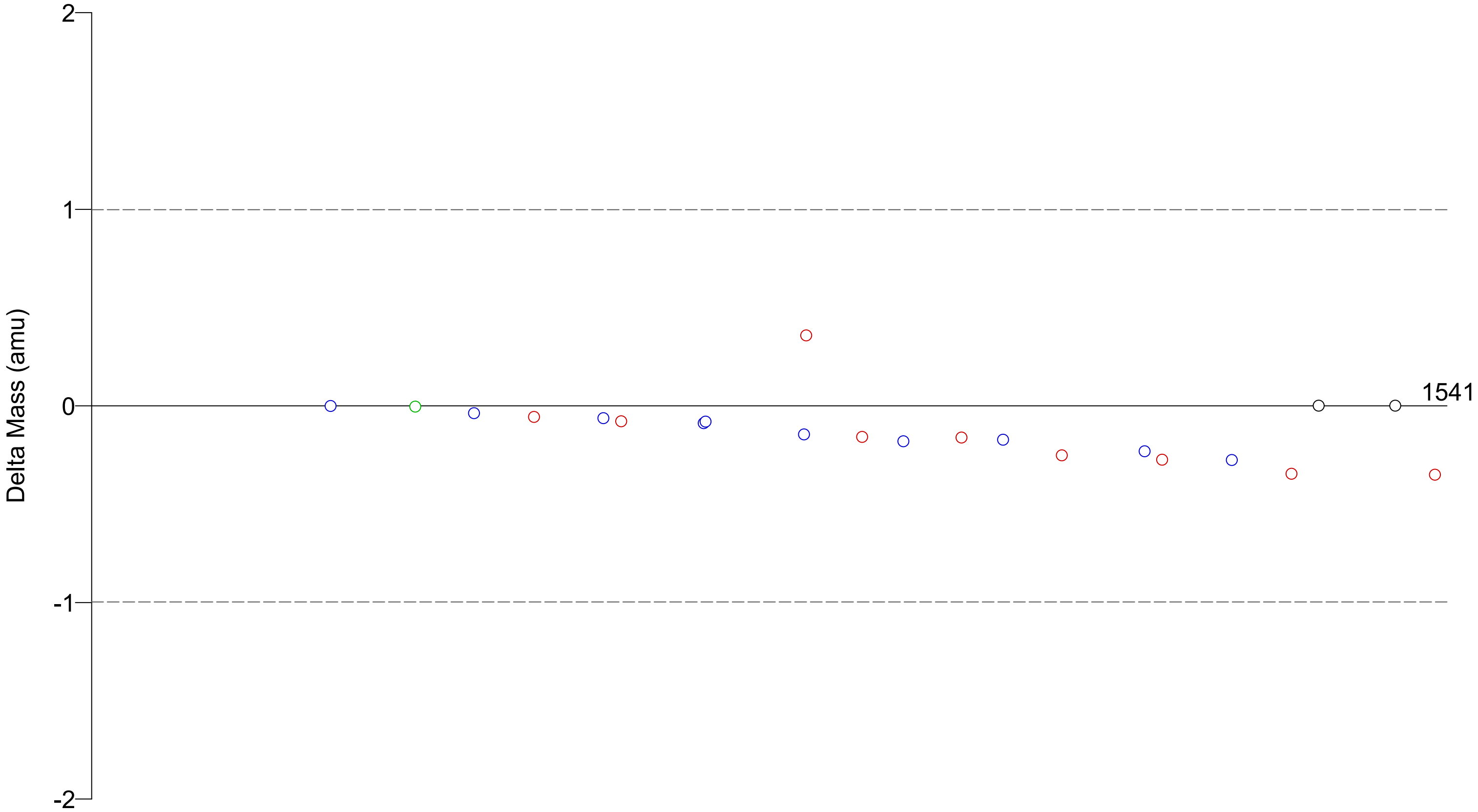
#19287468-1 NL: 6.55E4



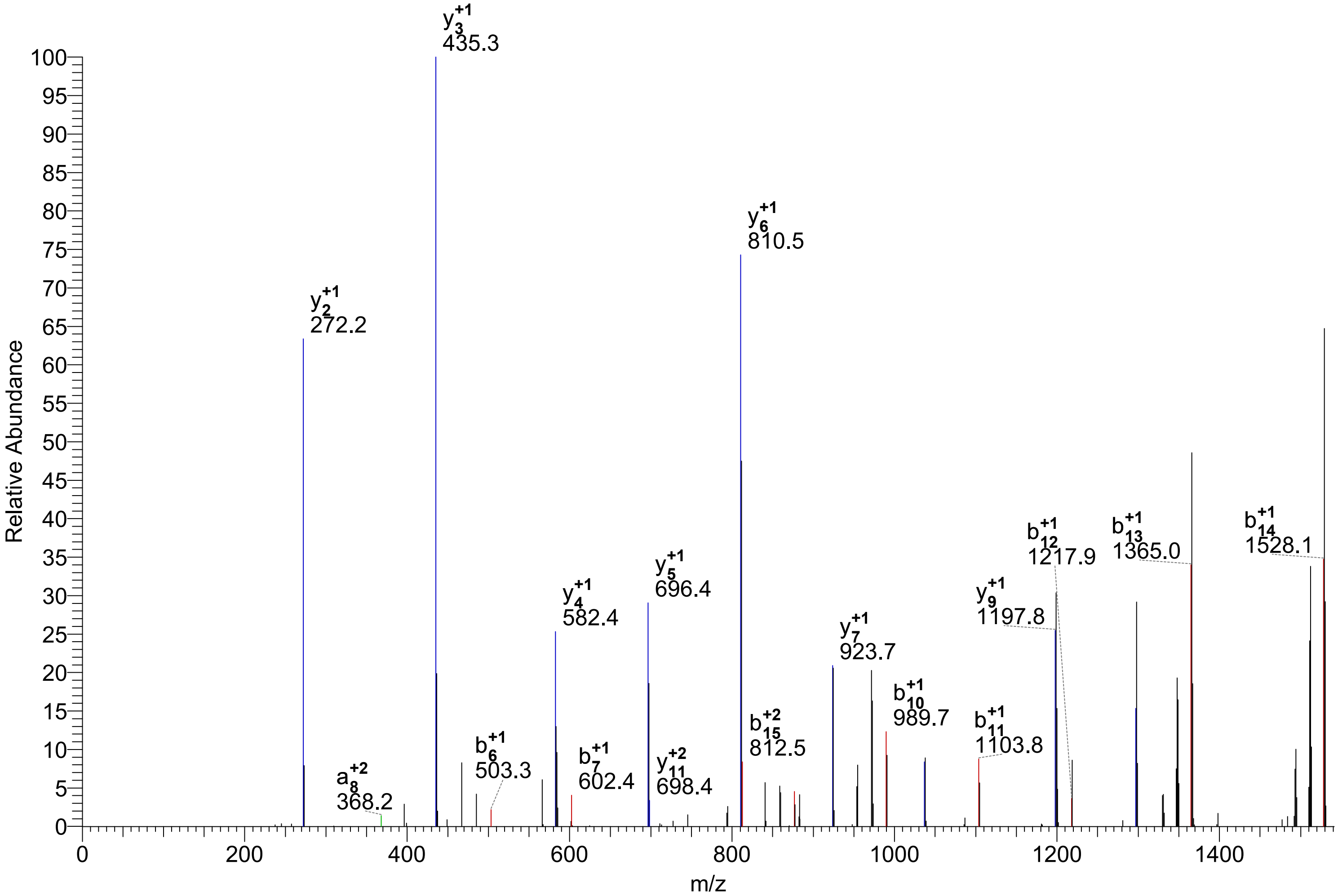
```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```



#19287468-1 NL: 2.53E6



```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

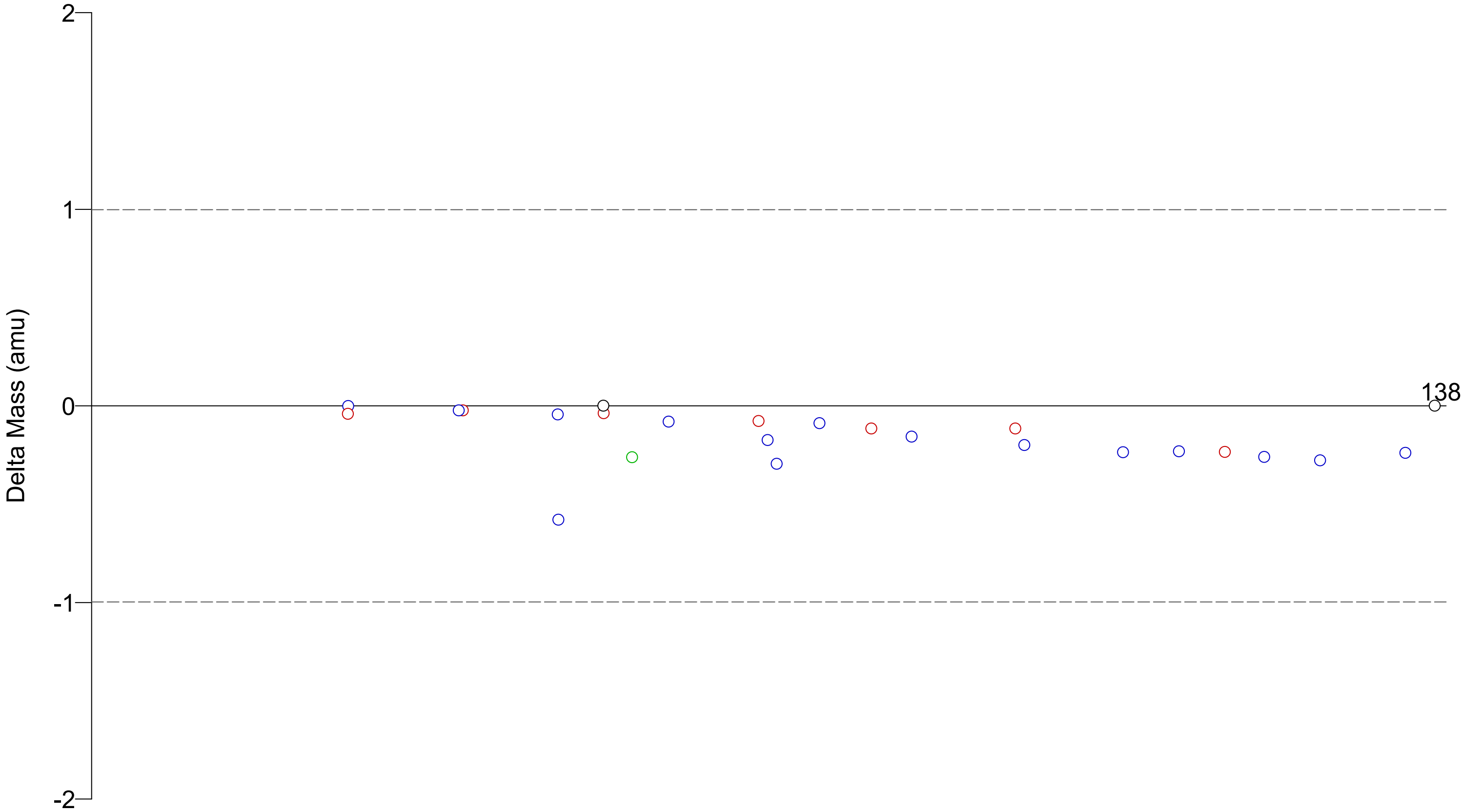
IPI:IPI00030205.3|SWISS-PROT:P18135|ENSEMBL:ENSP00000374790|VE     1e-006  10.2     0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                         1632.79   2  1e-006  3.219  0.589   674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

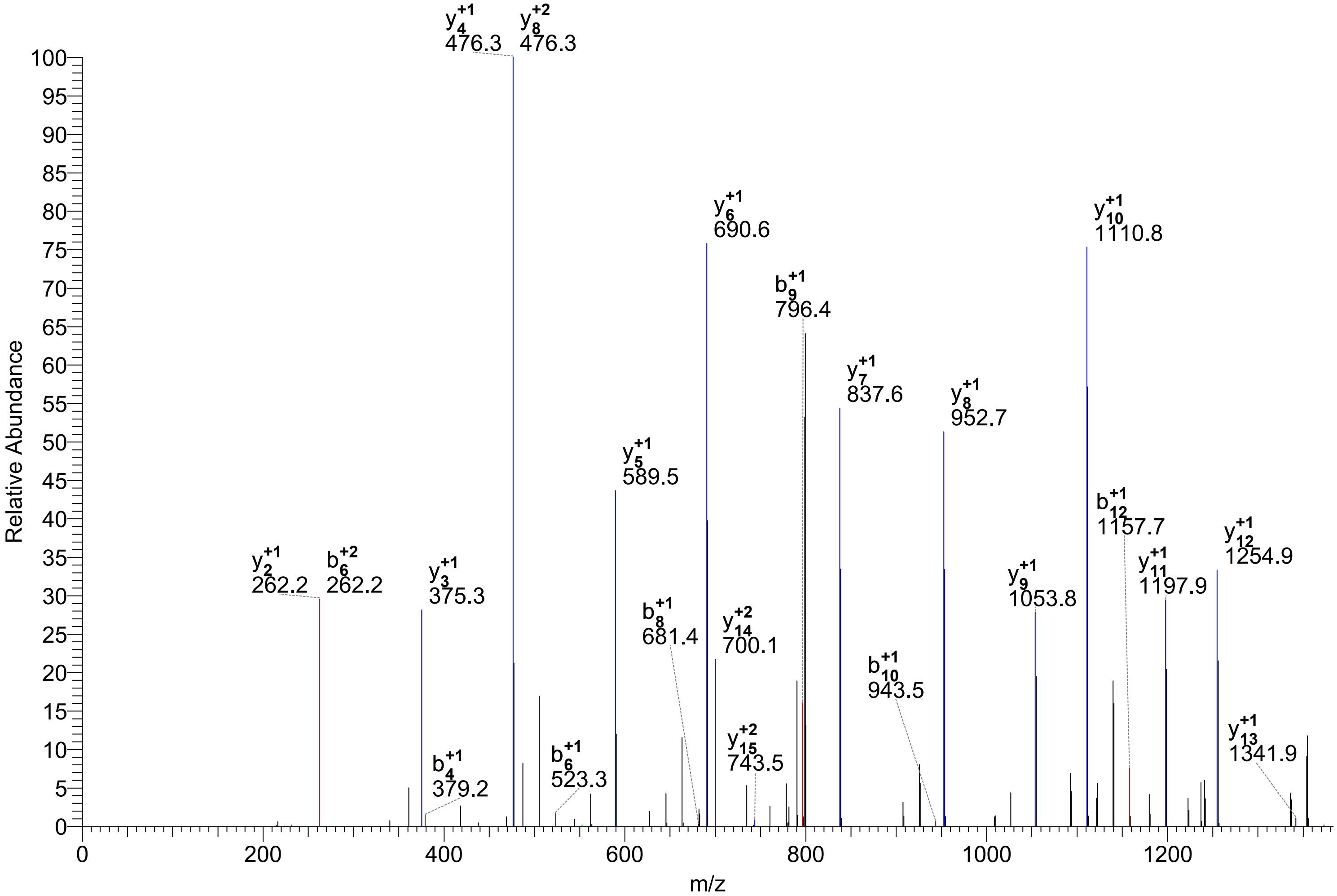
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



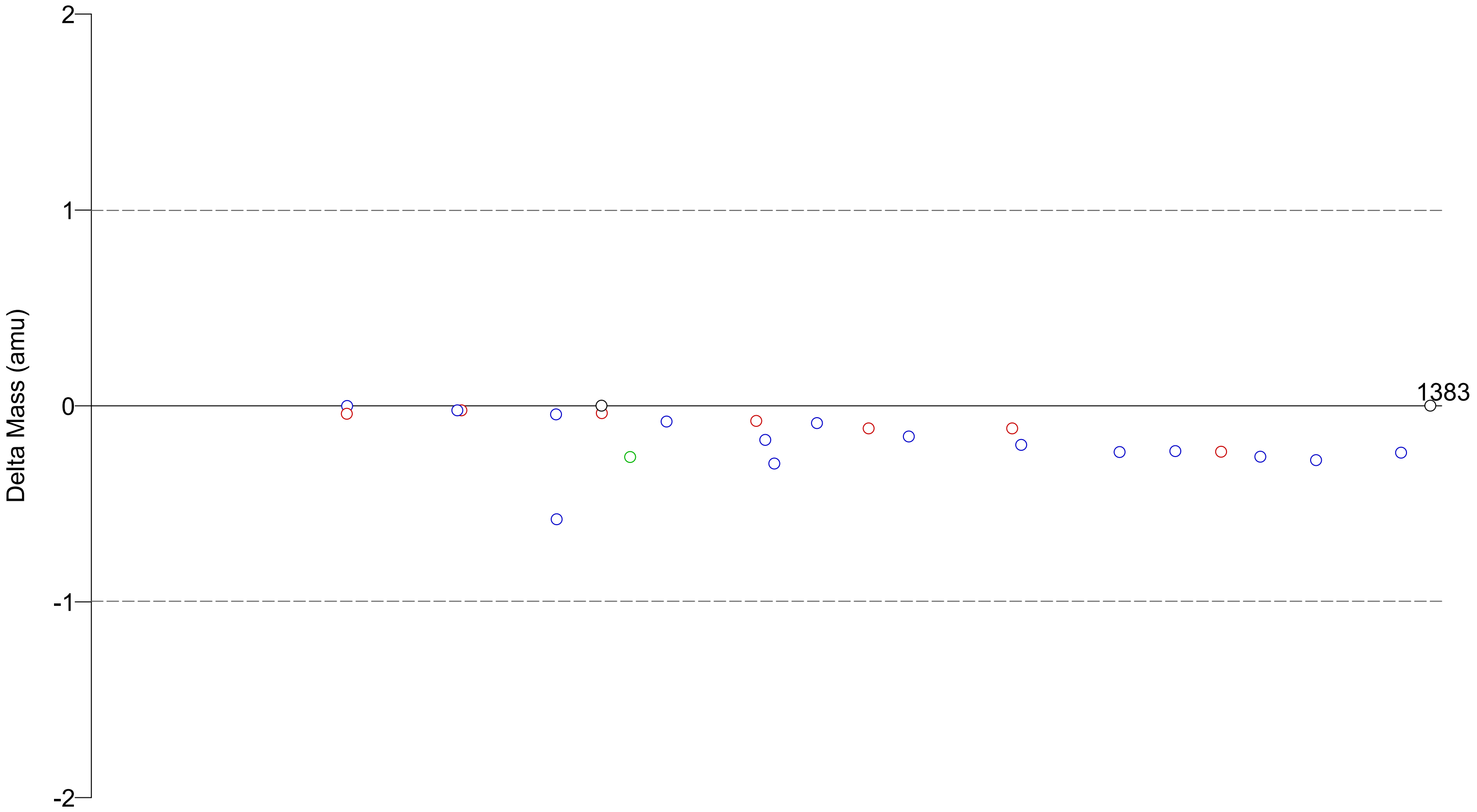
```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00384576.1|SWISS-PROT:P1813                                   1e-006  10.2      0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                       1632.79    2  1e-006  3.219  0.589    674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

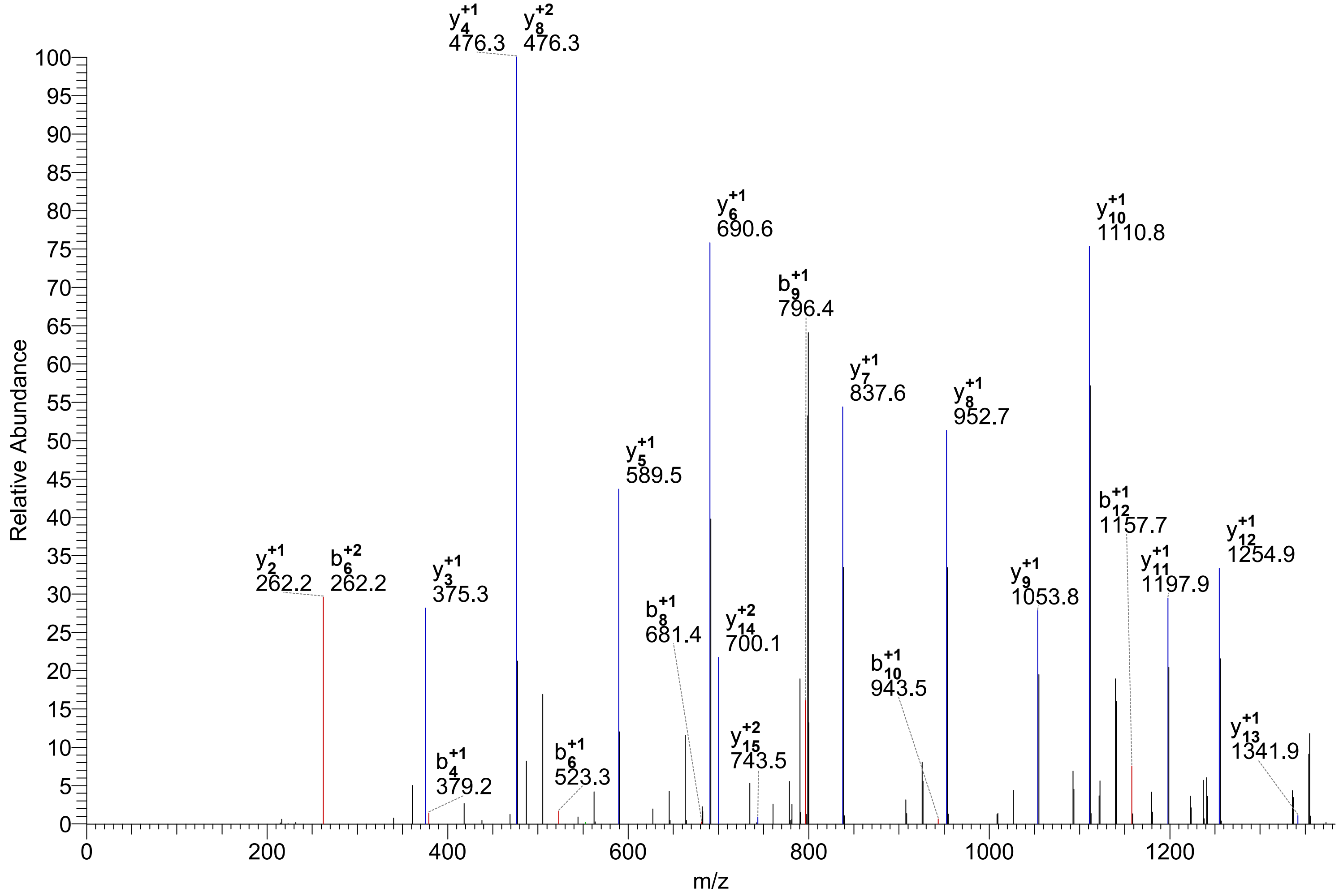
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



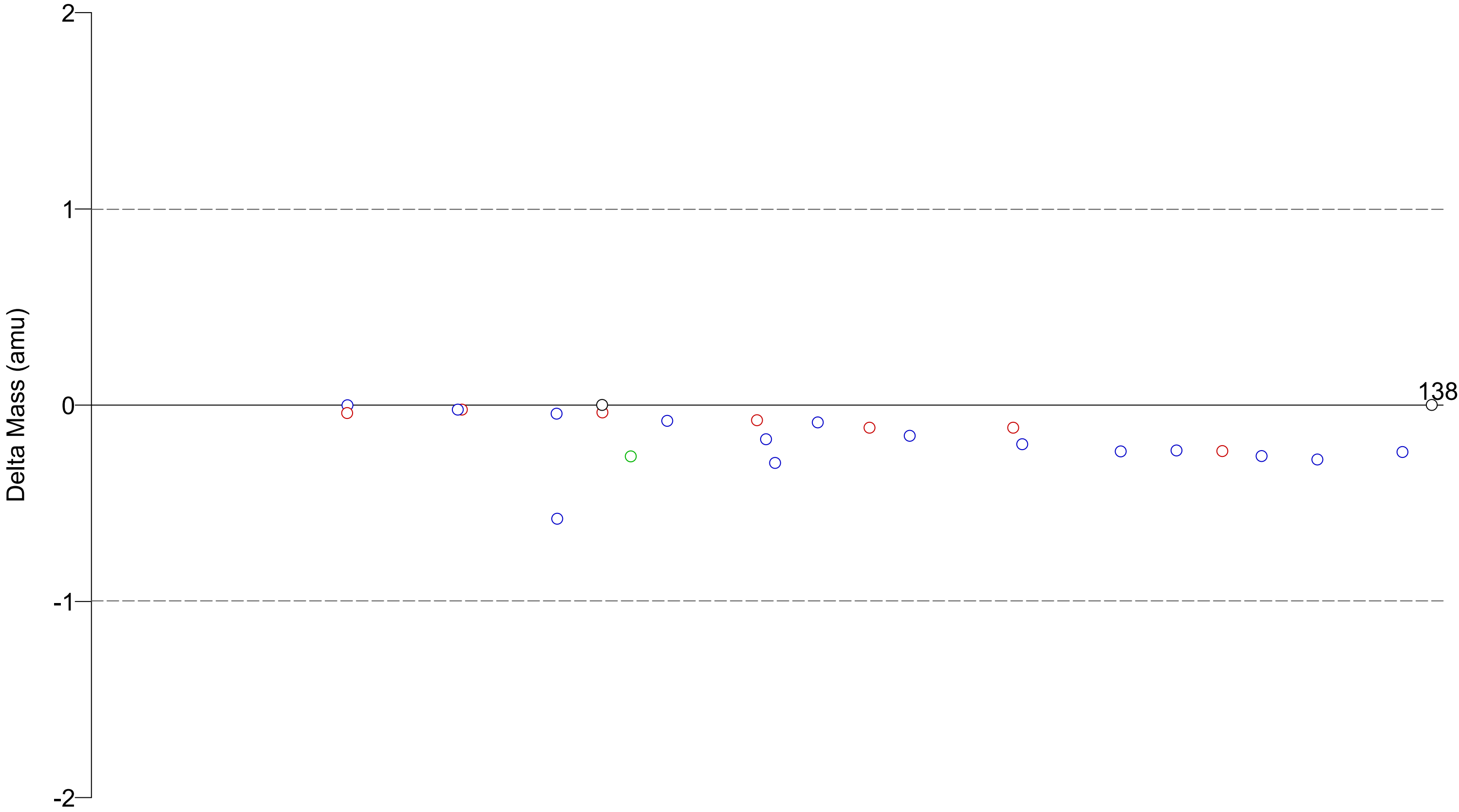
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                a     z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00385252.1|SWISS-PROT:P0420                                1e-006  10.2     0.0       0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                   1632.79   2  1e-006  3.219  0.589   674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

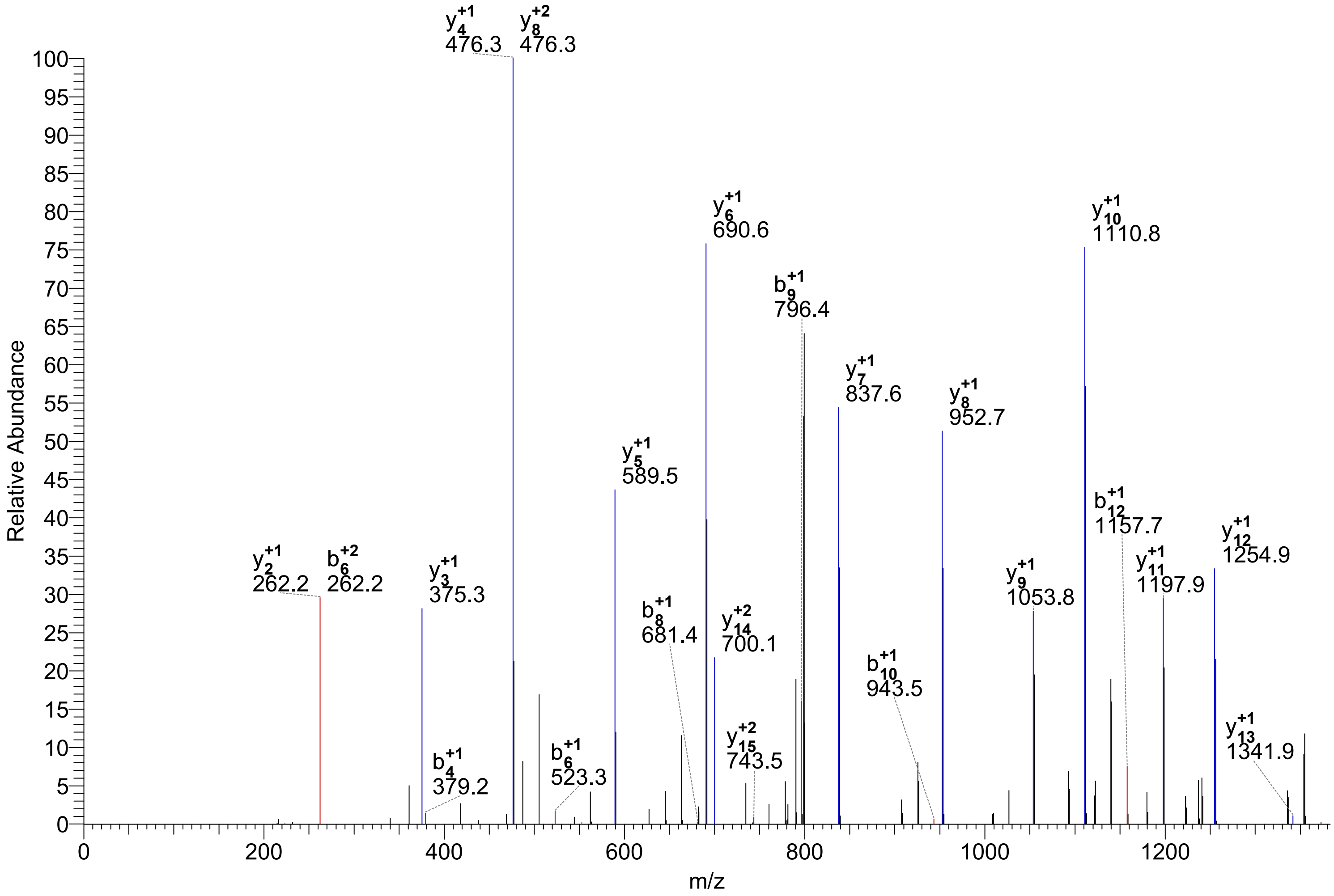
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                    1485.72
 G    264.13     292.13                                    1398.69
 S    351.17     379.16                                    1341.66
 G    408.19     436.18                                    1254.63
 S    495.22     523.21                                    1197.61
 G    552.24     580.24                                    1110.58
 T    653.29     681.28                                    1053.56
 D    768.32     796.31                                     952.51
 F    915.38     943.38                                     837.48
 T   1016.43    1044.43                                     690.41
 L   1129.52    1157.51                                     589.37
 T   1230.56    1258.56                                     476.28
 I   1343.65    1371.64                                     375.24
 S   1430.68    1458.67                                     262.15
 R                                                          175.12
```



#19287468-1 NL: 6.55E4



```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z     P        XC  DeltaCn    Sp    RSp  Ions   Count

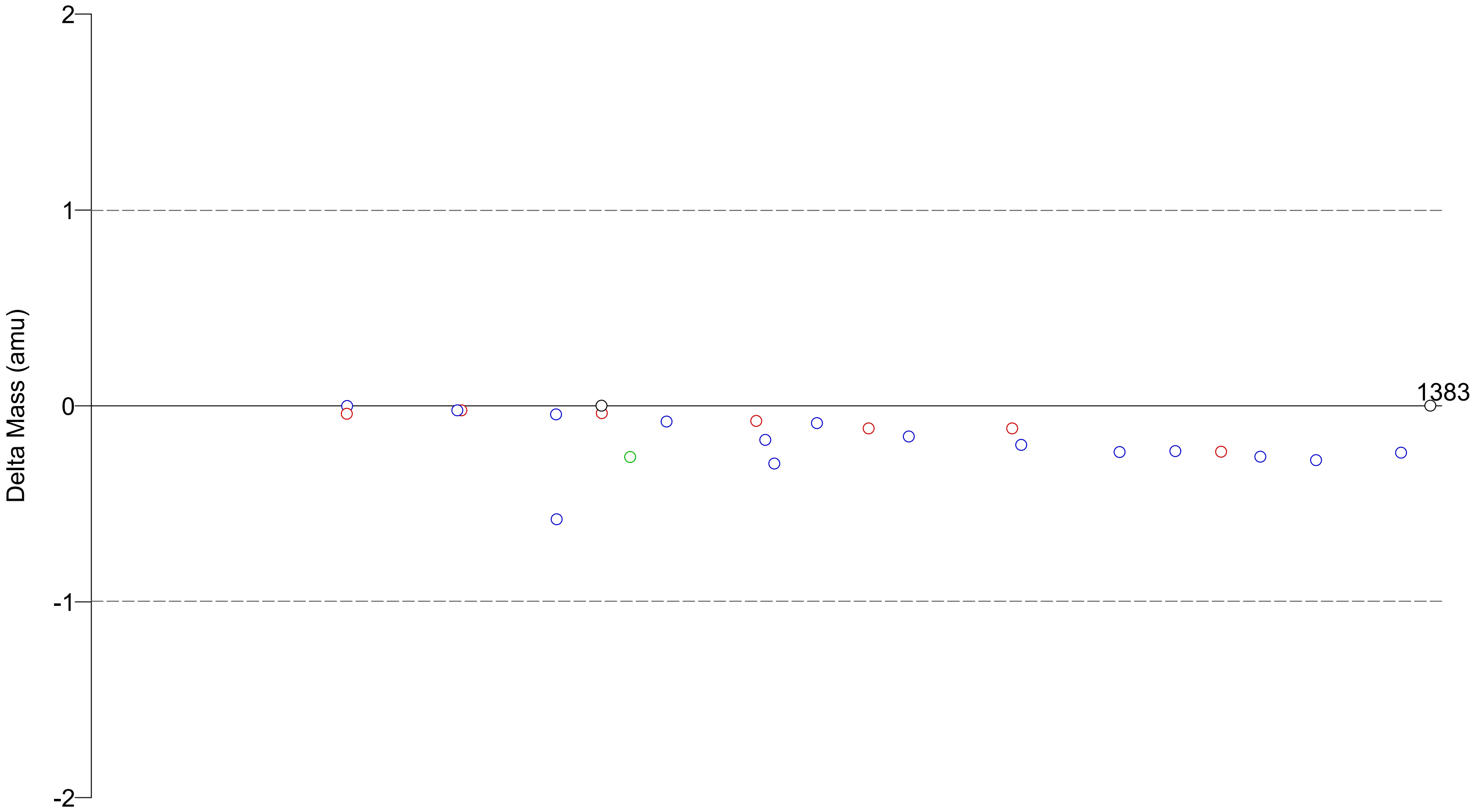
IPI:IPI00387115.1|SWISS-PROT:P0162                                     1e-006  10.2     0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                      1632.79    2  1e-006  3.219  0.589   674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

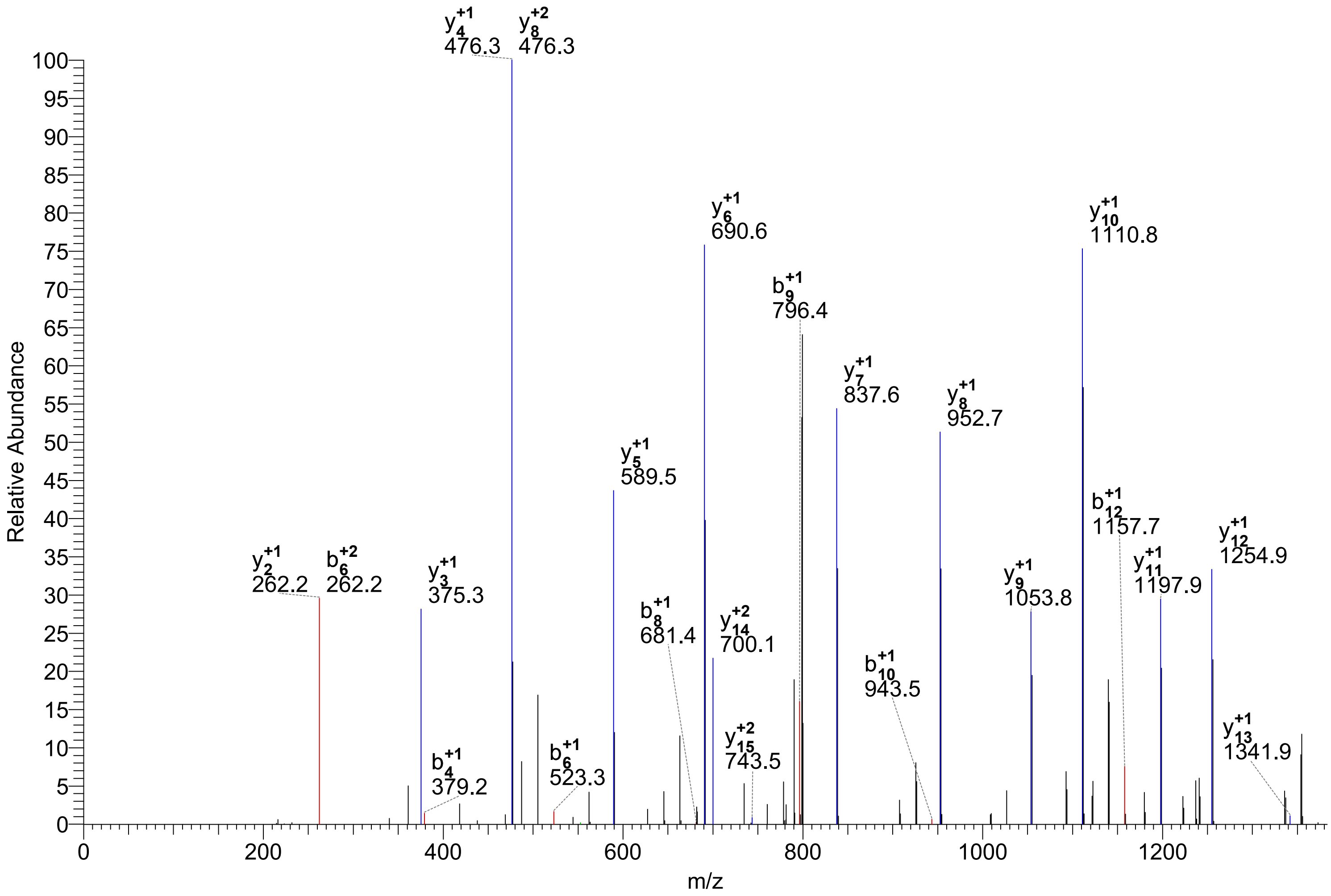
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z   P        XC  DeltaCn    Sp    RSp  Ions  Count

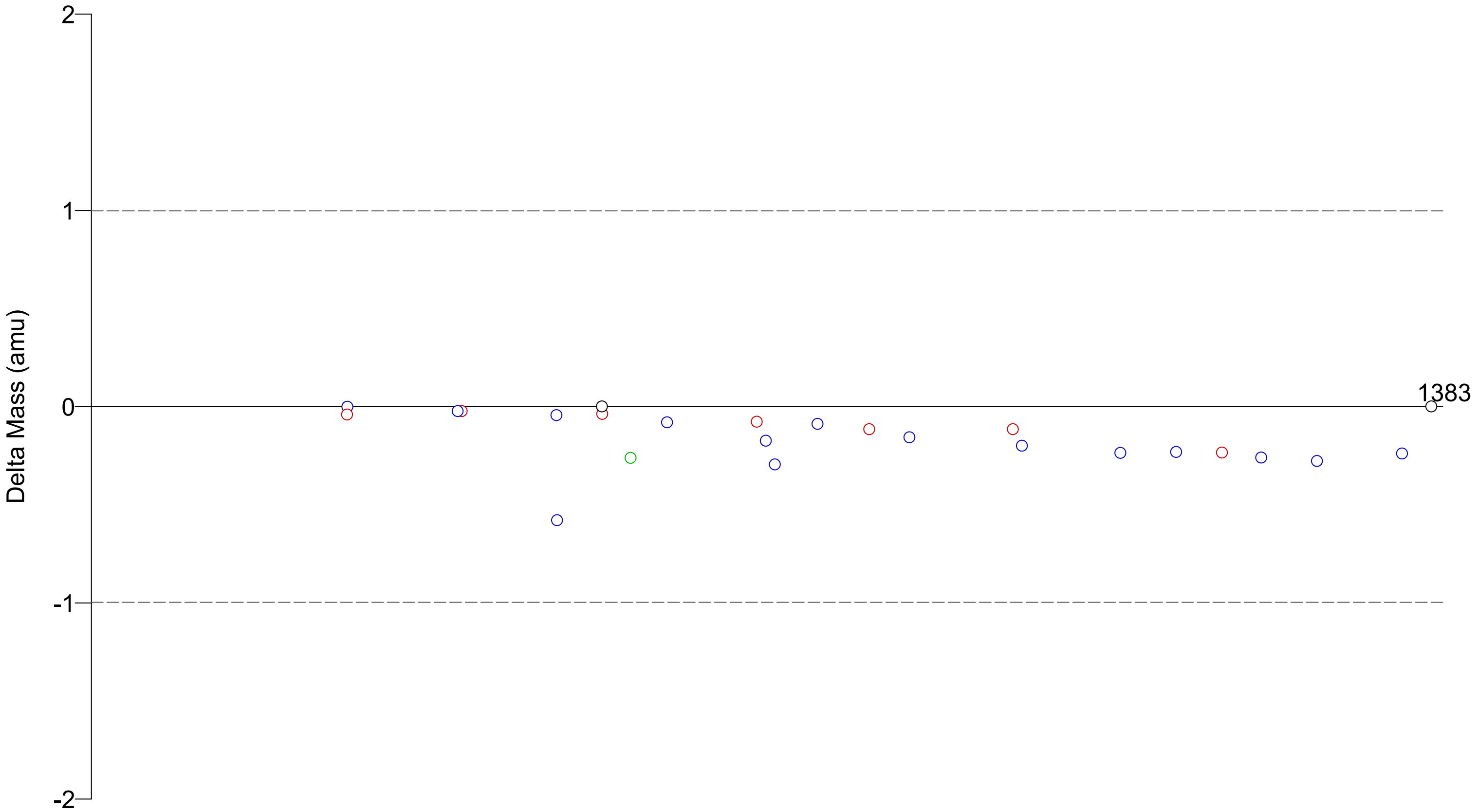
IPI:IPI00387117.5|SWISS-PROT:P0162                                    1e-006  10.2      0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                      1632.79    2  1e-006  3.219  0.589   674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

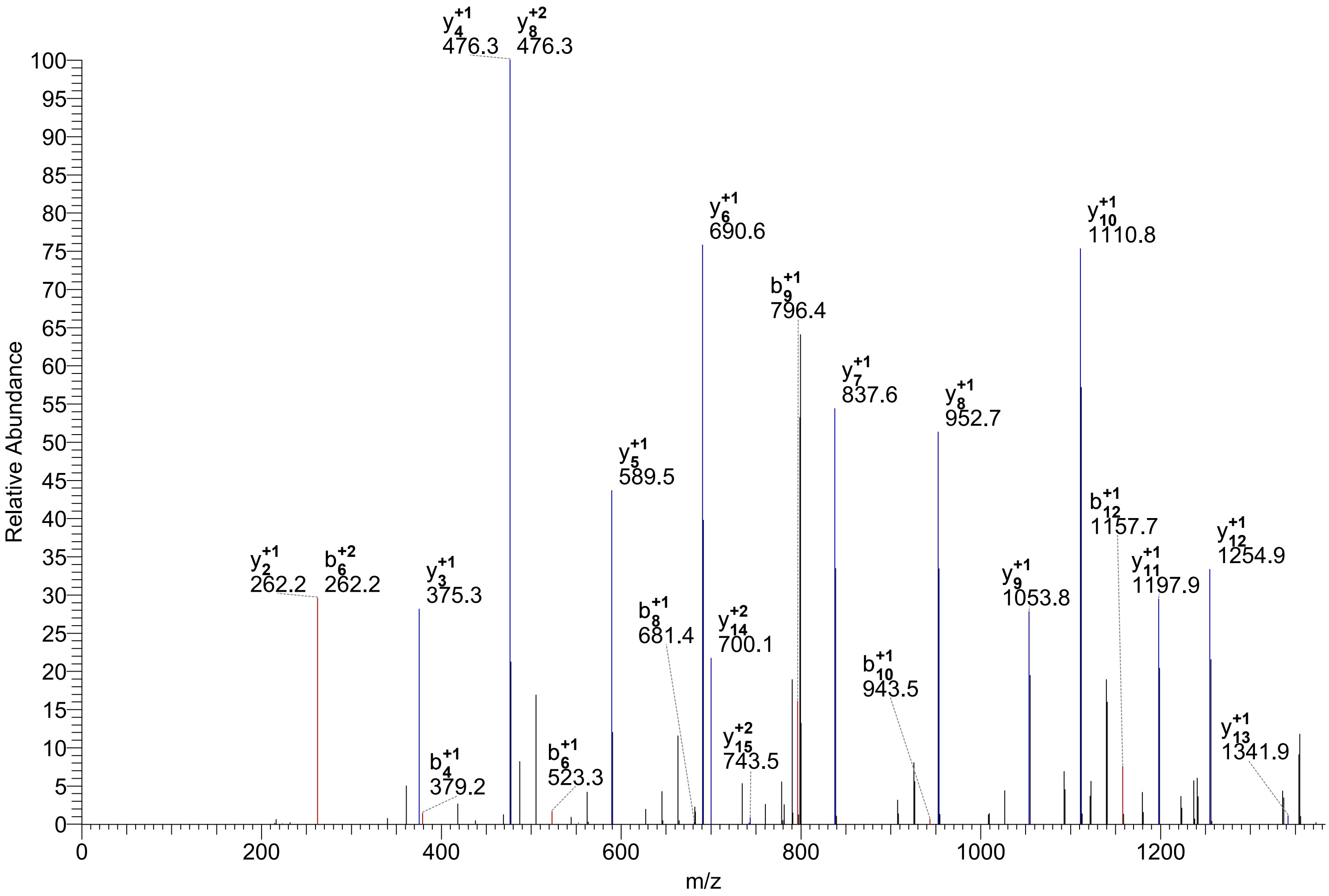
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



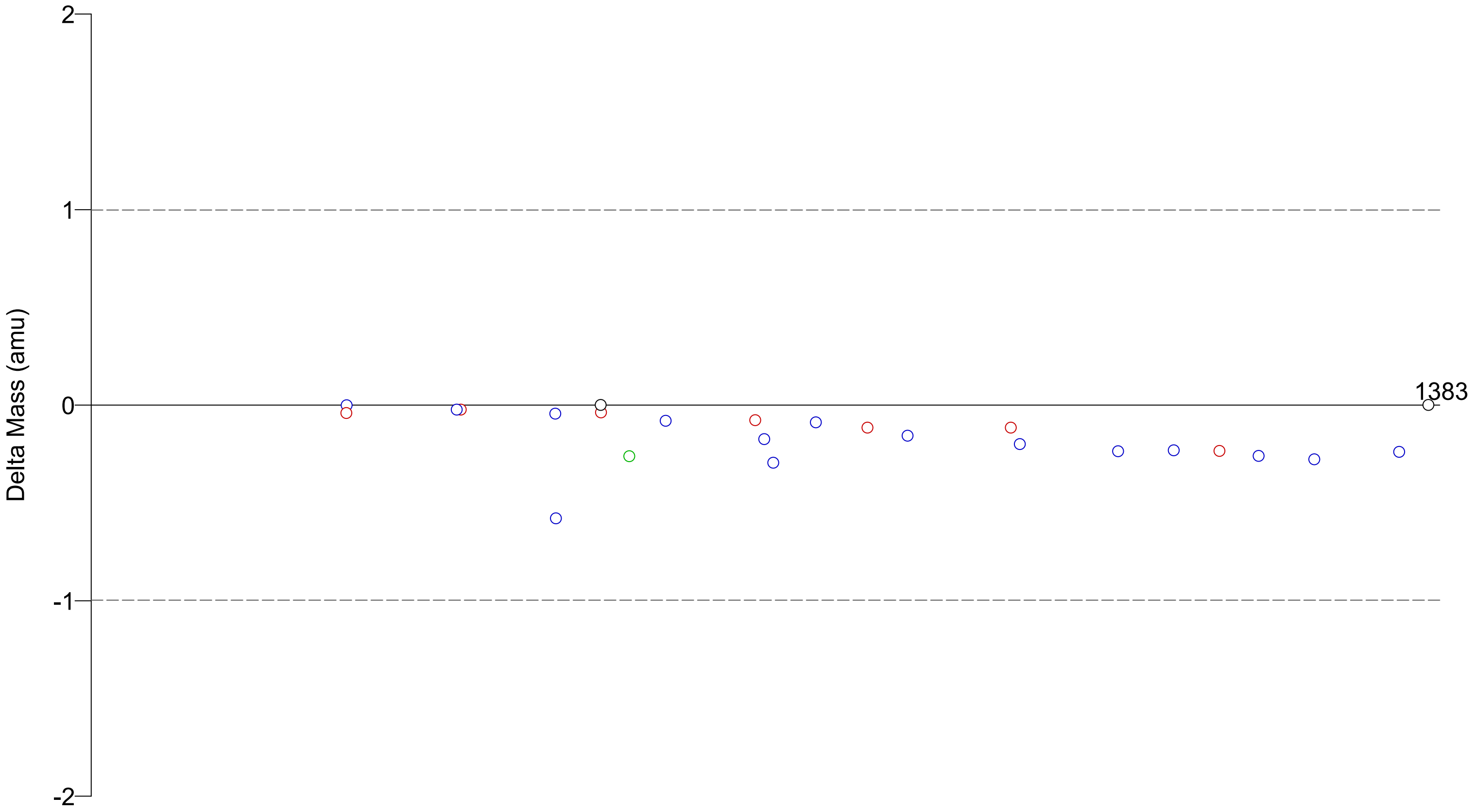
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00387118.1|SWISS-PROT:P0162                                 1e-006  10.2      0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                  1632.79    2  1e-006  3.219  0.589    674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

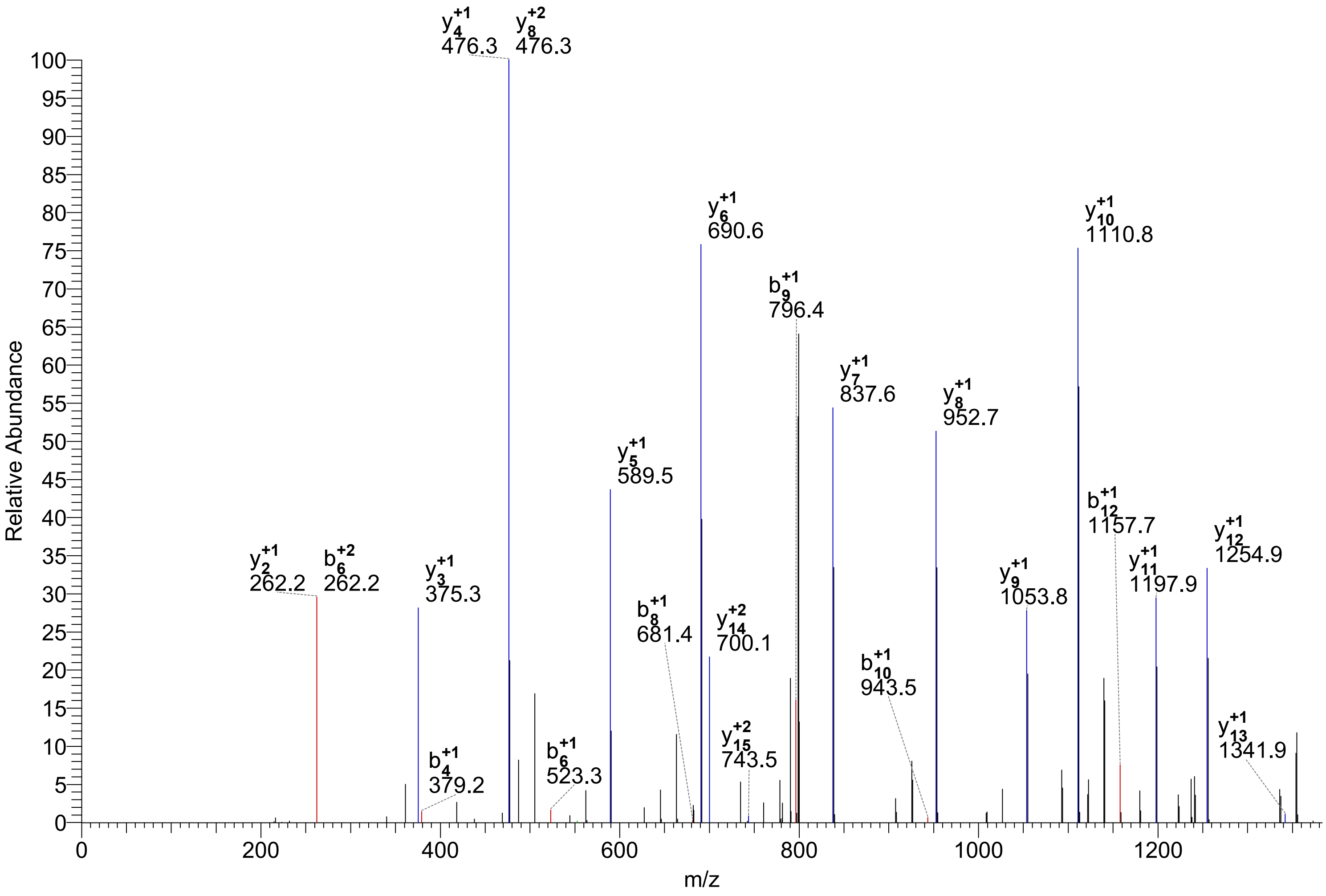
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



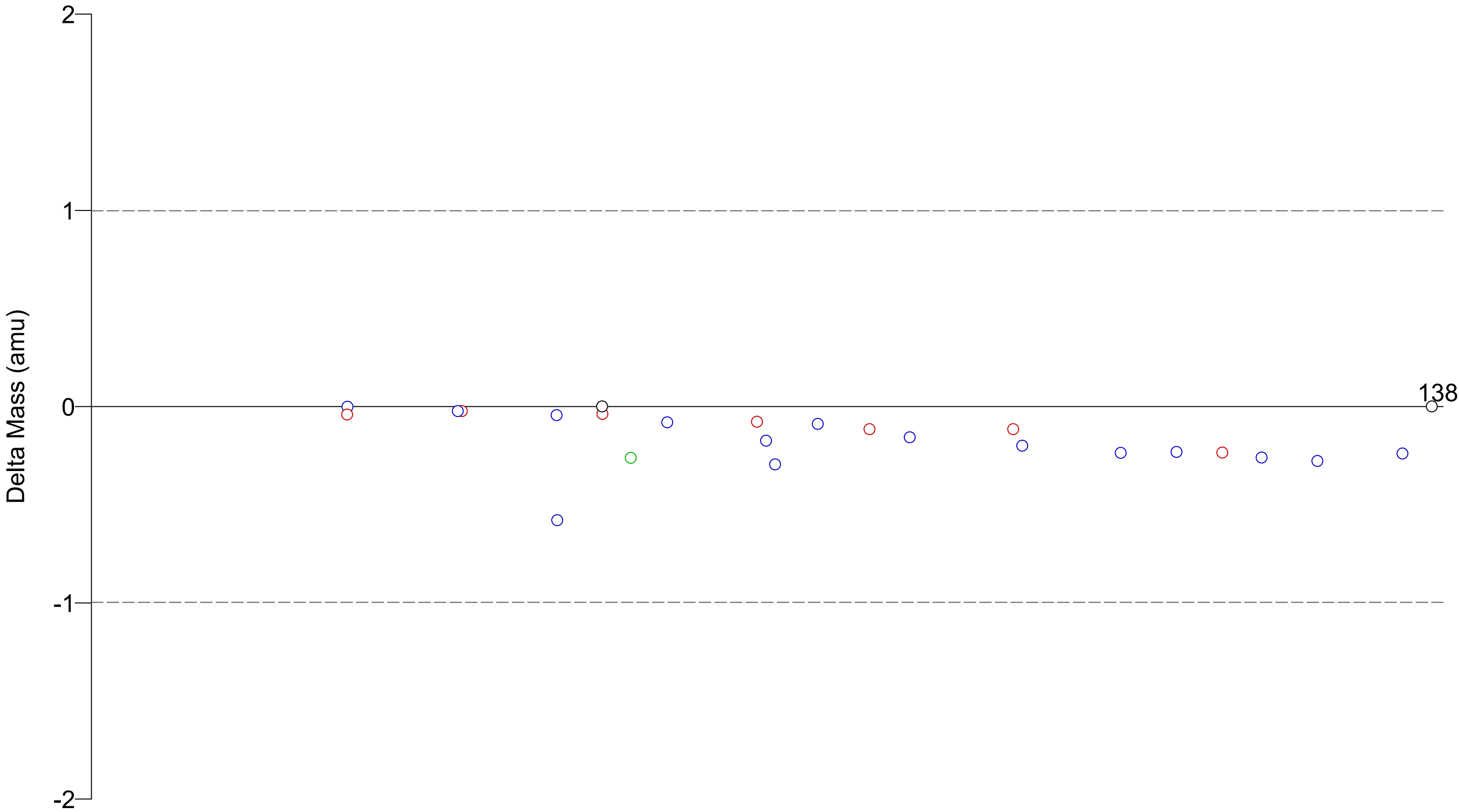
```
Reference                                                                 P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+        z     P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00827510.1|TREMBL:A2IPI5 Ta                                      1e-006  10.2      0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                     1632.79     2  1e-006  3.219  0.589    674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

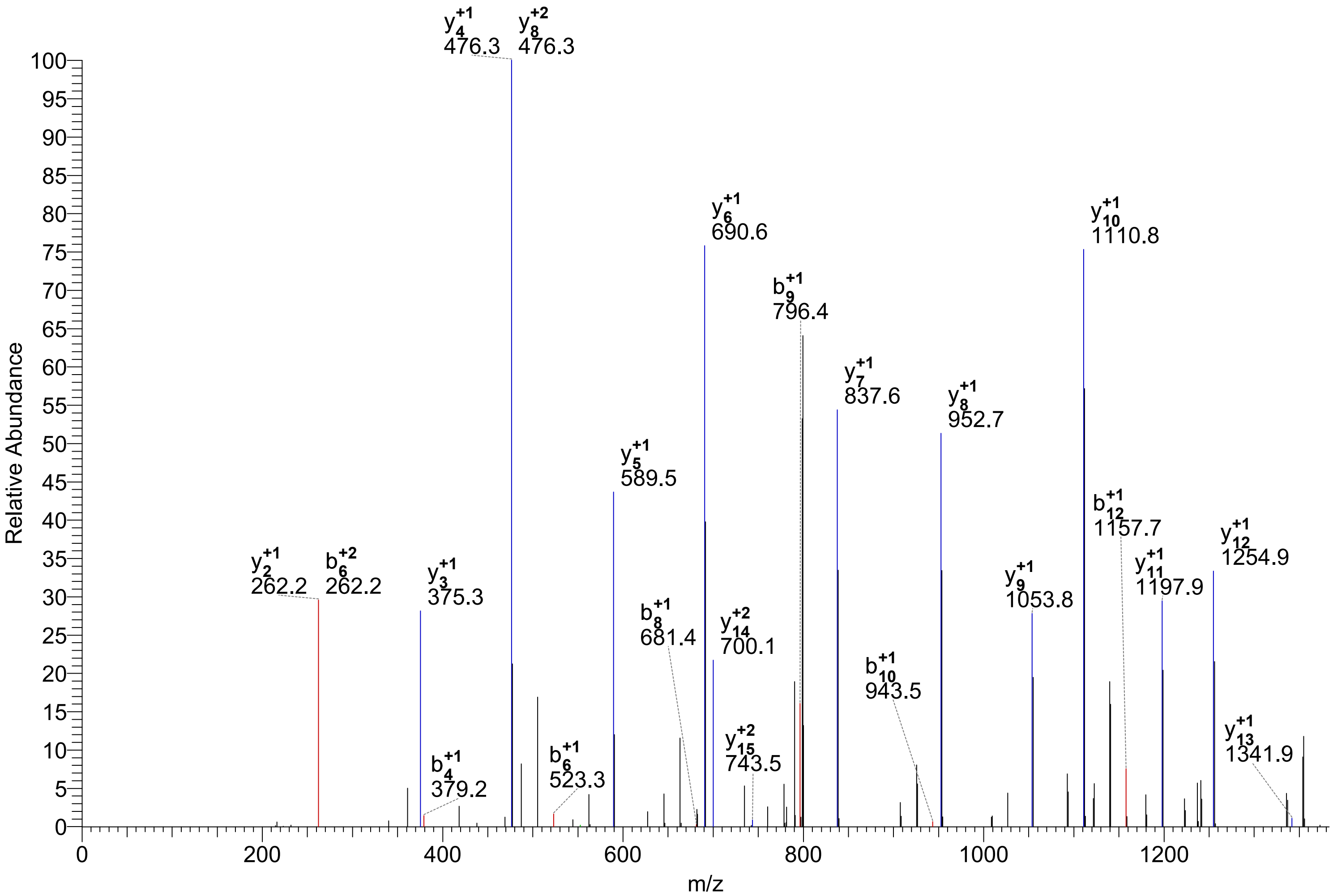
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



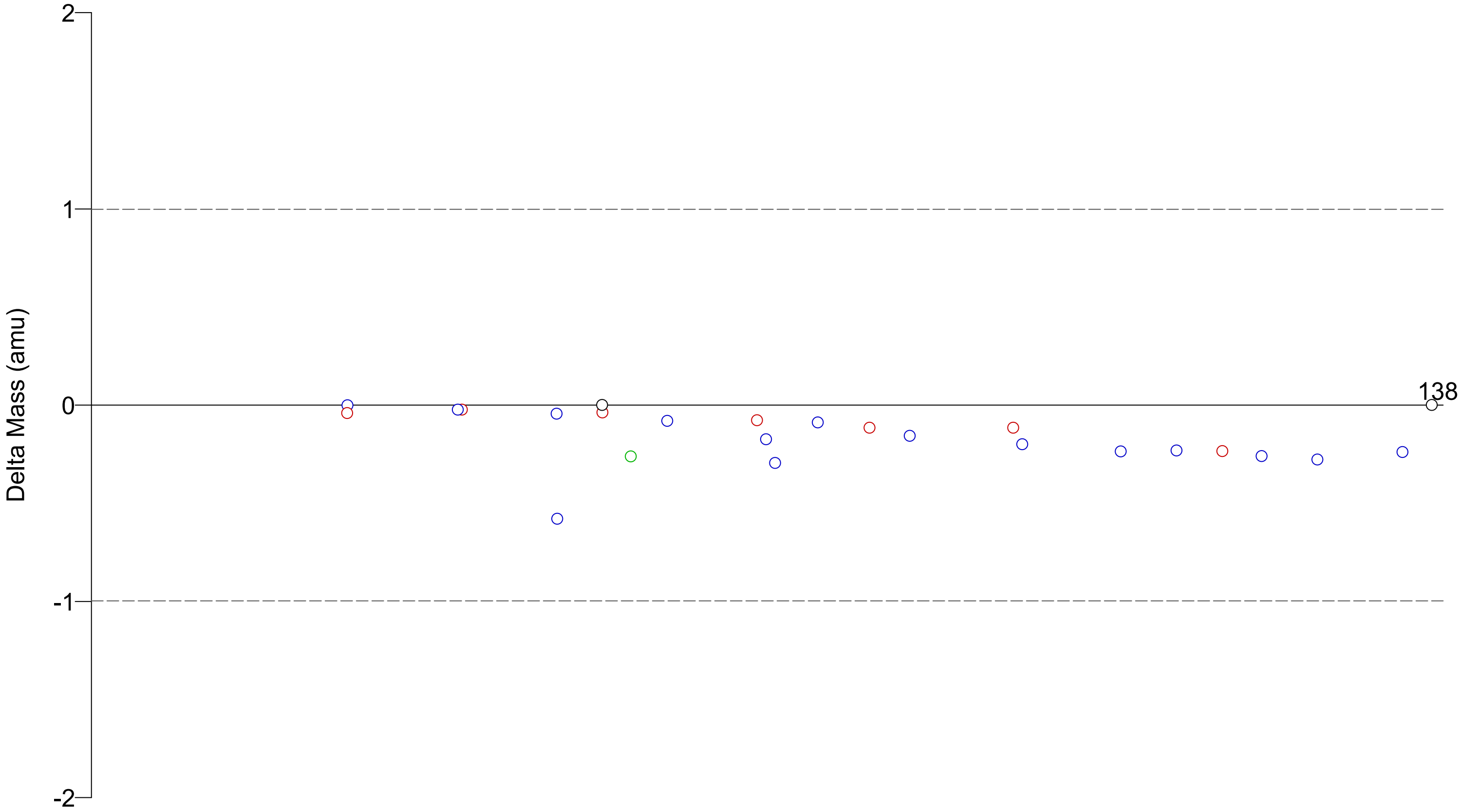
```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00827560.1|TREMBL:A2IPI2;A2                                       1e-006  10.2     0.0       0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                        1632.79    2  1e-006  3.219  0.589   674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

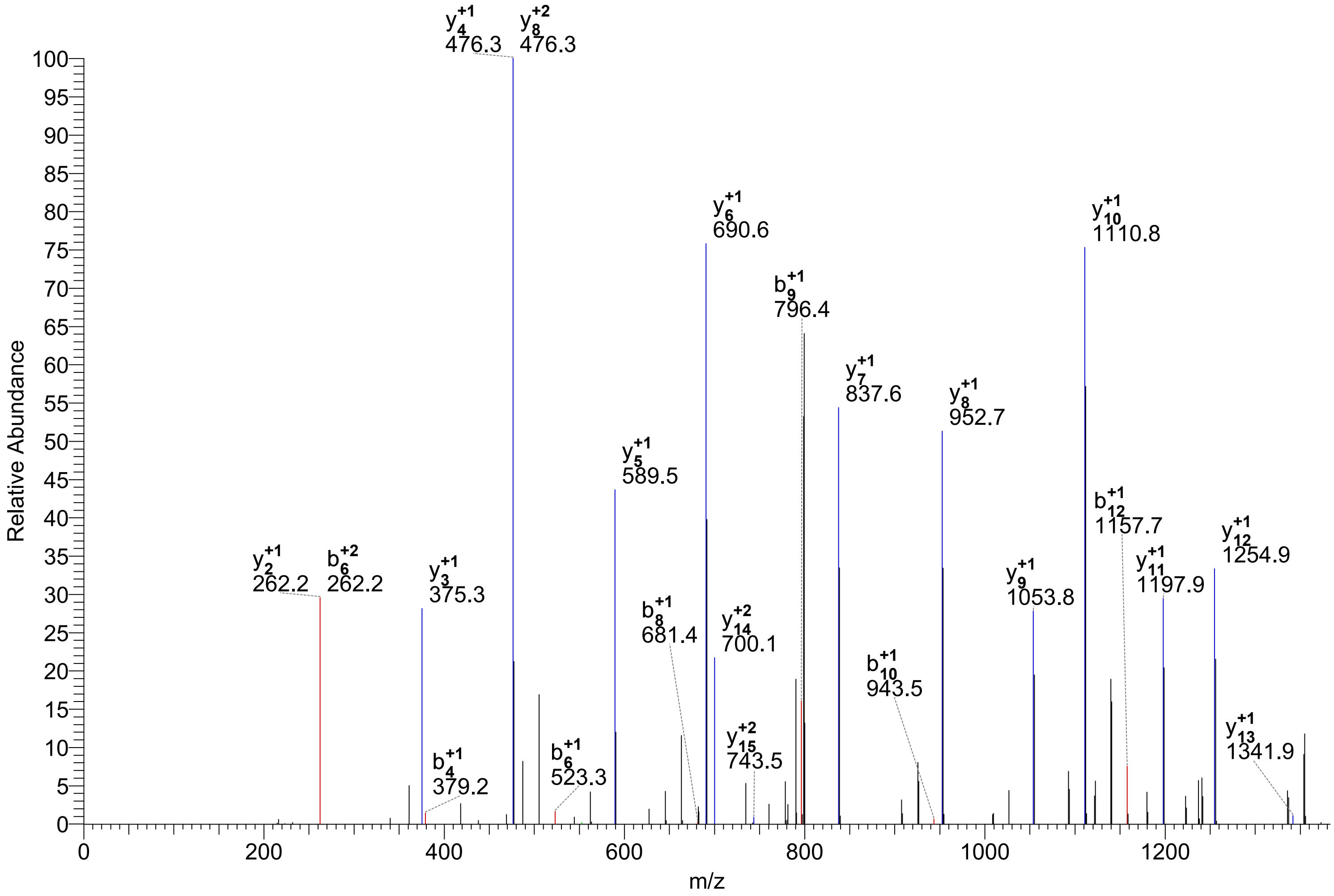
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                      1485.72
 G    264.13     292.13                                      1398.69
 S    351.17     379.16                                      1341.66
 G    408.19     436.18                                      1254.63
 S    495.22     523.21                                      1197.61
 G    552.24     580.24                                      1110.58
 T    653.29     681.28                                      1053.56
 D    768.32     796.31                                       952.51
 F    915.38     943.38                                       837.48
 T   1016.43    1044.43                                       690.41
 L   1129.52    1157.51                                       589.37
 T   1230.56    1258.56                                       476.28
 I   1343.65    1371.64                                       375.24
 S   1430.68    1458.67                                       262.15
 R                                                            175.12
```



#19287468-1 NL: 6.55E4



```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count

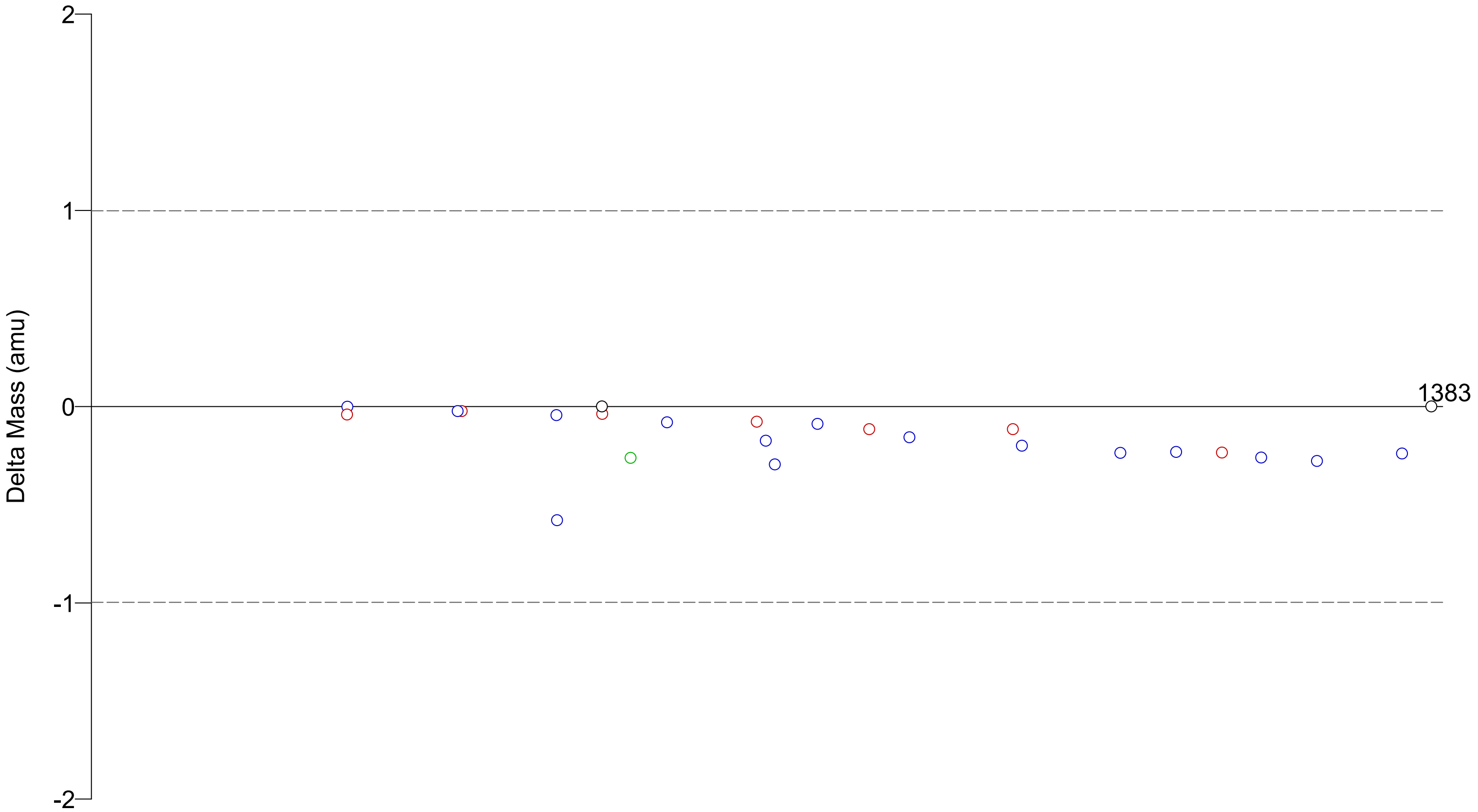
IPI:IPI00827637.1|TREMBL:A2NXP9 Ta                                        1e-006  10.2     0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                       1632.79    2  1e-006  3.219  0.589    674.9  1   19/45    14

1 of 1 peptide matches reported, 0 removed due to filtering
```

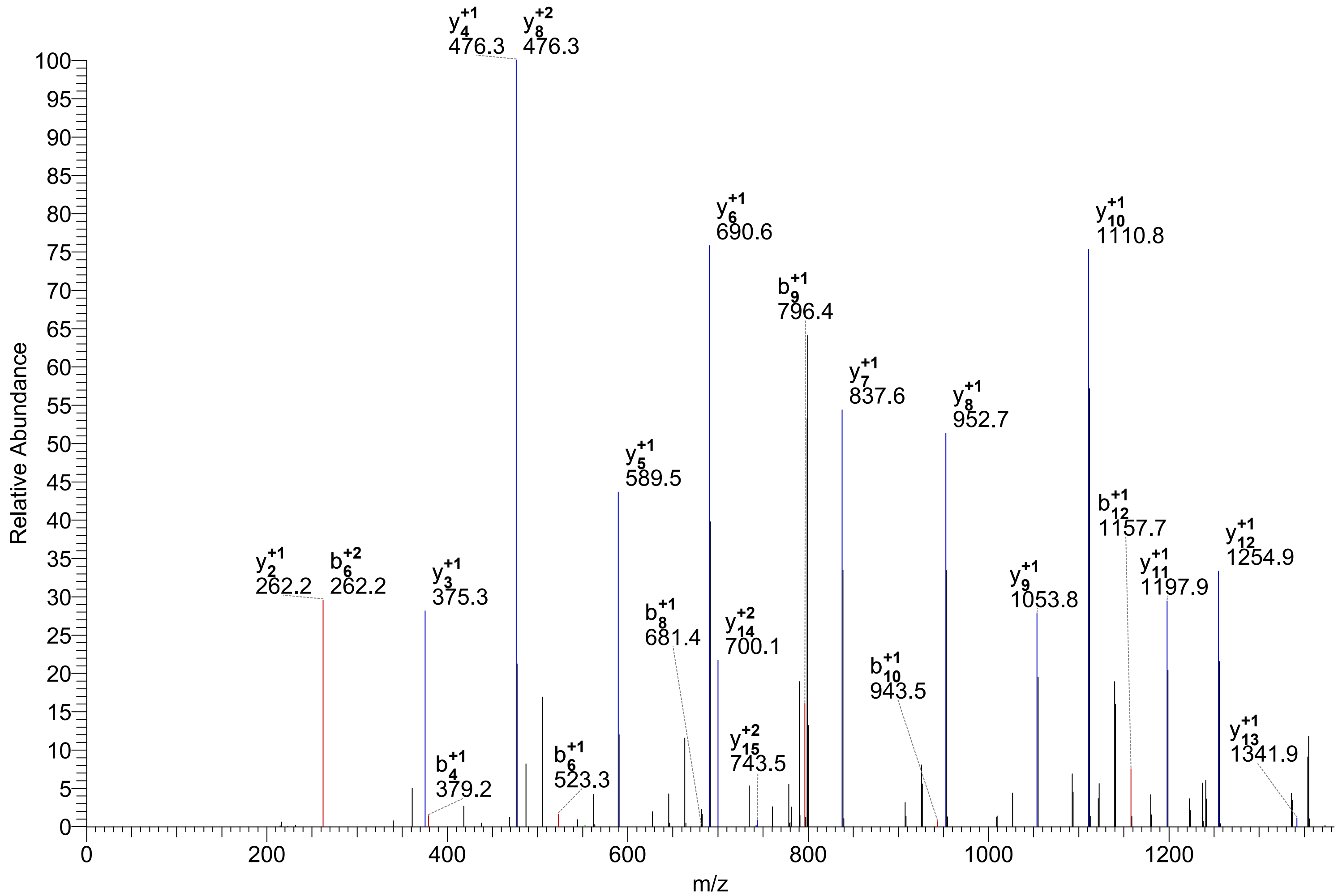
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



```
Reference                                                       P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z     P        XC  DeltaCn    Sp    RSp  Ions   Count

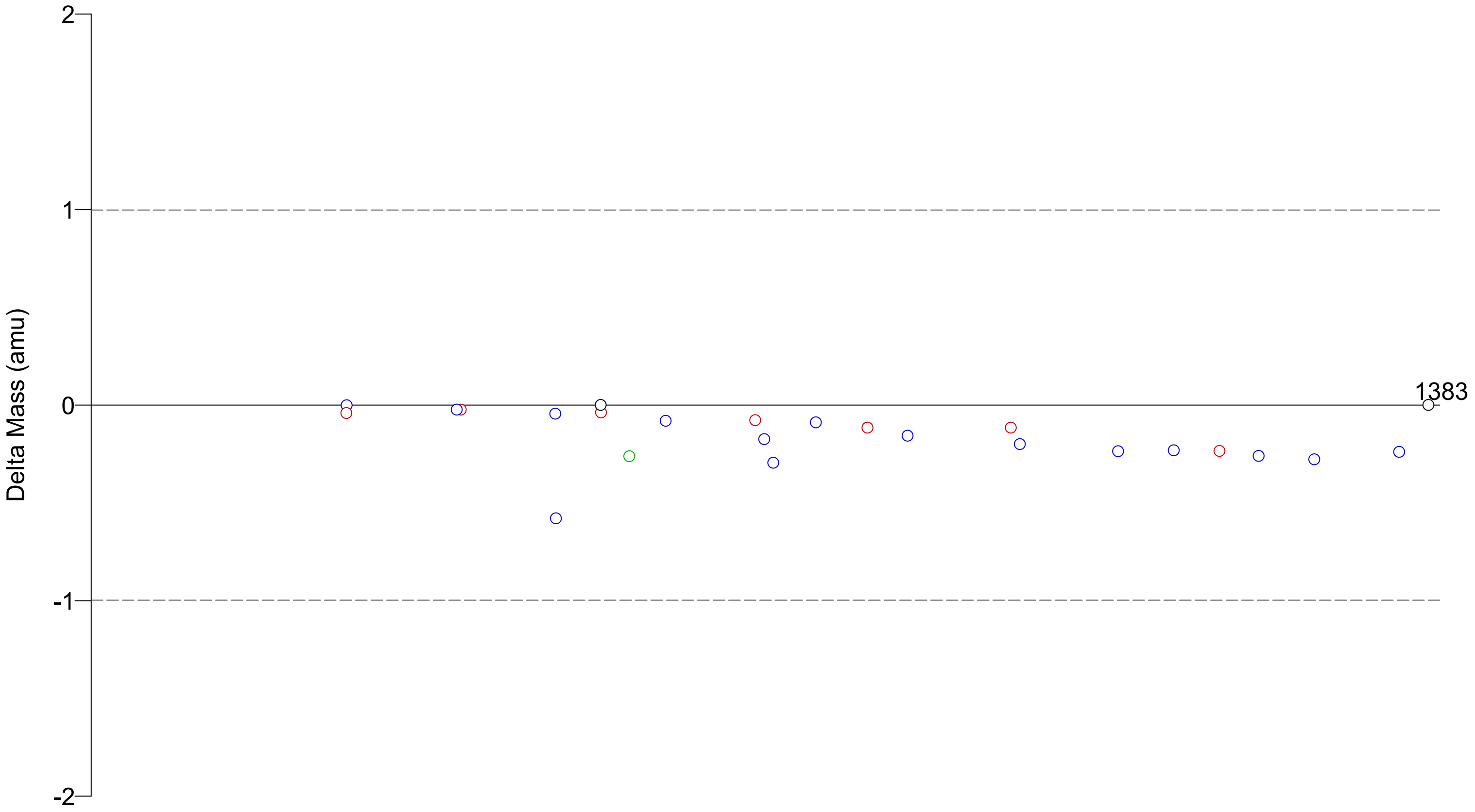
IPI:IPI00854644.2|TREMBL:A6NLY3|EN                                 1e-006  10.2      0.0        0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                    1632.79    2  1e-006  3.219  0.589    674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

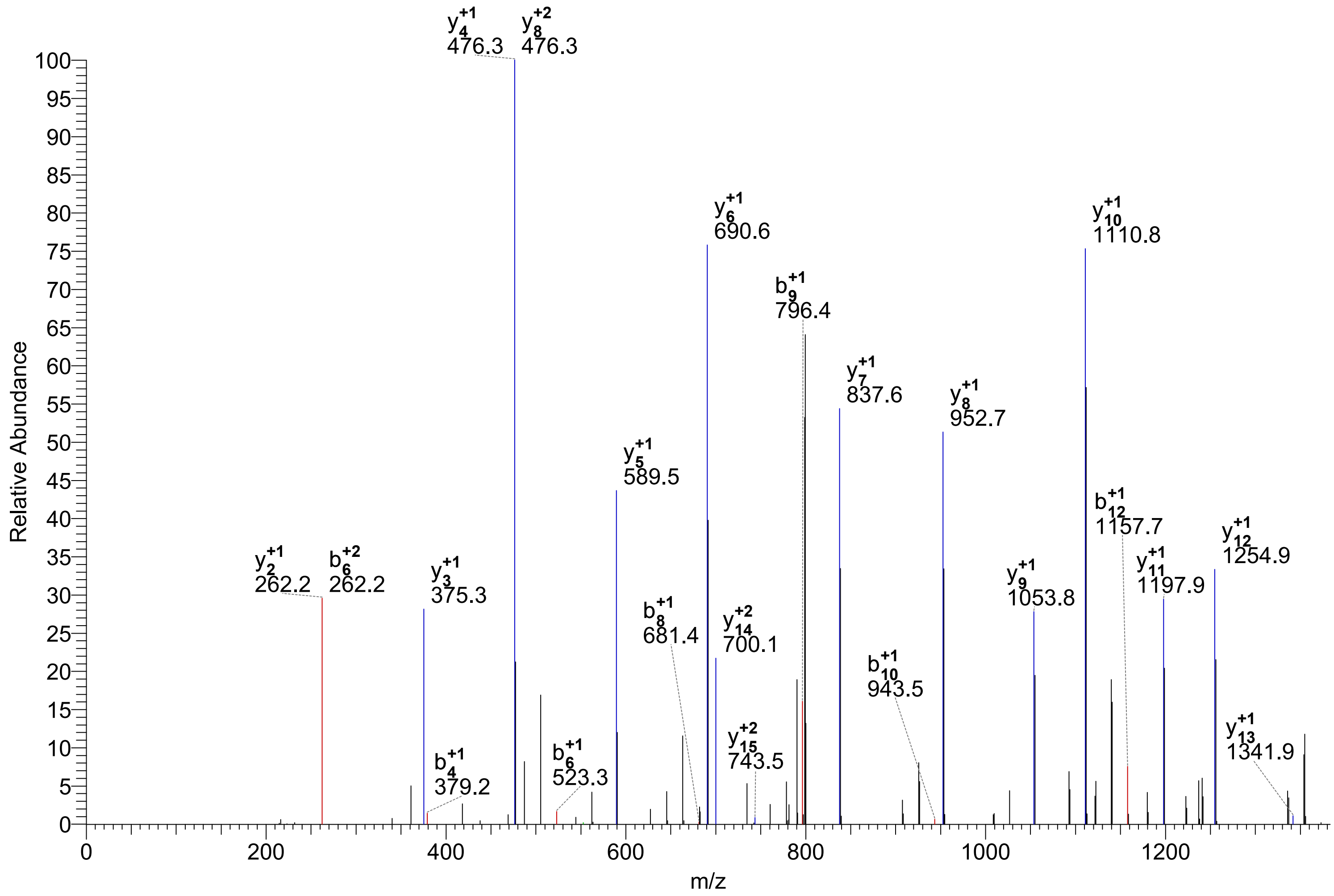
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

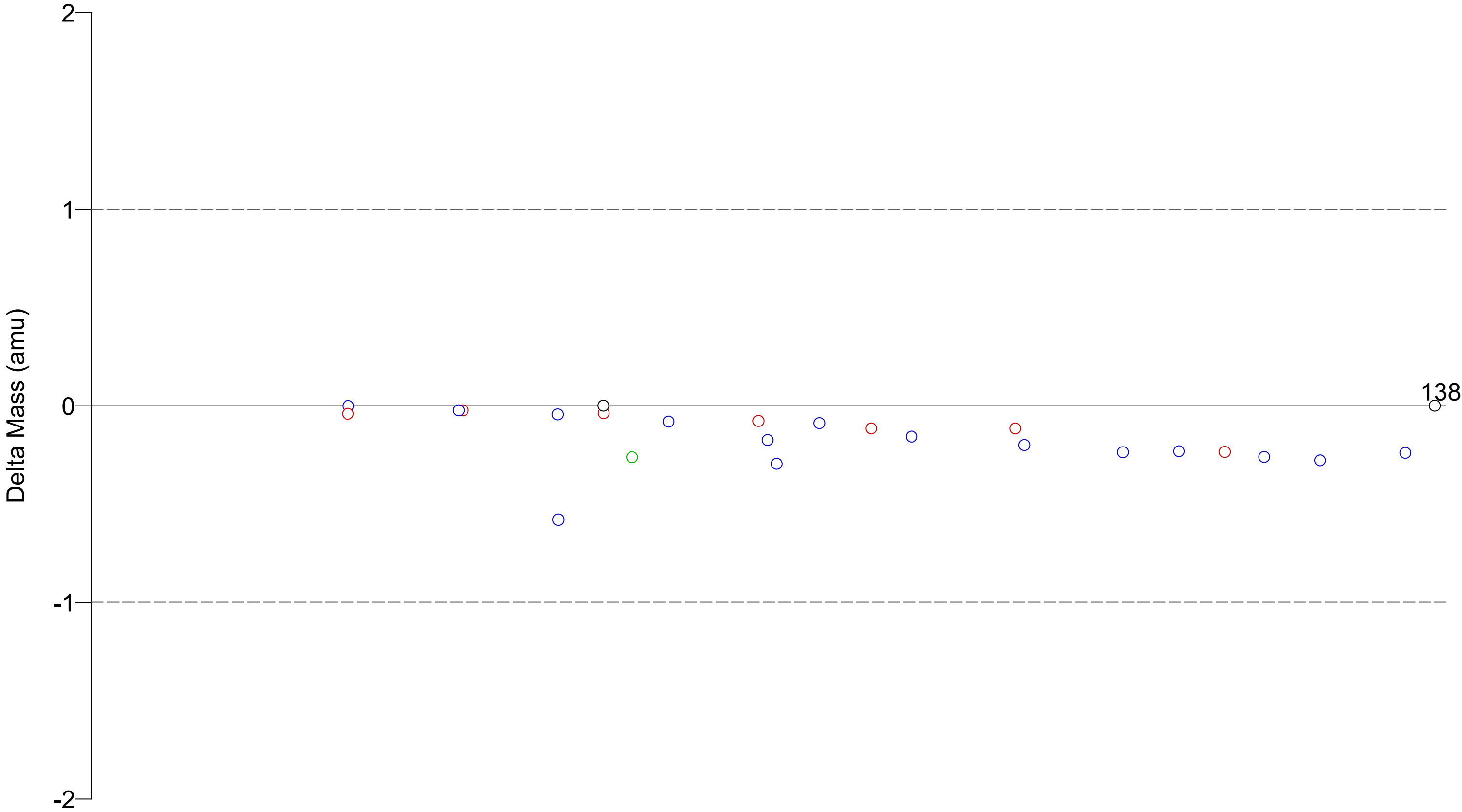
IPI:IPI00885193.1|TREMBL:Q9UL78 Ta                                1e-006  10.2     0.0       0
19287468 - 1  R.FSGSGSGTDFTLTISR.L                  1632.79   2  1e-006  3.219  0.589   674.9  1   19/45   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

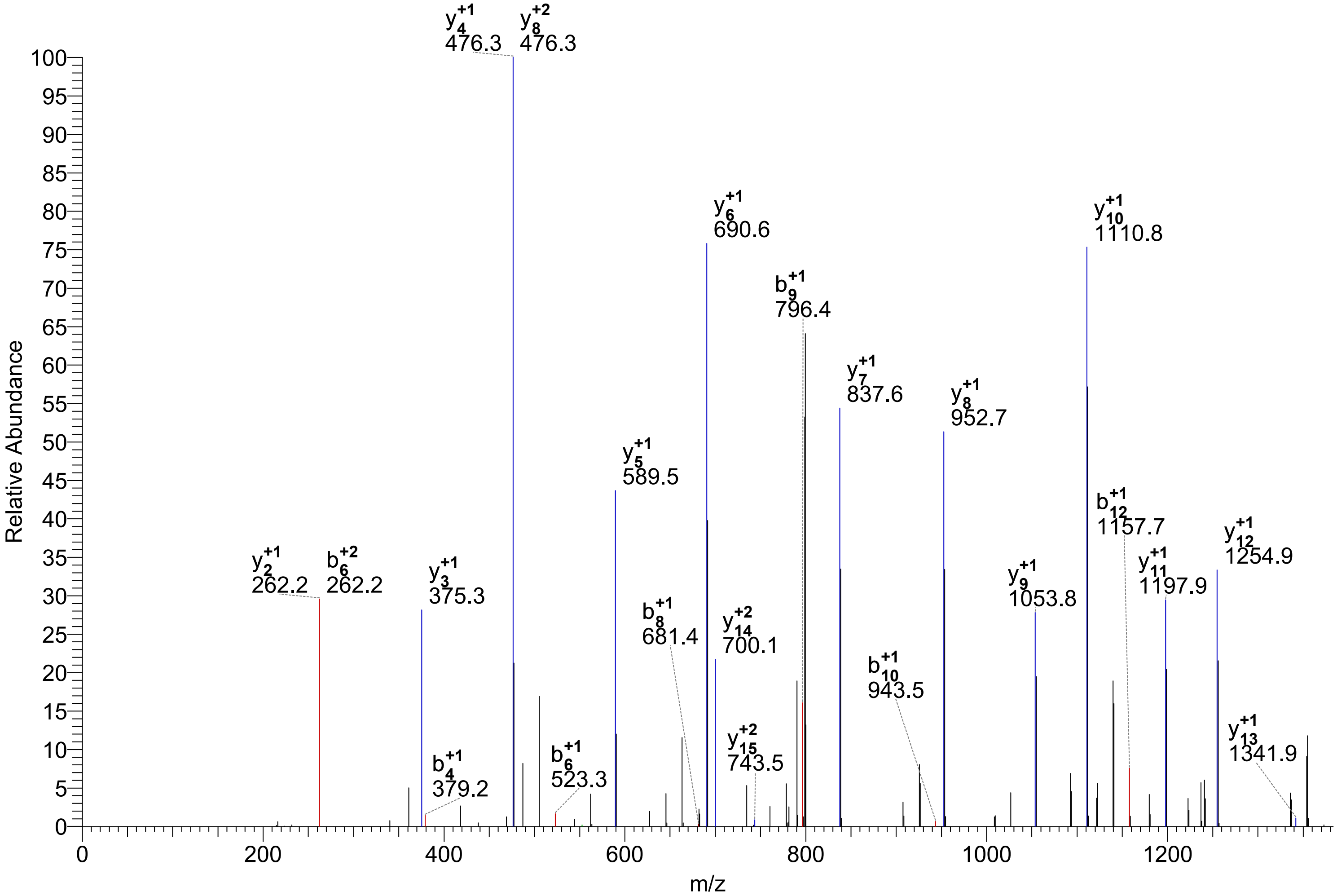
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
--------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                     1485.72
 G    264.13     292.13                                     1398.69
 S    351.17     379.16                                     1341.66
 G    408.19     436.18                                     1254.63
 S    495.22     523.21                                     1197.61
 G    552.24     580.24                                     1110.58
 T    653.29     681.28                                     1053.56
 D    768.32     796.31                                      952.51
 F    915.38     943.38                                      837.48
 T   1016.43    1044.43                                      690.41
 L   1129.52    1157.51                                      589.37
 T   1230.56    1258.56                                      476.28
 I   1343.65    1371.64                                      375.24
 S   1430.68    1458.67                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.55E4



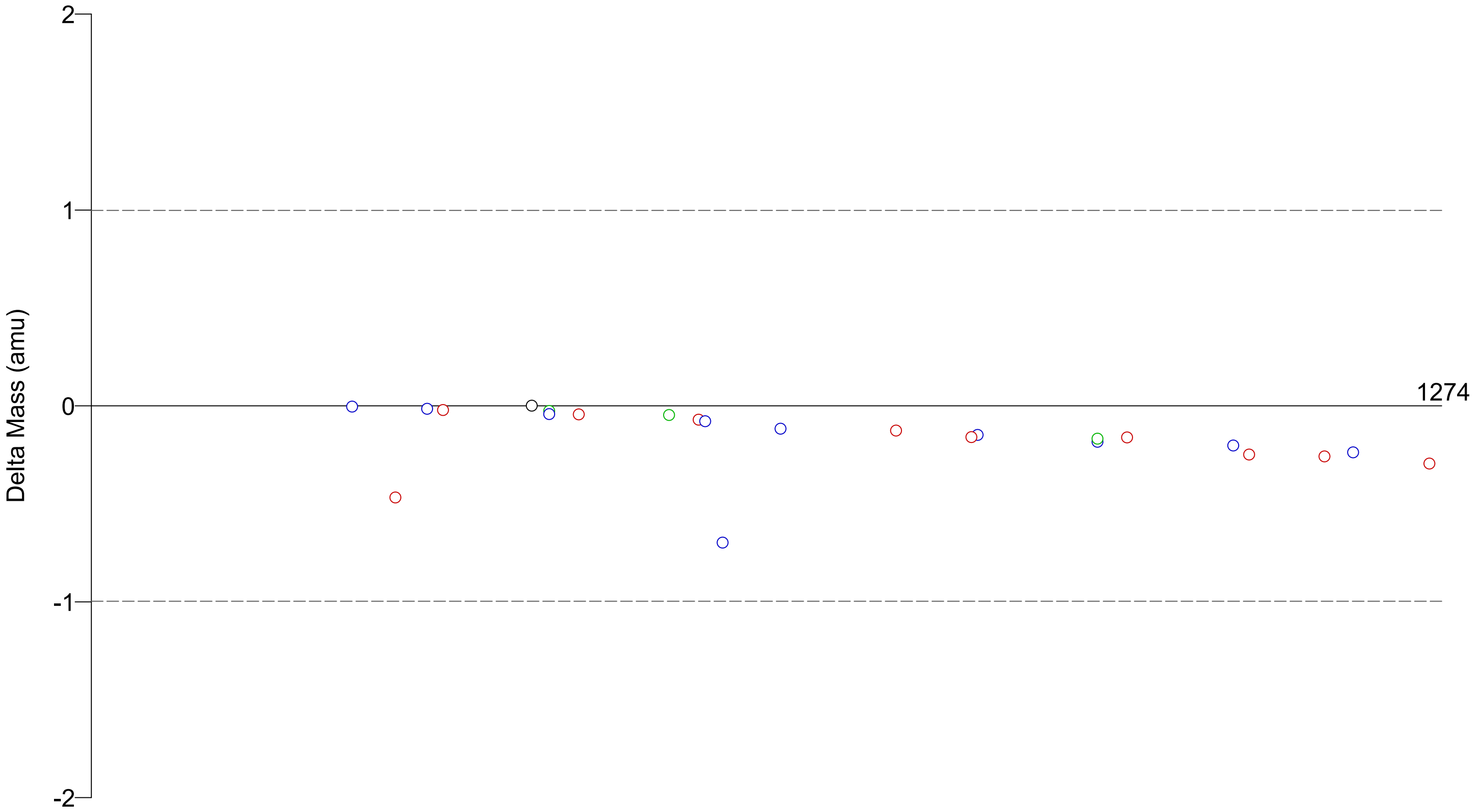
```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z     P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00022426.1|SWISS-PROT:P02760|TREMBL:P78492|ENSEMBL:ENSP     1e-006  10.2      0.0        0
19287468 - 1  R.AFIQLWAFDAVK.G                           1408.76   2  1e-006  3.585  0.380   1474.7 1   21/33

1 of 1 peptide matches reported, 0 removed due to filtering
```

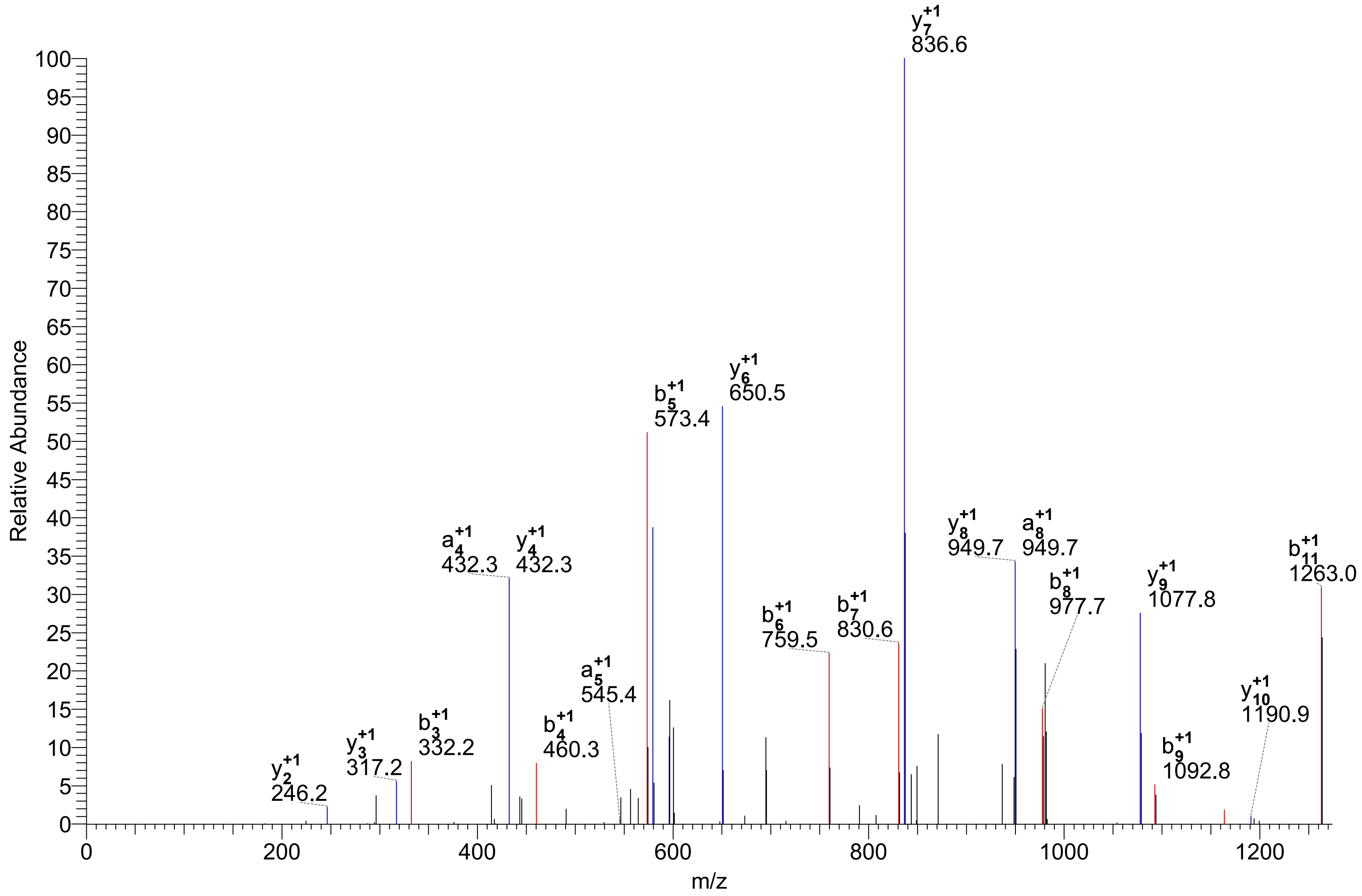
```
DTA for scans: 19287468-1
Precursor ion: 704.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 F    191.12     219.11                                      1337.73
 I    304.20     332.20                                      1190.66
 Q    432.26     460.26                                      1077.57
 L    545.34     573.34                                       949.51
 W    731.42     759.42                                       836.43
 A    802.46     830.46                                       650.35
 F    949.53     977.52                                       579.31
 D   1064.56    1092.55                                       432.25
 A   1135.59    1163.59                                       317.22
 V   1234.66    1262.66                                       246.18
 K                                                            147.11
```



#19287468-1 NL: 6.35E4



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

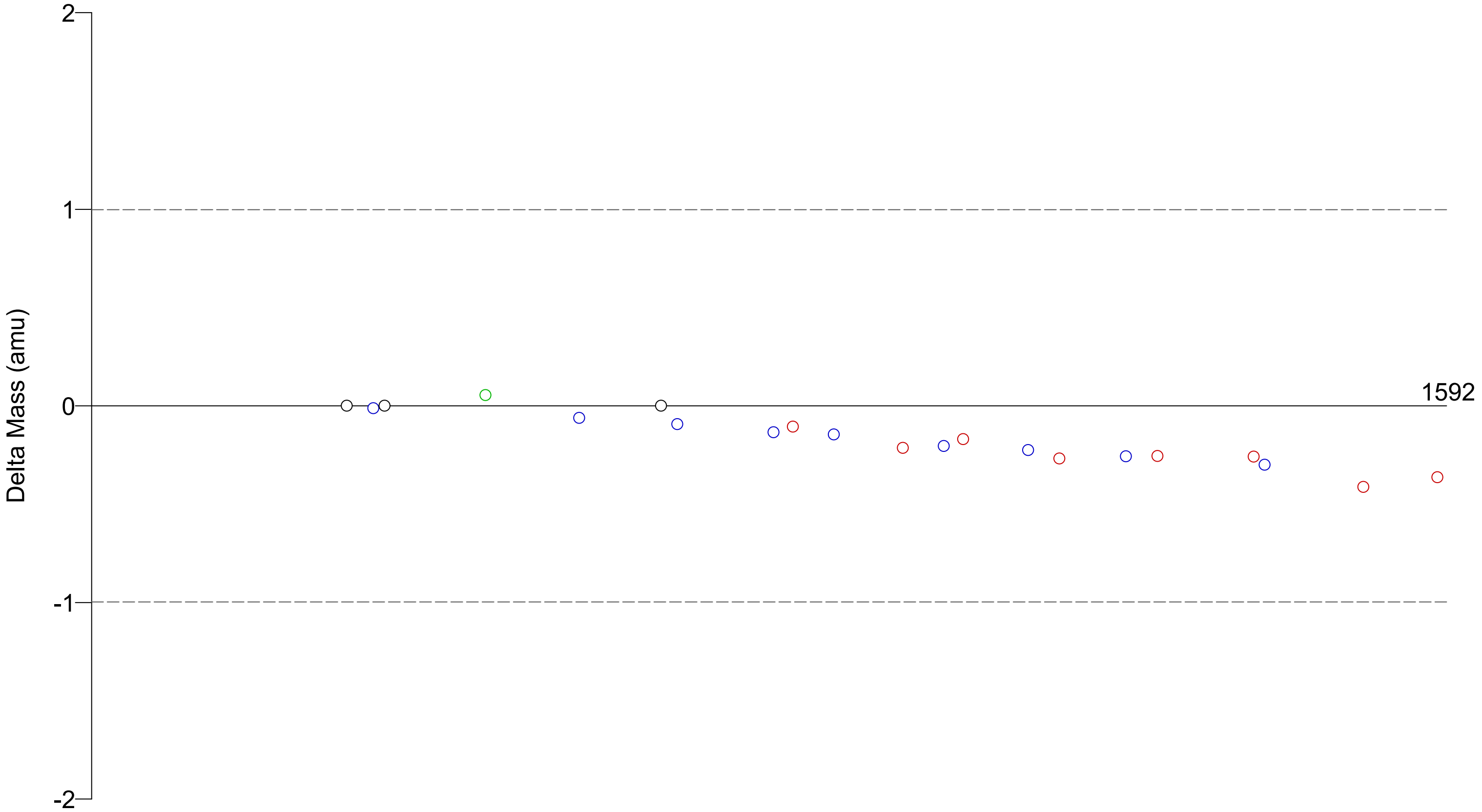
IPI:IPI00022371.1|SWISS-PROT:P04196|TREMBL:B2R8I2;B9EK35;Q68DR    2e-006  10.1     0.0       0
19287468 - 1  R.ADLFYDVEALDLESPK.N                   1824.89   2  2e-006  2.497  0.458   790.6  1   18/45

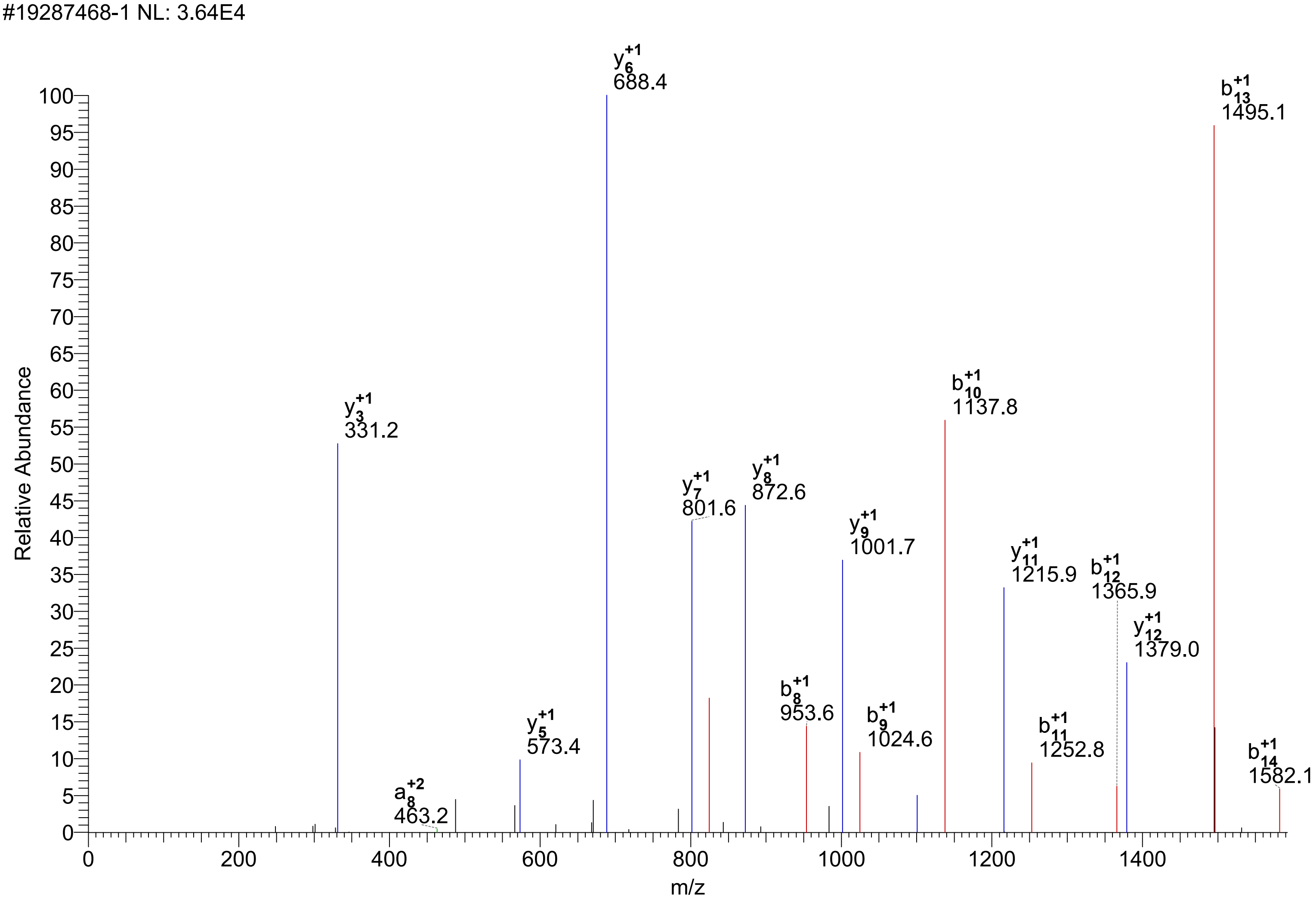
1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 912.95
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 D    159.08     187.07                                     1753.85
 L    272.16     300.16                                     1638.83
 F    419.23     447.22                                     1525.74
 Y    582.29     610.29                                     1378.67
 D    697.32     725.31                                     1215.61
 V    796.39     824.38                                     1100.58
 E    925.43     953.43                                     1001.51
 A    996.47    1024.46                                      872.47
 L   1109.55    1137.55                                      801.44
 D   1224.58    1252.57                                      688.35
 L   1337.66    1365.66                                      573.32
 E   1466.70    1494.70                                      460.24
 S   1553.74    1581.73                                      331.20
 P   1650.79    1678.78                                      244.17
 K                                                           147.11
```


Delta Mass (amu)
2
1
0
-1
-2
1592


#19287468-1 NL: 3.64E4
Relative Abundance
m/z
y3 +1 331.2
a8 +2 463.2
y5 +1 573.4
y6 +1 688.4
y7 +1 801.6
y8 +1 872.6
b8 +1 953.6
y9 +1 1001.7
b9 +1 1024.6
b10 +1 1137.8
y11 +1 1215.9
b11 +1 1252.8
b12 +1 1365.9
y12 +1 1379.0
b13 +1 1495.1
b14 +1 1582.1
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
0 200 400 600 800 1000 1200 1400

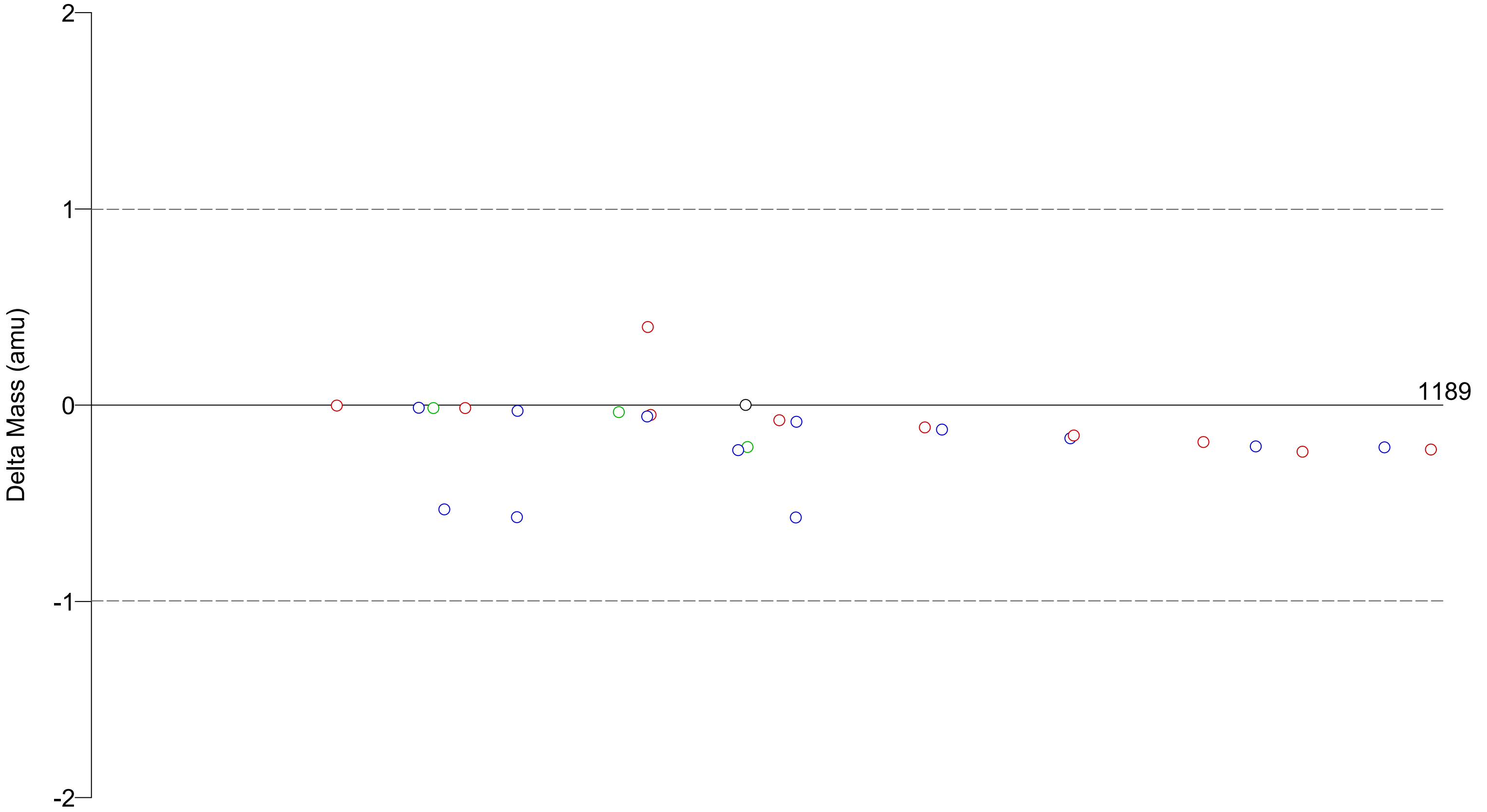
```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00828156.1|TREMBL:A2NKM6 Ta                                      3e-006  20.2      0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                            1352.70    2  3e-006  4.027  0.643    1526.5 1    20/30    39
2118291816 -  R.LSCAASGFTFR.S                            1217.56    2  6e-006  3.492  0.654    1231.4 1    20/30    3

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

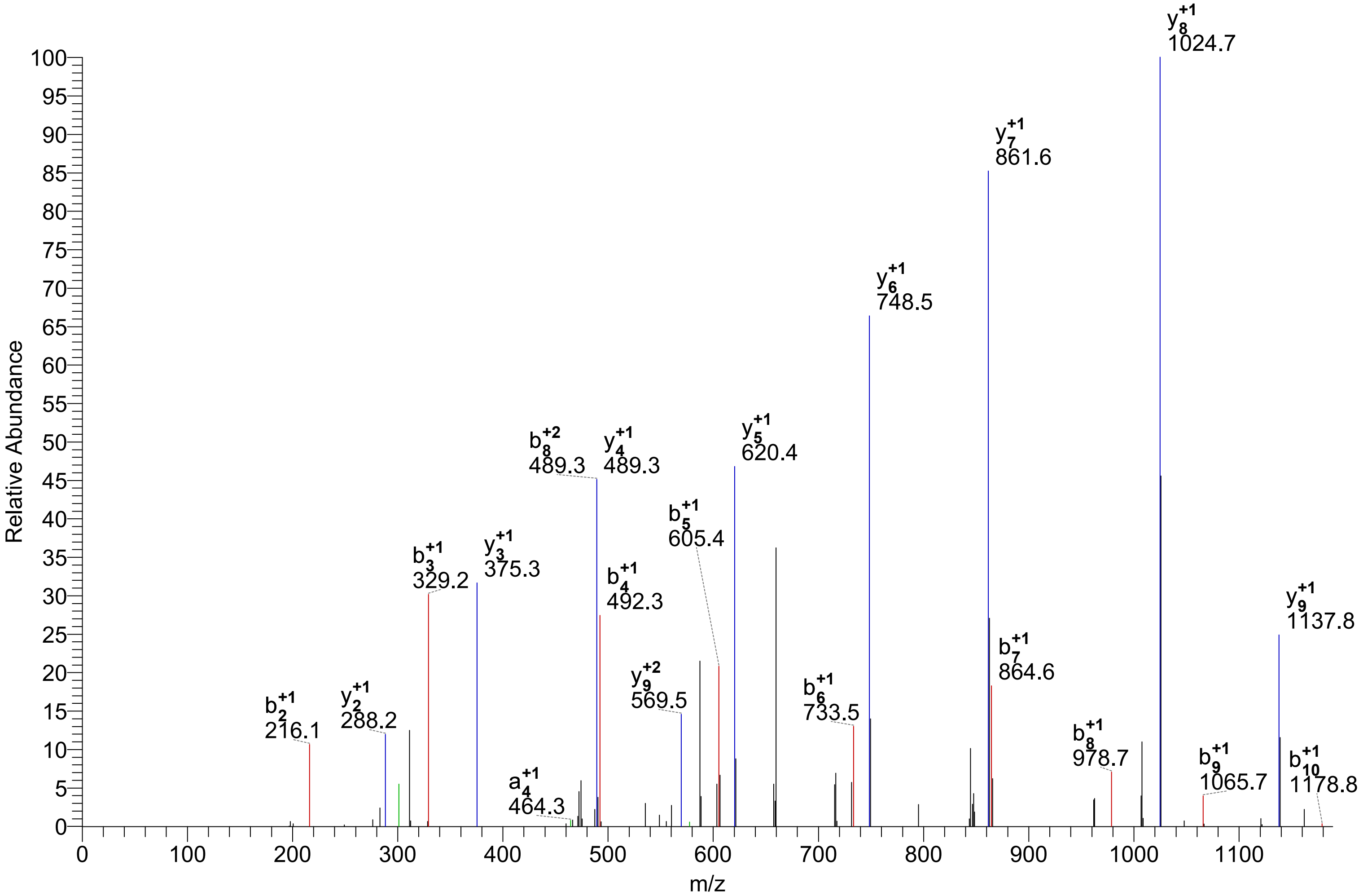
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



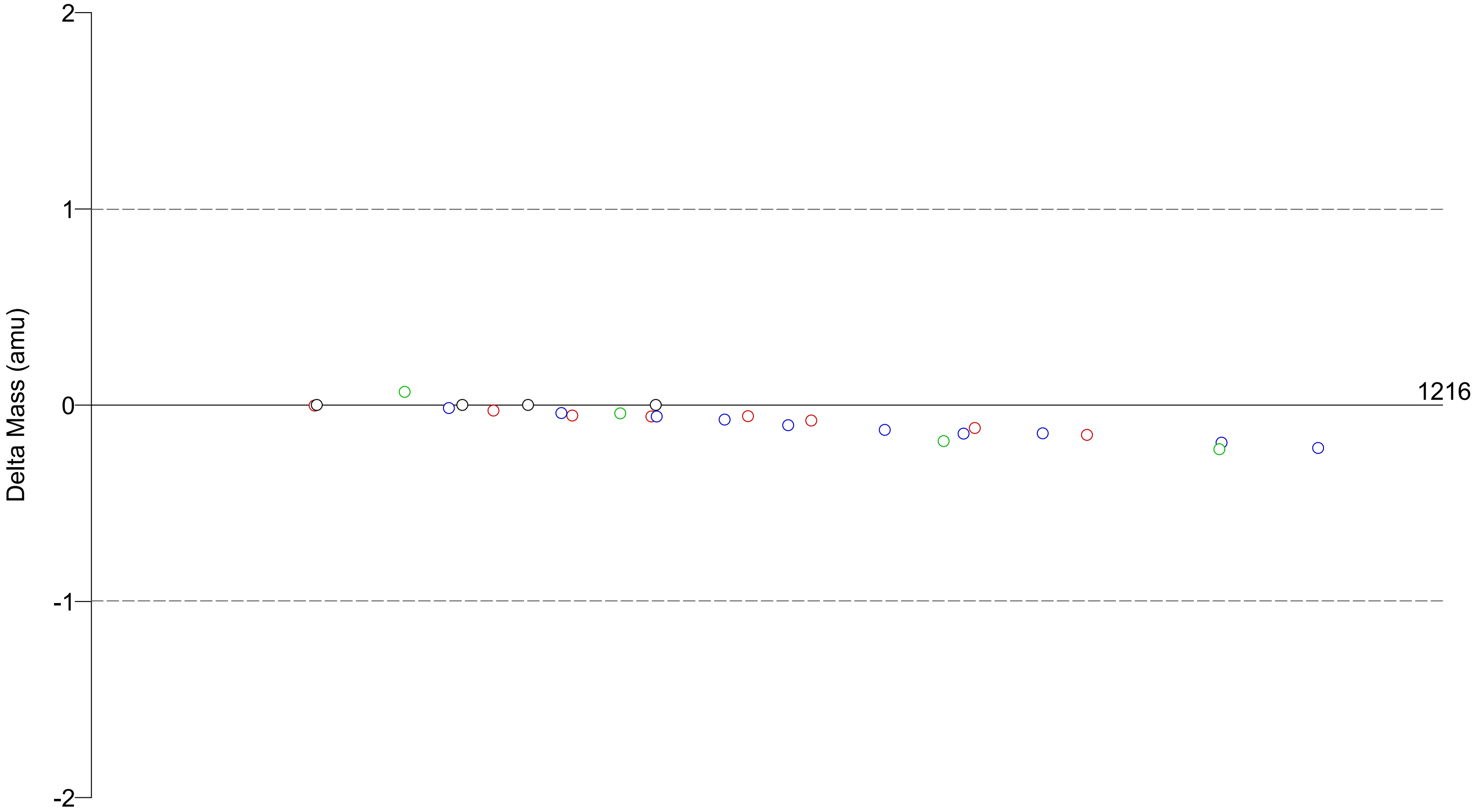
#19287468-1 NL: 1.01E5



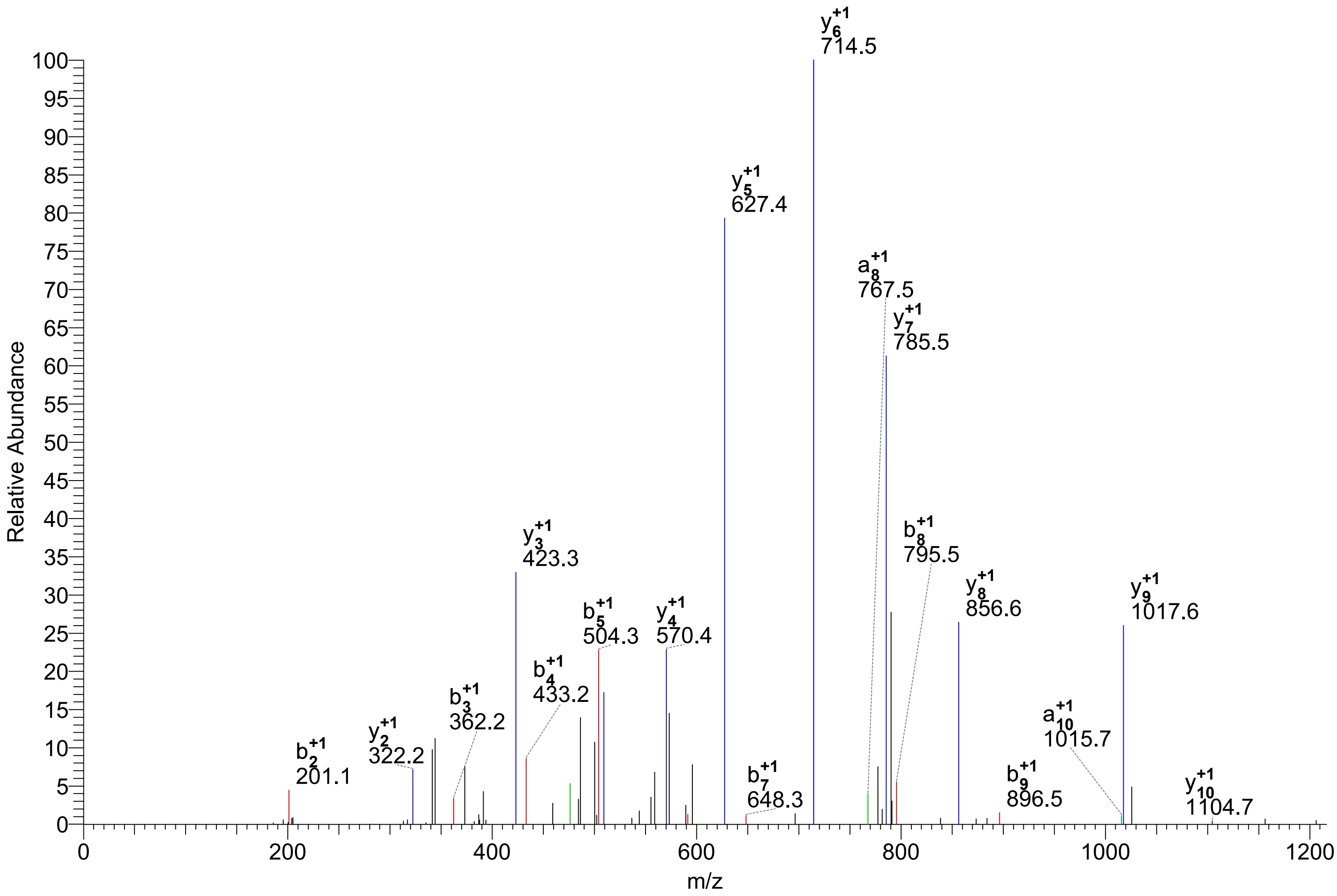
```
DTA for scans: 2118291816-26226248
Precursor ion: 609.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                      1104.48
 C    334.14     362.14                                      1017.45
 A    405.18     433.18                                       856.43
 A    476.22     504.21                                       785.39
 S    563.25     591.24                                       714.36
 G    620.27     648.27                                       627.32
 F    767.34     795.33                                       570.30
 T    868.39     896.38                                       423.24
 F   1015.46    1043.45                                       322.19
 R                                                            175.12
```



#2118291816-26226248 NL: 9.29E4



```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                        MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

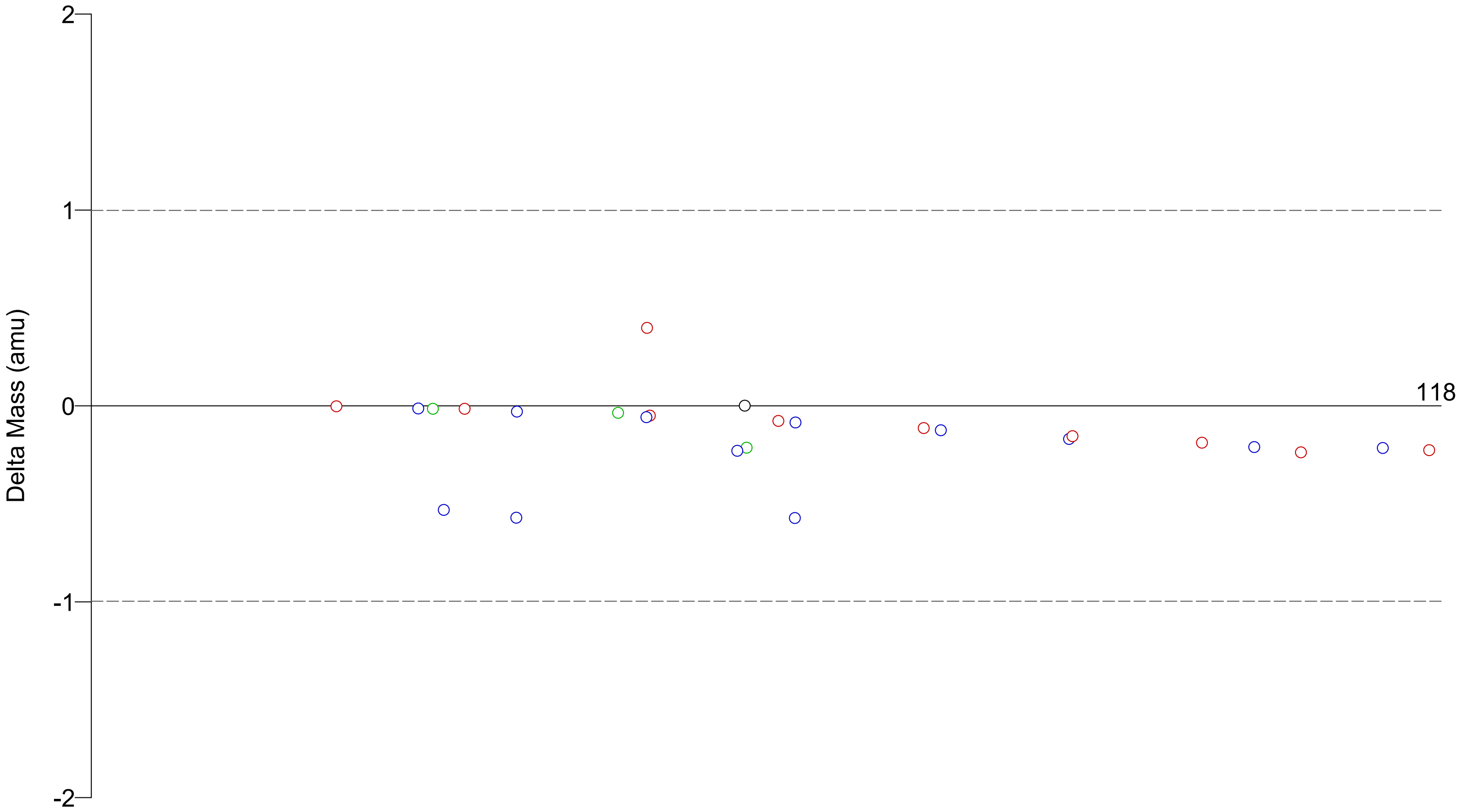
IPI:IPI00383887.1|TREMBL:Q9UGP3 Tax_Id=9606 Gene_Symbol=- Immu     3e-006  10.2     0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                              1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

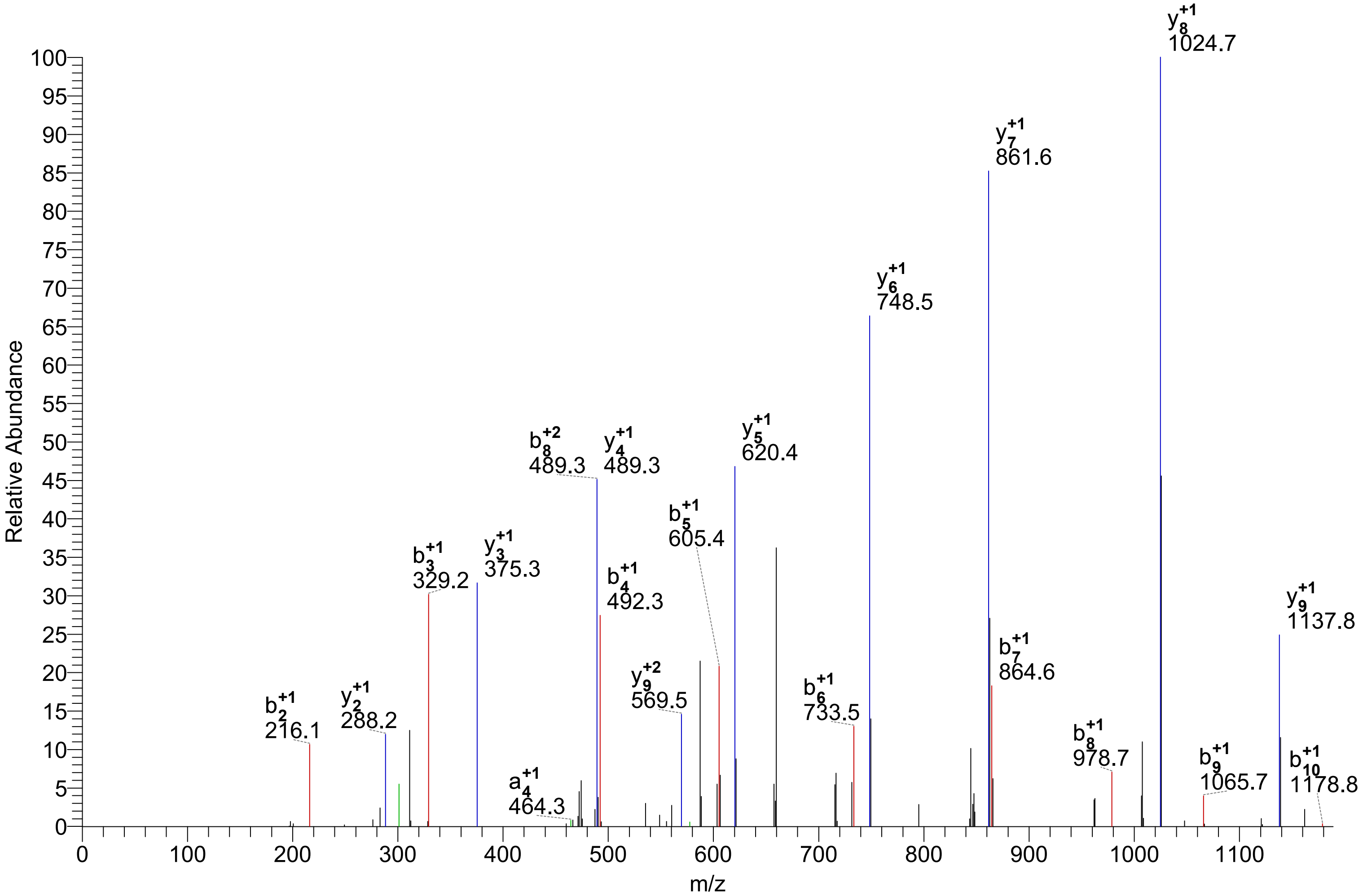
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



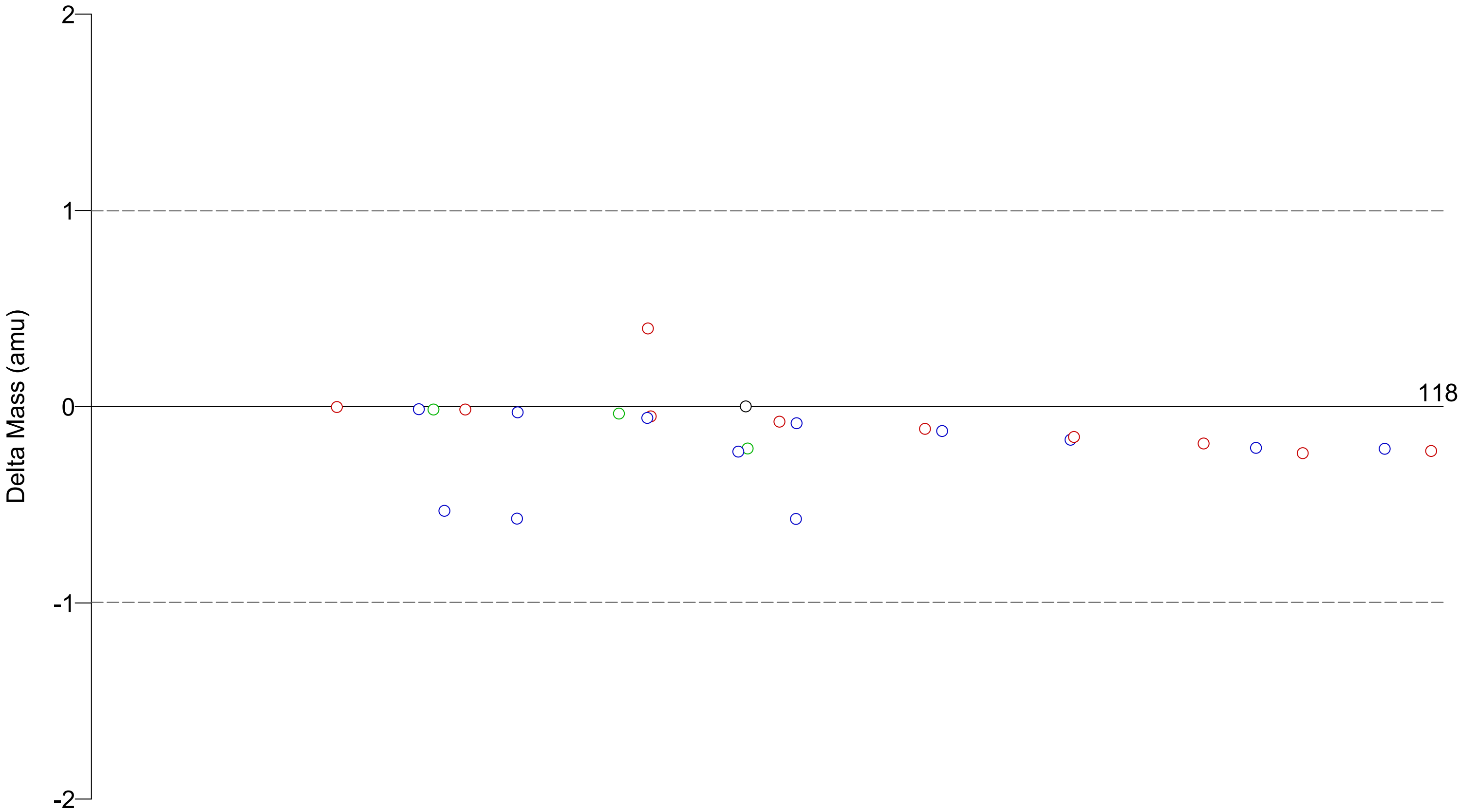
```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z   P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00384392.1|TREMBL:Q9UL72 Ta                                 3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                          1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

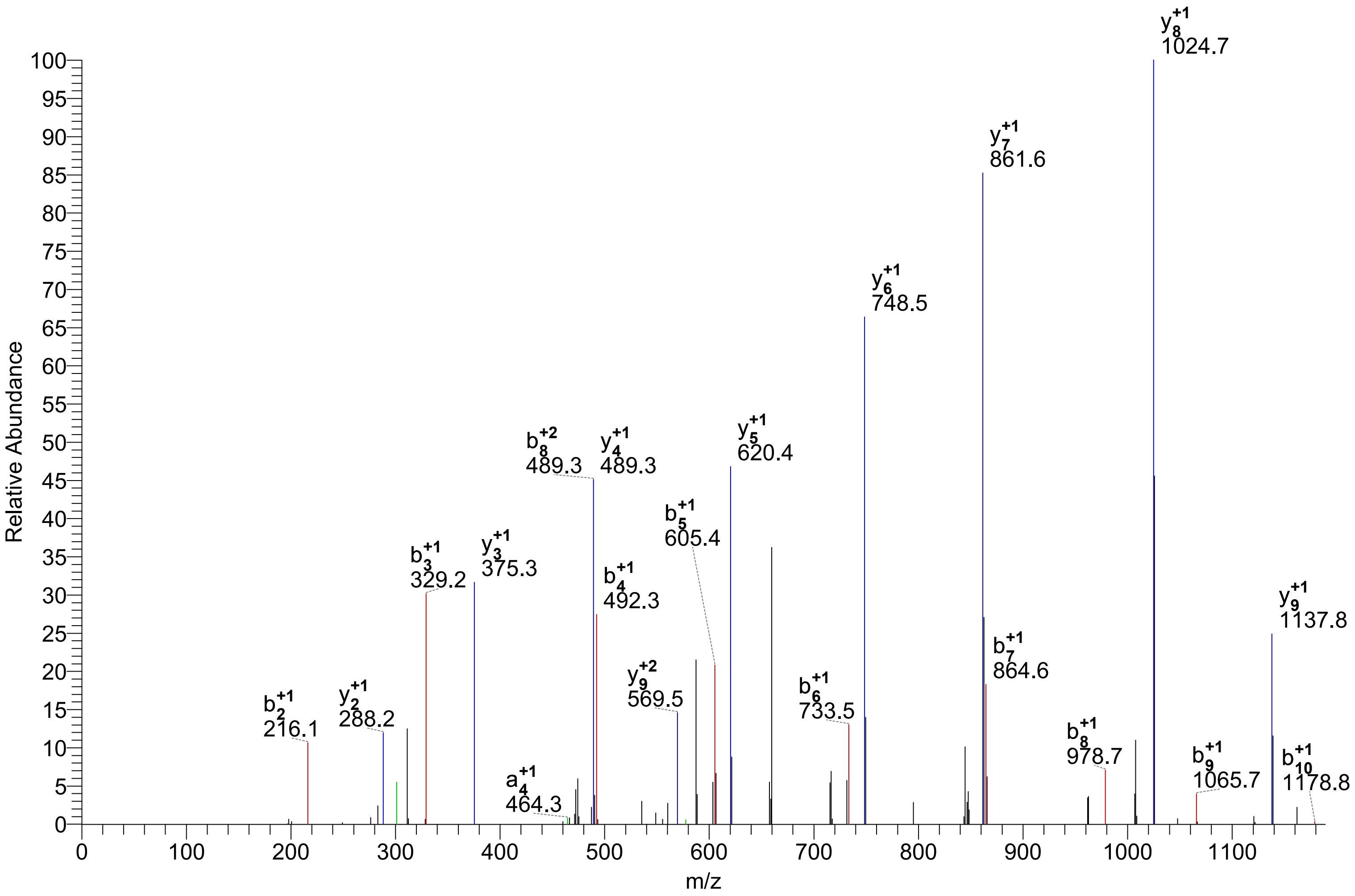
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



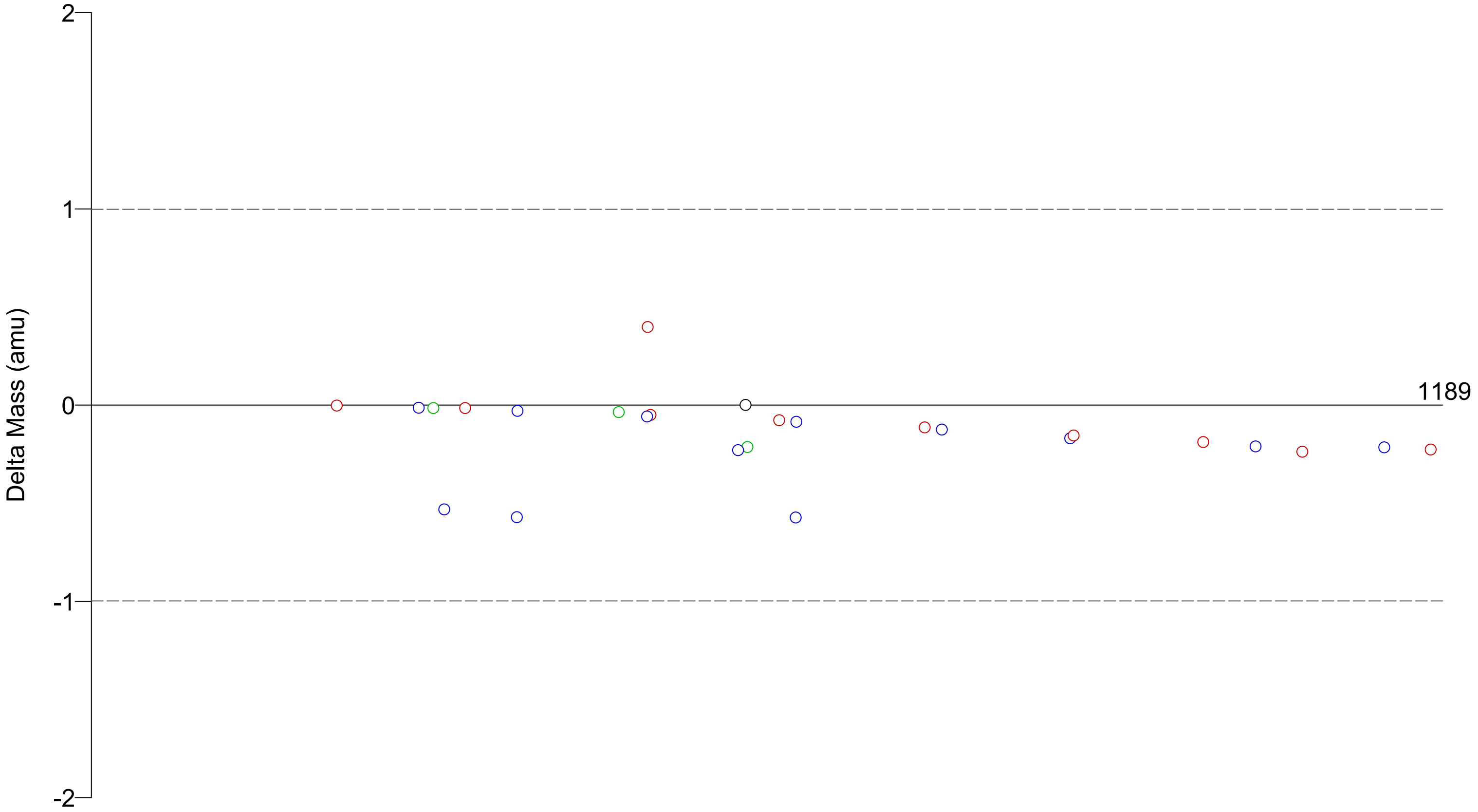
```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00413194.1|TREMBL:Q9UL93 Ta                                          3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                              1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

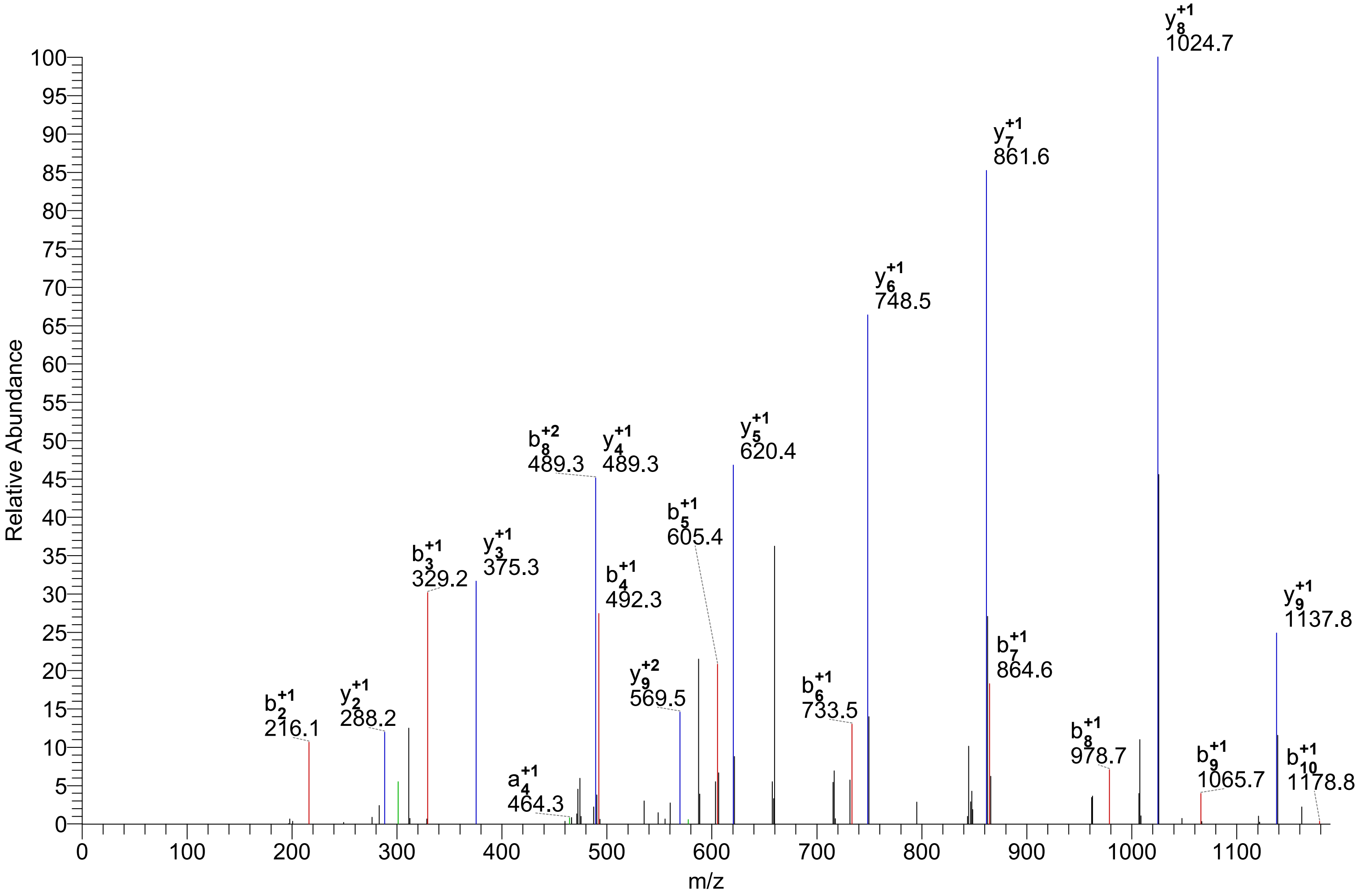
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



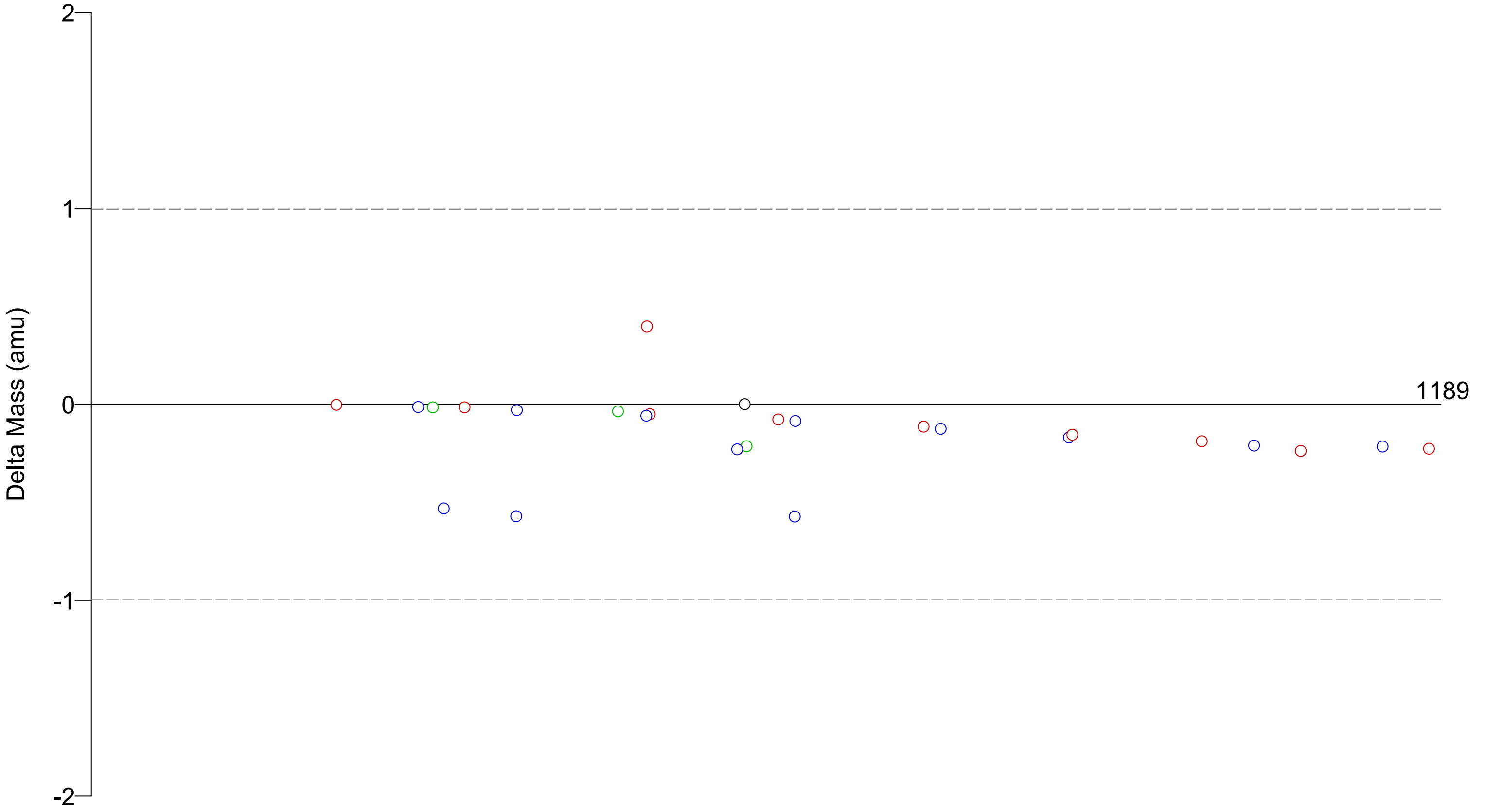
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00736507.2|TREMBL:Q0ZCG7;Q0                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

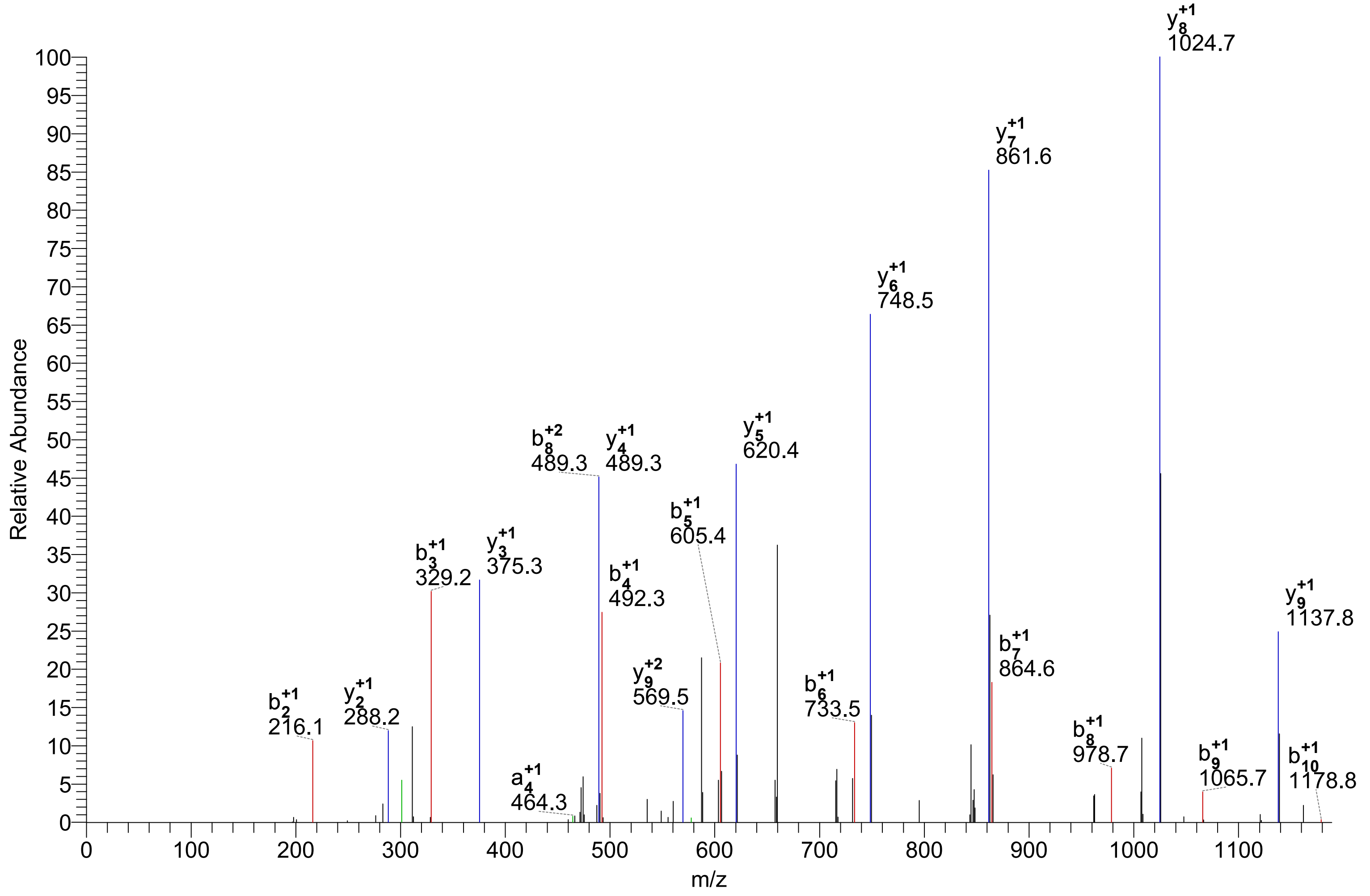
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

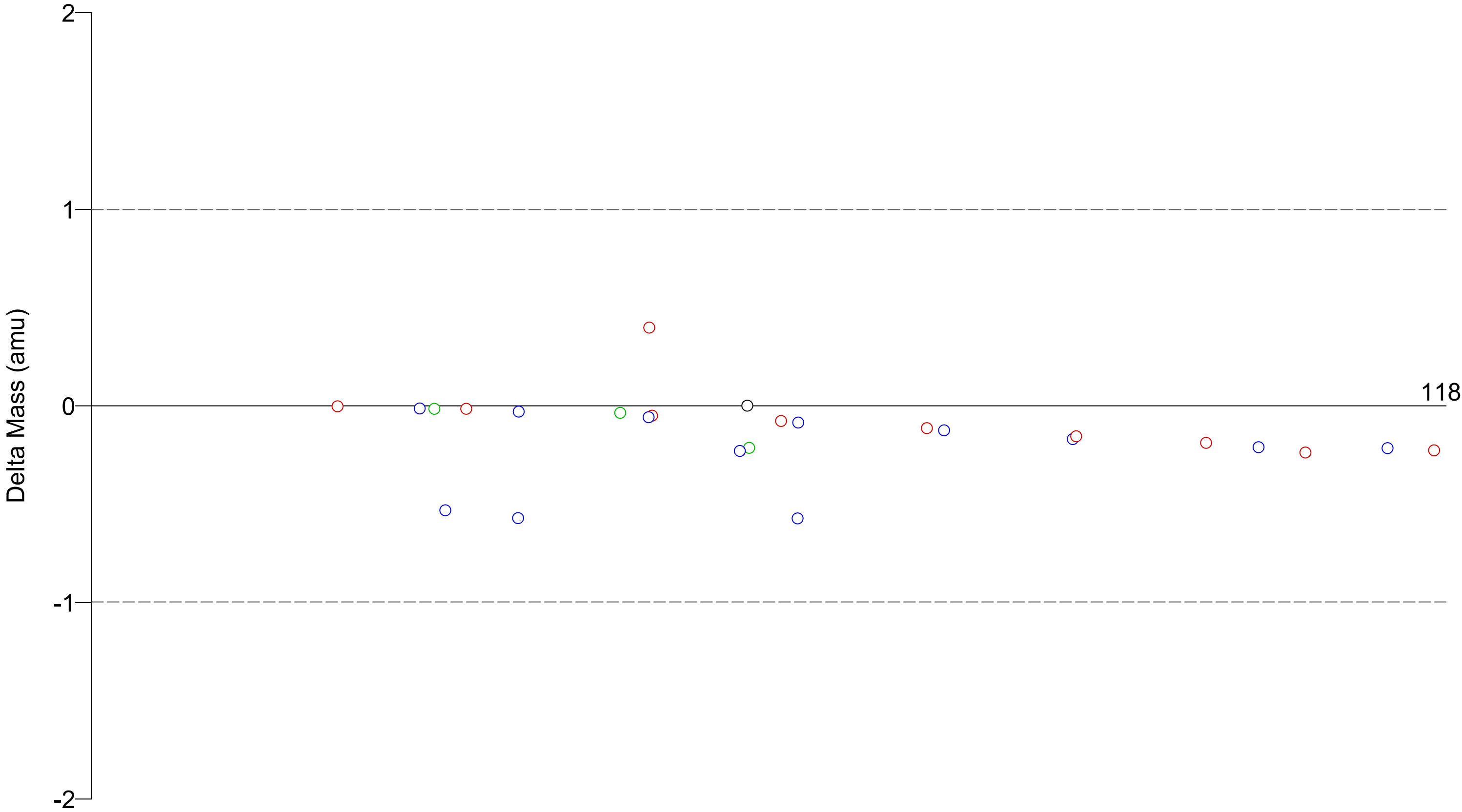
IPI:IPI00748665.3|TREMBL:A2J1N3;Q0                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                       1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

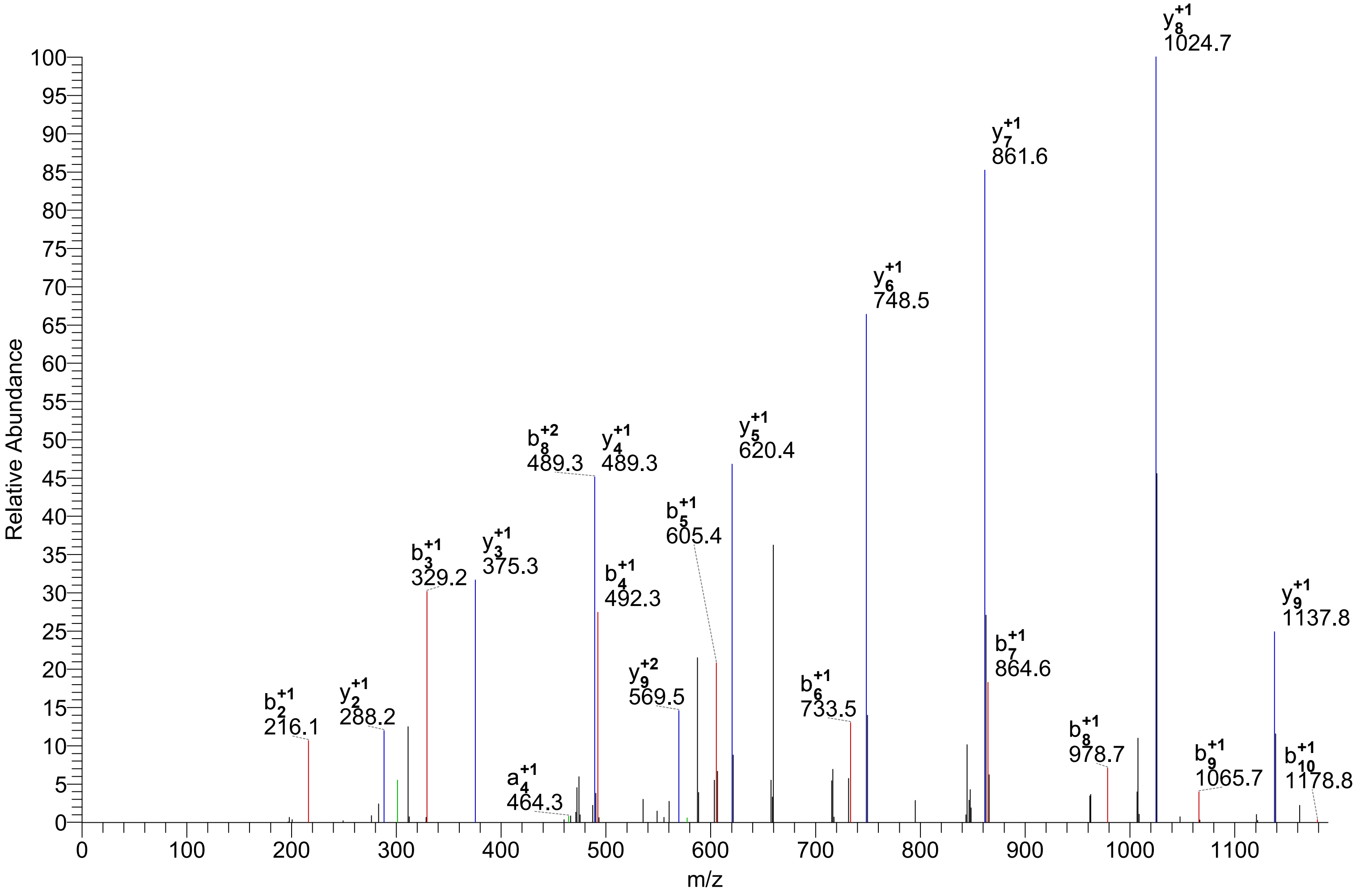
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions     Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10    216.10                                      1238.66
 L    301.19    329.18                                      1137.61
 Y    464.25    492.25                                      1024.52
 L    577.33    605.33                                       861.46
 Q    705.39    733.39                                       748.38
 M    836.43    864.43                                       620.32
 N    950.48    978.47                                       489.28
 S   1037.51   1065.50                                       375.24
 L   1150.59   1178.59                                       288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



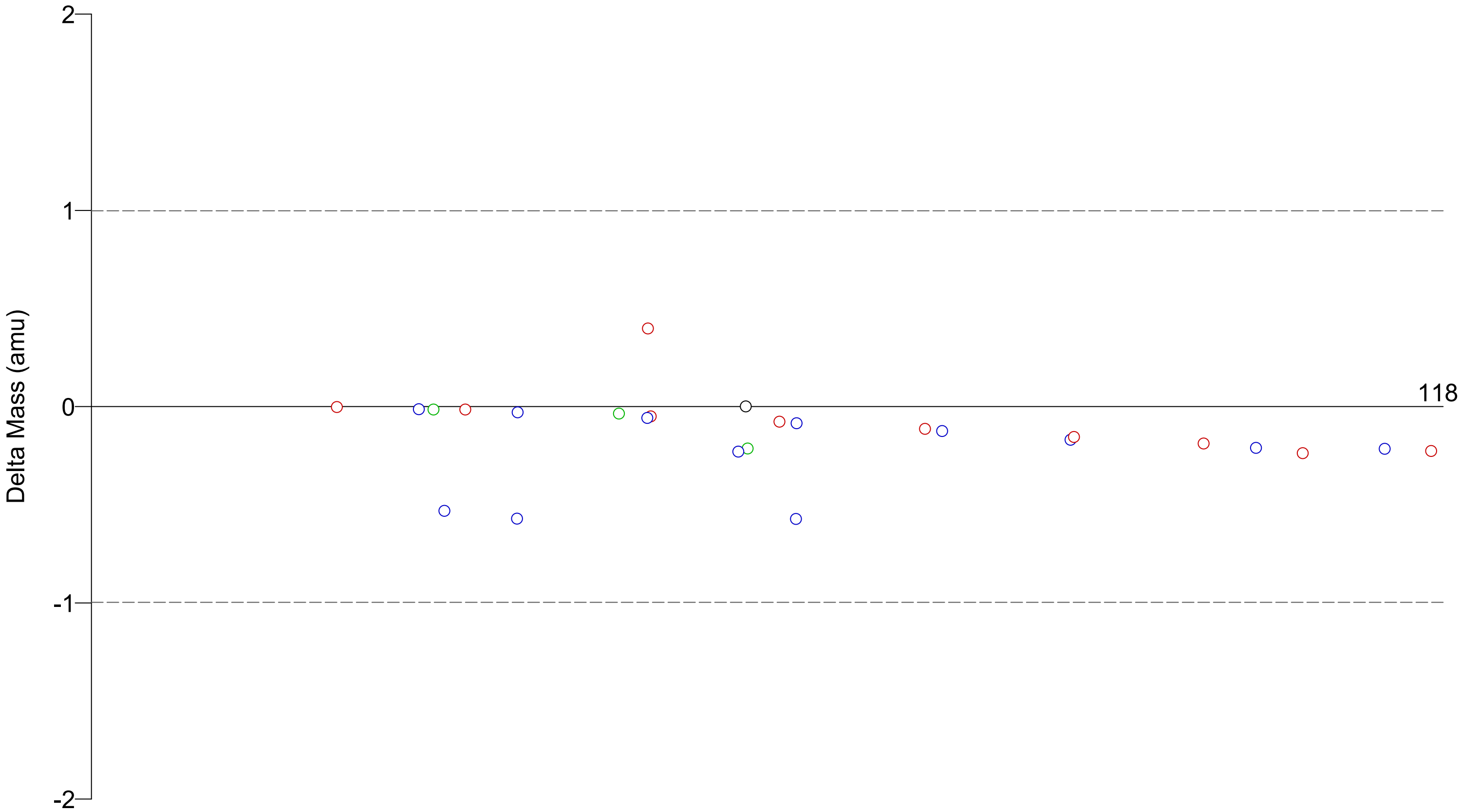
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                 МH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00748998.1|TREMBL:Q65ZC9 Ta                               3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39
```

1 of 1 peptide matches reported, 0 removed due to filtering

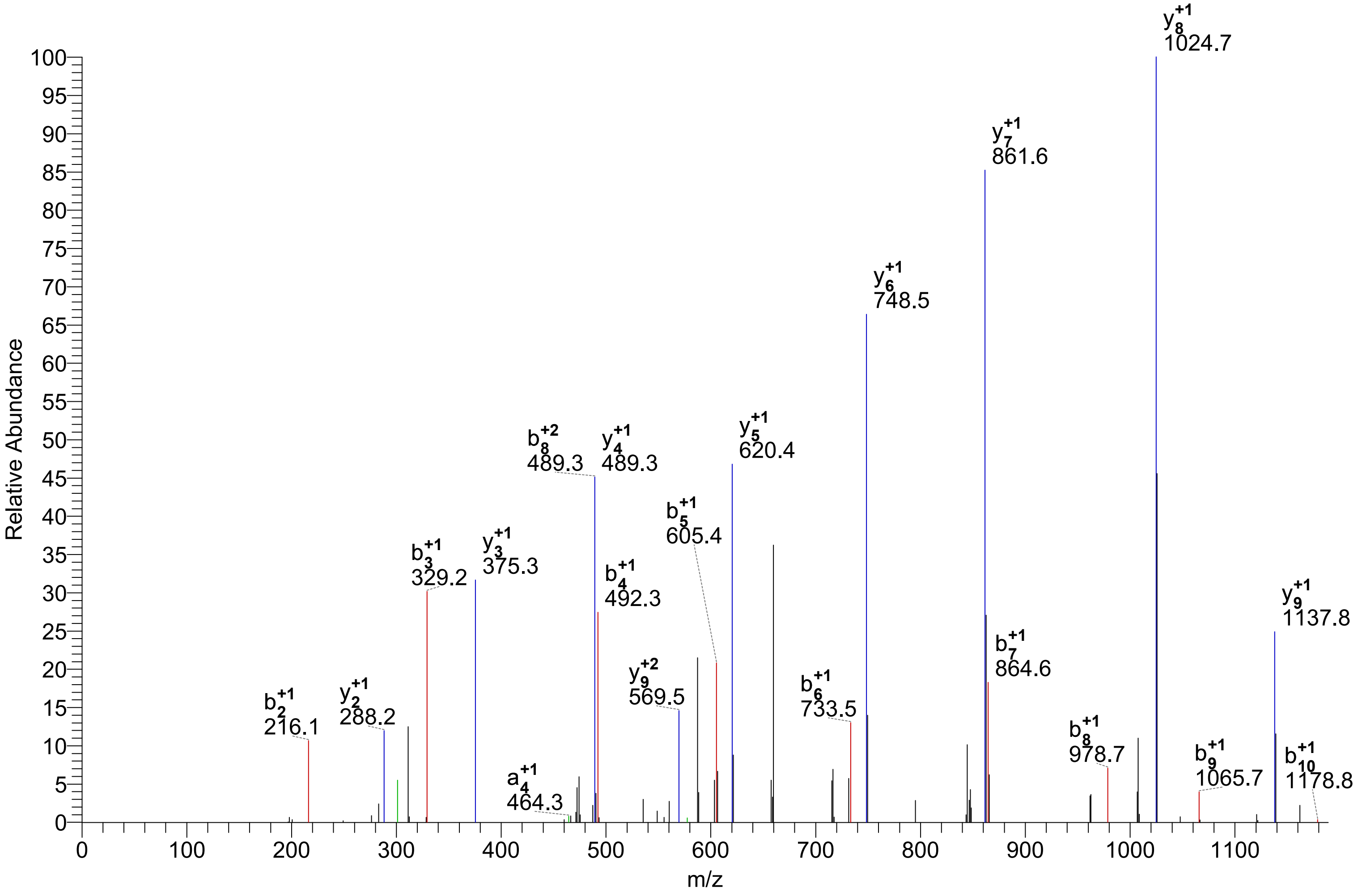
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
--------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00760721.3|ENSEMBL:ENSP0000                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```
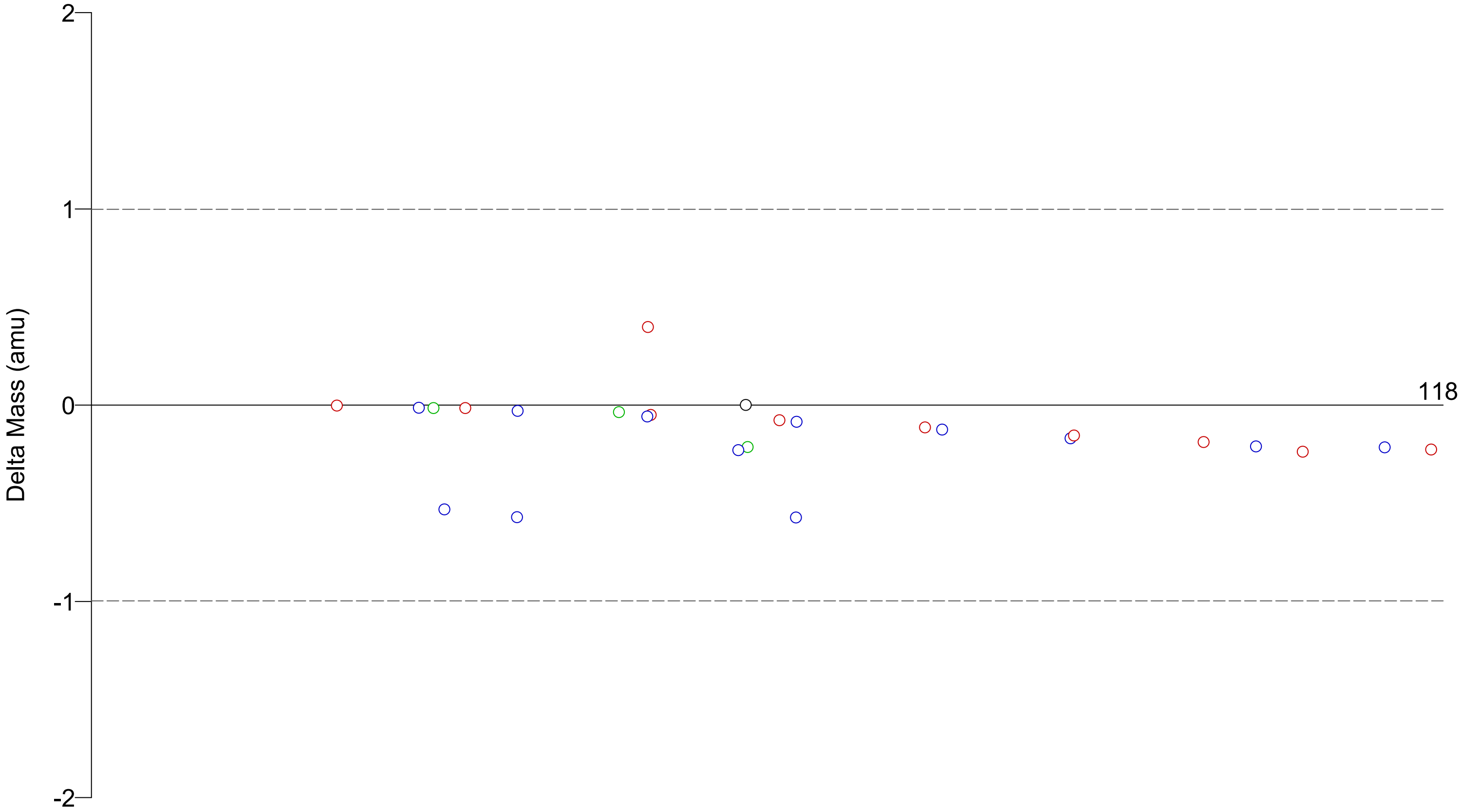
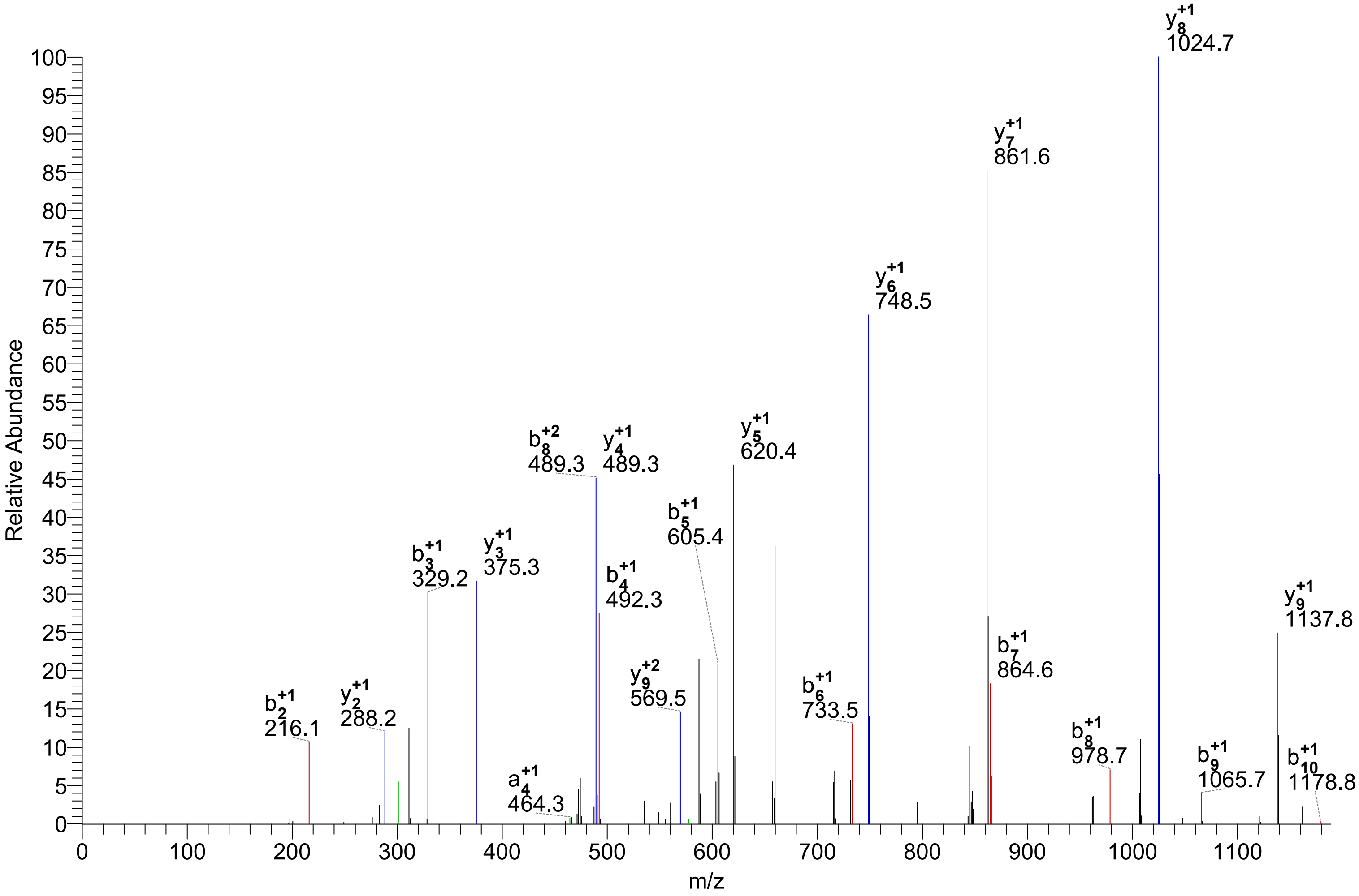

```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



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Reference                                                                 P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

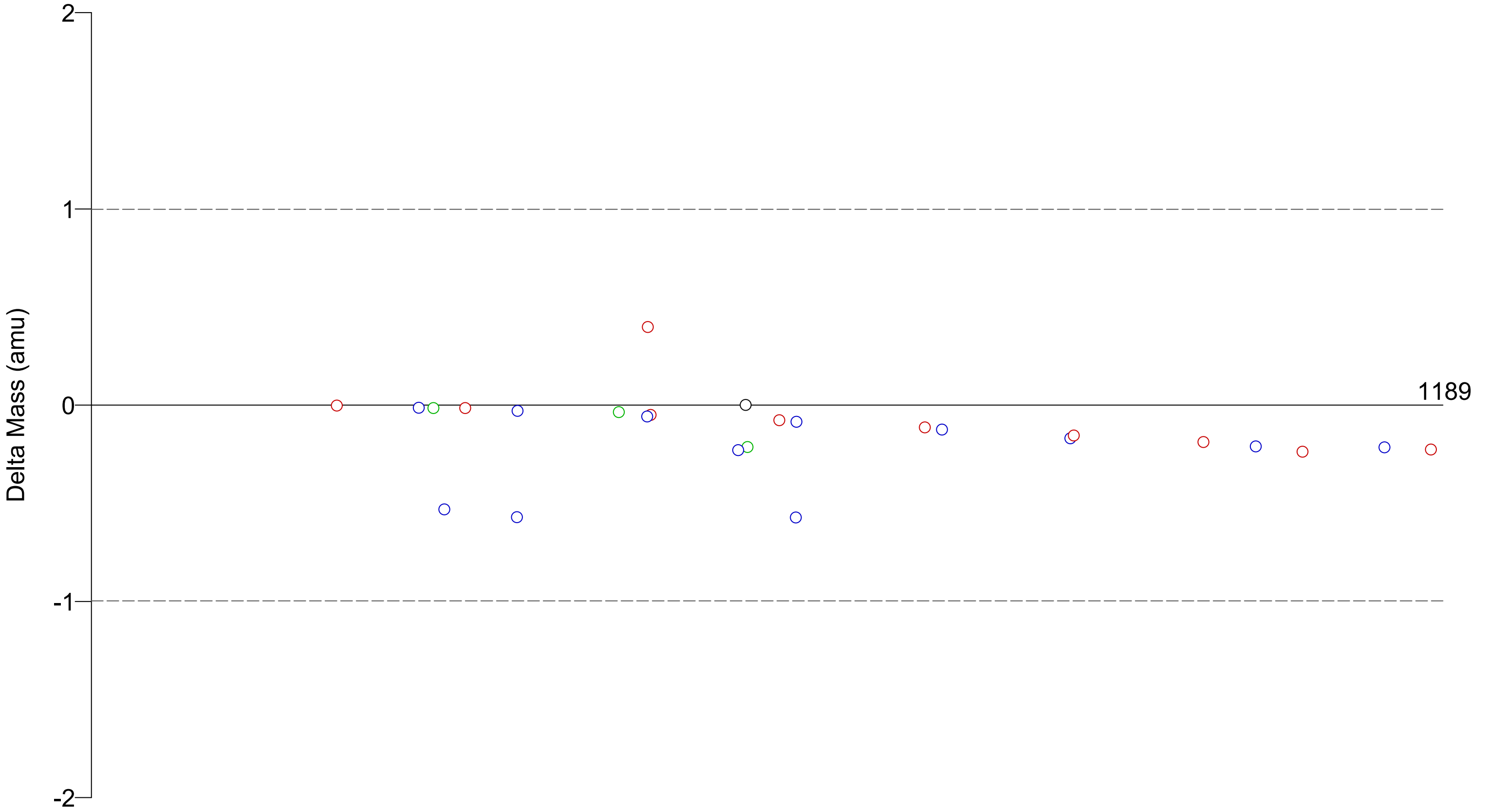
IPI:IPI00783094.1|TREMBL:Q0ZCG4;Q0                                     3e-006  10.2     0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                              1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

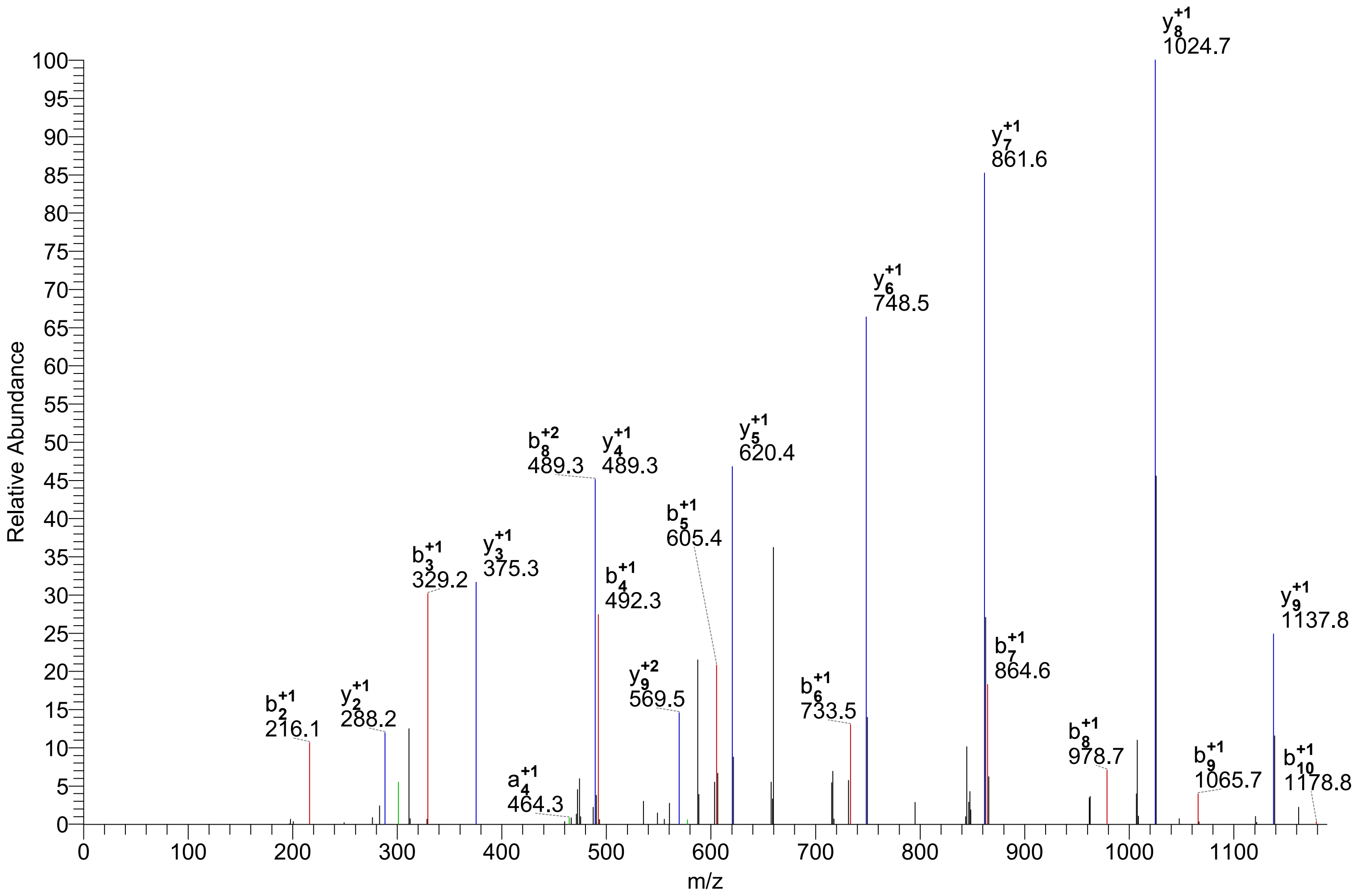
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions     Y ions     Y* ions     Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



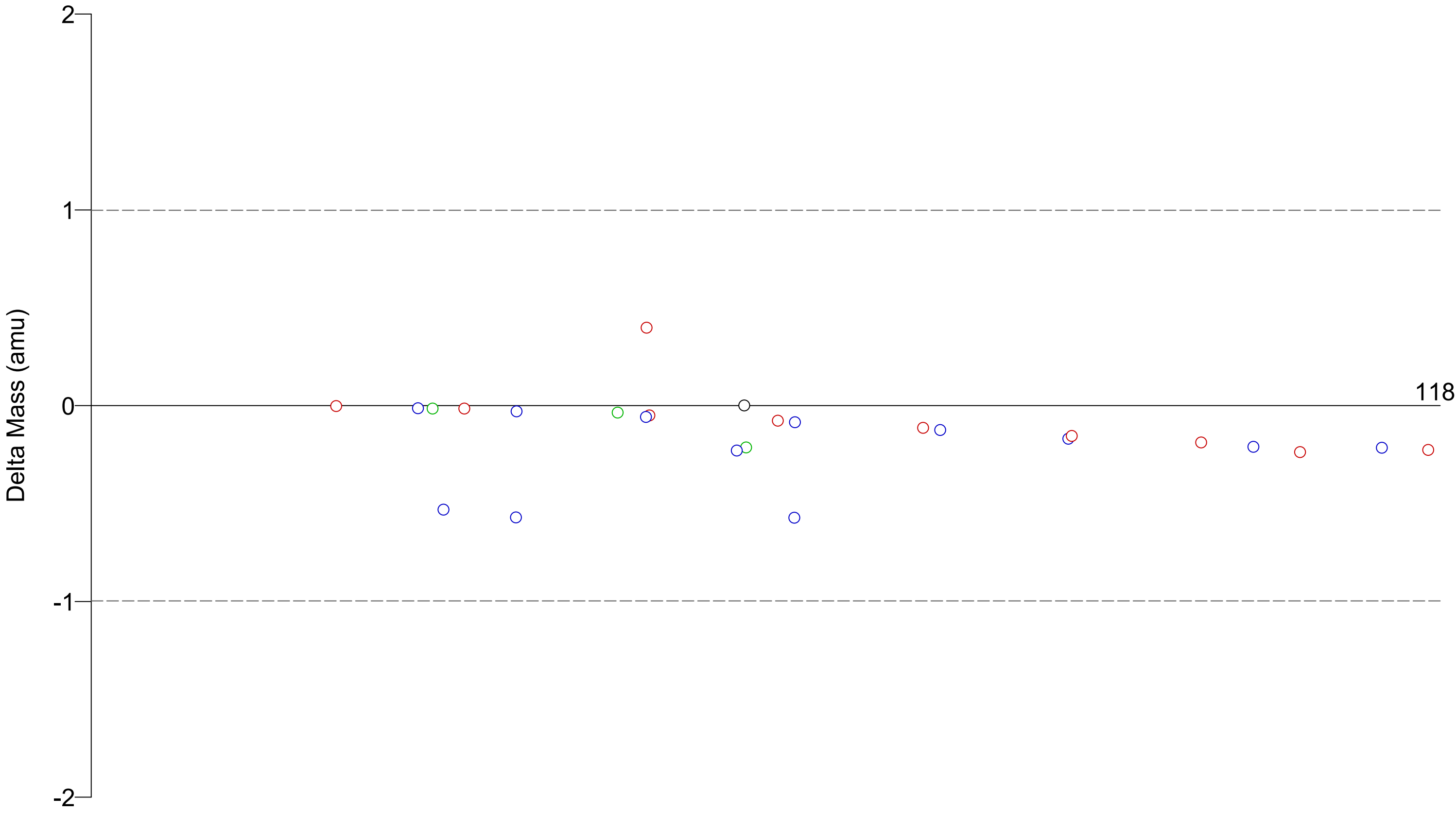
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00783116.1|TREMBL:Q0ZCI5 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

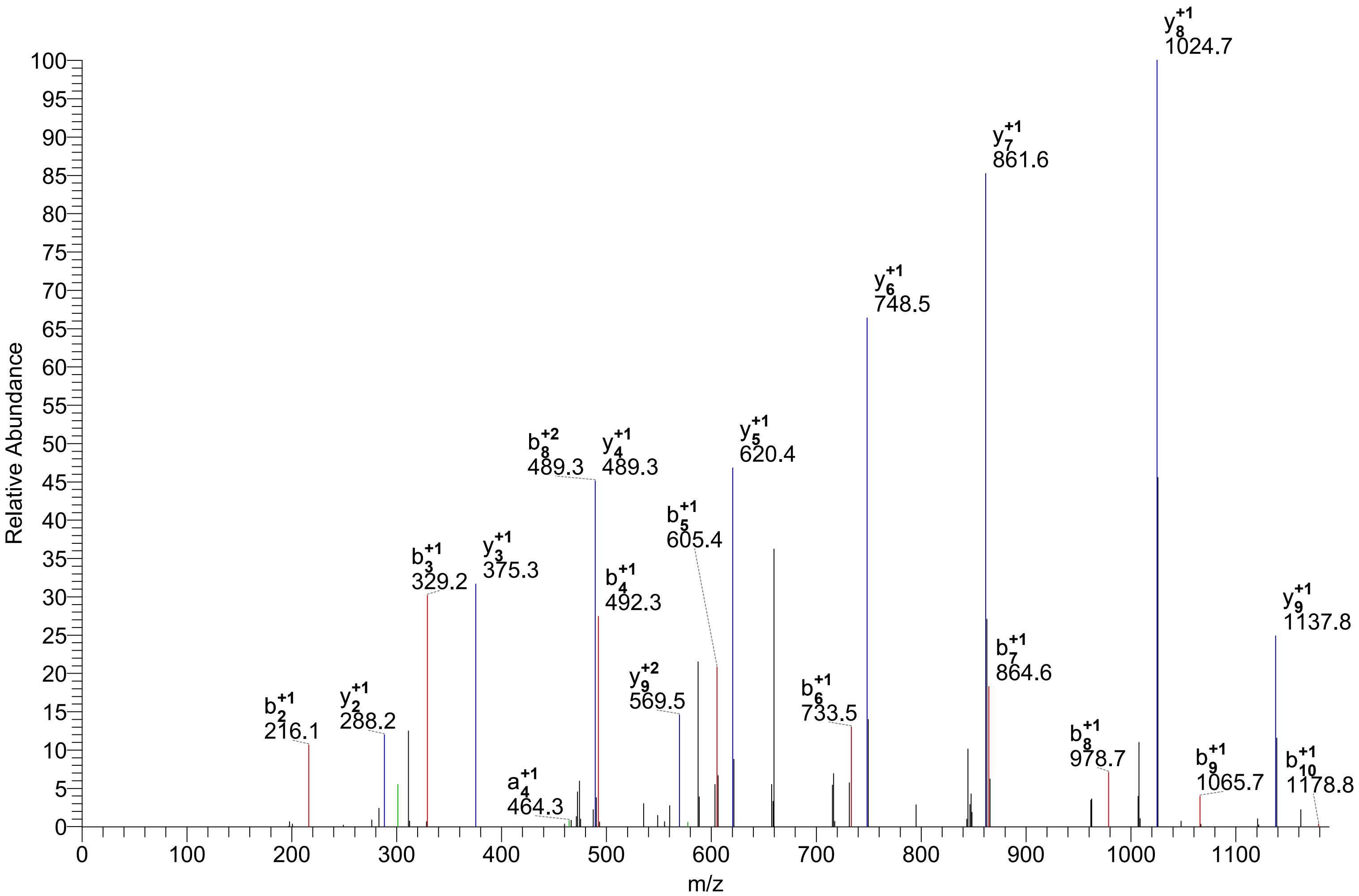
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



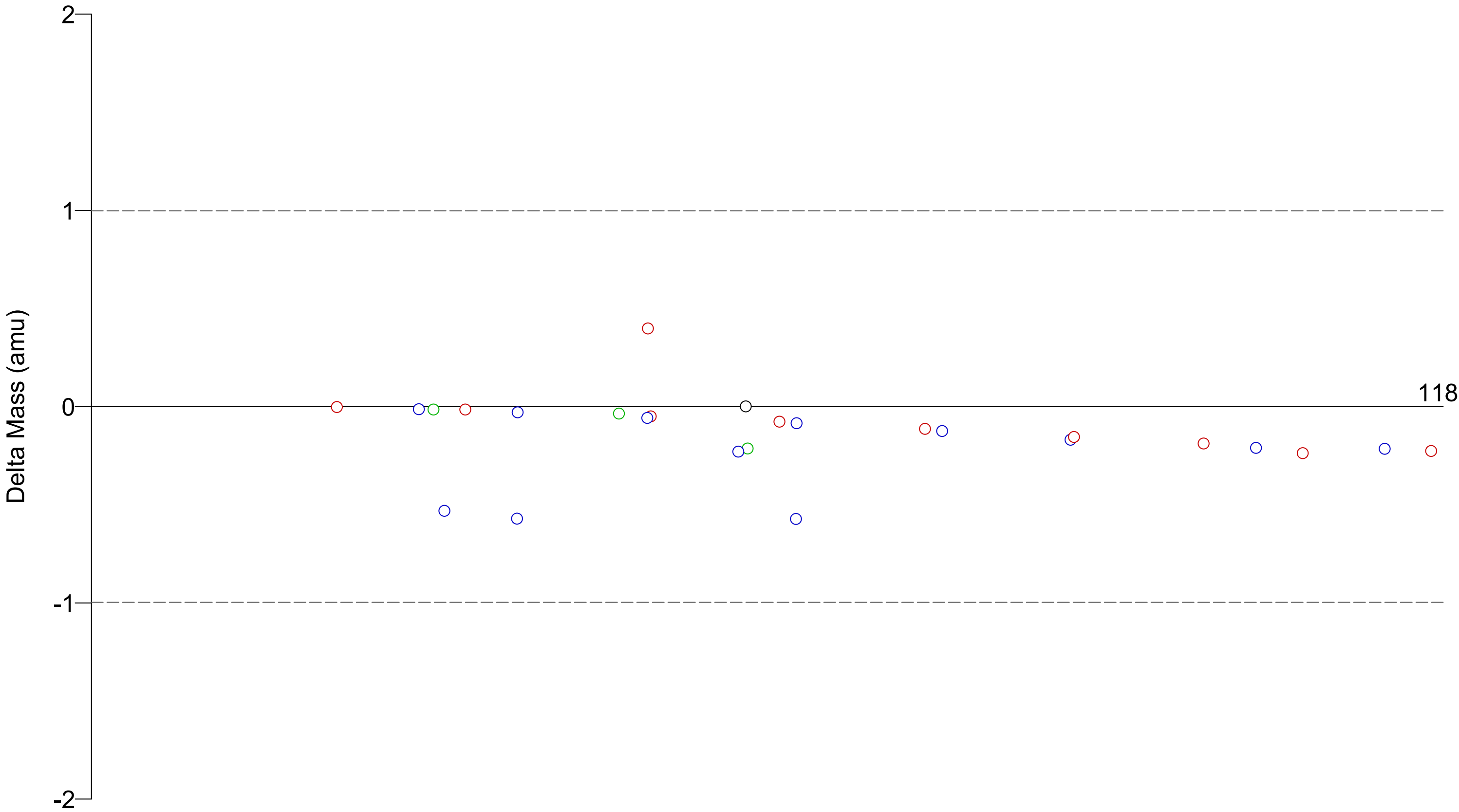
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                the  MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00783244.1|TREMBL:Q0ZCH1;Q0                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

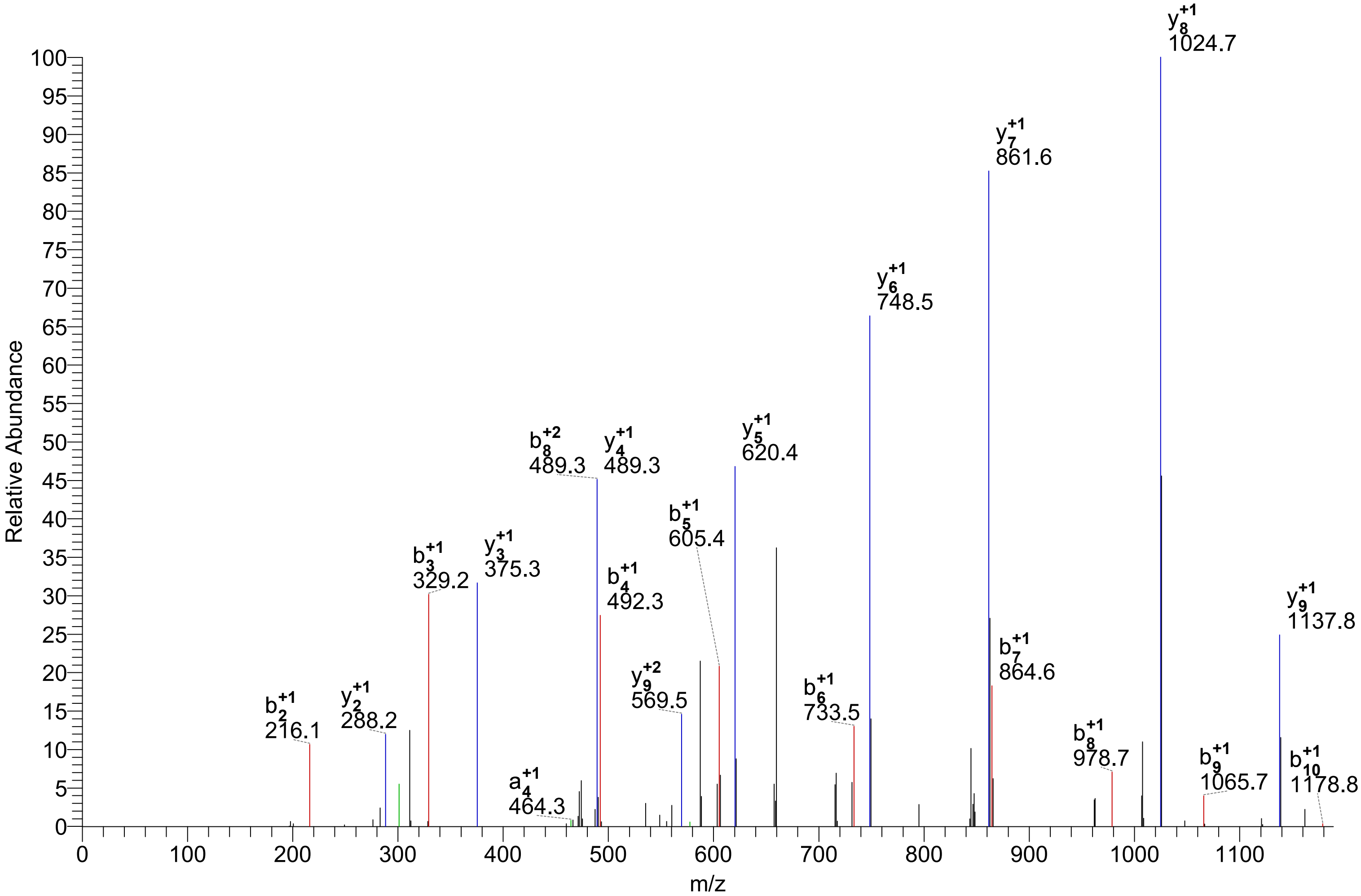
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



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Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00783393.1|TREMBL:Q0ZCI2 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```
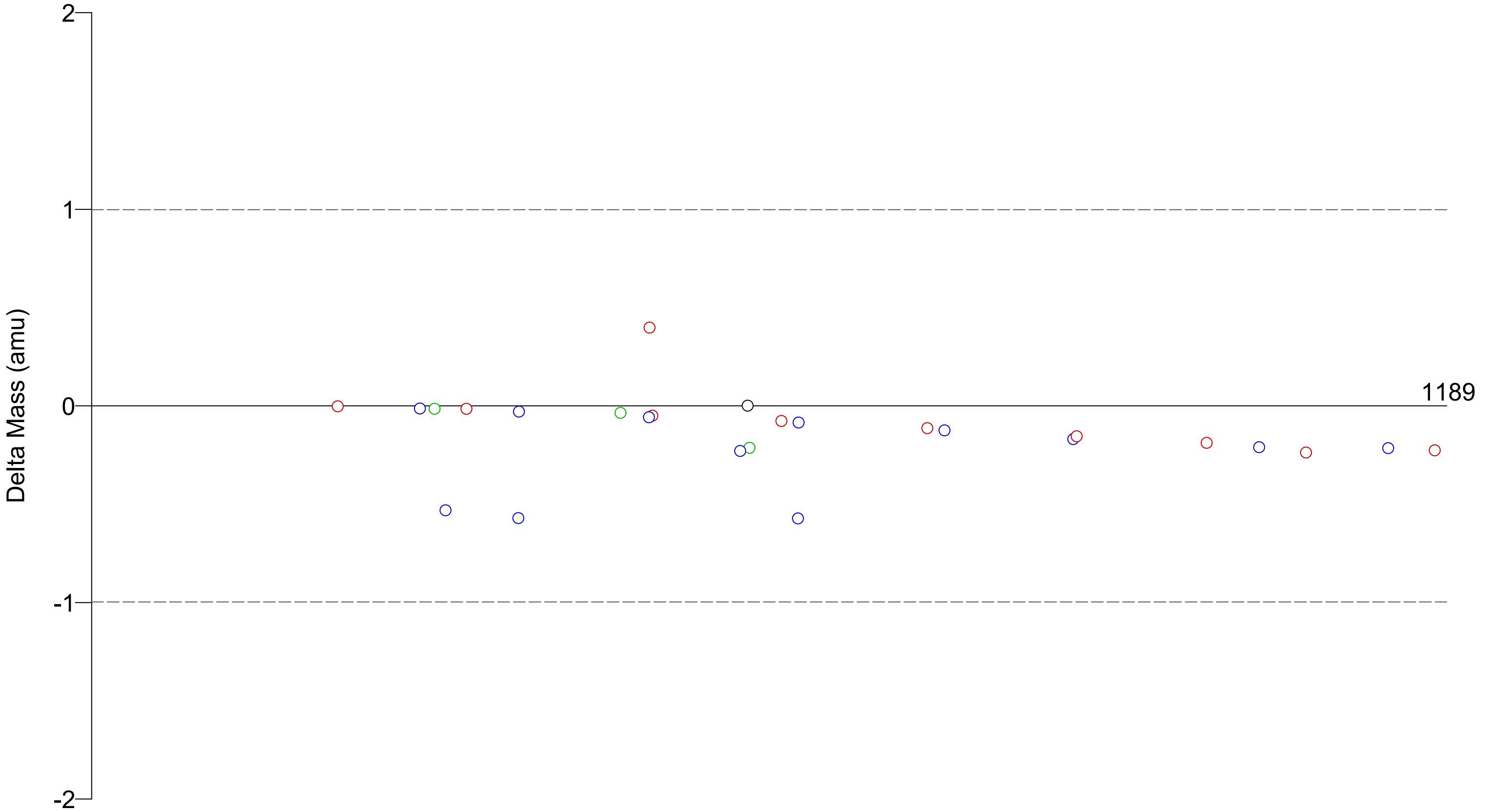
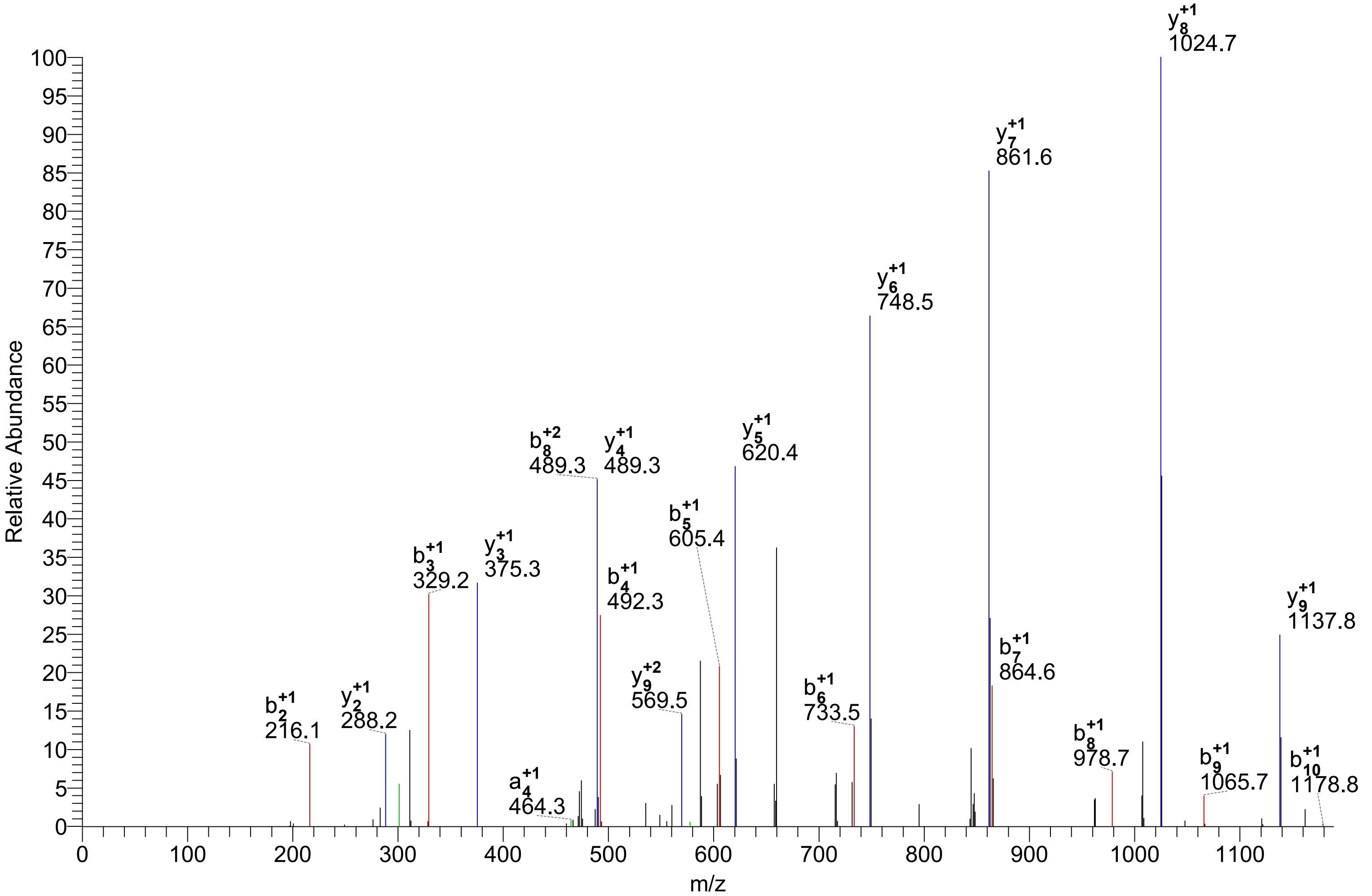

```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



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Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z   P        XC  DeltaCn    Sp   RSp  Ions  Count

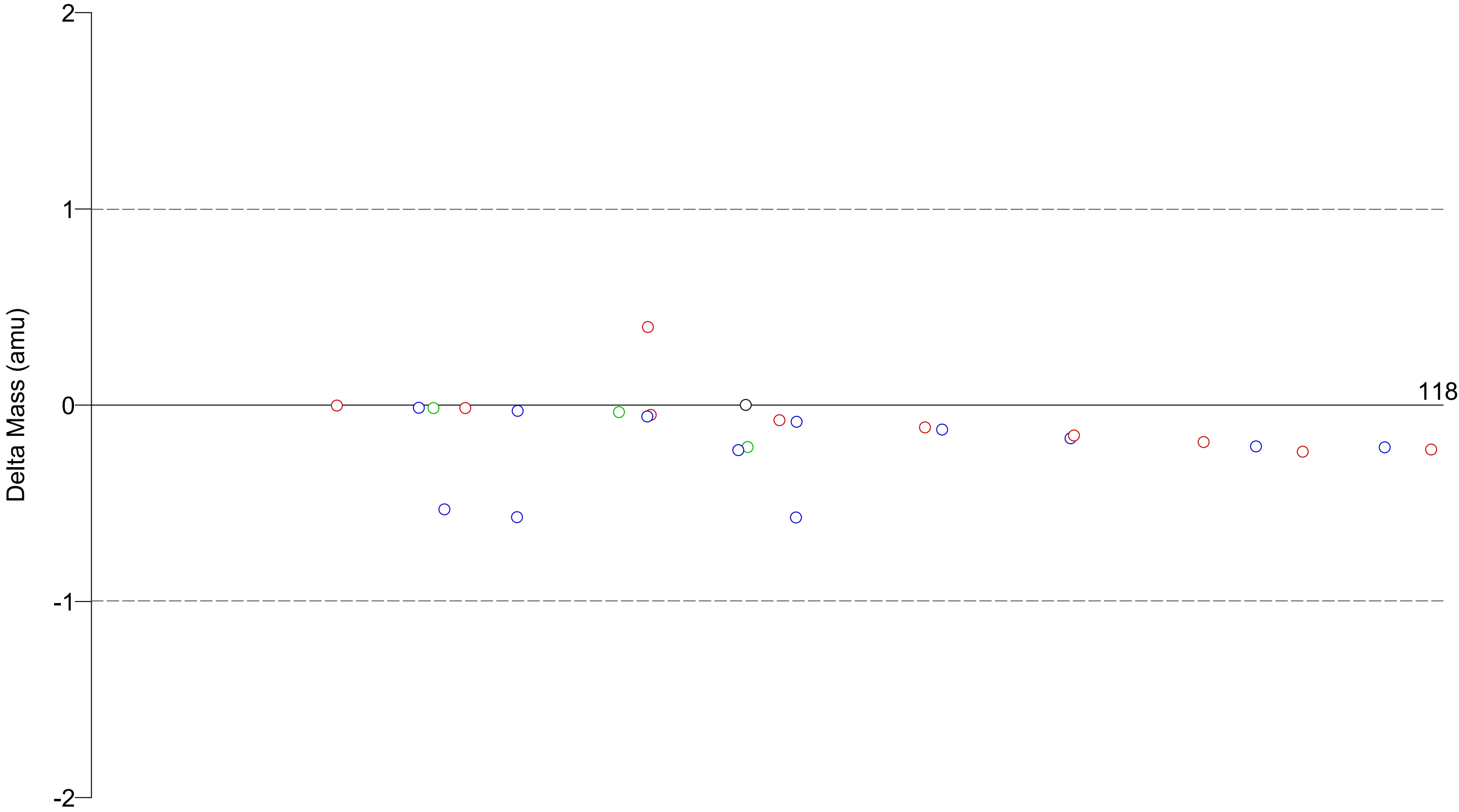
IPI:IPI00783818.1|TREMBL:Q0ZCJ1 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                       1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

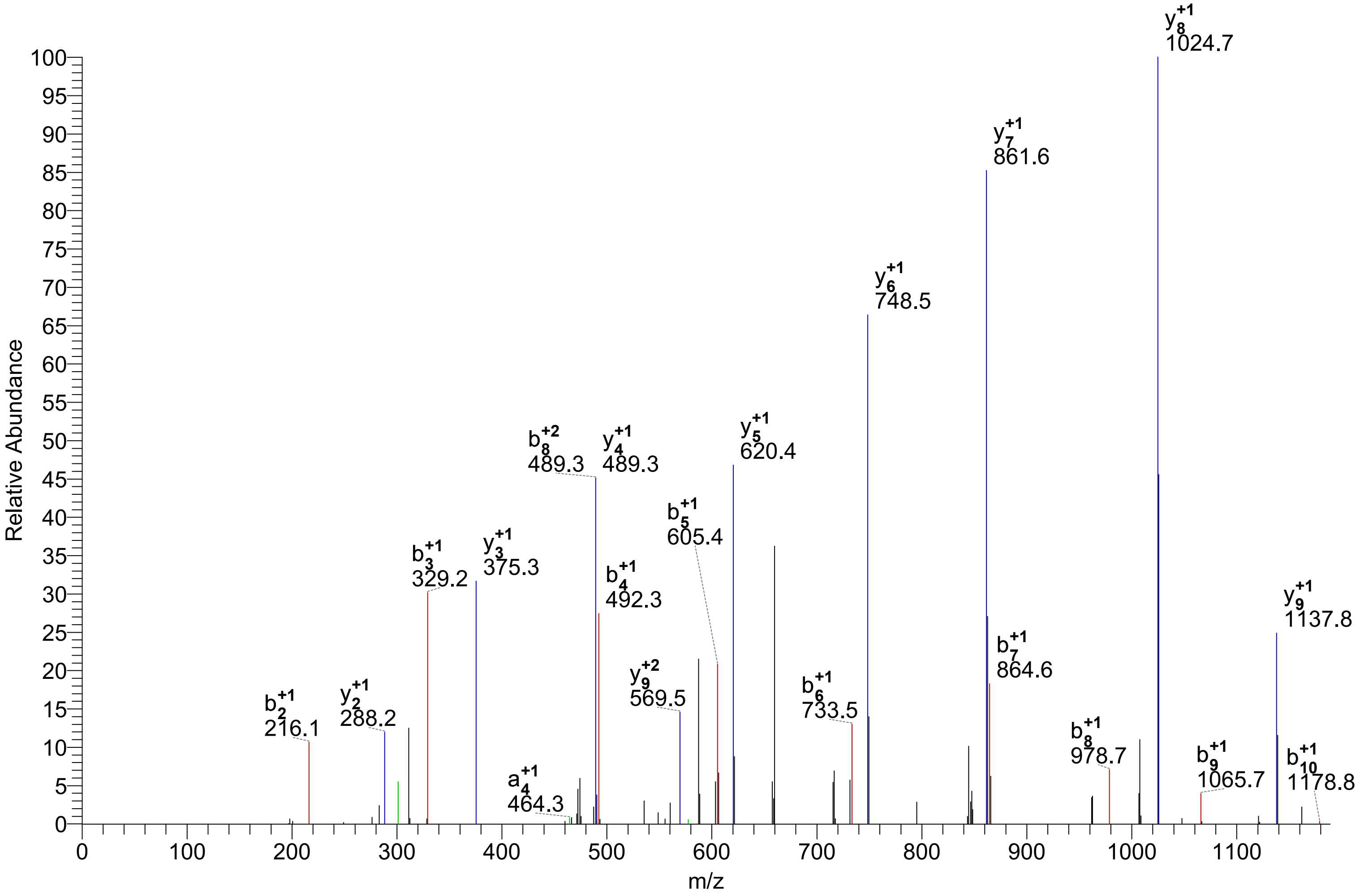
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn   Sp    RSp  Ions  Count

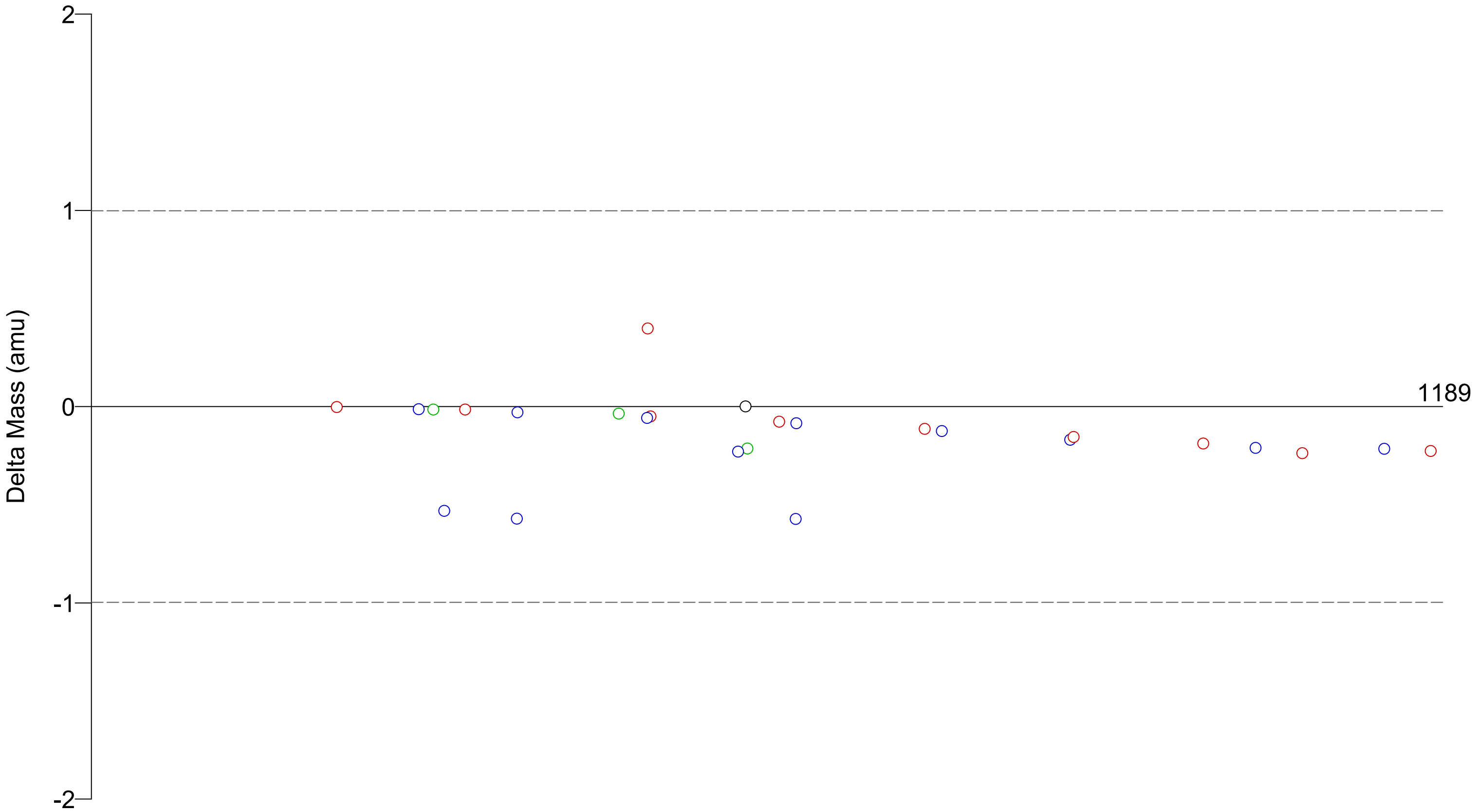
IPI:IPI00783909.1|TREMBL:Q0ZCH0 Ta                                        3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                            1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

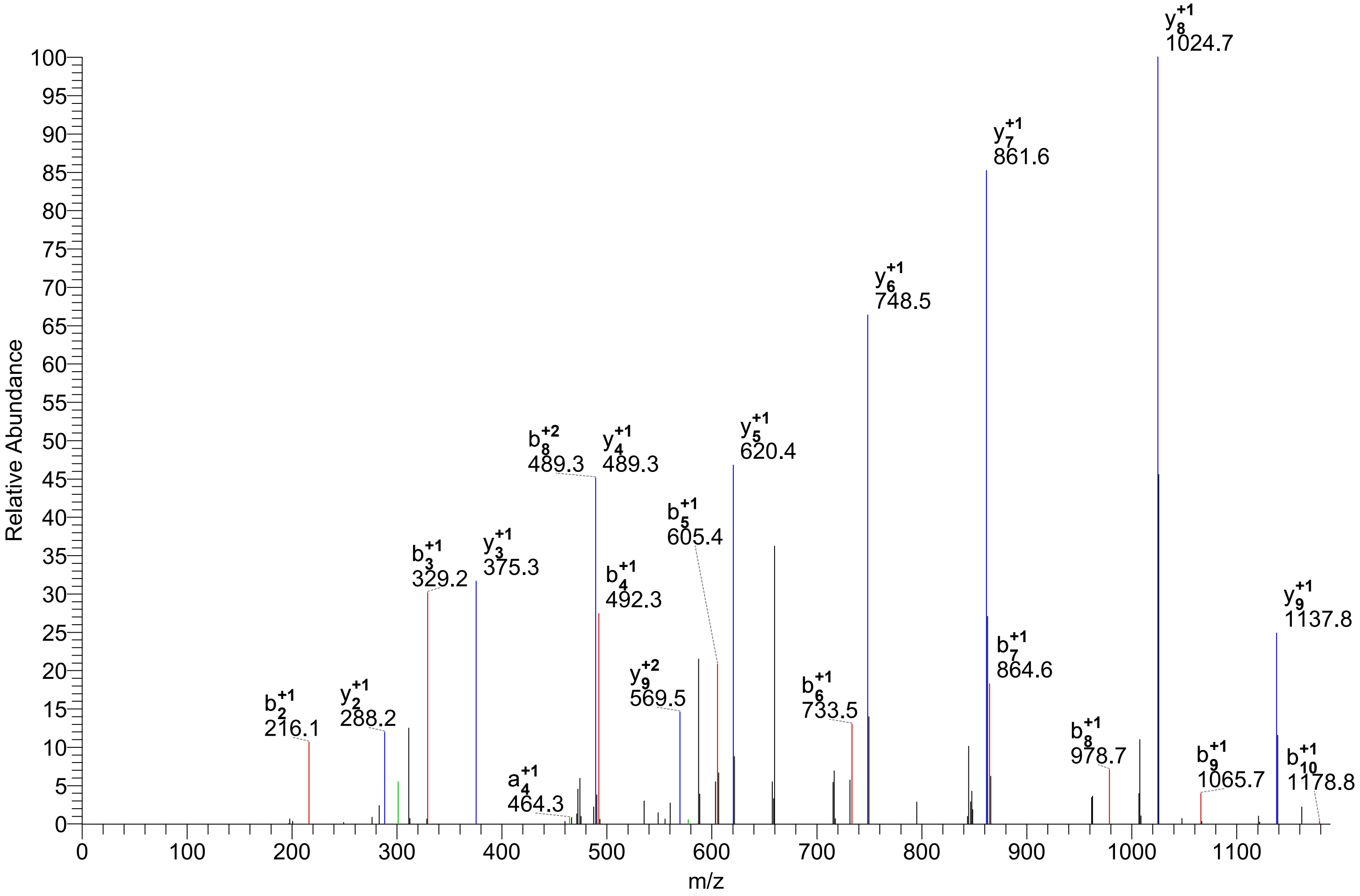
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                     P      Score   Coverage   Accession
Scan(s)       Sequence                          MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

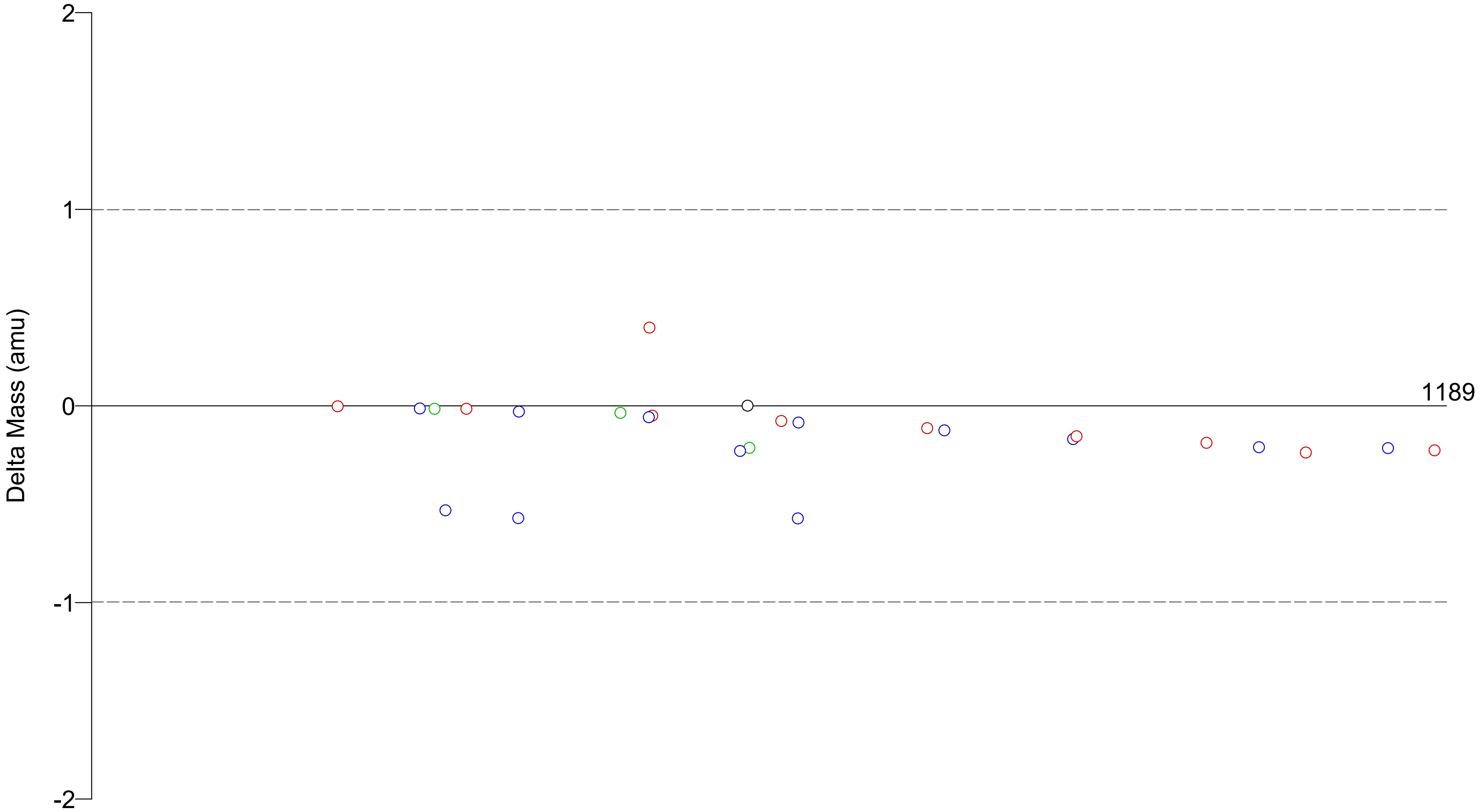
IPI:IPI00784513.1|TREMBL:Q0ZCI3 Ta                              3e-006  10.2     0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                  1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

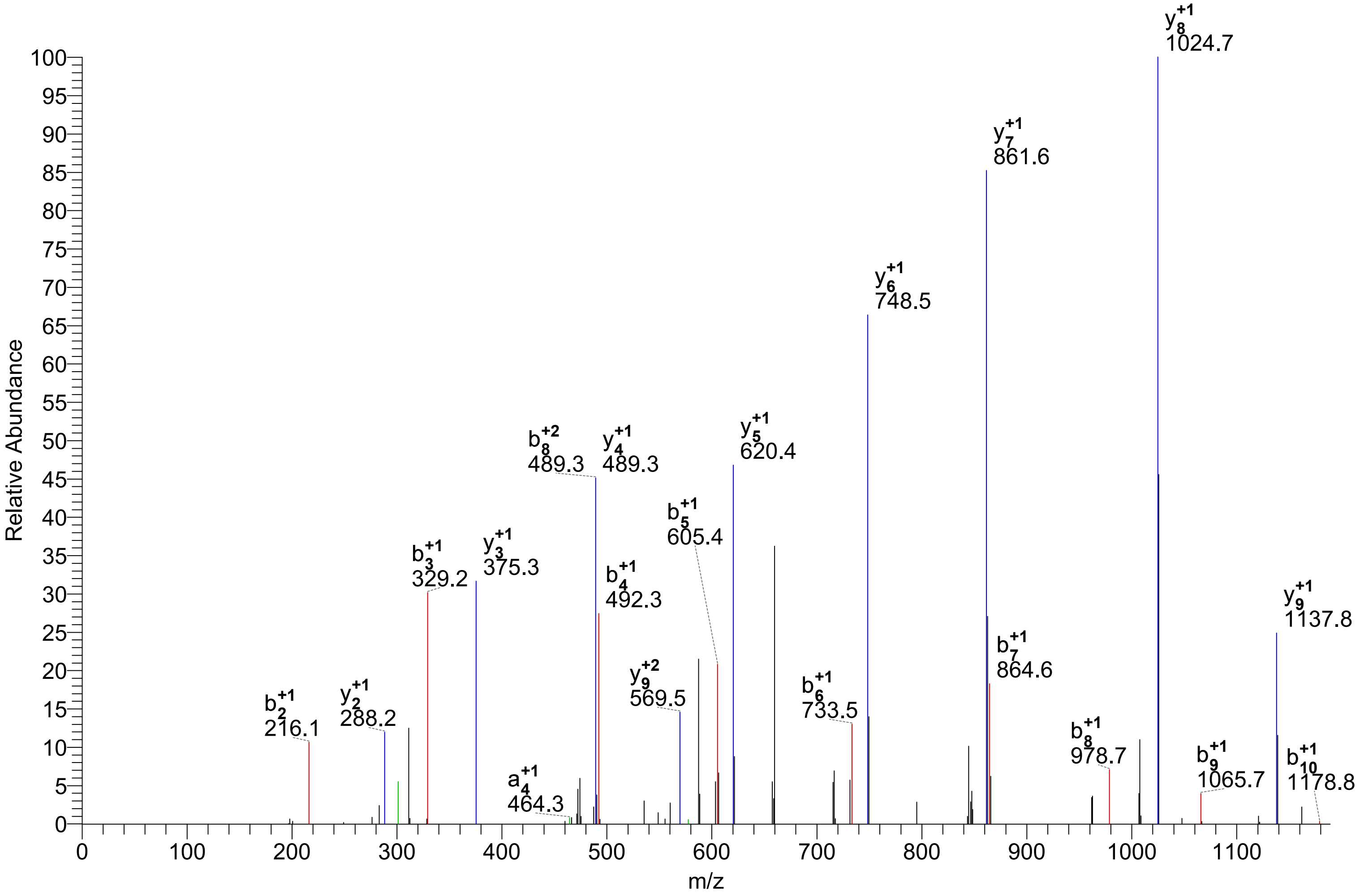
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

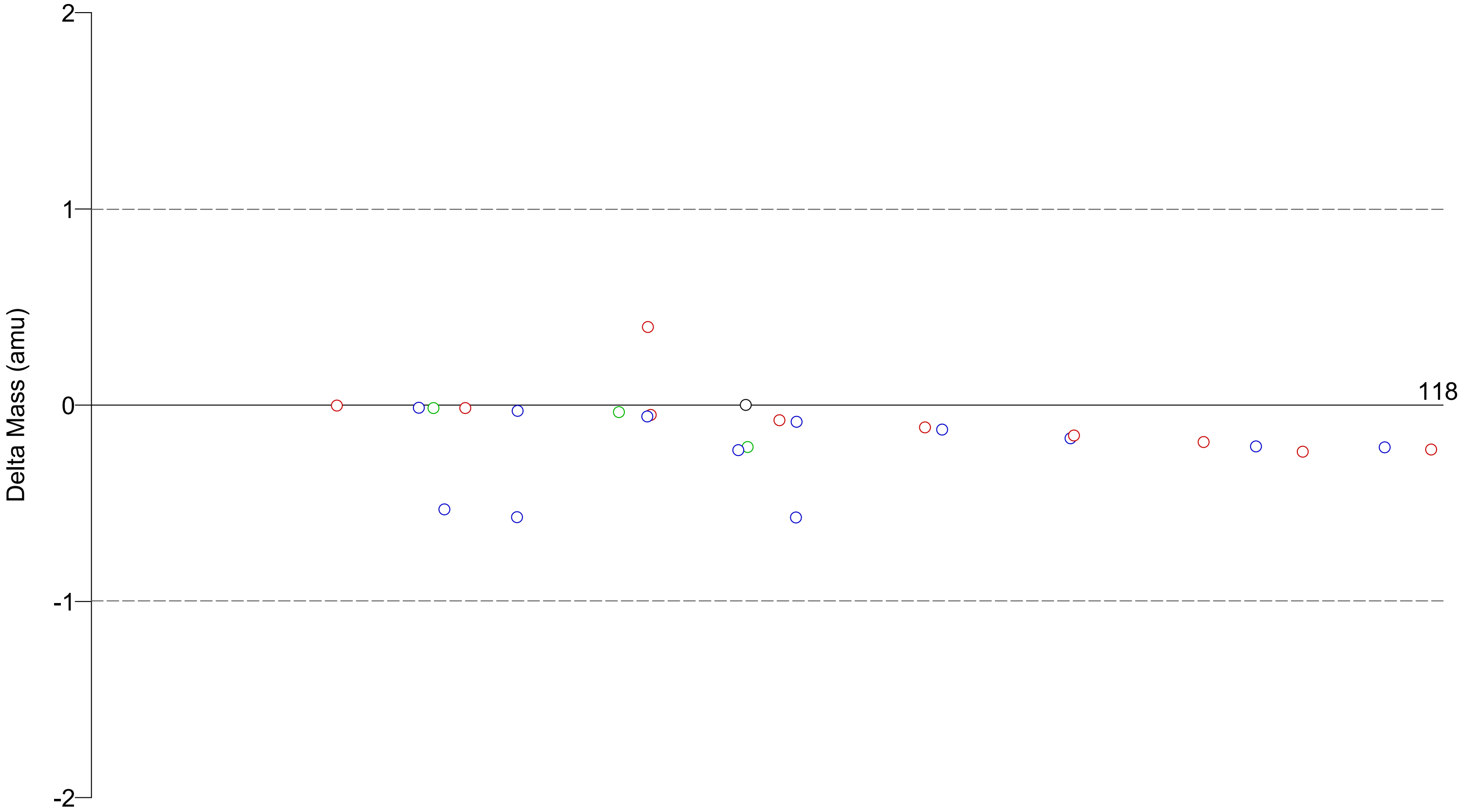
IPI:IPI00827581.1|TREMBL:A2NZ55 Ta                                   3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                            1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

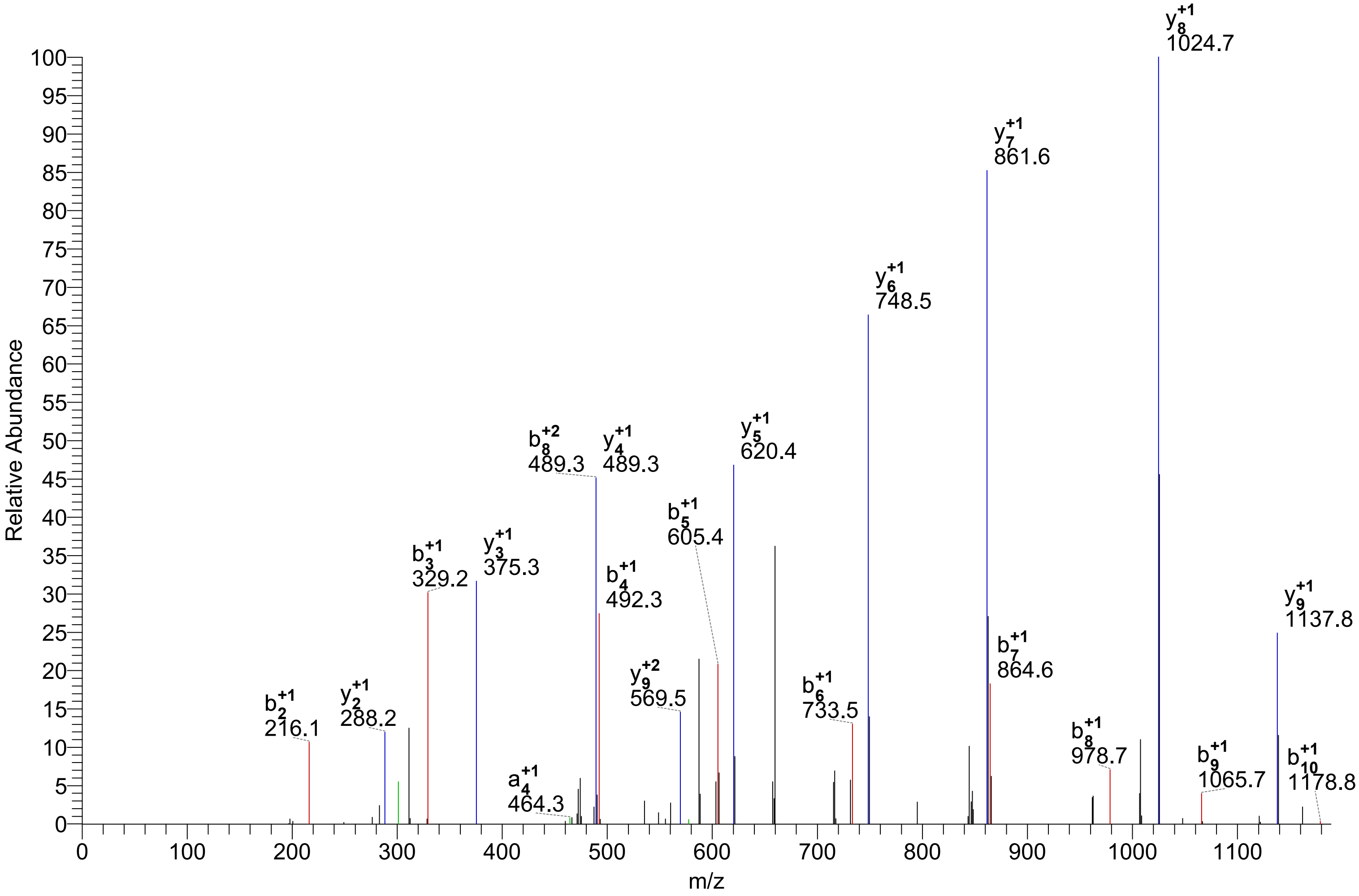
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



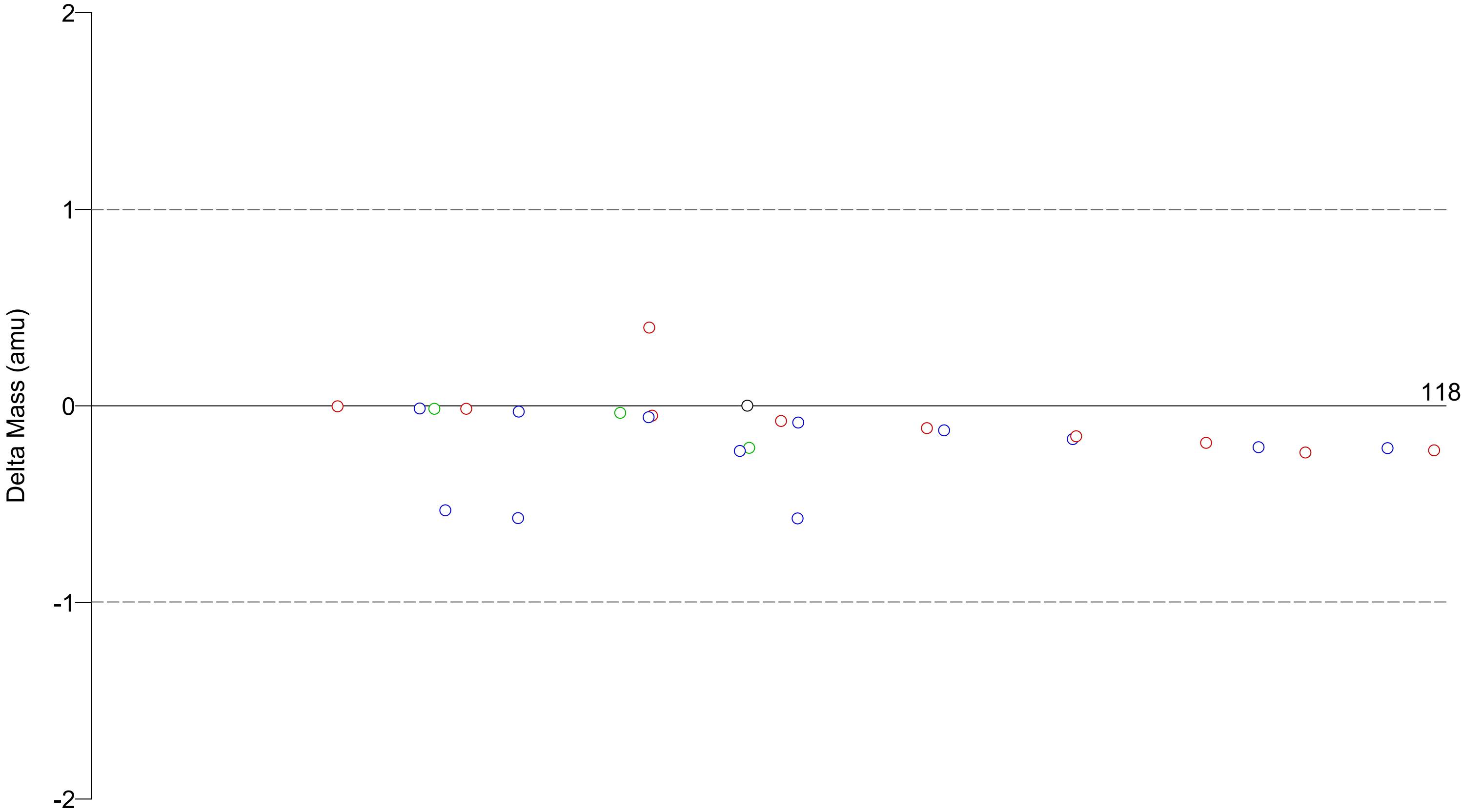
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00827589.1|TREMBL:A2NXP8 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

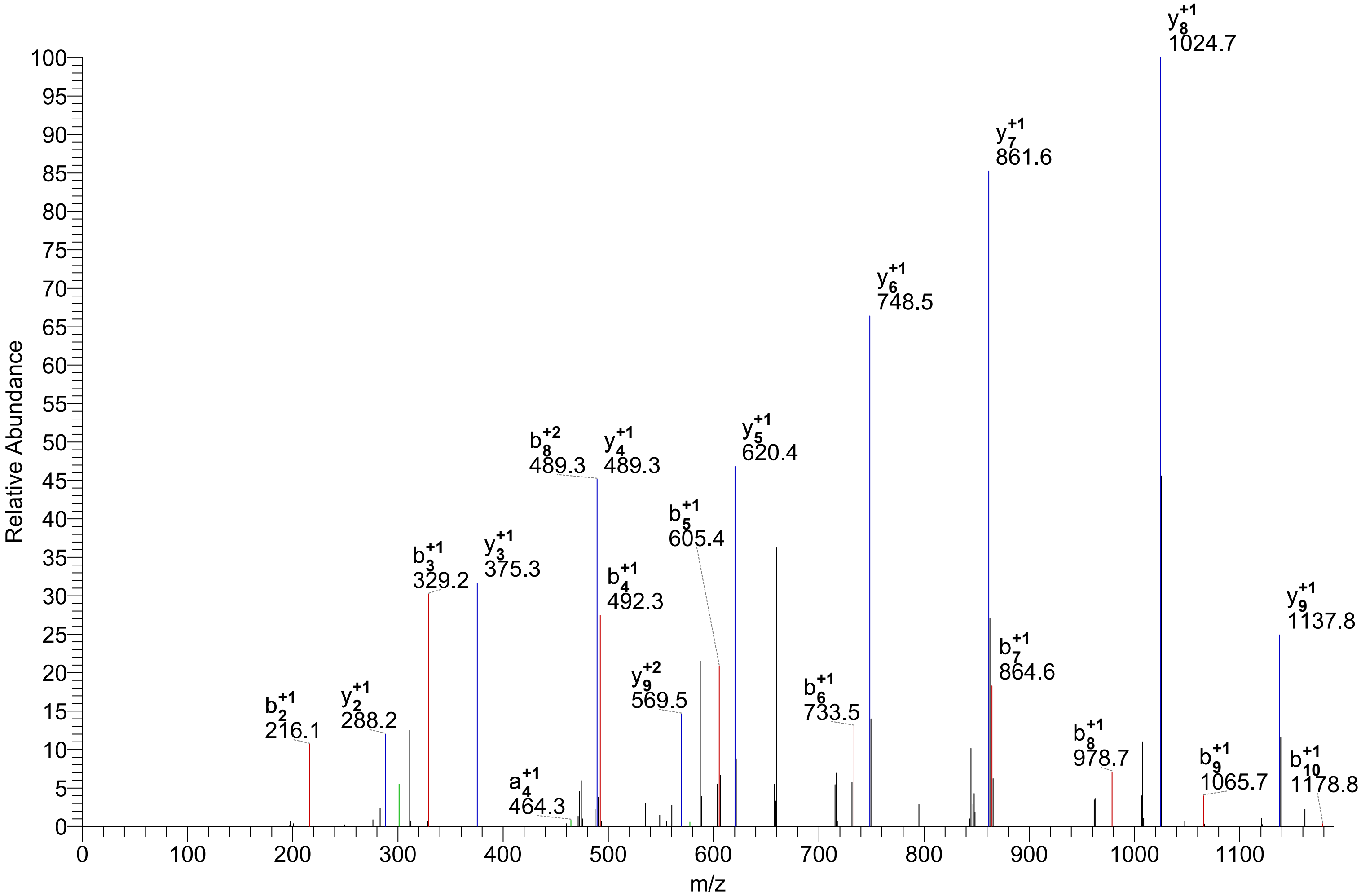
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



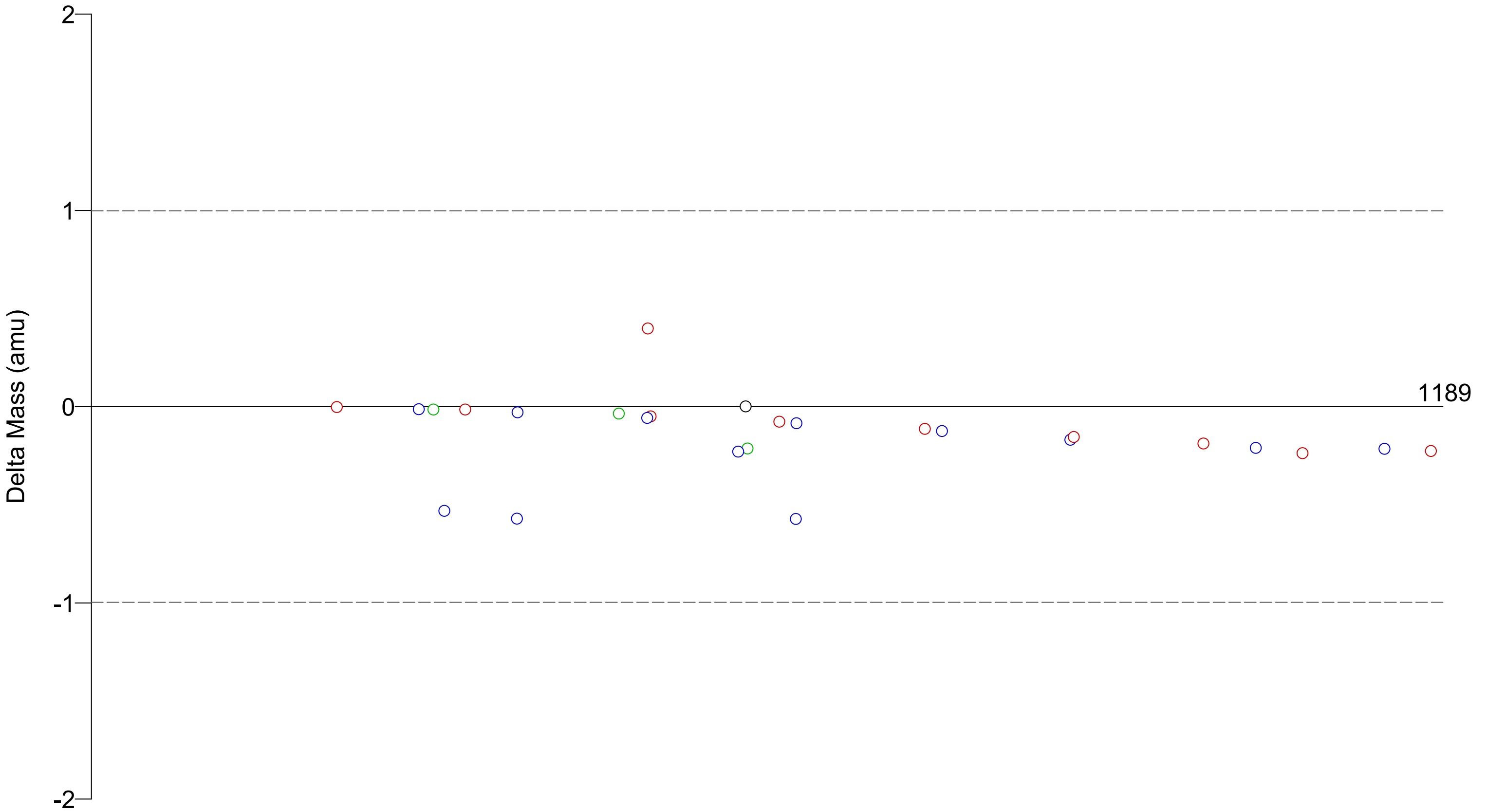
```
Reference                                                                P      Score   Coverage   Accession
Scan(s)        Sequence                                      MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00827678.1|TREMBL:A2NWX5 Ta                                         3e-006  10.2      0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                              1352.70    2  3e-006  4.027  0.643    1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

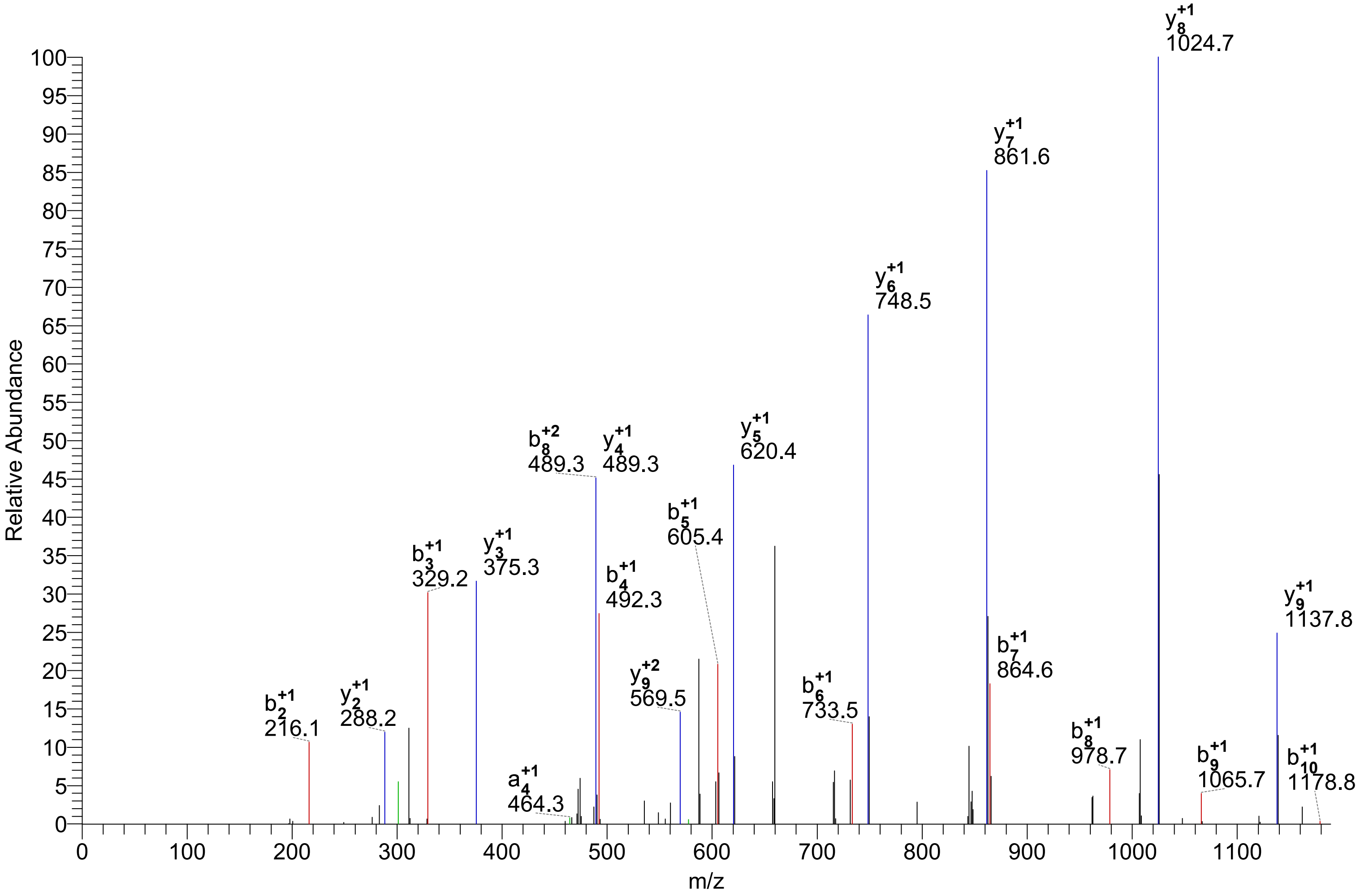
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



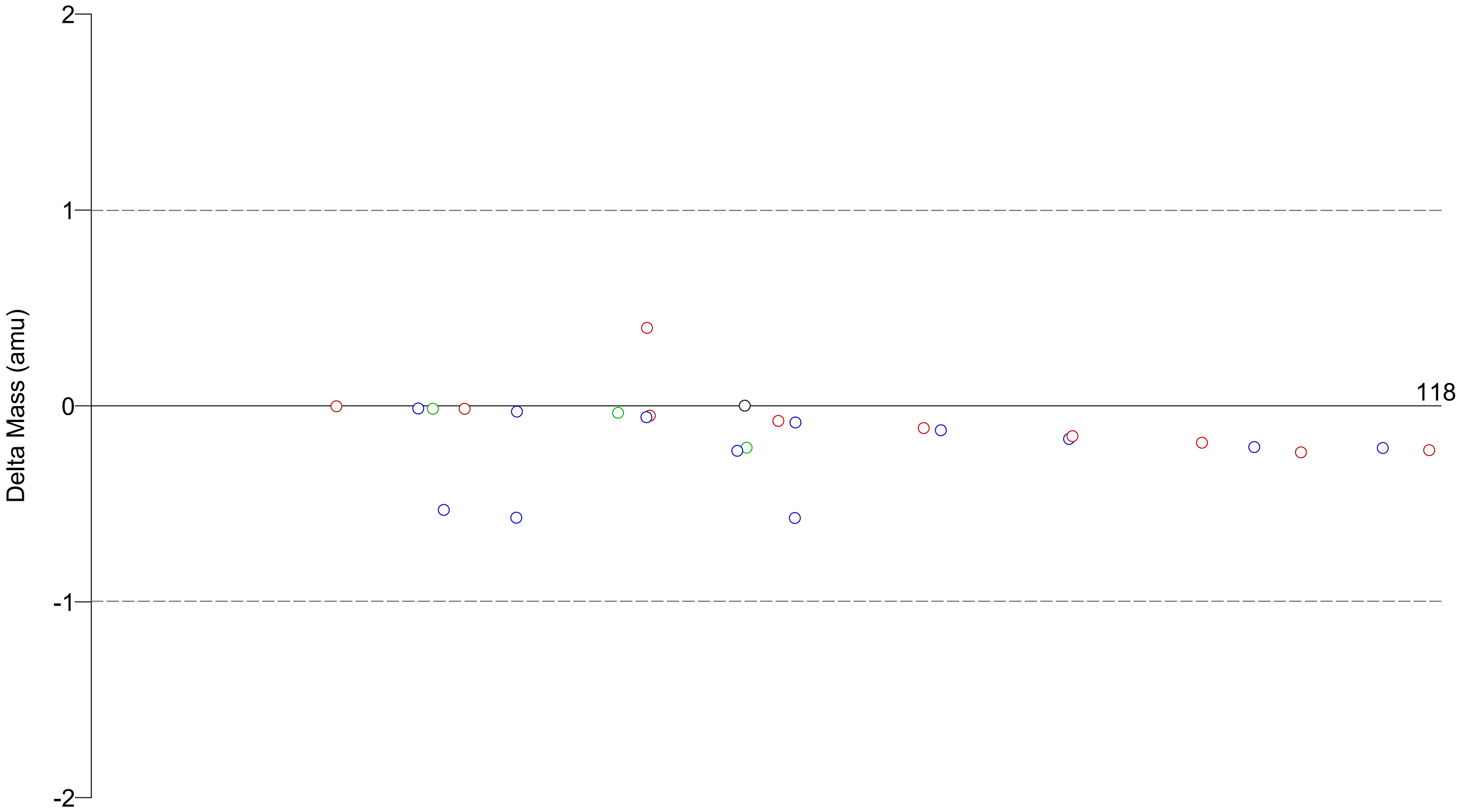
```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00827814.1|TREMBL:A2NWX1 Ta                                 3e-006  10.2      0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

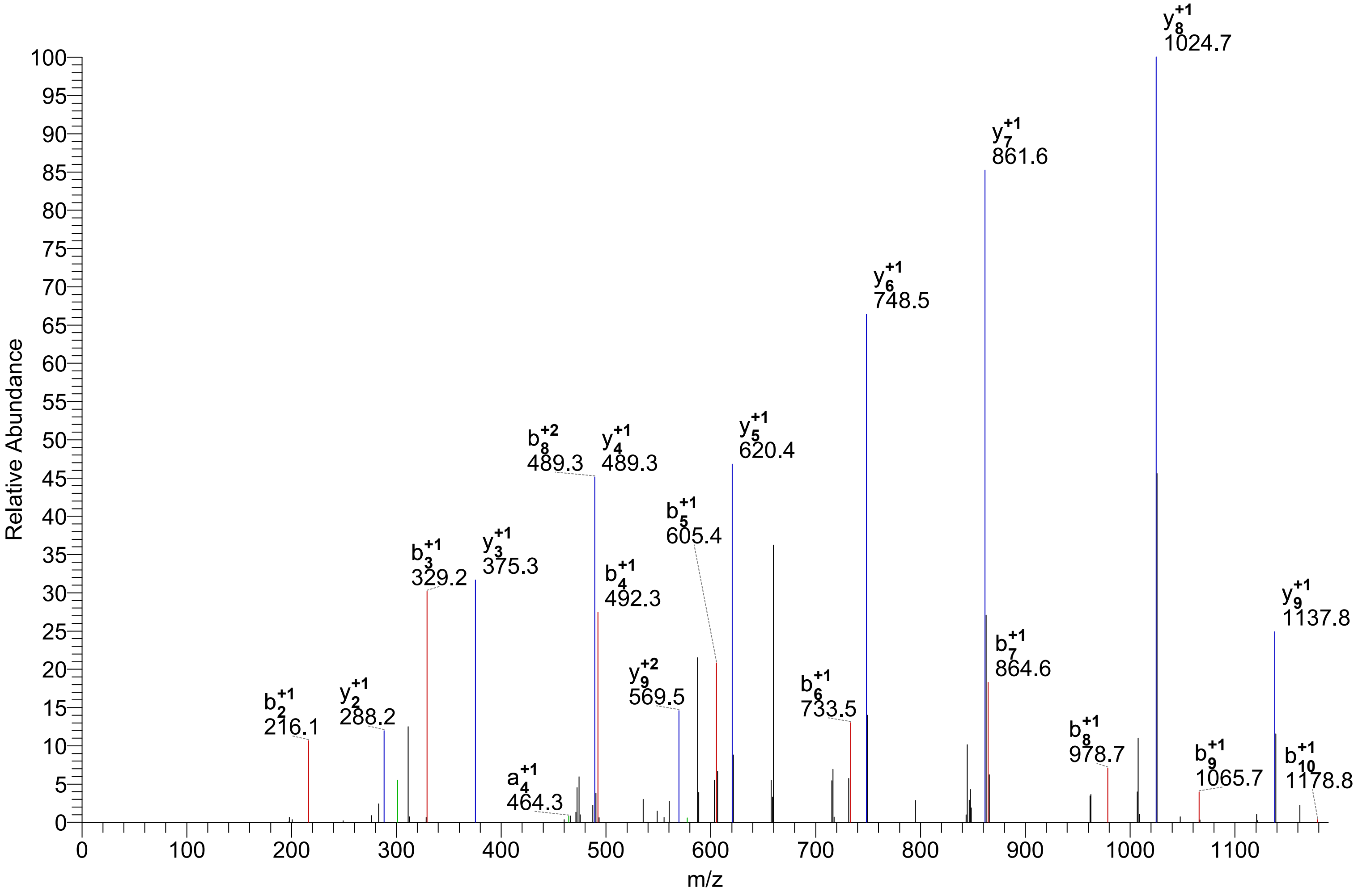
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                    1238.66
 L    301.19     329.18                                    1137.61
 Y    464.25     492.25                                    1024.52
 L    577.33     605.33                                     861.46
 Q    705.39     733.39                                     748.38
 M    836.43     864.43                                     620.32
 N    950.48     978.47                                     489.28
 S   1037.51    1065.50                                     375.24
 L   1150.59    1178.59                                     288.20
 R                                                          175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                               MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

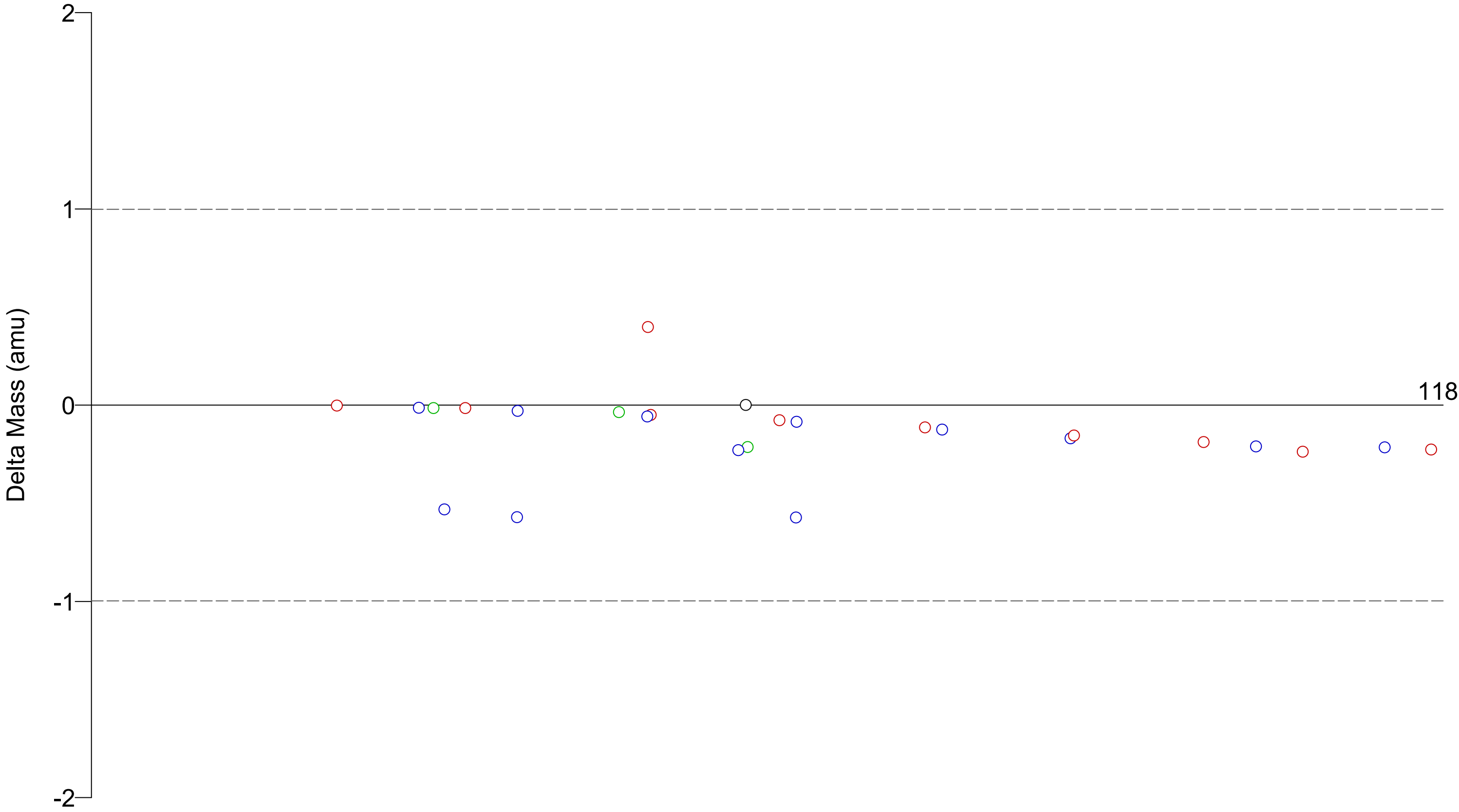
IPI:IPI00827929.1|TREMBL:A2NWW9 Ta                               3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                       1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30  39

1 of 1 peptide matches reported, 0 removed due to filtering
```

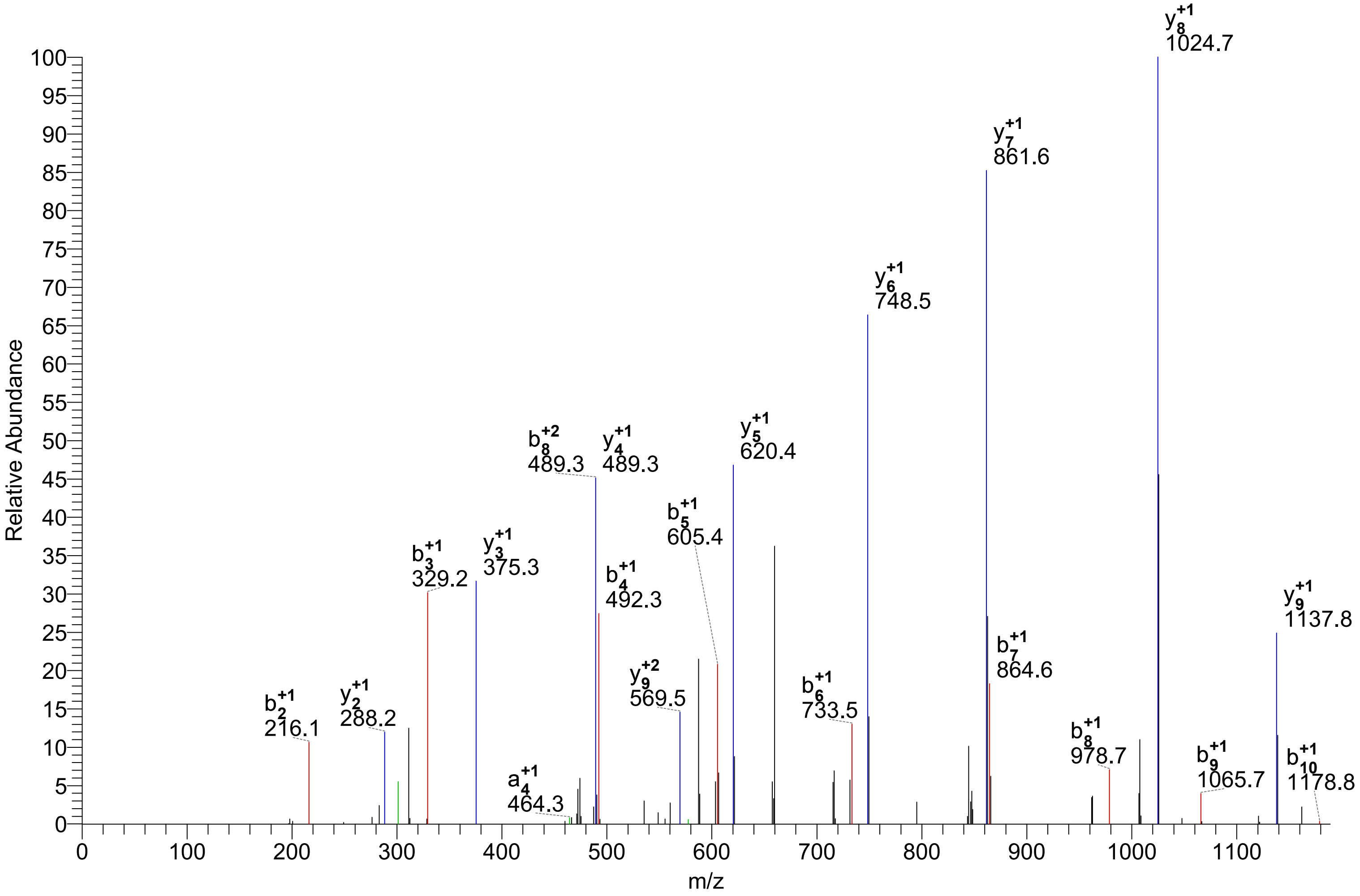
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06    115.05
 T    188.10    216.10                                     1238.66
 L    301.19    329.18                                     1137.61
 Y    464.25    492.25                                     1024.52
 L    577.33    605.33                                      861.46
 Q    705.39    733.39                                      748.38
 M    836.43    864.43                                      620.32
 N    950.48    978.47                                      489.28
 S   1037.51   1065.50                                      375.24
 L   1150.59   1178.59                                      288.20
 R                                                          175.12
```



#19287468-1 NL: 1.01E5



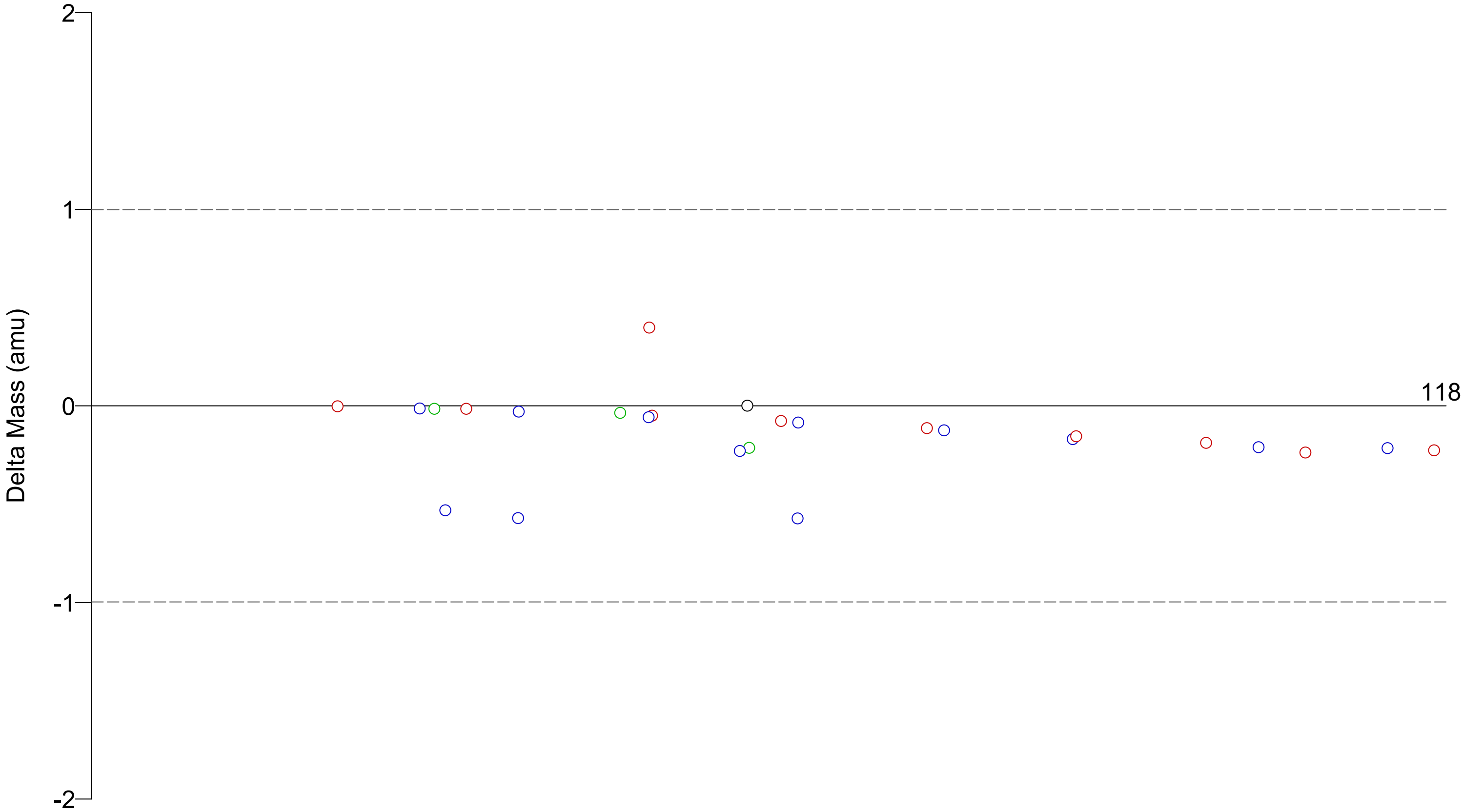
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                CMH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00827938.1|TREMBL:A2NWW5 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

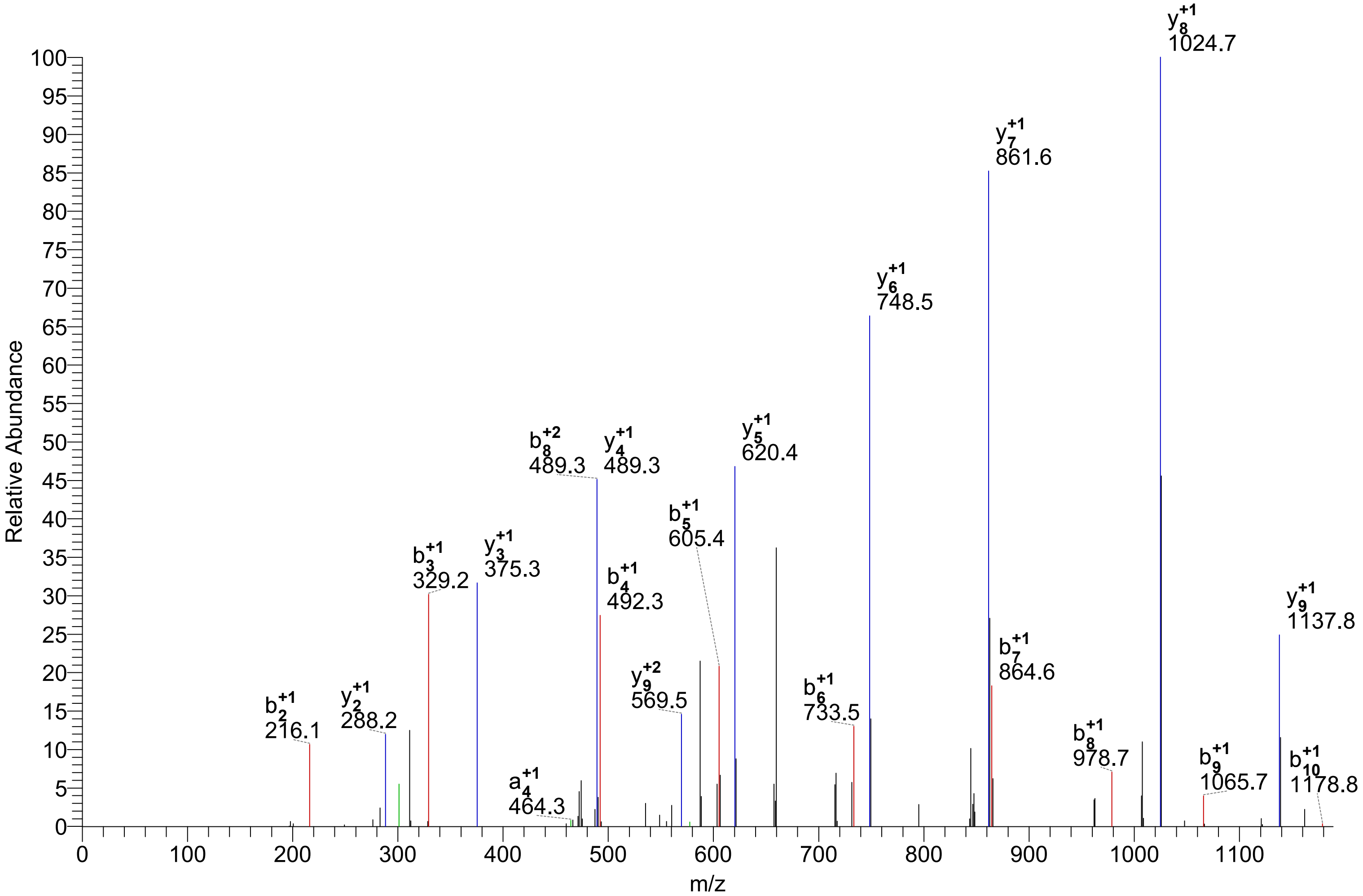
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10    216.10                                     1238.66
 L    301.19    329.18                                     1137.61
 Y    464.25    492.25                                     1024.52
 L    577.33    605.33                                      861.46
 Q    705.39    733.39                                      748.38
 M    836.43    864.43                                      620.32
 N    950.48    978.47                                      489.28
 S   1037.51   1065.50                                      375.24
 L   1150.59   1178.59                                      288.20
 R                                                          175.12
```



#19287468-1 NL: 1.01E5



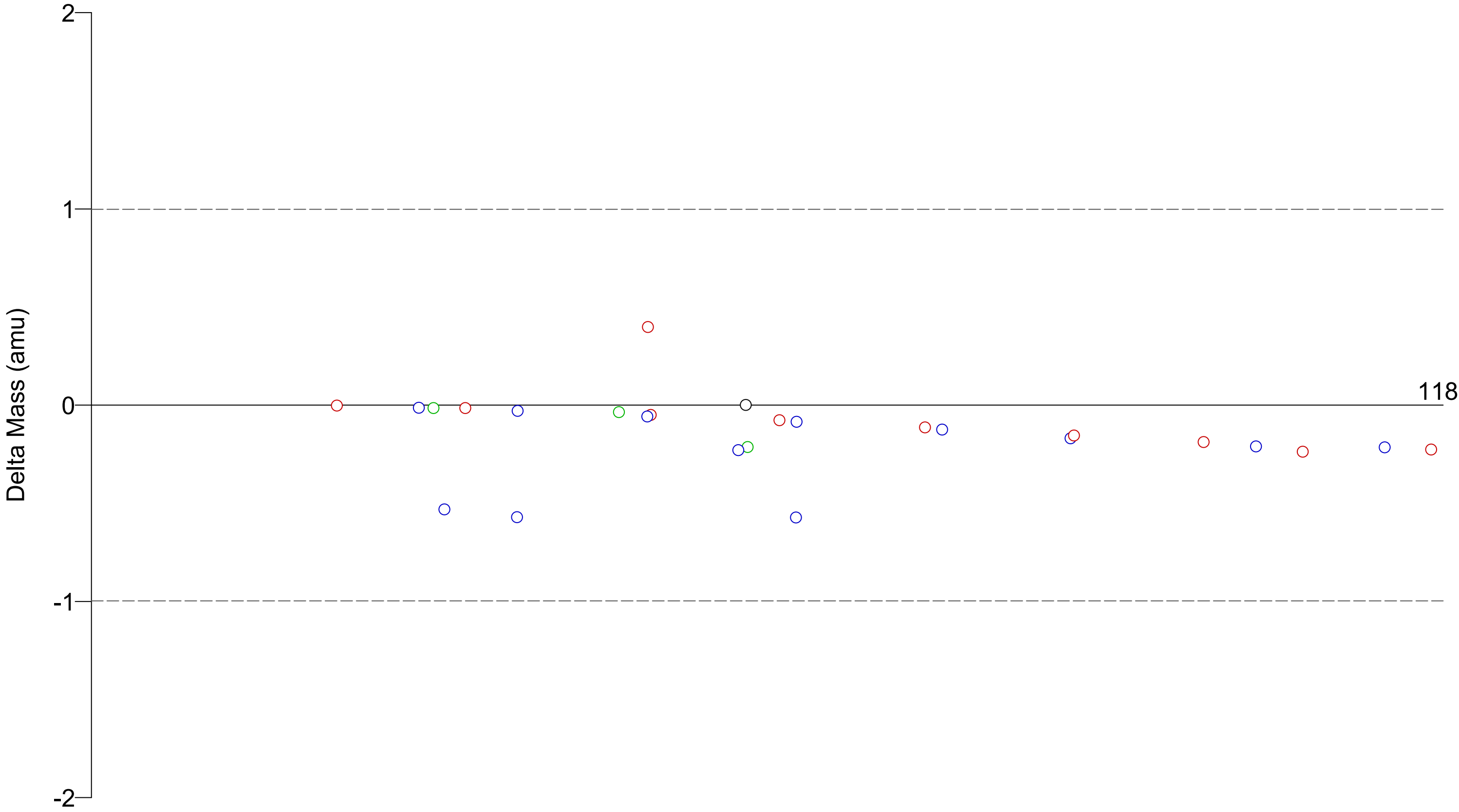
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00827940.1|SWISS-PROT:P0176                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

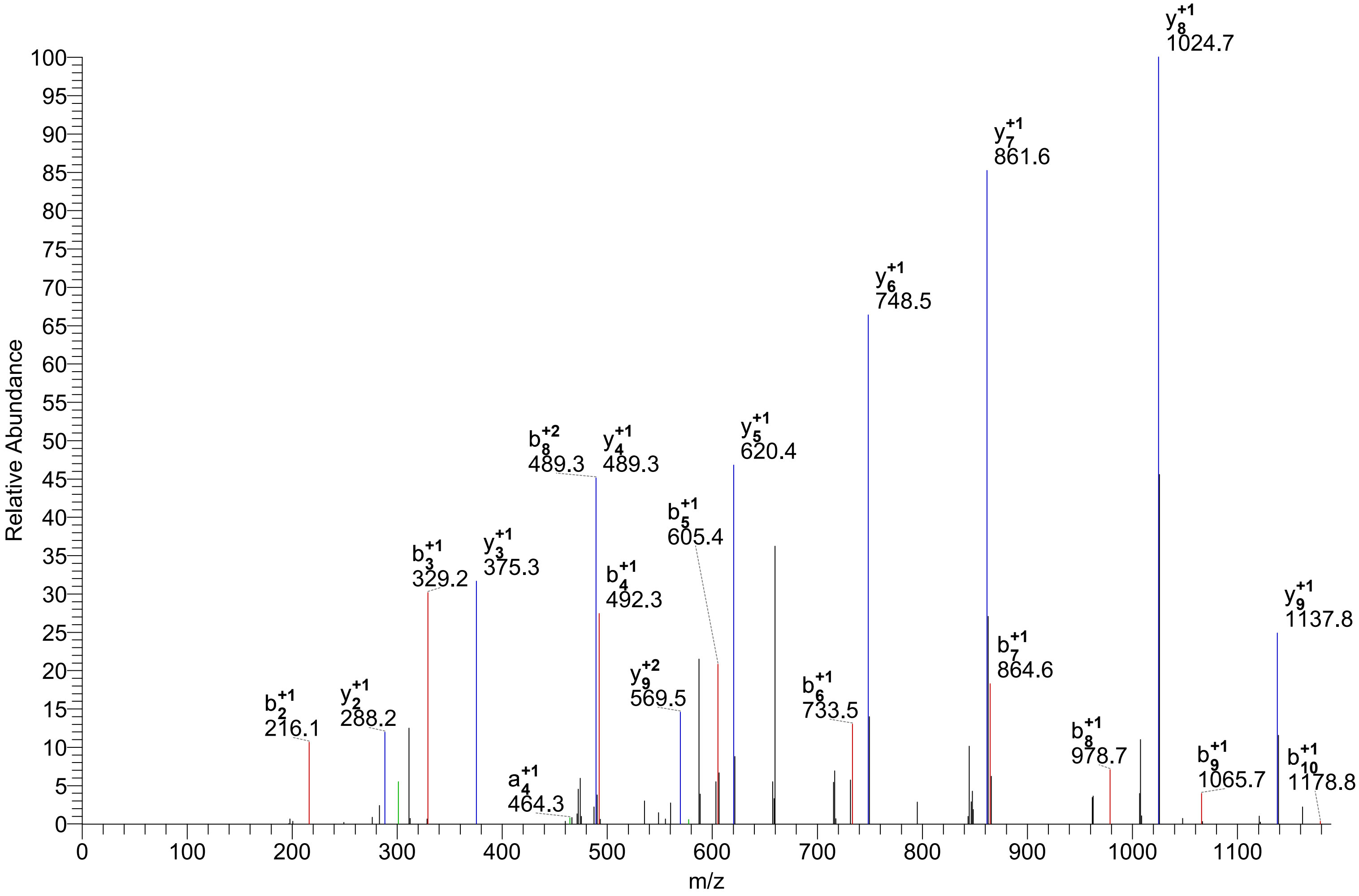
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count

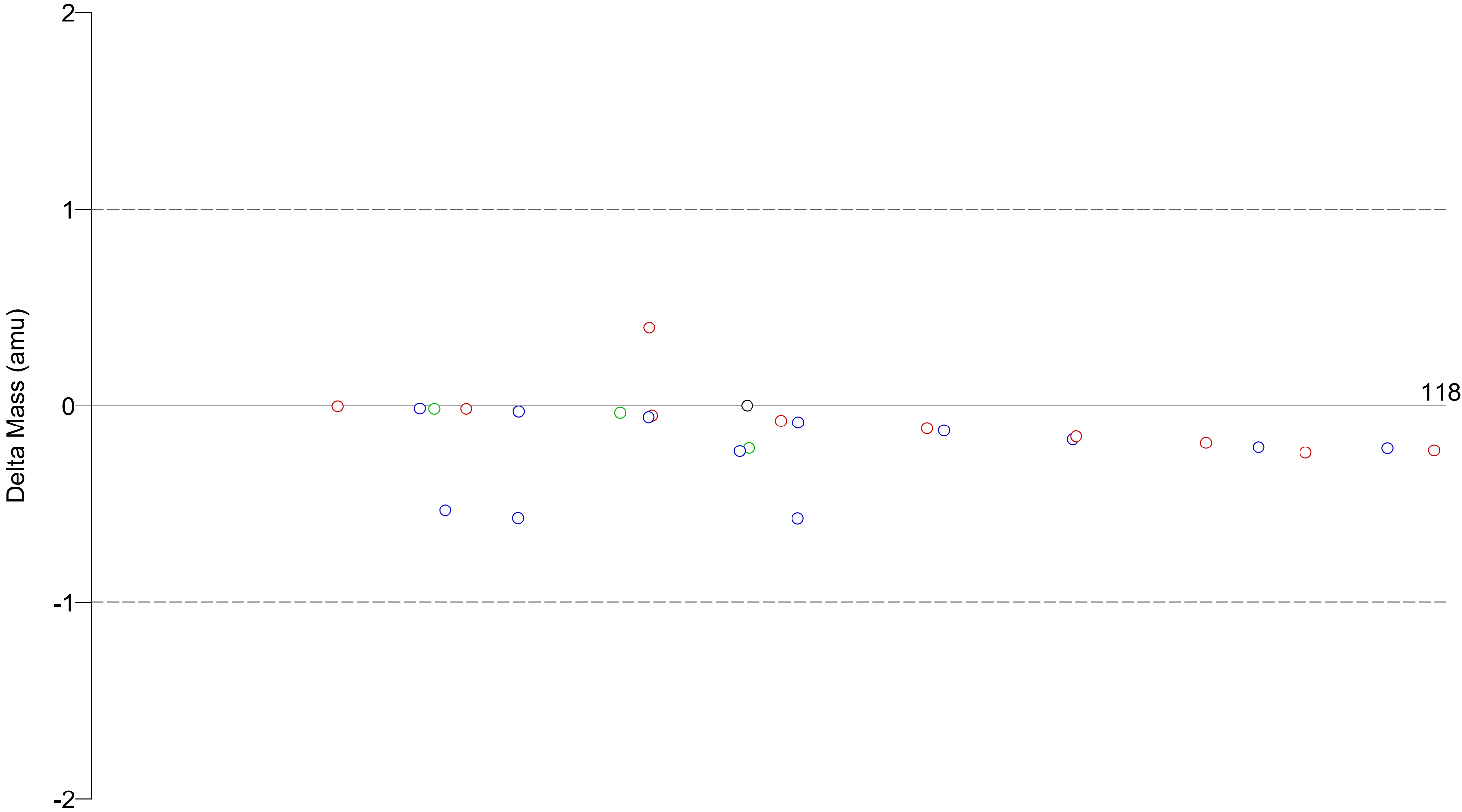
IPI:IPI00827989.1|TREMBL:A2NWW6 Ta                                   3e-006  10.2      0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                          1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

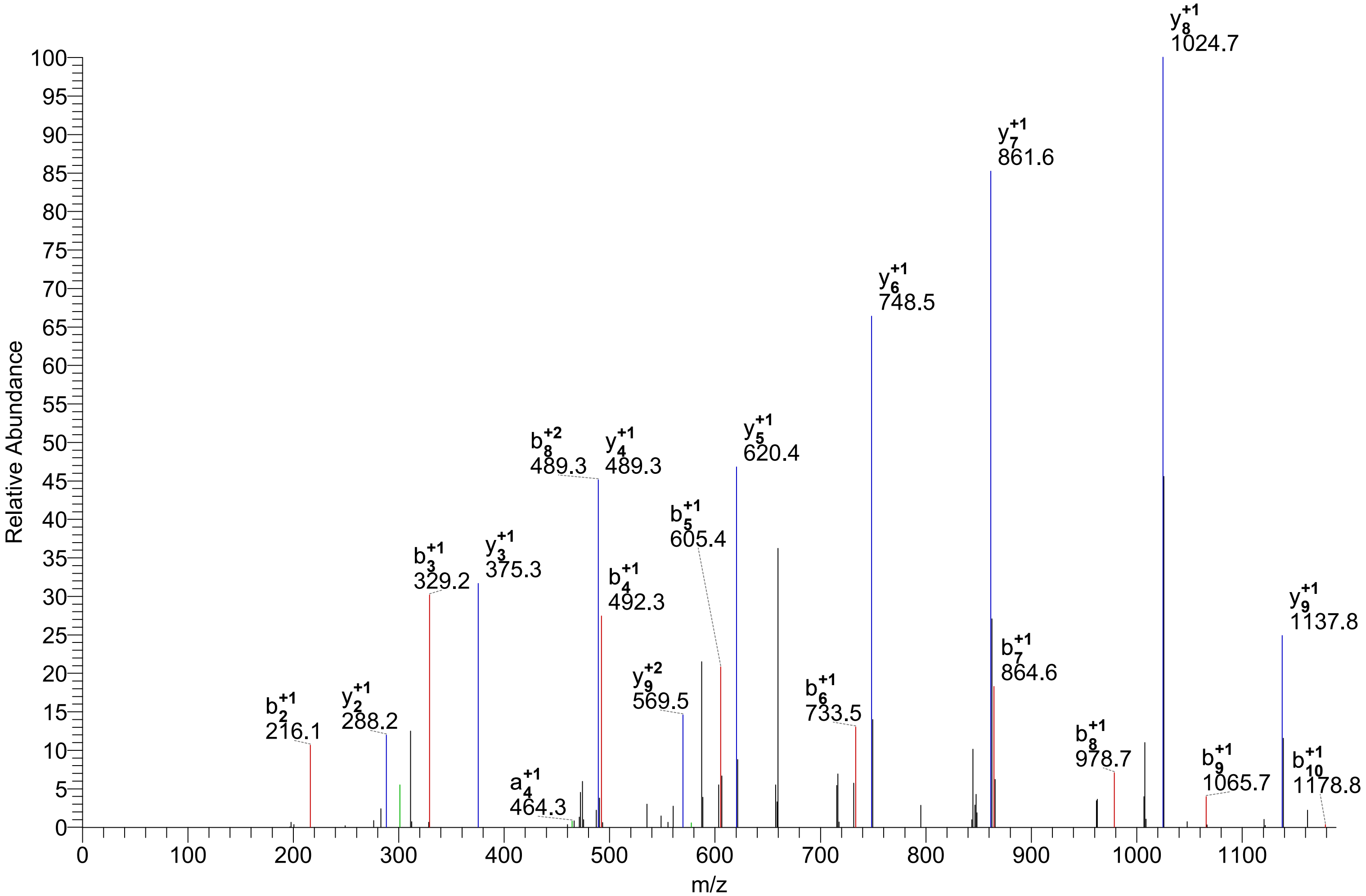
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



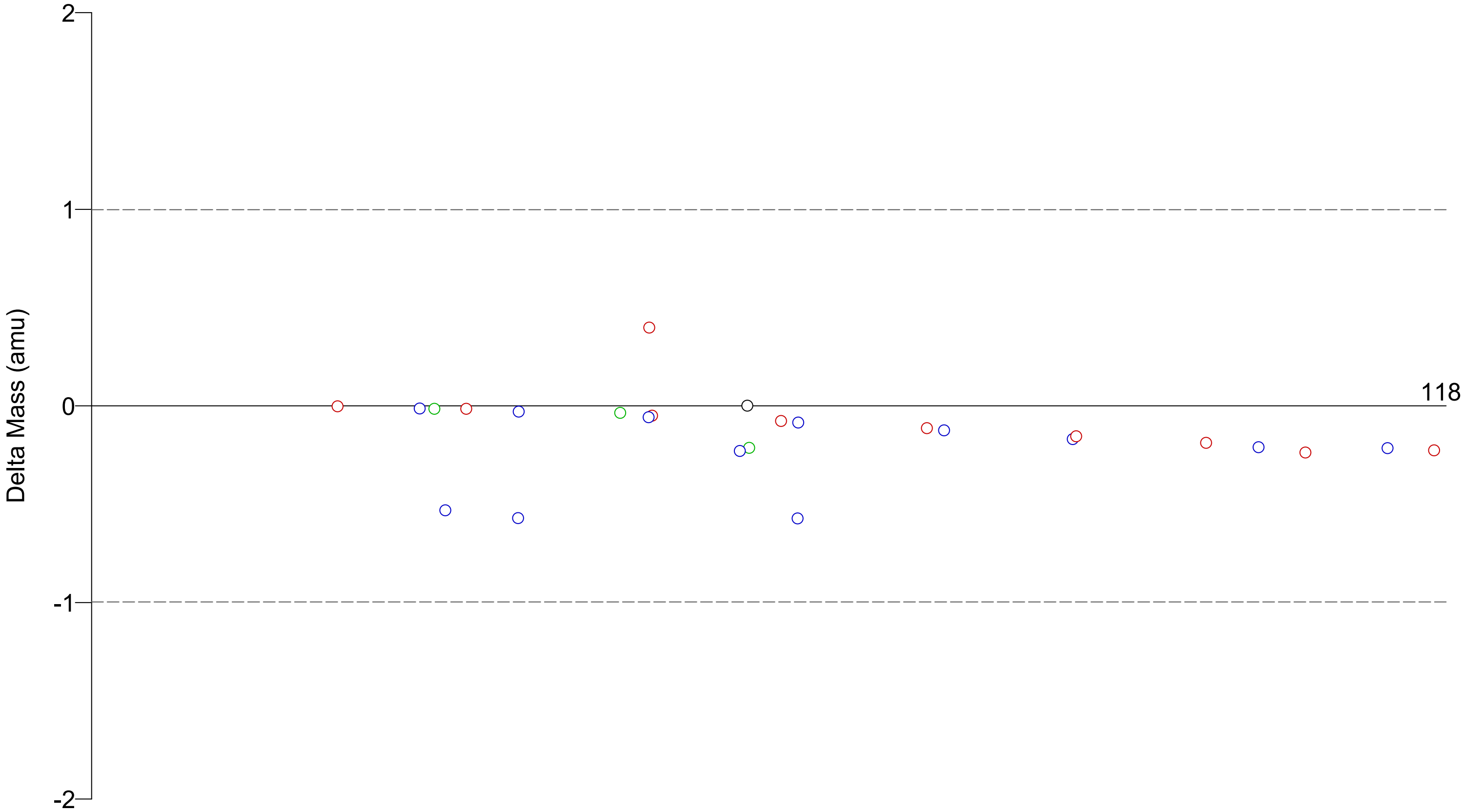
```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00828022.1|TREMBL:A2NWW7 Ta                                 3e-006  10.2     0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70    2  3e-006  4.027  0.643    1526.5 1    20/30    39

1 of 1 peptide matches reported, 0 removed due to filtering
```

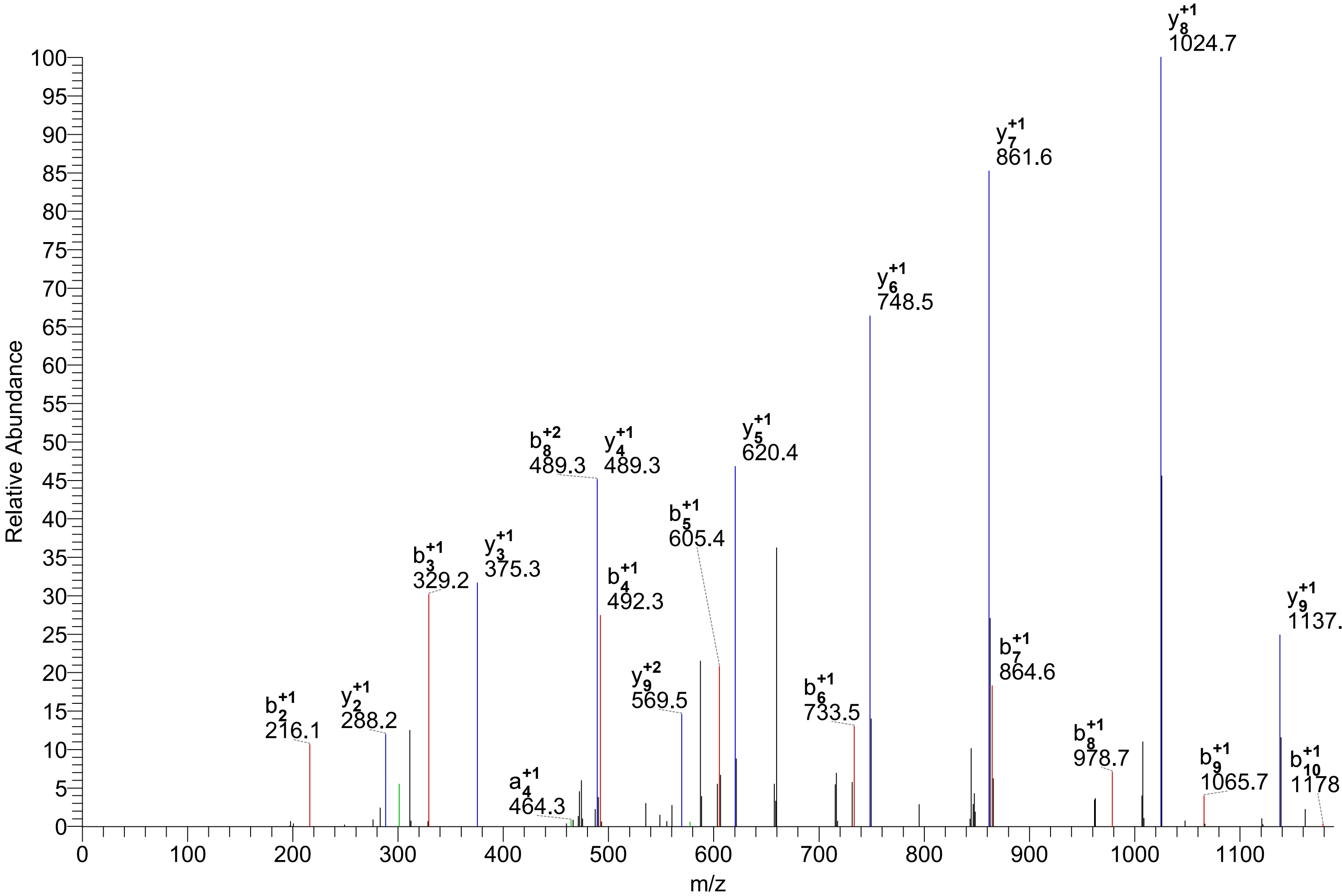
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00828061.1|TREMBL:A2JA14 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```
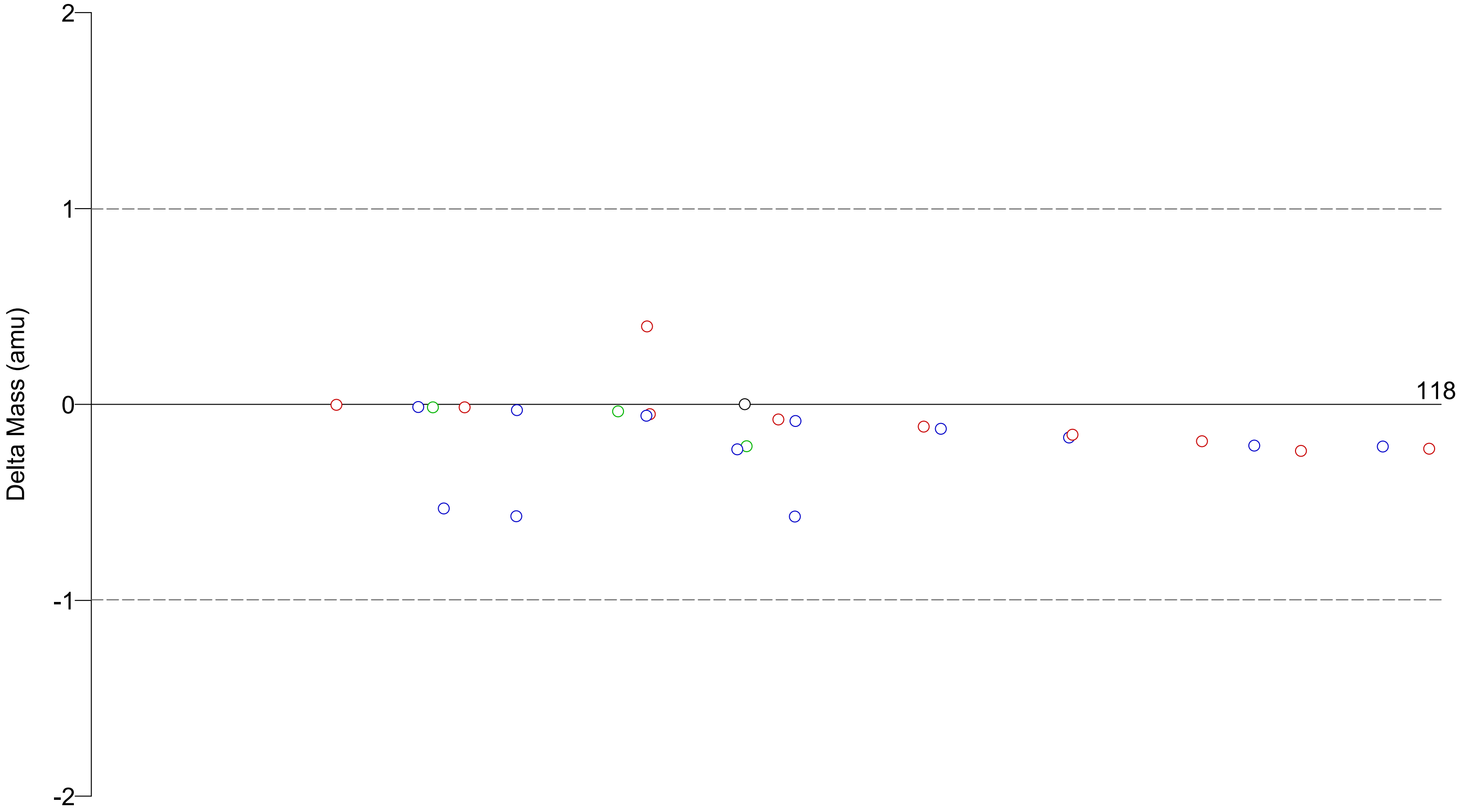
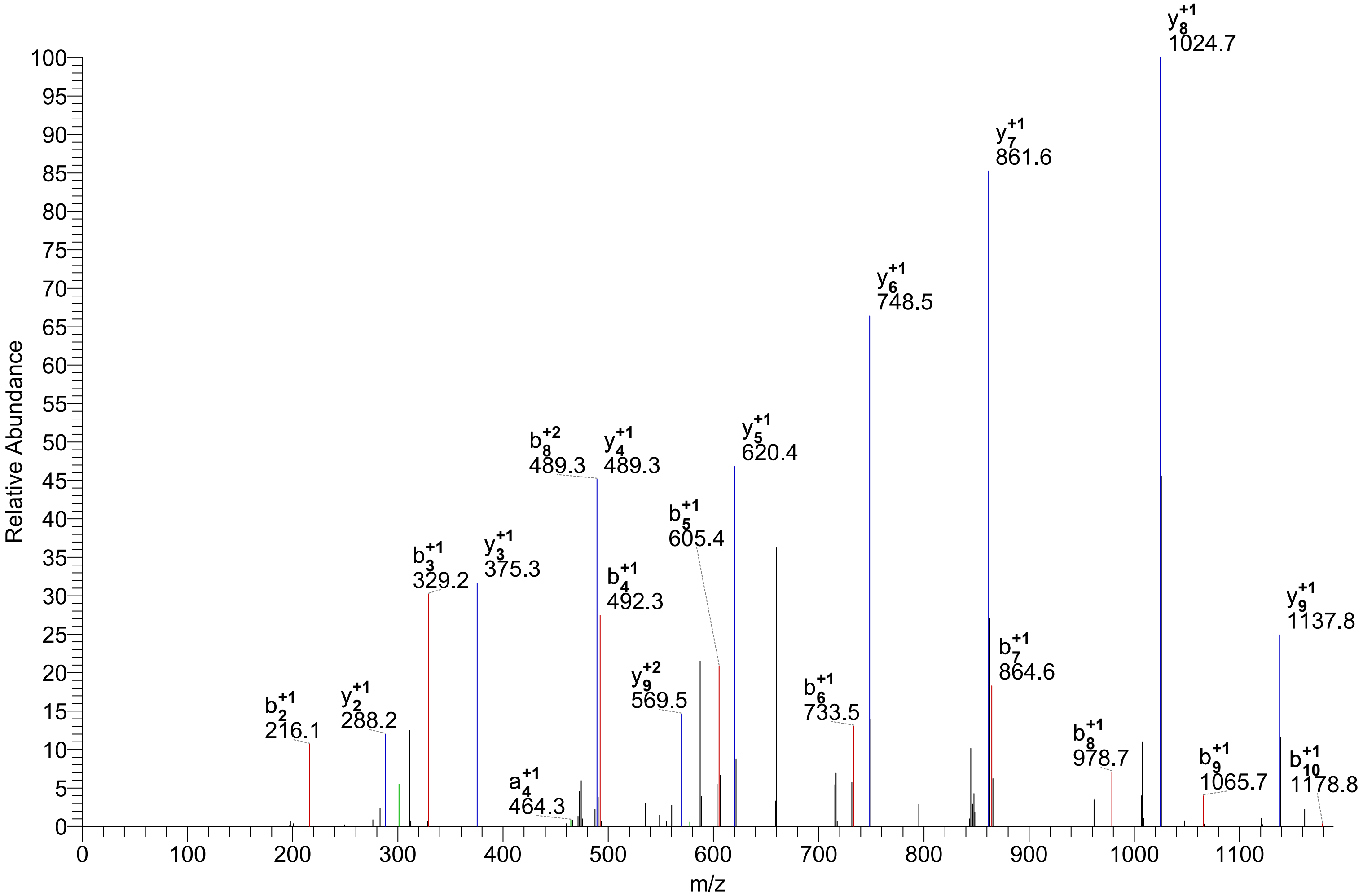

```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC DeltaCn   Sp   RSp  Ions  Count

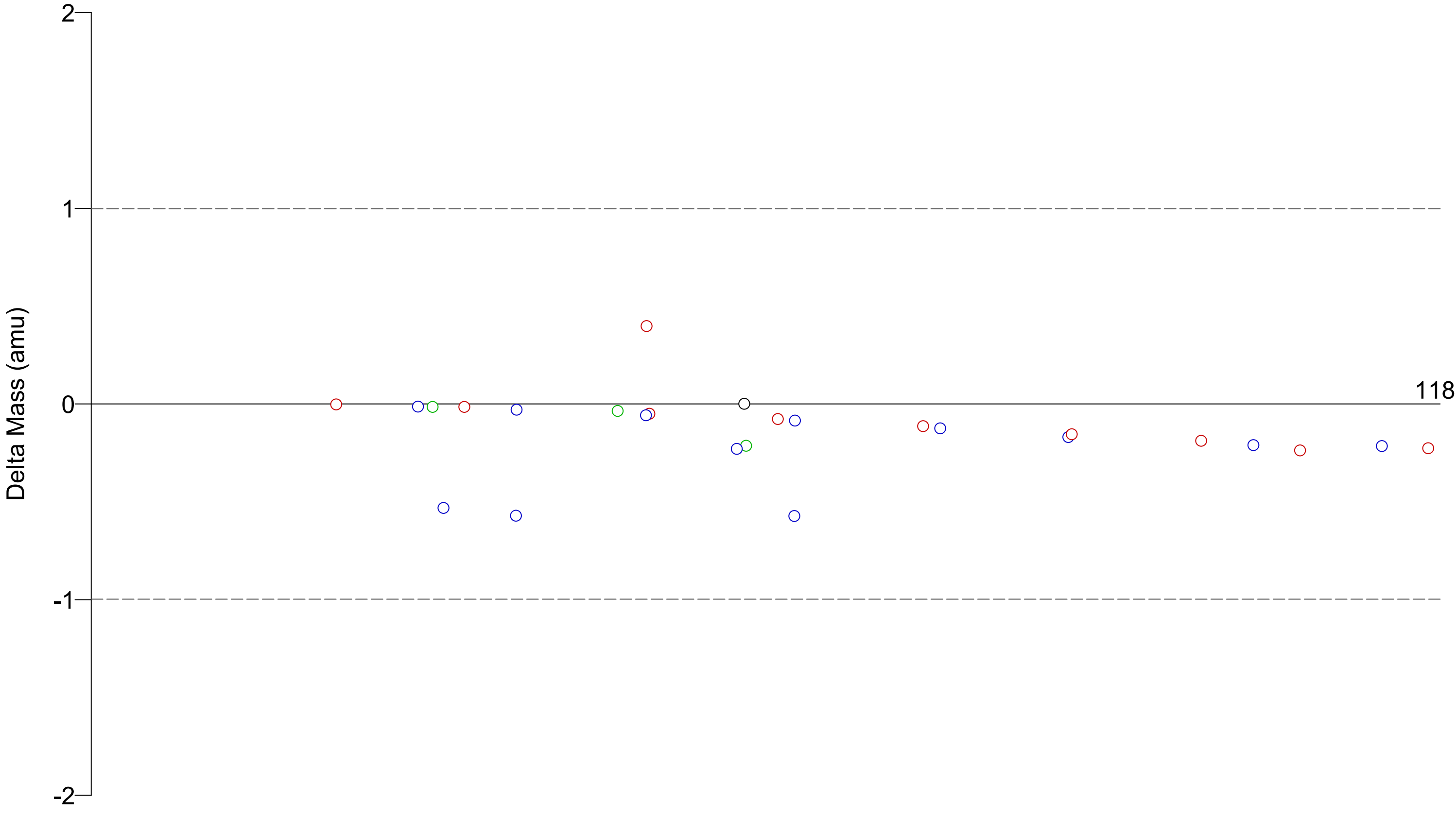
IPI:IPI00828085.1|TREMBL:A2NWW4 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

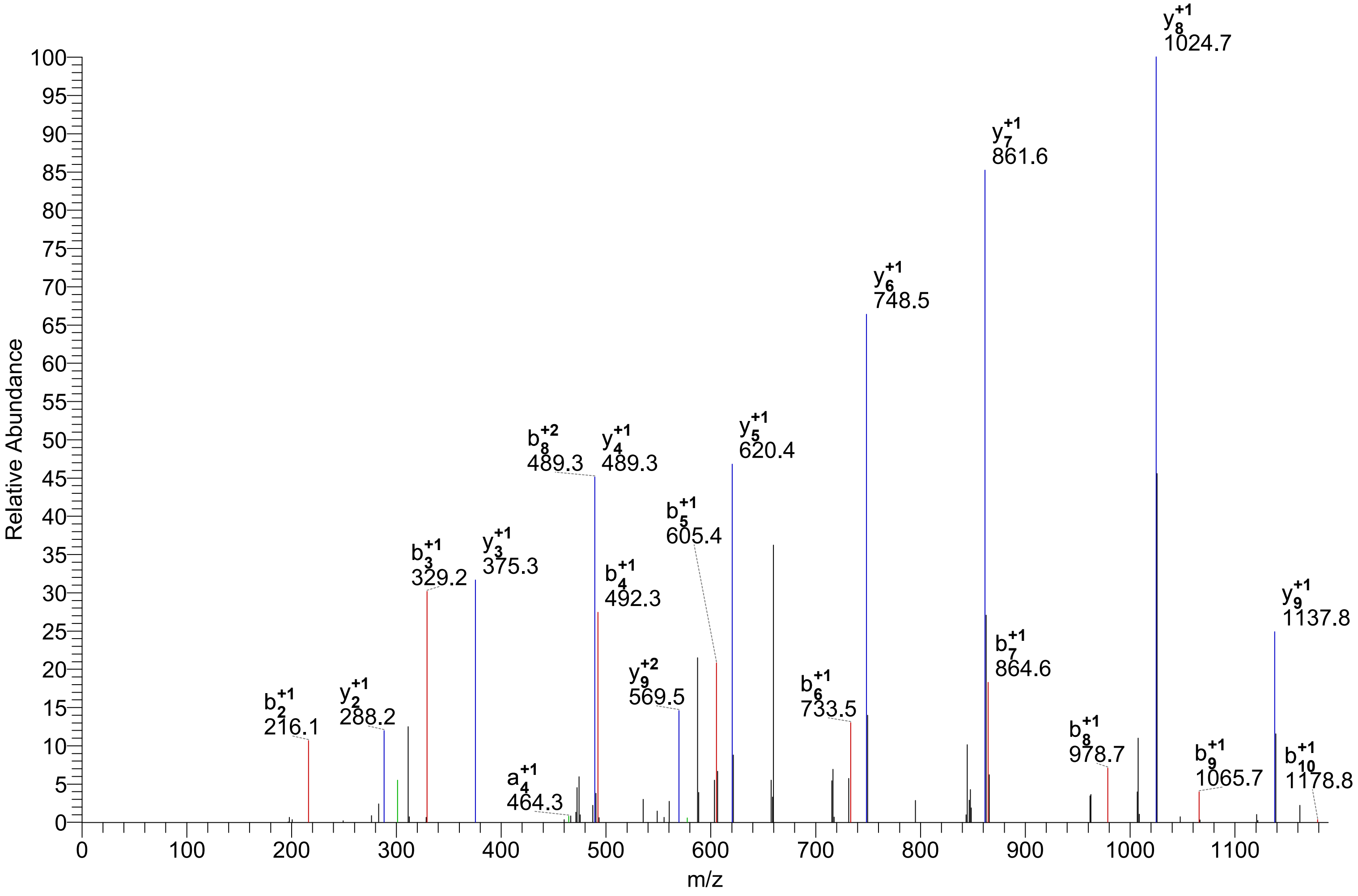
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10    216.10                                     1238.66
 L    301.19    329.18                                     1137.61
 Y    464.25    492.25                                     1024.52
 L    577.33    605.33                                      861.46
 Q    705.39    733.39                                      748.38
 M    836.43    864.43                                      620.32
 N    950.48    978.47                                      489.28
 S   1037.51   1065.50                                      375.24
 L   1150.59   1178.59                                      288.20
 R                                                          175.12
```



#19287468-1 NL: 1.01E5



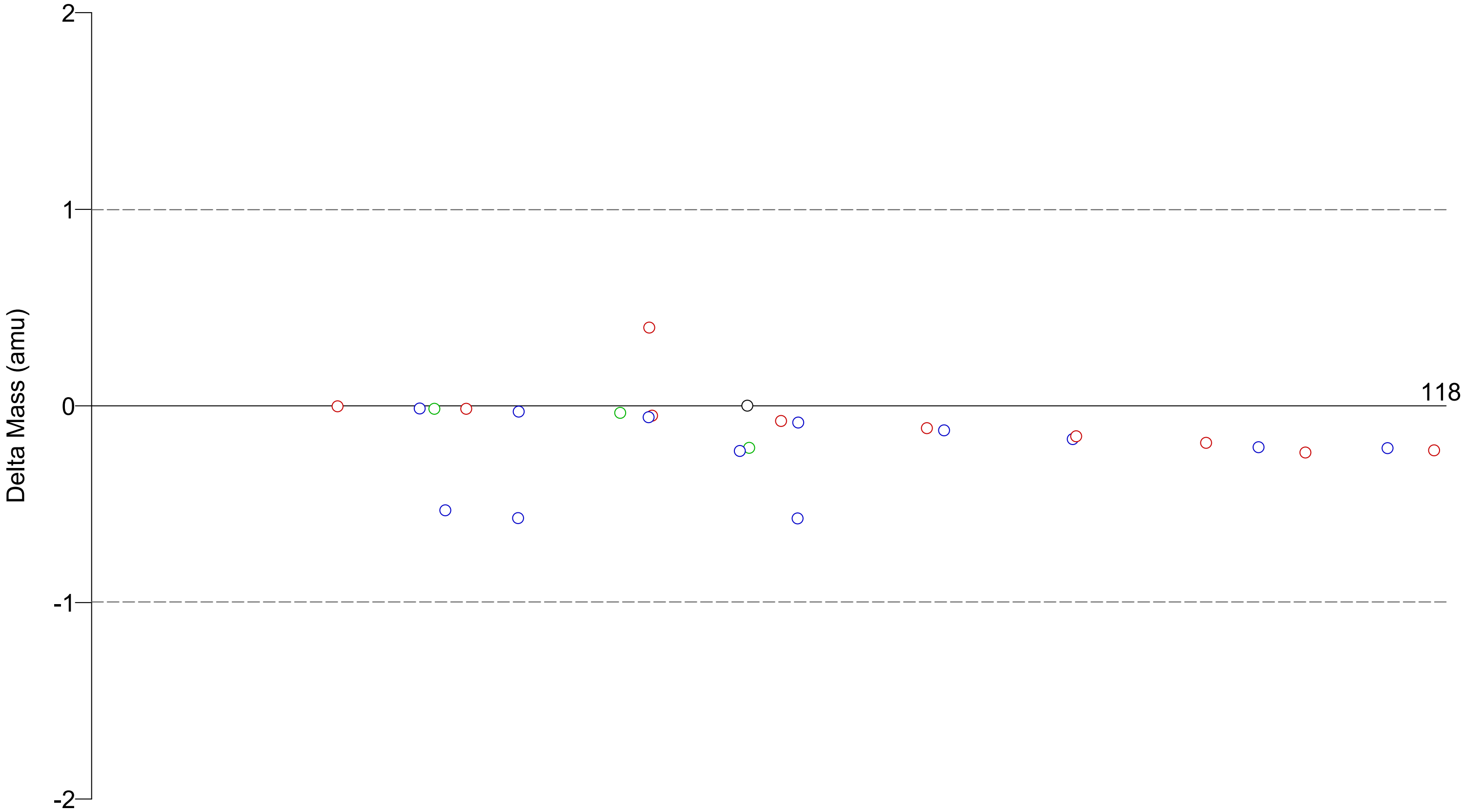
```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)       Sequence                                         MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00828099.1|TREMBL:A2KUC3 Ta                                         3e-006  10.2      0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                                1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

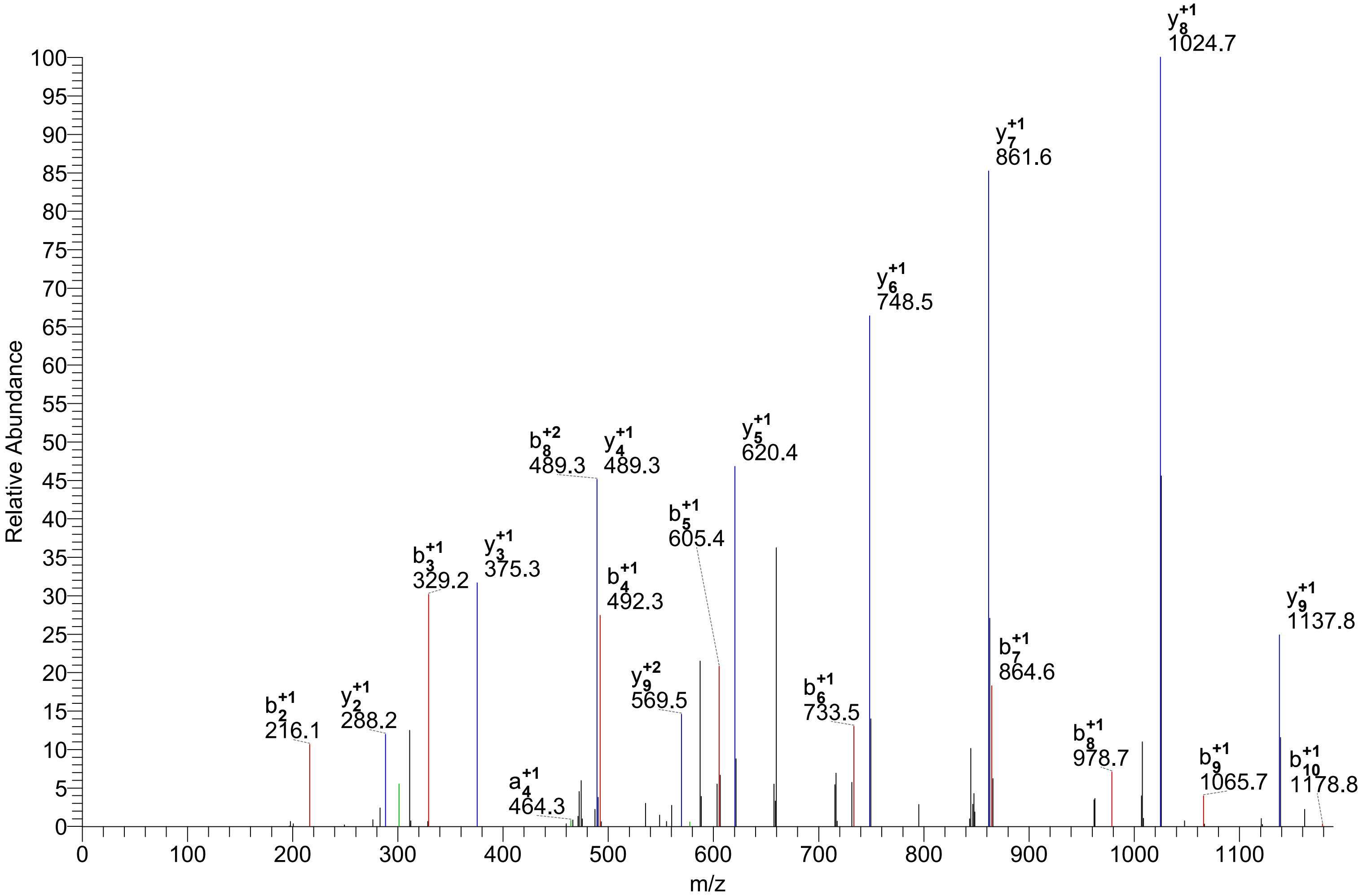
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                Kernel        MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count

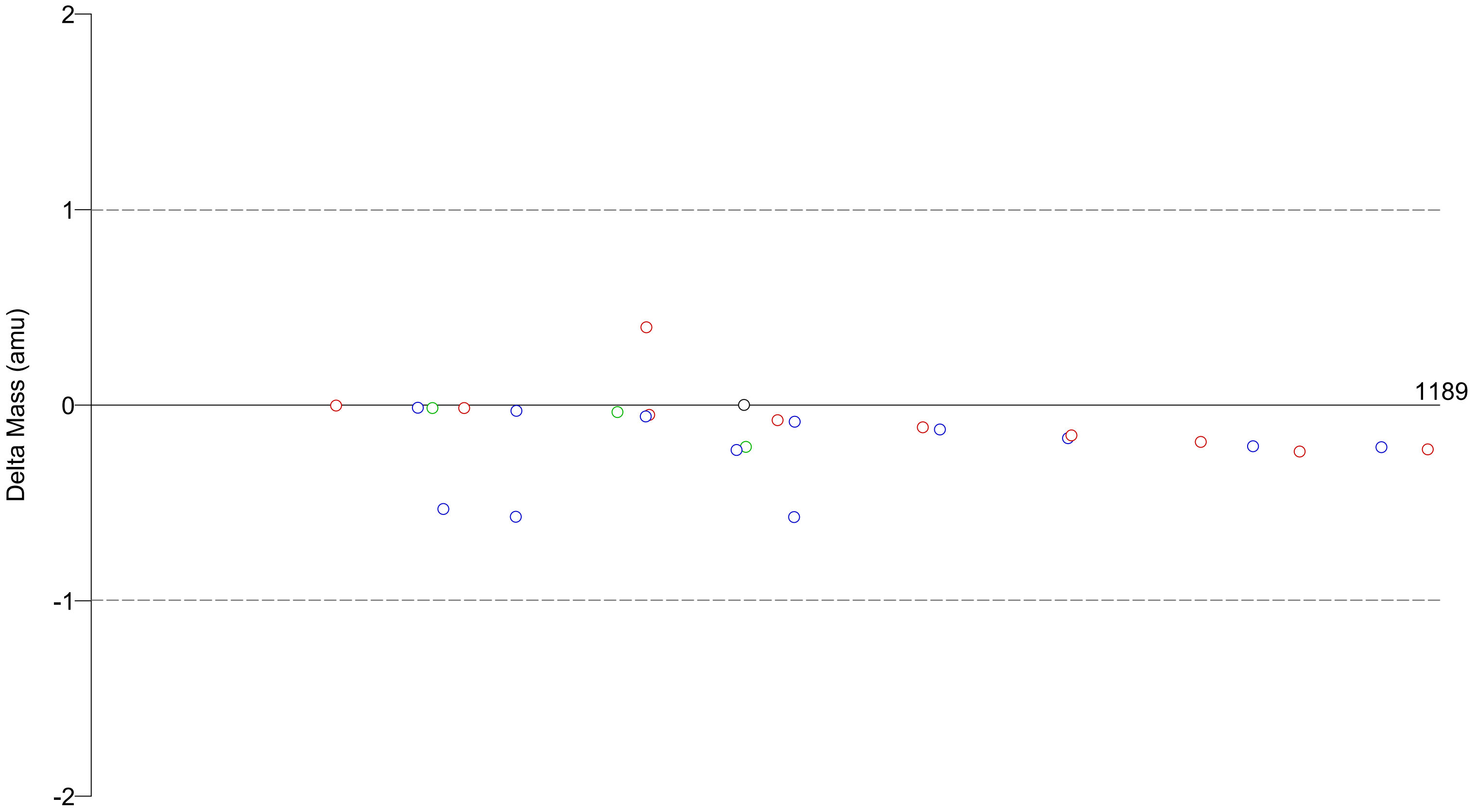
IPI:IPI00828105.1|TREMBL:A2J423 Ta                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

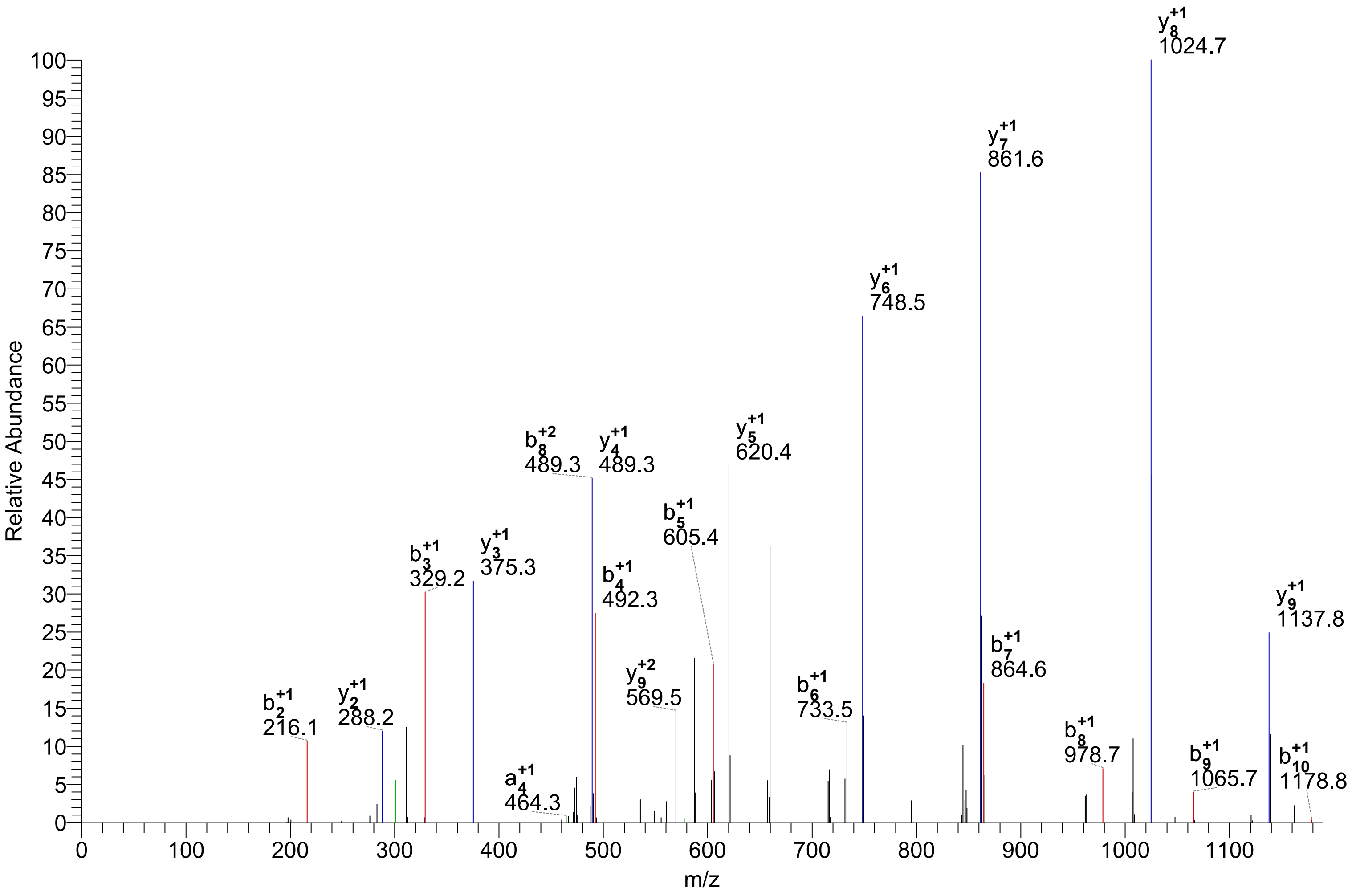
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

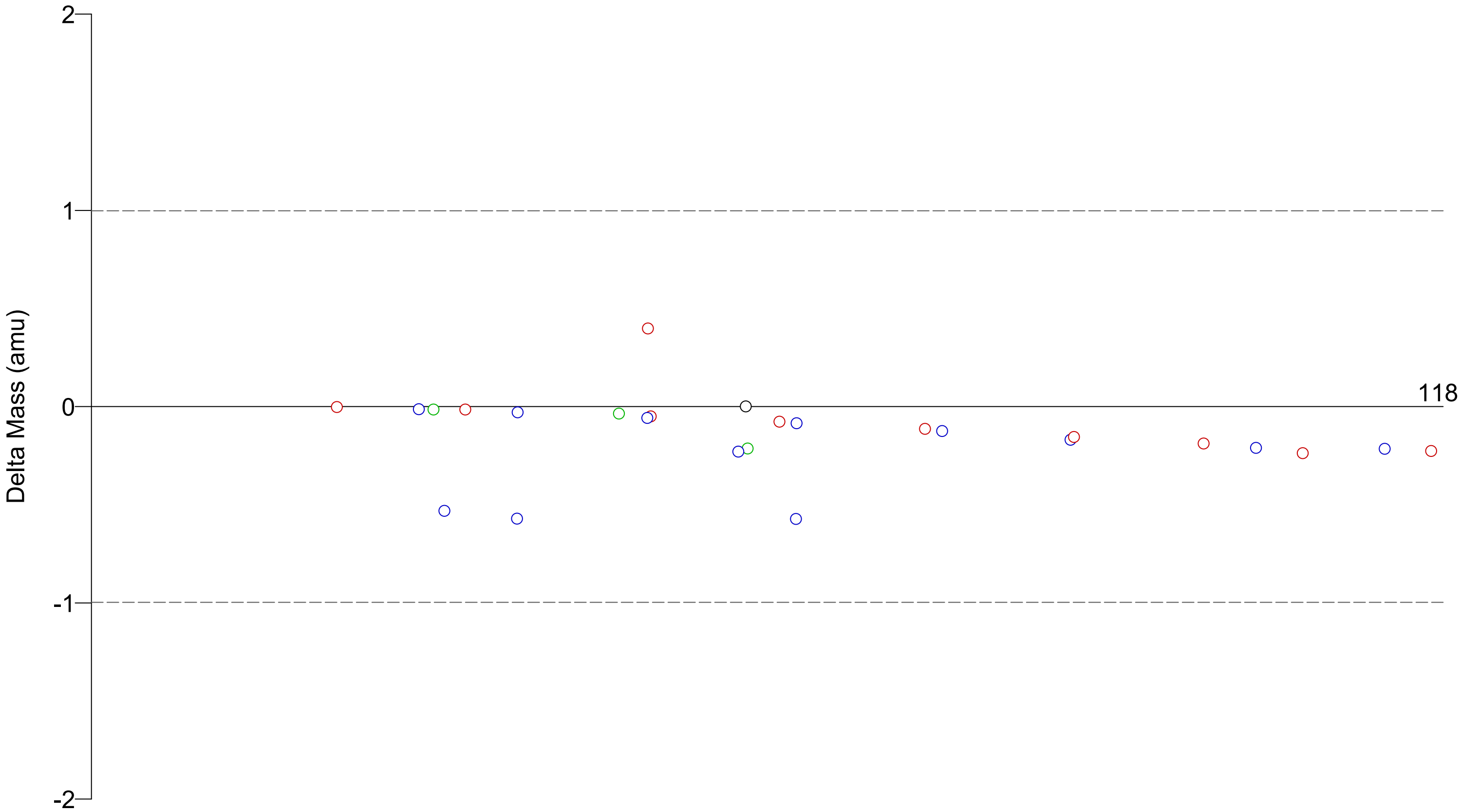
IPI:IPI00828153.1|TREMBL:A2NWW1 Ta                                     3e-006  10.2      0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                              1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

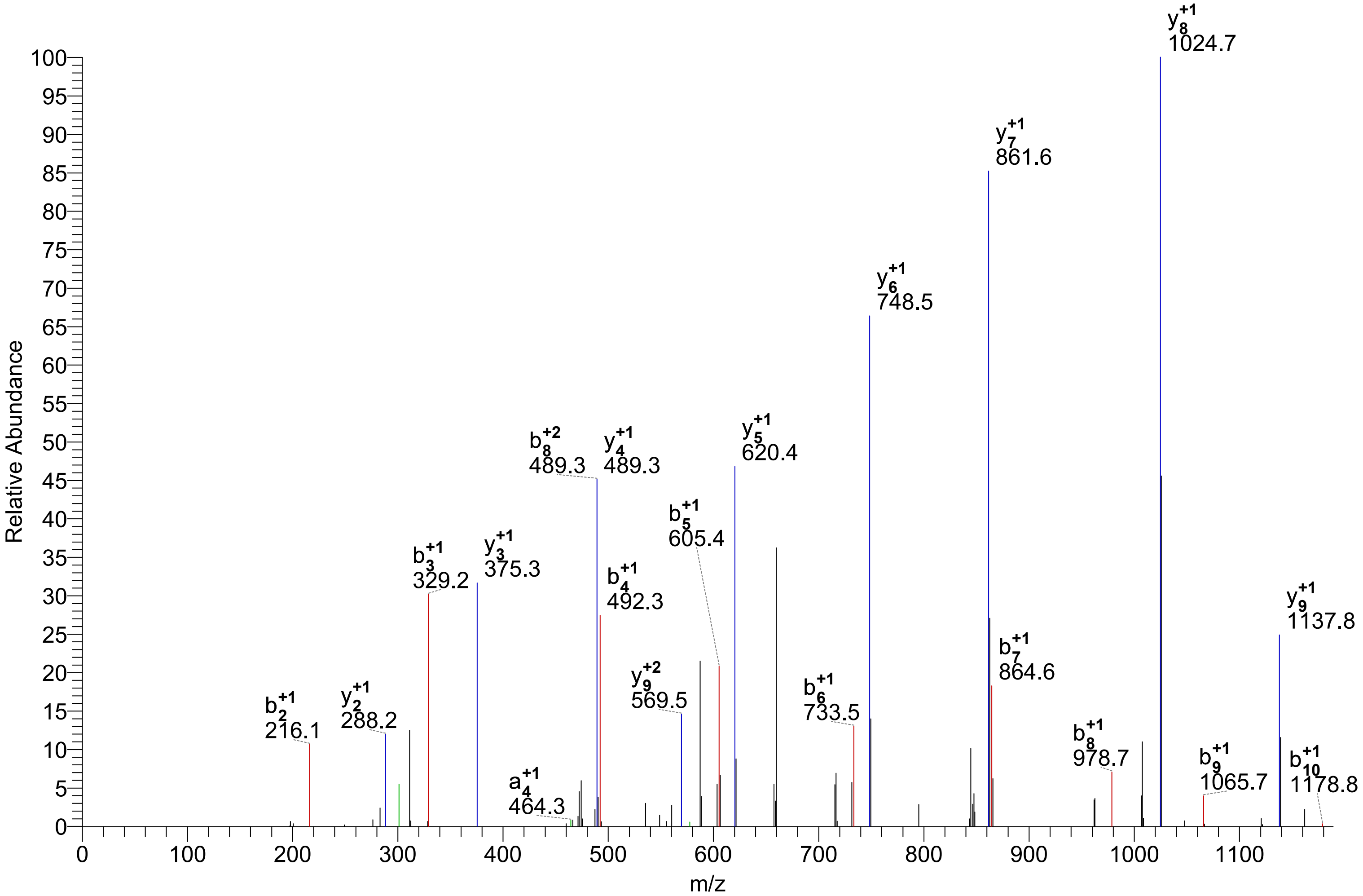
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



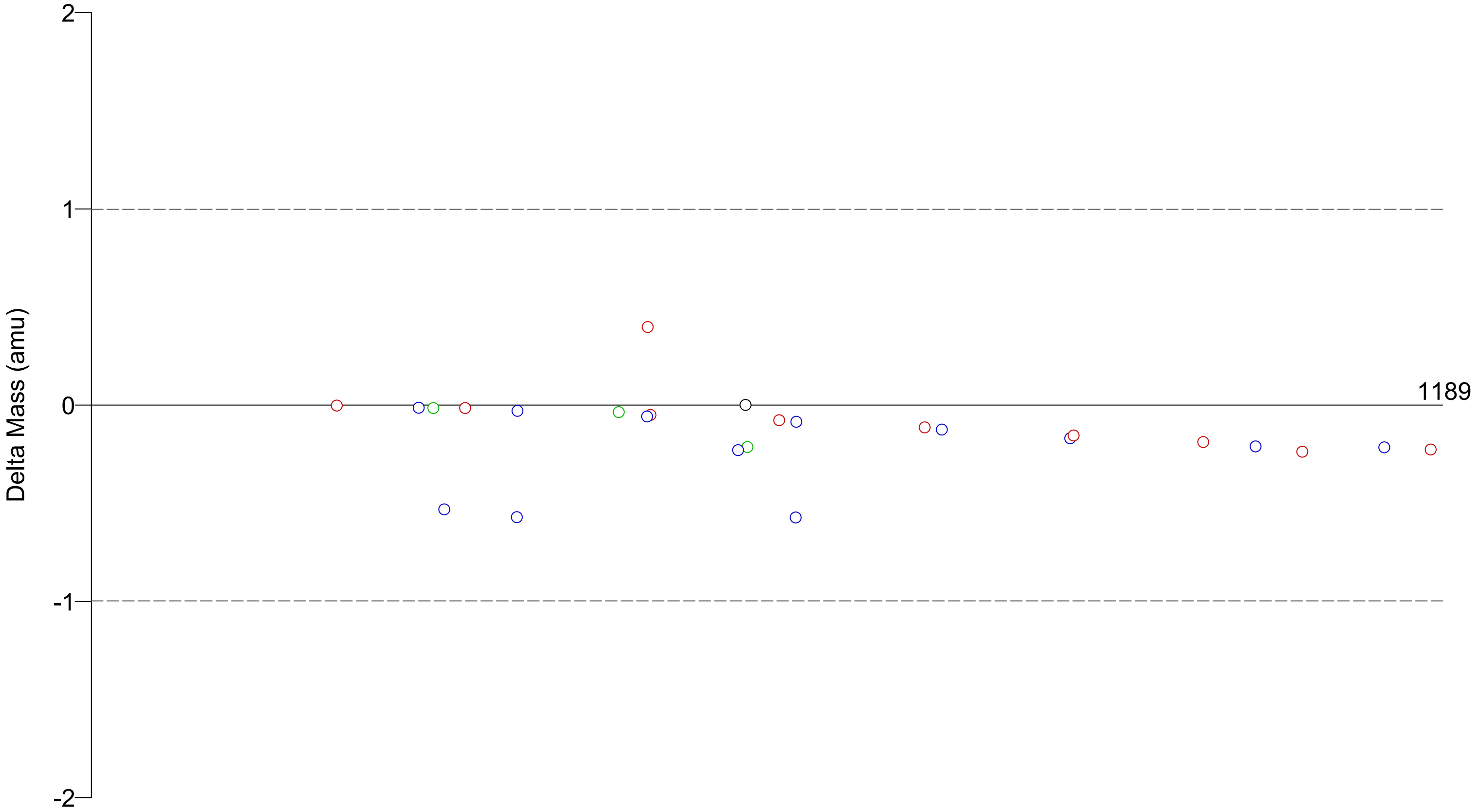
```
Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829724.1|TREMBL:A6NFJ8|EN                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

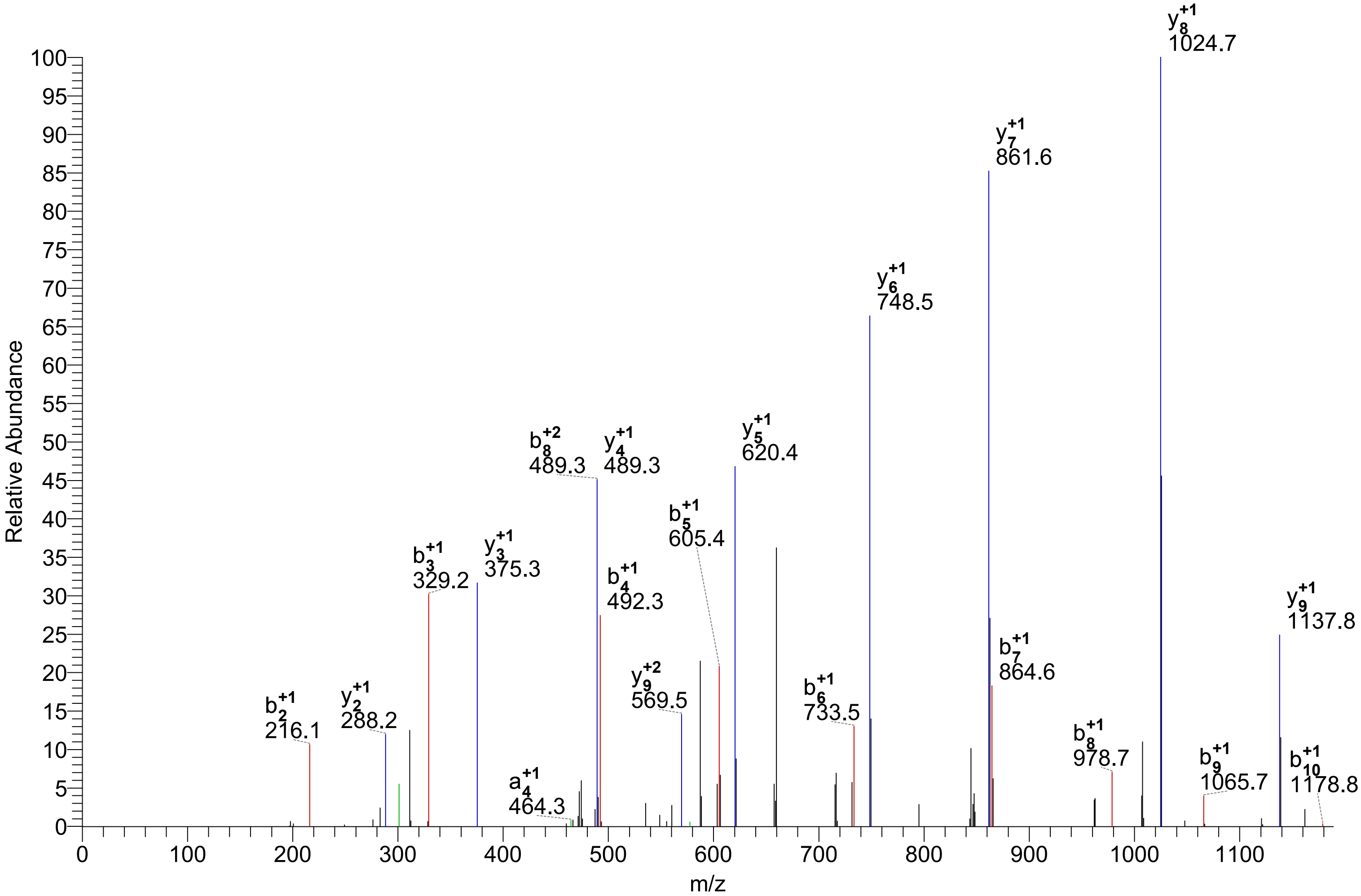
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

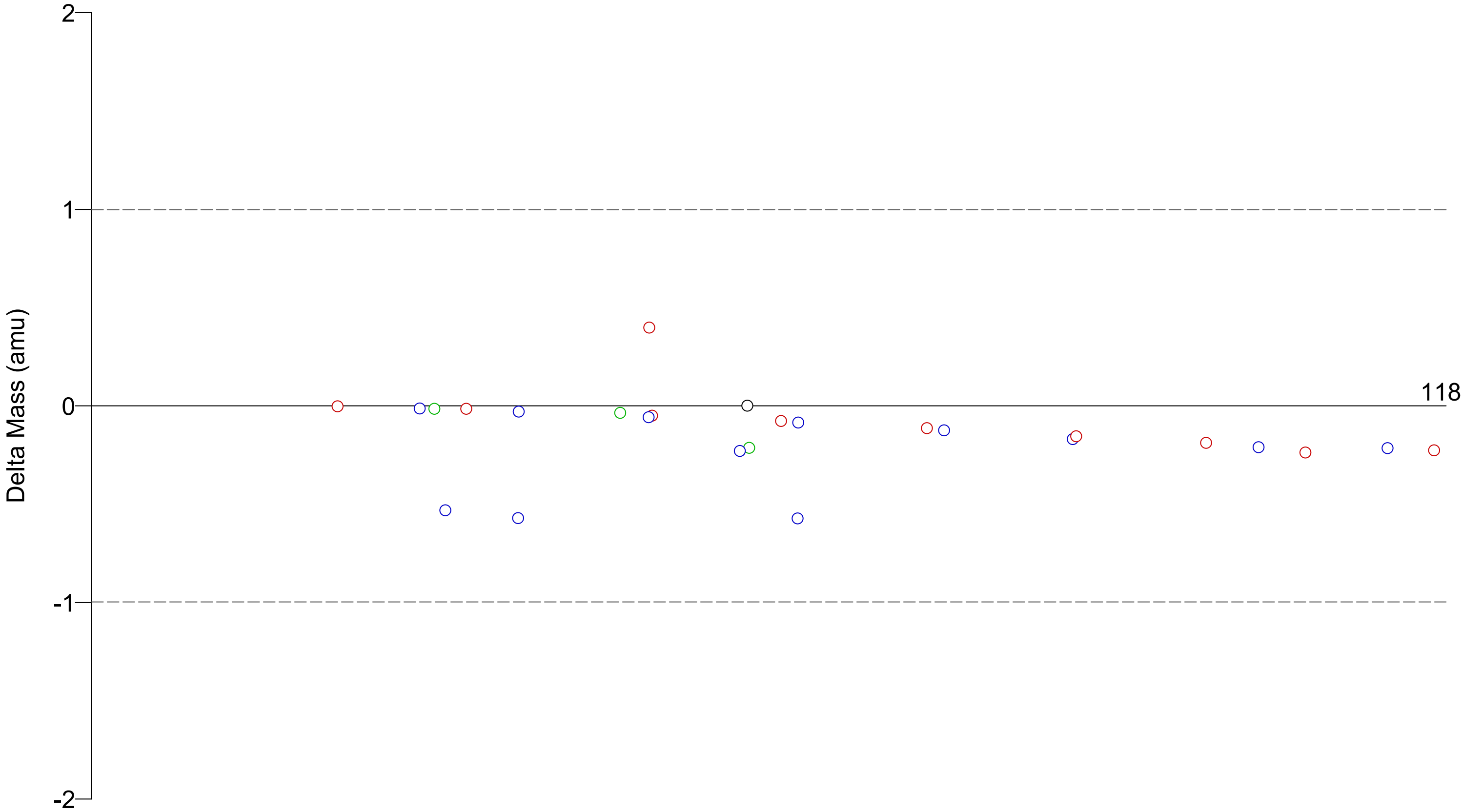
IPI:IPI00829747.2|ENSEMBL:ENSP0000                                 3e-006  10.2      0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                       1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

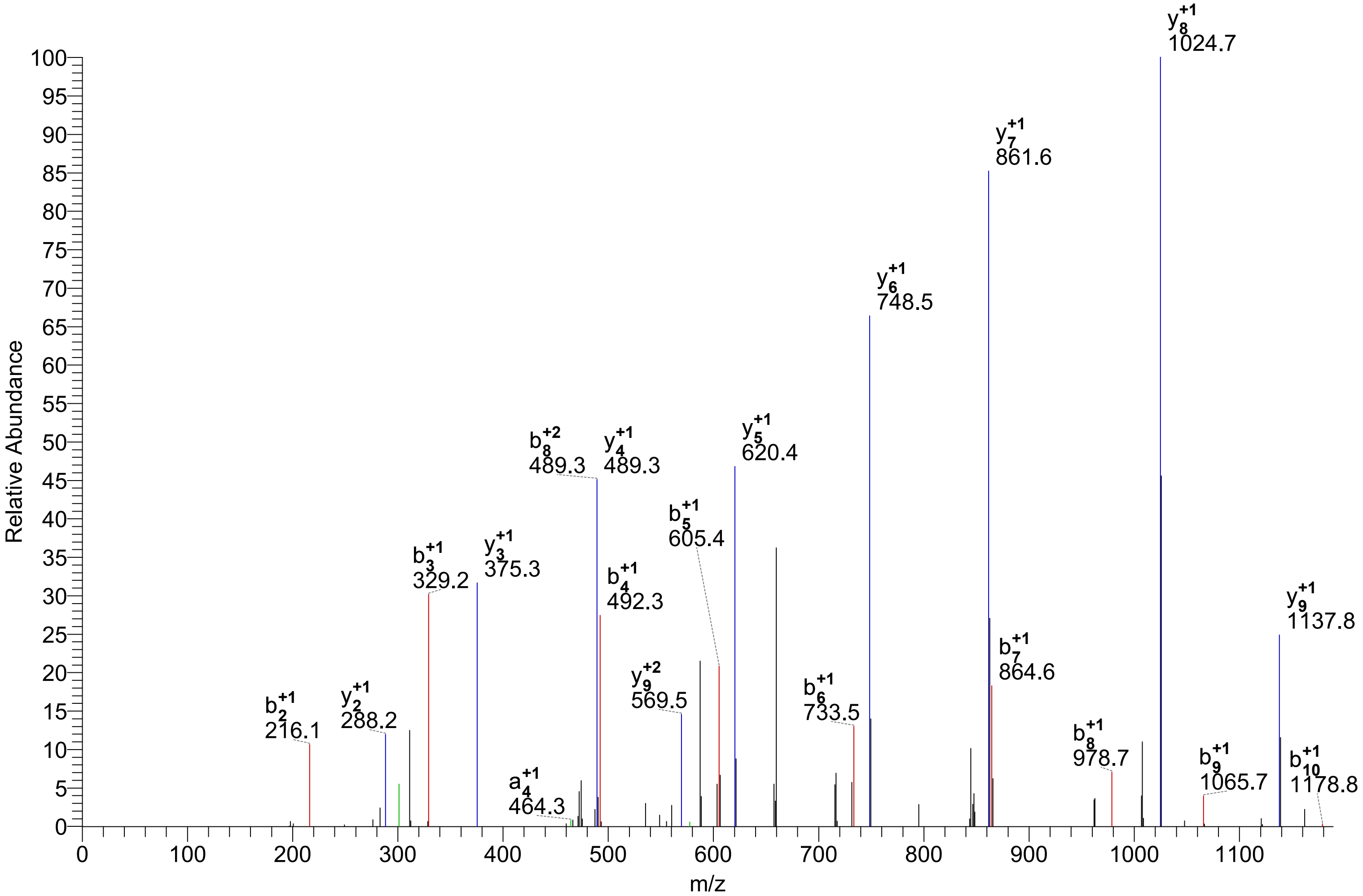
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                               P      Score   Coverage   Accession
Scan(s)        Sequence                                     MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

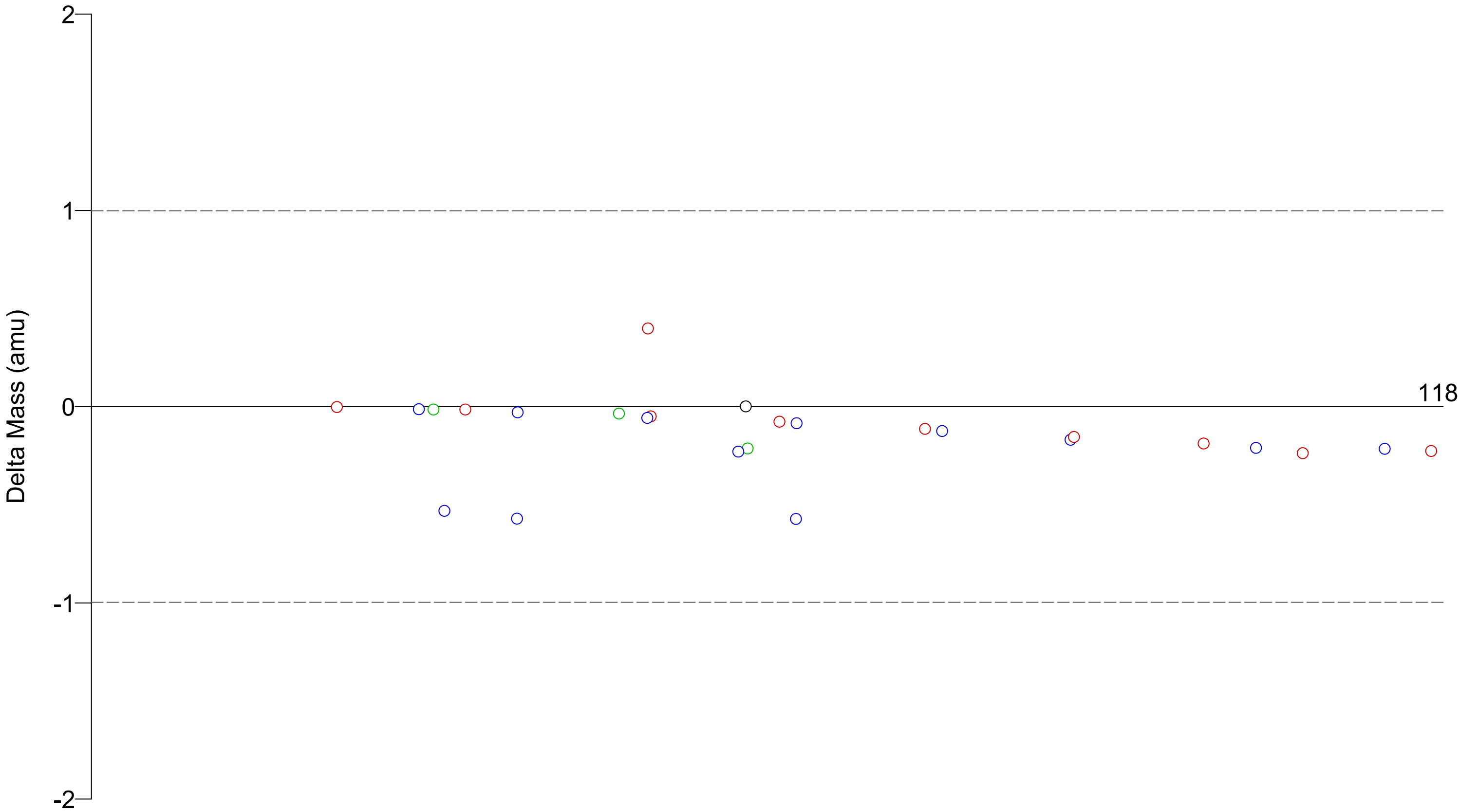
IPI:IPI00829806.1|TREMBL:Q0ZCH8;Q0                                       3e-006  10.2     0.0        0
19287468 - 1  K.NTLYLQMNSLR.A                             1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

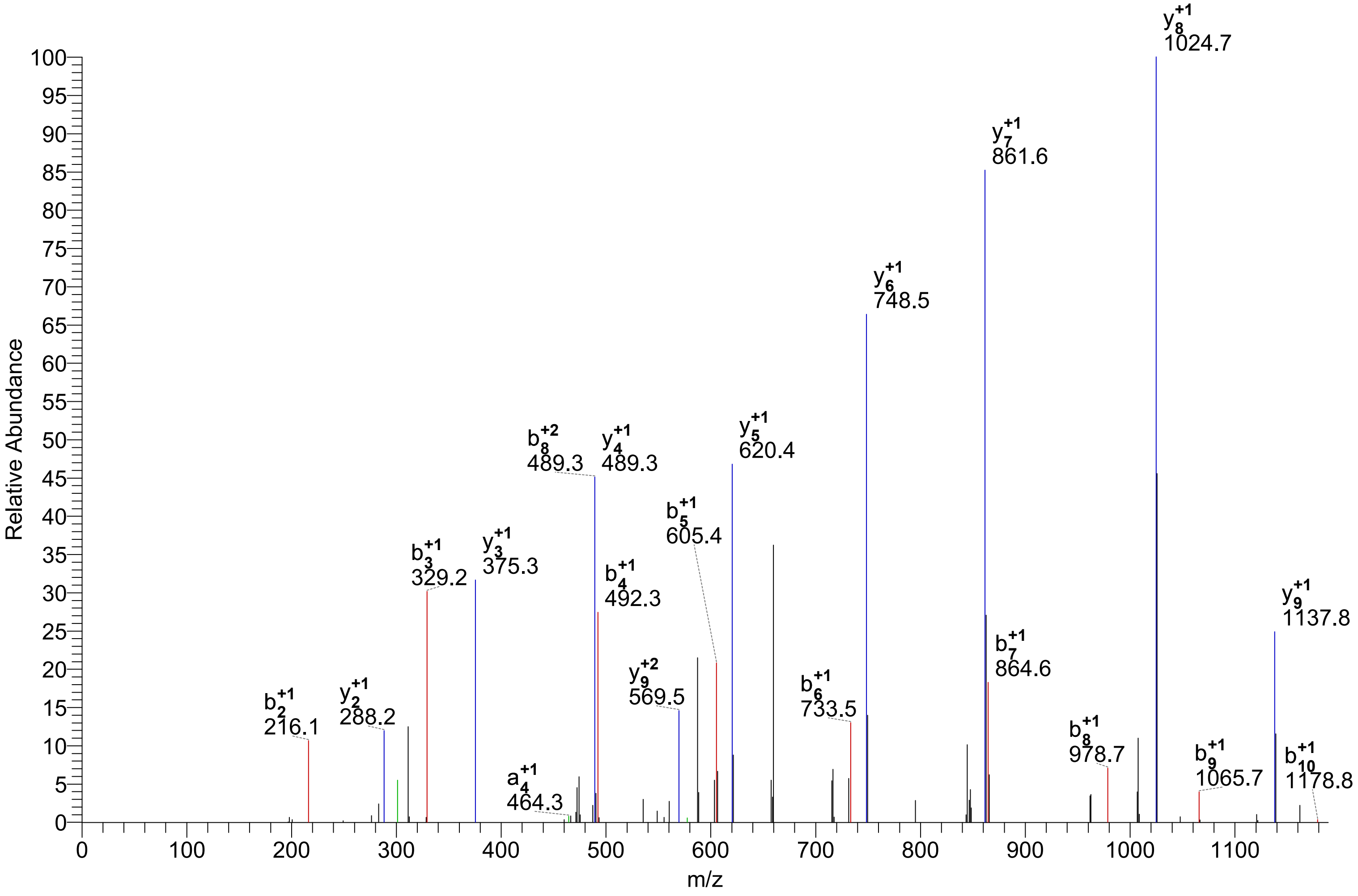
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

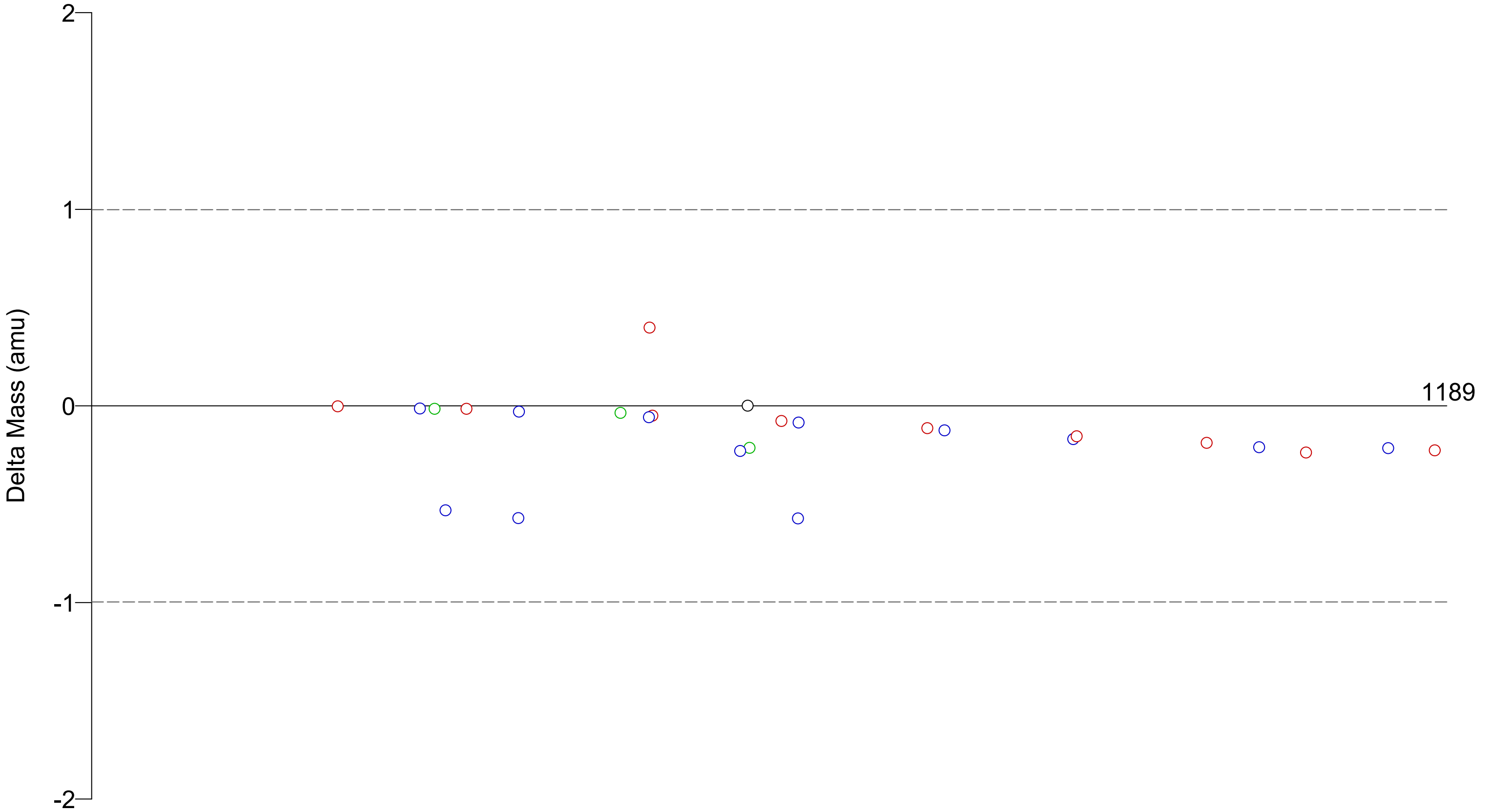
IPI:IPI00829976.1|TREMBL:A2N192|EN                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                       1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

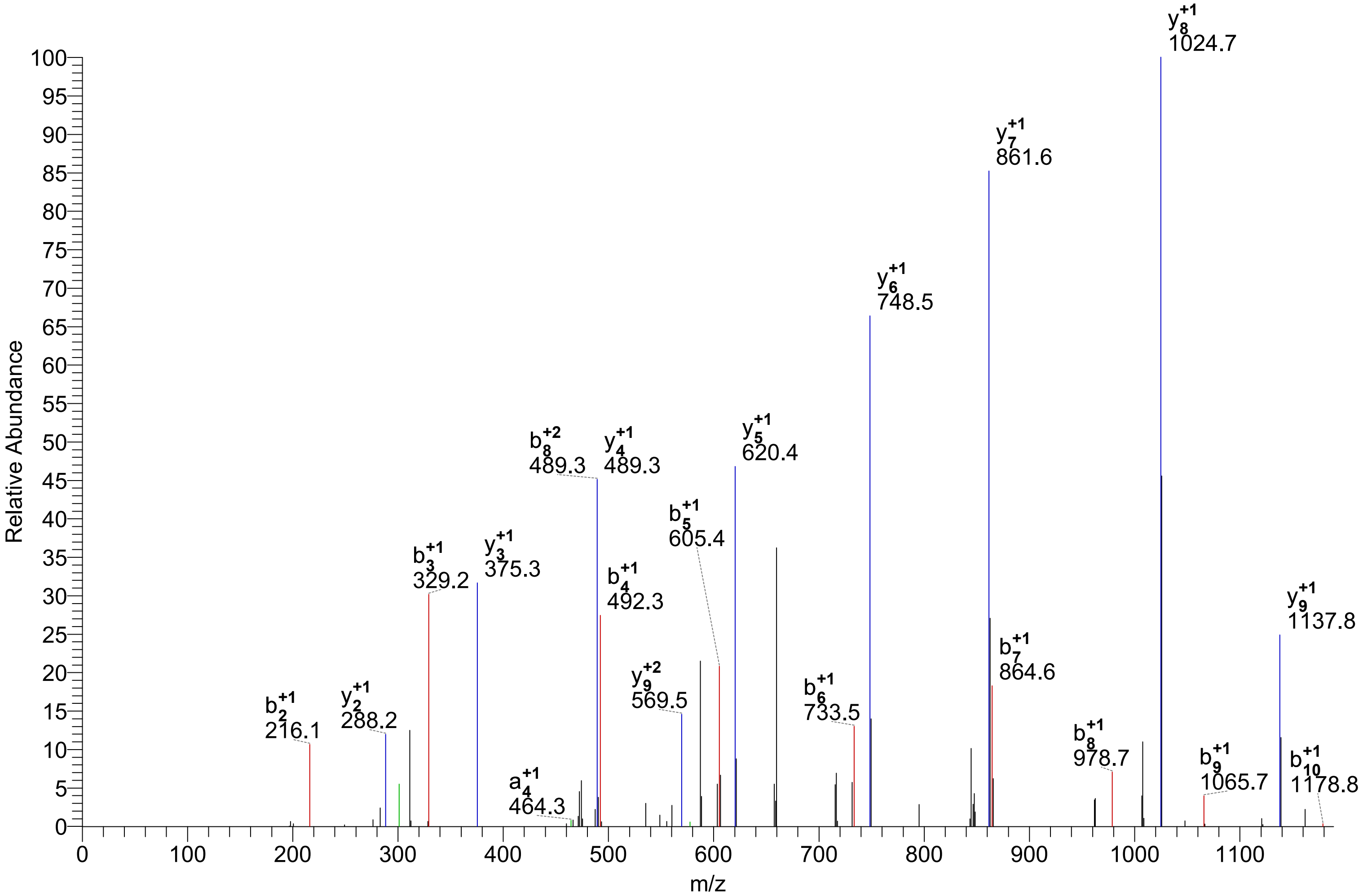
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                      1238.66
 L    301.19     329.18                                      1137.61
 Y    464.25     492.25                                      1024.52
 L    577.33     605.33                                       861.46
 Q    705.39     733.39                                       748.38
 M    836.43     864.43                                       620.32
 N    950.48     978.47                                       489.28
 S   1037.51    1065.50                                       375.24
 L   1150.59    1178.59                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

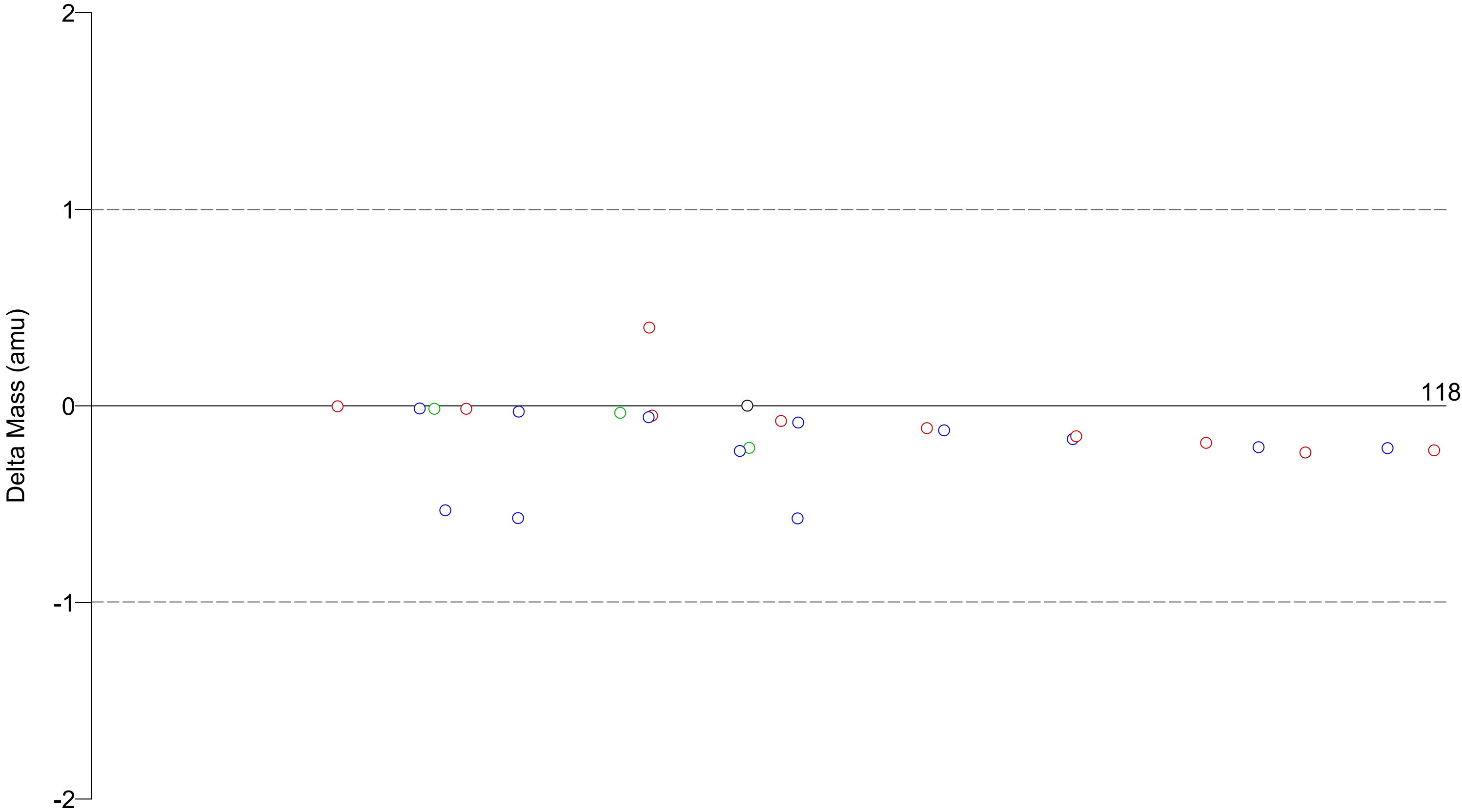
IPI:IPI00830088.1|ENSEMBL:ENSP0000                                  3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                           1352.70    2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

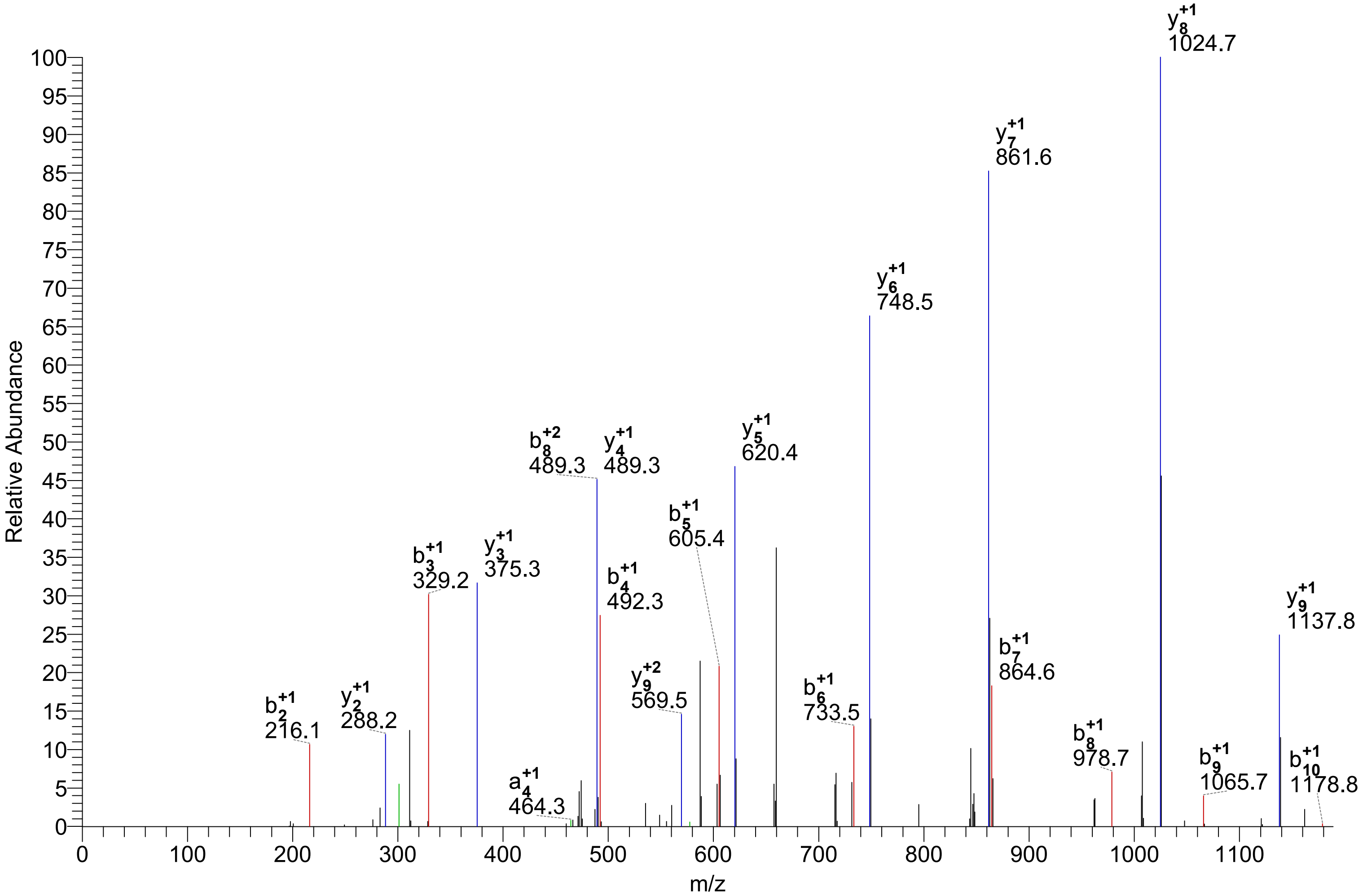
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



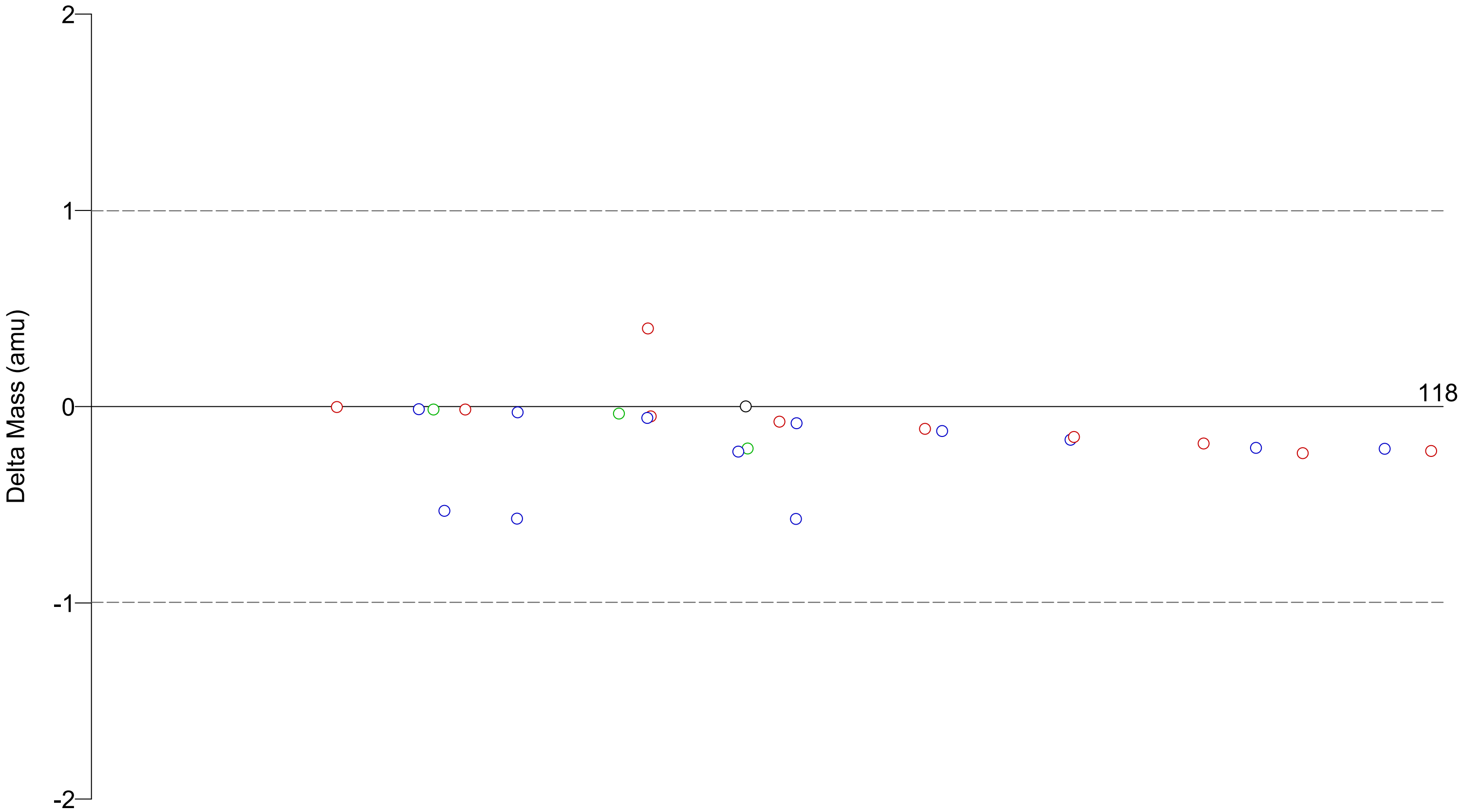
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                913    z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00854707.1|TREMBL:A2J1M5;Q0                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

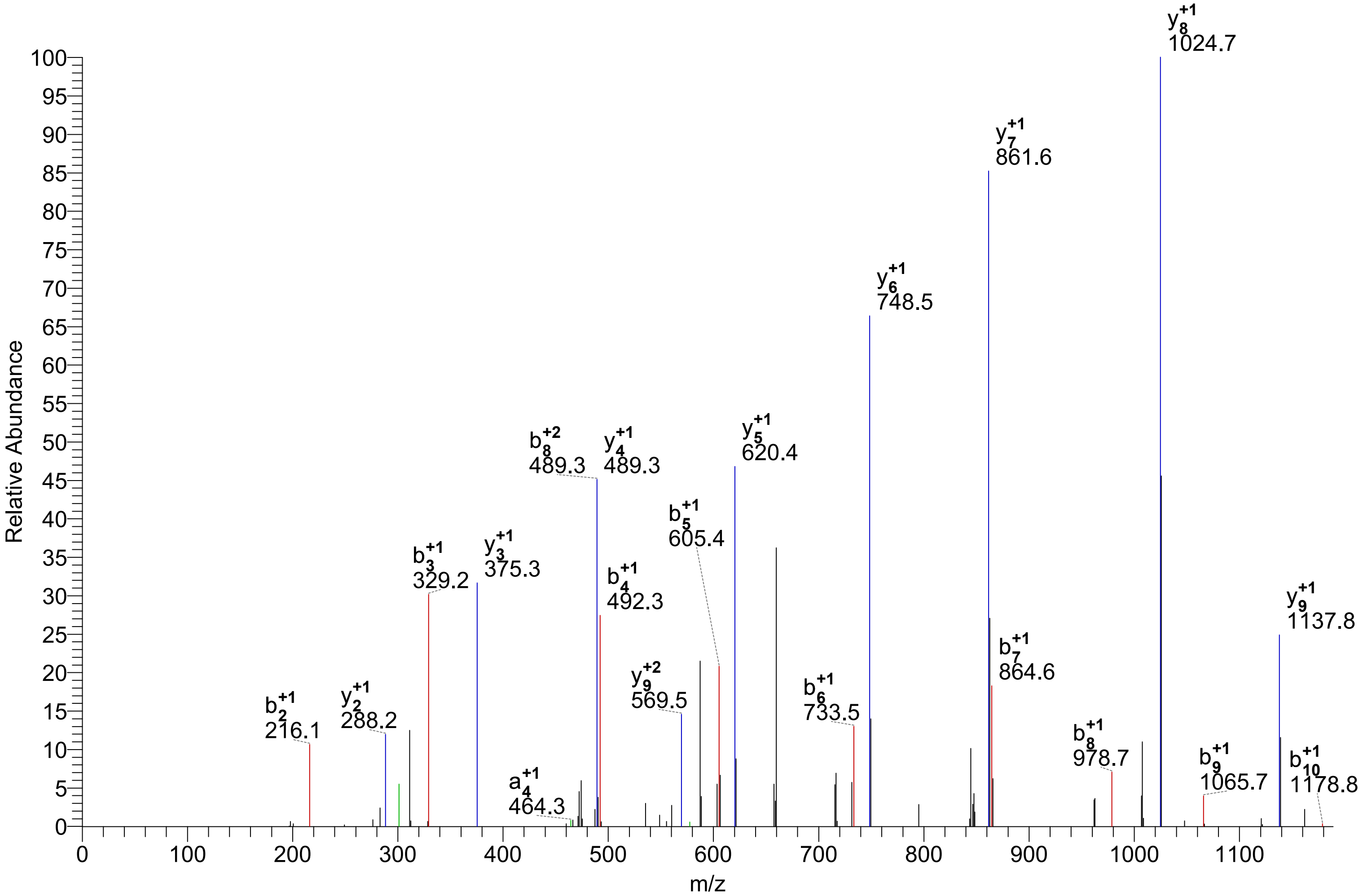
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



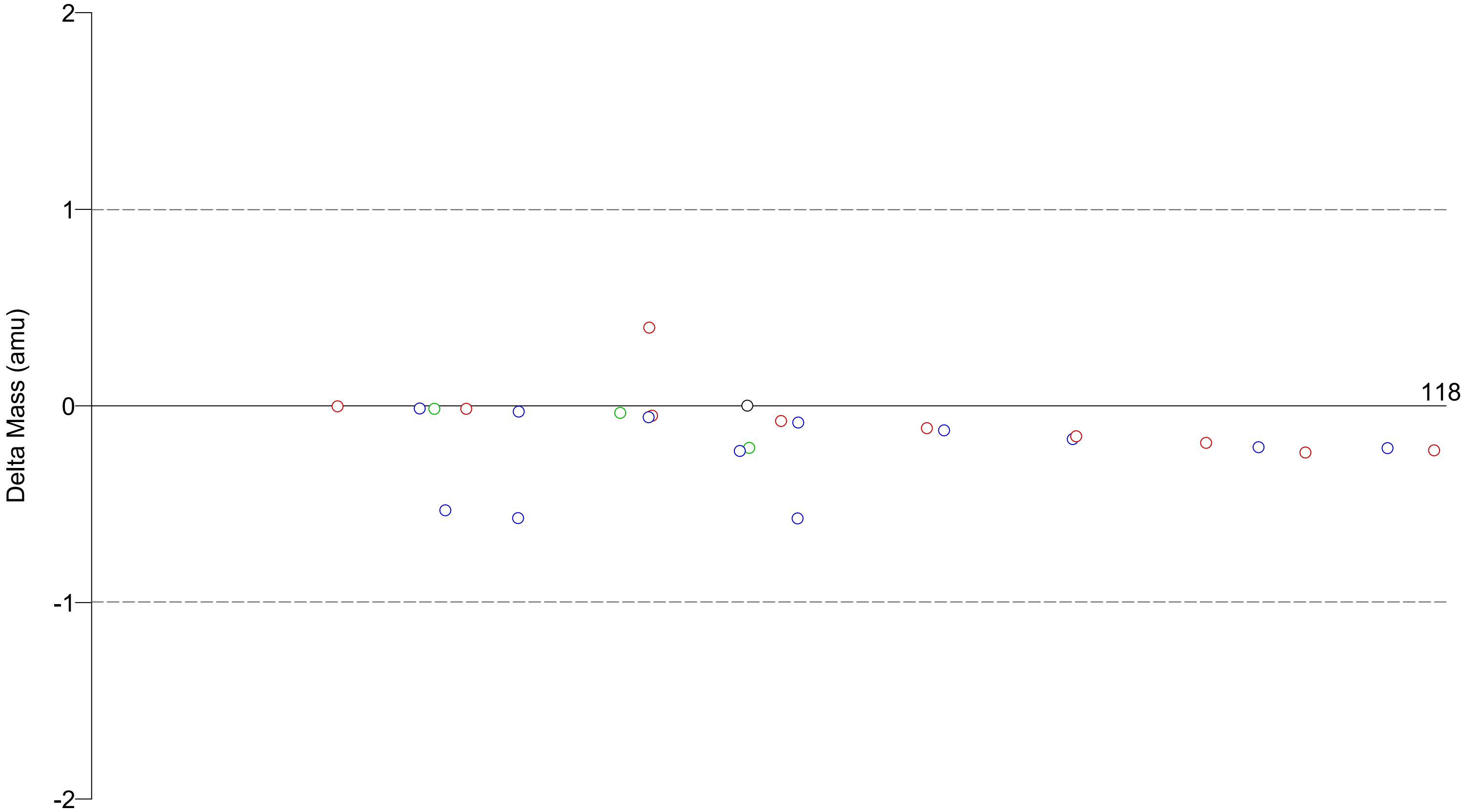
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00873155.2|TREMBL:A6NG04|EN                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

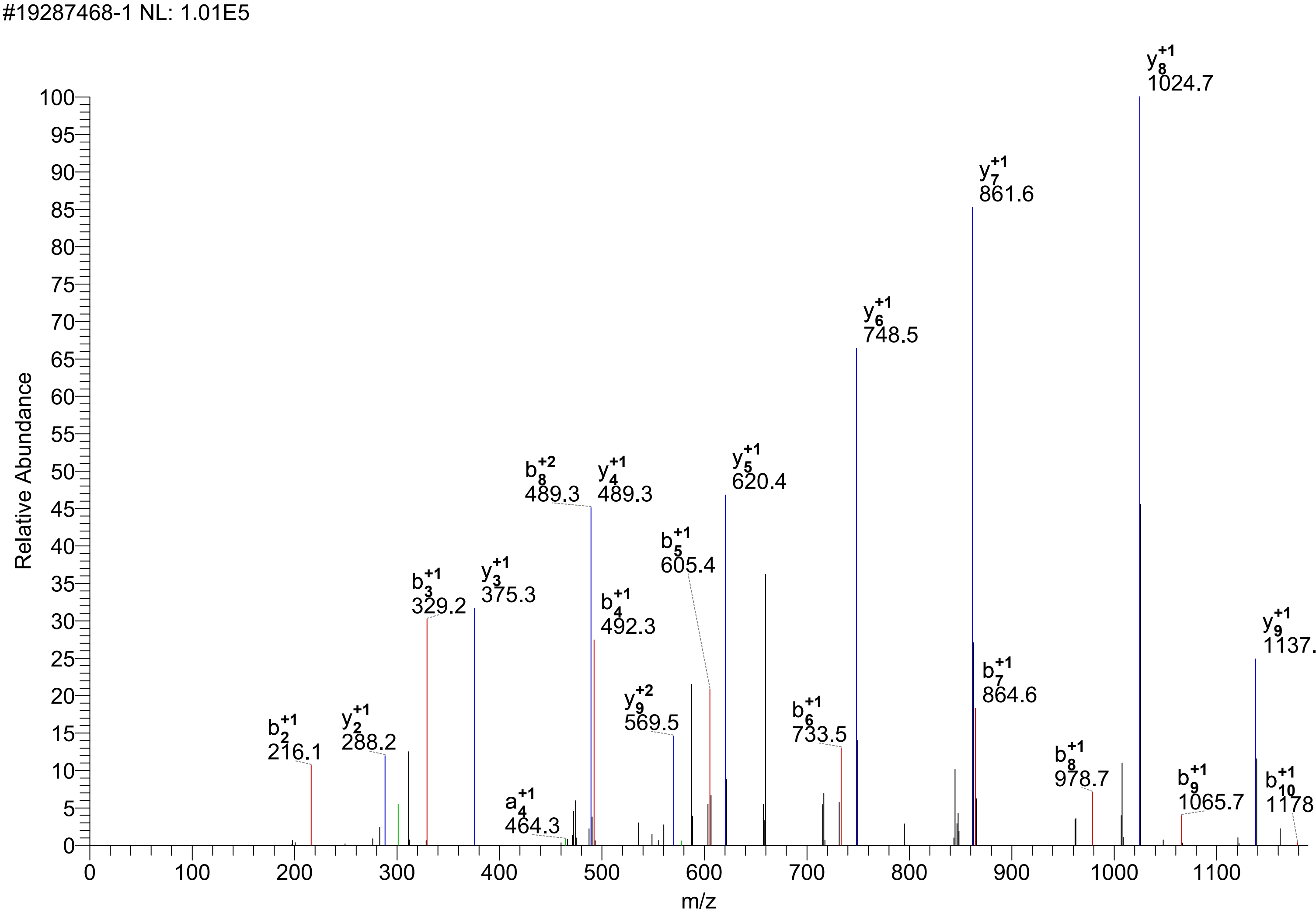
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



Delta Mass (amu)
2
1
0
-1
-2
1189



#19287468-1 NL: 1.01E5
Relative Abundance
m/z
y_8^{+1} 1024.7
y_7^{+1} 861.6
y_6^{+1} 748.5
y_5^{+1} 620.4
b_8^{+2} 489.3
y_4^{+1} 489.3
b_5^{+1} 605.4
b_3^{+1} 329.2
y_3^{+1} 375.3
b_4^{+1} 492.3
y_9^{+1} 1137.8
b_7^{+1} 864.6
y_9^{+2} 569.5
b_6^{+1} 733.5
b_2^{+1} 216.1
y_2^{+1} 288.2
b_8^{+1} 978.7
b_9^{+1} 1065.7
b_{10}^{+1} 1178.8
a_4^{+1} 464.3
0
100
200
300
400
500
600
700
800
900
1000
1100

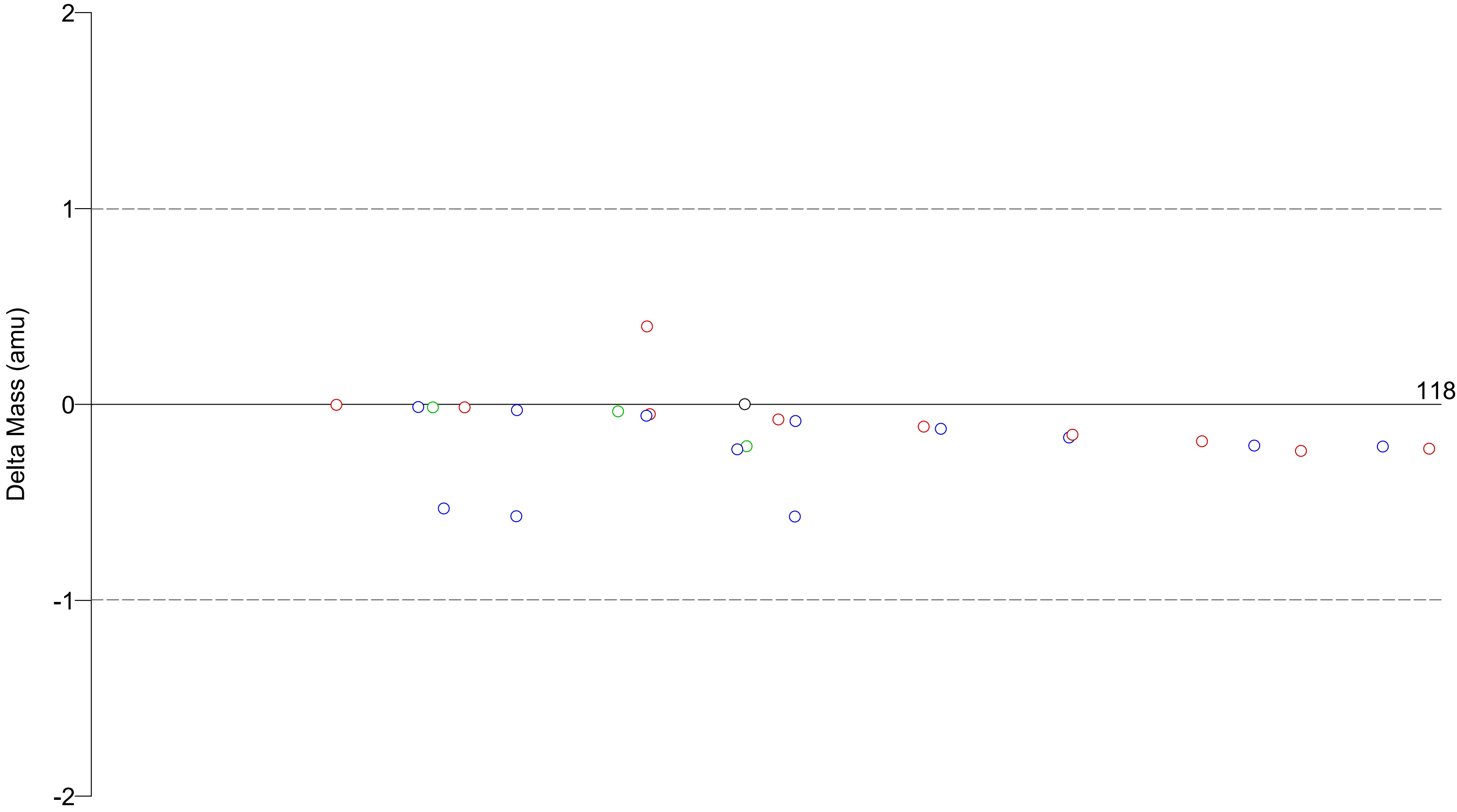
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00888191.1|REFSEQ:XP_001714                                3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                        1352.70   2  3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

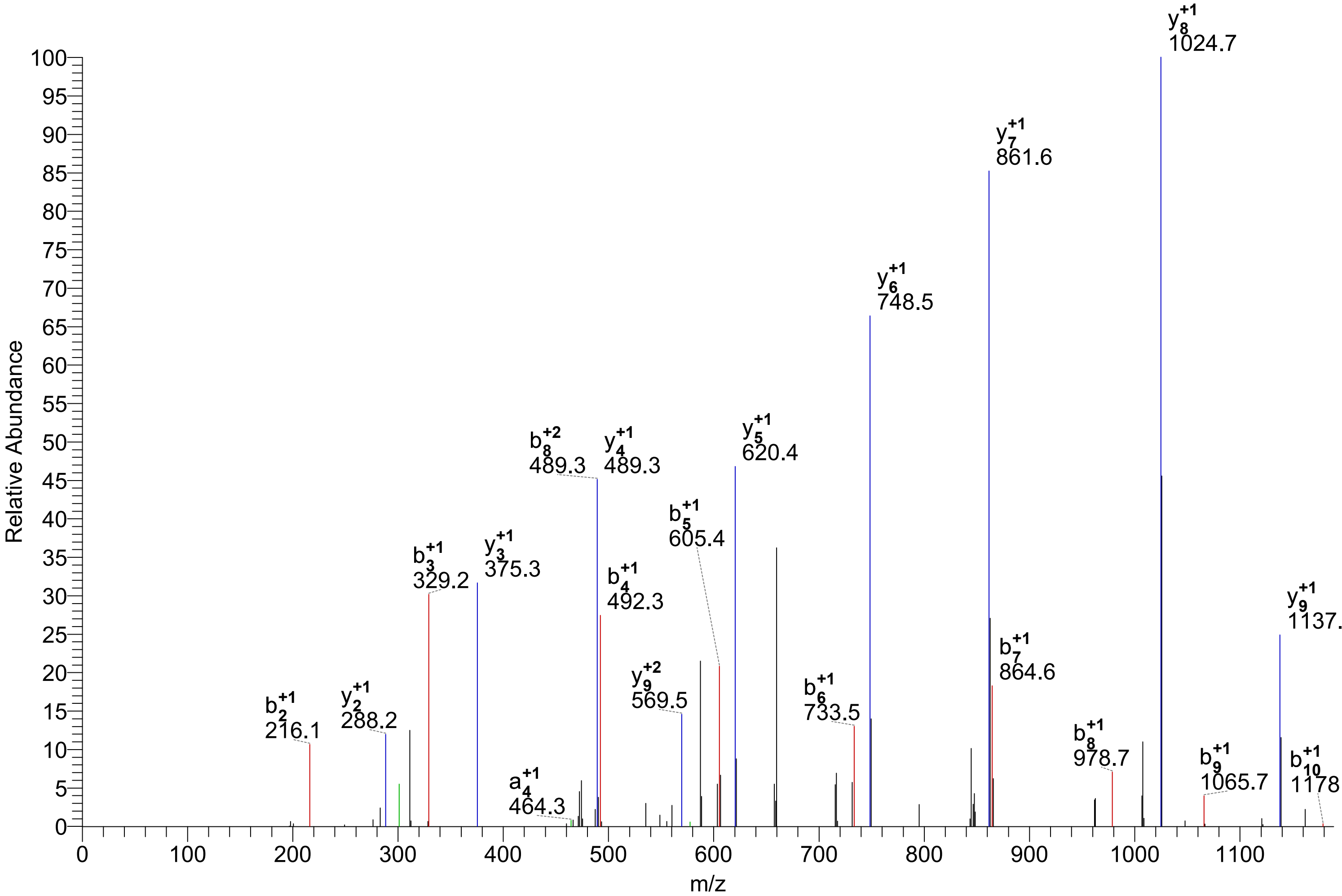
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count

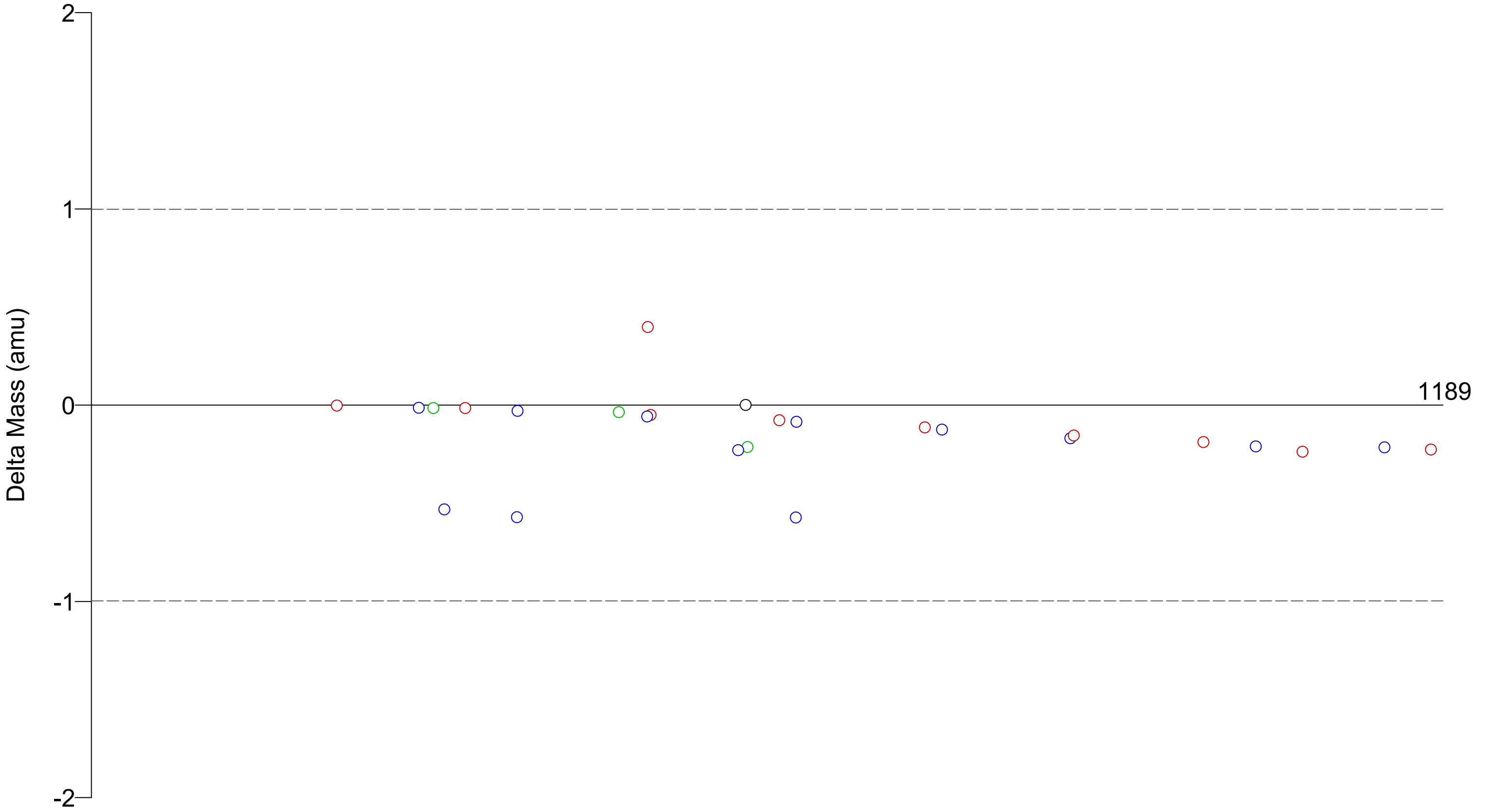
IPI:IPI00888954.1|REFSEQ:XP_001717                                     3e-006  10.2     0.0       0
19287468 - 1  K.NTLYLQMNSLR.A                            1352.70   2   3e-006  4.027  0.643   1526.5 1   20/30   39

