**Mzml #1 Mark Refat**

D:\computitionalbiologytry\venv\Scripts\python.exe D:/computitionalbiologytry/main.py

Proteins: 1

Peptides: 28

Processed peptides: 28

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 17 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 17 hits for 17 of 17 peptides.

Peptide hits passing enzyme filter: 17

... rejected by enzyme filter: 0

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Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 17 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 17

non-unique match (to >1 protein): 0

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Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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Peptide ID m/z: 879.953965193923

Peptide ID rt: 714.69732

Peptide scan index: 717

Peptide ID score type: hyperscore

- Peptide hit sequence: FDPELLFGVQFQYR

- Peptide hit monoisotopic m/z: 879.946133864821

comparsion score = 0.9999911002968204

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of FDPELLFGVQFQYR has 50 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

b5++ 2 301.64466708882094 301.26017670438114

y4++ 2 307.158275604771 307.2507959687359

b6++ 2 358.18669926427094 358.08212059196165

b3+ 1 360.155399136671 360.0529290653661

y5++ 2 371.187564732371 371.2168295293653

y6++ 2 420.72177187592104 420.3314837477067

b7++ 2 431.72090640782096 432.054415109658

y7++ 2 449.23250392377105 449.1368280486097

b8++ 2 460.231638455671 460.19204054052994

y3+ 1 466.2408604556711 466.1853308730071

b4+ 1 489.197993359971 489.07488216873315

y8++ 2 522.766711067321 523.0938174747348

y9++ 2 579.308743242771 579.1304942452058

y4+ 1 613.3092747427711 613.2141547028411

y11++ 2 700.372072529871 700.28964209934

y5+ 1 741.3678529979711 741.2215051676833

b10+ 1 1146.582992986871 1146.6234086189922

y10+ 1 1270.6942743696711 1270.6890619366652

b12+ 1 1421.709985529171 1422.0316664115555

b13+ 1 1584.773314816271 1584.9810296394353

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Peptide ID m/z: 563.331889799845

Peptide ID rt: 863.37624

Peptide scan index: 1710

Peptide ID score type: hyperscore

- Peptide hit sequence: QLPDAQLLAR

- Peptide hit monoisotopic m/z: 562.8247578225211

comparsion score = 0.9990997634138835

Spectrum 1 of QLPDAQLLAR has 34 peaks.

Number of matched peaks: 15

ion theo. m/z observed m/z

y5++ 2 300.69502524832103 300.7765851319063

b6++ 2 327.166298168571 327.1917022314419

y6++ 2 336.213582328071 336.4342068301714

b3+ 1 339.202683296171 339.20644385955126

y3+ 1 359.240131423771 359.082240721591

b7++ 2 383.708330344021 383.4666471632227

y7++ 2 393.727054407821 394.0690050717588

b8++ 2 440.250362519471 440.4748658771558

y8++ 2 442.253436519471 442.25349557110104

b9++ 2 475.768919599221 476.17618799181406

b5+ 1 525.266741615171 525.1810497765811

b6+ 1 653.325319870371 653.3233422326682

y6+ 1 671.4198881893709 671.8546348200912

b9+ 1 950.530562731671 950.2835865667752

y9+ 1 996.5836609230709 996.2122565759042

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Peptide ID m/z: 517.530726288532

Peptide ID rt: 962.98878

Peptide scan index: 1987

Peptide ID score type: hyperscore

- Peptide hit sequence: NSLRPSPSFTHFLLTHGR

- Peptide hit monoisotopic m/z: 517.527526607196

comparsion score = 0.9999938174079848

Spectrum 1 of NSLRPSPSFTHFLLTHGR has 66 peaks.

Number of matched peaks: 4

ion theo. m/z observed m/z

b3++ 2 158.086787317671 158.087346112084

y1+ 1 175.118952913371 175.11809620302006

y6++ 2 348.71120681212096 348.7090017596915

b7++ 2 376.70612181212095 376.31529285042245

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Peptide ID m/z: 595.641189443211

Peptide ID rt: 1145.2059

Peptide scan index: 3043

Peptide ID score type: hyperscore

- Peptide hit sequence: NM(Oxidation)DHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 595.6456697059377

comparsion score = 1.0000075217476665

Spectrum 1 of NM(Oxidation)DHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b2++ 2 131.546440571021 131.15312523704654

y1+ 1 175.118952913371 175.11824562951557

b7++ 2 439.20288922497105 439.6745697559204

b12++ 2 699.8327887832211 699.5114928019873

y13++ 2 762.4257022212711 762.4158423371539

b6+ 1 764.314437632271 764.3161488429691

b14++ 2 805.9090281022211 806.2261135949782

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Peptide ID m/z: 590.644783323966

Peptide ID rt: 1589.4443999999999

Peptide scan index: 5542

Peptide ID score type: hyperscore

- Peptide hit sequence: NMDHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 590.3140313726043

comparsion score = 0.9994400154531116

Spectrum 1 of NMDHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.1198714496573

y6++ 2 336.705590312121 337.11676267056157

y3+ 1 387.271431551371 387.6776198342007

b9++ 2 549.269094980171 549.2699484254894

y12++ 2 704.912230141521 705.2848303053871

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Peptide ID m/z: 885.461308410287

Peptide ID rt: 1595.97222

Peptide scan index: 5583

Peptide ID score type: hyperscore

- Peptide hit sequence: NMDHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 884.9674088255209

comparsion score = 0.999442212121439

Spectrum 1 of NMDHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 4

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.11929545446128

b4++ 2 249.59191126242098 249.211090806761

y5++ 2 301.187033232371 301.18486442454224

y5+ 1 601.366789997971 601.3708155870386

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Peptide ID m/z: 892.969266534774

Peptide ID rt: 1676.06574

Peptide scan index: 6025

Peptide ID score type: hyperscore

- Peptide hit sequence: NM(Oxidation)DHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 892.964866325521

comparsion score = 0.9999950723844394

Spectrum 1 of NM(Oxidation)DHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 26

ion theo. m/z observed m/z

y5++ 2 301.187033232371 301.15130991152597

y6++ 2 336.705590312121 337.14013286325513

b3+ 1 377.112548834771 377.1273757525636

b6++ 2 382.66085704952104 382.196396413731

y7++ 2 386.239797455671 386.2319568498063

y3+ 1 387.271431551371 387.4641348870918

b7++ 2 439.20288922497105 439.20355908734905

y8++ 2 454.769253567321 454.76900515731893

y4+ 1 502.29837571087097 502.2991223039556

b8++ 2 507.73234533662105 507.77008770318145

y9++ 2 511.311285742771 511.3126084474082

b4+ 1 514.171461058071 514.2593696969599

b9++ 2 557.2665524801711 557.3024453111484

y10++ 2 567.853317918221 567.8534442705976

b10++ 2 592.785109559921 592.816930611449

y5+ 1 601.366789997971 601.3661364444094

y11++ 2 636.382774029871 636.3768942564095

b11++ 2 642.319316703471 642.3176812209379

b5+ 1 651.230373281371 650.884403259828

b12++ 2 699.8327887832211 699.8348652504425

y12++ 2 704.912230141521 704.910496343924

y13++ 2 762.4257022212711 762.424580255184

b6+ 1 764.314437632271 764.3650108458869

b14++ 2 805.9090281022211 805.9102237841234

b9+ 1 1113.525828493571 1113.9004865056916

y10+ 1 1134.699359369671 1134.554376790511

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Peptide ID m/z: 595.647086265787

Peptide ID rt: 1683.37104

Peptide scan index: 6059

Peptide ID score type: hyperscore

- Peptide hit sequence: NM(Oxidation)DHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 595.6456697059377

comparsion score = 0.9999976218135168

Spectrum 1 of NM(Oxidation)DHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 14

ion theo. m/z observed m/z

b2++ 2 131.546440571021 131.1553267032453

y1+ 1 175.118952913371 175.11913374823868

y2+ 1 288.203017264271 288.2049634687388

y5++ 2 301.187033232371 301.2092948331985

y9++ 2 511.311285742771 511.3115937764871

y10++ 2 567.853317918221 568.2050512900927

b10++ 2 592.785109559921 592.7912464117028

y11++ 2 636.382774029871 636.3757853403063

b11++ 2 642.319316703471 642.3256921077511

b5+ 1 651.230373281371 651.2232781958838

y6+ 1 672.403904157471 672.4043264258659

b12++ 2 699.8327887832211 699.4376007098681

y12++ 2 704.912230141521 704.5002739127143

y9+ 1 1021.615295018771 1021.6132347915817

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Peptide ID m/z: 784.386017963093

Peptide ID rt: 2698.28928

Peptide scan index: 11343

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)HPNSIFGESM(Oxidation)IEIGAPFSLK

- Peptide hit monoisotopic m/z: 784.0450599881045

comparsion score = 0.9995653186477318

Spectrum 1 of C(Carbamidomethyl)HPNSIFGESM(Oxidation)IEIGAPFSLK has 78 peaks.

Number of matched peaks: 32

ion theo. m/z observed m/z

y3+ 1 347.228898423771 346.94245627490426

b6++ 2 355.157950033571 355.20660419782797

y7++ 2 360.207965828071 360.21293349117735

b3+ 1 395.14960189857095 395.1765198701117

y8++ 2 416.749998003521 416.7508787845392

b7++ 2 428.692157177121 428.7735874184384

b8++ 2 457.202889224971 457.235733154865

y9++ 2 481.27129511517103 481.2719519139881

y4+ 1 494.297312710871 494.3056447694805

b4+ 1 509.19253008997094 509.2712402355396

b9++ 2 521.724186336621 522.0245214738238

y10++ 2 537.813327290621 537.8029810379271

b10++ 2 565.240200916371 565.28916839595

y5+ 1 591.3500769341709 591.3517245327337

b5+ 1 596.224559249471 596.2680578074347

y11++ 2 611.3310272991711 611.3301095643853

b11++ 2 638.757900924921 638.8323602939784

y12++ 2 654.8470418789211 654.8473944218601

y6+ 1 662.3871910936709 662.3841993663193

b12++ 2 695.299933100371 695.3661043175927

b6+ 1 709.308623600371 709.3605229764826

y13++ 2 719.3683389905711 719.367697229471

y7+ 1 719.408655189371 719.4063063113873

y14++ 2 747.8790710384211 747.881377740834

b13++ 2 759.8212302120211 759.7725201488686

y15++ 2 821.4132781819711 821.6577184559162

y8+ 1 832.492719540271 832.4909206957244

b15++ 2 844.873994435321 844.5872615693796

b7+ 1 856.377037887471 856.4671797186859

b17++ 2 928.9189336267211 929.1108795144942

b18++ 2 1002.4531407702711 1002.4510319741864

y10+ 1 1074.619378114471 1074.5589725157208

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Peptide ID m/z: 562.819826671794

Peptide ID rt: 2838.6104400000004

Peptide scan index: 12097

Peptide ID score type: hyperscore

- Peptide hit sequence: QLPDAQLLAR

- Peptide hit monoisotopic m/z: 562.8247578225211

comparsion score = 1.0000087615085564

Spectrum 1 of QLPDAQLLAR has 34 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b2++ 2 121.57859776982102 121.09385512910585

y1+ 1 175.118952913371 175.11936481000393

y4++ 2 236.66573612072102 237.13826030823242

y3+ 1 359.240131423771 359.2415041276161

b7++ 2 383.708330344021 384.1394679501641

b8++ 2 440.250362519471 440.2586277800785

y4+ 1 472.324195774671 472.31969358609535

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Peptide ID m/z: 893.460688180545

Peptide ID rt: 2928.22548

Peptide scan index: 12621

Peptide ID score type: hyperscore

- Peptide hit sequence: NM(Oxidation)DHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 892.964866325521

comparsion score = 0.9994450546492049

Spectrum 1 of NM(Oxidation)DHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

b2++ 2 131.546440571021 131.1523647237734

y1+ 1 175.118952913371 175.11905228507354

b8++ 2 507.73234533662105 507.38648183320987

b13++ 2 749.3669959267711 749.3682906364224

b14++ 2 805.9090281022211 805.6141399243894

b13+ 1 1497.726715386771 1497.7018343984726

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Peptide ID m/z: 893.462040354719

Peptide ID rt: 2929.6058399999997

Peptide scan index: 12625

Peptide ID score type: hyperscore

- Peptide hit sequence: NM(Oxidation)DHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 892.964866325521

comparsion score = 0.9994435420793025

Spectrum 1 of NM(Oxidation)DHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

b2++ 2 131.546440571021 131.15522209015688

y1+ 1 175.118952913371 175.11919163183418

y5++ 2 301.187033232371 301.18922350243764

b3+ 1 377.112548834771 377.1109318552792

y8++ 2 454.769253567321 455.1981208850831

y4+ 1 502.29837571087097 502.2976791740804

b8++ 2 507.73234533662105 507.3537888633496

y9++ 2 511.311285742771 511.2715000269539

b4+ 1 514.171461058071 514.240520183669

y11++ 2 636.382774029871 636.3843727268677

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Peptide ID m/z: 689.696344560403

Peptide ID rt: 3511.27578

Peptide scan index: 15337

Peptide ID score type: hyperscore

- Peptide hit sequence: NSLRPSPSFTHFLLTHGR

- Peptide hit monoisotopic m/z: 689.7009433206712

comparsion score = 1.0000066678043236

Spectrum 1 of NSLRPSPSFTHFLLTHGR has 66 peaks.

Number of matched peaks: 19

ion theo. m/z observed m/z

y3+ 1 369.19932923237104 369.20151698745866

b7++ 2 376.70612181212095 376.28571093003467

b8++ 2 420.22213639187095 420.51689513334475

y4+ 1 470.24700845567105 470.6159084555624

b4+ 1 471.26740955137103 470.9816498214116

b9++ 2 493.7563435354209 493.9497059959941

y9++ 2 541.298709678971 541.3038777036677

b10++ 2 544.2801831470709 544.281210611551

b5+ 1 568.320173774671 568.3201394089515

y5+ 1 583.331072806571 583.3120317903553

y10++ 2 614.832916822521 614.8332923406983

y11++ 2 658.3489314022711 657.9092927685779

y6+ 1 696.415137157471 695.9430035955995

b7+ 1 752.404967157471 752.8698202640973

y14++ 2 798.9177102053212 798.5045914280602

b14++ 2 799.427910753171 799.4363160019789

y7+ 1 843.483551444571 843.4840453600268

b9+ 1 986.5054106040709 986.2829717094792

b10+ 1 1087.553089827371 1087.5562884429203

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Peptide ID m/z: 1034.040756515073

Peptide ID rt: 3518.37642

Peptide scan index: 15370

Peptide ID score type: hyperscore

- Peptide hit sequence: NSLRPSPSFTHFLLTHGR

- Peptide hit monoisotopic m/z: 1034.0477767476211

comparsion score = 1.0000067891255773

Spectrum 1 of NSLRPSPSFTHFLLTHGR has 66 peaks.

Number of matched peaks: 21

ion theo. m/z observed m/z

b2++ 2 101.544755142221 101.12161404804074

y2++ 2 116.573846737921 116.07967829601137

b3++ 2 158.086787317671 158.08678663221016

y1+ 1 175.118952913371 175.11949189046

b2+ 1 202.082233817671 202.1361588147574

y4++ 2 235.627142461221 235.13174183594256

b5++ 2 284.663725120721 284.6644419554481

y5++ 2 292.16917463667096 292.17082338658065

b3+ 1 315.166298168571 315.2250935322299

y3+ 1 369.19932923237104 369.2013847782177

b7++ 2 376.70612181212095 376.3340404708244

y4+ 1 470.24700845567105 470.2431726316373

y8++ 2 490.774870067321 490.3646075120804

b9++ 2 493.7563435354209 493.36357107813916

b5+ 1 568.320173774671 568.3199367946803

y5+ 1 583.331072806571 583.336841153642

b11++ 2 612.809639258721 612.4434825466179

y10++ 2 614.832916822521 614.4753783225595

y12++ 2 706.8753135139211 707.2741238619633

y14++ 2 798.9177102053212 798.61132476335

y16++ 2 933.5102980721712 933.513201121236

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Peptide ID m/z: 694.014256943625

Peptide ID rt: 4252.487279999999

Peptide scan index: 19010

Peptide ID score type: hyperscore

- Peptide hit sequence: TGYSGPNC(Carbamidomethyl)TIPGLWTWLR

- Peptide hit monoisotopic m/z: 693.675406521471

comparsion score = 0.99951175293769

Spectrum 1 of TGYSGPNC(Carbamidomethyl)TIPGLWTWLR has 66 peaks.

