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| STANDARD OPERATING PROCEDURE |
| |  |  | | --- | --- | | **Title: Repeatability/Validation Experiment for a Panel of Peptides from CPTAC Study 9** | | |  |  | | **Version #: 1** | **Author: Broad Inst Proteomics Platform** | | **Date: June 30, 2016** | **BRD-005** | |

**Purpose**

The purpose of this document is to describe the generation of a repeatability/validation experiment for a panel of peptides from CPTAC Study 9.

**Scope**

This procedure may be used to evaluate the repeatability/validation of and analysis by targeted mass spectrometry of peptides in a background of digested MARS-14 depleted human plasma.

**Responsibilities**

It is the responsibility of person(s) performing this procedure to be familiar with laboratory safety procedures. The interpretation of results must be done by a person trained in the procedure and familiar with such interpretation.

**Equipment**

1. Microcentrifuge
2. Quantiva TSQ Mass spectrometer (Thermo)
3. Easy NanoLC 1000 liquid chromatograph (Thermo)

# Reagents

**Standards: Refer to Appendix 1 for Phosphopeptide Sequences**

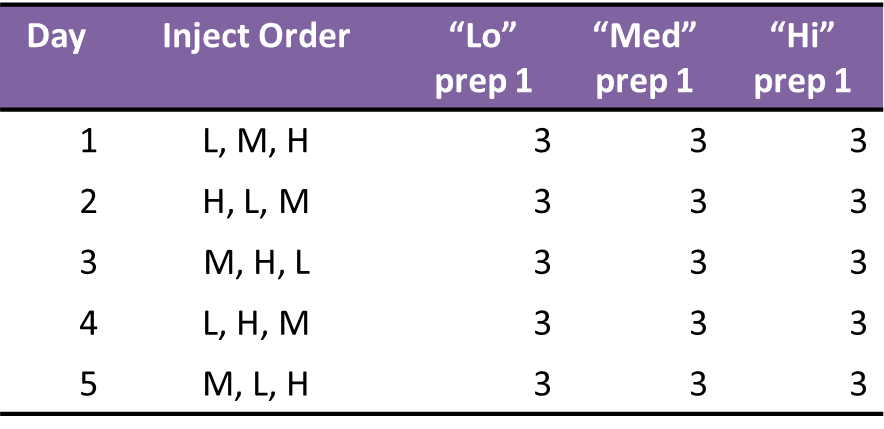
1. Study 9-1 kit (refer to SOP “**CPTAC Study 9-1 SOP\_0831\_2011\_v14**” and Appendix 1 for a complete list of proteins, peptides, background matrix and sample preparation)
2. System Suitability Sample (Study 9-1-SSS)
   1. Digest of 6 equimolar proteins (Michrom Bioresources, #PTD/00001/63) [Note: this product is no longer commercially available]
      1. Four 10 µL aliquots, 1 pmol/µL, supplied in 30% acetonitrile/0.1 % formic acid in water
3. Heavy-Only Peptide Mixture (in 25 fmol/uL Study 9-1-SSS 6 protein mix)
   1. 123 heavy peptides at 800 fmol/uL each
      1. Two 10 mL aliquots, supplied in 30% acetonitrile/0.1% formic acid
4. Light-Only Peptide Mixture (in 25 fmol/uL Study 9-1-SSS 6 protein mix)
   1. 123 light peptides at 800 fmol/uL each
      1. Two 10 mL aliquots, supplied in 30% acetonitrile/0.1% formic acid
5. Digested human plasma spiked with labeled IS peptides only, (Sample 9-1-A)
   1. Depleted plasma diluted to a final concentration after digestion of approximately 0.5 μg/µL
      1. 123 labeled IS peptides spiked at a concentration of 10 fmol/µL (Sample9-1-A)

# Procedure

1. **Determination of spike levels**
   1. Based on preliminary forward curve results and following the CPTAC assay characterization guidance document, three levels for “Hi”, “Med”, and “Lo” repeatability were determined.
      1. “Hi” = 80 fmol/uL
      2. “Med” = 15 fmol/uL
      3. “Lo” = 0.9 fmol/uL
   2. Five replicates of these samples were prepared by adding L-SIS peptides into digested, depleted plasma at each of the three concentration levels. These samples were then frozen. On each of 5 non-overlapping consecutive days, a set of samples were thawed and spiked with standard amount of H-SIS peptides and analyzed by targeted mass spectrometry.

*Three concentration levels (80 fmol/ug; 15 fmol/ug; 0.9 fmol/ug) were tested in a singlicate trial run of this protocol and were confirmed to be suitable appropriate concentrations for this experiment.*

1. **Preparation of Repeatability Samples - Completed for all Days prior to any analysis**
   1. Prepare 15 tubes, 5 labeled “Hi”, 5 labeled “Med”, and 5 labeled “Lo”.
   2. Aliquot 660 uL of 0.5 mg/mL depleted, digested, desalted plasma to each of the 15 tubes.
   3. Add L-SIS mixture to final concentration for each selected level (80 fmol/uL, 15 fmol/uL, 0.9 fmol/uL)
   4. Add heavy peptides to all tubes for final concentration of 10 fmol/uL
   5. Freeze all 15 sample tubes at -80C.
2. **Preparation of Sample Vials Plate – Performed each day 5 days**
   1. Remove and thaw one aliquot of each of the following previously prepped samples:
      1. “Hi” sample
      2. “Med” sample
      3. “Low” sample
   2. Centrifuge briefly (20 s at 2000 x g) to bring all the liquid to the bottom of the vial and place vial into HPLC autosampler.
3. **NanoLC-MRM-MS analysis**
   1. set up the TSQ-Quantiva MS with Easy NanoLC1000 and the following:
      1. Q1 resolution 0.2
      2. Q3 resolution 0.7
      3. 1.5 min cycle time
      4. CID gas 1.5
      5. 0.075 x 150 mm PicoFrit Reprosil C18, 3 um, 200 Å pore size, (Dr. Maisch GmBH) PicoFrit column
      6. mobile phase A: 3% acetonitrile/0.1% formic acid, mobile phase B: 90% acetonitrile/0.1% formic acid
      7. flowrate: 200 nL/min
      8. column temperature: 50 oC
      9. gradient: 0 – 6% B in 1 min, 6 – 30%B in 50 min, 30 – 60%B in 5 min, 60 – 90%B in 1 min, hold 90%B for 3 min. (60 min total time)
      10. injection volume: 1 uL
   2. Prior to analysis, a mixture of H-SIS peptides was injected onto the Quantiva to generate a CE calibration equation for Skyline suitable for the Quantiva. This set values were used with and without further optimization. The transitions previously selected for CPTAC study 9.1 were used with additional optimization or selection. See Appendix 2 for scheduled MRM method used to acquire the data.
4. **Run order**
   1. Samples are analyzed in random run order as described below:



1. **Data Analysis**
   1. Raw files were imported into Skyline.
   2. Extracted Ion chromatograms (XIC) of all transition ions were integrated using a Skyline document (Skyline daily version 2.6. <https://brendanx-uw1.gs.washington.edu/labkey/project/home/software/Skyline/begin.view>).
   3. Integrated peaks were manually inspected to confirm proper integration and detection of the transitions for the corresponding light and heavy peptides.

# Referenced Documents

[Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma.](http://www.ncbi.nlm.nih.gov/pubmed/25693799)

**Abbatiello SE**, Schilling B, Mani DR, Zimmerman LJ, Hall SC, MacLean B, Albertolle M, Allen S, Burgess M, Cusack MP, Gosh M, Hedrick V, Held JM, Inerowicz HD, Jackson A, Keshishian H, Kinsinger CR, Lyssand J, Makowski L, Mesri M, Rodriguez H, Rudnick P, Sadowski P, Sedransk N, Shaddox K, Skates SJ, Kuhn E, Smith D, Whiteaker JR, Whitwell C, Zhang S, Borchers CH, Fisher SJ, Gibson BW, Liebler DC, MacCoss MJ, Neubert TA, Paulovich AG, Regnier FE, Tempst P, Carr SA.

Mol Cell Proteomics. 2015 Sep;14(9):2357-74. doi: 10.1074/mcp.M114.047050. Epub 2015 Feb 18.