1 of 1 peptide matches reported, 0 removed due to filtering
```

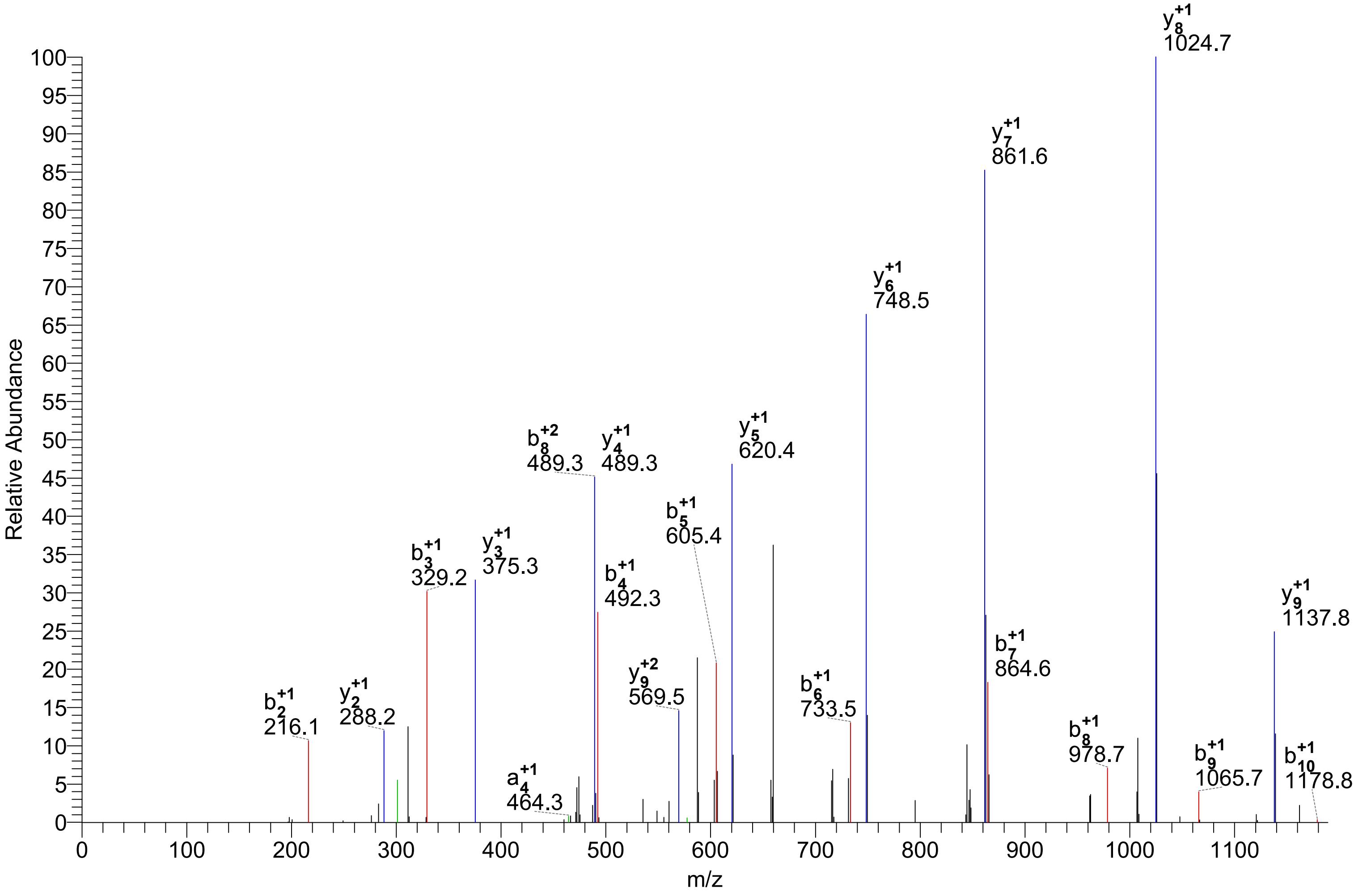
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1238.66
 L    301.19     329.18                                     1137.61
 Y    464.25     492.25                                     1024.52
 L    577.33     605.33                                      861.46
 Q    705.39     733.39                                      748.38
 M    836.43     864.43                                      620.32
 N    950.48     978.47                                      489.28
 S   1037.51    1065.50                                      375.24
 L   1150.59    1178.59                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.01E5



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

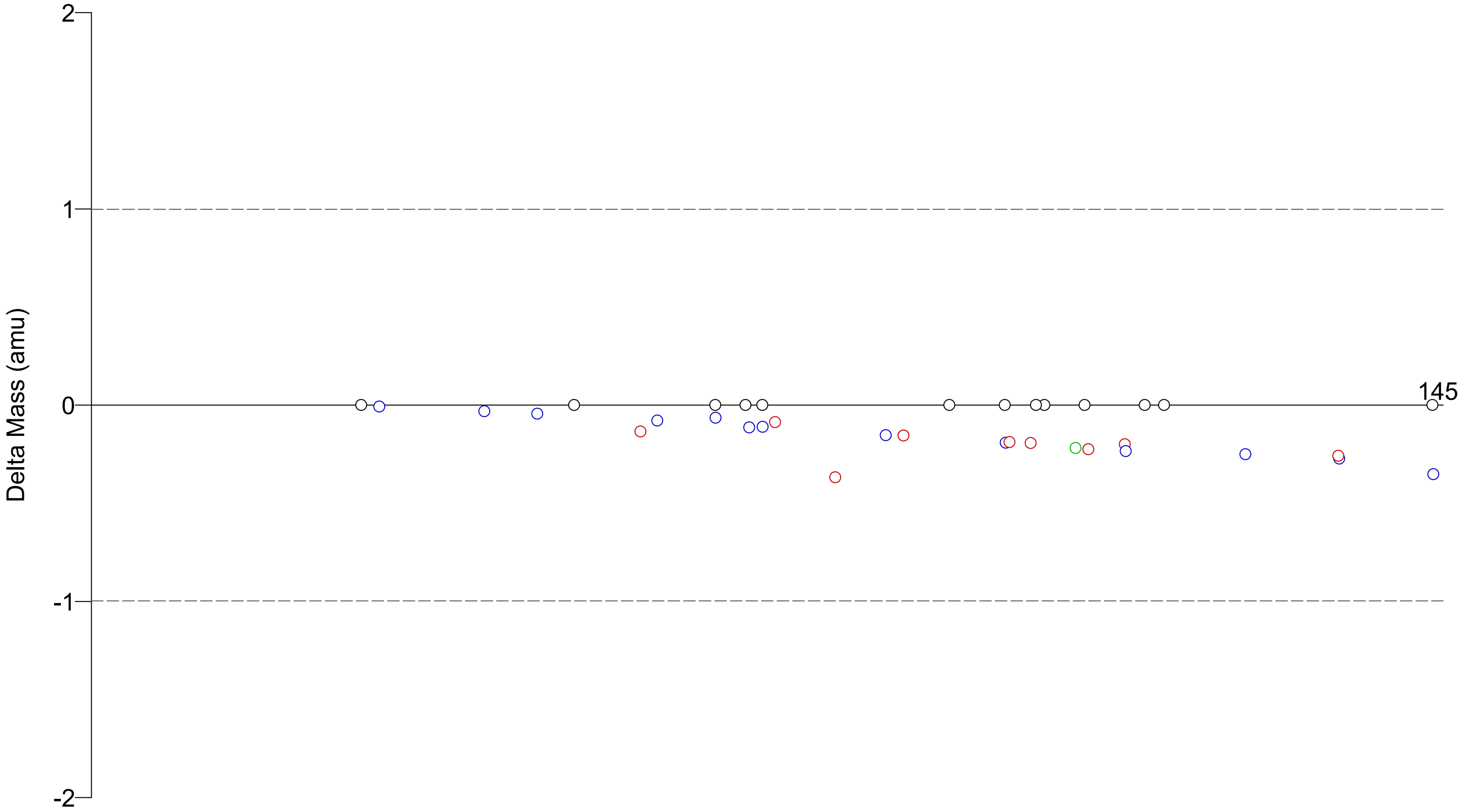
IPI:IPI00022432.1|SWISS-PROT:P02766|TREMBL:A6XMH1;Q53WY6;Q549C    3e-006  10.3     0.0       0
19287468 - 1  K.TSESGELHGLTTEEEFVEGIYK.V             2455.15   3  3e-006  5.015  0.570   946.8  1   30/126  2

1 of 1 peptide matches reported, 0 removed due to filtering
```

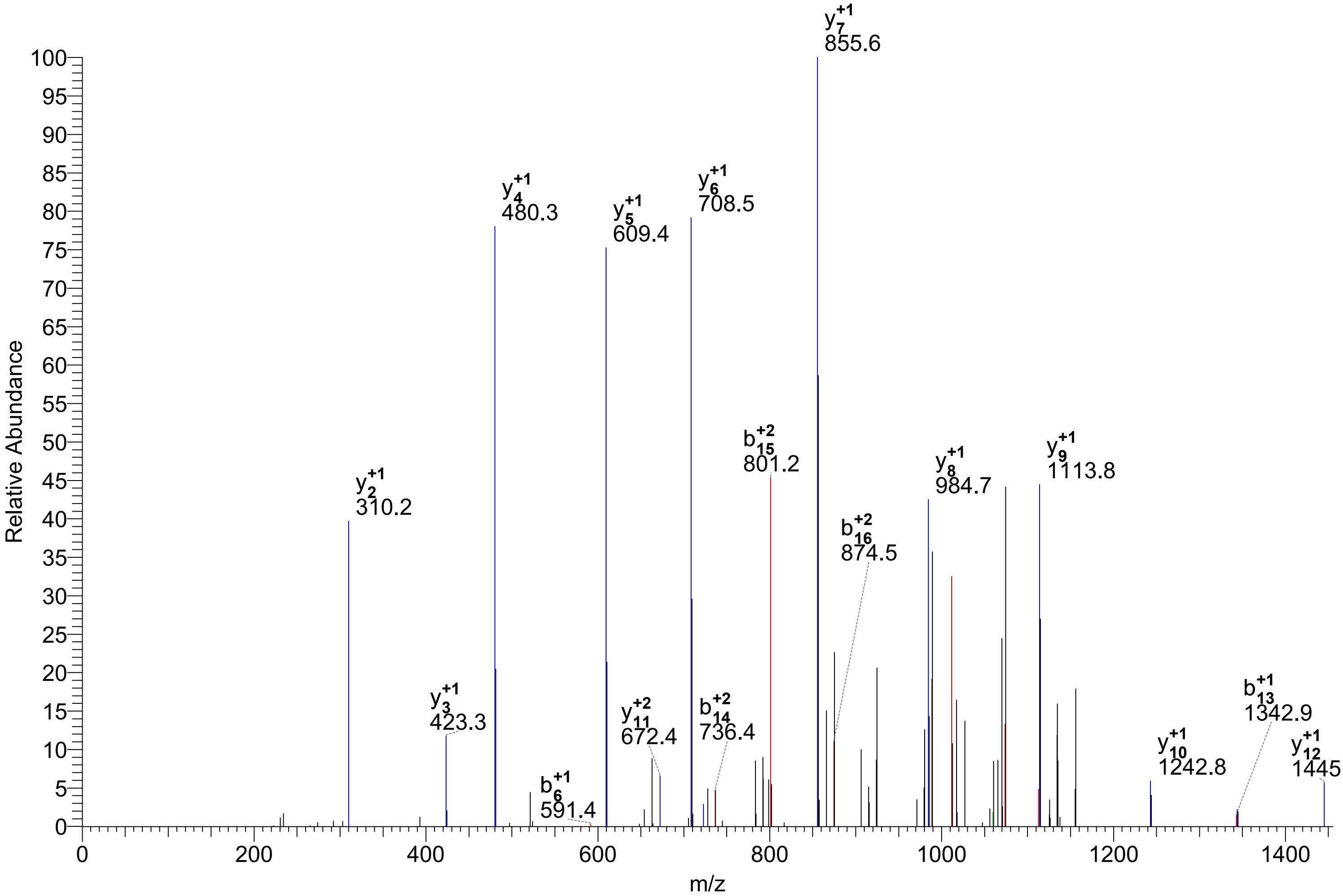
```
DTA for scans: 19287468-1
Precursor ion: 819.06
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 S    161.09     189.09                                     2354.10
 E    290.13     318.13                                     2267.07
 S    377.17     405.16                                     2138.03
 G    434.19     462.18                                     2051.00
 E    563.23     591.23                                     1993.98
 L    676.31     704.31                                     1864.93
 H    813.37     841.37                                     1751.85
 G    870.40     898.39                                     1614.79
 L    983.48    1011.47                                     1557.77
 T   1084.53    1112.52                                     1444.68
 T   1185.57    1213.57                                     1343.64
 E   1314.62    1342.61                                     1242.59
 E   1443.66    1471.65                                     1113.55
 E   1572.70    1600.70                                      984.50
 F   1719.77    1747.77                                      855.46
 V   1818.84    1846.83                                      708.39
 E   1947.88    1975.88                                      609.32
 G   2004.90    2032.90                                      480.28
 I   2117.99    2145.98                                      423.26
 Y   2281.05    2309.05                                      310.18
 K                                                           147.11
```



#19287468-1 NL: 6.24E5



```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                          MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

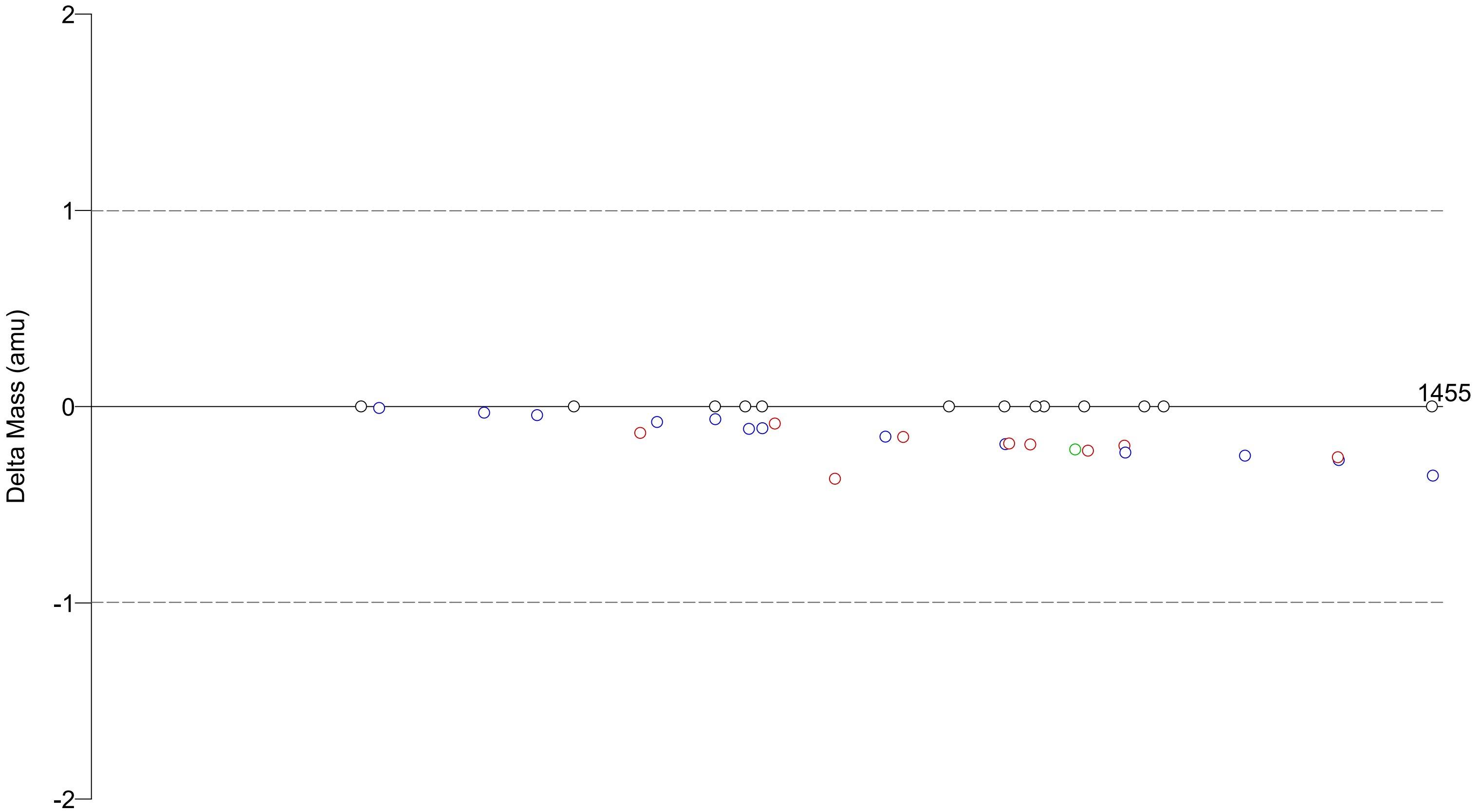
IPI:IPI00646384.1|VEGA:OTTHUMP0000                                           3e-006  10.3     0.0       0
19287468 - 1  K.TSESGELHGLTTEEEFVEGIYK.V                      2455.15    3  3e-006  5.015  0.570   946.8  1   30/126  2

1 of 1 peptide matches reported, 0 removed due to filtering
```

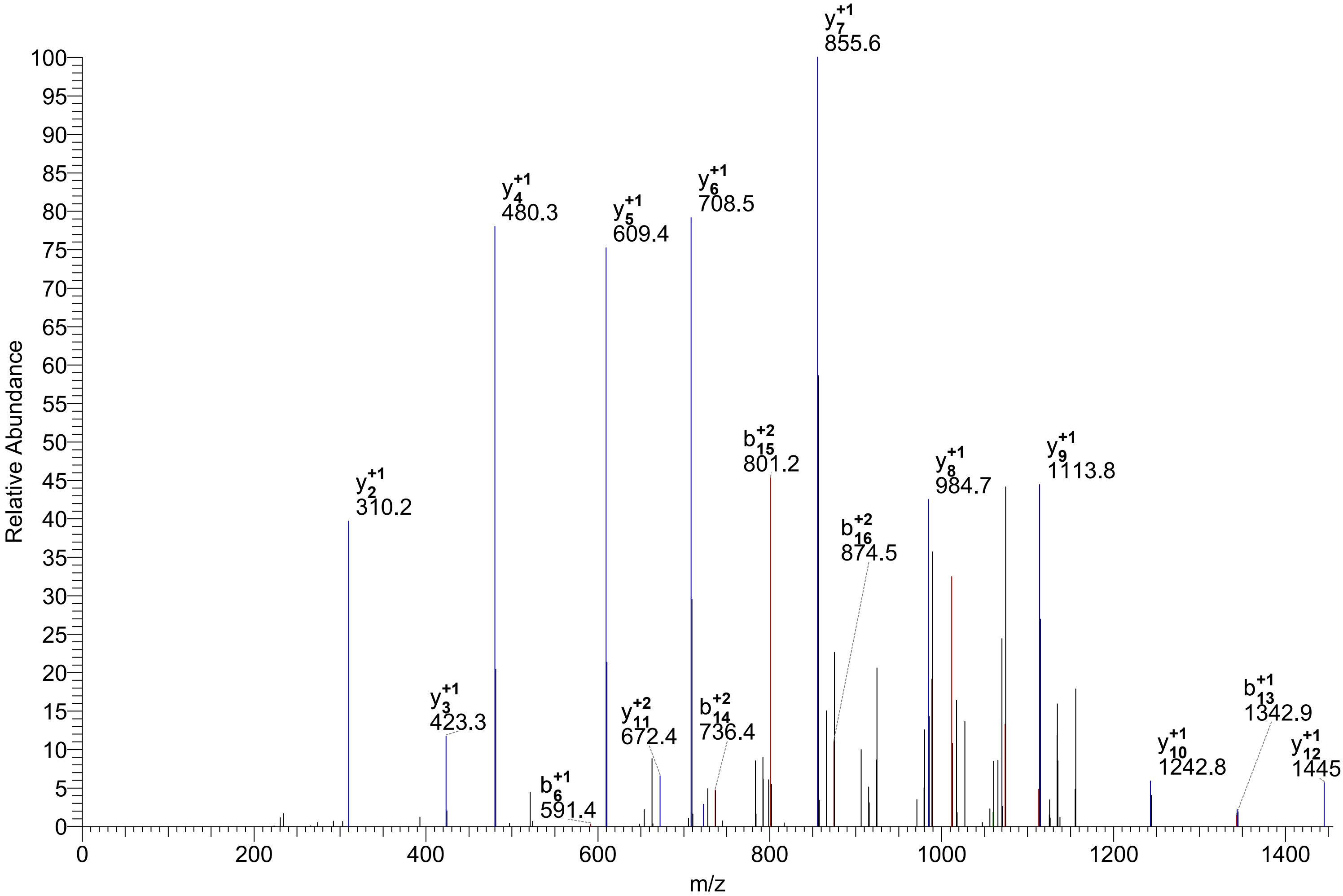
```
DTA for scans: 19287468-1
Precursor ion: 819.06
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 S    161.09     189.09                                     2354.10
 E    290.13     318.13                                     2267.07
 S    377.17     405.16                                     2138.03
 G    434.19     462.18                                     2051.00
 E    563.23     591.23                                     1993.98
 L    676.31     704.31                                     1864.93
 H    813.37     841.37                                     1751.85
 G    870.40     898.39                                     1614.79
 L    983.48    1011.47                                     1557.77
 T   1084.53    1112.52                                     1444.68
 T   1185.57    1213.57                                     1343.64
 E   1314.62    1342.61                                     1242.59
 E   1443.66    1471.65                                     1113.55
 E   1572.70    1600.70                                      984.50
 F   1719.77    1747.77                                      855.46
 V   1818.84    1846.83                                      708.39
 E   1947.88    1975.88                                      609.32
 G   2004.90    2032.90                                      480.28
 I   2117.99    2145.98                                      423.26
 Y   2281.05    2309.05                                      310.18
 K                                                           147.11
```



#19287468-1 NL: 6.24E5



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

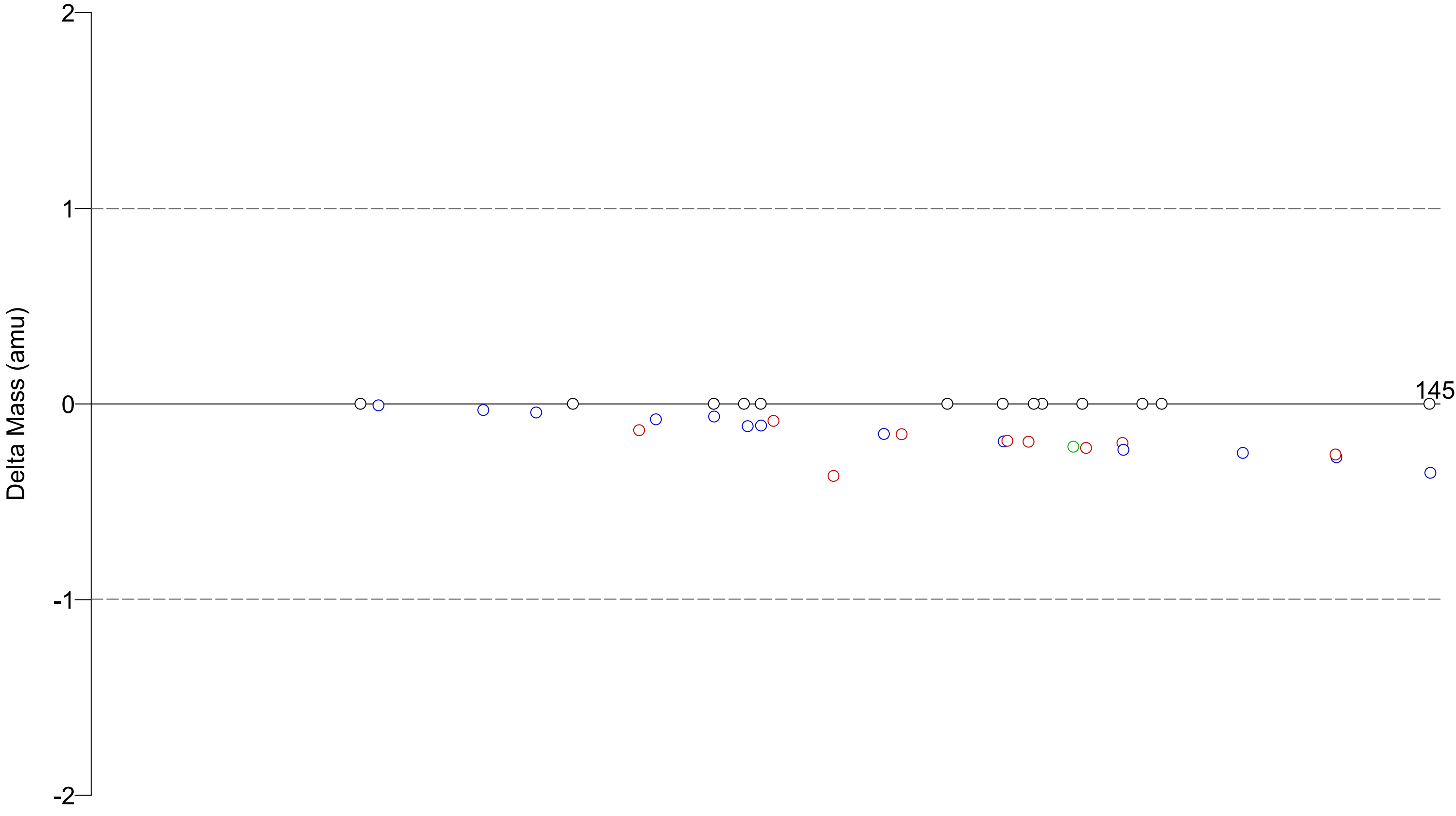
IPI:IPI00855916.1|TREMBL:A6XGL1 Ta                                3e-006  10.3     0.0       0
19287468 - 1  K.TSESGELHGLTTEEEFVEGIYK.V            2455.15    3  3e-006  5.015  0.570   946.8  1   30/126  2

1 of 1 peptide matches reported, 0 removed due to filtering
```

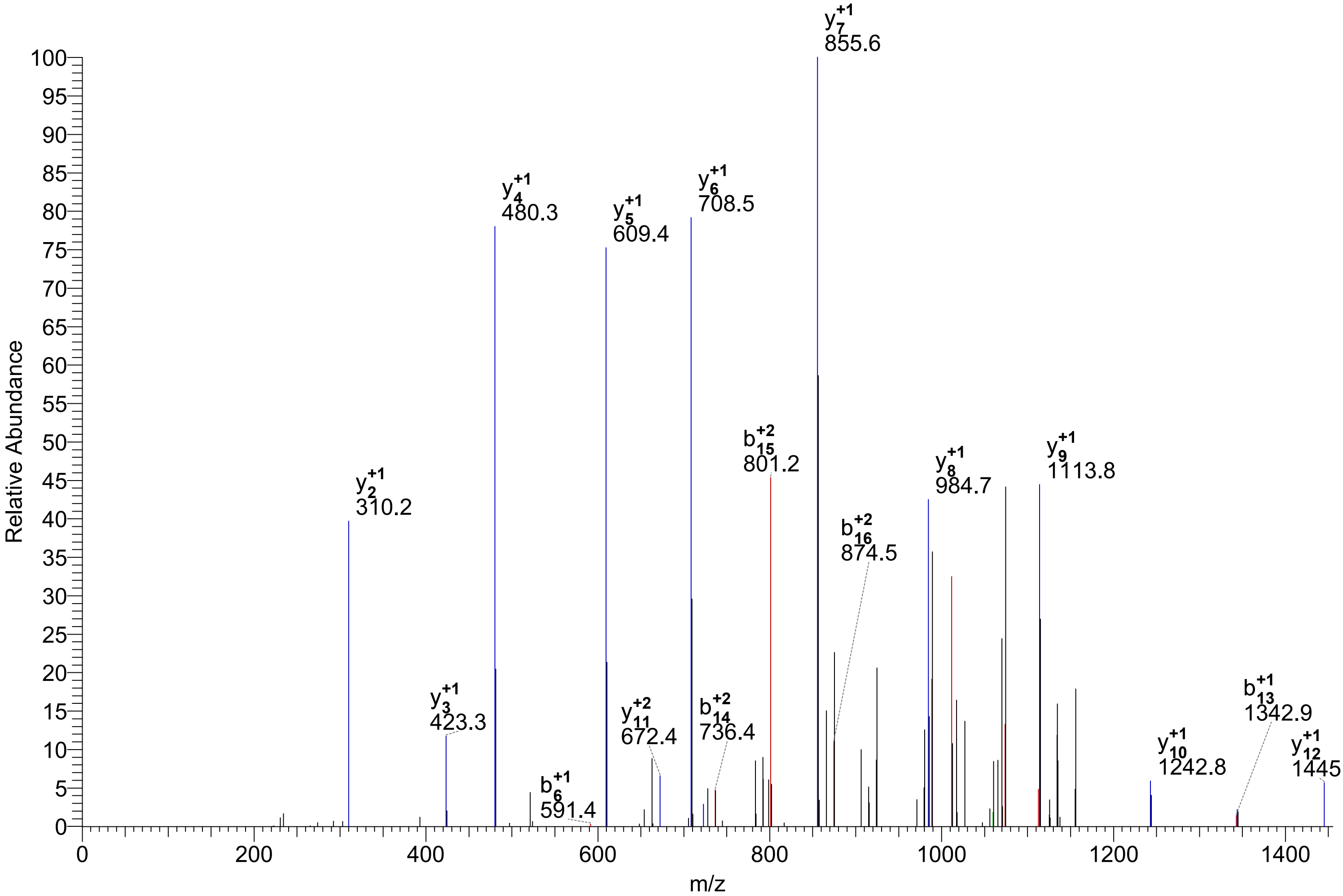
```
DTA for scans: 19287468-1
Precursor ion: 819.06
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 S    161.09     189.09                                     2354.10
 E    290.13     318.13                                     2267.07
 S    377.17     405.16                                     2138.03
 G    434.19     462.18                                     2051.00
 E    563.23     591.23                                     1993.98
 L    676.31     704.31                                     1864.93
 H    813.37     841.37                                     1751.85
 G    870.40     898.39                                     1614.79
 L    983.48    1011.47                                     1557.77
 T   1084.53    1112.52                                     1444.68
 T   1185.57    1213.57                                     1343.64
 E   1314.62    1342.61                                     1242.59
 E   1443.66    1471.65                                     1113.55
 E   1572.70    1600.70                                      984.50
 F   1719.77    1747.77                                      855.46
 V   1818.84    1846.83                                      708.39
 E   1947.88    1975.88                                      609.32
 G   2004.90    2032.90                                      480.28
 I   2117.99    2145.98                                      423.26
 Y   2281.05    2309.05                                      310.18
 K                                                           147.11
```



#19287468-1 NL: 6.24E5



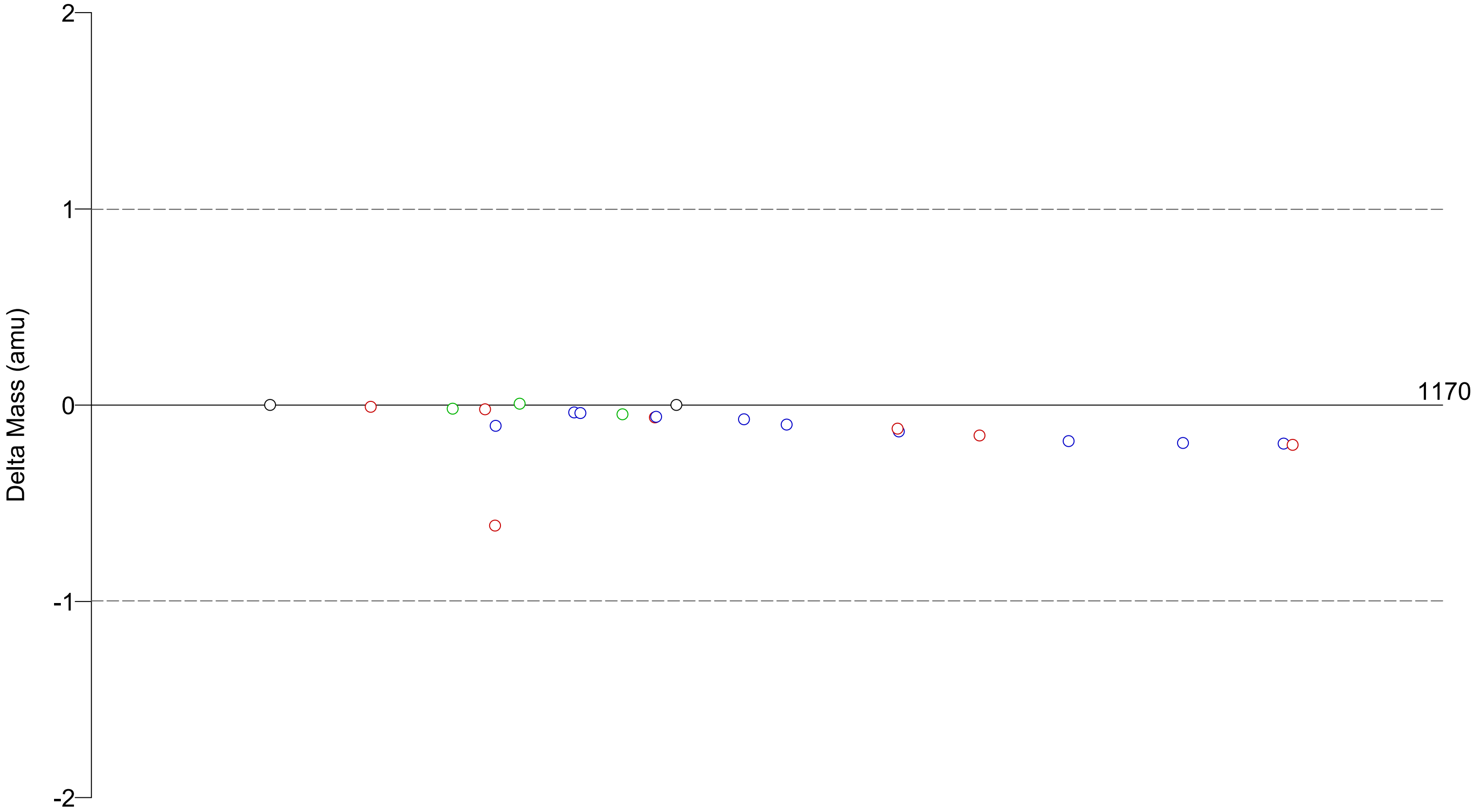
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00423463.1|TREMBL:Q6N094 Ta                                6e-006  20.2     0.0       0
2118291816 -  K.GPSVFPLAPSSK.S                       1186.65   2  0.02    2.948  0.348   465.0  1   15/33   14
2118291816 -  R.LSCAASGFTFR.S                        1217.56   2  6e-006  3.492  0.654   1231.4 1   20/30   3

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

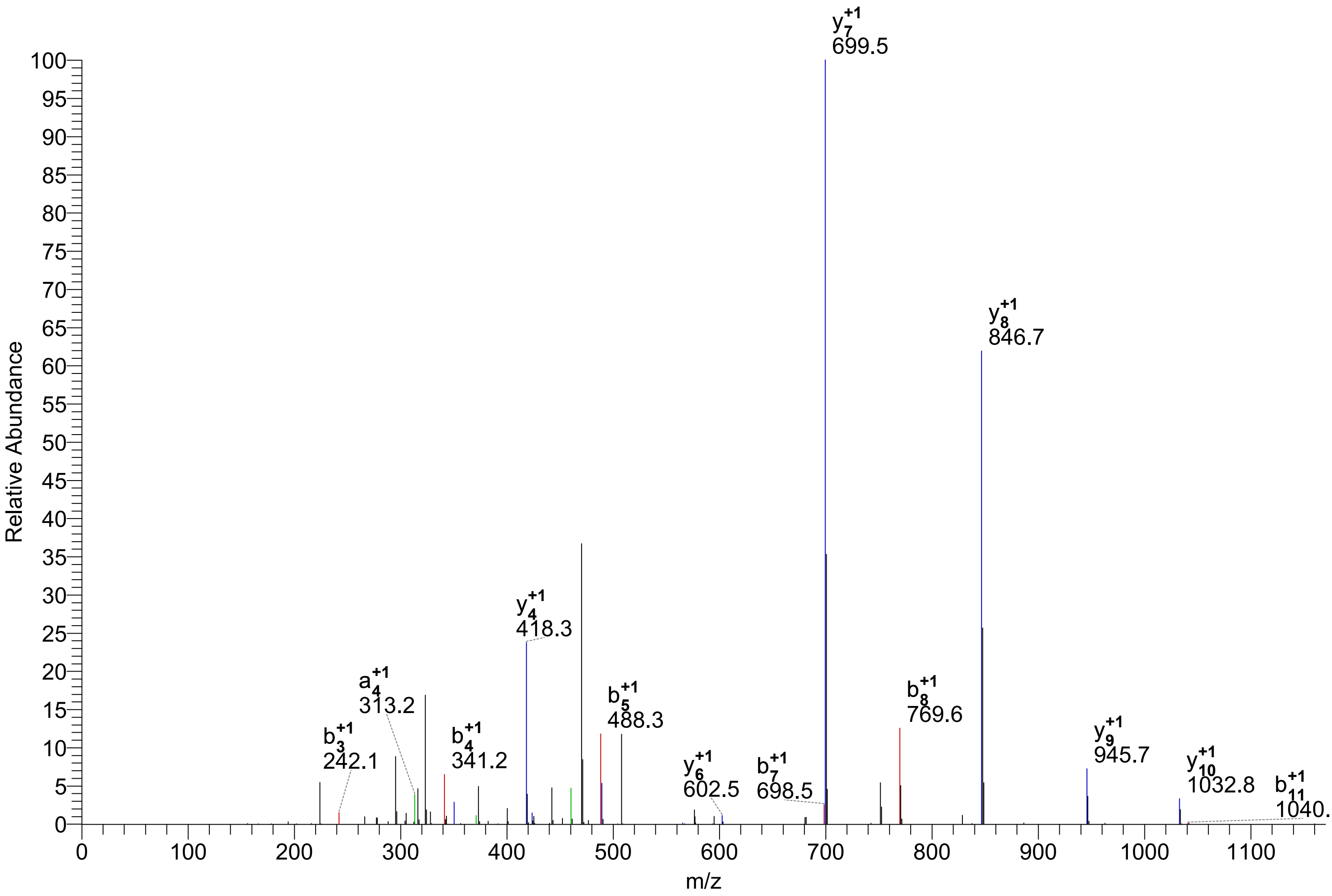
```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```



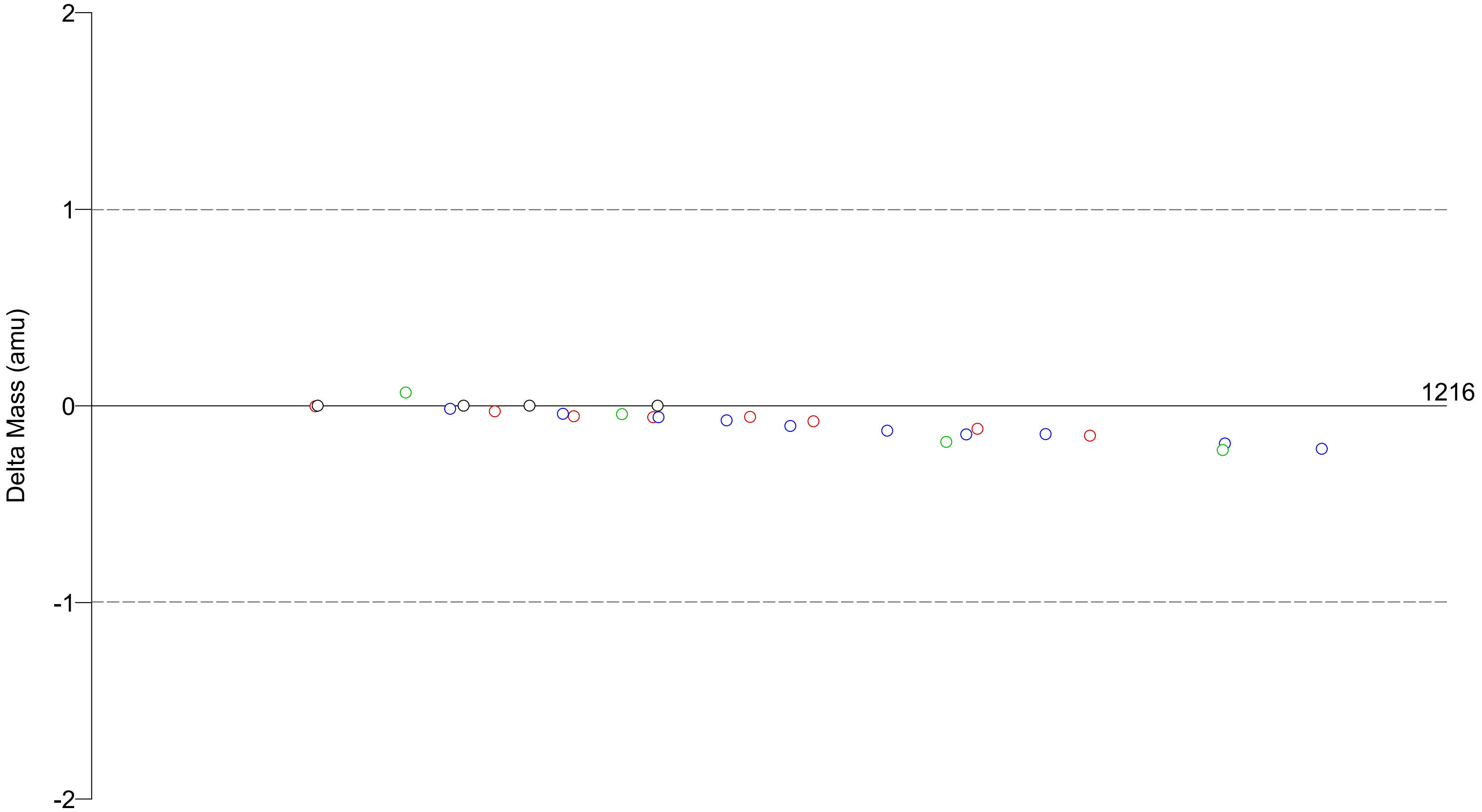
#2118291816-26226248 NL: 6.95E6



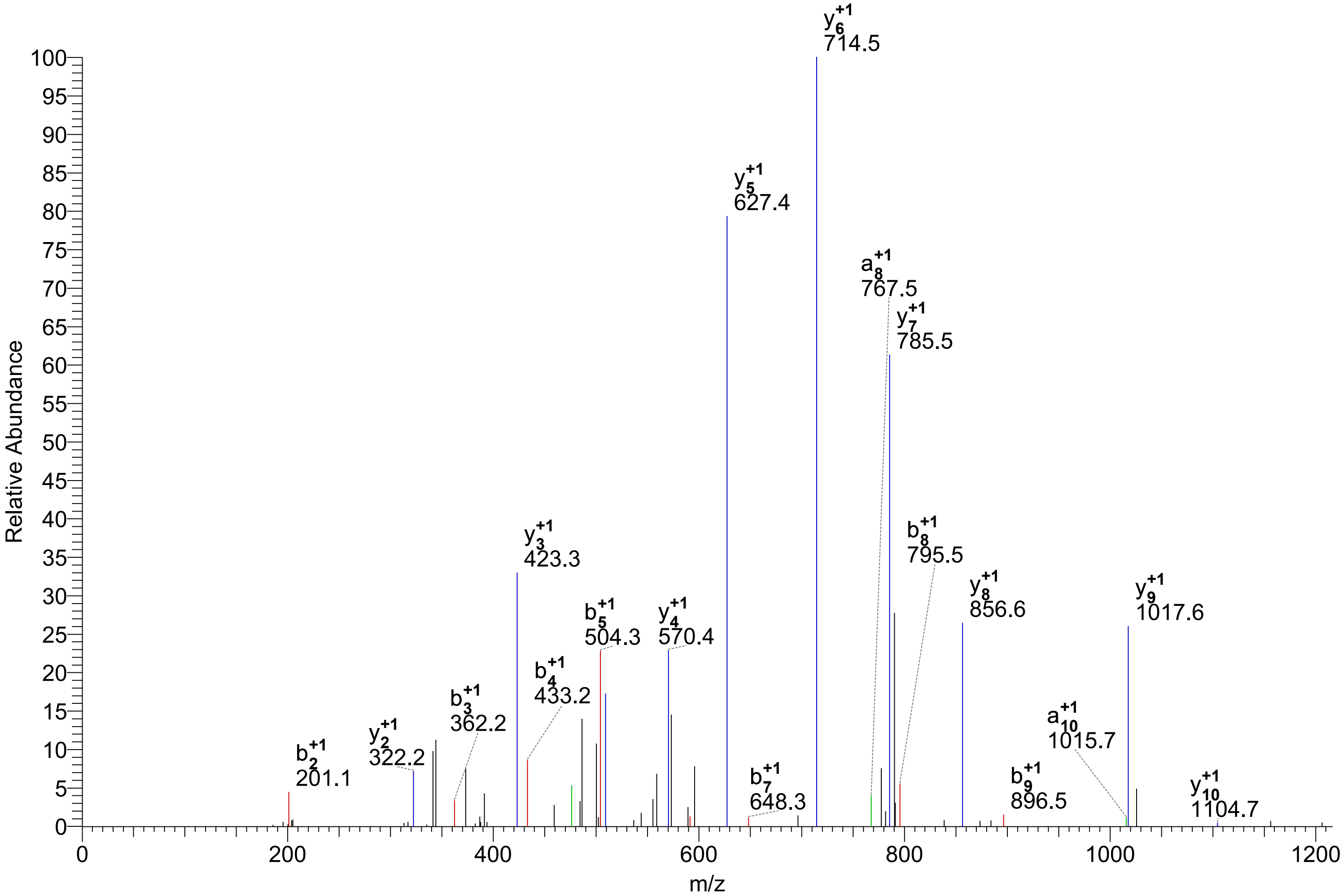
```
DTA for scans: 2118291816-26226248
Precursor ion: 609.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                     1104.48
 C    334.14     362.14                                     1017.45
 A    405.18     433.18                                      856.43
 A    476.22     504.21                                      785.39
 S    563.25     591.24                                      714.36
 G    620.27     648.27                                      627.32
 F    767.34     795.33                                      570.30
 T    868.39     896.38                                      423.24
 F   1015.46    1043.45                                      322.19
 R                                                           175.12
```



#2118291816-26226248 NL: 9.29E4



```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

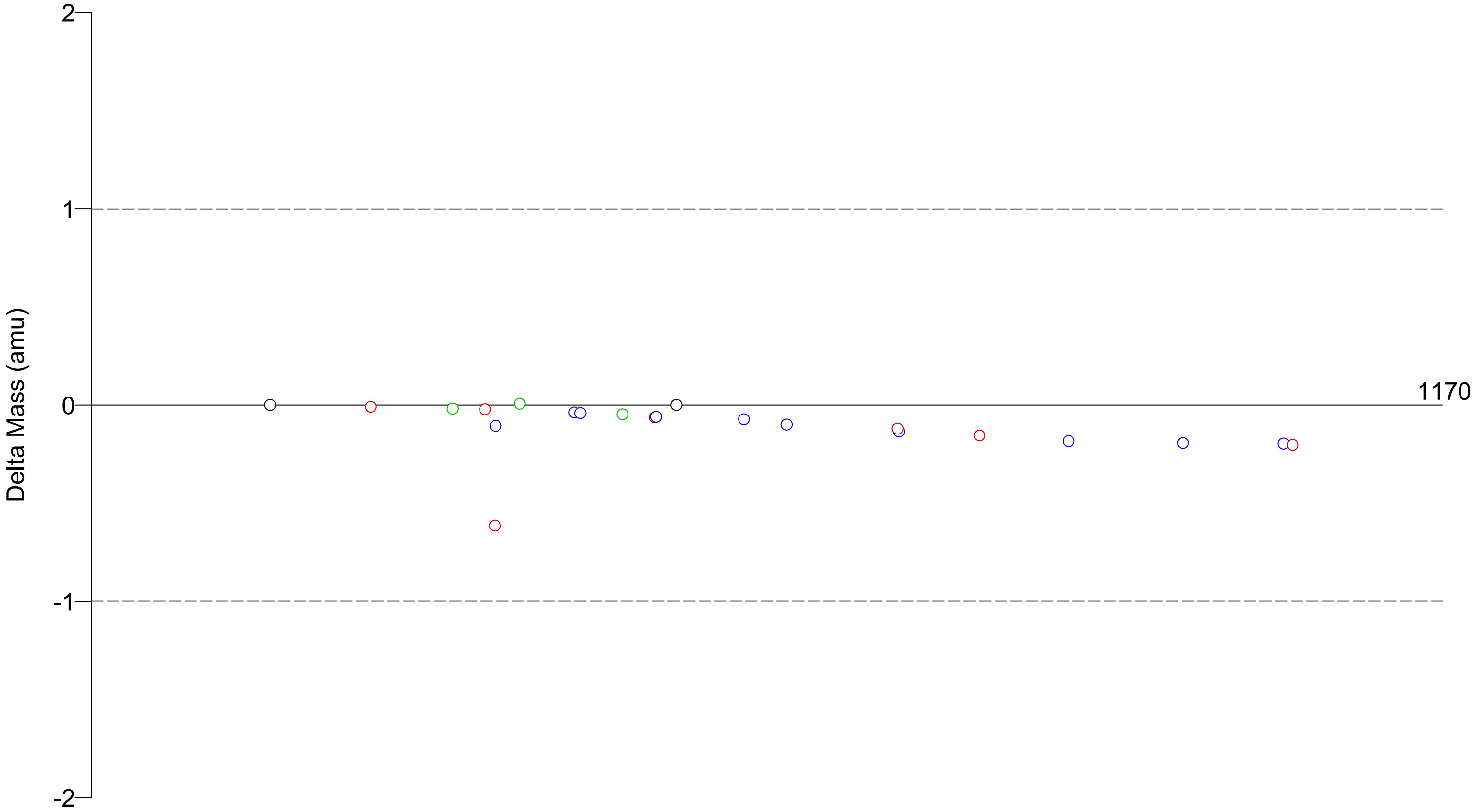
IPI:IPI00784842.1|TREMBL:Q6MZQ6 Ta                               6e-006  20.2     0.0        0
2118291816 -  K.GPSVFPLAPSSK.S                      1186.65   2  0.02     2.948  0.348    465.0  1    15/33   14
2118291816 -  R.LSCAASGFTFR.S                       1217.56   2  6e-006   3.492  0.654    1231.4 1    20/30   3

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

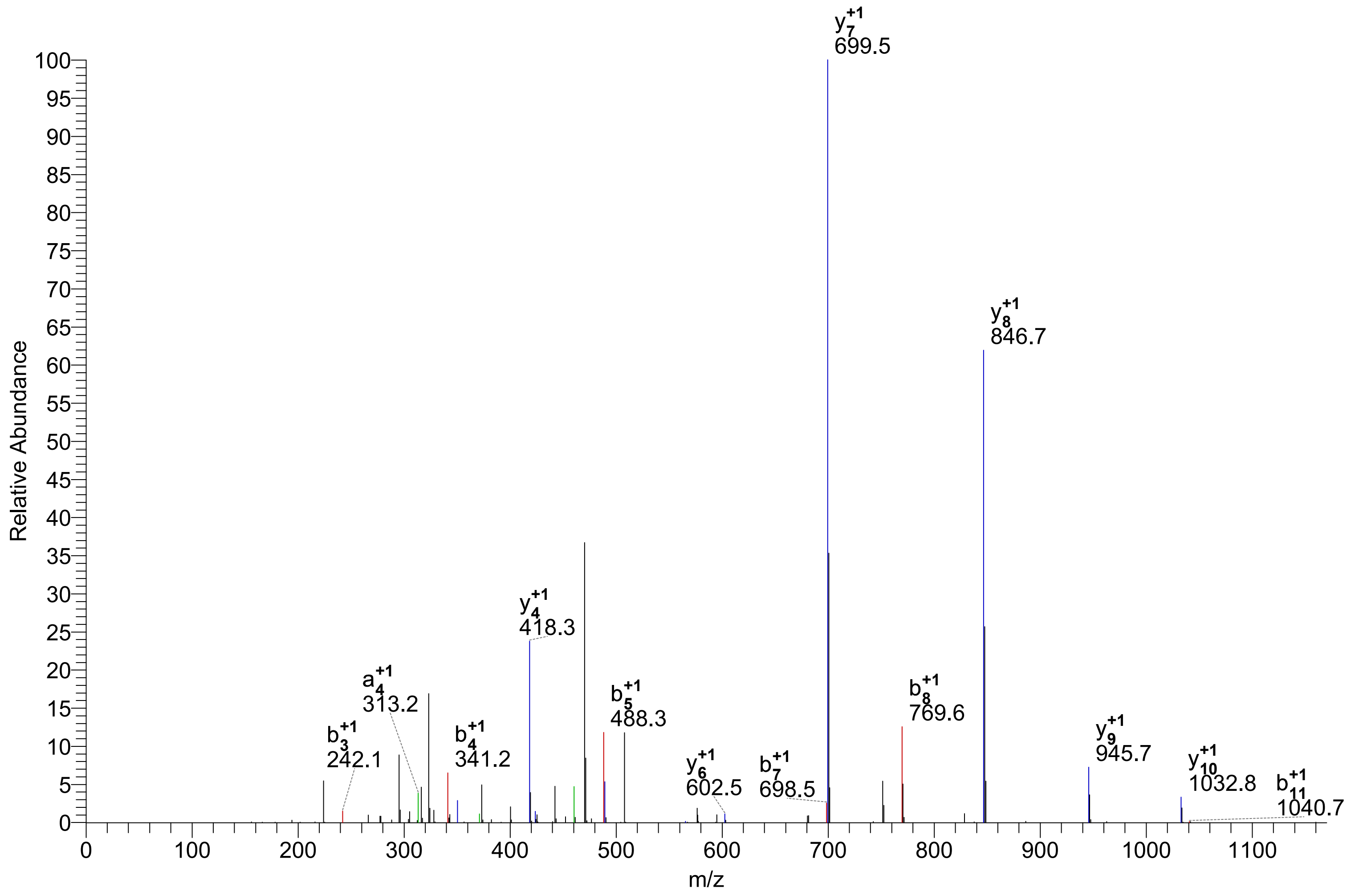
```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```



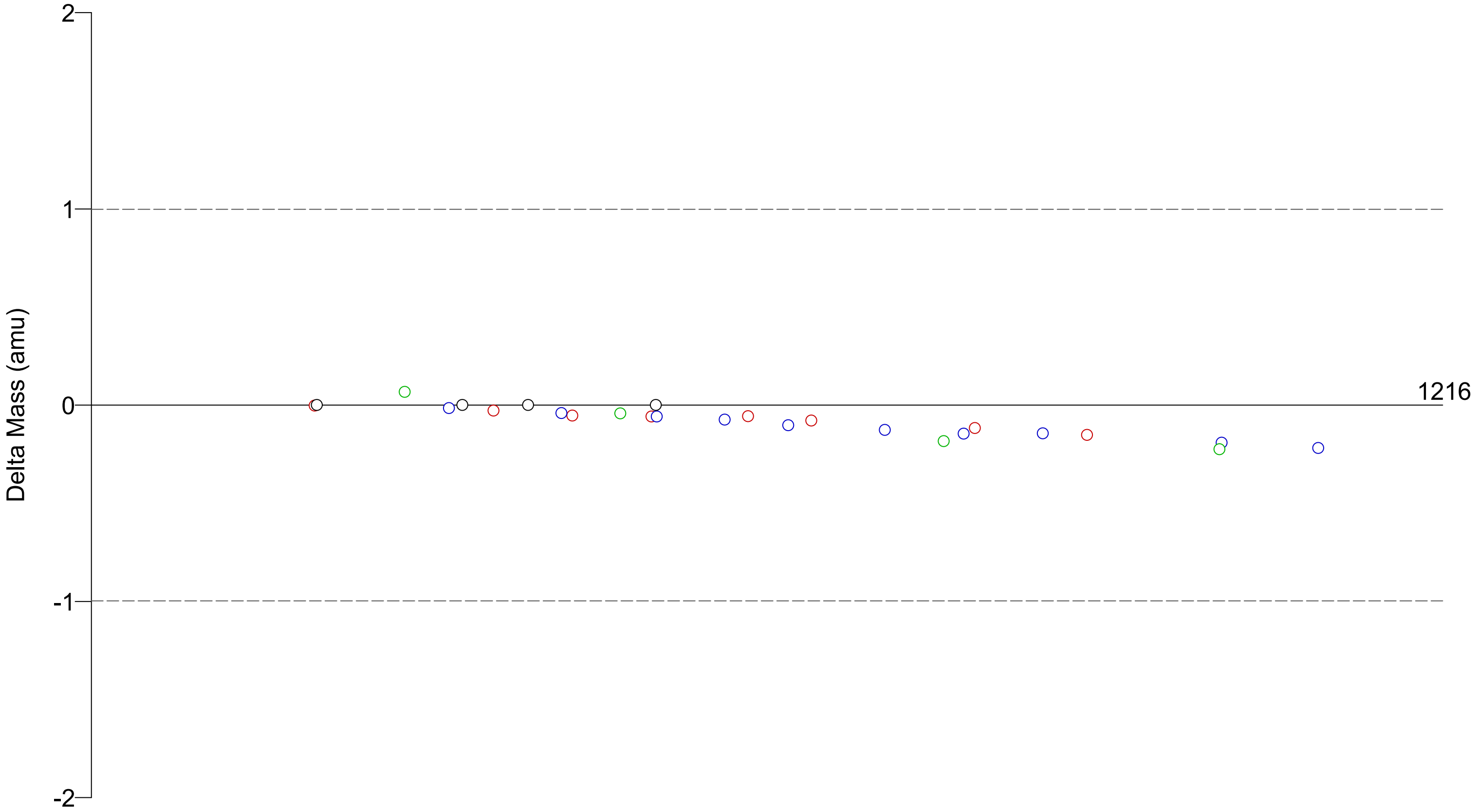
#2118291816-26226248 NL: 6.95E6



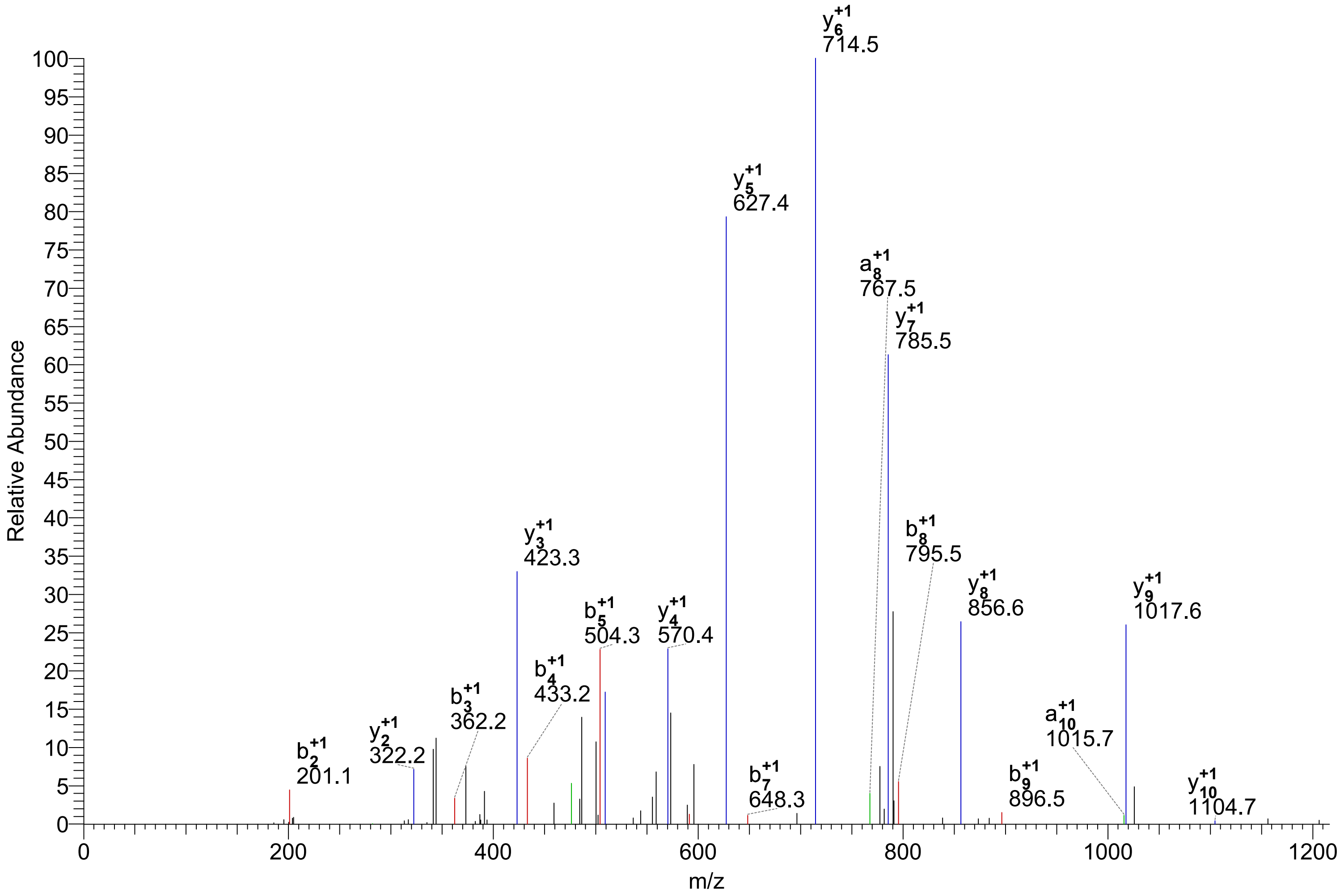
```
DTA for scans: 2118291816-26226248
Precursor ion: 609.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                     1104.48
 C    334.14     362.14                                     1017.45
 A    405.18     433.18                                      856.43
 A    476.22     504.21                                      785.39
 S    563.25     591.24                                      714.36
 G    620.27     648.27                                      627.32
 F    767.34     795.33                                      570.30
 T    868.39     896.38                                      423.24
 F   1015.46    1043.45                                      322.19
 R                                                           175.12
```



#2118291816-26226248 NL: 9.29E4



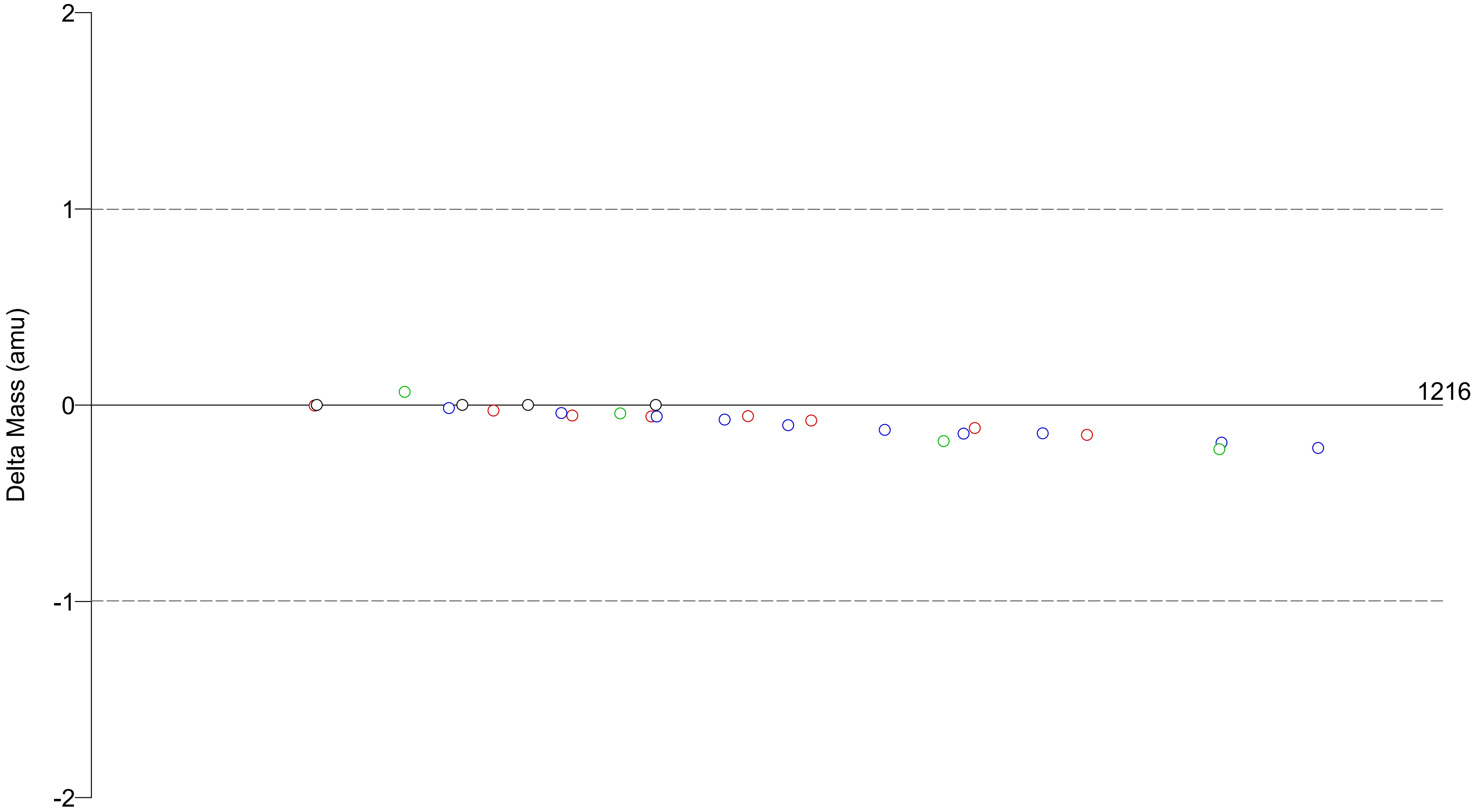
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00783023.1|TREMBL:Q0ZCI6 Ta                                        6e-006  10.2     0.0        0
2118291816 -  R.LSCAASGFTFR.S                            1217.56    2   6e-006  3.492  0.654   1231.4 1   20/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

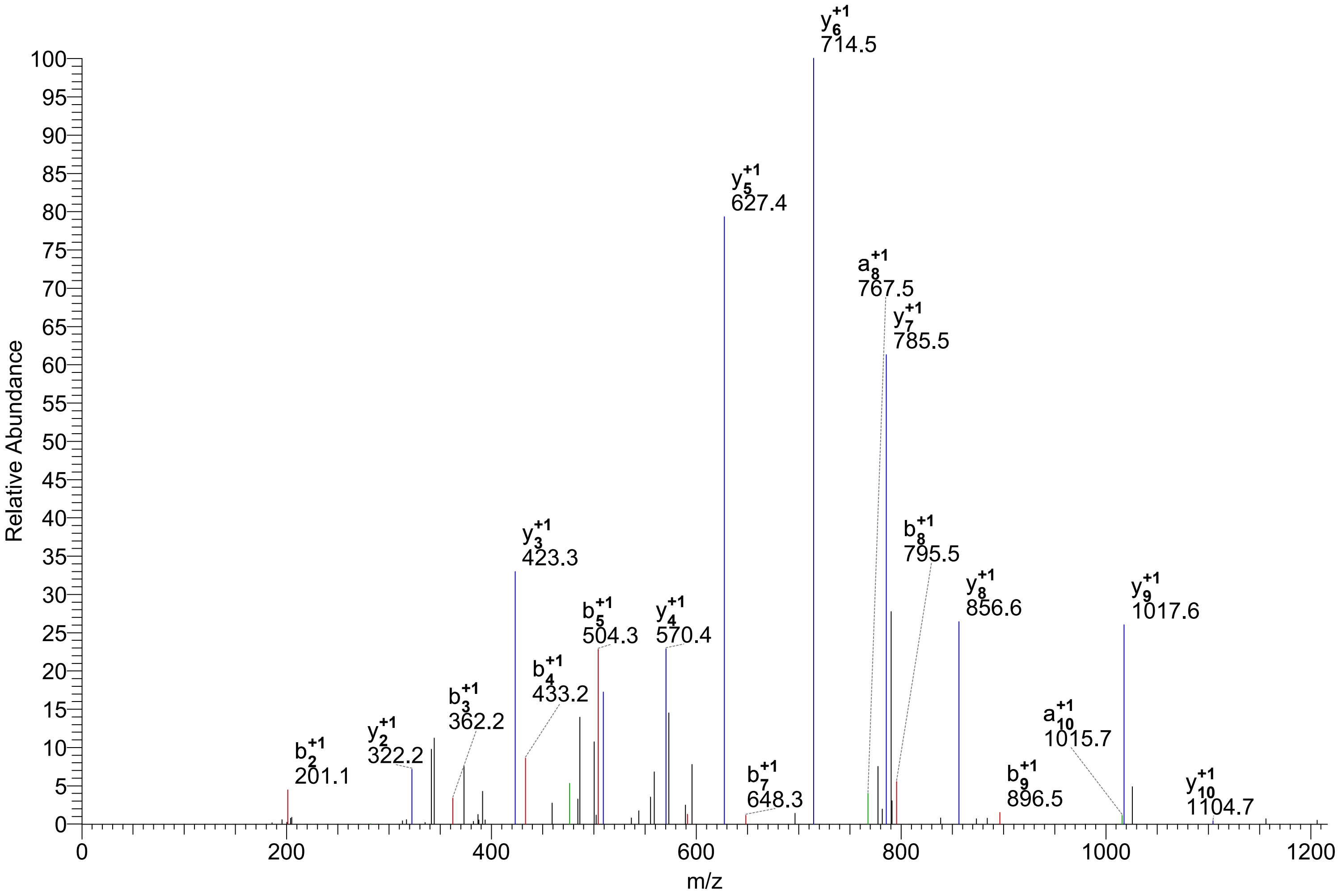
```
DTA for scans: 2118291816-26226248
Precursor ion: 609.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                     1104.48
 C    334.14     362.14                                     1017.45
 A    405.18     433.18                                      856.43
 A    476.22     504.21                                      785.39
 S    563.25     591.24                                      714.36
 G    620.27     648.27                                      627.32
 F    767.34     795.33                                      570.30
 T    868.39     896.38                                      423.24
 F   1015.46    1043.45                                      322.19
 R                                                           175.12
```



#2118291816-26226248 NL: 9.29E4



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)        Sequence                                 MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

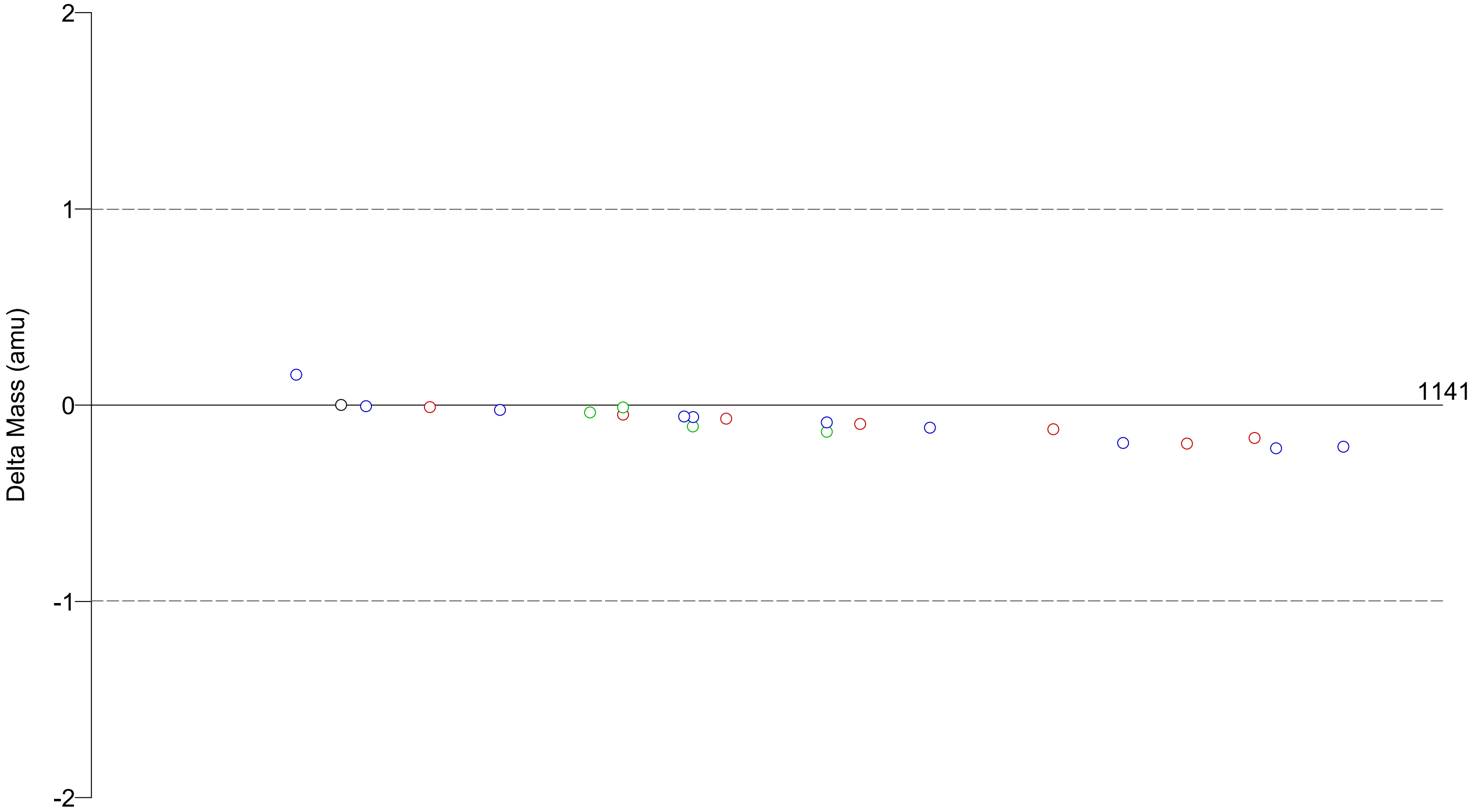
IPI:IPI00022391.1|SWISS-PROT:P02743|ENSEMBL:ENSP00000255040|RE     6e-006  10.2      0.0        0
19287468 - 1  R.VGEYSLYIGR.H                          1156.60    2  6e-006  3.220  0.492   1273.1 1   18/27

1 of 1 peptide matches reported, 0 removed due to filtering
```

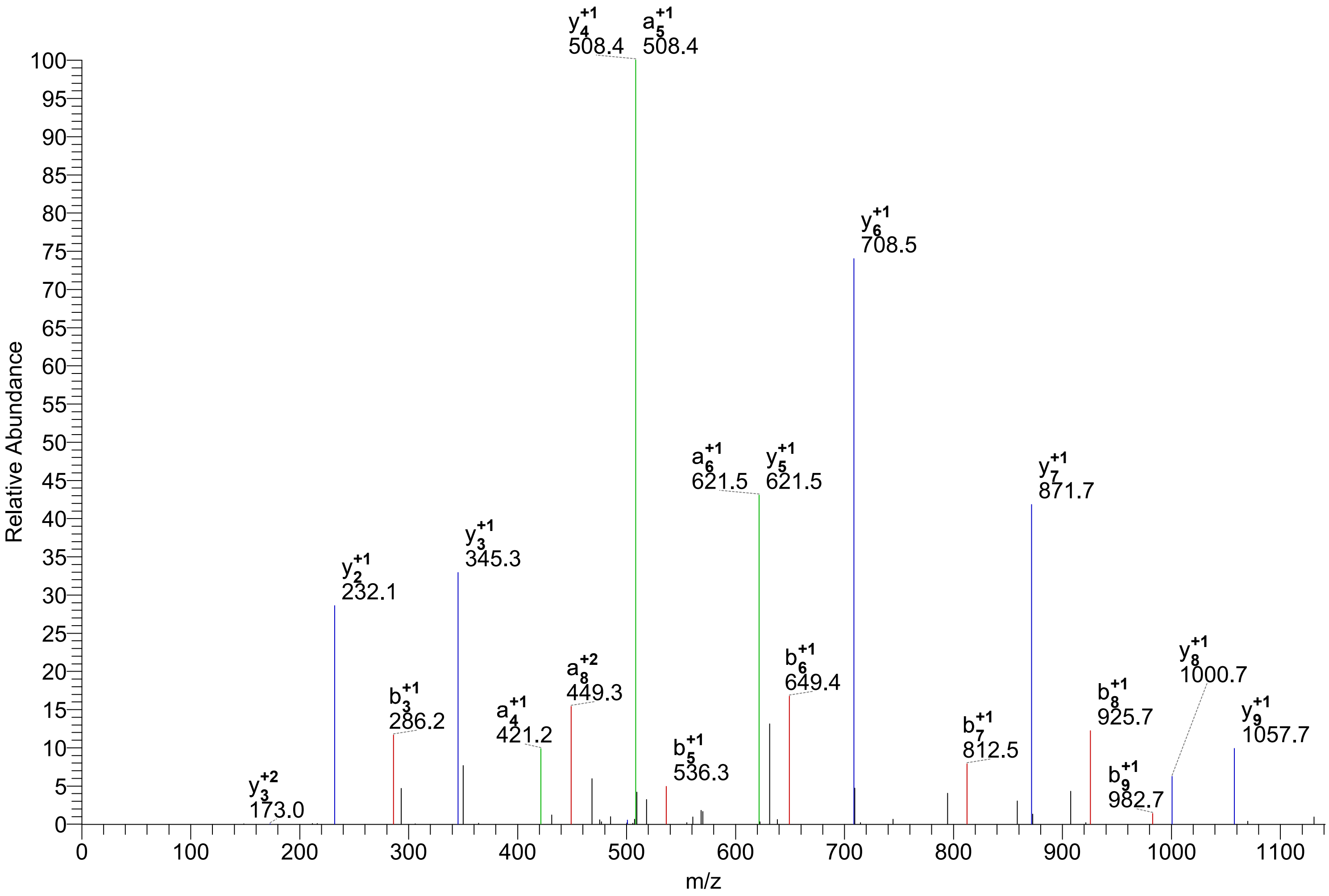
```
DTA for scans: 19287468-1
Precursor ion: 578.80
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 G    129.10     157.10                                      1057.53
 E    258.14     286.14                                      1000.51
 Y    421.21     449.20                                       871.47
 S    508.24     536.24                                       708.40
 L    621.32     649.32                                       621.37
 Y    784.39     812.38                                       508.29
 I    897.47     925.47                                       345.22
 G    954.49     982.49                                       232.14
 R                                                            175.12
```



#19287468-1 NL: 1.83E5



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Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+     z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00166729.4|SWISS-PROT:P25311|ENSEMBL:ENSP00000292401|RE     8e-006  10.1     0.0       0
2118291816 -  R.YSLTYIYTGLSK.H                           1408.74   2  8e-006  2.703  0.530   554.0  1   14/33   2

1 of 1 peptide matches reported, 0 removed due to filtering
```
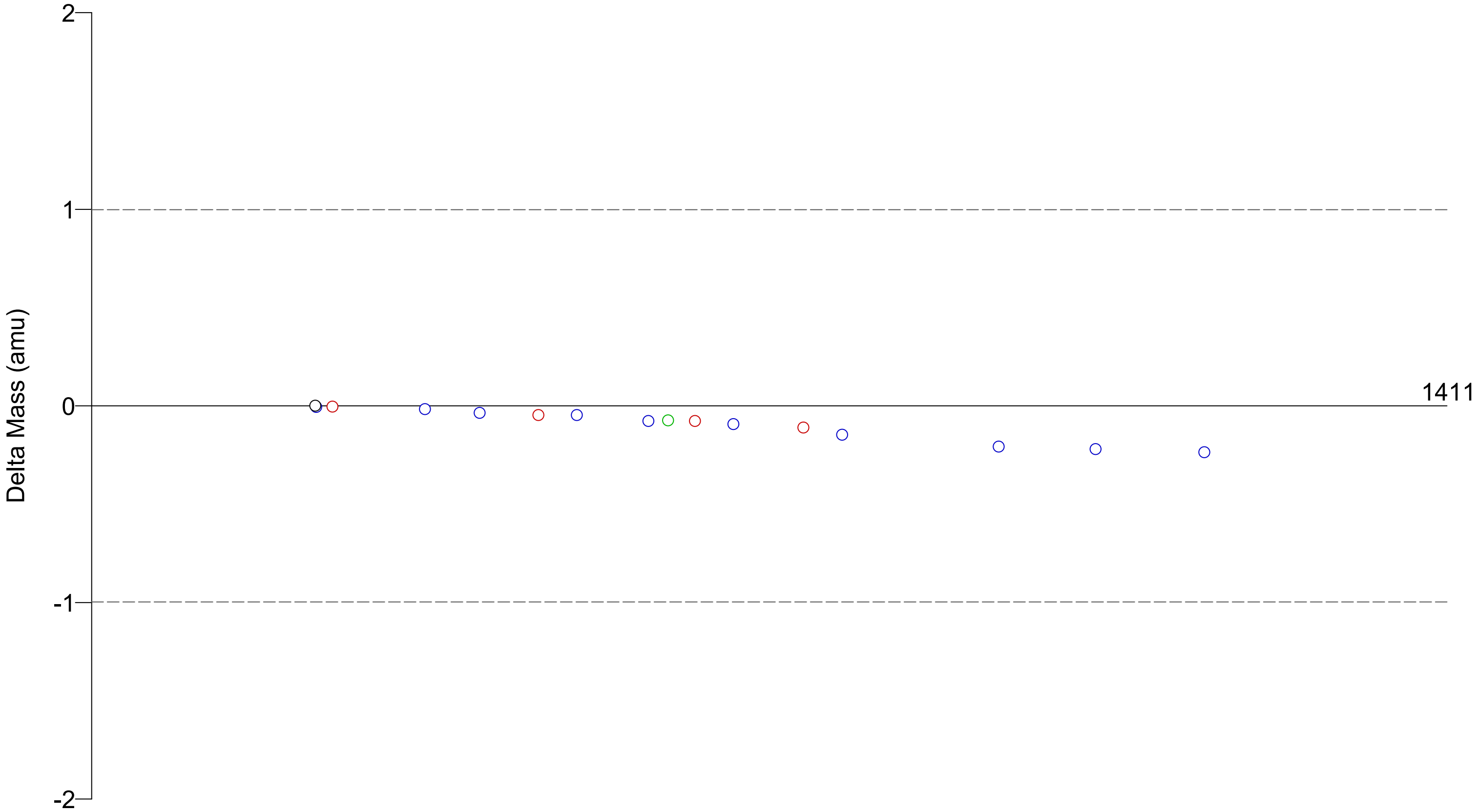
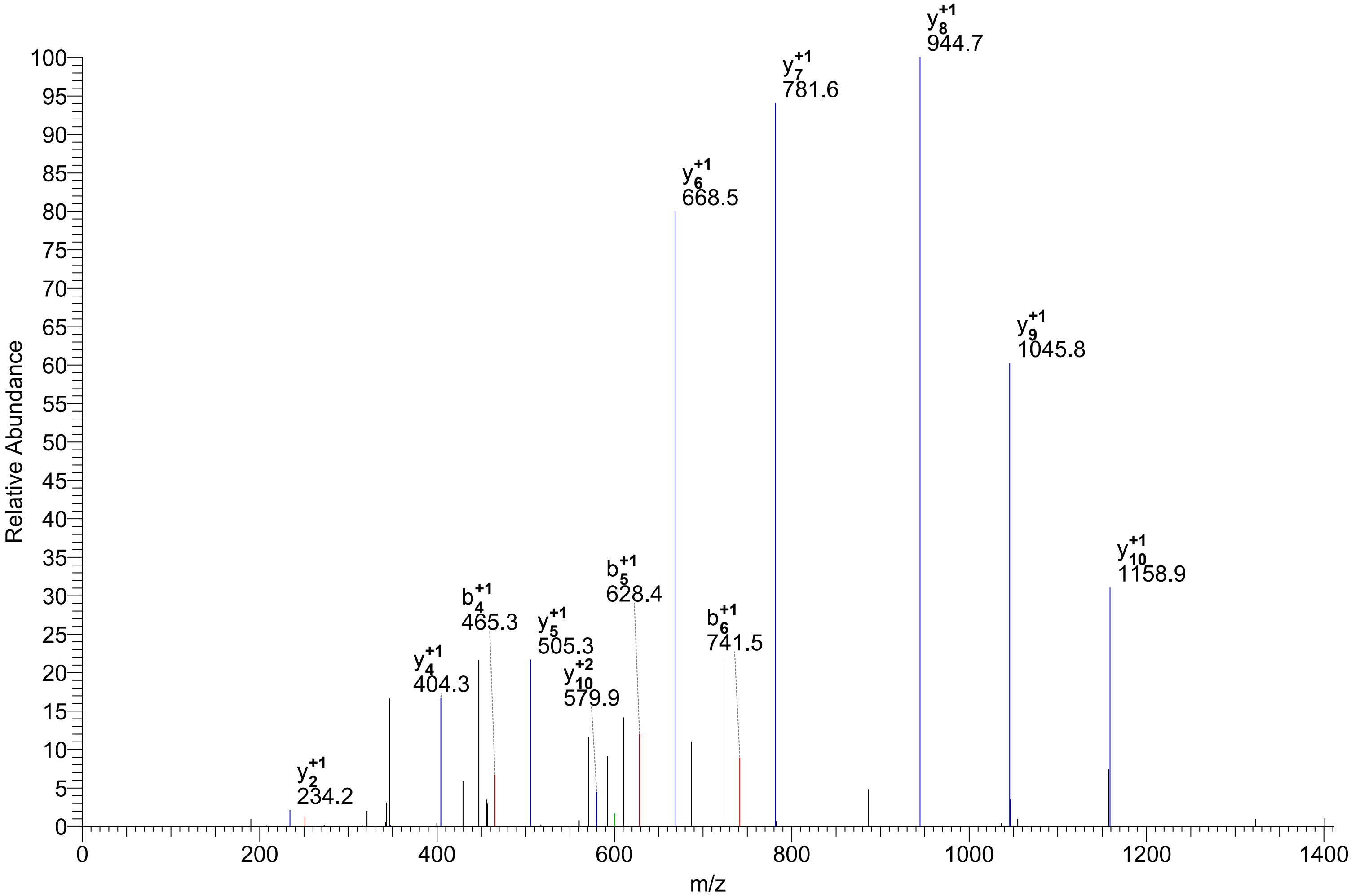

```
DTA for scans: 2118291816-26226248
Precursor ion: 704.87
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 S    223.11     251.10                                     1245.67
 L    336.19     364.19                                     1158.64
 T    437.24     465.23                                     1045.56
 Y    600.30     628.30                                      944.51
 I    713.39     741.38                                      781.45
 Y    876.45     904.45                                      668.36
 T    977.50    1005.49                                      505.30
 G   1034.52    1062.51                                      404.25
 L   1147.60    1175.60                                      347.23
 S   1234.64    1262.63                                      234.14
 K                                                           147.11
```

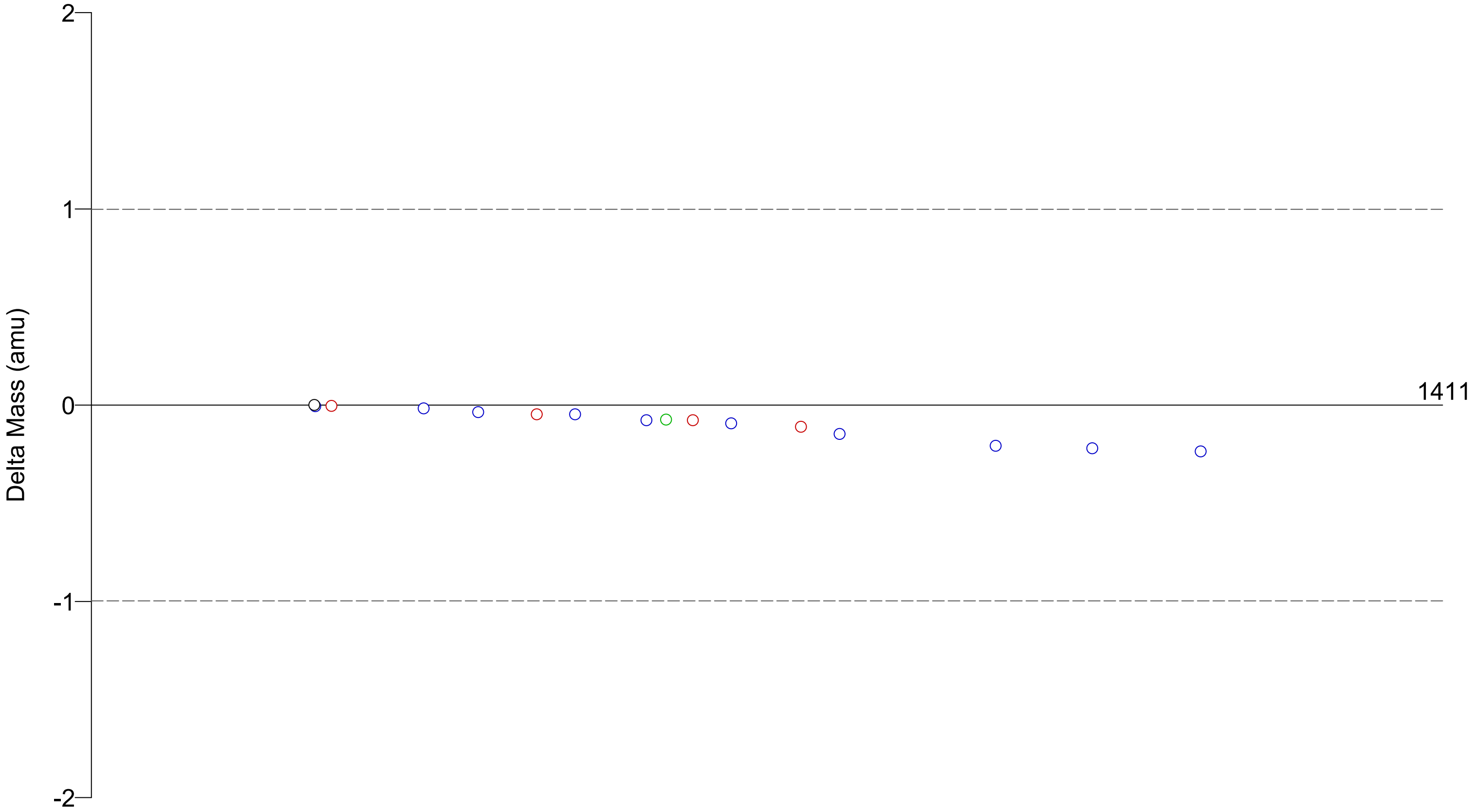


#2118291816-26226248 NL: 1.49E5

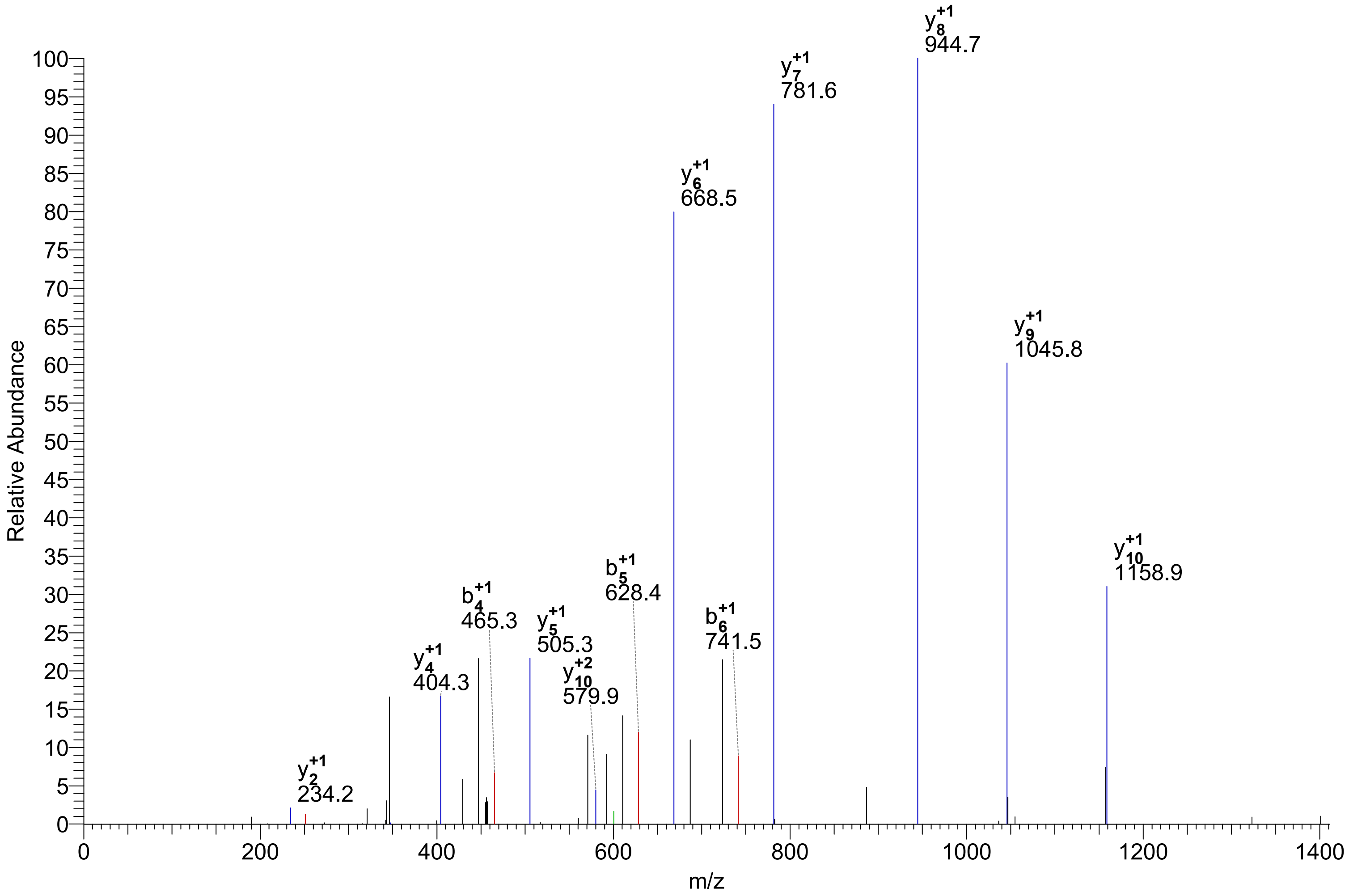


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00816309.1|TREMBL:A0JLQ0 Ta                                8e-006  10.1     0.0       0
2118291816 -  R.YSLTYIYTGLSK.H                       1408.74   2  8e-006  2.703  0.530    554.0 1   14/33   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 704.87
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 S    223.11     251.10                                     1245.67
 L    336.19     364.19                                     1158.64
 T    437.24     465.23                                     1045.56
 Y    600.30     628.30                                      944.51
 I    713.39     741.38                                      781.45
 Y    876.45     904.45                                      668.36
 T    977.50    1005.49                                      505.30
 G   1034.52    1062.51                                      404.25
 L   1147.60    1175.60                                      347.23
 S   1234.64    1262.63                                      234.14
 K                                                           147.11
```



#2118291816-26226248 NL: 1.49E5



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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count

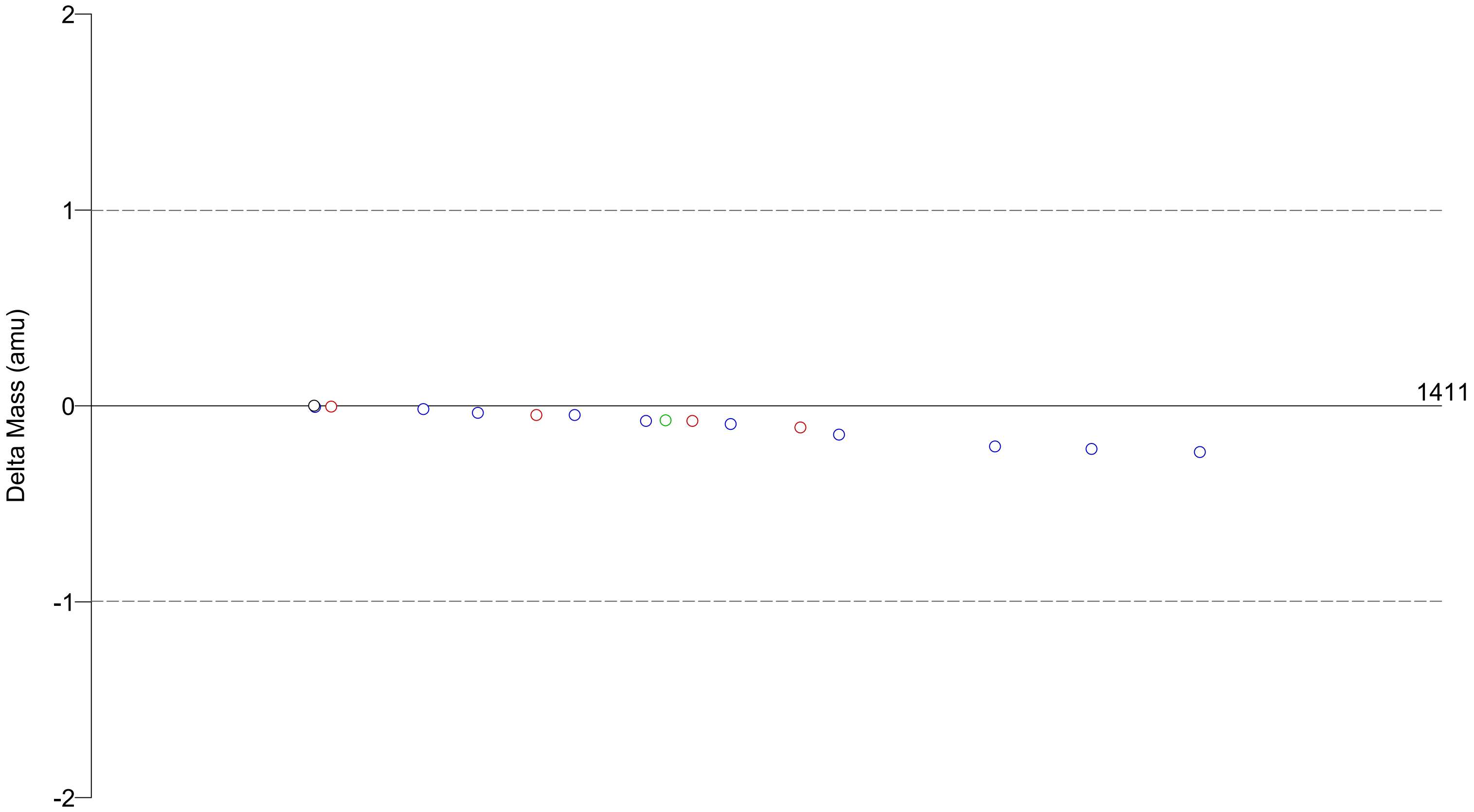
IPI:IPI00924948.1|VEGA:OTTHUMP0000                                8e-006  10.1     0.0       0
2118291816 -  R.YSLTYIYTGLSK.H                       1408.74   2  8e-006  2.703  0.530   554.0  1   14/33   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

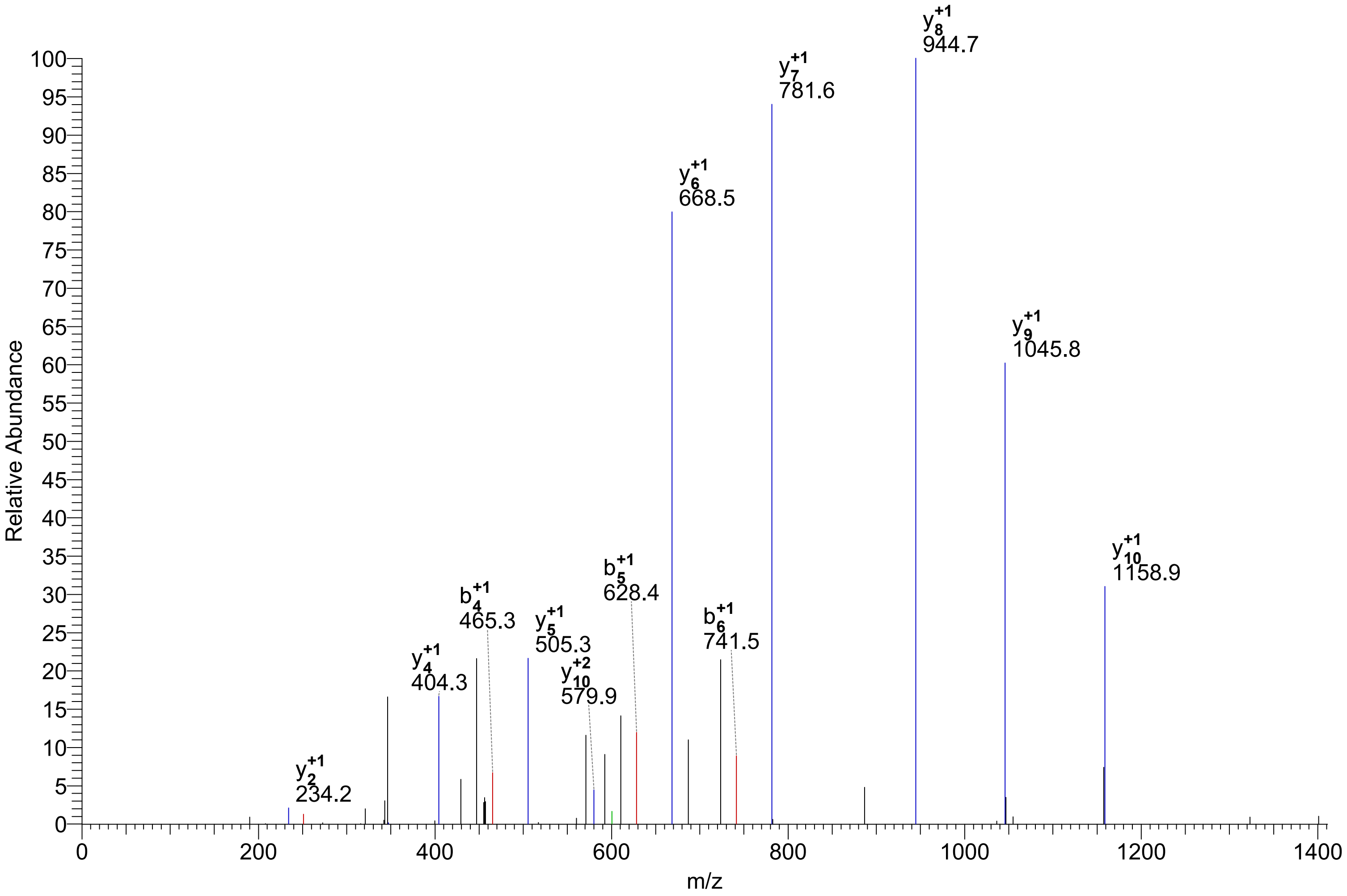
```
DTA for scans: 2118291816-26226248
Precursor ion: 704.87
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 S    223.11     251.10                                     1245.67
 L    336.19     364.19                                     1158.64
 T    437.24     465.23                                     1045.56
 Y    600.30     628.30                                      944.51
 I    713.39     741.38                                      781.45
 Y    876.45     904.45                                      668.36
 T    977.50    1005.49                                      505.30
 G   1034.52    1062.51                                      404.25
 L   1147.60    1175.60                                      347.23
 S   1234.64    1262.63                                      234.14
 K                                                           147.11
```



#2118291816-26226248 NL: 1.49E5



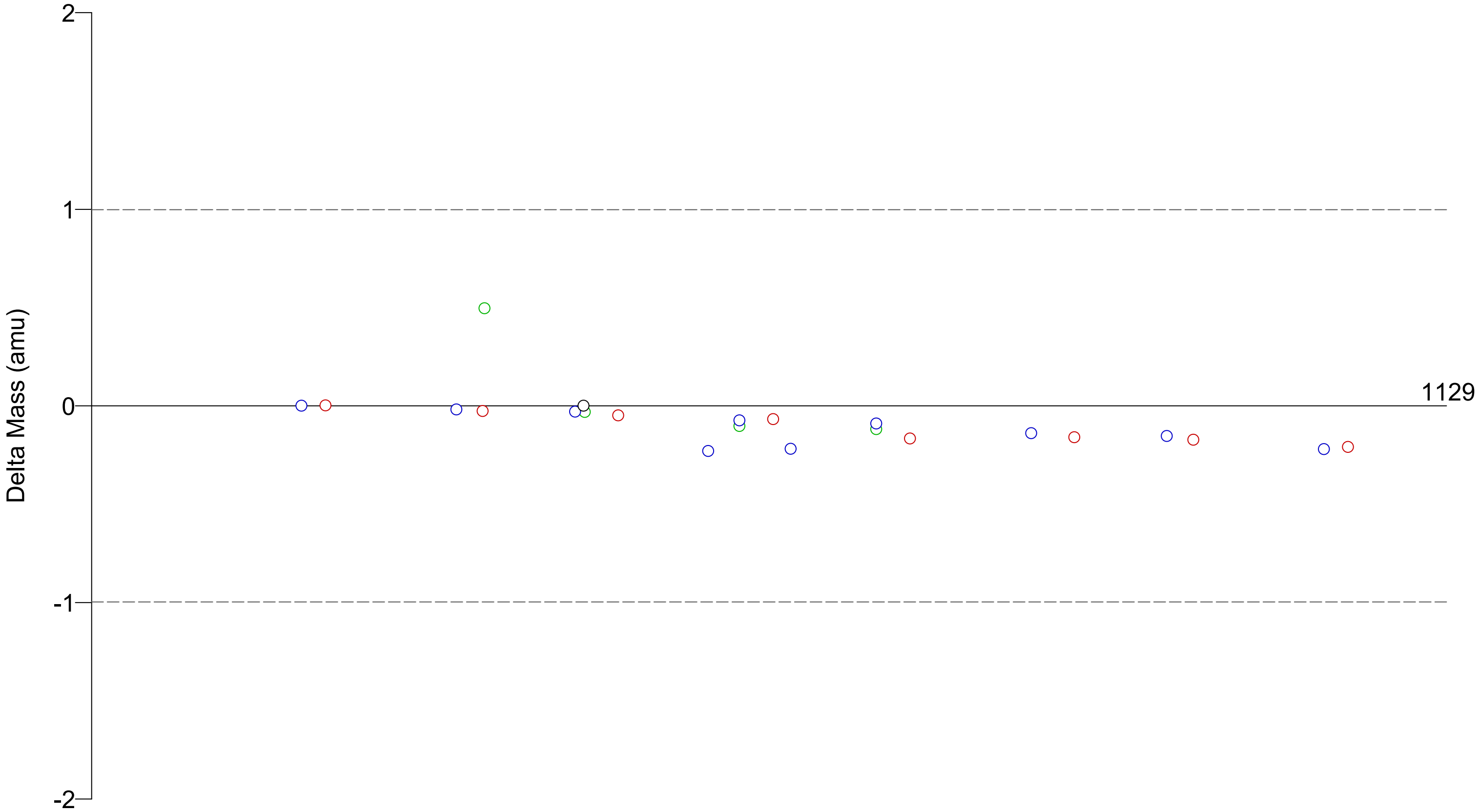
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00292530.1|SWISS-PROT:P19827|TREMBL:A8K9N5;B7Z539;B7Z54    1e-005  10.2     0.0       0
19682592 - 21 R.GHMLENHVER.L                         1221.58   2  1e-005  3.514  0.577   794.8  1   19/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

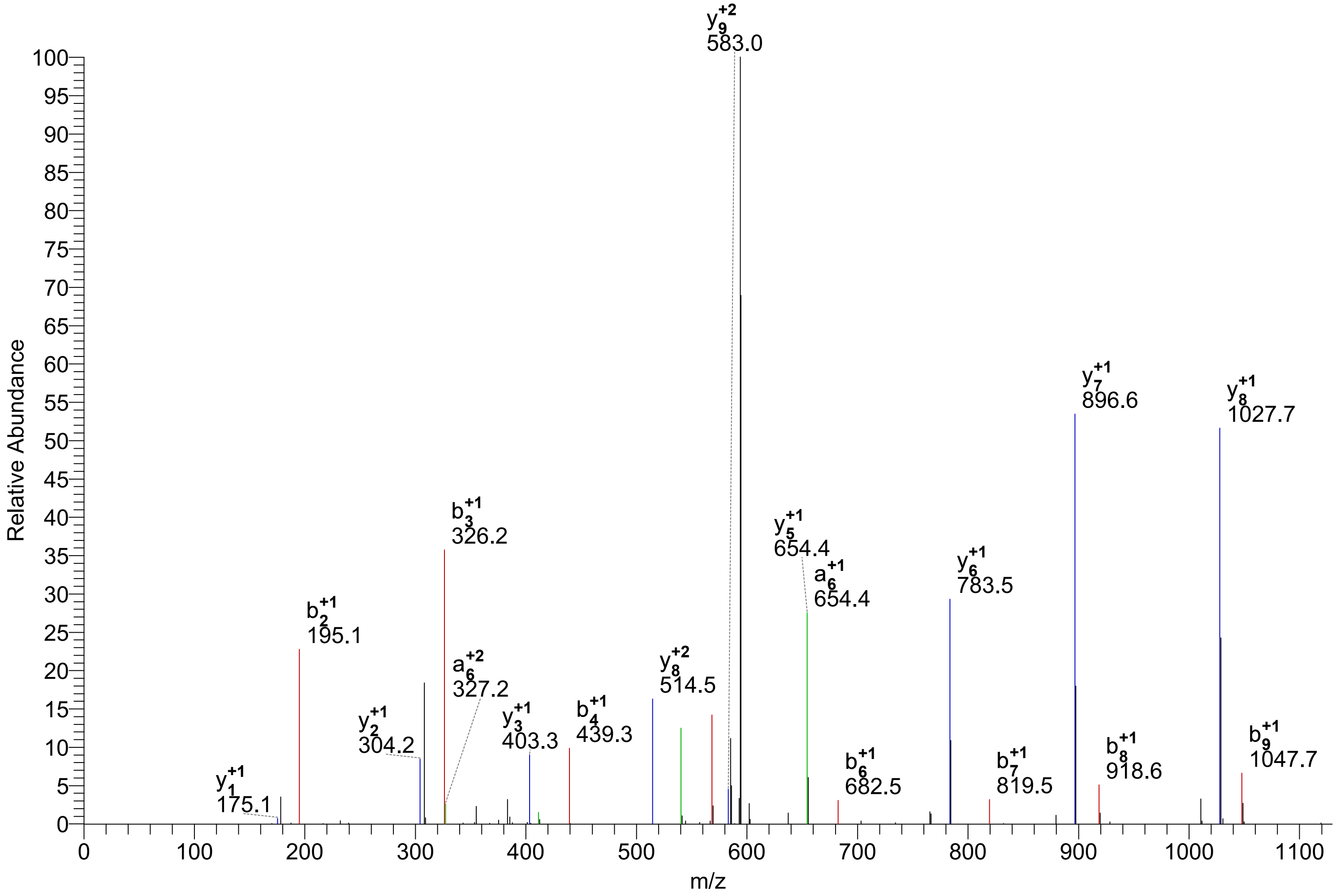
```
DTA for scans: 19682592-2147340288
Precursor ion: 611.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 H    167.09     195.09                                     1164.56
 M    298.13     326.13                                     1027.50
 L    411.22     439.21                                      896.46
 E    540.26     568.25                                      783.37
 N    654.30     682.30                                      654.33
 H    791.36     819.36                                      540.29
 V    890.43     918.43                                      403.23
 E   1019.47    1047.47                                      304.16
 R                                                           175.12
```



#19682592-2147340288 NL: 8.78E4



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

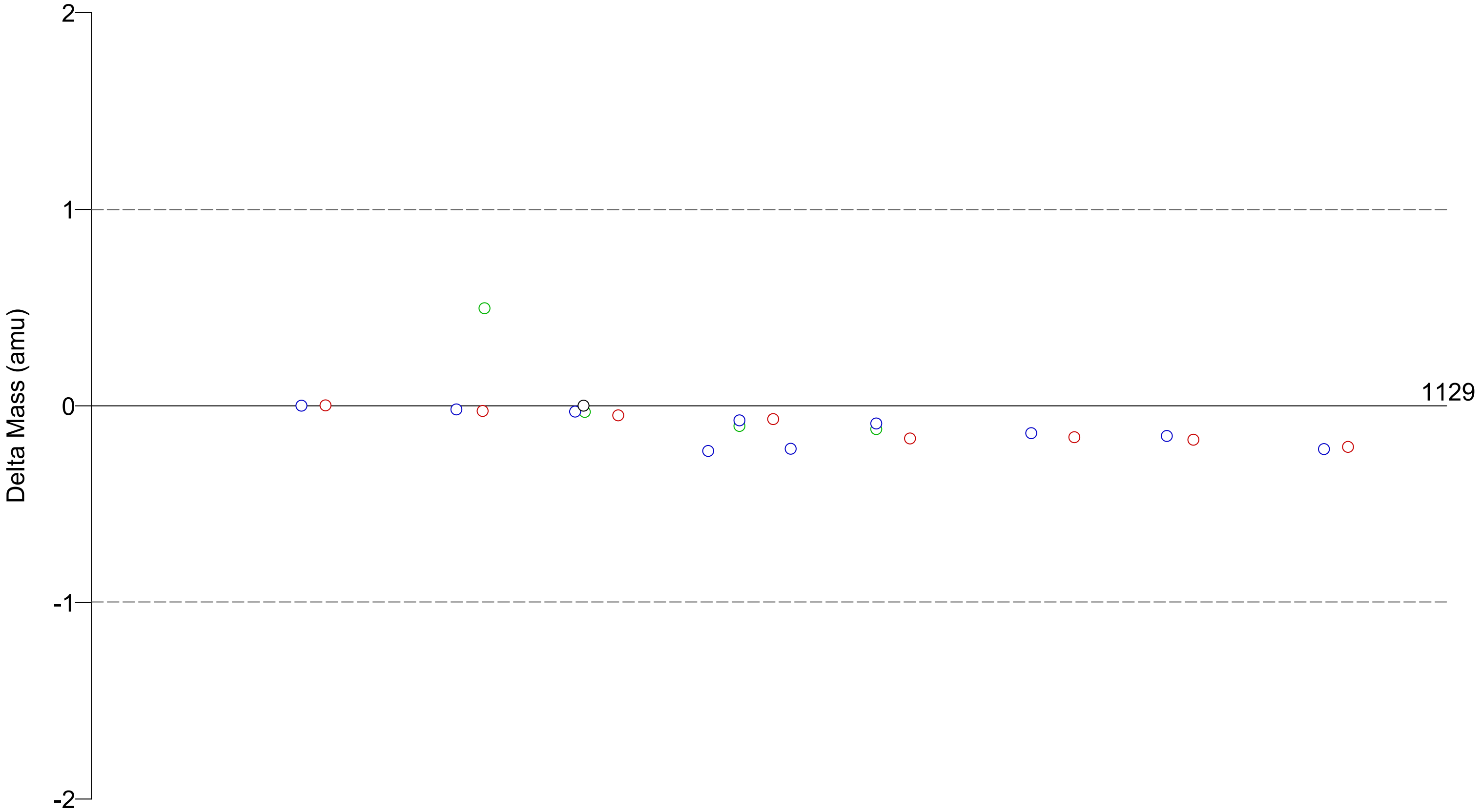
IPI:IPI00383338.1|TREMBL:Q9P1C5|VE                                1e-005  10.2     0.0        0
19682592 - 21 R.GHMLENHVER.L                         1221.58   2  1e-005  3.514  0.577    794.8  1   19/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

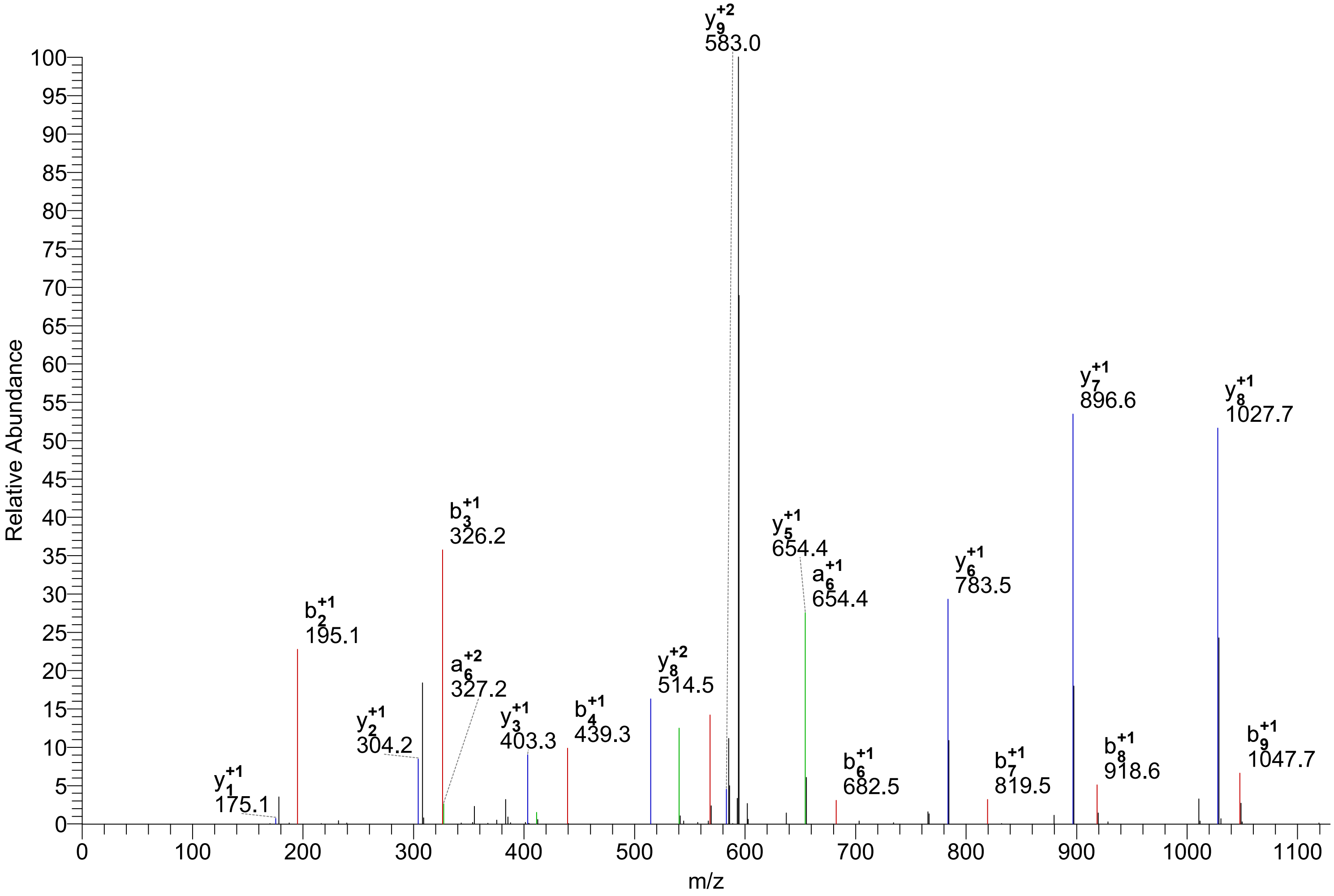
```
DTA for scans: 19682592-2147340288
Precursor ion: 611.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 H    167.09     195.09                                      1164.56
 M    298.13     326.13                                      1027.50
 L    411.22     439.21                                       896.46
 E    540.26     568.25                                       783.37
 N    654.30     682.30                                       654.33
 H    791.36     819.36                                       540.29
 V    890.43     918.43                                       403.23
 E   1019.47    1047.47                                       304.16
 R                                                            175.12
```



#19682592-2147340288 NL: 8.78E4



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z     P        XC  DeltaCn    Sp    RSp  Ions  Count

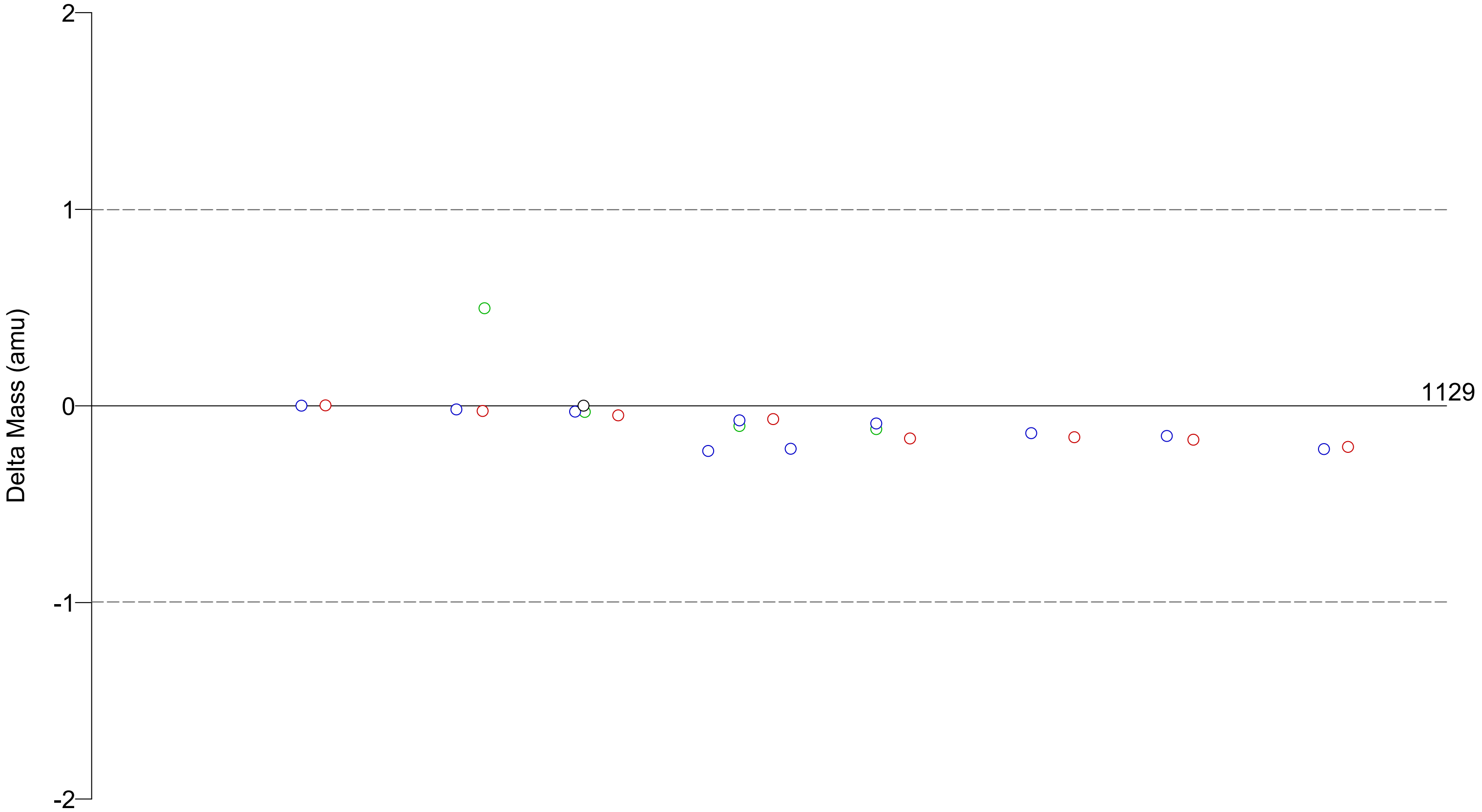
IPI:IPI00877852.1|VEGA:OTTHUMP0000                                1e-005  10.2      0.0       0
19682592 - 21 R.GHMLENHVER.L                          1221.58    2  1e-005  3.514  0.577   794.8  1   19/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

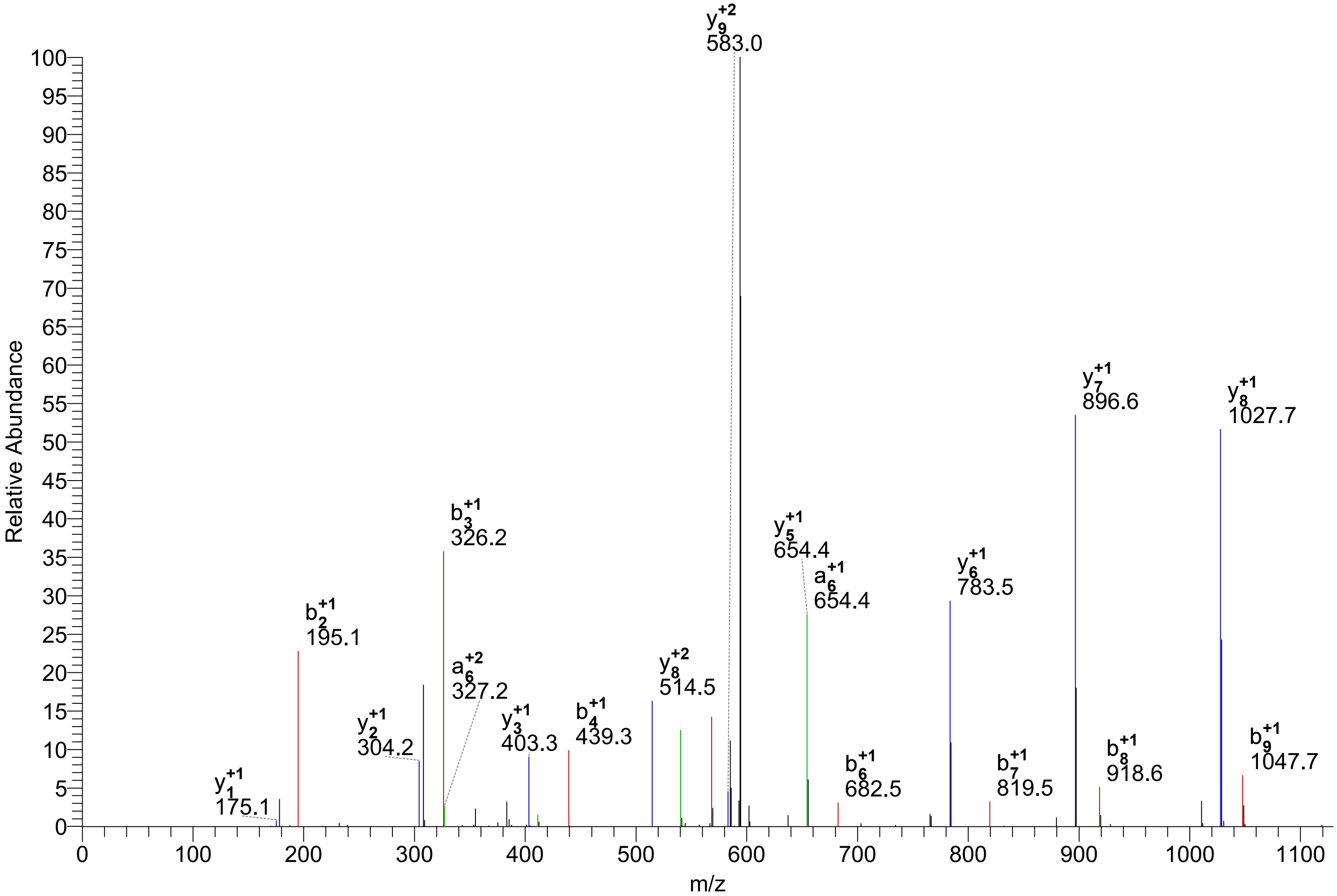
```
DTA for scans: 19682592-2147340288
Precursor ion: 611.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 H    167.09     195.09                                     1164.56
 M    298.13     326.13                                     1027.50
 L    411.22     439.21                                      896.46
 E    540.26     568.25                                      783.37
 N    654.30     682.30                                      654.33
 H    791.36     819.36                                      540.29
 V    890.43     918.43                                      403.23
 E   1019.47    1047.47                                      304.16
 R                                                           175.12
```



#19682592-2147340288 NL: 8.78E4



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z     P        XC  DeltaCn    Sp    RSp  Ions   Count

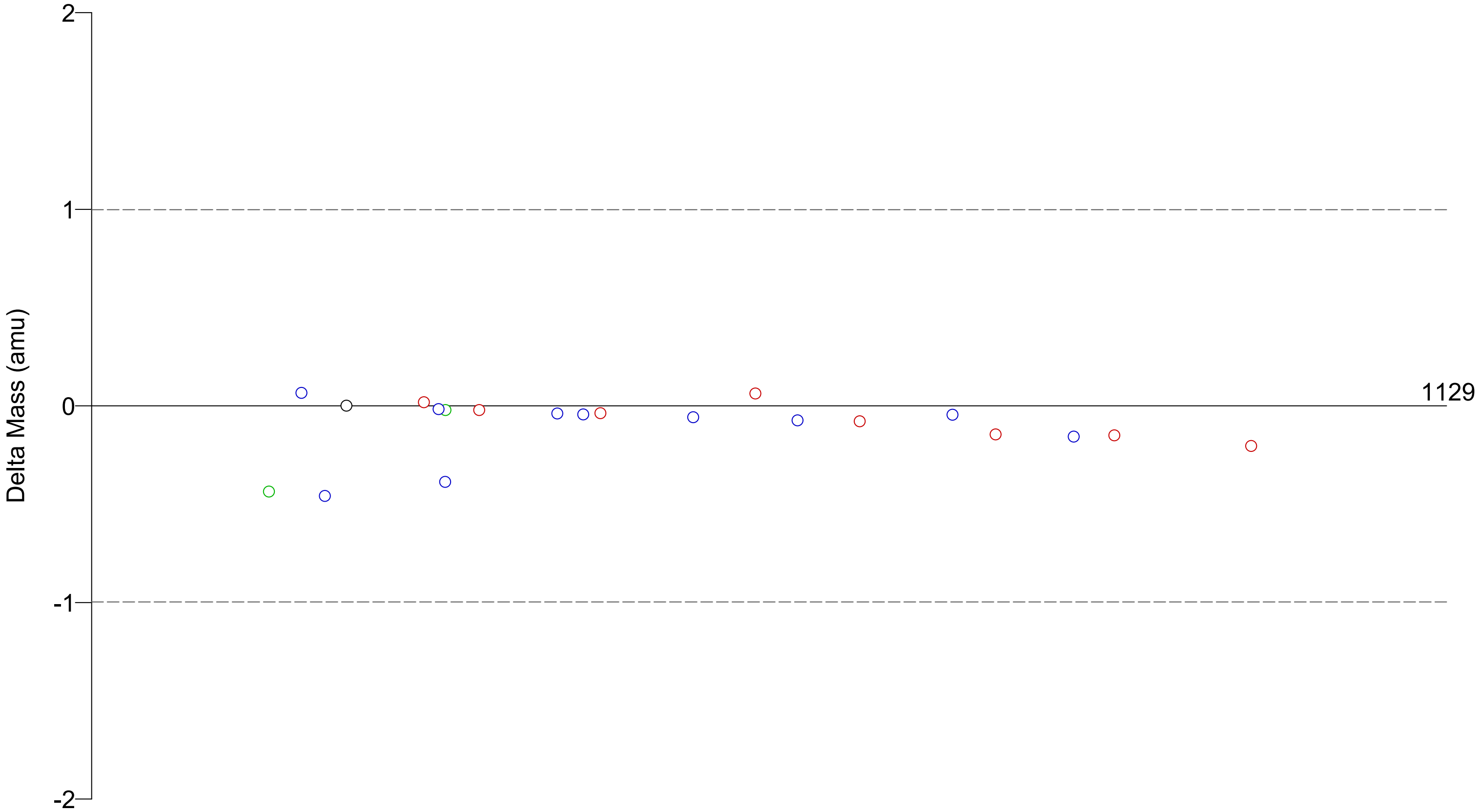
IPI:IPI00022434.4|TREMBL:A6NBZ8;B2RBS8;B4DPP6;Q56G89|ENSEMBL:E     2e-005  20.2     0.0       0
19287468 - 1  K.CCTESLVNR.R                               1140.47   2  0.0001  3.308  0.574   935.4  1   15/24   8
19287468 - 1  K.LVNEVTEFAK.T                              1149.62   2  2e-005  4.222  0.525   792.1  1   18/27   4

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

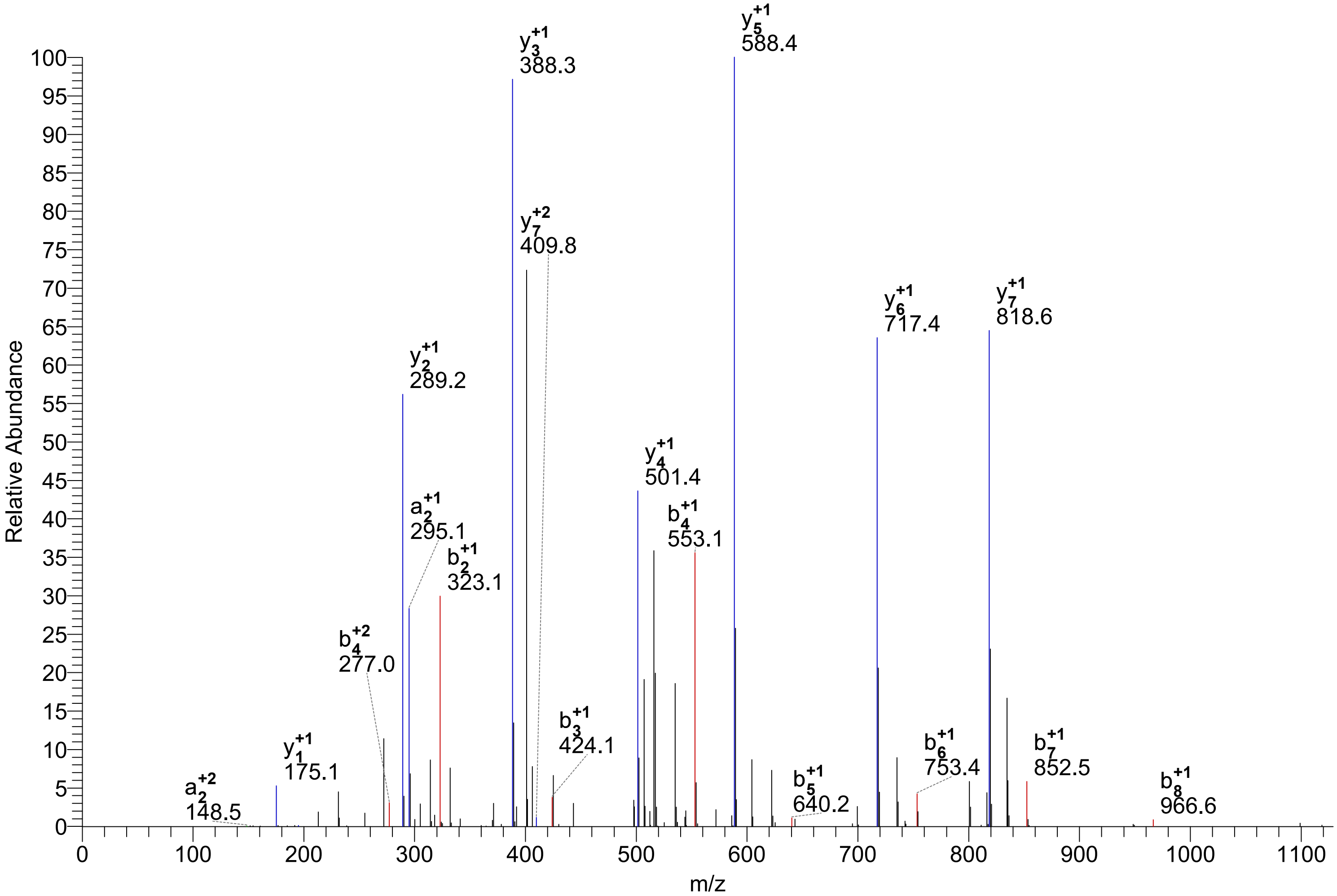
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions   Z ions
--------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                      979.45
 T    396.09     424.08                                      818.44
 E    525.13     553.13                                      717.39
 S    612.16     640.16                                      588.35
 L    725.25     753.24                                      501.31
 V    824.32     852.31                                      388.23
 N    938.36     966.35                                      289.16
 R                                                           175.12
```



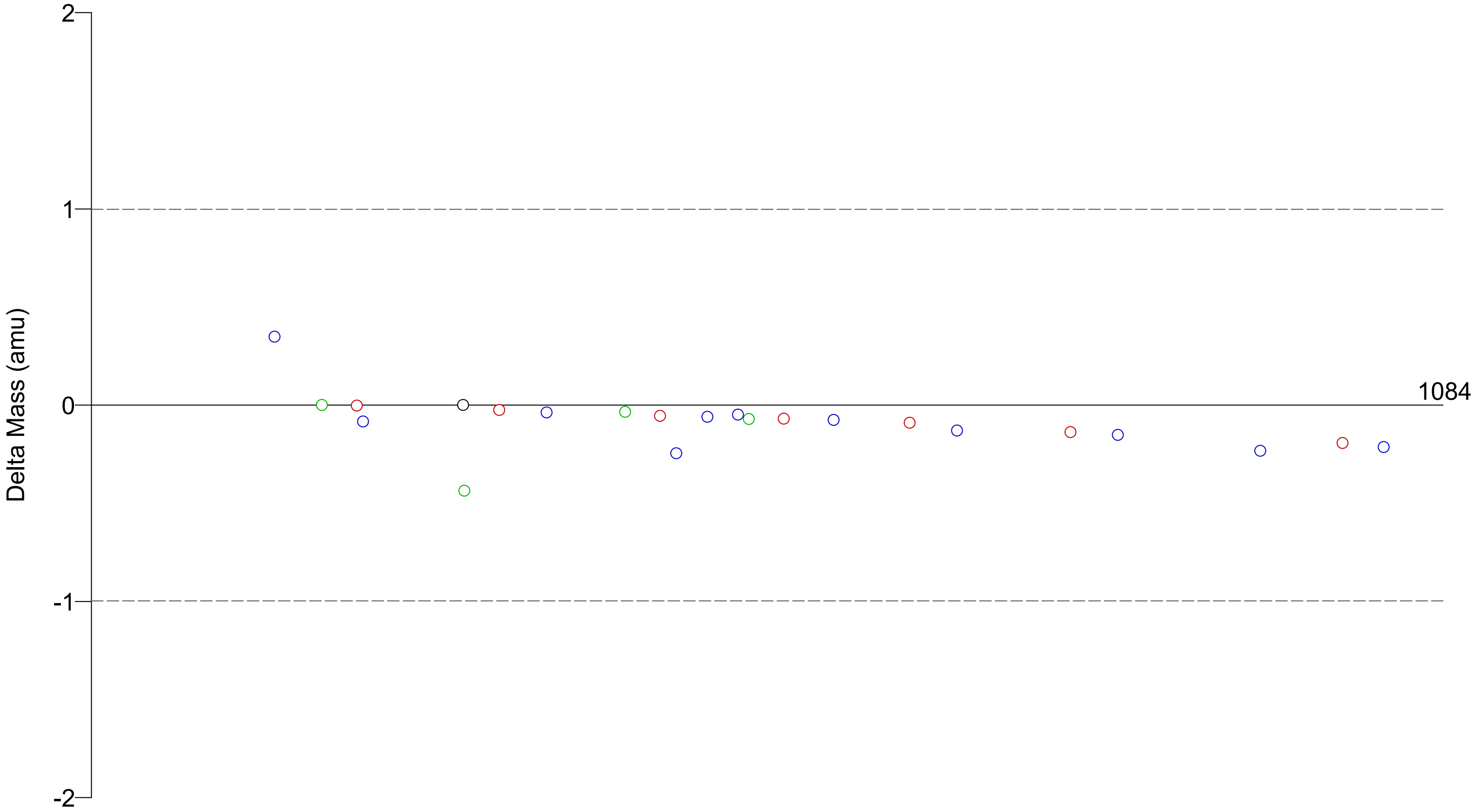
#19287468-1 NL: 8.98E6



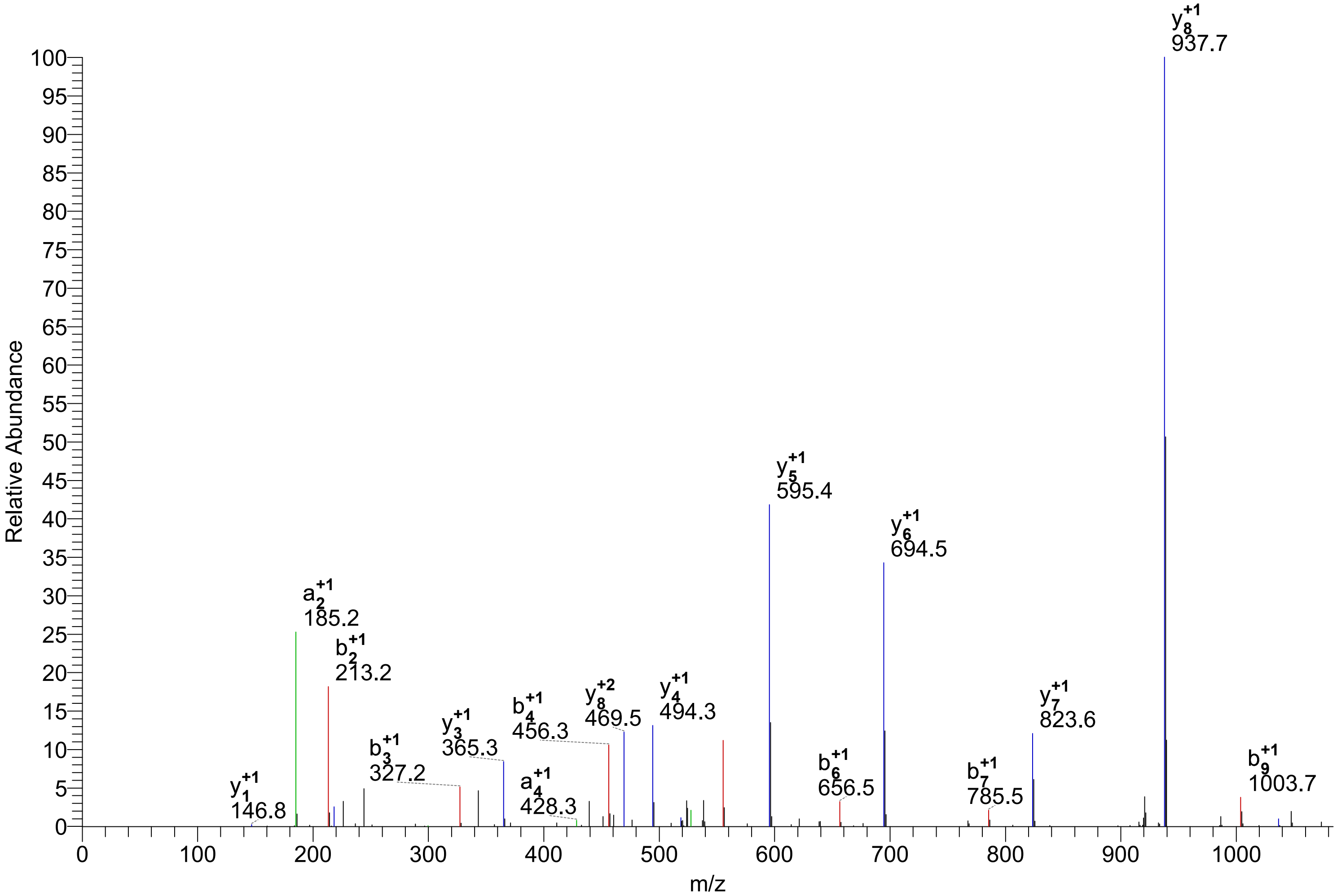
```
DTA for scans: 19287468-1
Precursor ion: 575.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 V    185.16     213.16                                     1036.53
 N    299.21     327.20                                      937.46
 E    428.25     456.25                                      823.42
 V    527.32     555.31                                      694.38
 T    628.37     656.36                                      595.31
 E    757.41     785.40                                      494.26
 F    904.48     932.47                                      365.22
 A    975.51    1003.51                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.94E6



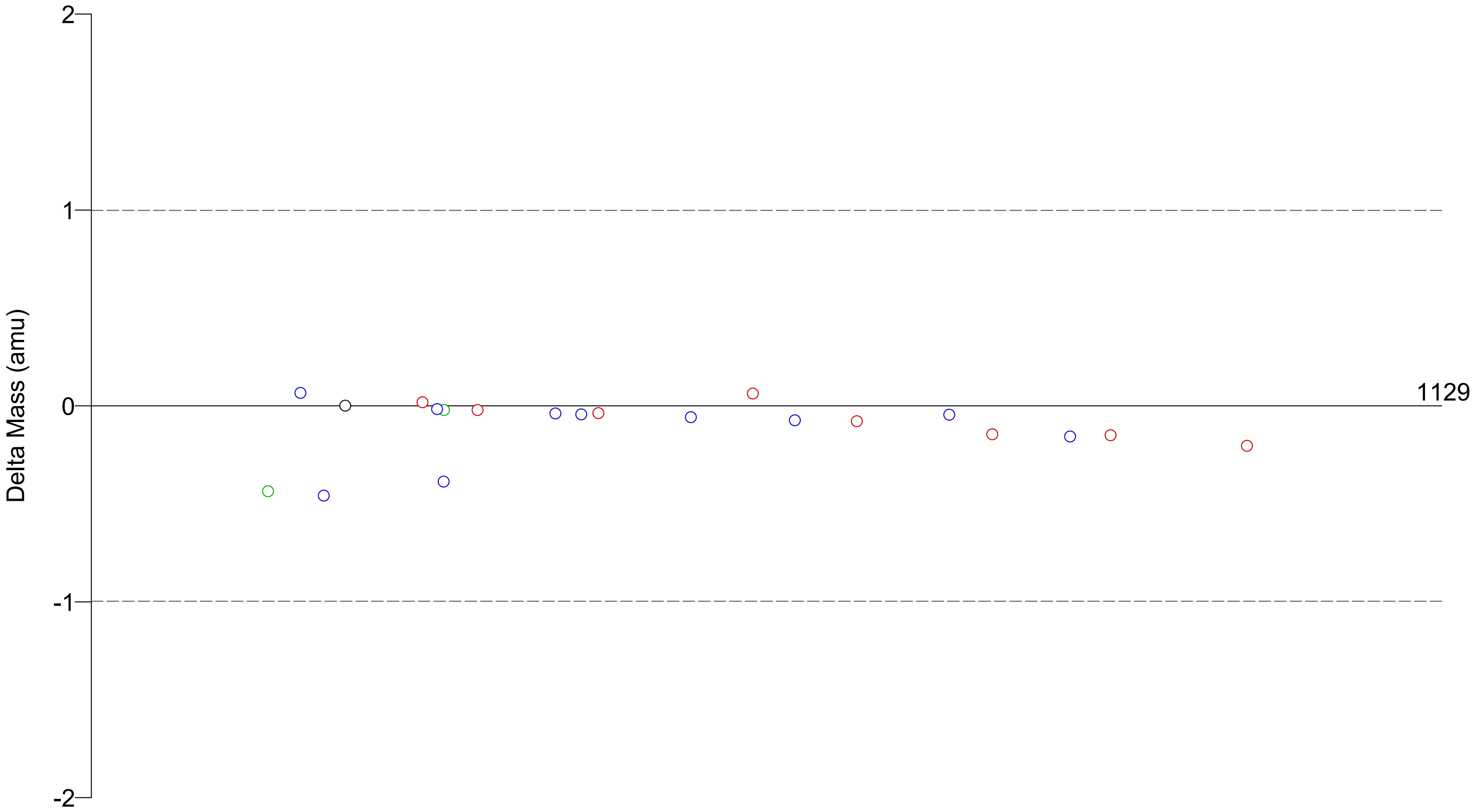
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00216773.4|TREMBL:Q8IUK7|EN                                2e-005  20.2     0.0       0
19287468 - 1  K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24   8
19287468 - 1  K.LVNEVTEFAK.T                         1149.62   2  2e-005  4.222  0.525   792.1  1   18/27   4

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

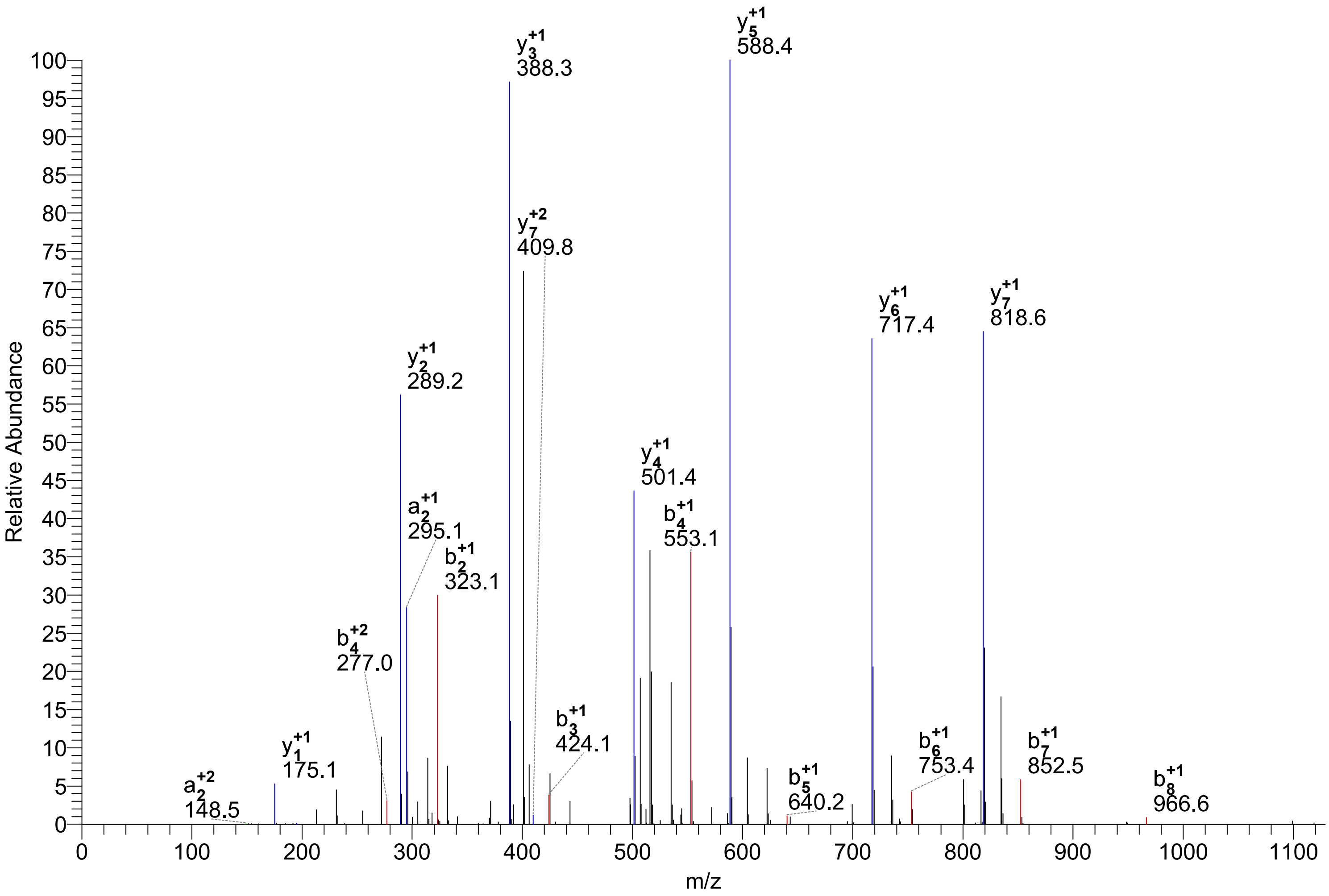
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                      979.45
 T    396.09     424.08                                      818.44
 E    525.13     553.13                                      717.39
 S    612.16     640.16                                      588.35
 L    725.25     753.24                                      501.31
 V    824.32     852.31                                      388.23
 N    938.36     966.35                                      289.16
 R                                                           175.12
```



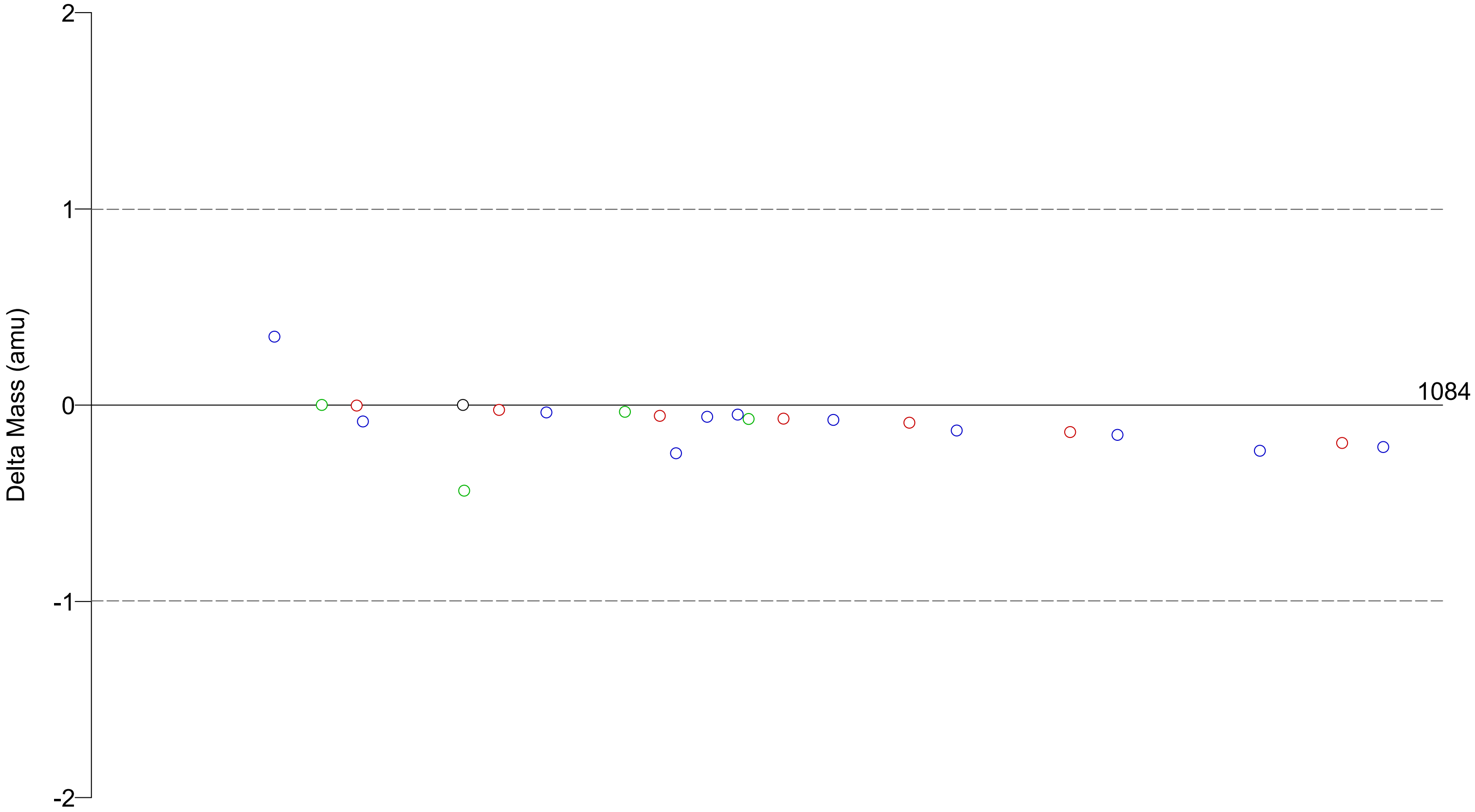
#19287468-1 NL: 8.98E6



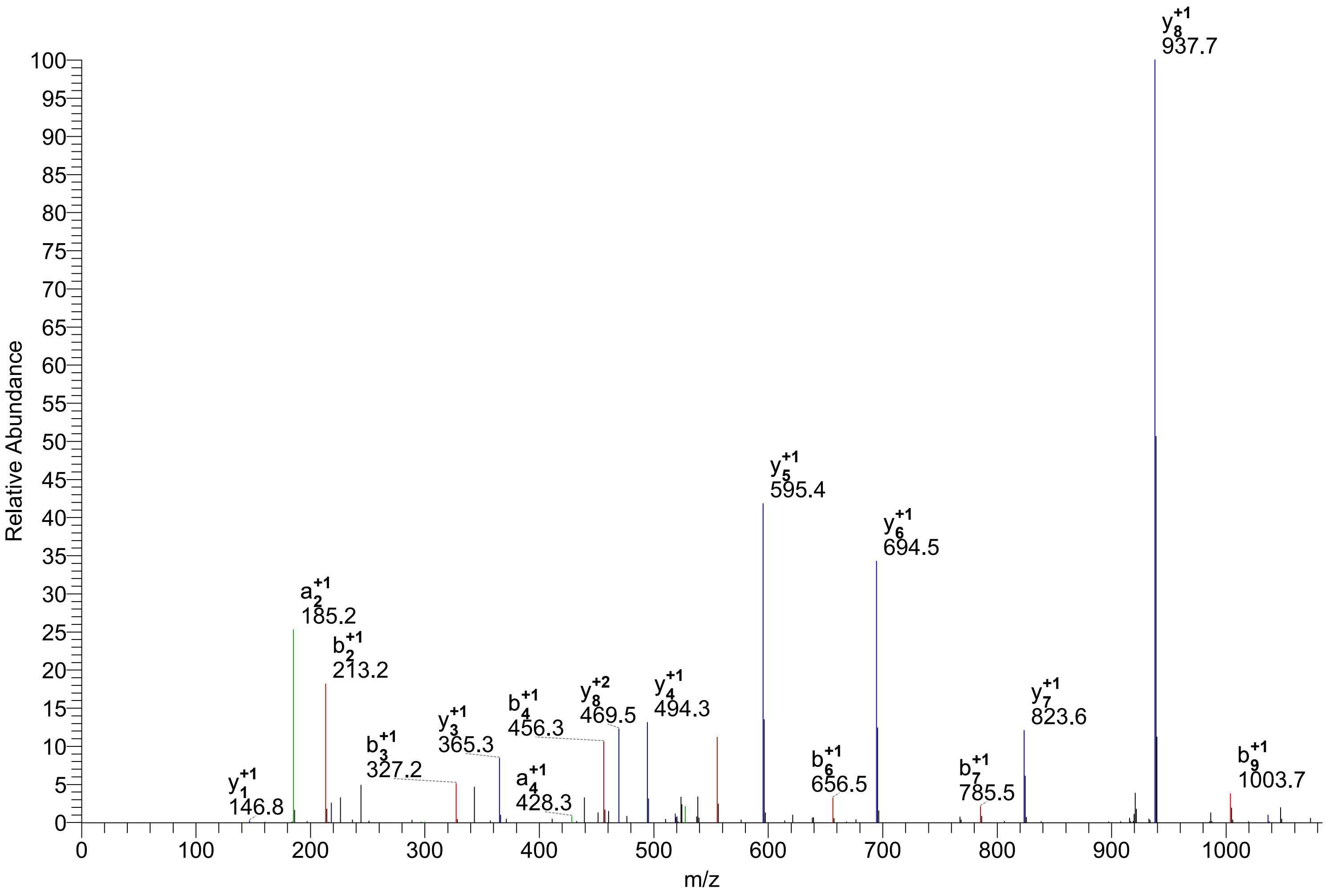
```
DTA for scans: 19287468-1
Precursor ion: 575.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 V    185.16    213.16                                     1036.53
 N    299.21    327.20                                      937.46
 E    428.25    456.25                                      823.42
 V    527.32    555.31                                      694.38
 T    628.37    656.36                                      595.31
 E    757.41    785.40                                      494.26
 F    904.48    932.47                                      365.22
 A    975.51   1003.51                                      218.15
 K                                                          147.11
```



#19287468-1 NL: 3.94E6



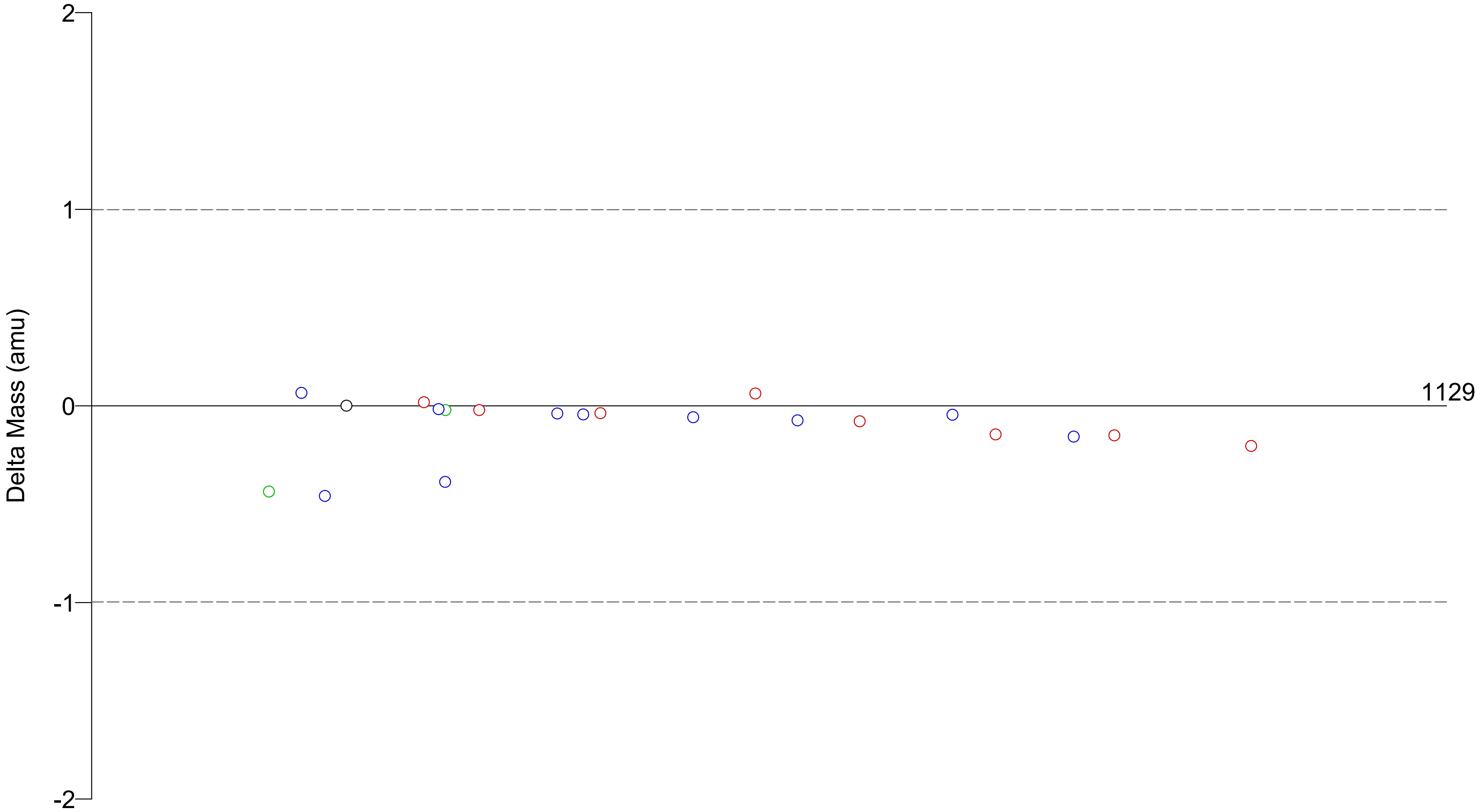
```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00745872.2|SWISS-PROT:P0276                                 2e-005  20.2      0.0        0
19287468 - 1  K.CCTESLVNR.R                          1140.47    2  0.0001  3.308  0.574    935.4  1    15/24    8
19287468 - 1  K.LVNEVTEFAK.T                         1149.62    2  2e-005  4.222  0.525    792.1  1    18/27    4

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

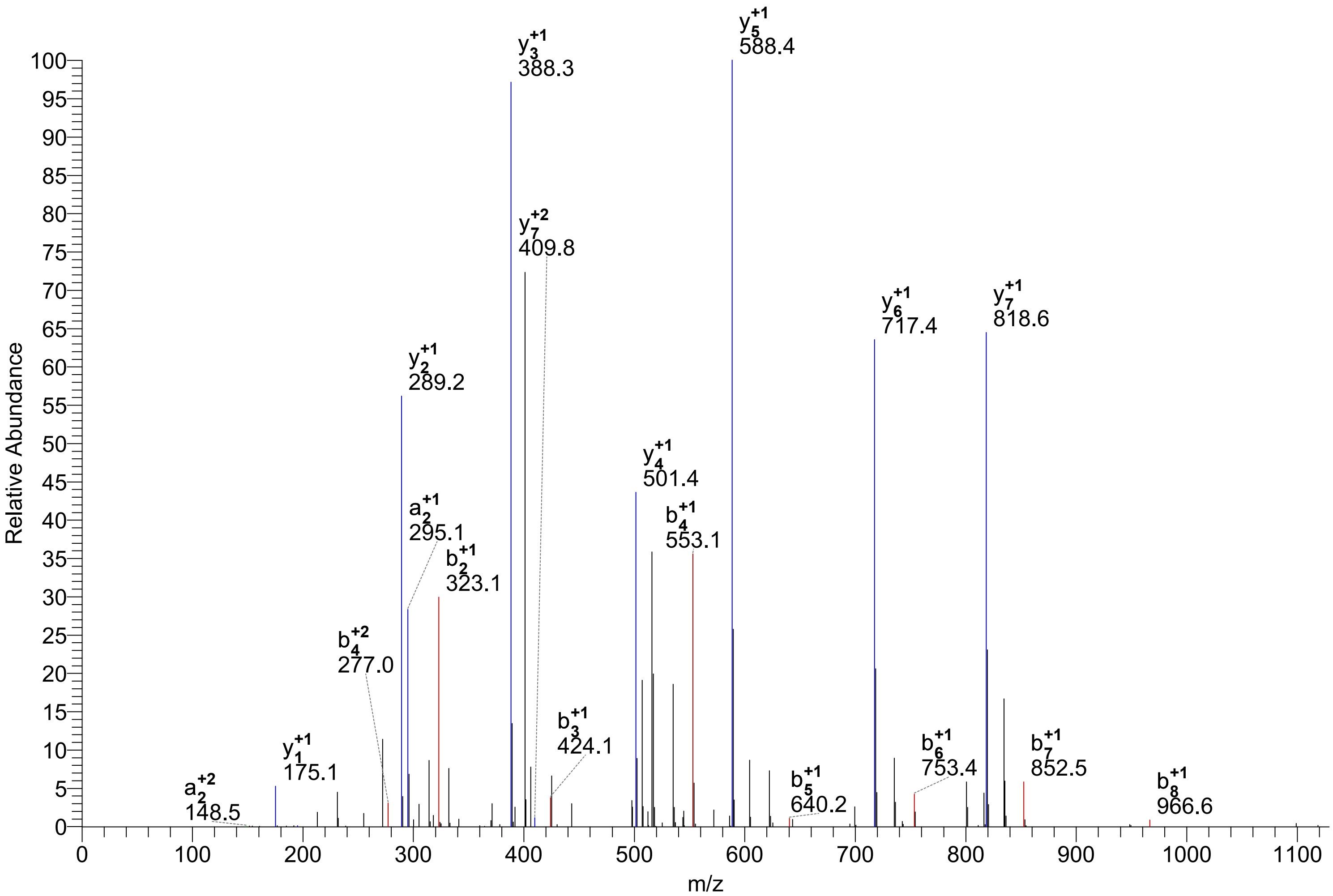
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                     979.45
 T    396.09     424.08                                     818.44
 E    525.13     553.13                                     717.39
 S    612.16     640.16                                     588.35
 L    725.25     753.24                                     501.31
 V    824.32     852.31                                     388.23
 N    938.36     966.35                                     289.16
 R                                                          175.12
```



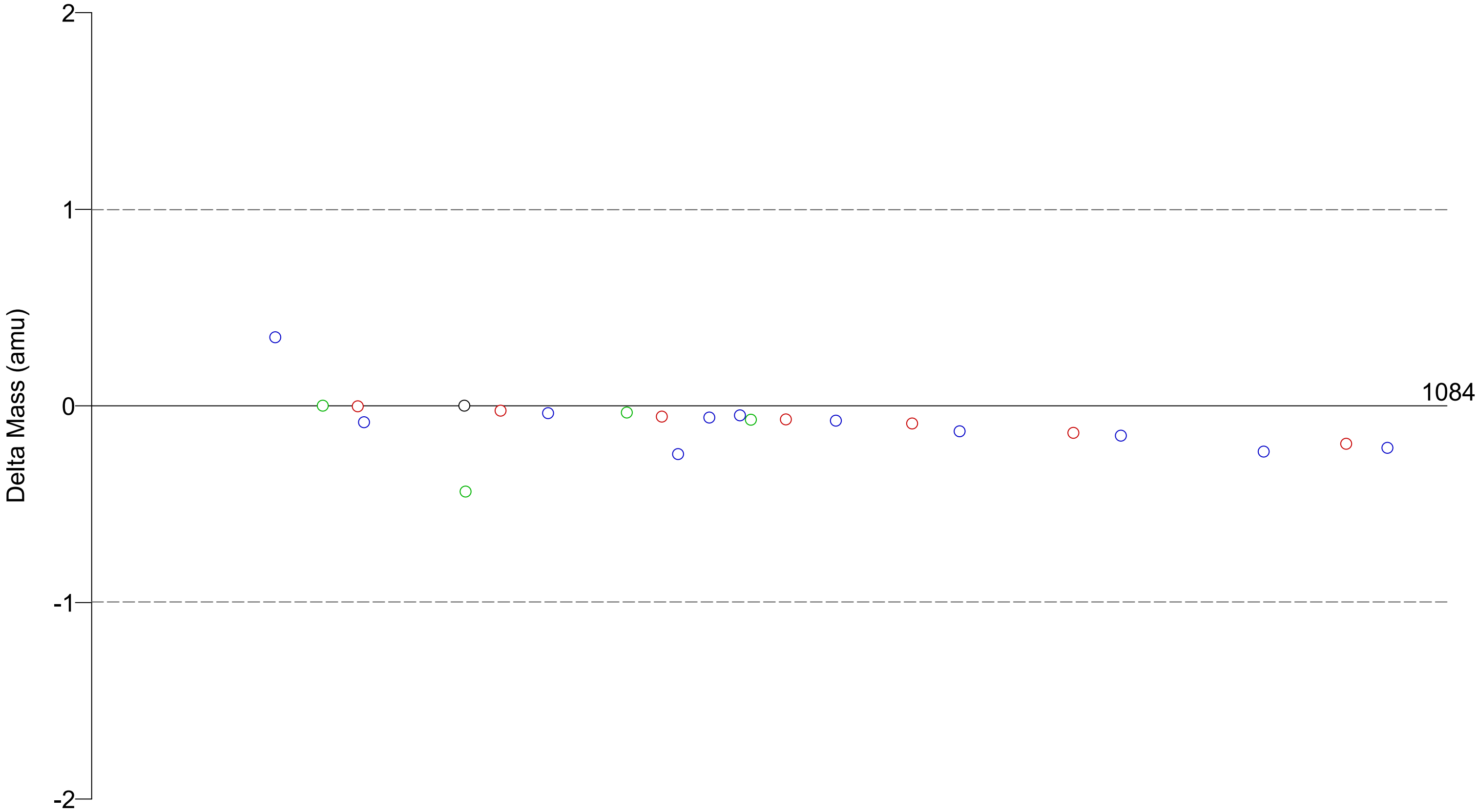
#19287468-1 NL: 8.98E6



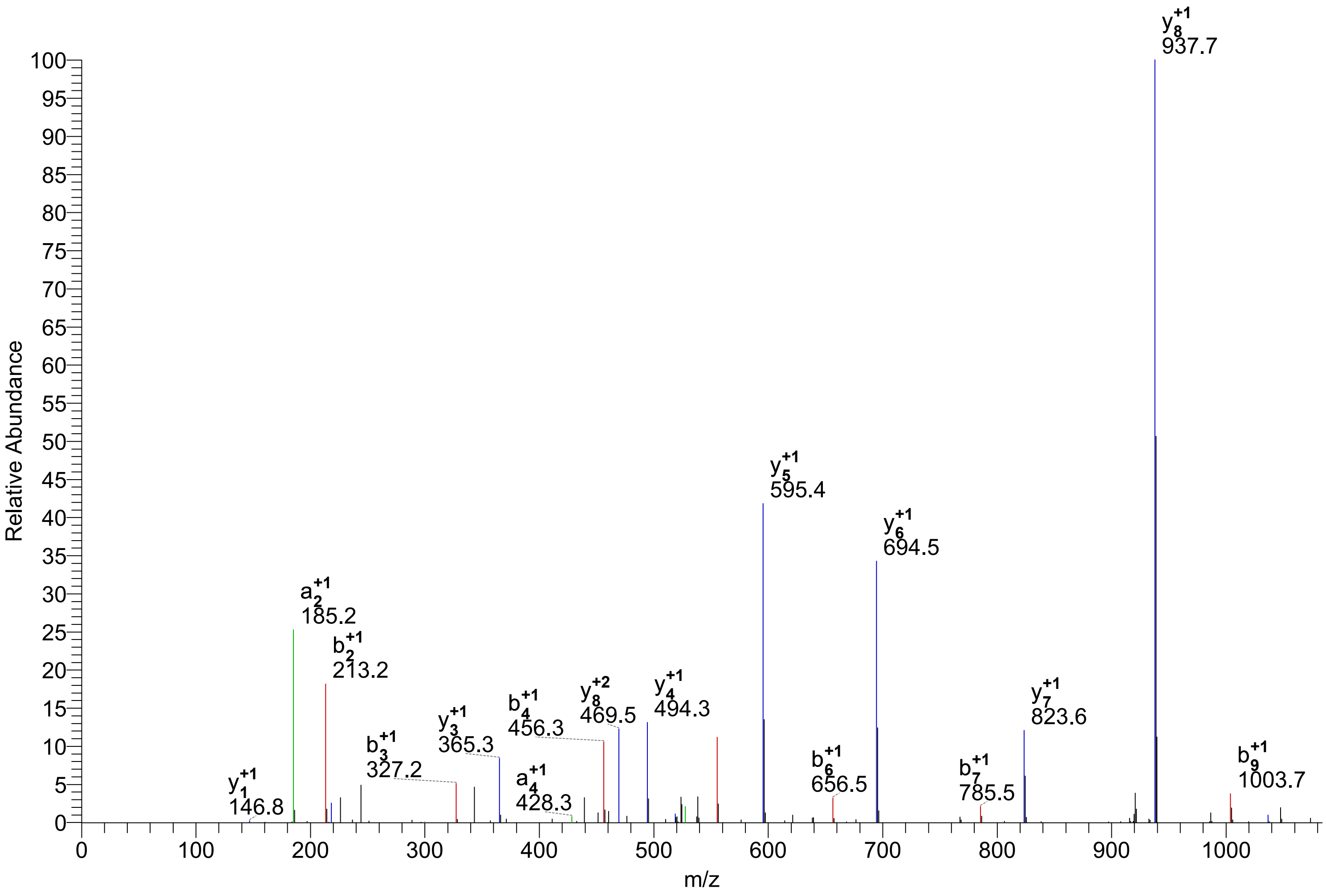
```
DTA for scans: 19287468-1
Precursor ion: 575.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 V    185.16     213.16                                     1036.53
 N    299.21     327.20                                      937.46
 E    428.25     456.25                                      823.42
 V    527.32     555.31                                      694.38
 T    628.37     656.36                                      595.31
 E    757.41     785.40                                      494.26
 F    904.48     932.47                                      365.22
 A    975.51    1003.51                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.94E6



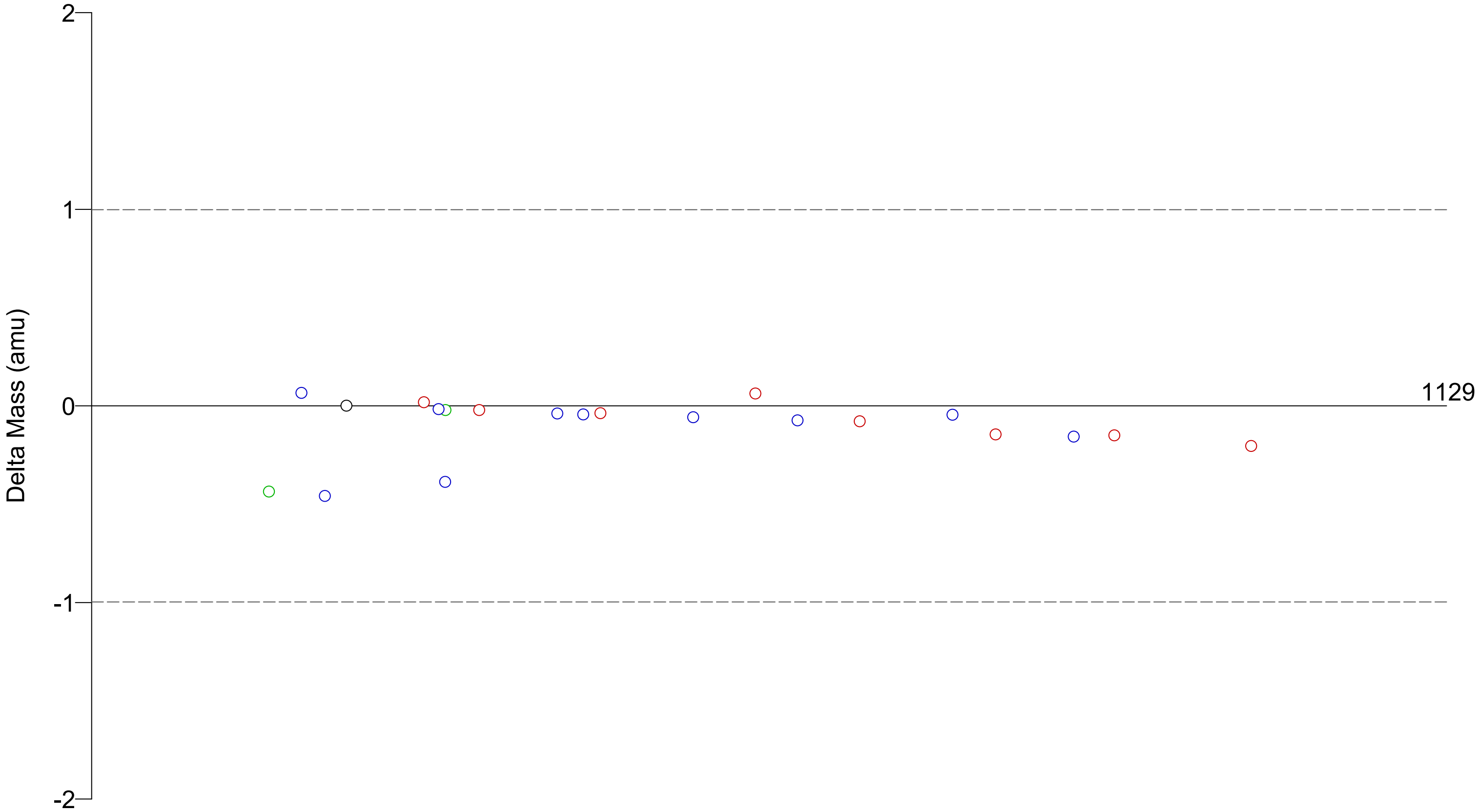
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                DH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
gi|113576|sp|P02768|ALBU_HUMAN SER                                2e-005  20.2     0.0       113576
19287468 - 1  K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24   8
19287468 - 1  K.LVNEVTEFAK.T                         1149.62   2  2e-005  4.222  0.525   792.1  1   18/27   4

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

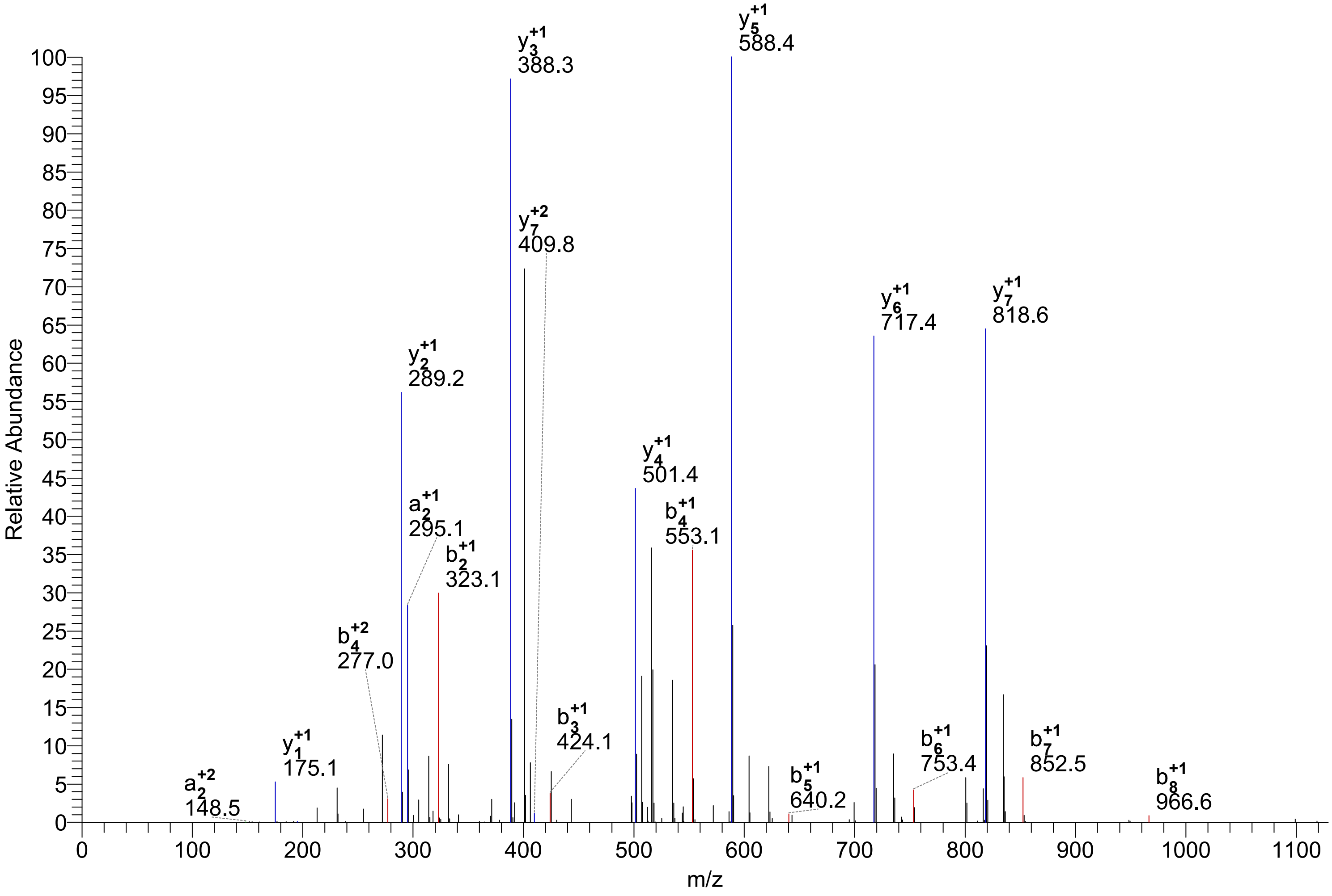
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                      979.45
 T    396.09     424.08                                      818.44
 E    525.13     553.13                                      717.39
 S    612.16     640.16                                      588.35
 L    725.25     753.24                                      501.31
 V    824.32     852.31                                      388.23
 N    938.36     966.35                                      289.16
 R                                                           175.12
```



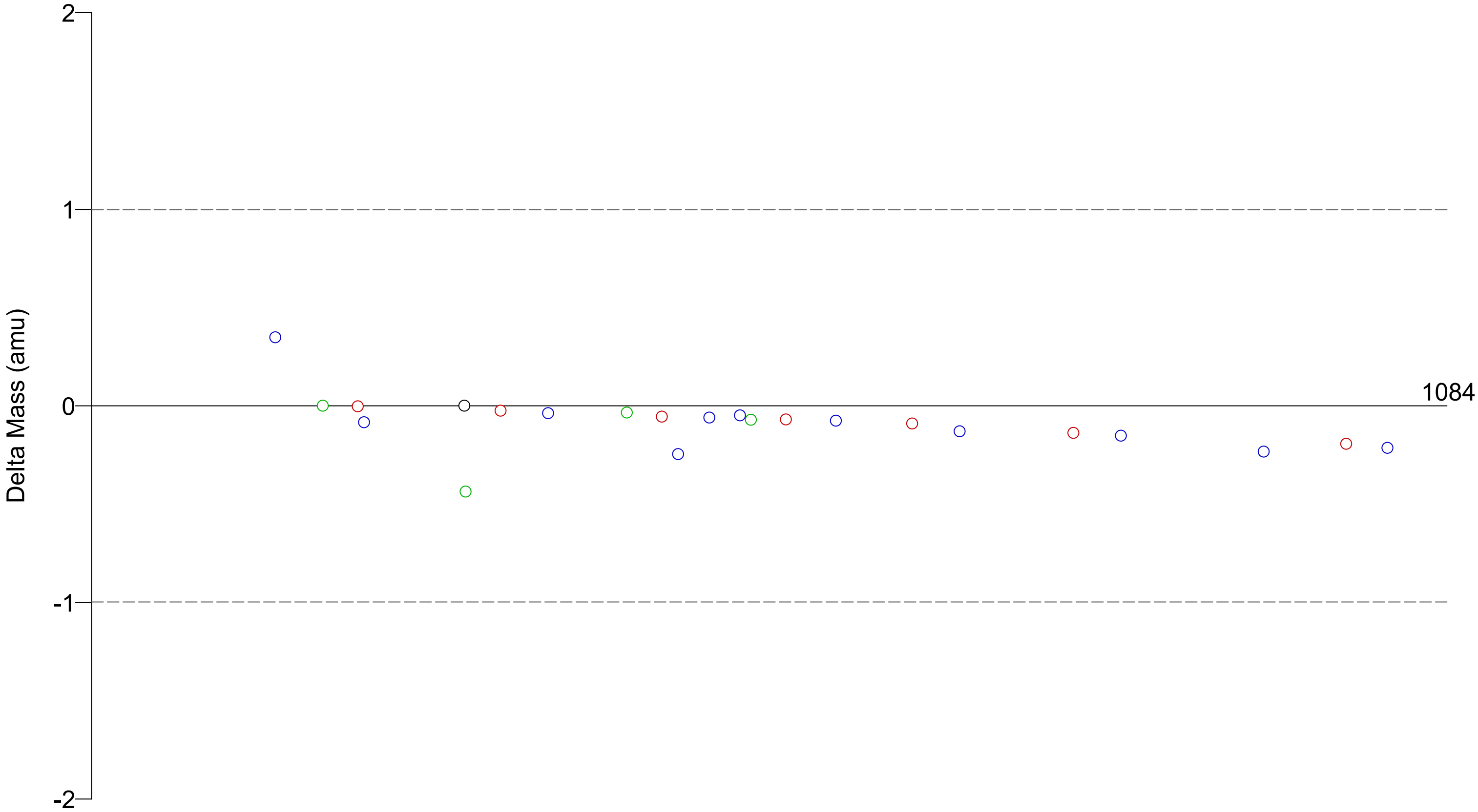
#19287468-1 NL: 8.98E6



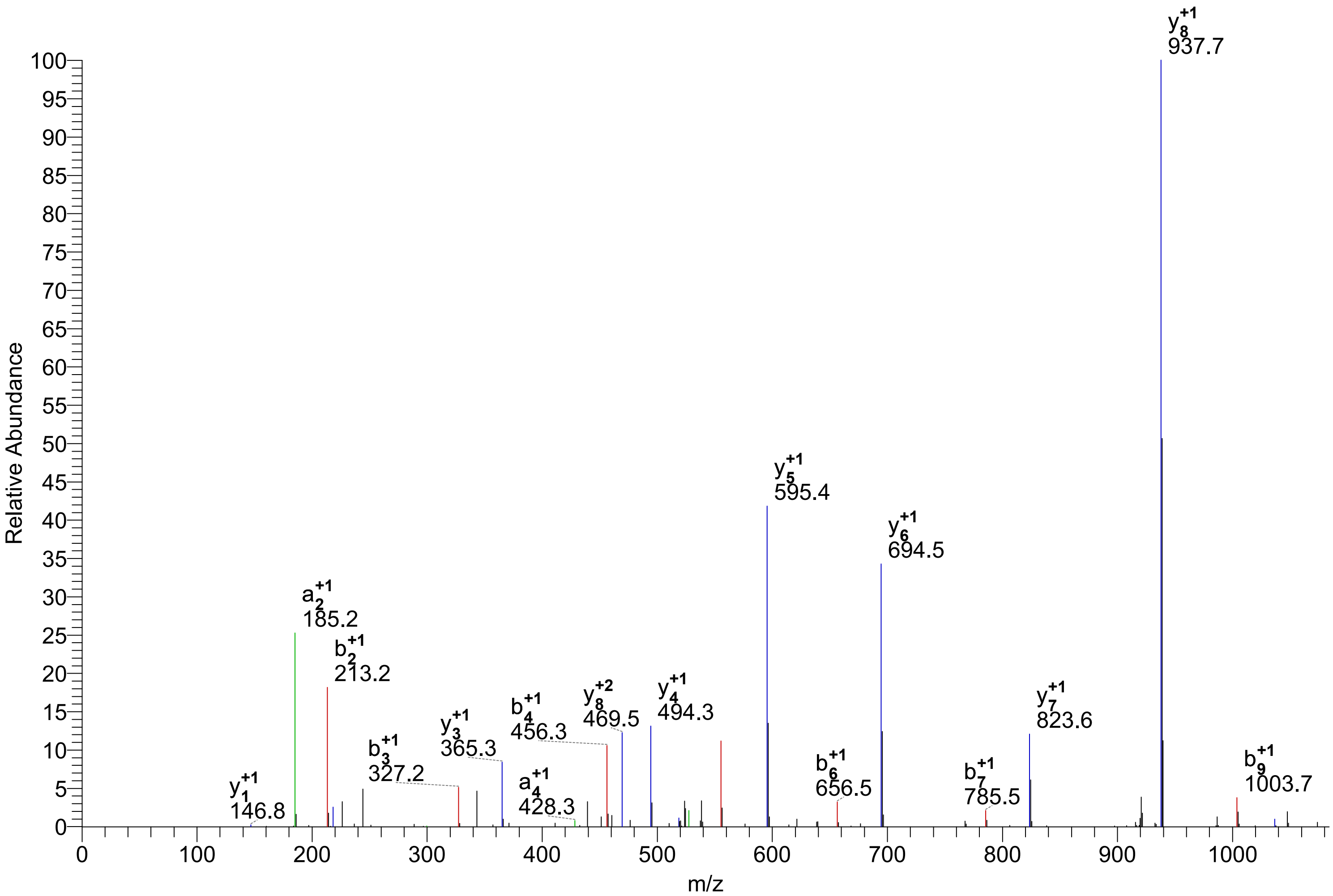
```
DTA for scans: 19287468-1
Precursor ion: 575.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 V    185.16    213.16                                     1036.53
 N    299.21    327.20                                      937.46
 E    428.25    456.25                                      823.42
 V    527.32    555.31                                      694.38
 T    628.37    656.36                                      595.31
 E    757.41    785.40                                      494.26
 F    904.48    932.47                                      365.22
 A    975.51   1003.51                                      218.15
 K                                                          147.11
```



#19287468-1 NL: 3.94E6



```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn   Sp    RSp  Ions  Count

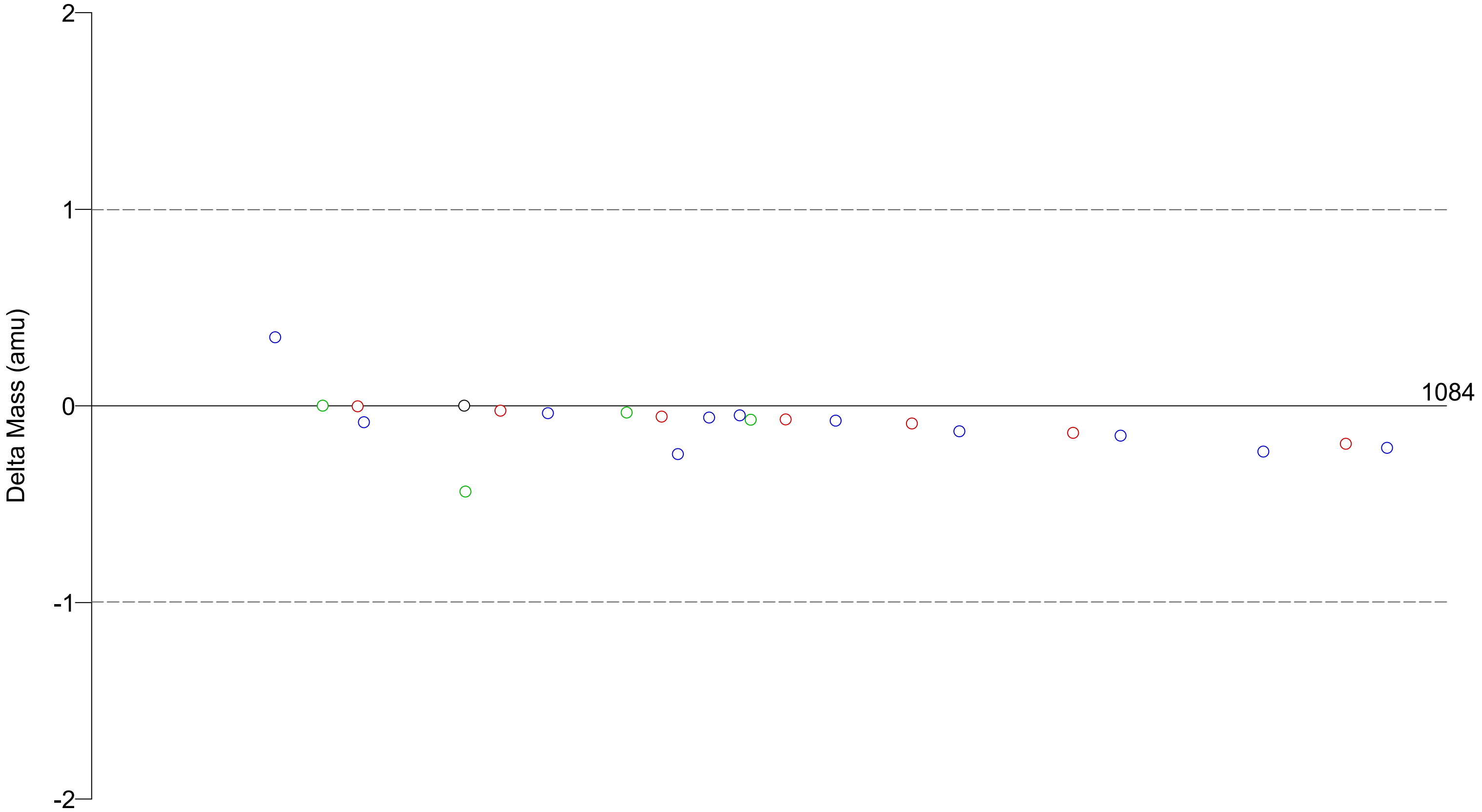
IPI:IPI00878282.1|VEGA:OTTHUMP0000                                    2e-005  10.2     0.0       0
19287468 - 1  K.LVNEVTEFAK.T                           1149.62   2  2e-005  4.222  0.525   792.1  1   18/27   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

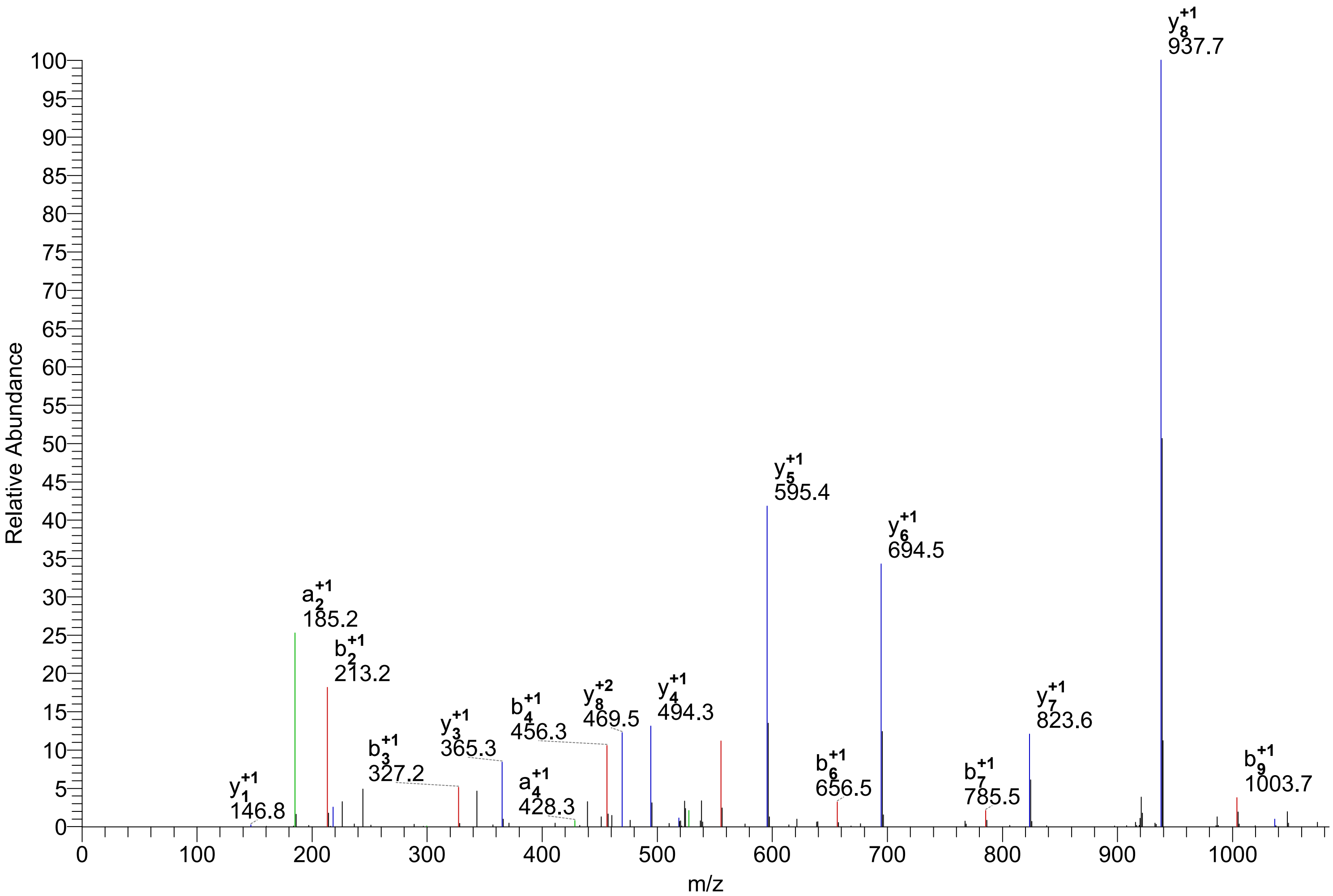
```
DTA for scans: 19287468-1
Precursor ion: 575.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 V    185.16     213.16                                     1036.53
 N    299.21     327.20                                      937.46
 E    428.25     456.25                                      823.42
 V    527.32     555.31                                      694.38
 T    628.37     656.36                                      595.31
 E    757.41     785.40                                      494.26
 F    904.48     932.47                                      365.22
 A    975.51    1003.51                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.94E6



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Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00418163.3|TREMBL:B4E344;Q6                                2e-005  20.2     0.0       0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126  8
2118291816 -  K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24   10

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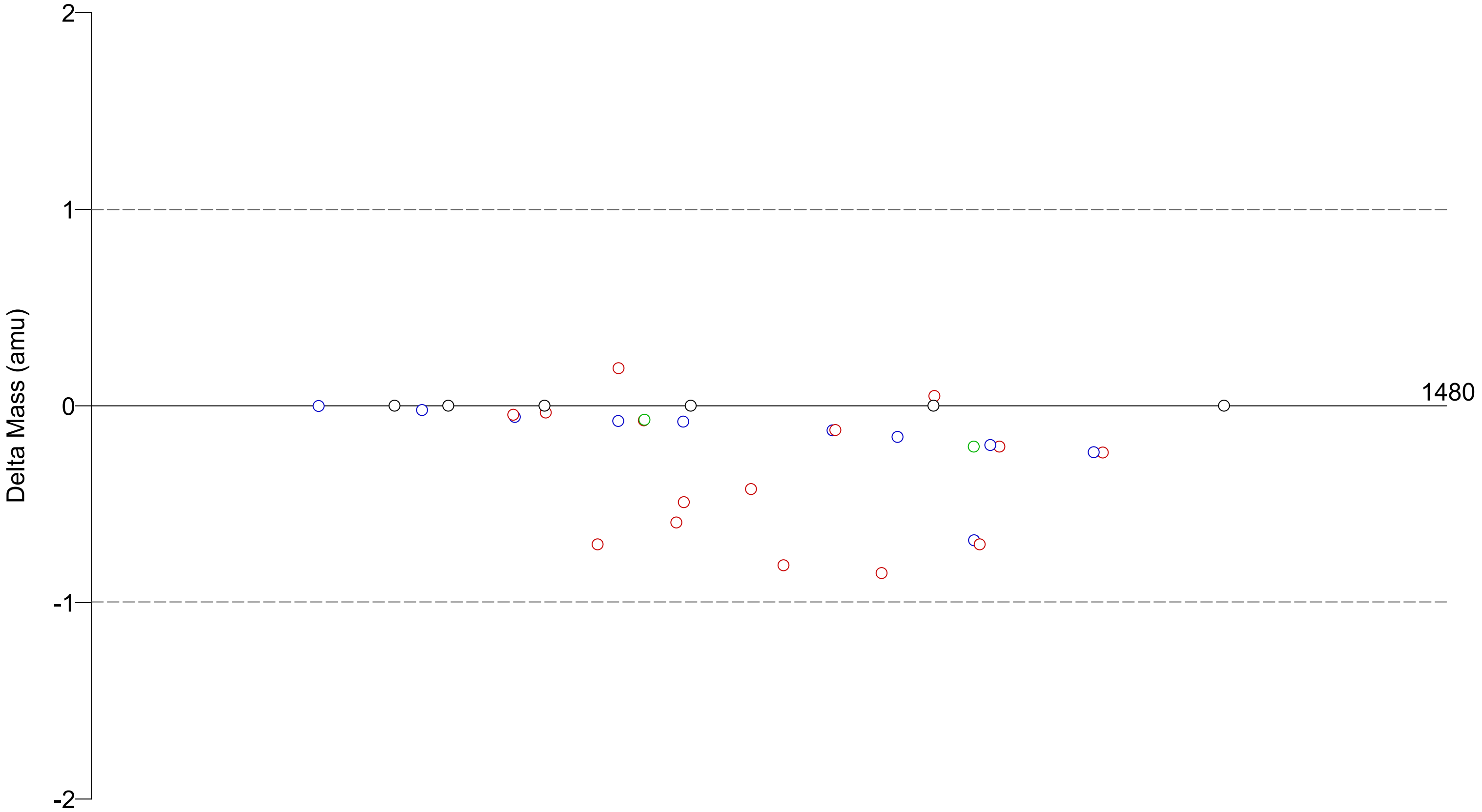
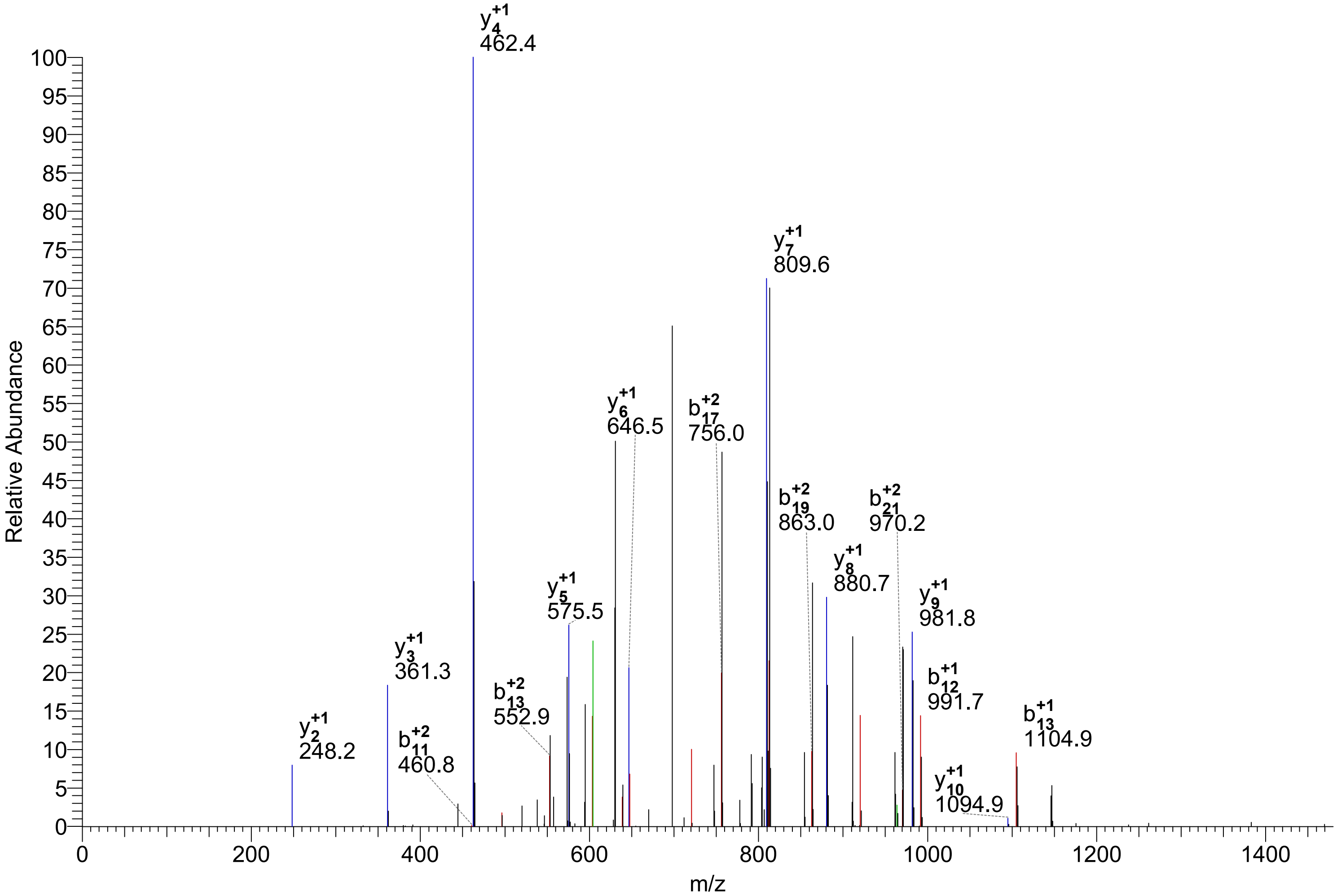
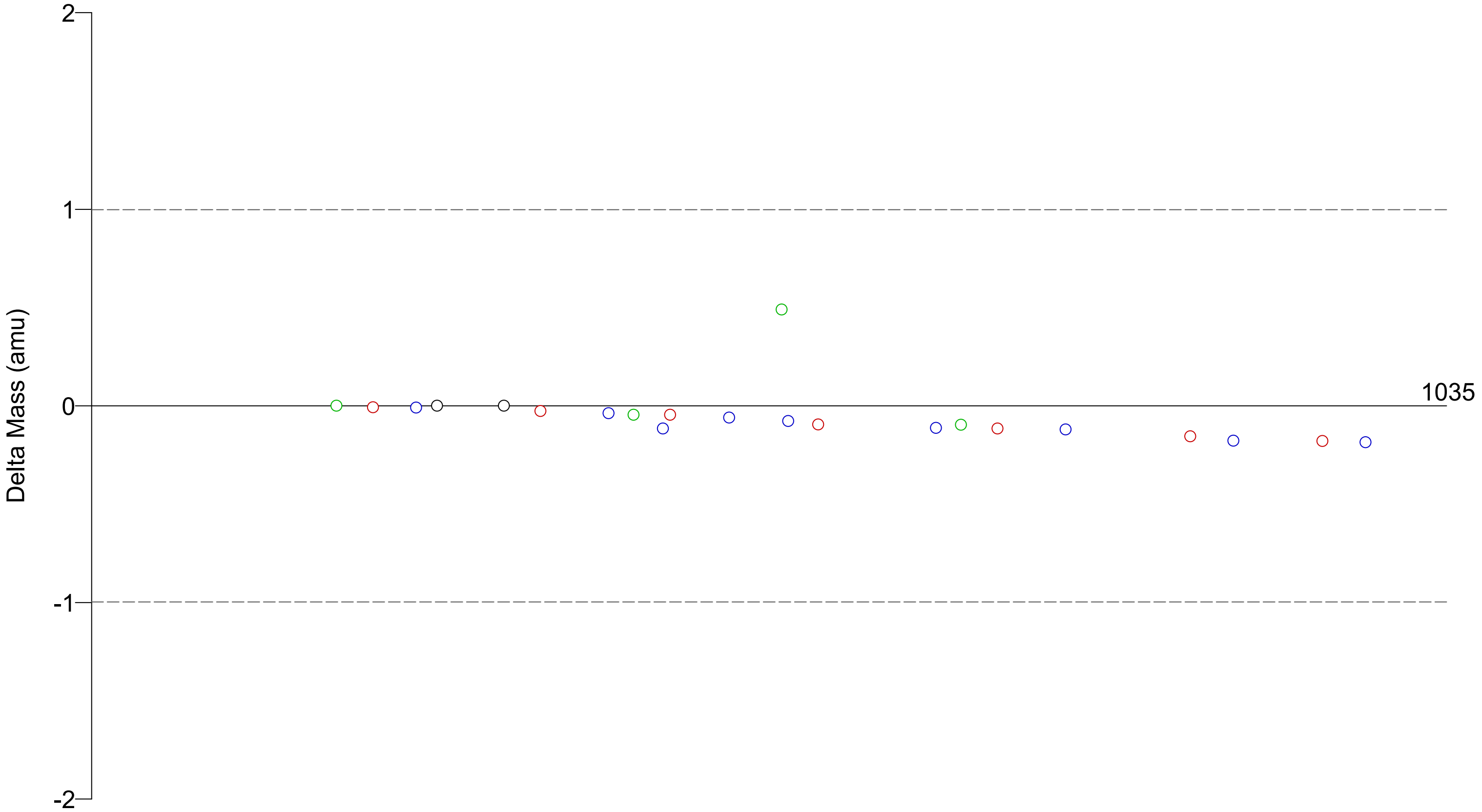

```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
--------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



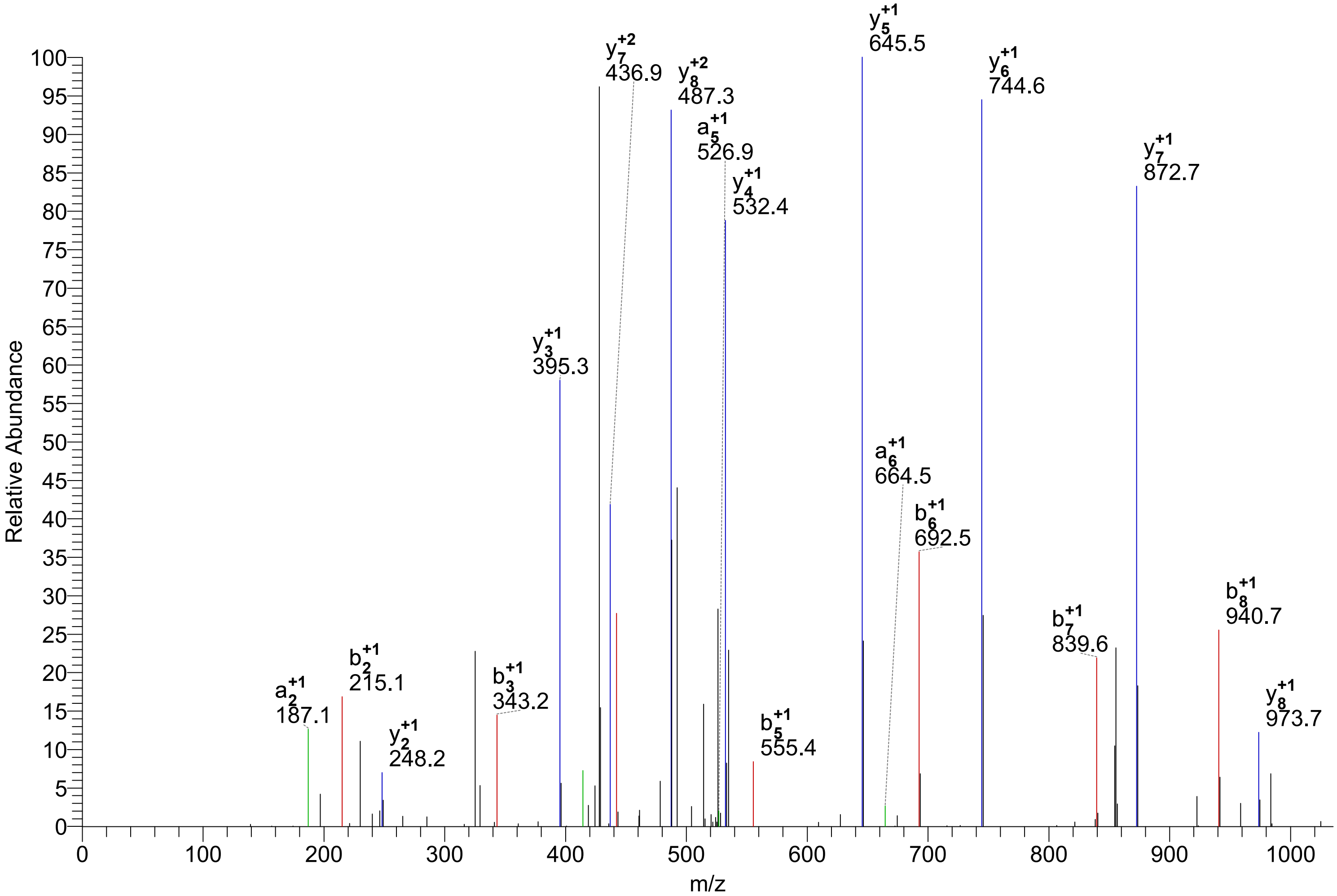
#19287468-1 NL: 5.80E4



```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```

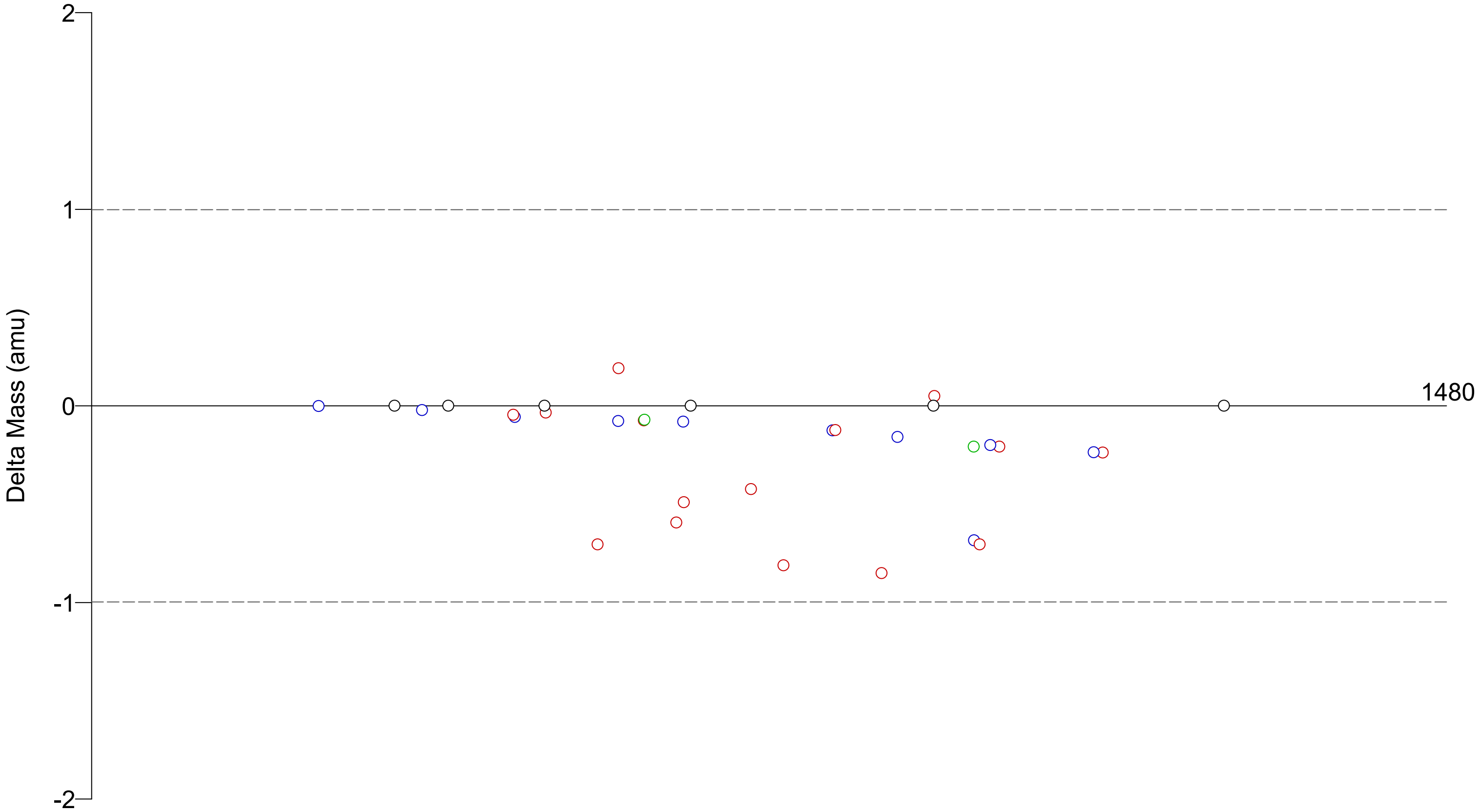


#2118291816-26226248 NL: 1.21E5

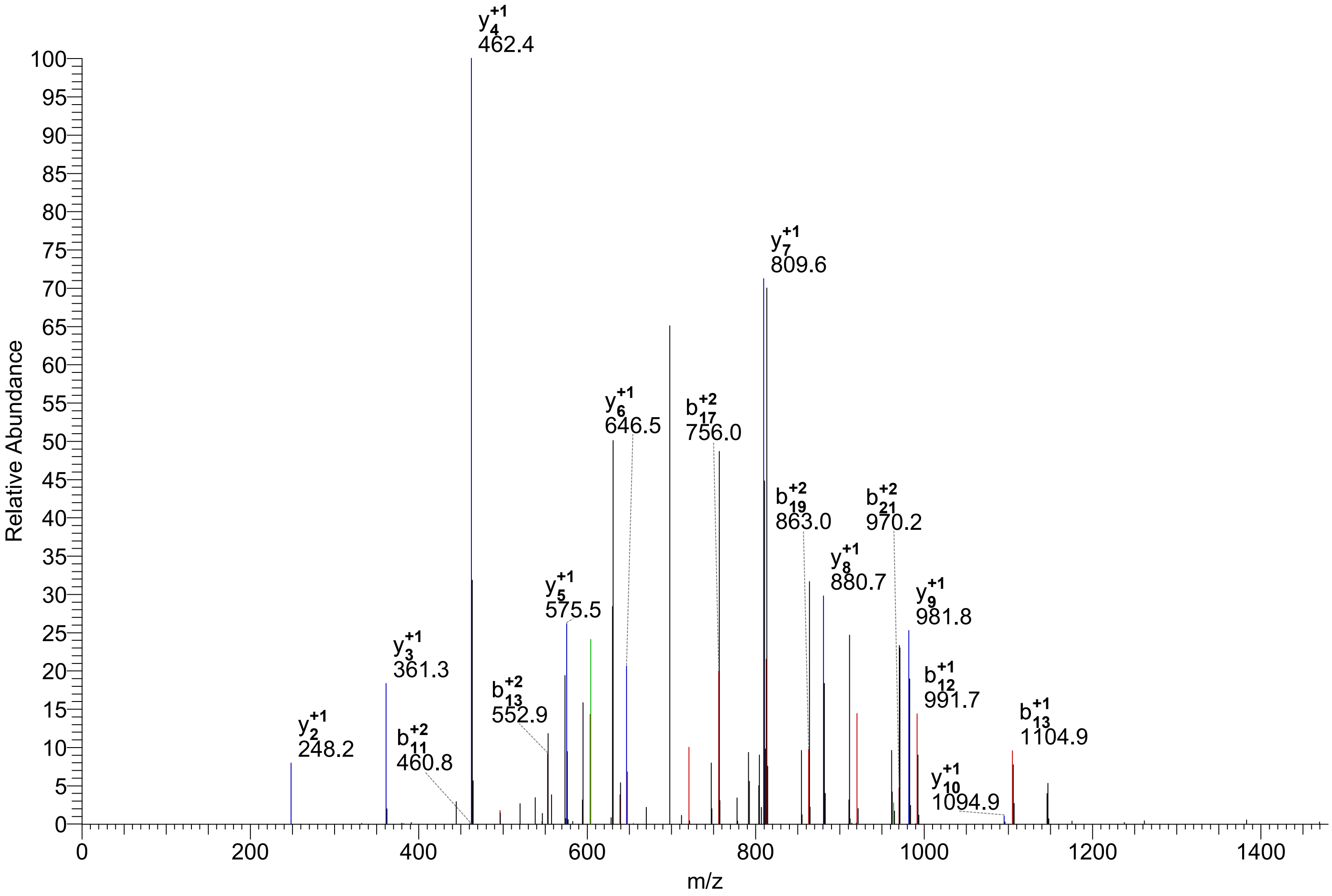


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+     z    P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00643525.1|TREMBL:A7E2V2;B4                               2e-005  20.2     0.0        0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126  8
2118291816 -  K.ITQVLHFTK.D                           1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24   10

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

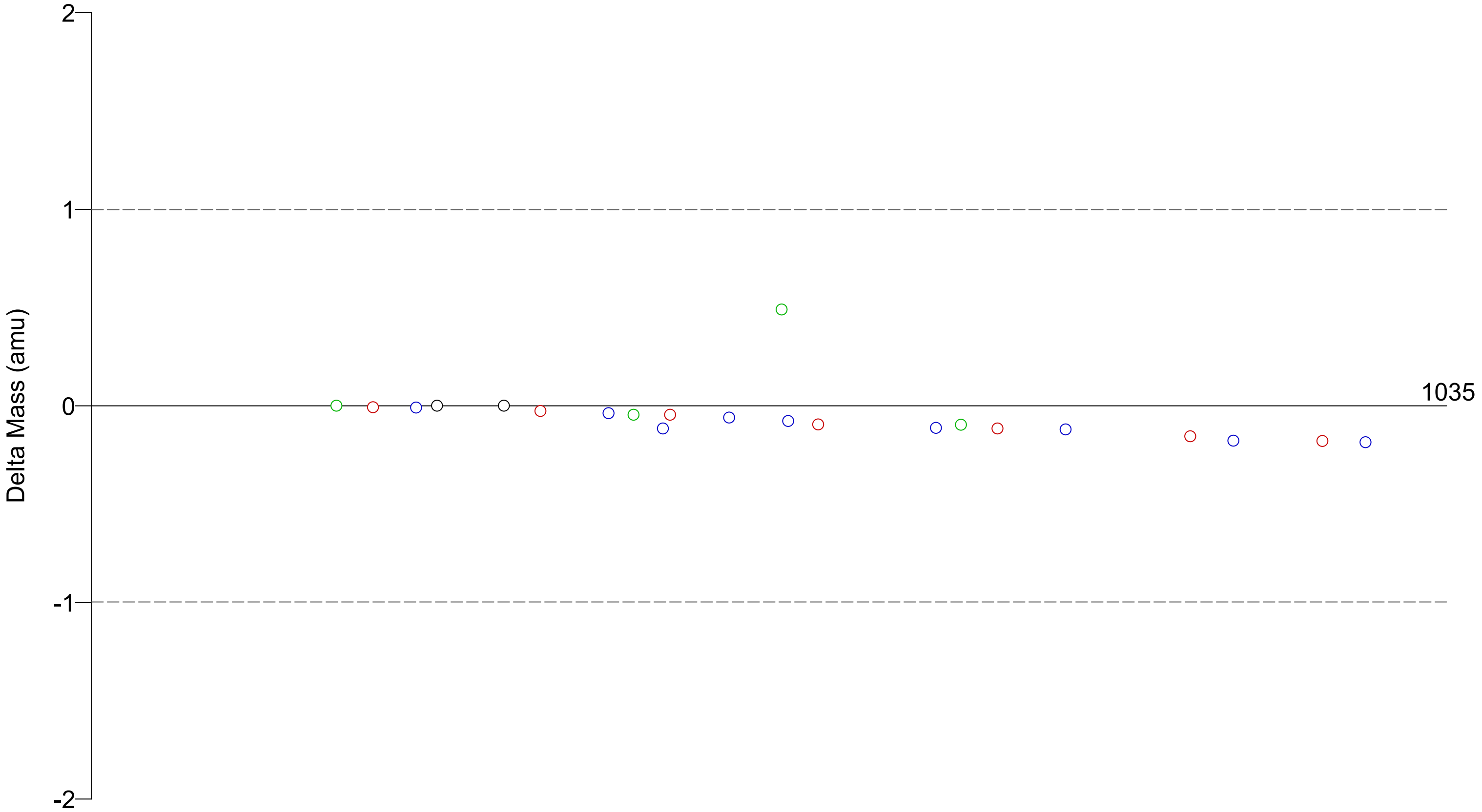
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
--------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



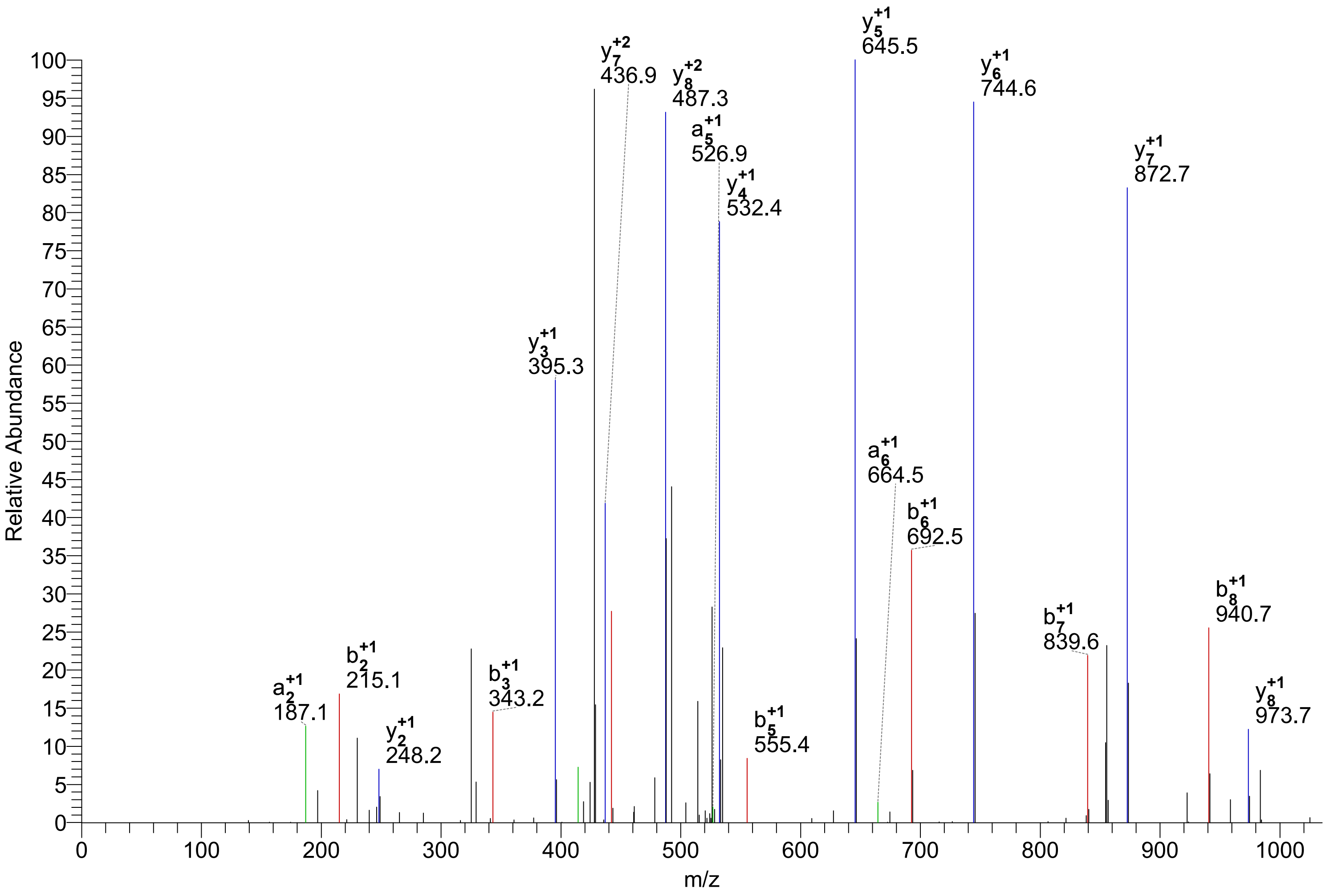
#19287468-1 NL: 5.80E4



```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```

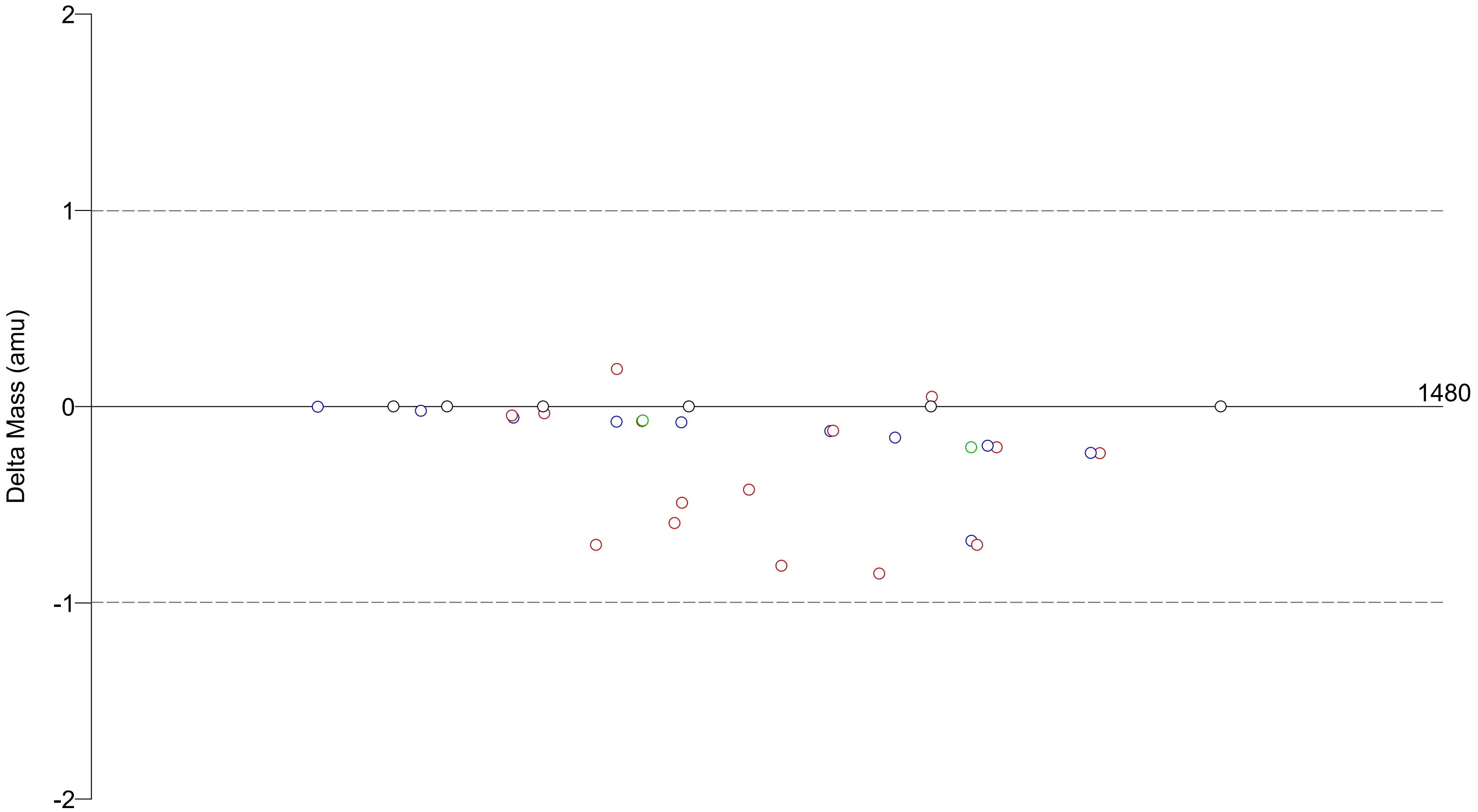


#2118291816-26226248 NL: 1.21E5

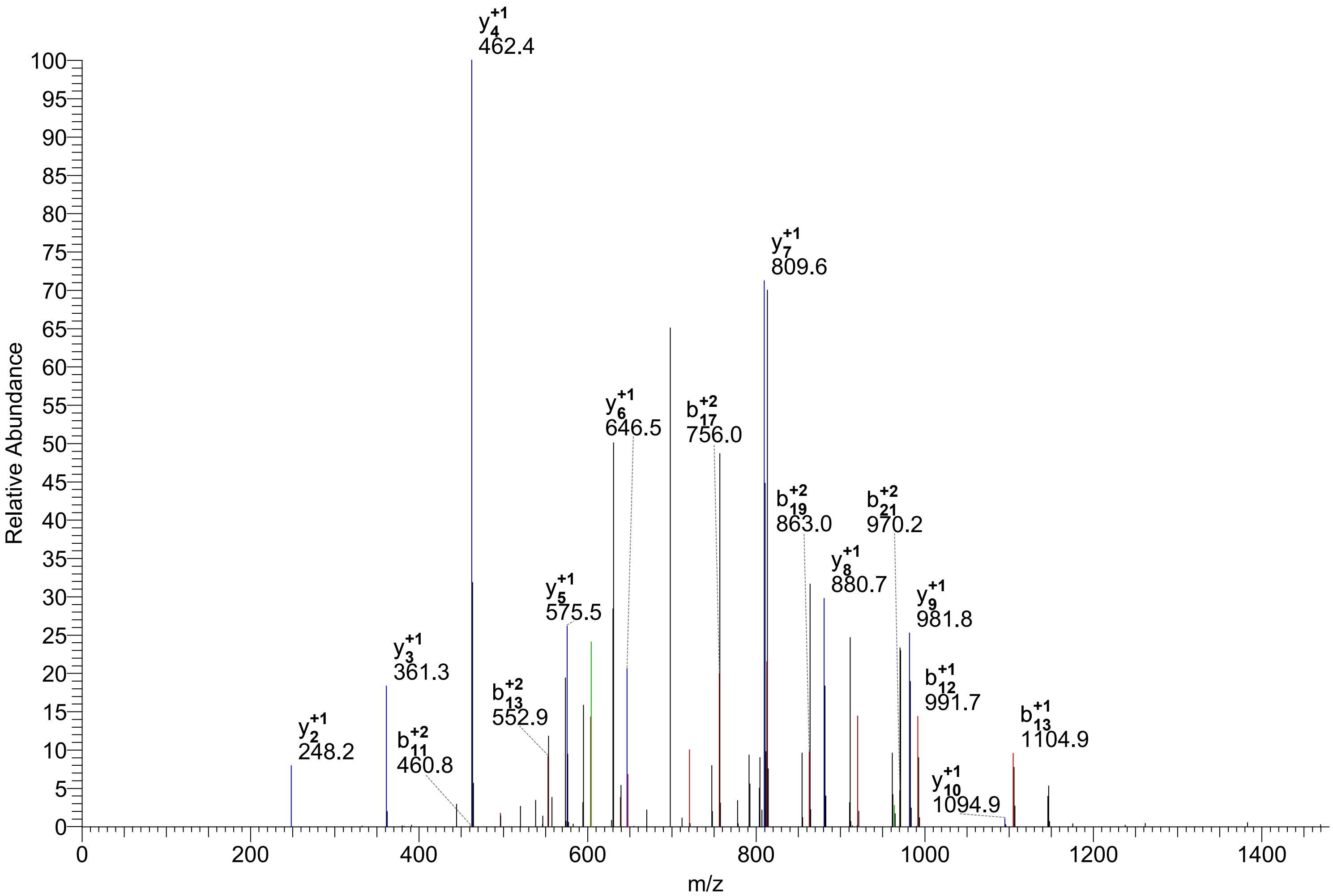


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)        Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00843913.3|TREMBL:B0V2C8;B2                                 2e-005  20.2     0.0       0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A              2085.17   3  2e-005  3.435  0.549   736.3  1    26/126  8
2118291816 -  K.ITQVLHFTK.D                           1086.63   2  0.0002  3.684  0.435   1215.2 1    18/24   10

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

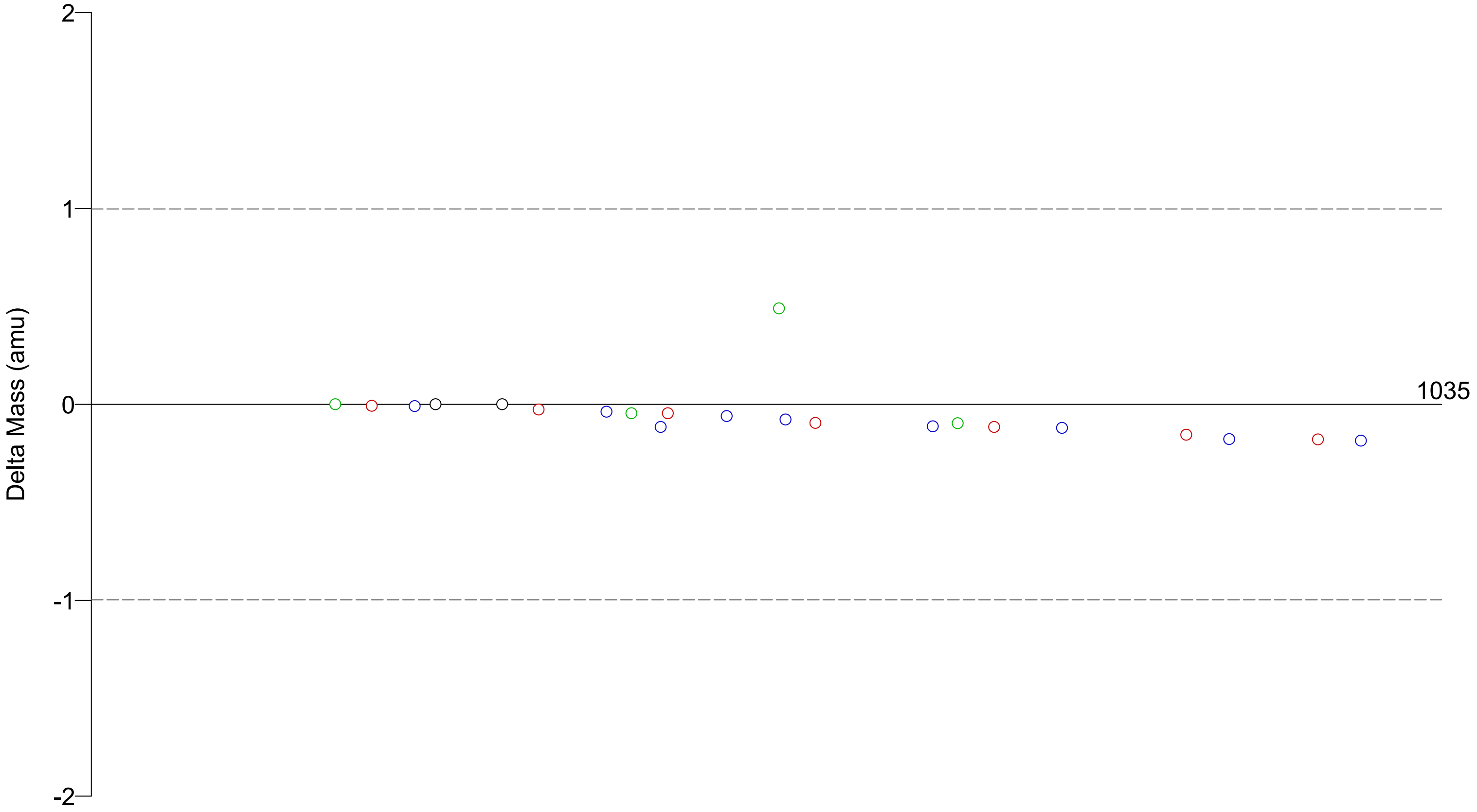
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
--------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



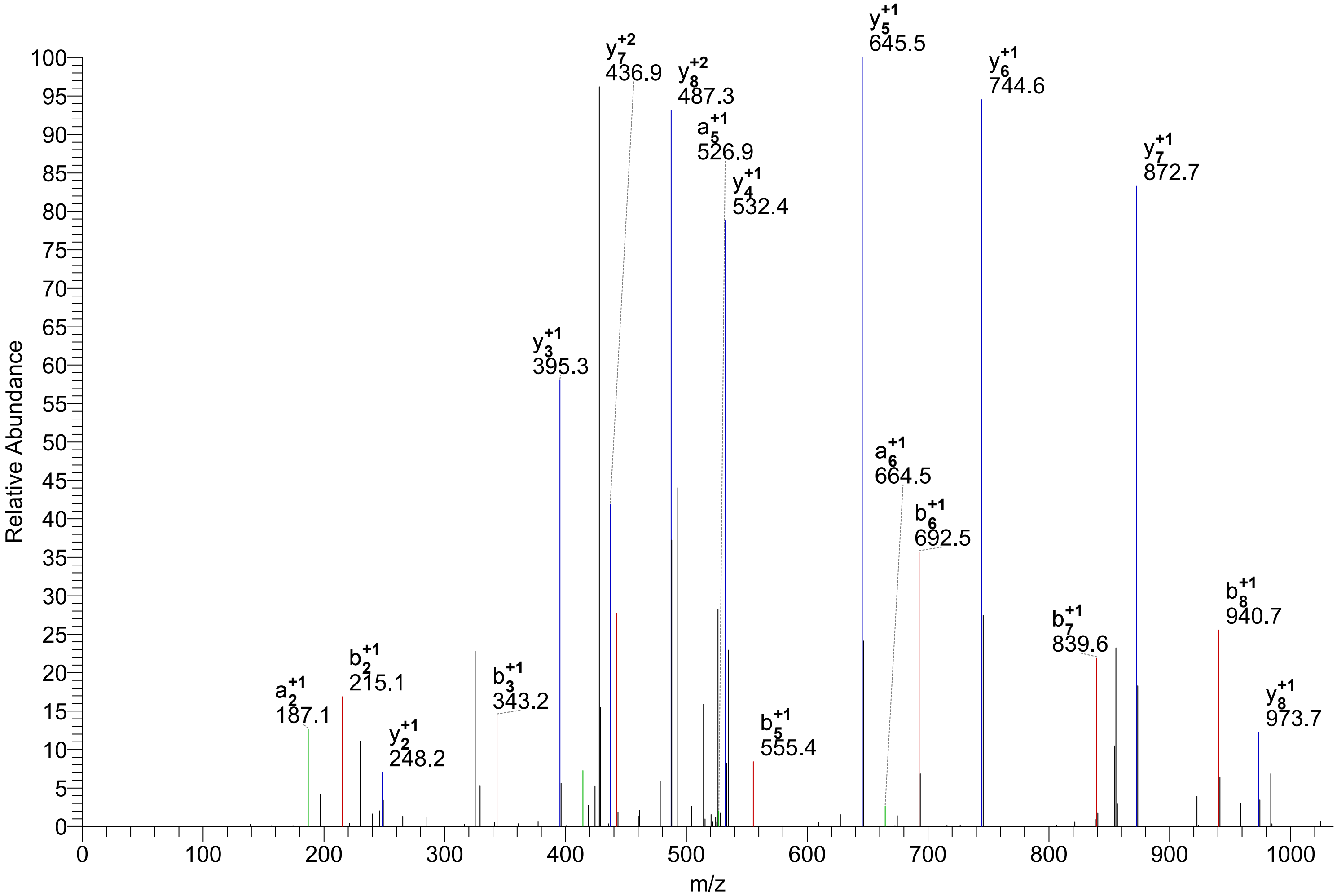
#19287468-1 NL: 5.80E4



```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```



#2118291816-26226248 NL: 1.21E5



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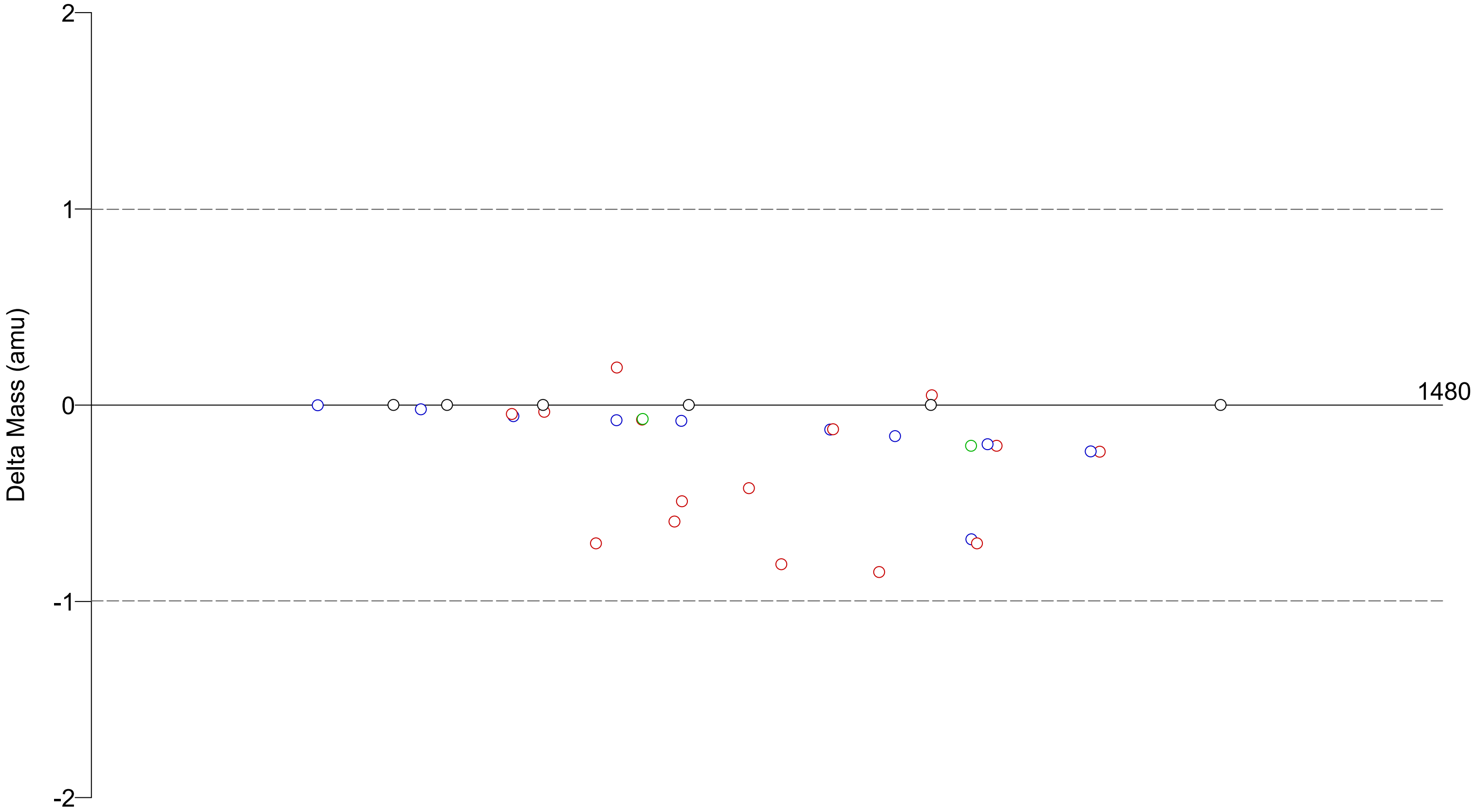
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00887154.2|TREMBL:B0UZ85;Q6                                2e-005  20.2     0.0       0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126  8
2118291816 -  K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24   10

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

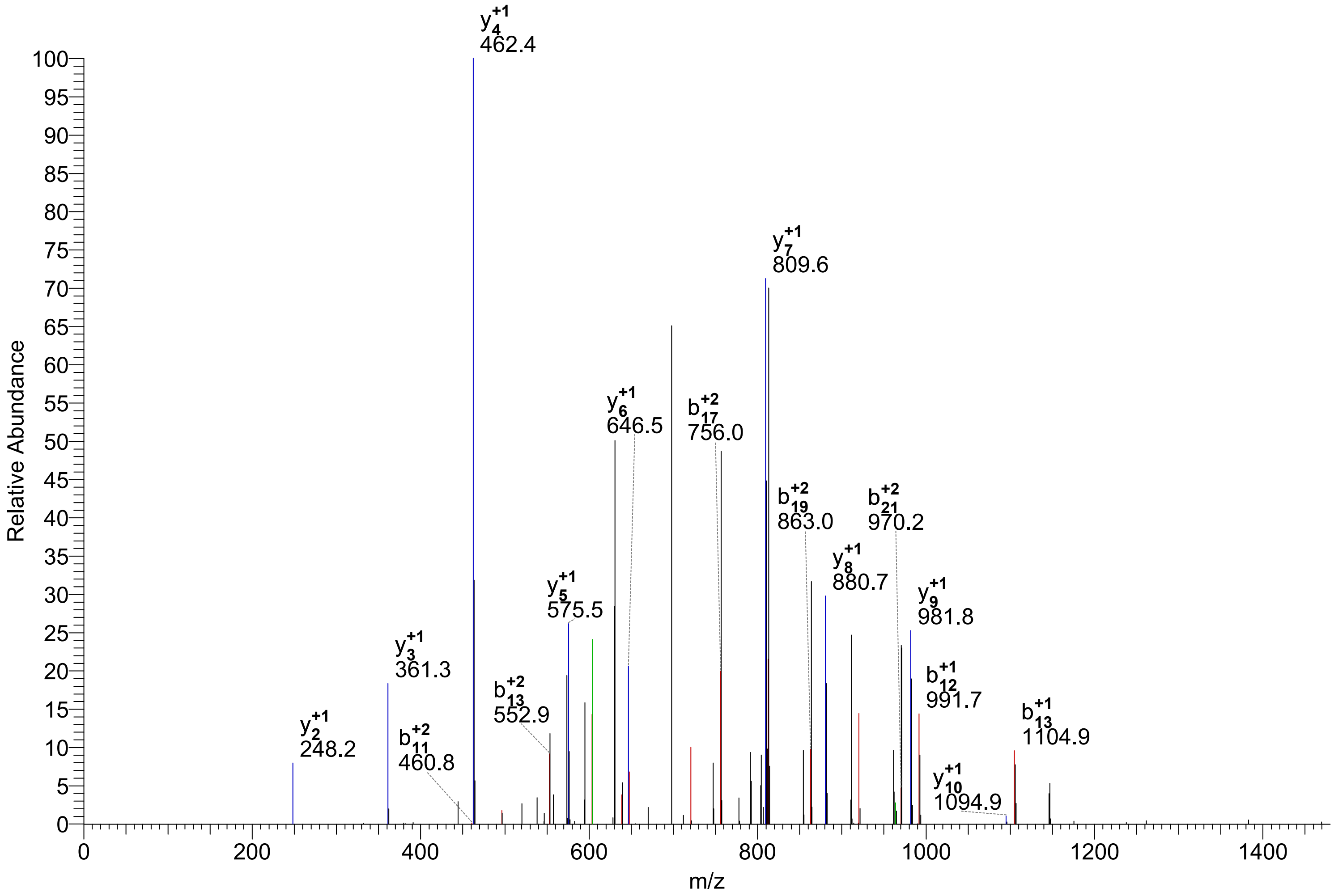
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



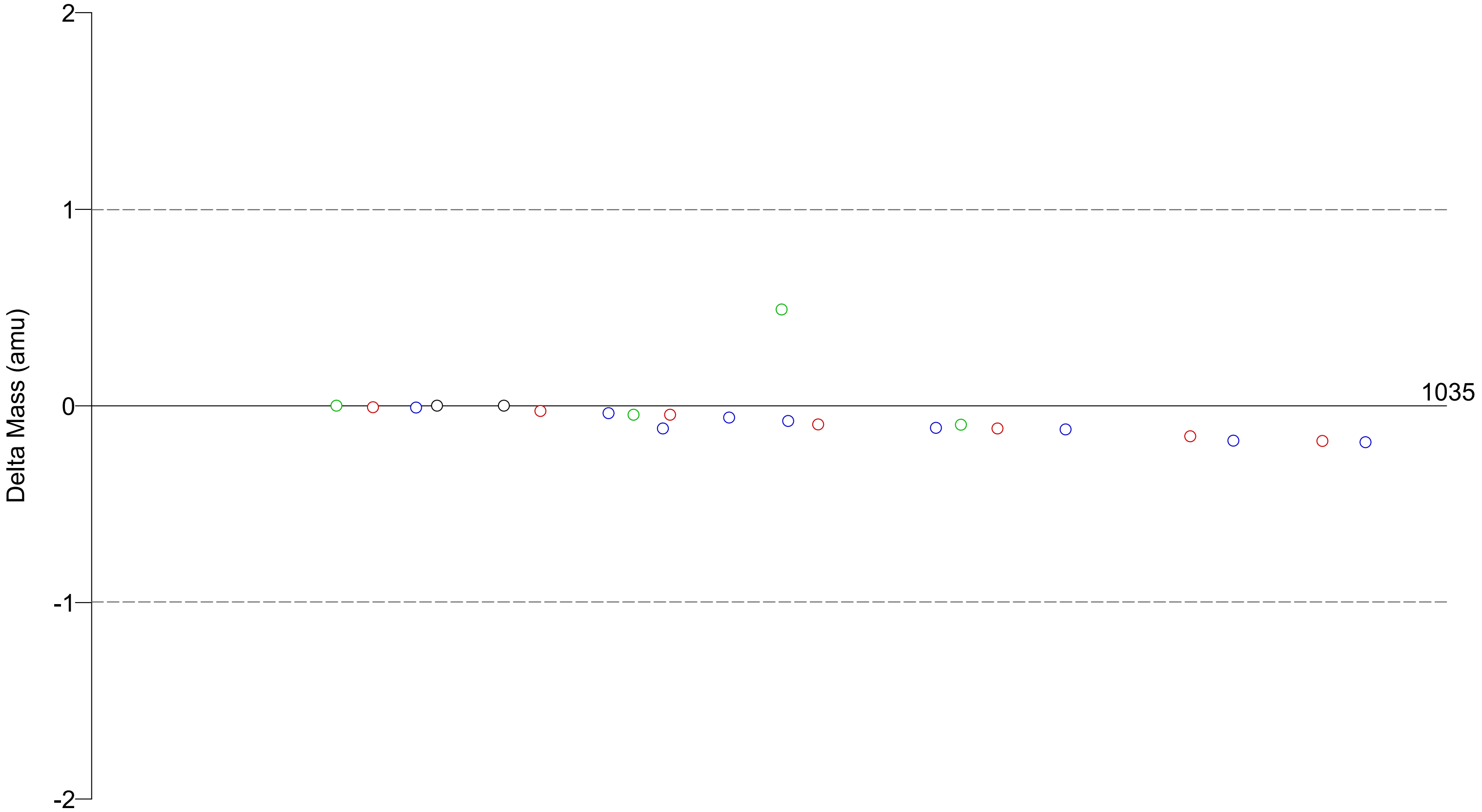
#19287468-1 NL: 5.80E4



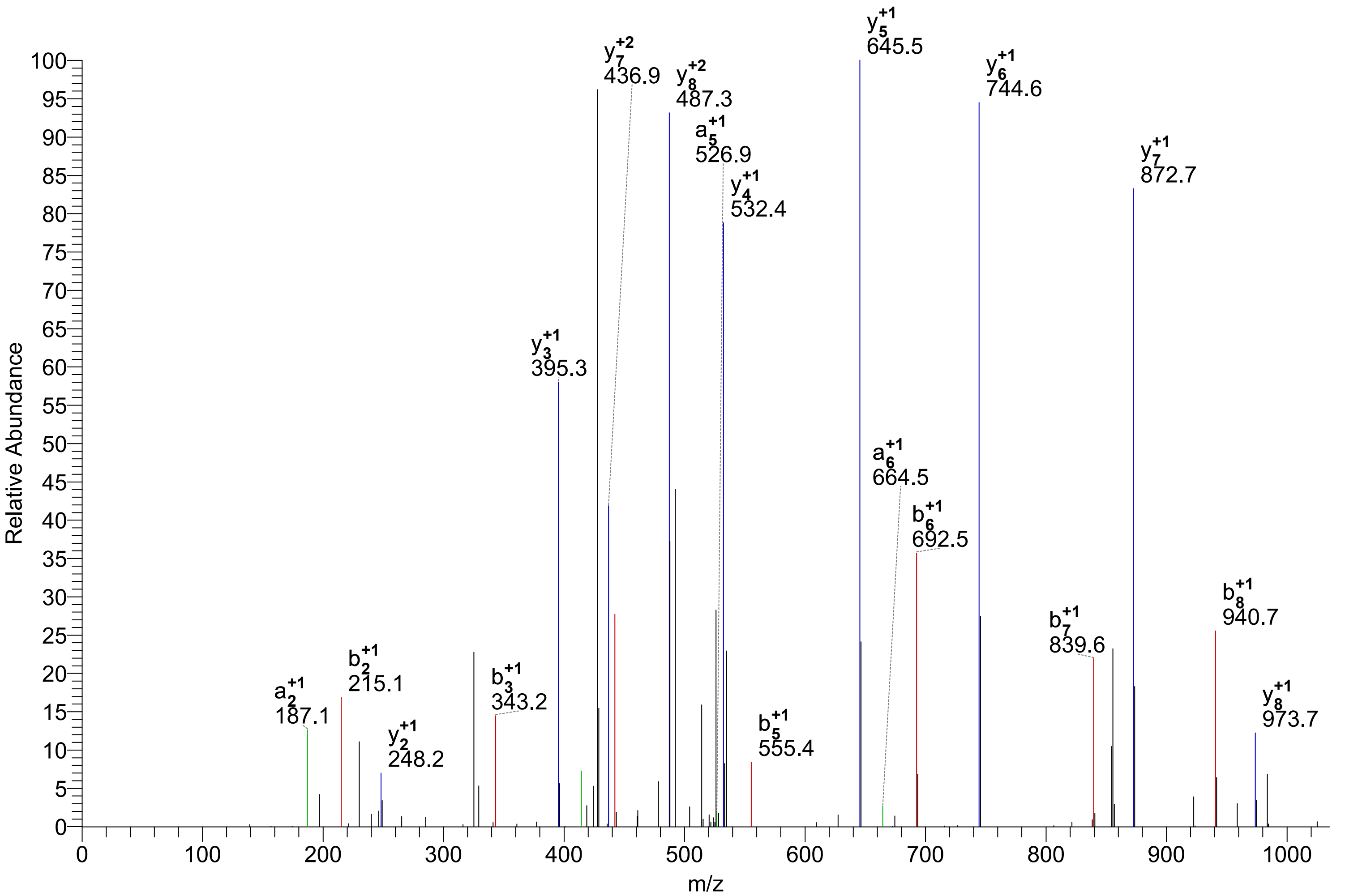
```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```



#2118291816-26226248 NL: 1.21E5



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z     P        XC  DeltaCn    Sp    RSp  Ions   Count

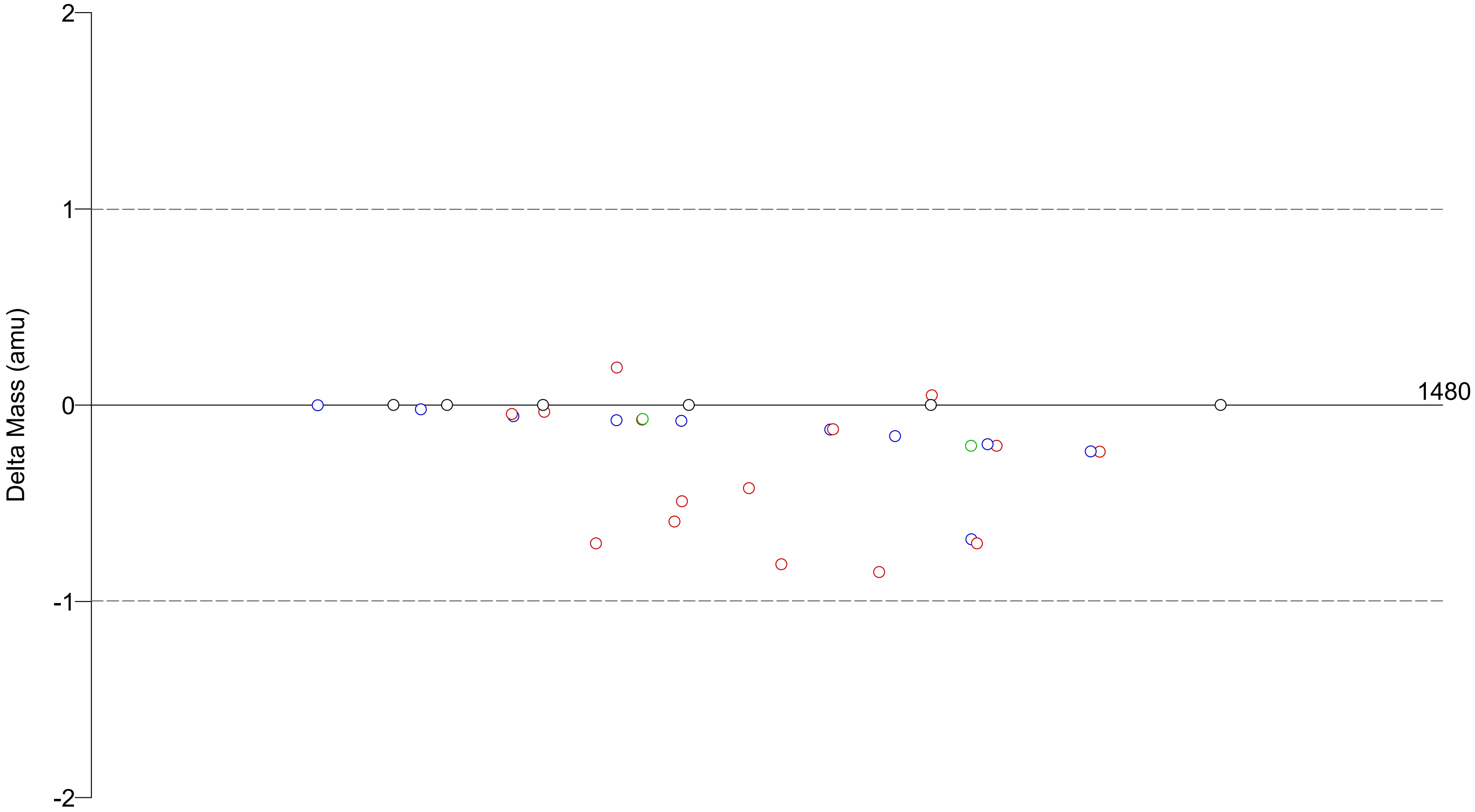
IPI:IPI00889723.1|TREMBL:B0QZR6;B4                                 2e-005  20.2     0.0       0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1    26/126  8
2118291816 -  K.ITQVLHFTK.D                           1086.63   2  0.0002  3.684  0.435   1215.2 1    18/24   10

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

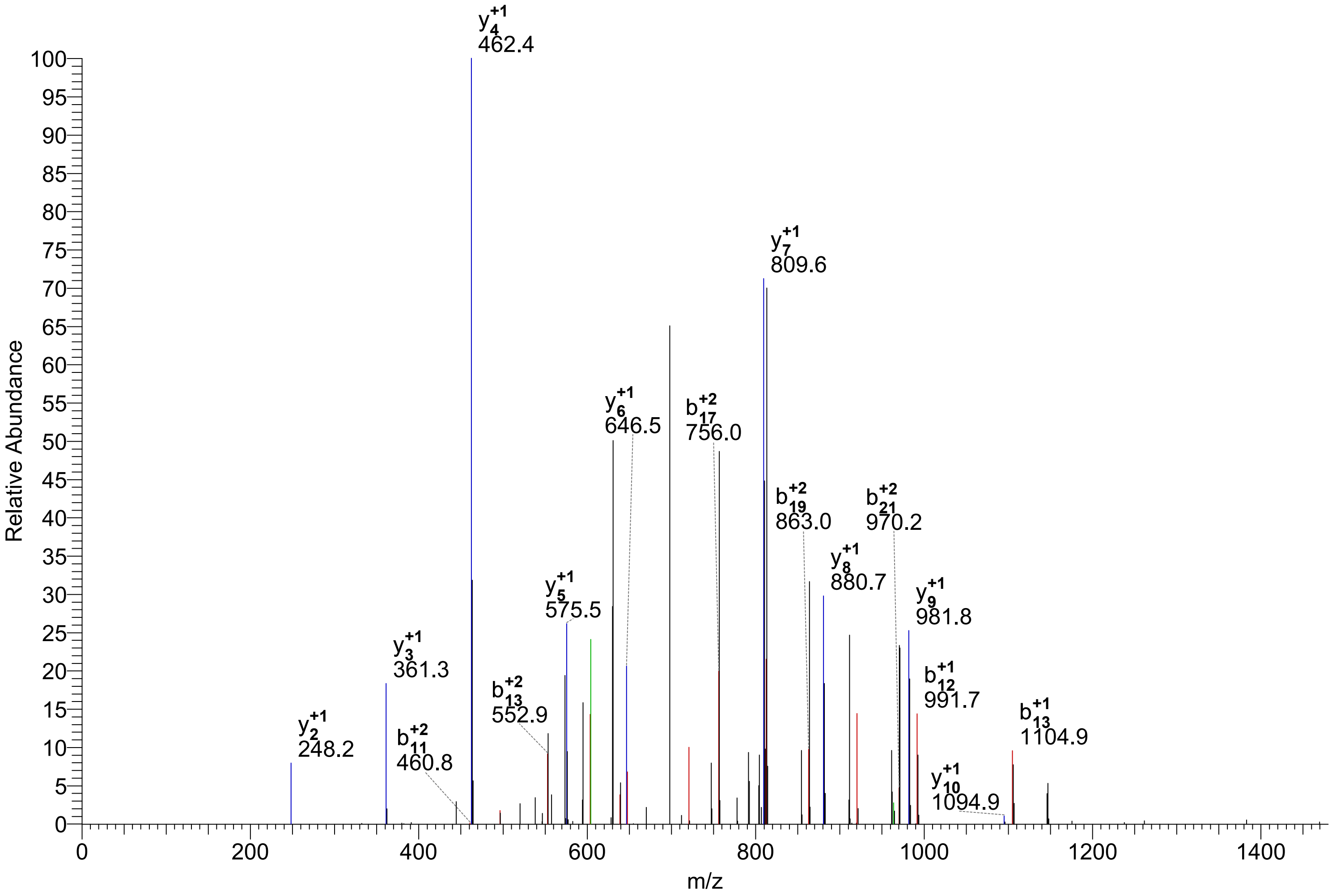
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



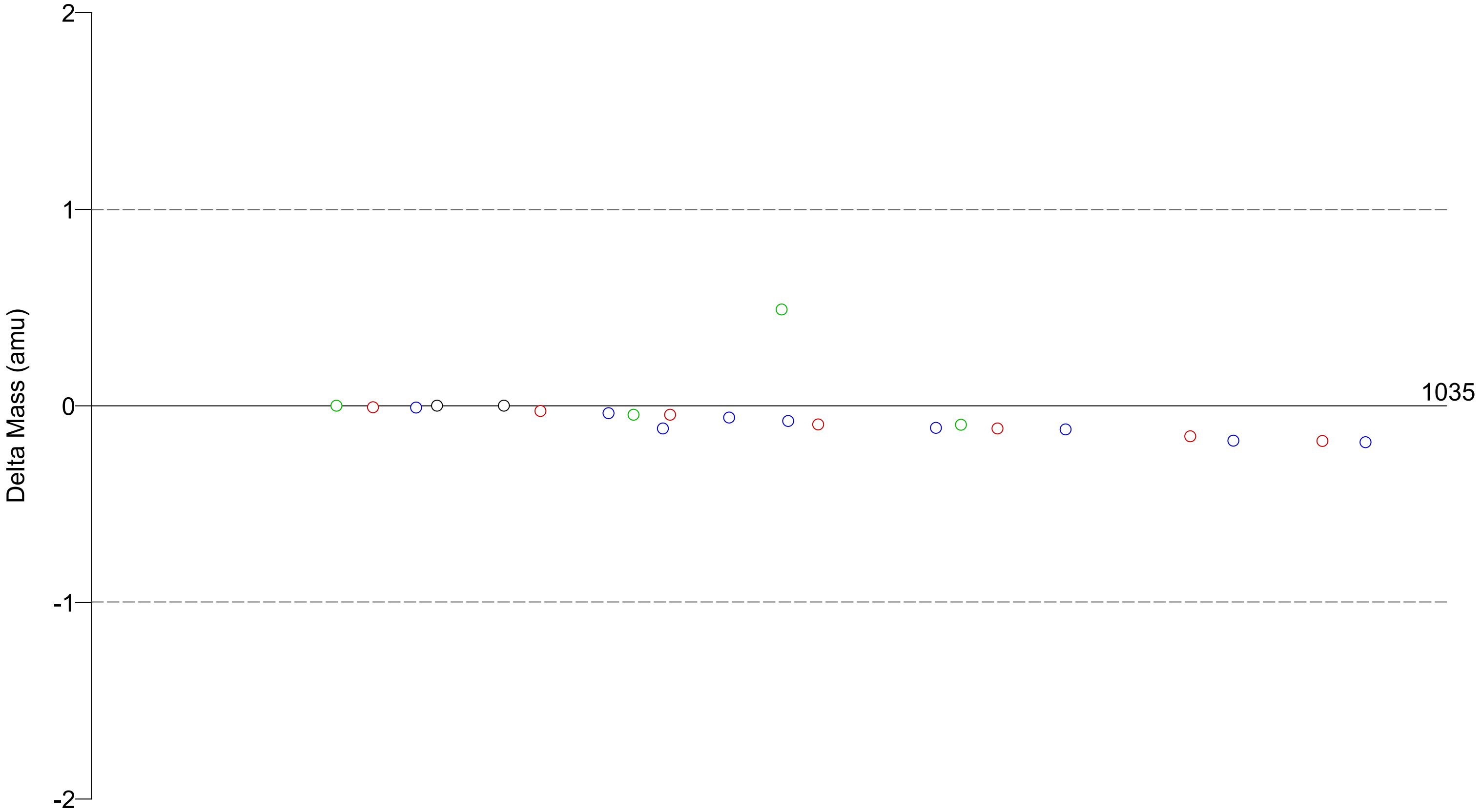
#19287468-1 NL: 5.80E4



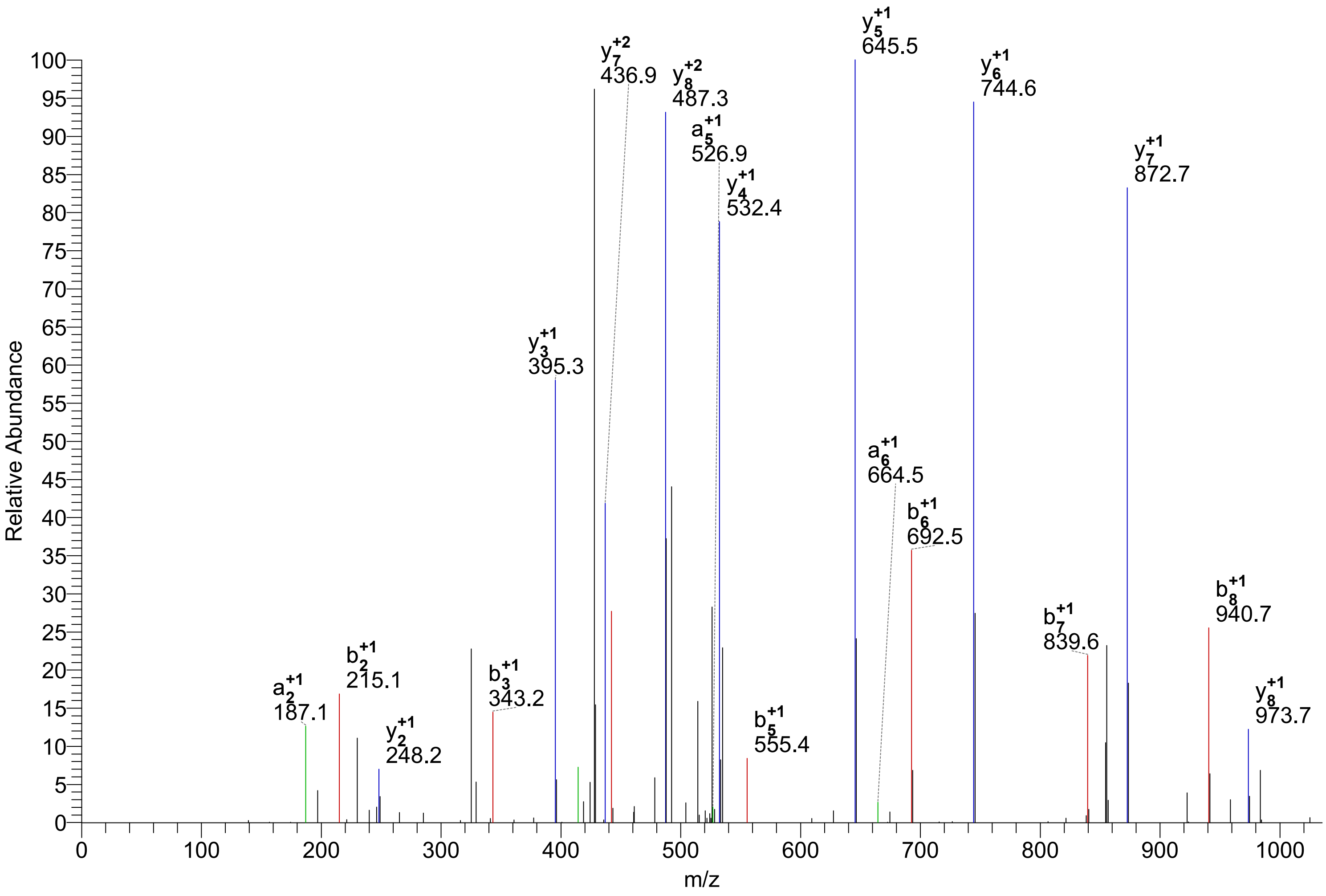
```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```



#2118291816-26226248 NL: 1.21E5



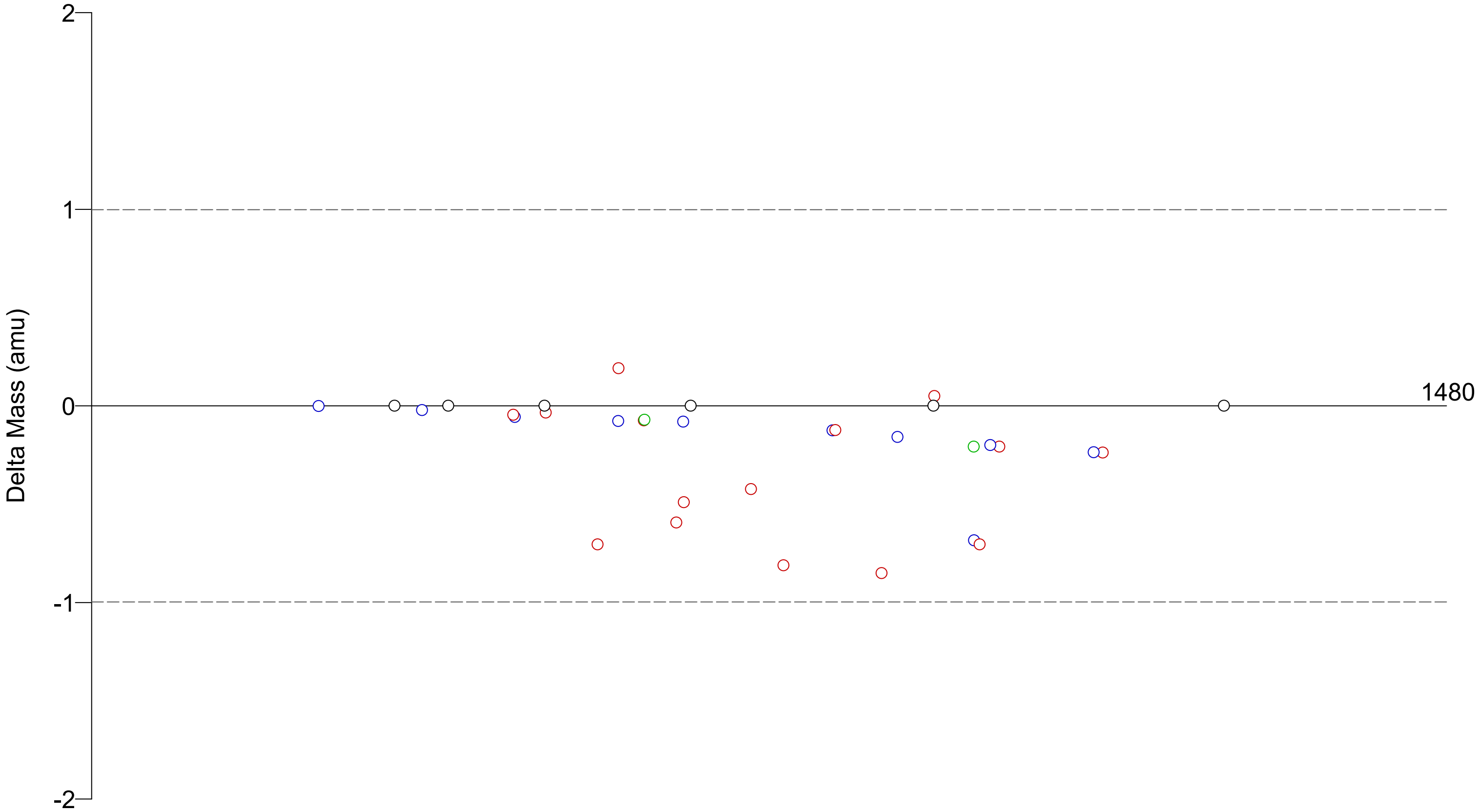
```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z     P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00892547.1|TREMBL:B0UZ83|RE                                  2e-005  20.2     0.0        0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A                  2085.17    3  2e-005  3.435  0.549   736.3  1   26/126  8
2118291816 -  K.ITQVLHFTK.D                               1086.63    2  0.0002  3.684  0.435   1215.2 1   18/24   10

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

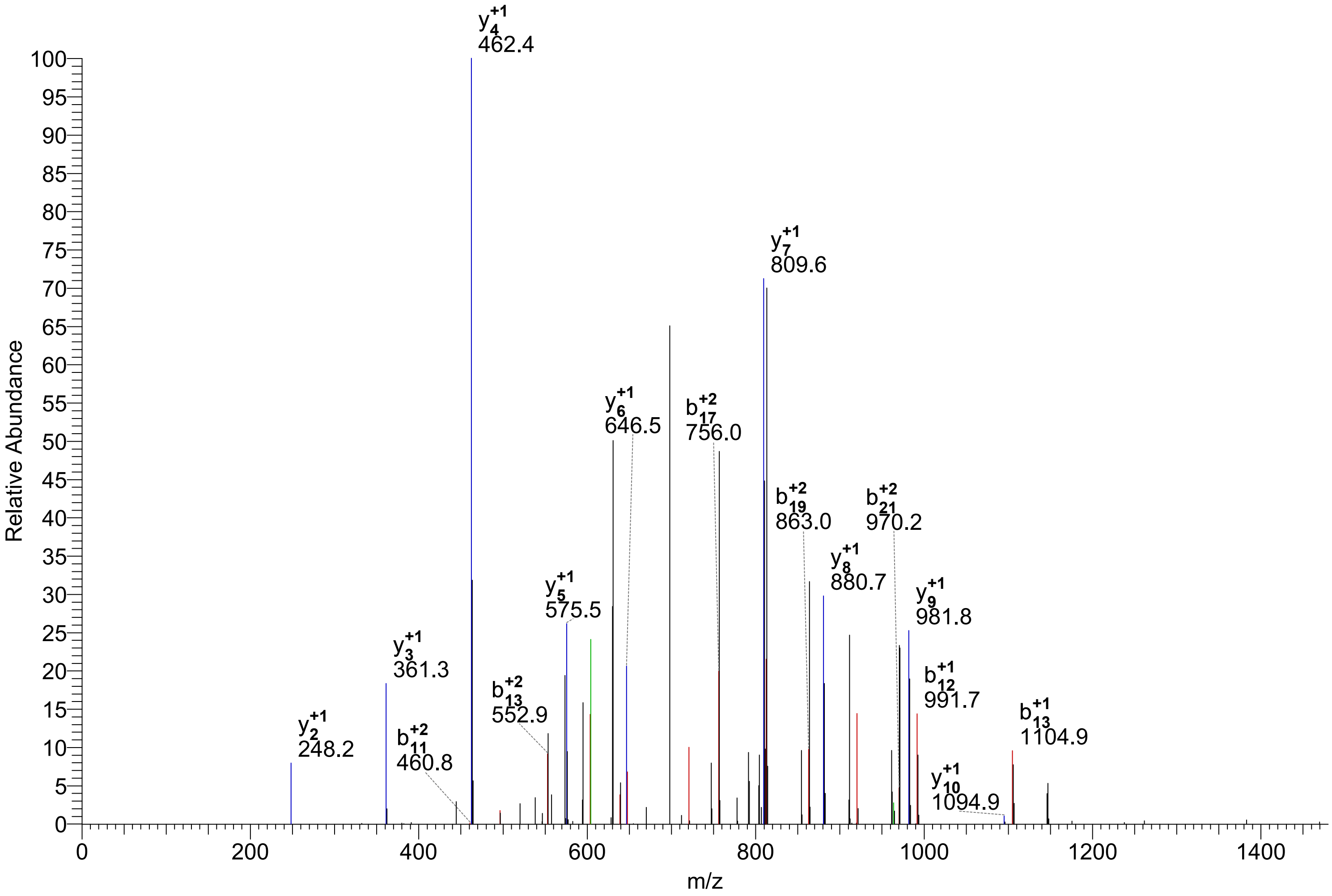
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



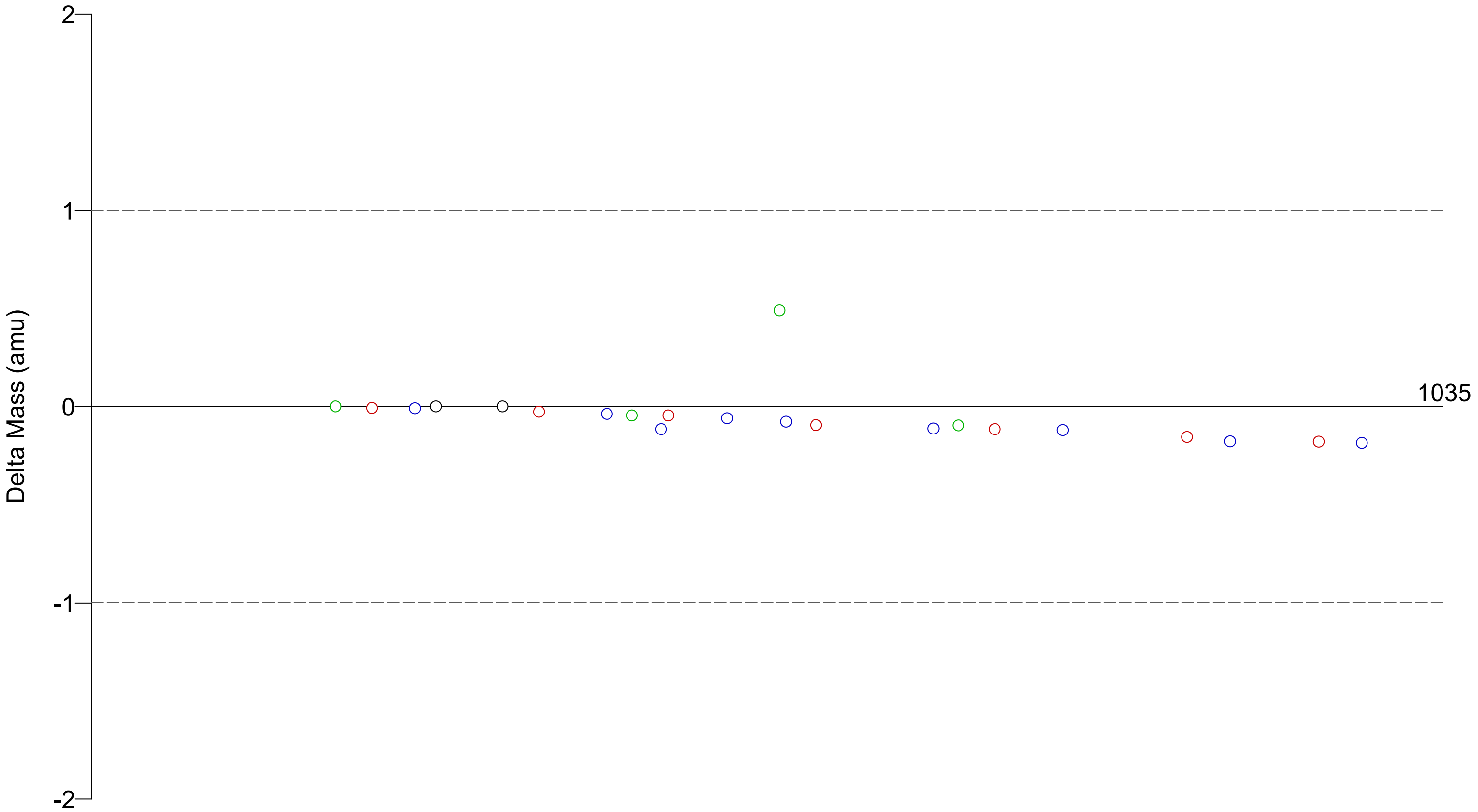
#19287468-1 NL: 5.80E4



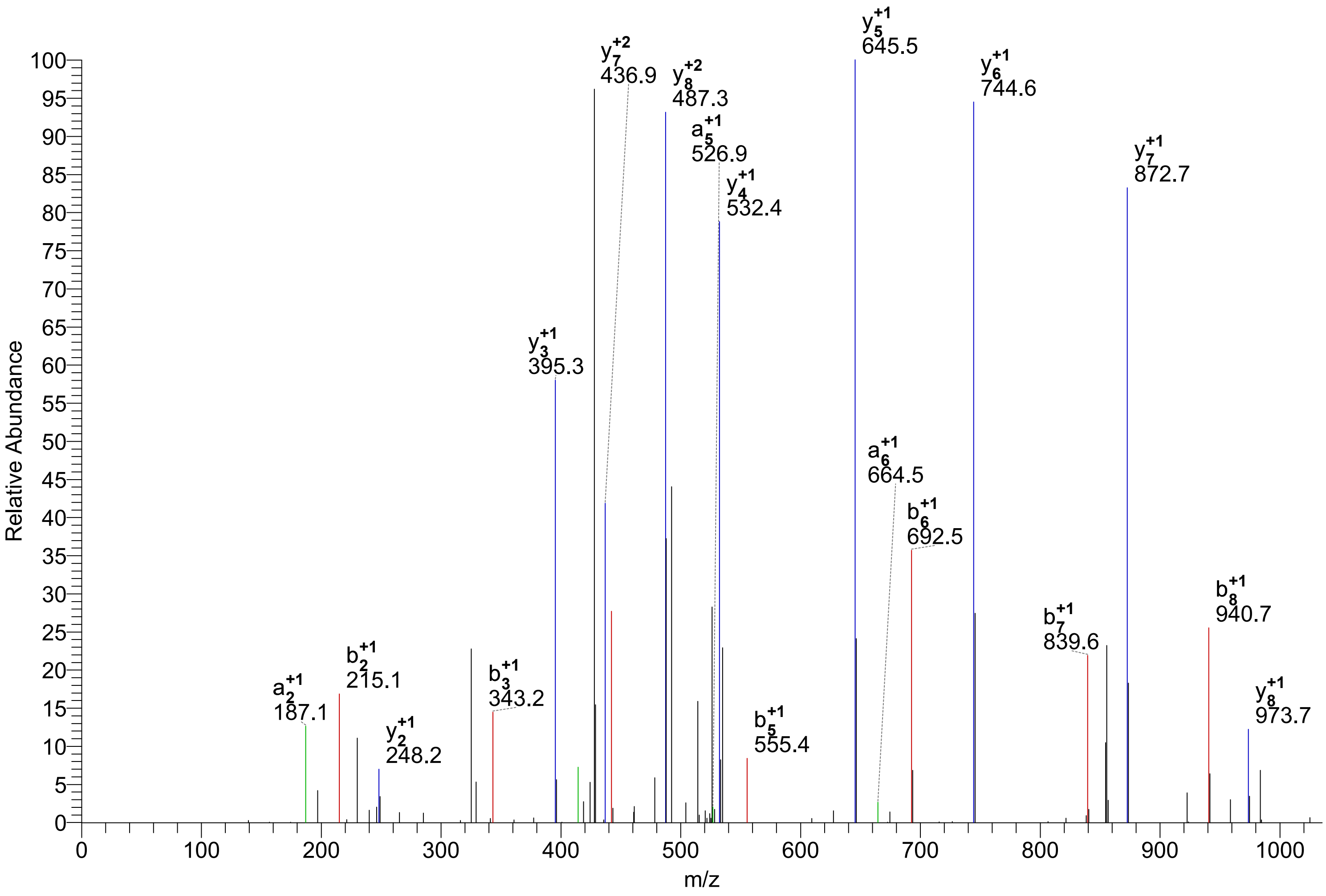
```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```



#2118291816-26226248 NL: 1.21E5



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Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00892604.1|TREMBL:A2BHY4;Q6                                2e-005  20.2     0.0       0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A             2085.17    3  2e-005  3.435  0.549   736.3  1   26/126  8
2118291816 -  K.ITQVLHFTK.D                          1086.63    2  0.0002  3.684  0.435   1215.2 1   18/24   10

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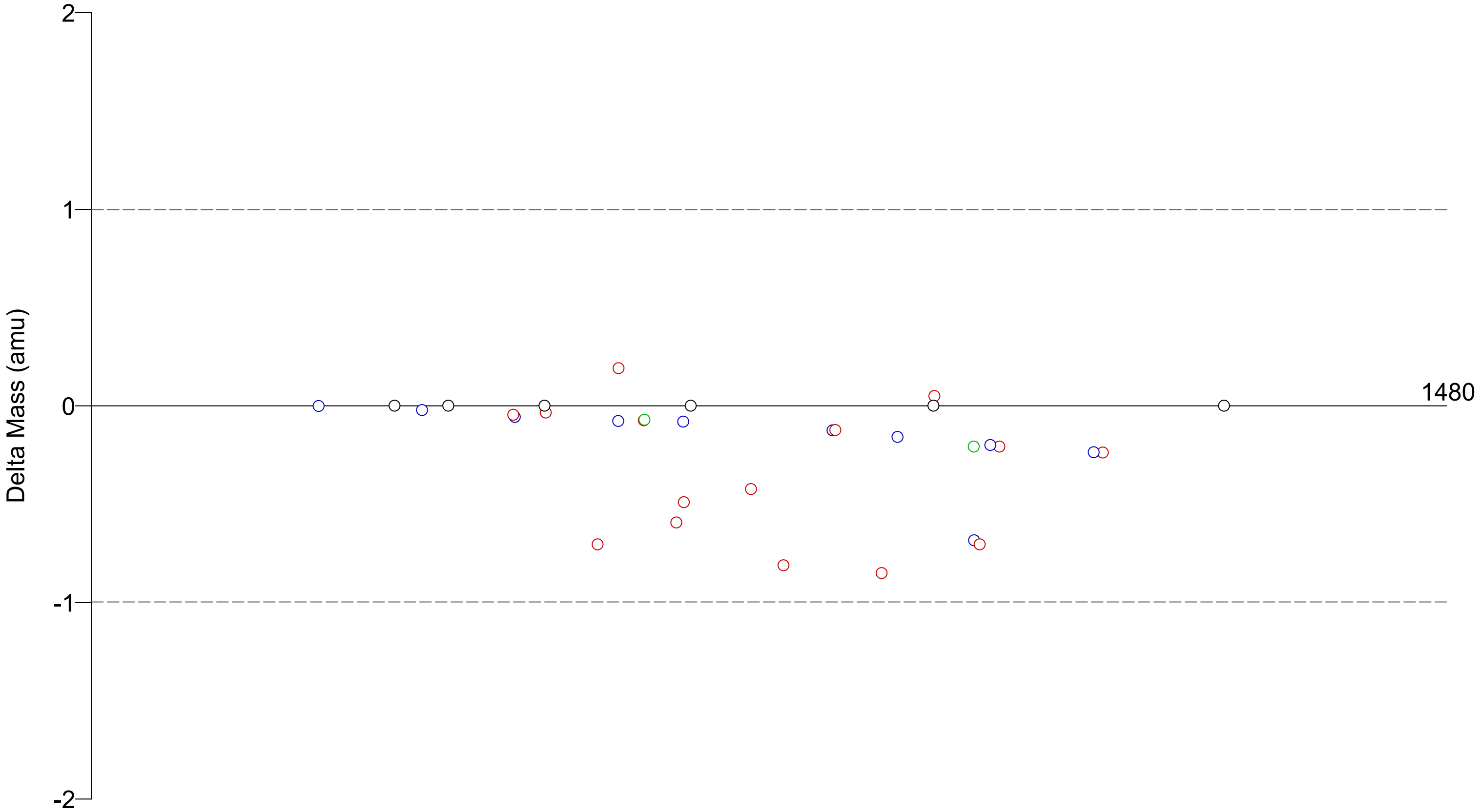
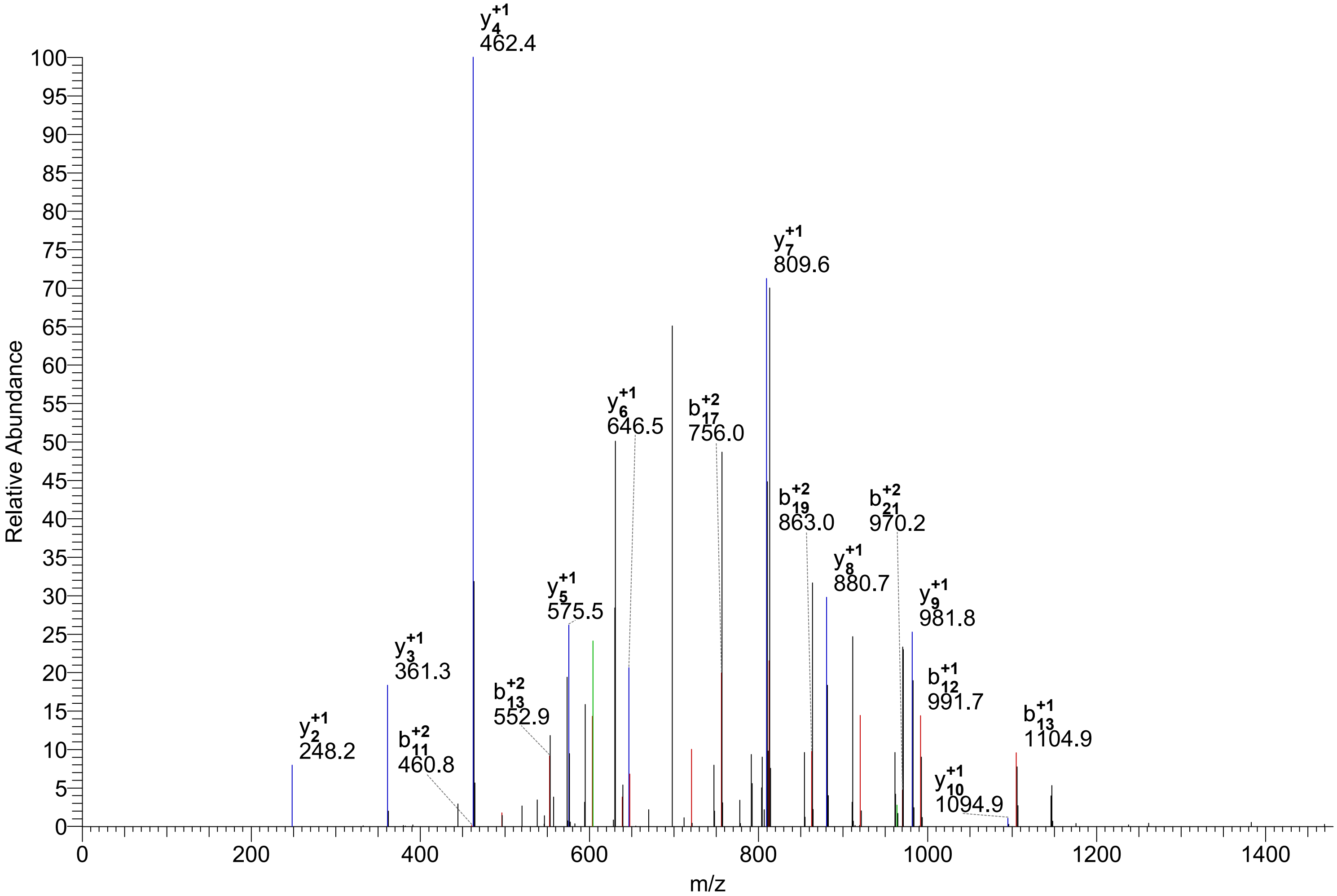
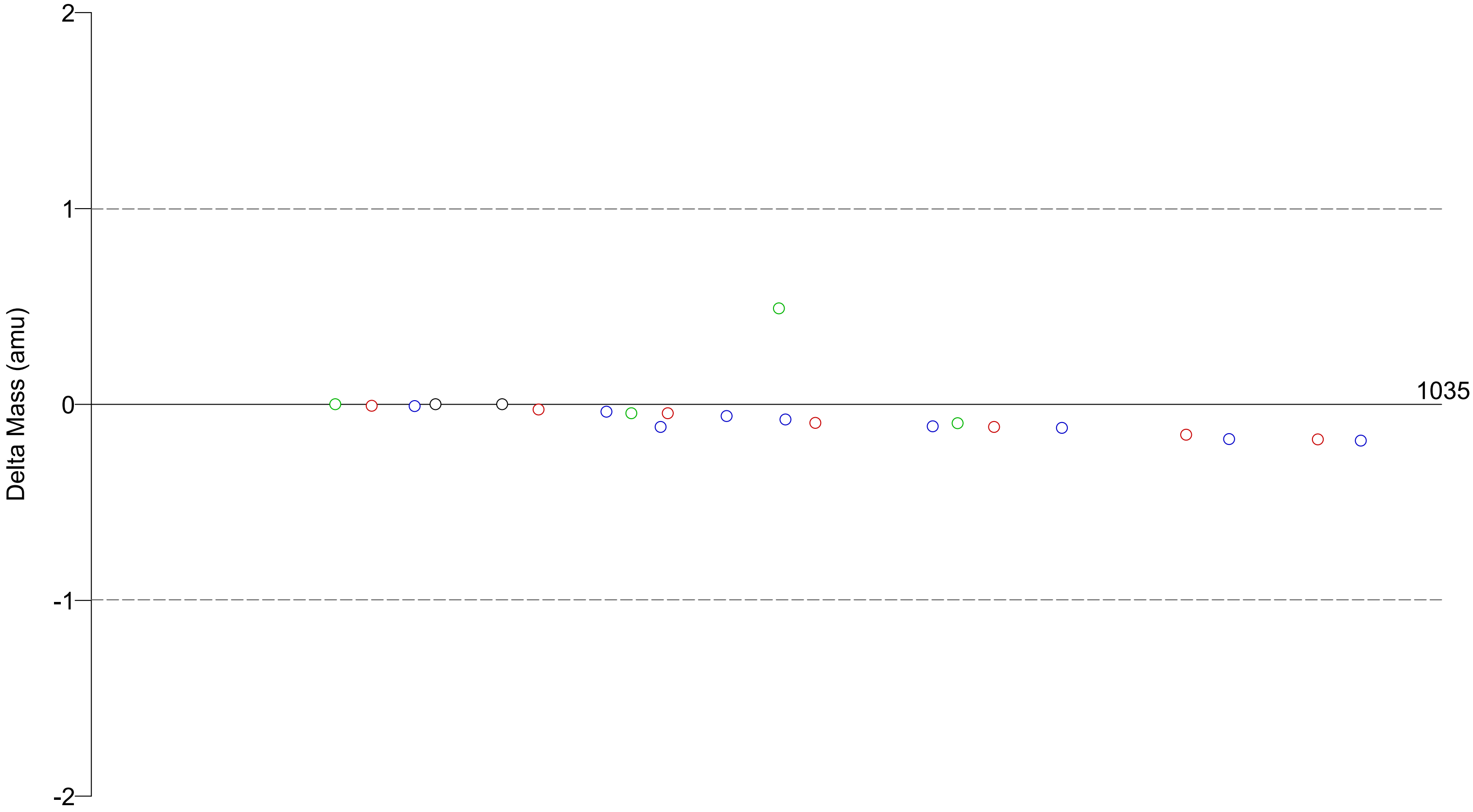

```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



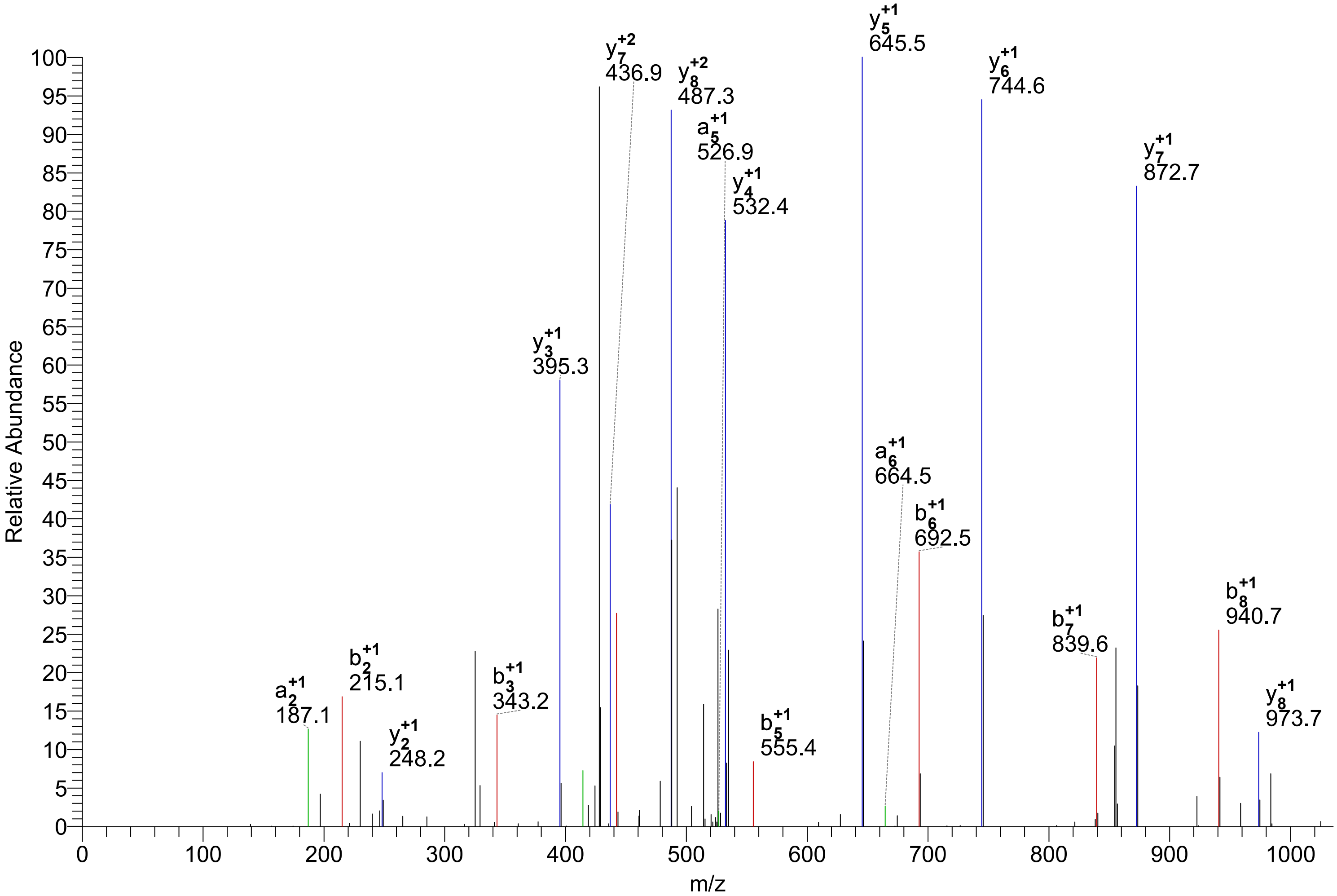
#19287468-1 NL: 5.80E4



```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
-----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```

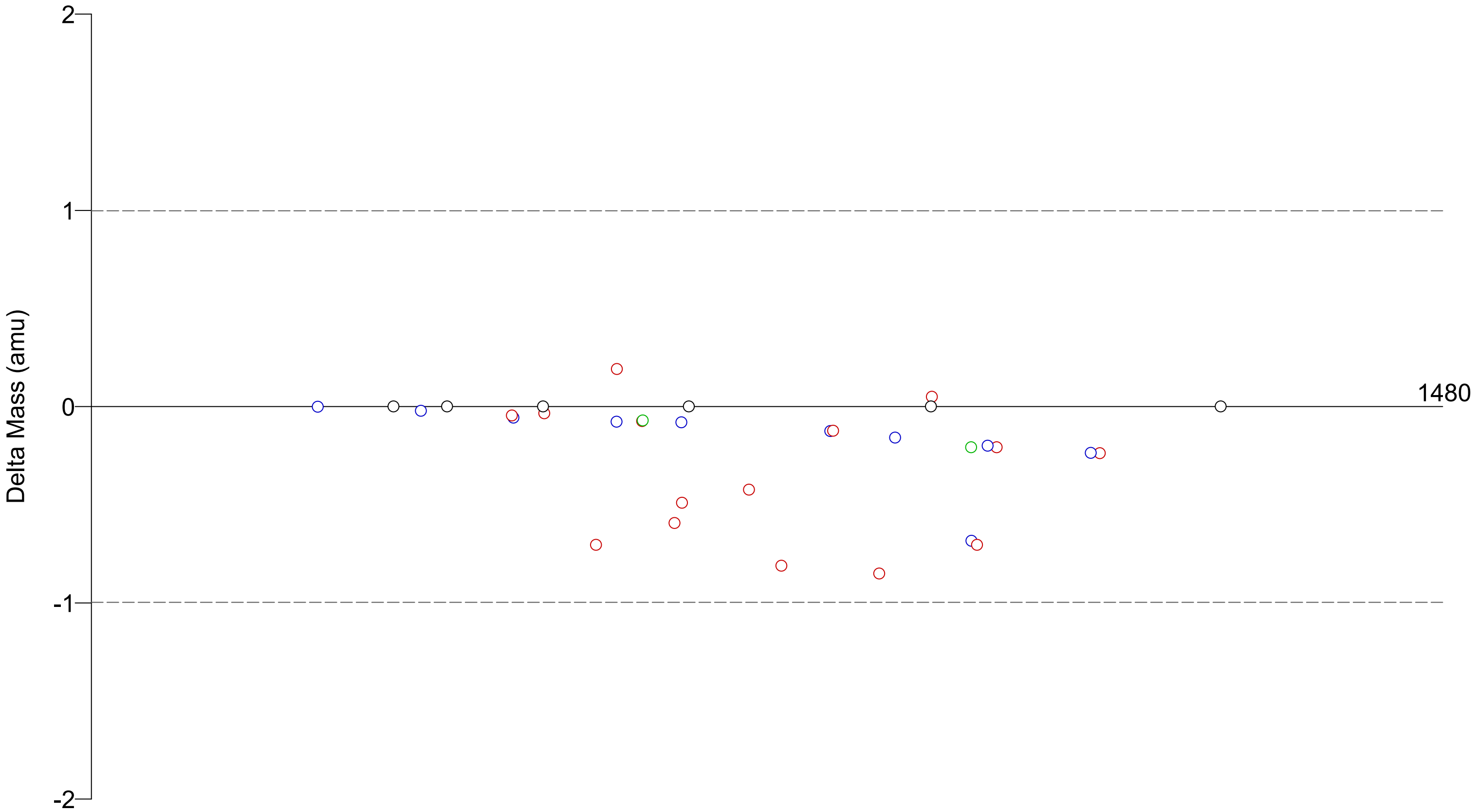


#2118291816-26226248 NL: 1.21E5

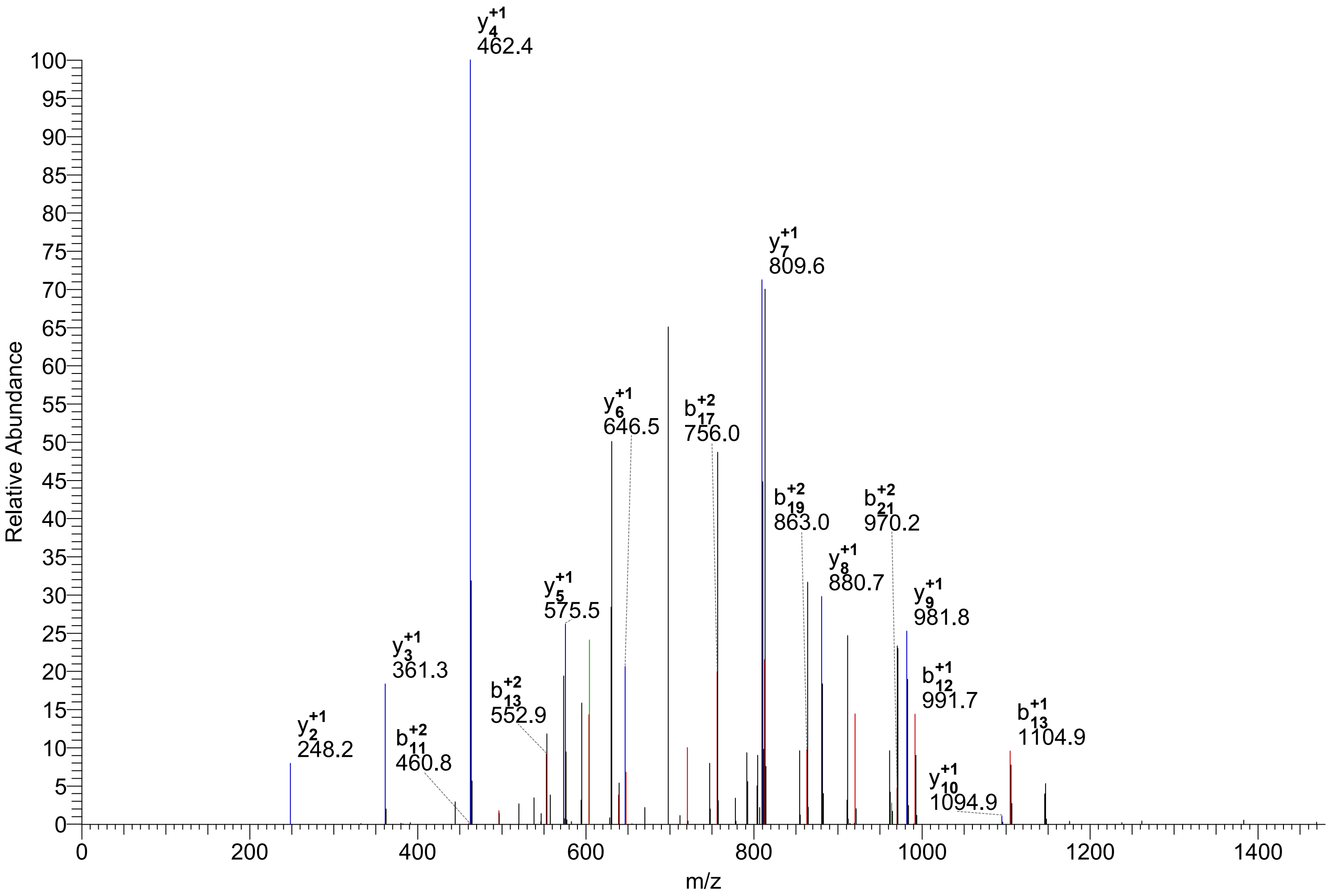


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00937598.1|TREMBL:A6H8M8|RE                                 2e-005  20.2     0.0        0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A             2085.17   3  2e-005  3.435  0.549   736.3  1   26/126  8
2118291816 -  K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24   10

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

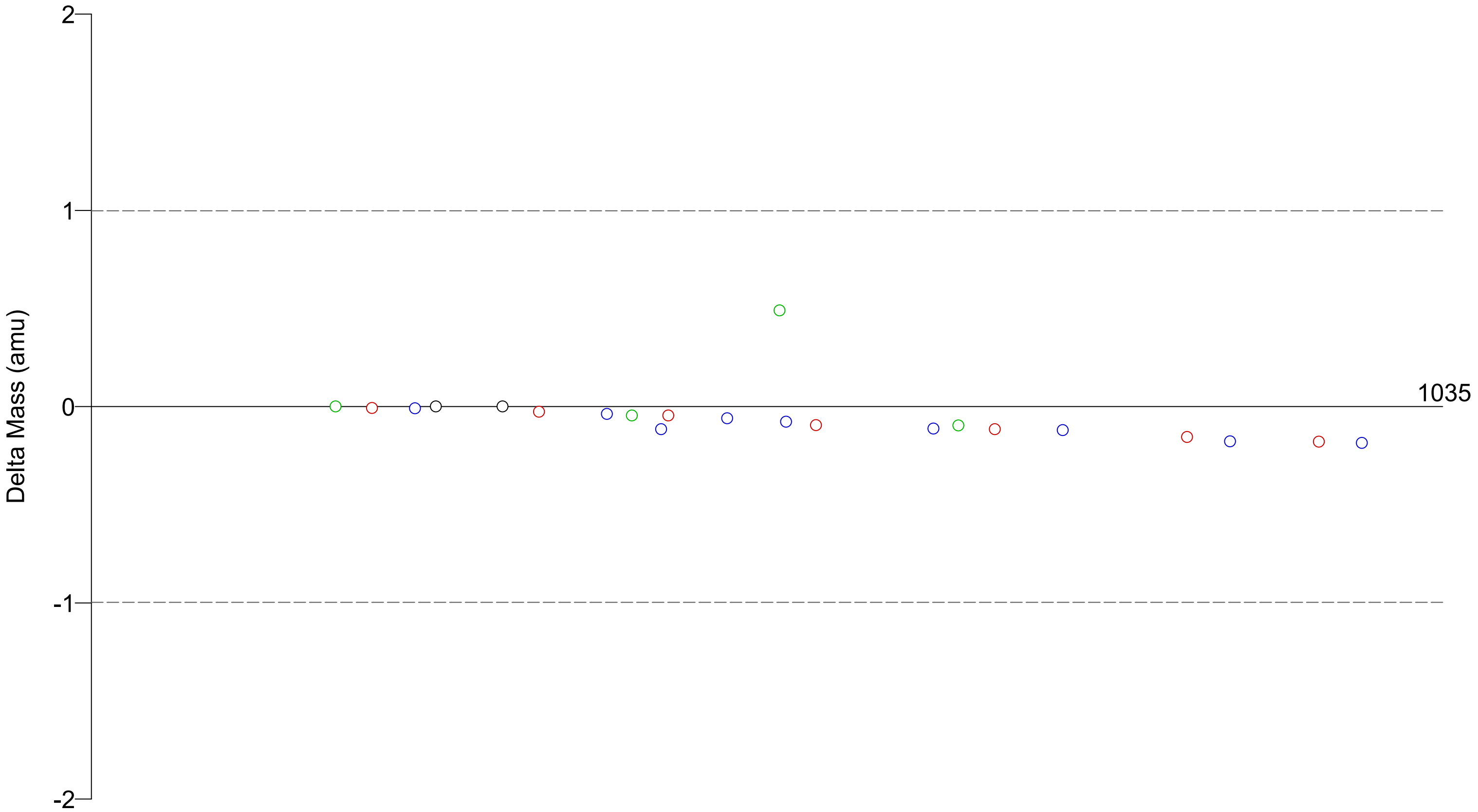
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```



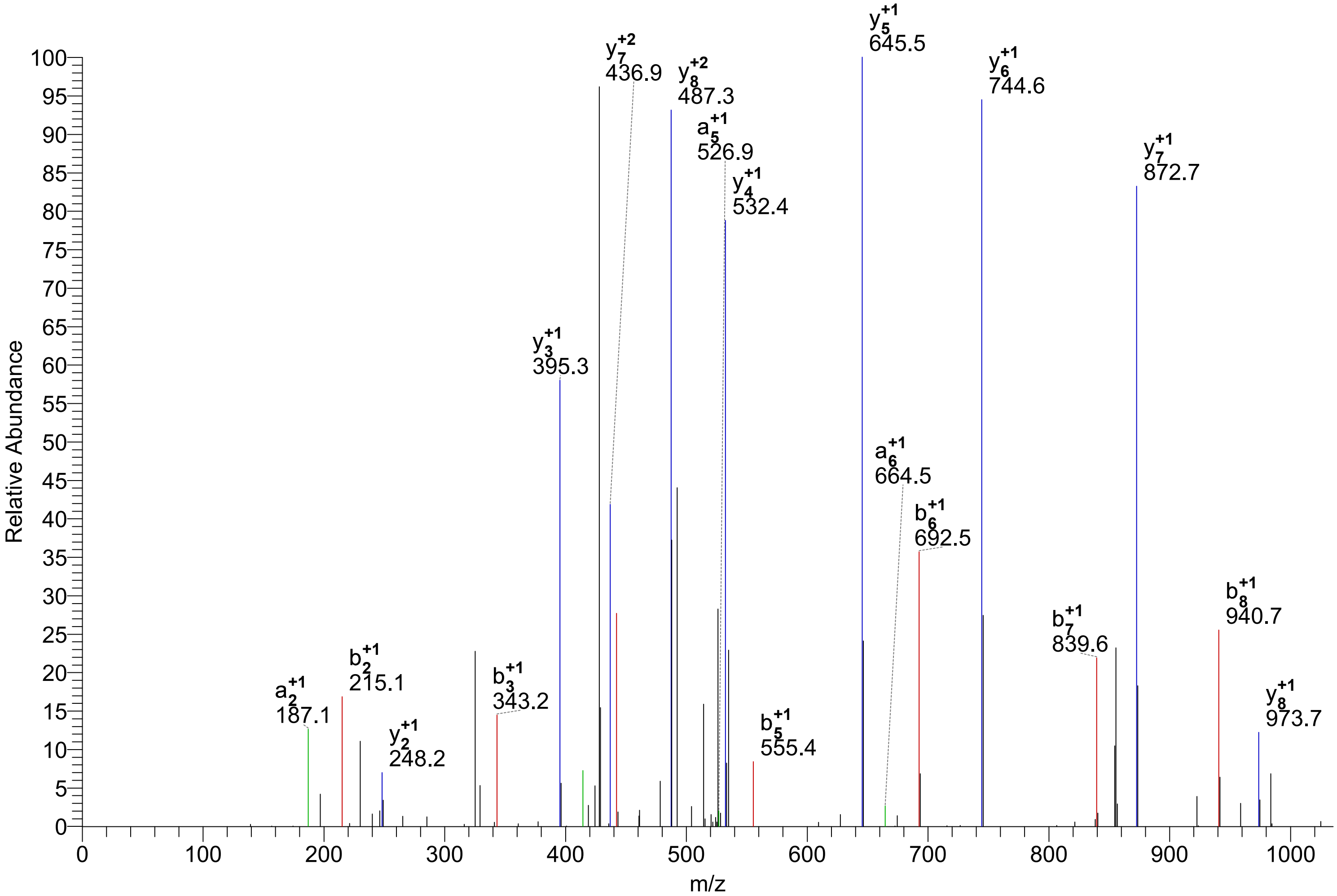
#19287468-1 NL: 5.80E4



```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```

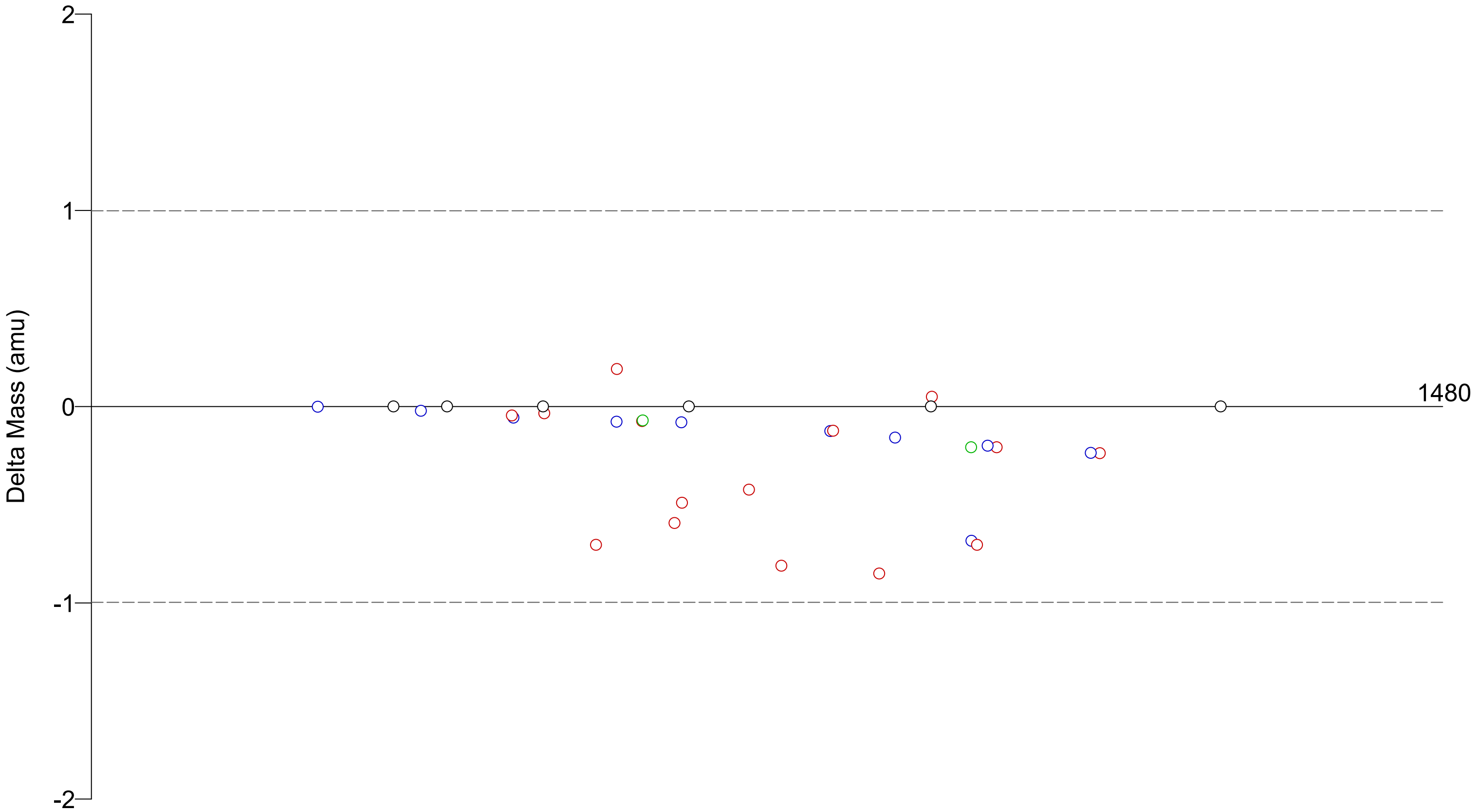


#2118291816-26226248 NL: 1.21E5

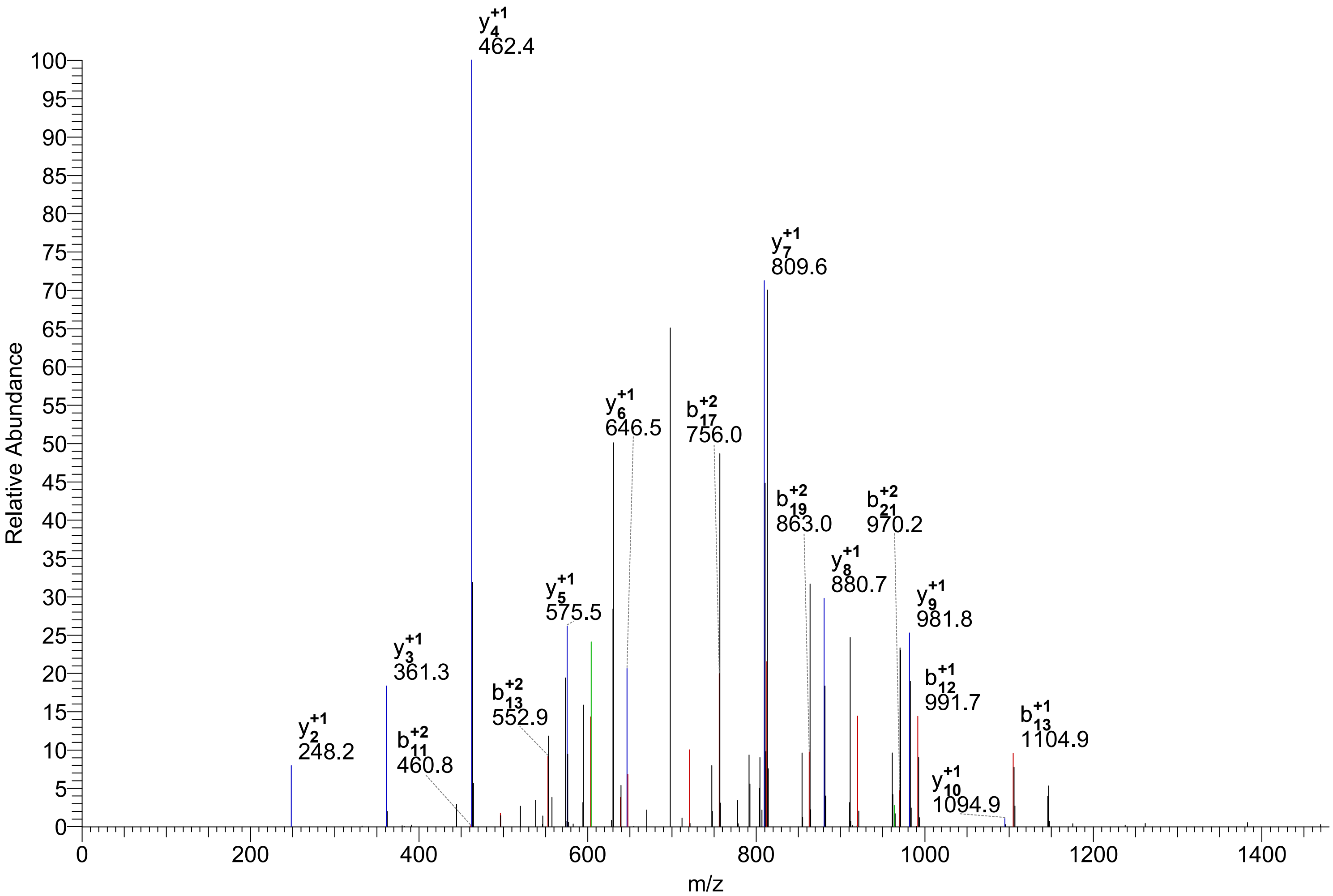


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)        Sequence                                    MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00922744.1|TREMBL:Q9UNU2 Ta                                    2e-005  10.2      0.0       0
19287468 - 1  K.ASAGLLGAHAAAITAYALTLTK.A               2085.17    3  2e-005  3.435  0.549   736.3  1   26/126  8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 S    131.08     159.08                                     2014.13
 A    202.12     230.11                                     1927.10
 G    259.14     287.13                                     1856.06
 L    372.22     400.22                                     1799.04
 L    485.31     513.30                                     1685.96
 G    542.33     570.32                                     1572.87
 A    613.37     641.36                                     1515.85
 H    750.43     778.42                                     1444.82
 A    821.46     849.46                                     1307.76
 A    892.50     920.49                                     1236.72
 A    963.54     991.53                                     1165.68
 I   1076.62    1104.62                                     1094.65
 T   1177.67    1205.66                                      981.56
 A   1248.71    1276.70                                      880.51
 Y   1411.77    1439.76                                      809.48
 A   1482.81    1510.80                                      646.41
 L   1595.89    1623.89                                      575.38
 T   1696.94    1724.93                                      462.29
 L   1810.02    1838.02                                      361.24
 T   1911.07    1939.06                                      248.16
 K                                                           147.11
```

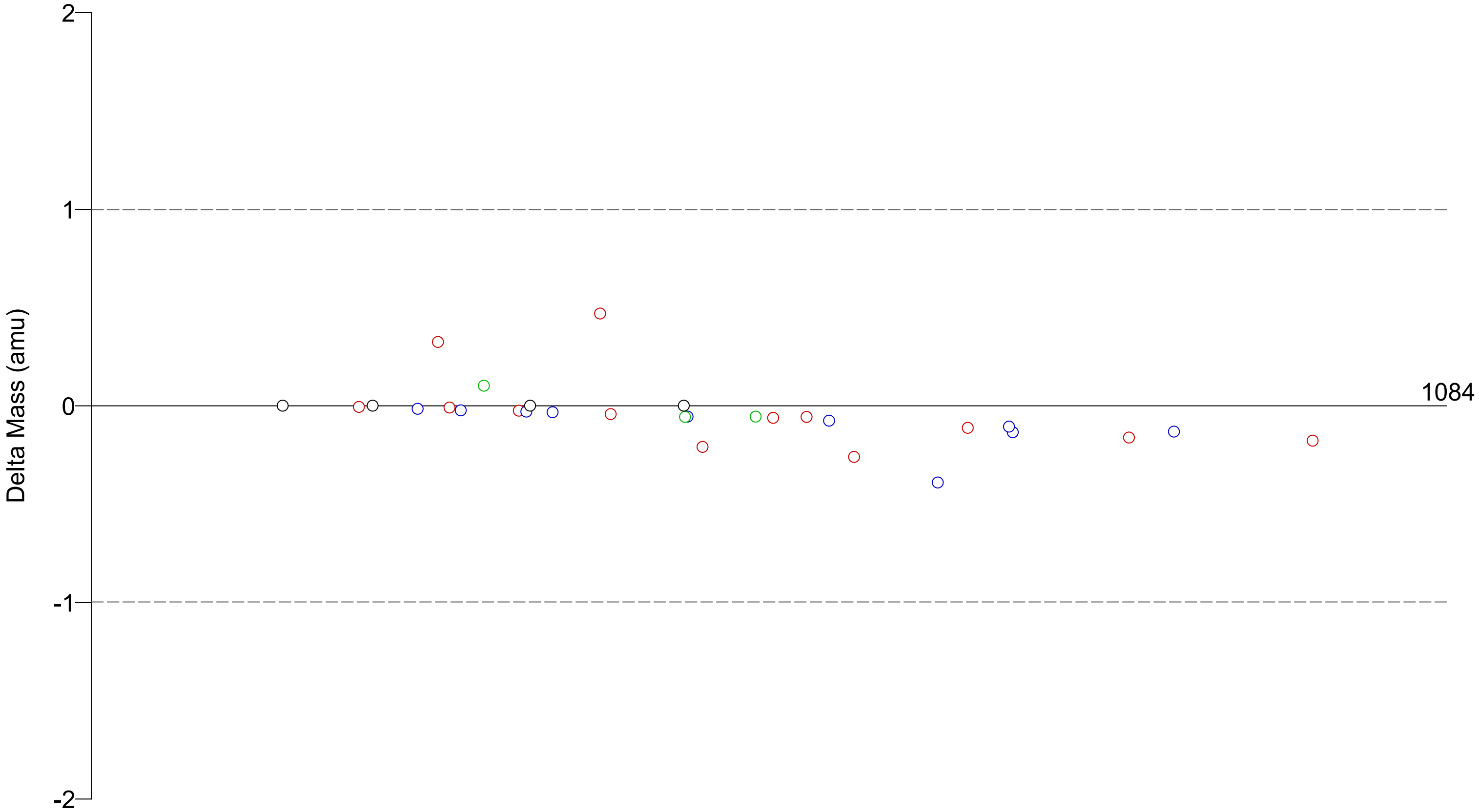


#19287468-1 NL: 5.80E4

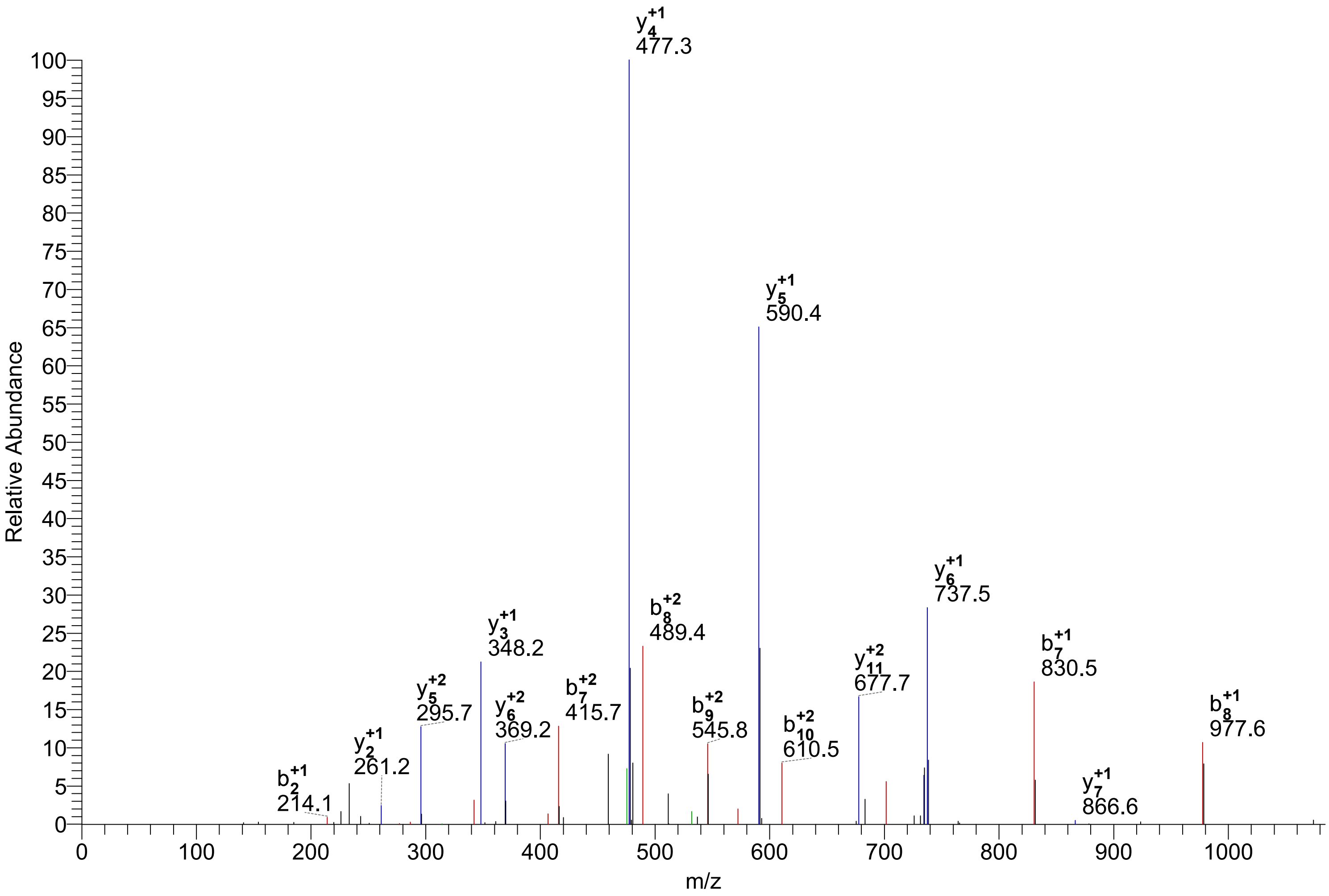


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00793108.1|VEGA:OTTHUMP0000                                 3e-005  10.2      0.0        0
2118291816 -  K.VNKDDEEFIESNK.M                        1566.73    3  3e-005  3.718  0.554    800.2  1    25/72   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 522.91
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 N    186.12     214.12                                    1467.66
 K    314.22     342.21                                    1353.62
 D    429.25     457.24                                    1225.52
 D    544.27     572.27                                    1110.49
 E    673.32     701.31                                     995.47
 E    802.36     830.35                                     866.43
 F    949.43     977.42                                     737.38
 I   1062.51    1090.51                                     590.31
 E   1191.55    1219.55                                     477.23
 S   1278.58    1306.58                                     348.19
 N   1392.63    1420.62                                     261.16
 K                                                          147.11
```

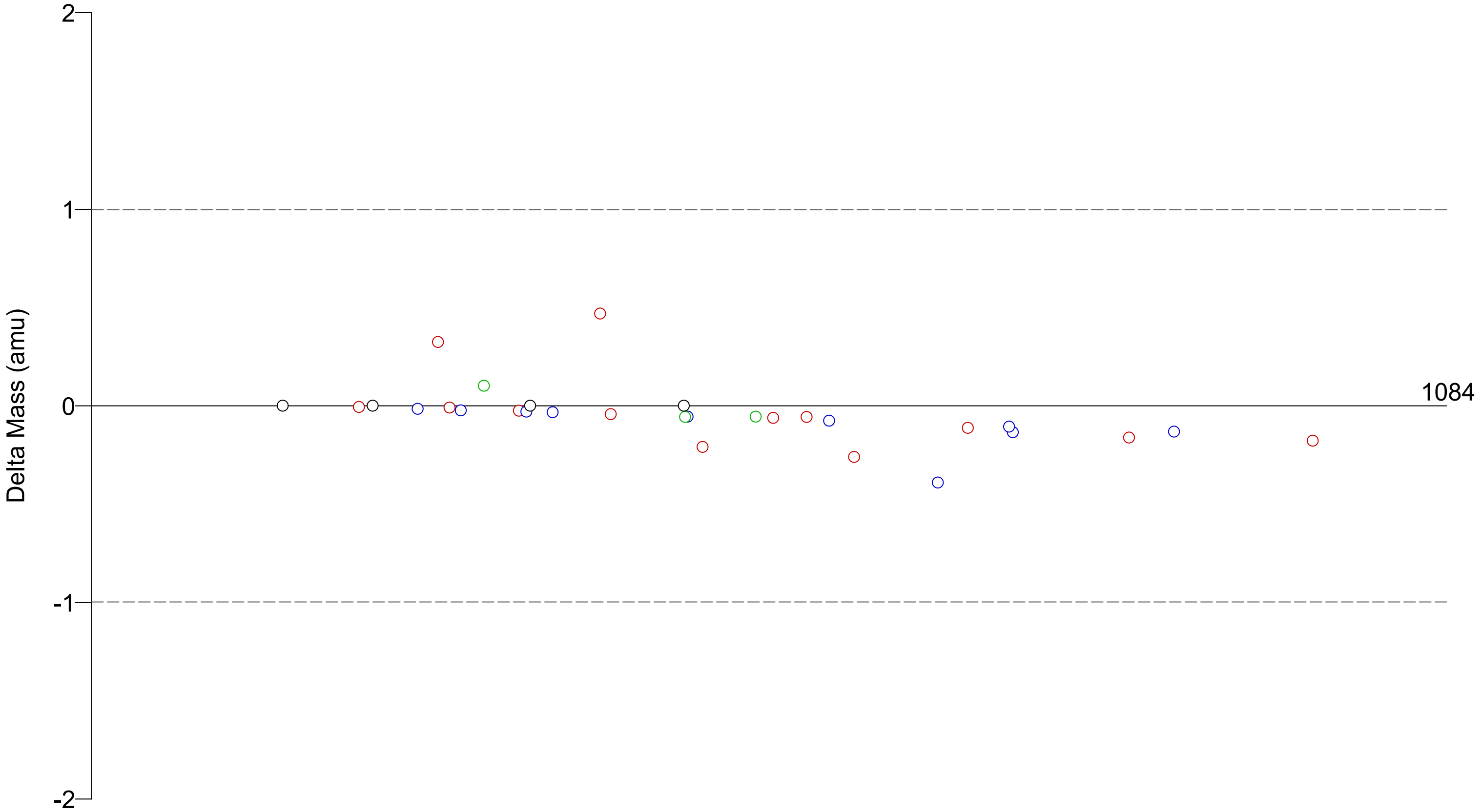


#2118291816-26226248 NL: 8.32E4

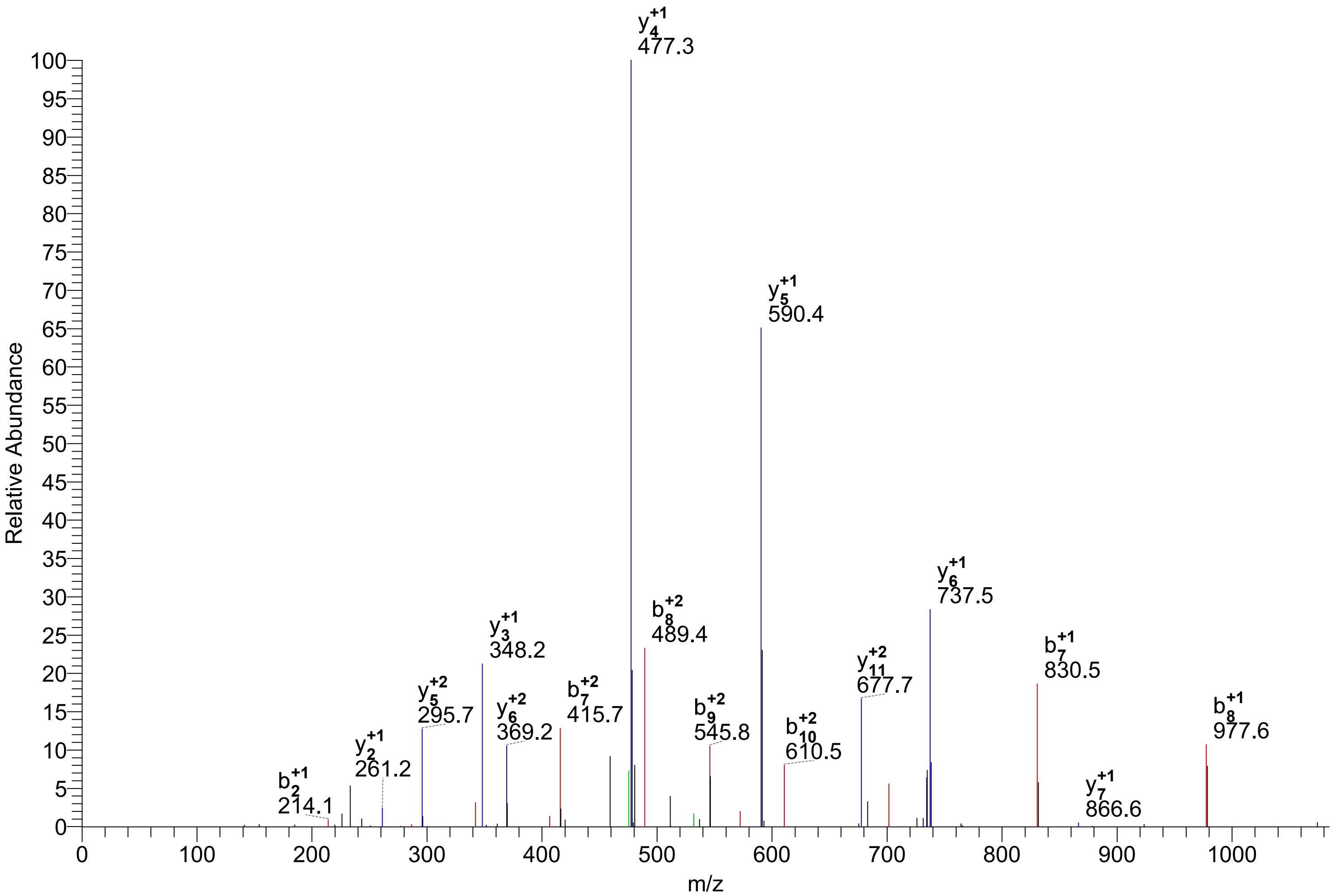


```
Reference                                                            P    Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z     P       XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00794184.1|TREMBL:B3KTA8|VE                                3e-005  10.2     0.0       0
2118291816 -  K.VNKDDEEFIESNK.M                      1566.73   3  3e-005  3.718  0.554   800.2  1   25/72   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 522.91
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 V     72.08     100.08
 N    186.12     214.12                                     1467.66
 K    314.22     342.21                                     1353.62
 D    429.25     457.24                                     1225.52
 D    544.27     572.27                                     1110.49
 E    673.32     701.31                                      995.47
 E    802.36     830.35                                      866.43
 F    949.43     977.42                                      737.38
 I   1062.51    1090.51                                      590.31
 E   1191.55    1219.55                                      477.23
 S   1278.58    1306.58                                      348.19
 N   1392.63    1420.62                                      261.16
 K                                                           147.11
```

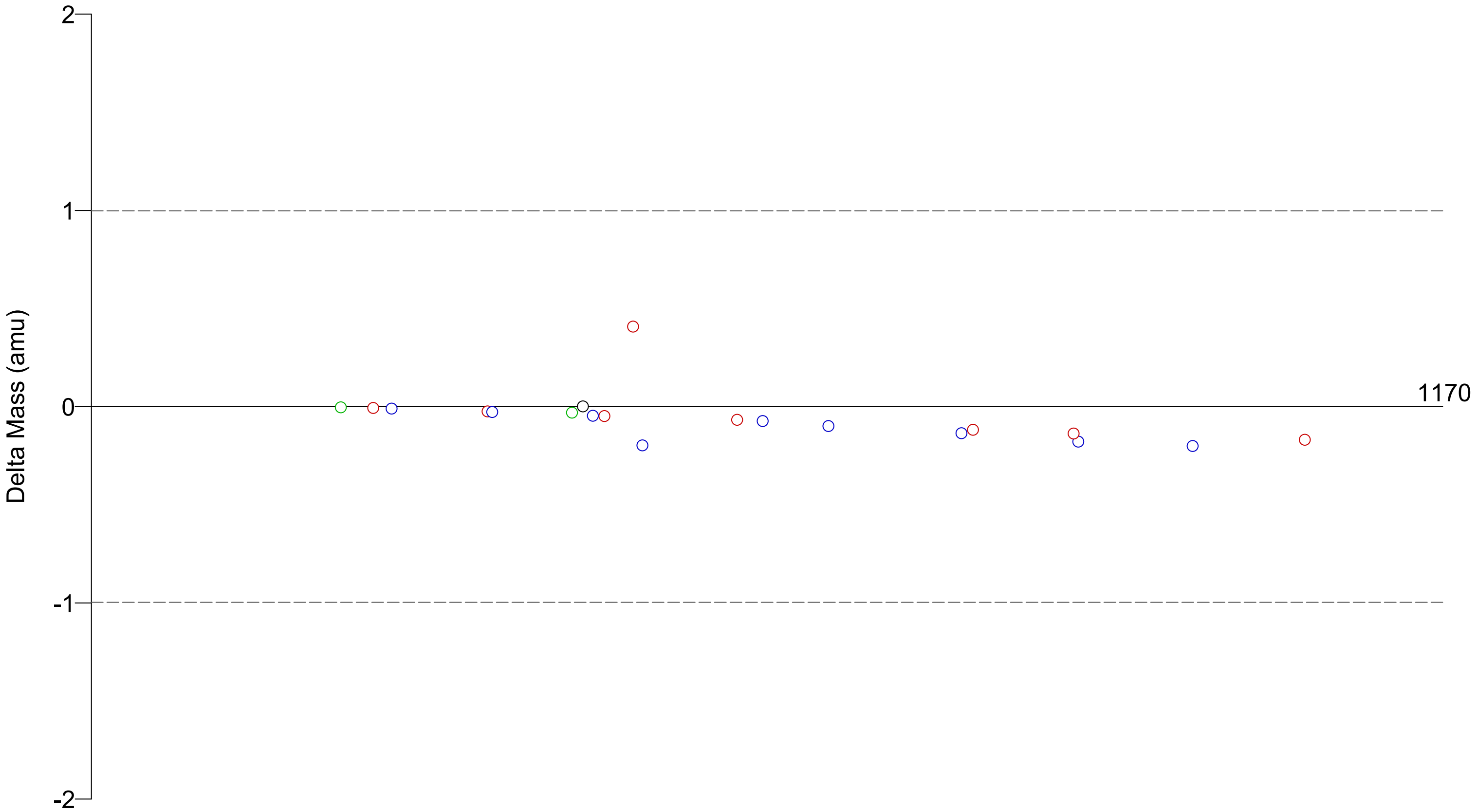


#2118291816-26226248 NL: 8.32E4

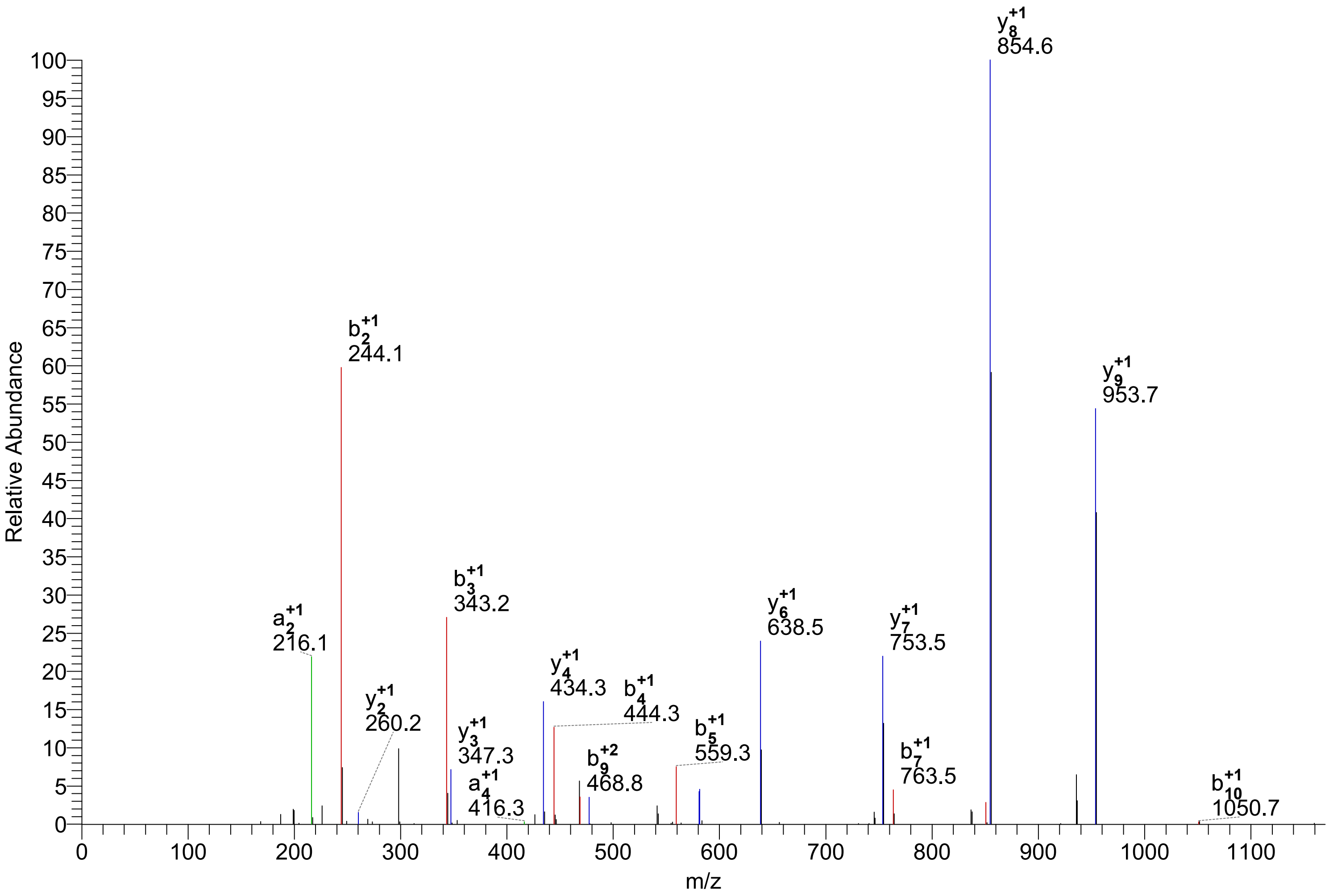


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00021857.1|SWISS-PROT:P02656|TREMBL:A3KPE2|ENSEMBL:ENSP     4e-005  10.2     0.0        0
19287468 - 1  R.GWVTDGFSSLK.D                        1196.59   2  4e-005  3.932  0.552   725.3  1   17/30   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 598.80
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 W    216.11     244.11                                     1139.57
 V    315.18     343.18                                      953.49
 T    416.23     444.22                                      854.43
 D    531.26     559.25                                      753.38
 G    588.28     616.27                                      638.35
 F    735.35     763.34                                      581.33
 S    822.38     850.37                                      434.26
 S    909.41     937.41                                      347.23
 L   1022.49    1050.49                                      260.20
 K                                                           147.11
```

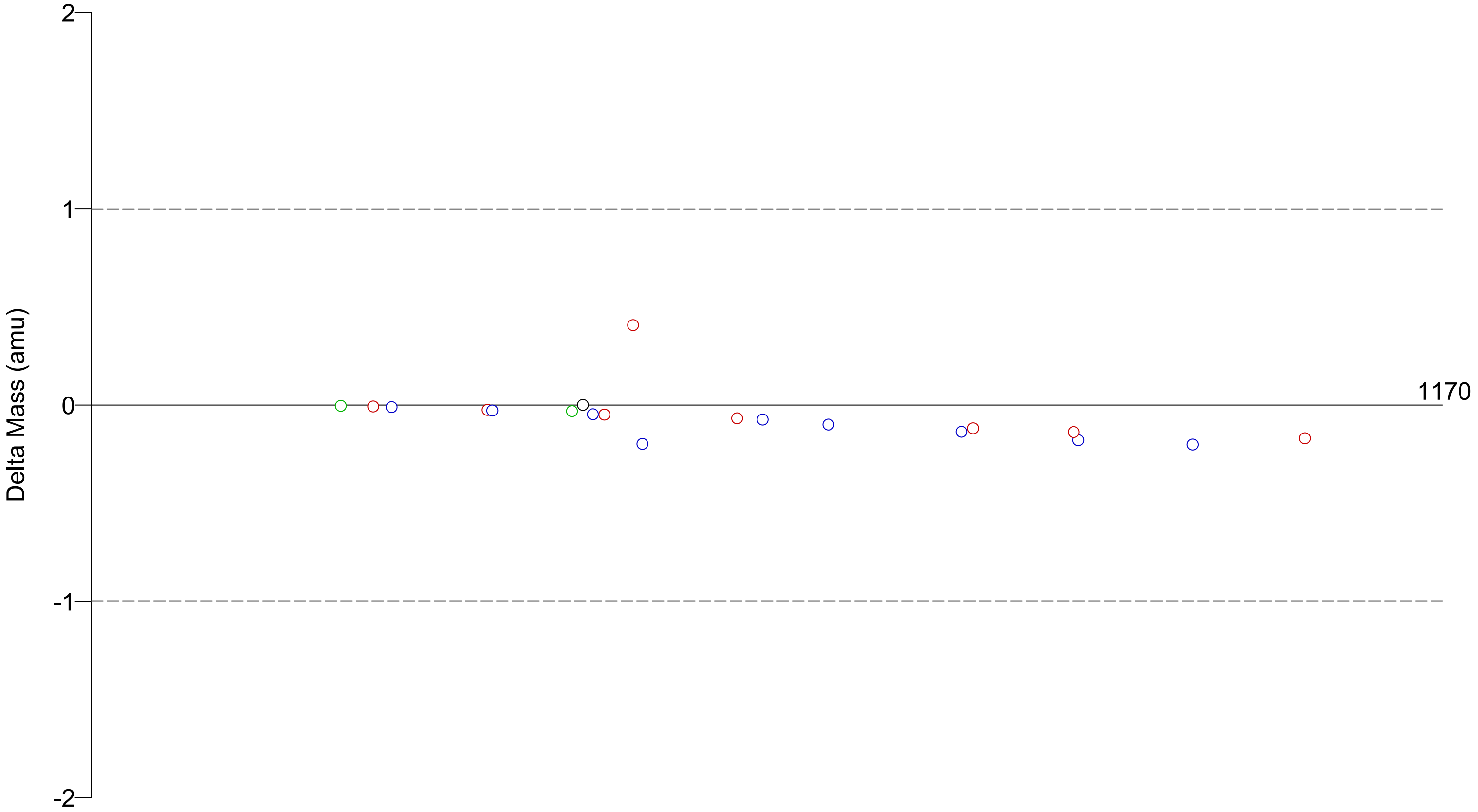


#19287468-1 NL: 9.45E4

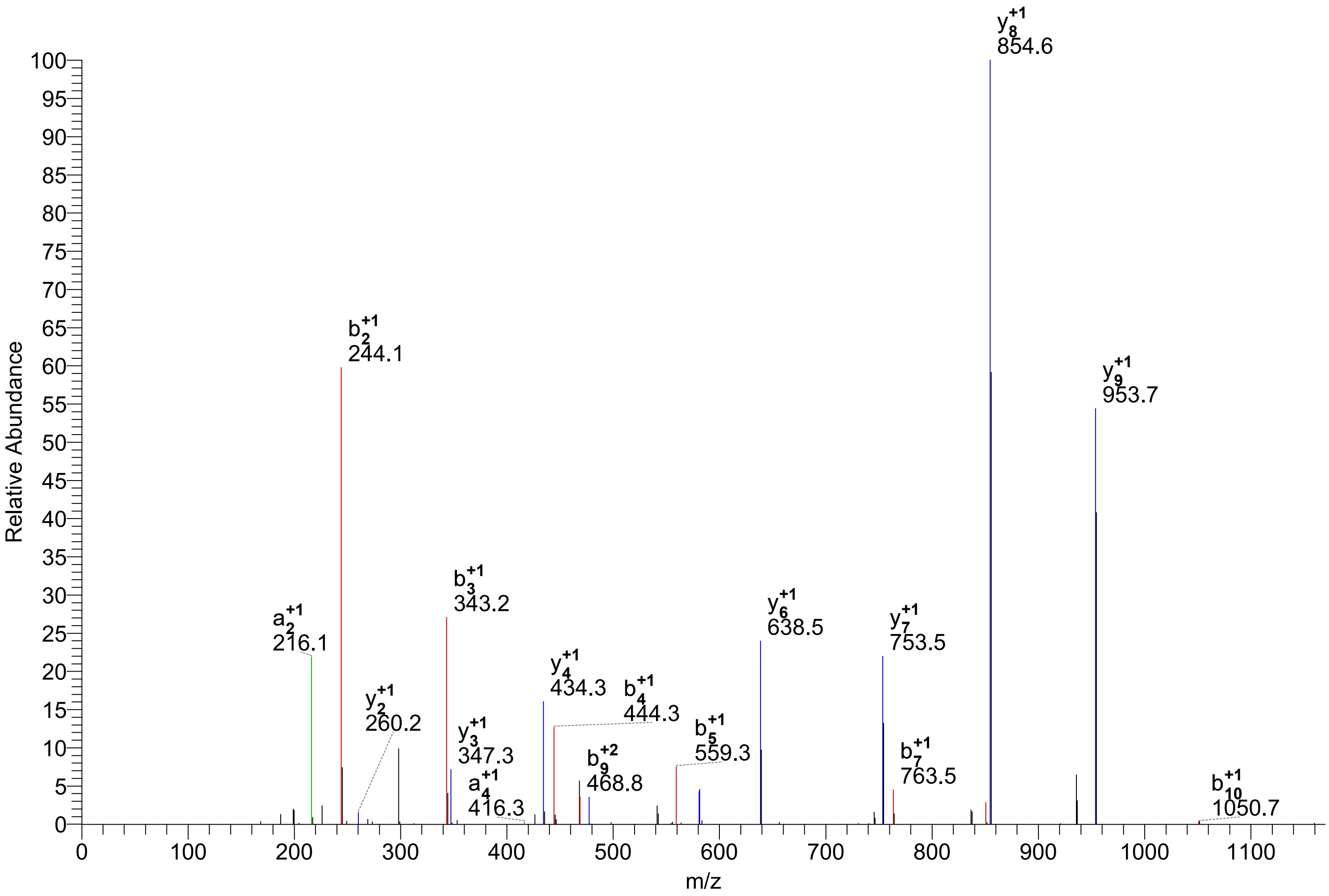


```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00657670.1|TREMBL:B0YIW2|EN                                          4e-005  10.2      0.0       0
19287468 - 1  R.GWVTDGFSSLK.D                              1196.59    2  4e-005  3.932  0.552   725.3  1   17/30   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 598.80
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 W    216.11     244.11                                     1139.57
 V    315.18     343.18                                      953.49
 T    416.23     444.22                                      854.43
 D    531.26     559.25                                      753.38
 G    588.28     616.27                                      638.35
 F    735.35     763.34                                      581.33
 S    822.38     850.37                                      434.26
 S    909.41     937.41                                      347.23
 L   1022.49    1050.49                                      260.20
 K                                                           147.11
```

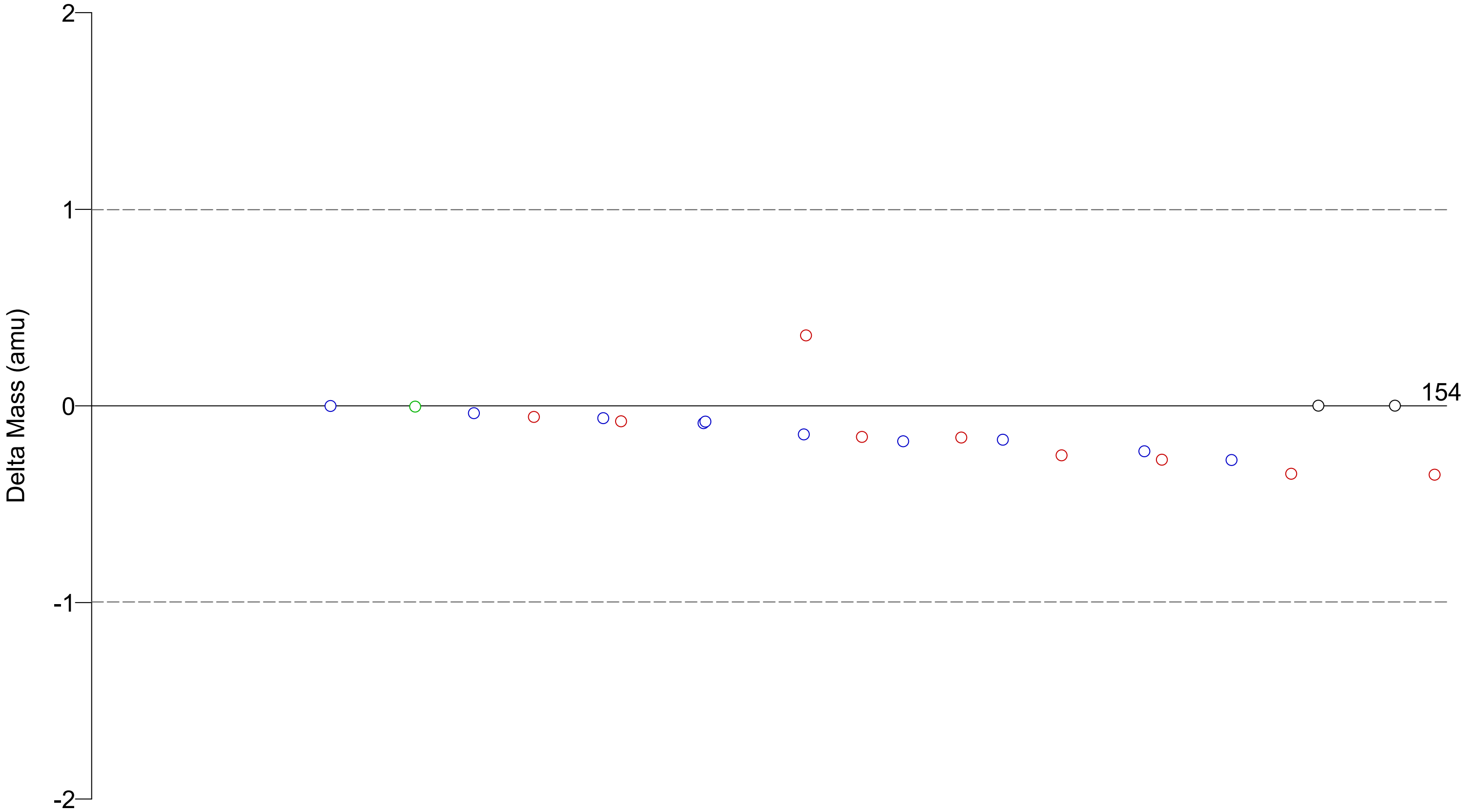


#19287468-1 NL: 9.45E4

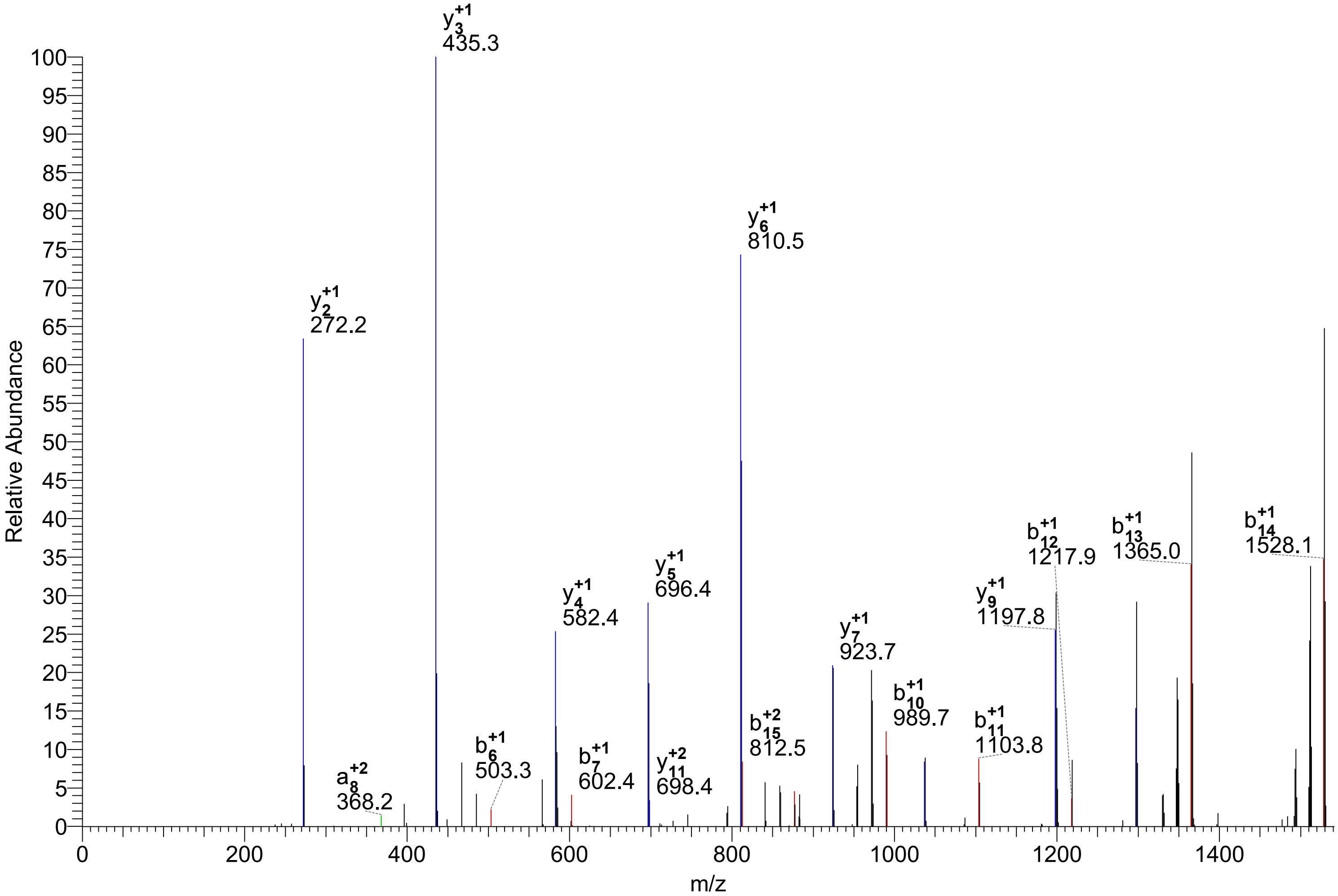


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z     P         XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00550731.2|SWISS-PROT:P06310|TREMBL:Q8TCD0|ENSEMBL:ENSP     5e-005  10.2      0.0        0
19287468 - 1  K.SGTASVVCLLNNFYPR.E                    1798.88   2  5e-005  3.485  0.433   766.8  1   17/45   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```

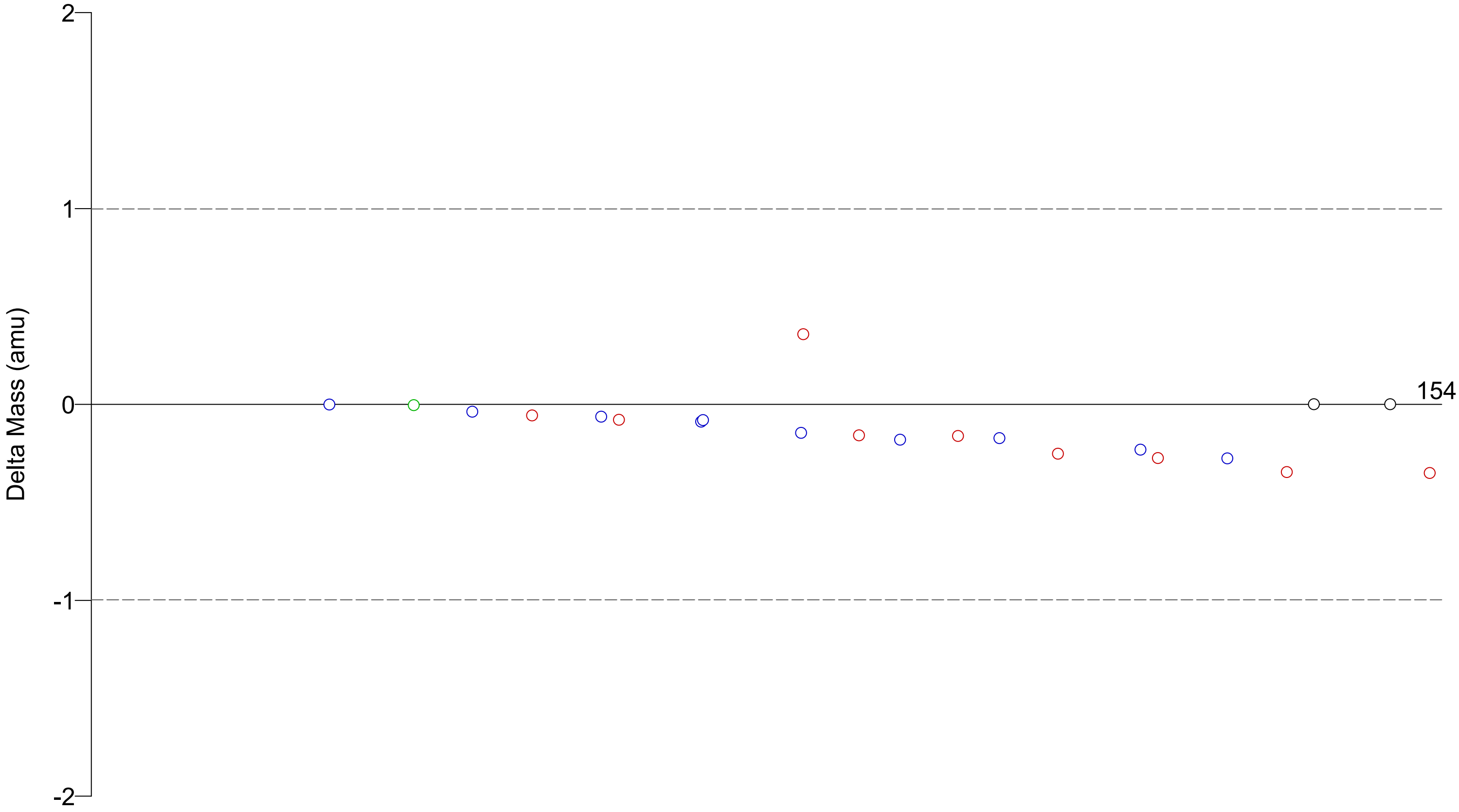


#19287468-1 NL: 2.53E6

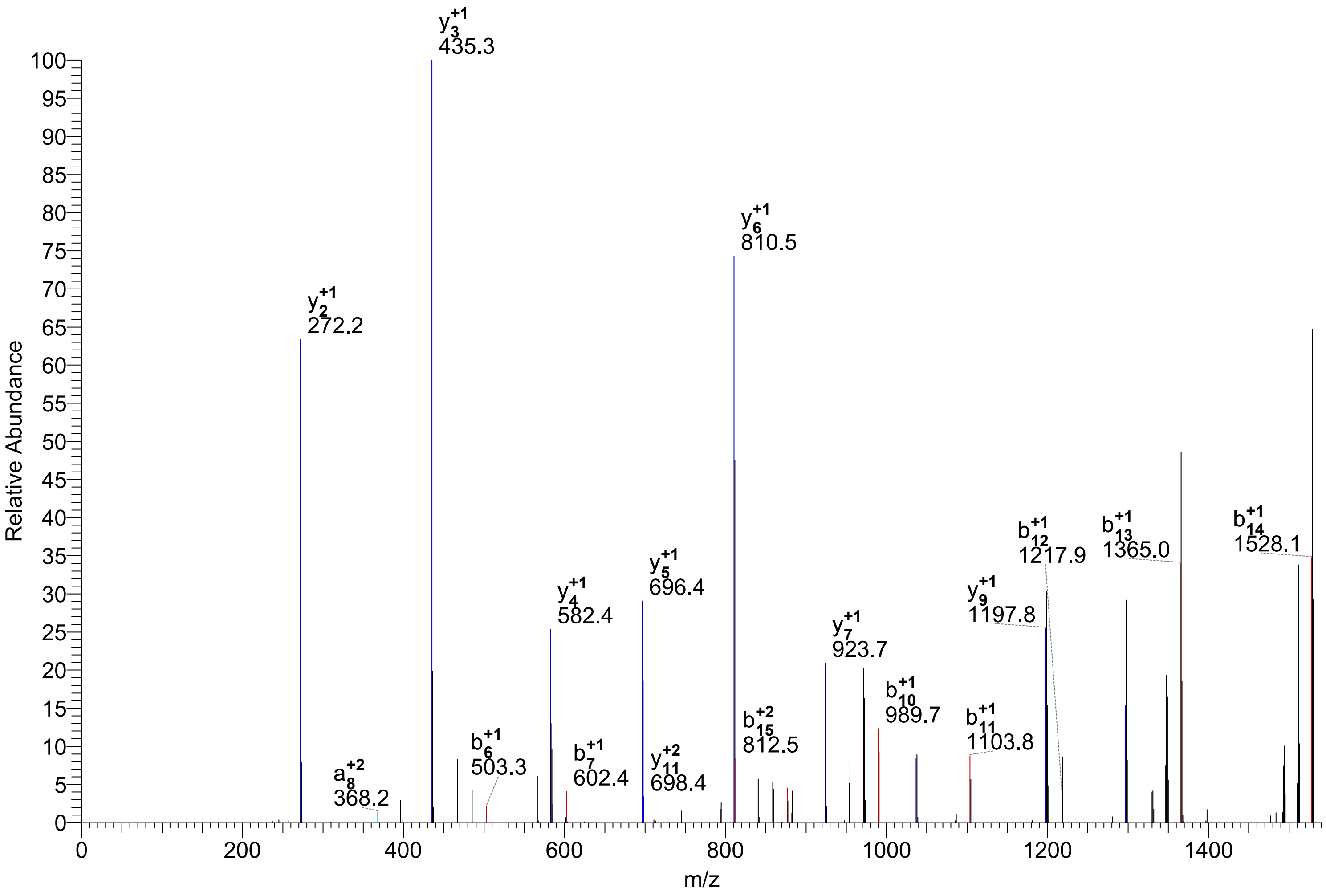


```
Reference                                                                 P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00556287.1|TREMBL:Q569I7 Ta                                      5e-005  10.2      0.0        0
19287468 - 1  K.SGTASVVCLLNNFYPR.E                       1798.88    2  5e-005  3.485  0.433   766.8  1   17/45   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```

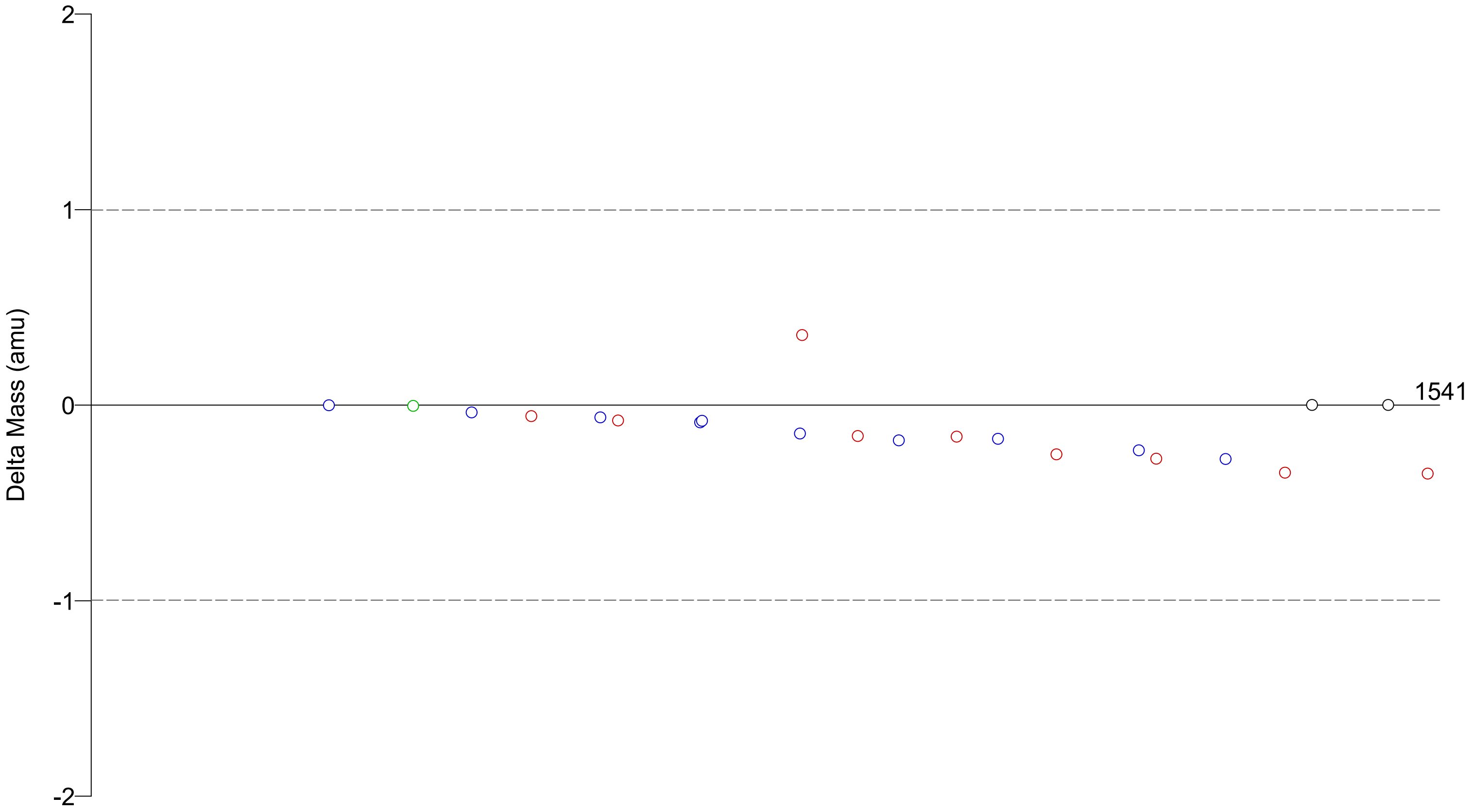


#19287468-1 NL: 2.53E6

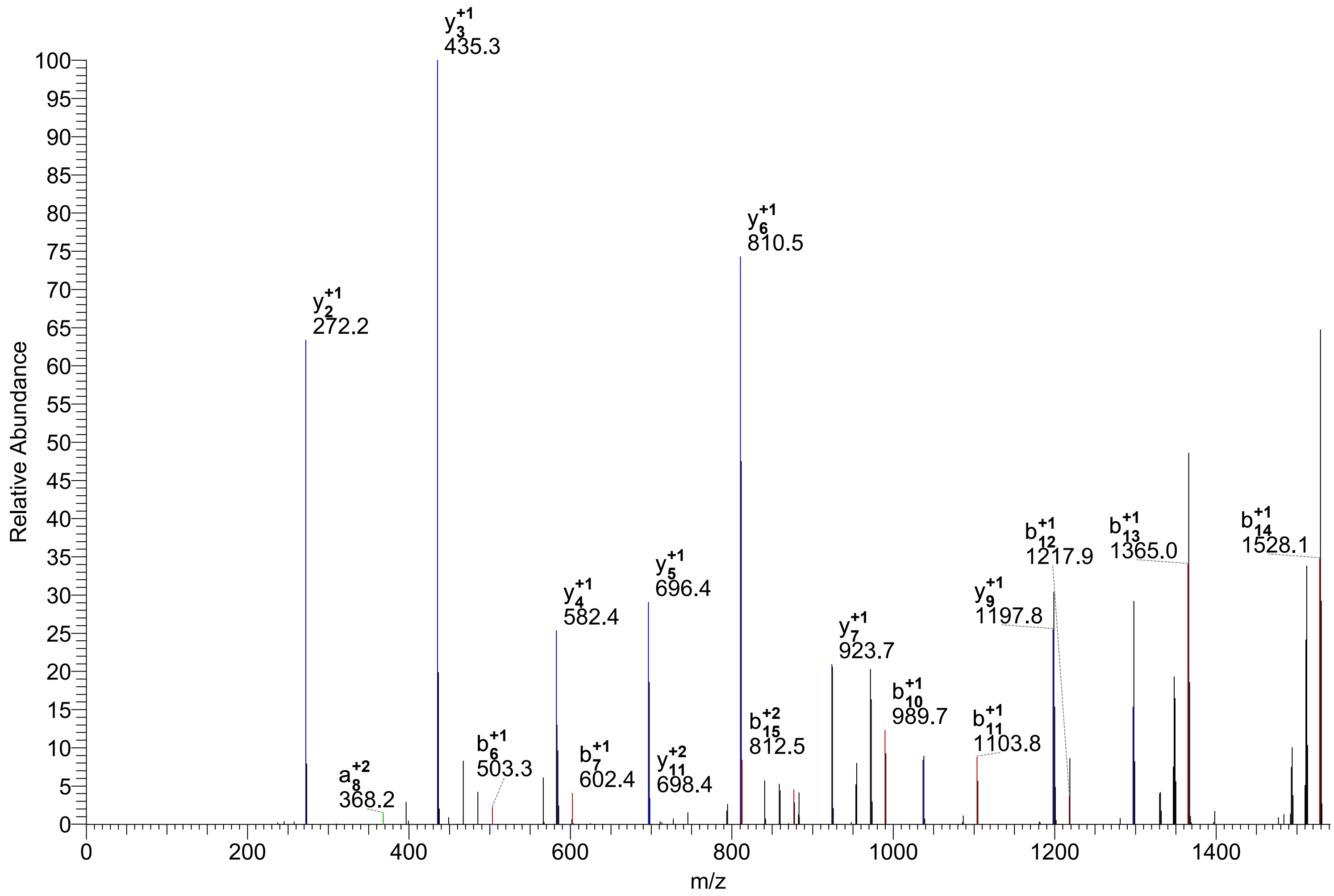


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00784773.7|TREMBL:Q7Z3Y4|EN                                     5e-005  10.2      0.0        0
19287468 - 1  K.SGTASVVCLLNNFYPR.E                       1798.88    2  5e-005  3.485  0.433   766.8  1   17/45   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```

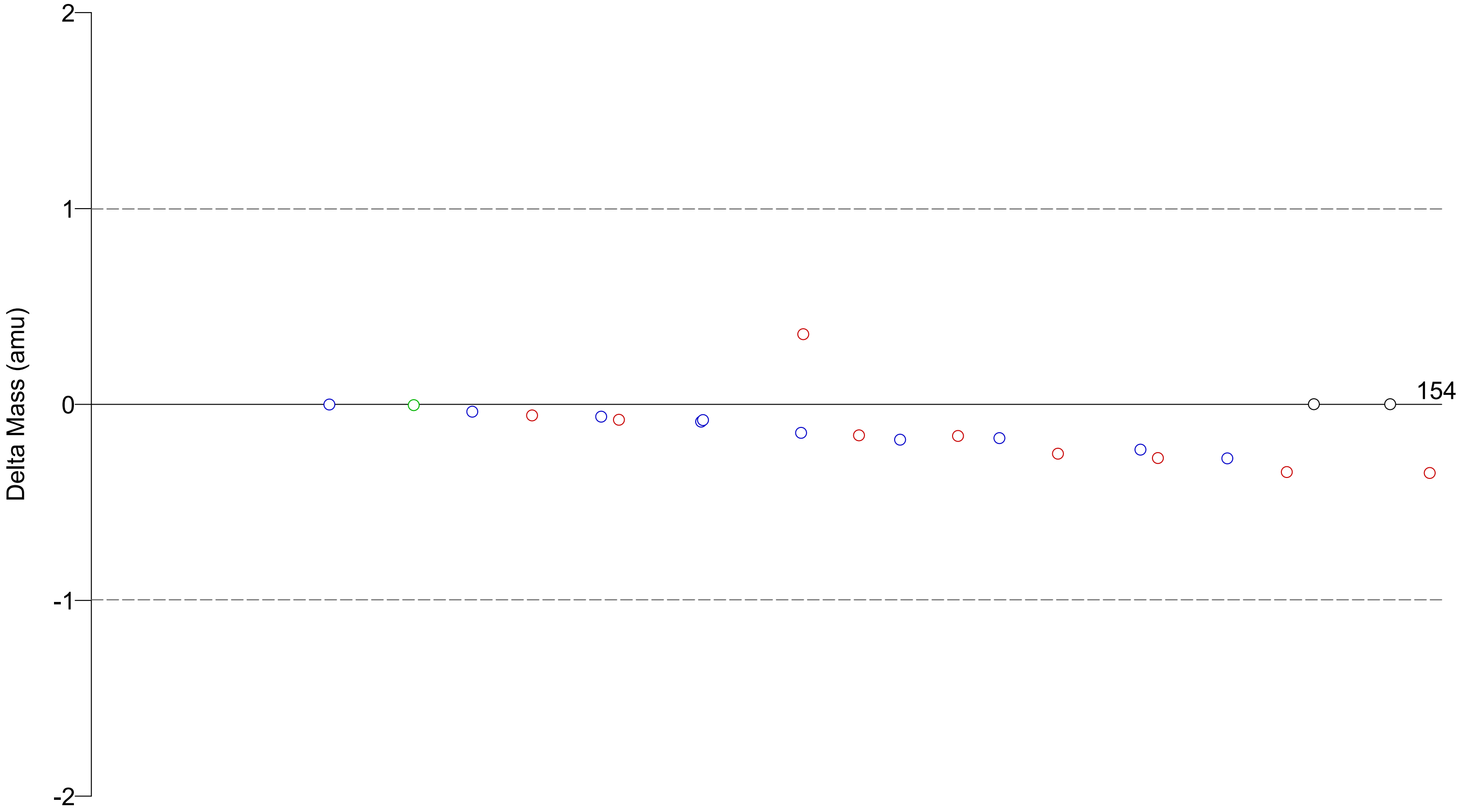


#19287468-1 NL: 2.53E6

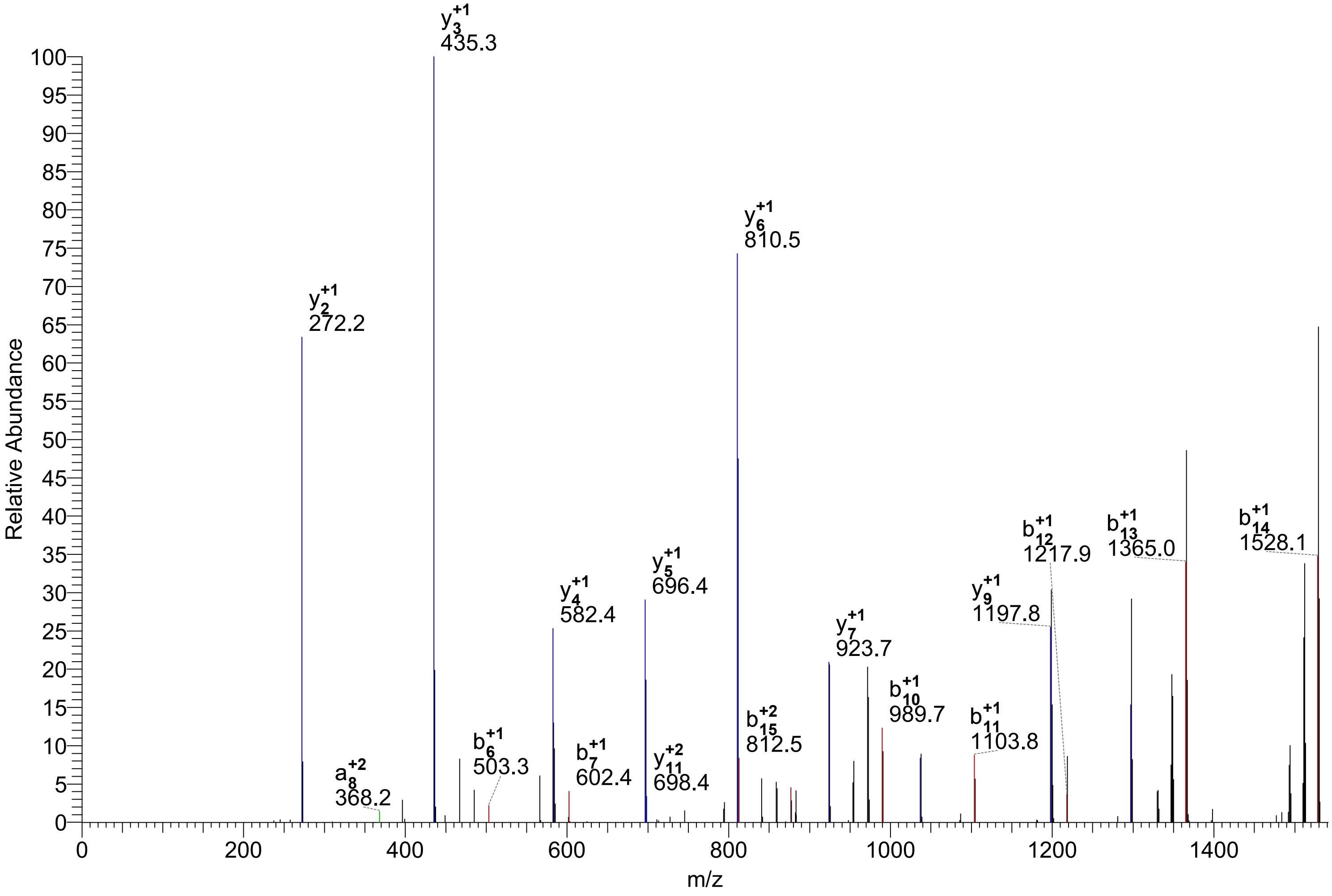


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00784865.1|TREMBL:Q6P5S8 Ta                                    5e-005  10.2     0.0        0
19287468 - 1  K.SGTASVVCLLNNFYPR.E                     1798.88    2  5e-005  3.485  0.433   766.8  1   17/45   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```

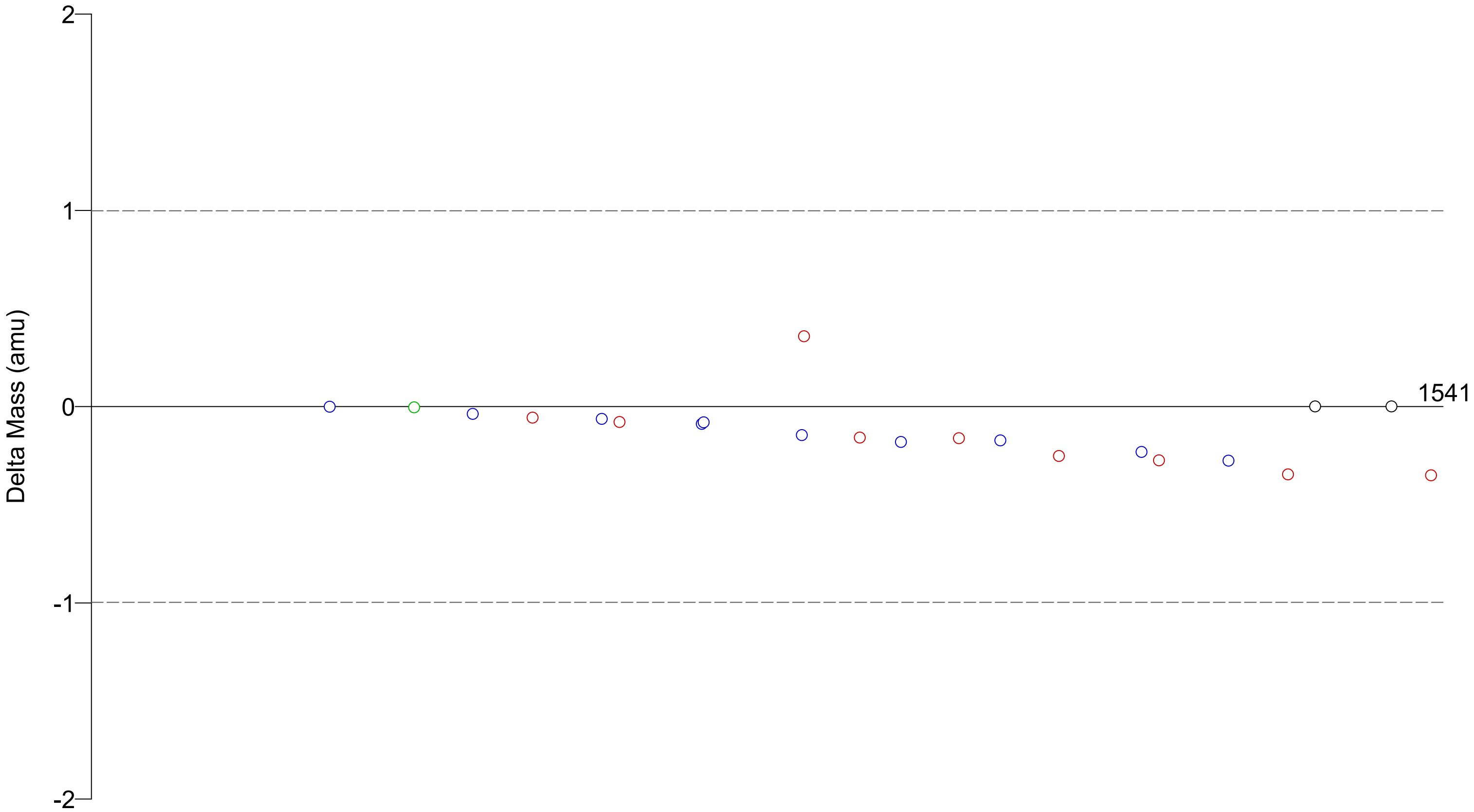


#19287468-1 NL: 2.53E6

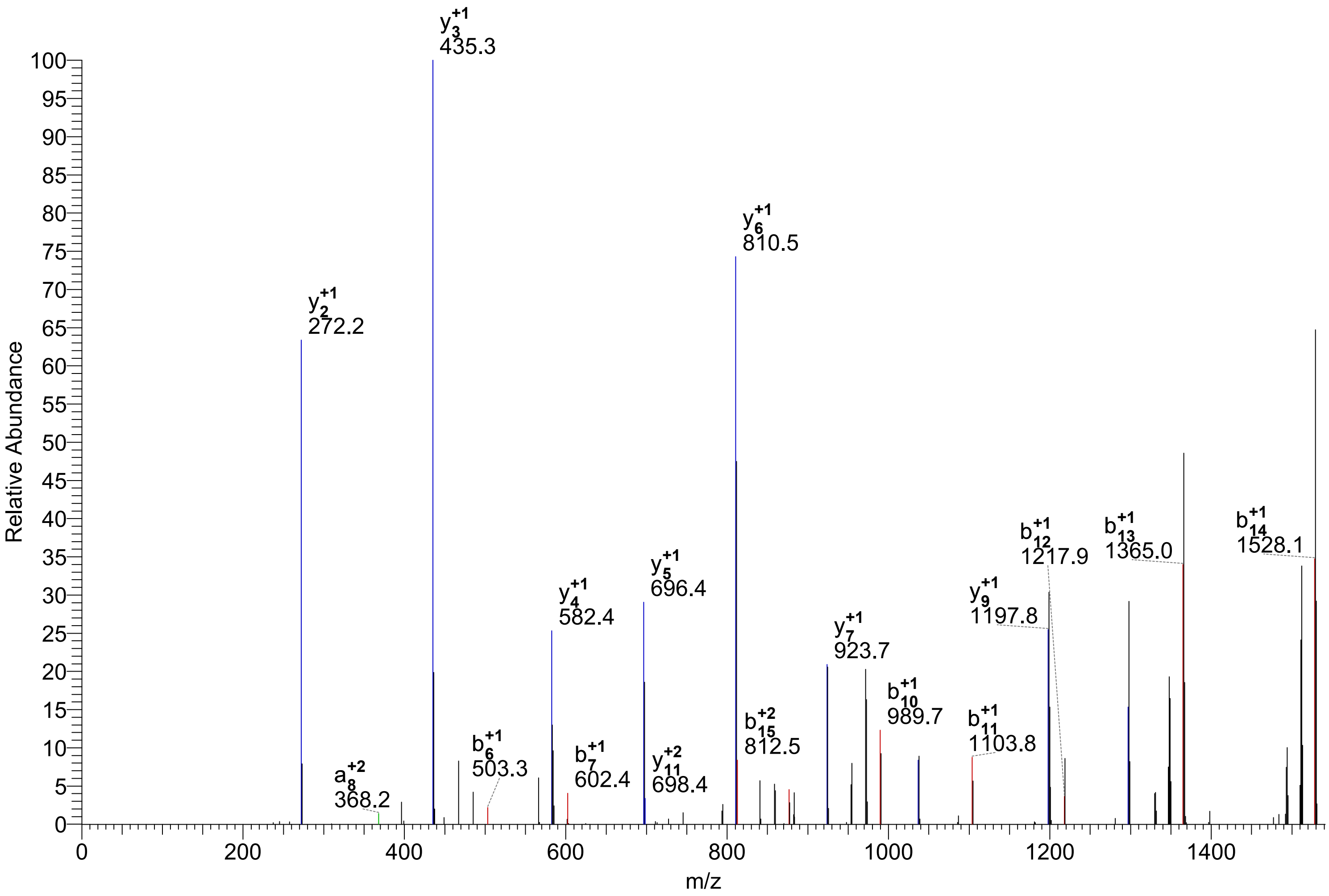


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)        Sequence                                MH+     z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00853045.1|TREMBL:Q5EFE6 Ta                               5e-005  10.2     0.0       0
19287468 - 1  K.SGTASVVCLLNNFYPR.E                   1798.88   2  5e-005  3.485  0.433   766.8  1   17/45   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```

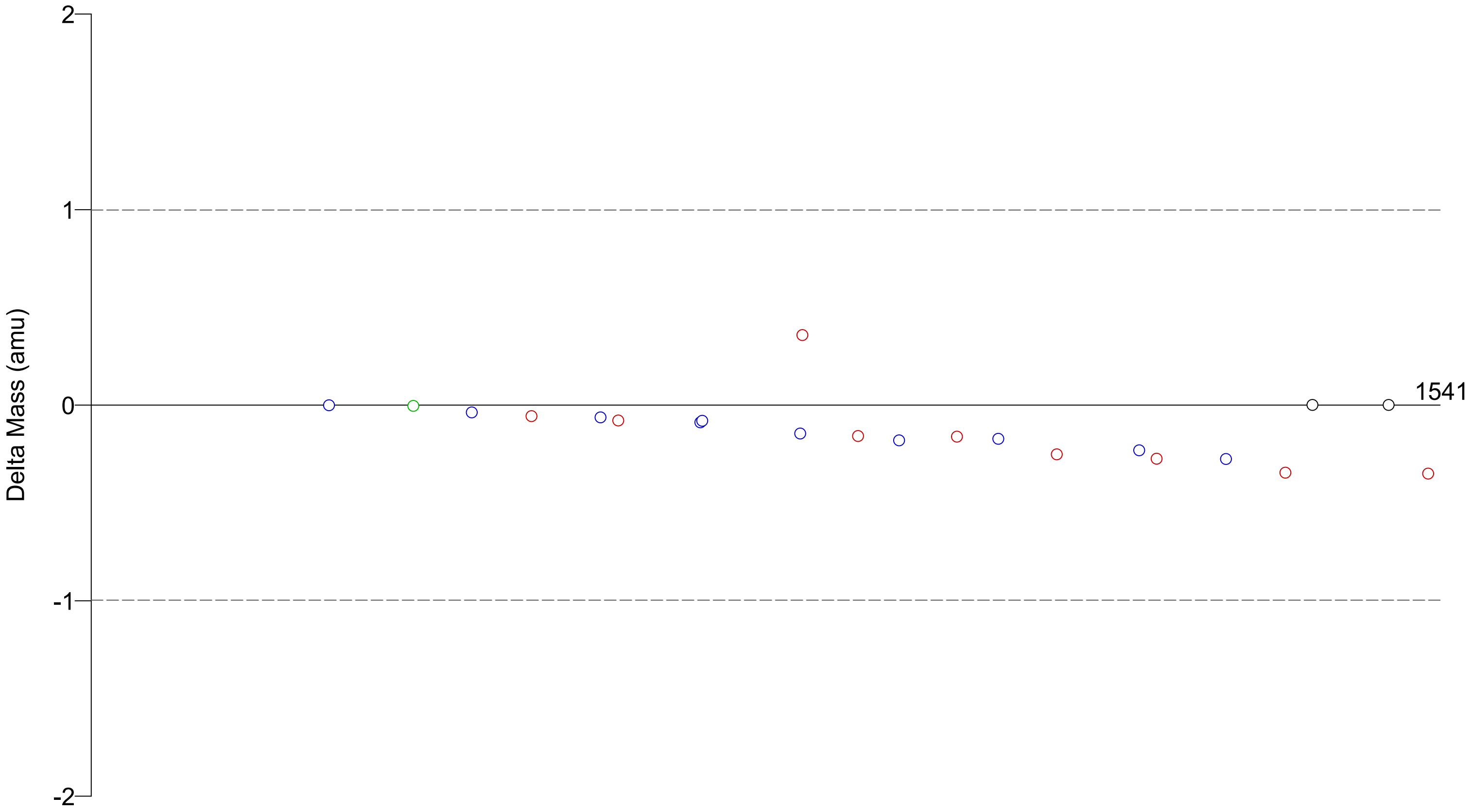


#19287468-1 NL: 2.53E6

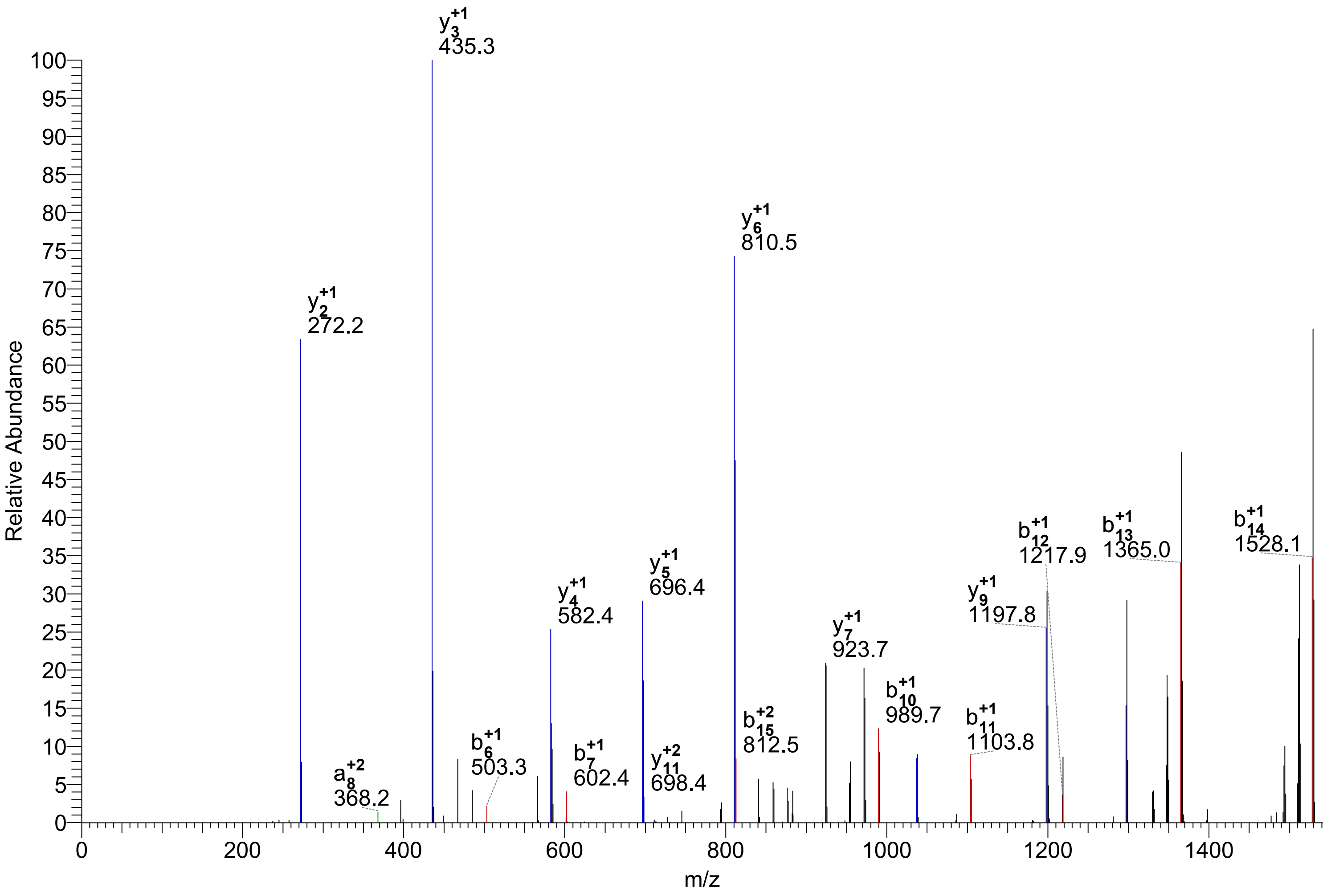


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count

IPI:IPI00909649.2|SWISS-PROT:P0183                                       5e-005  10.2      0.0        0
19287468 - 1  K.SGTASVVCLLNNFYPR.E                        1798.88   2  5e-005  3.485  0.433   766.8  1   17/45    7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1711.85
 T    218.11     246.11                                     1654.83
 A    289.15     317.15                                     1553.78
 S    376.18     404.18                                     1482.74
 V    475.25     503.25                                     1395.71
 V    574.32     602.31                                     1296.64
 C    735.33     763.33                                     1197.57
 L    848.42     876.41                                     1036.56
 L    961.50     989.50                                      923.47
 N   1075.55    1103.54                                      810.39
 N   1189.59    1217.58                                      696.35
 F   1336.66    1364.65                                      582.30
 Y   1499.72    1527.71                                      435.24
 P   1596.77    1624.77                                      272.17
 R                                                           175.12
```