Number of matched peaks: 32

ion theo. m/z observed m/z

b3+ 1 322.13974907287104 322.1391246025648

b4+ 1 409.171778232371 408.7473293375519

b8++ 2 419.163430097371 419.2133761433518

y6++ 2 437.750331971621 437.74938059541415

b5+ 1 466.19324232807105 466.51555954373896

y7++ 2 466.261064019471 466.51794869041635

y3+ 1 474.282330583271 474.28274824135354

y8++ 2 514.787446131121 514.8076928295574

b10++ 2 526.2293018844709 526.3449207868902

b6+ 1 563.246006551371 563.3134849420758

y9++ 2 571.329478306571 571.7957077272209

b11++ 2 574.755683996121 574.7836796620848

y4+ 1 575.330009806571 575.3299143156796

b12++ 2 603.2664160439709 603.3113289052503

y10++ 2 621.853317918221 621.8879261260872

b13++ 2 659.8084482194209 659.8380570156934

b7+ 1 677.2889347427711 677.3515037141416

y11++ 2 701.868642410821 701.8689002259675

b14++ 2 752.8481048789209 752.9026177896052

y12++ 2 758.8901065065211 758.7904684387486

y5+ 1 761.409323125571 761.4090025210462

b15++ 2 803.371944490571 803.4494372328761

y13++ 2 807.4164886181711 807.4169332810552

y14++ 2 835.9272206660211 835.9261287515923

b8+ 1 837.3195837279711 837.4008222527902

y15++ 2 879.4432352457711 879.4426083546879

b16++ 2 896.411601150071 896.4202091022202

y7+ 1 931.514851572171 931.5143537578695

y16++ 2 960.9748998893211 960.5271103731976

y17++ 2 989.4856319371711 989.4858807601968

b11+ 1 1148.504091525471 1148.5577356737836

b13+ 1 1318.609619972071 1318.7381233723293

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Peptide ID m/z: 1040.518677388702

Peptide ID rt: 4252.563

Peptide scan index: 19011

Peptide ID score type: hyperscore

- Peptide hit sequence: TGYSGPNC(Carbamidomethyl)TIPGLWTWLR

- Peptide hit monoisotopic m/z: 1040.009471548821

comparsion score = 0.9995106230662204

Spectrum 1 of TGYSGPNC(Carbamidomethyl)TIPGLWTWLR has 66 peaks.

Number of matched peaks: 31

ion theo. m/z observed m/z

b8++ 2 419.163430097371 419.21531115090534

y6++ 2 437.750331971621 437.7501778866635

b5+ 1 466.19324232807105 466.24320551101

y7++ 2 466.261064019471 466.25991528148006

b9++ 2 469.687269709021 469.9459423132754

y3+ 1 474.282330583271 474.2703909266136

y8++ 2 514.787446131121 514.3204756659103

b10++ 2 526.2293018844709 525.8812680366102

b6+ 1 563.246006551371 563.2939911666224

y9++ 2 571.329478306571 570.8789091492531

b11++ 2 574.755683996121 574.7867684427165

y4+ 1 575.330009806571 575.3300936563207

b12++ 2 603.2664160439709 603.35376374834

y10++ 2 621.853317918221 621.8848837373506

b13++ 2 659.8084482194209 659.8378993938503

b7+ 1 677.2889347427711 677.334622707416

y11++ 2 701.868642410821 701.8687325628647

b14++ 2 752.8481048789209 752.8779467357208

y12++ 2 758.8901065065211 758.8943722827056

y5+ 1 761.409323125571 761.403838942757

b15++ 2 803.371944490571 803.4493514847455

y13++ 2 807.4164886181711 807.4169656281102

y14++ 2 835.9272206660211 835.8056013314263

b8+ 1 837.3195837279711 837.3987874415444

y15++ 2 879.4432352457711 879.4426766592703

b16++ 2 896.411601150071 896.1591406007215

y7+ 1 931.514851572171 931.5151115723706

y16++ 2 960.9748998893211 960.7810358718016

y17++ 2 989.4856319371711 989.4851714058944

b11+ 1 1148.504091525471 1148.5574613021531

b13+ 1 1318.609619972071 1318.7390332669925

===================================

Peptide ID m/z: 724.066211682804

Peptide ID rt: 4374.09648

Peptide scan index: 19850

Peptide ID score type: hyperscore

- Peptide hit sequence: IVIEEYVQQLSGYFLQLK

- Peptide hit monoisotopic m/z: 724.0646658347711

comparsion score = 0.9999978650460303

Spectrum 1 of IVIEEYVQQLSGYFLQLK has 66 peaks.

Number of matched peaks: 4

ion theo. m/z observed m/z

y2++ 2 130.60207286552102 130.15682231384284

b5++ 2 292.668142184521 293.1309664889694

b7++ 2 423.73401397162104 423.23852323097066

y8++ 2 478.26601258327105 478.2668443947233

<Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!> occurred 17 times

Process finished with exit code 0

**Mzml #2 Mark Refat**

D:\computitionalbiologytry\venv\Scripts\python.exe D:/computitionalbiologytry/main.py

Proteins: 1

Peptides: 28

Processed peptides: 28

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 26 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 26 hits for 26 of 26 peptides.

Peptide hits passing enzyme filter: 26

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 26 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 26

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

-----------------------------------

===================================

Peptide ID m/z: 442.988403320313

Peptide ID rt: 1293.27185849502

Peptide scan index: 1093

Peptide ID score type: hyperscore

- Peptide hit sequence: NMDHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 442.98734264614603

comparsion score = 0.999997605638976

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of NMDHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

b7++ 2 431.20543172497105 431.0978869711383

y4+ 1 502.29837571087097 501.8525121889916

b13++ 2 741.3695384267712 741.2180287225208

===================================

Peptide ID m/z: 645.992797851563

Peptide ID rt: 1380.47748851202

Peptide scan index: 1697

Peptide ID score type: hyperscore

- Peptide hit sequence: ALGHGVDLGHIYGDNLER

- Peptide hit monoisotopic m/z: 645.9939041824376

comparsion score = 1.000001712605587

Spectrum 1 of ALGHGVDLGHIYGDNLER has 66 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

b9++ 2 410.71922937592103 410.246729005973

y3+ 1 417.245611487571 417.2453293921066

y7++ 2 433.70377684402104 433.3396306087151

b5+ 1 436.230295391871 436.2306022570102

b10++ 2 479.24868548757104 479.7198030259467

b6+ 1 535.298709678971 535.2008305631105

b11++ 2 535.790717663021 536.1507058745725

y12++ 2 701.341501434171 701.3778709293058

y13++ 2 750.8757085777211 750.712361990895

b15++ 2 760.3680505298711 759.8781812829301

b16++ 2 816.9100827053211 817.1928960483414

y7+ 1 866.4002772212709 866.8395884785118

b17++ 2 881.4313798169711 881.6981054703824

y17++ 2 932.968660960521 933.3166152318425

b10+ 1 957.490094508371 957.8142360769912

y8+ 1 979.4843415721709 979.296967772598

y9+ 1 1116.543253795471 1116.7377224249162

b12+ 1 1233.637488146371 1233.6354459059974

b13+ 1 1290.6589522420709 1290.4977773897044

b14+ 1 1405.685896401571 1405.6873504703278

===================================

Peptide ID m/z: 849.070739746094

Peptide ID rt: 1853.50003292802

Peptide scan index: 4342

Peptide ID score type: hyperscore

- Peptide hit sequence: IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK

- Peptide hit monoisotopic m/z: 849.0645657079377

comparsion score = 0.9999927284761243

Spectrum 1 of IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK has 74 peaks.

Number of matched peaks: 4

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11284164364685

y2++ 2 147.594247833621 147.11671133648957

y6++ 2 370.66781661332095 371.13846373092656

y8++ 2 475.73623090042094 476.17555195007293

===================================

Peptide ID m/z: 694.008911132813

Peptide ID rt: 2015.1393404149799

Peptide scan index: 5233

Peptide ID score type: hyperscore

- Peptide hit sequence: TGYSGPNC(Carbamidomethyl)TIPGLWTWLR

- Peptide hit monoisotopic m/z: 693.675406521471

comparsion score = 0.9995194519753391

Spectrum 1 of TGYSGPNC(Carbamidomethyl)TIPGLWTWLR has 66 peaks.

Number of matched peaks: 4

ion theo. m/z observed m/z

b2+ 1 159.076419785771 159.43381866899696

y1+ 1 175.118952913371 175.1188618212052

y10++ 2 621.853317918221 621.8202975762414

b13++ 2 659.8084482194209 659.4415383068917

===================================

Peptide ID m/z: 595.976135253906

Peptide ID rt: 2588.592498177

Peptide scan index: 8528

Peptide ID score type: hyperscore

- Peptide hit sequence: NM(Oxidation)DHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 595.6456697059377

comparsion score = 0.9994455054012733

Spectrum 1 of NM(Oxidation)DHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

y8++ 2 454.769253567321 454.76884324024275

y4+ 1 502.29837571087097 502.2950725659229

b8++ 2 507.73234533662105 507.77874767315404

y9++ 2 511.311285742771 511.2725684476395

b4+ 1 514.171461058071 514.2732490170886

b9++ 2 557.2665524801711 557.2667597961552

b10++ 2 592.785109559921 592.7052997697489

y5+ 1 601.366789997971 601.3215622084554

y11++ 2 636.382774029871 636.3698504543769

b11++ 2 642.319316703471 642.3196283470853

b5+ 1 651.230373281371 651.064148246299

y6+ 1 672.403904157471 672.3629336038201

b12++ 2 699.8327887832211 699.8578110304287

y12++ 2 704.912230141521 704.898061879882

b13++ 2 749.3669959267711 749.3842035883405

y13++ 2 762.4257022212711 762.903225929933

b6+ 1 764.314437632271 763.9016159213791

y7+ 1 771.472318444571 771.470961689901

b14++ 2 805.9090281022211 805.7299197398211

b7+ 1 877.3985019831711 877.4597562348616

===================================

Peptide ID m/z: 968.980773925781

Peptide ID rt: 3078.60749505498

Peptide scan index: 11224

Peptide ID score type: hyperscore

- Peptide hit sequence: ALGHGVDLGHIYGDNLER

- Peptide hit monoisotopic m/z: 968.4872180402712

comparsion score = 0.9994906442947157

Spectrum 1 of ALGHGVDLGHIYGDNLER has 66 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

b3++ 2 121.578597769821 121.08684848837662

y1+ 1 175.118952913371 175.1188336779875

y8++ 2 490.24580901947104 490.3366752398786

b12++ 2 617.3223823065711 617.3718224905133

y12++ 2 701.341501434171 701.3936290508217

y17++ 2 932.968660960521 933.3573891706234

===================================

Peptide ID m/z: 968.984619140625

Peptide ID rt: 3169.4951795830198

Peptide scan index: 11698

Peptide ID score type: hyperscore

- Peptide hit sequence: ALGHGVDLGHIYGDNLER

- Peptide hit monoisotopic m/z: 968.4872180402712

comparsion score = 0.9994866780230268

Spectrum 1 of ALGHGVDLGHIYGDNLER has 66 peaks.

Number of matched peaks: 24

ion theo. m/z observed m/z

y7++ 2 433.70377684402104 433.90775820505985

b10++ 2 479.24868548757104 479.2522695444688

y8++ 2 490.24580901947104 489.86810711866724

y4+ 1 531.288539678971 531.2882777206988

b6+ 1 535.298709678971 534.9685602015336

b11++ 2 535.790717663021 535.7796774089159

y9++ 2 558.775265131121 558.9474156133055

y10++ 2 587.285997178971 587.019981604118

b12++ 2 617.3223823065711 617.3222198813543

y11++ 2 643.828029354421 643.8885976117979

b13++ 2 645.833114354421 645.8331510275854

y5+ 1 646.315483838471 645.9014260890438

b7+ 1 650.325653838471 649.9088122290806

y12++ 2 701.341501434171 701.3407513172039

y6+ 1 703.336947934171 703.3637475888424

b14++ 2 703.3465864341711 703.3662505210191

b15++ 2 760.3680505298711 760.3705545377335

y14++ 2 779.386440625571 779.3861891697106

b16++ 2 816.9100827053211 816.9487691563625

b9+ 1 820.431182285071 820.4313068756333

y15++ 2 847.915896737221 847.9152015202136

y7+ 1 866.4002772212709 866.6858365373902

y16++ 2 876.426628785071 876.4283341707504

y17++ 2 932.968660960521 932.5255293913273

===================================

Peptide ID m/z: 968.980712890625

Peptide ID rt: 3239.73390401502

Peptide scan index: 12141

Peptide ID score type: hyperscore

- Peptide hit sequence: ALGHGVDLGHIYGDNLER

- Peptide hit monoisotopic m/z: 968.4872180402712

comparsion score = 0.9994907072516628

Spectrum 1 of ALGHGVDLGHIYGDNLER has 66 peaks.

Number of matched peaks: 14

ion theo. m/z observed m/z

b3++ 2 121.578597769821 121.08719318087297

y1+ 1 175.118952913371 175.1189729835748

b2+ 1 185.12845497717097 185.09902632097499

y3++ 2 209.12644397717102 209.09834891621574

b6++ 2 268.152993072871 268.13837939014843

y2+ 1 304.161547136671 304.1429408344721

b9++ 2 410.71922937592103 411.14592069145147

y7++ 2 433.70377684402104 434.2000005517155

b5+ 1 436.230295391871 435.73495697682876

y8++ 2 490.24580901947104 490.24714589205934

y4+ 1 531.288539678971 531.2813008594582

b11++ 2 535.790717663021 536.2406843229988

y16++ 2 876.426628785071 876.4253702770583

b10+ 1 957.490094508371 957.4218809189069

===================================

Peptide ID m/z: 1096.249267578125

Peptide ID rt: 3430.054758432

Peptide scan index: 13181

Peptide ID score type: hyperscore

- Peptide hit sequence: GIPPQSQMAVGQEVFGLLPGLMLYATLWLR

- Peptide hit monoisotopic m/z: 1095.9224088494043

comparsion score = 0.9997018390448343

Spectrum 1 of GIPPQSQMAVGQEVFGLLPGLMLYATLWLR has 114 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.11903213952053

b4++ 2 183.11280491337095 183.14309063777446

y2+ 1 288.203017264271 288.2033189185768

y5++ 2 344.71067531212094 345.1779149344091

y4+ 1 587.3663949341709 587.3688930816594

===================================

Peptide ID m/z: 646.322631835938

Peptide ID rt: 3456.9825525760198

Peptide scan index: 13333

Peptide ID score type: hyperscore

- Peptide hit sequence: ALGHGVDLGHIYGDNLER

- Peptide hit monoisotopic m/z: 645.9939041824376

comparsion score = 0.9994913876796074

Spectrum 1 of ALGHGVDLGHIYGDNLER has 66 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b3++ 2 121.578597769821 121.0877041441008

y1+ 1 175.118952913371 175.11883343532608

b5++ 2 218.618785929321 219.03516791132756

y4++ 2 266.147908072871 266.09521758314025

y7++ 2 433.70377684402104 433.2955780431321

y4+ 1 531.288539678971 531.2899287461081

b7+ 1 650.325653838471 650.3575803853097

===================================

Peptide ID m/z: 849.066345214844

Peptide ID rt: 3633.467140095

Peptide scan index: 14331

Peptide ID score type: hyperscore

- Peptide hit sequence: IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK

- Peptide hit monoisotopic m/z: 849.0645657079377

comparsion score = 0.9999979041603565

Spectrum 1 of IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK has 74 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

b4++ 2 231.106862842171 231.16563209198551

b3+ 1 332.163854994271 332.20756650031245

y7++ 2 427.20984878877096 427.657844481091

b4+ 1 461.206449217571 460.7273673390303

y8++ 2 475.73623090042094 475.7334297999657

===================================

Peptide ID m/z: 1023.192565917969

Peptide ID rt: 3649.85322689502

Peptide scan index: 14411

Peptide ID score type: hyperscore

- Peptide hit sequence: GLLGNPIC(Carbamidomethyl)SPEYWKPSTFGGEVGFNIVK

- Peptide hit monoisotopic m/z: 1022.8513076310379

comparsion score = 0.9996664769679744

Spectrum 1 of GLLGNPIC(Carbamidomethyl)SPEYWKPSTFGGEVGFNIVK has 106 peaks.