PMID: 25693799

**Appendix 1. Proteins, Peptides and Pathways**

|  |  |  |
| --- | --- | --- |
| Protein Targets | Peptide Sequences | Biological Pathway |
| sp|P09972|ALDOC\_HUMAN *Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2* | R.ALQASALNAWR.G [304, 314] | Glycolysis |
| sp|P09972|ALDOC\_HUMAN *Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2* | R.AEVNGLAAQGK.Y [331, 341] | Glycolysis |
| sp|P09972|ALDOC\_HUMAN *Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2* | K.ELSDIALR.I [14, 21] | Glycolysis |
| sp|P09972|ALDOC\_HUMAN *Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2* | R.TPSALAILENANVLAR.Y [157, 172] | Glycolysis |
| sp|P09972|ALDOC\_HUMAN *Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2* | R.QVLFSADDR.V [60, 68] | Glycolysis |
| sp|P04083|ANXA1\_HUMAN *Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2* | R.ALYEAGER.R [204, 211] | cell differentiation, receptor signal pathway, regulation, homeostasis, inflammatory response |
| sp|P04083|ANXA1\_HUMAN *Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2* | K.GTDVNVFNTILTTR.S [214, 227] | cell differentiation, receptor signal pathway, regulation, homeostasis, inflammatory response |
| sp|P04083|ANXA1\_HUMAN *Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2* | K.AAYLQETGKPLDETLK.K [81, 96] | cell differentiation, receptor signal pathway, regulation, homeostasis, inflammatory response |
| sp|P04083|ANXA1\_HUMAN *Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2* | K.TPAQFDADELR.A [113, 123] | cell differentiation, receptor signal pathway, regulation, homeostasis, inflammatory response |
| sp|P09525|ANXA4\_HUMAN *Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4* | R.VLVSLSAGGR.D [150, 159] | cell differentiation, negative regulation, signal transduction |
| sp|P09525|ANXA4\_HUMAN *Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4* | K.GLGTDEDAIISVLAYR.N [28, 43] | cell differentiation, negative regulation, signal transduction |
| sp|P09525|ANXA4\_HUMAN *Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4* | R.DEGNYLDDALVR.Q [160, 171] | cell differentiation, negative regulation, signal transduction |
| sp|P09525|ANXA4\_HUMAN *Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4* | K.GAGTDEGCLIEILASR.T [100, 115] | cell differentiation, negative regulation, signal transduction |
| sp|P20073|ANXA7\_HUMAN *Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3* | R.LYQAGEGR.L [348, 355] | autophagy, cell proliferation, hemostasis, cell differentiation |
| sp|P20073|ANXA7\_HUMAN *Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3* | R.SEIDLVQIK.Q [446, 454] | autophagy, cell proliferation, hemostasis, cell differentiation |
| sp|P20073|ANXA7\_HUMAN *Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3* | K.GAGTDDSTLVR.I [430, 440] | autophagy, cell proliferation, hemostasis, cell differentiation |
| sp|P20073|ANXA7\_HUMAN *Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3* | R.EFSGYVESGLK.T [397, 407] | autophagy, cell proliferation, hemostasis, cell differentiation |
| sp|P20073|ANXA7\_HUMAN *Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3* | K.GFGTDEQAIVDVVANR.S [199, 214] | autophagy, cell proliferation, hemostasis, cell differentiation |
| sp|Q53G71|Q53G71\_HUMAN *Calreticulin variant (Fragment) OS=Homo sapiens PE=2 SV=1* | R.QIDNPDYK.G [267, 274] | protein folding |
| sp|Q53G71|Q53G71\_HUMAN *Calreticulin variant (Fragment) OS=Homo sapiens PE=2 SV=1* | K.GLQTSQDAR.F [53, 61] | protein folding |
| sp|Q53G71|Q53G71\_HUMAN *Calreticulin variant (Fragment) OS=Homo sapiens PE=2 SV=1* | R.FYALSASFEPFSNK.G [62, 75] | protein folding |
| sp|Q53G71|Q53G71\_HUMAN *Calreticulin variant (Fragment) OS=Homo sapiens PE=2 SV=1* | K.EQFLDGDGWTSR.W [13, 24] | protein folding |
| sp|O00299|CLIC1\_HUMAN *Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4* | K.LHIVQVVCK.K [183, 191] | Ion transport, Transport |
| sp|O00299|CLIC1\_HUMAN *Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4* | R.YLSNAYAR.E [208, 215] | Ion transport, Transport |
| sp|O00299|CLIC1\_HUMAN *Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4* | K.IEEFLEAVLCPPR.Y [79, 91] | Ion transport, Transport |
| sp|O00299|CLIC1\_HUMAN *Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4* | K.GVTFNVTTVDTK.R [37, 48] | Ion transport, Transport |
| sp|O00299|CLIC1\_HUMAN *Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4* | R.GFTIPEAFR.G [195, 203] | Ion transport, Transport |
| sp|P15311|EZRI\_HUMAN *Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4* | R.IQVWHAEHR.G [171, 179] | Cell shape |
| sp|P15311|EZRI\_HUMAN *Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4* | K.EDEVEEWQHR.A [438, 447] | Cell shape |
| sp|P15311|EZRI\_HUMAN *Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4* | K.SGYLSSER.L [143, 150] | Cell shape |
| sp|P15311|EZRI\_HUMAN *Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4* | K.IALLEEAR.R [427, 434] | Cell shape |
| sp|P15311|EZRI\_HUMAN *Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4* | K.SQEQLAAELAEYTAK.I [412, 426] | Cell shape |
| sp|Q16658|FSCN1\_HUMAN *Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3* | K.YLTAEAFGFK.V [22, 31] | cell migration, proliferation |
| sp|Q16658|FSCN1\_HUMAN *Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3* | R.FLIVAHDDGR.W [90, 99] | cell migration, proliferation |
| sp|Q16658|FSCN1\_HUMAN *Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3* | R.YLAPSGPSGTLK.A [229, 240] | cell migration, proliferation |
| sp|Q16658|FSCN1\_HUMAN *Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3* | K.VTGTLDANR.S [399, 407] | cell migration, proliferation |
| sp|Q16658|FSCN1\_HUMAN *Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3* | R.LSCFAQTVSPAEK.W [118, 130] | cell migration, proliferation |
| sp|P02792|FRIL\_HUMAN *Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2* | R.LGGPEAGLGEYLFER.L [154, 168] | Iron storage |
| sp|P02792|FRIL\_HUMAN *Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2* | K.KPAEDEWGK.T [83, 91] | Iron storage |
| sp|P39748|FEN1\_HUMAN *Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1* | K.SIEEIVR.R [254, 260] | DNA damage, DNA repair, DNA replication |
| sp|P39748|FEN1\_HUMAN *Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1* | K.QLQQAQAAGAEQEVEK.F [109, 124] | DNA damage, DNA repair, DNA replication |
| sp|P39748|FEN1\_HUMAN *Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1* | K.LIADVAPSAIR.E [8, 18] | DNA damage, DNA repair, DNA replication |
| sp|P09211|GSTP1\_HUMAN *Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2* | K.FQDGDLTLYQSNTILR.H [55, 70] | glutathione metabolism, cellular response, negative regulation |
| sp|P09211|GSTP1\_HUMAN *Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2* | M.PPYTVVYFPVR.G [1, 11] | glutathione metabolism, cellular response, negative regulation |
| sp|P09211|GSTP1\_HUMAN *Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2* | K.ASCLYGQLPK.F [45, 54] | glutathione metabolism, cellular response, negative regulation |
| sp|Q04760|LGUL\_HUMAN *Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4* | K.FSLYFLAYEDK.N [67, 77] | metabolism, differentiation, regulation of transcription |
| sp|Q04760|LGUL\_HUMAN *Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4* | K.SLDFYTR.V [44, 50] | metabolism, differentiation, regulation of transcription |
| sp|Q04760|LGUL\_HUMAN *Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4* | K.IAWALSR.K [88, 94] | metabolism, differentiation, regulation of transcription |
| sp|Q04760|LGUL\_HUMAN *Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4* | R.GFGHIGIAVPDVYSACK.R [123, 139] | metabolism, differentiation, regulation of transcription |
| sp|Q04760|LGUL\_HUMAN *Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4* | R.FEELGVK.F [141, 147] | metabolism, differentiation, regulation of transcription |
| sp|P62993|GRB2\_HUMAN *Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1* | K.FNSLNELVDYHR.S [124, 135] | Host-virus interaction |
| sp|P62993|GRB2\_HUMAN *Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1* | K.FGNDVQHFK.V [100, 108] | Host-virus interaction |
| sp|P62993|GRB2\_HUMAN *Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1* | R.NYVTPVNR.N [207, 214] | Host-virus interaction |
| sp|P62993|GRB2\_HUMAN *Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1* | K.ATADDELSFK.R [10, 19] | Host-virus interaction |
| sp|P62993|GRB2\_HUMAN *Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1* | R.ESESAPGDFSLSVK.F [86, 99] | Host-virus interaction |
| sp|P04792|HSPB1\_HUMAN *Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2* | R.LFDQAFGLPR.L [27, 36] | Stress response |
| sp|P04792|HSPB1\_HUMAN *Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2* | R.AQLGGPEAAK.S [188, 197] | Stress response |
| sp|P04792|HSPB1\_HUMAN *Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2* | R.VSLDVNHFAPDELTVK.T [96, 111] | Stress response |
| sp|P04792|HSPB1\_HUMAN *Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2* | K.DGVVEITGK.H [114, 122] | Stress response |
| sp|P04792|HSPB1\_HUMAN *Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2* | R.QLSSGVSEIR.H [79, 88] | Stress response |
| sp|Q14116|IL18\_HUMAN *Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1* | K.EDELGDR.S [176, 182] | Angiogenesis, immune response |
| sp|Q14116|IL18\_HUMAN *Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1* | K.SDIIFFQR.S [132, 139] | Angiogenesis, immune response |
| sp|Q14116|IL18\_HUMAN *Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1* | R.TIFIISMYK.D [80, 88] | Angiogenesis, immune response |
| sp|Q14116|IL18\_HUMAN *Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1* | K.ISTLSCENK.I [106, 114] | Angiogenesis, immune response |
| sp|P09382|LEG1\_HUMAN *Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2* | K.DGGAWGTEQR.E [64, 73] | Apoptosis |
| sp|P09382|LEG1\_HUMAN *Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2* | K.DSNNLCLHFNPR.F [37, 48] | Apoptosis |
| sp|P09382|LEG1\_HUMAN *Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2* | R.FNAHGDANTIVCNSK.D [49, 63] | Apoptosis |
| sp|P09382|LEG1\_HUMAN *Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2* | K.SFVLNLGK.D [29, 36] | Apoptosis |
| sp|P09382|LEG1\_HUMAN *Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2* | K.LPDGYEFK.F [100, 107] | Apoptosis |
| sp|O00151|PDLI1\_HUMAN *PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4* | K.CGTGIVGVFVK.L [262, 272] | regulation of transcription, response to hypoxia |
| sp|O00151|PDLI1\_HUMAN *PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4* | K.GCTDNLTLTVAR.S [71, 82] | regulation of transcription, response to hypoxia |
| sp|O00151|PDLI1\_HUMAN *PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4* | K.VAASIGNAQK.L [246, 255] | regulation of transcription, response to hypoxia |
| sp|O00151|PDLI1\_HUMAN *PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4* | K.VWSPLVTEEGK.R [87, 97] | regulation of transcription, response to hypoxia |
| sp|O00151|PDLI1\_HUMAN *PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4* | K.DFEQPLAISR.V [22, 31] | regulation of transcription, response to hypoxia |
| sp|P32119|PRDX2\_HUMAN *Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5* | R.GLFIIDGK.G [127, 134] | cellular response to oxidative stress, regulation of apoptosis |
| sp|P32119|PRDX2\_HUMAN *Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5* | K.TDEGIAYR.G [119, 126] | cellular response to oxidative stress, regulation of apoptosis |
| sp|P32119|PRDX2\_HUMAN *Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5* | R.LSEDYGVLK.T [110, 118] | cellular response to oxidative stress, regulation of apoptosis |
| sp|P32119|PRDX2\_HUMAN *Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5* | K.ATAVVDGAFK.E [16, 25] | cellular response to oxidative stress, regulation of apoptosis |
| sp|Q13162|PRDX4\_HUMAN *Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1* | K.DYGVYLEDSGHTLR.G [186, 199] | Antioxidant, Oxidoreductase, Peroxidase |
| sp|Q13162|PRDX4\_HUMAN *Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1* | R.LVQAFQYTDK.H [230, 239] | Antioxidant, Oxidoreductase, Peroxidase |
| sp|Q13162|PRDX4\_HUMAN *Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1* | R.IPLLSDLTHQISK.D [173, 185] | Antioxidant, Oxidoreductase, Peroxidase |
| sp|Q13162|PRDX4\_HUMAN *Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1* | R.QITLNDLPVGR.S [212, 222] | Antioxidant, Oxidoreductase, Peroxidase |
| sp|P23297|S10A1\_HUMAN *Protein S100-A1 OS=Homo sapiens GN=S100A1 PE=1 SV=2* | K.ELLQTELSGFLDAQK.D [35, 49] | intracellular signal transduction |
| sp|P29034|S10A2\_HUMAN *Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=1 SV=3* | K.ELPSFVGEK.V [41, 49] | endothelial cell migration |
| sp|P04271|S100B\_HUMAN *Protein S100-B OS=Homo sapiens GN=S100B PE=1 SV=2* | K.AMVALIDVFHQYSGR.E [6, 20] | cell proliferation, differentiation, learning, CNS development |
| sp|P04271|S100B\_HUMAN *Protein S100-B OS=Homo sapiens GN=S100B PE=1 SV=2* | K.ELINNELSHFLEEIK.E [34, 48] | cell proliferation, differentiation, learning, CNS development |
| sp|P54727|RD23B\_HUMAN *UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1* | R.EQVIAALR.A [204, 211] | DNA damage, DNA repair, Ubl conjugation pathway |
| sp|P54727|RD23B\_HUMAN *UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1* | K.IDIDPEETVK.A [14, 23] | DNA damage, DNA repair, Ubl conjugation pathway |
| sp|P54727|RD23B\_HUMAN *UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1* | K.ILNDDTALK.E [51, 59] | DNA damage, DNA repair, Ubl conjugation pathway |
| sp|O76070|SYUG\_HUMAN *Gamma-synuclein OS=Homo sapiens GN=SNCG PE=1 SV=2* | K.EGVVGAVEK.T [12, 20] | cellular response to hydrostatic pressure, protein secretion, synaptic transmission |
| sp|O76070|SYUG\_HUMAN *Gamma-synuclein OS=Homo sapiens GN=SNCG PE=1 SV=2* | K.ENVVQSVTSVAEK.T [45, 57] | cellular response to hydrostatic pressure, protein secretion, synaptic transmission |
| sp|O76070|SYUG\_HUMAN *Gamma-synuclein OS=Homo sapiens GN=SNCG PE=1 SV=2* | K.TVEEAENIAVTSGVVR.K [80, 95] | cellular response to hydrostatic pressure, protein secretion, synaptic transmission |
| sp|P09493|TPM1\_HUMAN *Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2* | K.LVIIESDLER.A [168, 177] | cardiac muscle contraction, cytoskeleton organization, regulation and cellular response |
| sp|P09493|TPM1\_HUMAN *Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2* | K.SIDDLEDELYAQK.L [251, 263] | cardiac muscle contraction, cytoskeleton organization, regulation and cellular response |
| sp|P09493|TPM1\_HUMAN *Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2* | K.QLEDELVSLQK.K [37, 47] | cardiac muscle contraction, cytoskeleton organization, regulation and cellular response |
| sp|O00762|UBE2C\_HUMAN *Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1* | K.YLQETYSK.Q [164, 171] | Cell cycle, Cell division, Mitosis, Ubl conjugation pathway |
| sp|O00762|UBE2C\_HUMAN *Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1* | K.LSLEFPSGYPYNAPTVK.F [80, 96] | Cell cycle, Cell division, Mitosis, Ubl conjugation pathway |
| sp|O00762|UBE2C\_HUMAN *Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1* | R.DPAATSVAAAR.K [6, 16] | Cell cycle, Cell division, Mitosis, Ubl conjugation pathway |
| sp|O00762|UBE2C\_HUMAN *Ubiquitin-conjugating enzyme E2 C OS=Homo sapiens GN=UBE2C PE=1 SV=1* | K.GISAFPESDNLFK.W [48, 60] | Cell cycle, Cell division, Mitosis, Ubl conjugation pathway |
| sp|P63279|UBC9\_HUMAN *SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1* | K.DDYPSSPPK.C [65, 73] | Cell cycle, Cell division, Chromosome partition, Host-virus interaction, Mitosis, Ubl conjugation pathway |
| sp|P63279|UBC9\_HUMAN *SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1* | K.GTPWEGGLFK.L [49, 58] | Cell cycle, Cell division, Chromosome partition, Host-virus interaction, Mitosis, Ubl conjugation pathway |
| sp|P63279|UBC9\_HUMAN *SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1* | K.DWRPAITIK.Q [101, 109] | Cell cycle, Cell division, Chromosome partition, Host-virus interaction, Mitosis, Ubl conjugation pathway |
| sp|P63279|UBC9\_HUMAN *SUMO-conjugating enzyme UBC9 OS=Homo sapiens GN=UBE2I PE=1 SV=1* | K.DHPFGFVAVPTK.N [18, 29] | Cell cycle, Cell division, Chromosome partition, Host-virus interaction, Mitosis, Ubl conjugation pathway |