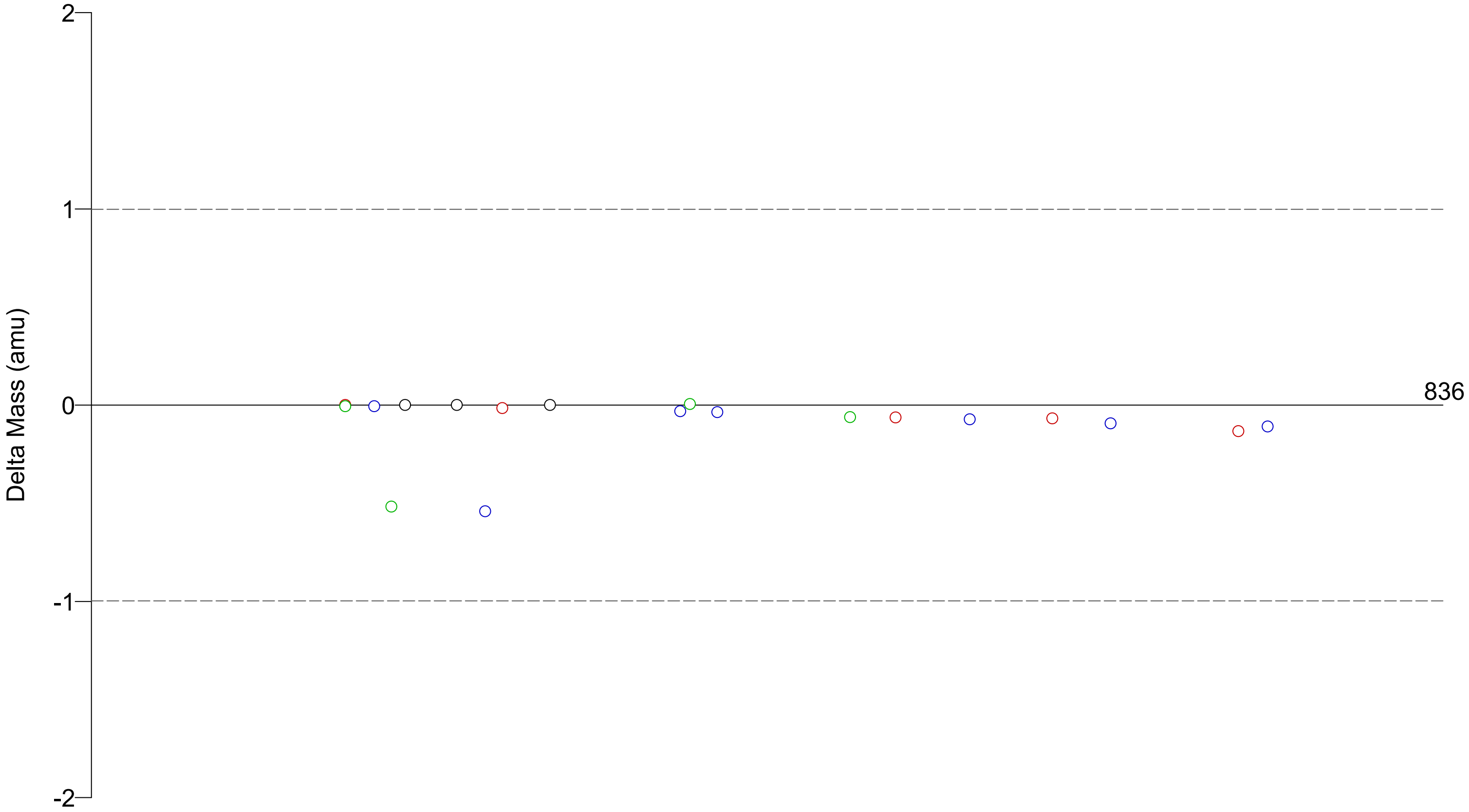


#19287468-1 NL: 2.53E6



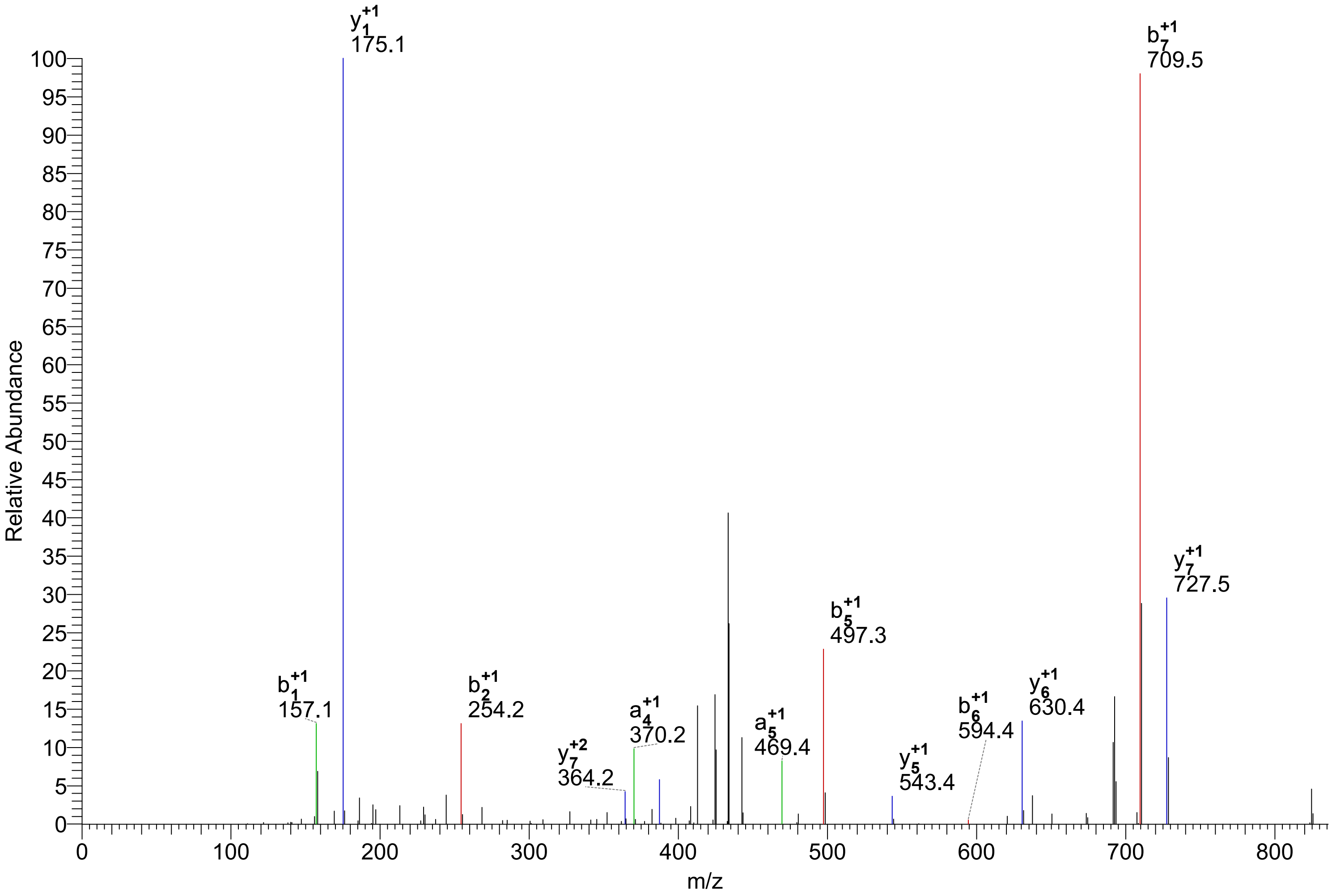
```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count

IPI:IPI00658130.1|TREMBL:Q5NV84;Q6                                 5e-005  20.2     0.0       0
              K.RPSGVPDR.F                            883.47    2  0.1     2.914  0.384   612.6  1    14/21   8
19287468 - 1  K.YAASSYLSLTPEQWK.S                     1743.86   2  5e-005  3.671  0.433   421.7  1    16/42   15

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

```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```



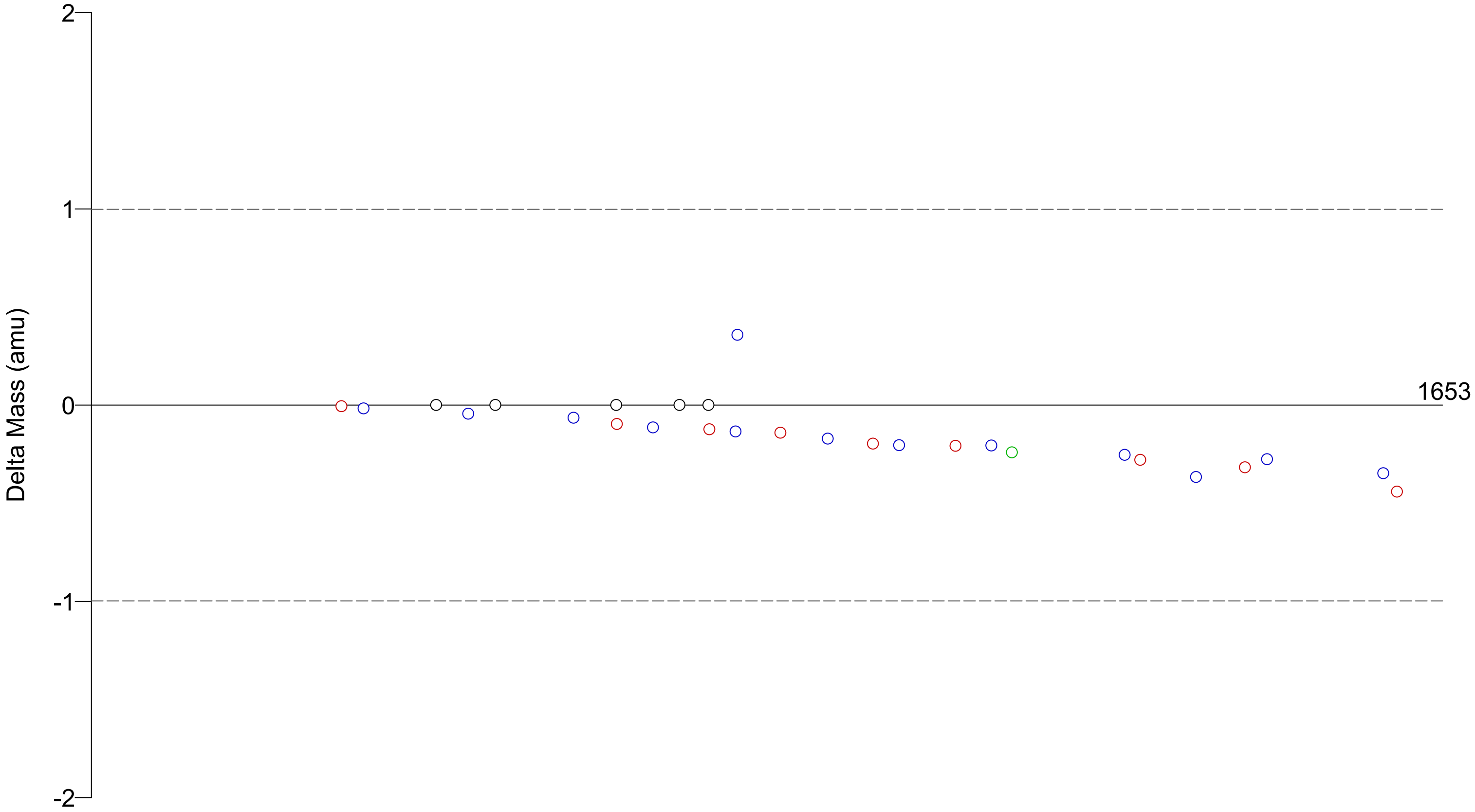
2
1
0
-1
-2
Delta Mass (amu)
836

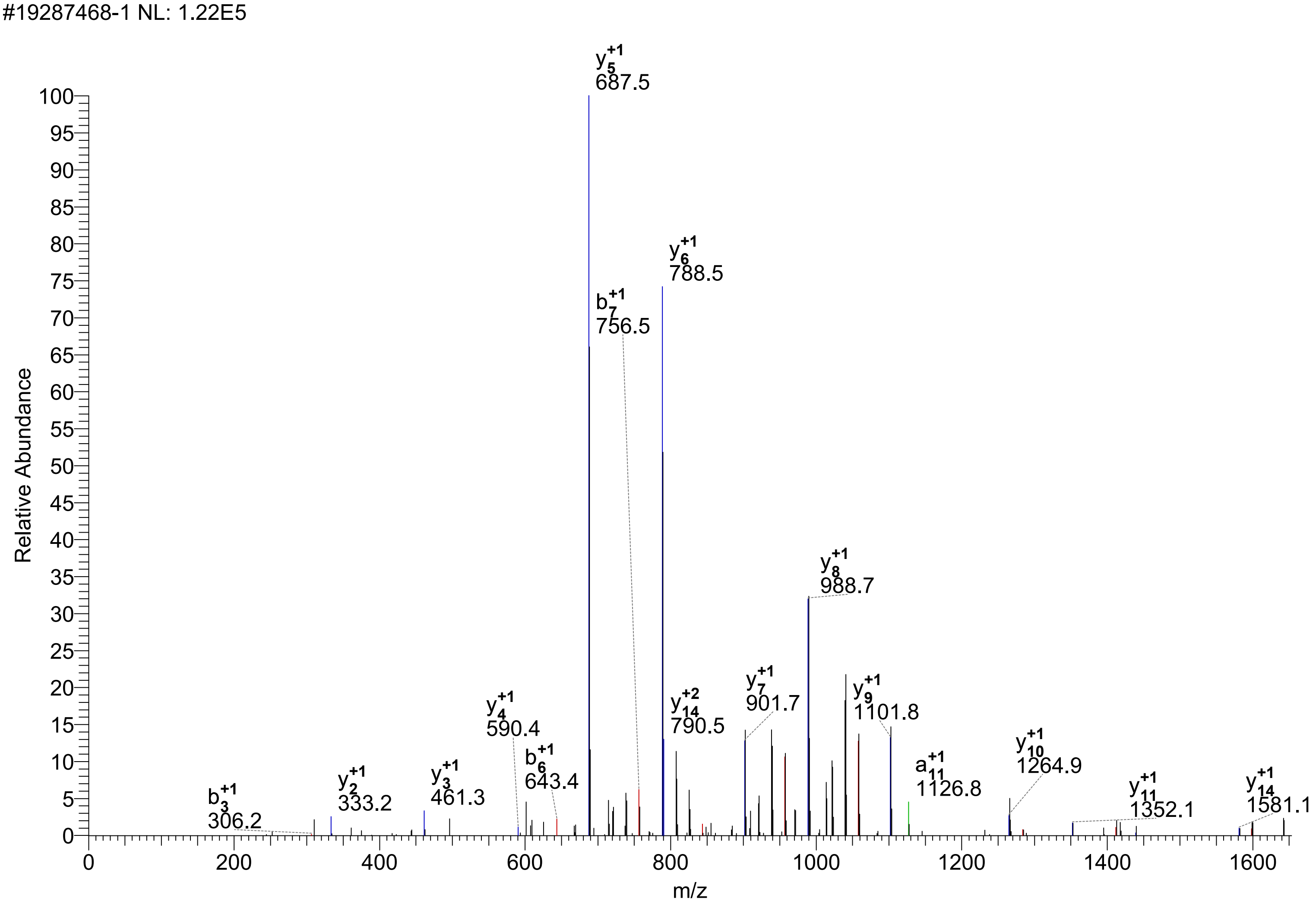
#0-0 NL: 6.35E5



Relative Abundance
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
y_1^{+1} 175.1
b_7^{+1} 709.5
y_7^{+1} 727.5
b_5^{+1} 497.3
b_1^{+1} 157.1
b_2^{+1} 254.2
a_4^{+1} 370.2
y_7^{+2} 364.2
a_5^{+1} 469.4
y_5^{+1} 543.4
b_6^{+1} 594.4
y_6^{+1} 630.4
0
100
200
300
400
500
600
700
800
m/z

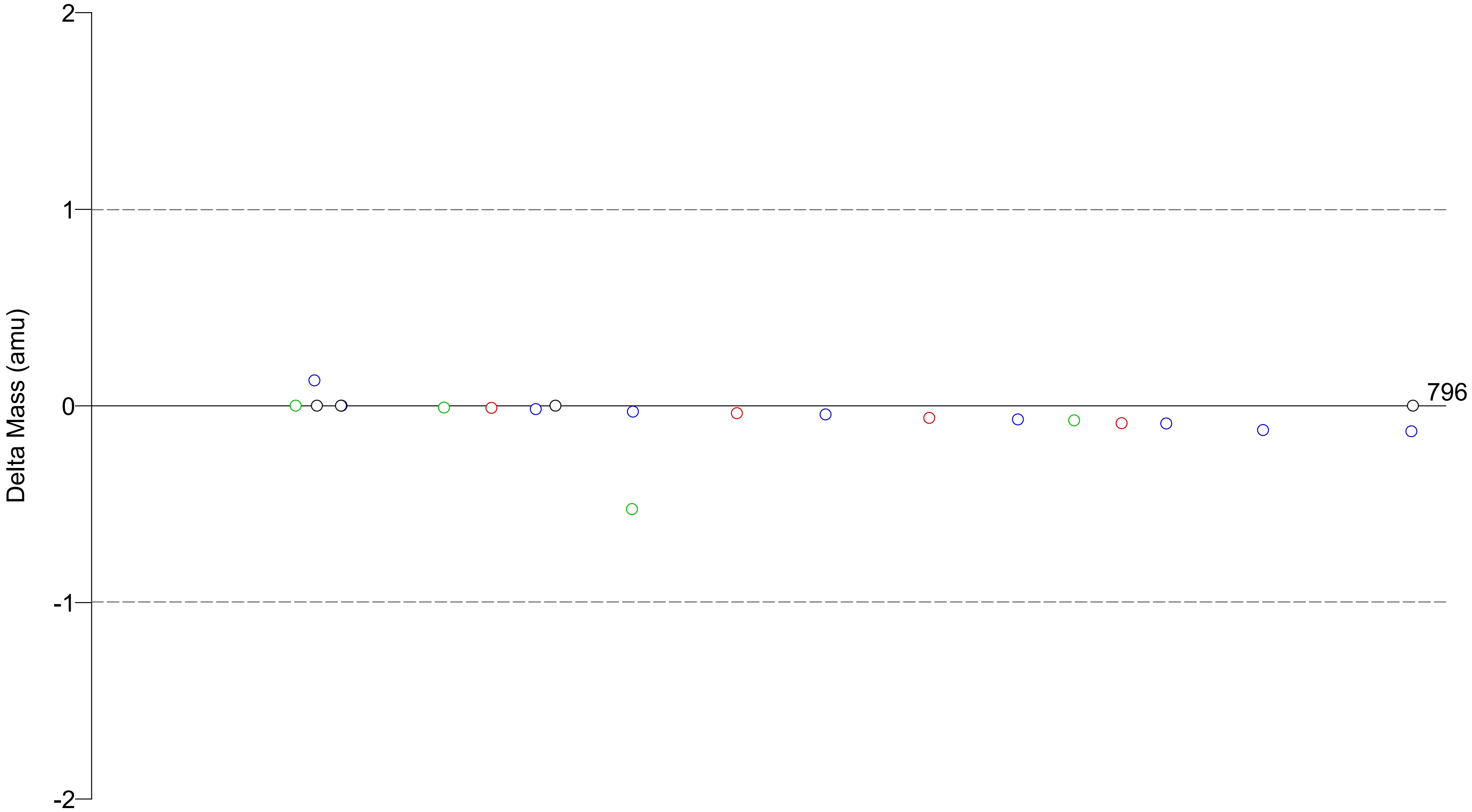
```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```


Delta Mass (amu)
2
1
0
-1
-2
1653

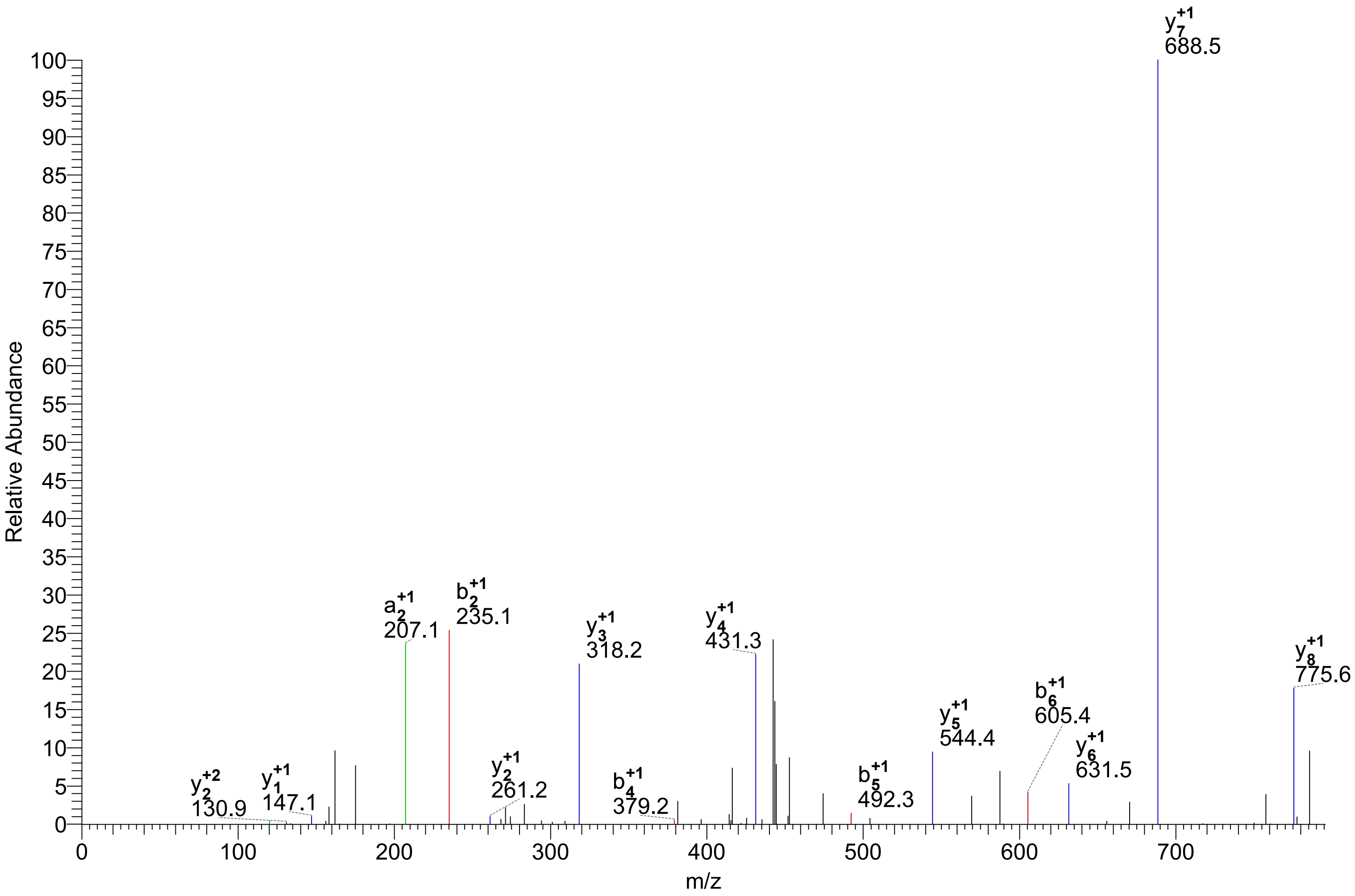

#19287468-1 NL: 1.22E5
Relative Abundance
m/z
y5 +1 687.5
y6 +1 788.5
b7 +1 756.5
y8 +1 988.7
y7 +1 901.7
y9 +1 1101.8
y14 +2 790.5
y4 +1 590.4
b6 +1 643.4
a11 +1 1126.8
y10 +1 1264.9
y3 +1 461.3
y2 +1 333.2
b3 +1 306.2
y11 +1 1352.1
y14 +1 1581.1
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
0
200
400
600
800
1000
1200
1400
1600

```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00807428.1|TREMBL:A0A5E4 Ta                                     5e-005  20.2     0.0       0
19287468 - 1  R.FSGSILGNK.A                              922.50     2  0.004   2.914  0.340   661.6  1   16/24   2
19287468 - 1  K.YAASSYLSLTPEQWK.S                       1743.86     2  5e-005  3.671  0.433   421.7  1   16/42   15

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

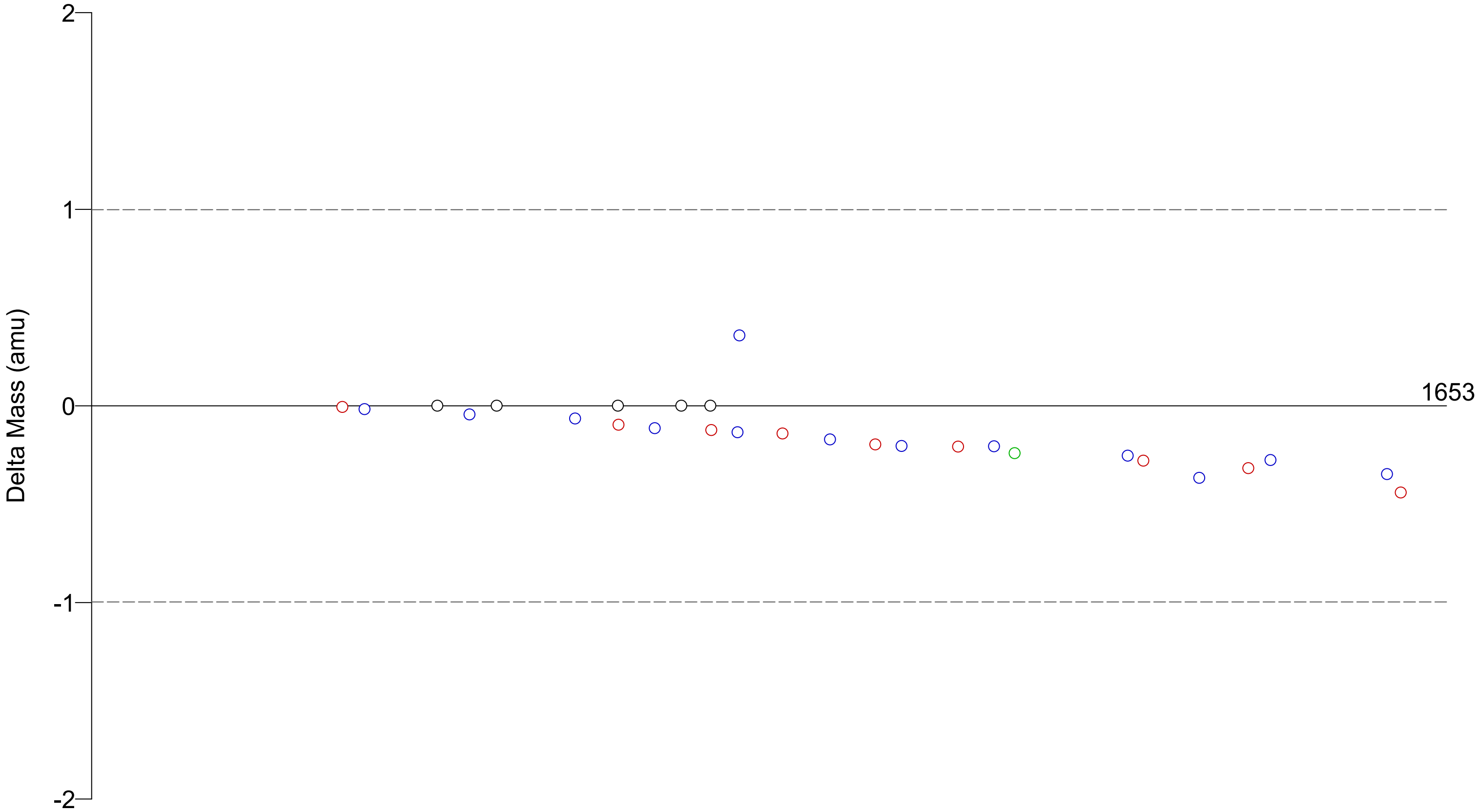
```
DTA for scans: 19287468-1
Precursor ion: 461.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                      775.43
 G    264.13     292.13                                      688.40
 S    351.17     379.16                                      631.38
 I    464.25     492.25                                      544.35
 L    577.33     605.33                                      431.26
 G    634.36     662.35                                      318.18
 N    748.40     776.39                                      261.16
 K                                                           147.11
```



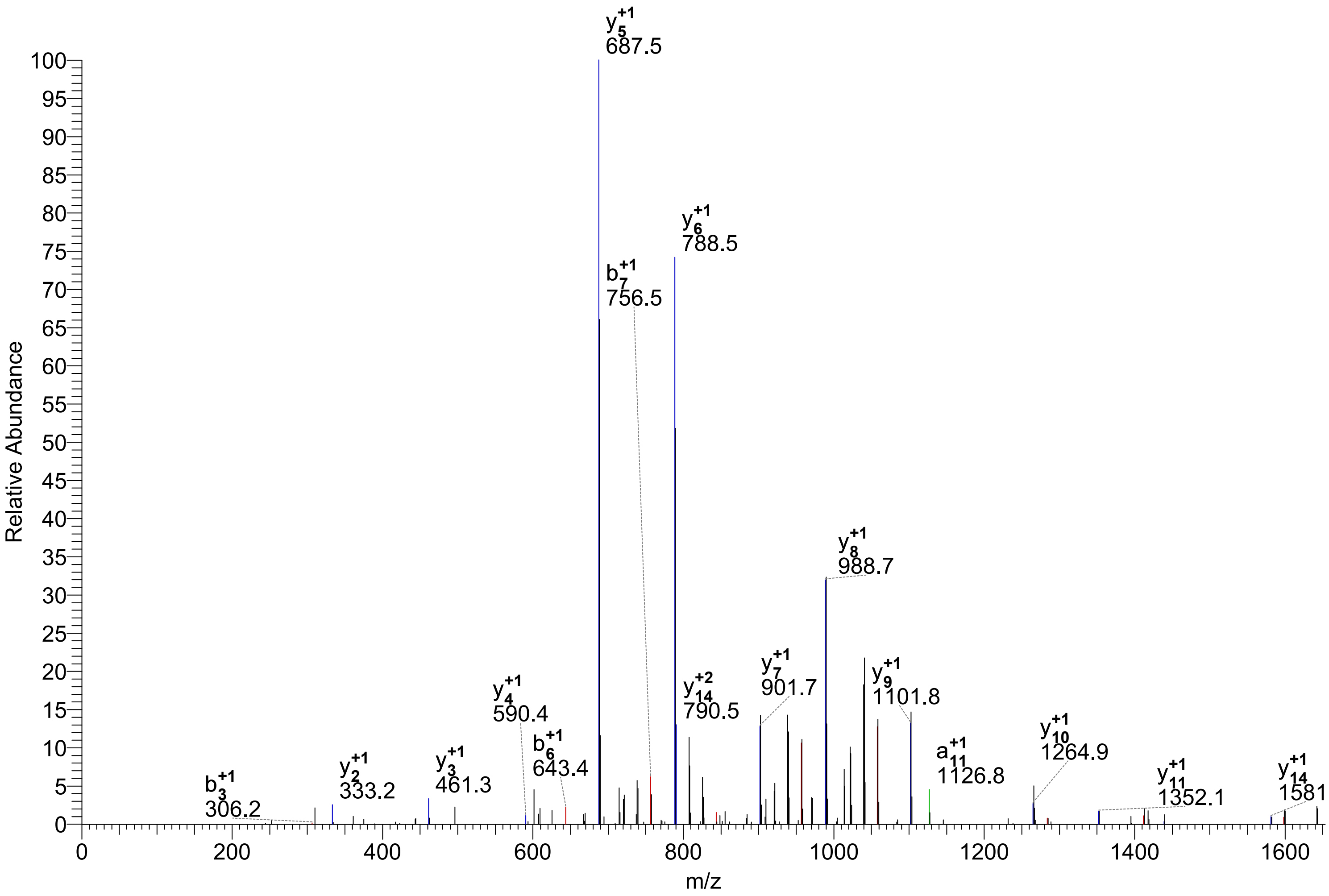
#19287468-1 NL: 1.73E5



```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

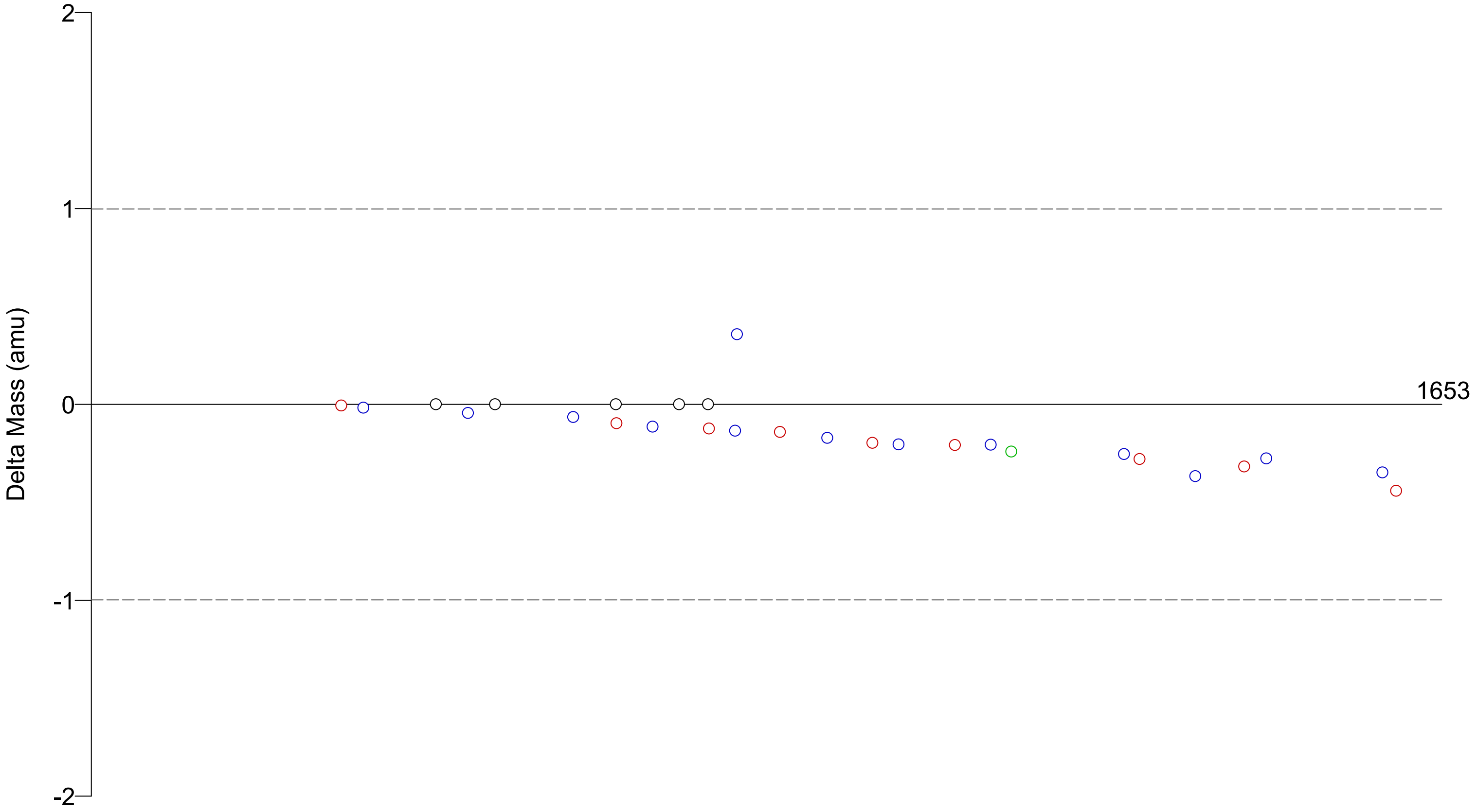


#19287468-1 NL: 1.22E5

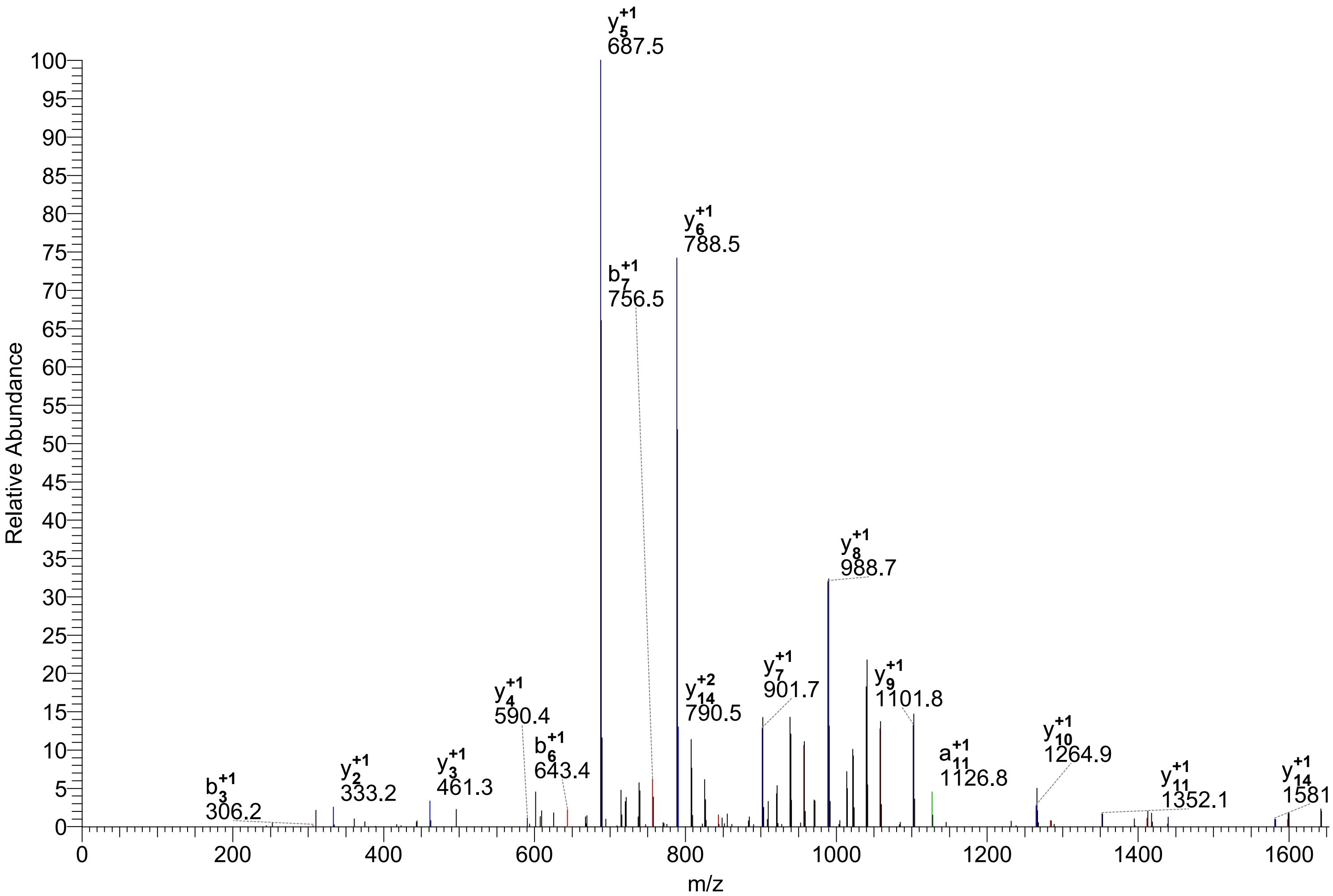


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+     z   P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00154742.6|SWISS-PROT:P01842|TREMBL:Q6PJR7;Q8N355;Q8TCJ     5e-005  10.2     0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                     1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

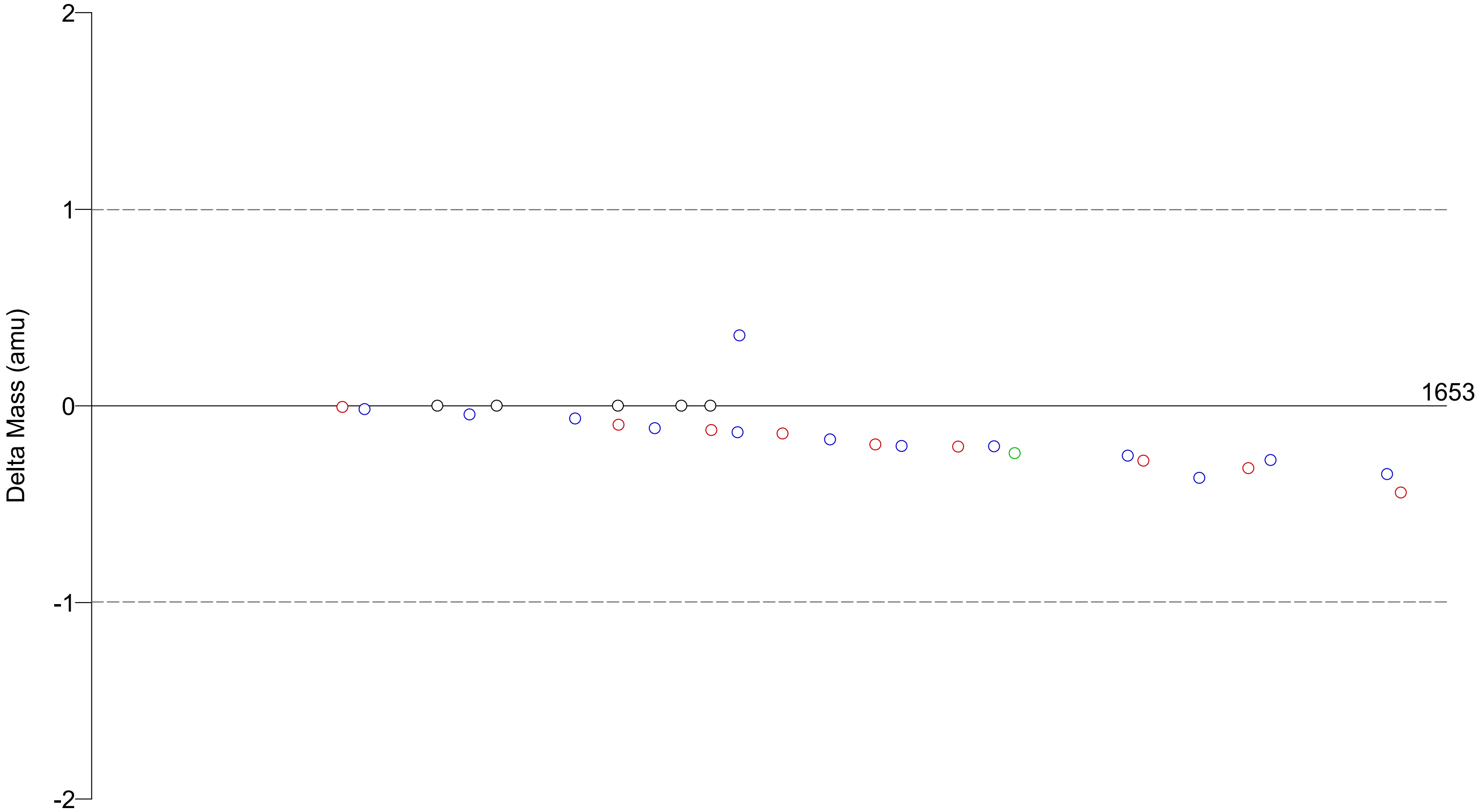


#19287468-1 NL: 1.22E5

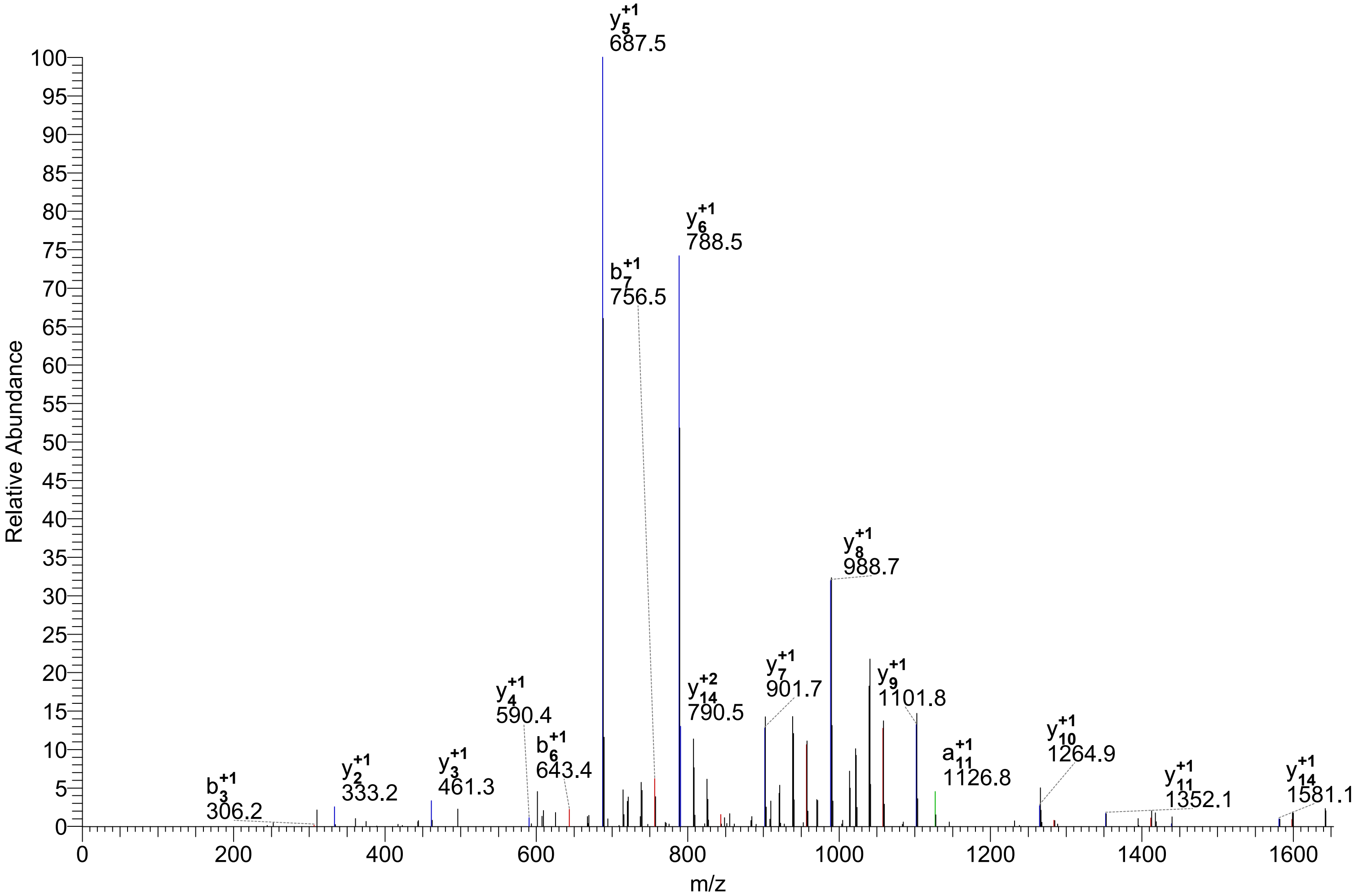


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00450309.1|TREMBL:Q6IN99 Ta                                   5e-005  10.2     0.0        0
19287468 - 1  K.YAASSYLSLTPEQWK.S                        1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

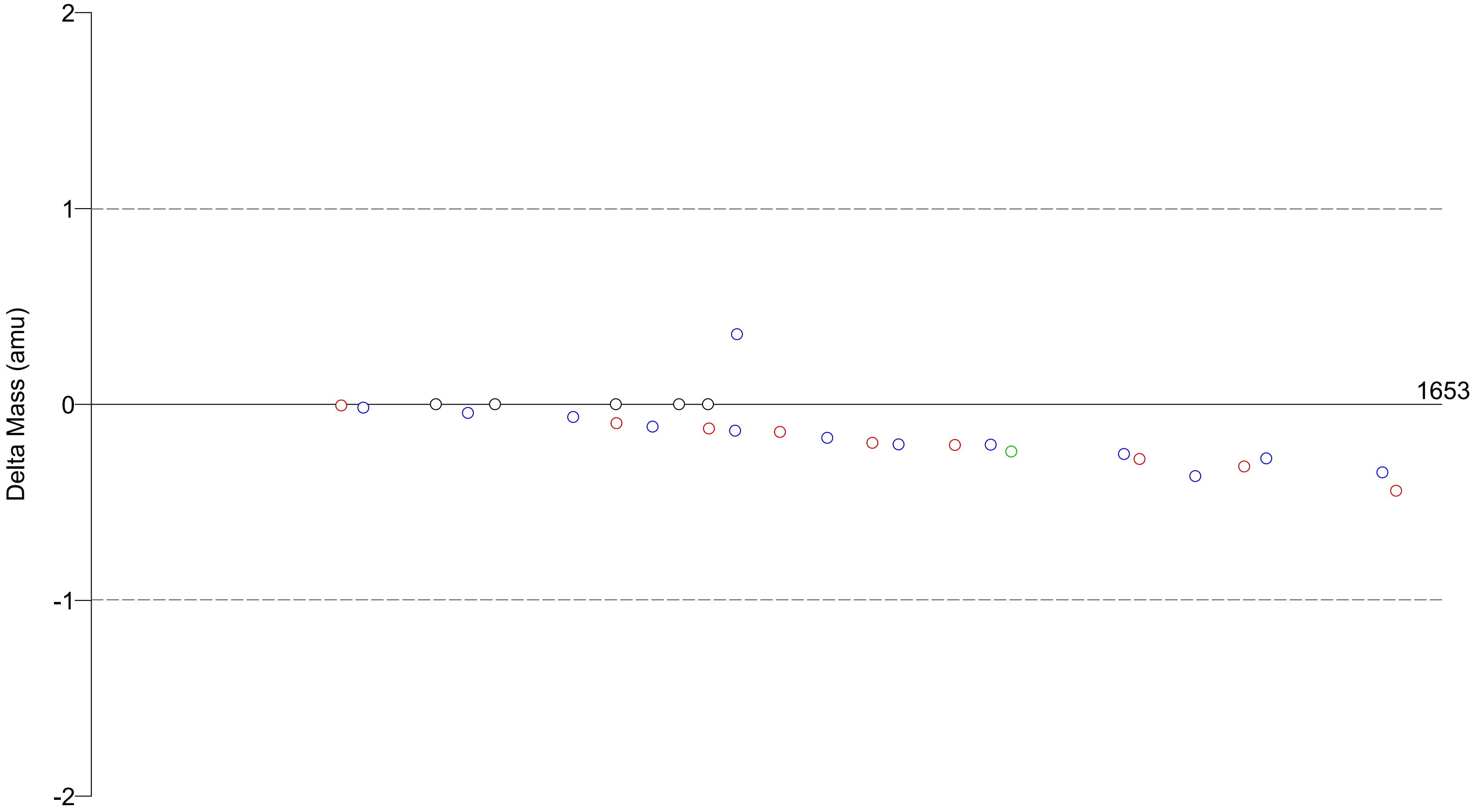


#19287468-1 NL: 1.22E5

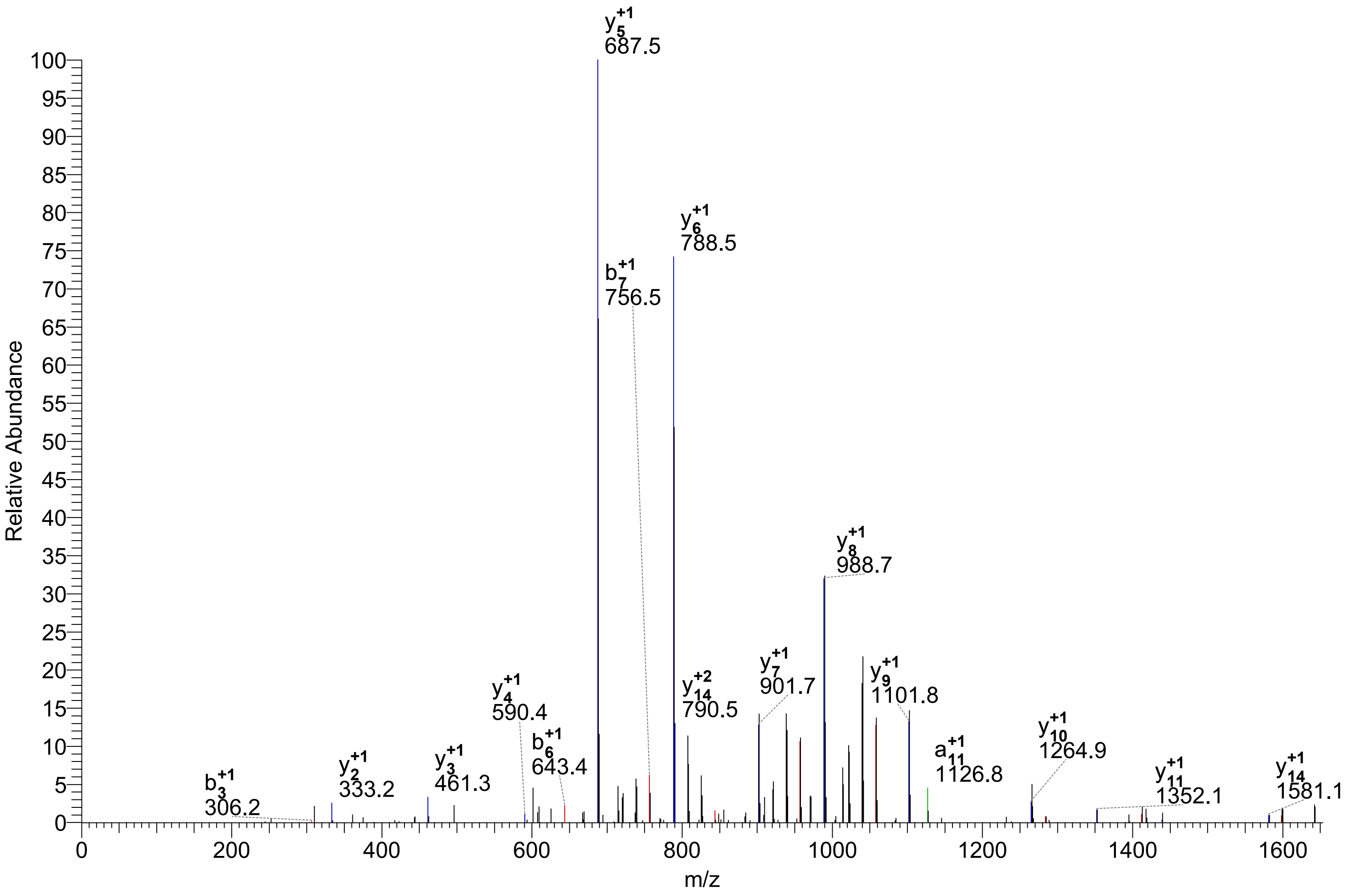


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00642632.1|TREMBL:A0M8Q6|EN                                   5e-005  10.2     0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                      1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

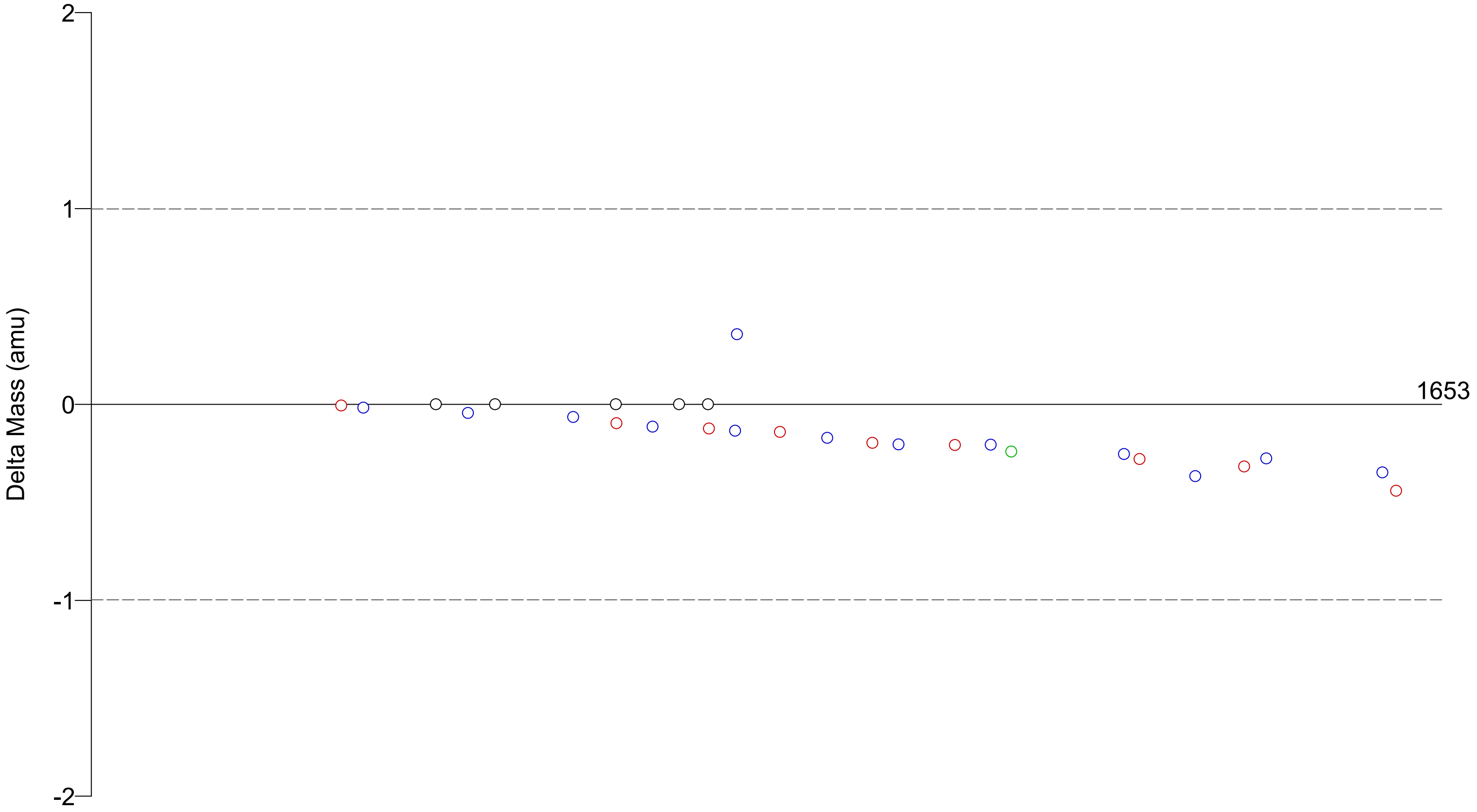


#19287468-1 NL: 1.22E5

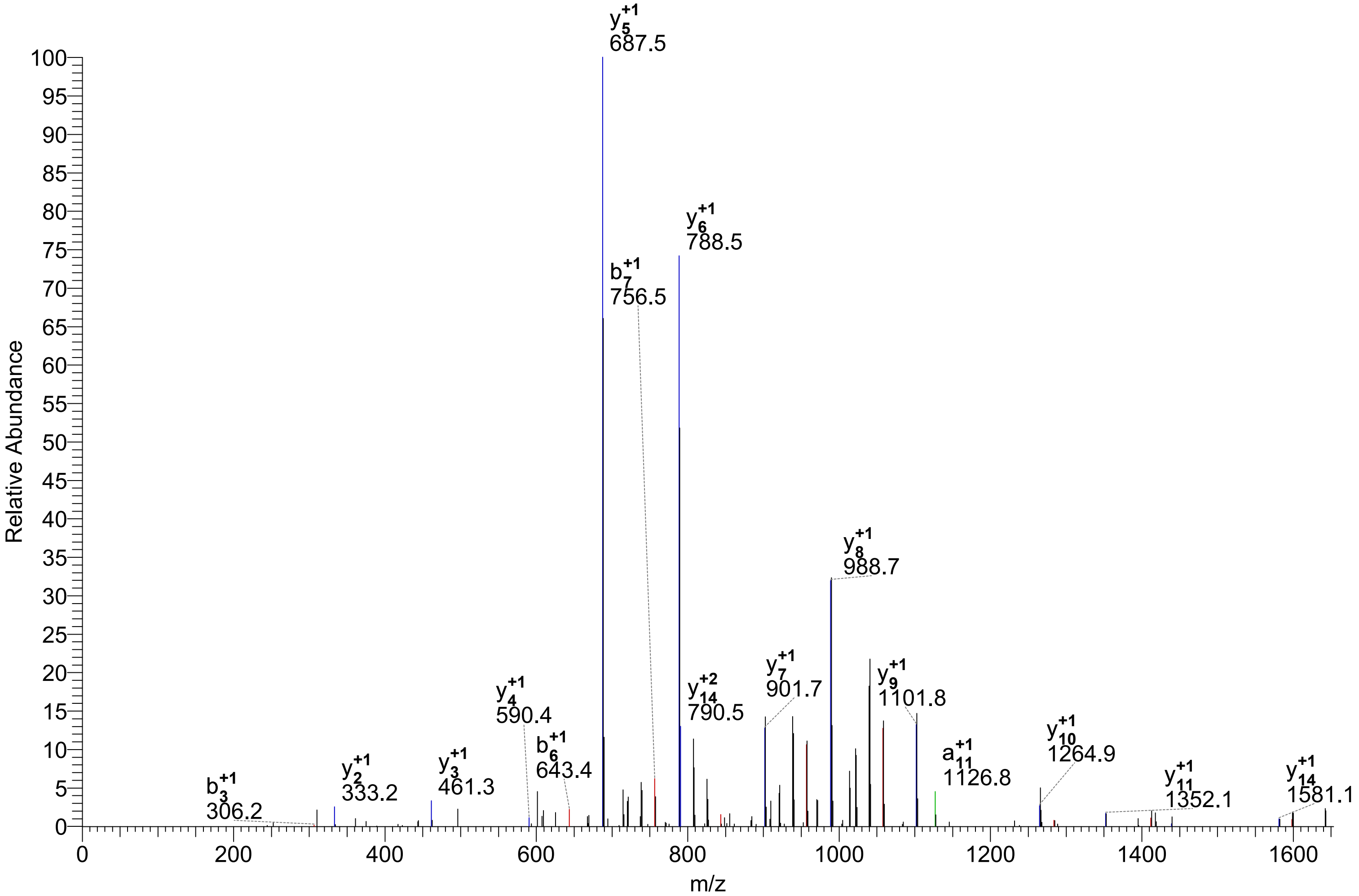


```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00719373.2|TREMBL:Q6NS95|EN                                   5e-005  10.2      0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                     1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

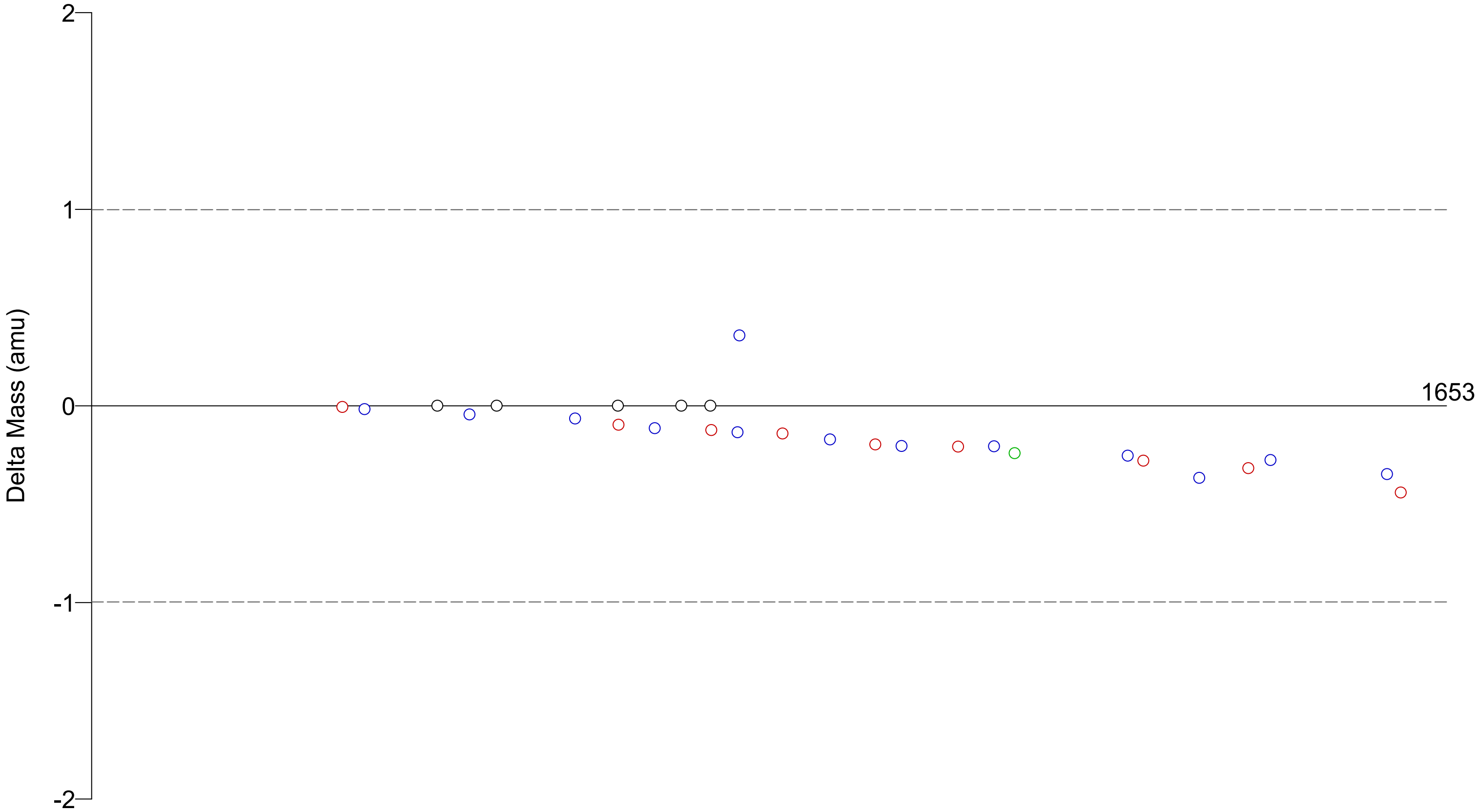


#19287468-1 NL: 1.22E5

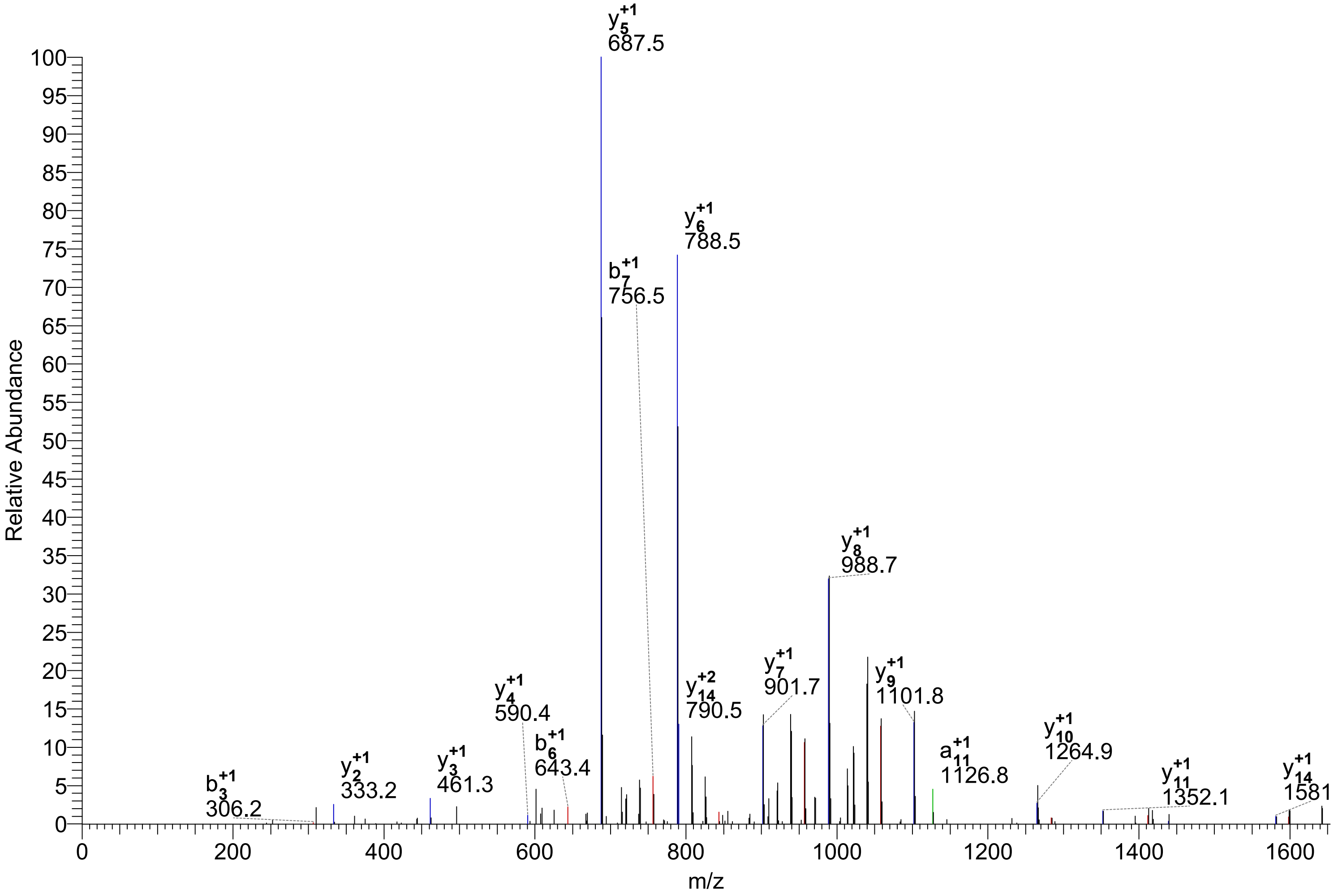


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00719452.1|TREMBL:Q5NV69;Q6                                    5e-005  10.2      0.0        0
19287468 - 1  K.YAASSYLSLTPEQWK.S                        1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

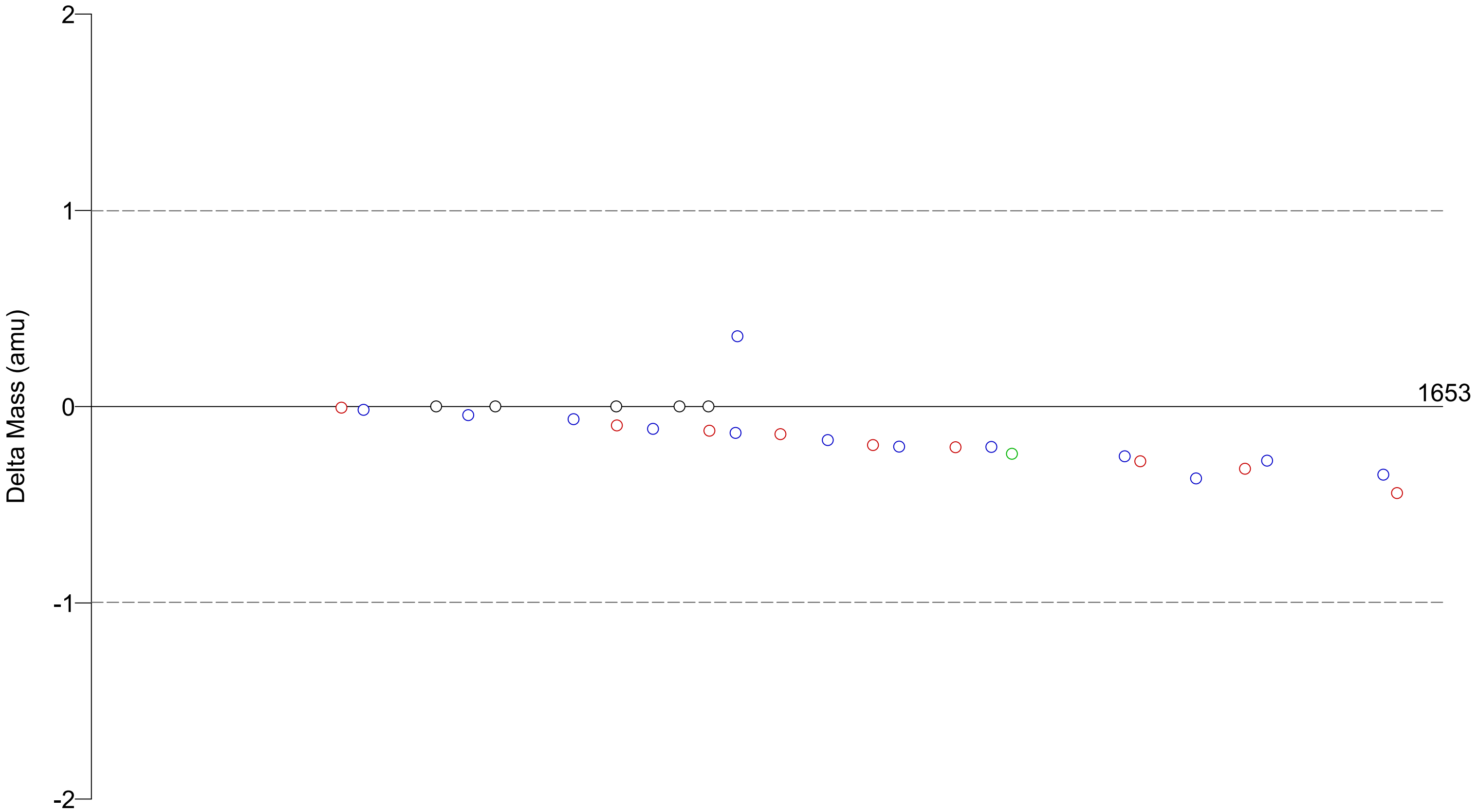


#19287468-1 NL: 1.22E5

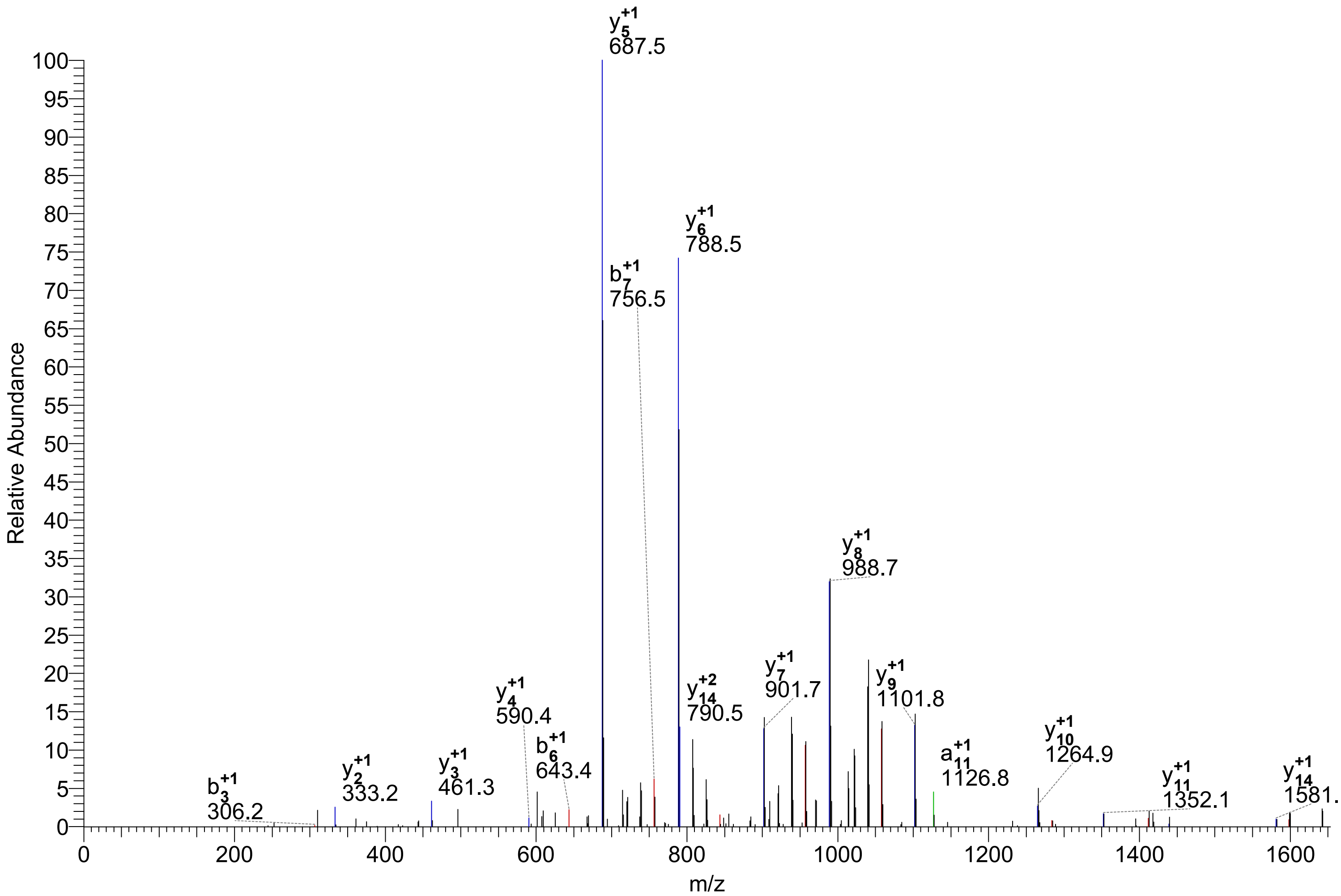


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00744476.6|TREMBL:A2MYD6;Q6                                   5e-005  10.2      0.0        0
19287468 - 1  K.YAASSYLSLTPEQWK.S                      1743.86    2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

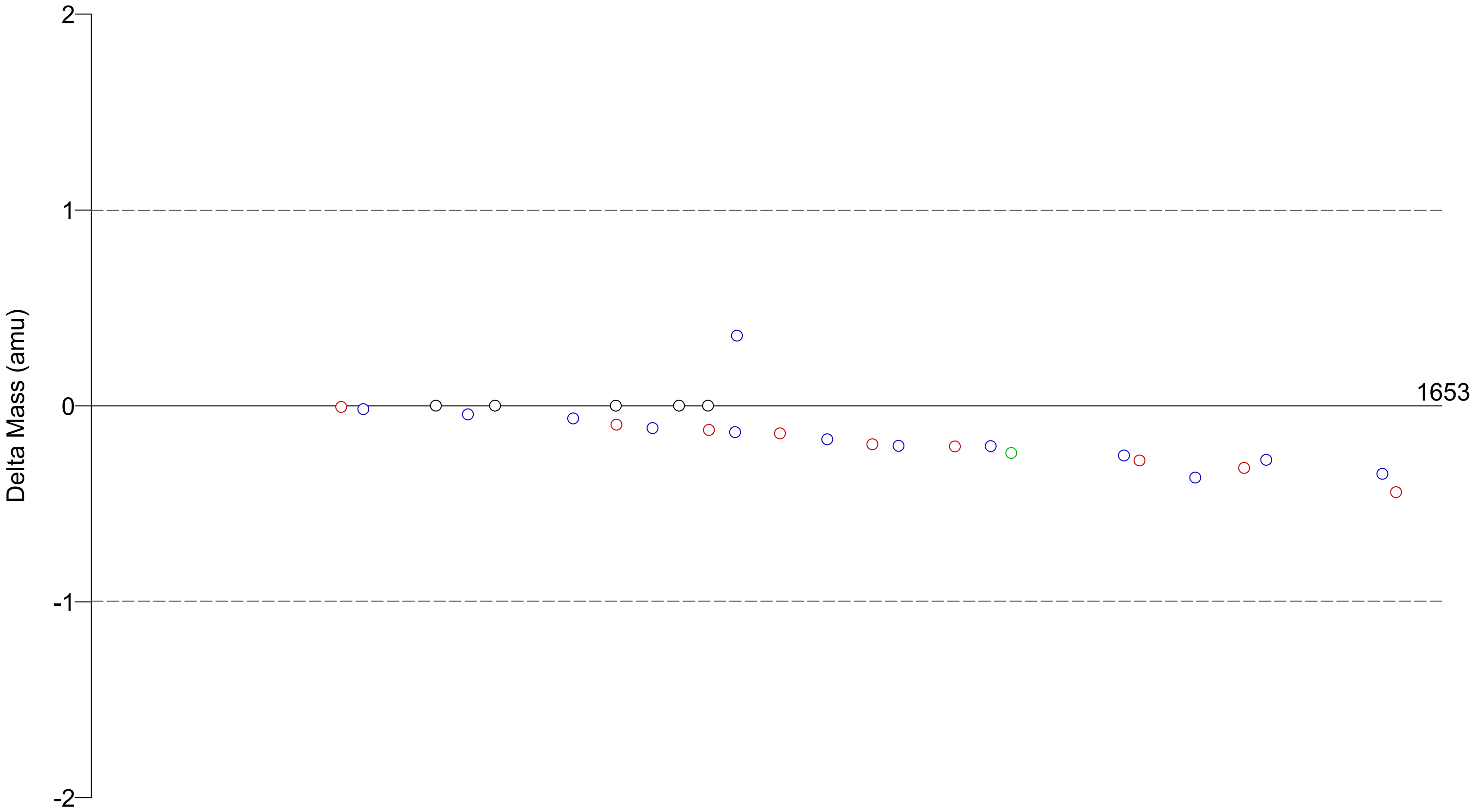


#19287468-1 NL: 1.22E5

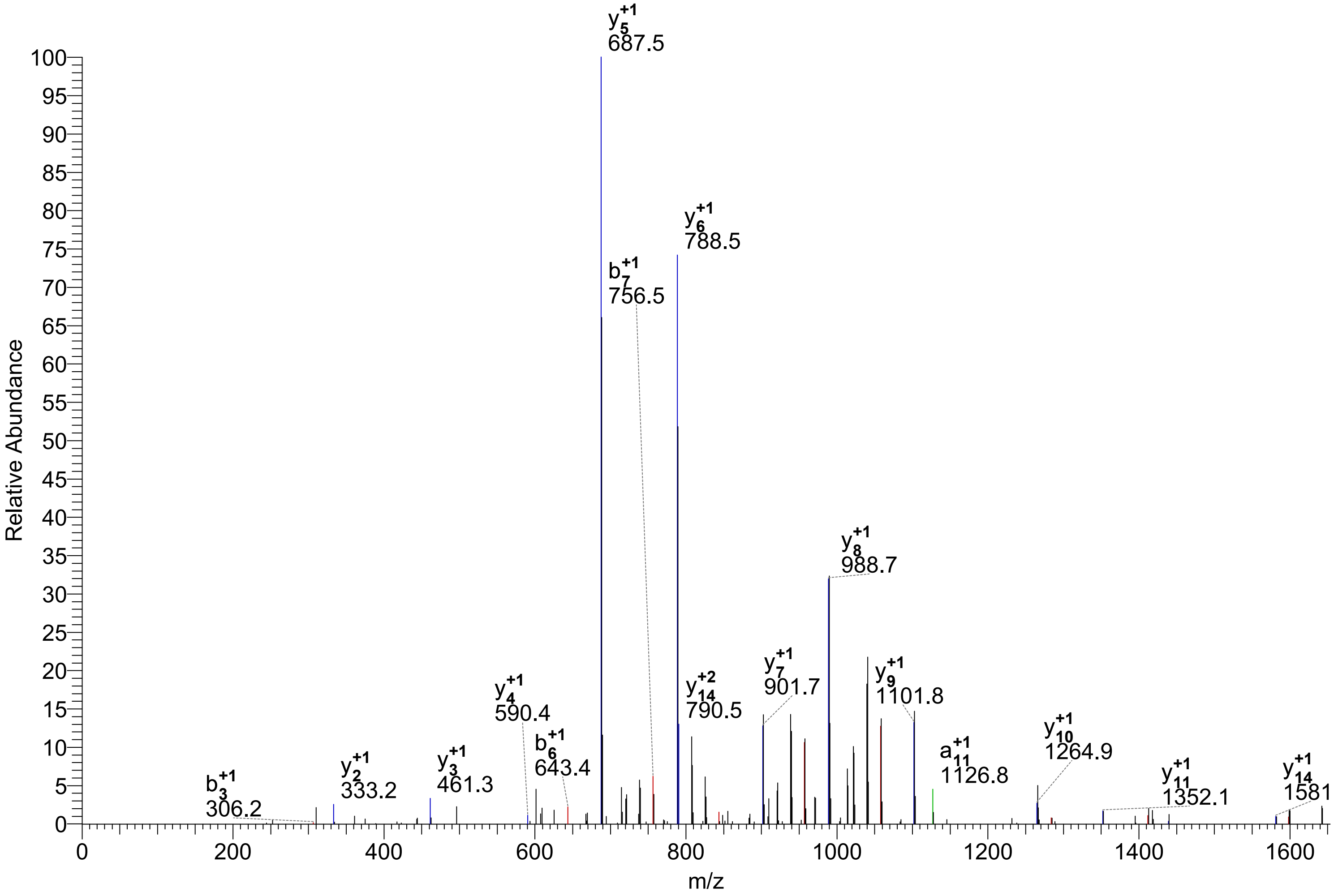


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00784935.1|TREMBL:Q6GMW3 Ta                                5e-005  10.2     0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

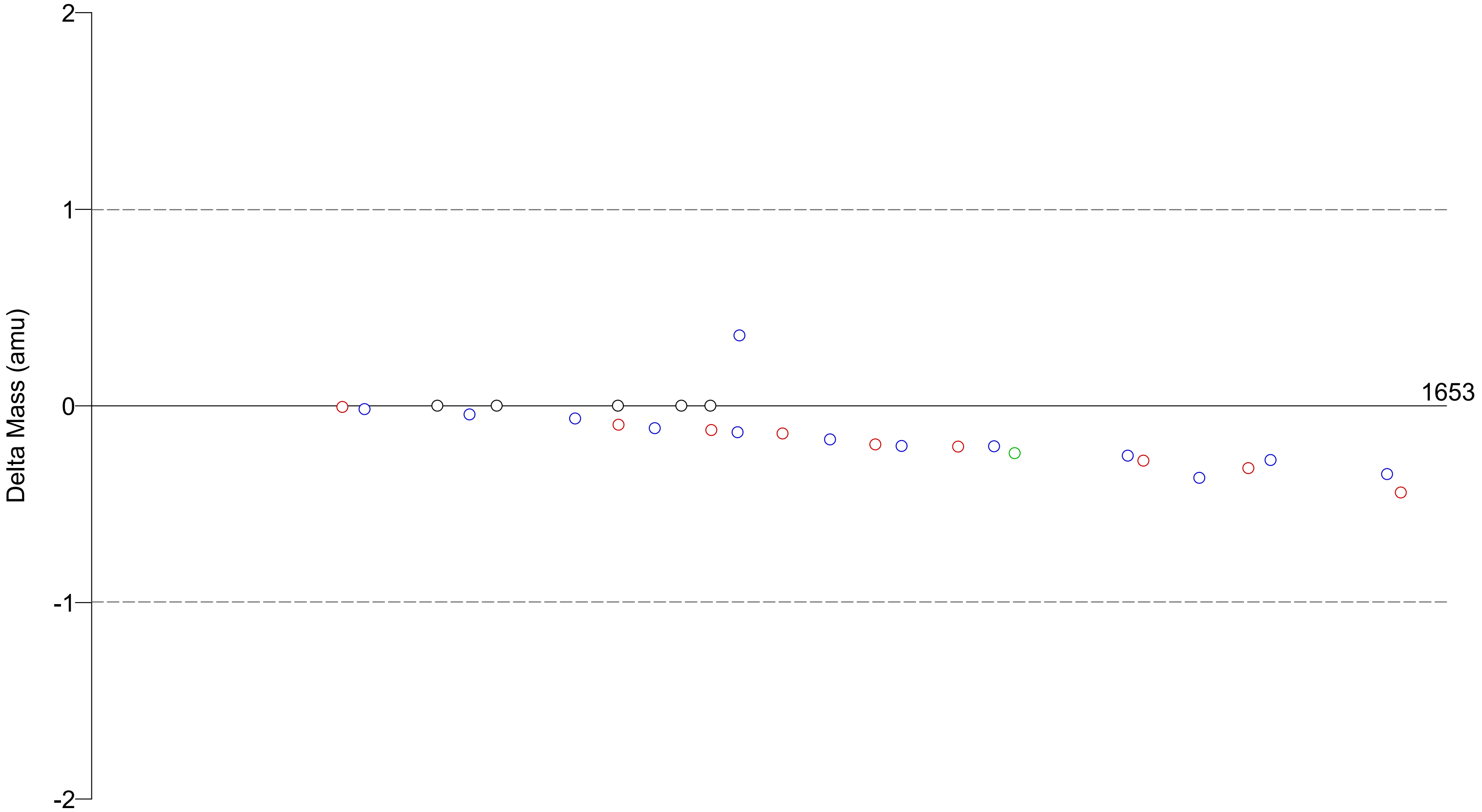


#19287468-1 NL: 1.22E5

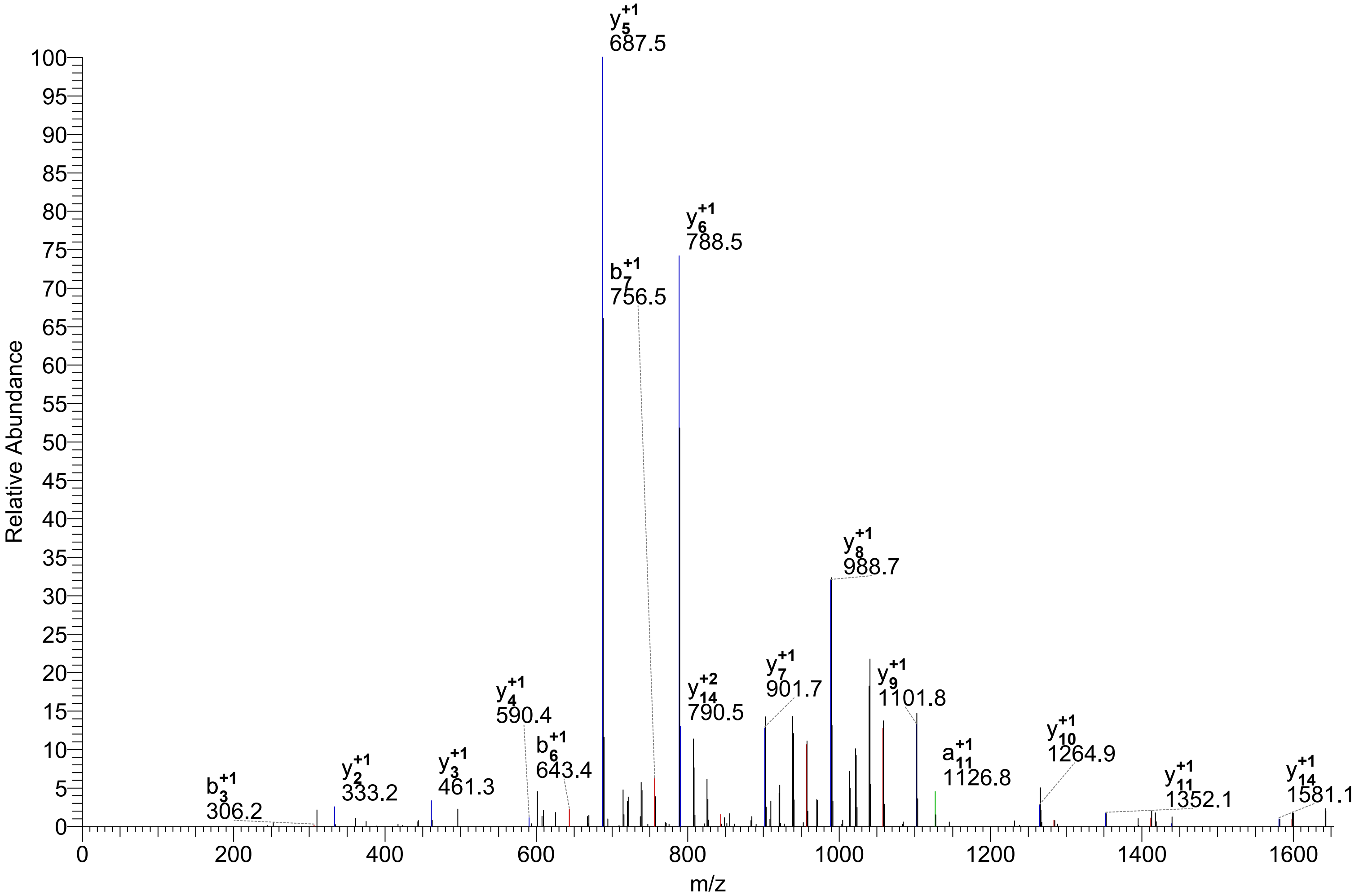


```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00788824.3|TREMBL:Q567P1;Q5                                     5e-005  10.2      0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                        1743.86    2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

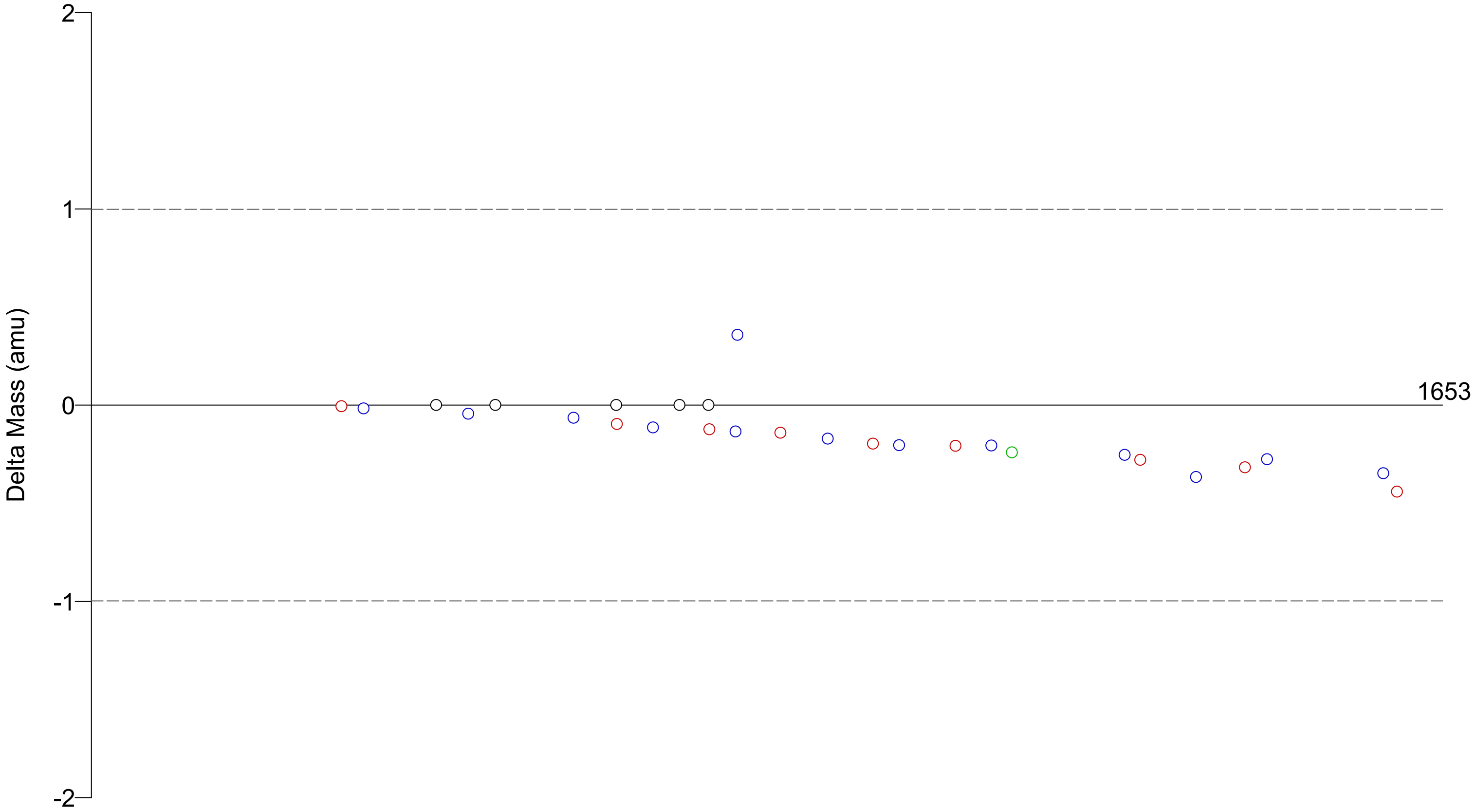


#19287468-1 NL: 1.22E5

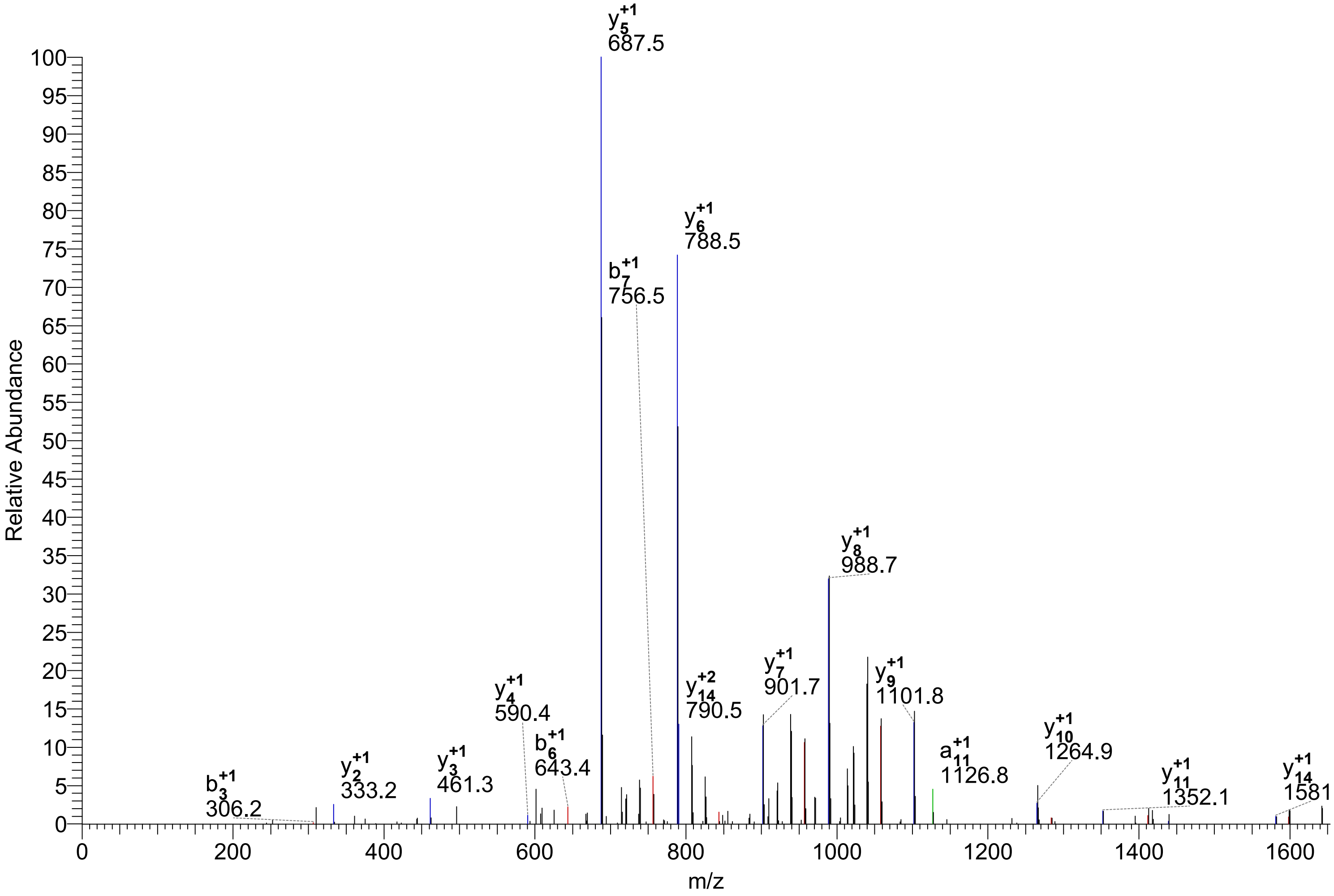


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00827875.1|TREMBL:A2MYD2;A2                                   5e-005  10.2     0.0        0
19287468 - 1  K.YAASSYLSLTPEQWK.S                       1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

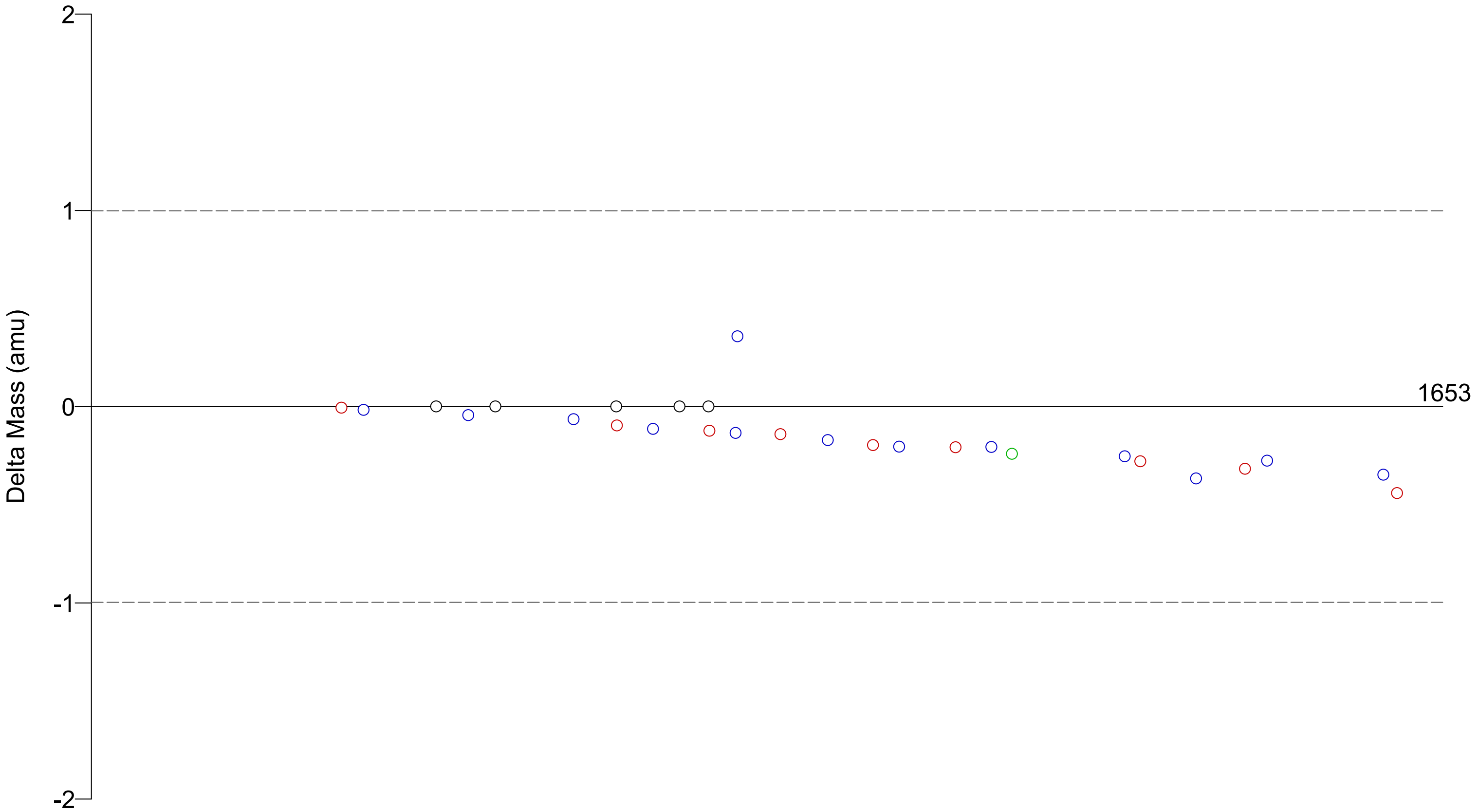


#19287468-1 NL: 1.22E5

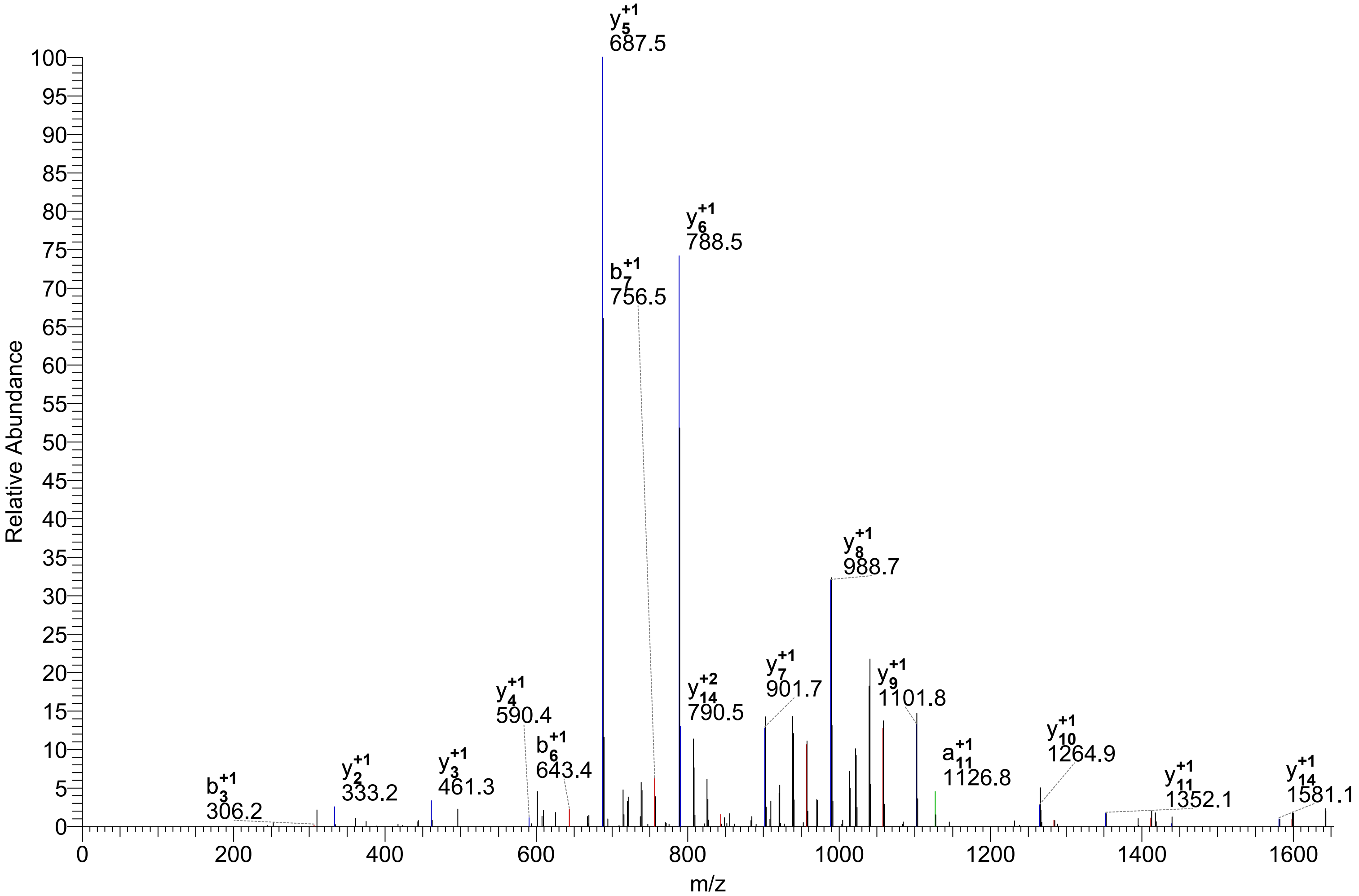


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                drawn    z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829640.1|TREMBL:Q6GMW4 Ta                                5e-005  10.2     0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                    1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

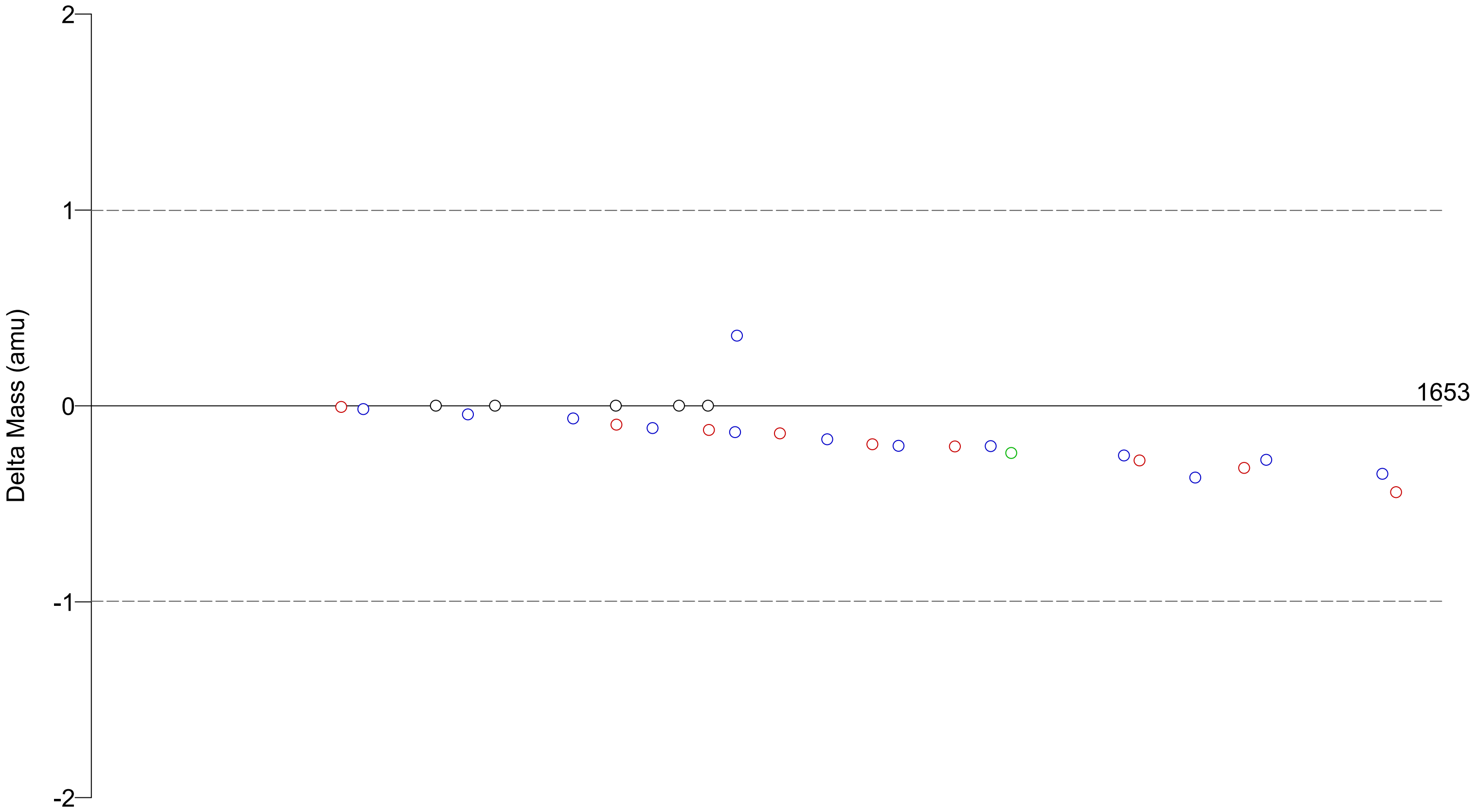


#19287468-1 NL: 1.22E5

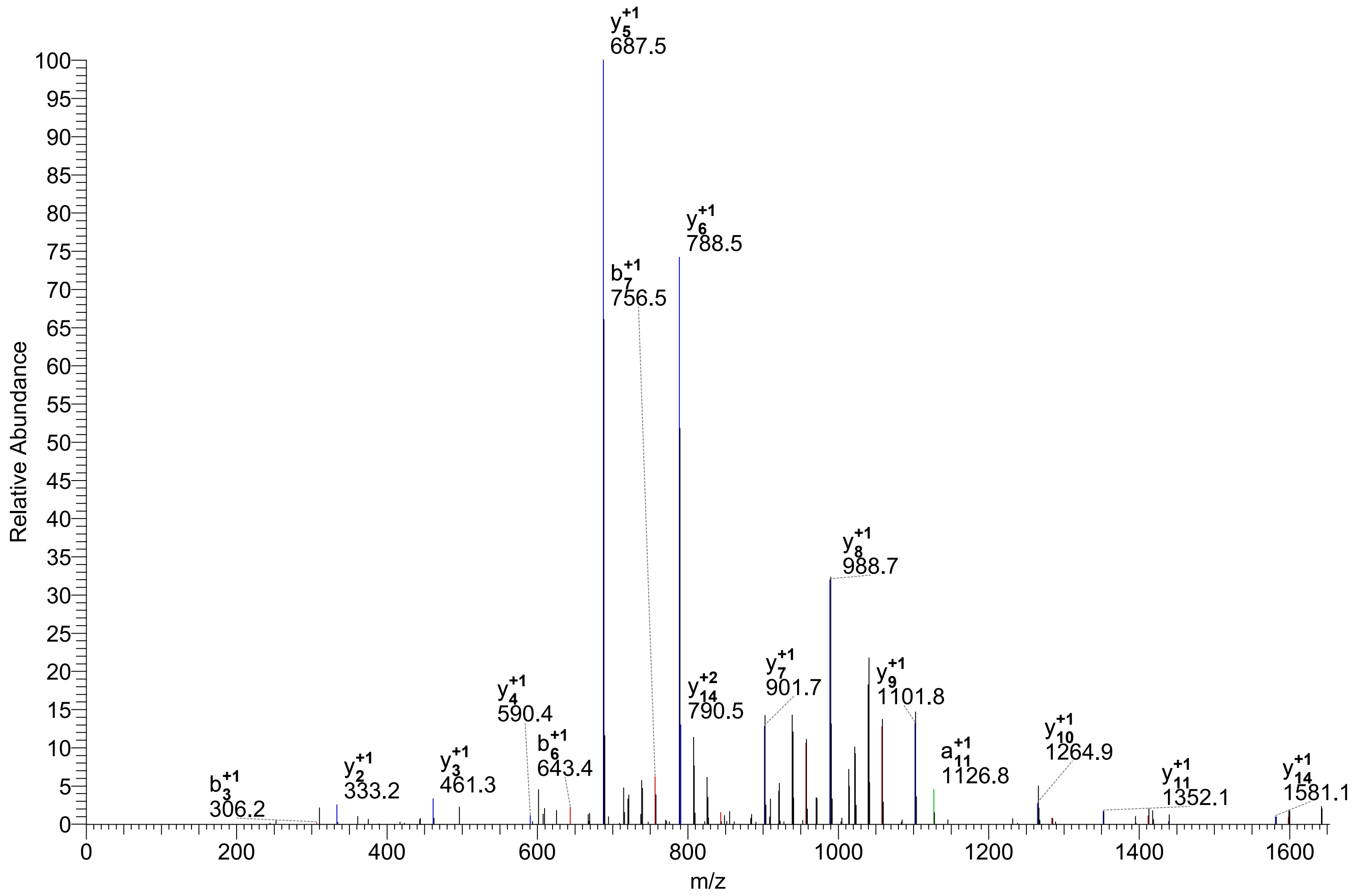


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00830047.1|TREMBL:A6NKU1|EN                                 5e-005  10.2     0.0        0
19287468 - 1  K.YAASSYLSLTPEQWK.S                      1743.86    2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                      1580.80
 A    278.15     306.14                                      1509.76
 S    365.18     393.18                                      1438.72
 S    452.21     480.21                                      1351.69
 Y    615.28     643.27                                      1264.66
 L    728.36     756.36                                      1101.59
 S    815.39     843.39                                       988.51
 L    928.48     956.47                                       901.48
 T   1029.53    1057.52                                       788.39
 P   1126.58    1154.57                                       687.35
 E   1255.62    1283.62                                       590.29
 Q   1383.68    1411.67                                       461.25
 W   1569.76    1597.75                                       333.19
 K                                                            147.11
```

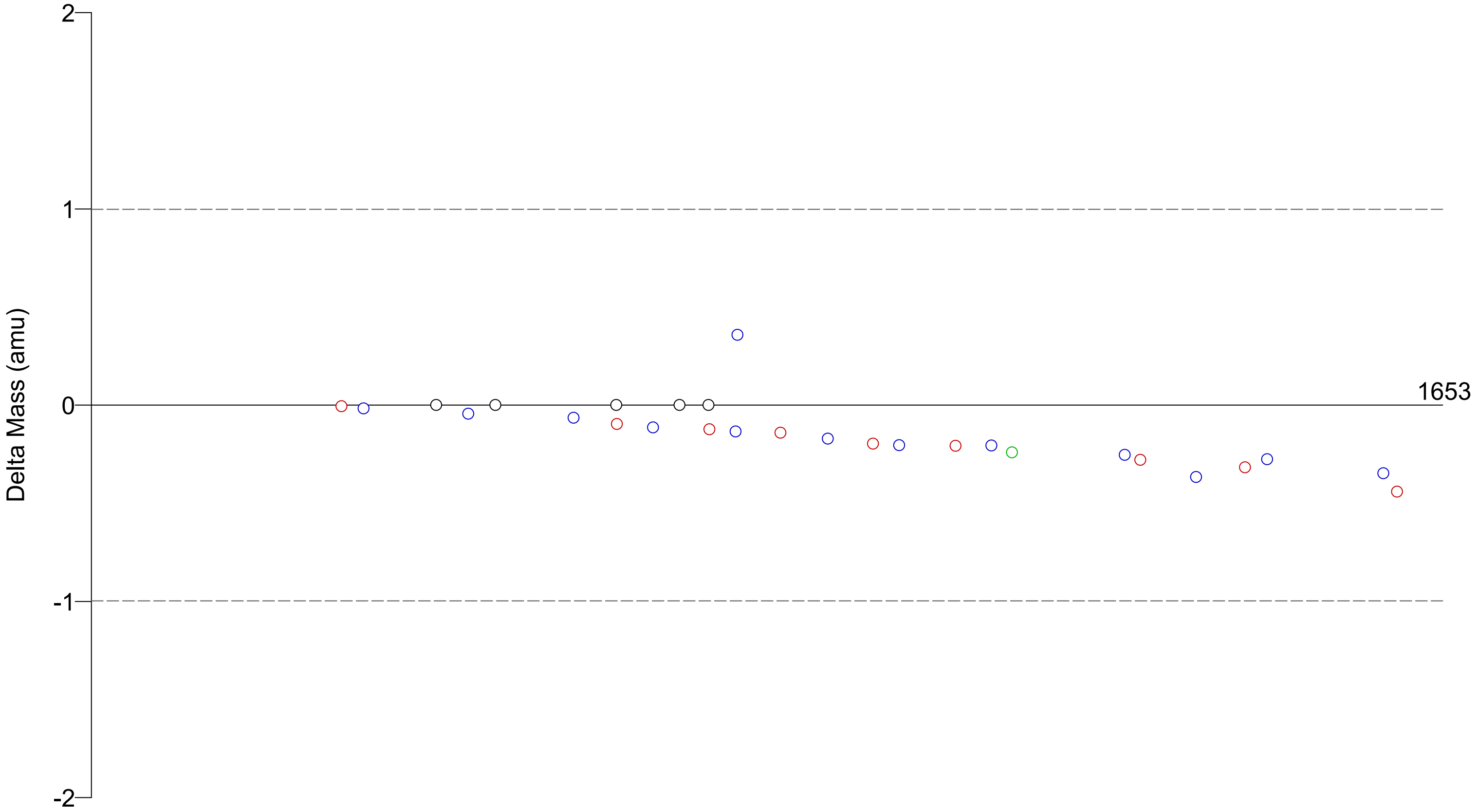


#19287468-1 NL: 1.22E5

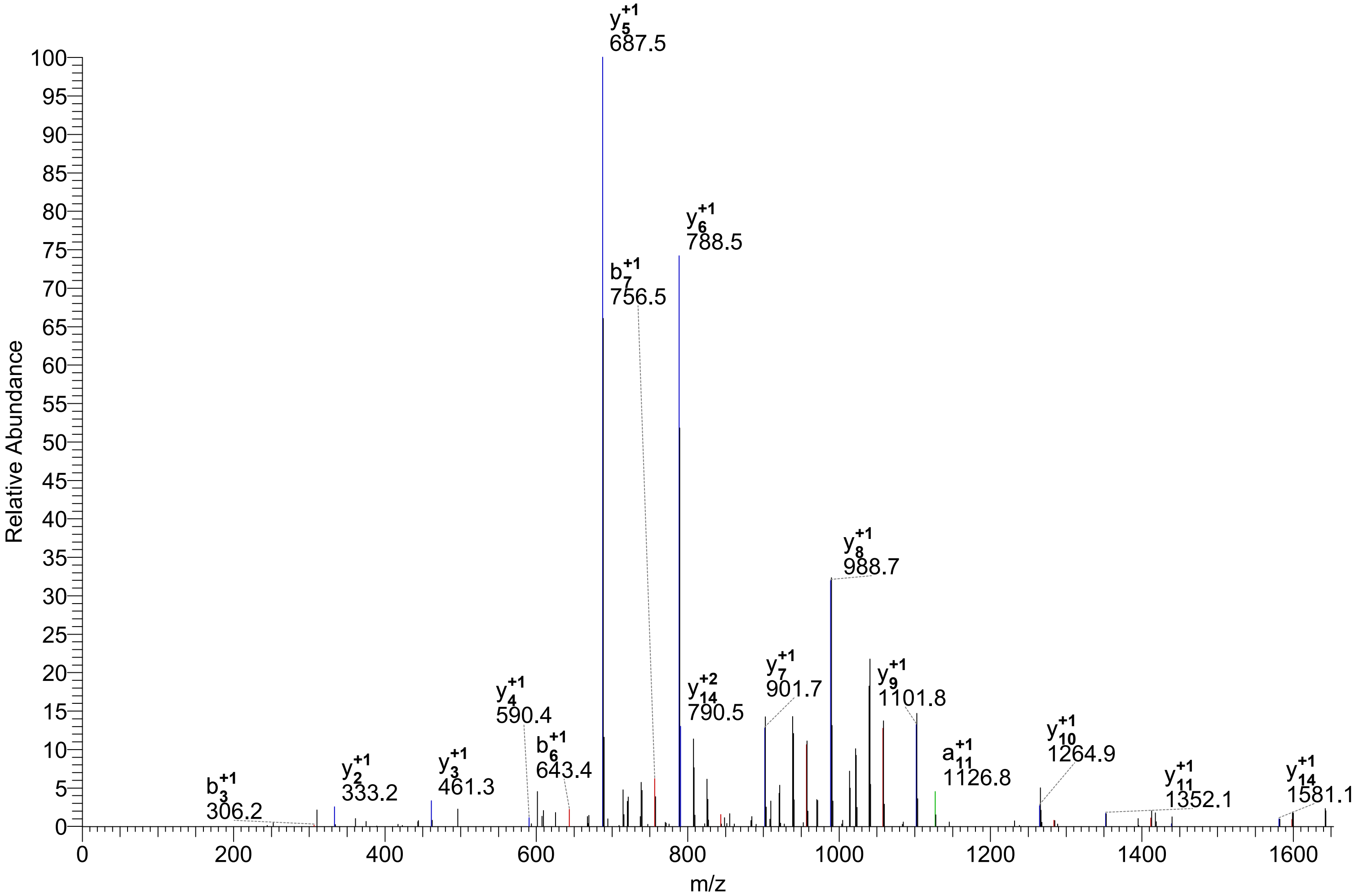


```
Reference                                                        P      Score   Coverage   Accession
Scan(s)        Sequence                              MH+      z    P       XC   DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00852577.2|TREMBL:A0M8Q9|EN                                 5e-005  10.2     0.0        0
19287468 - 1  K.YAASSYLSLTPEQWK.S                   1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

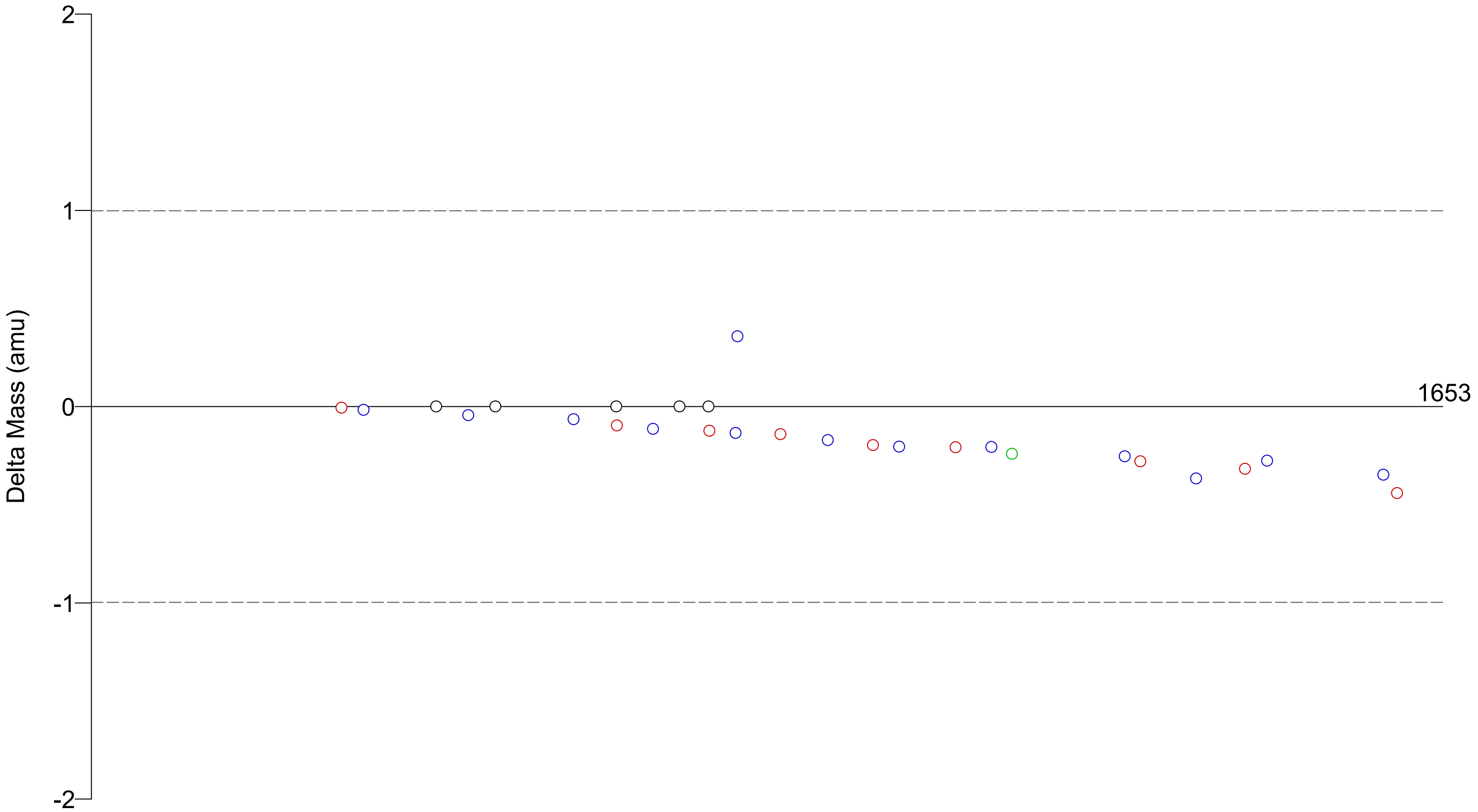


#19287468-1 NL: 1.22E5

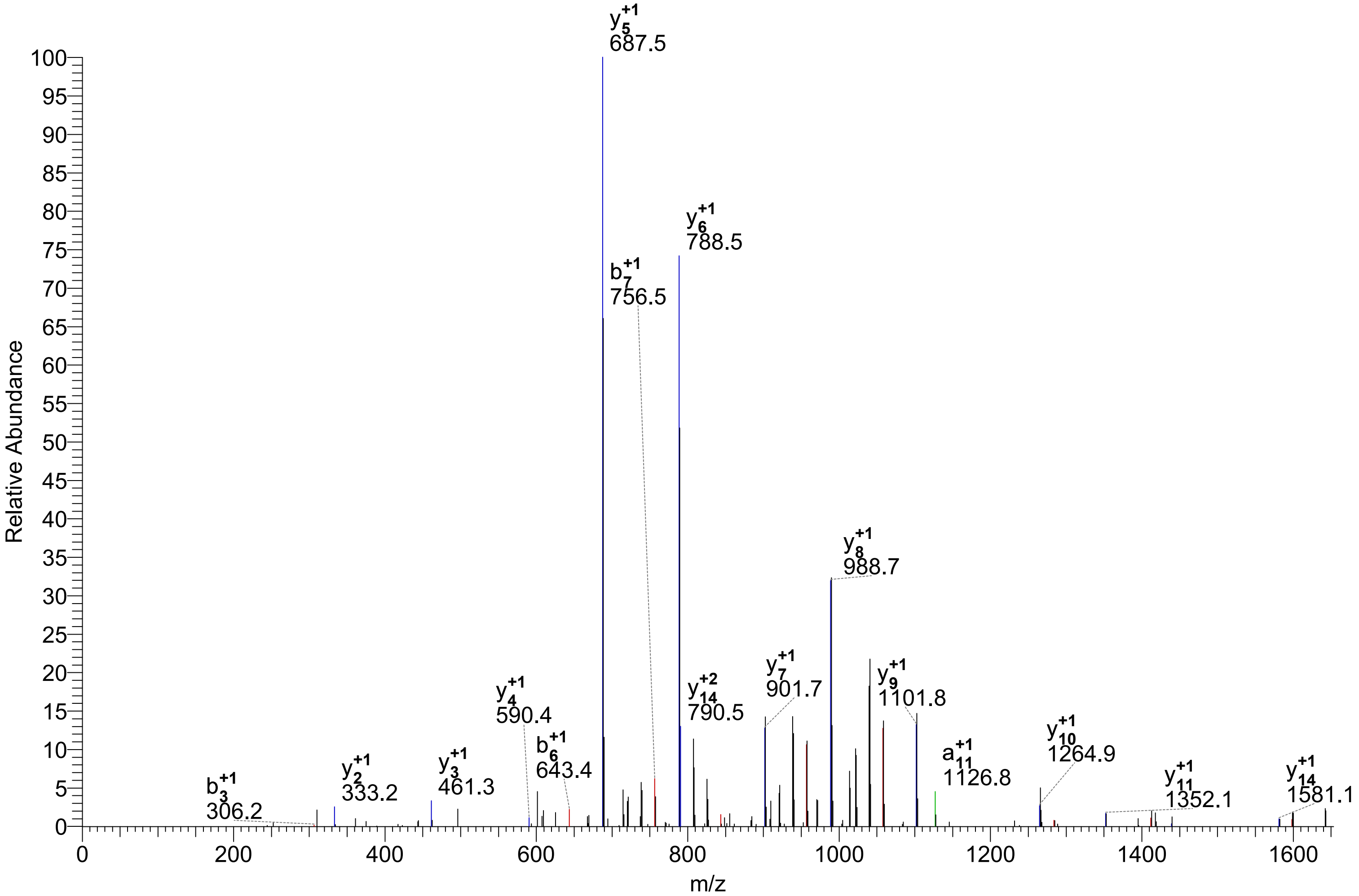


```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                              MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00887169.2|TREMBL:A2MYD0;A2                                5e-005  10.2     0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

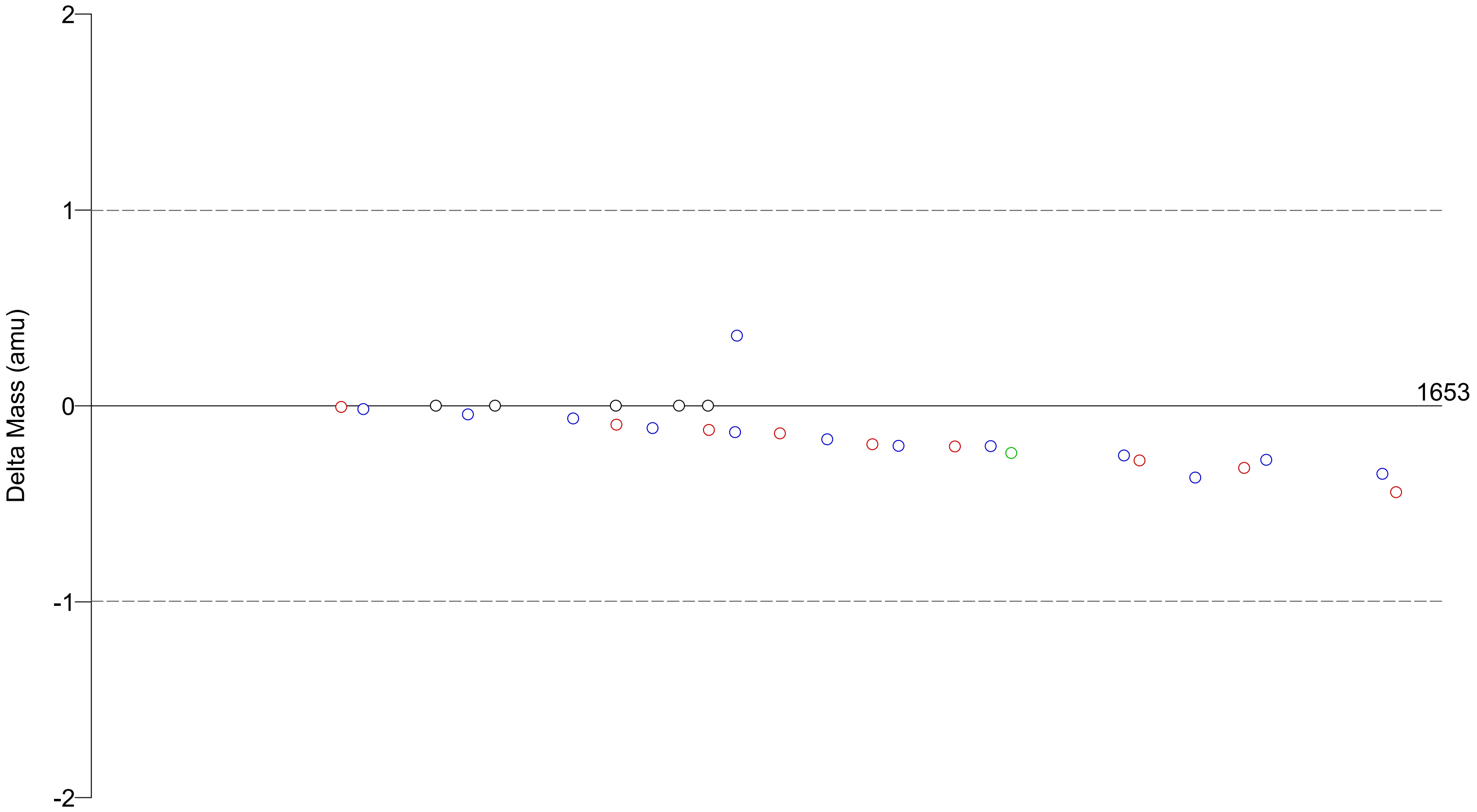


#19287468-1 NL: 1.22E5

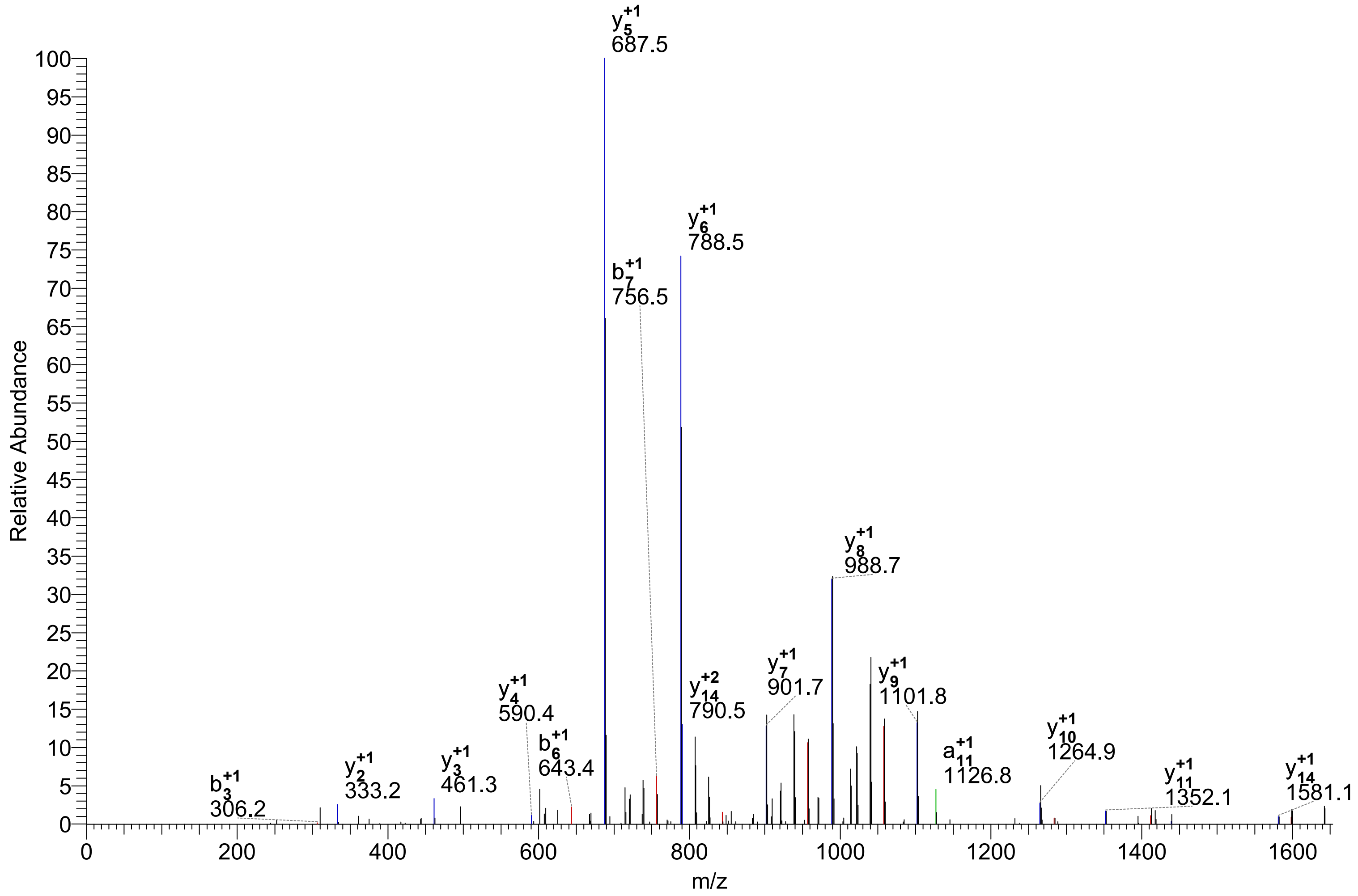


```
Reference                                                              P     Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00893178.1|ENSEMBL:ENSP0000                                   5e-005  10.2     0.0       0
19287468 - 1  K.YAASSYLSLTPEQWK.S                     1743.86   2  5e-005  3.671  0.433   421.7  1   16/42   15

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 A    207.11     235.11                                     1580.80
 A    278.15     306.14                                     1509.76
 S    365.18     393.18                                     1438.72
 S    452.21     480.21                                     1351.69
 Y    615.28     643.27                                     1264.66
 L    728.36     756.36                                     1101.59
 S    815.39     843.39                                      988.51
 L    928.48     956.47                                      901.48
 T   1029.53    1057.52                                      788.39
 P   1126.58    1154.57                                      687.35
 E   1255.62    1283.62                                      590.29
 Q   1383.68    1411.67                                      461.25
 W   1569.76    1597.75                                      333.19
 K                                                           147.11
```

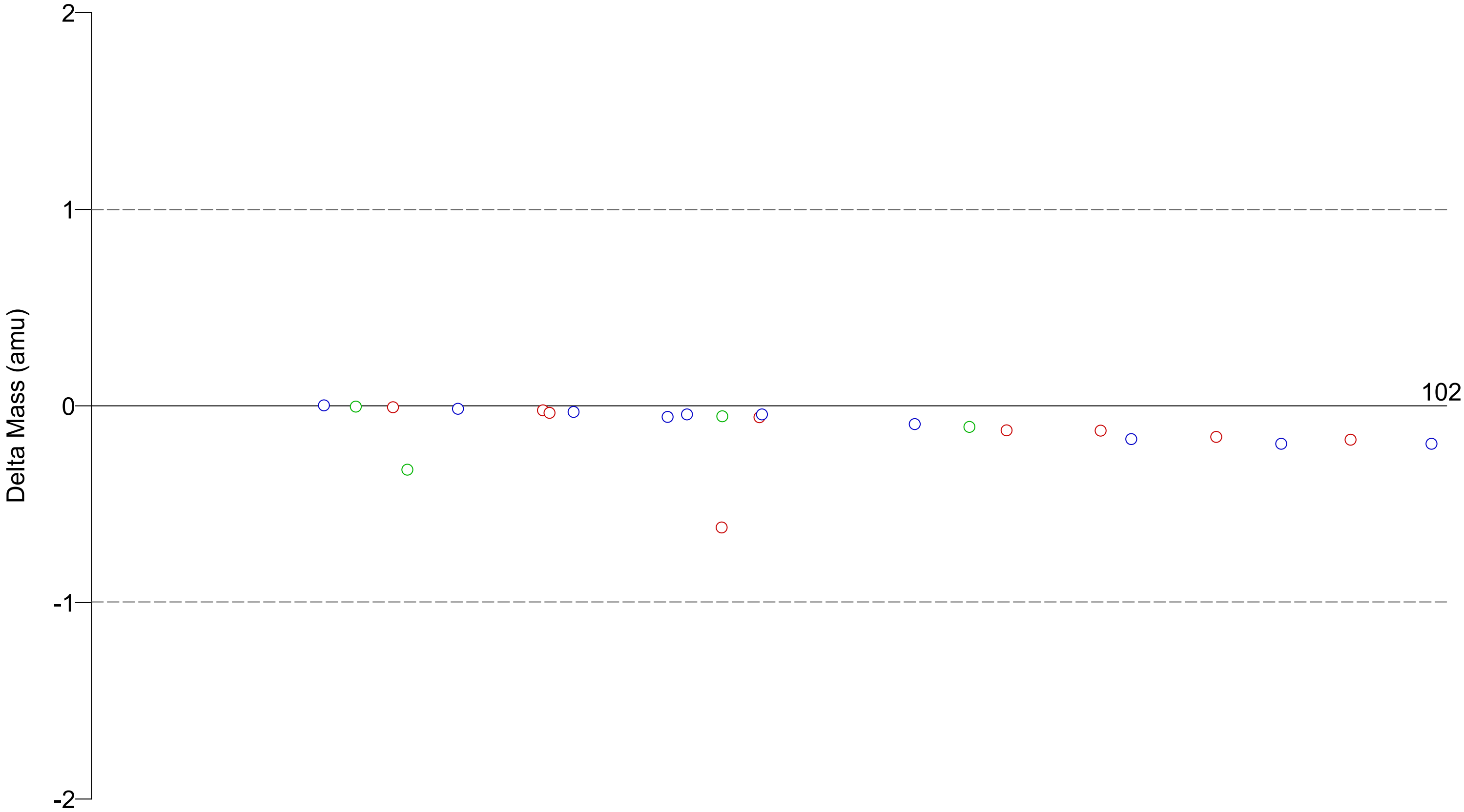


#19287468-1 NL: 1.22E5

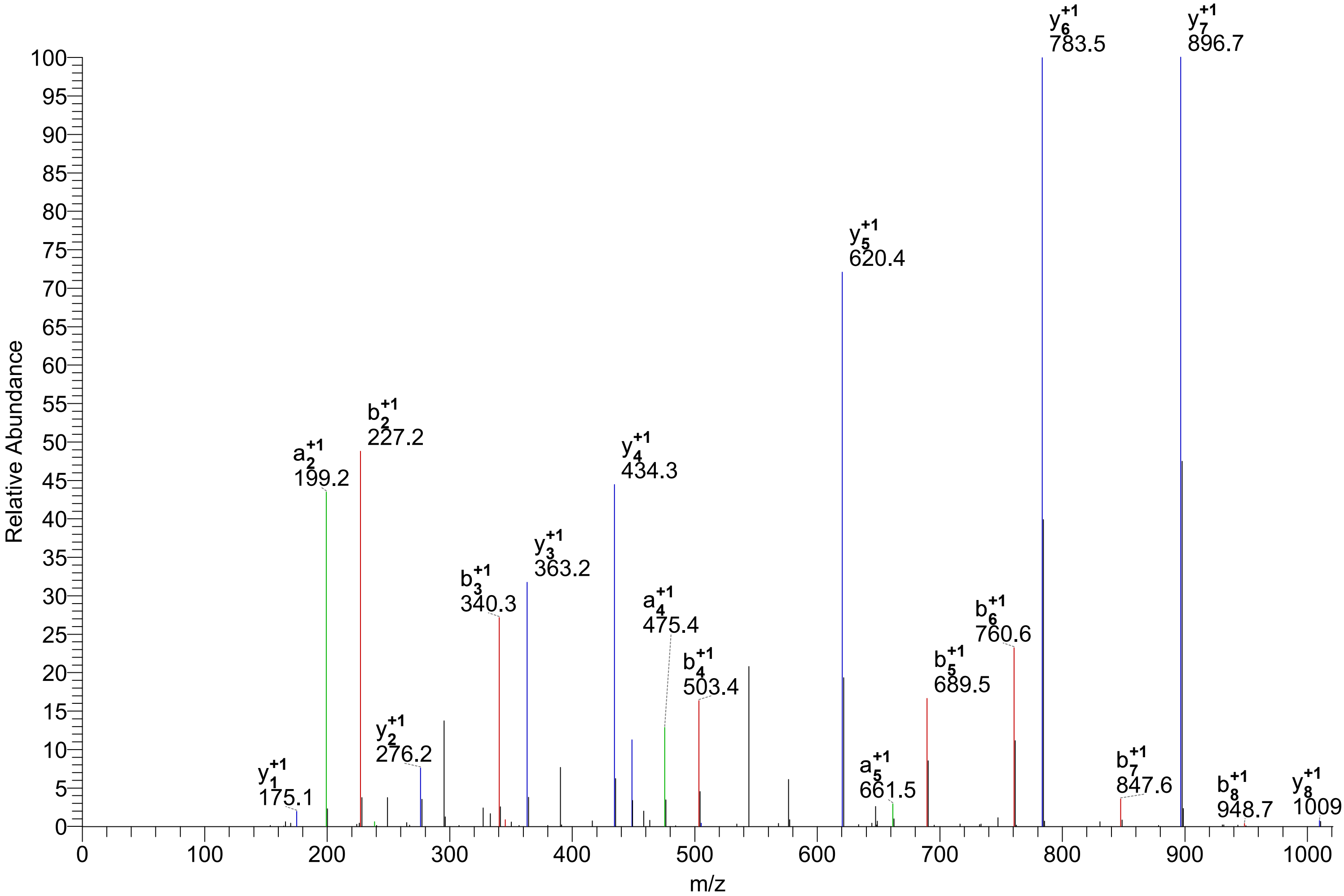


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z    P        XC  DeltaCn   Sp    RSp  Ions  Count

IPI:IPI00026197.7|SWISS-PROT:P06312|ENSEMBL:ENSP00000374778|H-     5e-005  10.2      0.0        0
2118291816 -  K.LLIYWASTR.E                            1122.63   2  5e-005  3.929  0.542   1464.4 1   19/24   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 561.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L    86.10     114.09
 L   199.18     227.18                                      1009.55
 I   312.26     340.26                                       896.46
 Y   475.33     503.32                                       783.38
 W   661.41     689.40                                       620.32
 A   732.44     760.44                                       434.24
 S   819.48     847.47                                       363.20
 T   920.52     948.52                                       276.17
 R                                                           175.12
```

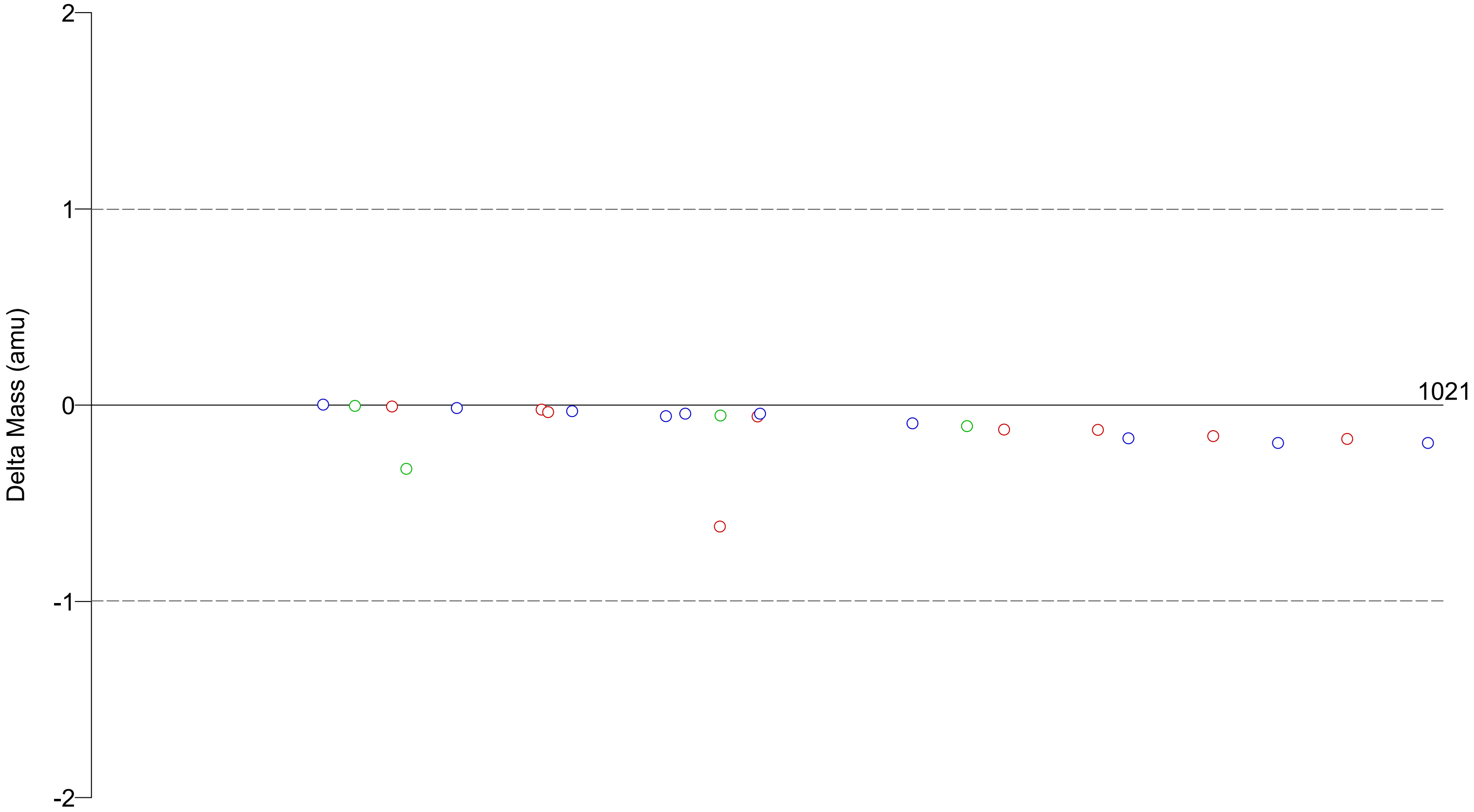


#2118291816-26226248 NL: 1.43E5

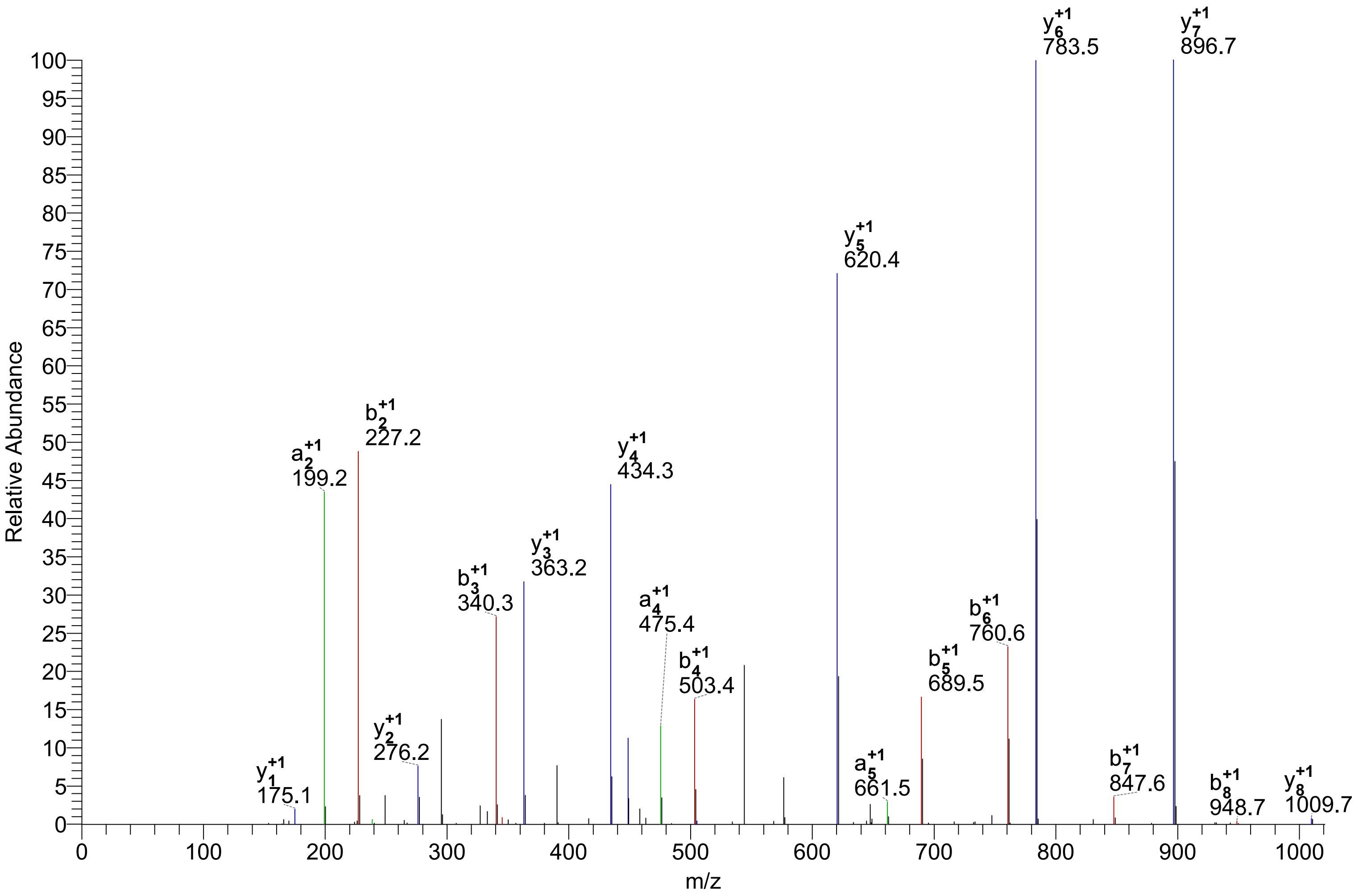


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00385143.1|TREMBL:Q9NP29 Ta                                   5e-005  10.2     0.0       0
2118291816 -  K.LLIYWASTR.E                           1122.63   2   5e-005  3.929  0.542   1464.4 1   19/24   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 561.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1009.55
 I    312.26     340.26                                      896.46
 Y    475.33     503.32                                      783.38
 W    661.41     689.40                                      620.32
 A    732.44     760.44                                      434.24
 S    819.48     847.47                                      363.20
 T    920.52     948.52                                      276.17
 R                                                           175.12
```

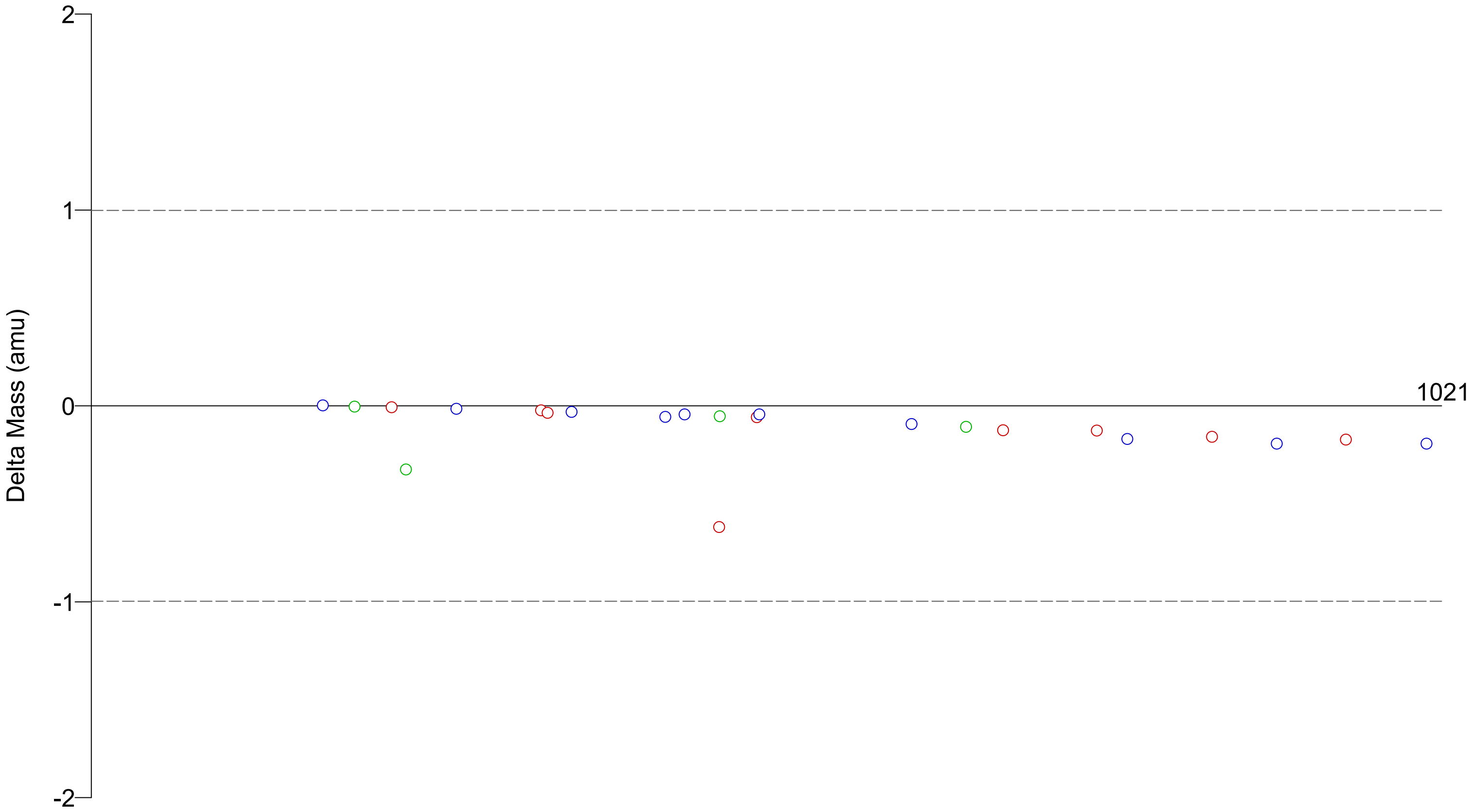


#2118291816-26226248 NL: 1.43E5

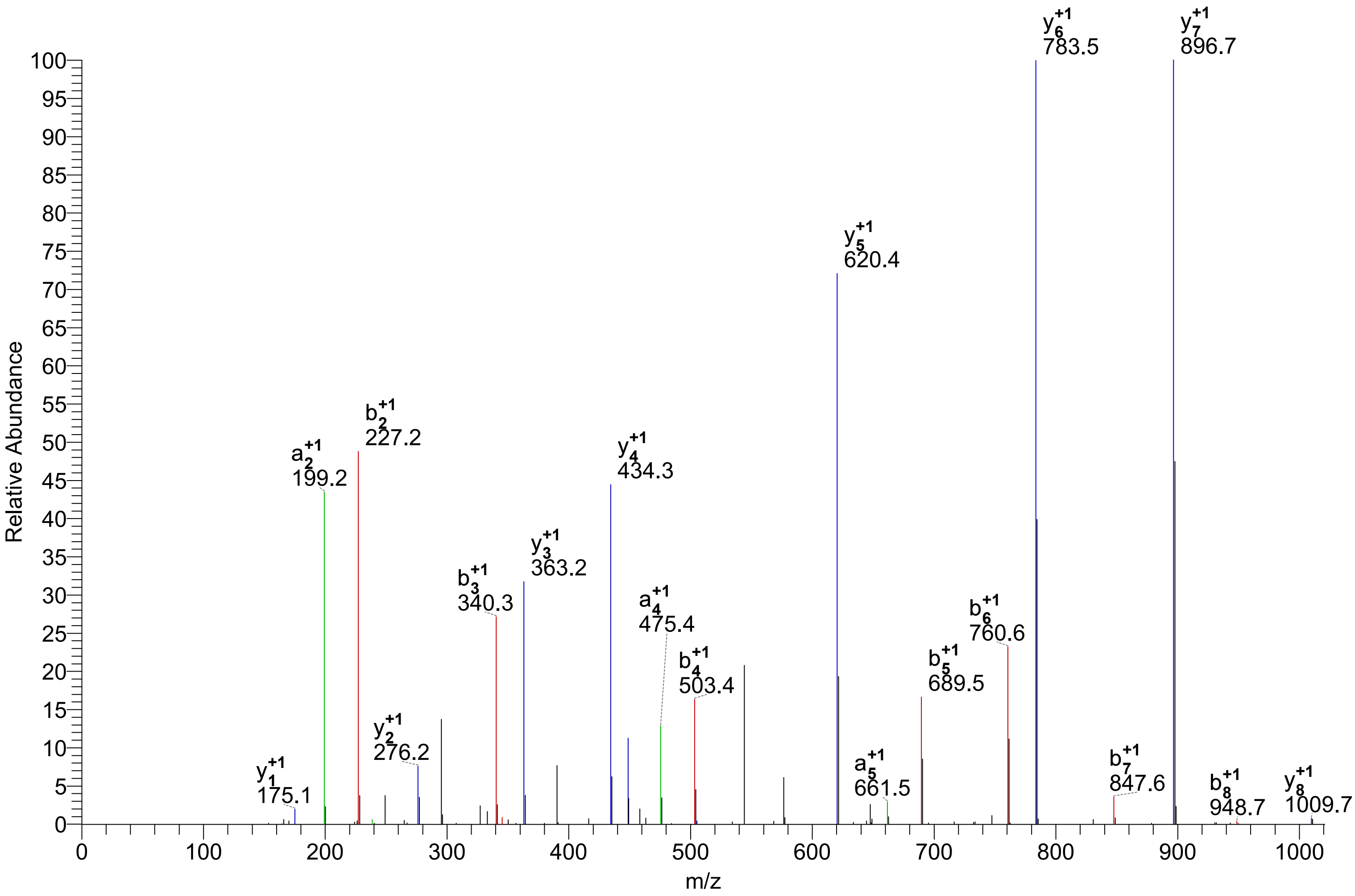


```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z     P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00386132.1|SWISS-PROT:P0631                                        5e-005  10.2     0.0       0
2118291816 -  K.LLIYWASTR.E                               1122.63    2  5e-005  3.929  0.542   1464.4 1   19/24   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 561.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions     Y ions     Y* ions     Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                      1009.55
 I    312.26     340.26                                       896.46
 Y    475.33     503.32                                       783.38
 W    661.41     689.40                                       620.32
 A    732.44     760.44                                       434.24
 S    819.48     847.47                                       363.20
 T    920.52     948.52                                       276.17
 R                                                            175.12
```

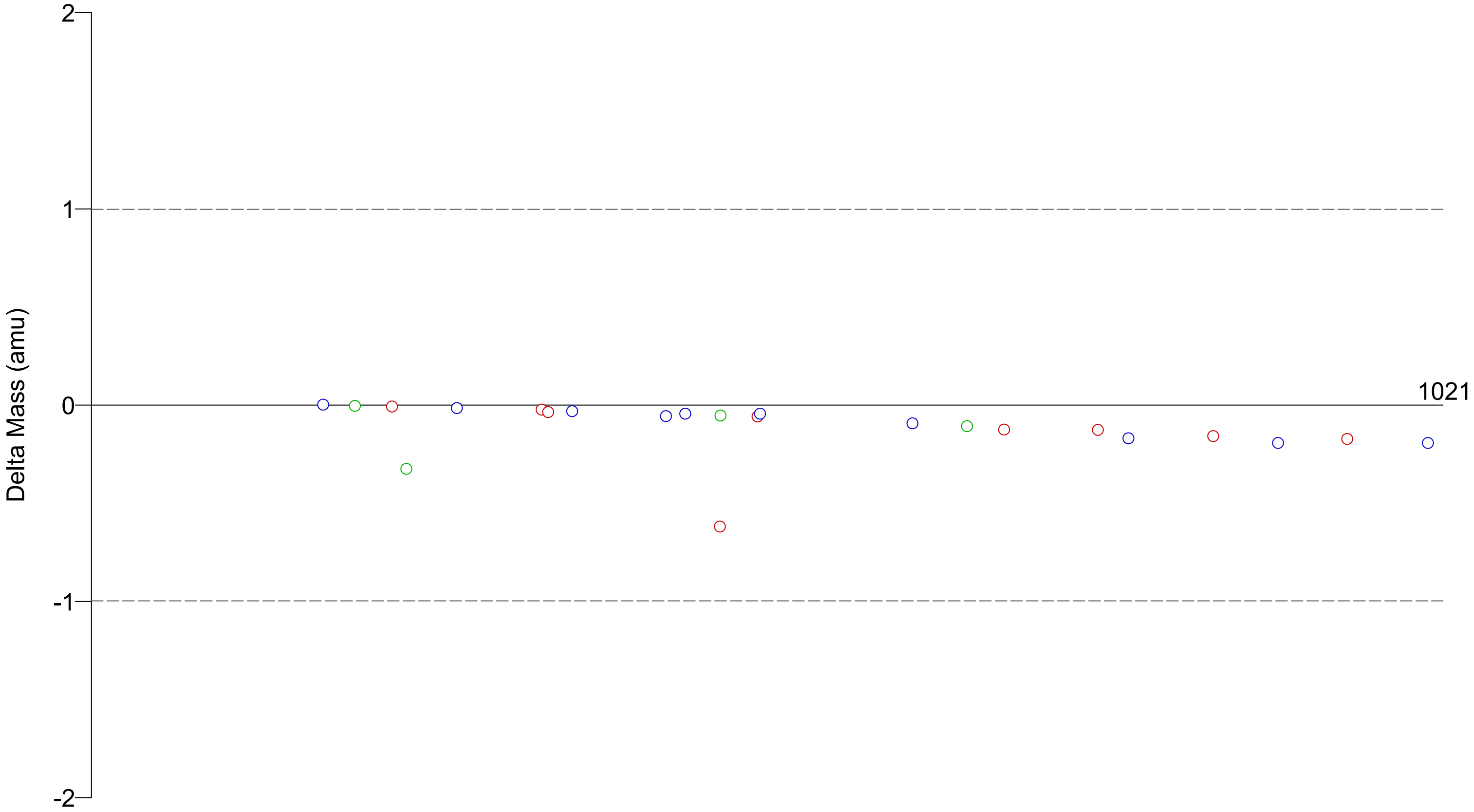


#2118291816-26226248 NL: 1.43E5

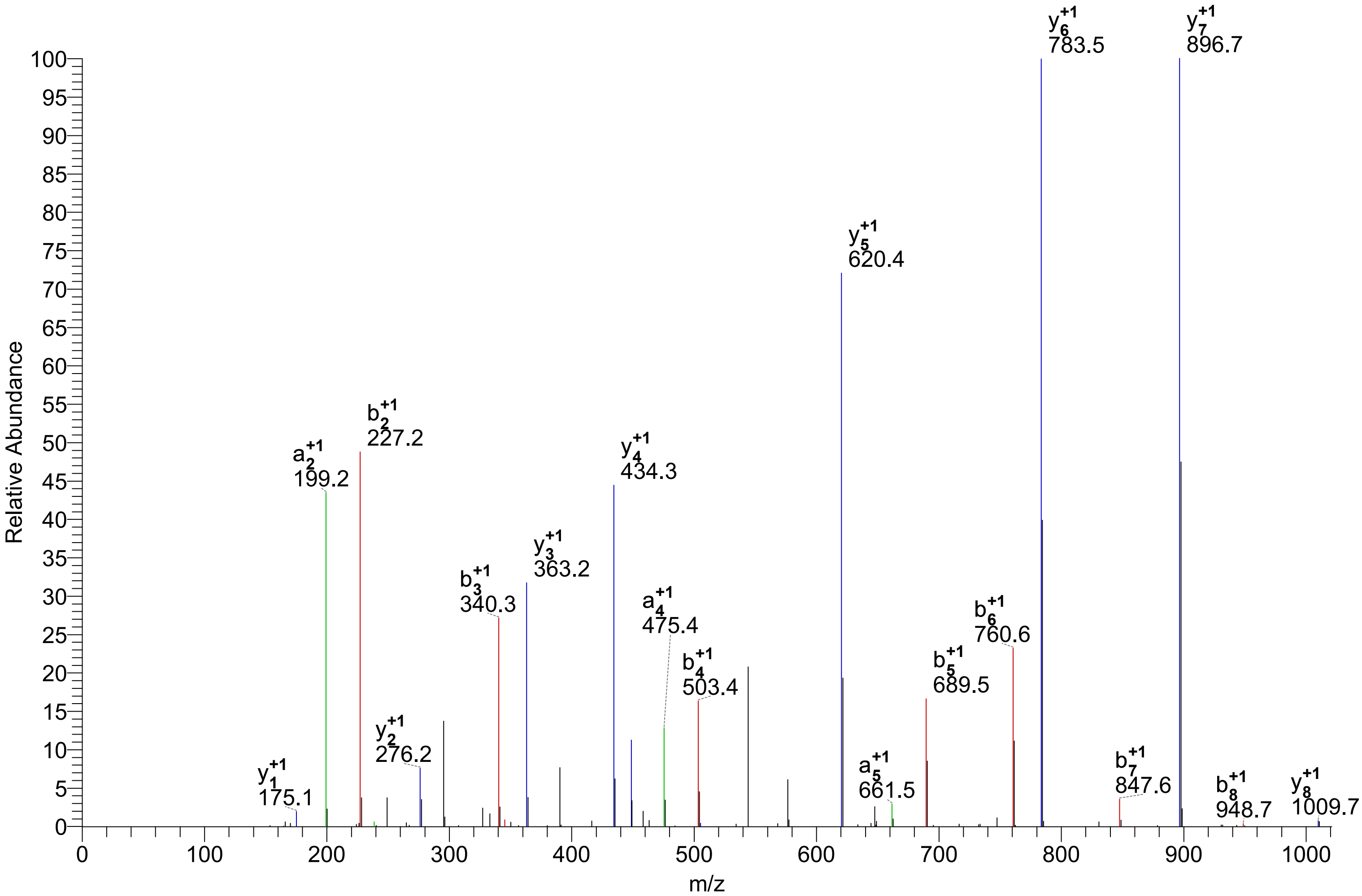


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00386133.1|SWISS-PROT:P0631                                   5e-005  10.2     0.0       0
2118291816 -  K.LLIYWASTR.E                           1122.63   2  5e-005  3.929  0.542   1464.4 1   19/24   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 561.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1009.55
 I    312.26     340.26                                      896.46
 Y    475.33     503.32                                      783.38
 W    661.41     689.40                                      620.32
 A    732.44     760.44                                      434.24
 S    819.48     847.47                                      363.20
 T    920.52     948.52                                      276.17
 R                                                           175.12
```

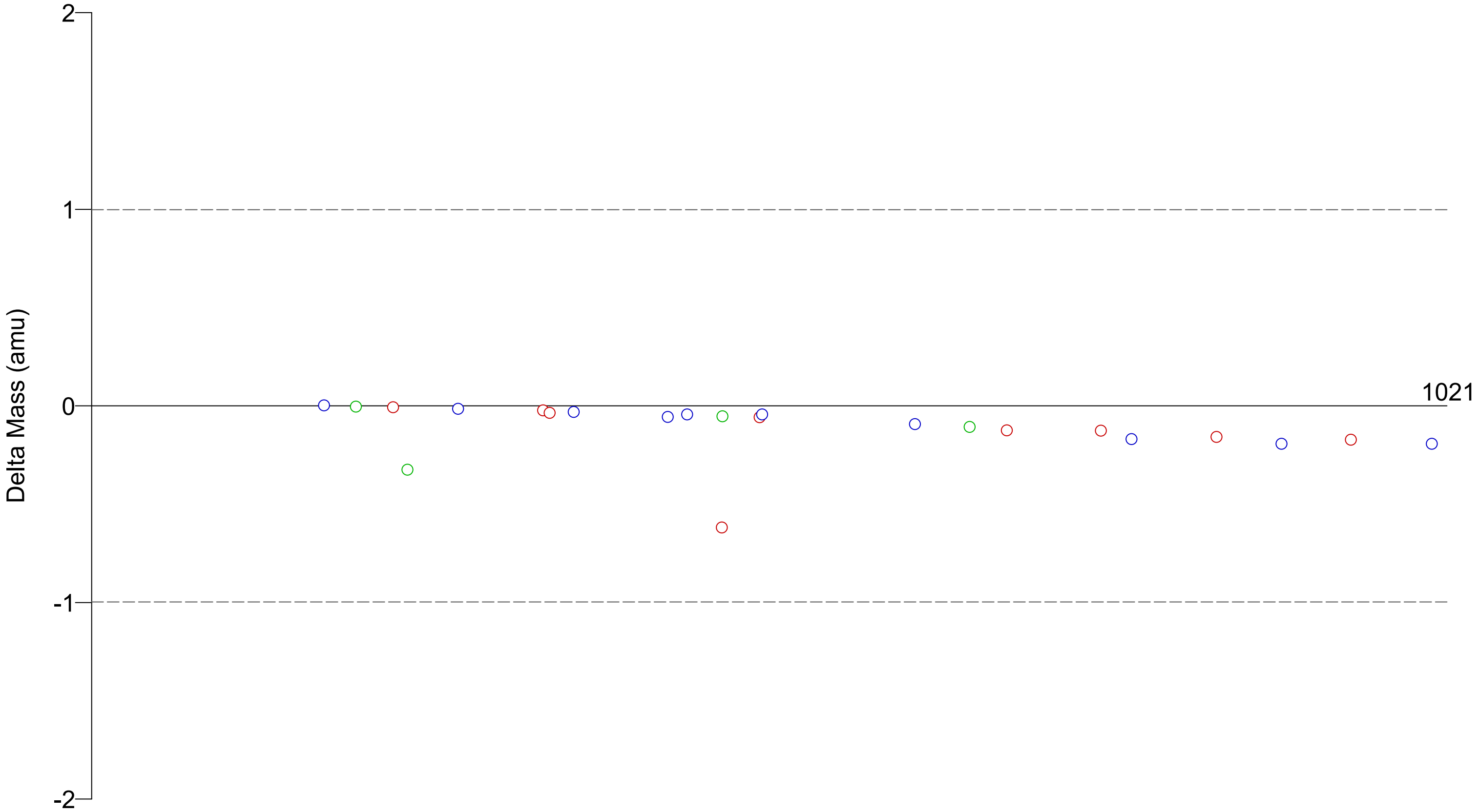


#2118291816-26226248 NL: 1.43E5

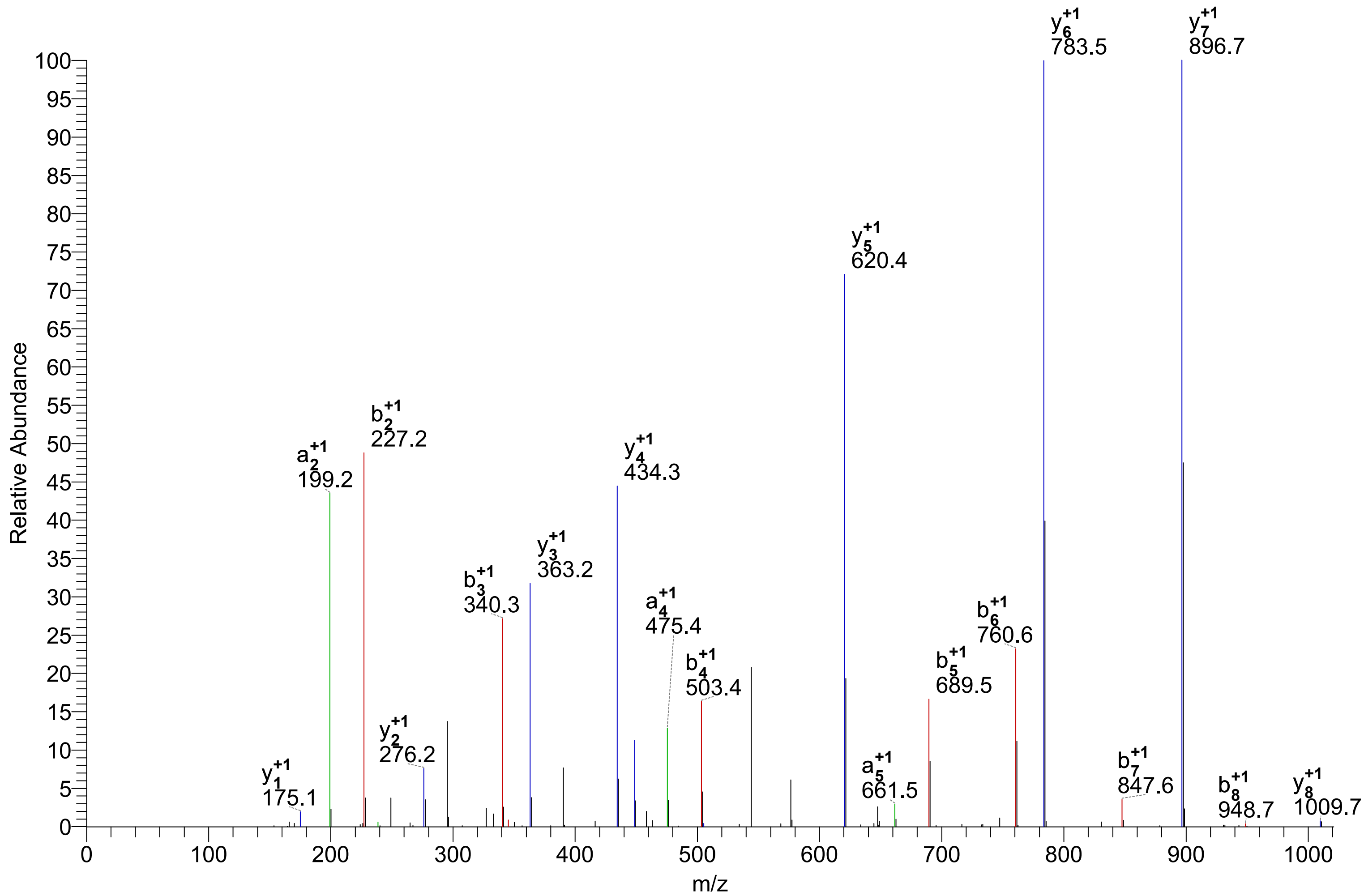


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00387120.1|SWISS-PROT:P0162                                5e-005  10.2     0.0       0
2118291816 -  K.LLIYWASTR.E                          1122.63   2  5e-005  3.929  0.542   1464.4 1   19/24   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 561.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions    Y ions    Y* ions     Yo ions     Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1009.55
 I    312.26     340.26                                      896.46
 Y    475.33     503.32                                      783.38
 W    661.41     689.40                                      620.32
 A    732.44     760.44                                      434.24
 S    819.48     847.47                                      363.20
 T    920.52     948.52                                      276.17
 R                                                           175.12
```

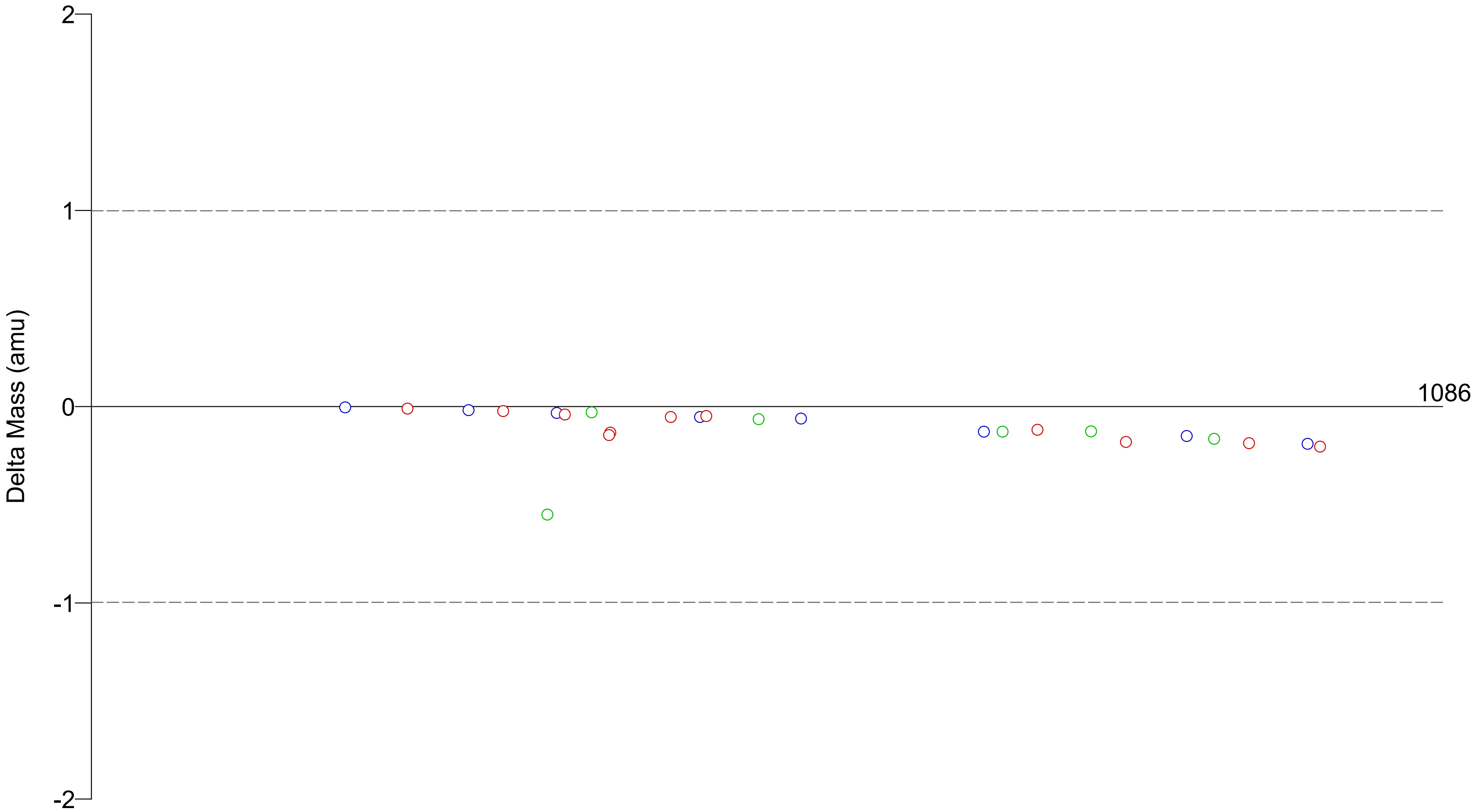


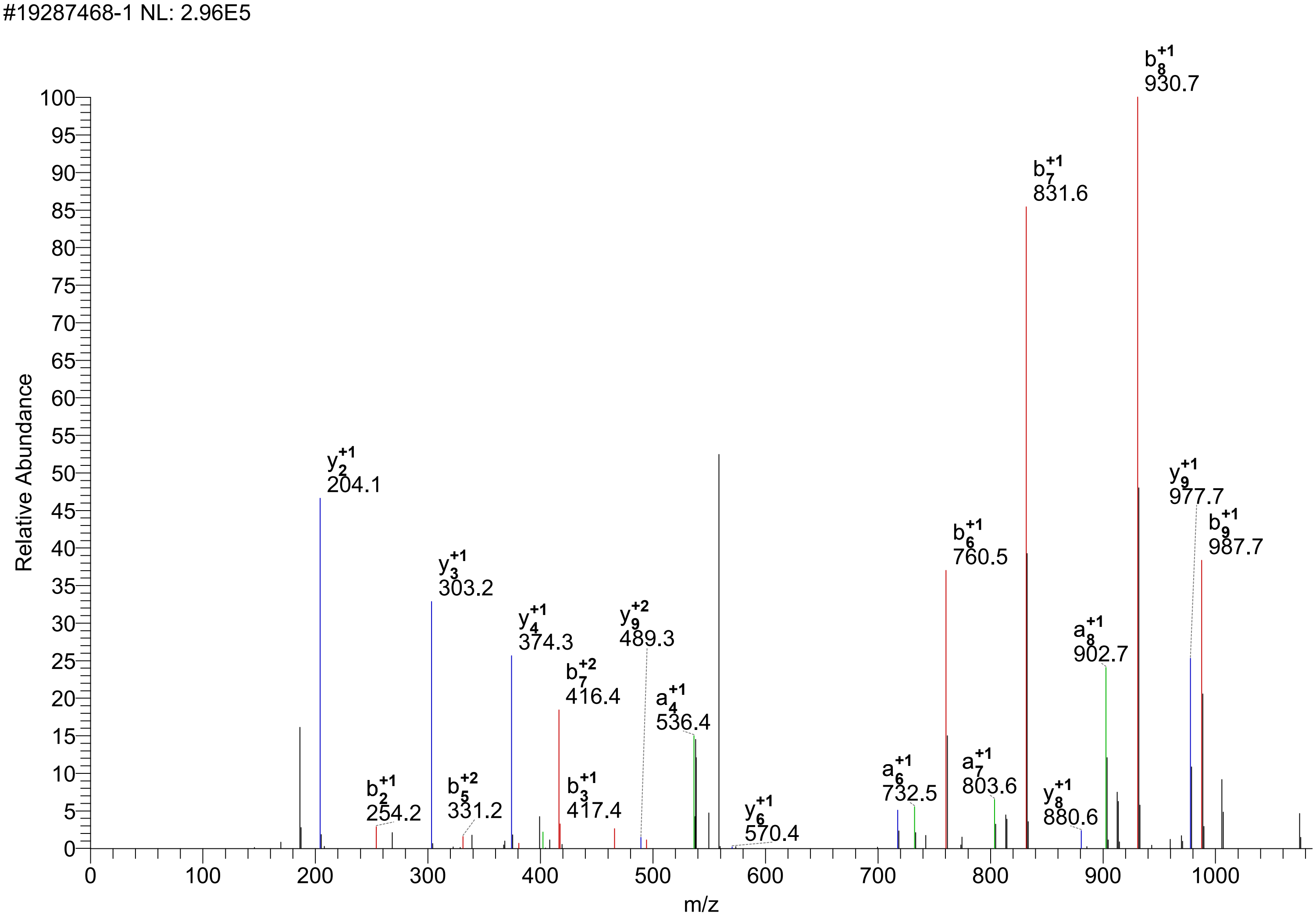
#2118291816-26226248 NL: 1.43E5



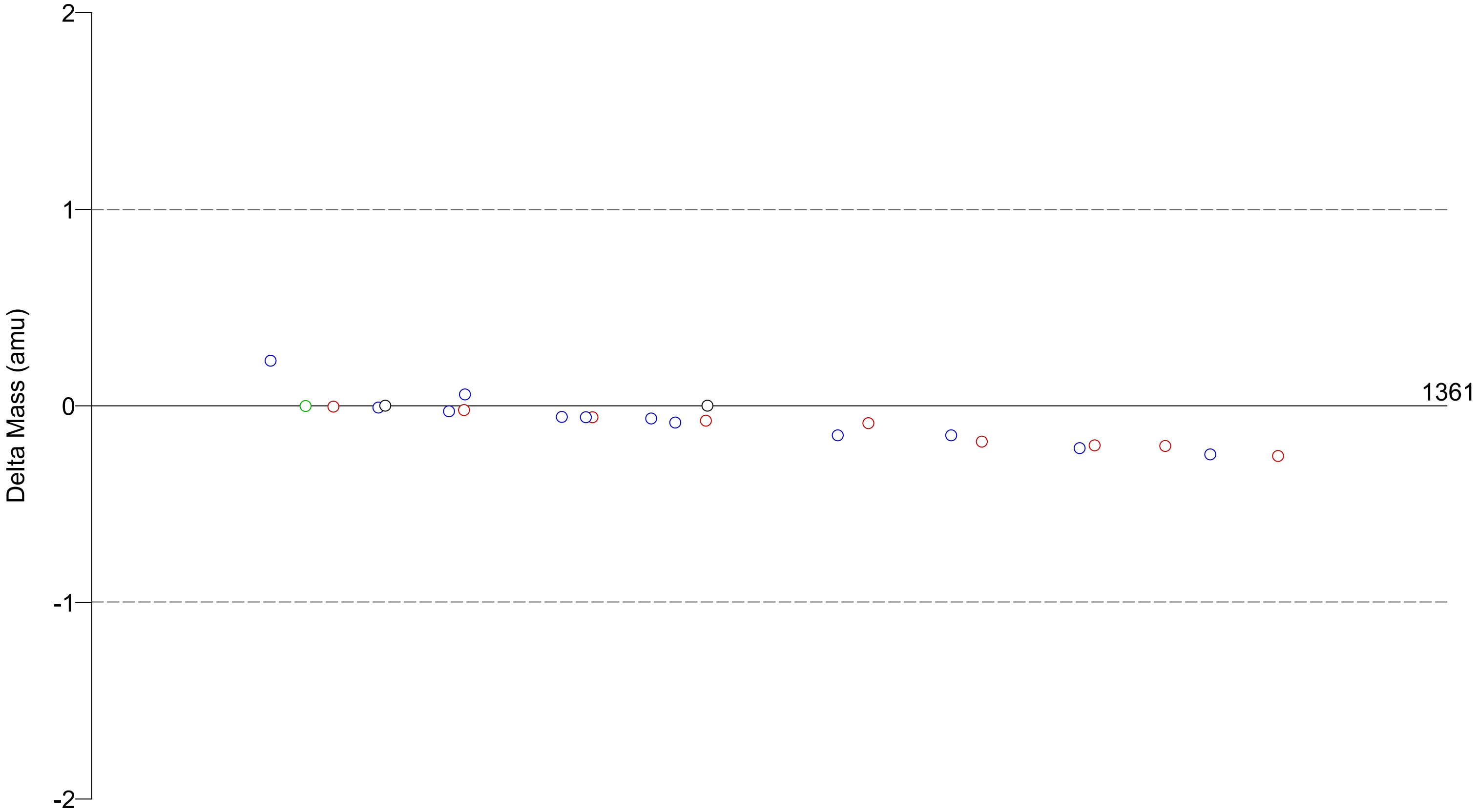
```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp    RSp  Ions  Count

IPI:IPI00029739.5|SWISS-PROT:P0860                                 5e-005  20.2     0.0       0
19287468 - 1  R.RPYFPVAVGK.Y                          1133.65   2  0.02    3.852  0.322   1065.5 1    18/27   6
19287468 - 1  R.EIMENYNIALR.W                         1365.68   2  5e-005  3.298  0.403   992.9  1    18/30   3

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

```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      977.55
 Y    389.23     417.22                                      880.49
 F    536.30     564.29                                      717.43
 P    633.35     661.35                                      570.36
 V    732.42     760.41                                      473.31
 A    803.46     831.45                                      374.24
 V    902.52     930.52                                      303.20
 G    959.55     987.54                                      204.13
 K                                                           147.11
```

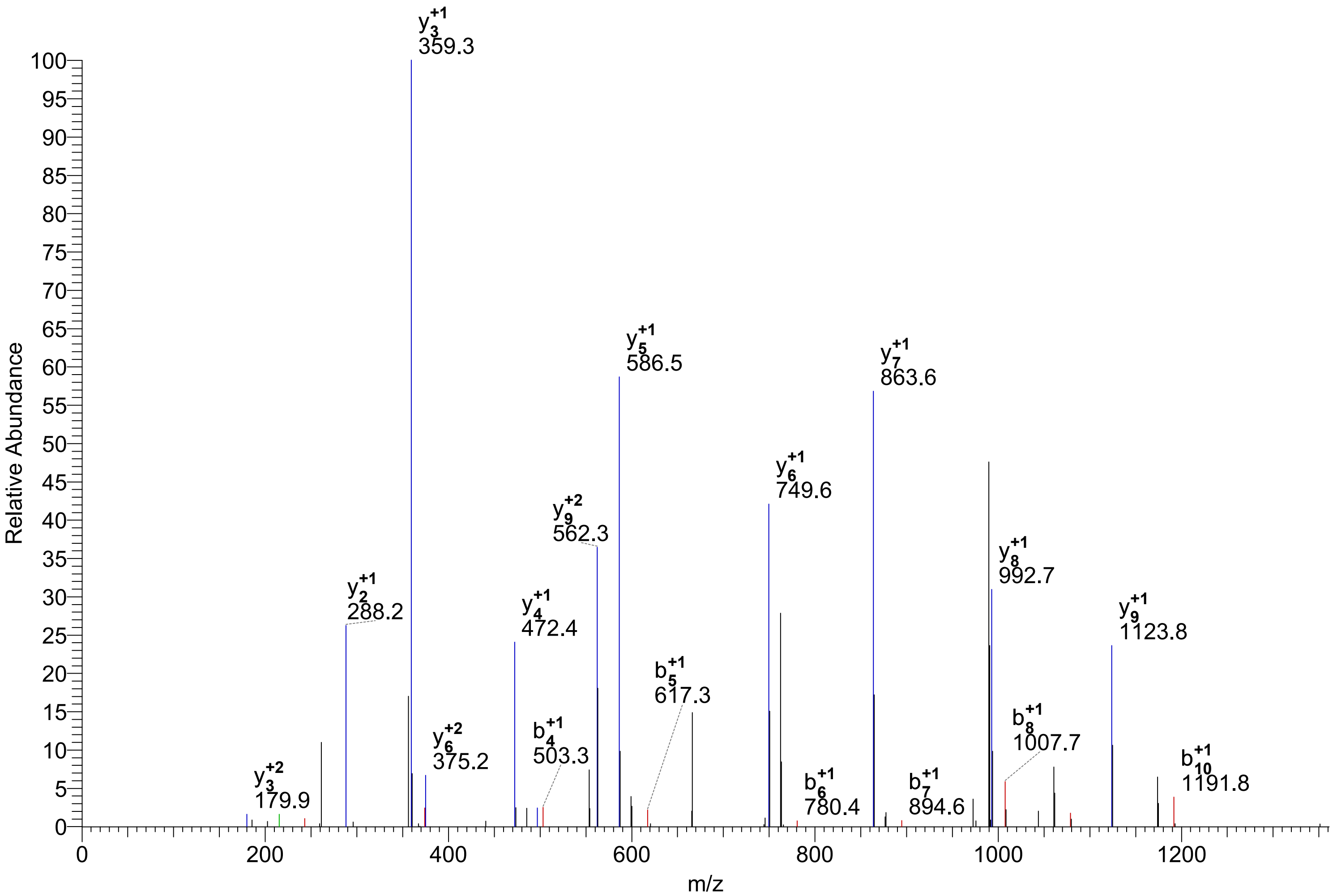

2
1
0
-1
-2
Delta Mass (amu)
1086


#19287468-1 NL: 2.96E5
Relative Abundance
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0
b_8^{+1} 930.7
b_7^{+1} 831.6
y_2^{+1} 204.1
y_9^{+1} 977.7
b_9^{+1} 987.7
b_6^{+1} 760.5
y_3^{+1} 303.2
y_4^{+1} 374.3
y_9^{+2} 489.3
a_8^{+1} 902.7
b_7^{+2} 416.4
a_4^{+1} 536.4
a_6^{+1} 732.5
a_7^{+1} 803.6
b_2^{+1} 254.2
b_5^{+2} 331.2
b_3^{+1} 417.4
y_6^{+1} 570.4
y_8^{+1} 880.6
0
100
200
300
400
500
600
700
800
900
1000
m/z

```
DTA for scans: 19287468-1
Precursor ion: 683.35
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 E    102.05     130.05
 I    215.14     243.13                                    1236.64
 M    346.18     374.17                                    1123.56
 E    475.22     503.22                                     992.52
 N    589.27     617.26                                     863.47
 Y    752.33     780.32                                     749.43
 N    866.37     894.37                                     586.37
 I    979.46    1007.45                                     472.32
 A   1050.49    1078.49                                     359.24
 L   1163.58    1191.57                                     288.20
 R                                                          175.12
```

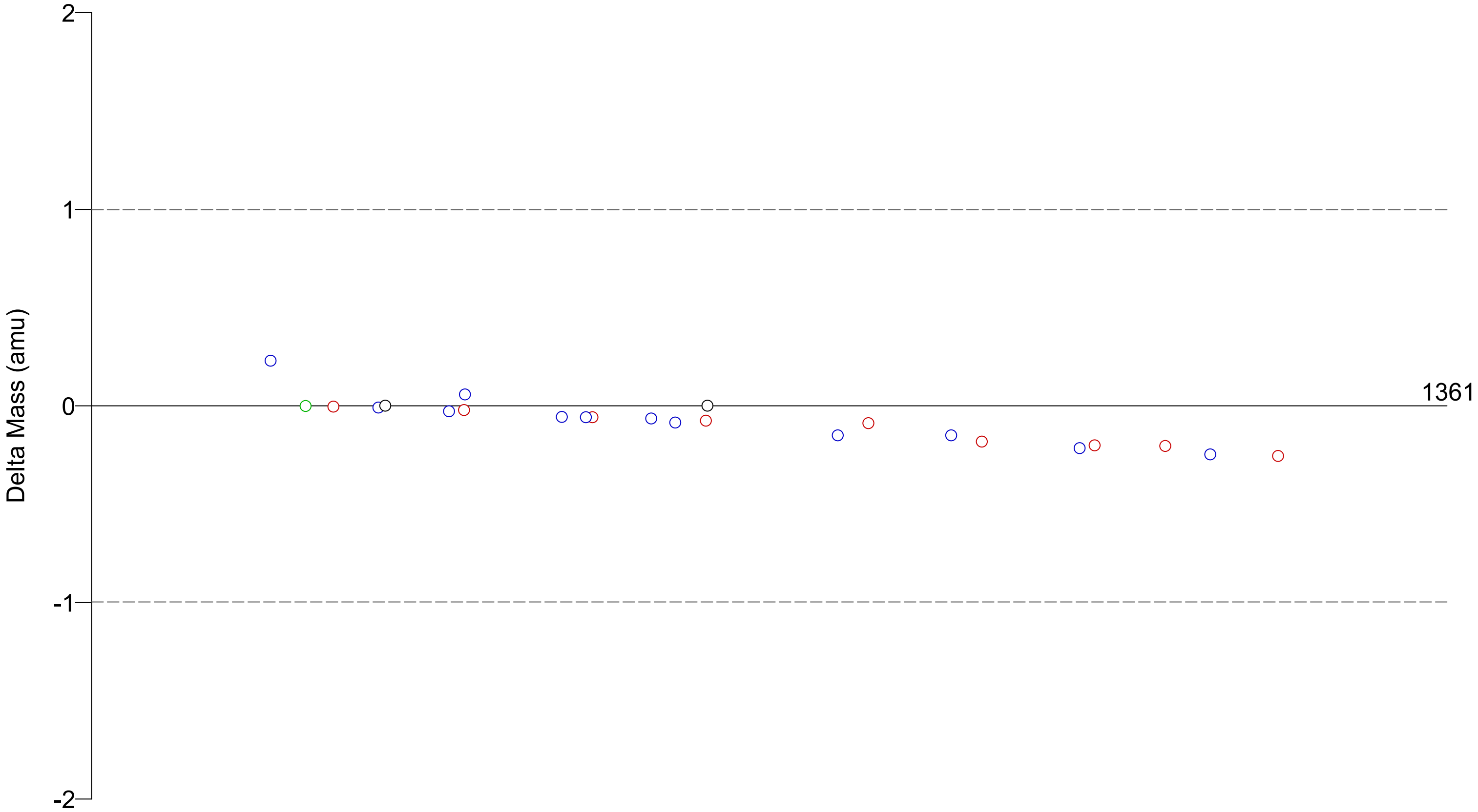


#19287468-1 NL: 1.28E5

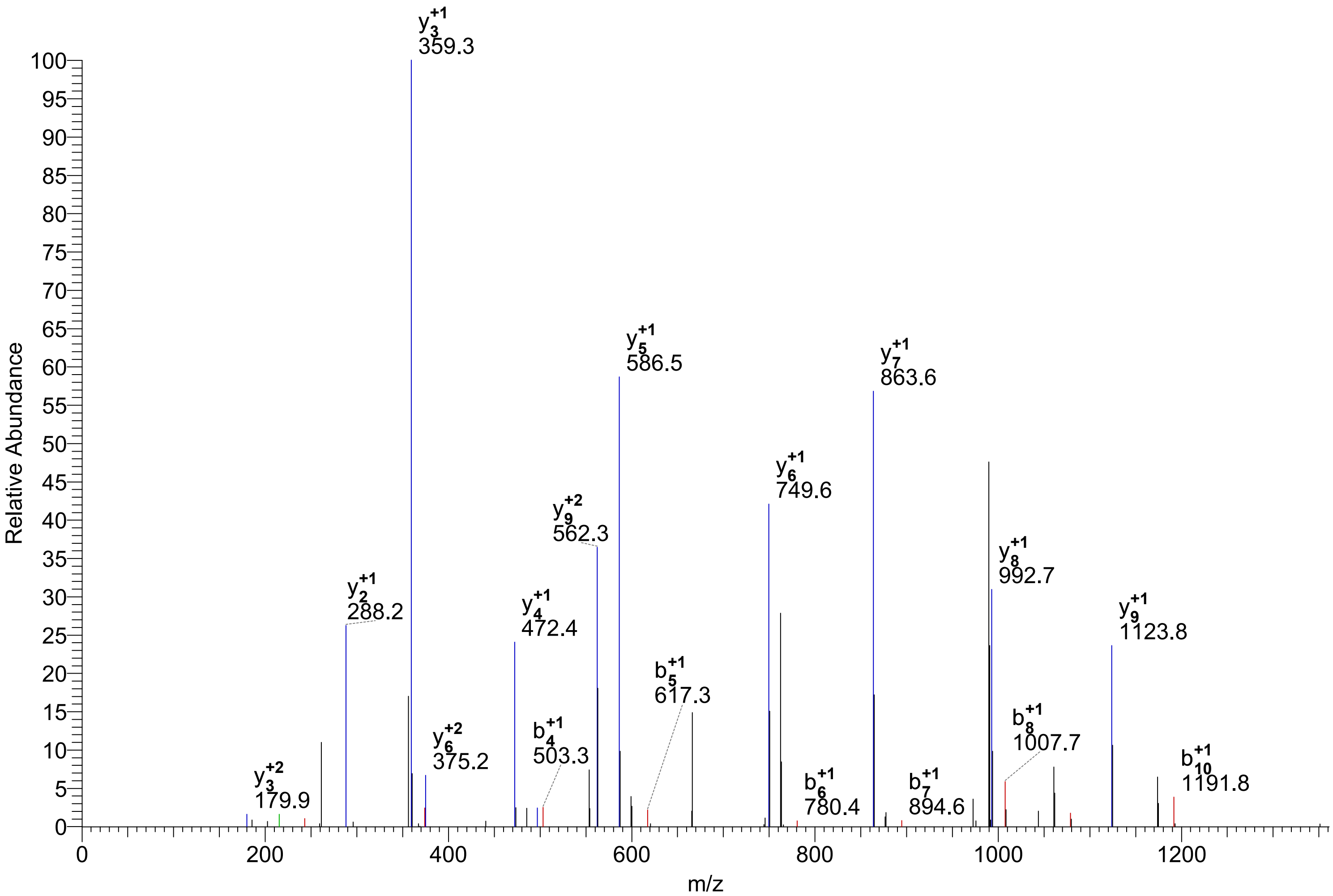


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00011264.2|SWISS-PROT:Q03591|ENSEMBL:ENSP00000314299|RE    5e-005  10.2     0.0       0
19287468 - 1   R.EIMENYNIALR.W                       1365.68   2  5e-005  3.298  0.403   992.9  1   18/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 683.35
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 E    102.05     130.05
 I    215.14     243.13                                    1236.64
 M    346.18     374.17                                    1123.56
 E    475.22     503.22                                     992.52
 N    589.27     617.26                                     863.47
 Y    752.33     780.32                                     749.43
 N    866.37     894.37                                     586.37
 I    979.46    1007.45                                     472.32
 A   1050.49    1078.49                                     359.24
 L   1163.58    1191.57                                     288.20
 R                                                          175.12
```

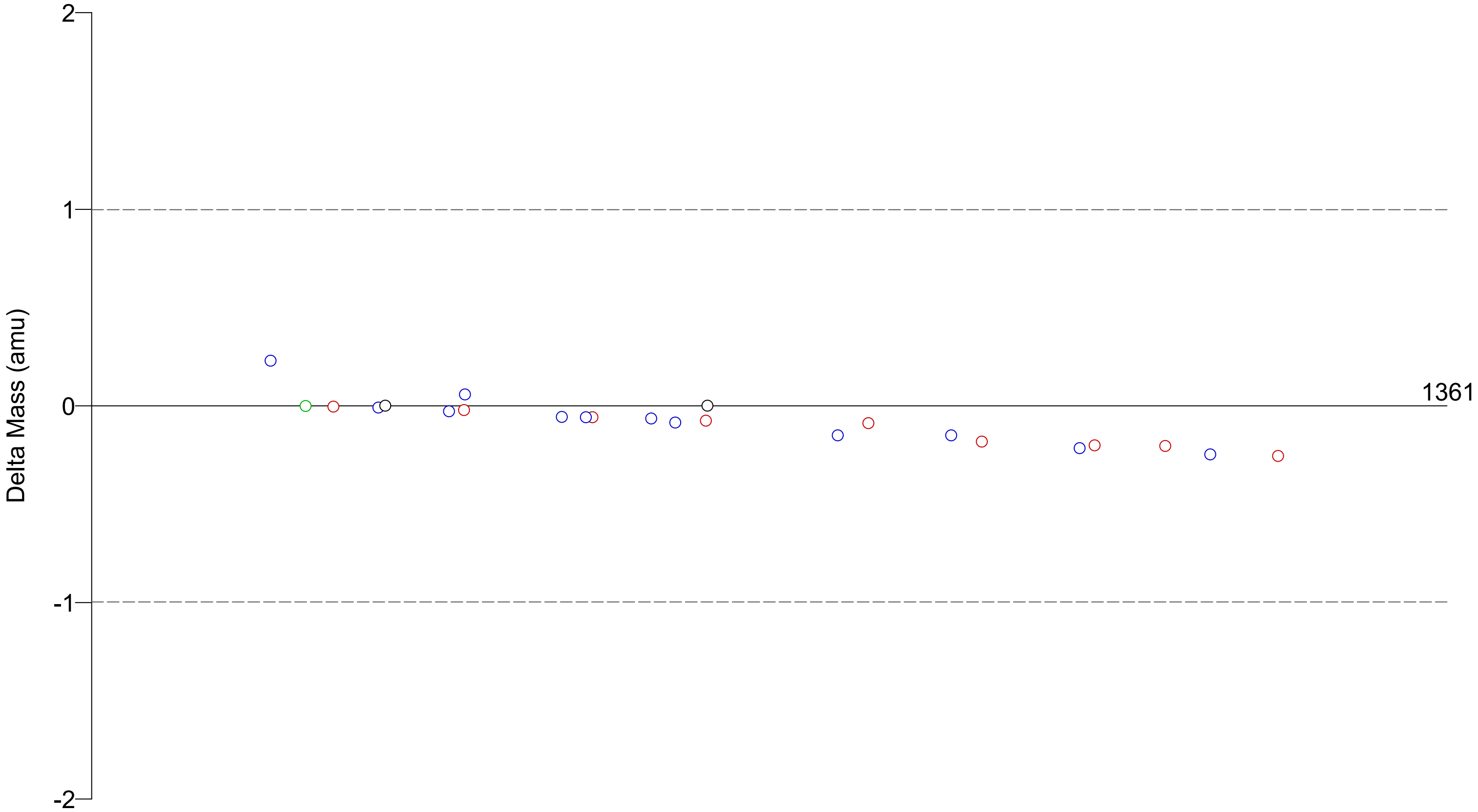


#19287468-1 NL: 1.28E5

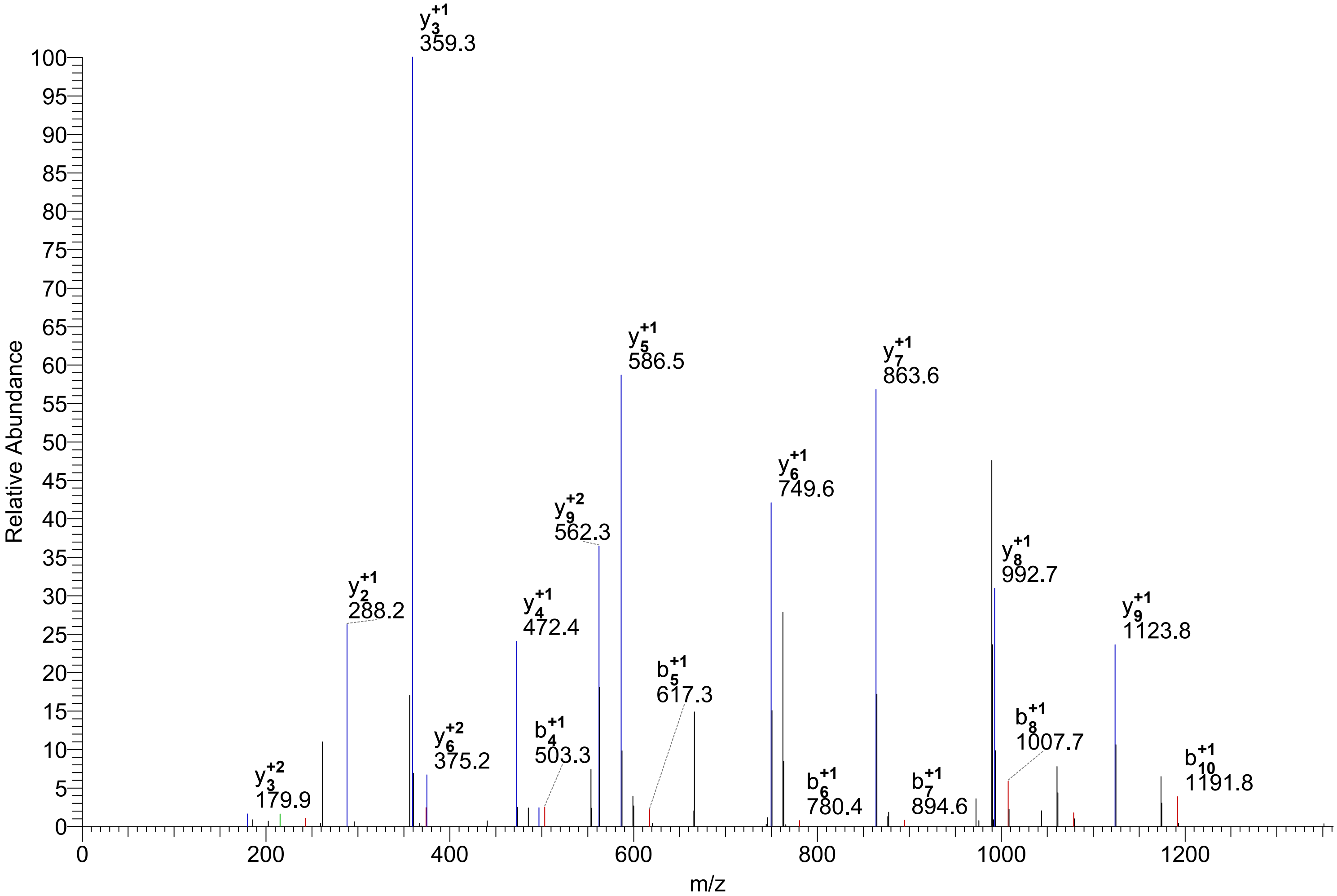


```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z     P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00513925.1|ENSEMBL:ENSP0000                                     5e-005  10.2      0.0        0
19287468 - 1  R.EIMENYNIALR.W                             1365.68    2  5e-005  3.298  0.403   992.9  1   18/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 683.35
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 E    102.05     130.05
 I    215.14     243.13                                     1236.64
 M    346.18     374.17                                     1123.56
 E    475.22     503.22                                      992.52
 N    589.27     617.26                                      863.47
 Y    752.33     780.32                                      749.43
 N    866.37     894.37                                      586.37
 I    979.46    1007.45                                      472.32
 A   1050.49    1078.49                                      359.24
 L   1163.58    1191.57                                      288.20
 R                                                           175.12
```

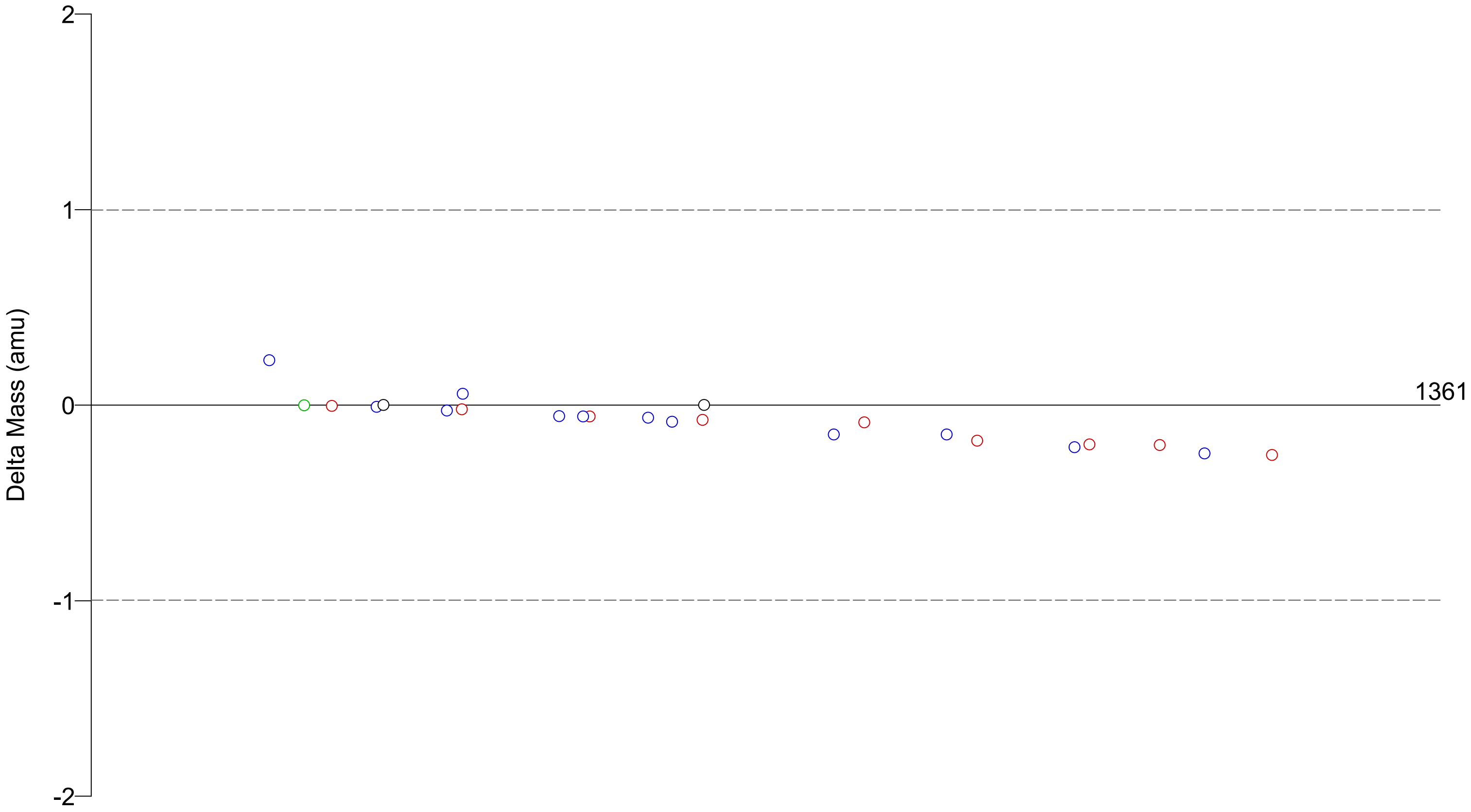


#19287468-1 NL: 1.28E5

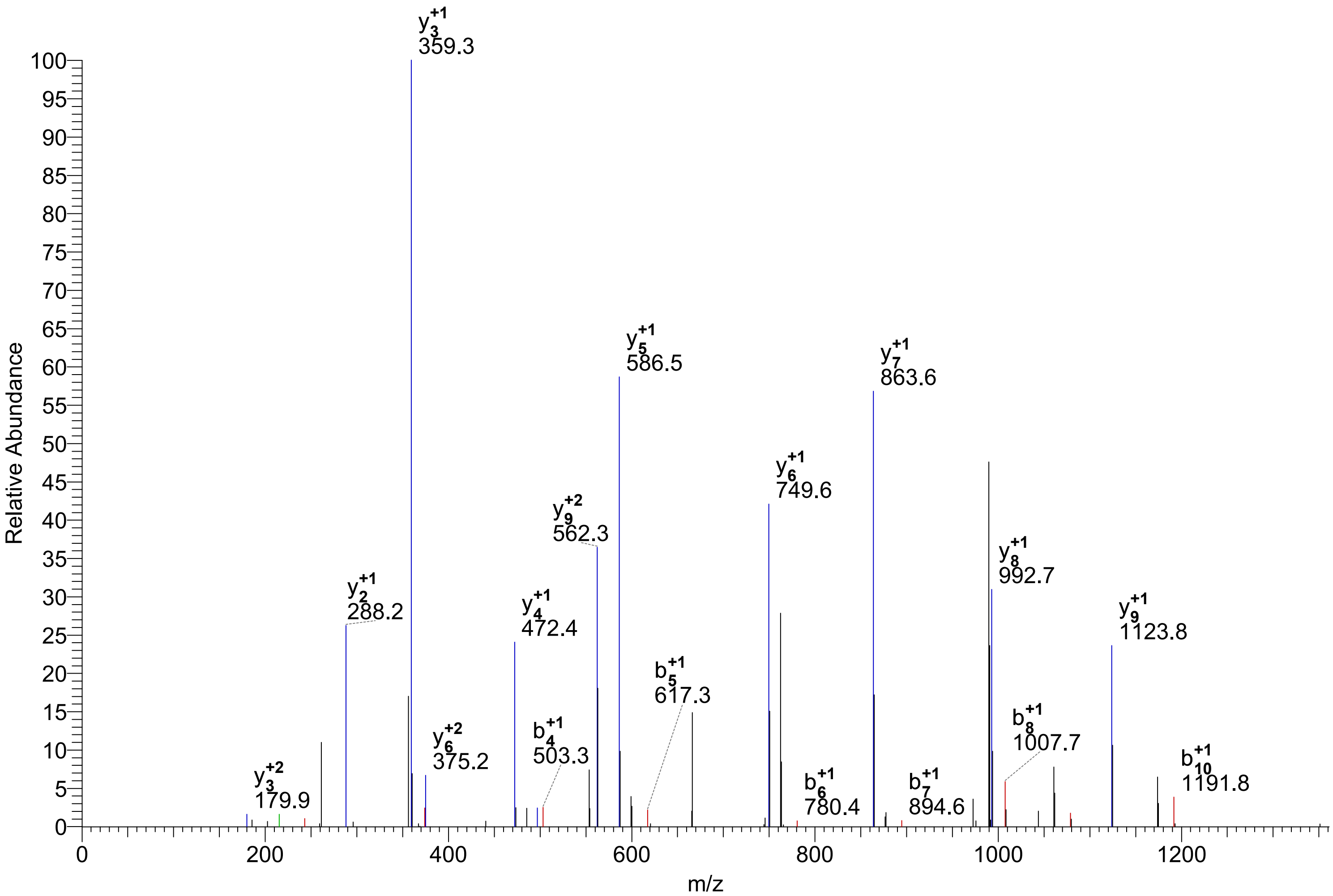


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00883722.1|TREMBL:B1AKG0;Q6                                5e-005  10.2     0.0       0
19287468 - 1  R.EIMENYNIALR.W                        1365.68   2  5e-005  3.298  0.403   992.9  1   18/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 683.35
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 E    102.05     130.05
 I    215.14     243.13                                     1236.64
 M    346.18     374.17                                     1123.56
 E    475.22     503.22                                      992.52
 N    589.27     617.26                                      863.47
 Y    752.33     780.32                                      749.43
 N    866.37     894.37                                      586.37
 I    979.46    1007.45                                      472.32
 A   1050.49    1078.49                                      359.24
 L   1163.58    1191.57                                      288.20
 R                                                           175.12
```

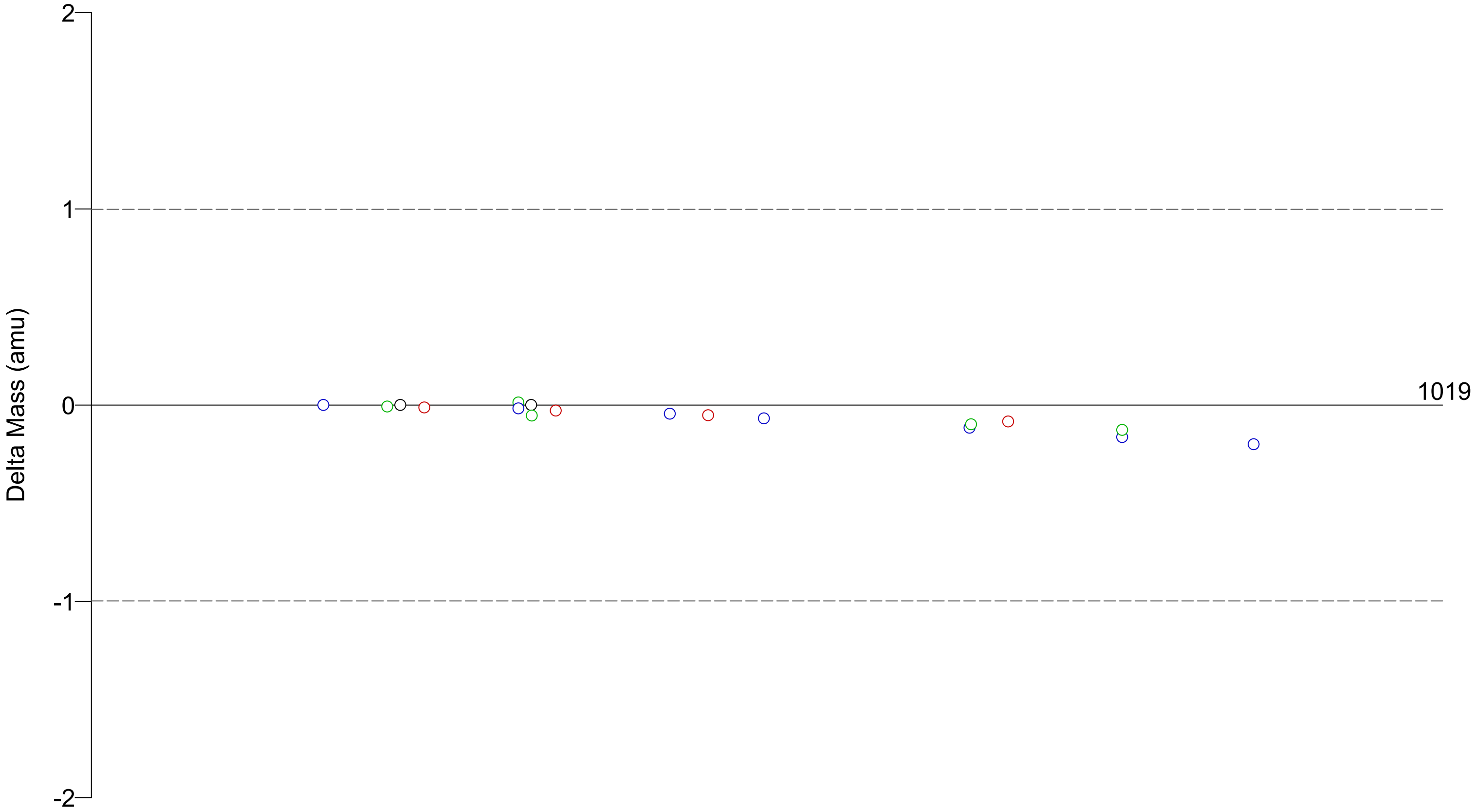


#19287468-1 NL: 1.28E5

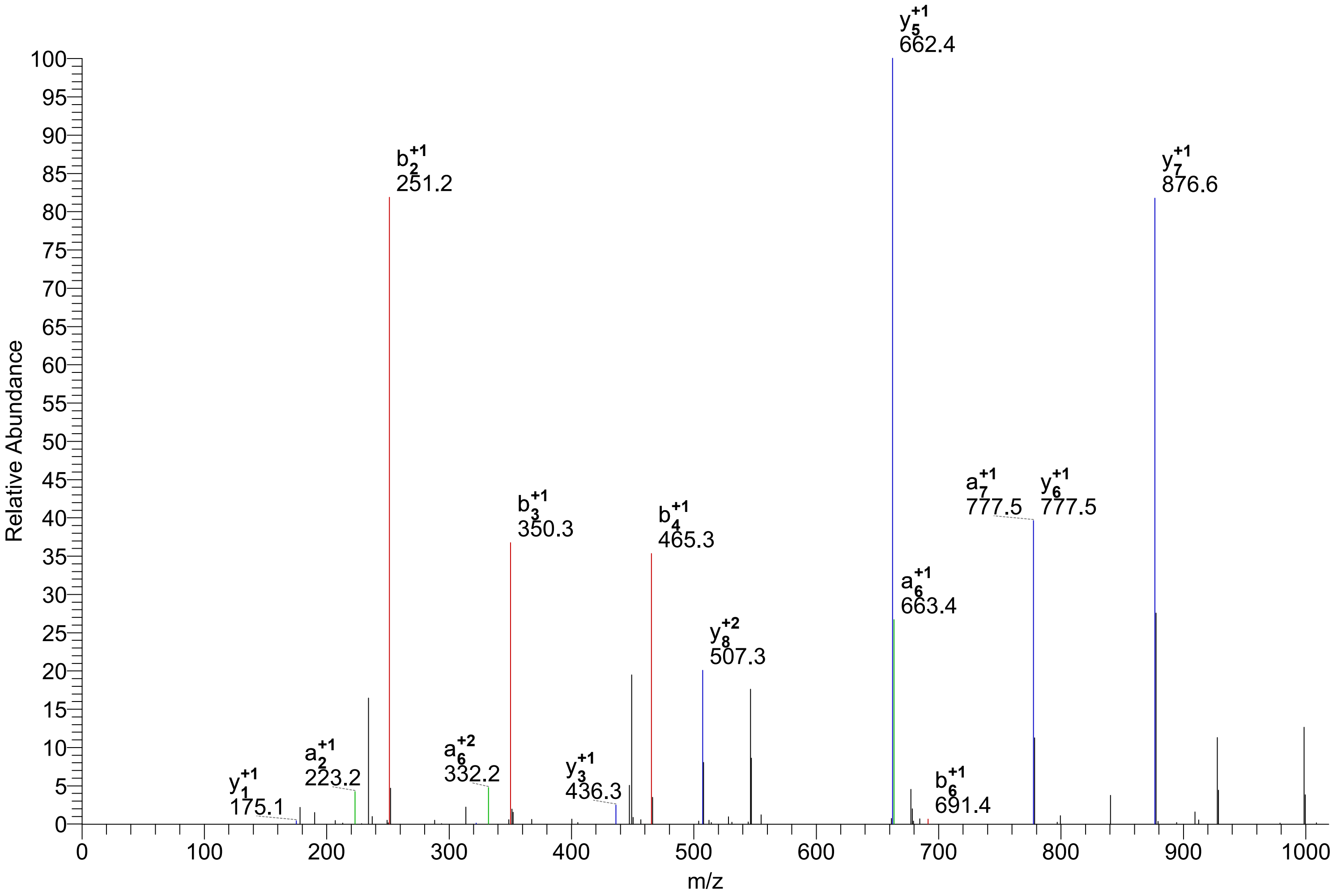


```
Reference                                                    P      Score   Coverage   Accession
Scan(s)       Sequence                             MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00654755.3|SWISS-PROT:P6887                                  6e-005  20.1     0.0        0
19287468 - 1  K.LHVDPENFR.L                      1126.56   2  0.06    2.171  0.417   654.7  1   14/24   5
19287468 - 1  R.LLGNVLVCVLAHHFGK.E               1777.98   3  6e-005  2.552  0.484   158.2  1   22/90   2

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

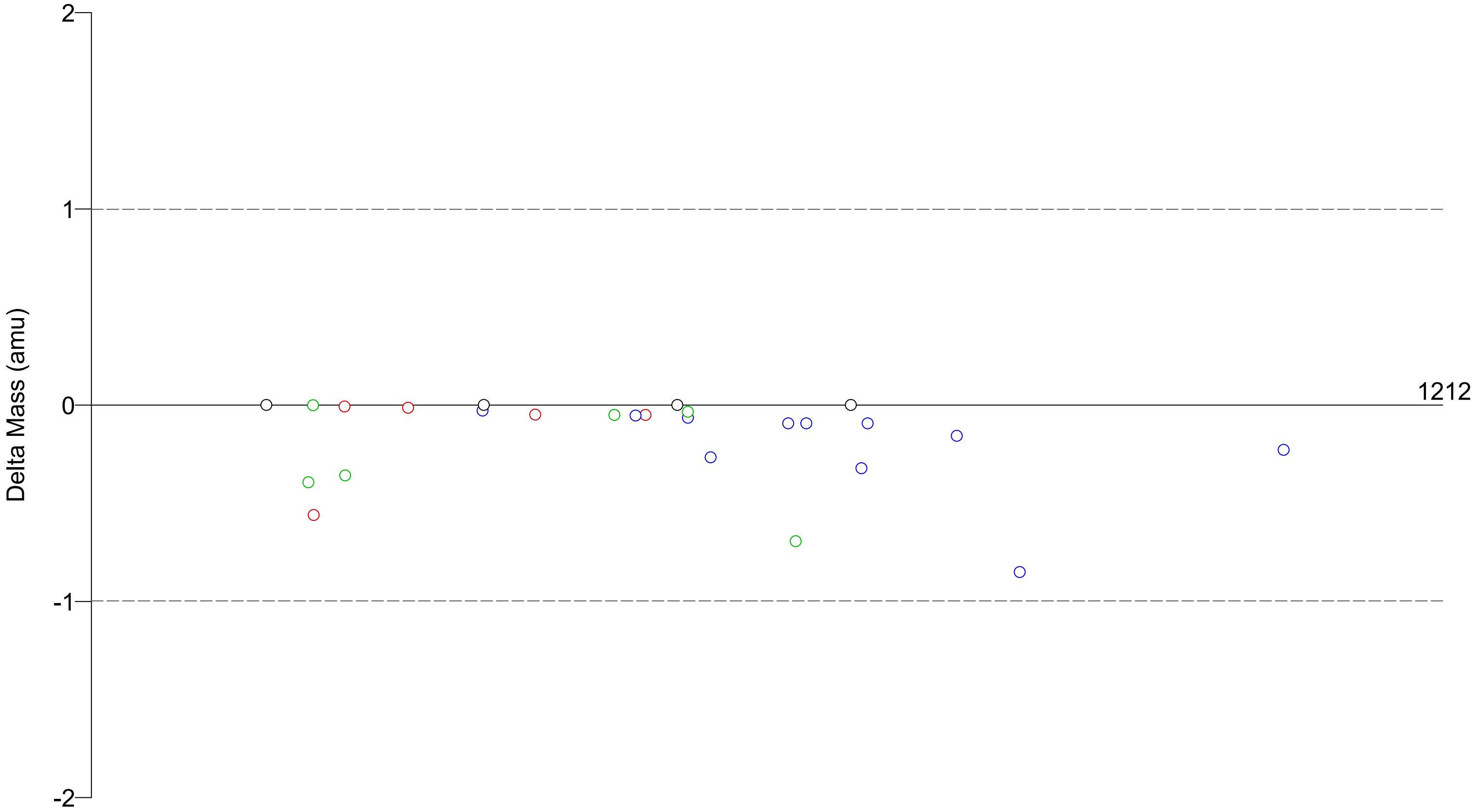
```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 H    223.16     251.15                                     1013.48
 V    322.22     350.22                                      876.42
 D    437.25     465.25                                      777.35
 P    534.30     562.30                                      662.33
 E    663.35     691.34                                      565.27
 N    777.39     805.38                                      436.23
 F    924.46     952.45                                      322.19
 R                                                           175.12
```



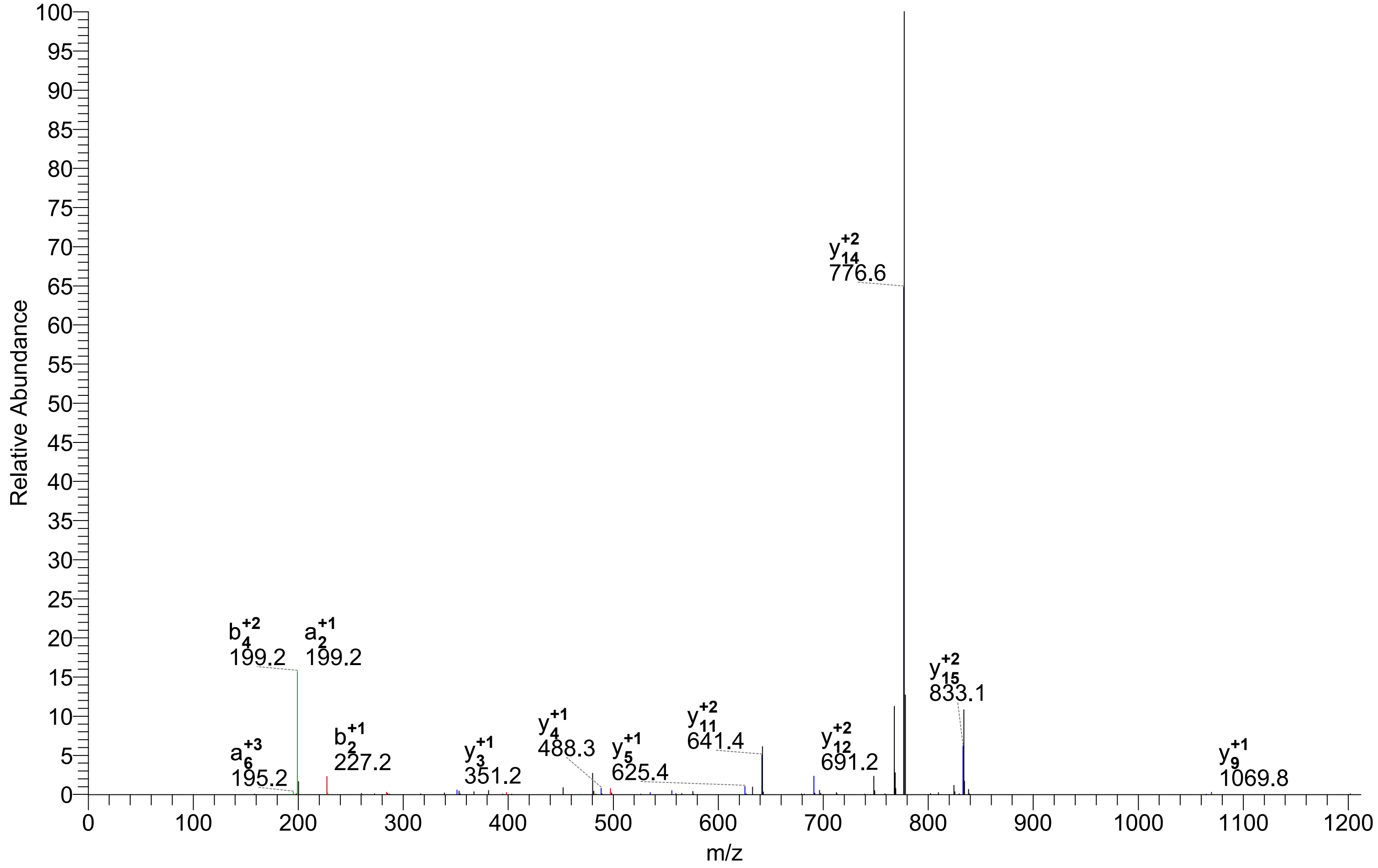
#19287468-1 NL: 7.10E5



```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1664.89
 G    256.20     284.20                                     1551.81
 N    370.24     398.24                                     1494.79
 V    469.31     497.31                                     1380.75
 L    582.40     610.39                                     1281.68
 V    681.47     709.46                                     1168.59
 C    842.48     870.48                                     1069.52
 V    941.55     969.54                                      908.51
 L   1054.63    1082.63                                      809.44
 A   1125.67    1153.66                                      696.36
 H   1262.73    1290.72                                      625.32
 H   1399.79    1427.78                                      488.26
 F   1546.86    1574.85                                      351.20
 G   1603.88    1631.87                                      204.13
 K                                                           147.11
```

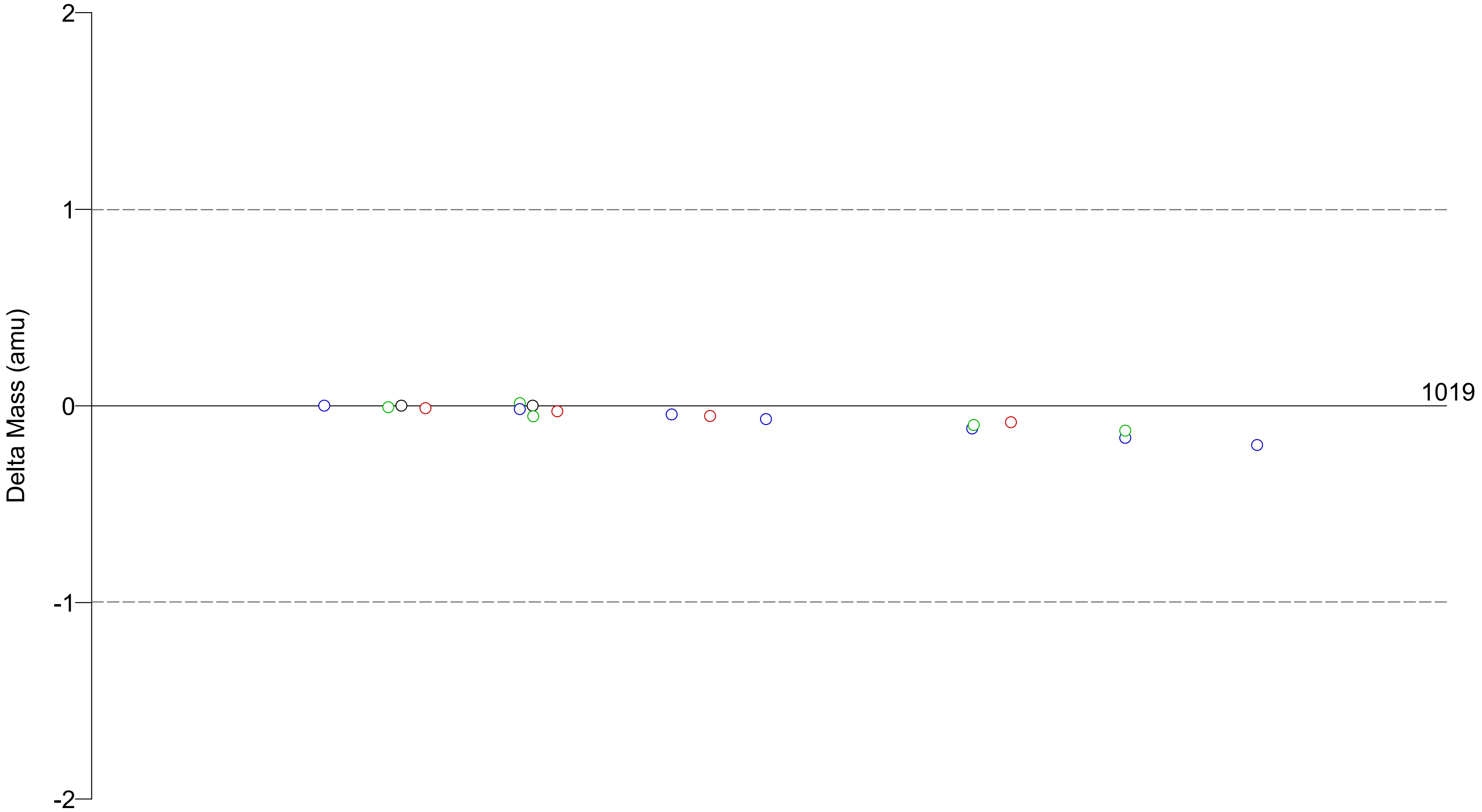


#19287468-1 NL: 6.49E5

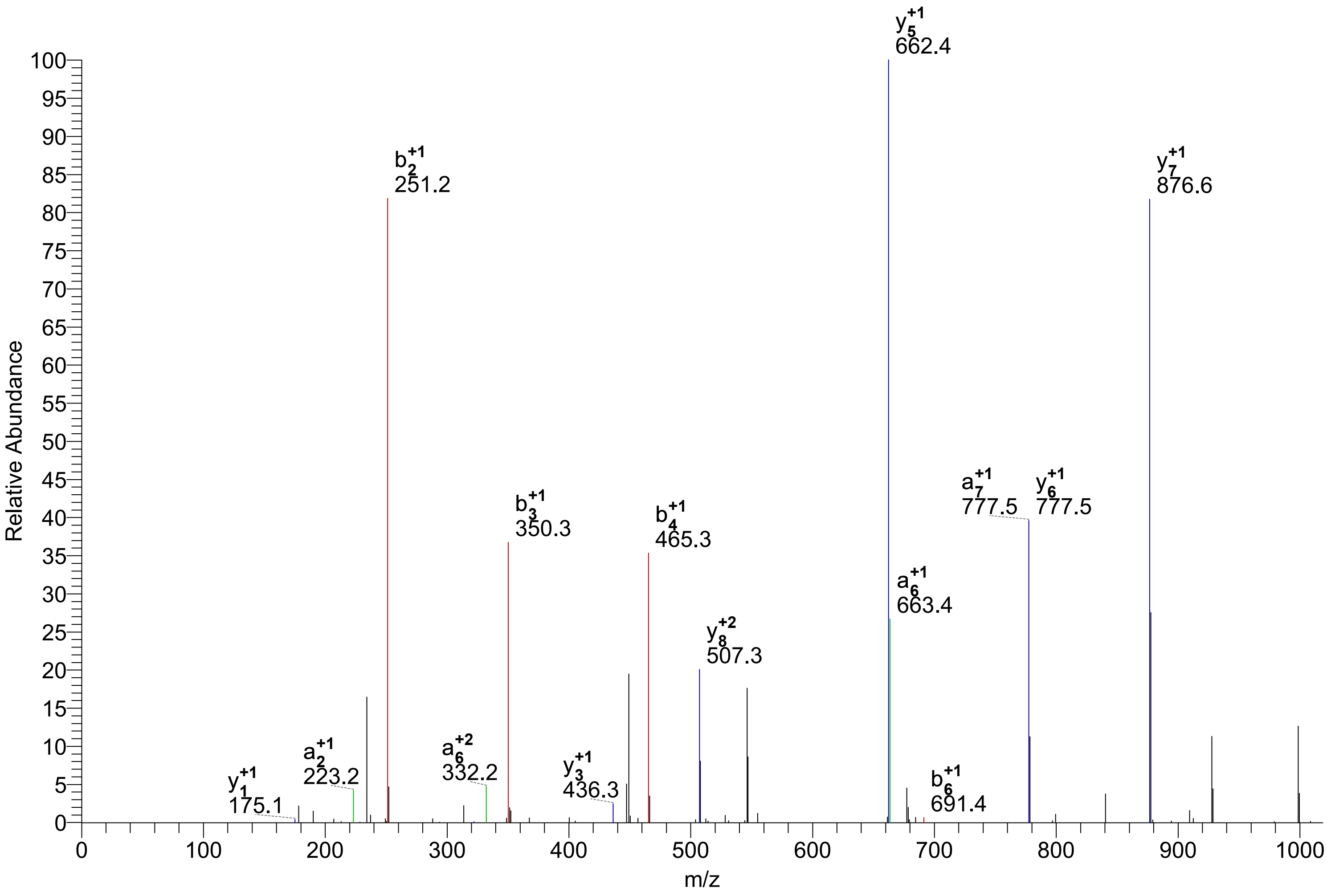


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00884107.1|TREMBL:Q14473 Ta                                6e-005  20.1     0.0       0
19287468 - 1  K.LHVDPENFR.L                          1126.56   2  0.06    2.171  0.417   654.7  1   14/24   5
19287468 - 1  R.LLGNVLVCVLAHHFGK.E                   1777.98   3  6e-005  2.552  0.484   158.2  1   22/90   2

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

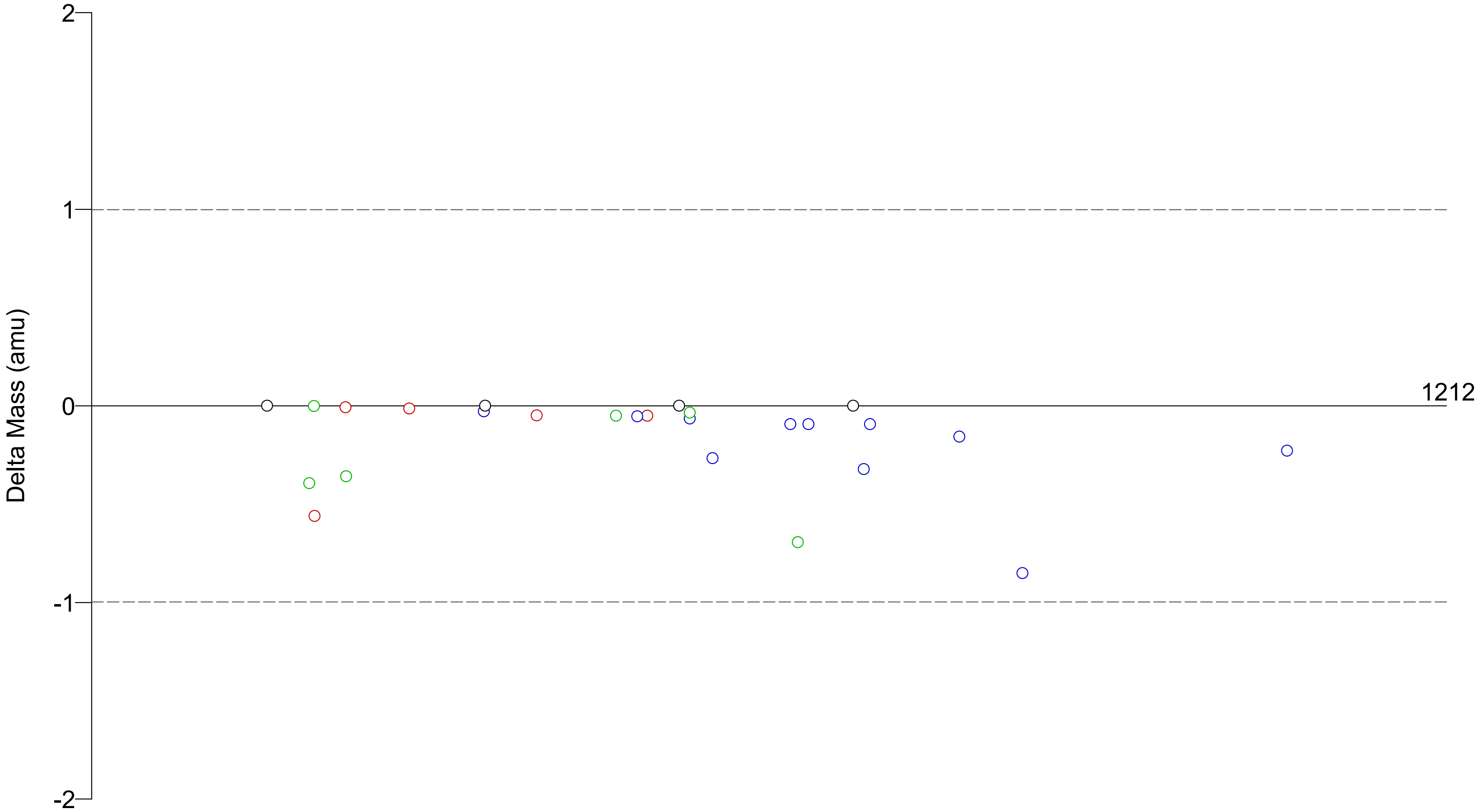
```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 H    223.16     251.15                                     1013.48
 V    322.22     350.22                                      876.42
 D    437.25     465.25                                      777.35
 P    534.30     562.30                                      662.33
 E    663.35     691.34                                      565.27
 N    777.39     805.38                                      436.23
 F    924.46     952.45                                      322.19
 R                                                           175.12
```



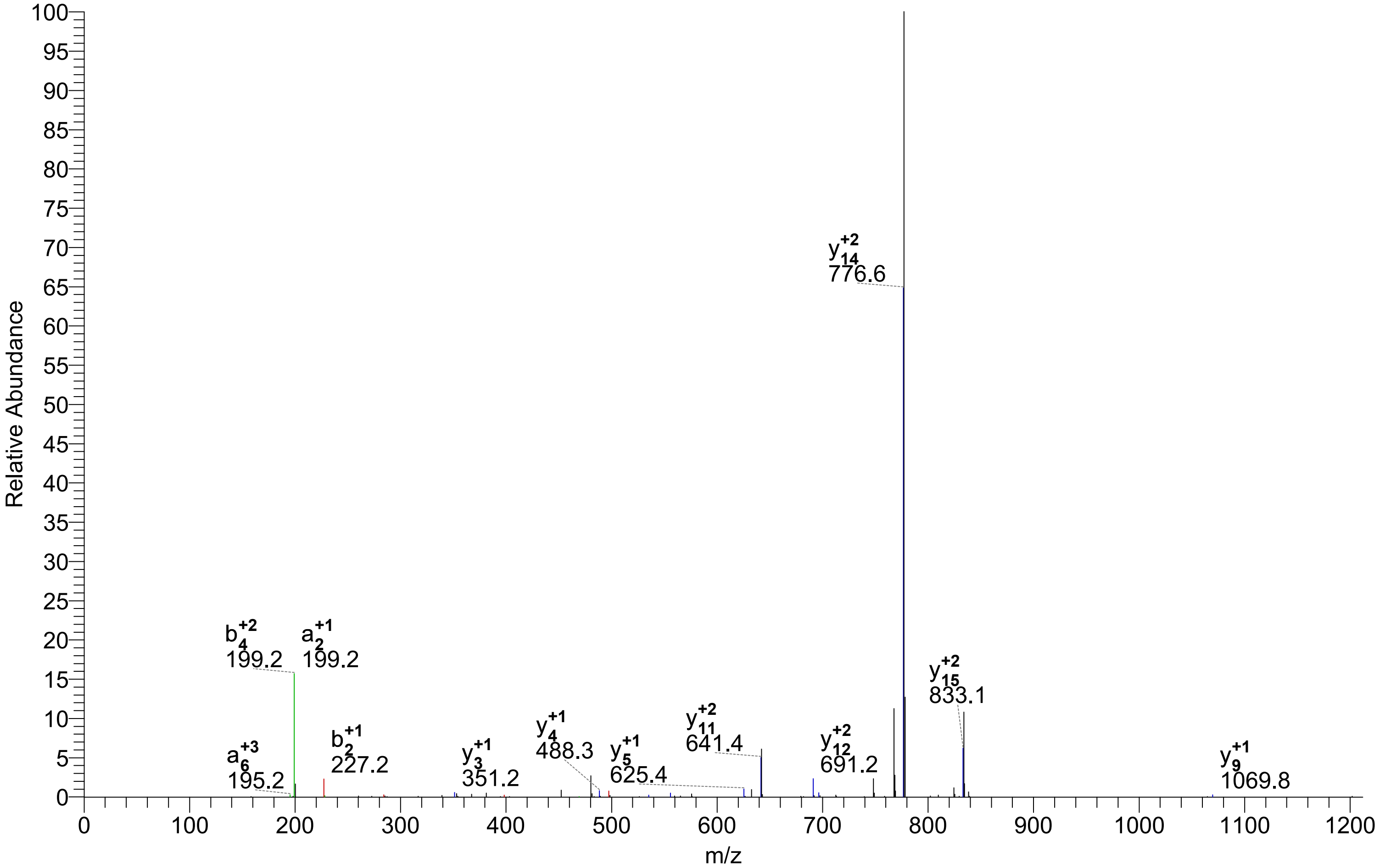
#19287468-1 NL: 7.10E5



```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1664.89
 G    256.20     284.20                                     1551.81
 N    370.24     398.24                                     1494.79
 V    469.31     497.31                                     1380.75
 L    582.40     610.39                                     1281.68
 V    681.47     709.46                                     1168.59
 C    842.48     870.48                                     1069.52
 V    941.55     969.54                                      908.51
 L   1054.63    1082.63                                      809.44
 A   1125.67    1153.66                                      696.36
 H   1262.73    1290.72                                      625.32
 H   1399.79    1427.78                                      488.26
 F   1546.86    1574.85                                      351.20
 G   1603.88    1631.87                                      204.13
 K                                                           147.11
```

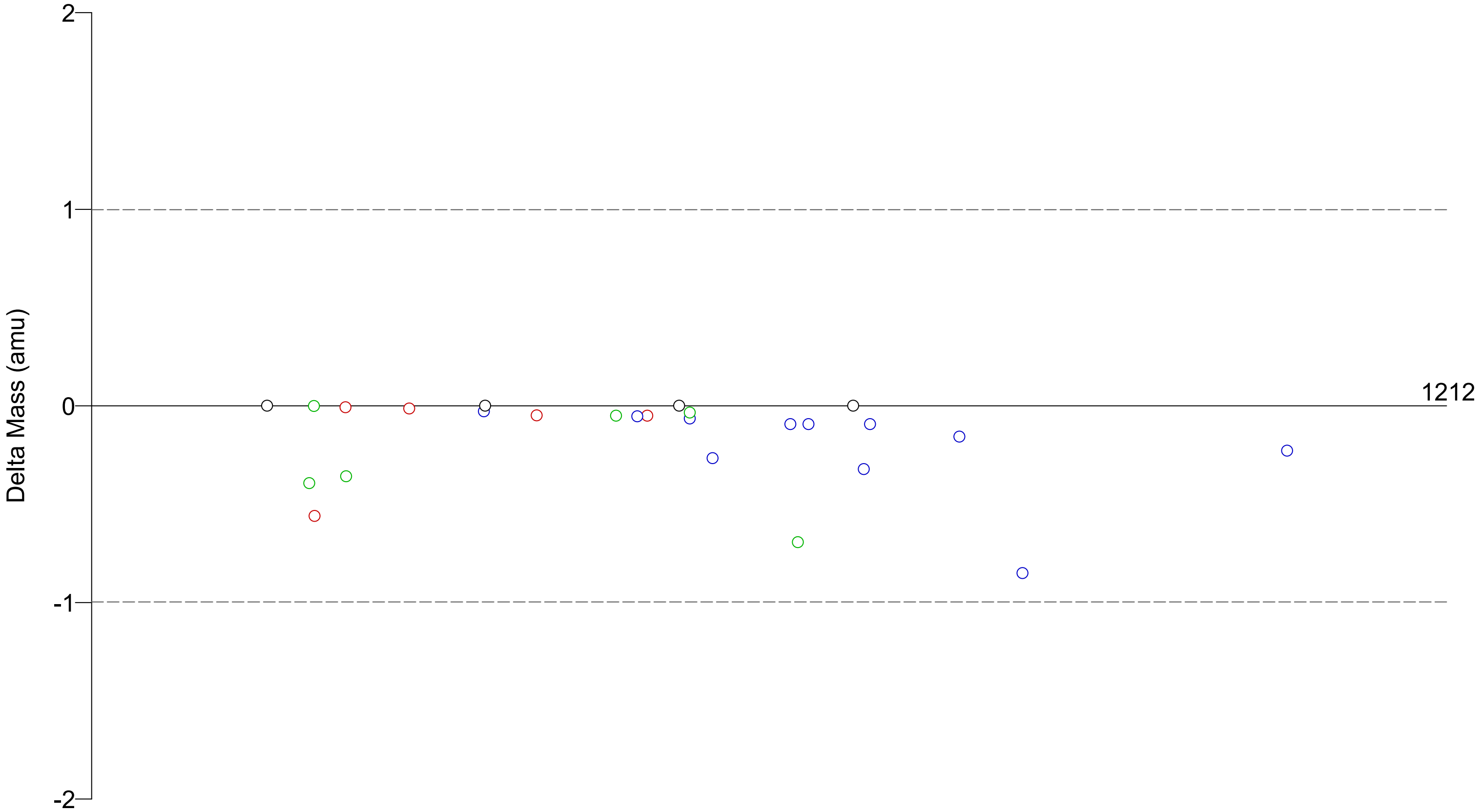


#19287468-1 NL: 6.49E5

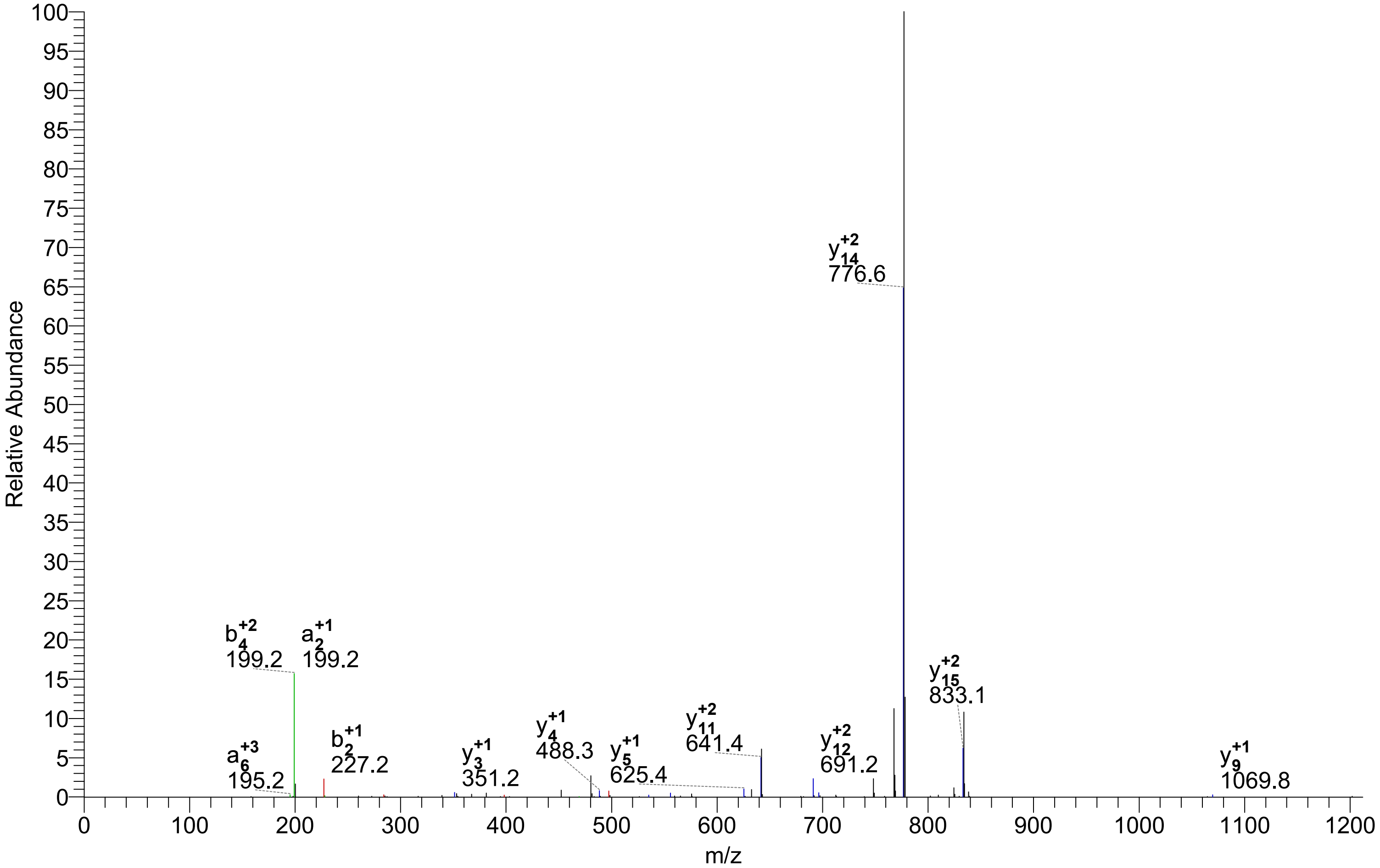


```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00816644.1|TREMBL:Q5GMQ1;Q9                              6e-005  10.1     0.0        0
19287468 - 1  R.LLGNVLVCVLAHHFGK.E                 1777.98   3  6e-005  2.552  0.484   158.2  1   22/90   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1664.89
 G    256.20     284.20                                     1551.81
 N    370.24     398.24                                     1494.79
 V    469.31     497.31                                     1380.75
 L    582.40     610.39                                     1281.68
 V    681.47     709.46                                     1168.59
 C    842.48     870.48                                     1069.52
 V    941.55     969.54                                      908.51
 L   1054.63    1082.63                                      809.44
 A   1125.67    1153.66                                      696.36
 H   1262.73    1290.72                                      625.32
 H   1399.79    1427.78                                      488.26
 F   1546.86    1574.85                                      351.20
 G   1603.88    1631.87                                      204.13
 K                                                           147.11
```

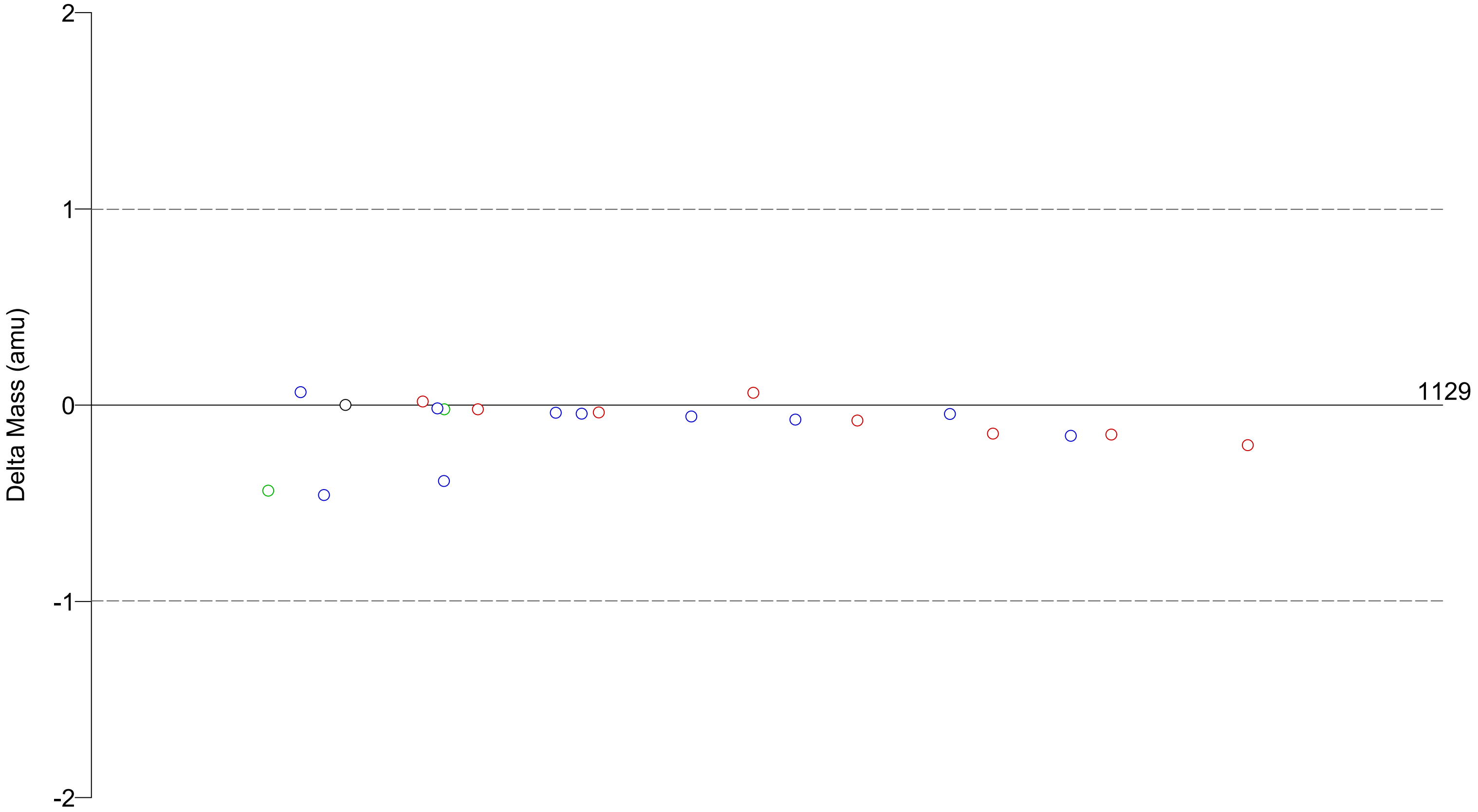


#19287468-1 NL: 6.49E5

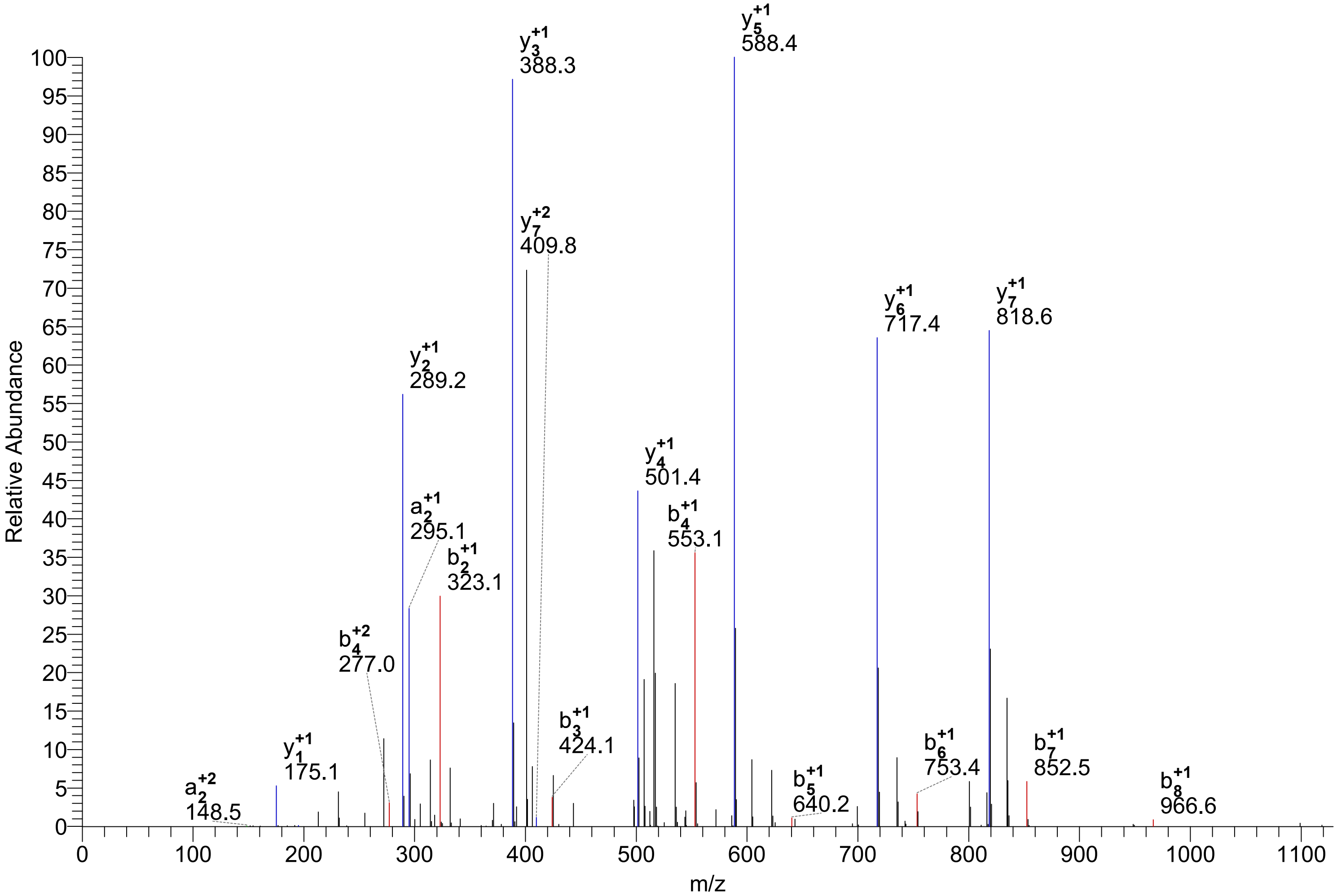


```
Reference                                                            P    Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z     P      XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00384697.2|SWISS-PROT:P0276                                0.0001  10.2     0.0       0
19287468 - 1  K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                      979.45
 T    396.09     424.08                                      818.44
 E    525.13     553.13                                      717.39
 S    612.16     640.16                                      588.35
 L    725.25     753.24                                      501.31
 V    824.32     852.31                                      388.23
 N    938.36     966.35                                      289.16
 R                                                           175.12
```

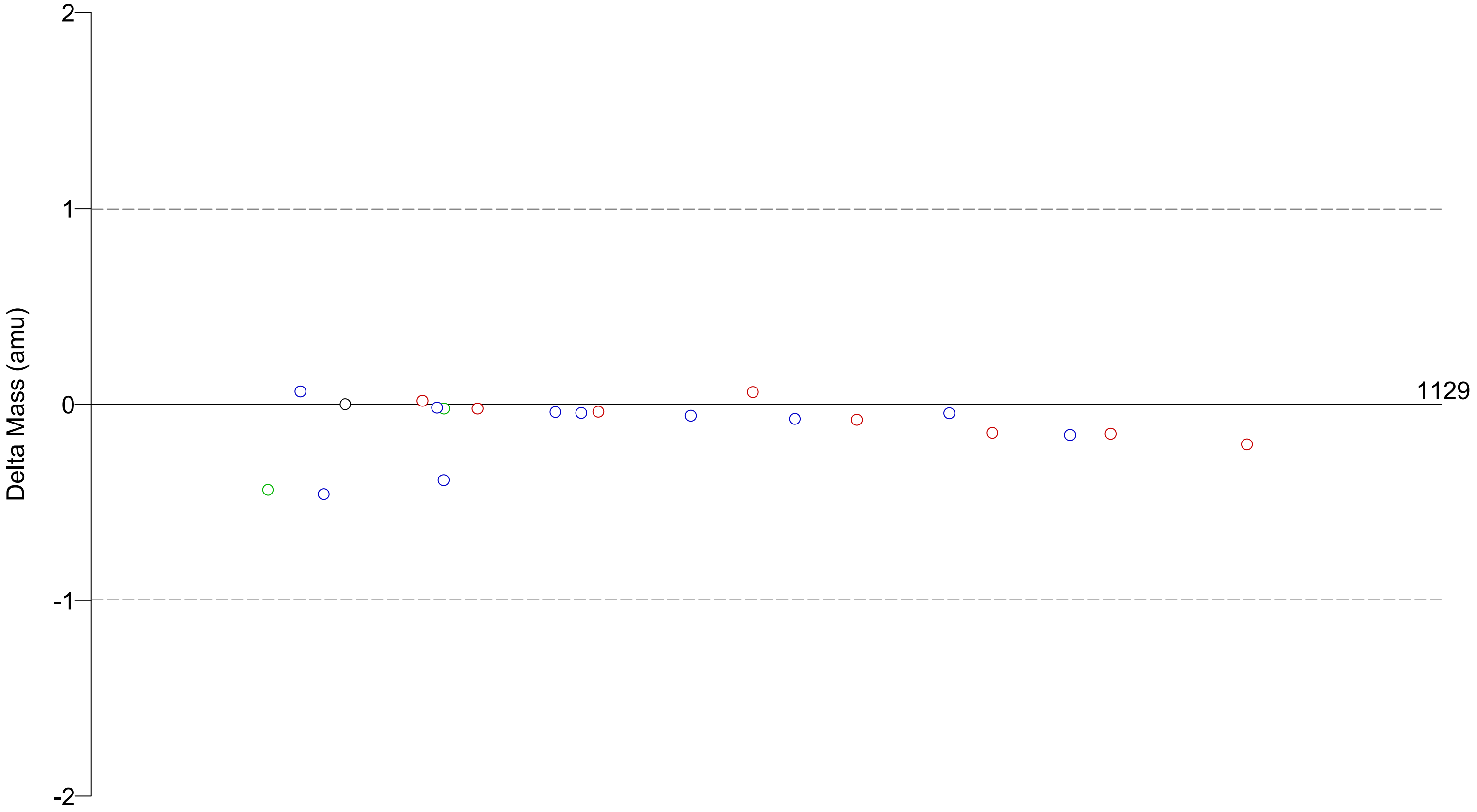


#19287468-1 NL: 8.98E6

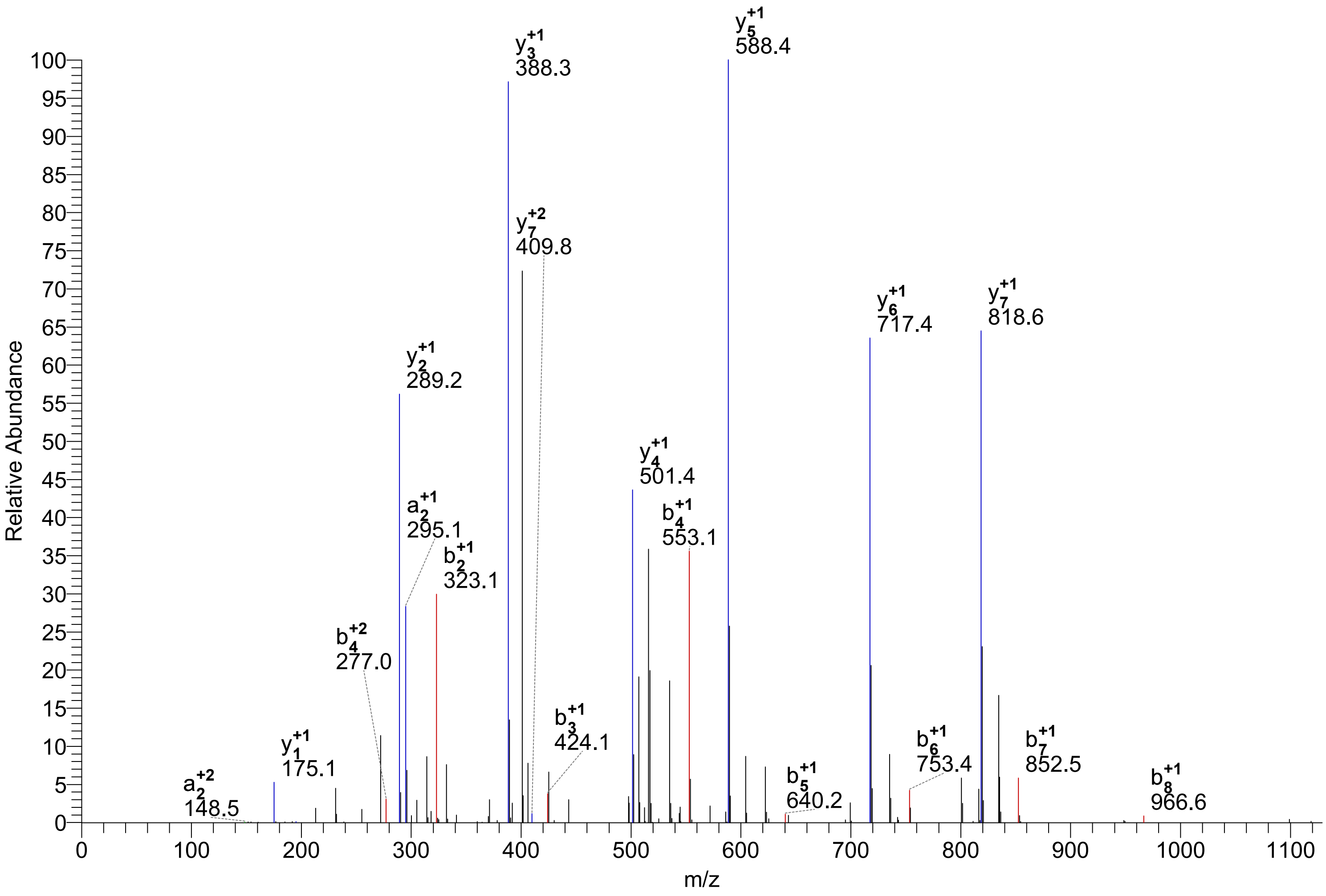


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P      XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00878517.1|TREMBL:B7WNR0|EN                                0.0001  10.2     0.0       0
19287468 - 1  K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                       979.45
 T    396.09     424.08                                       818.44
 E    525.13     553.13                                       717.39
 S    612.16     640.16                                       588.35
 L    725.25     753.24                                       501.31
 V    824.32     852.31                                       388.23
 N    938.36     966.35                                       289.16
 R                                                            175.12
```

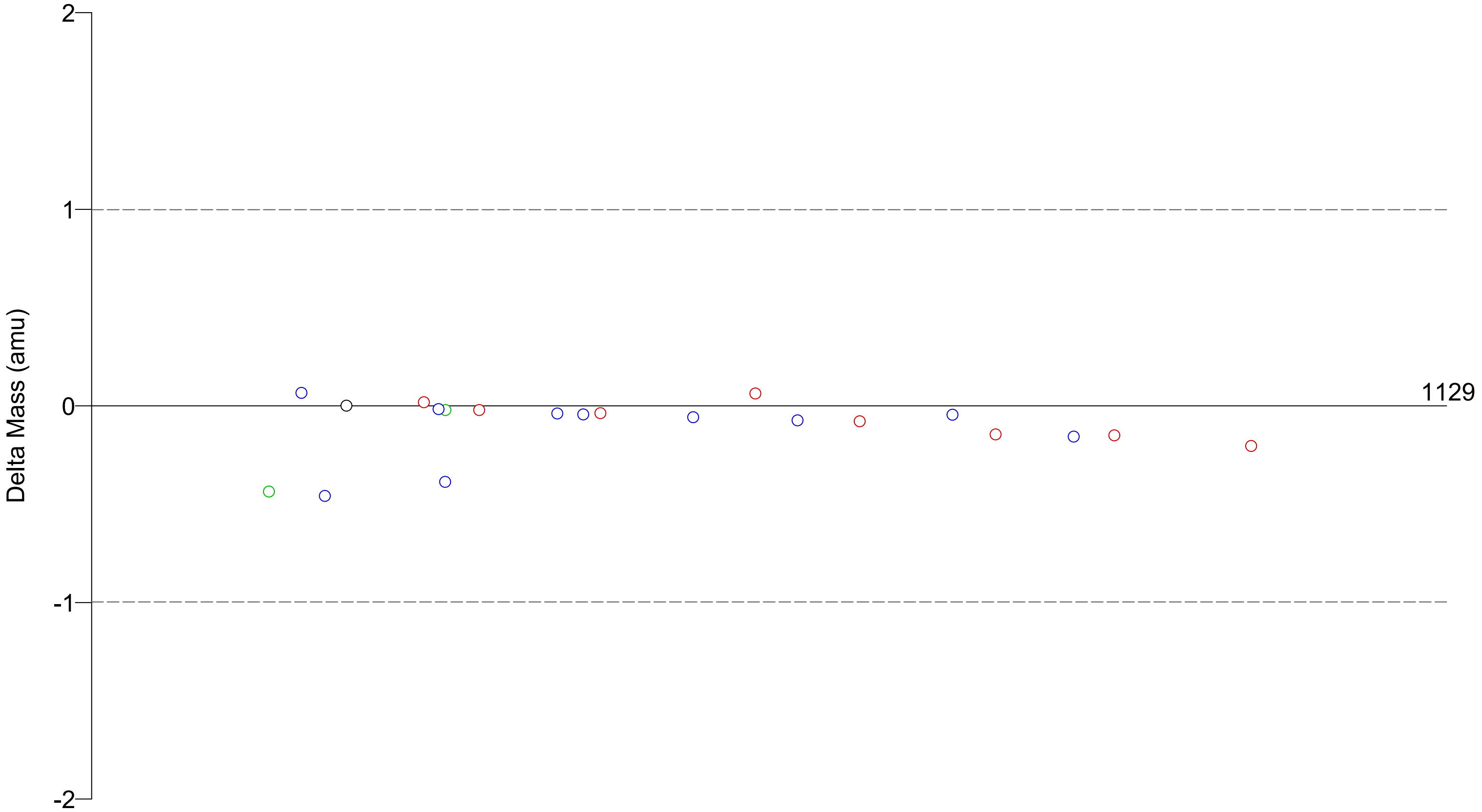


#19287468-1 NL: 8.98E6

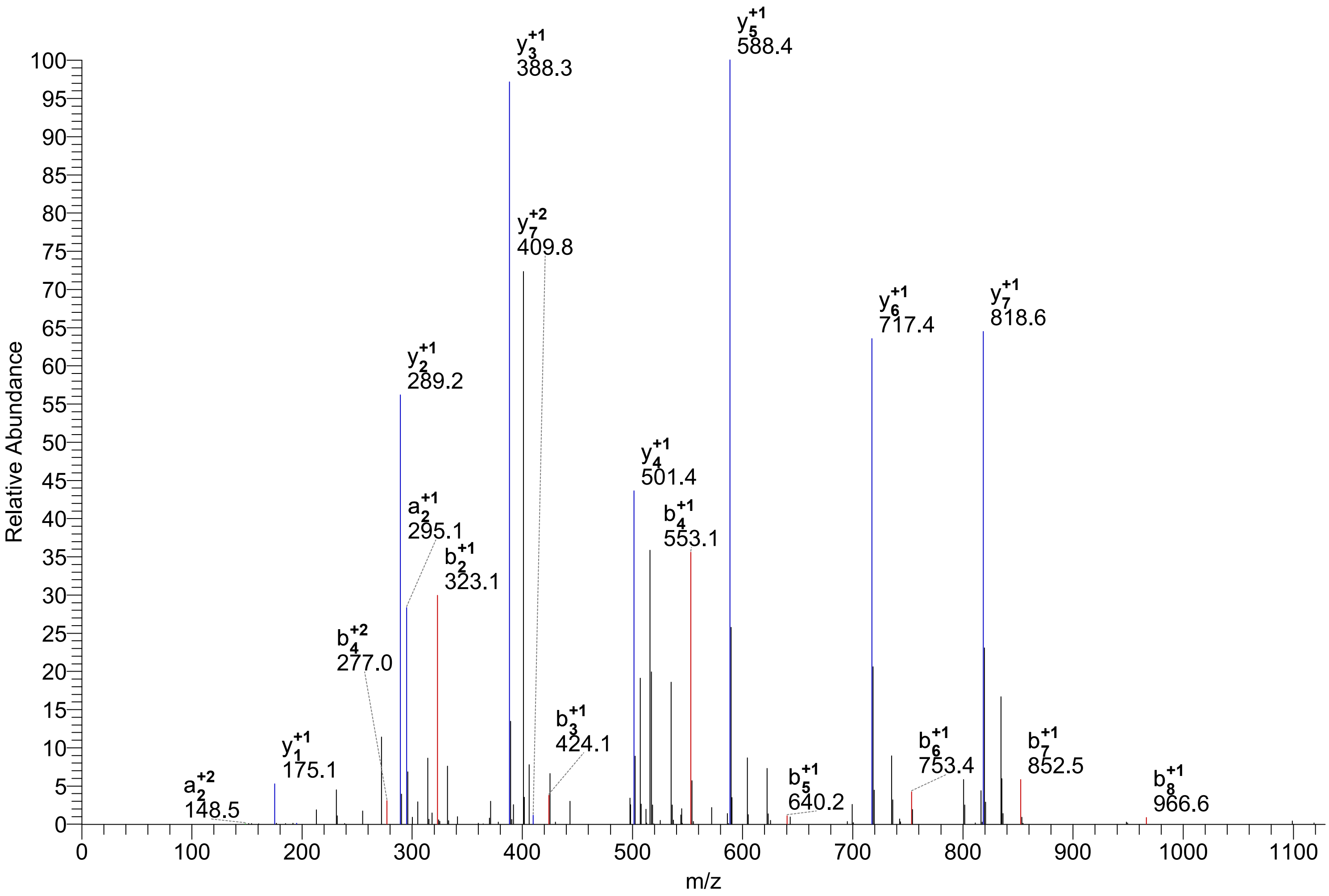


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00908876.1|TREMBL:B4DPR2 Ta                               0.0001  10.2     0.0       0
19287468 - 1  K.CCTESLVNR.R                          1140.47   2  0.0001  3.308  0.574   935.4  1   15/24   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                      979.45
 T    396.09     424.08                                      818.44
 E    525.13     553.13                                      717.39
 S    612.16     640.16                                      588.35
 L    725.25     753.24                                      501.31
 V    824.32     852.31                                      388.23
 N    938.36     966.35                                      289.16
 R                                                           175.12
```

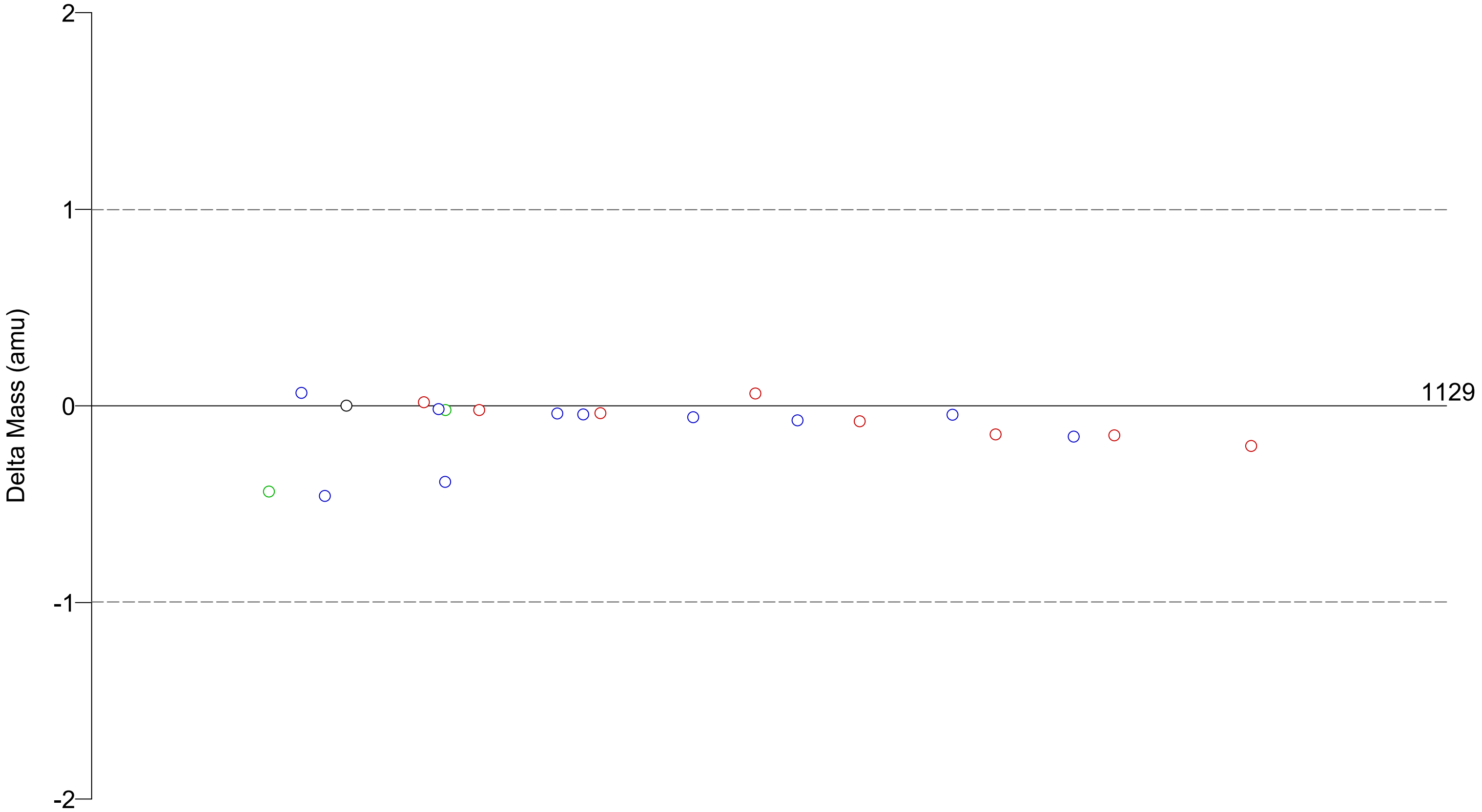


#19287468-1 NL: 8.98E6

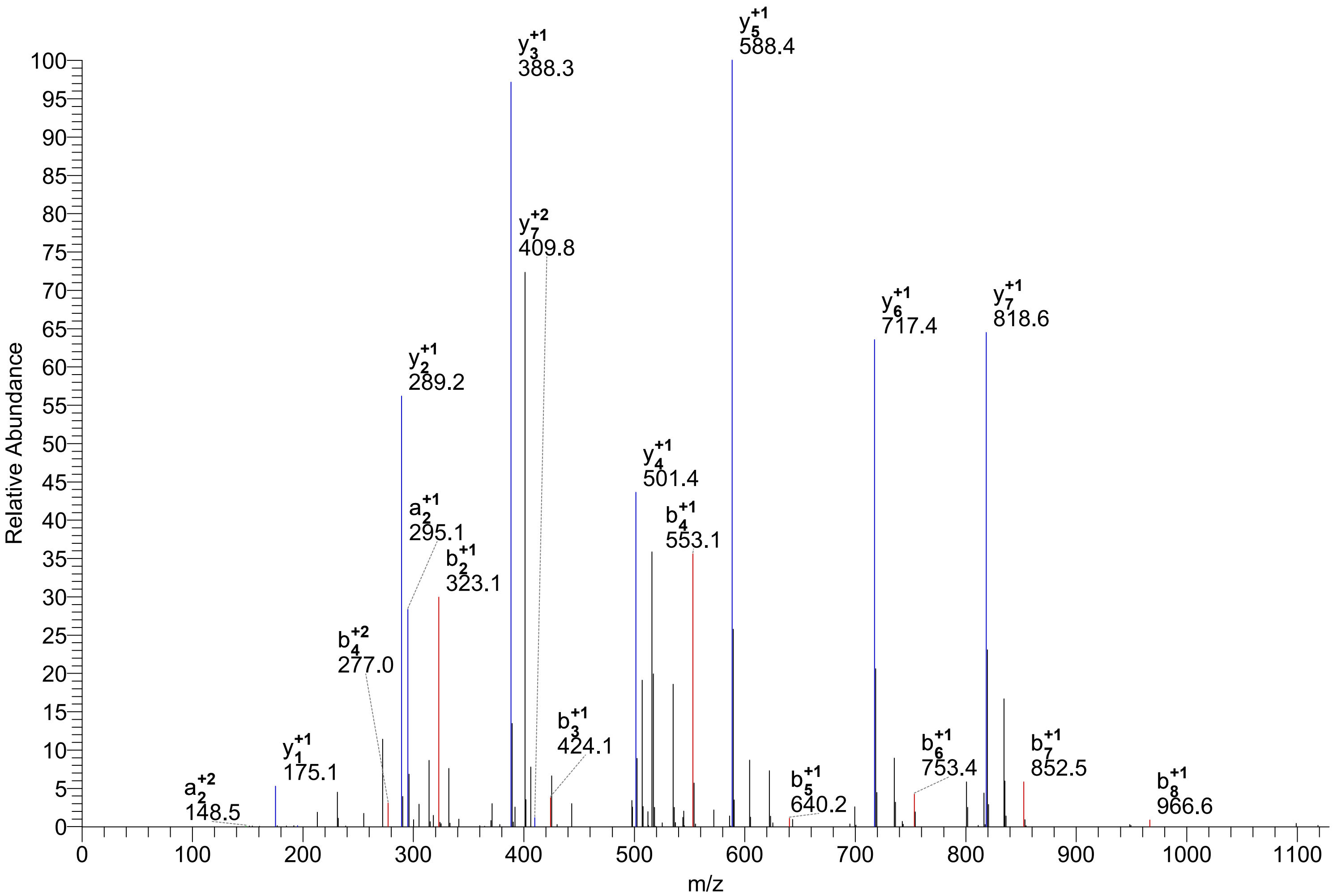


```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)        Sequence                                       MH+      z   P        XC  DeltaCn   Sp    RSp  Ions  Count

gi|229552|prf||754920A albumin [Bo                                       0.0001  10.2     0.0        229552
19287468 - 1  K.CCTESLVNR.R                                 1140.47    2  0.0001  3.308  0.574   935.4  1   15/24   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                      979.45
 T    396.09     424.08                                      818.44
 E    525.13     553.13                                      717.39
 S    612.16     640.16                                      588.35
 L    725.25     753.24                                      501.31
 V    824.32     852.31                                      388.23
 N    938.36     966.35                                      289.16
 R                                                           175.12
```

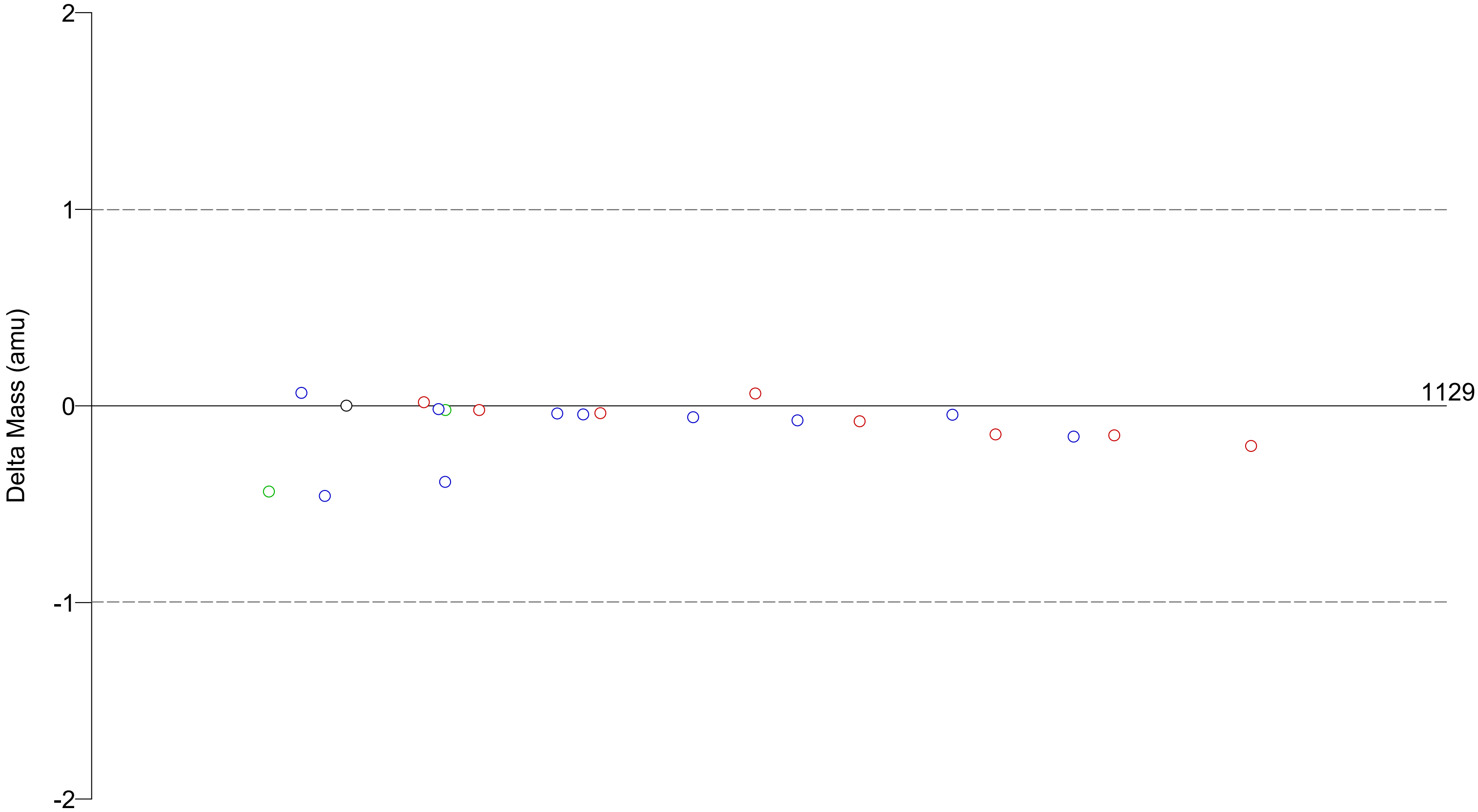


#19287468-1 NL: 8.98E6

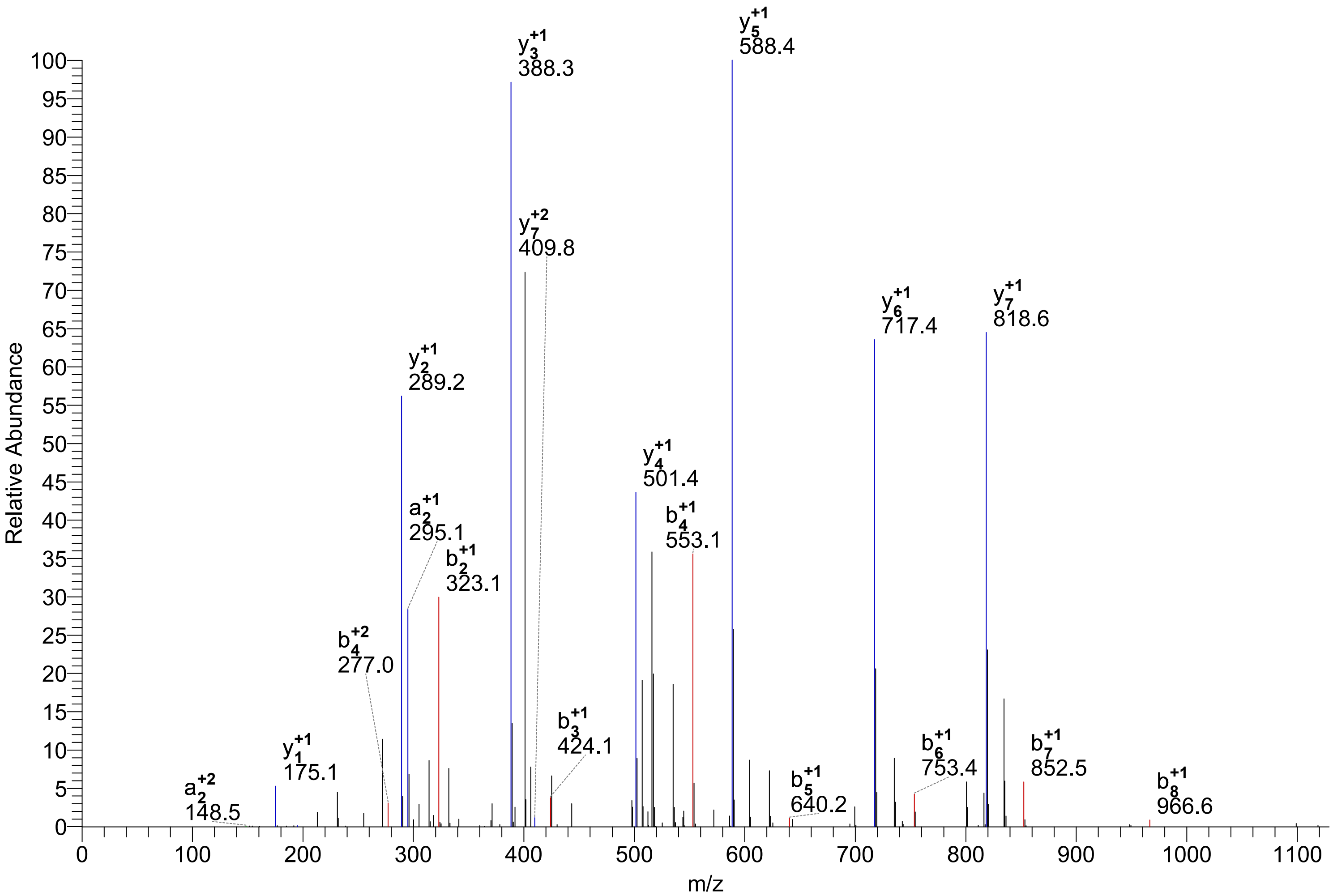


```
Reference                                                                    P      Score   Coverage   Accession
Scan(s)       Sequence                                        MH+       z    P        XC  DeltaCn   Sp    RSp  Ions  Count
gi|113574|sp|P02769|ALBU_BOVIN SER                                          0.0001  10.2     0.0        113574
19287468 - 1  K.CCTESLVNR.R                                 1140.47    2  0.0001  3.308  0.574   935.4  1   15/24   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 C    134.03     162.02
 C    295.04     323.04                                      979.45
 T    396.09     424.08                                      818.44
 E    525.13     553.13                                      717.39
 S    612.16     640.16                                      588.35
 L    725.25     753.24                                      501.31
 V    824.32     852.31                                      388.23
 N    938.36     966.35                                      289.16
 R                                                           175.12
```

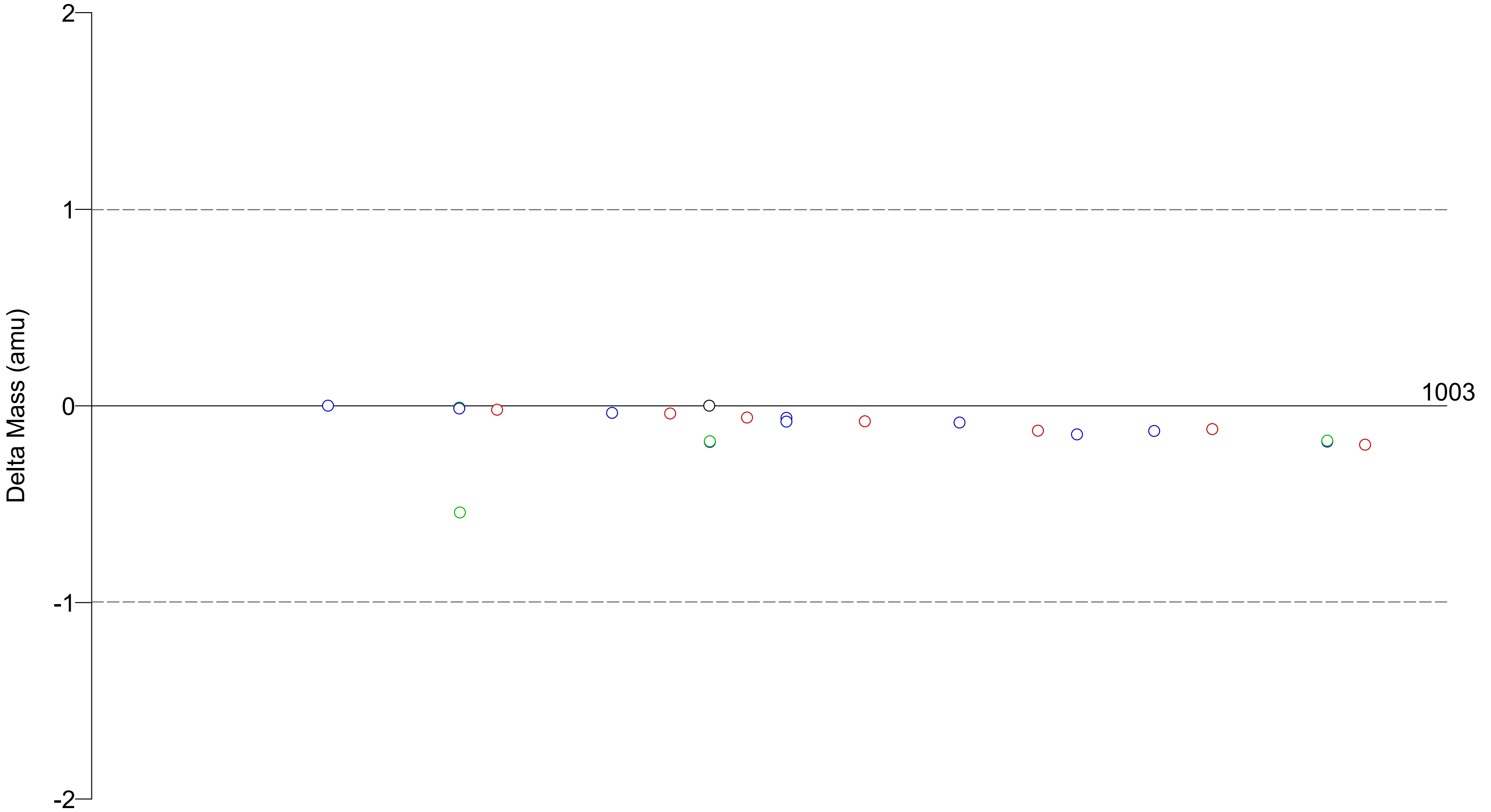


#19287468-1 NL: 8.98E6

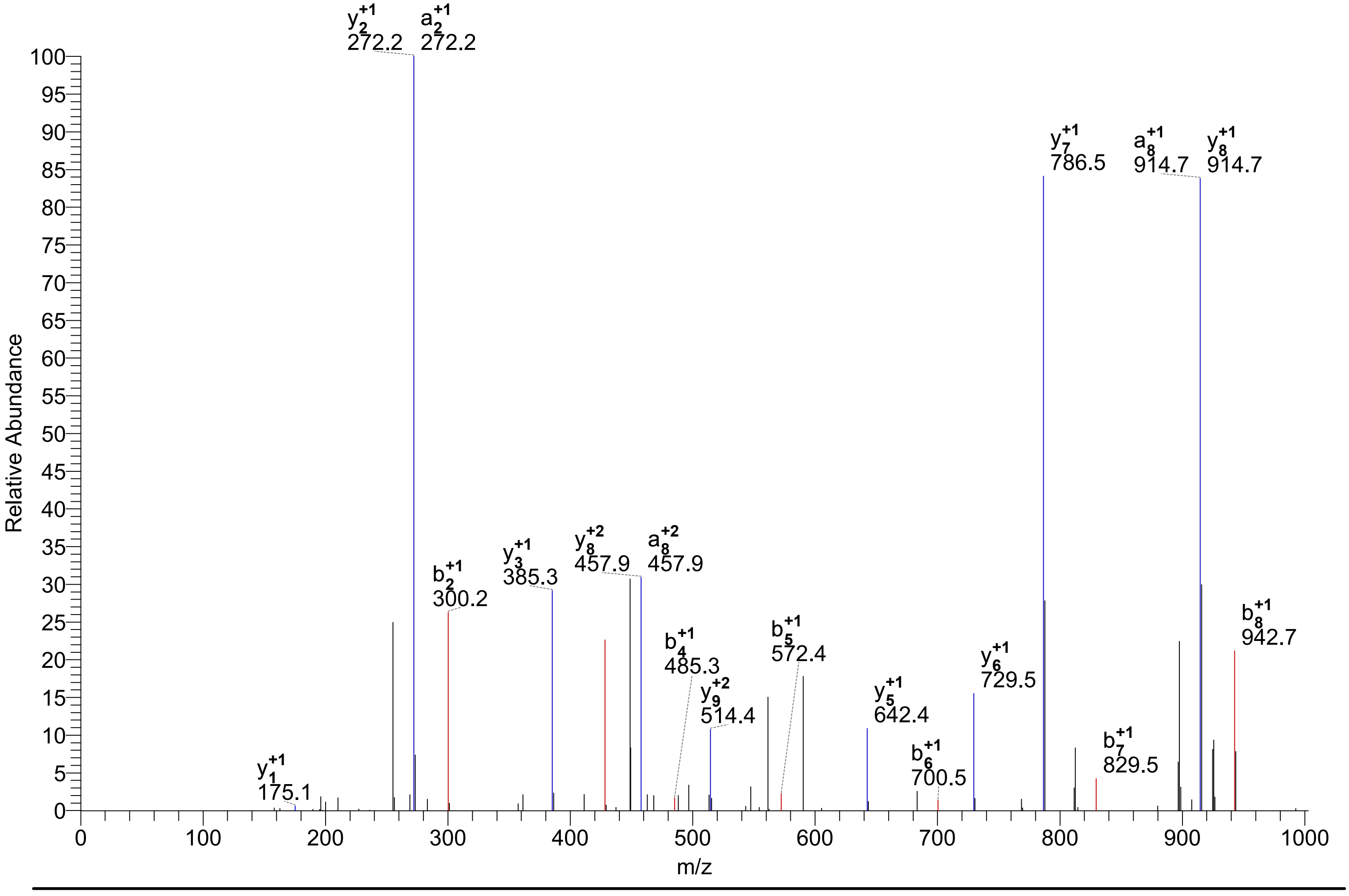


```
Reference                                                       P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00386879.1|TREMBL:Q96K68 Ta                                0.0001  18.2      0.0        0
19287468 - 1  R.WLQGSQELPR.E                        1213.63    2  0.0001  3.386  0.262   1272.1 1    18/27   19
19287468 - 1  K.NSLYLQM*NSLR.A                      1354.68    2  0.002   2.168  0.118   607.2  1    14/30   30

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

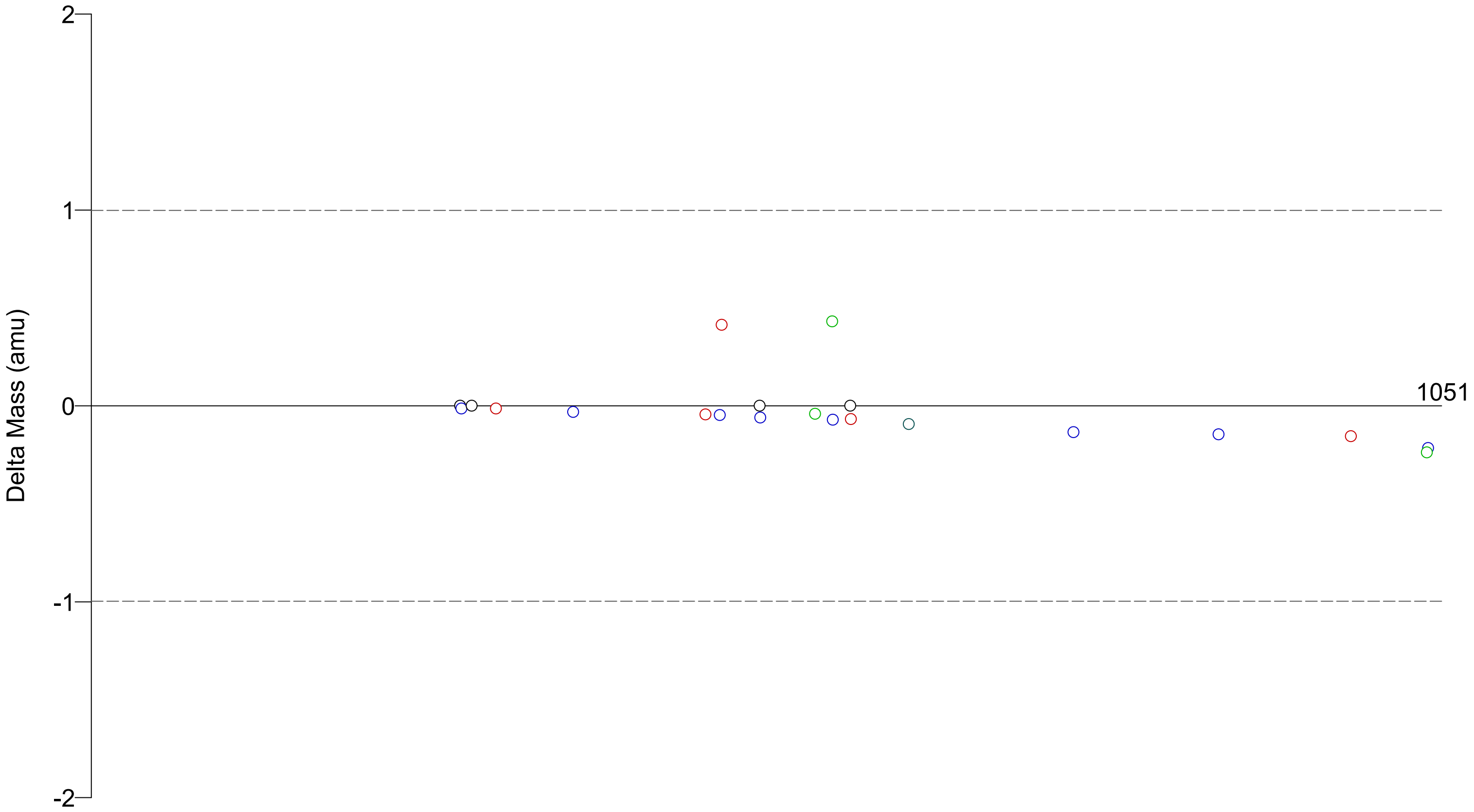
```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```



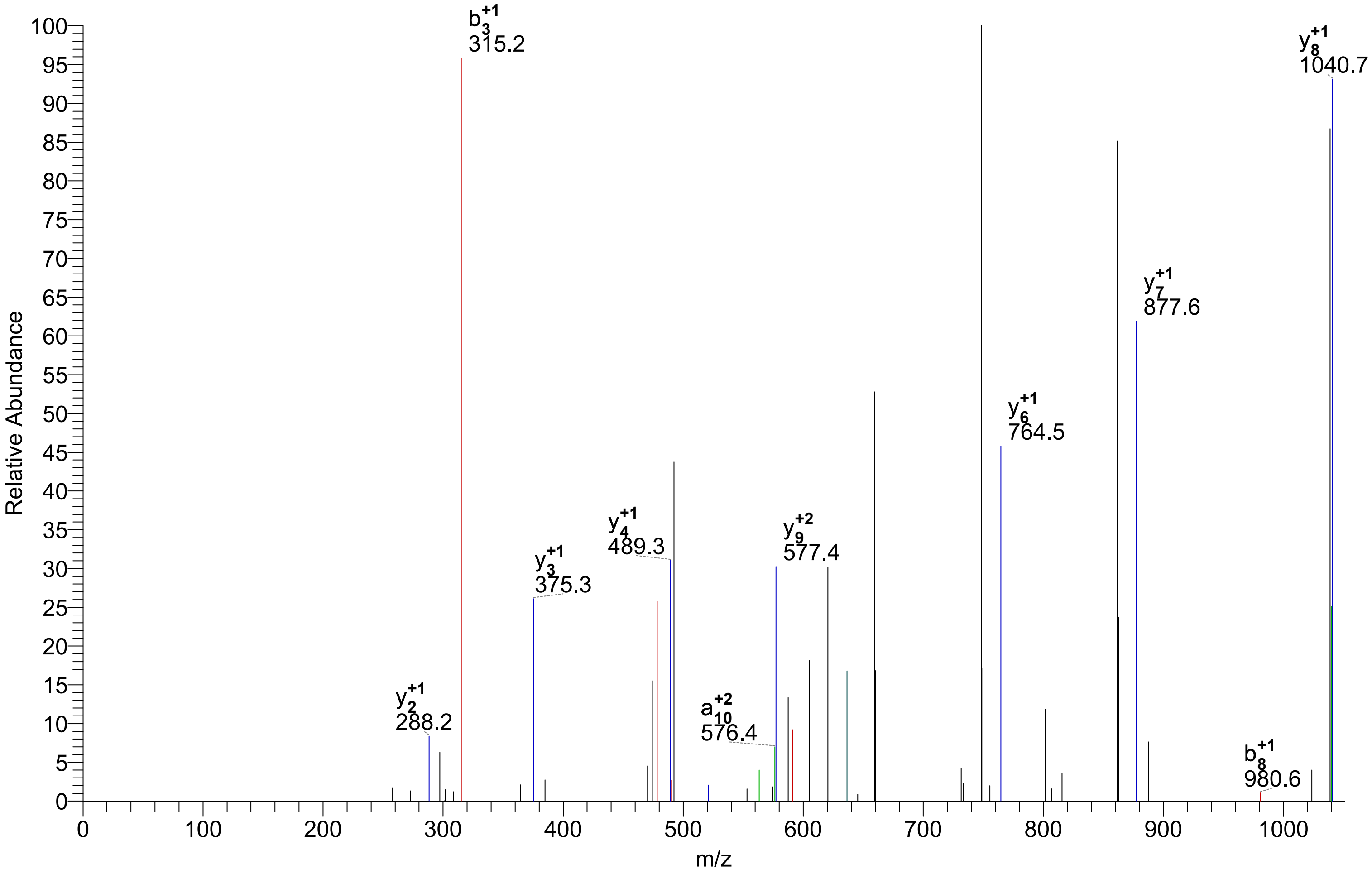
#19287468-1 NL: 1.26E5



```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N      87.06     115.05
 S     174.09     202.08                                    1240.64
 L     287.17     315.17                                    1153.60
 Y     450.23     478.23                                    1040.52
 L     563.32     591.31                                     877.46
 Q     691.38     719.37                                     764.37
 M*    838.41     866.41                                     636.31
 N     952.46     980.45                                     489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

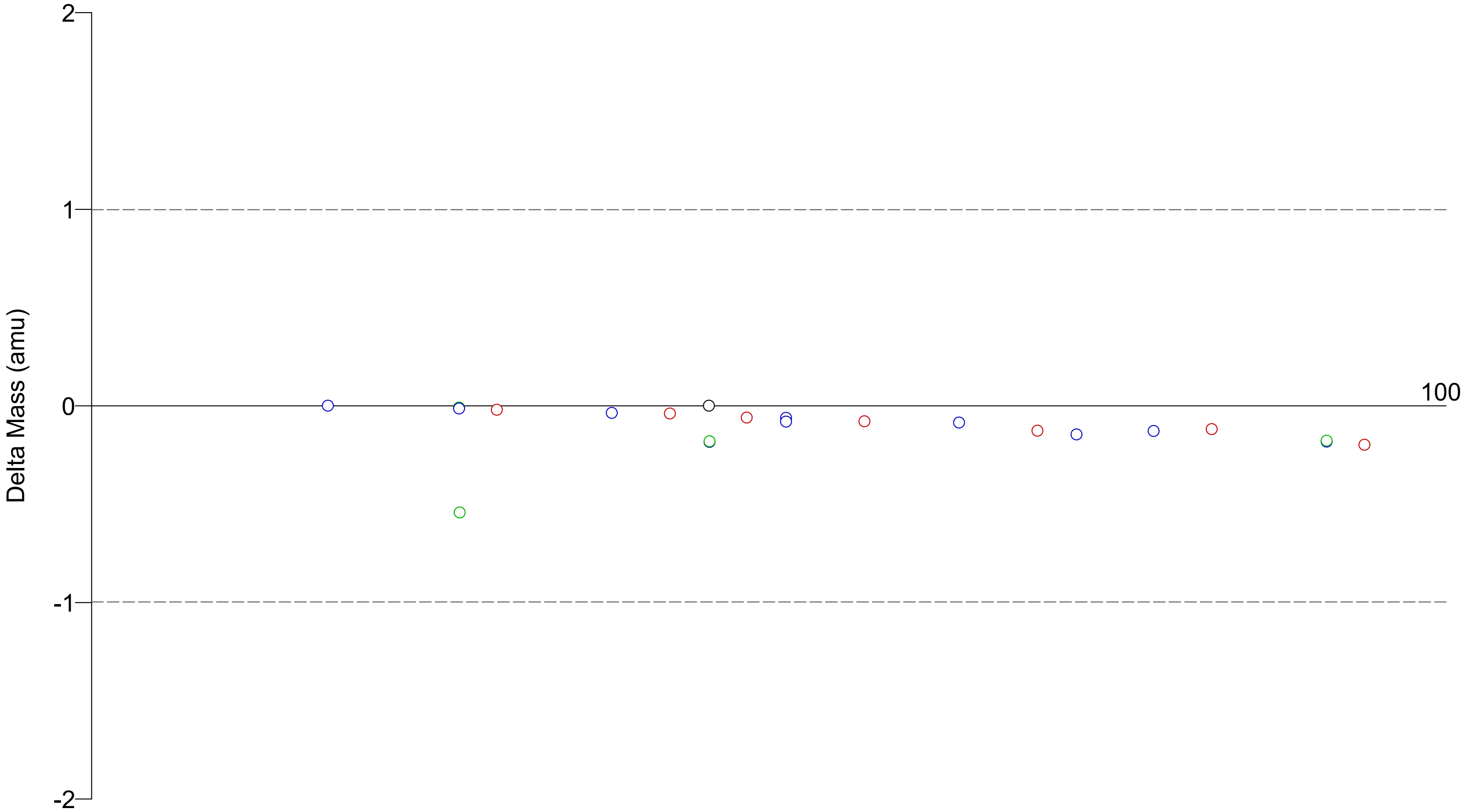


#19287468-1 NL: 8.93E4

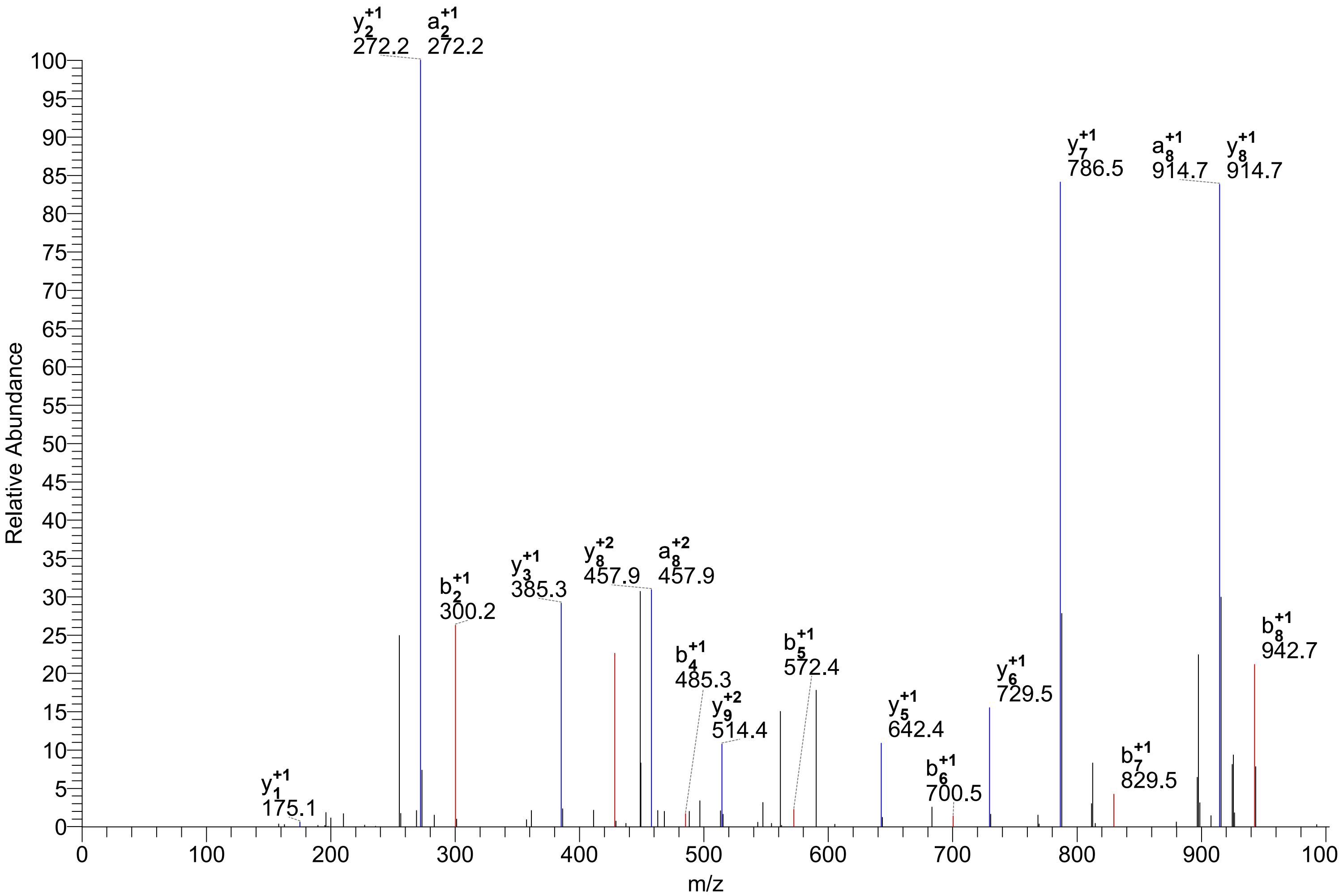


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00784950.1|TREMBL:Q6MZV6 Ta                                0.0001  18.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

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

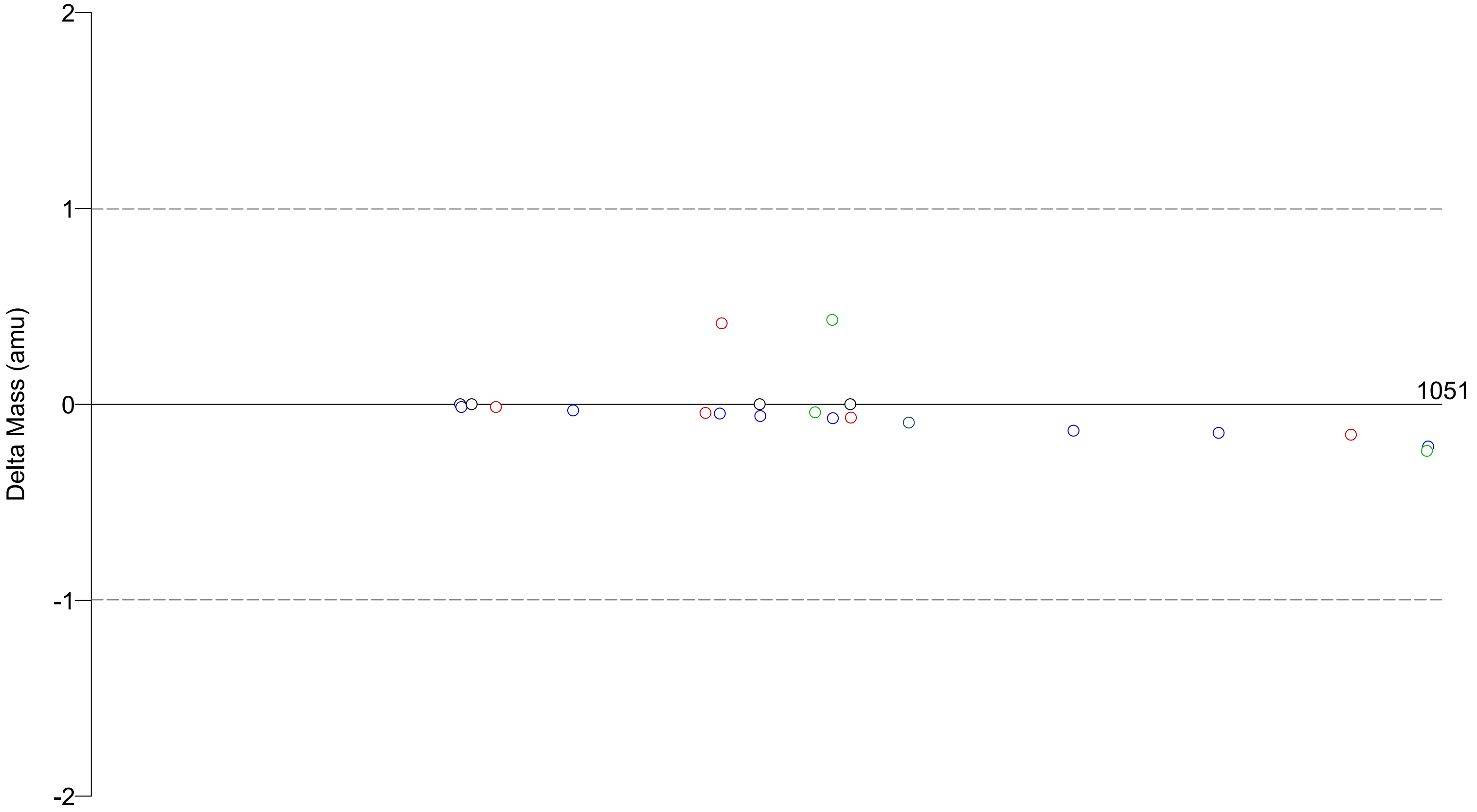
```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```



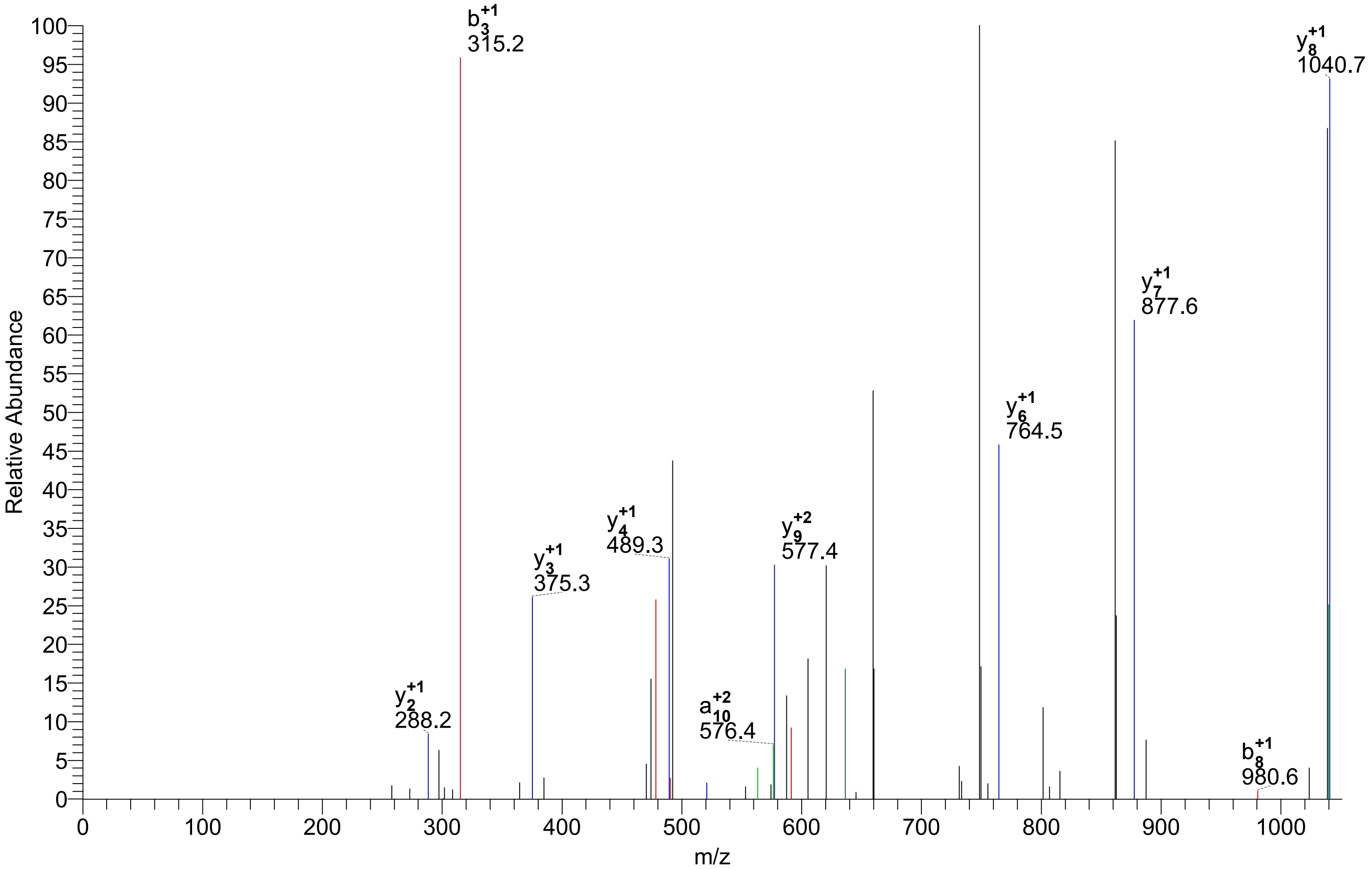
#19287468-1 NL: 1.26E5



```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

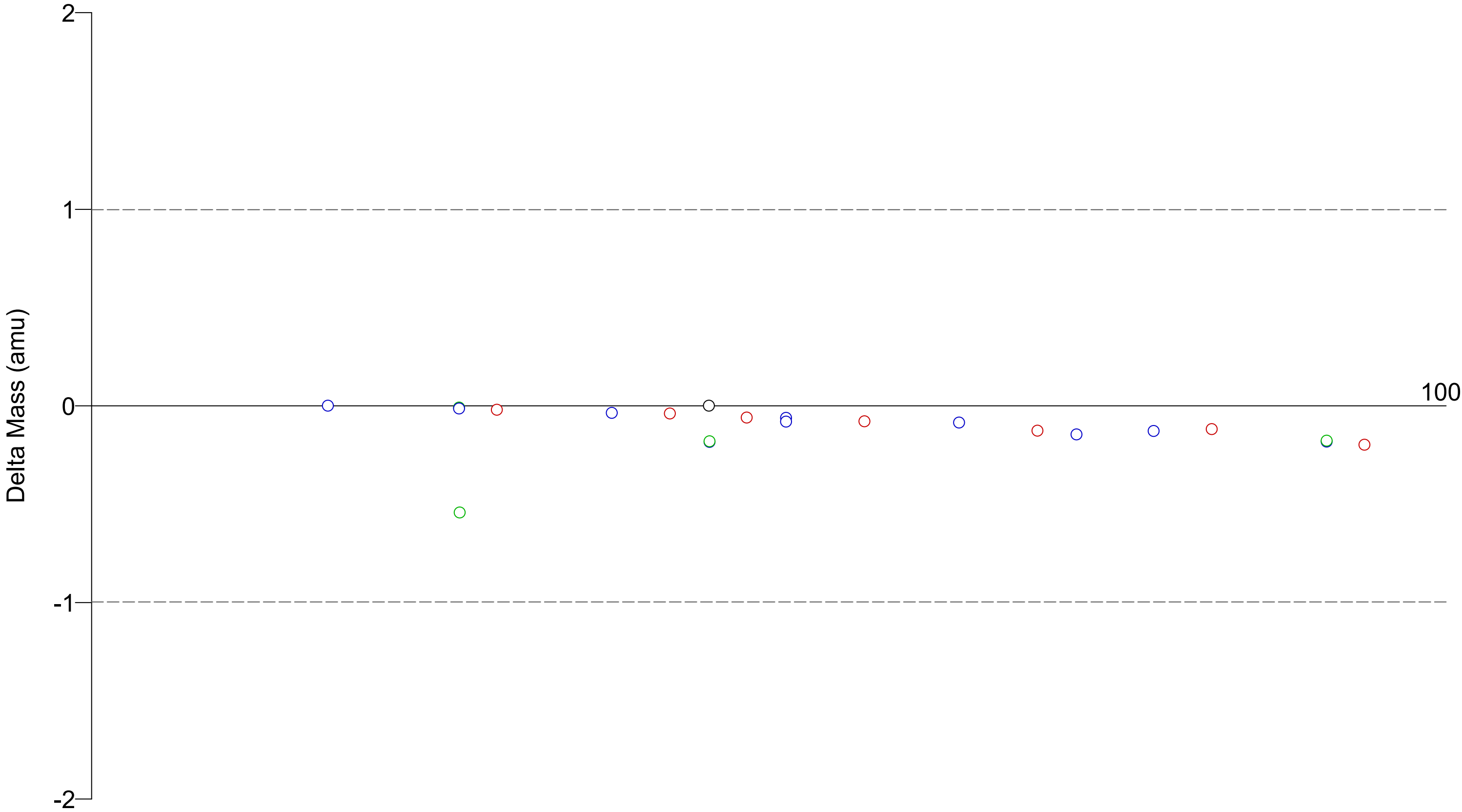


#19287468-1 NL: 8.93E4

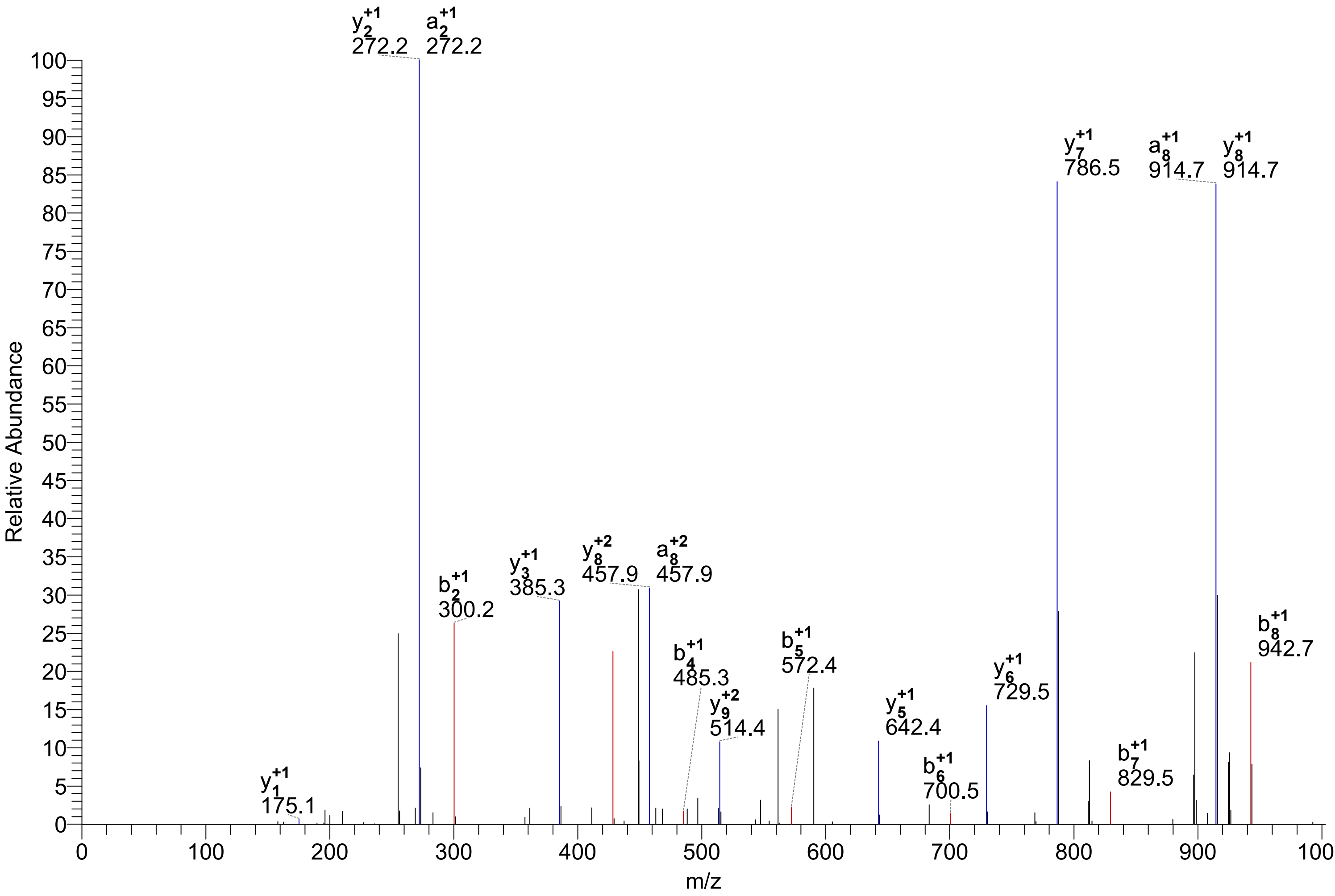


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00383164.1|TREMBL:Q8WY24 Tax_Id=9606 Gene_Symbol=IGHA1     0.0001  10.2      0.0        0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262    1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions    Y ions    Y* ions     Yo ions     Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

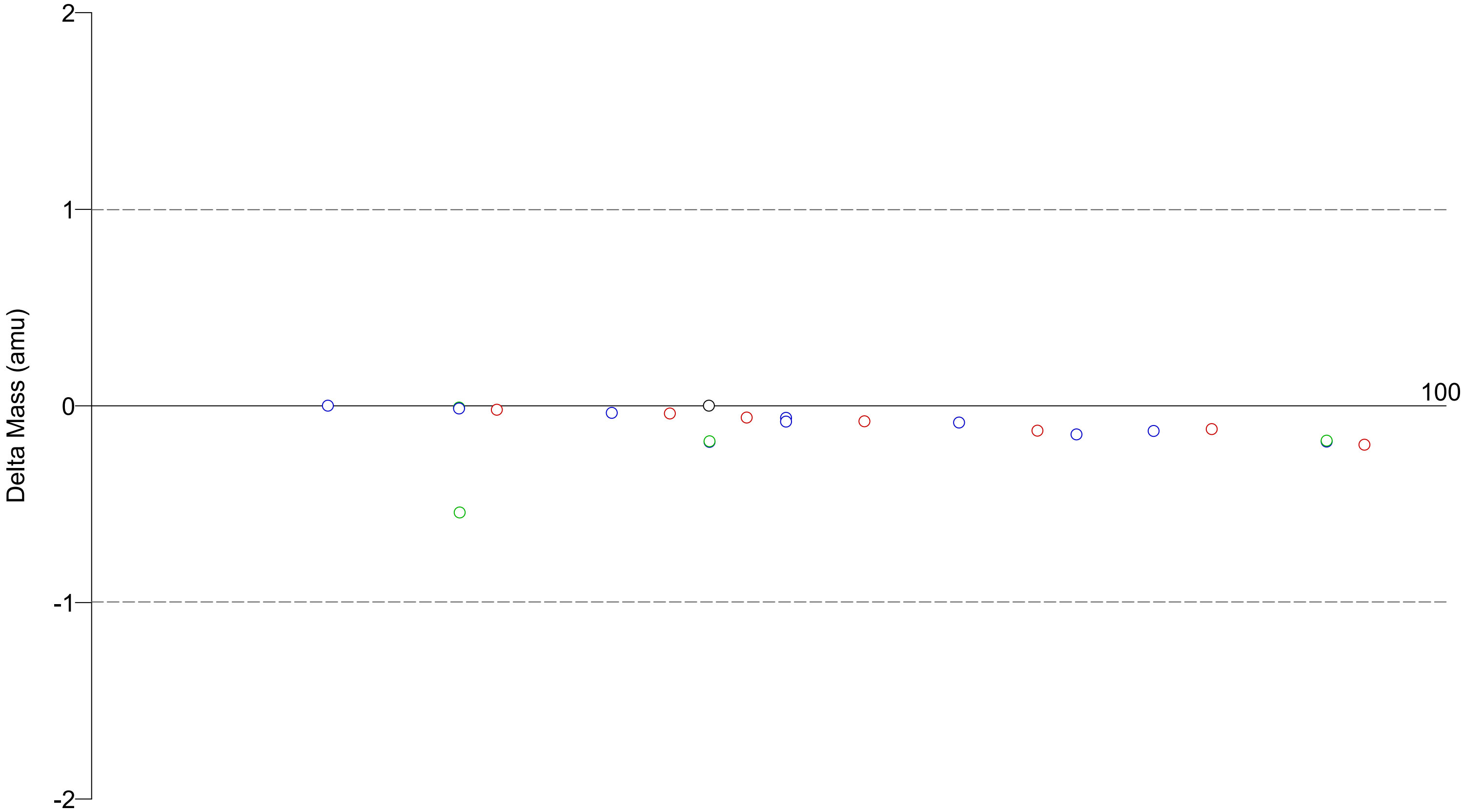


#19287468-1 NL: 1.26E5

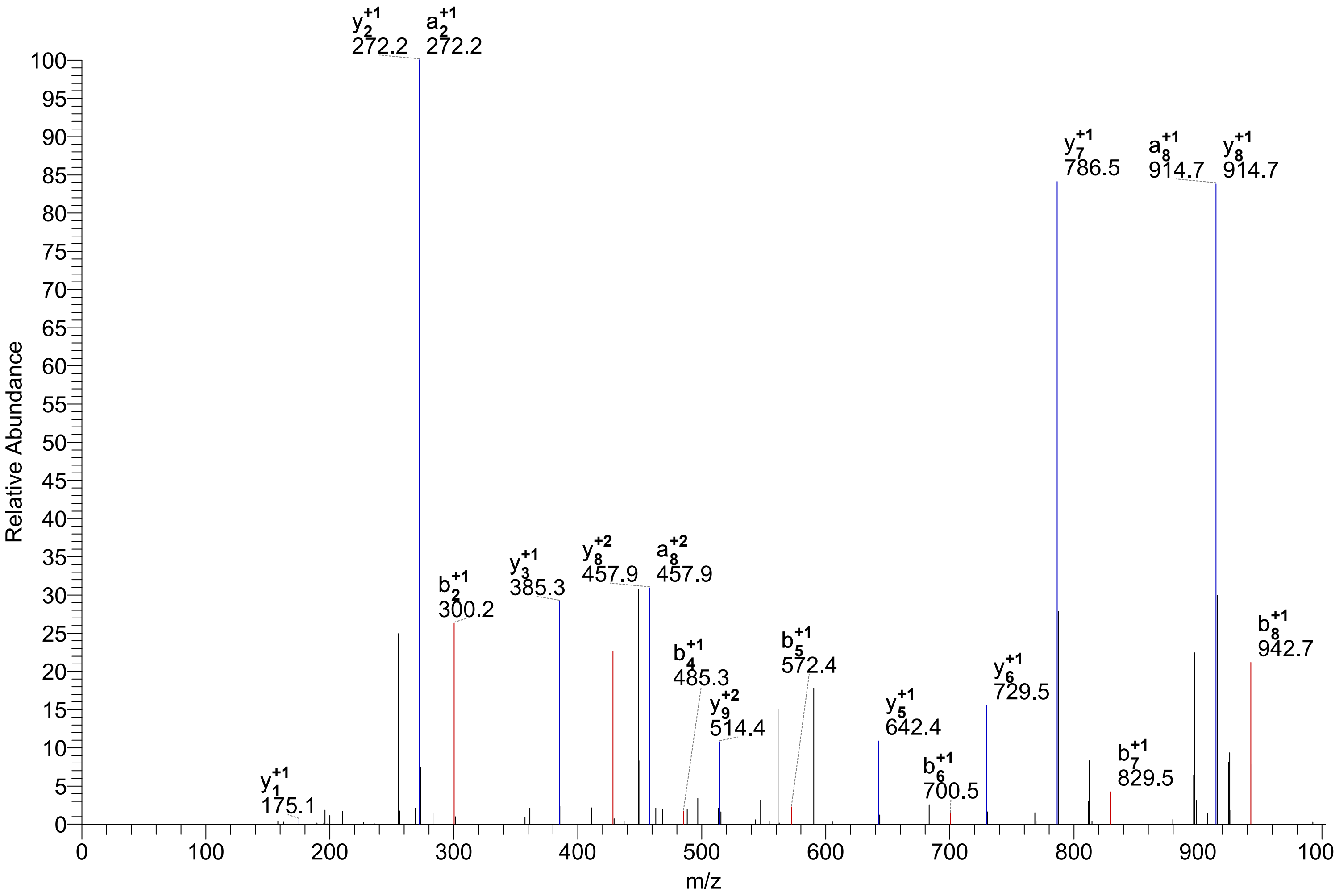


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00384952.1|TREMBL:Q7Z379 Ta                                0.0001  10.2      0.0        0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

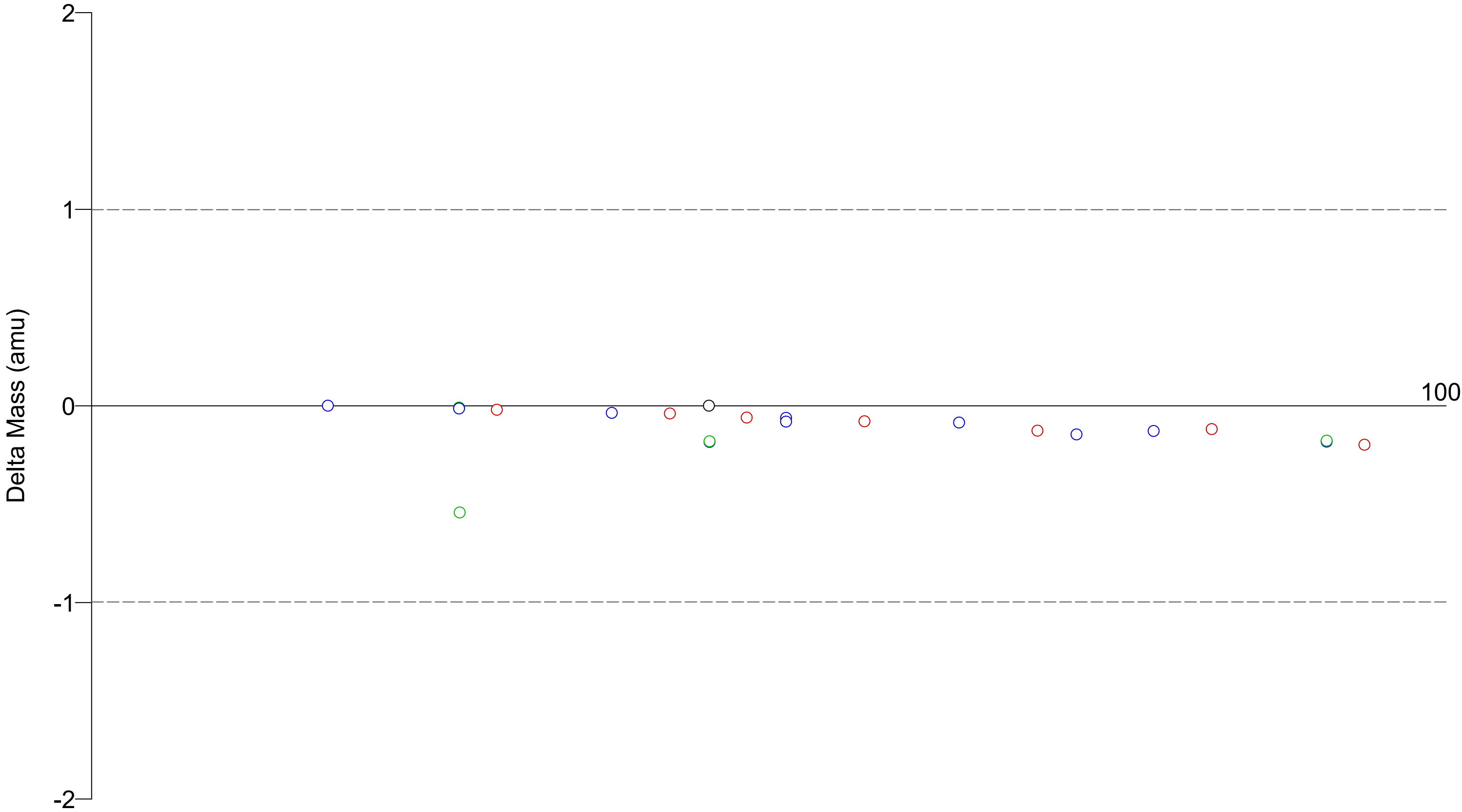


#19287468-1 NL: 1.26E5

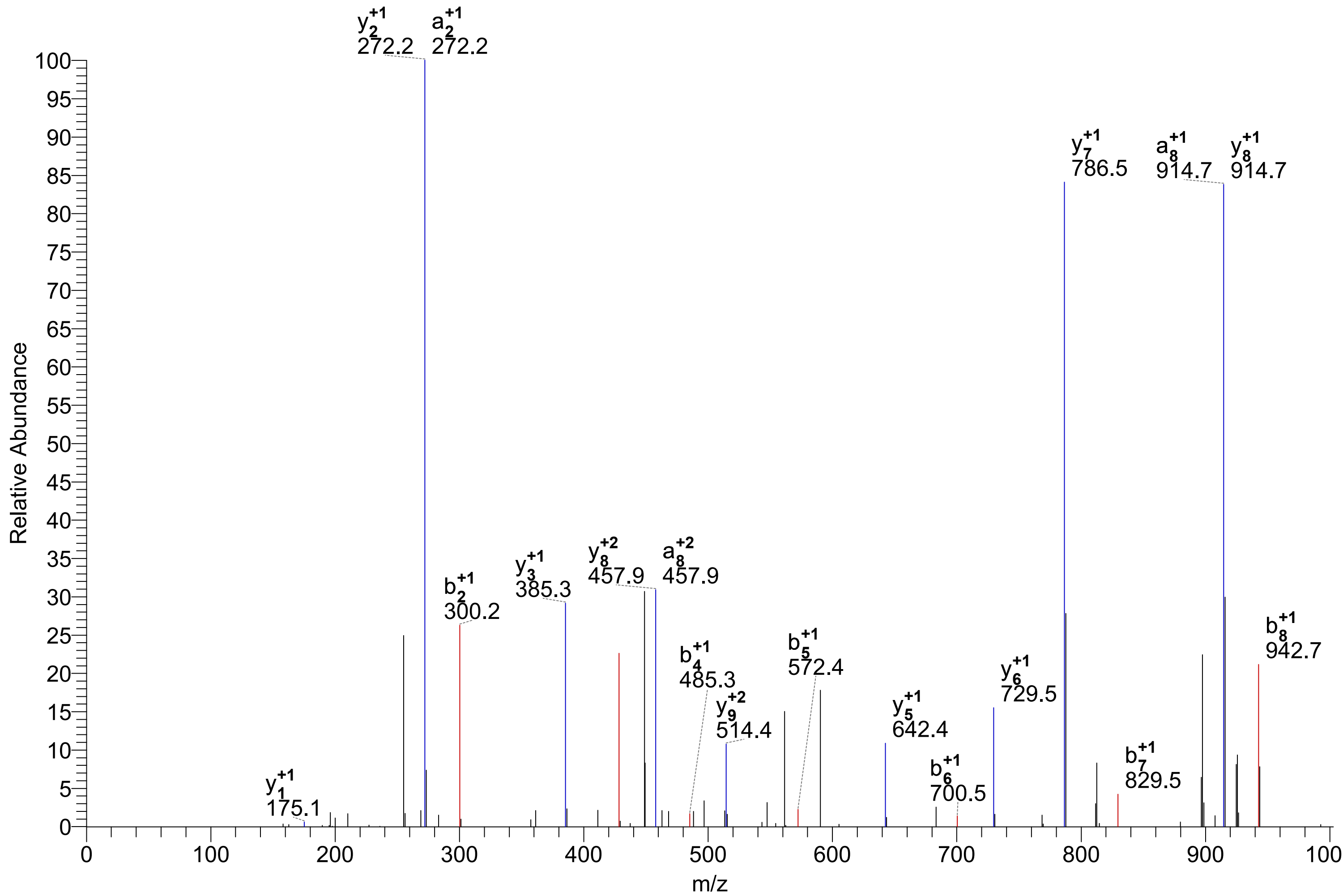


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                beadMH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00386524.3|TREMBL:Q96DK0 Ta                                0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions     Y ions     Y* ions     Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                       1027.55
 Q    400.23     428.23                                        914.47
 G    457.26     485.25                                        786.41
 S    544.29     572.28                                        729.39
 Q    672.35     700.34                                        642.36
 E    801.39     829.38                                        514.30
 L    914.47     942.47                                        385.26
 P   1011.53    1039.52                                        272.17
 R                                                             175.12
```

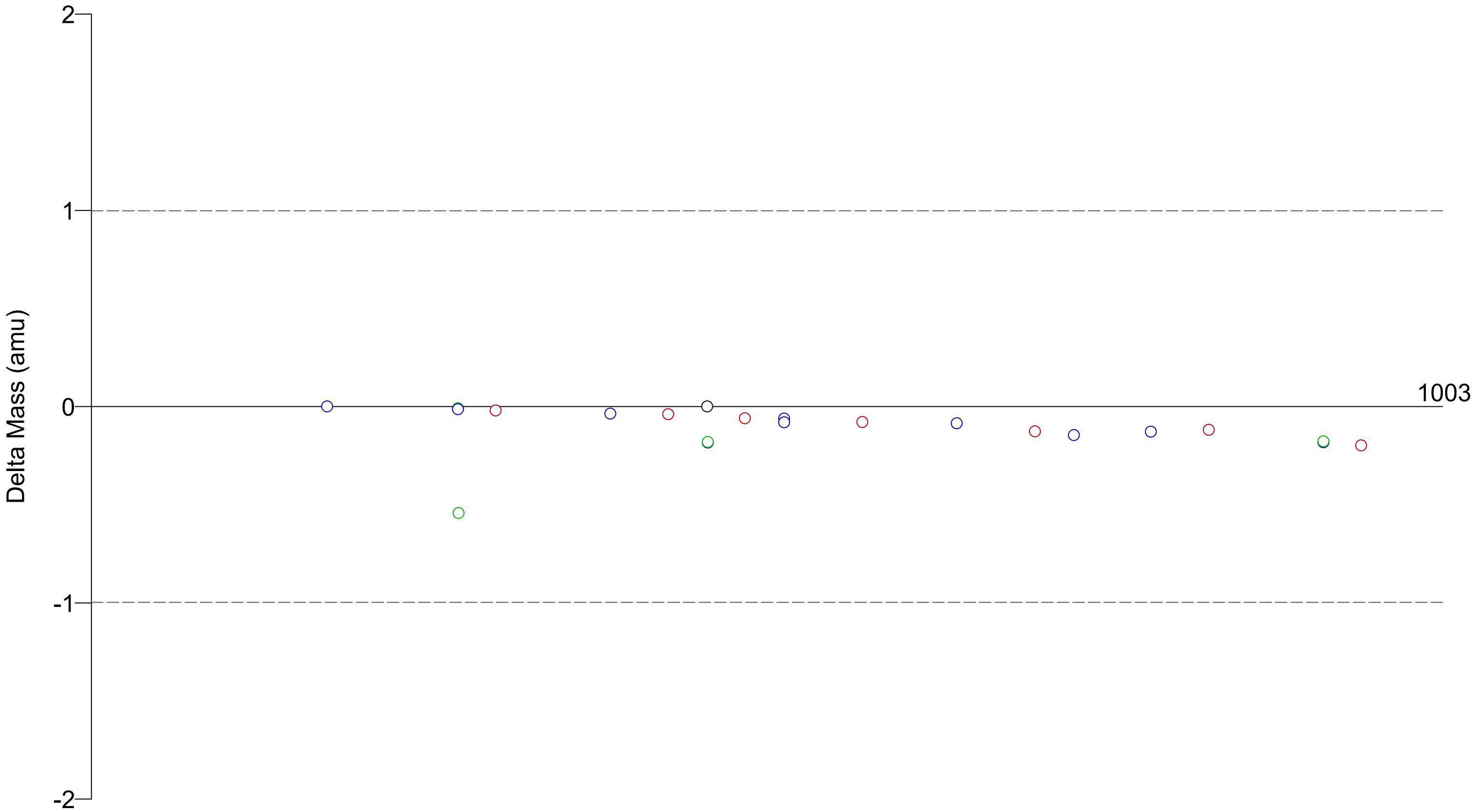


#19287468-1 NL: 1.26E5

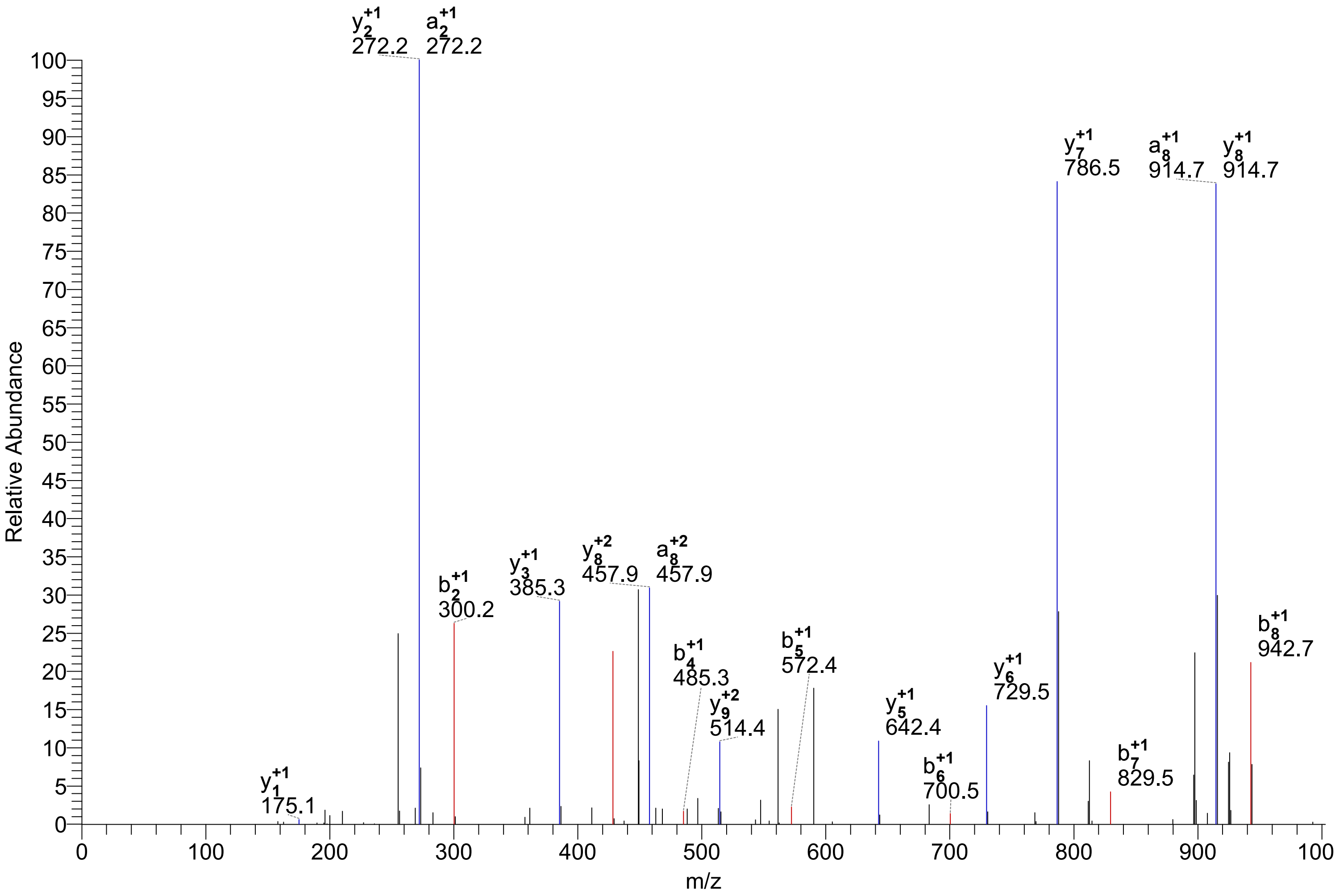


```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z    P         XC  DeltaCn   Sp    RSp  Ions  Count

IPI:IPI00423460.3|TREMBL:Q6N090 Ta                                       0.0001  10.2      0.0        0
19287468 - 1  R.WLQGSQELPR.E                             1213.63    2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

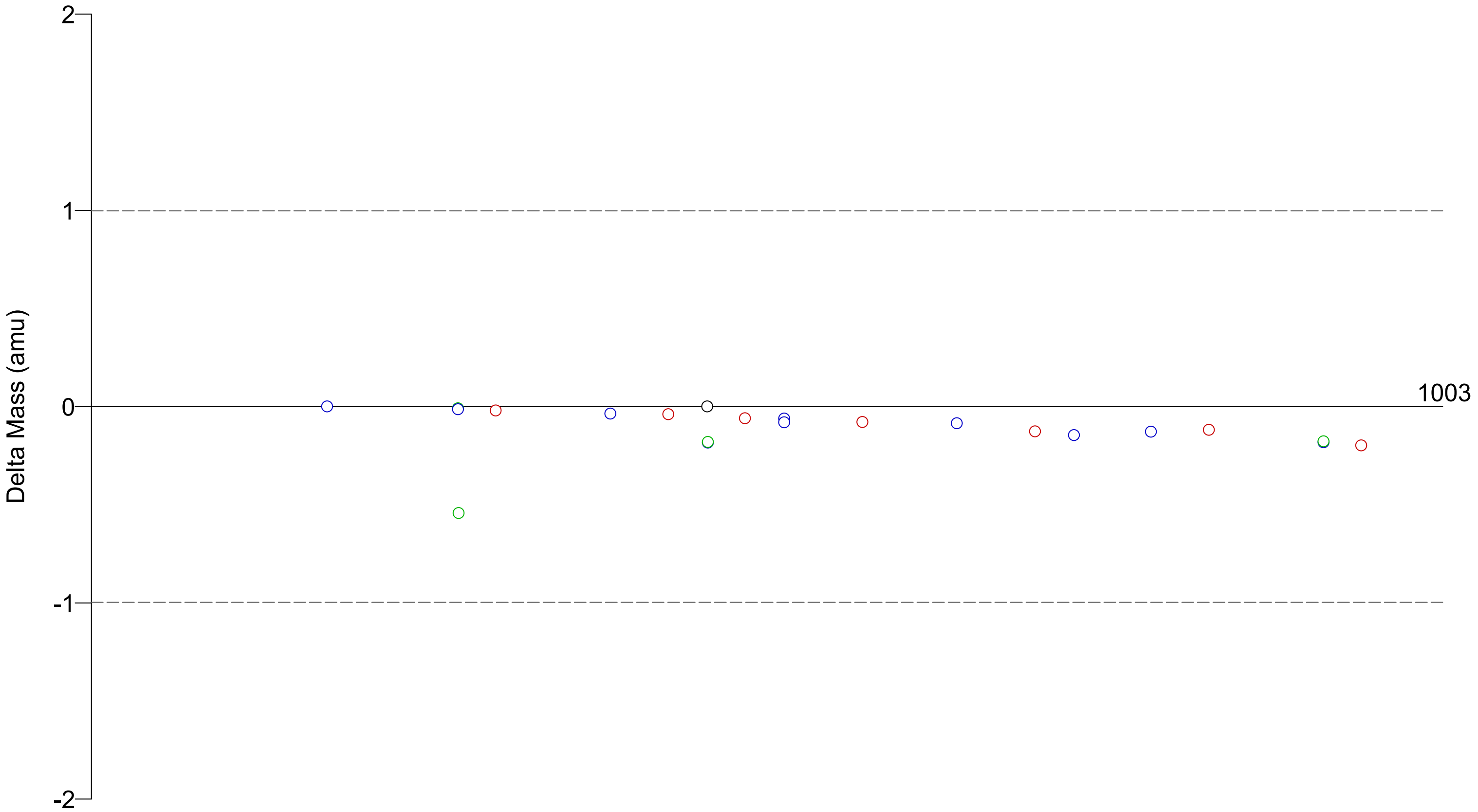


#19287468-1 NL: 1.26E5

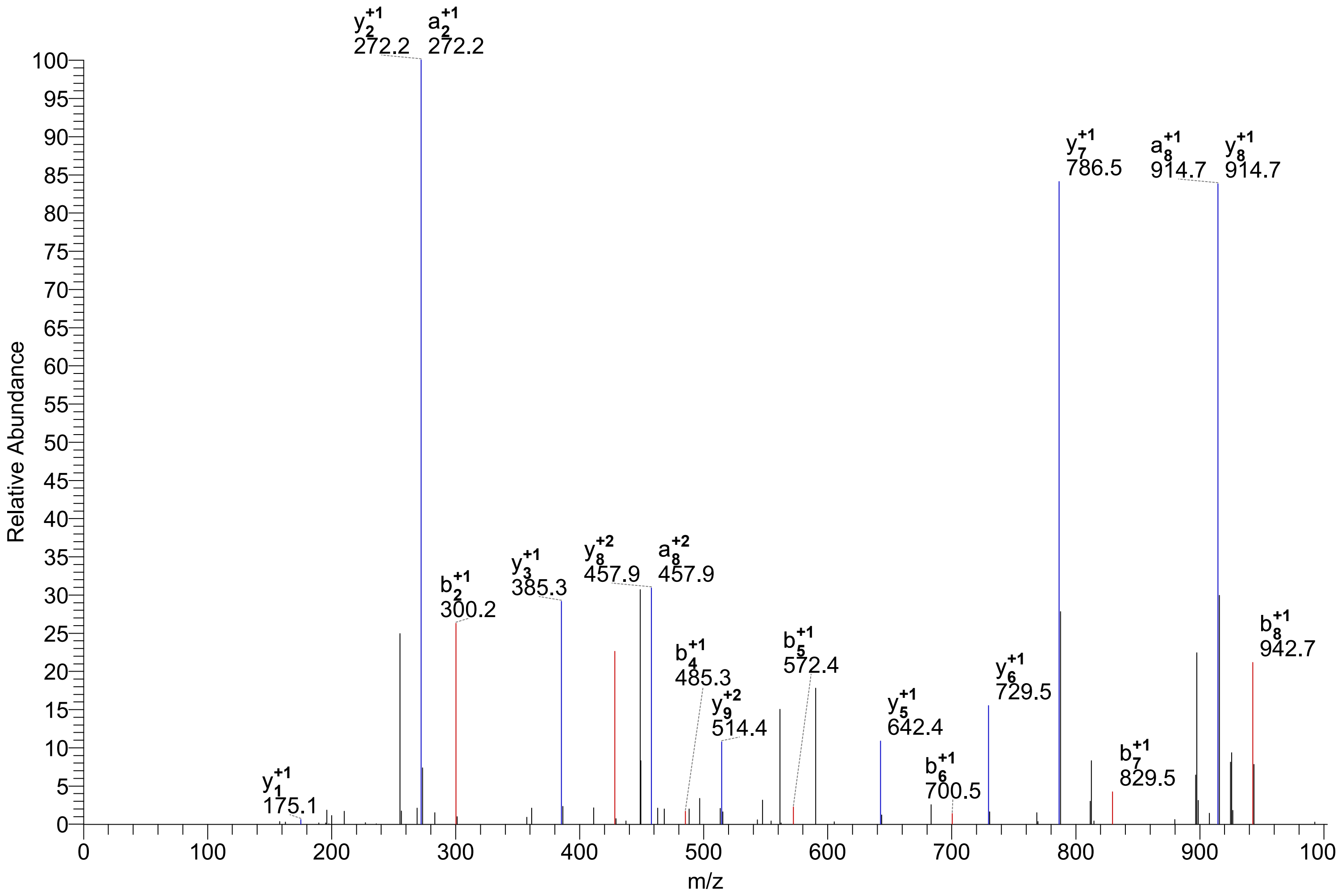


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00423461.3|TREMBL:Q6N091 Ta                               0.0001  10.2     0.0        0
19287468 - 1  R.WLQGSQELPR.E                       1213.63    2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

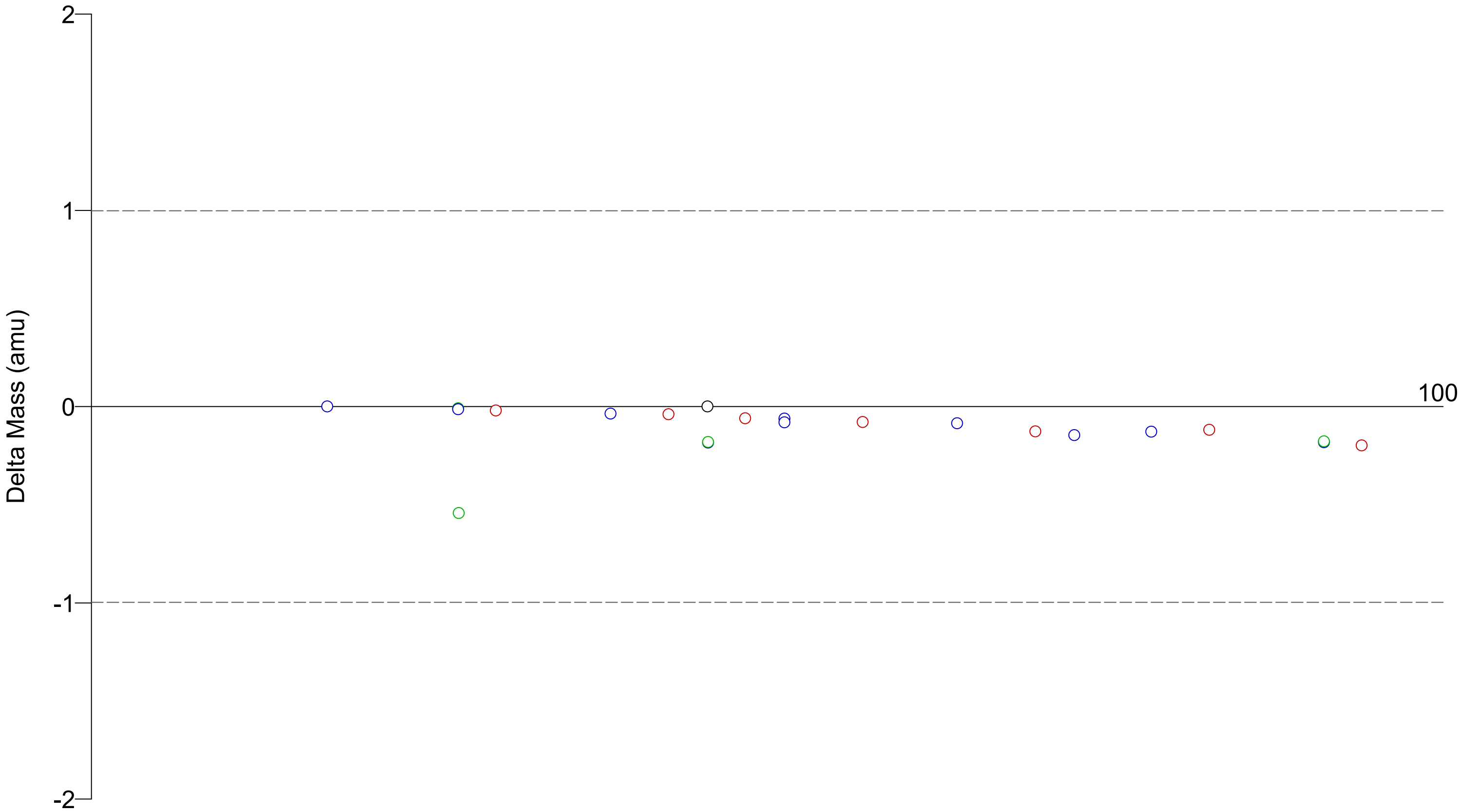


#19287468-1 NL: 1.26E5

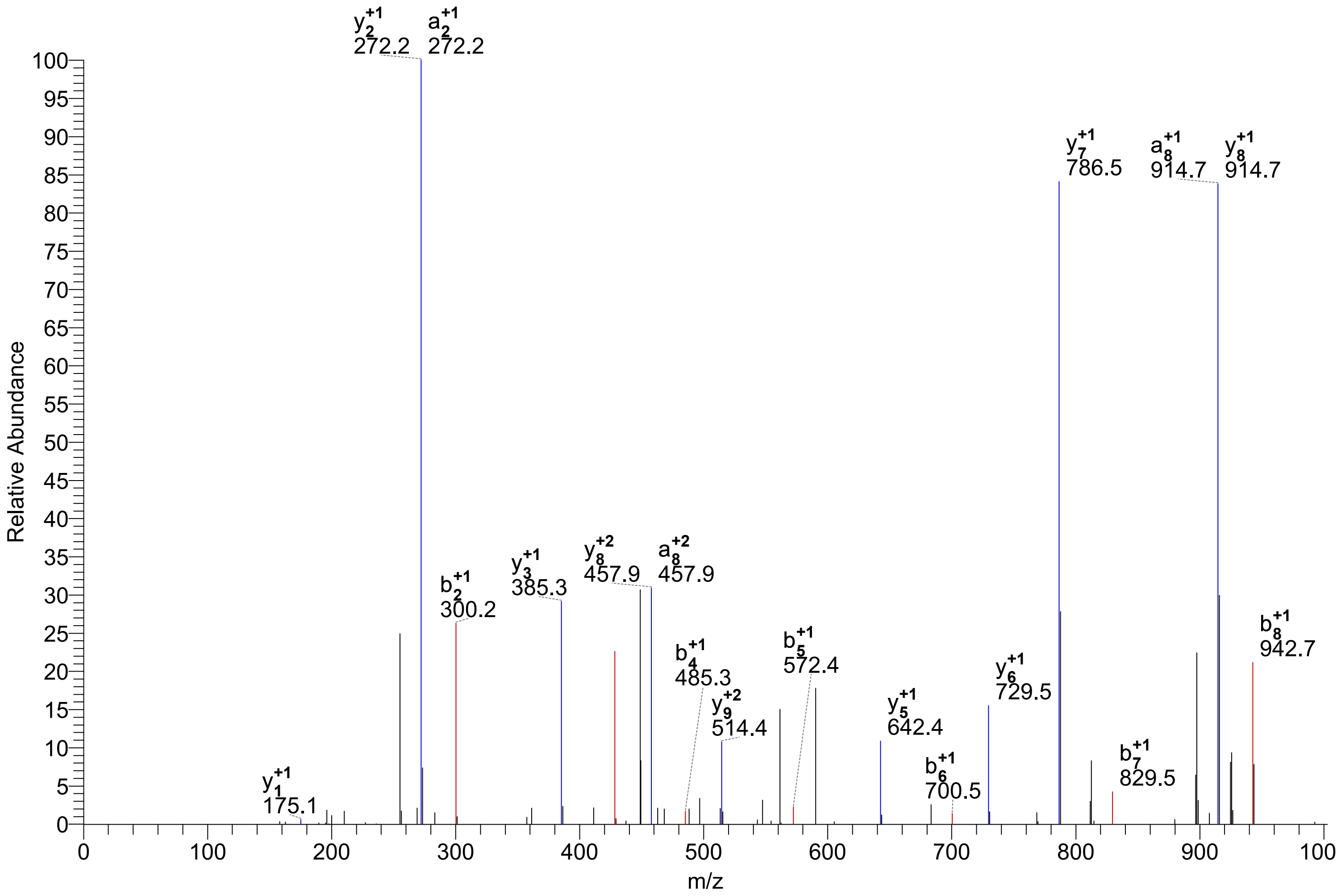


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp    RSp  Ions  Count

IPI:IPI00423462.5|TREMBL:Q6N092 Ta                                0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                      1027.55
 Q    400.23     428.23                                       914.47
 G    457.26     485.25                                       786.41
 S    544.29     572.28                                       729.39
 Q    672.35     700.34                                       642.36
 E    801.39     829.38                                       514.30
 L    914.47     942.47                                       385.26
 P   1011.53    1039.52                                       272.17
 R                                                            175.12
```

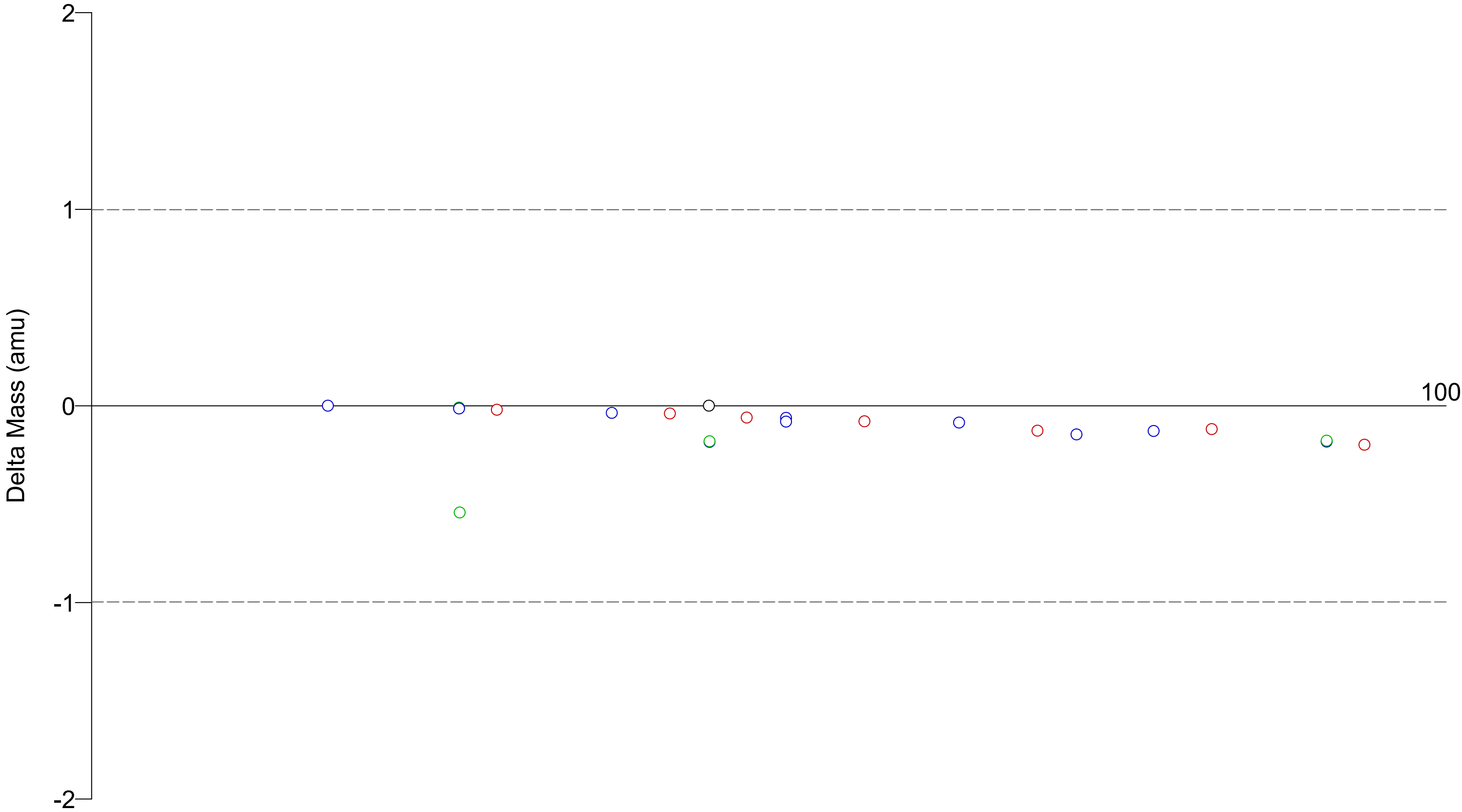


#19287468-1 NL: 1.26E5

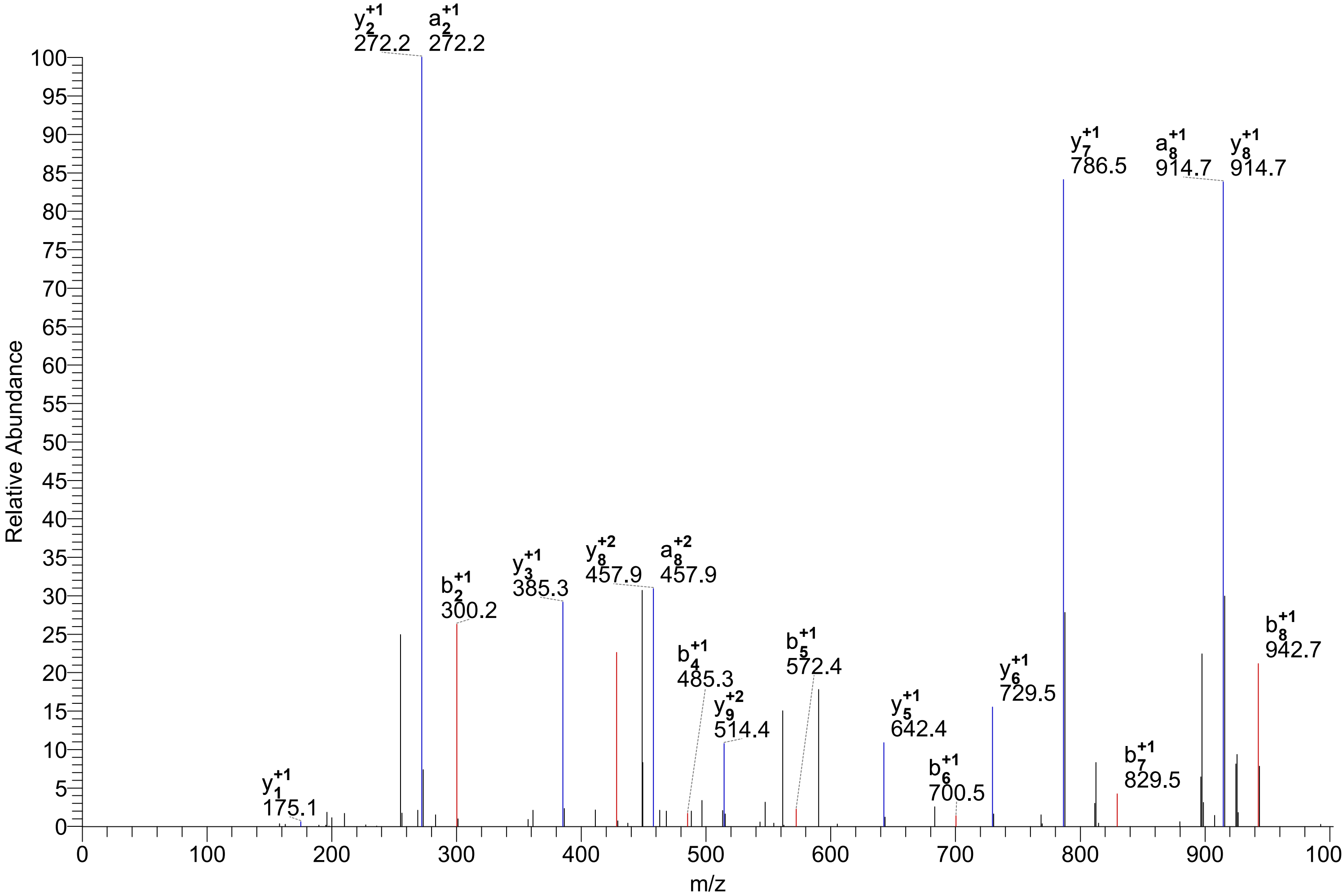


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P        XC DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00426060.3|TREMBL:Q6MZW0 Ta                                 0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63    2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

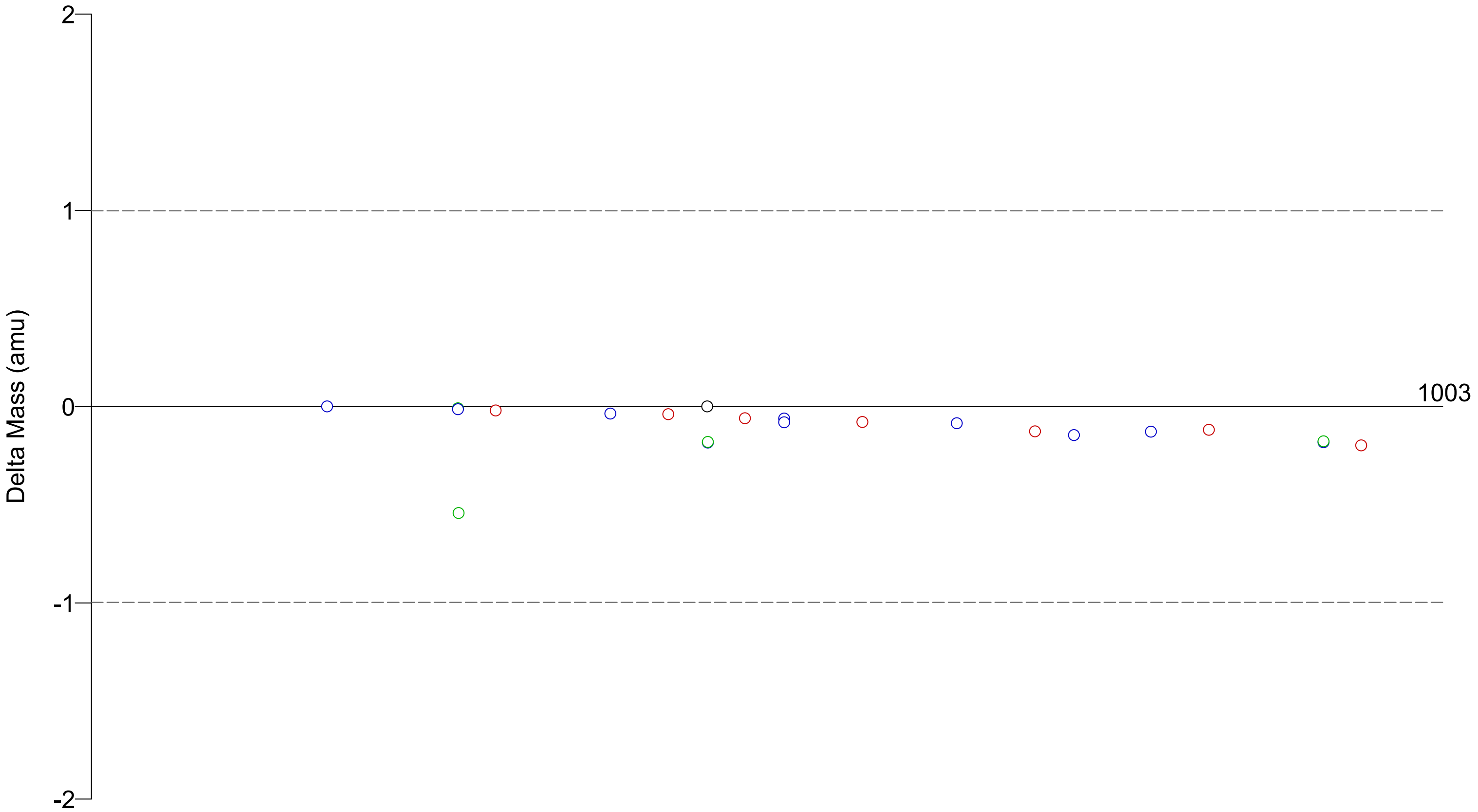


#19287468-1 NL: 1.26E5

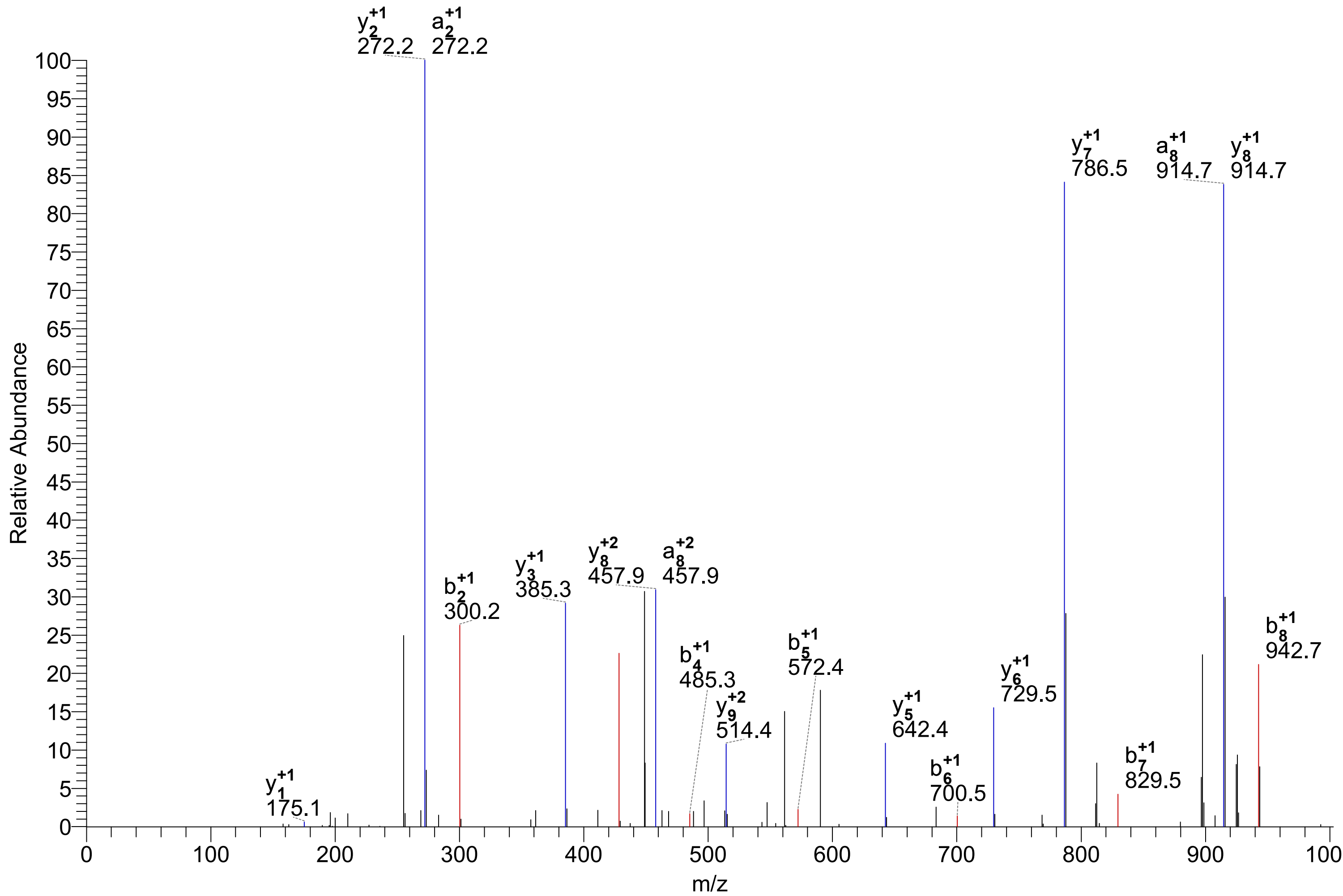


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count

IPI:IPI00449920.1|SWISS-PROT:P0187                                0.0001  10.2      0.0        0
19287468 - 1  R.WLQGSQELPR.E                          1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

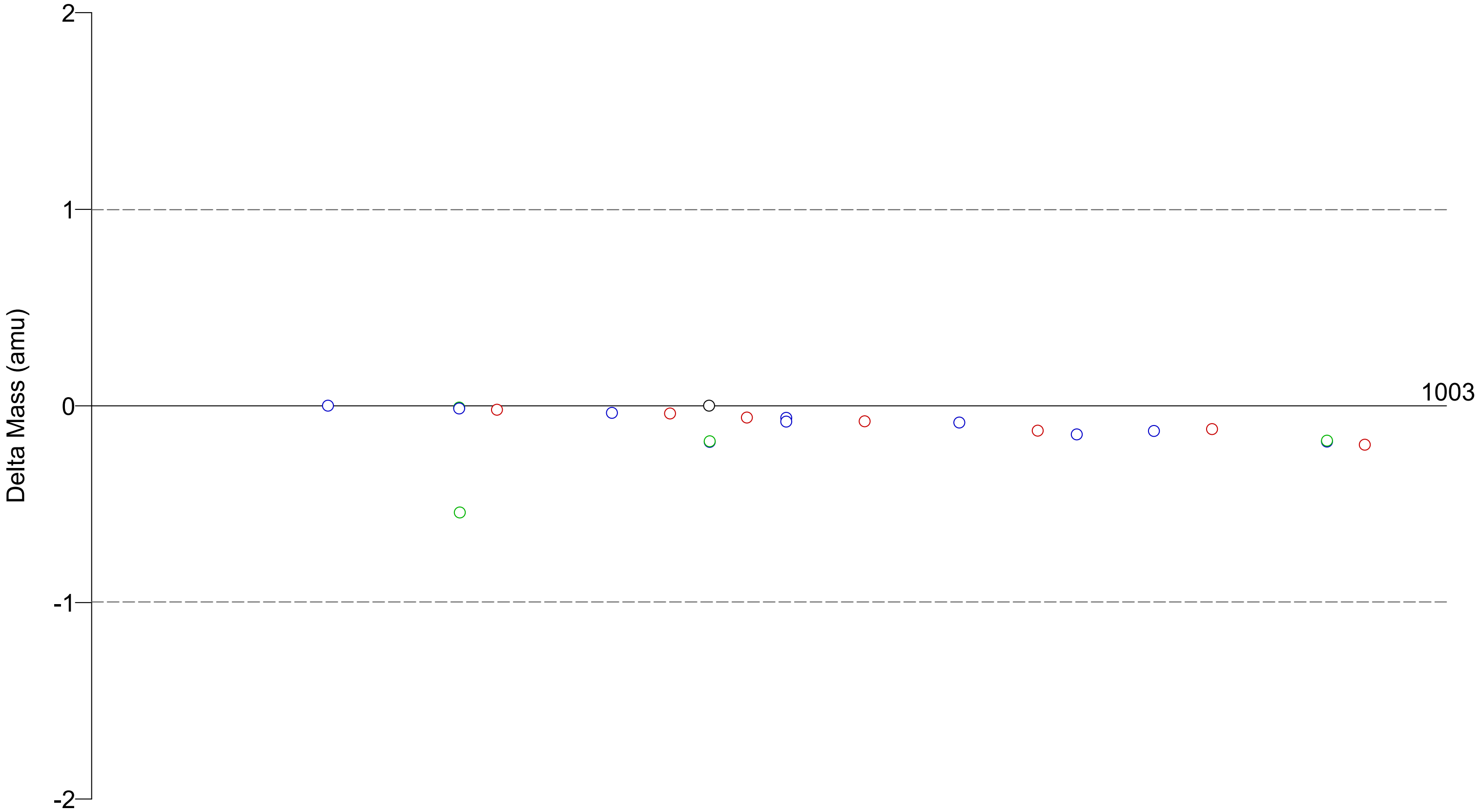


#19287468-1 NL: 1.26E5

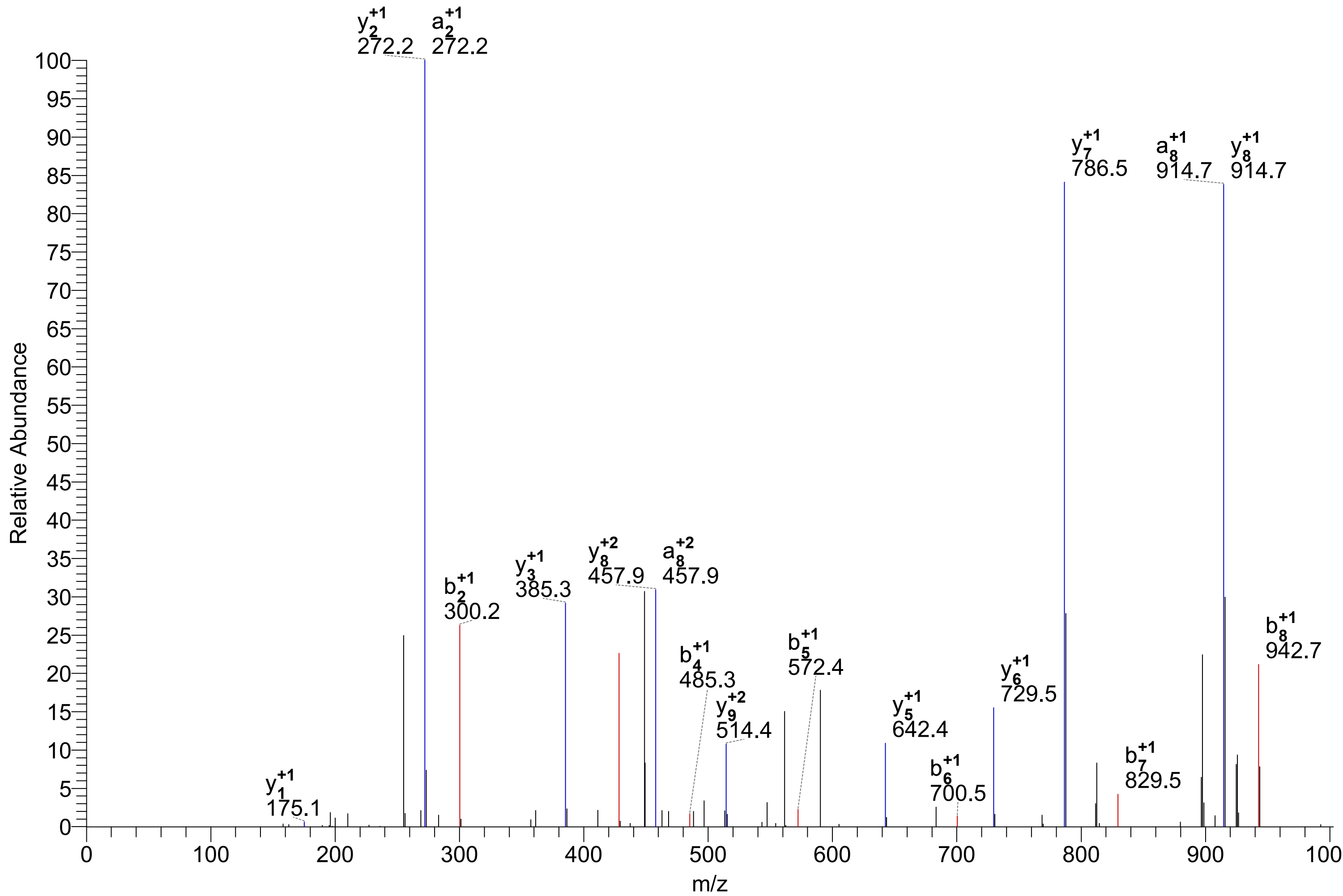


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00641229.4|SWISS-PROT:P0187                                0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                    1027.55
 Q    400.23     428.23                                     914.47
 G    457.26     485.25                                     786.41
 S    544.29     572.28                                     729.39
 Q    672.35     700.34                                     642.36
 E    801.39     829.38                                     514.30
 L    914.47     942.47                                     385.26
 P   1011.53    1039.52                                     272.17
 R                                                          175.12
```

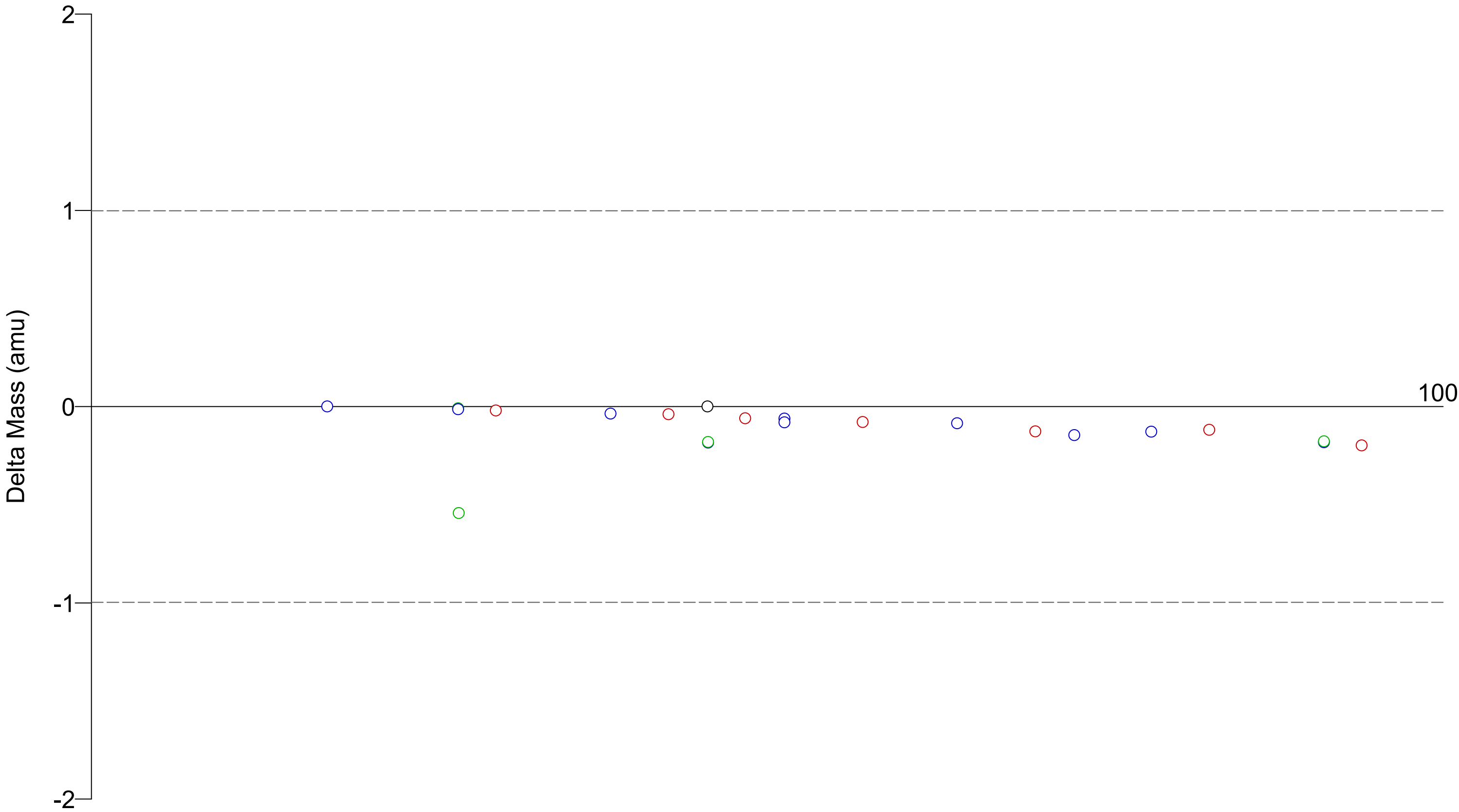


#19287468-1 NL: 1.26E5

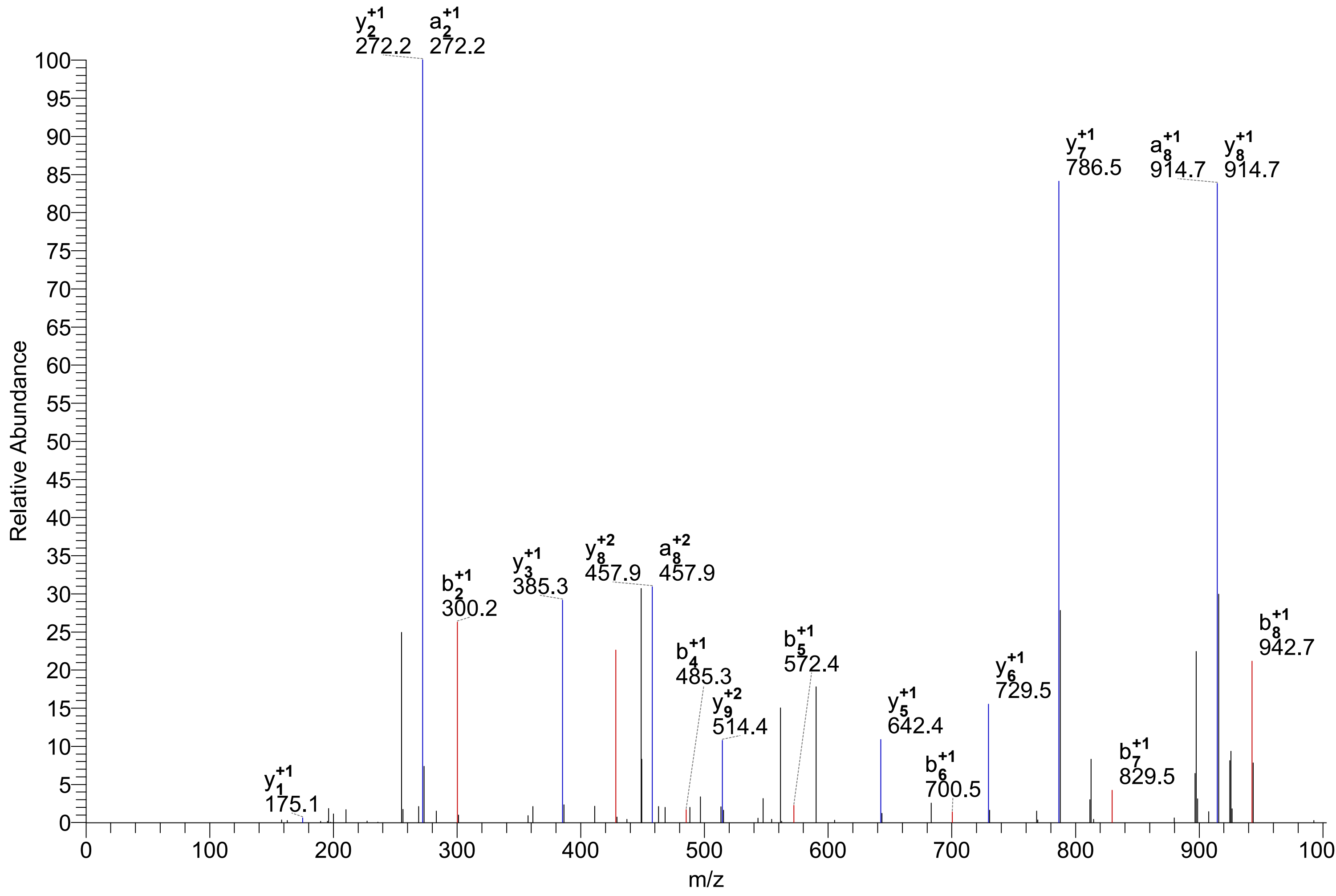


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00642017.1|TREMBL:Q7Z374|VE                                0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

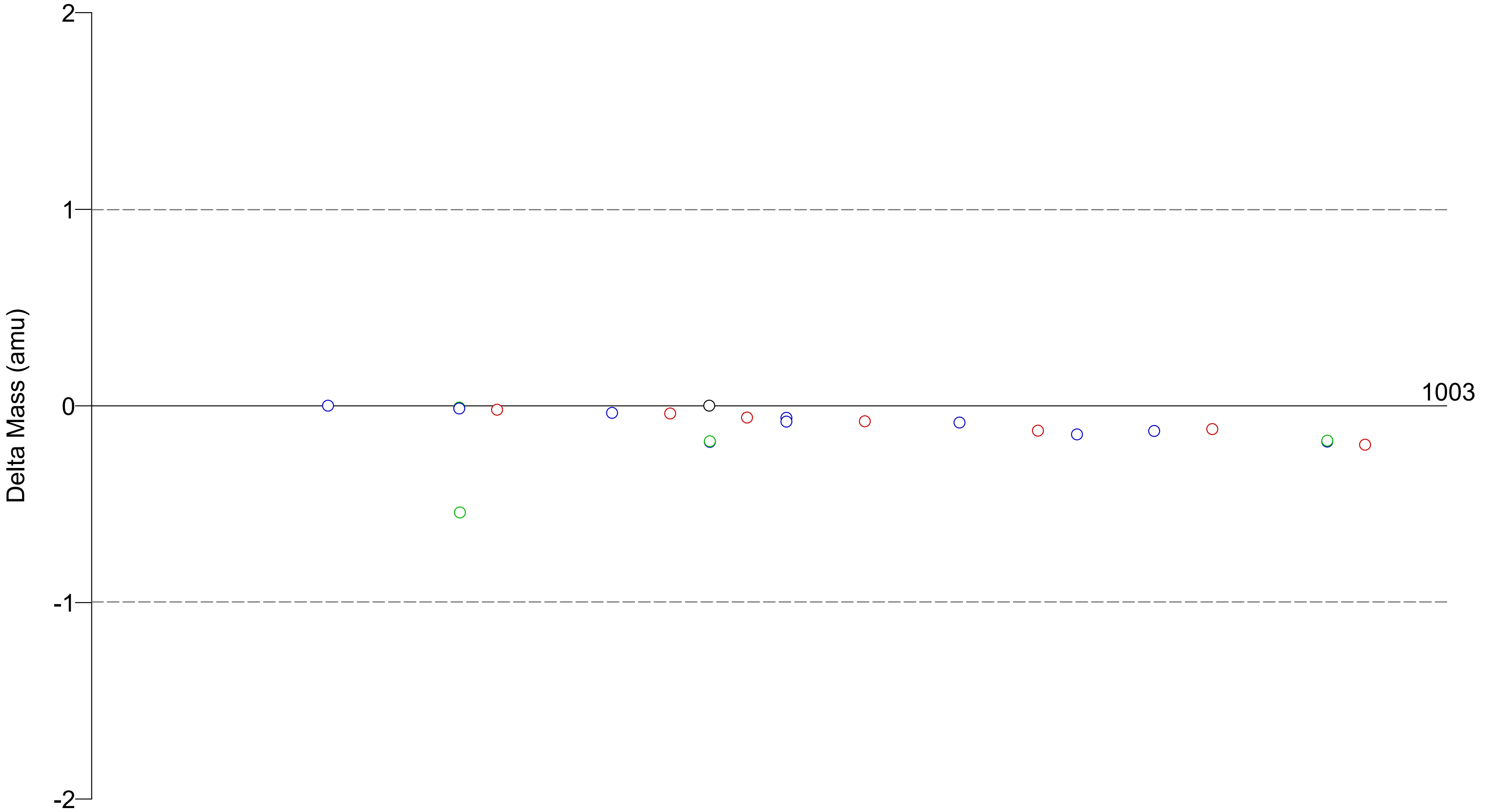


#19287468-1 NL: 1.26E5

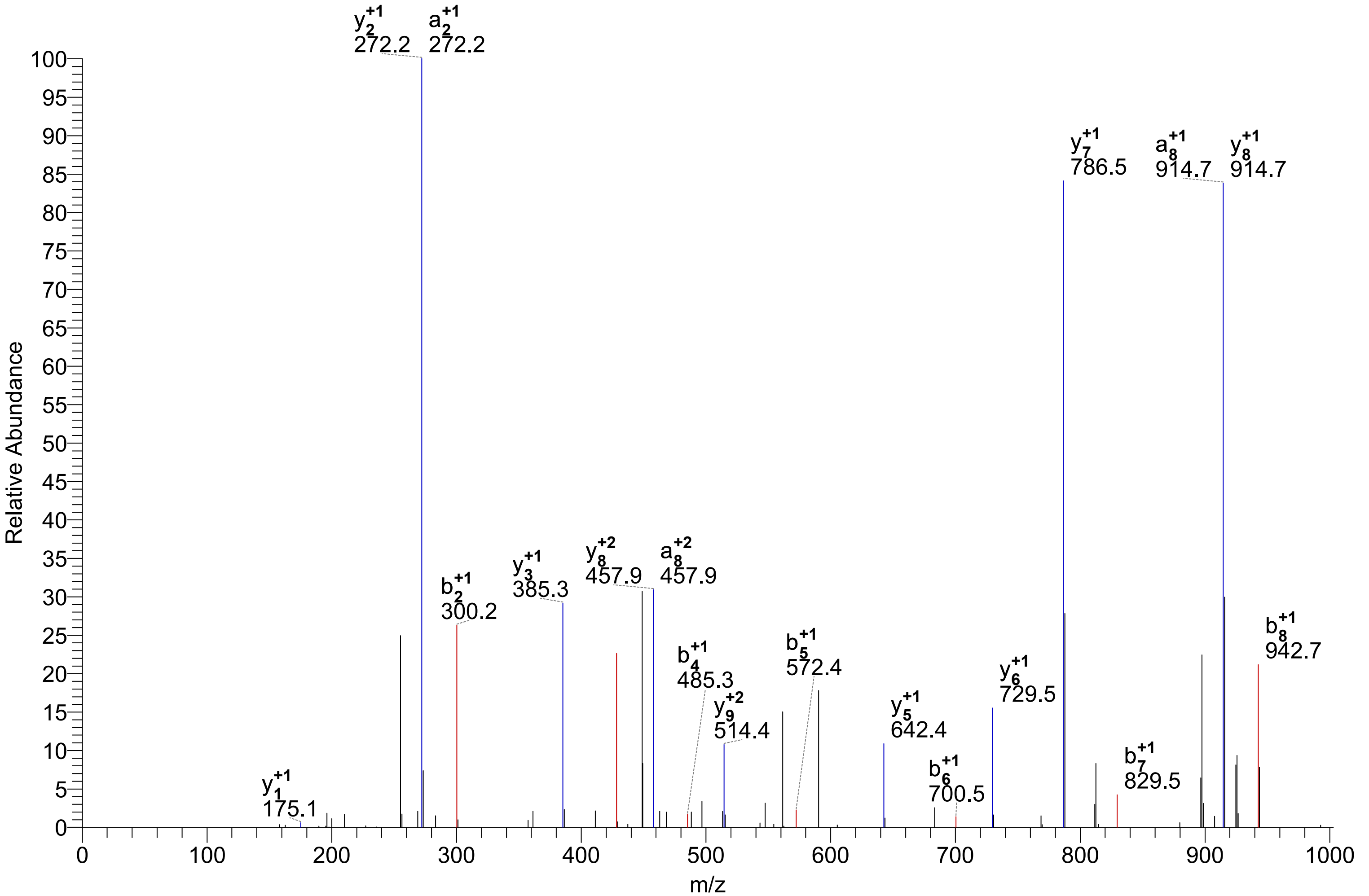


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00644497.4|H-INV:HIT0002157                                0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                    1027.55
 Q    400.23     428.23                                     914.47
 G    457.26     485.25                                     786.41
 S    544.29     572.28                                     729.39
 Q    672.35     700.34                                     642.36
 E    801.39     829.38                                     514.30
 L    914.47     942.47                                     385.26
 P   1011.53    1039.52                                     272.17
 R                                                          175.12
```