Number of matched peaks: 2

ion theo. m/z observed m/z

y3++ 2 180.13628000907102 180.1024893101398

b6++ 2 276.660651120721 276.16461201925307

===================================

Peptide ID m/z: 968.48193359375

Peptide ID rt: 3702.86331934302

Peptide scan index: 14737

Peptide ID score type: hyperscore

- Peptide hit sequence: ALGHGVDLGHIYGDNLER

- Peptide hit monoisotopic m/z: 968.4872180402712

comparsion score = 1.0000054564224048

Spectrum 1 of ALGHGVDLGHIYGDNLER has 66 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

b3++ 2 121.578597769821 121.41347204557363

y1+ 1 175.118952913371 175.11883337295424

b9++ 2 410.71922937592103 410.7202380410817

y11++ 2 643.828029354421 643.4048634234632

b8+ 1 763.409718189371 763.1137534827049

b17++ 2 881.4313798169711 881.4323255338794

===================================

Peptide ID m/z: 849.064147949219

Peptide ID rt: 3790.01564023902

Peptide scan index: 15249

Peptide ID score type: hyperscore

- Peptide hit sequence: IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK

- Peptide hit monoisotopic m/z: 849.0645657079377

comparsion score = 1.0000004920225636

Spectrum 1 of IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK has 74 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

b7++ 2 430.19199019307104 429.7308972973588

y8++ 2 475.73623090042094 475.3653381501966

b8++ 2 486.73402236852104 486.4957558582643

b9++ 2 568.265687012071 568.3116468635061

y5+ 1 593.2929567427709 593.3198020701604

b10++ 2 636.795143123721 636.354458963647

y11++ 2 705.834799783221 705.6288413122754

b6+ 1 722.317791696071 722.3225068606956

b11++ 2 729.834799783221 729.8674806808367

y6+ 1 740.328356759871 740.3879622829884

y12++ 2 787.366464426771 787.5992437377718

b12++ 2 798.364255894871 798.4180174567744

y13++ 2 843.908496602221 843.9293832937987

b13++ 2 846.890638006521 846.8906402132266

b7+ 1 859.376703919371 859.4188474867511

y14++ 2 912.437952713871 912.4365539013975

y15++ 2 969.459416809571 969.4617437236672

b15++ 2 976.9503701905211 976.8515156824885

b17++ 2 1082.990224381921 1082.8578836748618

y19++ 2 1216.5511781530713 1216.5531704785926

===================================

Peptide ID m/z: 849.066101074219

Peptide ID rt: 3852.21607260702

Peptide scan index: 15602

Peptide ID score type: hyperscore

- Peptide hit sequence: IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK

- Peptide hit monoisotopic m/z: 849.0645657079377

comparsion score = 0.9999981916999403

Spectrum 1 of IAM(Oxidation)EFNHLYHWHPLM(Oxidation)PDSFK has 74 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

b3++ 2 166.585565730521 167.04371310336978

y8++ 2 475.73623090042094 475.36976922899447

b18++ 2 1126.506238961671 1126.1520799347197

===================================

Peptide ID m/z: 940.775390625

Peptide ID rt: 3859.5730424959797

Peptide scan index: 15642

Peptide ID score type: hyperscore

- Peptide hit sequence: YQVLDGEMYPPSVEEAPVLMHYPR

- Peptide hit monoisotopic m/z: 940.7839056404379

comparsion score = 1.0000090510609894

Spectrum 1 of YQVLDGEMYPPSVEEAPVLMHYPR has 90 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

y6++ 2 408.71289224092095 409.00919280092836

y8++ 2 506.77348149612095 507.01707054805394

y4+ 1 572.2939586470709 571.9675630024414

y11++ 2 671.334632799171 671.3348676384186

b6+ 1 676.330070902271 676.3319170536196

y13++ 2 764.3848545224711 764.0758633698923

b14++ 2 804.8661610065212 805.0317935725056

b7+ 1 805.3726651255711 805.0685725860878

y15++ 2 861.4376187457711 861.4384742646716

b18++ 2 1002.9666044531214 1003.0319662160629

===================================

Peptide ID m/z: 941.111938476563

Peptide ID rt: 3865.42128940698

Peptide scan index: 15679

Peptide ID score type: hyperscore

- Peptide hit sequence: YQVLDGEMYPPSVEEAPVLMHYPR

- Peptide hit monoisotopic m/z: 940.7839056404379

comparsion score = 0.9996514412125553

Spectrum 1 of YQVLDGEMYPPSVEEAPVLMHYPR has 90 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

y2++ 2 136.589496801721 136.3490696091993

y3++ 2 218.12116144527099 217.9155709225434

b5++ 2 310.157941636671 310.161618280452

b20++ 2 1125.0288791371213 1125.028351051455

y20++ 2 1159.0350271371215 1158.6707059736198

===================================

Peptide ID m/z: 743.869384765625

Peptide ID rt: 4078.38349900698

Peptide scan index: 16992

Peptide ID score type: hyperscore

- Peptide hit sequence: EMAAELEELYGDIDALEFYPGLLLEK

- Peptide hit monoisotopic m/z: 743.6187828000961

comparsion score = 0.9996631102574441

Spectrum 1 of EMAAELEELYGDIDALEFYPGLLLEK has 98 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y4+ 1 502.3235278384711 502.3026829565923

b5+ 1 532.2071782494711 531.8264442975371

b10++ 2 590.2655505758711 590.3085086863762

y10++ 2 604.831717386321 604.8003771190372

b11++ 2 618.776282623721 618.744253973477

y11++ 2 661.373749561771 661.6524312135997

y6+ 1 672.429056285071 672.379162032456

b12++ 2 676.2897547034711 676.3360441106302

y12++ 2 696.892306641521 697.3088968077808

b7+ 1 774.3338368236712 774.1836807611479

b15++ 2 825.8638160384212 826.0697285471343

b8+ 1 903.3764310469712 903.6951805433858

===================================

Peptide ID m/z: 843.73486328125

Peptide ID rt: 4141.01956329498

Peptide scan index: 17385

Peptide ID score type: hyperscore

- Peptide hit sequence: IAM(Oxidation)EFNHLYHWHPLMPDSFK

- Peptide hit monoisotopic m/z: 843.7329273746045

comparsion score = 0.9999977055509619

Spectrum 1 of IAM(Oxidation)EFNHLYHWHPLMPDSFK has 74 peaks.

Number of matched peaks: 21

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.0803199930505

b3++ 2 166.585565730521 167.07564808334322

b2+ 1 185.12845497717097 185.09897102437517

b4++ 2 231.106862842171 231.1656326148388

y4++ 2 248.623734493121 249.11325473953426

y5++ 2 297.150116604771 297.15077901666314

b5++ 2 304.641069985721 304.17330508968524

b3+ 1 332.163854994271 332.164241171834

b6++ 2 361.66253408142103 361.2187363517706

y3+ 1 381.21324835997103 381.15829618921845

b4+ 1 461.206449217571 461.21610470132686

y8++ 2 467.73877340042094 467.24632887101603

b5+ 1 608.274863504671 608.2754867675541

b10++ 2 636.795143123721 636.7933520669782

y11++ 2 697.8373422832209 698.259600361171

b11++ 2 729.834799783221 729.4662464404198

b12++ 2 798.364255894871 798.3837568089965

y13++ 2 835.9110391022209 835.534599034316

b17++ 2 1074.9927668819212 1075.4510999183458

b19++ 2 1192.0429886052211 1191.7052627875055

b10+ 1 1272.583009780671 1272.5897179618669

===================================

Peptide ID m/z: 830.435974121094

Peptide ID rt: 4450.33496204802

Peptide scan index: 19116

Peptide ID score type: hyperscore

- Peptide hit sequence: GIPPQSQM(Oxidation)AVGQEVFGLLPGLM(Oxidation)LYATLWLR

- Peptide hit monoisotopic m/z: 830.1910832537459

comparsion score = 0.9997051056613879

Spectrum 1 of GIPPQSQM(Oxidation)AVGQEVFGLLPGLM(Oxidation)LYATLWLR has 114 peaks.

Number of matched peaks: 22

ion theo. m/z observed m/z

y7++ 2 461.76089703542095 462.13871260860725

y3+ 1 474.282330583271 474.2473762514449

b10++ 2 513.2578619801709 513.2975937611271

b11++ 2 541.7685940280209 541.272450067253

b12++ 2 605.7978831556209 605.8272100843243

y10++ 2 648.362661394871 648.5915529567837

b13++ 2 670.3191802672709 670.3452801030423

y11++ 2 676.873393442721 676.8567642303602

y5+ 1 688.4140741574708 688.4076632716656

b7+ 1 708.367519029871 708.3672582639754

b14++ 2 719.8533874108209 719.744590427706

y12++ 2 725.399775554371 725.3605642124213

b15++ 2 793.3875945543709 793.3886004684972

b16++ 2 821.8983266022209 821.948484983889

y14++ 2 838.483839905271 838.9170025872232

b17++ 2 878.4403587776709 878.5086220205653

y7+ 1 922.5145176040708 922.472426845869

b18++ 2 934.9823909531209 934.9811150701399

y16++ 2 940.528779096671 940.9437712055653

b19++ 2 983.5087730647709 983.0091949477379

y8+ 1 1035.5985819549708 1035.5040186641809

b12+ 1 1210.5884898444708 1210.5880686145738

===================================

Peptide ID m/z: 694.004760742188

Peptide ID rt: 4520.723150254979

Peptide scan index: 19537

Peptide ID score type: hyperscore

- Peptide hit sequence: TGYSGPNC(Carbamidomethyl)TIPGLWTWLR

- Peptide hit monoisotopic m/z: 693.675406521471

comparsion score = 0.9995254294504194

Spectrum 1 of TGYSGPNC(Carbamidomethyl)TIPGLWTWLR has 66 peaks.

Number of matched peaks: 17

ion theo. m/z observed m/z

b8++ 2 419.163430097371 418.73538143496575

b6+ 1 563.2460065513709 563.2923353409521

y9++ 2 571.329478306571 571.3183378726064

b11++ 2 574.755683996121 574.7565041807746

y4+ 1 575.330009806571 575.3300796077491

y10++ 2 621.853317918221 621.7060388158735

b13++ 2 659.8084482194209 659.3389104456144

y11++ 2 701.868642410821 702.0721941575308

b15++ 2 803.371944490571 803.4004442151522

y14++ 2 835.9272206660211 835.4644613716341

b8+ 1 837.3195837279709 837.4282287668619

y6+ 1 874.493387476471 874.958402998845

y15++ 2 879.4432352457711 879.4448621971445

y7+ 1 931.514851572171 931.4803741539171

y16++ 2 960.9748998893211 960.5498633217348

b10+ 1 1051.4513273021707 1051.8248466374405

b12+ 1 1205.5255556211707 1205.5396622881935

===================================

Peptide ID m/z: 939.453735351563

Peptide ID rt: 4603.76239985502

Peptide scan index: 19993

Peptide ID score type: hyperscore

- Peptide hit sequence: FGM(Oxidation)KPYTSFQELVGEK

- Peptide hit monoisotopic m/z: 938.961124389321

comparsion score = 0.999475641062774

Spectrum 1 of FGM(Oxidation)KPYTSFQELVGEK has 58 peaks.

Number of matched peaks: 25

ion theo. m/z observed m/z

y8++ 2 475.25310255137094 474.9327809804362

y9++ 2 518.769117131121 518.8141092308605

b9++ 2 538.249505448271 538.2739708123228

y5+ 1 545.329341870371 545.3266405496129

y10++ 2 569.2929567427709 569.0447697677773

b5+ 1 577.280282472771 577.2801328936607

b10++ 2 602.278794575871 602.291715394182

y11++ 2 650.8246213863209 650.8252076243971

b11++ 2 666.800091687521 666.8247792133169

y6+ 1 674.3719360936709 674.3690718964348

y12++ 2 699.351003497971 699.3506007873875

b12++ 2 723.342123862971 723.3418327842252

b6+ 1 740.343611759871 740.3633990224893

y13++ 2 763.398485189371 763.397635203039

b13++ 2 772.876331006521 772.7551090840377

b14++ 2 801.387063054371 801.3864983595829

y7+ 1 802.4305143488709 802.0017357224125

y14++ 2 836.916185197921 836.916491744643

b7+ 1 841.391290983171 841.4218958965228

y15++ 2 865.4269172457709 865.426783010925

b15++ 2 865.908360166021 865.9088907095021

b8+ 1 928.423320142671 928.4232368886436

y8+ 1 949.498928635971 949.4999267649549

b9+ 1 1075.491734429771 1075.7354554270091

b10+ 1 1203.550312684971 1203.5518700937841

===================================

Peptide ID m/z: 1011.8212890625

Peptide ID rt: 4826.610702111

Peptide scan index: 21322

Peptide ID score type: hyperscore

- Peptide hit sequence: FIPDPQGTNLM(Oxidation)FAFFAQHFTHQFFK

- Peptide hit monoisotopic m/z: 1011.4899324821712

comparsion score = 0.9996725147178551

Spectrum 1 of FIPDPQGTNLM(Oxidation)FAFFAQHFTHQFFK has 94 peaks.

Number of matched peaks: 13

ion theo. m/z observed m/z

b8++ 2 428.71361287592094 429.08072232010886

b4+ 1 473.2394634875709 473.2270226045515

b11++ 2 615.794809155621 615.7039516332253

y10++ 2 645.8225492906209 645.6832771033861

b12++ 2 689.329016299171 689.328595197

b6+ 1 698.3508059660709 698.3503431834588

y5+ 1 706.367123966071 706.0551106319172

y11++ 2 719.356756434171 719.3757021939336

b13++ 2 724.847573378921 724.8828806600757

y13++ 2 828.409520657471 828.4103033665823

b8+ 1 856.4199492850709 856.3989205177659

b18++ 2 1039.993289985021 1040.4745049620174

y19++ 2 1168.059495740221 1168.547846327251

===================================

Peptide ID m/z: 880.454650878906

Peptide ID rt: 4910.169459984

Peptide scan index: 21773

Peptide ID score type: hyperscore

- Peptide hit sequence: FDPELLFGVQFQYR

- Peptide hit monoisotopic m/z: 879.946133864821

comparsion score = 0.9994224381533139

Spectrum 1 of FDPELLFGVQFQYR has 50 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y2++ 2 169.594779333621 169.10194623113628

y1+ 1 175.118952913371 175.1190842979241

b3++ 2 180.58133780172096 180.28682667251857

b5++ 2 301.64466708882094 301.2580125730435

y5++ 2 371.187564732371 371.2024314077718

y6++ 2 420.72177187592104 421.1944569869365

b8++ 2 460.231638455671 460.6708189505195

b4+ 1 489.197993359971 489.3320148661768

b6+ 1 715.366122061771 715.3633560133333

y5+ 1 741.3678529979709 741.3680264329442

b7+ 1 862.434536348871 862.4367670322232

y7+ 1 897.457731380771 897.4142793208354

===================================

Peptide ID m/z: 892.963806152344

Peptide ID rt: 6043.34814607902

Peptide scan index: 27055

Peptide ID score type: hyperscore

- Peptide hit sequence: NM(Oxidation)DHHILHVAVDVIR

- Peptide hit monoisotopic m/z: 892.964866325521

comparsion score = 1.0000011872521257

Spectrum 1 of NM(Oxidation)DHHILHVAVDVIR has 54 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

b2++ 2 131.546440571021 131.14181883324605

y2++ 2 144.60514686552102 145.00964484771748

b3+ 1 377.112548834771 377.26362879496816

===================================

Peptide ID m/z: 879.9384765625

Peptide ID rt: 6381.48609670398

Peptide scan index: 27603

Peptide ID score type: hyperscore

- Peptide hit sequence: FDPELLFGVQFQYR

- Peptide hit monoisotopic m/z: 879.946133864821

comparsion score = 1.0000087020882993

Spectrum 1 of FDPELLFGVQFQYR has 50 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b2++ 2 132.05495569007098 132.1377699438118

b6++ 2 358.18669926427094 357.8914828388081

b3+ 1 360.155399136671 360.19902526120546

b8++ 2 460.231638455671 460.2322827643799

b10++ 2 573.7951347268211 573.378423893786

b5+ 1 602.282057710871 602.3237365810072

b6+ 1 715.366122061771 715.4116380020453

<Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!> occurred 26 times

Process finished with exit code 0

**Mzml #1 Mario Ehab**

Proteins: 1

Peptides: 4

Processed peptides: 4

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 11 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 11 hits for 11 of 11 peptides.