# Appendix 2. Scheduled MRM Method

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Compound | Start Time (min) | End Time (min) | Polarity | Precursor (m/z) | Product (m/z) | Collision Energy (V) |
| HLTASEAK | 5.6 | 13.6 | Positive | 428.729792 | 434.224539 | 16.9 |
| HLTASEAK | 5.6 | 13.6 | Positive | 428.729792 | 606.309331 | 16.9 |
| HLTASEAK | 5.6 | 13.6 | Positive | 428.729792 | 719.393395 | 16.9 |
| HLTASEAK | 5.6 | 13.6 | Positive | 432.736891 | 442.238738 | 16.9 |
| HLTASEAK | 5.6 | 13.6 | Positive | 432.736891 | 614.32353 | 16.9 |
| HLTASEAK | 5.6 | 13.6 | Positive | 432.736891 | 727.407594 | 16.9 |
| HIAEDADR | 8.76 | 16.76 | Positive | 463.719955 | 476.209952 | 18.1 |
| HIAEDADR | 8.76 | 16.76 | Positive | 463.719955 | 676.289659 | 18.1 |
| HIAEDADR | 8.76 | 16.76 | Positive | 463.719955 | 789.373723 | 18.1 |
| HIAEDADR | 8.76 | 16.76 | Positive | 468.72409 | 486.218221 | 18.1 |
| HIAEDADR | 8.76 | 16.76 | Positive | 468.72409 | 686.297928 | 18.1 |
| HIAEDADR | 8.76 | 16.76 | Positive | 468.72409 | 799.381992 | 18.1 |
| YSC[+57.0]QEGDK | 11.94 | 19.94 | Positive | 493.697831 | 576.262381 | 19.1 |
| YSC[+57.0]QEGDK | 11.94 | 19.94 | Positive | 493.697831 | 736.29303 | 19.1 |
| YSC[+57.0]QEGDK | 11.94 | 19.94 | Positive | 493.697831 | 823.325058 | 19.1 |
| YSC[+57.0]QEGDK | 11.94 | 19.94 | Positive | 496.707896 | 582.28251 | 19.1 |
| YSC[+57.0]QEGDK | 11.94 | 19.94 | Positive | 496.707896 | 742.313159 | 19.1 |
| YSC[+57.0]QEGDK | 11.94 | 19.94 | Positive | 496.707896 | 829.345187 | 19.1 |
| GLQTSQDAR | 24.64 | 32.64 | Positive | 488.246337 | 576.273615 | 18.9 |
| GLQTSQDAR | 24.64 | 32.64 | Positive | 488.246337 | 677.321293 | 18.9 |
| GLQTSQDAR | 24.64 | 32.64 | Positive | 488.246337 | 805.379871 | 18.9 |
| GLQTSQDAR | 24.64 | 32.64 | Positive | 493.250472 | 586.281884 | 18.9 |
| GLQTSQDAR | 24.64 | 32.64 | Positive | 493.250472 | 687.329562 | 18.9 |
| GLQTSQDAR | 24.64 | 32.64 | Positive | 493.250472 | 815.38814 | 18.9 |
| EDELGDR | 25.18 | 33.18 | Positive | 417.185414 | 460.251423 | 16.5 |
| EDELGDR | 25.18 | 33.18 | Positive | 417.185414 | 589.294016 | 16.5 |
| EDELGDR | 25.18 | 33.18 | Positive | 417.185414 | 704.320959 | 16.5 |
| EDELGDR | 25.18 | 33.18 | Positive | 422.189548 | 470.259692 | 16.5 |
| EDELGDR | 25.18 | 33.18 | Positive | 422.189548 | 599.302285 | 16.5 |
| EDELGDR | 25.18 | 33.18 | Positive | 422.189548 | 714.329228 | 16.5 |
| LYQAGEGR | 25.66 | 33.66 | Positive | 447.227416 | 489.241586 | 17.5 |
| LYQAGEGR | 25.66 | 33.66 | Positive | 447.227416 | 617.300164 | 17.5 |
| LYQAGEGR | 25.66 | 33.66 | Positive | 447.227416 | 780.363492 | 17.5 |
| LYQAGEGR | 25.66 | 33.66 | Positive | 452.231551 | 499.249855 | 17.5 |
| LYQAGEGR | 25.66 | 33.66 | Positive | 452.231551 | 627.308433 | 17.5 |
| LYQAGEGR | 25.66 | 33.66 | Positive | 452.231551 | 790.371761 | 17.5 |
| VAASIGNAQK | 25.94 | 33.94 | Positive | 479.769448 | 517.272886 | 18.6 |
| VAASIGNAQK | 25.94 | 33.94 | Positive | 479.769448 | 717.388979 | 18.6 |
| VAASIGNAQK | 25.94 | 33.94 | Positive | 479.769448 | 788.426093 | 18.6 |
| VAASIGNAQK | 25.94 | 33.94 | Positive | 483.776548 | 525.287085 | 18.6 |
| VAASIGNAQK | 25.94 | 33.94 | Positive | 483.776548 | 725.403178 | 18.6 |
| VAASIGNAQK | 25.94 | 33.94 | Positive | 483.776548 | 796.440292 | 18.6 |
| KPAEDEWGK | 26.11 | 34.11 | Positive | 353.841701 | 390.21358 | 12 |
| KPAEDEWGK | 26.11 | 34.11 | Positive | 353.841701 | 519.256174 | 12 |
| KPAEDEWGK | 26.11 | 34.11 | Positive | 353.841701 | 634.283117 | 12 |
| KPAEDEWGK | 26.11 | 34.11 | Positive | 355.848411 | 396.233709 | 12 |
| KPAEDEWGK | 26.11 | 34.11 | Positive | 355.848411 | 525.276303 | 12 |
| KPAEDEWGK | 26.11 | 34.11 | Positive | 355.848411 | 640.303246 | 12 |
| AQLGGPEAAK | 26.3 | 34.3 | Positive | 471.256174 | 572.303852 | 18.3 |
| AQLGGPEAAK | 26.3 | 34.3 | Positive | 471.256174 | 629.325316 | 18.3 |
| AQLGGPEAAK | 26.3 | 34.3 | Positive | 471.256174 | 742.40938 | 18.3 |
| AQLGGPEAAK | 26.3 | 34.3 | Positive | 475.263273 | 580.318051 | 18.3 |
| AQLGGPEAAK | 26.3 | 34.3 | Positive | 475.263273 | 637.339515 | 18.3 |
| AQLGGPEAAK | 26.3 | 34.3 | Positive | 475.263273 | 750.423579 | 18.3 |
| VTGTLDANR | 26.32 | 34.32 | Positive | 473.751255 | 475.225936 | 18.4 |
| VTGTLDANR | 26.32 | 34.32 | Positive | 473.751255 | 588.31 | 18.4 |
| VTGTLDANR | 26.32 | 34.32 | Positive | 473.751255 | 746.379142 | 18.4 |
| VTGTLDANR | 26.32 | 34.32 | Positive | 478.75539 | 485.234205 | 18.4 |
| VTGTLDANR | 26.32 | 34.32 | Positive | 478.75539 | 598.318269 | 18.4 |
| VTGTLDANR | 26.32 | 34.32 | Positive | 478.75539 | 756.387411 | 18.4 |
| INDISHTQSVSAK | 27.05 | 35.05 | Positive | 467.244045 | 472.74343 | 15.3 |
| INDISHTQSVSAK | 27.05 | 35.05 | Positive | 467.244045 | 529.285462 | 15.3 |
| INDISHTQSVSAK | 27.05 | 35.05 | Positive | 467.244045 | 643.820398 | 15.3 |
| INDISHTQSVSAK | 27.05 | 35.05 | Positive | 469.915445 | 476.75053 | 15.3 |
| INDISHTQSVSAK | 27.05 | 35.05 | Positive | 469.915445 | 533.292562 | 15.3 |
| INDISHTQSVSAK | 27.05 | 35.05 | Positive | 469.915445 | 647.827497 | 15.3 |
| ISTLSC[+57.0]ENK | 27.16 | 35.16 | Positive | 526.258056 | 637.261001 | 20.2 |
| ISTLSC[+57.0]ENK | 27.16 | 35.16 | Positive | 526.258056 | 851.392744 | 20.2 |
| ISTLSC[+57.0]ENK | 27.16 | 35.16 | Positive | 526.258056 | 938.424772 | 20.2 |
| ISTLSC[+57.0]ENK | 27.16 | 35.16 | Positive | 530.265156 | 645.2752 | 20.2 |
| ISTLSC[+57.0]ENK | 27.16 | 35.16 | Positive | 530.265156 | 859.406943 | 20.2 |
| ISTLSC[+57.0]ENK | 27.16 | 35.16 | Positive | 530.265156 | 946.438971 | 20.2 |
| QIDNPDYK | 27.53 | 35.53 | Positive | 496.737814 | 522.255839 | 19.2 |
| QIDNPDYK | 27.53 | 35.53 | Positive | 496.737814 | 636.298767 | 19.2 |
| QIDNPDYK | 27.53 | 35.53 | Positive | 496.737814 | 751.32571 | 19.2 |
| QIDNPDYK | 27.53 | 35.53 | Positive | 500.744913 | 530.270038 | 19.2 |
| QIDNPDYK | 27.53 | 35.53 | Positive | 500.744913 | 644.312966 | 19.2 |
| QIDNPDYK | 27.53 | 35.53 | Positive | 500.744913 | 759.339909 | 19.2 |
| SGYLSSER | 27.96 | 35.96 | Positive | 449.716881 | 478.225602 | 17.6 |
| SGYLSSER | 27.96 | 35.96 | Positive | 449.716881 | 591.309666 | 17.6 |
| SGYLSSER | 27.96 | 35.96 | Positive | 449.716881 | 754.372994 | 17.6 |
| SGYLSSER | 27.96 | 35.96 | Positive | 454.721016 | 488.233871 | 17.6 |
| SGYLSSER | 27.96 | 35.96 | Positive | 454.721016 | 601.317935 | 17.6 |
| SGYLSSER | 27.96 | 35.96 | Positive | 454.721016 | 764.381263 | 17.6 |
| AEVNGLAAQGK | 28.29 | 36.29 | Positive | 529.285462 | 474.267073 | 20.3 |
| AEVNGLAAQGK | 28.29 | 36.29 | Positive | 529.285462 | 644.3726 | 20.3 |
| AEVNGLAAQGK | 28.29 | 36.29 | Positive | 529.285462 | 758.415528 | 20.3 |
| AEVNGLAAQGK | 28.29 | 36.29 | Positive | 533.292562 | 482.281272 | 20.3 |
| AEVNGLAAQGK | 28.29 | 36.29 | Positive | 533.292562 | 652.386799 | 20.3 |
| AEVNGLAAQGK | 28.29 | 36.29 | Positive | 533.292562 | 766.429727 | 20.3 |
| DPAATSVAAAR | 28.54 | 36.54 | Positive | 515.269812 | 574.330736 | 19.8 |
| DPAATSVAAAR | 28.54 | 36.54 | Positive | 515.269812 | 675.378414 | 19.8 |
| DPAATSVAAAR | 28.54 | 36.54 | Positive | 515.269812 | 746.415528 | 19.8 |
| DPAATSVAAAR | 28.54 | 36.54 | Positive | 520.273947 | 584.339005 | 19.8 |
| DPAATSVAAAR | 28.54 | 36.54 | Positive | 520.273947 | 685.386683 | 19.8 |
| DPAATSVAAAR | 28.54 | 36.54 | Positive | 520.273947 | 756.423797 | 19.8 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 512.264446 | 275.171381 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 512.264446 | 391.687592 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 512.264446 | 404.213974 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 512.264446 | 473.219257 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 512.264446 | 567.277303 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 514.935846 | 283.18558 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 514.935846 | 395.694692 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 514.935846 | 412.228173 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 514.935846 | 477.226356 | 16.6 |
| YISLIYTNYEAGK | 28.57 | 36.57 | Positive | 514.935846 | 575.291502 | 16.6 |
| IQVWHAEHR | 28.76 | 36.76 | Positive | 392.540468 | 467.735743 | 13.1 |
| IQVWHAEHR | 28.76 | 36.76 | Positive | 392.540468 | 512.257571 | 13.1 |
| IQVWHAEHR | 28.76 | 36.76 | Positive | 392.540468 | 531.765031 | 13.1 |
| IQVWHAEHR | 28.76 | 36.76 | Positive | 395.876557 | 472.739877 | 13.1 |
| IQVWHAEHR | 28.76 | 36.76 | Positive | 395.876557 | 522.26584 | 13.1 |
| IQVWHAEHR | 28.76 | 36.76 | Positive | 395.876557 | 536.769166 | 13.1 |
| DDYPSSPPK | 28.77 | 36.77 | Positive | 503.229821 | 515.282388 | 19.4 |
| DDYPSSPPK | 28.77 | 36.77 | Positive | 503.229821 | 612.335152 | 19.4 |
| DDYPSSPPK | 28.77 | 36.77 | Positive | 503.229821 | 775.398481 | 19.4 |
| DDYPSSPPK | 28.77 | 36.77 | Positive | 507.236921 | 523.296587 | 19.4 |
| DDYPSSPPK | 28.77 | 36.77 | Positive | 507.236921 | 620.349351 | 19.4 |
| DDYPSSPPK | 28.77 | 36.77 | Positive | 507.236921 | 783.41268 | 19.4 |
| ALYEAGER | 29.27 | 37.27 | Positive | 454.727249 | 419.208692 | 17.8 |
| ALYEAGER | 29.27 | 37.27 | Positive | 454.727249 | 432.220122 | 17.8 |
| ALYEAGER | 29.27 | 37.27 | Positive | 454.727249 | 561.262716 | 17.8 |
| ALYEAGER | 29.27 | 37.27 | Positive | 459.731383 | 424.212827 | 17.8 |
| ALYEAGER | 29.27 | 37.27 | Positive | 459.731383 | 442.228391 | 17.8 |
| ALYEAGER | 29.27 | 37.27 | Positive | 459.731383 | 571.270985 | 17.8 |
| GAGTDDSTLVR | 29.3 | 37.3 | Positive | 546.270009 | 575.351137 | 20.9 |
| GAGTDDSTLVR | 29.3 | 37.3 | Positive | 546.270009 | 690.37808 | 20.9 |
| GAGTDDSTLVR | 29.3 | 37.3 | Positive | 546.270009 | 805.405023 | 20.9 |