#19287468-1 NL: 1.26E5



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Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z    P        XC  DeltaCn   Sp    RSp  Ions  Count

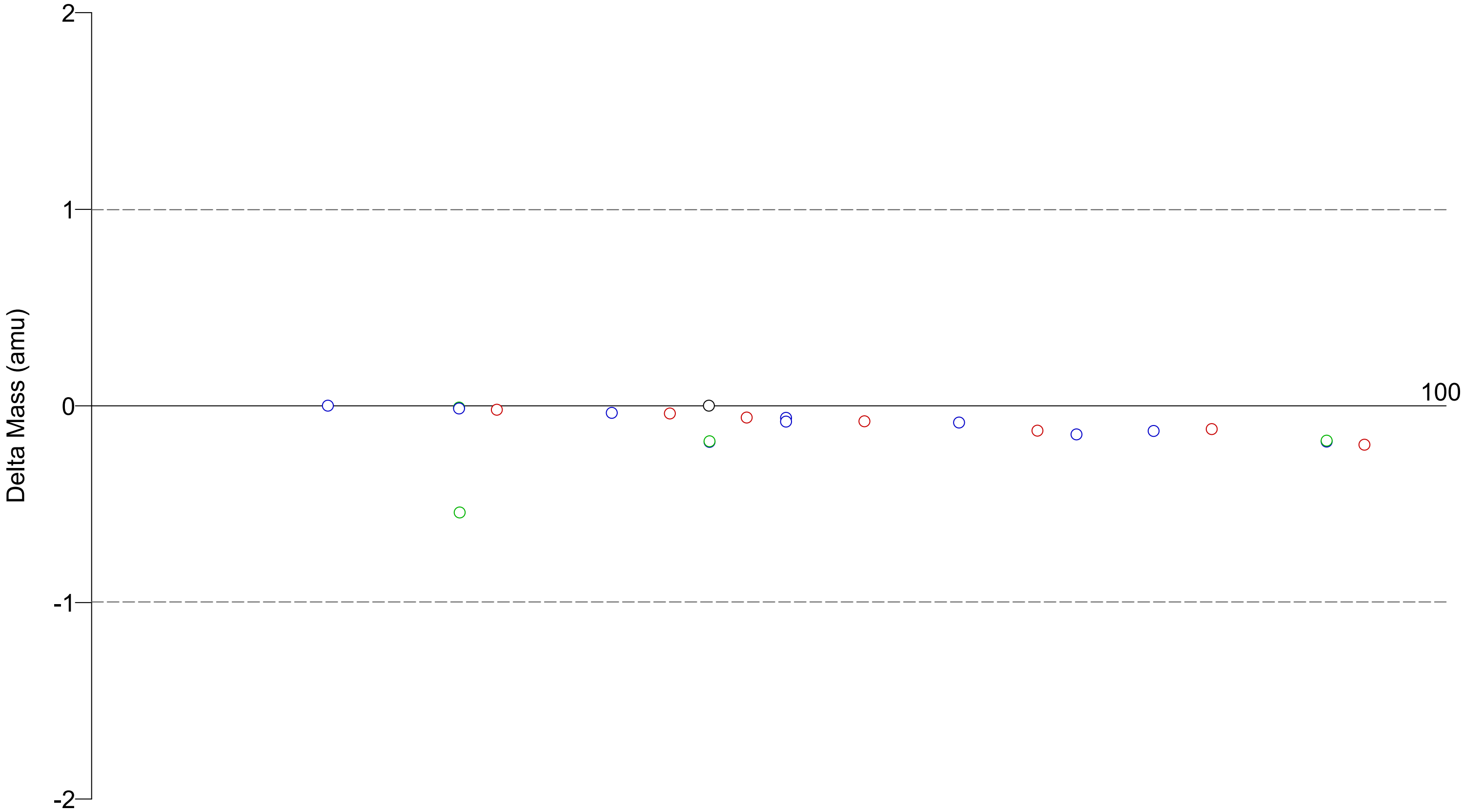
IPI:IPI00647704.1|TREMBL:Q6ZW64 Ta                                 0.0001  10.2      0.0       0
19287468 - 1  R.WLQGSQELPR.E                        1213.63    2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

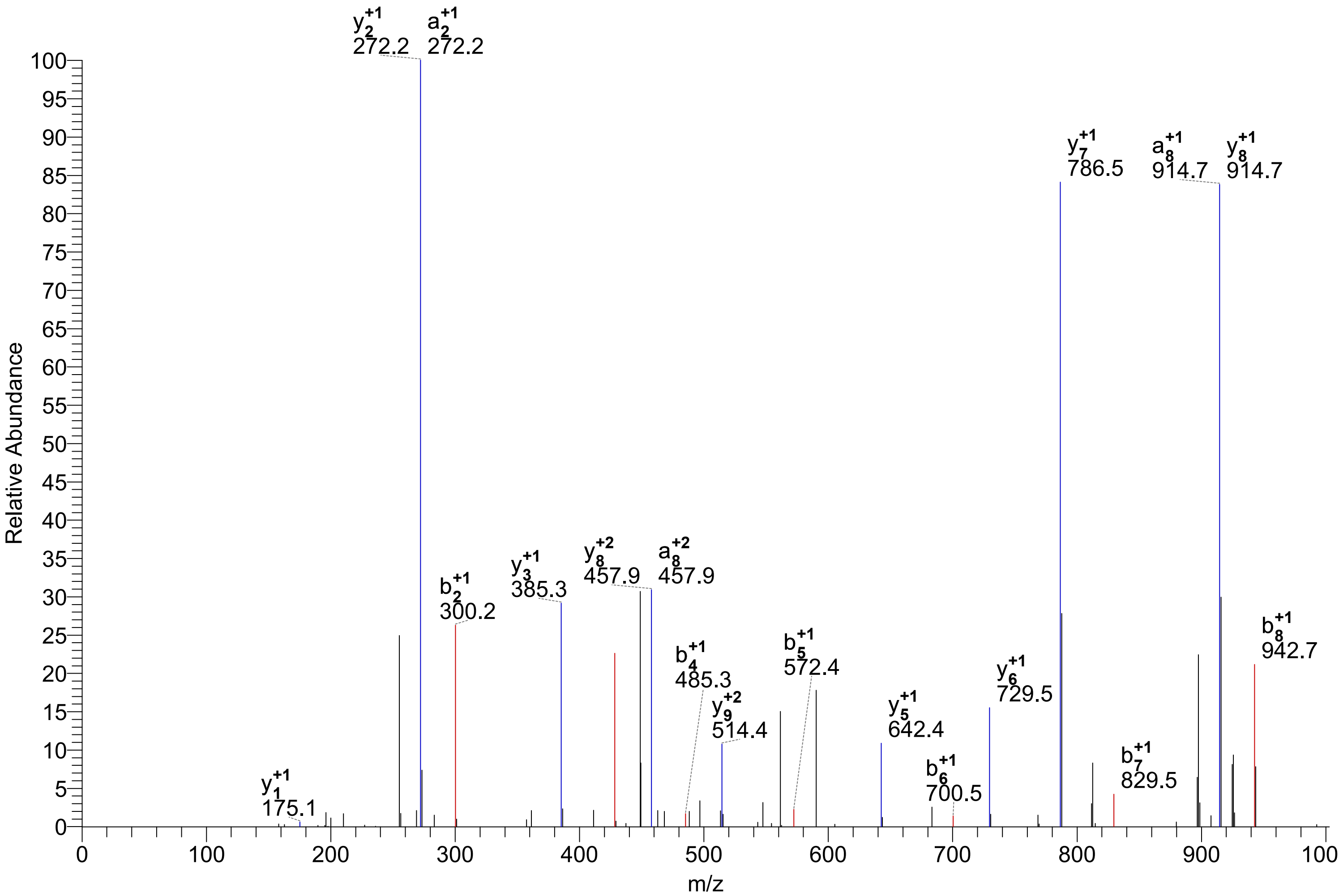
```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```



#19287468-1 NL: 1.26E5



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Reference                                                              P      Score   Coverage   Accession
Scan(s)        Sequence                                      MH+       z     P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00784758.1|TREMBL:Q6MZX9 Ta                                         0.0001  10.2      0.0        0
19287468 - 1  R.WLQGSQELPR.E                               1213.63    2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```
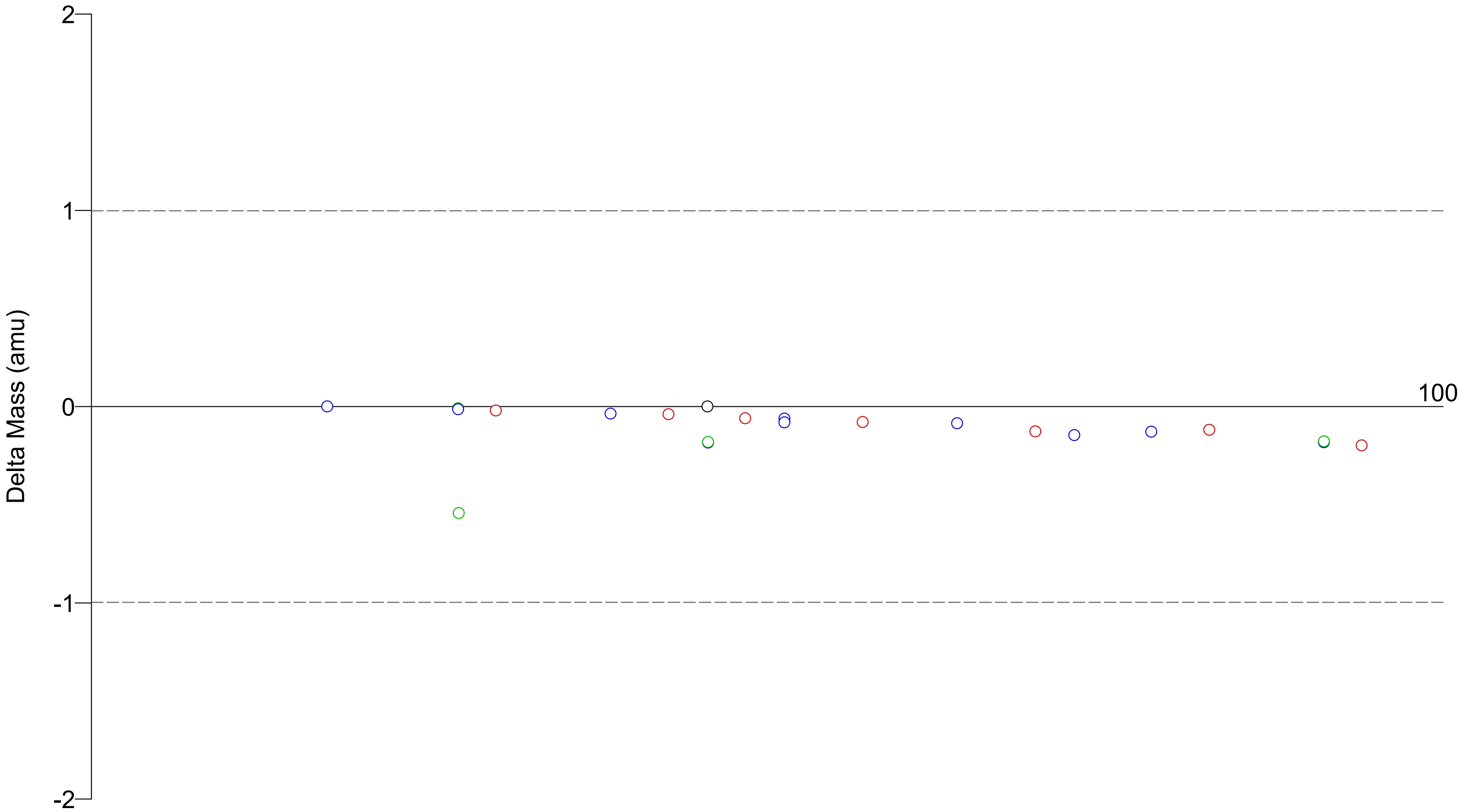
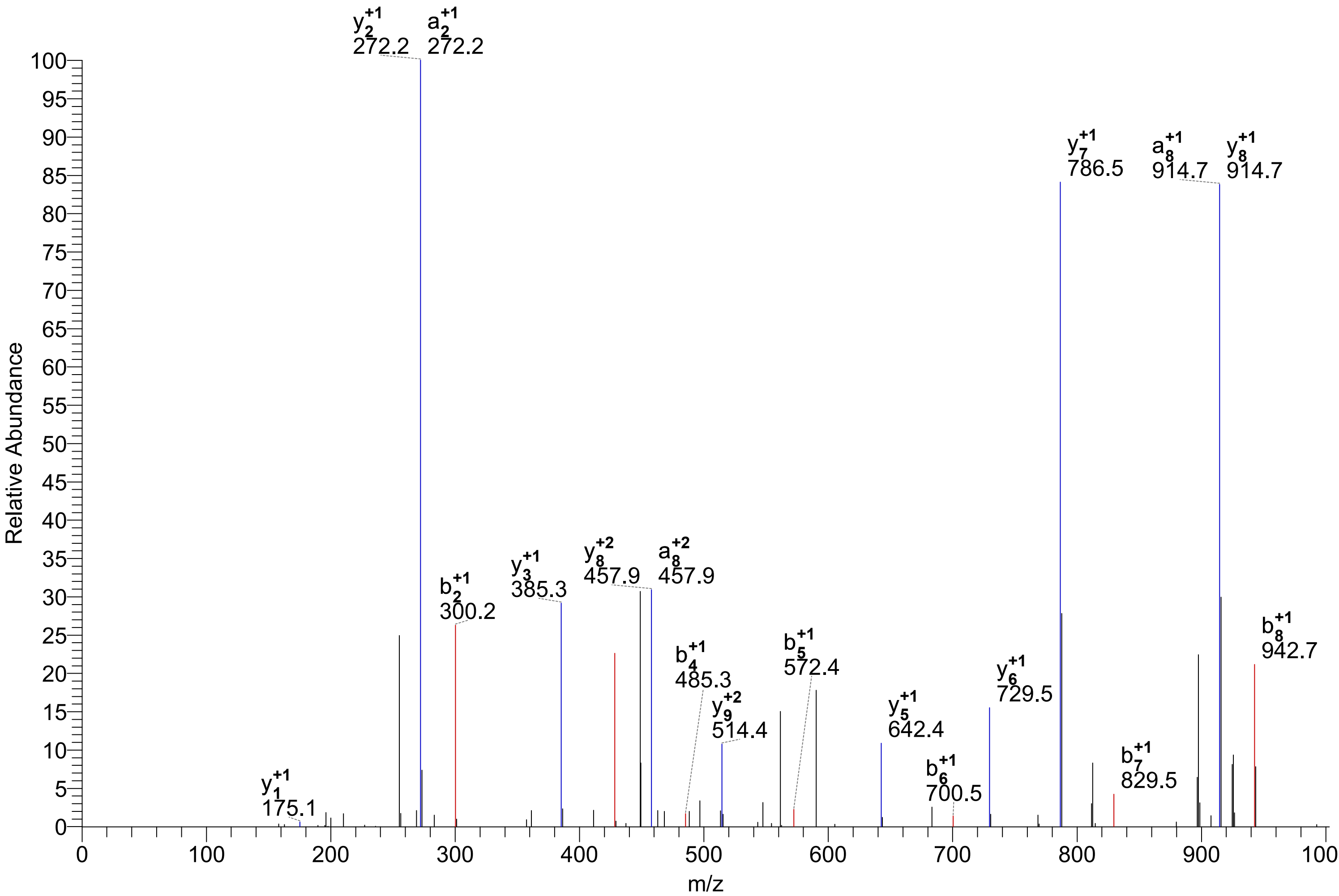

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

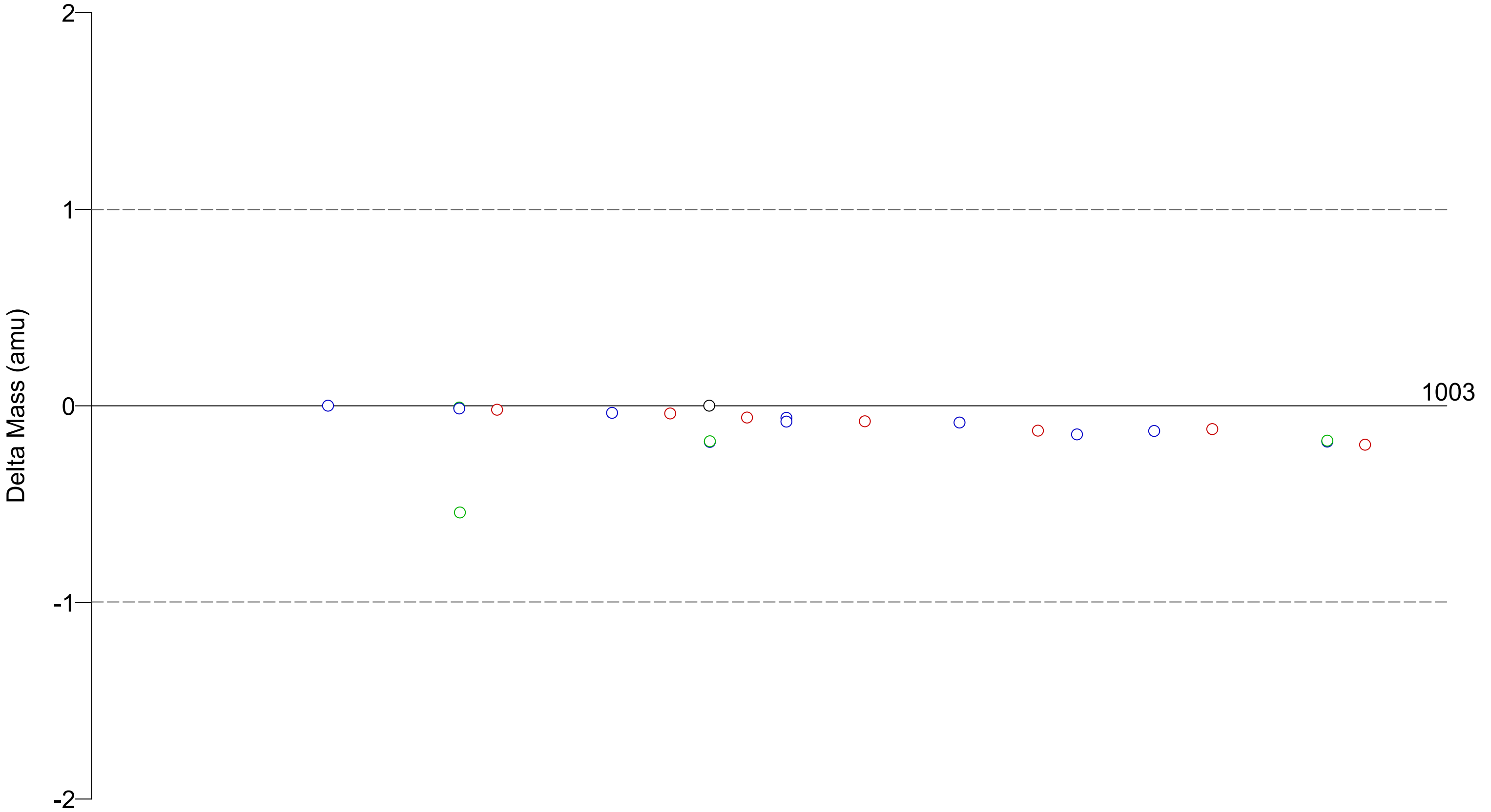


#19287468-1 NL: 1.26E5

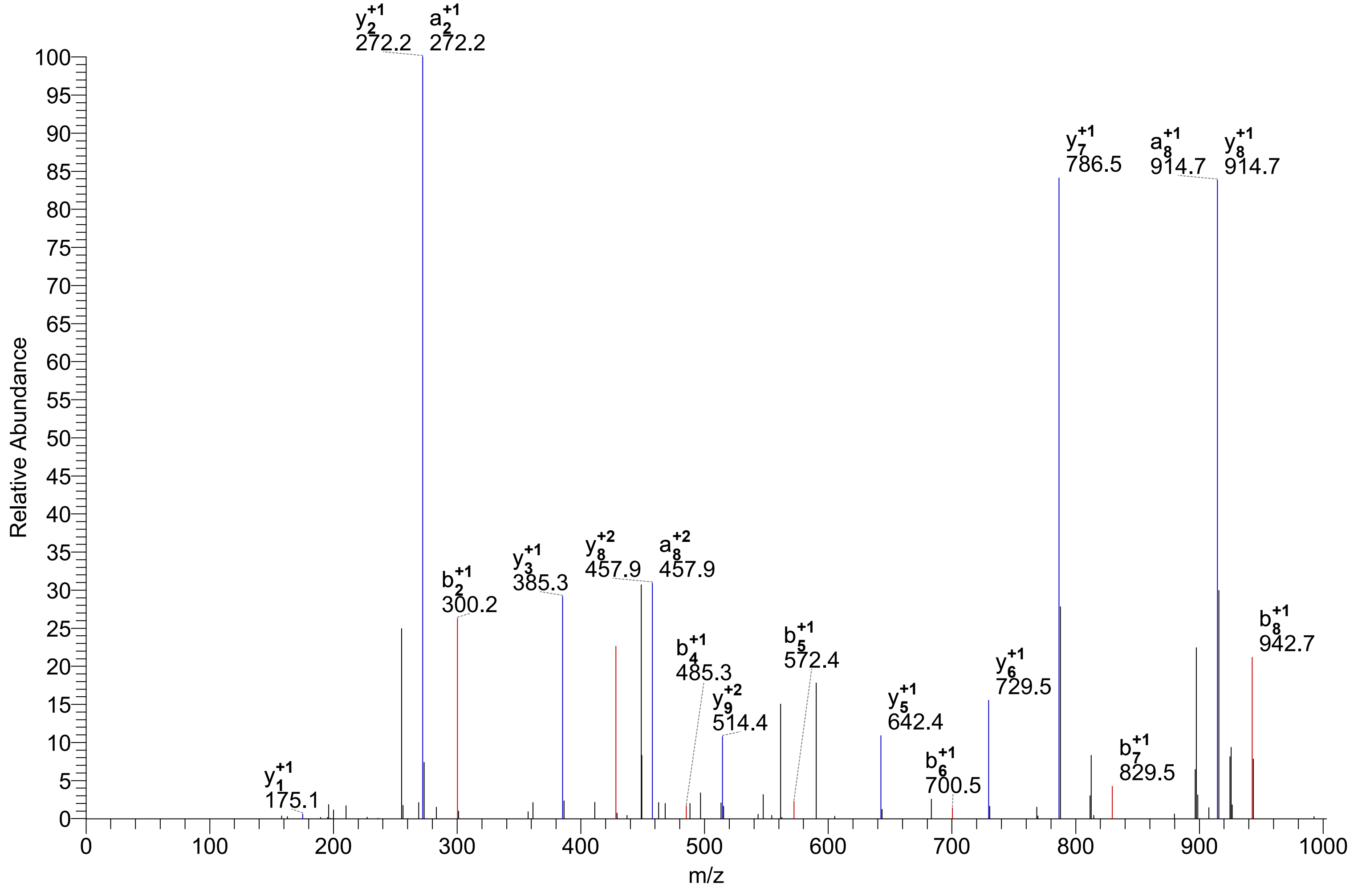


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00784830.1|TREMBL:Q6ZVX0 Ta                                0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63   2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

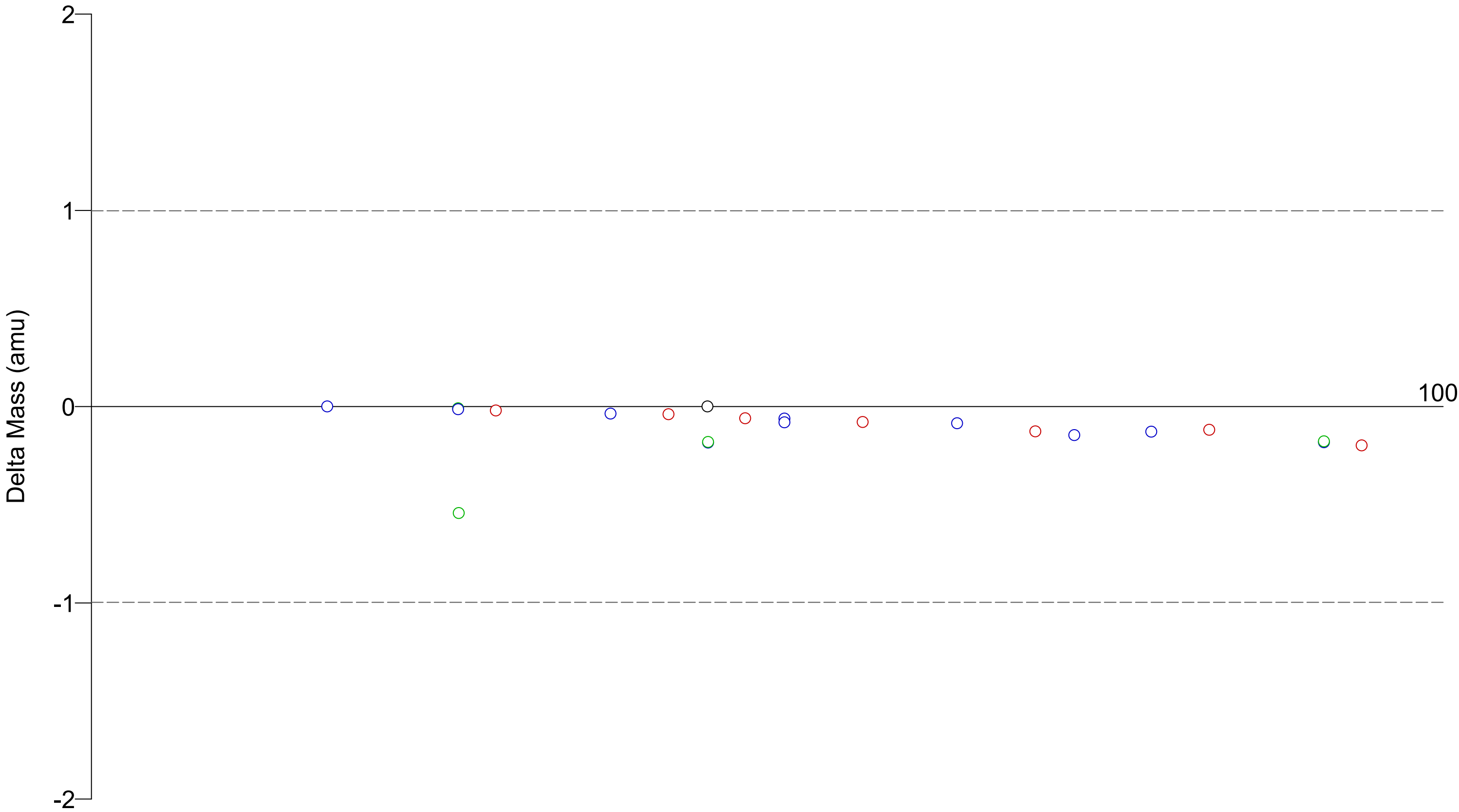


#19287468-1 NL: 1.26E5

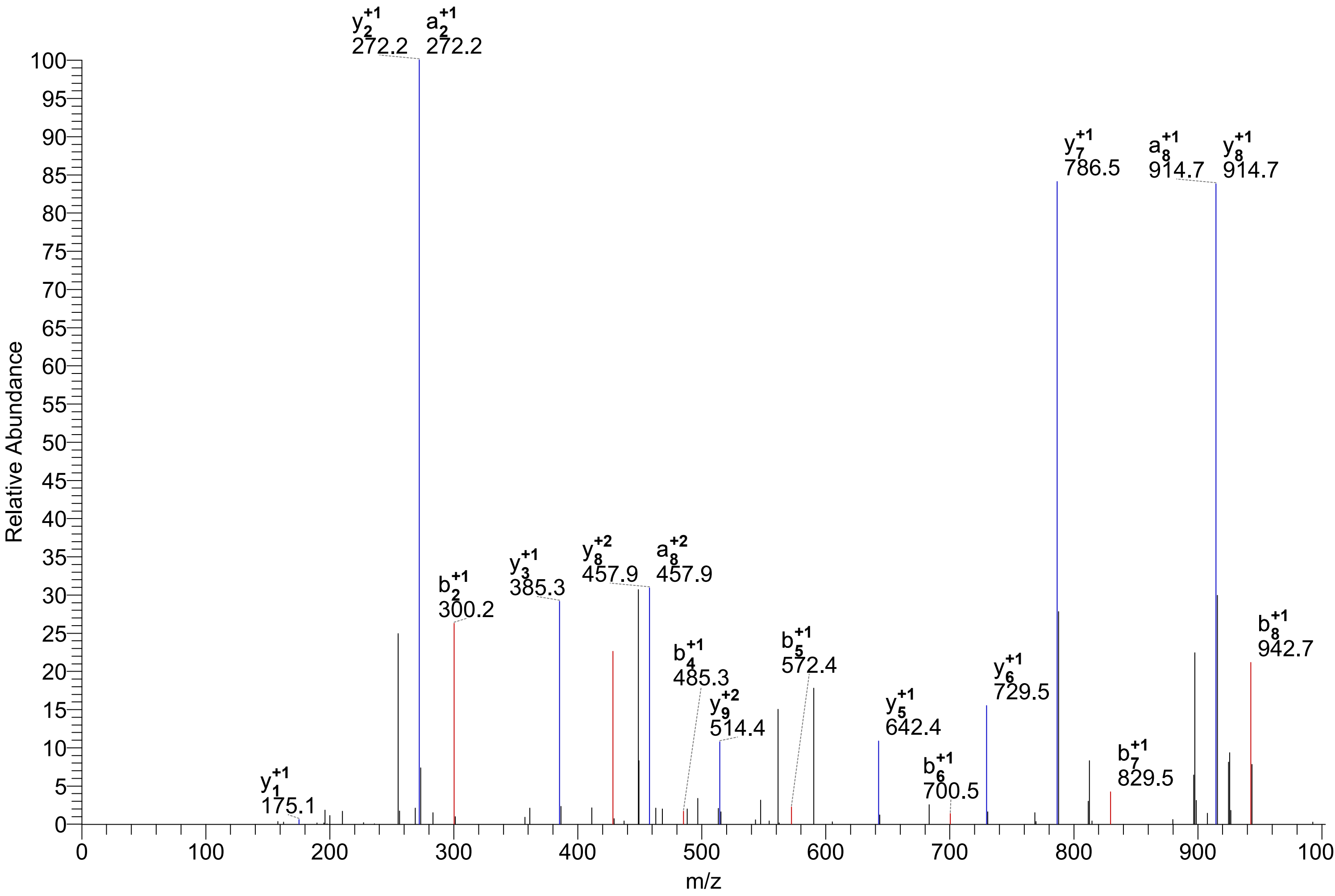


```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00785067.1|TREMBL:Q6P089 Ta                                     0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                             1213.63    2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

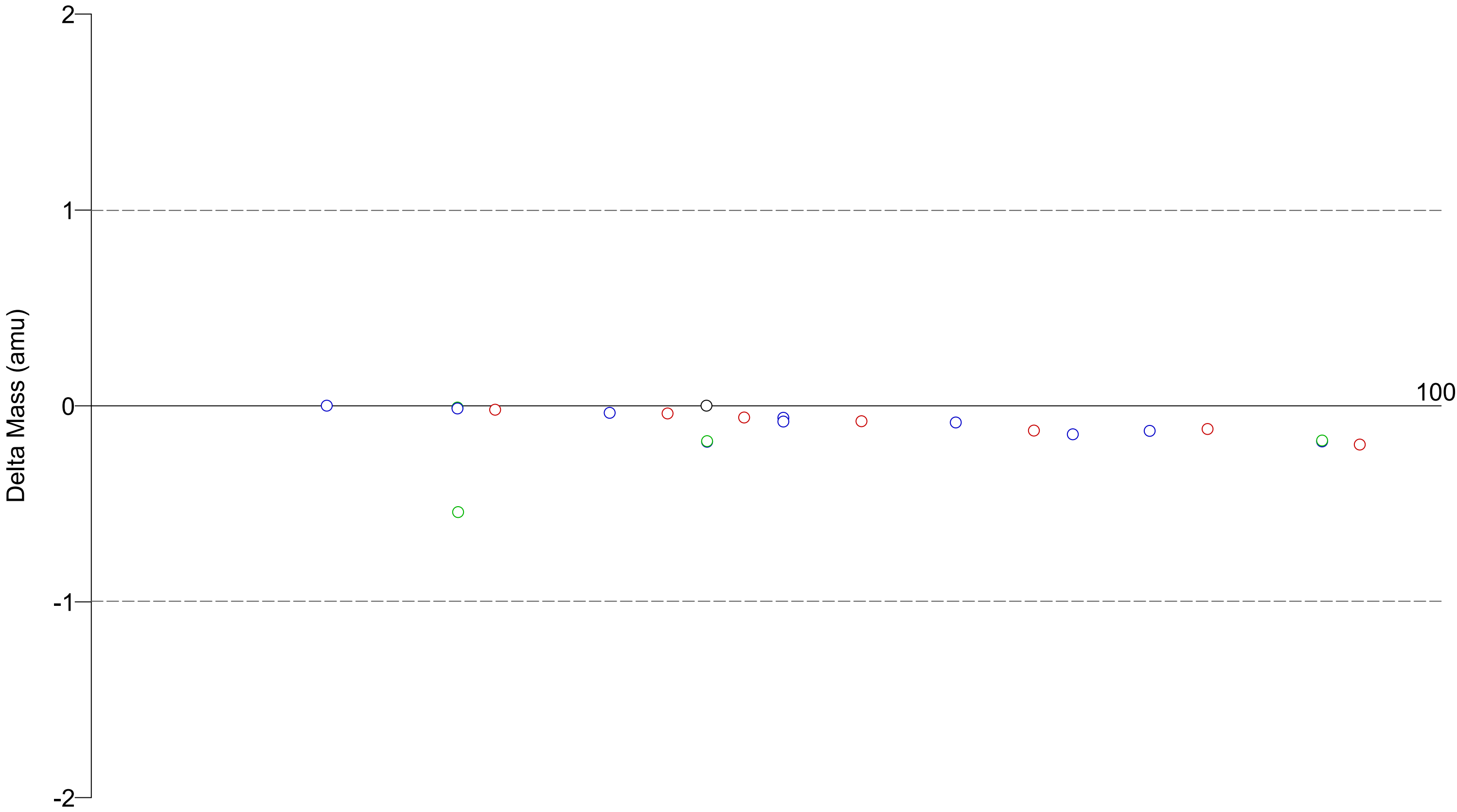


#19287468-1 NL: 1.26E5

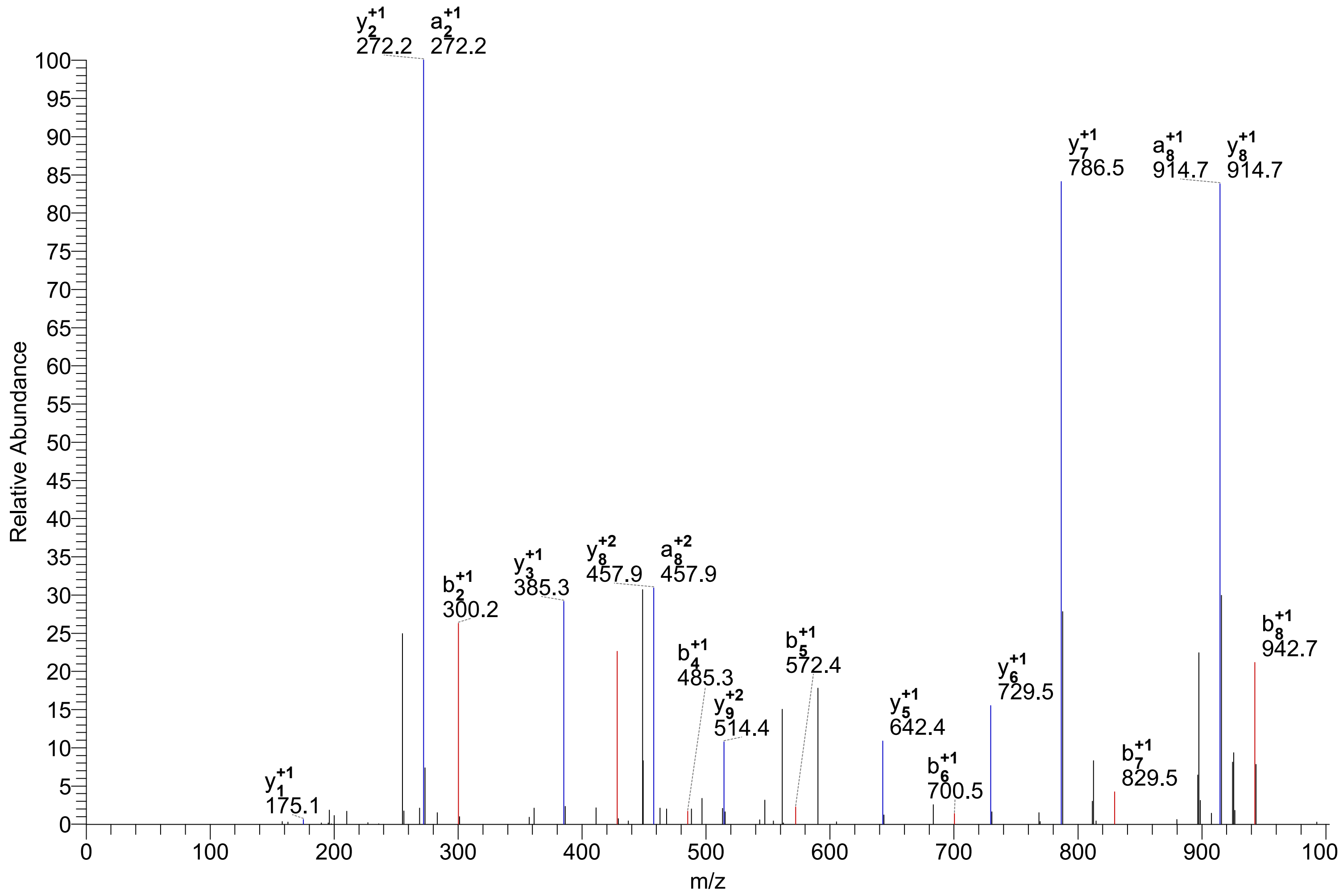


```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00829711.1|TREMBL:A6NE94|EN                                 0.0001  10.2     0.0        0
19287468 - 1  R.WLQGSQELPR.E                       1213.63    2  0.0001  3.386  0.262    1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

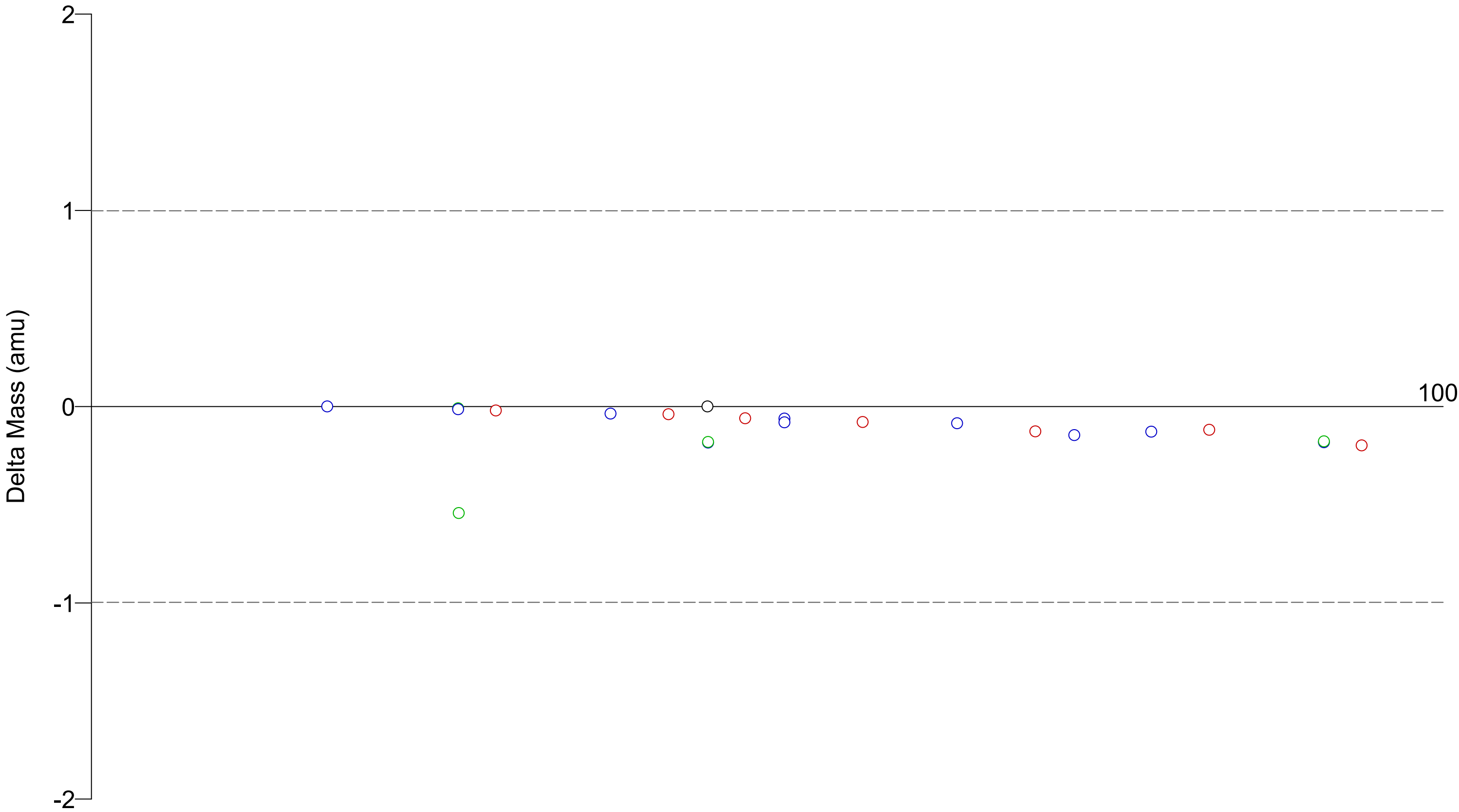


#19287468-1 NL: 1.26E5

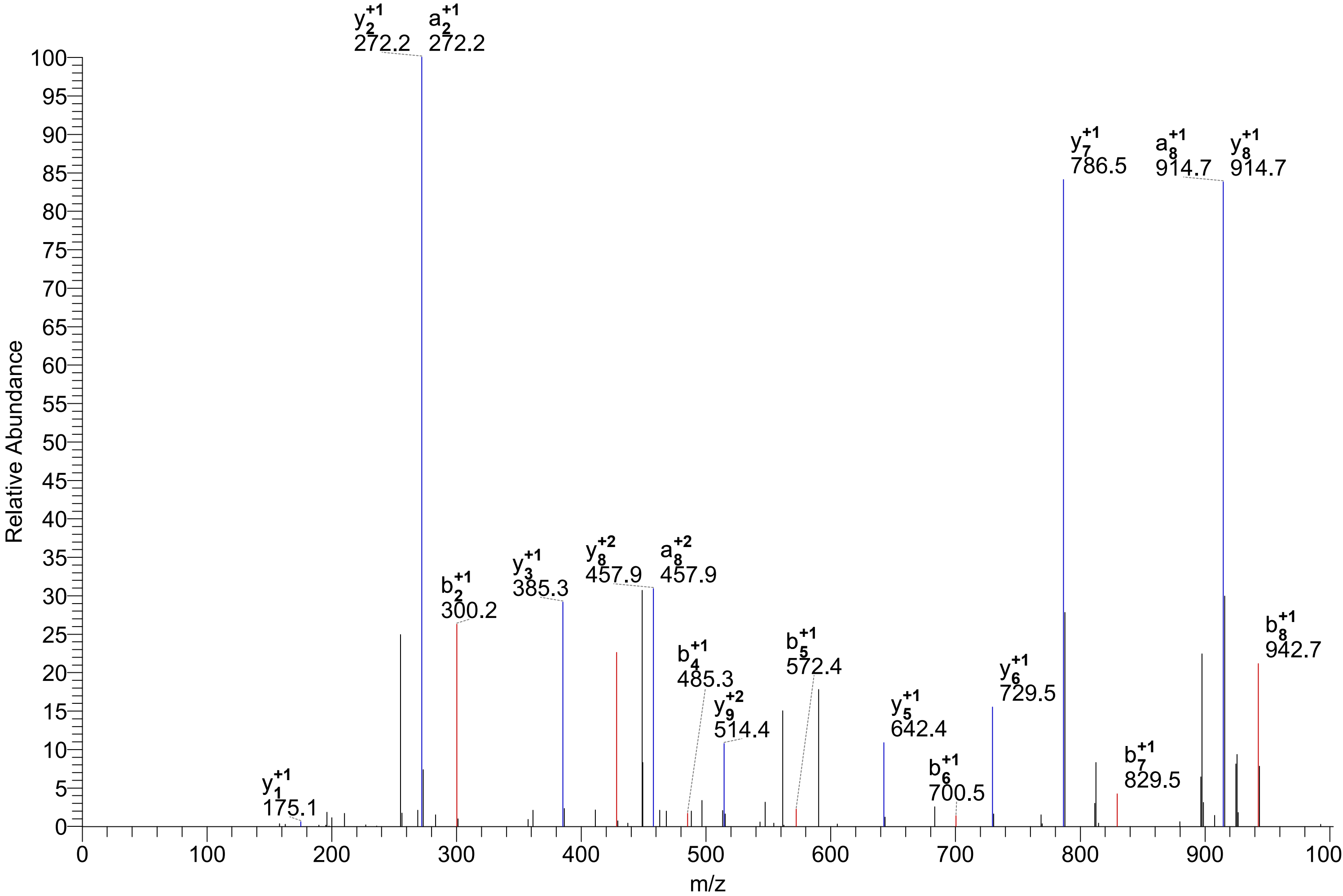


```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00893853.1|VEGA:OTTHUMP0000                              0.0001  10.2     0.0        0
19287468 - 1  R.WLQGSQELPR.E                       1213.63   2  0.0001  3.386  0.262    1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                     1027.55
 Q    400.23     428.23                                      914.47
 G    457.26     485.25                                      786.41
 S    544.29     572.28                                      729.39
 Q    672.35     700.34                                      642.36
 E    801.39     829.38                                      514.30
 L    914.47     942.47                                      385.26
 P   1011.53    1039.52                                      272.17
 R                                                           175.12
```

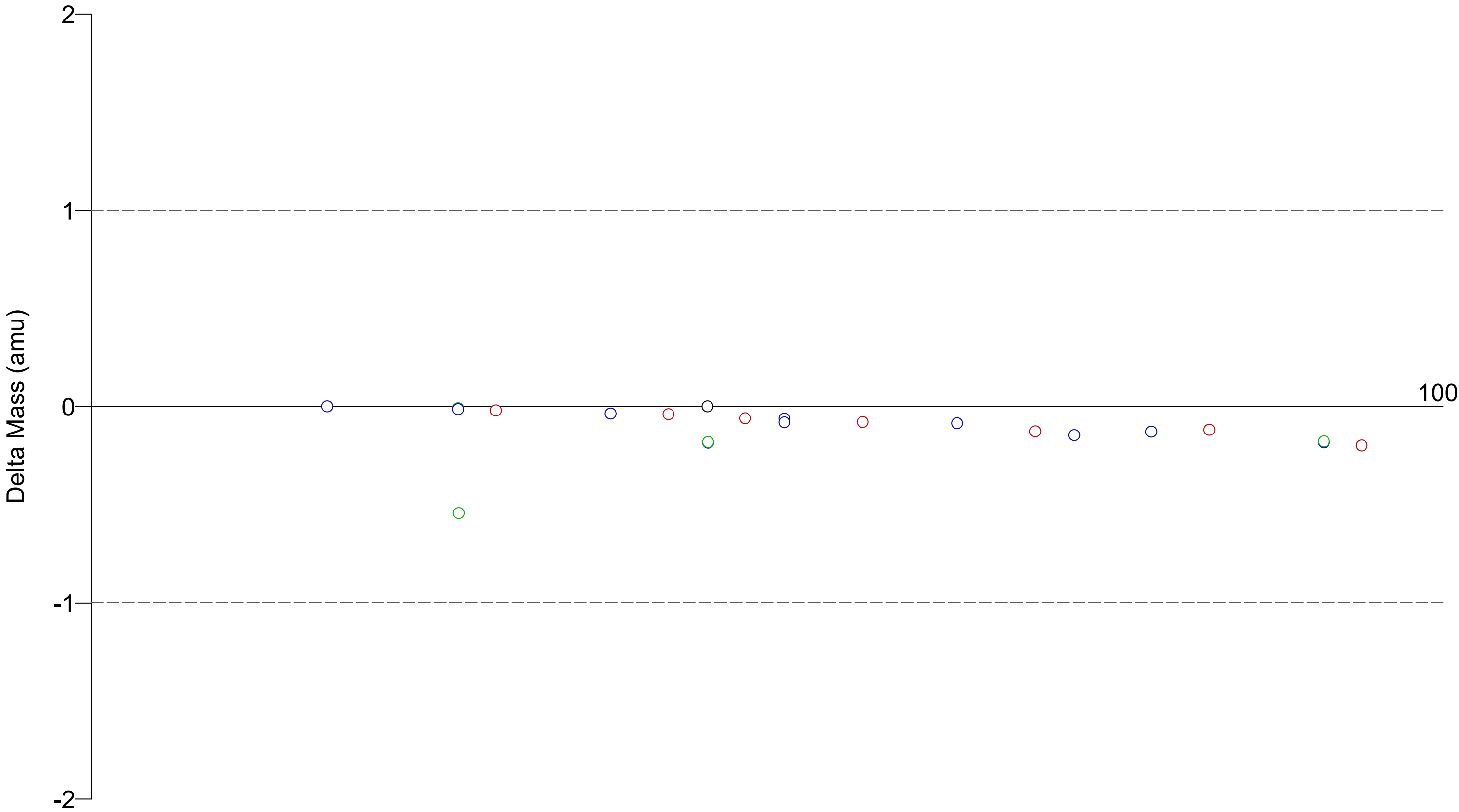


#19287468-1 NL: 1.26E5

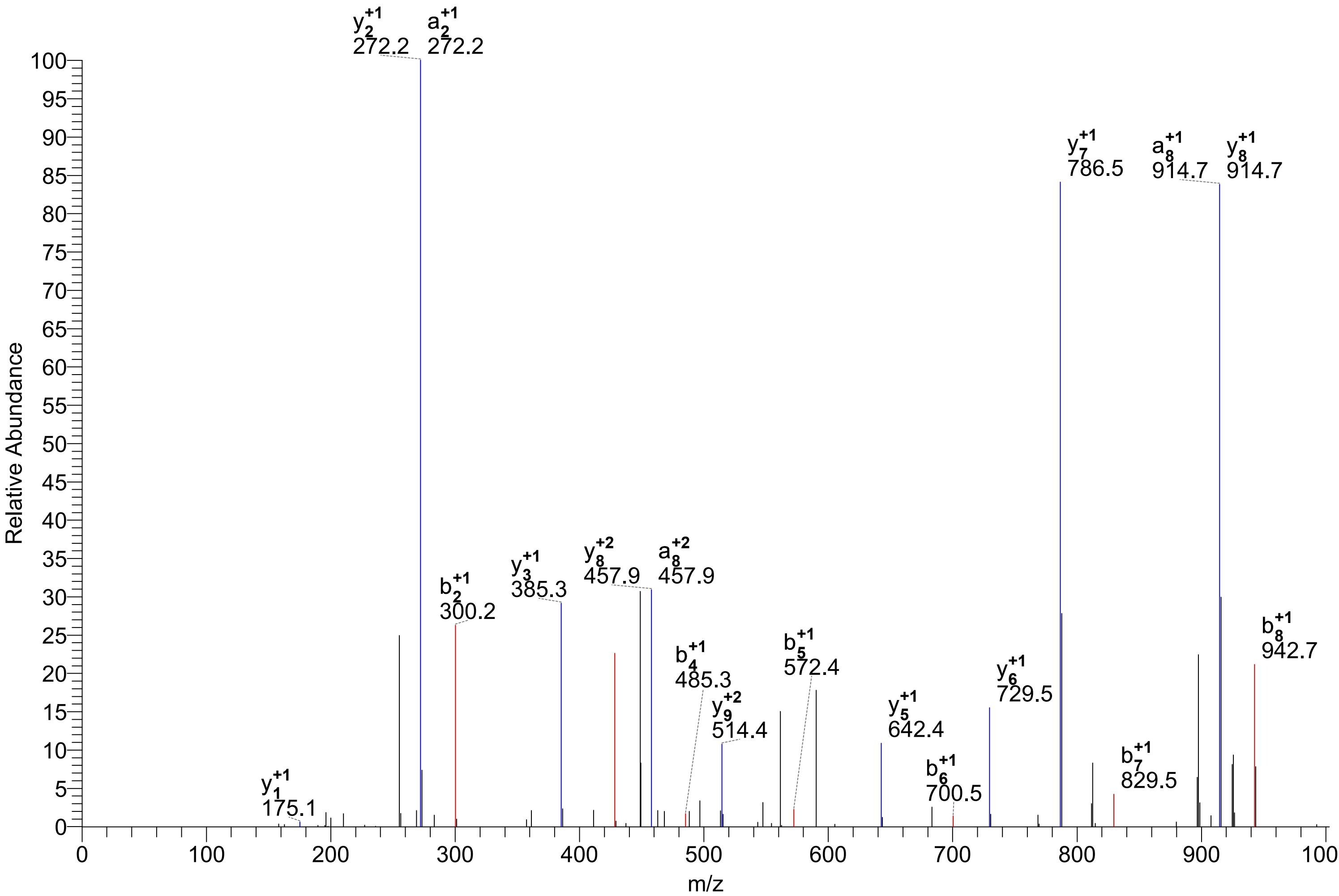


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp    RSp  Ions  Count

IPI:IPI00894384.1|TREMBL:Q6N041;Q9                                 0.0001  10.2     0.0       0
19287468 - 1  R.WLQGSQELPR.E                         1213.63    2  0.0001  3.386  0.262   1272.1 1   18/27   19

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 L    272.18     300.17                                      1027.55
 Q    400.23     428.23                                       914.47
 G    457.26     485.25                                       786.41
 S    544.29     572.28                                       729.39
 Q    672.35     700.34                                       642.36
 E    801.39     829.38                                       514.30
 L    914.47     942.47                                       385.26
 P   1011.53    1039.52                                       272.17
 R                                                            175.12
```

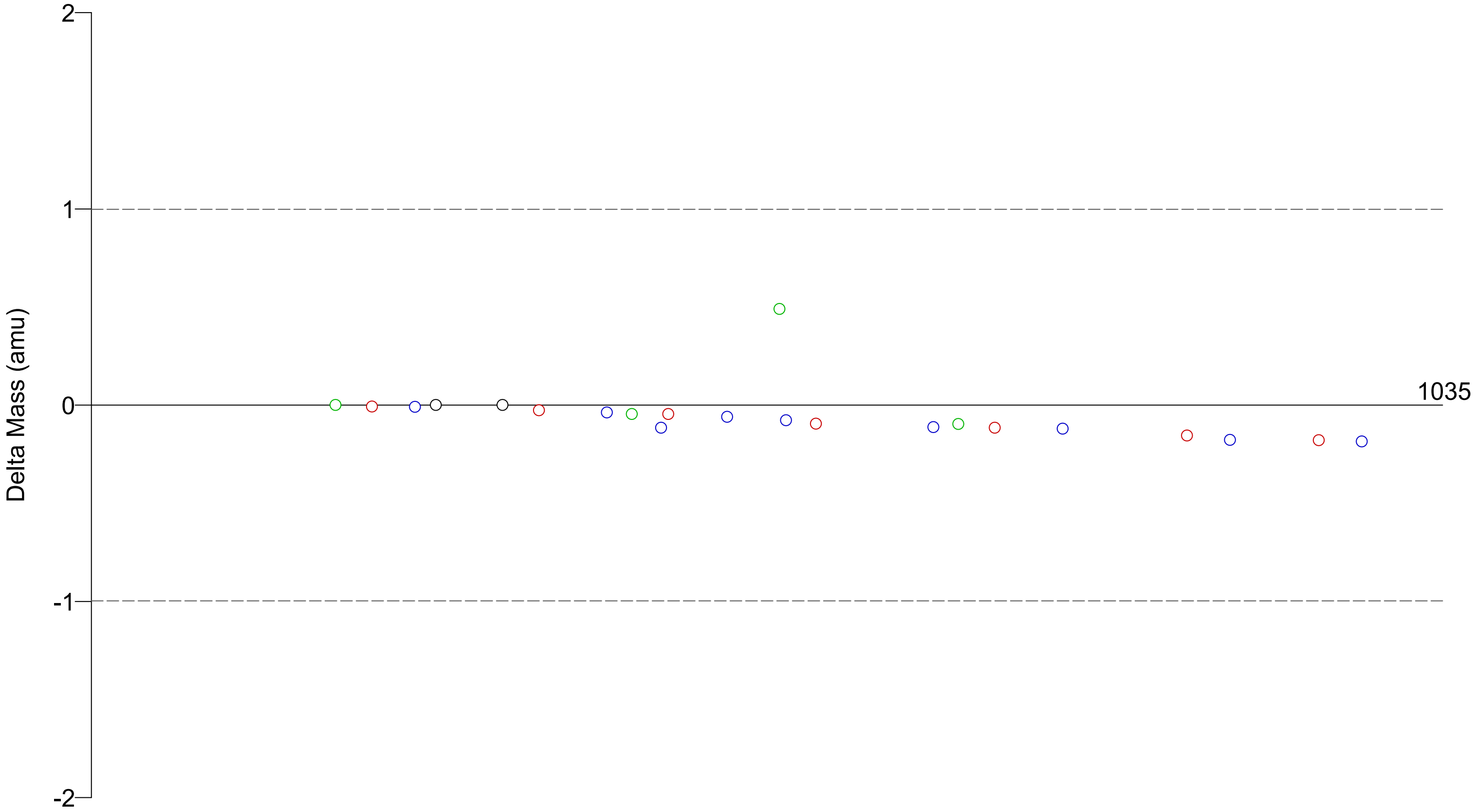


#19287468-1 NL: 1.26E5

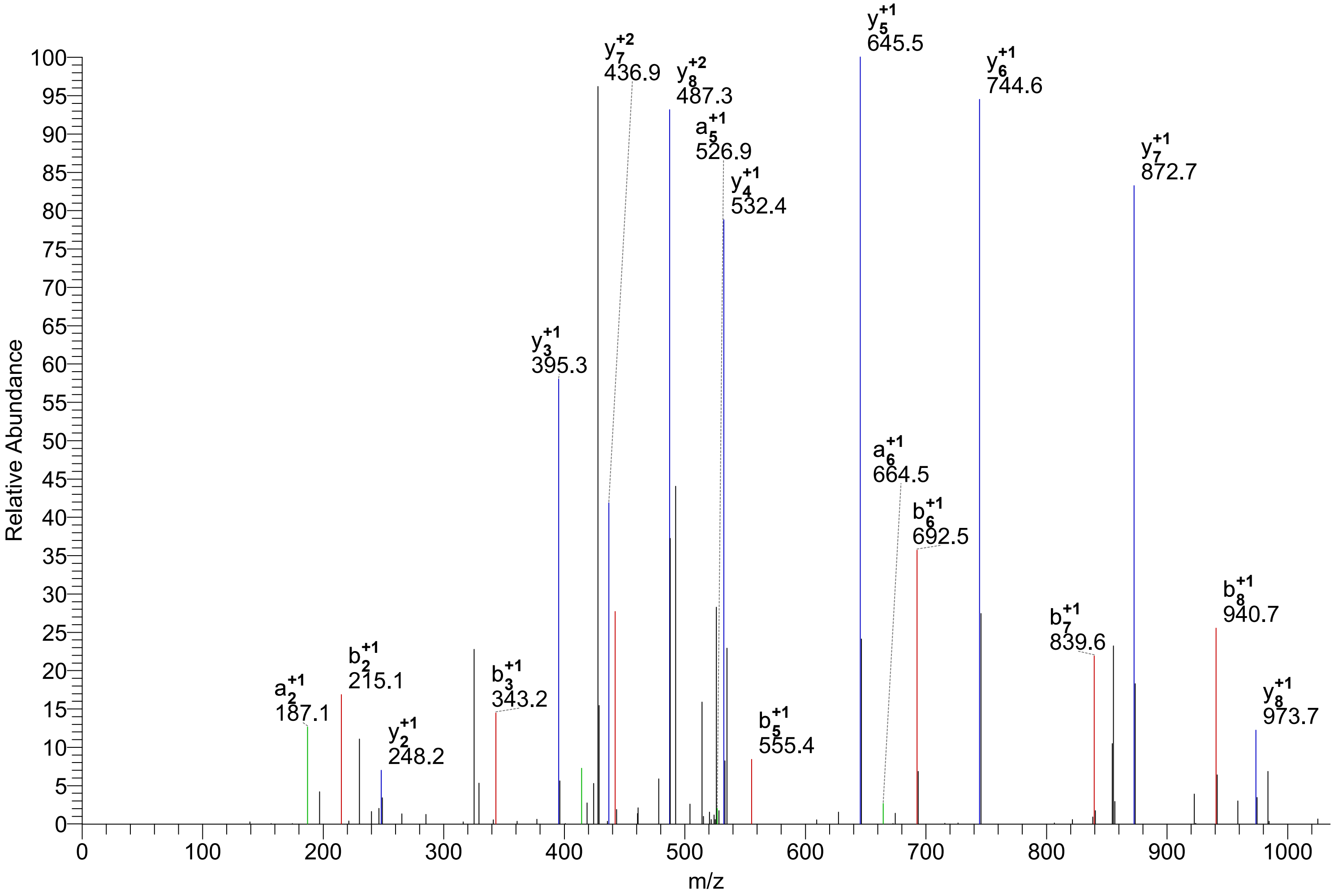


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+     z     P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00032258.4|SWISS-PROT:P0C0L4 Tax_Id=9606 Gene_Symbol=C4     0.0002  10.2      0.0        0
2118291816 -  K.ITQVLHFTK.D                             1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24   10

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```

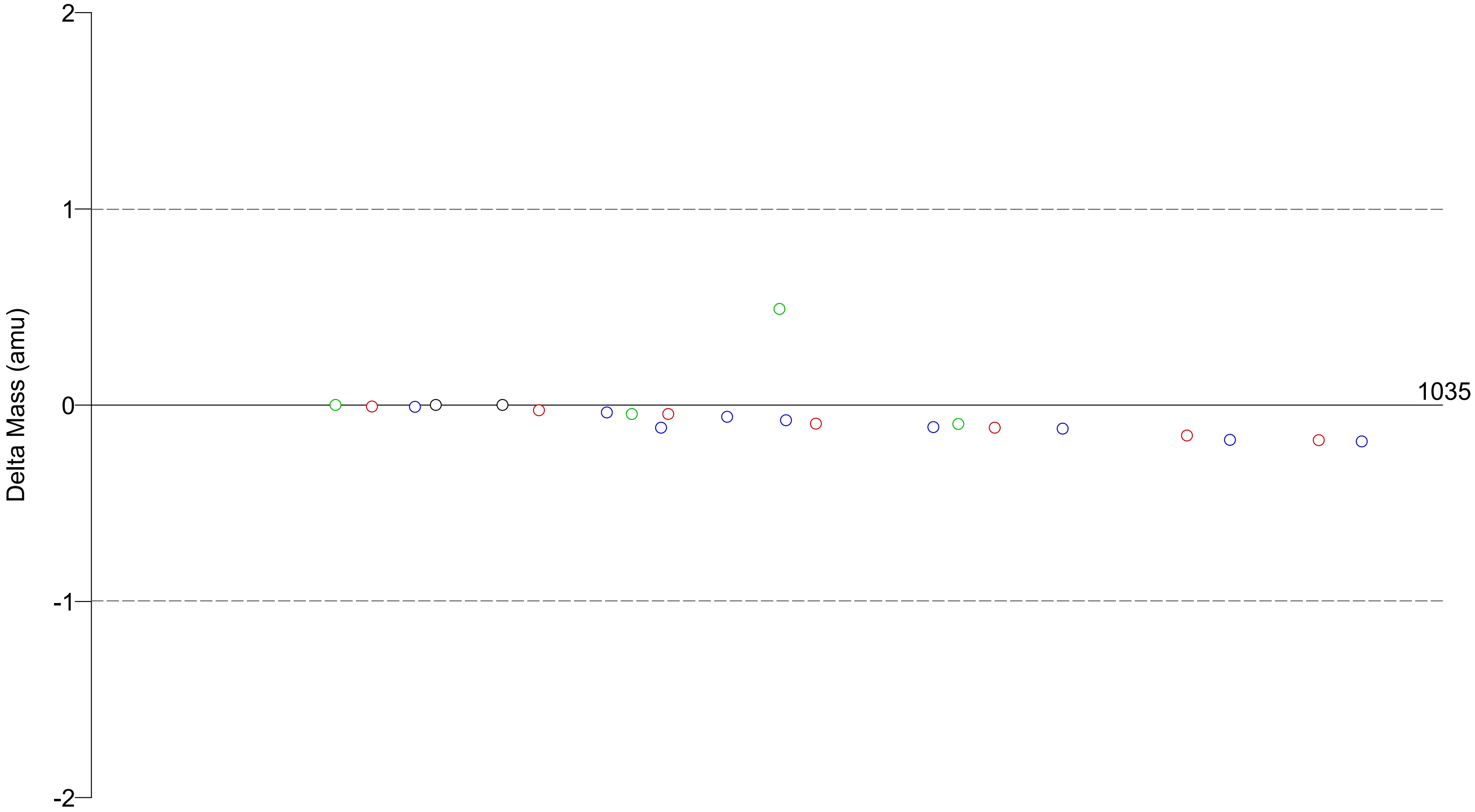


#2118291816-26226248 NL: 1.21E5

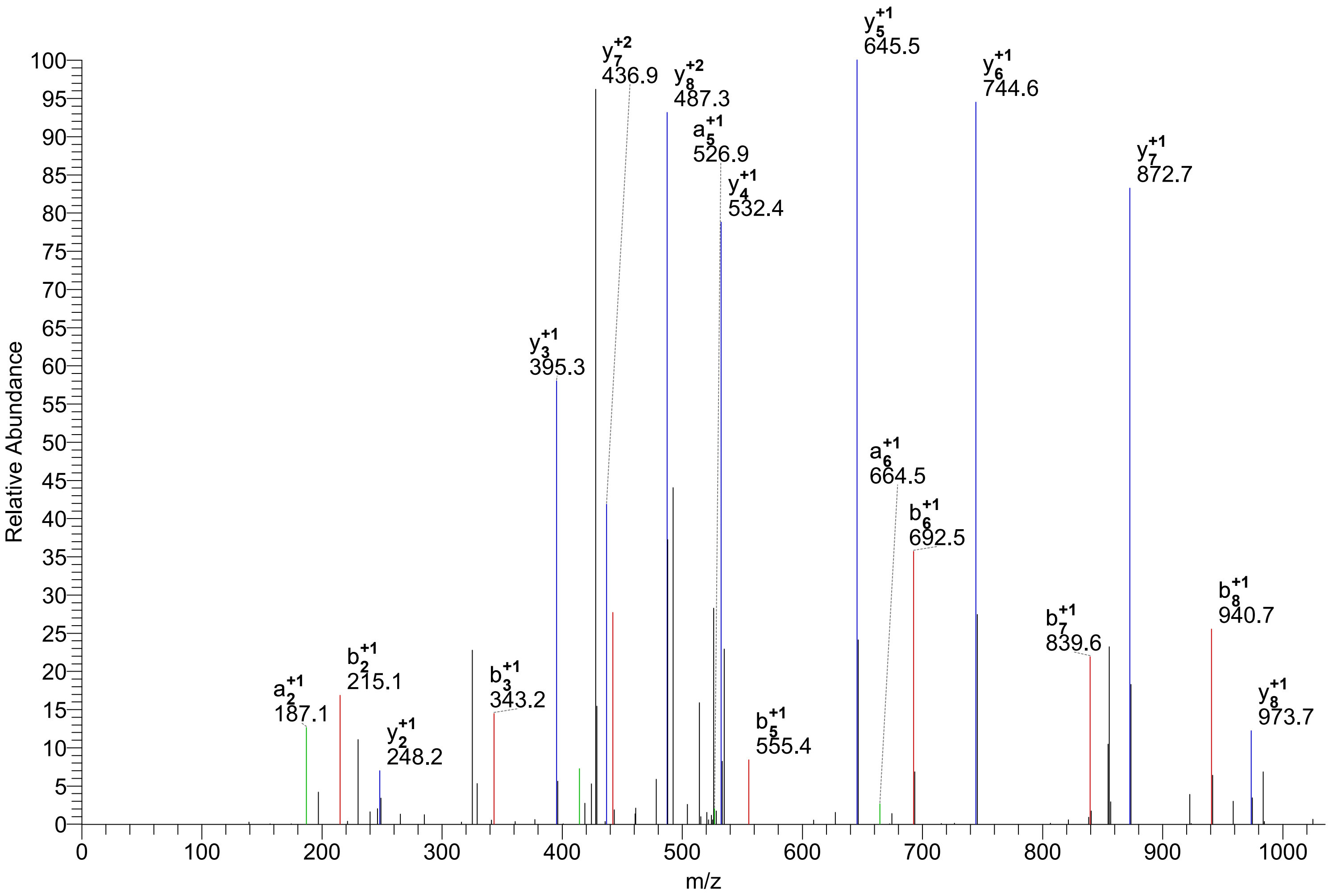


```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)       Sequence                                          MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00654875.1|SWISS-PROT:P0C0L                                          0.0002  10.2     0.0       0
2118291816 -  K.ITQVLHFTK.D                                   1086.63    2  0.0002  3.684  0.435   1215.2 1   18/24   10

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                       973.55
 Q    315.20     343.20                                       872.50
 V    414.27     442.27                                       744.44
 L    527.36     555.35                                       645.37
 H    664.41     692.41                                       532.29
 F    811.48     839.48                                       395.23
 T    912.53     940.53                                       248.16
 K                                                            147.11
```

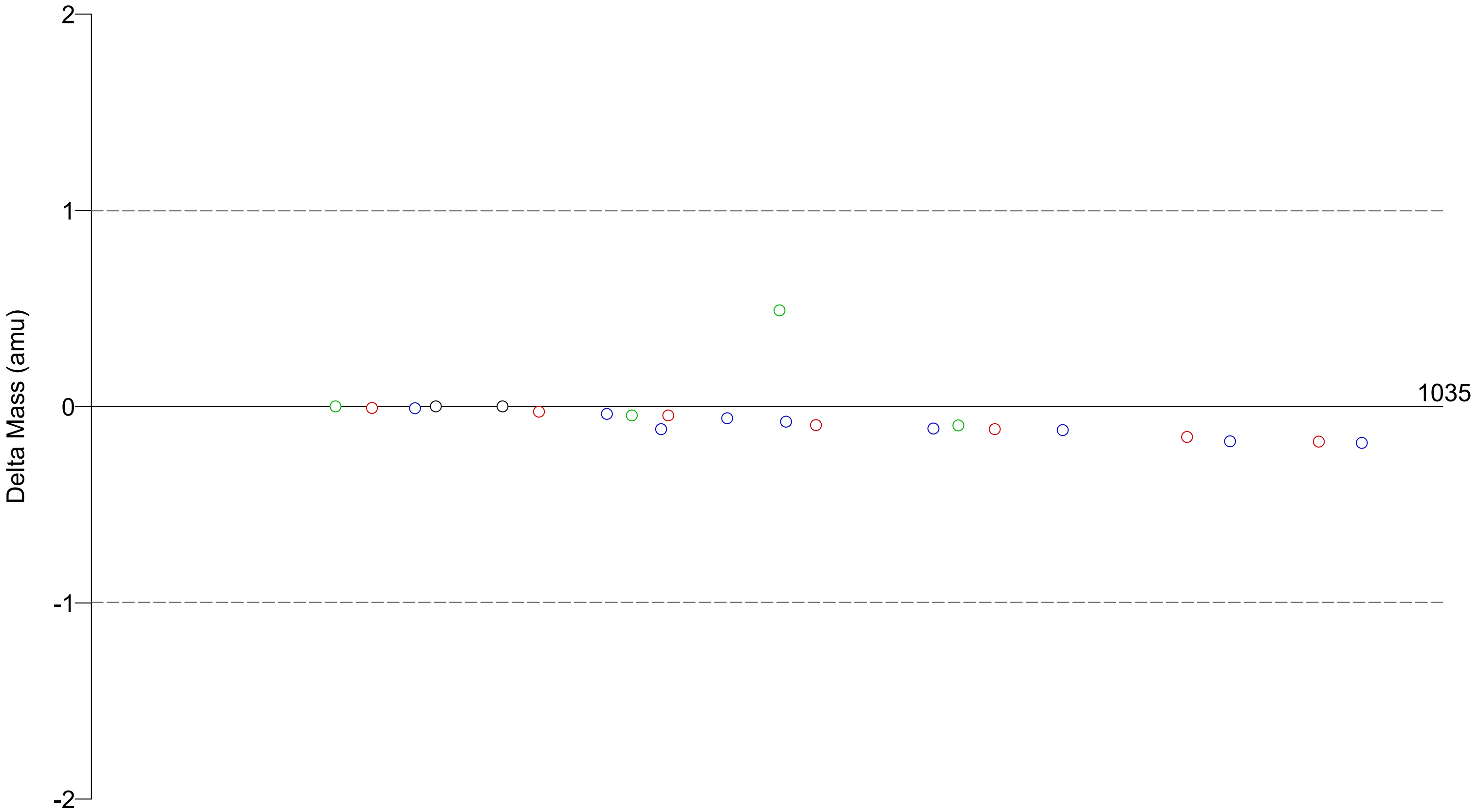


#2118291816-26226248 NL: 1.21E5

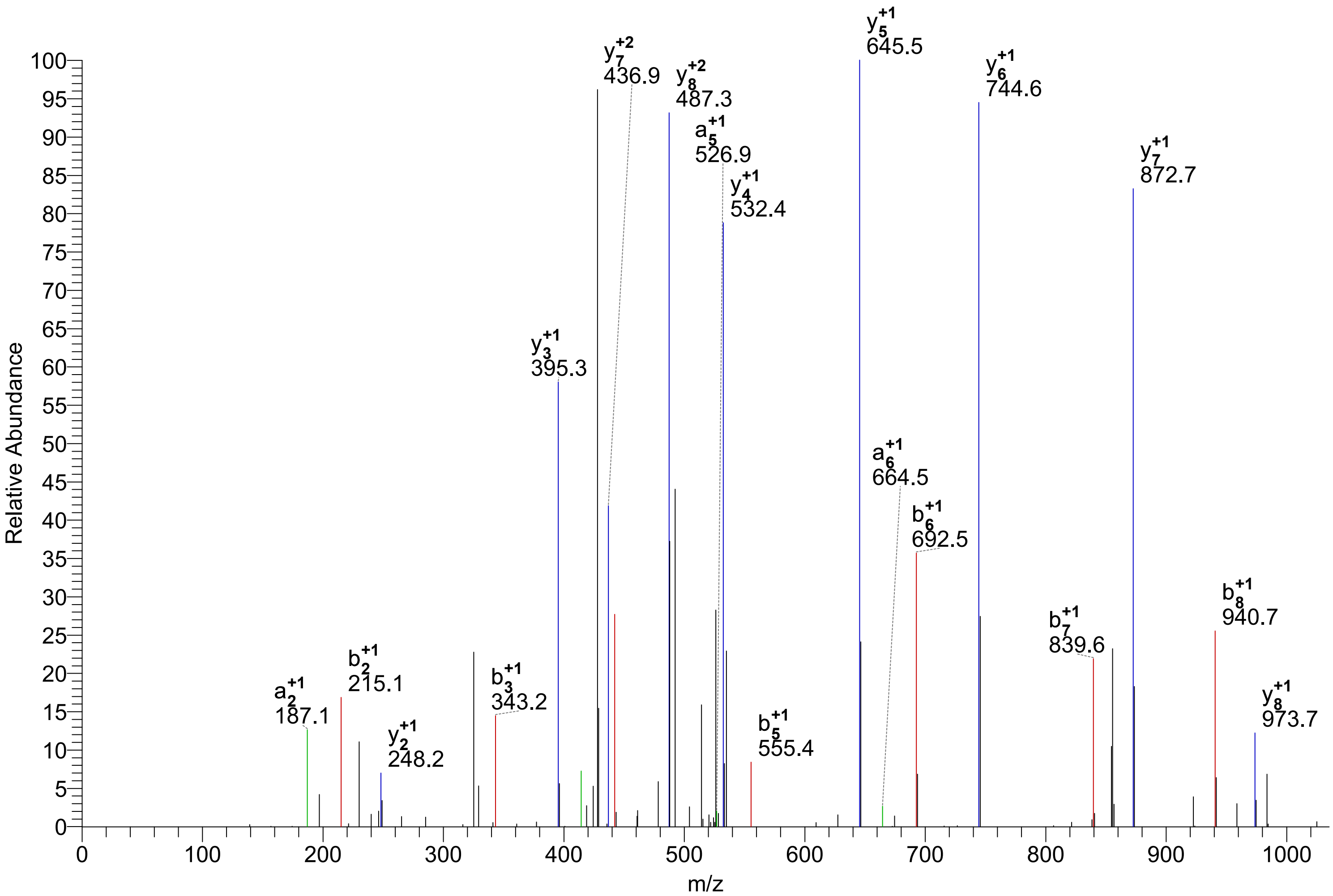


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00935601.1|TREMBL:Q9UM89|EN                                0.0002  10.2     0.0       0
2118291816 -  K.ITQVLHFTK.D                          1086.63   2  0.0002  3.684  0.435   1215.2 1   18/24   10

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 T    187.14     215.14                                      973.55
 Q    315.20     343.20                                      872.50
 V    414.27     442.27                                      744.44
 L    527.36     555.35                                      645.37
 H    664.41     692.41                                      532.29
 F    811.48     839.48                                      395.23
 T    912.53     940.53                                      248.16
 K                                                           147.11
```

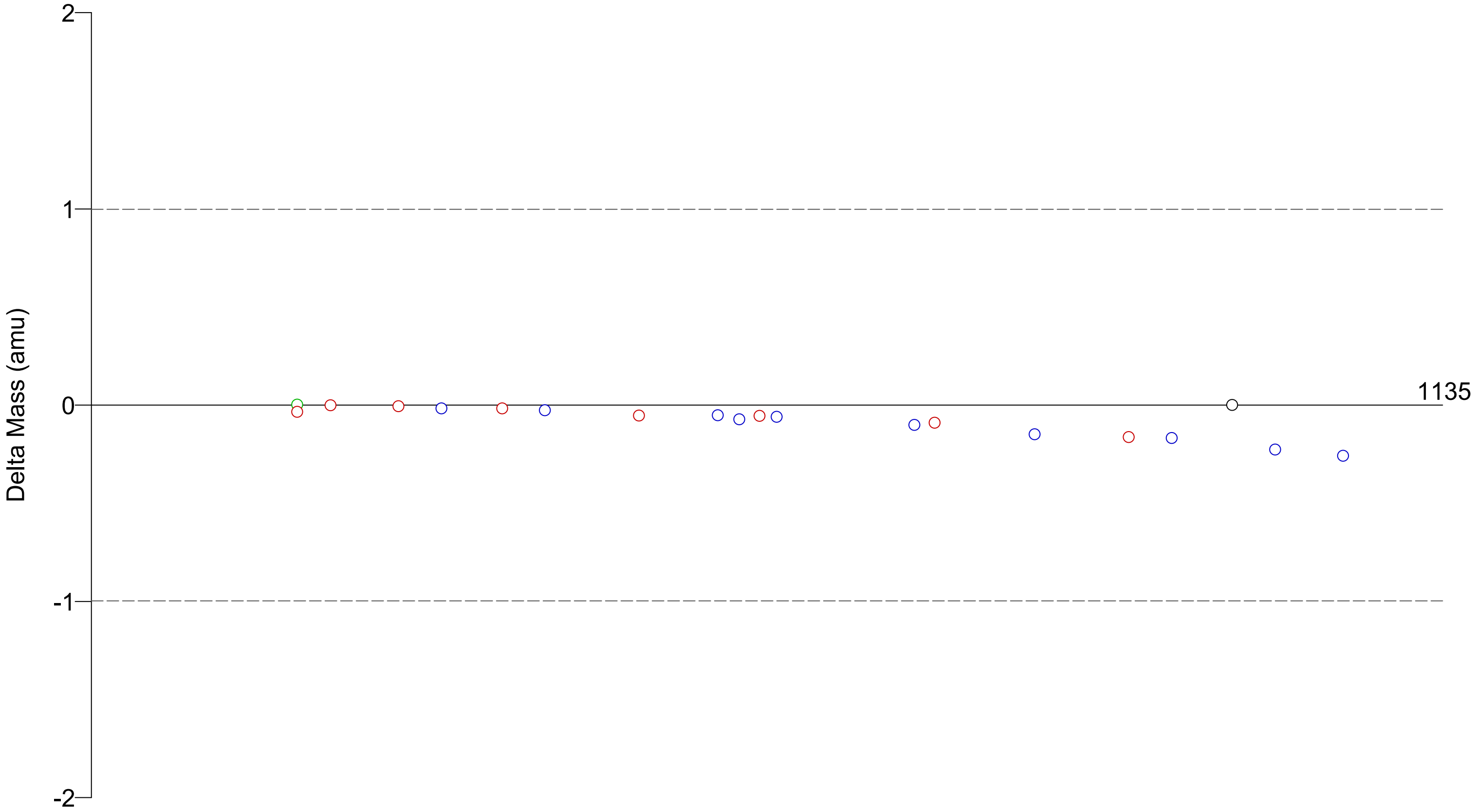


#2118291816-26226248 NL: 1.21E5

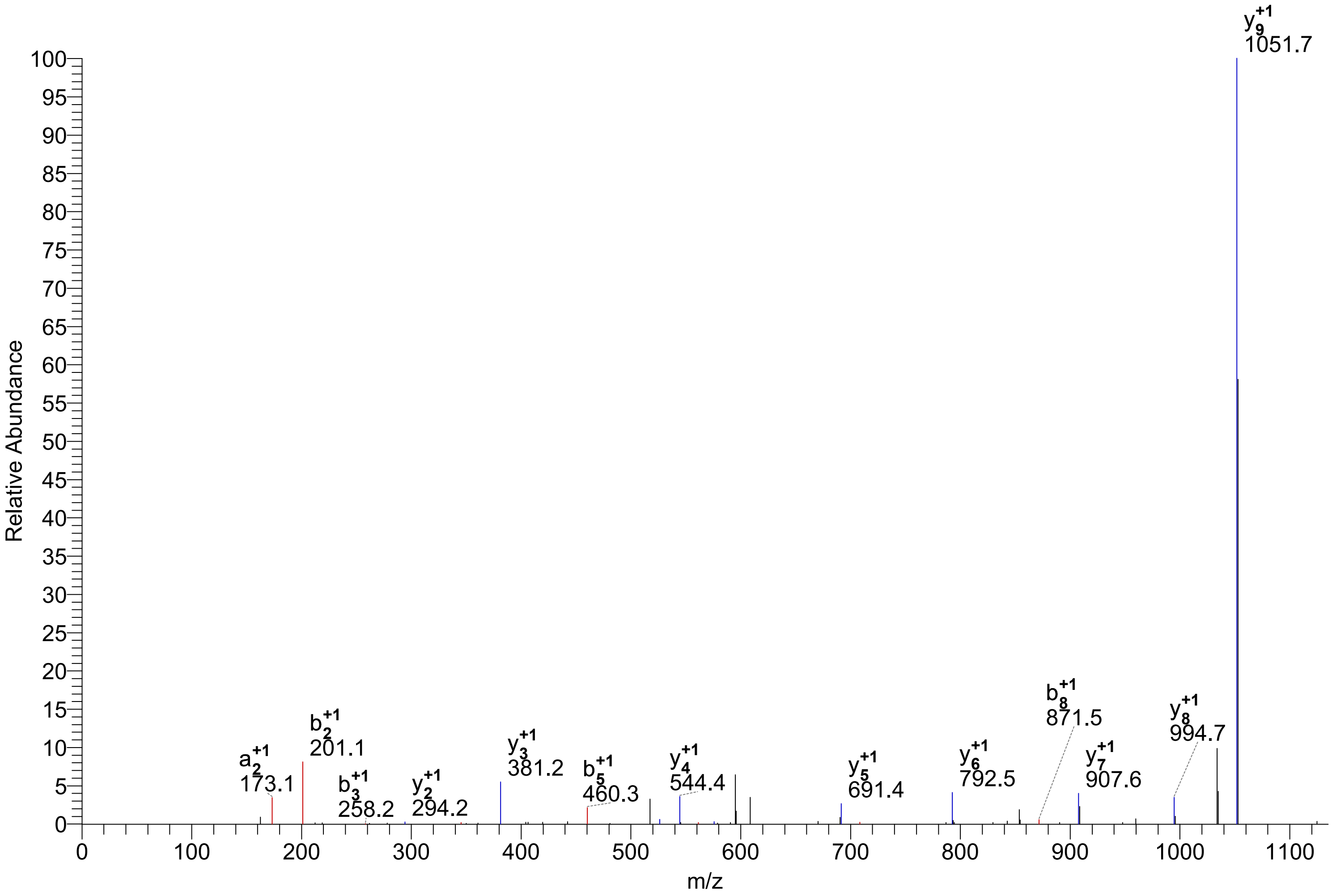


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00032328.2|SWISS-PROT:P01042-1|TREMBL:B4E1C2|ENSEMBL:EN    0.0003  10.2     0.0       0
2118291816 -  K.TVGSDTFYSFK.Y                        1251.59   2  0.0003  3.649  0.643   417.3  1   18/30   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 626.30
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 V    173.13    201.12                                     1150.54
 G    230.15    258.14                                     1051.47
 S    317.18    345.18                                      994.45
 D    432.21    460.20                                      907.42
 T    533.26    561.25                                      792.39
 F    680.32    708.32                                      691.34
 Y    843.39    871.38                                      544.28
 S    930.42    958.42                                      381.21
 F   1077.49   1105.48                                      294.18
 K                                                          147.11
```

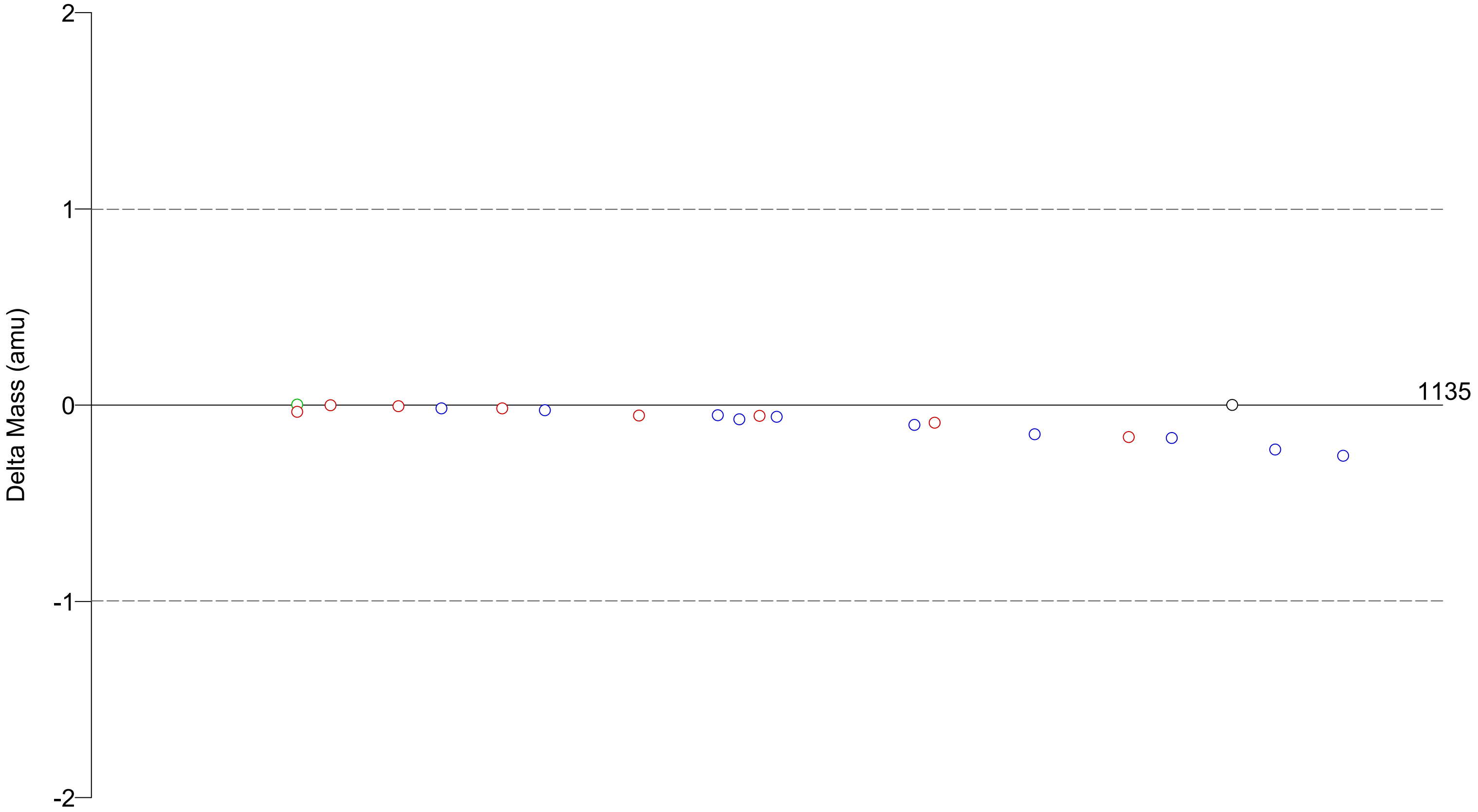


#2118291816-26226248 NL: 2.31E5

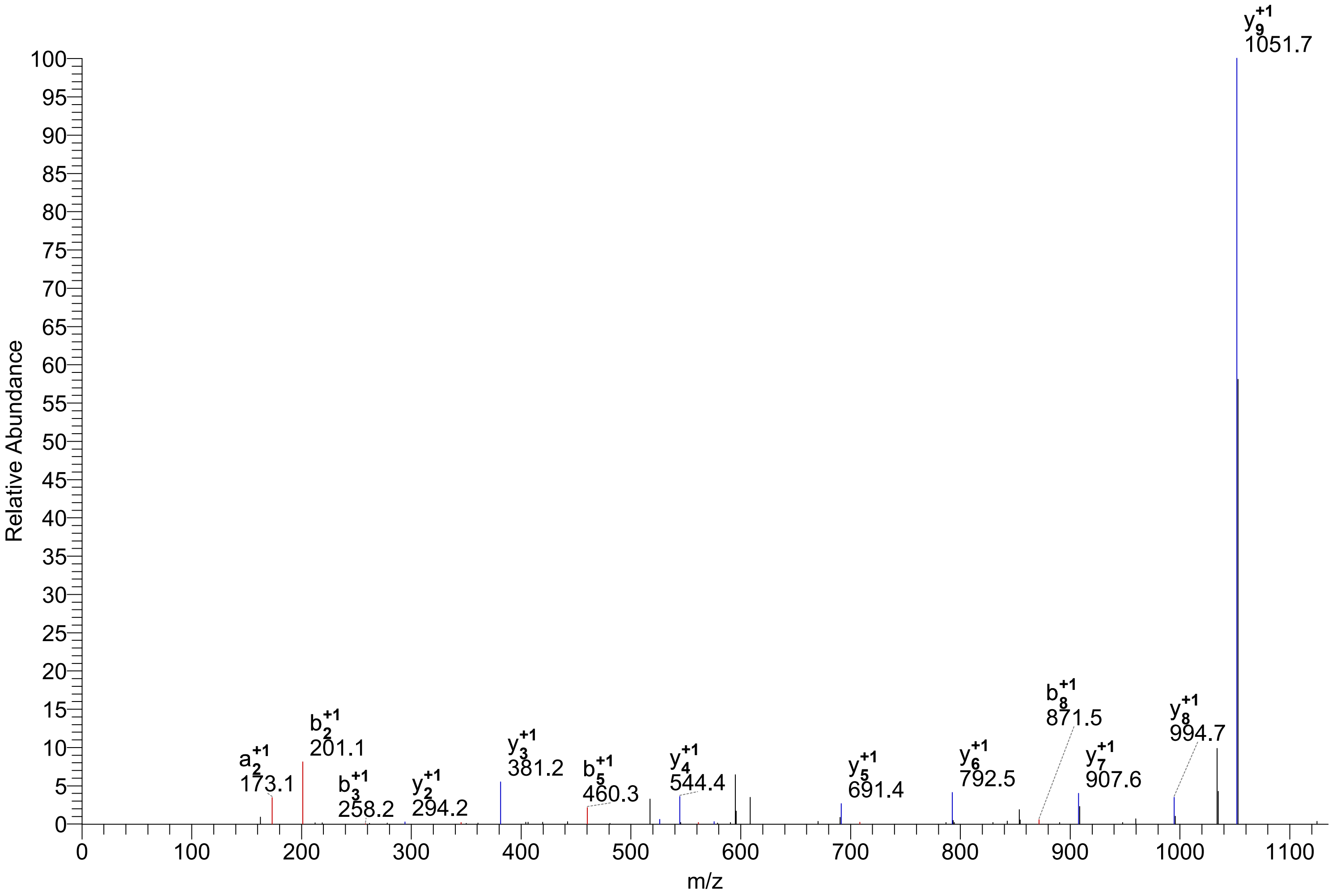


```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                              MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00215894.1|SWISS-PROT:P0104                               0.0003  10.2     0.0       0
2118291816 -  K.TVGSDTFYSFK.Y                     1251.59   2  0.0003  3.649  0.643   417.3  1   18/30   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 626.30
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions     Y ions     Y* ions     Yo ions     Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 V    173.13     201.12                                     1150.54
 G    230.15     258.14                                     1051.47
 S    317.18     345.18                                      994.45
 D    432.21     460.20                                      907.42
 T    533.26     561.25                                      792.39
 F    680.32     708.32                                      691.34
 Y    843.39     871.38                                      544.28
 S    930.42     958.42                                      381.21
 F   1077.49    1105.48                                      294.18
 K                                                           147.11
```

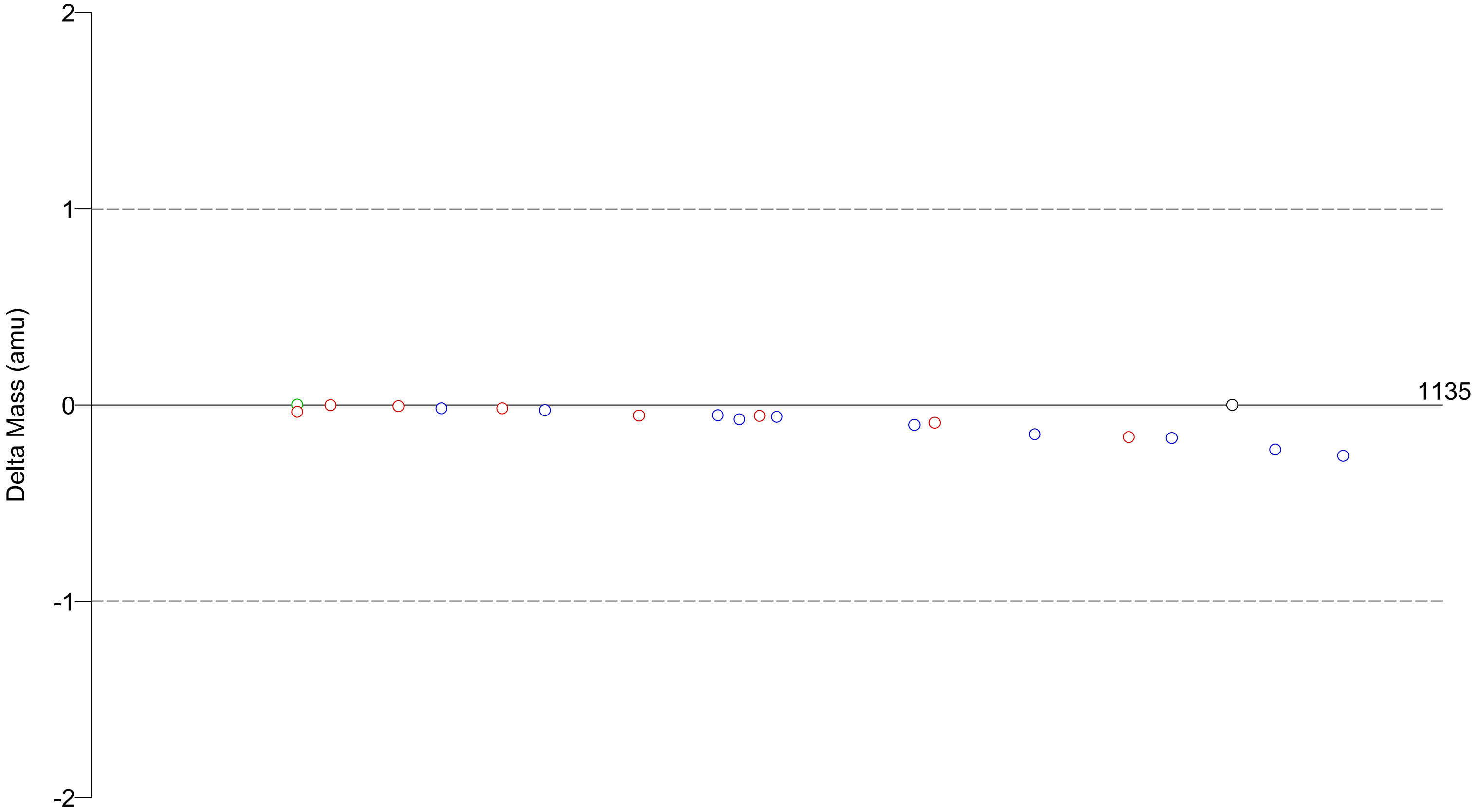


#2118291816-26226248 NL: 2.31E5

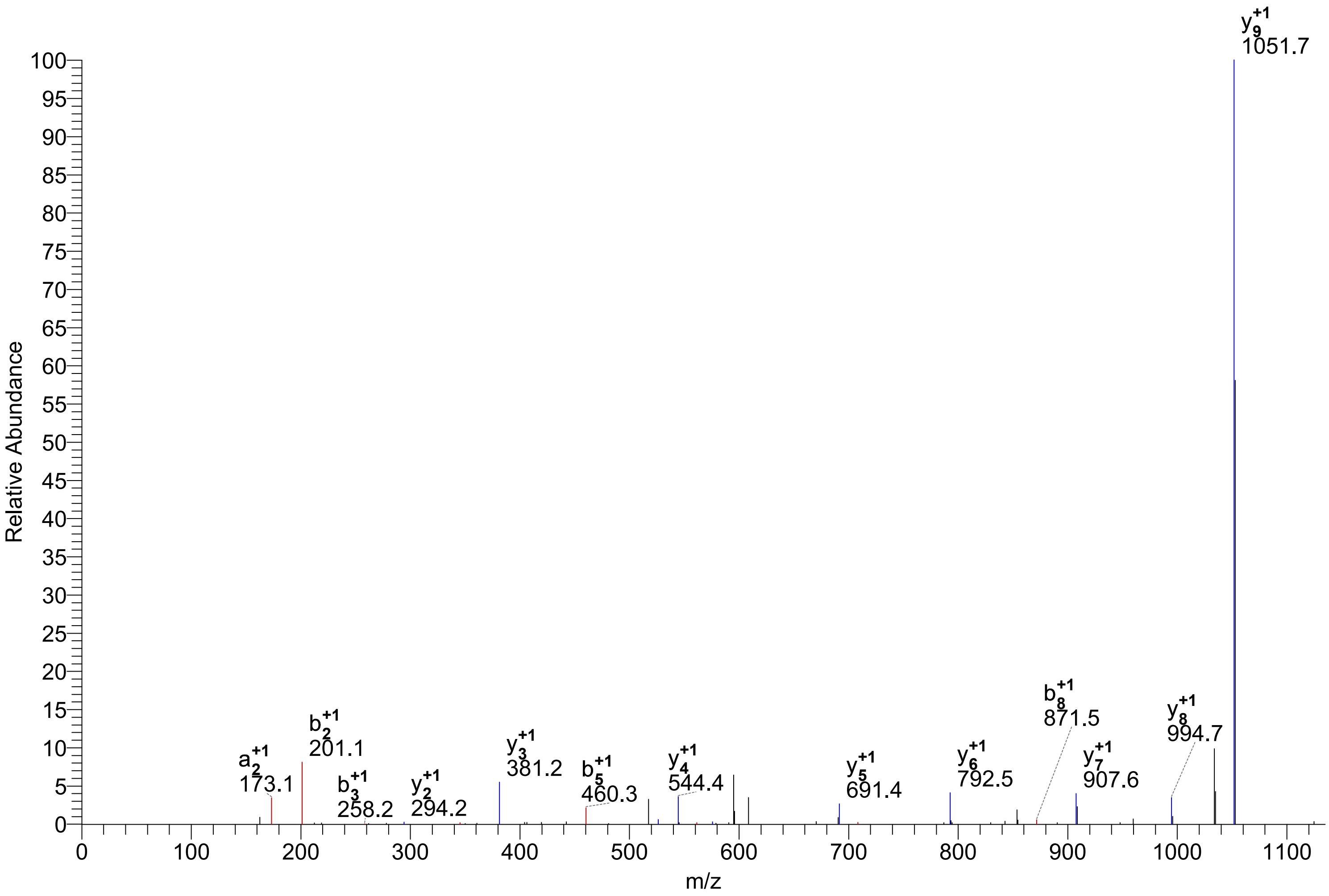


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00797097.1|VEGA:OTTHUMP0000                                0.0003  10.2     0.0       0
2118291816 -  K.TVGSDTFYSFK.Y                        1251.59   2  0.0003  3.649  0.643   417.3  1   18/30   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 626.30
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 V    173.13     201.12                                    1150.54
 G    230.15     258.14                                    1051.47
 S    317.18     345.18                                     994.45
 D    432.21     460.20                                     907.42
 T    533.26     561.25                                     792.39
 F    680.32     708.32                                     691.34
 Y    843.39     871.38                                     544.28
 S    930.42     958.42                                     381.21
 F   1077.49    1105.48                                     294.18
 K                                                          147.11
```

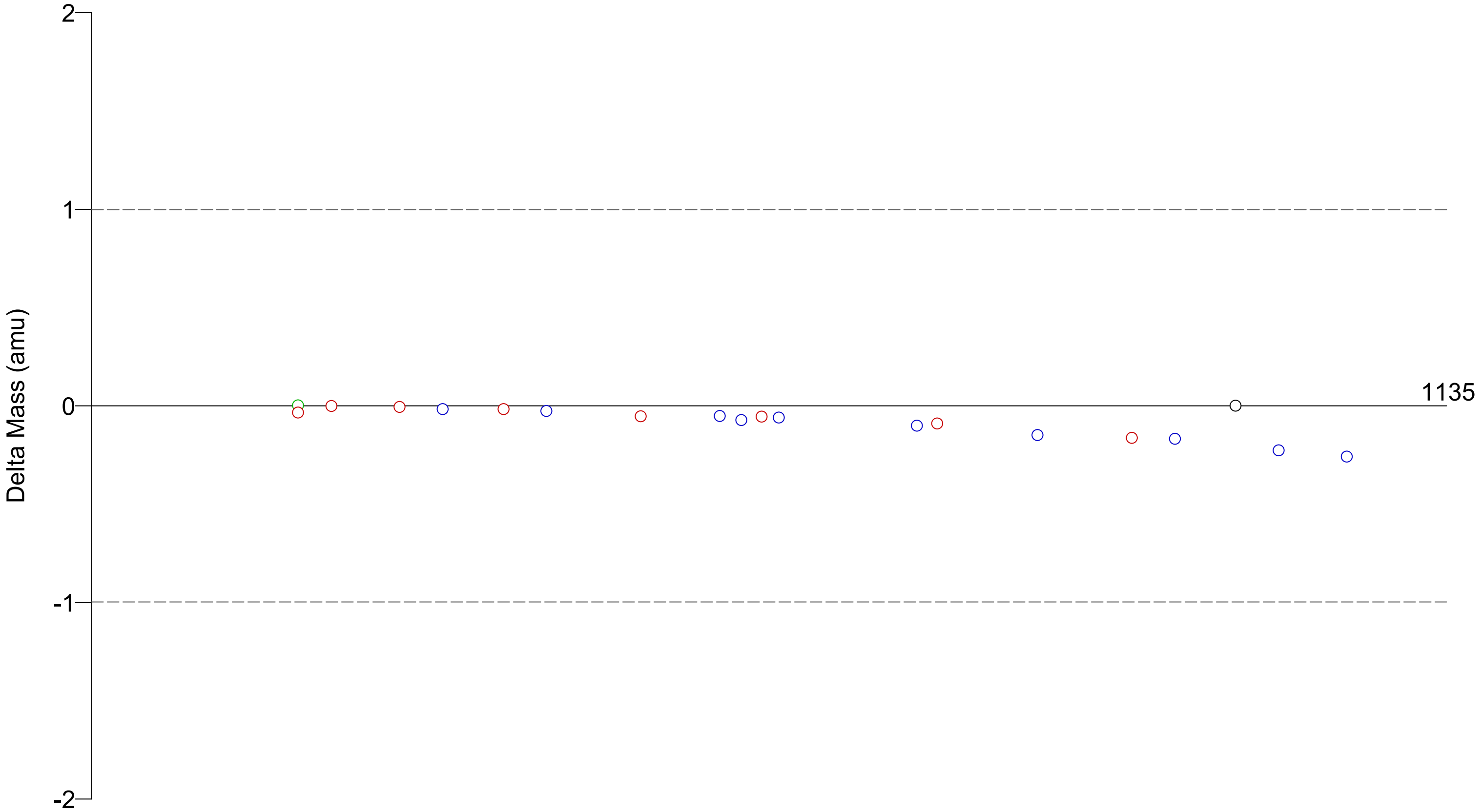


#2118291816-26226248 NL: 2.31E5

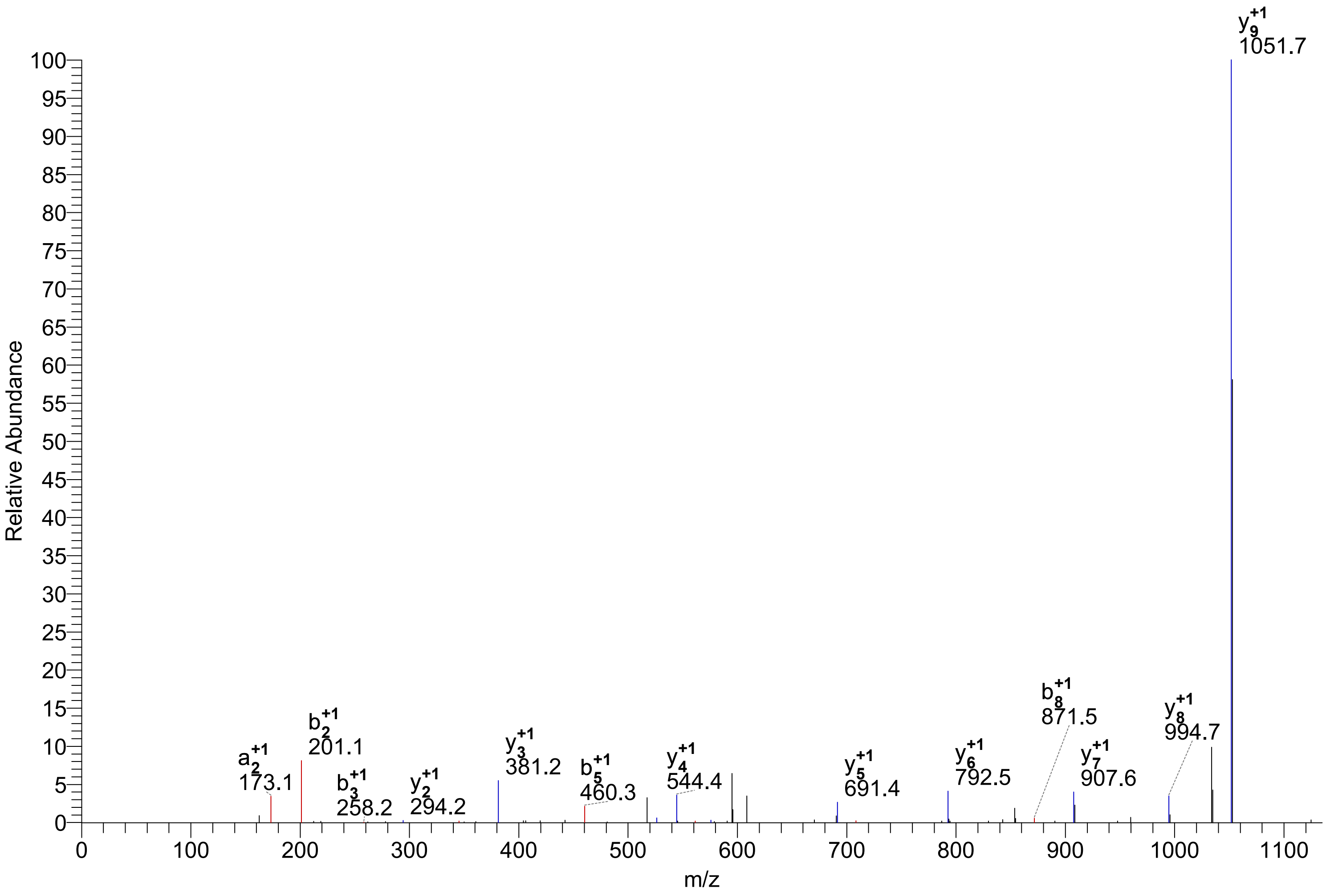


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00797833.4|VEGA:OTTHUMP0000                                   0.0003  10.2     0.0        0
2118291816 -  K.TVGSDTFYSFK.Y                          1251.59    2  0.0003  3.649  0.643   417.3  1   18/30   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 626.30
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 V    173.13     201.12                                     1150.54
 G    230.15     258.14                                     1051.47
 S    317.18     345.18                                      994.45
 D    432.21     460.20                                      907.42
 T    533.26     561.25                                      792.39
 F    680.32     708.32                                      691.34
 Y    843.39     871.38                                      544.28
 S    930.42     958.42                                      381.21
 F   1077.49    1105.48                                      294.18
 K                                                           147.11
```

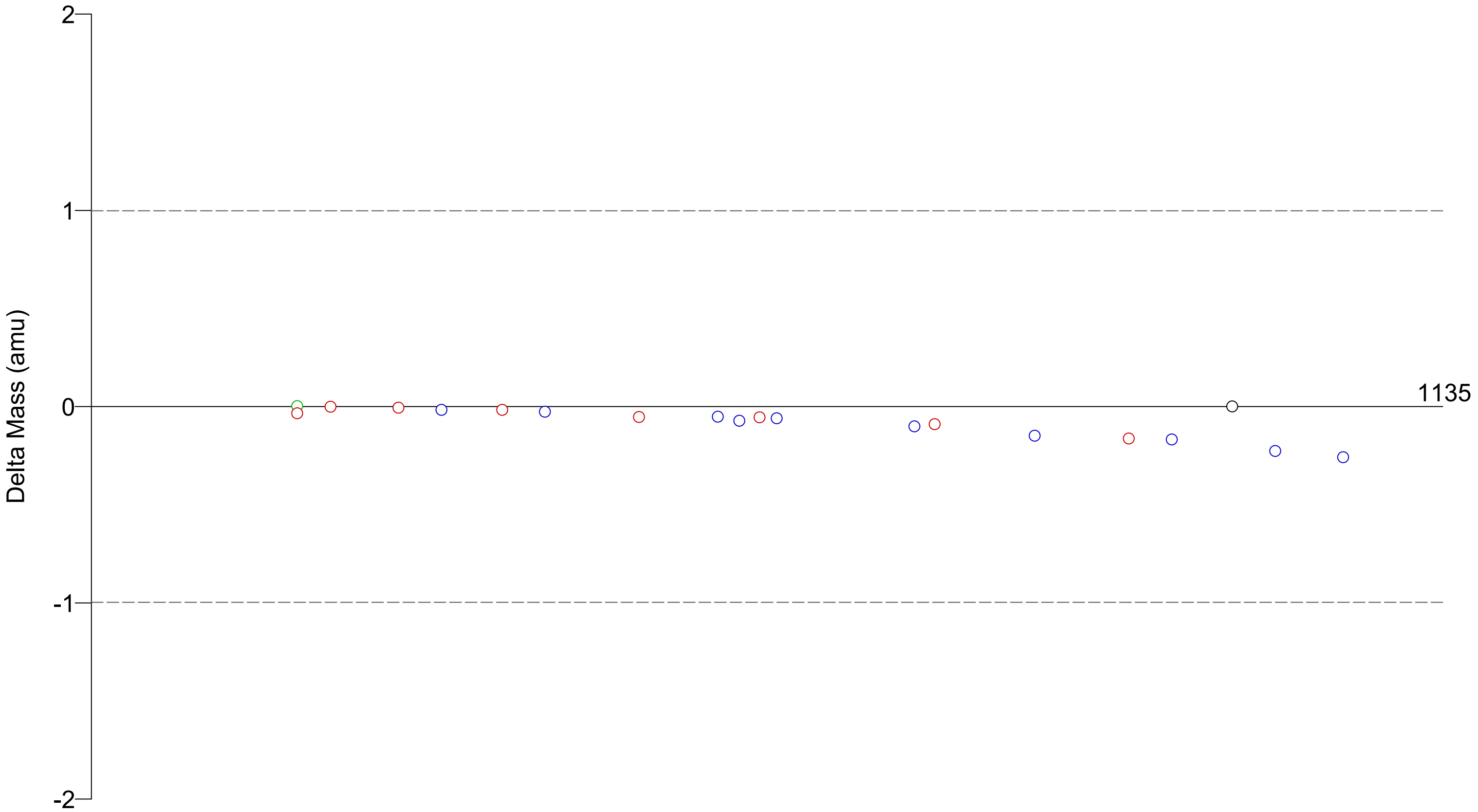


#2118291816-26226248 NL: 2.31E5

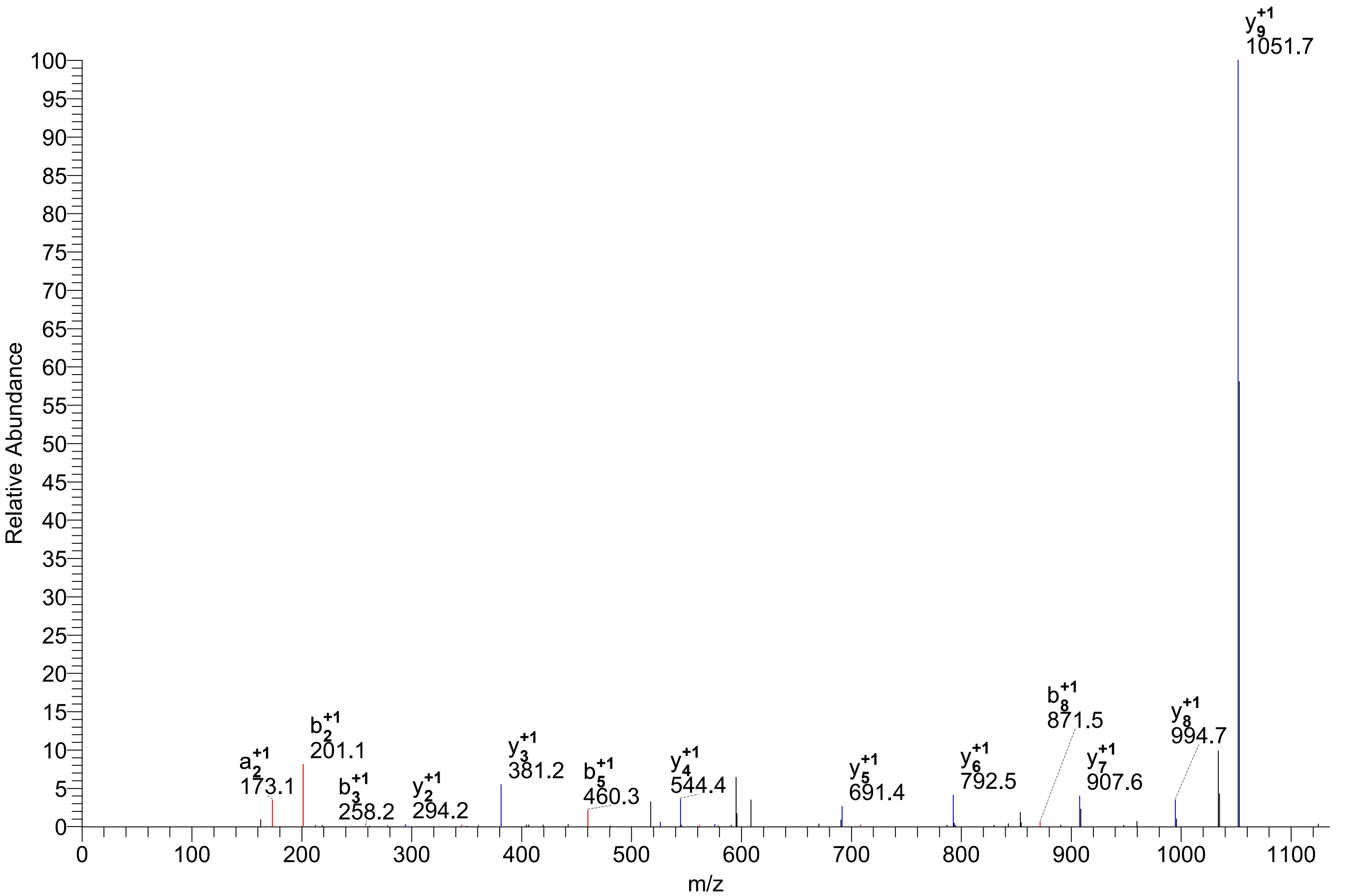


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)        Sequence                                  MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00924859.1|VEGA:OTTHUMP0000                                  0.0003  10.2     0.0        0
2118291816 -  K.TVGSDTFYSFK.Y                          1251.59   2  0.0003  3.649  0.643   417.3  1   18/30   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 626.30
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 V    173.13     201.12                                     1150.54
 G    230.15     258.14                                     1051.47
 S    317.18     345.18                                      994.45
 D    432.21     460.20                                      907.42
 T    533.26     561.25                                      792.39
 F    680.32     708.32                                      691.34
 Y    843.39     871.38                                      544.28
 S    930.42     958.42                                      381.21
 F   1077.49    1105.48                                      294.18
 K                                                           147.11
```

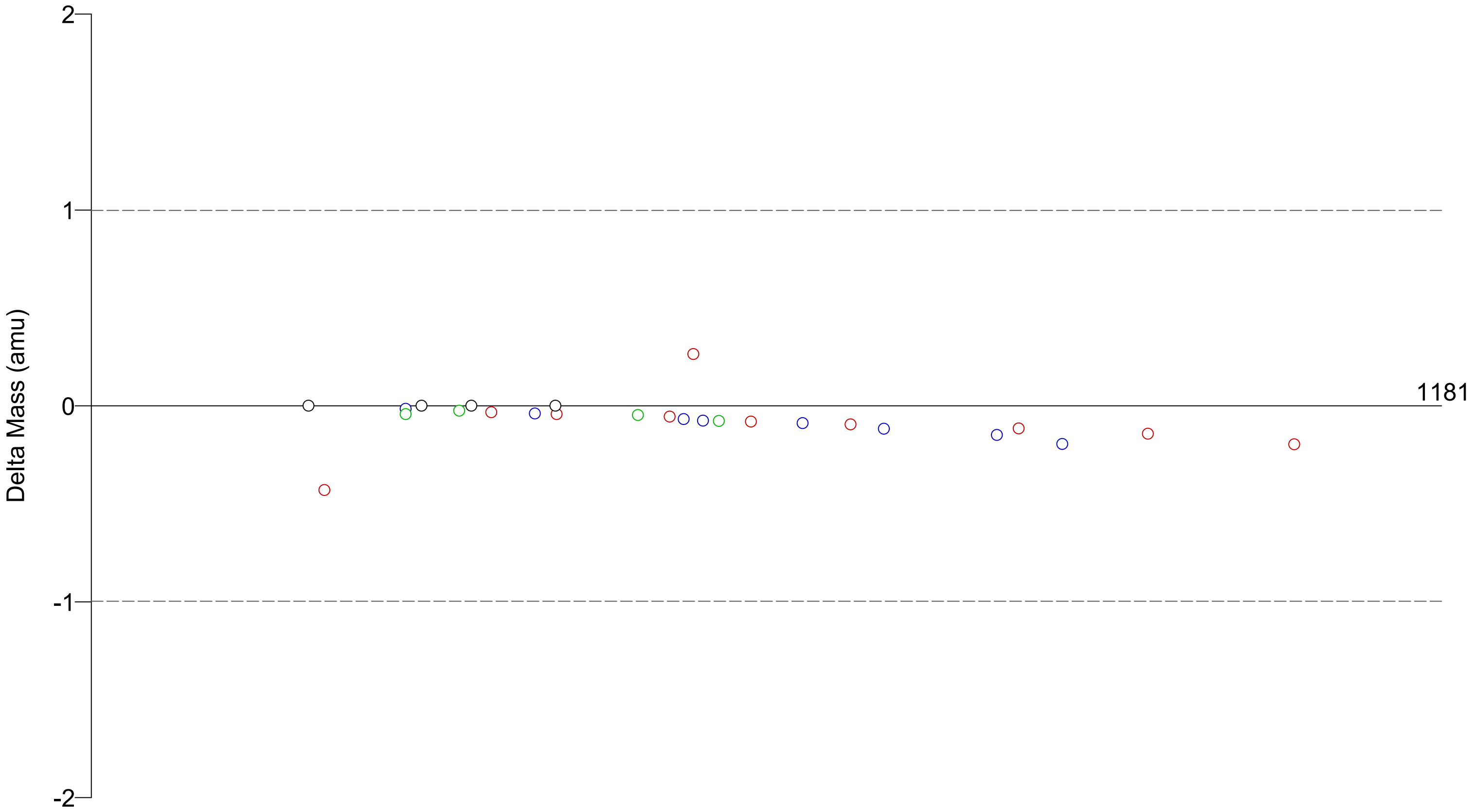


#2118291816-26226248 NL: 2.31E5

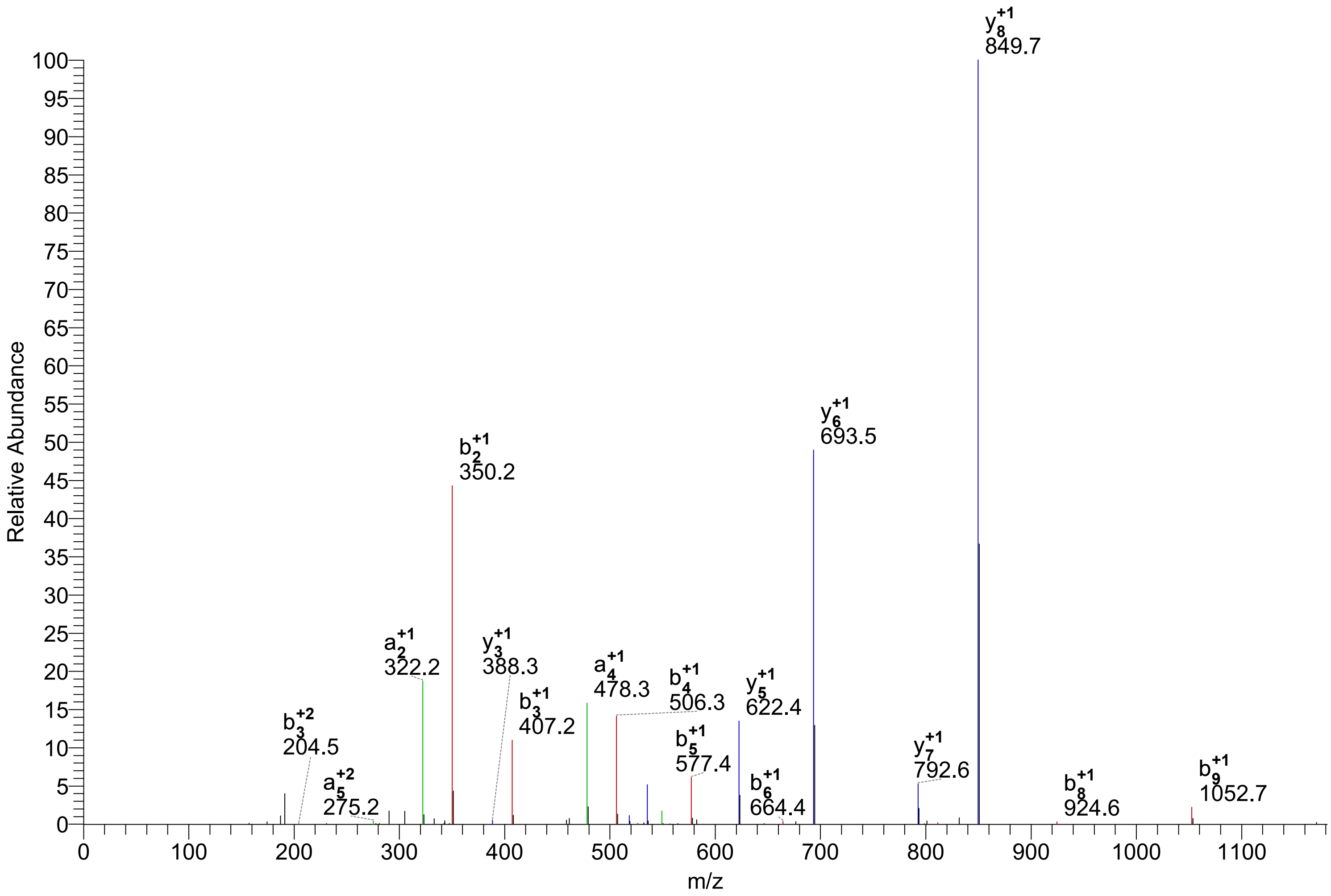


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00022420.3|SWISS-PROT:P02753|ENSEMBL:ENSP00000360519;EN    0.0003  10.2     0.0       0
19287468 - 1  K.YWGVASFLQK.G                         1198.63   2  0.0003  3.463  0.383   766.9  1   18/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 599.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 W    322.16     350.15                                     1035.56
 G    379.18     407.17                                      849.48
 V    478.24     506.24                                      792.46
 A    549.28     577.28                                      693.39
 S    636.31     664.31                                      622.36
 F    783.38     811.38                                      535.32
 L    896.47     924.46                                      388.26
 Q   1024.53    1052.52                                      275.17
 K                                                           147.11
```

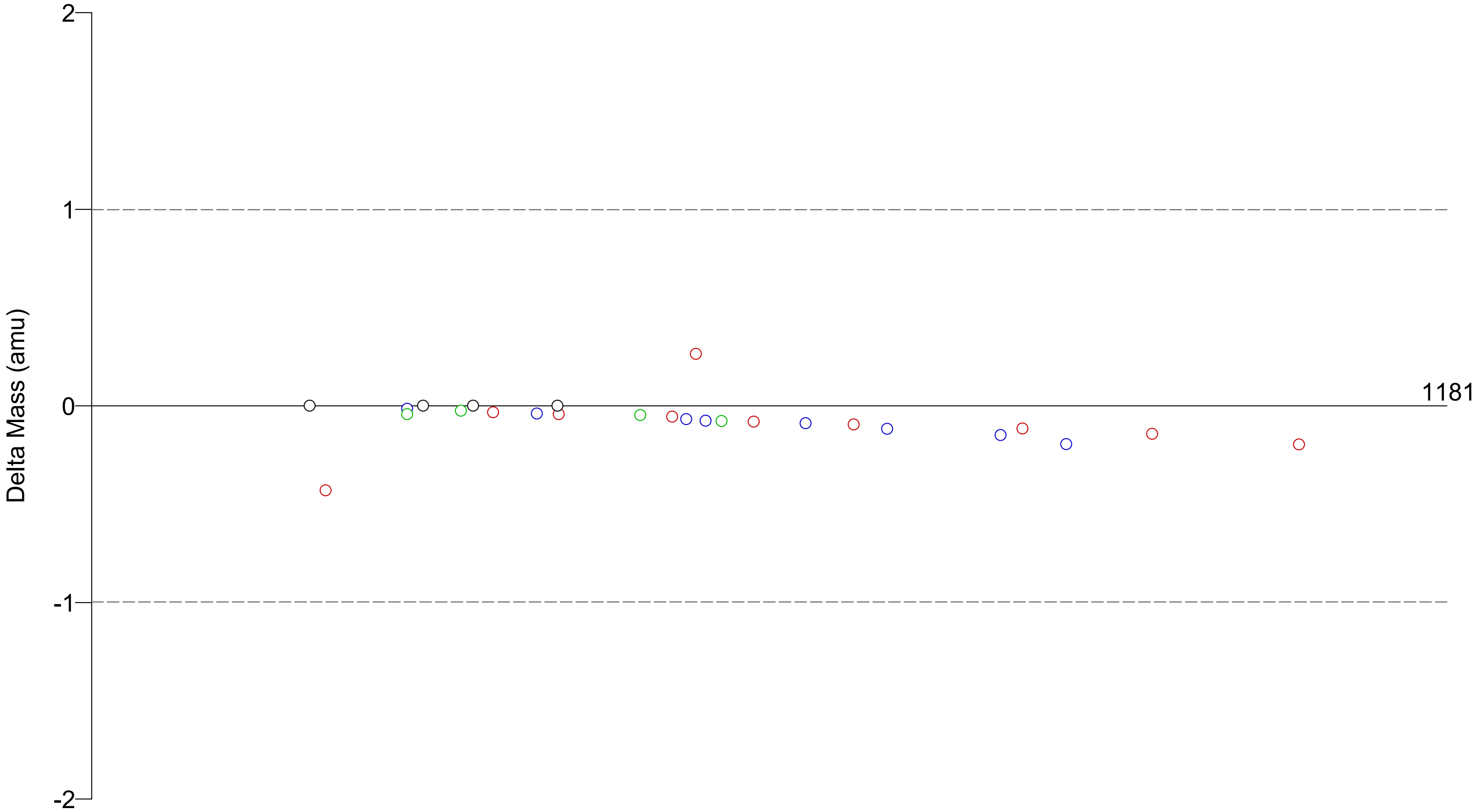


#19287468-1 NL: 2.47E6

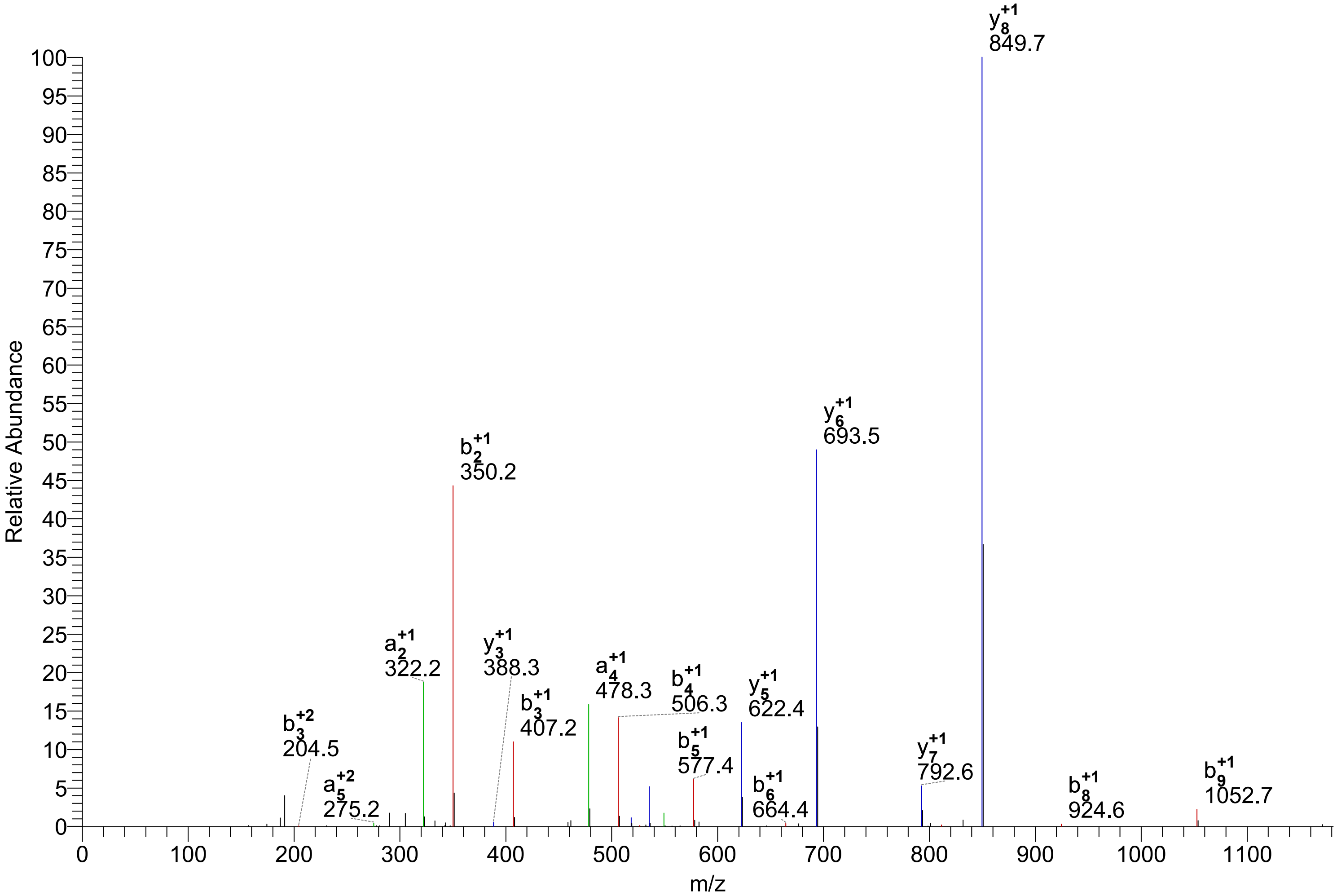


```
Reference                                                       P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+      z     P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00480192.1|TREMBL:Q5VY30|EN                                0.0003  10.2     0.0        0
19287468 - 1  K.YWGVASFLQK.G                      1198.63   2  0.0003  3.463  0.383   766.9  1   18/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 599.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 W    322.16     350.15                                    1035.56
 G    379.18     407.17                                     849.48
 V    478.24     506.24                                     792.46
 A    549.28     577.28                                     693.39
 S    636.31     664.31                                     622.36
 F    783.38     811.38                                     535.32
 L    896.47     924.46                                     388.26
 Q   1024.53    1052.52                                     275.17
 K                                                          147.11
```

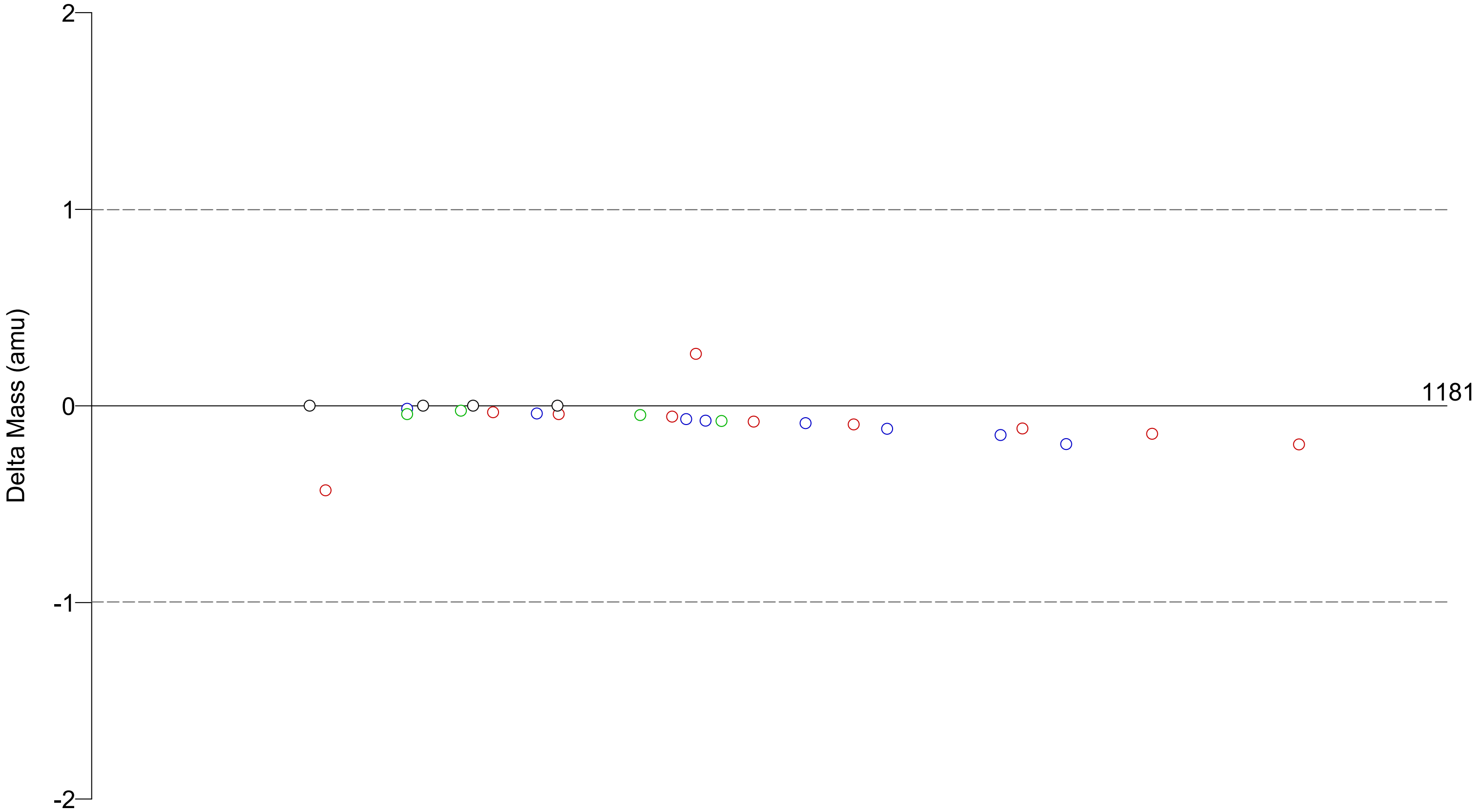


#19287468-1 NL: 2.47E6

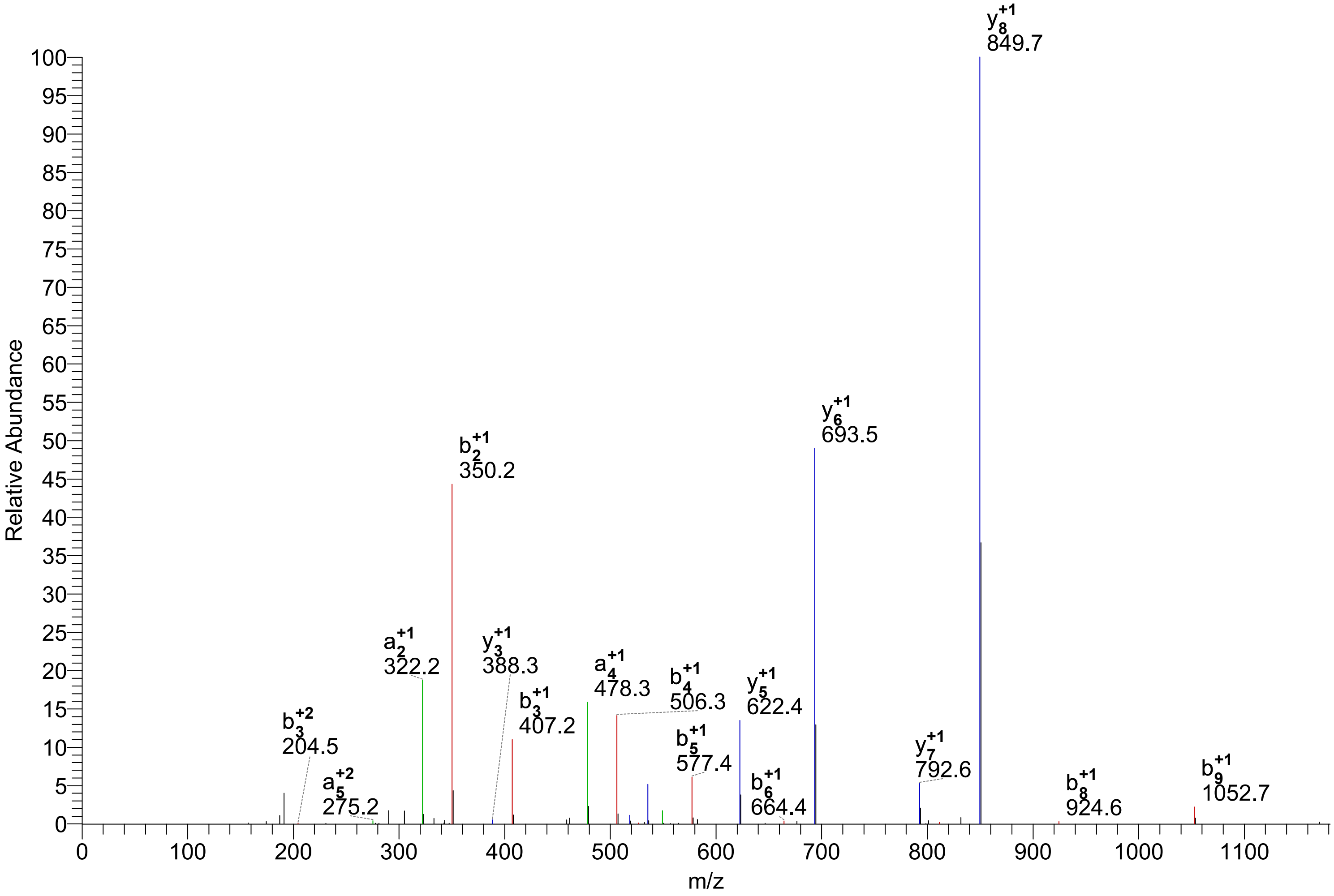


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00844536.2|TREMBL:A6NCP9|EN                                 0.0003  10.2      0.0        0
19287468 - 1  K.YWGVASFLQK.G                        1198.63    2  0.0003  3.463  0.383   766.9  1   18/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 599.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 W    322.16     350.15                                      1035.56
 G    379.18     407.17                                       849.48
 V    478.24     506.24                                       792.46
 A    549.28     577.28                                       693.39
 S    636.31     664.31                                       622.36
 F    783.38     811.38                                       535.32
 L    896.47     924.46                                       388.26
 Q   1024.53    1052.52                                       275.17
 K                                                            147.11
```

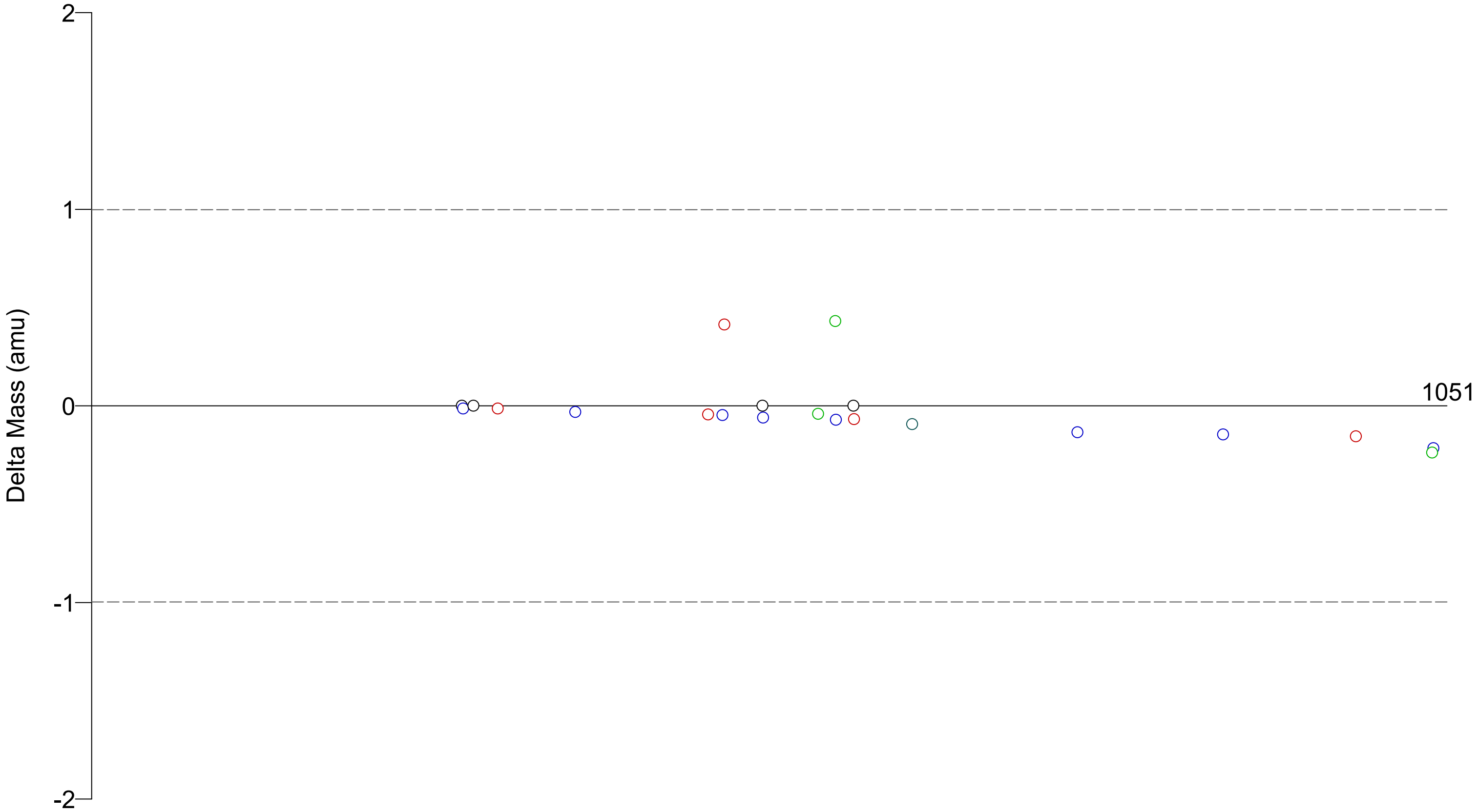


#19287468-1 NL: 2.47E6

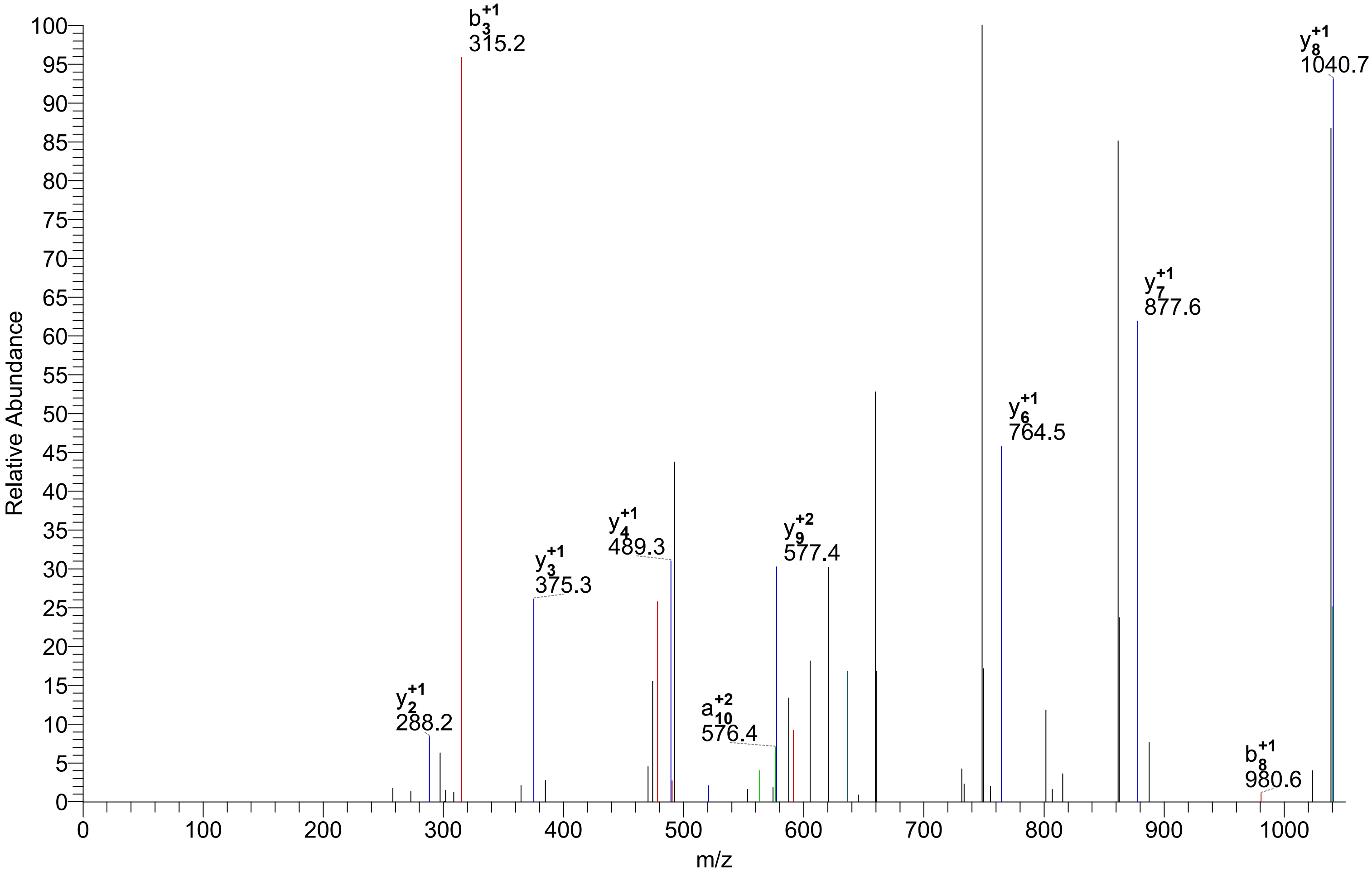


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z    P       XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00426051.3|TREMBL:Q6MZU6 Ta                                 0.0004  18.2     0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68    2  0.002   2.168  0.118   607.2  1   14/30   30
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64    2  0.0004  3.377  0.600   416.0  1   16/33   13

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

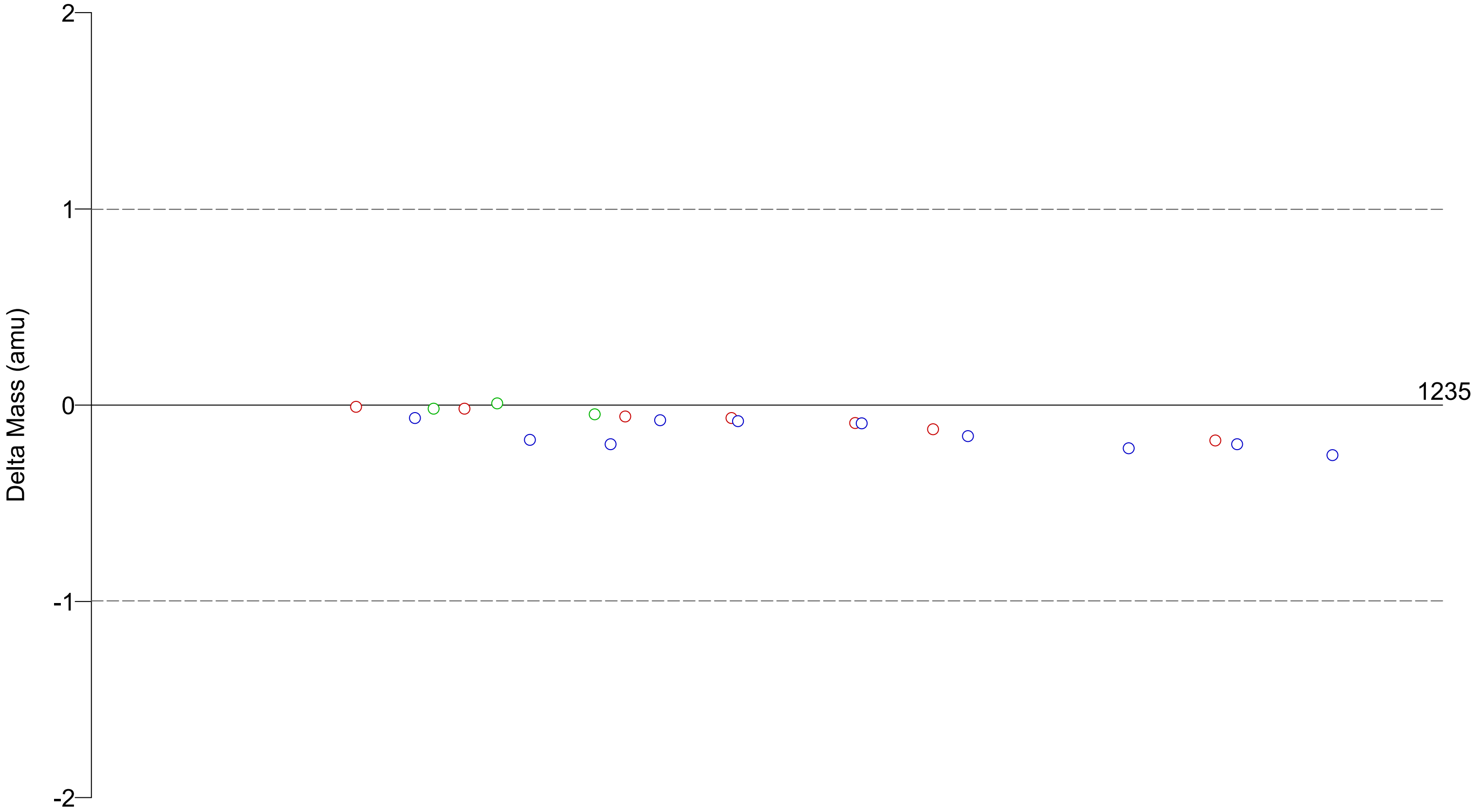
```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```



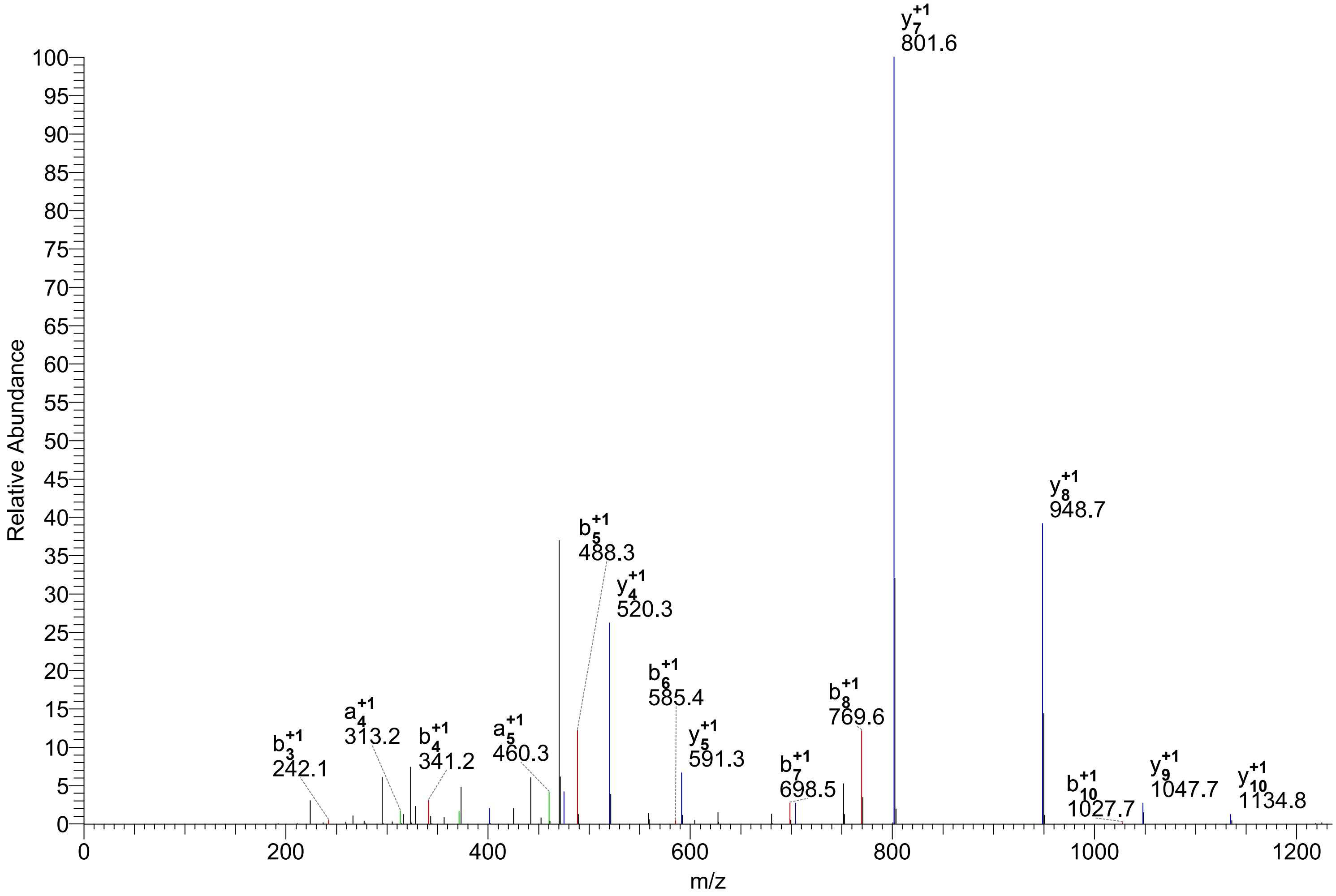
#19287468-1 NL: 8.93E4



```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

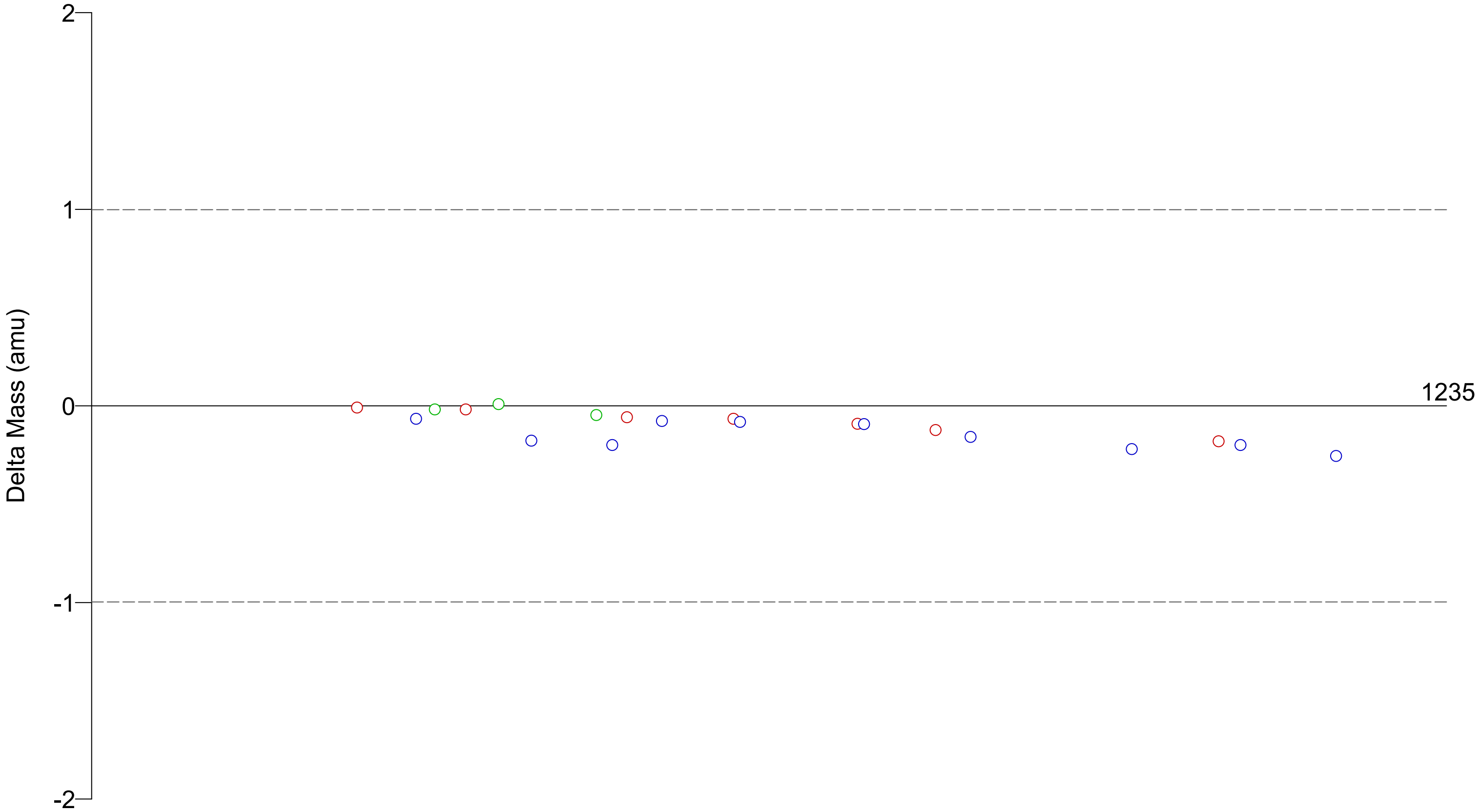


#19287468-1 NL: 4.16E6

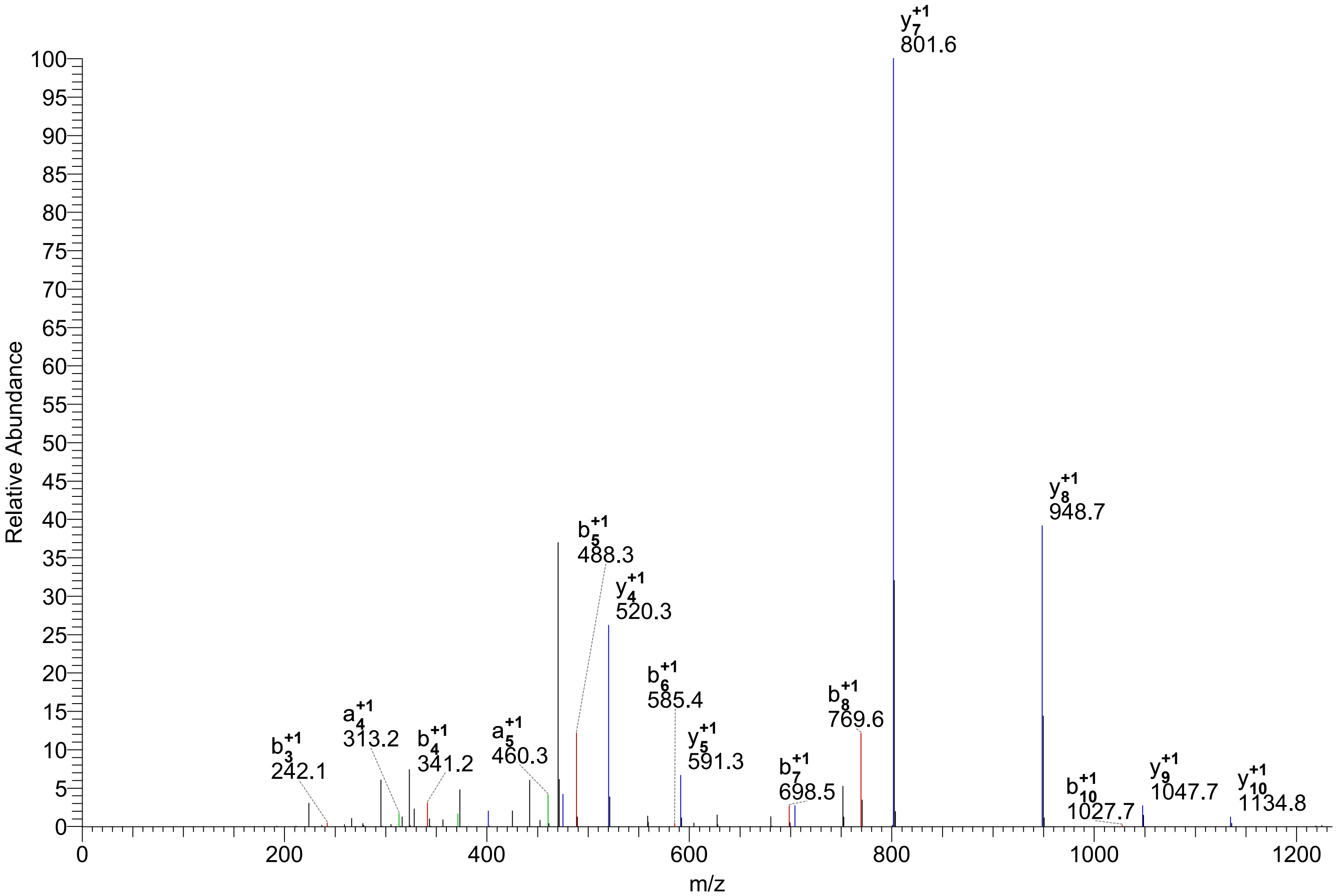


```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00168728.1|TREMBL:Q8NF17|ENSEMBL:ENSP00000374992 Tax_Id     0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                        1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

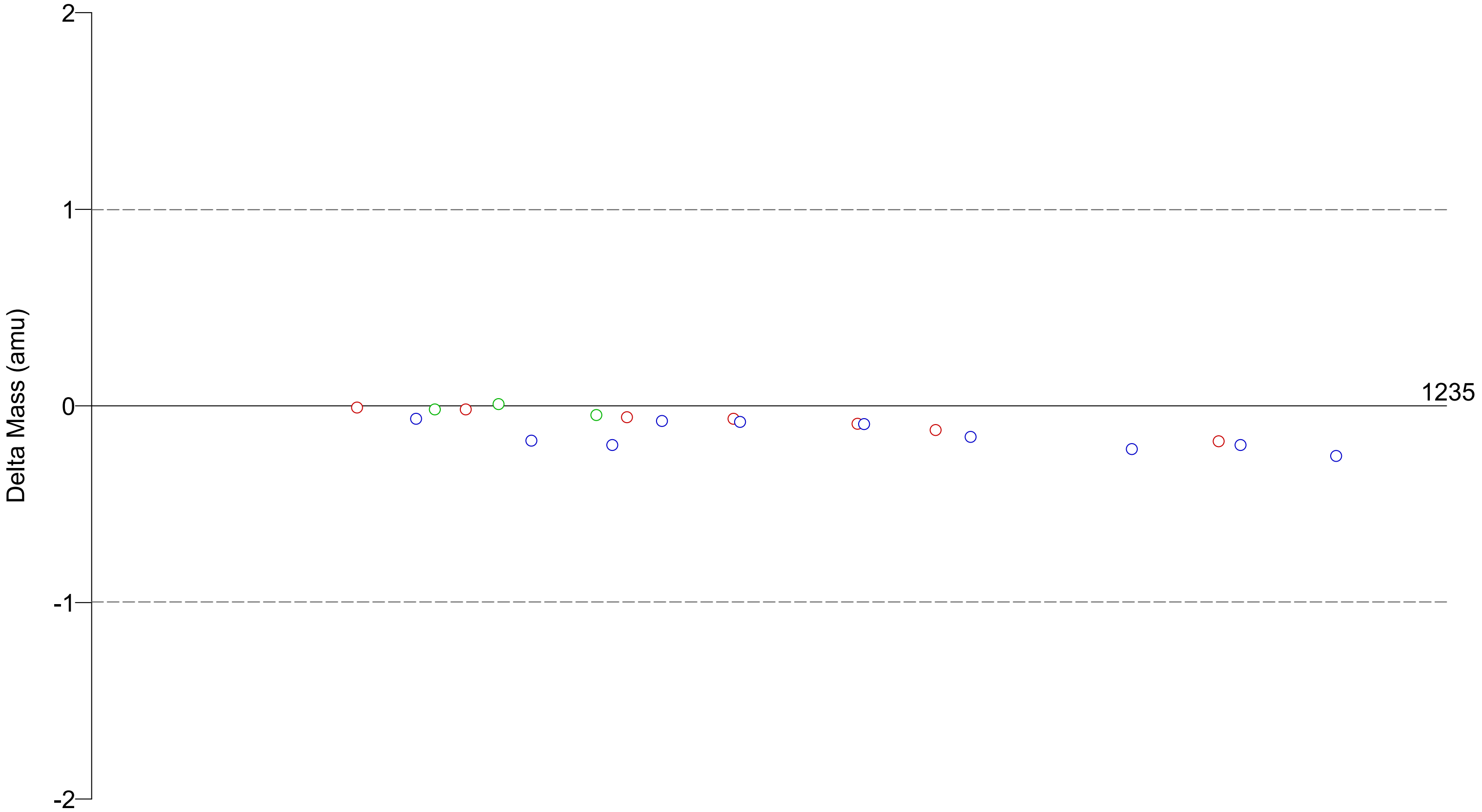


#19287468-1 NL: 4.16E6

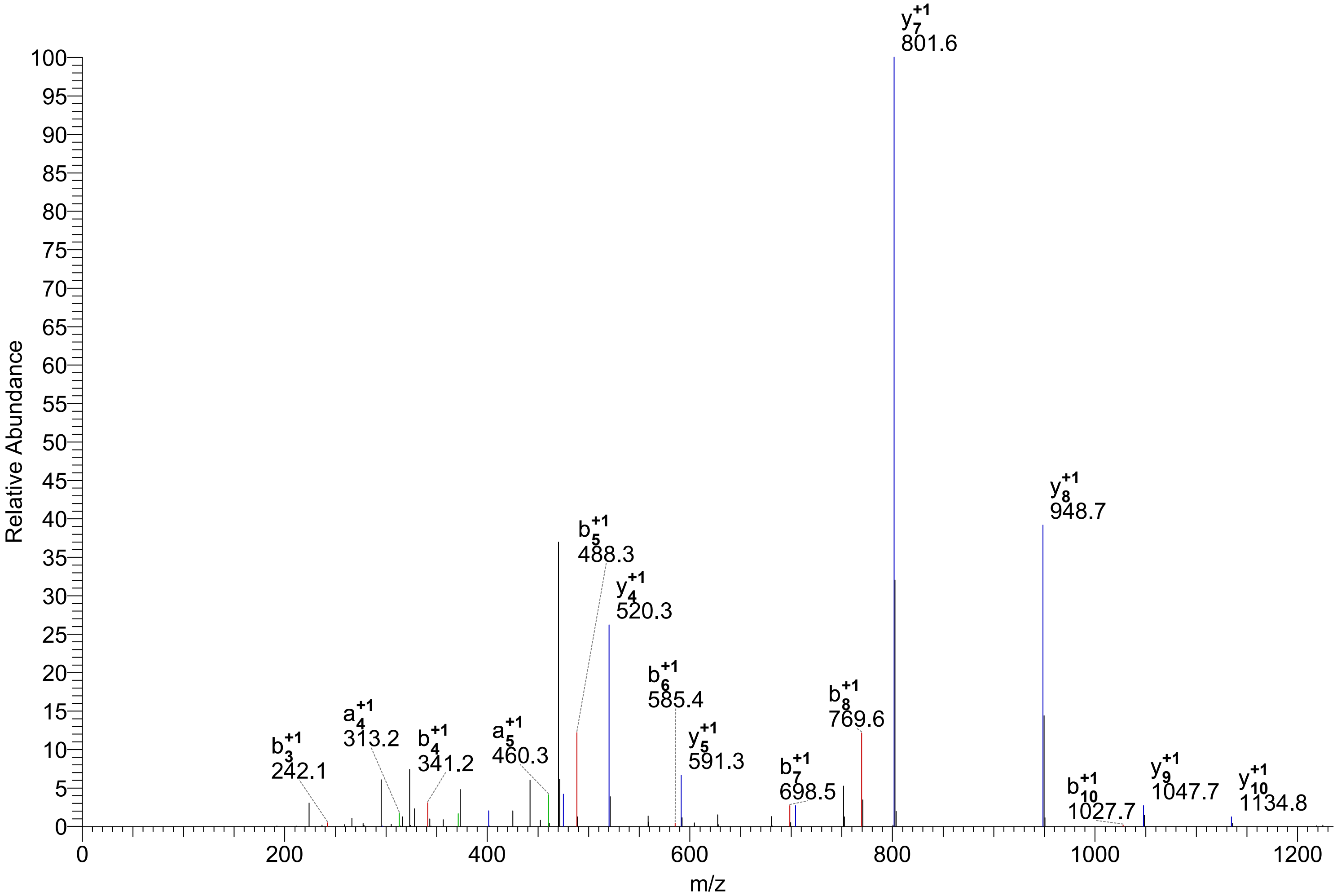


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00383957.1|TREMBL:O95978 Ta                                 0.0004  10.2      0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64    2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

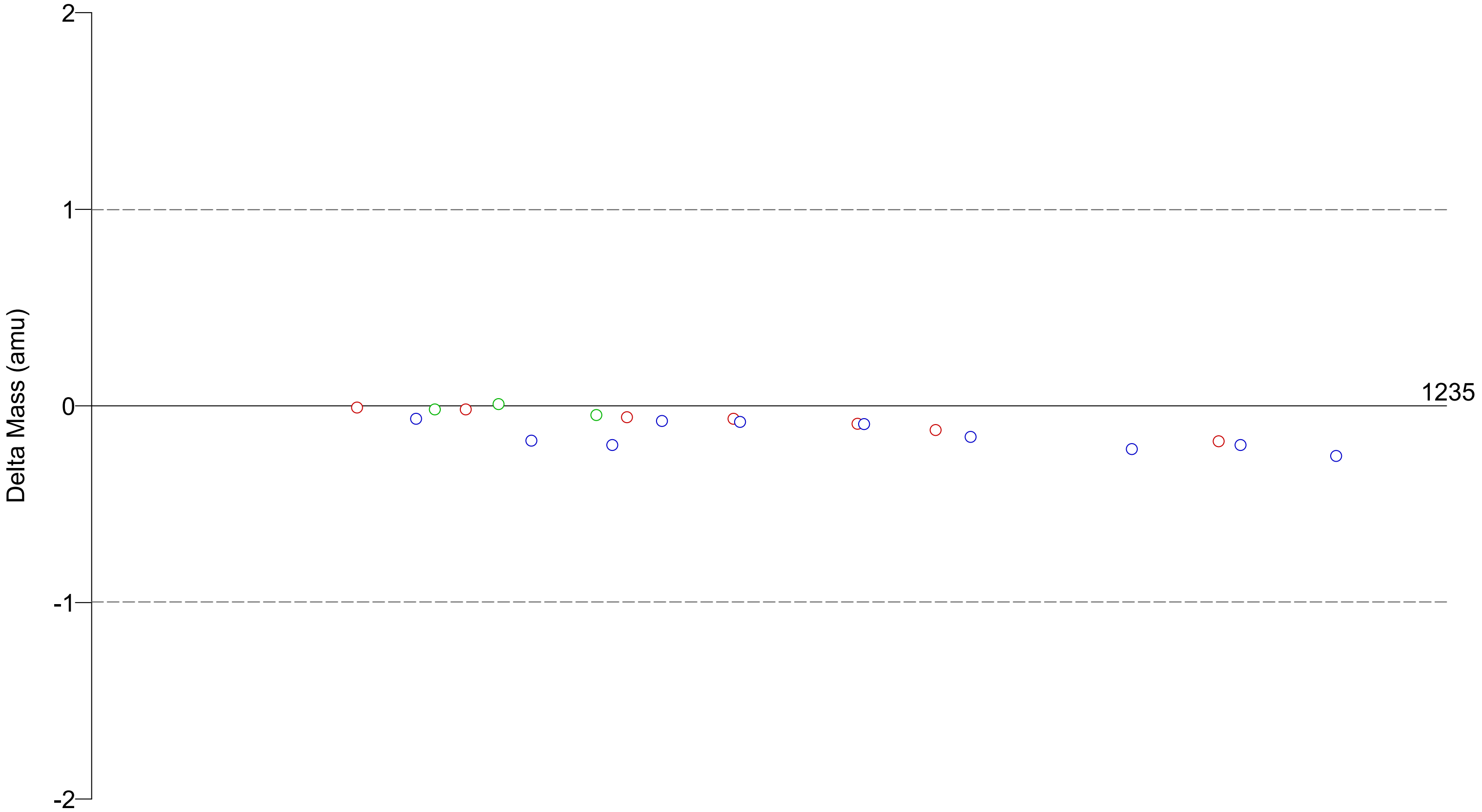


#19287468-1 NL: 4.16E6

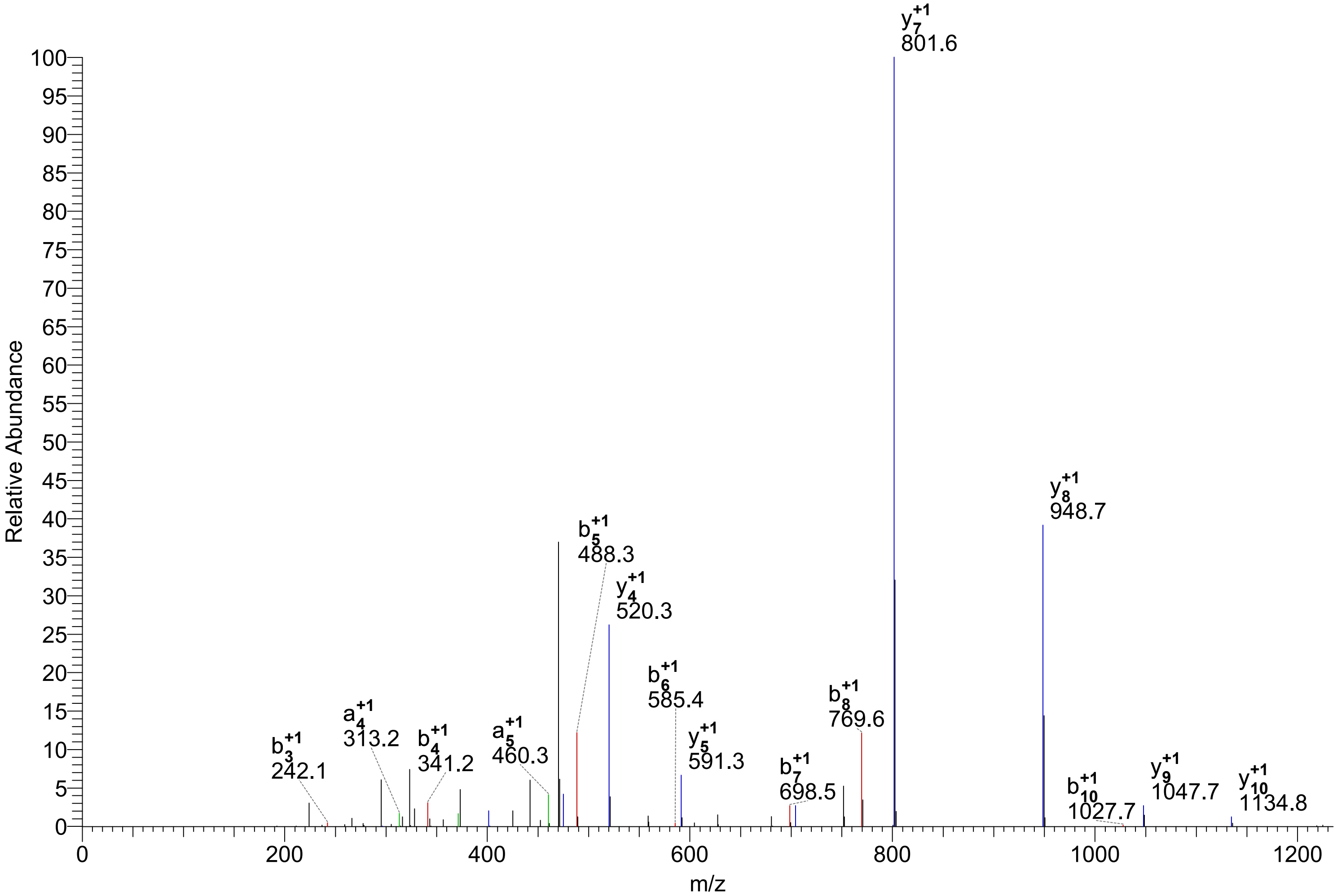


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00399007.7|SWISS-PROT:P0185                                0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

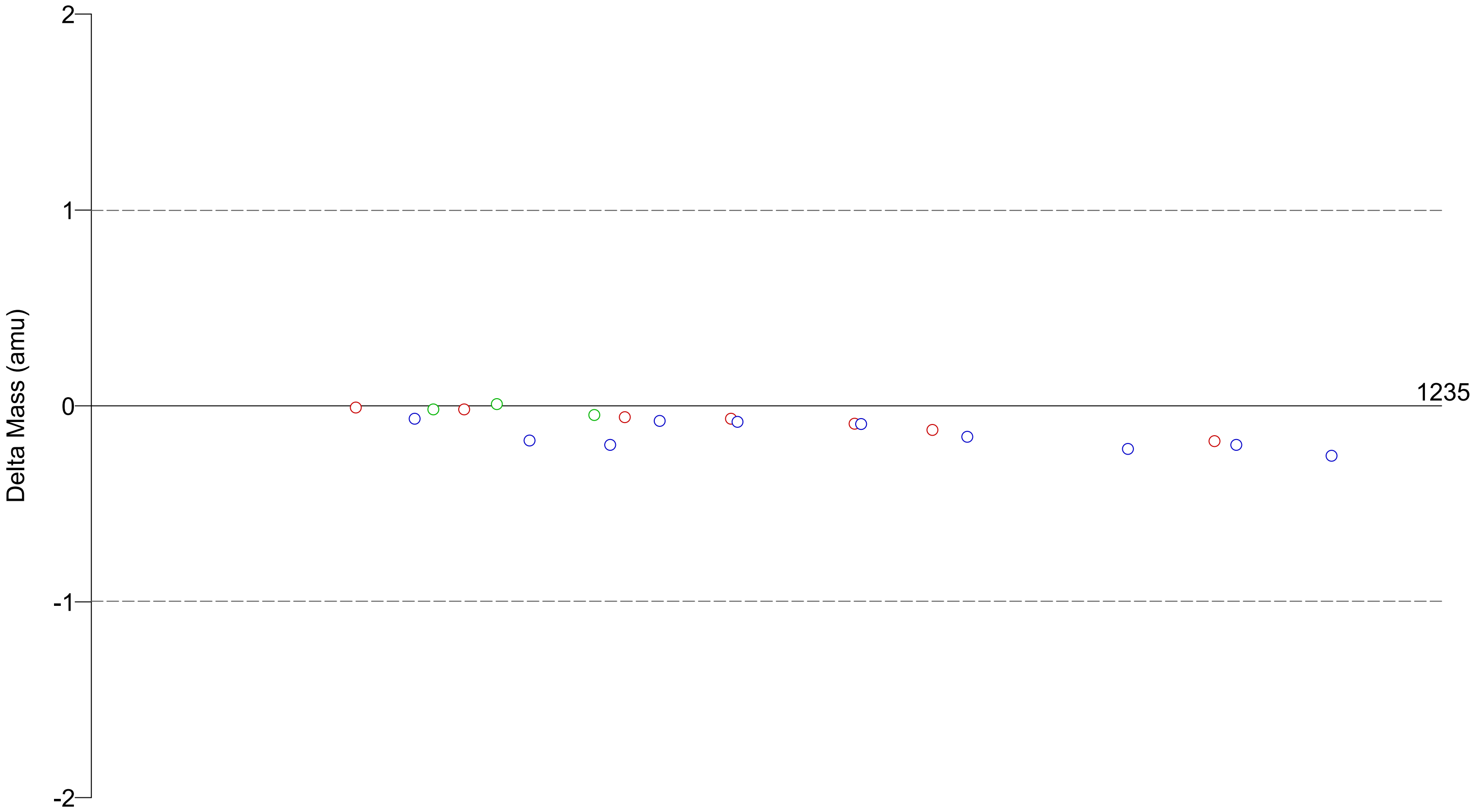


#19287468-1 NL: 4.16E6

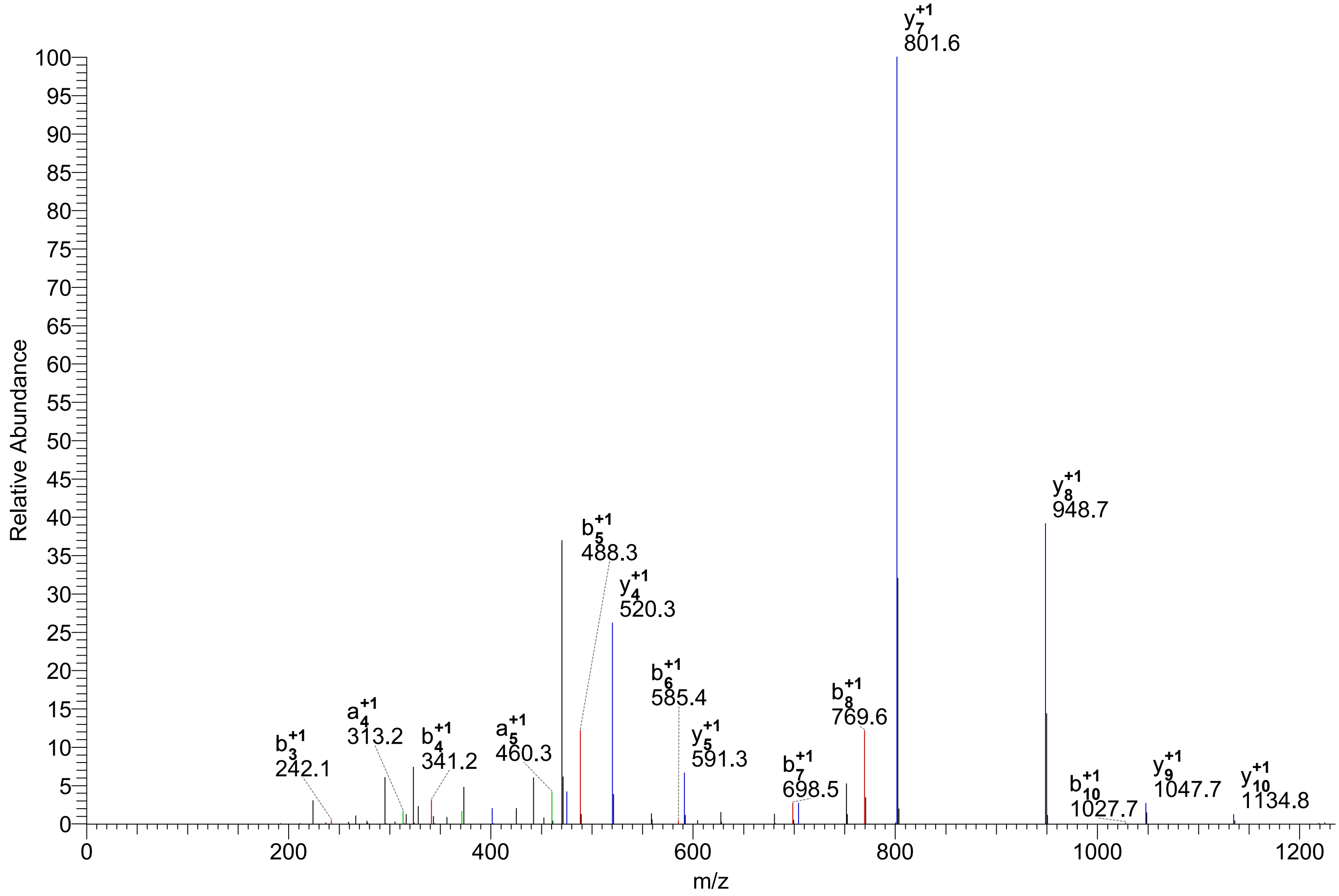


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                926      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00418153.1|TREMBL:Q6N030 Ta                                0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

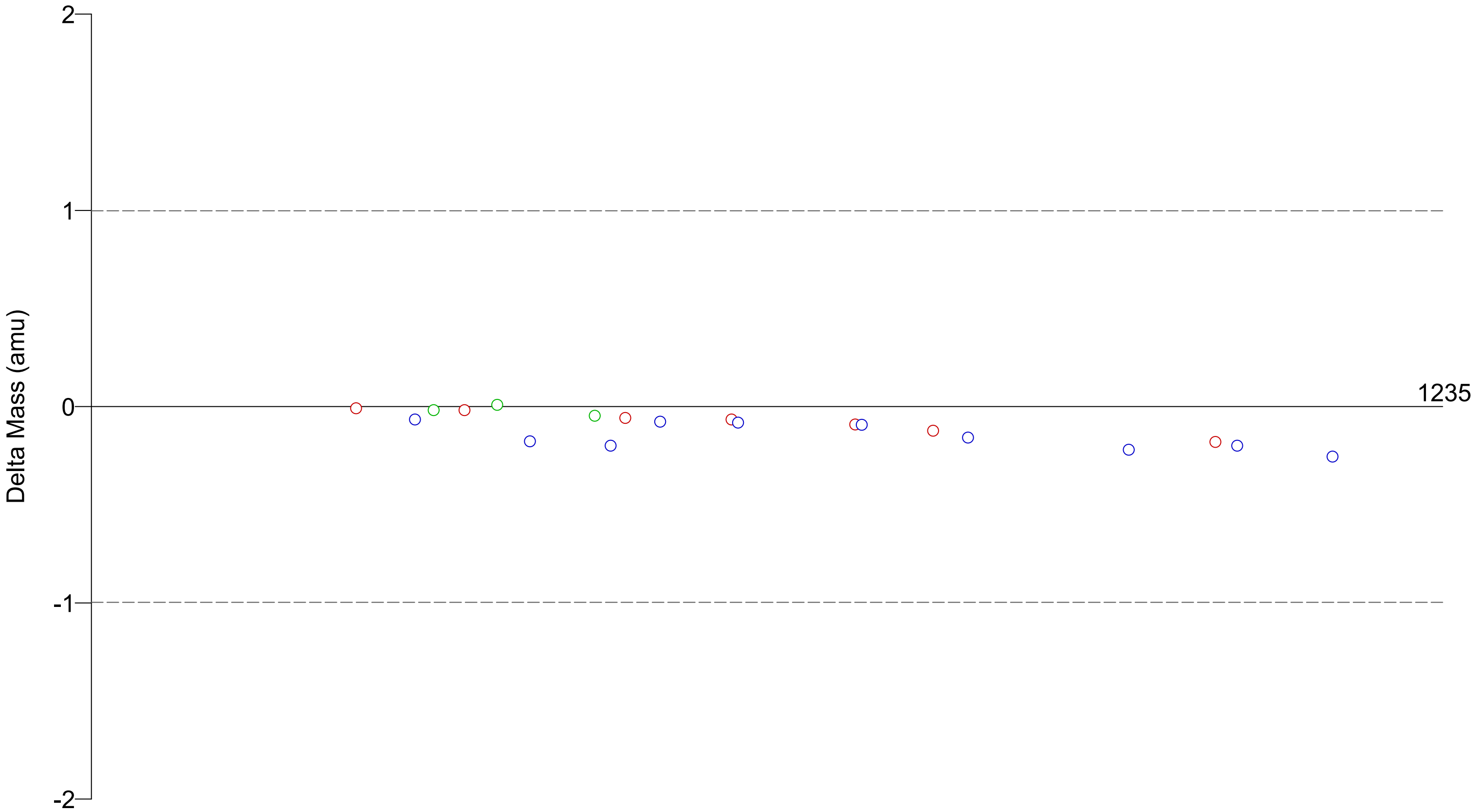


#19287468-1 NL: 4.16E6

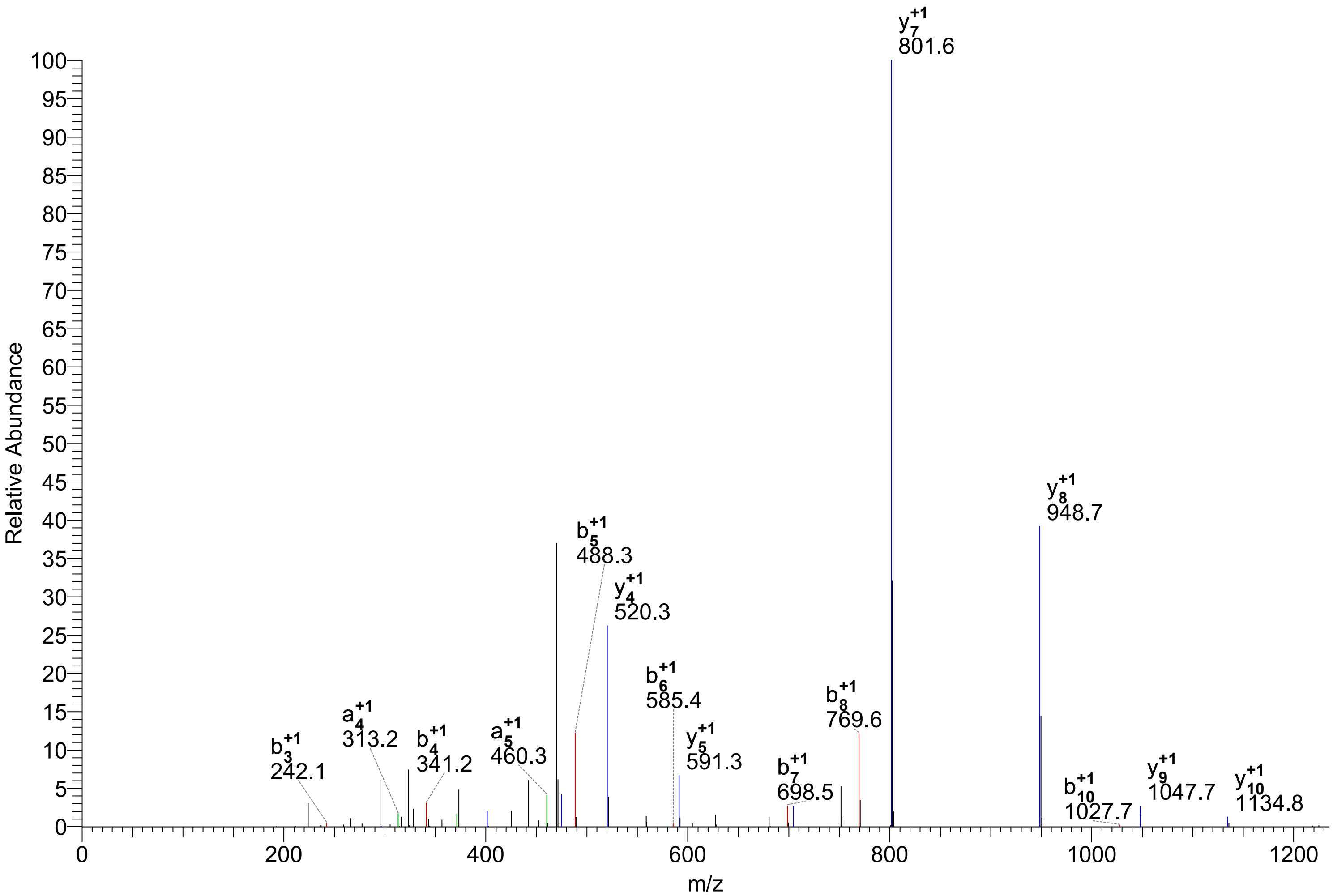


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00827754.3|SWISS-PROT:P0186                              0.0004  10.2      0.0        0
19287468 - 1  K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600    416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

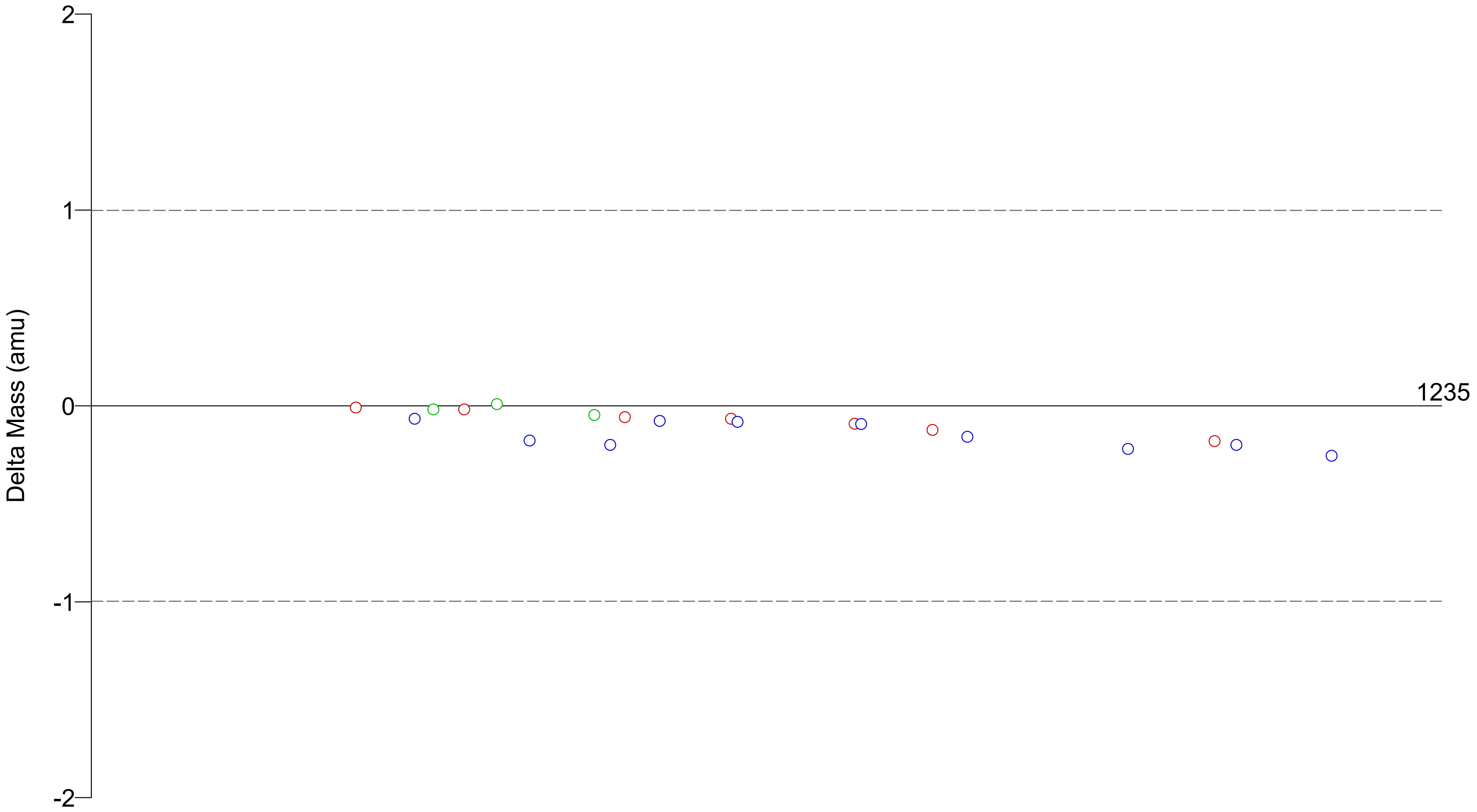


#19287468-1 NL: 4.16E6

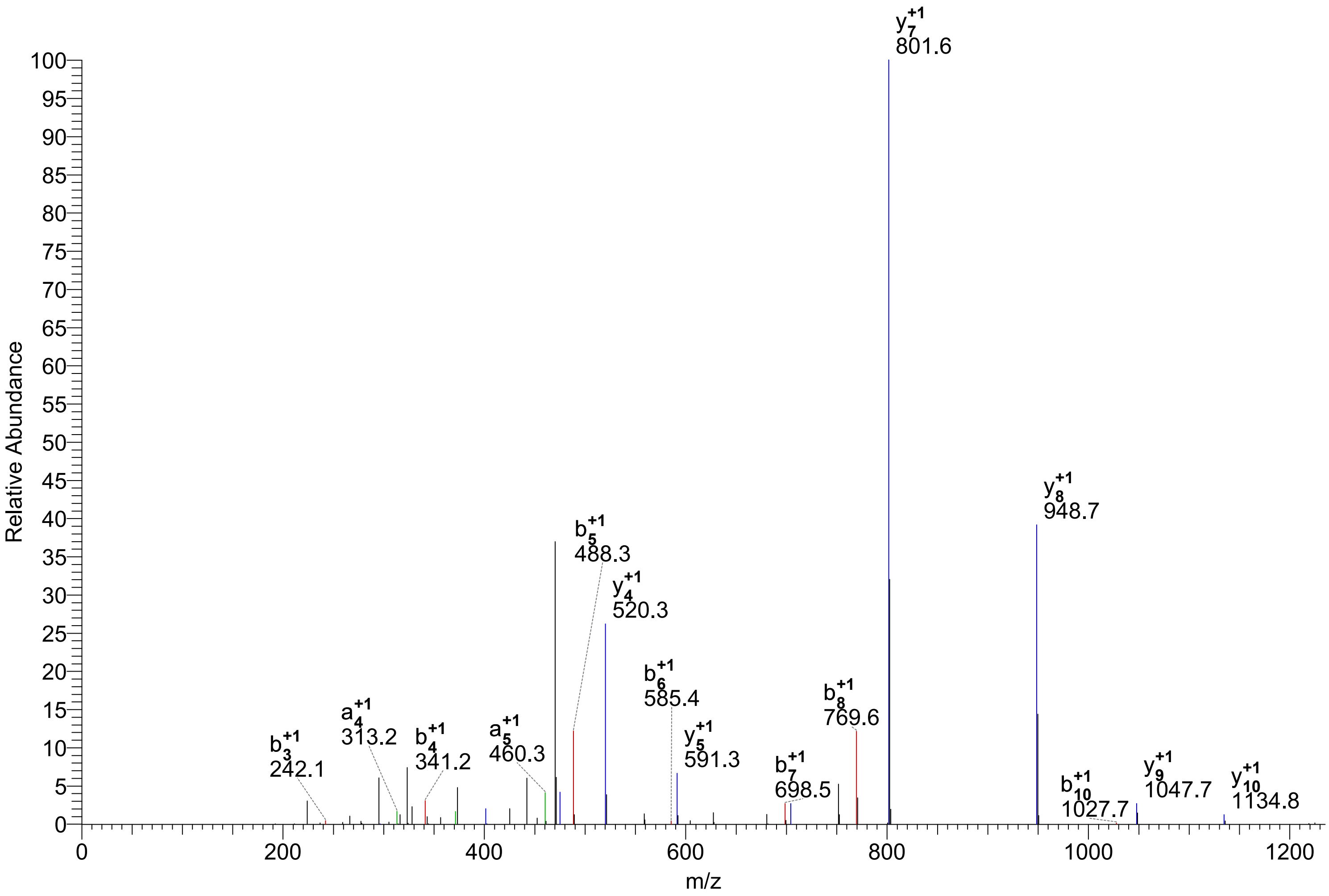


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829716.2|TREMBL:A6NJI8|EN                                0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 4.16E6



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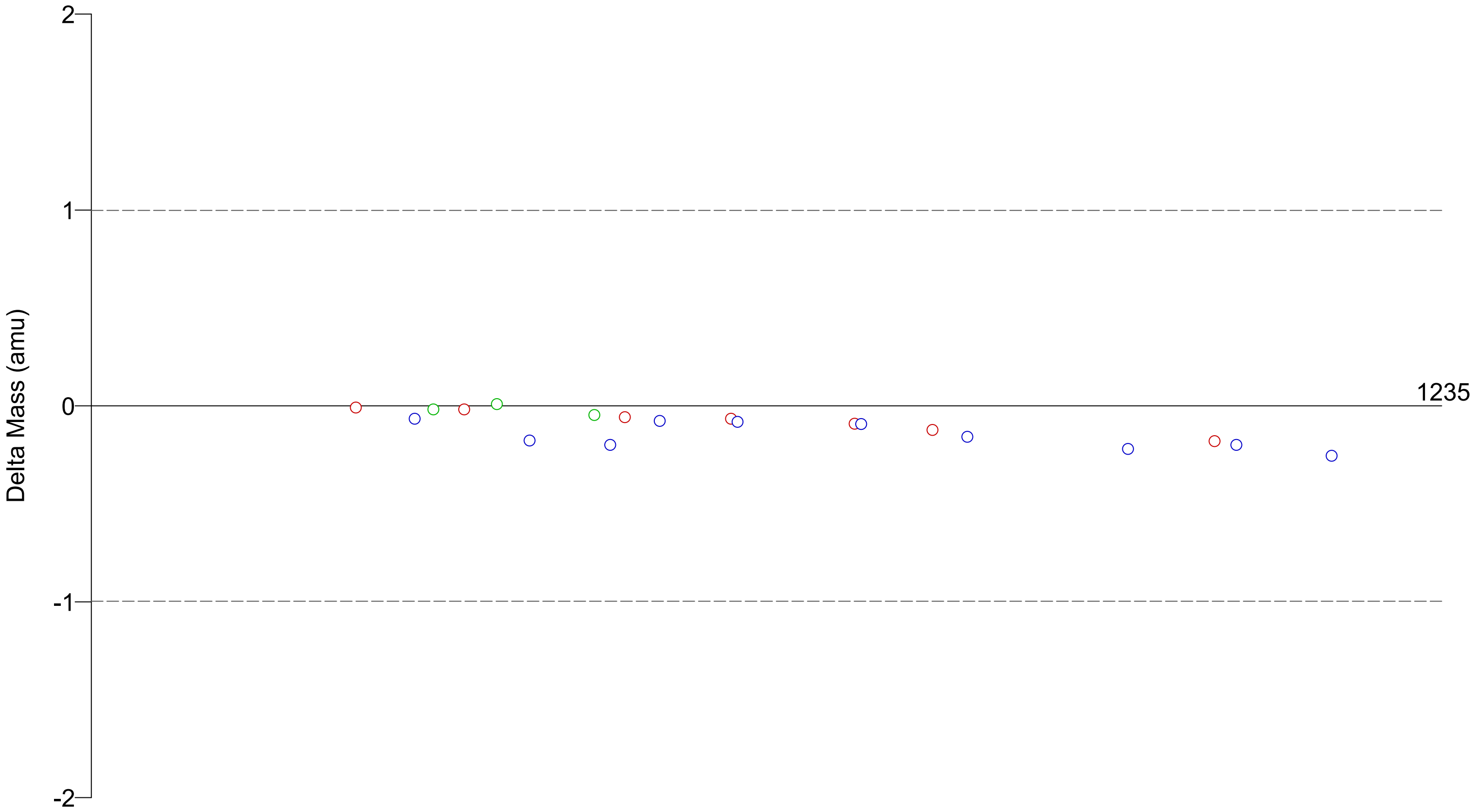
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                              MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829814.1|SWISS-PROT:P0186                                0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

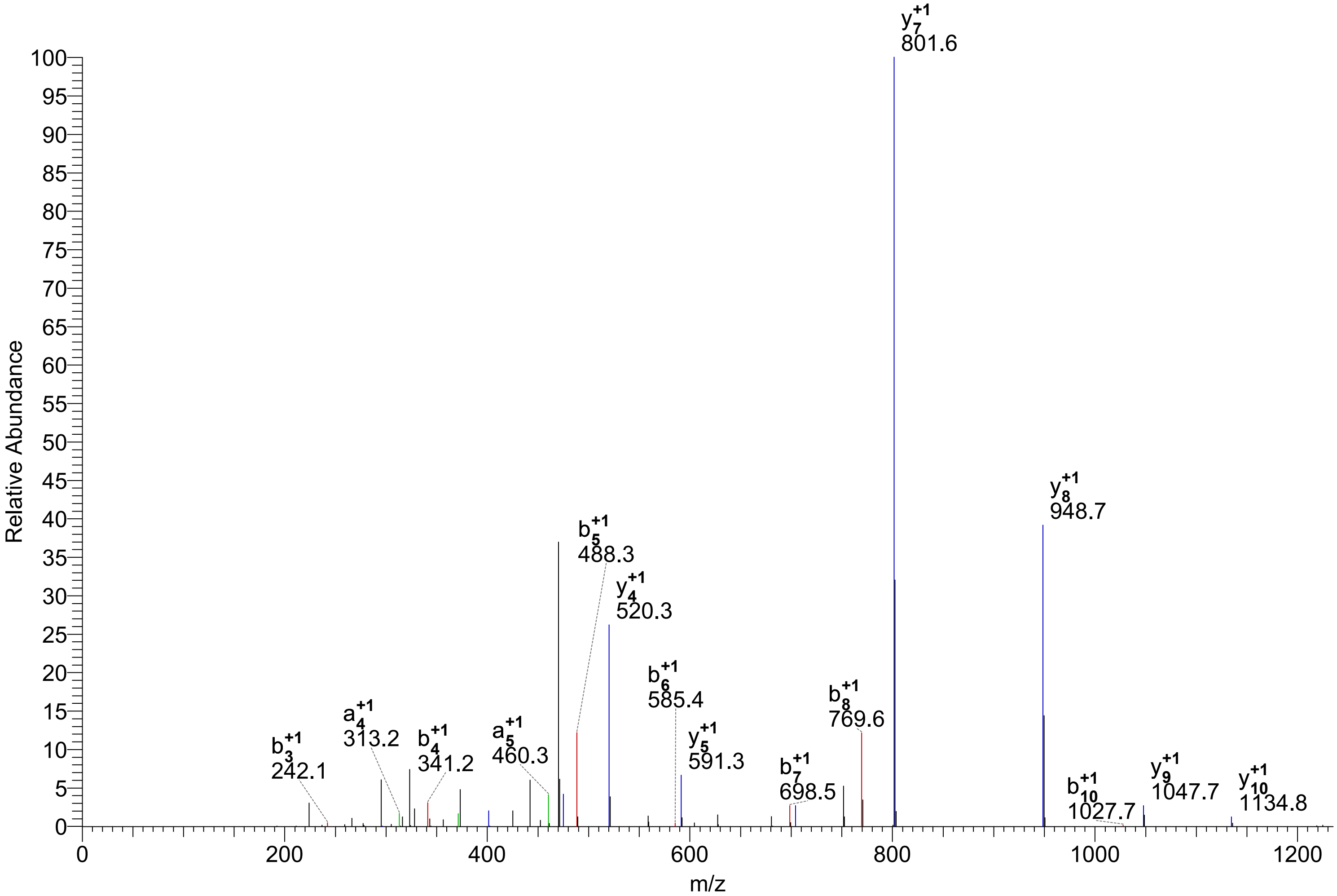
```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 4.16E6



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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829940.1|TREMBL:A6NGU3|EN                                0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```
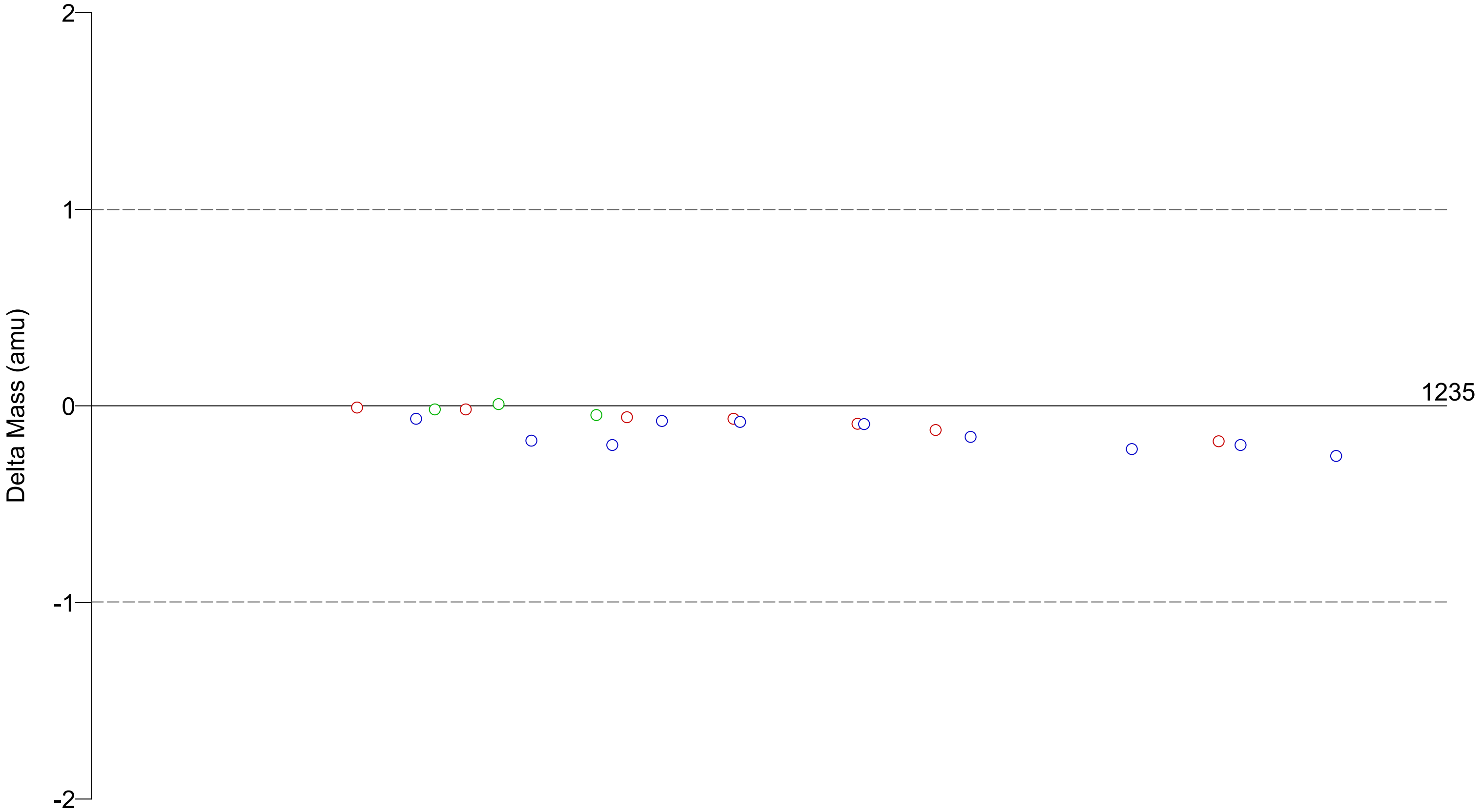
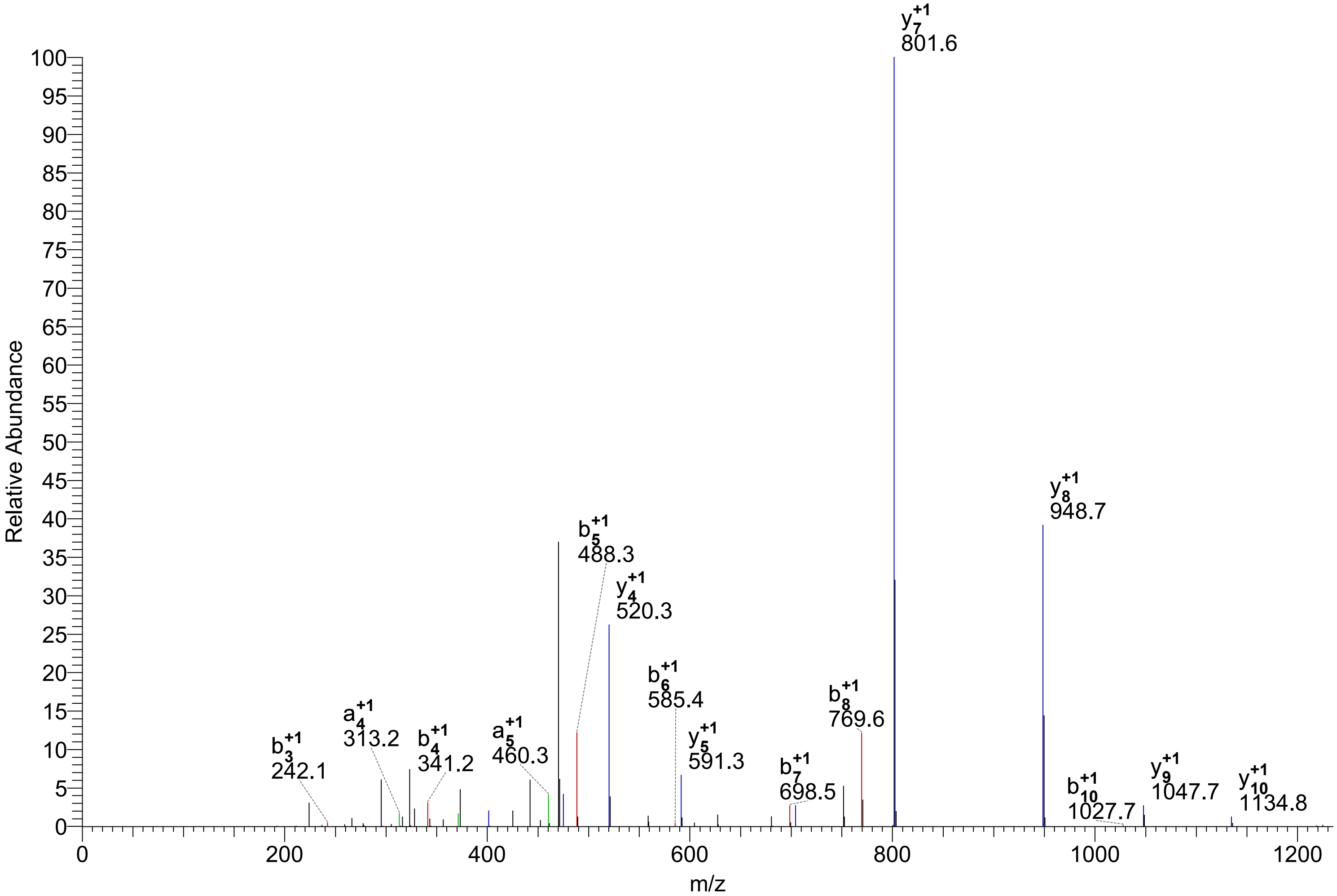

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

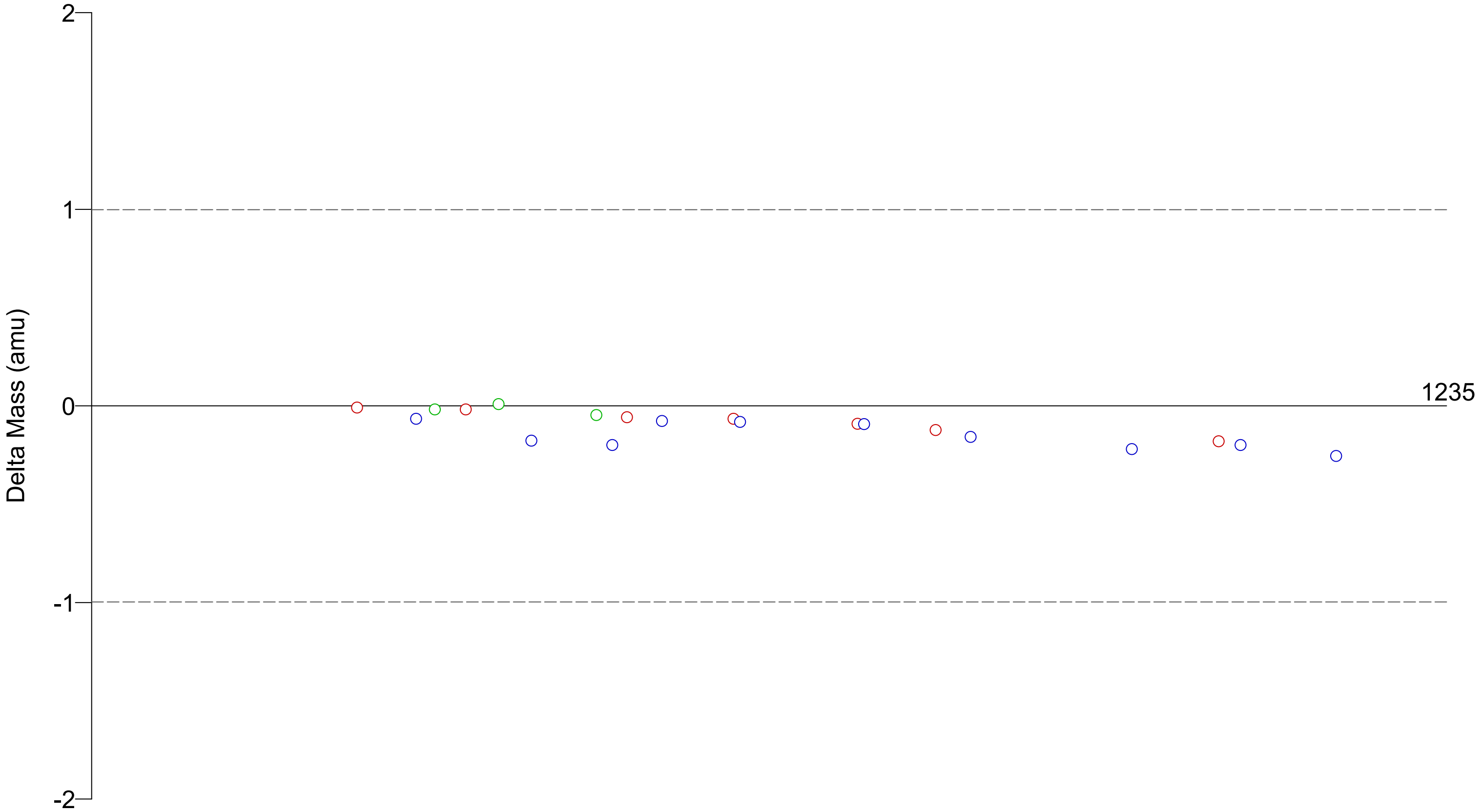


#19287468-1 NL: 4.16E6

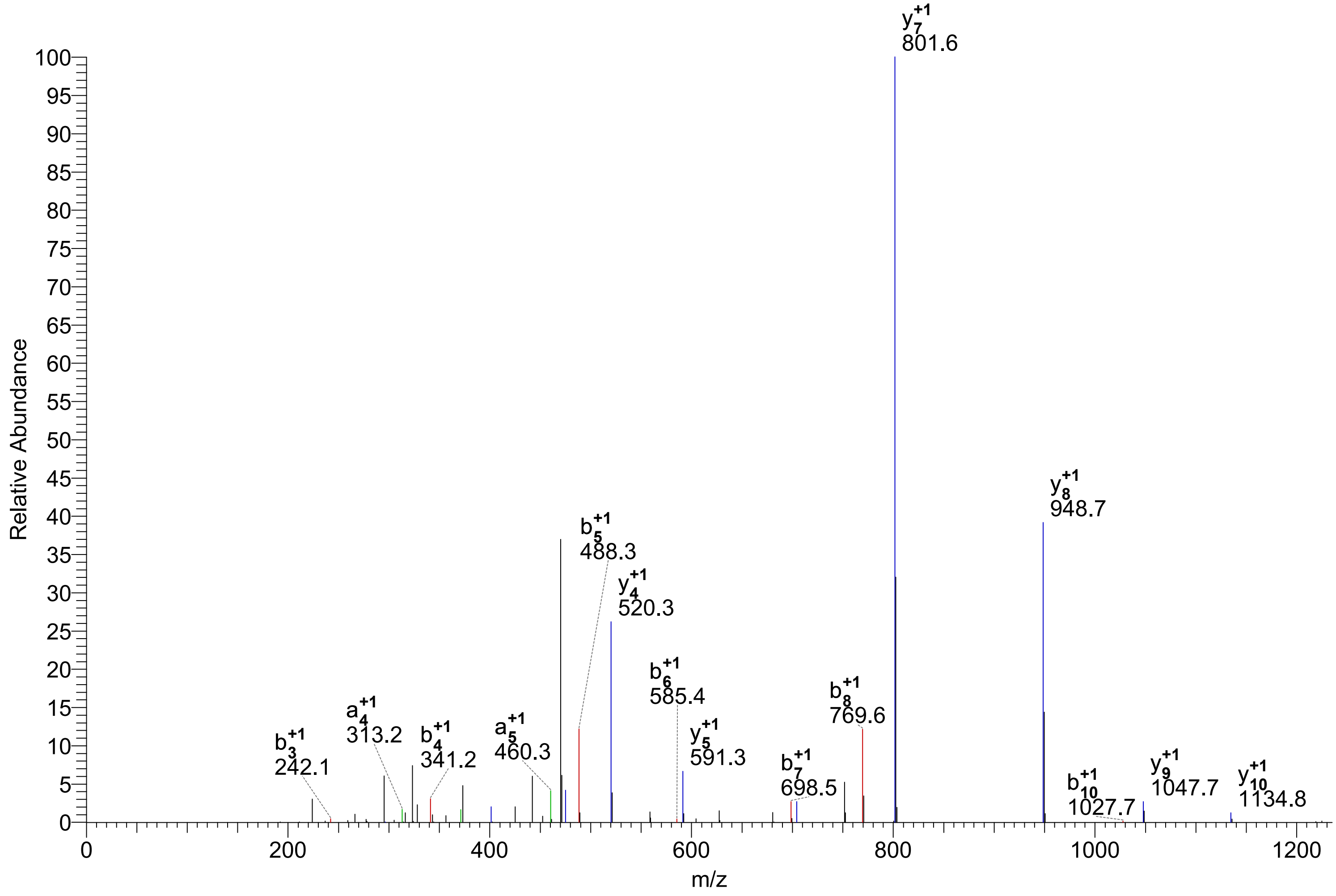


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00830132.1|TREMBL:A6NNZ4|EN                                0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                       1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                    1231.61
 S    214.12     242.11                                    1134.56
 V    313.19     341.18                                    1047.53
 F    460.26     488.25                                     948.46
 P    557.31     585.30                                     801.39
 L    670.39     698.39                                     704.34
 A    741.43     769.42                                     591.26
 P    838.48     866.48                                     520.22
 C    999.50    1027.49                                     423.17
 S   1086.53    1114.52                                     262.15
 R                                                          175.12
```



#19287468-1 NL: 4.16E6



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Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count

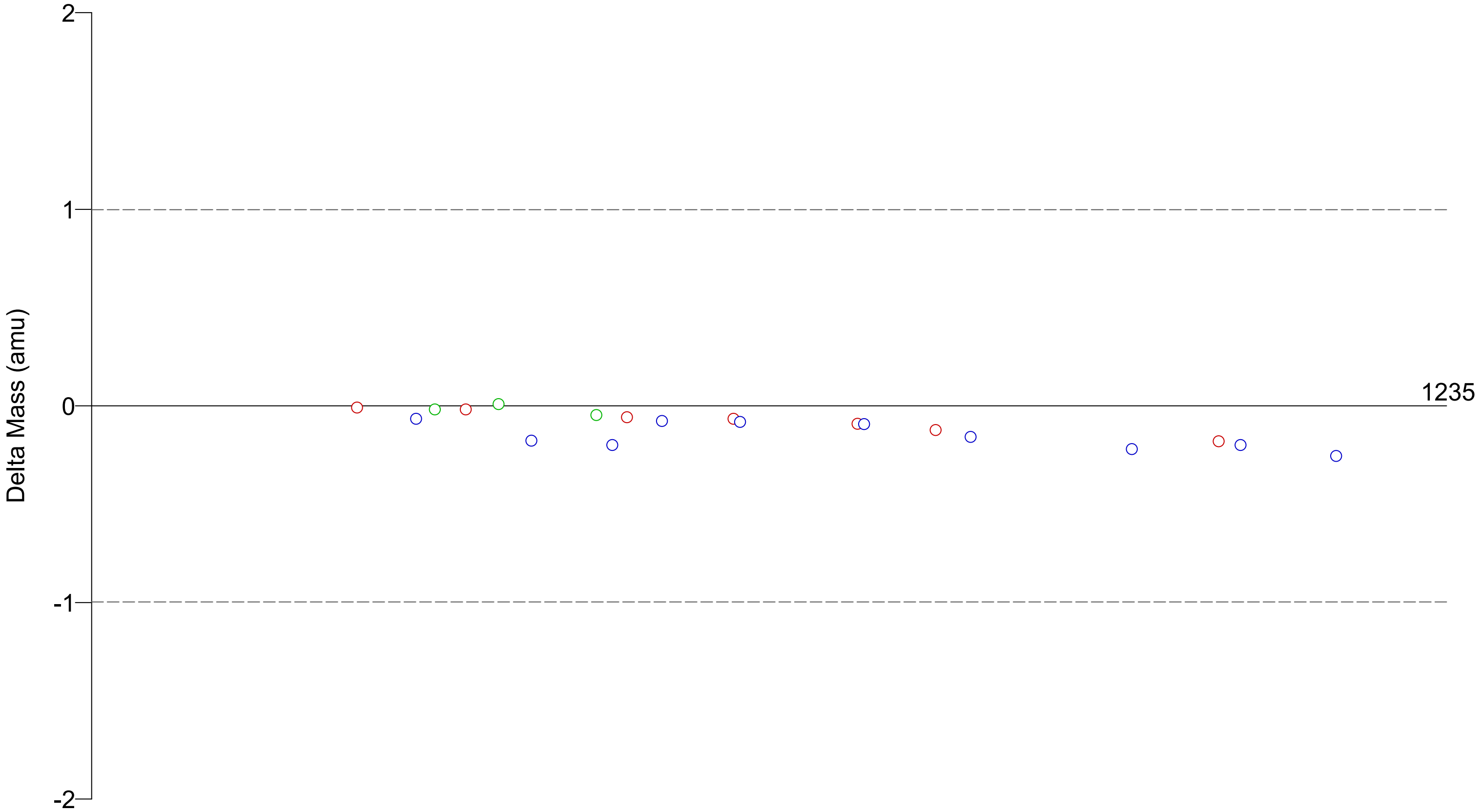
IPI:IPI00930072.1|TREMBL:Q68CN4 Ta                                  0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                      1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

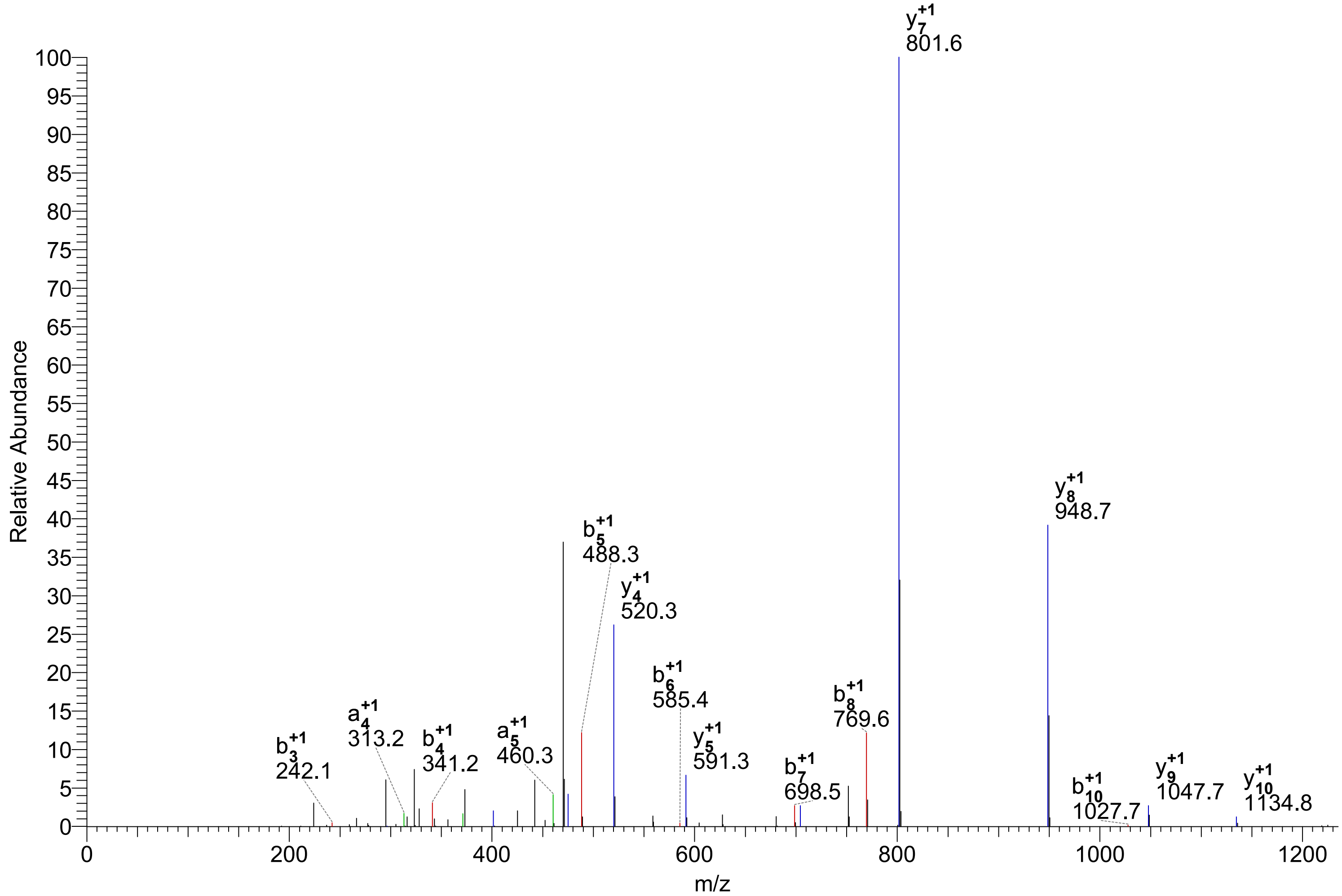
```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 4.16E6



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Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00930442.1|TREMBL:Q6MZX7 Ta                                   0.0004  10.2     0.0       0
19287468 - 1  K.GPSVFPLAPCSR.S                         1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```
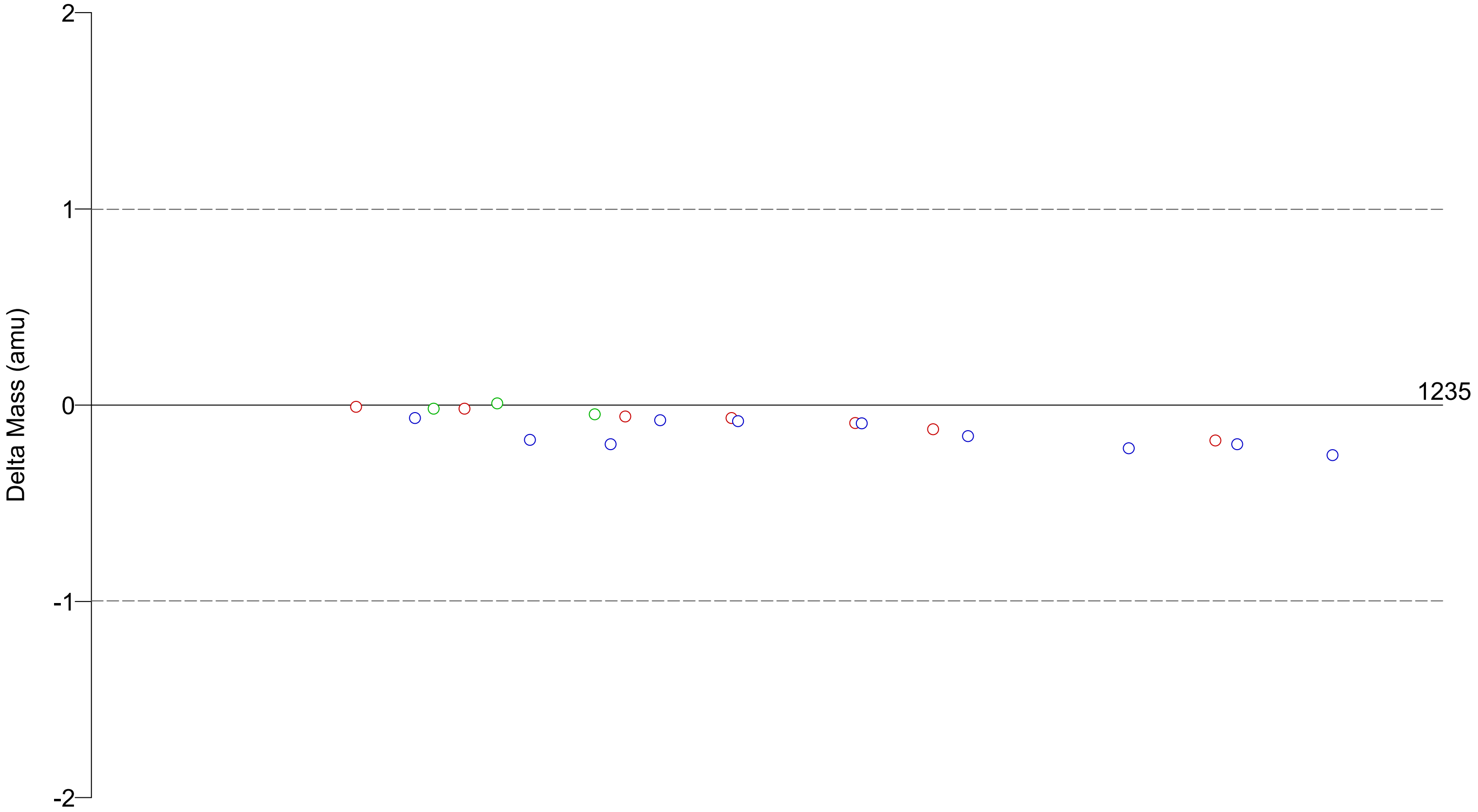
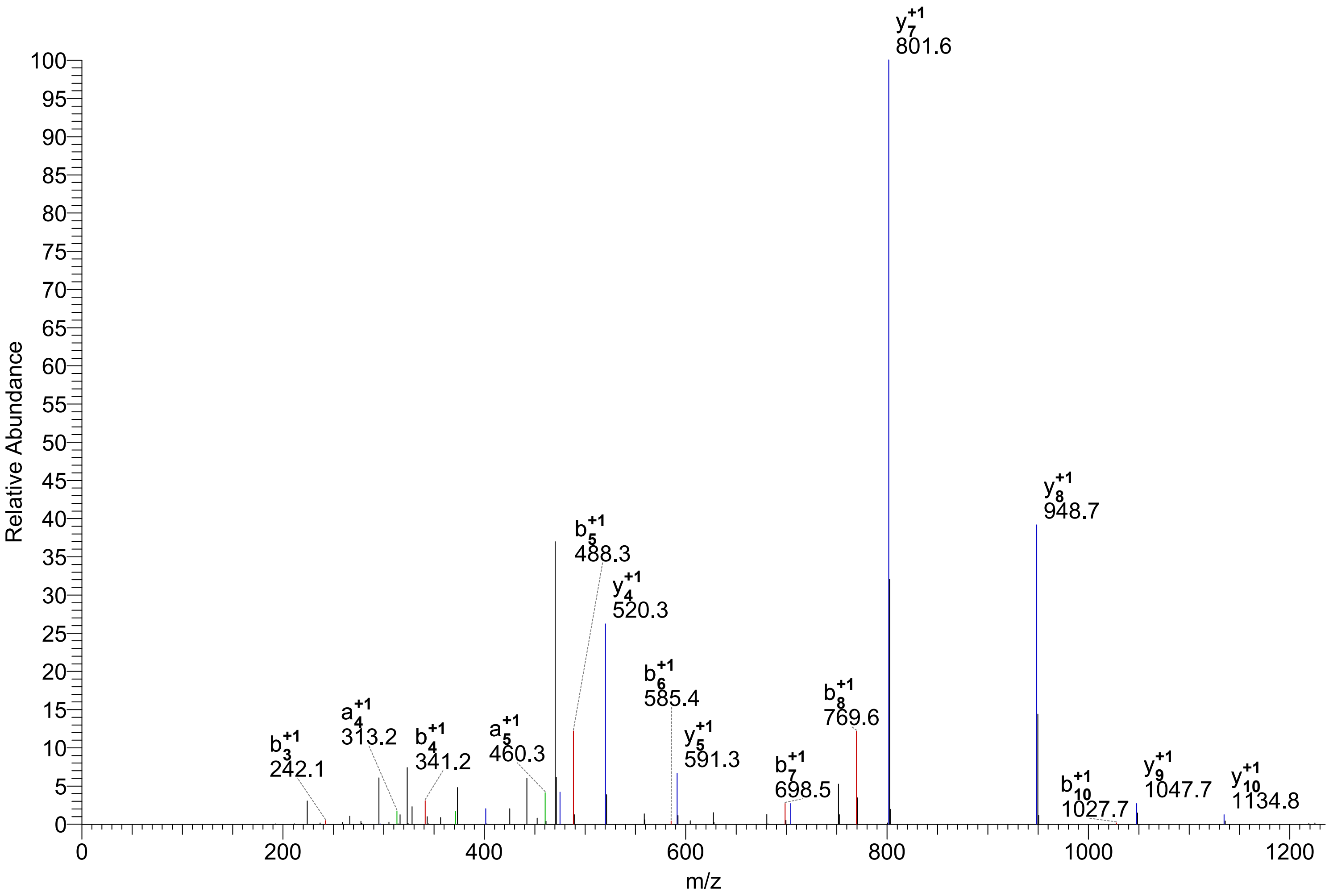

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

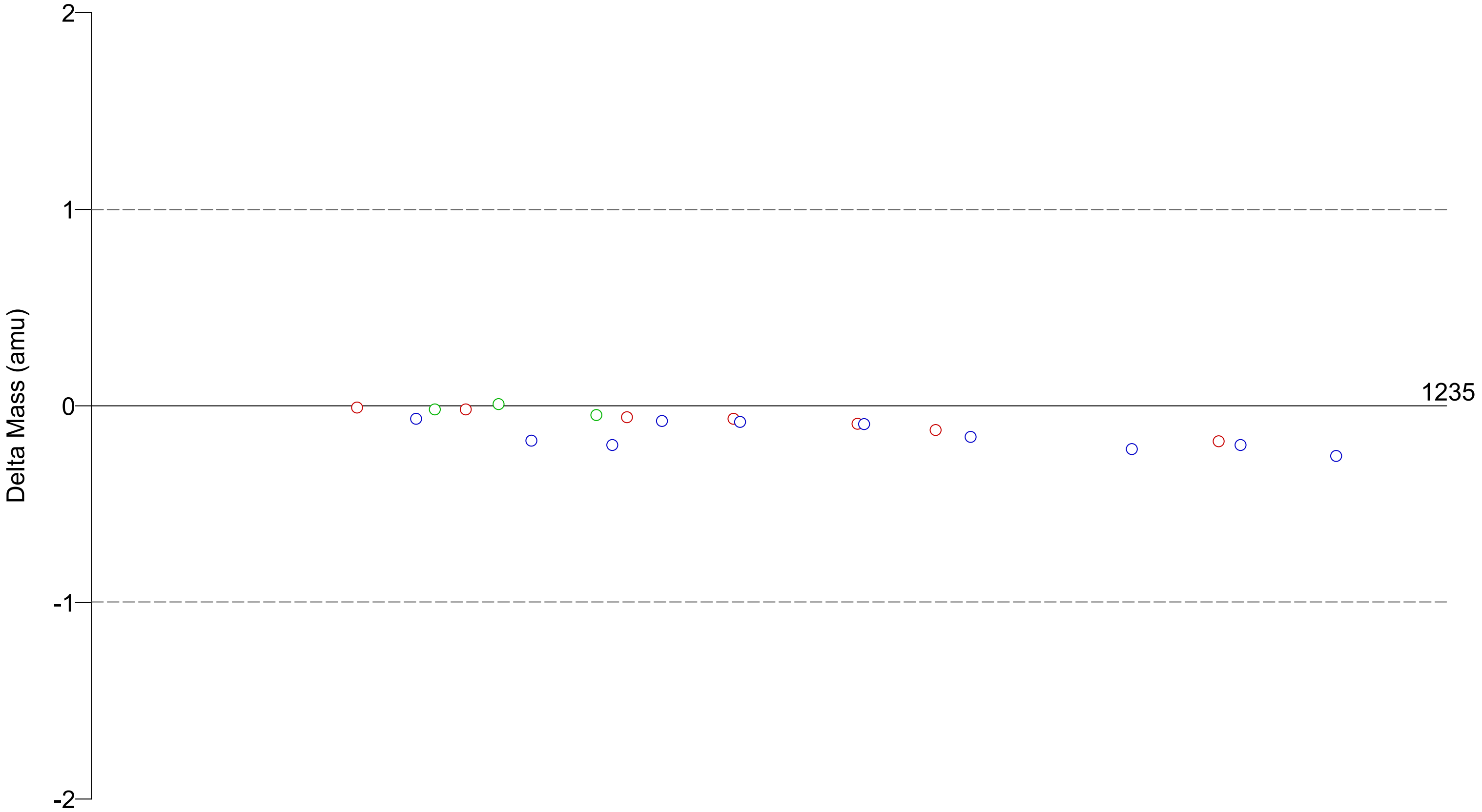


#19287468-1 NL: 4.16E6

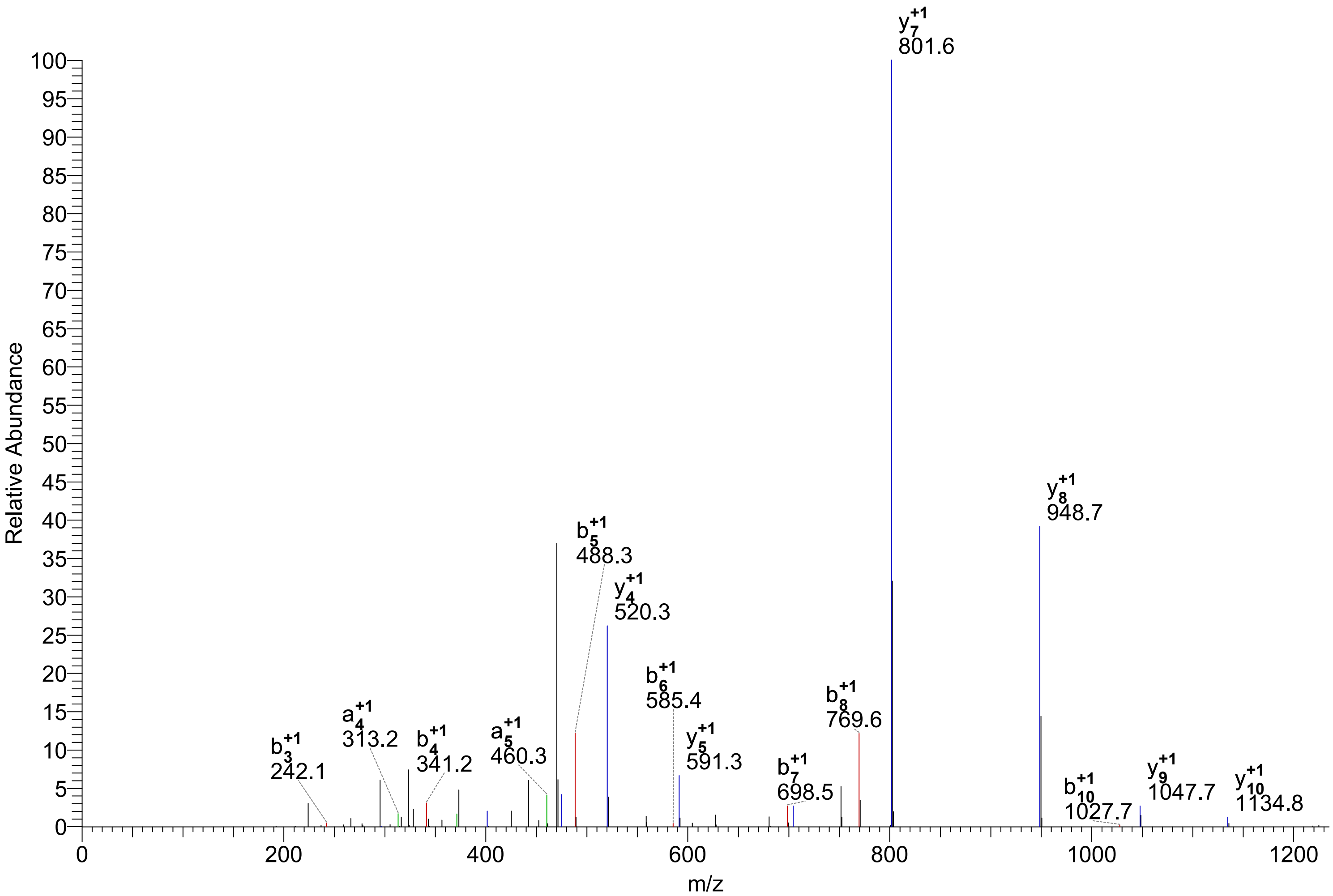


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00930684.1|TREMBL:Q5EBM2 Ta                                0.0004  10.2     0.0        0
19287468 - 1  K.GPSVFPLAPCSR.S                    1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

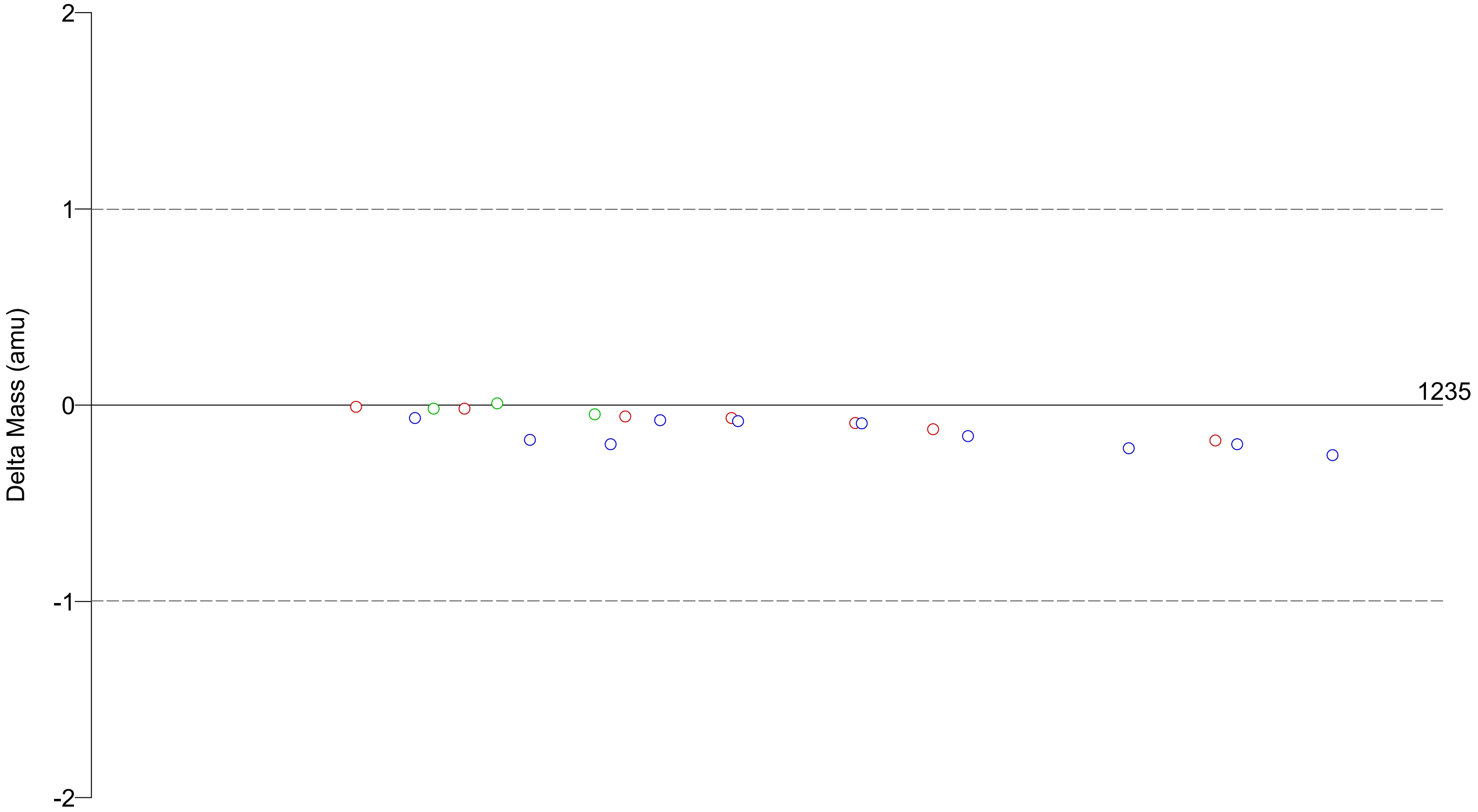


#19287468-1 NL: 4.16E6

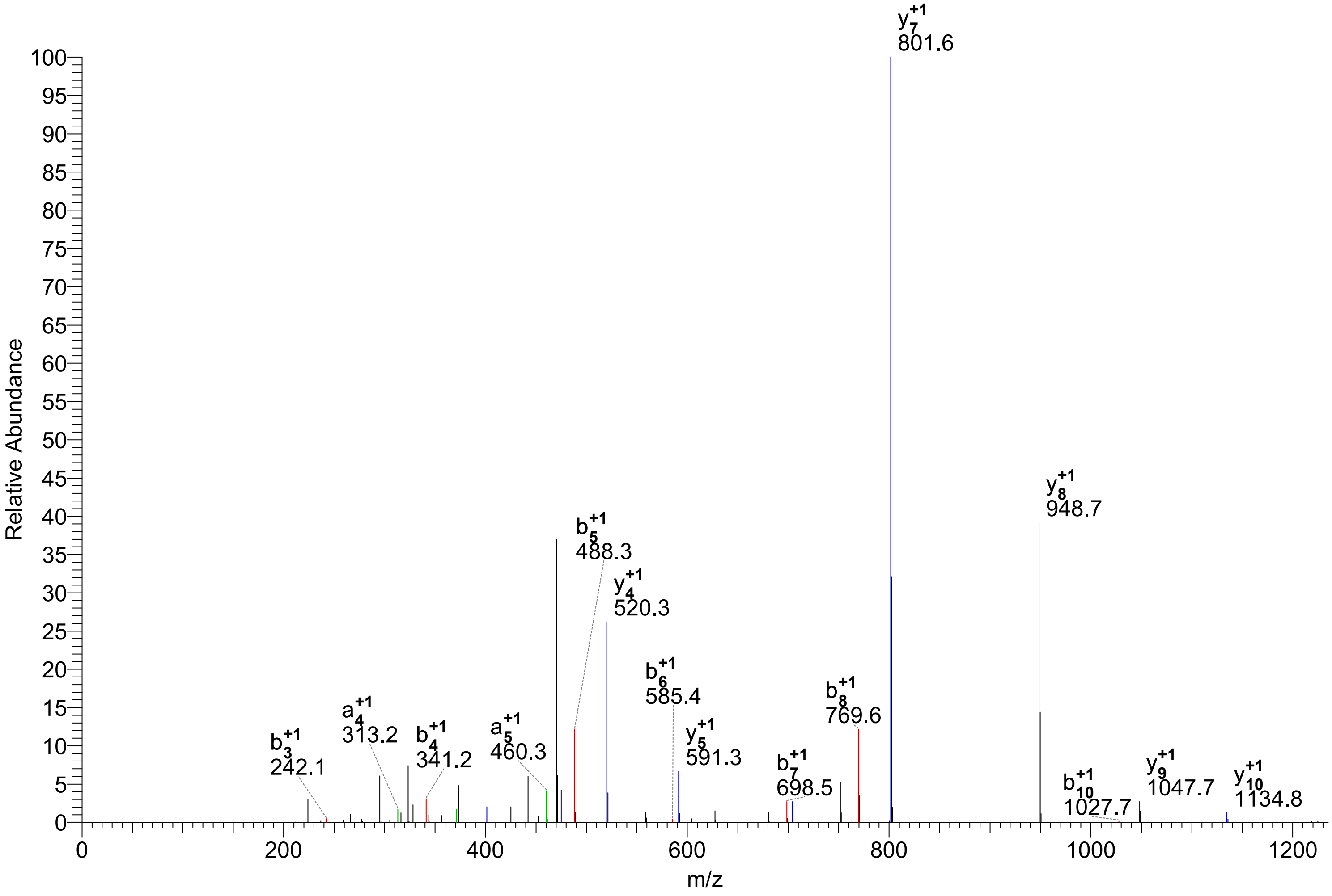


```
Reference                                                       P      Score   Coverage   Accession
Scan(s)       Sequence                              MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00936490.1|REFSEQ:XP_002348                             0.0004  10.2     0.0        0
19287468 - 1  K.GPSVFPLAPCSR̅.S                    1288.64   2  0.0004  3.377  0.600   416.0  1   16/33   13

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1231.61
 S    214.12     242.11                                     1134.56
 V    313.19     341.18                                     1047.53
 F    460.26     488.25                                      948.46
 P    557.31     585.30                                      801.39
 L    670.39     698.39                                      704.34
 A    741.43     769.42                                      591.26
 P    838.48     866.48                                      520.22
 C    999.50    1027.49                                      423.17
 S   1086.53    1114.52                                      262.15
 R                                                           175.12
```

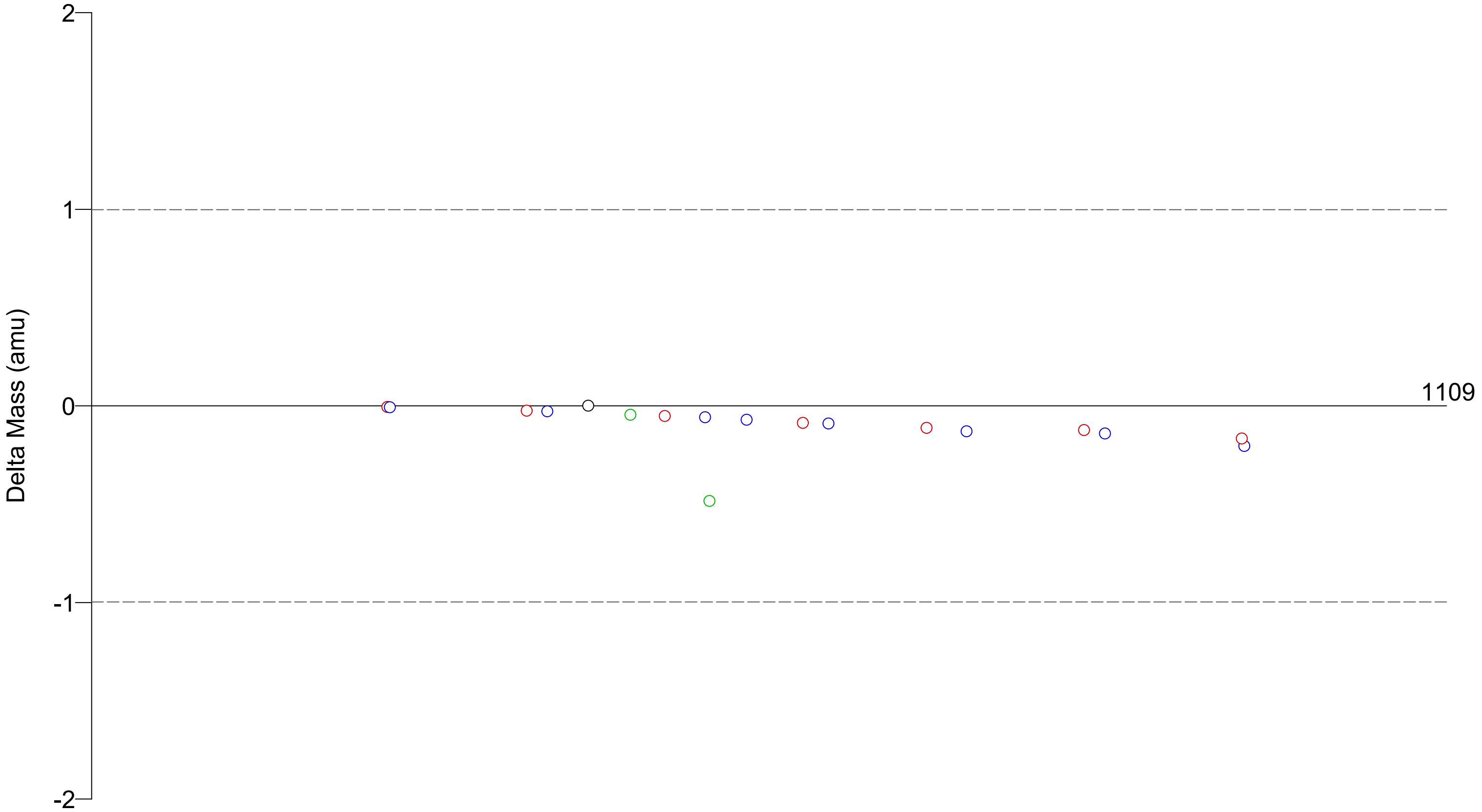


#19287468-1 NL: 4.16E6

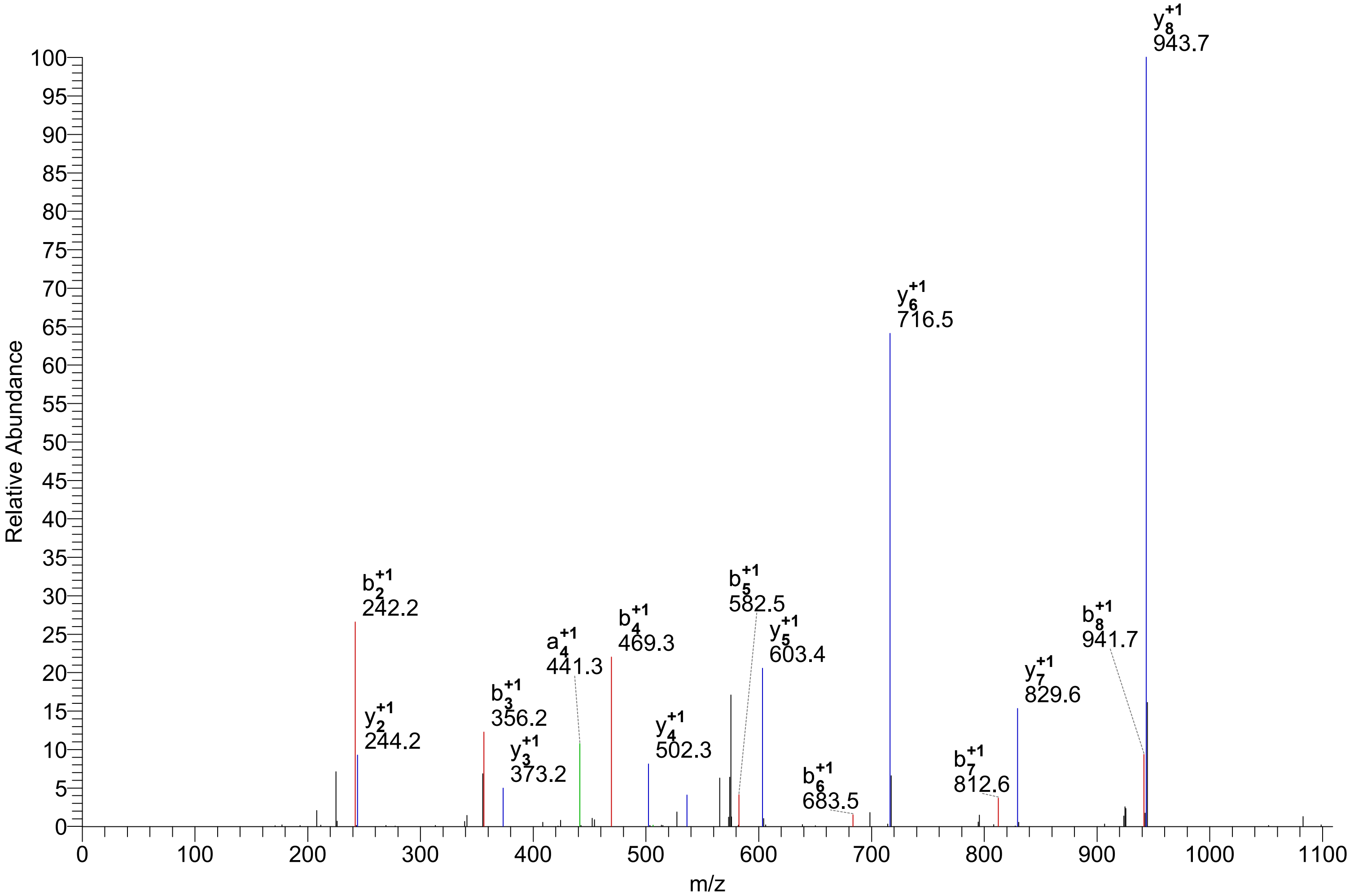


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp   RSp   Ions  Count
IPI:IPI00218732.3|SWISS-PROT:P27169|TREMBL:B4DX19;Q96P89;Q96P9    0.0005  24.2     0.0       0
19287468 - 1  R.IQNILTEEPK.V                          1184.65   2  0.001   3.049  0.518   731.0  1    15/27
19287468 - 1  K.LLIGTVFHK.A                           1027.63   2  0.0005  2.467  0.391   636.3  1    16/24
19287468 - 1  K.LLIGTVFHKALYCEL.-                     1777.96   3  0.02    1.300  0.501    63.0  3    14/84

3 of 3 peptide matches reported, 0 removed due to filtering
```

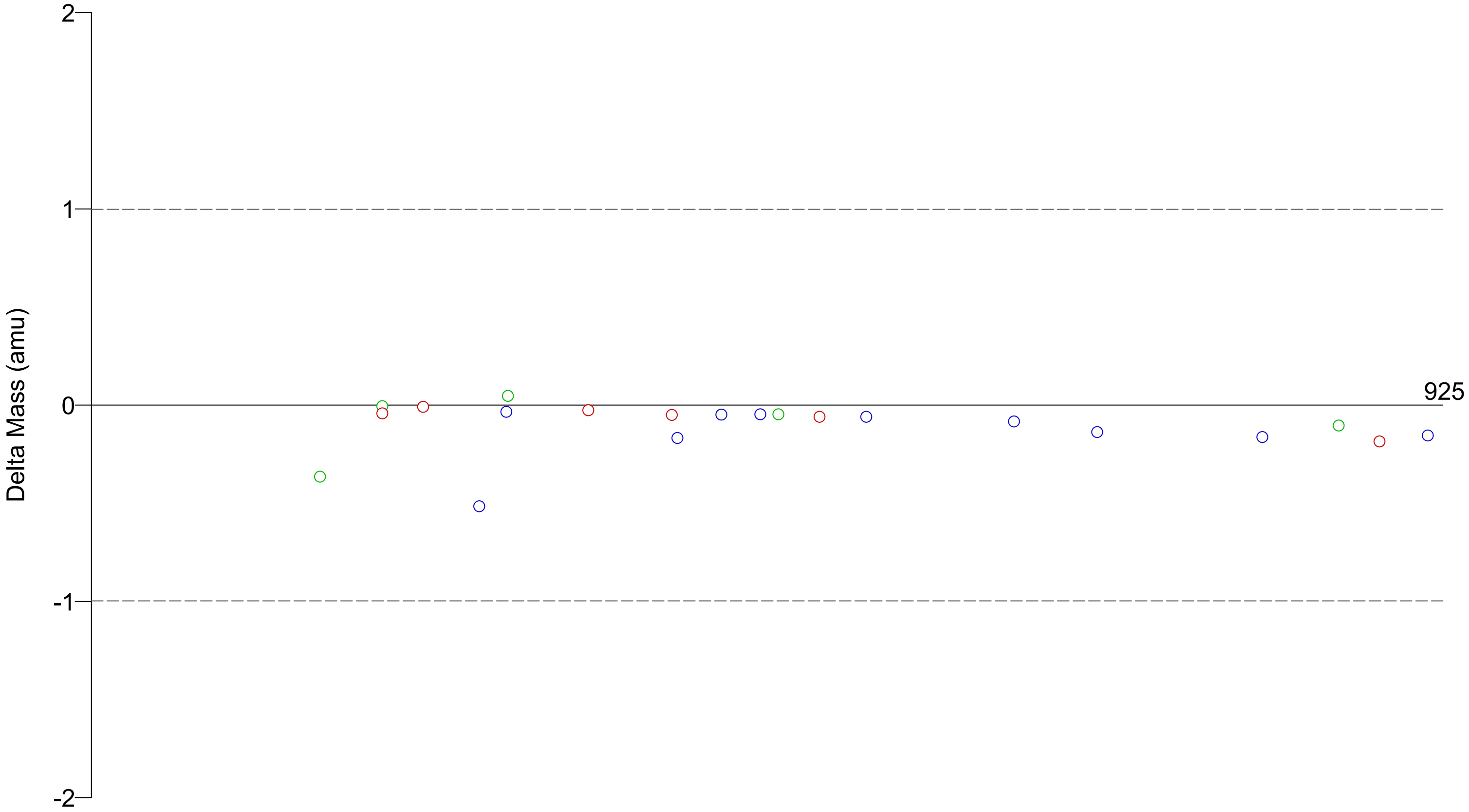
```
DTA for scans: 19287468-1
Precursor ion: 592.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 Q    214.16     242.15                                     1071.57
 N    328.20     356.19                                      943.51
 I    441.28     469.28                                      829.47
 L    554.37     582.36                                      716.38
 T    655.41     683.41                                      603.30
 E    784.46     812.45                                      502.25
 E    913.50     941.49                                      373.21
 P   1010.55    1038.55                                      244.17
 K                                                           147.11
```



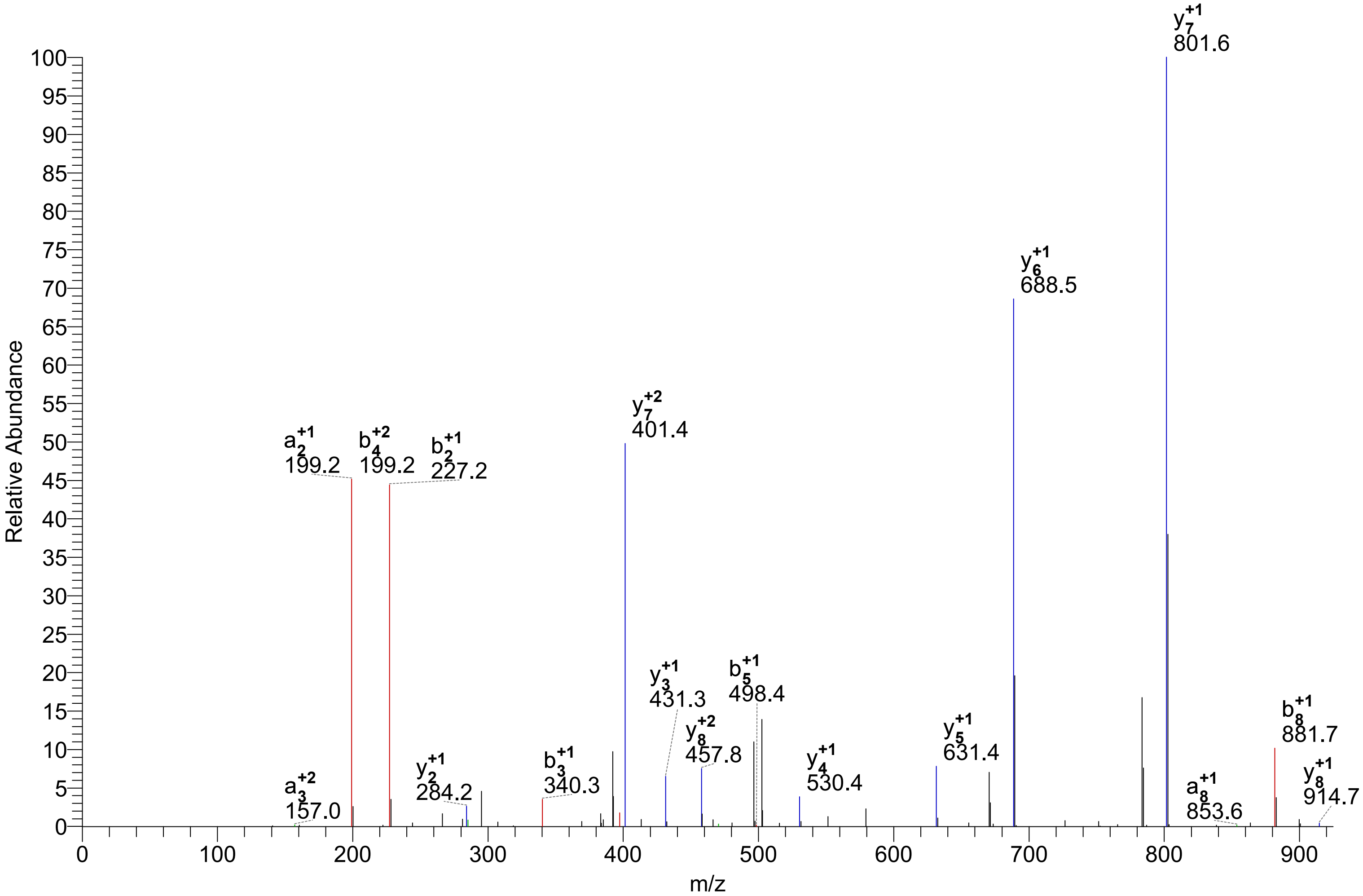
#19287468-1 NL: 1.66E5



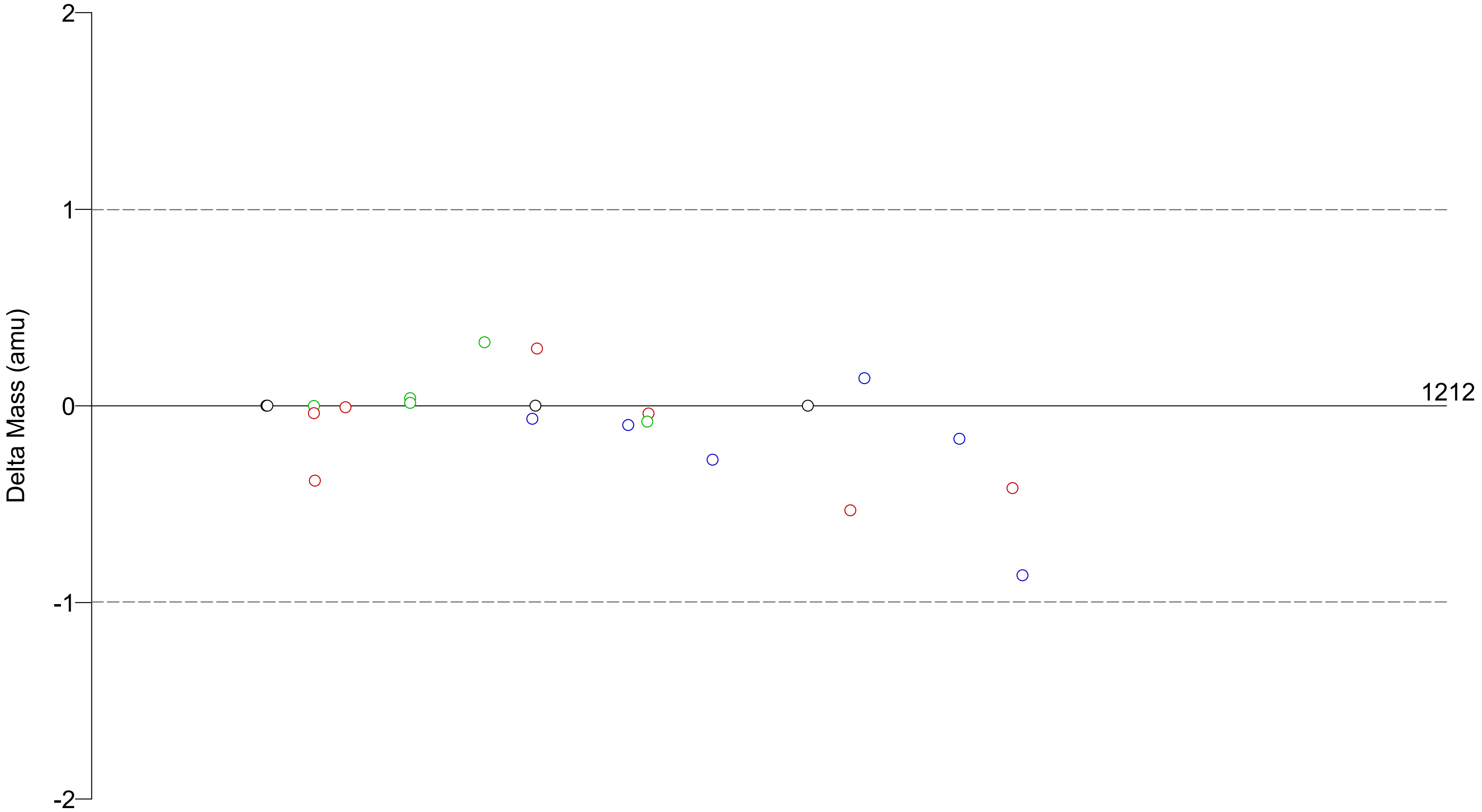
```
DTA for scans: 19287468-1
Precursor ion: 514.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                      914.55
 I    312.26     340.26                                      801.46
 G    369.29     397.28                                      688.38
 T    470.33     498.33                                      631.36
 V    569.40     597.40                                      530.31
 F    716.47     744.47                                      431.24
 H    853.53     881.52                                      284.17
 K                                                           147.11
```



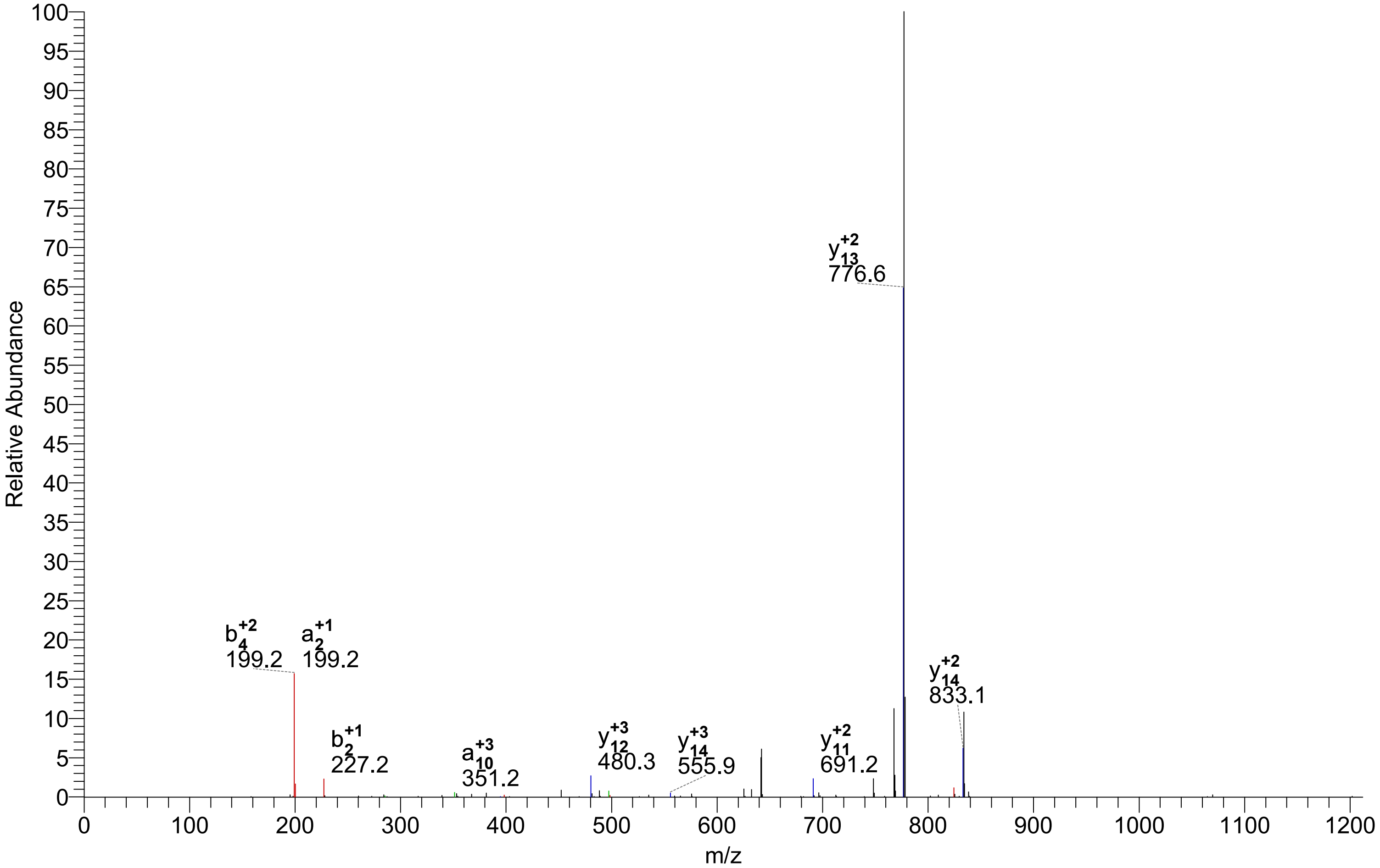
#19287468-1 NL: 2.17E5



```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1664.87
 I    312.26     340.26                                     1551.79
 G    369.29     397.28                                     1438.70
 T    470.33     498.33                                     1381.68
 V    569.40     597.40                                     1280.63
 F    716.47     744.47                                     1181.57
 H    853.53     881.52                                     1034.50
 K    981.62    1009.62                                      897.44
 A   1052.66    1080.66                                      769.34
 L   1165.75    1193.74                                      698.31
 Y   1328.81    1356.80                                      585.22
 C   1489.82    1517.82                                      422.16
 E   1618.87    1646.86                                      261.14
 L                                                           132.10
```

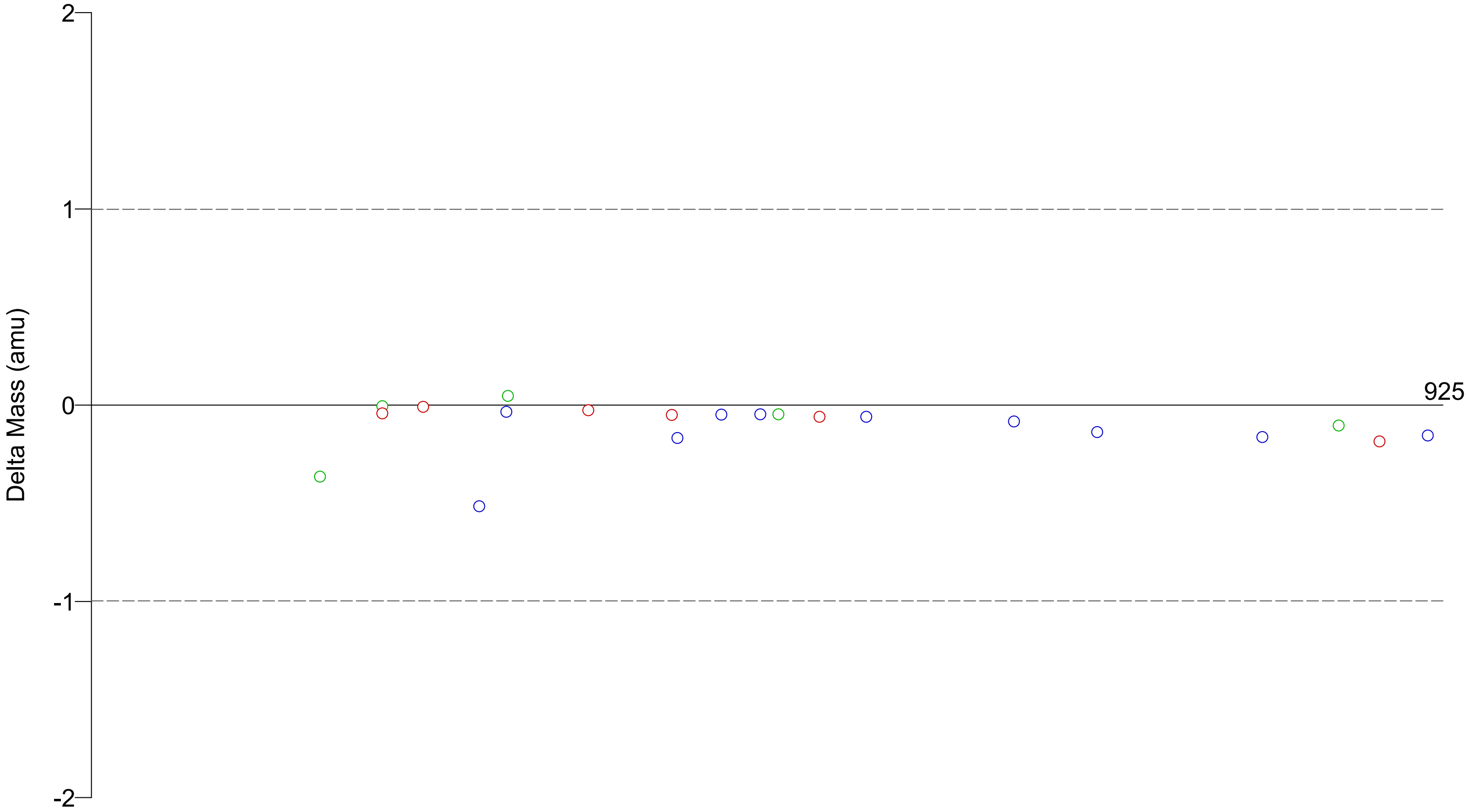


#19287468-1 NL: 6.49E5

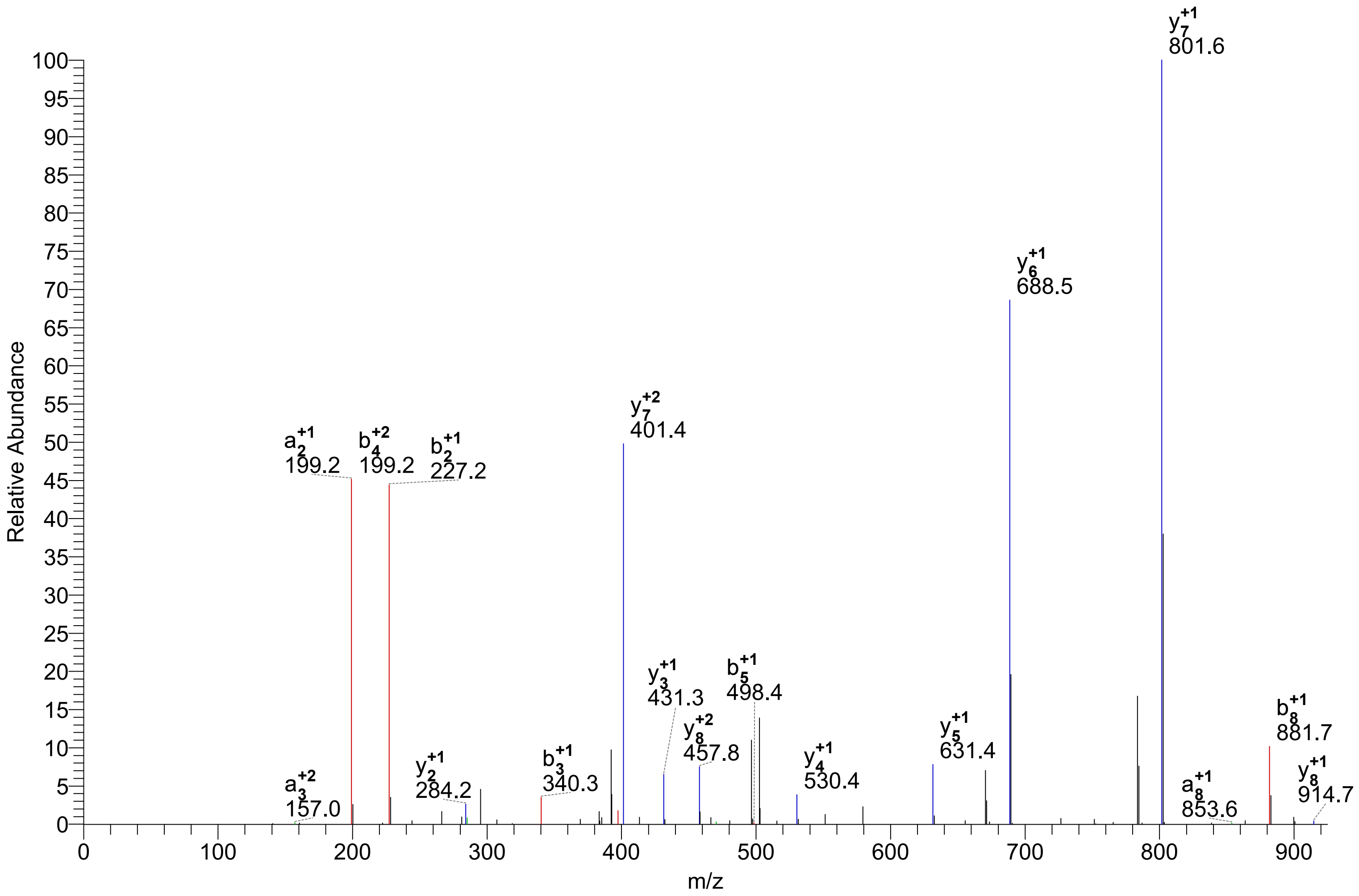


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                        MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00299778.2|SWISS-PROT:Q15166|TREMBL:A4D1H8|ENSEMBL:ENSP     0.0005  10.1     0.0       0
19287468 - 1  K.ILIGTVFHK.T                                  1027.63   2  0.0005  2.467  0.000   636.3  1   16/24   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 514.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18     227.18                                     914.55
 I    312.26     340.26                                     801.46
 G    369.29     397.28                                     688.38
 T    470.33     498.33                                     631.36
 V    569.40     597.40                                     530.31
 F    716.47     744.47                                     431.24
 H    853.53     881.52                                     284.17
 K                                                          147.11
```

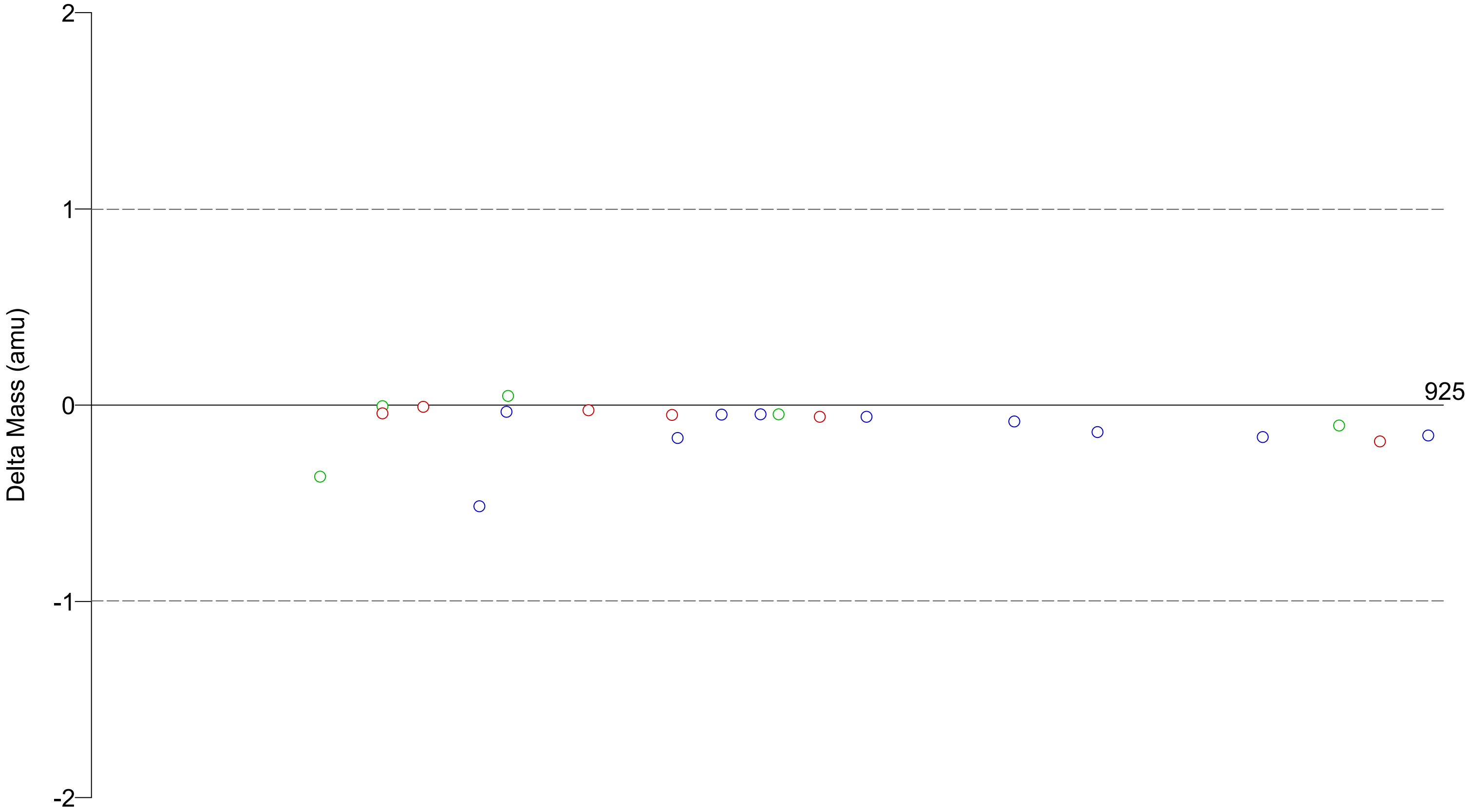


#19287468-1 NL: 2.17E5

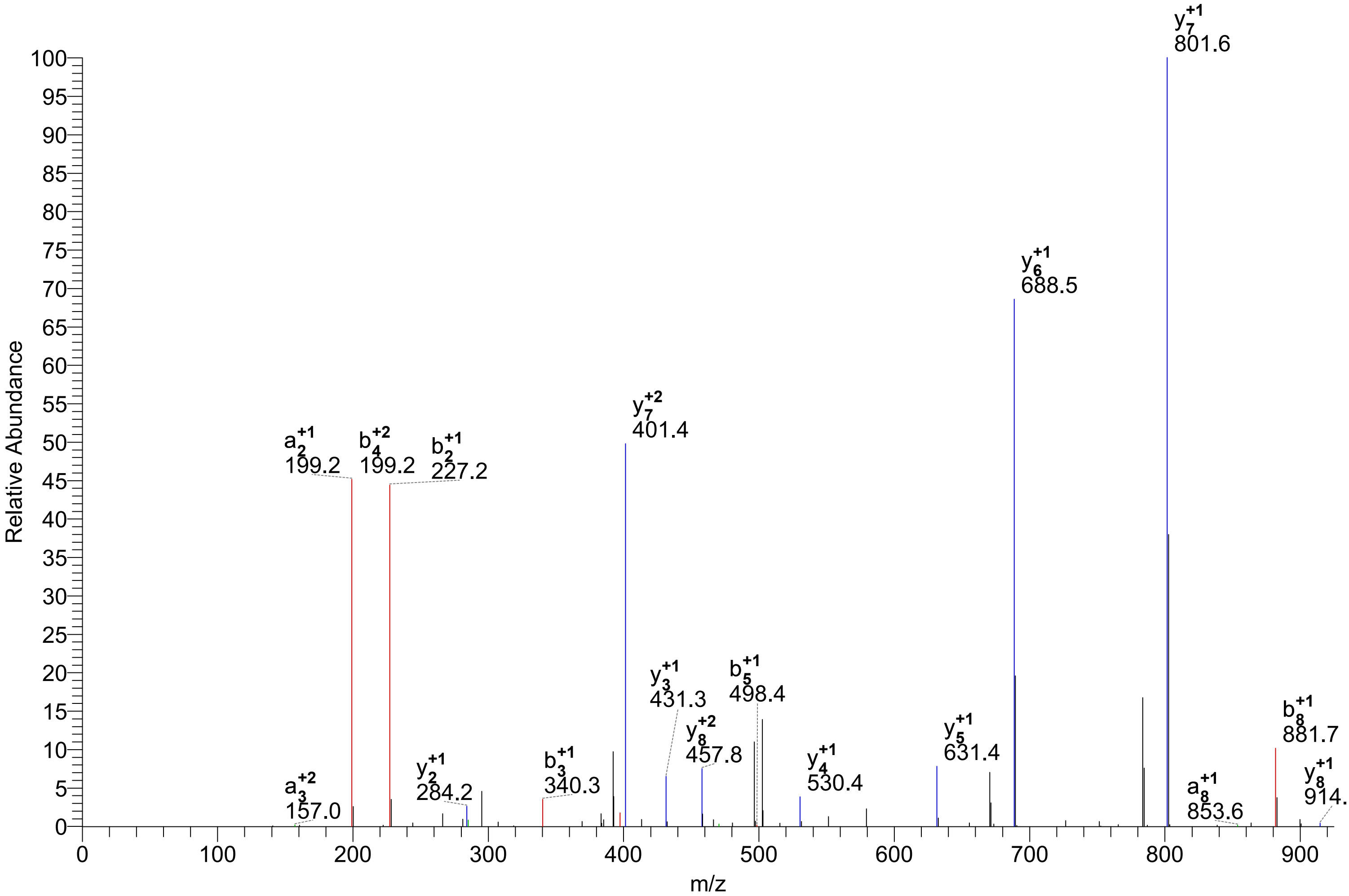


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00925751.1|VEGA:OTTHUMP0000                                0.0005  10.1     0.0       0
19287468 - 1  K.ILIGTVFHK.T                          1027.63   2  0.0005  2.467  0.000   636.3  1   16/24   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 514.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18     227.18                                      914.55
 I    312.26     340.26                                      801.46
 G    369.29     397.28                                      688.38
 T    470.33     498.33                                      631.36
 V    569.40     597.40                                      530.31
 F    716.47     744.47                                      431.24
 H    853.53     881.52                                      284.17
 K                                                           147.11
```

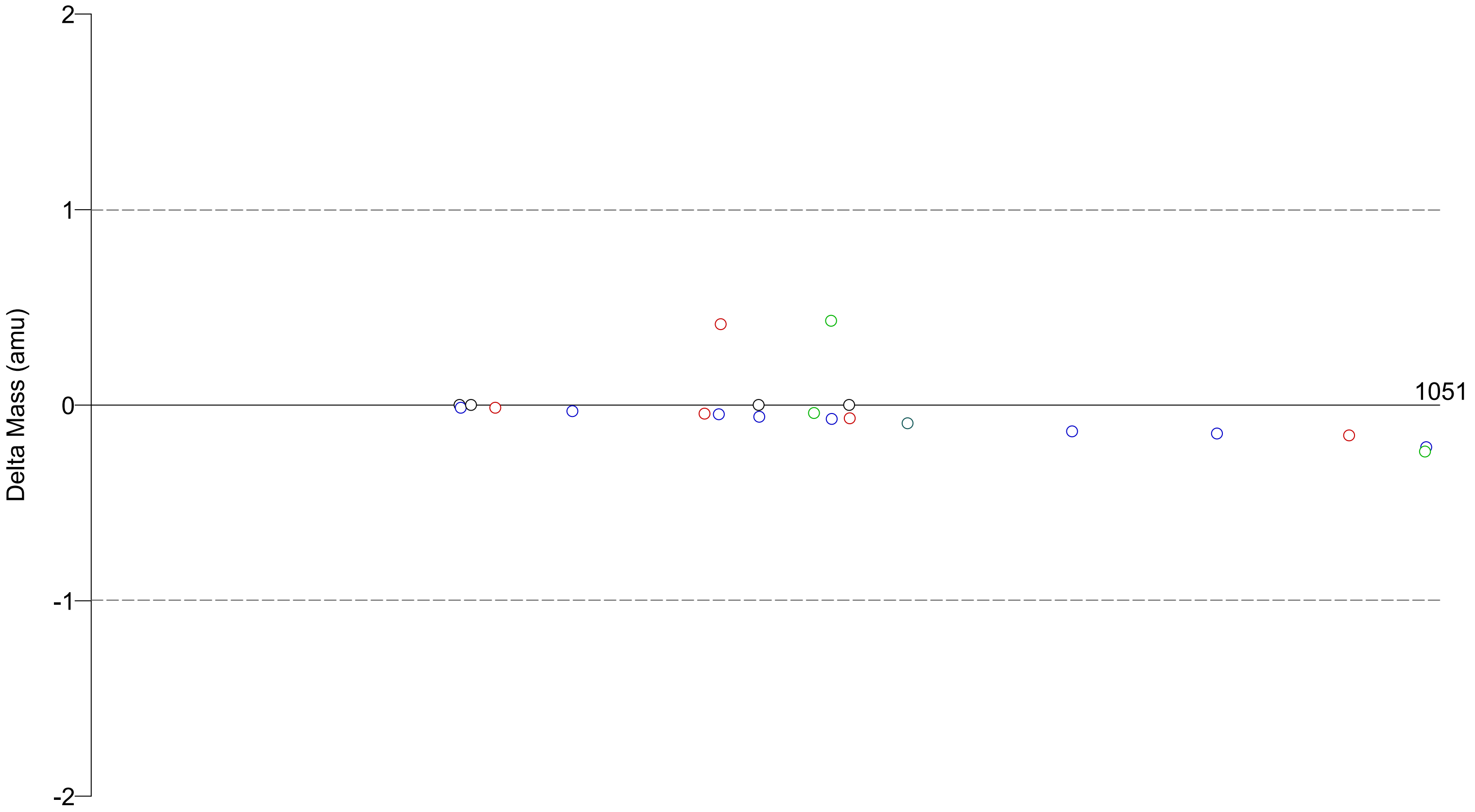


#19287468-1 NL: 2.17E5

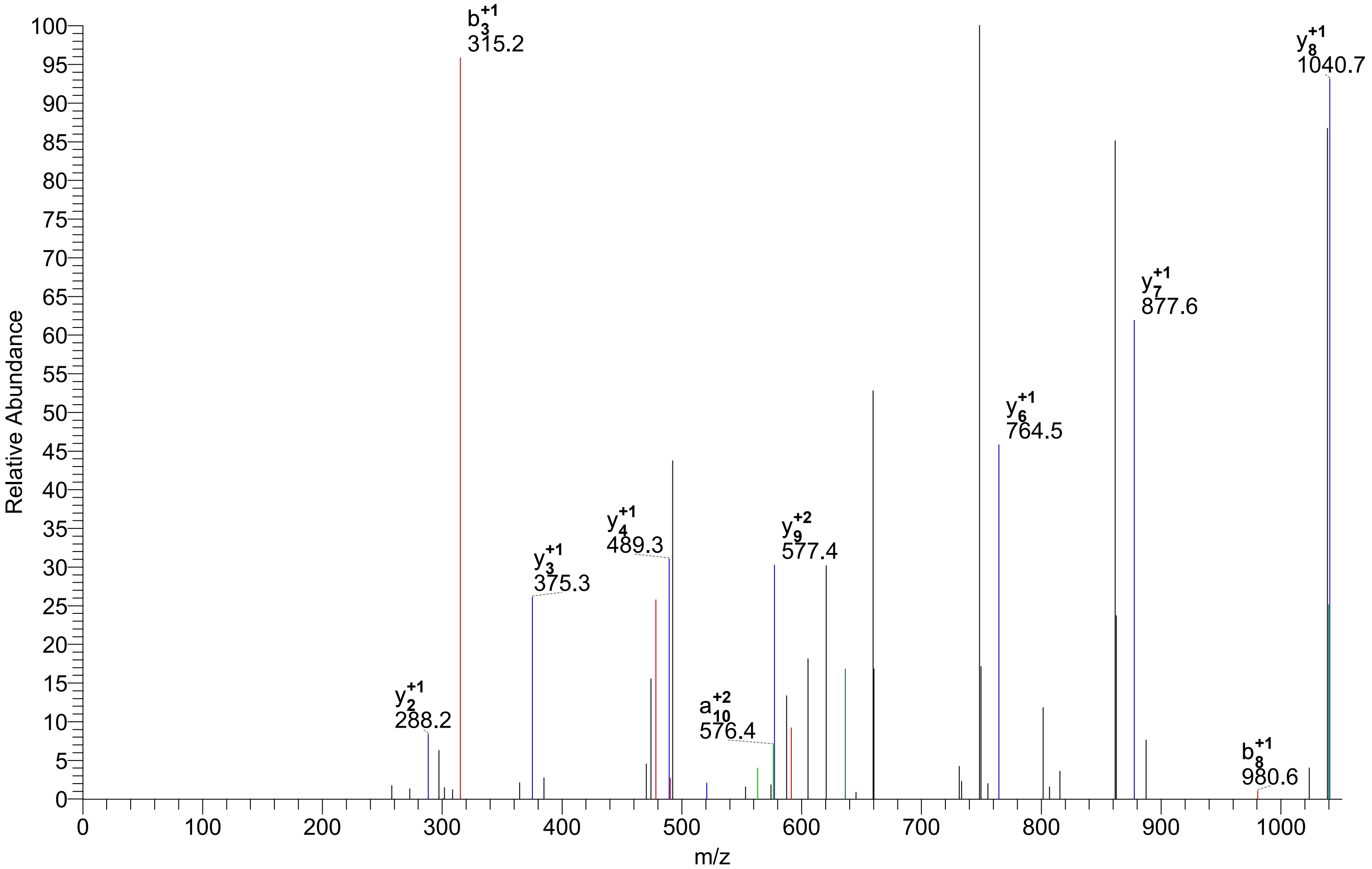


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z     P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00645363.2|TREMBL:Q6N089 Ta                                    0.1      18.1     0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                        1354.68    2  0.002    2.168  0.118   607.2  1    14/30   30
2118291816 -  K.GPSVFPLAPSSK.S                        1186.65    2  0.02     2.948  0.348   465.0  1    15/33   14

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

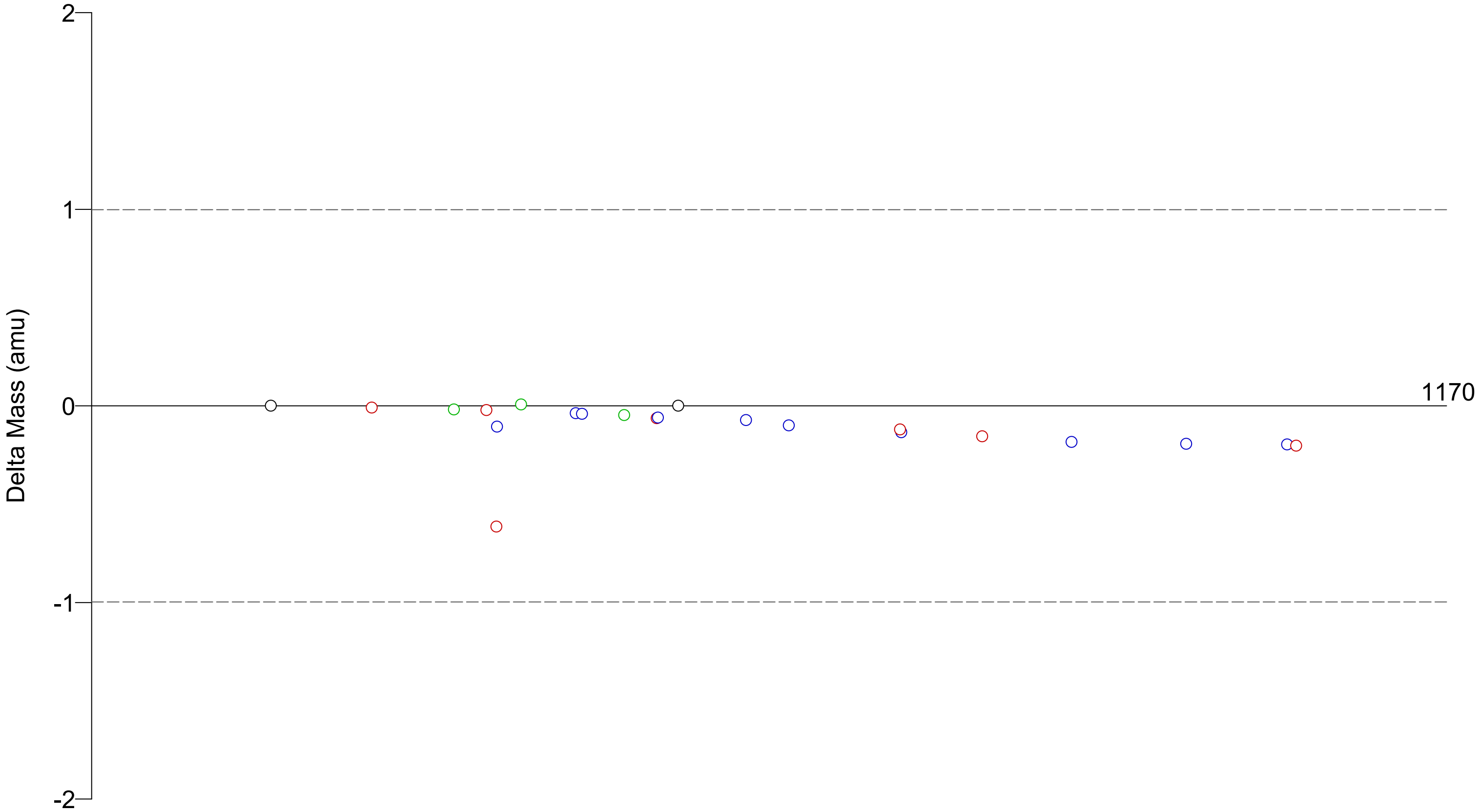
```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09    202.08                                     1240.64
 L    287.17    315.17                                     1153.60
 Y    450.23    478.23                                     1040.52
 L    563.32    591.31                                      877.46
 Q    691.38    719.37                                      764.37
 M*   838.41    866.41                                      636.31
 N    952.46    980.45                                      489.28
 S   1039.49   1067.48                                      375.24
 L   1152.57   1180.57                                      288.20
 R                                                          175.12
```



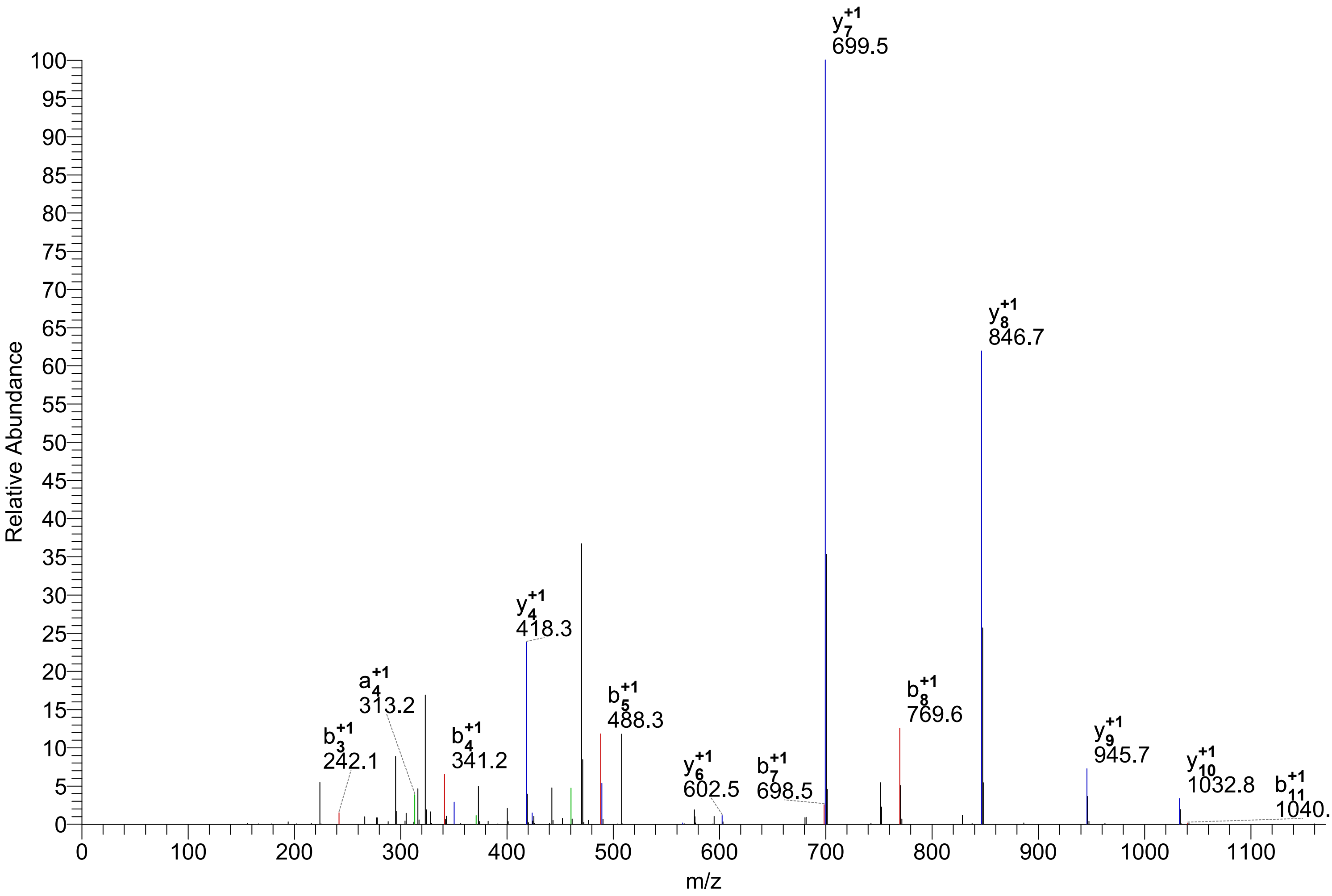
#19287468-1 NL: 8.93E4



```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

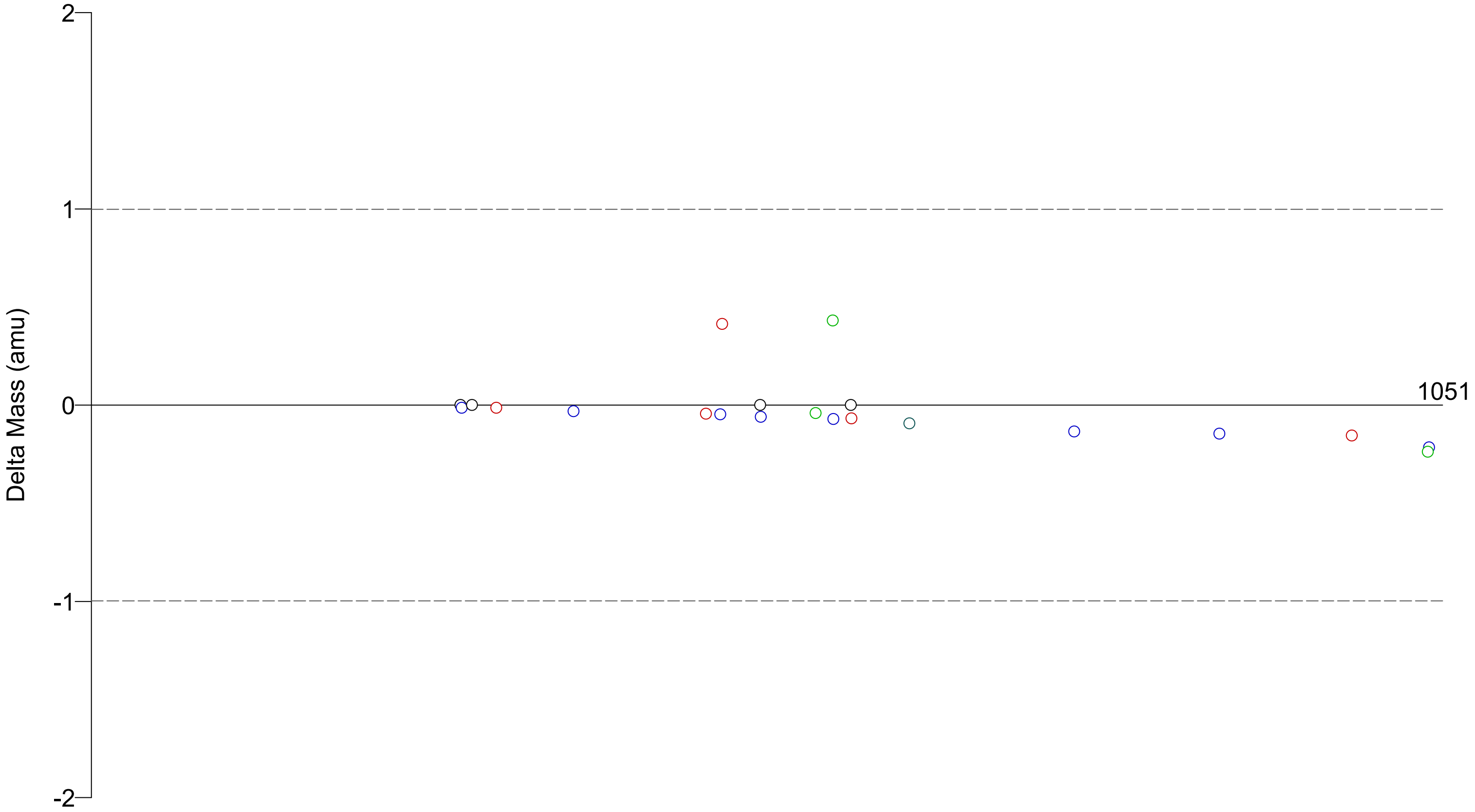


#2118291816-26226248 NL: 6.95E6

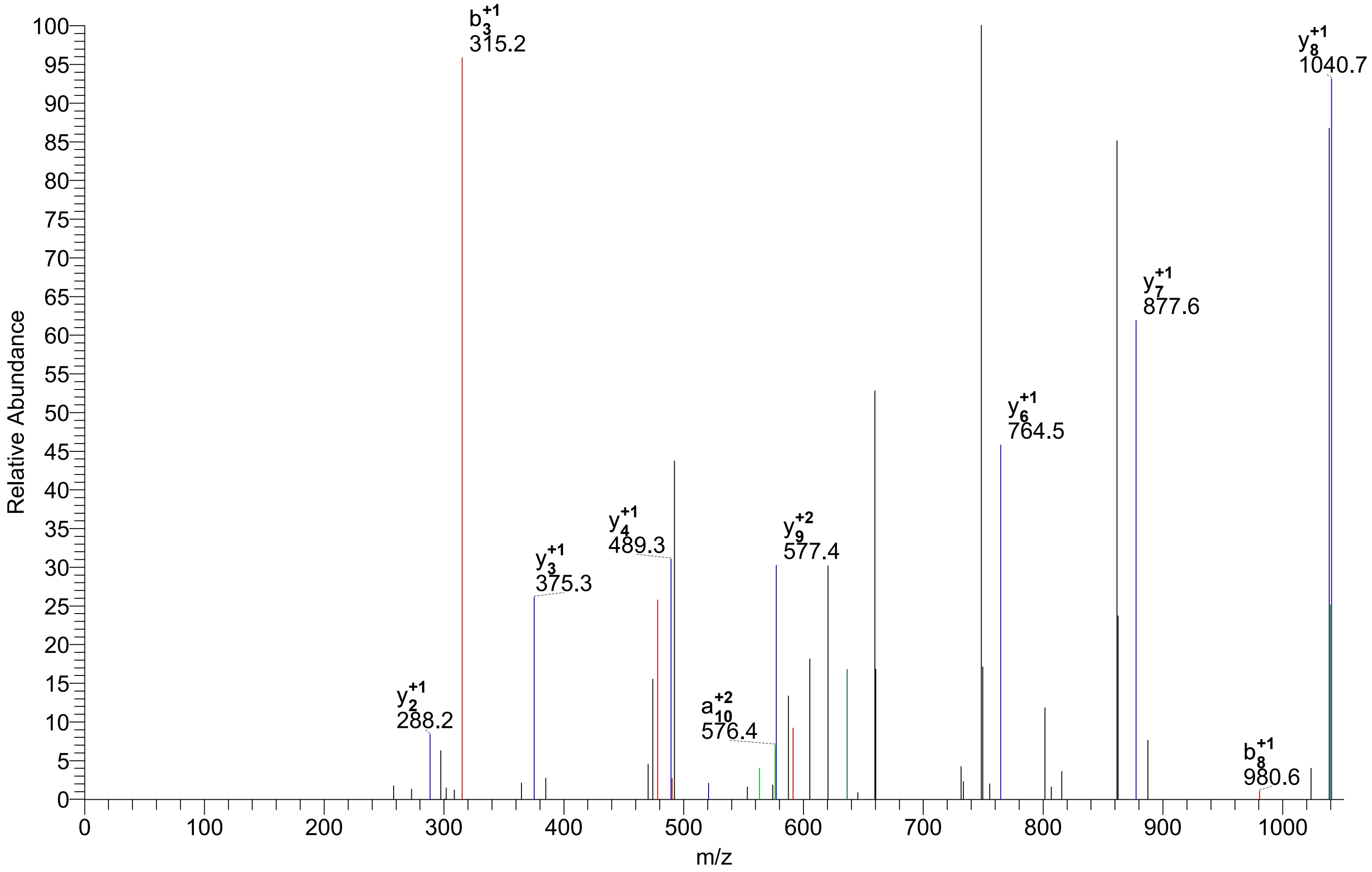


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00930124.1|TREMBL:Q6MZV7 Ta                                0.1      18.1     0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30
2118291816 -  K.GPSVFPLAPSSK.S                       1186.65    2  0.02     2.948  0.348   465.0  1   15/33   14

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

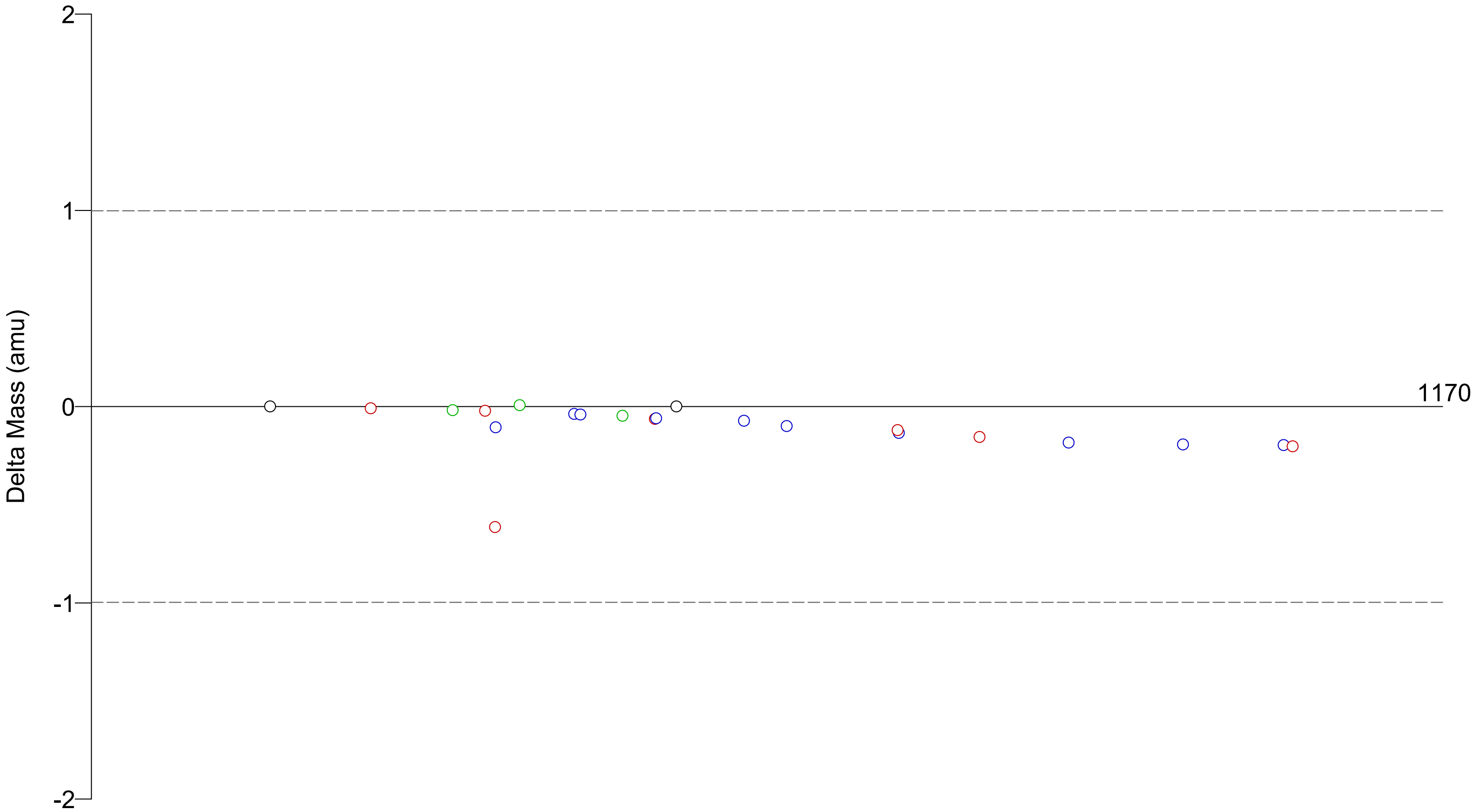
```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```



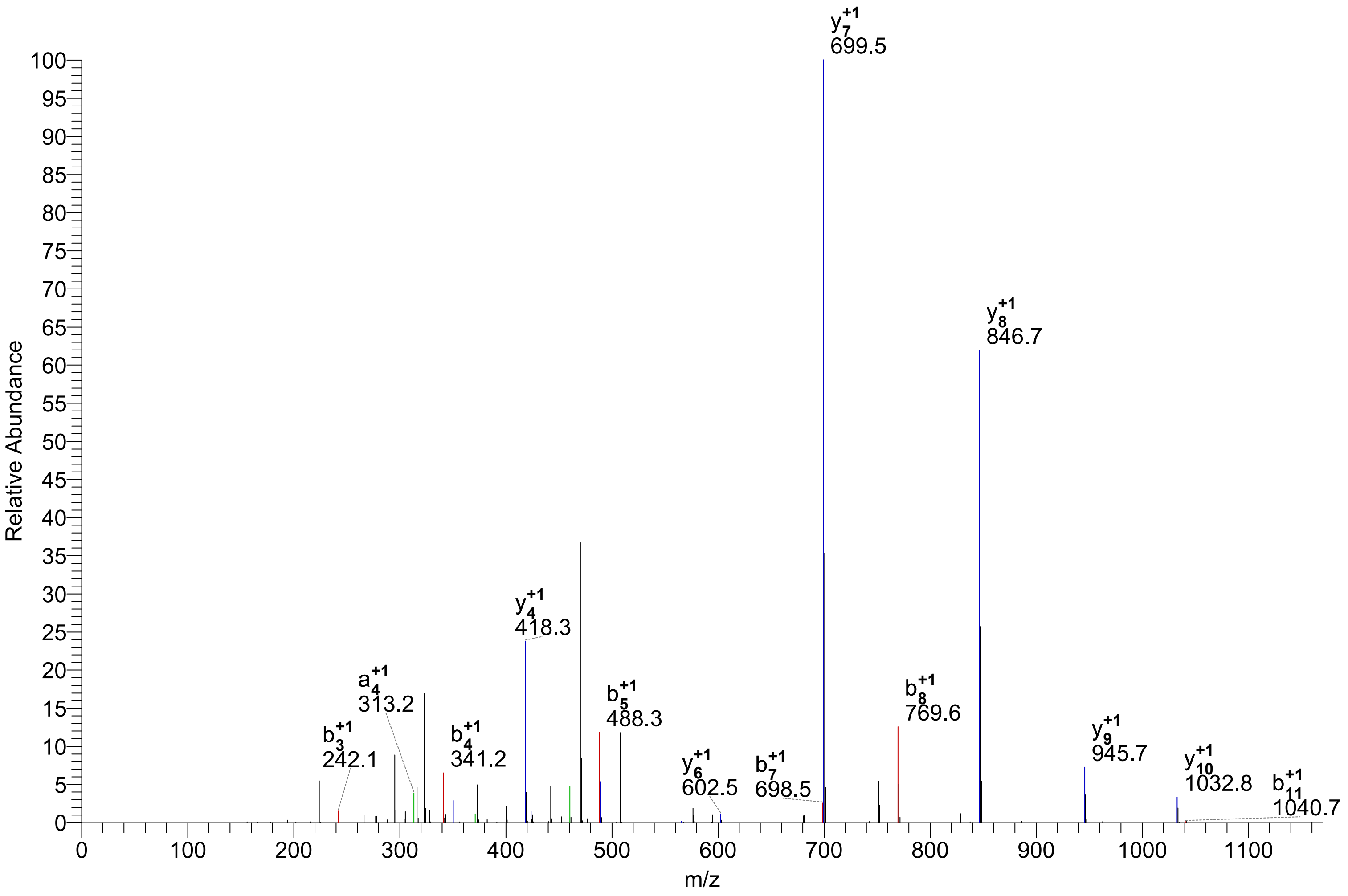
#19287468-1 NL: 8.93E4



```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

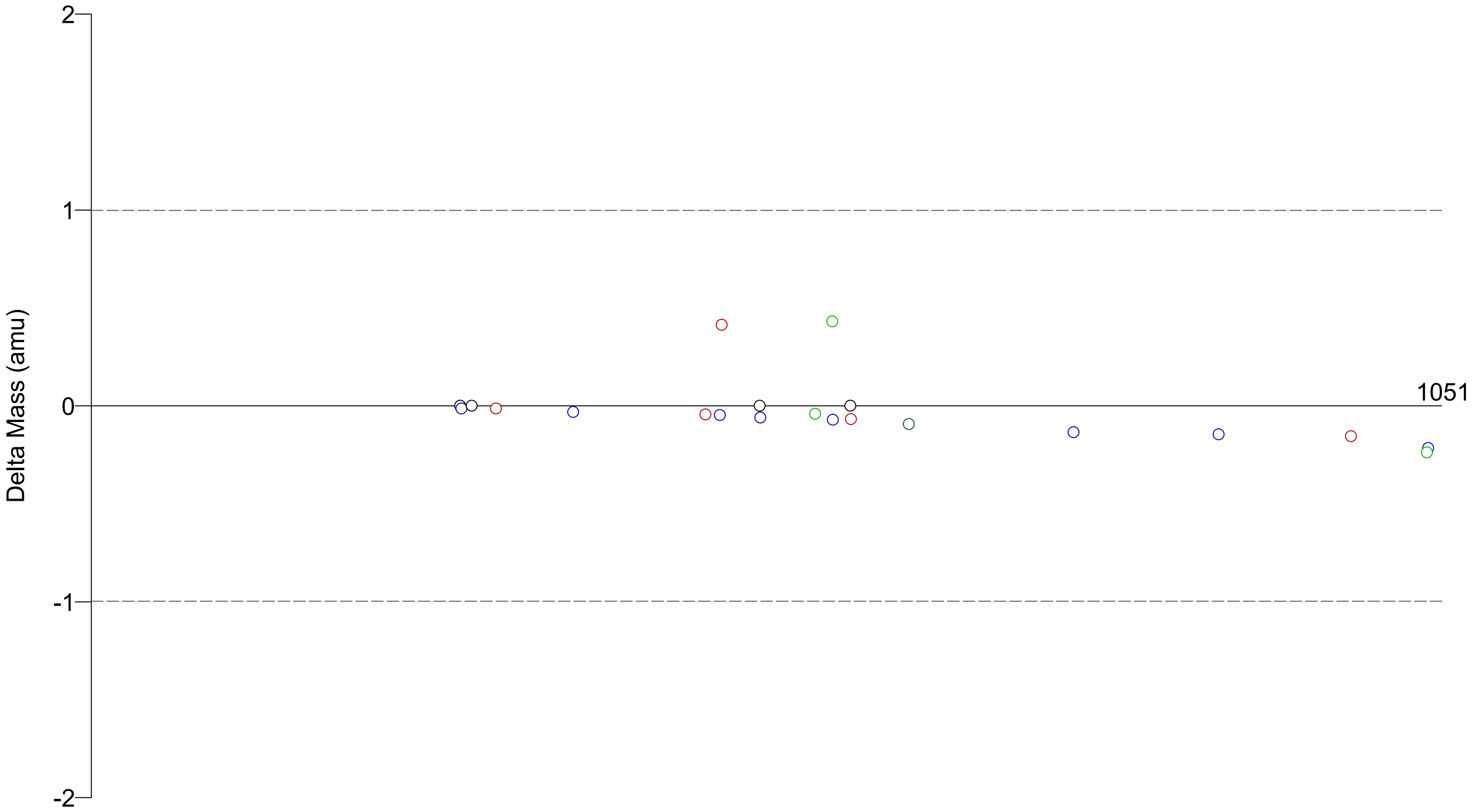


#2118291816-26226248 NL: 6.95E6

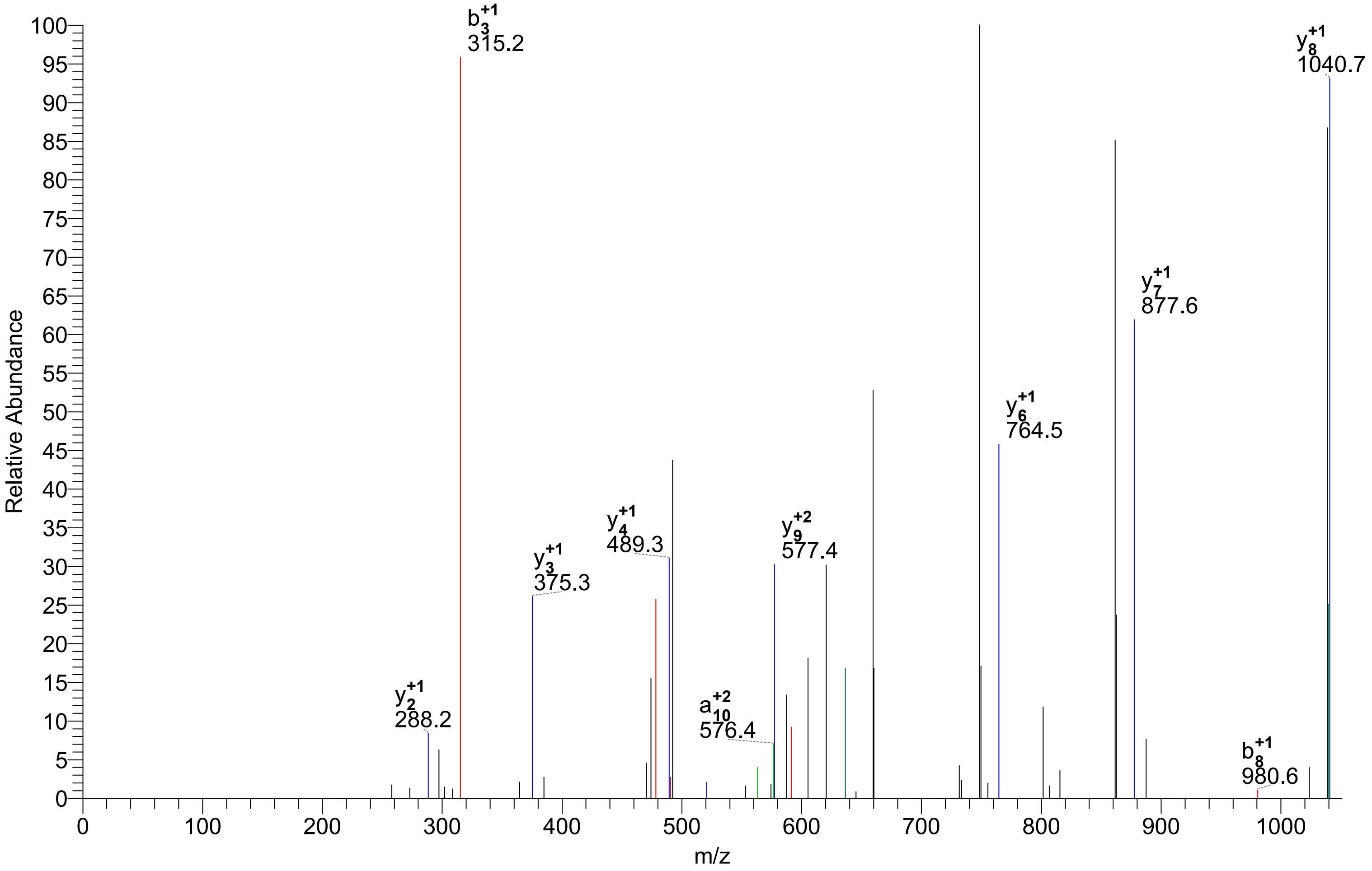


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00007899.4|TREMBL:Q9HCC1 Tax_Id=9606 Gene_Symbol=- Sing     0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                           1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

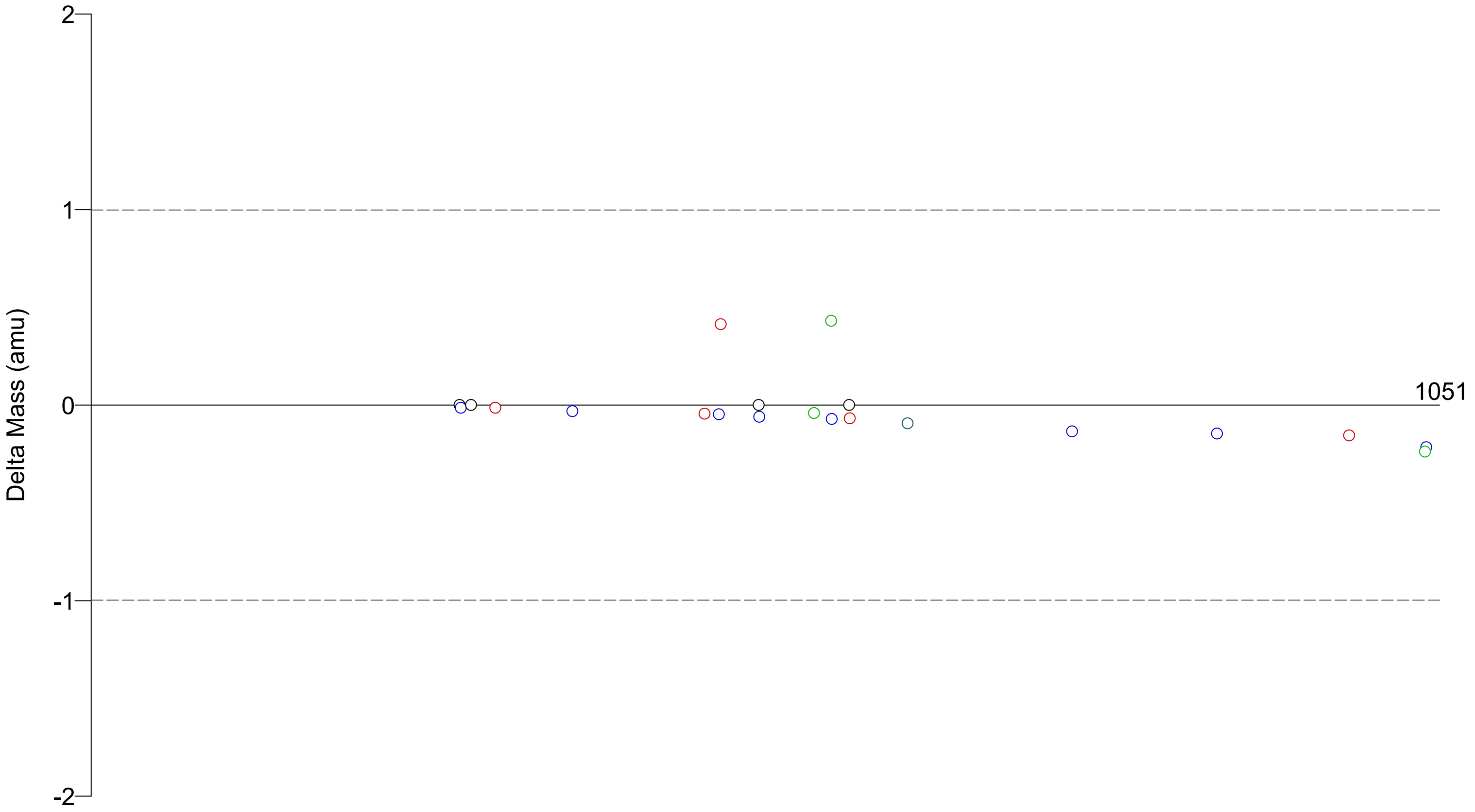


#19287468-1 NL: 8.93E4

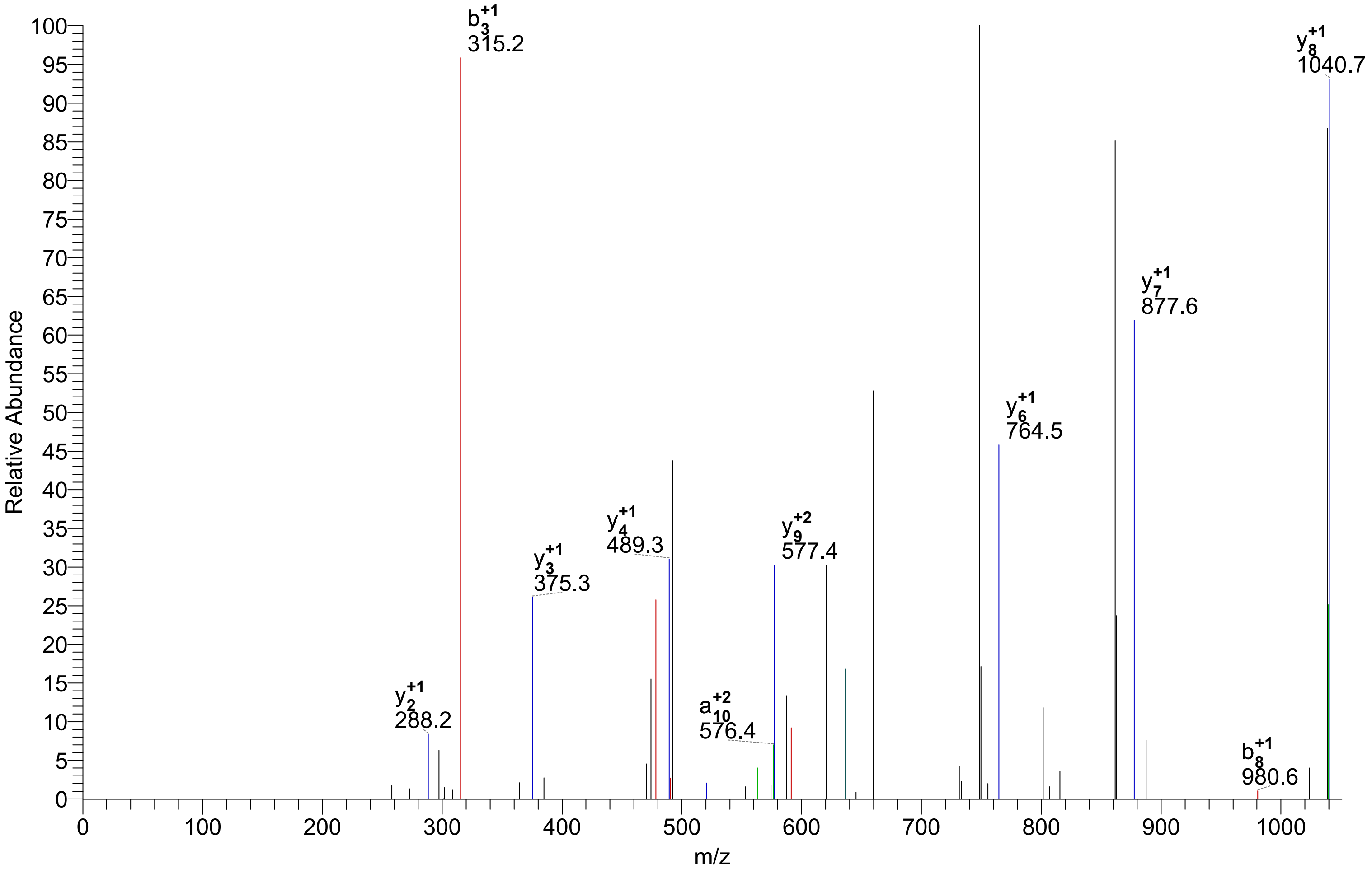


```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z   P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00382500.1|SWISS-PROT:P0178                                      0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                           1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

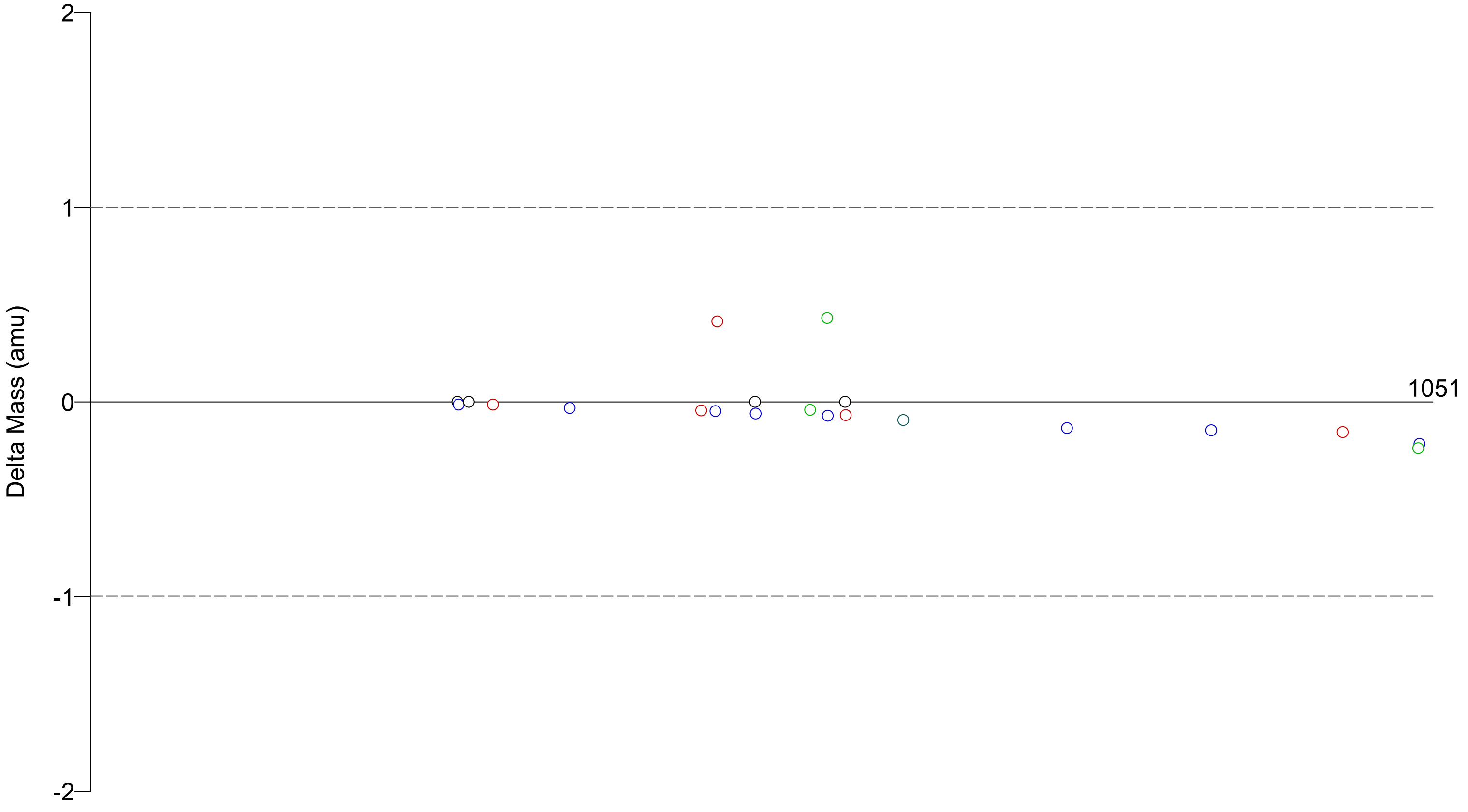


#19287468-1 NL: 8.93E4

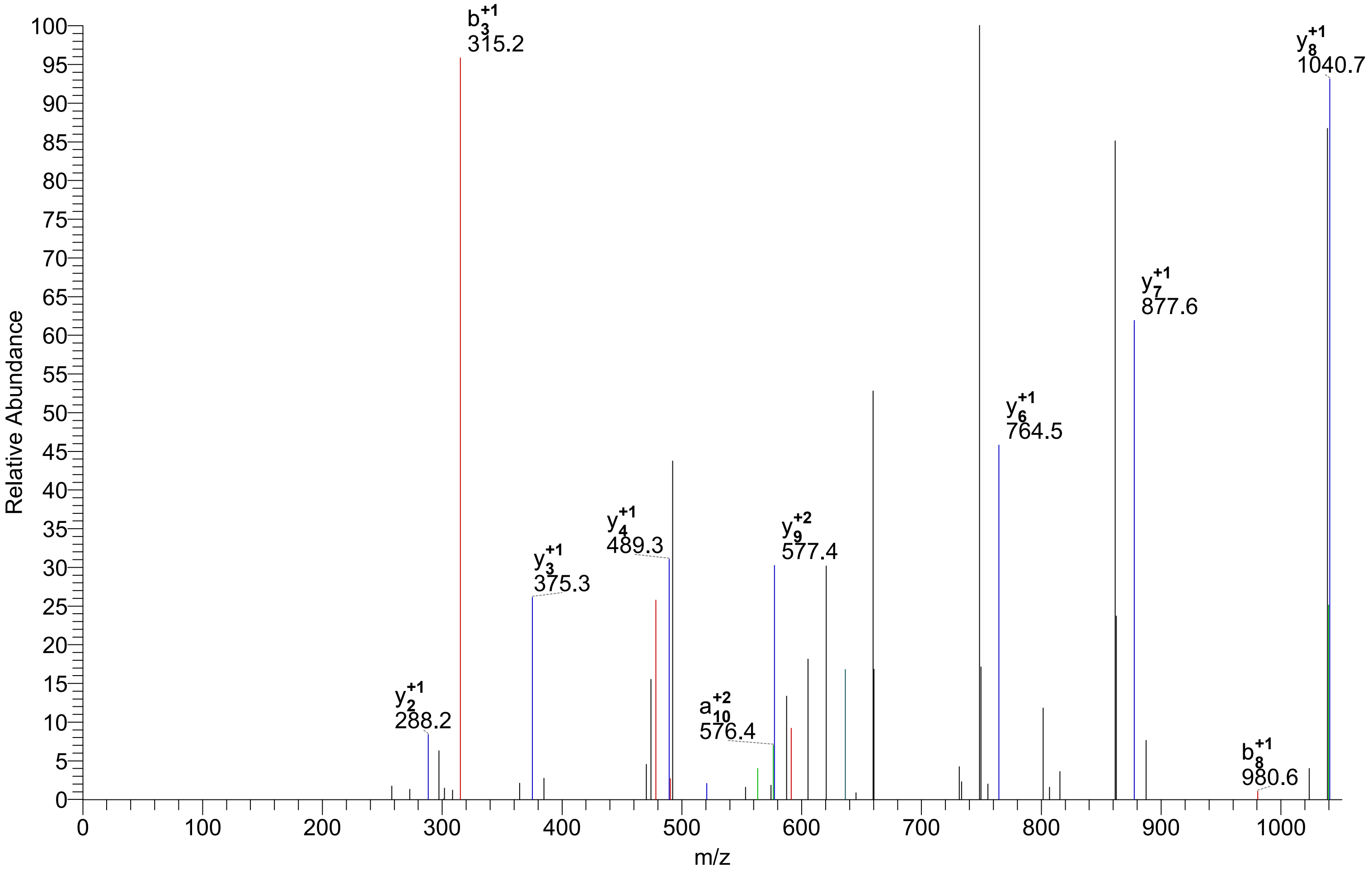


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00384391.1|TREMBL:Q9UL71 Ta                                0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2  0.002    2.168  0.118    607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

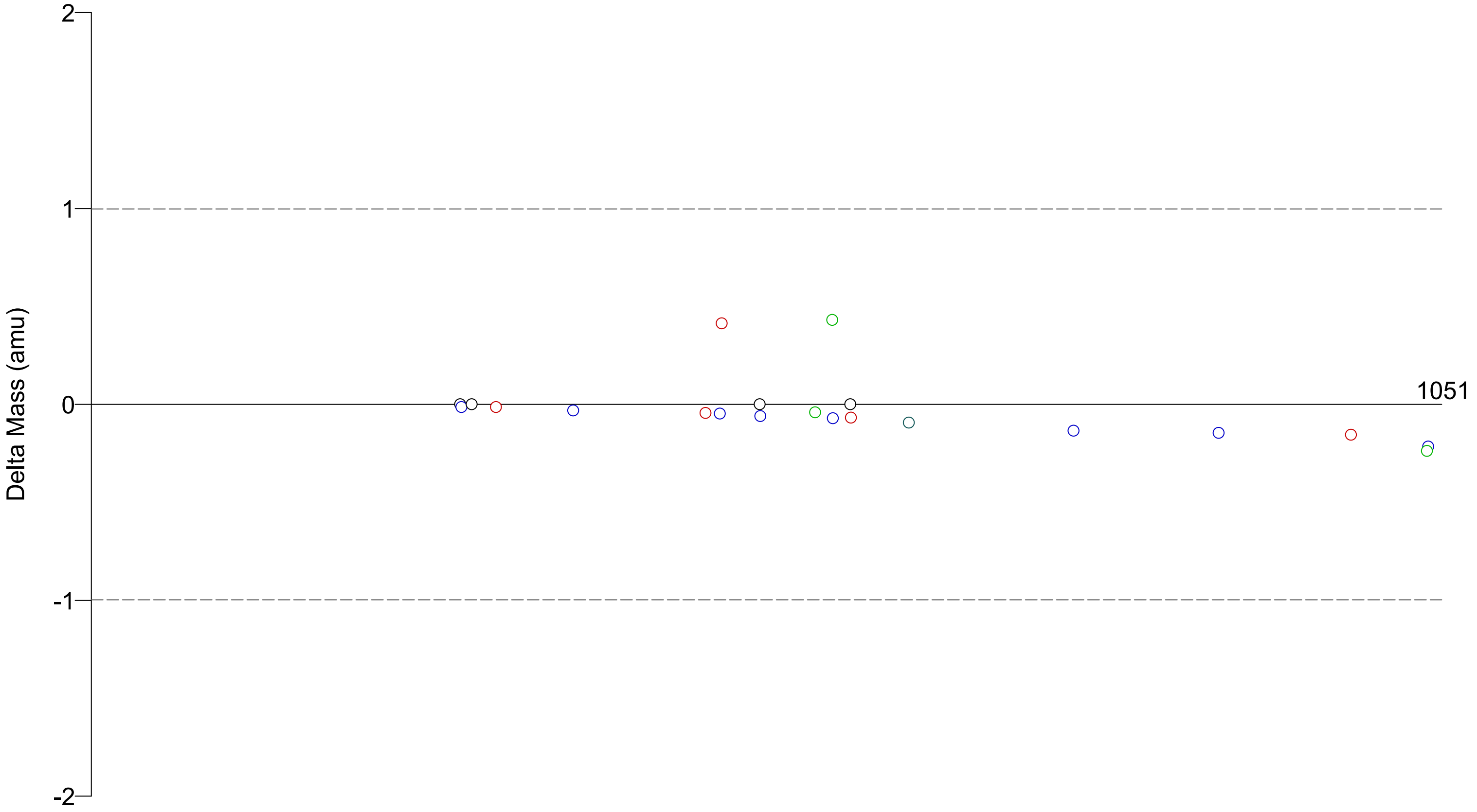


#19287468-1 NL: 8.93E4

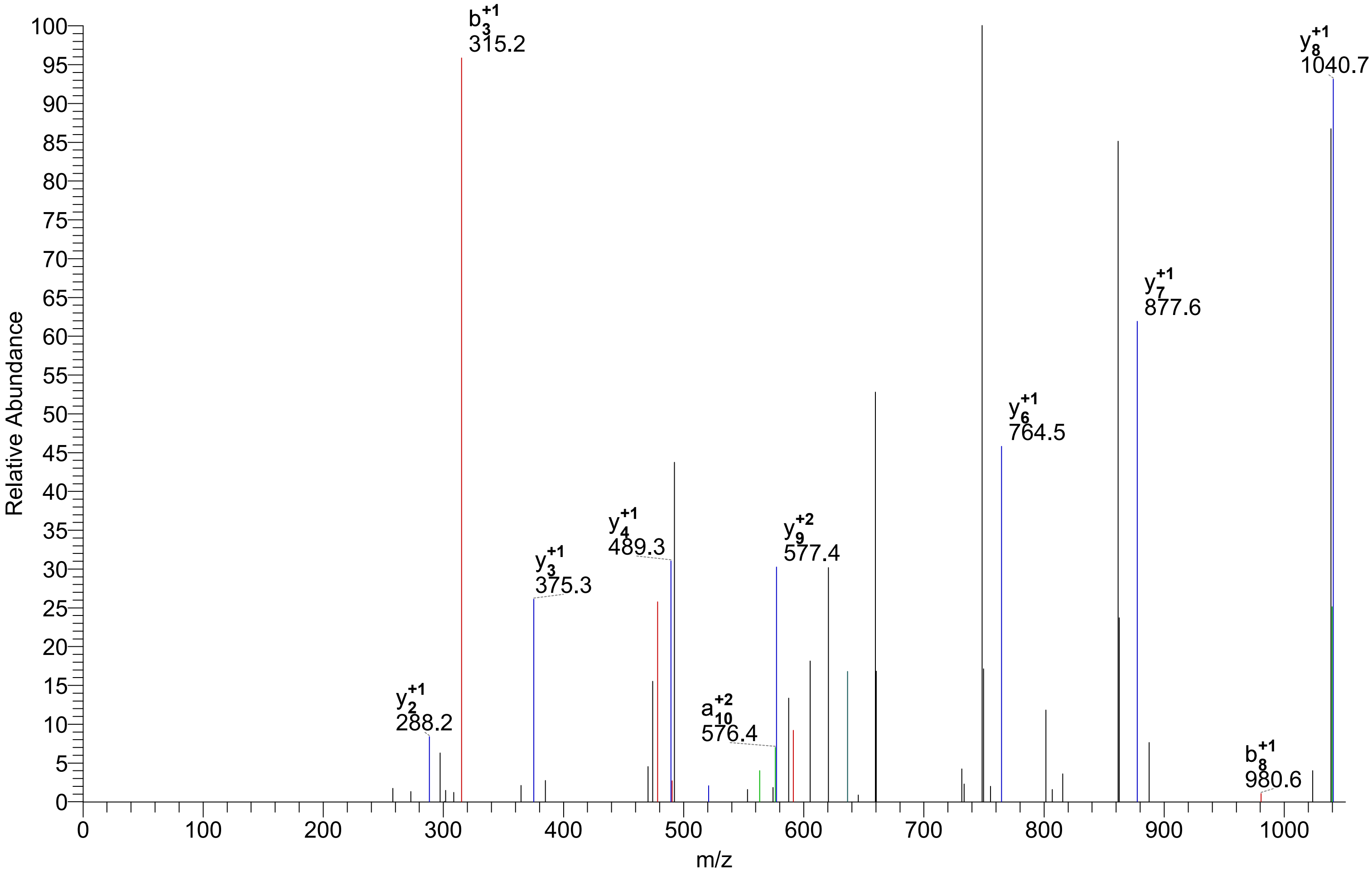


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00555872.5|TREMBL:Q9UL91 Ta                                0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

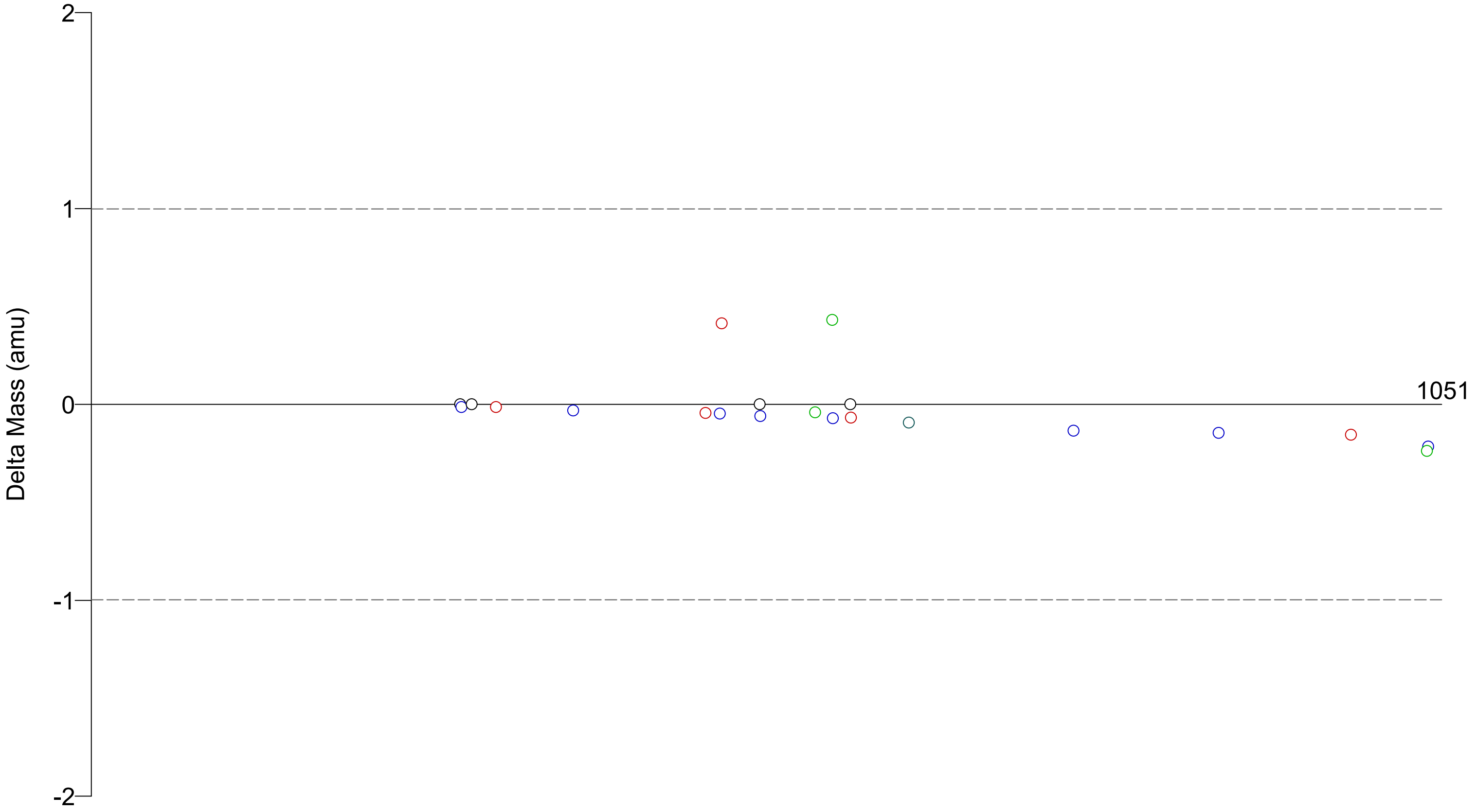


#19287468-1 NL: 8.93E4

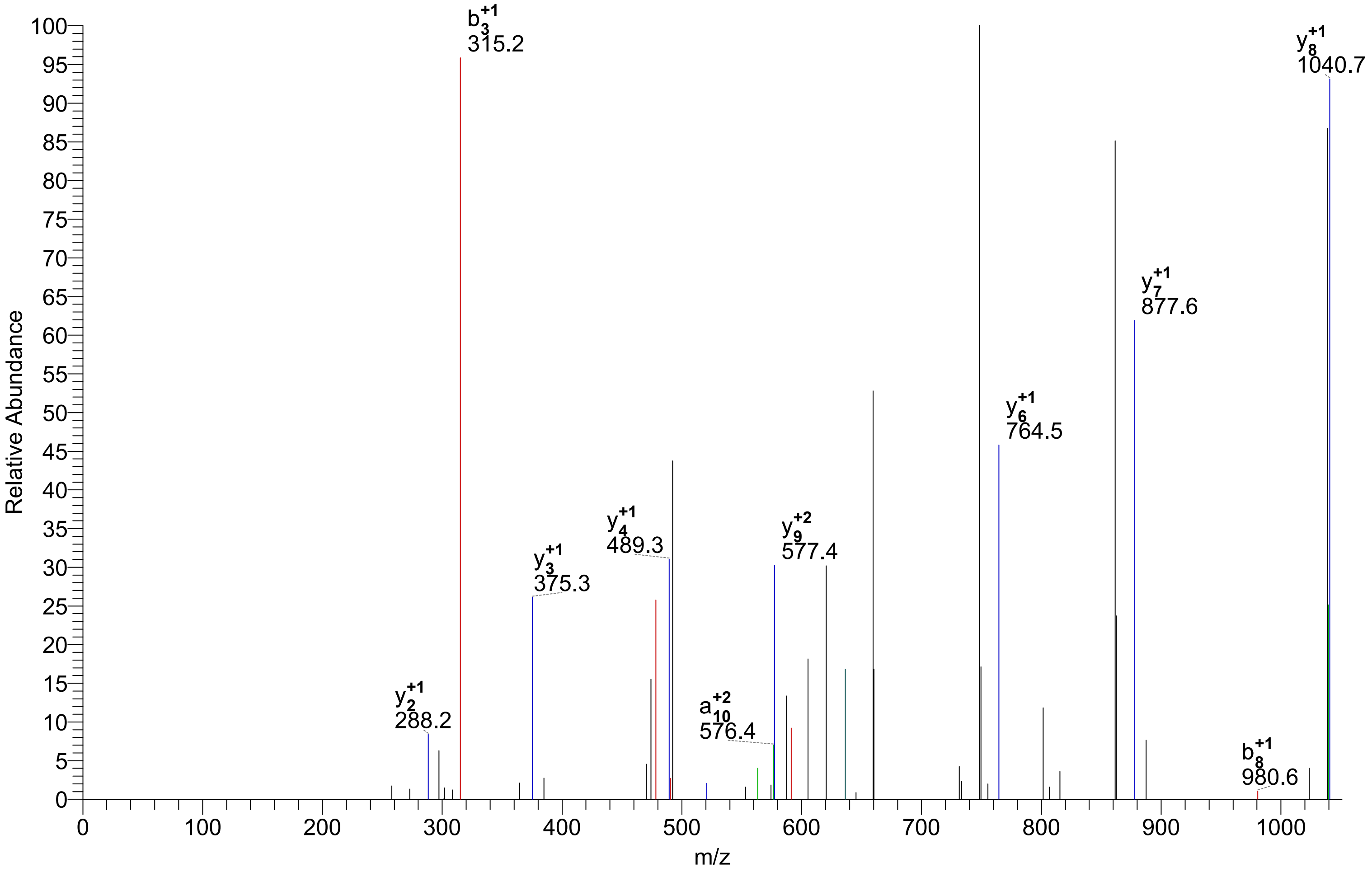


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00782983.2|TREMBL:Q0ZCH4;Q0                                   0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                        1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

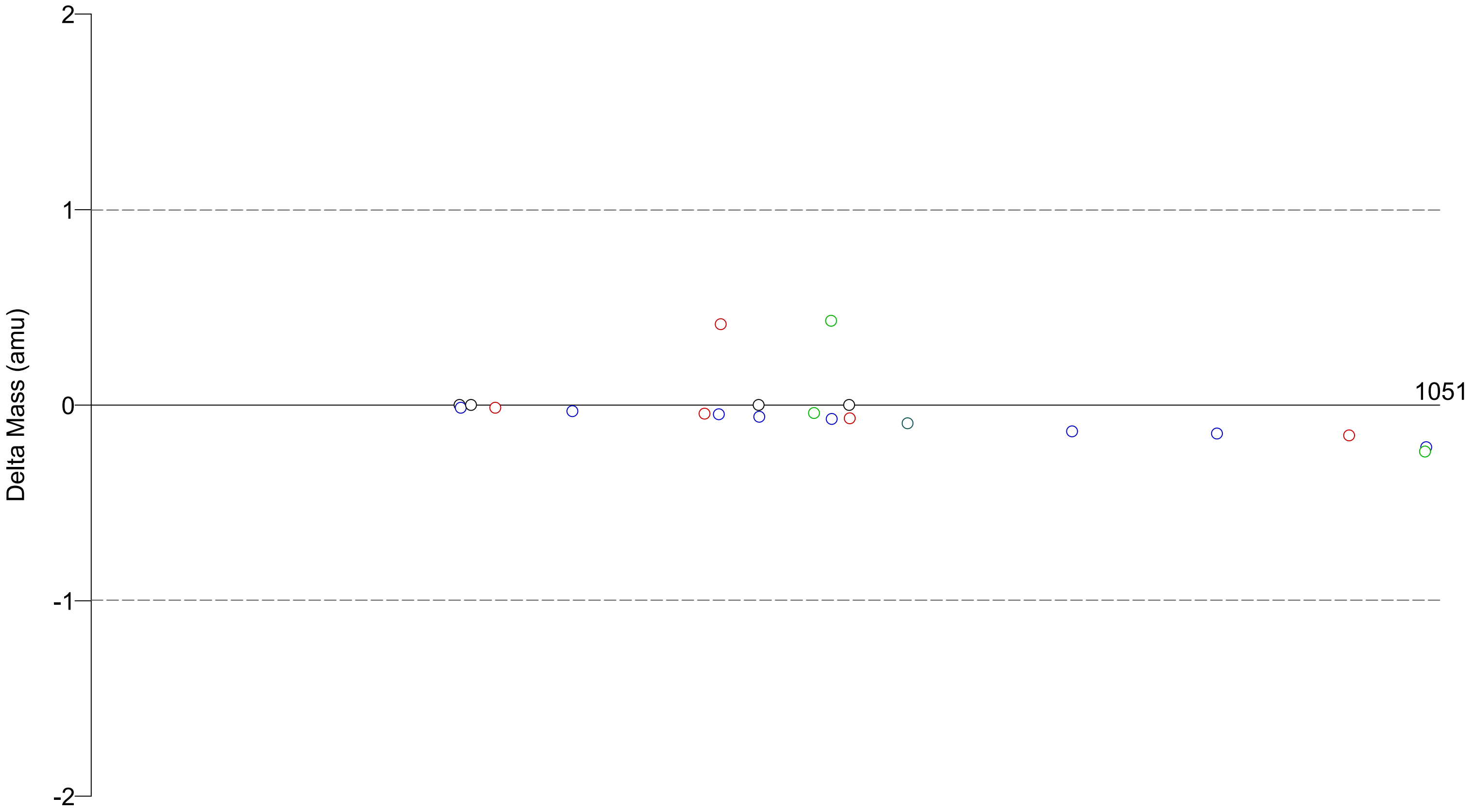


#19287468-1 NL: 8.93E4

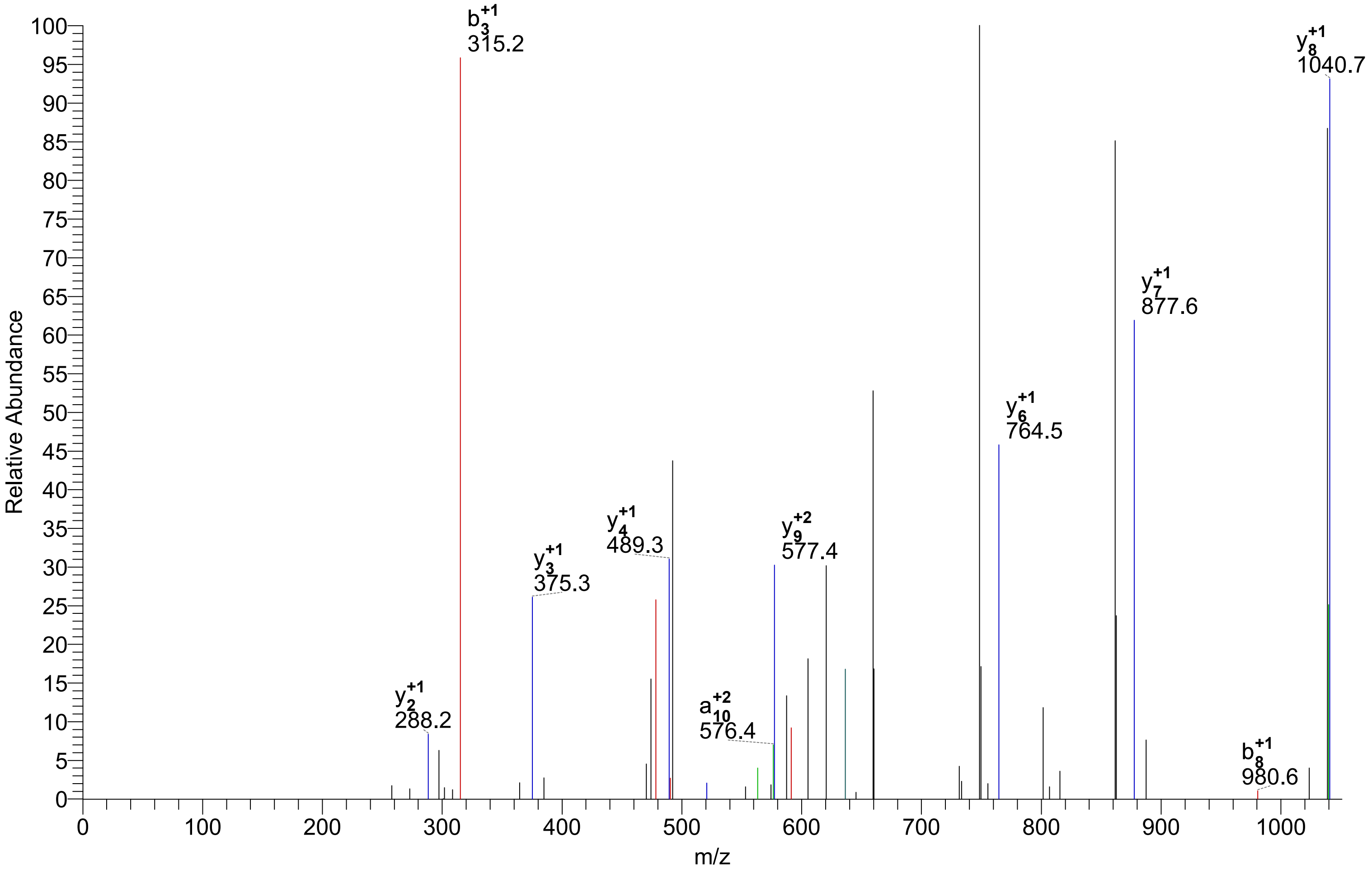


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z     P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00783287.1|TREMBL:Q0ZCH9 Ta                                 0.1    8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2   0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

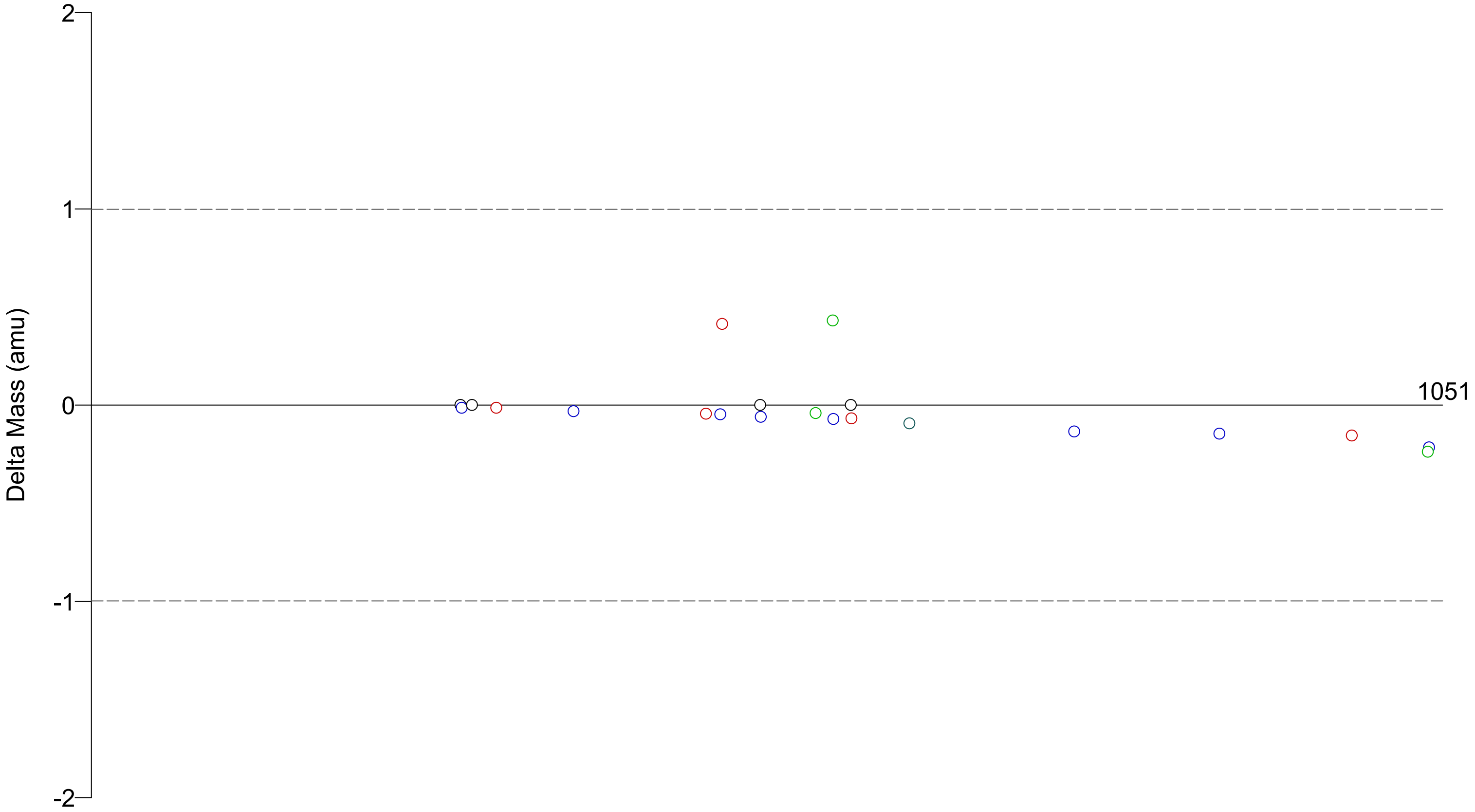


#19287468-1 NL: 8.93E4

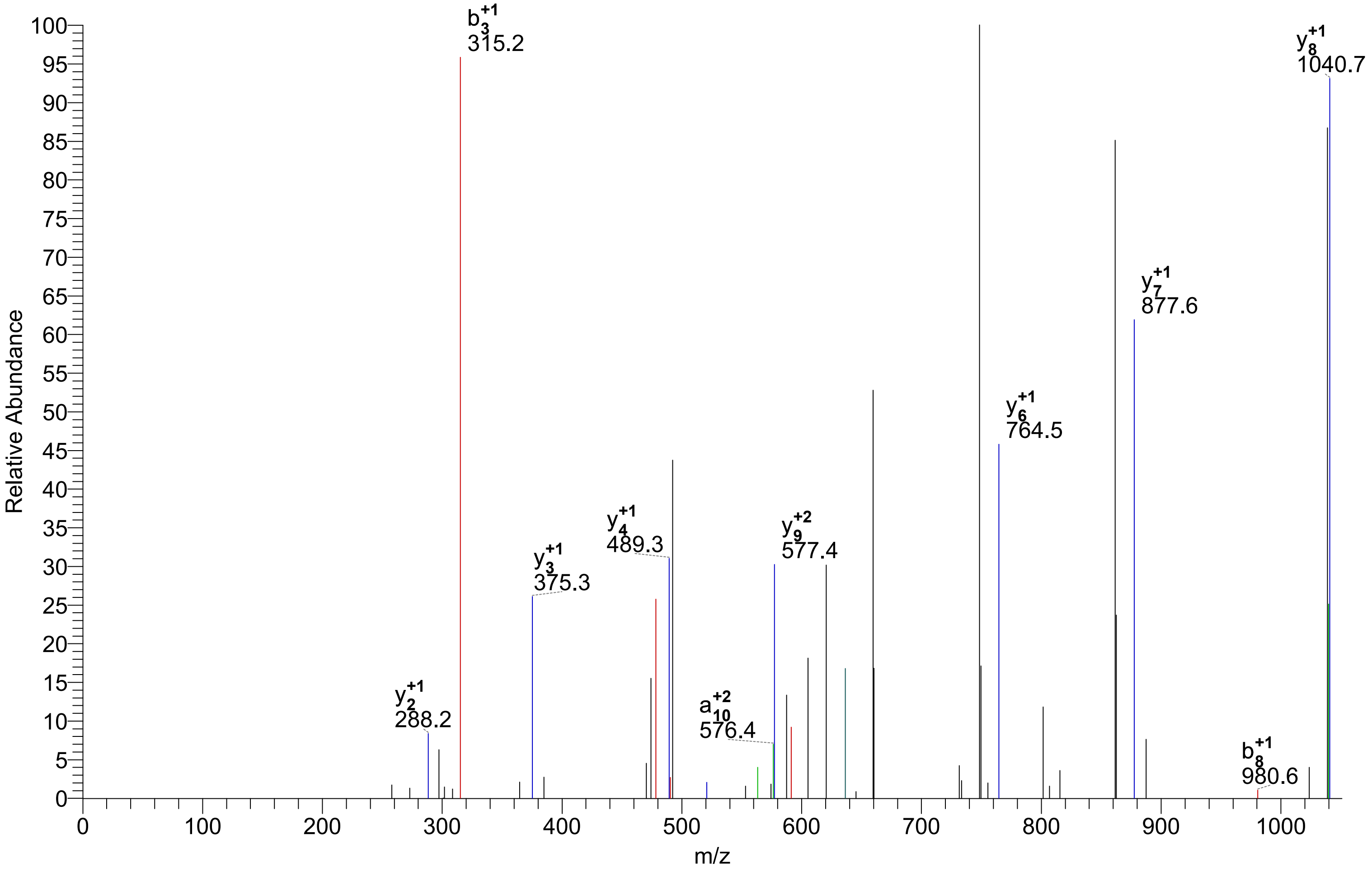


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                ств MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00783451.1|TREMBL:Q0ZCJ5 Ta                                0.1    8.1       0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

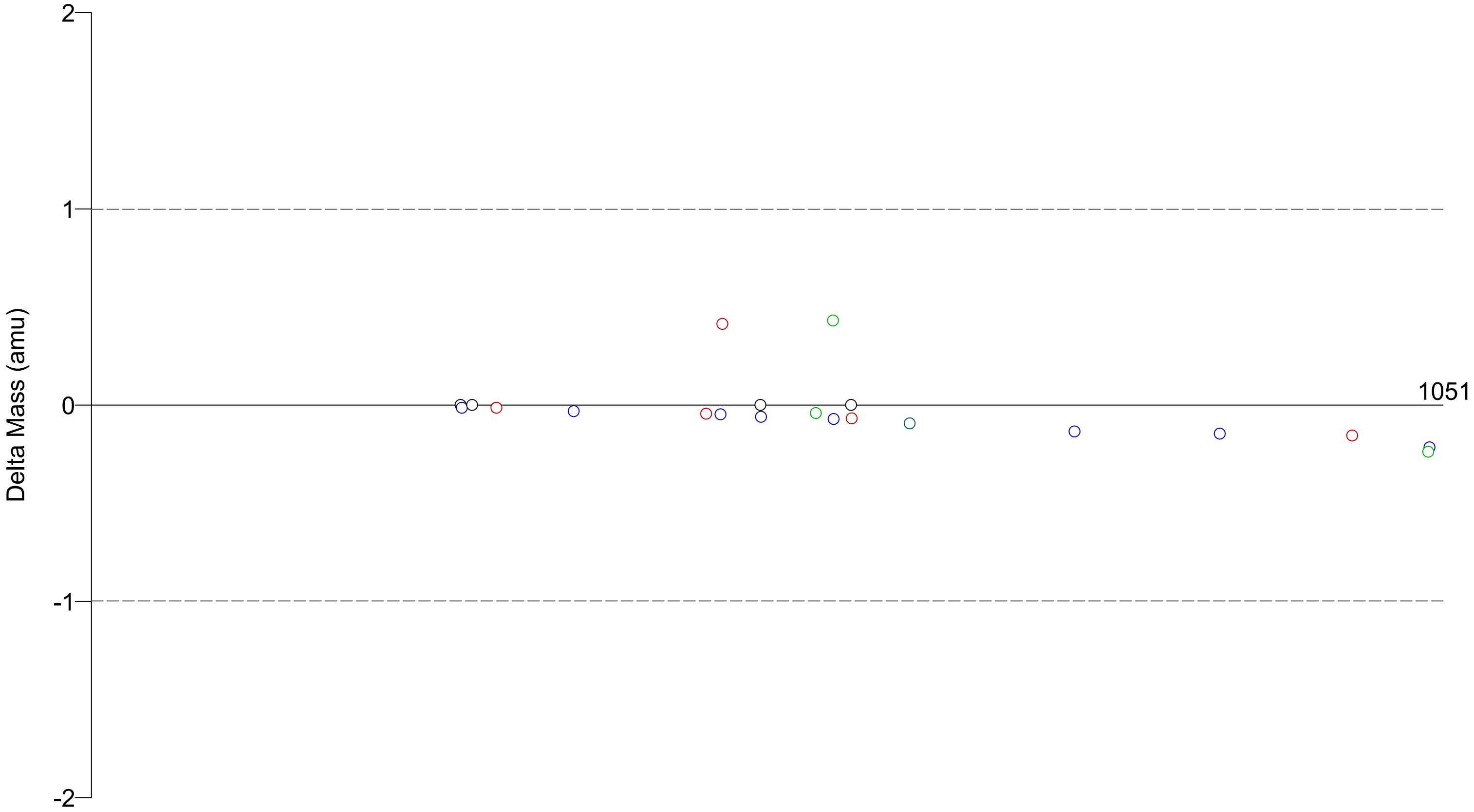


#19287468-1 NL: 8.93E4

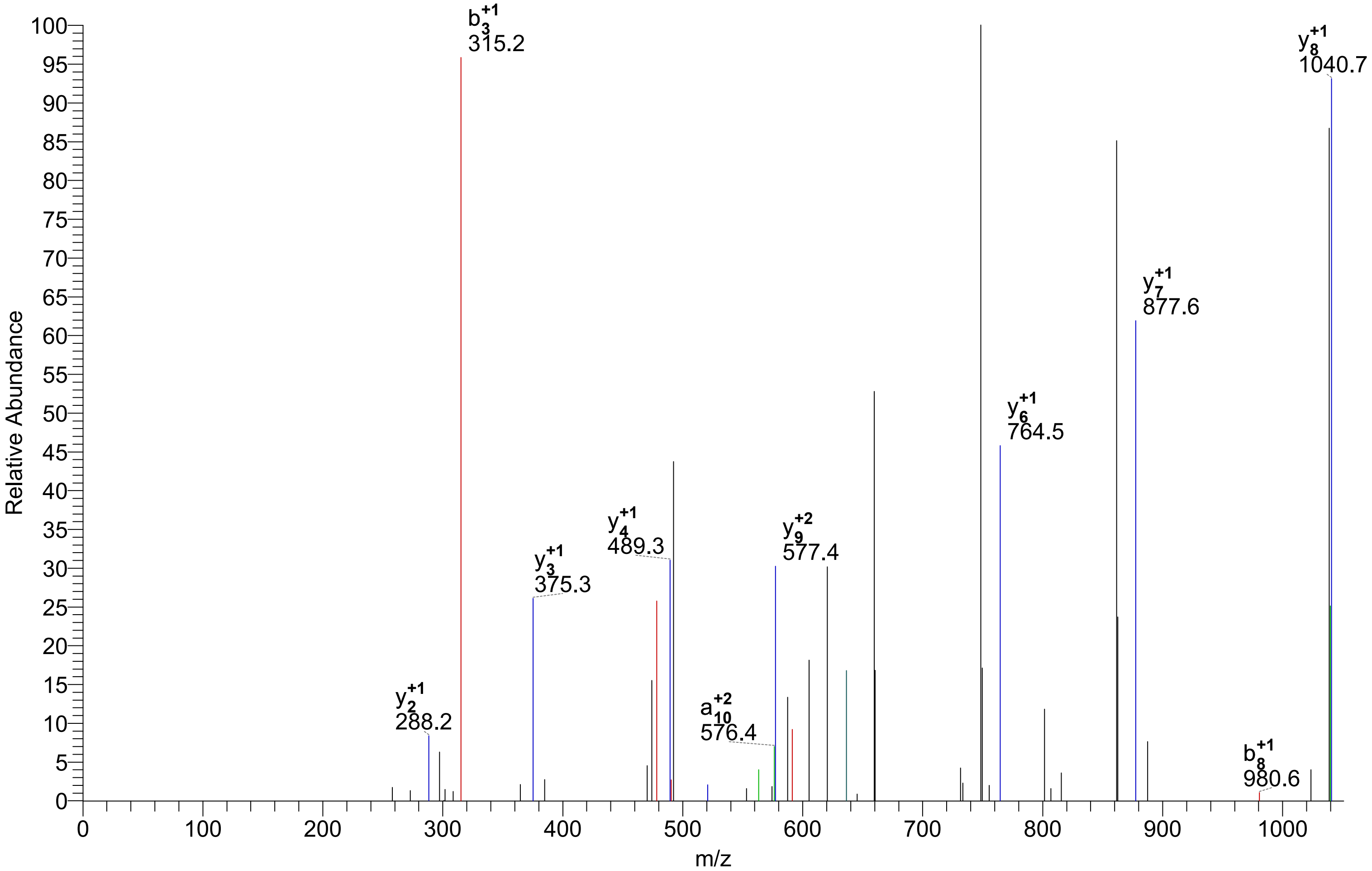


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00783689.1|TREMBL:Q0ZCF9;Q0                                     0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                           1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N      87.06     115.05
 S     174.09     202.08                                     1240.64
 L     287.17     315.17                                     1153.60
 Y     450.23     478.23                                     1040.52
 L     563.32     591.31                                      877.46
 Q     691.38     719.37                                      764.37
 M*    838.41     866.41                                      636.31
 N     952.46     980.45                                      489.28
 S    1039.49    1067.48                                      375.24
 L    1152.57    1180.57                                      288.20
 R                                                            175.12
```

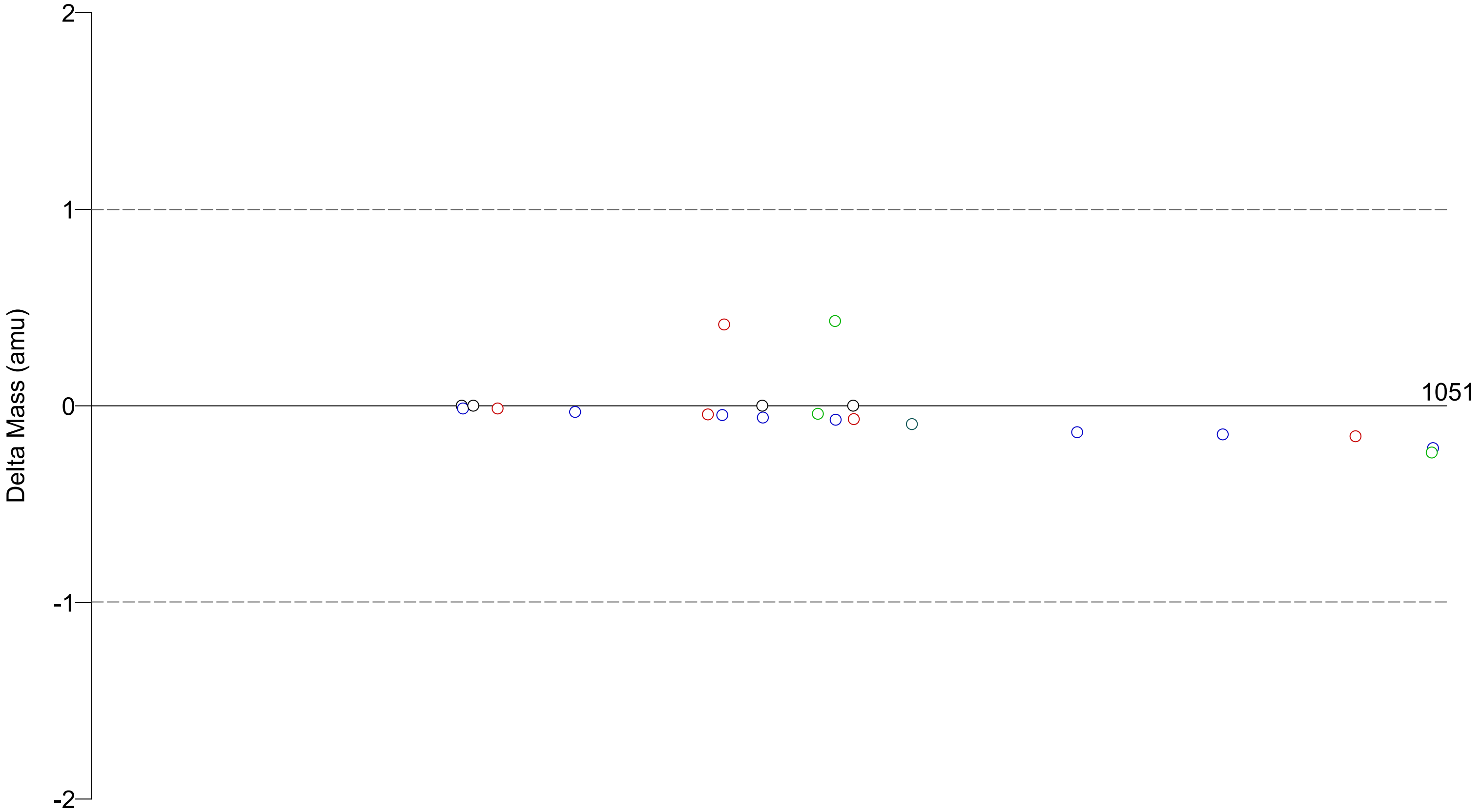


#19287468-1 NL: 8.93E4

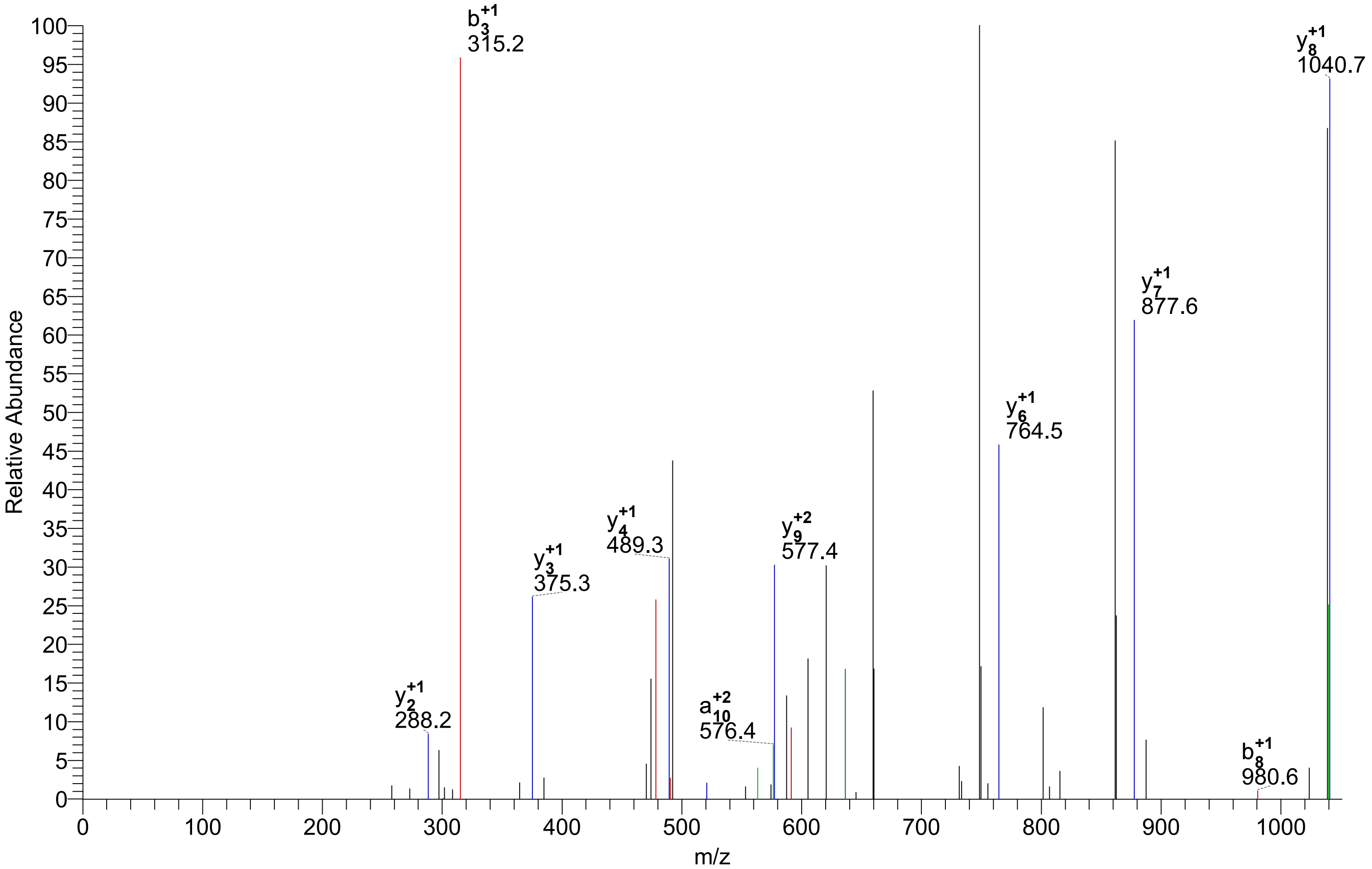


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z   P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00827690.1|TREMBL:A2NWX2 Ta                                0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                      1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

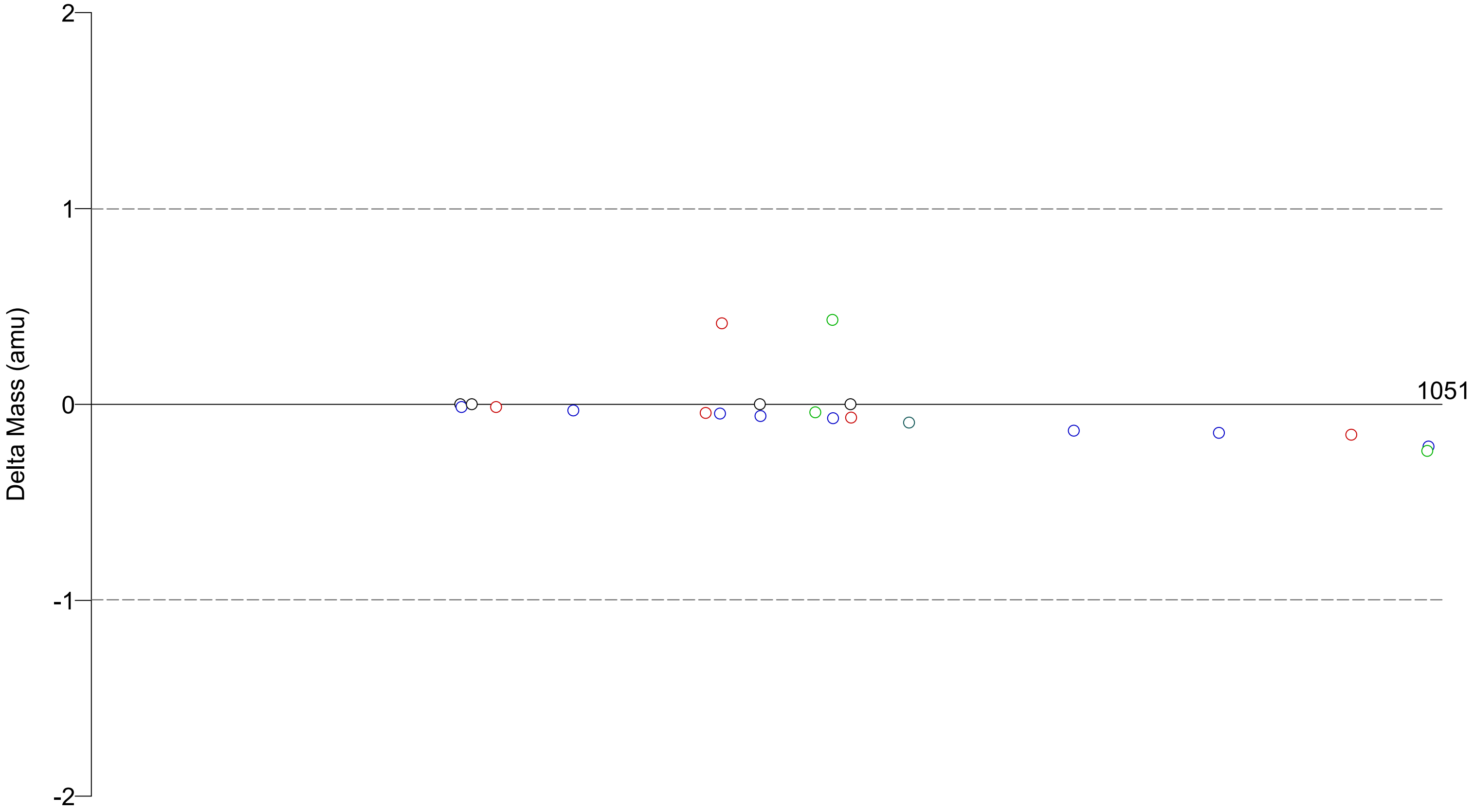


#19287468-1 NL: 8.93E4

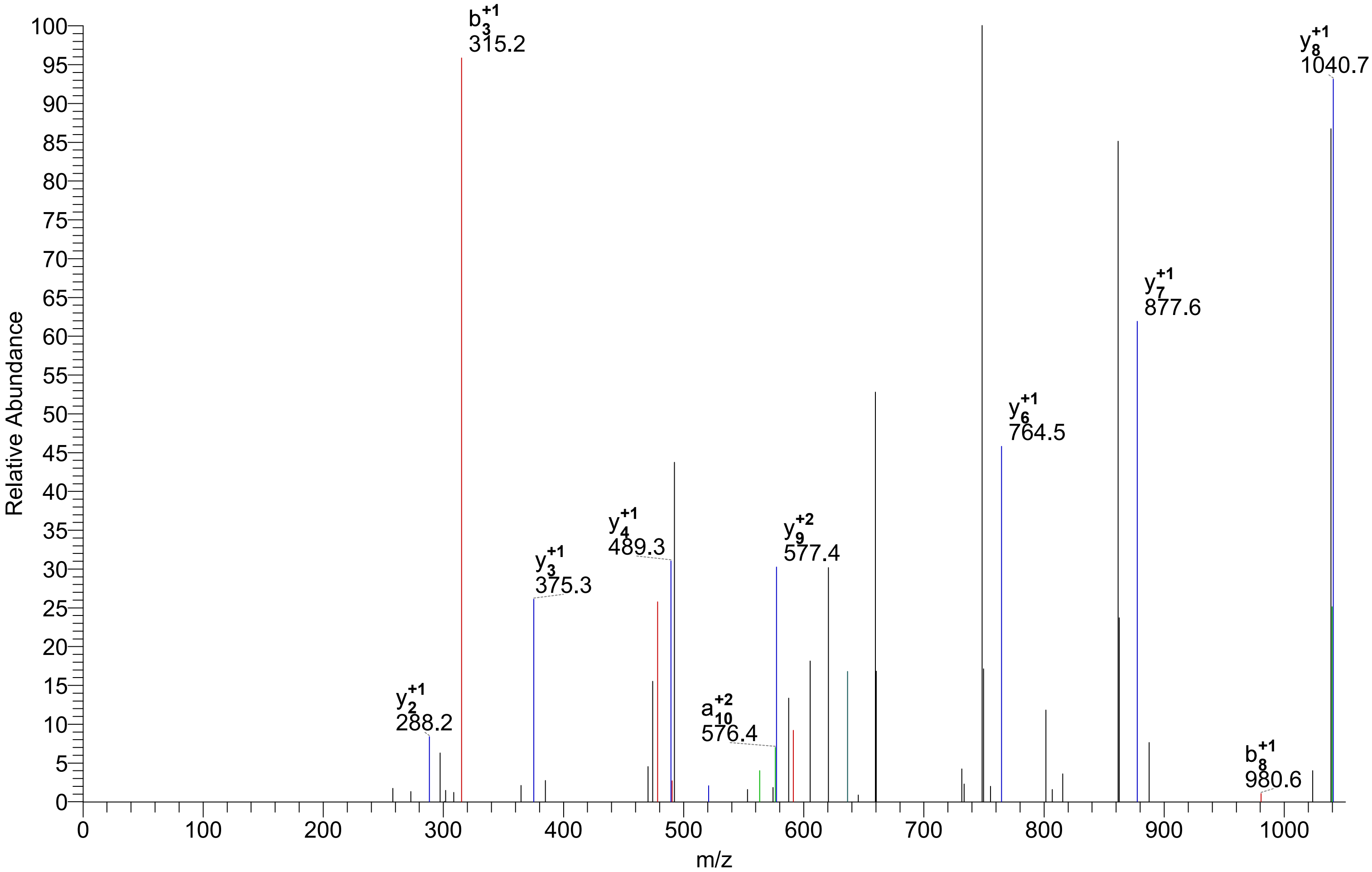


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+     z    P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00827733.1|TREMBL:A2NWX3 Ta                                0.1     8.1     0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                      1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                    1240.64
 L    287.17     315.17                                    1153.60
 Y    450.23     478.23                                    1040.52
 L    563.32     591.31                                     877.46
 Q    691.38     719.37                                     764.37
 M*   838.41     866.41                                     636.31
 N    952.46     980.45                                     489.28
 S   1039.49    1067.48                                     375.24
 L   1152.57    1180.57                                     288.20
 R                                                          175.12
```