Peptide hits passing enzyme filter: 11

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 11 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 11

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 475.768047598774

Peptide ID rt: 346.478346

Peptide scan index: 1609

Peptide ID score type: hyperscore

- Peptide hit sequence: TVVTSSISR

- Peptide hit monoisotopic m/z: 475.269284115171

comparsion score = 0.9989516667079257

Spectrum 1 of TVVTSSISR has 15 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.11866760253906

b6++ 2 288.155399136671 288.0375671386719

y6++ 2 325.677030216421 325.8769836425781

===================================

Peptide ID m/z: 541.608287687596

Peptide ID rt: 400.579644

Peptide scan index: 2018

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 541.278652943571

comparsion score = 0.9993913779542918

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 1

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.11871337890625

===================================

Peptide ID m/z: 406.461711099558

Peptide ID rt: 463.32383999999996

Peptide scan index: 2553

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 406.210808824371

comparsion score = 0.9993827160878

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

y2++ 2 136.589496801721 137.04571533203125

y1+ 1 175.118952913371 175.0384979248047

b4++ 2 208.131195009071 208.07147216796875

b3+ 1 314.207434328071 313.8747253417969

b13++ 2 675.8321208470211 676.0333862304688

b9+ 1 860.4723795402709 860.1744384765625

===================================

Peptide ID m/z: 541.61386986937

Peptide ID rt: 463.42315199999996

Peptide scan index: 2554

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 541.278652943571

comparsion score = 0.9993810776561542

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y2++ 2 136.589496801721 137.06504821777344

b3++ 2 157.607355397421 157.10821533203125

y1+ 1 175.118952913371 175.11898803710938

b4++ 2 208.131195009071 208.07164001464844

y5++ 2 308.164089636671 308.0359802246094

b11++ 2 547.7735425918211 547.8406372070312

y10++ 2 560.7744080599209 560.3824462890625

b12++ 2 611.8028317194211 612.0721435546875

y5+ 1 615.320902806571 615.0629272460938

y8+ 1 950.436011206471 950.542724609375

b11+ 1 1094.539808716871 1094.67529296875

===================================

Peptide ID m/z: 541.276794433594

Peptide ID rt: 1332.25518

Peptide scan index: 9567

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 541.278652943571

comparsion score = 1.0000034335667003

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

b3++ 2 157.607355397421 158.0921173095703

y1+ 1 175.118952913371 175.1188201904297

y2+ 1 272.171717136671 272.1717834472656

b4+ 1 415.255113551371 415.2427673339844

y7++ 2 432.20562925687096 432.2427978515625

y8++ 2 475.72164383662096 475.58453369140625

b10++ 2 504.257528012071 503.764404296875

y4+ 1 528.288873647071 528.6150512695312

y9++ 2 532.263676012071 532.6300659179688

y13++ 2 711.356294426771 711.3781127929688

===================================

Peptide ID m/z: 811.41552734375

Peptide ID rt: 1861.0308

Peptide scan index: 13642

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 811.414341181971

comparsion score = 0.9999985381574065

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

b3++ 2 157.607355397421 157.13275146484375

y1+ 1 175.118952913371 175.11898803710938

b4++ 2 208.131195009071 208.10789489746094

b5++ 2 251.647209588821 252.13414001464844

b6++ 2 280.157941636671 280.2195129394531

b4+ 1 415.255113551371 415.25177001953125

b5+ 1 502.28714271087097 502.3632507324219

b6+ 1 559.308606806571 559.433349609375

y11++ 2 604.290422639671 603.9955444335938

y5+ 1 615.320902806571 615.333740234375

b9+ 1 860.4723795402709 860.5899658203125

y14+ 1 1534.789376737671 1534.907470703125

===================================

Peptide ID m/z: 811.913513183594

Peptide ID rt: 2279.95476

Peptide scan index: 16774

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 811.414341181971

comparsion score = 0.999385190671768

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.1190185546875

b6+ 1 559.308606806571 559.43310546875

b13++ 2 675.8321208470211 675.4423828125

===================================

Peptide ID m/z: 541.611572265625

Peptide ID rt: 2285.4748200000004

Peptide scan index: 16815

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 541.278652943571

comparsion score = 0.9993853171920583

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b3++ 2 157.607355397421 157.1327667236328

y1+ 1 175.118952913371 175.11886596679688

b5++ 2 251.647209588821 251.24269104003906

y5++ 2 308.164089636671 307.6908264160156

b3+ 1 314.207434328071 314.3739929199219

b7+ 1 672.392671157471 672.4133911132812

b8+ 1 759.424700316971 759.880615234375

===================================

Peptide ID m/z: 803.4091796875

Peptide ID rt: 2316.78738

Peptide scan index: 17033

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTMSQQPR

- Peptide hit monoisotopic m/z: 803.4168836819712

comparsion score = 1.0000095891292582

Spectrum 1 of SLITSGLSTMSQQPR has 27 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

b3++ 2 157.607355397421 157.13270568847656

y1+ 1 175.118952913371 175.11862182617188

y5++ 2 308.164089636671 308.0140075683594

y3+ 1 400.23029539187104 400.2743225097656

b4+ 1 415.255113551371 415.2861328125

b9++ 2 430.739828003521 430.30126953125

b6+ 1 559.308606806571 559.4324340820312

y5+ 1 615.320902806571 614.8861694335938

===================================

Peptide ID m/z: 811.408949590093

Peptide ID rt: 2702.5785

Peptide scan index: 19930

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 811.414341181971

comparsion score = 1.000006644728137

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b3++ 2 157.607355397421 157.13272094726562

y1+ 1 175.118952913371 175.11891174316406

y2+ 1 272.171717136671 272.1715087890625

b4+ 1 415.255113551371 415.2861328125

y7++ 2 432.20562925687096 432.15057373046875

b10++ 2 504.257528012071 504.3340759277344

b11++ 2 547.7735425918211 548.1384887695312

===================================

Peptide ID m/z: 811.417053222656

Peptide ID rt: 3160.2839400000003

Peptide scan index: 23315

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 811.414341181971

comparsion score = 0.9999966576488943

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.11886596679688

y2+ 1 272.171717136671 272.1714172363281

y8++ 2 475.72164383662096 475.3440856933594

b10++ 2 504.257528012071 504.3341369628906

y13++ 2 711.356294426771 711.2900390625

**Mzml #2 Mario Ehab**

Proteins: 1

Peptides: 4

Processed peptides: 4

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 3 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 3 hits for 3 of 3 peptides.

Peptide hits passing enzyme filter: 3

... rejected by enzyme filter: 0

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Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 3 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 3

non-unique match (to >1 protein): 0

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Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 535.949035644531

Peptide ID rt: 2457.588

Peptide scan index: 6213

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTMSQQPR

- Peptide hit monoisotopic m/z: 535.9470146102377

comparsion score = 0.9999962290550801

Spectrum 1 of SLITSGLSTMSQQPR has 27 peaks.

Number of matched peaks: 14

ion theo. m/z observed m/z

b5++ 2 251.647209588821 252.0948944091797

y2+ 1 272.171717136671 272.18115234375

b6++ 2 280.157941636671 280.0599670410156

b7++ 2 336.699973812121 337.0863037109375

y3+ 1 400.23029539187104 400.24932861328125

b4+ 1 415.255113551371 415.3231201171875

y8++ 2 467.72418633662096 467.3618469238281

b5+ 1 502.28714271087097 502.27056884765625

y4+ 1 528.288873647071 528.279296875

y10++ 2 552.7769505599209 553.191162109375

b6+ 1 559.308606806571 559.3509521484375

b12++ 2 603.8053742194211 603.3605346679688

y6+ 1 746.3613878236711 746.2835693359375

y7+ 1 847.409067046971 847.515625

===================================

Peptide ID m/z: 811.416931152344

Peptide ID rt: 2756.75680000002

Peptide scan index: 7753

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTM(Oxidation)SQQPR

- Peptide hit monoisotopic m/z: 811.414341181971

comparsion score = 0.9999968080893146

Spectrum 1 of SLITSGLSTM(Oxidation)SQQPR has 27 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

y2+ 1 272.171717136671 272.16229248046875

b6++ 2 280.157941636671 280.15936279296875

y5++ 2 308.164089636671 307.91021728515625

b3+ 1 314.207434328071 313.8955383300781

y3+ 1 400.23029539187104 400.00714111328125

y7++ 2 432.20562925687096 432.24810791015625

y8++ 2 475.72164383662096 475.232177734375

b10++ 2 504.257528012071 504.20111083984375

y4+ 1 528.288873647071 528.3497314453125

b11++ 2 547.7735425918211 548.2500610351562

y11++ 2 604.290422639671 604.5910034179688

y12++ 2 654.814262251321 654.4549560546875

b7+ 1 672.392671157471 672.248779296875

b13++ 2 675.8321208470211 676.2929077148438

y13++ 2 711.356294426771 711.194580078125

b14++ 2 724.3585029586711 724.3201904296875

b8+ 1 759.424700316971 759.5009765625

y14++ 2 767.898326602221 767.5531005859375

b12+ 1 1222.598386972071 1222.634765625

y12+ 1 1308.621248035871 1308.6646728515625

===================================

Peptide ID m/z: 803.420227050781

Peptide ID rt: 3403.07980000002

Peptide scan index: 10976

Peptide ID score type: hyperscore

- Peptide hit sequence: SLITSGLSTMSQQPR

- Peptide hit monoisotopic m/z: 803.4168836819712

comparsion score = 0.9999958385802382

Spectrum 1 of SLITSGLSTMSQQPR has 27 peaks.

Number of matched peaks: 28

ion theo. m/z observed m/z

b6++ 2 280.157941636671 280.1026611328125

b3+ 1 314.207434328071 314.2640380859375

y6++ 2 373.684332145221 373.2401123046875

b8++ 2 380.215988391871 379.8348693847656

y3+ 1 400.23029539187104 400.60491943359375

b4+ 1 415.255113551371 414.95574951171875

y7++ 2 424.20817175687097 424.5203857421875

y8++ 2 467.72418633662096 467.34918212890625

b10++ 2 496.260070512071 496.27740478515625

b5+ 1 502.28714271087097 502.2120056152344

y9++ 2 524.266218512071 524.2136840820312

b11++ 2 539.7760850918211 539.2985229492188

y10++ 2 552.7769505599209 552.337158203125

b6+ 1 559.308606806571 559.347900390625

b13++ 2 667.8346633470211 667.492919921875

b7+ 1 672.392671157471 672.568603515625

y13++ 2 703.358836926771 703.477783203125

b14++ 2 716.3610454586711 716.2583618164062

y6+ 1 746.3613878236711 746.3548583984375

b8+ 1 759.424700316971 759.254150390625

y7+ 1 847.409067046971 847.5394287109375

b9+ 1 860.4723795402709 860.379150390625

b10+ 1 991.5128645573709 991.641357421875

b11+ 1 1078.544893716871 1078.7418212890625

y10+ 1 1104.546624653071 1104.6700439453125

y12+ 1 1292.626333035871 1292.7816162109375

b13+ 1 1334.662050227271 1334.6793212890625

b14+ 1 1431.714814450571 1431.7398681640625

**Mzml #1 Kerolos Onsy**

C:\Users\ONSY\PycharmProjects\pythonProject\venv\Scripts\python.exe C:/Users/ONSY/PycharmProjects/pythonProject/main.py

Hi, PyCharm

Proteins: 1

Peptides: 20

Processed peptides: 20

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 888 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 888 hits for 888 of 888 peptides.

Peptide hits passing enzyme filter: 888

... rejected by enzyme filter: 0

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Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 888 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 888

non-unique match (to >1 protein): 0

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Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 59.423835

Peptide scan index: 319

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 437.484018

Peptide scan index: 2359

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 1

ion theo. m/z observed m/z

y3++ 2 187.62353696122102 187.69301907479633

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 722.57652

Peptide scan index: 3931

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 36

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.08176249360145

y1+ 1 147.112804913371 147.11307976234926

b2+ 1 187.107719913371 187.1081672392759

y3++ 2 187.62353696122102 187.13728965858388

y4++ 2 223.14209404097102 223.1419825993857

b4++ 2 224.596662294321 225.0318322055346

y2+ 1 261.15573310477106 261.1456861243232

y5++ 2 271.668476152621 272.0549471288232

b5++ 2 275.12050190597097 275.1237358893516

b3+ 1 288.155399136671 288.1509914231478

y6++ 2 315.184490732371 315.1836192509479

b6++ 2 356.652166549521 356.1872112739957

y3+ 1 374.23979745567107 374.20132777907355

y7++ 2 396.71615537592095 397.07305331110507

b7++ 2 400.168181129271 400.1679032654677

y4+ 1 445.27691161517106 445.24206016090284

y8++ 2 447.2399949875709 447.240315999433

b4+ 1 448.186048121871 448.19274075197103

b8++ 2 448.69456324092096 448.6926299434194

b9++ 2 484.21312032067095 484.21452920075563

y9++ 2 527.2553194801709 527.2555428339233

b10++ 2 540.7551524961209 540.7535724047946

y5+ 1 542.329675838471 542.2727765575169

y10++ 2 577.7791590918209 577.779369076211

b11++ 2 597.7766165918209 597.7791408398798

y11++ 2 627.313366235371 627.2801630425539

y6+ 1 629.361704997971 629.3041229421726

b6+ 1 712.297056632271 712.2968609507523

y7+ 1 792.425034285071 792.7500177168316

b7+ 1 799.329085791771 799.3328828814632

y8+ 1 893.4727135083709 893.4323370509564

b8+ 1 896.381850015071 896.3777330215422

b9+ 1 967.418964174571 967.4231638492244

y9+ 1 1053.5033624935709 1053.4968965924609

b10+ 1 1080.5030285254709 1080.5048544294118

y10+ 1 1154.551041716871 1154.559813232517

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 724.82136

Peptide scan index: 3943

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 34

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.0831904296559

b3++ 2 144.581337801721 145.01026258365212

y1+ 1 147.112804913371 147.11311206700623

b2+ 1 187.107719913371 187.10821659958378

y3++ 2 187.62353696122102 187.13734440612947

y4++ 2 223.14209404097102 223.14204146713496

b4++ 2 224.596662294321 224.14920576799193

y2+ 1 261.15573310477106 261.1557646155497

y5++ 2 271.668476152621 272.05501889618483

b5++ 2 275.12050190597097 275.123808467166

b3+ 1 288.155399136671 288.15110096265346

y6++ 2 315.184490732371 315.1837082687279

b6++ 2 356.652166549521 356.18435342502823

y3+ 1 374.23979745567107 374.1978713033585

y7++ 2 396.71615537592095 397.0731580630731

y4+ 1 445.27691161517106 445.24217762637005

y8++ 2 447.2399949875709 447.24016854852425

b4+ 1 448.186048121871 448.19735876743823

b8++ 2 448.69456324092096 448.38179302737126

b9++ 2 484.21312032067095 484.2151384074251

y9++ 2 527.2553194801709 527.2327172147056

b10++ 2 540.7551524961209 540.7550370123545

y5+ 1 542.329675838471 542.2726457697888

y10++ 2 577.7791590918209 577.7795228160675

b11++ 2 597.7766165918209 598.1884426800724

y11++ 2 627.313366235371 627.2877790470219

b6+ 1 712.297056632271 712.2954615020346

b7+ 1 799.329085791771 799.328777749415

y8+ 1 893.4727135083709 893.4325743564673

b8+ 1 896.381850015071 896.3779694931312

b9+ 1 967.418964174571 967.4210225871839

y9+ 1 1053.5033624935709 1053.4971745607809

b10+ 1 1080.5030285254709 1080.5005699320218

y10+ 1 1154.551041716871 1154.5601160760598

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 726.93876

Peptide scan index: 3955

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

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Peptide ID m/z: 670.835327148438