| GAGTDDSTLVR | 29.3 | 37.3 | Positive | 551.274144 | 585.359406 | 20.9 |
| GAGTDDSTLVR | 29.3 | 37.3 | Positive | 551.274144 | 700.386349 | 20.9 |
| GAGTDDSTLVR | 29.3 | 37.3 | Positive | 551.274144 | 815.413292 | 20.9 |
| EGVVGAVEK | 29.57 | 37.57 | Positive | 444.245275 | 446.260925 | 17.4 |
| EGVVGAVEK | 29.57 | 37.57 | Positive | 444.245275 | 503.282388 | 17.4 |
| EGVVGAVEK | 29.57 | 37.57 | Positive | 444.245275 | 602.350802 | 17.4 |
| EGVVGAVEK | 29.57 | 37.57 | Positive | 448.252374 | 454.275124 | 17.4 |
| EGVVGAVEK | 29.57 | 37.57 | Positive | 448.252374 | 511.296587 | 17.4 |
| EGVVGAVEK | 29.57 | 37.57 | Positive | 448.252374 | 610.365001 | 17.4 |
| YLQETYSK | 29.68 | 37.68 | Positive | 516.255839 | 397.208161 | 19.9 |
| YLQETYSK | 29.68 | 37.68 | Positive | 516.255839 | 498.255839 | 19.9 |
| YLQETYSK | 29.68 | 37.68 | Positive | 516.255839 | 755.35701 | 19.9 |
| YLQETYSK | 29.68 | 37.68 | Positive | 520.262939 | 405.22236 | 19.9 |
| YLQETYSK | 29.68 | 37.68 | Positive | 520.262939 | 506.270038 | 19.9 |
| YLQETYSK | 29.68 | 37.68 | Positive | 520.262939 | 763.371209 | 19.9 |
| HGFLPR | 29.74 | 37.74 | Positive | 363.705923 | 385.25578 | 14.7 |
| HGFLPR | 29.74 | 37.74 | Positive | 363.705923 | 532.324194 | 14.7 |
| HGFLPR | 29.74 | 37.74 | Positive | 363.705923 | 589.345657 | 14.7 |
| HGFLPR | 29.74 | 37.74 | Positive | 366.715987 | 391.275909 | 14.7 |
| HGFLPR | 29.74 | 37.74 | Positive | 366.715987 | 538.344323 | 14.7 |
| HGFLPR | 29.74 | 37.74 | Positive | 366.715987 | 595.365786 | 14.7 |
| TDEGIAYR | 29.82 | 37.82 | Positive | 462.724706 | 522.303458 | 18 |
| TDEGIAYR | 29.82 | 37.82 | Positive | 462.724706 | 579.324922 | 18 |
| TDEGIAYR | 29.82 | 37.82 | Positive | 462.724706 | 708.367515 | 18 |
| TDEGIAYR | 29.82 | 37.82 | Positive | 467.728841 | 532.311727 | 18 |
| TDEGIAYR | 29.82 | 37.82 | Positive | 467.728841 | 589.333191 | 18 |
| TDEGIAYR | 29.82 | 37.82 | Positive | 467.728841 | 718.375784 | 18 |
| DGGAWGTEQR | 29.86 | 37.86 | Positive | 538.741419 | 590.289265 | 20.6 |
| DGGAWGTEQR | 29.86 | 37.86 | Positive | 538.741419 | 776.368578 | 20.6 |
| DGGAWGTEQR | 29.86 | 37.86 | Positive | 538.741419 | 847.405691 | 20.6 |
| DGGAWGTEQR | 29.86 | 37.86 | Positive | 543.745553 | 600.297534 | 20.6 |
| DGGAWGTEQR | 29.86 | 37.86 | Positive | 543.745553 | 786.376847 | 20.6 |
| DGGAWGTEQR | 29.86 | 37.86 | Positive | 543.745553 | 857.41396 | 20.6 |
| NYVTPVNR | 30.03 | 38.03 | Positive | 481.756341 | 485.283057 | 18.7 |
| NYVTPVNR | 30.03 | 38.03 | Positive | 481.756341 | 586.330736 | 18.7 |
| NYVTPVNR | 30.03 | 38.03 | Positive | 481.756341 | 685.399149 | 18.7 |
| NYVTPVNR | 30.03 | 38.03 | Positive | 486.760475 | 495.291326 | 18.7 |
| NYVTPVNR | 30.03 | 38.03 | Positive | 486.760475 | 596.339005 | 18.7 |
| NYVTPVNR | 30.03 | 38.03 | Positive | 486.760475 | 695.407418 | 18.7 |
| YLSNAYAR | 30.83 | 38.83 | Positive | 479.243066 | 594.299435 | 18.6 |
| YLSNAYAR | 30.83 | 38.83 | Positive | 479.243066 | 681.331464 | 18.6 |
| YLSNAYAR | 30.83 | 38.83 | Positive | 479.243066 | 794.415528 | 18.6 |
| YLSNAYAR | 30.83 | 38.83 | Positive | 484.247201 | 604.307704 | 18.6 |
| YLSNAYAR | 30.83 | 38.83 | Positive | 484.247201 | 691.339733 | 18.6 |
| YLSNAYAR | 30.83 | 38.83 | Positive | 484.247201 | 804.423797 | 18.6 |
| FGNDVQHFK | 30.9 | 38.9 | Positive | 364.513807 | 329.687199 | 12.3 |
| FGNDVQHFK | 30.9 | 38.9 | Positive | 364.513807 | 444.222134 | 12.3 |
| FGNDVQHFK | 30.9 | 38.9 | Positive | 364.513807 | 559.298707 | 12.3 |
| FGNDVQHFK | 30.9 | 38.9 | Positive | 367.185207 | 333.694298 | 12.3 |
| FGNDVQHFK | 30.9 | 38.9 | Positive | 367.185207 | 448.229233 | 12.3 |
| FGNDVQHFK | 30.9 | 38.9 | Positive | 367.185207 | 567.312906 | 12.3 |
| FNAHGDANTIVC[+57.0]NSK | 31.92 | 39.92 | Positive | 549.922977 | 508.218408 | 17.7 |
| FNAHGDANTIVC[+57.0]NSK | 31.92 | 39.92 | Positive | 549.922977 | 607.286822 | 17.7 |
| FNAHGDANTIVC[+57.0]NSK | 31.92 | 39.92 | Positive | 549.922977 | 720.370886 | 17.7 |
| FNAHGDANTIVC[+57.0]NSK | 31.92 | 39.92 | Positive | 552.594377 | 516.232607 | 17.7 |
| FNAHGDANTIVC[+57.0]NSK | 31.92 | 39.92 | Positive | 552.594377 | 615.301021 | 17.7 |
| FNAHGDANTIVC[+57.0]NSK | 31.92 | 39.92 | Positive | 552.594377 | 728.385085 | 17.7 |
| QLQQAQAAGAEQEVEK | 33.14 | 41.14 | Positive | 576.623473 | 480.735271 | 18.5 |
| QLQQAQAAGAEQEVEK | 33.14 | 41.14 | Positive | 576.623473 | 632.324982 | 18.5 |
| QLQQAQAAGAEQEVEK | 33.14 | 41.14 | Positive | 576.623473 | 761.367575 | 18.5 |
| QLQQAQAAGAEQEVEK | 33.14 | 41.14 | Positive | 579.294873 | 484.74237 | 18.5 |
| QLQQAQAAGAEQEVEK | 33.14 | 41.14 | Positive | 579.294873 | 640.339181 | 18.5 |
| QLQQAQAAGAEQEVEK | 33.14 | 41.14 | Positive | 579.294873 | 769.381774 | 18.5 |
| QLSSGVSEIR | 33.94 | 41.94 | Positive | 538.290745 | 660.367515 | 20.6 |
| QLSSGVSEIR | 33.94 | 41.94 | Positive | 538.290745 | 747.399543 | 20.6 |
| QLSSGVSEIR | 33.94 | 41.94 | Positive | 538.290745 | 834.431572 | 20.6 |
| QLSSGVSEIR | 33.94 | 41.94 | Positive | 543.294879 | 670.375784 | 20.6 |
| QLSSGVSEIR | 33.94 | 41.94 | Positive | 543.294879 | 757.407812 | 20.6 |
| QLSSGVSEIR | 33.94 | 41.94 | Positive | 543.294879 | 844.439841 | 20.6 |
| EDEVEEWQHR | 34.18 | 42.18 | Positive | 452.865345 | 378.182812 | 14.9 |
| EDEVEEWQHR | 34.18 | 42.18 | Positive | 452.865345 | 442.704108 | 14.9 |
| EDEVEEWQHR | 34.18 | 42.18 | Positive | 452.865345 | 626.315754 | 14.9 |
| EDEVEEWQHR | 34.18 | 42.18 | Positive | 456.201435 | 383.186946 | 14.9 |
| EDEVEEWQHR | 34.18 | 42.18 | Positive | 456.201435 | 447.708243 | 14.9 |
| EDEVEEWQHR | 34.18 | 42.18 | Positive | 456.201435 | 636.324023 | 14.9 |
| LFTGHPETLEK | 34.63 | 42.63 | Positive | 424.559193 | 506.258913 | 14 |
| LFTGHPETLEK | 34.63 | 42.63 | Positive | 424.559193 | 579.79312 | 14 |
| LFTGHPETLEK | 34.63 | 42.63 | Positive | 424.559193 | 716.382496 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 424.894242 | 388.213443 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 424.894242 | 472.258382 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 424.894242 | 536.779679 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 424.894242 | 580.295693 | 14 |
| LFTGHPETLEK | 34.63 | 42.63 | Positive | 427.230593 | 510.266013 | 14 |
| LFTGHPETLEK | 34.63 | 42.63 | Positive | 427.230593 | 583.80022 | 14 |
| LFTGHPETLEK | 34.63 | 42.63 | Positive | 427.230593 | 724.396695 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 427.565641 | 392.220543 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 427.565641 | 476.265481 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 427.565641 | 540.786778 | 14 |
| LSEPAELTDAVK | 34.63 | 42.63 | Positive | 427.565641 | 584.302792 | 14 |
| ILNDDTALK | 34.77 | 42.77 | Positive | 501.776939 | 662.335546 | 19.4 |
| ILNDDTALK | 34.77 | 42.77 | Positive | 501.776939 | 776.378474 | 19.4 |
| ILNDDTALK | 34.77 | 42.77 | Positive | 501.776939 | 889.462538 | 19.4 |
| ILNDDTALK | 34.77 | 42.77 | Positive | 505.784038 | 670.349745 | 19.4 |
| ILNDDTALK | 34.77 | 42.77 | Positive | 505.784038 | 784.392673 | 19.4 |
| ILNDDTALK | 34.77 | 42.77 | Positive | 505.784038 | 897.476737 | 19.4 |
| DGVVEITGK | 34.96 | 42.96 | Positive | 459.250557 | 547.308603 | 17.9 |
| DGVVEITGK | 34.96 | 42.96 | Positive | 459.250557 | 646.377017 | 17.9 |
| DGVVEITGK | 34.96 | 42.96 | Positive | 459.250557 | 745.445431 | 17.9 |
| DGVVEITGK | 34.96 | 42.96 | Positive | 463.257656 | 555.322802 | 17.9 |
| DGVVEITGK | 34.96 | 42.96 | Positive | 463.257656 | 654.391216 | 17.9 |
| DGVVEITGK | 34.96 | 42.96 | Positive | 463.257656 | 753.45963 | 17.9 |
| IVGGWEC[+57.0]EK | 35.8 | 43.8 | Positive | 539.255316 | 436.186045 | 20.6 |
| IVGGWEC[+57.0]EK | 35.8 | 43.8 | Positive | 539.255316 | 865.350879 | 20.6 |
| IVGGWEC[+57.0]EK | 35.8 | 43.8 | Positive | 539.255316 | 964.419293 | 20.6 |
| IVGGWEC[+57.0]EK | 35.8 | 43.8 | Positive | 541.763703 | 436.186045 | 20.6 |
| IVGGWEC[+57.0]EK | 35.8 | 43.8 | Positive | 541.763703 | 865.350879 | 20.6 |
| IVGGWEC[+57.0]EK | 35.8 | 43.8 | Positive | 541.763703 | 969.436067 | 20.6 |
| ATAVVDGAFK | 36.05 | 44.05 | Positive | 489.766374 | 636.335152 | 19 |
| ATAVVDGAFK | 36.05 | 44.05 | Positive | 489.766374 | 735.403566 | 19 |
| ATAVVDGAFK | 36.05 | 44.05 | Positive | 489.766374 | 806.44068 | 19 |
| ATAVVDGAFK | 36.05 | 44.05 | Positive | 493.773474 | 644.349351 | 19 |
| ATAVVDGAFK | 36.05 | 44.05 | Positive | 493.773474 | 743.417765 | 19 |
| ATAVVDGAFK | 36.05 | 44.05 | Positive | 493.773474 | 814.454879 | 19 |
| FEELGVK | 36.15 | 44.15 | Positive | 411.223811 | 303.202681 | 16.3 |
| FEELGVK | 36.15 | 44.15 | Positive | 411.223811 | 416.286745 | 16.3 |
| FEELGVK | 36.15 | 44.15 | Positive | 411.223811 | 545.329339 | 16.3 |
| FEELGVK | 36.15 | 44.15 | Positive | 415.23091 | 311.21688 | 16.3 |
| FEELGVK | 36.15 | 44.15 | Positive | 415.23091 | 424.300944 | 16.3 |
| FEELGVK | 36.15 | 44.15 | Positive | 415.23091 | 553.343538 | 16.3 |
| LHIVQVVC[+57.0]K | 36.27 | 44.27 | Positive | 365.882955 | 307.143452 | 12.3 |
| LHIVQVVC[+57.0]K | 36.27 | 44.27 | Positive | 365.882955 | 406.211866 | 12.3 |
| LHIVQVVC[+57.0]K | 36.27 | 44.27 | Positive | 365.882955 | 505.28028 | 12.3 |
| LHIVQVVC[+57.0]K | 36.27 | 44.27 | Positive | 368.554354 | 315.157651 | 12.3 |
| LHIVQVVC[+57.0]K | 36.27 | 44.27 | Positive | 368.554354 | 414.226065 | 12.3 |
| LHIVQVVC[+57.0]K | 36.27 | 44.27 | Positive | 368.554354 | 513.294479 | 12.3 |
| ESDTSYVSLK | 36.41 | 44.41 | Positive | 564.774593 | 609.360639 | 21.5 |
| ESDTSYVSLK | 36.41 | 44.41 | Positive | 564.774593 | 696.392667 | 21.5 |
| ESDTSYVSLK | 36.41 | 44.41 | Positive | 564.774593 | 797.440346 | 21.5 |