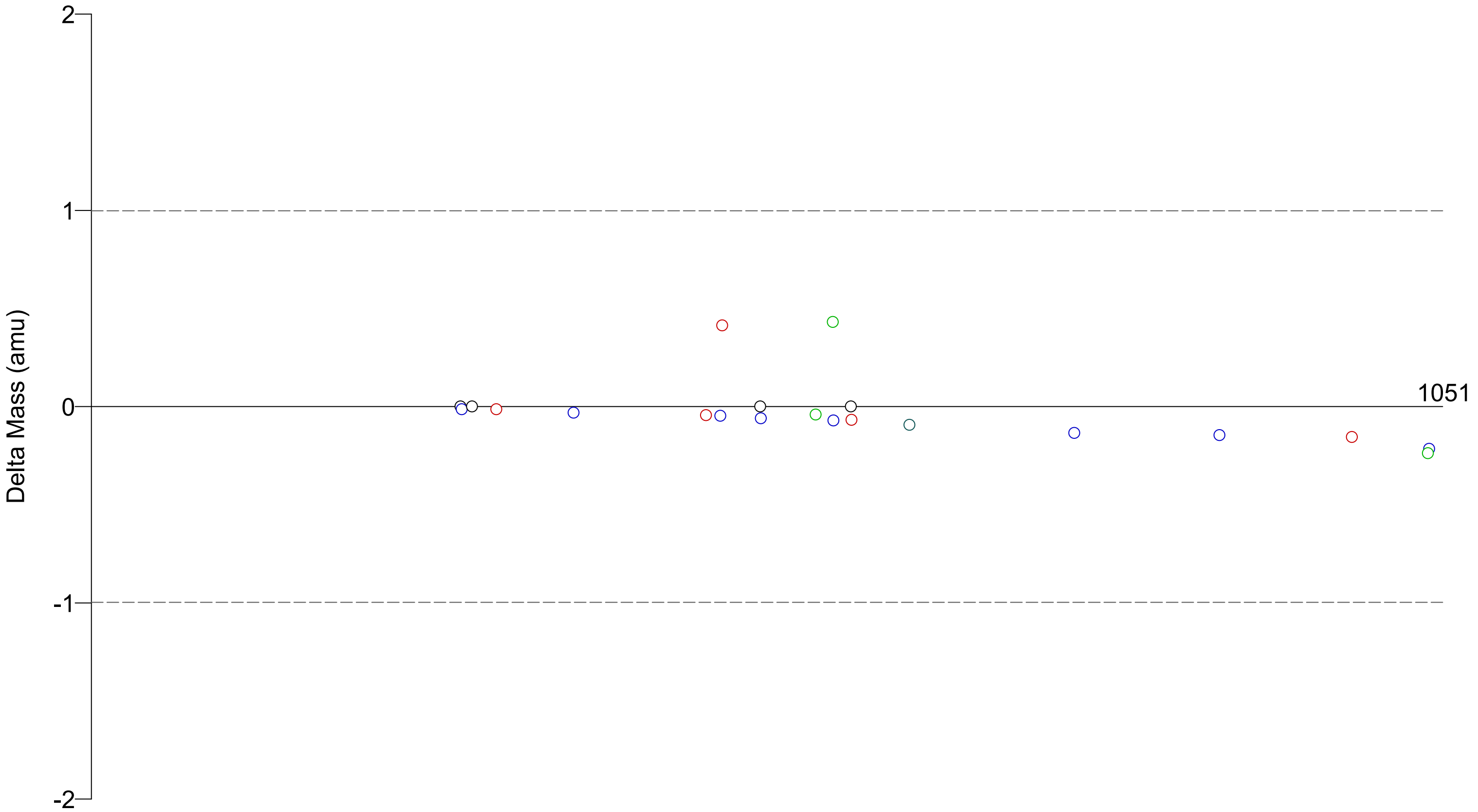


#19287468-1 NL: 8.93E4

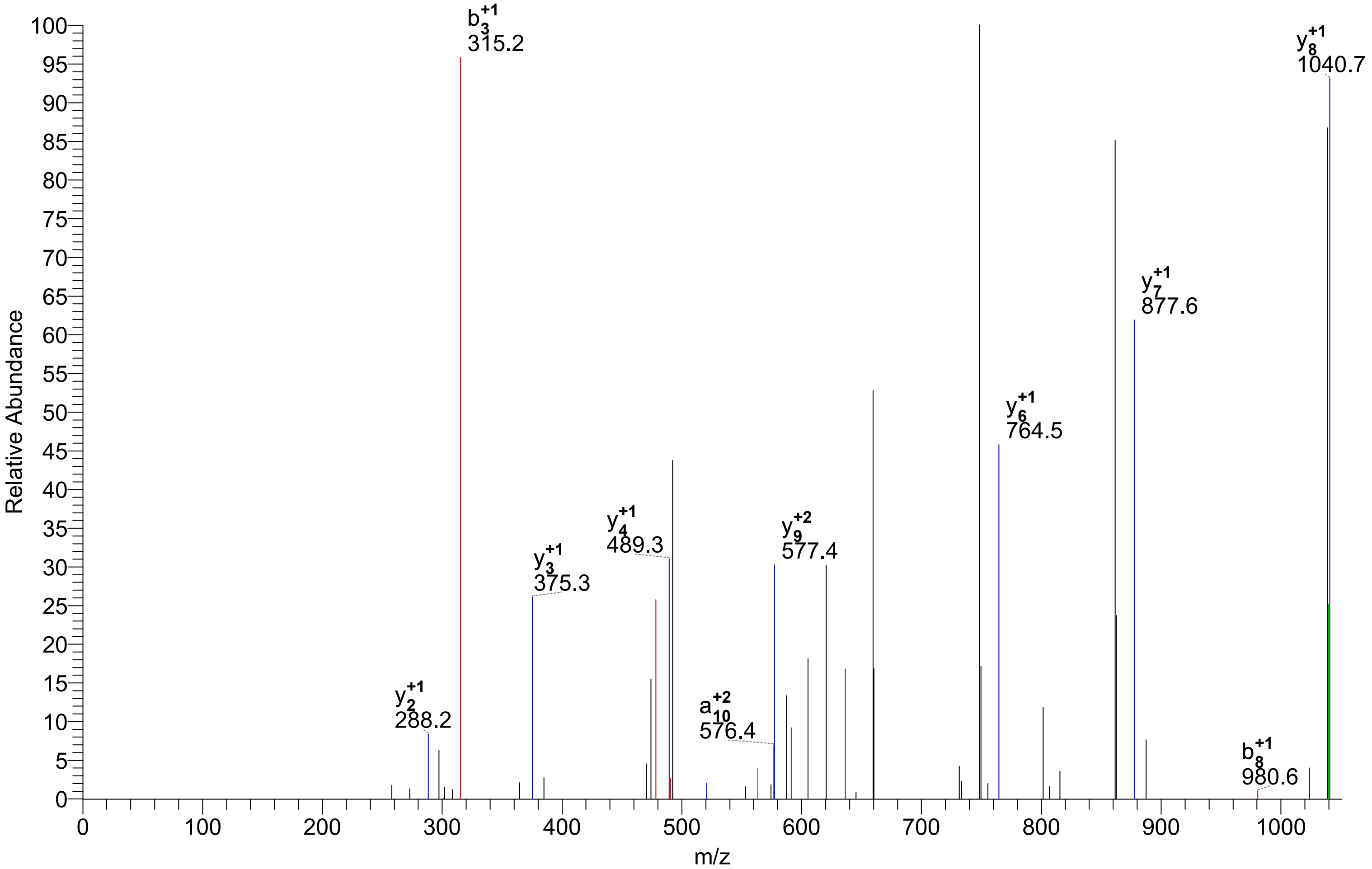


```
Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829752.1|TREMBL:A6NK61|EN                                0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

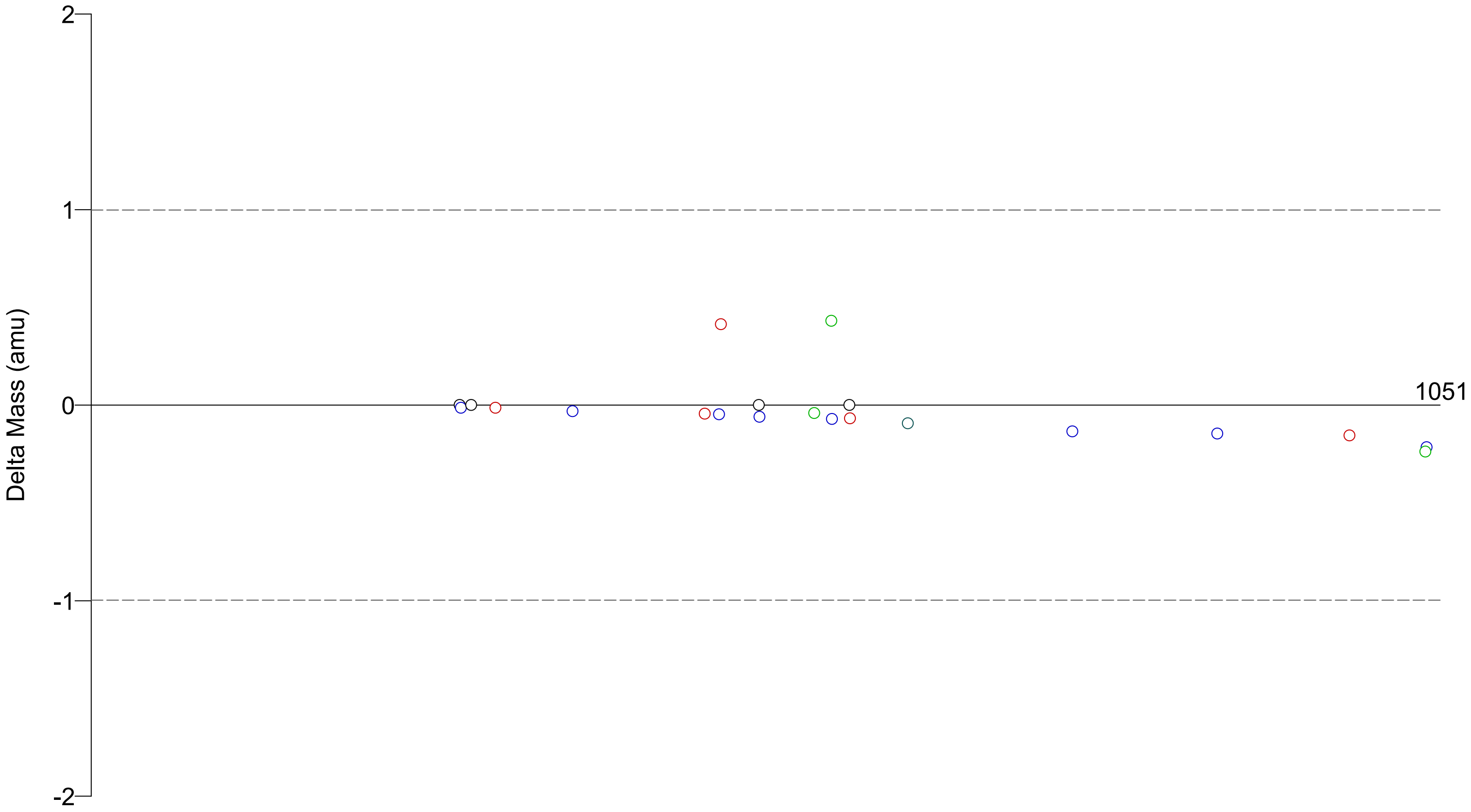


#19287468-1 NL: 8.93E4

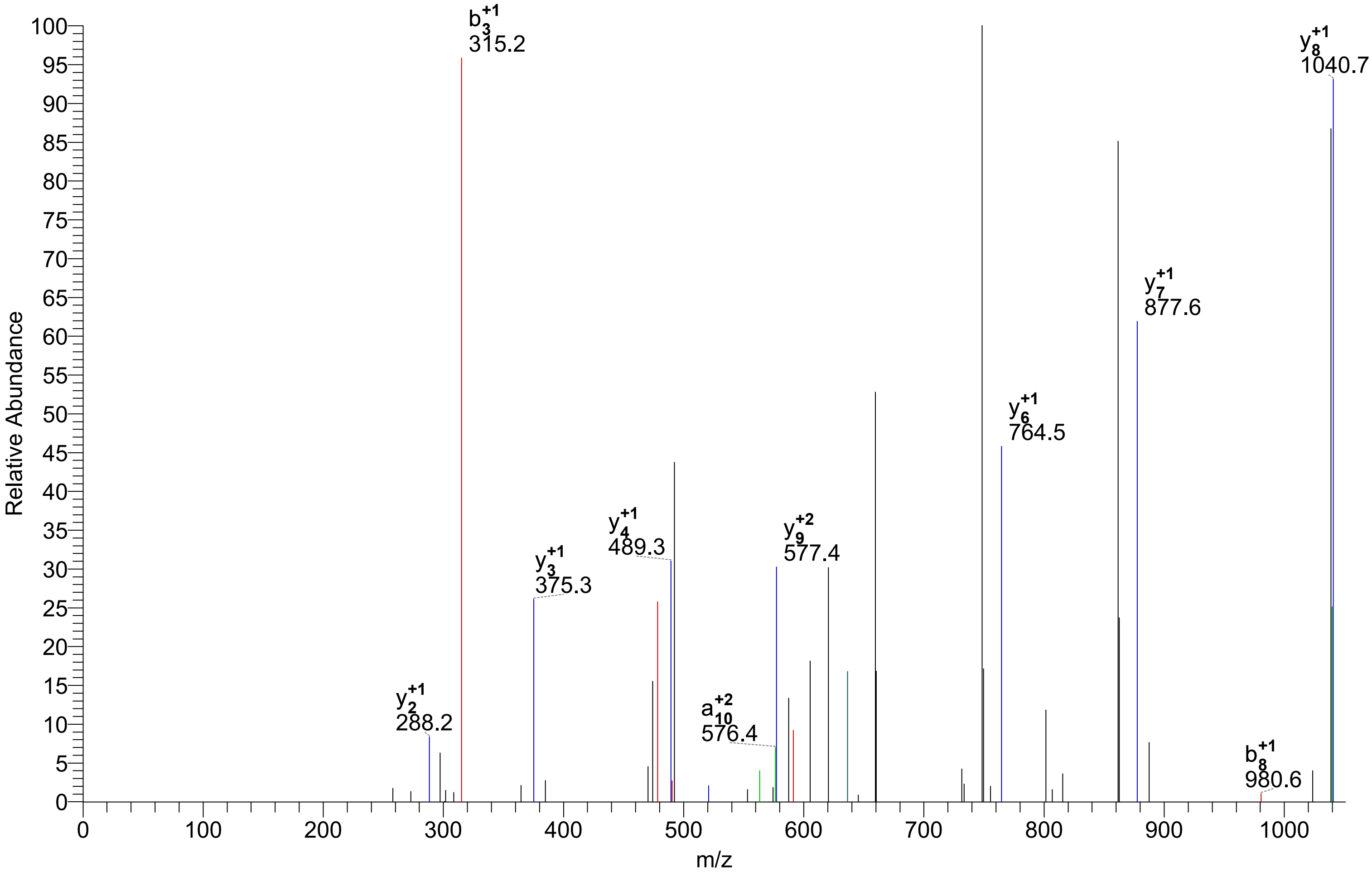


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)        Sequence                                 MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00829812.2|TREMBL:A6NHF5|EN                                 0.1      8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                        1354.68   2  0.002    2.168  0.118    607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions     Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                      1240.64
 L    287.17     315.17                                      1153.60
 Y    450.23     478.23                                      1040.52
 L    563.32     591.31                                       877.46
 Q    691.38     719.37                                       764.37
 M*   838.41     866.41                                       636.31
 N    952.46     980.45                                       489.28
 S   1039.49    1067.48                                       375.24
 L   1152.57    1180.57                                       288.20
 R                                                            175.12
```

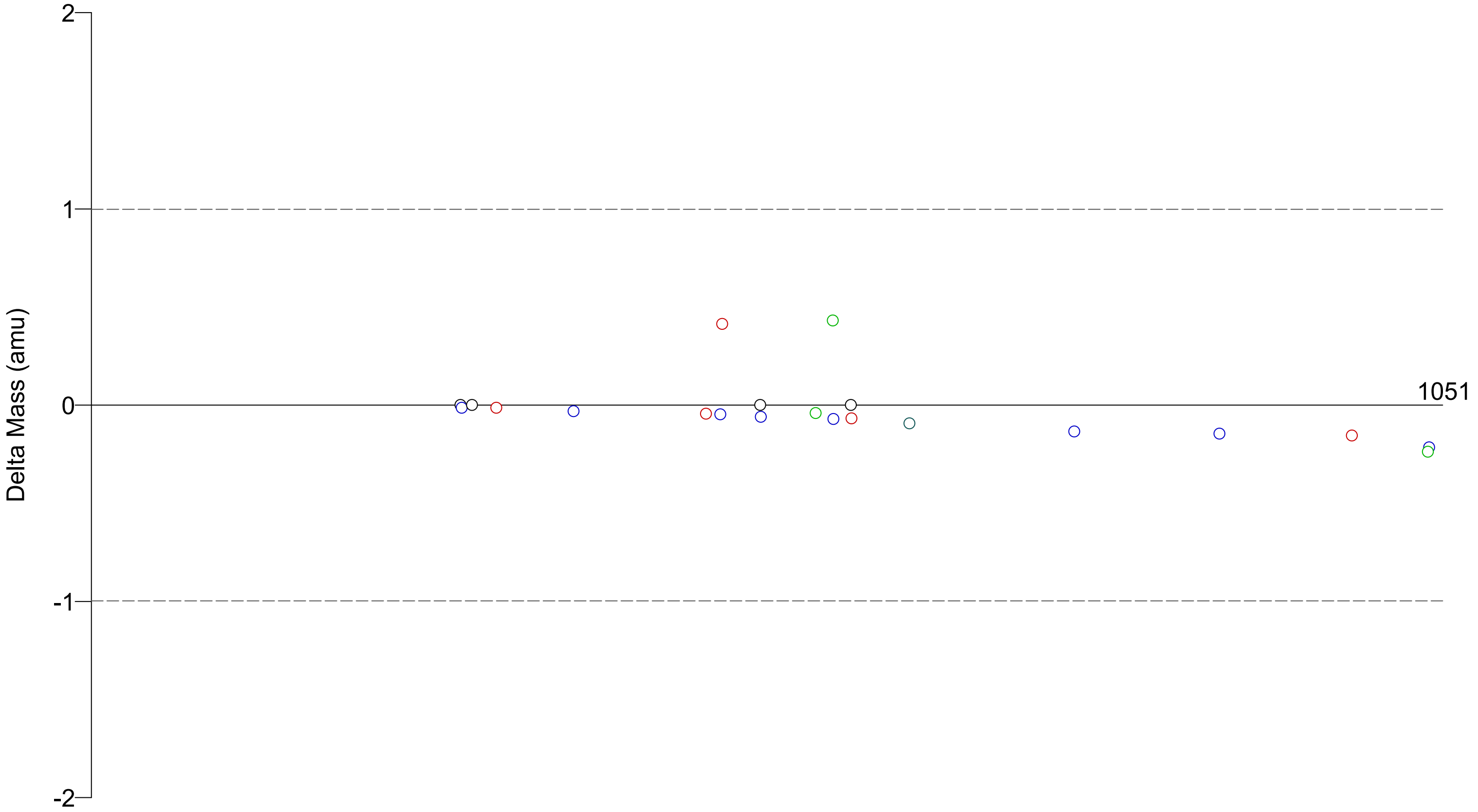


#19287468-1 NL: 8.93E4

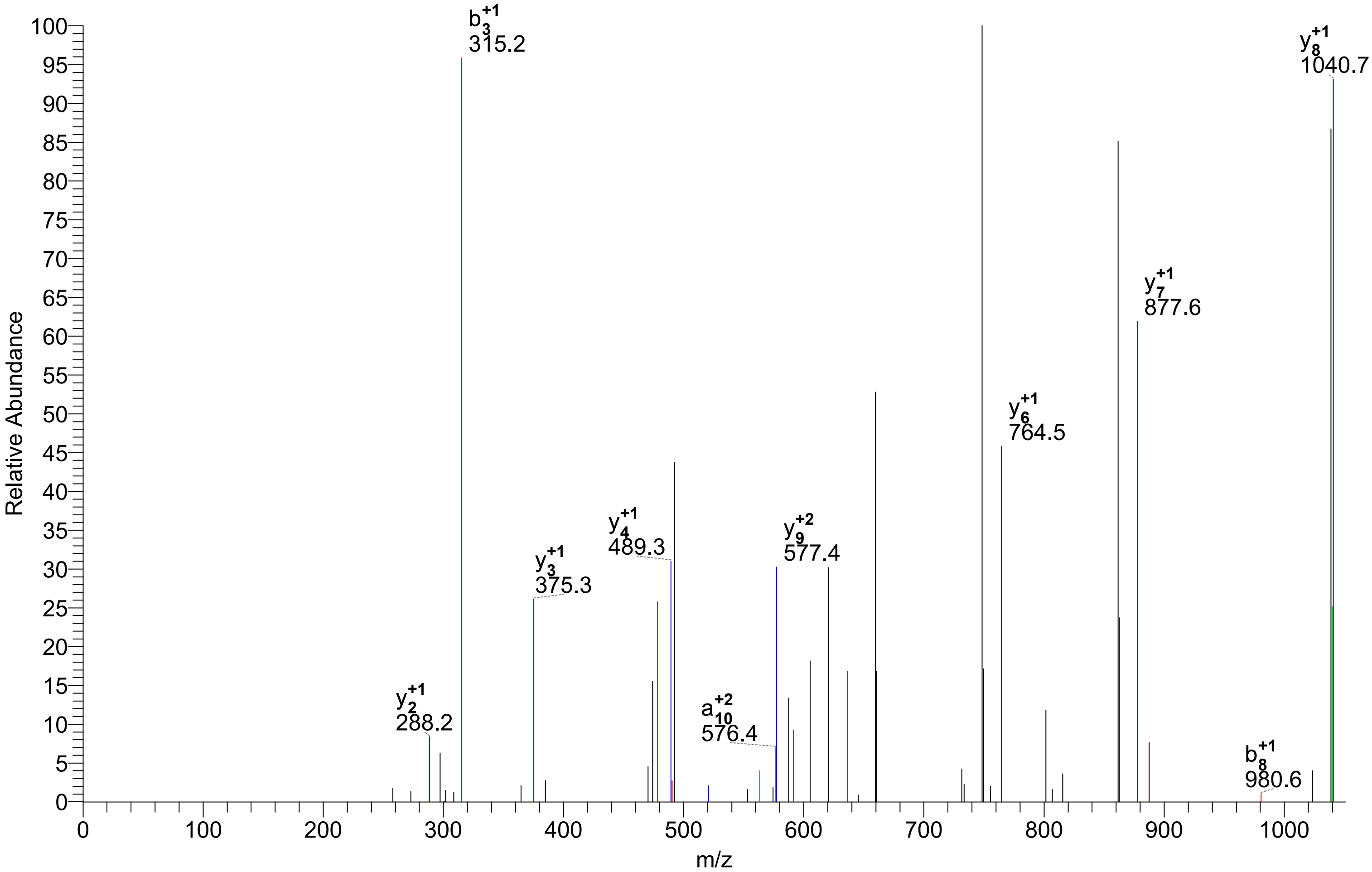


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00854667.1|TREMBL:A6NKU8|EN                                   0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68    2  0.002    2.168  0.118    607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

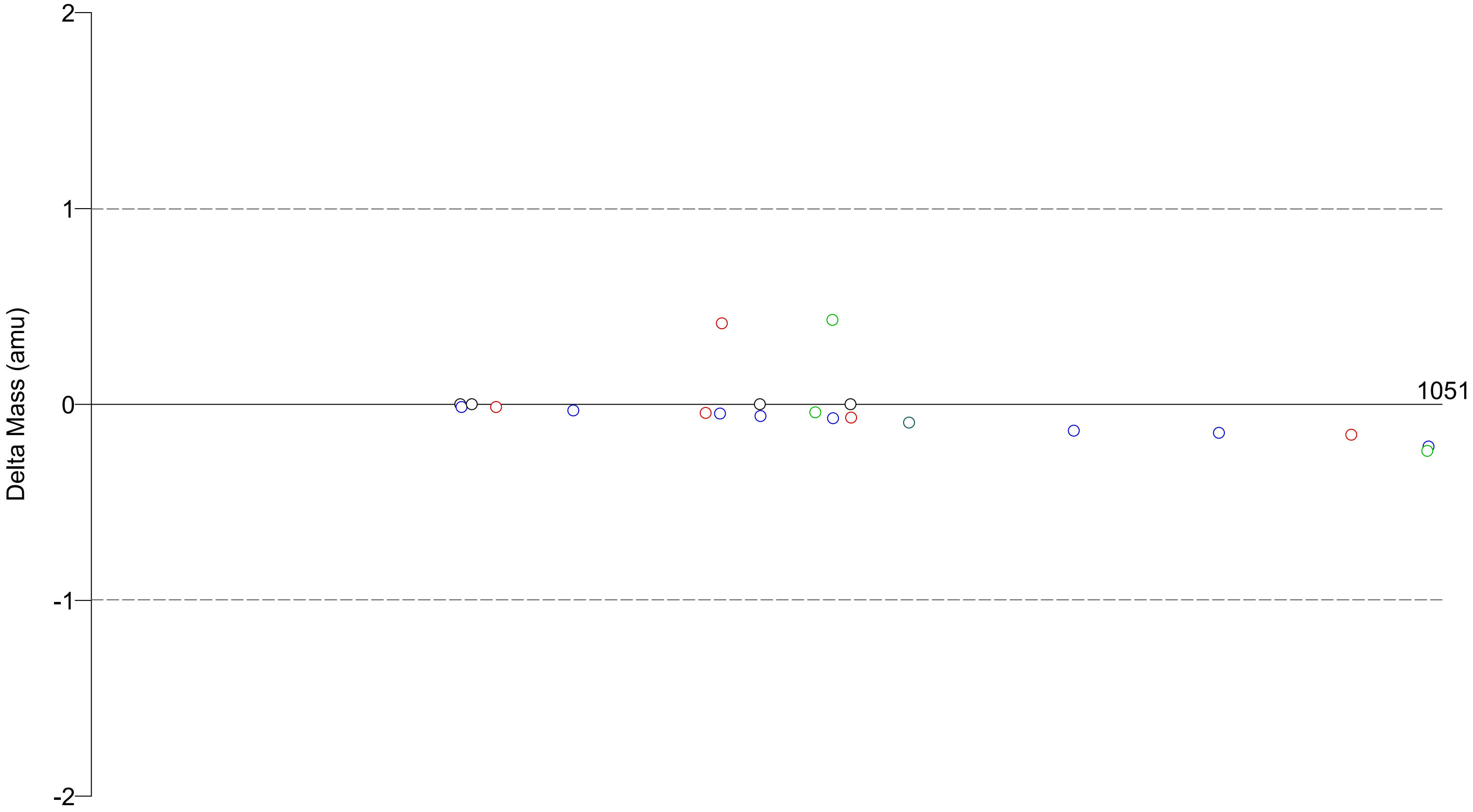


#19287468-1 NL: 8.93E4

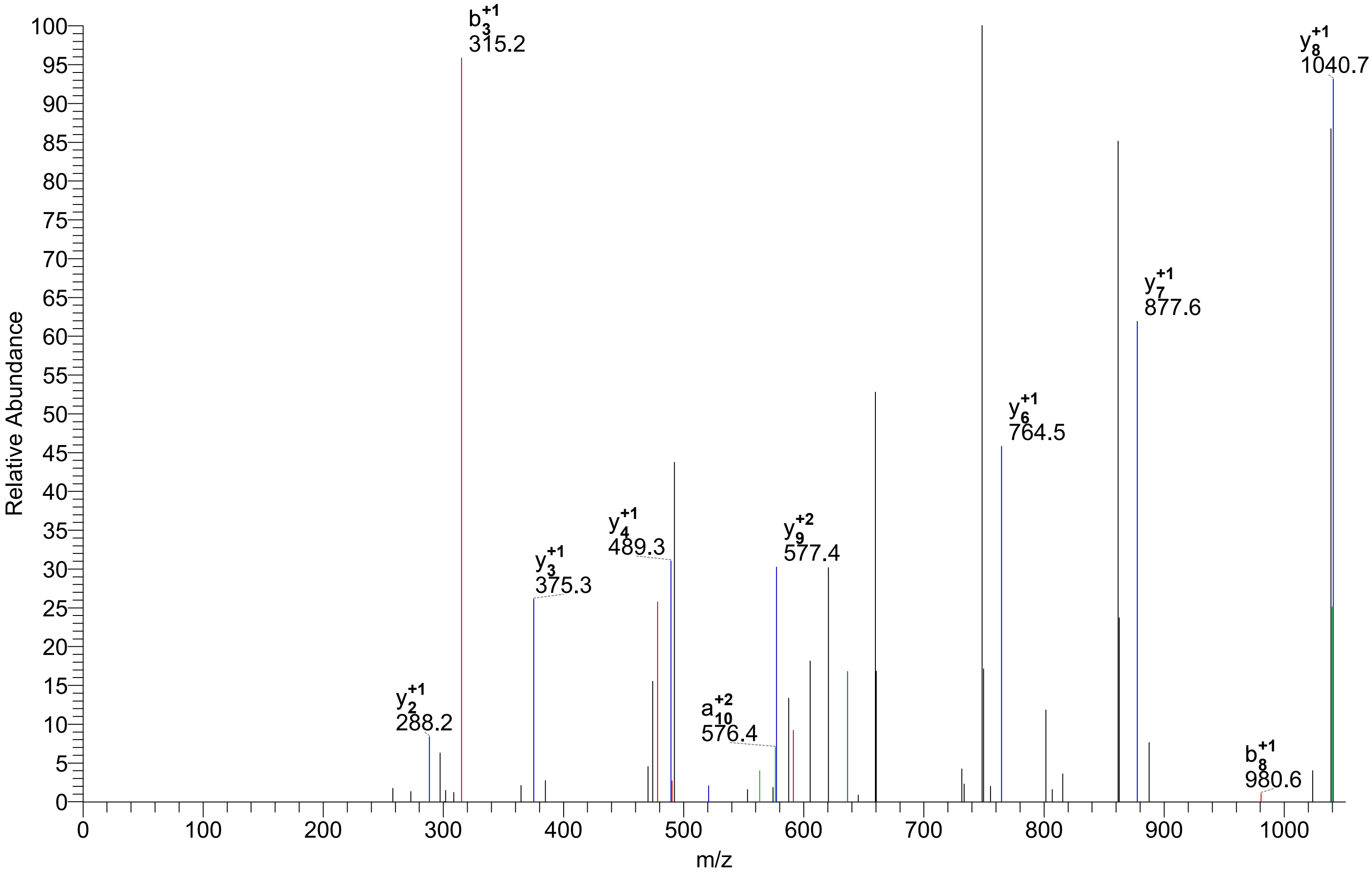


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00854841.1|TREMBL:A6NL39|EN                                 0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                         1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

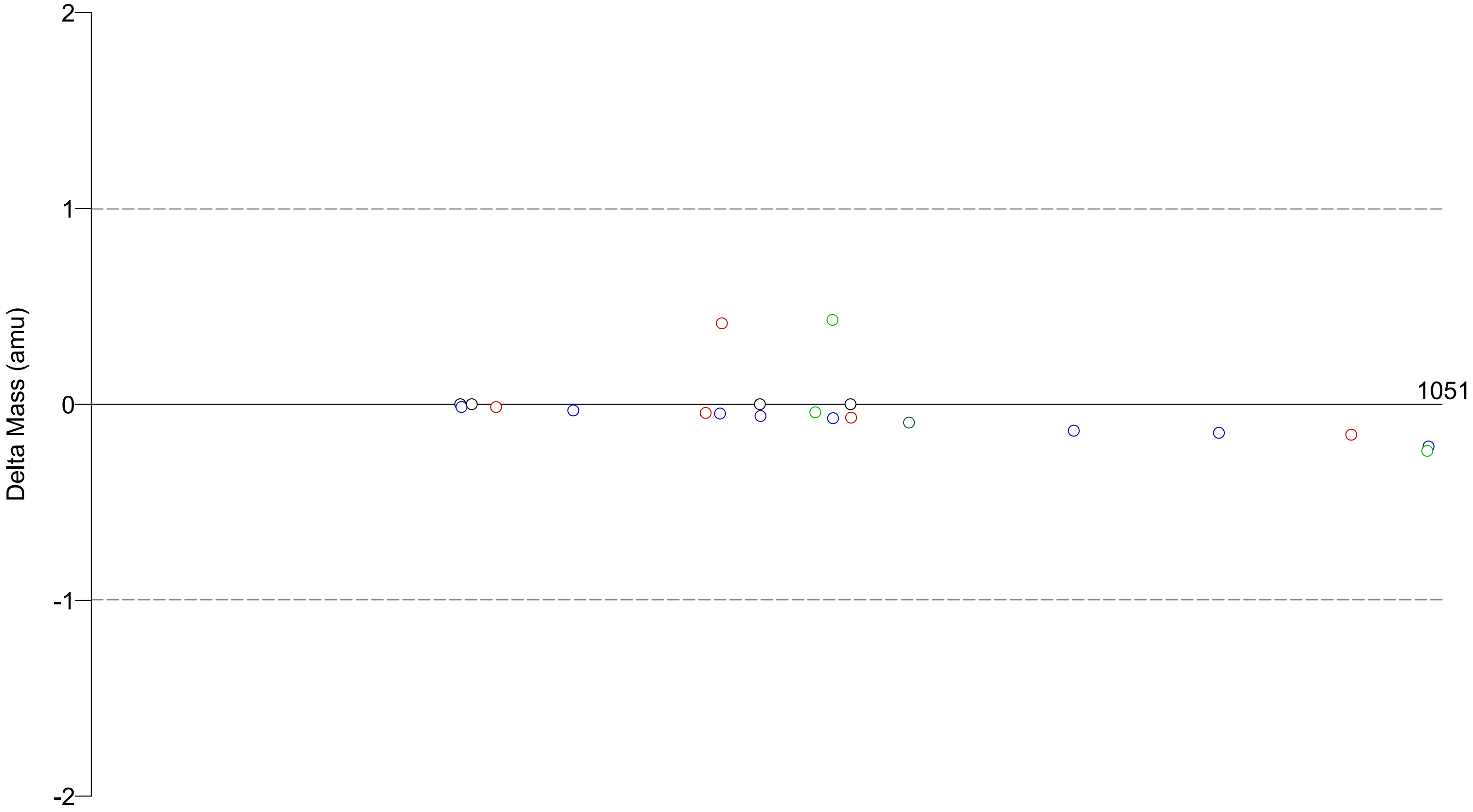


#19287468-1 NL: 8.93E4

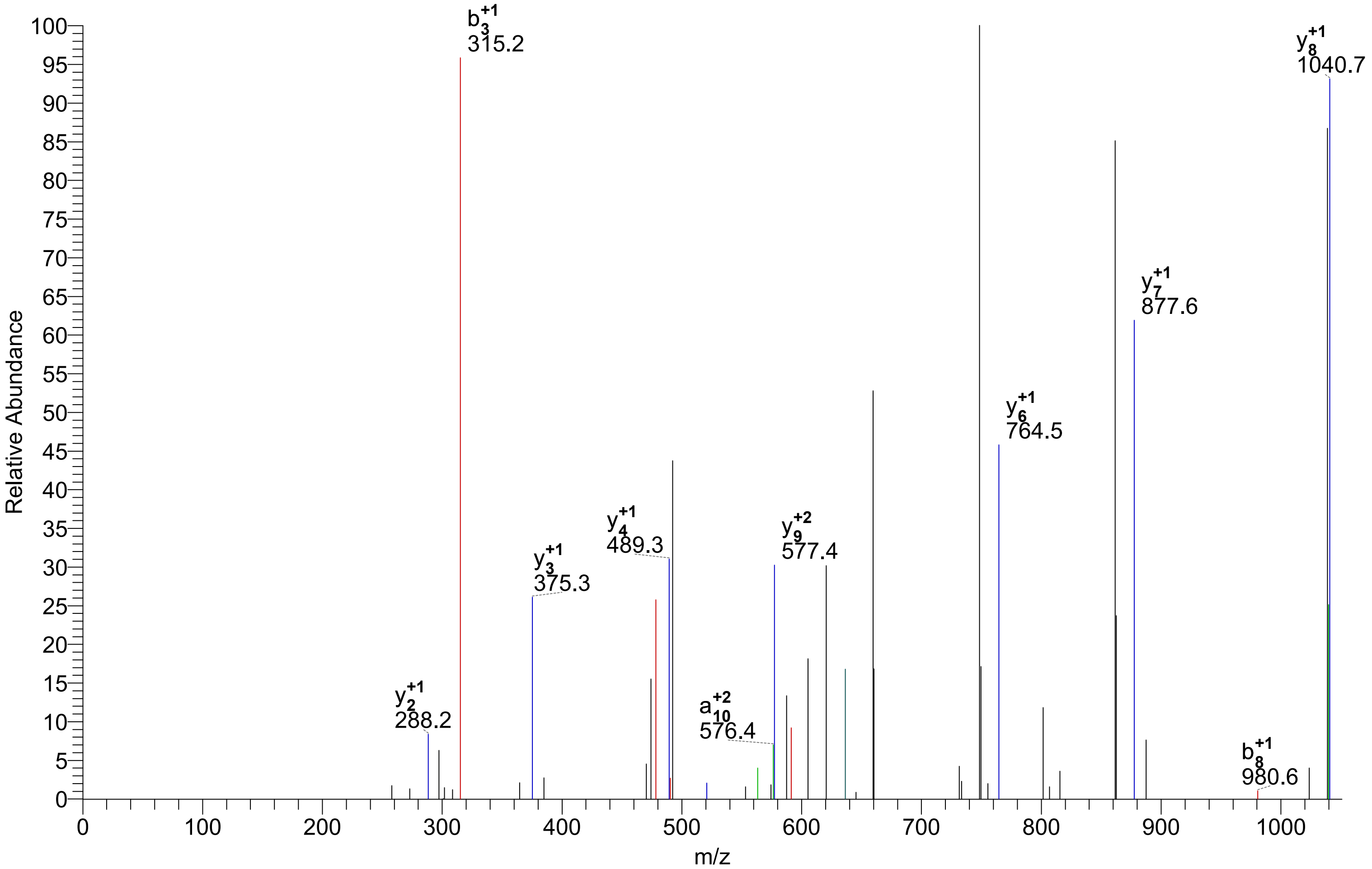


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00884078.2|TREMBL:A2J1N2|EN                                       0.1      8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                            1354.68   2  0.002    2.168  0.118    607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                      1240.64
 L    287.17     315.17                                      1153.60
 Y    450.23     478.23                                      1040.52
 L    563.32     591.31                                       877.46
 Q    691.38     719.37                                       764.37
 M*   838.41     866.41                                       636.31
 N    952.46     980.45                                       489.28
 S   1039.49    1067.48                                       375.24
 L   1152.57    1180.57                                       288.20
 R                                                            175.12
```

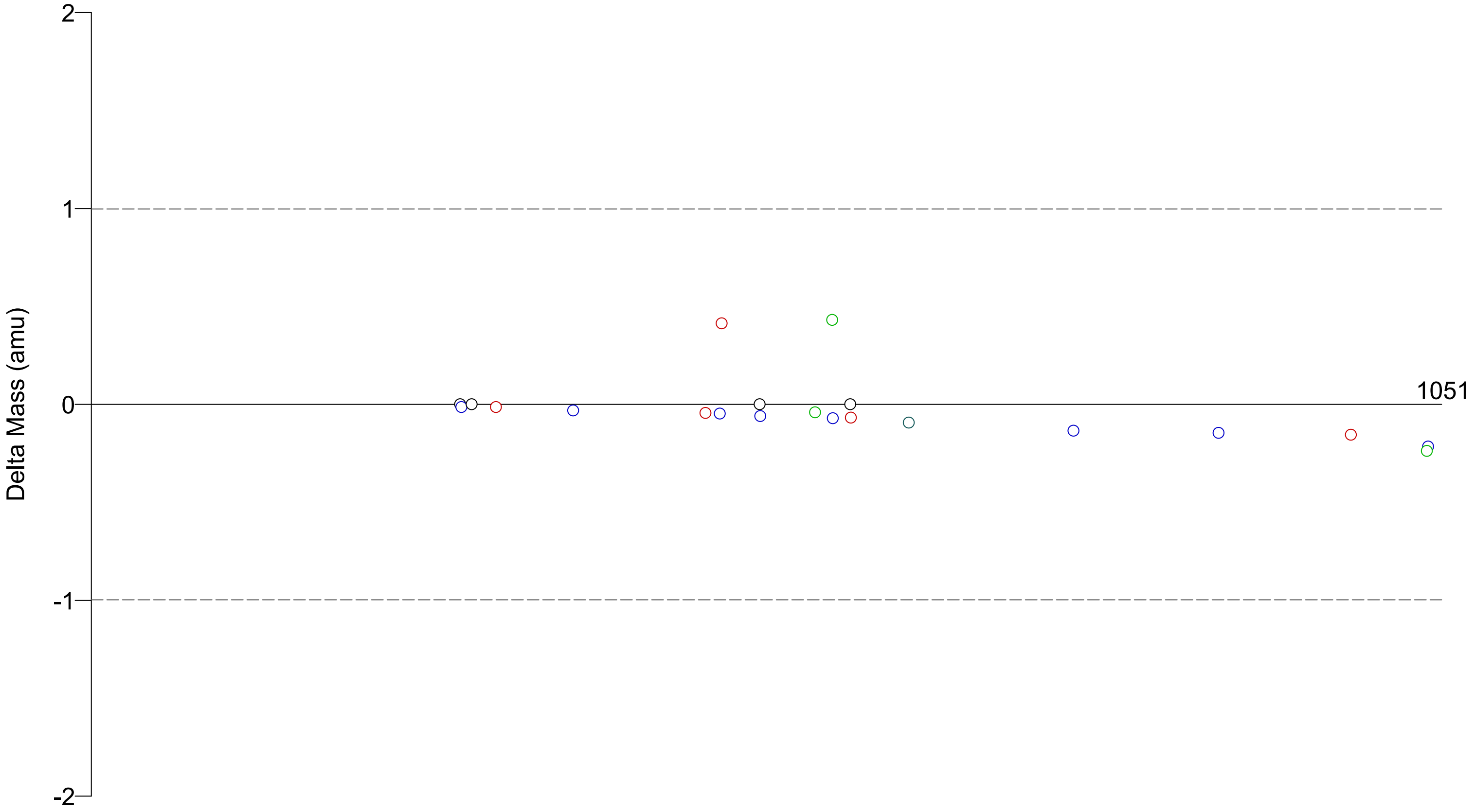


#19287468-1 NL: 8.93E4

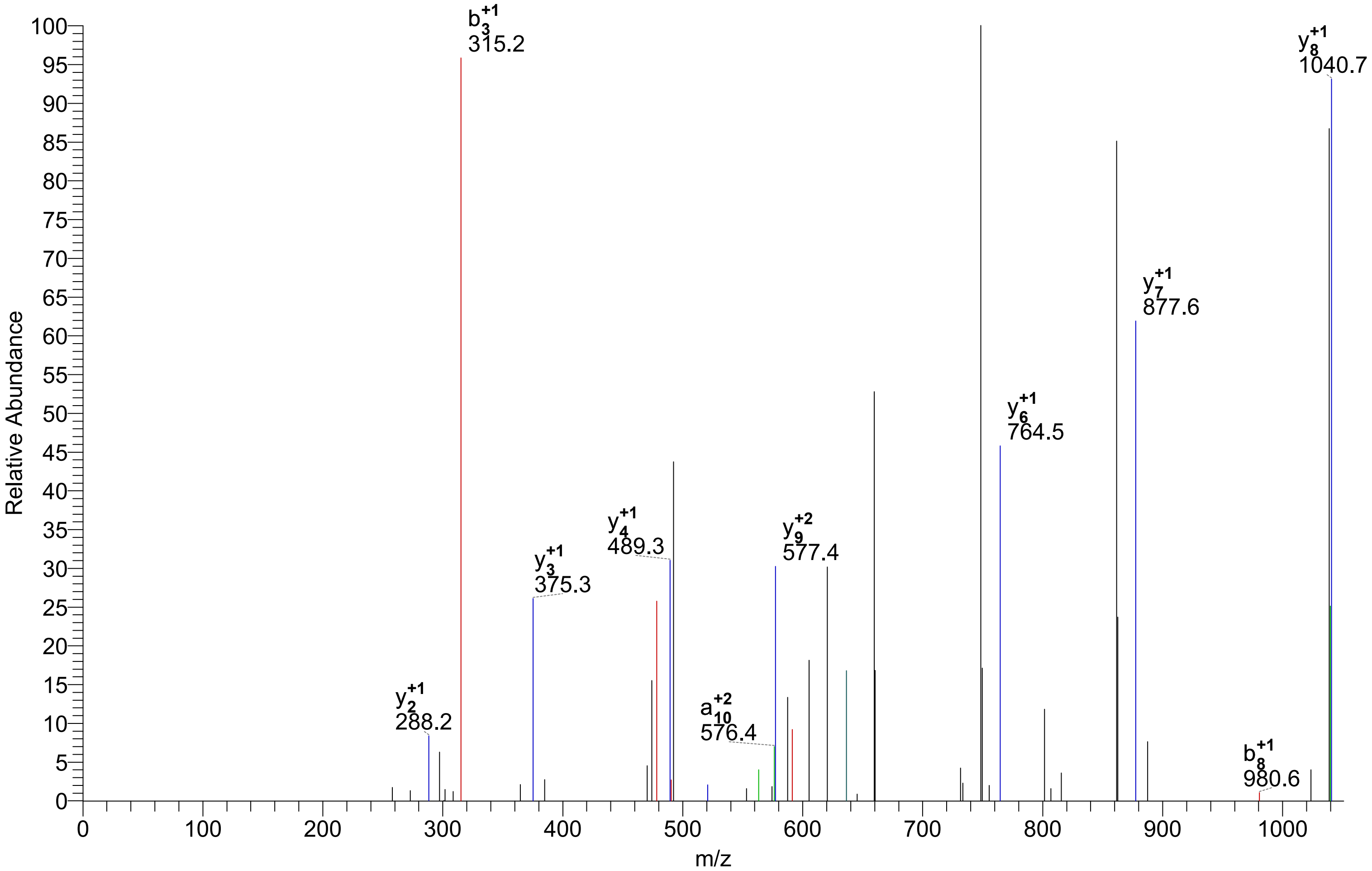


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)        Sequence                                      MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00884183.1|TREMBL:Q9ULB6 Ta                                    0.1     8.1      0.0        0
19287468 - 1  K.NSLYLQM*NSLR.A                            1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

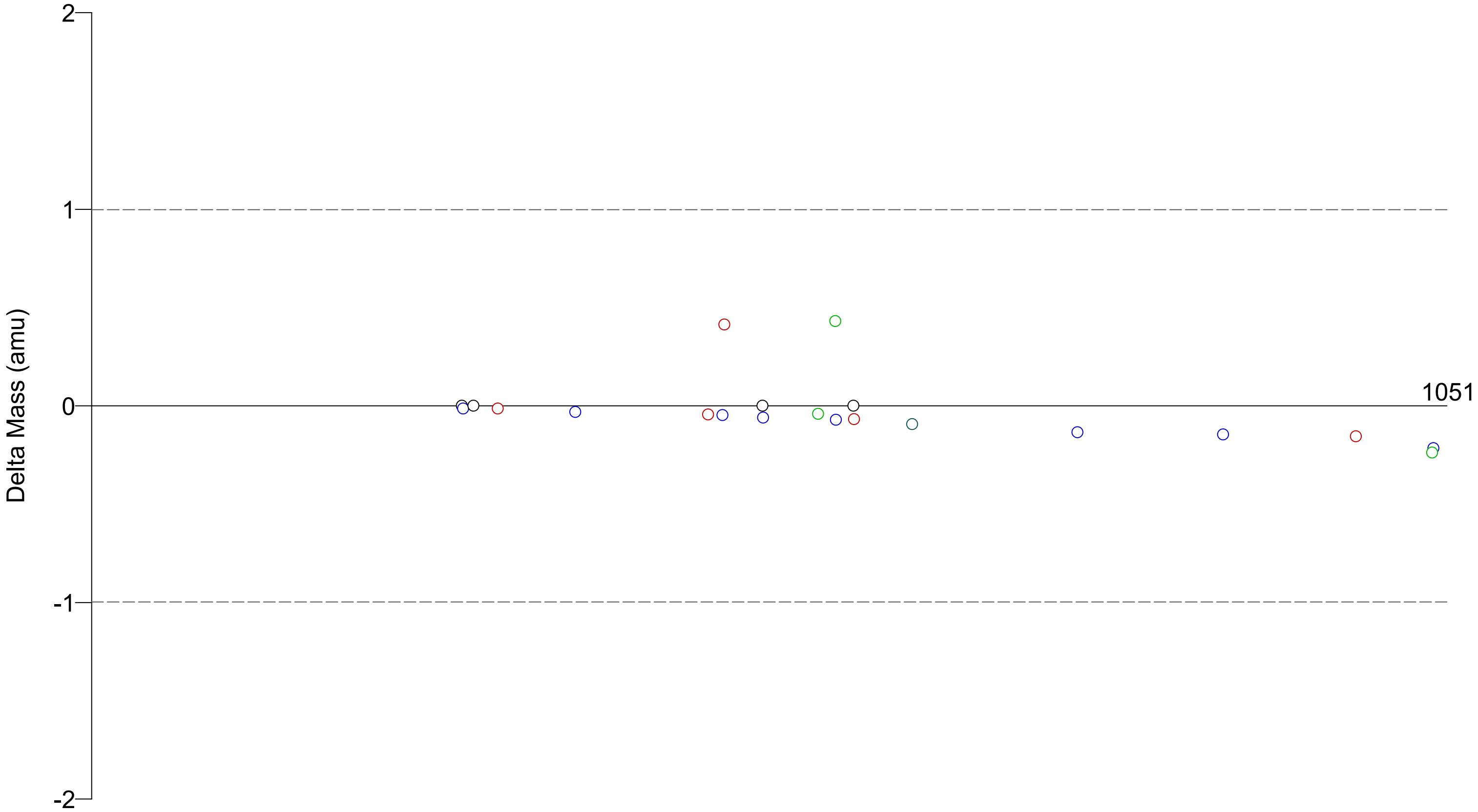


#19287468-1 NL: 8.93E4

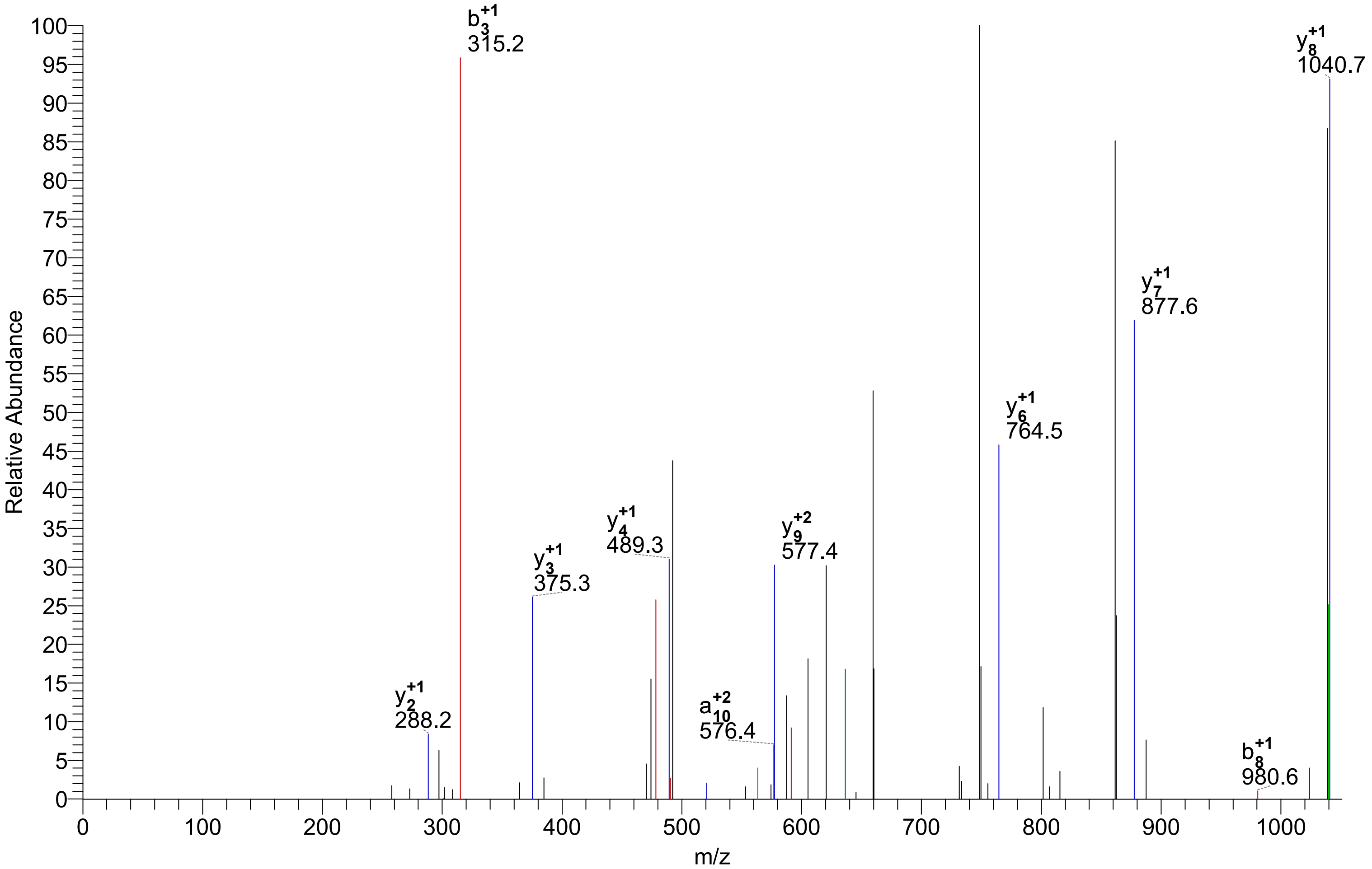


```
Reference                                                    P      Score   Coverage   Accession
Scan(s)        Sequence                         MH+       z   P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00894177.2|TREMBL:Q9UL87|VE                            0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                1354.68   2  0.002    2.168  0.118    607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

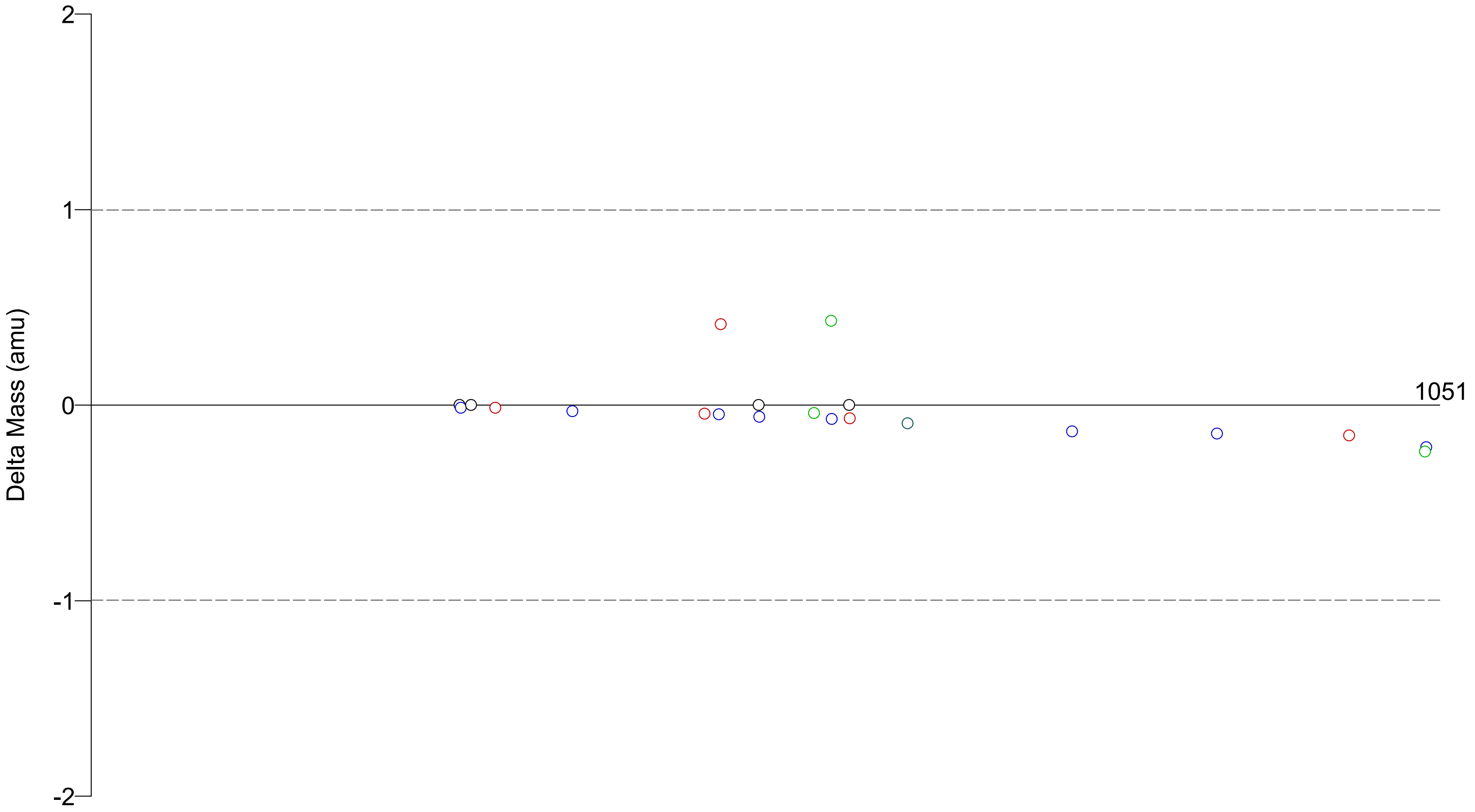


#19287468-1 NL: 8.93E4

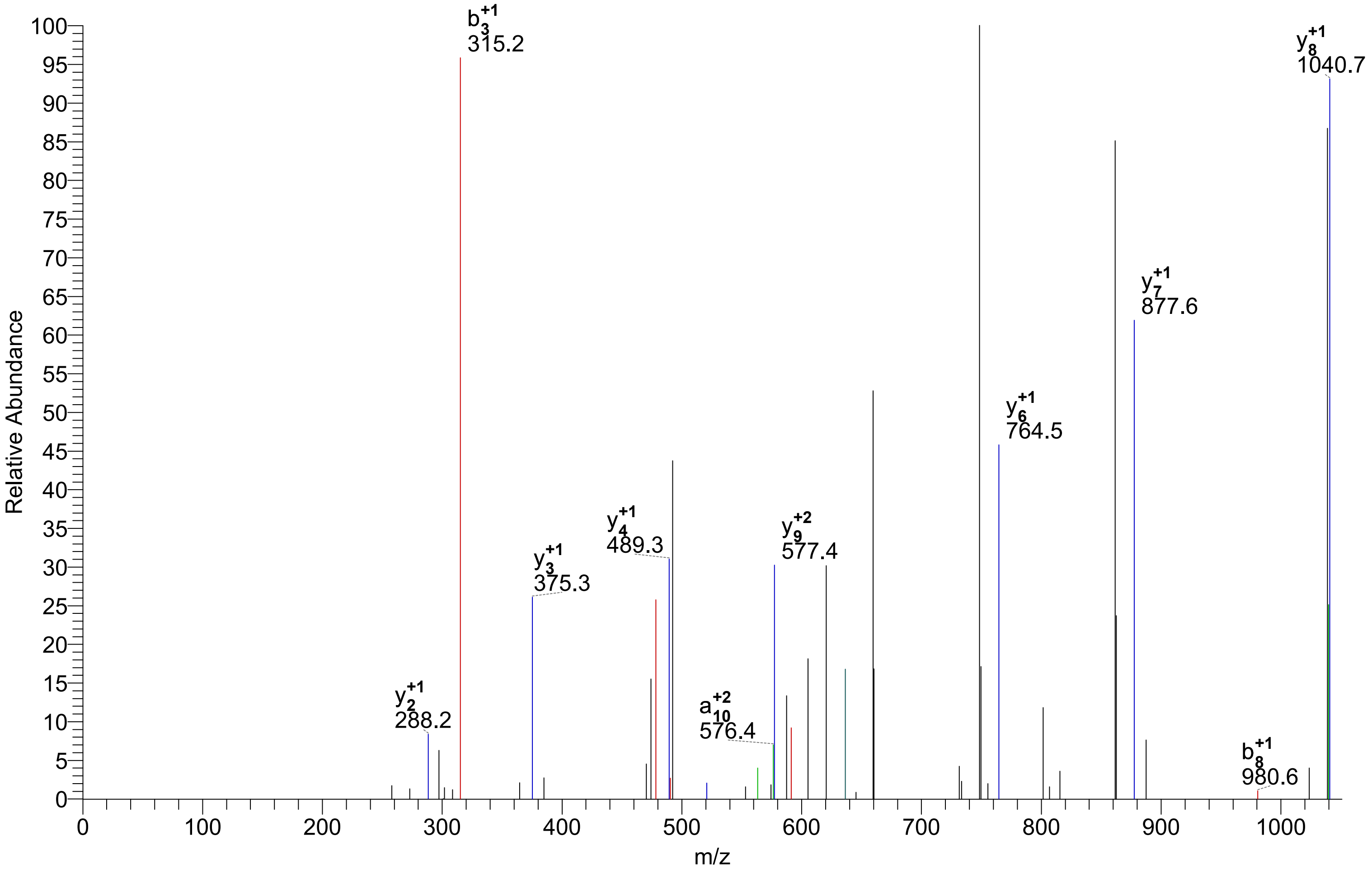


```
Reference                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                            MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00914985.1|TREMBL:B6EDE2 Ta                            0.1      8.1      0.0        0
19287468 - 1  K.NSLYLQM*NSLR.A                 1354.68    2  0.002    2.168  0.118    607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

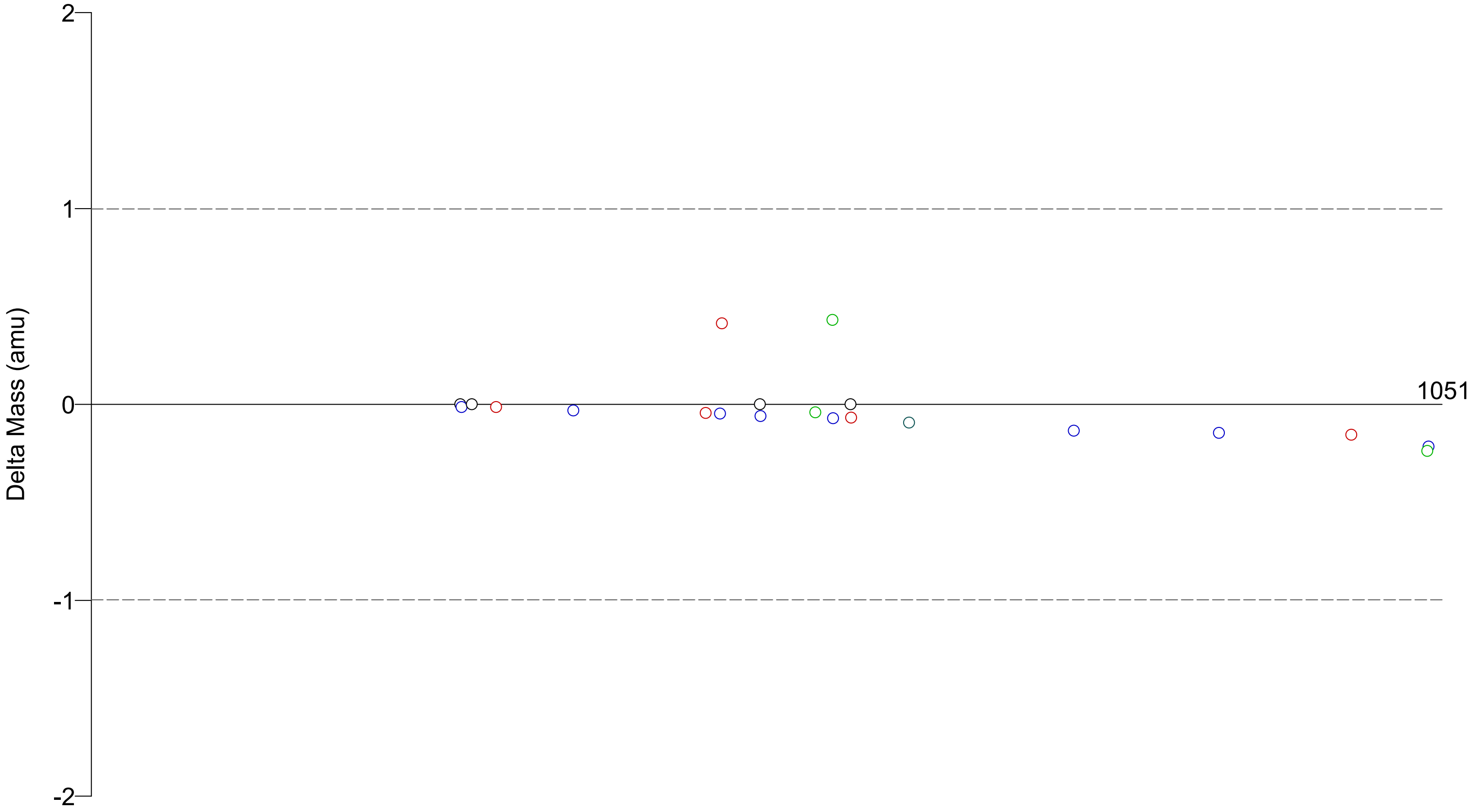


#19287468-1 NL: 8.93E4

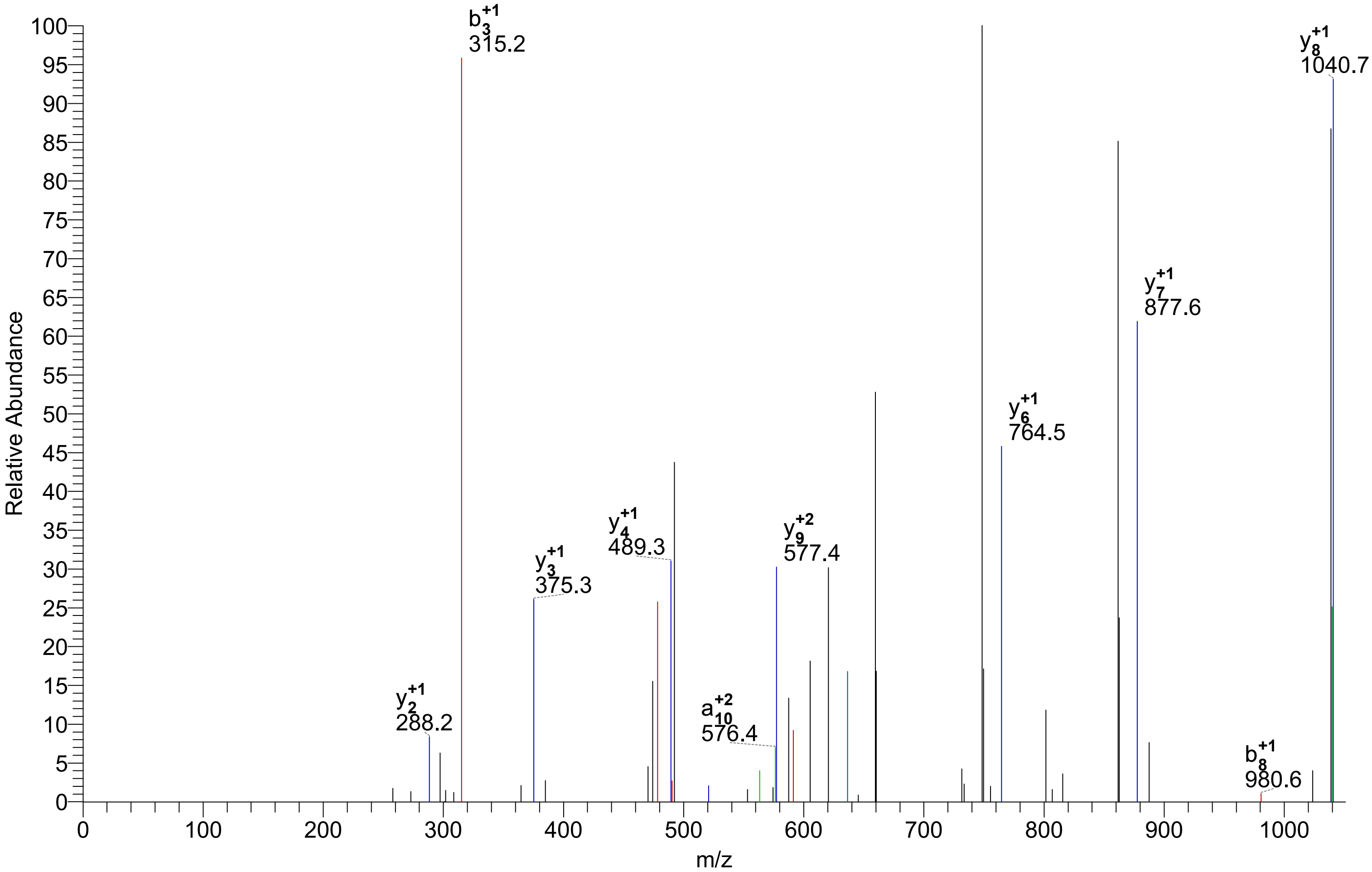


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00915820.1|TREMBL:A2NYQ9 Ta                                       0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                             1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

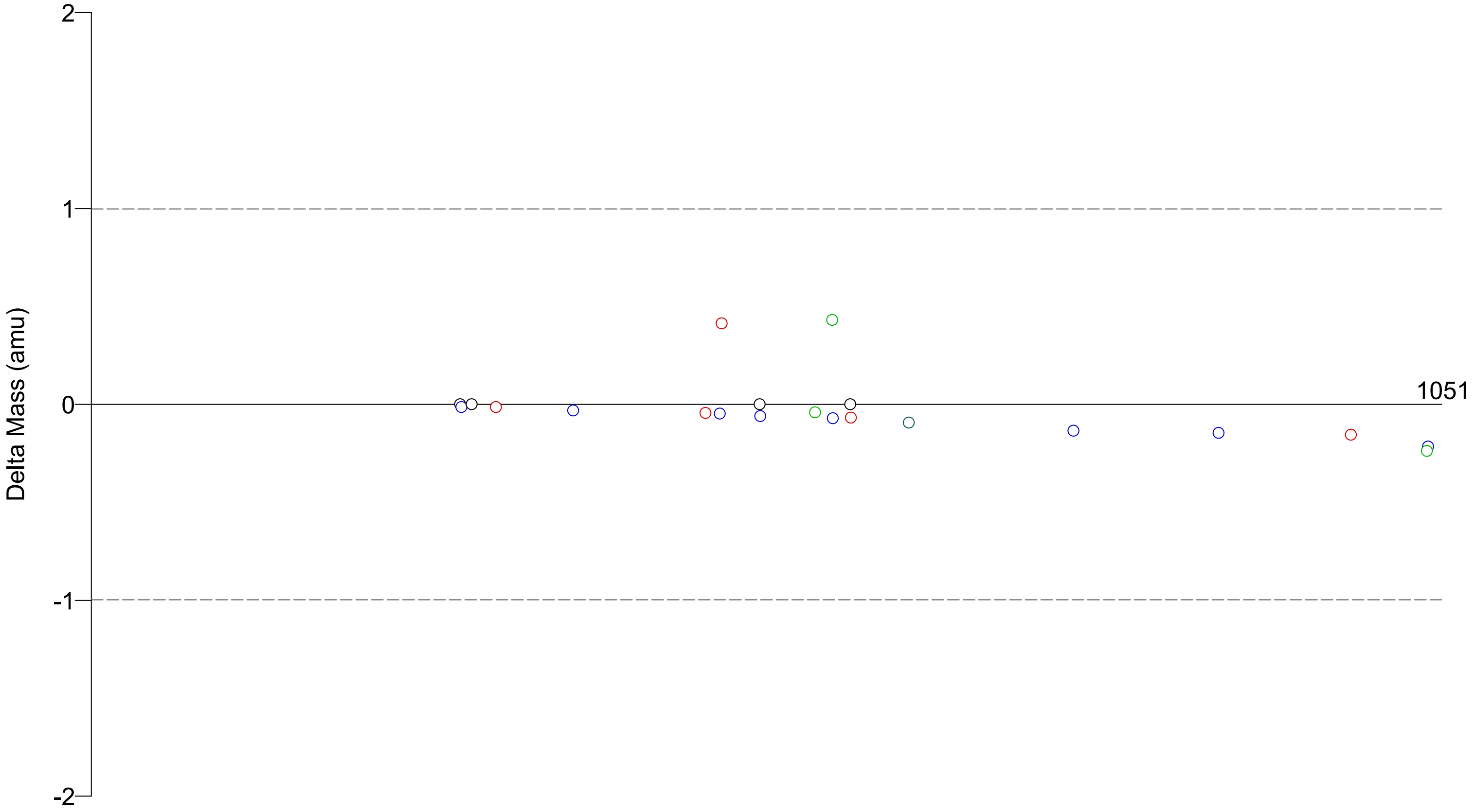


#19287468-1 NL: 8.93E4

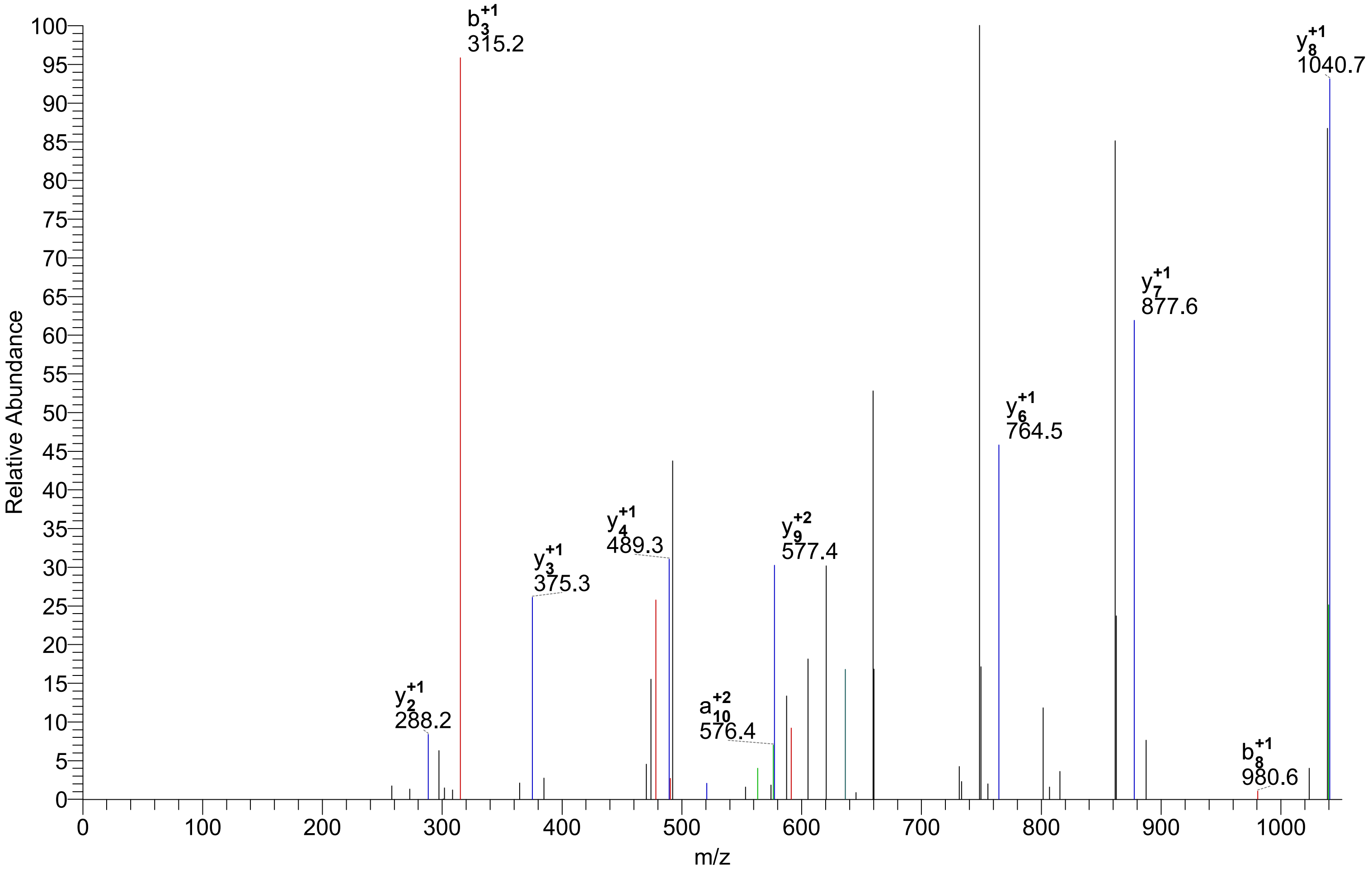


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00936563.1|ENSEMBL:ENSP0000                                  0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68    2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
-----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

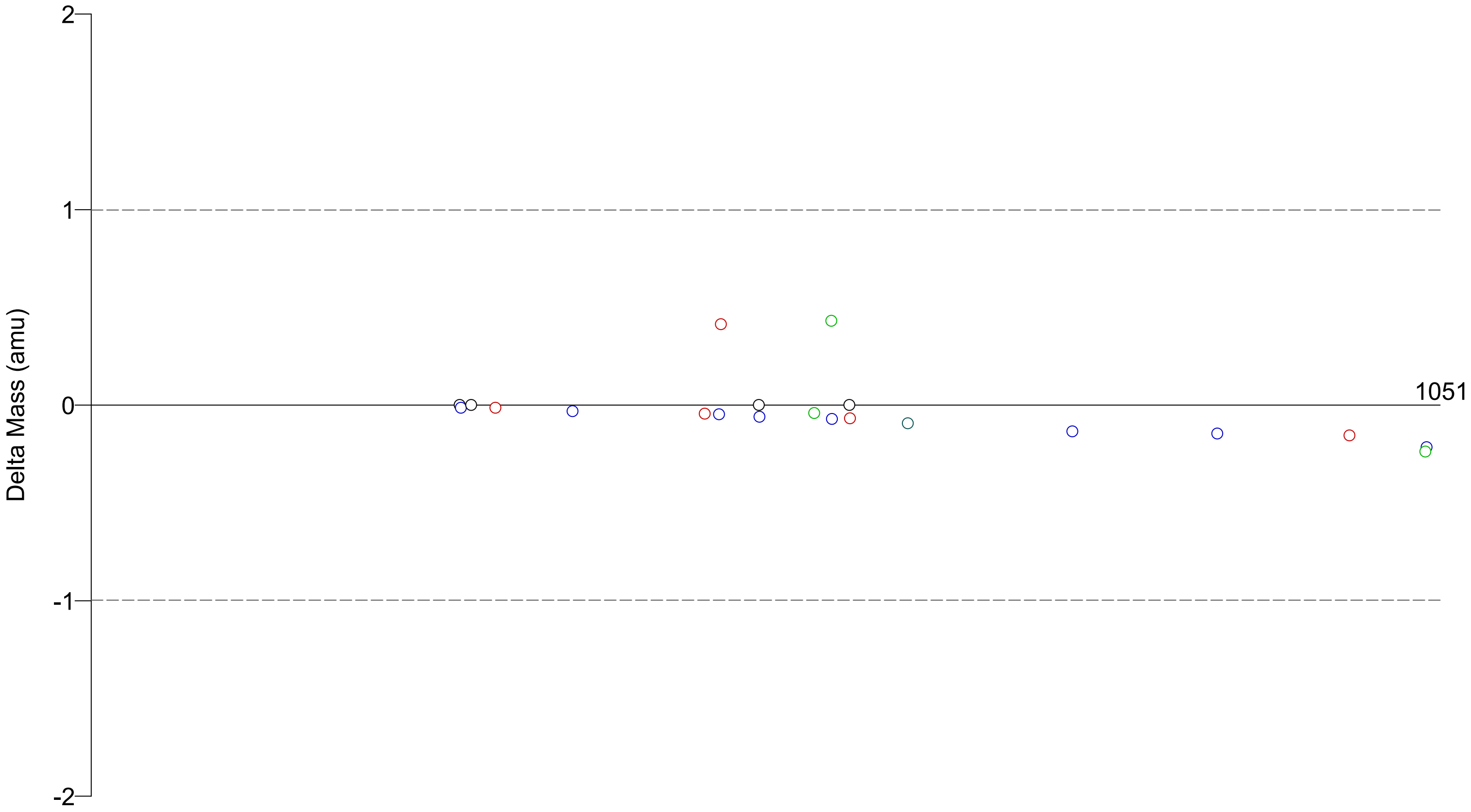


#19287468-1 NL: 8.93E4

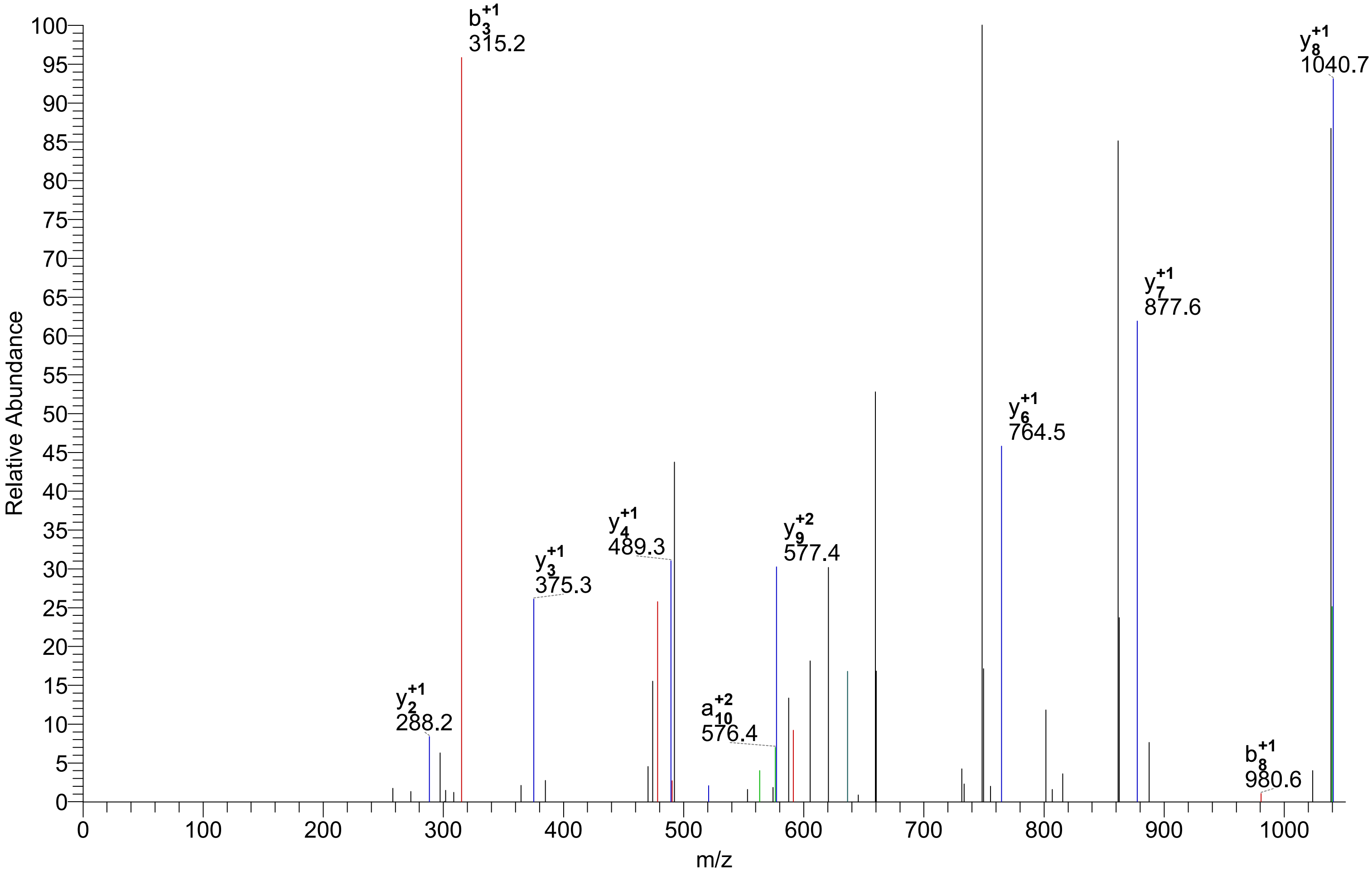


```
Reference                                                            P    Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z     P       XC DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00936661.1|REFSEQ:XP_001718                                0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

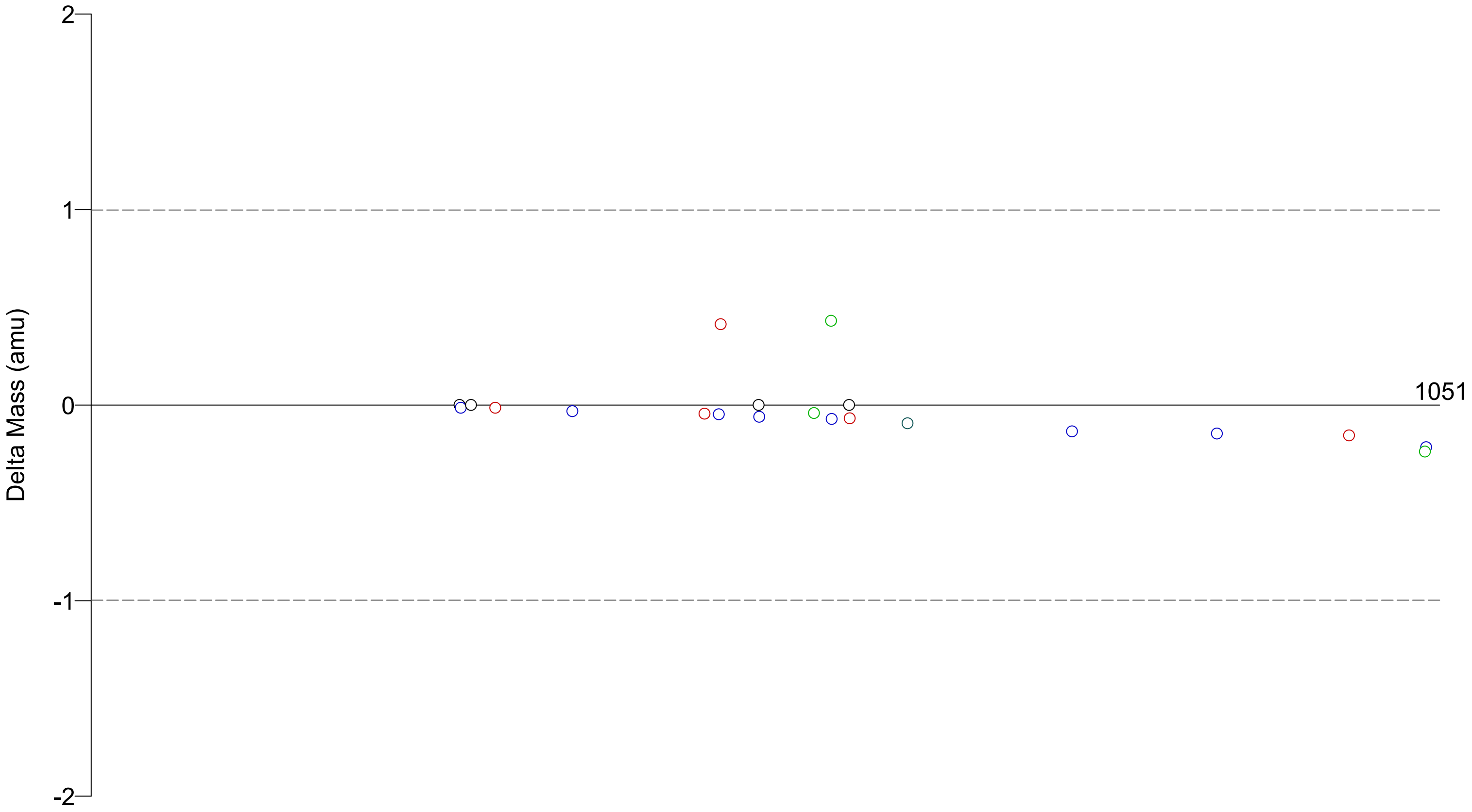


#19287468-1 NL: 8.93E4

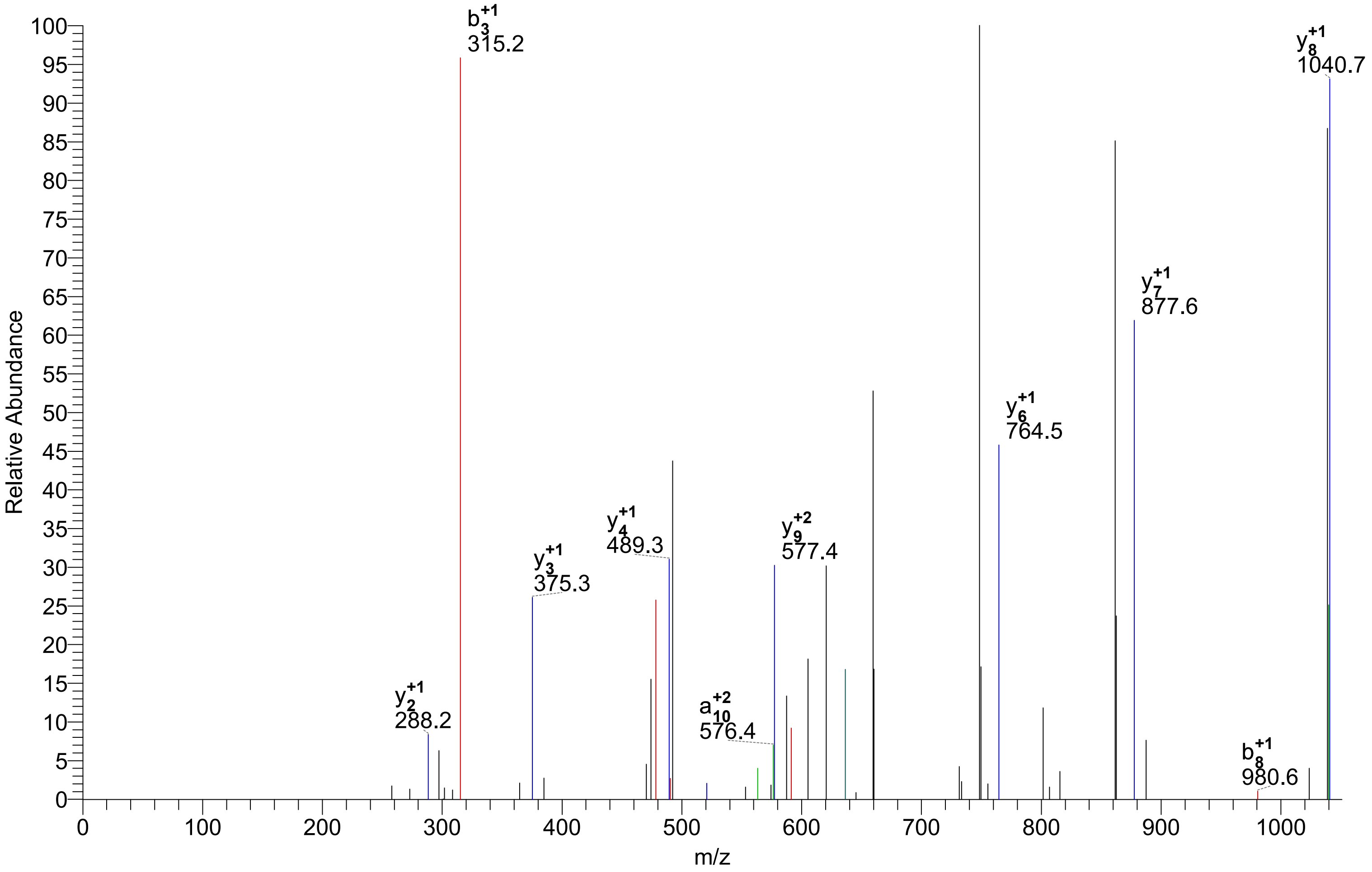


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z   P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00937119.1|REFSEQ:XP_002344                                 0.1      8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                       1354.68   2  0.002    2.168  0.118    607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09    202.08                                     1240.64
 L    287.17    315.17                                     1153.60
 Y    450.23    478.23                                     1040.52
 L    563.32    591.31                                      877.46
 Q    691.38    719.37                                      764.37
 M*   838.41    866.41                                      636.31
 N    952.46    980.45                                      489.28
 S   1039.49   1067.48                                      375.24
 L   1152.57   1180.57                                      288.20
 R                                                          175.12
```

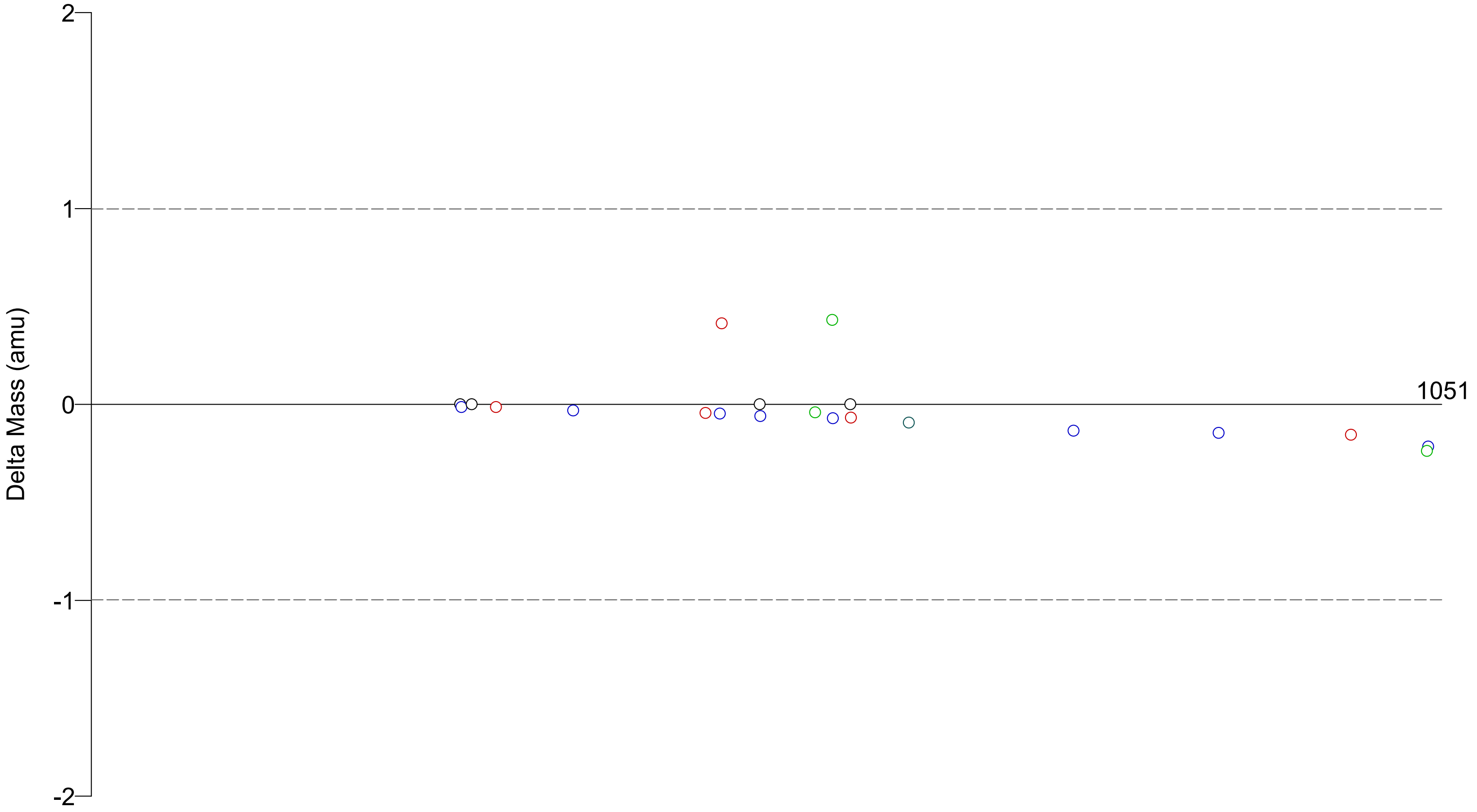


#19287468-1 NL: 8.93E4

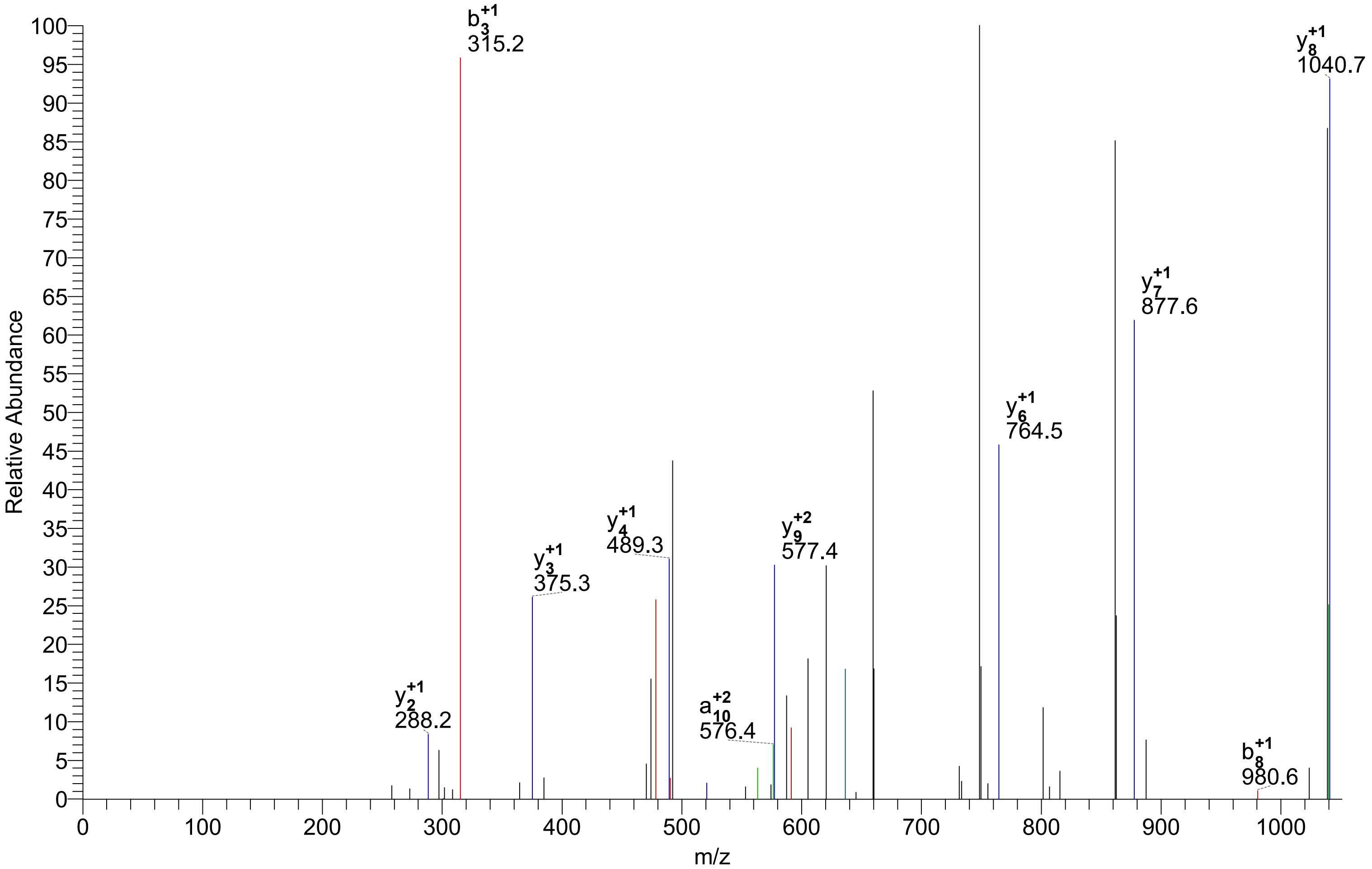


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00937583.1|TREMBL:A0N5G2|EN                                   0.1      8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                         1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N      87.06     115.05
 S     174.09     202.08                                     1240.64
 L     287.17     315.17                                     1153.60
 Y     450.23     478.23                                     1040.52
 L     563.32     591.31                                      877.46
 Q     691.38     719.37                                      764.37
 M*    838.41     866.41                                      636.31
 N     952.46     980.45                                      489.28
 S    1039.49    1067.48                                      375.24
 L    1152.57    1180.57                                      288.20
 R                                                            175.12
```

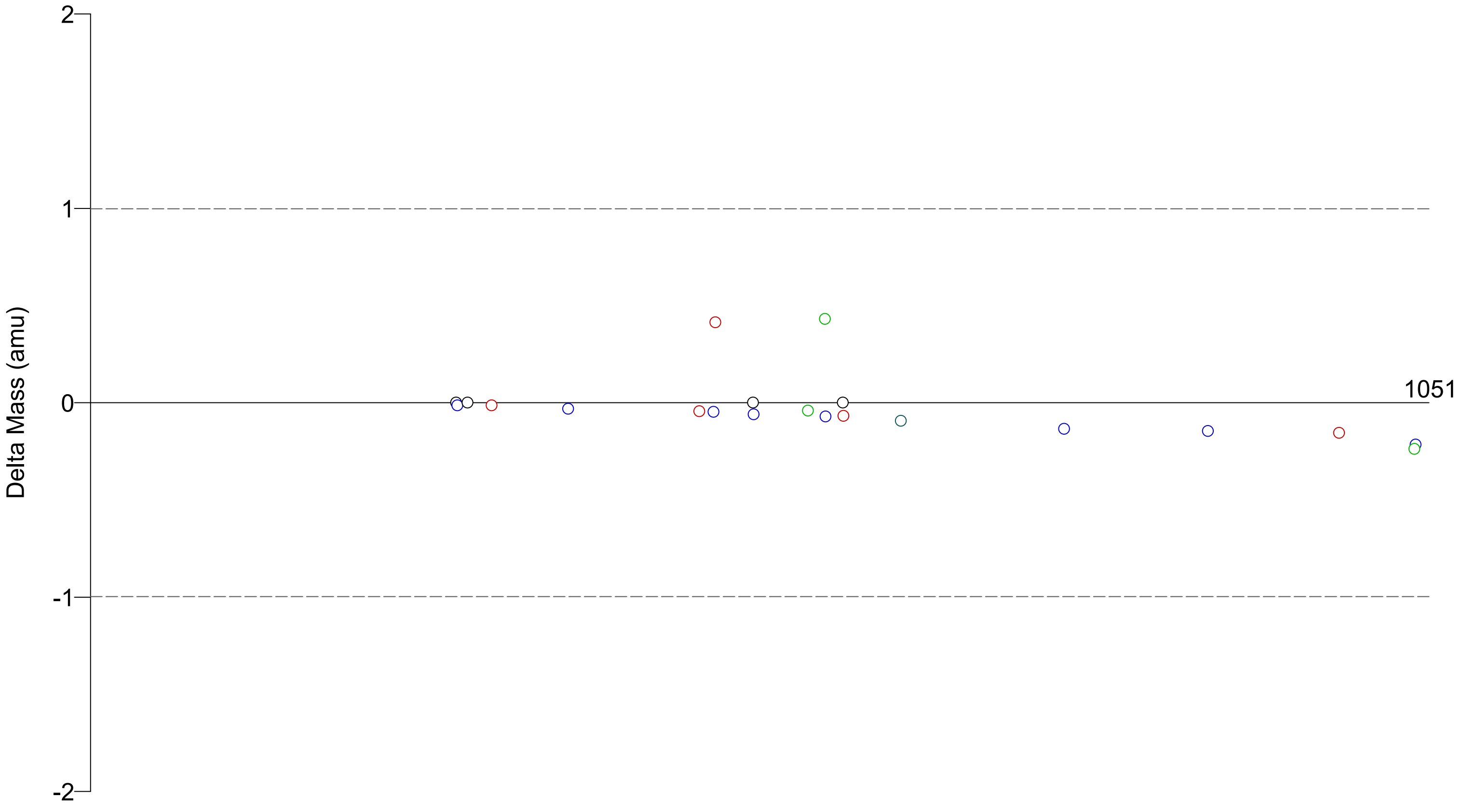


#19287468-1 NL: 8.93E4

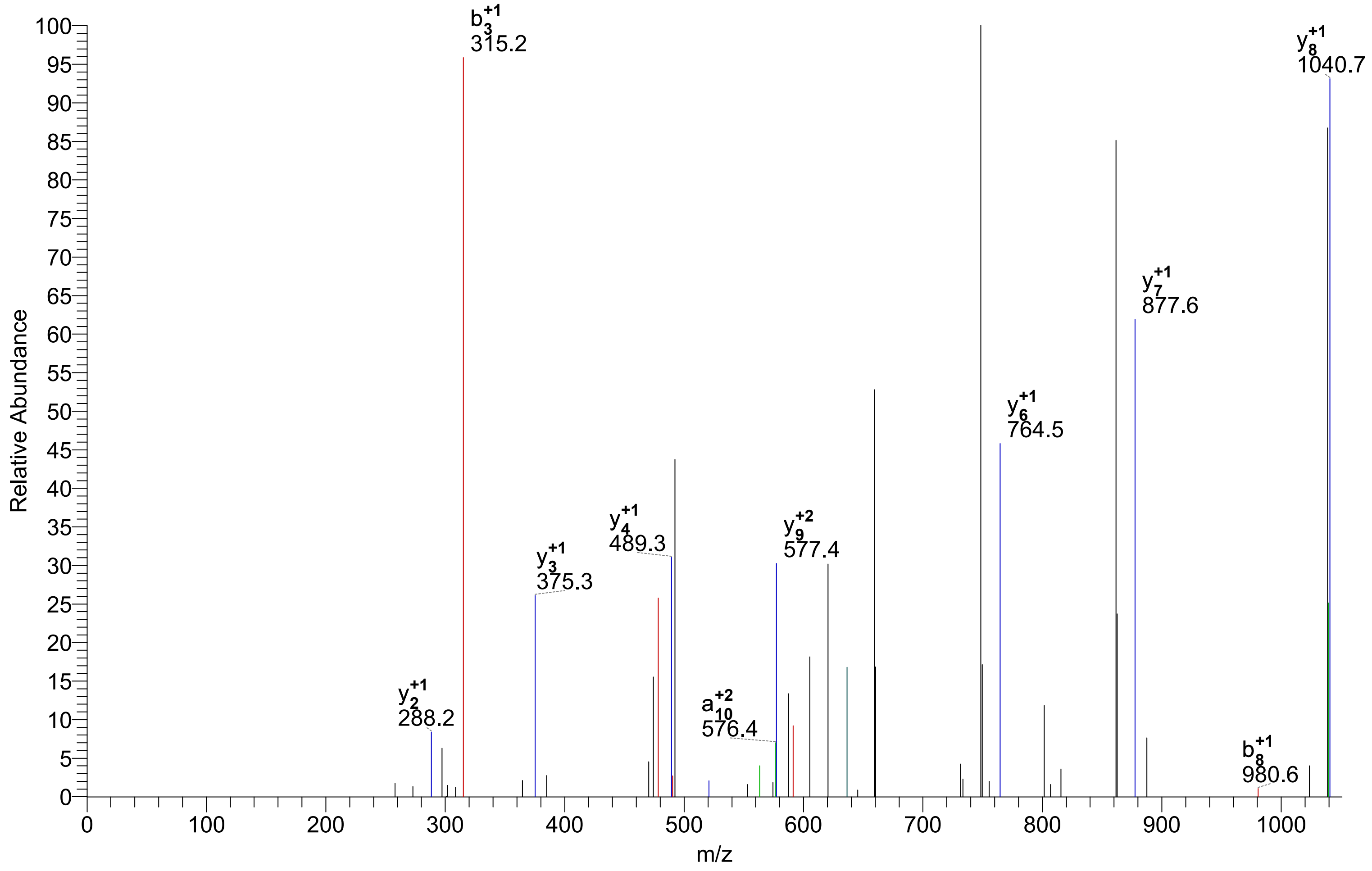


```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00937669.1|REFSEQ:XP_002343                               0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                    1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA    A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                      1240.64
 L    287.17     315.17                                      1153.60
 Y    450.23     478.23                                      1040.52
 L    563.32     591.31                                       877.46
 Q    691.38     719.37                                       764.37
 M*   838.41     866.41                                       636.31
 N    952.46     980.45                                       489.28
 S   1039.49    1067.48                                       375.24
 L   1152.57    1180.57                                       288.20
 R                                                            175.12
```

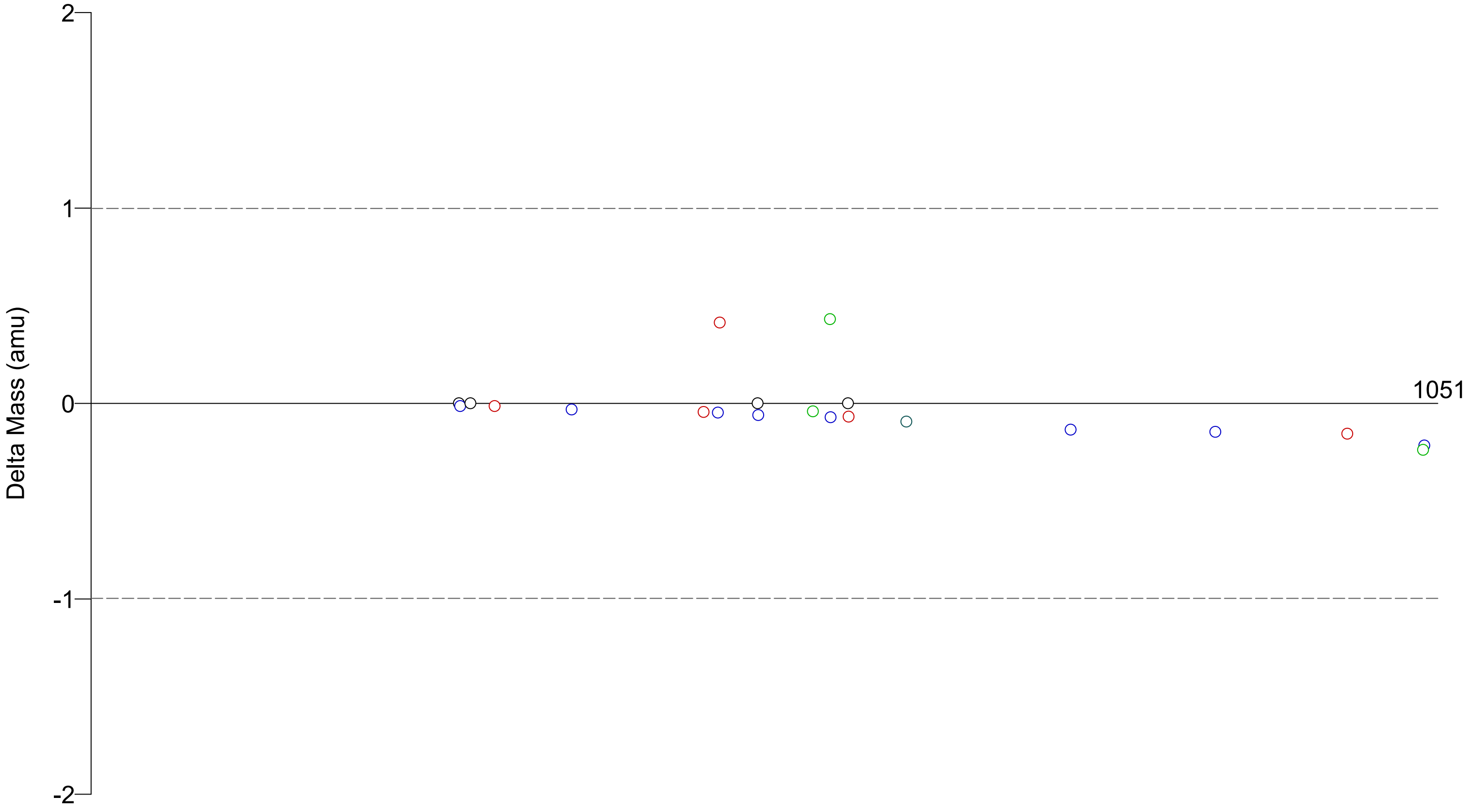


#19287468-1 NL: 8.93E4

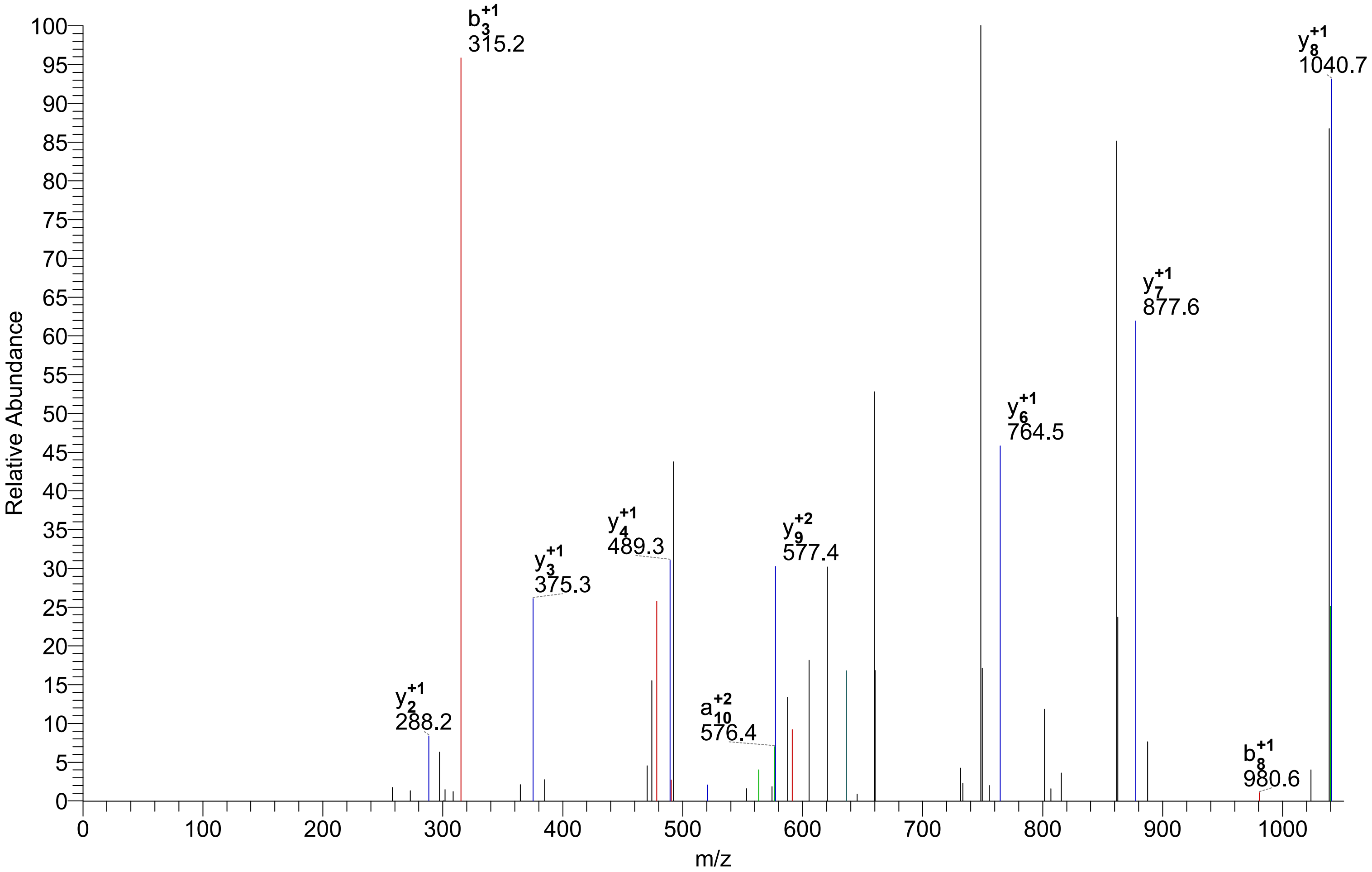


```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00937796.1|TREMBL:A2J1N1;Q0                                      0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                            1354.68    2  0.002    2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N      87.06     115.05
 S     174.09     202.08                                    1240.64
 L     287.17     315.17                                    1153.60
 Y     450.23     478.23                                    1040.52
 L     563.32     591.31                                     877.46
 Q     691.38     719.37                                     764.37
 M*    838.41     866.41                                     636.31
 N     952.46     980.45                                     489.28
 S    1039.49    1067.48                                     375.24
 L    1152.57    1180.57                                     288.20
 R                                                           175.12
```

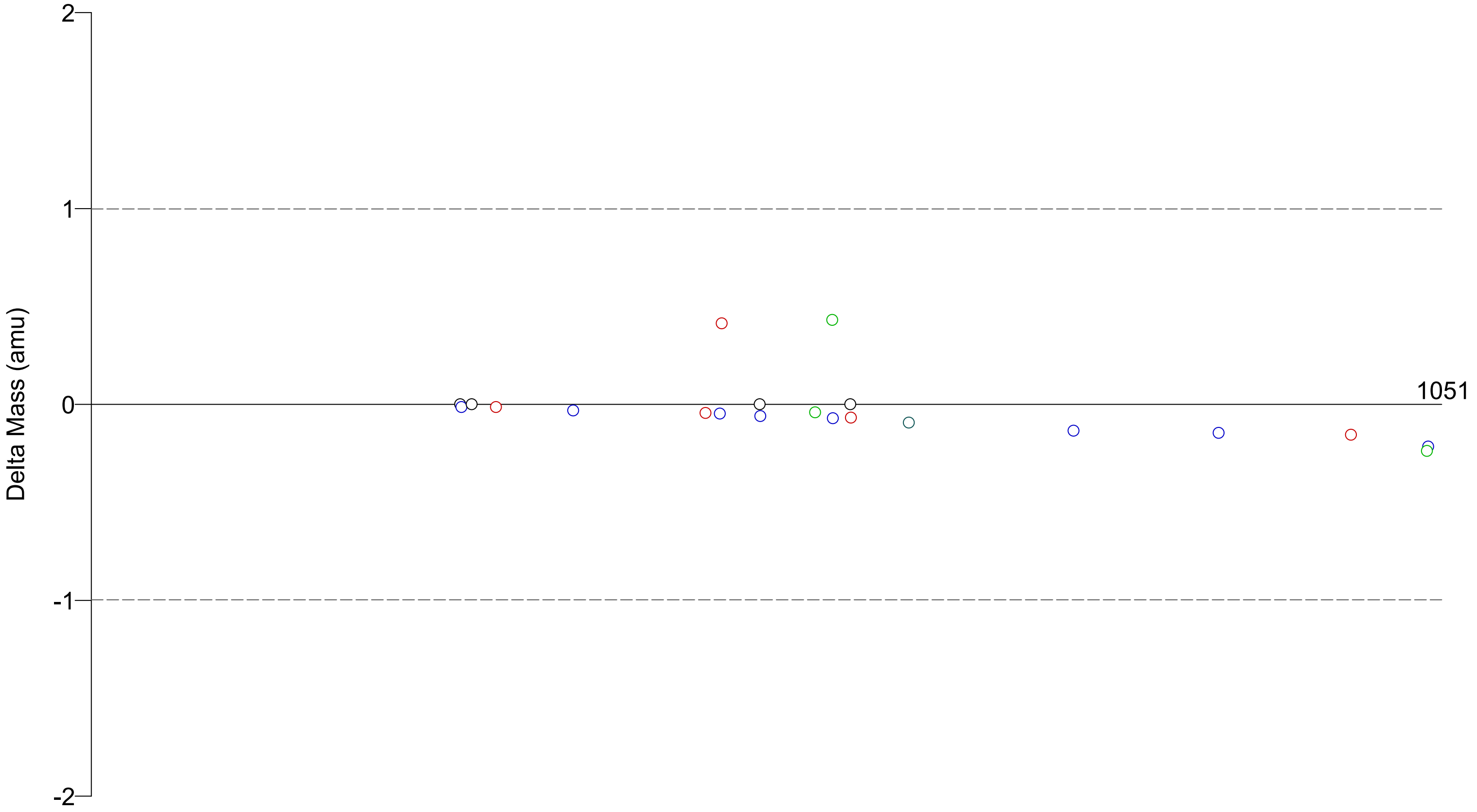


#19287468-1 NL: 8.93E4

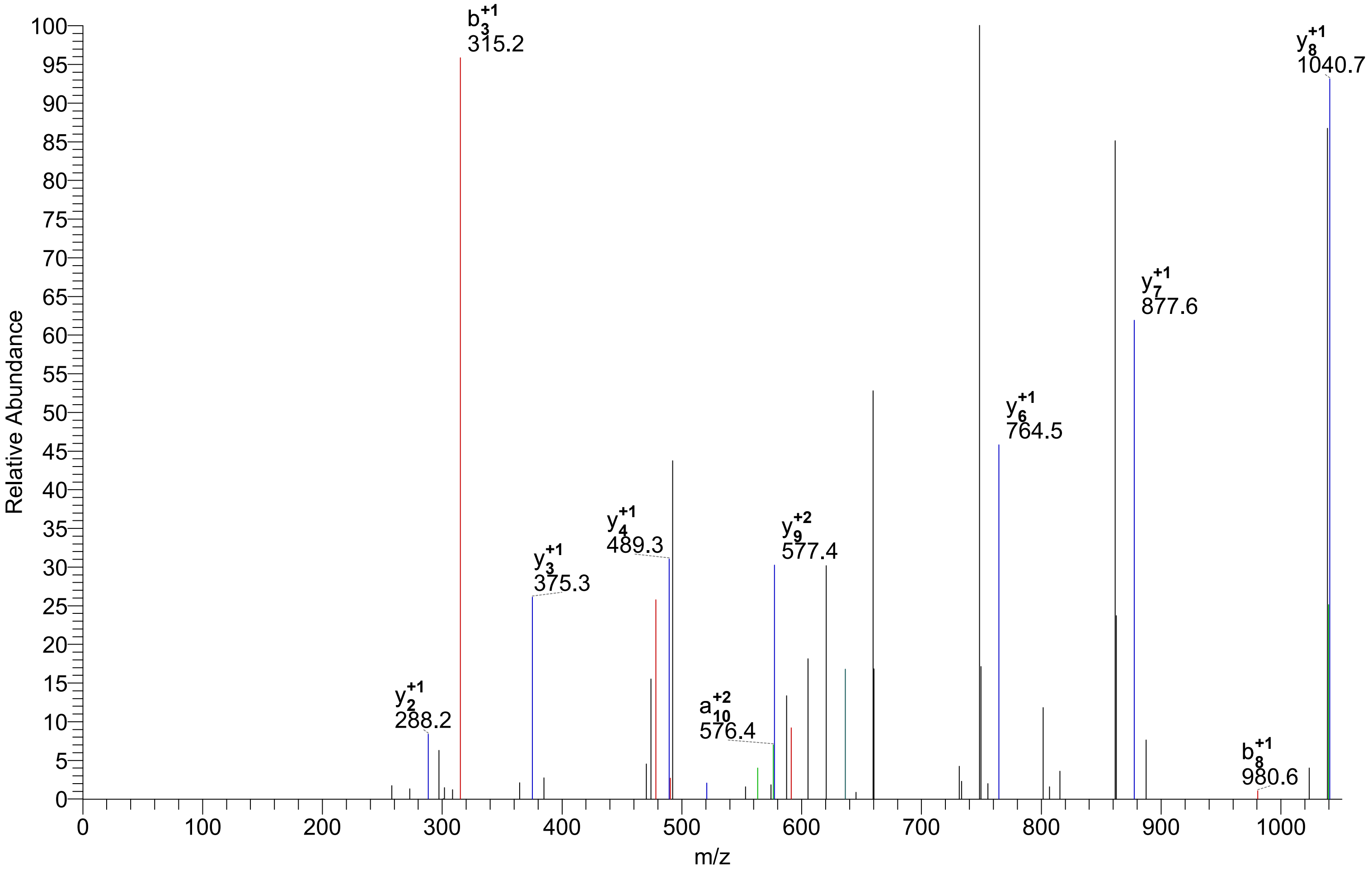


```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00937964.1|REFSEQ:XP_002346                                   0.1     8.1      0.0       0
19287468 - 1  K.NSLYLQM*NSLR.A                         1354.68   2  0.002   2.168  0.118   607.2  1   14/30   30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 S    174.09     202.08                                     1240.64
 L    287.17     315.17                                     1153.60
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```

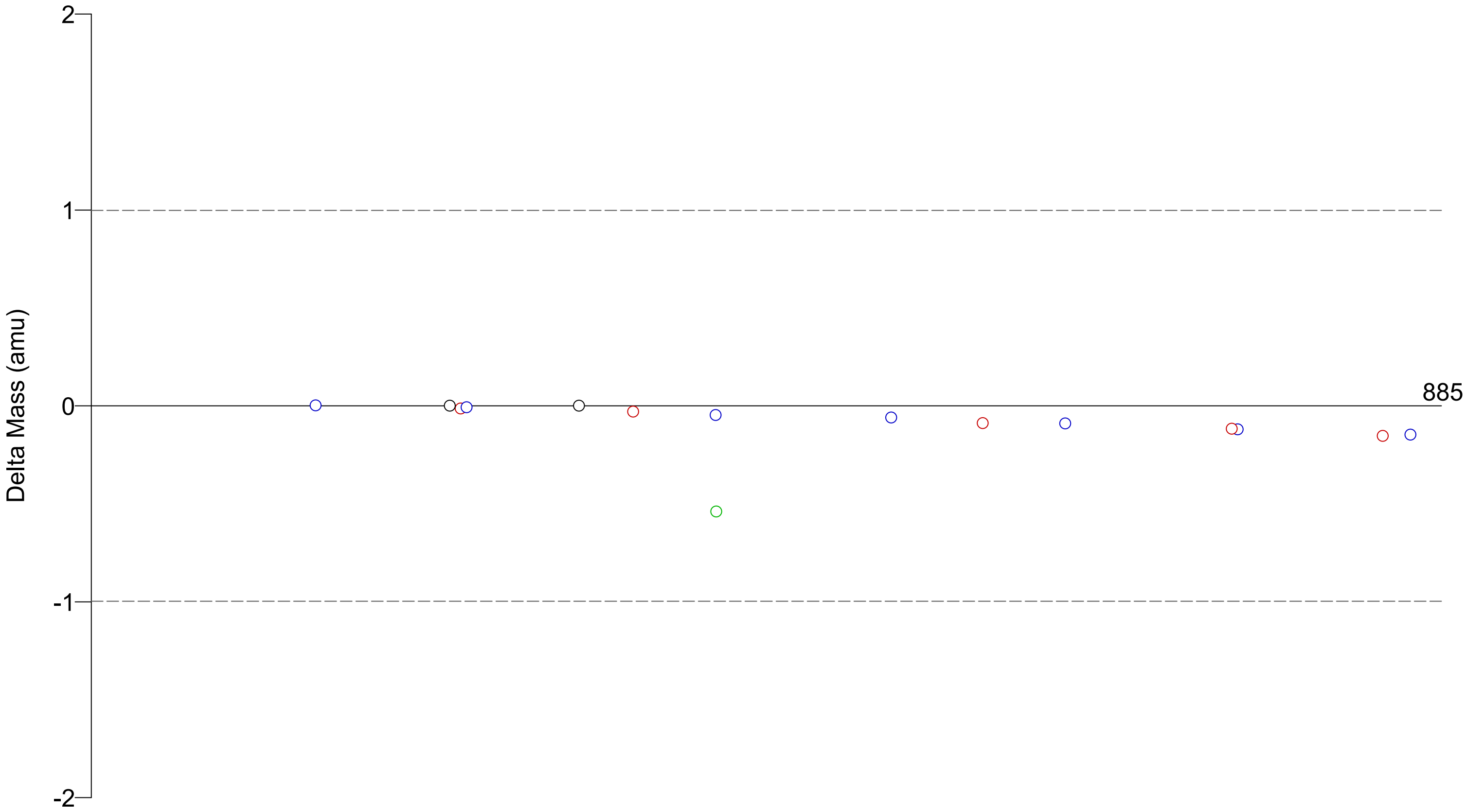


#19287468-1 NL: 8.93E4

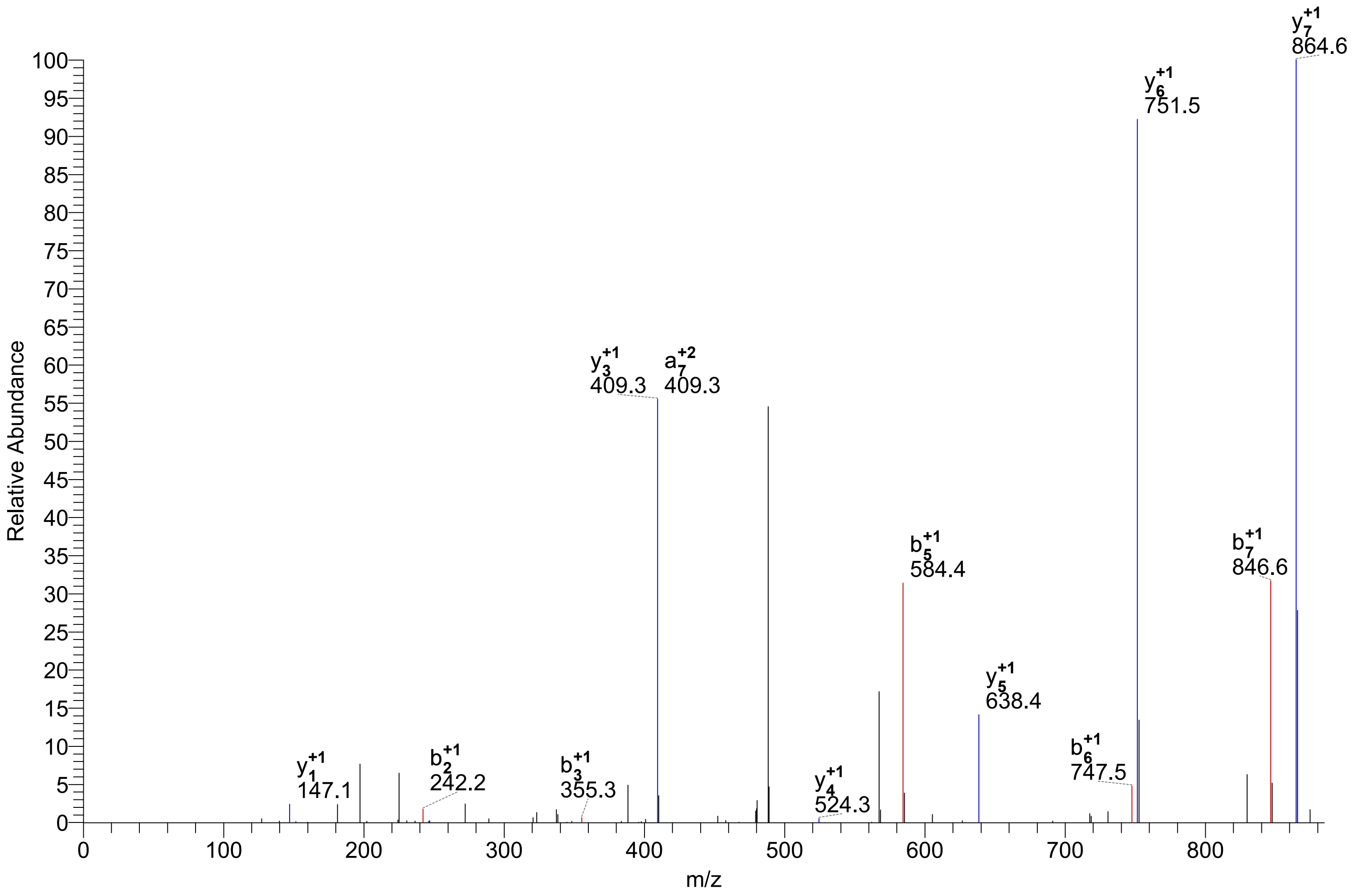


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00550991.3|SWISS-PROT:P01011-2|TREMBL:B3KS79|ENSEMBL:EN      0.3      10.1     0.0        0
19287468 - 1  K.KLINDYVK.N                              992.58    2  0.004    2.401  0.272    505.2  1    12/21   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 496.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 K    101.11     129.10
 L    214.19     242.19                                      864.48
 I    327.28     355.27                                      751.40
 N    441.32     469.31                                      638.31
 D    556.35     584.34                                      524.27
 Y    719.41     747.40                                      409.24
 V    818.48     846.47                                      246.18
 K                                                           147.11
```

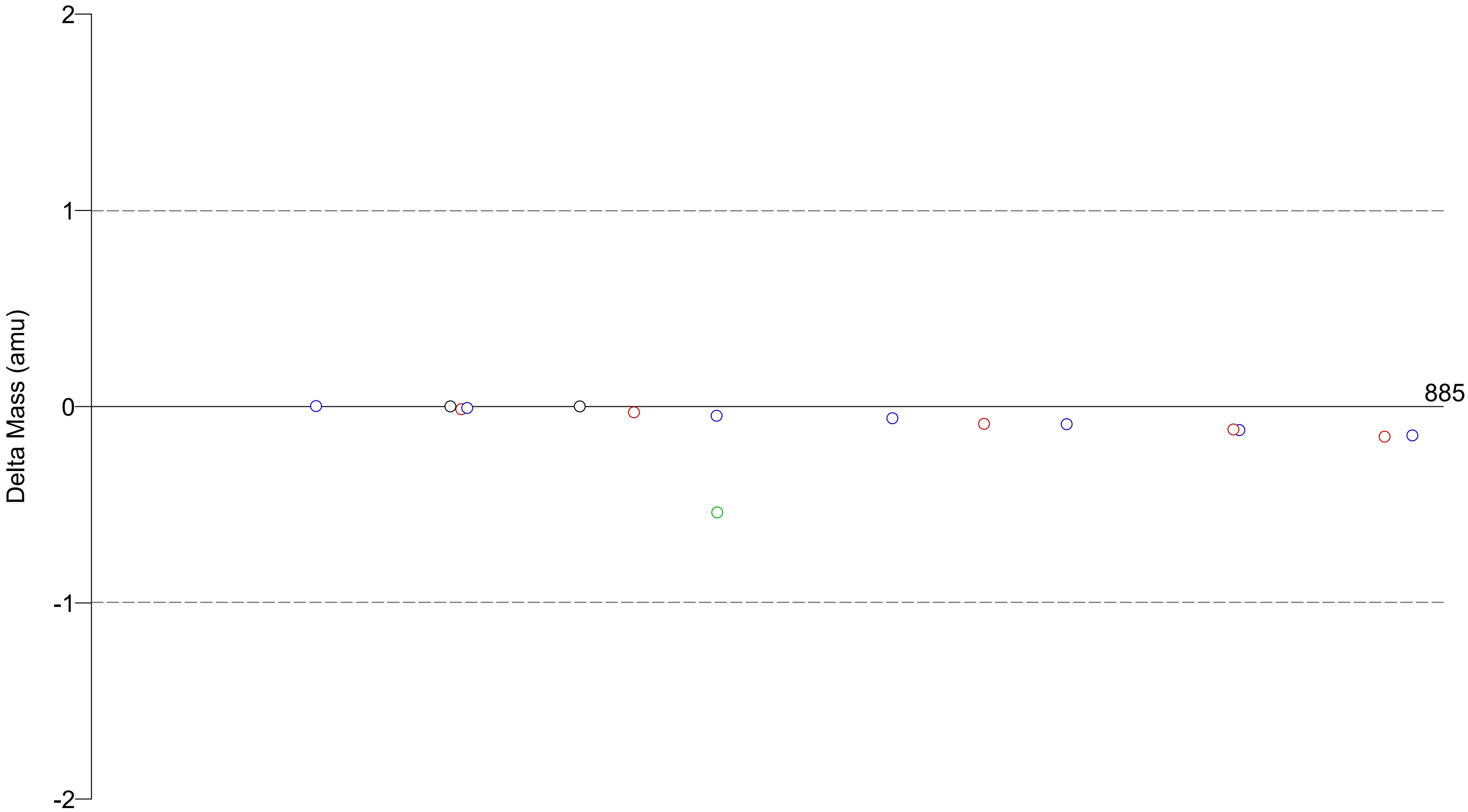


#19287468-1 NL: 1.35E5

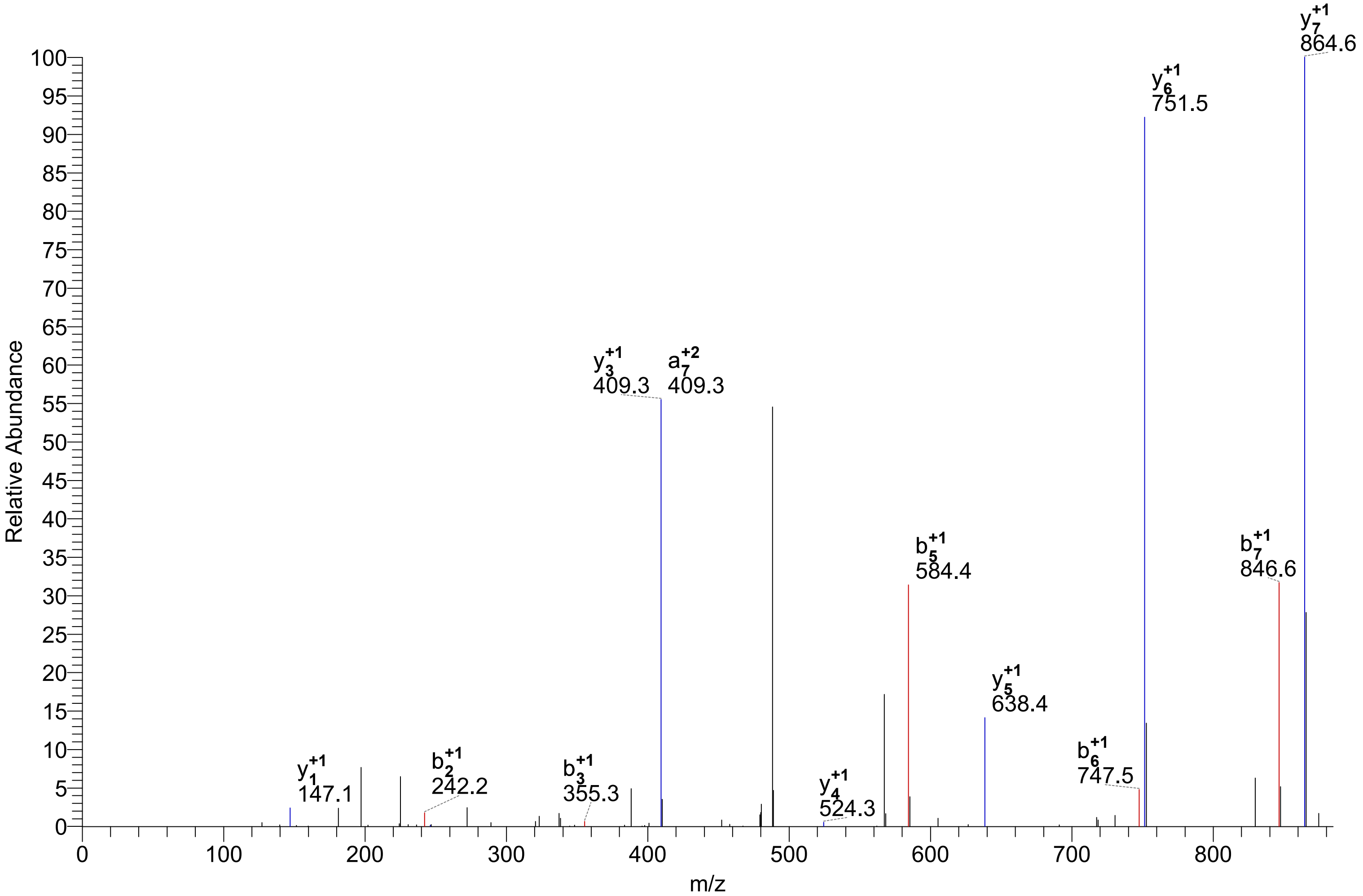


```
Reference                                                       P      Score   Coverage   Accession
Scan(s)       Sequence                              MH+      z     P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00847635.1|SWISS-PROT:P0101                              0.3      10.1     0.0       0
19287468 - 1  K.KLINDYVK.N                        992.58    2  0.004    2.401  0.272   505.2  1   12/21   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 496.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 K    101.11     129.10
 L    214.19     242.19                                      864.48
 I    327.28     355.27                                      751.40
 N    441.32     469.31                                      638.31
 D    556.35     584.34                                      524.27
 Y    719.41     747.40                                      409.24
 V    818.48     846.47                                      246.18
 K                                                           147.11
```

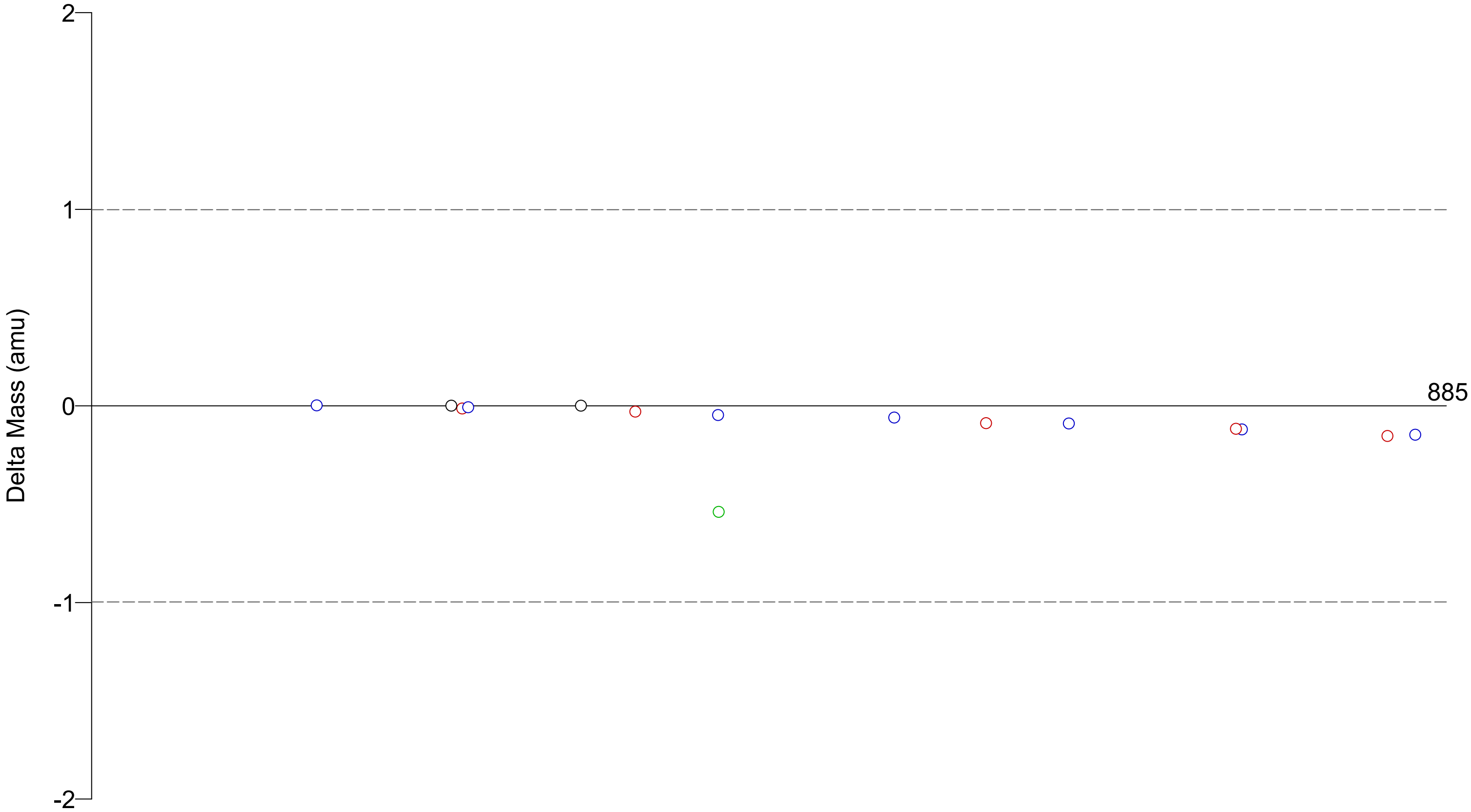


#19287468-1 NL: 1.35E5

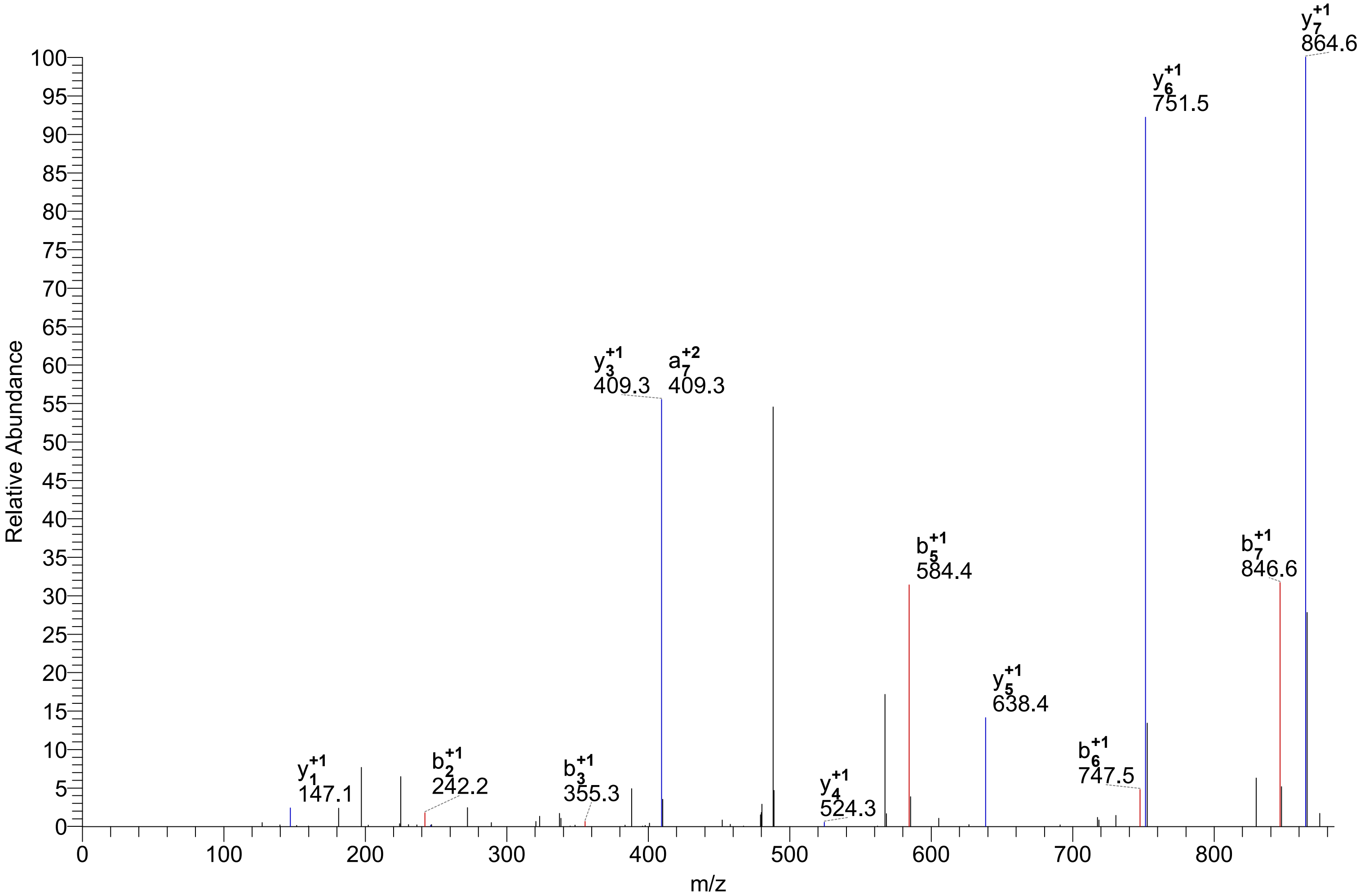


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00935915.1|ENSEMBL:ENSP0000                                0.3     10.1     0.0       0
19287468 - 1  K.KLINDYVK.N                           992.58    2  0.004   2.401  0.272   505.2  1   12/21   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 496.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 K    101.11     129.10
 L    214.19     242.19                                      864.48
 I    327.28     355.27                                      751.40
 N    441.32     469.31                                      638.31
 D    556.35     584.34                                      524.27
 Y    719.41     747.40                                      409.24
 V    818.48     846.47                                      246.18
 K                                                           147.11
```

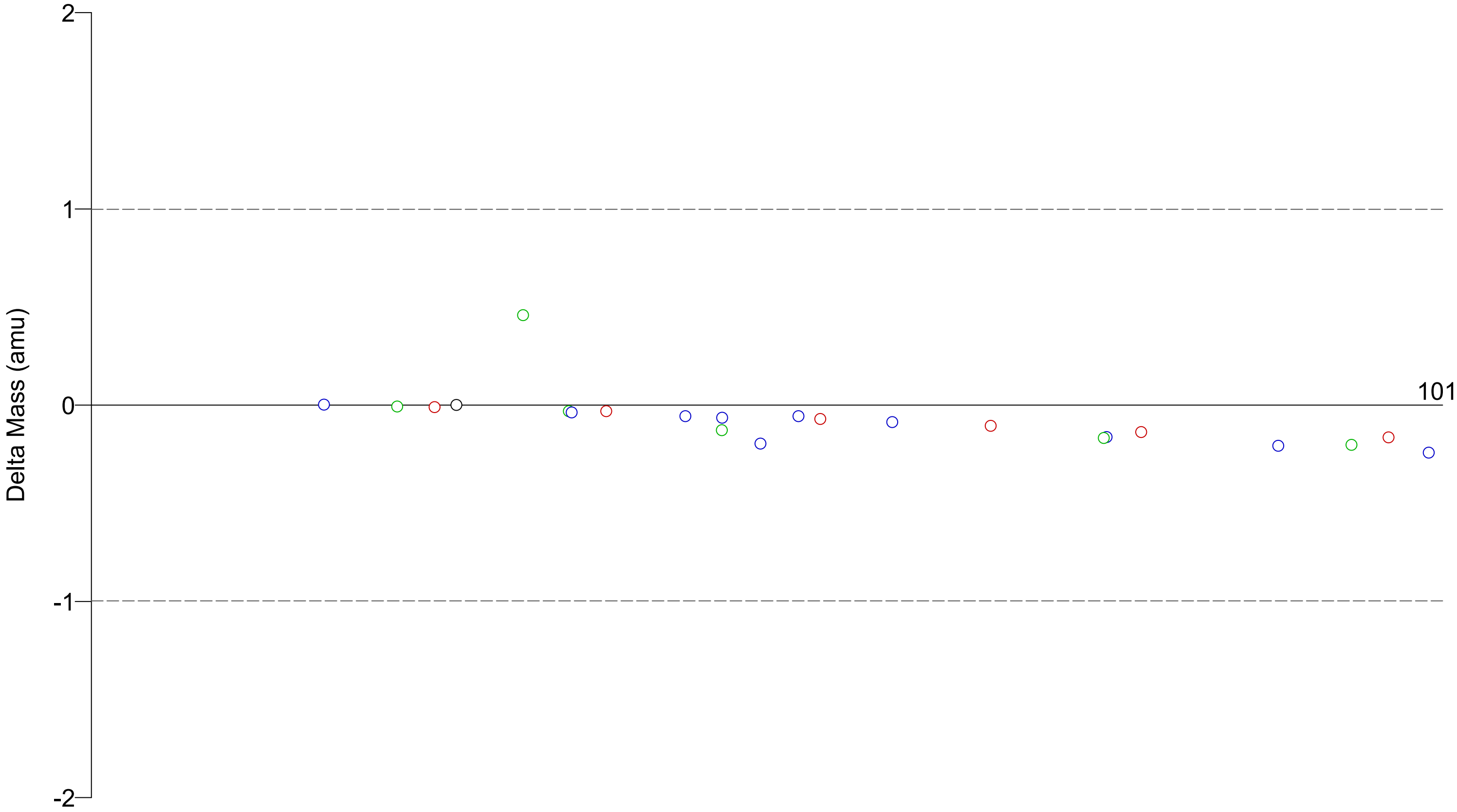


#19287468-1 NL: 1.35E5

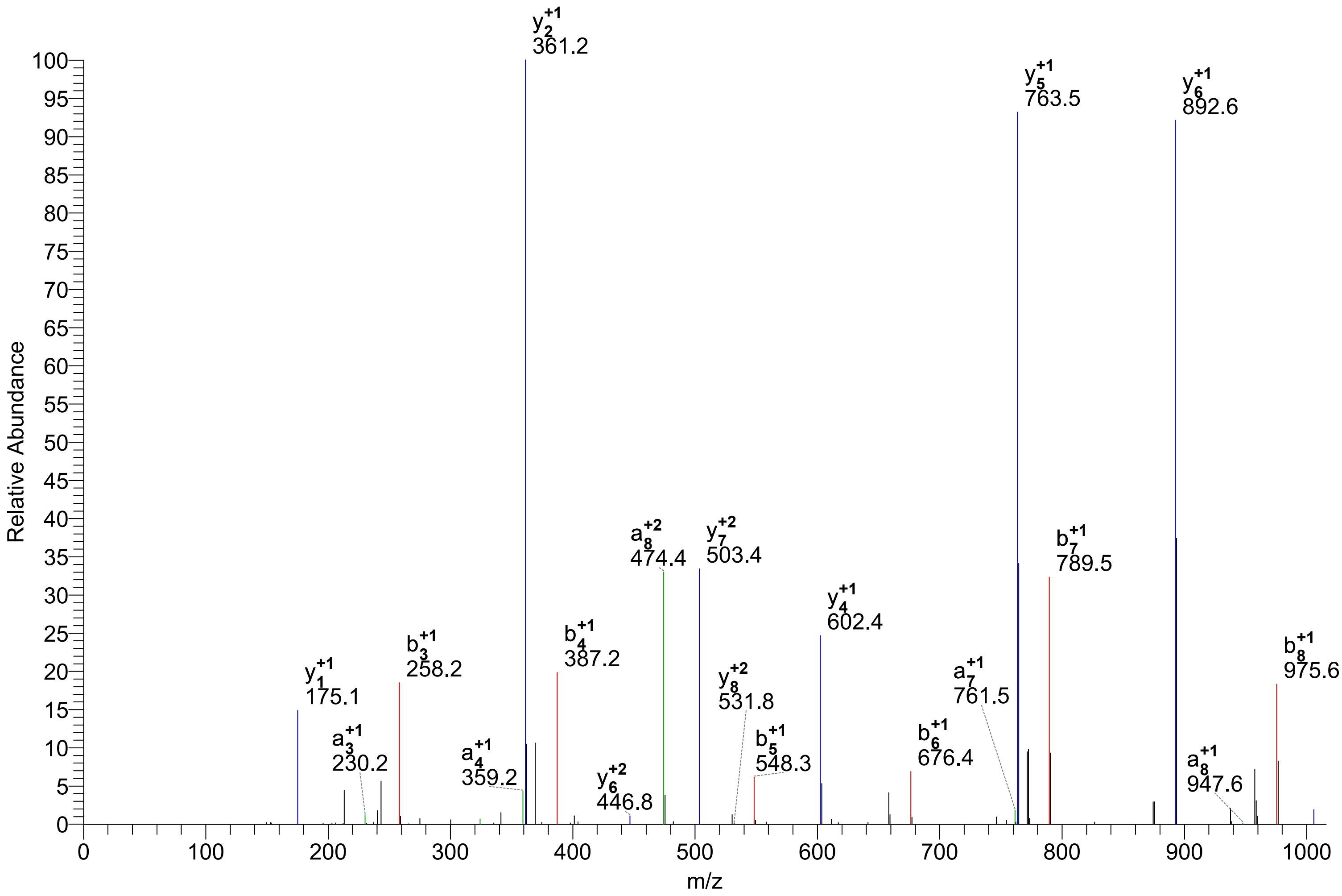


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00019568.1|SWISS-PROT:P00734|TREMBL:B4DDT3;Q15253;Q69EZ    0.3     10.2     0.0       0
19287468 - 1  R.SGIECQLWR.S                          1149.54   2  0.004   3.490  0.339   1292.4 1   17/24   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 575.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                    1062.50
 I    230.15     258.14                                    1005.48
 E    359.19     387.19                                     892.40
 C    520.21     548.20                                     763.36
 Q    648.27     676.26                                     602.34
 L    761.35     789.34                                     474.28
 W    947.43     975.42                                     361.20
 R                                                          175.12
```

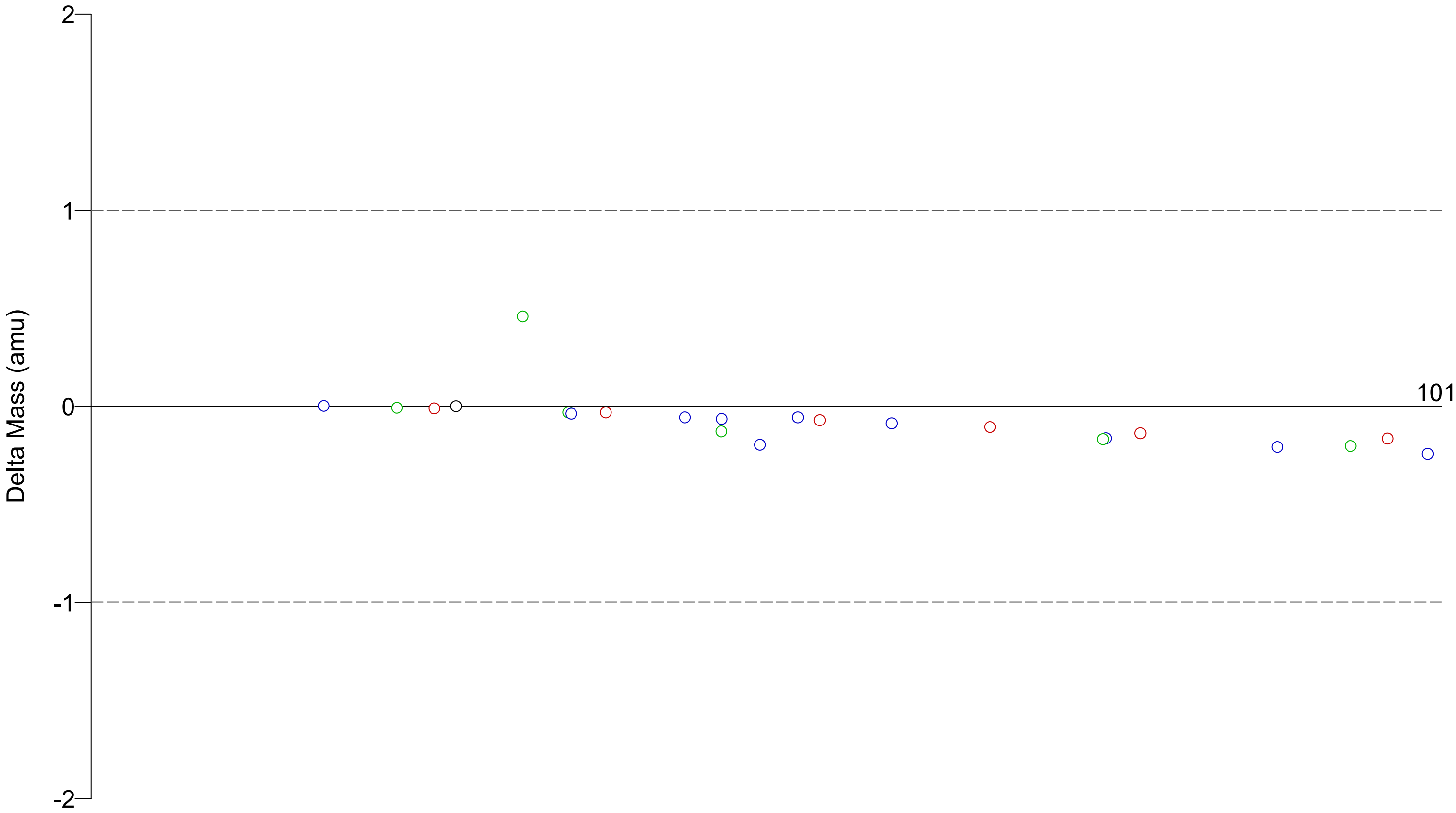


#19287468-1 NL: 1.42E5

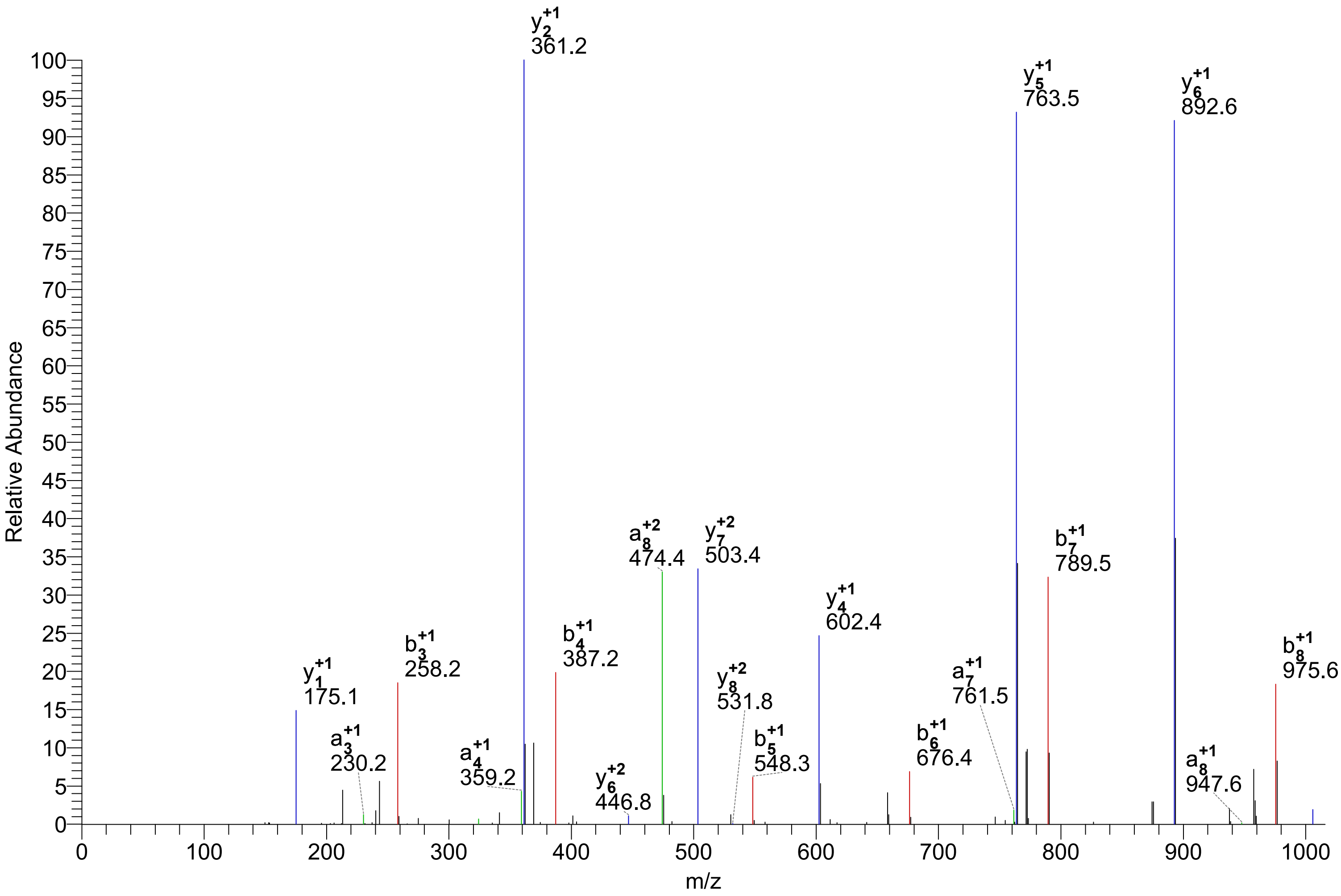


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z   P        XC  DeltaCn   Sp    RSp  Ions  Count

IPI:IPI00877967.1|VEGA:OTTHUMP0000                                   0.3      10.2     0.0       0
19287468 - 1  R.SGIECQLWR.S                             1149.54   2  0.004    3.490  0.339   1292.4 1   17/24   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 575.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 G    117.07     145.06                                     1062.50
 I    230.15     258.14                                     1005.48
 E    359.19     387.19                                      892.40
 C    520.21     548.20                                      763.36
 Q    648.27     676.26                                      602.34
 L    761.35     789.34                                      474.28
 W    947.43     975.42                                      361.20
 R                                                           175.12
```

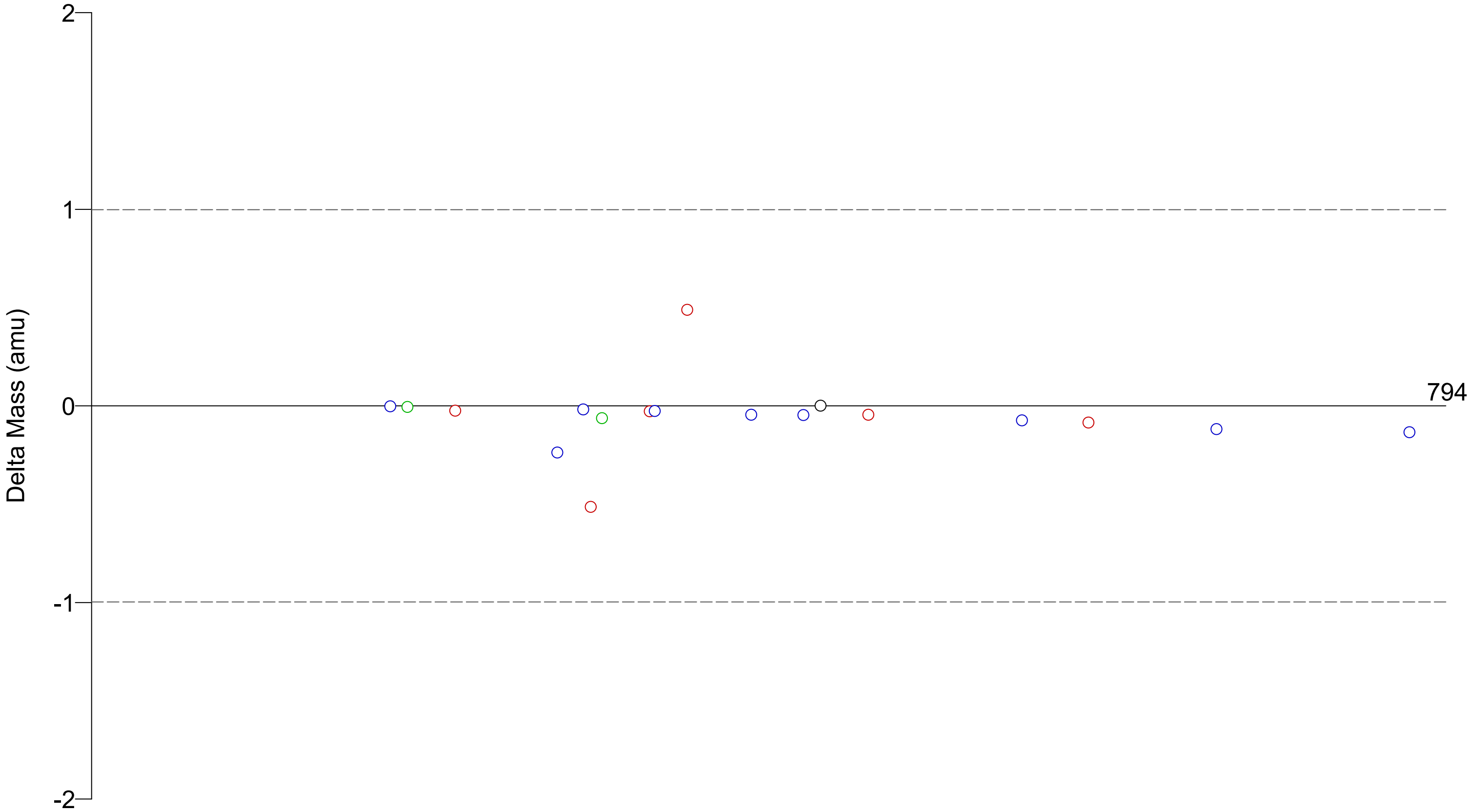


#19287468-1 NL: 1.42E5

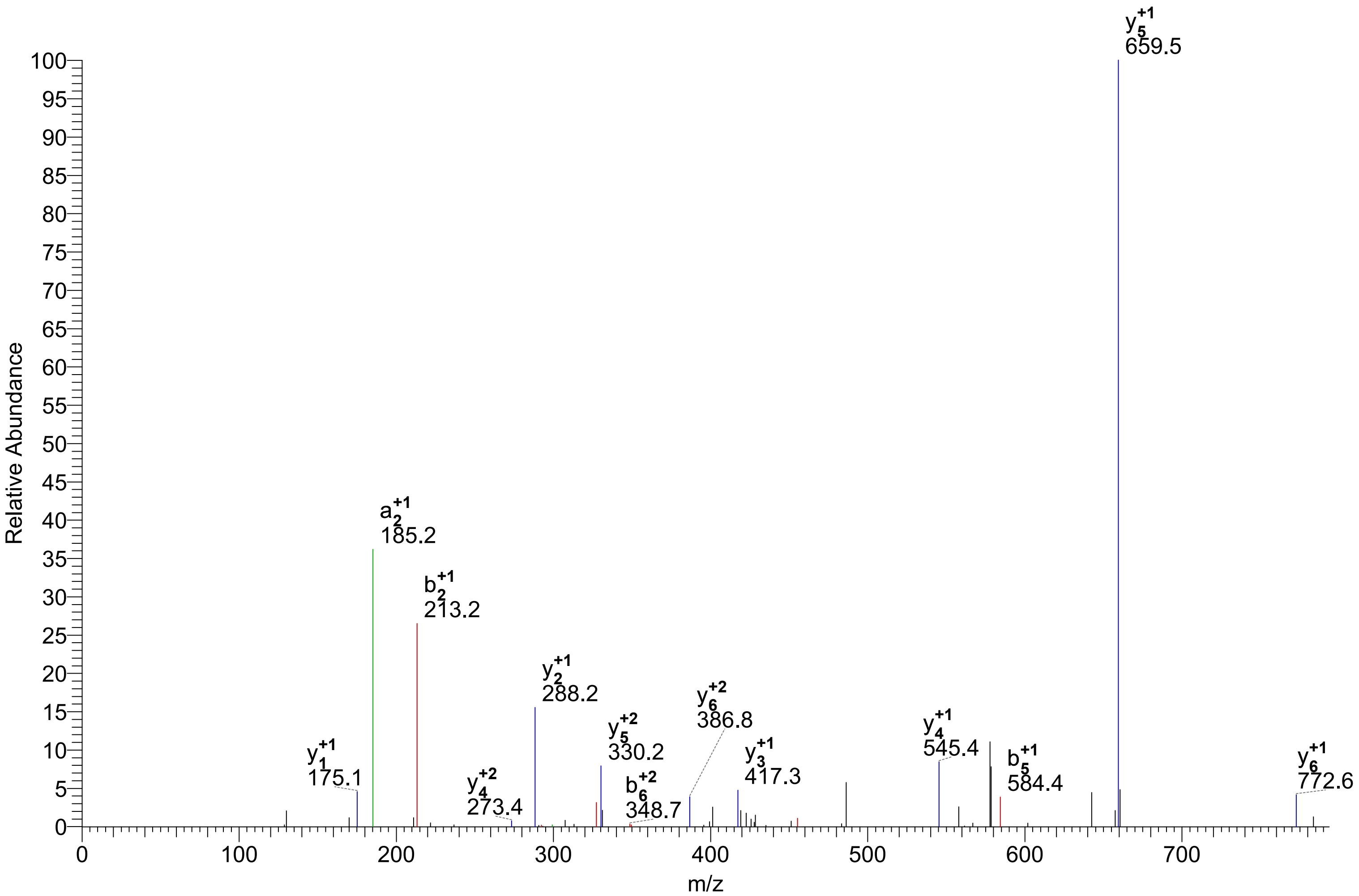


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00006662.1|SWISS-PROT:P05090|TREMBL:B2R579|ENSEMBL:ENSP    0.3     10.1      0.0        0
19287468 - 1  K.VLNQELR.A                                 871.50    2  0.004    2.210  0.309   564.0  1   13/18   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 436.25
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 L    185.16     213.16                                      772.43
 N    299.21     327.20                                      659.35
 Q    427.27     455.26                                      545.30
 E    556.31     584.30                                      417.25
 L    669.39     697.39                                      288.20
 R                                                           175.12
```

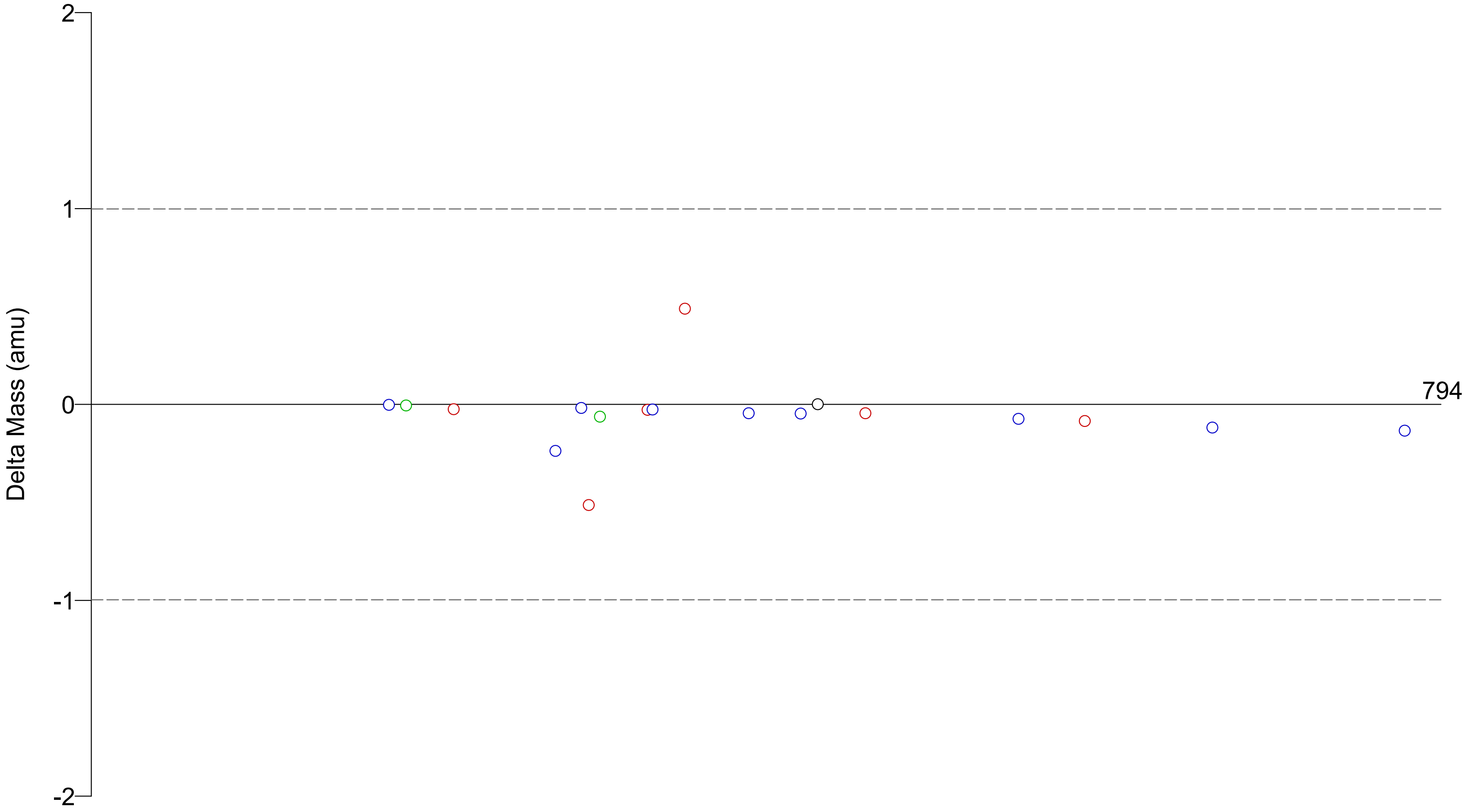


#19287468-1 NL: 5.11E5

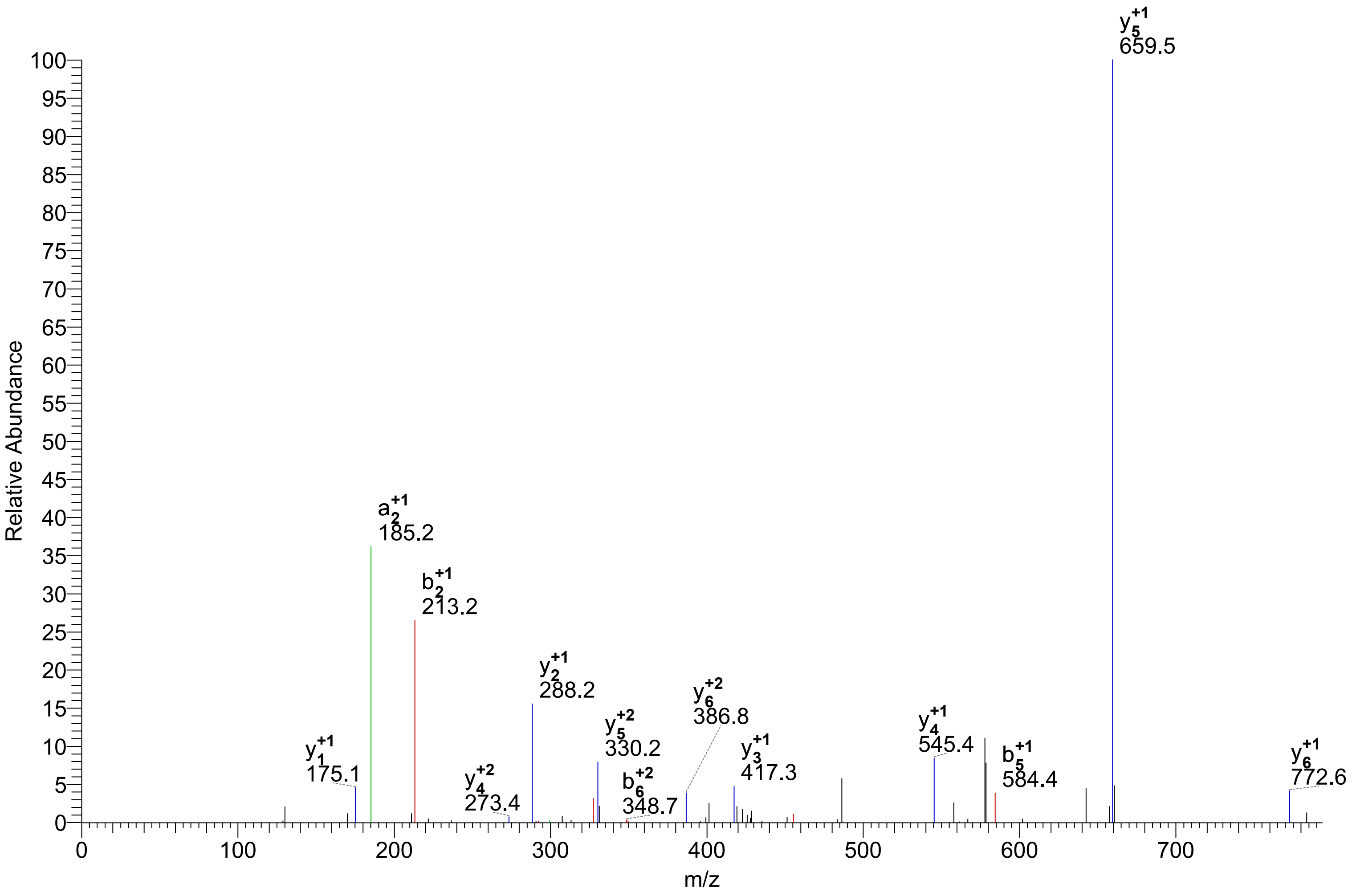


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00910432.1|TREMBL:B4DGC3 Ta                                  0.3     10.1     0.0        0
19287468 - 1  K.VLNQELR.A                              871.50    2  0.004    2.210  0.309    564.0  1   13/18   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 436.25
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 L    185.16     213.16                                      772.43
 N    299.21     327.20                                      659.35
 Q    427.27     455.26                                      545.30
 E    556.31     584.30                                      417.25
 L    669.39     697.39                                      288.20
 R                                                           175.12
```

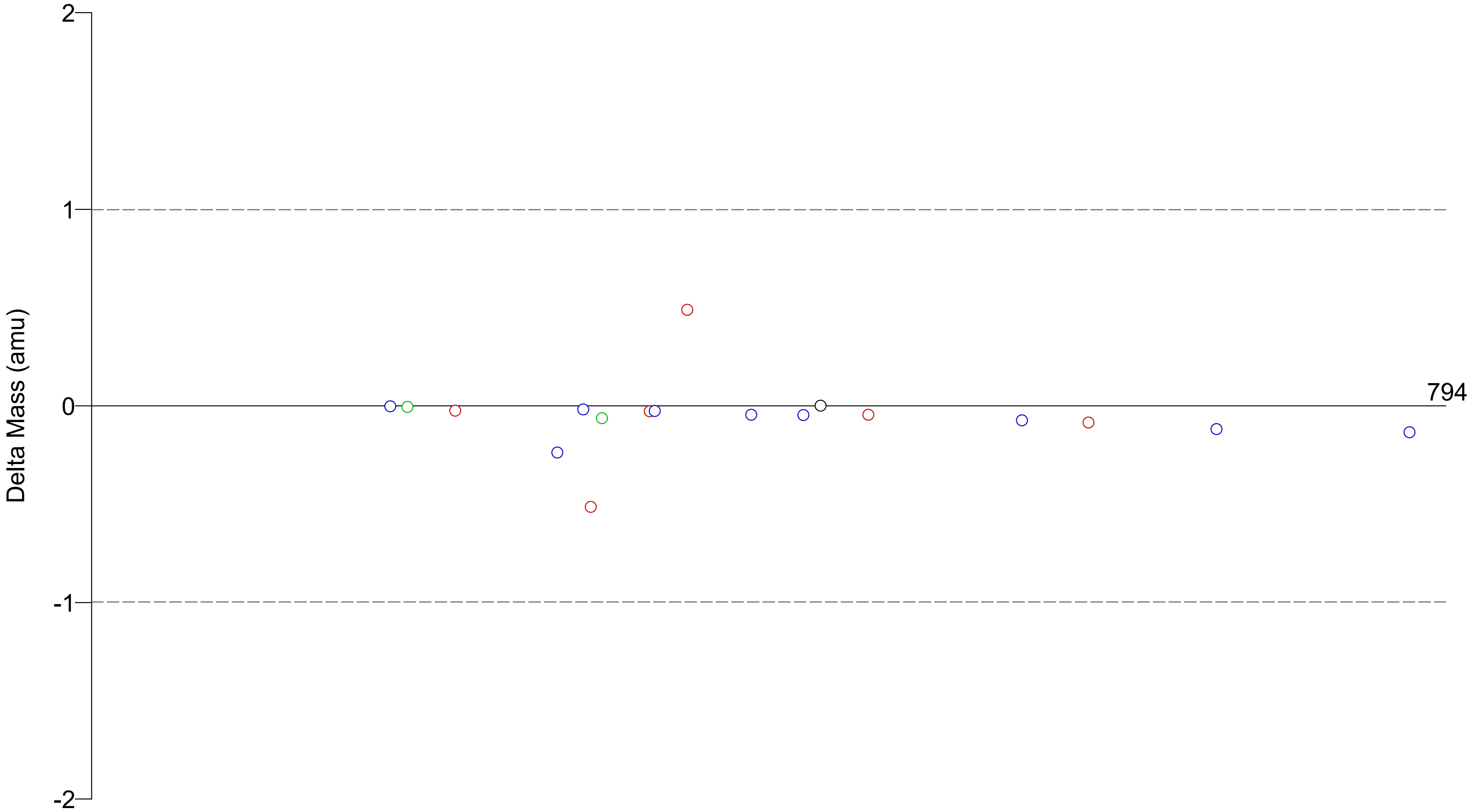


#19287468-1 NL: 5.11E5

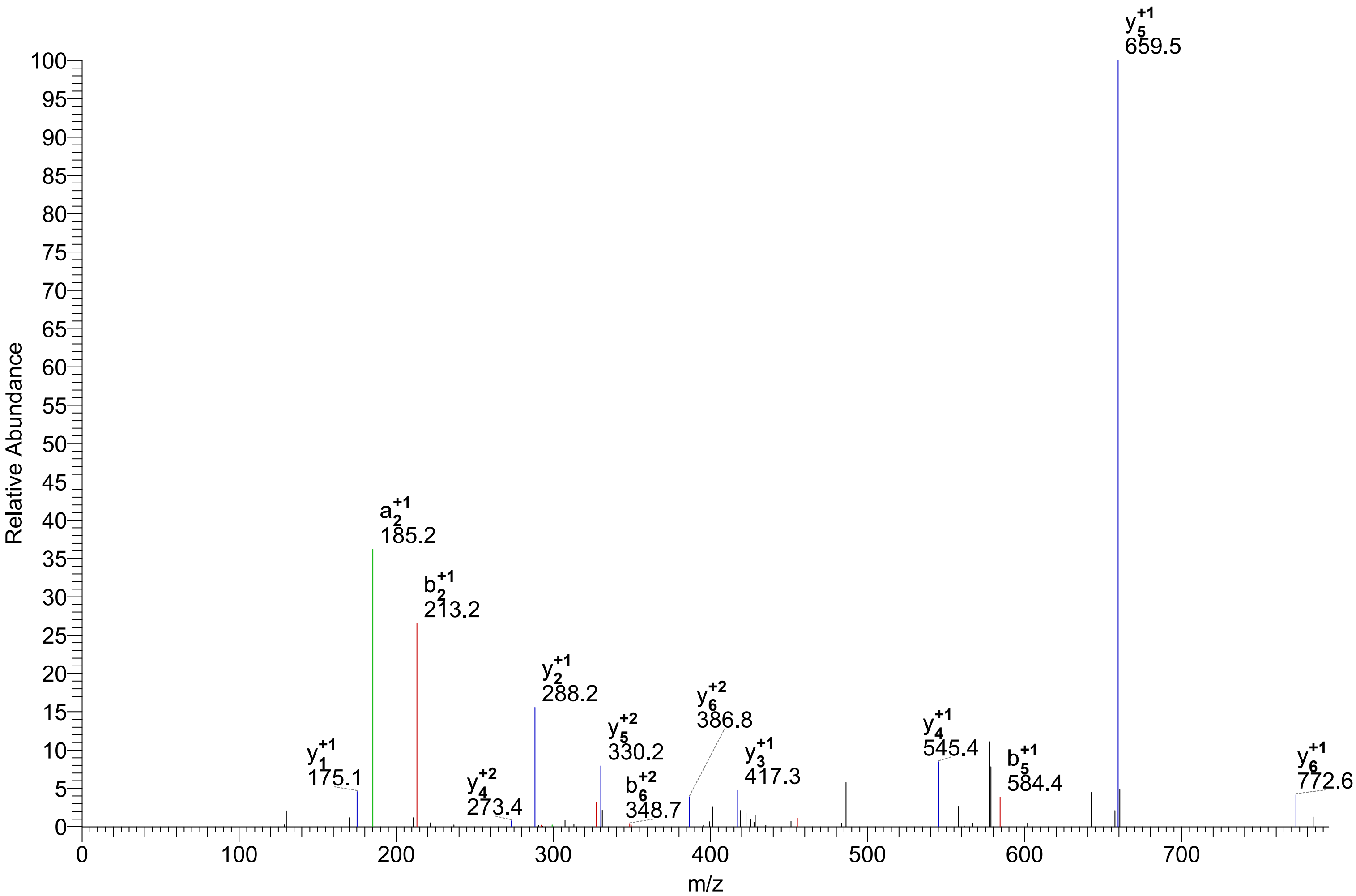


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00924574.1|VEGA:OTTHUMP0000                                0.3     10.1     0.0       0
19287468 - 1  K.VLNQELR.A                            871.50    2  0.004   2.210  0.309   564.0  1   13/18   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 436.25
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 L    185.16     213.16                                      772.43
 N    299.21     327.20                                      659.35
 Q    427.27     455.26                                      545.30
 E    556.31     584.30                                      417.25
 L    669.39     697.39                                      288.20
 R                                                           175.12
```

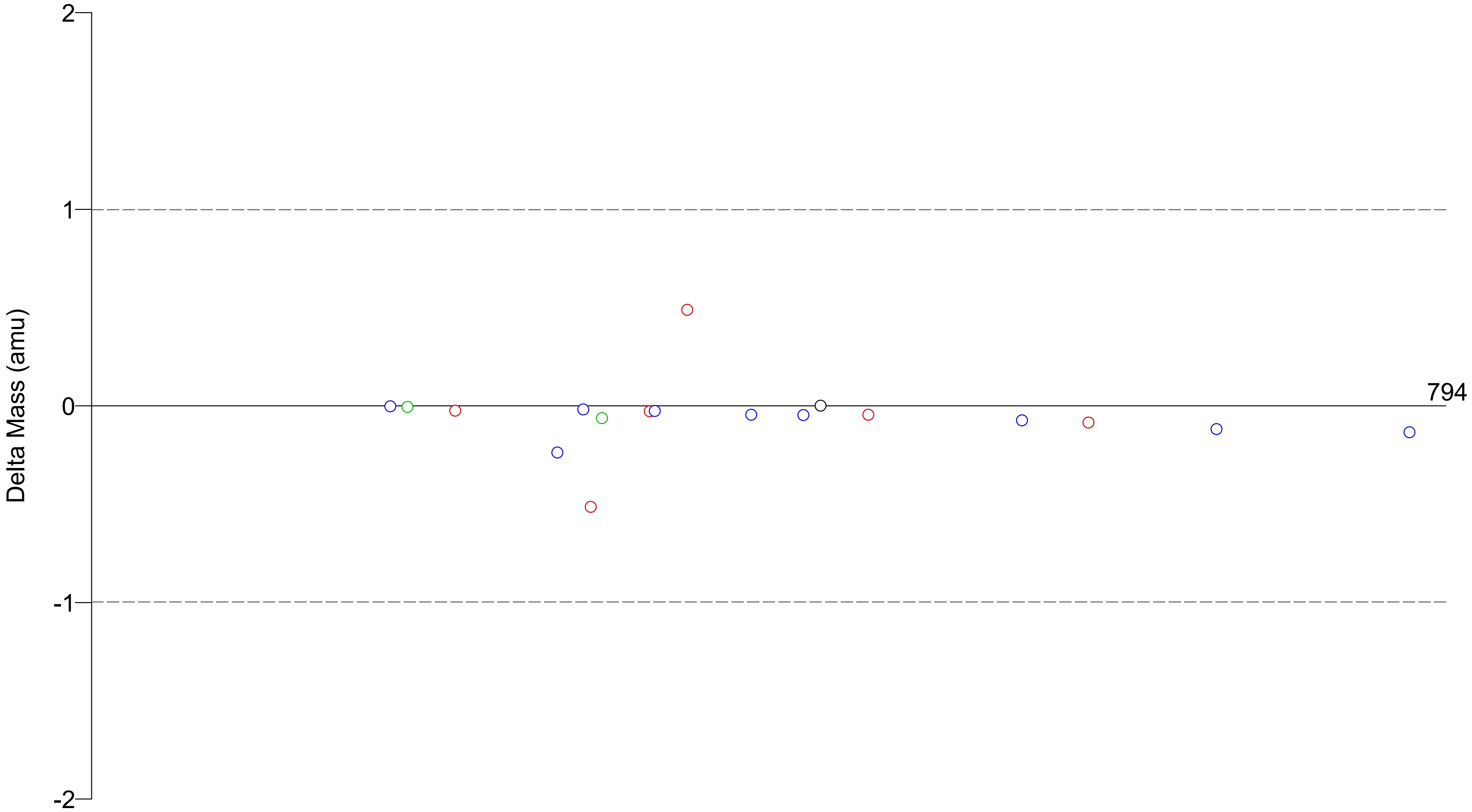


#19287468-1 NL: 5.11E5

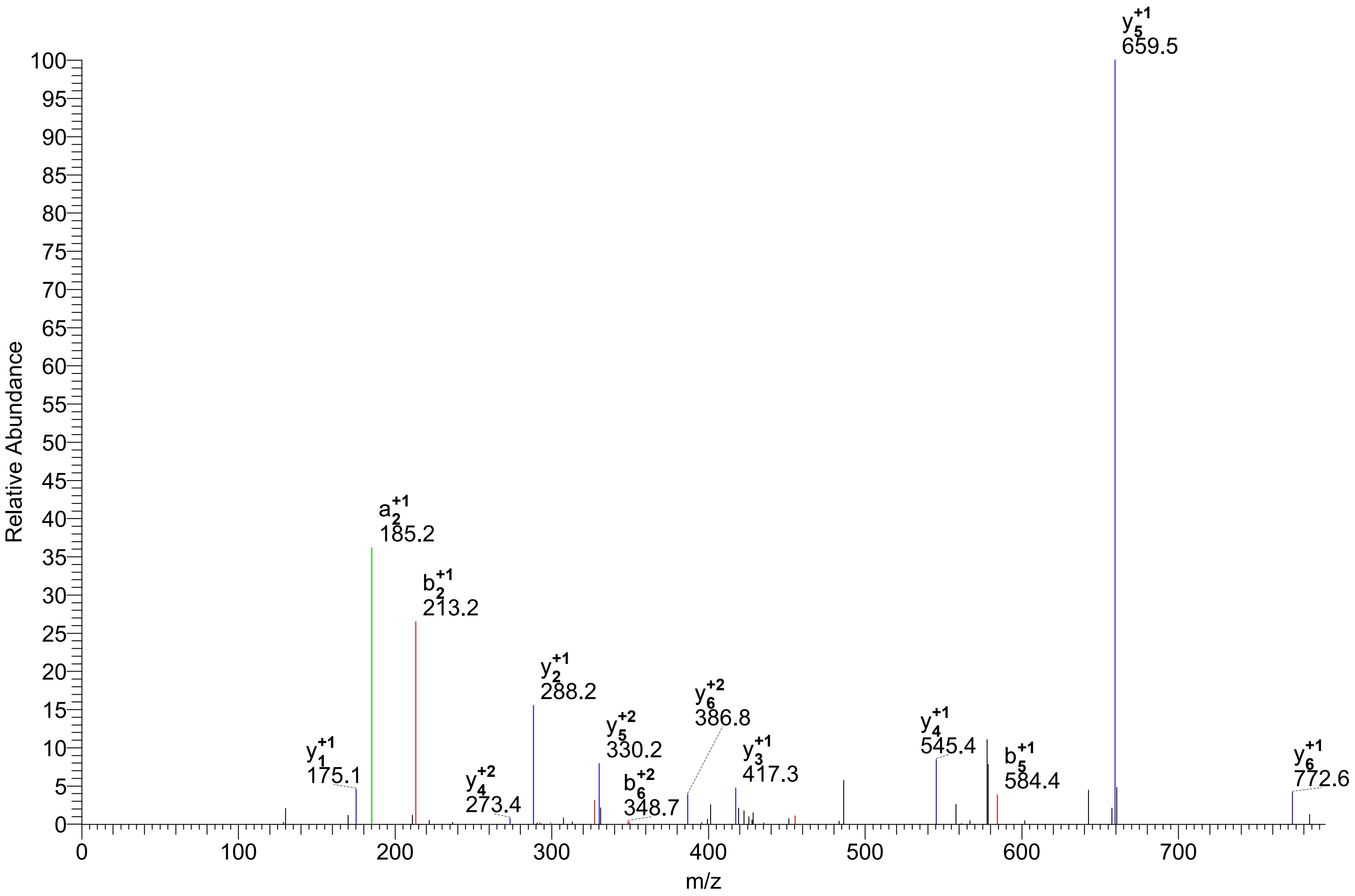


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00927914.1|VEGA:OTTHUMP0000                                  0.3     10.1     0.0        0
19287468 - 1  K.VLNQELR.A                              871.50    2  0.004    2.210  0.309    564.0  1   13/18   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 436.25
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions      B ions      B* ions     Bo ions      C ions     Y ions     Y* ions     Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 L    185.16     213.16                                       772.43
 N    299.21     327.20                                       659.35
 Q    427.27     455.26                                       545.30
 E    556.31     584.30                                       417.25
 L    669.39     697.39                                       288.20
 R                                                            175.12
```

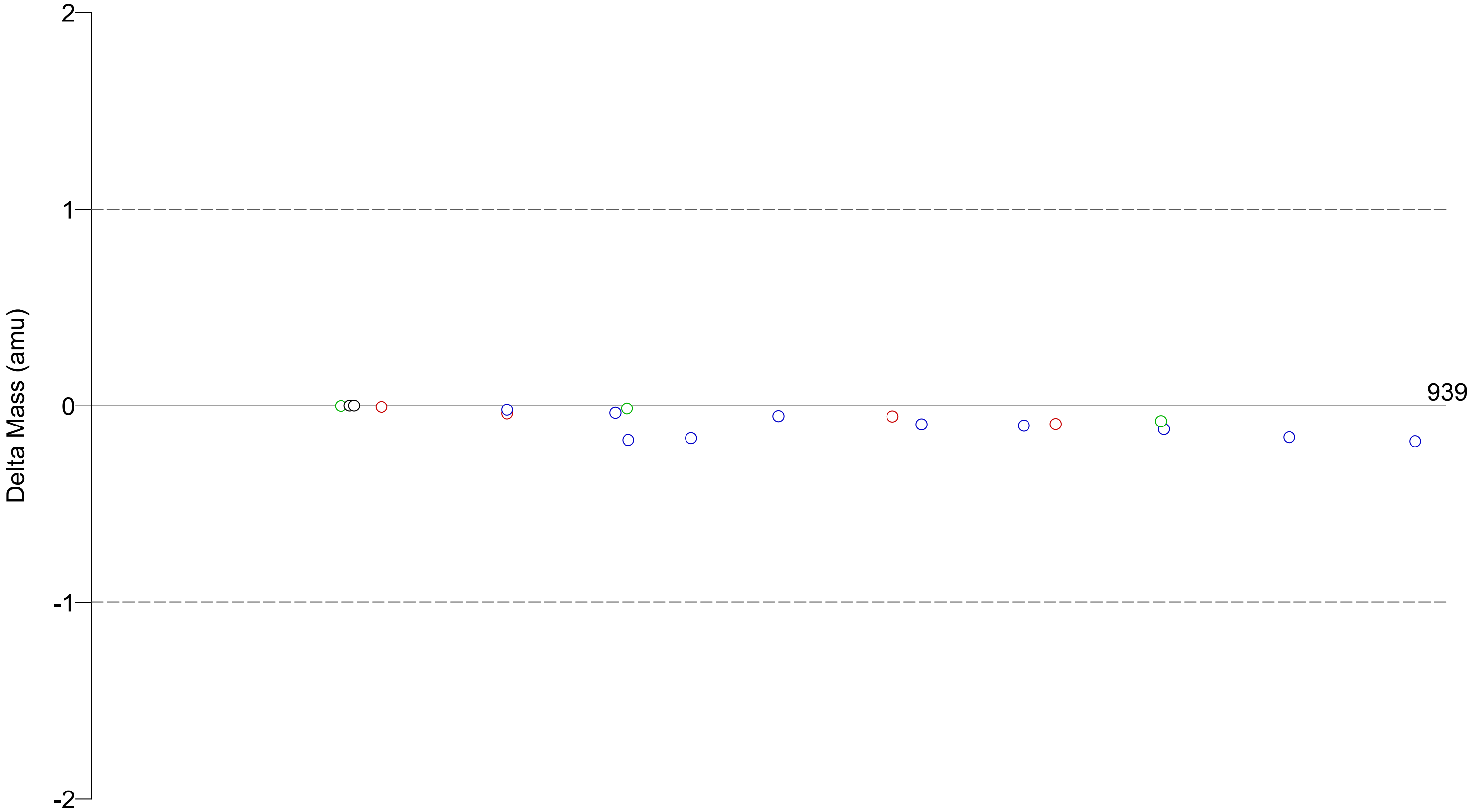


#19287468-1 NL: 5.11E5

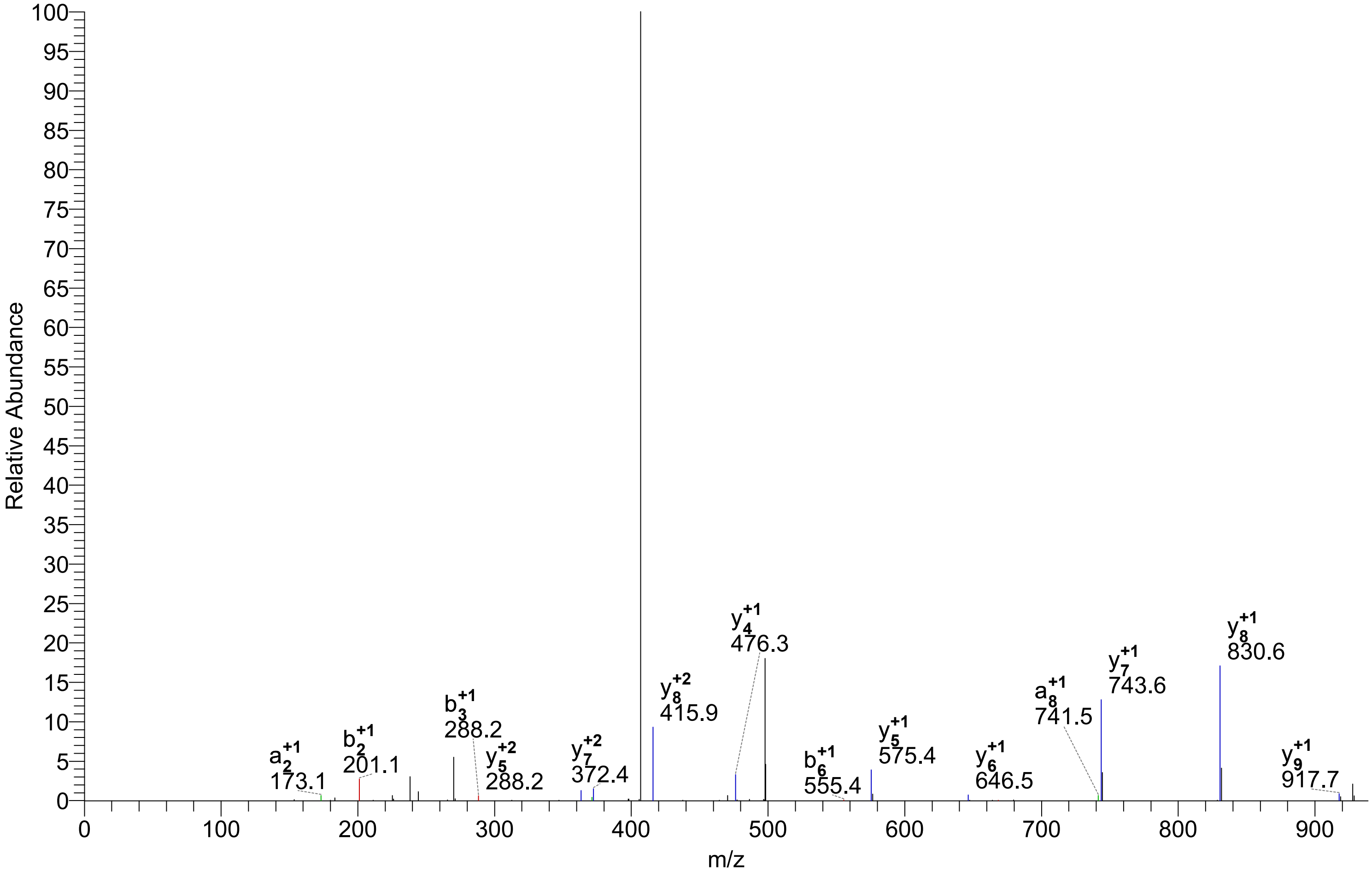


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00019580.1|SWISS-PROT:P00747|TREMBL:B2R7F8;B4DPH4;Q68DS    0.3     10.1     0.0       0
19287468 - 1  K.LSSPAVITDK.V                         1030.58   2  0.004   2.679  0.346   201.9  1   13/27

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 515.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13    201.12                                       917.49
 S    260.16    288.16                                       830.46
 P    357.21    385.21                                       743.43
 A    428.25    456.25                                       646.38
 V    527.32    555.31                                       575.34
 I    640.40    668.40                                       476.27
 T    741.45    769.45                                       363.19
 D    856.48    884.47                                       262.14
 K                                                           147.11
```

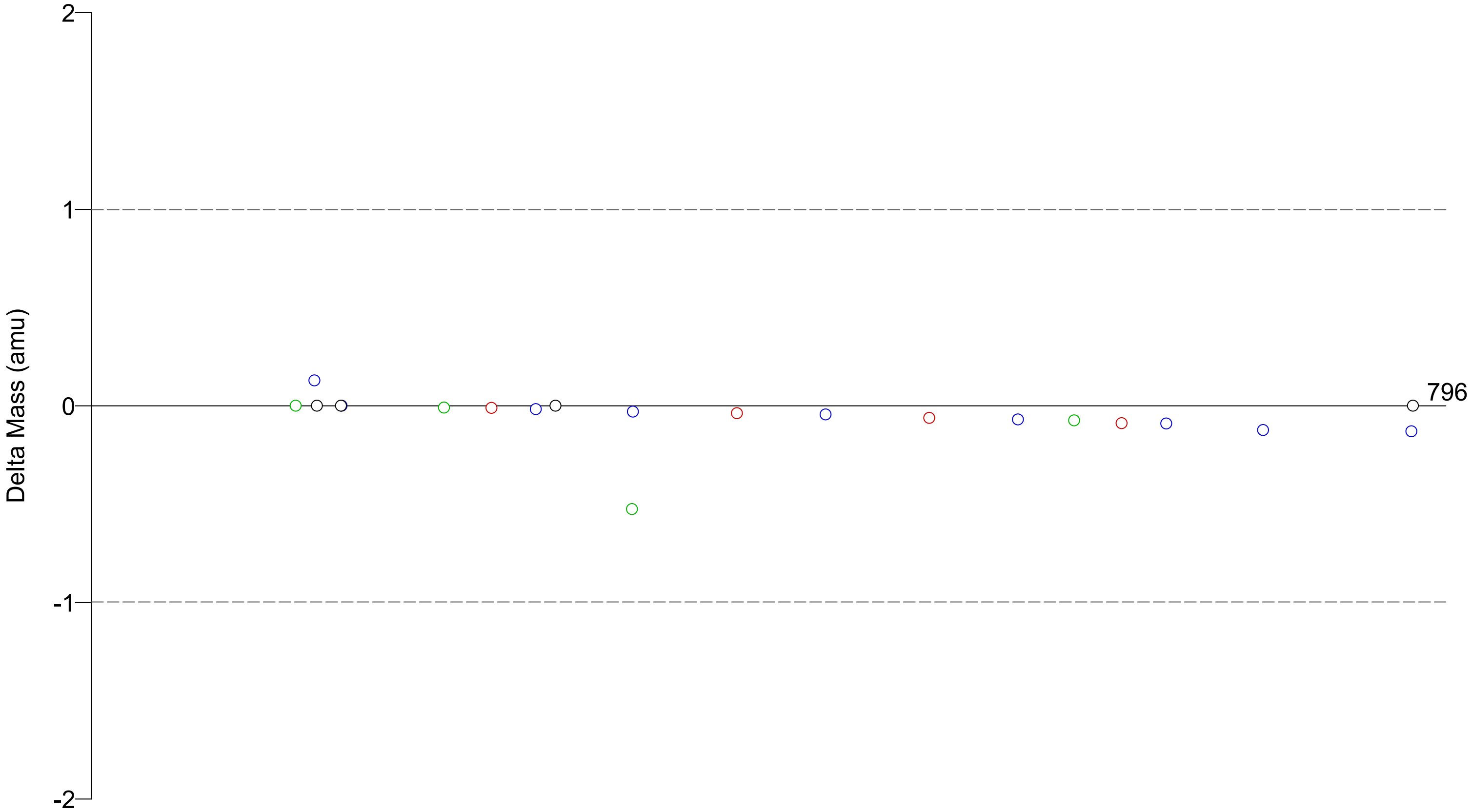


#19287468-1 NL: 6.13E5

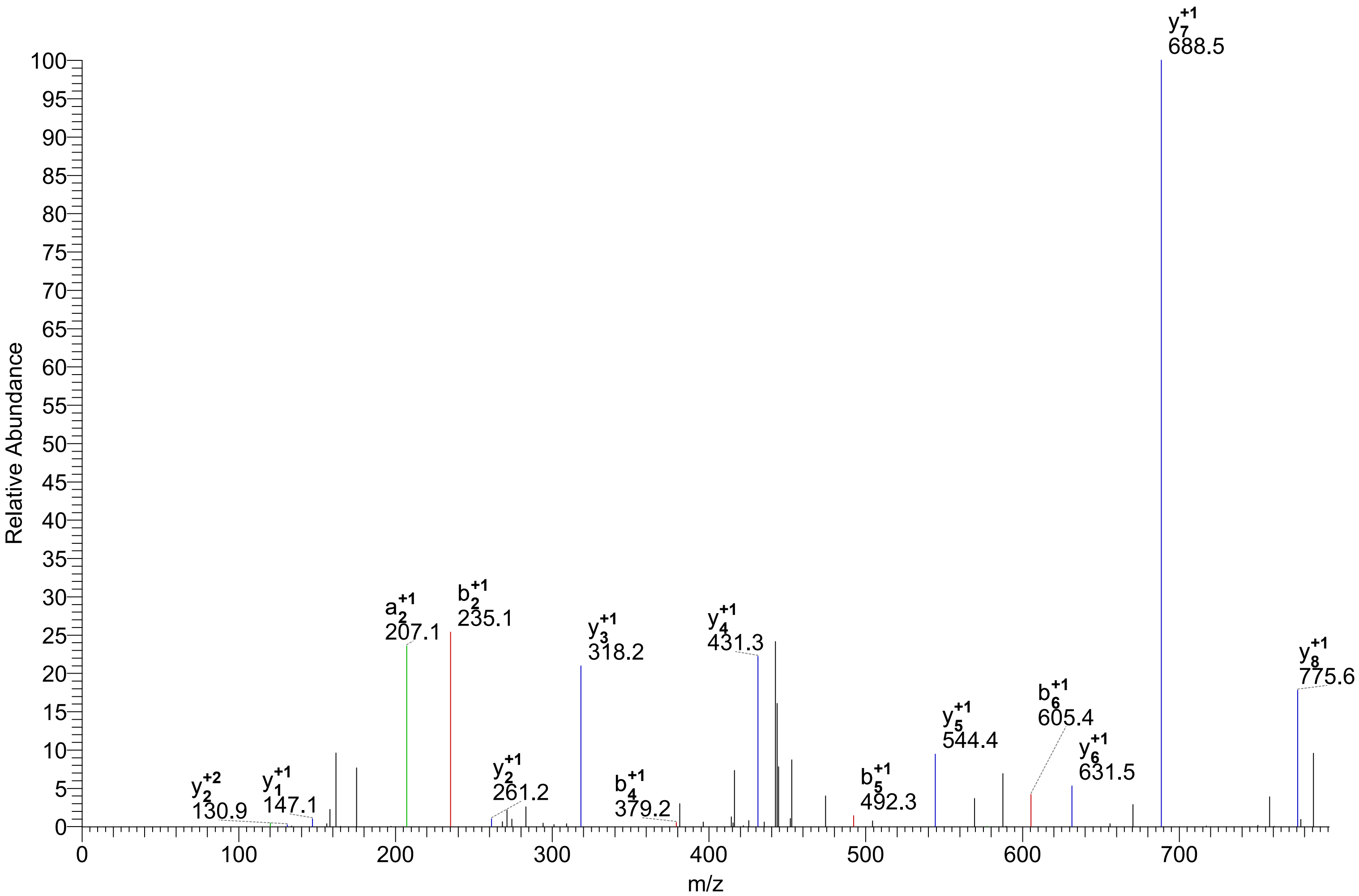


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00477714.5|TREMBL:Q5NV62|ENSEMBL:ENSP00000374818|VEGA:O    0.3     10.1     0.0        0
19287468 - 1  R.FSGSILGNK.A                           922.50    2  0.004    2.914  0.340   661.6  1   16/24   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 461.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                      775.43
 G    264.13     292.13                                      688.40
 S    351.17     379.16                                      631.38
 I    464.25     492.25                                      544.35
 L    577.33     605.33                                      431.26
 G    634.36     662.35                                      318.18
 N    748.40     776.39                                      261.16
 K                                                           147.11
```

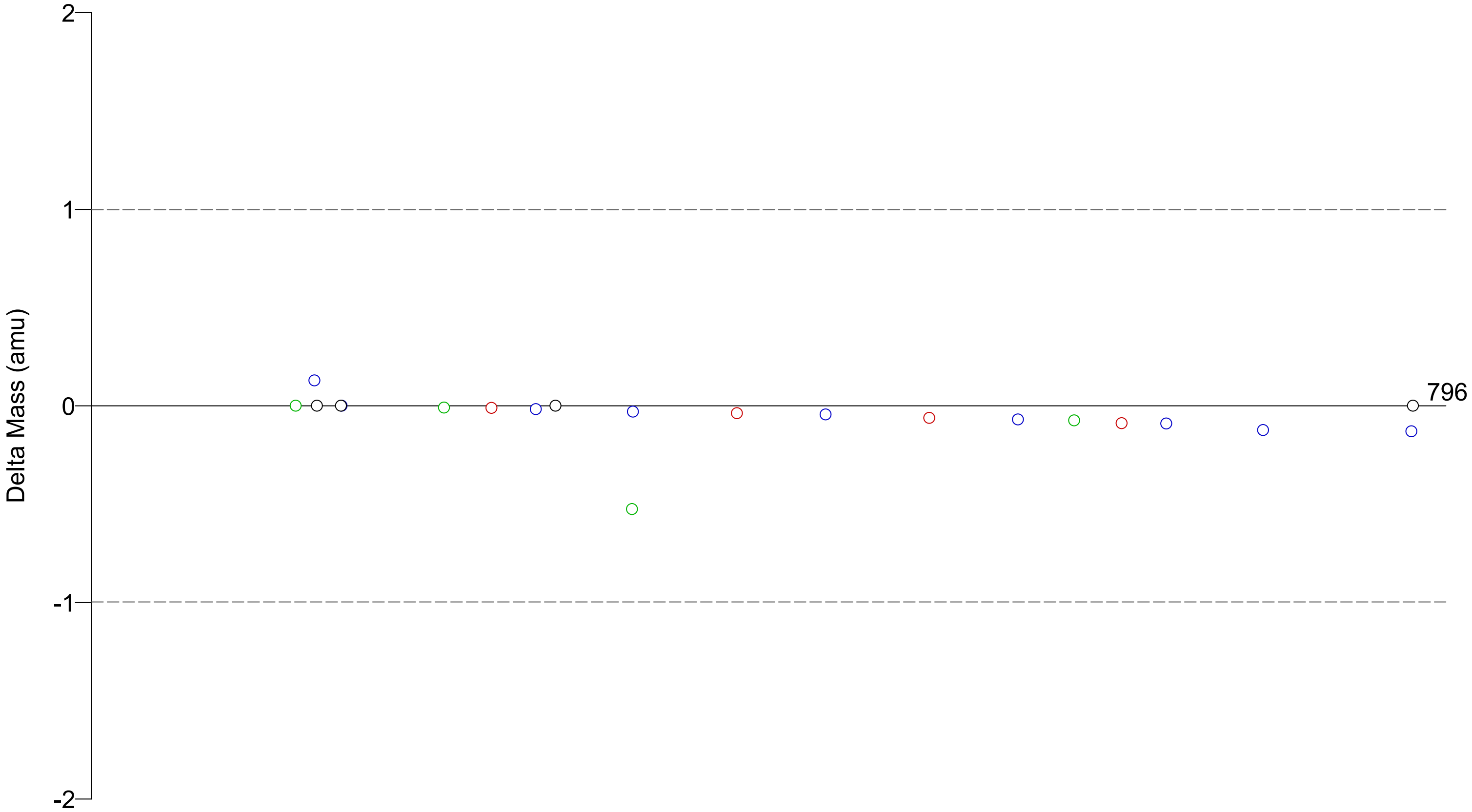


#19287468-1 NL: 1.73E5

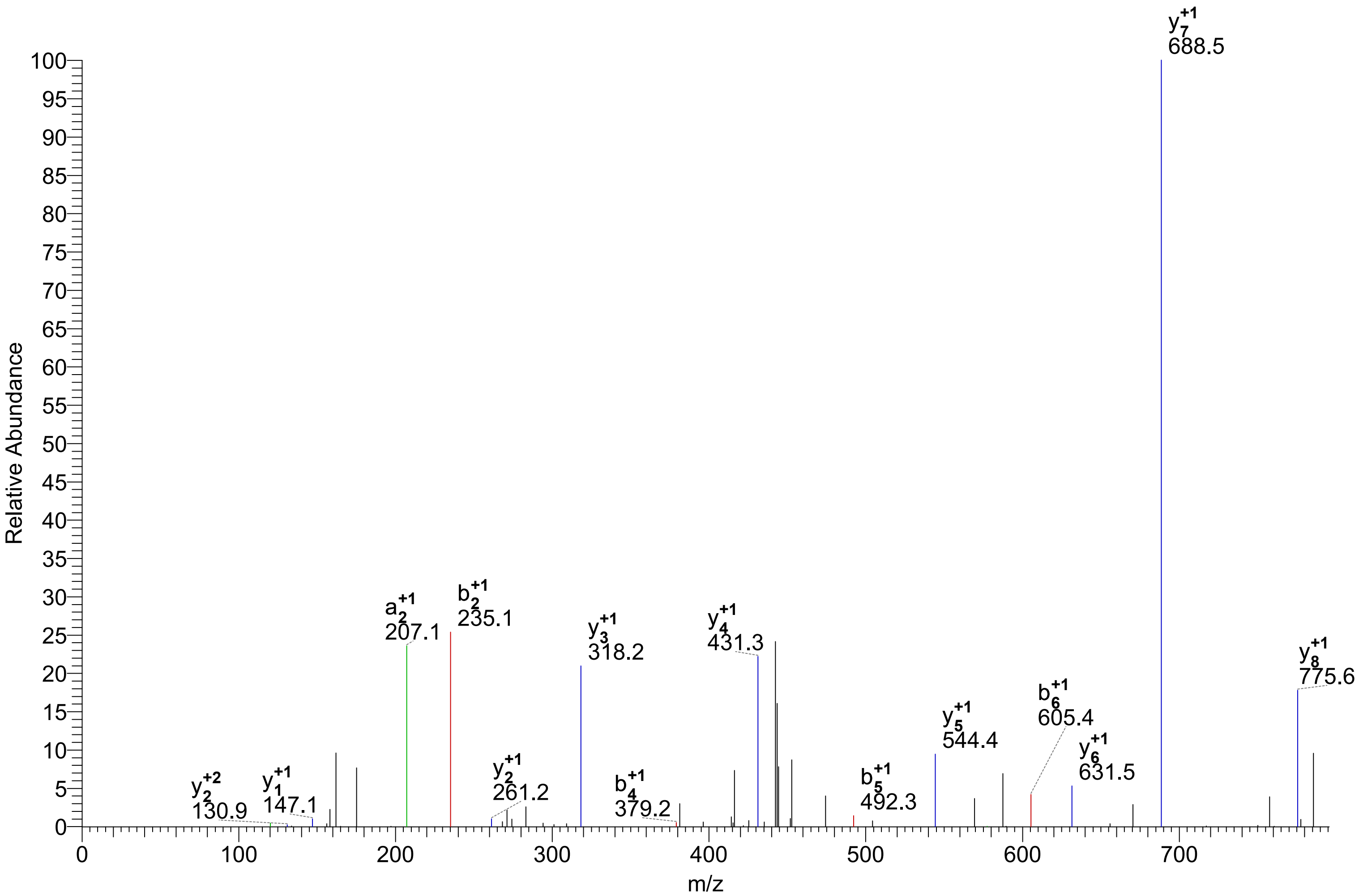


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z  P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00873719.1|TREMBL:A8MXK2|EN                                0.3      10.1     0.0       0
19287468 - 1  R.FSGSILGNK.A                           922.50    2  0.004    2.914  0.340   661.6  1   16/24   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 461.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 S    207.11     235.11                                      775.43
 G    264.13     292.13                                      688.40
 S    351.17     379.16                                      631.38
 I    464.25     492.25                                      544.35
 L    577.33     605.33                                      431.26
 G    634.36     662.35                                      318.18
 N    748.40     776.39                                      261.16
 K                                                           147.11
```

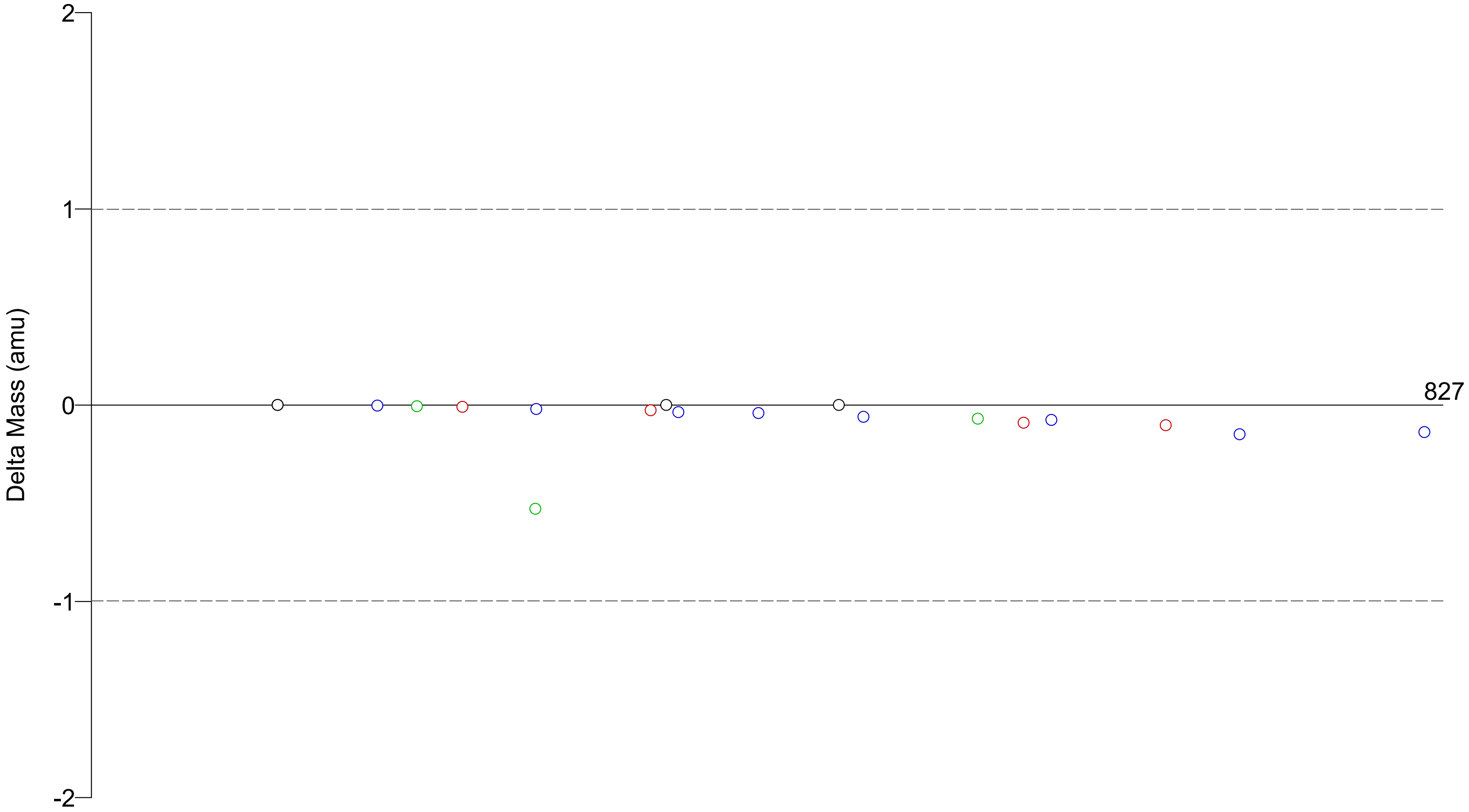


#19287468-1 NL: 1.73E5

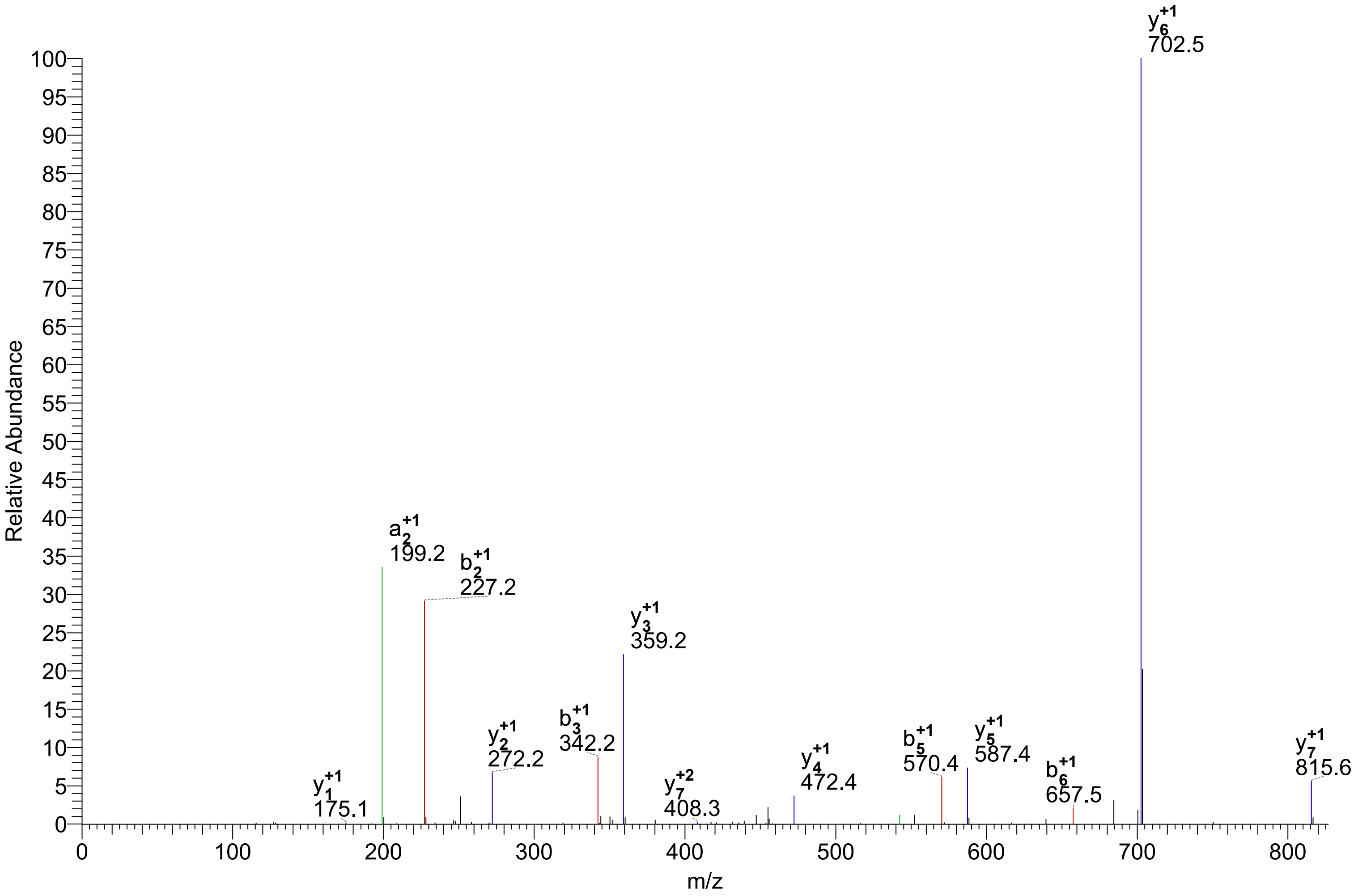


```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+     z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00218192.3|SWISS-PROT:Q14624-2|TREMBL:B7Z544|ENSEMBL:EN    0.3     10.1     0.0       0
19287468 - 1  K.ILDDLSPR.D                          928.51    2  0.005    2.464  0.419   541.6  1   14/21   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 464.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18     227.18                                      815.43
 D    314.21     342.20                                      702.34
 D    429.23     457.23                                      587.31
 L    542.32     570.31                                      472.29
 S    629.35     657.35                                      359.20
 P    726.40     754.40                                      272.17
 R                                                           175.12
```

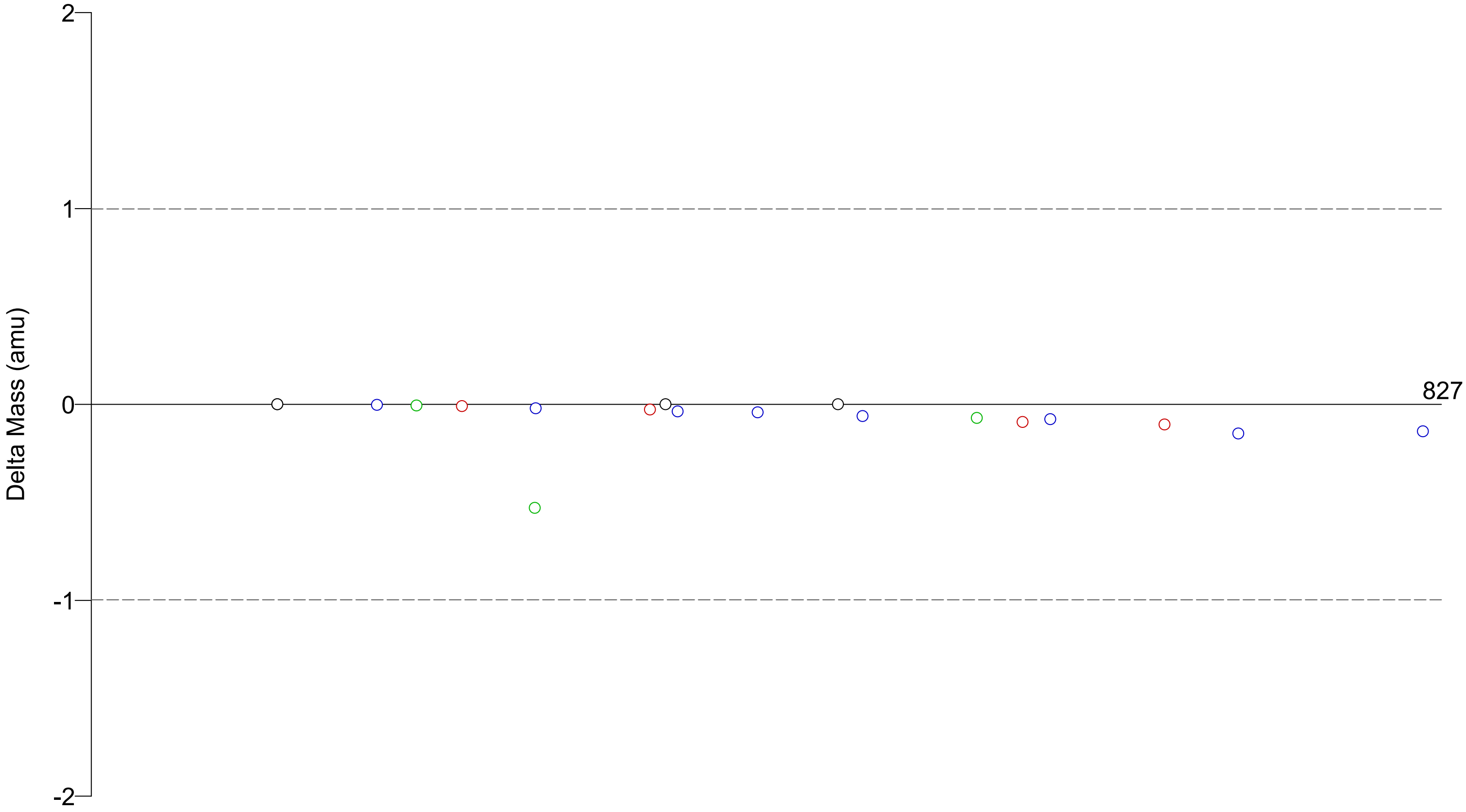


#19287468-1 NL: 1.36E6

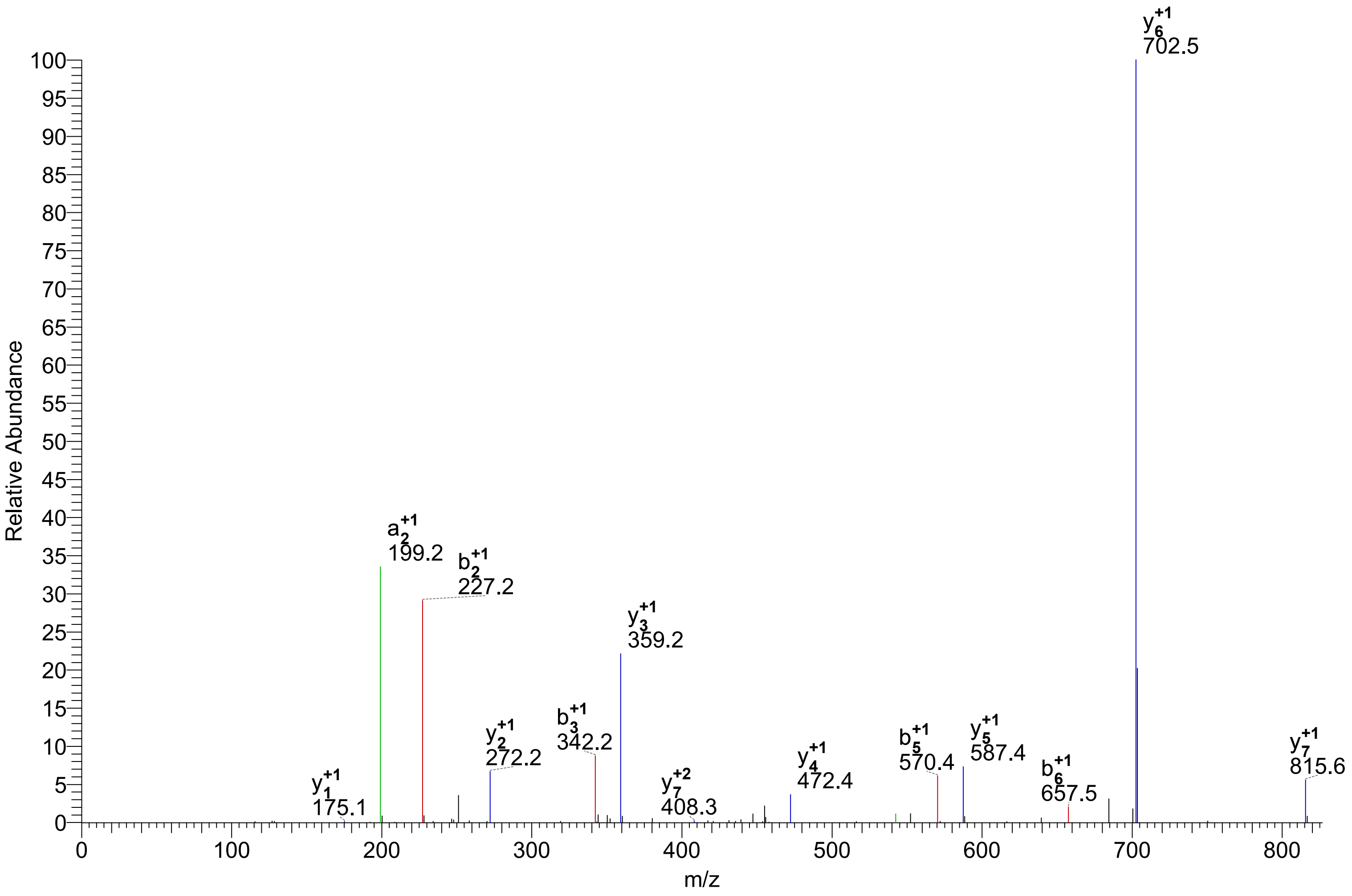


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00791097.2|TREMBL:B7Z8Q7|VE                                0.3     10.1     0.0       0
19287468 - 1  K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 464.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18     227.18                                      815.43
 D    314.21     342.20                                      702.34
 D    429.23     457.23                                      587.31
 L    542.32     570.31                                      472.29
 S    629.35     657.35                                      359.20
 P    726.40     754.40                                      272.17
 R                                                           175.12
```

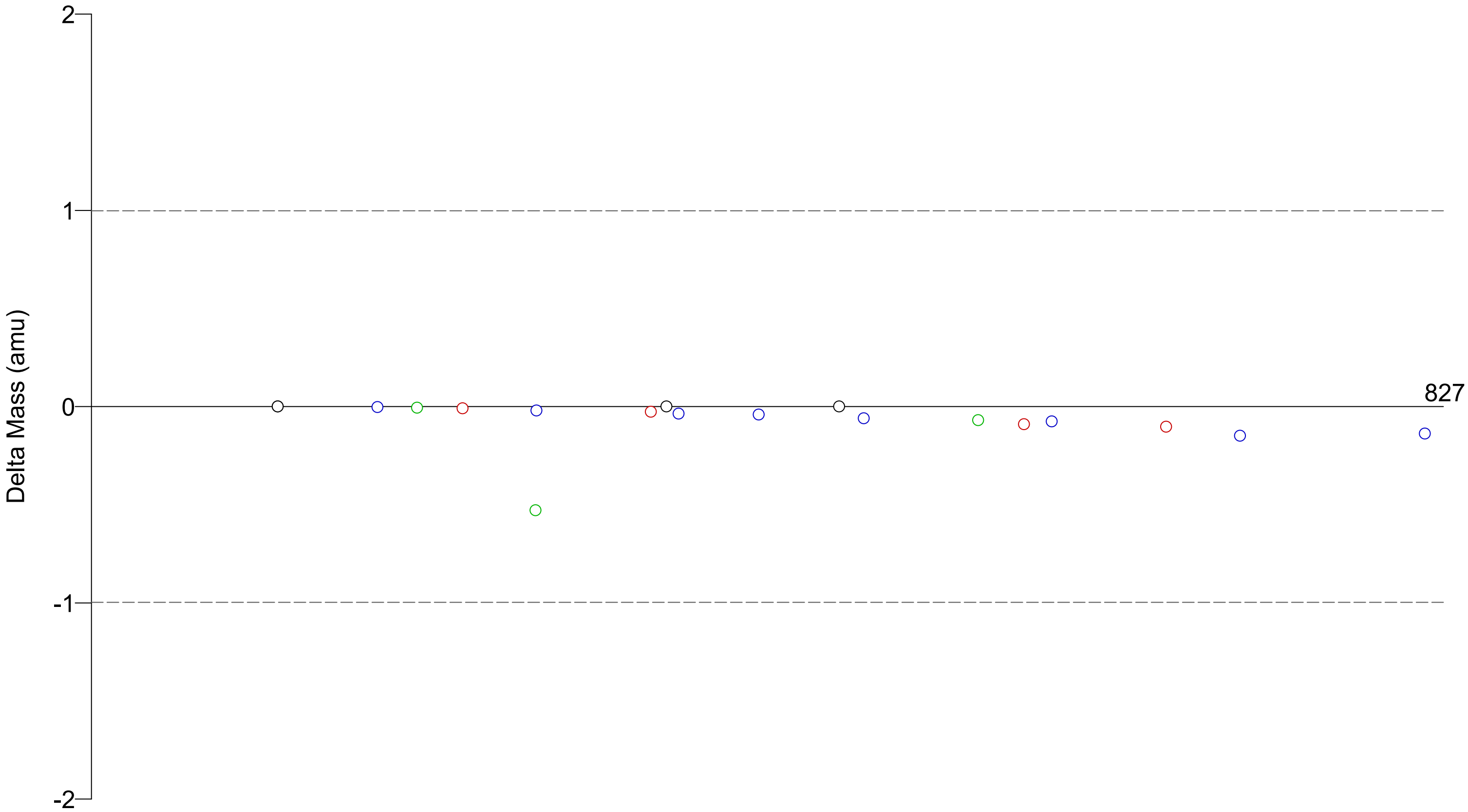


#19287468-1 NL: 1.36E6

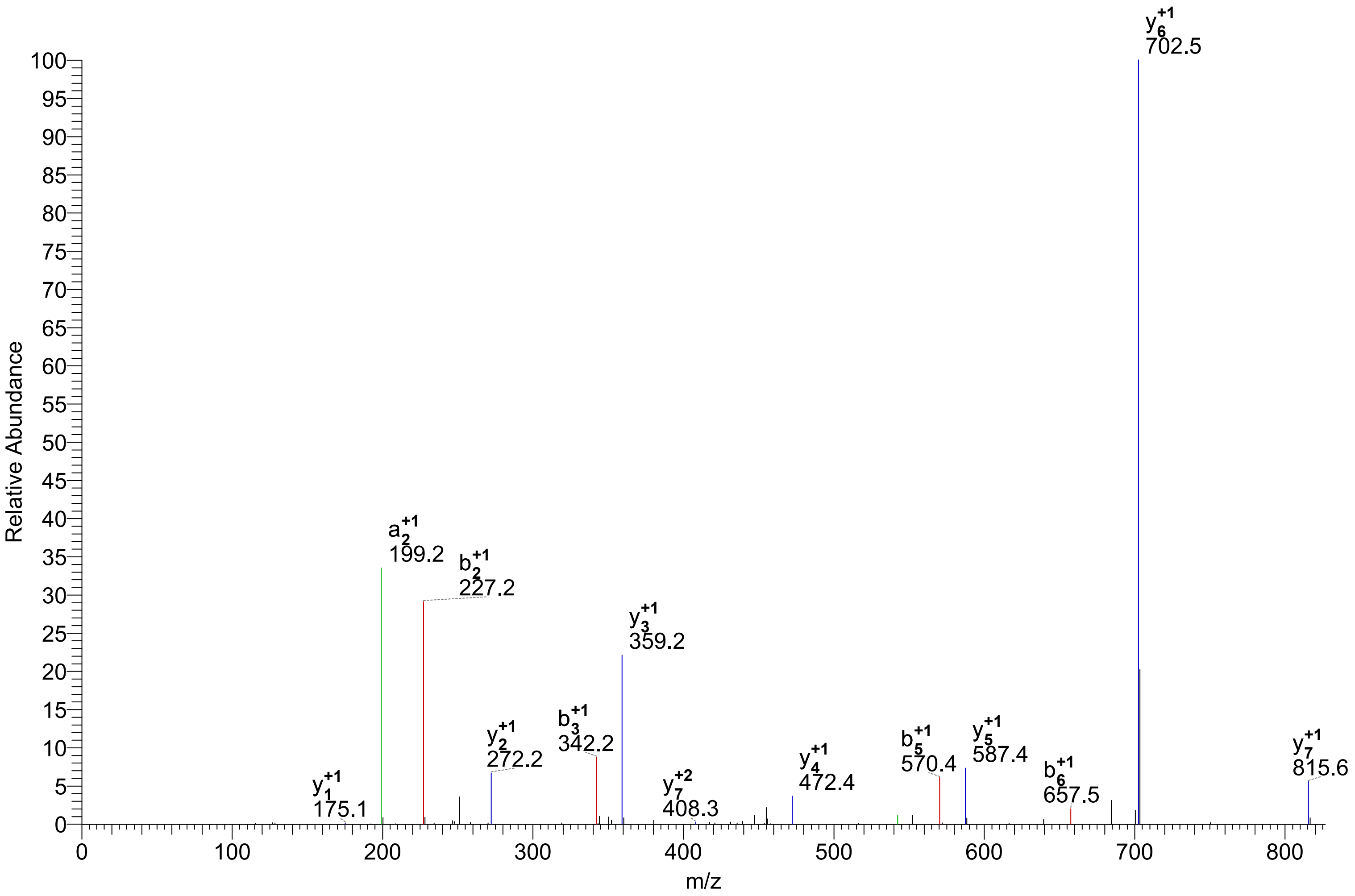


```
Reference                                                    P      Score   Coverage   Accession
Scan(s)       Sequence                            MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00798006.1|VEGA:OTTHUMP0000                           0.3     10.1     0.0       0
19287468 - 1  K.ILDDLSPR.D                      928.51     2  0.005    2.464  0.419   541.6  1   14/21   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 464.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18     227.18                                      815.43
 D    314.21     342.20                                      702.34
 D    429.23     457.23                                      587.31
 L    542.32     570.31                                      472.29
 S    629.35     657.35                                      359.20
 P    726.40     754.40                                      272.17
 R                                                           175.12
```

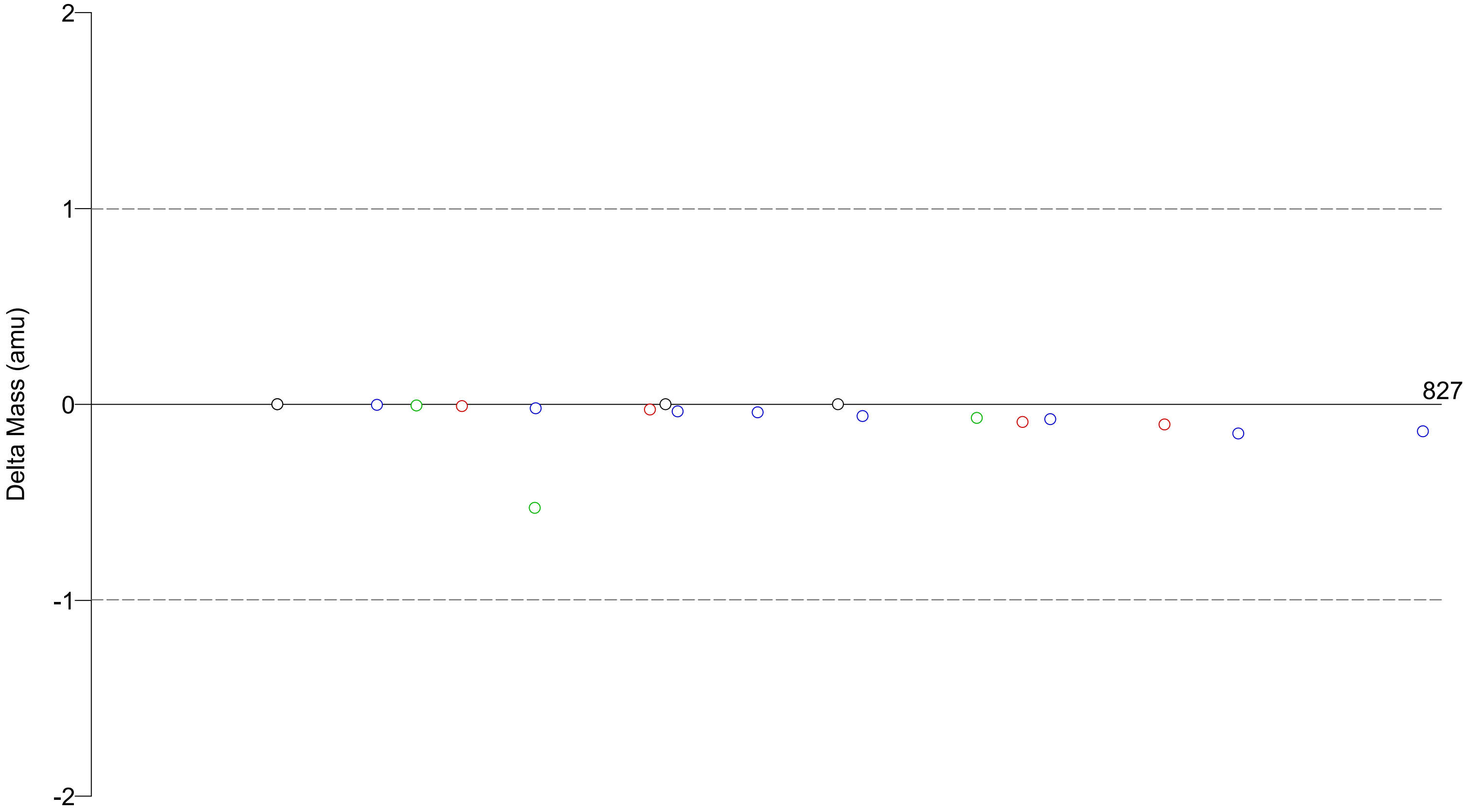


#19287468-1 NL: 1.36E6

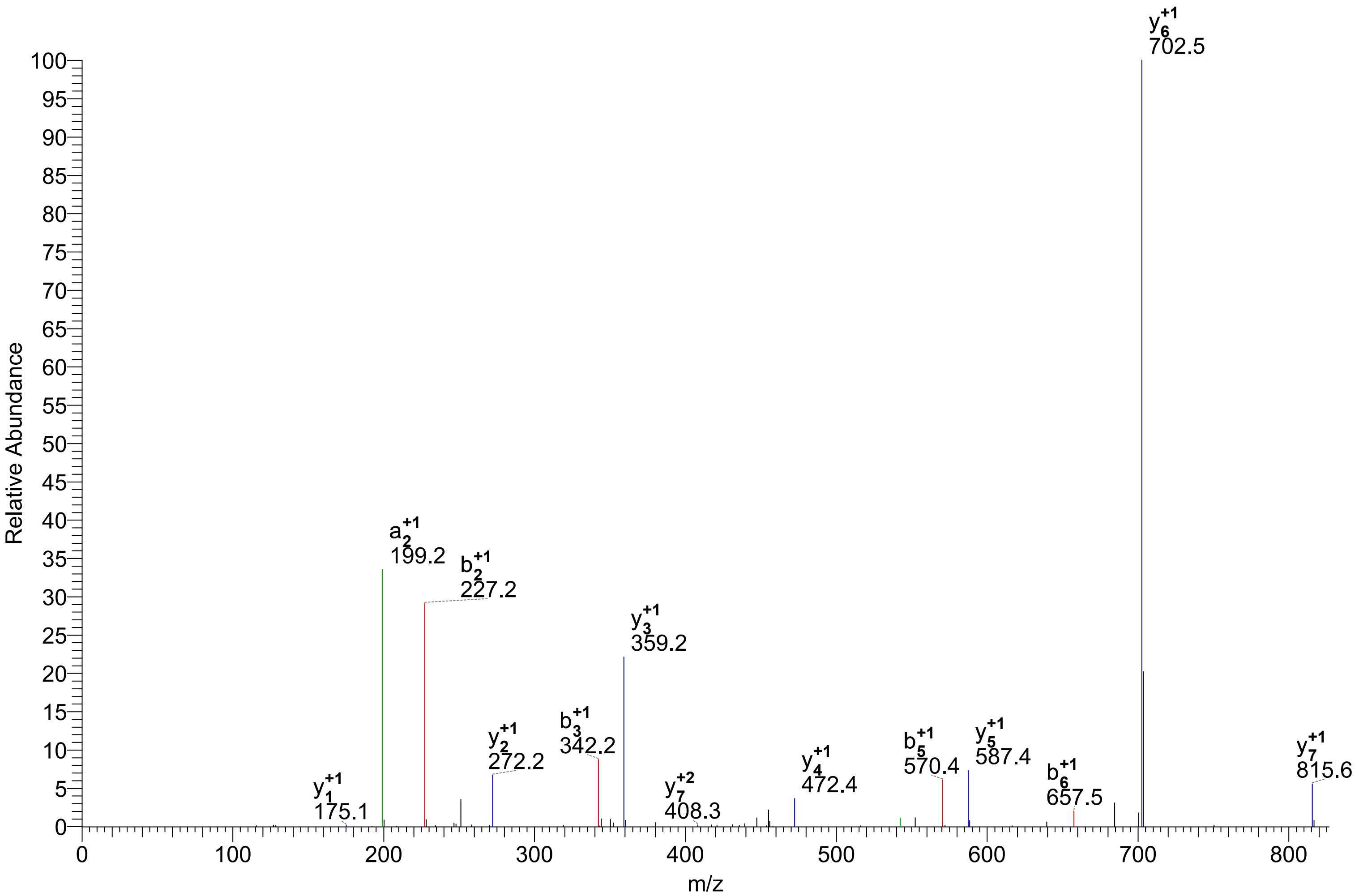


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00896413.1|ENSEMBL:ENSP0000                                0.3     10.1     0.0       0
19287468 - 1  K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 464.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18     227.18                                      815.43
 D    314.21     342.20                                      702.34
 D    429.23     457.23                                      587.31
 L    542.32     570.31                                      472.29
 S    629.35     657.35                                      359.20
 P    726.40     754.40                                      272.17
 R                                                           175.12
```

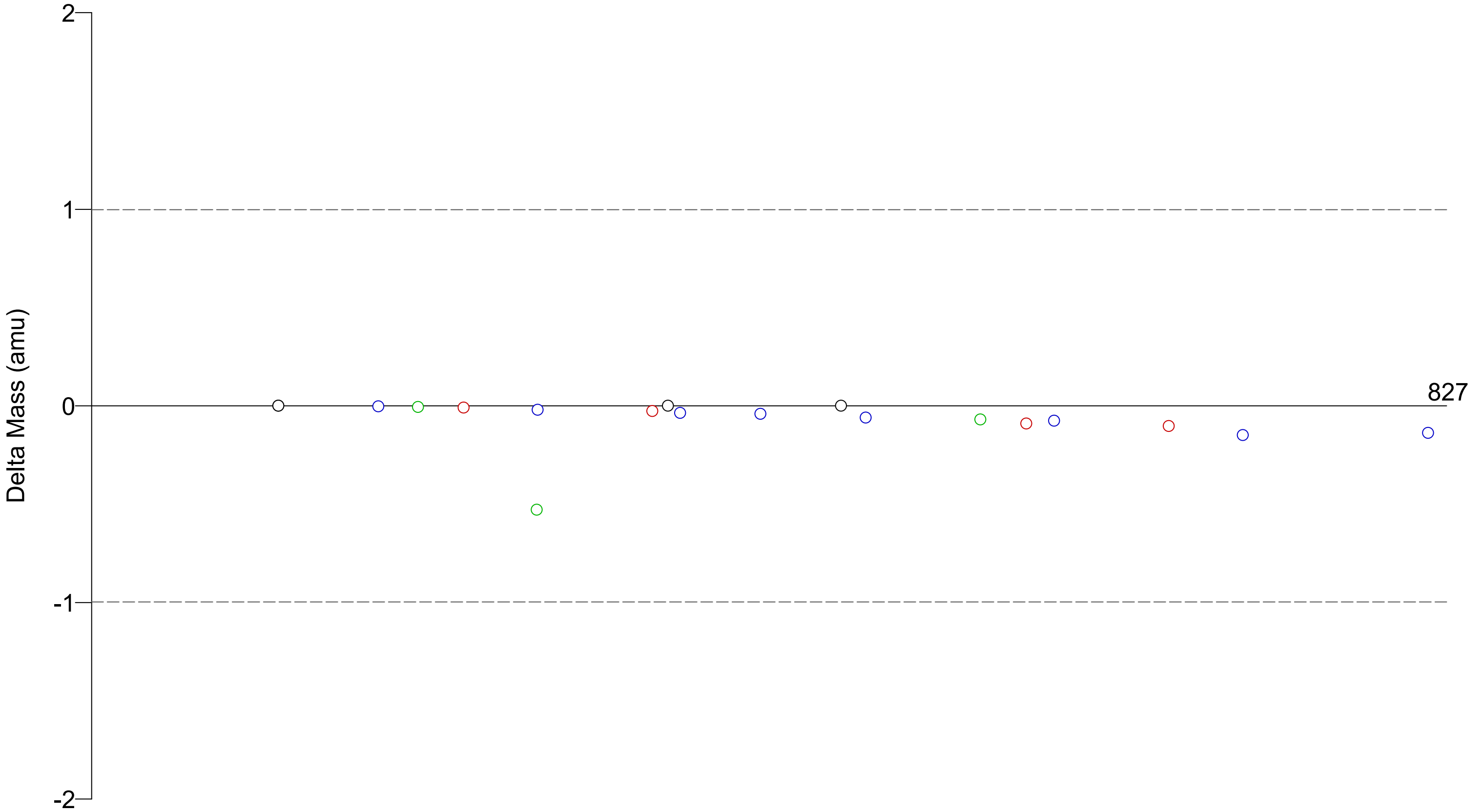


#19287468-1 NL: 1.36E6

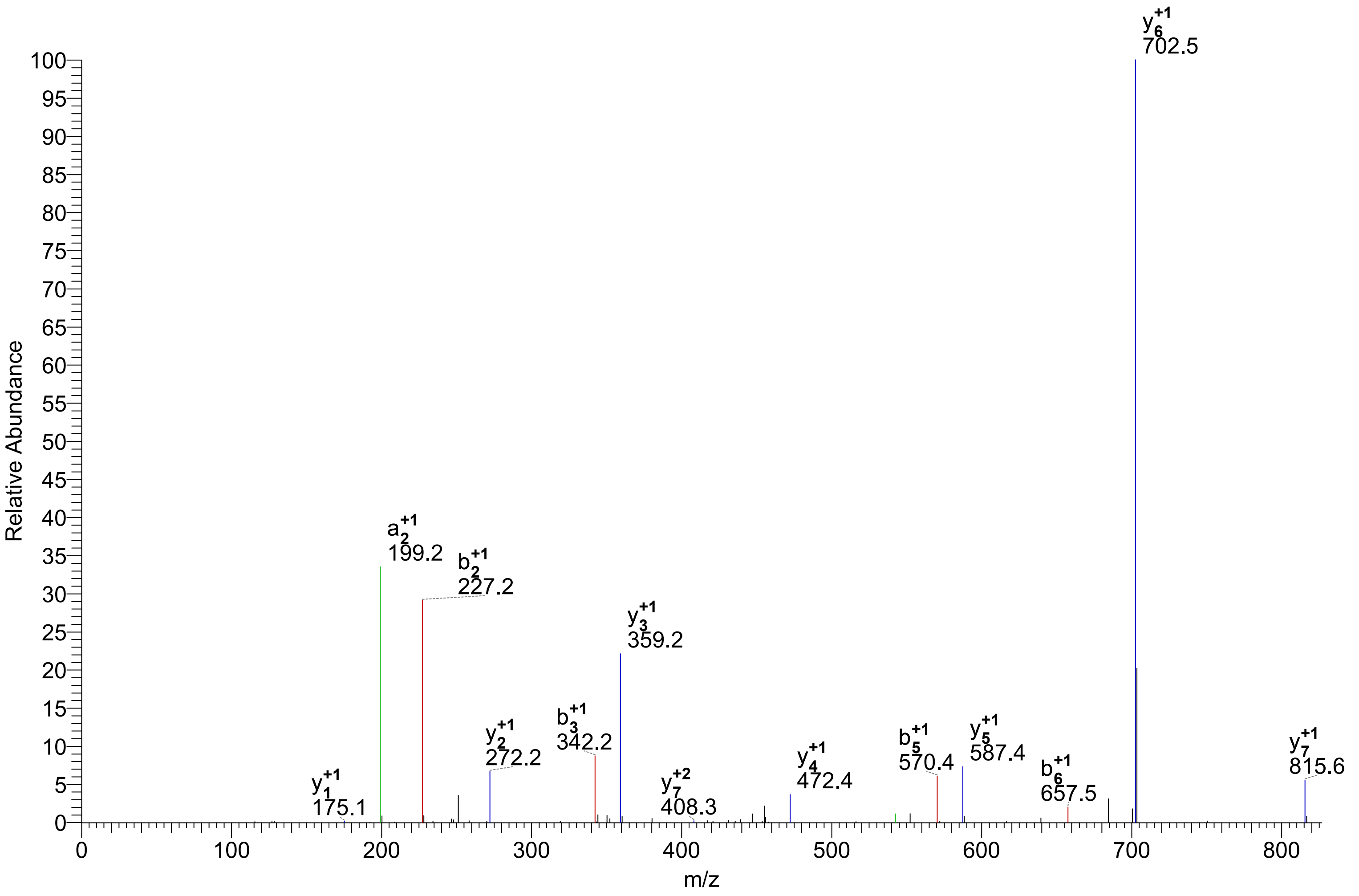


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                make+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00896419.2|SWISS-PROT:Q1462                                0.3     10.1     0.0       0
19287468 - 1  K.ILDDLSPR.D                           928.51    2  0.005   2.464  0.419   541.6  1   14/21   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 464.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18     227.18                                       815.43
 D    314.21     342.20                                       702.34
 D    429.23     457.23                                       587.31
 L    542.32     570.31                                       472.29
 S    629.35     657.35                                       359.20
 P    726.40     754.40                                       272.17
 R                                                            175.12
```

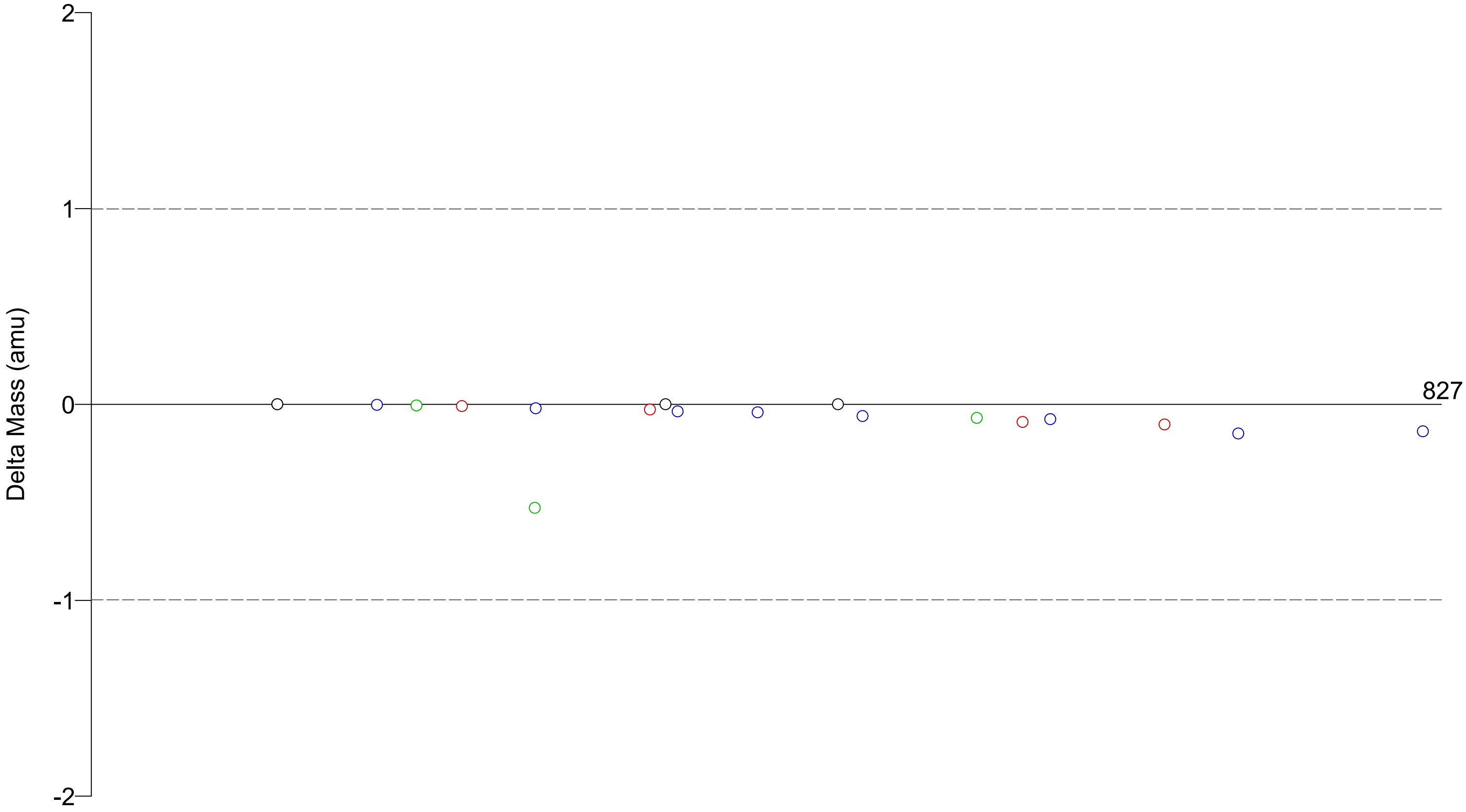


#19287468-1 NL: 1.36E6

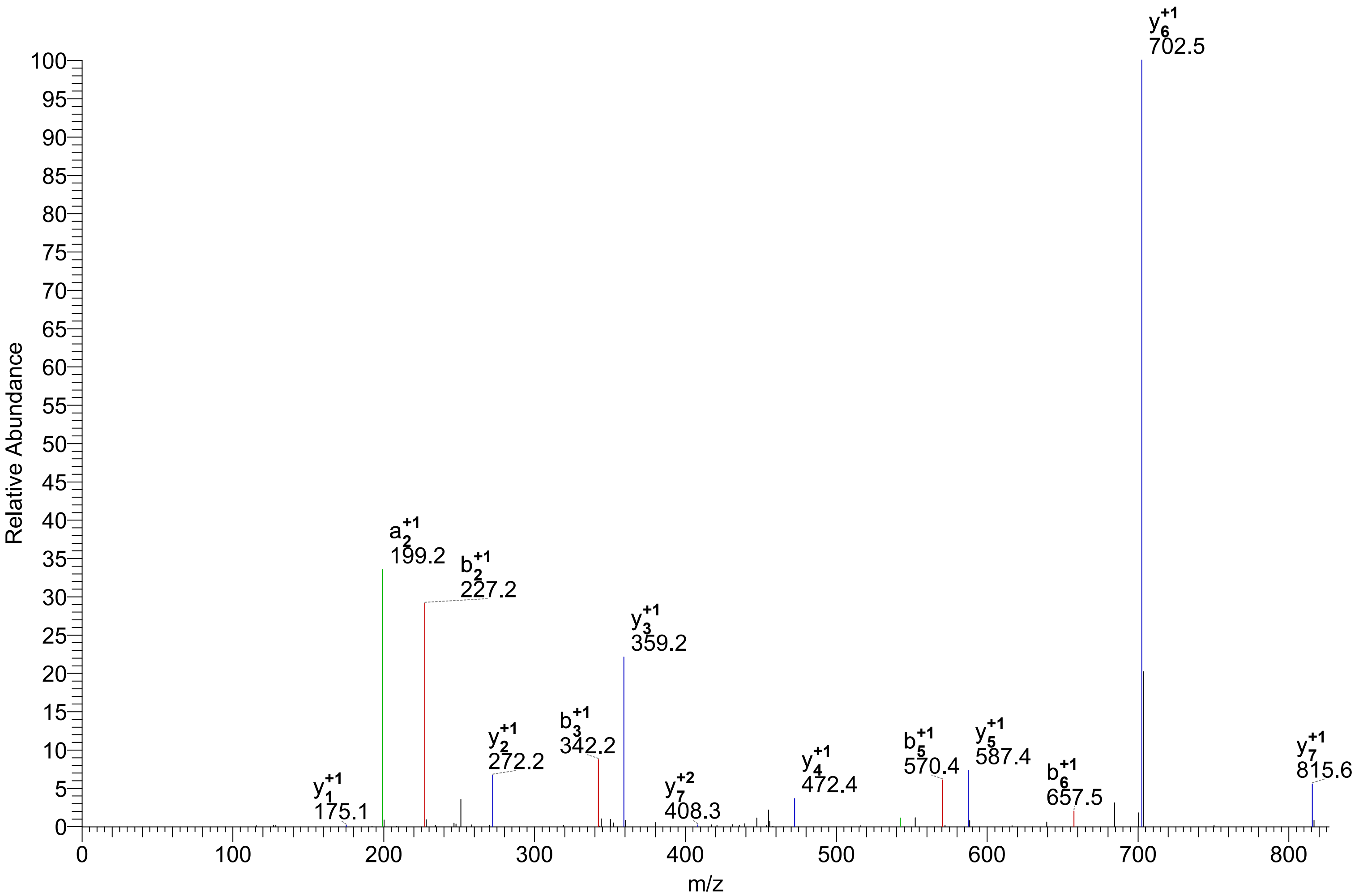


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00922043.1|VEGA:OTTHUMP0000                                    0.3     10.1     0.0       0
19287468 - 1  K.ILDDLSPR.D                                 928.51    2  0.005   2.464  0.419   541.6  1   14/21   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 464.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 L    199.18    227.18                                      815.43
 D    314.21    342.20                                      702.34
 D    429.23    457.23                                      587.31
 L    542.32    570.31                                      472.29
 S    629.35    657.35                                      359.20
 P    726.40    754.40                                      272.17
 R                                                          175.12
```

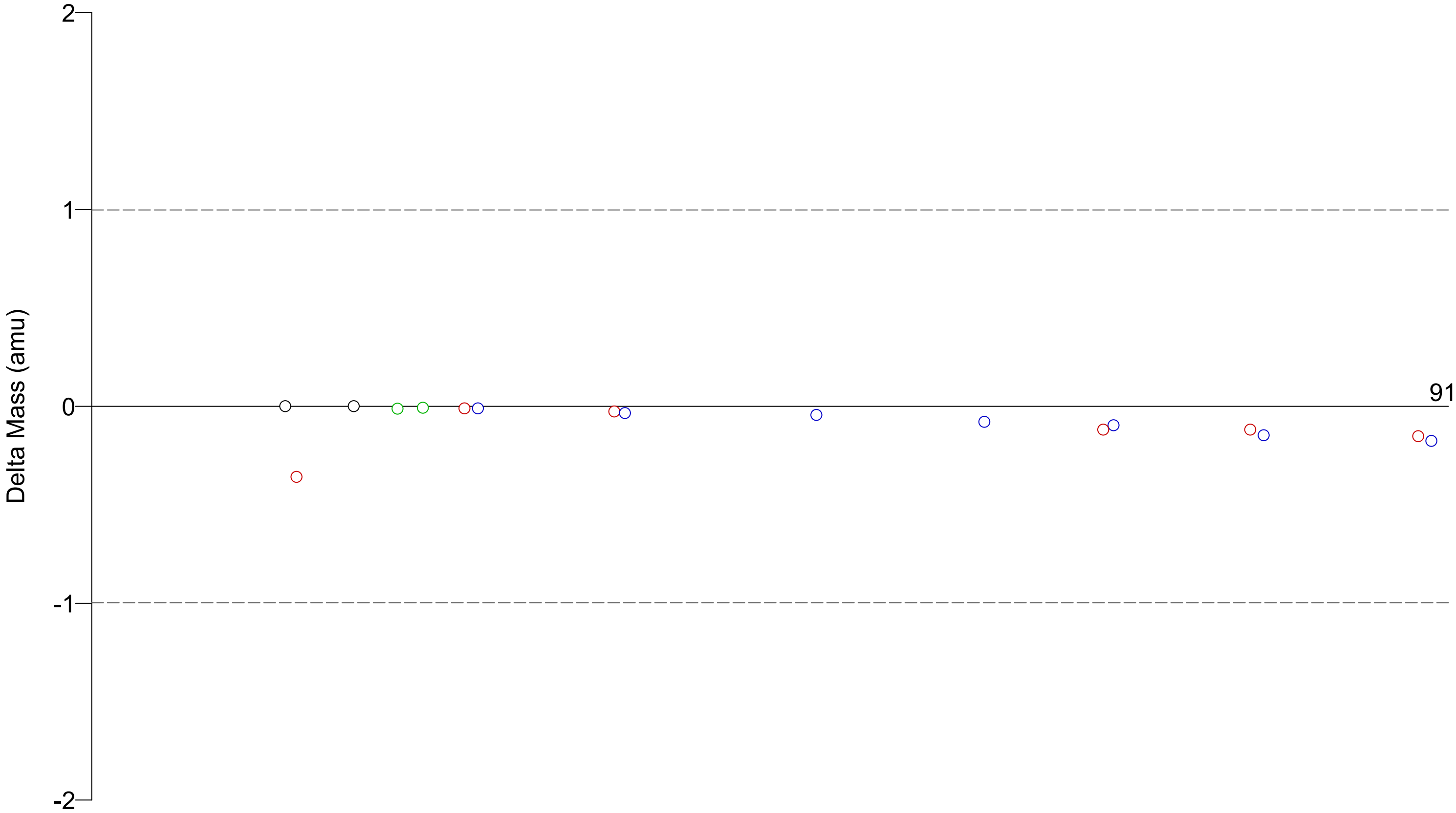


#19287468-1 NL: 1.36E6

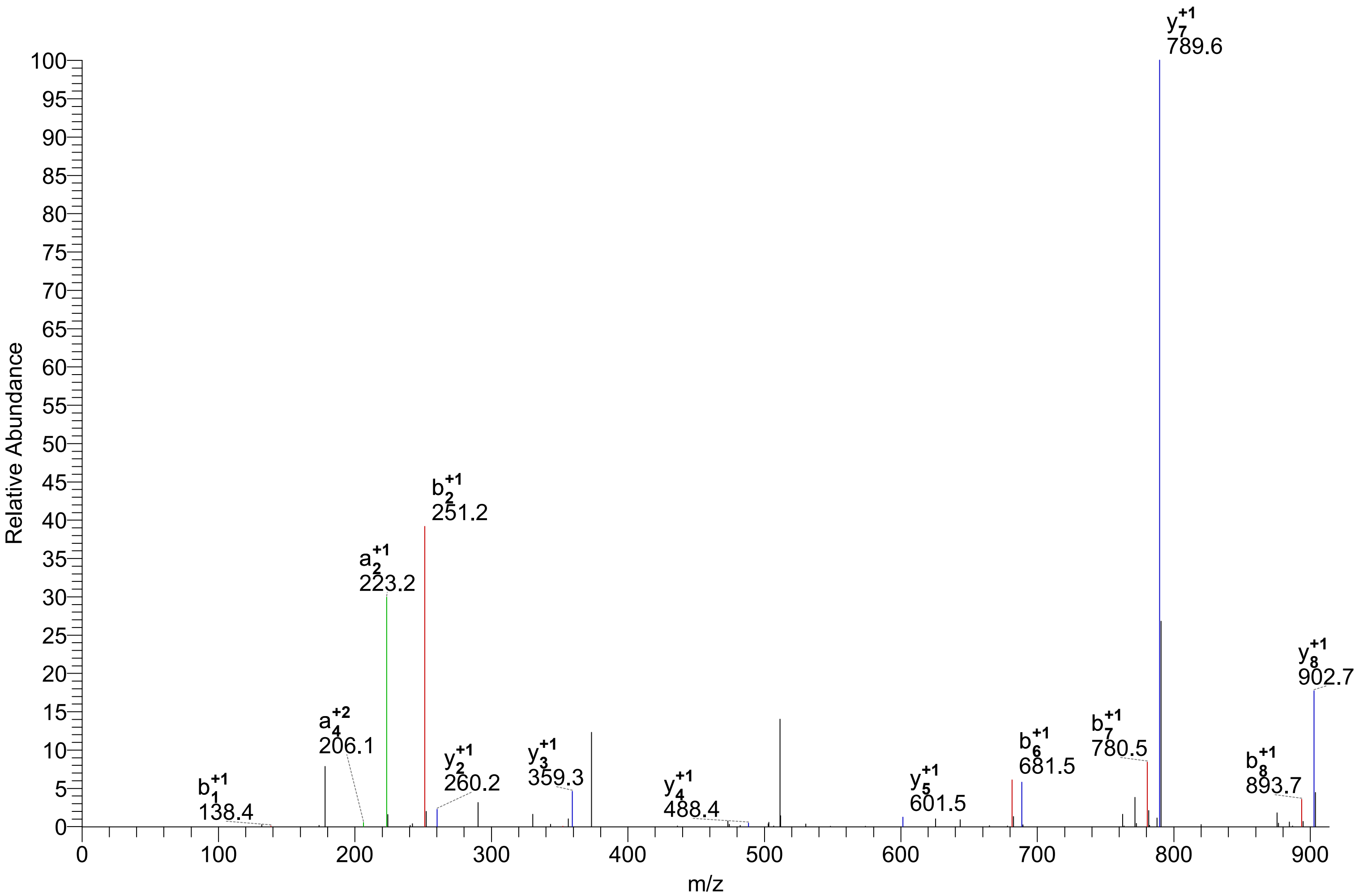


```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00022295.1|SWISS-PROT:P10720|TREMBL:A1L4S0|ENSEMBL:ENSP     0.5     10.1     0.0       0
2118291816 -  R.HITSLEVIK.A                            1039.61   2  0.01     2.472  0.301   457.5  1   14/24   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 520.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 H    110.07     138.07
 I    223.16     251.15                                      902.56
 T    324.20     352.20                                      789.47
 S    411.24     439.23                                      688.42
 L    524.32     552.31                                      601.39
 E    653.36     681.36                                      488.31
 V    752.43     780.43                                      359.27
 I    865.51     893.51                                      260.20
 K                                                           147.11
```

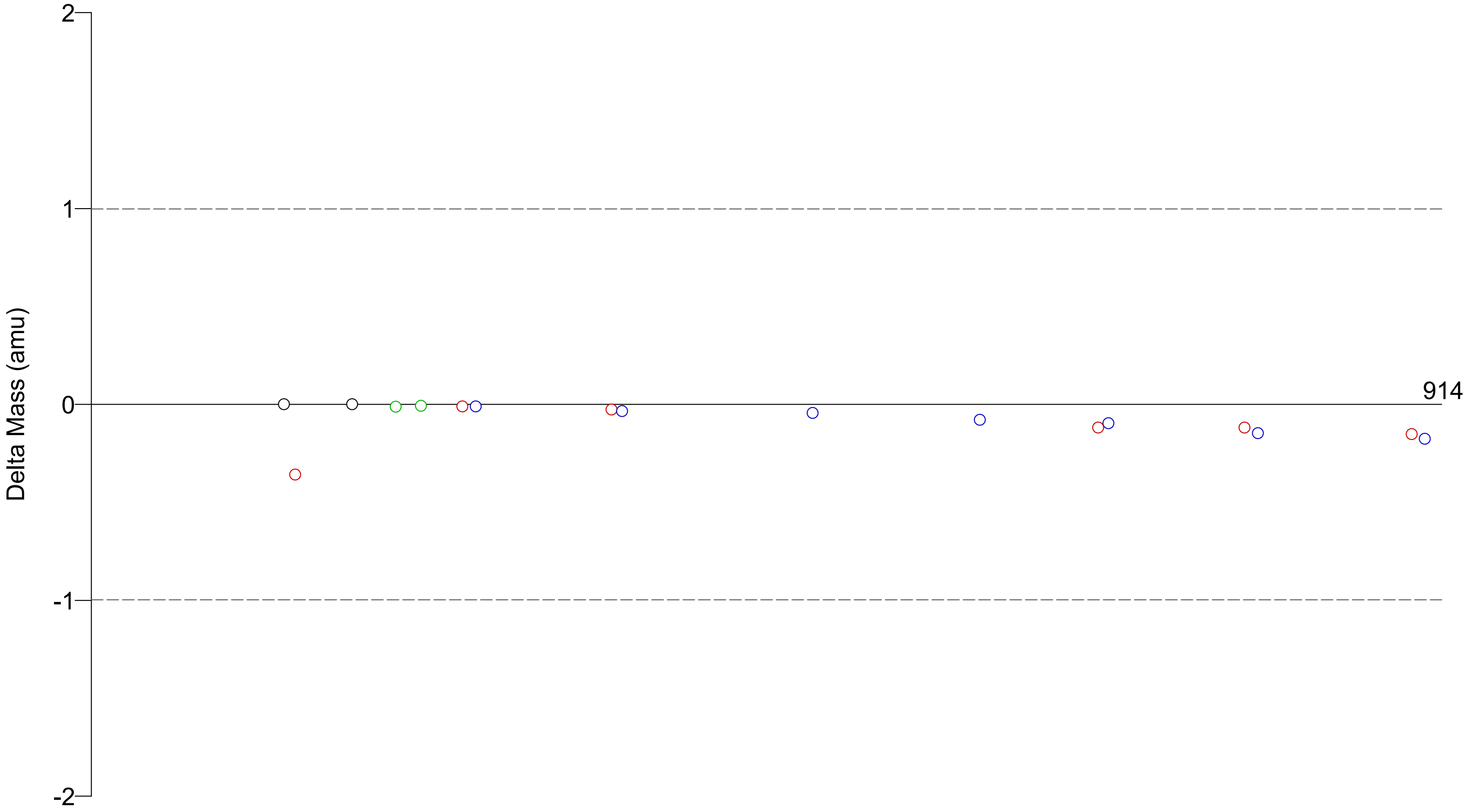


#2118291816-26226248 NL: 1.52E5

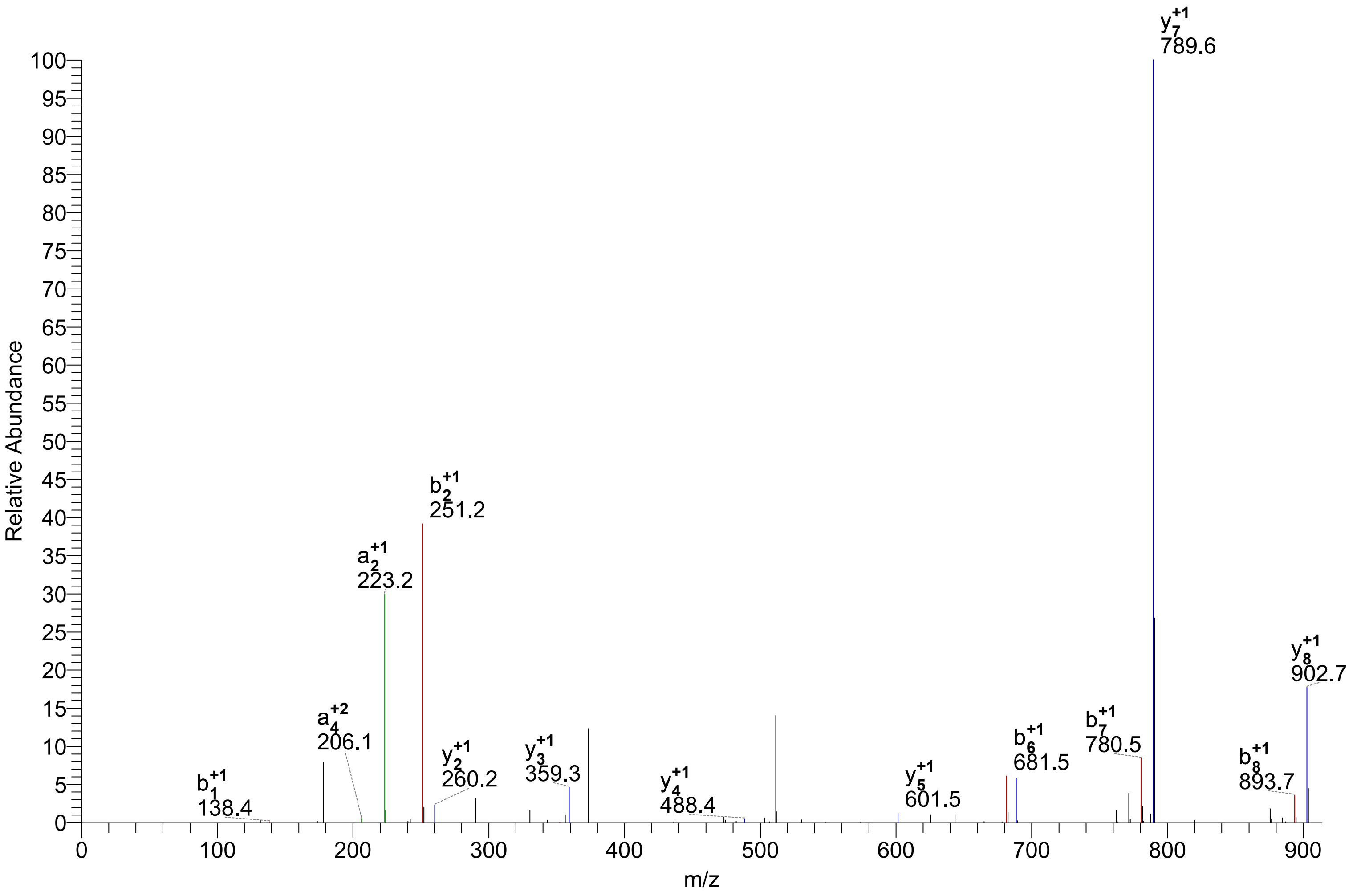


```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00022446.1|SWISS-PROT:P0277                                     0.5      10.1      0.0       0
2118291816 -  R.HITSLEVIK.A                             1039.61   2  0.01     2.472  0.301   457.5  1   14/24   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 520.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
------------------------------------------------------------------------------------------------------
 H    110.07     138.07
 I    223.16     251.15                                       902.56
 T    324.20     352.20                                       789.47
 S    411.24     439.23                                       688.42
 L    524.32     552.31                                       601.39
 E    653.36     681.36                                       488.31
 V    752.43     780.43                                       359.27
 I    865.51     893.51                                       260.20
 K                                                            147.11
```

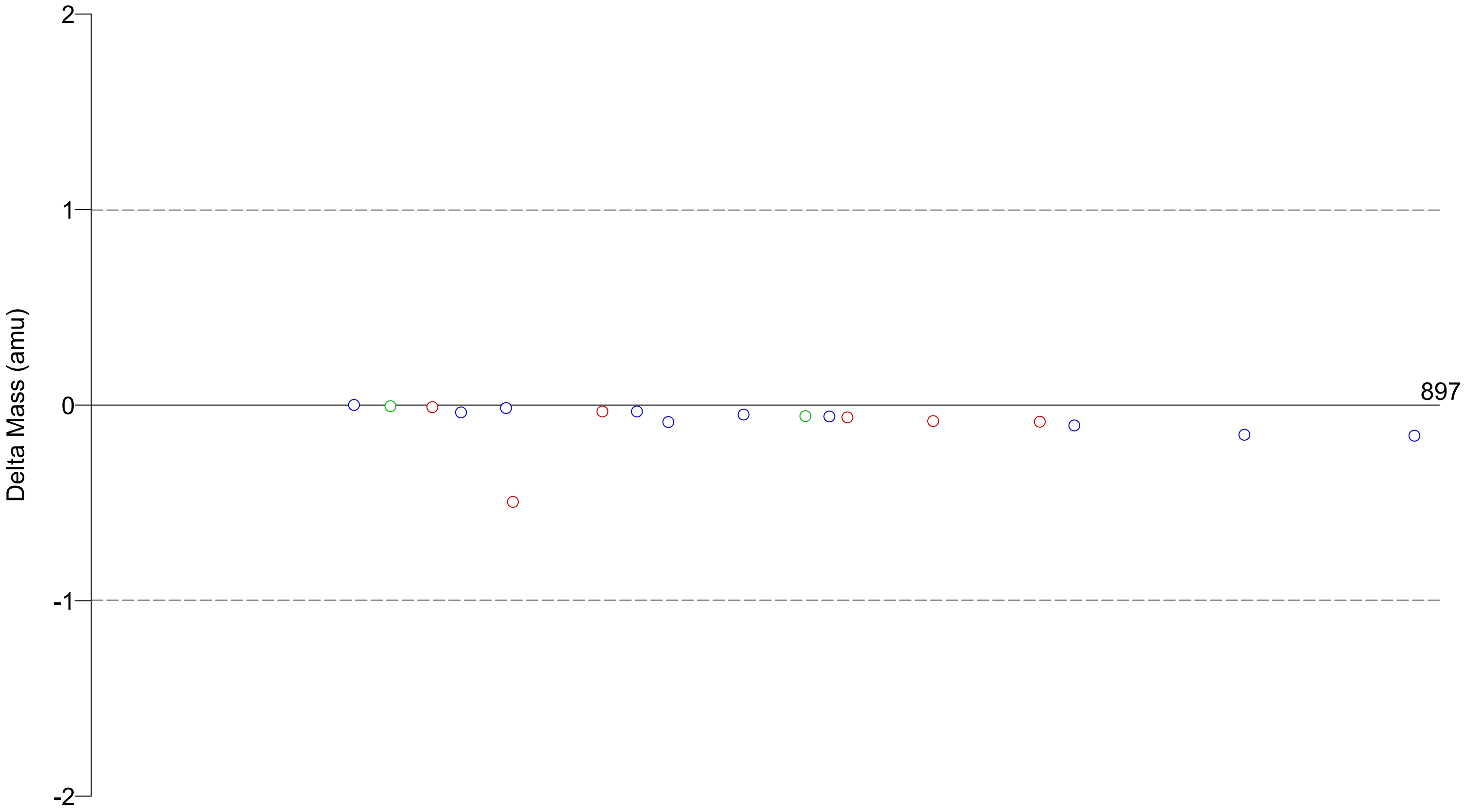


#2118291816-26226248 NL: 1.52E5

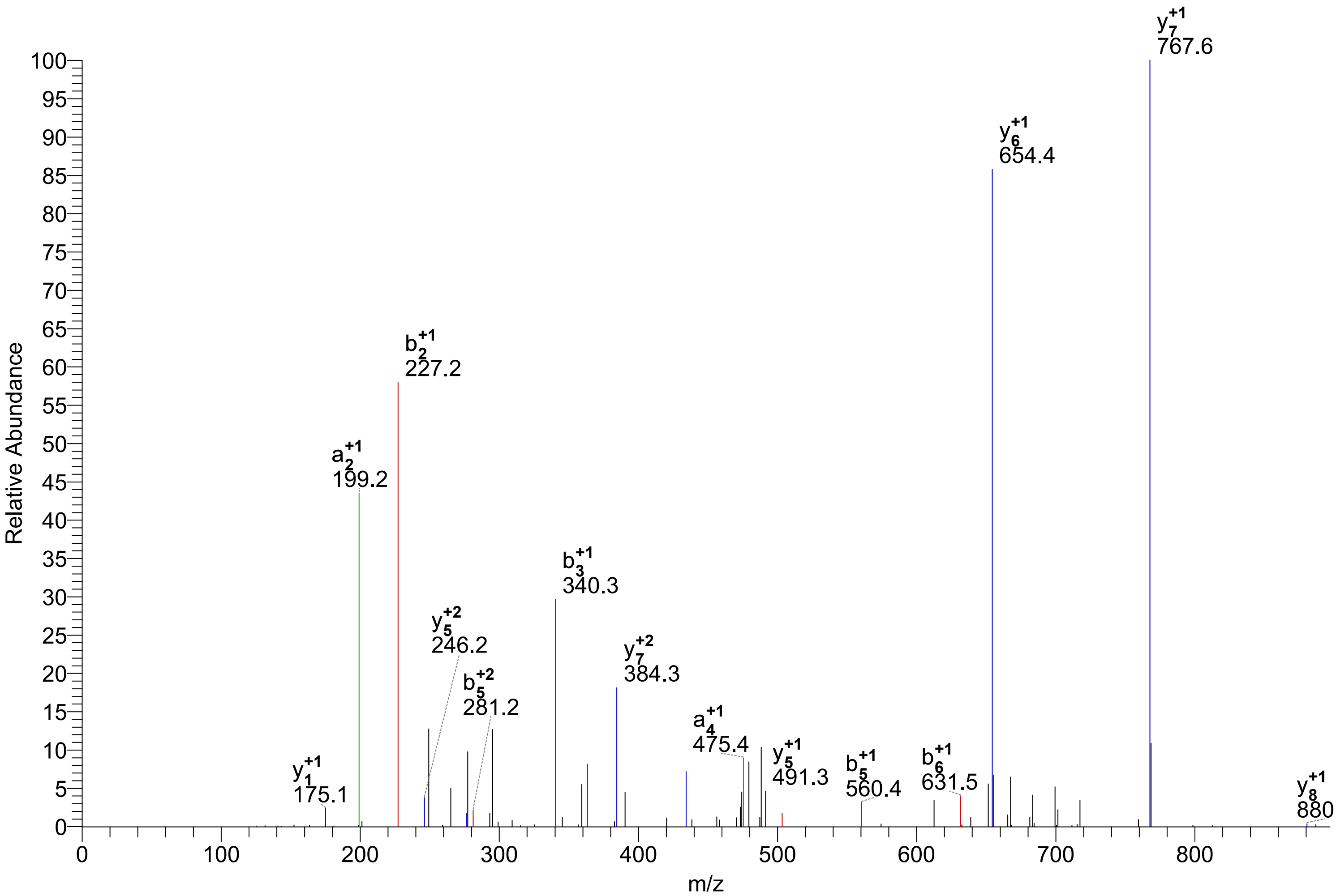


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00384401.1|TREMBL:Q9UL85 Tax_Id=9606 Gene_Symbol=- Myos     0.5      10.1      0.0        0
19287468 - 1  R.LLIYGASTR.A                             993.57    2  0.01     2.977  0.065   715.8  1   15/24   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18    227.18                                      880.49
 I    312.26    340.26                                      767.40
 Y    475.33    503.32                                      654.32
 G    532.35    560.34                                      491.26
 A    603.39    631.38                                      434.24
 S    690.42    718.41                                      363.20
 T    791.47    819.46                                      276.17
 R                                                          175.12
```

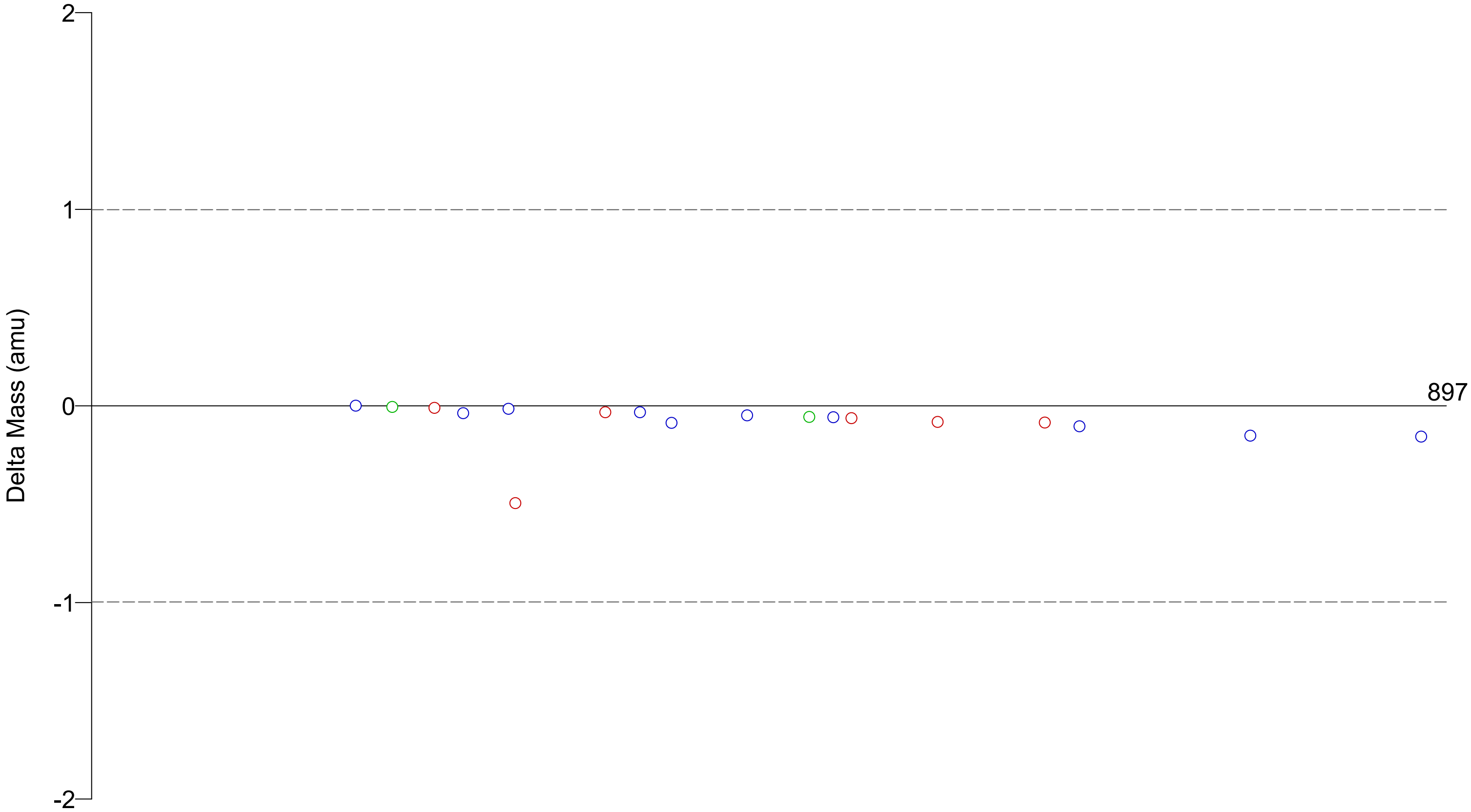


#19287468-1 NL: 1.29E6

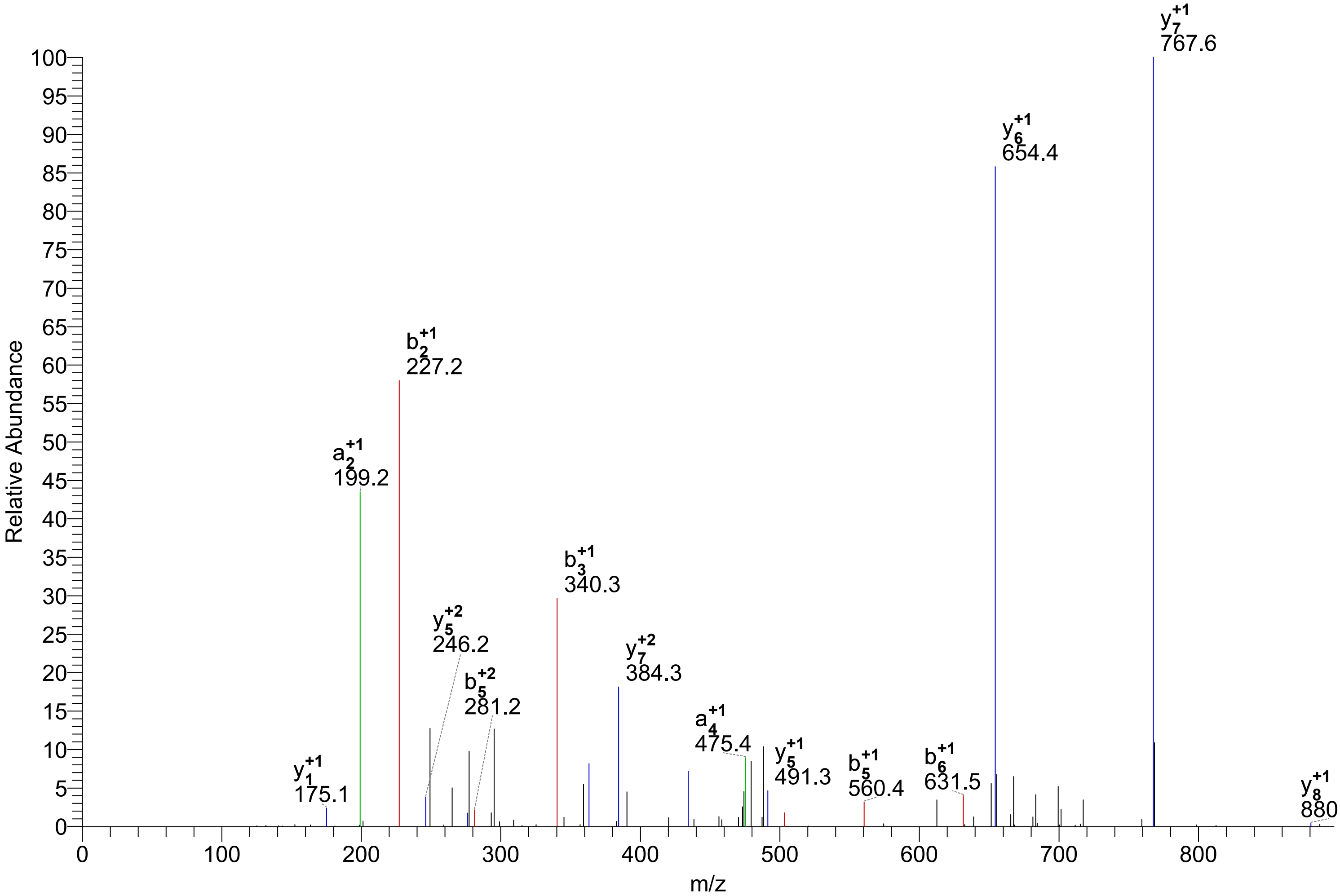


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00385253.1|SWISS-PROT:P0420                                 0.5     10.1     0.0        0
19287468 - 1  R.LLIYGASTR.A                           993.57     2  0.01     2.977  0.065   715.8  1   15/24   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                       880.49
 I    312.26     340.26                                       767.40
 Y    475.33     503.32                                       654.32
 G    532.35     560.34                                       491.26
 A    603.39     631.38                                       434.24
 S    690.42     718.41                                       363.20
 T    791.47     819.46                                       276.17
 R                                                            175.12
```

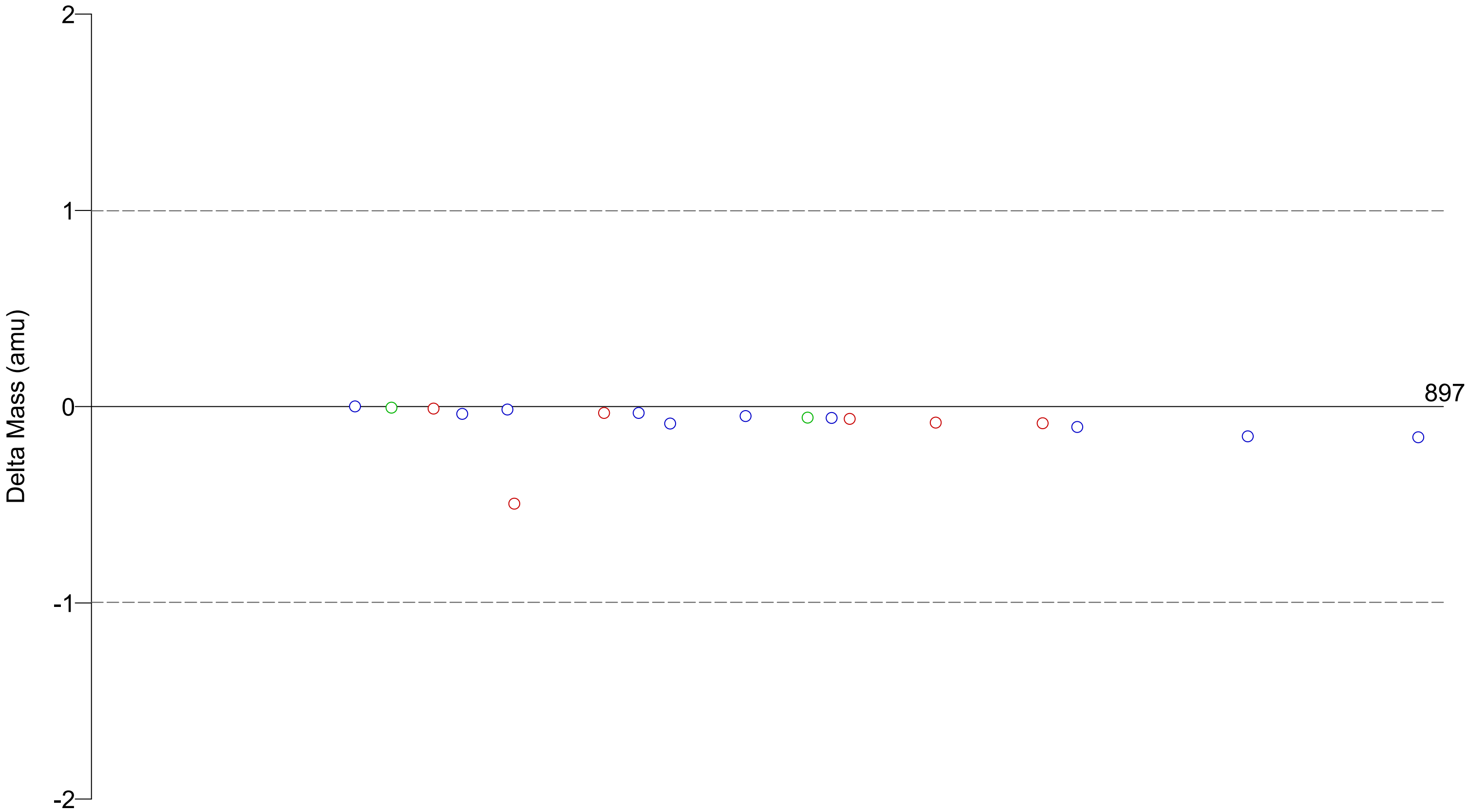


#19287468-1 NL: 1.29E6

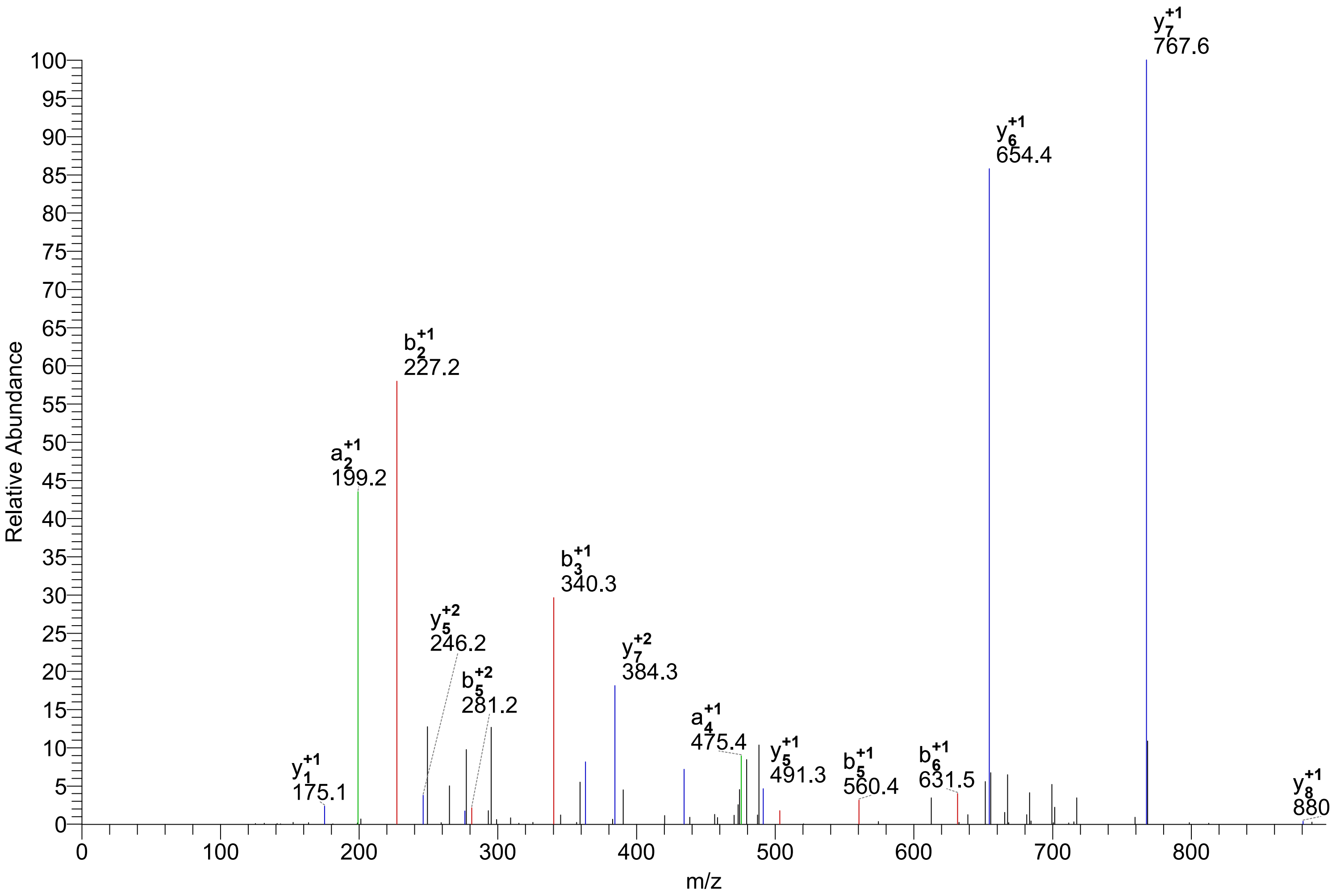


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                90       z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00387097.1|SWISS-PROT:P0160                                0.5     10.1     0.0       0
19287468 - 1  R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                      880.49
 I    312.26     340.26                                      767.40
 Y    475.33     503.32                                      654.32
 G    532.35     560.34                                      491.26
 A    603.39     631.38                                      434.24
 S    690.42     718.41                                      363.20
 T    791.47     819.46                                      276.17
 R                                                           175.12
```

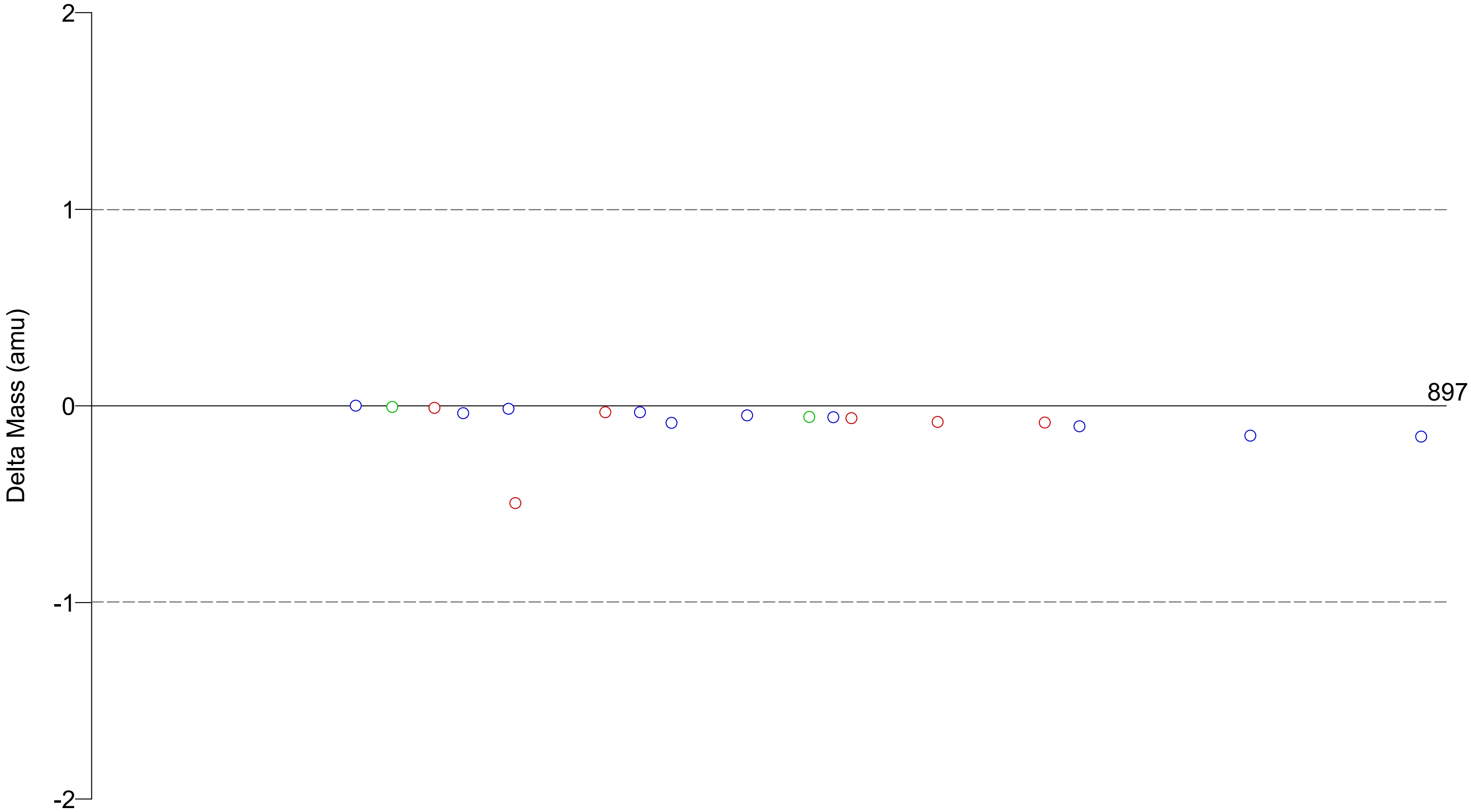


#19287468-1 NL: 1.29E6

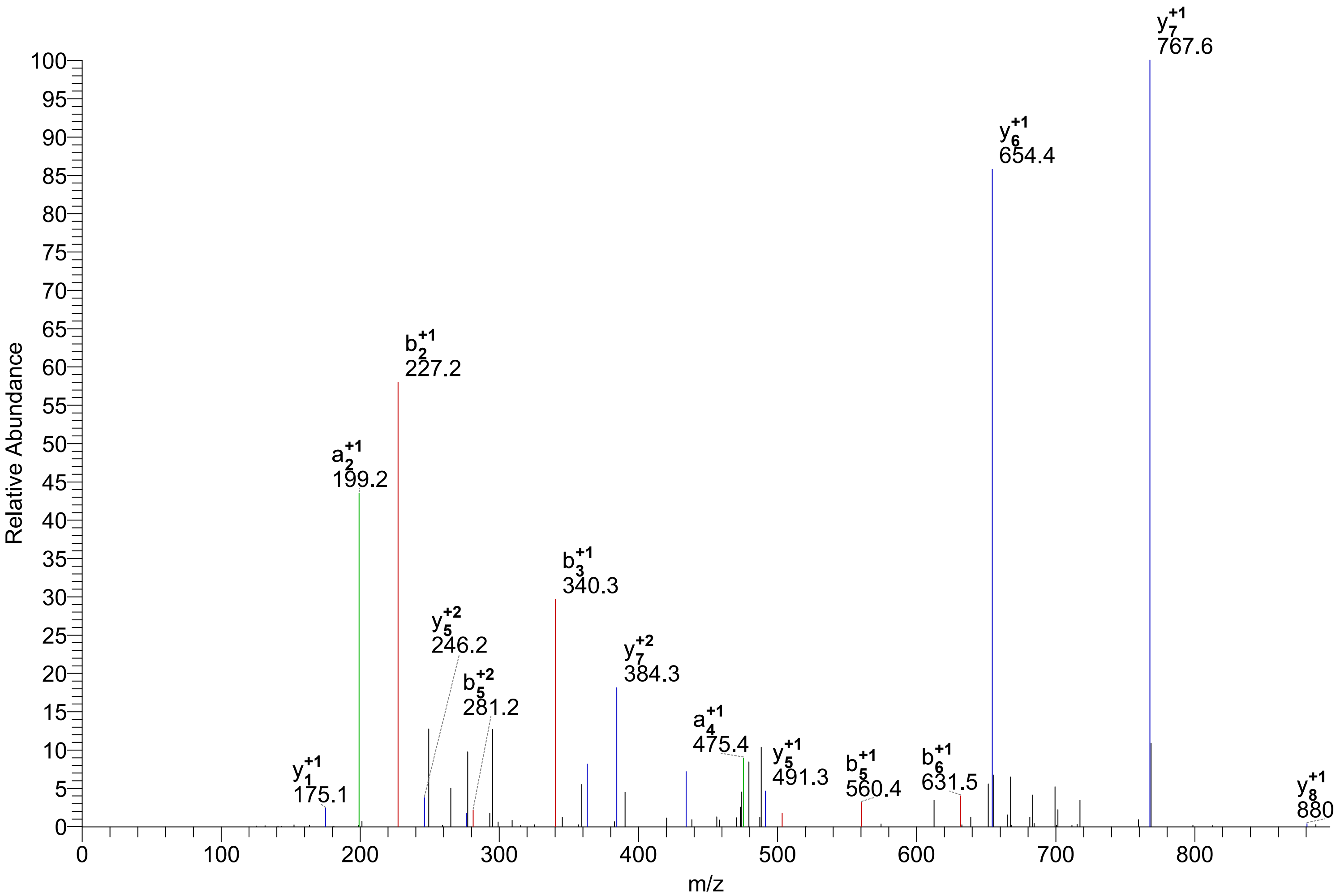


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00387119.1|SWISS-PROT:P0162                                0.5     10.1     0.0       0
19287468 - 1  R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L    86.10     114.09
 L   199.18     227.18                                      880.49
 I   312.26     340.26                                      767.40
 Y   475.33     503.32                                      654.32
 G   532.35     560.34                                      491.26
 A   603.39     631.38                                      434.24
 S   690.42     718.41                                      363.20
 T   791.47     819.46                                      276.17
 R                                                          175.12
```



#19287468-1 NL: 1.29E6



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Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+     z   P        XC  DeltaCn    Sp   RSp  Ions  Count

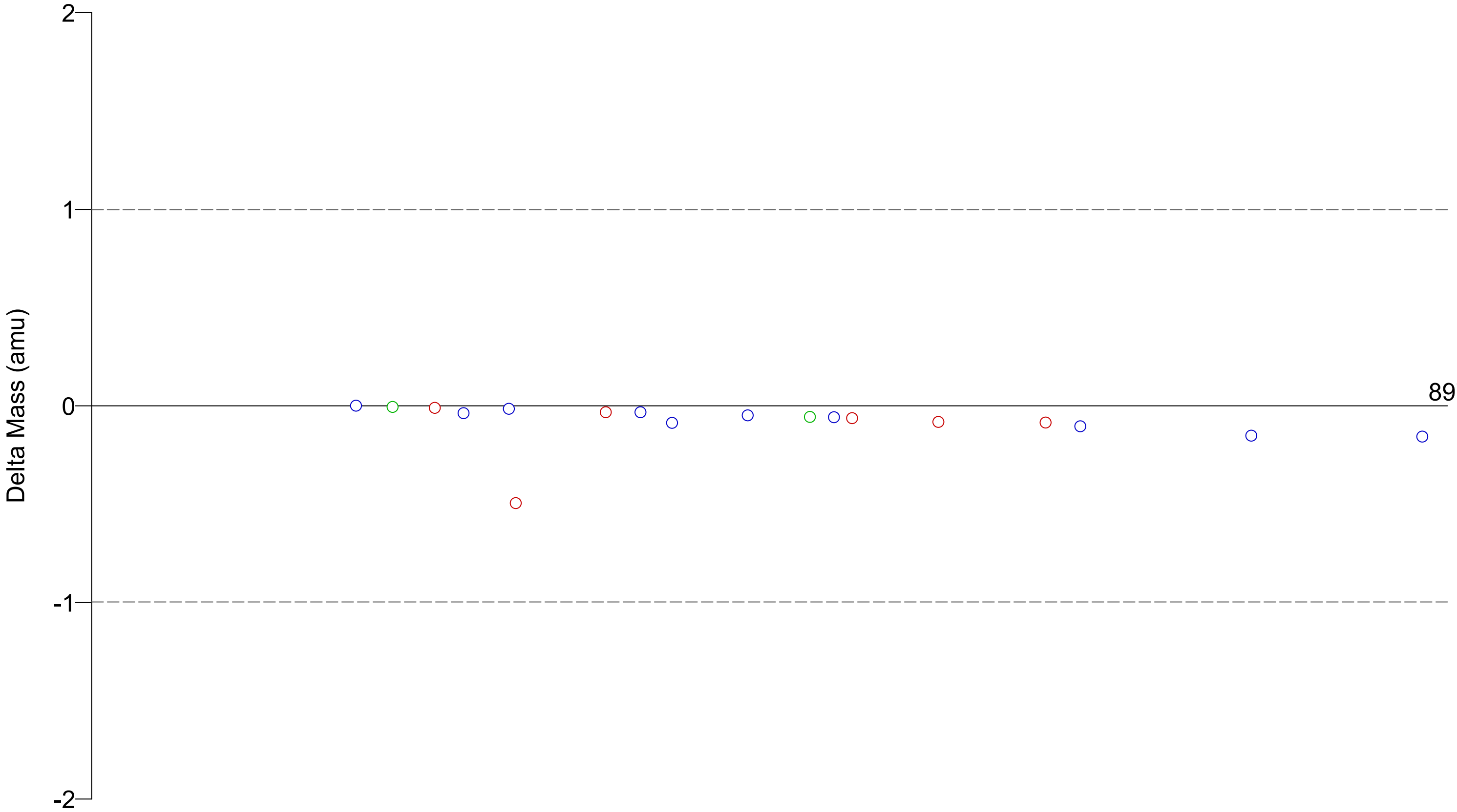
IPI:IPI00549330.4|TREMBL:Q9UL83|EN                                0.5     10.1     0.0       0
19287468 - 1  R.LLIYGASTR.A                          993.57    2  0.01     2.977  0.065   715.8  1   15/24   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

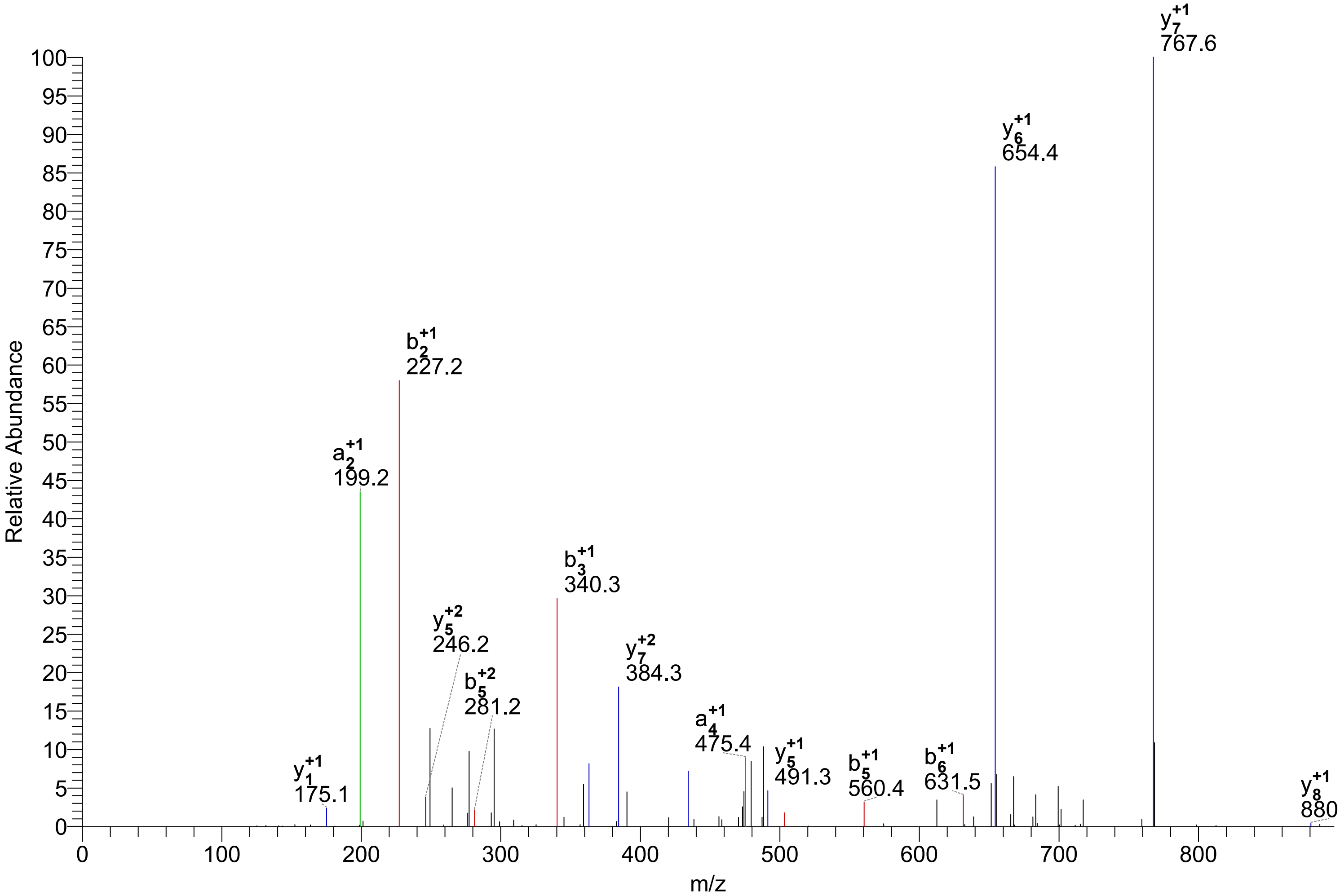
```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
-----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                       880.49
 I    312.26     340.26                                       767.40
 Y    475.33     503.32                                       654.32
 G    532.35     560.34                                       491.26
 A    603.39     631.38                                       434.24
 S    690.42     718.41                                       363.20
 T    791.47     819.46                                       276.17
 R                                                            175.12
```



#19287468-1 NL: 1.29E6



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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                X        z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829834.1|SWISS-PROT:P0443                                0.5     10.1     0.0       0
19287468 - 1  R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24   7

1 of 1 peptide matches reported, 0 removed due to filtering
```
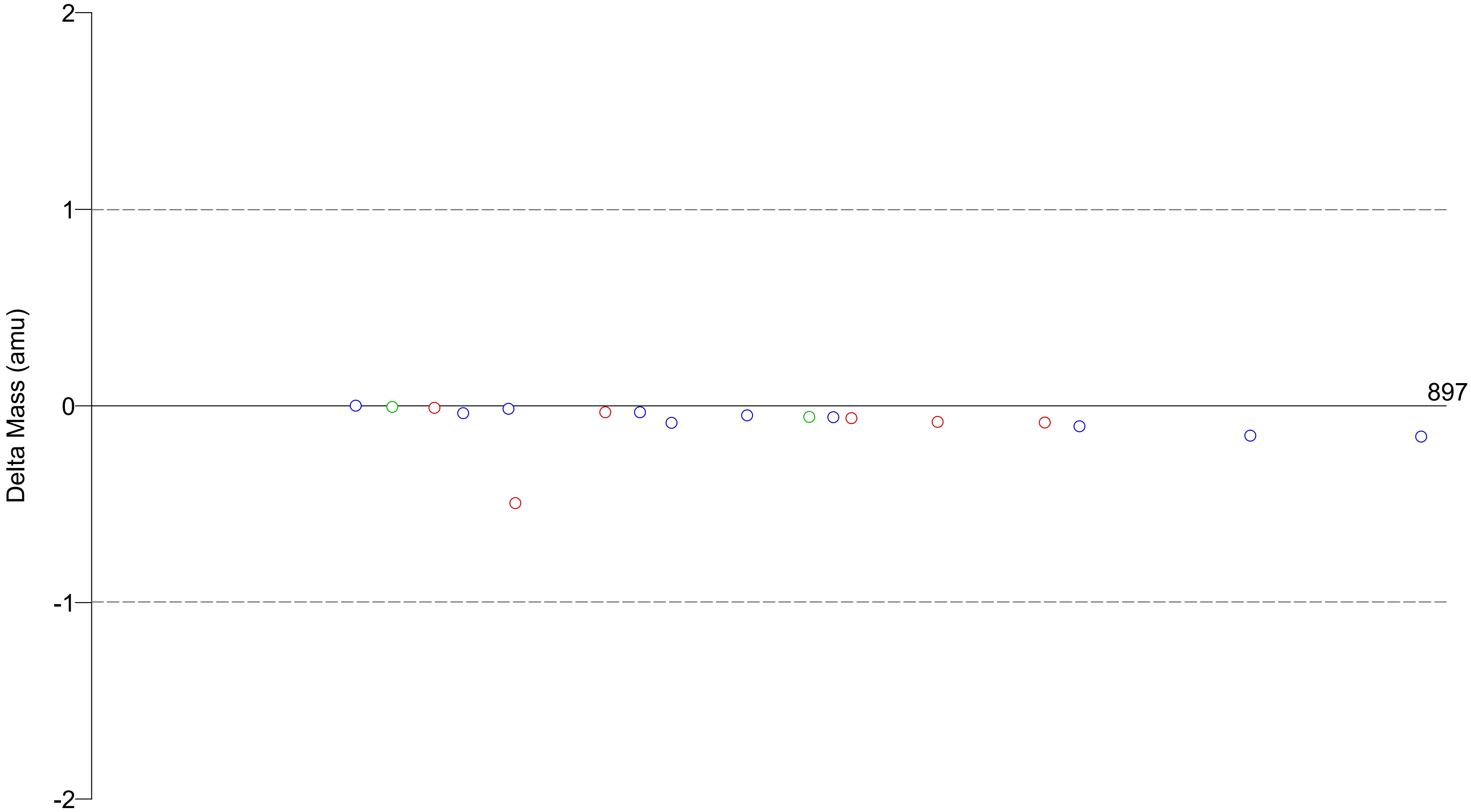
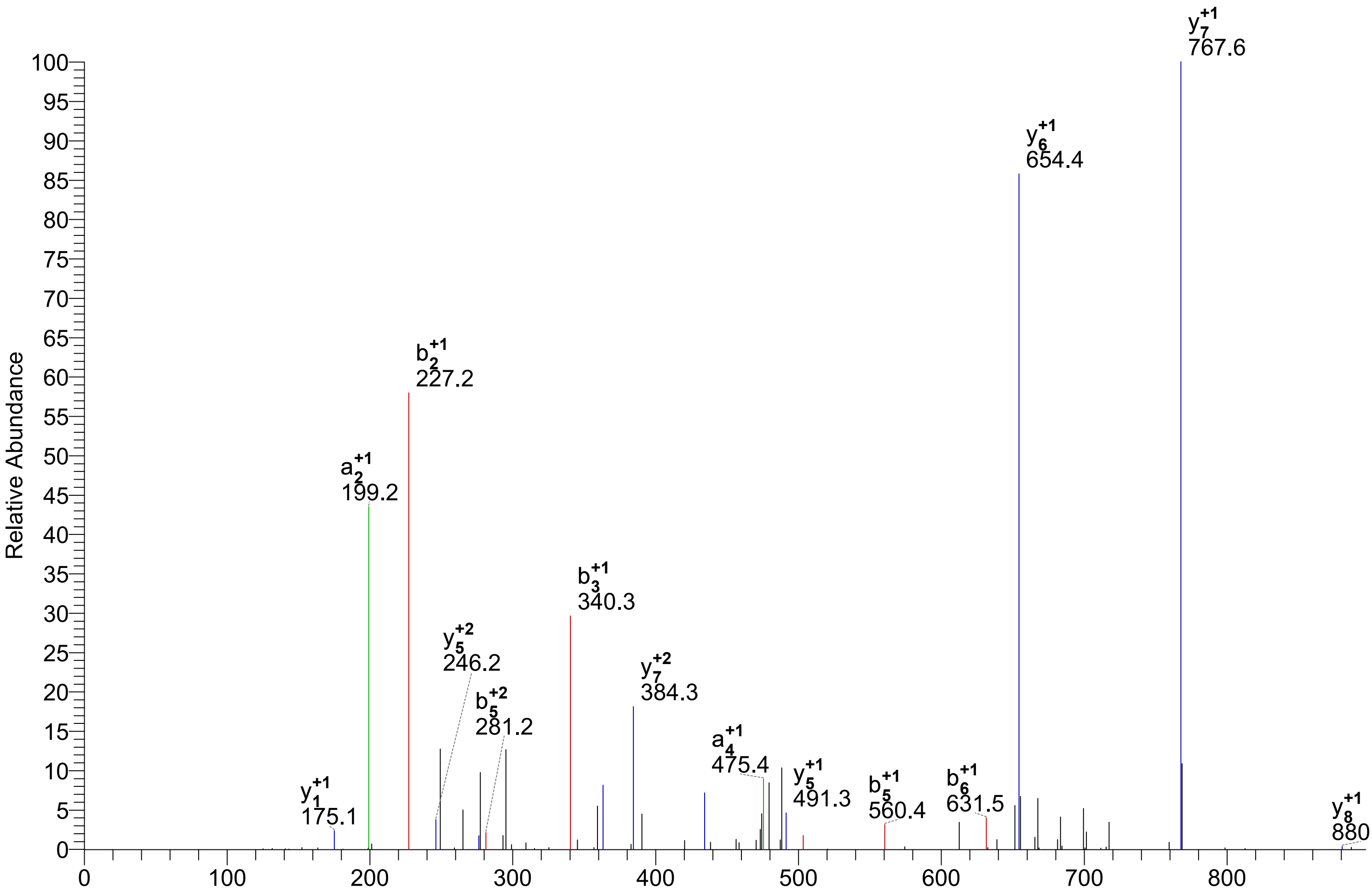

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                       880.49
 I    312.26     340.26                                       767.40
 Y    475.33     503.32                                       654.32
 G    532.35     560.34                                       491.26
 A    603.39     631.38                                       434.24
 S    690.42     718.41                                       363.20
 T    791.47     819.46                                       276.17
 R                                                            175.12
```

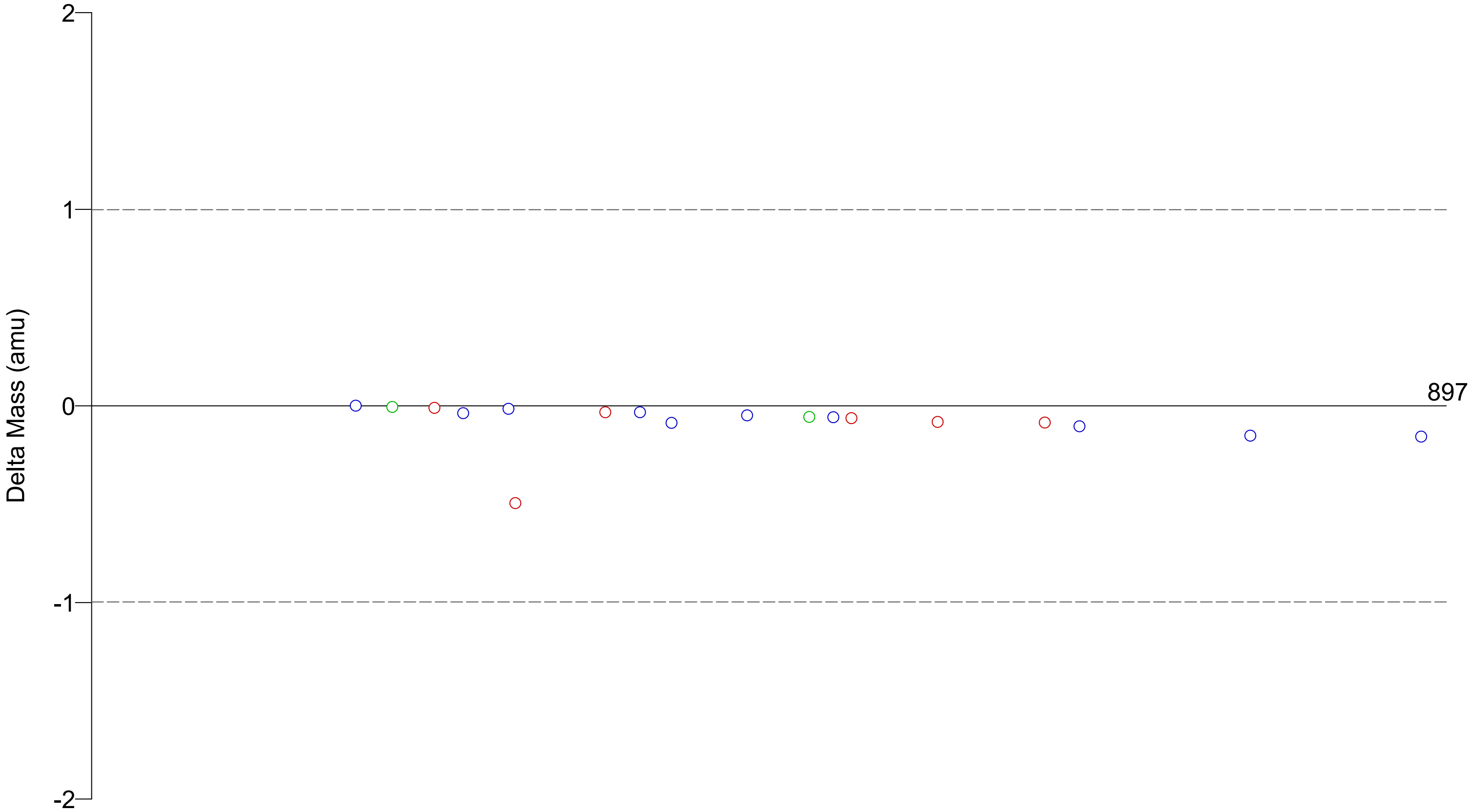


#19287468-1 NL: 1.29E6

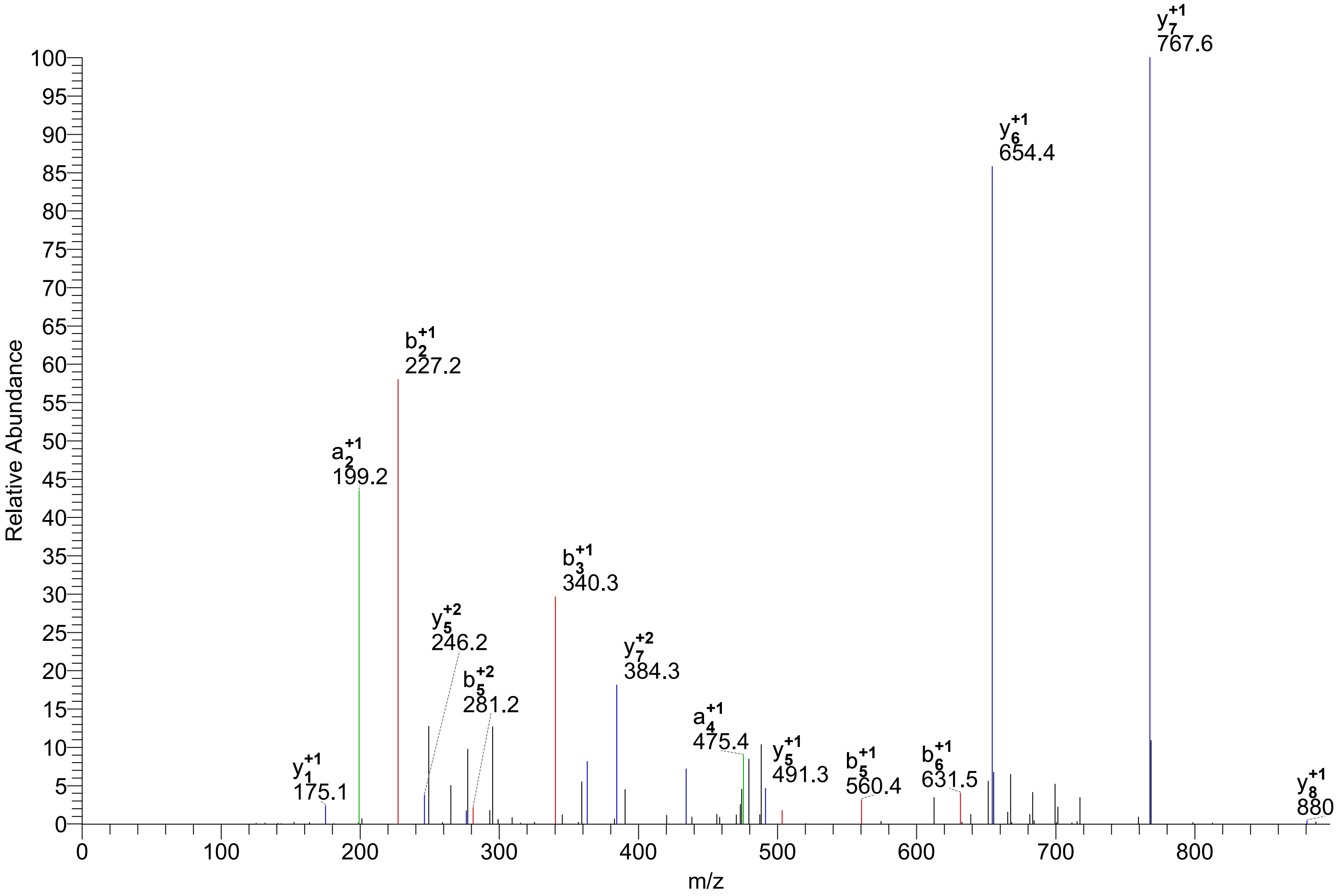


```
Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00892594.1|TREMBL:A6NGI0|EN                                0.5     10.1     0.0       0
19287468 - 1  R.LLIYGASTR.A                          993.57    2  0.01    2.977  0.065   715.8  1   15/24   7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions      C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                       880.49
 I    312.26     340.26                                       767.40
 Y    475.33     503.32                                       654.32
 G    532.35     560.34                                       491.26
 A    603.39     631.38                                       434.24
 S    690.42     718.41                                       363.20
 T    791.47     819.46                                       276.17
 R                                                            175.12
```

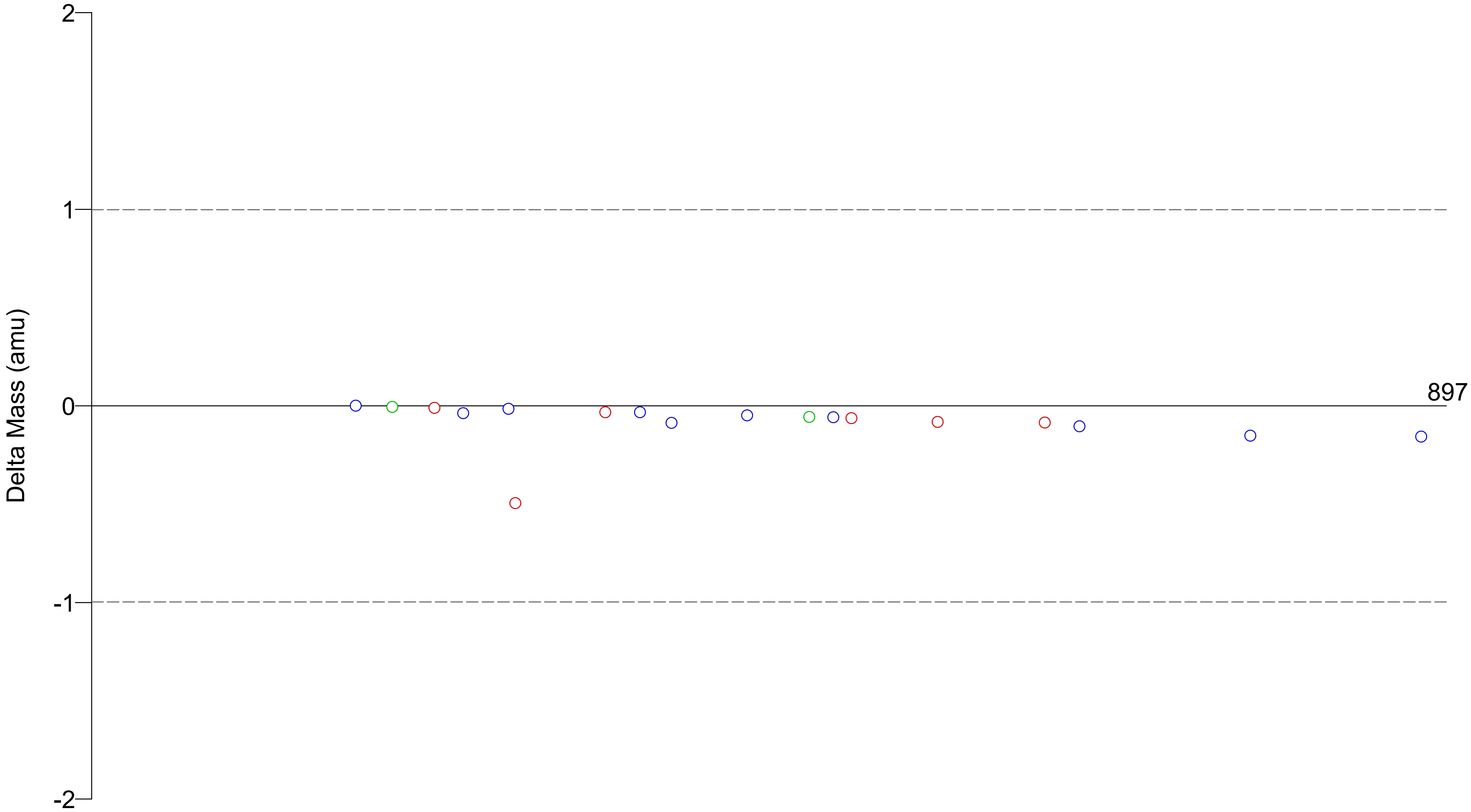


#19287468-1 NL: 1.29E6

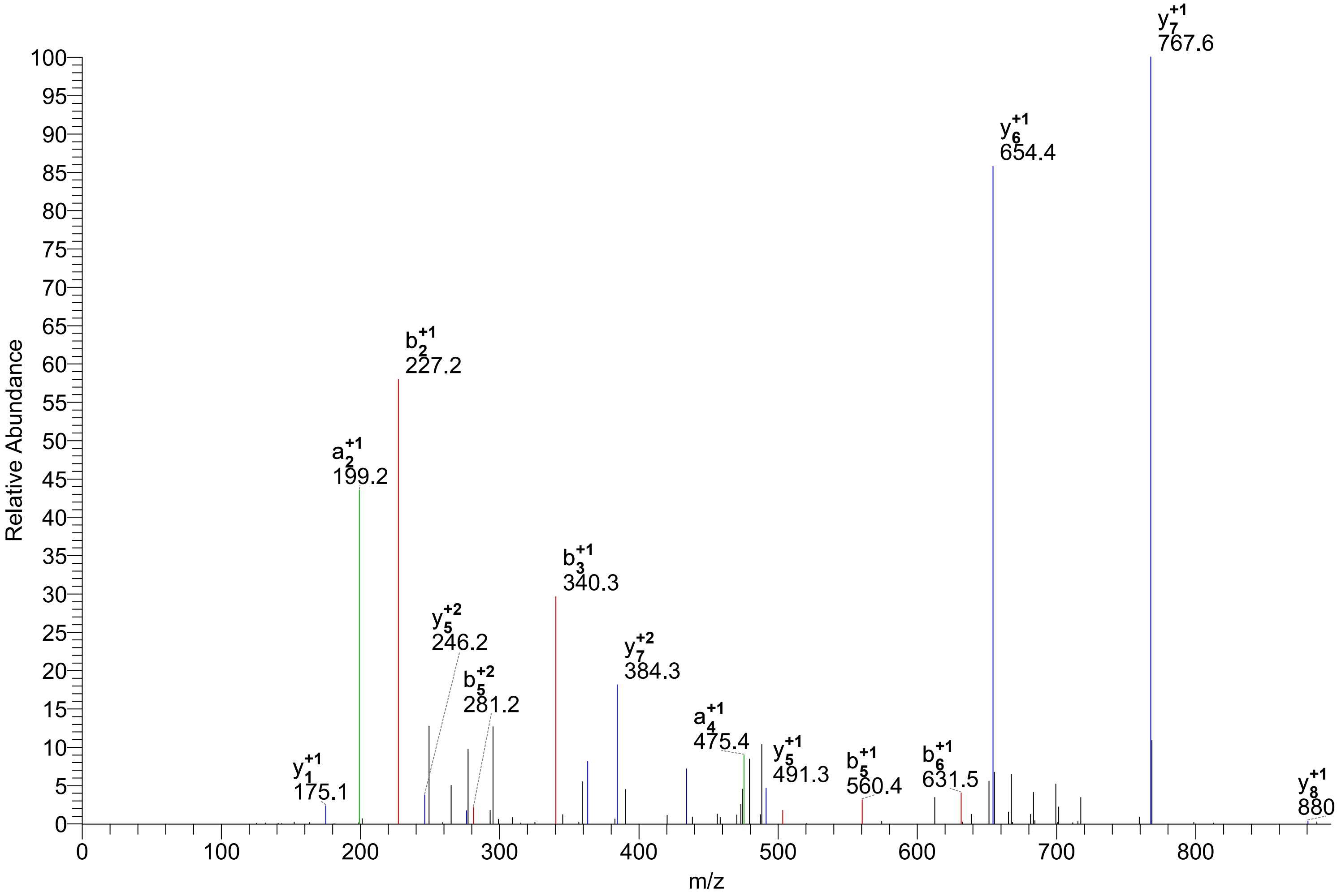


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00936553.1|REFSEQ:XP_002345                                   0.5     10.1     0.0        0
19287468 - 1  R.LLIYGASTR.A                             993.57     2  0.01     2.977  0.065   715.8  1   15/24    7

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L    86.10     114.09
 L   199.18     227.18                                      880.49
 I   312.26     340.26                                      767.40
 Y   475.33     503.32                                      654.32
 G   532.35     560.34                                      491.26
 A   603.39     631.38                                      434.24
 S   690.42     718.41                                      363.20
 T   791.47     819.46                                      276.17
 R                                                          175.12
```

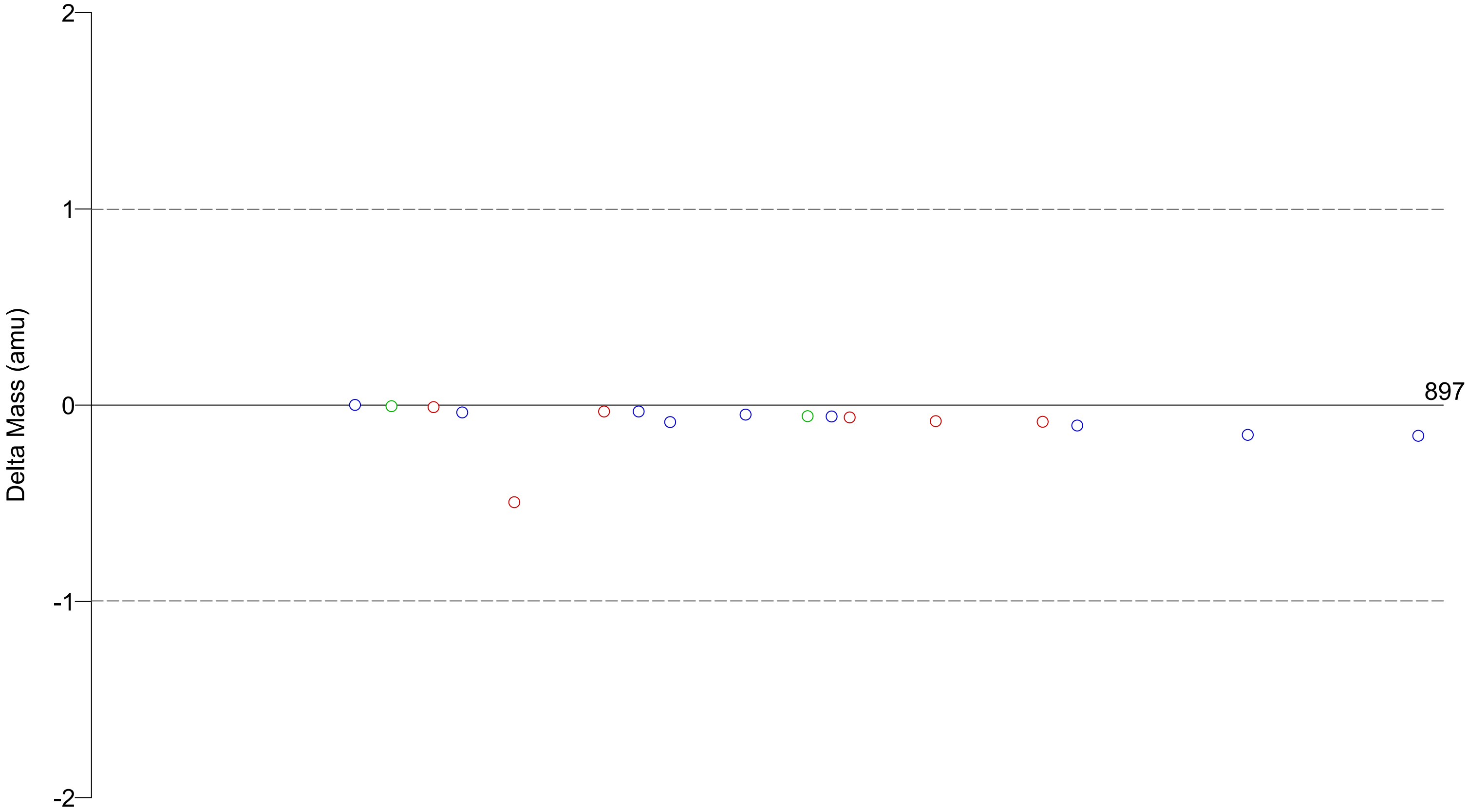


#19287468-1 NL: 1.29E6

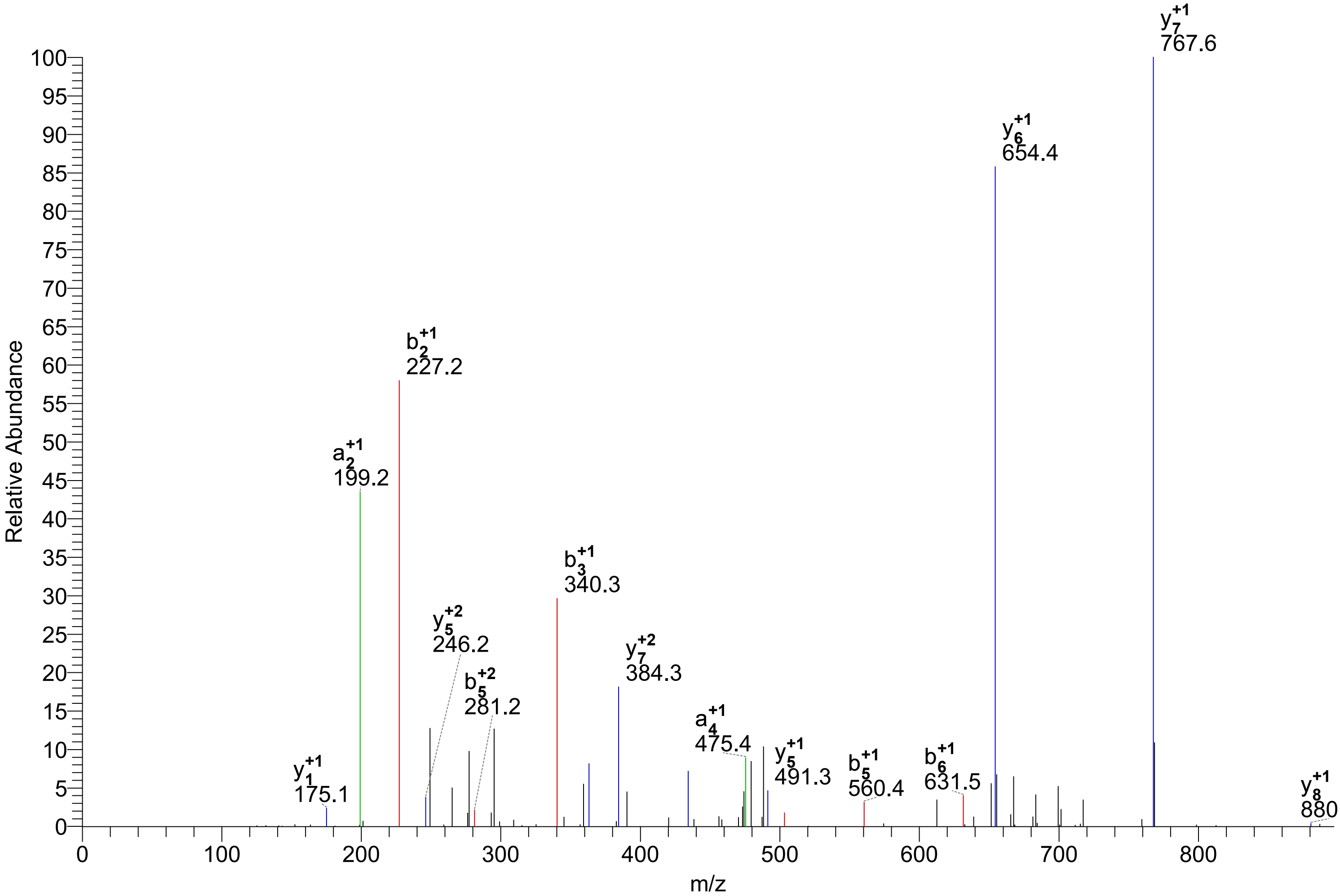


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00387116.1|SWISS-PROT:P01621 Tax_Id=9606 Gene_Symbol=-     0.5     8.1      0.0       0
19287468 - 1  R.LLIYGATSR.A                                993.57    2  0.01     2.784  0.369   580.4  2   14/24

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 497.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                       880.49
 I    312.26     340.26                                       767.40
 Y    475.33     503.32                                       654.32
 G    532.35     560.34                                       491.26
 A    603.39     631.38                                       434.24
 T    704.43     732.43                                       363.20
 S    791.47     819.46                                       262.15
 R                                                            175.12
```

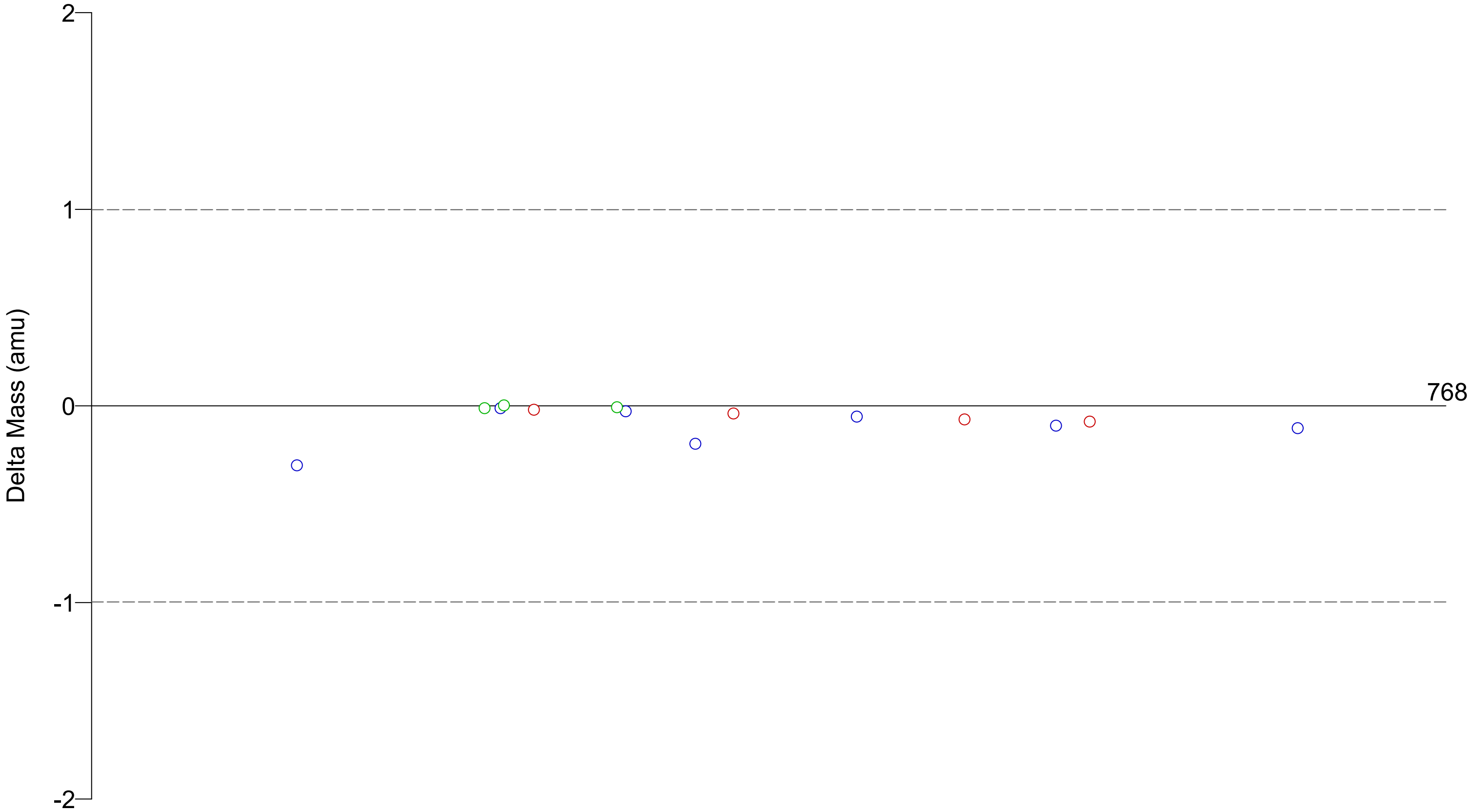


#19287468-1 NL: 1.29E6

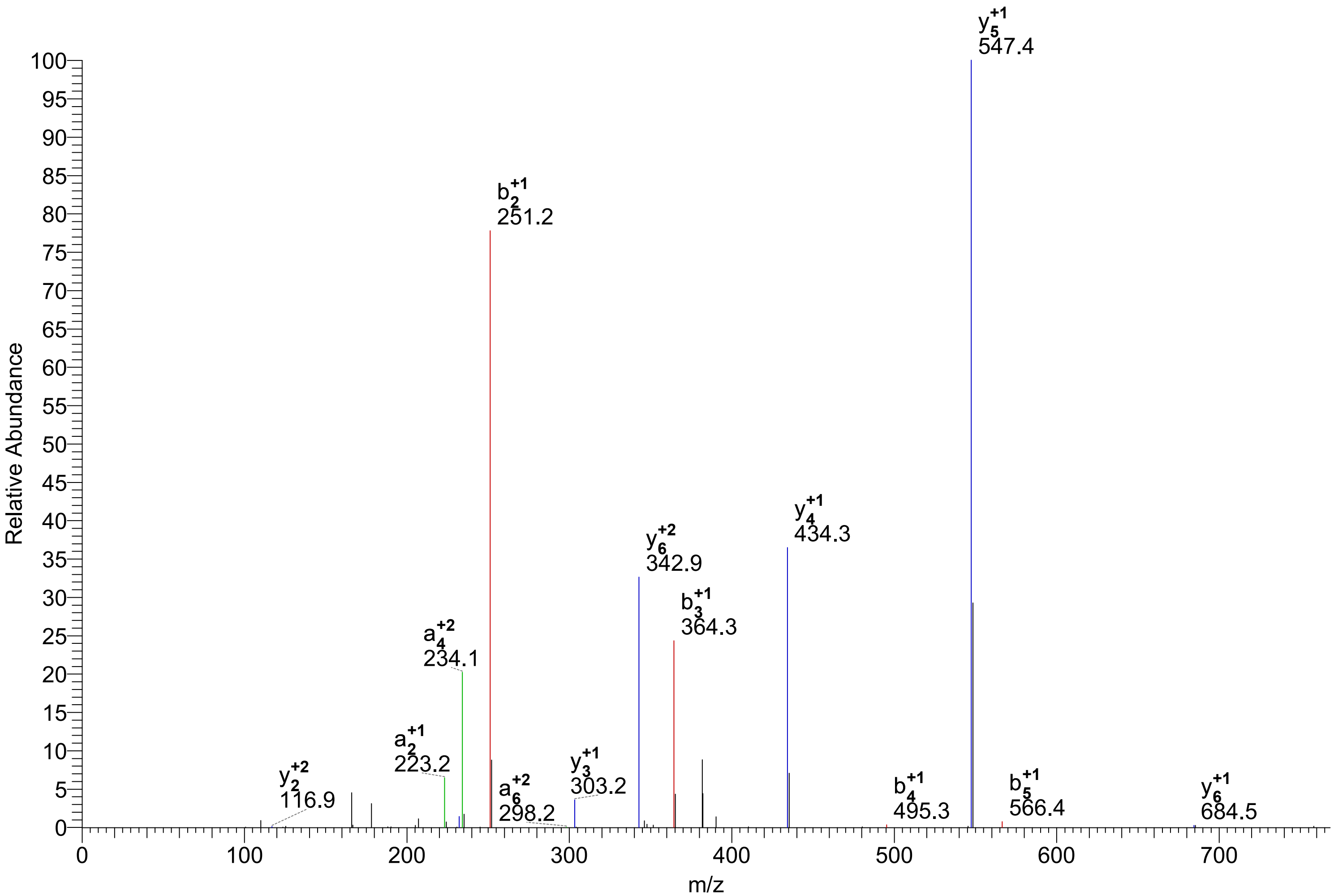


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)        Sequence                                 MH+     z    P         XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00022488.1|SWISS-PROT:P02790|TREMBL:Q9BS19|ENSEMBL:ENSP  0.6      18.1     0.0       0
19287468 - 1  R.LHIMAGR.R                              797.45   2  0.07     2.141  0.129   350.3  1   10/18
19287468 - 1  K.NFPSPVDAAFR.Q                          1220.61   2  0.01     2.871  0.432   324.9  1   16/30   1

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

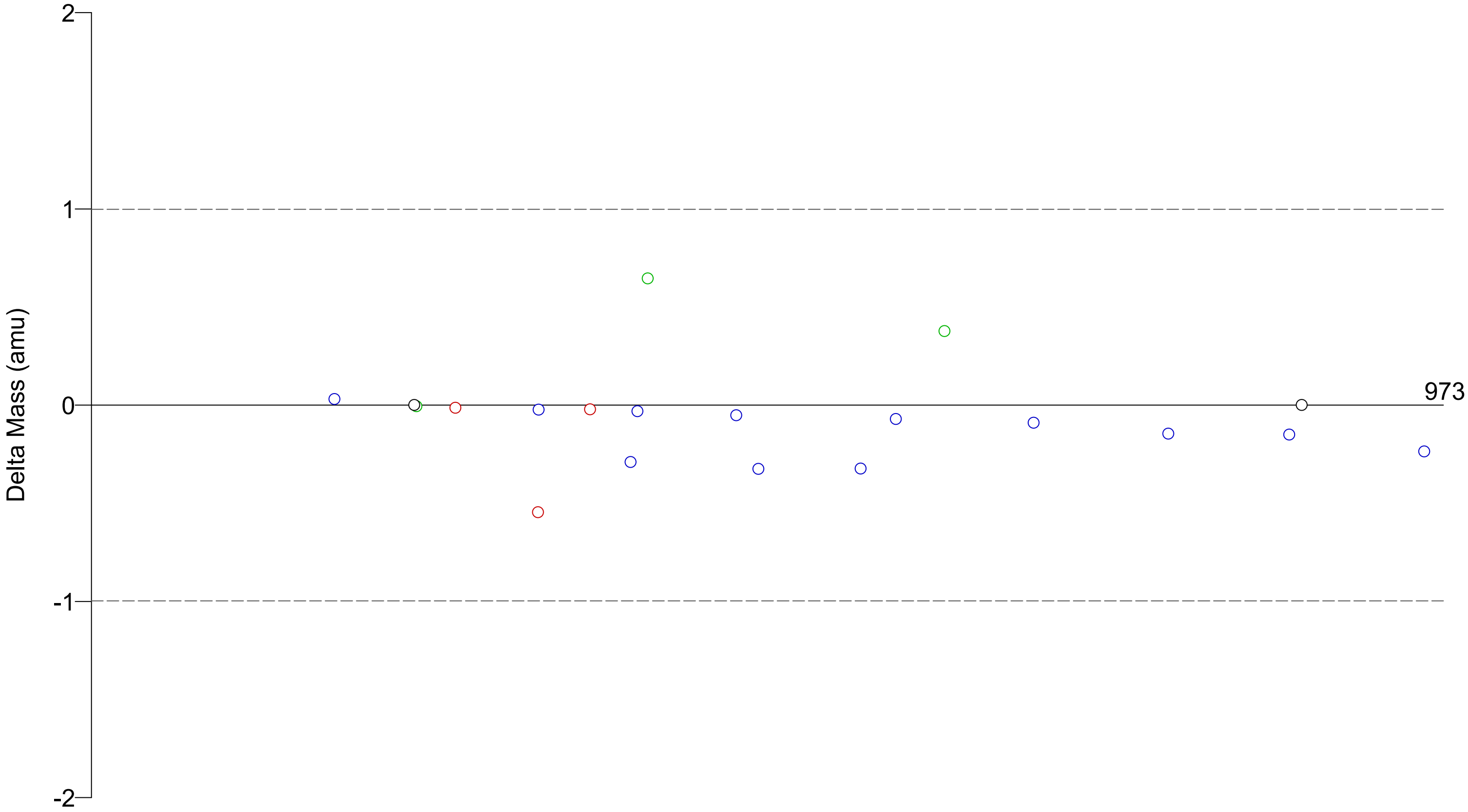
```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 H    223.16    251.15                                      684.36
 I    336.24    364.23                                      547.30
 M    467.28    495.27                                      434.22
 A    538.32    566.31                                      303.18
 G    595.34    623.33                                      232.14
 R                                                          175.12
```



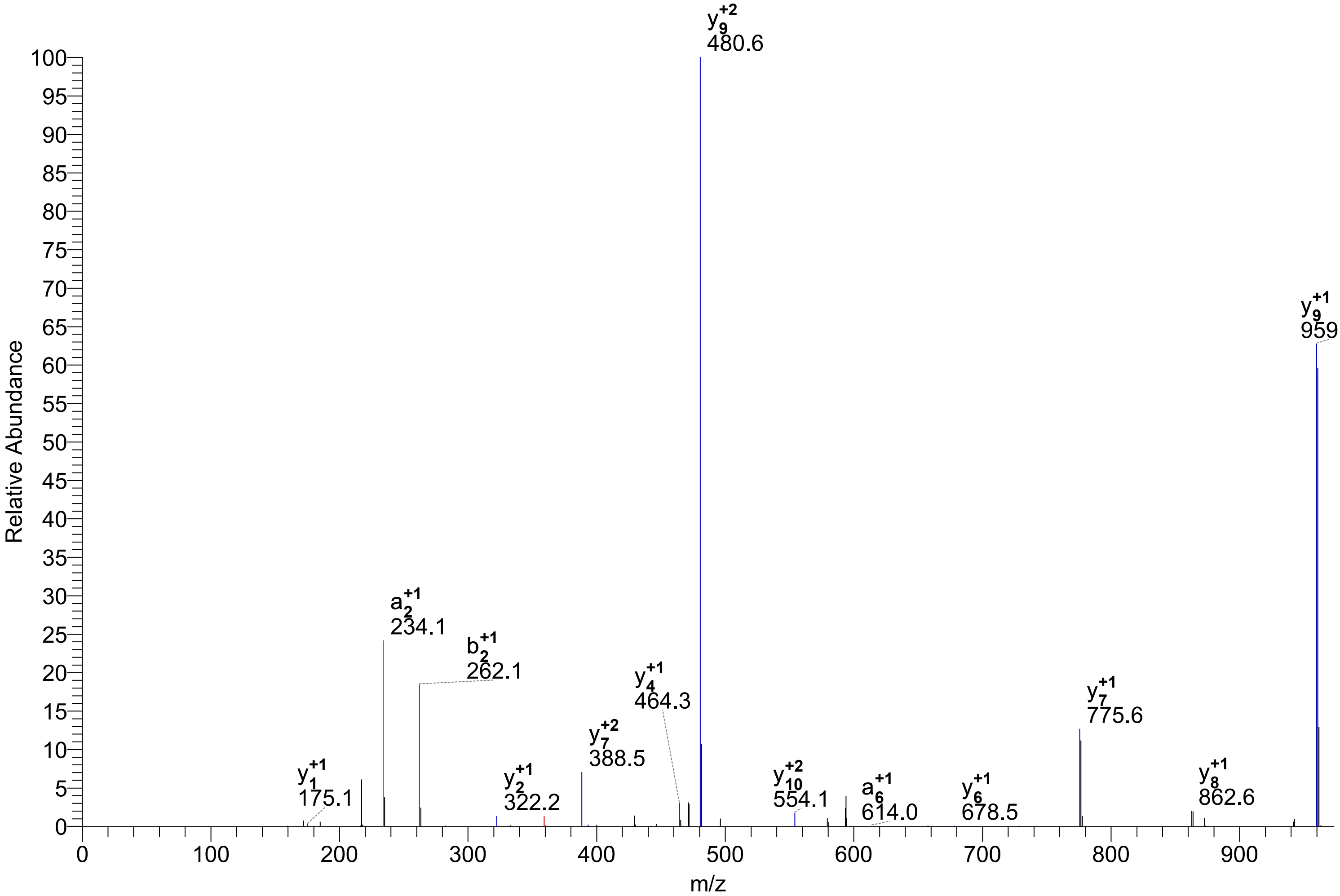
#19287468-1 NL: 3.32E5



```
DTA for scans: 19287468-1
Precursor ion: 610.81
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 F    234.12     262.12                                     1106.56
 P    331.18     359.17                                      959.49
 S    418.21     446.20                                      862.44
 P    515.26     543.26                                      775.41
 V    614.33     642.32                                      678.36
 D    729.36     757.35                                      579.29
 A    800.39     828.39                                      464.26
 A    871.43     899.43                                      393.22
 F   1018.50    1046.49                                      322.19
 R                                                           175.12
```

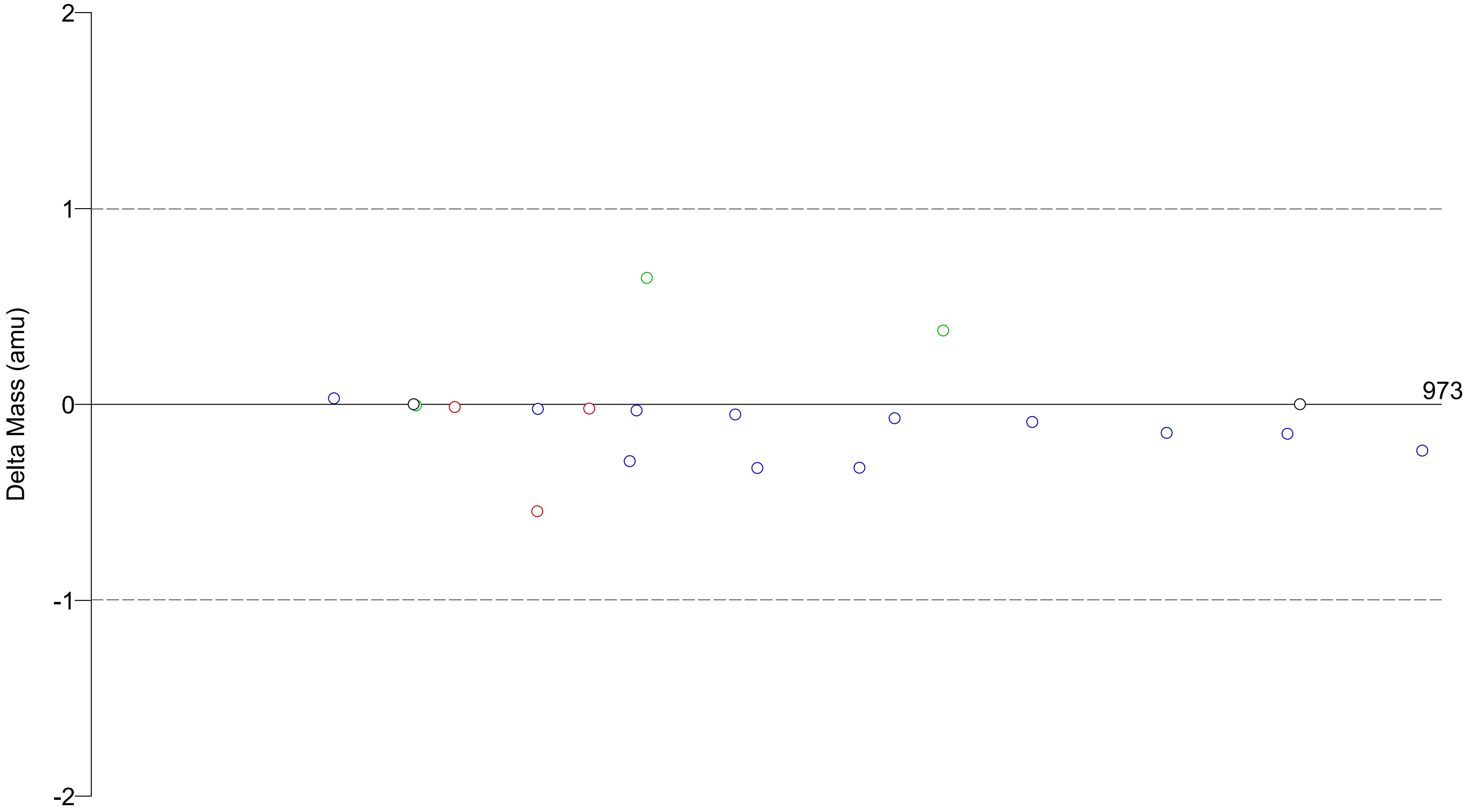


#19287468-1 NL: 1.83E6

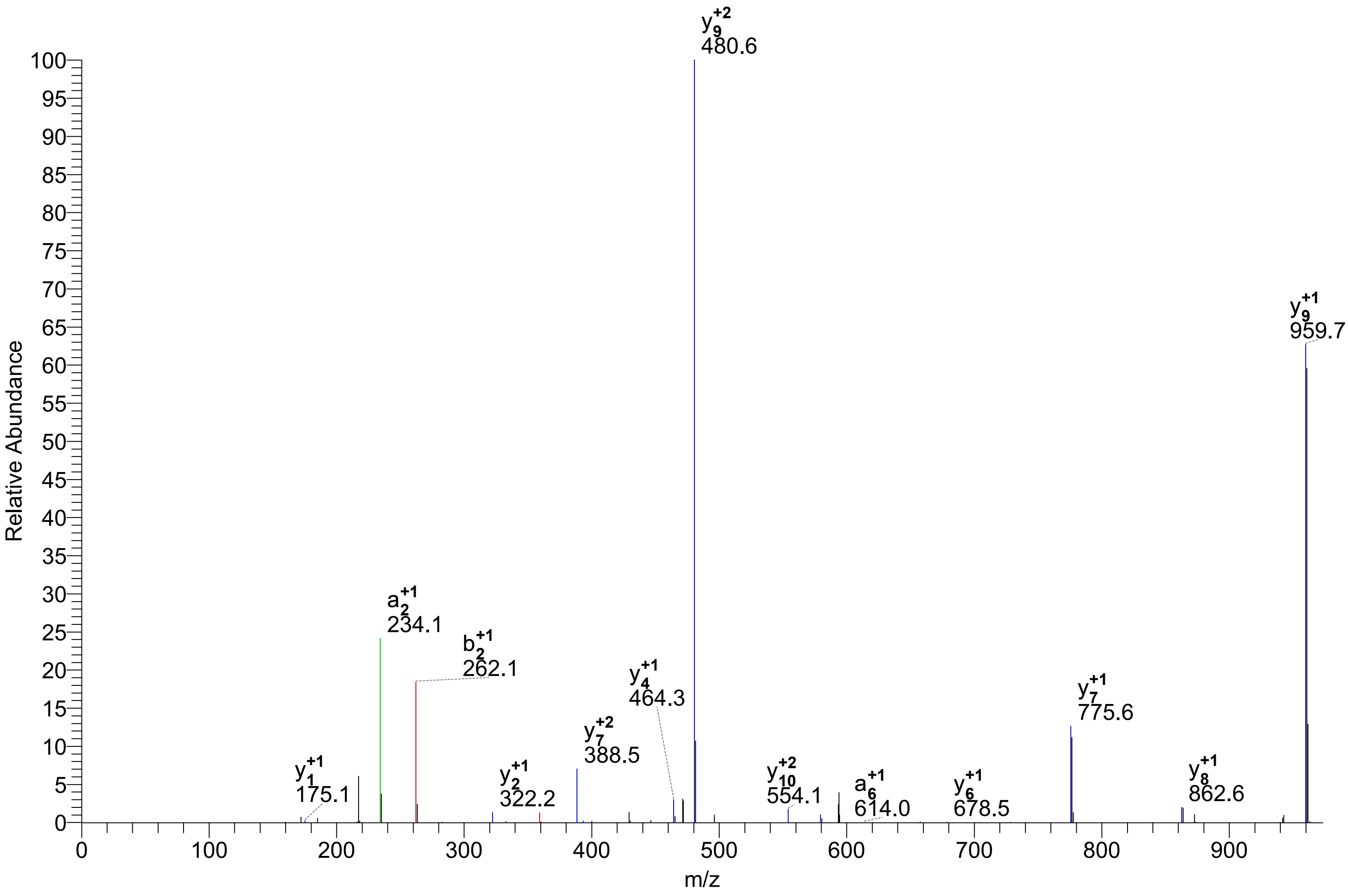


```
Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00922564.1|TREMBL:B7Z8Q4 Ta                                0.6     10.1     0.0       0
19287468 - 1  K.NFPSPVDAAFR.Q                        1220.61   2  0.01    2.871  0.432   324.9  1   16/30   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 610.81
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 F    234.12     262.12                                     1106.56
 P    331.18     359.17                                      959.49
 S    418.21     446.20                                      862.44
 P    515.26     543.26                                      775.41
 V    614.33     642.32                                      678.36
 D    729.36     757.35                                      579.29
 A    800.39     828.39                                      464.26
 A    871.43     899.43                                      393.22
 F   1018.50    1046.49                                      322.19
 R                                                           175.12
```

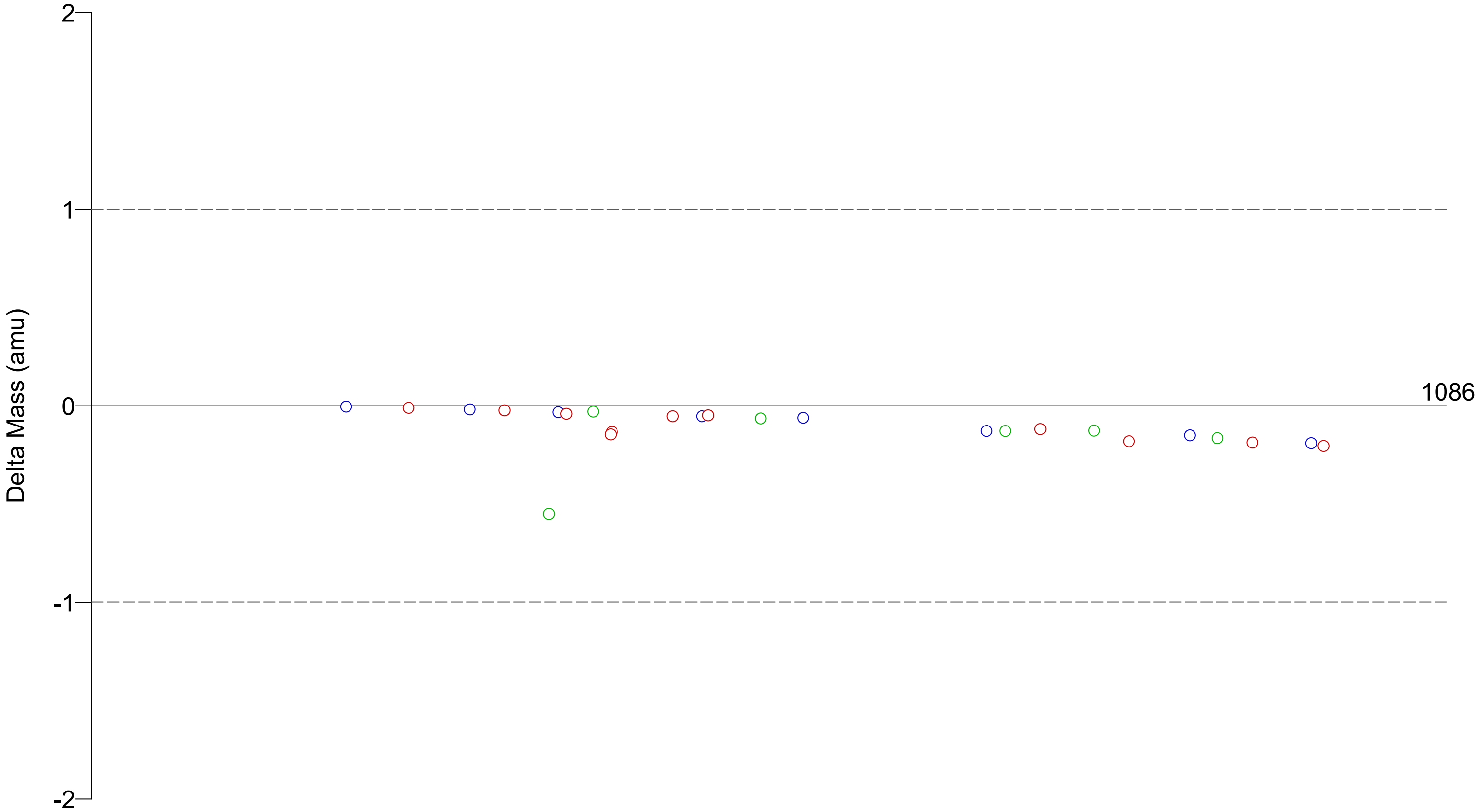


#19287468-1 NL: 1.83E6

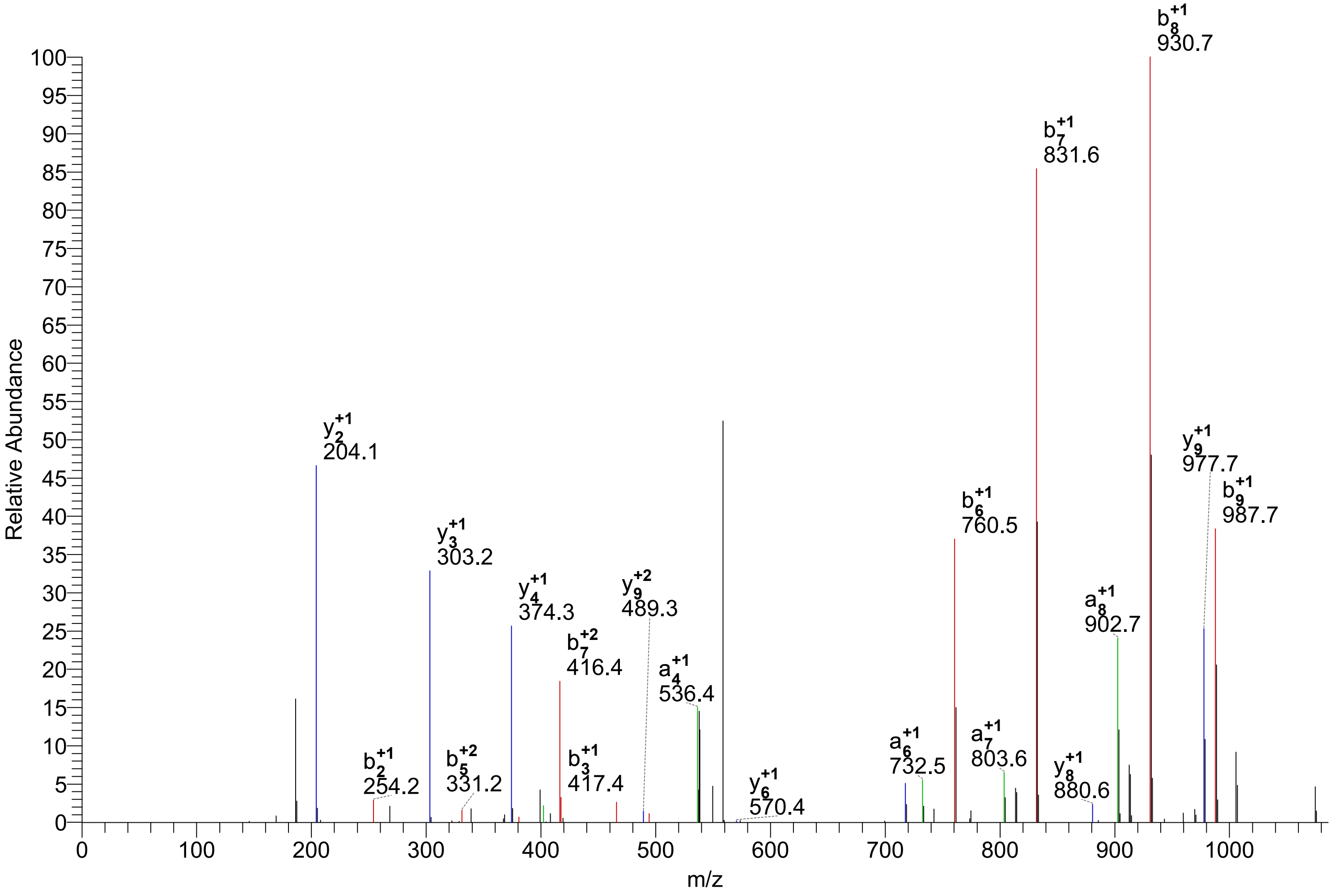


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00027507.1|SWISS-PROT:Q02985|ENSEMBL:ENSP00000356395|RE    0.8     10.2     0.0        0
19287468 - 1  R.RPYFPVAVGK.Y                            1133.65   2  0.02     3.852  0.322   1065.5 1   18/27   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      977.55
 Y    389.23     417.22                                      880.49
 F    536.30     564.29                                      717.43
 P    633.35     661.35                                      570.36
 V    732.42     760.41                                      473.31
 A    803.46     831.45                                      374.24
 V    902.52     930.52                                      303.20
 G    959.55     987.54                                      204.13
 K                                                           147.11
```

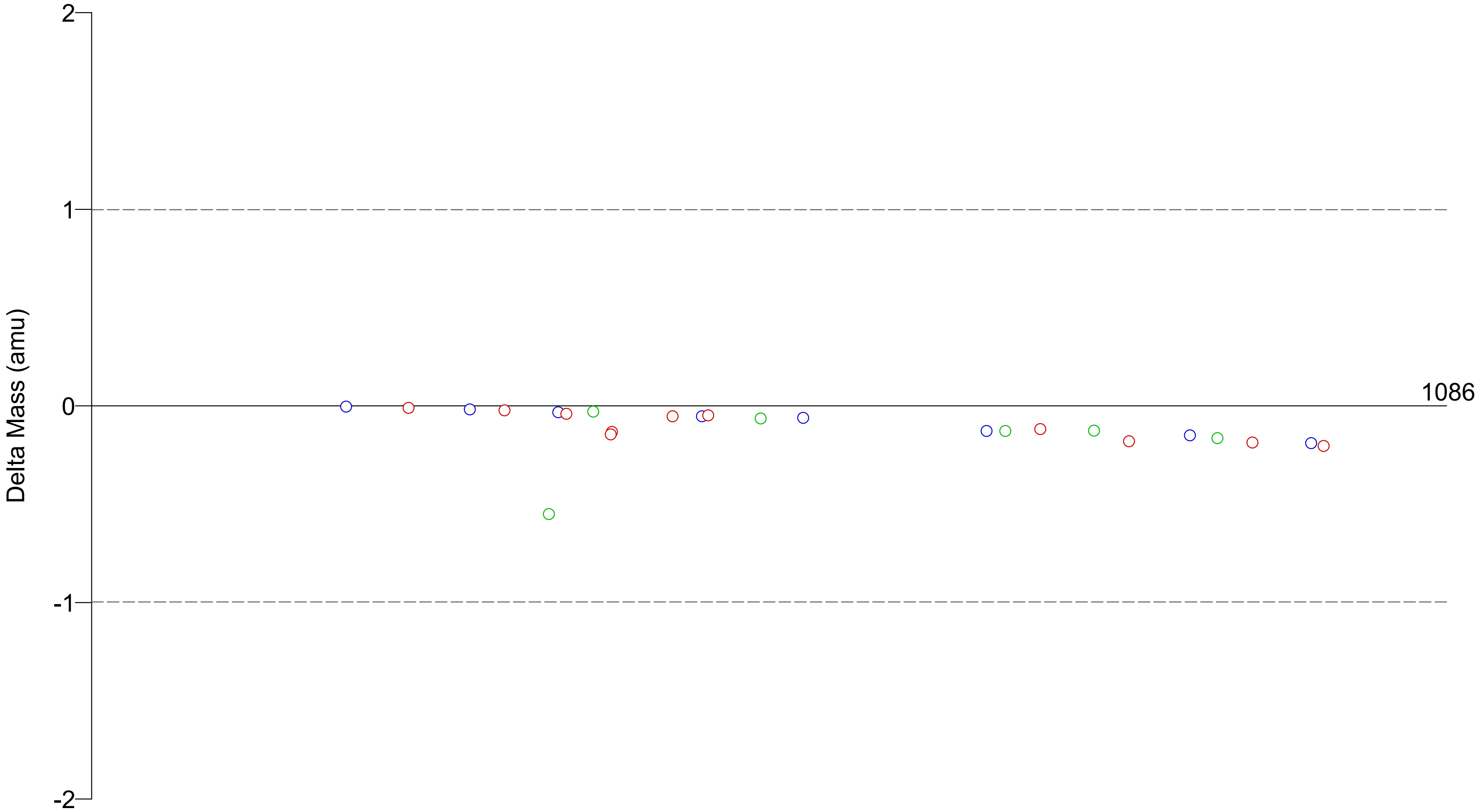


#19287468-1 NL: 2.96E5

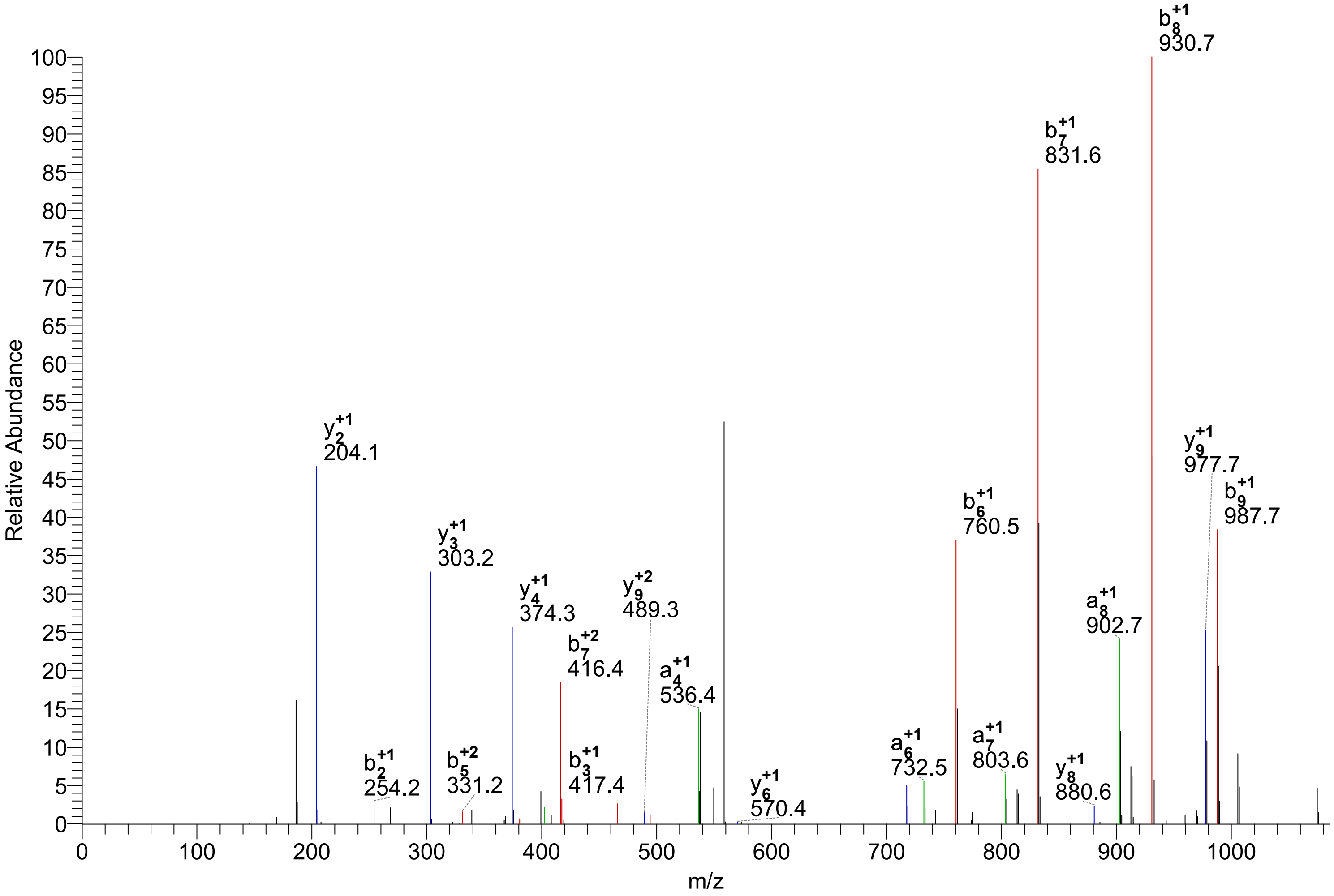


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+     z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00218999.2|SWISS-PROT:P0860                               0.8      10.2     0.0       0
19287468 - 1  R.RPYFPVAVGK.Y                         1133.65   2  0.02     3.852  0.322   1065.5 1   18/27   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      977.55
 Y    389.23     417.22                                      880.49
 F    536.30     564.29                                      717.43
 P    633.35     661.35                                      570.36
 V    732.42     760.41                                      473.31
 A    803.46     831.45                                      374.24
 V    902.52     930.52                                      303.20
 G    959.55     987.54                                      204.13
 K                                                           147.11
```