Peptide ID rt: 3442.9123799999998

Peptide scan index: 18931

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.07452856389307

b3++ 2 144.581337801721 145.0556111410215

y1+ 1 147.112804913371 147.11284924892385

b2+ 1 187.107719913371 187.1078027348197

y4++ 2 223.14209404097102 223.14175724972074

b4++ 2 224.596662294321 224.16767513946655

y2+ 1 261.15573310477106 261.15487962046166

b3+ 1 288.155399136671 288.1548366150346

y7++ 2 396.71615537592095 396.2543721161552

b4+ 1 448.186048121871 448.235275626714

b8++ 2 448.69456324092096 448.2982869345553

y10++ 2 577.7791590918209 577.3738671444033

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 3445.1971200000003

Peptide scan index: 18943

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 27

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.08159752341234

b3++ 2 144.581337801721 145.05555777158753

y1+ 1 147.112804913371 147.11275191535634

b2+ 1 187.107719913371 187.10767494218567

y3++ 2 187.62353696122102 187.1538592909341

y4++ 2 223.14209404097102 223.12868291877646

b4++ 2 224.596662294321 224.14849407816953

y2+ 1 261.15573310477106 261.1564413051546

y5++ 2 271.668476152621 272.05608184145996

b5++ 2 275.12050190597097 275.11634238719563

b3+ 1 288.155399136671 288.15009118140597

y6++ 2 315.184490732371 315.18524507590996

y3+ 1 374.23979745567107 374.24065277128494

y7++ 2 396.71615537592095 397.1835486010455

b7++ 2 400.168181129271 400.15438716271245

y4+ 1 445.27691161517106 445.27065080267755

y8++ 2 447.2399949875709 447.24218138491466

y9++ 2 527.2553194801709 527.2577419902386

y5+ 1 542.329675838471 542.3289404667202

y10++ 2 577.7791590918209 577.3736508351807

b11++ 2 597.7766165918209 597.3452129726736

y11++ 2 627.313366235371 627.3125821104657

y7+ 1 792.425034285071 792.002313471124

b7+ 1 799.329085791771 799.3249404391996

y8+ 1 893.4727135083709 893.4740571445083

b8+ 1 896.381850015071 896.3814718227597

b11+ 1 1194.545956716871 1194.545685846212

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 3447.3297

Peptide scan index: 18955

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 28

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.08160712893843

b3++ 2 144.581337801721 145.01415229748568

y1+ 1 147.112804913371 147.11279879869602

b2+ 1 187.107719913371 187.10776232518975

y3++ 2 187.62353696122102 187.1538730058615

y4++ 2 223.14209404097102 223.1176350868369

b4++ 2 224.596662294321 224.1851185219171

y2+ 1 261.15573310477106 261.155007116621

y5++ 2 271.668476152621 272.056101779477

b5++ 2 275.12050190597097 275.0947236964837

b3+ 1 288.155399136671 288.1501122978314

y6++ 2 315.184490732371 315.1852664938565

b6++ 2 356.652166549521 356.23654755713

y3+ 1 374.23979745567107 374.2406801988765

y7++ 2 396.71615537592095 397.18357770947836

b7++ 2 400.168181129271 400.19617675603104

y4+ 1 445.27691161517106 445.26622766803587

y8++ 2 447.2399949875709 447.24221414998595

b4+ 1 448.186048121871 448.2306432180411

b8++ 2 448.69456324092096 448.28465137507686

b9++ 2 484.21312032067095 484.21198105761476

y10++ 2 577.7791590918209 577.3671139796345

b11++ 2 597.7766165918209 597.3452567462283

y11++ 2 627.313366235371 627.312628086732

y8+ 1 893.4727135083709 893.4741234671176

b8+ 1 896.381850015071 896.3831067657876

b9+ 1 967.418964174571 967.1147539581921

b11+ 1 1194.545956716871 1194.550679747686

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 3449.5956

Peptide scan index: 18967

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 21

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.0837104985874

y1+ 1 147.112804913371 147.11277615935873

b2+ 1 187.107719913371 187.10790392554853

y3++ 2 187.62353696122102 187.15138801337653

y4++ 2 223.14209404097102 223.0796345579412

y2+ 1 261.15573310477106 261.15475924237984

b5++ 2 275.12050190597097 275.1898312225299

y6++ 2 315.184490732371 315.15338635349536

b6++ 2 356.652166549521 356.2396703690333

y3+ 1 374.23979745567107 374.24045254581864

b7++ 2 400.168181129271 400.23404890338975

y4+ 1 445.27691161517106 445.2750315469955

y8++ 2 447.2399949875709 447.3183678407992

b4+ 1 448.186048121871 448.22153421784407

b8++ 2 448.69456324092096 448.72147059056505

b9++ 2 484.21312032067095 484.21186381583215

y9++ 2 527.2553194801709 527.257652964294

b5+ 1 549.233727345171 548.8069538307547

b11++ 2 597.7766165918209 597.7746017861595

b6+ 1 712.297056632271 712.3341870599002

b8+ 1 896.381850015071 896.3846890818005

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 3451.5768

Peptide scan index: 18979

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 21

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.08442318686912

y1+ 1 147.112804913371 147.11279005330542

b2+ 1 187.107719913371 187.1077036572923

y3++ 2 187.62353696122102 187.15138937310806

y2+ 1 261.15573310477106 261.1547612243966

b5++ 2 275.12050190597097 275.18764275096134

y6++ 2 315.184490732371 315.1533495025441

b6++ 2 356.652166549521 356.23646180591476

y3+ 1 374.23979745567107 374.2398255097935

y7++ 2 396.71615537592095 396.2279804209164

b7++ 2 400.168181129271 400.169507660348

y4+ 1 445.27691161517106 445.2750347811497

y8++ 2 447.2399949875709 447.2421091167949

b4+ 1 448.186048121871 448.2215374732421

b8++ 2 448.69456324092096 448.7214738496996

b9++ 2 484.21312032067095 484.21186733249664

y9++ 2 527.2553194801709 527.2576591797604

y5+ 1 542.329675838471 542.2809387449125

y10++ 2 577.7791590918209 577.7816852229254

b11++ 2 597.7766165918209 597.7746061230516

b8+ 1 896.381850015071 896.3940542183456

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 3458.2655400000003

Peptide scan index: 19015

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 35

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.08126038249907

b3++ 2 144.581337801721 145.0540752486155

y1+ 1 147.112804913371 147.1124931241242

b2+ 1 187.107719913371 187.10732354576686

y3++ 2 187.62353696122102 188.06594879255175

y4++ 2 223.14209404097102 223.14233938355105

b4++ 2 224.596662294321 224.18612801614893

y2+ 1 261.15573310477106 261.1560070943646

y5++ 2 271.668476152621 272.05325410499285

b5++ 2 275.12050190597097 275.12160175849584

b3+ 1 288.155399136671 288.1563092040947

y6++ 2 315.184490732371 315.18432421683644

b6++ 2 356.652166549521 356.248359900037

y3+ 1 374.23979745567107 374.20264498409796

y7++ 2 396.71615537592095 397.13752988376245

b7++ 2 400.168181129271 400.1685430826623

y4+ 1 445.27691161517106 445.24556303839955

y8++ 2 447.2399949875709 447.24103109117857

b4+ 1 448.186048121871 448.1844580063804

b8++ 2 448.69456324092096 448.38250656365017

b9++ 2 484.21312032067095 484.2107001941181

y9++ 2 527.2553194801709 527.2527544255756

b10++ 2 540.7551524961209 540.7557586543388

y5+ 1 542.329675838471 542.3035873044859

b5+ 1 549.233727345171 549.2326738671424

y10++ 2 577.7791590918209 577.7802928910451

b11++ 2 597.7766165918209 597.4172801577992

y6+ 1 629.361704997971 629.3650243487241

b6+ 1 712.297056632271 712.2964125279079

b7+ 1 799.329085791771 799.3336017065035

y8+ 1 893.4727135083709 893.4695259526468

b8+ 1 896.381850015071 896.3838181326942

y9+ 1 1053.5033624935709 1053.4985811283204

b11+ 1 1194.545956716871 1194.841263117805

y11+ 1 1253.619456003971 1253.628169033659

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 3460.5302399999996

Peptide scan index: 19027

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 31

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.08152680226462

b3++ 2 144.581337801721 145.0438809343836

y1+ 1 147.112804913371 147.1127477519913

b2+ 1 187.107719913371 187.10761097338911

y3++ 2 187.62353696122102 187.15375795752763

y4++ 2 223.14209404097102 223.1424915020622

b4++ 2 224.596662294321 224.1849807528253

y2+ 1 261.15573310477106 261.1565984313162

y5++ 2 271.668476152621 272.053806517493

b5++ 2 275.12050190597097 275.12040624655555

b3+ 1 288.155399136671 288.154574610509

y6++ 2 315.184490732371 315.1850727736781

b6++ 2 356.652166549521 356.220386189296

y3+ 1 374.23979745567107 374.1958203883333

y7++ 2 396.71615537592095 397.17957972995345

b7++ 2 400.168181129271 400.169355648999

y4+ 1 445.27691161517106 445.2755059172592

y8++ 2 447.2399949875709 447.3143551067657

b4+ 1 448.186048121871 448.1898677125381

b8++ 2 448.69456324092096 448.37891434505207

b9++ 2 484.21312032067095 484.2116834050683

y9++ 2 527.2553194801709 527.26319803664

b10++ 2 540.7551524961209 540.7568570392449

y5+ 1 542.329675838471 542.71816542688

y10++ 2 577.7791590918209 577.3470222125254

b11++ 2 597.7766165918209 597.7743794118848

y11++ 2 627.313366235371 627.3135745022038

b7+ 1 799.329085791771 799.3566597352722

y8+ 1 893.4727135083709 893.4735751814509

b8+ 1 896.381850015071 896.3809864387243

y11+ 1 1253.619456003971 1253.6149826766919

===================================

Peptide ID m/z: 670.835327148438

Peptide ID rt: 3462.51138

Peptide scan index: 19039

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999911359269907

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 29

ion theo. m/z observed m/z

y2++ 2 131.08150478577102 131.08158485093742

b3++ 2 144.581337801721 144.12625167994076

y1+ 1 147.112804913371 147.11278670890036

b2+ 1 187.107719913371 187.10764334502306

y3++ 2 187.62353696122102 188.06653283087684

y4++ 2 223.14209404097102 223.14280761749933

b4++ 2 224.596662294321 224.1865878160448

y2+ 1 261.15573310477106 261.1564920238751

y5++ 2 271.668476152621 272.05382497078426

b5++ 2 275.12050190597097 275.1204249111217

b3+ 1 288.155399136671 288.1545941530373

y6++ 2 315.184490732371 315.18487254769855

b6++ 2 356.652166549521 356.2204103789061

y3+ 1 374.23979745567107 374.23360810903097

y7++ 2 396.71615537592095 397.1495780530043

b7++ 2 400.168181129271 400.1693827829975

y8++ 2 447.2399949875709 447.31506945467834

b4+ 1 448.186048121871 448.2258978136637

b8++ 2 448.69456324092096 448.6987961991102

b9++ 2 484.21312032067095 484.21171624940513

y9++ 2 527.2553194801709 527.2574922411383

b10++ 2 540.7551524961209 540.3158736346712

b11++ 2 597.7766165918209 597.7744199612491

y11++ 2 627.313366235371 627.3122850268676

b6+ 1 712.297056632271 712.2979071917312

y8+ 1 893.4727135083709 893.6636427648748

b8+ 1 896.381850015071 896.3876127520014

b9+ 1 967.418964174571 967.7706464978409

y11+ 1 1253.619456003971 1253.6130599448552

===================================

**Mzml #2 Kerolos Onsy**

C:\Users\ONSY\PycharmProjects\pythonProject\venv\Scripts\python.exe C:/Users/ONSY/PycharmProjects/pythonProject/main.py

Hi, PyCharm

Proteins: 1

Peptides: 20

Processed peptides: 20

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 96 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 96 hits for 96 of 96 peptides.

Peptide hits passing enzyme filter: 96

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 96 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 96

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 556.274865625713

Peptide ID rt: 1809.7037400000002

Peptide scan index: 6089

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 555.9386305677043

comparsion score = 0.9993955594998338

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 14

ion theo. m/z observed m/z

y6++ 2 382.23230639187096 381.8745422363281

y3+ 1 401.287081615171 401.3790588378906

b8++ 2 403.652895581421 403.8127136230469

y7++ 2 430.75868850352094 430.7705383300781

b4+ 1 450.128927930471 450.1146240234375

b9++ 2 452.17927769307096 452.1529846191406

y8++ 2 466.27724558327094 466.76885986328125

b10++ 2 500.70565980472094 500.7884521484375

y9++ 2 522.8192777587209 522.796142578125

y4+ 1 538.345993838471 538.1641845703125

y10++ 2 551.3300098065708 551.2189331054688

y11++ 2 608.8434818863209 609.2086181640625

y14++ 2 753.388983125571 753.6195678710938

b8+ 1 806.298514696071 806.6339111328125

===================================

Peptide ID m/z: 556.274087555469

Peptide ID rt: 1830.99708

Peptide scan index: 6267

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 555.9386305677043

comparsion score = 0.9993969573717898

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y6++ 2 382.23230639187096 381.8753967285156

b8++ 2 403.652895581421 403.8121337890625

y7++ 2 430.75868850352094 430.7691955566406

b4+ 1 450.128927930471 450.11566162109375

b9++ 2 452.17927769307096 451.8854675292969

y8++ 2 466.27724558327094 466.1428527832031

y9++ 2 522.8192777587209 522.9160766601562

y4+ 1 538.345993838471 538.1637573242188

y10++ 2 551.3300098065708 551.2181396484375

y11++ 2 608.8434818863209 609.2069702148438

y12++ 2 652.3594964660709 652.739501953125

b8+ 1 806.298514696071 806.5910034179688

===================================

Peptide ID m/z: 417.458314820585

Peptide ID rt: 1835.39604

Peptide scan index: 6304

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 417.20579204247093

comparsion score = 0.9993950946258608

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 447.897295462304

Peptide ID rt: 1875.35556

Peptide scan index: 6690

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 447.5650101223376

comparsion score = 0.9992581215753414

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 13

ion theo. m/z observed m/z

b8++ 2 393.19304479617097 393.09466552734375

b4+ 1 396.224147391871 396.07940673828125

y8++ 2 416.2139773918709 415.80615234375

b9++ 2 436.70905937592096 436.8796081542969

y4+ 1 469.27691161517106 469.3292236328125

b10++ 2 485.23544148757094 485.0755920410156

b5+ 1 510.267075583271 510.6565856933594

y10++ 2 530.256905583271 530.6749267578125

y5+ 1 556.308940774671 556.1749877929688

y11++ 2 578.783287694921 579.1057739257812

b6+ 1 611.3147548065709 611.1854858398438

y12++ 2 635.325319870371 635.755859375

y7+ 1 730.372999093671 730.2593994140625

===================================

Peptide ID m/z: 556.275901830626

Peptide ID rt: 1961.74206

Peptide scan index: 7438

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 555.9386305677043

comparsion score = 0.9993936978722037

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y6++ 2 382.23230639187096 382.07275390625

b8++ 2 403.652895581421 403.2319030761719

y7++ 2 430.75868850352094 430.77056884765625

b4+ 1 450.128927930471 450.11505126953125

y8++ 2 466.27724558327094 466.1417541503906

y9++ 2 522.8192777587209 523.1336059570312

y4+ 1 538.345993838471 538.1630249023438

y10++ 2 551.3300098065708 551.2181396484375

y11++ 2 608.8434818863209 609.2097778320312

y6+ 1 763.457336316971 763.175048828125

y8+ 1 931.547214699771 931.7730102539062

===================================

Peptide ID m/z: 417.458557128906

Peptide ID rt: 1963.08792

Peptide scan index: 7450

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 417.20579204247093

comparsion score = 0.9993945145401414

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

y6++ 2 382.23230639187096 382.07293701171875

b8++ 2 403.652895581421 403.8149108886719

y7++ 2 430.75868850352094 430.7701416015625

b4+ 1 450.128927930471 450.1144714355469

y8++ 2 466.27724558327094 466.14154052734375

y9++ 2 522.8192777587209 523.134765625

y4+ 1 538.345993838471 538.1630249023438

y10++ 2 551.3300098065708 551.2183837890625

b13++ 2 689.806437219421 690.158935546875

b8+ 1 806.298514696071 806.2688598632812

===================================

Peptide ID m/z: 447.897191988056

Peptide ID rt: 1984.09716

Peptide scan index: 7635

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 447.5650101223376

comparsion score = 0.9992583524262699

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 671.344197221523

Peptide ID rt: 1986.47064

Peptide scan index: 7656

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 670.843876950121

comparsion score = 0.9992547484979051

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

b8++ 2 393.19304479617097 393.2977600097656

b4+ 1 396.224147391871 396.1059265136719

y8++ 2 416.2139773918709 416.0964660644531

y4+ 1 469.27691161517106 469.3291015625

b10++ 2 485.23544148757094 485.0743103027344

b5+ 1 510.267075583271 510.74493408203125

y5+ 1 556.308940774671 556.1732788085938

y11++ 2 578.783287694921 578.9254150390625

b6+ 1 611.3147548065709 611.1856079101562

y10+ 1 1059.506534699771 1059.64599609375

===================================

Peptide ID m/z: 462.564397715187

Peptide ID rt: 1989.0912600000001

Peptide scan index: 7679

Peptide ID score type: hyperscore

- Peptide hit sequence: GEPHHELPPGSTK

- Peptide hit monoisotopic m/z: 462.5651214450377

comparsion score = 1.0000015646034461

Spectrum 1 of GEPHHELPPGSTK has 46 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y4+ 1 392.21397739187097 392.18743896484375

y8++ 2 414.7267204397209 415.03692626953125

b4+ 1 421.183011232371 421.32244873046875

b8++ 2 449.21431135997096 449.1134338378906

y9++ 2 483.2561765513709 483.1514892578125

y5+ 1 489.26674161517093 489.0276184082031

b9++ 2 497.74069347162094 497.8331298828125

y10++ 2 551.7856326630209 552.2152099609375

===================================

Peptide ID m/z: 693.343078613281

Peptide ID rt: 1995.9865800000002

Peptide scan index: 7748

Peptide ID score type: hyperscore

- Peptide hit sequence: GEPHHELPPGSTK

- Peptide hit monoisotopic m/z: 693.3440439341709

comparsion score = 1.0000013922701758

Spectrum 1 of GEPHHELPPGSTK has 46 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y4+ 1 392.21397739187097 392.28741455078125

b7++ 2 400.687929248321 400.3507995605469

y8++ 2 414.7267204397209 414.7139587402344

b4+ 1 421.183011232371 421.3223571777344

b8++ 2 449.21431135997096 449.11346435546875

y9++ 2 483.2561765513709 483.1525573730469

y5+ 1 489.26674161517093 489.0545959472656

b9++ 2 497.74069347162094 497.83514404296875

b10++ 2 526.2514255194709 525.8641357421875

y10++ 2 551.7856326630209 552.2160034179688

b8+ 1 897.421346253171 897.477783203125

===================================

Peptide ID m/z: 670.845032554492

Peptide ID rt: 2002.5384600000002

Peptide scan index: 7823

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 670.843876950121

comparsion score = 0.9999982773899857

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 9

ion theo. m/z observed m/z

b8++ 2 393.19304479617097 393.11346435546875

b4+ 1 396.224147391871 396.0818786621094

y8++ 2 416.2139773918709 416.1497497558594

b9++ 2 436.70905937592096 436.83984375

y4+ 1 469.27691161517106 469.3291320800781

b10++ 2 485.23544148757094 485.0736083984375

y5+ 1 556.308940774671 556.1734619140625

y11++ 2 578.783287694921 578.8378295898438

b6+ 1 611.3147548065709 611.185302734375

===================================

Peptide ID m/z: 462.565093994141

Peptide ID rt: 2020.9174199999998

Peptide scan index: 8011

Peptide ID score type: hyperscore

- Peptide hit sequence: GEPHHELPPGSTK

- Peptide hit monoisotopic m/z: 462.5651214450377

comparsion score = 1.0000000593449376

Spectrum 1 of GEPHHELPPGSTK has 46 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y4+ 1 392.21397739187097 392.2213439941406