| ESDTSYVSLK | 36.41 | 44.41 | Positive | 568.781693 | 617.374838 | 21.5 |
| ESDTSYVSLK | 36.41 | 44.41 | Positive | 568.781693 | 704.406866 | 21.5 |
| ESDTSYVSLK | 36.41 | 44.41 | Positive | 568.781693 | 805.454545 | 21.5 |
| YLAPSGPSGTLK | 36.77 | 44.77 | Positive | 595.82442 | 746.404294 | 22.6 |
| YLAPSGPSGTLK | 36.77 | 44.77 | Positive | 595.82442 | 843.457058 | 22.6 |
| YLAPSGPSGTLK | 36.77 | 44.77 | Positive | 595.82442 | 914.494172 | 22.6 |
| YLAPSGPSGTLK | 36.77 | 44.77 | Positive | 599.83152 | 754.418493 | 22.6 |
| YLAPSGPSGTLK | 36.77 | 44.77 | Positive | 599.83152 | 851.471257 | 22.6 |
| YLAPSGPSGTLK | 36.77 | 44.77 | Positive | 599.83152 | 922.508371 | 22.6 |
| FLIVAHDDGR | 36.85 | 44.85 | Positive | 381.536612 | 300.130245 | 12.8 |
| FLIVAHDDGR | 36.85 | 44.85 | Positive | 381.536612 | 385.183009 | 12.8 |
| FLIVAHDDGR | 36.85 | 44.85 | Positive | 381.536612 | 441.725041 | 12.8 |
| FLIVAHDDGR | 36.85 | 44.85 | Positive | 384.872701 | 305.134379 | 12.8 |
| FLIVAHDDGR | 36.85 | 44.85 | Positive | 384.872701 | 390.187143 | 12.8 |
| FLIVAHDDGR | 36.85 | 44.85 | Positive | 384.872701 | 446.729175 | 12.8 |
| SIEEIVR | 36.88 | 44.88 | Positive | 423.239992 | 516.314023 | 16.7 |
| SIEEIVR | 36.88 | 44.88 | Positive | 423.239992 | 645.356616 | 16.7 |
| SIEEIVR | 36.88 | 44.88 | Positive | 423.239992 | 758.44068 | 16.7 |
| SIEEIVR | 36.88 | 44.88 | Positive | 428.244127 | 526.322292 | 16.7 |
| SIEEIVR | 36.88 | 44.88 | Positive | 428.244127 | 655.364885 | 16.7 |
| SIEEIVR | 36.88 | 44.88 | Positive | 428.244127 | 768.448949 | 16.7 |
| YLASASTMDHAR | 38.6 | 46.6 | Positive | 441.543438 | 488.219265 | 14.5 |
| YLASASTMDHAR | 38.6 | 46.6 | Positive | 441.543438 | 523.737822 | 14.5 |
| YLASASTMDHAR | 38.6 | 46.6 | Positive | 441.543438 | 817.362112 | 14.5 |
| YLASASTMDHAR | 38.6 | 46.6 | Positive | 443.550147 | 491.22933 | 14.5 |
| YLASASTMDHAR | 38.6 | 46.6 | Positive | 443.550147 | 526.747887 | 14.5 |
| YLASASTMDHAR | 38.6 | 46.6 | Positive | 443.550147 | 823.382241 | 14.5 |
| QVLFSADDR | 38.68 | 46.68 | Positive | 525.764363 | 563.24198 | 20.2 |
| QVLFSADDR | 38.68 | 46.68 | Positive | 525.764363 | 710.310394 | 20.2 |
| QVLFSADDR | 38.68 | 46.68 | Positive | 525.764363 | 823.394458 | 20.2 |
| QVLFSADDR | 38.68 | 46.68 | Positive | 530.768497 | 573.250249 | 20.2 |
| QVLFSADDR | 38.68 | 46.68 | Positive | 530.768497 | 720.318663 | 20.2 |
| QVLFSADDR | 38.68 | 46.68 | Positive | 530.768497 | 833.402727 | 20.2 |
| ATADDELSFK | 38.68 | 46.68 | Positive | 548.761486 | 738.366846 | 21 |
| ATADDELSFK | 38.68 | 46.68 | Positive | 548.761486 | 853.393789 | 21 |
| ATADDELSFK | 38.68 | 46.68 | Positive | 548.761486 | 924.430903 | 21 |
| ATADDELSFK | 38.68 | 46.68 | Positive | 552.768585 | 746.381045 | 21 |
| ATADDELSFK | 38.68 | 46.68 | Positive | 552.768585 | 861.407988 | 21 |
| ATADDELSFK | 38.68 | 46.68 | Positive | 552.768585 | 932.445102 | 21 |
| EQVIAALR | 38.82 | 46.82 | Positive | 450.269084 | 430.277243 | 17.6 |
| EQVIAALR | 38.82 | 46.82 | Positive | 450.269084 | 543.361307 | 17.6 |
| EQVIAALR | 38.82 | 46.82 | Positive | 450.269084 | 642.429721 | 17.6 |
| EQVIAALR | 38.82 | 46.82 | Positive | 455.273219 | 440.285512 | 17.6 |
| EQVIAALR | 38.82 | 46.82 | Positive | 455.273219 | 553.369576 | 17.6 |
| EQVIAALR | 38.82 | 46.82 | Positive | 455.273219 | 652.43799 | 17.6 |
| LSC[+57.0]FAQTVSPAEK | 39.09 | 47.09 | Positive | 719.355759 | 531.277303 | 26.7 |
| LSC[+57.0]FAQTVSPAEK | 39.09 | 47.09 | Positive | 719.355759 | 731.393395 | 26.7 |
| LSC[+57.0]FAQTVSPAEK | 39.09 | 47.09 | Positive | 719.355759 | 930.489087 | 26.7 |
| LSC[+57.0]FAQTVSPAEK | 39.09 | 47.09 | Positive | 723.362858 | 539.291502 | 26.7 |
| LSC[+57.0]FAQTVSPAEK | 39.09 | 47.09 | Positive | 723.362858 | 739.407594 | 26.7 |
| LSC[+57.0]FAQTVSPAEK | 39.09 | 47.09 | Positive | 723.362858 | 938.503286 | 26.7 |
| VLVSLSAGGR | 39.48 | 47.48 | Positive | 479.787641 | 447.231021 | 18.6 |
| VLVSLSAGGR | 39.48 | 47.48 | Positive | 479.787641 | 647.347114 | 18.6 |
| VLVSLSAGGR | 39.48 | 47.48 | Positive | 479.787641 | 746.415528 | 18.6 |
| VLVSLSAGGR | 39.48 | 47.48 | Positive | 484.791775 | 457.23929 | 18.6 |
| VLVSLSAGGR | 39.48 | 47.48 | Positive | 484.791775 | 657.355383 | 18.6 |
| VLVSLSAGGR | 39.48 | 47.48 | Positive | 484.791775 | 756.423797 | 18.6 |
| LSEDYGVLK | 39.76 | 47.76 | Positive | 512.271489 | 694.377017 | 19.7 |
| LSEDYGVLK | 39.76 | 47.76 | Positive | 512.271489 | 823.41961 | 19.7 |
| LSEDYGVLK | 39.76 | 47.76 | Positive | 512.271489 | 910.451639 | 19.7 |
| LSEDYGVLK | 39.76 | 47.76 | Positive | 516.278589 | 702.391216 | 19.7 |
| LSEDYGVLK | 39.76 | 47.76 | Positive | 516.278589 | 831.433809 | 19.7 |
| LSEDYGVLK | 39.76 | 47.76 | Positive | 516.278589 | 918.465838 | 19.7 |
| GLGTDDNTLIR | 40.04 | 48.04 | Positive | 587.806759 | 502.334758 | 22.3 |
| GLGTDDNTLIR | 40.04 | 48.04 | Positive | 587.806759 | 559.296027 | 22.3 |
| GLGTDDNTLIR | 40.04 | 48.04 | Positive | 587.806759 | 731.404629 | 22.3 |
| GLGTDDNTLIR | 40.04 | 48.04 | Positive | 592.810893 | 512.343027 | 22.3 |
| GLGTDDNTLIR | 40.04 | 48.04 | Positive | 592.810893 | 564.300162 | 22.3 |
| GLGTDDNTLIR | 40.04 | 48.04 | Positive | 592.810893 | 741.412898 | 22.3 |
| ASC[+57.0]LYGQLPK | 40.17 | 48.17 | Positive | 568.792066 | 542.329673 | 21.6 |
| ASC[+57.0]LYGQLPK | 40.17 | 48.17 | Positive | 568.792066 | 705.393001 | 21.6 |
| ASC[+57.0]LYGQLPK | 40.17 | 48.17 | Positive | 568.792066 | 818.477066 | 21.6 |
| C[+57.0]GTGIVGVFVK | 40.17 | 48.17 | Positive | 568.810259 | 488.794935 | 21.6 |
| C[+57.0]GTGIVGVFVK | 40.17 | 48.17 | Positive | 568.810259 | 549.339509 | 21.6 |
| C[+57.0]GTGIVGVFVK | 40.17 | 48.17 | Positive | 568.810259 | 818.513451 | 21.6 |
| ASC[+57.0]LYGQLPK | 40.17 | 48.17 | Positive | 572.799166 | 550.343872 | 21.6 |
| ASC[+57.0]LYGQLPK | 40.17 | 48.17 | Positive | 572.799166 | 713.4072 | 21.6 |
| ASC[+57.0]LYGQLPK | 40.17 | 48.17 | Positive | 572.799166 | 826.491265 | 21.6 |
| C[+57.0]GTGIVGVFVK | 40.17 | 48.17 | Positive | 572.817358 | 492.802034 | 21.6 |
| C[+57.0]GTGIVGVFVK | 40.17 | 48.17 | Positive | 572.817358 | 557.353708 | 21.6 |
| C[+57.0]GTGIVGVFVK | 40.17 | 48.17 | Positive | 572.817358 | 826.52765 | 21.6 |
| LVQAFQYTDK | 40.65 | 48.65 | Positive | 606.816595 | 801.377745 | 22.9 |
| LVQAFQYTDK | 40.65 | 48.65 | Positive | 606.816595 | 872.414859 | 22.9 |
| LVQAFQYTDK | 40.65 | 48.65 | Positive | 606.816595 | 1000.473437 | 22.9 |
| LVQAFQYTDK | 40.65 | 48.65 | Positive | 610.823695 | 809.391944 | 22.9 |
| LVQAFQYTDK | 40.65 | 48.65 | Positive | 610.823695 | 880.429058 | 22.9 |
| LVQAFQYTDK | 40.65 | 48.65 | Positive | 610.823695 | 1008.487636 | 22.9 |
| GMAVTISVK | 40.68 | 48.68 | Positive | 453.25987 | 547.344989 | 17.7 |
| GMAVTISVK | 40.68 | 48.68 | Positive | 453.25987 | 646.413403 | 17.7 |
| GMAVTISVK | 40.68 | 48.68 | Positive | 453.25987 | 717.450516 | 17.7 |
| GMAVTISVK | 40.68 | 48.68 | Positive | 457.26697 | 555.359188 | 17.7 |
| GMAVTISVK | 40.68 | 48.68 | Positive | 457.26697 | 654.427602 | 17.7 |
| GMAVTISVK | 40.68 | 48.68 | Positive | 457.26697 | 725.464715 | 17.7 |
| LPDGYEFK | 40.94 | 48.94 | Positive | 484.739825 | 428.197793 | 18.8 |
| LPDGYEFK | 40.94 | 48.94 | Positive | 484.739825 | 758.335546 | 18.8 |
| LPDGYEFK | 40.94 | 48.94 | Positive | 484.739825 | 855.38831 | 18.8 |
| LPDGYEFK | 40.94 | 48.94 | Positive | 488.746925 | 432.204893 | 18.8 |
| LPDGYEFK | 40.94 | 48.94 | Positive | 488.746925 | 766.349745 | 18.8 |
| LPDGYEFK | 40.94 | 48.94 | Positive | 488.746925 | 863.402509 | 18.8 |
| SLDFYTR | 41.11 | 49.11 | Positive | 451.224342 | 586.298373 | 17.7 |
| SLDFYTR | 41.11 | 49.11 | Positive | 451.224342 | 701.325316 | 17.7 |
| SLDFYTR | 41.11 | 49.11 | Positive | 451.224342 | 814.40938 | 17.7 |
| SLDFYTR | 41.11 | 49.11 | Positive | 456.228477 | 596.306642 | 17.7 |
| SLDFYTR | 41.11 | 49.11 | Positive | 456.228477 | 711.333585 | 17.7 |
| SLDFYTR | 41.11 | 49.11 | Positive | 456.228477 | 824.417649 | 17.7 |
| TPAQFDADELR | 41.13 | 49.13 | Positive | 631.804216 | 718.336609 | 23.8 |
| TPAQFDADELR | 41.13 | 49.13 | Positive | 631.804216 | 865.405023 | 23.8 |
| TPAQFDADELR | 41.13 | 49.13 | Positive | 631.804216 | 1064.500714 | 23.8 |
| TPAQFDADELR | 41.13 | 49.13 | Positive | 636.808351 | 728.344878 | 23.8 |
| TPAQFDADELR | 41.13 | 49.13 | Positive | 636.808351 | 875.413292 | 23.8 |
| TPAQFDADELR | 41.13 | 49.13 | Positive | 636.808351 | 1074.508983 | 23.8 |
| ELSDIALR | 41.21 | 49.21 | Positive | 458.758549 | 472.324194 | 17.9 |
| ELSDIALR | 41.21 | 49.21 | Positive | 458.758549 | 587.351137 | 17.9 |
| ELSDIALR | 41.21 | 49.21 | Positive | 458.758549 | 674.383165 | 17.9 |
| ELSDIALR | 41.21 | 49.21 | Positive | 463.762684 | 482.332463 | 17.9 |
| ELSDIALR | 41.21 | 49.21 | Positive | 463.762684 | 597.359406 | 17.9 |
| ELSDIALR | 41.21 | 49.21 | Positive | 463.762684 | 684.391434 | 17.9 |
| IDIDPEETVK | 41.58 | 49.58 | Positive | 579.798068 | 702.366846 | 22 |
| IDIDPEETVK | 41.58 | 49.58 | Positive | 579.798068 | 817.393789 | 22 |
| IDIDPEETVK | 41.58 | 49.58 | Positive | 579.798068 | 930.477853 | 22 |
| IDIDPEETVK | 41.58 | 49.58 | Positive | 583.805168 | 710.381045 | 22 |
| IDIDPEETVK | 41.58 | 49.58 | Positive | 583.805168 | 825.407988 | 22 |
| IDIDPEETVK | 41.58 | 49.58 | Positive | 583.805168 | 938.492052 | 22 |
| GC[+57.0]TDNLTLTVAR | 41.61 | 49.61 | Positive | 660.832451 | 559.356222 | 24.8 |
| GC[+57.0]TDNLTLTVAR | 41.61 | 49.61 | Positive | 660.832451 | 660.403901 | 24.8 |
| GC[+57.0]TDNLTLTVAR | 41.61 | 49.61 | Positive | 660.832451 | 1103.605514 | 24.8 |
| GC[+57.0]TDNLTLTVAR | 41.61 | 49.61 | Positive | 665.836585 | 569.364491 | 24.8 |
| GC[+57.0]TDNLTLTVAR | 41.61 | 49.61 | Positive | 665.836585 | 670.41217 | 24.8 |