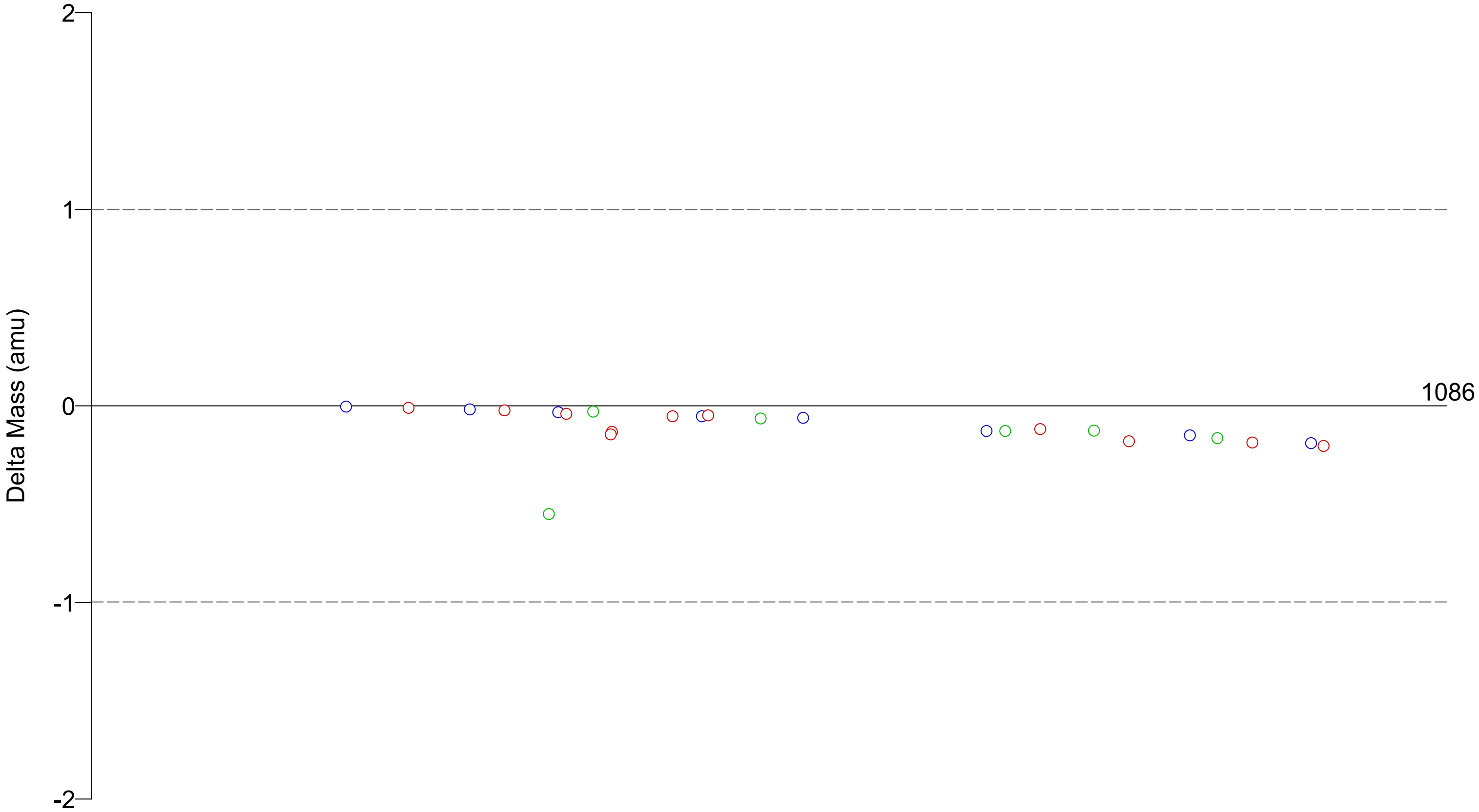


#19287468-1 NL: 2.96E5

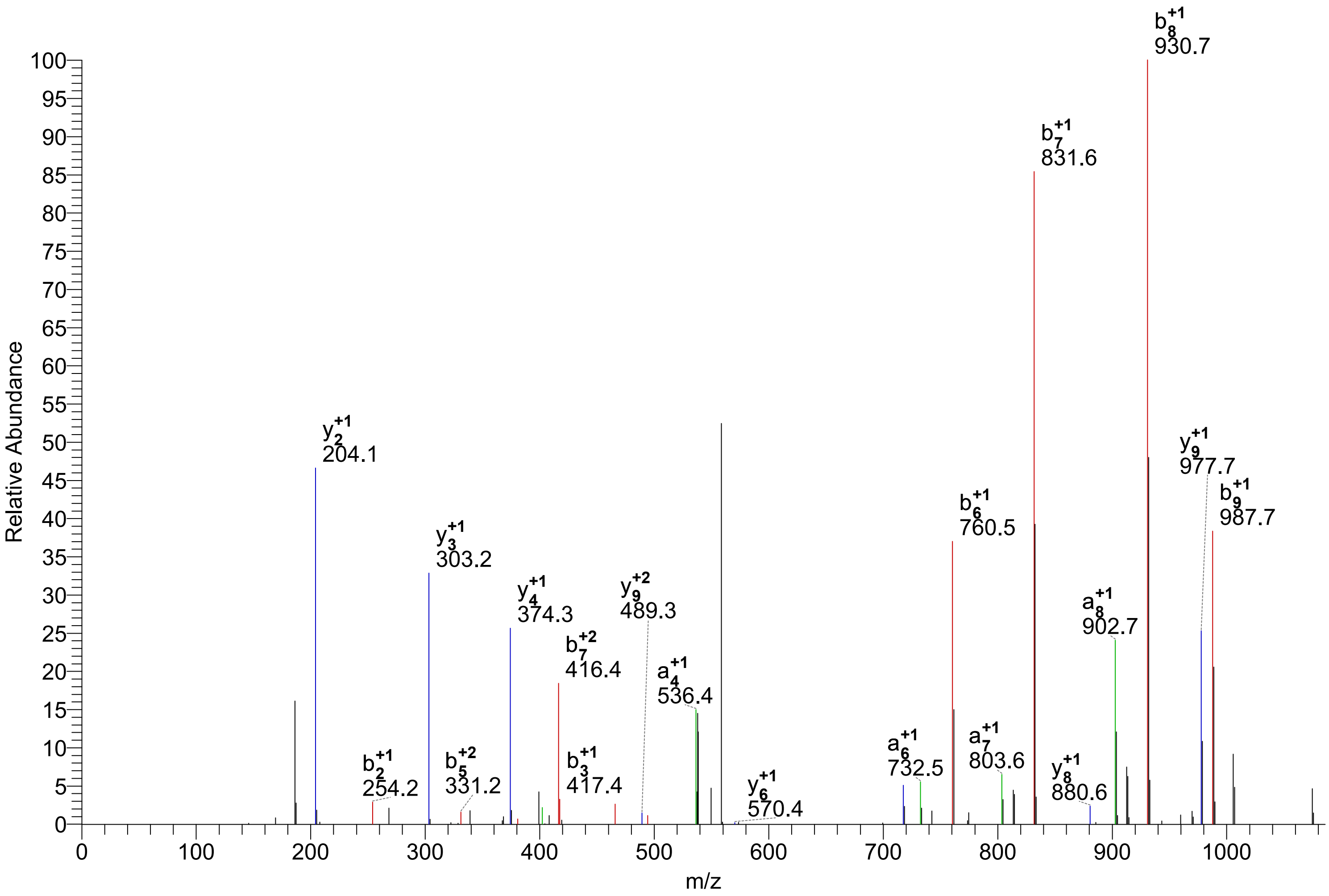


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00515041.5|TREMBL:A8MPQ4;Q5                                0.8     10.2     0.0       0
19287468 - 1  R.RPYFPVAVGK.Y                         1133.65   2  0.02    3.852  0.322   1065.5 1   18/27   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      977.55
 Y    389.23     417.22                                      880.49
 F    536.30     564.29                                      717.43
 P    633.35     661.35                                      570.36
 V    732.42     760.41                                      473.31
 A    803.46     831.45                                      374.24
 V    902.52     930.52                                      303.20
 G    959.55     987.54                                      204.13
 K                                                           147.11
```

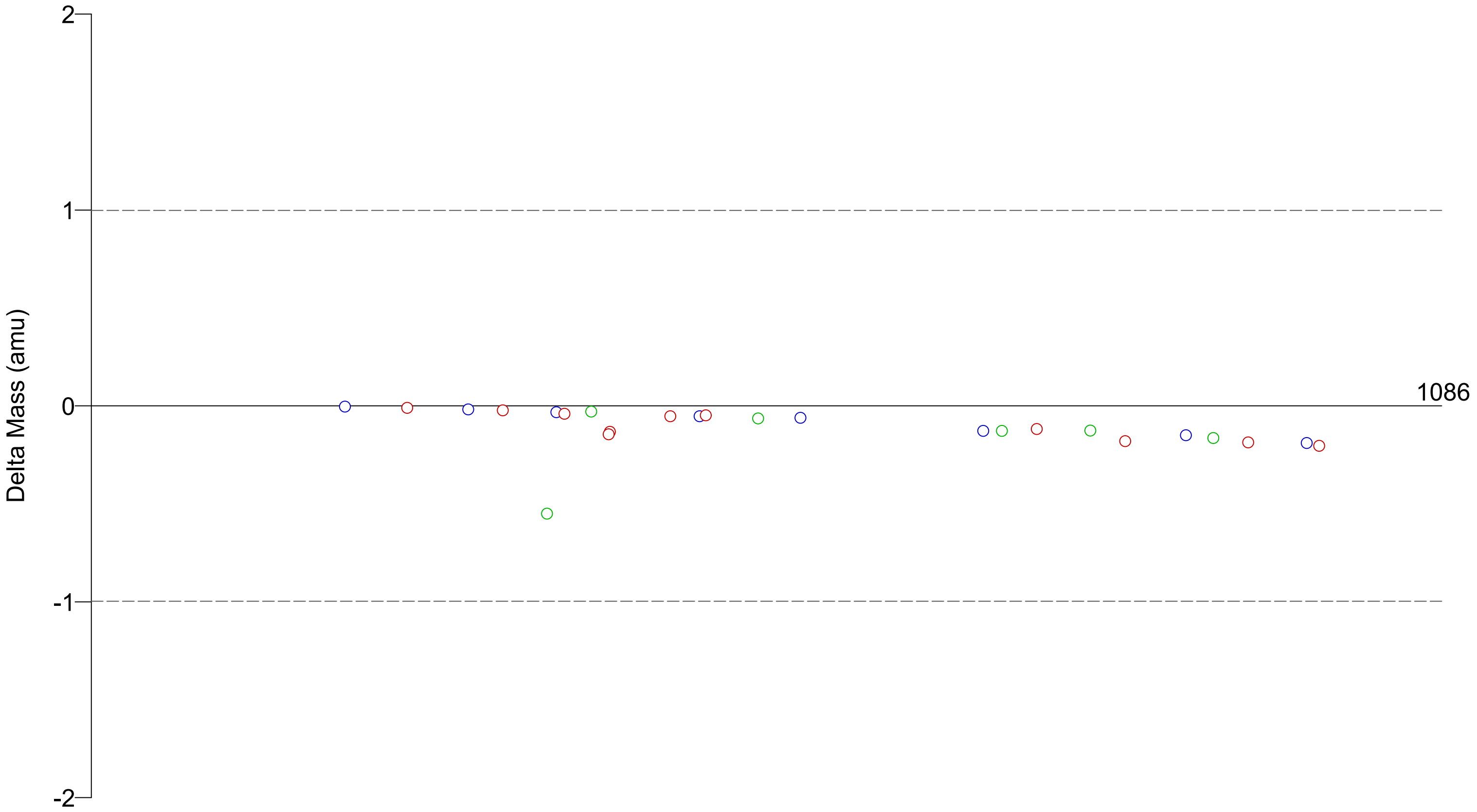


#19287468-1 NL: 2.96E5

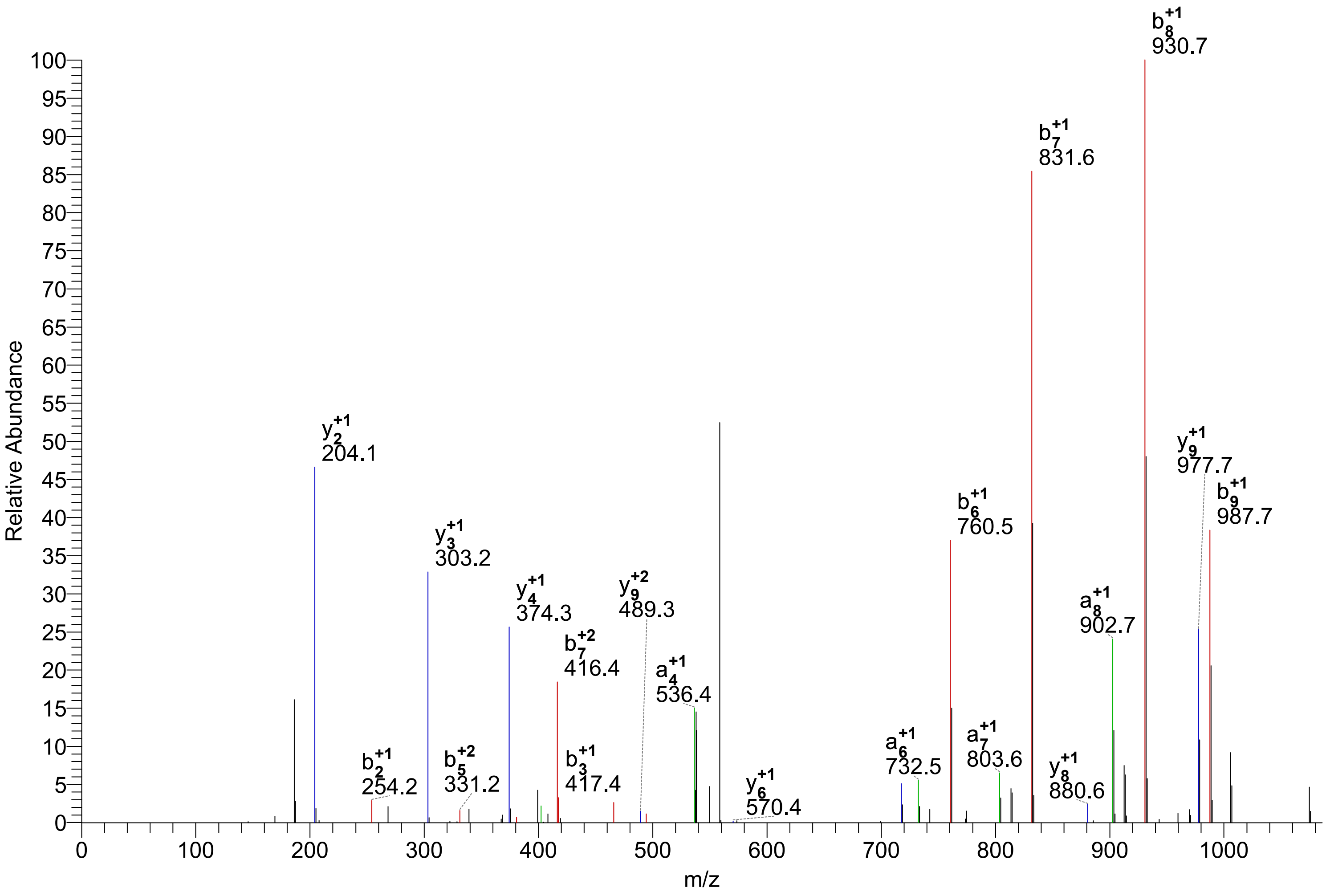


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00654723.1|TREMBL:B1AKF8;Q8                                0.8     10.2     0.0       0
19287468 - 1  R.RPYFPVAVGK.Y                         1133.65   2  0.02    3.852  0.322   1065.5 1   18/27   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      977.55
 Y    389.23     417.22                                      880.49
 F    536.30     564.29                                      717.43
 P    633.35     661.35                                      570.36
 V    732.42     760.41                                      473.31
 A    803.46     831.45                                      374.24
 V    902.52     930.52                                      303.20
 G    959.55     987.54                                      204.13
 K                                                           147.11
```

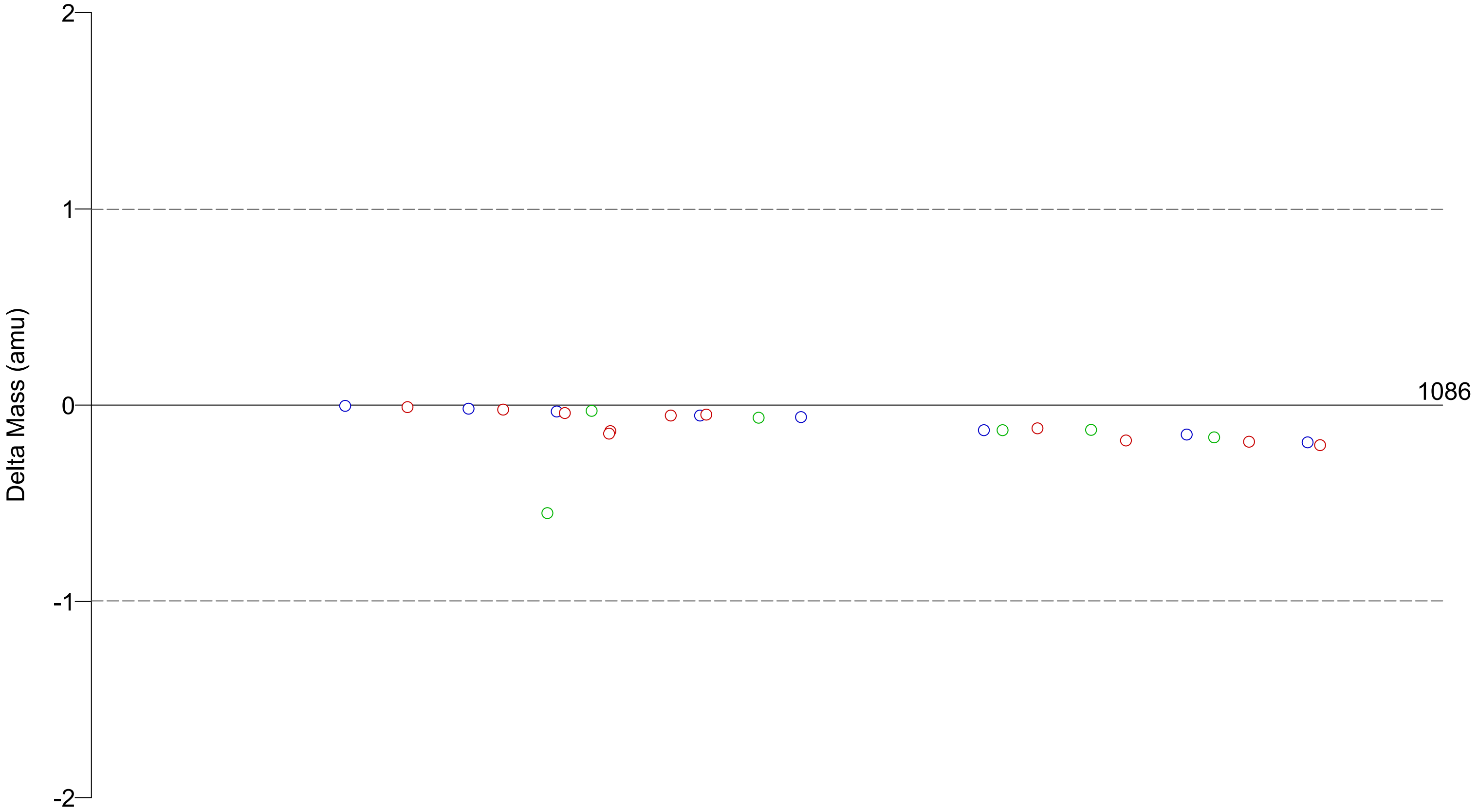


#19287468-1 NL: 2.96E5

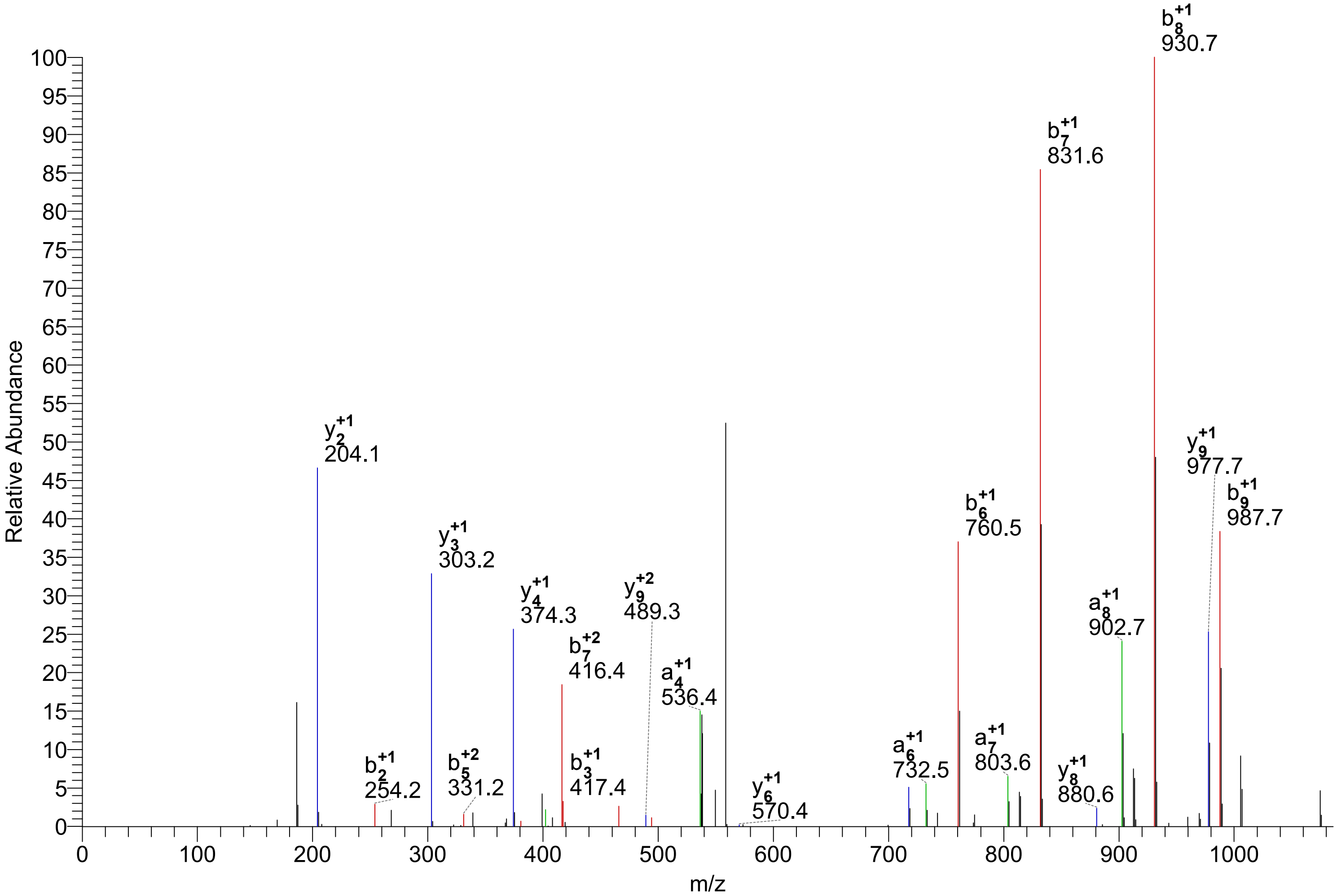


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00844262.1|TREMBL:Q6NSD3|EN                                       0.8      10.2     0.0        0
19287468 - 1  R.RPYFPVAVGK.Y                               1133.65    2  0.02     3.852  0.322   1065.5 1   18/27   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                       977.55
 Y    389.23     417.22                                       880.49
 F    536.30     564.29                                       717.43
 P    633.35     661.35                                       570.36
 V    732.42     760.41                                       473.31
 A    803.46     831.45                                       374.24
 V    902.52     930.52                                       303.20
 G    959.55     987.54                                       204.13
 K                                                            147.11
```

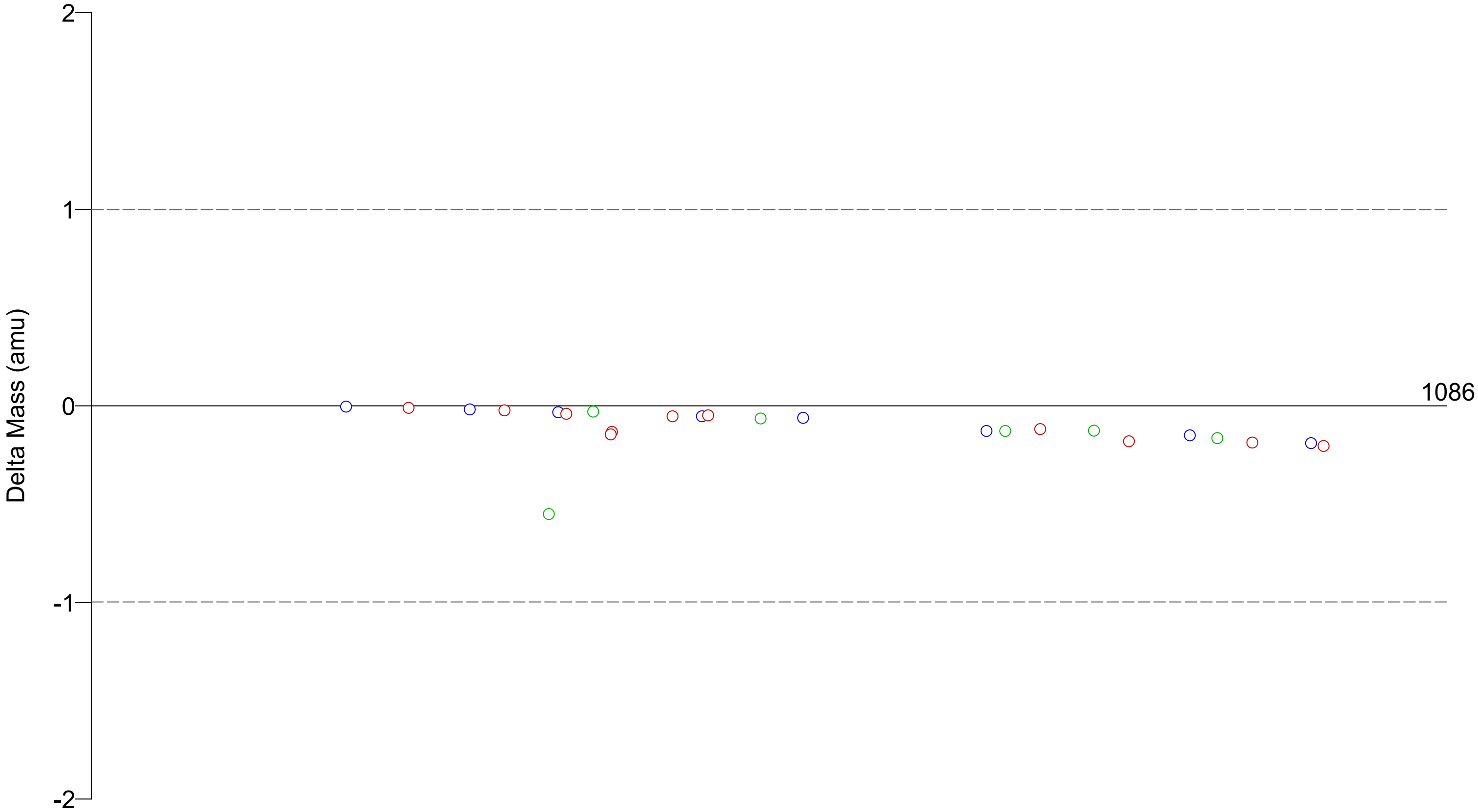


#19287468-1 NL: 2.96E5

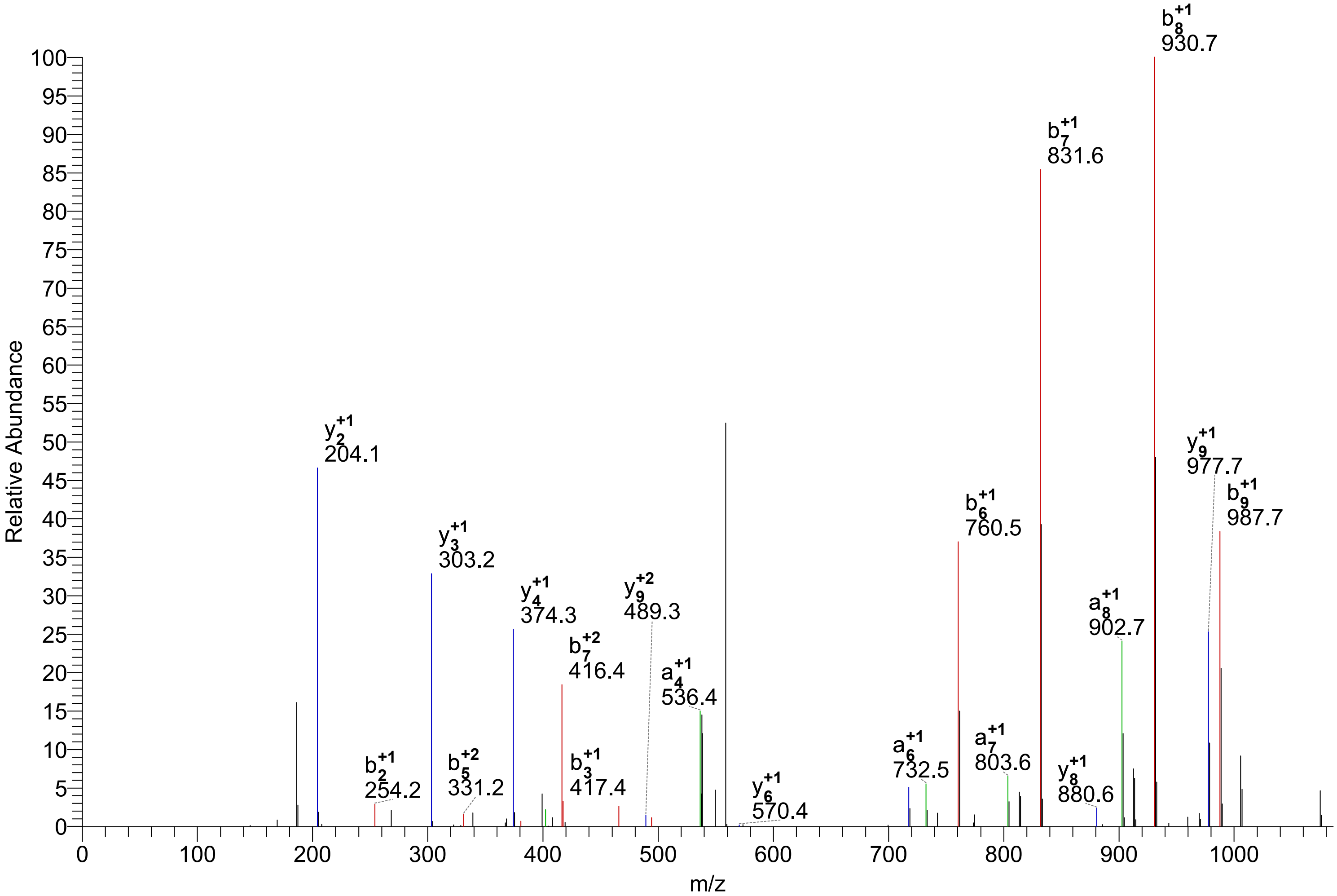


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00908535.1|TREMBL:B4DPR0 Ta                                0.8     10.2     0.0       0
19287468 - 1  R.RPYFPVAVGK.Y                         1133.65   2  0.02    3.852  0.322   1065.5 1   18/27   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                       977.55
 Y    389.23     417.22                                       880.49
 F    536.30     564.29                                       717.43
 P    633.35     661.35                                       570.36
 V    732.42     760.41                                       473.31
 A    803.46     831.45                                       374.24
 V    902.52     930.52                                       303.20
 G    959.55     987.54                                       204.13
 K                                                            147.11
```

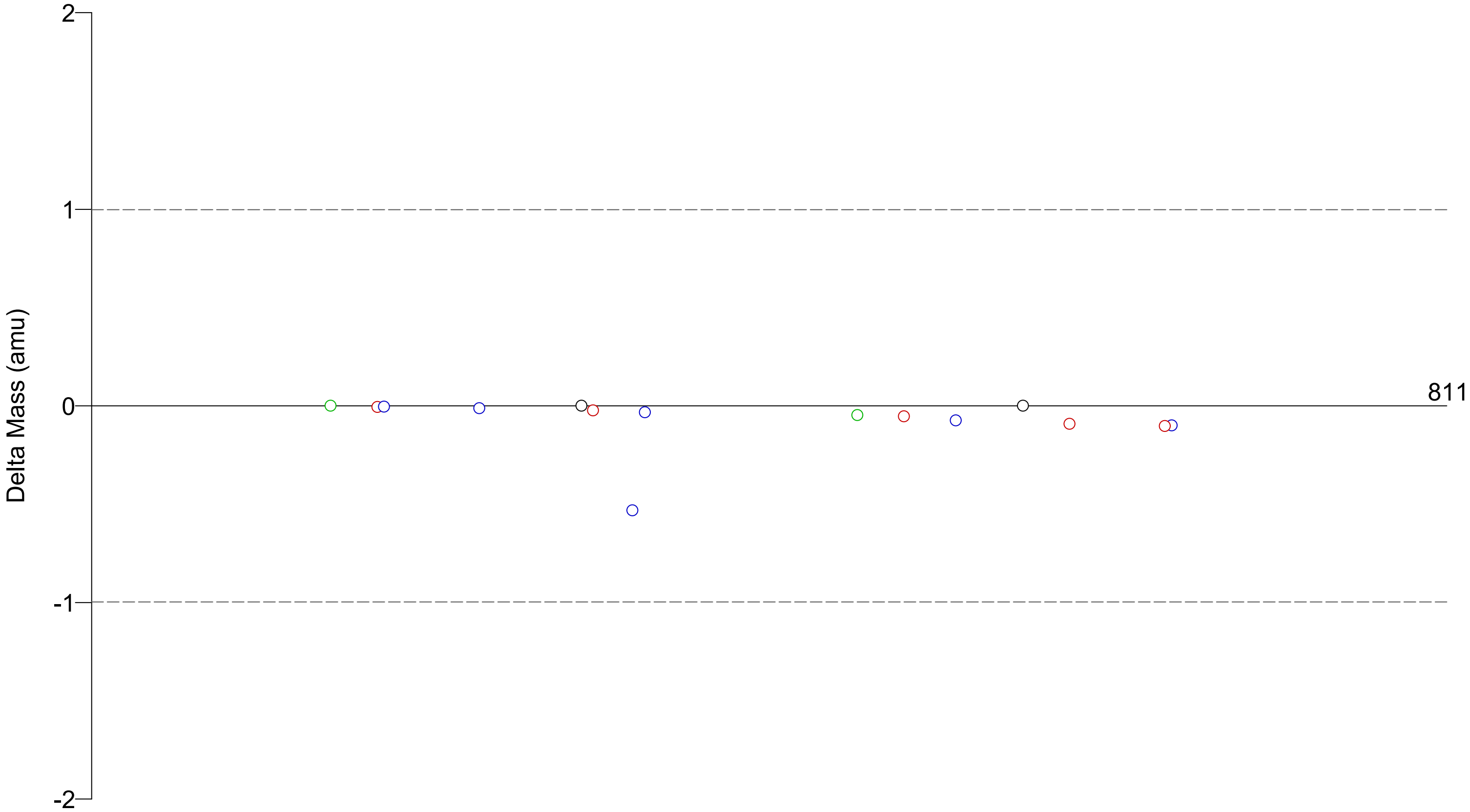


#19287468-1 NL: 2.96E5

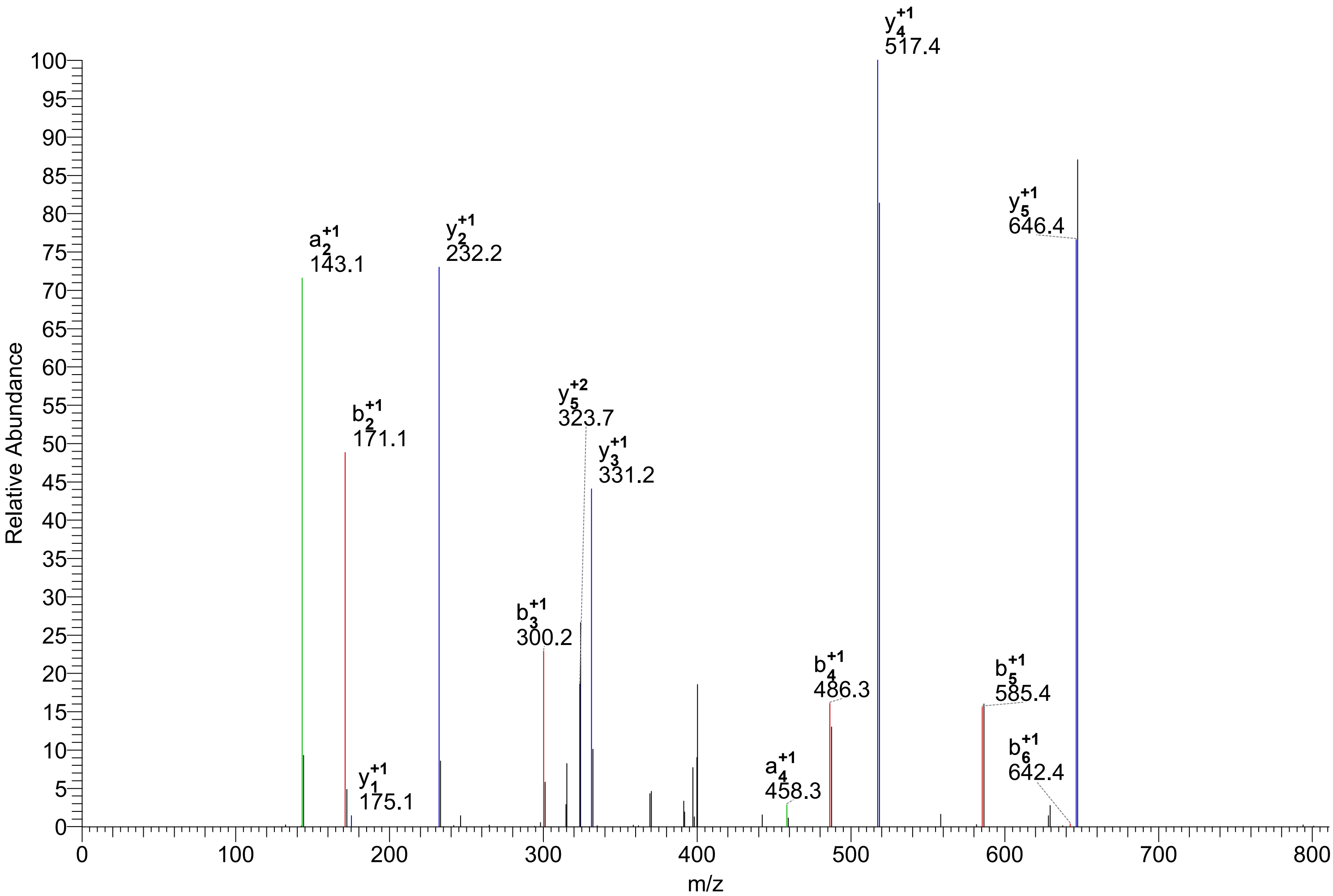


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)        Sequence                                   MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00876888.1|TREMBL:A8K008 Ta                                     0.8     20.1     0.0        0
19287468 - 1  K.GLEWVGR.I                                816.44    2  0.4     2.817  0.203   839.1  1   13/18   8
2118291816 -  K.GPSVFPLAPSSK.S                           1186.65   2  0.02    2.948  0.348   465.0  1   15/33   14

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

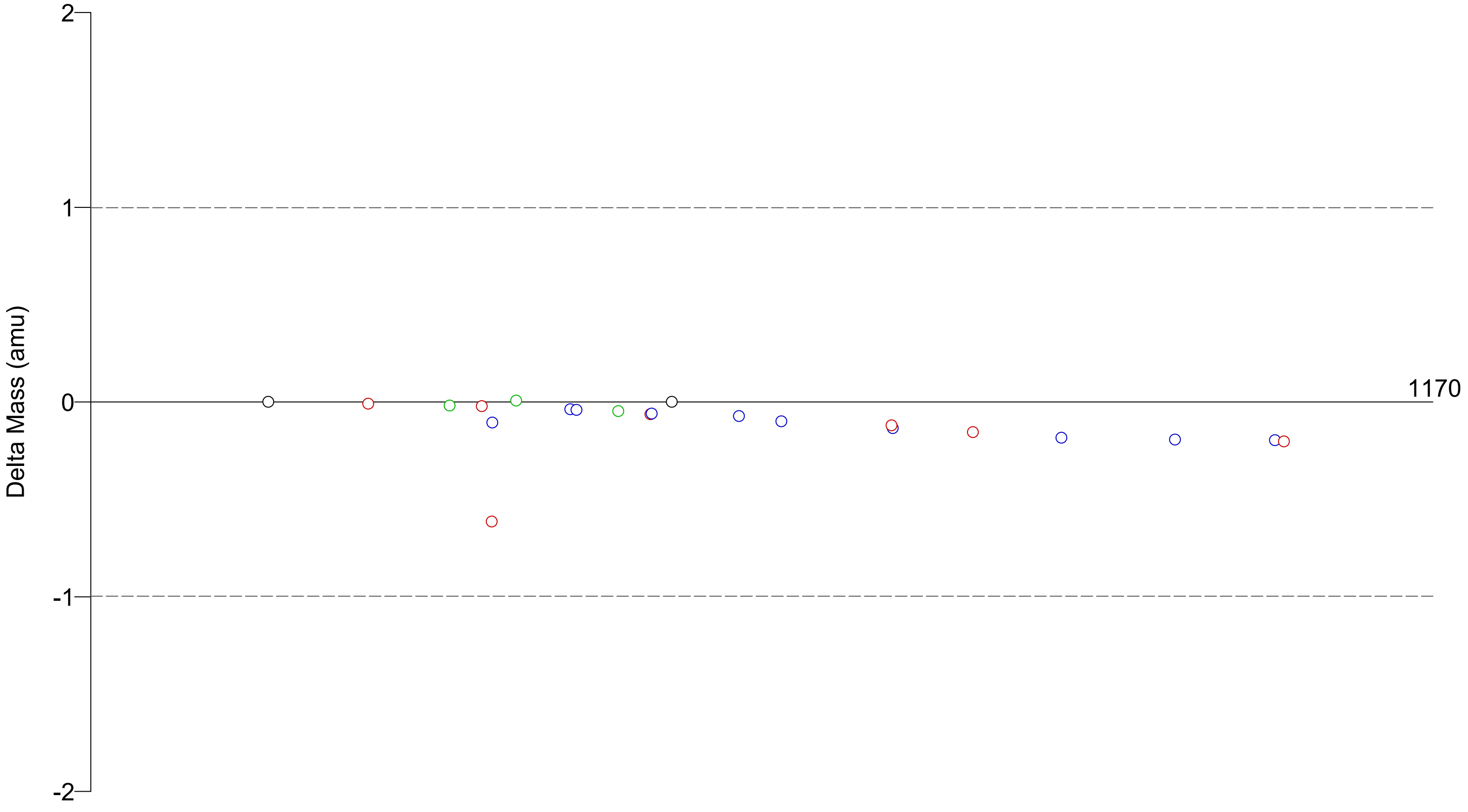
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                      759.41
 E    272.16     300.16                                      646.33
 W    458.24     486.23                                      517.29
 V    557.31     585.30                                      331.21
 G    614.33     642.32                                      232.14
 R                                                           175.12
```



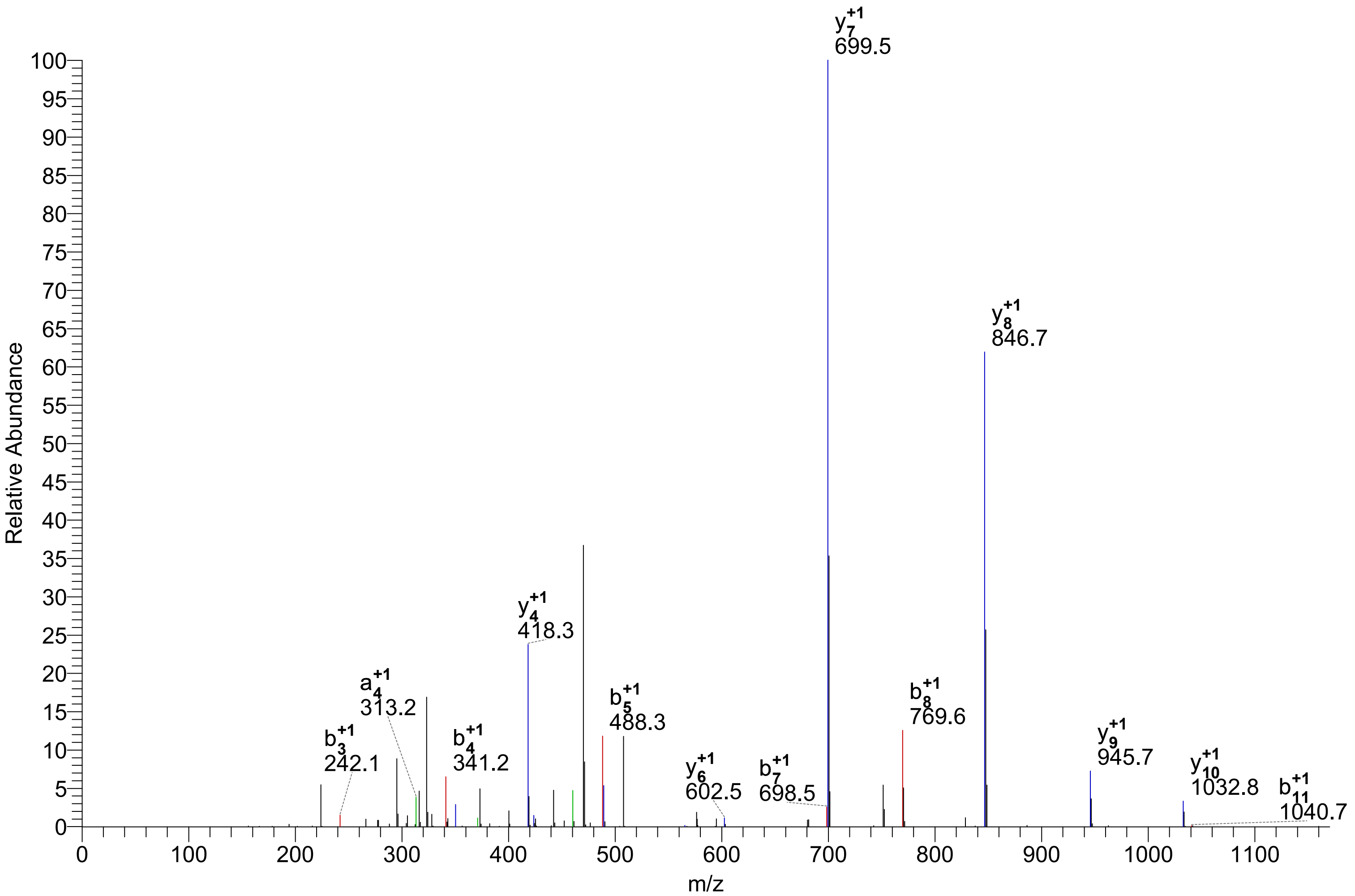
#19287468-1 NL: 1.30E5



```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

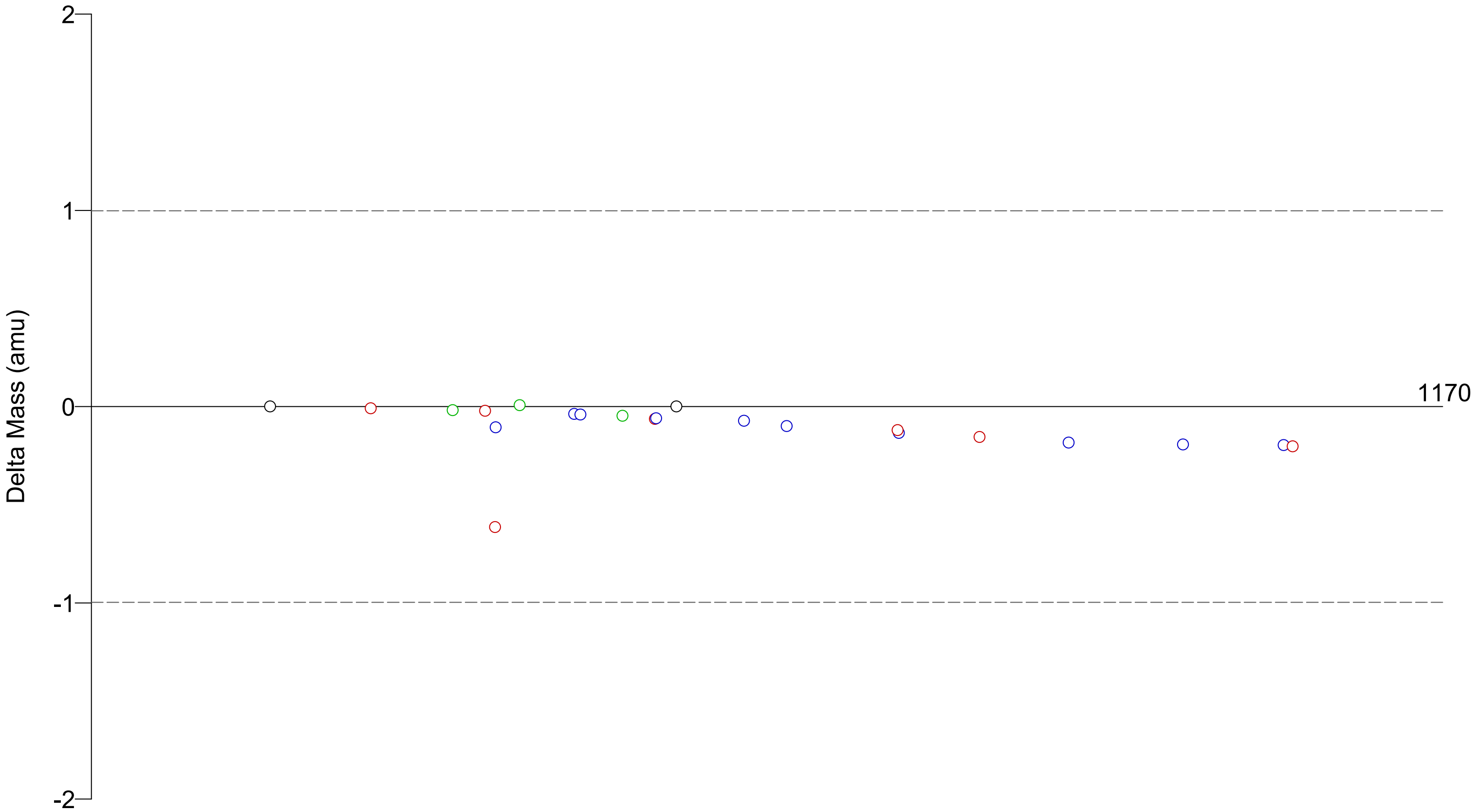


#2118291816-26226248 NL: 6.95E6

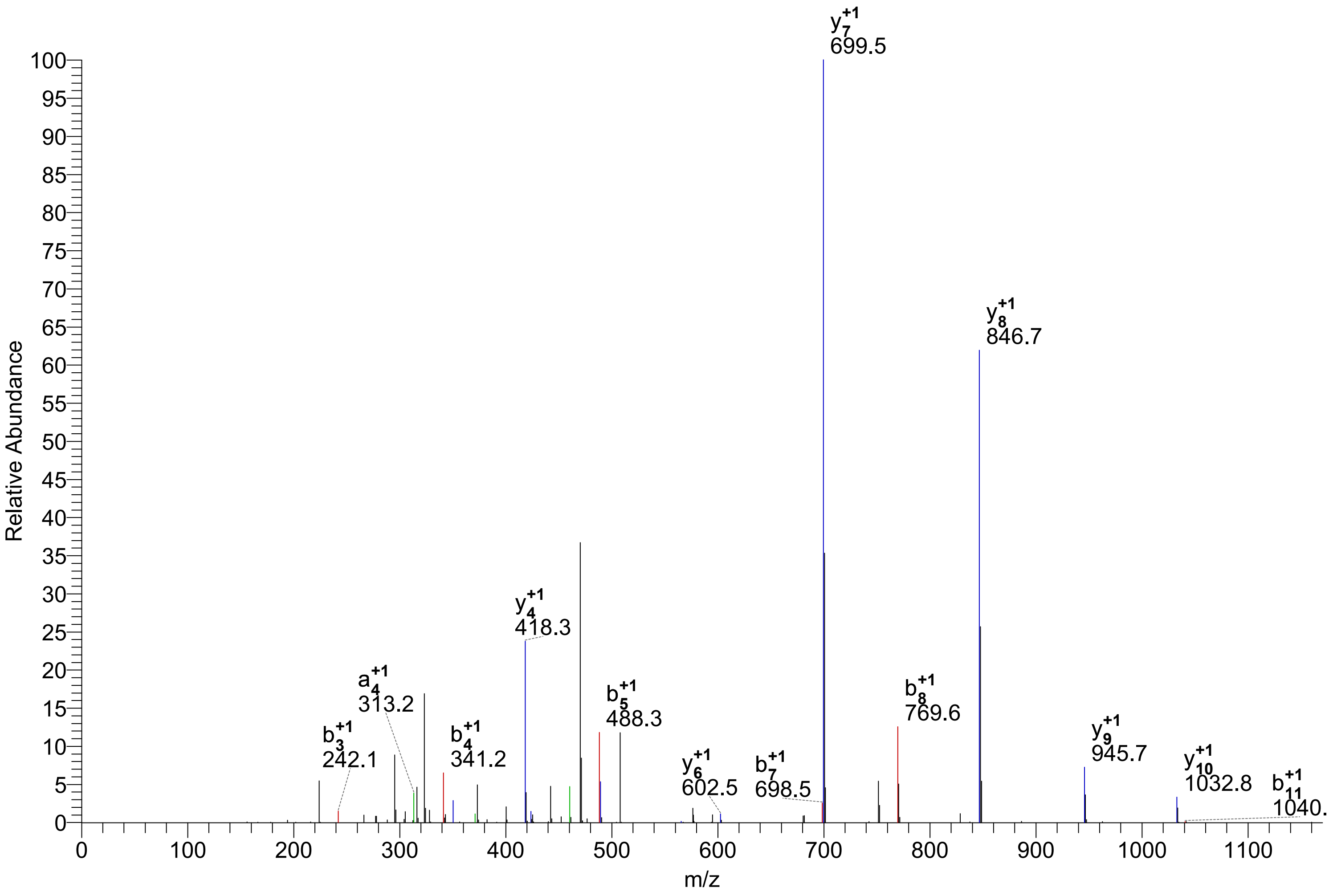


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z     P       XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00383732.1|TREMBL:Q9Y509 Tax_Id=9606 Gene_Symbol=- VH3      0.8     10.1     0.0        0
2118291816 -  K.GPSVFPLAPSSK.S                            1186.65   2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

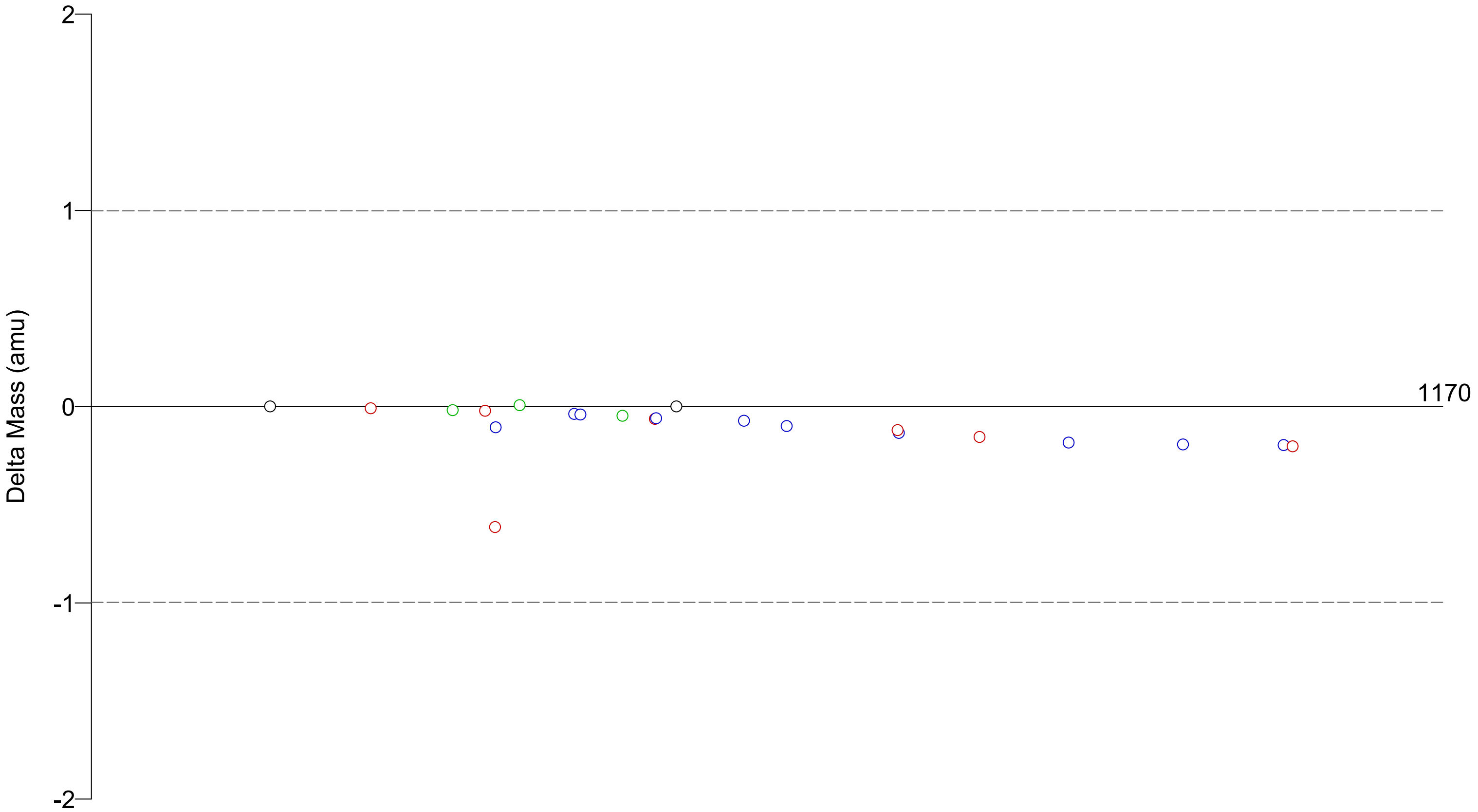


#2118291816-26226248 NL: 6.95E6

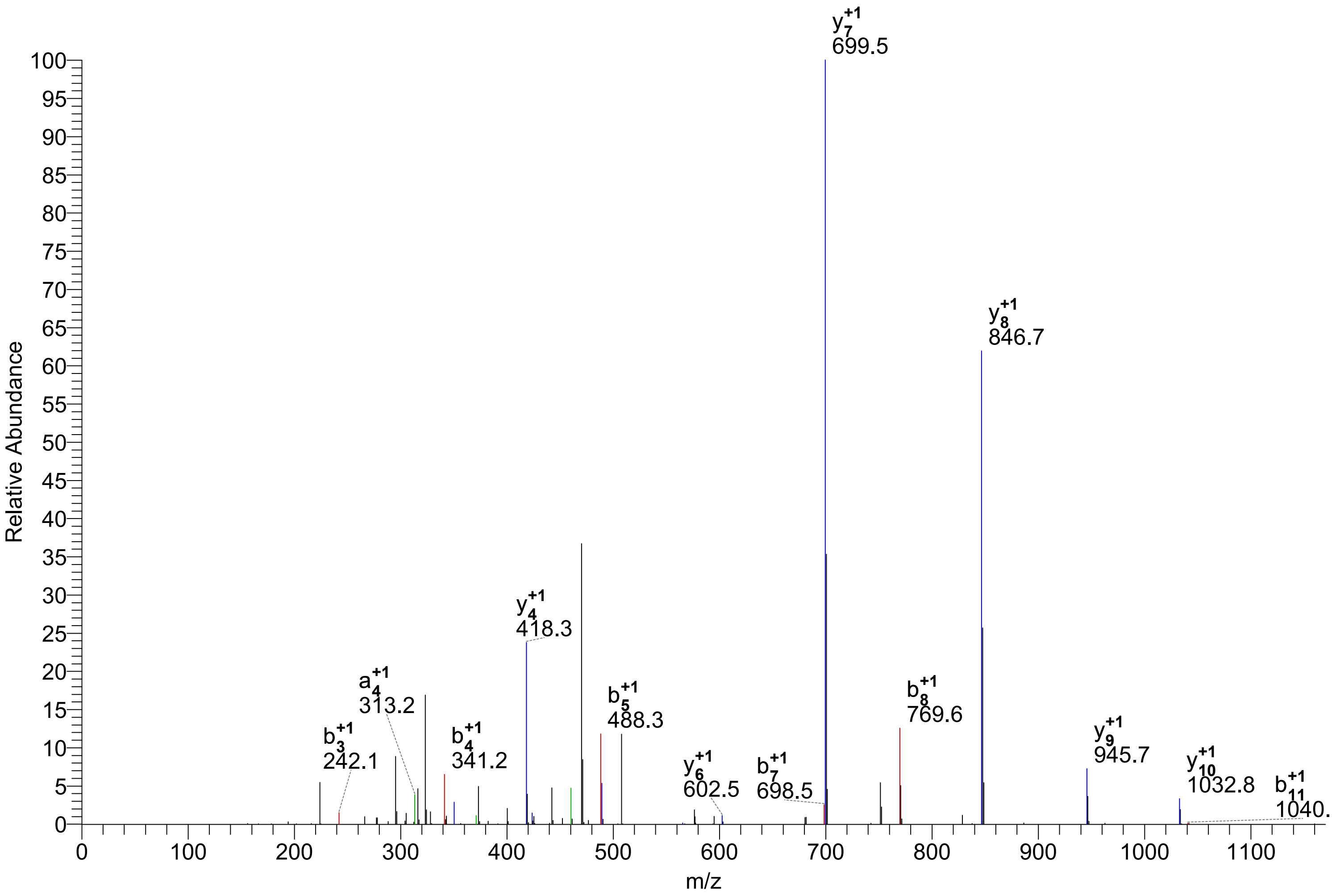


```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z     P        XC  DeltaCn    Sp    RSp  Ions   Count

IPI:IPI00384938.1|TREMBL:Q7Z351 Ta                                   0.8      10.1     0.0        0
2118291816 -  K.GPSVFPLAPSSK.S                       1186.65    2  0.02      2.948  0.348    465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                    1129.63
 S    214.12     242.11                                    1032.57
 V    313.19     341.18                                     945.54
 F    460.26     488.25                                     846.47
 P    557.31     585.30                                     699.40
 L    670.39     698.39                                     602.35
 A    741.43     769.42                                     489.27
 P    838.48     866.48                                     418.23
 S    925.51     953.51                                     321.18
 S   1012.55    1040.54                                     234.14
 K                                                          147.11
```

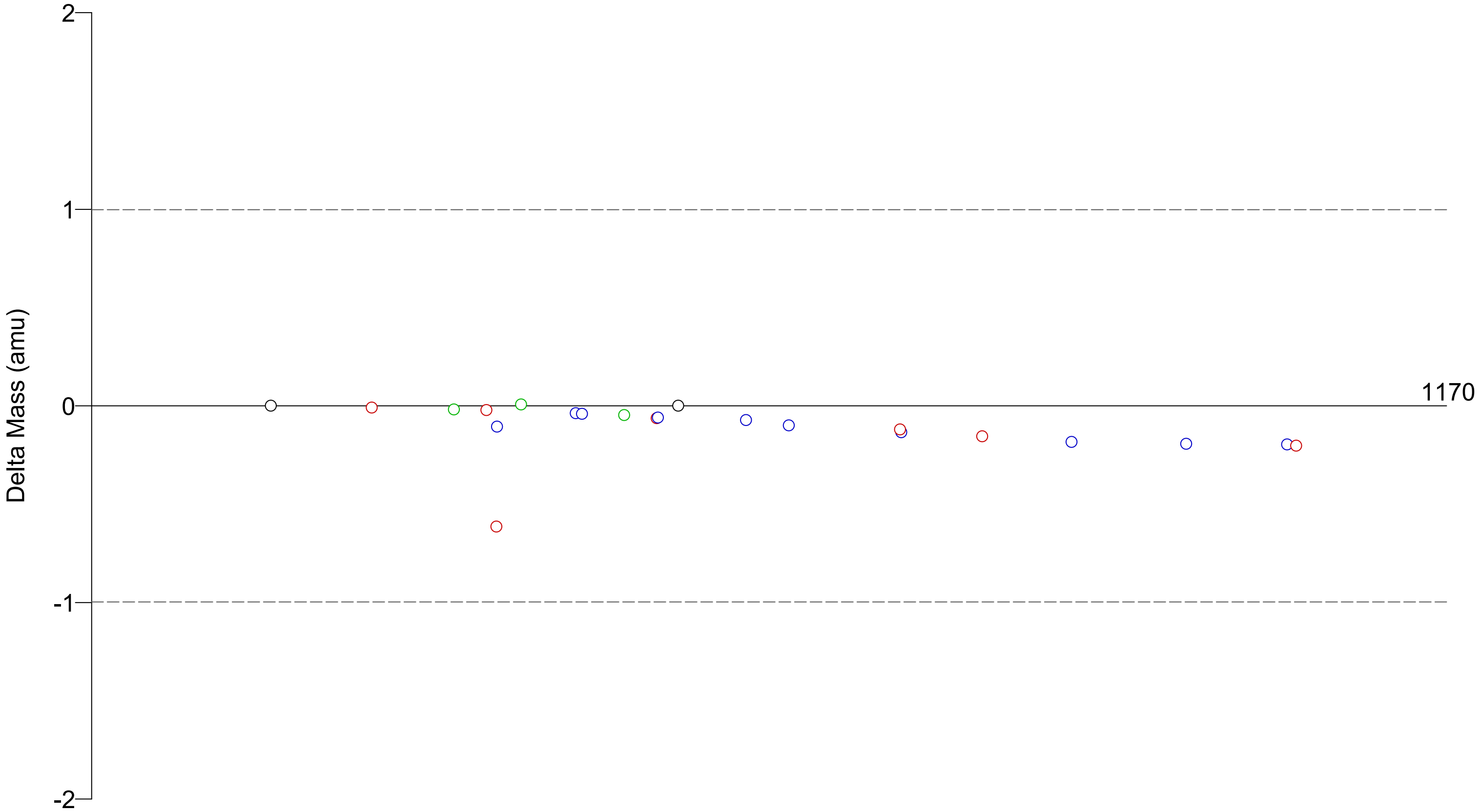


#2118291816-26226248 NL: 6.95E6

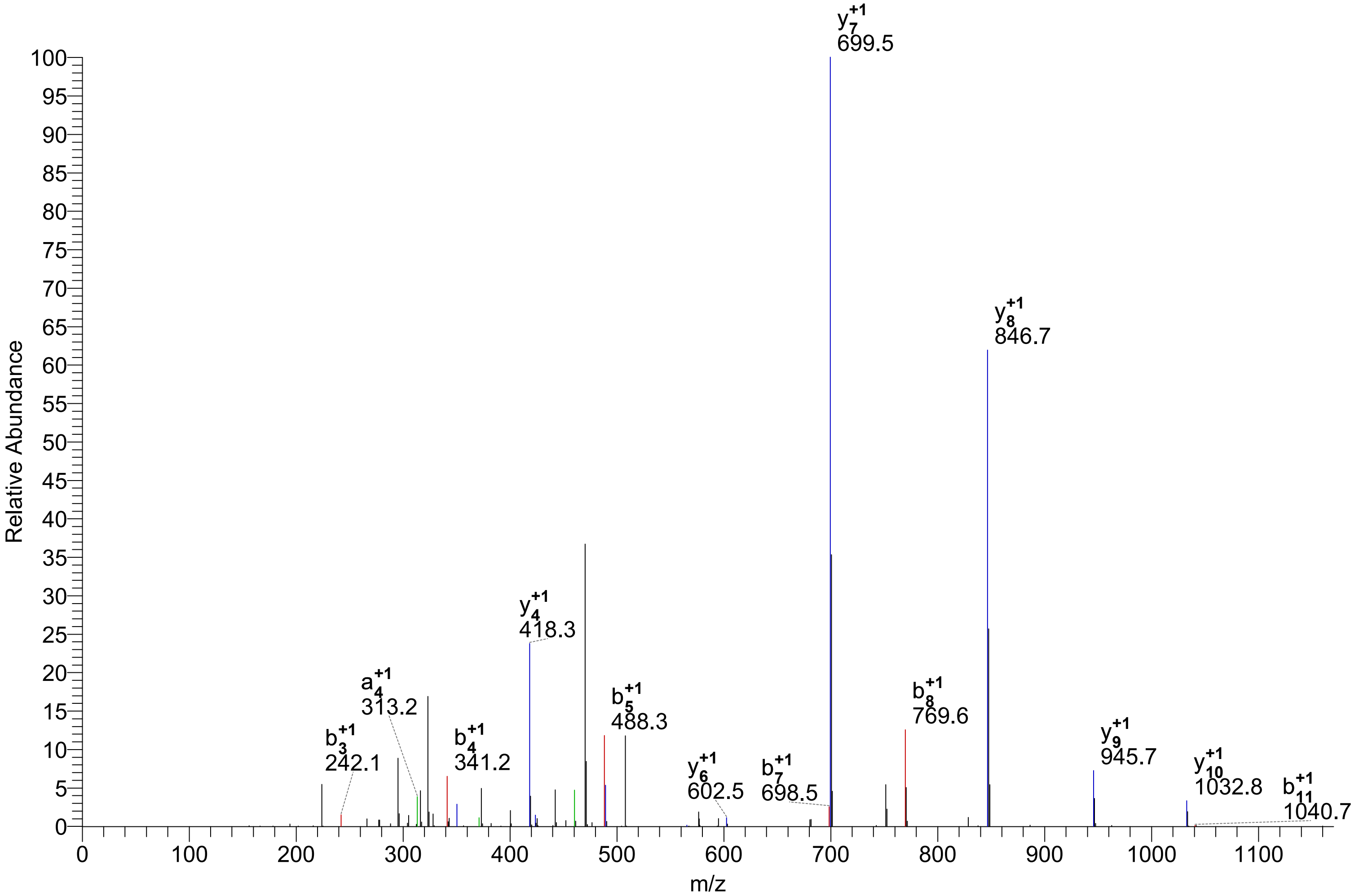


```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z   P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00423464.1|TREMBL:Q6N095 Ta                               0.8      10.1     0.0        0
2118291816 -  K.GPSVFPLAPSSK.S                      1186.65   2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

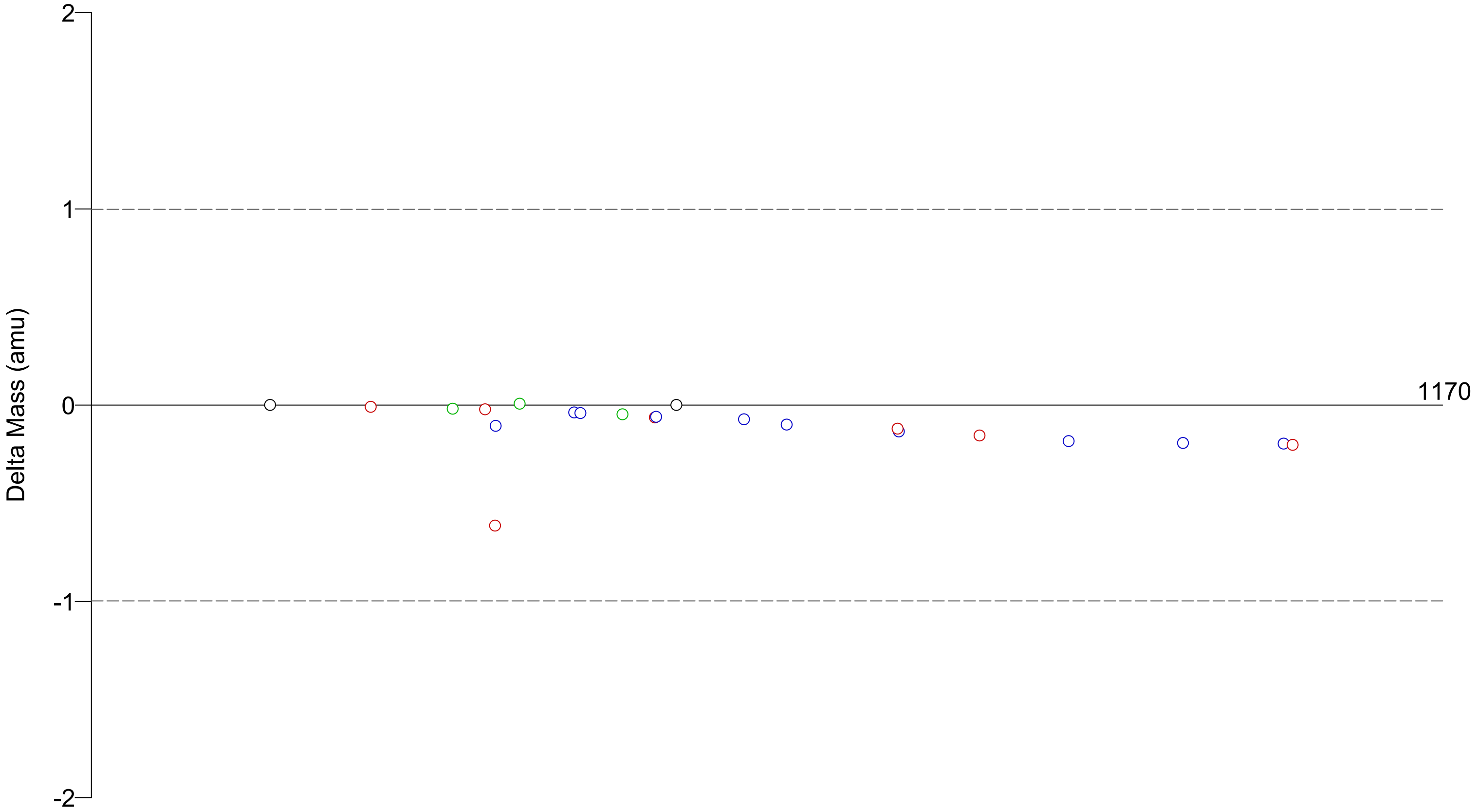


#2118291816-26226248 NL: 6.95E6

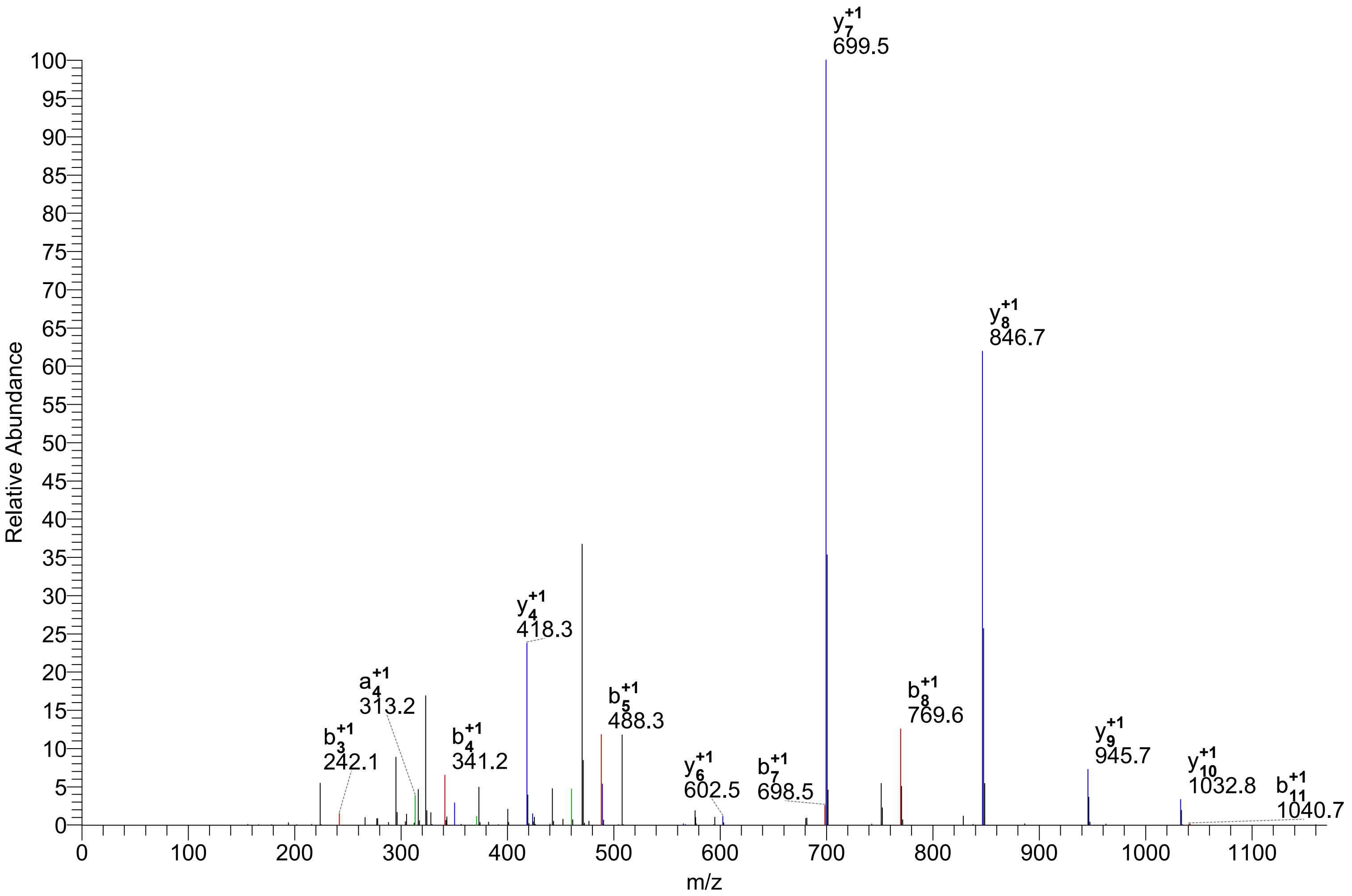


```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)        Sequence                                         MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00423466.1|TREMBL:Q6N097 Ta                                          0.8      10.1     0.0        0
2118291816 -  K.GPSVFPLAPSSK.S                               1186.65    2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G    30.03      58.03
 P   127.09     155.08                                      1129.63
 S   214.12     242.11                                      1032.57
 V   313.19     341.18                                       945.54
 F   460.26     488.25                                       846.47
 P   557.31     585.30                                       699.40
 L   670.39     698.39                                       602.35
 A   741.43     769.42                                       489.27
 P   838.48     866.48                                       418.23
 S   925.51     953.51                                       321.18
 S  1012.55    1040.54                                       234.14
 K                                                           147.11
```

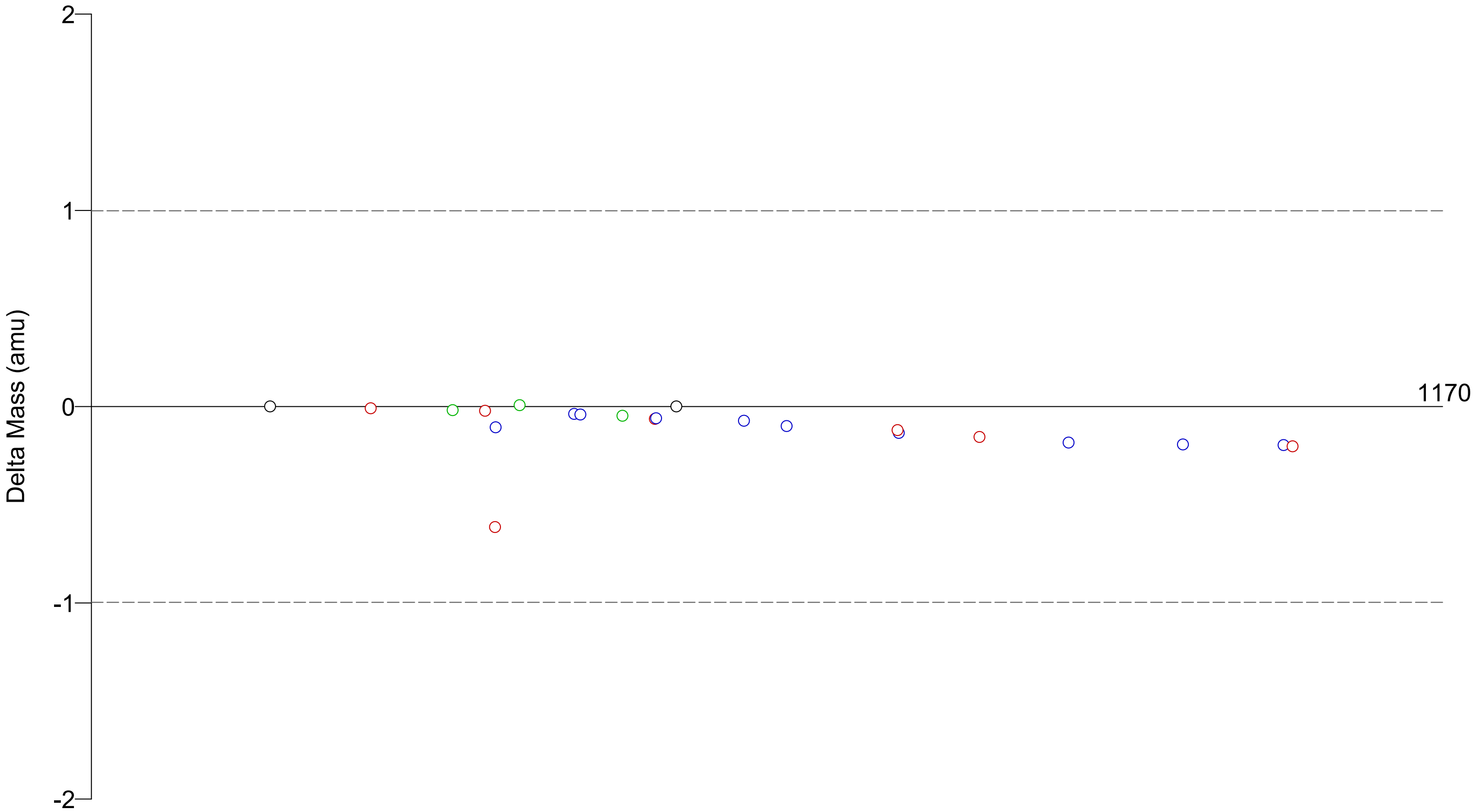


#2118291816-26226248 NL: 6.95E6

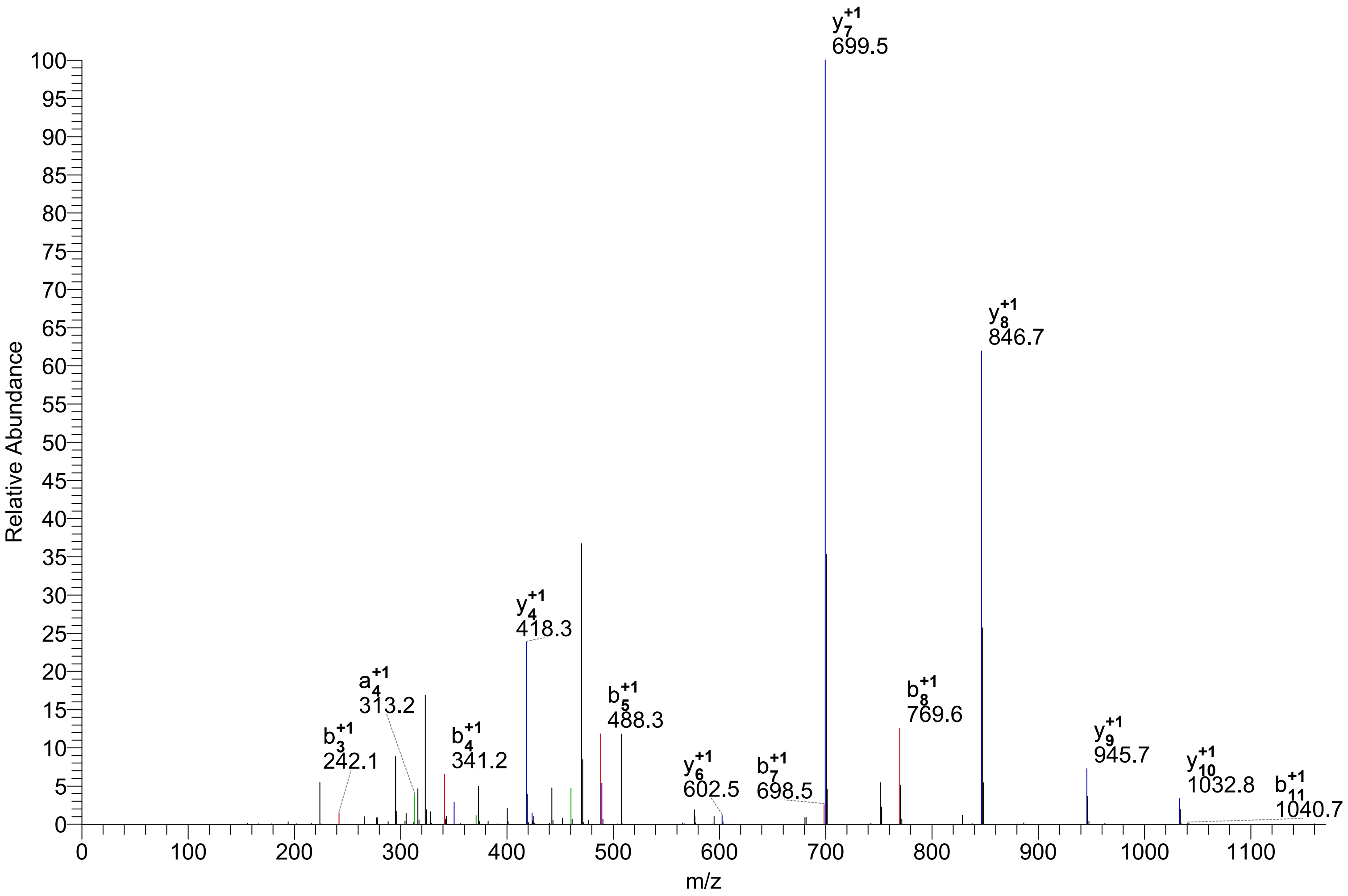


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00442911.1|TREMBL:Q6ZP87 Ta                                   0.8      10.1     0.0       0
2118291816 -  K.GPSVFPLAPSSK.S                        1186.65    2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

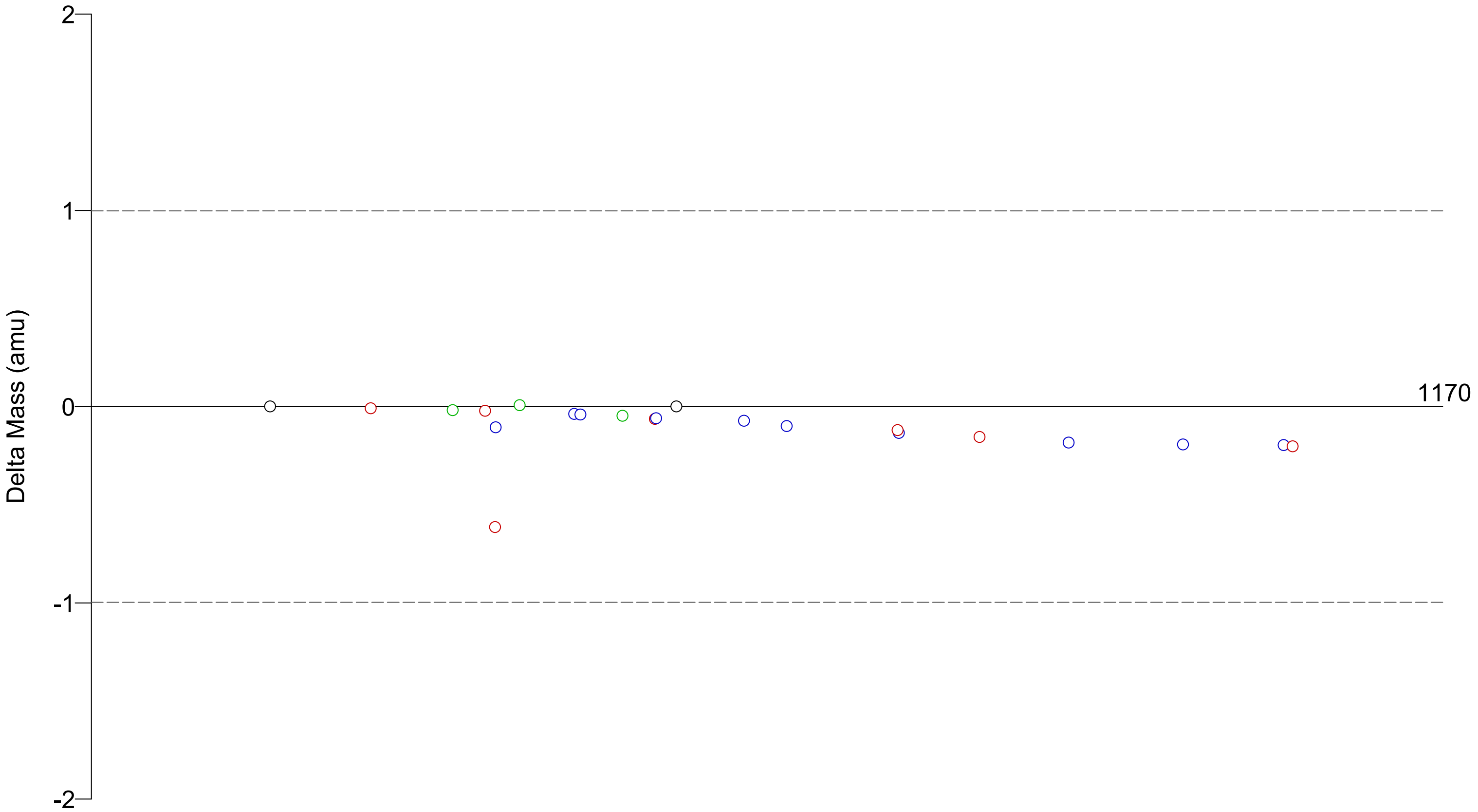


#2118291816-26226248 NL: 6.95E6

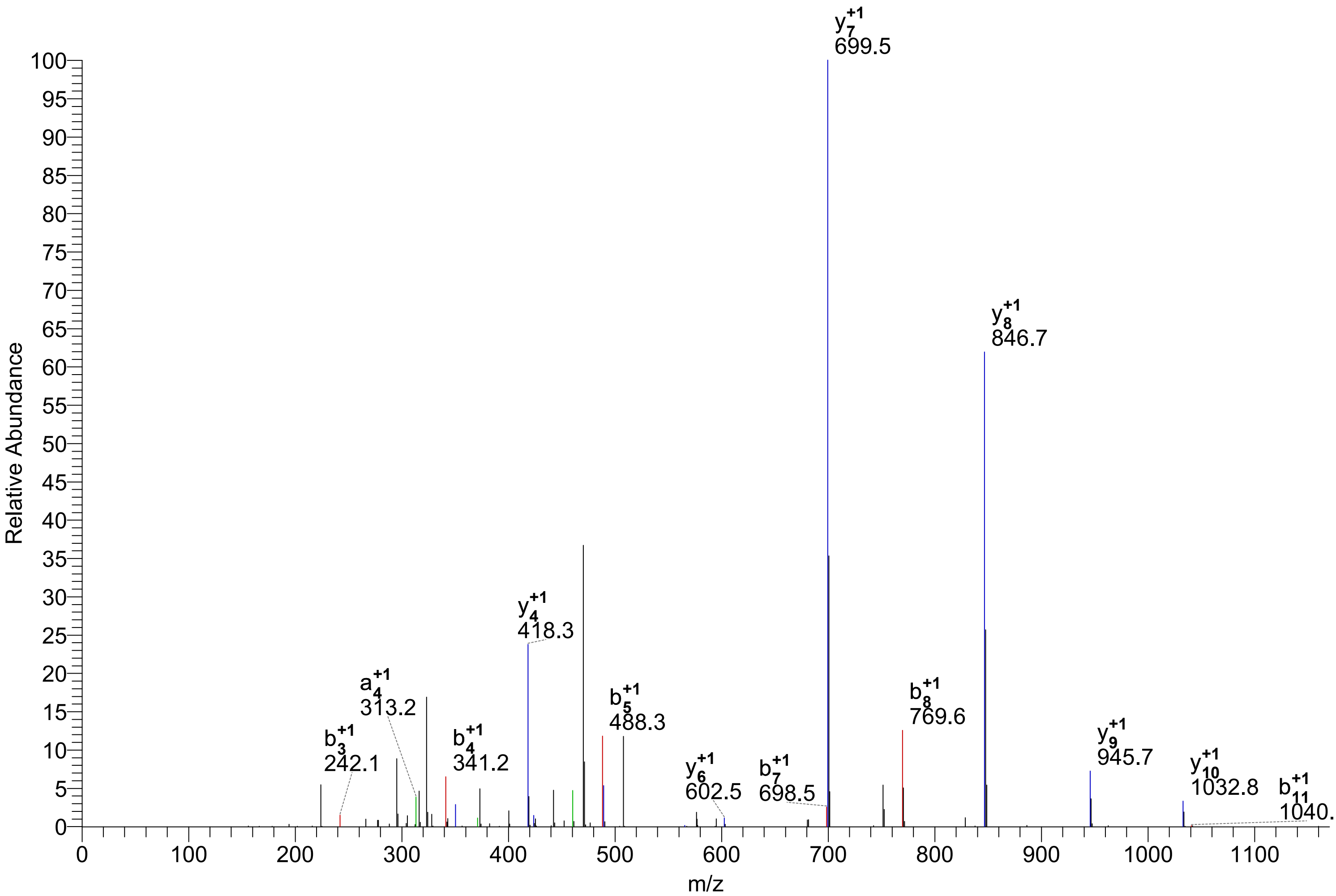


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00784817.1|TREMBL:Q5EFE5 Ta                                    0.8      10.1     0.0       0
2118291816 -  K.GPSVFPLAPSSK.S                          1186.65   2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

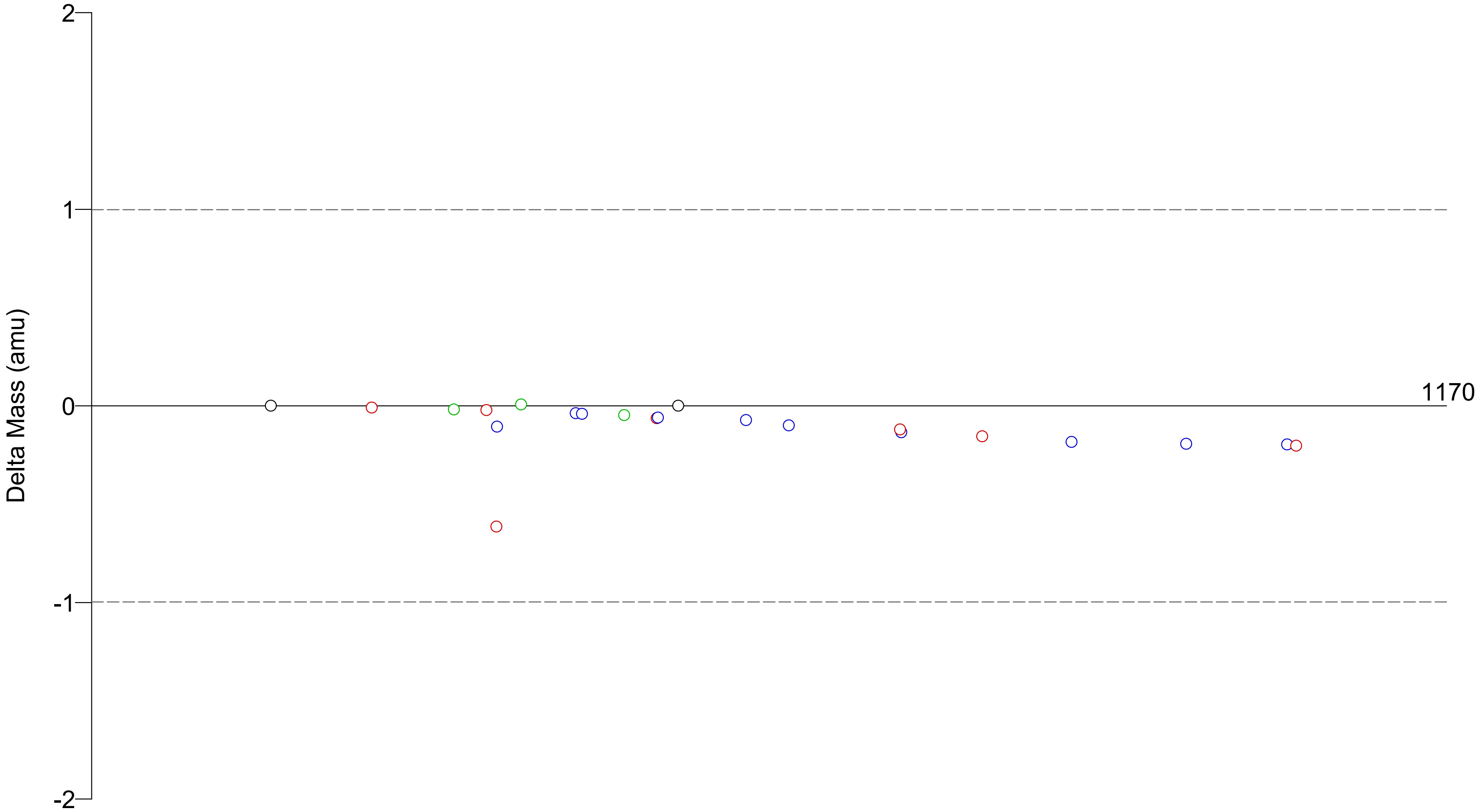


#2118291816-26226248 NL: 6.95E6

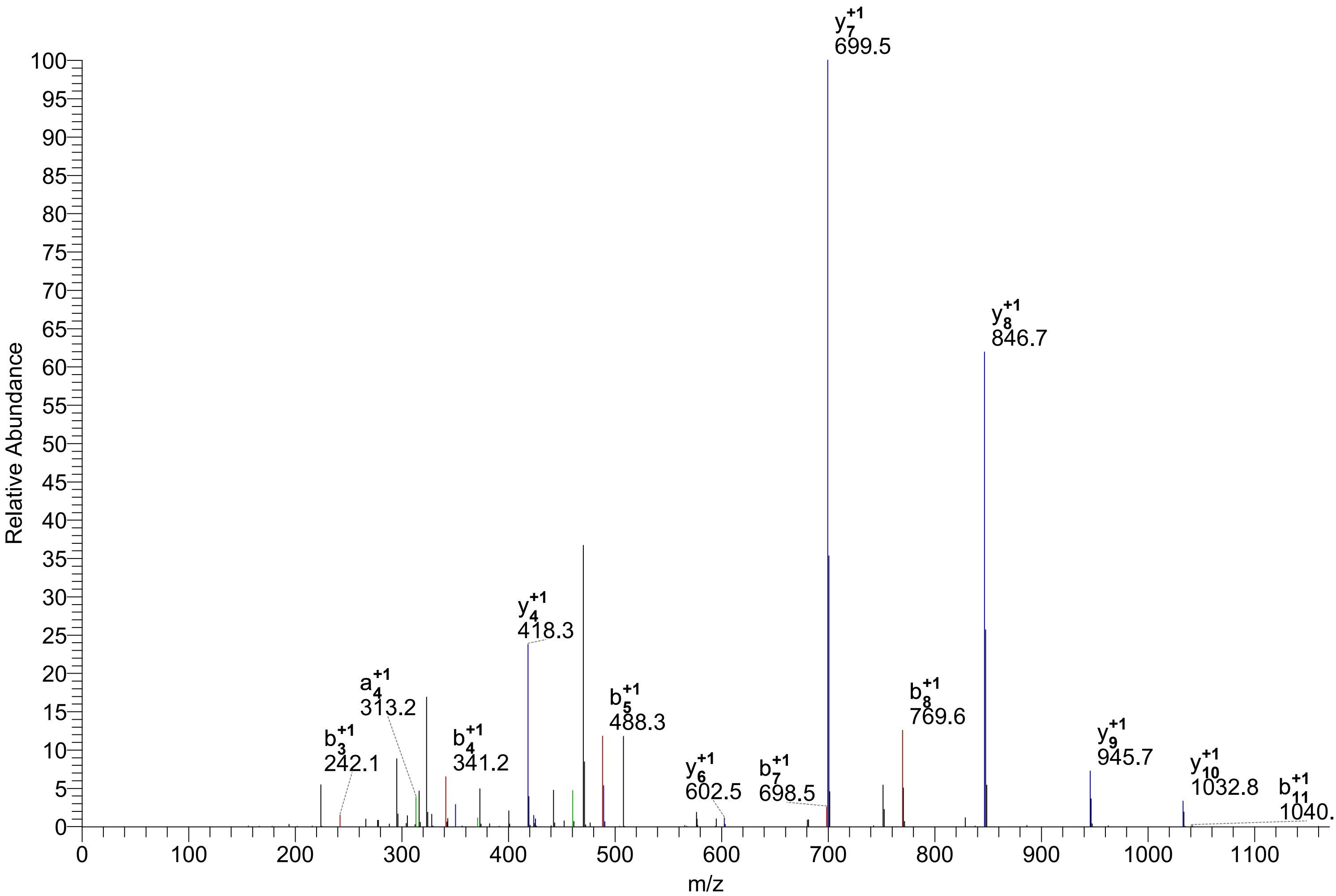


```
Reference                                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                                          MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00785084.2|SWISS-PROT:P0185                                           0.8      10.1     0.0        0
2118291816 -  K.GPSVFPLAPSSK.S                               1186.65   2  0.02     2.948  0.348    465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                    1129.63
 S    214.12     242.11                                    1032.57
 V    313.19     341.18                                     945.54
 F    460.26     488.25                                     846.47
 P    557.31     585.30                                     699.40
 L    670.39     698.39                                     602.35
 A    741.43     769.42                                     489.27
 P    838.48     866.48                                     418.23
 S    925.51     953.51                                     321.18
 S   1012.55    1040.54                                     234.14
 K                                                          147.11
```

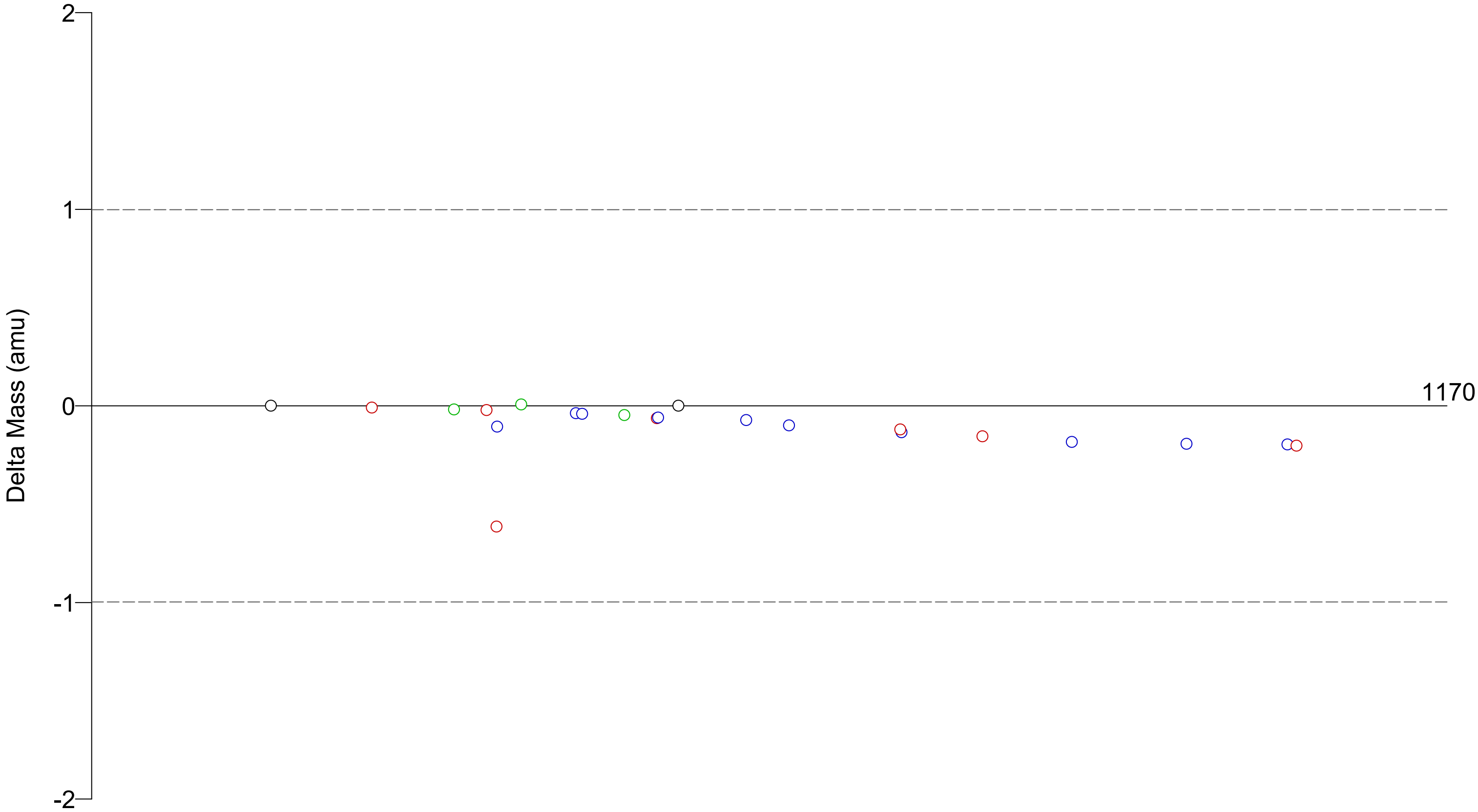


#2118291816-26226248 NL: 6.95E6

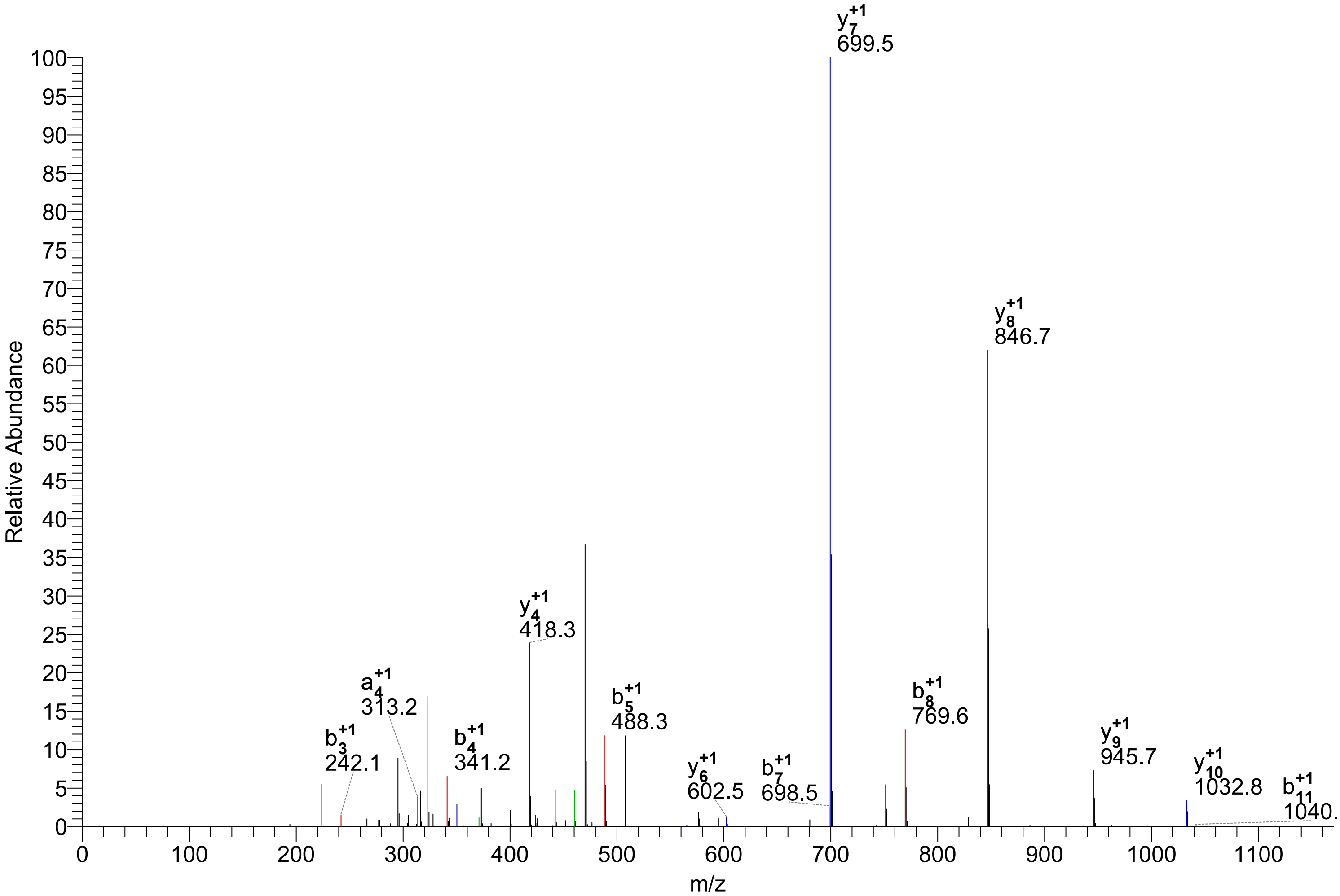


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z     P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00816314.1|TREMBL:Q6N096 Ta                                  0.8     10.1     0.0        0
2118291816 -  K.GPSVFPLAPSSK.S                         1186.65   2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```



#2118291816-26226248 NL: 6.95E6



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Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count

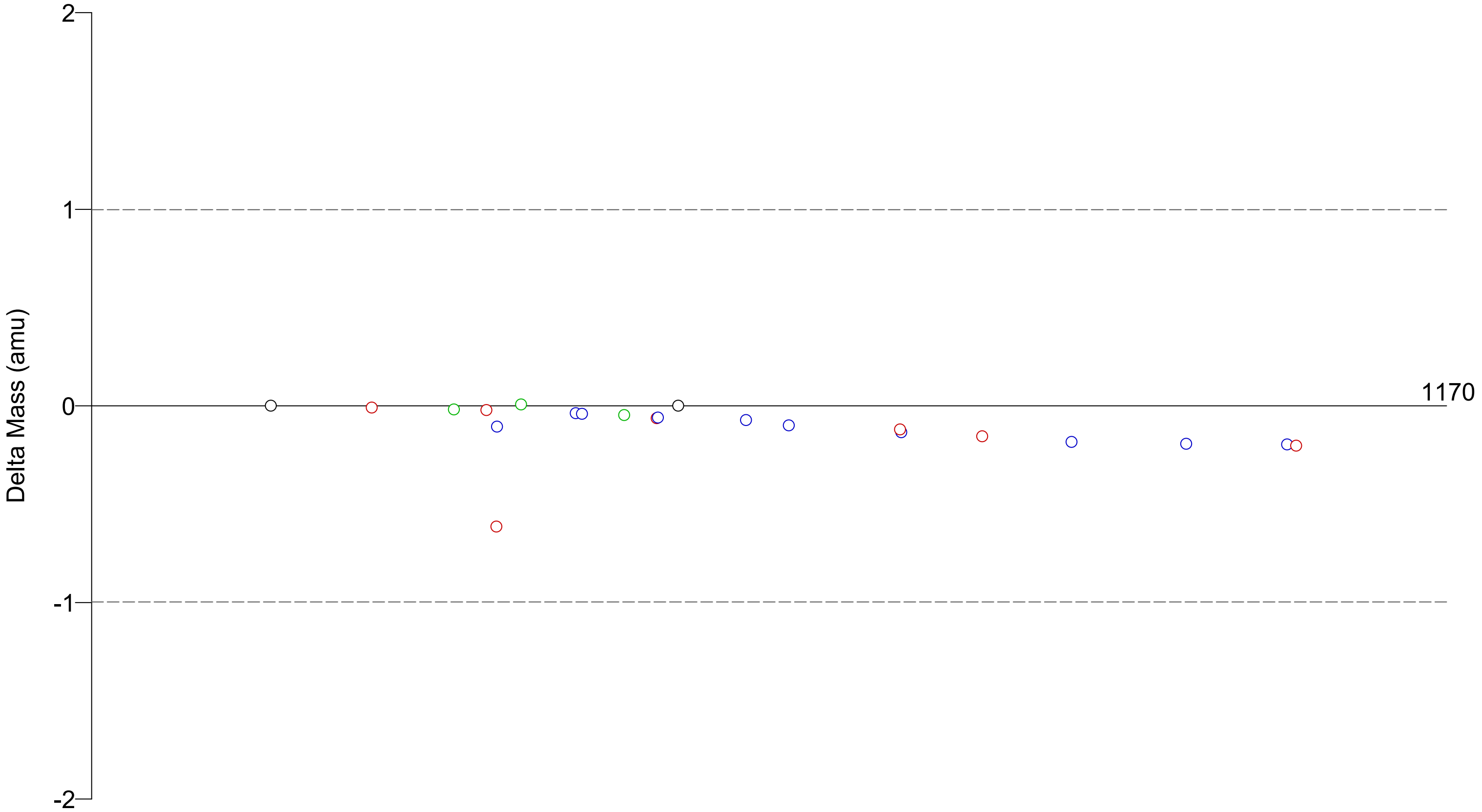
IPI:IPI00844239.1|TREMBL:A4F255 Ta                                0.8      10.1     0.0       0
2118291816 -  K.GPSVFPLAPSSK.S                        1186.65   2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```

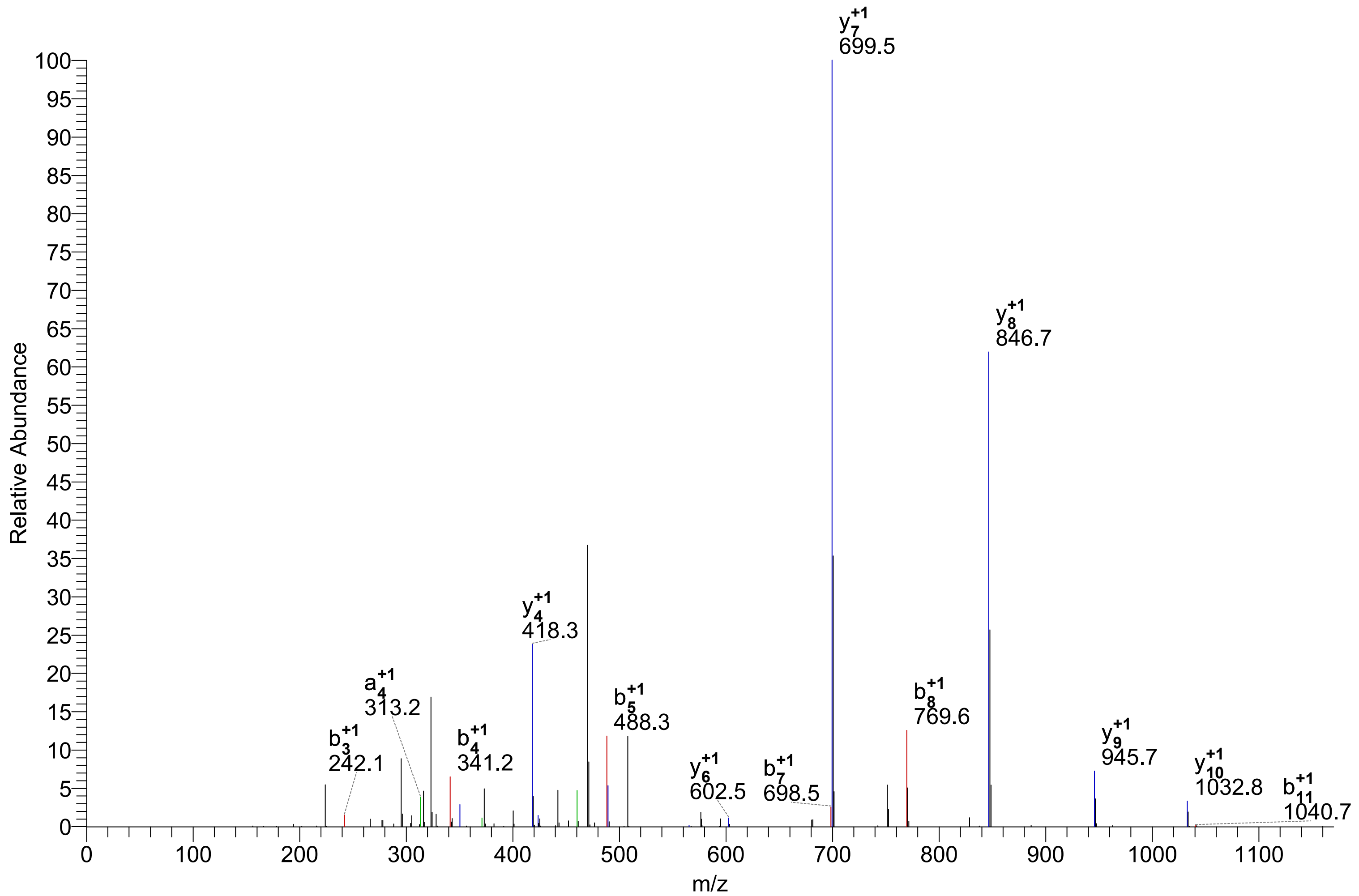
```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                    1129.63
 S    214.12     242.11                                    1032.57
 V    313.19     341.18                                     945.54
 F    460.26     488.25                                     846.47
 P    557.31     585.30                                     699.40
 L    670.39     698.39                                     602.35
 A    741.43     769.42                                     489.27
 P    838.48     866.48                                     418.23
 S    925.51     953.51                                     321.18
 S   1012.55    1040.54                                     234.14
 K                                                          147.11
```



#2118291816-26226248 NL: 6.95E6



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Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00892671.1|VEGA:OTTHUMP0000                                   0.8     10.1     0.0       0
2118291816 -  K.GPSVFPLAPSSK.S                         1186.65   2  0.02     2.948  0.348   465.0  1   15/33   14

1 of 1 peptide matches reported, 0 removed due to filtering
```
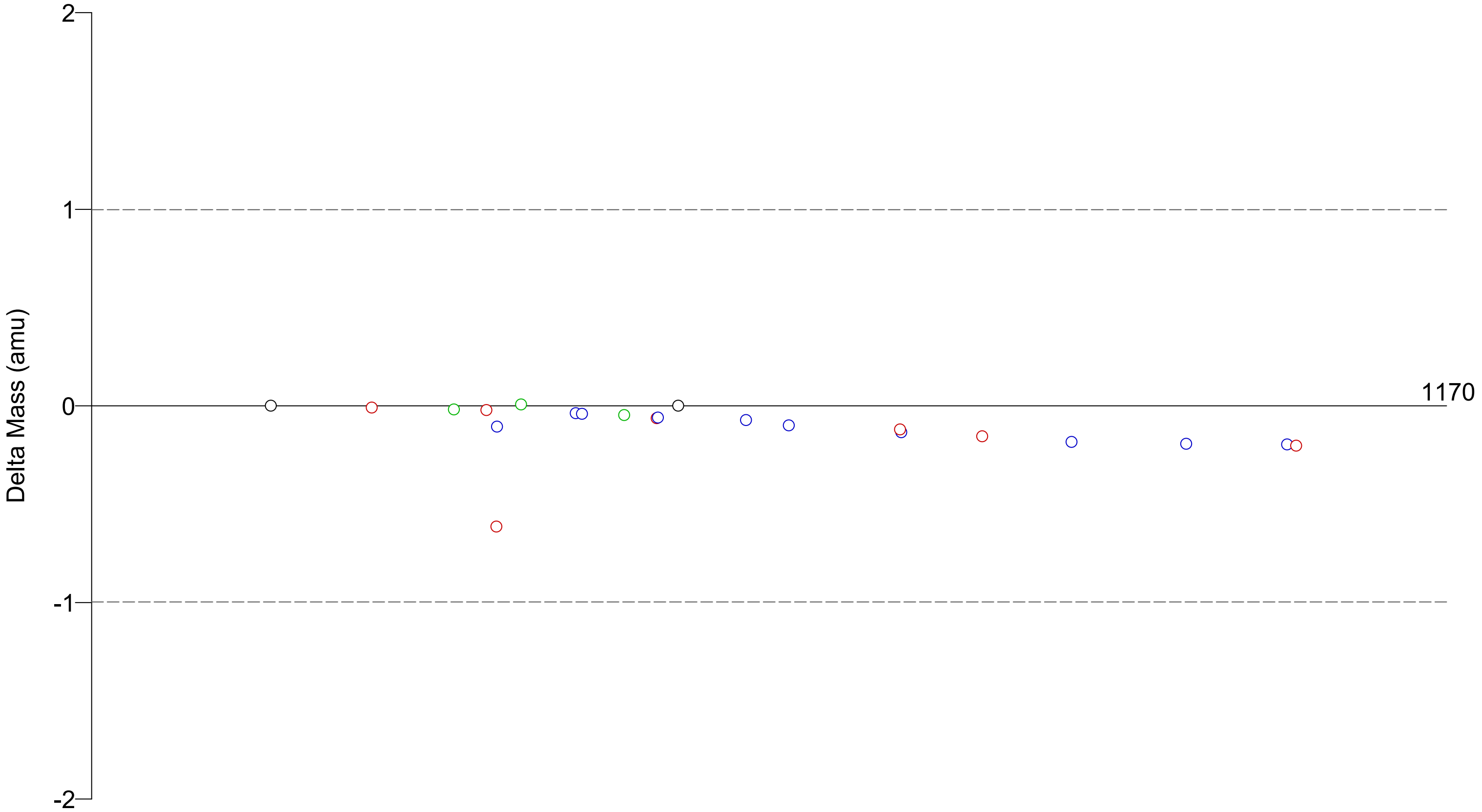
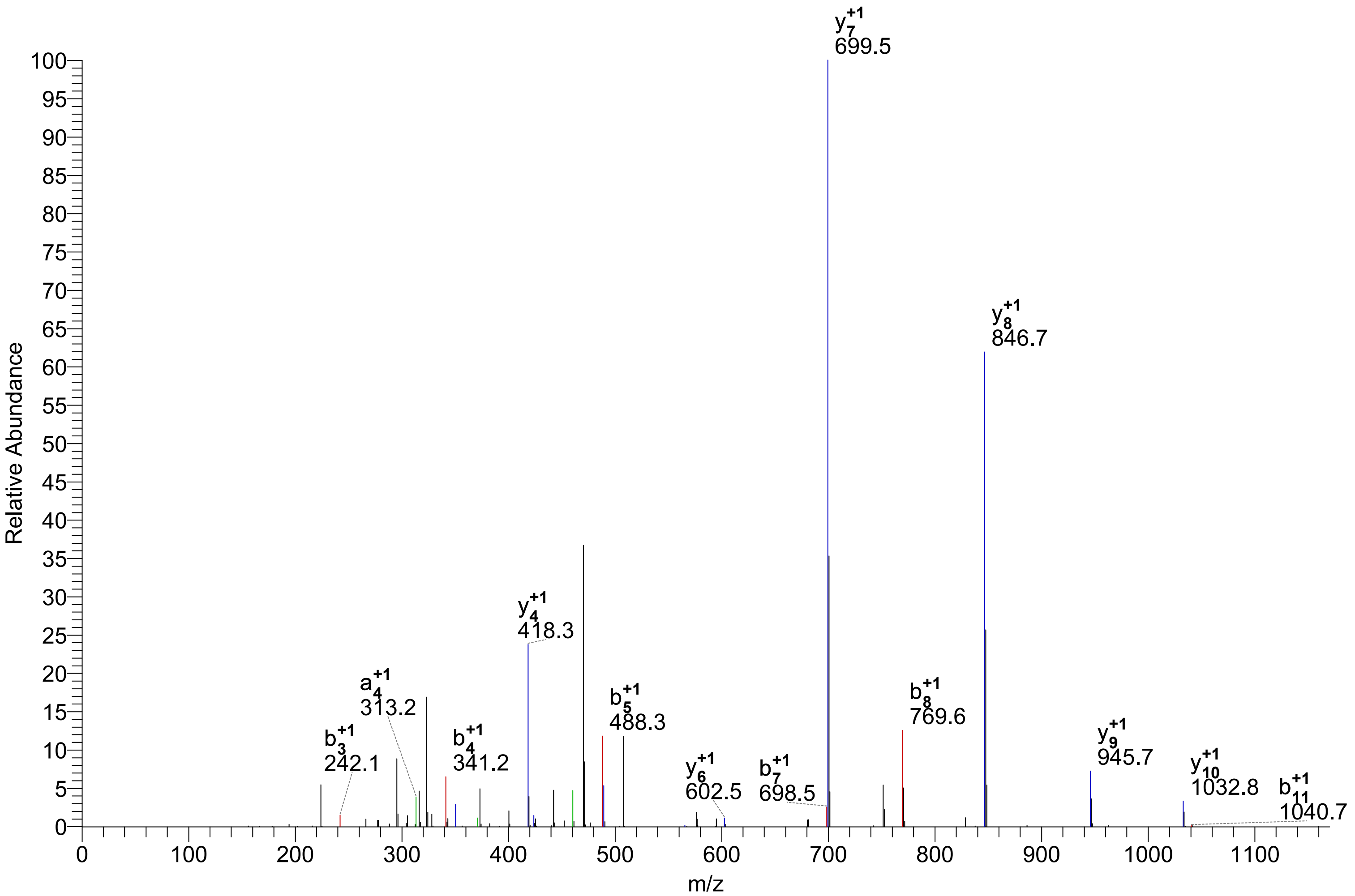

```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     1129.63
 S    214.12     242.11                                     1032.57
 V    313.19     341.18                                      945.54
 F    460.26     488.25                                      846.47
 P    557.31     585.30                                      699.40
 L    670.39     698.39                                      602.35
 A    741.43     769.42                                      489.27
 P    838.48     866.48                                      418.23
 S    925.51     953.51                                      321.18
 S   1012.55    1040.54                                      234.14
 K                                                           147.11
```

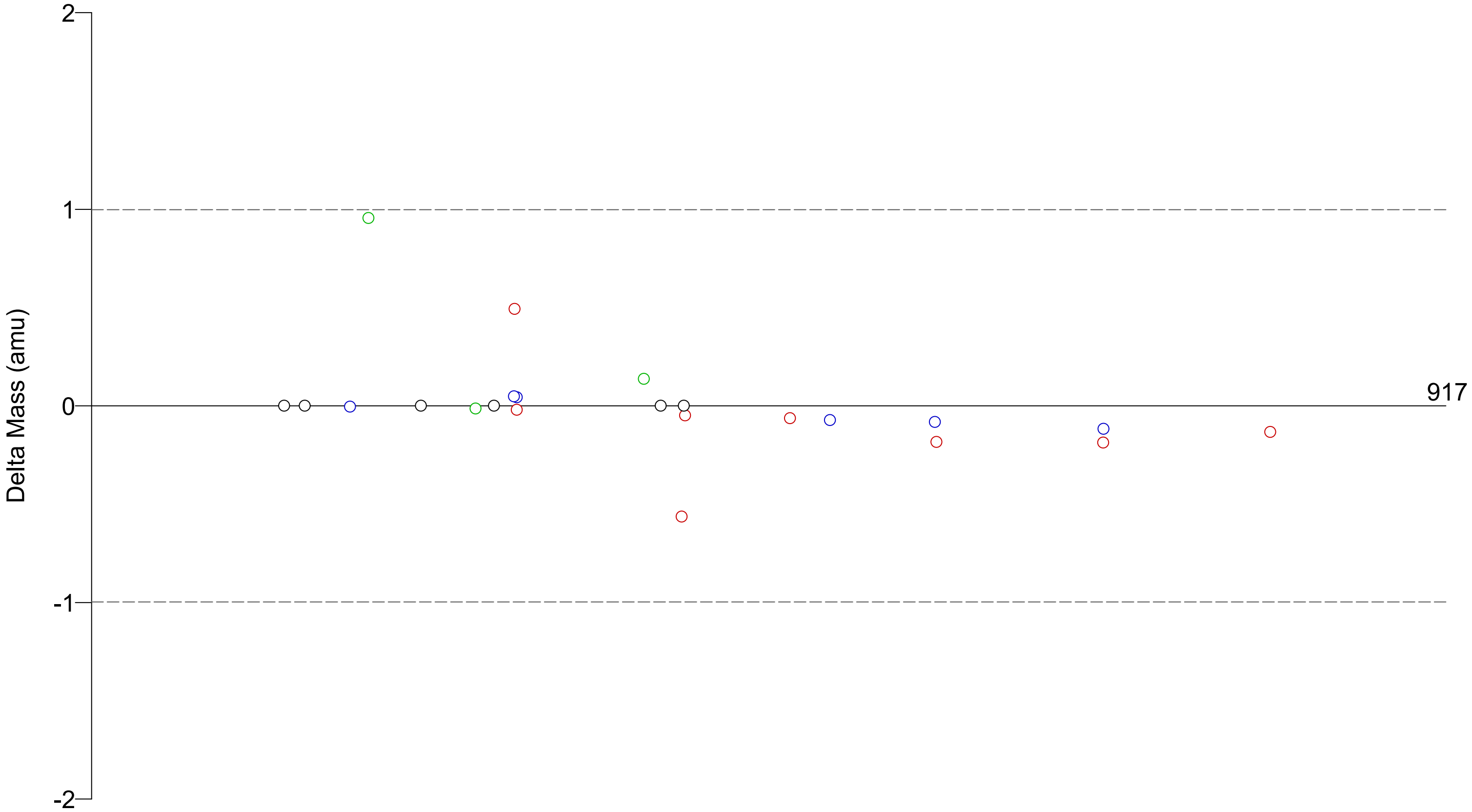


#2118291816-26226248 NL: 6.95E6

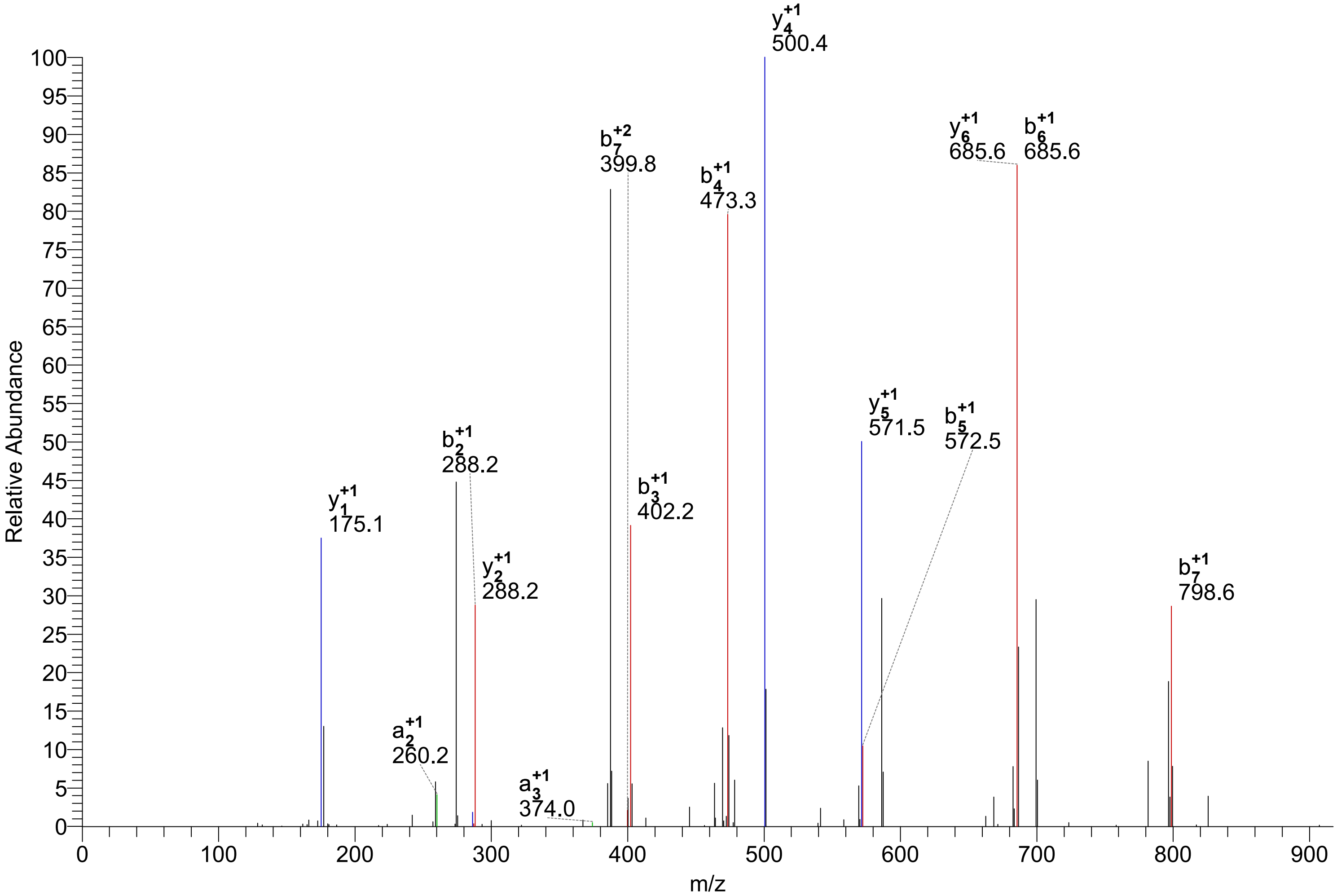


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00030229.4|TREMBL:Q5QPP4|ENSEMBL:ENSP00000363622|VEGA:O    0.9     10.1     0.0       0
19287468 - 1  K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 486.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 T     74.06     102.05
 W    260.14     288.13                                      871.51
 N    374.18     402.18                                      685.44
 A    445.22     473.21                                      571.39
 V    544.29     572.28                                      500.36
 L    657.37     685.37                                      401.29
 L    770.46     798.45                                      288.20
 R                                                           175.12
```

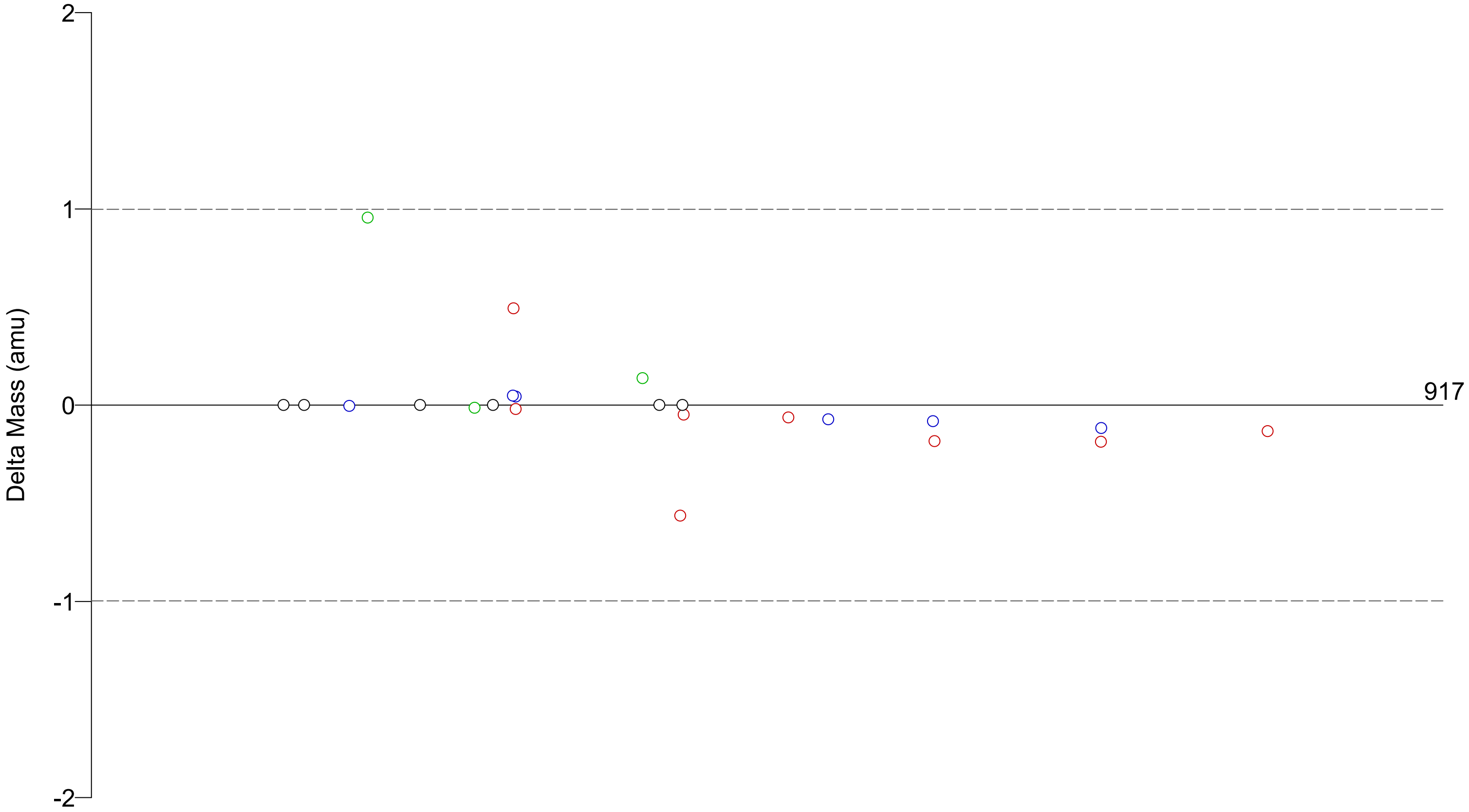


#19287468-1 NL: 1.90E5

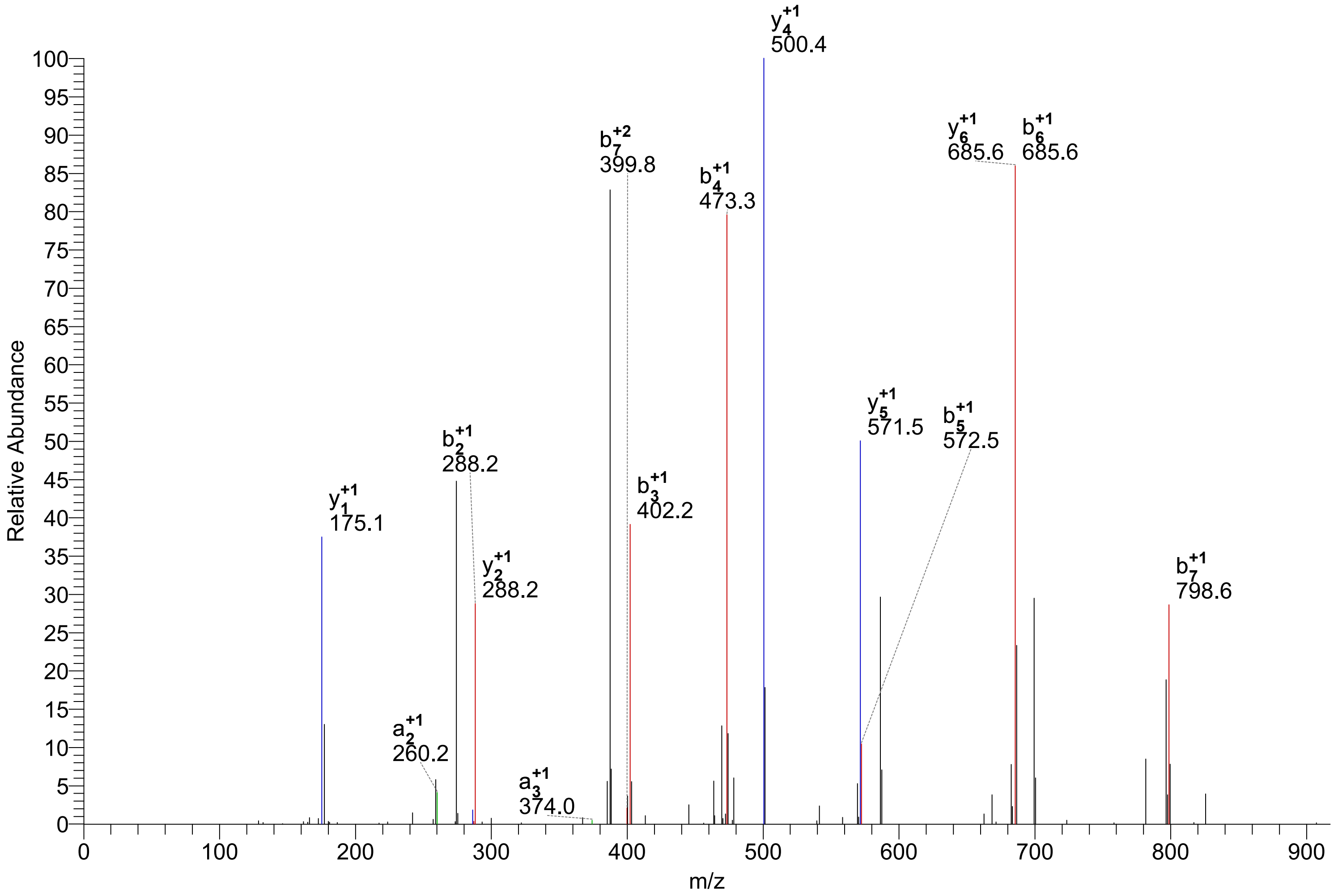


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00553131.2|SWISS-PROT:Q1437                                0.9     10.1     0.0       0
19287468 - 1  K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 486.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions   Z ions
---------------------------------------------------------------------------------------------------
 T     74.06     102.05
 W    260.14     288.13                                      871.51
 N    374.18     402.18                                      685.44
 A    445.22     473.21                                      571.39
 V    544.29     572.28                                      500.36
 L    657.37     685.37                                      401.29
 L    770.46     798.45                                      288.20
 R                                                           175.12
```

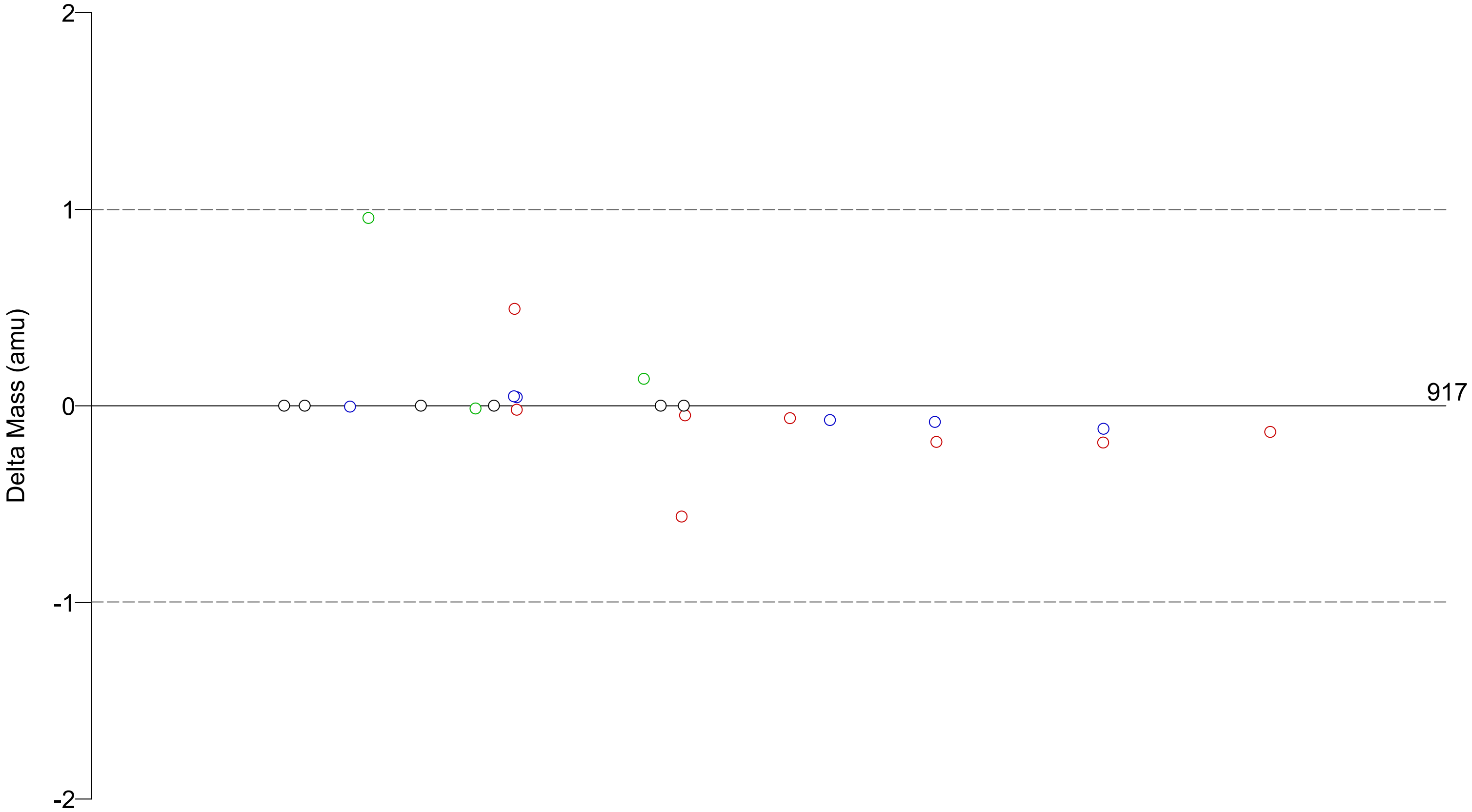


#19287468-1 NL: 1.90E5

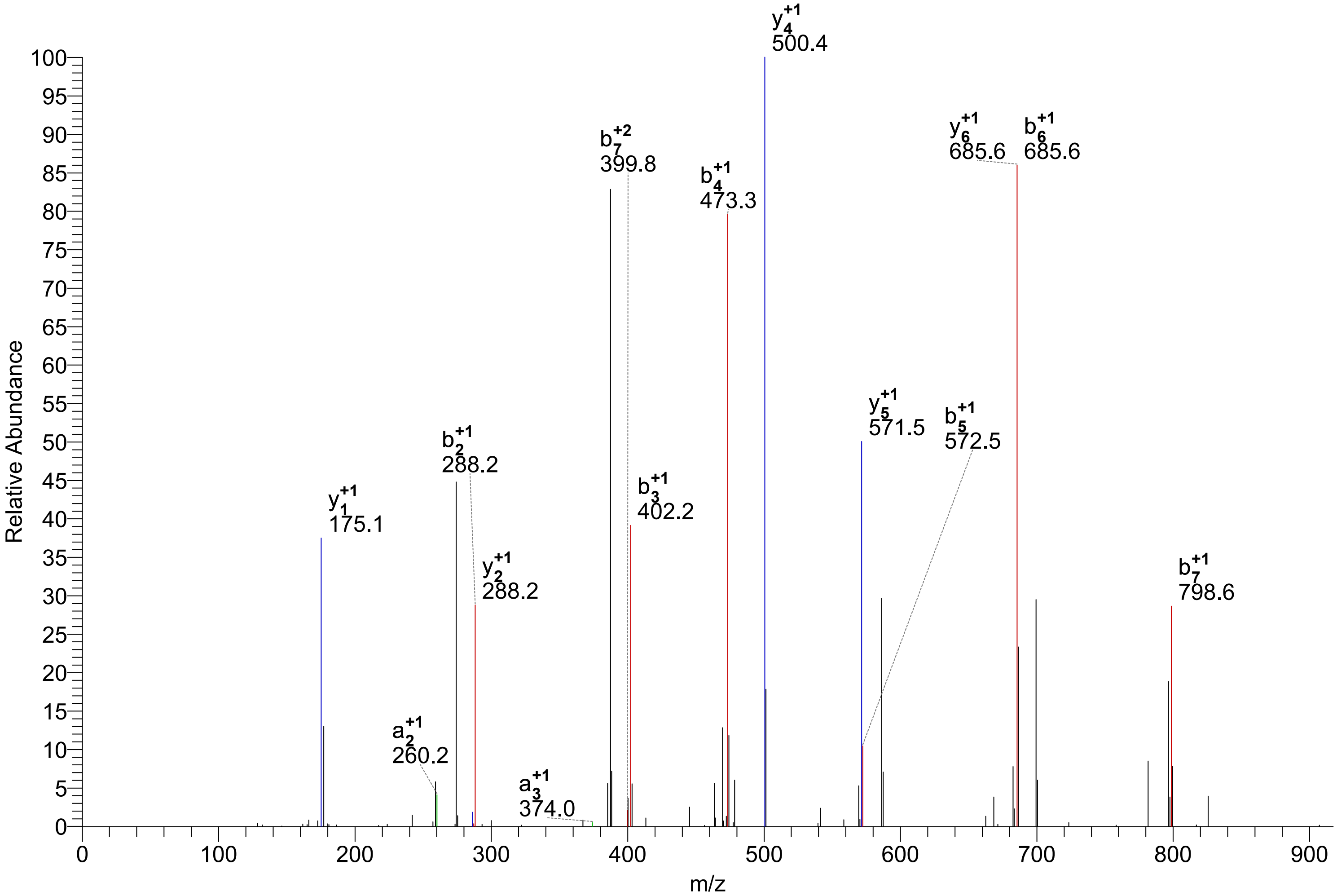


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00641123.1|TREMBL:Q5QPP1|VE                                0.9     10.1     0.0       0
19287468 - 1  K.TWNAVLLR.Y                           972.56    2  0.03    2.663  0.089   1273.6 1   15/21   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 486.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 T     74.06     102.05
 W    260.14     288.13                                      871.51
 N    374.18     402.18                                      685.44
 A    445.22     473.21                                      571.39
 V    544.29     572.28                                      500.36
 L    657.37     685.37                                      401.29
 L    770.46     798.45                                      288.20
 R                                                           175.12
```

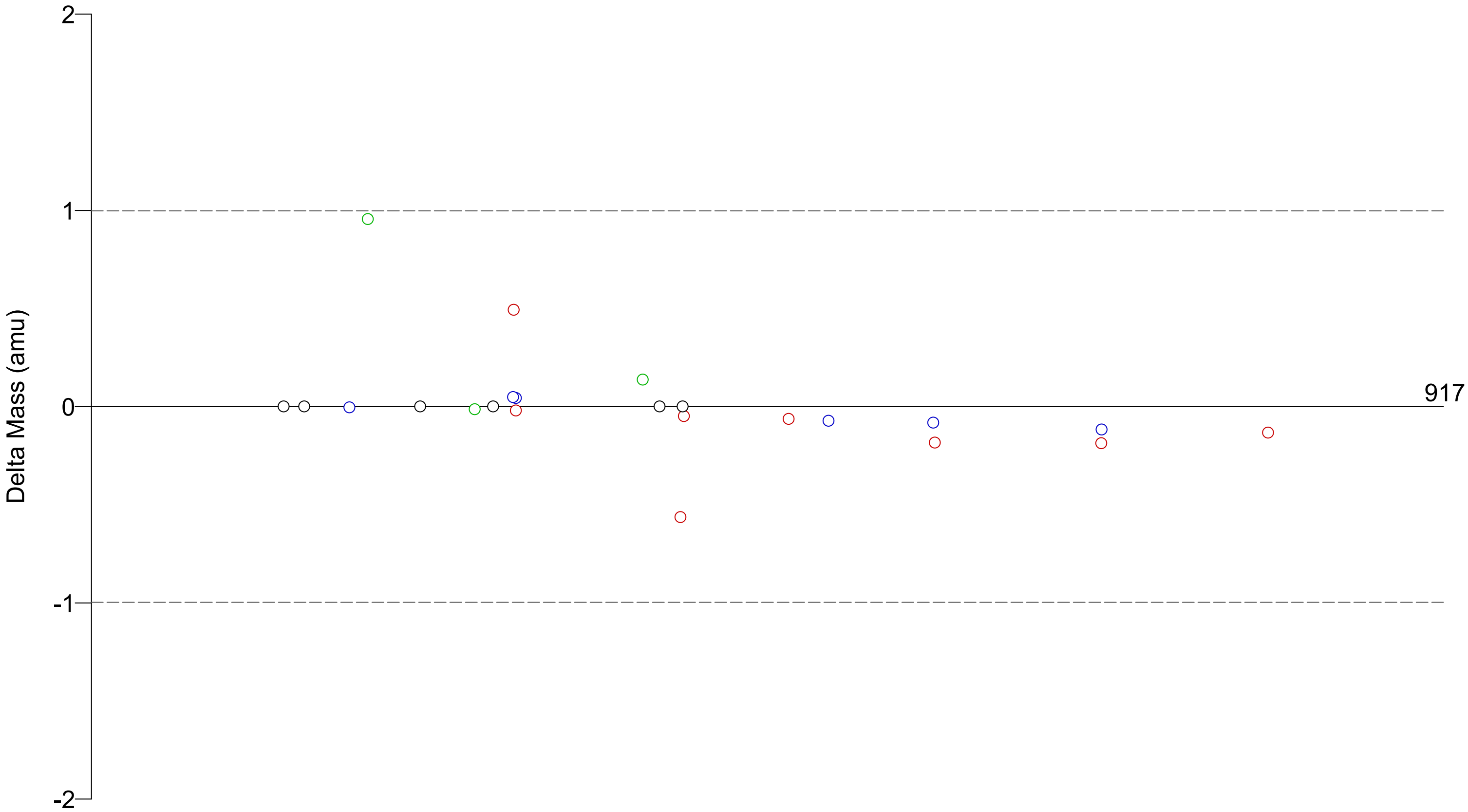


#19287468-1 NL: 1.90E5

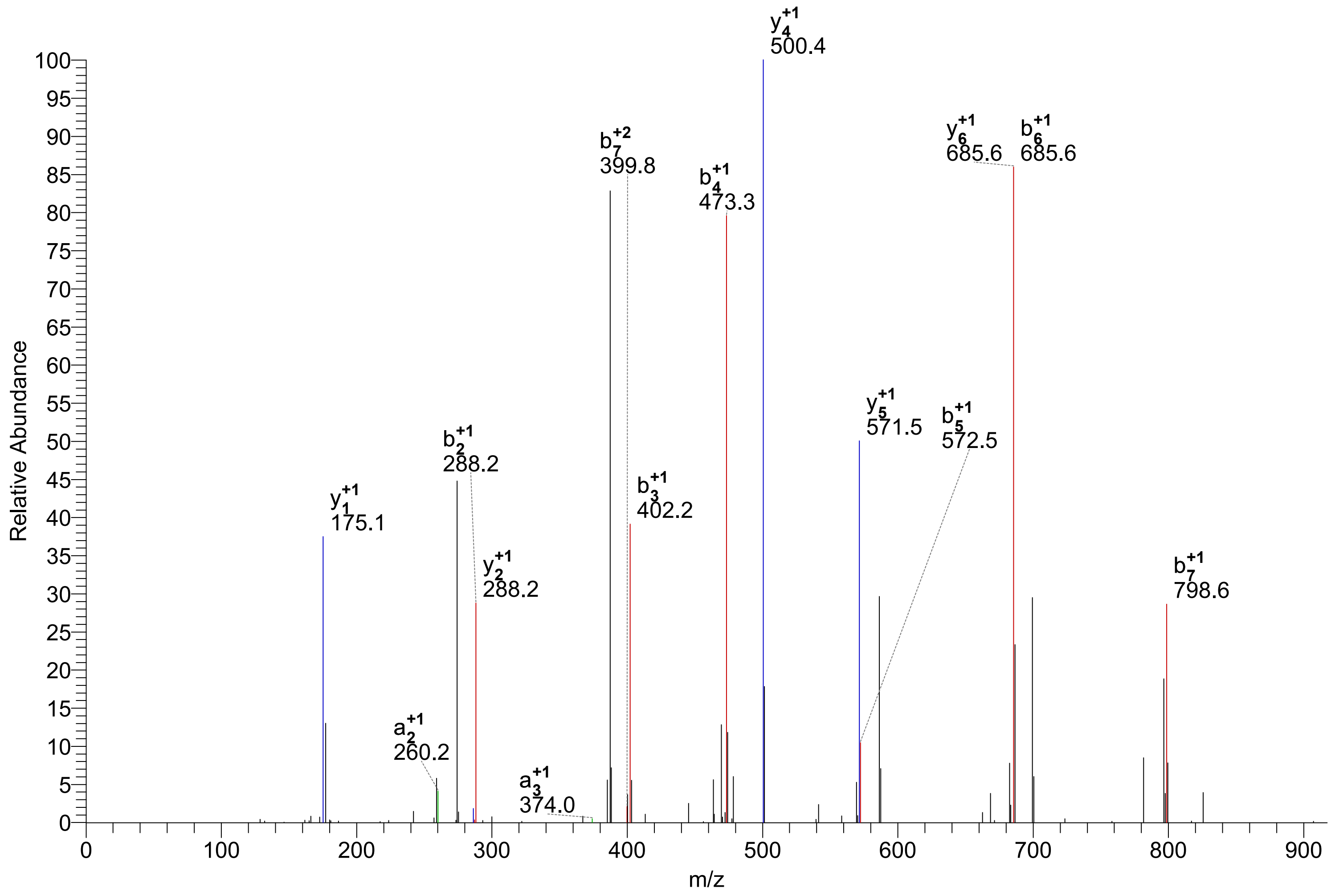


```
Reference                                                               P      Score   Coverage   Accession
Scan(s)        Sequence                                    MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00644339.1|TREMBL:Q5QPP3|VE                                   0.9     10.1     0.0       0
19287468 - 1  K.TWNAVLLR.Y                               972.56    2  0.03     2.663  0.089   1273.6 1   15/21   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 486.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 T     74.06     102.05
 W    260.14     288.13                                       871.51
 N    374.18     402.18                                       685.44
 A    445.22     473.21                                       571.39
 V    544.29     572.28                                       500.36
 L    657.37     685.37                                       401.29
 L    770.46     798.45                                       288.20
 R                                                            175.12
```

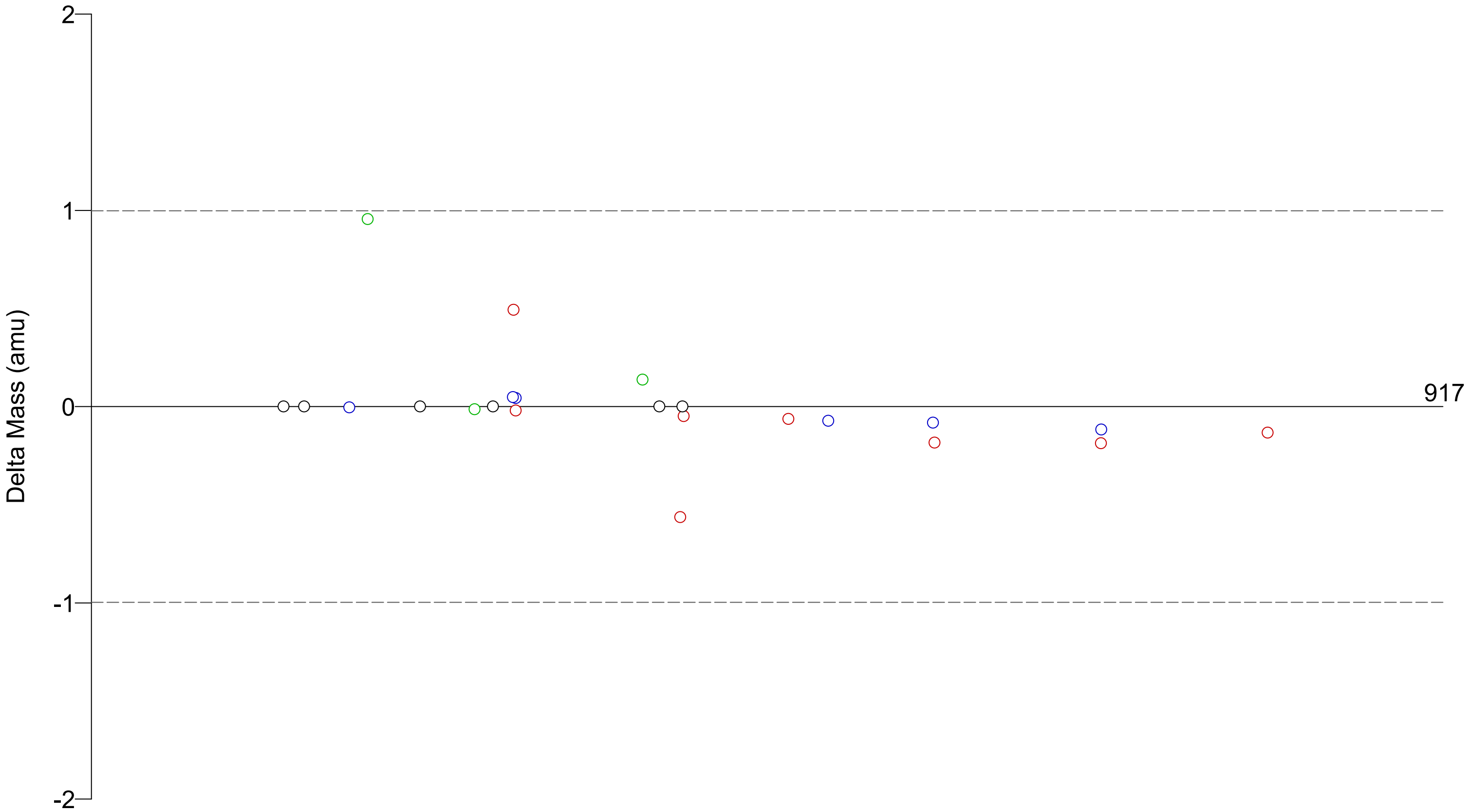


#19287468-1 NL: 1.90E5

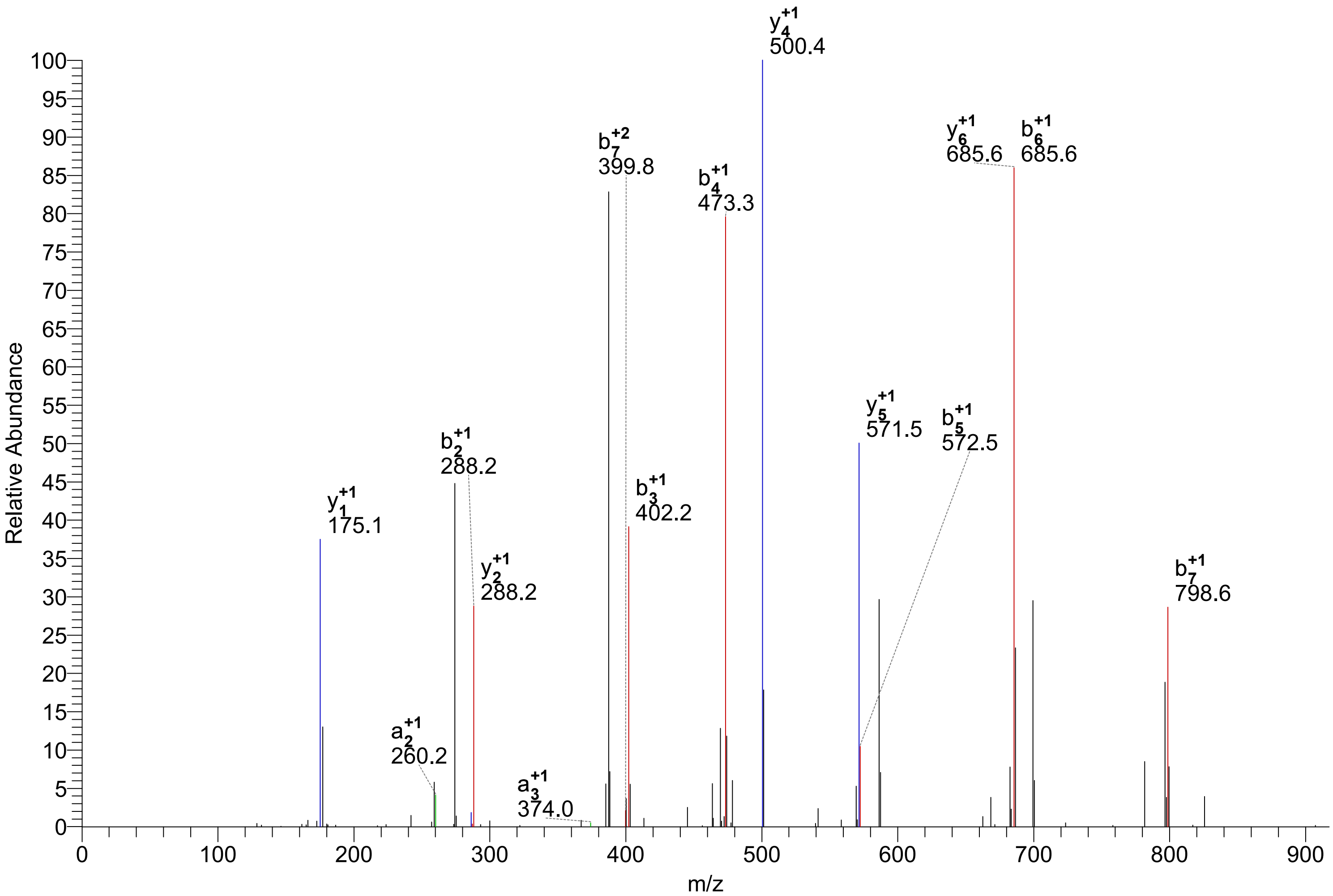


```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00644364.1|TREMBL:Q5QPP2|VE                                0.9     10.1     0.0        0
19287468 - 1  K.TWNAVLLR.Y                             972.56    2  0.03     2.663  0.089   1273.6 1   15/21   4

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 486.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 T     74.06     102.05
 W    260.14     288.13                                      871.51
 N    374.18     402.18                                      685.44
 A    445.22     473.21                                      571.39
 V    544.29     572.28                                      500.36
 L    657.37     685.37                                      401.29
 L    770.46     798.45                                      288.20
 R                                                           175.12
```

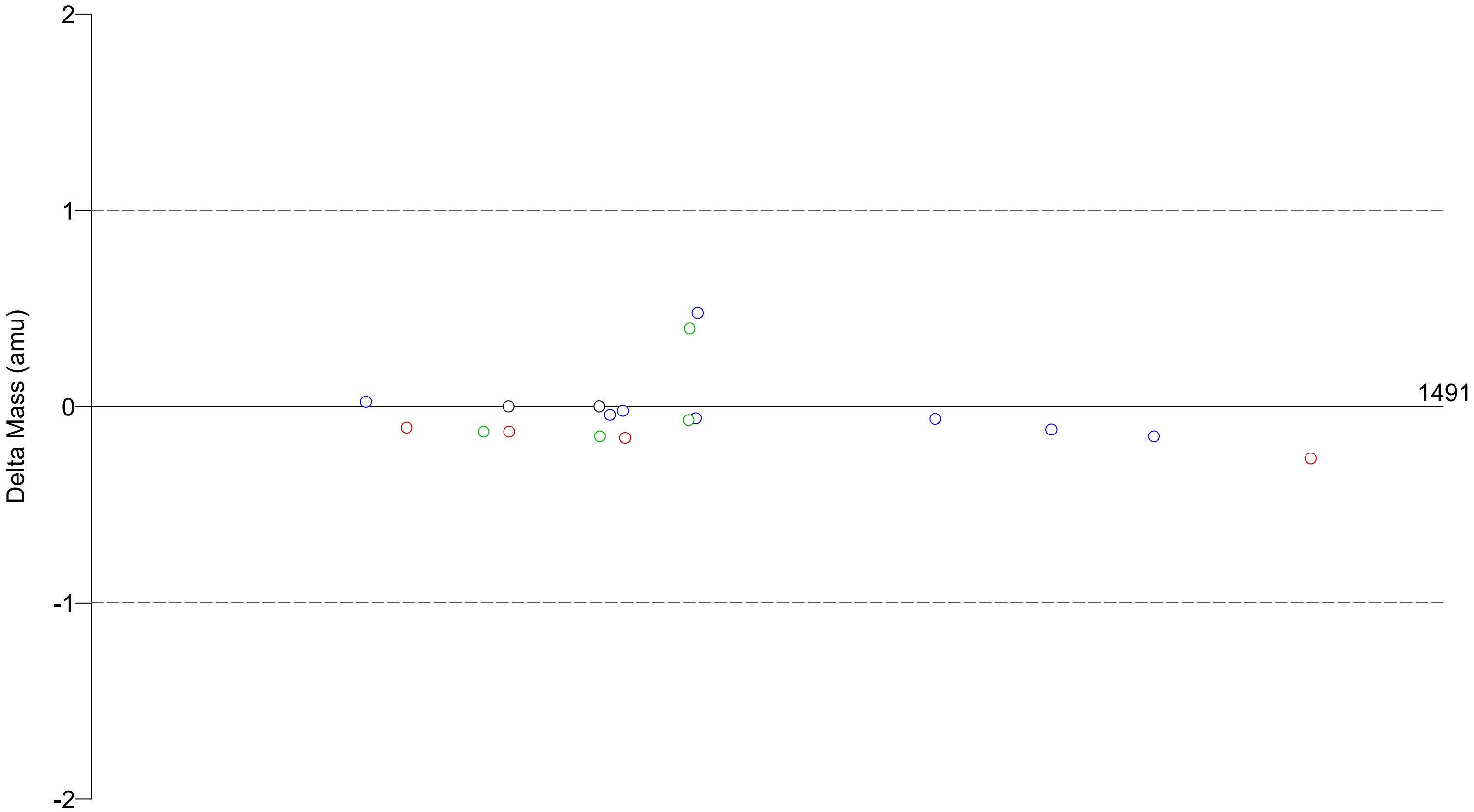


#19287468-1 NL: 1.90E5

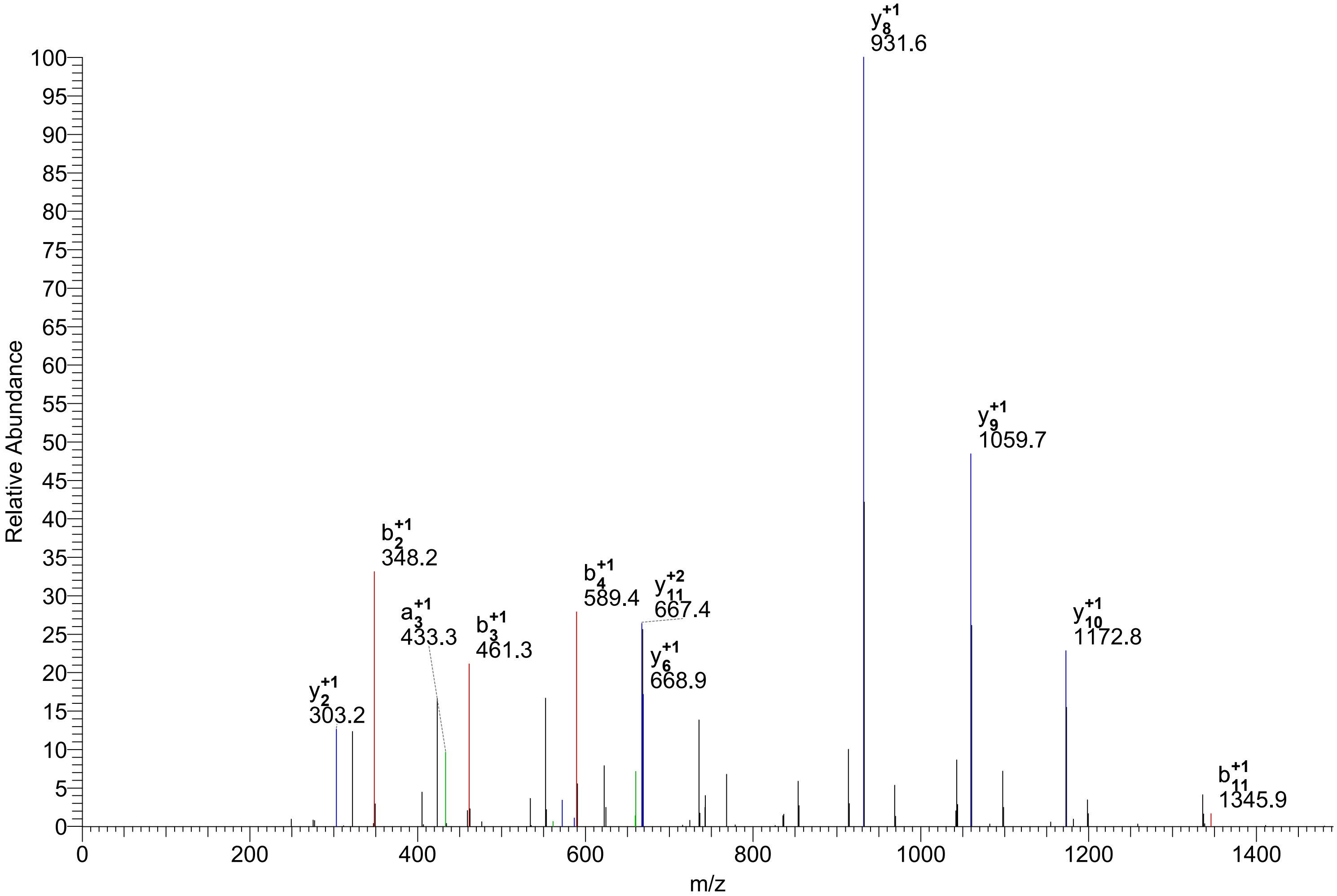


```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00414914.3|SWISS-PROT:P61580 Tax_Id=9606 Gene_Symbol=-      0.9      8.1       0.0       0
19287468 - 1  R.WCLQVYPTAPKR.Q                          1519.77   2  0.04     2.492  0.609   380.1  2   13/33   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 760.38
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 C    320.11     348.10                                      1333.69
 L    433.19     461.19                                      1172.68
 Q    561.25     589.24                                      1059.59
 V    660.32     688.31                                       931.54
 Y    823.38     851.38                                       832.47
 P    920.43     948.43                                       669.40
 T   1021.48    1049.48                                       572.35
 A   1092.52    1120.51                                       471.30
 P   1189.57    1217.57                                       400.27
 K   1317.67    1345.66                                       303.21
 R                                                            175.12
```

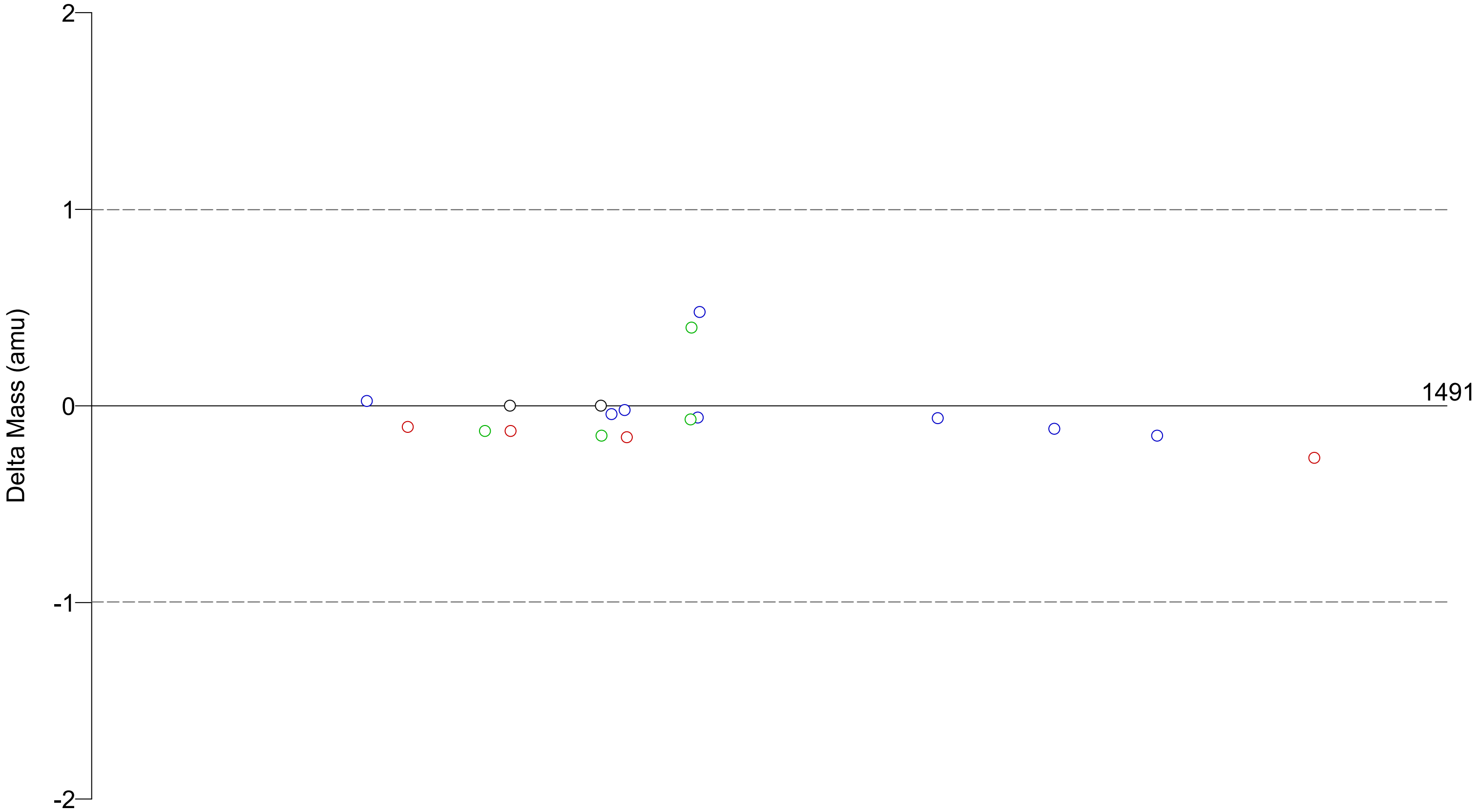


#19287468-1 NL: 6.47E4

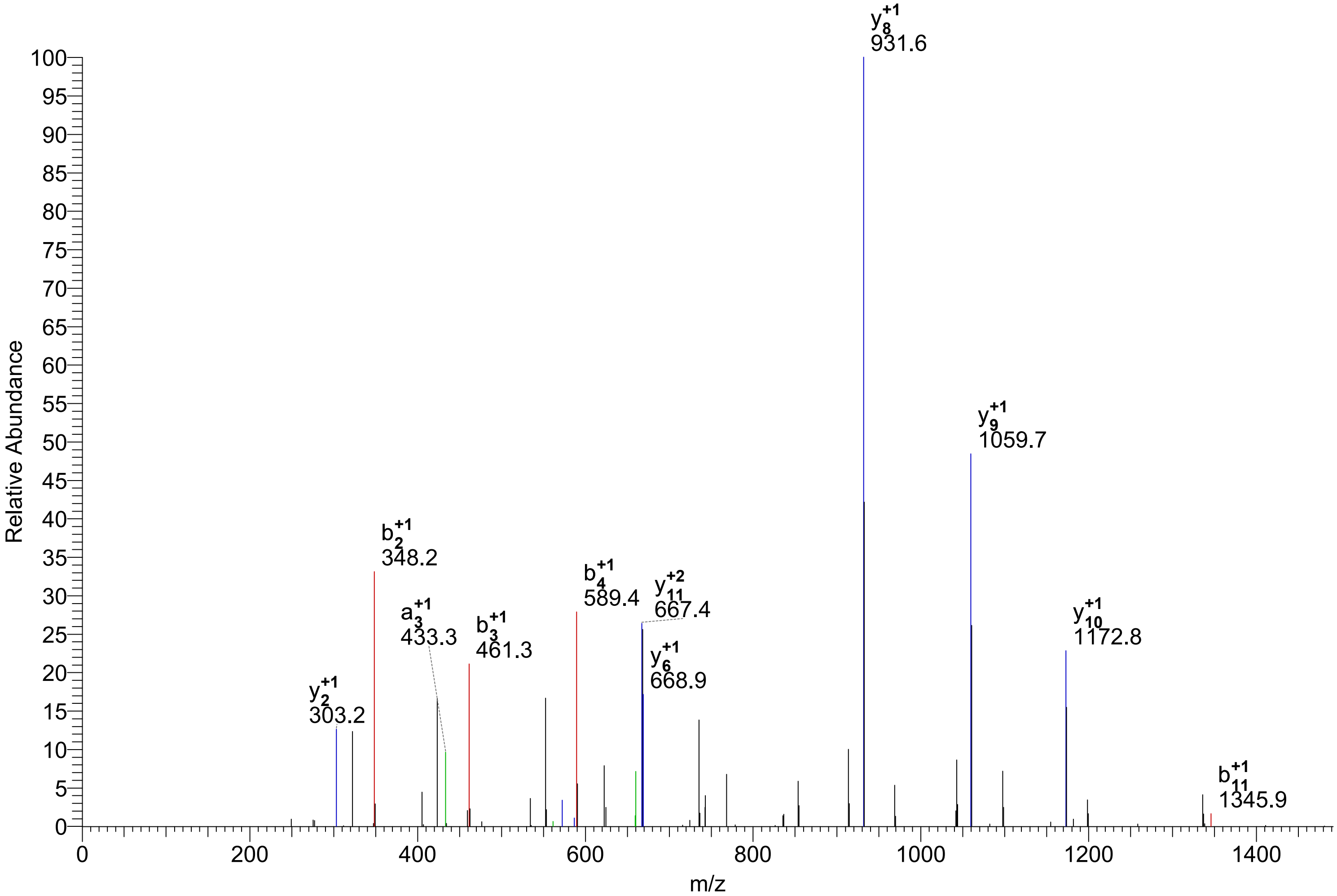


```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+       z     P        XC  DeltaCn   Sp    RSp  Ions  Count

IPI:IPI00414915.1|SWISS-PROT:P6158                                        0.9      8.1      0.0        0
19287468 - 1  R.WCLQVYPTAPKR.Q                         1519.77    2  0.04     2.492  0.609   380.1  2   13/33   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 760.38
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 C    320.11     348.10                                     1333.69
 L    433.19     461.19                                     1172.68
 Q    561.25     589.24                                     1059.59
 V    660.32     688.31                                      931.54
 Y    823.38     851.38                                      832.47
 P    920.43     948.43                                      669.40
 T   1021.48    1049.48                                      572.35
 A   1092.52    1120.51                                      471.30
 P   1189.57    1217.57                                      400.27
 K   1317.67    1345.66                                      303.21
 R                                                           175.12
```

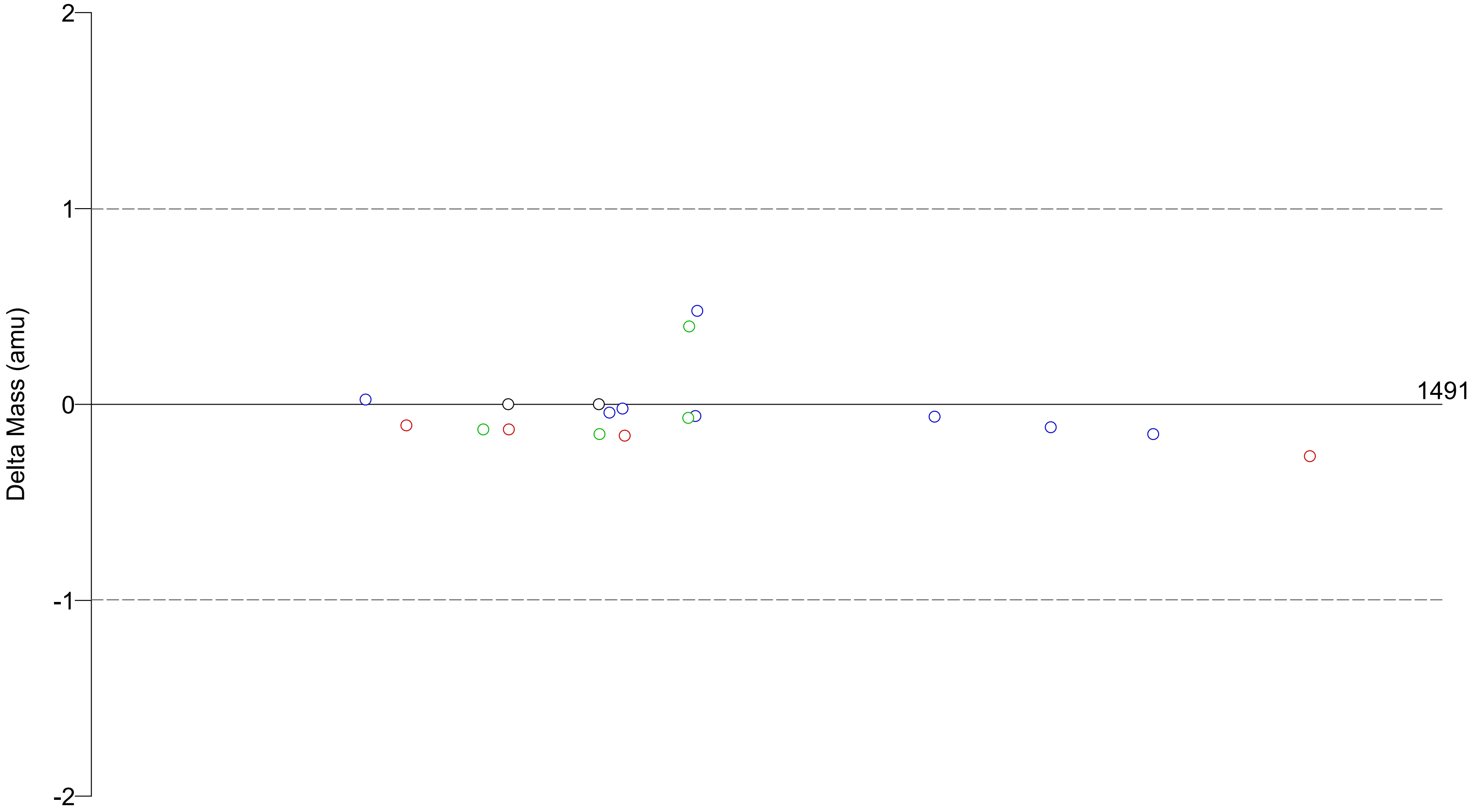


#19287468-1 NL: 6.47E4

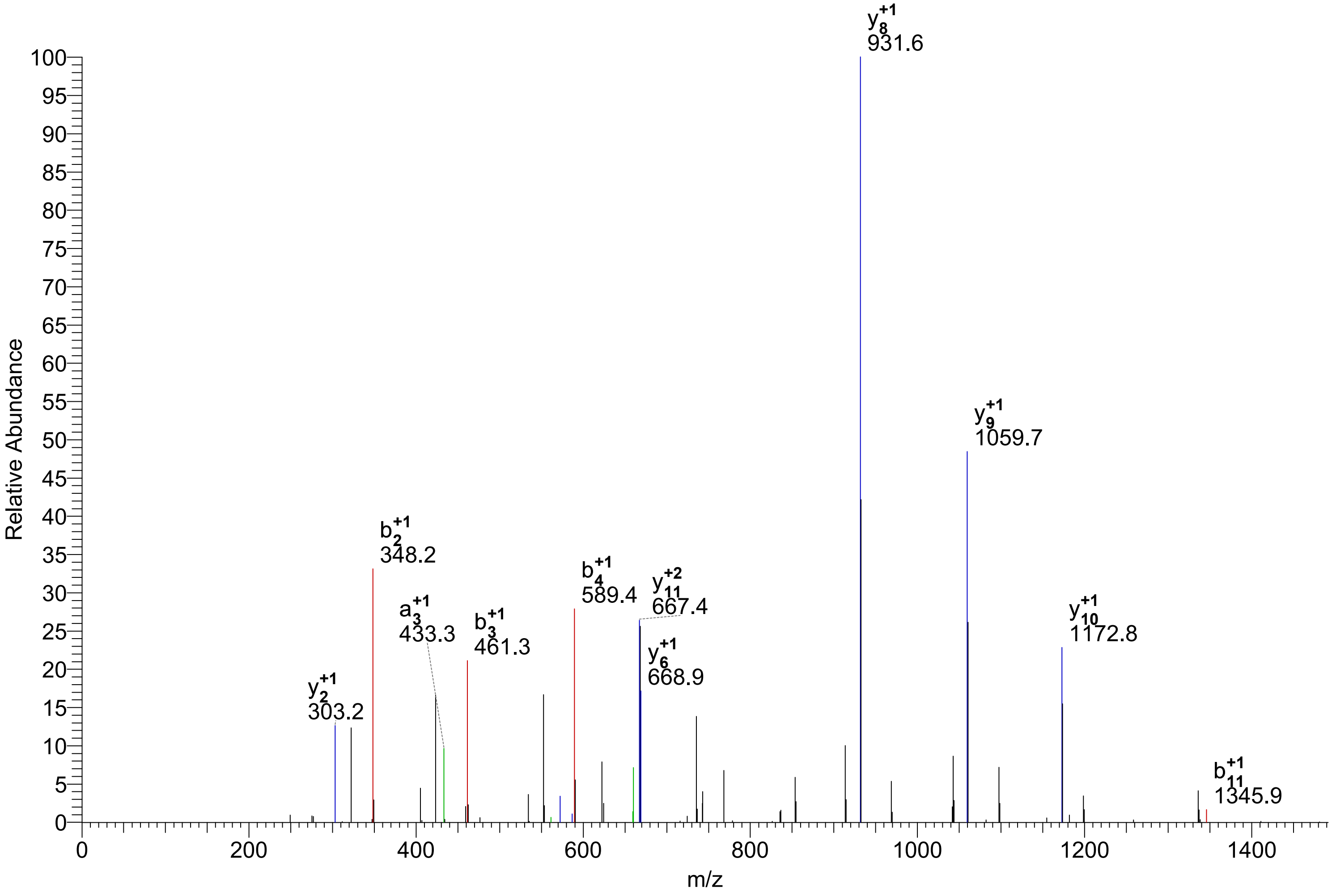


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00414916.3|SWISS-PROT:P6158                                  0.9     8.1      0.0       0
19287468 - 1  R.WCLQVYPTAPKR.Q                           1519.77   2  0.04     2.492  0.609   380.1  2   13/33   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 760.38
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 C    320.11     348.10                                     1333.69
 L    433.19     461.19                                     1172.68
 Q    561.25     589.24                                     1059.59
 V    660.32     688.31                                      931.54
 Y    823.38     851.38                                      832.47
 P    920.43     948.43                                      669.40
 T   1021.48    1049.48                                      572.35
 A   1092.52    1120.51                                      471.30
 P   1189.57    1217.57                                      400.27
 K   1317.67    1345.66                                      303.21
 R                                                           175.12
```

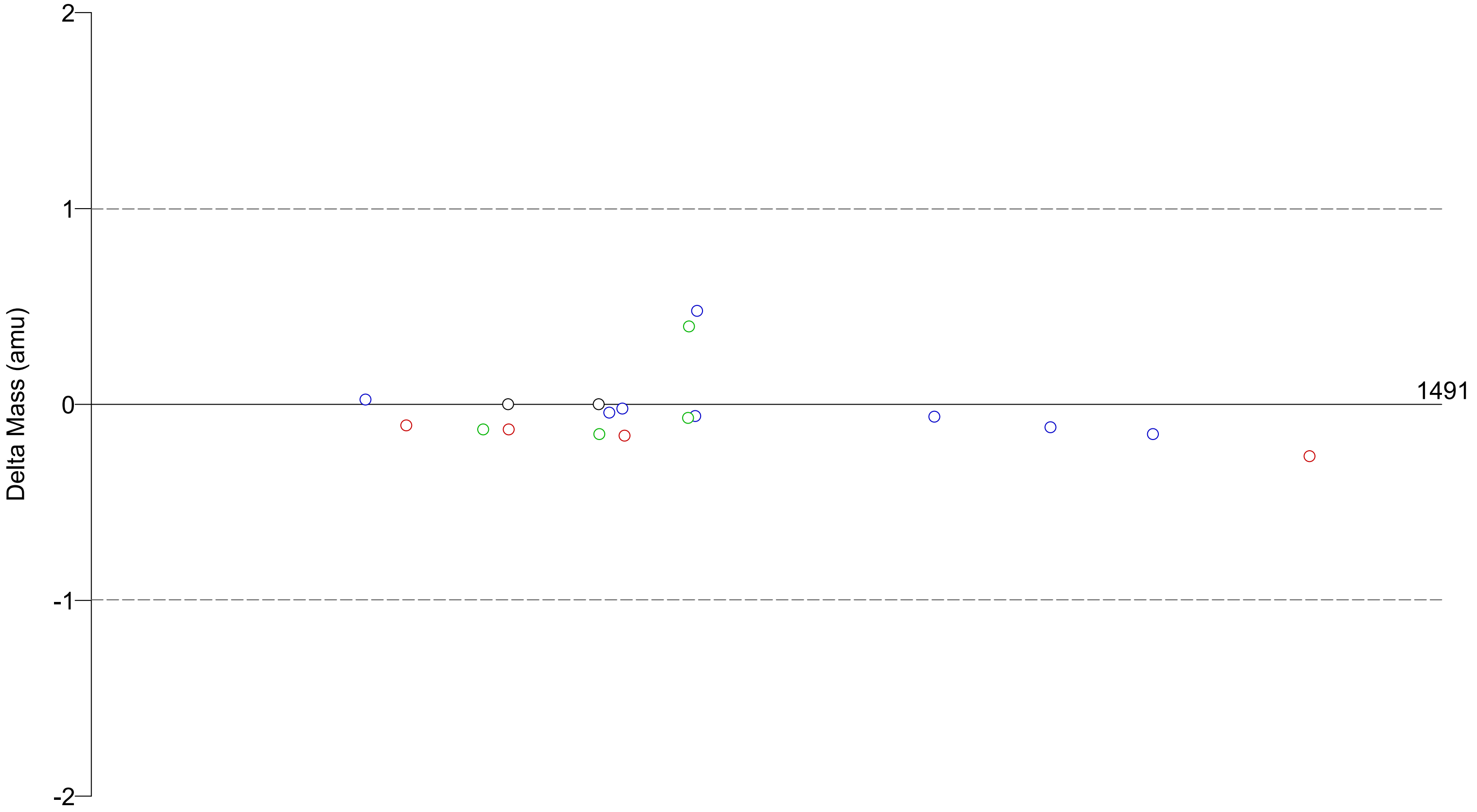


#19287468-1 NL: 6.47E4

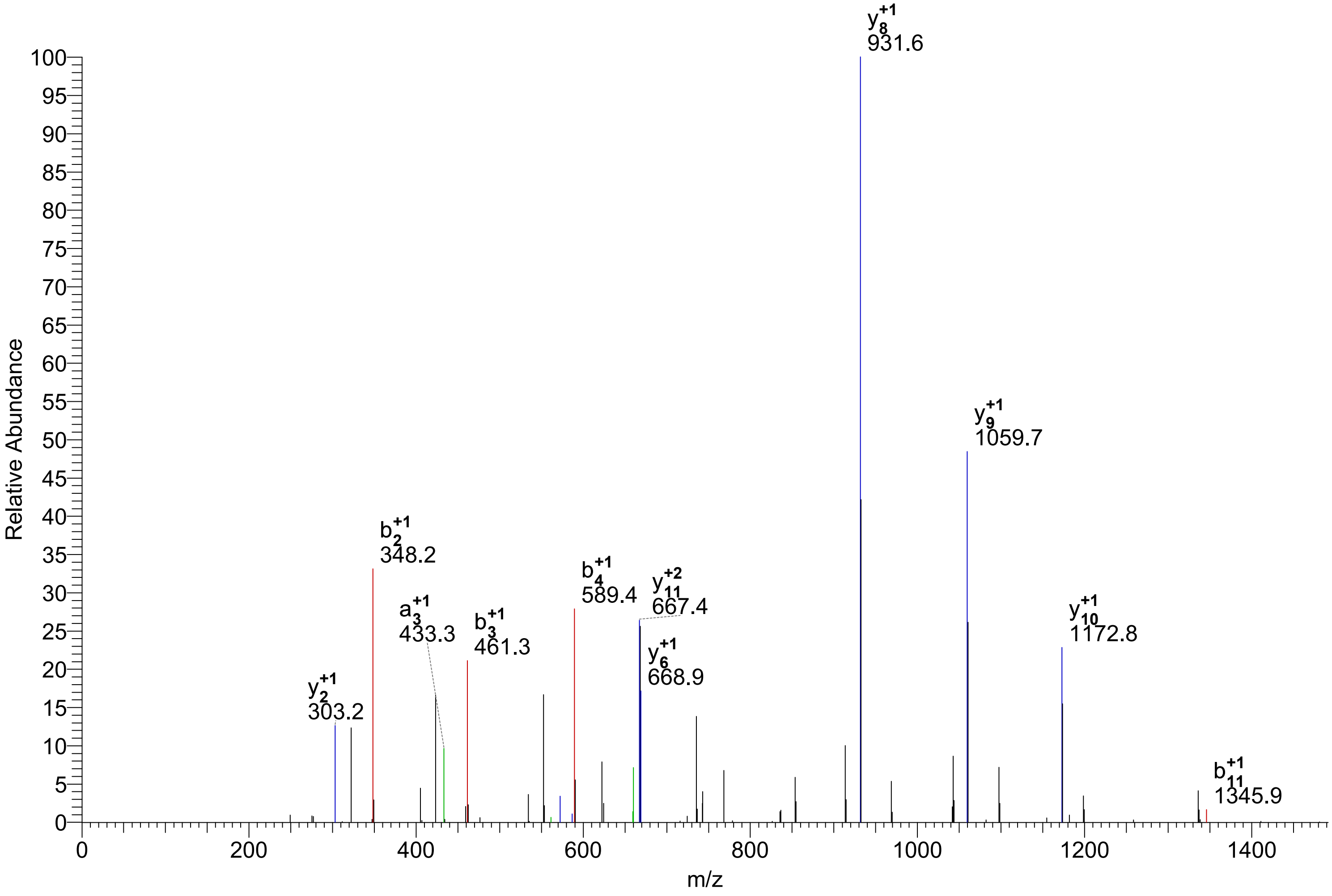


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00414917.1|SWISS-PROT:P6158                                 0.9     8.1      0.0       0
19287468 - 1  R.WCLQVYPTAPKR.Q                      1519.77    2  0.04     2.492  0.609   380.1  2   13/33   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 760.38
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 W    159.09     187.09
 C    320.11     348.10                                     1333.69
 L    433.19     461.19                                     1172.68
 Q    561.25     589.24                                     1059.59
 V    660.32     688.31                                      931.54
 Y    823.38     851.38                                      832.47
 P    920.43     948.43                                      669.40
 T   1021.48    1049.48                                      572.35
 A   1092.52    1120.51                                      471.30
 P   1189.57    1217.57                                      400.27
 K   1317.67    1345.66                                      303.21
 R                                                           175.12
```

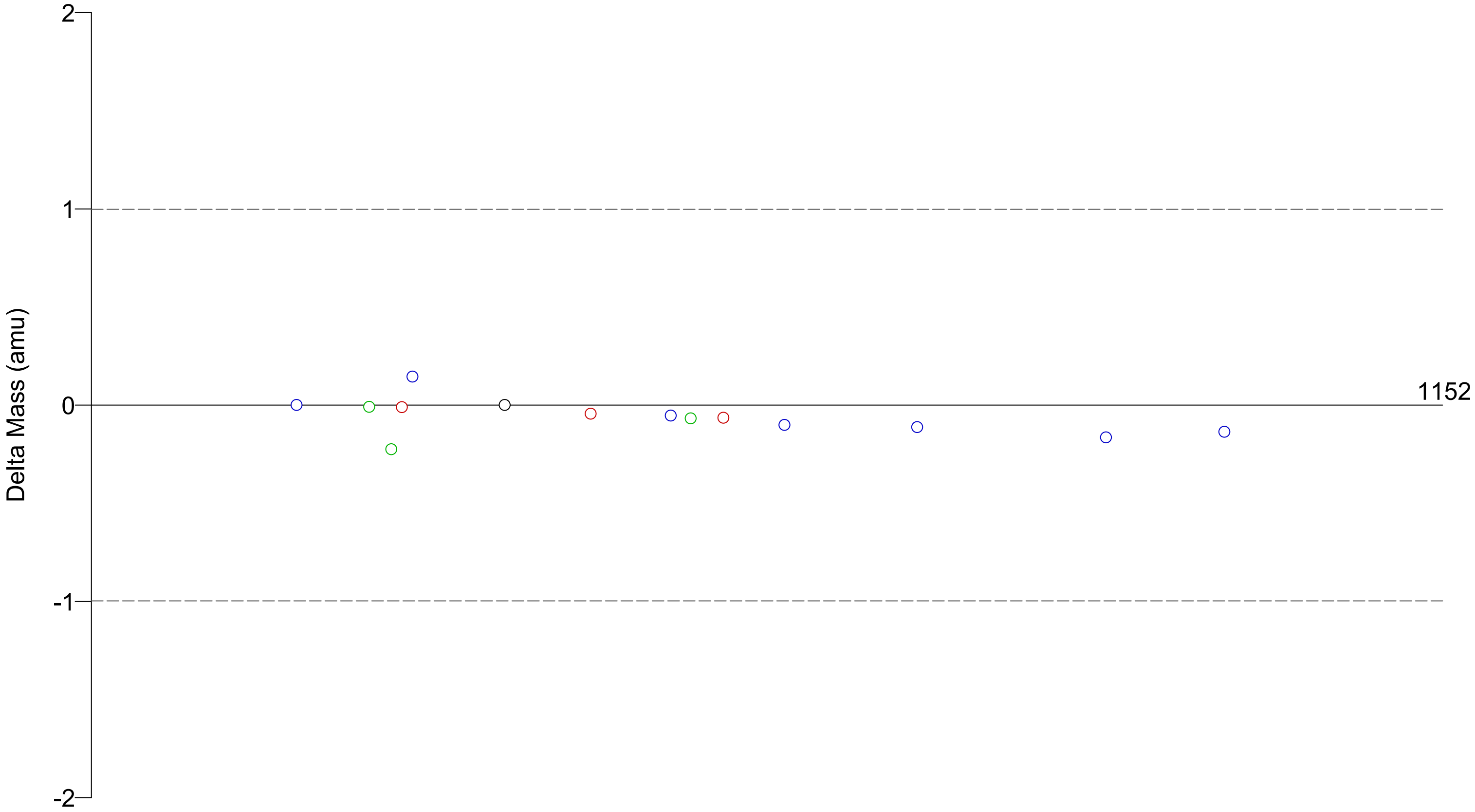


#19287468-1 NL: 6.47E4

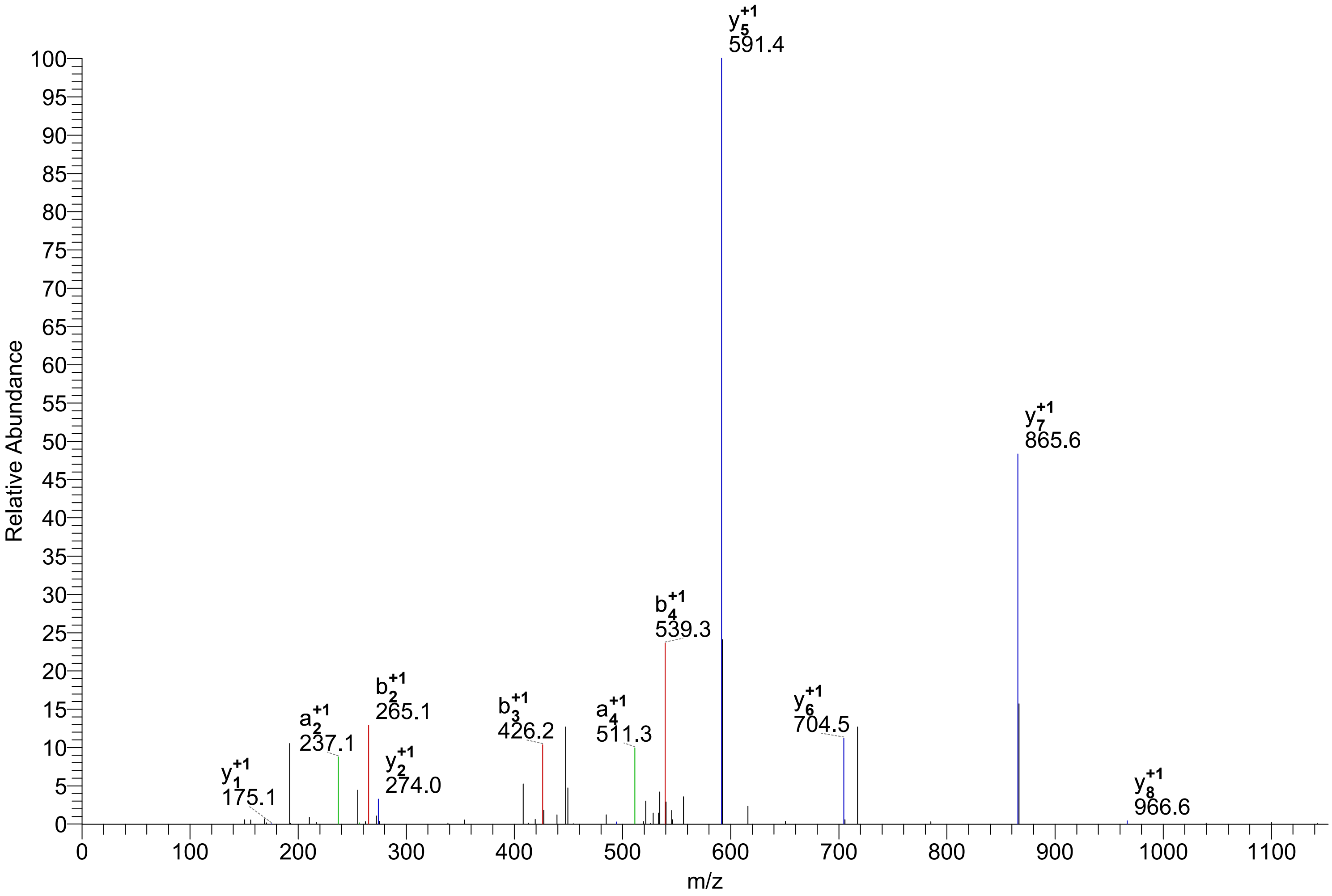


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00021727.1|SWISS-PROT:P04003|TREMBL:B4E1D8;B4E1E1;Q5VVQ    1       10.1     0.0       0
19287468 - 1  K.YTCLPGYVR.S                          1129.53   2  0.05    2.580  0.512   346.1  1   12/24   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 565.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 T    237.12     265.12                                      966.47
 C    398.14     426.13                                      865.42
 L    511.22     539.22                                      704.41
 P    608.27     636.27                                      591.32
 G    665.30     693.29                                      494.27
 Y    828.36     856.35                                      437.25
 V    927.43     955.42                                      274.19
 R                                                           175.12
```

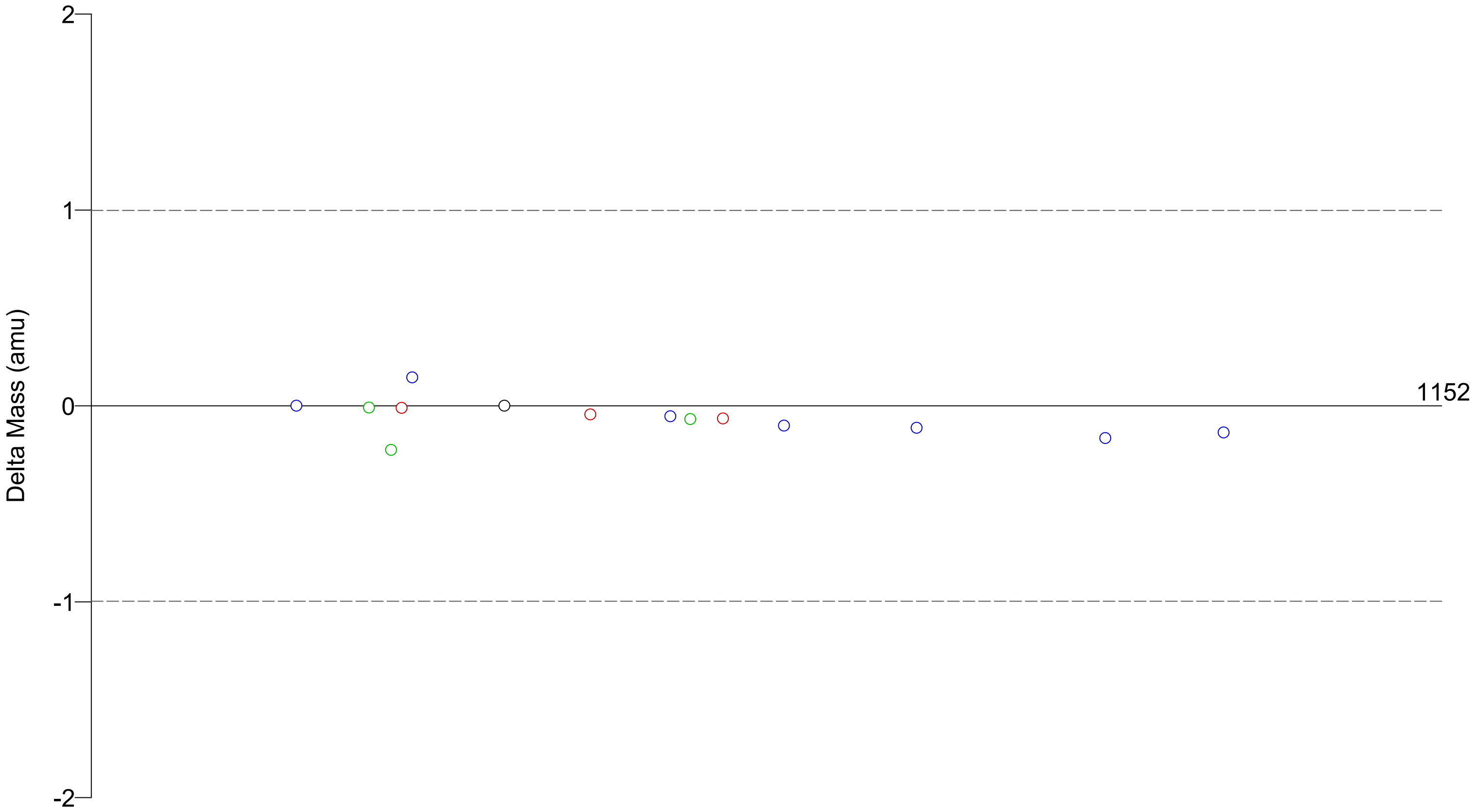


#19287468-1 NL: 1.65E5

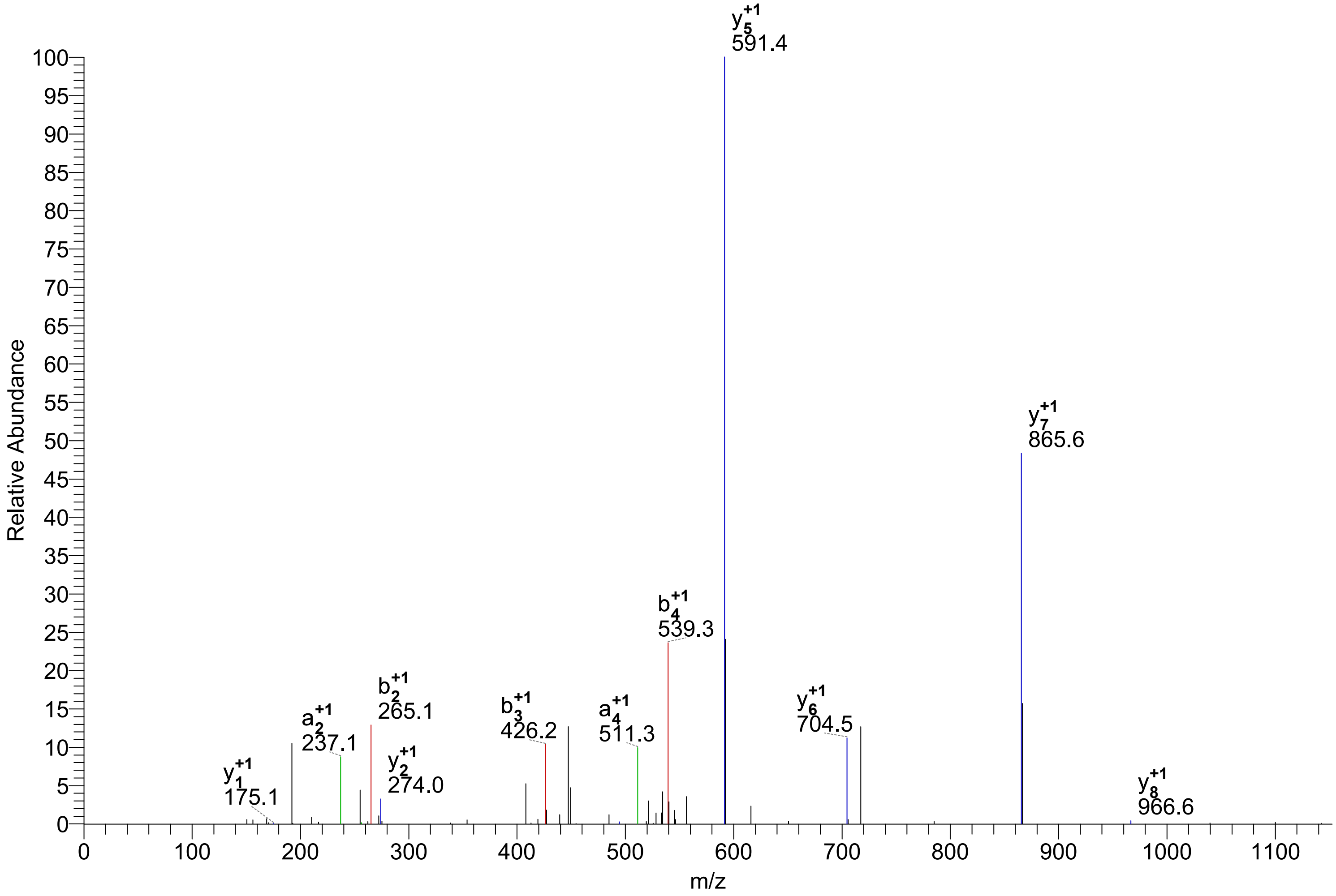


```
Reference                                                   P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00855766.1|VEGA:OTTHUMP0000                                1       10.1     0.0       0
19287468 - 1  K.YTCLPGYVR.S                          1129.53   2  0.05    2.580  0.512   346.1  1   12/24   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 565.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 T    237.12     265.12                                      966.47
 C    398.14     426.13                                      865.42
 L    511.22     539.22                                      704.41
 P    608.27     636.27                                      591.32
 G    665.30     693.29                                      494.27
 Y    828.36     856.35                                      437.25
 V    927.43     955.42                                      274.19
 R                                                           175.12
```

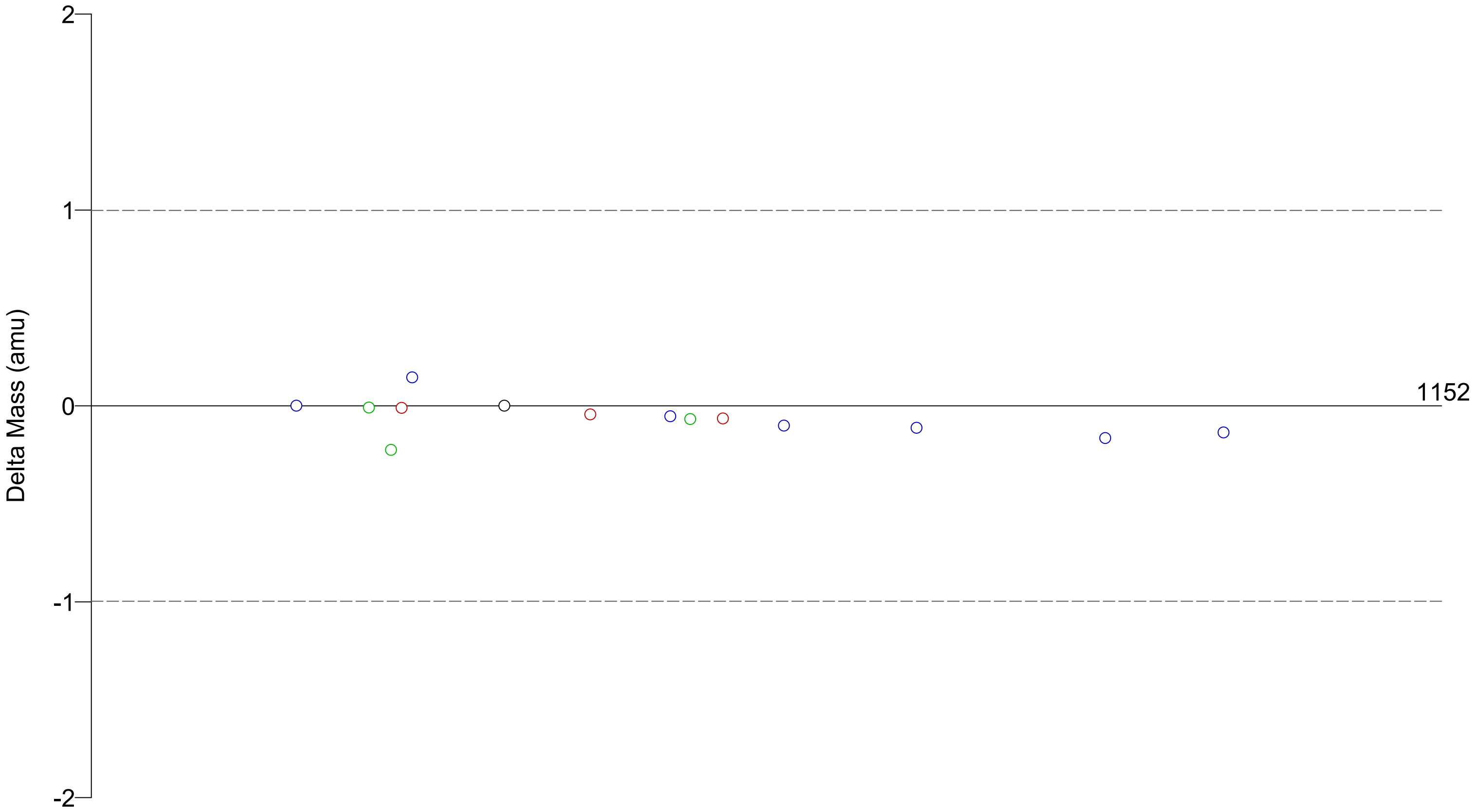


#19287468-1 NL: 1.65E5

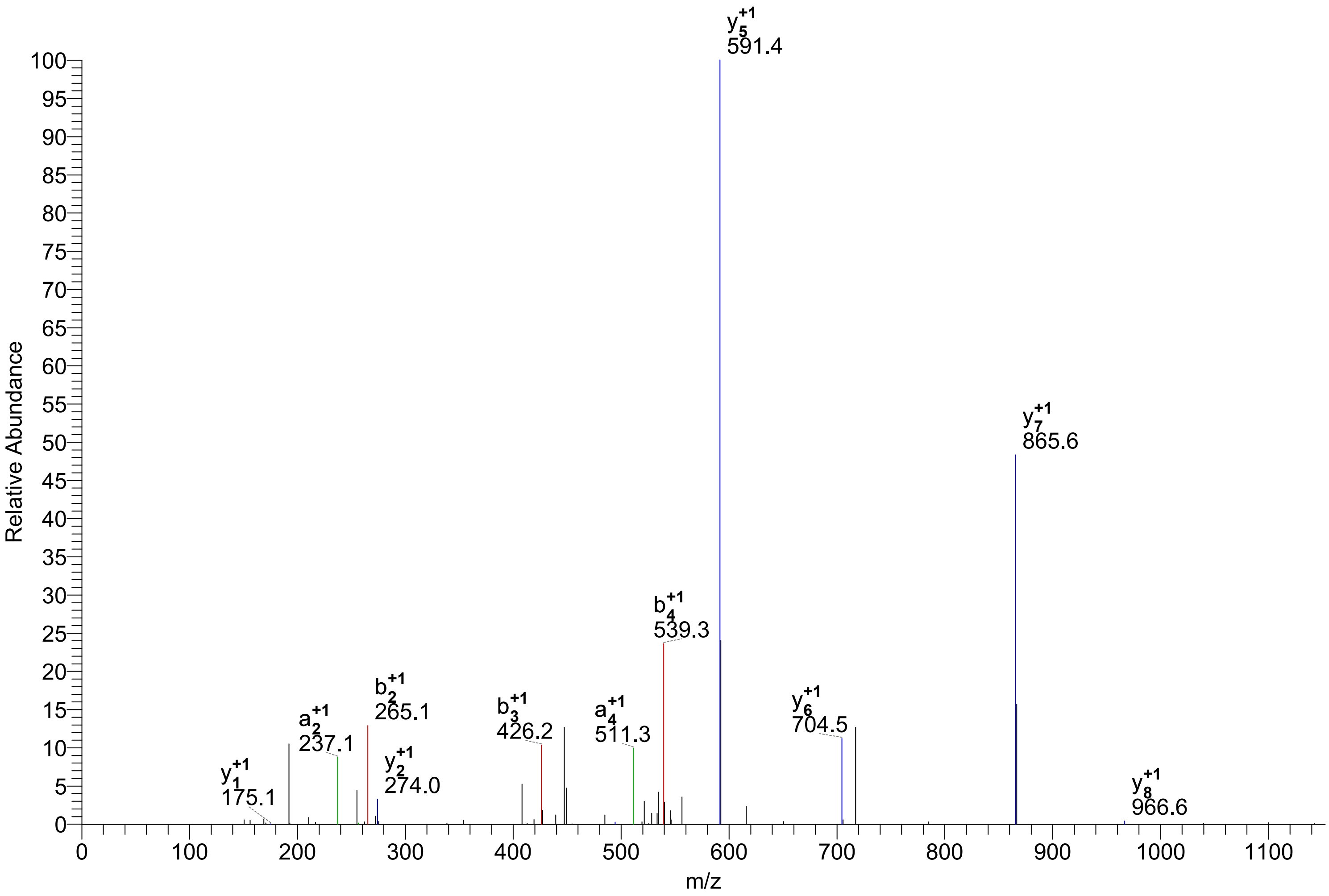


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp   RSp  Ions   Count
IPI:IPI00872510.1|TREMBL:A8MVU6|EN                                 1       10.1     0.0       0
19287468 - 1  K.YTCLPGYVR.S                           1129.53   2  0.05    2.580  0.512   346.1  1   12/24   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 565.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 T    237.12     265.12                                      966.47
 C    398.14     426.13                                      865.42
 L    511.22     539.22                                      704.41
 P    608.27     636.27                                      591.32
 G    665.30     693.29                                      494.27
 Y    828.36     856.35                                      437.25
 V    927.43     955.42                                      274.19
 R                                                           175.12
```

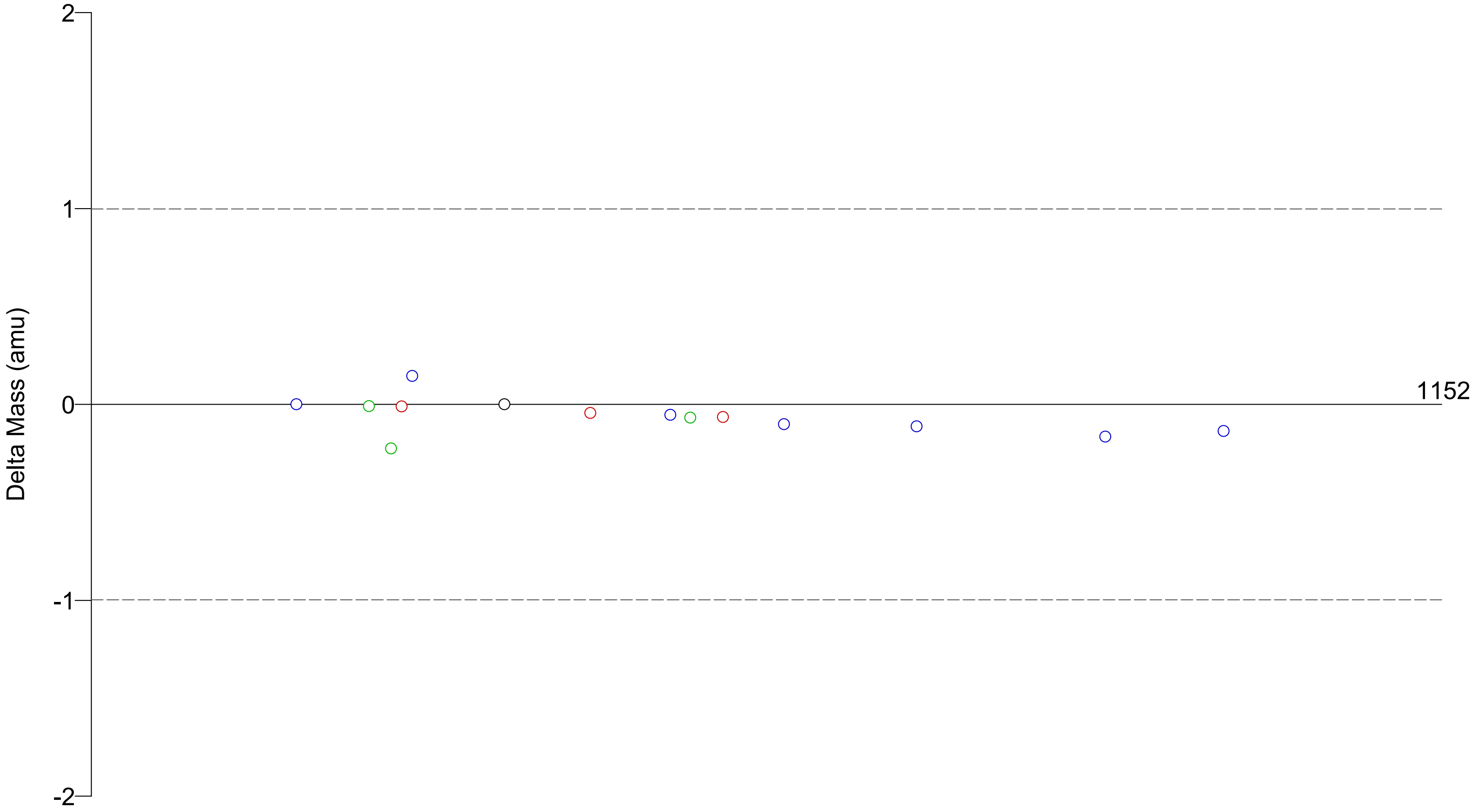


#19287468-1 NL: 1.65E5

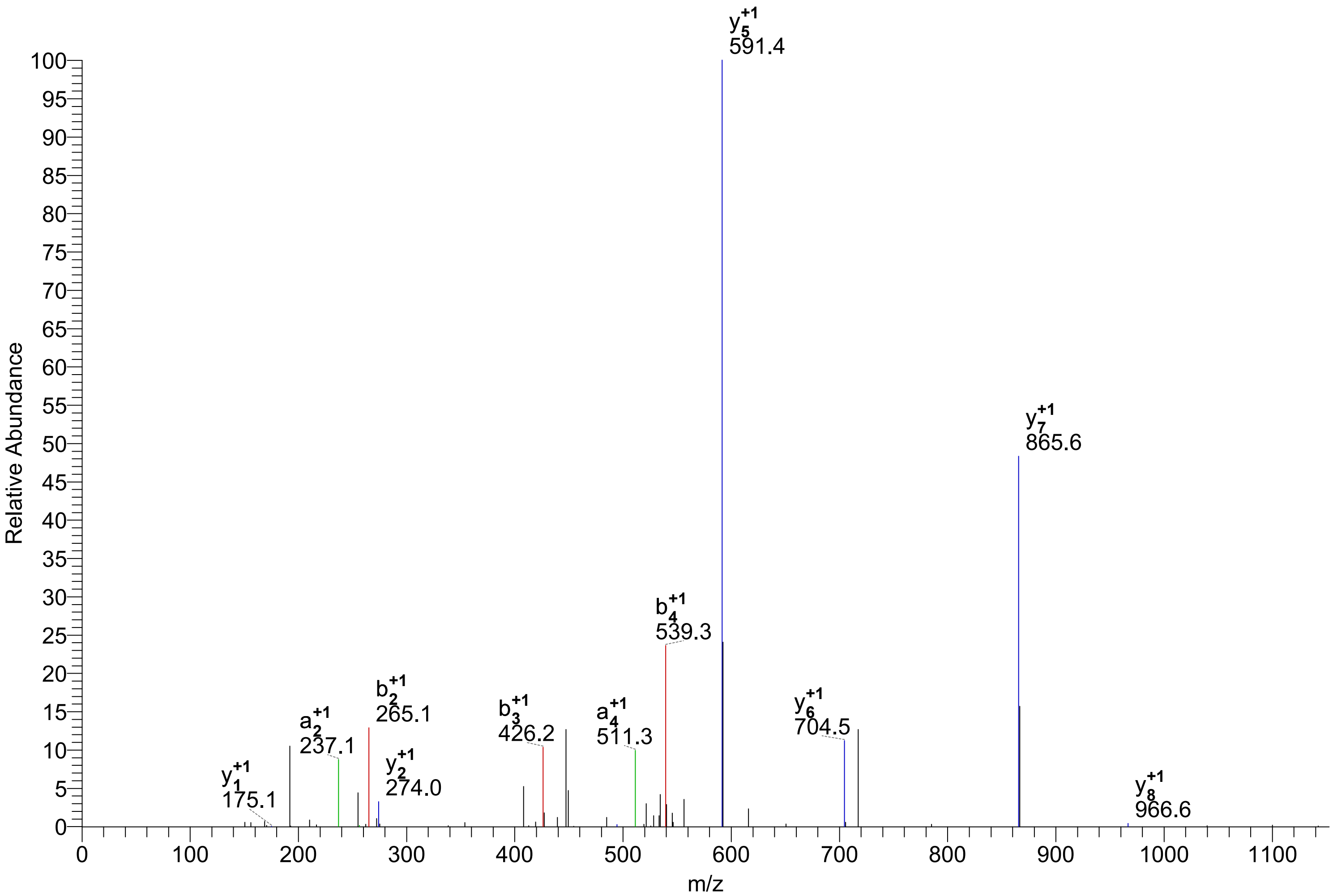


```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00880200.1|TREMBL:A6PVY5|VE                                1       10.1     0.0       0
19287468 - 1  K.YTCLPGYVR.S                        1129.53   2  0.05     2.580  0.512   346.1  1   12/24   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 565.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Y    136.08     164.07
 T    237.12     265.12                                      966.47
 C    398.14     426.13                                      865.42
 L    511.22     539.22                                      704.41
 P    608.27     636.27                                      591.32
 G    665.30     693.29                                      494.27
 Y    828.36     856.35                                      437.25
 V    927.43     955.42                                      274.19
 R                                                           175.12
```

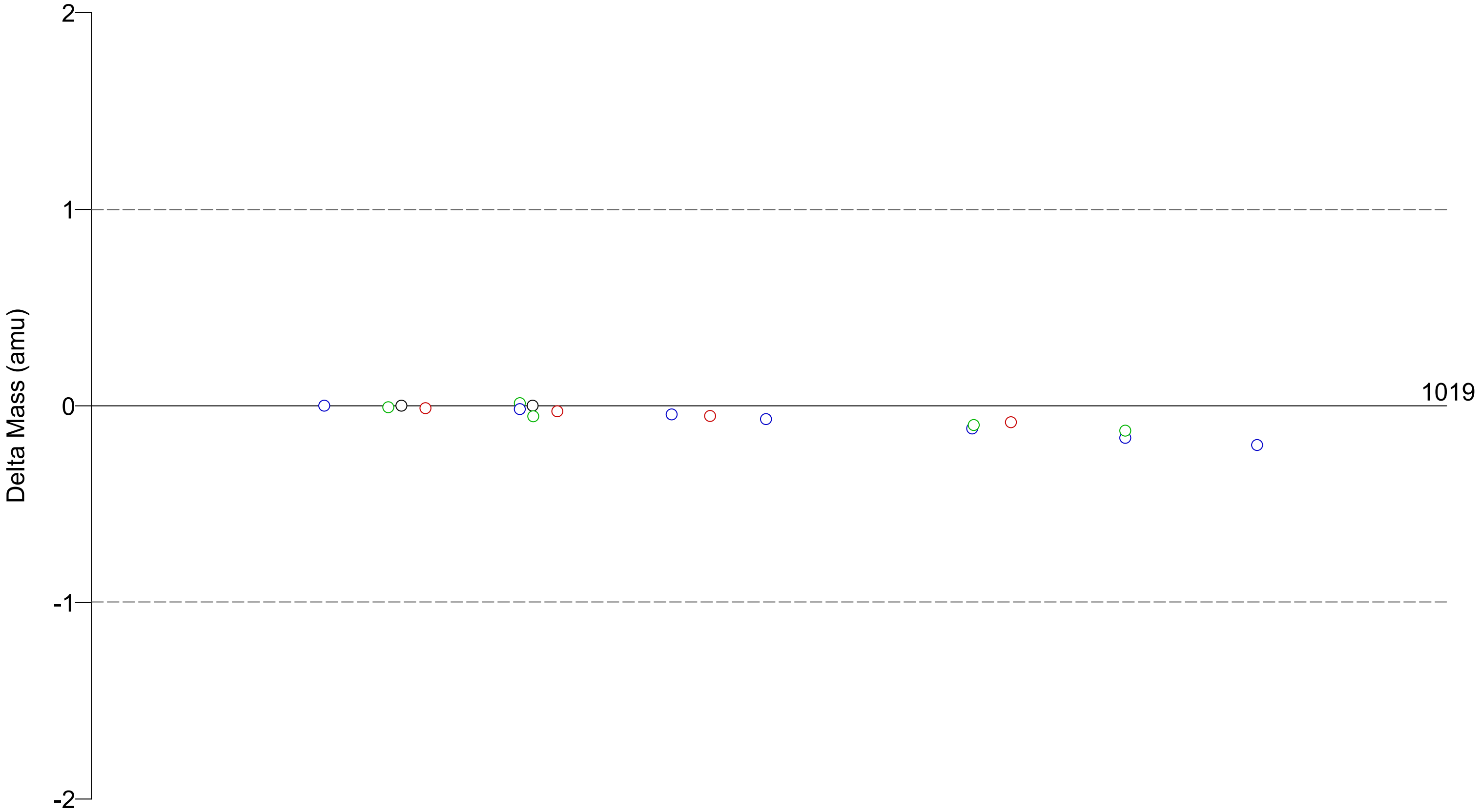


#19287468-1 NL: 1.65E5

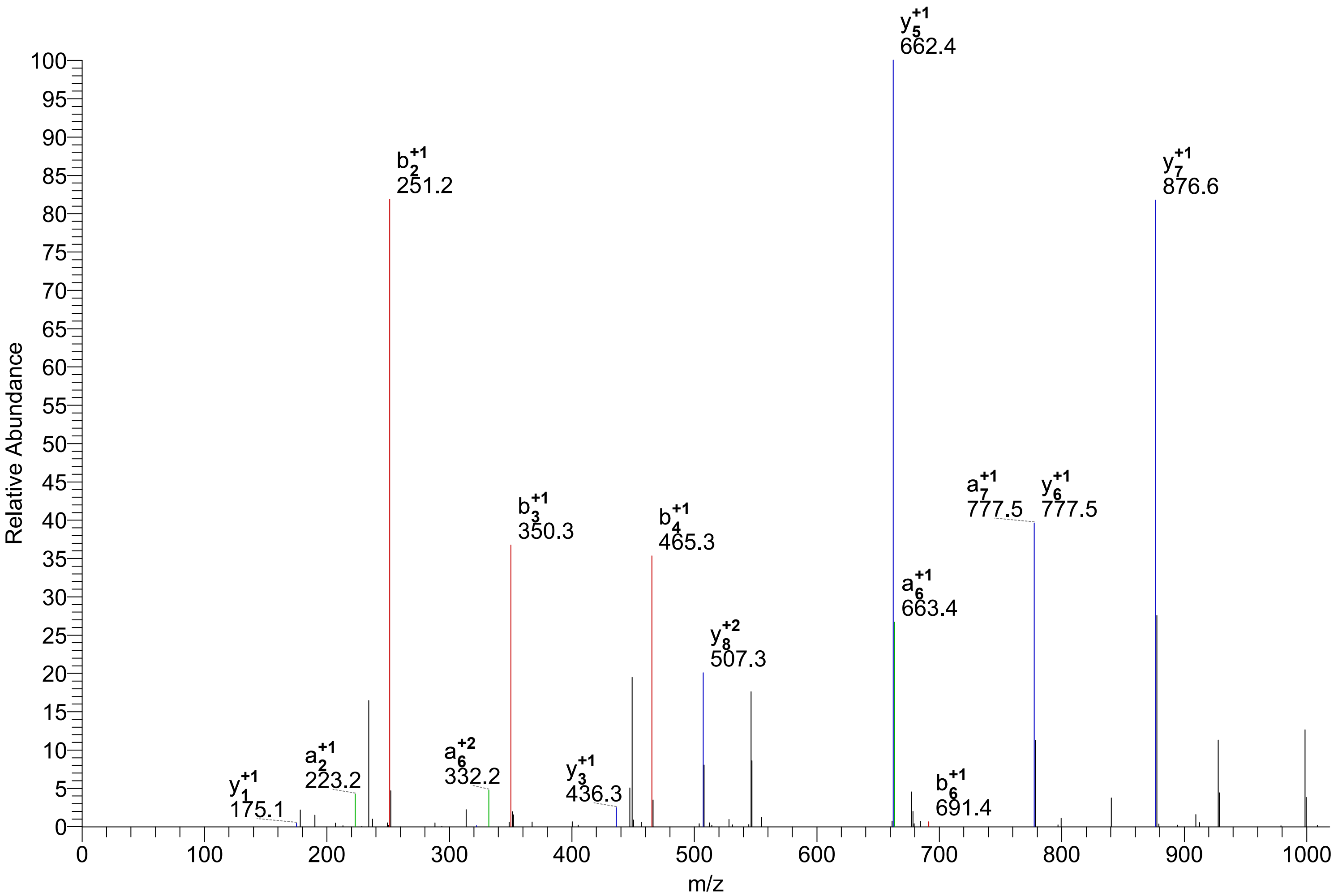


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00473011.3|SWISS-PROT:P02042|TREMBL:A0N071|ENSEMBL:ENSP    1        10.1     0.0        0
19287468 - 1  K.LHVDPENFR.L                           1126.56   2  0.06     2.171  0.417   654.7  1   14/24   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 H    223.16     251.15                                     1013.48
 V    322.22     350.22                                      876.42
 D    437.25     465.25                                      777.35
 P    534.30     562.30                                      662.33
 E    663.35     691.34                                      565.27
 N    777.39     805.38                                      436.23
 F    924.46     952.45                                      322.19
 R                                                           175.12
```

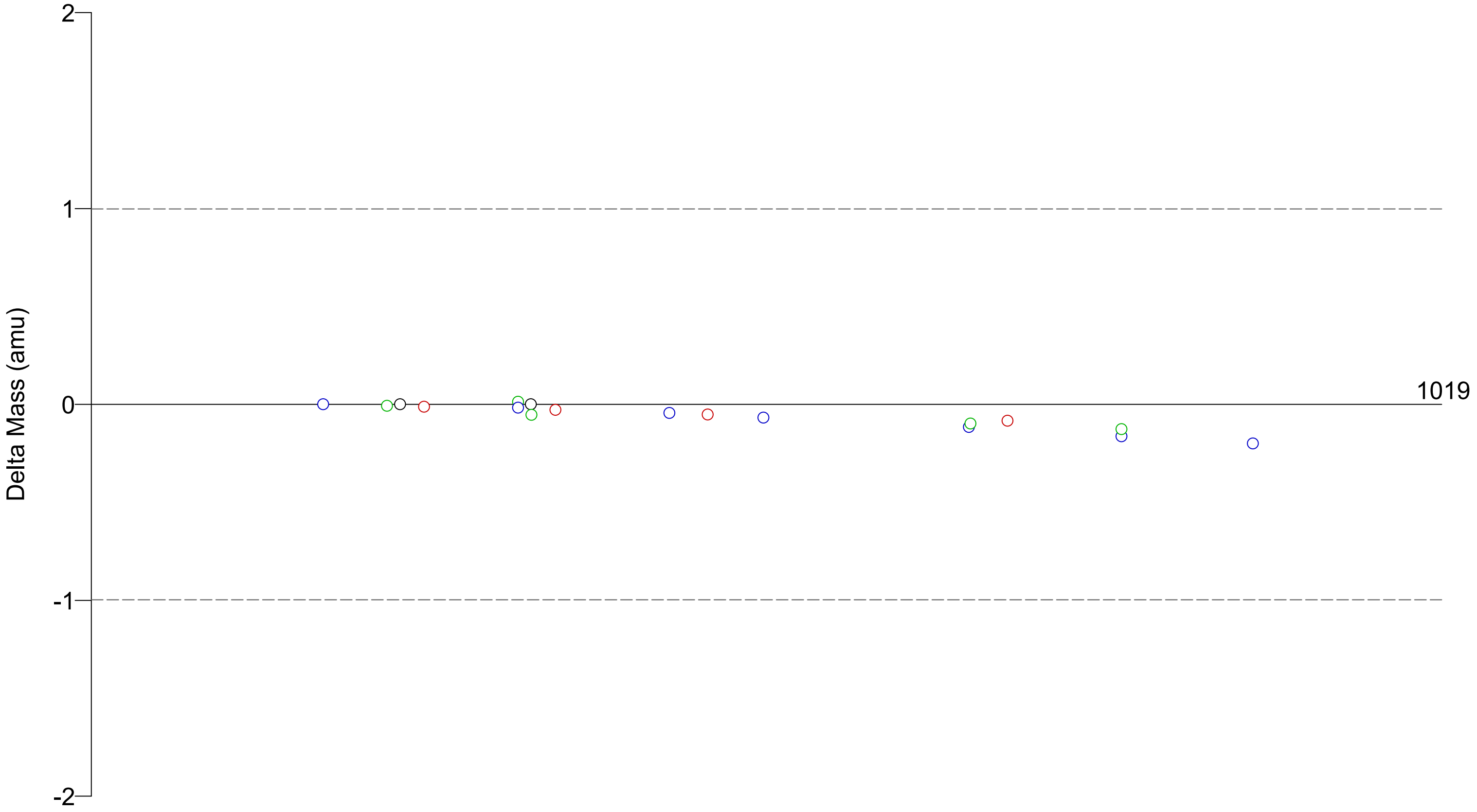


#19287468-1 NL: 7.10E5

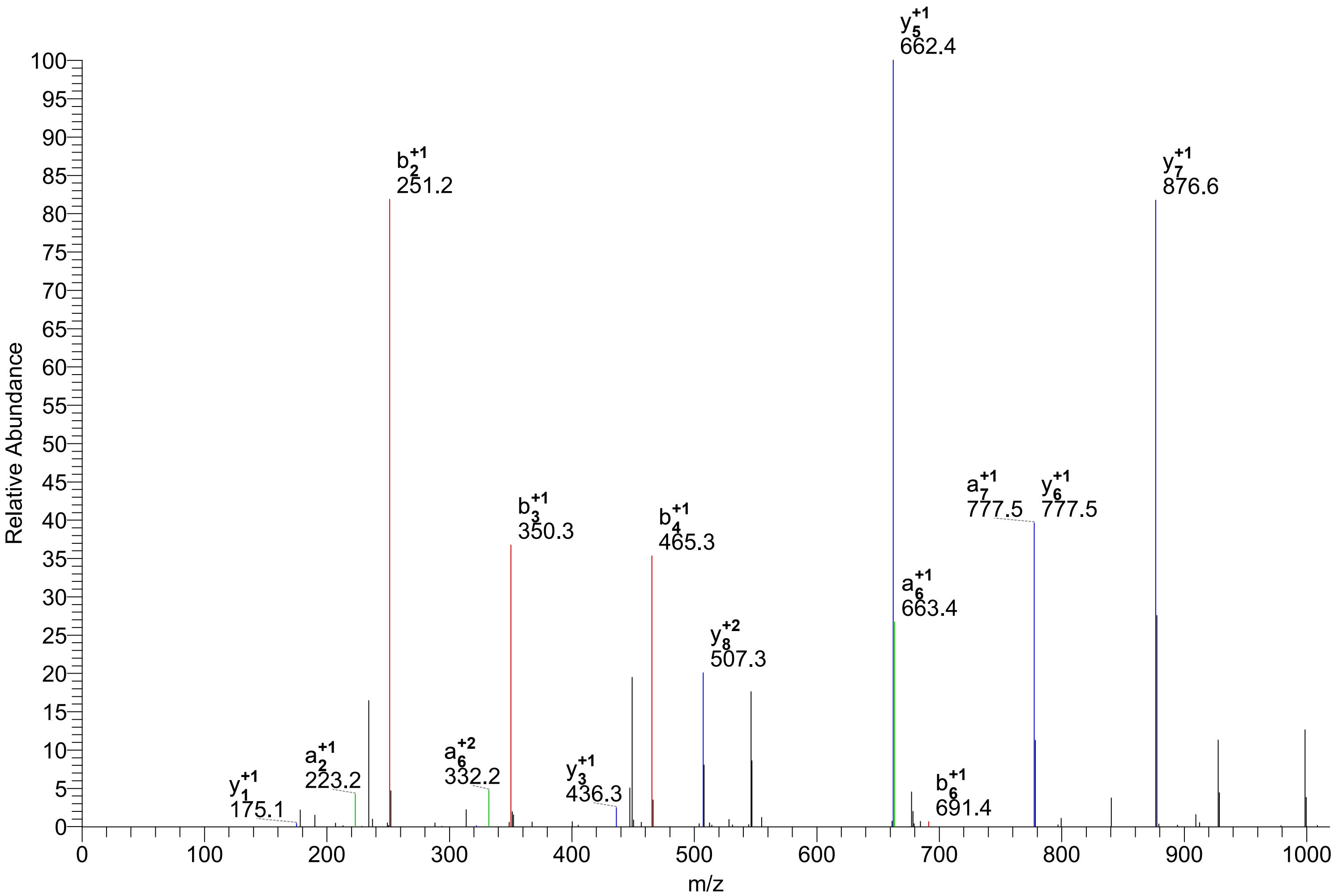


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00657660.1|ENSEMBL:ENSP0000                                1       10.1     0.0       0
19287468 - 1  K.LHVDPENFR.L                          1126.56   2  0.06    2.171 0.417   654.7  1   14/24   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 H    223.16    251.15                                     1013.48
 V    322.22    350.22                                      876.42
 D    437.25    465.25                                      777.35
 P    534.30    562.30                                      662.33
 E    663.35    691.34                                      565.27
 N    777.39    805.38                                      436.23
 F    924.46    952.45                                      322.19
 R                                                          175.12
```

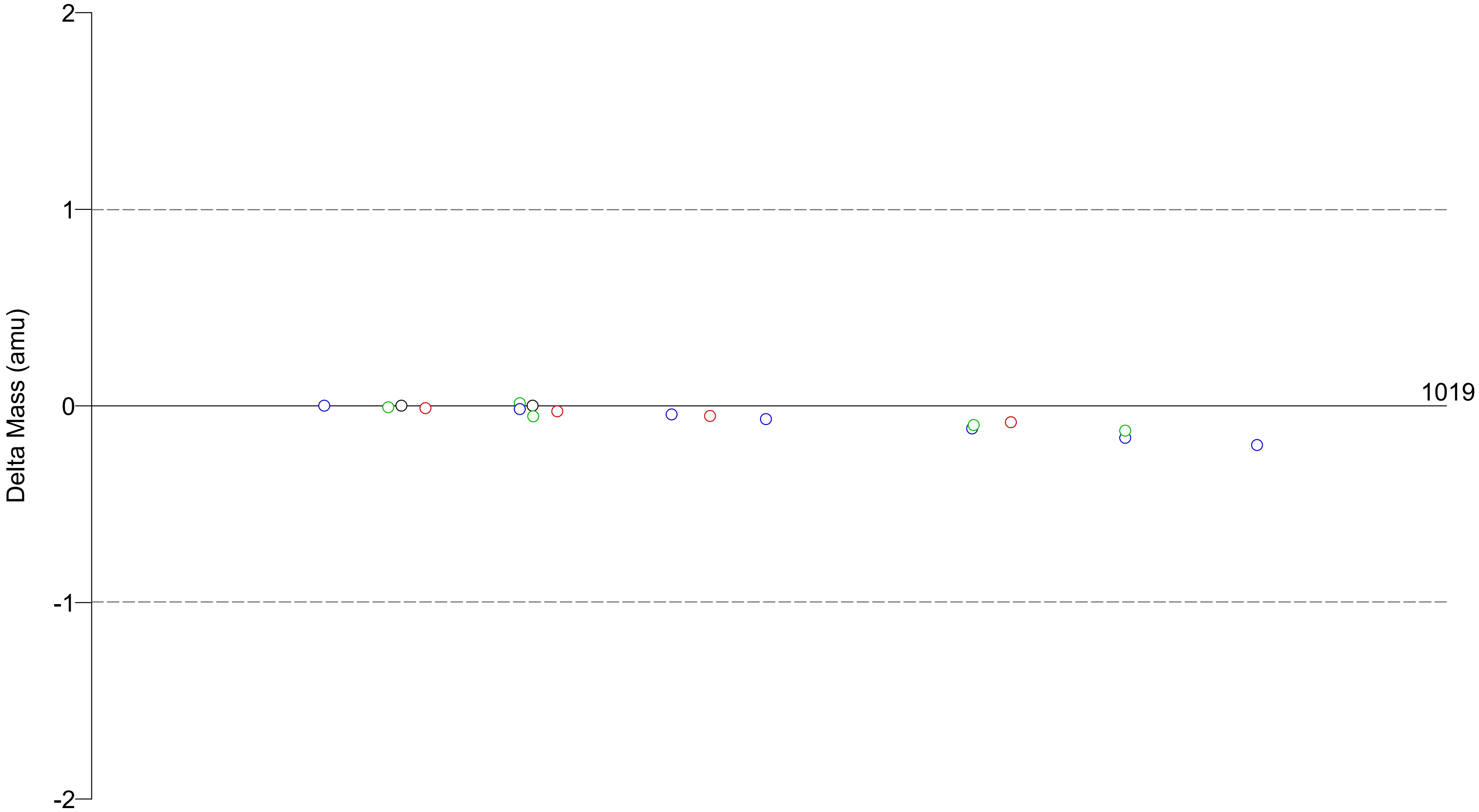


#19287468-1 NL: 7.10E5

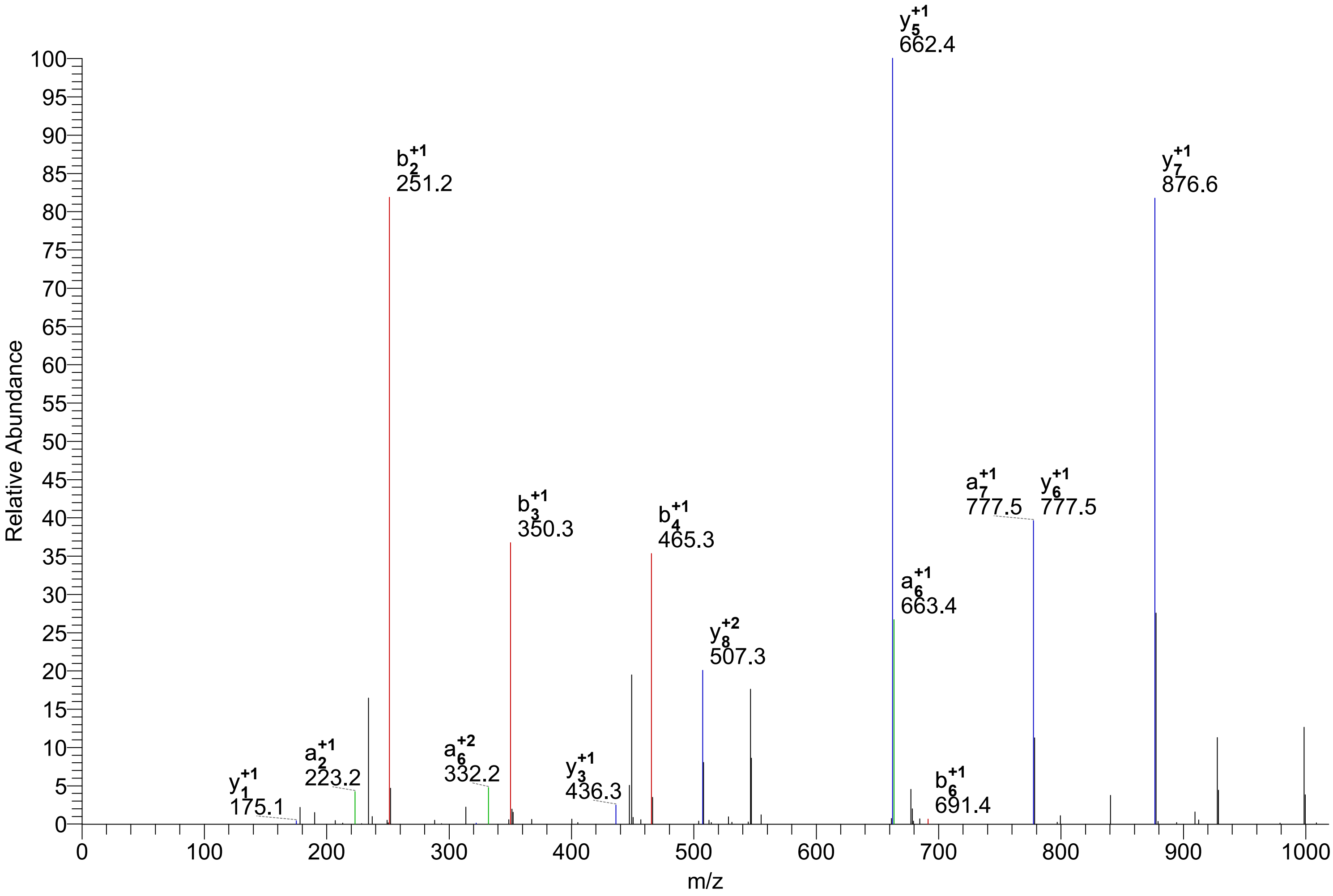


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00796636.14|TREMBL:A9YUX2;B                                1       10.1     0.0       0
19287468 - 1  K.LHVDPENFR.L                          1126.56   2  0.06    2.171  0.417   654.7  1   14/24   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 H    223.16     251.15                                     1013.48
 V    322.22     350.22                                      876.42
 D    437.25     465.25                                      777.35
 P    534.30     562.30                                      662.33
 E    663.35     691.34                                      565.27
 N    777.39     805.38                                      436.23
 F    924.46     952.45                                      322.19
 R                                                           175.12
```

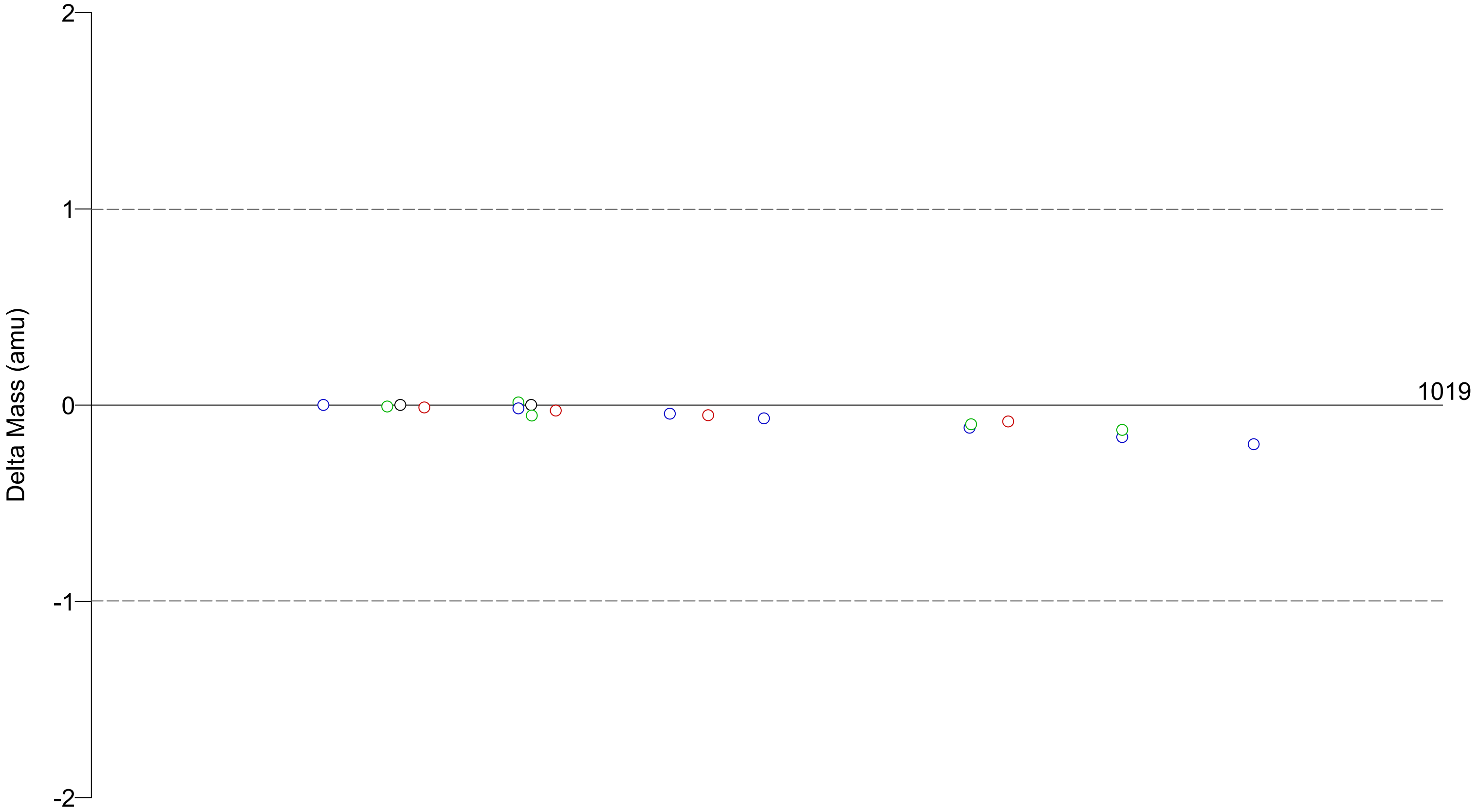


#19287468-1 NL: 7.10E5

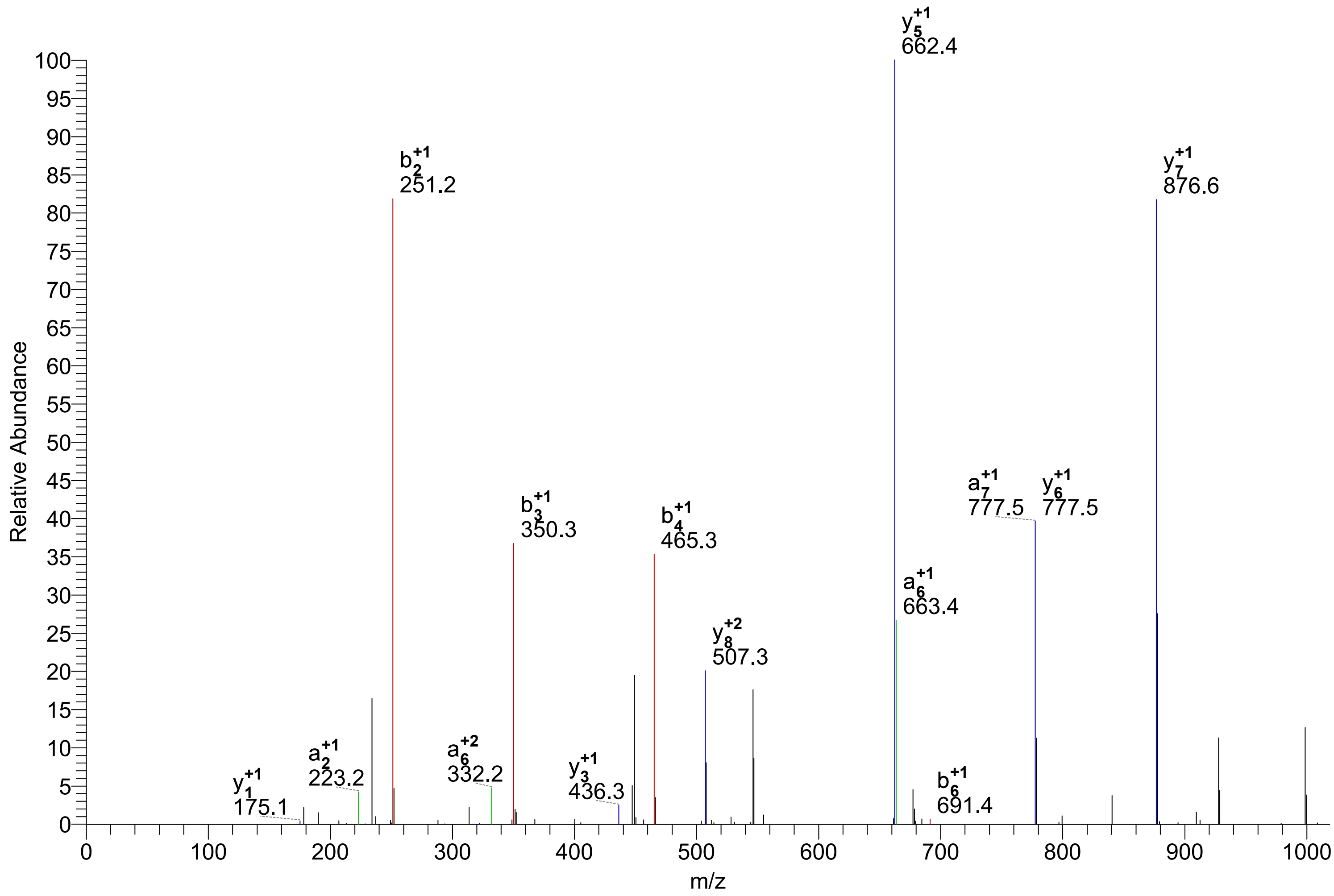


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829896.1|TREMBL:Q670S4 Ta                                 1       10.1     0.0       0
19287468 - 1  K.LHVDPENFR.L                          1126.56    2  0.06    2.171  0.417   654.7  1   14/24   5

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 H    223.16     251.15                                     1013.48
 V    322.22     350.22                                      876.42
 D    437.25     465.25                                      777.35
 P    534.30     562.30                                      662.33
 E    663.35     691.34                                      565.27
 N    777.39     805.38                                      436.23
 F    924.46     952.45                                      322.19
 R                                                           175.12
```

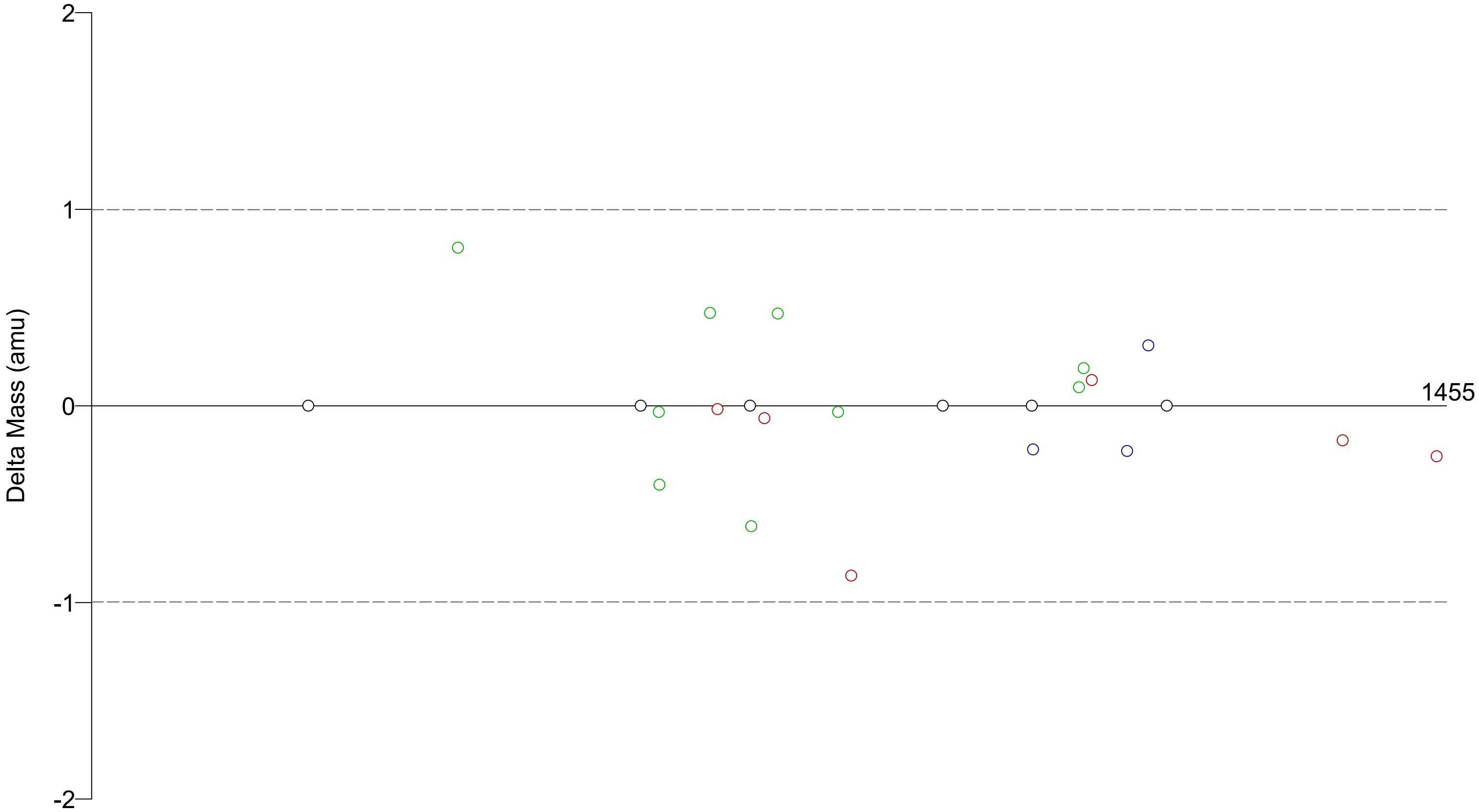


#19287468-1 NL: 7.10E5

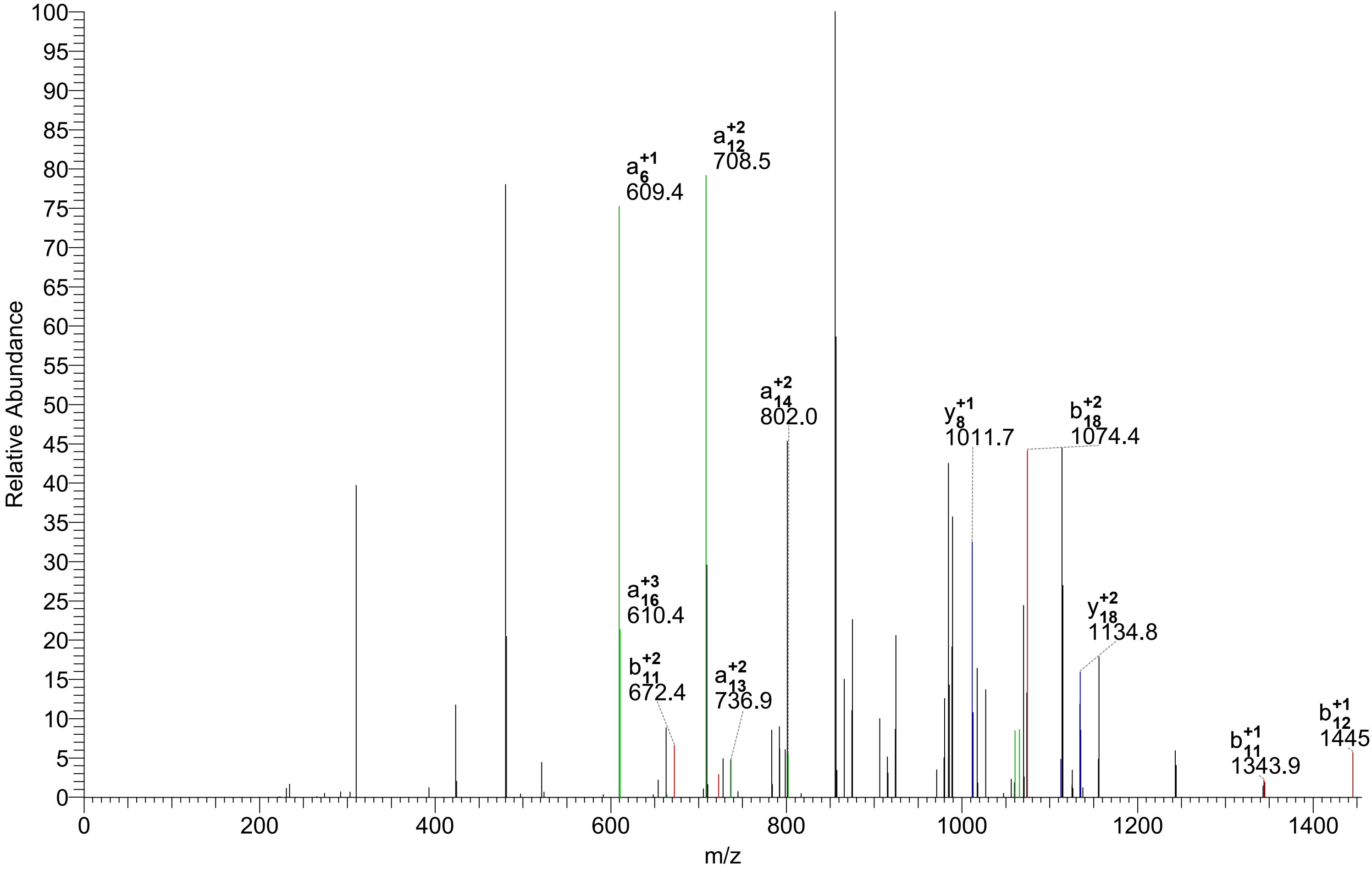


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00871791.2|SWISS-PROT:Q96NG8|TREMBL:B4DQZ9;B7Z9R3|ENSEM    1       8.1      0.0       0
19287468 - 1  R.VSHLTVHYRIHTGEKPYECK.E               2455.22   3  1       2.157  0.637   199.9  2   17/114

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 819.06
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 V     72.08     100.08
 S    159.11     187.11                                     2356.15
 H    296.17     324.17                                     2269.12
 L    409.26     437.25                                     2132.06
 T    510.30     538.30                                     2018.98
 V    609.37     637.37                                     1917.93
 H    746.43     774.43                                     1818.86
 Y    909.49     937.49                                     1681.80
 R   1065.60    1093.59                                     1518.74
 I   1178.68    1206.67                                     1362.64
 H   1315.74    1343.73                                     1249.55
 T   1416.79    1444.78                                     1112.49
 G   1473.81    1501.80                                     1011.45
 E   1602.85    1630.84                                      954.42
 K   1730.94    1758.94                                      825.38
 P   1828.00    1855.99                                      697.29
 Y   1991.06    2019.06                                      600.23
 E   2120.10    2148.10                                      437.17
 C   2281.12    2309.11                                      308.13
 K                                                           147.11
```

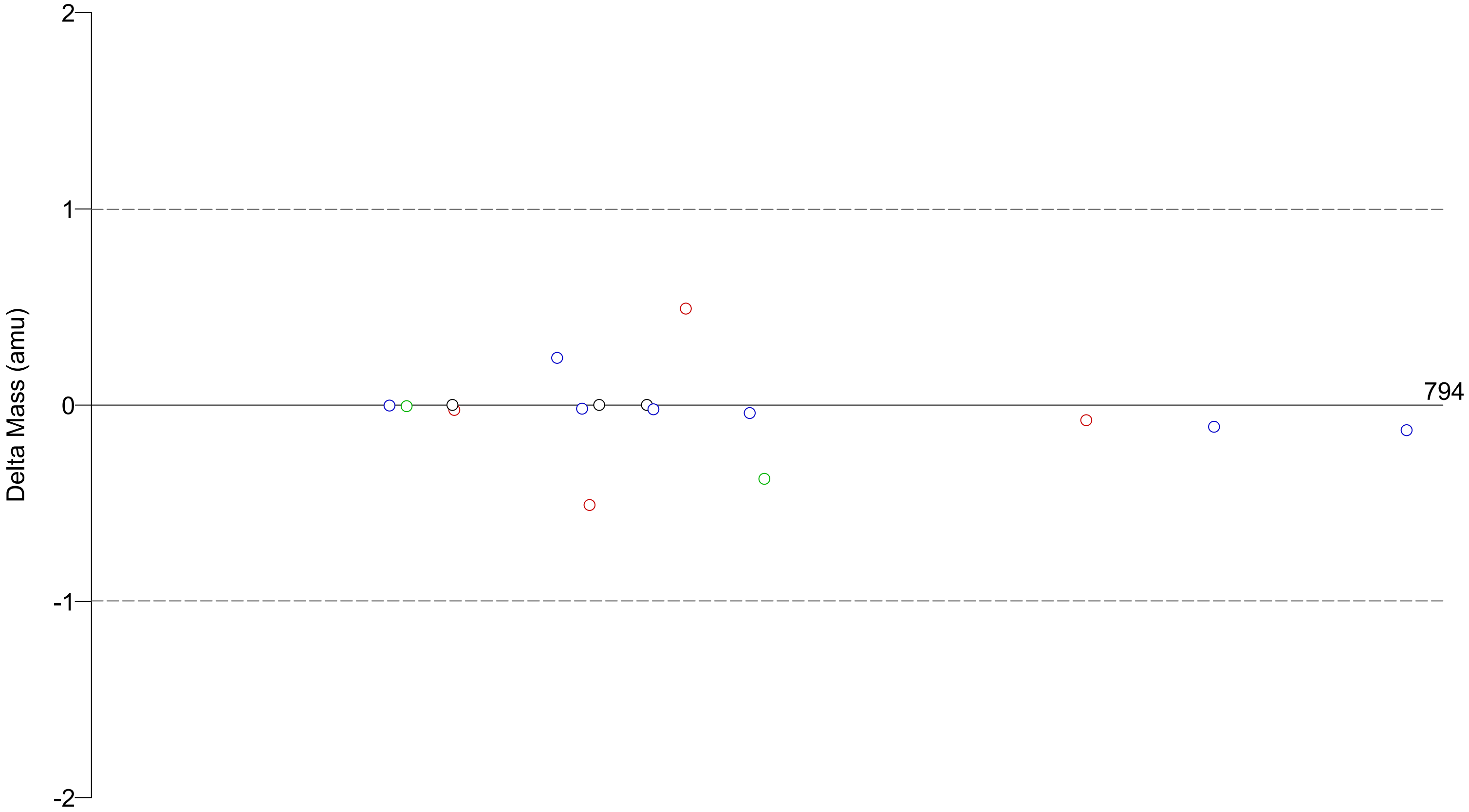


#19287468-1 NL: 6.24E5

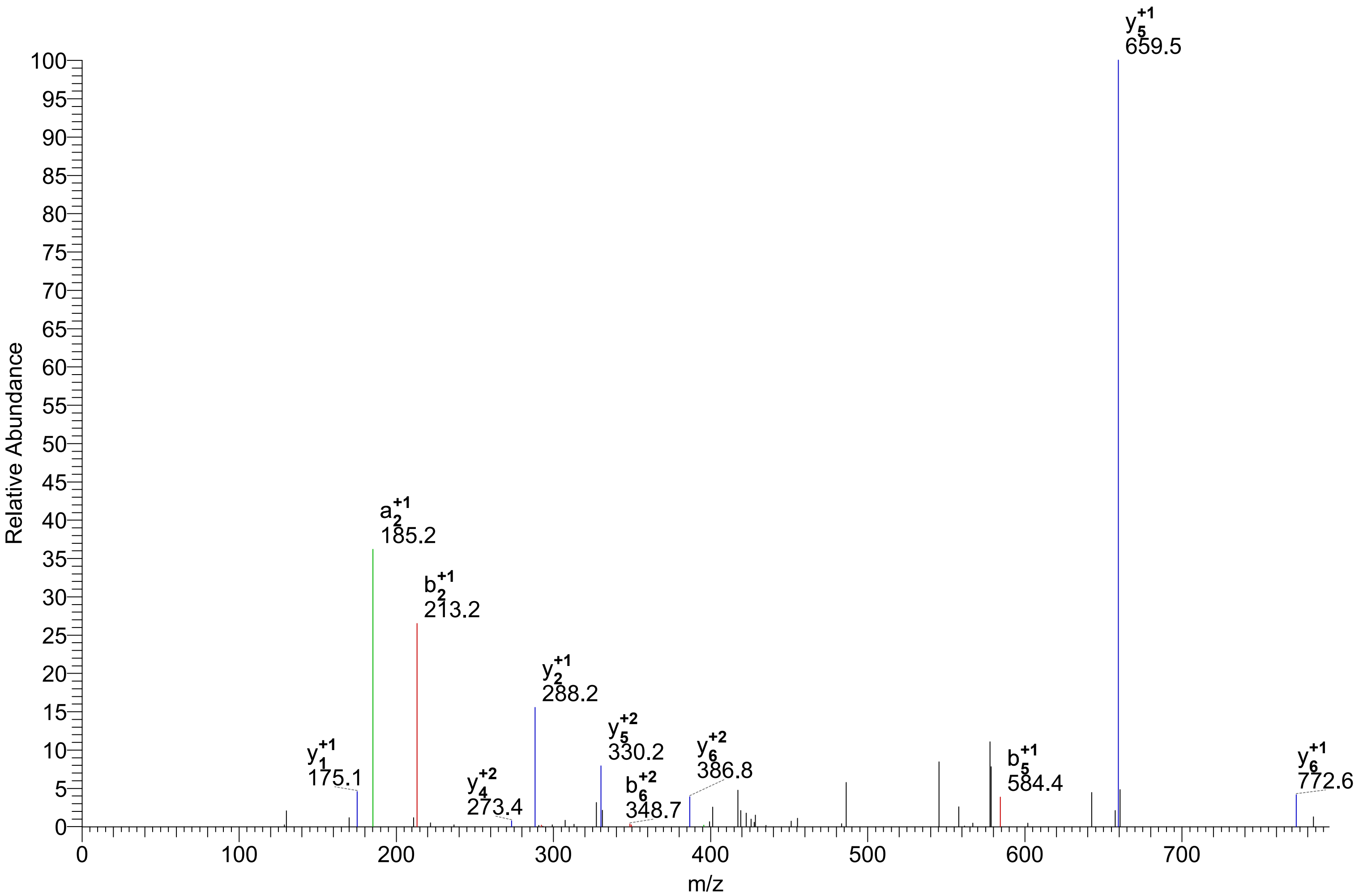


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00888034.1|REFSEQ:XP_001732886 Tax_Id=9606 Gene_Symbol=    1       8.1      0.0       0
19287468 - 1  K.VXXPCXR.R                            871.51    2  0.06    1.526  0.312   361.0  2   11/18

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 436.25
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 X    185.16     213.16                                      772.44
 X    298.25     326.24                                      659.35
 P    395.30     423.30                                      546.27
 C    556.32     584.31                                      449.22
 X    669.40     697.40                                      288.20
 R                                                           175.12
```

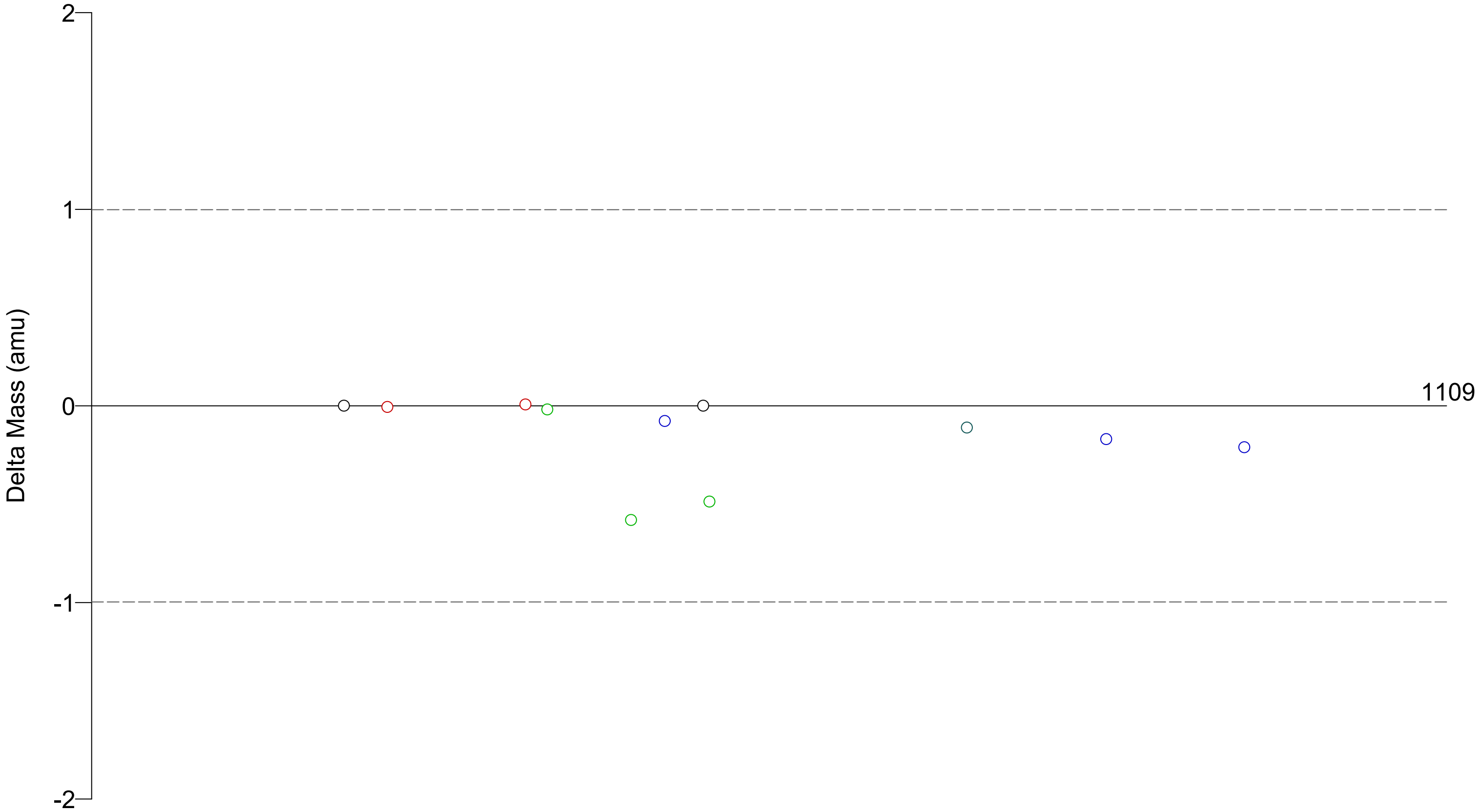


#19287468-1 NL: 5.11E5

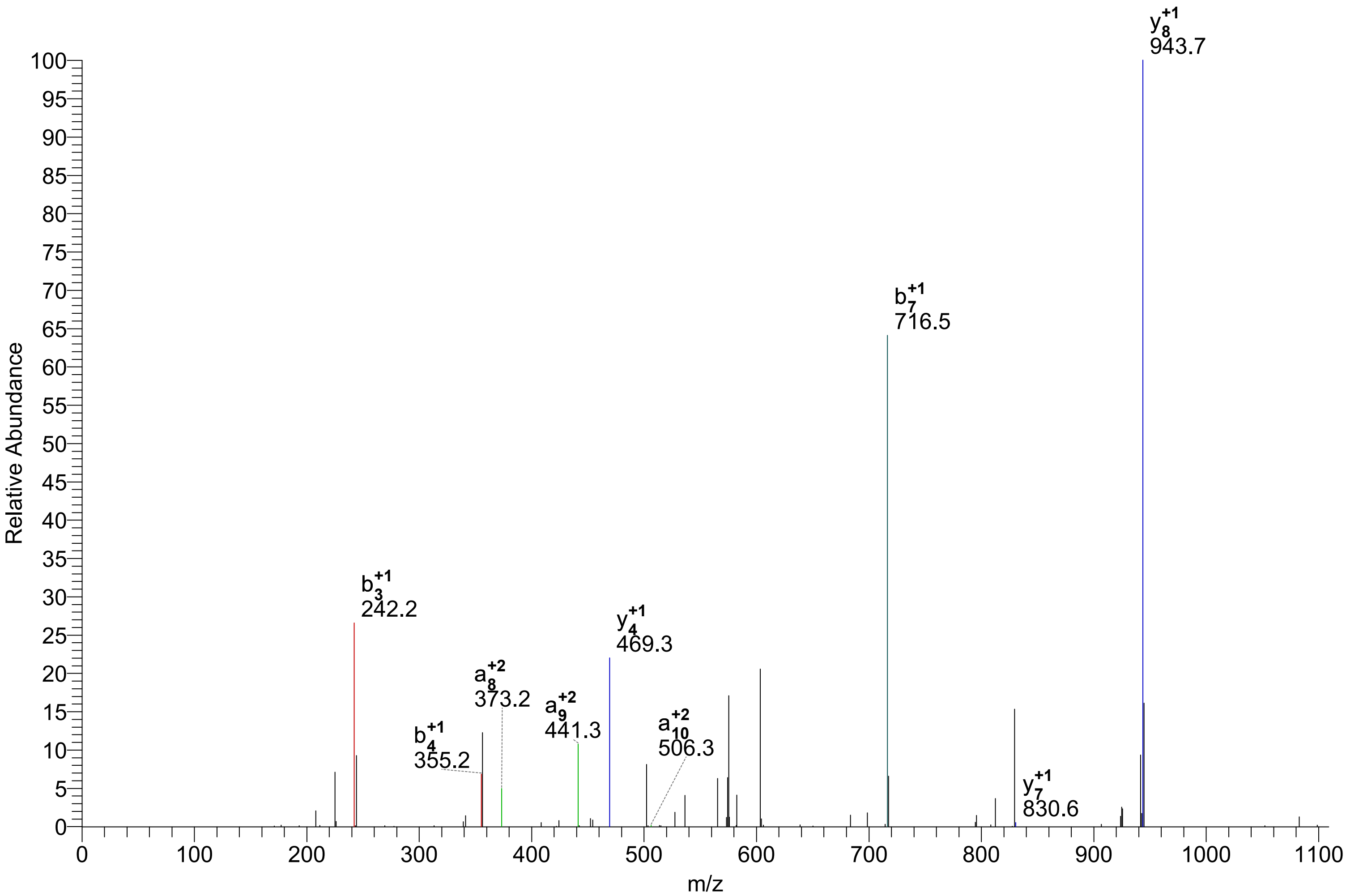


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00021274.2|SWISS-PROT:P29322|ENSEMBL:ENSP00000166244|RE    1       8.1      0.0       0
19287468 - 1  R.ALGITLM*GHQK.K                       1184.65   2  1       1.470  0.526   80.2   12  6/30

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 592.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 L    157.13     185.13                                     1113.61
 G    214.16     242.15                                     1000.52
 I    327.24     355.23                                      943.50
 T    428.29     456.28                                      830.42
 L    541.37     569.37                                      729.37
 M*   688.41     716.40                                      616.29
 G    745.43     773.42                                      469.25
 H    882.49     910.48                                      412.23
 Q   1010.55    1038.54                                      275.17
 K                                                           147.11
```

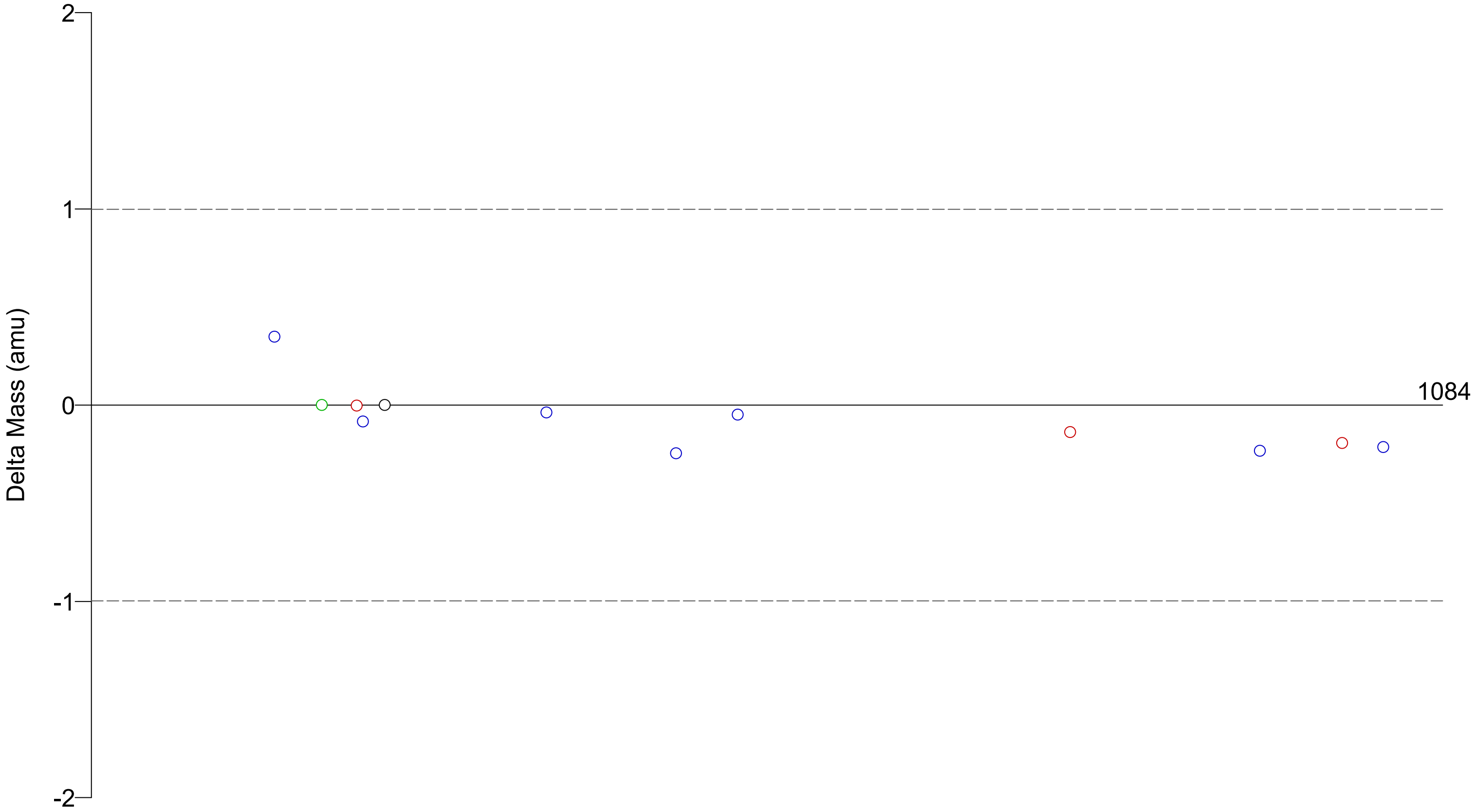


#19287468-1 NL: 1.66E5

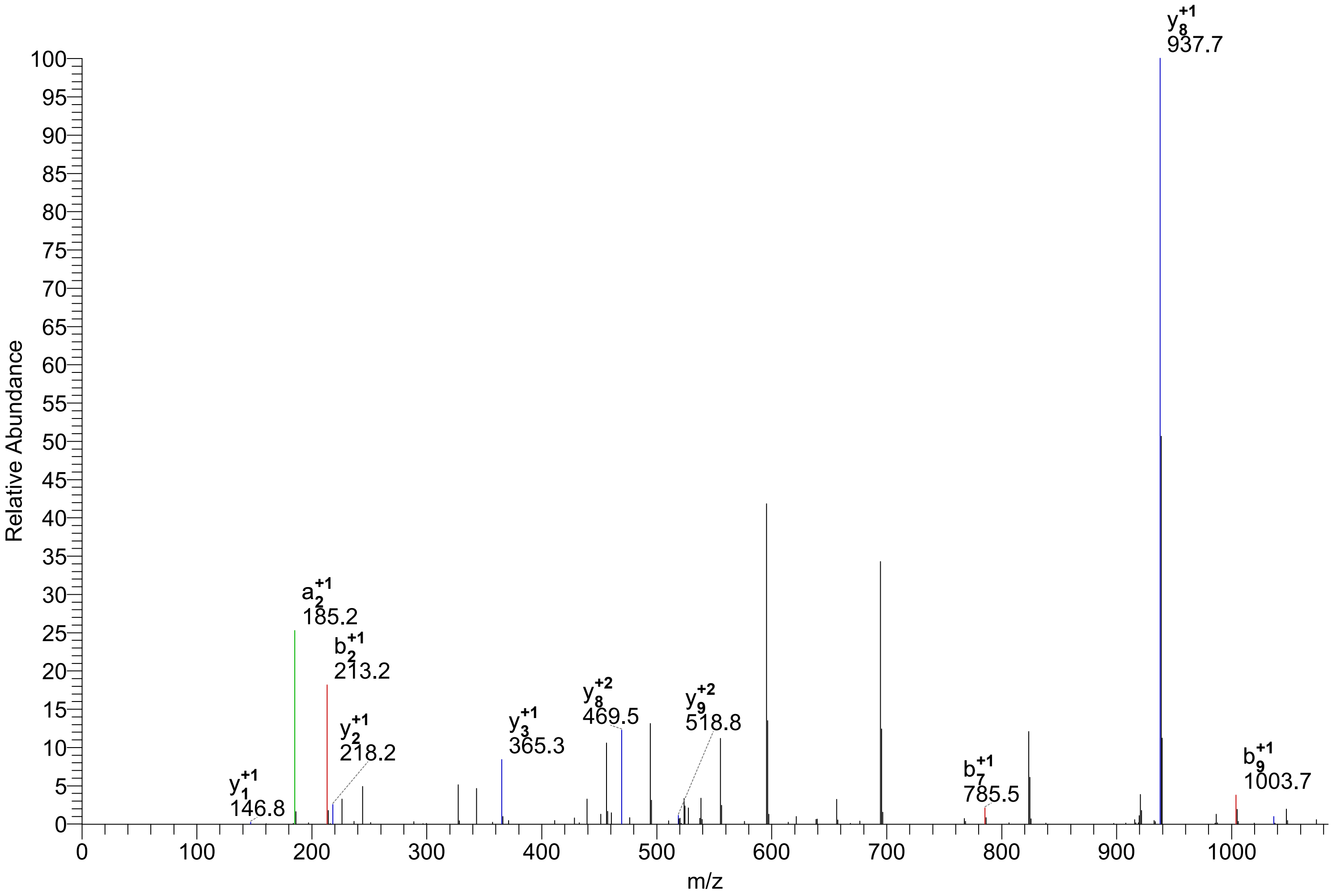


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
gi|113580|sp|P02770|ALBU_RAT SERUM ALBUMIN PRECURSOR. [MASS=68    1       8.1      0.0       113580
19287468 - 1  K.LVQEVTDFAK.T                              1149.62   2  1       2.007  0.529   95.0   6   8/27

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 575.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 V    185.16     213.16                                     1036.53
 Q    313.22     341.22                                      937.46
 E    442.27     470.26                                      809.40
 V    541.33     569.33                                      680.36
 T    642.38     670.38                                      581.29
 D    757.41     785.40                                      480.25
 F    904.48     932.47                                      365.22
 A    975.51    1003.51                                      218.15
 K                                                           147.11
```

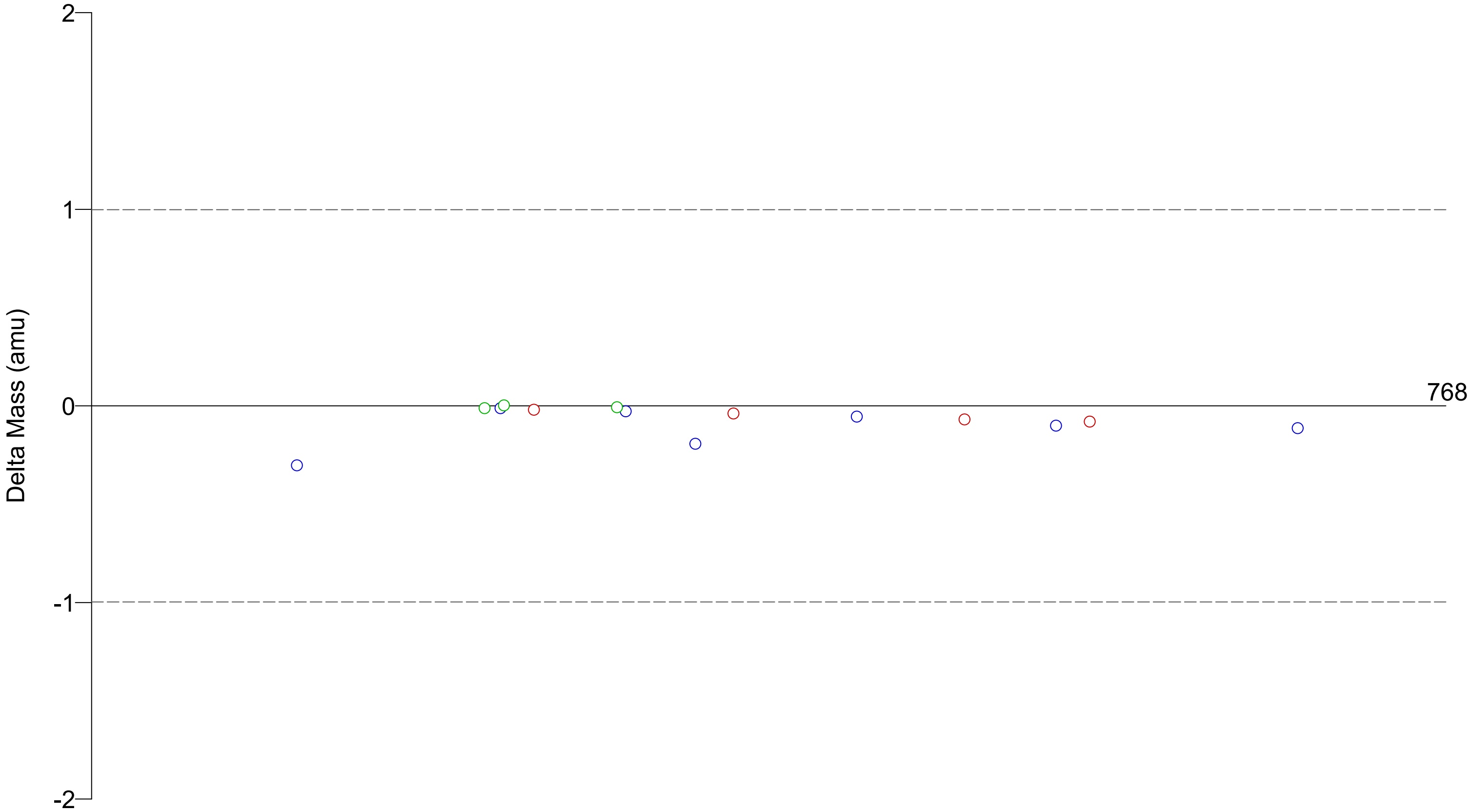


#19287468-1 NL: 3.94E6

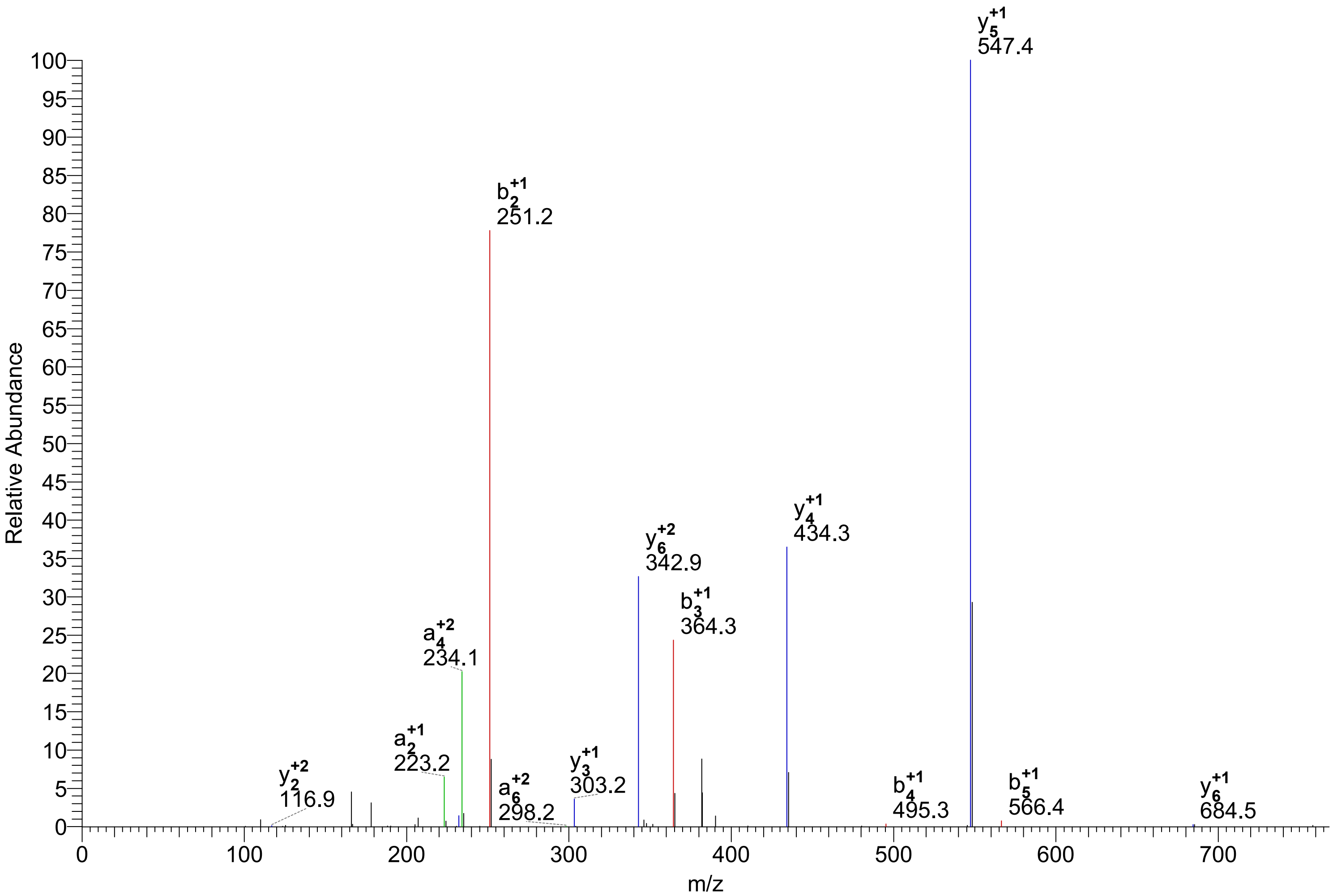


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00382748.2|SWISS-PROT:Q5T013-3|TREMBL:A8MSM3|ENSEMBL:EN    1       10.1     0.0       0
19287468 - 1 R.IHLMAGR.V                             797.45    2  0.07    2.141  0.000   350.3  1   10/18   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                     684.36
 L    336.24     364.23                                     547.30
 M    467.28     495.27                                     434.22
 A    538.32     566.31                                     303.18
 G    595.34     623.33                                     232.14
 R                                                          175.12
```

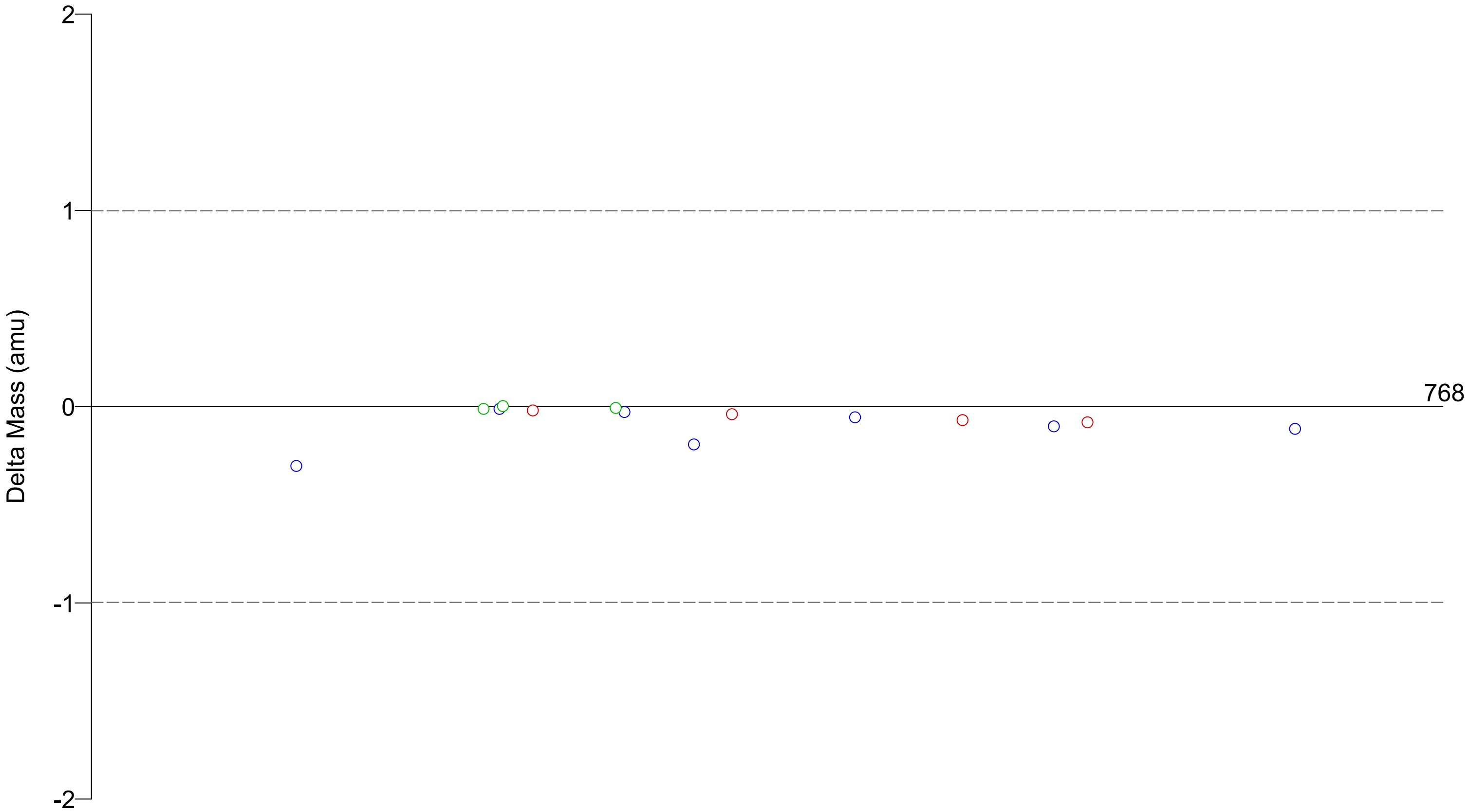


#19287468-1 NL: 3.32E5

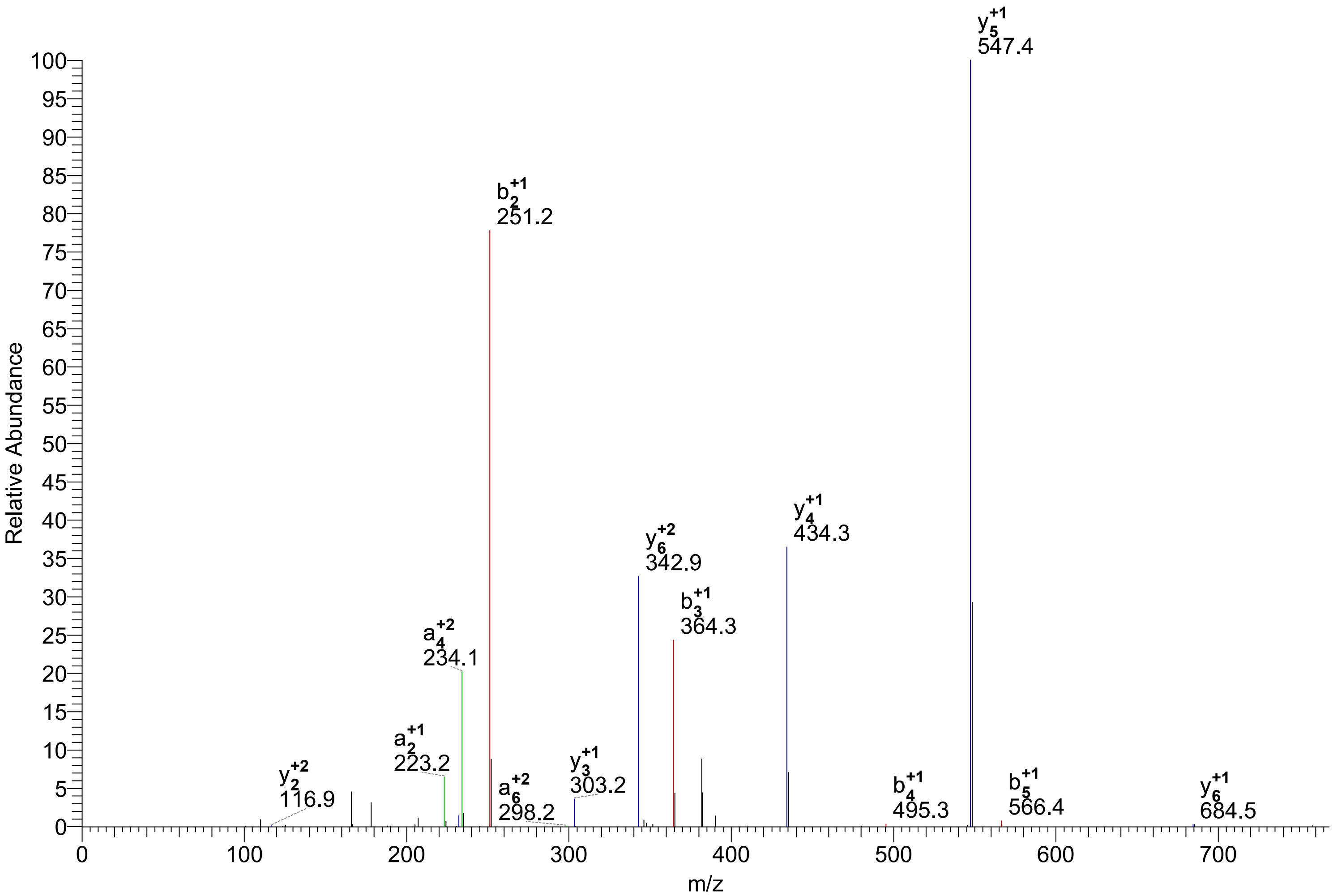


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                ME+      z    P        XC DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00465271.2|SWISS-PROT:Q5T01                                1       10.1     0.0       0
19287468 - 1 R.IHLMAGR.V                             797.45    2  0.07    2.141  0.000   350.3  1   10/18   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                      684.36
 L    336.24     364.23                                      547.30
 M    467.28     495.27                                      434.22
 A    538.32     566.31                                      303.18
 G    595.34     623.33                                      232.14
 R                                                           175.12
```

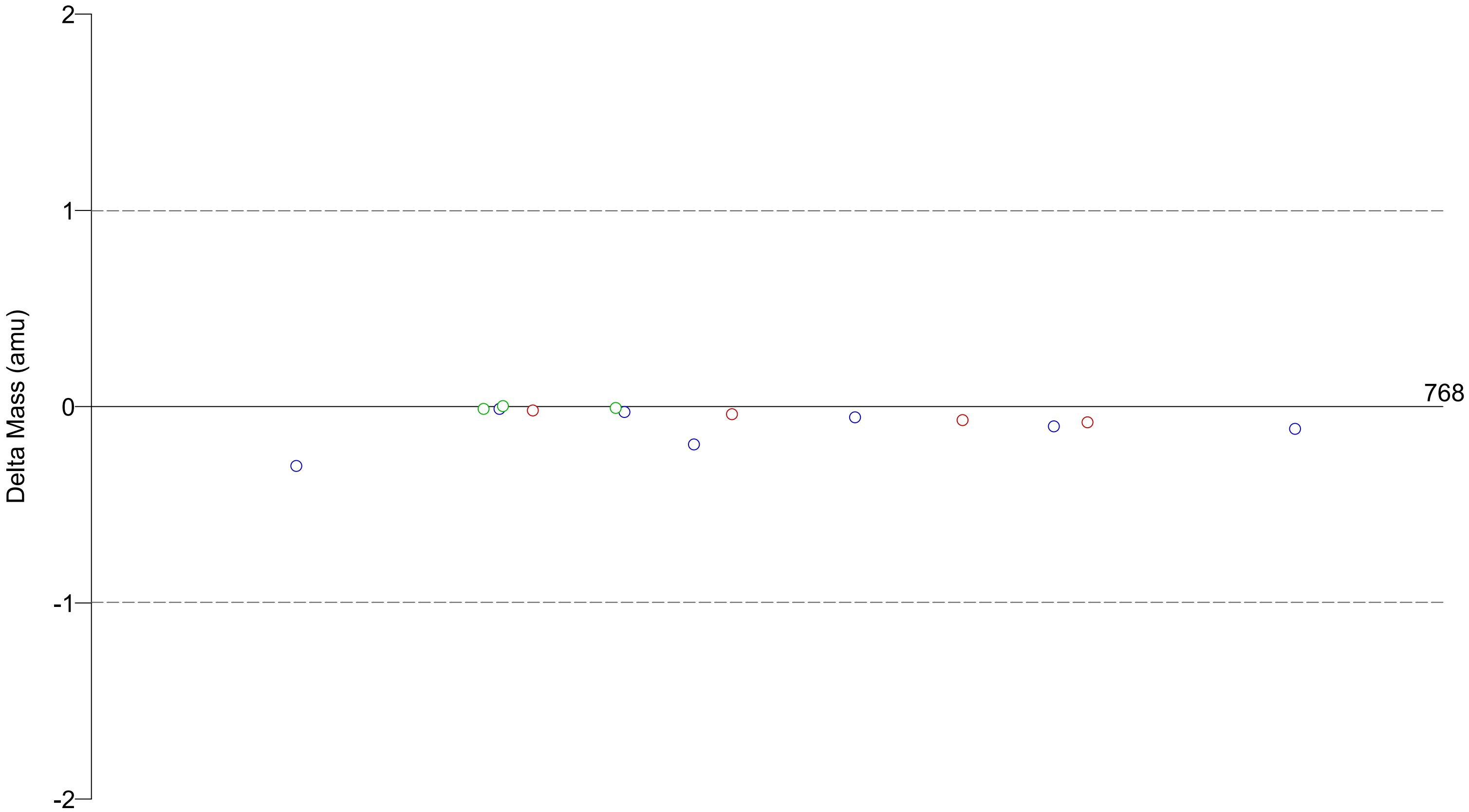


#19287468-1 NL: 3.32E5

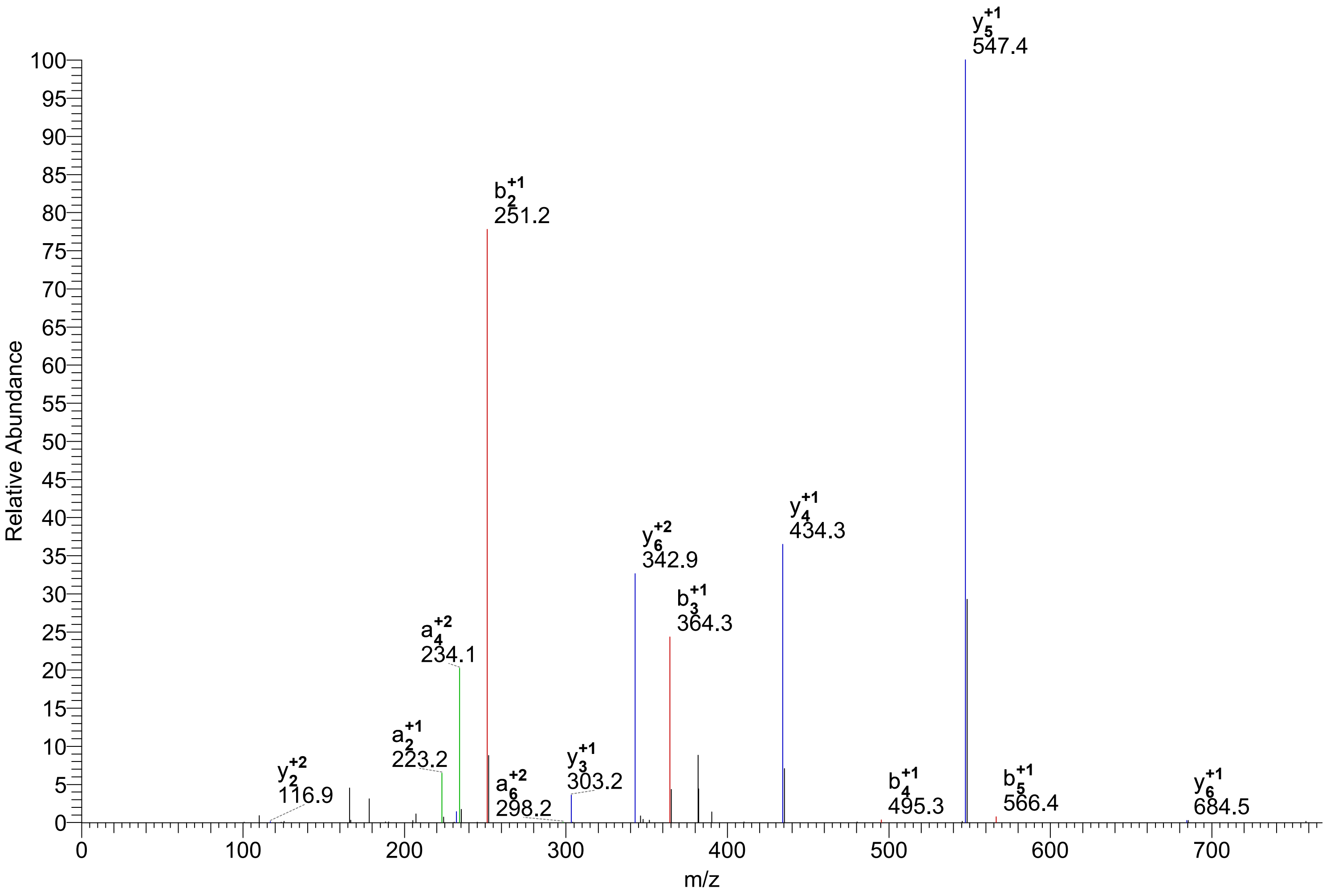


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00514542.1|TREMBL:Q5T017|EN                                 1       10.1     0.0       0
19287468 - 1  R.IHLMAGR.V                            797.45     2  0.07    2.141  0.000   350.3  1   10/18   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                       684.36
 L    336.24     364.23                                       547.30
 M    467.28     495.27                                       434.22
 A    538.32     566.31                                       303.18
 G    595.34     623.33                                       232.14
 R                                                            175.12
```

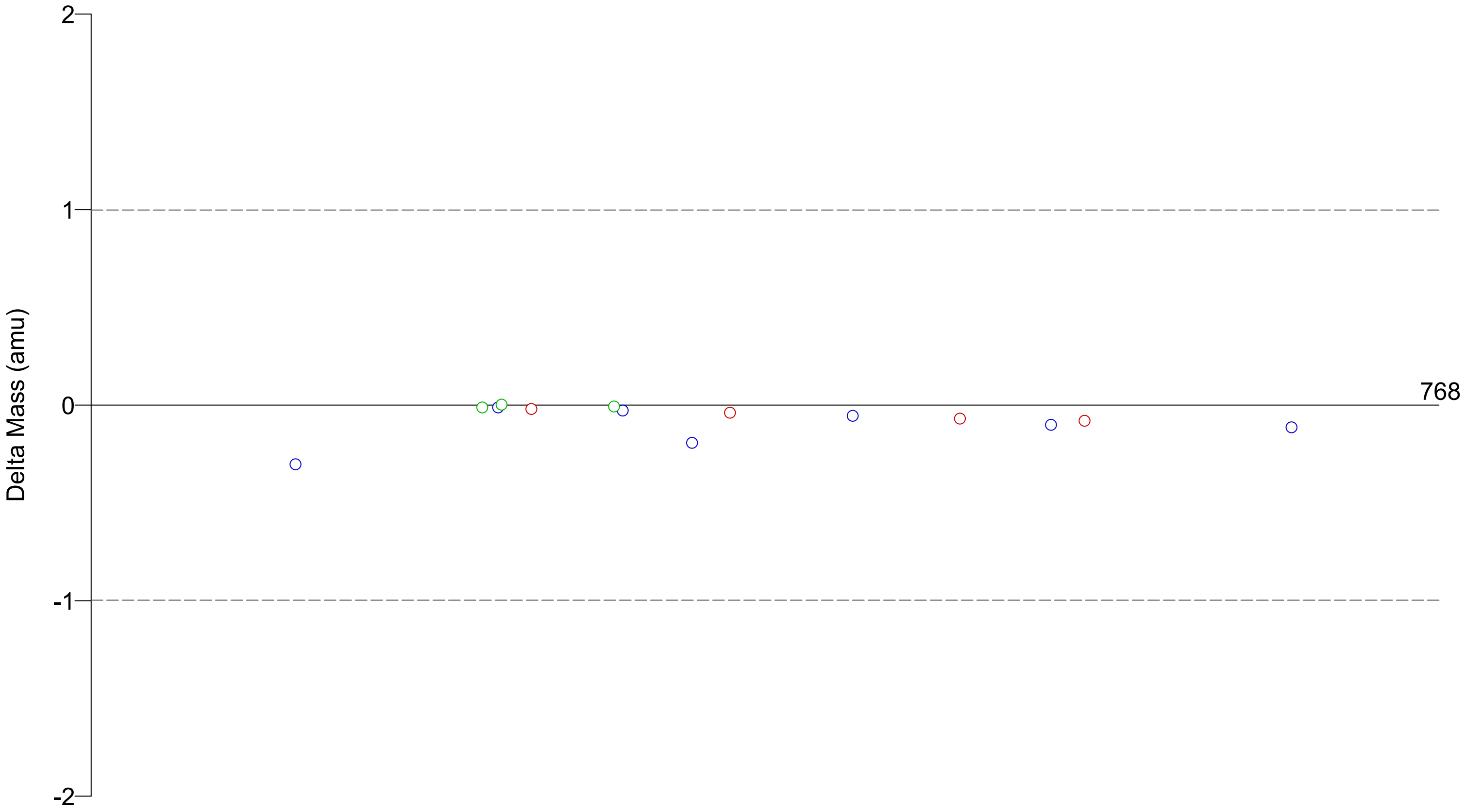


#19287468-1 NL: 3.32E5

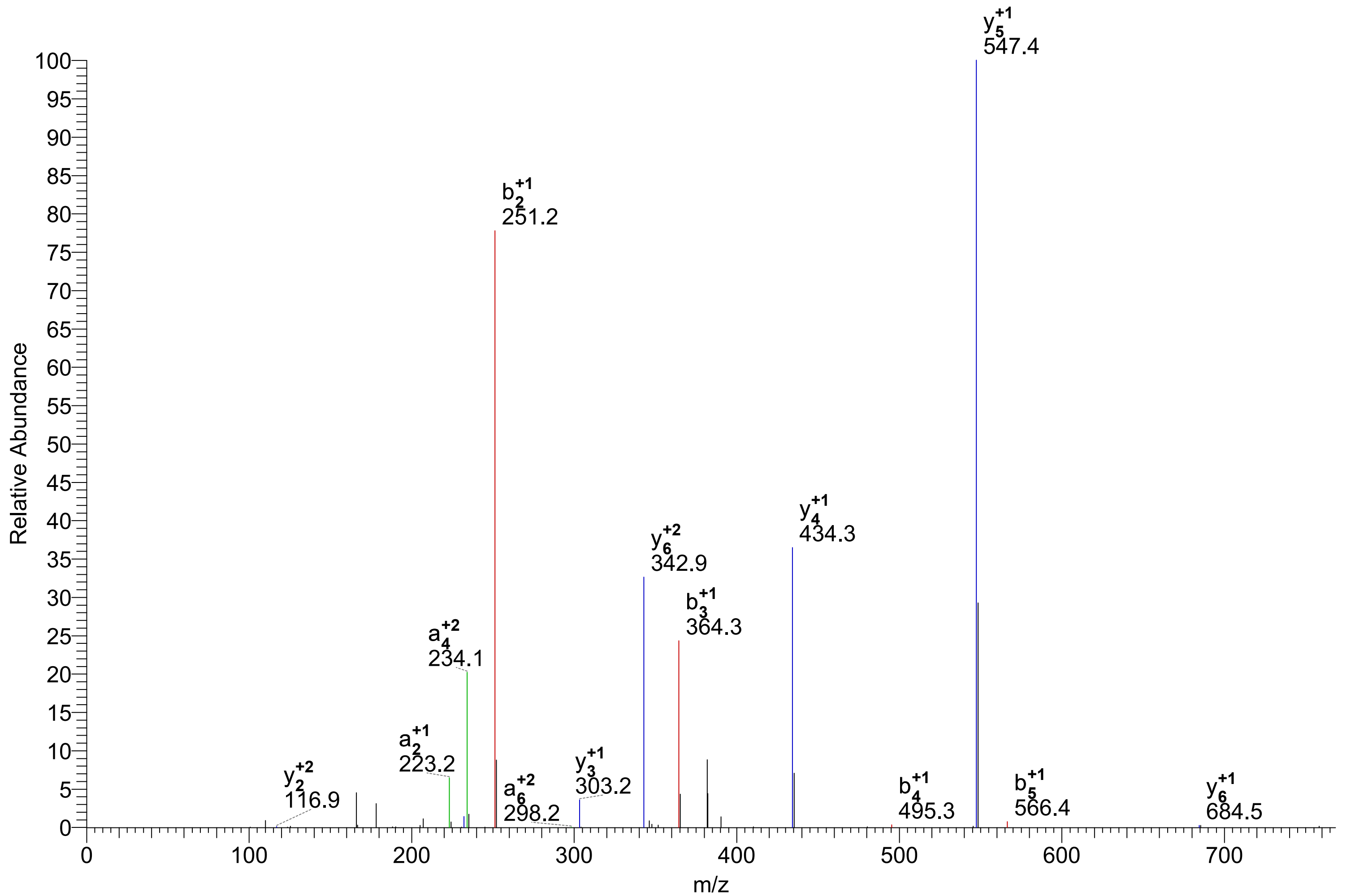


```
Reference                                                    P      Score   Coverage   Accession
Scan(s)       Sequence                              MH+      z     P       XC  DeltaCn    Sp    RSp  Ions   Count

IPI:IPI00647220.1|TREMBL:Q5T014|EN                                  1       10.1     0.0        0
19287468 - 1  R.IHLMAGR.V                         797.45     2  0.07     2.141  0.000   350.3  1   10/18   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                      684.36
 L    336.24     364.23                                      547.30
 M    467.28     495.27                                      434.22
 A    538.32     566.31                                      303.18
 G    595.34     623.33                                      232.14
 R                                                           175.12
```

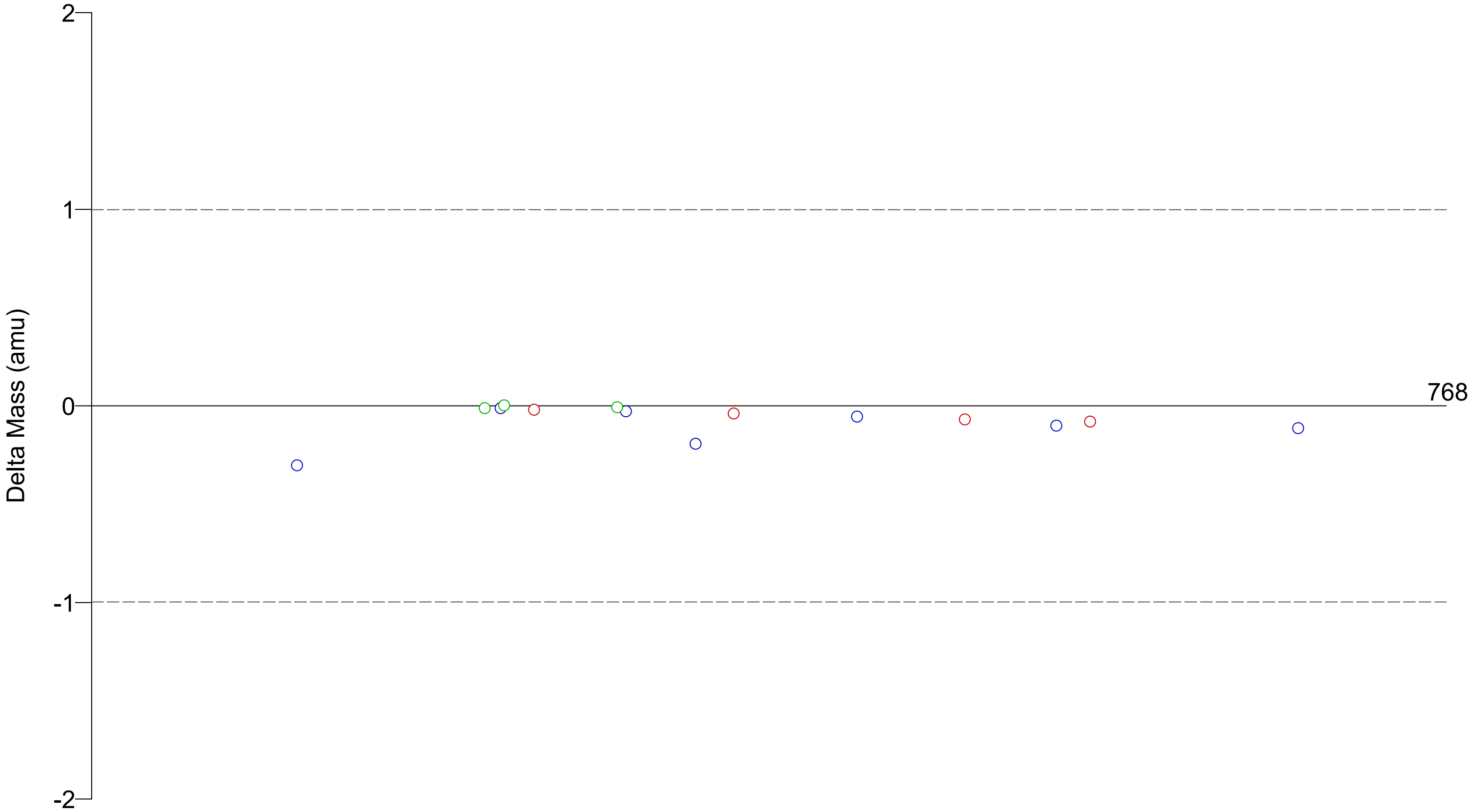


#19287468-1 NL: 3.32E5

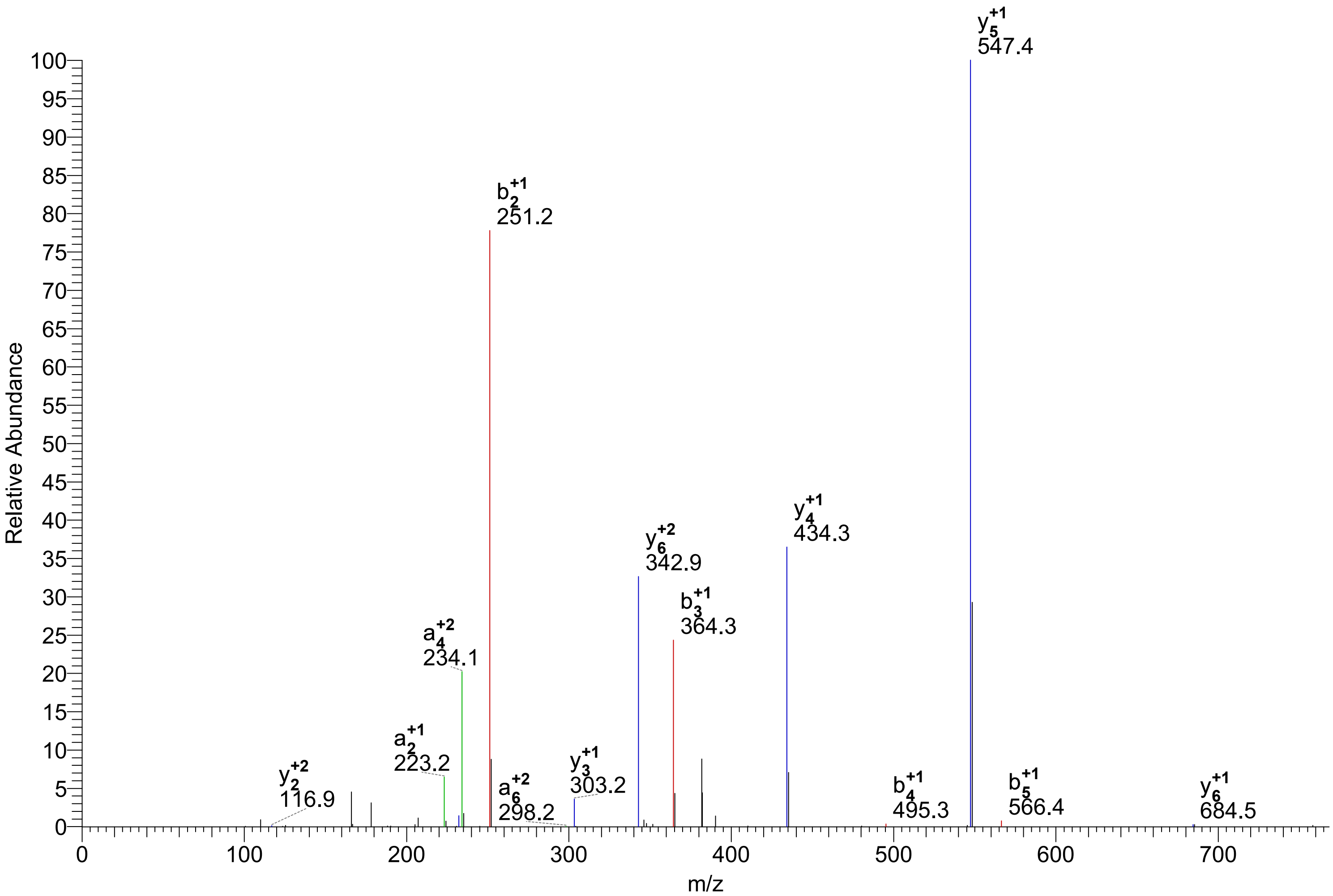


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)        Sequence                                 MH+       z    P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00743712.1|ENSEMBL:ENSP0000                                   1       10.1      0.0       0
19287468 - 1  R.IHLMAGR.V                              797.45     2  0.07     2.141  0.000   350.3  1   10/18    6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                     684.36
 L    336.24     364.23                                     547.30
 M    467.28     495.27                                     434.22
 A    538.32     566.31                                     303.18
 G    595.34     623.33                                     232.14
 R                                                          175.12
```

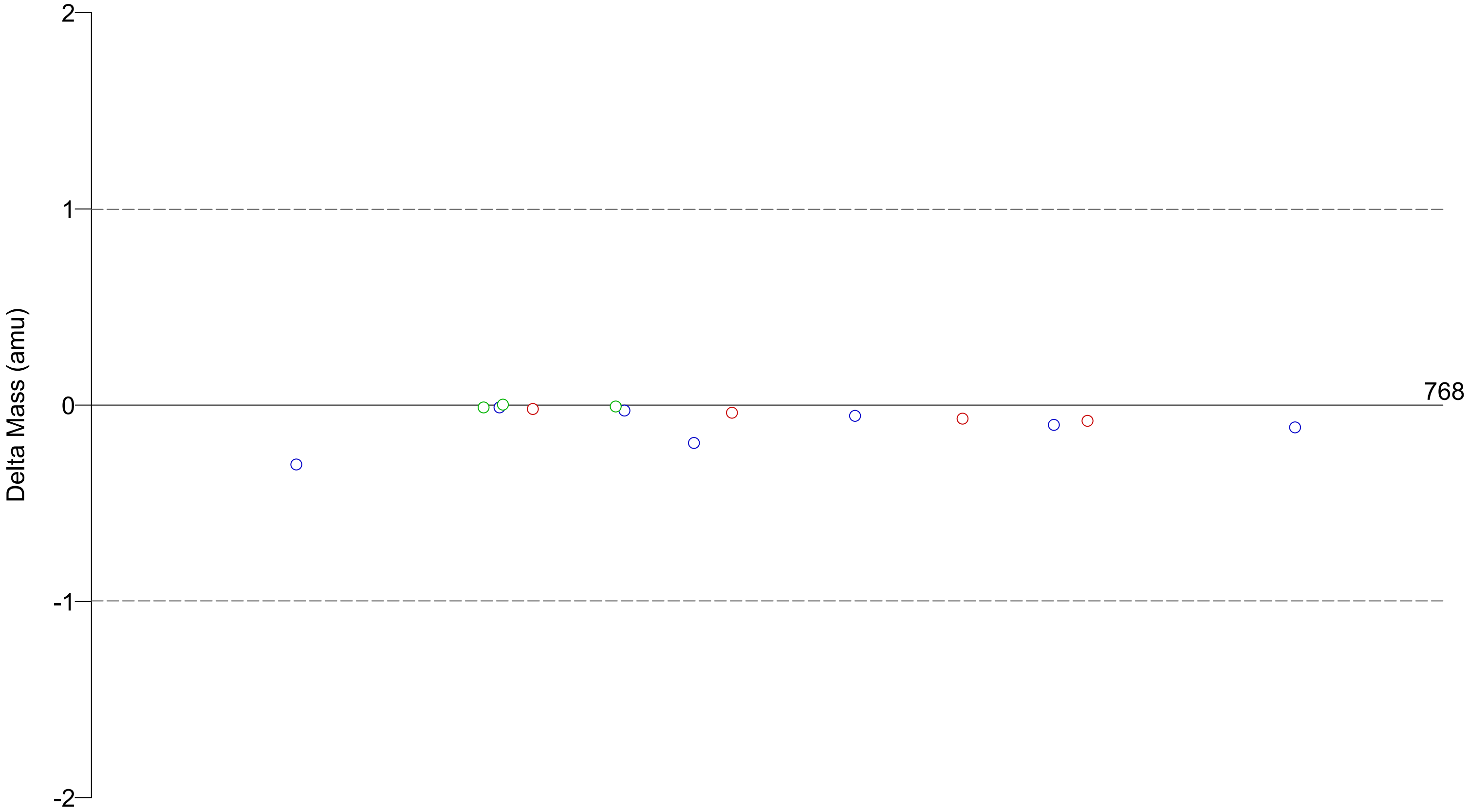


#19287468-1 NL: 3.32E5

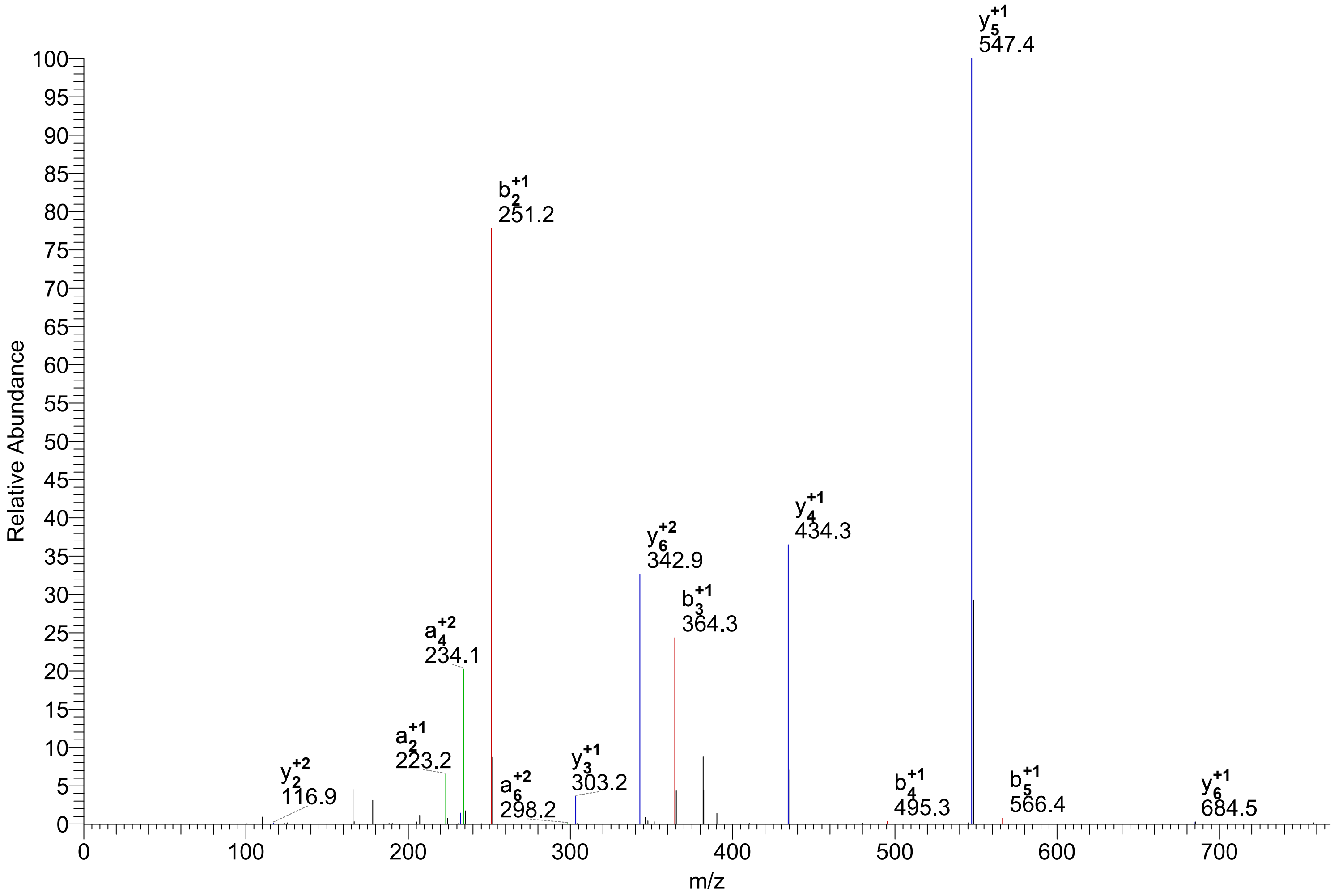


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P       XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00847938.1|SWISS-PROT:Q5T01                                     1       10.1     0.0        0
19287468 - 1  R.IHLMAGR.V                               797.45     2  0.07     2.141  0.000   350.3  1   10/18   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                      684.36
 L    336.24     364.23                                      547.30
 M    467.28     495.27                                      434.22
 A    538.32     566.31                                      303.18
 G    595.34     623.33                                      232.14
 R                                                           175.12
```

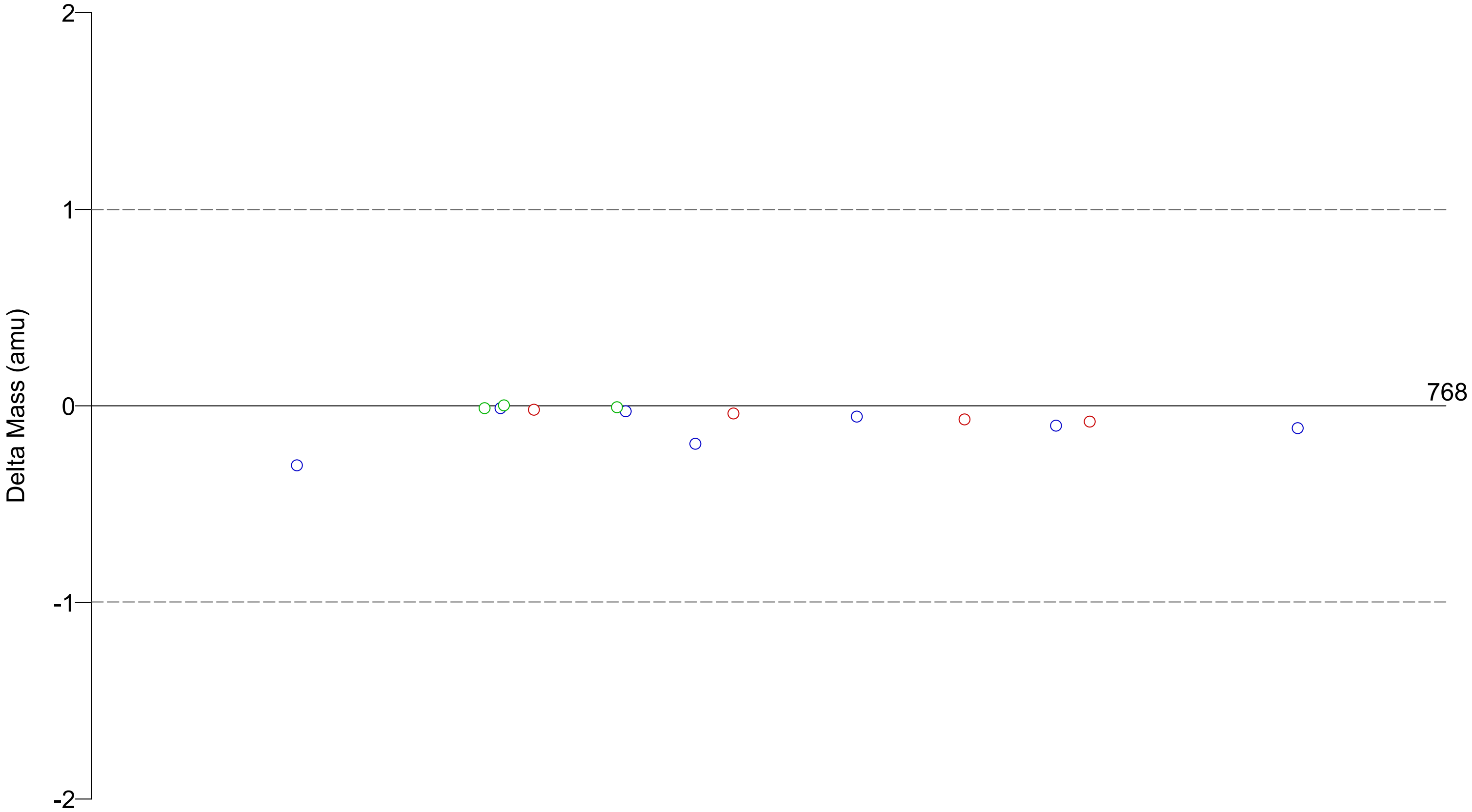


#19287468-1 NL: 3.32E5

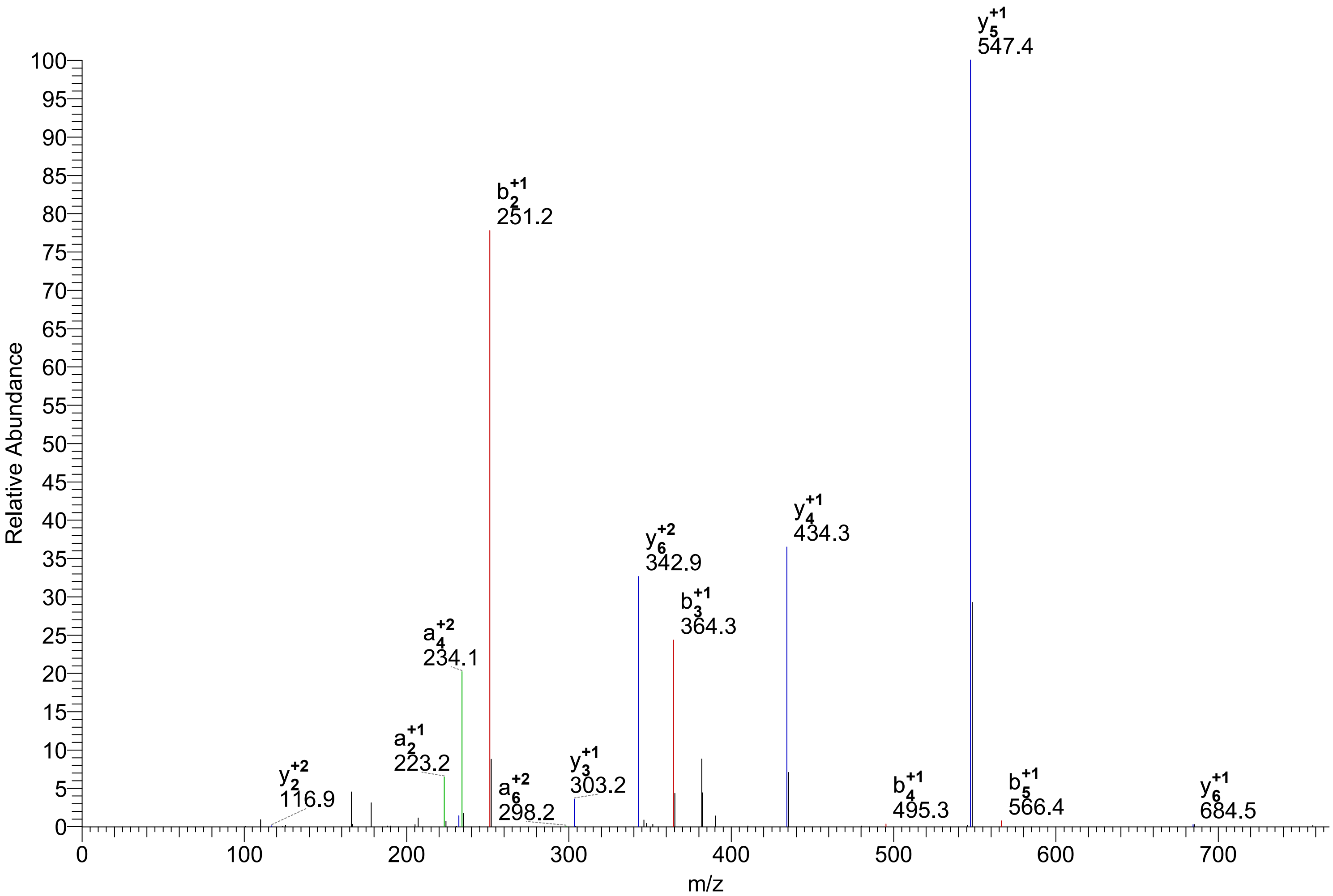


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00848045.1|SWISS-PROT:Q5T01                                1       10.1     0.0       0
19287468 - 1  R.IHLMAGR.V                            797.45    2  0.07    2.141  0.000   350.3  1   10/18   6

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 399.23
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                      684.36
 L    336.24     364.23                                      547.30
 M    467.28     495.27                                      434.22
 A    538.32     566.31                                      303.18
 G    595.34     623.33                                      232.14
 R                                                           175.12
```

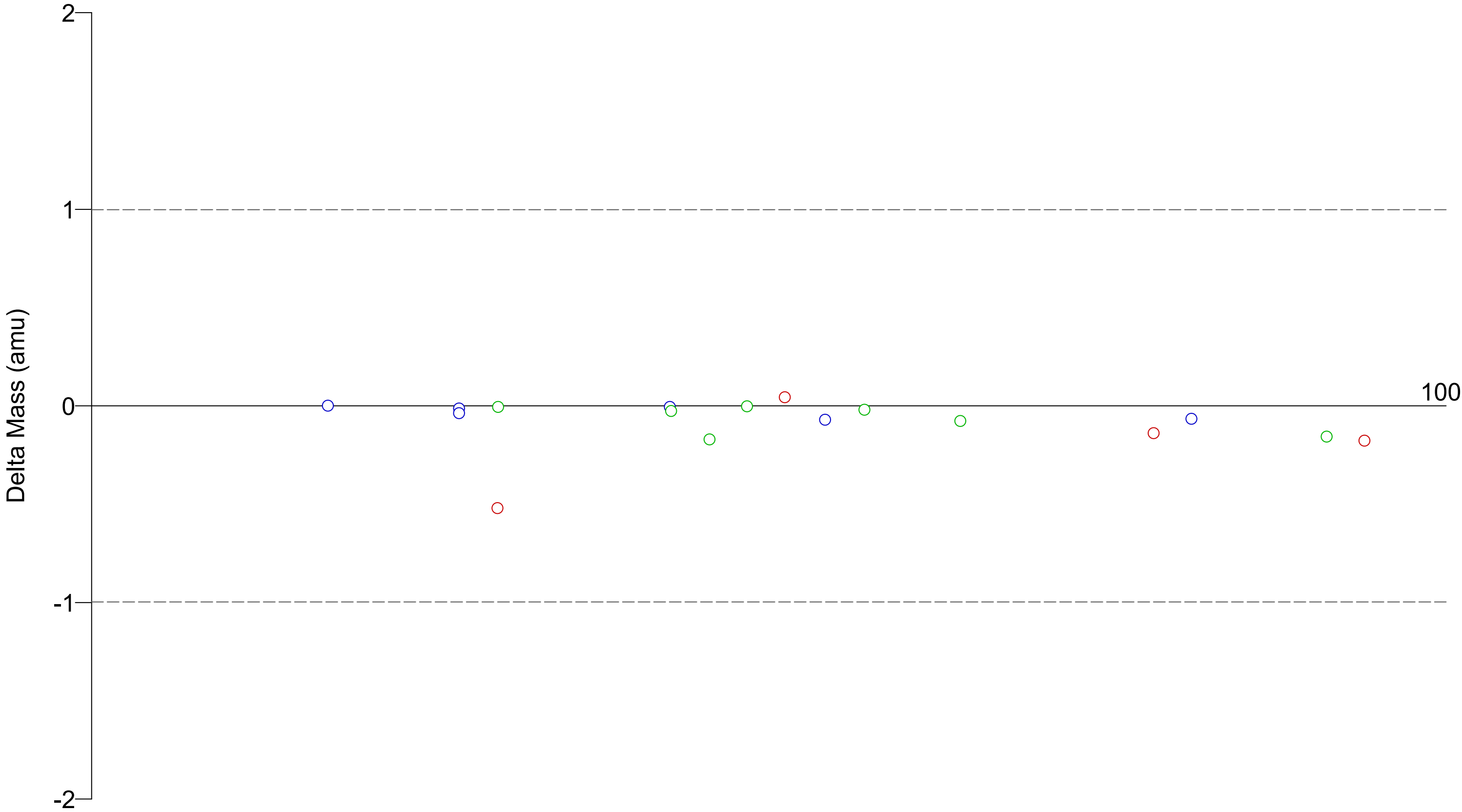


#19287468-1 NL: 3.32E5

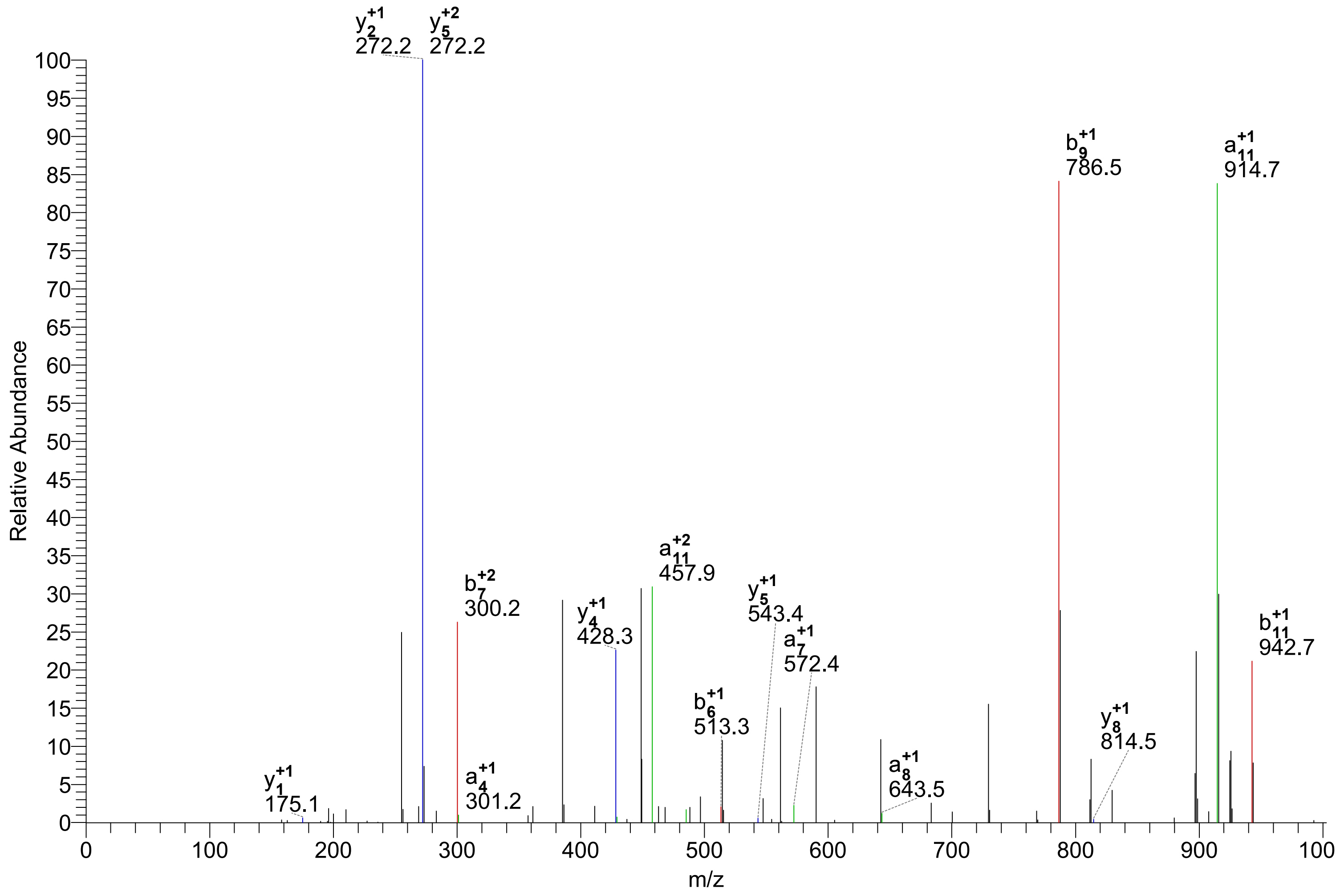


```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00655605.1|TREMBL:Q3C2D8|ENSEMBL:ENSP00000356952|REFSEQ    1       8.1      0.0       0
19287468 - 1  R.GTGIALSADVGPR.K                       1213.65   2  1       2.499  0.397   295.1  4   13/36   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03     58.03
 T    131.08    159.08                                     1156.63
 G    188.10    216.10                                     1055.58
 I    301.19    329.18                                      998.56
 A    372.22    400.22                                      885.48
 L    485.31    513.30                                      814.44
 S    572.34    600.34                                      701.36
 A    643.38    671.37                                      614.33
 D    758.40    786.40                                      543.29
 V    857.47    885.47                                      428.26
 G    914.49    942.49                                      329.19
 P   1011.55   1039.54                                      272.17
 R                                                          175.12
```

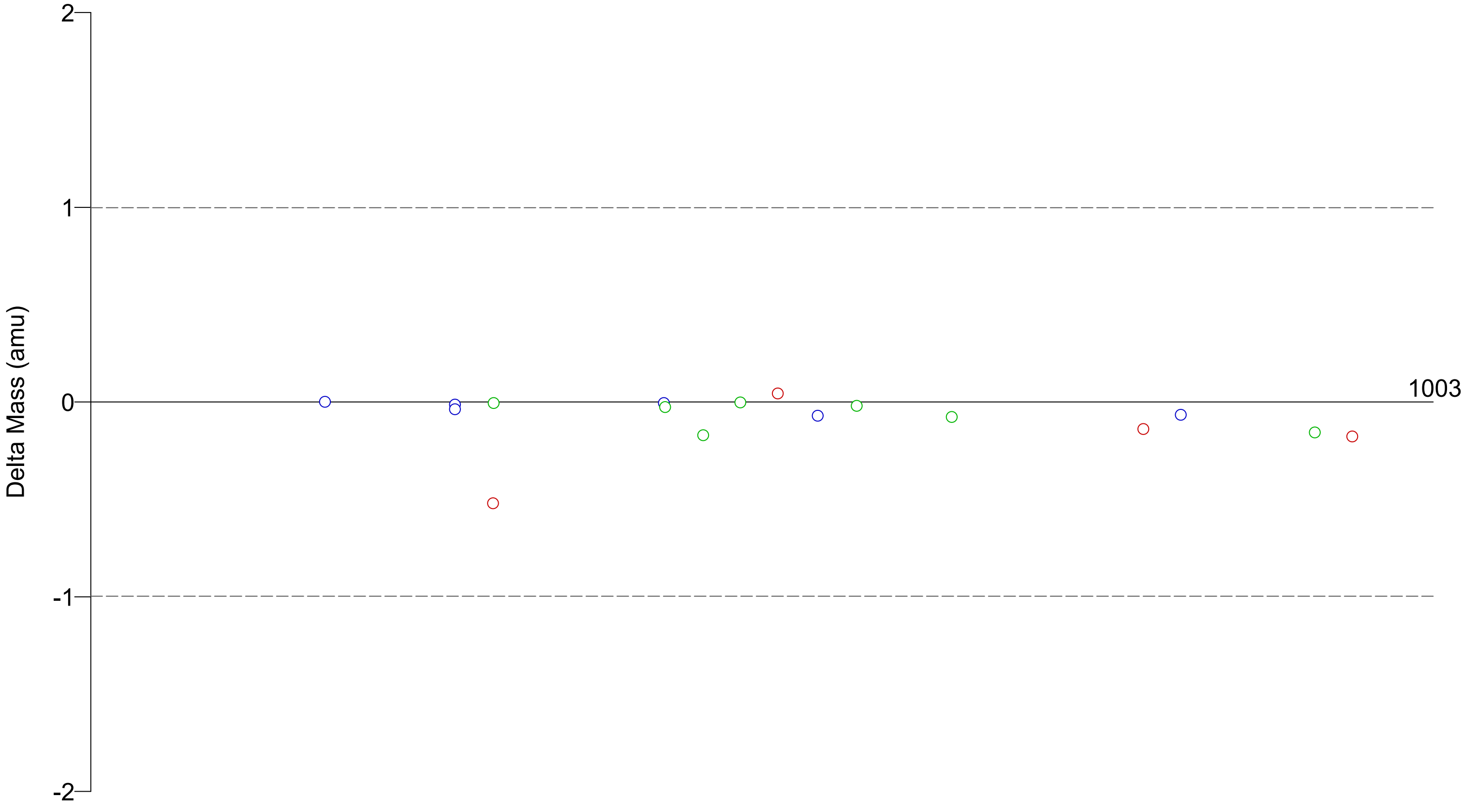


#19287468-1 NL: 1.26E5

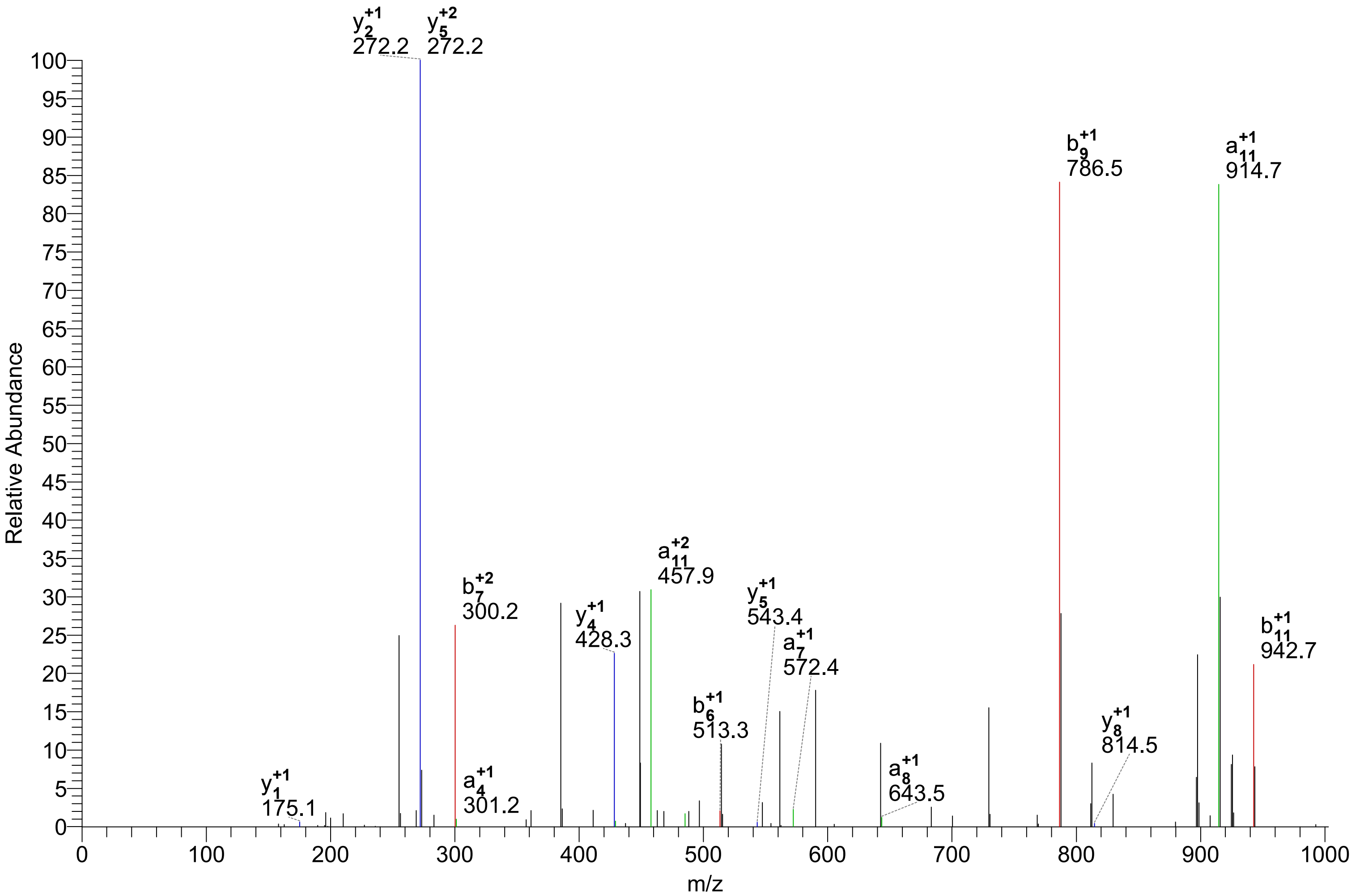


```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00655889.1|TREMBL:Q3C259|RE                                       1       8.1      0.0       0
19287468 - 1  R.GTGIALSADVGPR.K                          1213.65   2  1       2.499  0.397   295.1  4   13/36   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 607.32
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 T    131.08     159.08                                     1156.63
 G    188.10     216.10                                     1055.58
 I    301.19     329.18                                      998.56
 A    372.22     400.22                                      885.48
 L    485.31     513.30                                      814.44
 S    572.34     600.34                                      701.36
 A    643.38     671.37                                      614.33
 D    758.40     786.40                                      543.29
 V    857.47     885.47                                      428.26
 G    914.49     942.49                                      329.19
 P   1011.55    1039.54                                      272.17
 R                                                           175.12
```

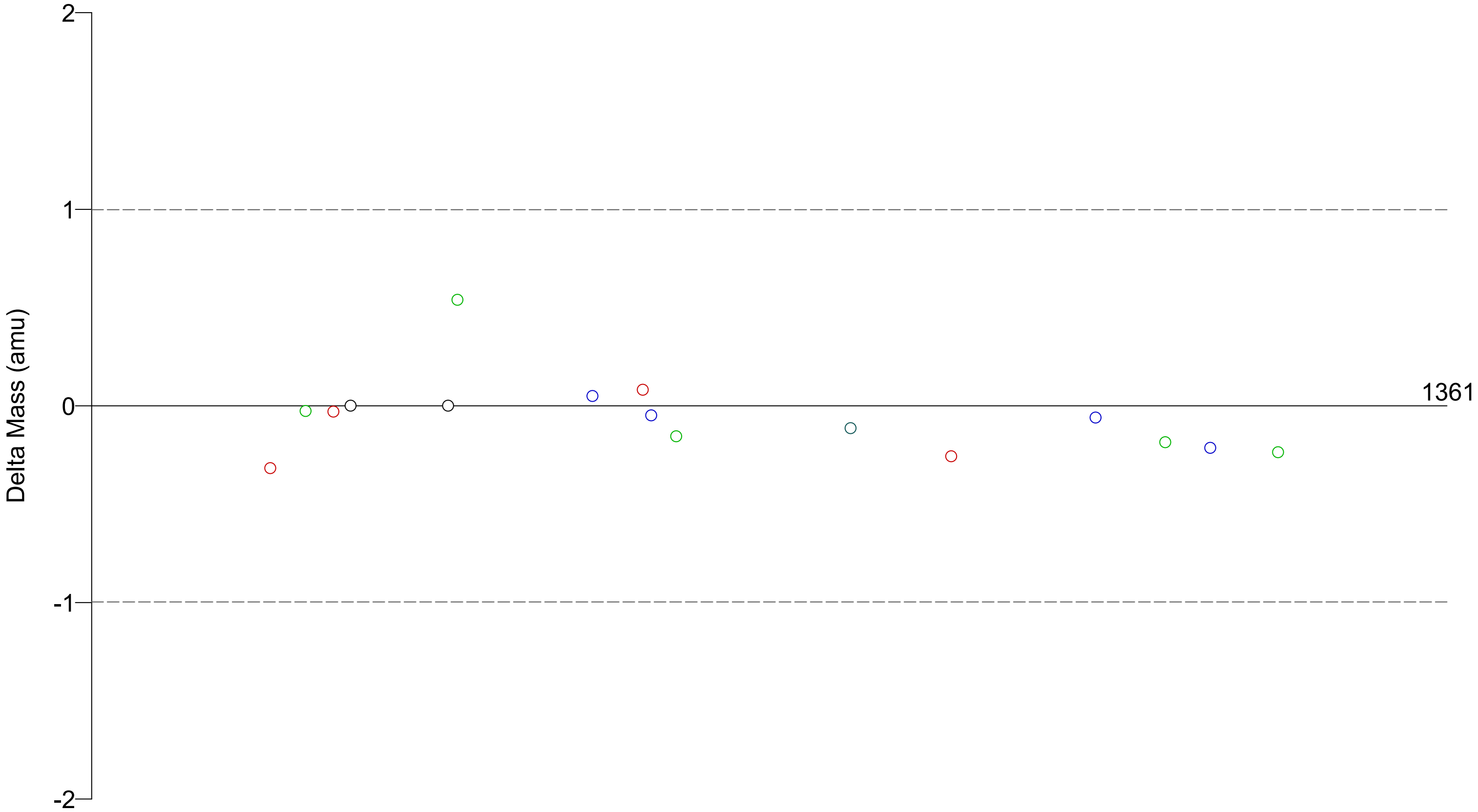


#19287468-1 NL: 1.26E5

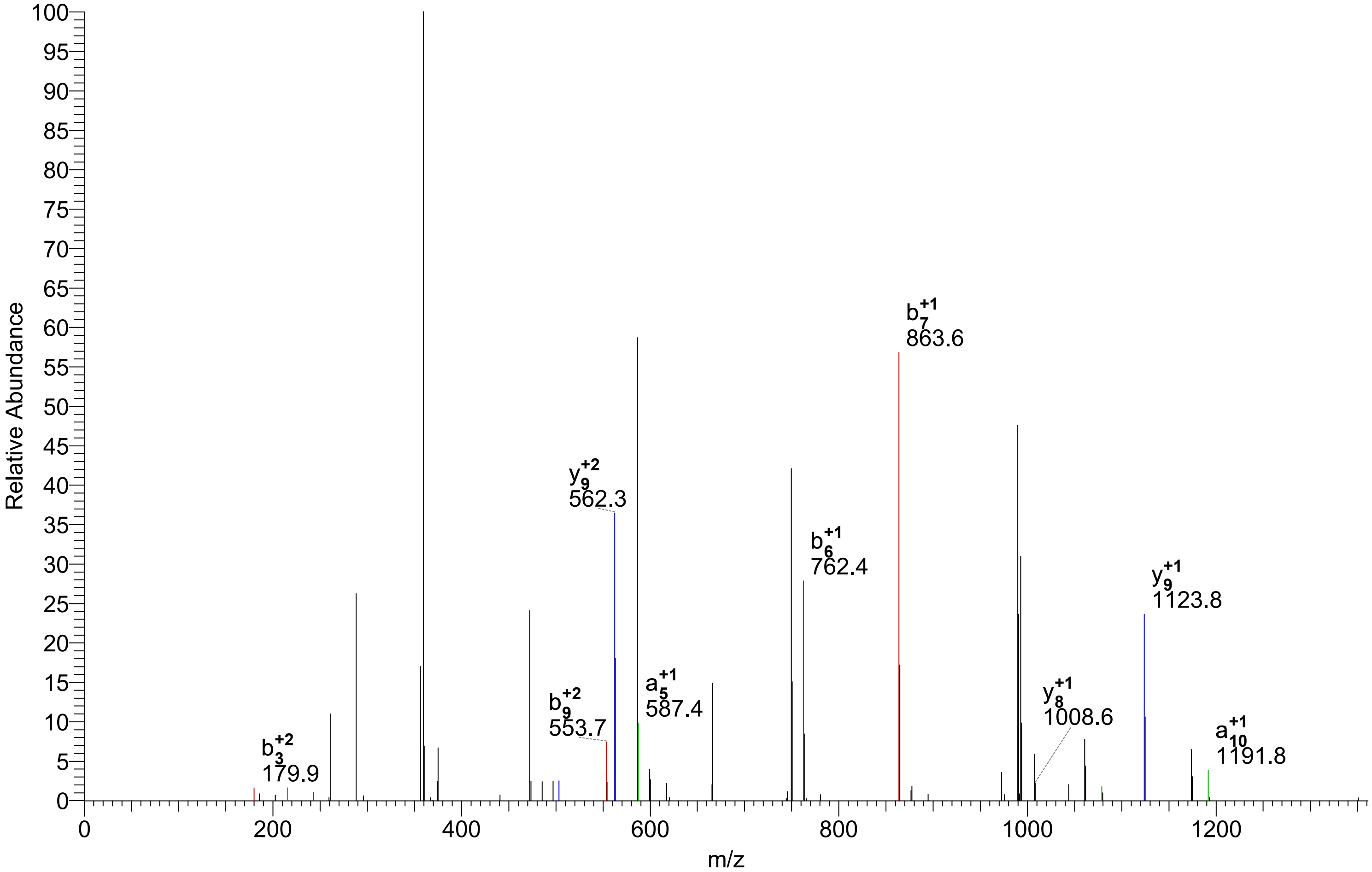


```
Reference                                                              P      Score   Coverage   Accession
Scan(s)        Sequence                                     MH+      z     P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00740527.3|SWISS-PROT:A8MUQ0|REFSEQ:XP_001717830 Tax_Id     1        8.1      0.0        0
19287468 - 1  R.NQDTRM*TSRLK.F                           1365.69   2  1        1.969  0.491   279.0  2   12/30   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 683.35
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 Q    215.11    243.11                                     1251.65
 D    330.14    358.14                                     1123.59
 T    431.19    459.18                                     1008.56
 R    587.29    615.28                                      907.51
 M*   734.33    762.32                                      751.41
 T    835.37    863.37                                      604.38
 S    922.40    950.40                                      503.33
 R   1078.51   1106.50                                      416.30
 L   1191.59   1219.58                                      260.20
 K                                                          147.11
```

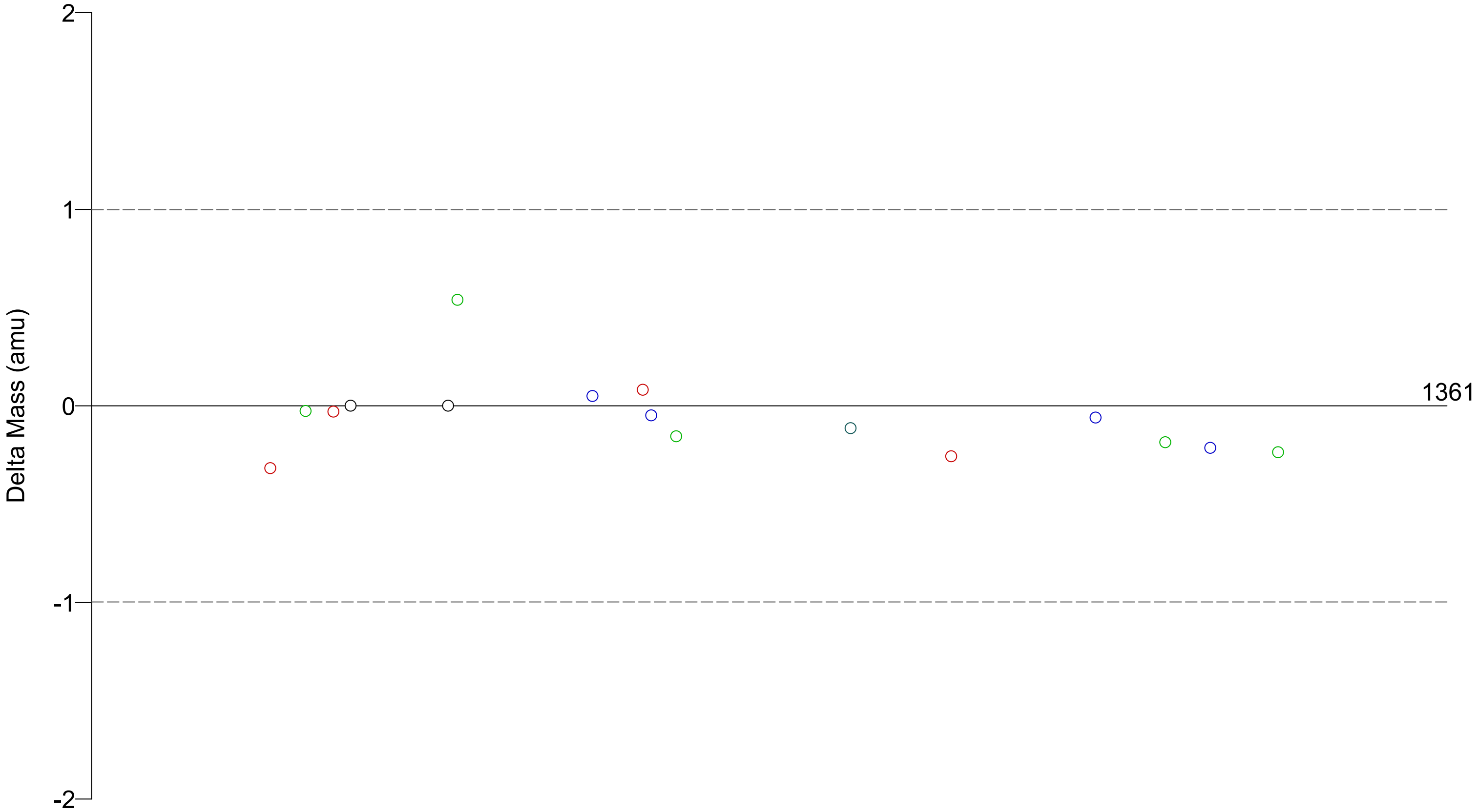


#19287468-1 NL: 1.28E5

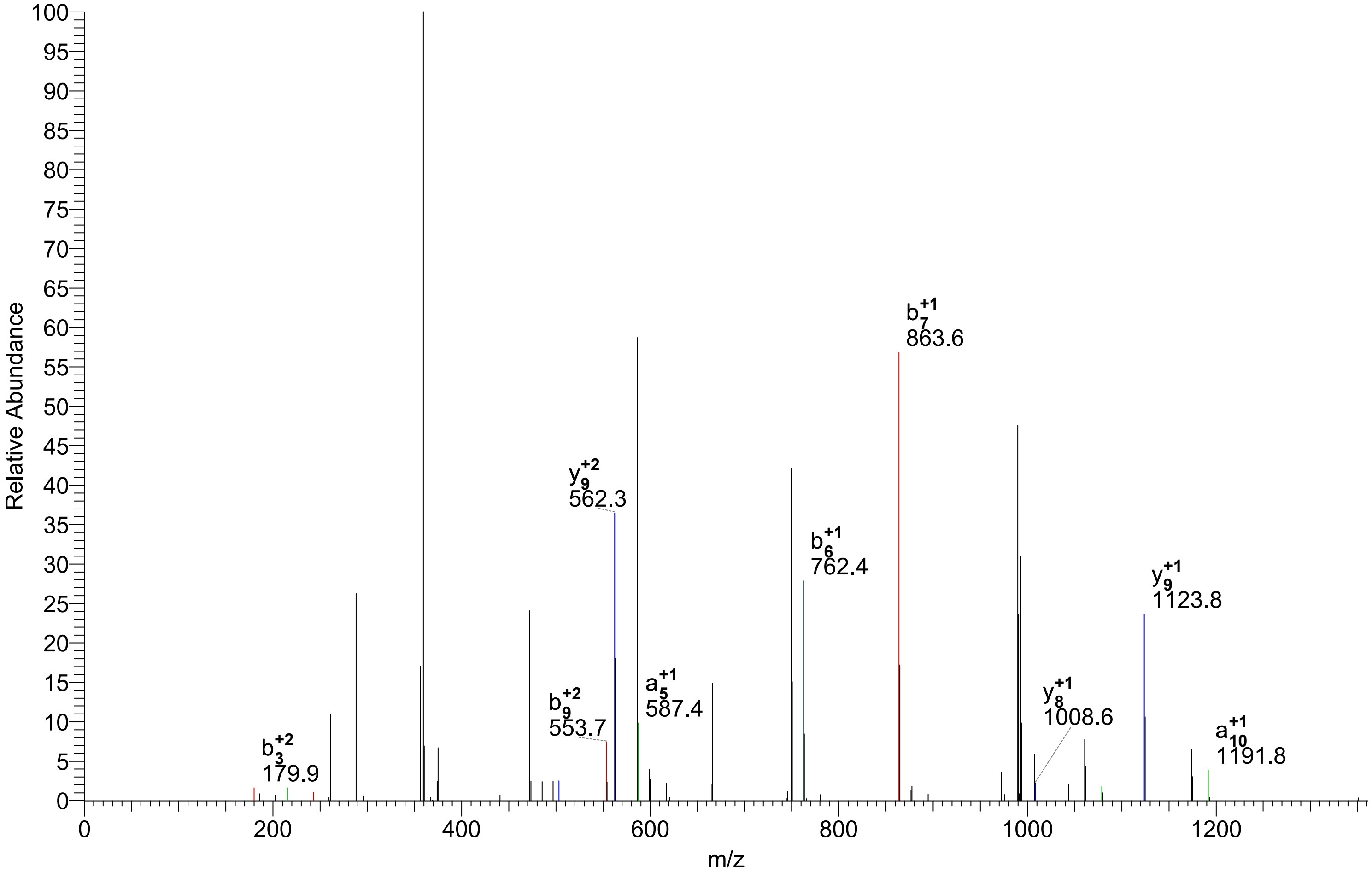


```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

IPI:IPI00888926.1|REFSEQ:XP_943402                                        1       8.1      0.0       0
19287468 - 1  R.NQDTRM*TSRLK.F                            1365.69   2  1       1.969  0.491   279.0  2   12/30   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 683.35
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 N     87.06     115.05
 Q    215.11     243.11                                     1251.65
 D    330.14     358.14                                     1123.59
 T    431.19     459.18                                     1008.56
 R    587.29     615.28                                      907.51
 M*   734.33     762.32                                      751.41
 T    835.37     863.37                                      604.38
 S    922.40     950.40                                      503.33
 R   1078.51    1106.50                                      416.30
 L   1191.59    1219.58                                      260.20
 K                                                           147.11
```

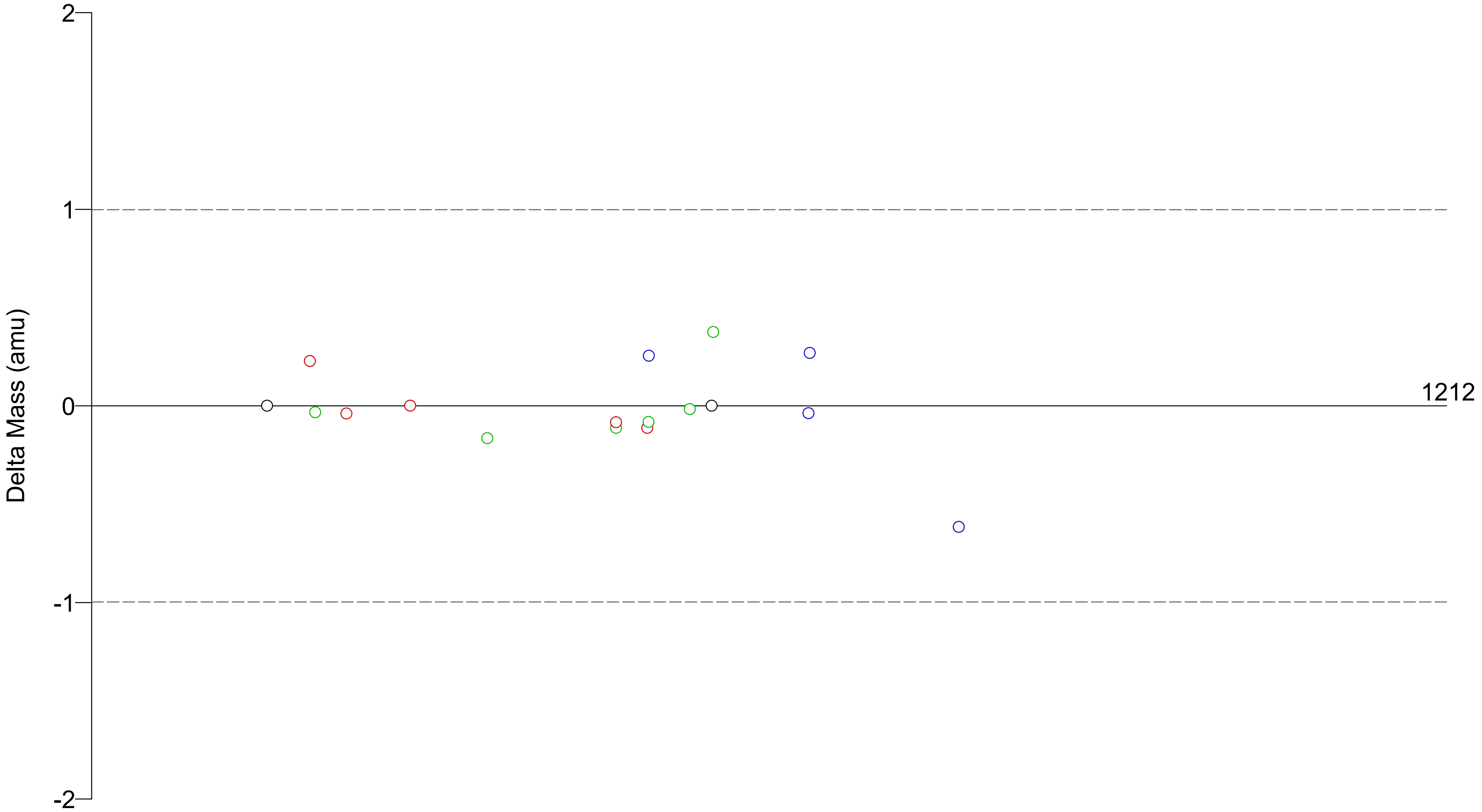


#19287468-1 NL: 1.28E5

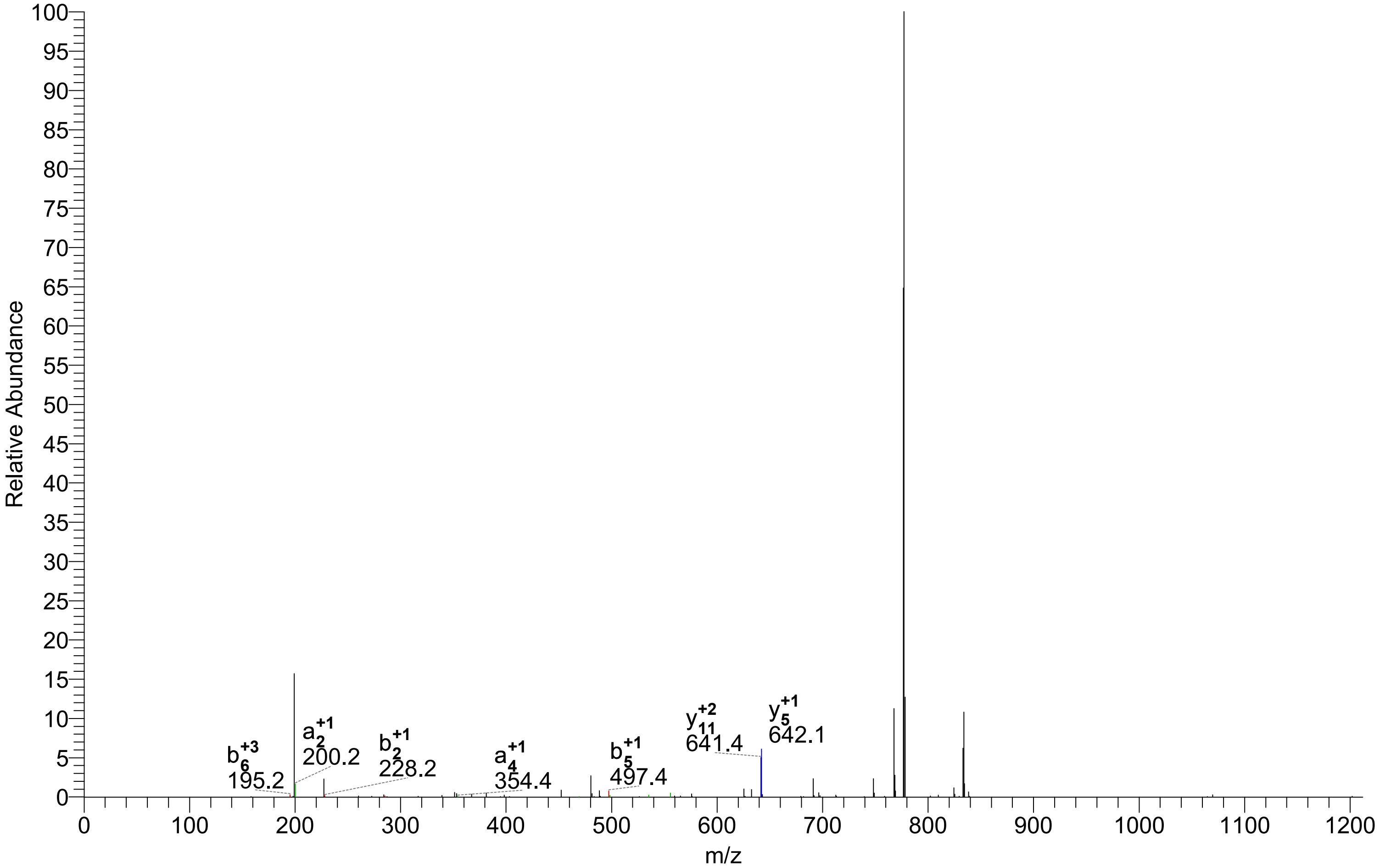


```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00103871.3|SWISS-PROT:Q8WZ75-1|ENSEMBL:ENSP00000304945|    1       8.1      0.0       0
19287468 - 1  R.ARGPDSNVLLLRLPEK.V                     1778.03   3  1       1.316  0.491   55.0   6   14/90   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 R    200.15     228.15                                     1706.99
 G    257.17     285.17                                     1550.89
 P    354.22     382.22                                     1493.87
 D    469.25     497.25                                     1396.82
 S    556.28     584.28                                     1281.79
 N    670.33     698.32                                     1194.76
 V    769.40     797.39                                     1080.71
 L    882.48     910.47                                      981.65
 L    995.56    1023.56                                      868.56
 L   1108.65    1136.64                                      755.48
 R   1264.75    1292.74                                      642.39
 L   1377.83    1405.83                                      486.29
 P   1474.89    1502.88                                      373.21
 E   1603.93    1631.92                                      276.16
 K                                                           147.11
```

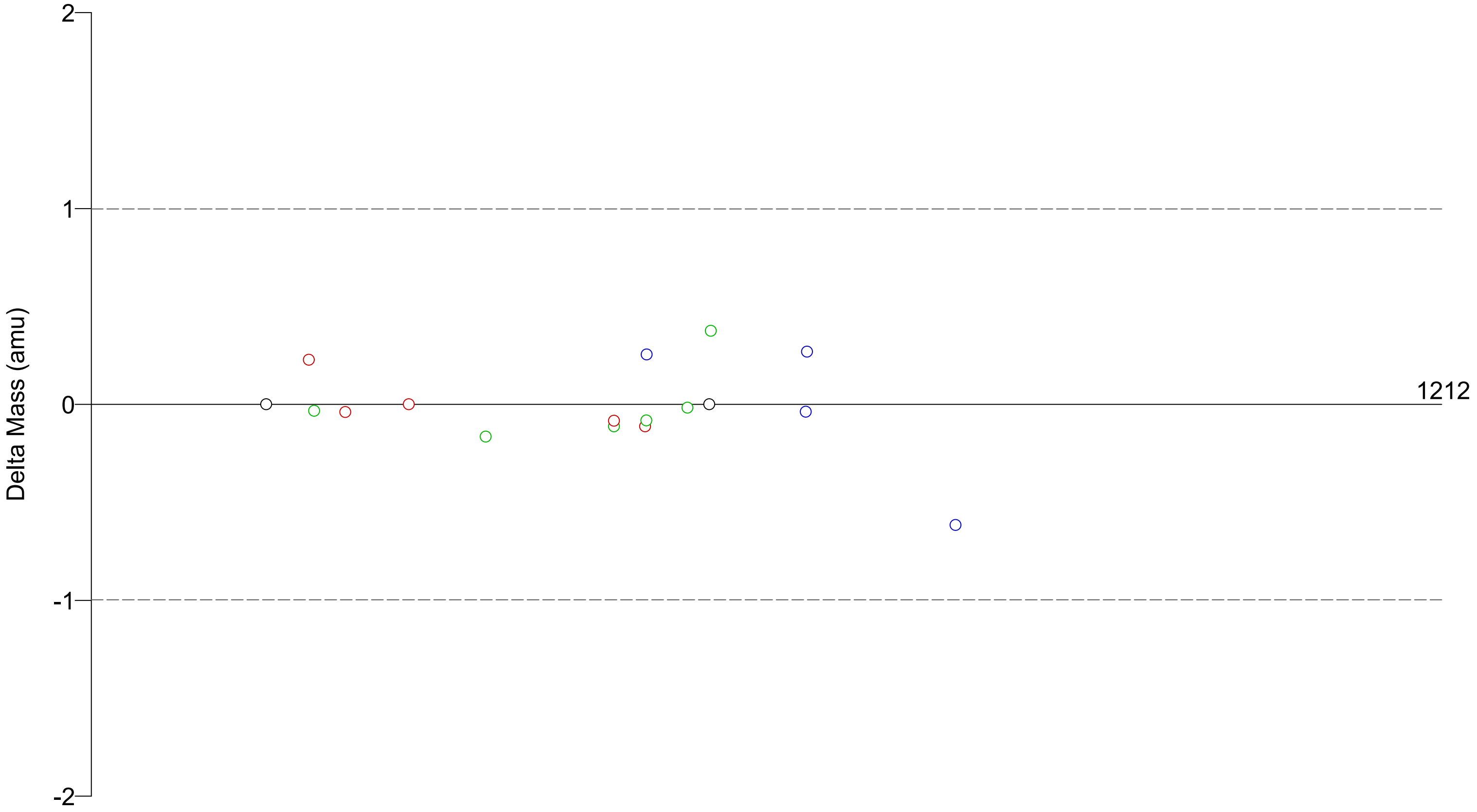


#19287468-1 NL: 6.49E5

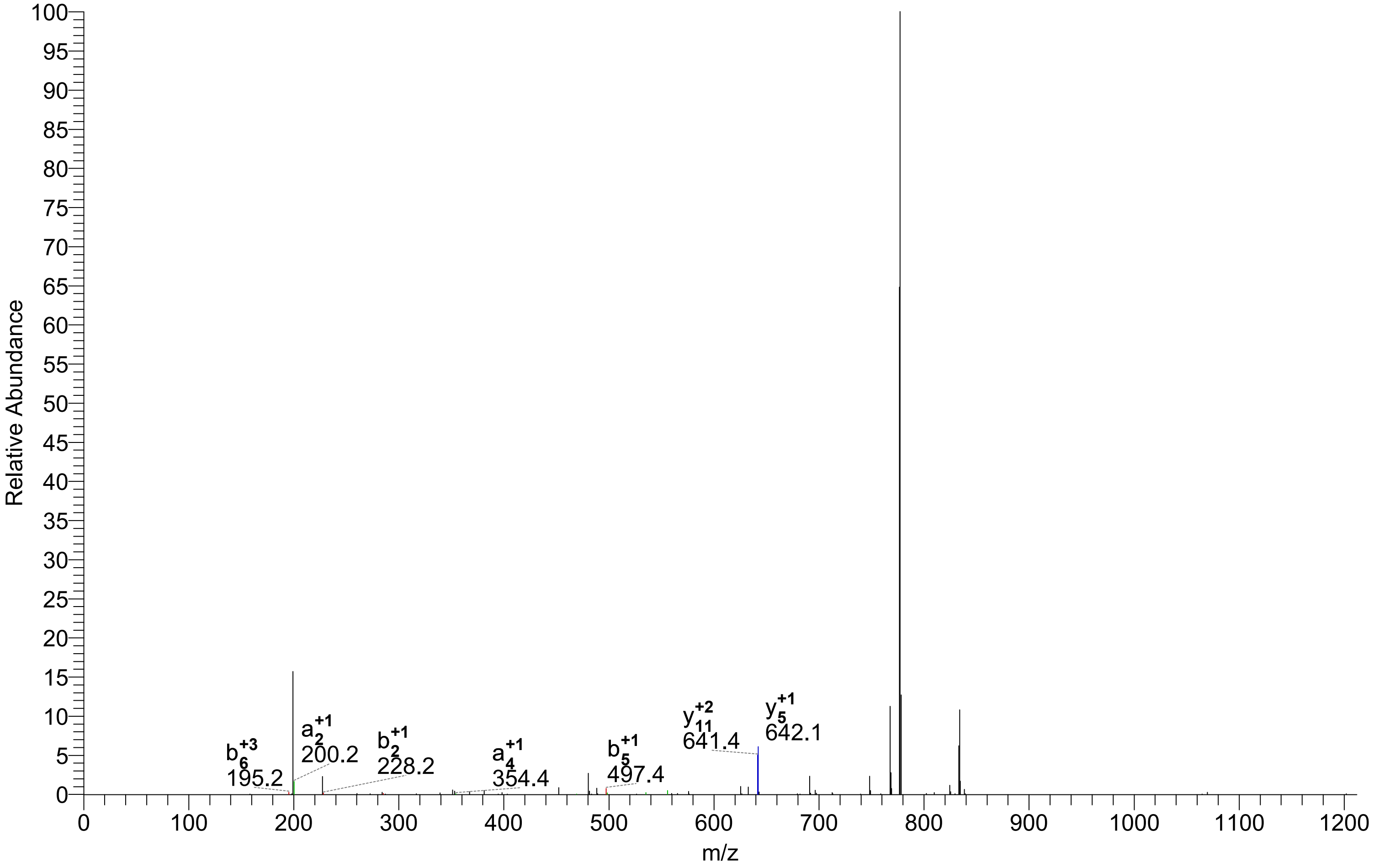


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00179778.1|TREMBL:B4DNB7;B5                                1       8.1      0.0       0
19287468 - 1  R.ARGPDSNVLLLRLPEK.V                   1778.03   3  1       1.316  0.491   55.0   6   14/90   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 R    200.15     228.15                                     1706.99
 G    257.17     285.17                                     1550.89
 P    354.22     382.22                                     1493.87
 D    469.25     497.25                                     1396.82
 S    556.28     584.28                                     1281.79
 N    670.33     698.32                                     1194.76
 V    769.40     797.39                                     1080.71
 L    882.48     910.47                                      981.65
 L    995.56    1023.56                                      868.56
 L   1108.65    1136.64                                      755.48
 R   1264.75    1292.74                                      642.39
 L   1377.83    1405.83                                      486.29
 P   1474.89    1502.88                                      373.21
 E   1603.93    1631.92                                      276.16
 K                                                           147.11
```

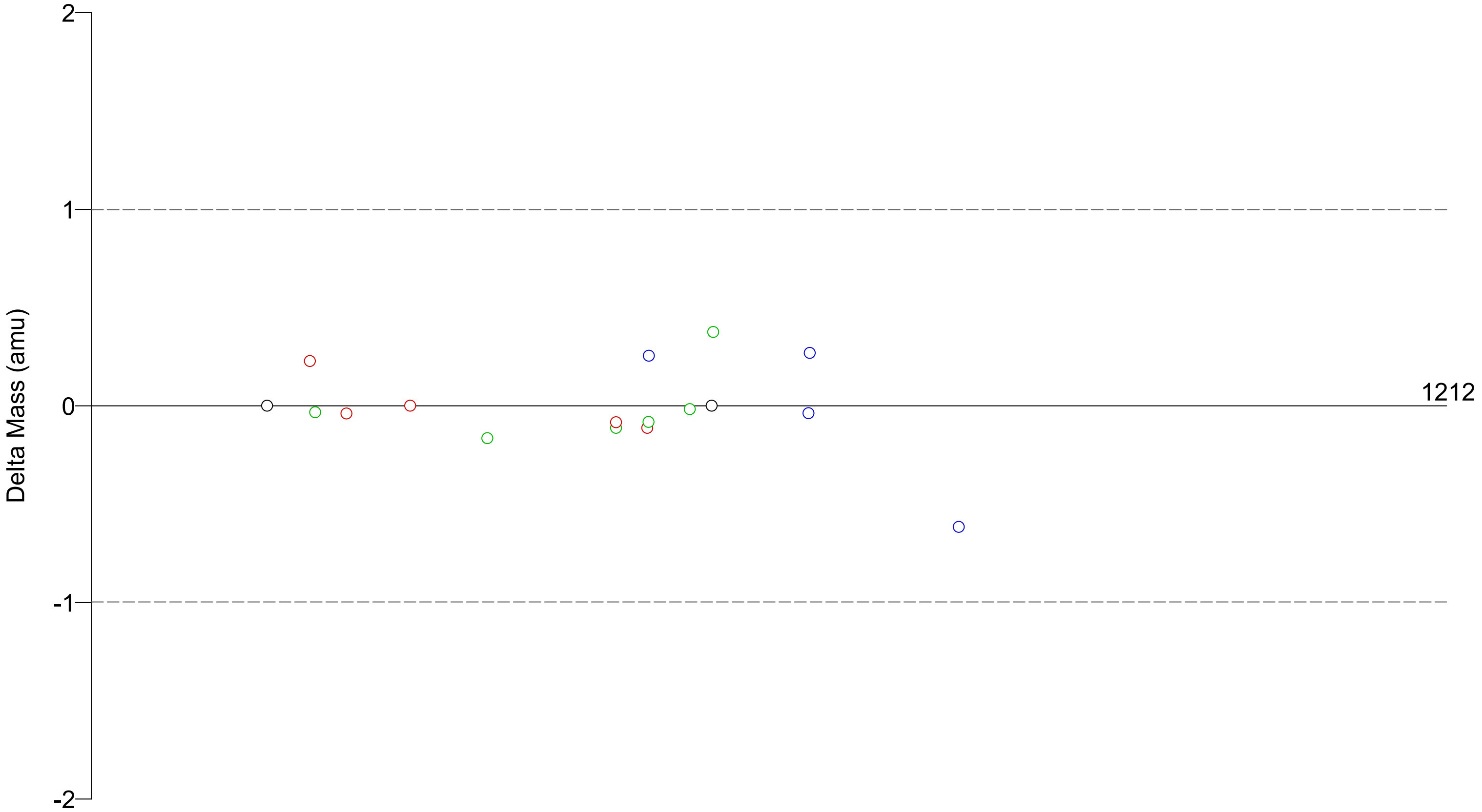


#19287468-1 NL: 6.49E5

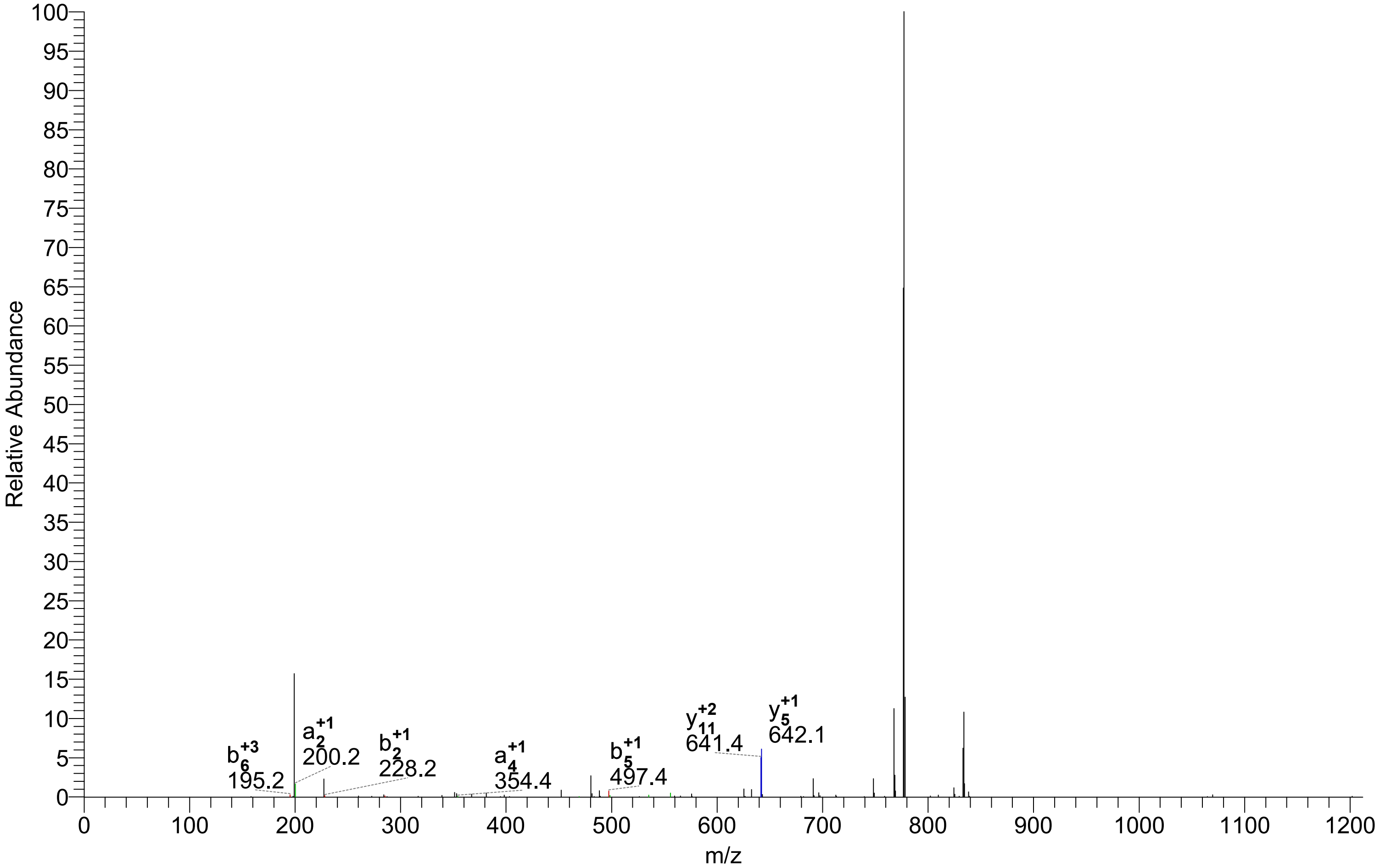


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00418144.1|SWISS-PROT:Q8WZ7                                1       8.1      0.0       0
19287468 - 1  R.ARGPDSNVLLLRLPEK.V                   1778.03   3  1       1.316  0.491   55.0  6   14/90   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 R    200.15     228.15                                     1706.99
 G    257.17     285.17                                     1550.89
 P    354.22     382.22                                     1493.87
 D    469.25     497.25                                     1396.82
 S    556.28     584.28                                     1281.79
 N    670.33     698.32                                     1194.76
 V    769.40     797.39                                     1080.71
 L    882.48     910.47                                      981.65
 L    995.56    1023.56                                      868.56
 L   1108.65    1136.64                                      755.48
 R   1264.75    1292.74                                      642.39
 L   1377.83    1405.83                                      486.29
 P   1474.89    1502.88                                      373.21
 E   1603.93    1631.92                                      276.16
 K                                                           147.11
```

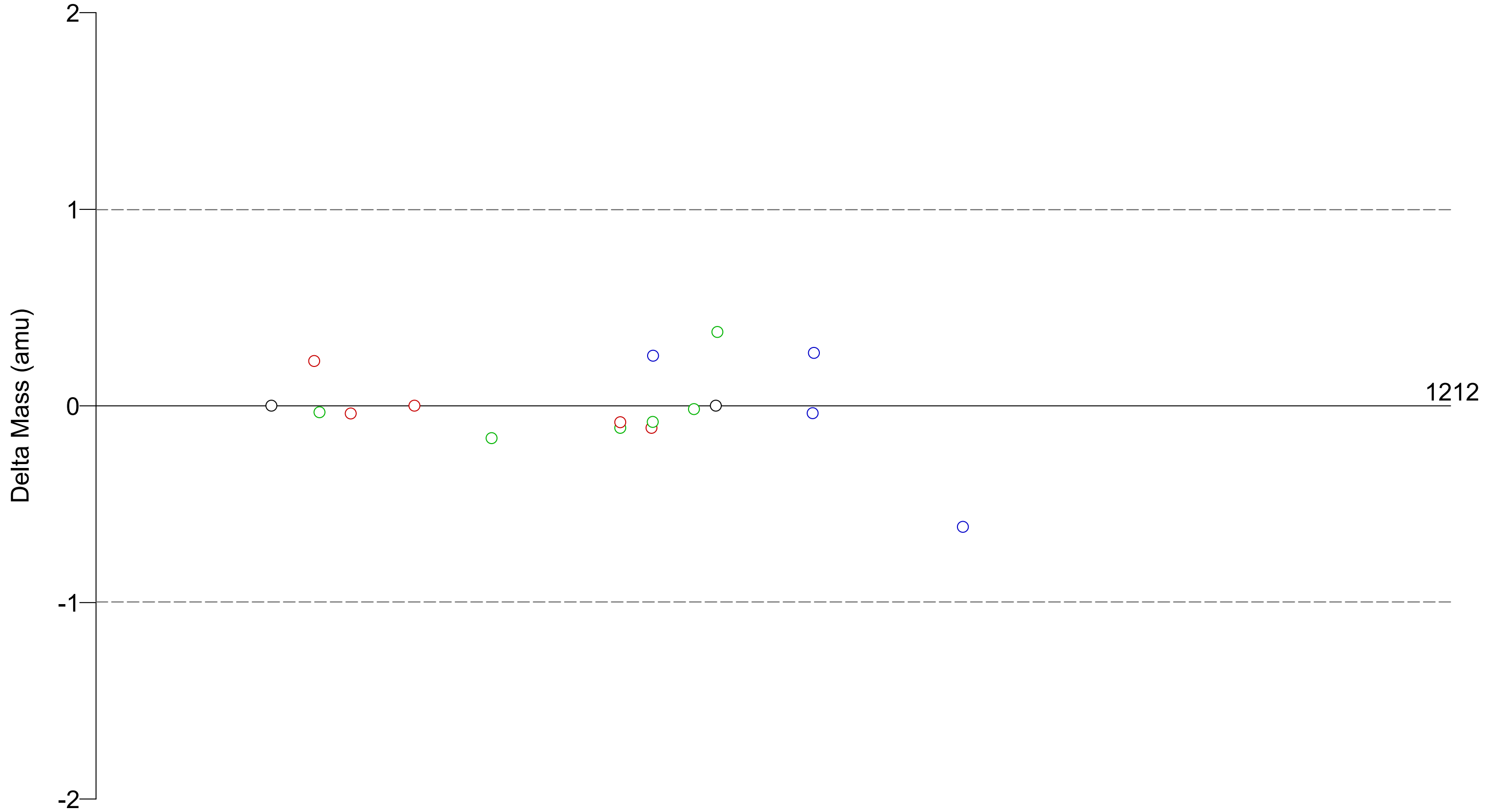


#19287468-1 NL: 6.49E5

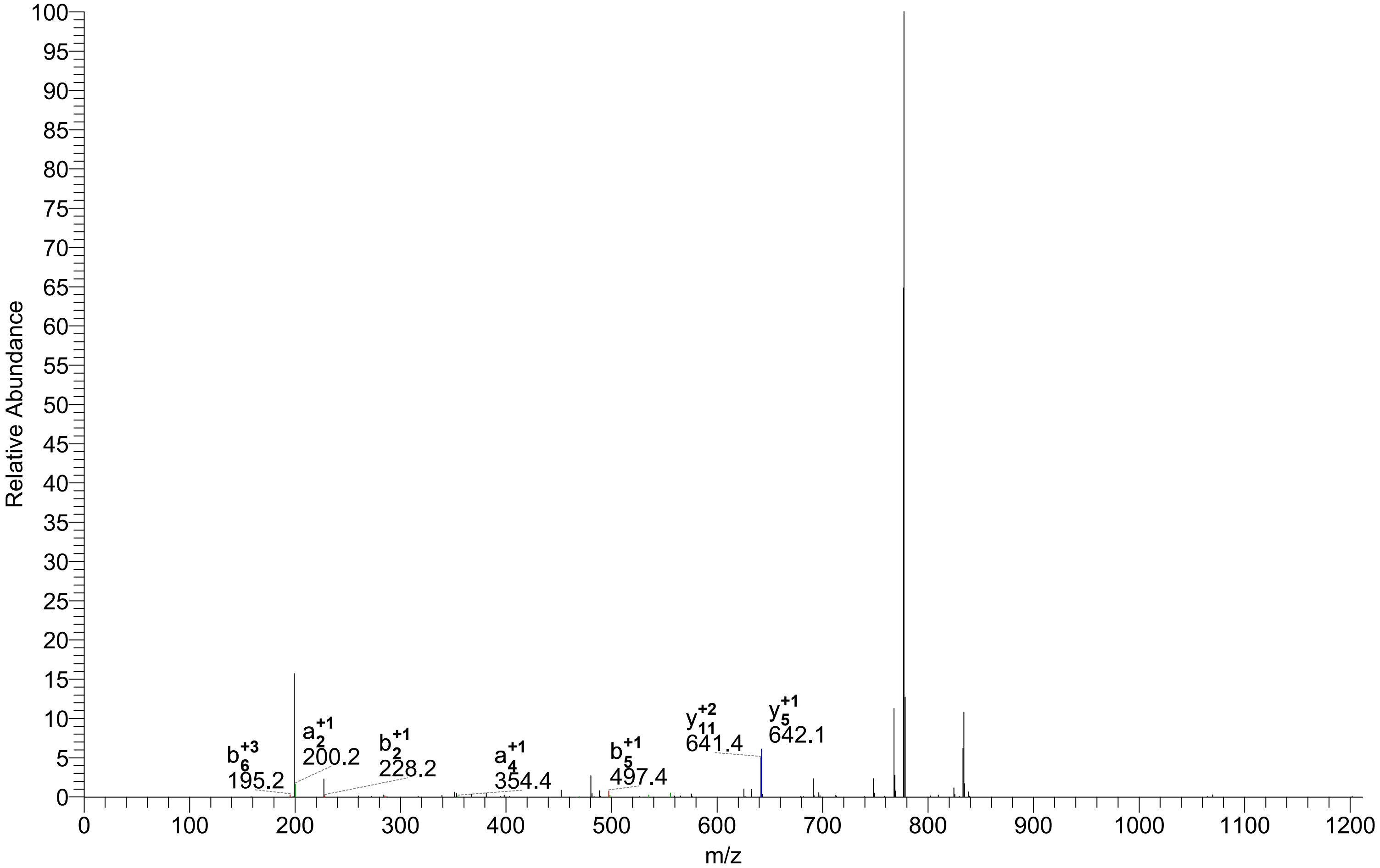


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00418145.4|SWISS-PROT:Q8WZ7                                 1       8.1      0.0       0
19287468 - 1  R.ARGPDSNVLLLRLPEK.V                    1778.03   3  1       1.316  0.491   55.0   6   14/90   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 R    200.15     228.15                                     1706.99
 G    257.17     285.17                                     1550.89
 P    354.22     382.22                                     1493.87
 D    469.25     497.25                                     1396.82
 S    556.28     584.28                                     1281.79
 N    670.33     698.32                                     1194.76
 V    769.40     797.39                                     1080.71
 L    882.48     910.47                                      981.65
 L    995.56    1023.56                                      868.56
 L   1108.65    1136.64                                      755.48
 R   1264.75    1292.74                                      642.39
 L   1377.83    1405.83                                      486.29
 P   1474.89    1502.88                                      373.21
 E   1603.93    1631.92                                      276.16
 K                                                           147.11
```