b7++ 2 400.687929248321 400.89263916015625

y8++ 2 414.7267204397209 415.0365905761719

b4+ 1 421.183011232371 421.32275390625

b8++ 2 449.21431135997096 449.1159973144531

y9++ 2 483.2561765513709 483.1506042480469

y5+ 1 489.26674161517093 489.0286560058594

b9++ 2 497.74069347162094 497.8335876464844

y10++ 2 551.7856326630209 552.2158813476562

b6+ 1 687.284517678971 687.2015380859375

b7+ 1 800.368582029871 800.7515869140625

b11+ 1 1138.527603731671 1138.488037109375

===================================

Peptide ID m/z: 447.89754576665

Peptide ID rt: 2070.37512

Peptide scan index: 8461

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 447.5650101223376

comparsion score = 0.9992575631470736

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 2

ion theo. m/z observed m/z

b5++ 2 255.637176025021 256.08111572265625

y7++ 2 365.69013778022094 366.08770751953125

===================================

Peptide ID m/z: 447.555395760738

Peptide ID rt: 2100.24366

Peptide scan index: 8749

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 447.5553460323376

comparsion score = 0.9999998888888373

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 2

ion theo. m/z observed m/z

y4++ 2 223.14209404097102 223.06202697753906

b4++ 2 224.596662294321 225.04254150390625

===================================

Peptide ID m/z: 693.841432497186

Peptide ID rt: 2126.5168799999997

Peptide scan index: 9020

Peptide ID score type: hyperscore

- Peptide hit sequence: GEPHHELPPGSTK

- Peptide hit monoisotopic m/z: 693.3440439341709

comparsion score = 0.999283137991306

Spectrum 1 of GEPHHELPPGSTK has 46 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

b2+ 1 187.071334785771 187.0711212158203

y3+ 1 335.192513296171 335.0960998535156

y8++ 2 414.7267204397209 415.0377197265625

===================================

Peptide ID m/z: 670.838851300851

Peptide ID rt: 2150.3392200000003

Peptide scan index: 9262

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 670.843876950121

comparsion score = 1.0000074915894632

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 555.935403422745

Peptide ID rt: 2150.72982

Peptide scan index: 9265

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 555.9386305677043

comparsion score = 1.0000058048919702

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 540.254967101639

Peptide ID rt: 2178.73602

Peptide scan index: 9537

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9990676465800579

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 417.204782192402

Peptide ID rt: 2302.42842

Peptide scan index: 10819

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 417.20579204247093

comparsion score = 1.0000024205141265

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y2++ 2 144.60514686552102 145.0974578857422

y1+ 1 175.118952913371 175.1197967529297

y4++ 2 269.676635152621 270.14483642578125

b5++ 2 283.08157427837097 283.1398620605469

b7++ 2 368.134338501671 368.1719665527344

b8++ 2 403.652895581421 403.706298828125

y4+ 1 538.345993838471 538.2857666015625

b5+ 1 565.155872089971 565.272216796875

y12++ 2 652.3594964660709 652.3384399414062

y13++ 2 709.872968545821 710.3306274414062

b7+ 1 735.261400536571 735.3414306640625

y14++ 2 753.388983125571 753.364013671875

===================================

Peptide ID m/z: 417.204304538267

Peptide ID rt: 2324.6889

Peptide scan index: 11045

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 417.20579204247093

comparsion score = 1.0000035654095314

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.03977966308594

y1+ 1 175.118952913371 175.11895751953125

y3++ 2 201.14717904097103 201.12319946289062

y4++ 2 269.676635152621 270.1445617675781

y3+ 1 401.287081615171 401.48858642578125

y8++ 2 466.27724558327094 465.94195556640625

b10++ 2 500.70565980472094 500.6188049316406

b6+ 1 622.177336185671 622.3253173828125

===================================

Peptide ID m/z: 833.396457363808

Peptide ID rt: 2334.45246

Peptide scan index: 11154

Peptide ID score type: hyperscore

- Peptide hit sequence: C(Carbamidomethyl)SDSDGLAPPQHLIR

- Peptide hit monoisotopic m/z: 833.404307618171

comparsion score = 1.0000094195917124

Spectrum 1 of C(Carbamidomethyl)SDSDGLAPPQHLIR has 54 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.0400390625

y1+ 1 175.118952913371 175.11886596679688

b5++ 2 283.08157427837097 283.17572021484375

y3+ 1 401.287081615171 401.2143249511719

b10++ 2 500.70565980472094 500.9604187011719

y11++ 2 608.8434818863209 608.7966918945312

b6+ 1 622.177336185671 622.3219604492188

===================================

Peptide ID m/z: 670.826554591169

Peptide ID rt: 2388.2160000000003

Peptide scan index: 11734

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 1.0000042130472213

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11280822753906

b2+ 1 187.107719913371 187.07215881347656

b5++ 2 275.12050190597097 275.1266174316406

b7++ 2 400.168181129271 400.25726318359375

b4+ 1 448.186048121871 448.2615051269531

b5+ 1 549.233727345171 549.30126953125

y10++ 2 577.7791590918209 578.2645263671875

y6+ 1 629.361704997971 629.3140258789062

===================================

Peptide ID m/z: 527.623641166899

Peptide ID rt: 2403.48786

Peptide scan index: 11899

Peptide ID score type: hyperscore

- Peptide hit sequence: KPLDGEYFTLQIR

- Peptide hit monoisotopic m/z: 527.2874766789711

comparsion score = 0.999362870687173

Spectrum 1 of KPLDGEYFTLQIR has 46 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

y3++ 2 208.63443599312103 209.09132385253906

b2+ 1 226.155004072871 226.11843872070312

y5++ 2 315.70030778022095 316.11865234375

b10++ 2 582.800417258721 583.1248779296875

y10++ 2 621.311680806571 621.6854248046875

y5+ 1 630.393339093671 630.695068359375

b11++ 2 646.829706386321 646.7077026367188

b12++ 2 703.371738561771 703.2123413085938

y12++ 2 726.380095093671 726.2293701171875

b11+ 1 1292.6521363058712 1292.4285888671875

===================================

Peptide ID m/z: 615.802890896013

Peptide ID rt: 2415.7839

Peptide scan index: 12023

Peptide ID score type: hyperscore

- Peptide hit sequence: QSQHM(Oxidation)TEVVR

- Peptide hit monoisotopic m/z: 615.7984146556211

comparsion score = 0.9999927310500517

Spectrum 1 of QSQHM(Oxidation)TEVVR has 34 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y6++ 2 375.694365709021 375.9481506347656

b7++ 2 429.674162145221 429.7226867675781

y4+ 1 502.298375710871 502.2581481933594

y8++ 2 508.253110948271 508.26715087890625

b9++ 2 528.742576432321 528.7700805664062

b5+ 1 628.2507743770711 628.3018798828125

b6+ 1 729.2984536003711 729.2822875976562

y6+ 1 750.381454951271 750.4212036132812

===================================

Peptide ID m/z: 527.284015716255

Peptide ID rt: 2470.81194

Peptide scan index: 12606

Peptide ID score type: hyperscore

- Peptide hit sequence: KPLDGEYFTLQIR

- Peptide hit monoisotopic m/z: 527.2874766789711

comparsion score = 1.000006563754282

Spectrum 1 of KPLDGEYFTLQIR has 46 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.11903381347656

y3++ 2 208.63443599312103 209.0931396484375

b2+ 1 226.155004072871 226.12078857421875

y4+ 1 529.345659870371 529.2684326171875

y8++ 2 535.287476678971 535.301025390625

b6+ 1 640.330070902271 640.323486328125

b12++ 2 703.371738561771 703.3367309570312

y6+ 1 777.4617533807709 777.3699951171875

===================================

Peptide ID m/z: 790.420769226467

Peptide ID rt: 2474.9964

Peptide scan index: 12652

Peptide ID score type: hyperscore

- Peptide hit sequence: KPLDGEYFTLQIR

- Peptide hit monoisotopic m/z: 790.427576785071

comparsion score = 1.000008612575566

Spectrum 1 of KPLDGEYFTLQIR has 46 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.03996276855469

y1+ 1 175.118952913371 175.11880493164062

b2+ 1 226.155004072871 226.11875915527344

b5++ 2 256.147376572871 256.0927734375

y5++ 2 315.70030778022095 316.1499328613281

y6++ 2 389.2345149237709 389.1290283203125

b7++ 2 402.200338328071 402.1964111328125

y7++ 2 470.76617956732093 470.71087646484375

b5+ 1 511.28747667897096 511.2243957519531

y4+ 1 529.345659870371 529.2374267578125

b7+ 1 803.393400189371 803.3740844726562

y7+ 1 940.525082667871 940.422607421875

===================================

Peptide ID m/z: 527.28353118361

Peptide ID rt: 2491.75506

Peptide scan index: 12836

Peptide ID score type: hyperscore

- Peptide hit sequence: KPLDGEYFTLQIR

- Peptide hit monoisotopic m/z: 527.2874766789711

comparsion score = 1.0000074826827081

Spectrum 1 of KPLDGEYFTLQIR has 46 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.03997802734375

y1+ 1 175.118952913371 175.11911010742188

y3++ 2 208.63443599312103 209.05682373046875

b2+ 1 226.155004072871 226.15414428710938

y3+ 1 416.26159551947103 416.2889709472656

b4+ 1 454.266012583271 454.22991943359375

y7++ 2 470.76617956732093 470.9187316894531

b8++ 2 475.734545471621 475.92401123046875

b9++ 2 526.258385083271 526.1910400390625

y8++ 2 535.287476678971 535.2635498046875

y9++ 2 563.7982087268209 564.2926025390625

===================================

Peptide ID m/z: 405.540253333047

Peptide ID rt: 2515.82826

Peptide scan index: 13079

Peptide ID score type: hyperscore

- Peptide hit sequence: QSQHMTEVVR

- Peptide hit monoisotopic m/z: 405.53639692600433

comparsion score = 0.9999904906923271

Spectrum 1 of QSQHMTEVVR has 34 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

b7++ 2 421.676704645221 421.5439453125

y7++ 2 436.22636432067094 436.22625732421875

b8++ 2 471.210911788771 471.2373962402344

b4+ 1 481.21537435997107 481.2304382324219

y8++ 2 500.25565344827095 500.258544921875

y4+ 1 502.298375710871 502.2503662109375

b9++ 2 520.745118932321 520.5037841796875

y9++ 2 543.7716680280209 543.7831420898438

y5+ 1 603.346054934171 603.2864379882812

b5+ 1 612.255859377071 612.2664184570312

b6+ 1 713.303538600371 712.8424682617188

y6+ 1 734.386539951271 734.2689208984375

===================================

Peptide ID m/z: 447.564428298566

Peptide ID rt: 2562.58344

Peptide scan index: 13581

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 447.5650101223376

comparsion score = 1.00000129997769

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 17

ion theo. m/z observed m/z

b3++ 2 141.594247833621 141.10227966308594

y1+ 1 147.112804913371 147.1129913330078

b2+ 1 185.12845497717097 185.09283447265625

y3++ 2 186.615711929321 187.0712432861328

b4++ 2 198.615711929321 199.10775756835938

y2+ 1 244.16556913667102 244.1301727294922

b5++ 2 255.637176025021 256.129638671875

b6++ 2 306.161015636671 306.18023681640625

y6++ 2 322.17412320047094 322.1548156738281

y7++ 2 365.69013778022094 366.1401062011719

y3+ 1 372.22414739187104 372.49139404296875

y8++ 2 416.2139773918709 416.2259216308594

b9++ 2 436.70905937592096 436.6773986816406

y9++ 2 473.23544148757094 473.2799377441406

b5+ 1 510.267075583271 510.1952819824219

y10++ 2 530.256905583271 530.3005981445312

y11++ 2 578.783287694921 578.8250122070312

===================================

Peptide ID m/z: 671.337647736492

Peptide ID rt: 2590.0037399999997

Peptide scan index: 13889

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9992429041882503

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

b3++ 2 144.581337801721 145.0493621826172

y1+ 1 147.112804913371 147.1132049560547

b2+ 1 187.107719913371 187.07107543945312

y3++ 2 187.62353696122102 187.1448974609375

y4++ 2 223.14209404097102 223.15505981445312

y10++ 2 577.7791590918209 577.2916259765625

===================================

Peptide ID m/z: 607.7950522022

Peptide ID rt: 2606.9914200000003

Peptide scan index: 14071

Peptide ID score type: hyperscore

- Peptide hit sequence: QSQHMTEVVR

- Peptide hit monoisotopic m/z: 607.800957155621

comparsion score = 1.0000097153693495

Spectrum 1 of QSQHMTEVVR has 34 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

b7++ 2 421.676704645221 421.5844421386719

y7++ 2 436.22636432067094 436.22552490234375

b8++ 2 471.210911788771 470.98040771484375

b4+ 1 481.21537435997107 481.2750244140625

y8++ 2 500.25565344827095 500.242919921875

y4+ 1 502.298375710871 502.26129150390625

b9++ 2 520.745118932321 520.7296752929688

y9++ 2 543.7716680280209 543.6356811523438

y5+ 1 603.346054934171 603.28564453125

b5+ 1 612.255859377071 612.243896484375

y6+ 1 734.386539951271 734.3491821289062

b7+ 1 842.346132823671 841.888671875

===================================

Peptide ID m/z: 539.75481875297

Peptide ID rt: 2616.92736

Peptide scan index: 14177

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999934040096998

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

y4++ 2 271.63971852502095 272.12225341796875

y5++ 2 315.15573310477095 315.161865234375

y2+ 1 322.187367200471 322.07183837890625

b3+ 1 393.176863232371 393.1087341308594

y8++ 2 489.227418923771 489.17169189453125

b5+ 1 537.2303564875709 537.7058715820312

y4+ 1 542.272160583271 542.2084350585938

b6+ 1 700.2936857746708 700.63916015625

y7+ 1 814.384232093671 814.3529663085938

y8+ 1 977.447561380771 977.3809814453125

===================================

Peptide ID m/z: 670.832889566932

Peptide ID rt: 2668.0896

Peptide scan index: 14723

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9999947695590576

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 9

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.1132354736328

b2+ 1 187.107719913371 187.14474487304688

y3+ 1 374.23979745567107 374.1478576660156

y7++ 2 396.71615537592095 396.6600036621094

b7++ 2 400.168181129271 400.1816711425781

y8++ 2 447.2399949875709 447.71697998046875

b4+ 1 448.186048121871 448.2098083496094

y11++ 2 627.313366235371 627.2523803710938

b7+ 1 799.329085791771 799.3408203125

===================================

Peptide ID m/z: 671.343126148887

Peptide ID rt: 2705.67888

Peptide scan index: 15151

Peptide ID score type: hyperscore

- Peptide hit sequence: ALPNNTSSSPQPK

- Peptide hit monoisotopic m/z: 670.843876950121

comparsion score = 0.9992563427265131

Spectrum 1 of ALPNNTSSSPQPK has 46 peaks.

Number of matched peaks: 22

ion theo. m/z observed m/z

b3++ 2 141.594247833621 142.06910705566406

y1+ 1 147.112804913371 147.11302185058594

b2+ 1 185.12845497717097 185.12811279296875

y3++ 2 186.615711929321 187.07167053222656

b4++ 2 198.615711929321 199.0716552734375

y2+ 1 244.16556913667102 244.1663360595703

b3+ 1 282.181219200471 282.10992431640625

b7++ 2 349.677030216421 350.15087890625

y7++ 2 365.69013778022094 365.65966796875

y3+ 1 372.22414739187104 372.201416015625

b8++ 2 393.19304479617097 393.1792297363281

b4+ 1 396.224147391871 396.19873046875

y8++ 2 416.2139773918709 416.178466796875

y4+ 1 469.27691161517106 469.2308044433594

b10++ 2 485.23544148757094 485.1976623535156

b5+ 1 510.267075583271 509.9107971191406

y11++ 2 578.783287694921 579.25830078125

b12++ 2 597.791112726821 597.7947998046875

b7+ 1 698.3467839660709 698.3453979492188

y7+ 1 730.372999093671 730.3327026367188

b8+ 1 785.3788131255709 785.3536376953125

y8+ 1 831.4206783169709 831.4596557617188

===================================

Peptide ID m/z: 637.987284242971

Peptide ID rt: 2751.6424199999997

Peptide scan index: 15653

Peptide ID score type: hyperscore

- Peptide hit sequence: TC(Carbamidomethyl)PVQLWVDSTPPPGTR

- Peptide hit monoisotopic m/z: 637.6524904364045

comparsion score = 0.9994752343583716

Spectrum 1 of TC(Carbamidomethyl)PVQLWVDSTPPPGTR has 62 peaks.