| GC[+57.0]TDNLTLTVAR | 41.61 | 49.61 | Positive | 665.836585 | 1113.613783 | 24.8 |
| DSNNLC[+57.0]LHFNPR | 42.23 | 50.23 | Positive | 496.233375 | 472.231979 | 16.2 |
| DSNNLC[+57.0]LHFNPR | 42.23 | 50.23 | Positive | 496.233375 | 528.774011 | 16.2 |
| DSNNLC[+57.0]LHFNPR | 42.23 | 50.23 | Positive | 496.233375 | 642.816938 | 16.2 |
| DSNNLC[+57.0]LHFNPR | 42.23 | 50.23 | Positive | 499.569464 | 477.236113 | 16.2 |
| DSNNLC[+57.0]LHFNPR | 42.23 | 50.23 | Positive | 499.569464 | 533.778145 | 16.2 |
| DSNNLC[+57.0]LHFNPR | 42.23 | 50.23 | Positive | 499.569464 | 647.821073 | 16.2 |
| IALLEEAR | 42.3 | 50.3 | Positive | 457.768917 | 504.241252 | 17.9 |
| IALLEEAR | 42.3 | 50.3 | Positive | 457.768917 | 617.325316 | 17.9 |
| IALLEEAR | 42.3 | 50.3 | Positive | 457.768917 | 801.446494 | 17.9 |
| IALLEEAR | 42.3 | 50.3 | Positive | 462.773051 | 514.249521 | 17.9 |
| IALLEEAR | 42.3 | 50.3 | Positive | 462.773051 | 627.333585 | 17.9 |
| IALLEEAR | 42.3 | 50.3 | Positive | 462.773051 | 811.454763 | 17.9 |
| AAYLQETGKPLDETLK | 42.46 | 50.46 | Positive | 592.98412 | 679.861731 | 19 |
| AAYLQETGKPLDETLK | 42.46 | 50.46 | Positive | 592.98412 | 736.403763 | 19 |
| AAYLQETGKPLDETLK | 42.46 | 50.46 | Positive | 592.98412 | 817.935427 | 19 |
| AAYLQETGKPLDETLK | 42.46 | 50.46 | Positive | 595.655519 | 683.868831 | 19 |
| AAYLQETGKPLDETLK | 42.46 | 50.46 | Positive | 595.655519 | 740.410863 | 19 |
| AAYLQETGKPLDETLK | 42.46 | 50.46 | Positive | 595.655519 | 821.942527 | 19 |
| SSDLVALSGGHTFGK | 42.73 | 50.73 | Positive | 492.587812 | 487.756341 | 16 |
| SSDLVALSGGHTFGK | 42.73 | 50.73 | Positive | 492.587812 | 537.290548 | 16 |
| SSDLVALSGGHTFGK | 42.73 | 50.73 | Positive | 492.587812 | 651.346051 | 16 |
| SSDLVALSGGHTFGK | 42.73 | 50.73 | Positive | 495.259211 | 491.76344 | 16 |
| SSDLVALSGGHTFGK | 42.73 | 50.73 | Positive | 495.259211 | 541.297647 | 16 |
| SSDLVALSGGHTFGK | 42.73 | 50.73 | Positive | 495.259211 | 655.353151 | 16 |
| EFSGYVESGLK | 42.74 | 50.74 | Positive | 608.298235 | 533.292953 | 23 |
| EFSGYVESGLK | 42.74 | 50.74 | Positive | 608.298235 | 632.361367 | 23 |
| EFSGYVESGLK | 42.74 | 50.74 | Positive | 608.298235 | 939.478188 | 23 |
| EFSGYVESGLK | 42.74 | 50.74 | Positive | 612.305335 | 541.307152 | 23 |
| EFSGYVESGLK | 42.74 | 50.74 | Positive | 612.305335 | 640.375566 | 23 |
| EFSGYVESGLK | 42.74 | 50.74 | Positive | 612.305335 | 947.492387 | 23 |
| ELPSFVGEK | 43.23 | 51.23 | Positive | 503.266207 | 432.245275 | 19.4 |
| ELPSFVGEK | 43.23 | 51.23 | Positive | 503.266207 | 579.313689 | 19.4 |
| ELPSFVGEK | 43.23 | 51.23 | Positive | 503.266207 | 763.398481 | 19.4 |
| ELPSFVGEK | 43.23 | 51.23 | Positive | 506.276271 | 438.265404 | 19.4 |
| ELPSFVGEK | 43.23 | 51.23 | Positive | 506.276271 | 585.333818 | 19.4 |
| ELPSFVGEK | 43.23 | 51.23 | Positive | 506.276271 | 769.41861 | 19.4 |
| GVTFNVTTVDTK | 43.85 | 51.85 | Positive | 641.337892 | 664.351196 | 24.1 |
| GVTFNVTTVDTK | 43.85 | 51.85 | Positive | 641.337892 | 763.41961 | 24.1 |
| GVTFNVTTVDTK | 43.85 | 51.85 | Positive | 641.337892 | 877.462538 | 24.1 |
| GVTFNVTTVDTK | 43.85 | 51.85 | Positive | 645.344991 | 672.365395 | 24.1 |
| GVTFNVTTVDTK | 43.85 | 51.85 | Positive | 645.344991 | 771.433809 | 24.1 |
| GVTFNVTTVDTK | 43.85 | 51.85 | Positive | 645.344991 | 885.476737 | 24.1 |
| LIADVAPSAIR | 43.89 | 51.89 | Positive | 563.334955 | 543.324922 | 21.5 |
| LIADVAPSAIR | 43.89 | 51.89 | Positive | 563.334955 | 614.362036 | 21.5 |
| LIADVAPSAIR | 43.89 | 51.89 | Positive | 563.334955 | 899.494506 | 21.5 |
| LIADVAPSAIR | 43.89 | 51.89 | Positive | 568.33909 | 553.333191 | 21.5 |
| LIADVAPSAIR | 43.89 | 51.89 | Positive | 568.33909 | 624.370305 | 21.5 |
| LIADVAPSAIR | 43.89 | 51.89 | Positive | 568.33909 | 909.502775 | 21.5 |
| IAWALSR | 44.03 | 52.03 | Positive | 408.739962 | 375.235044 | 16.2 |
| IAWALSR | 44.03 | 52.03 | Positive | 408.739962 | 446.272158 | 16.2 |
| IAWALSR | 44.03 | 52.03 | Positive | 408.739962 | 703.388585 | 16.2 |
| IAWALSR | 44.03 | 52.03 | Positive | 413.744097 | 385.243313 | 16.2 |
| IAWALSR | 44.03 | 52.03 | Positive | 413.744097 | 456.280427 | 16.2 |
| IAWALSR | 44.03 | 52.03 | Positive | 413.744097 | 713.396854 | 16.2 |
| GQTLVVQFTVK | 44.06 | 52.06 | Positive | 407.239684 | 246.181218 | 13.5 |
| GQTLVVQFTVK | 44.06 | 52.06 | Positive | 407.239684 | 347.228896 | 13.5 |
| GQTLVVQFTVK | 44.06 | 52.06 | Positive | 407.239684 | 494.29731 | 13.5 |
| GQTLVVQFTVK | 44.06 | 52.06 | Positive | 409.911083 | 254.195417 | 13.5 |
| GQTLVVQFTVK | 44.06 | 52.06 | Positive | 409.911083 | 355.243095 | 13.5 |
| GQTLVVQFTVK | 44.06 | 52.06 | Positive | 409.911083 | 502.311509 | 13.5 |
| DWRPAITIK | 44.74 | 52.74 | Positive | 367.213469 | 321.712882 | 12.3 |
| DWRPAITIK | 44.74 | 52.74 | Positive | 367.213469 | 399.763438 | 12.3 |
| DWRPAITIK | 44.74 | 52.74 | Positive | 367.213469 | 492.803094 | 12.3 |
| DWRPAITIK | 44.74 | 52.74 | Positive | 369.884869 | 325.719981 | 12.3 |
| DWRPAITIK | 44.74 | 52.74 | Positive | 369.884869 | 403.770537 | 12.3 |
| DWRPAITIK | 44.74 | 52.74 | Positive | 369.884869 | 496.810193 | 12.3 |
| AGLC[+57.0]QTFVYGGC[+57.0]R | 44.76 | 52.76 | Positive | 744.839753 | 612.255856 | 27.6 |
| AGLC[+57.0]QTFVYGGC[+57.0]R | 44.76 | 52.76 | Positive | 744.839753 | 858.392684 | 27.6 |
| AGLC[+57.0]QTFVYGGC[+57.0]R | 44.76 | 52.76 | Positive | 744.839753 | 959.440363 | 27.6 |
| AGLC[+57.0]QTFVYGGC[+57.0]R | 44.76 | 52.76 | Positive | 747.34814 | 612.255856 | 27.6 |
| AGLC[+57.0]QTFVYGGC[+57.0]R | 44.76 | 52.76 | Positive | 747.34814 | 863.409458 | 27.6 |
| AGLC[+57.0]QTFVYGGC[+57.0]R | 44.76 | 52.76 | Positive | 747.34814 | 964.457137 | 27.6 |
| ESESAPGDFSLSVK | 44.83 | 52.83 | Positive | 726.846278 | 949.498923 | 27 |
| ESESAPGDFSLSVK | 44.83 | 52.83 | Positive | 726.846278 | 1020.536037 | 27 |
| ESESAPGDFSLSVK | 44.83 | 52.83 | Positive | 726.846278 | 1107.568065 | 27 |
| ESESAPGDFSLSVK | 44.83 | 52.83 | Positive | 730.853378 | 957.513122 | 27 |
| ESESAPGDFSLSVK | 44.83 | 52.83 | Positive | 730.853378 | 1028.550236 | 27 |
| ESESAPGDFSLSVK | 44.83 | 52.83 | Positive | 730.853378 | 1115.582264 | 27 |
| DYGVYLEDSGHTLR | 45.05 | 53.05 | Positive | 542.258243 | 514.261987 | 17.5 |
| DYGVYLEDSGHTLR | 45.05 | 53.05 | Positive | 542.258243 | 595.793652 | 17.5 |
| DYGVYLEDSGHTLR | 45.05 | 53.05 | Positive | 542.258243 | 914.432635 | 17.5 |
| DYGVYLEDSGHTLR | 45.05 | 53.05 | Positive | 545.594332 | 519.266122 | 17.5 |
| DYGVYLEDSGHTLR | 45.05 | 53.05 | Positive | 545.594332 | 600.797786 | 17.5 |
| DYGVYLEDSGHTLR | 45.05 | 53.05 | Positive | 545.594332 | 924.440904 | 17.5 |
| WSEPNEEELIK | 45.46 | 53.46 | Positive | 687.332807 | 631.366118 | 25.7 |
| WSEPNEEELIK | 45.46 | 53.46 | Positive | 687.332807 | 971.504403 | 25.7 |
| WSEPNEEELIK | 45.46 | 53.46 | Positive | 687.332807 | 1100.546996 | 25.7 |
| WSEPNEEELIK | 45.46 | 53.46 | Positive | 691.339906 | 639.380317 | 25.7 |
| WSEPNEEELIK | 45.46 | 53.46 | Positive | 691.339906 | 979.518602 | 25.7 |
| WSEPNEEELIK | 45.46 | 53.46 | Positive | 691.339906 | 1108.561195 | 25.7 |
| WSALYDVR | 45.58 | 53.58 | Positive | 505.258716 | 389.214309 | 19.5 |
| WSALYDVR | 45.58 | 53.58 | Positive | 505.258716 | 552.277637 | 19.5 |
| WSALYDVR | 45.58 | 53.58 | Positive | 505.258716 | 665.361701 | 19.5 |
| WSALYDVR | 45.58 | 53.58 | Positive | 510.262851 | 399.222578 | 19.5 |
| WSALYDVR | 45.58 | 53.58 | Positive | 510.262851 | 562.285906 | 19.5 |
| WSALYDVR | 45.58 | 53.58 | Positive | 510.262851 | 675.36997 | 19.5 |
| TVEEAENIAVTSGVVR | 45.99 | 53.99 | Positive | 558.628336 | 517.309272 | 18 |
| TVEEAENIAVTSGVVR | 45.99 | 53.99 | Positive | 558.628336 | 618.35695 | 18 |
| TVEEAENIAVTSGVVR | 45.99 | 53.99 | Positive | 558.628336 | 717.425364 | 18 |
| TVEEAENIAVTSGVVR | 45.99 | 53.99 | Positive | 561.964425 | 527.317541 | 18 |
| TVEEAENIAVTSGVVR | 45.99 | 53.99 | Positive | 561.964425 | 628.365219 | 18 |
| TVEEAENIAVTSGVVR | 45.99 | 53.99 | Positive | 561.964425 | 727.433633 | 18 |
| ENVVQSVTSVAEK | 45.99 | 53.99 | Positive | 695.364638 | 820.441074 | 25.9 |
| ENVVQSVTSVAEK | 45.99 | 53.99 | Positive | 695.364638 | 948.499651 | 25.9 |
| ENVVQSVTSVAEK | 45.99 | 53.99 | Positive | 695.364638 | 1047.568065 | 25.9 |
| ENVVQSVTSVAEK | 45.99 | 53.99 | Positive | 699.371737 | 828.455273 | 25.9 |
| ENVVQSVTSVAEK | 45.99 | 53.99 | Positive | 699.371737 | 956.51385 | 25.9 |
| ENVVQSVTSVAEK | 45.99 | 53.99 | Positive | 699.371737 | 1055.582264 | 25.9 |
| DFEQPLAISR | 46.27 | 54.27 | Positive | 588.306395 | 446.272158 | 22.3 |
| DFEQPLAISR | 46.27 | 54.27 | Positive | 588.306395 | 656.408986 | 22.3 |
| DFEQPLAISR | 46.27 | 54.27 | Positive | 588.306395 | 784.467563 | 22.3 |
| DFEQPLAISR | 46.27 | 54.27 | Positive | 593.310529 | 456.280427 | 22.3 |
| DFEQPLAISR | 46.27 | 54.27 | Positive | 593.310529 | 666.417255 | 22.3 |
| DFEQPLAISR | 46.27 | 54.27 | Positive | 593.310529 | 794.475832 | 22.3 |
| VWSPLVTEEGK | 46.42 | 54.42 | Positive | 622.829703 | 563.267132 | 23.5 |
| VWSPLVTEEGK | 46.42 | 54.42 | Positive | 622.829703 | 872.472374 | 23.5 |
| VWSPLVTEEGK | 46.42 | 54.42 | Positive | 622.829703 | 959.504403 | 23.5 |
| VWSPLVTEEGK | 46.42 | 54.42 | Positive | 626.836802 | 571.281331 | 23.5 |
| VWSPLVTEEGK | 46.42 | 54.42 | Positive | 626.836802 | 880.486573 | 23.5 |
| VWSPLVTEEGK | 46.42 | 54.42 | Positive | 626.836802 | 967.518602 | 23.5 |
| SEIDLVQIK | 46.46 | 54.46 | Positive | 522.800414 | 600.407923 | 20.1 |
| SEIDLVQIK | 46.46 | 54.46 | Positive | 522.800414 | 715.434866 | 20.1 |
| SEIDLVQIK | 46.46 | 54.46 | Positive | 522.800414 | 828.51893 | 20.1 |
| SEIDLVQIK | 46.46 | 54.46 | Positive | 526.807513 | 608.422122 | 20.1 |