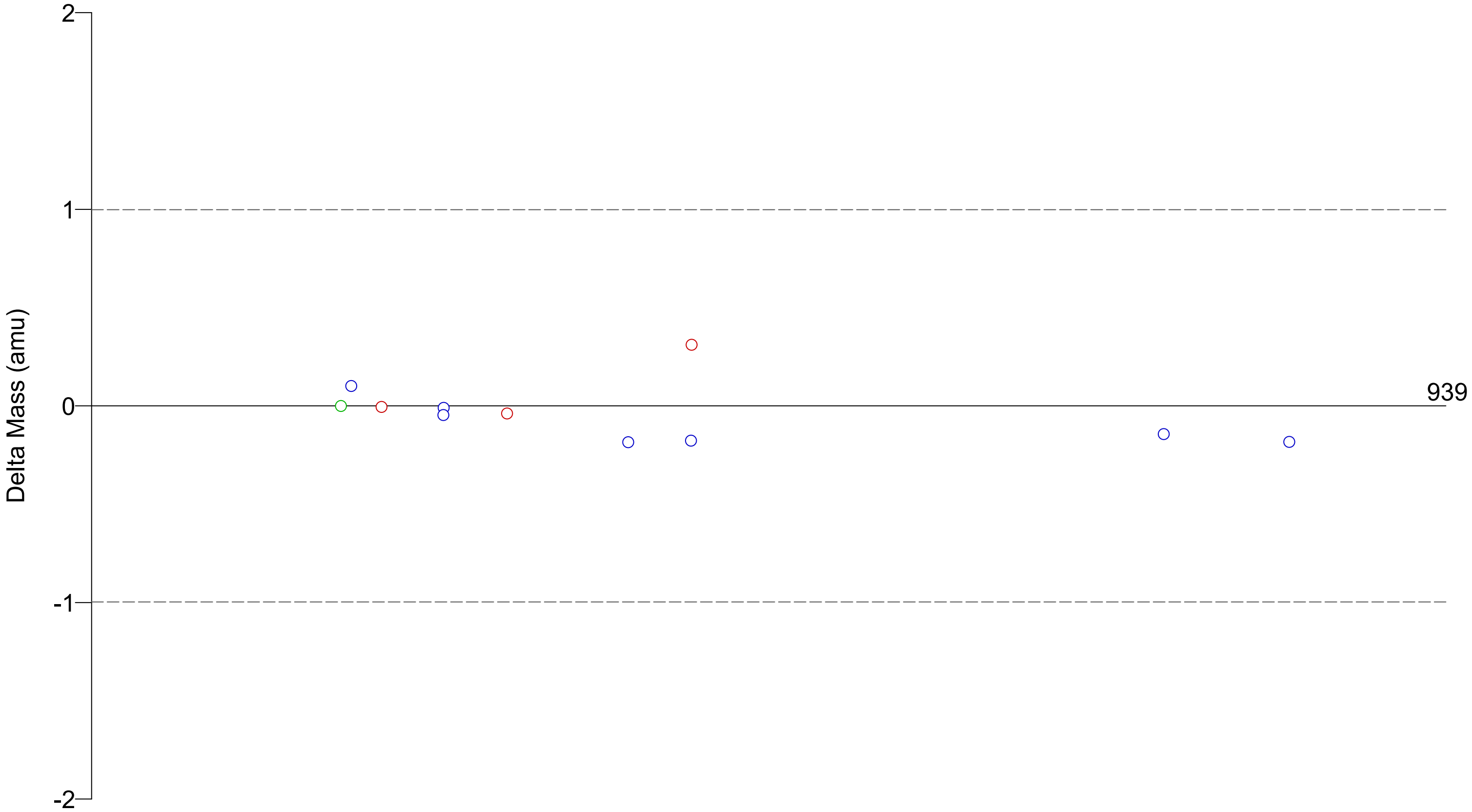


#19287468-1 NL: 6.49E5

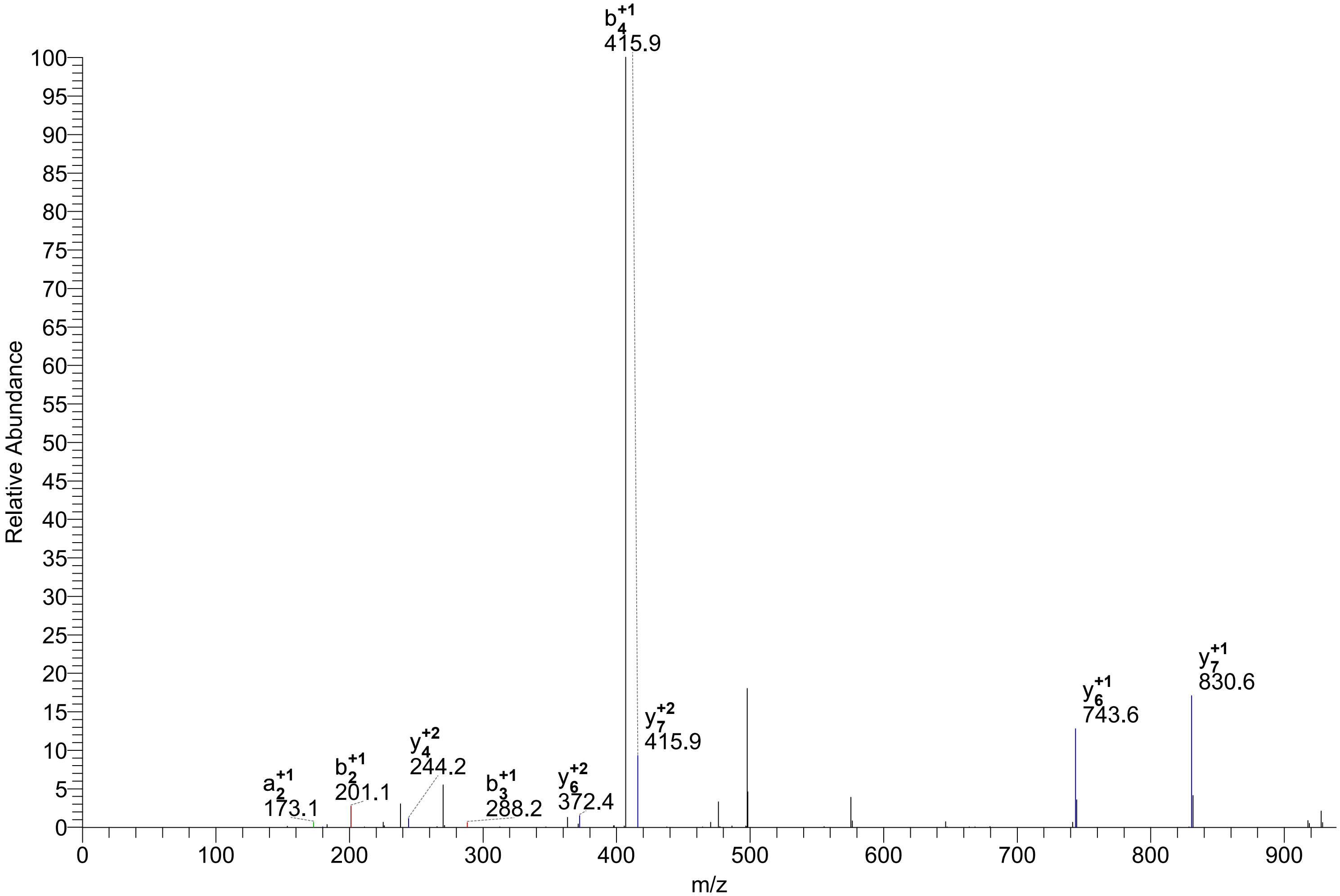


```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00782966.1|SWISS-PROT:Q9H2Y7|TREMBL:B4DGC7;B4DZ40;Q05C4    1       4.1      0.0       0
19287468 - 1  K.SLSQKQDPK.N                          1030.55   2  1       1.289  0.531   59.0   19  7/24
19287468 - 1  K.LIKGGKVTTSTWEDSR.T                   1777.94   3  1       1.235  -       42.4   23  12/90   1

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

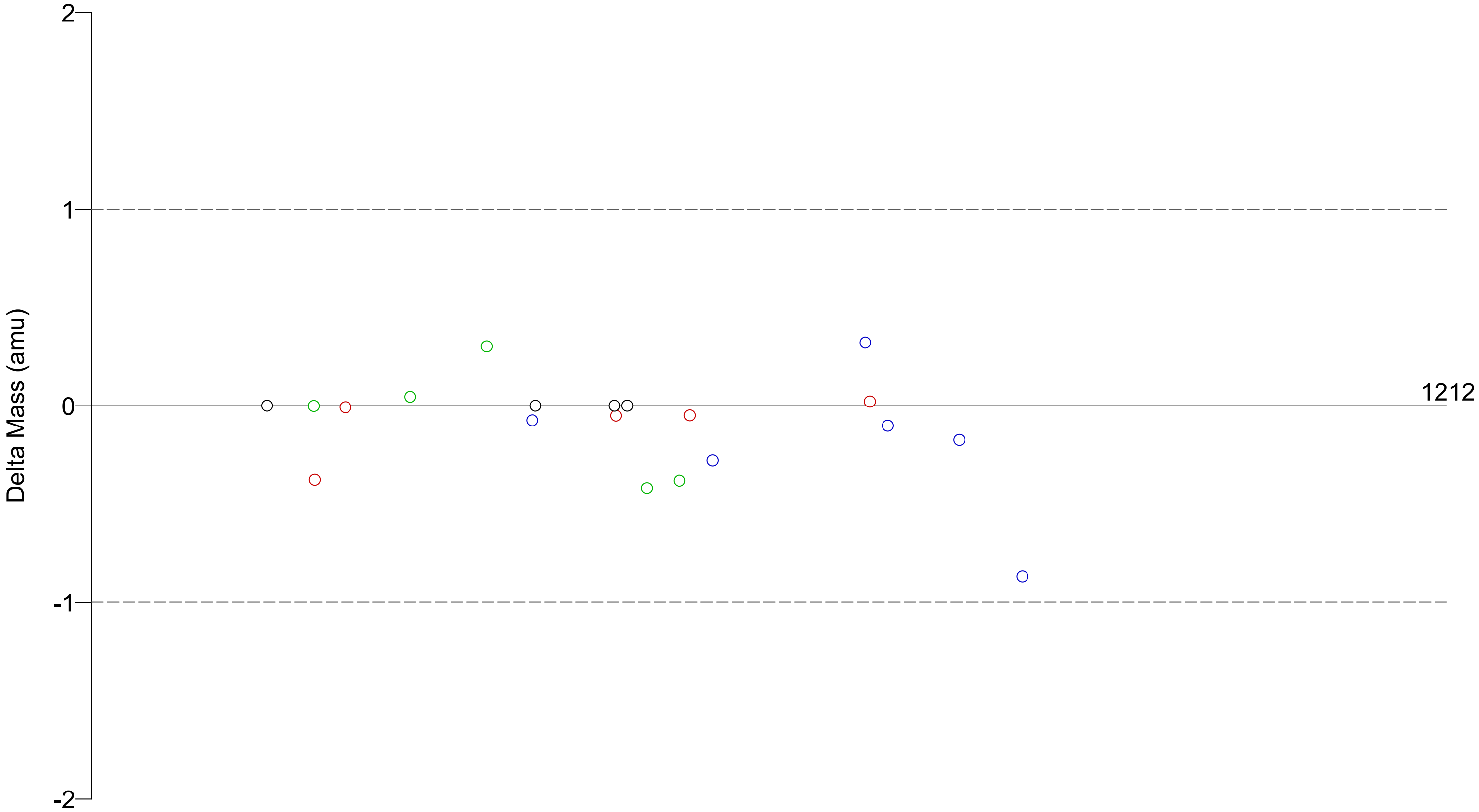
```
DTA for scans: 19287468-1
Precursor ion: 515.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 L    173.13     201.12                                      943.52
 S    260.16     288.16                                      830.44
 Q    388.22     416.21                                      743.40
 K    516.31     544.31                                      615.35
 Q    644.37     672.37                                      487.25
 D    759.40     787.39                                      359.19
 P    856.45     884.45                                      244.17
 K                                                           147.11
```



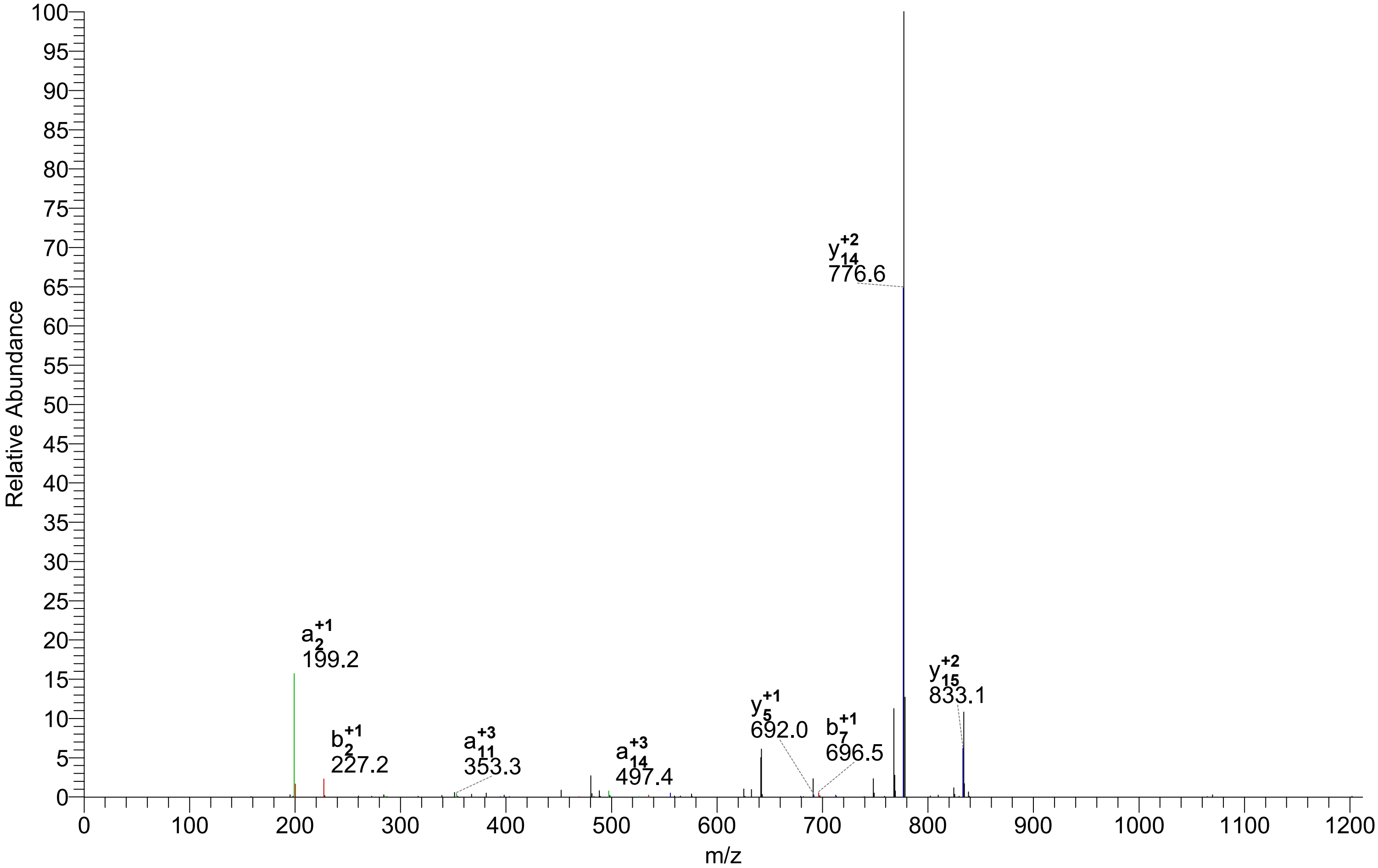
#19287468-1 NL: 6.13E5



```
DTA for scans: 19287468-1
Precursor ion: 593.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
-----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 I    199.18     227.18                                     1664.86
 K    327.28     355.27                                     1551.78
 G    384.30     412.29                                     1423.68
 G    441.32     469.31                                     1366.66
 K    569.41     597.41                                     1309.64
 V    668.48     696.48                                     1181.54
 T    769.53     797.52                                     1082.47
 T    870.58     898.57                                      981.43
 S    957.61     985.60                                      880.38
 T   1058.66    1086.65                                      793.35
 W   1244.74    1272.73                                      692.30
 E   1373.78    1401.77                                      506.22
 D   1488.81    1516.80                                      377.18
 S   1575.84    1603.83                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 6.49E5



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Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

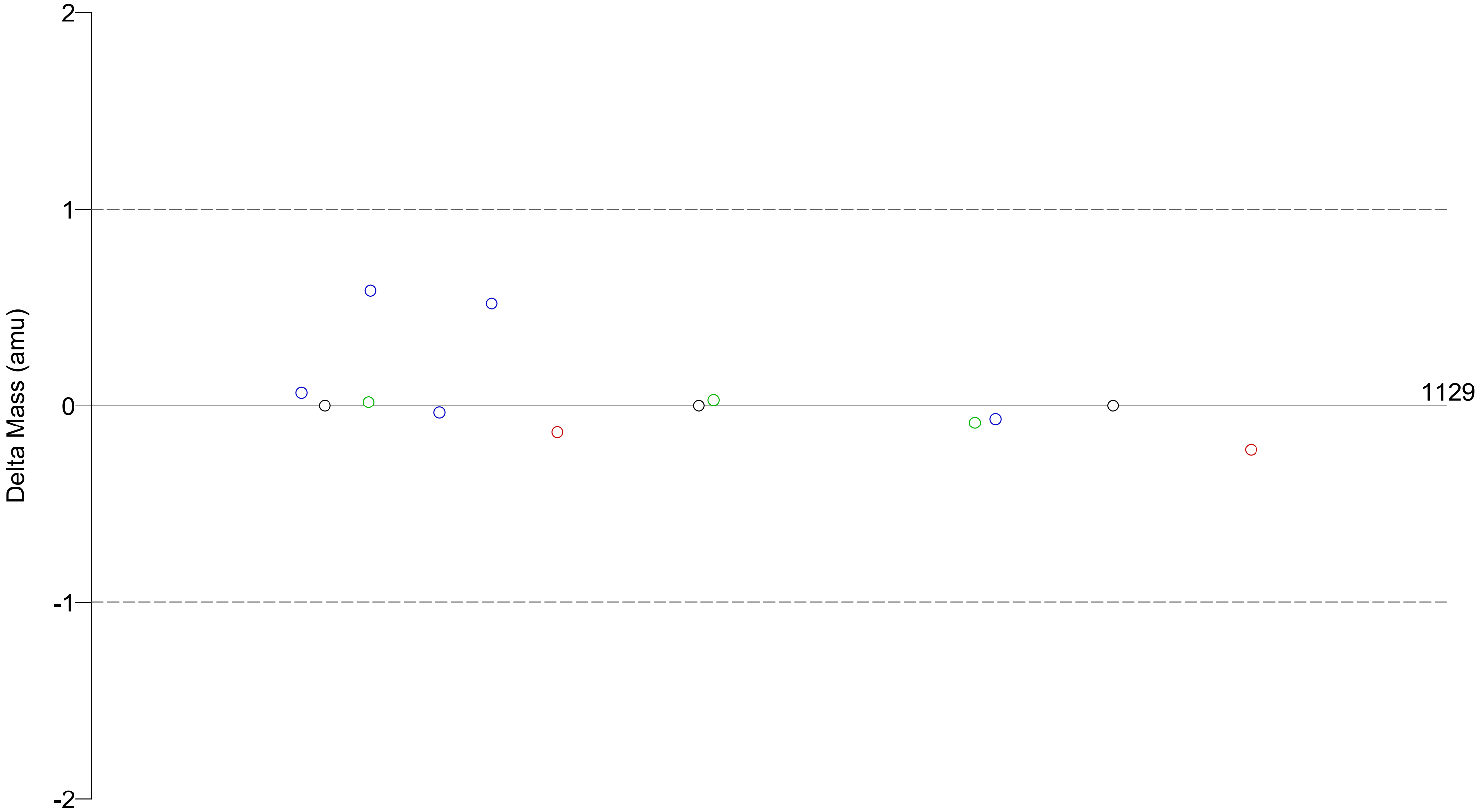
IPI:IPI00166518.6|SWISS-PROT:Q6WCQ1-3|TREMBL:Q5ZEZ6;Q96EE5|ENS    1       8.1      0.0       0
19287468 - 1  K.EEESAMSSDR.M                         1140.45   2  1       1.408  0.594   105.5  5   8/27    4

1 of 1 peptide matches reported, 0 removed due to filtering
```

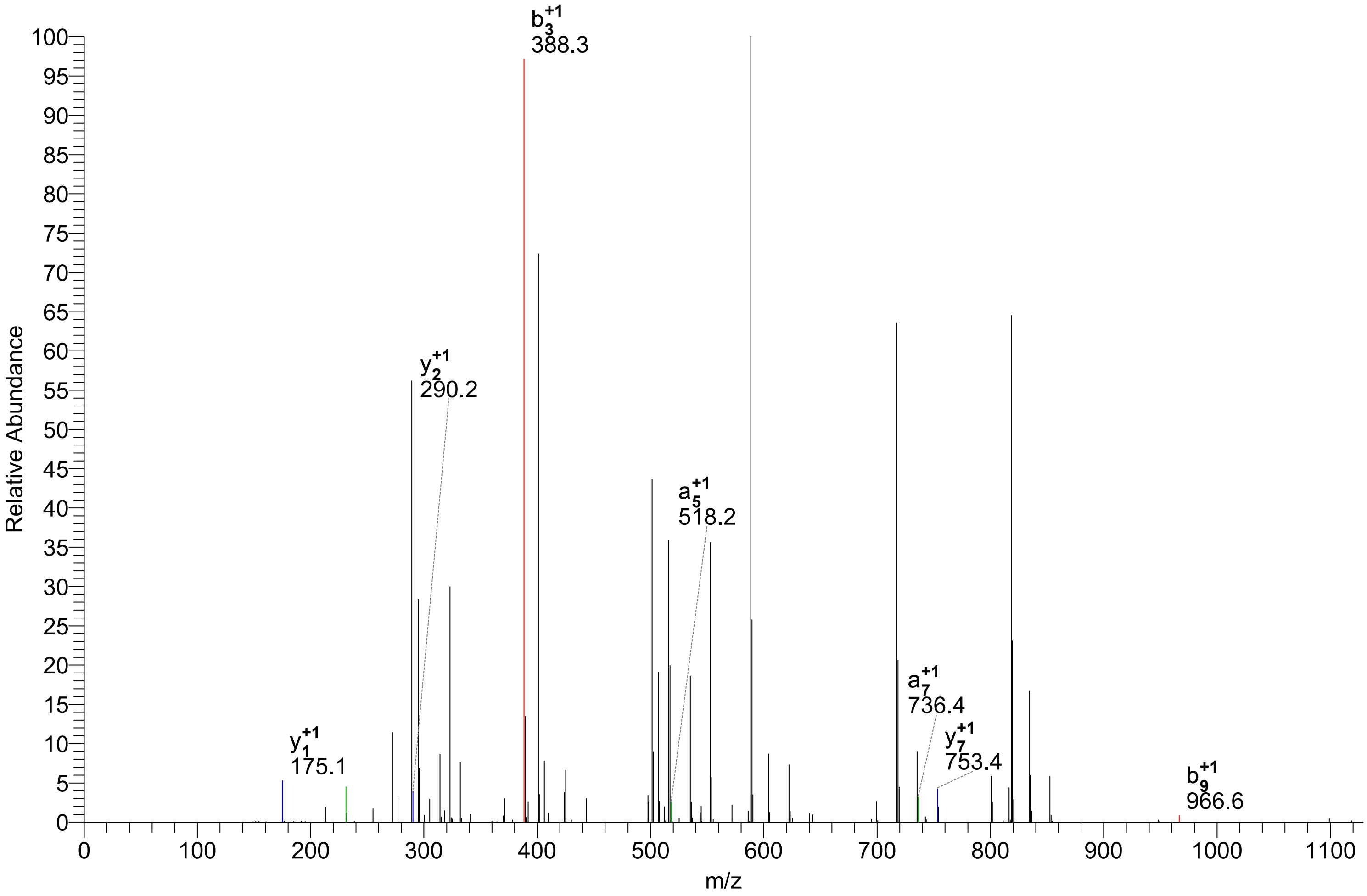
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 E    102.05     130.05
 E    231.10     259.09                                     1011.40
 E    360.14     388.14                                      882.36
 S    447.17     475.17                                      753.32
 A    518.21     546.20                                      666.29
 M    649.25     677.24                                      595.25
 S    736.28     764.28                                      464.21
 S    823.31     851.31                                      377.18
 D    938.34     966.34                                      290.15
 R                                                           175.12
```



#19287468-1 NL: 8.98E6



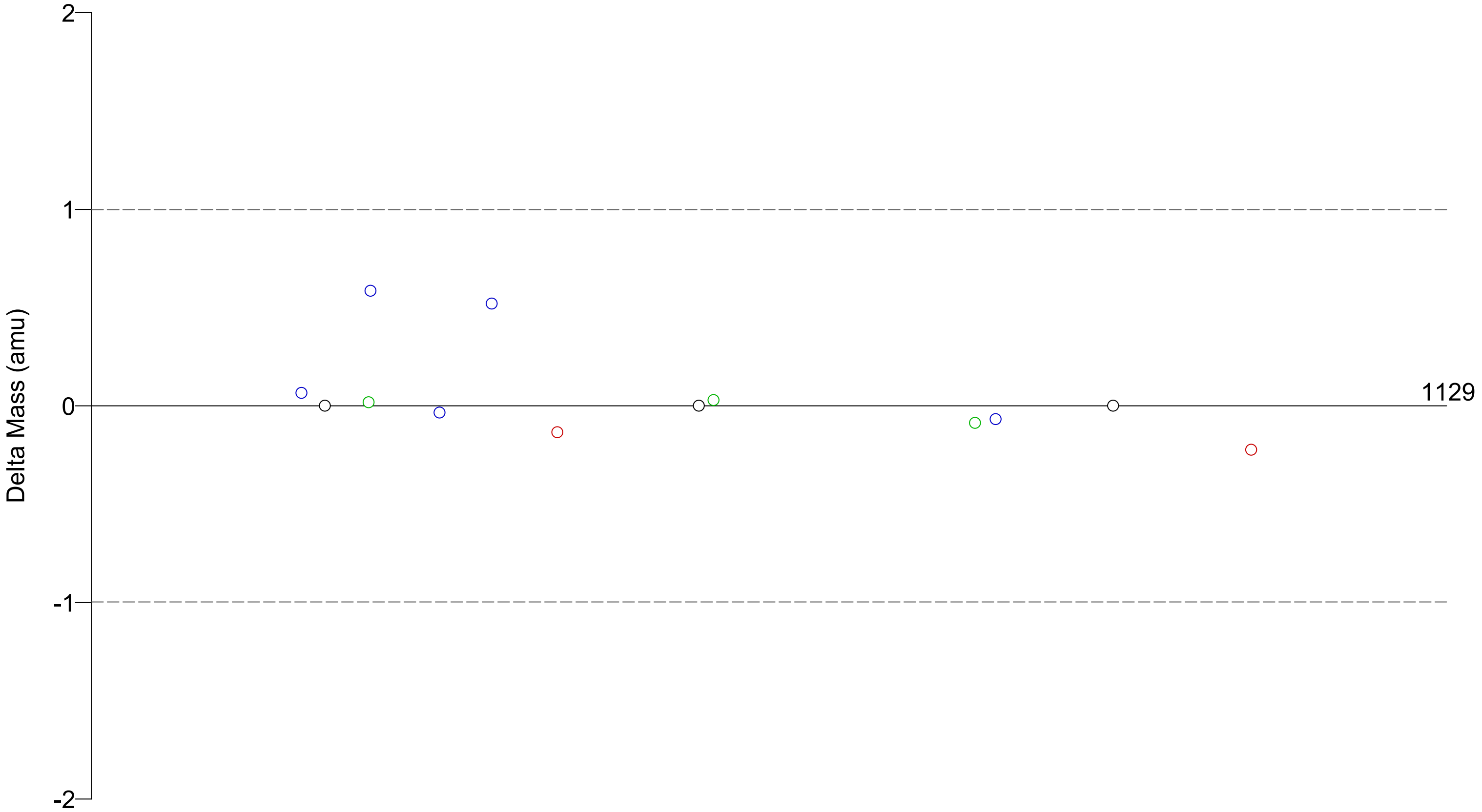
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00295457.6|SWISS-PROT:Q6WCQ                                 1        8.1      0.0       0
19287468 - 1  K.EEESAMSSDR.M                          1140.45    2  1        1.408  0.594   105.5  5   8/27    4

1 of 1 peptide matches reported, 0 removed due to filtering
```

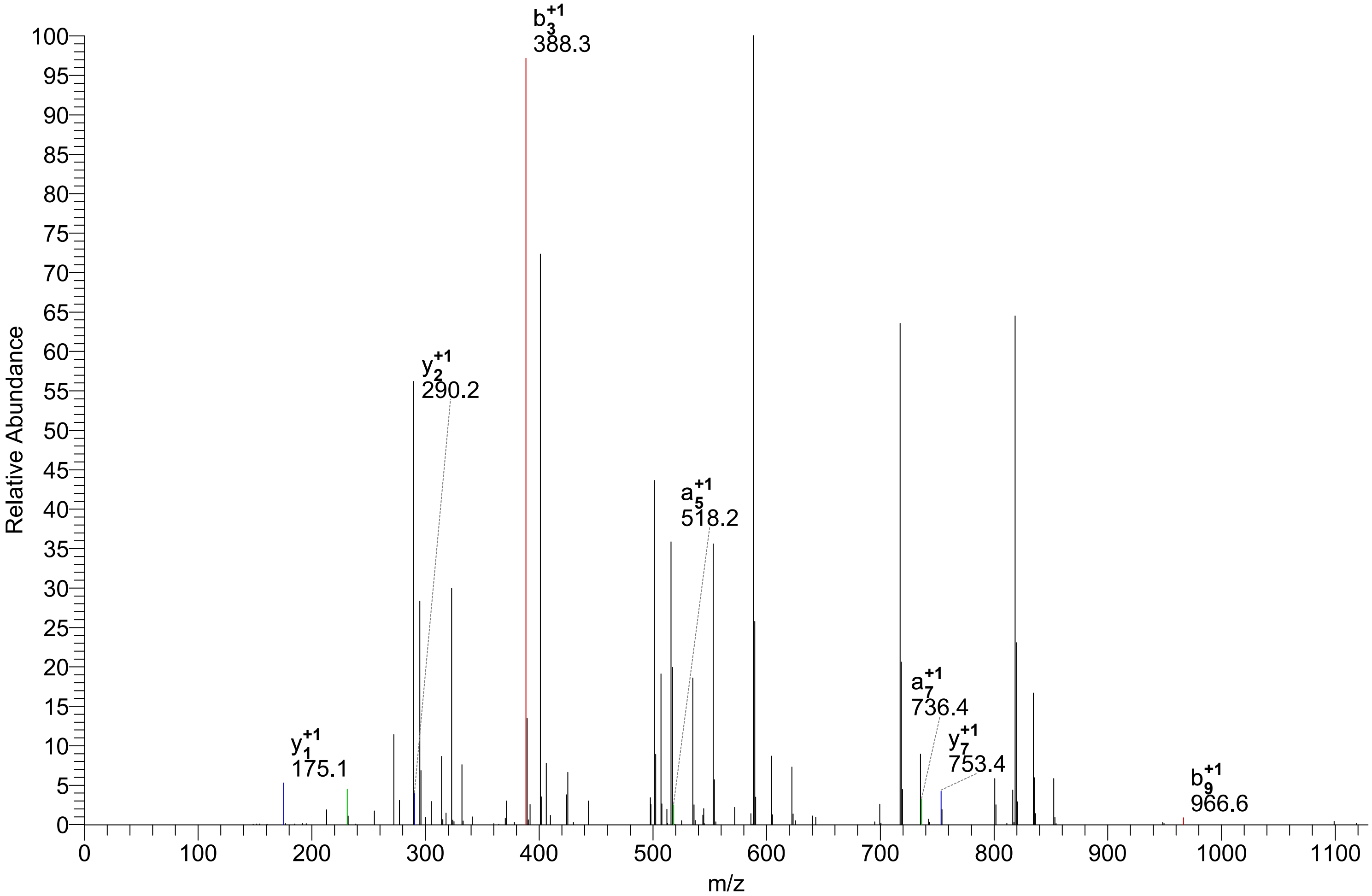
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 E    102.05     130.05
 E    231.10     259.09                                     1011.40
 E    360.14     388.14                                      882.36
 S    447.17     475.17                                      753.32
 A    518.21     546.20                                      666.29
 M    649.25     677.24                                      595.25
 S    736.28     764.28                                      464.21
 S    823.31     851.31                                      377.18
 D    938.34     966.34                                      290.15
 R                                                           175.12
```



#19287468-1 NL: 8.98E6



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count

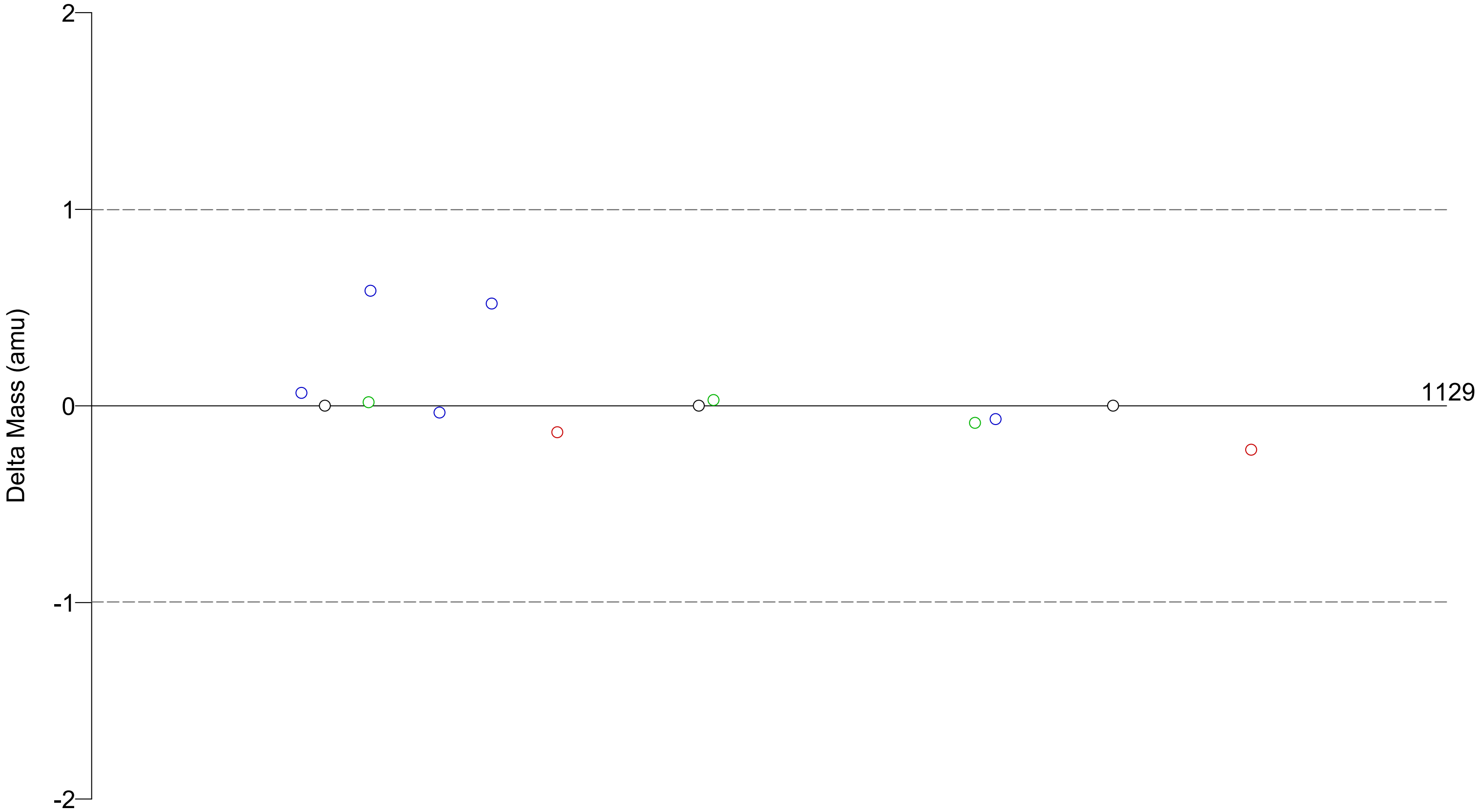
IPI:IPI00305344.7|SWISS-PROT:Q6WCQ                                 1       8.1      0.0       0
19287468 - 1  K.EEESAMSSDR.M                          1140.45   2  1       1.408  0.594   105.5  5   8/27    4

1 of 1 peptide matches reported, 0 removed due to filtering
```

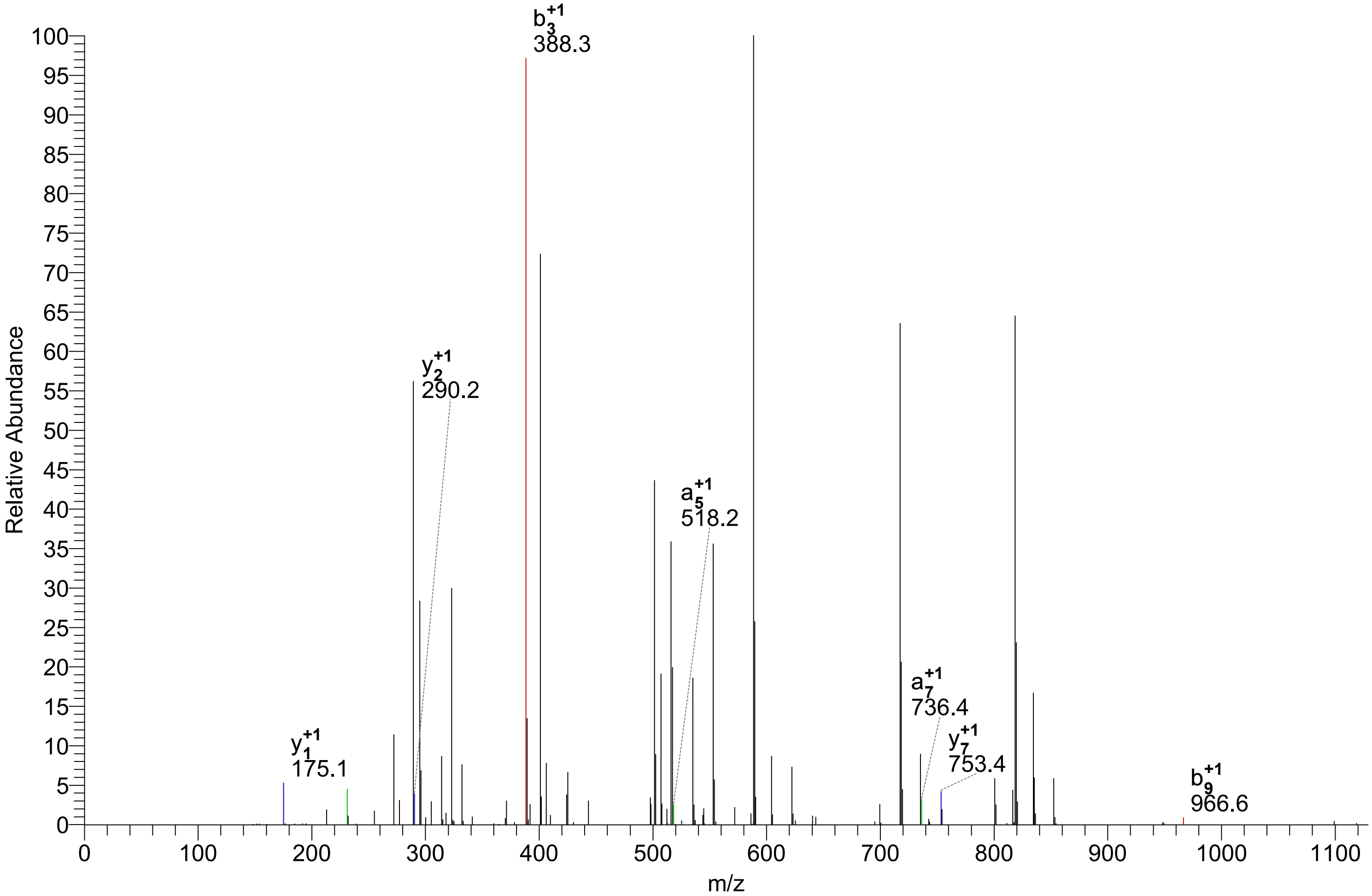
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 E    102.05     130.05
 E    231.10     259.09                                     1011.40
 E    360.14     388.14                                      882.36
 S    447.17     475.17                                      753.32
 A    518.21     546.20                                      666.29
 M    649.25     677.24                                      595.25
 S    736.28     764.28                                      464.21
 S    823.31     851.31                                      377.18
 D    938.34     966.34                                      290.15
 R                                                           175.12
```



#19287468-1 NL: 8.98E6



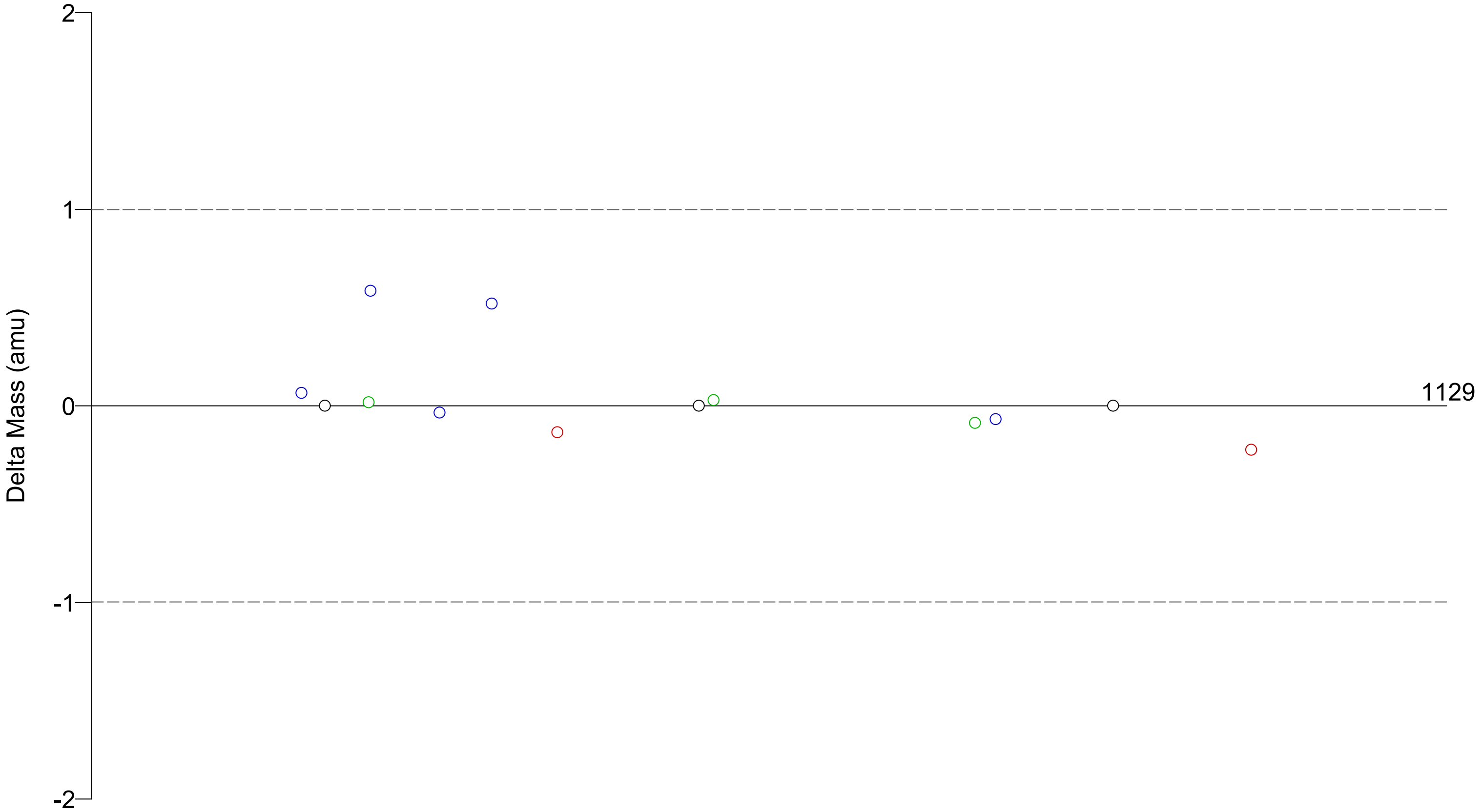
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                Mh+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00796460.1|TREMBL:A8MTJ7|VE                                1        8.1     0.0       0
19287468 - 1  K.EEESAMSSDR.M                         1140.45   2  1       1.408  0.594   105.5  5   8/27    4

1 of 1 peptide matches reported, 0 removed due to filtering
```

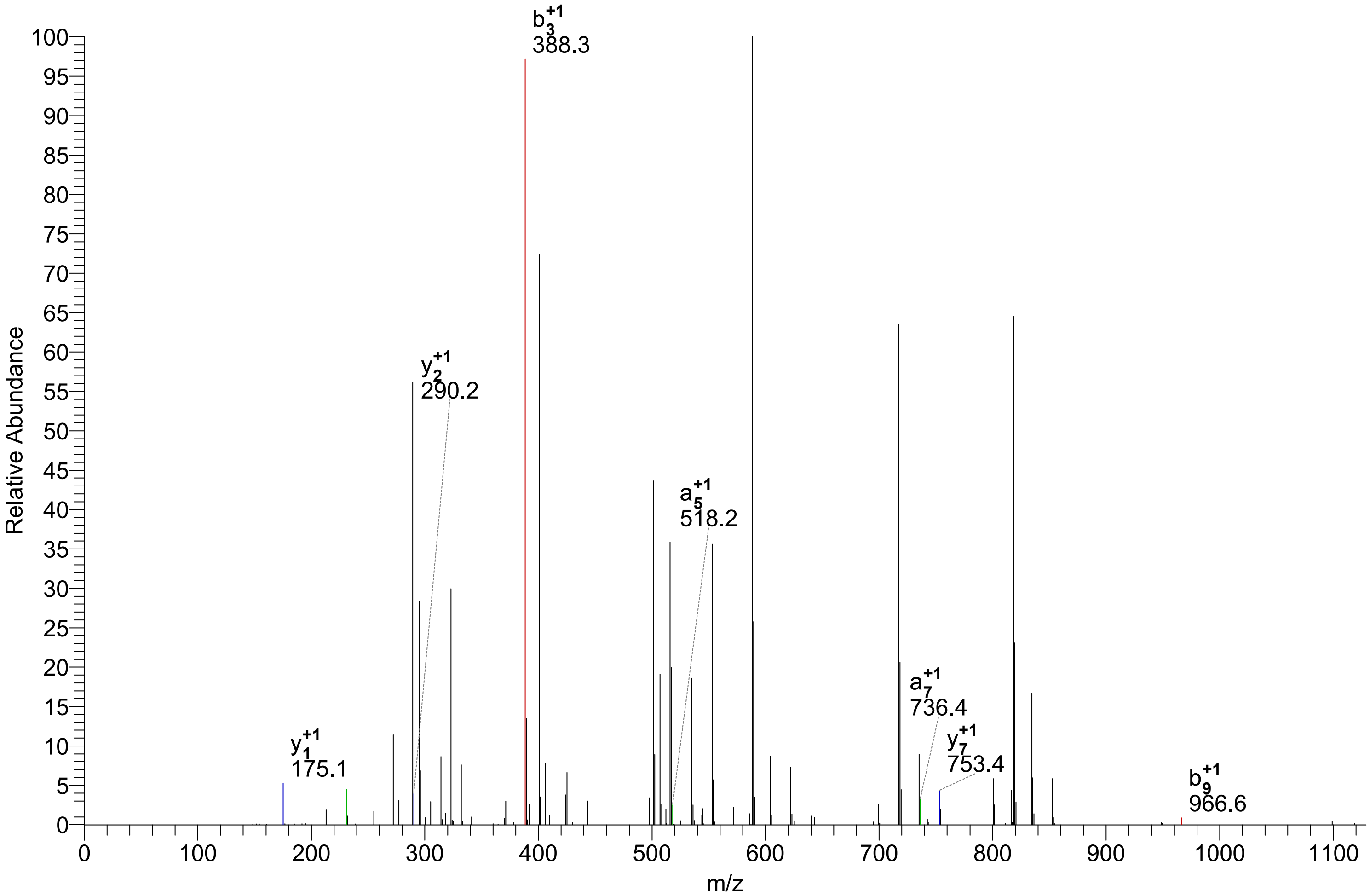
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 E    102.05     130.05
 E    231.10     259.09                                     1011.40
 E    360.14     388.14                                      882.36
 S    447.17     475.17                                      753.32
 A    518.21     546.20                                      666.29
 M    649.25     677.24                                      595.25
 S    736.28     764.28                                      464.21
 S    823.31     851.31                                      377.18
 D    938.34     966.34                                      290.15
 R                                                           175.12
```



#19287468-1 NL: 8.98E6



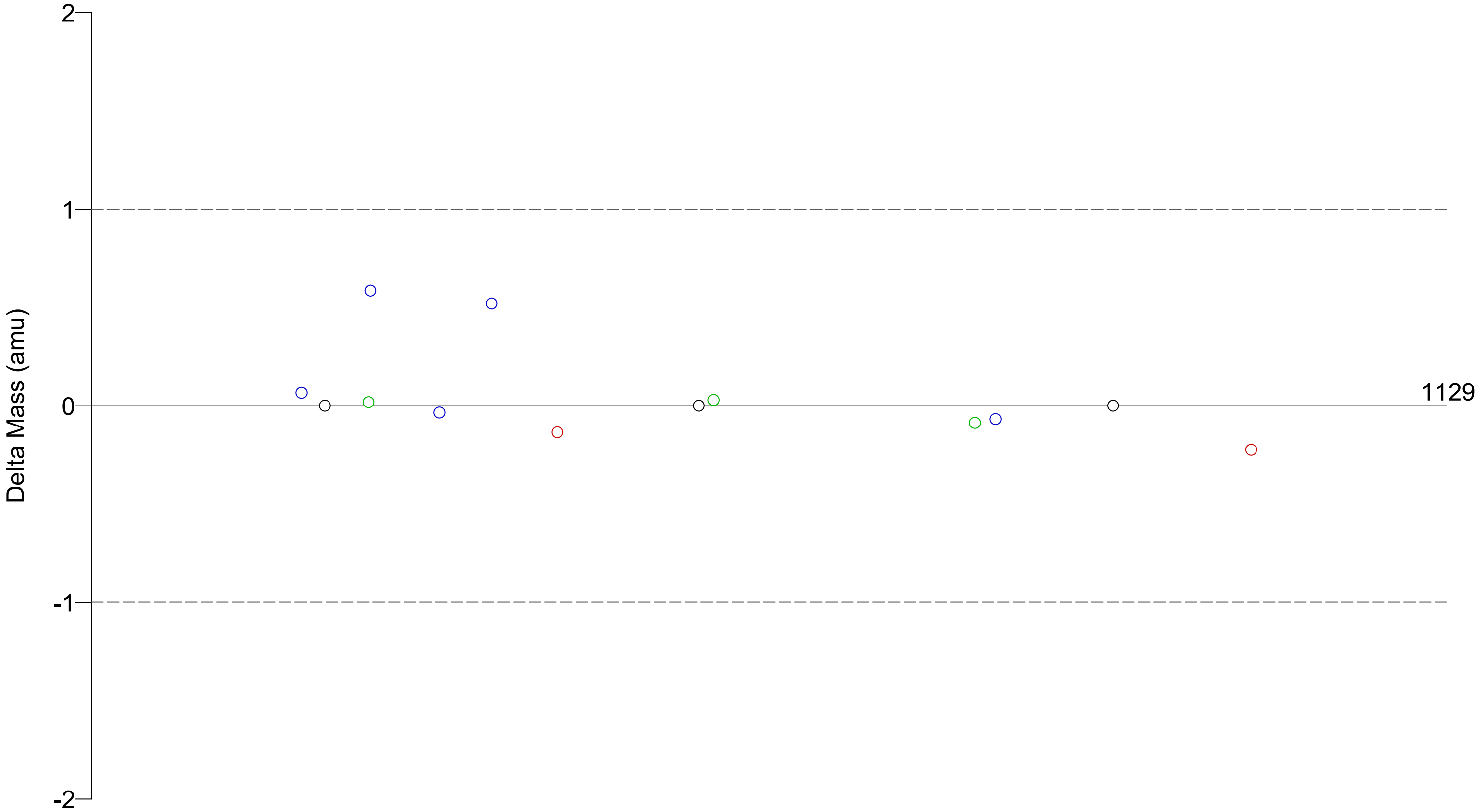
```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z     P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00797228.1|VEGA:OTTHUMP0000                                  1       8.1      0.0       0
19287468 - 1  K.EEESAMSSDR.M                        1140.45   2  1       1.408  0.594   105.5  5   8/27    4

1 of 1 peptide matches reported, 0 removed due to filtering
```

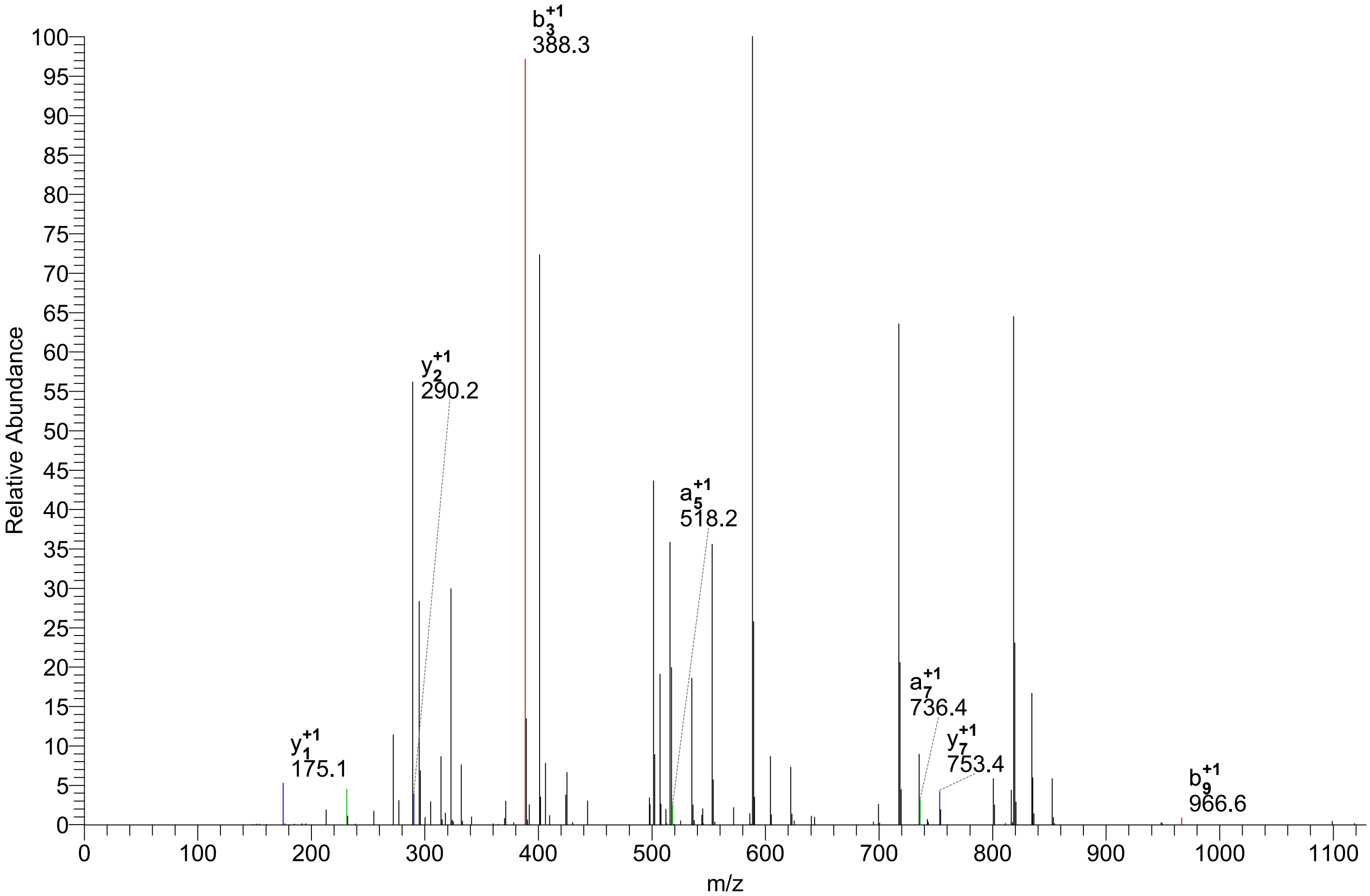
```
DTA for scans: 19287468-1
Precursor ion: 570.74
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 E    102.05     130.05
 E    231.10     259.09                                     1011.40
 E    360.14     388.14                                      882.36
 S    447.17     475.17                                      753.32
 A    518.21     546.20                                      666.29
 M    649.25     677.24                                      595.25
 S    736.28     764.28                                      464.21
 S    823.31     851.31                                      377.18
 D    938.34     966.34                                      290.15
 R                                                           175.12
```



#19287468-1 NL: 8.98E6



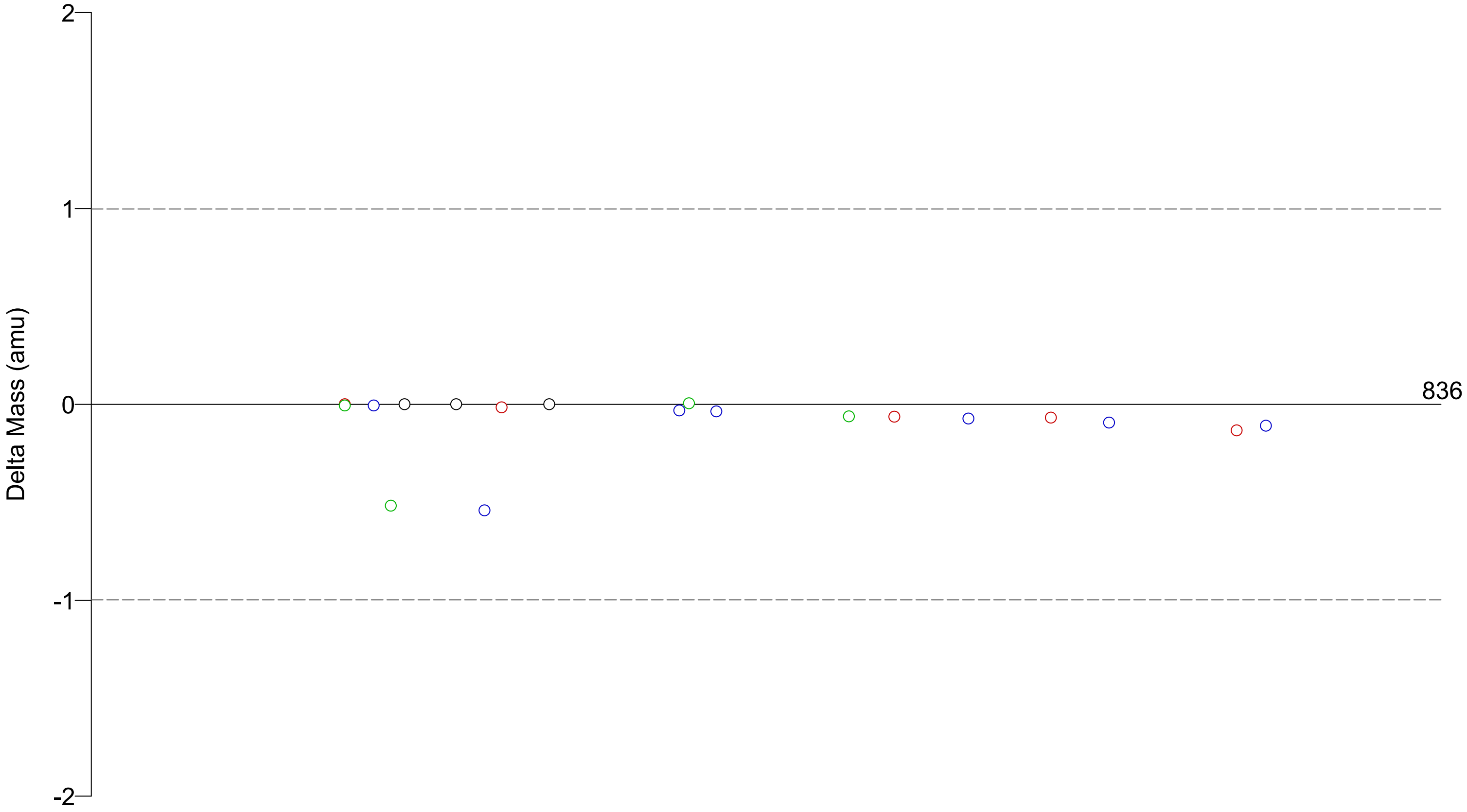
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00382420.1|SWISS-PROT:P01700 Tax_Id=9606 Gene_Symbol=-    1       10.1     0.0       0
              K.RPSGVPDR.F                           883.47    2  0.1     2.914  0.384   612.6  1   14/21   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

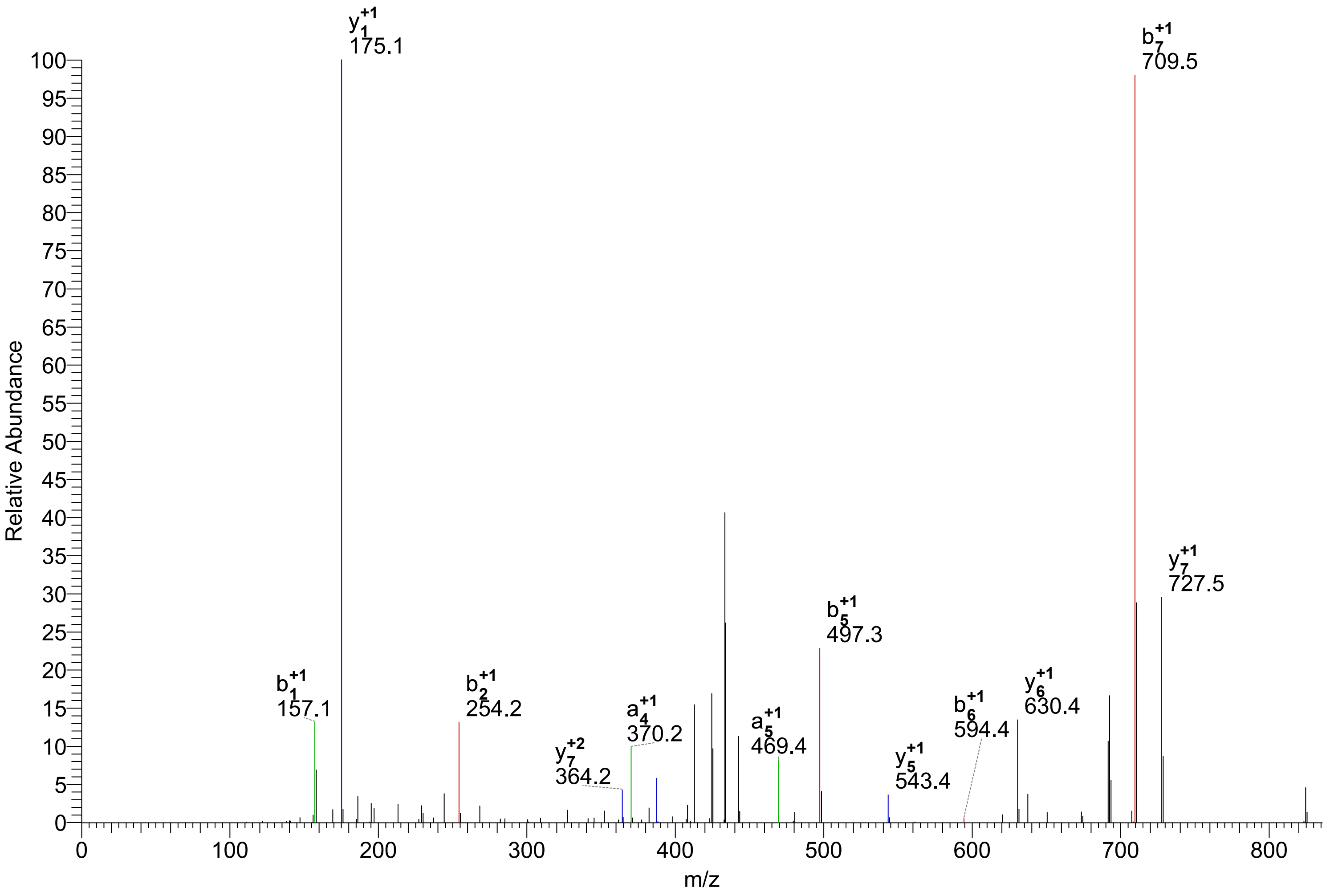
```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```


2
1
0
-1
-2
Delta Mass (amu)
836

#0-0 NL: 6.35E5


Relative Abundance
m/z
y1 +1 175.1
b7 +1 709.5
y7 +1 727.5
b5 +1 497.3
b1 +1 157.1
b2 +1 254.2
a4 +1 370.2
a5 +1 469.4
y7 +2 364.2
y5 +1 543.4
b6 +1 594.4
y6 +1 630.4
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
0
100
200
300
400
500
600
700
800

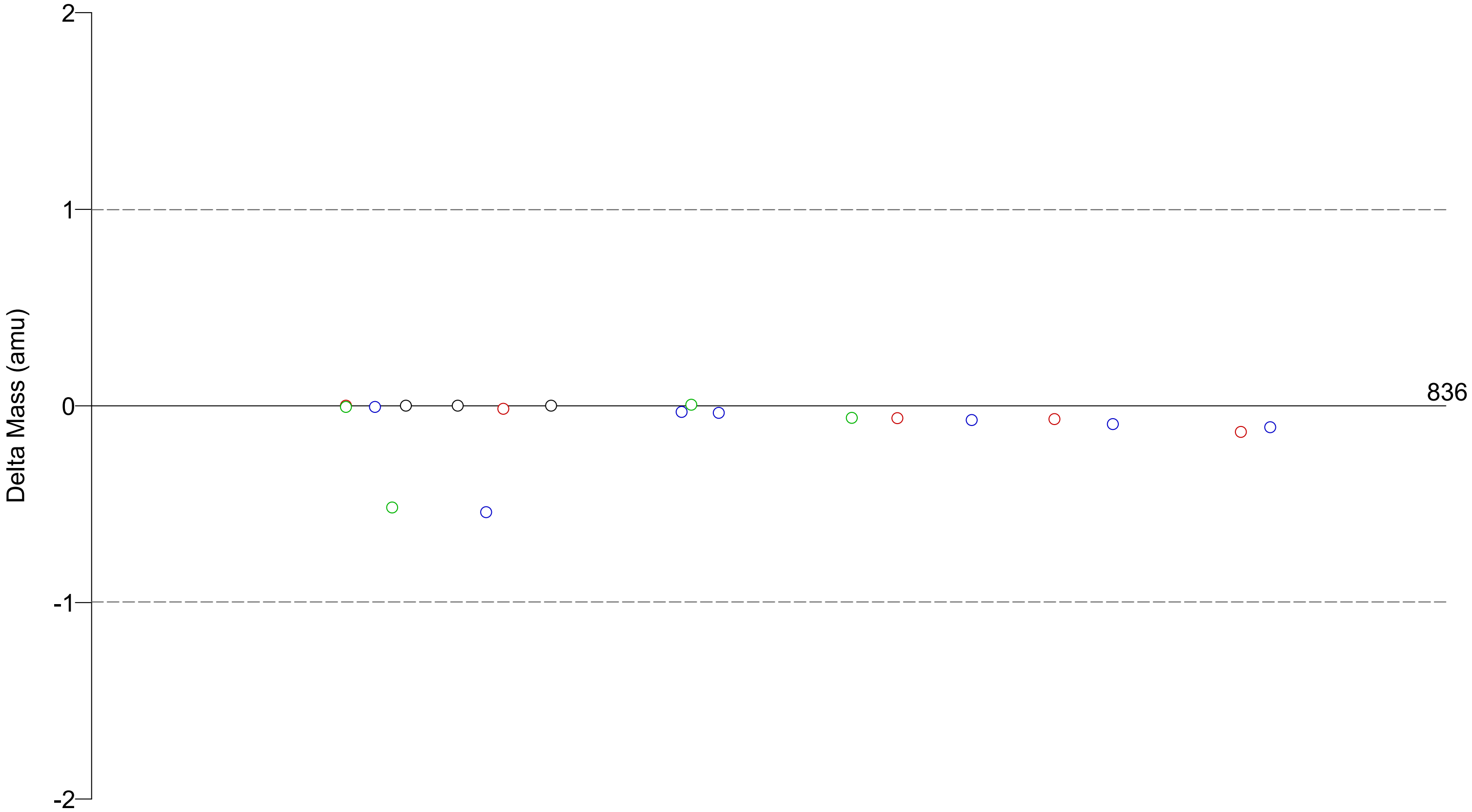
```
Reference                                                                 P      Score   Coverage   Accession
Scan(s)       Sequence                                        MH+       z     P        XC  DeltaCn    Sp    RSp  Ions   Count
IPI:IPI00382426.1|SWISS-PROT:P0170                                          1       10.1      0.0        0
              K.RPSGVPDR.F                                   883.47     2  0.1      2.914  0.384    612.6  1    14/21    8

1 of 1 peptide matches reported, 0 removed due to filtering
```

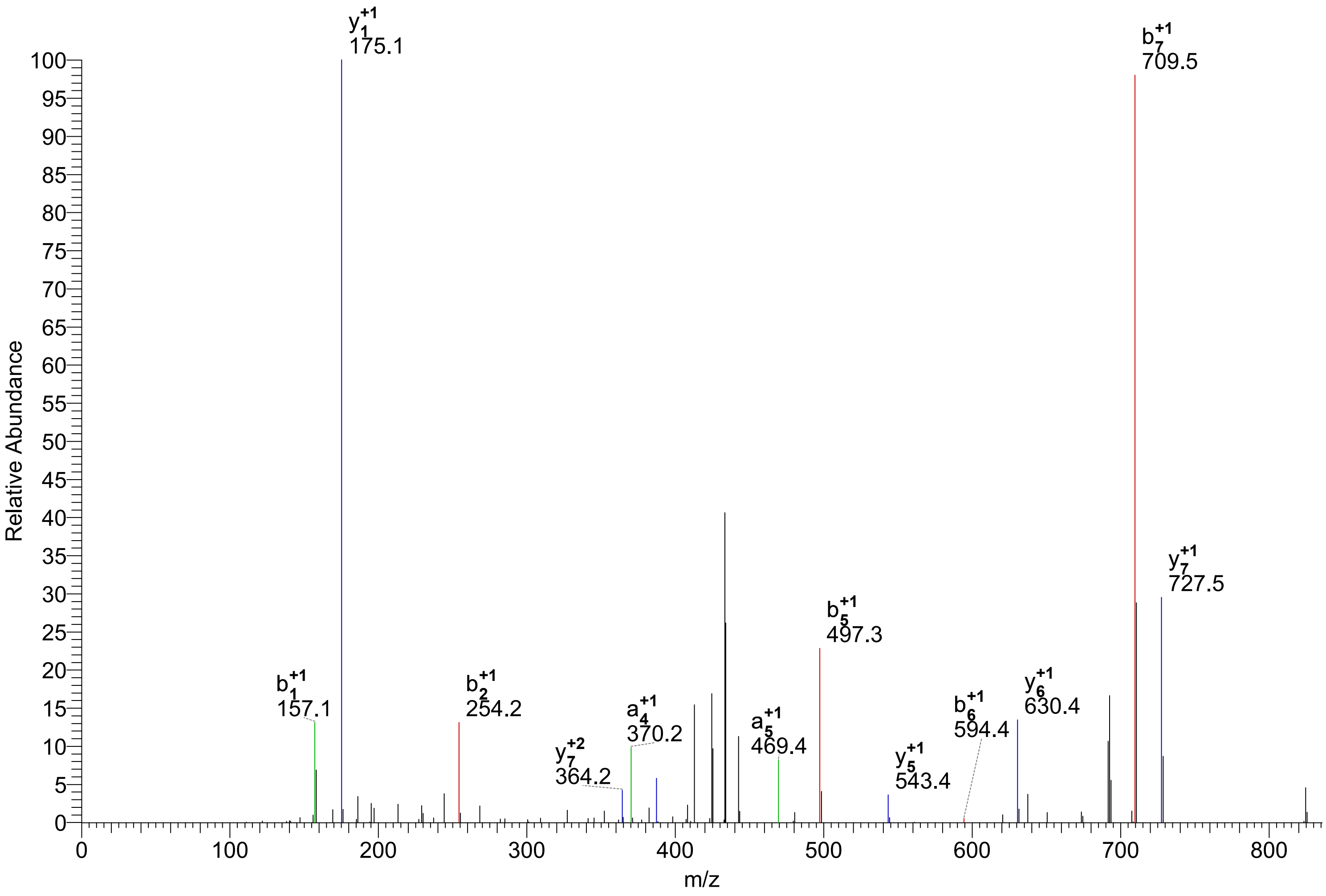
```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```


Delta Mass (amu)
2
1
0
-1
-2
836

#0-0 NL: 6.35E5


Relative Abundance
m/z
y_1^{+1} 175.1
b_7^{+1} 709.5
y_7^{+1} 727.5
b_5^{+1} 497.3
b_1^{+1} 157.1
b_2^{+1} 254.2
y_7^{+2} 364.2
a_4^{+1} 370.2
a_5^{+1} 469.4
y_5^{+1} 543.4
b_6^{+1} 594.4
y_6^{+1} 630.4
0
100
200
300
400
500
600
700
800

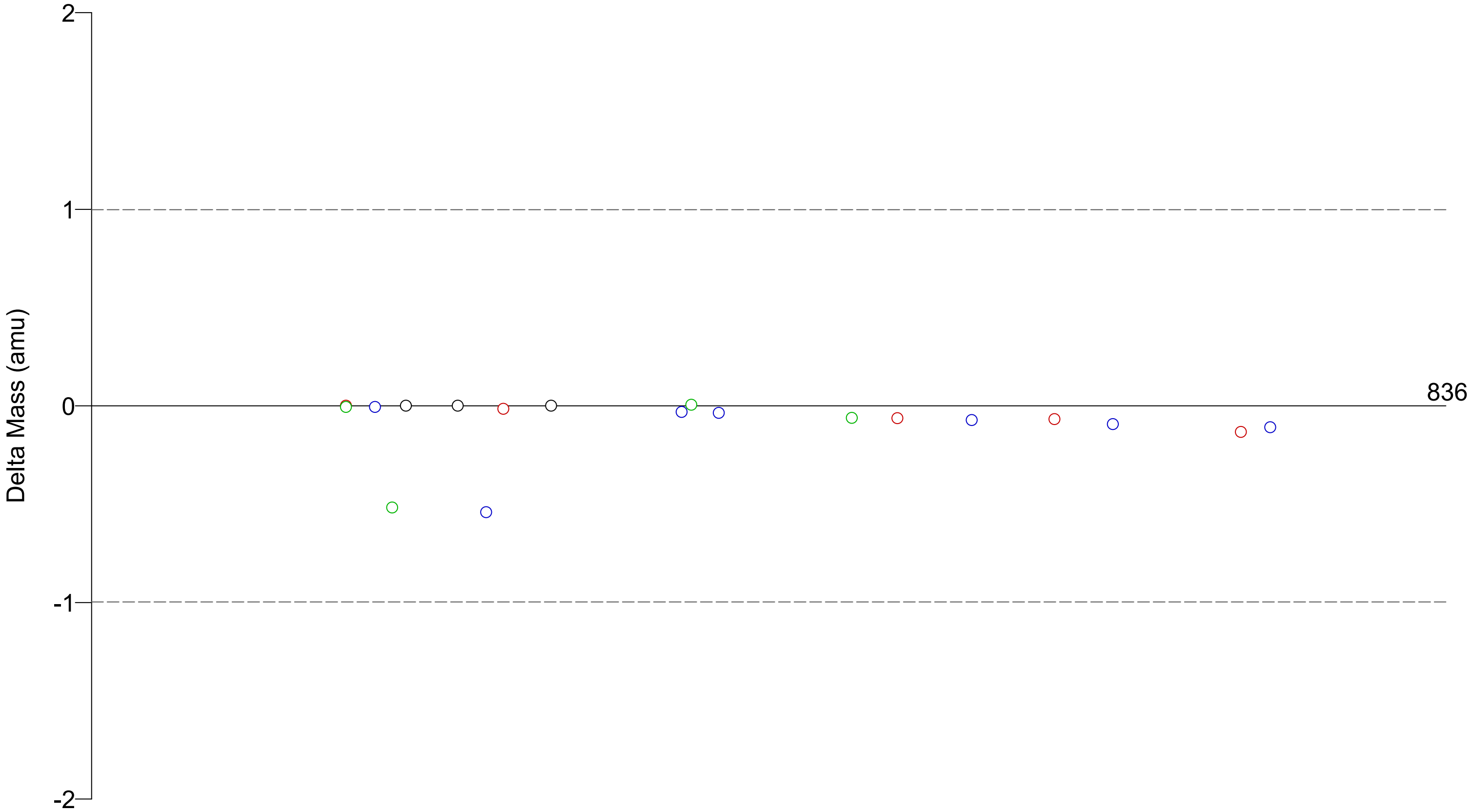
```
Reference                                                                    P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+       z     P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00382427.1|SWISS-PROT:P0170                                         1       10.1     0.0       0
              K.RPSGVPDR.F                                  883.47     2  0.1      2.914  0.384   612.6  1   14/21   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

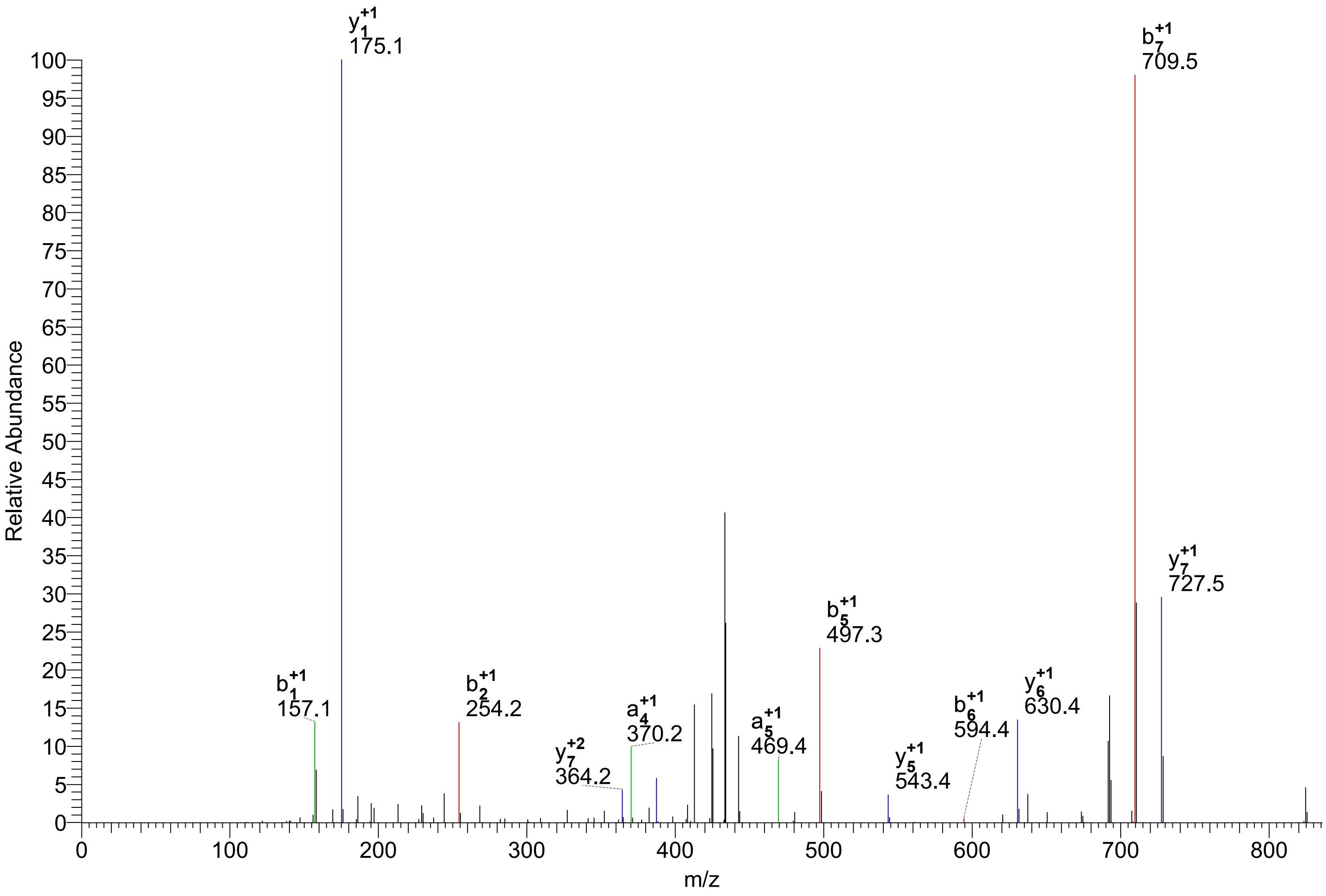
```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```


2
1
0
-1
-2
Delta Mass (amu)
836

#0-0 NL: 6.35E5


y1 +1 175.1
b7 +1 709.5
y7 +1 727.5
b5 +1 497.3
b1 +1 157.1
b2 +1 254.2
y7 +2 364.2
a4 +1 370.2
a5 +1 469.4
y5 +1 543.4
b6 +1 594.4
y6 +1 630.4
Relative Abundance
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
0
100
200
300
400
500
600
700
800
m/z

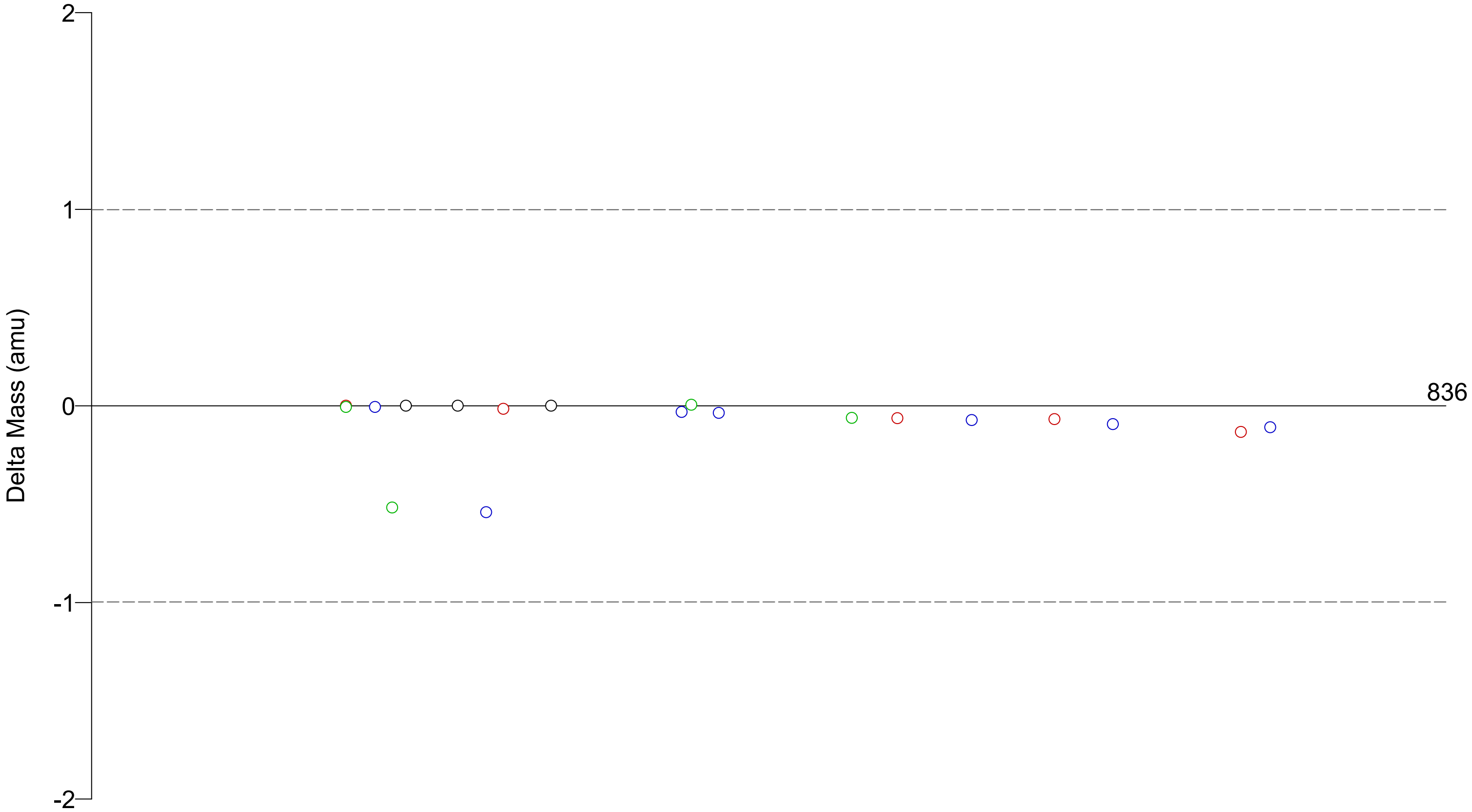
```
Reference                                                   P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00382434.1|SWISS-PROT:P0171                                1       10.1     0.0       0
              K.RPSGVPDR.F                           883.47    2  0.1     2.914  0.384   612.6  1   14/21   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

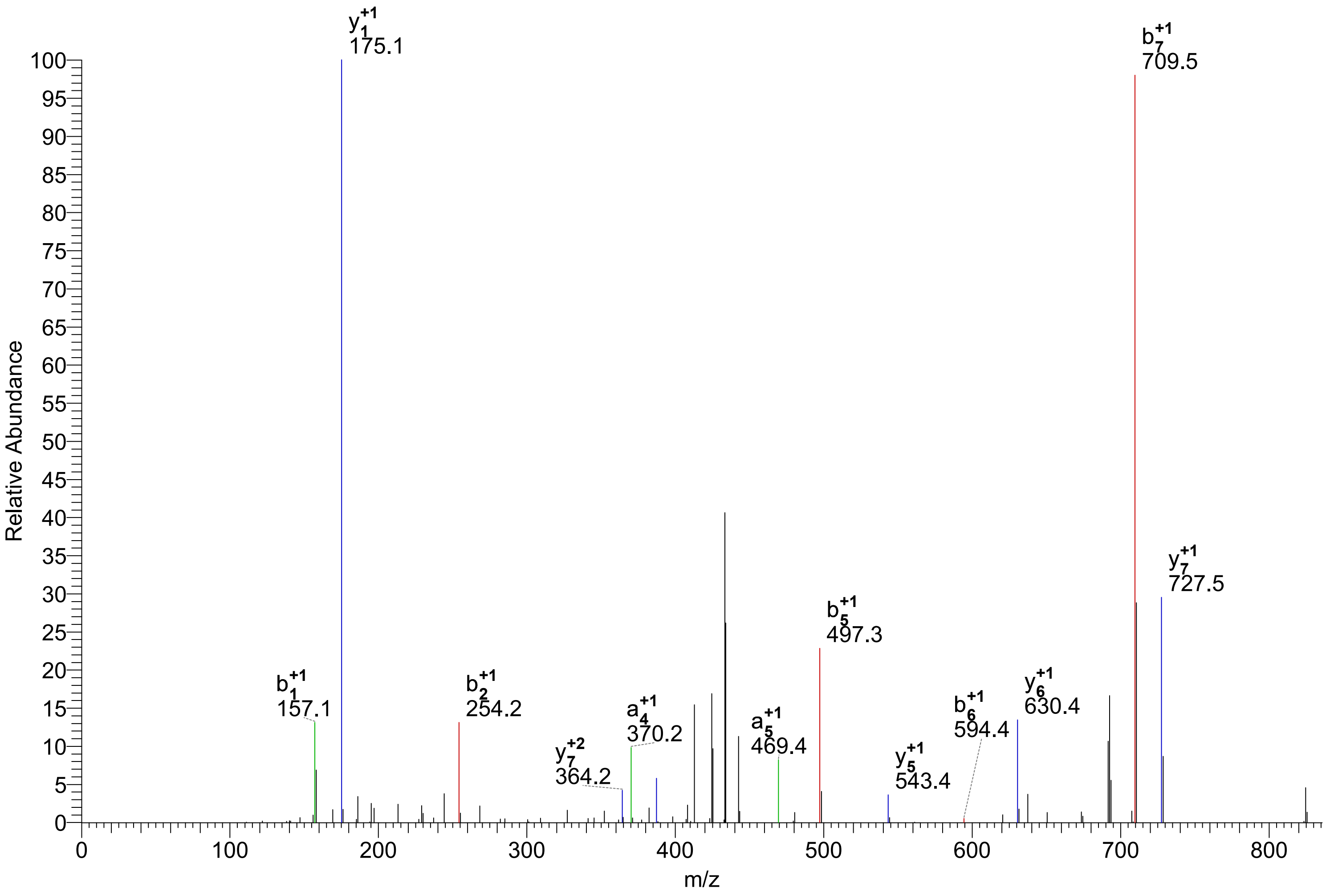
```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```


Delta Mass (amu)
2
1
0
-1
-2
836

#0-0 NL: 6.35E5


Relative Abundance
m/z
y1+1 175.1
b7+1 709.5
y7+1 727.5
b5+1 497.3
b1+1 157.1
b2+1 254.2
y7+2 364.2
a4+1 370.2
a5+1 469.4
y5+1 543.4
b6+1 594.4
y6+1 630.4
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
0
100
200
300
400
500
600
700
800

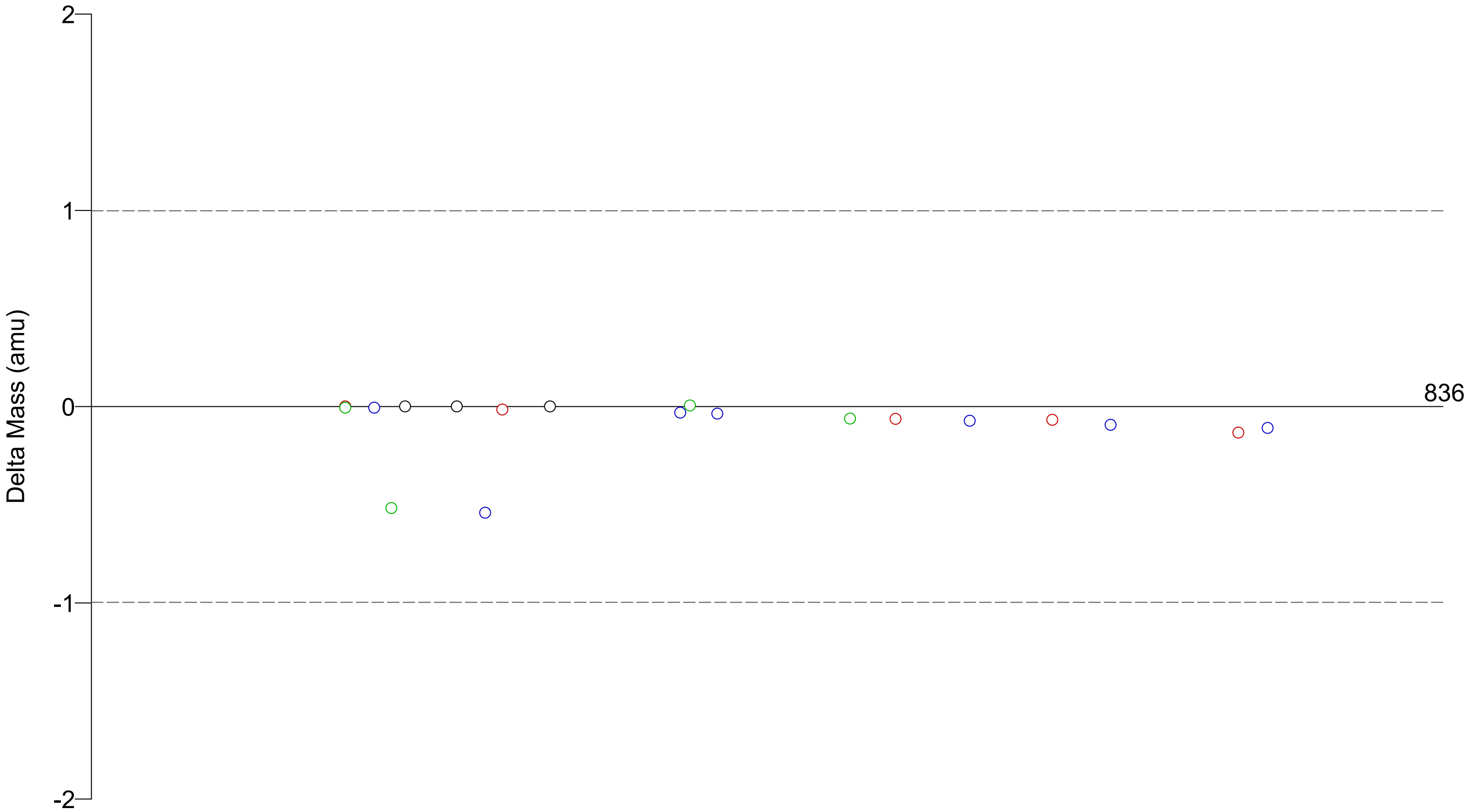
```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00383016.1|TREMBL:Q8TE63 Ta                                       1      10.1     0.0       0
              K.RPSGVPDR.F                                  883.47     2  0.1      2.914  0.384   612.6  1   14/21   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

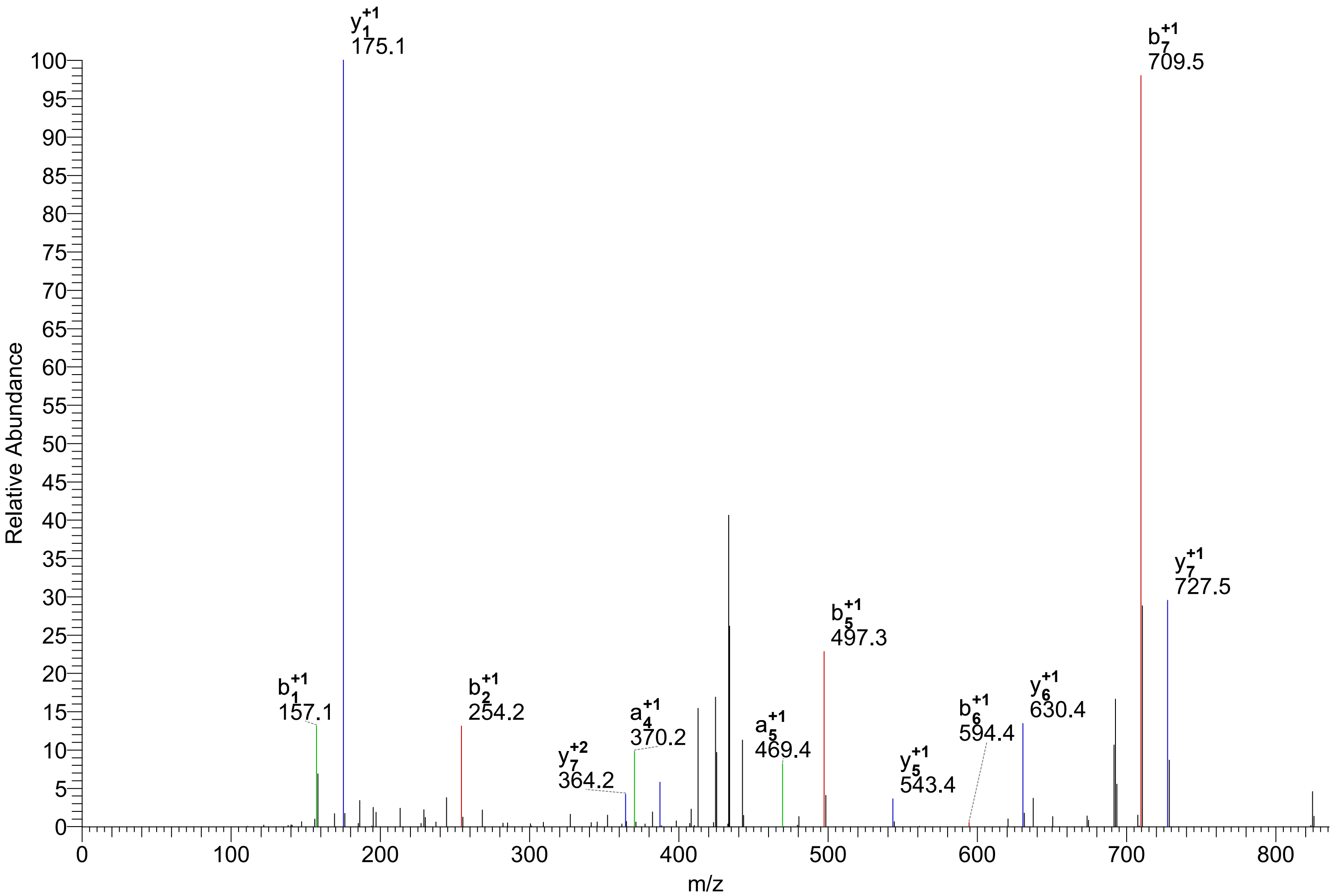
```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```


2
1
0
-1
-2
Delta Mass (amu)
836

#0-0 NL: 6.35E5


Relative Abundance
m/z
y1 +1 175.1
b7 +1 709.5
y7 +1 727.5
b5 +1 497.3
b1 +1 157.1
b2 +1 254.2
a4 +1 370.2
y7 +2 364.2
a5 +1 469.4
y5 +1 543.4
b6 +1 594.4
y6 +1 630.4
0
100
200
300
400
500
600
700
800

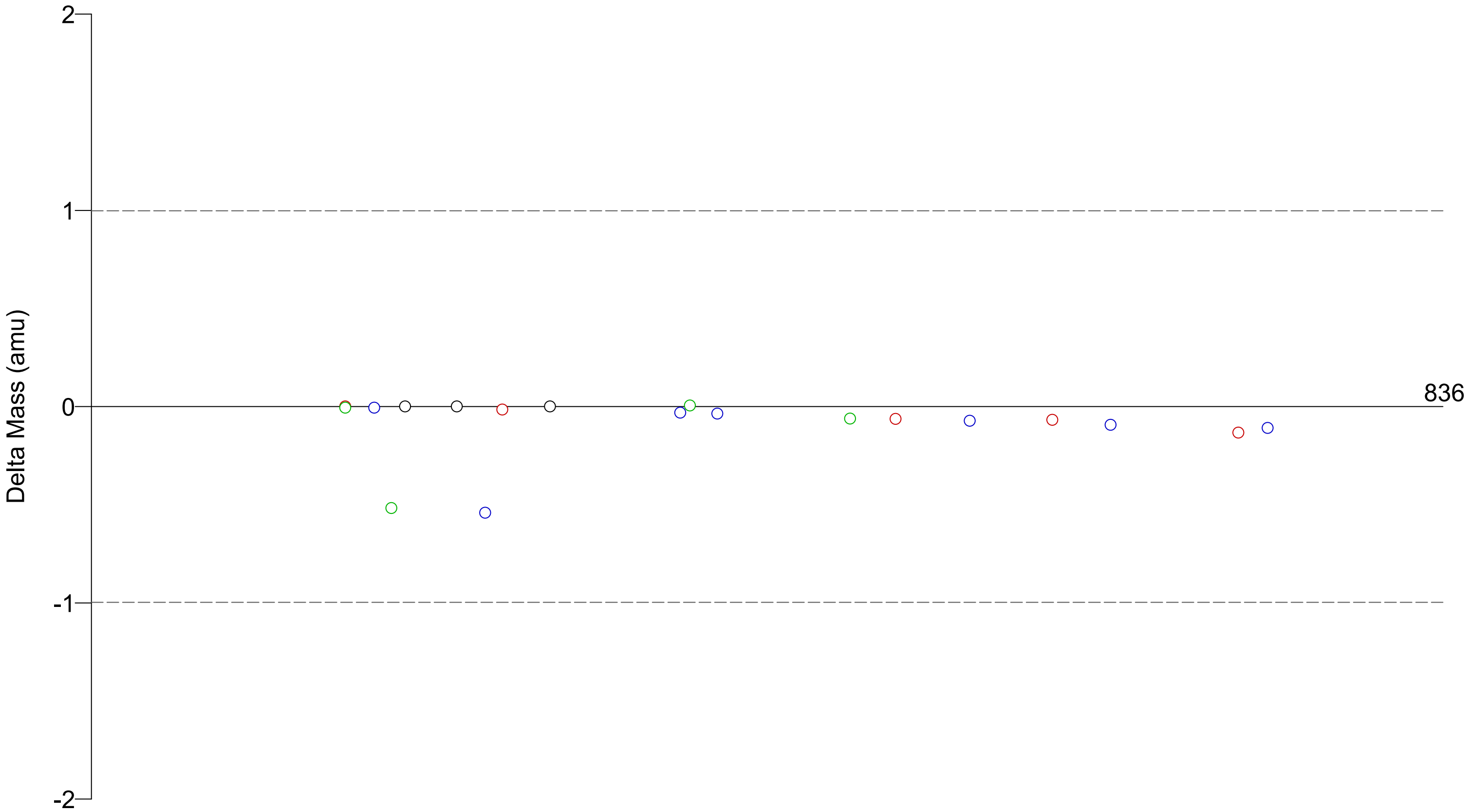
```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z    P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00827815.1|TREMBL:A2NYV4 Ta                                      1        10.1     0.0       0
              K.RPSGVPDR.F                                883.47     2  0.1      2.914  0.384   612.6  1   14/21   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

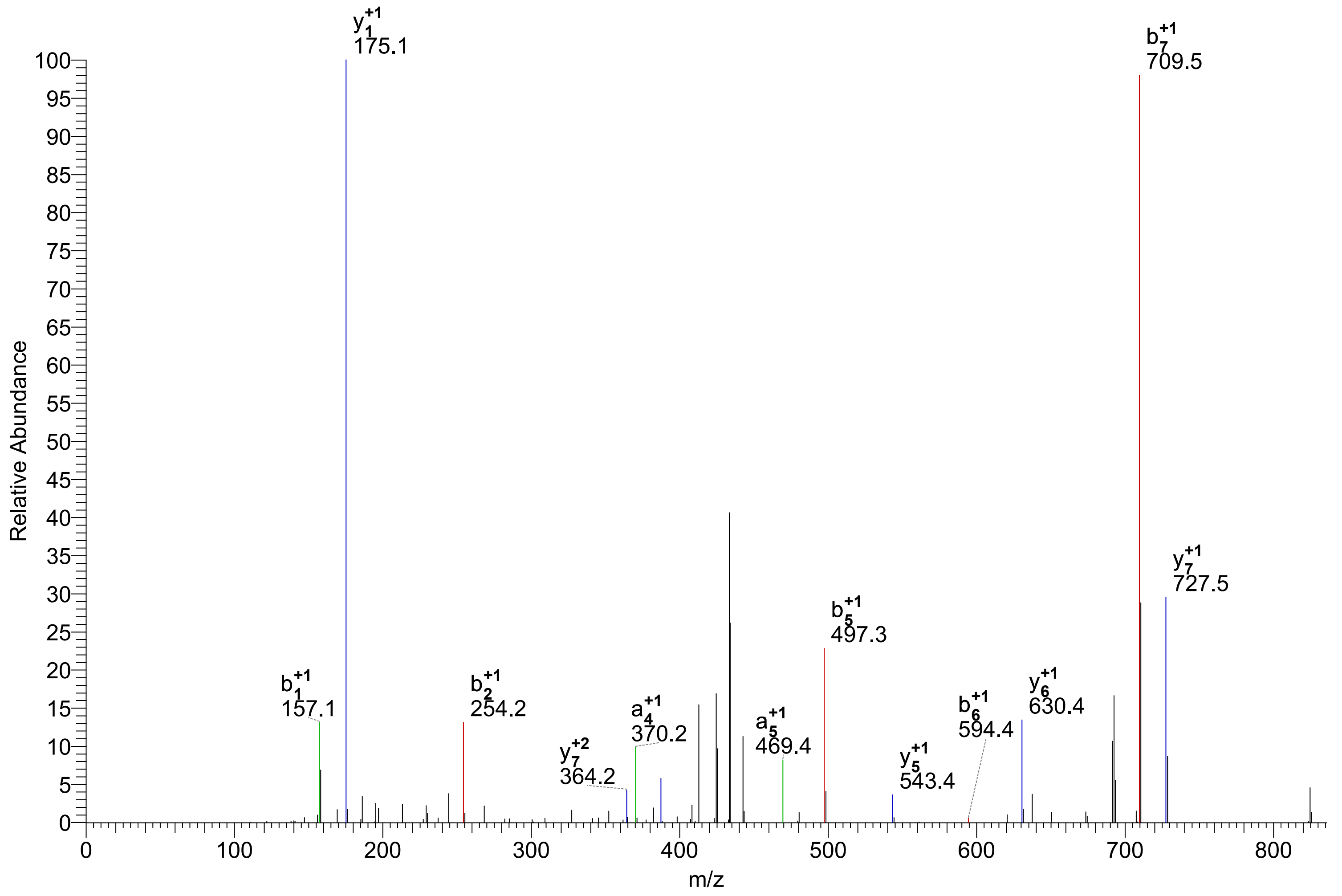
Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```



Delta Mass (amu)
2
1
0
-1
-2
836

#0-0 NL: 6.35E5



Relative Abundance
m/z
y1+1 175.1
b7+1 709.5
y7+1 727.5
b5+1 497.3
b1+1 157.1
b2+1 254.2
y7+2 364.2
a4+1 370.2
a5+1 469.4
y5+1 543.4
b6+1 594.4
y6+1 630.4
0
100
200
300
400
500
600
700
800

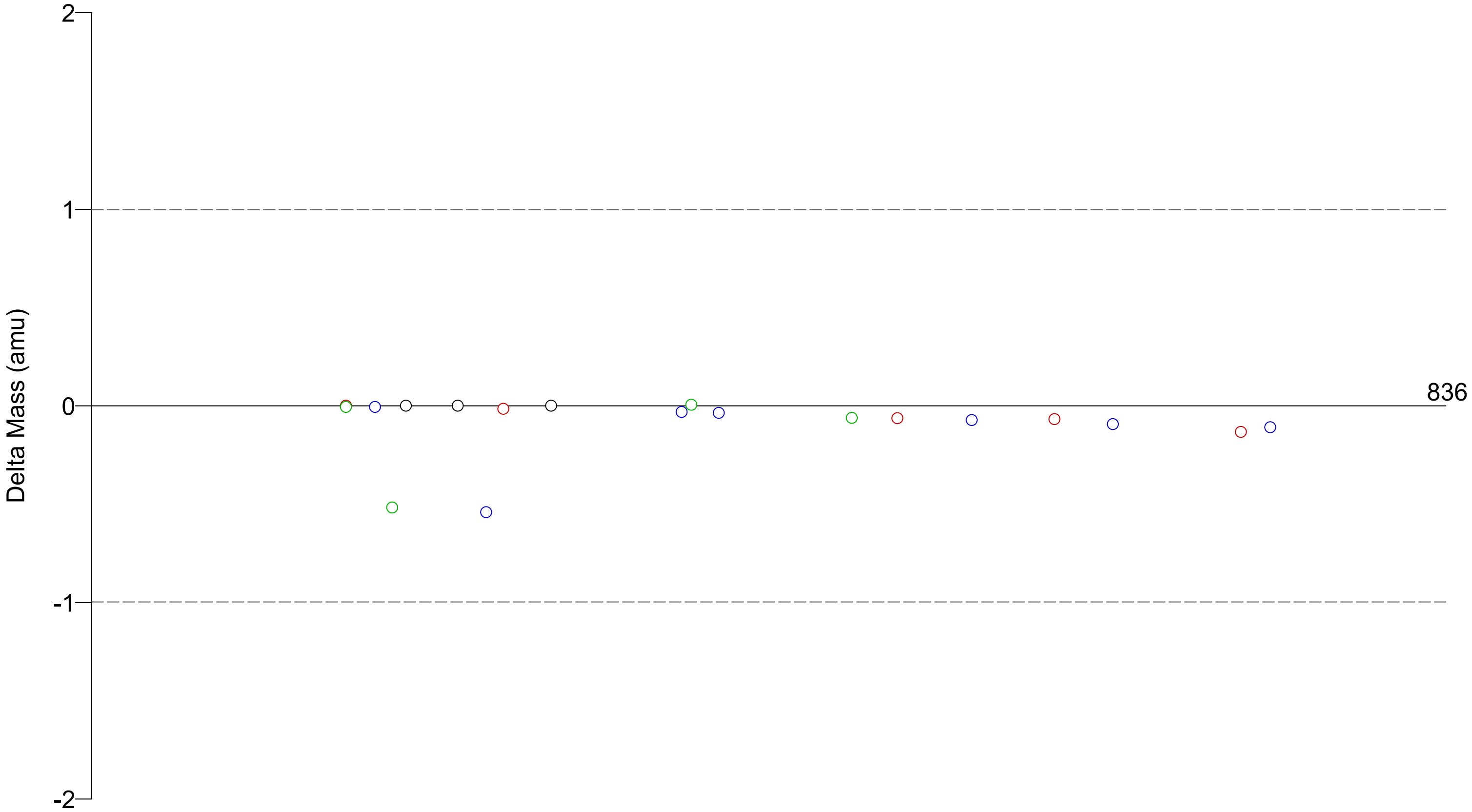
```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+      z     P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00828048.1|TREMBL:A2KUC4 Ta                                       1       10.1     0.0       0
              K.RPSGVPDR.F                                883.47    2  0.1      2.914  0.384   612.6  1   14/21   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

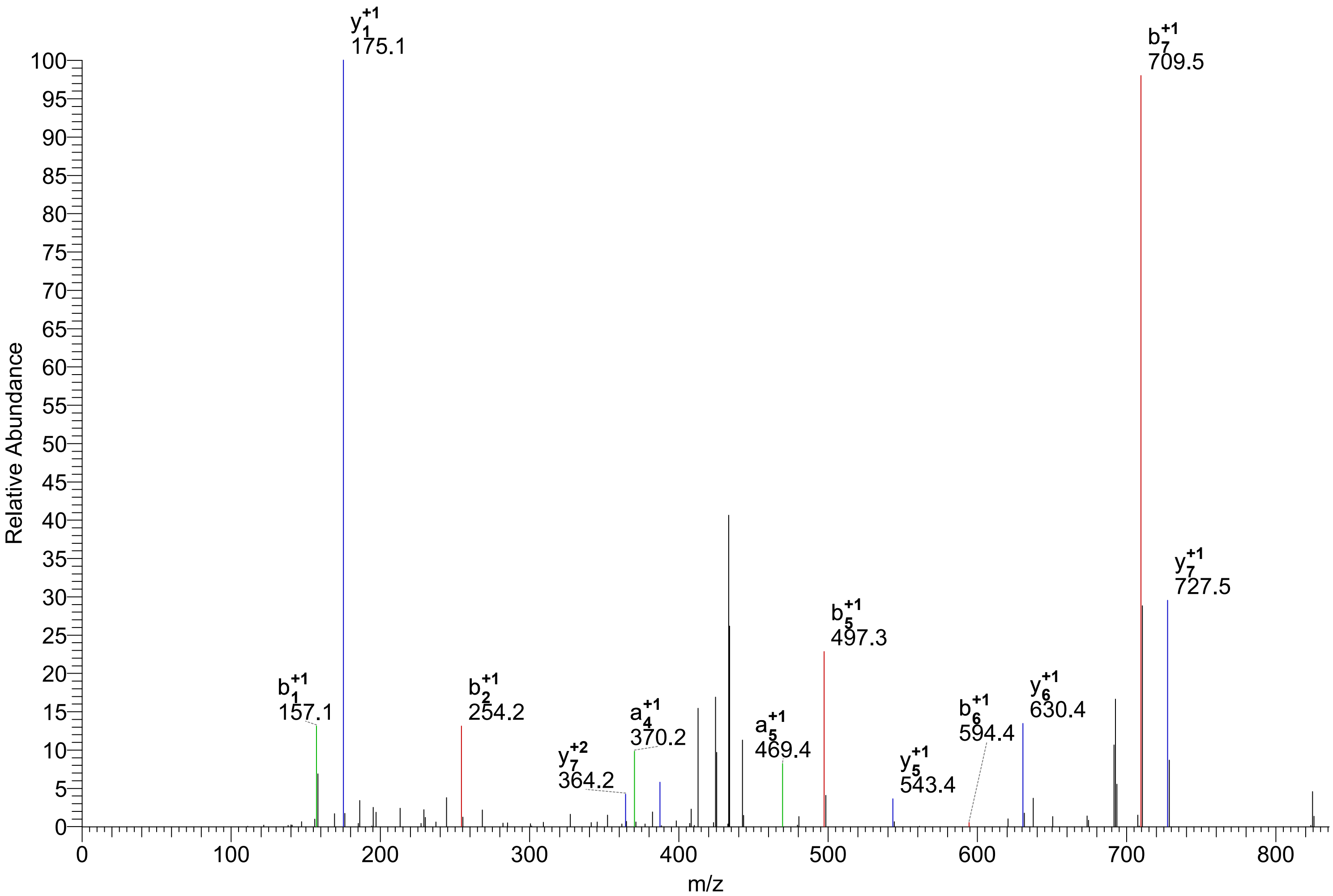
Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```



2
1
0
-1
-2
Delta Mass (amu)
836

#0-0 NL: 6.35E5



y1 +1 175.1
b7 +1 709.5
y7 +1 727.5
b5 +1 497.3
b1 +1 157.1
b2 +1 254.2
a4 +1 370.2
y7 +2 364.2
a5 +1 469.4
y5 +1 543.4
b6 +1 594.4
y6 +1 630.4
Relative Abundance
0
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
95
100
0
100
200
300
400
500
600
700
800
m/z

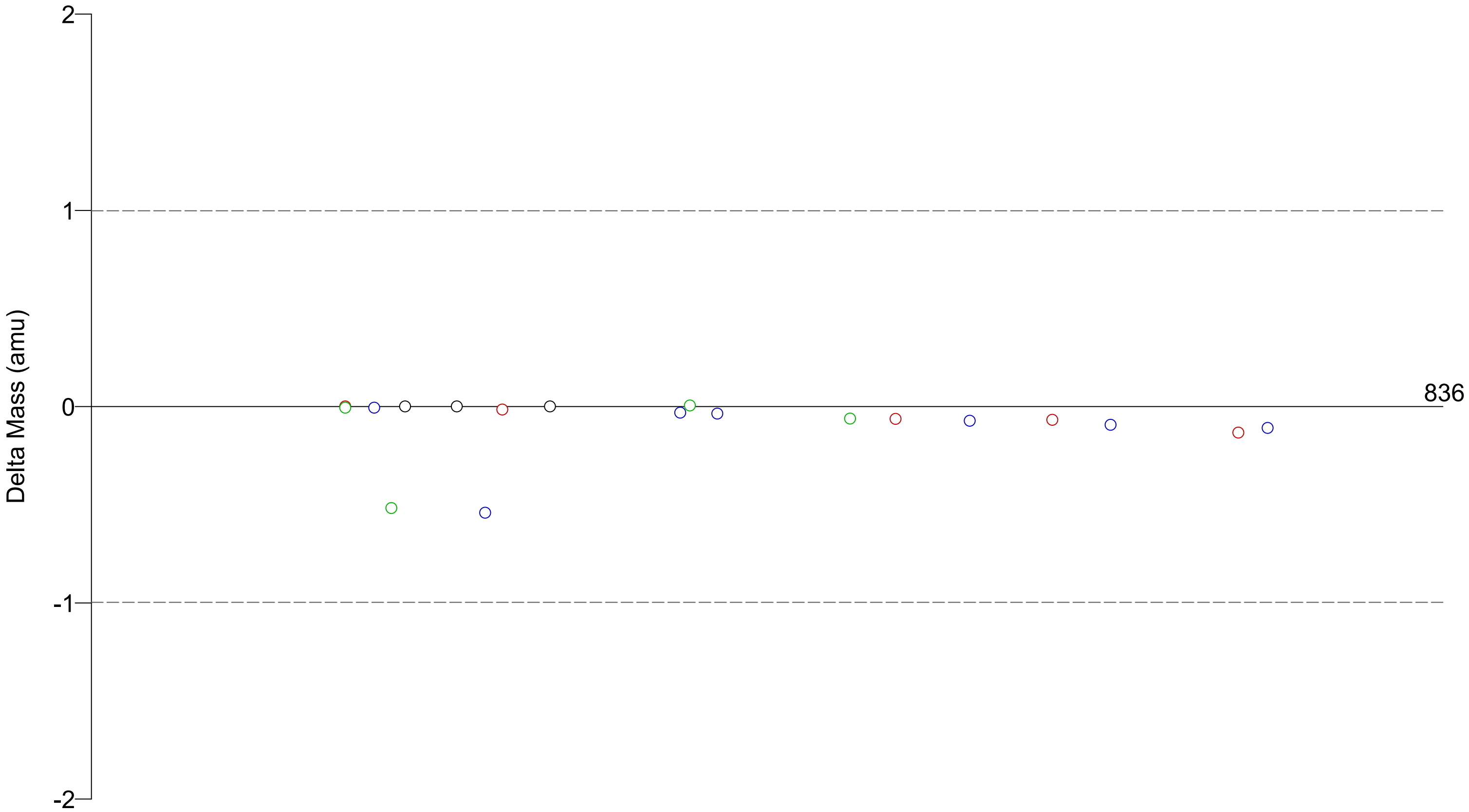
```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+        z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00828149.1|TREMBL:A2NYQ8 Ta                                    1        10.1     0.0       0
              K.RPSGVPDR.F                             883.47     2  0.1      2.914  0.384   612.6  1   14/21   8

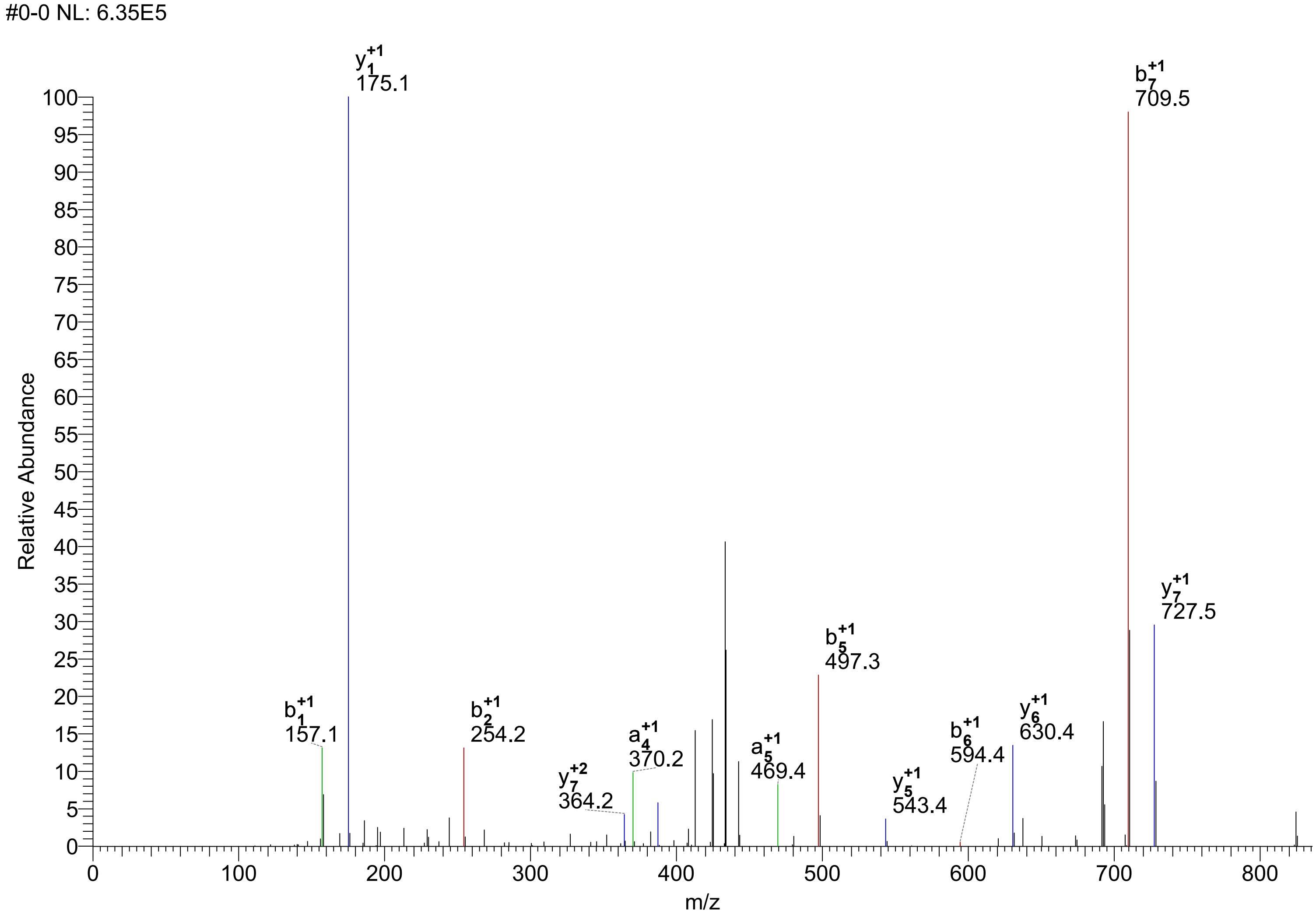
1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 S    313.20     341.19                                      630.32
 G    370.22     398.21                                      543.29
 V    469.29     497.28                                      486.27
 P    566.34     594.34                                      387.20
 D    681.37     709.36                                      290.15
 R                                                           175.12
```


Delta Mass (amu)
2
1
0
-1
-2
836


#0-0 NL: 6.35E5
Relative Abundance
m/z
y_1^{+1} 175.1
b_7^{+1} 709.5
y_7^{+1} 727.5
b_5^{+1} 497.3
b_1^{+1} 157.1
b_2^{+1} 254.2
y_7^{+2} 364.2
a_4^{+1} 370.2
a_5^{+1} 469.4
y_5^{+1} 543.4
b_6^{+1} 594.4
y_6^{+1} 630.4
0 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100
0 100 200 300 400 500 600 700 800

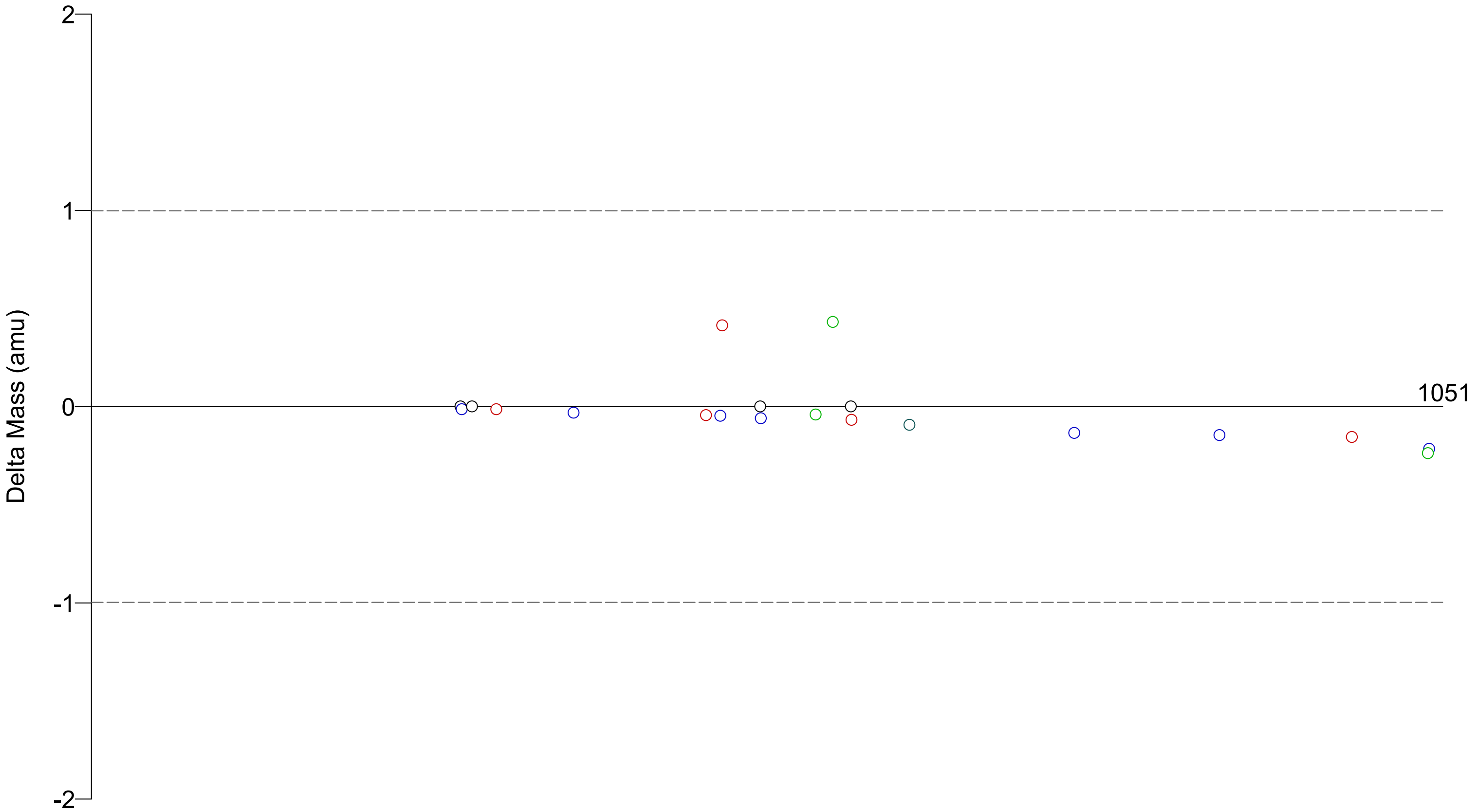
```
Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00890754.1|TREMBL:B1N7B6 Tax_Id=9606 Gene_Symbol=- Cryo    1       10.1     0.0       0
19287468 - 1  K.NTVYLQM*NSLR.A                       1354.68   2  0.1     2.168  0.000   607.2  1   14/30

1 of 1 peptide matches reported, 0 removed due to filtering
```

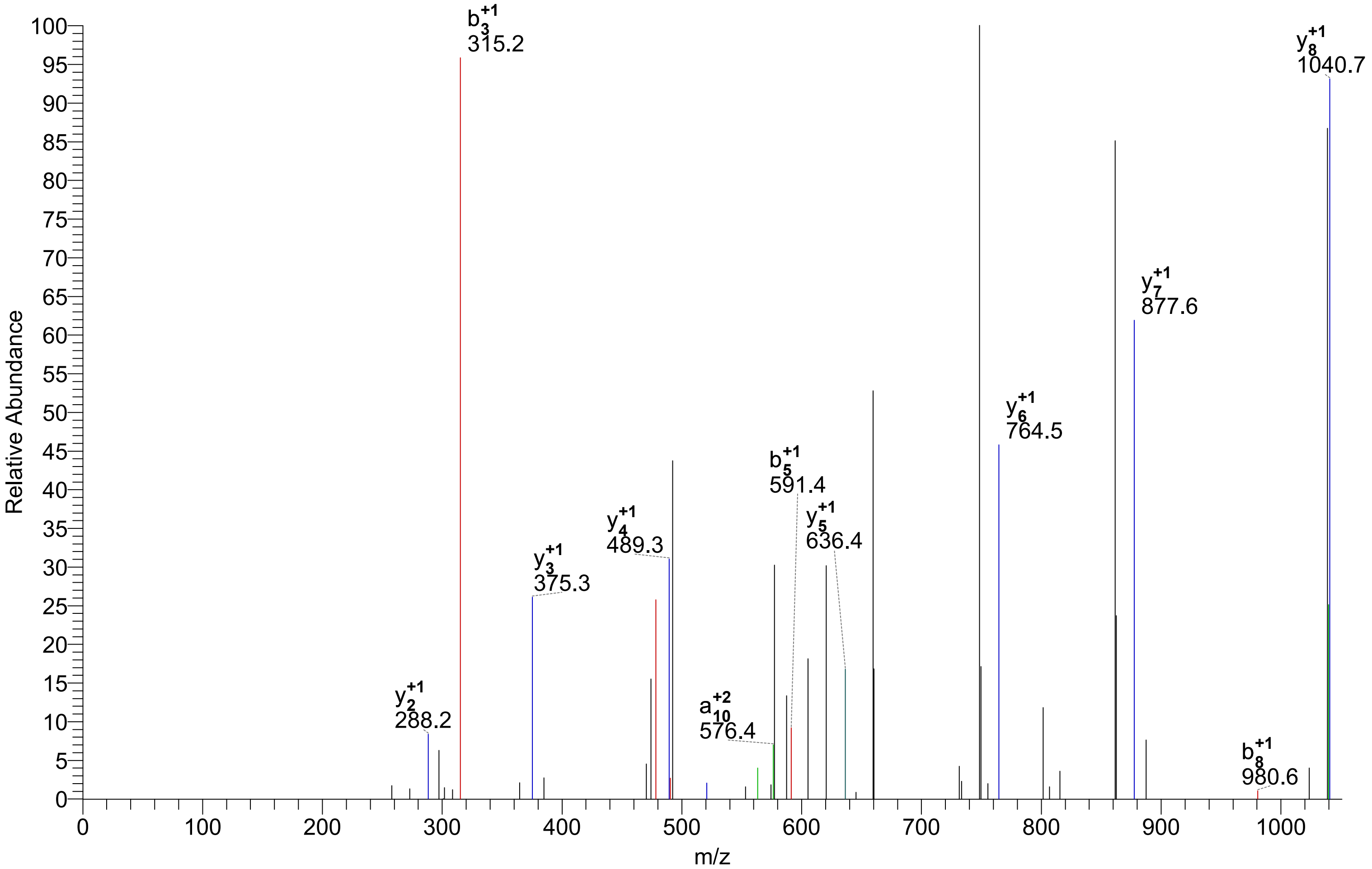
```
DTA for scans: 19287468-1
Precursor ion: 677.84
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 N     87.06     115.05
 T    188.10     216.10                                     1240.64
 V    287.17     315.17                                     1139.59
 Y    450.23     478.23                                     1040.52
 L    563.32     591.31                                      877.46
 Q    691.38     719.37                                      764.37
 M*   838.41     866.41                                      636.31
 N    952.46     980.45                                      489.28
 S   1039.49    1067.48                                      375.24
 L   1152.57    1180.57                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 8.93E4



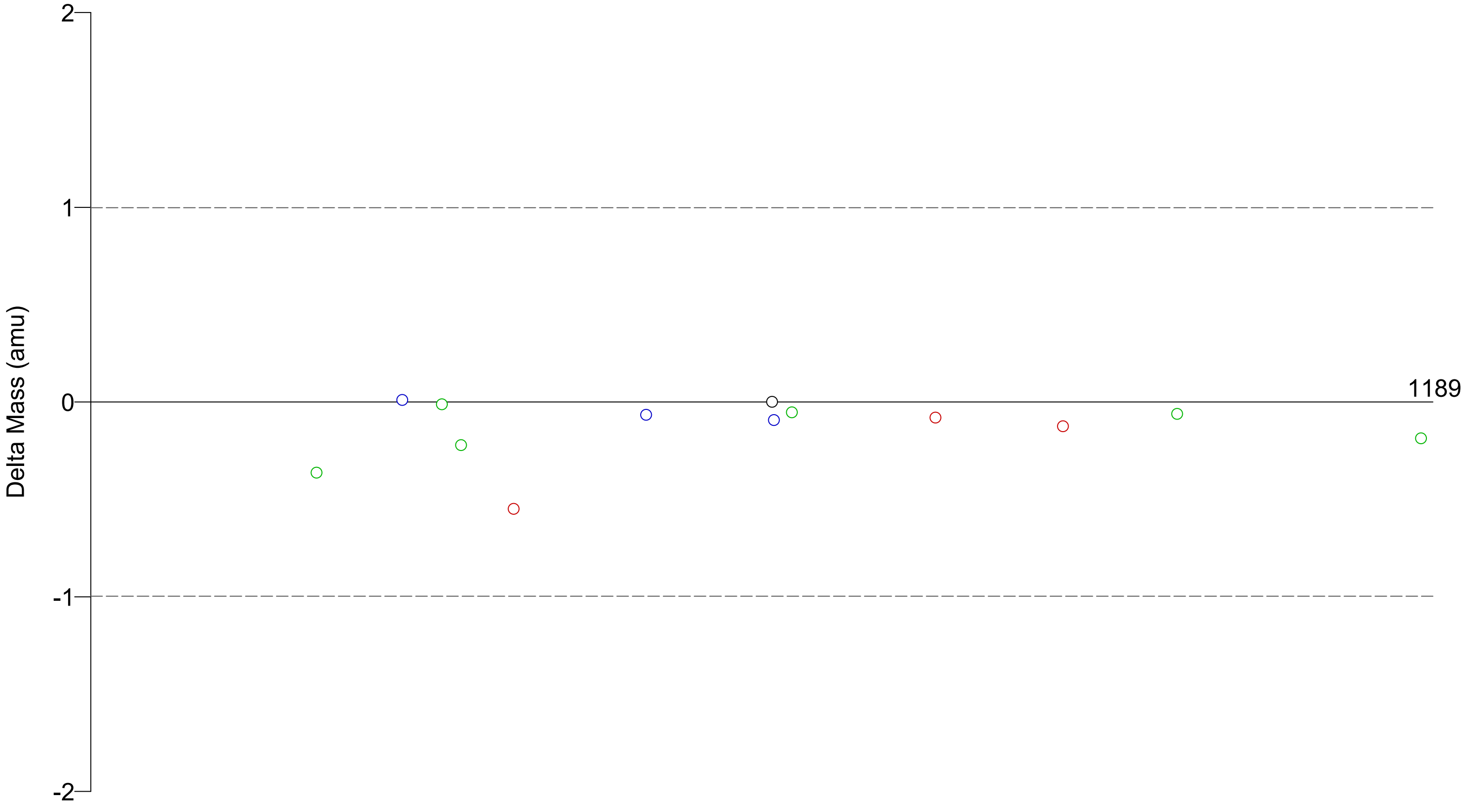
```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC DeltaCn   Sp   RSp   Ions  Count
IPI:IPI00022438.1|SWISS-PROT:O75444-1|TREMBL:Q8IX32|ENSEMBL:EN    1       8.1      0.0        0
19287468 - 1  R.VQQRHVLESEK.N                         1352.73   2  1       1.436  0.647   201.9   2   10/30   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

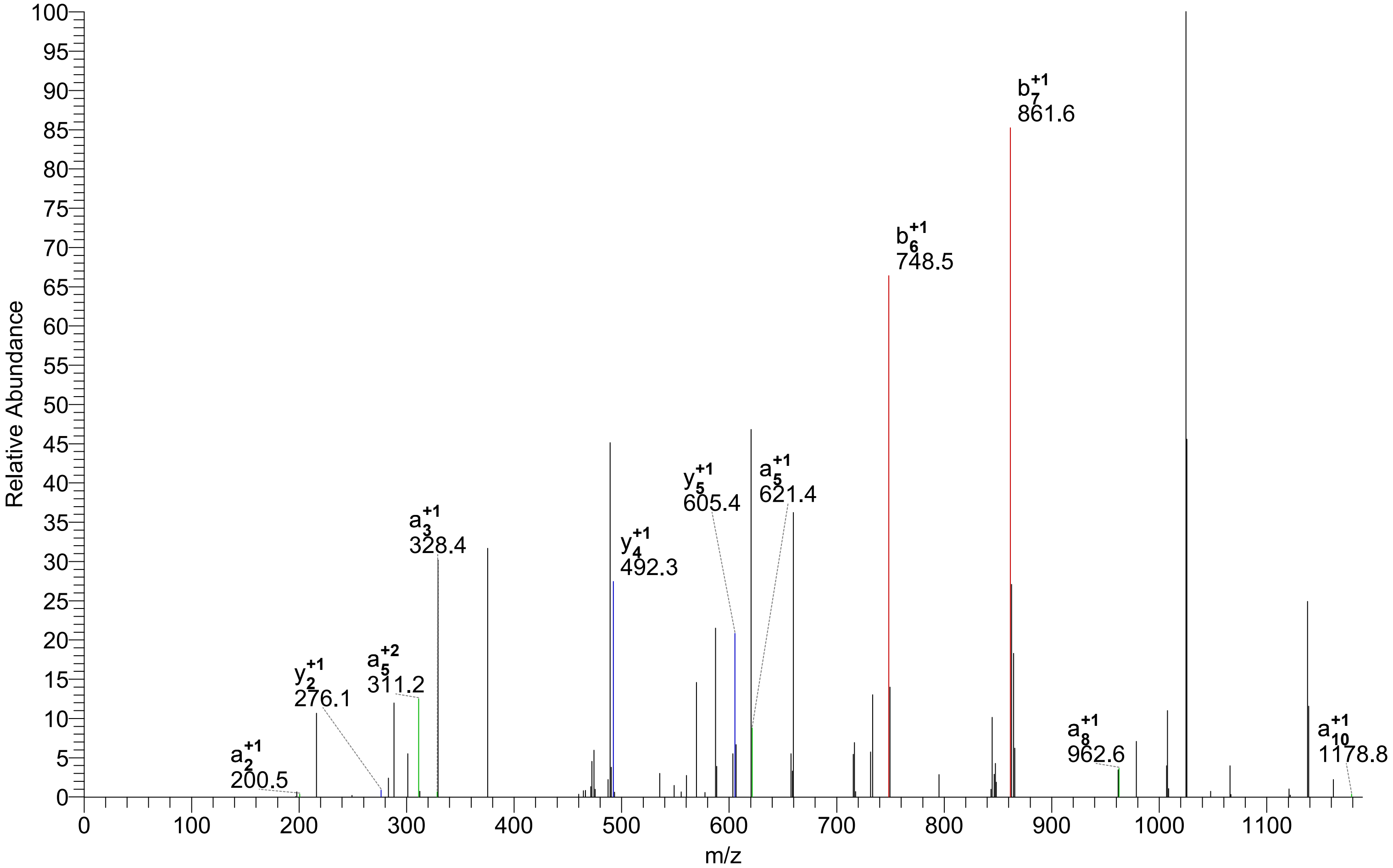
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 V     72.08     100.08
 Q    200.14     228.13                                     1253.66
 Q    328.20     356.19                                     1125.60
 R    484.30     512.29                                      997.54
 H    621.36     649.35                                      841.44
 V    720.43     748.42                                      704.38
 L    833.51     861.51                                      605.31
 E    962.55     990.55                                      492.23
 S   1049.59    1077.58                                      363.19
 E   1178.63    1206.62                                      276.16
 K                                                           147.11
```



#19287468-1 NL: 1.01E5



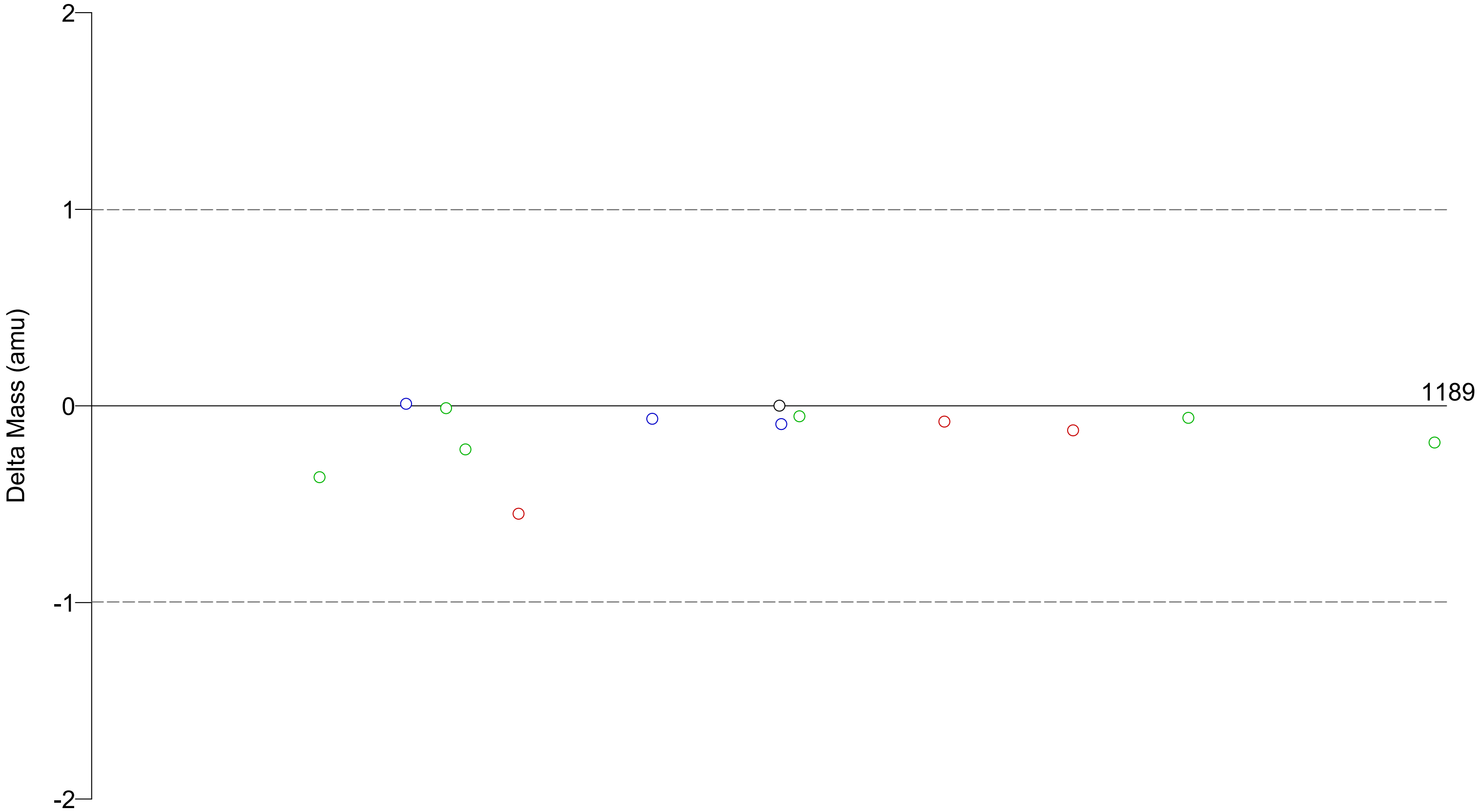
```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00219060.1|SWISS-PROT:O7544                                 1        8.1      0.0        0
19287468 - 1  R.VQQRHVLESEK.N                        1352.73    2  1        1.436  0.647   201.9  2   10/30   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

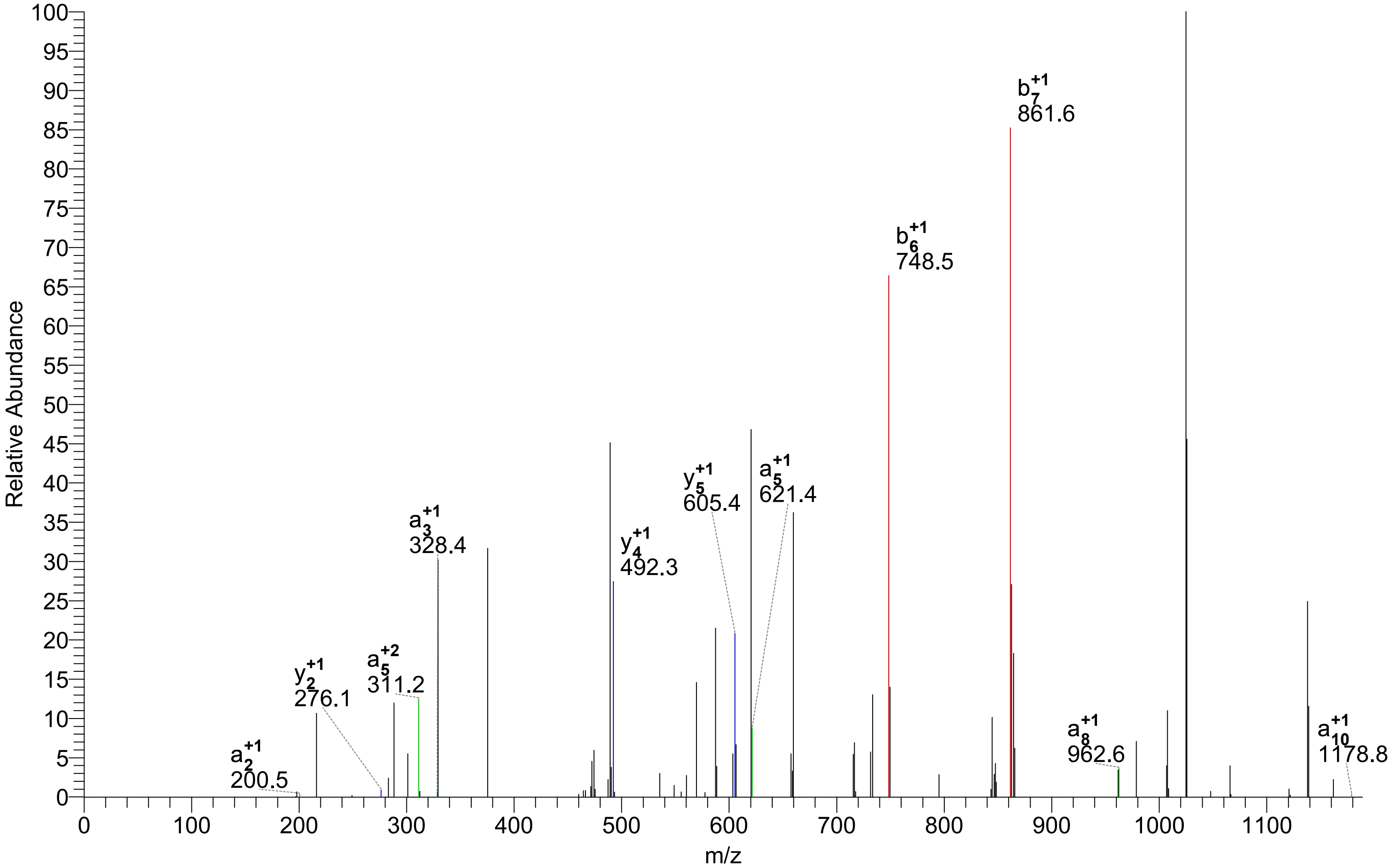
```
DTA for scans: 19287468-1
Precursor ion: 676.85
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 V     72.08     100.08
 Q    200.14     228.13                                     1253.66
 Q    328.20     356.19                                     1125.60
 R    484.30     512.29                                      997.54
 H    621.36     649.35                                      841.44
 V    720.43     748.42                                      704.38
 L    833.51     861.51                                      605.31
 E    962.55     990.55                                      492.23
 S   1049.59    1077.58                                      363.19
 E   1178.63    1206.62                                      276.16
 K                                                           147.11
```



#19287468-1 NL: 1.01E5



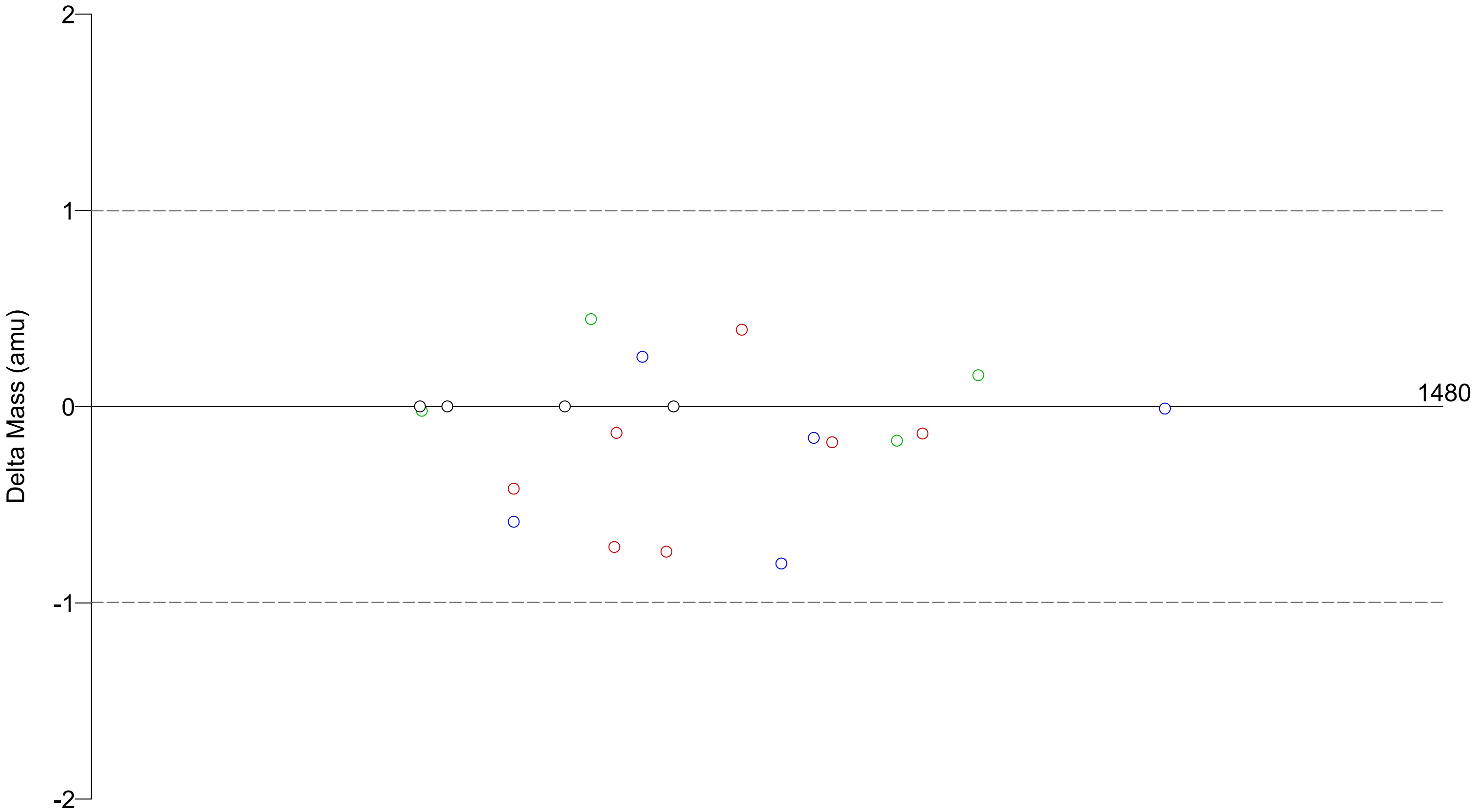
```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00445079.1|TREMBL:Q6ZTG6|REFSEQ:XP_001714376;XP_0017207    1       8.1      0.0       0
19287468 - 1  R.LYLNAHVVPGPPQSSRPRP.-             2085.14   3  0.1      1.550  0.564   118.3  8   13/108  1

1 of 1 peptide matches reported, 0 removed due to filtering
```

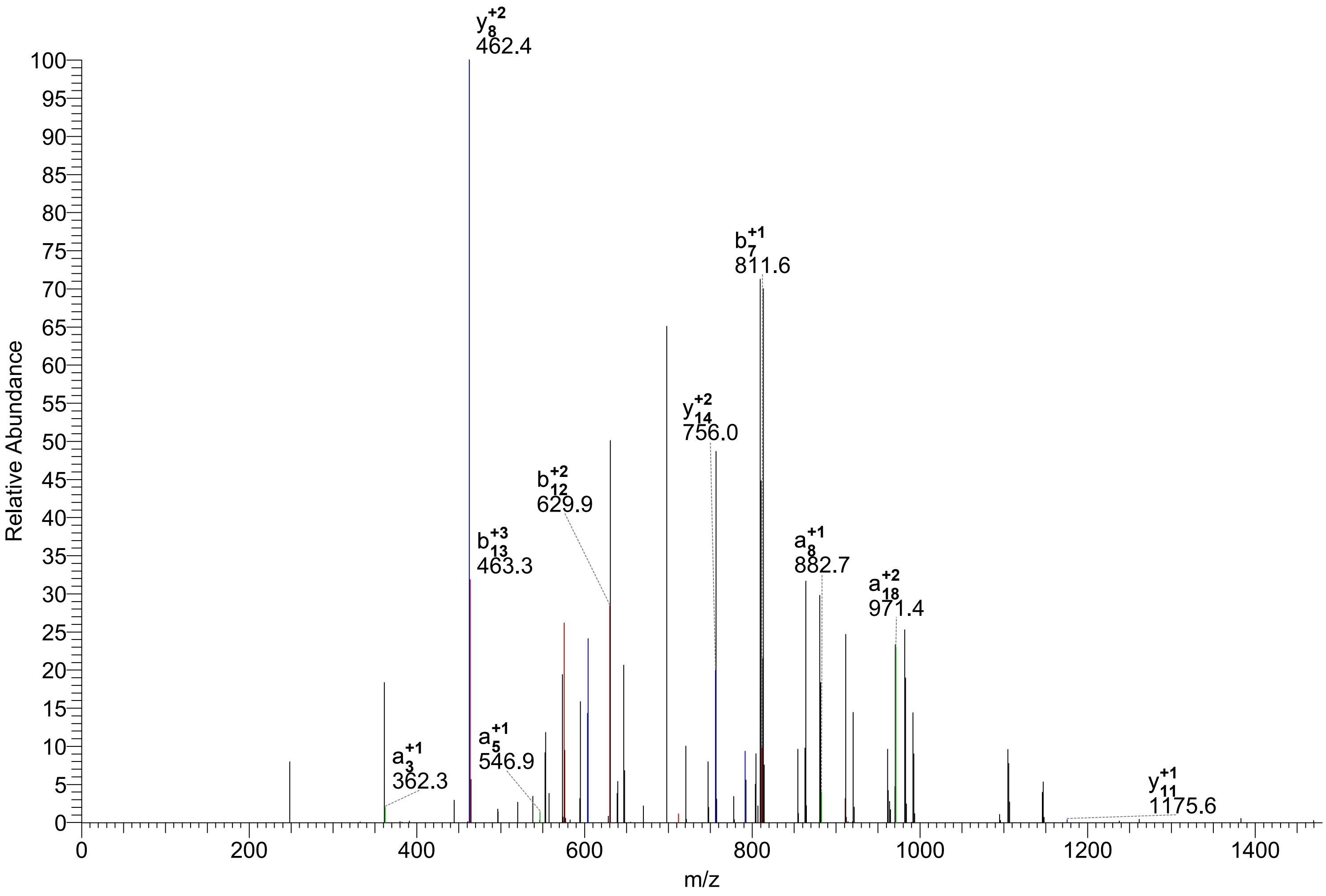
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 Y    249.16     277.15                                     1972.05
 L    362.24     390.24                                     1808.99
 N    476.29     504.28                                     1695.90
 A    547.32     575.32                                     1581.86
 H    684.38     712.38                                     1510.82
 V    783.45     811.45                                     1373.76
 V    882.52     910.51                                     1274.70
 P    979.57    1007.57                                     1175.63
 G   1036.59    1064.59                                     1078.58
 P   1133.65    1161.64                                     1021.55
 P   1230.70    1258.69                                      924.50
 Q   1358.76    1386.75                                      827.45
 S   1445.79    1473.78                                      699.39
 S   1532.82    1560.82                                      612.36
 R   1688.92    1716.92                                      525.33
 P   1785.98    1813.97                                      369.22
 R   1942.08    1970.07                                      272.17
 P                                                           116.07
```



#19287468-1 NL: 5.80E4



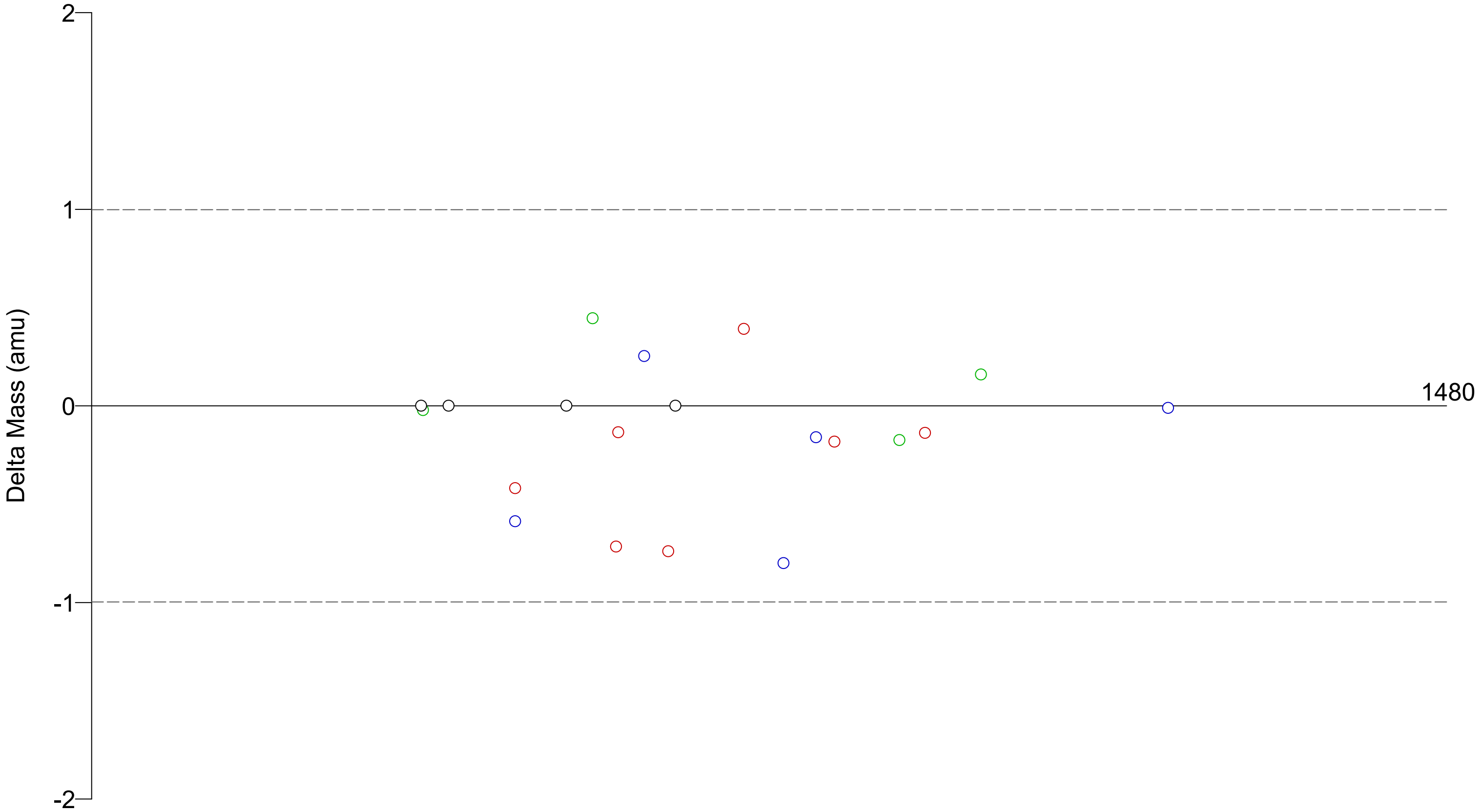
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00935923.1|REFSEQ:XP_002342                                 1       8.1      0.0       0
19287468 - 1  R.LYLNAHVVPGPPQSSRPRP.-              2085.14    3  0.1      1.550  0.564   118.3  8   13/108  1

1 of 1 peptide matches reported, 0 removed due to filtering
```

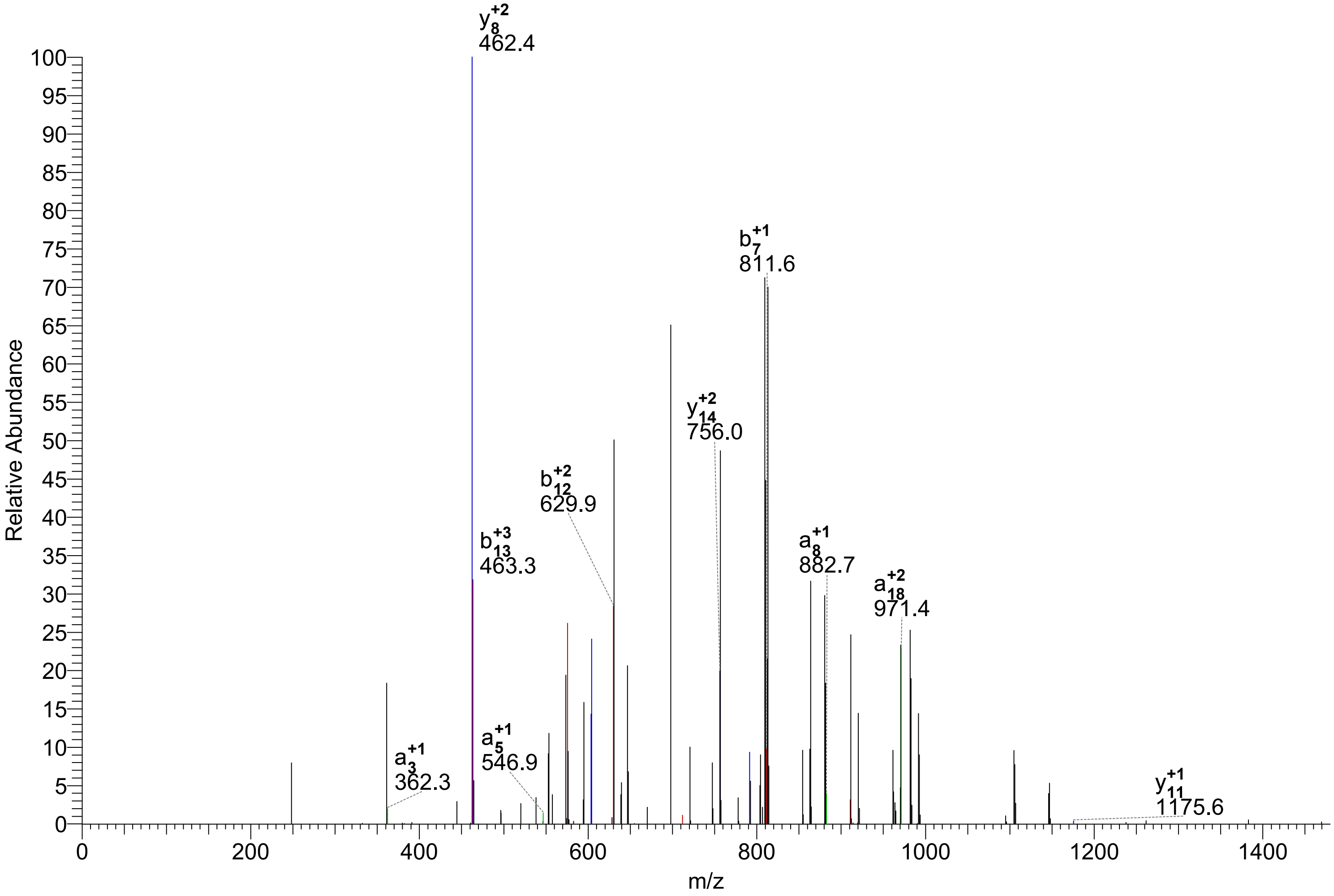
```
DTA for scans: 19287468-1
Precursor ion: 695.73
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 Y    249.16    277.15                                     1972.05
 L    362.24    390.24                                     1808.99
 N    476.29    504.28                                     1695.90
 A    547.32    575.32                                     1581.86
 H    684.38    712.38                                     1510.82
 V    783.45    811.45                                     1373.76
 V    882.52    910.51                                     1274.70
 P    979.57   1007.57                                     1175.63
 G   1036.59   1064.59                                     1078.58
 P   1133.65   1161.64                                     1021.55
 P   1230.70   1258.69                                      924.50
 Q   1358.76   1386.75                                      827.45
 S   1445.79   1473.78                                      699.39
 S   1532.82   1560.82                                      612.36
 R   1688.92   1716.92                                      525.33
 P   1785.98   1813.97                                      369.22
 R   1942.08   1970.07                                      272.17
 P                                                          116.07
```



#19287468-1 NL: 5.80E4



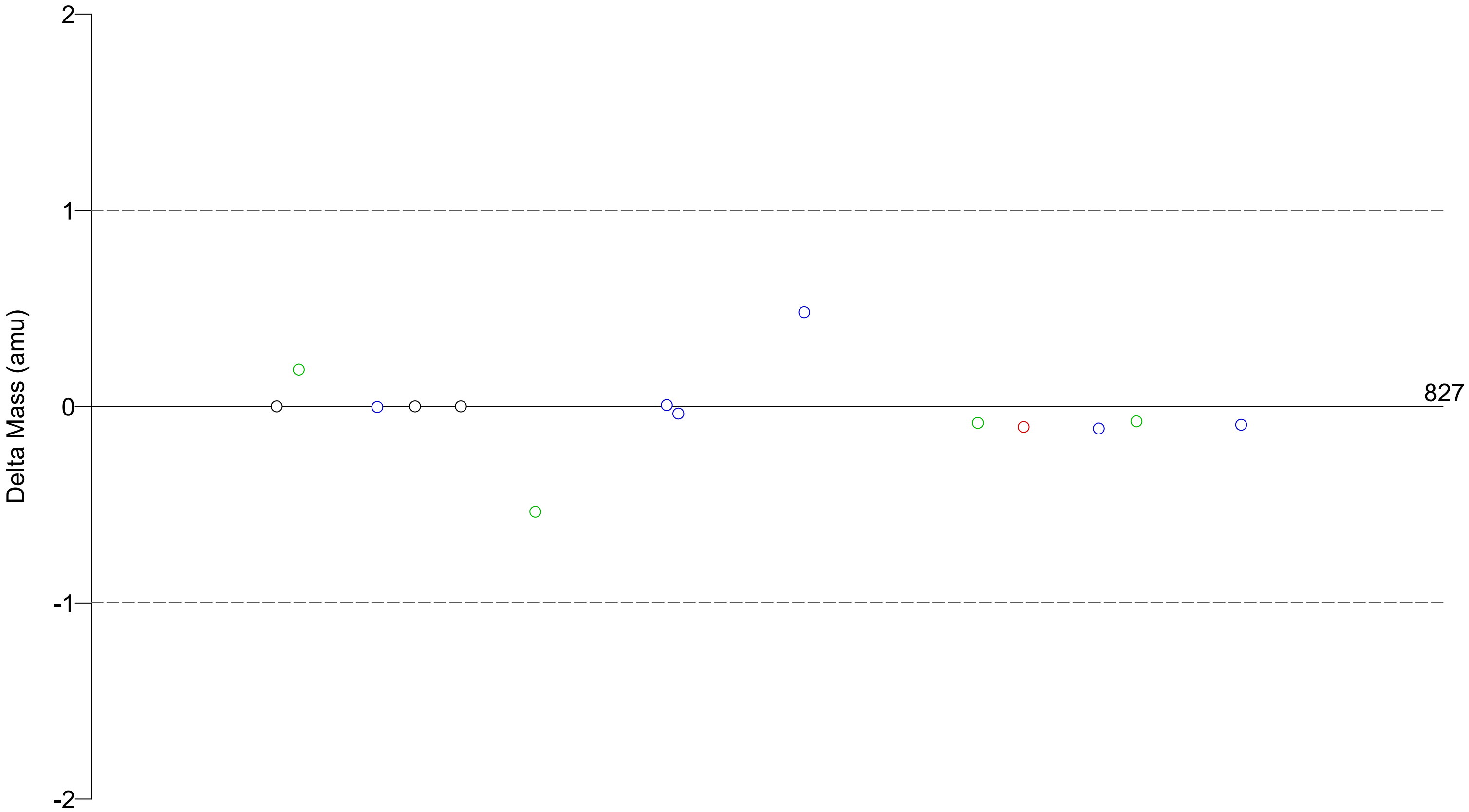
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00418845.1|TREMBL:Q6ZS85|H-INV:HIT000047515 Tax_Id=9606    1        8.1      0.0       0
19287468 - 1  R.GPASRTPSR.A                              928.50    2  1       1.431  0.467   166.7  10  10/24

1 of 1 peptide matches reported, 0 removed due to filtering
```

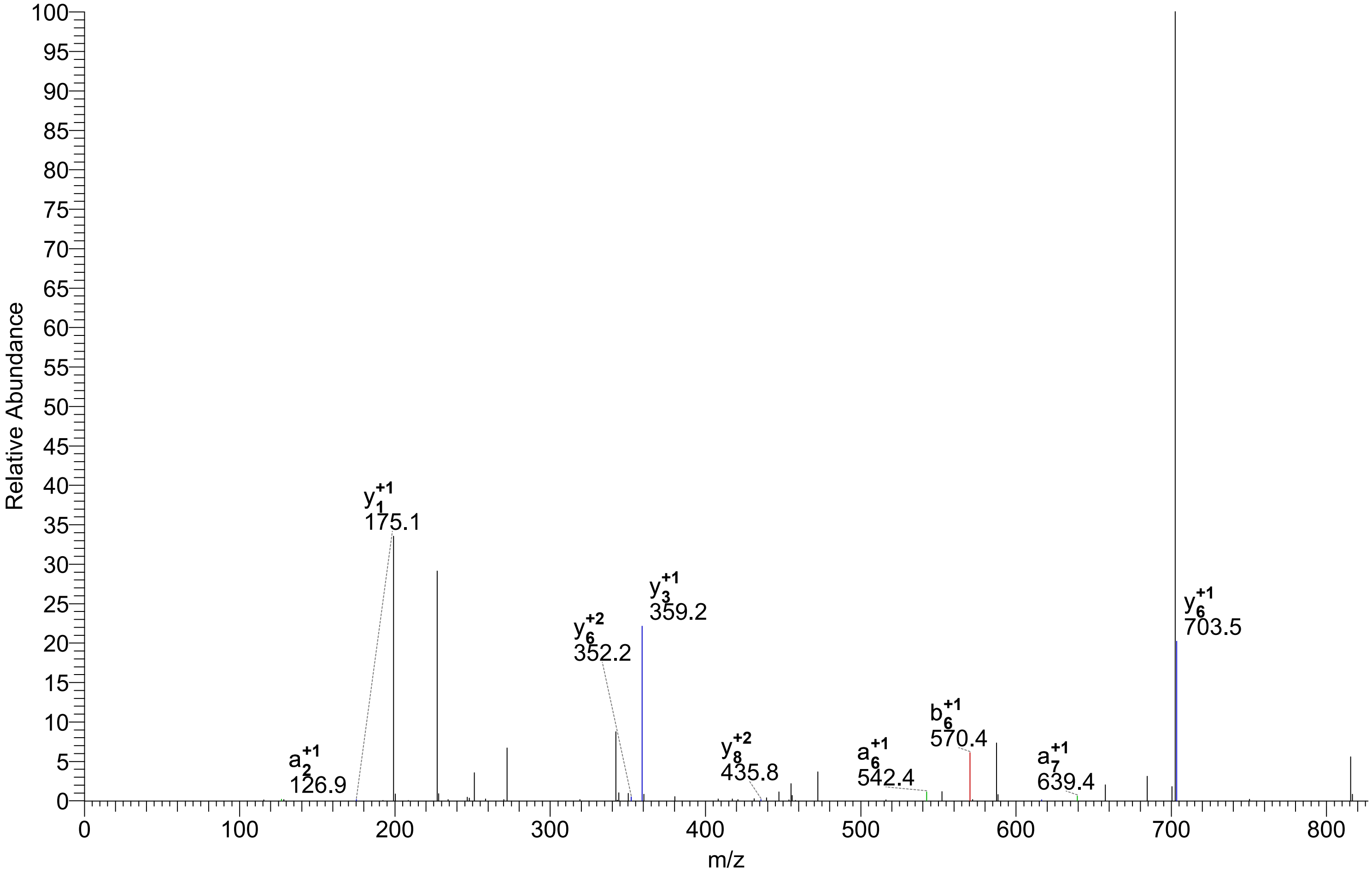
```
DTA for scans: 19287468-1
Precursor ion: 464.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 P    127.09     155.08                                     871.47
 A    198.12     226.12                                     774.42
 S    285.16     313.15                                     703.38
 R    441.26     469.25                                     616.35
 T    542.30     570.30                                     460.25
 P    639.36     667.35                                     359.20
 S    726.39     754.38                                     262.15
 R                                                          175.12
```



#19287468-1 NL: 1.36E6



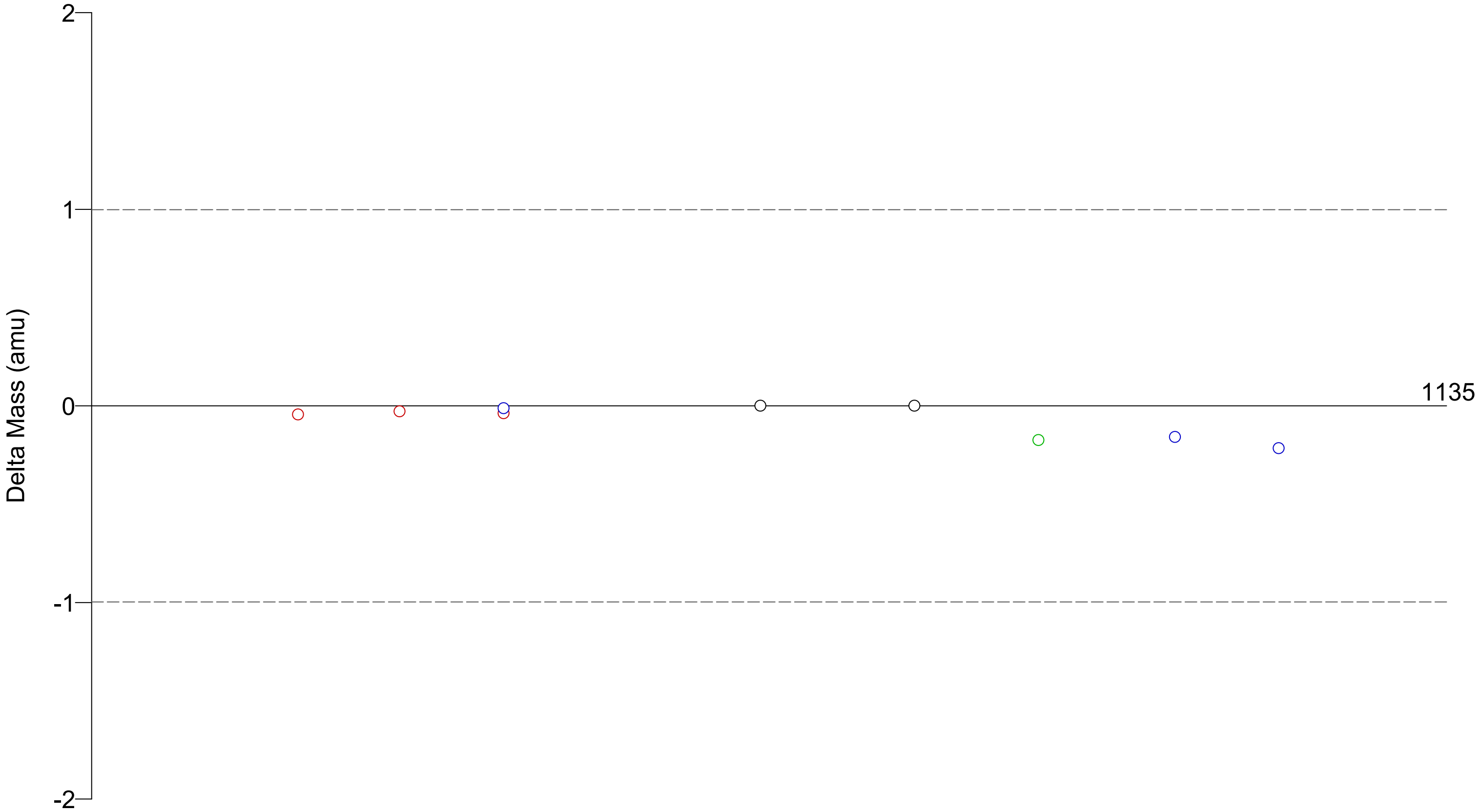
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn  Sp    RSp  Ions  Count
IPI:IPI00069817.2|SWISS-PROT:Q9UIG0-1|ENSEMBL:ENSP00000342434;    1       8.1      0.0       0
2118291816 -  R.WASMSEEQRK.E                         1251.58   2  1       1.301  0.654   32.9   10  7/27    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

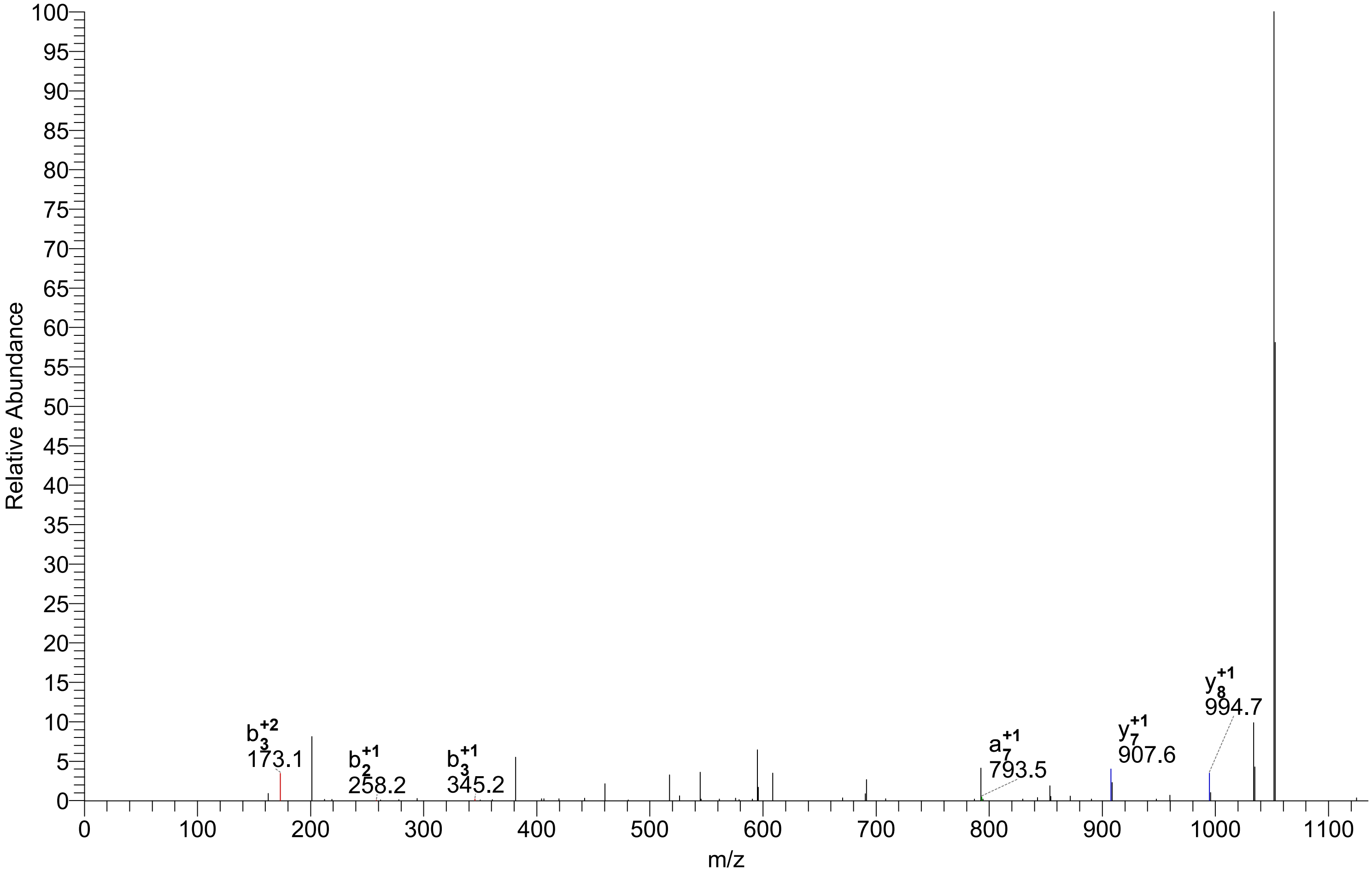
```
DTA for scans: 2118291816-26226248
Precursor ion: 626.30
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 A    230.13     258.12                                    1065.50
 S    317.16     345.16                                     994.46
 M    448.20     476.20                                     907.43
 S    535.23     563.23                                     776.39
 E    664.28     692.27                                     689.36
 E    793.32     821.31                                     560.32
 Q    921.38     949.37                                     431.27
 R   1077.48    1105.47                                     303.21
 K                                                          147.11
```



#2118291816-26226248 NL: 2.31E5



```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

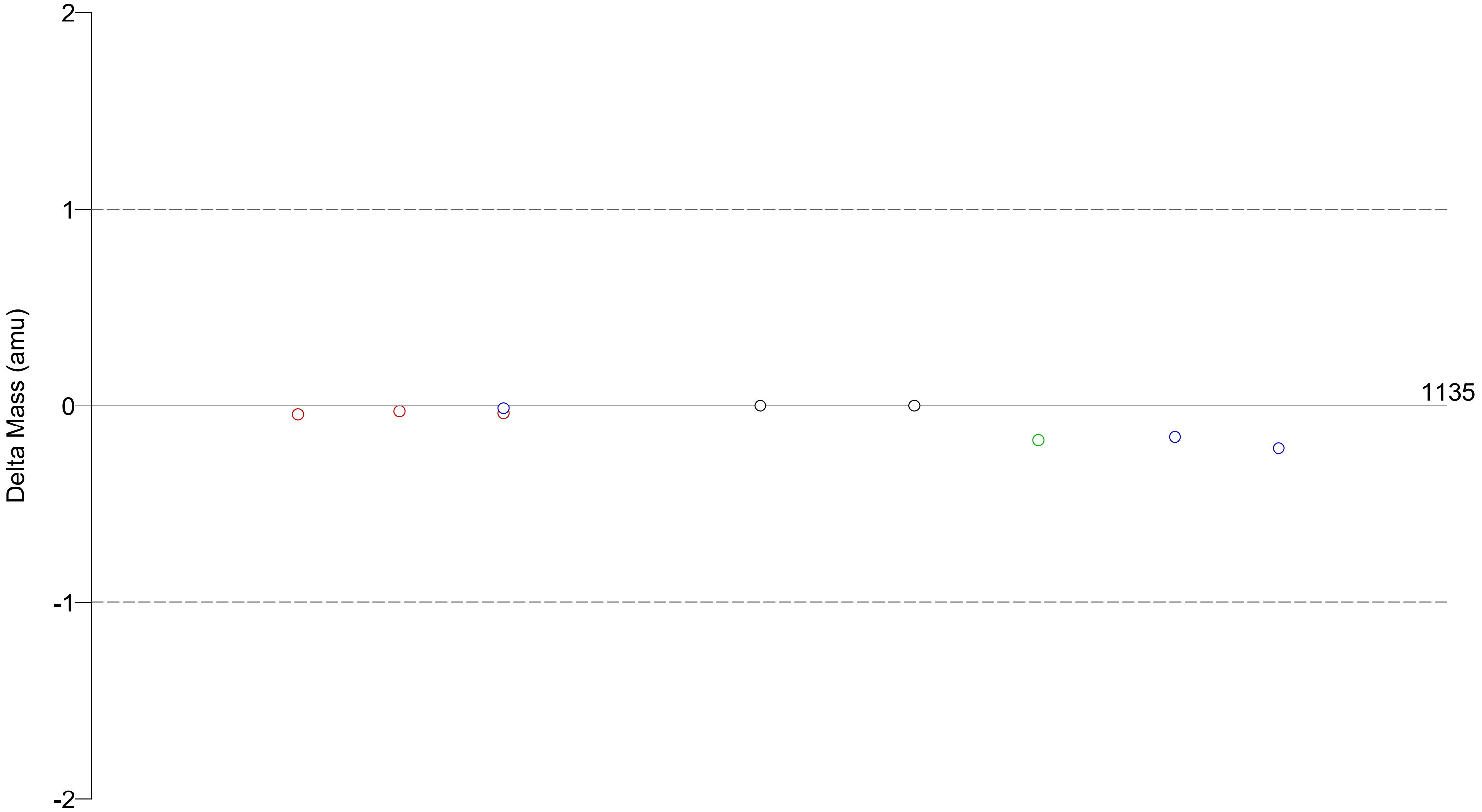
IPI:IPI00216695.1|SWISS-PROT:Q9UIG                                1       8.1      0.0       0
2118291816 -  R.WASMSEEQRK.E                        1251.58   2  1       1.301  0.654   32.9   10  7/27    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

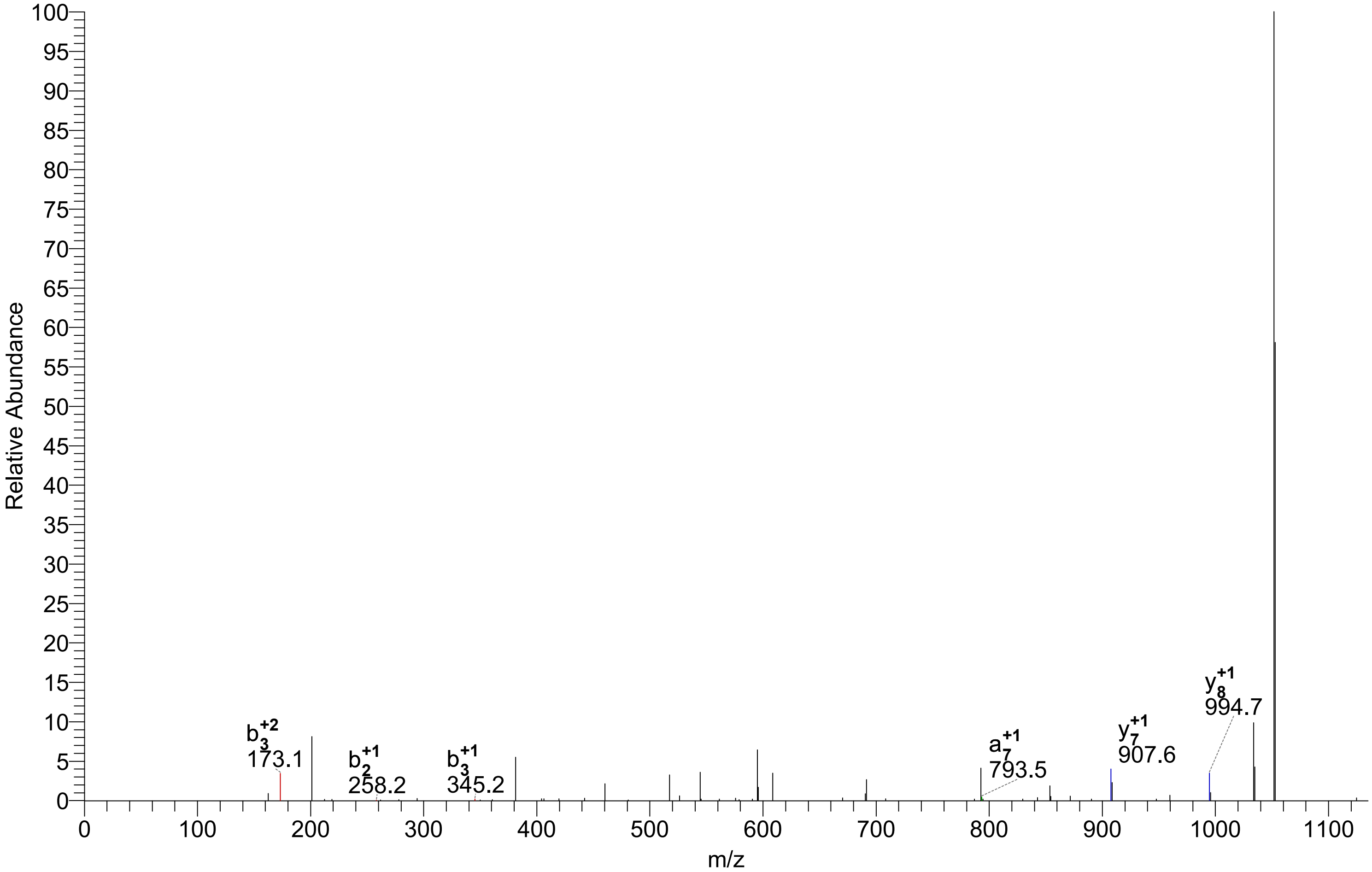
```
DTA for scans: 2118291816-26226248
Precursor ion: 626.30
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 W    159.09     187.09
 A    230.13     258.12                                     1065.50
 S    317.16     345.16                                      994.46
 M    448.20     476.20                                      907.43
 S    535.23     563.23                                      776.39
 E    664.28     692.27                                      689.36
 E    793.32     821.31                                      560.32
 Q    921.38     949.37                                      431.27
 R   1077.48    1105.47                                      303.21
 K                                                           147.11
```



#2118291816-26226248 NL: 2.31E5



```
Reference                                                                    P      Score   Coverage   Accession
Scan(s)       Sequence                                         MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

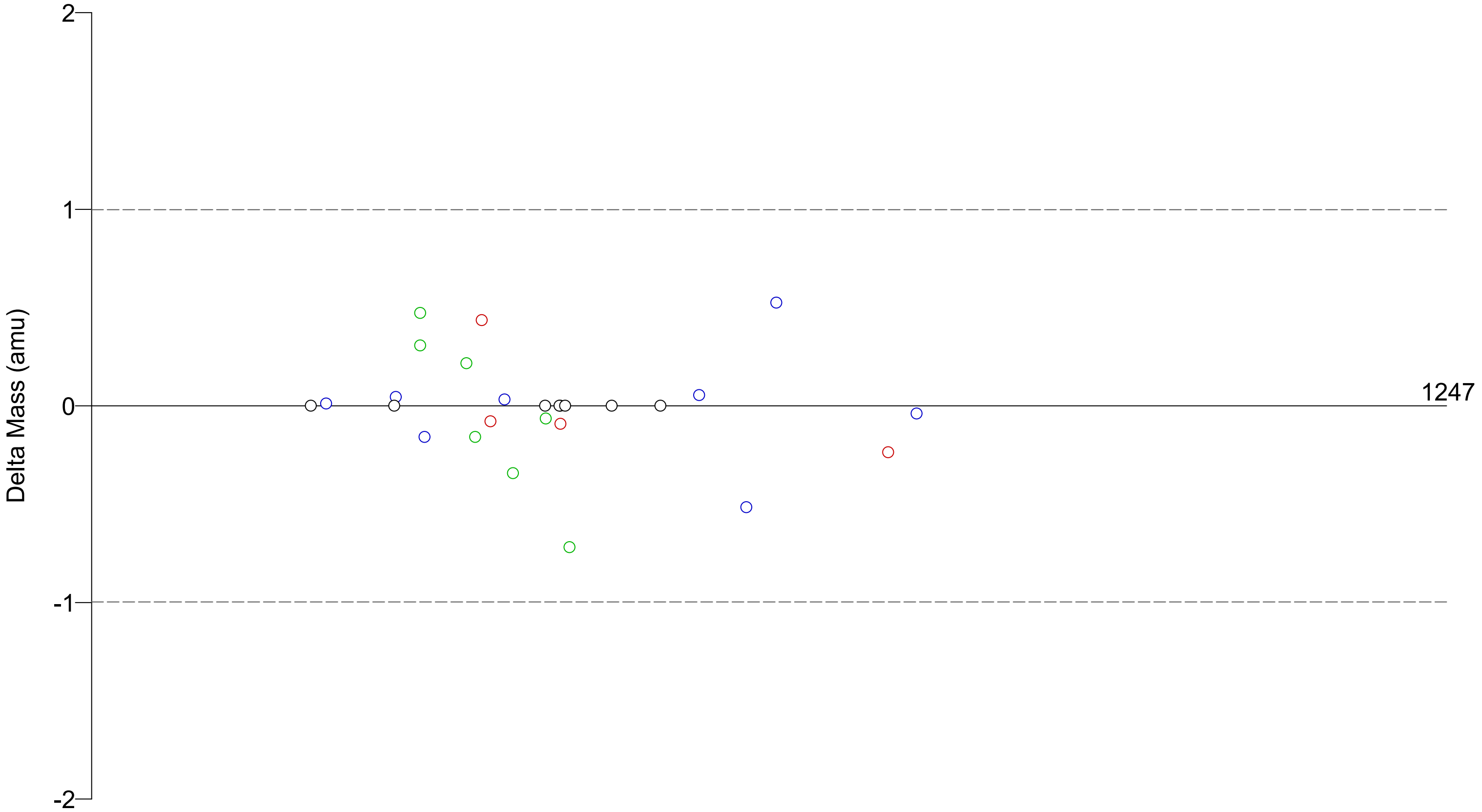
IPI:IPI00411614.1|SWISS-PROT:O75717|TREMBL:A8KAE0;Q05DR3|ENSEM     1       8.1      0.0       0
19287468 - 1  K.GETASEGTEAKKRK.R                            1491.78   3  1       1.815  0.629   168.0  2   16/78   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

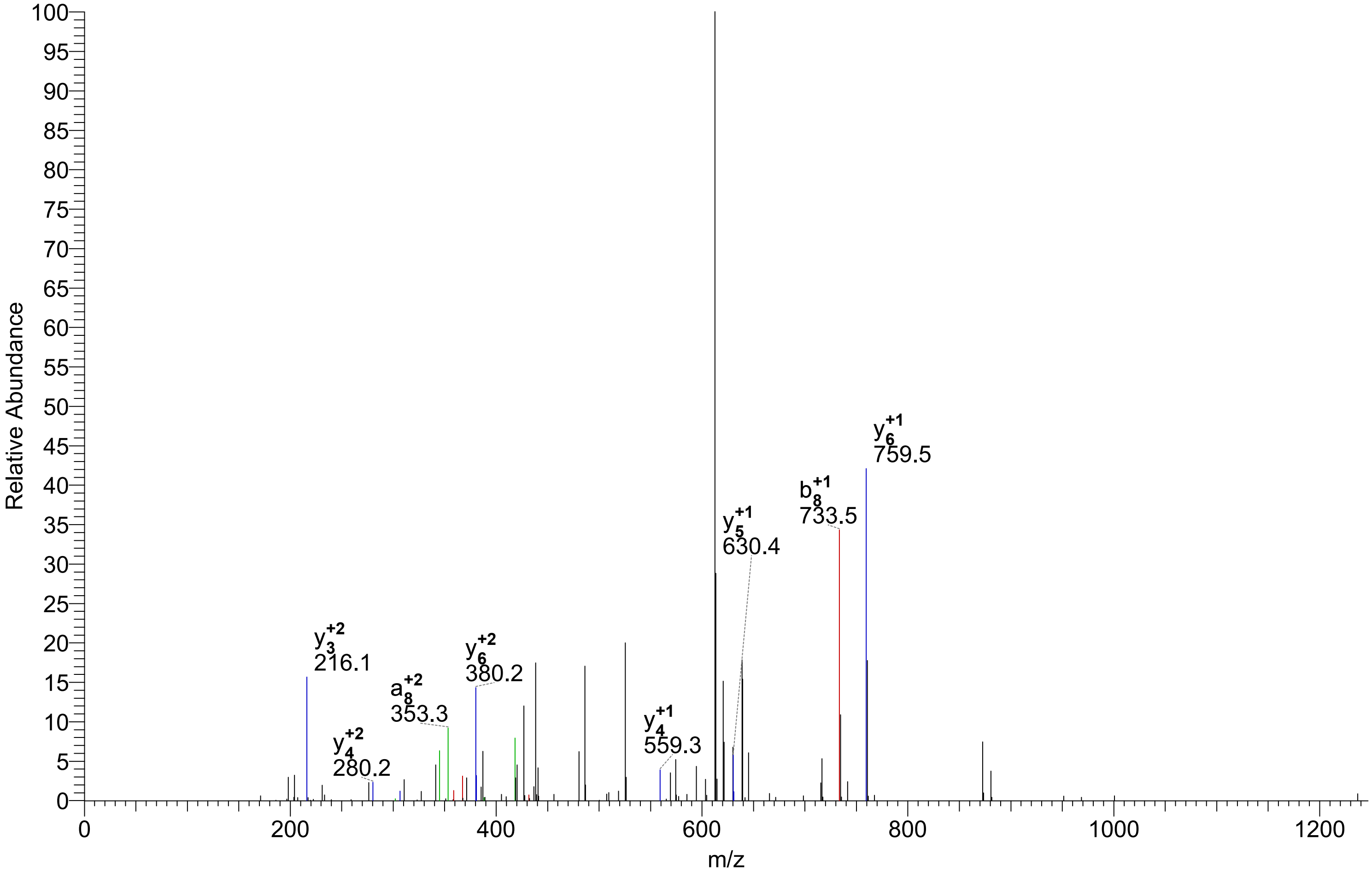
```
DTA for scans: 19287468-1
Precursor ion: 497.93
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 E    159.08     187.07                                     1434.75
 T    260.12     288.12                                     1305.71
 A    331.16     359.16                                     1204.66
 S    418.19     446.19                                     1133.63
 E    547.24     575.23                                     1046.60
 G    604.26     632.25                                      917.55
 T    705.30     733.30                                      860.53
 E    834.35     862.34                                      759.48
 A    905.38     933.38                                      630.44
 K   1033.48    1061.47                                      559.40
 K   1161.57    1189.57                                      431.31
 R   1317.68    1345.67                                      303.21
 K                                                           147.11
```



#19287468-1 NL: 3.10E6



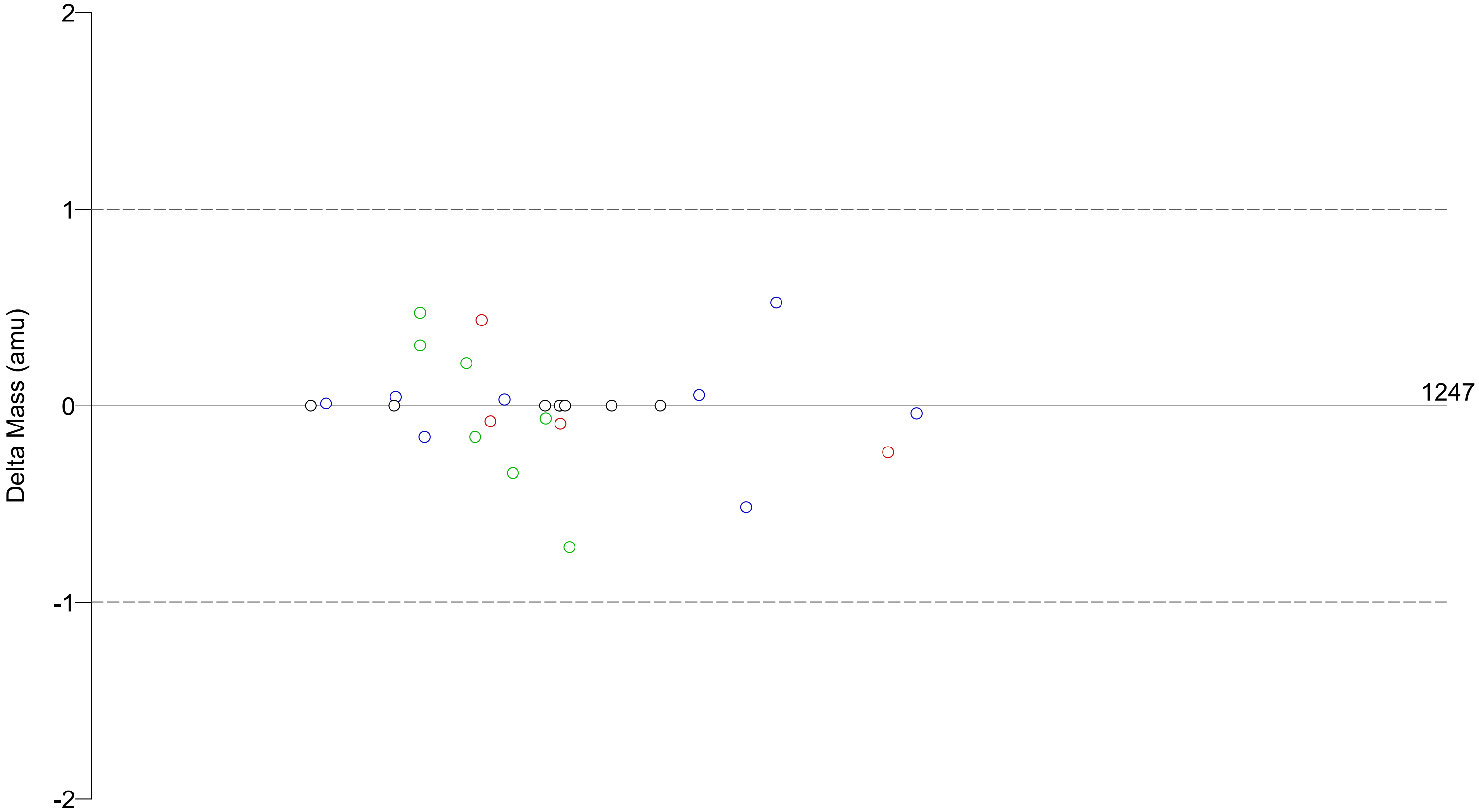
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00513835.1|TREMBL:A8MRA5;B3                                1       8.1      0.0       0
19287468 - 1  K.GETASEGTEAKKRK.R                     1491.78   3  1       1.815  0.629   168.0  2   16/78   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

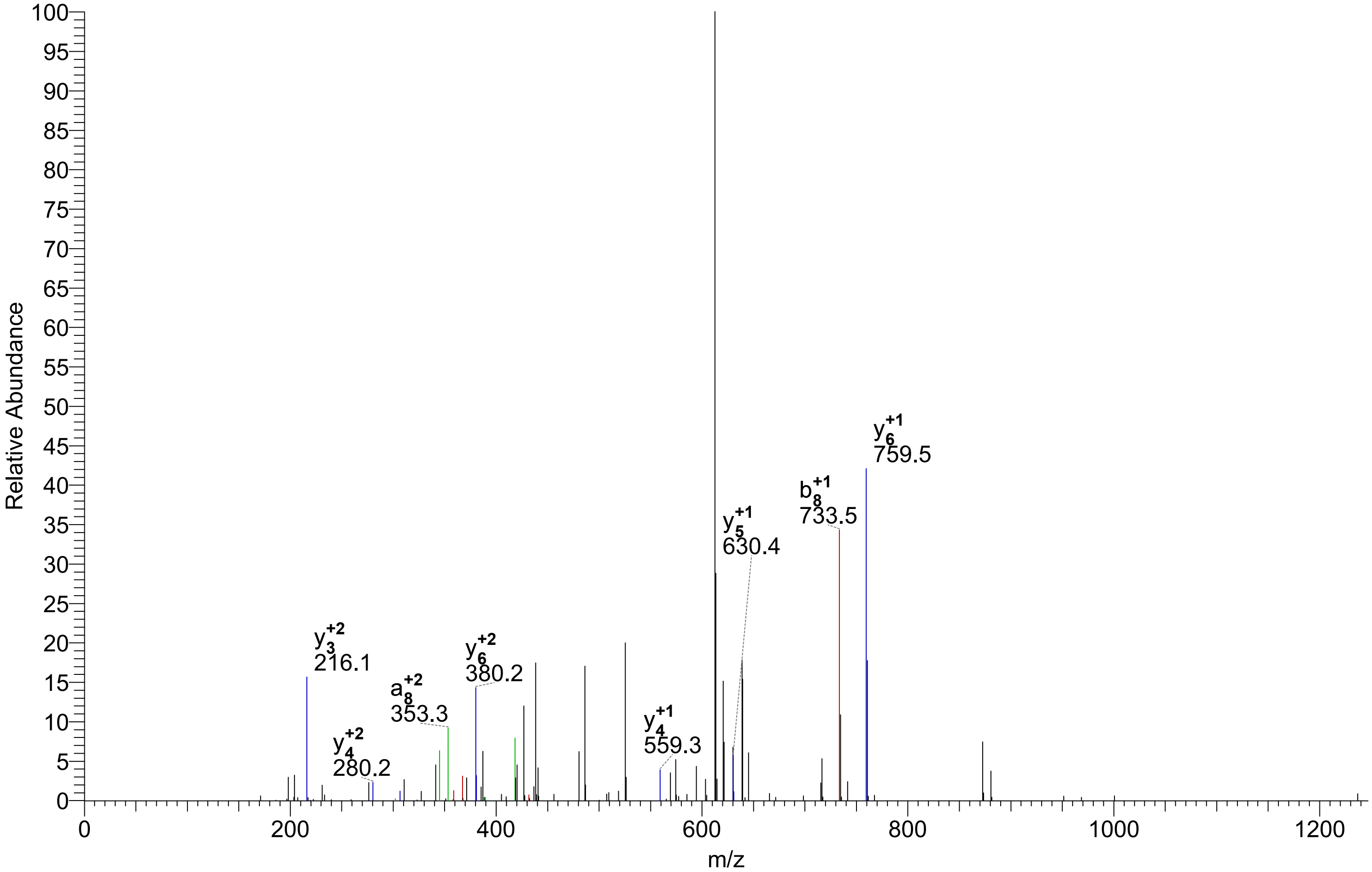
```
DTA for scans: 19287468-1
Precursor ion: 497.93
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 E    159.08     187.07                                    1434.75
 T    260.12     288.12                                    1305.71
 A    331.16     359.16                                    1204.66
 S    418.19     446.19                                    1133.63
 E    547.24     575.23                                    1046.60
 G    604.26     632.25                                     917.55
 T    705.30     733.30                                     860.53
 E    834.35     862.34                                     759.48
 A    905.38     933.38                                     630.44
 K   1033.48    1061.47                                     559.40
 K   1161.57    1189.57                                     431.31
 R   1317.68    1345.67                                     303.21
 K                                                          147.11
```



#19287468-1 NL: 3.10E6



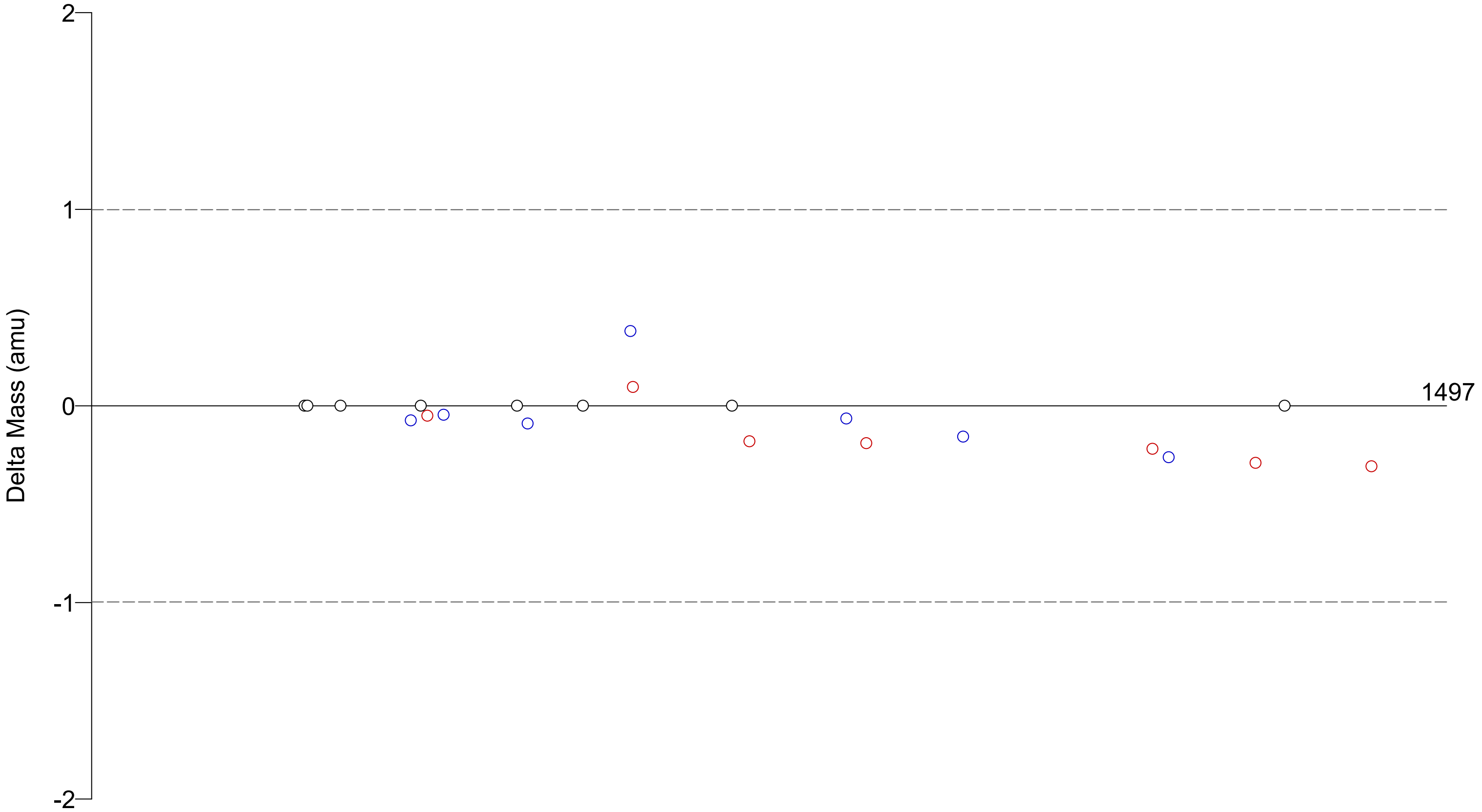
```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z    P        XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00418991.5|SWISS-PROT:Q2KHR3-1|TREMBL:B3KWV1|ENSEMBL:EN     1       10.1     0.0        0
19287468 - 1  K.GKGQVKEEDNSNQK.Q                       1560.76   2  0.2      2.747  0.382   212.8  1   11/39   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

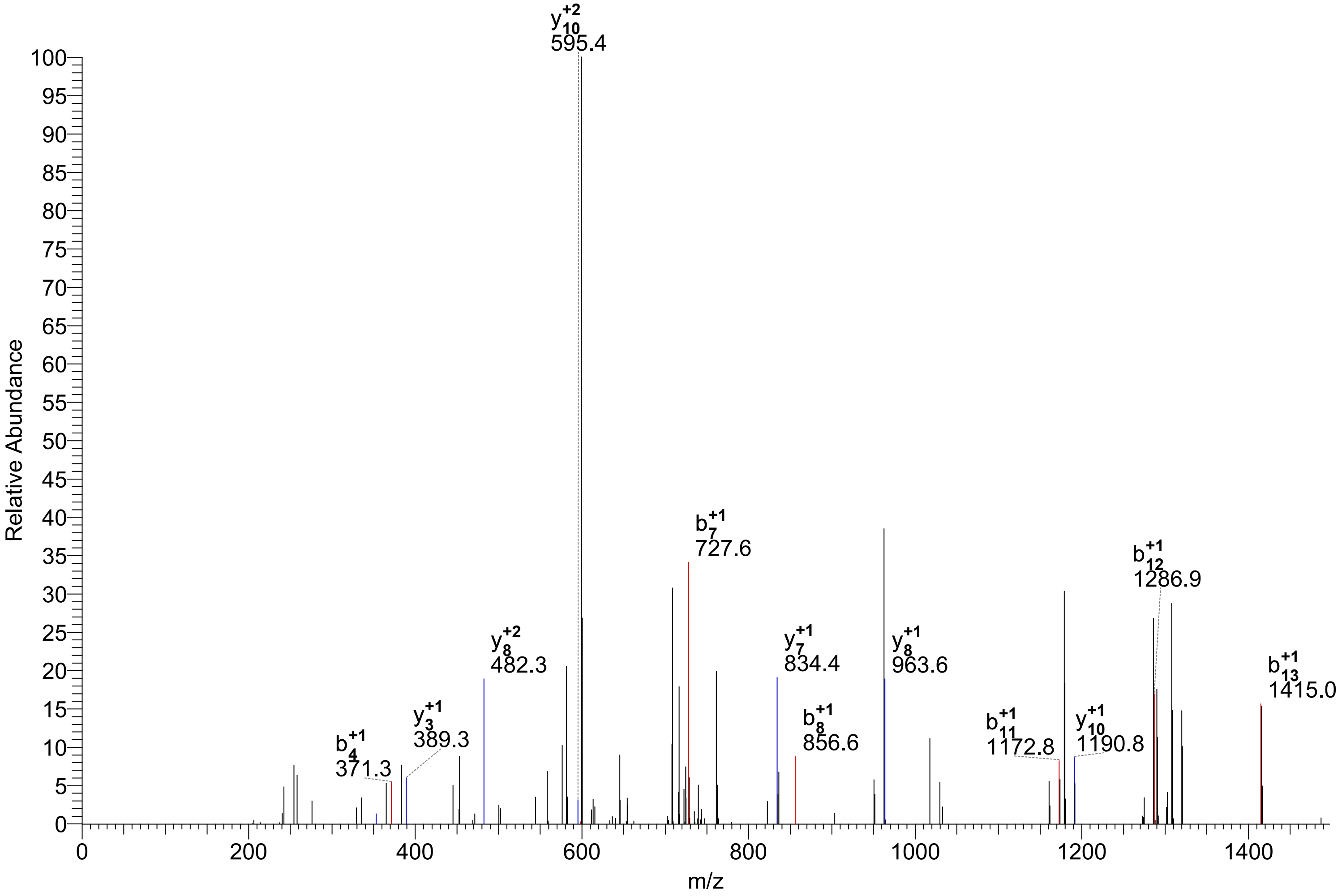
```
DTA for scans: 19287468-1
Precursor ion: 780.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 K    158.13     186.12                                     1503.74
 G    215.15     243.15                                     1375.64
 Q    343.21     371.20                                     1318.62
 V    442.28     470.27                                     1190.56
 K    570.37     598.37                                     1091.50
 E    699.41     727.41                                      963.40
 E    828.46     856.45                                      834.36
 D    943.48     971.48                                      705.32
 N   1057.53    1085.52                                      590.29
 S   1144.56    1172.55                                      476.25
 N   1258.60    1286.60                                      389.21
 Q   1386.66    1414.66                                      275.17
 K                                                           147.11
```



#19287468-1 NL: 6.84E4



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count

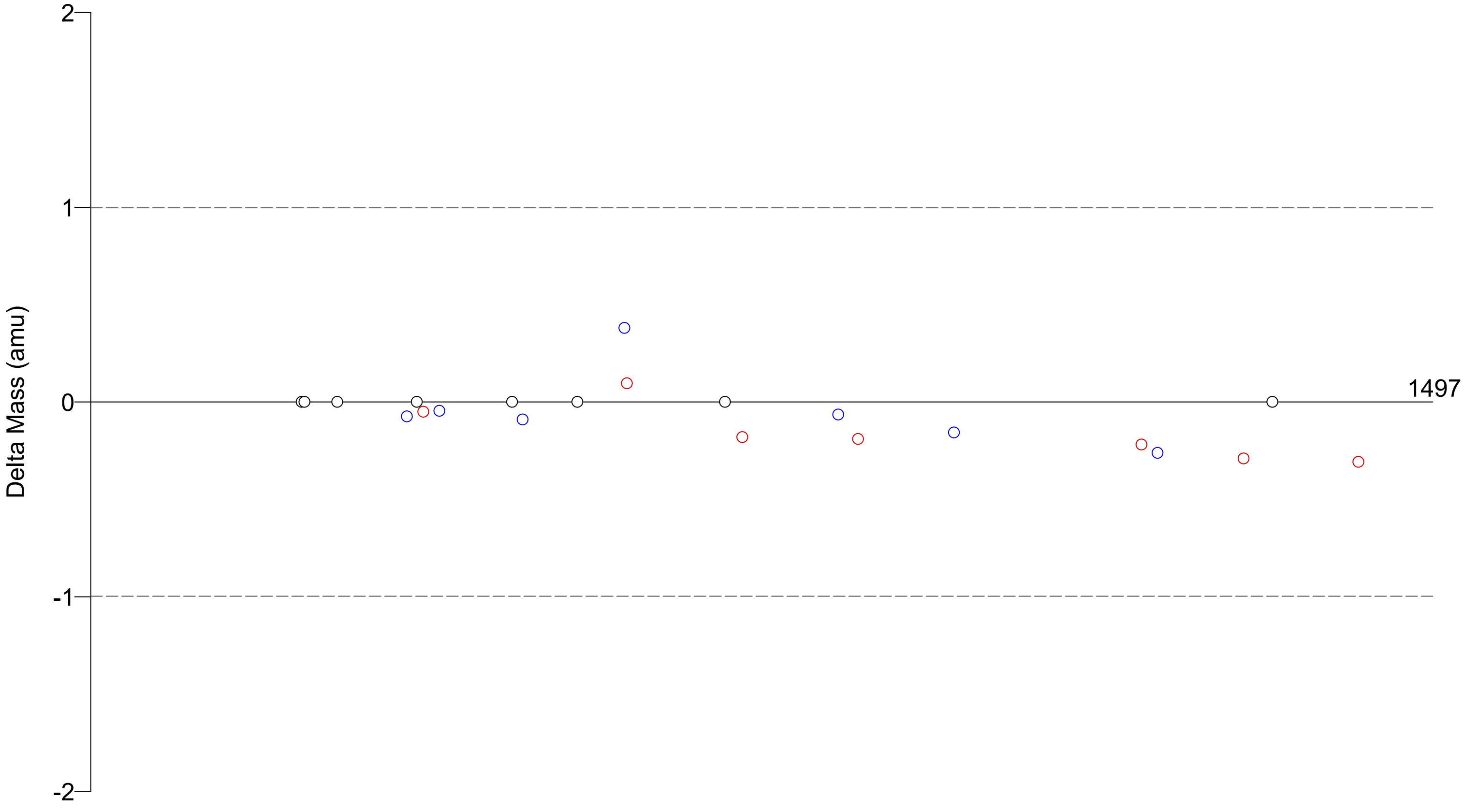
IPI:IPI00745241.1|TREMBL:Q9H6S7 Ta                                    1       10.1     0.0       0
19287468 - 1  K.GKGQVKEEDNSNQK.Q                       1560.76   2  0.2      2.747  0.382   212.8  1   11/39   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

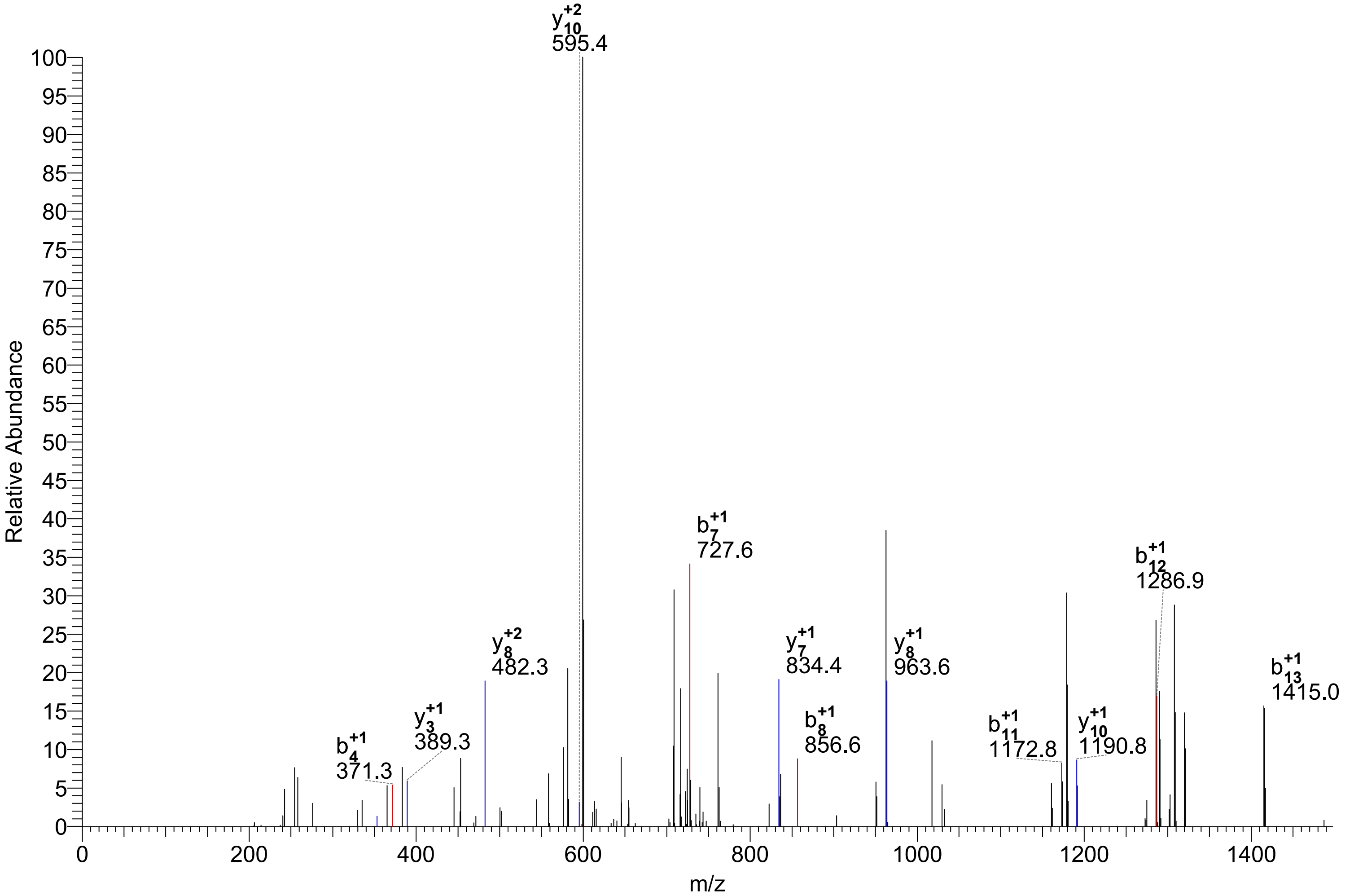
```
DTA for scans: 19287468-1
Precursor ion: 780.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 K    158.13     186.12                                     1503.74
 G    215.15     243.15                                     1375.64
 Q    343.21     371.20                                     1318.62
 V    442.28     470.27                                     1190.56
 K    570.37     598.37                                     1091.50
 E    699.41     727.41                                      963.40
 E    828.46     856.45                                      834.36
 D    943.48     971.48                                      705.32
 N   1057.53    1085.52                                      590.29
 S   1144.56    1172.55                                      476.25
 N   1258.60    1286.60                                      389.21
 Q   1386.66    1414.66                                      275.17
 K                                                           147.11
```



#19287468-1 NL: 6.84E4



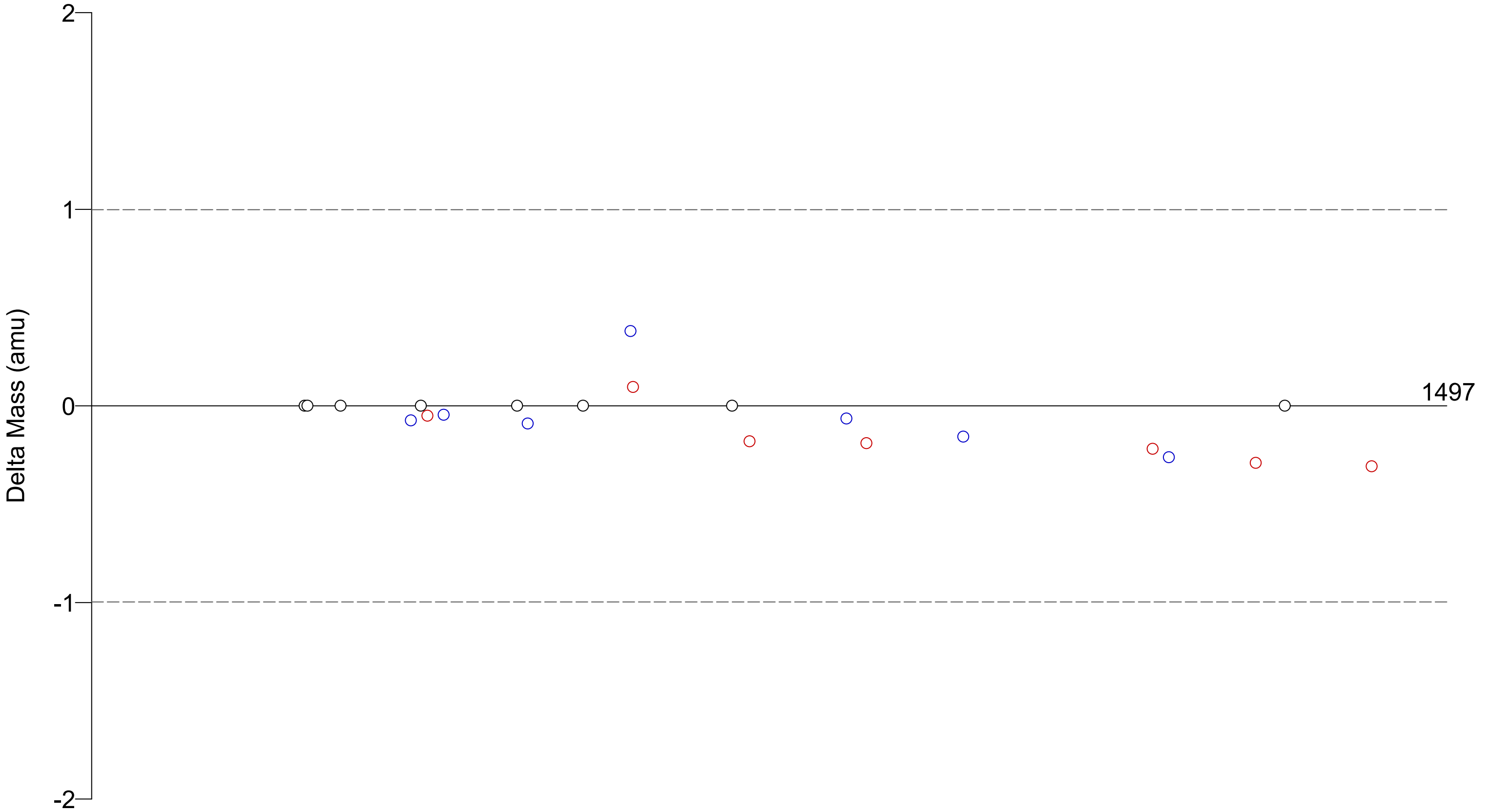
```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00847870.1|SWISS-PROT:Q2KHR                                     1        10.1     0.0        0
19287468 - 1  K.GKGQVKEEDNSNQK.Q                       1560.76    2  0.2      2.747  0.382   212.8  1   11/39   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

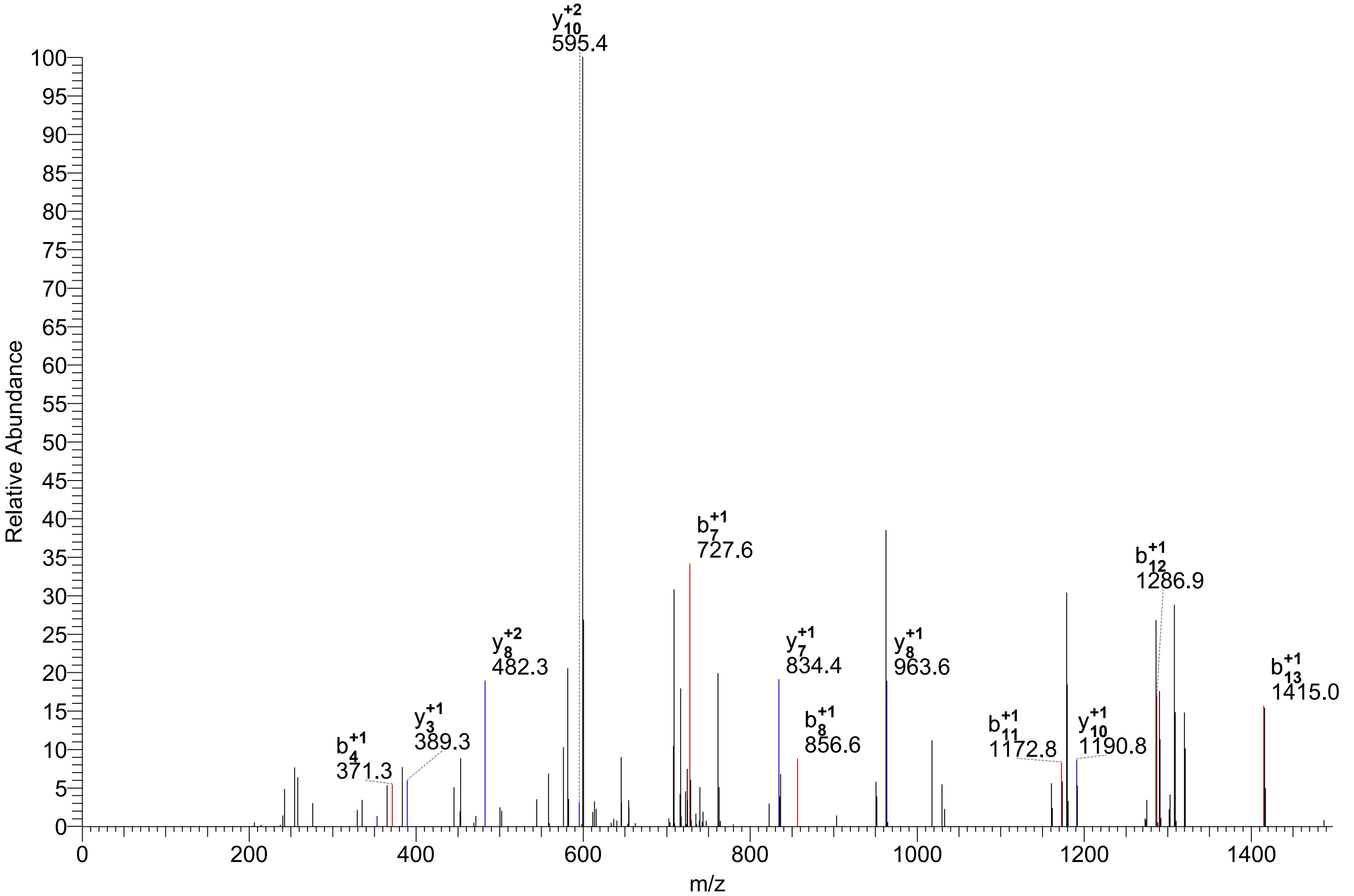
```
DTA for scans: 19287468-1
Precursor ion: 780.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 K    158.13     186.12                                      1503.74
 G    215.15     243.15                                      1375.64
 Q    343.21     371.20                                      1318.62
 V    442.28     470.27                                      1190.56
 K    570.37     598.37                                      1091.50
 E    699.41     727.41                                       963.40
 E    828.46     856.45                                       834.36
 D    943.48     971.48                                       705.32
 N   1057.53    1085.52                                       590.29
 S   1144.56    1172.55                                       476.25
 N   1258.60    1286.60                                       389.21
 Q   1386.66    1414.66                                       275.17
 K                                                            147.11
```



#19287468-1 NL: 6.84E4



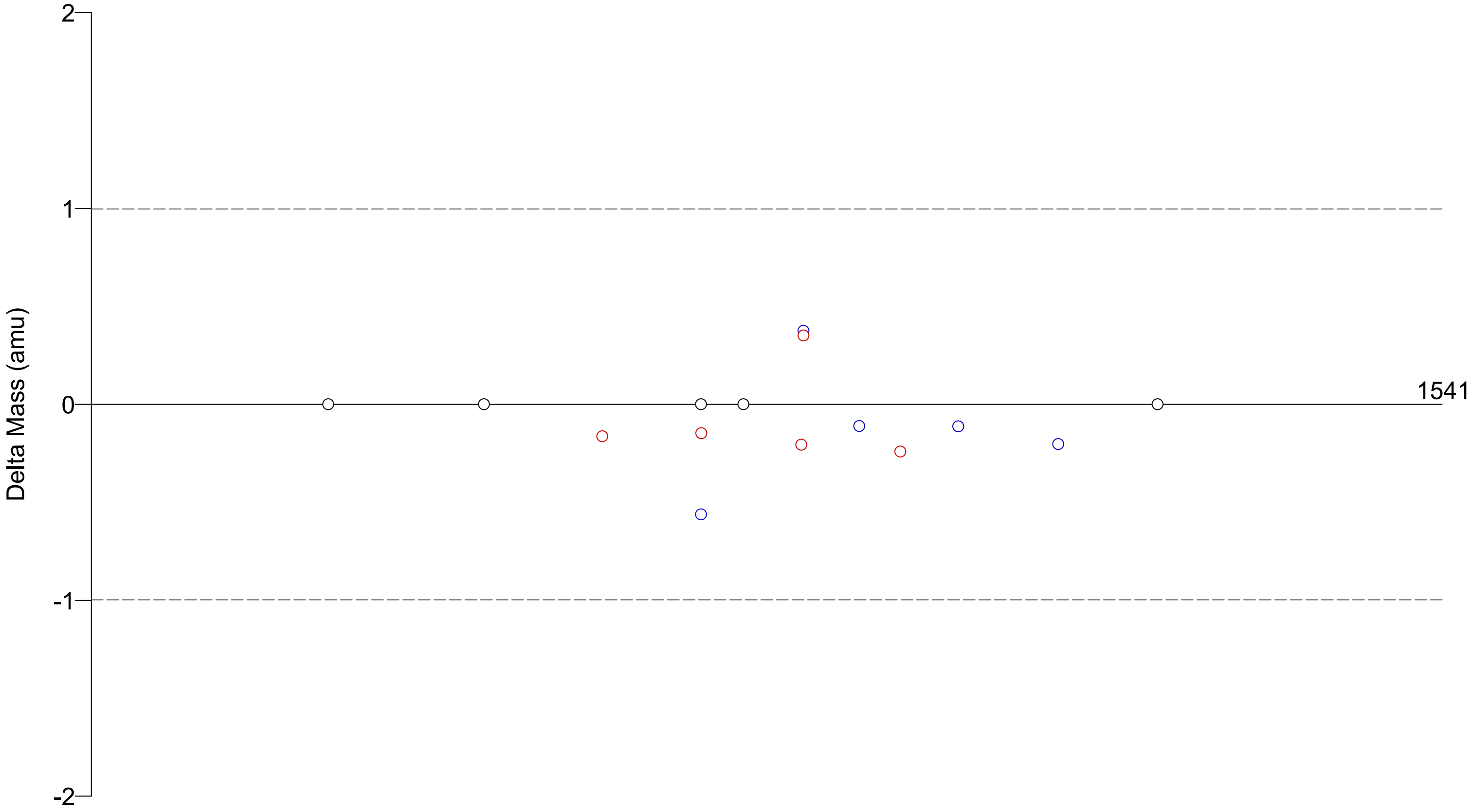
```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00003330.4|SWISS-PROT:Q9NTU4|ENSEMBL:ENSP00000330877|RE     1       8.1      0.0        0
19287468 - 1  K.SSSM*SSLNIAKHMPHR.A                     1798.87   2  0.2      1.976  0.523   81.9   6   7/45

1 of 1 peptide matches reported, 0 removed due to filtering
```

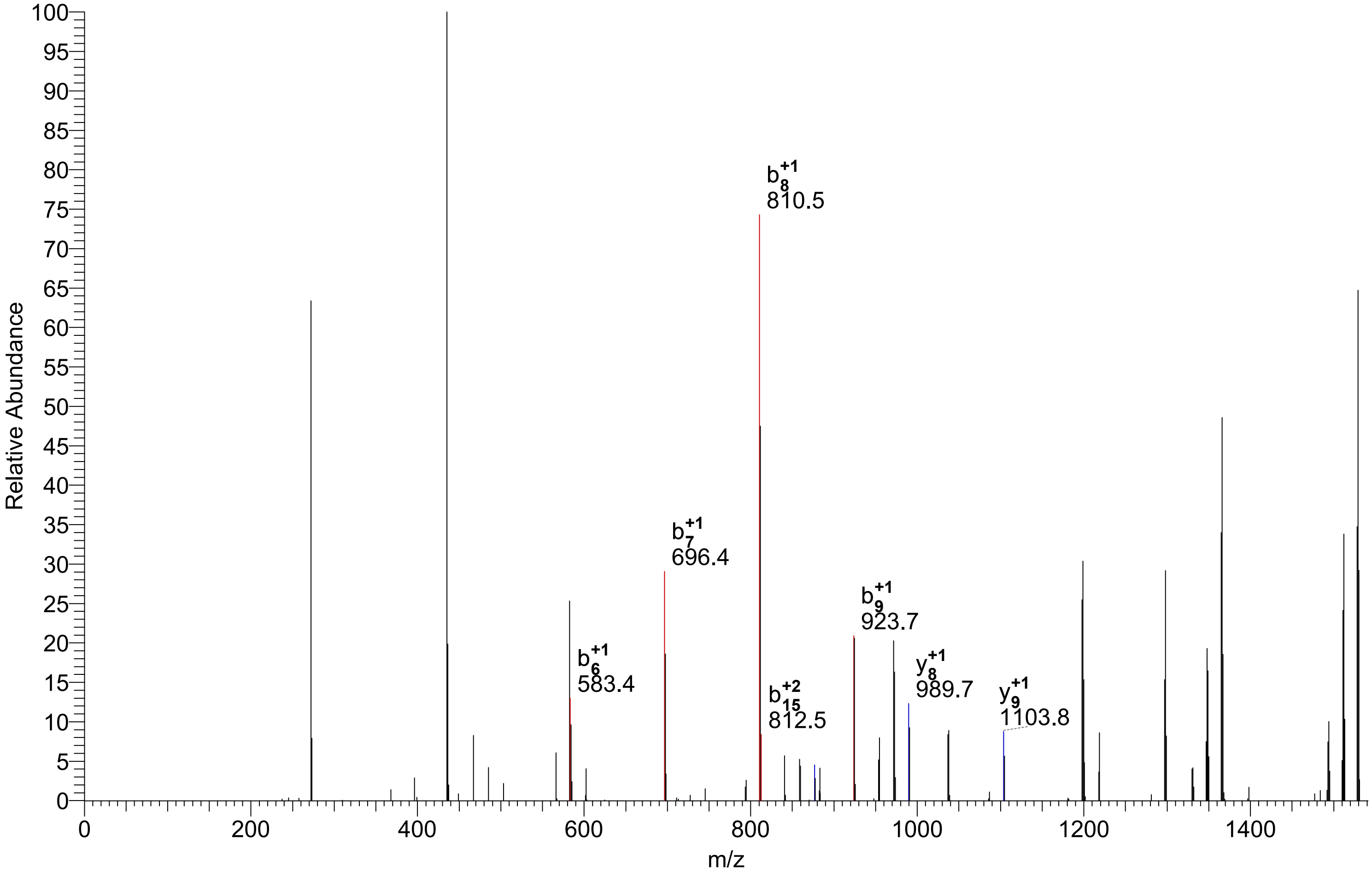
```
DTA for scans: 19287468-1
Precursor ion: 899.94
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 S    147.08     175.07                                      1711.84
 S    234.11     262.10                                      1624.80
 M*   381.14     409.14                                      1537.77
 S    468.18     496.17                                      1390.74
 S    555.21     583.20                                      1303.71
 L    668.29     696.29                                      1216.67
 N    782.33     810.33                                      1103.59
 I    895.42     923.41                                       989.55
 A    966.46     994.45                                       876.46
 K   1094.55    1122.55                                       805.42
 H   1231.61    1259.60                                       677.33
 M   1362.65    1390.65                                       540.27
 P   1459.70    1487.70                                       409.23
 H   1596.76    1624.76                                       312.18
 R                                                            175.12
```



#19287468-1 NL: 2.53E6



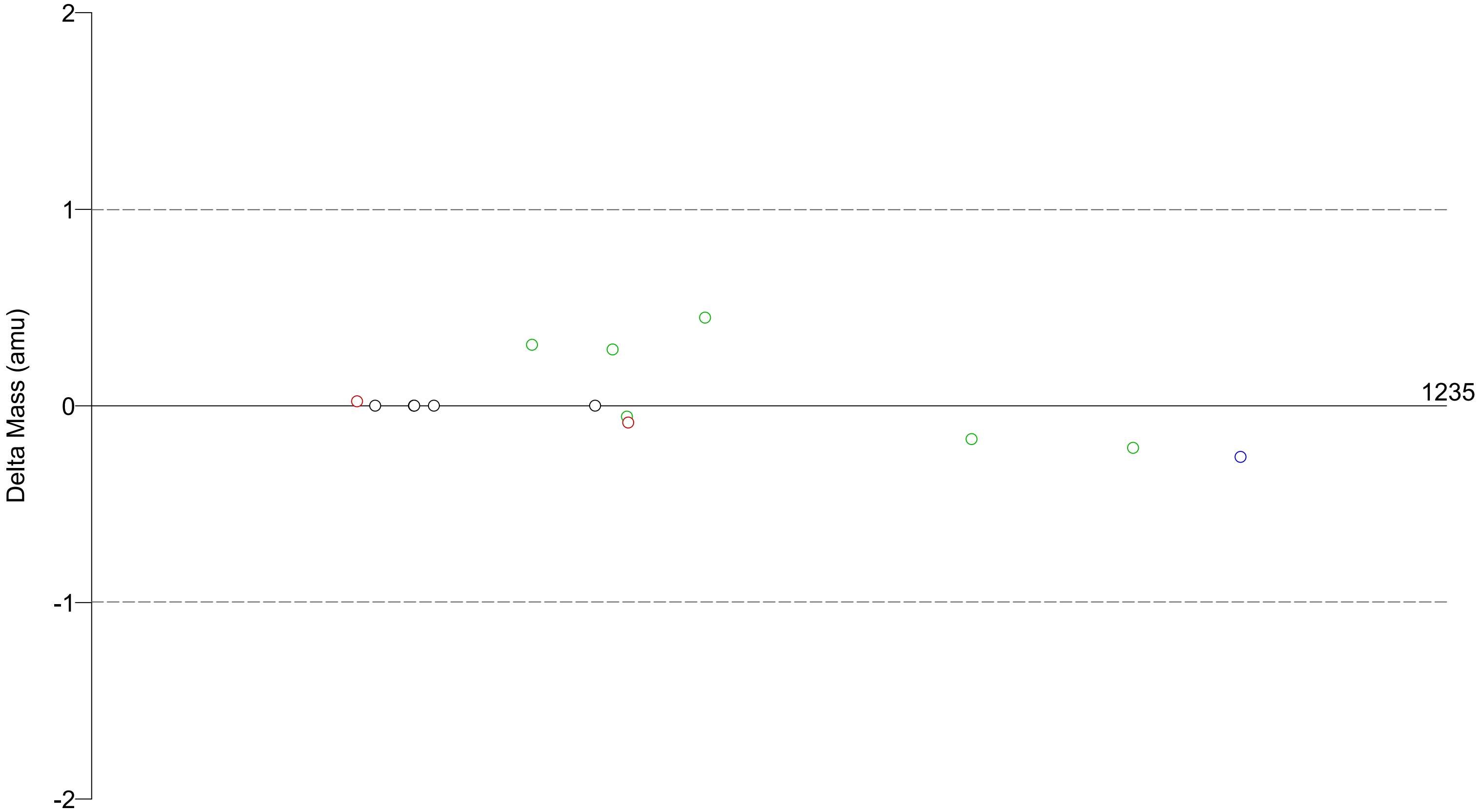
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00477176.1|SWISS-PROT:Q96LC9-1|ENSEMBL:ENSP00000346697;     1       8.1      0.0       0
19287468 - 1  K.LQCIADQFHR.L                           1288.61   2  1       1.350  0.621   61.6   3   6/27

1 of 1 peptide matches reported, 0 removed due to filtering
```

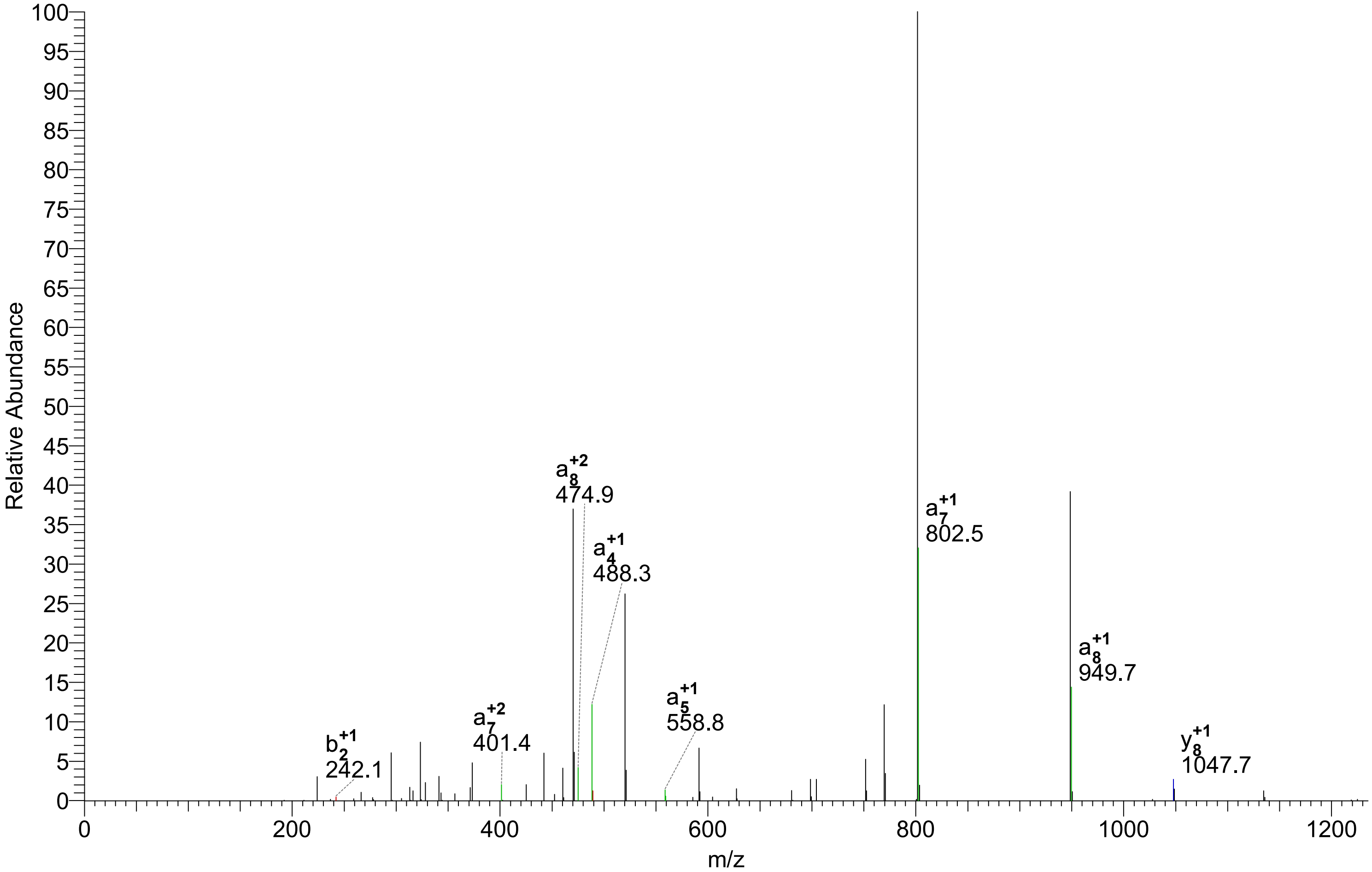
```
DTA for scans: 19287468-1
Precursor ion: 644.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 Q    214.16     242.15                                     1175.53
 C    375.17     403.16                                     1047.47
 I    488.25     516.25                                      886.45
 A    559.29     587.29                                      773.37
 D    674.32     702.31                                      702.33
 Q    802.38     830.37                                      587.30
 F    949.44     977.44                                      459.25
 H   1086.50    1114.50                                      312.18
 R                                                           175.12
```



#19287468-1 NL: 4.16E6



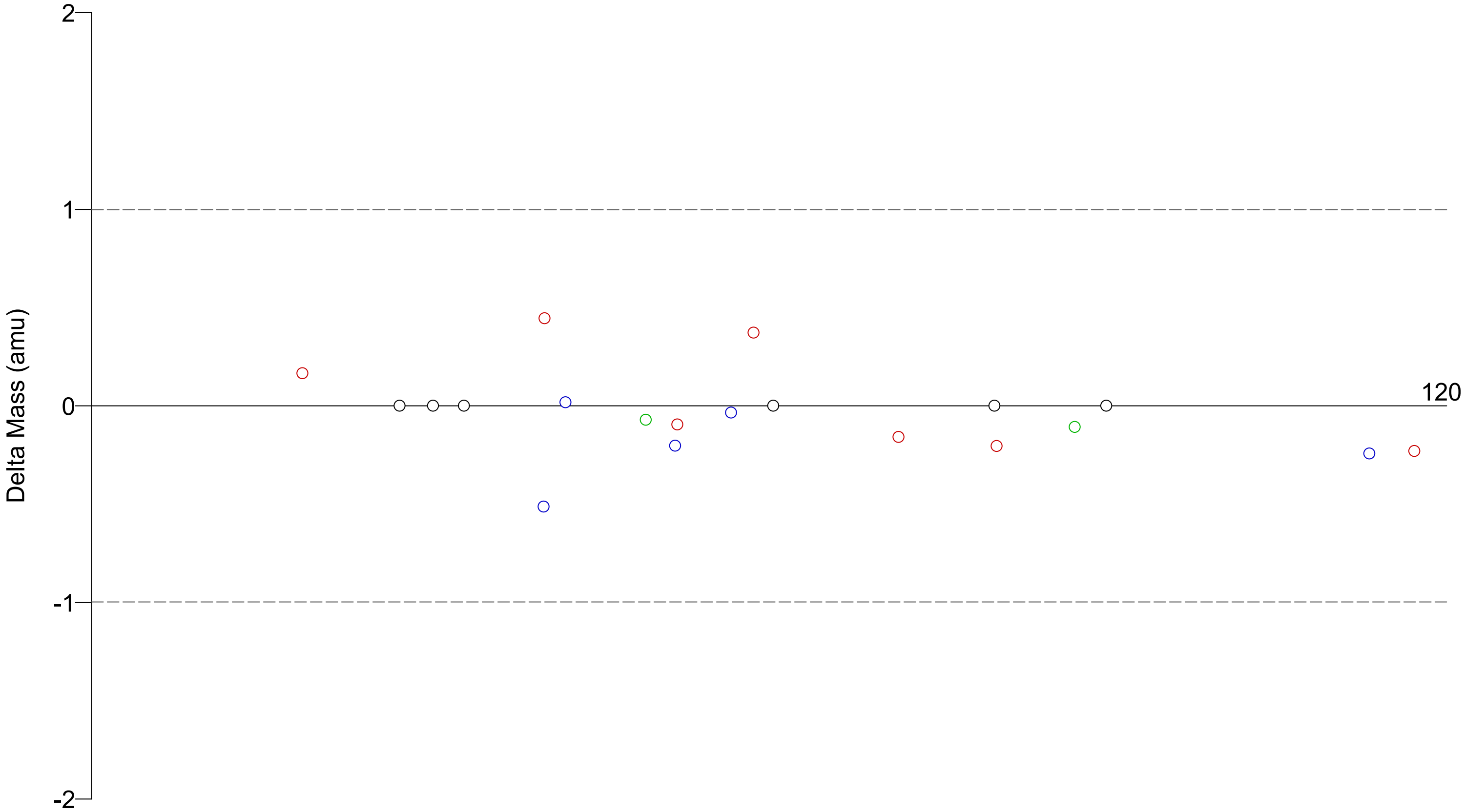
```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00783294.1|SWISS-PROT:Q9P267-1|TREMBL:B4E2U1|ENSEMBL:EN     1        8.1       0.0        0
19287468 - 1  K.SVNGCVPSPSDAK.S                         1318.59   2  0.2      2.111  0.618   149.8  3   10/36   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

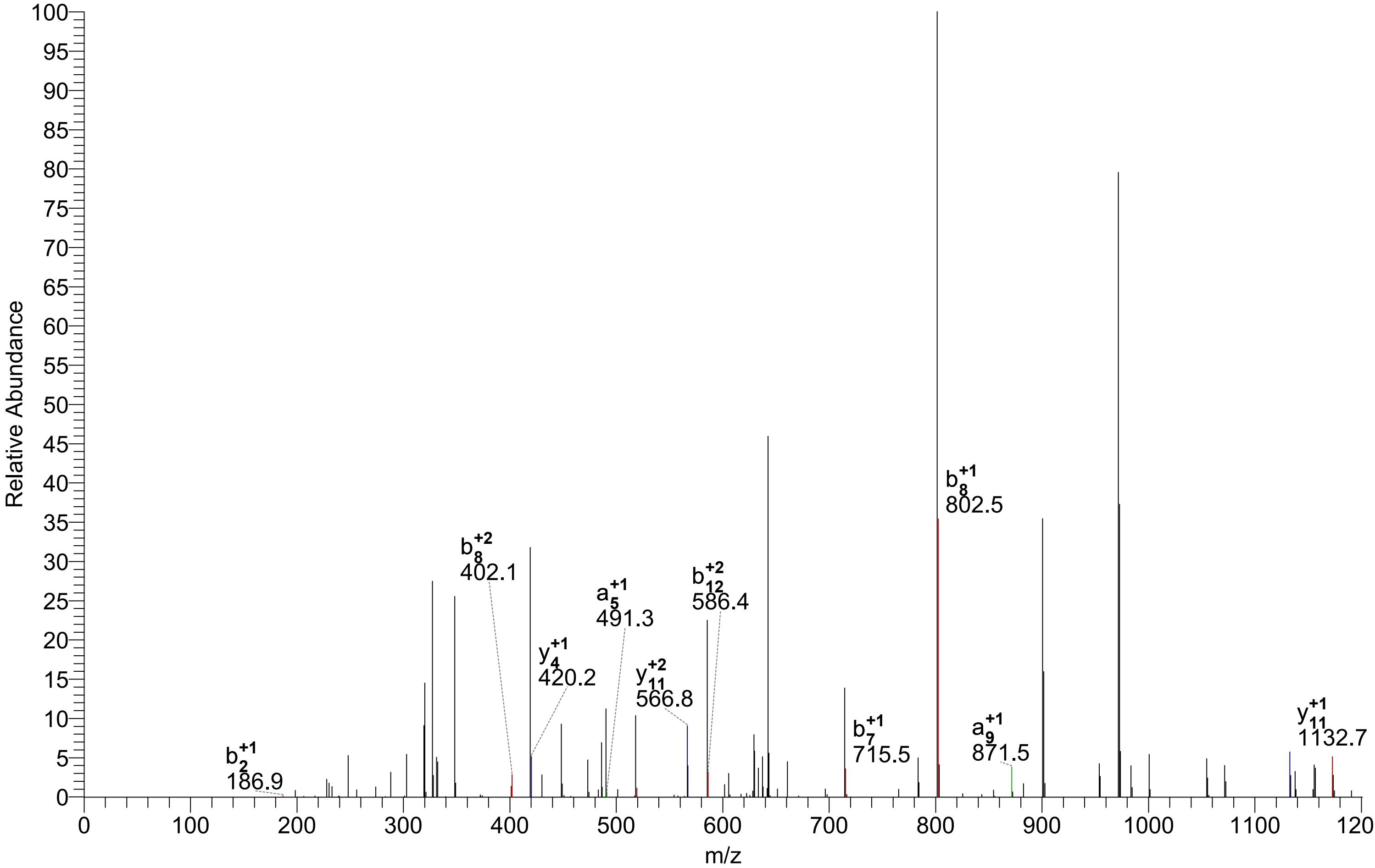
```
DTA for scans: 19287468-1
Precursor ion: 659.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 V    159.11     187.11                                     1231.56
 N    273.16     301.15                                     1132.49
 G    330.18     358.17                                     1018.45
 C    491.19     519.19                                      961.43
 V    590.26     618.26                                      800.41
 P    687.31     715.31                                      701.35
 S    774.35     802.34                                      604.29
 P    871.40     899.39                                      517.26
 S    958.43     986.42                                      420.21
 D   1073.46    1101.45                                      333.18
 A   1144.49    1172.49                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 2.05E5



```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

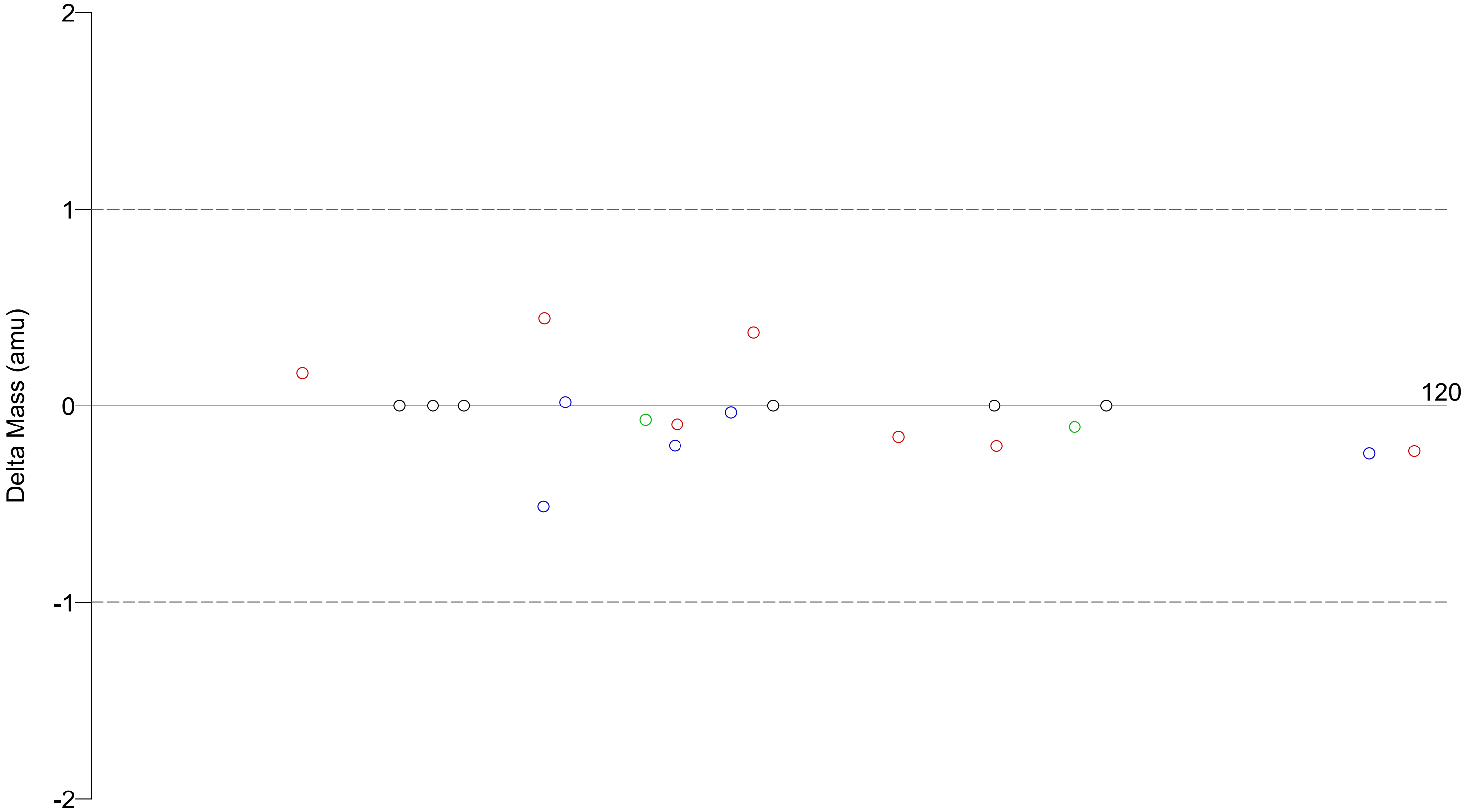
IPI:IPI00879134.1|TREMBL:B3KQW0|EN                               1      8.1      0.0        0
19287468 - 1  K.SVNGCVPSPSDAK.S                    1318.59   2  0.2      2.111  0.618   149.8  3   10/36   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

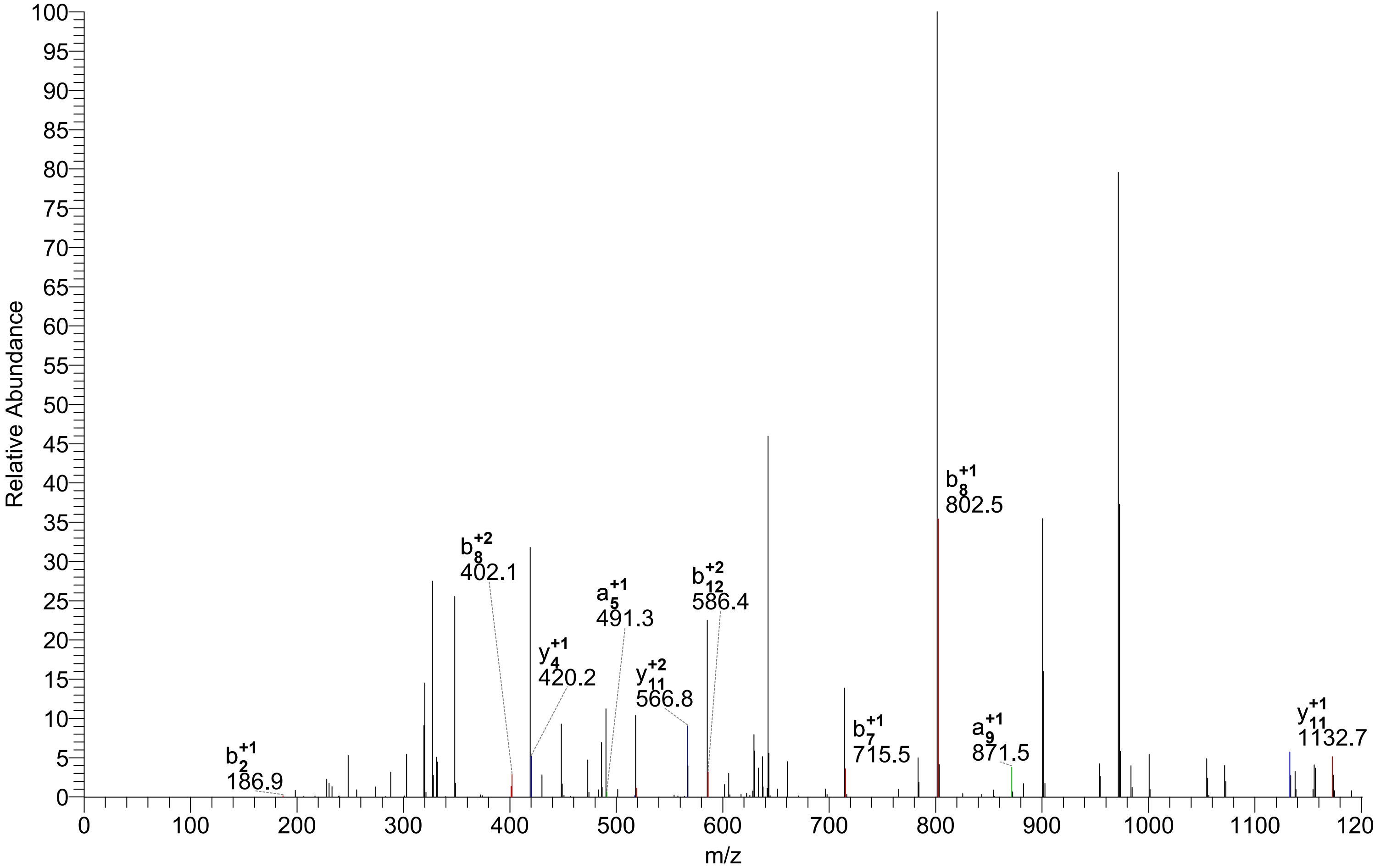
```
DTA for scans: 19287468-1
Precursor ion: 659.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 V    159.11     187.11                                     1231.56
 N    273.16     301.15                                     1132.49
 G    330.18     358.17                                     1018.45
 C    491.19     519.19                                      961.43
 V    590.26     618.26                                      800.41
 P    687.31     715.31                                      701.35
 S    774.35     802.34                                      604.29
 P    871.40     899.39                                      517.26
 S    958.43     986.42                                      420.21
 D   1073.46    1101.45                                      333.18
 A   1144.49    1172.49                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 2.05E5



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

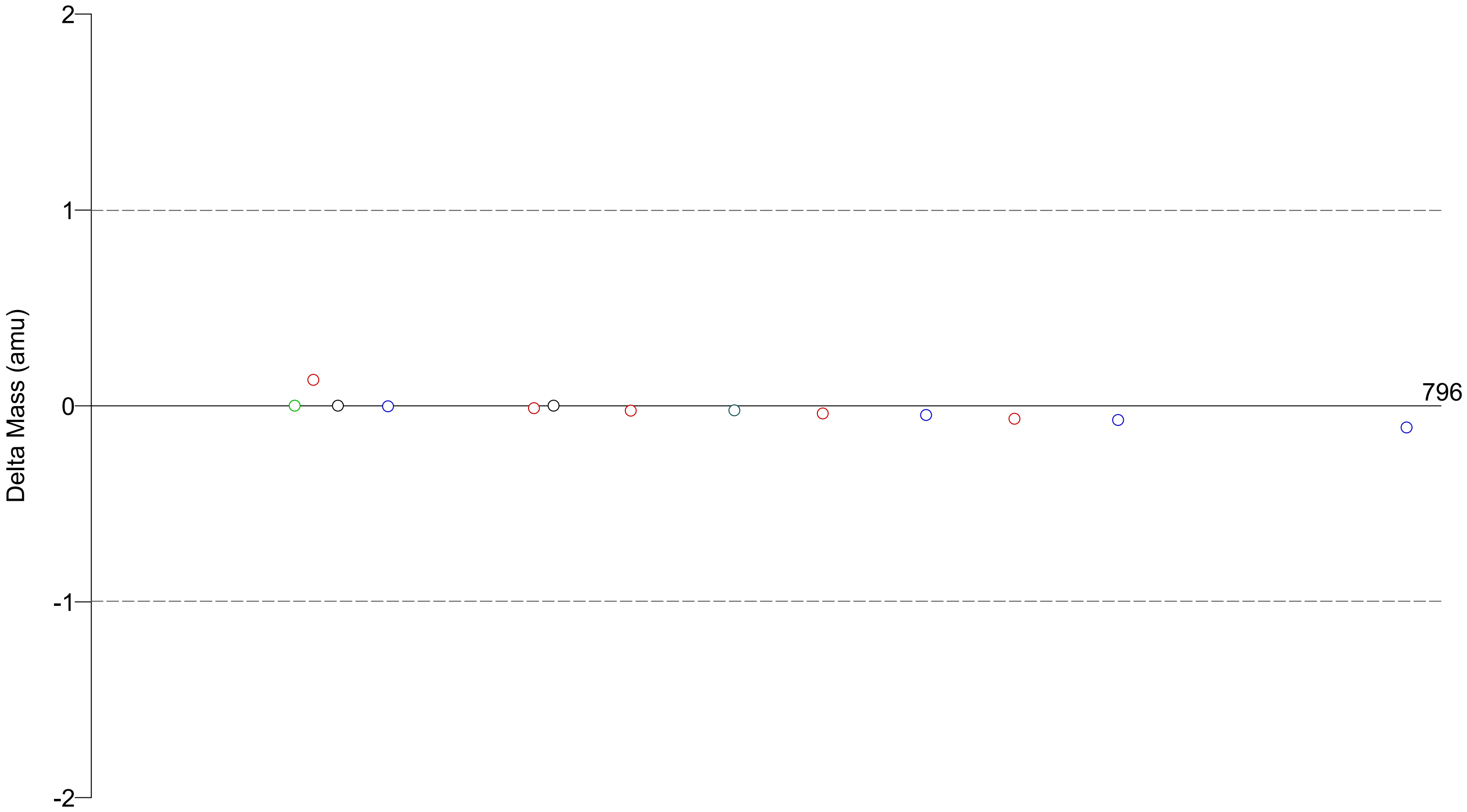
IPI:IPI00936423.1|REFSEQ:XP_002343325 Tax_Id=9606 Gene_Symbol=   1       8.1      0.0       0
19287468 - 1  K.FLGLIM*GR.G                         922.52    2  0.3     1.924  0.405   193.5  3   10/21   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

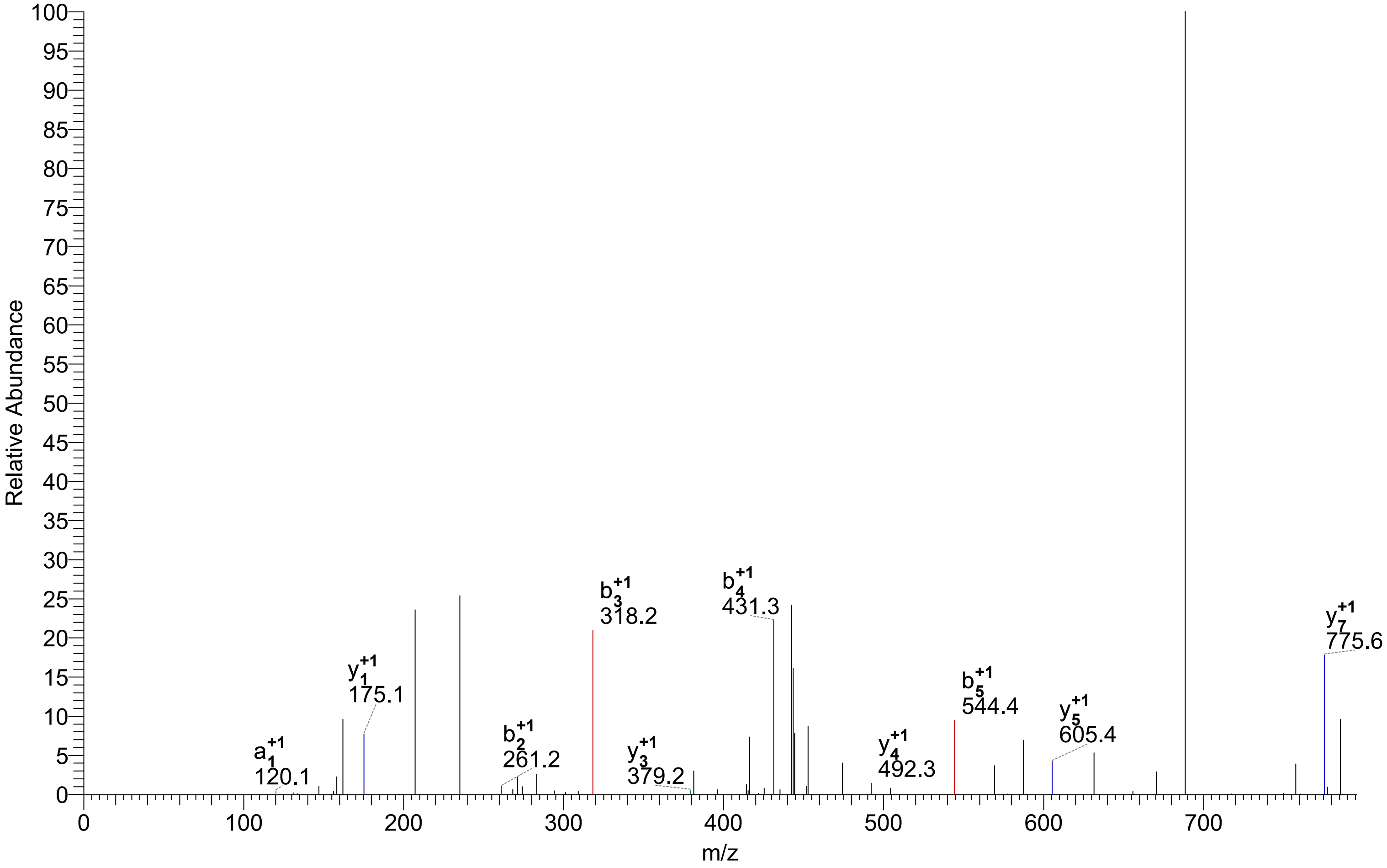
```
DTA for scans: 19287468-1
Precursor ion: 461.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 L    233.16     261.16                                      775.45
 G    290.19     318.18                                      662.37
 L    403.27     431.27                                      605.34
 I    516.35     544.35                                      492.26
 M*   663.39     691.38                                      379.18
 G    720.41     748.41                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.73E5



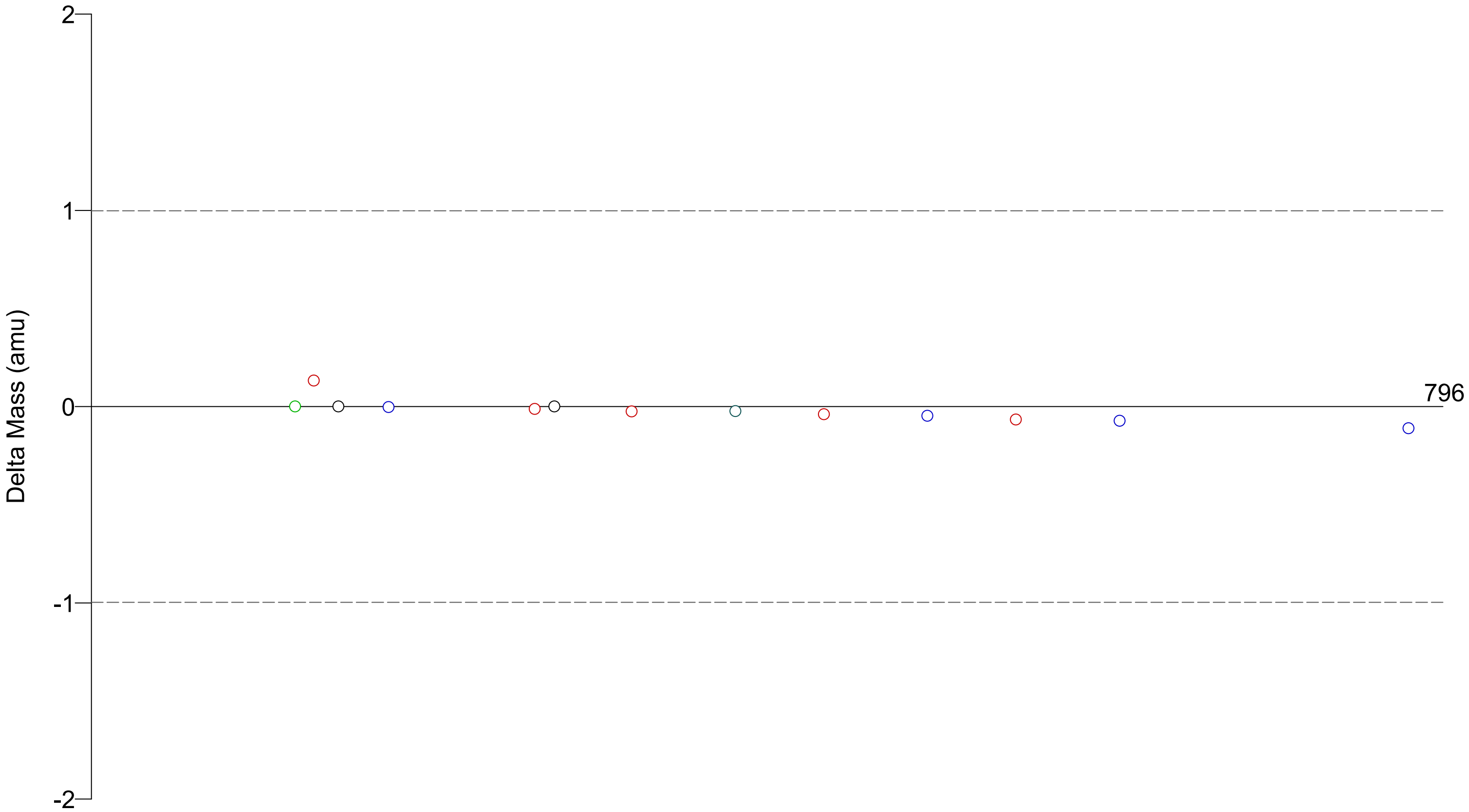
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)        Sequence                                   MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00937991.1|REFSEQ:XP_002347                                 1      8.1      0.0       0
19287468 - 1  K.FLGLIM*GR.G                              922.52    2  0.3      1.924  0.405   193.5  3   10/21   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

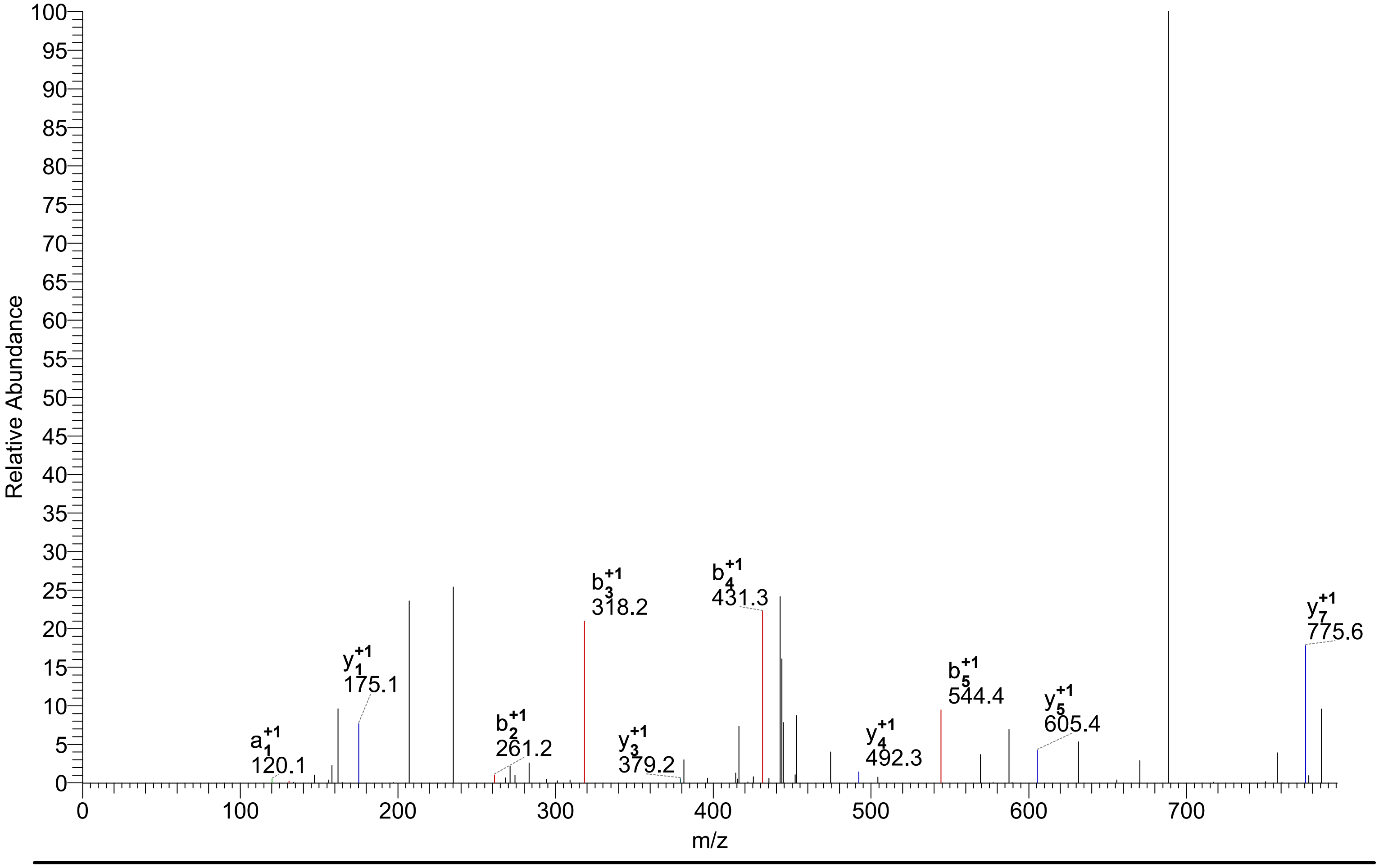
```
DTA for scans: 19287468-1
Precursor ion: 461.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 F    120.08     148.08
 L    233.16     261.16                                      775.45
 G    290.19     318.18                                      662.37
 L    403.27     431.27                                      605.34
 I    516.35     544.35                                      492.26
 M*   663.39     691.38                                      379.18
 G    720.41     748.41                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.73E5



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z  P        XC  DeltaCn   Sp   RSp  Ions  Count

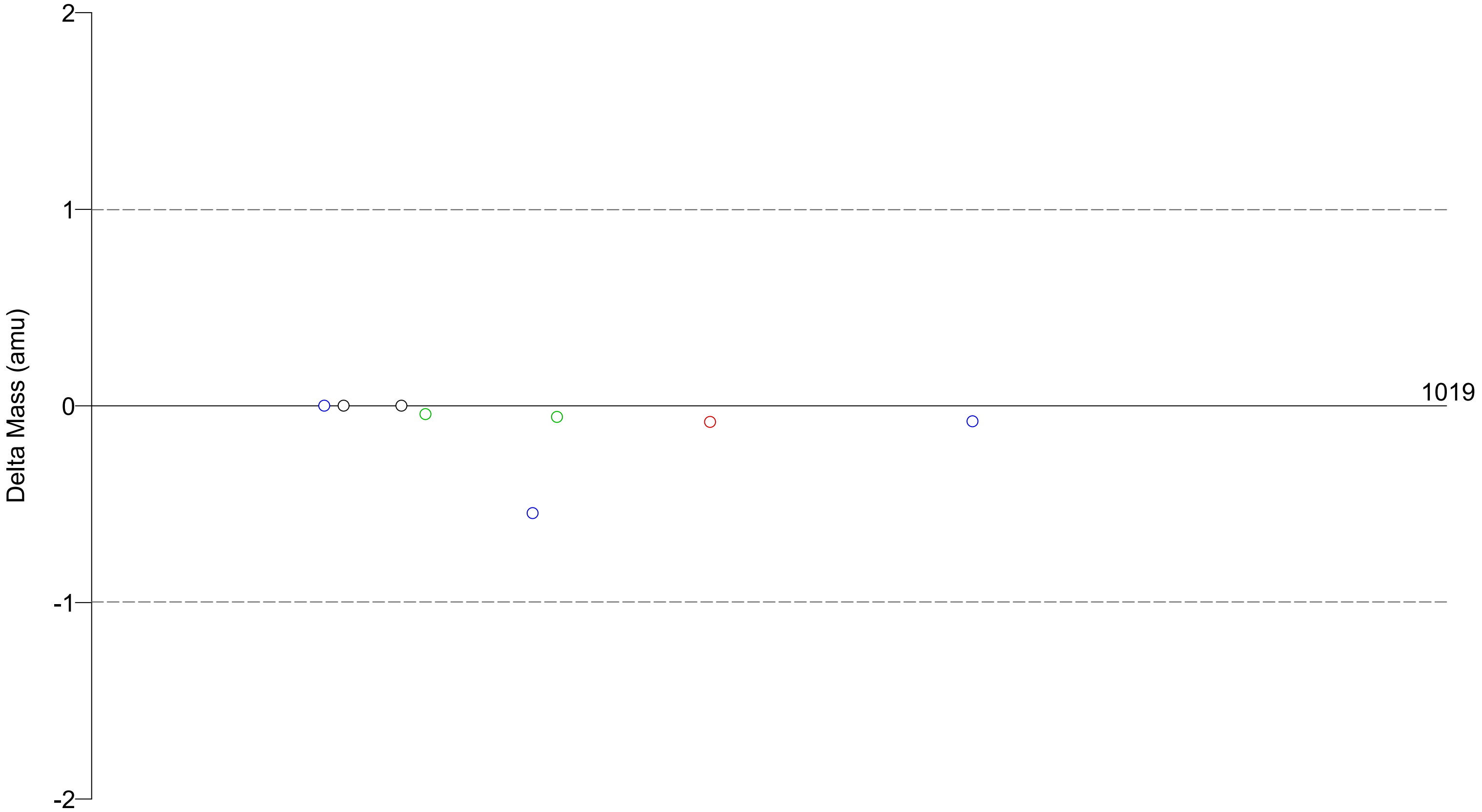
IPI:IPI00893555.1|VEGA:OTTHUMP00000201682 Tax_Id=9606 Gene_Sym    1       8.1      0.0        0
19287468 - 1  R.MFVSTVWTR.M                            1126.57   2  1       1.265  0.427   69.9   27  5/24

1 of 1 peptide matches reported, 0 removed due to filtering
```

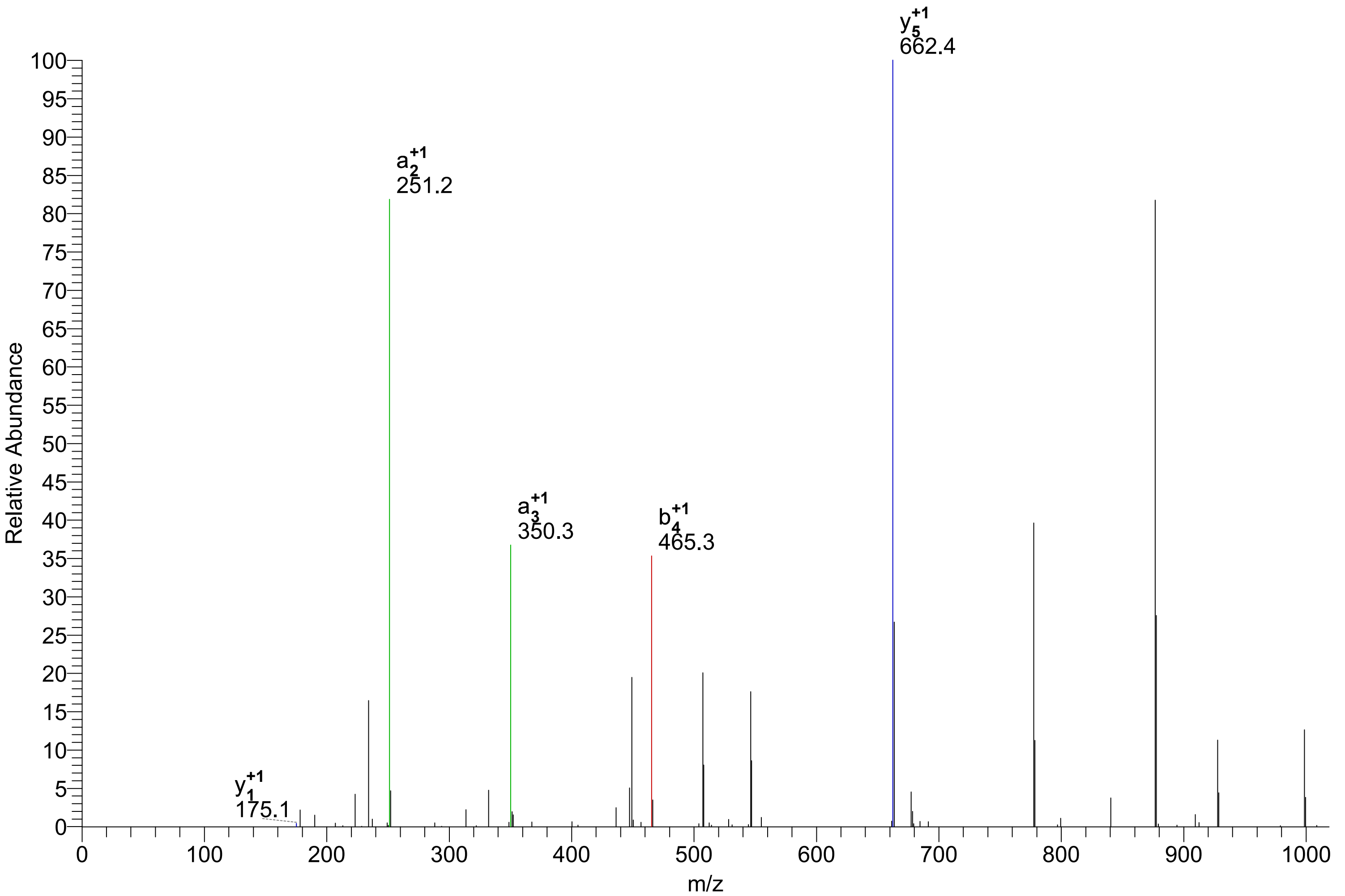
```
DTA for scans: 19287468-1
Precursor ion: 563.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 M    104.05     132.05
 F    251.12     279.12                                      995.53
 V    350.19     378.18                                      848.46
 S    437.22     465.22                                      749.39
 T    538.27     566.26                                      662.36
 V    637.34     665.33                                      561.31
 W    823.42     851.41                                      462.25
 T    924.46     952.46                                      276.17
 R                                                           175.12
```



#19287468-1 NL: 7.10E5



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

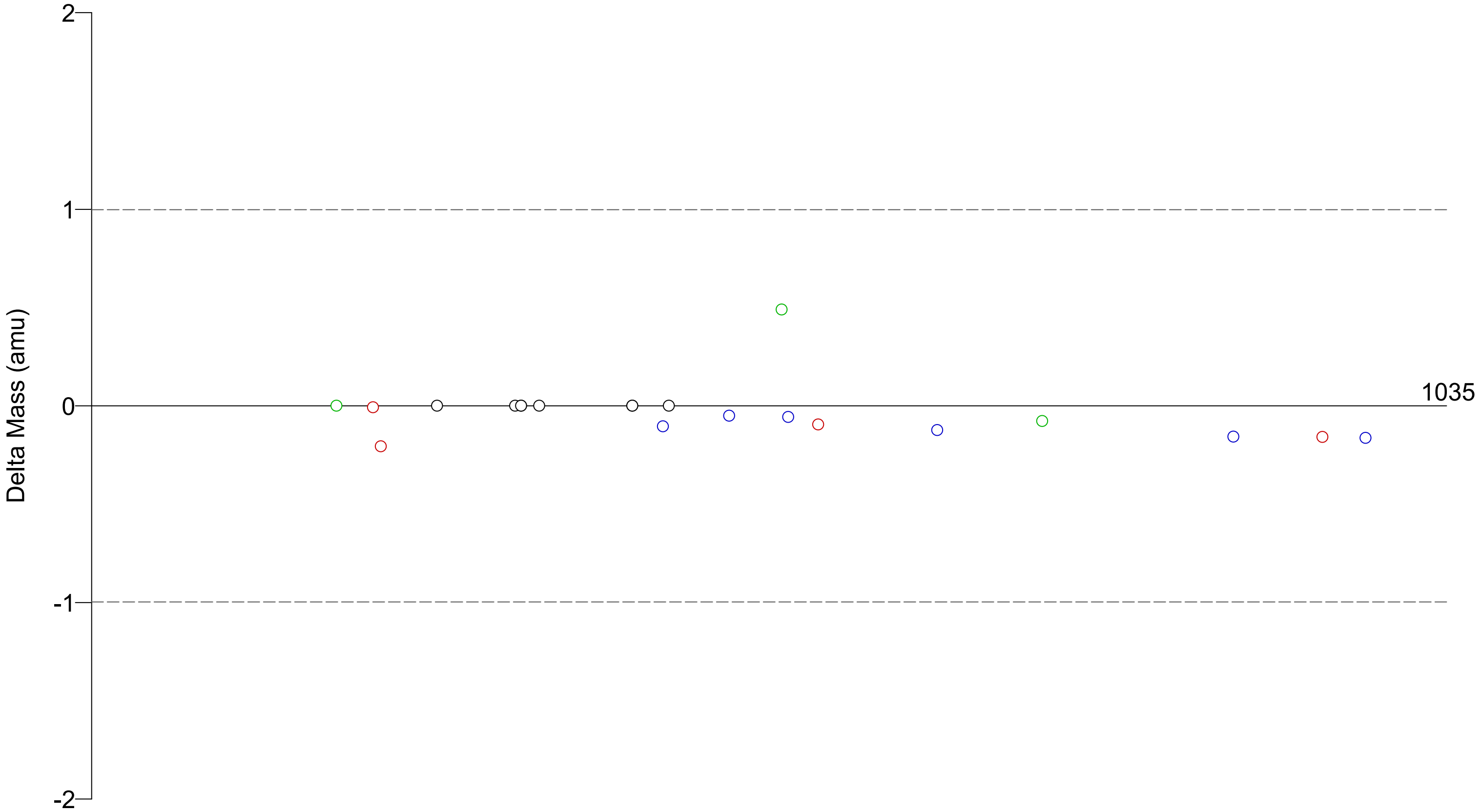
IPI:IPI00328929.3|SWISS-PROT:Q86VM9-1|ENSEMBL:ENSP00000301011|     1       8.1      0.0       0
2118291816 -  K.LTLLNKAADK.G                          1086.65   2  0.4      2.083  0.466   185.2  3   10/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

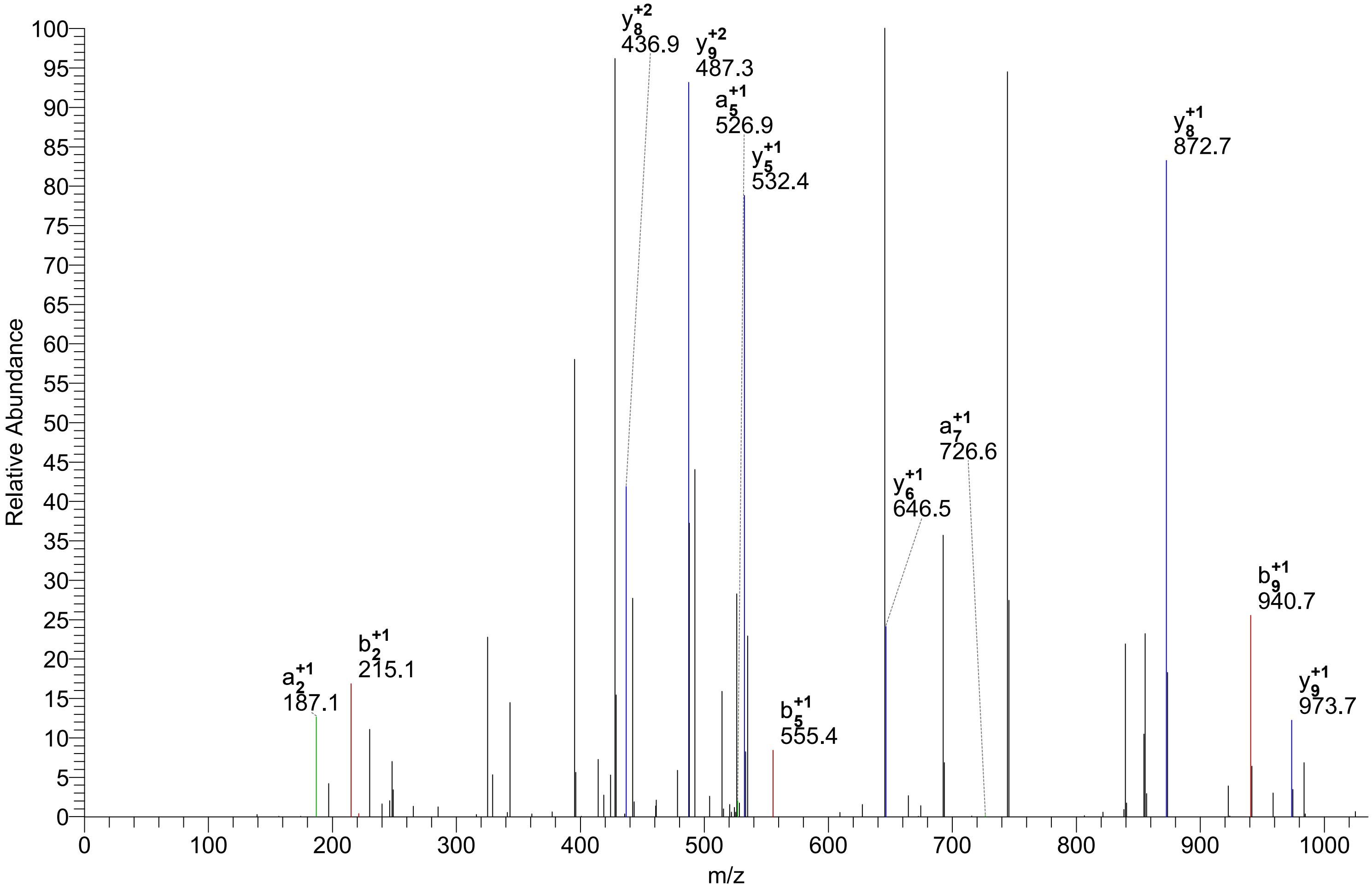
```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 T    187.14    215.14                                      973.57
 L    300.23    328.22                                      872.52
 L    413.31    441.31                                      759.44
 N    527.36    555.35                                      646.35
 K    655.45    683.45                                      532.31
 A    726.49    754.48                                      404.21
 A    797.52    825.52                                      333.18
 D    912.55    940.55                                      262.14
 K                                                          147.11
```



#2118291816-26226248 NL: 1.21E5



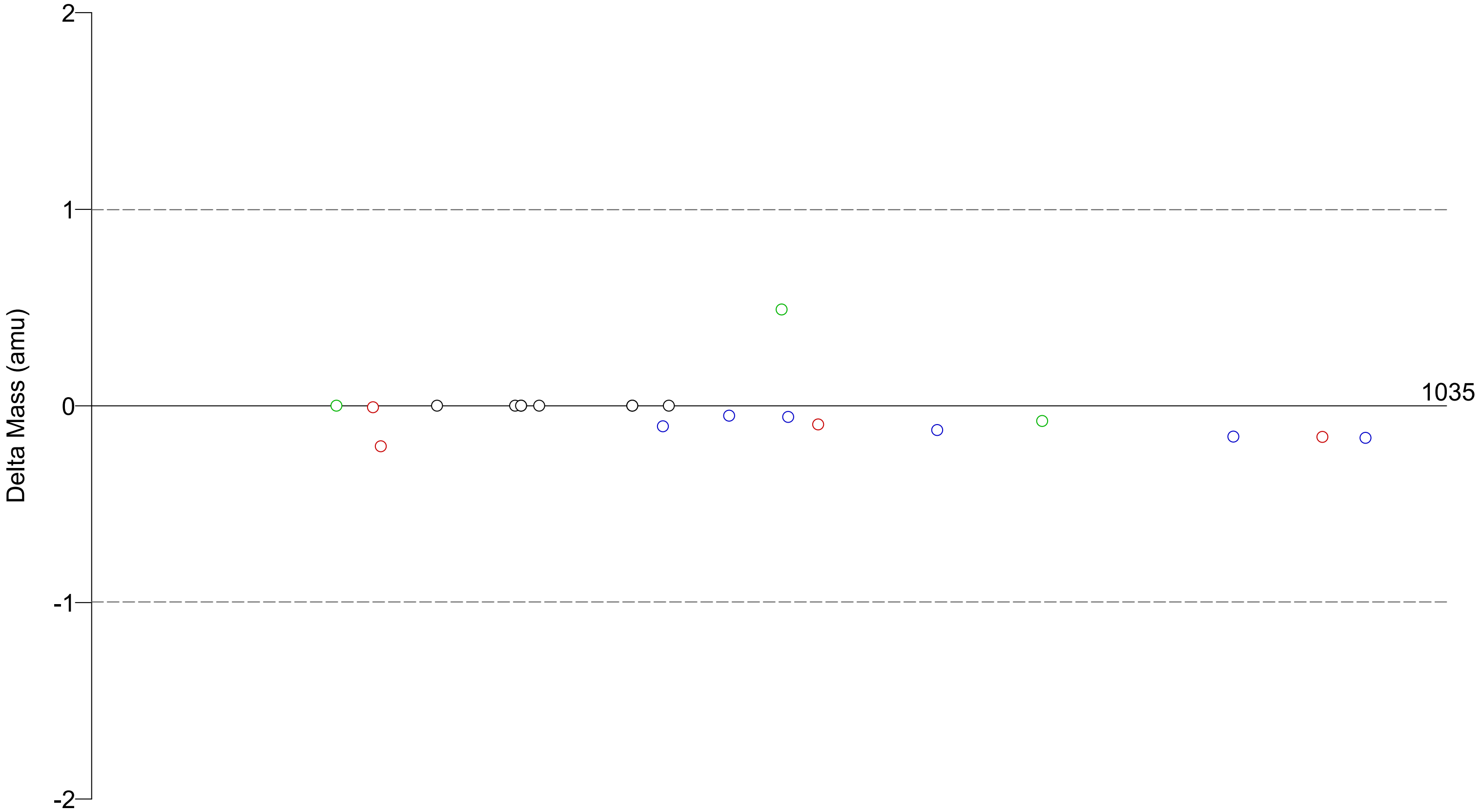
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00642285.1|TREMBL:B3KRL4|VE                                1       8.1      0.0       0
2118291816 -  K.LTLLNKAADK.G                         1086.65   2  0.4     2.083  0.466   185.2  3   10/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

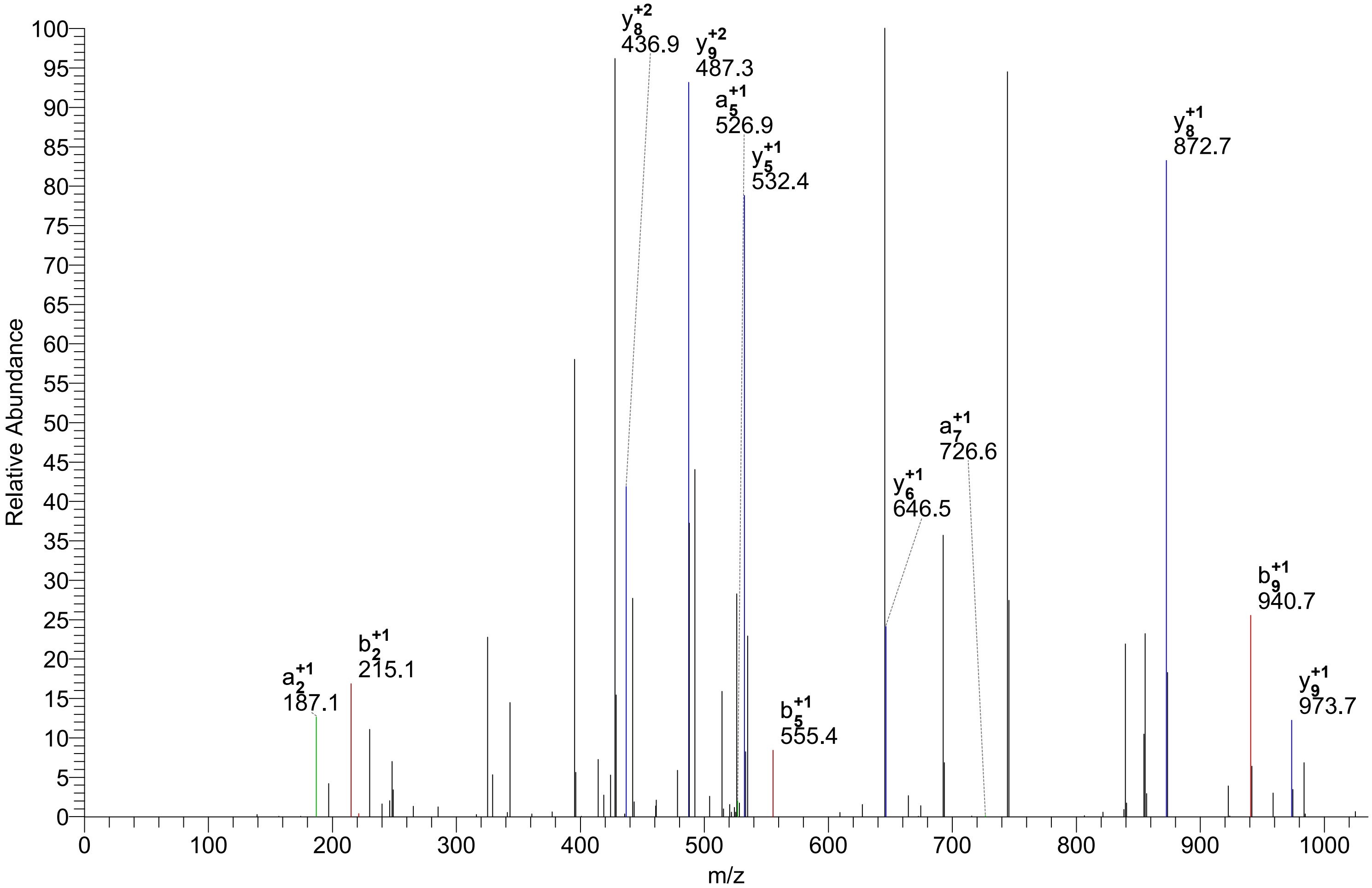
```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 T    187.14     215.14                                      973.57
 L    300.23     328.22                                      872.52
 L    413.31     441.31                                      759.44
 N    527.36     555.35                                      646.35
 K    655.45     683.45                                      532.31
 A    726.49     754.48                                      404.21
 A    797.52     825.52                                      333.18
 D    912.55     940.55                                      262.14
 K                                                           147.11
```



#2118291816-26226248 NL: 1.21E5



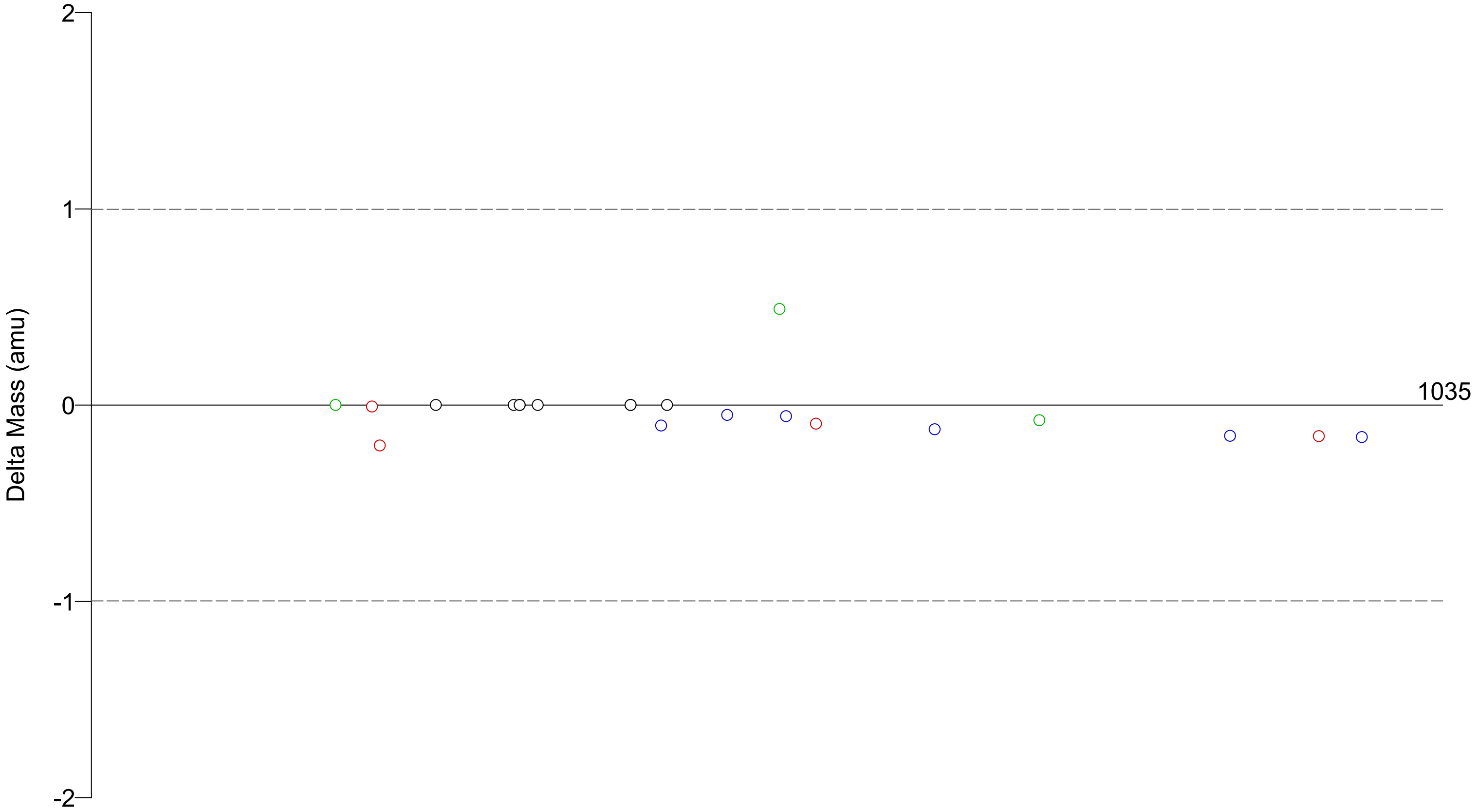
```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00908725.1|TREMBL:B4DTK7 Ta                                  1       8.1      0.0        0
2118291816 -  K.LTLLNKAADK.G                           1086.65   2  0.4      2.083  0.466   185.2  3   10/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

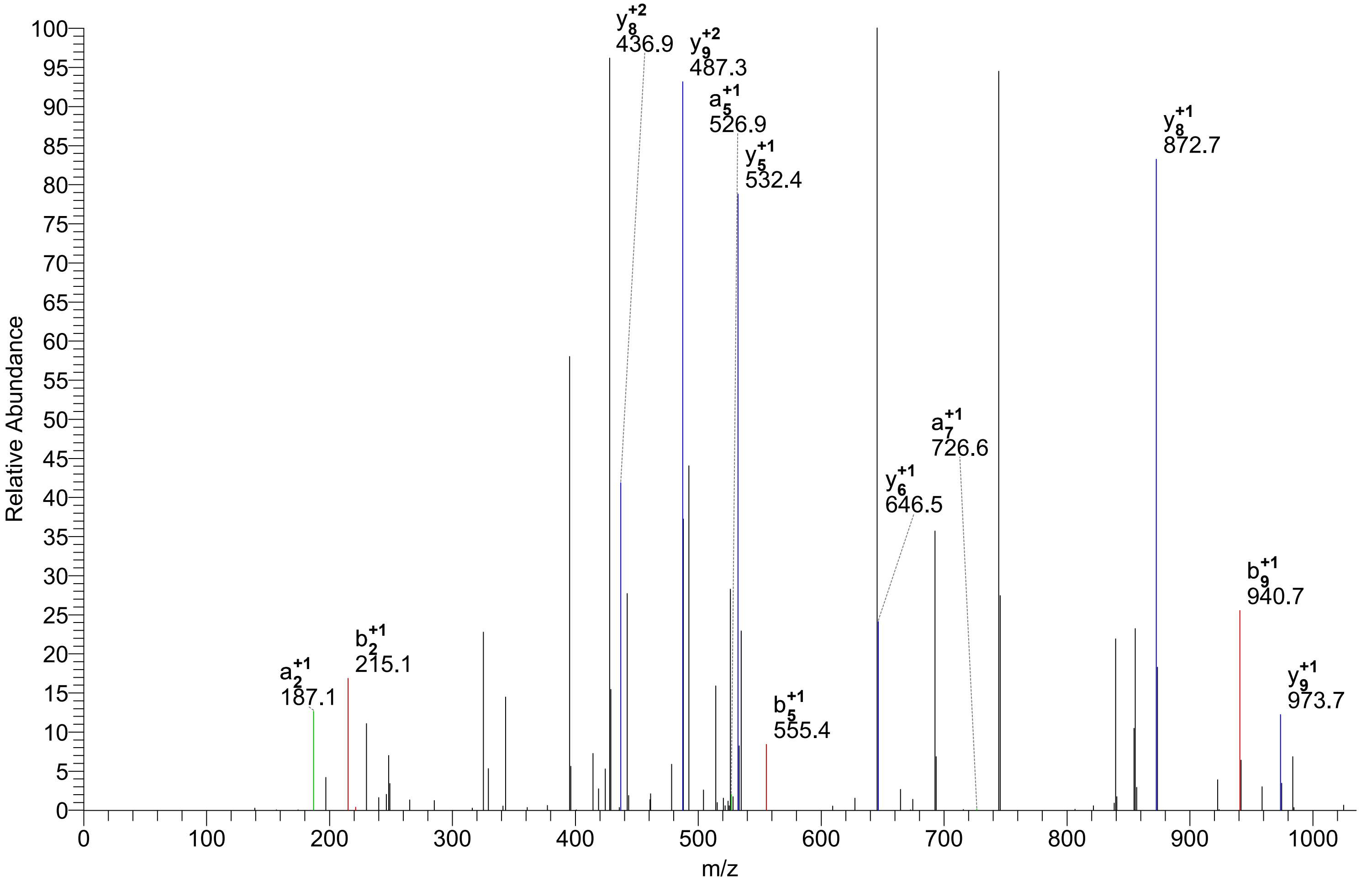
```
DTA for scans: 2118291816-26226248
Precursor ion: 543.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10    114.09
 T    187.14    215.14                                      973.57
 L    300.23    328.22                                      872.52
 L    413.31    441.31                                      759.44
 N    527.36    555.35                                      646.35
 K    655.45    683.45                                      532.31
 A    726.49    754.48                                      404.21
 A    797.52    825.52                                      333.18
 D    912.55    940.55                                      262.14
 K                                                          147.11
```



#2118291816-26226248 NL: 1.21E5



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

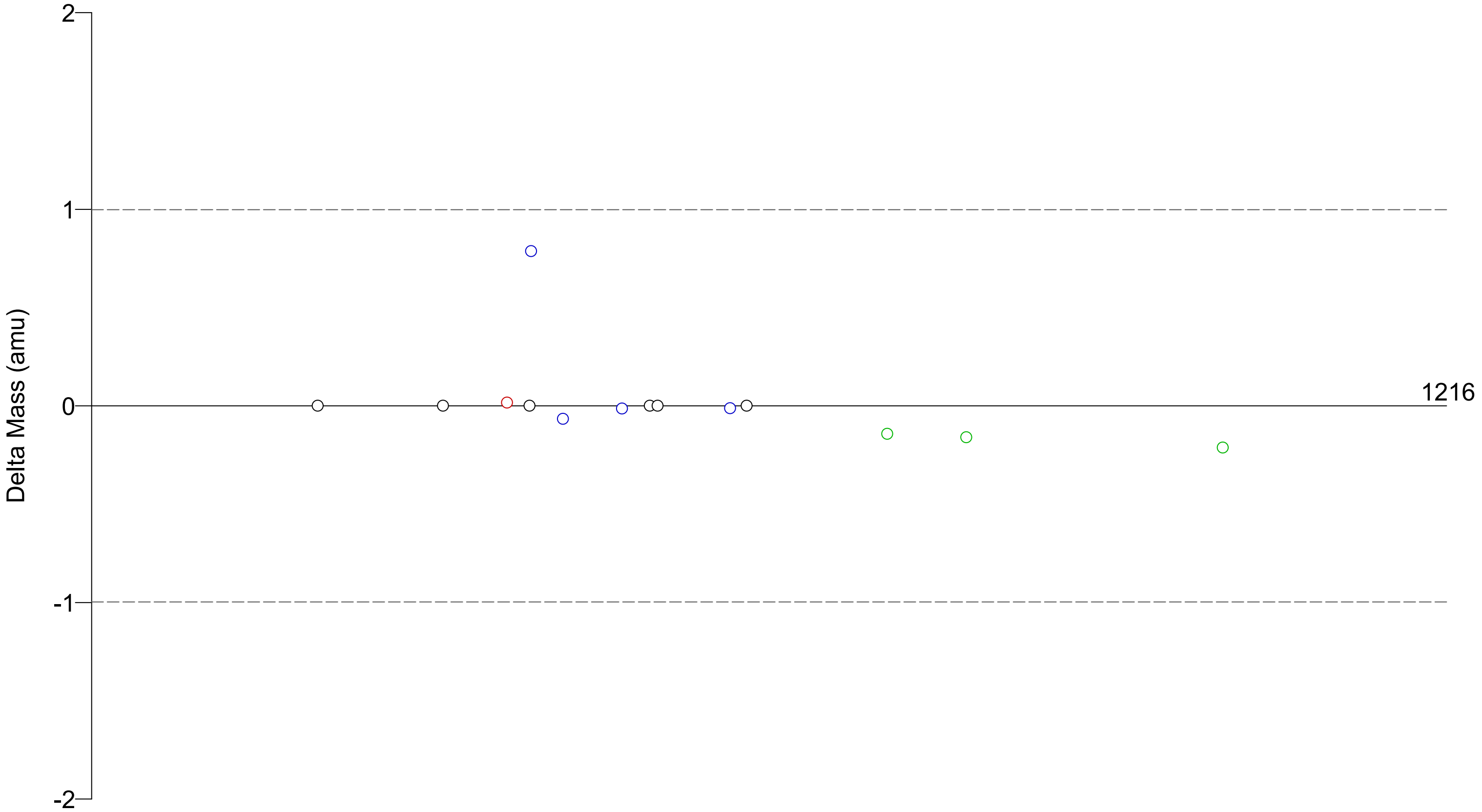
IPI:IPI00065529.1|TREMBL:Q96MJ9|H-INV:HIT000013428 Tax_Id=9606    1       8.1      0.0       0
2118291816 -  R.GDLSGASGPAETR.G                      1217.58   2  1       1.209  0.711   107.4  3   8/36

1 of 1 peptide matches reported, 0 removed due to filtering
```

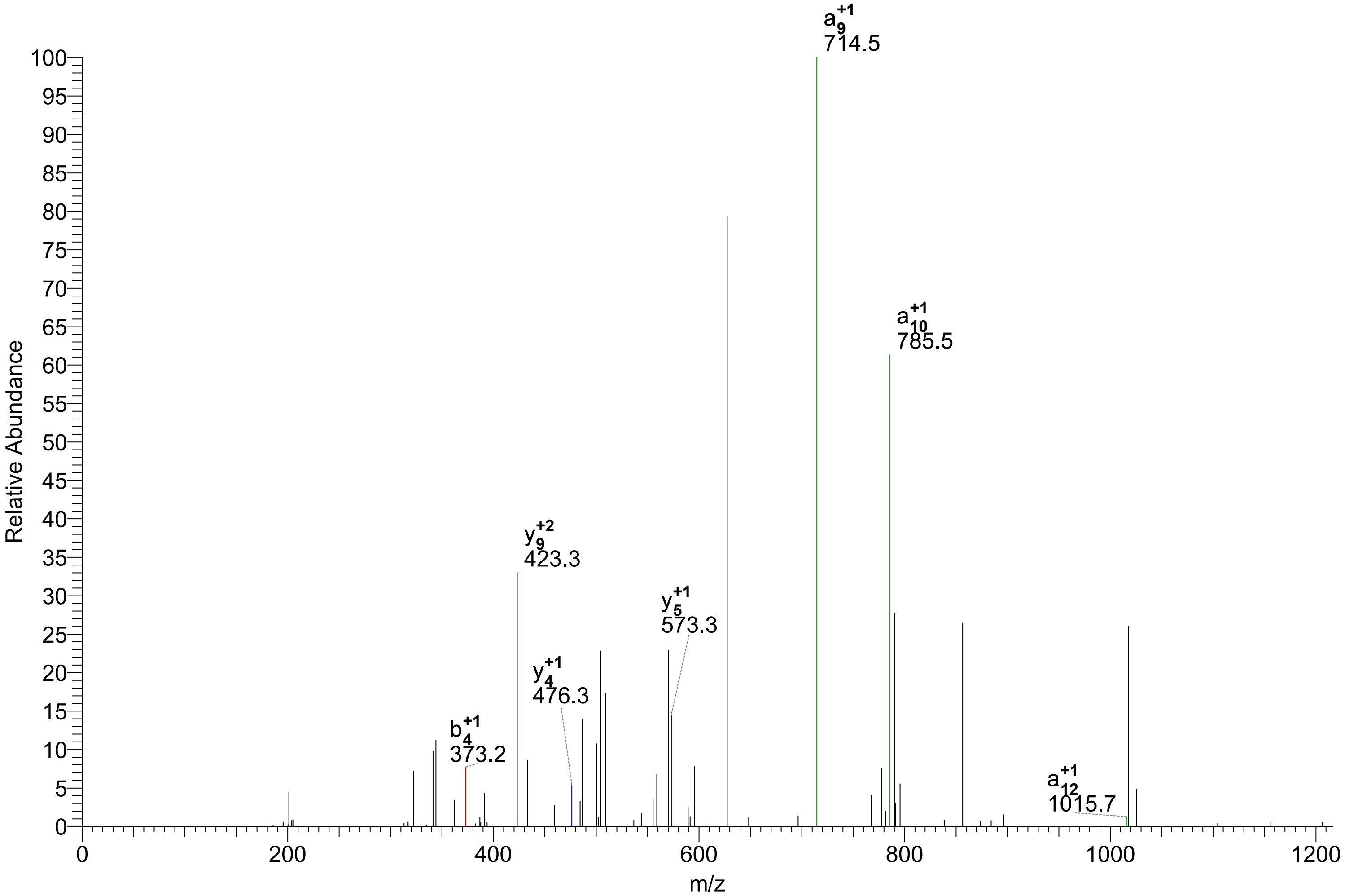
```
DTA for scans: 2118291816-26226248
Precursor ion: 609.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 D    145.06     173.06                                     1160.55
 L    258.14     286.14                                     1045.53
 S    345.18     373.17                                      932.44
 G    402.20     430.19                                      845.41
 A    473.24     501.23                                      788.39
 S    560.27     588.26                                      717.35
 G    617.29     645.28                                      630.32
 P    714.34     742.34                                      573.30
 A    785.38     813.37                                      476.25
 E    914.42     942.42                                      405.21
 T   1015.47    1043.46                                      276.17
 R                                                           175.12
```



#2118291816-26226248 NL: 9.29E4



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

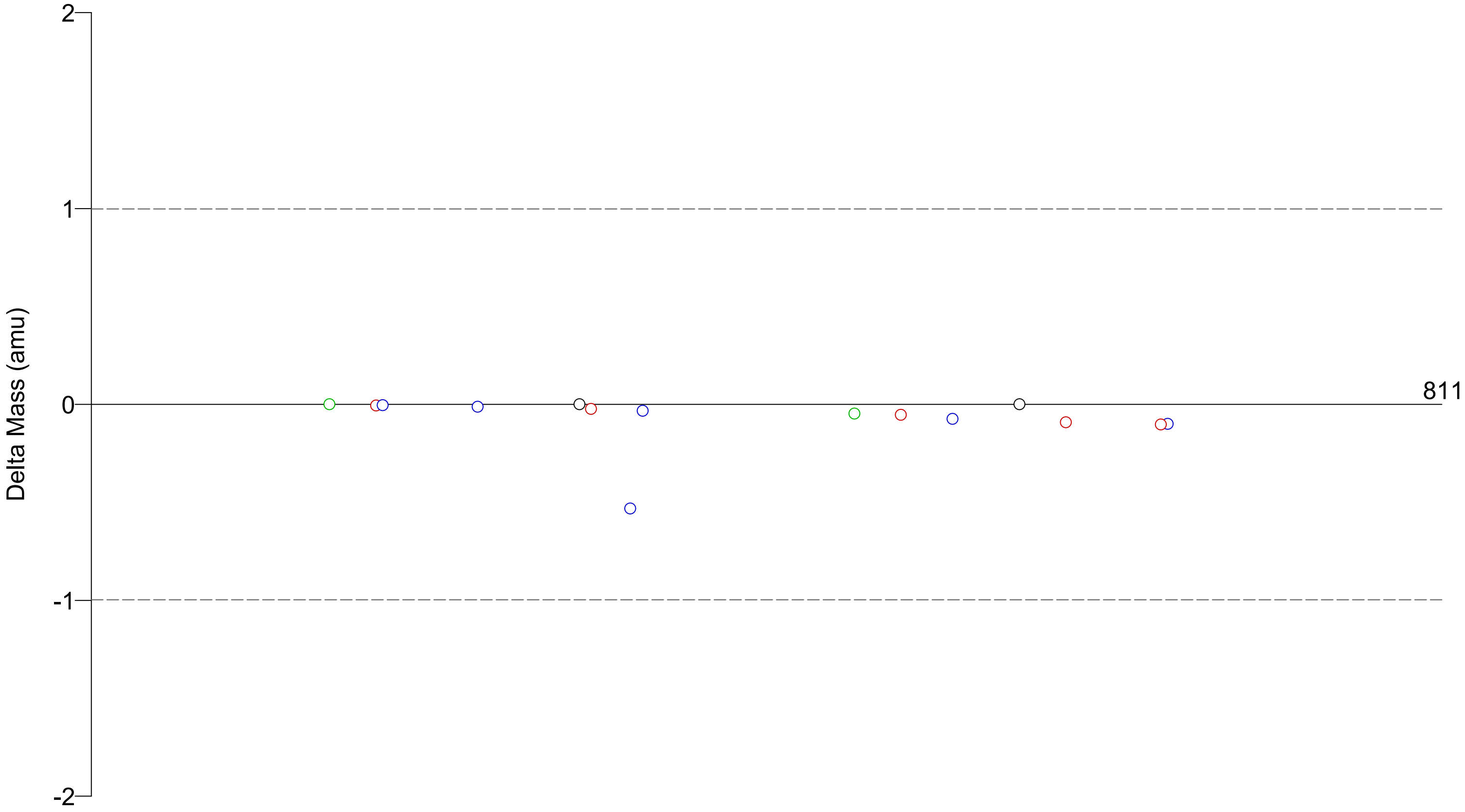
IPI:IPI00384404.4|TREMBL:A2J1N6 Tax_Id=9606 Gene_Symbol=- Rheu     1       10.1     0.0       0
19287468 - 1  K.GLEWVGR.I                                 816.44    2  0.4     2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

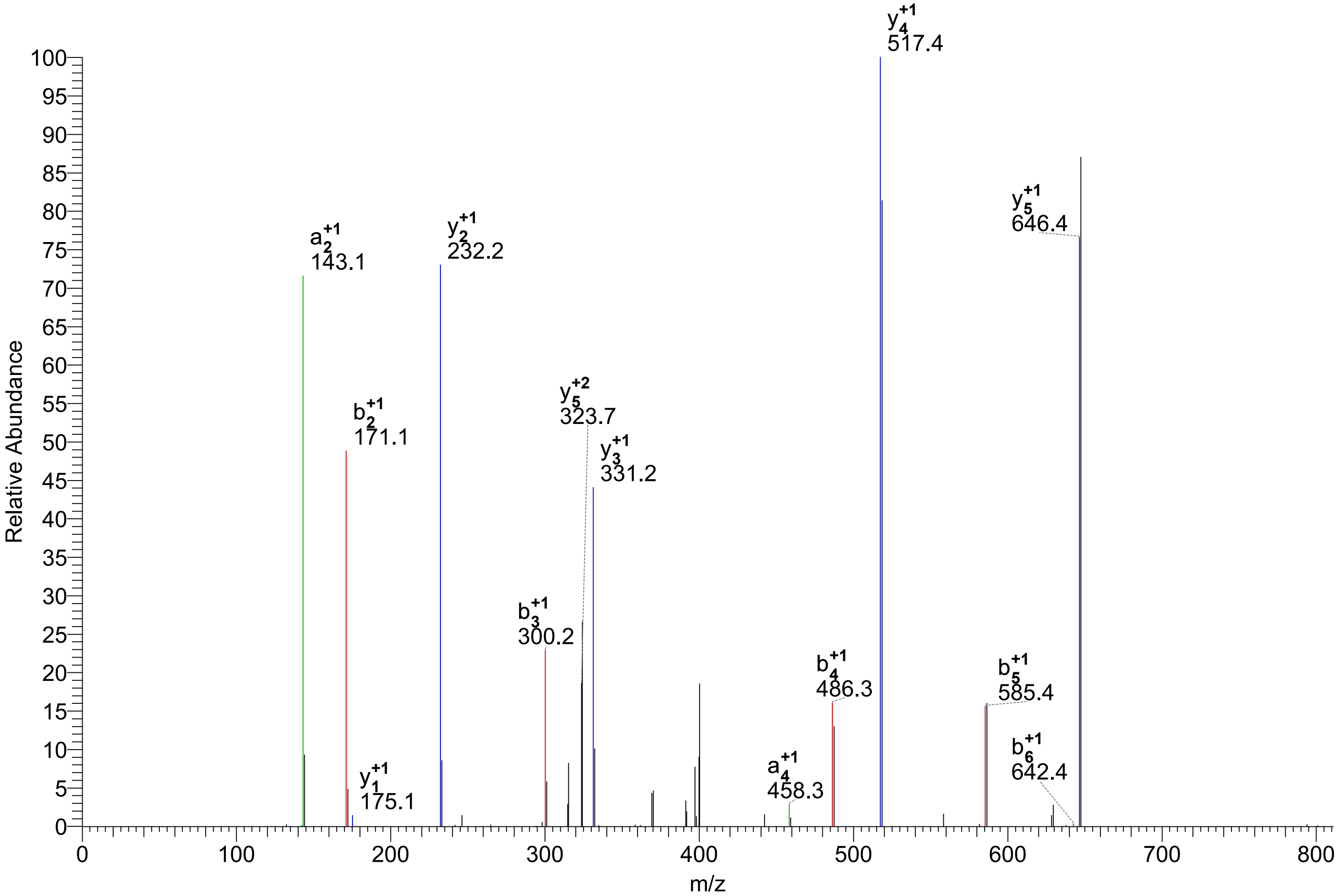
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                       759.41
 E    272.16     300.16                                       646.33
 W    458.24     486.23                                       517.29
 V    557.31     585.30                                       331.21
 G    614.33     642.32                                       232.14
 R                                                            175.12
```



#19287468-1 NL: 1.30E5



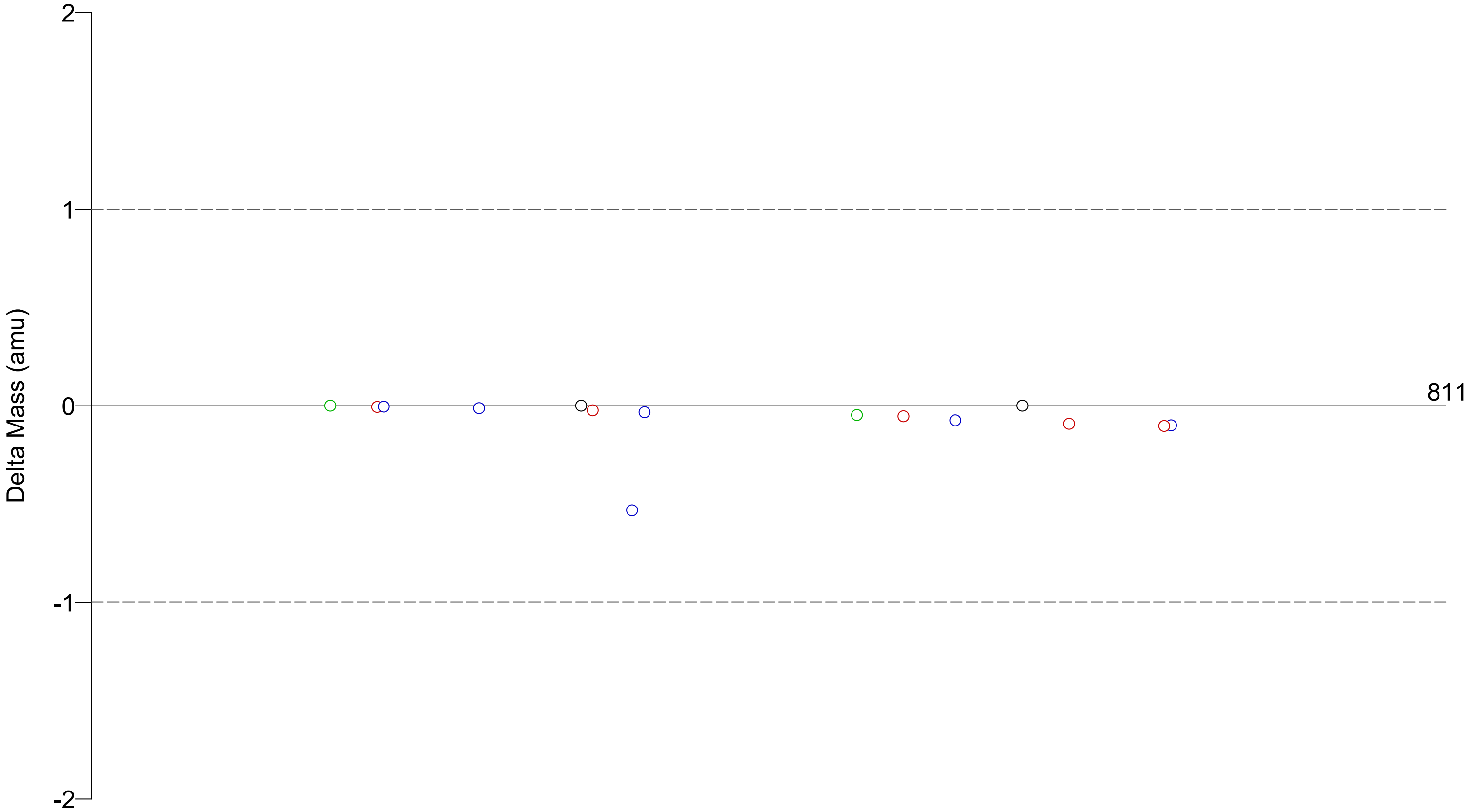
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00783024.1|TREMBL:Q9UL88 Ta                                1       10.1     0.0       0
19287468 - 1  K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

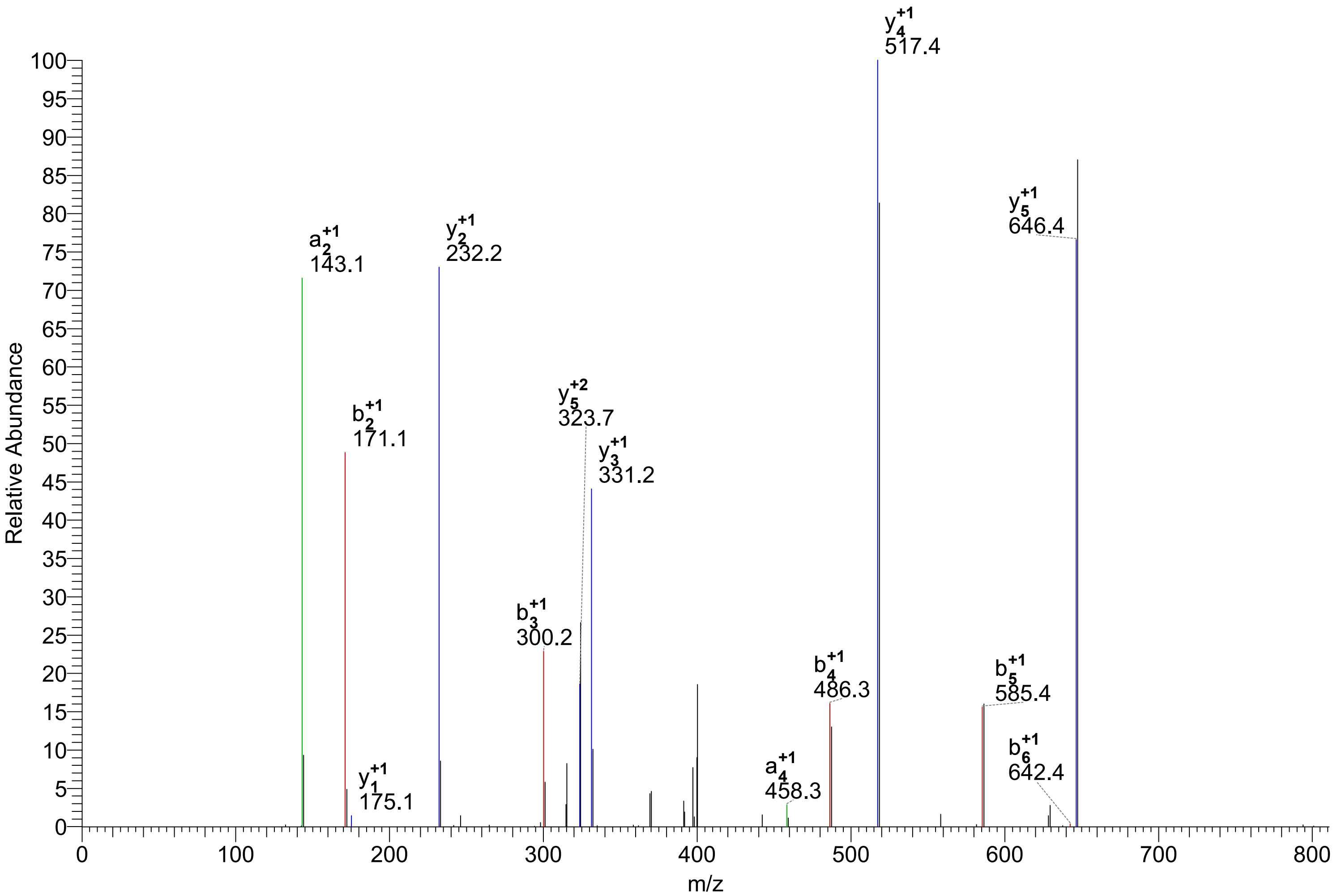
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                      759.41
 E    272.16     300.16                                      646.33
 W    458.24     486.23                                      517.29
 V    557.31     585.30                                      331.21
 G    614.33     642.32                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.30E5



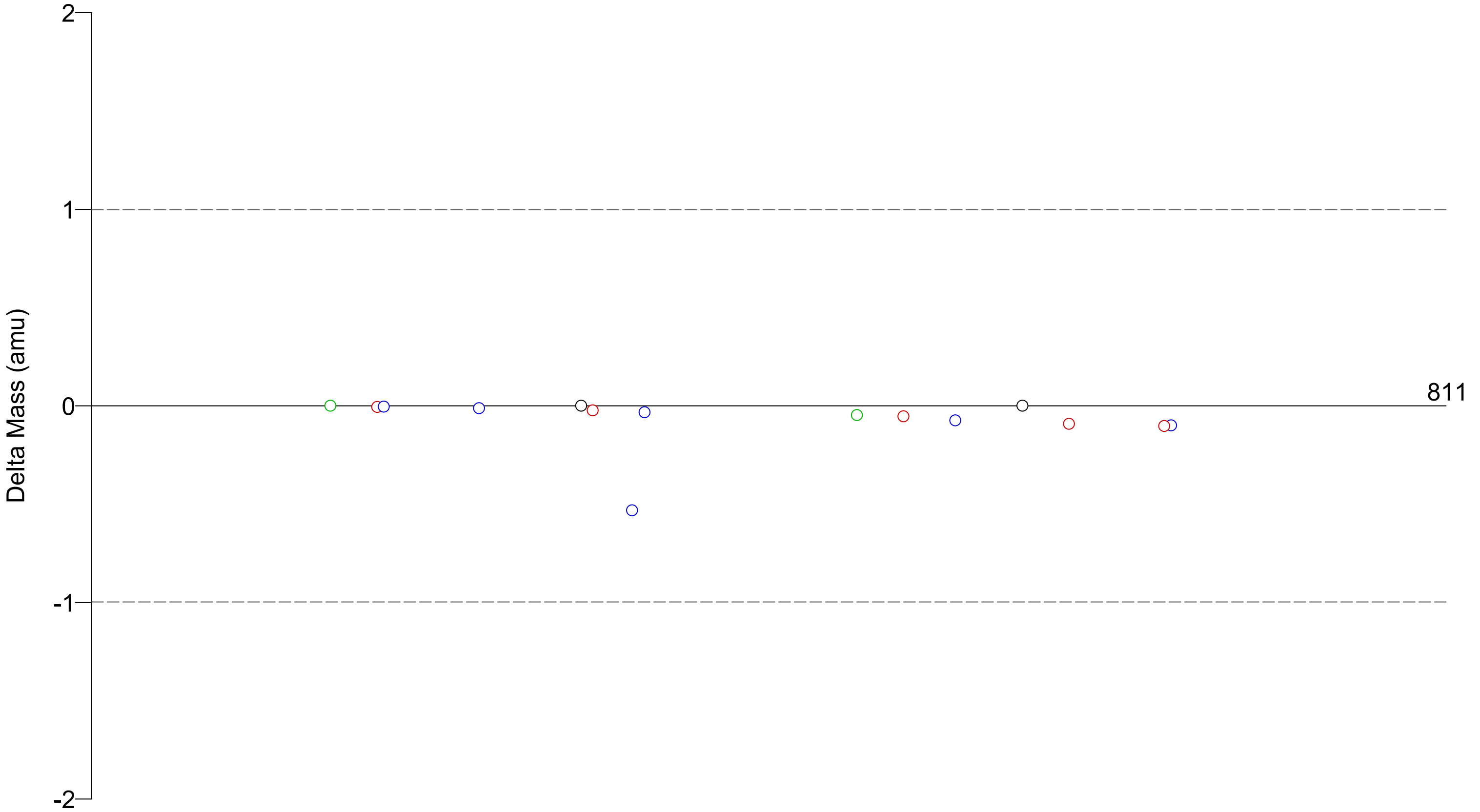
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00783184.1|TREMBL:Q0ZCI0 Ta                                1       10.1     0.0       0
19287468 - 1  K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

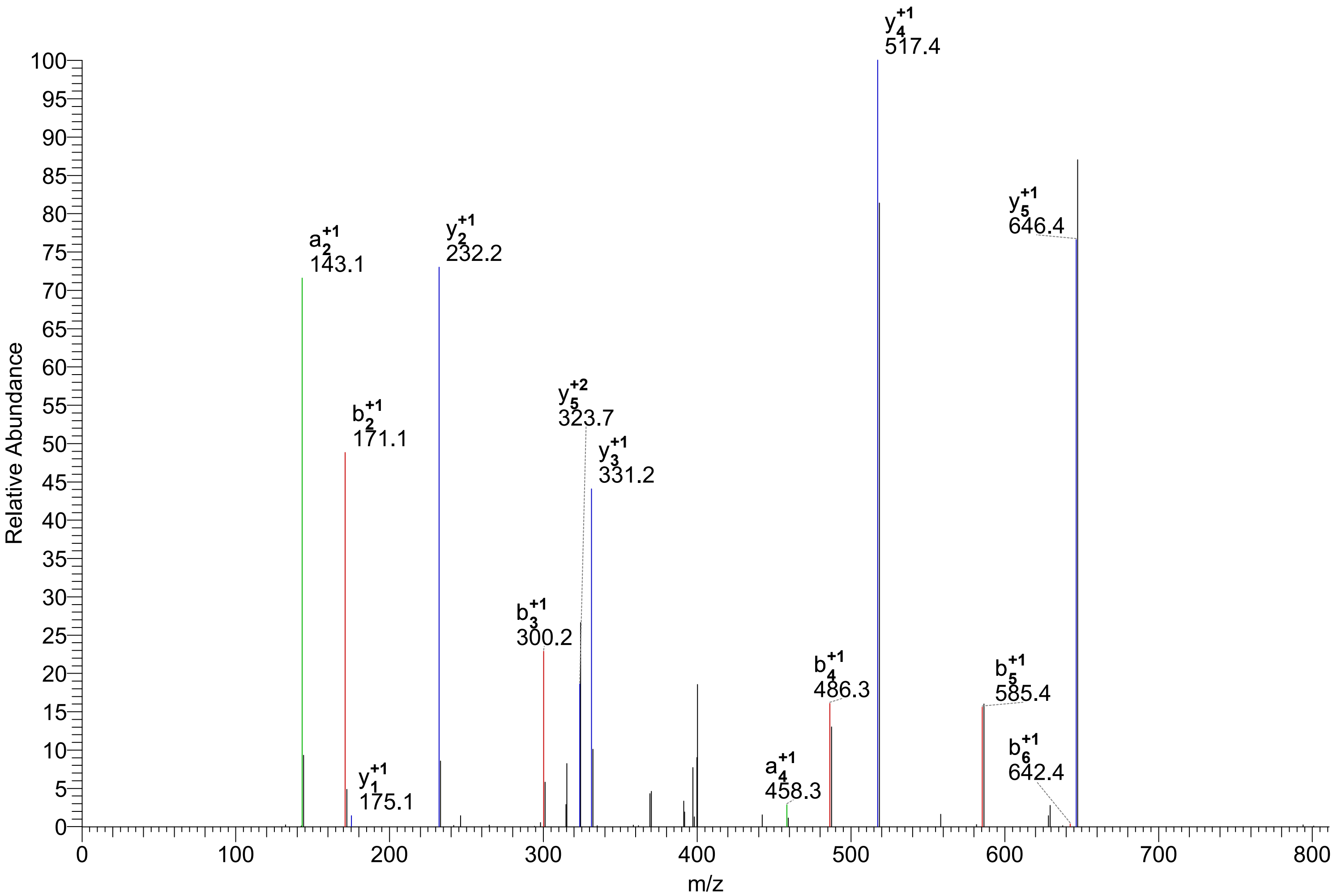
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                      759.41
 E    272.16     300.16                                      646.33
 W    458.24     486.23                                      517.29
 V    557.31     585.30                                      331.21
 G    614.33     642.32                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.30E5



```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+        z     P        XC  DeltaCn   Sp    RSp  Ions  Count

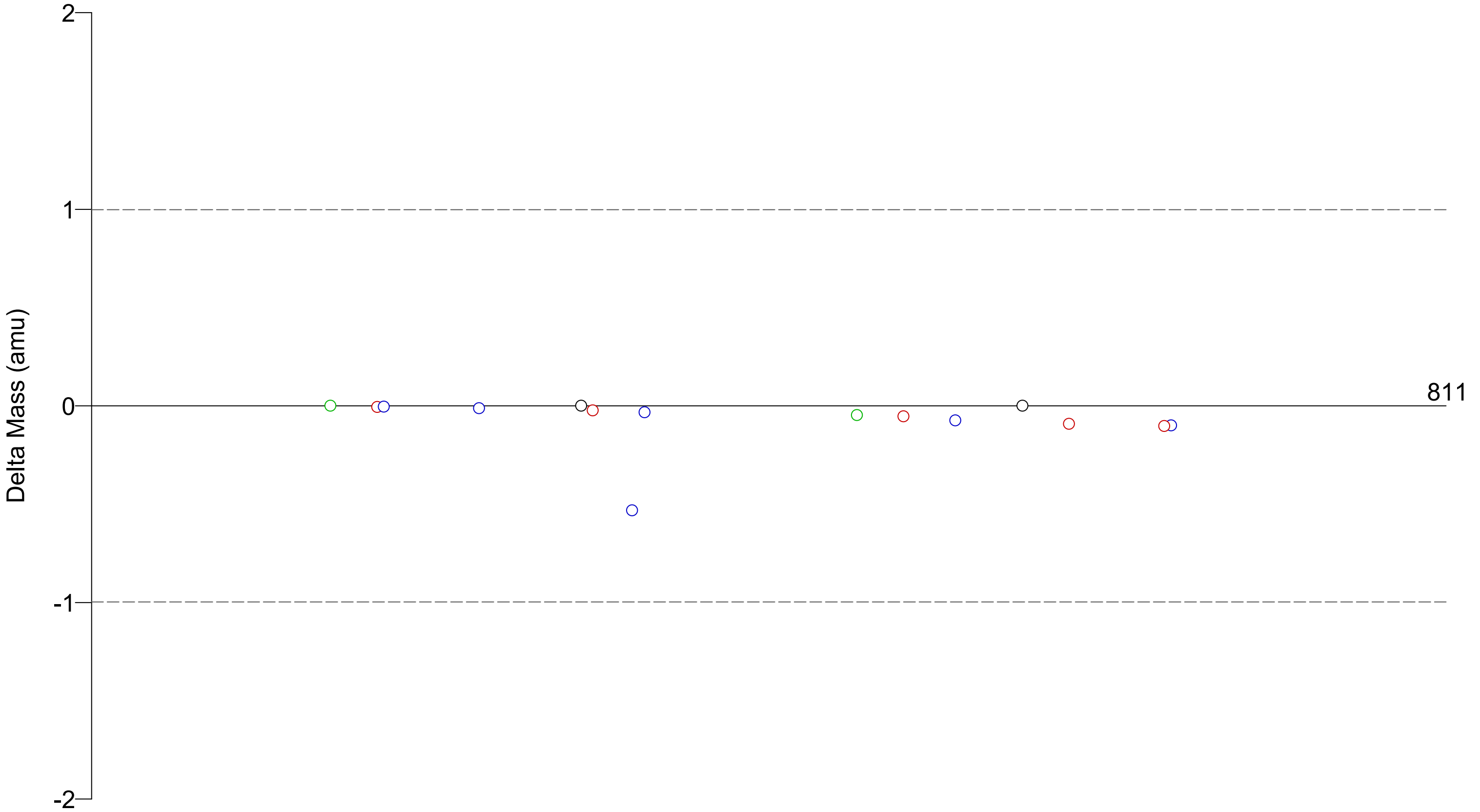
IPI:IPI00827892.1|TREMBL:A2N2G5 Ta                                       1        10.1     0.0       0
19287468 - 1  K.GLEWVGR.I                               816.44     2  0.4      2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

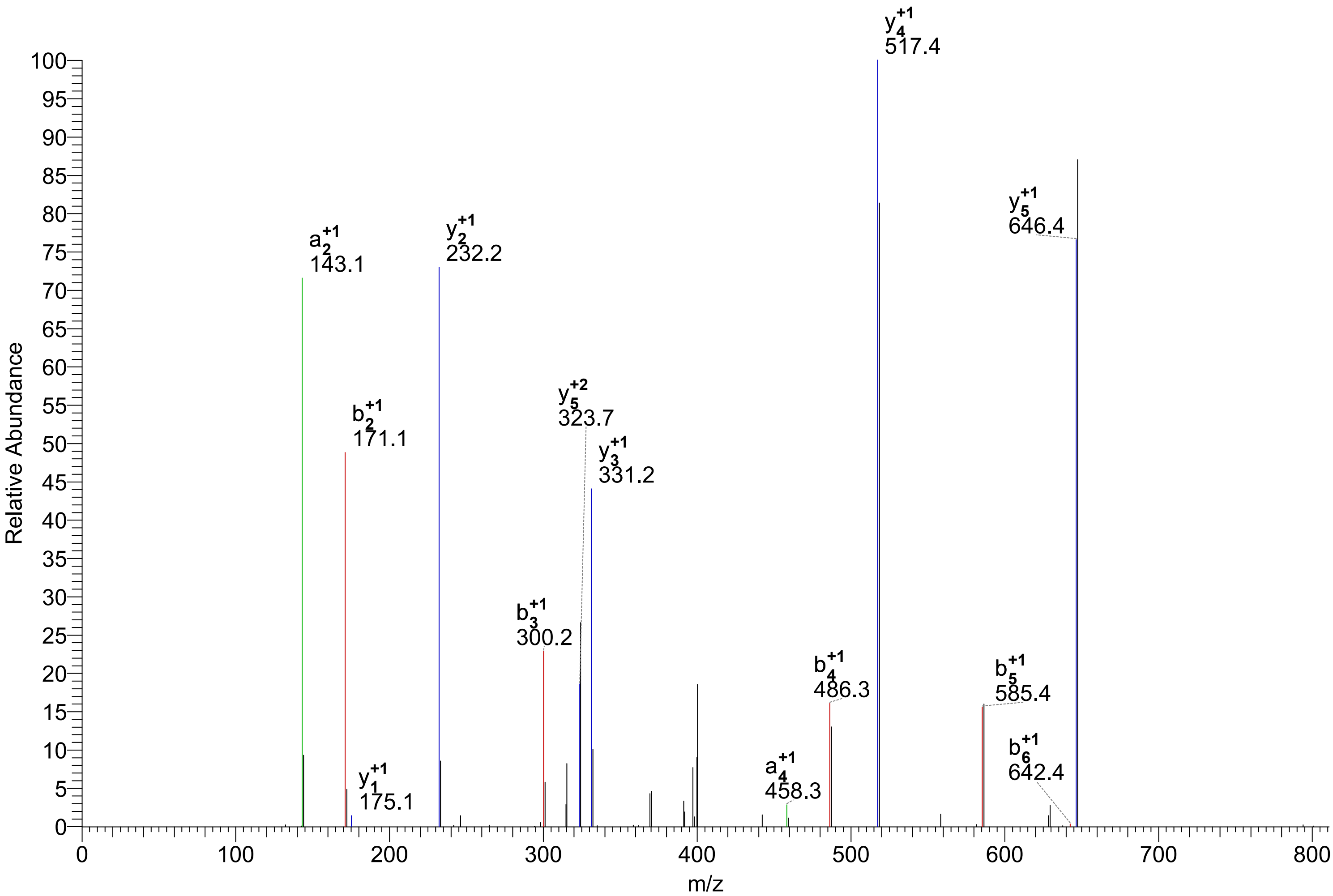
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                      759.41
 E    272.16     300.16                                      646.33
 W    458.24     486.23                                      517.29
 V    557.31     585.30                                      331.21
 G    614.33     642.32                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.30E5



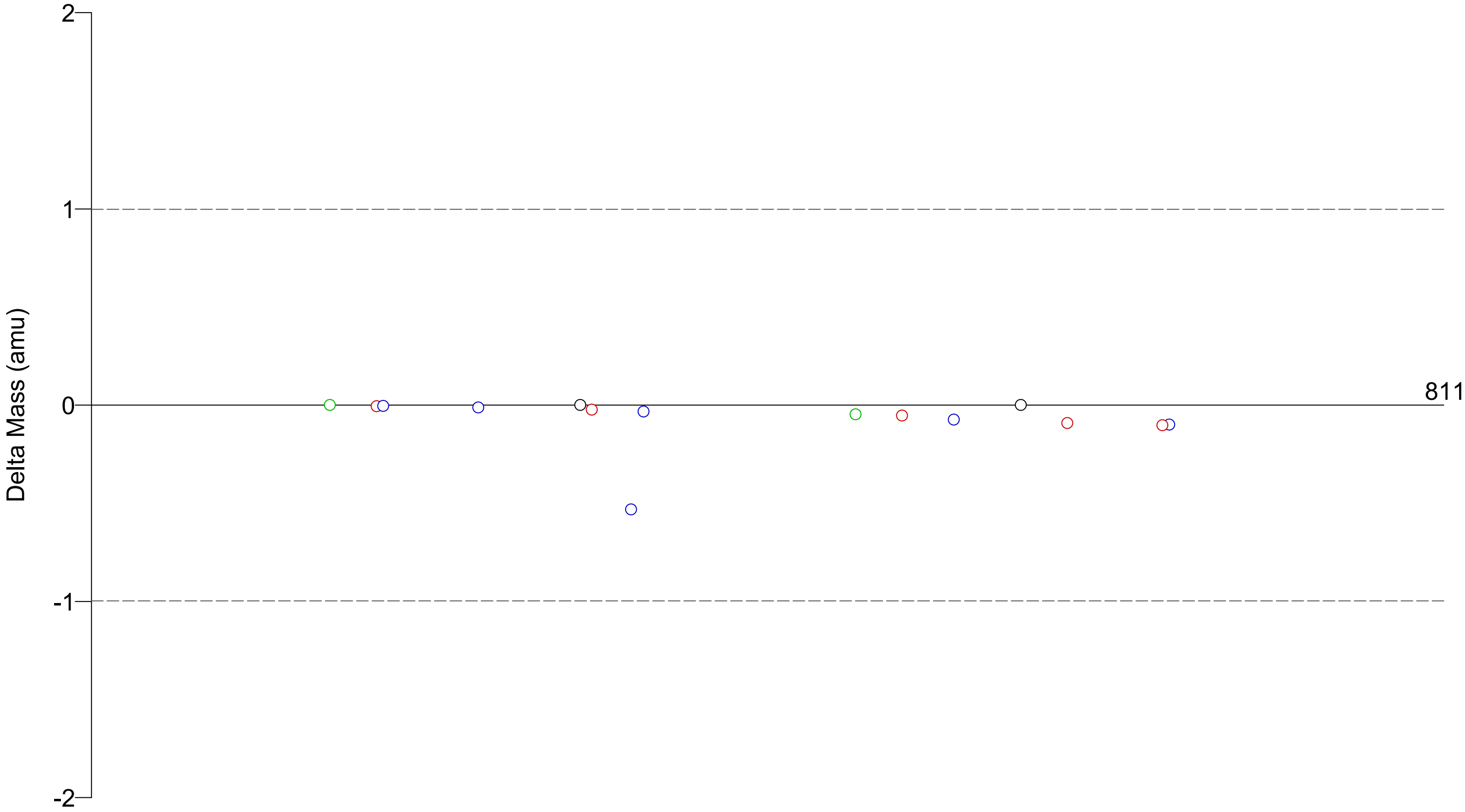
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                Mh+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829590.1|TREMBL:A6NNW3|EN                                1       10.1     0.0       0
19287468 - 1  K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

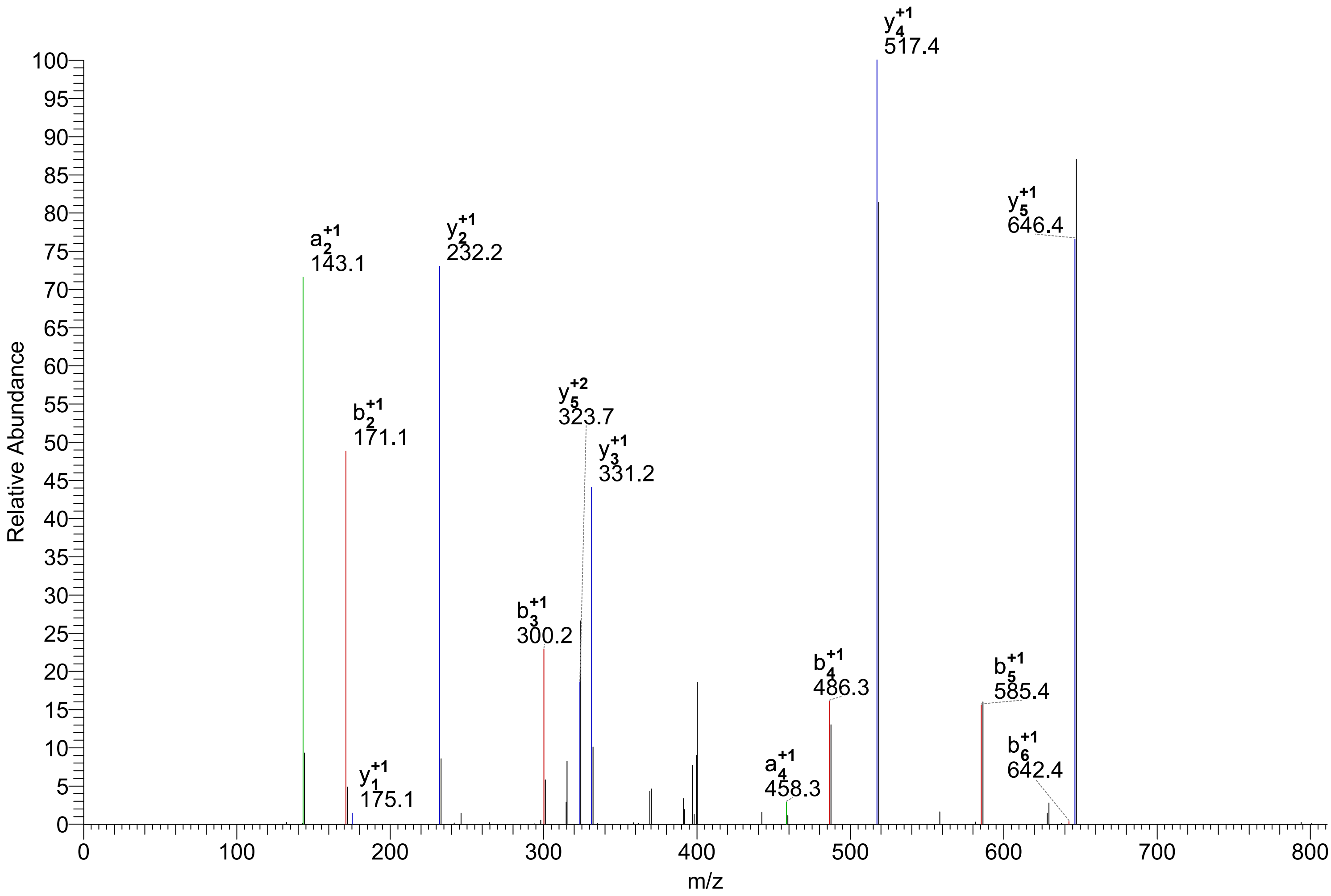
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions      C ions     Y ions     Y* ions     Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                        759.41
 E    272.16     300.16                                        646.33
 W    458.24     486.23                                        517.29
 V    557.31     585.30                                        331.21
 G    614.33     642.32                                        232.14
 R                                                             175.12
```



#19287468-1 NL: 1.30E5



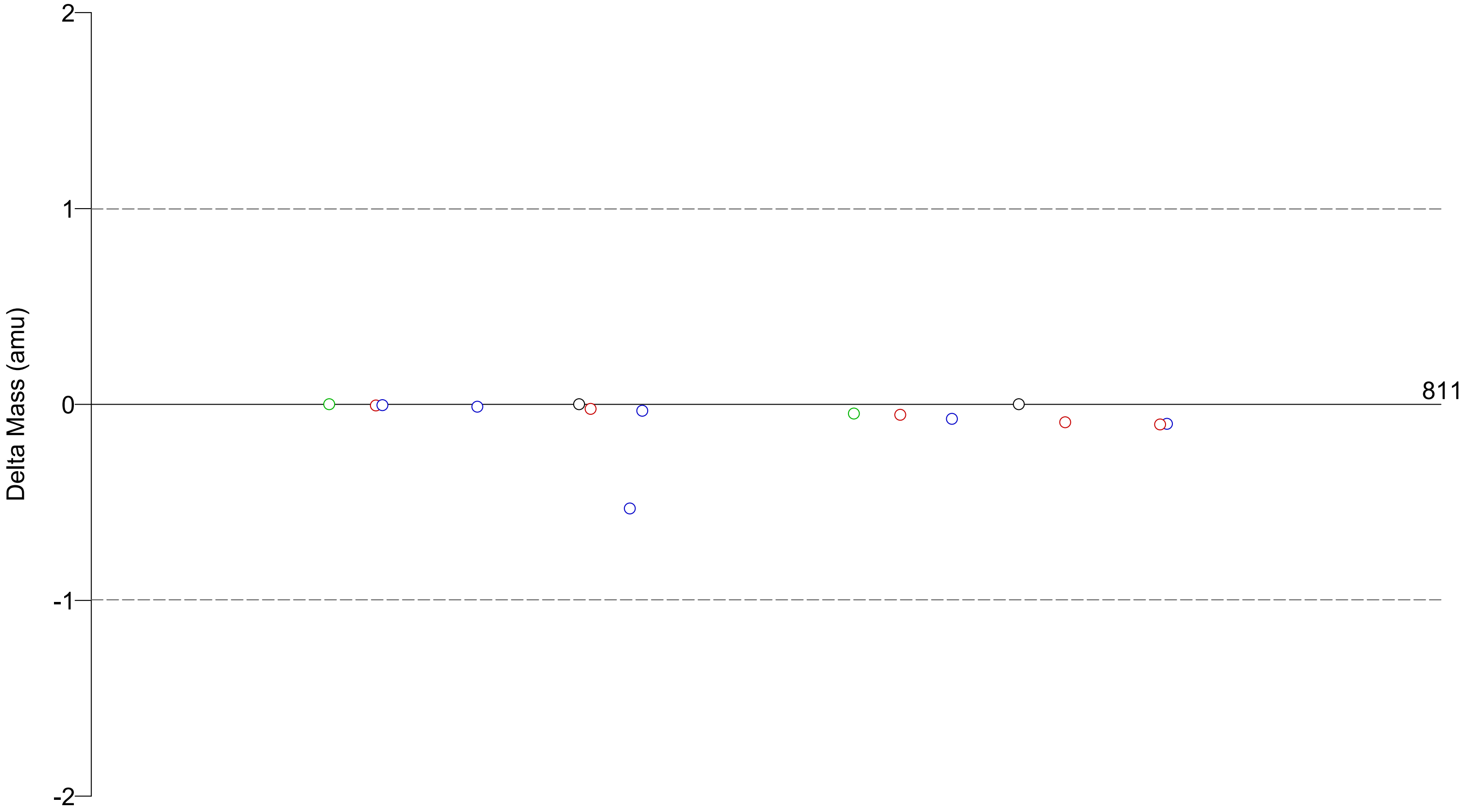
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00829841.1|ENSEMBL:ENSP0000                                1       10.1     0.0       0
19287468 - 1  K.GLEWVGR.I                            816.44    2  0.4     2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

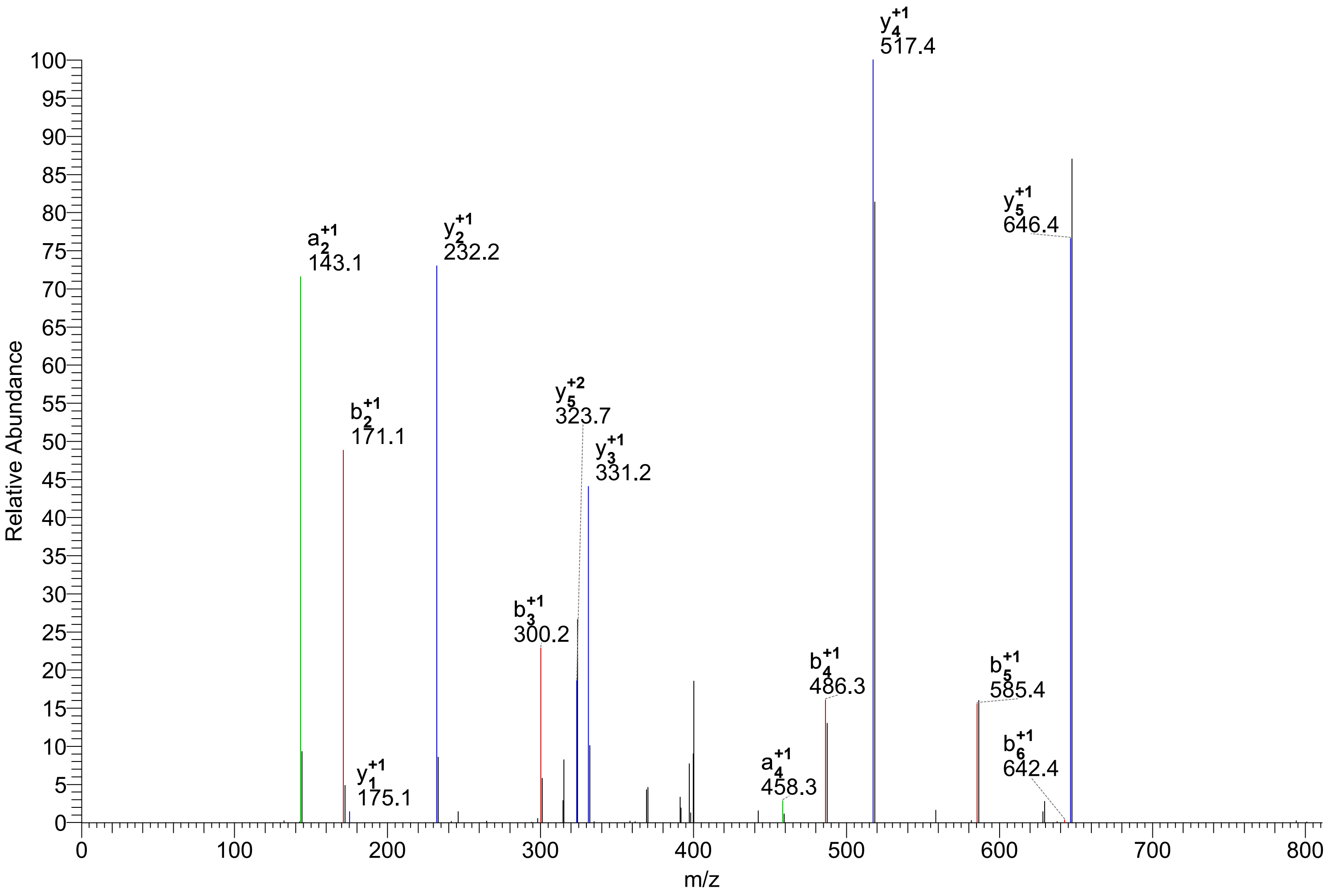
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                      759.41
 E    272.16     300.16                                      646.33
 W    458.24     486.23                                      517.29
 V    557.31     585.30                                      331.21
 G    614.33     642.32                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.30E5



```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

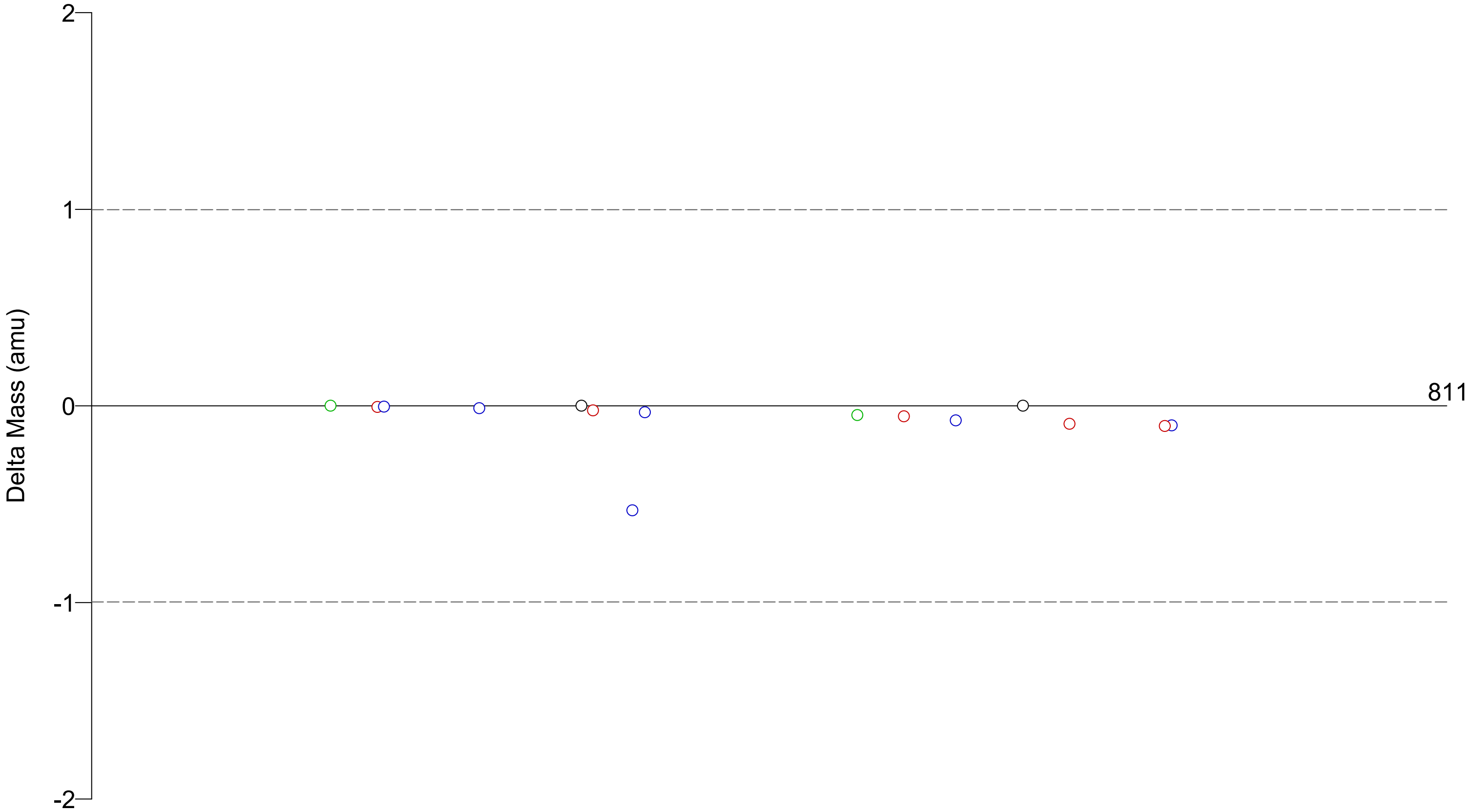
IPI:IPI00921238.1|H-INV:HIT0003928                                       1      10.1     0.0        0
19287468 - 1  K.GLEWVGR.I                                 816.44     2  0.4      2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

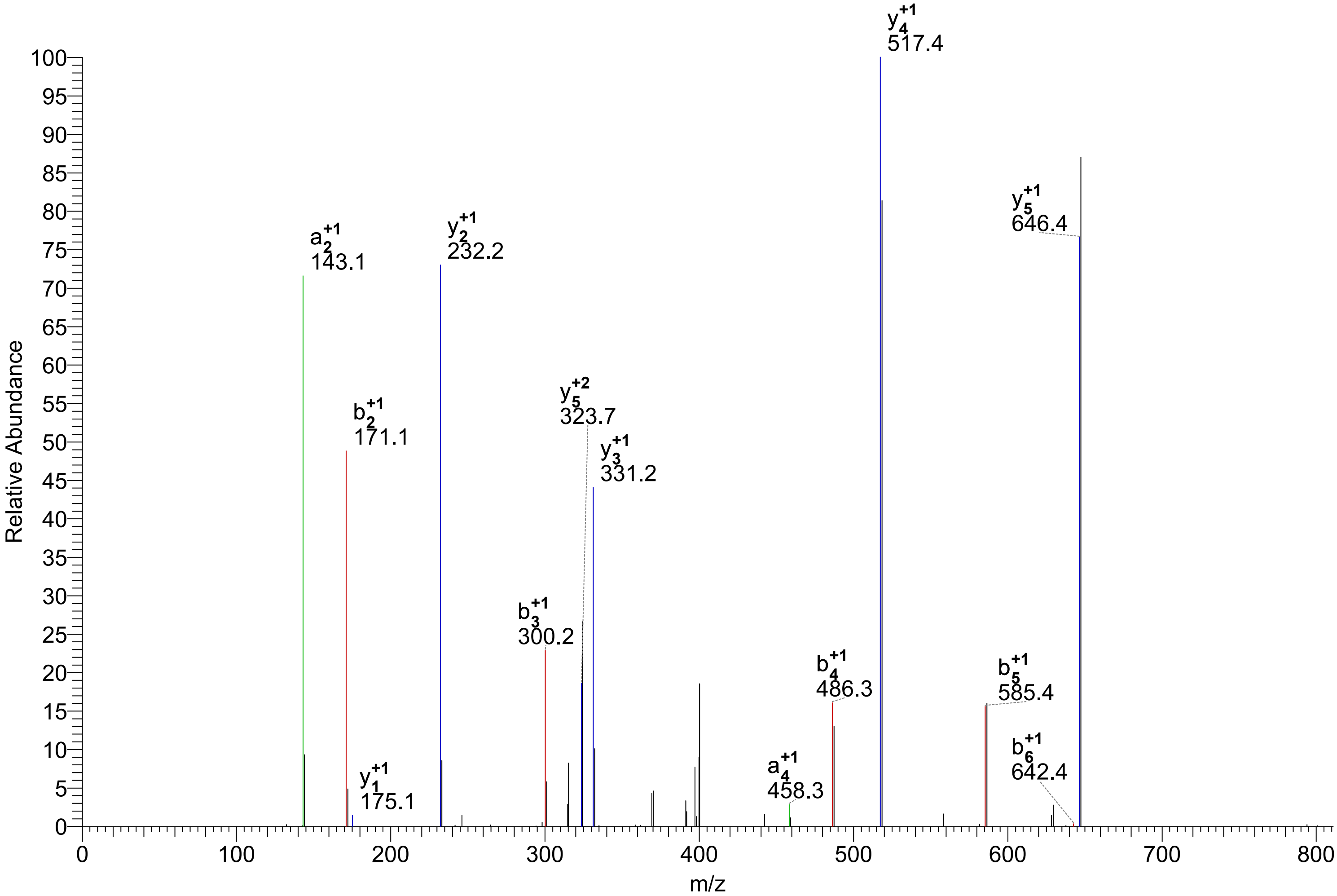
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G     30.03      58.03
 L    143.12     171.11                                      759.41
 E    272.16     300.16                                      646.33
 W    458.24     486.23                                      517.29
 V    557.31     585.30                                      331.21
 G    614.33     642.32                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.30E5



```
Reference                                                                 P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

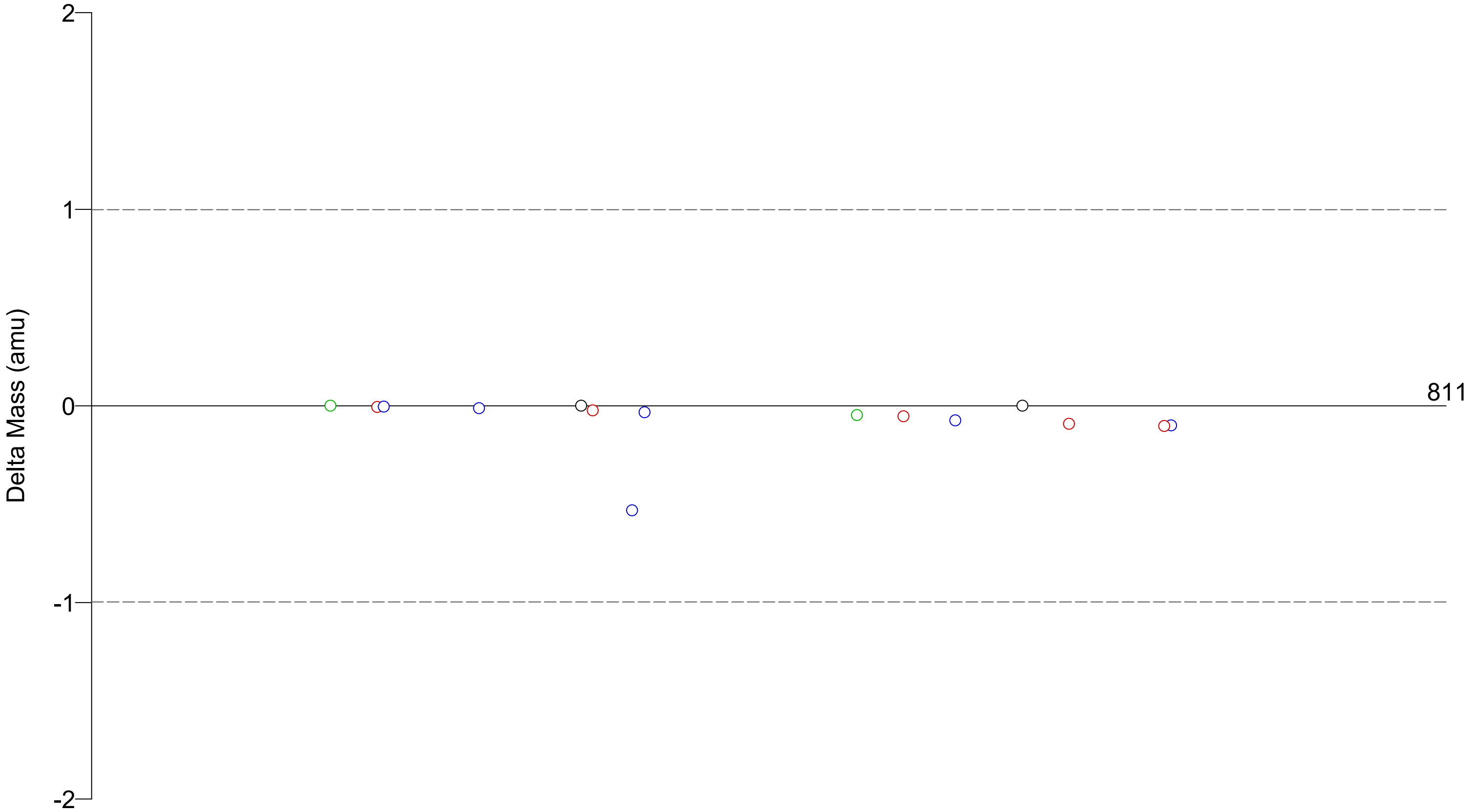
IPI:IPI00936370.1|TREMBL:Q0ZCJ6|EN                                   1       10.1     0.0       0
19287468 - 1  K.GLEWVGR.I                                816.44     2  0.4      2.817  0.203   839.1  1   13/18   8

1 of 1 peptide matches reported, 0 removed due to filtering
```

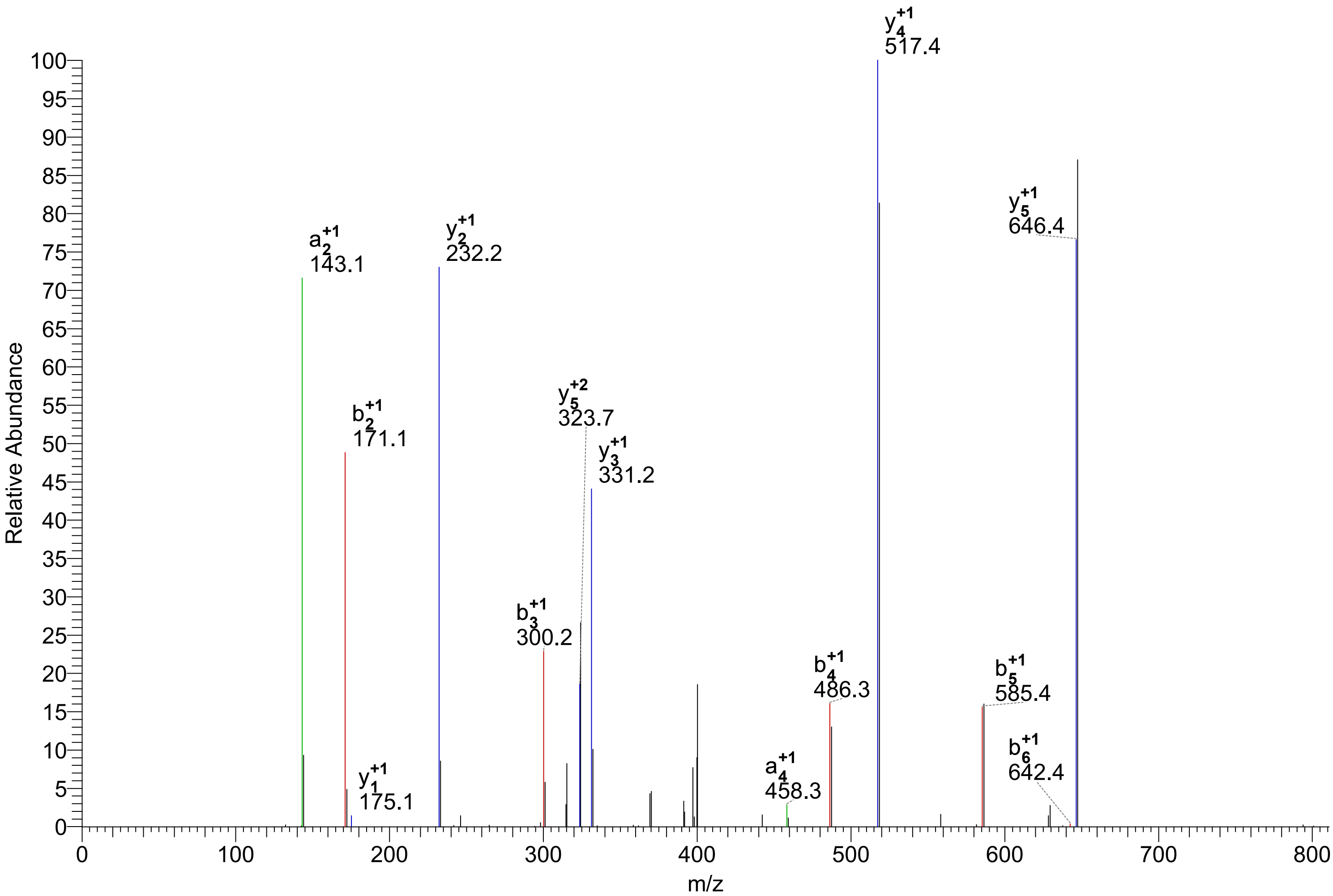
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 G    30.03      58.03
 L   143.12     171.11                                      759.41
 E   272.16     300.16                                      646.33
 W   458.24     486.23                                      517.29
 V   557.31     585.30                                      331.21
 G   614.33     642.32                                      232.14
 R                                                          175.12
```



#19287468-1 NL: 1.30E5



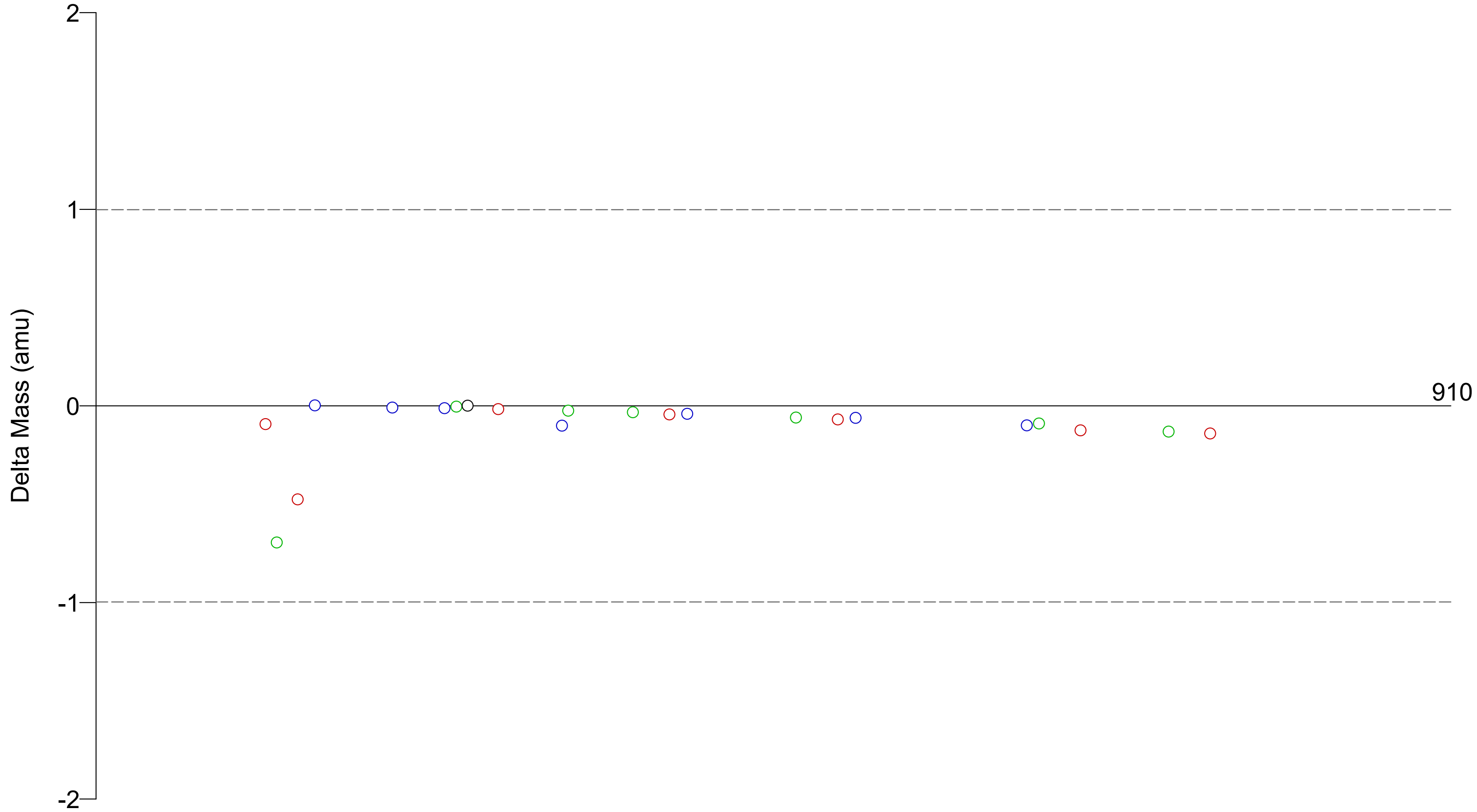
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)        Sequence                                 MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00021856.3|SWISS-PROT:P02655|TREMBL:C0JYY4;Q6P163|ENSEM     1        10.1     0.0        0
19287468 - 1  K.LRDLYSK.S                              894.50    2  0.6      2.716  0.205   1098.8 1   15/18

1 of 1 peptide matches reported, 0 removed due to filtering
```

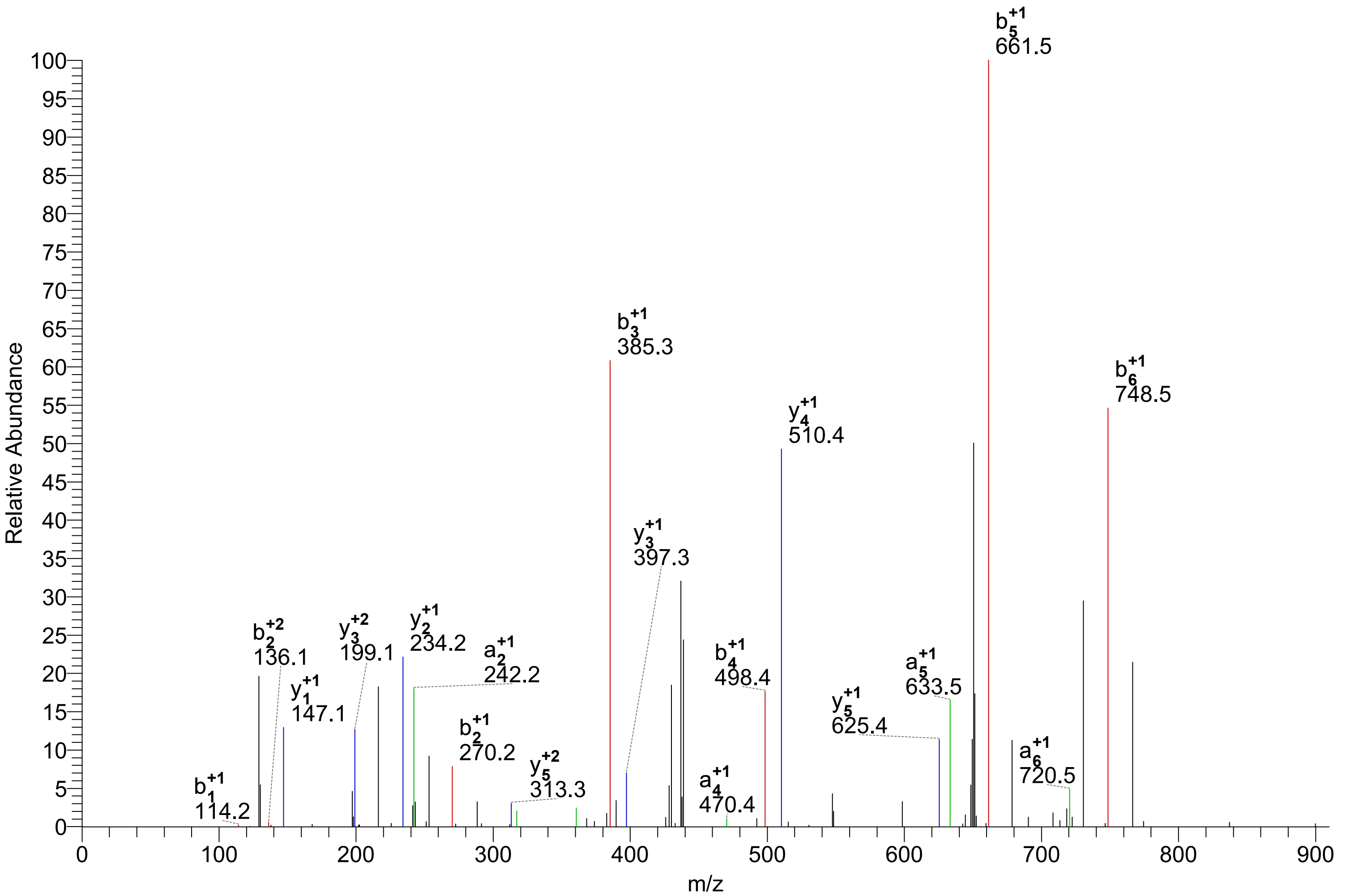
```
DTA for scans: 19287468-1
Precursor ion: 447.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 R    242.20     270.19                                      781.42
 D    357.22     385.22                                      625.32
 L    470.31     498.30                                      510.29
 Y    633.37     661.37                                      397.21
 S    720.40     748.40                                      234.14
 K                                                           147.11
```



#19287468-1 NL: 1.39E5



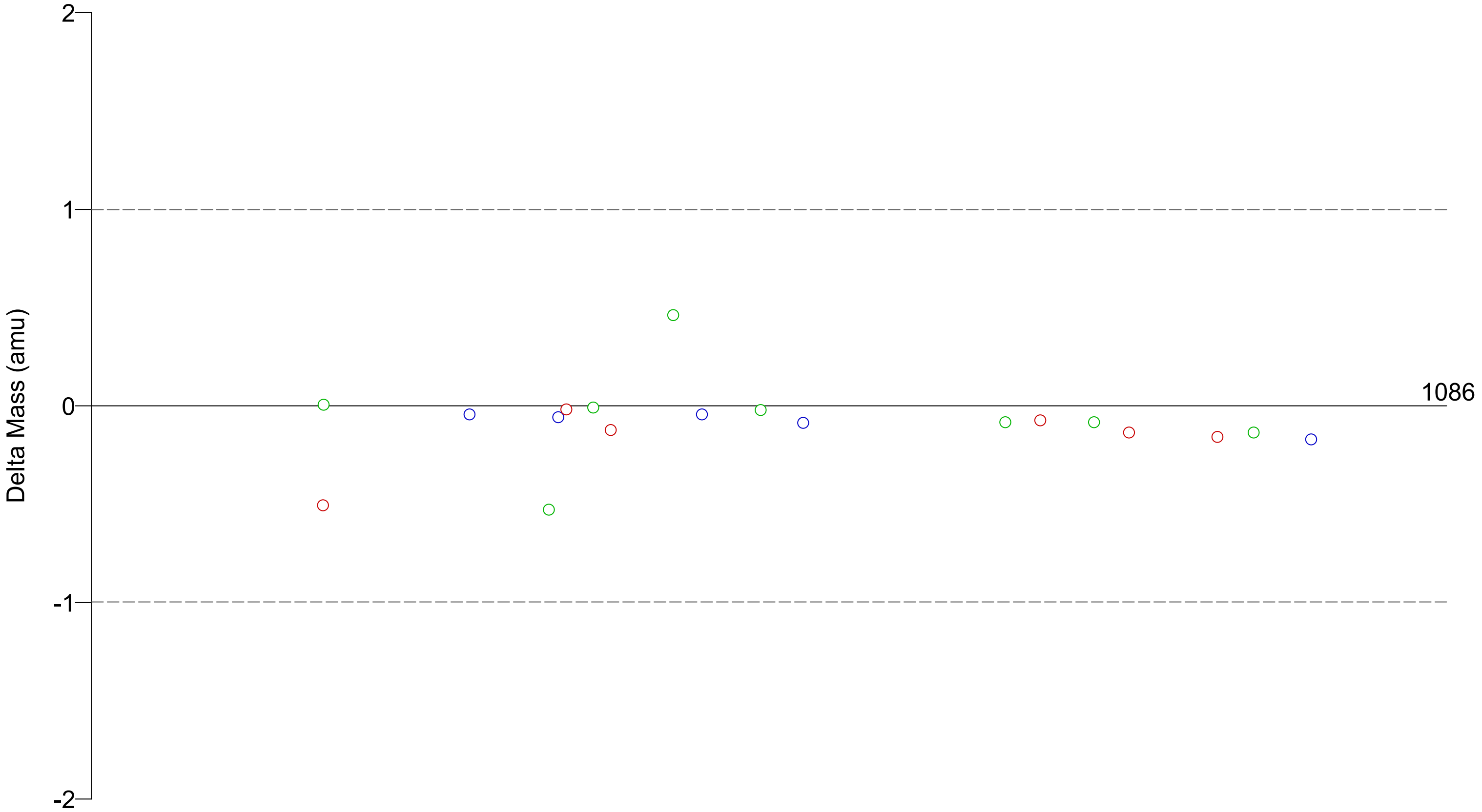
```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00555595.1|TREMBL:Q59GS1 Tax_Id=9606 Gene_Symbol=UCHL1          1        8.1      0.0        0
19287468 - 1  R.RGRPPVPAAGR.D                           1133.67   2  1        2.610  0.428   386.9  2   13/30

1 of 1 peptide matches reported, 0 removed due to filtering
```

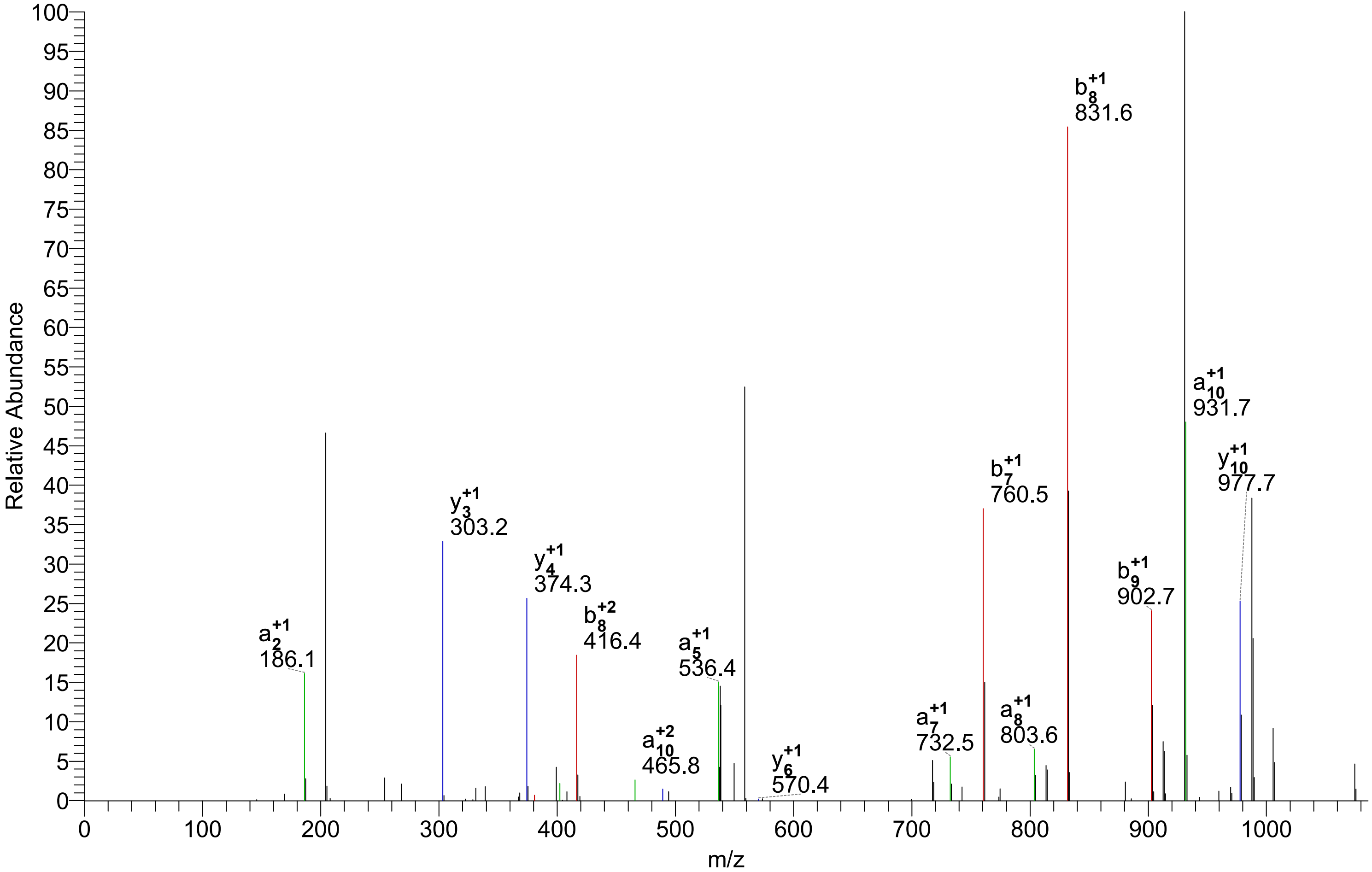
```
DTA for scans: 19287468-1
Precursor ion: 567.33
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 G    186.13     214.13                                      977.56
 R    342.24     370.23                                      920.54
 P    439.29     467.28                                      764.44
 P    536.34     564.34                                      667.39
 V    635.41     663.40                                      570.34
 P    732.46     760.46                                      471.27
 A    803.50     831.49                                      374.21
 A    874.54     902.53                                      303.18
 G    931.56     959.55                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 2.96E5



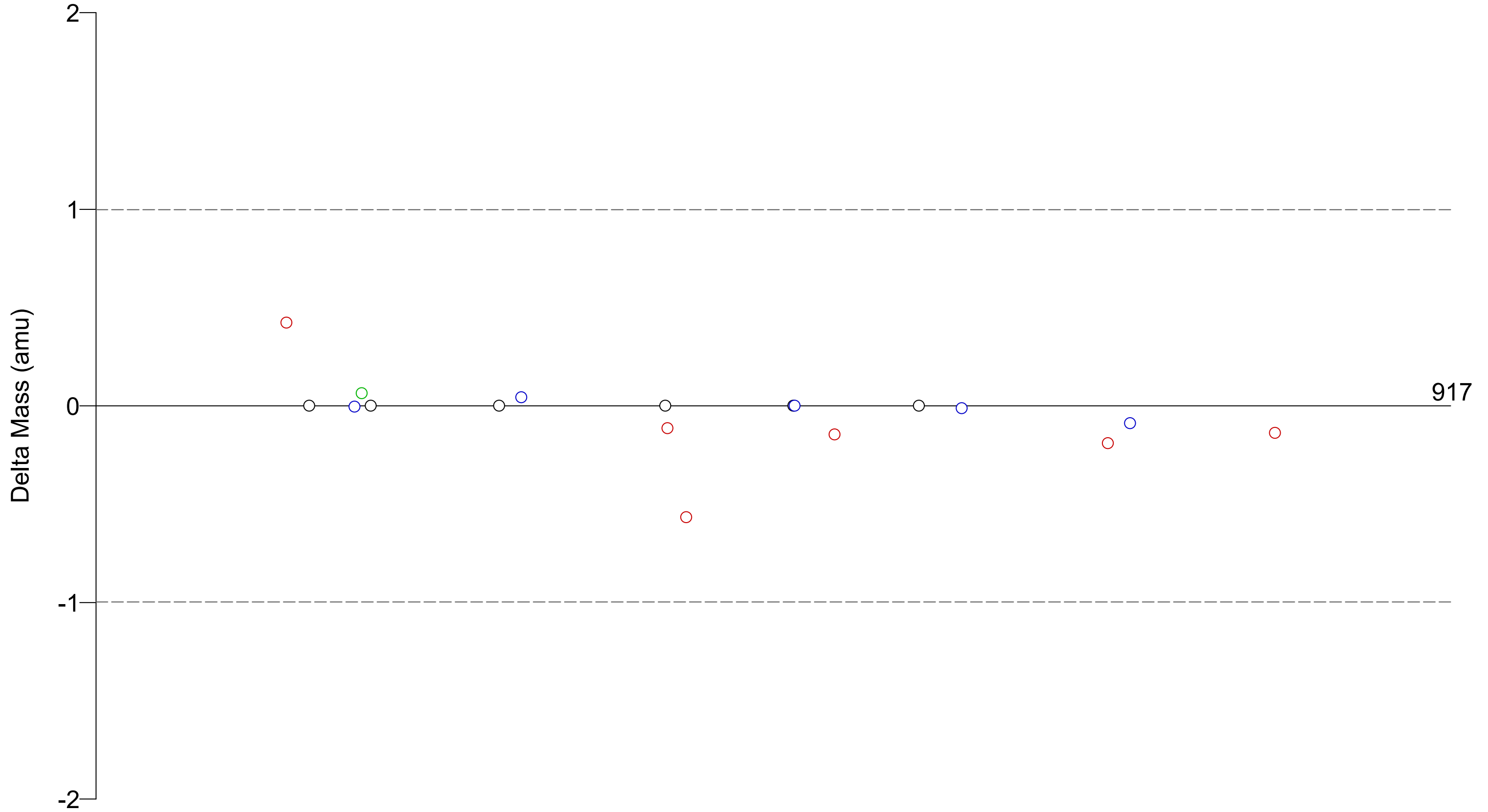
```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00937422.1|REFSEQ:XP_002346542 Tax_Id=9606 Gene_Symbol=    1       8.1      0.0       0
19287468 - 1  R.KGSNIGQLR.P                            972.56    2  0.4     2.427  0.100   721.2  2   13/24

1 of 1 peptide matches reported, 0 removed due to filtering
```