Number of matched peaks: 9

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.0396728515625

b2++ 2 131.546440571021 131.11790466308594

y1+ 1 175.118952913371 175.11883544921875

y4++ 2 215.62406846122101 215.13946533203125

y2+ 1 276.166632136671 276.16998291015625

b5++ 2 293.63631895382105 293.172119140625

y3+ 1 333.18809623237104 333.2055358886719

y7++ 2 363.2006722961709 363.2010803222656

y10++ 2 513.764366099221 513.8895874023438

===================================

Peptide ID m/z: 607.80527419843

Peptide ID rt: 2803.4972399999997

Peptide scan index: 16200

Peptide ID score type: hyperscore

- Peptide hit sequence: QSQHMTEVVR

- Peptide hit monoisotopic m/z: 607.800957155621

comparsion score = 0.9999928973258504

Spectrum 1 of QSQHMTEVVR has 34 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.0399398803711

y2++ 2 137.597321833621 138.09156799316406

y1+ 1 175.118952913371 175.11924743652344

b4++ 2 241.11132541337102 241.1404571533203

b6++ 2 357.155407533571 357.21441650390625

y6++ 2 367.69690820902093 368.19256591796875

y8++ 2 500.25565344827095 500.25152587890625

y4+ 1 502.298375710871 502.7542724609375

b9++ 2 520.745118932321 520.2764892578125

y9++ 2 543.7716680280209 543.751953125

b5+ 1 612.255859377071 612.2623901367188

===================================

Peptide ID m/z: 410.871998887604

Peptide ID rt: 2889.17292

Peptide scan index: 17146

Peptide ID score type: hyperscore

- Peptide hit sequence: QSQHM(Oxidation)TEVVR

- Peptide hit monoisotopic m/z: 410.8680352593378

comparsion score = 0.9999903531312015

Spectrum 1 of QSQHM(Oxidation)TEVVR has 34 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.1189727783203

y3++ 2 187.131528977171 187.14356994628906

y4++ 2 251.652826088821 252.1092987060547

y5++ 2 302.17666570047095 302.1169128417969

y4+ 1 502.298375710871 502.2723388671875

y5+ 1 603.346054934171 603.2597045898438

===================================

Peptide ID m/z: 615.800533596807

Peptide ID rt: 2890.6677600000003

Peptide scan index: 17165

Peptide ID score type: hyperscore

- Peptide hit sequence: QSQHM(Oxidation)TEVVR

- Peptide hit monoisotopic m/z: 615.7984146556211

comparsion score = 0.9999965590462003

Spectrum 1 of QSQHM(Oxidation)TEVVR has 34 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

b3++ 2 172.581869301721 172.10806274414062

y1+ 1 175.118952913371 175.11898803710938

y3++ 2 187.131528977171 187.07241821289062

y5+ 1 603.346054934171 603.2462158203125

b5+ 1 628.2507743770711 628.2838745117188

b6+ 1 729.2984536003711 729.3565673828125

======================================================================

Peptide ID m/z: 671.325827712541

Peptide ID rt: 3006.0769800000003

Peptide scan index: 18434

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9992604978433324

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 16

ion theo. m/z observed m/z

y1++ 2 74.06004069007102 74.06092071533203

y2++ 2 131.08150478577102 131.11810302734375

b3++ 2 144.581337801721 145.0613555908203

y1+ 1 147.112804913371 147.11294555664062

b2+ 1 187.107719913371 187.0889129638672

y3++ 2 187.62353696122102 187.1428680419922

y4++ 2 223.14209404097102 223.10874938964844

y5++ 2 271.668476152621 271.1784362792969

b3+ 1 288.155399136671 288.2037048339844

y6++ 2 315.184490732371 315.17010498046875

b6++ 2 356.652166549521 356.1946716308594

b4+ 1 448.186048121871 448.1854553222656

y9++ 2 527.2553194801709 526.8174438476562

y5+ 1 542.329675838471 542.2559204101562

b11++ 2 597.7766165918209 597.3460693359375

b6+ 1 712.297056632271 712.3785400390625

**Mzml #1 Felopater Nashat**

Proteins: 1

Peptides: 5

Processed peptides: 5

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 14 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 14 hits for 14 of 14 peptides.

Peptide hits passing enzyme filter: 14

... rejected by enzyme filter: 0

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Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 14 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 14

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 447.556593470872

Peptide ID rt: 2266.18218

Peptide scan index: 7894

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 447.5553460323376

comparsion score = 0.9999972127803443

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 1

ion theo. m/z observed m/z

b4++ 2 224.596662294321 225.0431671142578

===================================

Peptide ID m/z: 670.827145144315

Peptide ID rt: 2473.43304

Peptide scan index: 9775

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 1.0000033327077207

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 1

ion theo. m/z observed m/z

y9+ 1 1053.5033624935709 1053.3505859375

===================================

Peptide ID m/z: 516.291782109927

Peptide ID rt: 2508.33468

Peptide scan index: 10104

Peptide ID score type: hyperscore

- Peptide hit sequence: LGFLHSGTAK

- Peptide hit monoisotopic m/z: 515.787643663021

comparsion score = 0.9990235396642461

Spectrum 1 of LGFLHSGTAK has 34 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.1129150390625

b2+ 1 171.112804913371 171.11270141601562

y4++ 2 188.613169429321 189.08778381347656

b4++ 2 216.136280009071 216.0988006591797

y7++ 2 357.200672296171 357.2101135253906

b9++ 2 442.734879439721 442.24432373046875

b9+ 1 884.462482412671 884.3914794921875

===================================

Peptide ID m/z: 447.554456421661

Peptide ID rt: 2572.9204799999998

Peptide scan index: 10703

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 447.5553460323376

comparsion score = 1.0000019877149335

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

b3++ 2 144.581337801721 145.06150817871094

y1+ 1 147.112804913371 147.11288452148438

b2+ 1 187.107719913371 187.0721435546875

b4++ 2 224.596662294321 224.10401916503906

y5++ 2 271.668476152621 271.1768798828125

b5++ 2 275.12050190597097 275.1398620605469

b8++ 2 448.69456324092096 448.7316589355469

b9++ 2 484.21312032067095 484.2742004394531

b10++ 2 540.7551524961209 540.3018188476562

y5+ 1 542.329675838471 542.2839965820312

b11++ 2 597.7766165918209 597.8001098632812

y11++ 2 627.313366235371 627.3248901367188

===================================

Peptide ID m/z: 671.329281128051

Peptide ID rt: 2722.38438

Peptide scan index: 12062

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.999255357501925

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

b2+ 1 187.107719913371 187.0718536376953

b5++ 2 275.12050190597097 275.1253356933594

b7++ 2 400.168181129271 400.1465759277344

b9++ 2 484.21312032067095 483.8694152832031

y9++ 2 527.2553194801709 527.2135009765625

b10++ 2 540.7551524961209 540.7409057617188

y6+ 1 629.361704997971 629.2830200195312

y9+ 1 1053.5033624935709 1053.4267578125

===================================

Peptide ID m/z: 447.557065088355

Peptide ID rt: 2817.99414

Peptide scan index: 12956

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 447.5553460323376

comparsion score = 0.9999961590238396

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 4

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.1132049560547

b2+ 1 187.107719913371 187.07205200195312

b3+ 1 288.155399136671 287.88507080078125

b11++ 2 597.7766165918209 597.795654296875

===================================

Peptide ID m/z: 671.326931323989

Peptide ID rt: 3124.69608

Peptide scan index: 15942

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9992588551335385

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 16

ion theo. m/z observed m/z

y1++ 2 74.06004069007102 74.06089782714844

y2++ 2 131.08150478577102 131.08177185058594

b3++ 2 144.581337801721 145.0608673095703

y1+ 1 147.112804913371 147.11309814453125

b2+ 1 187.107719913371 187.10848999023438

y3++ 2 187.62353696122102 187.14488220214844

b4++ 2 224.596662294321 224.1018829345703

y2+ 1 261.15573310477106 261.1259460449219

y5++ 2 271.668476152621 271.6677551269531

b5++ 2 275.12050190597097 275.1719055175781

y3+ 1 374.23979745567107 374.244140625

y7++ 2 396.71615537592095 396.2260437011719

y4+ 1 445.27691161517106 445.2740173339844

y8++ 2 447.2399949875709 447.27154541015625

b4+ 1 448.186048121871 447.7720031738281

y5+ 1 542.329675838471 542.329833984375

===================================

Peptide ID m/z: 539.756374773576

Peptide ID rt: 3356.3947799999996

Peptide scan index: 18171

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999905212084672

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

b7++ 2 379.161213168571 378.7222595214844

y3+ 1 379.208831296171 379.69940185546875

b3+ 1 393.176863232371 393.1441345214844

y7++ 2 407.69575428022097 407.74444580078125

b4+ 1 450.19832732807095 450.239013671875

b8++ 2 452.695420312121 452.74066162109375

y8++ 2 489.227418923771 489.2350158691406

b5+ 1 537.2303564875709 537.2208251953125

y5+ 1 629.304189742771 629.3104248046875

y6+ 1 686.325653838471 686.2893676757812

y7+ 1 814.384232093671 814.6766967773438

===================================

Peptide ID m/z: 539.756601484496

Peptide ID rt: 3379.86528

Peptide scan index: 18401

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999901011880906

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.04015350341797

y1+ 1 175.118952913371 175.1193389892578

y3++ 2 190.10805388147102 190.08653259277344

b3++ 2 197.092069849571 197.12876892089844

y2+ 1 322.187367200471 322.13873291015625

b6++ 2 350.650481120721 350.1805114746094

b3+ 1 393.176863232371 393.1776428222656

===================================

Peptide ID m/z: 539.755570520461

Peptide ID rt: 3414.18564

Peptide scan index: 18738

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999920112264227

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

b2++ 2 133.062780721971 133.0435333251953

y1+ 1 175.118952913371 175.11920166015625

y4++ 2 271.63971852502095 272.1243591308594

y5++ 2 315.15573310477095 315.1683654785156

y6++ 2 343.66646515262096 343.2030944824219

y7++ 2 407.69575428022097 407.70361328125

b8++ 2 452.695420312121 452.709228515625

b5+ 1 537.2303564875709 537.272216796875

b6+ 1 700.2936857746708 700.3485717773438

b7+ 1 757.3151498703709 757.3587036132812

y7+ 1 814.384232093671 814.3998413085938

===================================

Peptide ID m/z: 539.754991942626

Peptide ID rt: 3439.39824

Peptide scan index: 18986

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999930831446476

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.0400619506836

y1+ 1 175.118952913371 175.1194305419922

b3++ 2 197.092069849571 197.12850952148438

b2+ 1 265.11828497717096 265.1197814941406

y4++ 2 271.63971852502095 271.1759338378906

y6++ 2 343.66646515262096 343.6782531738281

y3+ 1 379.208831296171 379.1922912597656

b4+ 1 450.19832732807095 450.22320556640625

y8++ 2 489.227418923771 488.7804260253906

y6+ 1 686.325653838471 686.345947265625

b7+ 1 757.3151498703709 757.3624877929688

===================================

Peptide ID m/z: 515.789103610151

Peptide ID rt: 4047.05202

Peptide scan index: 24578

Peptide ID score type: hyperscore

- Peptide hit sequence: LGFLHSGTAK

- Peptide hit monoisotopic m/z: 515.787643663021

comparsion score = 0.9999971694882273

Spectrum 1 of LGFLHSGTAK has 34 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

b5++ 2 284.665736120721 285.1213073730469

y4+ 1 376.219062391871 376.1544189453125

b5+ 1 568.324195774671 568.2680053710938

y6+ 1 600.3100037746709 600.2891235351562

b8+ 1 813.425368253171 813.3399047851562

y8+ 1 860.4624824126709 860.36865234375

b9+ 1 884.462482412671 884.3670654296875

y9+ 1 917.4839465083709 917.153076171875

===================================

Peptide ID m/z: 516.288429156491

Peptide ID rt: 4132.37634

Peptide scan index: 25365

Peptide ID score type: hyperscore

- Peptide hit sequence: LGFLHSGTAK

- Peptide hit monoisotopic m/z: 515.787643663021

comparsion score = 0.9990300276644041

Spectrum 1 of LGFLHSGTAK has 34 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11318969726562

b4++ 2 216.136280009071 216.1007537841797

b7++ 2 356.692482748321 356.23065185546875

y7++ 2 357.200672296171 357.17730712890625

b7+ 1 712.377689029871 712.3920288085938

b8+ 1 813.425368253171 812.942626953125

y9+ 1 917.4839465083709 917.4591064453125

===================================

Peptide ID m/z: 671.334209335461

Peptide ID rt: 5425.69548

Peptide scan index: 36357

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9992480220532187

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 13

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11326599121094

b2+ 1 187.107719913371 187.14431762695312

y2+ 1 261.15573310477106 261.1249694824219

y6++ 2 315.184490732371 315.1431579589844

y7++ 2 396.71615537592095 397.2083740234375

y4+ 1 445.27691161517106 445.2333068847656

b9++ 2 484.21312032067095 484.2408752441406

y9++ 2 527.2553194801709 527.192626953125

y10++ 2 577.7791590918209 577.8037719726562

b11++ 2 597.7766165918209 597.3300170898438

y11++ 2 627.313366235371 627.3140869140625

y6+ 1 629.361704997971 629.303955078125

y7+ 1 792.425034285071 792.39306640625

**Mzml #2 Felopater Nashat**

Proteins: 1

Peptides: 5

Processed peptides: 5

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 15 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 15 hits for 15 of 15 peptides.

Peptide hits passing enzyme filter: 15

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 15 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 15

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

-----------------------------------

===================================

Peptide ID m/z: 447.557456432476

Peptide ID rt: 2148.65916

Peptide scan index: 7879

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 447.5553460323376

comparsion score = 0.9999952846274639

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 670.826327473161

Peptide ID rt: 2363.22906

Peptide scan index: 9836

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 1.0000045516131895

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 2

ion theo. m/z observed m/z

b10++ 2 540.7551524961209 540.2828369140625

b7+ 1 799.329085791771 798.8320922851562

===================================

Peptide ID m/z: 447.554772660961

Peptide ID rt: 2462.37126

Peptide scan index: 10765

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 447.5553460323376

comparsion score = 1.0000012811200139

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 1

ion theo. m/z observed m/z

b10++ 2 540.7551524961209 540.2853393554688

===================================

Peptide ID m/z: 447.556909149619

Peptide ID rt: 2718.88944

Peptide scan index: 13162

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 447.5553460323376

comparsion score = 0.9999965074446412

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 16

ion theo. m/z observed m/z

y1++ 2 74.06004069007102 74.06089782714844

y2++ 2 131.08150478577102 131.11758422851562

y1+ 1 147.112804913371 147.11306762695312

b2+ 1 187.107719913371 187.12628173828125

y3++ 2 187.62353696122102 187.4943084716797

y4++ 2 223.14209404097102 223.0710906982422

b4++ 2 224.596662294321 225.04348754882812

b5++ 2 275.12050190597097 275.1768798828125

b3+ 1 288.155399136671 288.0831604003906

y6++ 2 315.184490732371 315.1675720214844

b7++ 2 400.168181129271 400.2325439453125

b4+ 1 448.186048121871 448.67828369140625

b8++ 2 448.69456324092096 449.18157958984375

b9++ 2 484.21312032067095 484.1943664550781

b10++ 2 540.7551524961209 541.2254028320312

y10++ 2 577.7791590918209 577.7151489257812

===================================

Peptide ID m/z: 671.327261231626

Peptide ID rt: 3039.02268

Peptide scan index: 16256

Peptide ID score type: hyperscore

- Peptide hit sequence: SVTC(Carbamidomethyl)TYSPALNK

- Peptide hit monoisotopic m/z: 670.8293808151209

comparsion score = 0.9992583640718065

Spectrum 1 of SVTC(Carbamidomethyl)TYSPALNK has 42 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

b6++ 2 356.652166549521 356.1985778808594

y7++ 2 396.71615537592095 397.13616943359375

b11++ 2 597.7766165918209 597.354736328125

===================================

Peptide ID m/z: 539.756561546599

Peptide ID rt: 3230.28306

Peptide scan index: 18133

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999901751797834

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 2

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.1201934814453

y6++ 2 343.66646515262096 343.2359313964844

===================================

Peptide ID m/z: 515.783155743246

Peptide ID rt: 3296.74446

Peptide scan index: 18763

Peptide ID score type: hyperscore

- Peptide hit sequence: LGFLHSGTAK

- Peptide hit monoisotopic m/z: 515.787643663021

comparsion score = 1.0000087011755328

Spectrum 1 of LGFLHSGTAK has 34 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y1++ 2 74.06004069007102 74.06107330322266

b2++ 2 86.06004069007099 86.09721374511719

y2++ 2 109.57859776982102 110.0718002319336

y1+ 1 147.112804913371 147.11297607421875

b2+ 1 171.112804913371 171.1143035888672

b4++ 2 216.136280009071 216.09915161132812

y6++ 2 300.658640120721 300.69317626953125

b9++ 2 442.734879439721 442.23992919921875

y9++ 2 459.245611487571 459.2620849609375

y6+ 1 600.3100037746709 600.3770751953125

b6+ 1 655.356224934171 655.3936767578125

===================================

Peptide ID m/z: 539.756325605729

Peptide ID rt: 3345.10776

Peptide scan index: 19232

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999906123002777

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

y1++ 2 88.06311469007102 88.04008483886719

b2++ 2 133.062780721971 133.04295349121094

y1+ 1 175.118952913371 175.11929321289062

b3++ 2 197.092069849571 197.1283721923828

b4++ 2 225.602801897421 226.08151245117188

y4++ 2 271.63971852502095 271.1766662597656

===================================

Peptide ID m/z: 539.756079067891

Peptide ID rt: 3373.35948

Peptide scan index: 19514

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999910690538616

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b2++ 2 133.062780721971 133.04307556152344

y1+ 1 175.118952913371 175.119873046875

b3++ 2 197.092069849571 197.12945556640625

b4++ 2 225.602801897421 225.12313842773438

y4++ 2 271.63971852502095 272.0712585449219

b8++ 2 452.695420312121 452.3217468261719

y8++ 2 489.227418923771 489.3163757324219

===================================

Peptide ID m/z: 539.75658139794

Peptide ID rt: 3454.30632

Peptide scan index: 20303

Peptide ID score type: hyperscore

- Peptide hit sequence: TYQGSYGFR

- Peptide hit monoisotopic m/z: 539.751258535421

comparsion score = 0.9999901384018234

Spectrum 1 of TYQGSYGFR has 30 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

b2++ 2 133.062780721971 133.04312133789062

y1+ 1 175.118952913371 175.1195831298828

b5++ 2 269.118816477171 269.1253356933594

y6++ 2 343.66646515262096 344.1585693359375

y4+ 1 542.272160583271 542.1964111328125

===================================

Peptide ID m/z: 516.287505169677

Peptide ID rt: 3879.81882

Peptide scan index: 24211

Peptide ID score type: hyperscore

- Peptide hit sequence: LGFLHSGTAK

- Peptide hit monoisotopic m/z: 515.787643663021

comparsion score = 0.9990318156034169

Spectrum 1 of LGFLHSGTAK has 34 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11322021484375

b4++ 2 216.136280009071 216.1348876953125

y2+ 1 218.149919072871 218.15097045898438

b3+ 1 318.181219200471 318.2264404296875

y7++ 2 357.200672296171 357.2505798339844

y9++ 2 459.245611487571 459.20550537109375

b5+ 1 568.324195774671 568.2700805664062

y8+ 1 860.4624824126709 860.404052734375

===================================

Peptide ID m/z: 515.789182755602

Peptide ID rt: 3988.12872

Peptide scan index: 25150

Peptide ID score type: hyperscore

- Peptide hit sequence: LGFLHSGTAK

- Peptide hit monoisotopic m/z: 515.787643663021

comparsion score = 0.9999970160433128

Spectrum 1 of LGFLHSGTAK has 34 peaks.