| SEIDLVQIK | 46.46 | 54.46 | Positive | 526.807513 | 723.449065 | 20.1 |
| SEIDLVQIK | 46.46 | 54.46 | Positive | 526.807513 | 836.533129 | 20.1 |
| ALQASALNAWR | 46.47 | 54.47 | Positive | 600.827829 | 659.36237 | 22.7 |
| ALQASALNAWR | 46.47 | 54.47 | Positive | 600.827829 | 817.431512 | 22.7 |
| ALQASALNAWR | 46.47 | 54.47 | Positive | 600.827829 | 888.468626 | 22.7 |
| ALQASALNAWR | 46.47 | 54.47 | Positive | 605.831963 | 669.370639 | 22.7 |
| ALQASALNAWR | 46.47 | 54.47 | Positive | 605.831963 | 827.439781 | 22.7 |
| ALQASALNAWR | 46.47 | 54.47 | Positive | 605.831963 | 898.476895 | 22.7 |
| DHPFGFVAVPTK | 46.96 | 54.96 | Positive | 438.89955 | 444.28166 | 14.5 |
| DHPFGFVAVPTK | 46.96 | 54.96 | Positive | 438.89955 | 515.318774 | 14.5 |
| DHPFGFVAVPTK | 46.96 | 54.96 | Positive | 438.89955 | 614.387188 | 14.5 |
| DHPFGFVAVPTK | 46.96 | 54.96 | Positive | 441.57095 | 452.295859 | 14.5 |
| DHPFGFVAVPTK | 46.96 | 54.96 | Positive | 441.57095 | 523.332973 | 14.5 |
| DHPFGFVAVPTK | 46.96 | 54.96 | Positive | 441.57095 | 622.401387 | 14.5 |
| LVIIESDLER | 47.4 | 55.4 | Positive | 593.837528 | 748.347174 | 22.5 |
| LVIIESDLER | 47.4 | 55.4 | Positive | 593.837528 | 861.431238 | 22.5 |
| LVIIESDLER | 47.4 | 55.4 | Positive | 593.837528 | 974.515302 | 22.5 |
| LVIIESDLER | 47.4 | 55.4 | Positive | 598.841662 | 758.355443 | 22.5 |
| LVIIESDLER | 47.4 | 55.4 | Positive | 598.841662 | 871.439507 | 22.5 |
| LVIIESDLER | 47.4 | 55.4 | Positive | 598.841662 | 984.523571 | 22.5 |
| FNSLNELVDYHR | 47.49 | 55.49 | Positive | 502.91604 | 590.268135 | 16.3 |
| FNSLNELVDYHR | 47.49 | 55.49 | Positive | 502.91604 | 623.314751 | 16.3 |
| FNSLNELVDYHR | 47.49 | 55.49 | Positive | 502.91604 | 689.336549 | 16.3 |
| FNSLNELVDYHR | 47.49 | 55.49 | Positive | 506.25213 | 600.276404 | 16.3 |
| FNSLNELVDYHR | 47.49 | 55.49 | Positive | 506.25213 | 628.318886 | 16.3 |
| FNSLNELVDYHR | 47.49 | 55.49 | Positive | 506.25213 | 699.344818 | 16.3 |
| EQFLDGDGWTSR | 47.51 | 55.51 | Positive | 705.817855 | 778.347842 | 26.3 |
| EQFLDGDGWTSR | 47.51 | 55.51 | Positive | 705.817855 | 893.374785 | 26.3 |
| EQFLDGDGWTSR | 47.51 | 55.51 | Positive | 705.817855 | 1153.527263 | 26.3 |
| EQFLDGDGWTSR | 47.51 | 55.51 | Positive | 710.821989 | 788.356111 | 26.3 |
| EQFLDGDGWTSR | 47.51 | 55.51 | Positive | 710.821989 | 903.383054 | 26.3 |
| EQFLDGDGWTSR | 47.51 | 55.51 | Positive | 710.821989 | 1163.535532 | 26.3 |
| QLEDELVSLQK | 47.55 | 55.55 | Positive | 651.350999 | 475.287474 | 24.4 |
| QLEDELVSLQK | 47.55 | 55.55 | Positive | 651.350999 | 574.355888 | 24.4 |
| QLEDELVSLQK | 47.55 | 55.55 | Positive | 651.350999 | 687.439952 | 24.4 |
| QLEDELVSLQK | 47.55 | 55.55 | Positive | 655.358099 | 483.301673 | 24.4 |
| QLEDELVSLQK | 47.55 | 55.55 | Positive | 655.358099 | 582.370087 | 24.4 |
| QLEDELVSLQK | 47.55 | 55.55 | Positive | 655.358099 | 695.454151 | 24.4 |
| SFVLNLGK | 47.92 | 55.92 | Positive | 439.260728 | 431.261259 | 17.3 |
| SFVLNLGK | 47.92 | 55.92 | Positive | 439.260728 | 544.345323 | 17.3 |
| SFVLNLGK | 47.92 | 55.92 | Positive | 439.260728 | 643.413737 | 17.3 |
| SFVLNLGK | 47.92 | 55.92 | Positive | 443.267827 | 439.275458 | 17.3 |
| SFVLNLGK | 47.92 | 55.92 | Positive | 443.267827 | 552.359522 | 17.3 |
| SFVLNLGK | 47.92 | 55.92 | Positive | 443.267827 | 651.427936 | 17.3 |
| EEVVTVETWQEGSLK | 49.15 | 57.15 | Positive | 867.433249 | 948.478522 | 31.8 |
| EEVVTVETWQEGSLK | 49.15 | 57.15 | Positive | 867.433249 | 1077.521115 | 31.8 |
| EEVVTVETWQEGSLK | 49.15 | 57.15 | Positive | 867.433249 | 1277.637208 | 31.8 |
| EEVVTVETWQEGSLK | 49.15 | 57.15 | Positive | 871.440348 | 956.492721 | 31.8 |
| EEVVTVETWQEGSLK | 49.15 | 57.15 | Positive | 871.440348 | 1085.535314 | 31.8 |
| EEVVTVETWQEGSLK | 49.15 | 57.15 | Positive | 871.440348 | 1285.651407 | 31.8 |
| QITLNDLPVGR | 49.29 | 57.29 | Positive | 613.348594 | 428.261593 | 23.2 |
| QITLNDLPVGR | 49.29 | 57.29 | Positive | 613.348594 | 541.345657 | 23.2 |
| QITLNDLPVGR | 49.29 | 57.29 | Positive | 613.348594 | 770.415528 | 23.2 |
| QITLNDLPVGR | 49.29 | 57.29 | Positive | 618.352728 | 438.269862 | 23.2 |
| QITLNDLPVGR | 49.29 | 57.29 | Positive | 618.352728 | 551.353926 | 23.2 |
| QITLNDLPVGR | 49.29 | 57.29 | Positive | 618.352728 | 780.423797 | 23.2 |
| GYSIFSYATK | 49.41 | 57.41 | Positive | 568.784764 | 569.292953 | 21.6 |
| GYSIFSYATK | 49.41 | 57.41 | Positive | 568.784764 | 716.361367 | 21.6 |
| GYSIFSYATK | 49.41 | 57.41 | Positive | 568.784764 | 916.477459 | 21.6 |
| GYSIFSYATK | 49.41 | 57.41 | Positive | 572.791863 | 577.307152 | 21.6 |
| GYSIFSYATK | 49.41 | 57.41 | Positive | 572.791863 | 724.375566 | 21.6 |
| GYSIFSYATK | 49.41 | 57.41 | Positive | 572.791863 | 924.491658 | 21.6 |
| DEGNYLDDALVR | 50.05 | 58.05 | Positive | 690.325513 | 688.36243 | 25.8 |
| DEGNYLDDALVR | 50.05 | 58.05 | Positive | 690.325513 | 801.446494 | 25.8 |
| DEGNYLDDALVR | 50.05 | 58.05 | Positive | 690.325513 | 964.509822 | 25.8 |
| DEGNYLDDALVR | 50.05 | 58.05 | Positive | 695.329647 | 698.370699 | 25.8 |
| DEGNYLDDALVR | 50.05 | 58.05 | Positive | 695.329647 | 811.454763 | 25.8 |
| DEGNYLDDALVR | 50.05 | 58.05 | Positive | 695.329647 | 974.518091 | 25.8 |
| GLFIIDGK | 50.23 | 58.23 | Positive | 431.755278 | 319.161211 | 17 |
| GLFIIDGK | 50.23 | 58.23 | Positive | 431.755278 | 545.329339 | 17 |
| GLFIIDGK | 50.23 | 58.23 | Positive | 431.755278 | 692.397753 | 17 |
| GLFIIDGK | 50.23 | 58.23 | Positive | 435.762378 | 327.17541 | 17 |
| GLFIIDGK | 50.23 | 58.23 | Positive | 435.762378 | 553.343538 | 17 |
| GLFIIDGK | 50.23 | 58.23 | Positive | 435.762378 | 700.411952 | 17 |
| SDIIFFQR | 51.1 | 59.1 | Positive | 513.274366 | 597.314357 | 19.8 |
| SDIIFFQR | 51.1 | 59.1 | Positive | 513.274366 | 710.398421 | 19.8 |
| SDIIFFQR | 51.1 | 59.1 | Positive | 513.274366 | 823.482485 | 19.8 |
| SDIIFFQR | 51.1 | 59.1 | Positive | 518.278501 | 607.322626 | 19.8 |
| SDIIFFQR | 51.1 | 59.1 | Positive | 518.278501 | 720.40669 | 19.8 |
| SDIIFFQR | 51.1 | 59.1 | Positive | 518.278501 | 833.490754 | 19.8 |
| GTPWEGGLFK | 51.15 | 59.15 | Positive | 546.279649 | 650.350802 | 20.9 |
| GTPWEGGLFK | 51.15 | 59.15 | Positive | 546.279649 | 836.430115 | 20.9 |
| GTPWEGGLFK | 51.15 | 59.15 | Positive | 546.279649 | 933.482879 | 20.9 |
| GTPWEGGLFK | 51.15 | 59.15 | Positive | 550.286748 | 658.365001 | 20.9 |
| GTPWEGGLFK | 51.15 | 59.15 | Positive | 550.286748 | 844.444314 | 20.9 |
| GTPWEGGLFK | 51.15 | 59.15 | Positive | 550.286748 | 941.497078 | 20.9 |
| VSLDVNHFAPDELTVK | 51.38 | 59.38 | Positive | 595.312348 | 742.87263 | 19.1 |
| VSLDVNHFAPDELTVK | 51.38 | 59.38 | Positive | 595.312348 | 799.414662 | 19.1 |
| VSLDVNHFAPDELTVK | 51.38 | 59.38 | Positive | 595.312348 | 842.930676 | 19.1 |
| VSLDVNHFAPDELTVK | 51.38 | 59.38 | Positive | 597.983747 | 746.87973 | 19.1 |
| VSLDVNHFAPDELTVK | 51.38 | 59.38 | Positive | 597.983747 | 803.421762 | 19.1 |
| VSLDVNHFAPDELTVK | 51.38 | 59.38 | Positive | 597.983747 | 846.937776 | 19.1 |
| GFGHIGIAVPDVYSAC[+57.0]K | 51.53 | 59.53 | Positive | 597.634656 | 628.275923 | 19.1 |
| GFGHIGIAVPDVYSAC[+57.0]K | 51.53 | 59.53 | Positive | 597.634656 | 727.344337 | 19.1 |
| GFGHIGIAVPDVYSAC[+57.0]K | 51.53 | 59.53 | Positive | 597.634656 | 939.424044 | 19.1 |
| GFGHIGIAVPDVYSAC[+57.0]K | 51.53 | 59.53 | Positive | 600.306056 | 636.290122 | 19.1 |
| GFGHIGIAVPDVYSAC[+57.0]K | 51.53 | 59.53 | Positive | 600.306056 | 735.358536 | 19.1 |
| GFGHIGIAVPDVYSAC[+57.0]K | 51.53 | 59.53 | Positive | 600.306056 | 947.438243 | 19.1 |
| SIDDLEDELYAQK | 51.77 | 59.77 | Positive | 769.864668 | 866.425424 | 28.5 |
| SIDDLEDELYAQK | 51.77 | 59.77 | Positive | 769.864668 | 995.468017 | 28.5 |
| SIDDLEDELYAQK | 51.77 | 59.77 | Positive | 769.864668 | 1338.605967 | 28.5 |
| SIDDLEDELYAQK | 51.77 | 59.77 | Positive | 773.871767 | 874.439623 | 28.5 |
| SIDDLEDELYAQK | 51.77 | 59.77 | Positive | 773.871767 | 1003.482216 | 28.5 |
| SIDDLEDELYAQK | 51.77 | 59.77 | Positive | 773.871767 | 1346.620166 | 28.5 |
| EQANAVSEAVVSSVNTVATK | 52.09 | 60.09 | Positive | 668.679647 | 819.457058 | 21.2 |
| EQANAVSEAVVSSVNTVATK | 52.09 | 60.09 | Positive | 668.679647 | 906.489087 | 21.2 |
| EQANAVSEAVVSSVNTVATK | 52.09 | 60.09 | Positive | 668.679647 | 1005.557501 | 21.2 |
| EQANAVSEAVVSSVNTVATK | 52.09 | 60.09 | Positive | 671.351047 | 827.471257 | 21.2 |
| EQANAVSEAVVSSVNTVATK | 52.09 | 60.09 | Positive | 671.351047 | 914.503286 | 21.2 |
| EQANAVSEAVVSSVNTVATK | 52.09 | 60.09 | Positive | 671.351047 | 1013.5717 | 21.2 |
| SQEQLAAELAEYTAK | 52.41 | 60.41 | Positive | 551.277303 | 611.303518 | 17.8 |
| SQEQLAAELAEYTAK | 52.41 | 60.41 | Positive | 551.277303 | 682.340632 | 17.8 |
| SQEQLAAELAEYTAK | 52.41 | 60.41 | Positive | 551.277303 | 795.424696 | 17.8 |
| SQEQLAAELAEYTAK | 52.41 | 60.41 | Positive | 553.948703 | 619.317717 | 17.8 |
| SQEQLAAELAEYTAK | 52.41 | 60.41 | Positive | 553.948703 | 690.354831 | 17.8 |
| SQEQLAAELAEYTAK | 52.41 | 60.41 | Positive | 553.948703 | 803.438895 | 17.8 |
| YLTAEAFGFK | 52.46 | 60.46 | Positive | 573.795132 | 569.308209 | 21.8 |
| YLTAEAFGFK | 52.46 | 60.46 | Positive | 573.795132 | 769.387916 | 21.8 |
| YLTAEAFGFK | 52.46 | 60.46 | Positive | 573.795132 | 870.435595 | 21.8 |
| YLTAEAFGFK | 52.46 | 60.46 | Positive | 577.802231 | 577.322408 | 21.8 |
| YLTAEAFGFK | 52.46 | 60.46 | Positive | 577.802231 | 777.402115 | 21.8 |
| YLTAEAFGFK | 52.46 | 60.46 | Positive | 577.802231 | 878.449794 | 21.8 |
| GFTIPEAFR | 52.84 | 60.84 | Positive | 519.274366 | 619.319837 | 20 |
| GFTIPEAFR | 52.84 | 60.84 | Positive | 519.274366 | 732.403901 | 20 |
| GFTIPEAFR | 52.84 | 60.84 | Positive | 519.274366 | 833.451579 | 20 |
| GFTIPEAFR | 52.84 | 60.84 | Positive | 524.278501 | 629.328106 | 20 |