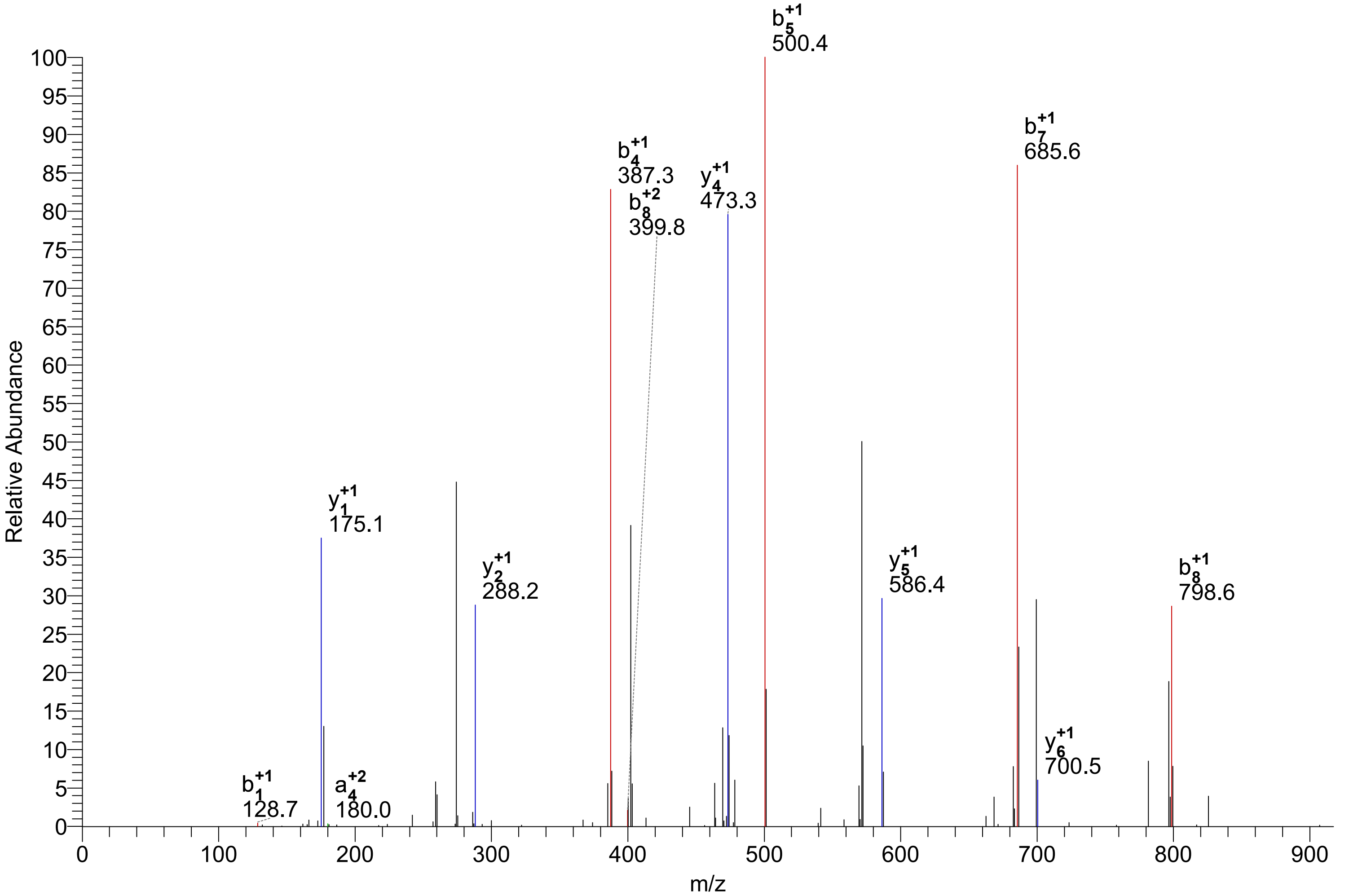
```
DTA for scans: 19287468-1
Precursor ion: 486.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 K    101.11     129.10
 G    158.13     186.12                                      844.46
 S    245.16     273.16                                      787.44
 N    359.20     387.20                                      700.41
 I    472.29     500.28                                      586.37
 G    529.31     557.30                                      473.28
 Q    657.37     685.36                                      416.26
 L    770.45     798.45                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.90E5



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

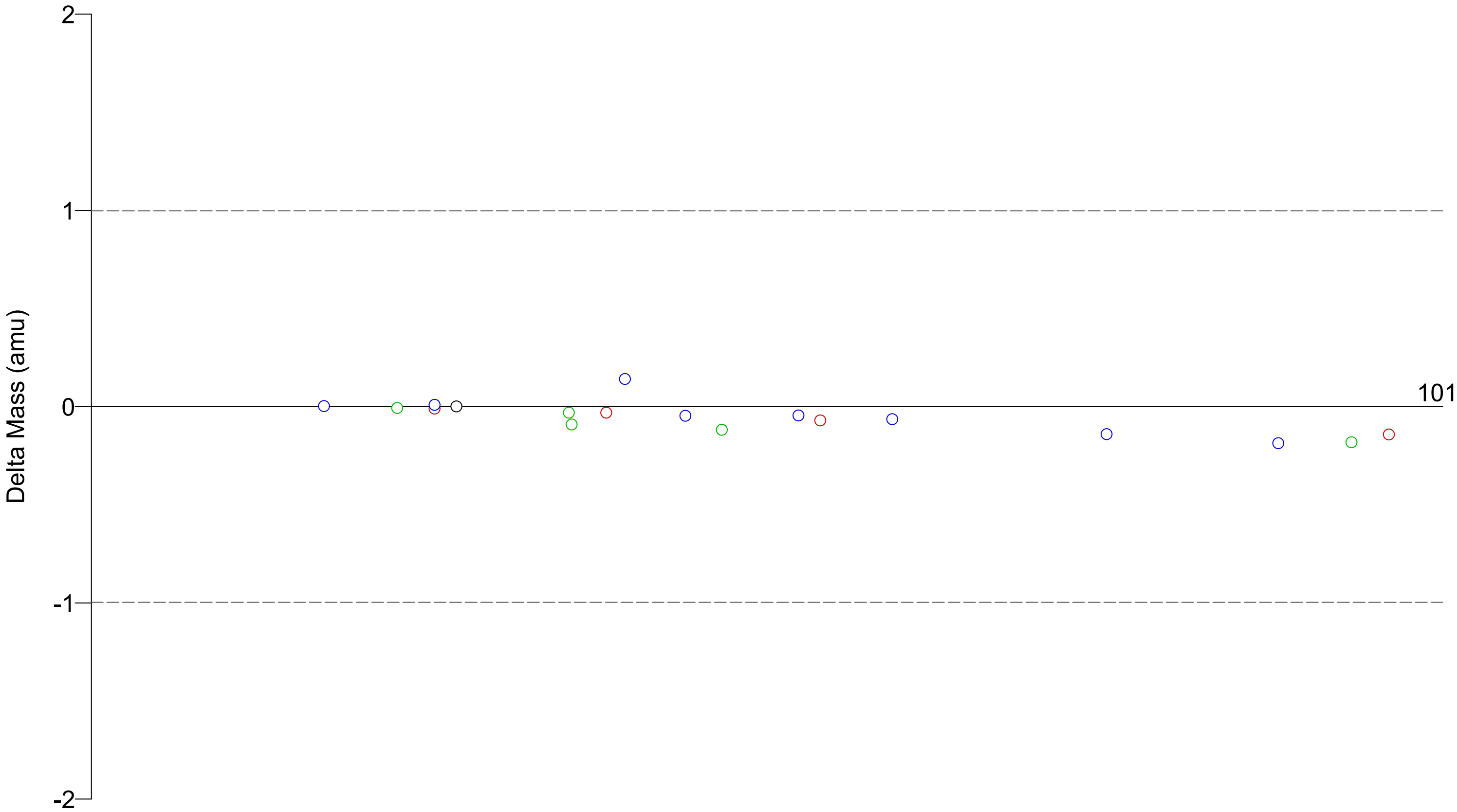
IPI:IPI00168913.1|SWISS-PROT:Q86UK5-2|TREMBL:Q4W5A4;Q4W5B1|ENS     1       8.1      0.0       0
19287468 - 1  R.SAVECSNLLR.T                              1149.56   2  0.4     2.306  0.370   355.1  4   12/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

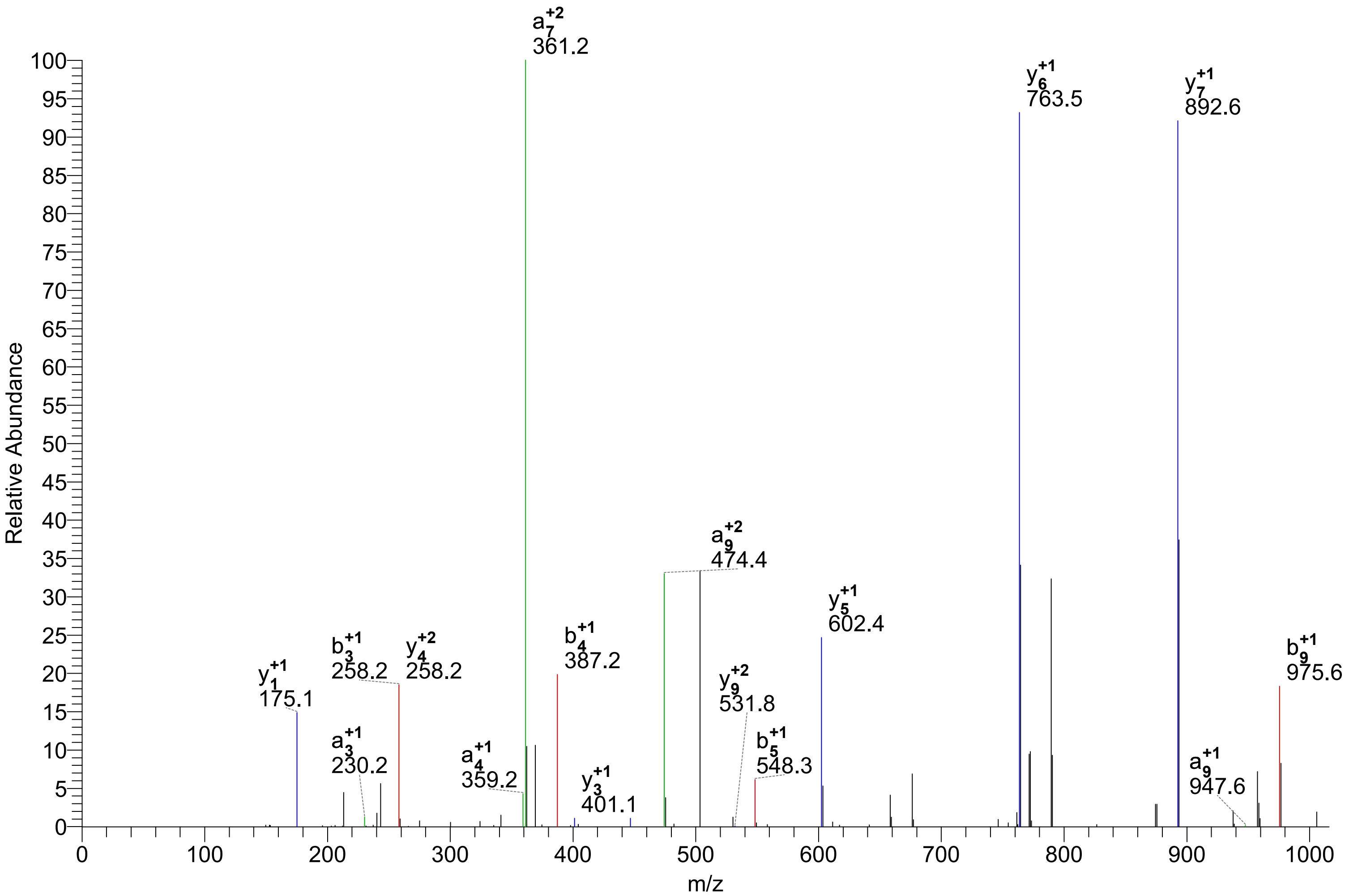
```
DTA for scans: 19287468-1
Precursor ion: 575.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 A    131.08     159.08                                     1062.52
 V    230.15     258.14                                      991.49
 E    359.19     387.19                                      892.42
 C    520.21     548.20                                      763.38
 S    607.24     635.23                                      602.36
 N    721.28     749.28                                      515.33
 L    834.37     862.36                                      401.29
 L    947.45     975.45                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.42E5



```
Reference                                                          P     Score   Coverage   Accession
Scan(s)       Sequence                                  MH+       z    P       XC  DeltaCn    Sp   RSp  Ions  Count

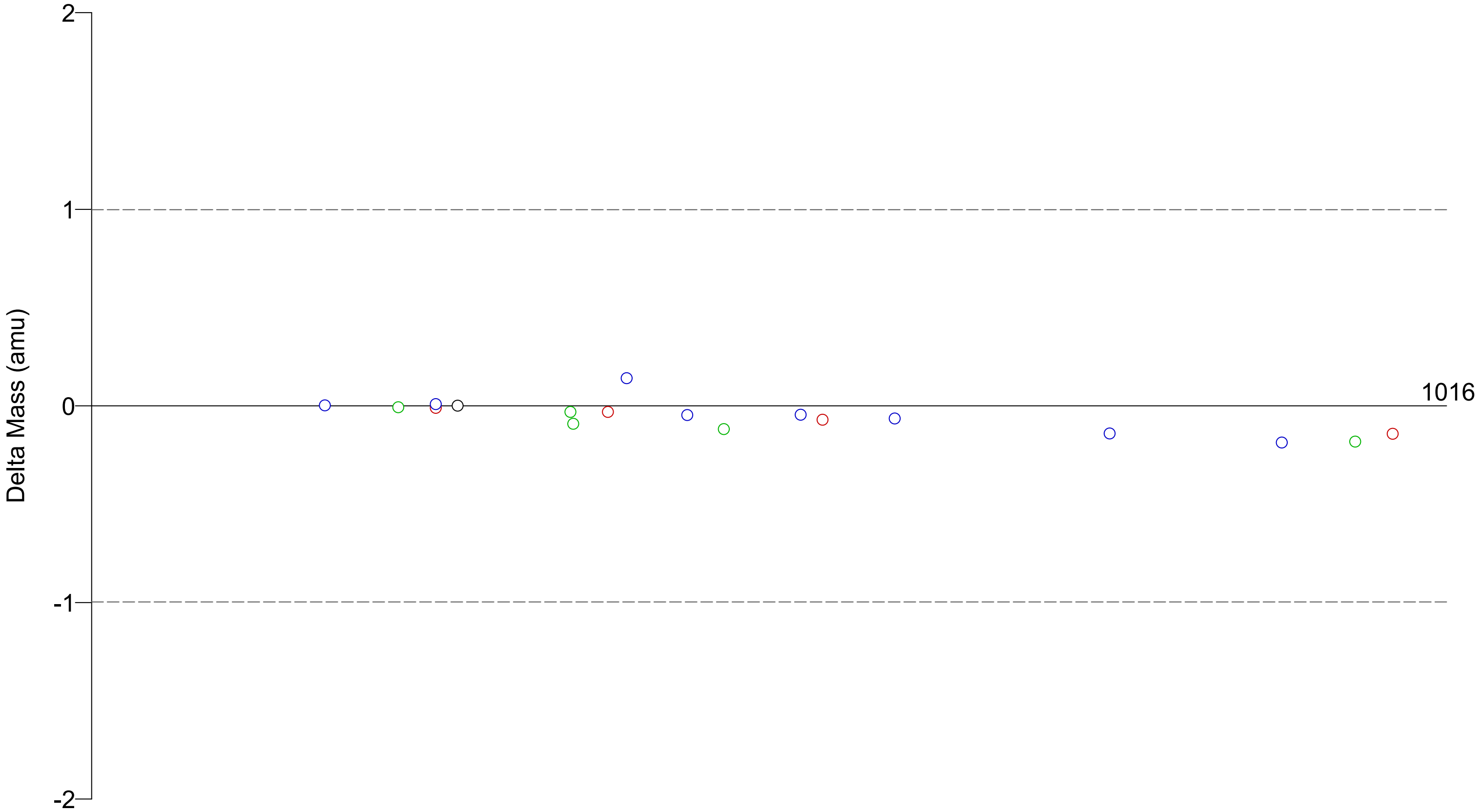
IPI:IPI00382523.1|SWISS-PROT:Q86UK                                   1       8.1      0.0       0
19287468 - 1  R.SAVECSNLLR.T                          1149.56    2  0.4      2.306  0.370   355.1  4   12/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

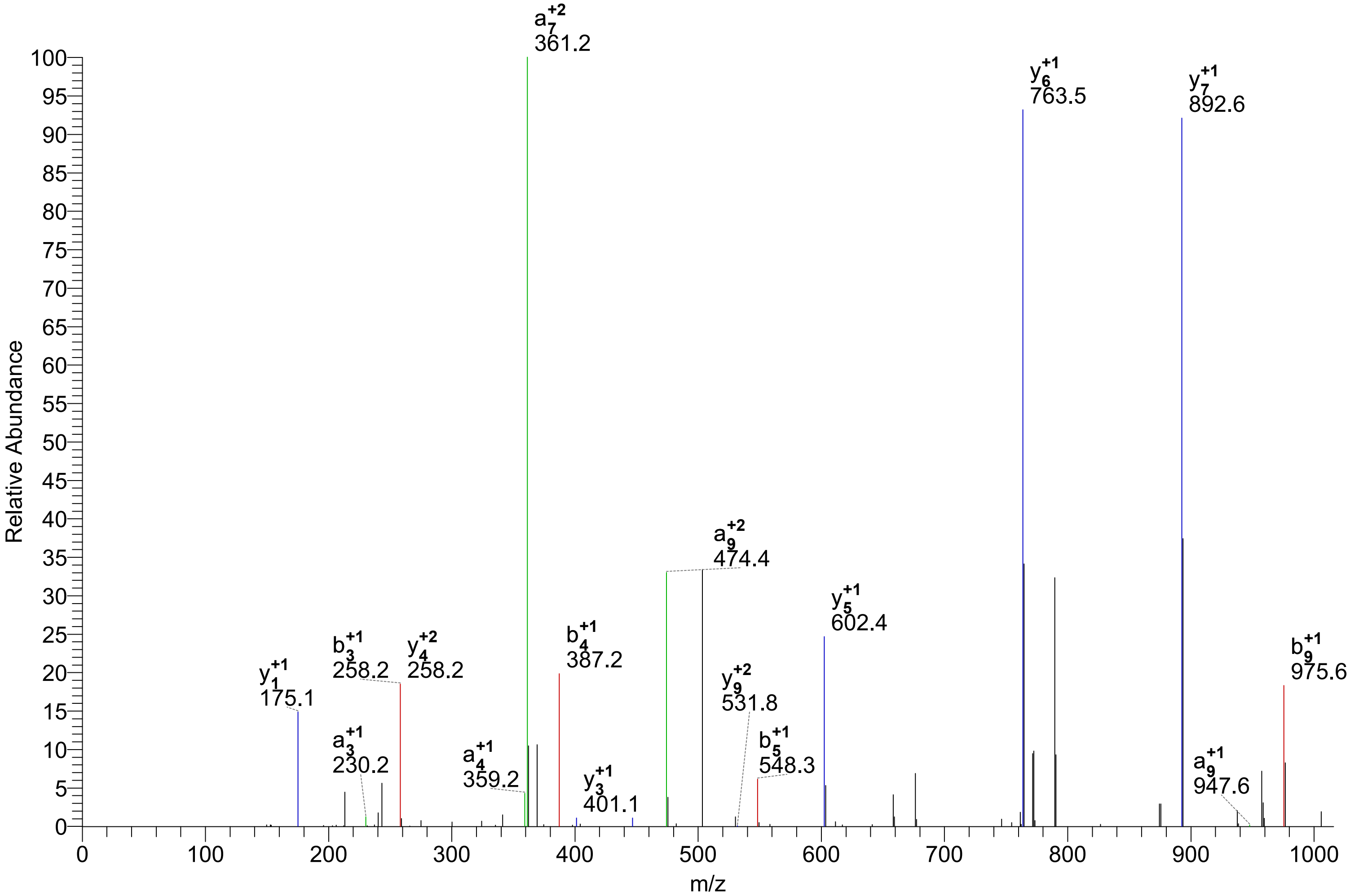
```
DTA for scans: 19287468-1
Precursor ion: 575.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 S     60.04      88.04
 A    131.08     159.08                                      1062.52
 V    230.15     258.14                                       991.49
 E    359.19     387.19                                       892.42
 C    520.21     548.20                                       763.38
 S    607.24     635.23                                       602.36
 N    721.28     749.28                                       515.33
 L    834.37     862.36                                       401.29
 L    947.45     975.45                                       288.20
 R                                                            175.12
```



#19287468-1 NL: 1.42E5



```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

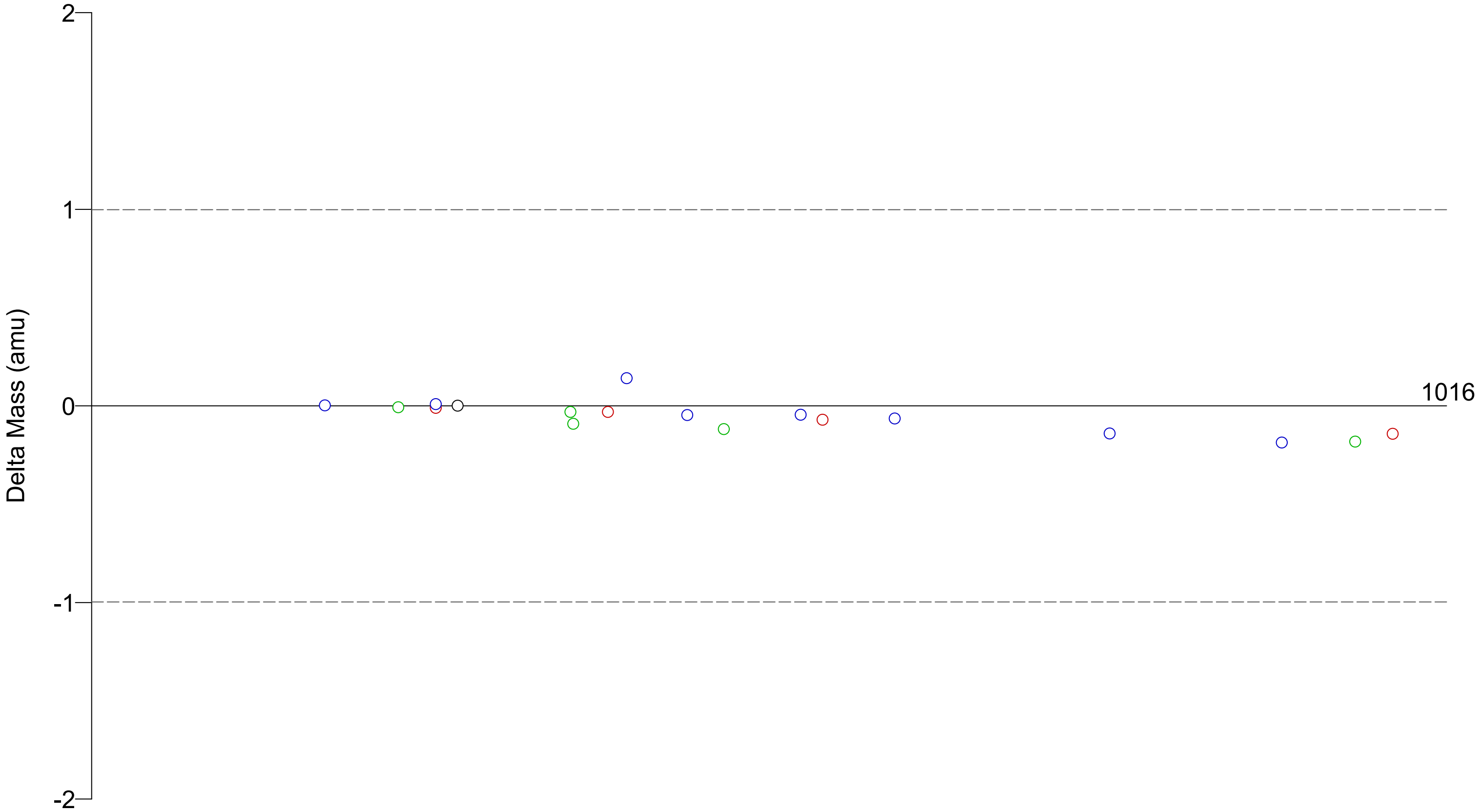
IPI:IPI00382525.1|SWISS-PROT:Q86UK                                   1       8.1      0.0       0
19287468 - 1  R.SAVECSNLLR.T                            1149.56   2  0.4      2.306  0.370   355.1  4   12/27   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

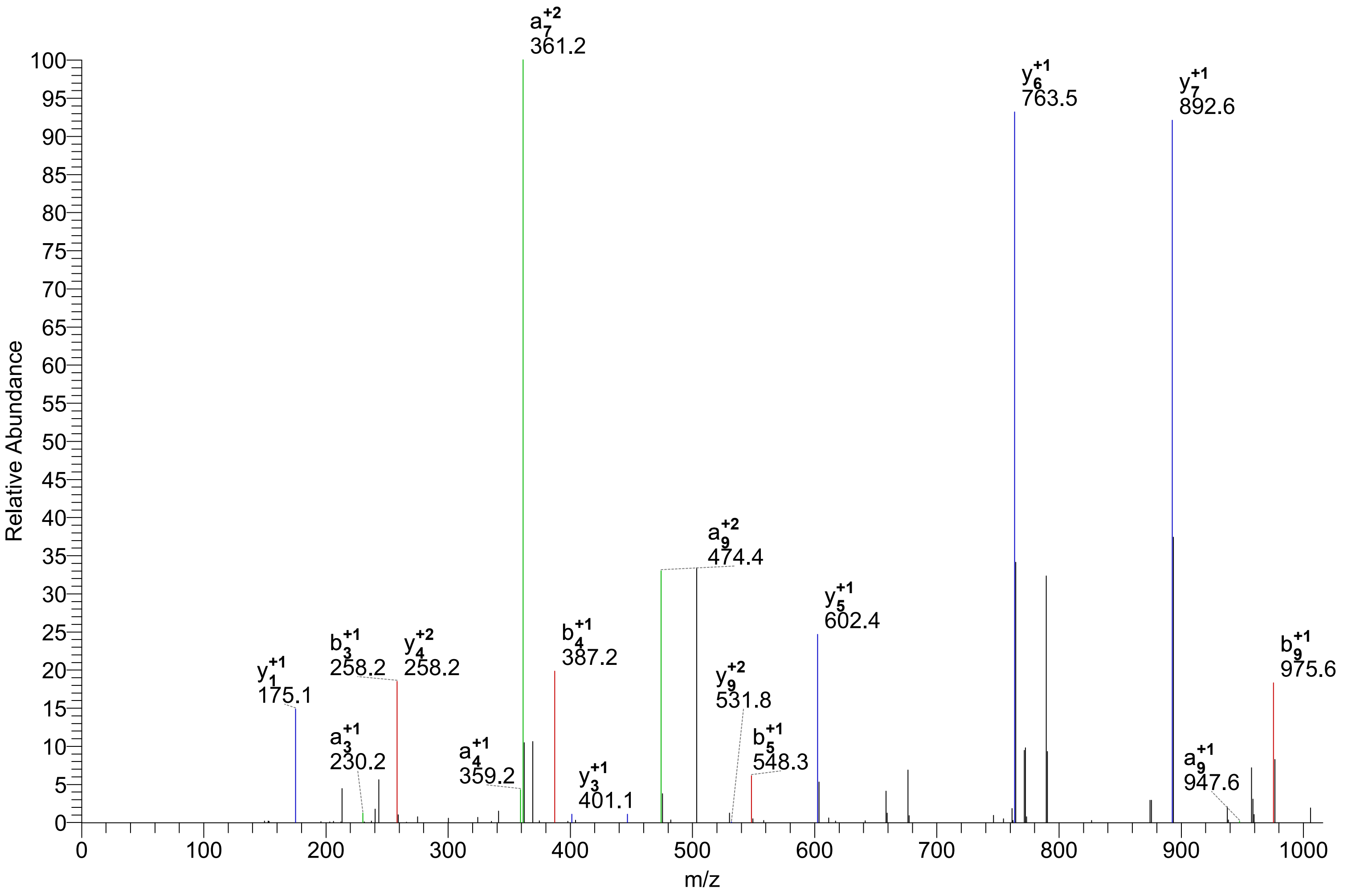
```
DTA for scans: 19287468-1
Precursor ion: 575.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 A    131.08     159.08                                     1062.52
 V    230.15     258.14                                      991.49
 E    359.19     387.19                                      892.42
 C    520.21     548.20                                      763.38
 S    607.24     635.23                                      602.36
 N    721.28     749.28                                      515.33
 L    834.37     862.36                                      401.29
 L    947.45     975.45                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 1.42E5



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z    P        XC  DeltaCn   Sp    RSp  Ions  Count

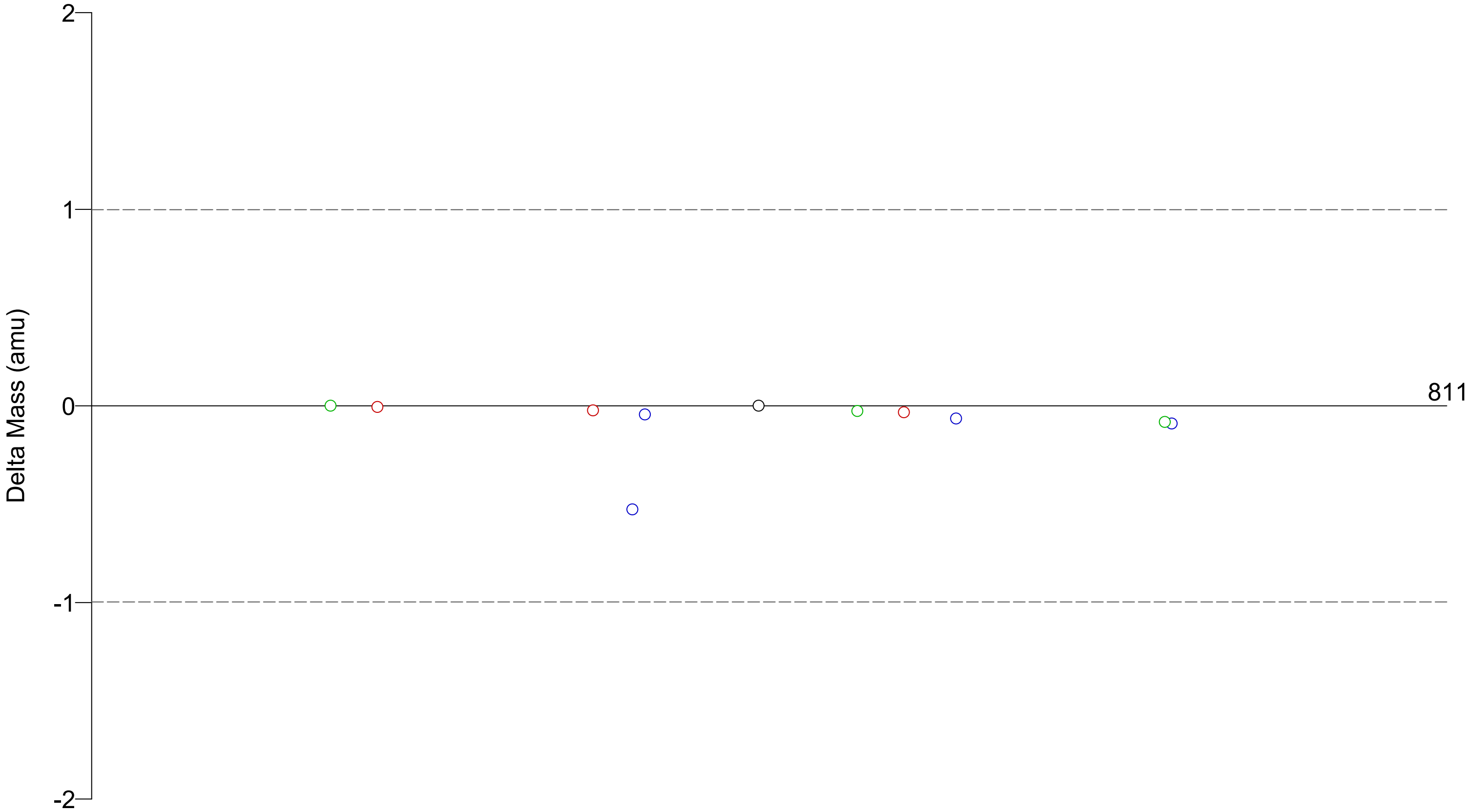
IPI:IPI00375358.2|SWISS-PROT:P35251-1|TREMBL:A8K6E7|ENSEMBL:EN     1        8.1      0.0       0
19287468 - 1  K.IGEVSSPK.A                                 816.45    2  0.6      2.245  0.317   420.5  3   11/21   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

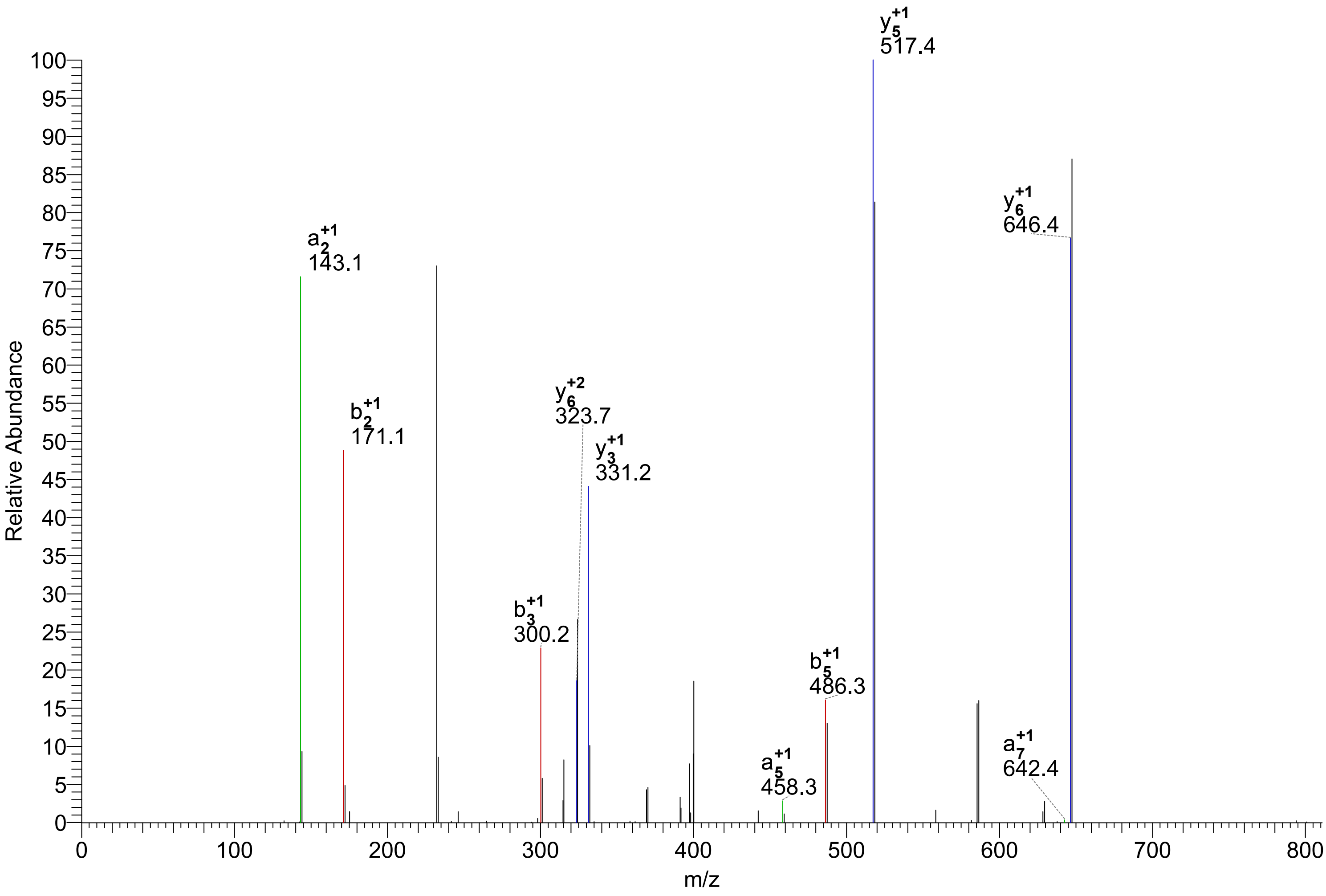
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 G    143.12     171.11                                       703.36
 E    272.16     300.16                                       646.34
 V    371.23     399.22                                       517.30
 S    458.26     486.26                                       418.23
 S    545.29     573.29                                       331.20
 P    642.35     670.34                                       244.17
 K                                                            147.11
```



#19287468-1 NL: 1.30E5



```
Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count

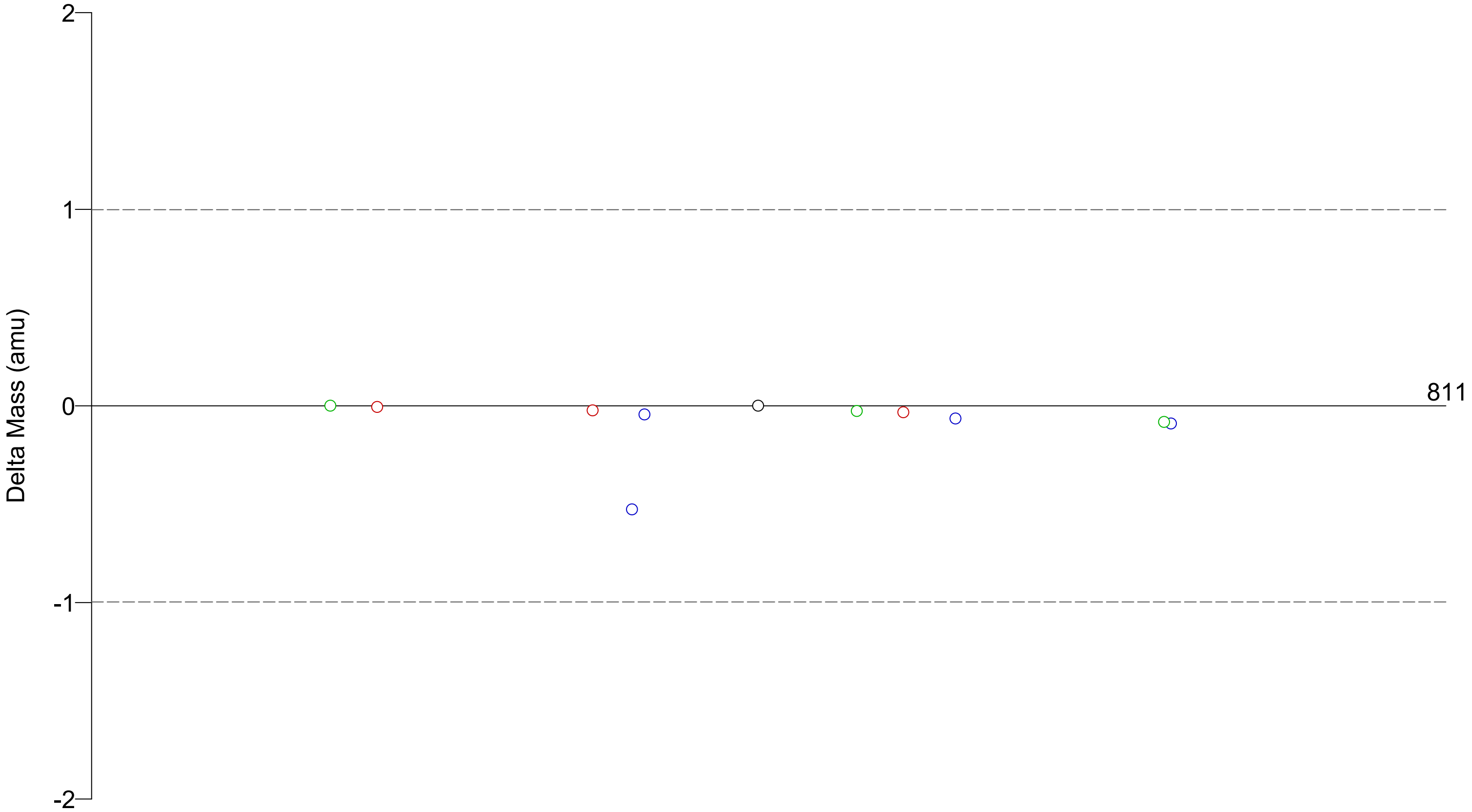
IPI:IPI00375359.2|SWISS-PROT:P3525                                     1       8.1      0.0       0
19287468 - 1  K.IGEVSSPK.A                              816.45    2  0.6      2.245  0.317   420.5  3   11/21   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

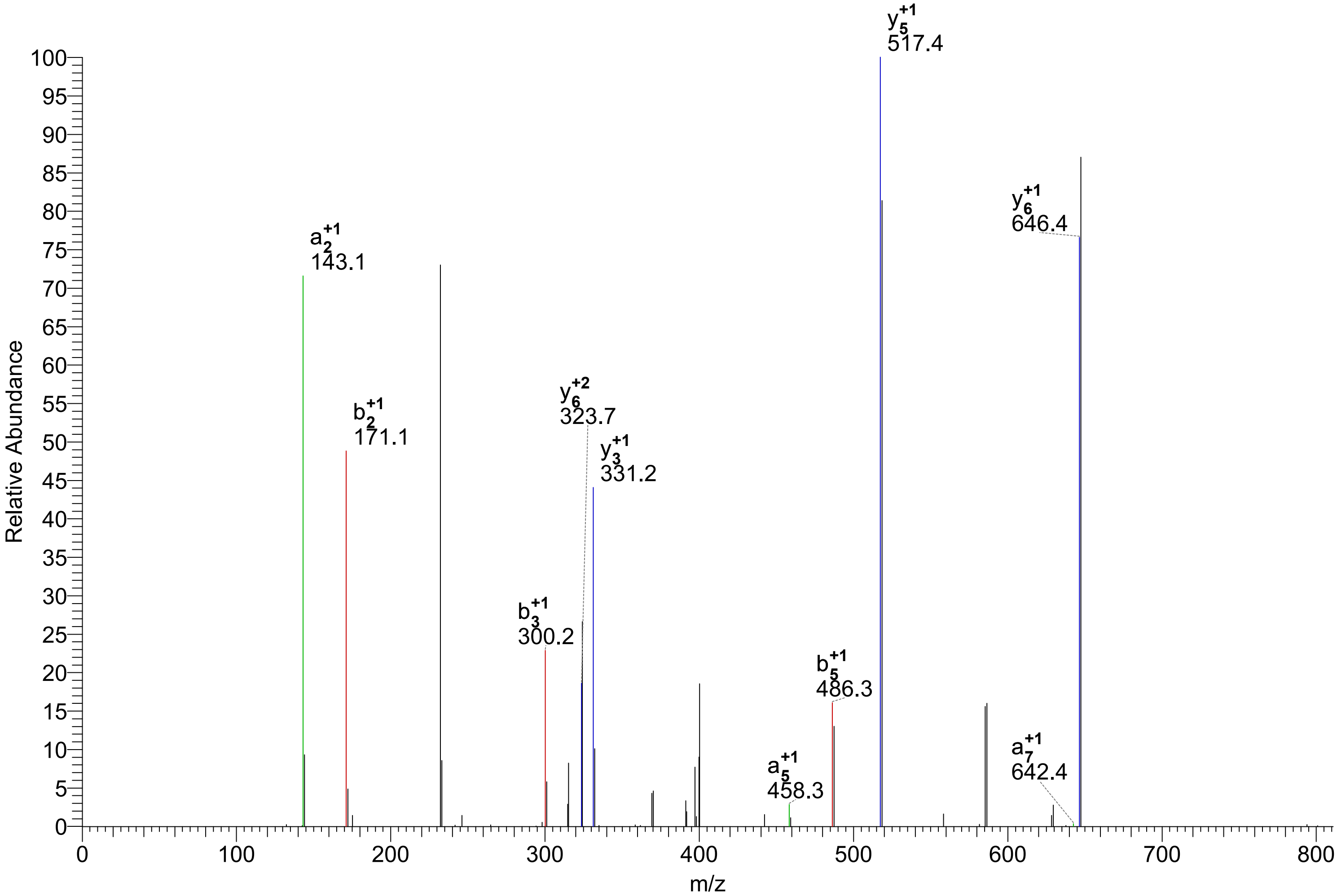
```
DTA for scans: 19287468-1
Precursor ion: 408.72
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 I     86.10     114.09
 G    143.12    171.11                                      703.36
 E    272.16    300.16                                      646.34
 V    371.23    399.22                                      517.30
 S    458.26    486.26                                      418.23
 S    545.29    573.29                                      331.20
 P    642.35    670.34                                      244.17
 K                                                          147.11
```



#19287468-1 NL: 1.30E5



```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

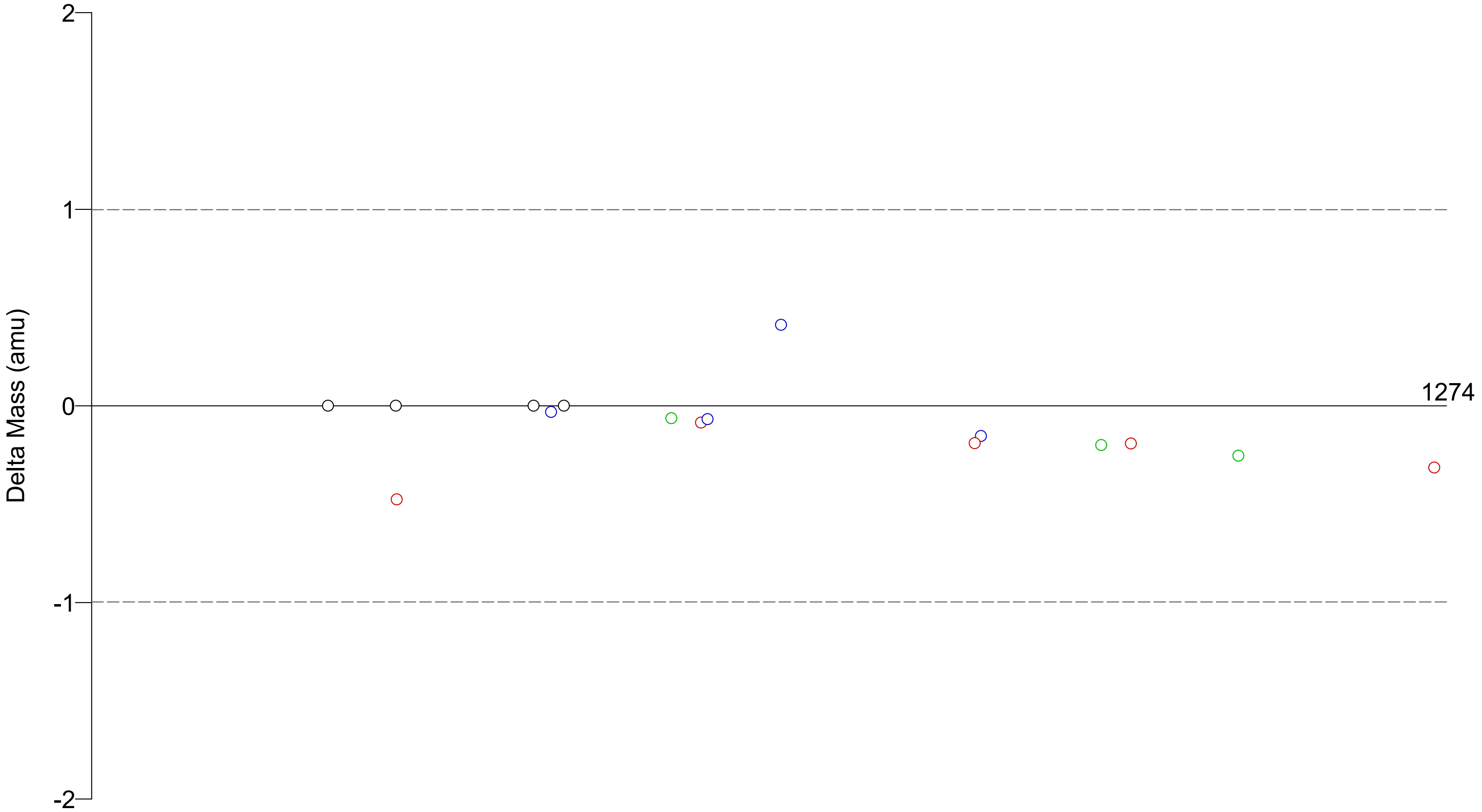
IPI:IPI00065348.2|TREMBL:B1AL16;Q05BG6;Q96LW0|ENSEMBL:ENSP0000    1       8.1      0.0        0
19287468 - 1  R.LSITGTEQFERK.L                        1408.74   2  0.7      2.224  0.498   271.7  3   11/33   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

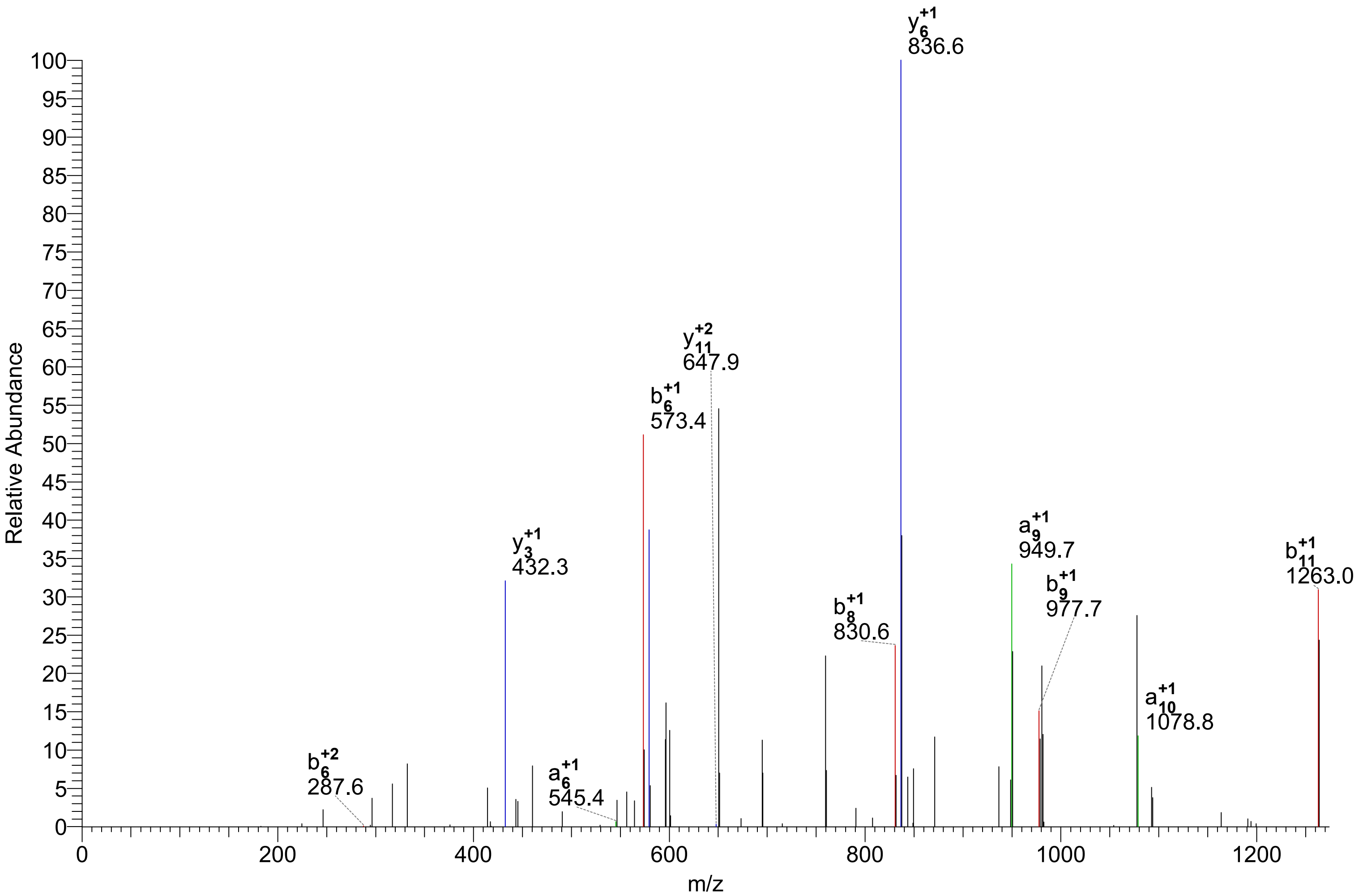
```
DTA for scans: 19287468-1
Precursor ion: 704.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                     1295.66
 I    286.21     314.21                                     1208.63
 T    387.26     415.26                                     1095.54
 G    444.28     472.28                                      994.50
 T    545.33     573.32                                      937.47
 E    674.37     702.37                                      836.43
 Q    802.43     830.43                                      707.38
 F    949.50     977.49                                      579.32
 E   1078.54    1106.54                                      432.26
 R   1234.64    1262.64                                      303.21
 K                                                           147.11
```



#19287468-1 NL: 6.35E4



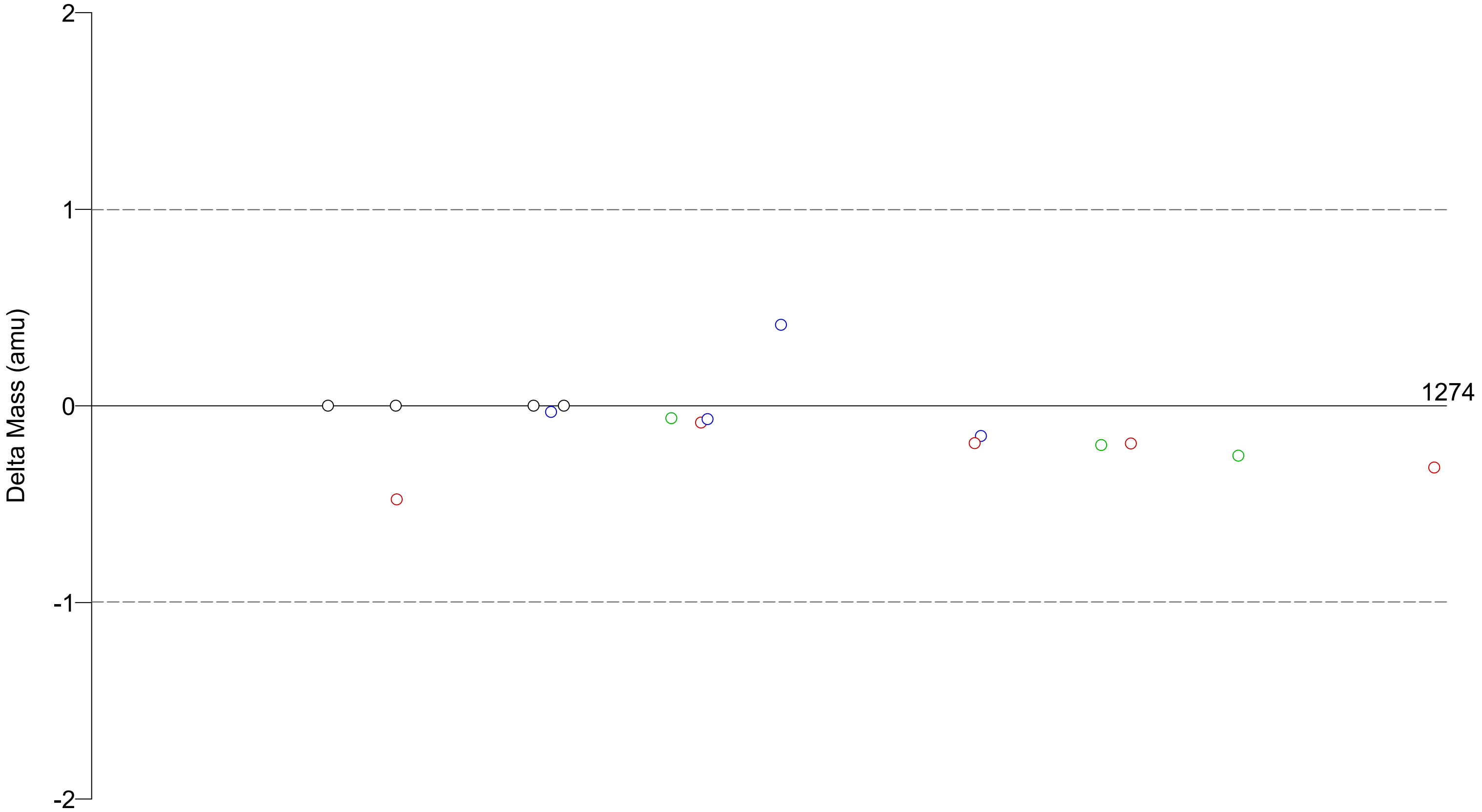
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                purfMH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00293188.5|SWISS-PROT:Q8IX2                                1       8.1      0.0       0
19287468 - 1  R.LSITGTEQFERK.L                       1408.74   2  0.7     2.224  0.498   271.7  3   11/33   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

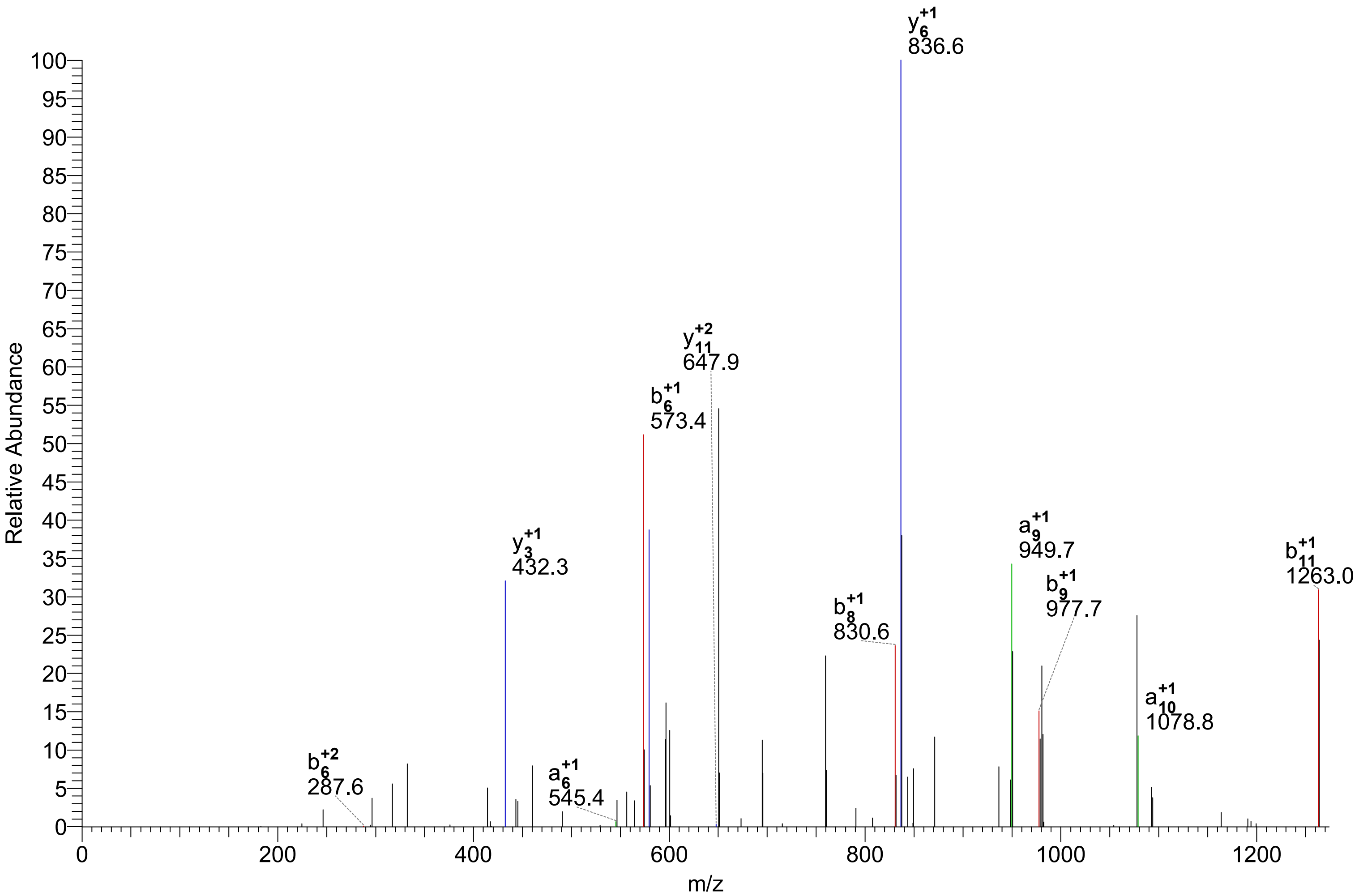
```
DTA for scans: 19287468-1
Precursor ion: 704.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions      B ions      B* ions     Bo ions      C ions     Y ions     Y* ions     Yo ions     Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                     1295.66
 I    286.21     314.21                                     1208.63
 T    387.26     415.26                                     1095.54
 G    444.28     472.28                                      994.50
 T    545.33     573.32                                      937.47
 E    674.37     702.37                                      836.43
 Q    802.43     830.43                                      707.38
 F    949.50     977.49                                      579.32
 E   1078.54    1106.54                                      432.26
 R   1234.64    1262.64                                      303.21
 K                                                           147.11
```



#19287468-1 NL: 6.35E4



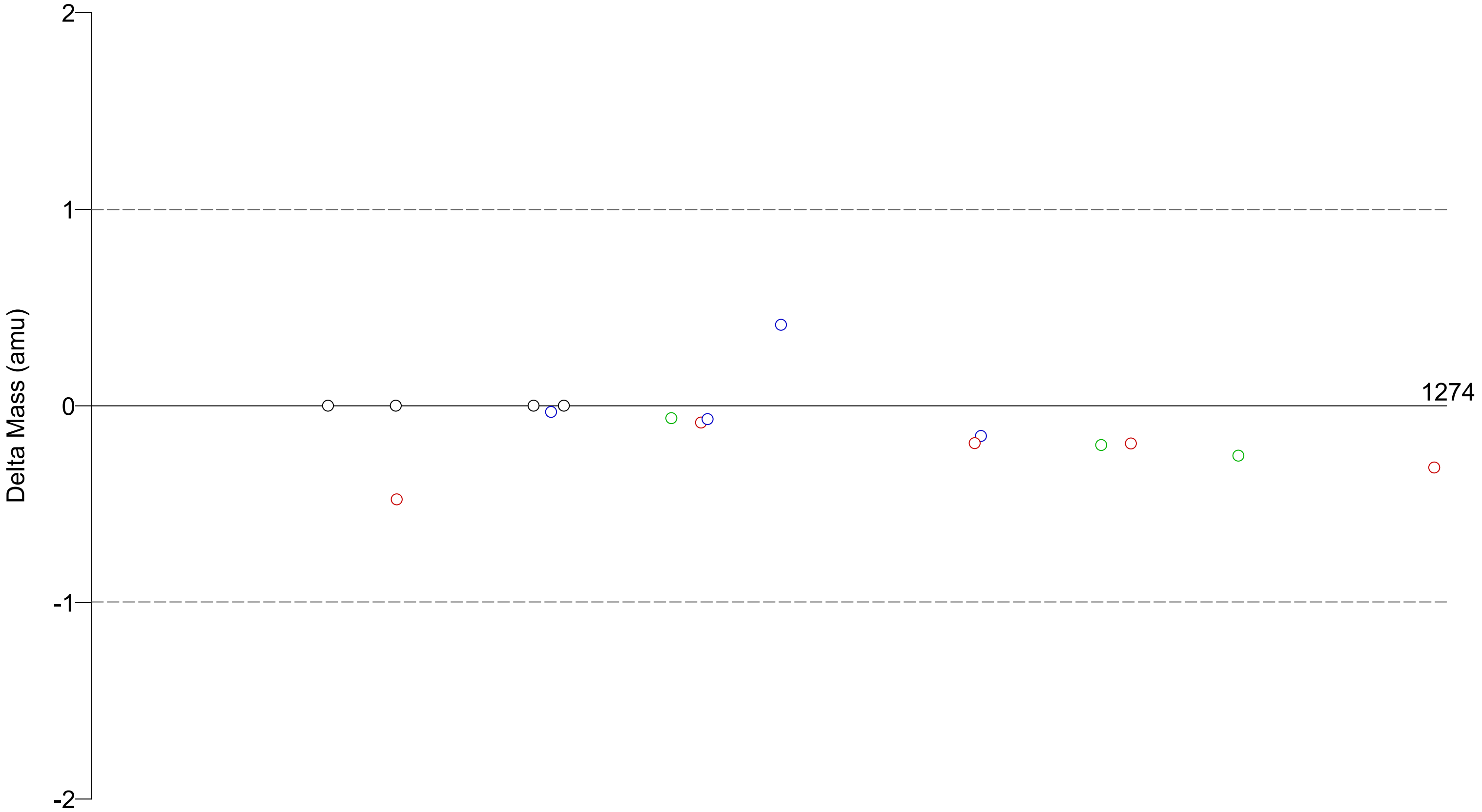
```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+     z    P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00640126.1|TREMBL:B1AL17|EN                                1       8.1      0.0        0
19287468 - 1  R.LSITGTEQFERK.L                         1408.74   2  0.7      2.224  0.498   271.7  3   11/33   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

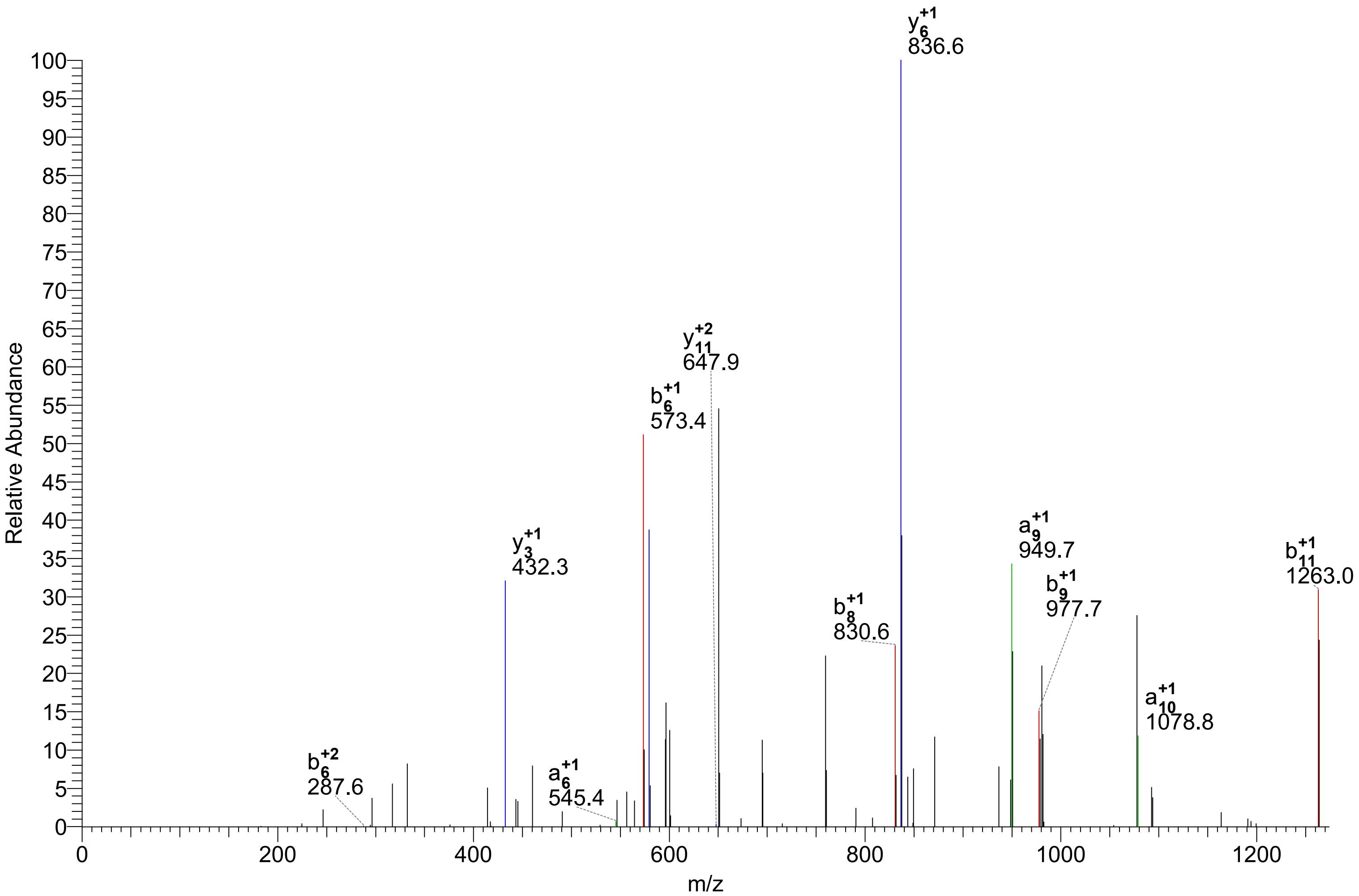
```
DTA for scans: 19287468-1
Precursor ion: 704.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                     1295.66
 I    286.21     314.21                                     1208.63
 T    387.26     415.26                                     1095.54
 G    444.28     472.28                                      994.50
 T    545.33     573.32                                      937.47
 E    674.37     702.37                                      836.43
 Q    802.43     830.43                                      707.38
 F    949.50     977.49                                      579.32
 E   1078.54    1106.54                                      432.26
 R   1234.64    1262.64                                      303.21
 K                                                           147.11
```



#19287468-1 NL: 6.35E4



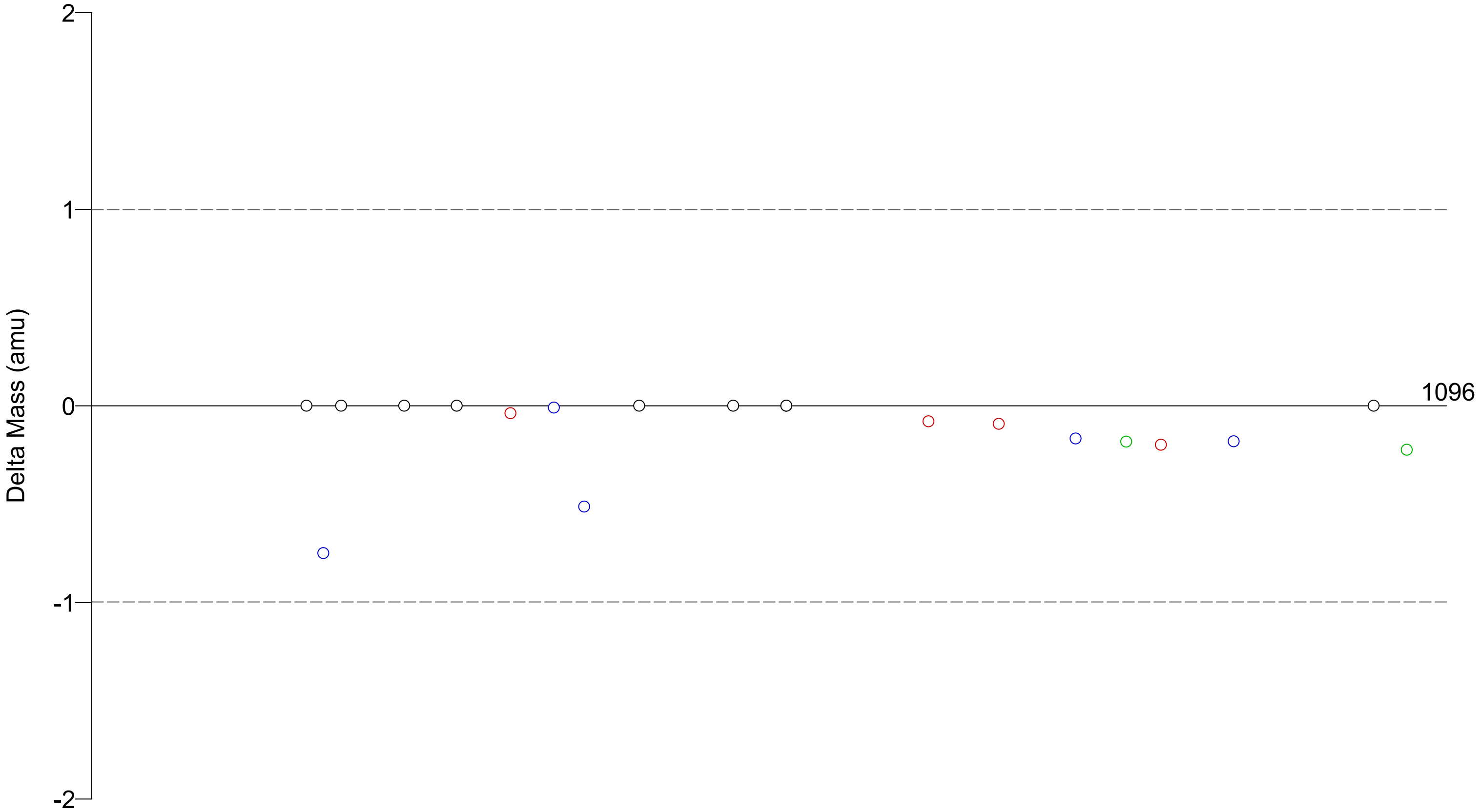
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00217895.4|SWISS-PROT:Q6S5L8-1|TREMBL:B3KWT2|ENSEMBL:EN     1       8.1      0.0       0
2118291816 -  K.SNLQFSGMNIK.L                            1238.62   2  0.8      2.210  0.498   104.6  16  8/30

1 of 1 peptide matches reported, 0 removed due to filtering
```

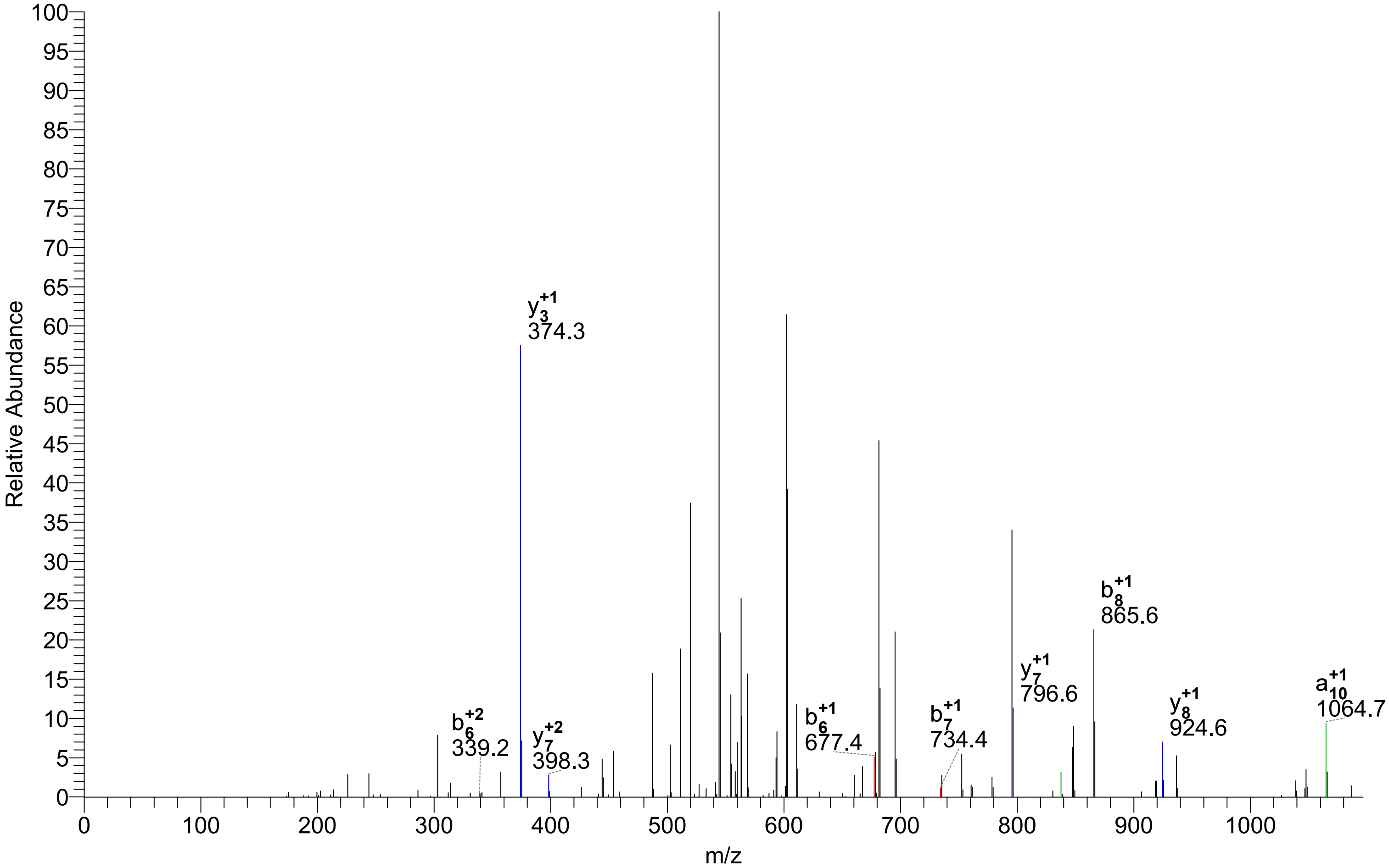
```
DTA for scans: 2118291816-26226248
Precursor ion: 619.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 S     60.04      88.04
 N    174.09     202.08                                     1151.59
 L    287.17     315.17                                     1037.54
 Q    415.23     443.22                                      924.46
 F    562.30     590.29                                      796.40
 S    649.33     677.33                                      649.33
 G    706.35     734.35                                      562.30
 M    837.39     865.39                                      505.28
 N    951.44     979.43                                      374.24
 I   1064.52    1092.51                                      260.20
 K                                                           147.11
```



#2118291816-26226248 NL: 2.79E5



```
Reference                                                                   P      Score   Coverage   Accession
Scan(s)       Sequence                                        MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count

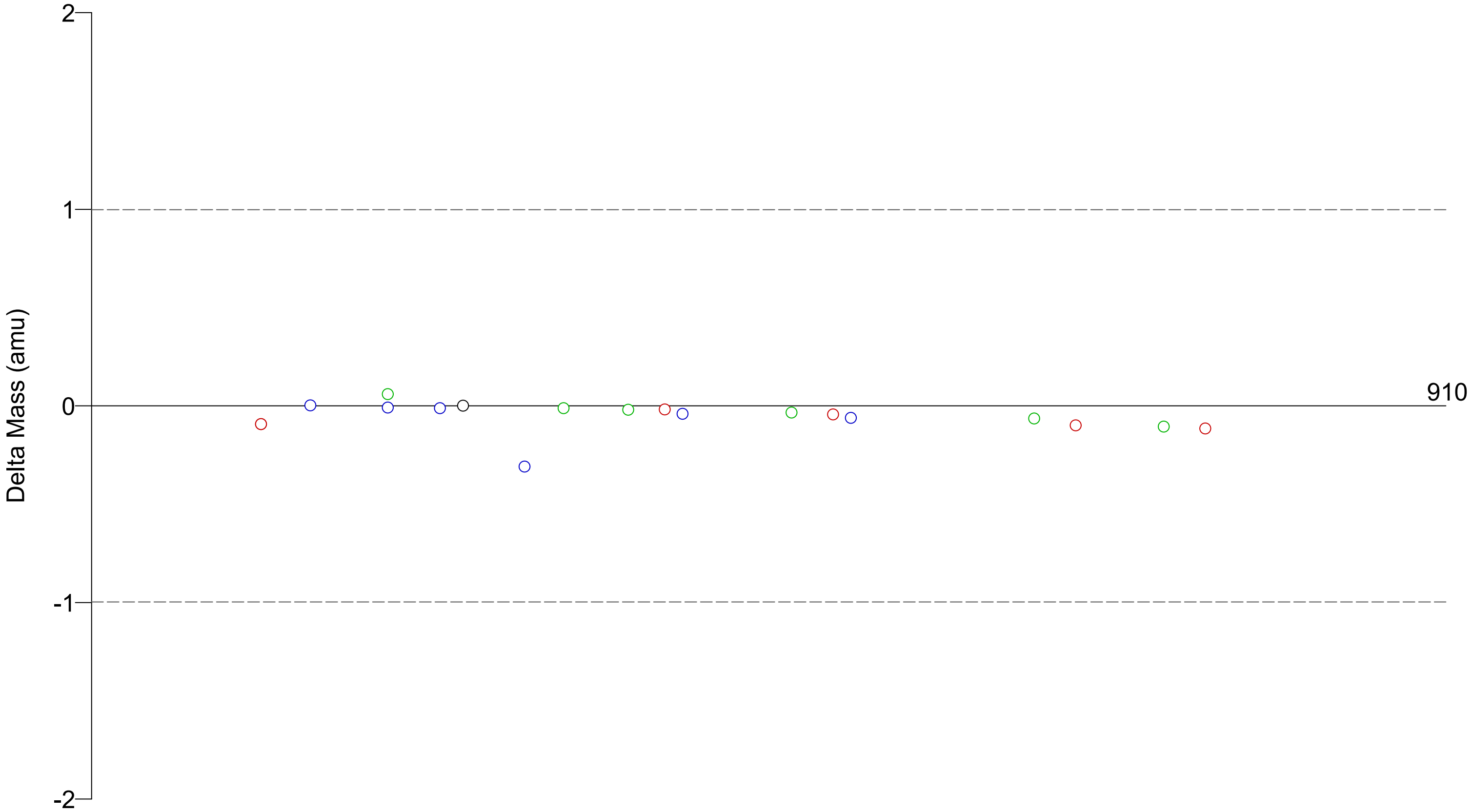
IPI:IPI00043430.5|SWISS-PROT:Q8IUR5-2|TREMBL:B3KVW1|ENSEMBL:EN      1        8.1      0.0       0
19287468 - 1  R.LLSAIYSK.Q                                   894.53    2  0.8      2.159  0.253   634.7  2   13/21   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

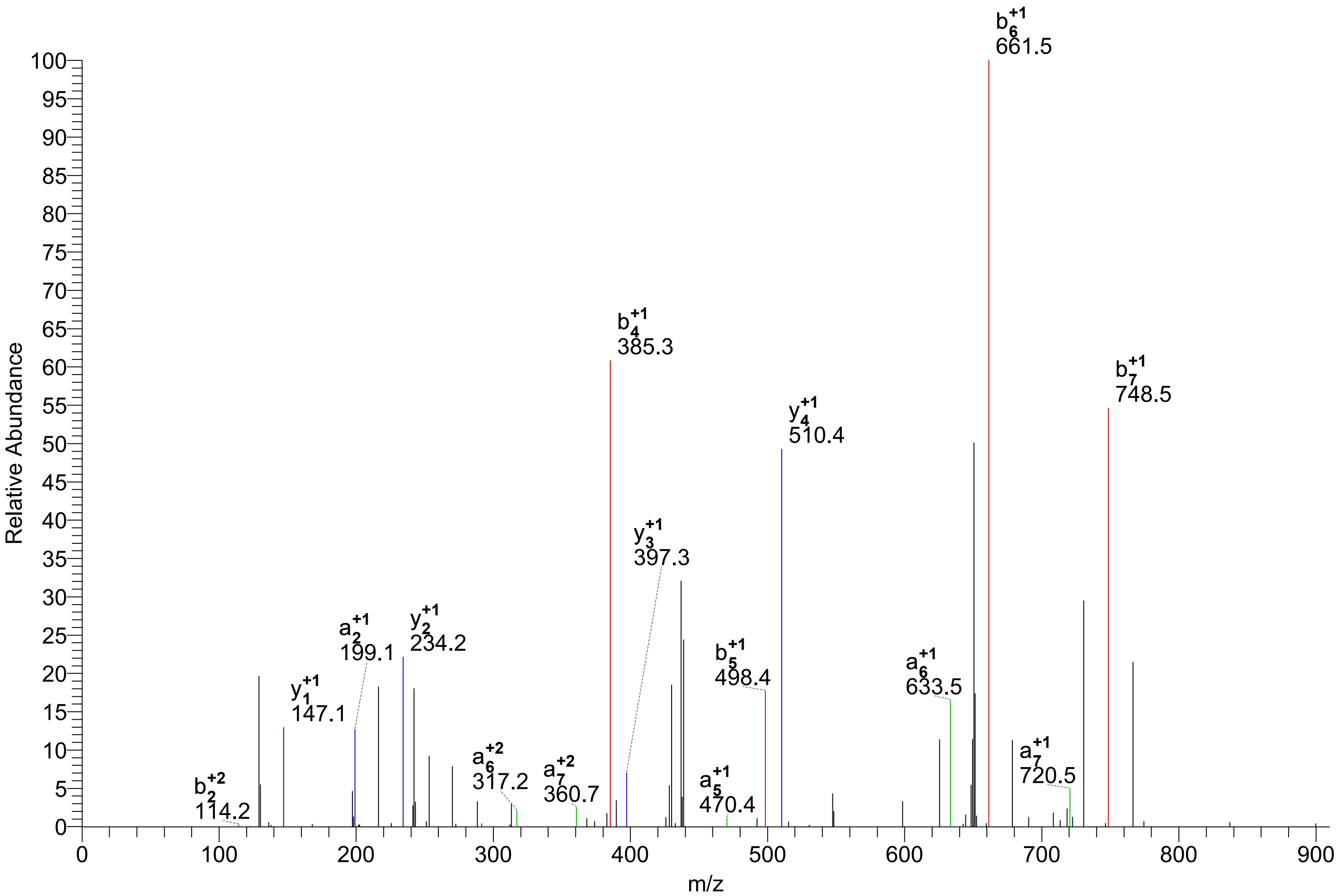
```
DTA for scans: 19287468-1
Precursor ion: 447.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                      781.45
 S    286.21     314.21                                      668.36
 A    357.25     385.24                                      581.33
 I    470.33     498.33                                      510.29
 Y    633.40     661.39                                      397.21
 S    720.43     748.42                                      234.14
 K                                                           147.11
```



#19287468-1 NL: 1.39E5



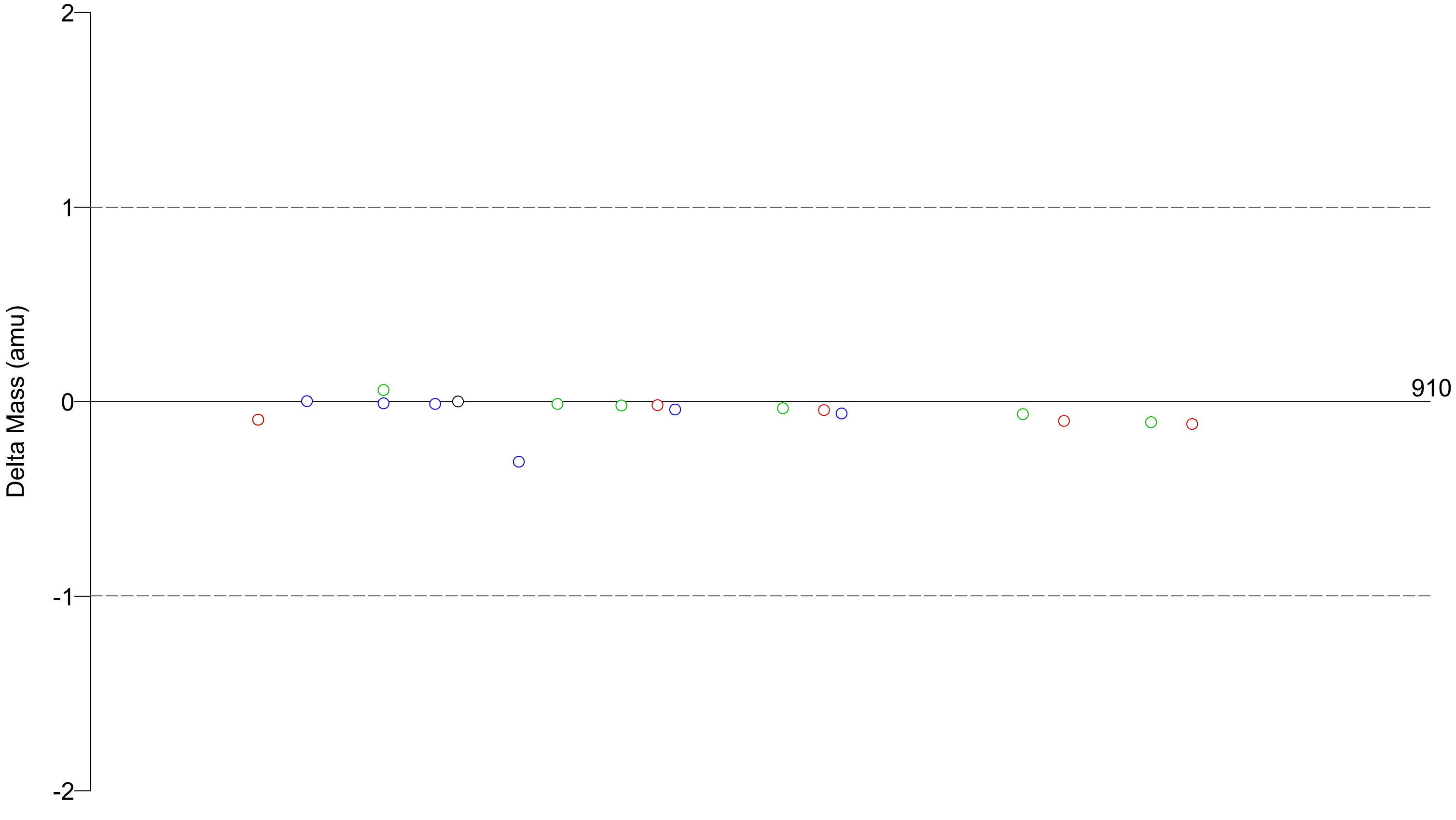
```
Reference                                                         P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z     P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00216822.3|SWISS-PROT:Q8IUR                                  1       8.1      0.0        0
19287468 - 1  R.LLSAIYSK.Q                             894.53     2  0.8      2.159  0.253   634.7  2   13/21   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

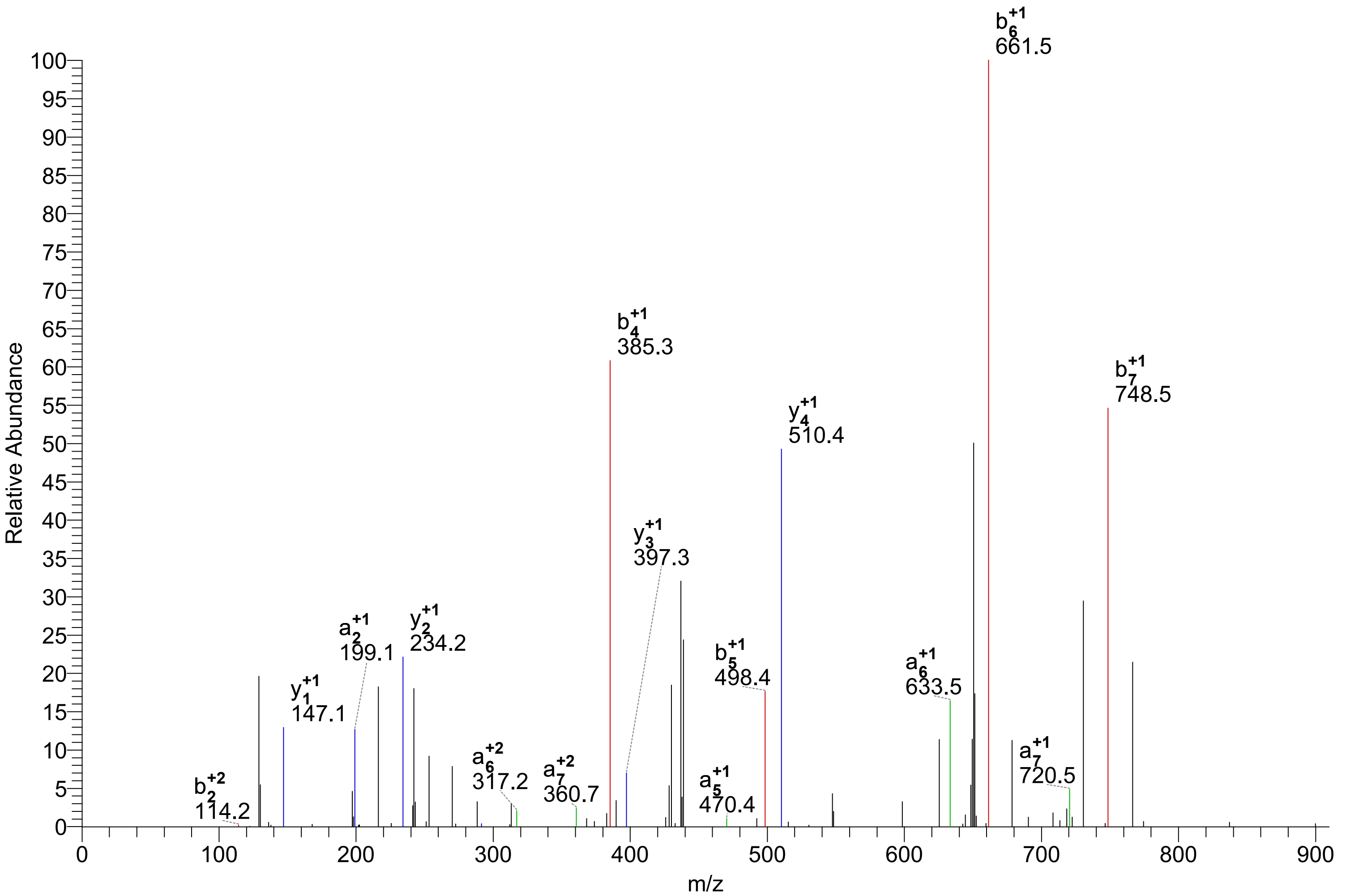
```
DTA for scans: 19287468-1
Precursor ion: 447.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                      781.45
 S    286.21     314.21                                      668.36
 A    357.25     385.24                                      581.33
 I    470.33     498.33                                      510.29
 Y    633.40     661.39                                      397.21
 S    720.43     748.42                                      234.14
 K                                                           147.11
```



#19287468-1 NL: 1.39E5



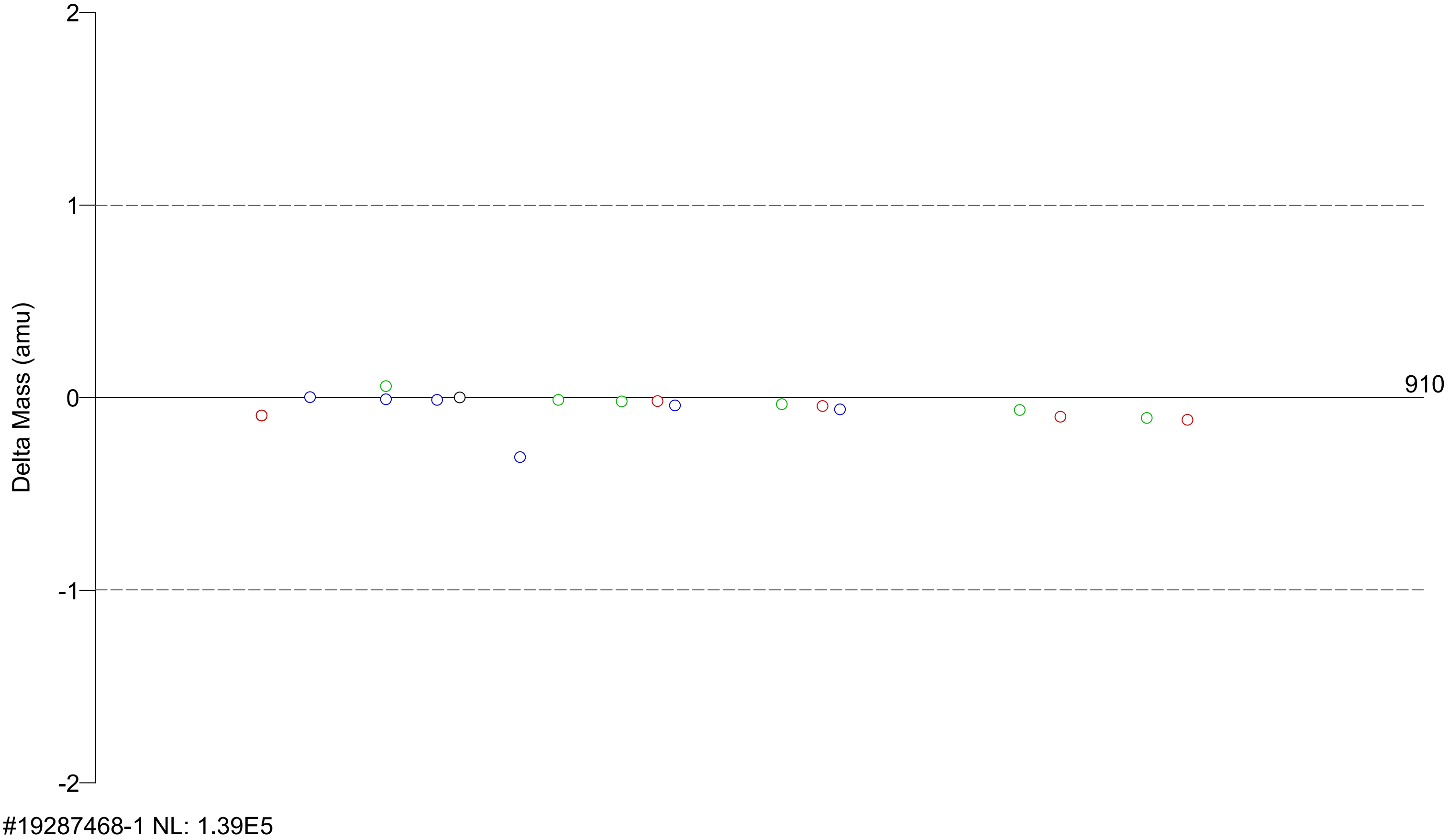
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00795924.2|SWISS-PROT:Q8IUR                                1       8.1      0.0       0
19287468 - 1  R.LLSAIYSK.Q                           894.53    2  0.8     2.159  0.253   634.7  2   13/21   2

1 of 1 peptide matches reported, 0 removed due to filtering
```

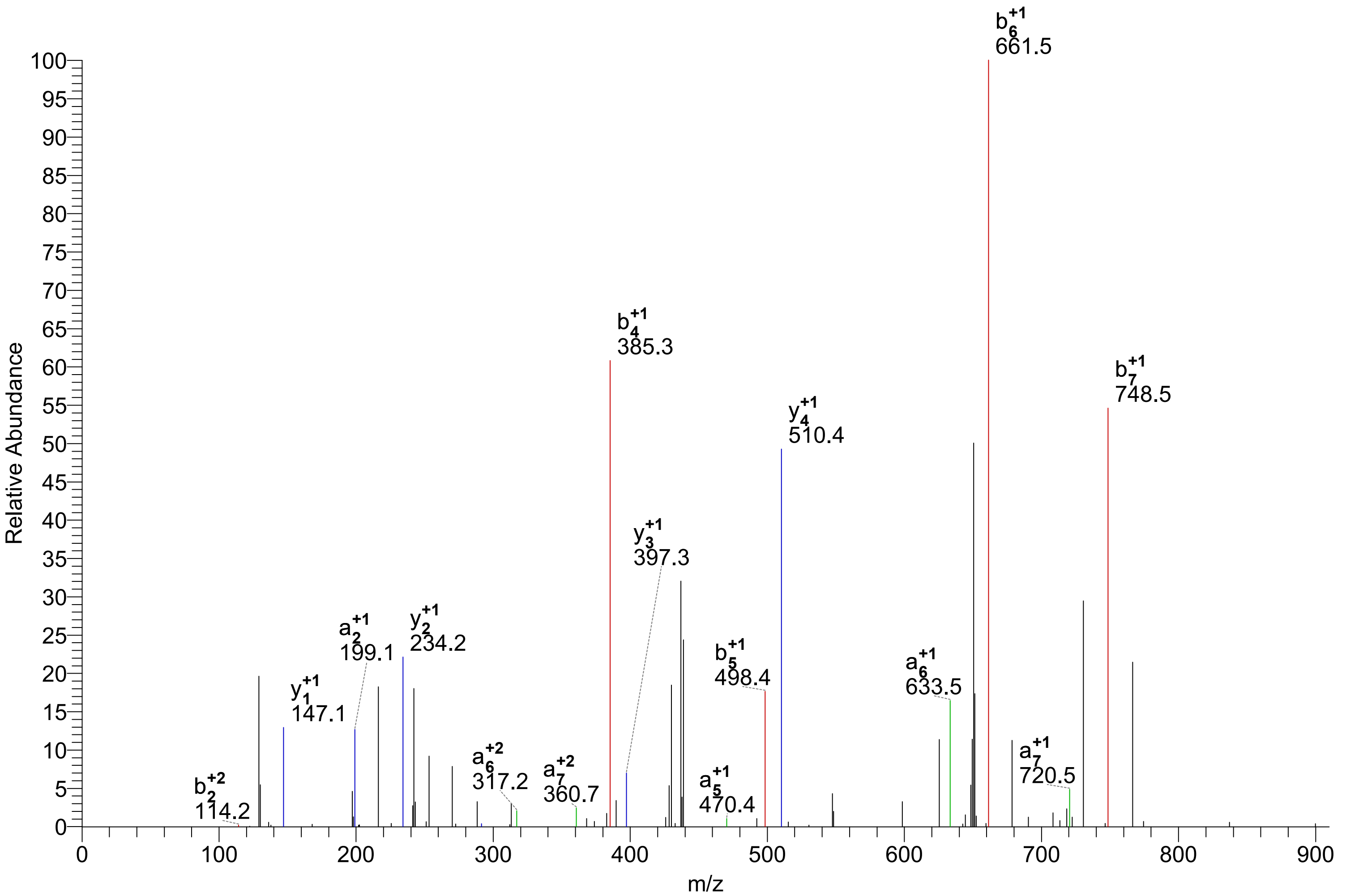
```
DTA for scans: 19287468-1
Precursor ion: 447.76
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                      781.45
 S    286.21     314.21                                      668.36
 A    357.25     385.24                                      581.33
 I    470.33     498.33                                      510.29
 Y    633.40     661.39                                      397.21
 S    720.43     748.42                                      234.14
 K                                                           147.11
```



#19287468-1 NL: 1.39E5



```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count

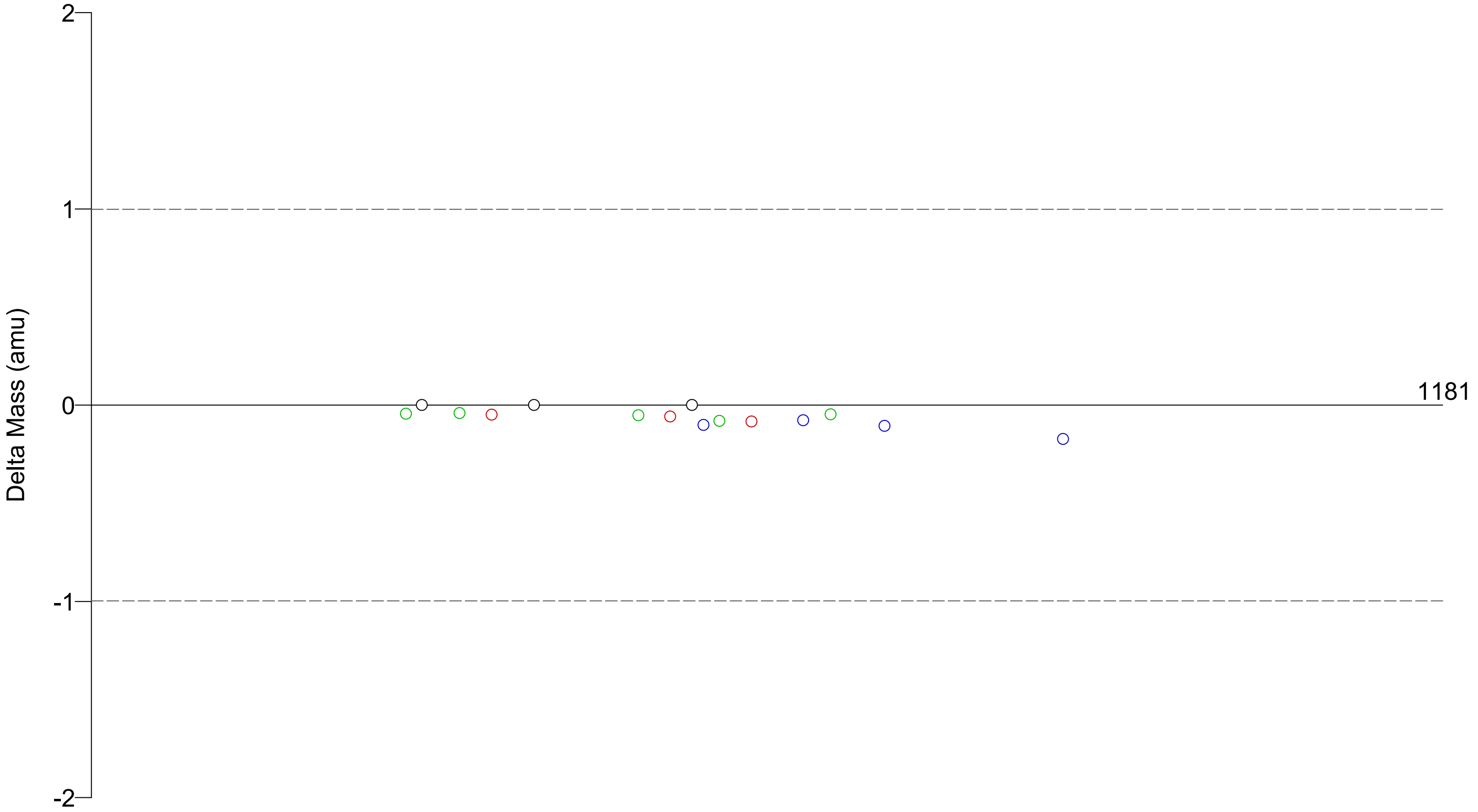
IPI:IPI00433499.6|SWISS-PROT:Q6PJF5-1|ENSEMBL:ENSP00000322775|   1       8.1      0.0       0
19287468 - 1  K.EYGRAPVPGPR.R                       1198.63   2  0.8      2.135  0.461   245.0  3   11/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

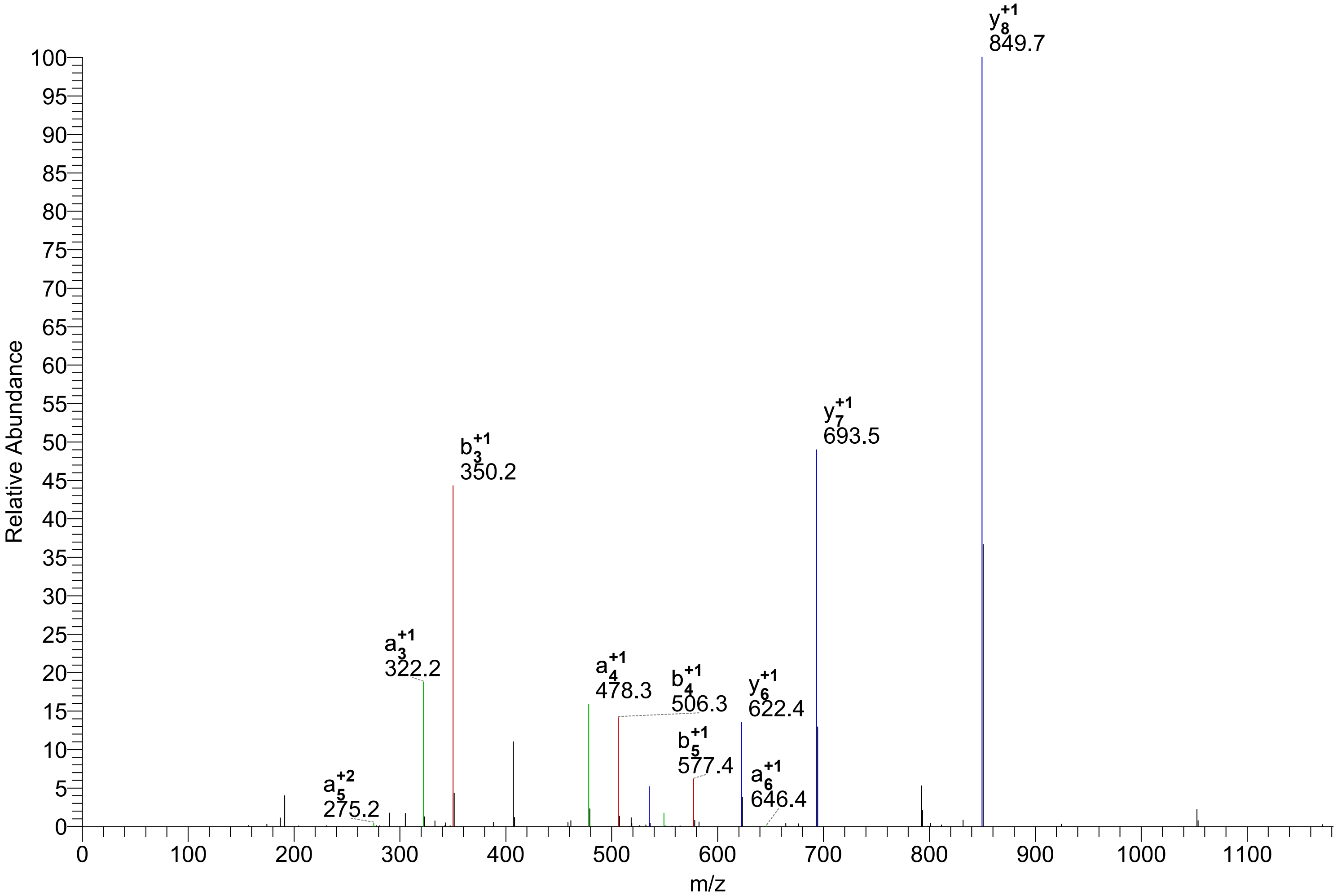
```
DTA for scans: 19287468-1
Precursor ion: 599.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 E    102.05     130.05
 Y    265.12     293.11                                     1069.59
 G    322.14     350.13                                      906.53
 R    478.24     506.24                                      849.51
 A    549.28     577.27                                      693.40
 P    646.33     674.33                                      622.37
 V    745.40     773.39                                      525.31
 P    842.45     870.45                                      426.25
 G    899.47     927.47                                      329.19
 P    996.53    1024.52                                      272.17
 R                                                           175.12
```



#19287468-1 NL: 2.47E6



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

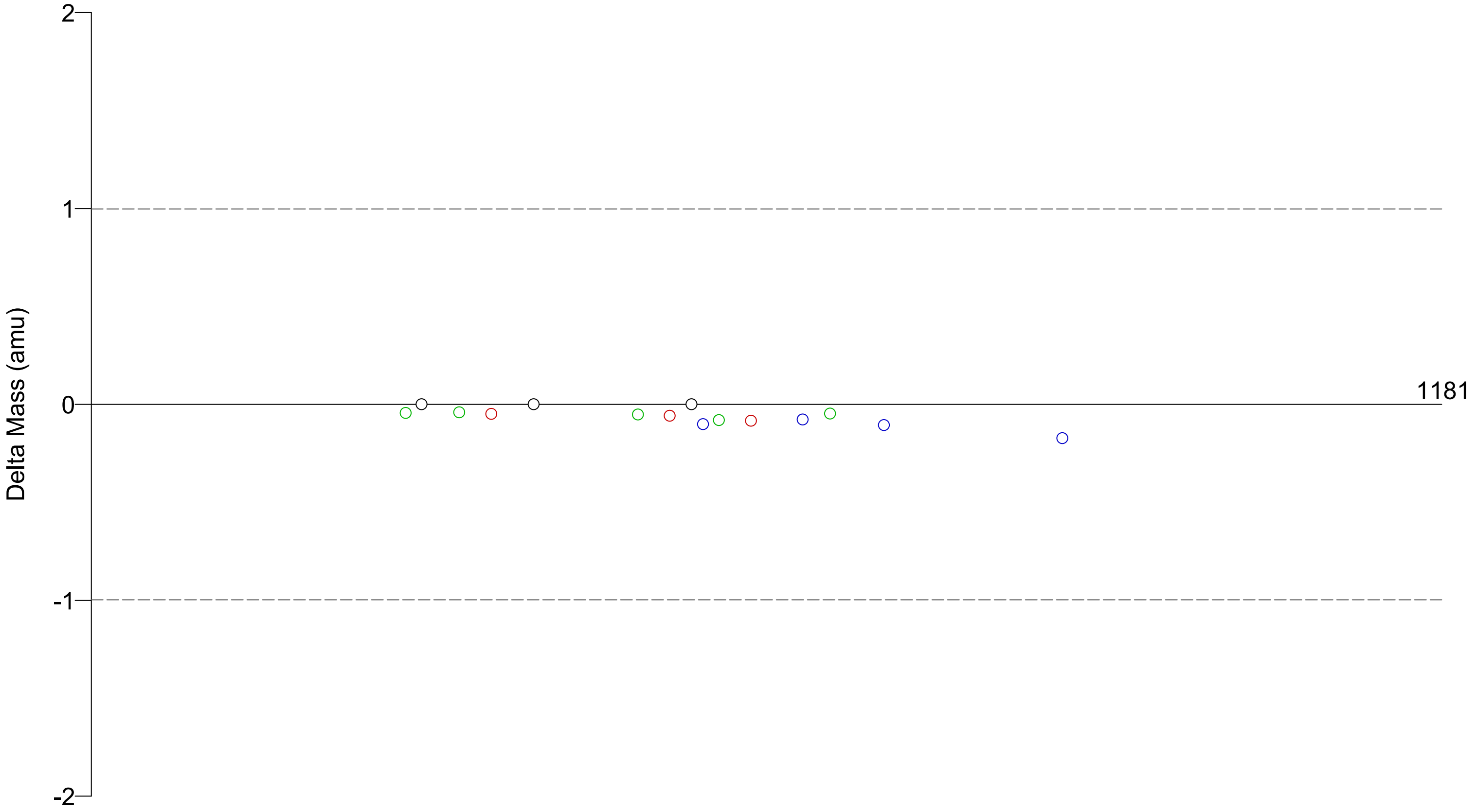
IPI:IPI00446876.3|TREMBL:Q6ZWP8|EN                                1       8.1      0.0       0
19287468 - 1  K.EYGRAPVPGPR.R                        1198.63   2  0.8     2.135  0.461   245.0  3   11/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

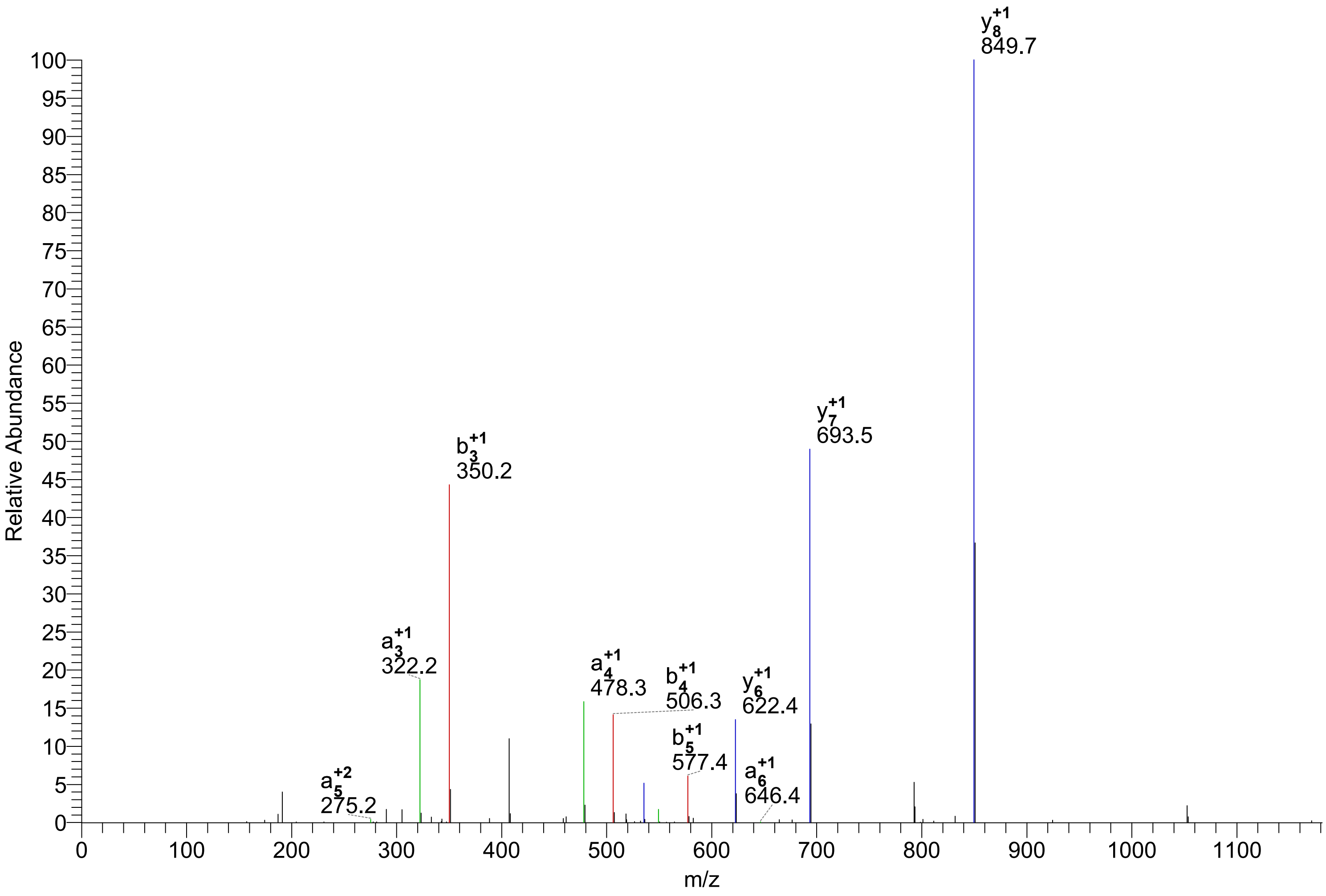
```
DTA for scans: 19287468-1
Precursor ion: 599.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions     Y ions     Y* ions     Yo ions     Z ions
---------------------------------------------------------------------------------------------------
 E    102.05     130.05
 Y    265.12     293.11                                     1069.59
 G    322.14     350.13                                      906.53
 R    478.24     506.24                                      849.51
 A    549.28     577.27                                      693.40
 P    646.33     674.33                                      622.37
 V    745.40     773.39                                      525.31
 P    842.45     870.45                                      426.25
 G    899.47     927.47                                      329.19
 P    996.53    1024.52                                      272.17
 R                                                           175.12
```



#19287468-1 NL: 2.47E6



```
Reference                                                               P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

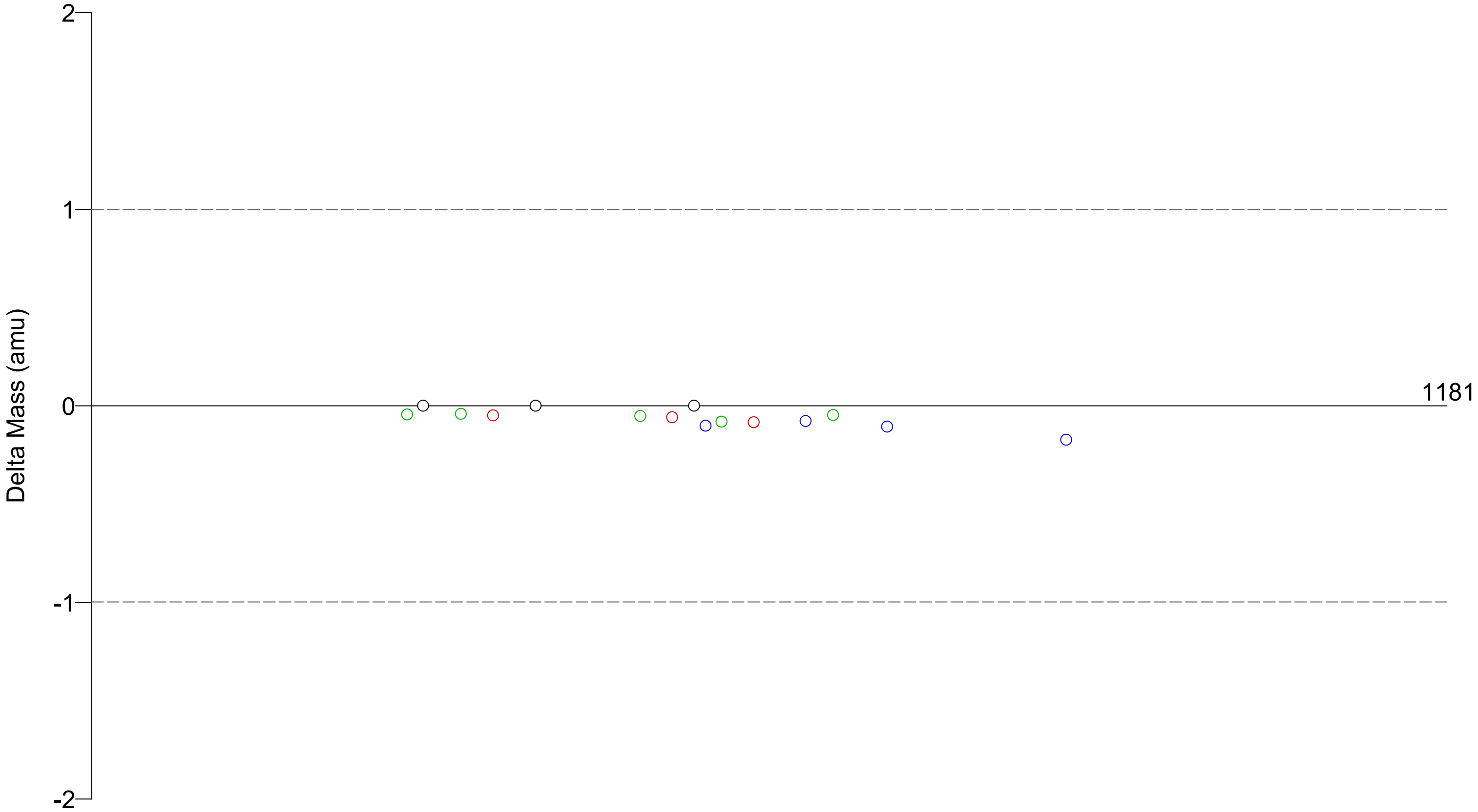
IPI:IPI00470604.2|SWISS-PROT:Q6PJF                                    1       8.1      0.0       0
19287468 - 1  K.EYGRAPVPGPR.R                           1198.63   2  0.8      2.135  0.461   245.0  3   11/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

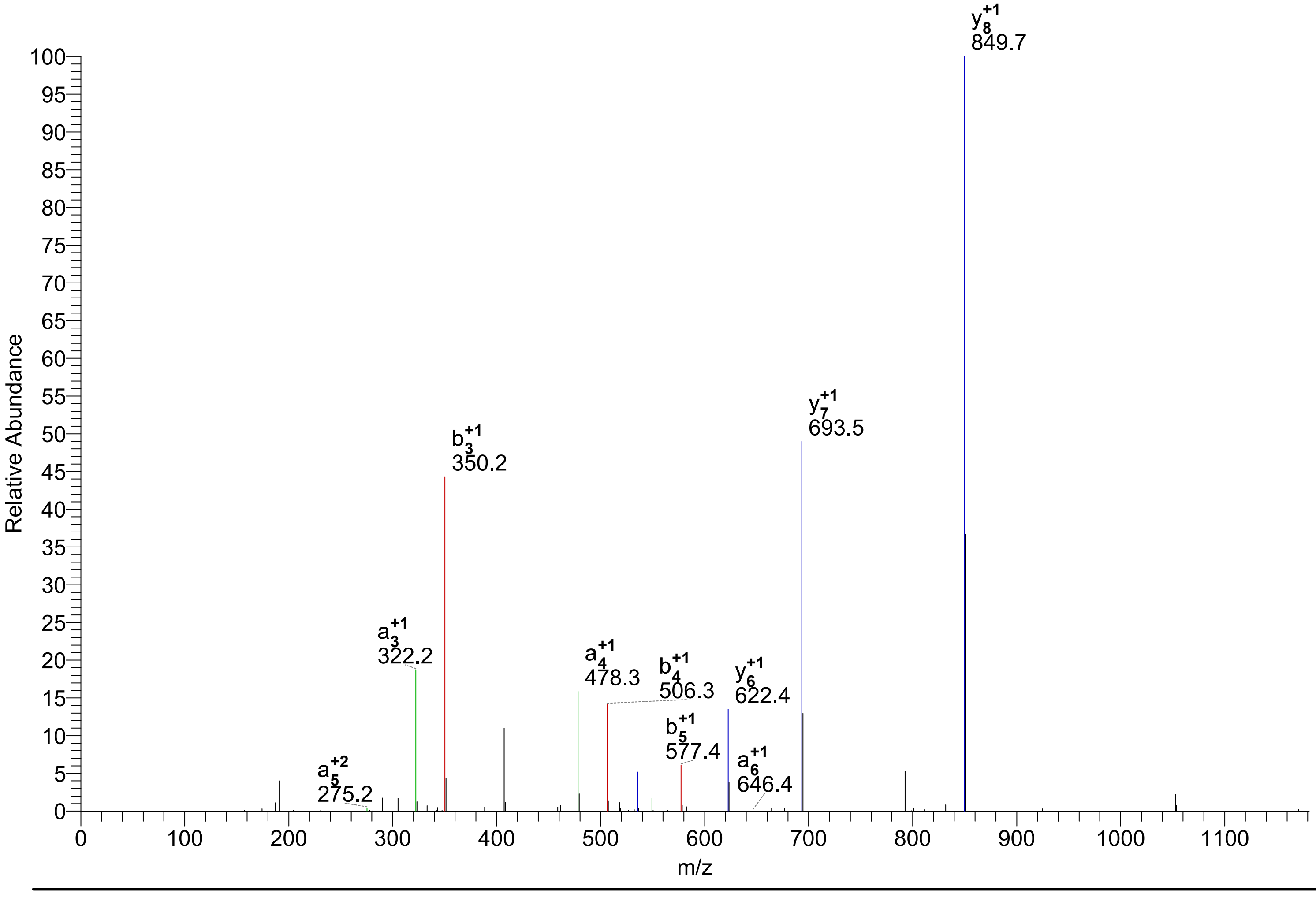
```
DTA for scans: 19287468-1
Precursor ion: 599.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 E    102.05     130.05
 Y    265.12     293.11                                     1069.59
 G    322.14     350.13                                      906.53
 R    478.24     506.24                                      849.51
 A    549.28     577.27                                      693.40
 P    646.33     674.33                                      622.37
 V    745.40     773.39                                      525.31
 P    842.45     870.45                                      426.25
 G    899.47     927.47                                      329.19
 P    996.53    1024.52                                      272.17
 R                                                           175.12
```



#19287468-1 NL: 2.47E6



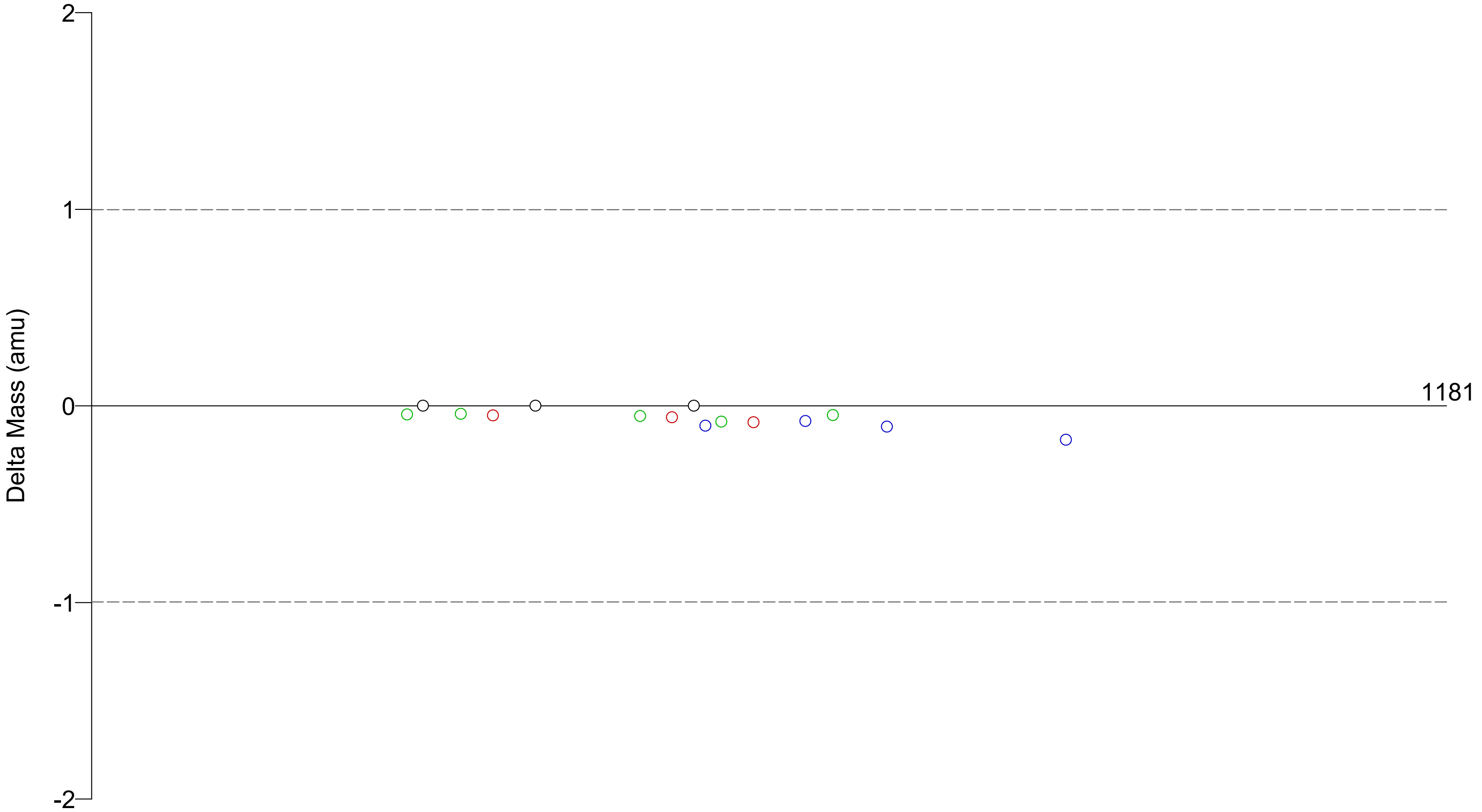
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00922473.1|TREMBL:B7Z8H4 Ta                                  1      8.1      0.0       0
19287468 - 1  K.EYGRAPVPGPR.R                          1198.63   2  0.8      2.135  0.461   245.0  3   11/30   3

1 of 1 peptide matches reported, 0 removed due to filtering
```

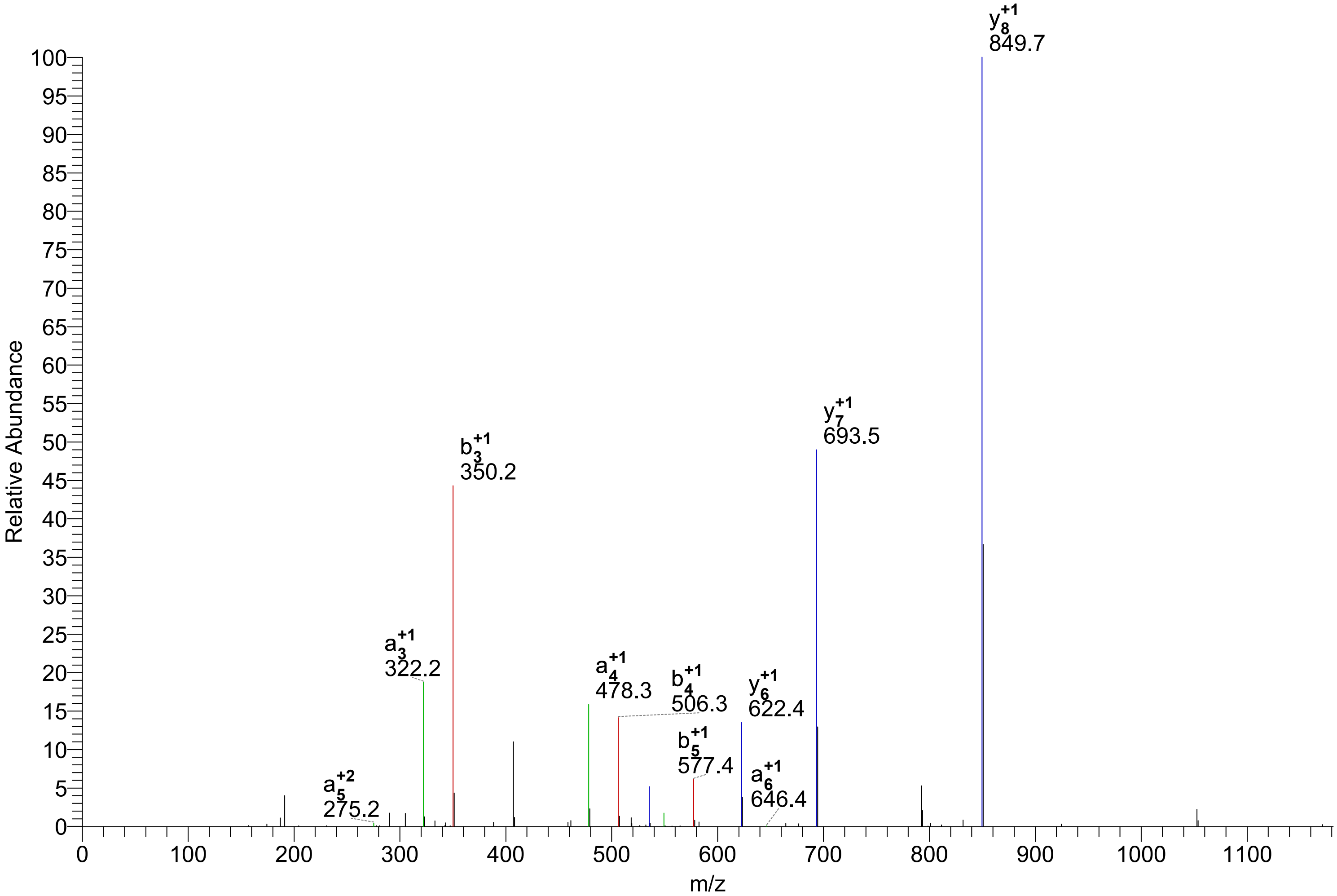
```
DTA for scans: 19287468-1
Precursor ion: 599.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 E    102.05     130.05
 Y    265.12     293.11                                     1069.59
 G    322.14     350.13                                      906.53
 R    478.24     506.24                                      849.51
 A    549.28     577.27                                      693.40
 P    646.33     674.33                                      622.37
 V    745.40     773.39                                      525.31
 P    842.45     870.45                                      426.25
 G    899.47     927.47                                      329.19
 P    996.53    1024.52                                      272.17
 R                                                           175.12
```



#19287468-1 NL: 2.47E6



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp    RSp  Ions  Count

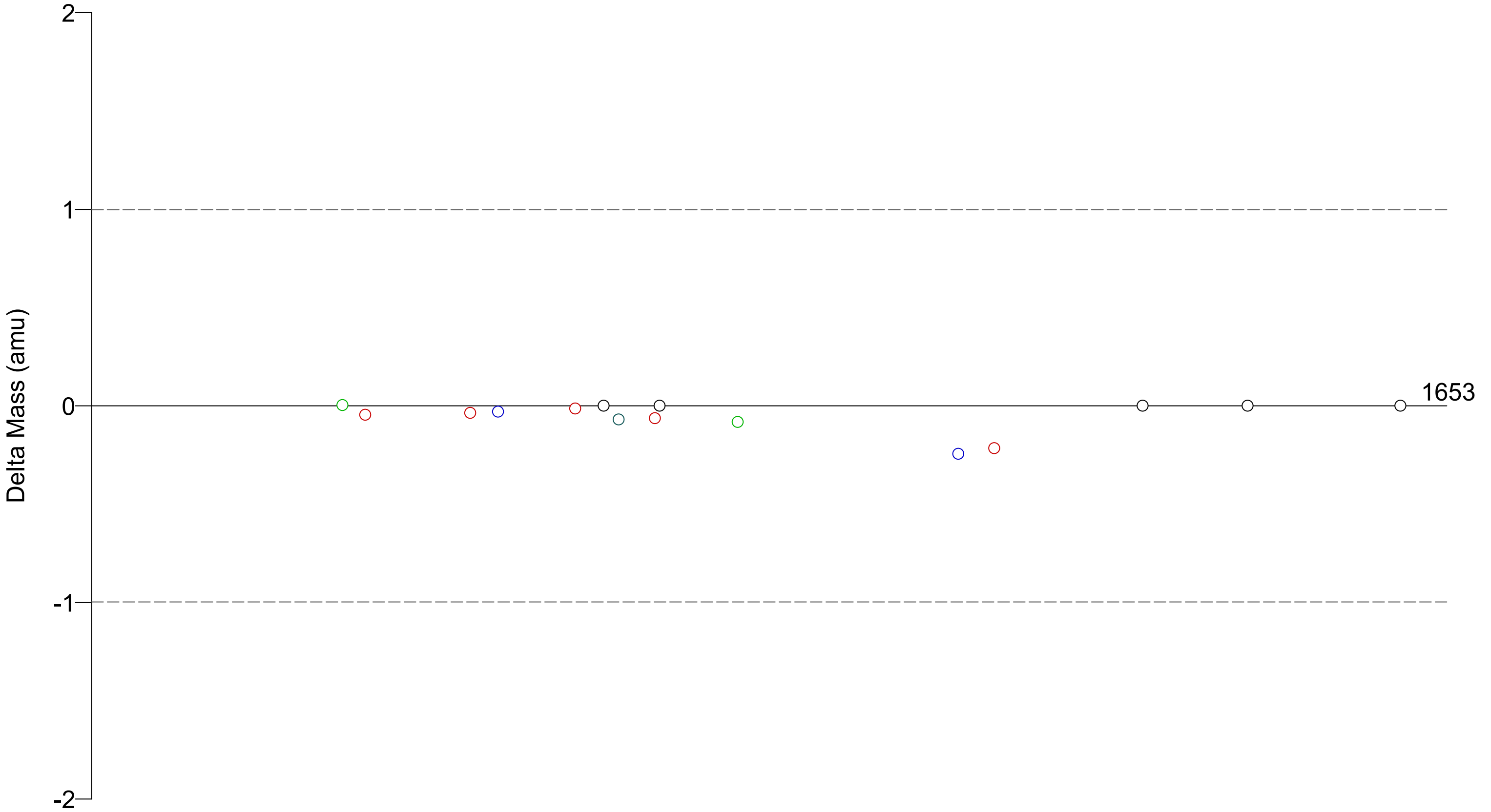
IPI:IPI00023129.1|SWISS-PROT:O95813|TREMBL:Q3SY34|ENSEMBL:ENSP     1        8.1      0.0        0
19287468 - 1  R.FWKKPEREM*HPSR.D                        1743.87   2  1        2.081  0.445   89.0   4   8/36

1 of 1 peptide matches reported, 0 removed due to filtering
```

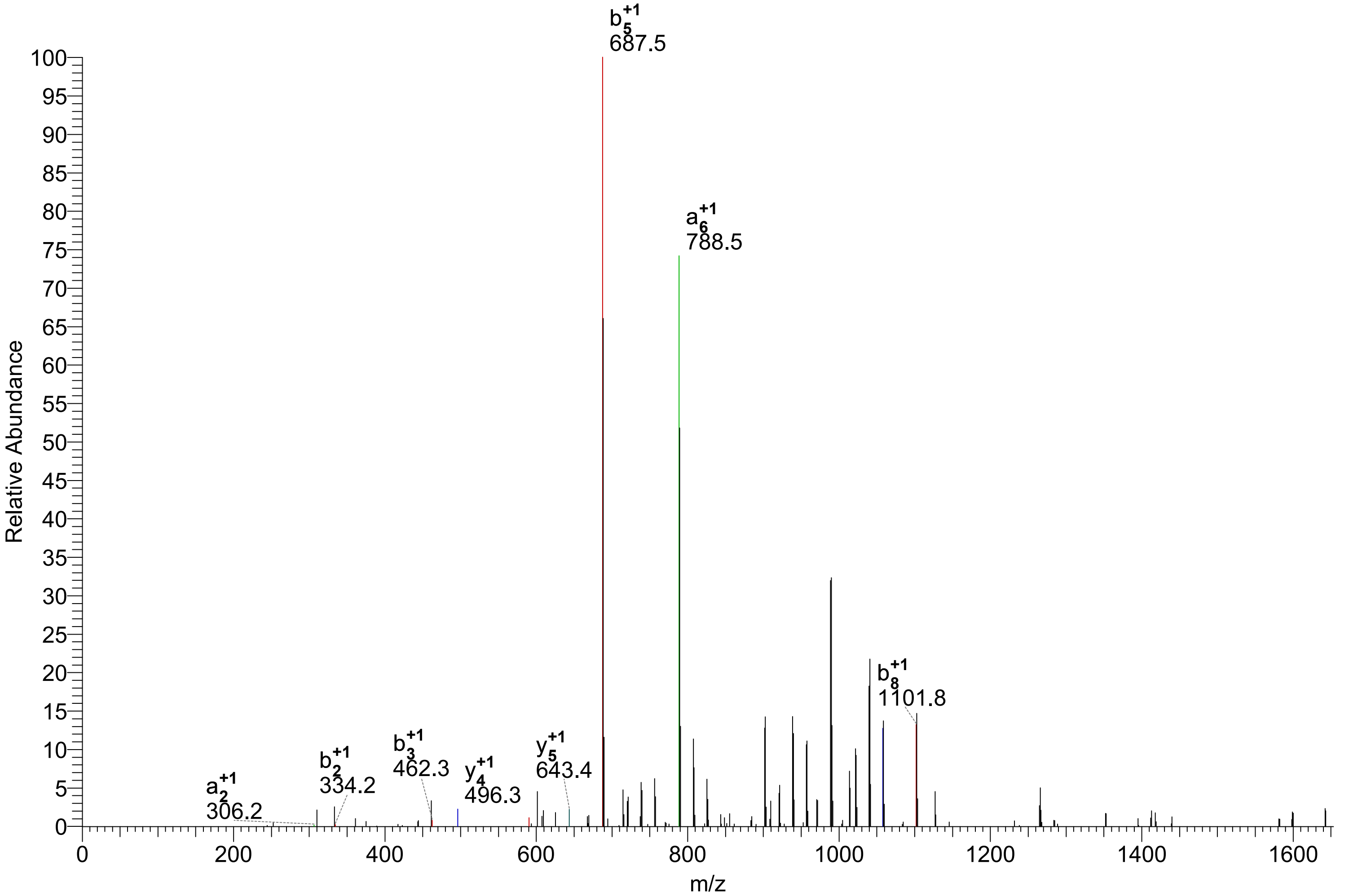
```
DTA for scans: 19287468-1
Precursor ion: 872.44
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 F    120.08     148.08
 W    306.16     334.16                                     1596.81
 K    434.26     462.25                                     1410.73
 K    562.35     590.34                                     1282.63
 P    659.40     687.40                                     1154.54
 E    788.45     816.44                                     1057.48
 R    944.55     972.54                                      928.44
 E   1073.59    1101.58                                      772.34
 M*  1220.62    1248.62                                      643.30
 H   1357.68    1385.68                                      496.26
 P   1454.74    1482.73                                      359.20
 S   1541.77    1569.76                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 1.22E5



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+     z   P        XC  DeltaCn    Sp   RSp  Ions  Count

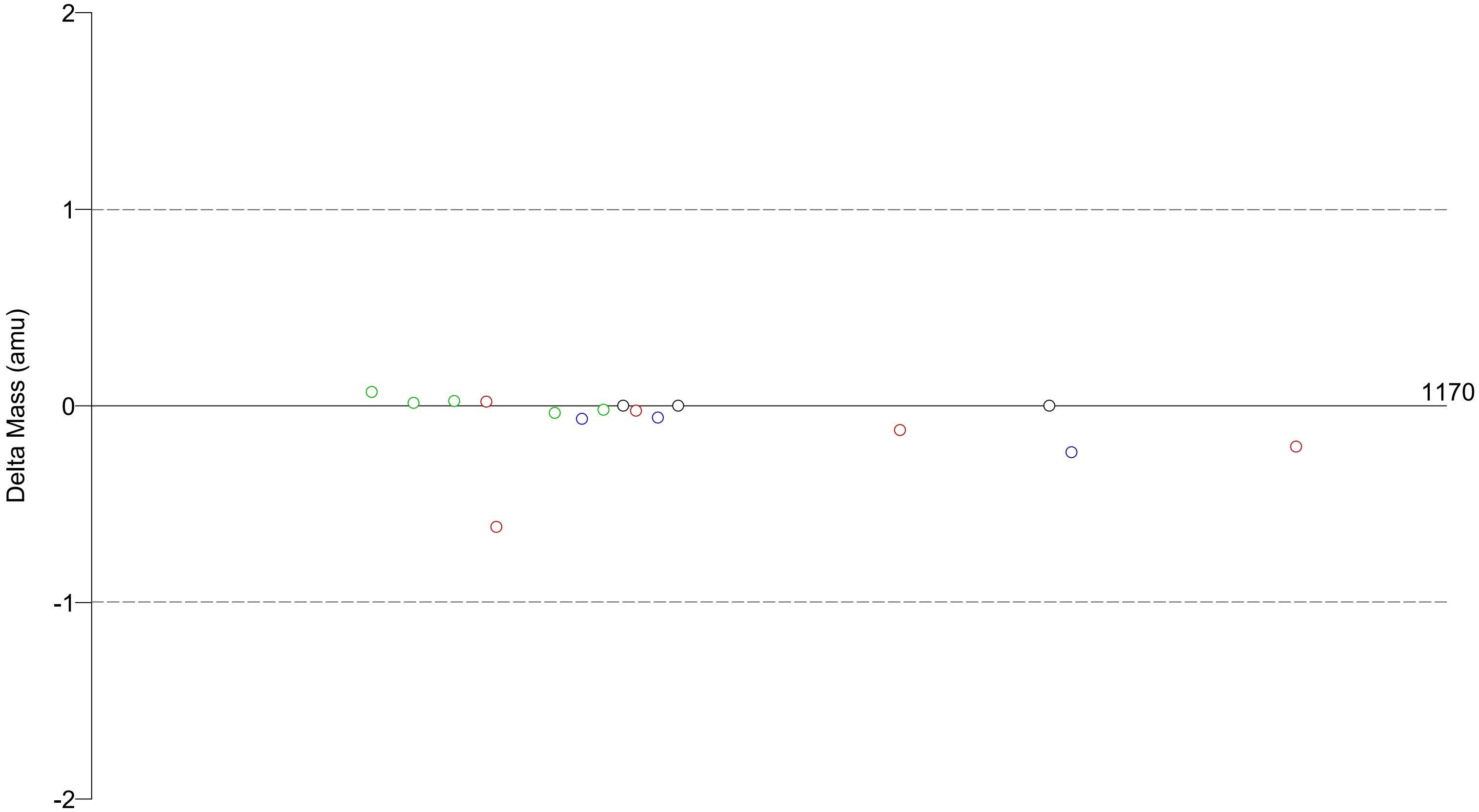
IPI:IPI00009771.6|H-INV:HIT000278695|VEGA:OTTHUMP00000077225 T    1       8.1      0.0       0
2118291816 -  K.LRAELDEVNK.S                            1186.64   2  1       1.923  0.445   146.4  3   9/27    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

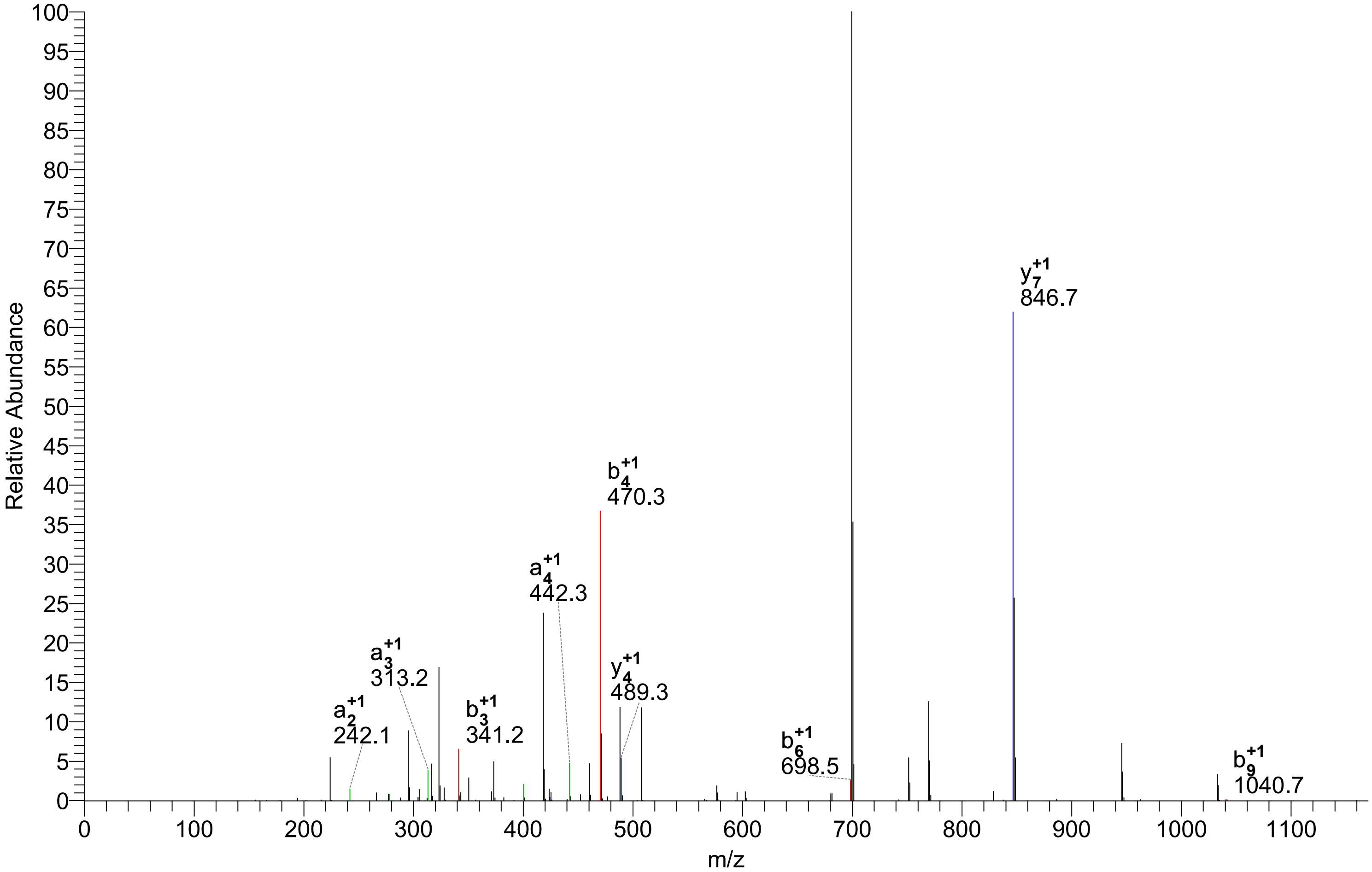
```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 R    242.20     270.19                                     1073.56
 A    313.23     341.23                                      917.46
 E    442.28     470.27                                      846.42
 L    555.36     583.36                                      717.38
 D    670.39     698.38                                      604.29
 E    799.43     827.43                                      489.27
 V    898.50     926.49                                      360.22
 N   1012.54    1040.54                                      261.16
 K                                                           147.11
```



#2118291816-26226248 NL: 6.95E6



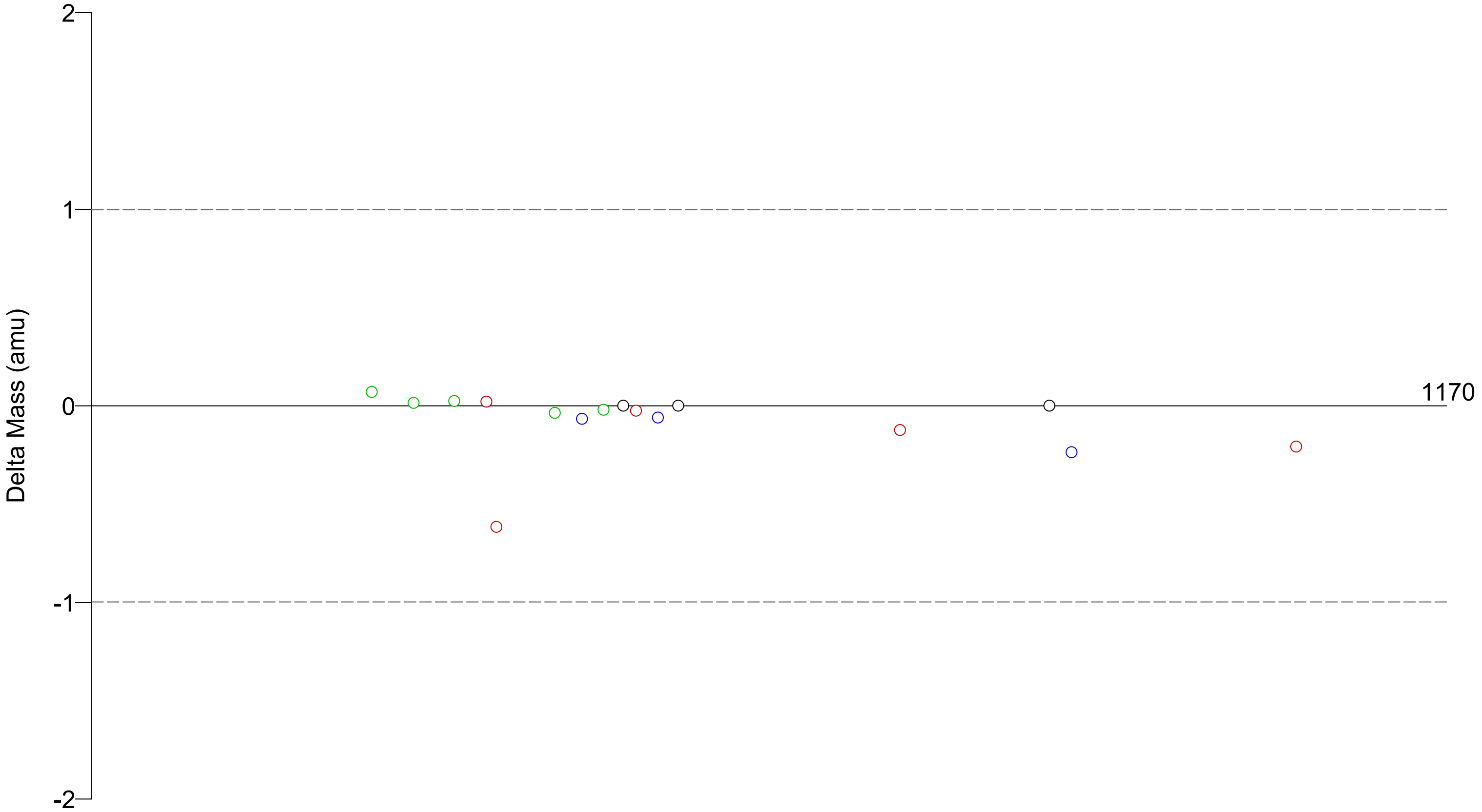
```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z   P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00879819.1|SWISS-PROT:Q0325                                 1       8.1      0.0        0
2118291816 -  K.LRAELDEVNK.S                         1186.64   2  1       1.923  0.445   146.4  3   9/27    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

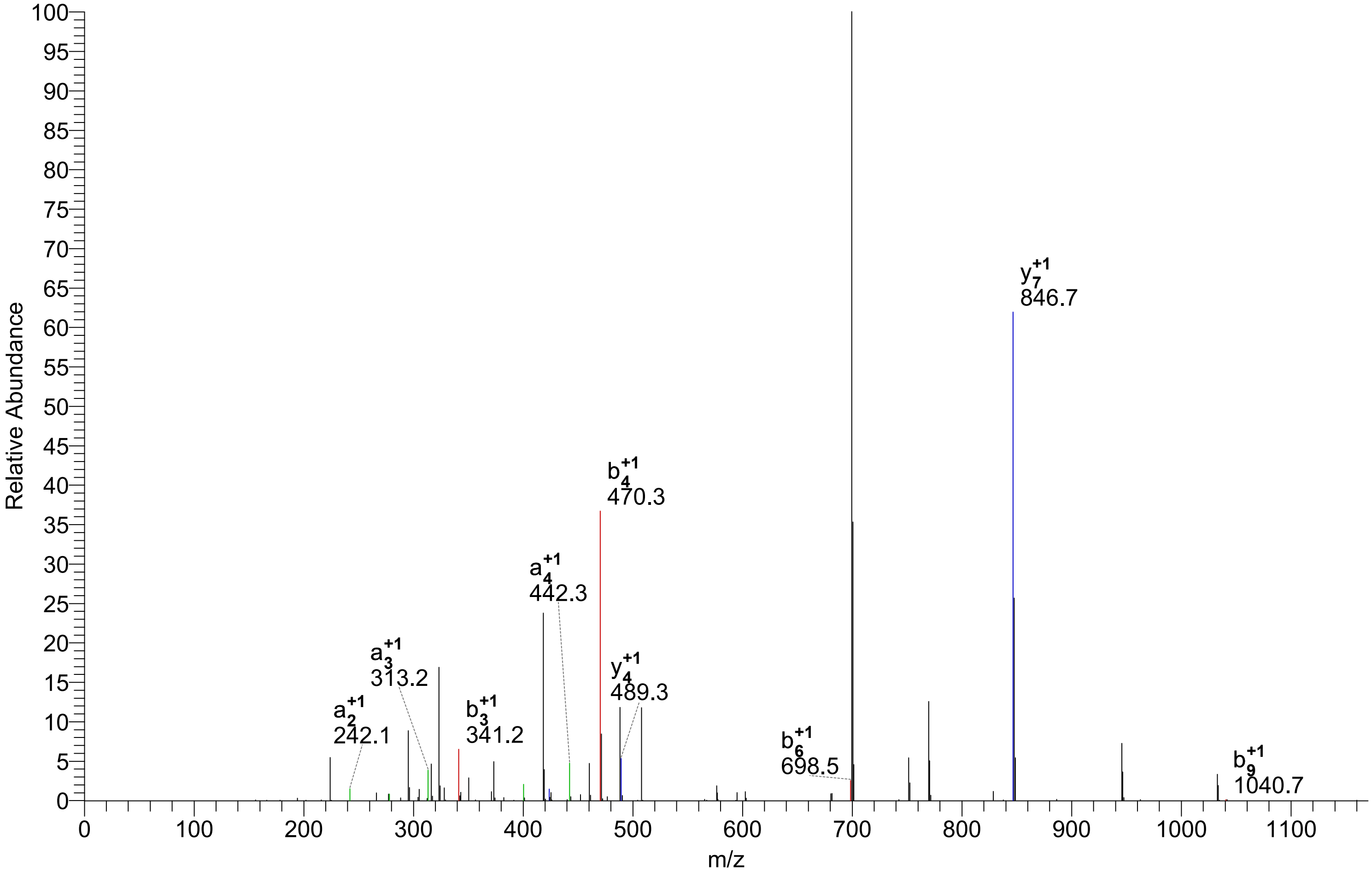
```
DTA for scans: 2118291816-26226248
Precursor ion: 593.83
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 R    242.20     270.19                                     1073.56
 A    313.23     341.23                                      917.46
 E    442.28     470.27                                      846.42
 L    555.36     583.36                                      717.38
 D    670.39     698.38                                      604.29
 E    799.43     827.43                                      489.27
 V    898.50     926.49                                      360.22
 N   1012.54    1040.54                                      261.16
 K                                                           147.11
```



#2118291816-26226248 NL: 6.95E6



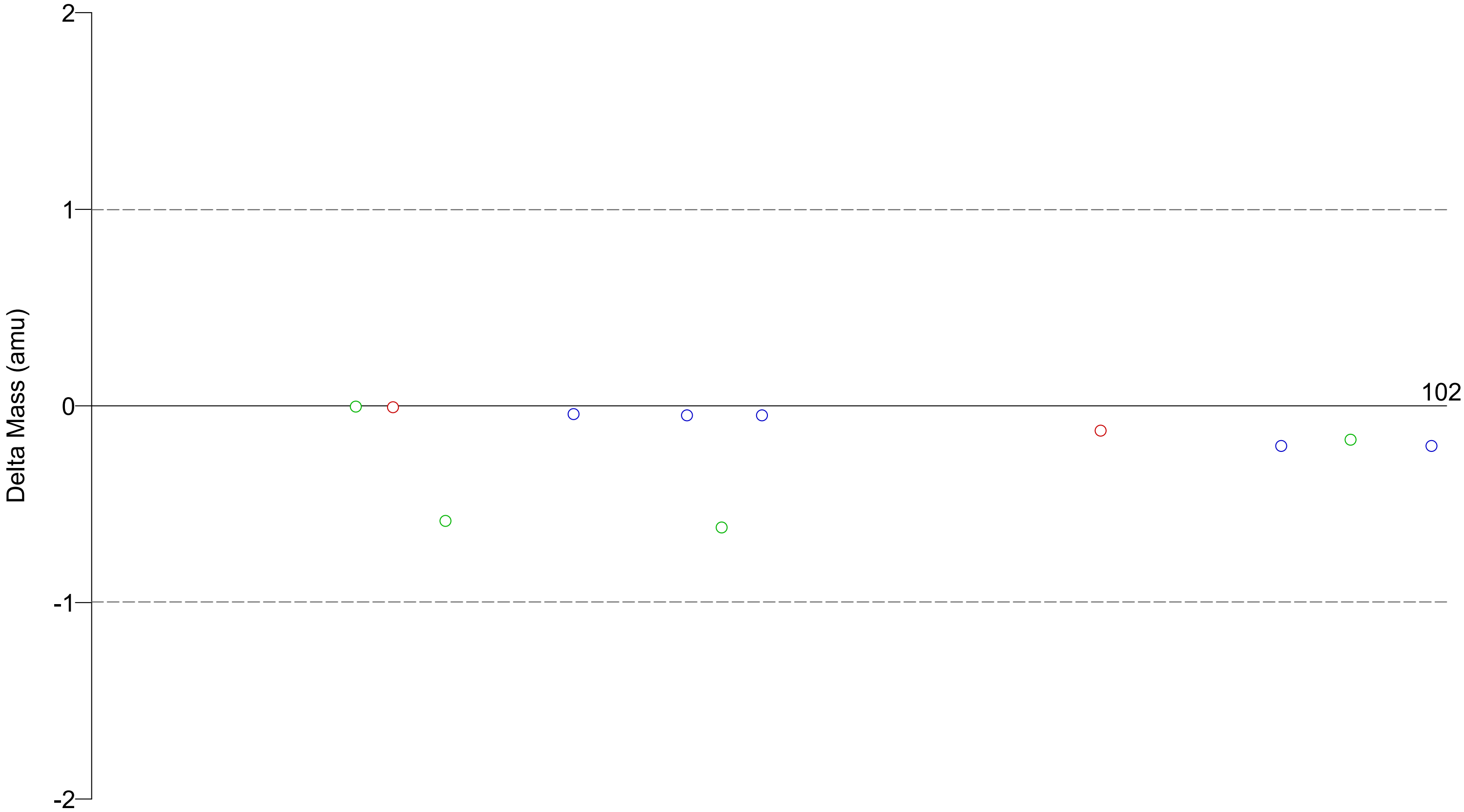
```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00032087.4|SWISS-PROT:Q9Y2E4|TREMBL:Q86XV3|ENSEMBL:ENSP    1        8.1      0.0       0
2118291816 -  K.LLWFVTESK.H                           1122.62   2  1        1.798  0.549   133.1  18  8/24    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

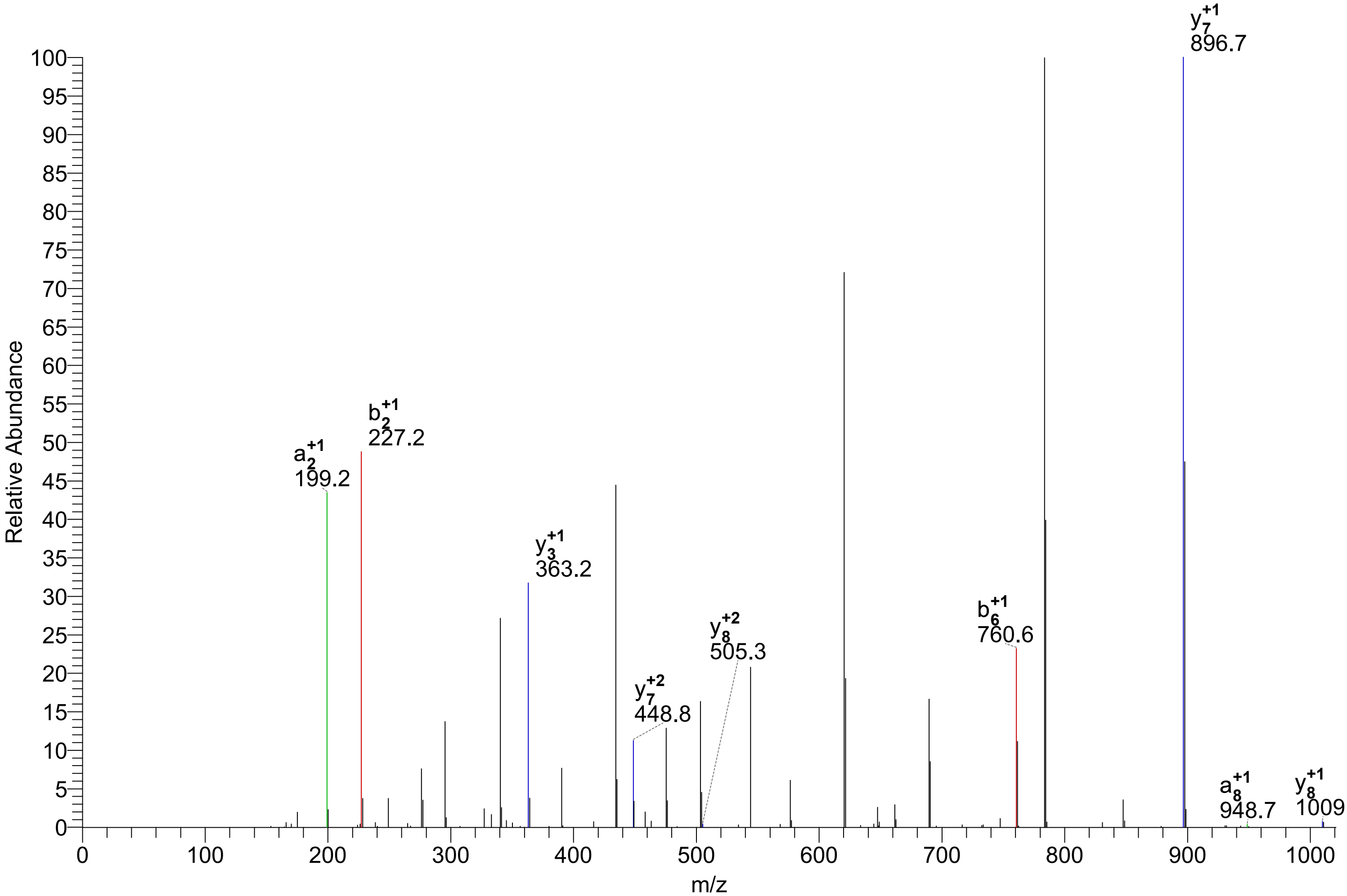
```
DTA for scans: 2118291816-26226248
Precursor ion: 561.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1009.54
 W    385.26     413.25                                      896.45
 F    532.33     560.32                                      710.37
 V    631.40     659.39                                      563.30
 T    732.44     760.44                                      464.24
 E    861.49     889.48                                      363.19
 S    948.52     976.51                                      234.14
 K                                                           147.11
```



#2118291816-26226248 NL: 1.43E5



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count

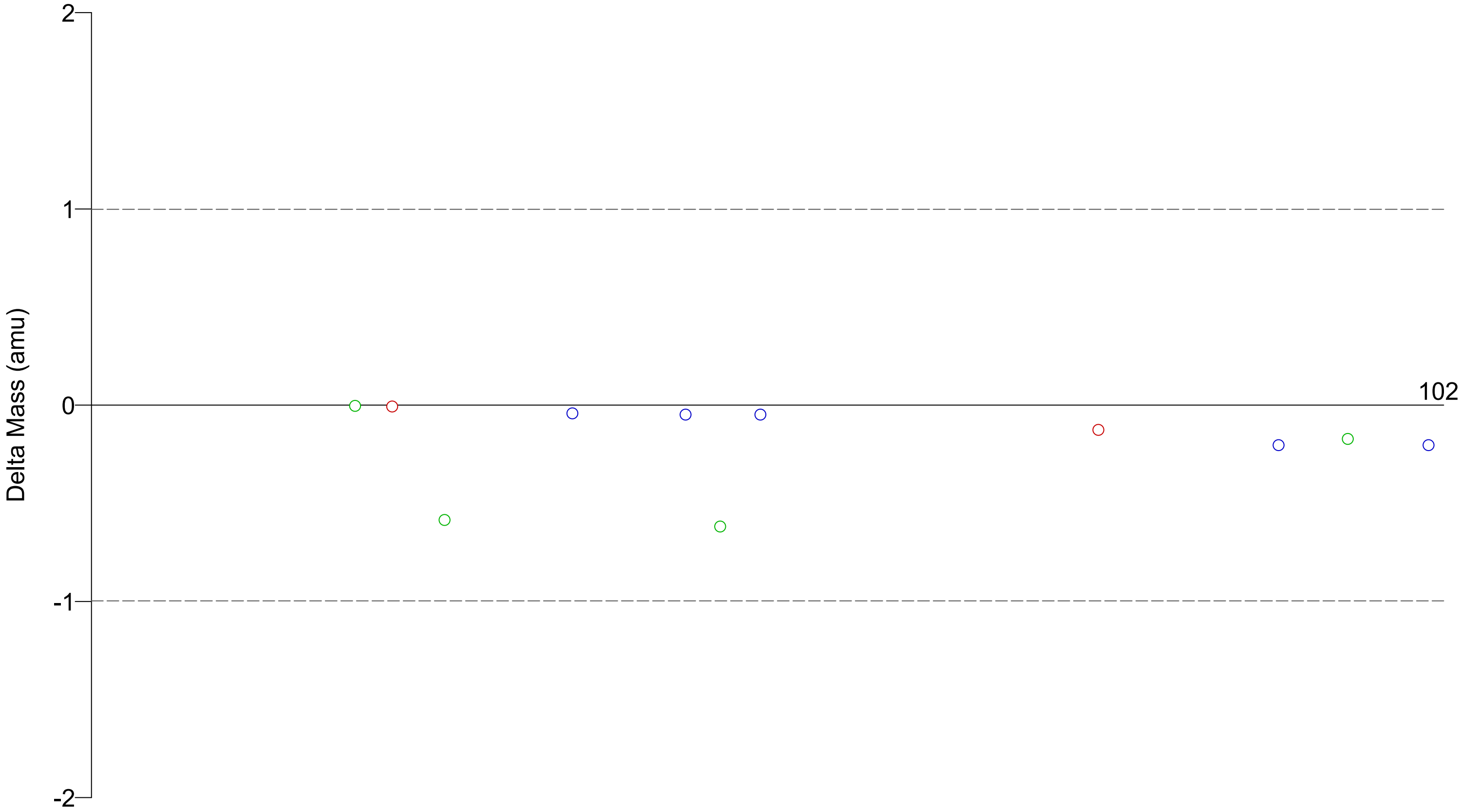
IPI:IPI00643330.5|TREMBL:B3KWX2;Q5                                 1       8.1      0.0       0
2118291816 -  K.LLWFVTESK.H                          1122.62   2  1       1.798  0.549   133.1  18  8/24    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

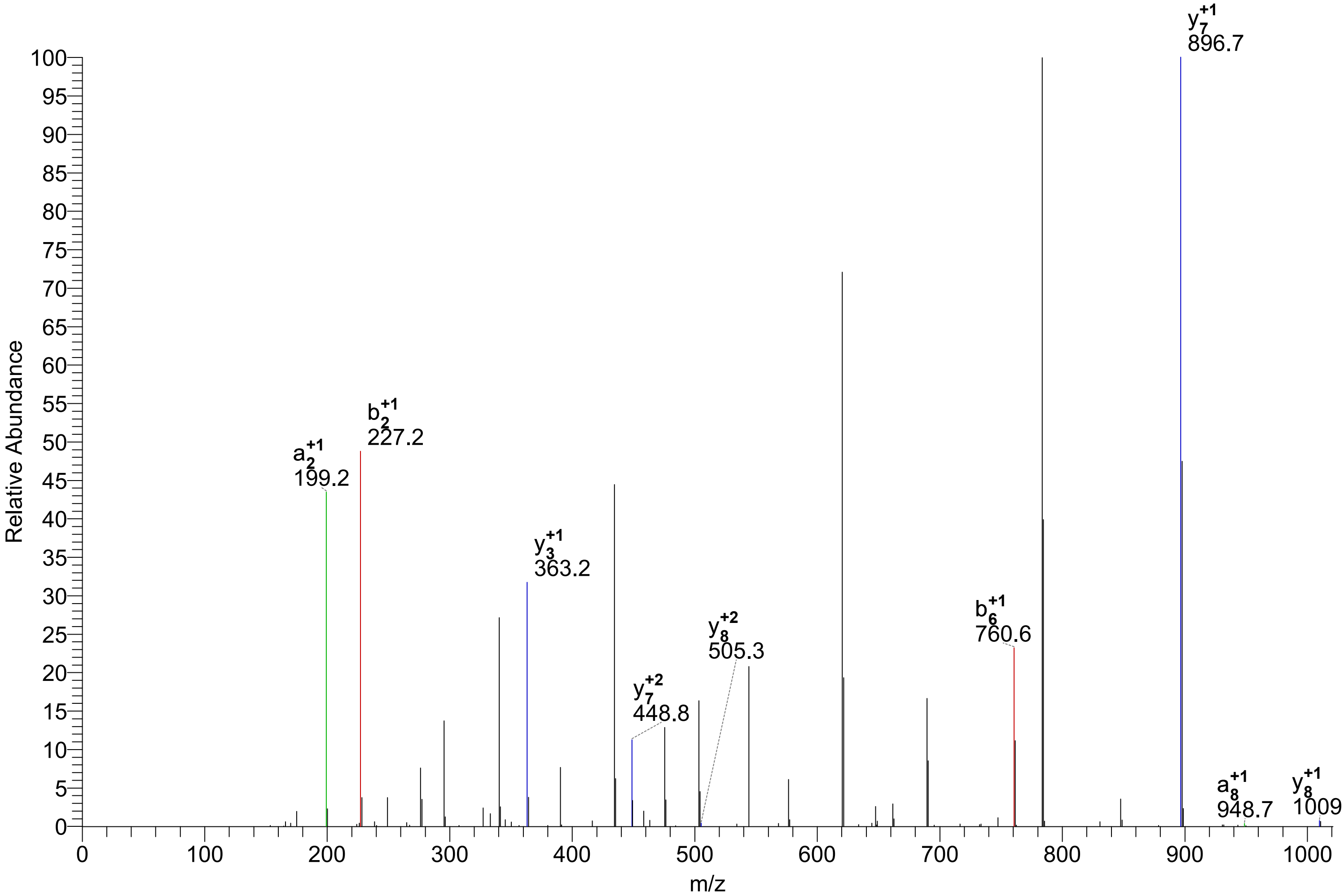
```
DTA for scans: 2118291816-26226248
Precursor ion: 561.82
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 L    199.18     227.18                                     1009.54
 W    385.26     413.25                                      896.45
 F    532.33     560.32                                      710.37
 V    631.40     659.39                                      563.30
 T    732.44     760.44                                      464.24
 E    861.49     889.48                                      363.19
 S    948.52     976.51                                      234.14
 K                                                           147.11
```



#2118291816-26226248 NL: 1.43E5



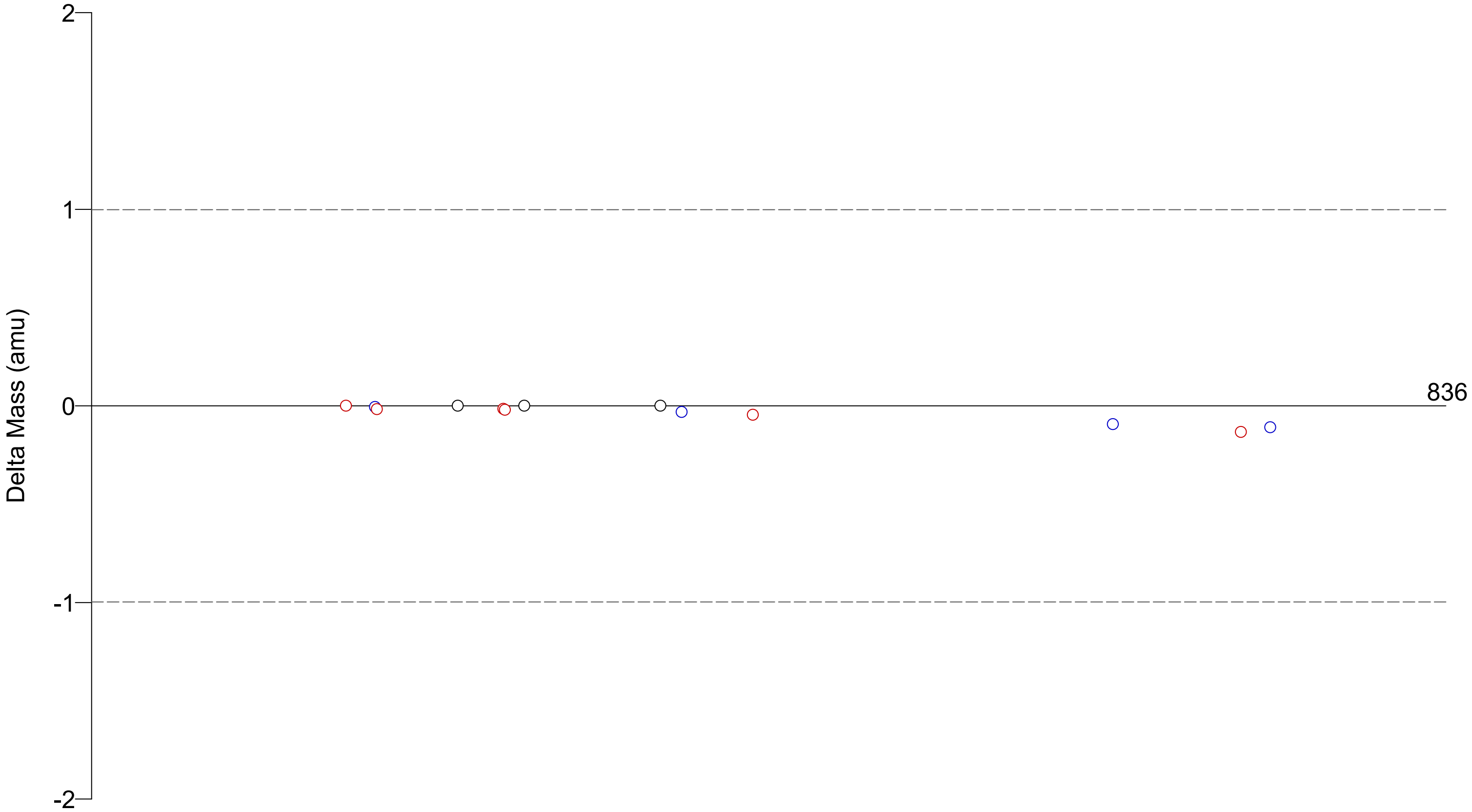
```
Reference                                                                  P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z     P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00018279.7|SWISS-PROT:P25940|TREMBL:Q59GD4|ENSEMBL:ENSP    1       8.1      0.0       0
              R.RPPGTAER.P                                883.47    2  1       1.794  0.387   146.8  6   7/21

1 of 1 peptide matches reported, 0 removed due to filtering
```

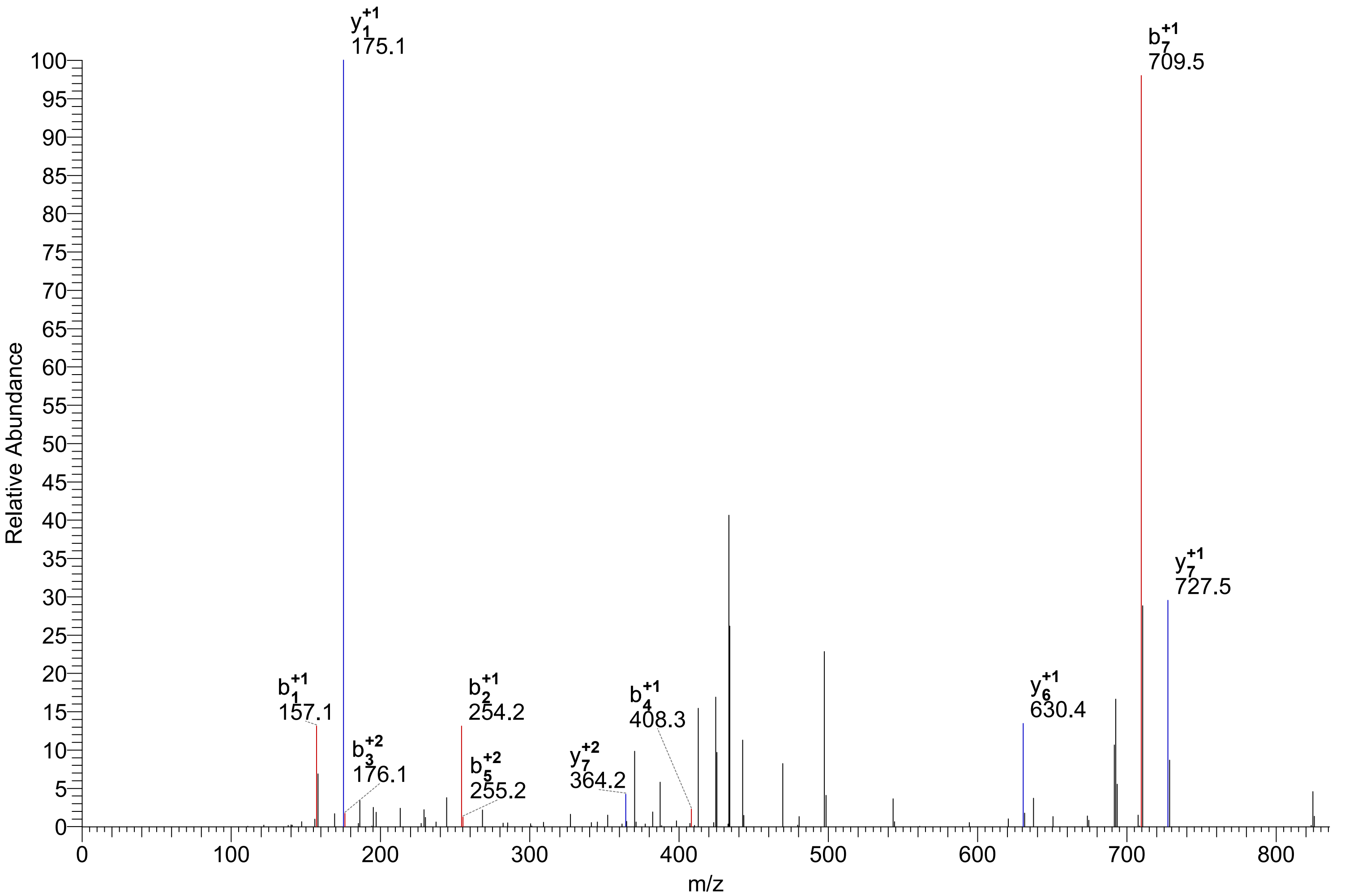
```
DTA for scan: 0
Precursor ion: 442.24
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 P    226.17     254.16                                      727.37
 P    323.22     351.21                                      630.32
 G    380.24     408.24                                      533.27
 T    481.29     509.28                                      476.25
 A    552.33     580.32                                      375.20
 E    681.37     709.36                                      304.16
 R                                                           175.12
```


Delta Mass (amu)
2
1
0
-1
-2
836

#0-0 NL: 6.35E5


Relative Abundance
m/z
y1+1 175.1
b7+1 709.5
y7+1 727.5
b1+1 157.1
b3+2 176.1
b2+1 254.2
b5+2 255.2
y7+2 364.2
b4+1 408.3
y6+1 630.4
0
100
200
300
400
500
600
700
800
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
0

```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                   MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

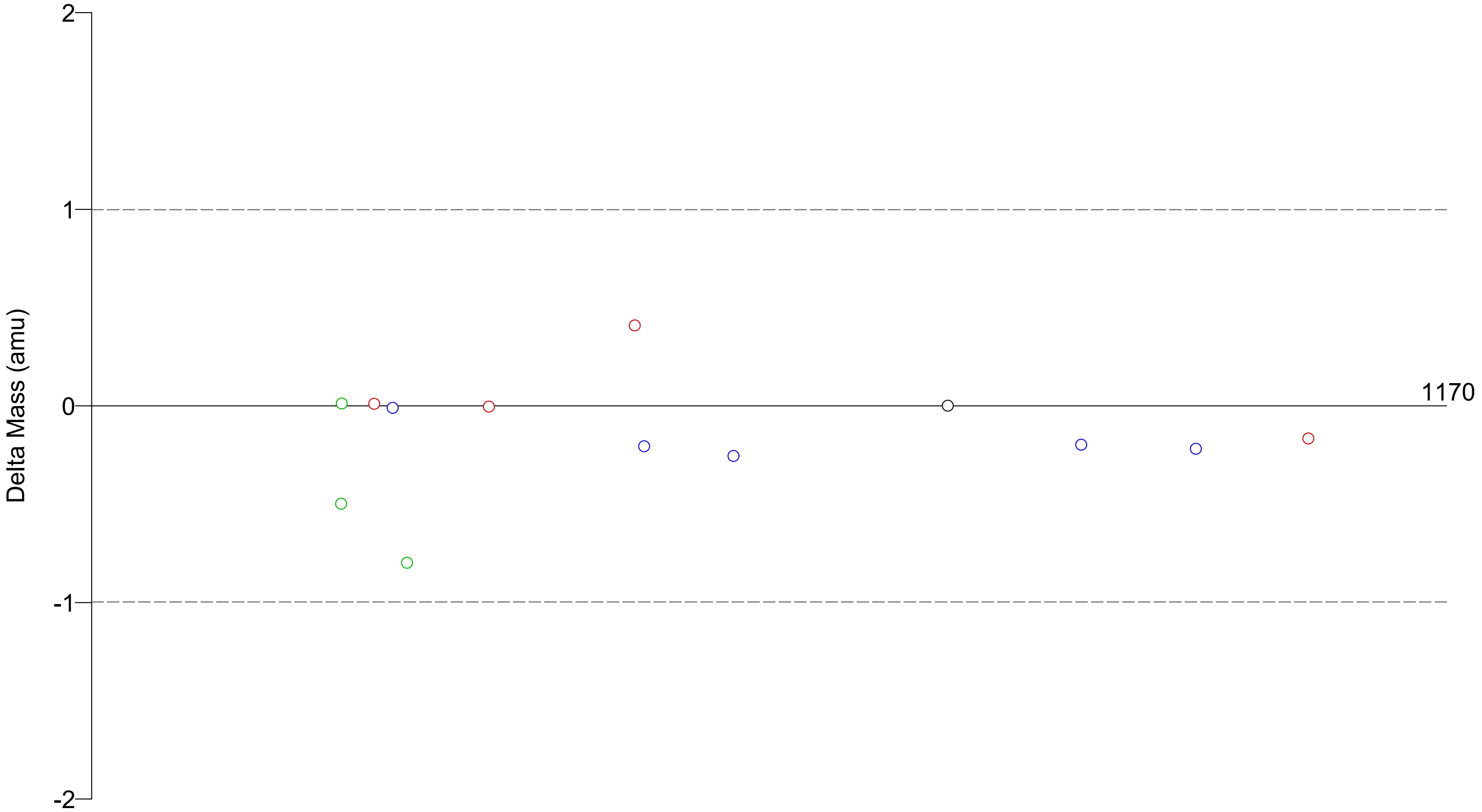
IPI:IPI00021304.1|SWISS-PROT:P35908|ENSEMBL:ENSP00000310861|RE     1       8.1      0.0        0
19287468 - 1  K.KDVDNAYMIK.V                            1196.60   2  1       1.761  0.589   130.6  4   8/27    2

1 of 1 peptide matches reported, 0 removed due to filtering
```

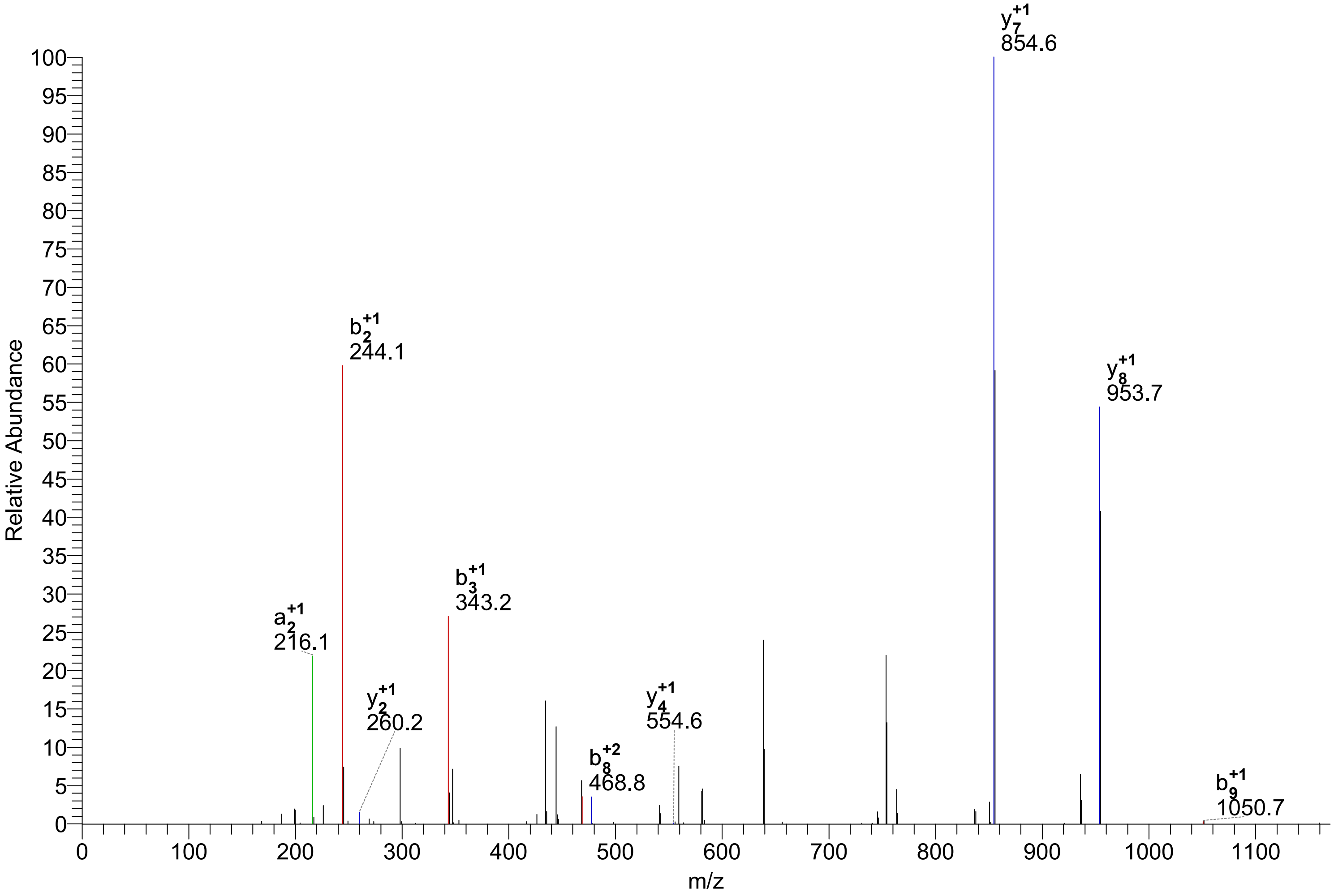
```
DTA for scans: 19287468-1
Precursor ion: 598.80
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 K    101.11     129.10
 D    216.13     244.13                                     1068.50
 V    315.20     343.20                                      953.48
 D    430.23     458.22                                      854.41
 N    544.27     572.27                                      739.38
 A    615.31     643.30                                      625.34
 Y    778.37     806.37                                      554.30
 M    909.41     937.41                                      391.24
 I   1022.50    1050.49                                      260.20
 K                                                           147.11
```



#19287468-1 NL: 9.45E4



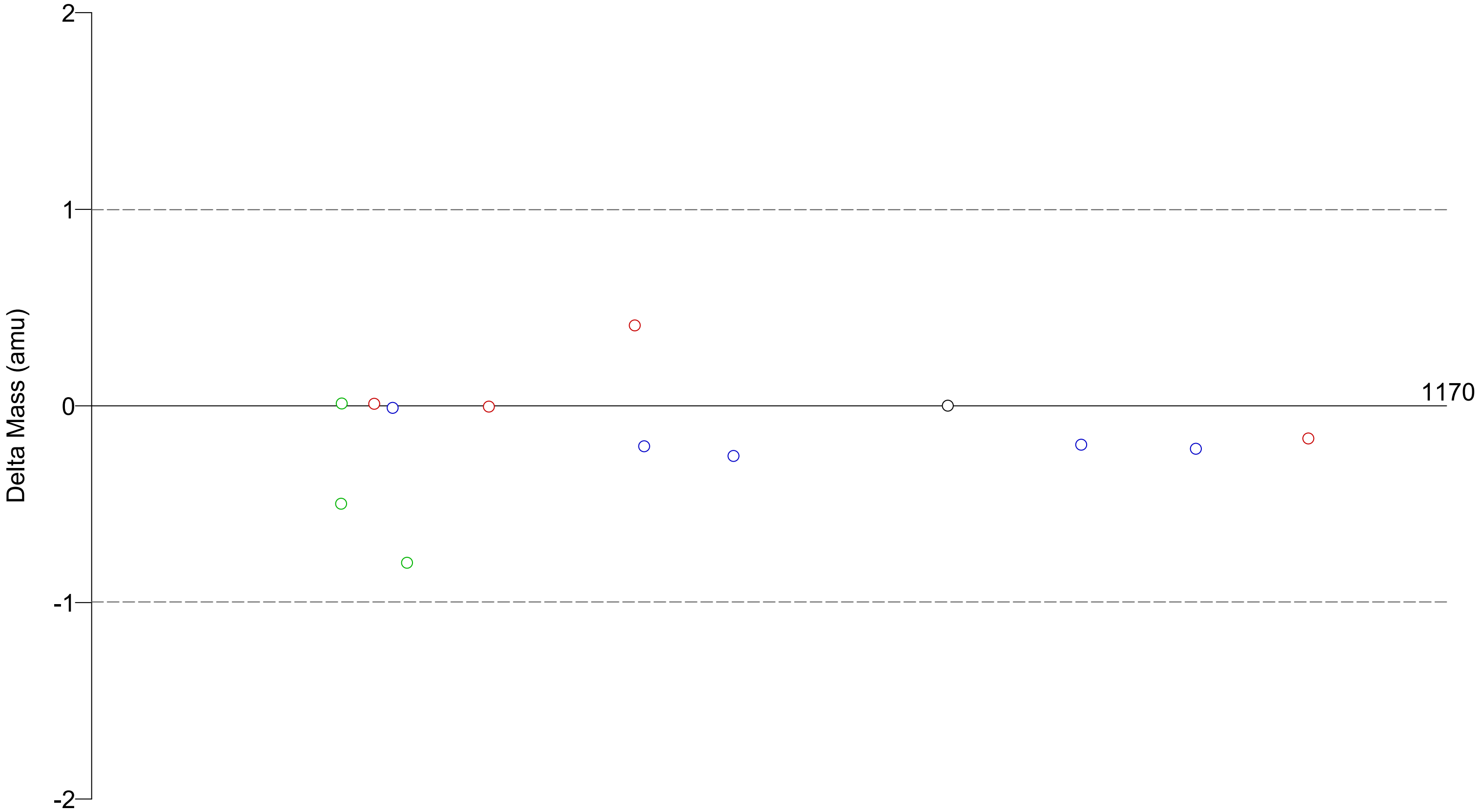
```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z     P        XC  DeltaCn   Sp    RSp  Ions  Count
gi|254622|bbs|112352 (S43646) cyto                                  1       8.1      0.0       254622
19287468 - 1  K.KDVDNAYMIK.V                              1196.60   2  1       1.761  0.589   130.6  4   8/27    2

1 of 1 peptide matches reported, 0 removed due to filtering
```

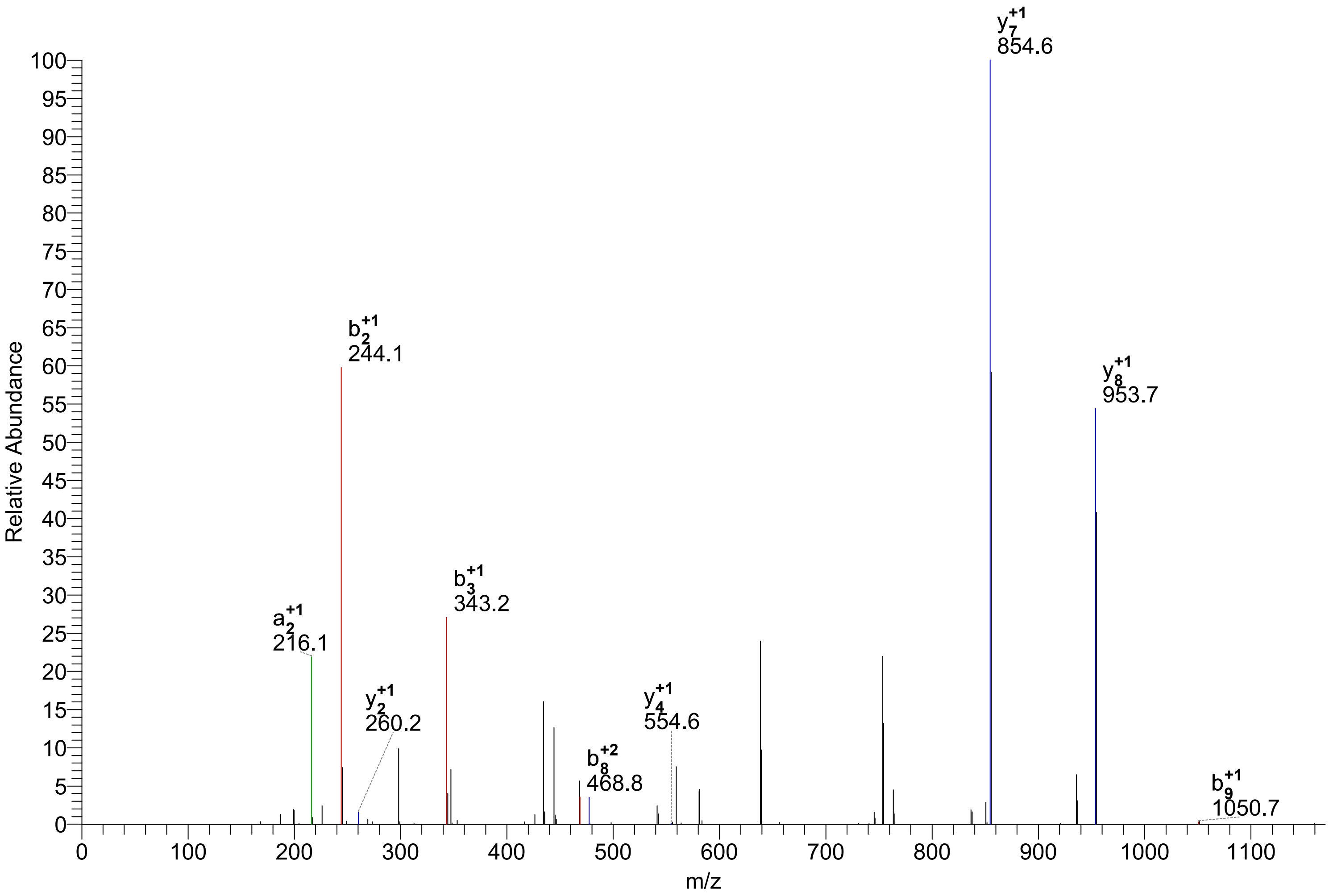
```
DTA for scans: 19287468-1
Precursor ion: 598.80
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 K    101.11     129.10
 D    216.13     244.13                                     1068.50
 V    315.20     343.20                                      953.48
 D    430.23     458.22                                      854.41
 N    544.27     572.27                                      739.38
 A    615.31     643.30                                      625.34
 Y    778.37     806.37                                      554.30
 M    909.41     937.41                                      391.24
 I   1022.50    1050.49                                      260.20
 K                                                           147.11
```



#19287468-1 NL: 9.45E4



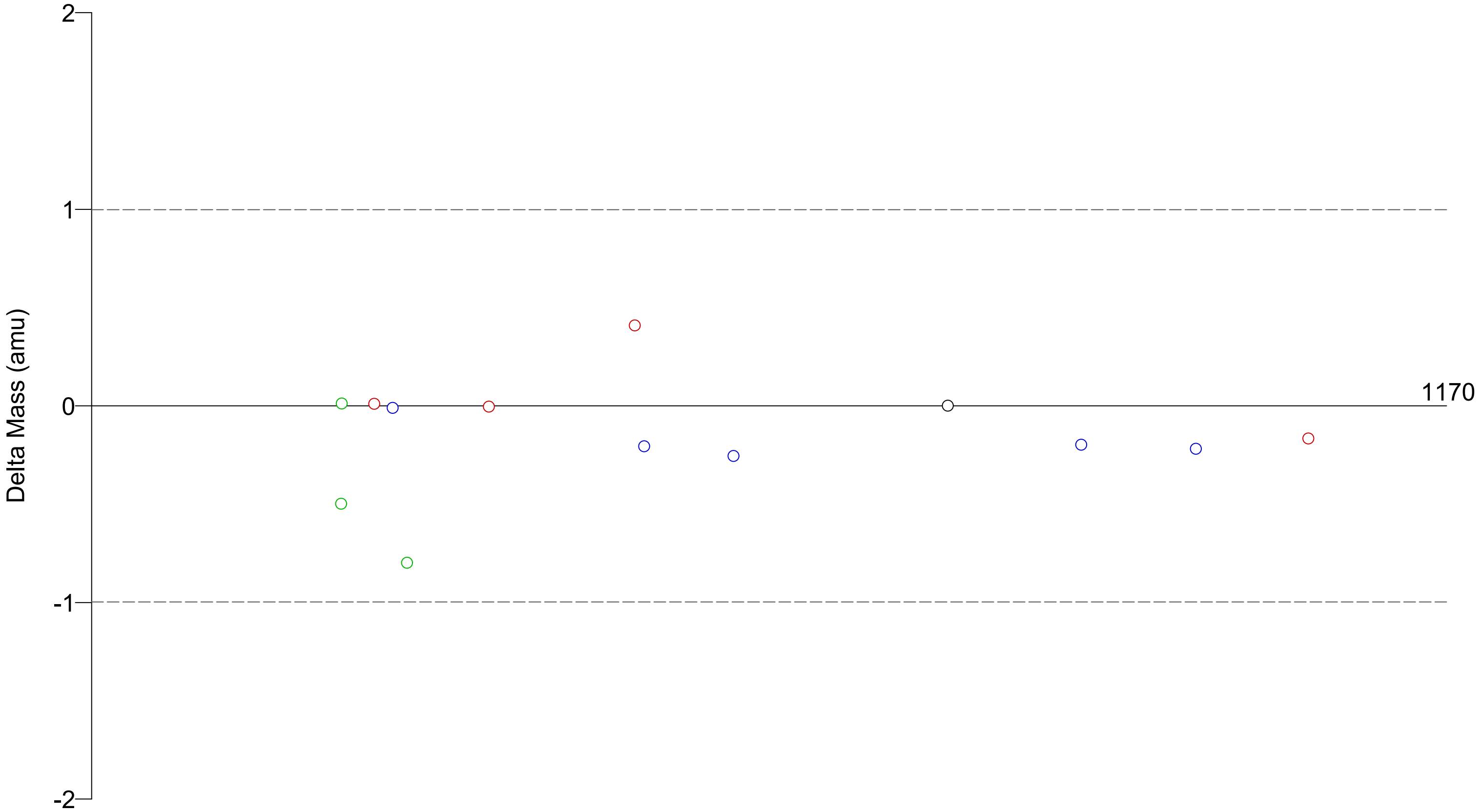
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                  MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count
gi|547754|sp|P35908|K22E_HUMAN KER                                 1        8.1      0.0       547754
19287468 - 1  K.KDVDNAYMIK.V                         1196.60    2  1        1.761  0.589   130.6  4   8/27    2

1 of 1 peptide matches reported, 0 removed due to filtering
```

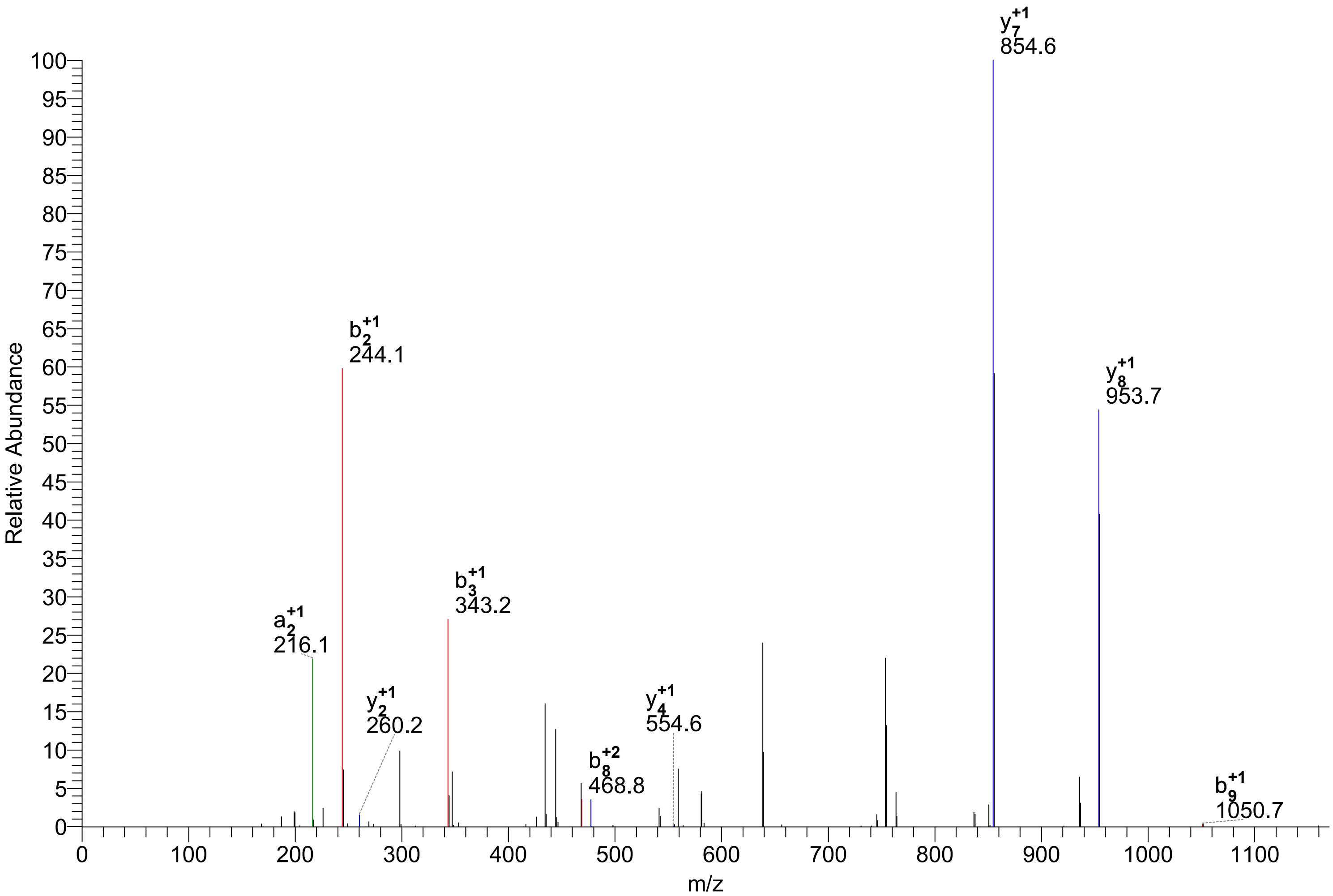
```
DTA for scans: 19287468-1
Precursor ion: 598.80
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 K    101.11     129.10
 D    216.13     244.13                                     1068.50
 V    315.20     343.20                                      953.48
 D    430.23     458.22                                      854.41
 N    544.27     572.27                                      739.38
 A    615.31     643.30                                      625.34
 Y    778.37     806.37                                      554.30
 M    909.41     937.41                                      391.24
 I   1022.50    1050.49                                      260.20
 K                                                           147.11
```



#19287468-1 NL: 9.45E4



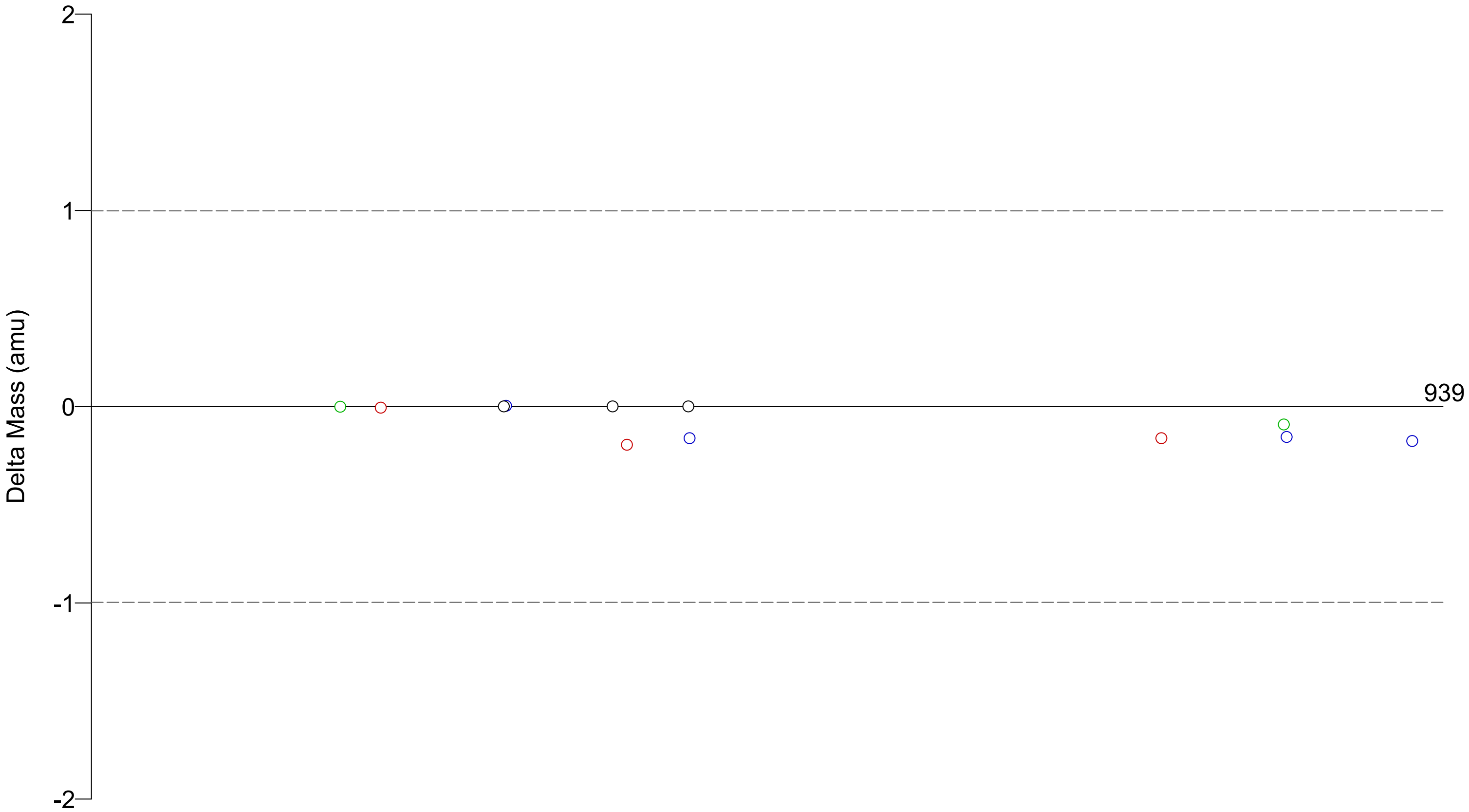
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00418876.3|SWISS-PROT:Q70Z35-1|TREMBL:B4DFX0|ENSEMBL:EN     1        8.1      0.0       0
19287468 - 1  K.LSCPKRLR.L                            1030.58   2  0.9      1.753  0.426   105.7  3   9/21    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

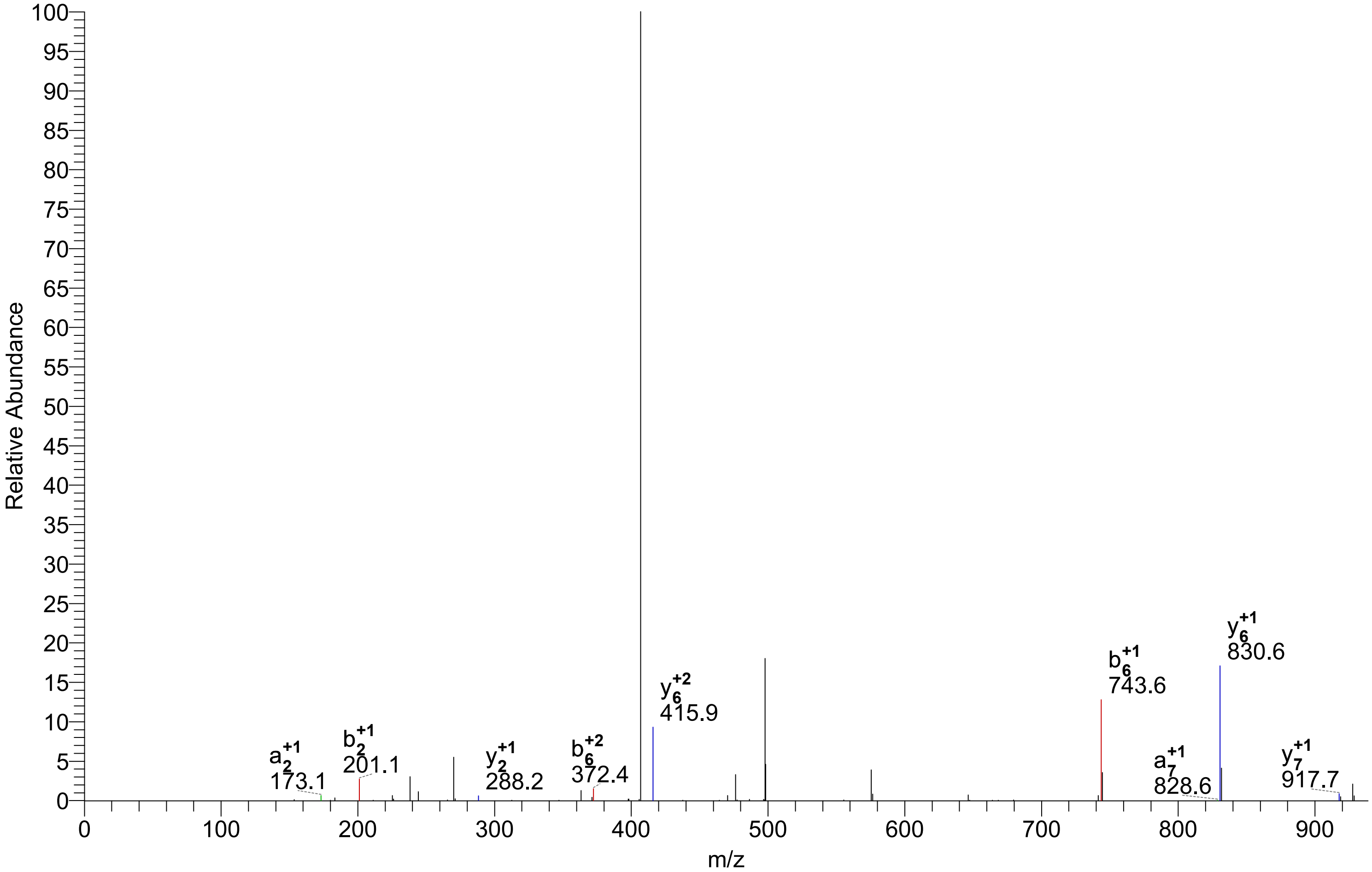
```
DTA for scans: 19287468-1
Precursor ion: 515.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                      917.50
 C    334.14     362.14                                      830.47
 P    431.20     459.19                                      669.45
 K    559.29     587.29                                      572.40
 R    715.39     743.39                                      444.30
 L    828.48     856.47                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 6.13E5



```
Reference                                                        P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z   P        XC  DeltaCn   Sp   RSp  Ions  Count

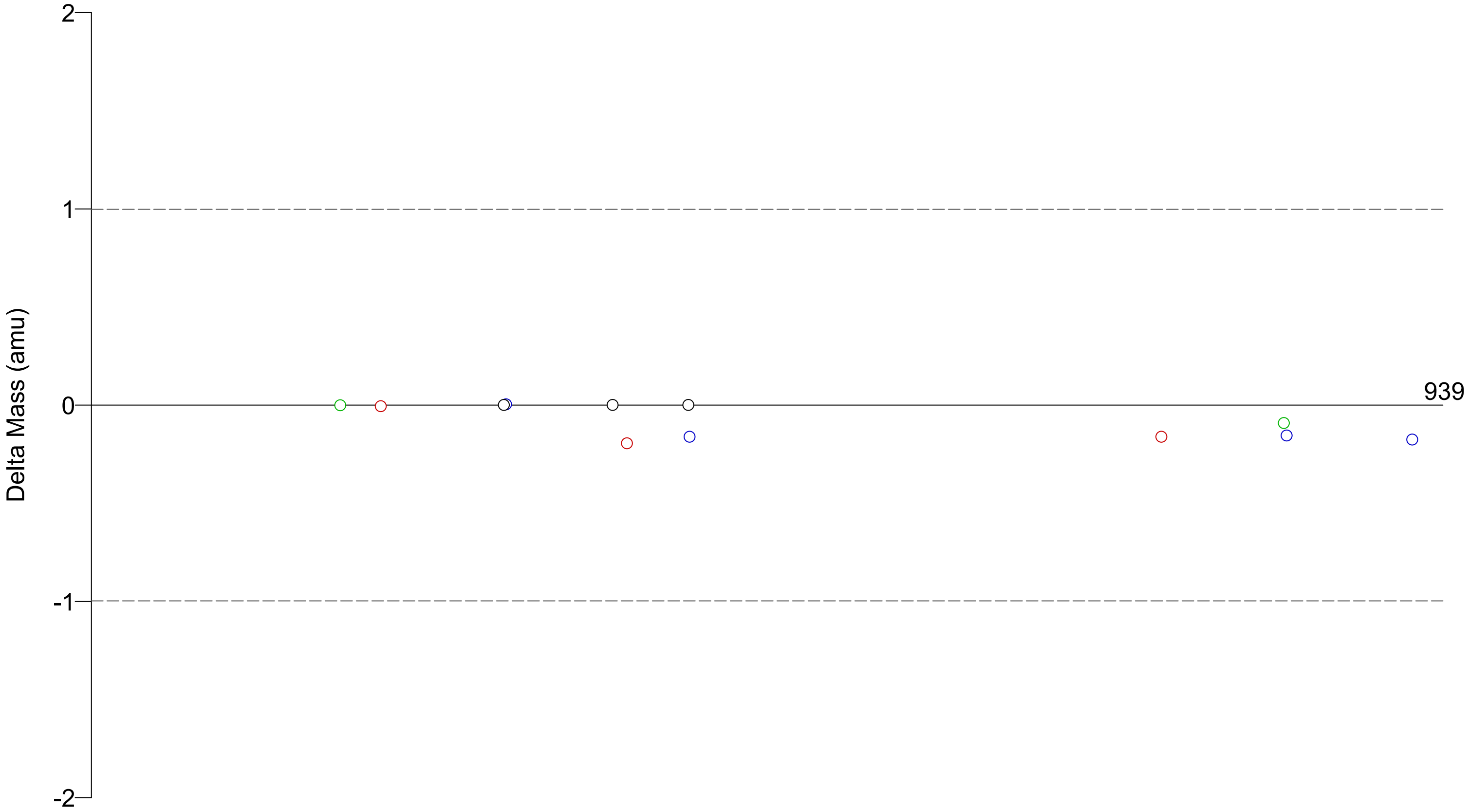
IPI:IPI00845229.1|SWISS-PROT:Q70Z3                            1       8.1      0.0       0
19287468 - 1  K.LSCPKRLR.L                         1030.58   2  0.9      1.753  0.426   105.7  3   9/21    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

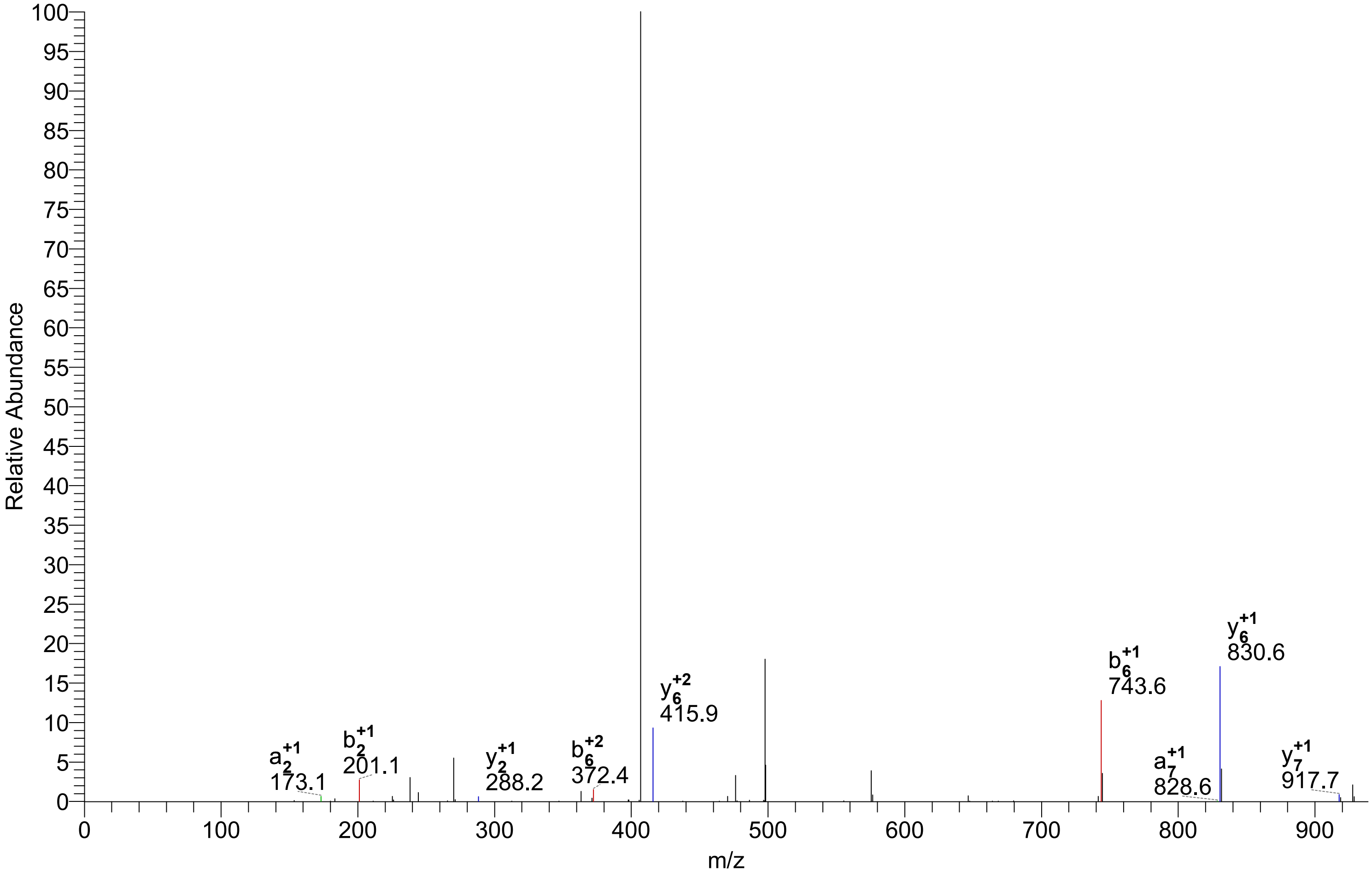
```
DTA for scans: 19287468-1
Precursor ion: 515.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 L     86.10     114.09
 S    173.13     201.12                                      917.50
 C    334.14     362.14                                      830.47
 P    431.20     459.19                                      669.45
 K    559.29     587.29                                      572.40
 R    715.39     743.39                                      444.30
 L    828.48     856.47                                      288.20
 R                                                           175.12
```



#19287468-1 NL: 6.13E5



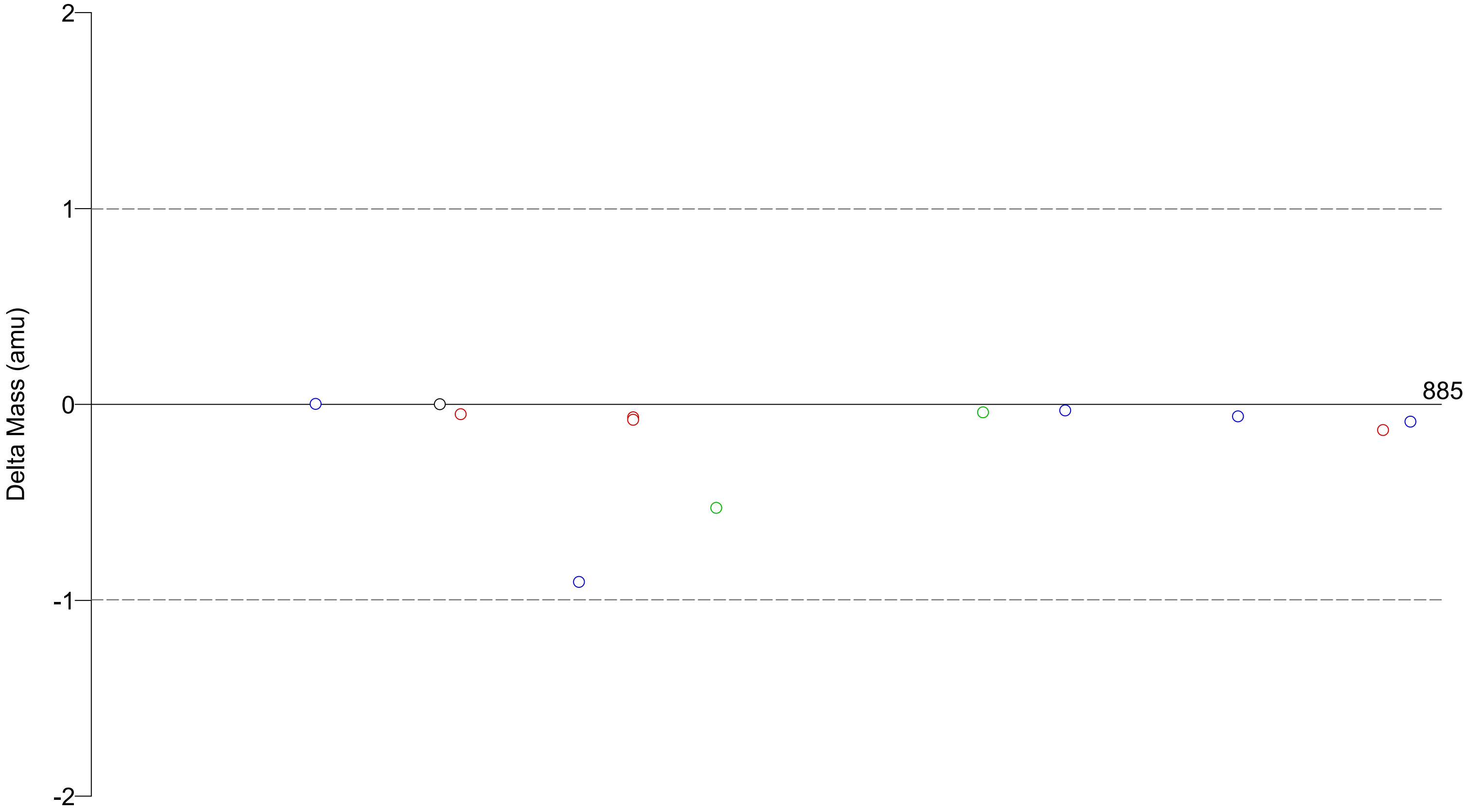
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z     P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00294519.2|SWISS-PROT:Q99973-1|ENSEMBL:ENSP00000262715|     1        8.1      0.0       0
19287468 - 1  R.QLLTRPHK.A                                992.60    2  0.8      1.747  0.306   184.8  5   8/21    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

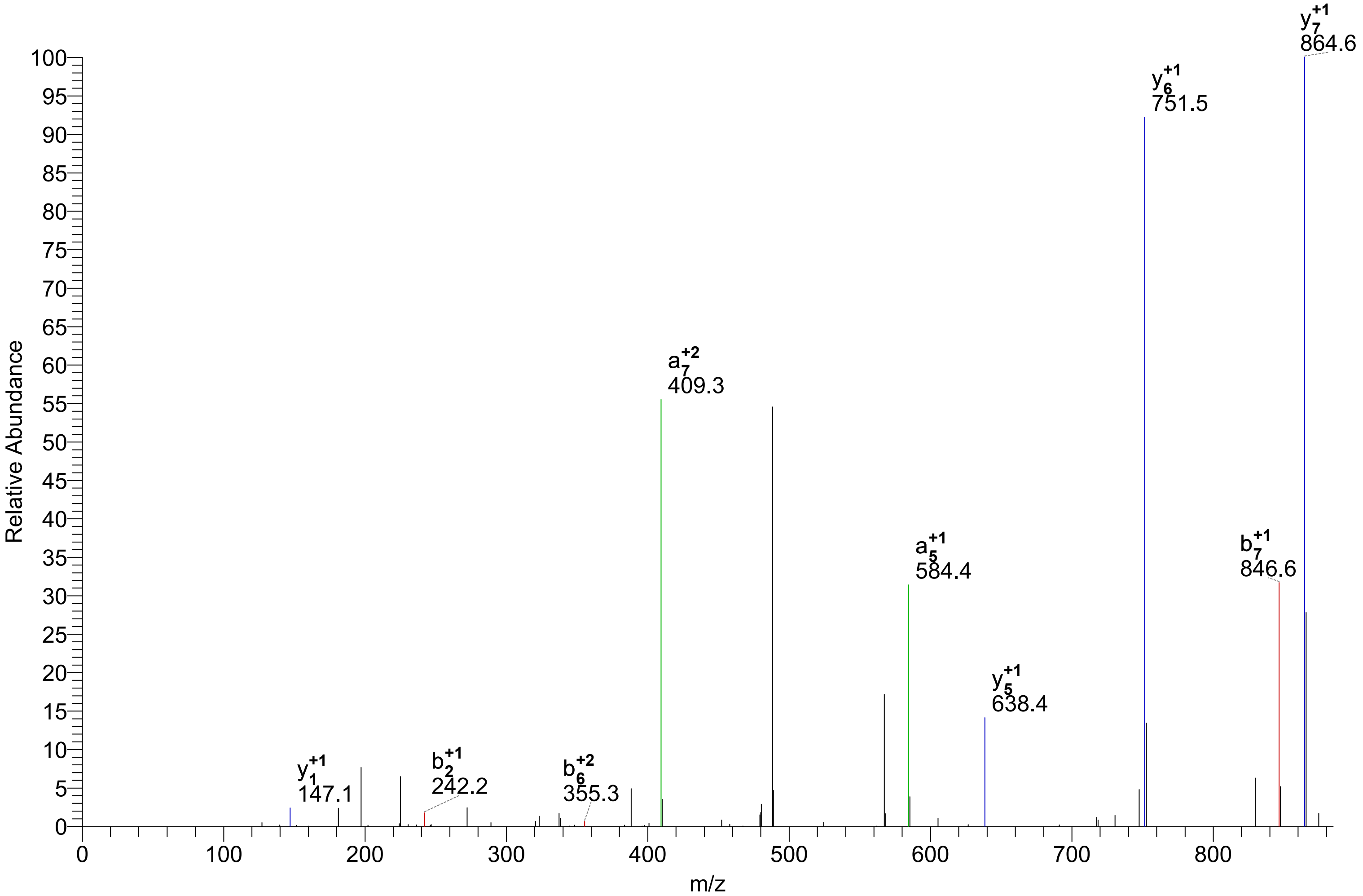
```
DTA for scans: 19287468-1
Precursor ion: 496.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 Q    101.07     129.07
 L    214.16     242.15                                      864.54
 L    327.24     355.23                                      751.46
 T    428.29     456.28                                      638.37
 R    584.39     612.38                                      537.33
 P    681.44     709.44                                      381.22
 H    818.50     846.49                                      284.17
 K                                                           147.11
```



#19287468-1 NL: 1.35E5



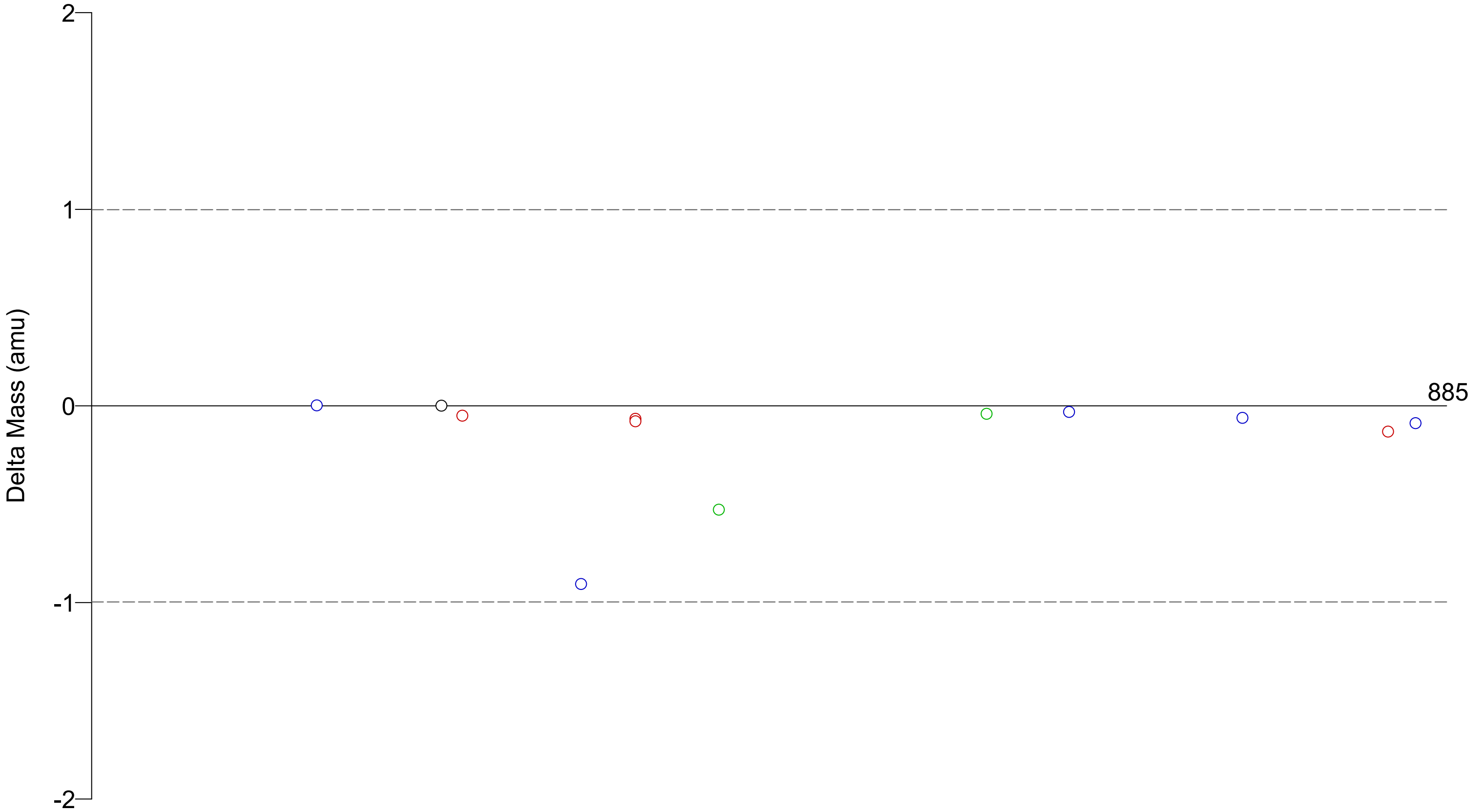
```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00413874.2|SWISS-PROT:Q9997                                   1       8.1      0.0       0
19287468 - 1  R.QLLTRPHK.A                              992.60     2  0.8      1.747  0.306   184.8  5   8/21    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

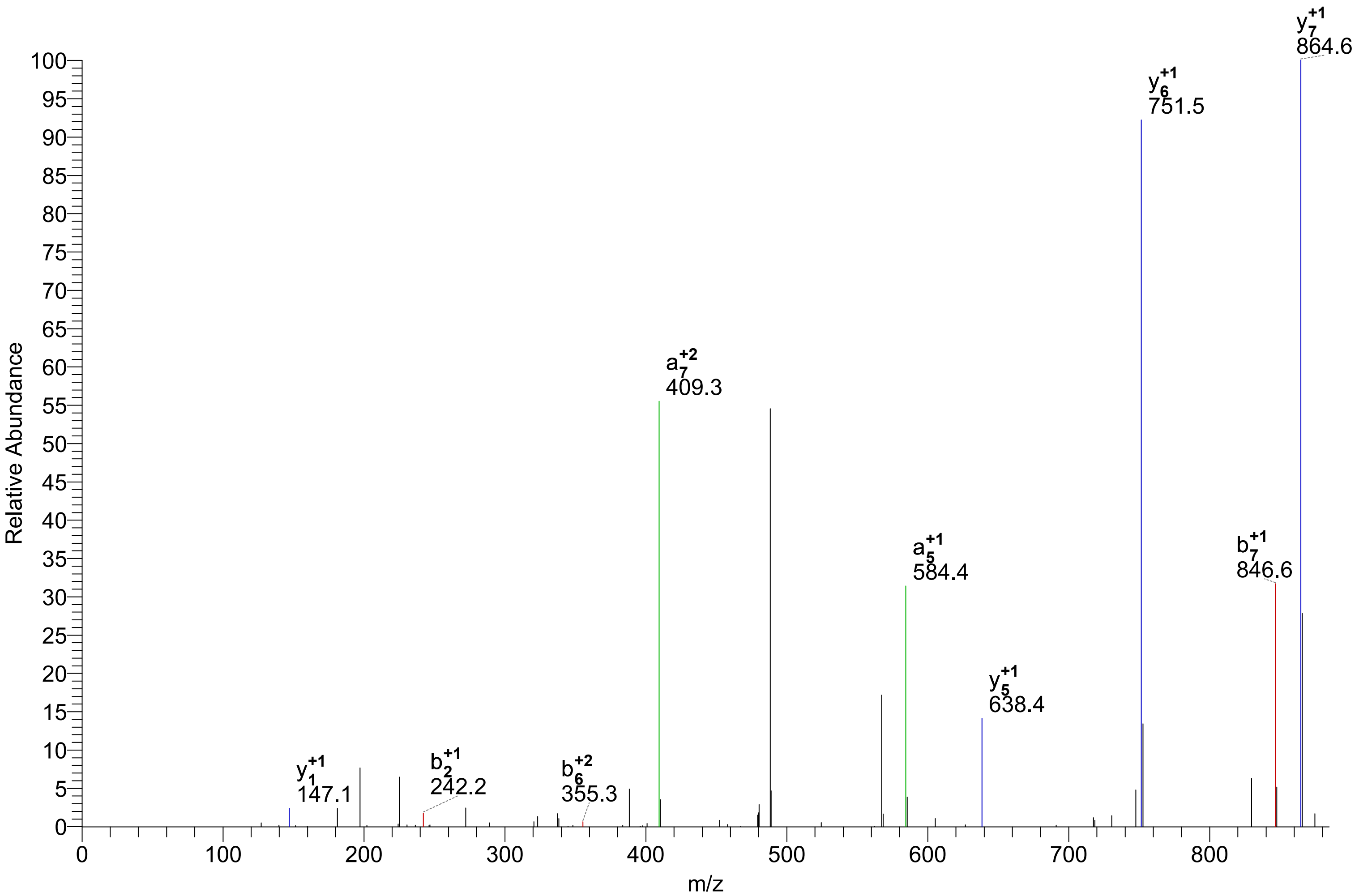
```
DTA for scans: 19287468-1
Precursor ion: 496.79
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 Q    101.07     129.07
 L    214.16     242.15                                      864.54
 L    327.24     355.23                                      751.46
 T    428.29     456.28                                      638.37
 R    584.39     612.38                                      537.33
 P    681.44     709.44                                      381.22
 H    818.50     846.49                                      284.17
 K                                                           147.11
```



#19287468-1 NL: 1.35E5



```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

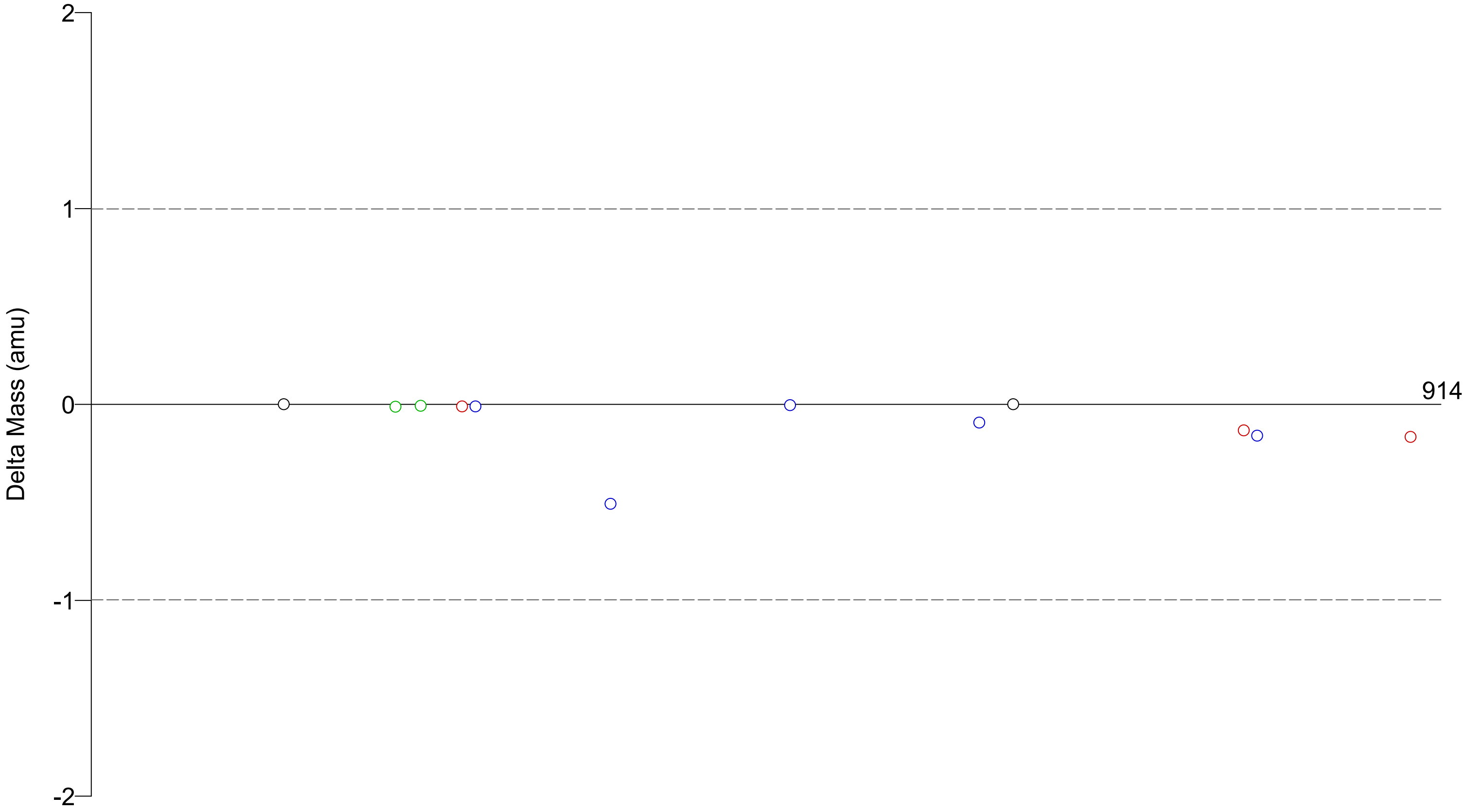
IPI:IPI00448364.1|TREMBL:Q6IEV0|H-INV:HIT000391565 Tax_Id=9606    1       8.1      0.0       0
2118291816 -  R.IHSTQGRIK.V                          1039.60   2  0.4      1.729  0.349   149.9  3   9/24

1 of 1 peptide matches reported, 0 removed due to filtering
```

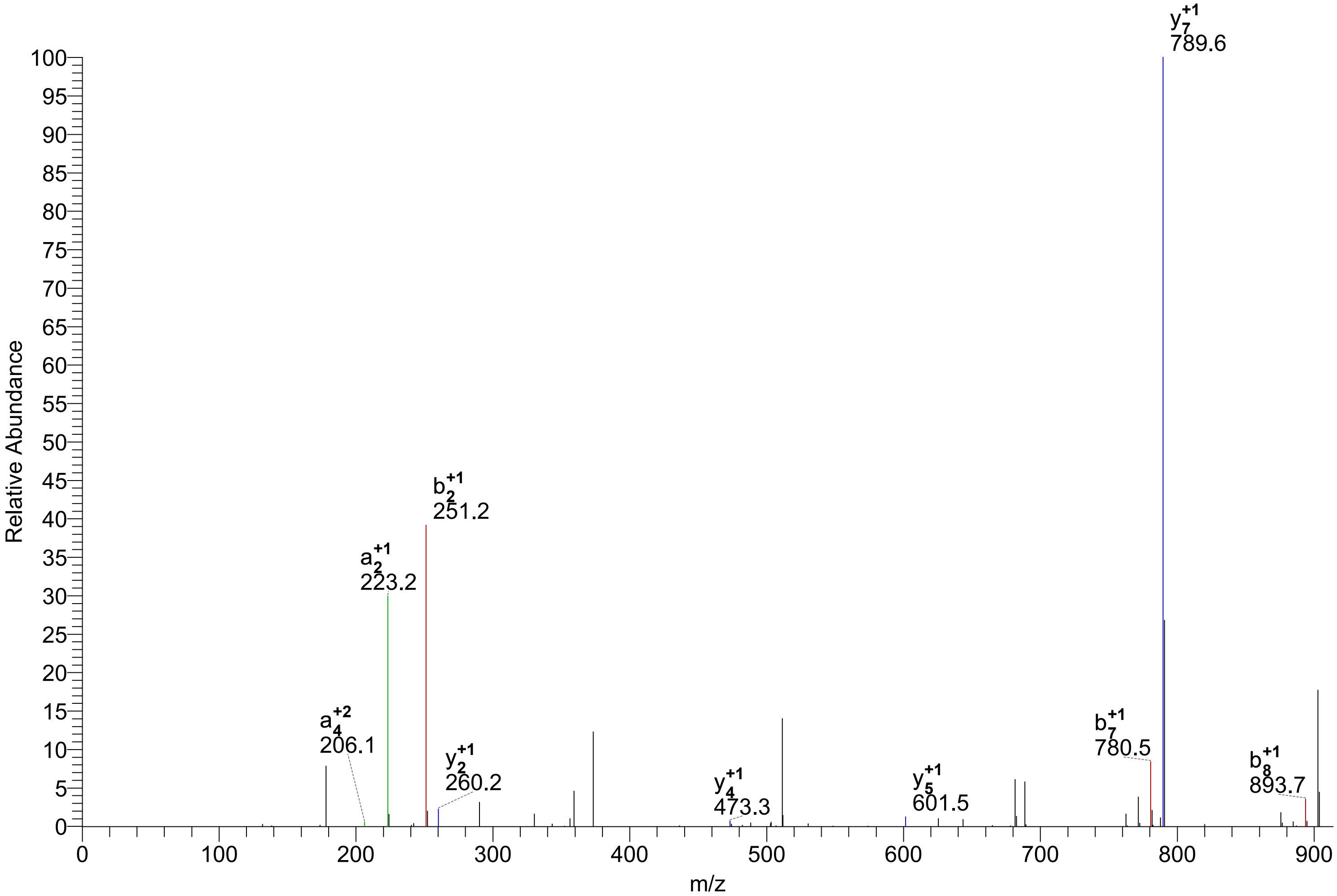
```
DTA for scans: 2118291816-26226248
Precursor ion: 520.31
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 I     86.10     114.09
 H    223.16     251.15                                        926.52
 S    310.19     338.18                                        789.46
 T    411.24     439.23                                        702.43
 Q    539.29     567.29                                        601.38
 G    596.32     624.31                                        473.32
 R    752.42     780.41                                        416.30
 I    865.50     893.50                                        260.20
 K                                                             147.11
```



#2118291816-26226248 NL: 1.52E5



```
Reference                                                              P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+       z   P        XC  DeltaCn   Sp   RSp  Ions  Count

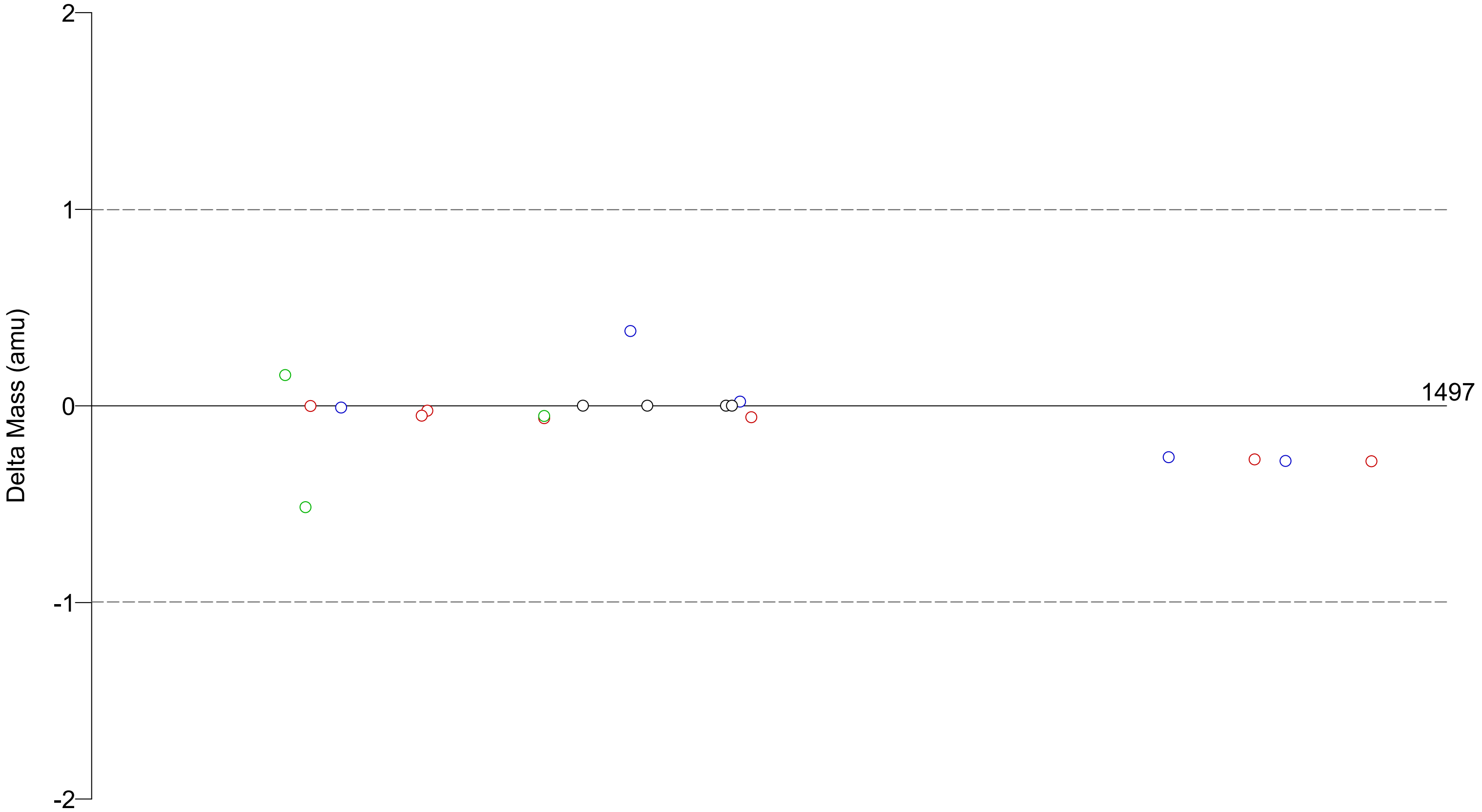
IPI:IPI00307200.9|SWISS-PROT:Q9UH65|TREMBL:B4E245|ENSEMBL:ENSP    1       8.1      0.0       0
19287468 - 1  K.KLEEAASRAAEEEK.K                         1560.79   2  1       1.699  0.383   106.1  4   9/39    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

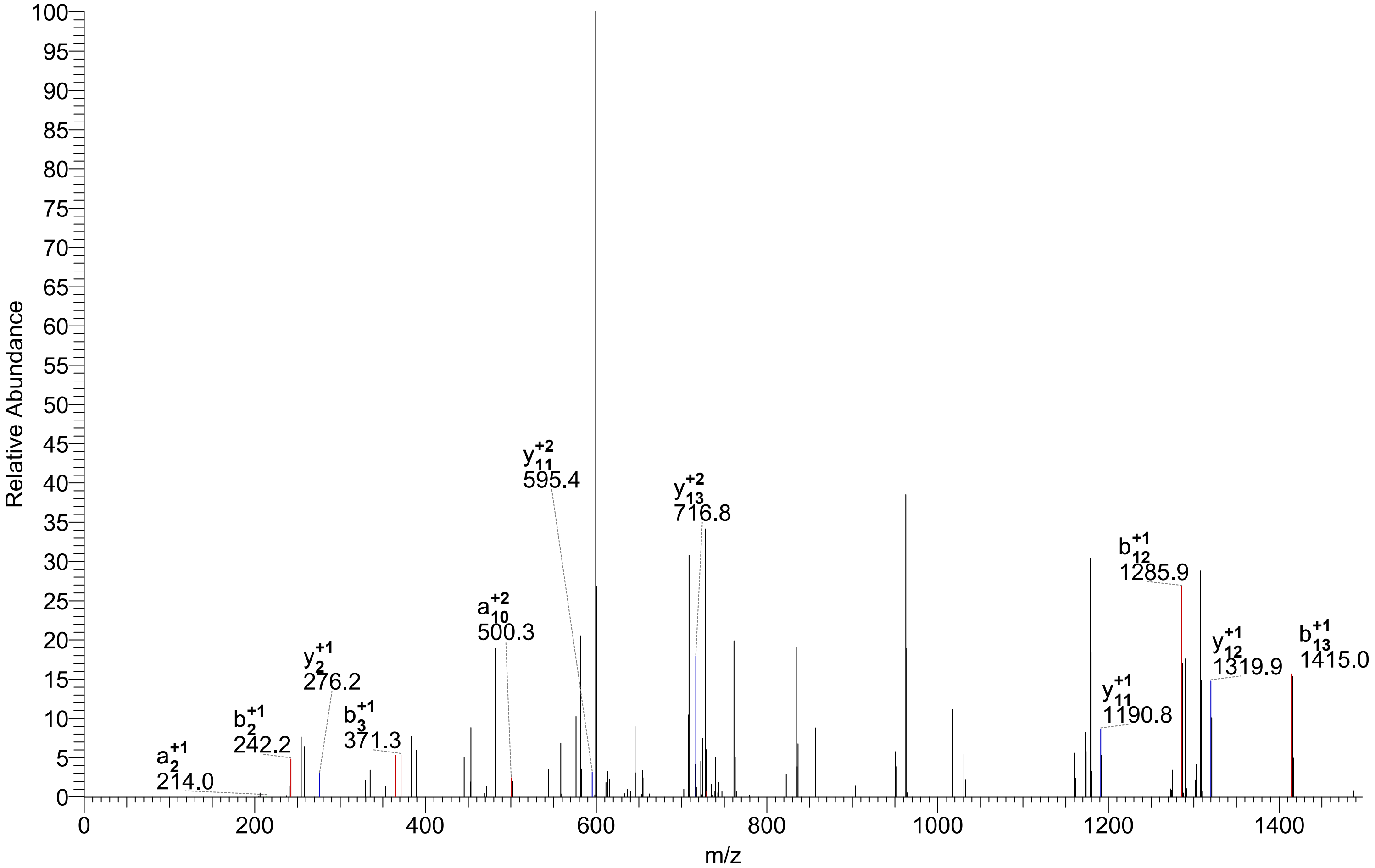
```
DTA for scans: 19287468-1
Precursor ion: 780.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 K    101.11     129.10
 L    214.19     242.19                                     1432.69
 E    343.23     371.23                                     1319.61
 E    472.28     500.27                                     1190.56
 A    543.31     571.31                                     1061.52
 A    614.35     642.35                                      990.49
 S    701.38     729.38                                      919.45
 R    857.48     885.48                                      832.42
 A    928.52     956.52                                      676.31
 A    999.56    1027.55                                      605.28
 E   1128.60    1156.60                                      534.24
 E   1257.64    1285.64                                      405.20
 E   1386.69    1414.68                                      276.16
 K                                                           147.11
```



#19287468-1 NL: 6.84E4



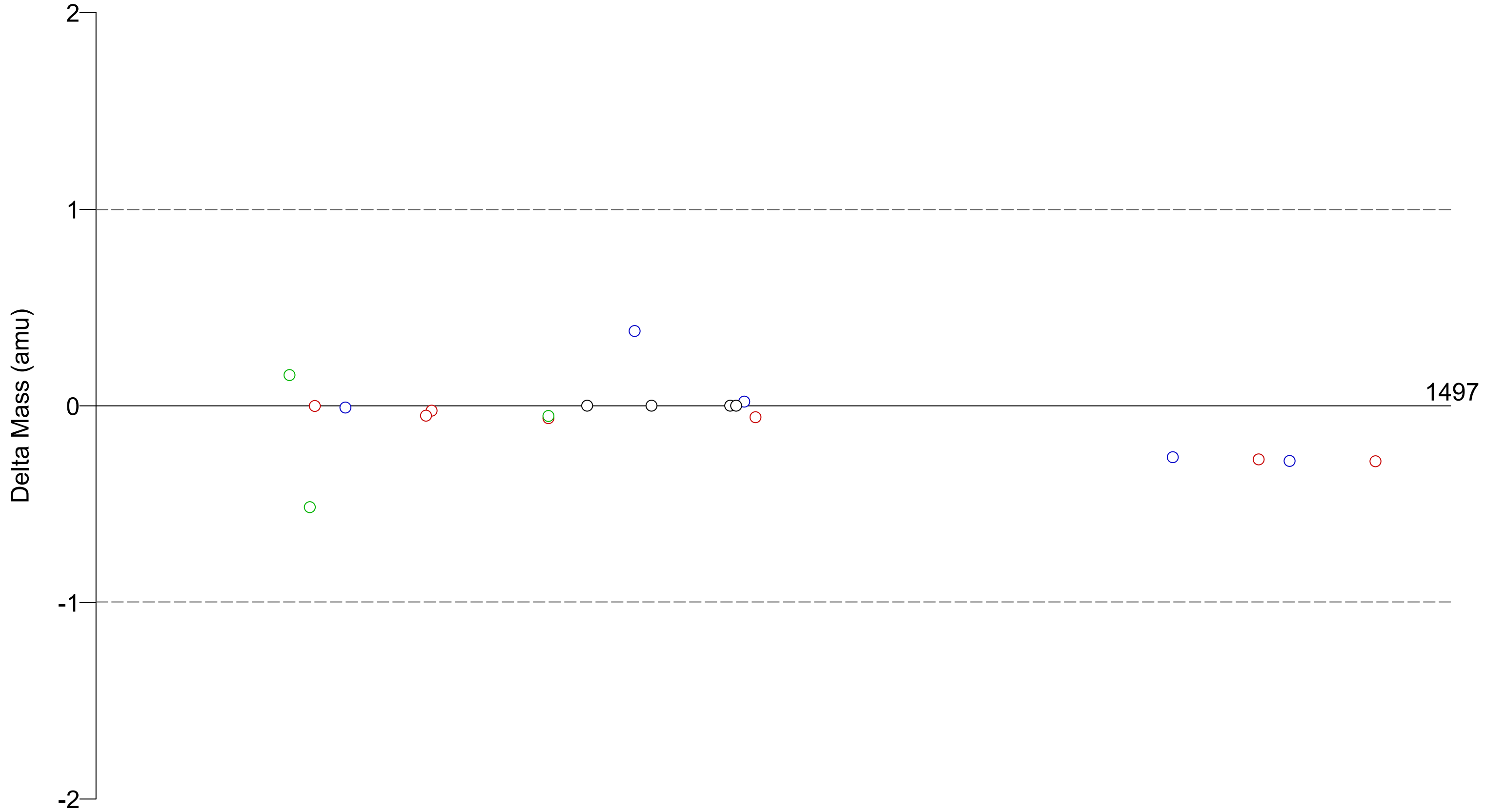
```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00903155.1|TREMBL:B3KUB9 Ta                                 1       8.1      0.0       0
19287468 - 1  K.KLEEAASRAAEEEK.K                        1560.79   2  1       1.699  0.383   106.1  4   9/39    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

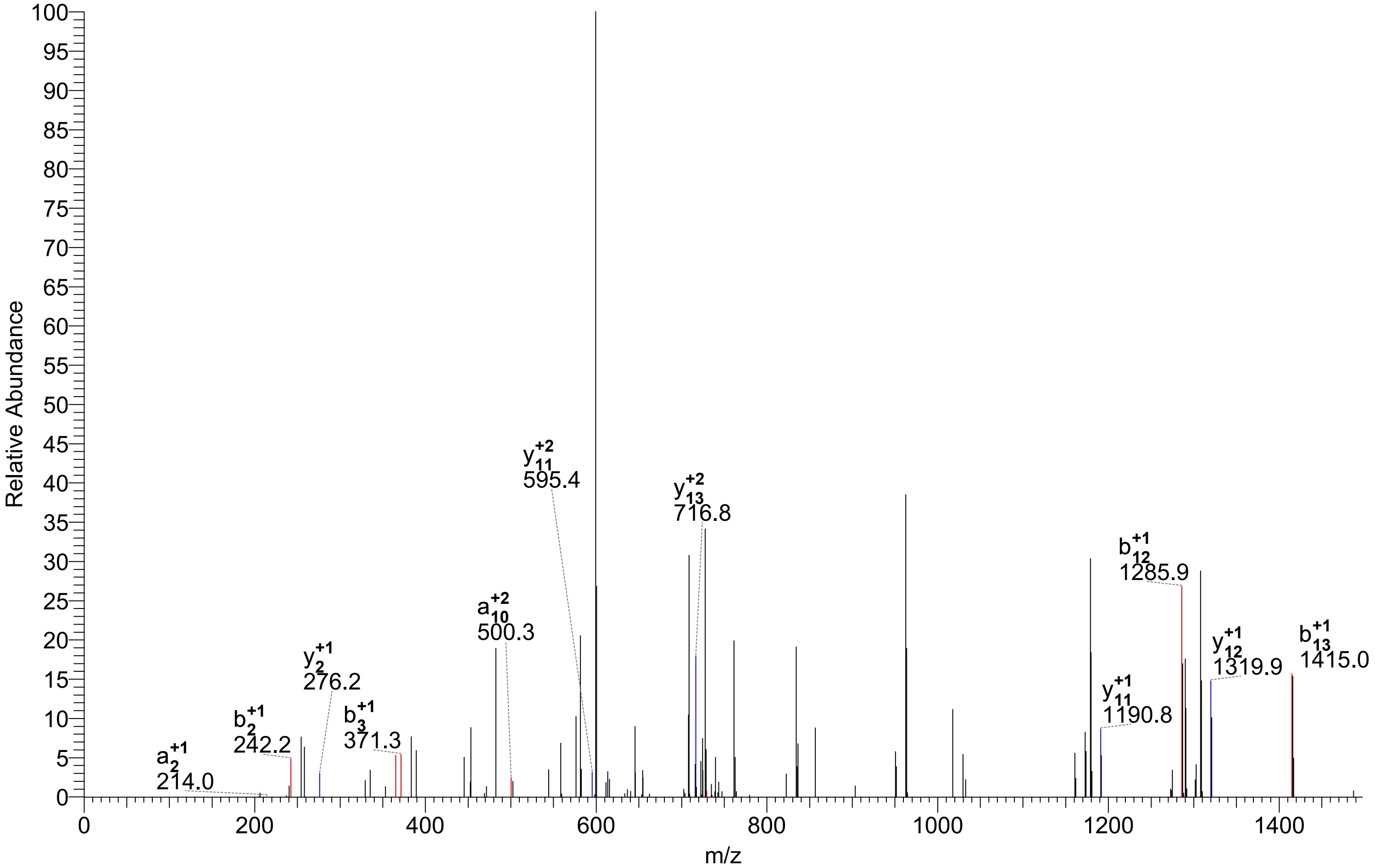
```
DTA for scans: 19287468-1
Precursor ion: 780.88
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 K    101.11     129.10
 L    214.19     242.19                                     1432.69
 E    343.23     371.23                                     1319.61
 E    472.28     500.27                                     1190.56
 A    543.31     571.31                                     1061.52
 A    614.35     642.35                                      990.49
 S    701.38     729.38                                      919.45
 R    857.48     885.48                                      832.42
 A    928.52     956.52                                      676.31
 A    999.56    1027.55                                      605.28
 E   1128.60    1156.60                                      534.24
 E   1257.64    1285.64                                      405.20
 E   1386.69    1414.68                                      276.16
 K                                                           147.11
```



#19287468-1 NL: 6.84E4



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                       MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

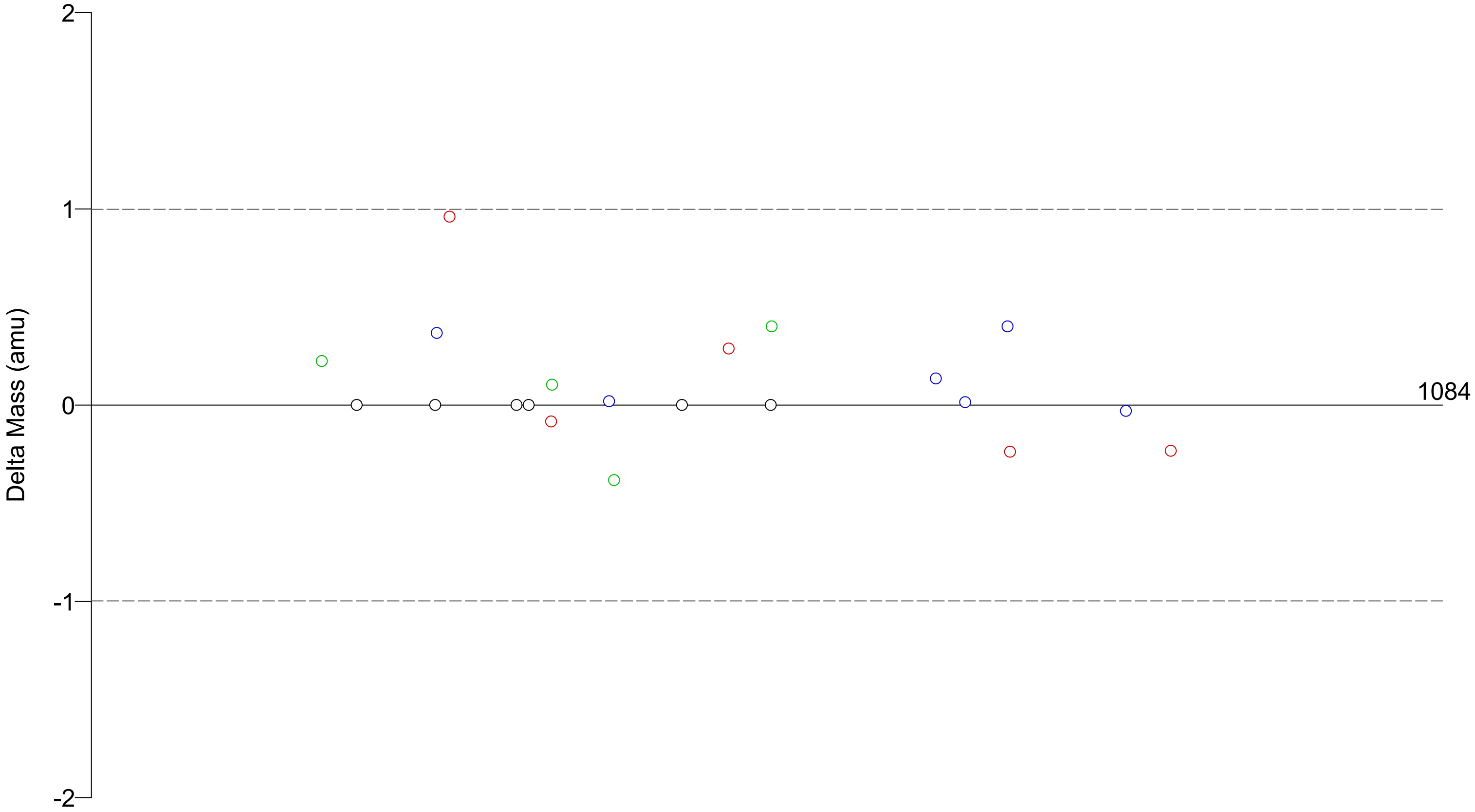
IPI:IPI00022963.3|SWISS-PROT:O95926|TREMBL:B2RBX8;B4E0Y8|ENSEM     1       8.1      0.0       0
2118291816 -  K.PDMETYERLREK.H                             1566.76   3  0.5      1.657  0.583   147.7  12  14/66   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

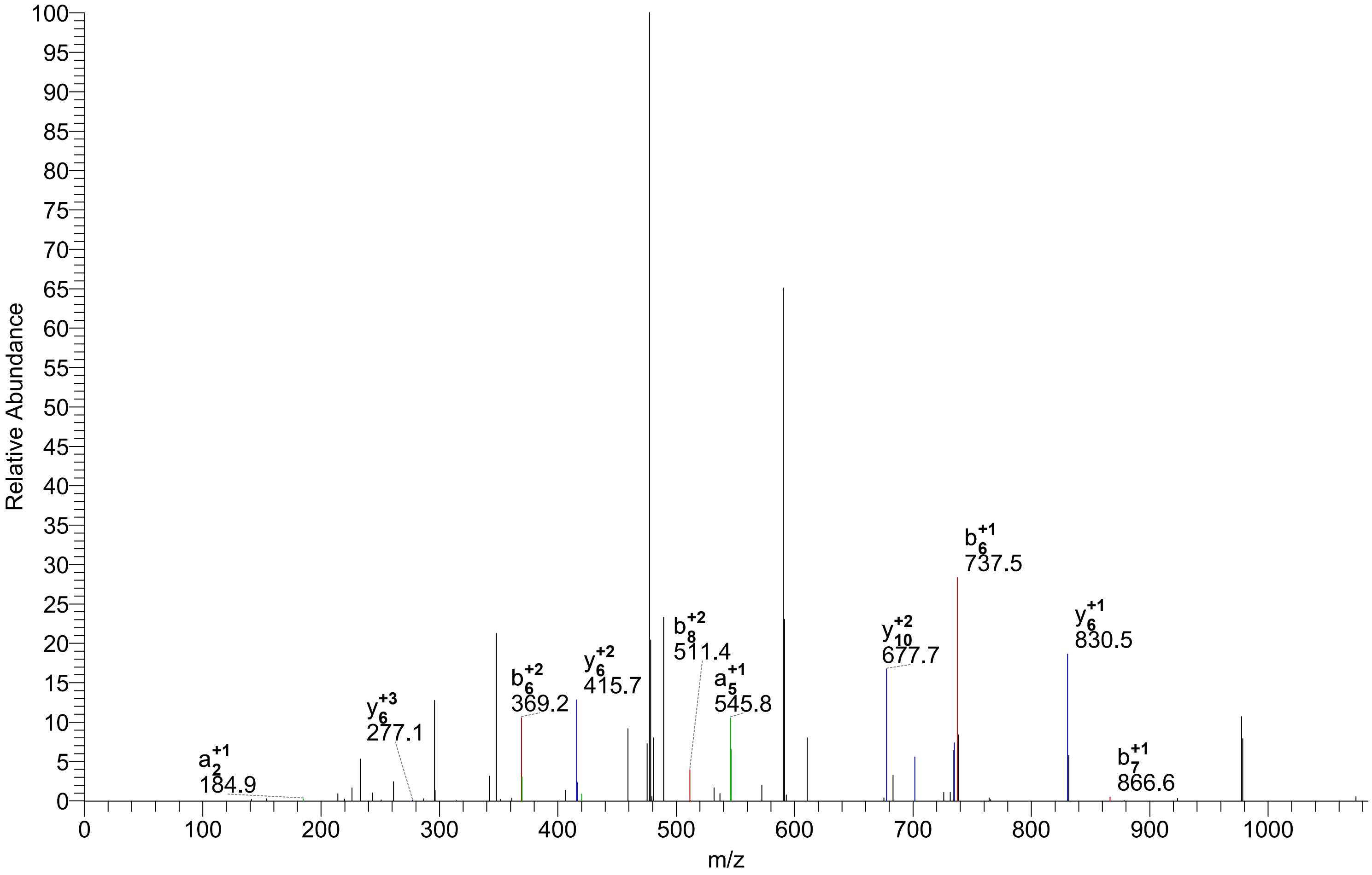
```
DTA for scans: 2118291816-26226248
Precursor ion: 522.91
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 P     70.07      98.06
 D    185.09     213.09                                     1469.71
 M    316.13     344.13                                     1354.68
 E    445.18     473.17                                     1223.64
 T    546.22     574.22                                     1094.60
 Y    709.29     737.28                                      993.55
 E    838.33     866.32                                      830.48
 R    994.43    1022.42                                      701.44
 L   1107.51    1135.51                                      545.34
 R   1263.62    1291.61                                      432.26
 E   1392.66    1420.65                                      276.16
 K                                                           147.11
```



#2118291816-26226248 NL: 8.32E4



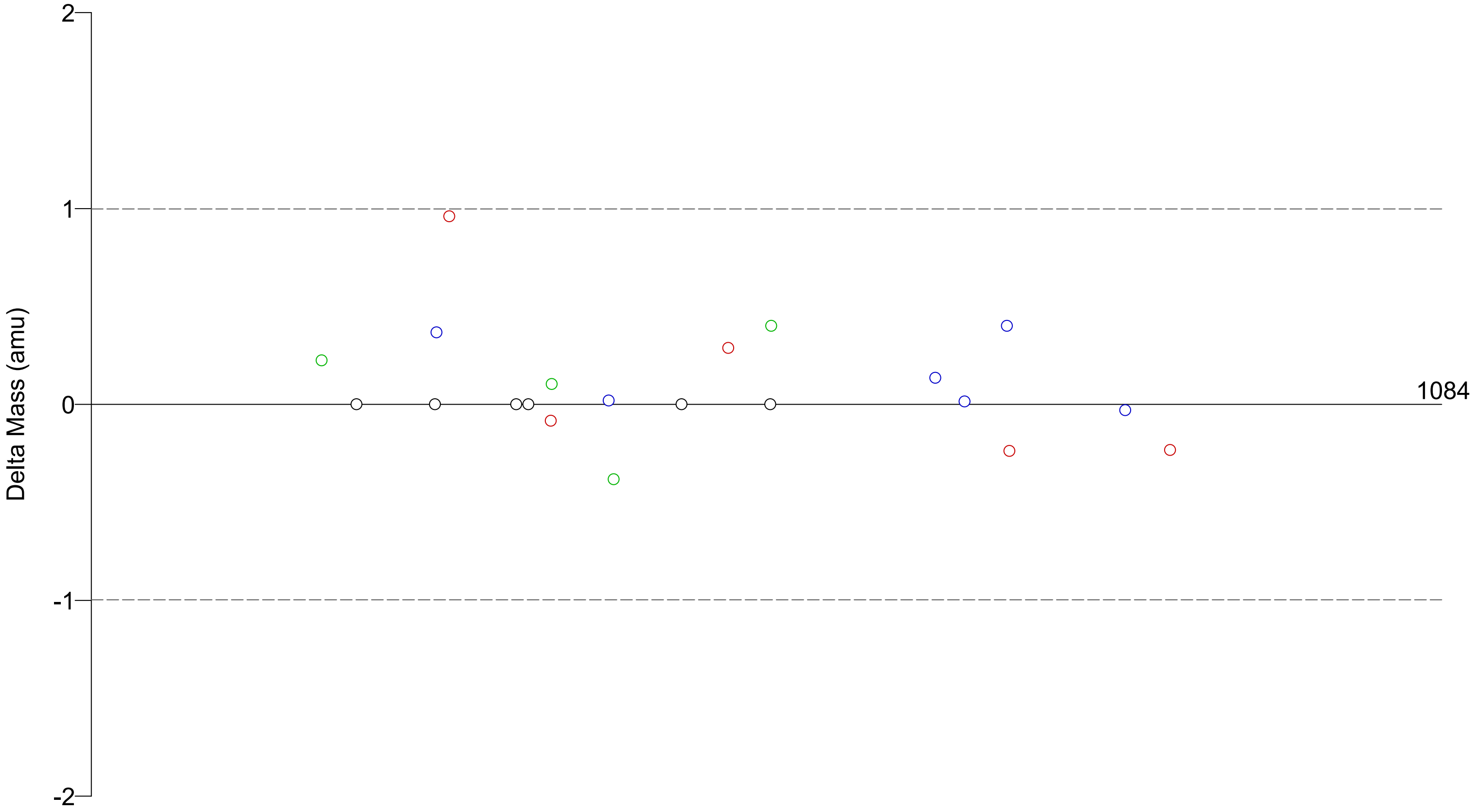
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00410388.1|ENSEMBL:ENSP0000                                1       8.1      0.0       0
2118291816 -  K.PDMETYERLREK.H                       1566.76   3  0.5     1.657  0.583   147.7  12  14/66   1

1 of 1 peptide matches reported, 0 removed due to filtering
```

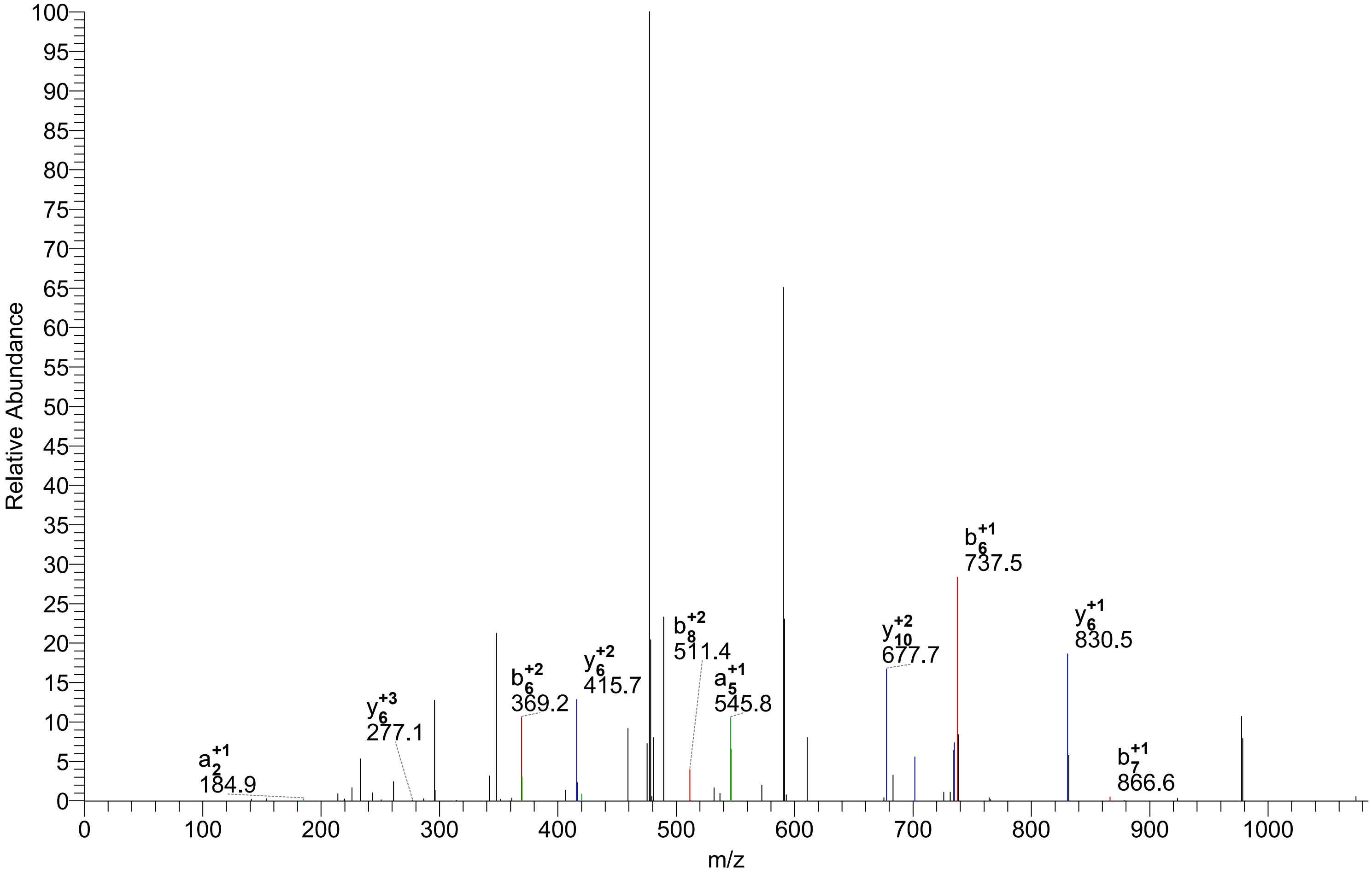
```
DTA for scans: 2118291816-26226248
Precursor ion: 522.91
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 P     70.07      98.06
 D    185.09     213.09                                     1469.71
 M    316.13     344.13                                     1354.68
 E    445.18     473.17                                     1223.64
 T    546.22     574.22                                     1094.60
 Y    709.29     737.28                                      993.55
 E    838.33     866.32                                      830.48
 R    994.43    1022.42                                      701.44
 L   1107.51    1135.51                                      545.34
 R   1263.62    1291.61                                      432.26
 E   1392.66    1420.65                                      276.16
 K                                                           147.11
```



#2118291816-26226248 NL: 8.32E4



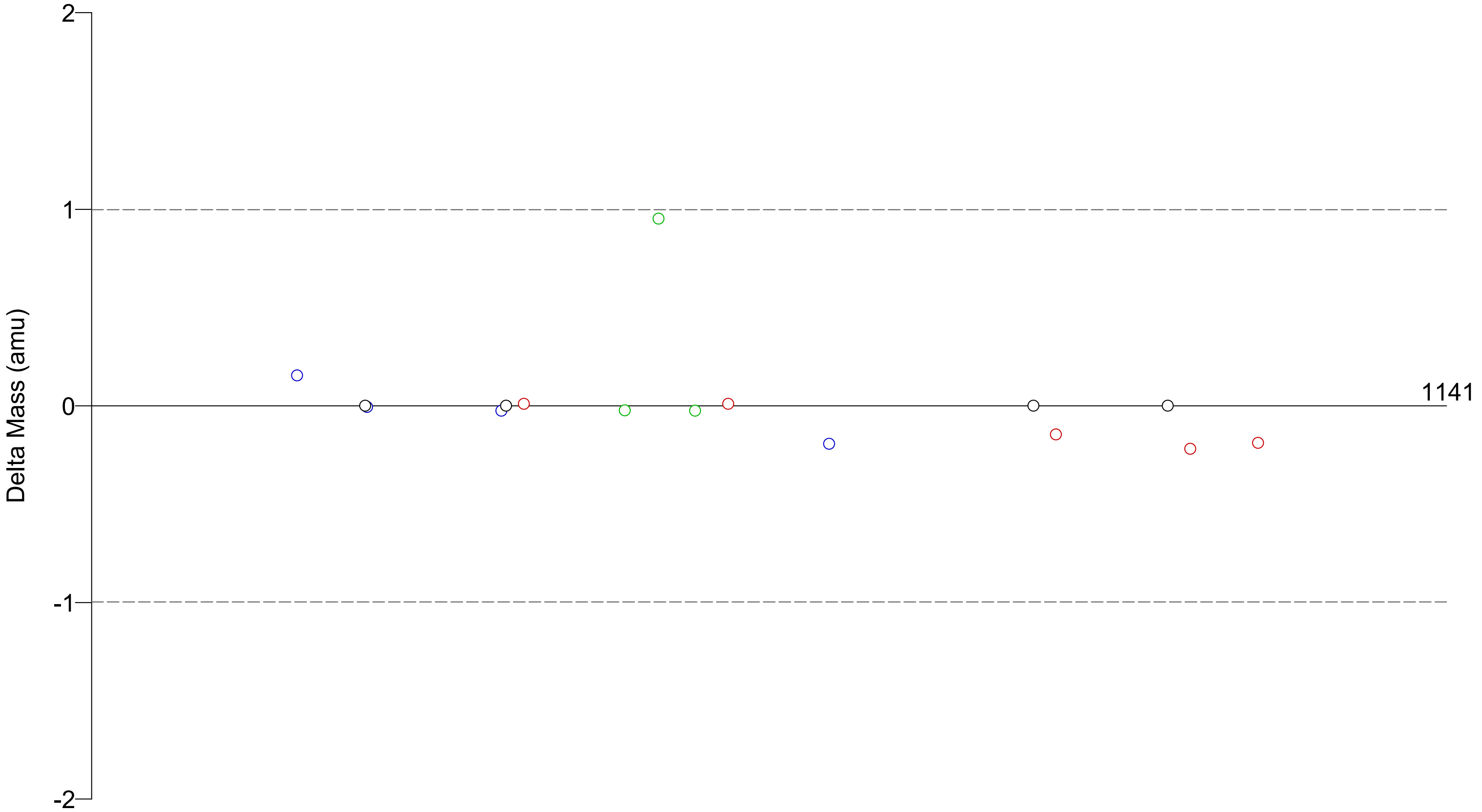
```
Reference                                                           P      Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P        XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00929282.1|H-INV:HIT000046184 Tax_Id=9606 Gene_Symbol=N    1       8.1      0.0       0
19287468 - 1  R.HLLATCDLGR.S                         1156.58   2  0.6      1.635  0.619   232.9  3   11/27

1 of 1 peptide matches reported, 0 removed due to filtering
```

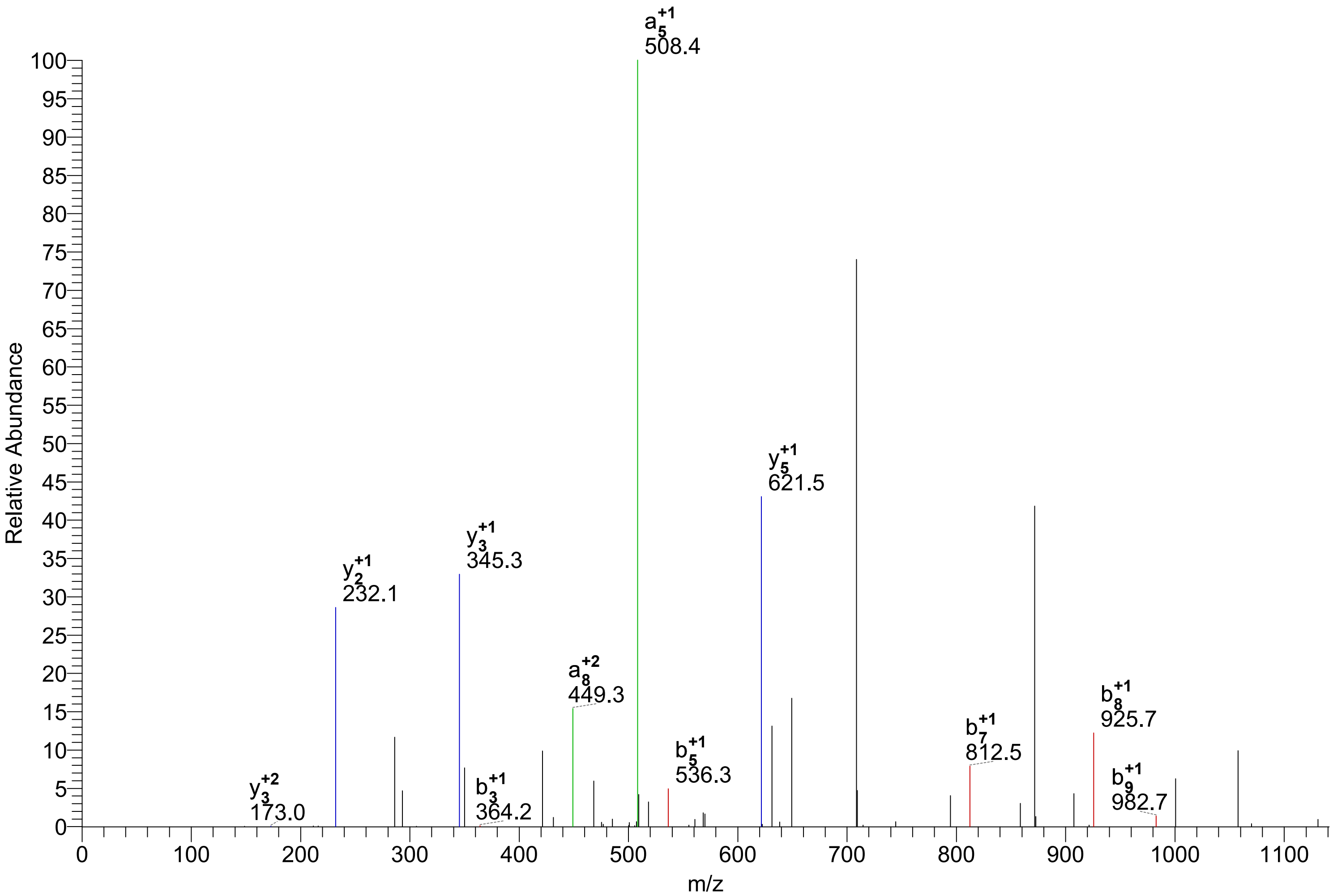
```
DTA for scans: 19287468-1
Precursor ion: 578.80
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 H    110.07     138.07
 L    223.16     251.15                                     1019.52
 L    336.24     364.23                                      906.43
 A    407.28     435.27                                      793.35
 T    508.32     536.32                                      722.31
 C    669.34     697.33                                      621.27
 D    784.37     812.36                                      460.25
 L    897.45     925.44                                      345.22
 G    954.47     982.47                                      232.14
 R                                                           175.12
```



#19287468-1 NL: 1.83E5



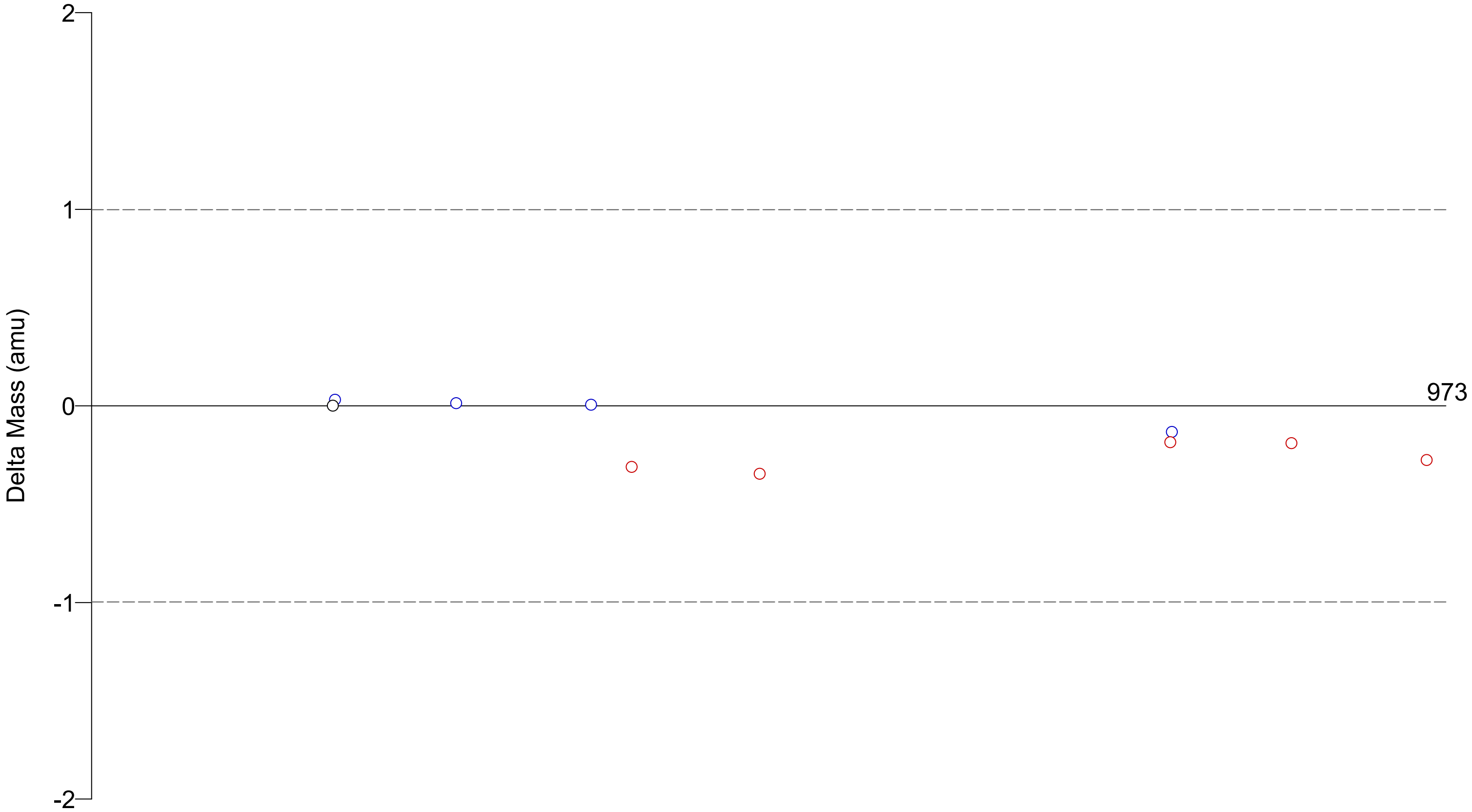
```
Reference                                                      P      Score   Coverage   Accession
Scan(s)       Sequence                               MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00937649.1|REFSEQ:XP_002343712 Tax_Id=9606 Gene_Symbol=    1       8.1      0.0       0
19287468 - 1  R.GSQTARSSSPSR.A                      1220.60   2  0.6      1.630  0.445   83.5   9   8/33

1 of 1 peptide matches reported, 0 removed due to filtering
```

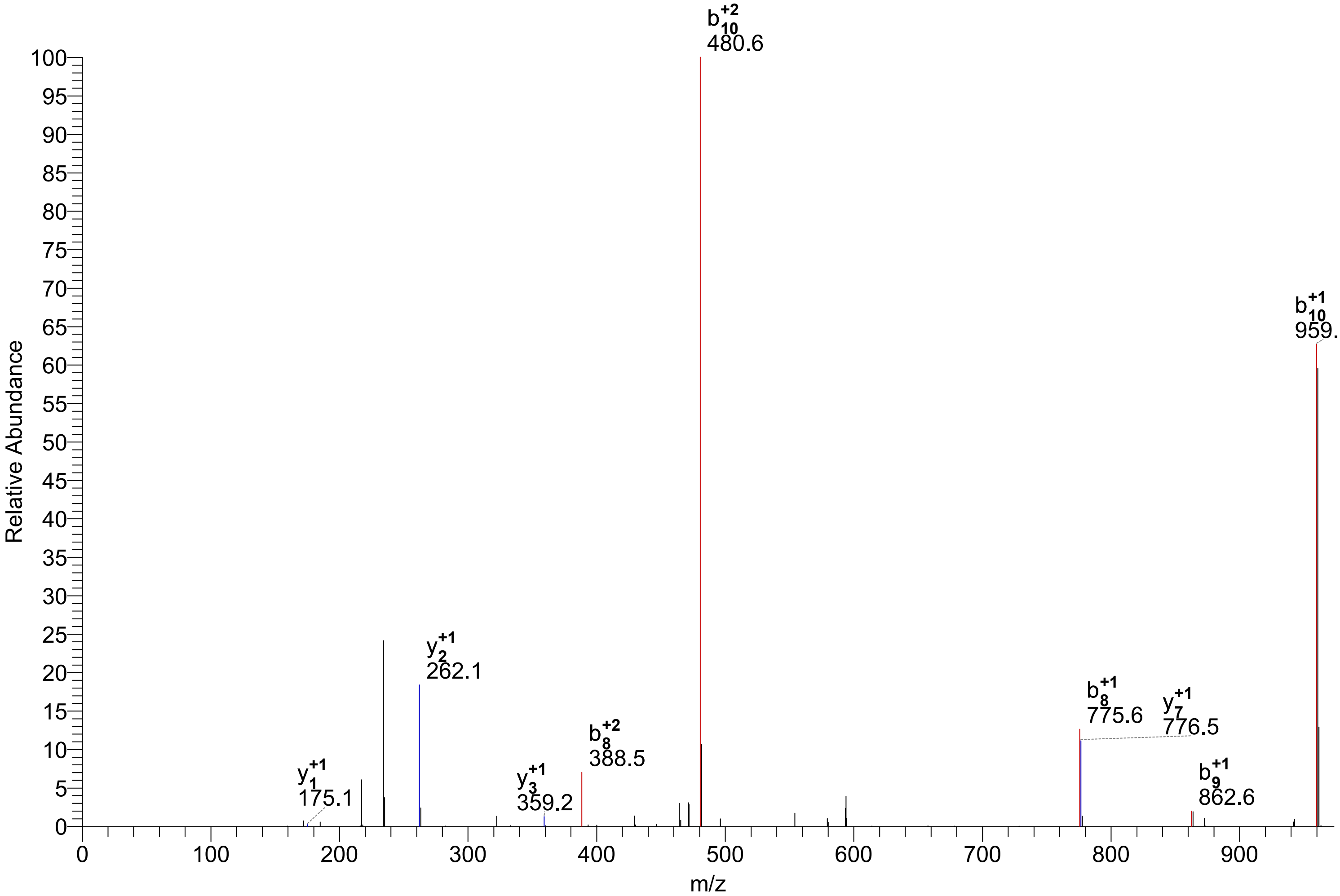
```
DTA for scans: 19287468-1
Precursor ion: 610.81
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 G     30.03      58.03
 S    117.07     145.06                                     1163.58
 Q    245.12     273.12                                     1076.54
 T    346.17     374.17                                      948.49
 A    417.21     445.20                                      847.44
 R    573.31     601.31                                      776.40
 S    660.34     688.34                                      620.30
 S    747.37     775.37                                      533.27
 S    834.41     862.40                                      446.24
 P    931.46     959.45                                      359.20
 S   1018.49    1046.49                                      262.15
 R                                                           175.12
```



#19287468-1 NL: 1.83E6



```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+      z    P        XC  DeltaCn   Sp   RSp  Ions  Count

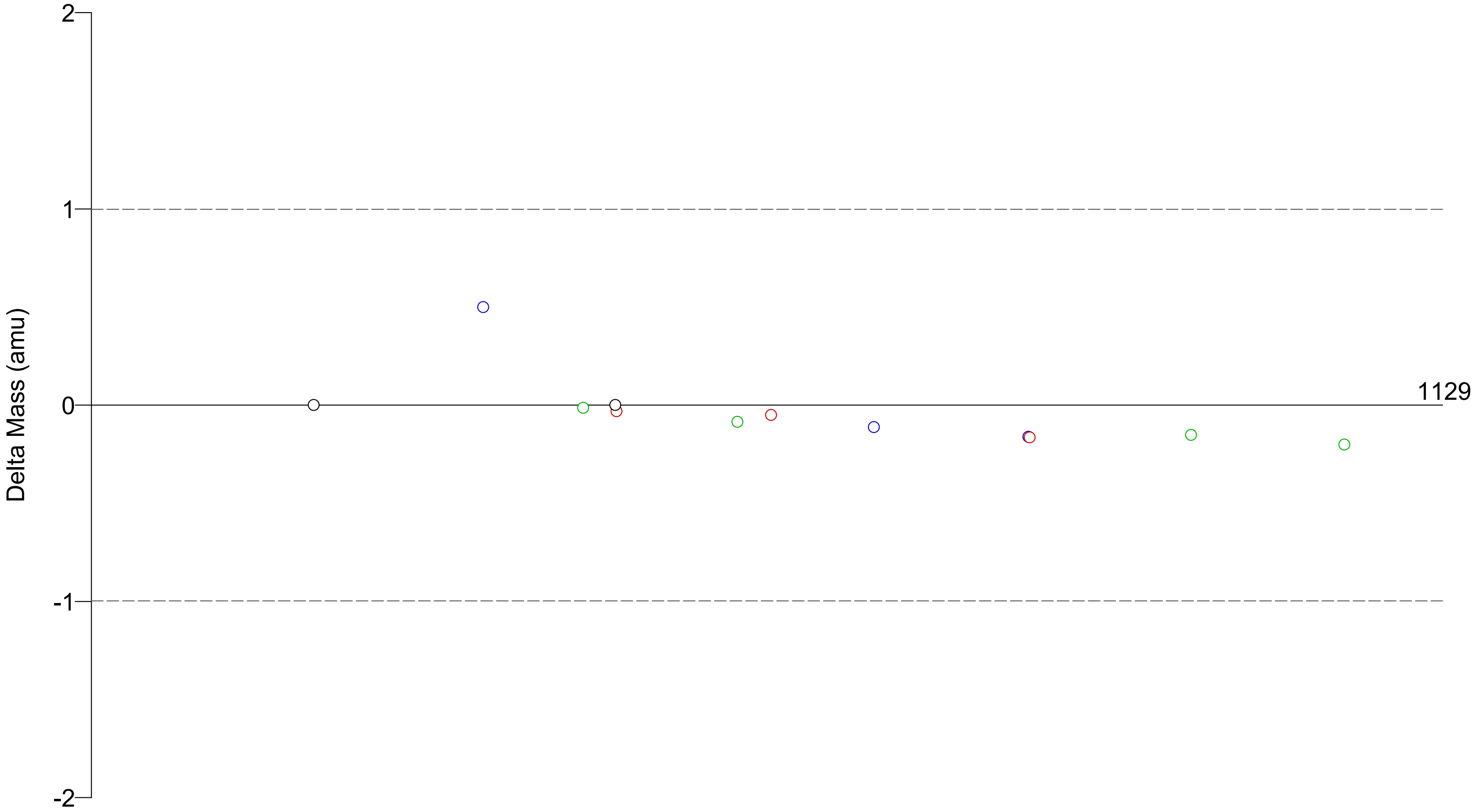
IPI:IPI00016604.1|SWISS-PROT:Q07343-1|TREMBL:Q5TEK6|ENSEMBL:EN     1       8.1      0.0       0
19682592 - 21 R.VNPQEESYQK.L                             1221.57   2  0.8     1.486  0.615   103.8  3   9/27    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

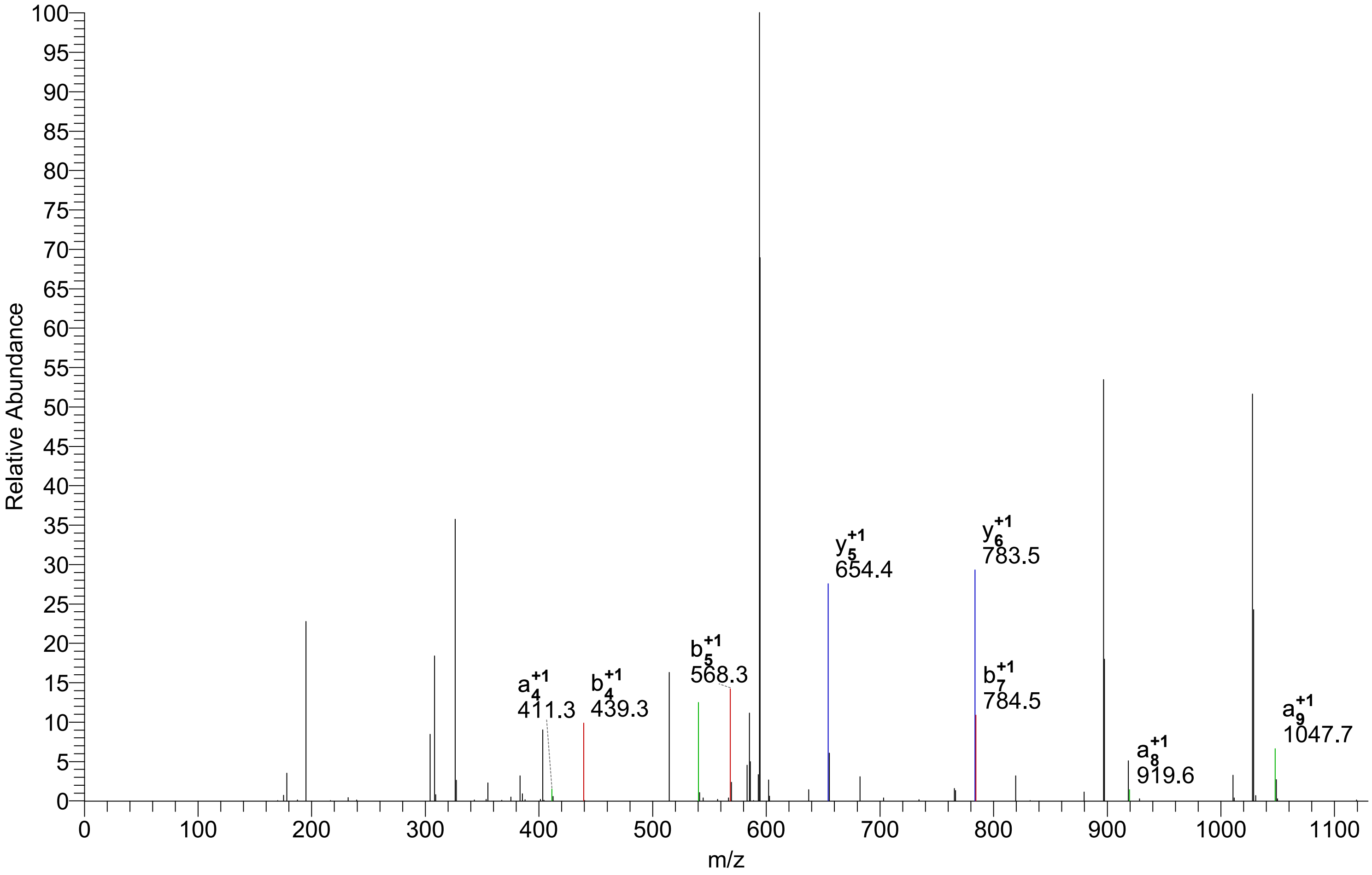
```
DTA for scans: 19682592-2147340288
Precursor ion: 611.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 V     72.08     100.08
 N    186.12     214.12                                      1122.51
 P    283.18     311.17                                      1008.46
 Q    411.24     439.23                                       911.41
 E    540.28     568.27                                       783.35
 E    669.32     697.32                                       654.31
 S    756.35     784.35                                       525.27
 Y    919.42     947.41                                       438.23
 Q   1047.47    1075.47                                       275.17
 K                                                            147.11
```



#19682592-2147340288 NL: 8.78E4



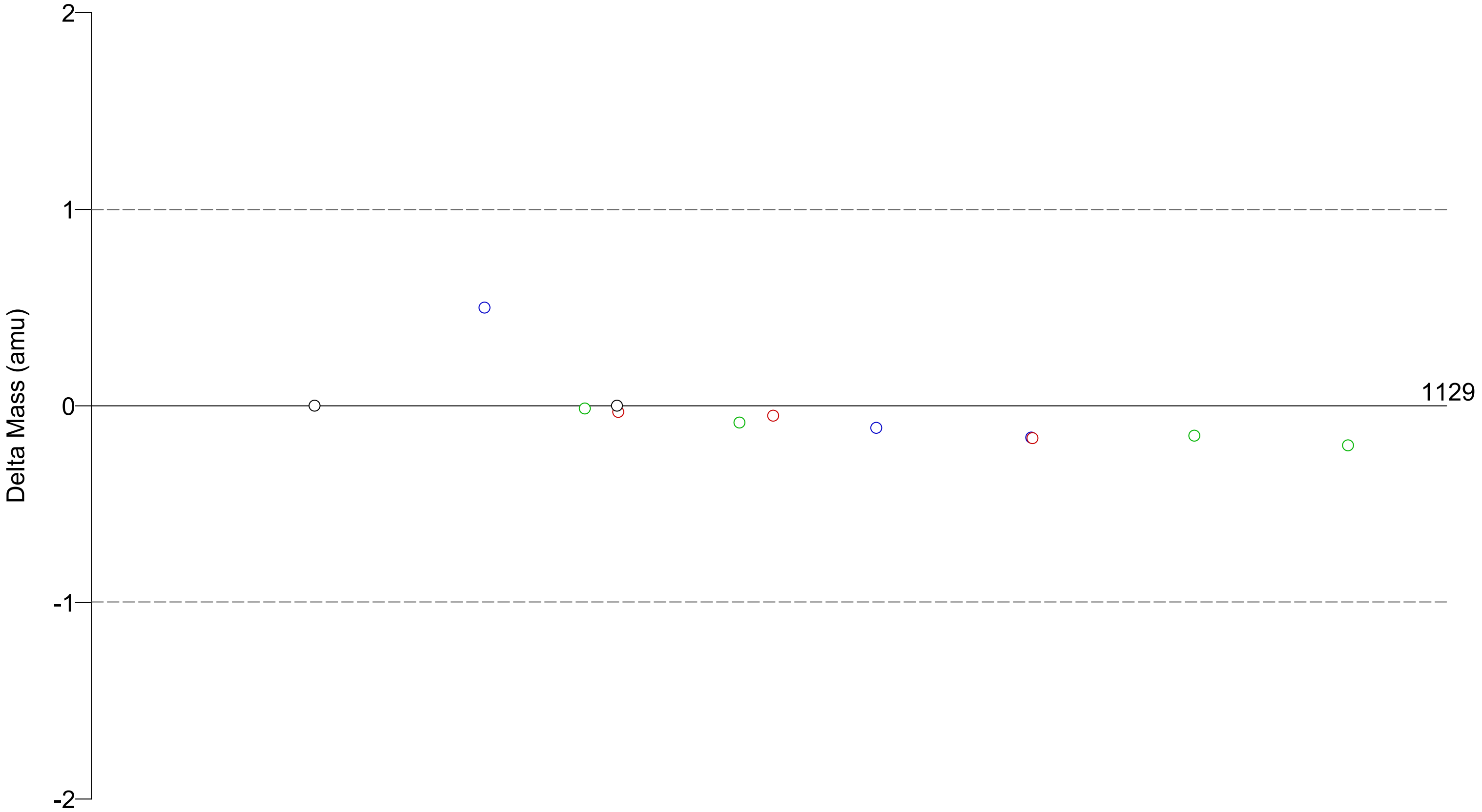
```
Reference                                                                    P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+       z      P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00220621.1|SWISS-PROT:Q0734                                         1        8.1       0.0        0
19682592 - 21 R.VNPQEESYQK.L                              1221.57    2   0.8      1.486  0.615   103.8  3    9/27    1

1 of 1 peptide matches reported, 0 removed due to filtering
```

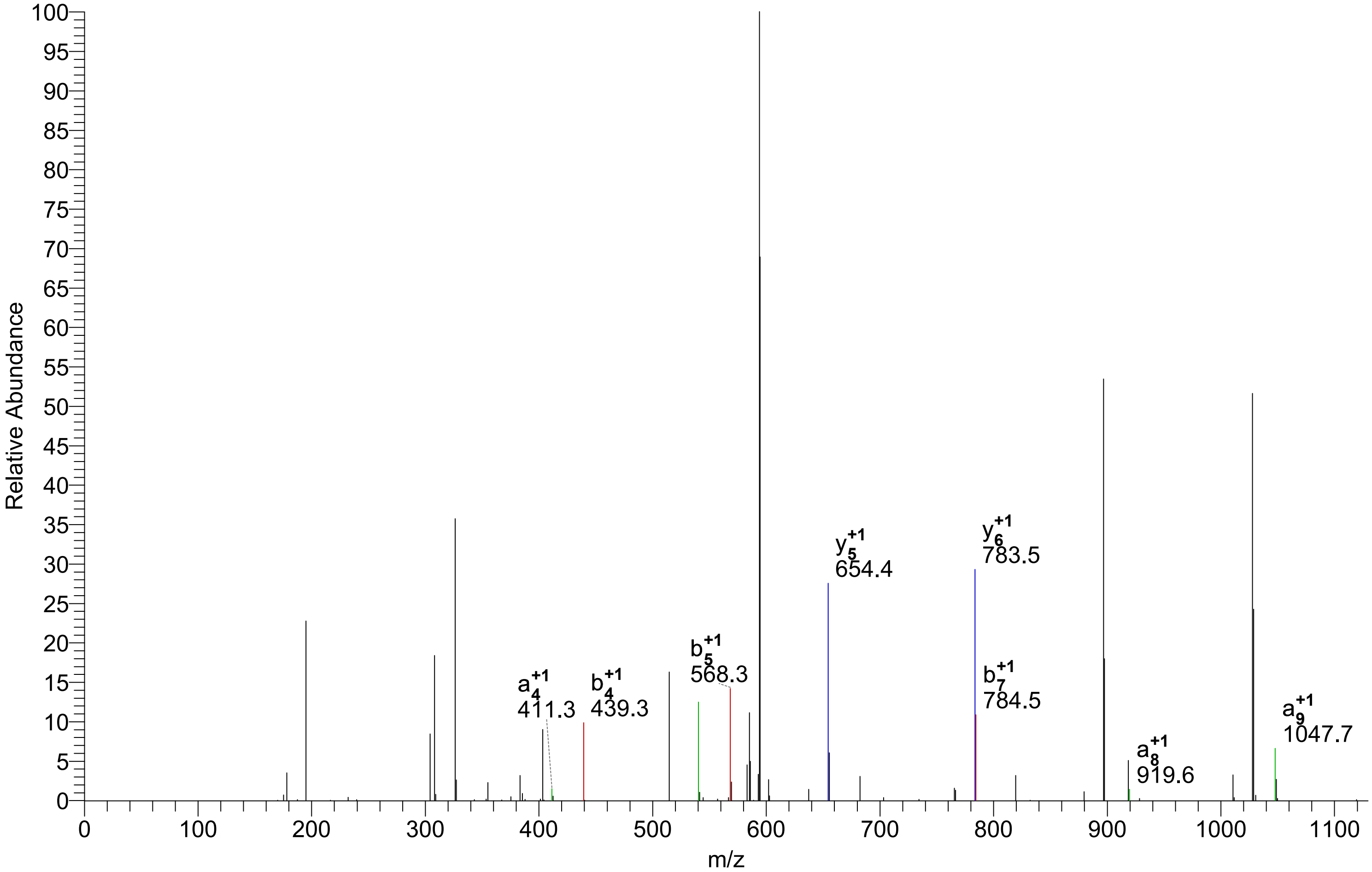
```
DTA for scans: 19682592-2147340288
Precursor ion: 611.29
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 V     72.08     100.08
 N    186.12    214.12                                     1122.51
 P    283.18    311.17                                     1008.46
 Q    411.24    439.23                                      911.41
 E    540.28    568.27                                      783.35
 E    669.32    697.32                                      654.31
 S    756.35    784.35                                      525.27
 Y    919.42    947.41                                      438.23
 Q   1047.47   1075.47                                      275.17
 K                                                          147.11
```



#19682592-2147340288 NL: 8.78E4



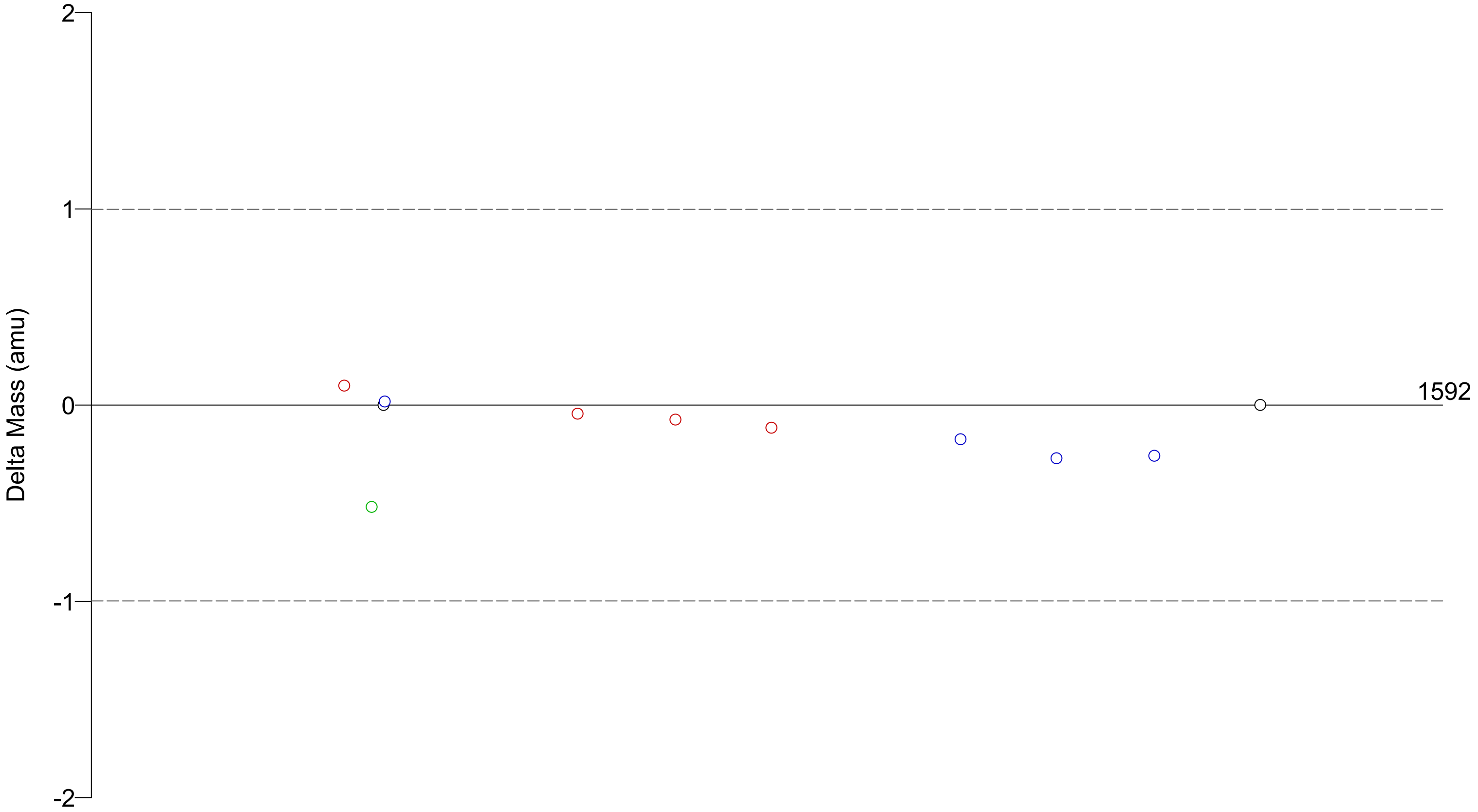
```
Reference                                                             P      Score   Coverage   Accession
Scan(s)       Sequence                                      MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count
IPI:IPI00329088.4|SWISS-PROT:Q86WJ1-1|ENSEMBL:ENSP00000358262|     1       8.1      0.0       0
19287468 - 1  K.AILM*KDLDAFENETAK.K                       1824.90   2  0.6      1.353  0.548   73.7   15  7/45    5

1 of 1 peptide matches reported, 0 removed due to filtering
```

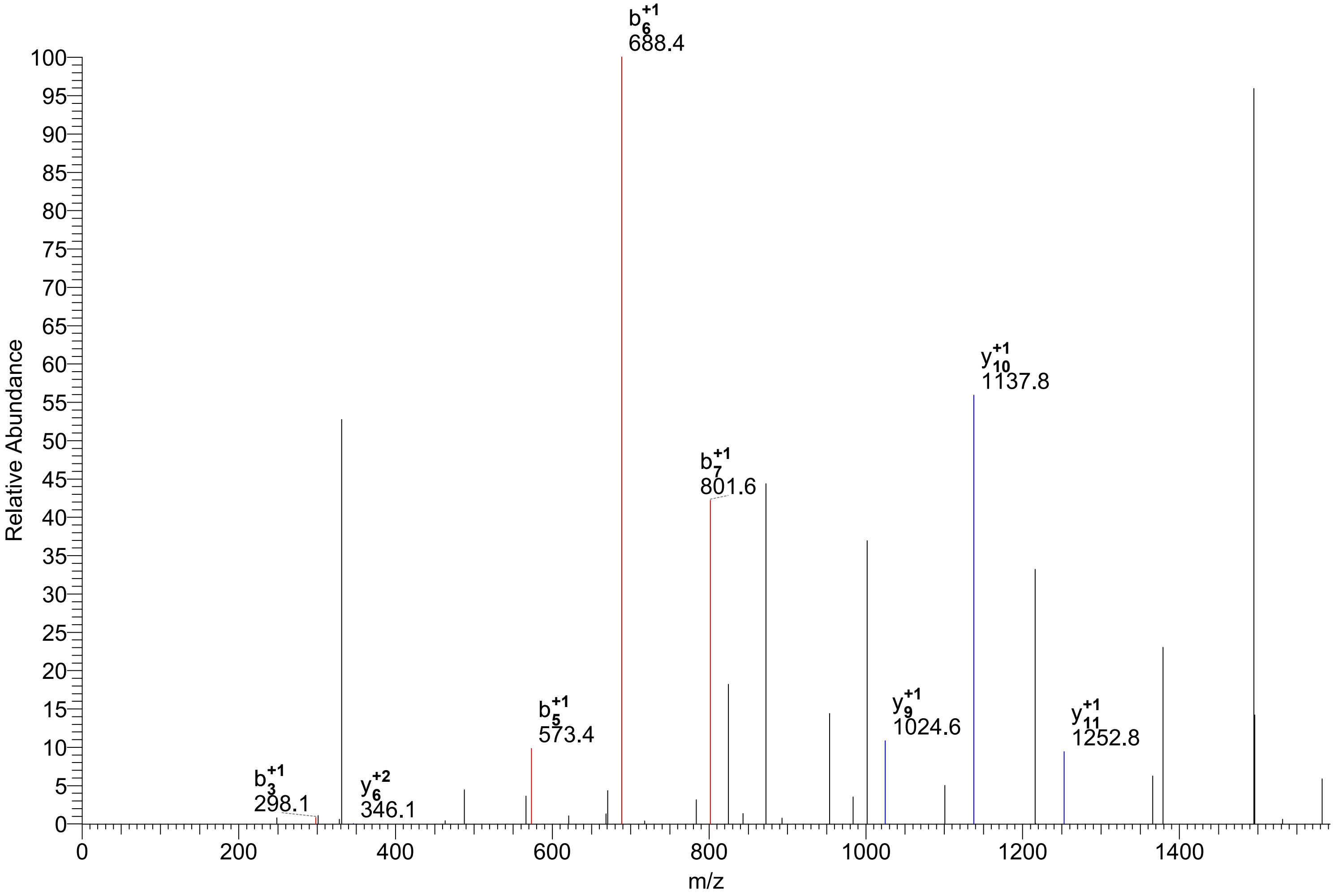
```
DTA for scans: 19287468-1
Precursor ion: 912.95
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 A     44.05      72.04
 I    157.13     185.13                                     1753.87
 L    270.22     298.21                                     1640.78
 M*   417.25     445.25                                     1527.70
 K    545.35     573.34                                     1380.66
 D    660.37     688.37                                     1252.57
 L    773.46     801.45                                     1137.54
 D    888.49     916.48                                     1024.46
 A    959.52     987.52                                      909.43
 F   1106.59    1134.59                                      838.39
 E   1235.63    1263.63                                      691.33
 N   1349.68    1377.67                                      562.28
 E   1478.72    1506.71                                      448.24
 T   1579.77    1607.76                                      319.20
 A   1650.80    1678.80                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.64E4



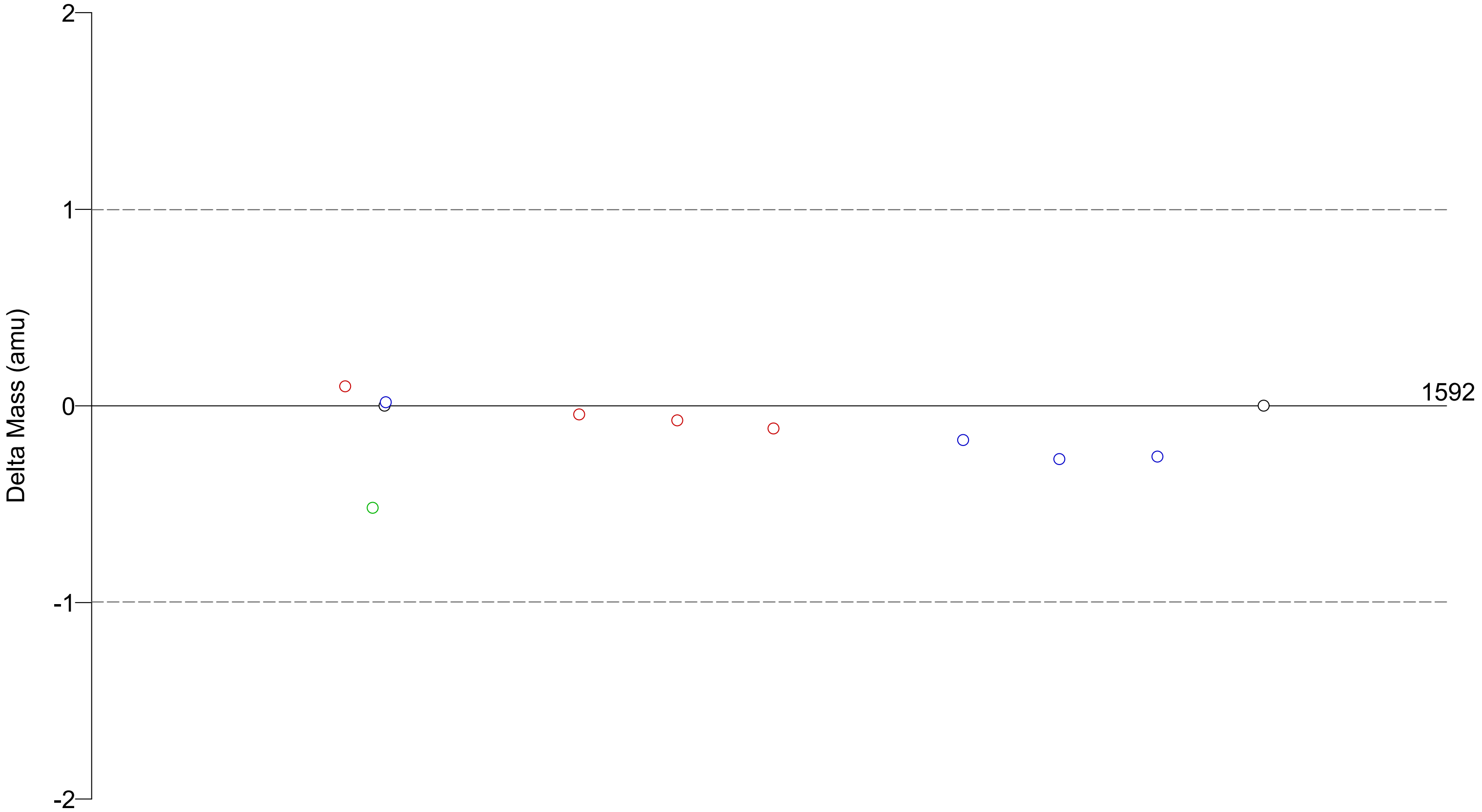
```
Reference                                                        P     Score   Coverage   Accession
Scan(s)       Sequence                              MH+      z   P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00400835.6|TREMBL:B5MDZ7|EN                             1       8.1      0.0       0
19287468 - 1  K.AILM*KDLDAFENETAK.K               1824.90    2  0.6     1.353  0.548   73.7   15  7/45    5

1 of 1 peptide matches reported, 0 removed due to filtering
```

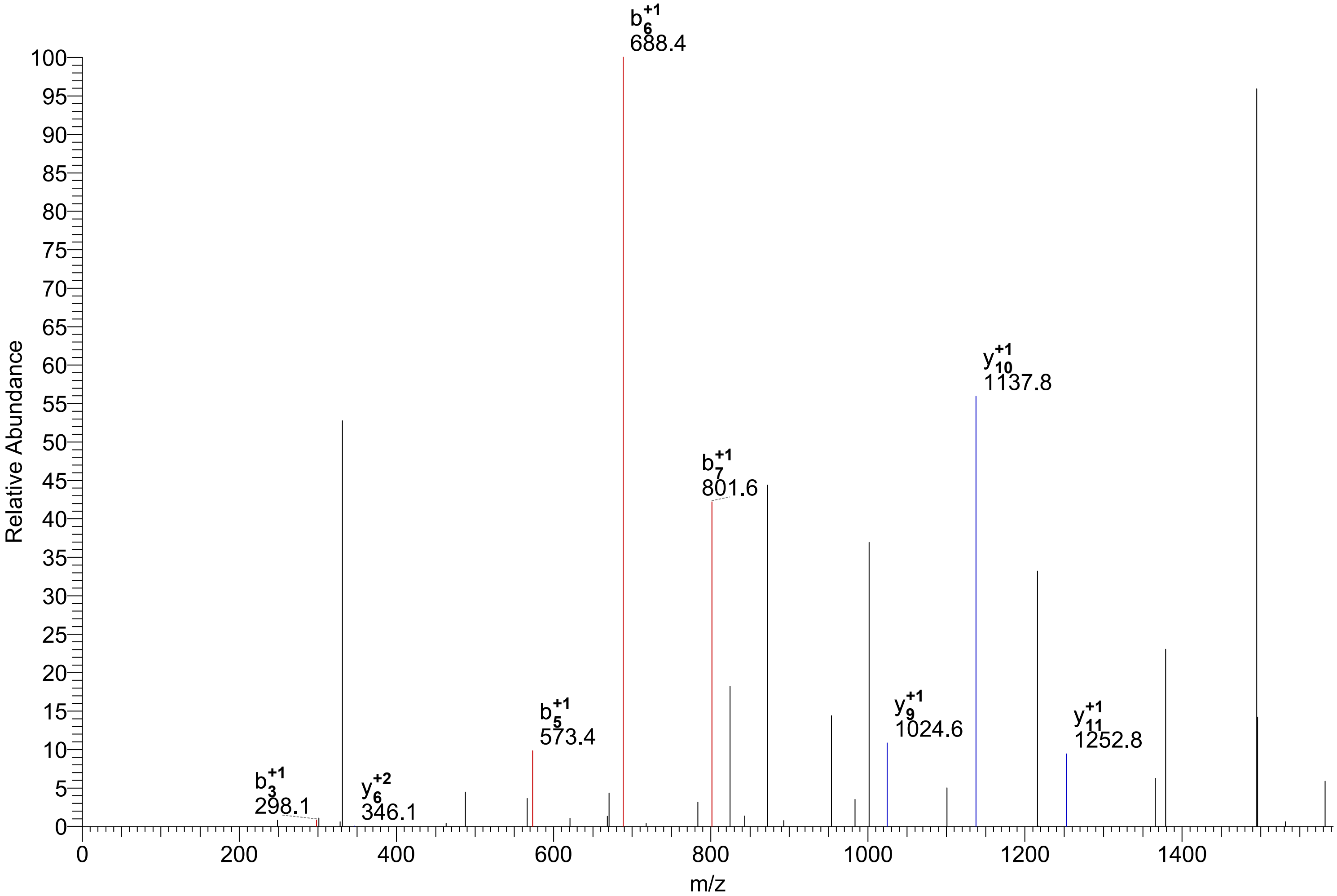
```
DTA for scans: 19287468-1
Precursor ion: 912.95
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 I    157.13     185.13                                     1753.87
 L    270.22     298.21                                     1640.78
 M*   417.25     445.25                                     1527.70
 K    545.35     573.34                                     1380.66
 D    660.37     688.37                                     1252.57
 L    773.46     801.45                                     1137.54
 D    888.49     916.48                                     1024.46
 A    959.52     987.52                                      909.43
 F   1106.59    1134.59                                      838.39
 E   1235.63    1263.63                                      691.33
 N   1349.68    1377.67                                      562.28
 E   1478.72    1506.71                                      448.24
 T   1579.77    1607.76                                      319.20
 A   1650.80    1678.80                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.64E4



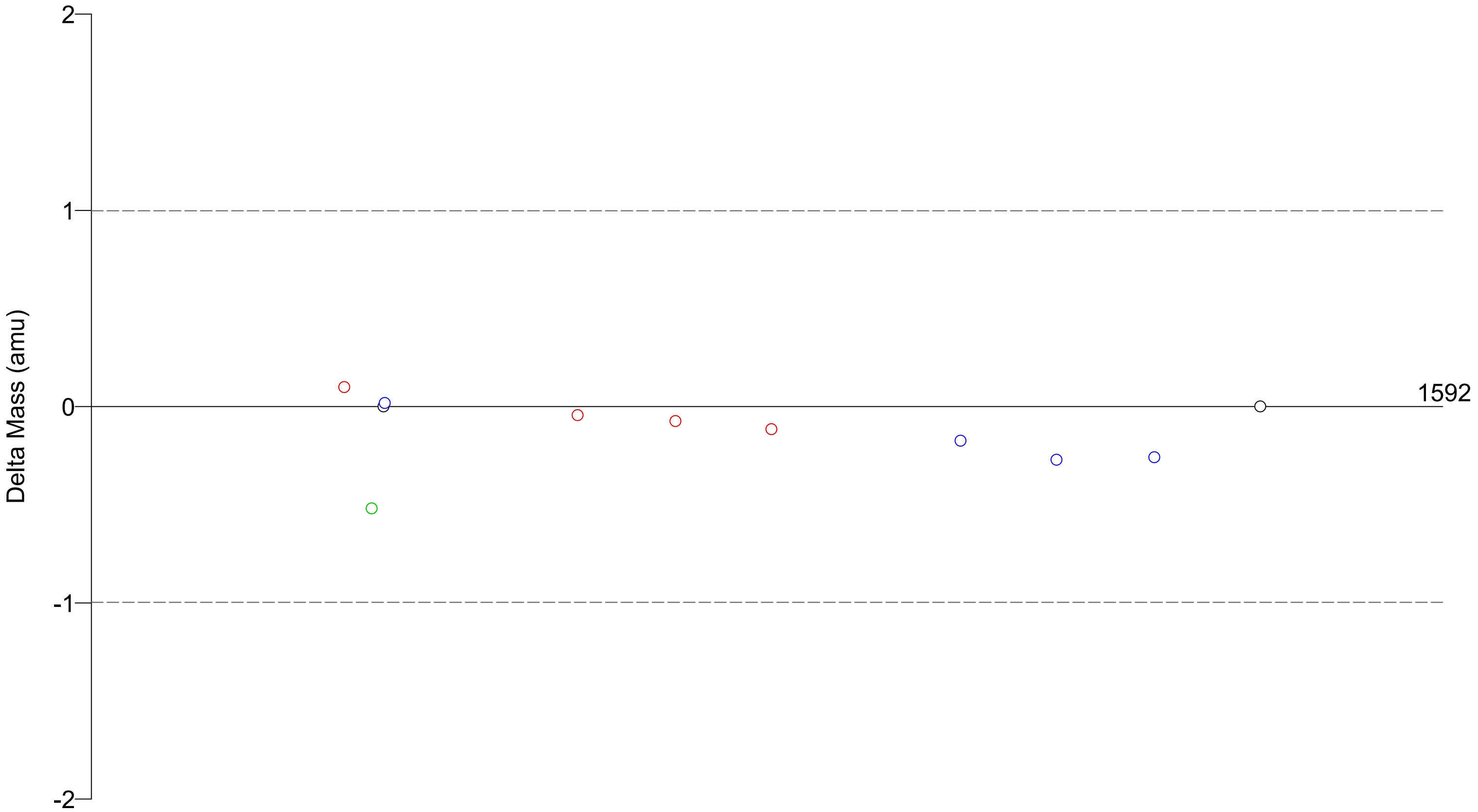
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00854584.1|SWISS-PROT:Q86WJ                                1       8.1      0.0       0
19287468 - 1  K.AILM*KDLDAFENETAK.K                  1824.90   2  0.6     1.353  0.548   73.7   15  7/45    5

1 of 1 peptide matches reported, 0 removed due to filtering
```

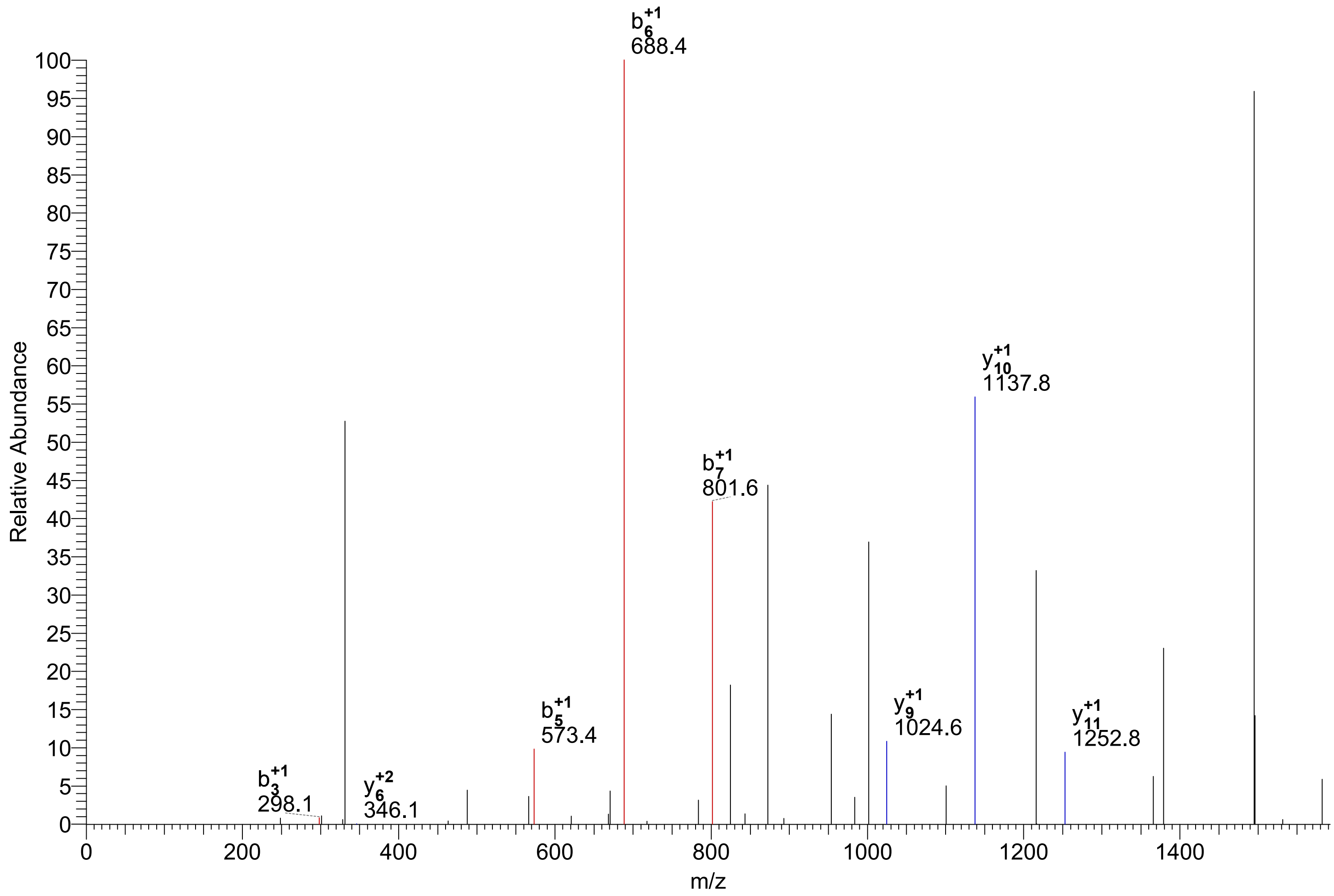
```
DTA for scans: 19287468-1
Precursor ion: 912.95
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 I    157.13     185.13                                     1753.87
 L    270.22     298.21                                     1640.78
 M*   417.25     445.25                                     1527.70
 K    545.35     573.34                                     1380.66
 D    660.37     688.37                                     1252.57
 L    773.46     801.45                                     1137.54
 D    888.49     916.48                                     1024.46
 A    959.52     987.52                                      909.43
 F   1106.59    1134.59                                      838.39
 E   1235.63    1263.63                                      691.33
 N   1349.68    1377.67                                      562.28
 E   1478.72    1506.71                                      448.24
 T   1579.77    1607.76                                      319.20
 A   1650.80    1678.80                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.64E4



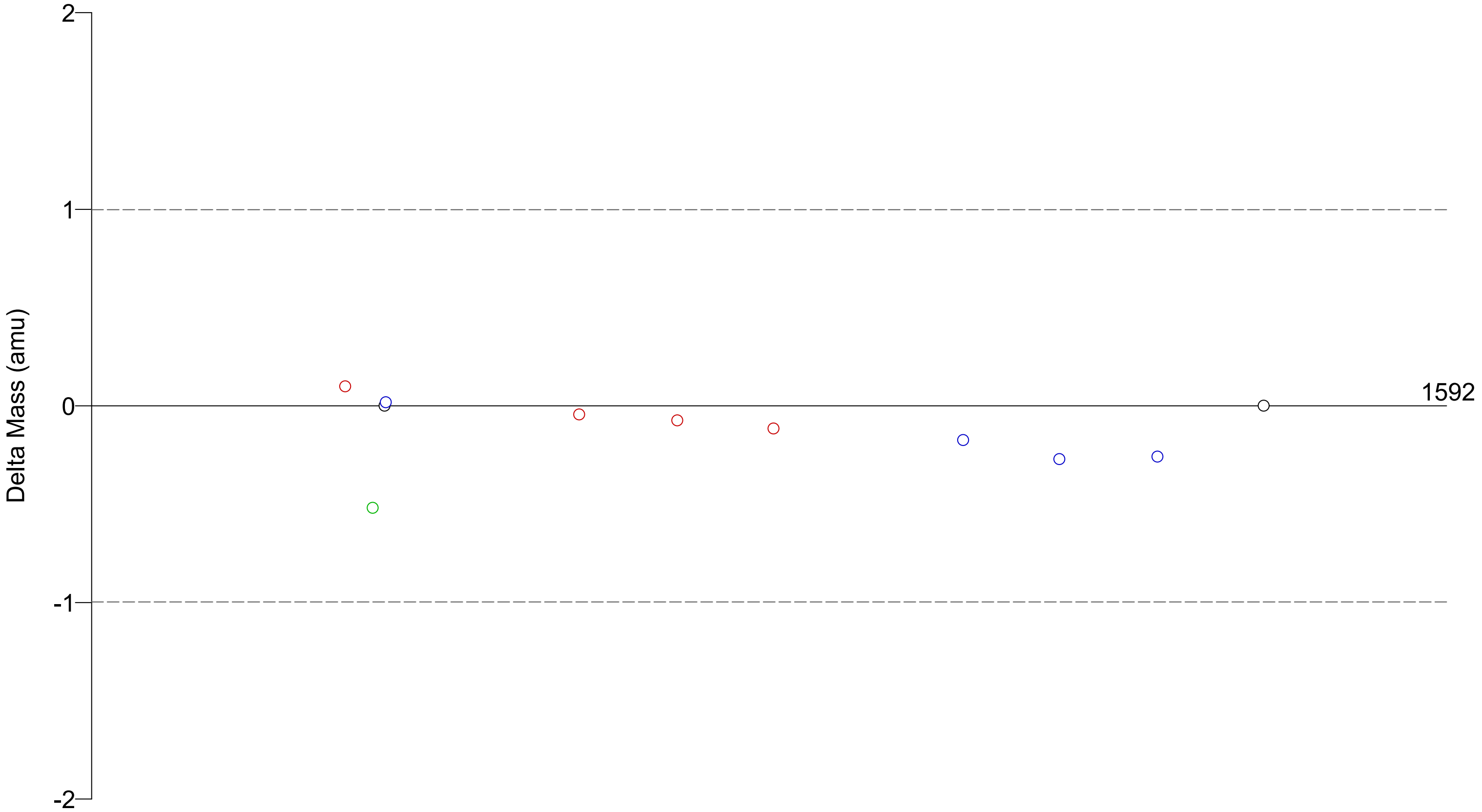
```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00890729.1|SWISS-PROT:Q86WJ                                1       8.1      0.0       0
19287468 - 1  K.AILM*KDLDAFENETAK.K                  1824.90   2  0.6     1.353  0.548   73.7   15  7/45    5

1 of 1 peptide matches reported, 0 removed due to filtering
```

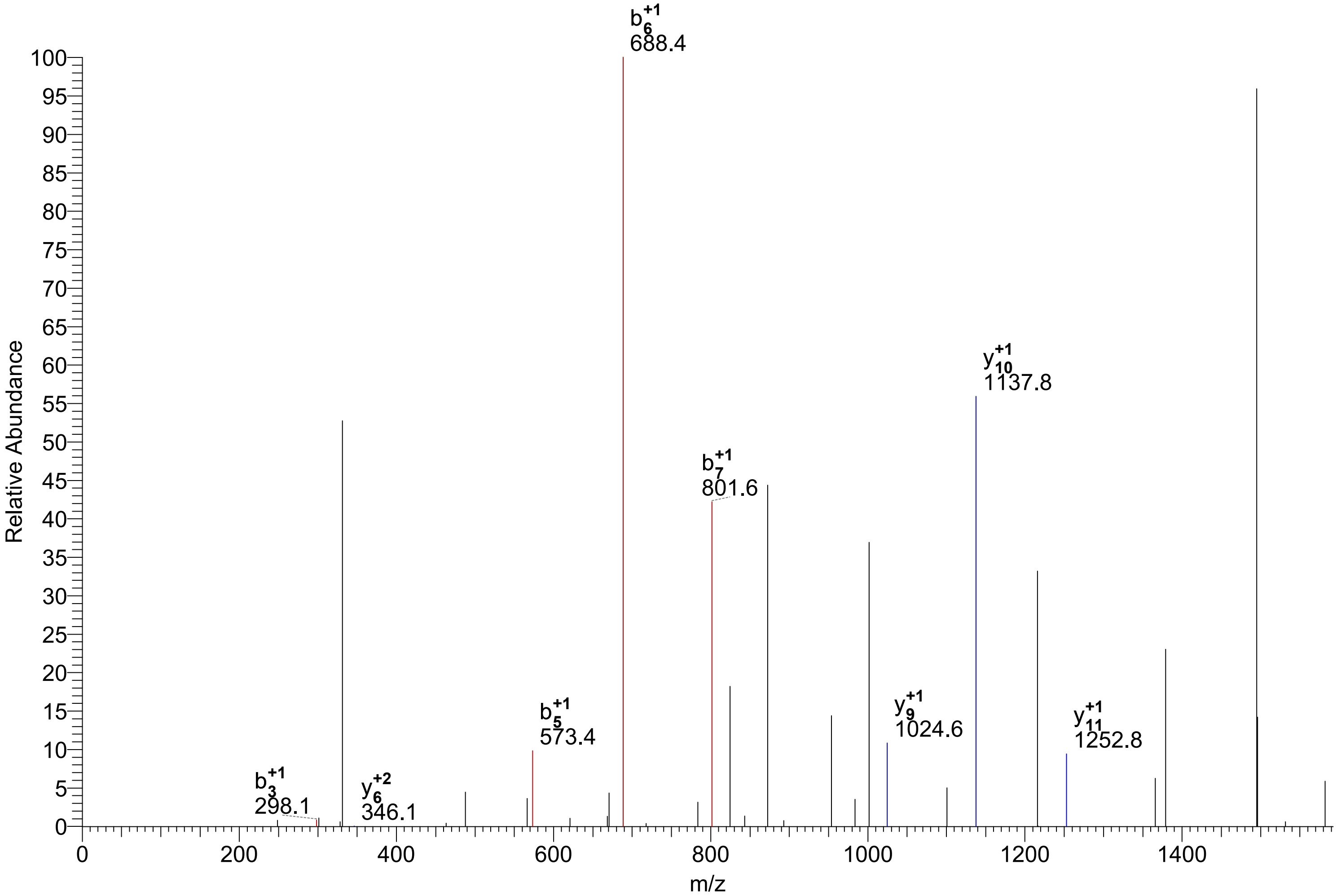
```
DTA for scans: 19287468-1
Precursor ion: 912.95
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 I    157.13     185.13                                     1753.87
 L    270.22     298.21                                     1640.78
 M*   417.25     445.25                                     1527.70
 K    545.35     573.34                                     1380.66
 D    660.37     688.37                                     1252.57
 L    773.46     801.45                                     1137.54
 D    888.49     916.48                                     1024.46
 A    959.52     987.52                                      909.43
 F   1106.59    1134.59                                      838.39
 E   1235.63    1263.63                                      691.33
 N   1349.68    1377.67                                      562.28
 E   1478.72    1506.71                                      448.24
 T   1579.77    1607.76                                      319.20
 A   1650.80    1678.80                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.64E4



```
Reference                                                          P      Score   Coverage   Accession
Scan(s)       Sequence                                 MH+       z    P        XC  DeltaCn    Sp   RSp  Ions  Count

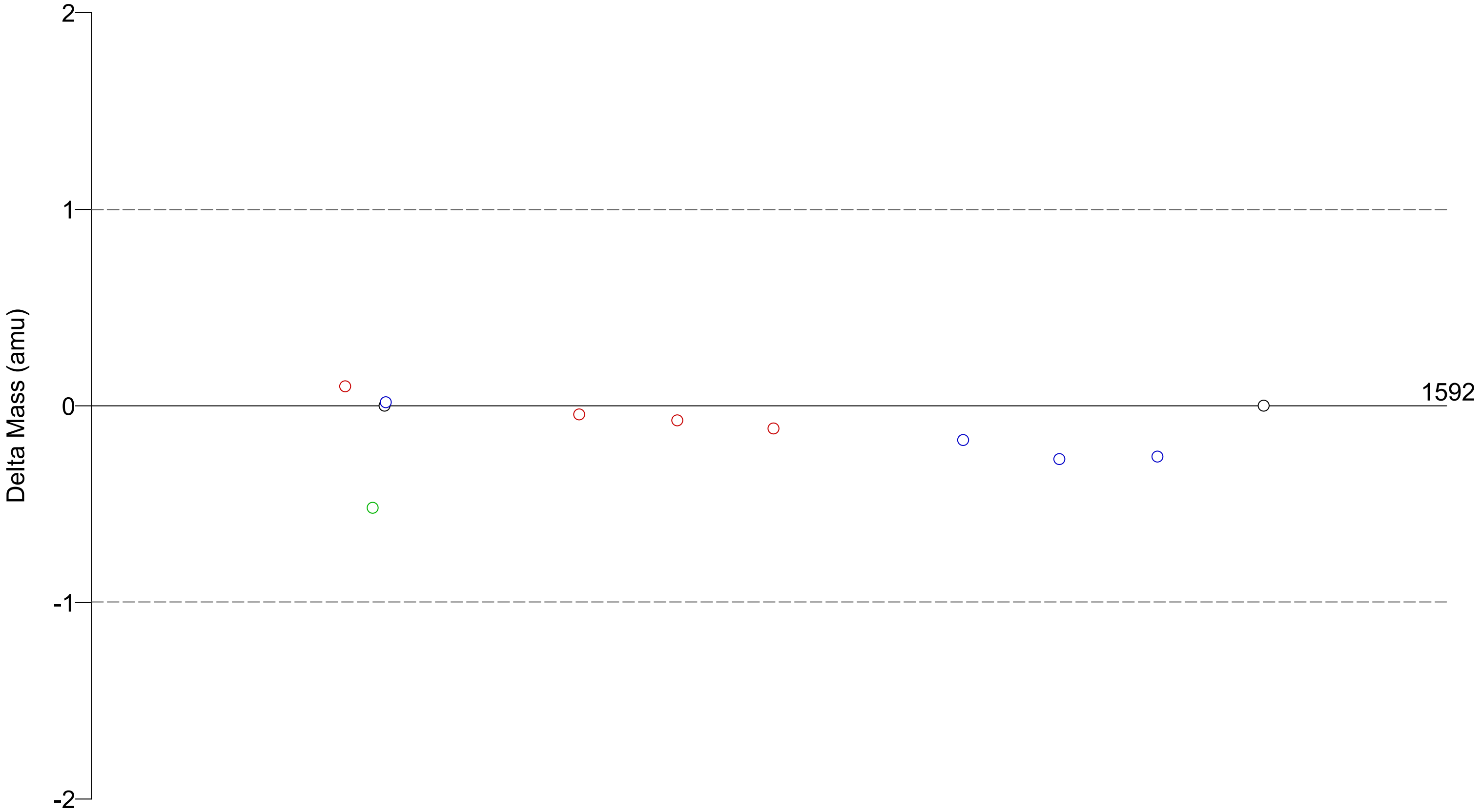
IPI:IPI00890749.1|SWISS-PROT:Q86WJ                                 1       8.1      0.0        0
19287468 - 1  K.AILM*KDLDAFENETAK.K                  1824.90   2  0.6      1.353  0.548   73.7    15  7/45    5

1 of 1 peptide matches reported, 0 removed due to filtering
```

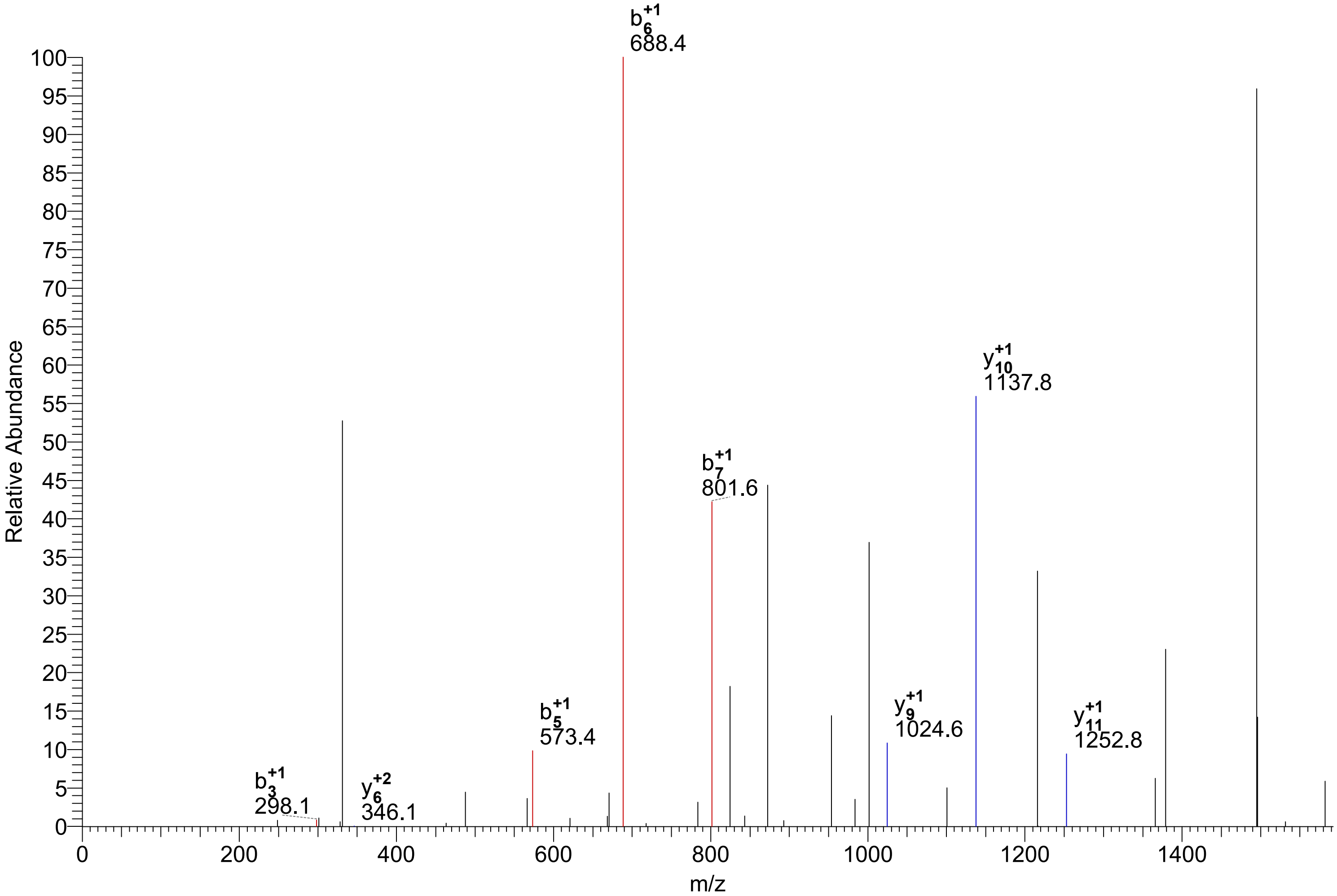
```
DTA for scans: 19287468-1
Precursor ion: 912.95
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 I    157.13     185.13                                     1753.87
 L    270.22     298.21                                     1640.78
 M*   417.25     445.25                                     1527.70
 K    545.35     573.34                                     1380.66
 D    660.37     688.37                                     1252.57
 L    773.46     801.45                                     1137.54
 D    888.49     916.48                                     1024.46
 A    959.52     987.52                                      909.43
 F   1106.59    1134.59                                      838.39
 E   1235.63    1263.63                                      691.33
 N   1349.68    1377.67                                      562.28
 E   1478.72    1506.71                                      448.24
 T   1579.77    1607.76                                      319.20
 A   1650.80    1678.80                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.64E4



```
Reference                                                           P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+      z    P        XC DeltaCn   Sp   RSp  Ions  Count

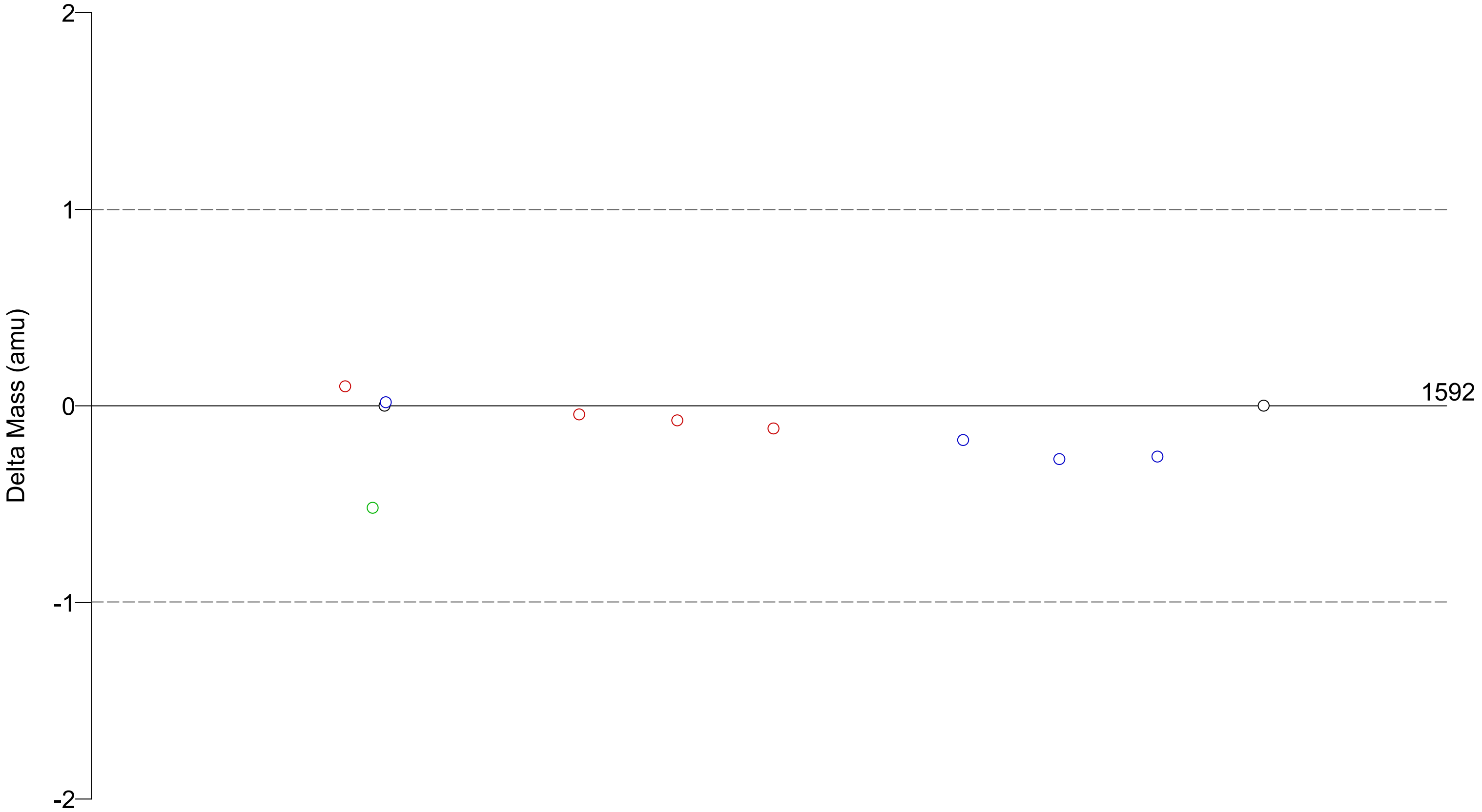
IPI:IPI00909123.1|TREMBL:B4DPN5 Ta                                1       8.1      0.0       0
19287468 - 1  K.AILM*KDLDAFENETAK.K                  1824.90   2  0.6     1.353  0.548   73.7   15  7/45    5

1 of 1 peptide matches reported, 0 removed due to filtering
```

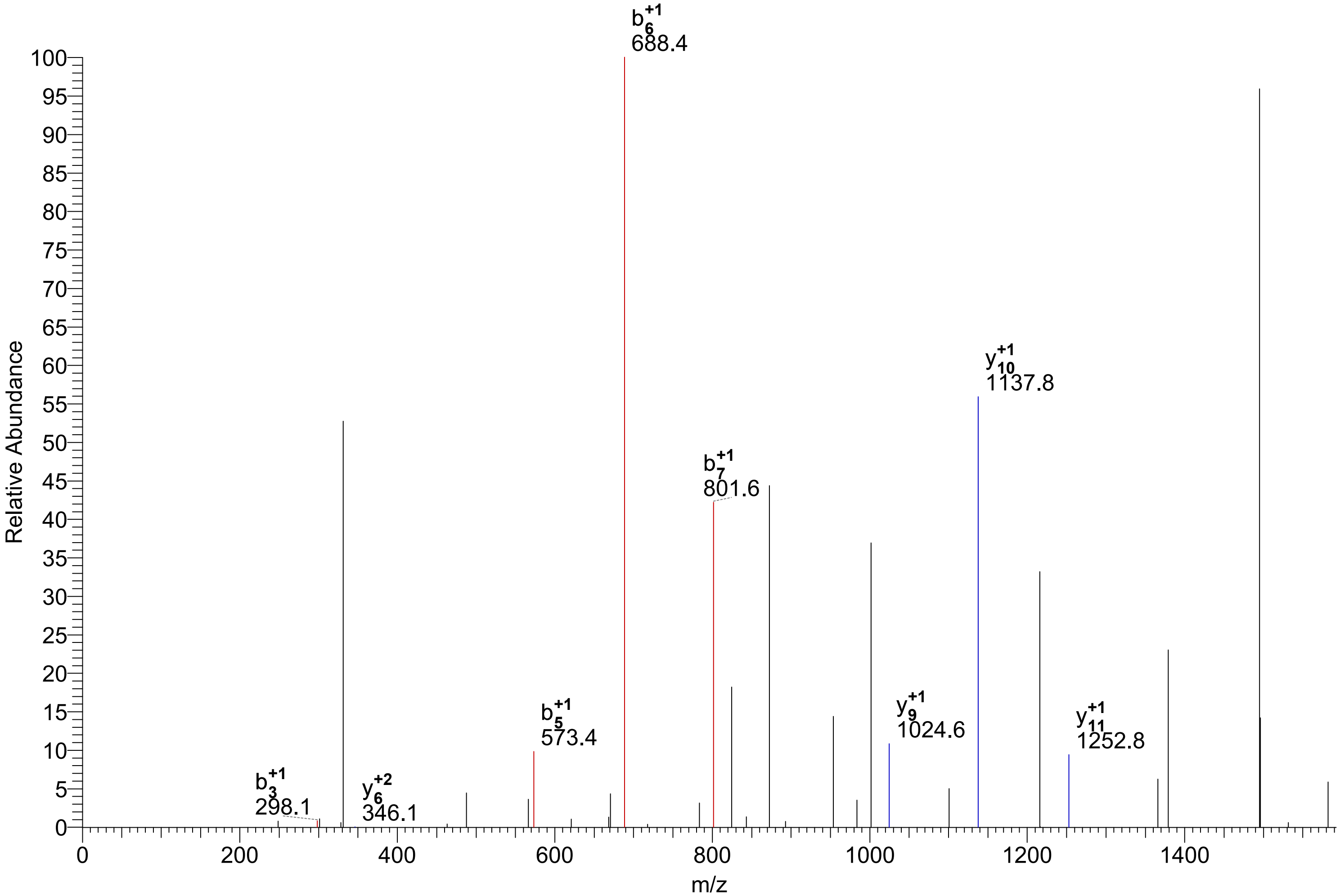
```
DTA for scans: 19287468-1
Precursor ion: 912.95
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 A     44.05      72.04
 I    157.13     185.13                                     1753.87
 L    270.22     298.21                                     1640.78
 M*   417.25     445.25                                     1527.70
 K    545.35     573.34                                     1380.66
 D    660.37     688.37                                     1252.57
 L    773.46     801.45                                     1137.54
 D    888.49     916.48                                     1024.46
 A    959.52     987.52                                      909.43
 F   1106.59    1134.59                                      838.39
 E   1235.63    1263.63                                      691.33
 N   1349.68    1377.67                                      562.28
 E   1478.72    1506.71                                      448.24
 T   1579.77    1607.76                                      319.20
 A   1650.80    1678.80                                      218.15
 K                                                           147.11
```



#19287468-1 NL: 3.64E4



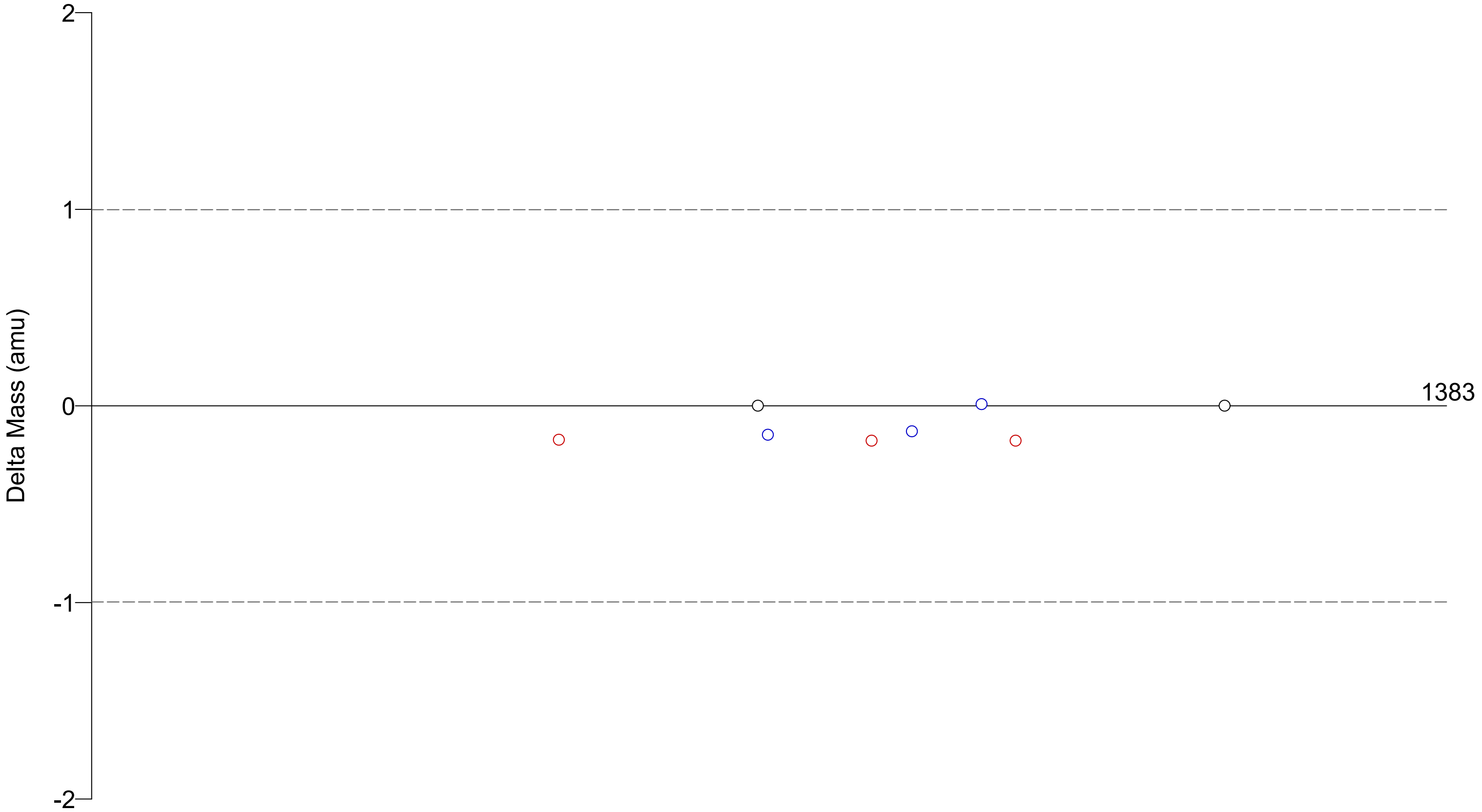
```
Reference                                                                  P      Score    Coverage   Accession
Scan(s)        Sequence                                       MH+       z     P        XC  DeltaCn    Sp    RSp  Ions  Count
IPI:IPI00007775.1|SWISS-PROT:Q9UKT6|TREMBL:Q3KPF8|ENSEMBL:ENSP     1       8.1      0.0        0
19287468 - 1  K.CEVSCSAFIRFVR.L                            1632.75   2  1       1.324  0.637   67.0   3   6/36

1 of 1 peptide matches reported, 0 removed due to filtering
```

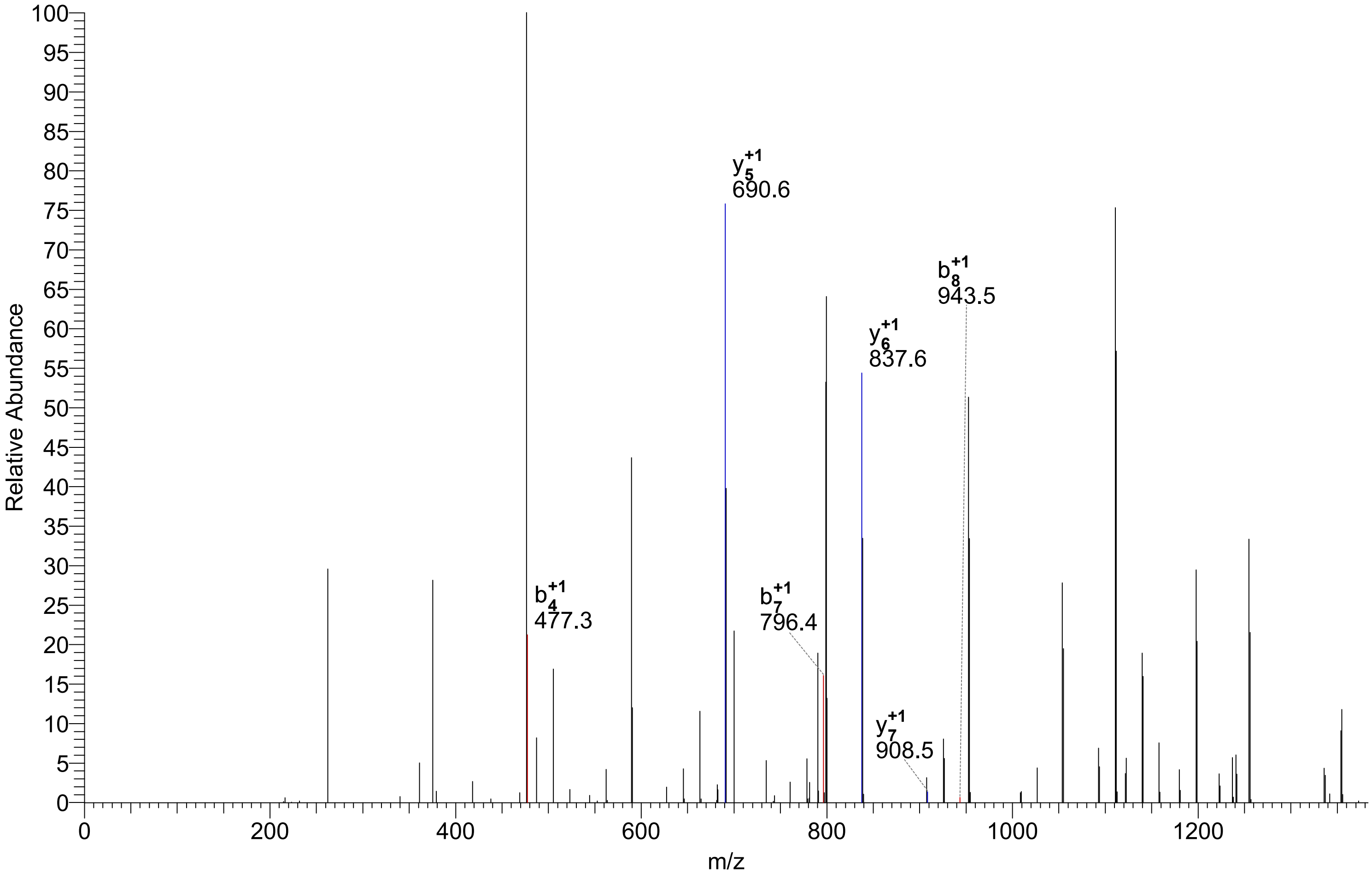
```
DTA for scans: 19287468-1
Precursor ion: 816.90
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions      C ions    Y ions    Y* ions    Yo ions    Z ions
----------------------------------------------------------------------------------------------------
 C    134.03     162.02
 E    263.07     291.06                                      1471.74
 V    362.14     390.13                                      1342.69
 S    449.17     477.16                                      1243.63
 C    610.18     638.18                                      1156.59
 S    697.22     725.21                                       995.58
 A    768.25     796.25                                       908.55
 F    915.32     943.32                                       837.51
 I   1028.41    1056.40                                       690.44
 R   1184.51    1212.50                                       577.36
 F   1331.58    1359.57                                       421.26
 V   1430.64    1458.64                                       274.19
 R                                                            175.12
```



#19287468-1 NL: 6.55E4



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Reference                                                                P      Score   Coverage   Accession
Scan(s)       Sequence                                    MH+       z    P        XC  DeltaCn    Sp    RSp  Ions  Count

IPI:IPI00003519.1|SWISS-PROT:Q15029|TREMBL:A8KAP3;B3KX19;B4DMC     1        8.1      0.0        0
2118291816 -  K.RLWGDIYFNPK.T                            1408.74   2  0.6      1.270  0.699   132.3  2   8/30    2

1 of 1 peptide matches reported, 0 removed due to filtering
```
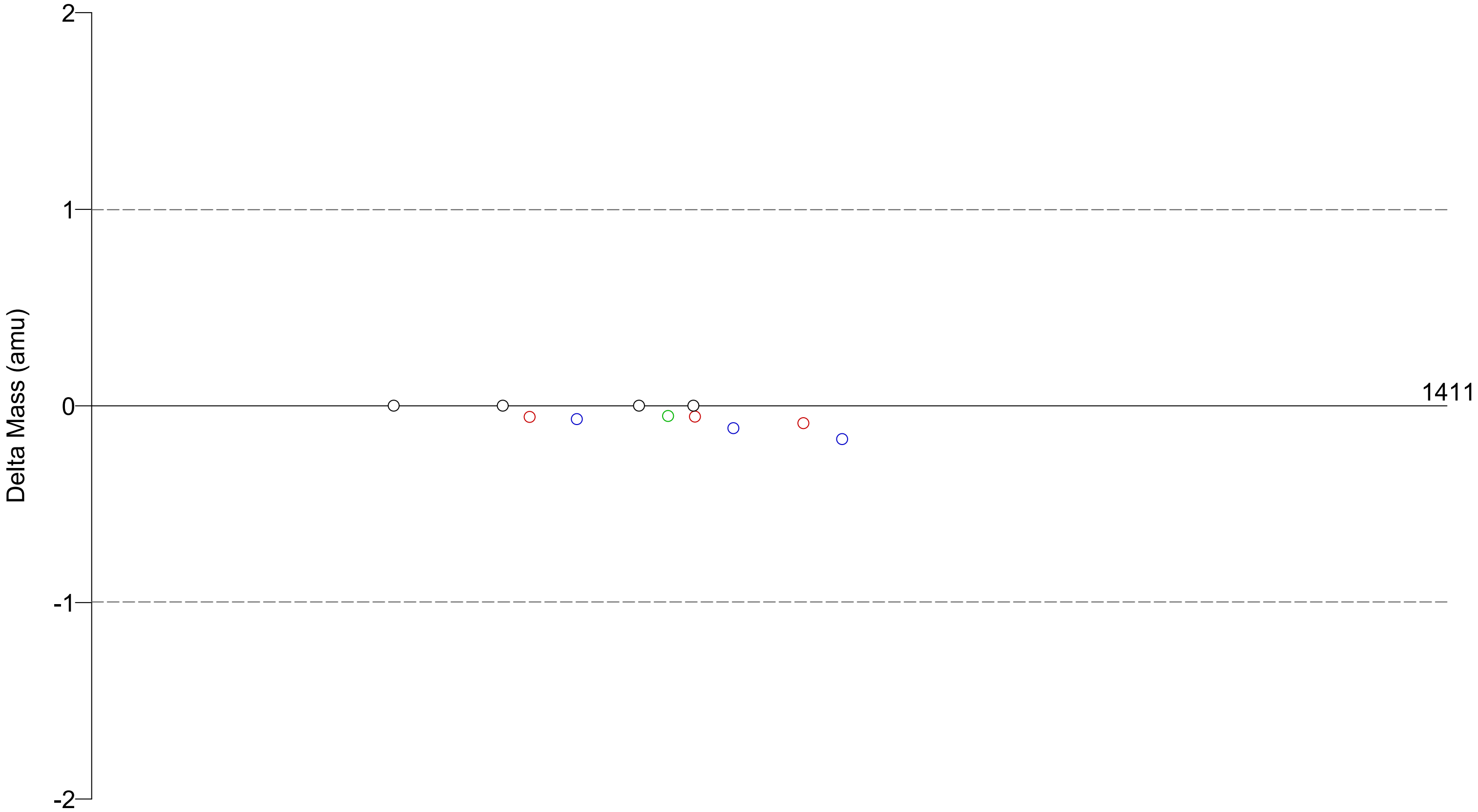
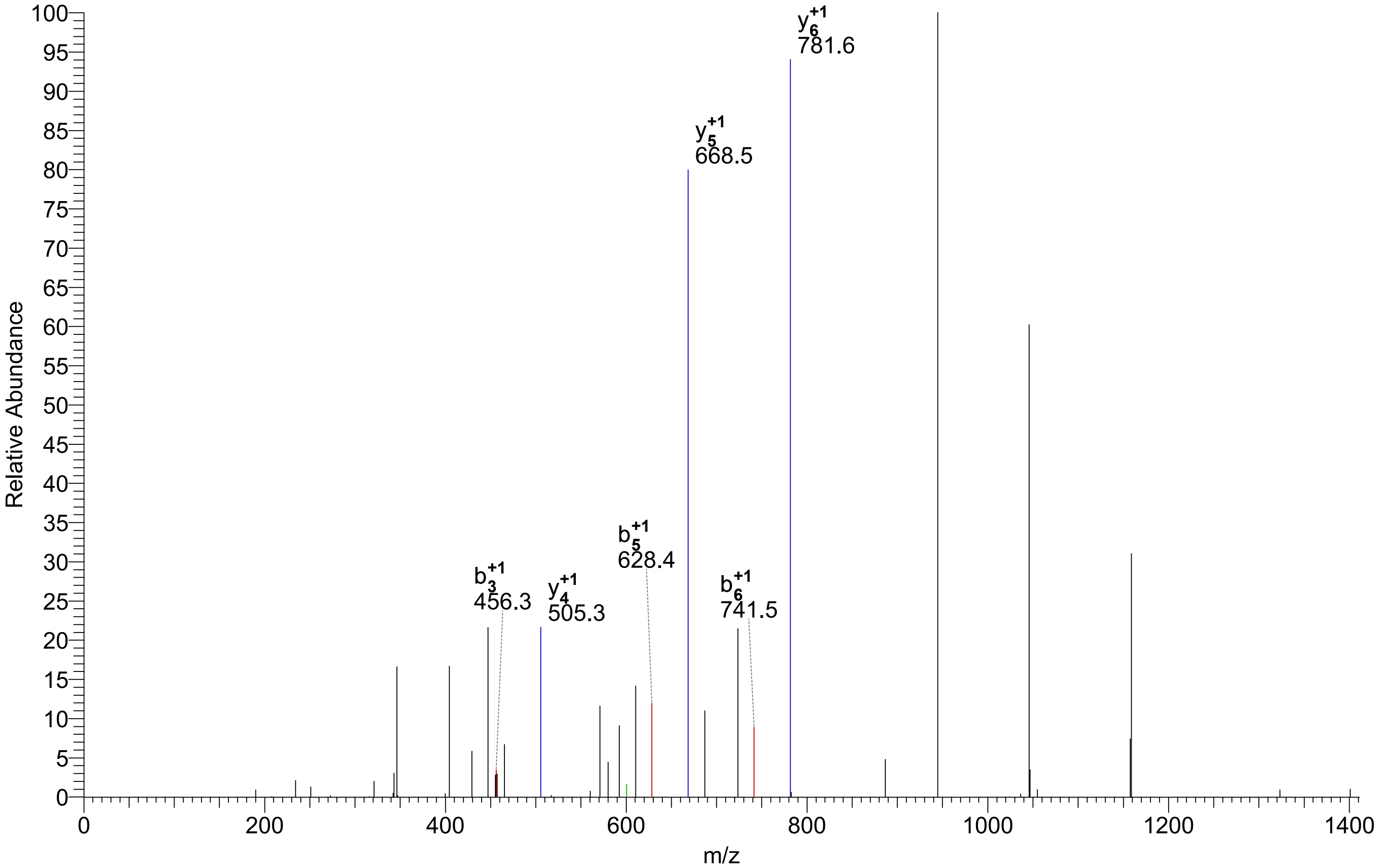

```
DTA for scans: 2118291816-26226248
Precursor ion: 704.87
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 L    242.20     270.19                                     1252.64
 W    428.28     456.27                                     1139.55
 G    485.30     513.29                                      953.47
 D    600.33     628.32                                      896.45
 I    713.41     741.40                                      781.42
 Y    876.47     904.47                                      668.34
 F   1023.54    1051.54                                      505.28
 N   1137.58    1165.58                                      358.21
 P   1234.64    1262.63                                      244.17
 K                                                           147.11
```

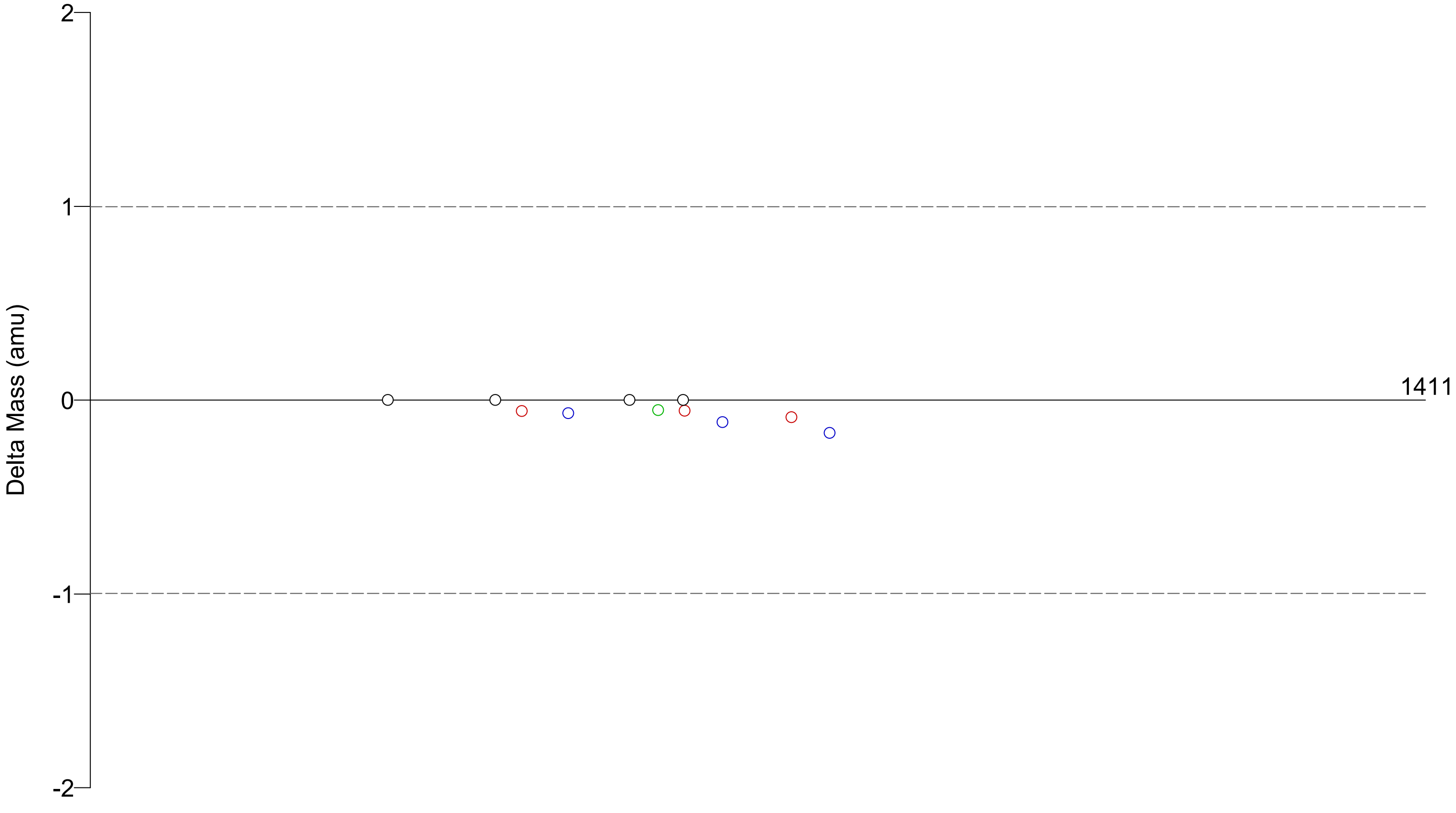


#2118291816-26226248 NL: 1.49E5

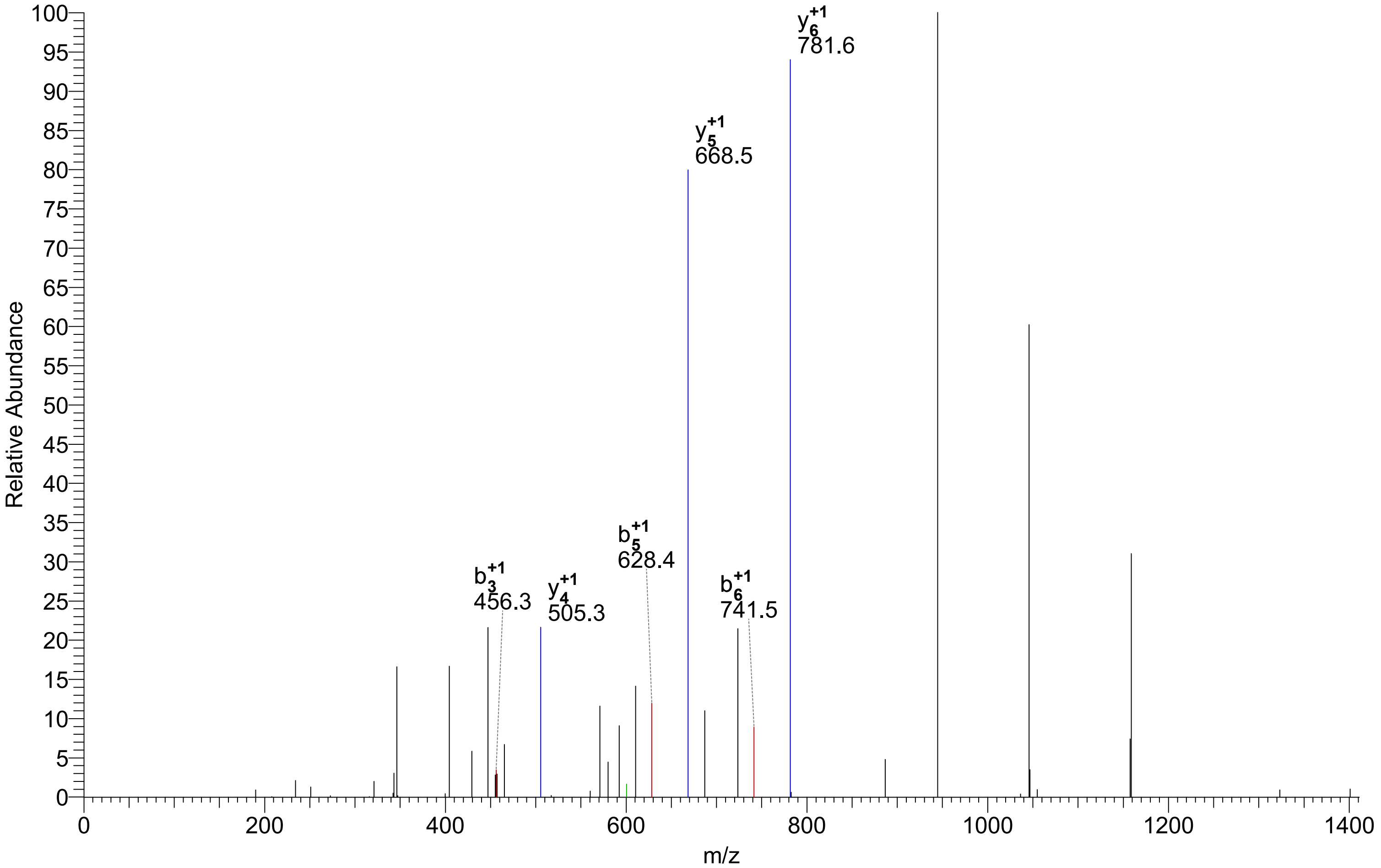


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                 MH+      z    P       XC  DeltaCn   Sp    RSp  Ions  Count
IPI:IPI00903143.1|TREMBL:B3KWY2 Ta                                 1       8.1      0.0        0
2118291816 -  K.RLWGDIYFNPK.T                         1408.74   2  0.6     1.270  0.699   132.3  2    8/30    2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 704.87
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions    Y ions    Y* ions    Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 R    129.11     157.11
 L    242.20     270.19                                     1252.64
 W    428.28     456.27                                     1139.55
 G    485.30     513.29                                      953.47
 D    600.33     628.32                                      896.45
 I    713.41     741.40                                      781.42
 Y    876.47     904.47                                      668.34
 F   1023.54    1051.54                                      505.28
 N   1137.58    1165.58                                      358.21
 P   1234.64    1262.63                                      244.17
 K                                                           147.11
```

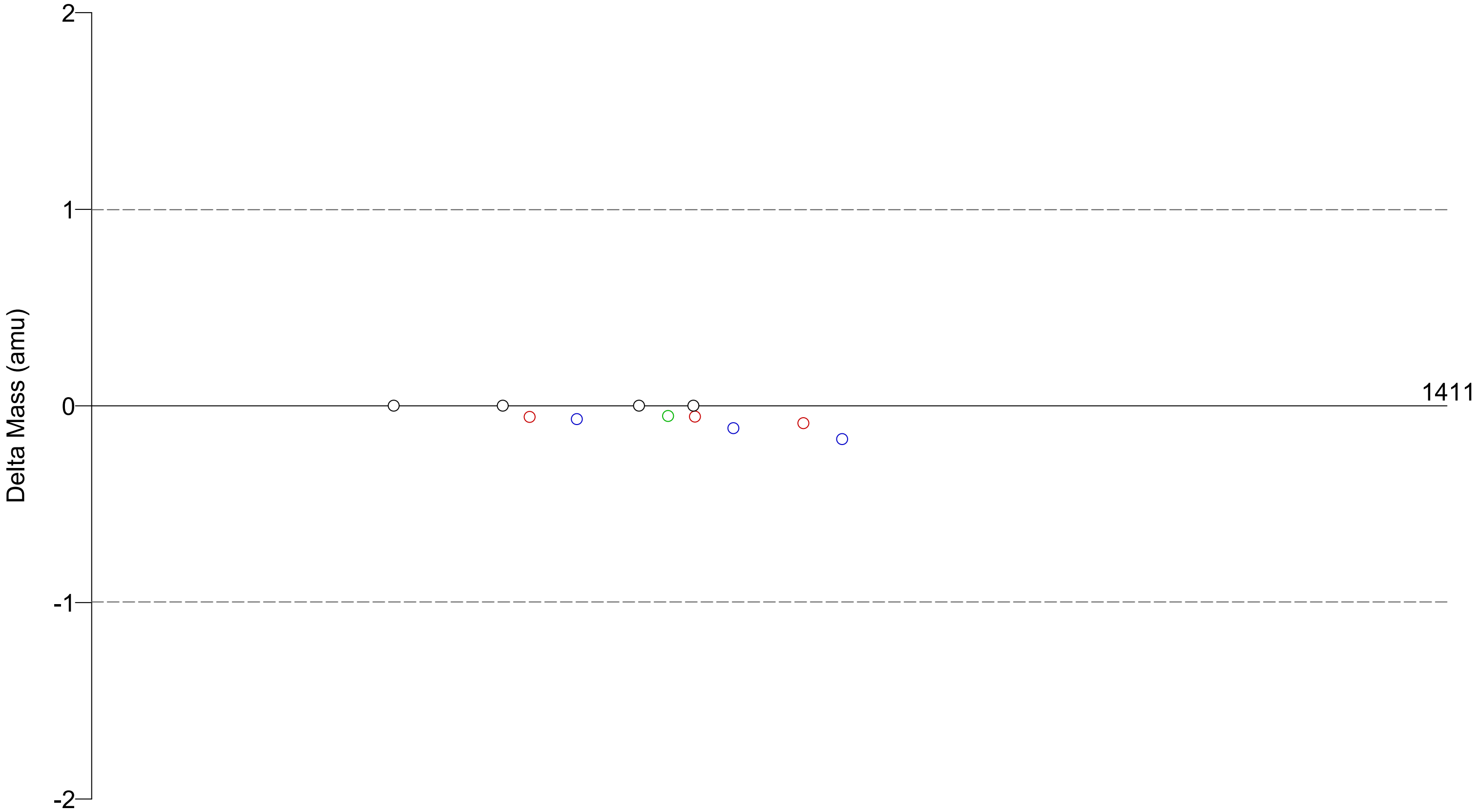


#2118291816-26226248 NL: 1.49E5

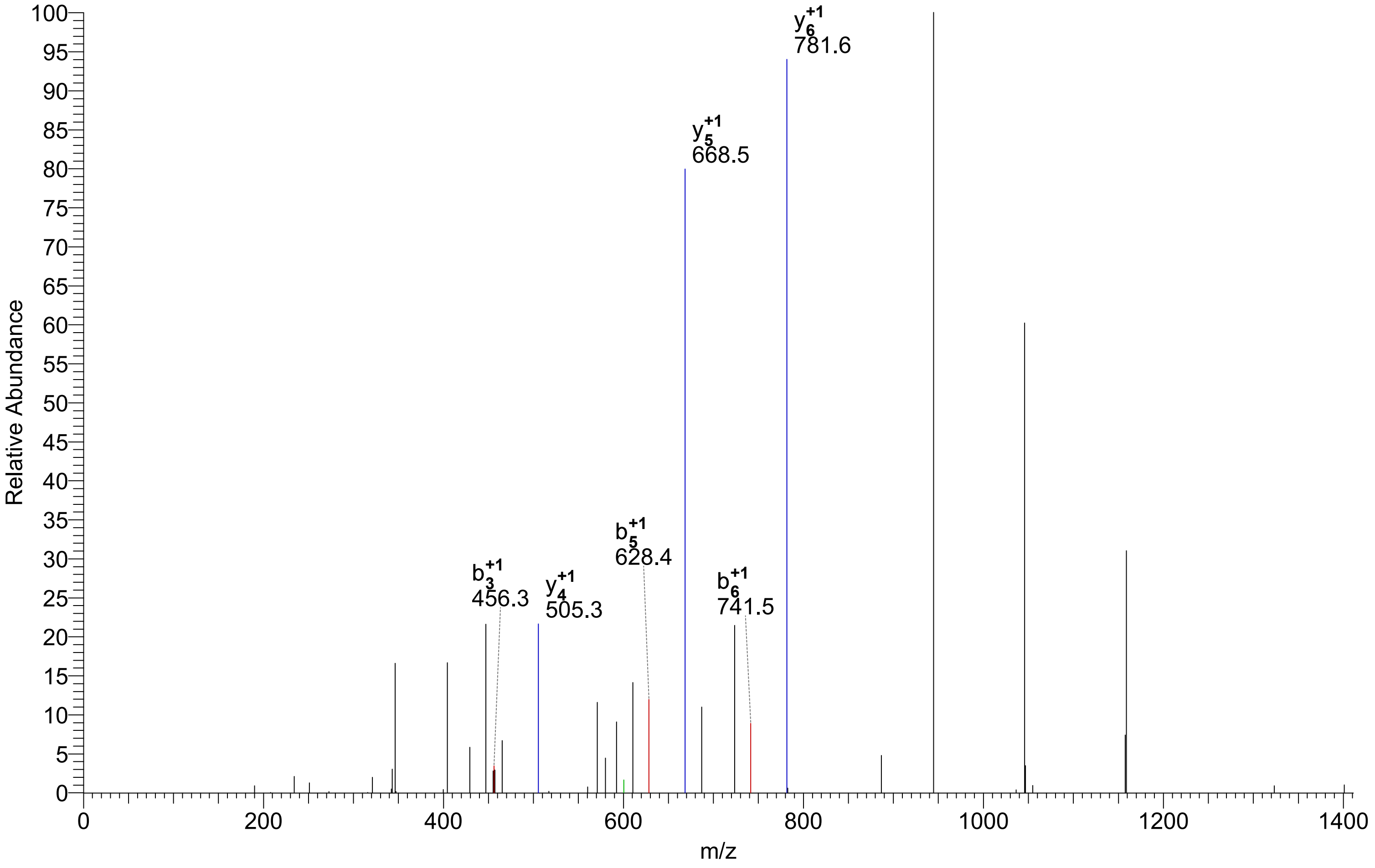


```
Reference                                                            P     Score   Coverage   Accession
Scan(s)       Sequence                                MH+       z    P       XC  DeltaCn   Sp   RSp  Ions  Count
IPI:IPI00917777.1|TREMBL:B4DK30;B4                                 1       8.1      0.0       0
2118291816 -  K.RLWGDIYFNPK.T                        1408.74    2  0.6     1.270  0.699   132.3  2   8/30    2

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 2118291816-26226248
Precursor ion: 704.87
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions    Bo ions     C ions     Y ions     Y* ions    Yo ions    Z ions
---------------------------------------------------------------------------------------------------
 R    129.11     157.11
 L    242.20     270.19                                     1252.64
 W    428.28     456.27                                     1139.55
 G    485.30     513.29                                      953.47
 D    600.33     628.32                                      896.45
 I    713.41     741.40                                      781.42
 Y    876.47     904.47                                      668.34
 F   1023.54    1051.54                                      505.28
 N   1137.58    1165.58                                      358.21
 P   1234.64    1262.63                                      244.17
 K                                                           147.11
```

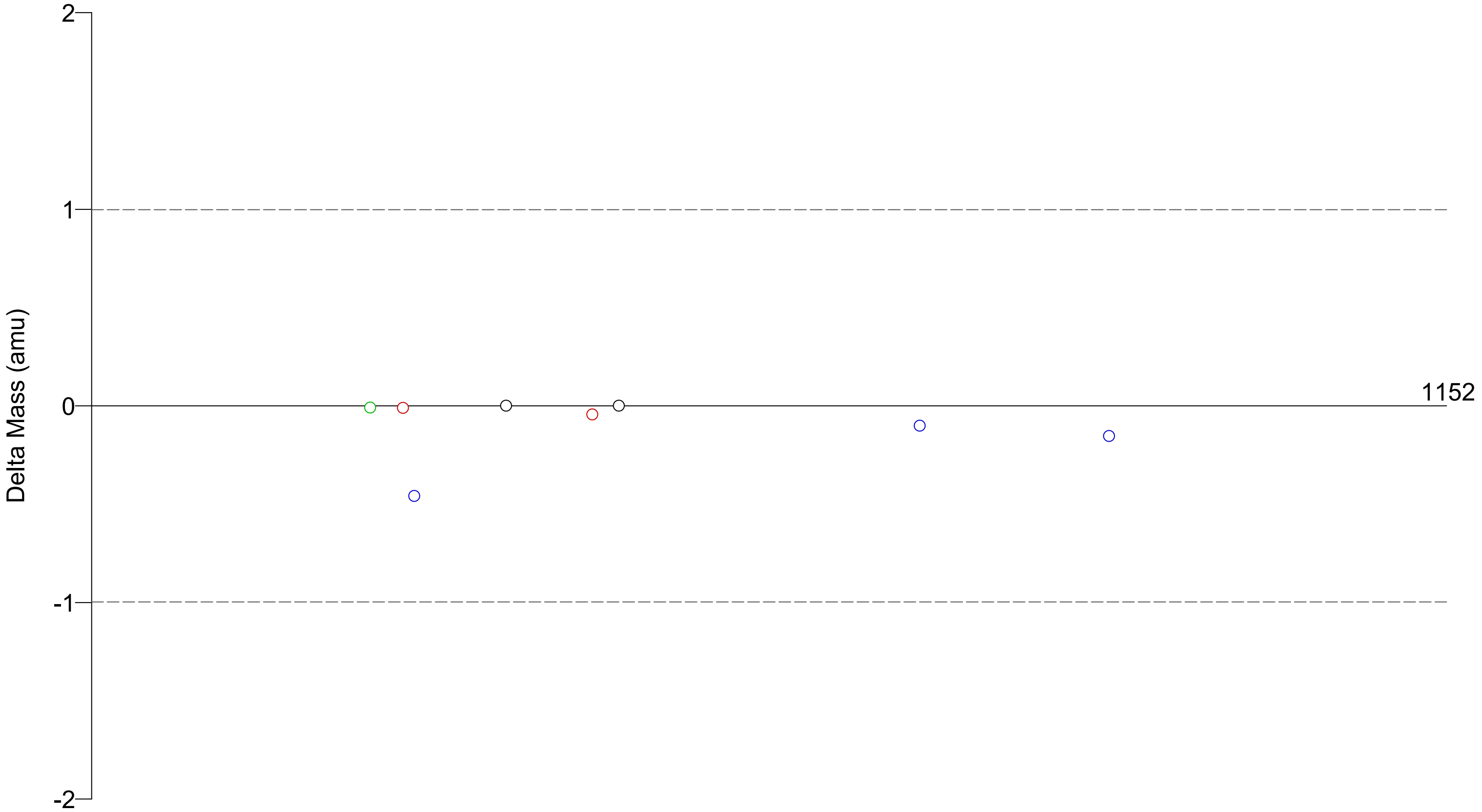


#2118291816-26226248 NL: 1.49E5



```
Reference                                                            P      Score   Coverage   Accession
Scan(s)       Sequence                                     MH+      z    P        XC  DeltaCn    Sp   RSp  Ions  Count

IPI:IPI00028954.1|SWISS-PROT:O60318|TREMBL:B3KT88;B3KWZ4;B3KXE     1        8.1      0.0        0
19287468 - 1  R.TYCRWKSK.S                                1129.55   2  0.9      1.258  0.606   56.9   5   5/21

1 of 1 peptide matches reported, 0 removed due to filtering
```

```
DTA for scans: 19287468-1
Precursor ion: 565.27
Mass type: mono
Mod's:  (M* +15.99492) C=161.01468

Ion series for charge: +1

AA   A ions     B ions     B* ions     Bo ions     C ions     Y ions     Y* ions     Yo ions     Z ions
----------------------------------------------------------------------------------------------------
 T     74.06     102.05
 Y    237.12     265.12                                      1028.50
 C    398.14     426.13                                       865.43
 R    554.24     582.23                                       704.42
 W    740.32     768.31                                       548.32
 K    868.41     896.41                                       362.24
 S    955.45     983.44                                       234.14
 K                                                            147.11
```



#19287468-1 NL: 1.65E5