| GFTIPEAFR | 52.84 | 60.84 | Positive | 524.278501 | 742.41217 | 20 |
| GFTIPEAFR | 52.84 | 60.84 | Positive | 524.278501 | 843.459848 | 20 |
| LFDQAFGLPR | 53.93 | 61.93 | Positive | 582.314023 | 589.345657 | 22.1 |
| LFDQAFGLPR | 53.93 | 61.93 | Positive | 582.314023 | 660.382771 | 22.1 |
| LFDQAFGLPR | 53.93 | 61.93 | Positive | 582.314023 | 903.468292 | 22.1 |
| LFDQAFGLPR | 53.93 | 61.93 | Positive | 587.318157 | 599.353926 | 22.1 |
| LFDQAFGLPR | 53.93 | 61.93 | Positive | 587.318157 | 670.39104 | 22.1 |
| LFDQAFGLPR | 53.93 | 61.93 | Positive | 587.318157 | 913.476561 | 22.1 |
| GISAFPESDNLFK | 54.08 | 62.08 | Positive | 712.856449 | 949.462538 | 26.5 |
| GISAFPESDNLFK | 54.08 | 62.08 | Positive | 712.856449 | 1096.530952 | 26.5 |
| GISAFPESDNLFK | 54.08 | 62.08 | Positive | 712.856449 | 1254.600094 | 26.5 |
| GISAFPESDNLFK | 54.08 | 62.08 | Positive | 716.863548 | 957.476737 | 26.5 |
| GISAFPESDNLFK | 54.08 | 62.08 | Positive | 716.863548 | 1104.545151 | 26.5 |
| GISAFPESDNLFK | 54.08 | 62.08 | Positive | 716.863548 | 1262.614293 | 26.5 |
| FQDGDLTLYQSNTILR | 54.26 | 62.26 | Positive | 942.478522 | 994.53162 | 34.3 |
| FQDGDLTLYQSNTILR | 54.26 | 62.26 | Positive | 942.478522 | 1107.615684 | 34.3 |
| FQDGDLTLYQSNTILR | 54.26 | 62.26 | Positive | 942.478522 | 1208.663363 | 34.3 |
| FQDGDLTLYQSNTILR | 54.26 | 62.26 | Positive | 947.482657 | 1004.539889 | 34.3 |
| FQDGDLTLYQSNTILR | 54.26 | 62.26 | Positive | 947.482657 | 1117.623953 | 34.3 |
| FQDGDLTLYQSNTILR | 54.26 | 62.26 | Positive | 947.482657 | 1218.671632 | 34.3 |
| PPYTVVYFPVR | 54.38 | 62.38 | Positive | 669.366255 | 681.371872 | 25.1 |
| PPYTVVYFPVR | 54.38 | 62.38 | Positive | 669.366255 | 780.440286 | 25.1 |
| PPYTVVYFPVR | 54.38 | 62.38 | Positive | 669.366255 | 980.556378 | 25.1 |
| PPYTVVYFPVR | 54.38 | 62.38 | Positive | 674.37039 | 691.380141 | 25.1 |
| PPYTVVYFPVR | 54.38 | 62.38 | Positive | 674.37039 | 790.448555 | 25.1 |
| PPYTVVYFPVR | 54.38 | 62.38 | Positive | 674.37039 | 990.564647 | 25.1 |
| IPLLSDLTHQISK | 54.8 | 62.8 | Positive | 488.952203 | 571.31422 | 15.9 |
| IPLLSDLTHQISK | 54.8 | 62.8 | Positive | 488.952203 | 627.856252 | 15.9 |
| IPLLSDLTHQISK | 54.8 | 62.8 | Positive | 488.952203 | 676.382634 | 15.9 |
| IPLLSDLTHQISK | 54.8 | 62.8 | Positive | 491.623602 | 575.321319 | 15.9 |
| IPLLSDLTHQISK | 54.8 | 62.8 | Positive | 491.623602 | 631.863351 | 15.9 |
| IPLLSDLTHQISK | 54.8 | 62.8 | Positive | 491.623602 | 680.389733 | 15.9 |
| LSLEFPSGYPYNAPTVK | 56.4 | 64.4 | Positive | 941.982909 | 889.477794 | 34.3 |
| LSLEFPSGYPYNAPTVK | 56.4 | 64.4 | Positive | 941.982909 | 1293.647378 | 34.3 |
| LSLEFPSGYPYNAPTVK | 56.4 | 64.4 | Positive | 941.982909 | 1440.715792 | 34.3 |
| LSLEFPSGYPYNAPTVK | 56.4 | 64.4 | Positive | 945.990008 | 897.491993 | 34.3 |
| LSLEFPSGYPYNAPTVK | 56.4 | 64.4 | Positive | 945.990008 | 1301.661577 | 34.3 |
| LSLEFPSGYPYNAPTVK | 56.4 | 64.4 | Positive | 945.990008 | 1448.729991 | 34.3 |
| GFGTDEQAIVDVVANR | 56.43 | 64.43 | Positive | 845.923383 | 772.431178 | 31 |
| GFGTDEQAIVDVVANR | 56.43 | 64.43 | Positive | 845.923383 | 885.515242 | 31 |
| GFGTDEQAIVDVVANR | 56.43 | 64.43 | Positive | 845.923383 | 956.552356 | 31 |
| GFGTDEQAIVDVVANR | 56.43 | 64.43 | Positive | 850.927517 | 782.439447 | 31 |
| GFGTDEQAIVDVVANR | 56.43 | 64.43 | Positive | 850.927517 | 895.523511 | 31 |
| GFGTDEQAIVDVVANR | 56.43 | 64.43 | Positive | 850.927517 | 966.560625 | 31 |
| TIFIISMYK | 56.87 | 64.87 | Positive | 558.312103 | 641.332709 | 21.3 |
| TIFIISMYK | 56.87 | 64.87 | Positive | 558.312103 | 754.416773 | 21.3 |
| TIFIISMYK | 56.87 | 64.87 | Positive | 558.312103 | 901.485187 | 21.3 |
| TIFIISMYK | 56.87 | 64.87 | Positive | 562.319202 | 649.346908 | 21.3 |
| TIFIISMYK | 56.87 | 64.87 | Positive | 562.319202 | 762.430972 | 21.3 |
| TIFIISMYK | 56.87 | 64.87 | Positive | 562.319202 | 909.499386 | 21.3 |
| LGGPEAGLGEYLFER | 58.12 | 66.12 | Positive | 804.406837 | 913.441408 | 29.6 |
| LGGPEAGLGEYLFER | 58.12 | 66.12 | Positive | 804.406837 | 1083.546936 | 29.6 |
| LGGPEAGLGEYLFER | 58.12 | 66.12 | Positive | 804.406837 | 1154.58405 | 29.6 |
| LGGPEAGLGEYLFER | 58.12 | 66.12 | Positive | 807.416902 | 919.461537 | 29.6 |
| LGGPEAGLGEYLFER | 58.12 | 66.12 | Positive | 807.416902 | 1089.567065 | 29.6 |
| LGGPEAGLGEYLFER | 58.12 | 66.12 | Positive | 807.416902 | 1160.604179 | 29.6 |
| FYALSASFEPFSNK | 58.32 | 66.32 | Positive | 804.390656 | 592.308937 | 29.6 |
| FYALSASFEPFSNK | 58.32 | 66.32 | Positive | 804.390656 | 955.451973 | 29.6 |
| FYALSASFEPFSNK | 58.32 | 66.32 | Positive | 804.390656 | 1026.489087 | 29.6 |
| FYALSASFEPFSNK | 58.32 | 66.32 | Positive | 808.397755 | 600.323136 | 29.6 |
| FYALSASFEPFSNK | 58.32 | 66.32 | Positive | 808.397755 | 963.466172 | 29.6 |
| FYALSASFEPFSNK | 58.32 | 66.32 | Positive | 808.397755 | 1034.503286 | 29.6 |
| GTDVNVFNTILTTR | 58.9 | 66.9 | Positive | 775.912287 | 818.473043 | 28.7 |
| GTDVNVFNTILTTR | 58.9 | 66.9 | Positive | 775.912287 | 965.541457 | 28.7 |
| GTDVNVFNTILTTR | 58.9 | 66.9 | Positive | 775.912287 | 1178.652798 | 28.7 |
| GTDVNVFNTILTTR | 58.9 | 66.9 | Positive | 780.916421 | 828.481312 | 28.7 |
| GTDVNVFNTILTTR | 58.9 | 66.9 | Positive | 780.916421 | 975.549726 | 28.7 |
| GTDVNVFNTILTTR | 58.9 | 66.9 | Positive | 780.916421 | 1188.661067 | 28.7 |
| GAGTDEGC[+57.0]LIEILASR | 59.83 | 67.83 | Positive | 831.411794 | 688.398815 | 30.5 |
| GAGTDEGC[+57.0]LIEILASR | 59.83 | 67.83 | Positive | 831.411794 | 801.482879 | 30.5 |
| GAGTDEGC[+57.0]LIEILASR | 59.83 | 67.83 | Positive | 831.411794 | 1131.619055 | 30.5 |
| GAGTDEGC[+57.0]LIEILASR | 59.83 | 67.83 | Positive | 836.415928 | 698.407084 | 30.5 |
| GAGTDEGC[+57.0]LIEILASR | 59.83 | 67.83 | Positive | 836.415928 | 811.491148 | 30.5 |
| GAGTDEGC[+57.0]LIEILASR | 59.83 | 67.83 | Positive | 836.415928 | 1141.627324 | 30.5 |
| AMVALIDVFHQYSGR | 60.25 | 68.25 | Positive | 569.627613 | 611.304186 | 18.3 |
| AMVALIDVFHQYSGR | 60.25 | 68.25 | Positive | 569.627613 | 703.364775 | 18.3 |
| AMVALIDVFHQYSGR | 60.25 | 68.25 | Positive | 569.627613 | 752.898982 | 18.3 |
| AMVALIDVFHQYSGR | 60.25 | 68.25 | Positive | 571.634323 | 614.314251 | 18.3 |
| AMVALIDVFHQYSGR | 60.25 | 68.25 | Positive | 571.634323 | 706.37484 | 18.3 |
| AMVALIDVFHQYSGR | 60.25 | 68.25 | Positive | 571.634323 | 755.909047 | 18.3 |
| FSLYFLAYEDK | 62.55 | 70.55 | Positive | 698.345186 | 738.366846 | 26 |
| FSLYFLAYEDK | 62.55 | 70.55 | Positive | 698.345186 | 885.43526 | 26 |
| FSLYFLAYEDK | 62.55 | 70.55 | Positive | 698.345186 | 1048.498589 | 26 |
| FSLYFLAYEDK | 62.55 | 70.55 | Positive | 702.352285 | 746.381045 | 26 |
| FSLYFLAYEDK | 62.55 | 70.55 | Positive | 702.352285 | 893.449459 | 26 |
| FSLYFLAYEDK | 62.55 | 70.55 | Positive | 702.352285 | 1056.512788 | 26 |
| ELLQTELSGFLDAQK | 62.88 | 70.88 | Positive | 846.446159 | 865.441408 | 31.1 |
| ELLQTELSGFLDAQK | 62.88 | 70.88 | Positive | 846.446159 | 978.525472 | 31.1 |
| ELLQTELSGFLDAQK | 62.88 | 70.88 | Positive | 846.446159 | 1208.615744 | 31.1 |
| ELLQTELSGFLDAQK | 62.88 | 70.88 | Positive | 849.456224 | 871.461537 | 31.1 |
| ELLQTELSGFLDAQK | 62.88 | 70.88 | Positive | 849.456224 | 984.545601 | 31.1 |
| ELLQTELSGFLDAQK | 62.88 | 70.88 | Positive | 849.456224 | 1214.635873 | 31.1 |
| IEEFLEAVLC[+57.0]PPR | 64.25 | 72.25 | Positive | 524.941198 | 529.255128 | 17 |
| IEEFLEAVLC[+57.0]PPR | 64.25 | 72.25 | Positive | 524.941198 | 642.339192 | 17 |
| IEEFLEAVLC[+57.0]PPR | 64.25 | 72.25 | Positive | 524.941198 | 741.407606 | 17 |
| IEEFLEAVLC[+57.0]PPR | 64.25 | 72.25 | Positive | 528.277287 | 539.263397 | 17 |
| IEEFLEAVLC[+57.0]PPR | 64.25 | 72.25 | Positive | 528.277287 | 652.347461 | 17 |
| IEEFLEAVLC[+57.0]PPR | 64.25 | 72.25 | Positive | 528.277287 | 751.415875 | 17 |
| TPSALAILENANVLAR | 64.54 | 72.54 | Positive | 826.970136 | 757.431512 | 30.4 |
| TPSALAILENANVLAR | 64.54 | 72.54 | Positive | 826.970136 | 1112.642233 | 30.4 |
| TPSALAILENANVLAR | 64.54 | 72.54 | Positive | 826.970136 | 1183.679347 | 30.4 |
| TPSALAILENANVLAR | 64.54 | 72.54 | Positive | 831.97427 | 767.439781 | 30.4 |
| TPSALAILENANVLAR | 64.54 | 72.54 | Positive | 831.97427 | 1122.650502 | 30.4 |
| TPSALAILENANVLAR | 64.54 | 72.54 | Positive | 831.97427 | 1193.687616 | 30.4 |
| GLGTDEDAIISVLAYR | 64.9 | 72.9 | Positive | 846.943784 | 708.403901 | 31.1 |
| GLGTDEDAIISVLAYR | 64.9 | 72.9 | Positive | 846.943784 | 821.487965 | 31.1 |
| GLGTDEDAIISVLAYR | 64.9 | 72.9 | Positive | 846.943784 | 934.572029 | 31.1 |
| GLGTDEDAIISVLAYR | 64.9 | 72.9 | Positive | 851.947918 | 718.41217 | 31.1 |
| GLGTDEDAIISVLAYR | 64.9 | 72.9 | Positive | 851.947918 | 831.496234 | 31.1 |
| GLGTDEDAIISVLAYR | 64.9 | 72.9 | Positive | 851.947918 | 944.580298 | 31.1 |
| GVDEATIIDILTK | 65.2 | 73.2 | Positive | 694.387582 | 702.439617 | 25.9 |
| GVDEATIIDILTK | 65.2 | 73.2 | Positive | 694.387582 | 815.523681 | 25.9 |
| GVDEATIIDILTK | 65.2 | 73.2 | Positive | 694.387582 | 916.57136 | 25.9 |
| GVDEATIIDILTK | 65.2 | 73.2 | Positive | 698.394681 | 710.453816 | 25.9 |
| GVDEATIIDILTK | 65.2 | 73.2 | Positive | 698.394681 | 823.53788 | 25.9 |
| GVDEATIIDILTK | 65.2 | 73.2 | Positive | 698.394681 | 924.585559 | 25.9 |
| ELINNELSHFLEEIK | 66.28 | 74.28 | Positive | 609.987753 | 679.851166 | 19.5 |
| ELINNELSHFLEEIK | 66.28 | 74.28 | Positive | 609.987753 | 736.87263 | 19.5 |
| ELINNELSHFLEEIK | 66.28 | 74.28 | Positive | 609.987753 | 793.414662 | 19.5 |
| ELINNELSHFLEEIK | 66.28 | 74.28 | Positive | 611.994462 | 682.861231 | 19.5 |
| ELINNELSHFLEEIK | 66.28 | 74.28 | Positive | 611.994462 | 739.882695 | 19.5 |
| ELINNELSHFLEEIK | 66.28 | 74.28 | Positive | 611.994462 | 796.424727 | 19.5 |