Number of matched peaks: 13

ion theo. m/z observed m/z

y4+ 1 376.219062391871 376.2136535644531

b8++ 2 407.216322359971 407.2024230957031

y8++ 2 430.734879439721 430.7353820800781

b4+ 1 431.265283551371 431.25360107421875

b9++ 2 442.734879439721 442.7170715332031

y9++ 2 459.245611487571 458.75811767578125

y5+ 1 463.25109155137096 463.2430114746094

b5+ 1 568.324195774671 568.2955322265625

y6+ 1 600.3100037746709 600.317626953125

b6+ 1 655.356224934171 655.308837890625

y7+ 1 713.3940681255709 713.3377685546875

b8+ 1 813.425368253171 813.162841796875

y8+ 1 860.4624824126709 860.9594116210938

===================================

Peptide ID m/z: 699.072822843574

Peptide ID rt: 4018.6894199999997

Peptide scan index: 25407

Peptide ID score type: hyperscore

- Peptide hit sequence: M(Oxidation)EEPQSDPSVEPPLSQETFSDLWK

- Peptide hit monoisotopic m/z: 698.8206448507211

comparsion score = 0.9996392679208624

Spectrum 1 of M(Oxidation)EEPQSDPSVEPPLSQETFSDLWK has 90 peaks.

Number of matched peaks: 2

ion theo. m/z observed m/z

y2++ 2 167.09969734957102 167.11837768554688

y5++ 2 324.671216184521 324.1739501953125

===================================

Peptide ID m/z: 516.287877042875

Peptide ID rt: 4074.02718

Peptide scan index: 25893

Peptide ID score type: hyperscore

- Peptide hit sequence: LGFLHSGTAK

- Peptide hit monoisotopic m/z: 515.787643663021

comparsion score = 0.9990310960181377

Spectrum 1 of LGFLHSGTAK has 34 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

y2++ 2 109.57859776982102 110.07182312011719

y1+ 1 147.112804913371 147.11329650878906

b3++ 2 159.59424783362098 159.11386108398438

b2+ 1 171.112804913371 171.11337280273438

y2+ 1 218.149919072871 218.14981079101562

b5++ 2 284.665736120721 285.1571350097656

b6++ 2 328.181750700471 328.1983642578125

b7++ 2 356.692482748321 356.1934509277344

y7++ 2 357.200672296171 357.19818115234375

y7+ 1 713.3940681255709 713.3638305664062

b9+ 1 884.462482412671 884.4447631835938

===================================

Peptide ID m/z: 1148.604125976562

Peptide ID rt: 6429.8634

Peptide scan index: 45138

Peptide ID score type: hyperscore

- Peptide hit sequence: MPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQK

- Peptide hit monoisotopic m/z: 1148.5937862940045

comparsion score = 0.9999909980450847

Spectrum 1 of MPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQK has 138 peaks.

Number of matched peaks: 19

ion theo. m/z observed m/z

b4++ 2 215.09375527837096 215.1037139892578

b2+ 1 229.10052570717096 229.11892700195312

y4++ 2 230.131726509071 230.1173858642578

y2+ 1 275.171383168571 275.10418701171875

b6++ 2 299.13869446977094 299.1417236328125

y6++ 2 323.181948232371 323.1389465332031

b7++ 2 347.6650765814209 348.1600646972656

y7++ 2 366.697962812121 367.1552734375

y5+ 1 558.324590838471 558.2627563476562

y11++ 2 608.322048338471 608.3455810546875

y6+ 1 645.3566199979709 645.300537109375

y12++ 2 651.838062918221 651.861083984375

b7+ 1 694.3228766960709 694.3385009765625

b8+ 1 793.391290983171 793.3814697265625

b18++ 2 819.421437181971 819.523193359375

y17++ 2 868.4543234126712 868.4310913085938

y9+ 1 932.5047426678709 932.4872436523438

b24++ 2 1071.5562547561713 1071.5203857421875

y23++ 2 1122.5865984868715 1122.56494140625

Mzml #1 Beshoy Atef

C:\Users\besho\PycharmProjects\pythonProject1\venv\Scripts\python.exe C:/Users/besho/PycharmProjects/pythonProject1/main.py

Proteins: 1

Peptides: 14

Processed peptides: 14

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 19 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 19 hits for 19 of 19 peptides.

Peptide hits passing enzyme filter: 19

... rejected by enzyme filter: 0

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Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 19 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 19

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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Peptide ID m/z: 567.949279785156

Peptide ID rt: 1096.23408

Peptide scan index: 671

Peptide ID score type: hyperscore

- Peptide hit sequence: ISYPSLHEEALGEEK

- Peptide hit monoisotopic m/z: 567.949190033571

comparsion score = 0.9999998419725348

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of ISYPSLHEEALGEEK has 54 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

b7++ 2 399.710872844021 400.1861542530676

y3+ 1 405.19799335997106 405.1767162557992

y8++ 2 452.716550439721 452.8537618918077

b4+ 1 461.23946348757096 461.1900803350791

y4+ 1 462.21945745567103 462.18059868308006

b8++ 2 464.232169955671 464.16868480287206

y9++ 2 521.246006551371 521.1676046231199

y5+ 1 575.303521806571 574.8107455403191

y10++ 2 577.788038726821 577.7891066308018

b12++ 2 649.324788370371 649.8148518543965

b6+ 1 661.355556997971 661.6771232078871

y12++ 2 669.8304354182211 669.8892099240132

===================================

Peptide ID m/z: 552.7763671875

Peptide ID rt: 1111.2679799999999

Peptide scan index: 799

Peptide ID score type: hyperscore

- Peptide hit sequence: NHFPDIFSK

- Peptide hit monoisotopic m/z: 552.777276131121

comparsion score = 1.0000016443243143

Spectrum 1 of NHFPDIFSK has 30 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y7++ 2 427.22635592377094 427.3115627089237

b7++ 2 436.20849732807096 435.9007465739229

b8++ 2 479.72451190782095 479.8356005251774

y4+ 1 494.29731271087104 493.88170430617004

y8++ 2 495.75581203542094 495.8140506886708

b4+ 1 496.23029539187104 495.85554013702085

y5+ 1 609.324256870371 609.3236149965572

b5+ 1 611.2572395513711 611.2258793173369

===================================

Peptide ID m/z: 496.999237060547

Peptide ID rt: 1269.6805200000001

Peptide scan index: 2015

Peptide ID score type: hyperscore

- Peptide hit sequence: LLTQEWVQENYLEYR

- Peptide hit monoisotopic m/z: 496.7507270354211

comparsion score = 0.9994999790611437

Spectrum 1 of LLTQEWVQENYLEYR has 54 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 538.260131835938

Peptide ID rt: 1390.79352

Peptide scan index: 2891

Peptide ID score type: hyperscore

- Peptide hit sequence: ASEC(Carbamidomethyl)M(Oxidation)QVIFGIDVK

- Peptide hit monoisotopic m/z: 538.2618341550043

comparsion score = 1.0000031626326484

Spectrum 1 of ASEC(Carbamidomethyl)M(Oxidation)QVIFGIDVK has 50 peaks.

Number of matched peaks: 13

ion theo. m/z observed m/z

y1++ 2 74.06004069007102 74.06058502197266

y1+ 1 147.112804913371 147.11289978027344

b2+ 1 159.076419785771 159.0768280029297

y3++ 2 181.107719913371 181.09695434570312

y2+ 1 246.18121920047105 246.15481567382812

y5++ 2 266.16048413667096 266.11419677734375

b3+ 1 288.119014009071 288.119140625

y6++ 2 339.6946912802209 340.1901550292969

y3+ 1 361.208163359971 361.1885681152344

y7++ 2 396.2367234556709 396.2064514160156

b11++ 2 626.788669552521 626.367919921875

y12++ 2 727.854541339621 727.3616333007812

b7+ 1 822.3120555536711 822.408935546875

===================================

Peptide ID m/z: 463.741148263078

Peptide ID rt: 1403.5014

Peptide scan index: 2985

Peptide ID score type: hyperscore

- Peptide hit sequence: QAPGSDPVR

- Peptide hit monoisotopic m/z: 463.738150971621

comparsion score = 0.9999935367144619

Spectrum 1 of QAPGSDPVR has 30 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y2++ 2 137.597321833621 138.06617736816406

y1+ 1 175.118952913371 175.11907958984375

y4++ 2 243.637176025021 244.13197326660156

y2+ 1 274.18736720047104 274.1862487792969

y6++ 2 315.663922652621 315.20257568359375

b7++ 2 327.148105604771 327.1659851074219

y5+ 1 573.299104742771 573.3358764648438

===================================

Peptide ID m/z: 538.262023925781

Peptide ID rt: 1491.57834

Peptide scan index: 3663

Peptide ID score type: hyperscore

- Peptide hit sequence: ASEC(Carbamidomethyl)M(Oxidation)QVIFGIDVK

- Peptide hit monoisotopic m/z: 538.2618341550043

comparsion score = 0.9999996474379237

Spectrum 1 of ASEC(Carbamidomethyl)M(Oxidation)QVIFGIDVK has 50 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11279296875

b4++ 2 224.578469730521 224.1026611328125

y6++ 2 339.6946912802209 340.1313171386719

b6++ 2 362.125458866671 362.1466979980469

y7+ 1 791.4661704445709 791.4329833984375

b7+ 1 822.3120555536711 821.9047241210938

y8+ 1 890.534584731671 890.5007934570312

===================================

Peptide ID m/z: 426.762933422334

Peptide ID rt: 1542.40074

Peptide scan index: 4040

Peptide ID score type: hyperscore

- Peptide hit sequence: VLEHVVR

- Peptide hit monoisotopic m/z: 426.258521519471

comparsion score = 0.9988180512800913

Spectrum 1 of VLEHVVR has 22 peaks.

Number of matched peaks: 10

ion theo. m/z observed m/z

b3++ 2 171.604812897421 171.11257934570312

y1+ 1 175.118952913371 175.11907958984375

y3++ 2 187.131528977171 187.1439666748047

b2+ 1 213.159755104771 213.16036987304688

b4++ 2 240.134269009071 240.13421630859375

y4++ 2 255.660985088821 256.1275634765625

y2+ 1 274.18736720047104 274.1584777832031

y5++ 2 320.182282200471 320.1589660644531

b4+ 1 479.26126155137104 479.24200439453125

y5+ 1 639.3572879341709 639.2974243164062

===================================

Peptide ID m/z: 807.3984375

Peptide ID rt: 1616.33322

Peptide scan index: 4631

Peptide ID score type: hyperscore

- Peptide hit sequence: ASEC(Carbamidomethyl)M(Oxidation)QVIFGIDVK

- Peptide hit monoisotopic m/z: 806.889112999121

comparsion score = 0.999369178243079

Spectrum 1 of ASEC(Carbamidomethyl)M(Oxidation)QVIFGIDVK has 50 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11248779296875

b2+ 1 159.076419785771 159.0918731689453

y2+ 1 246.18121920047105 246.16949462890625

y3+ 1 361.208163359971 361.1535949707031

b4+ 1 448.149662994271 448.1352233886719

b5+ 1 595.1850630113711 595.2515869140625

y6+ 1 678.3821060936709 678.3204956054688

y7+ 1 791.4661704445709 791.3421630859375

===================================

Peptide ID m/z: 491.765942260428

Peptide ID rt: 1619.6693400000001

Peptide scan index: 4662

Peptide ID score type: hyperscore

- Peptide hit sequence: ALAETSYVK

- Peptide hit monoisotopic m/z: 491.266210115171

comparsion score = 0.9989838008241076

Spectrum 1 of ALAETSYVK has 30 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

b3++ 2 128.586422801721 128.10684204101562

y1+ 1 147.112804913371 147.11264038085938

y3++ 2 205.125912477171 205.33258056640625

b5++ 2 243.631559525021 244.0926971435547

b3+ 1 256.165569136671 256.130615234375

b6+ 1 573.287871742771 573.1461181640625

===================================

Peptide ID m/z: 552.776957667471

Peptide ID rt: 1645.01574

Peptide scan index: 4892

Peptide ID score type: hyperscore

- Peptide hit sequence: NHFPDIFSK

- Peptide hit monoisotopic m/z: 552.777276131121

comparsion score = 1.0000005761160002

Spectrum 1 of NHFPDIFSK has 30 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y1+ 1 147.112804913371 147.11277770996094

y2+ 1 234.14483407287105 234.6138916015625

b4++ 2 248.618785929321 249.10105895996094

b2+ 1 252.10911688147104 252.09625244140625

y3+ 1 381.21324835997103 381.1932067871094

b3+ 1 399.177531168571 399.1591491699219

y4+ 1 494.29731271087104 494.24908447265625

===================================

Peptide ID m/z: 534.270701565131

Peptide ID rt: 1731.43392

Peptide scan index: 5528

Peptide ID score type: hyperscore

- Peptide hit sequence: YEFLWGPR

- Peptide hit monoisotopic m/z: 534.2690865832709

comparsion score = 0.9999969772217429

Spectrum 1 of YEFLWGPR has 26 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

b3+ 1 440.181614264271 440.2394396228193

b7++ 2 447.213248359971 447.4905848927839

y7++ 2 452.737421939721 452.8718527207112

y4+ 1 515.272494551371 515.2717915690378

b4+ 1 553.2656786151709 553.631277331398

y5+ 1 628.356558902271 628.2825750415323

b5+ 1 739.3449919341709 739.0644363903237

b7+ 1 893.4192202531709 893.4204734339096

===================================

Peptide ID m/z: 851.424926757813

Peptide ID rt: 1757.37222

Peptide scan index: 5778

Peptide ID score type: hyperscore

- Peptide hit sequence: ISYPSLHEEALGEEK

- Peptide hit monoisotopic m/z: 851.420146816971

comparsion score = 0.9999943859514895

Spectrum 1 of ISYPSLHEEALGEEK has 54 peaks.

Number of matched peaks: 6

ion theo. m/z observed m/z

b6++ 2 331.181416732371 331.23345947265625

y8++ 2 452.716550439721 452.2276611328125

b11++ 2 620.8140563225211 620.869140625

b13++ 2 713.8460854820211 713.9750366210938

y13++ 2 751.3621000617711 751.306884765625

y8+ 1 904.4258244126711 904.4512939453125

===================================

Peptide ID m/z: 567.953308105469

Peptide ID rt: 1834.43628

Peptide scan index: 6427

Peptide ID score type: hyperscore

- Peptide hit sequence: ISYPSLHEEALGEEK

- Peptide hit monoisotopic m/z: 567.949190033571

comparsion score = 0.9999927492773804

Spectrum 1 of ISYPSLHEEALGEEK has 54 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y2++ 2 138.58133780172102 139.04942321777344

y1+ 1 147.112804913371 147.11334228515625

b2+ 1 201.123369977171 201.12405395507812

y3++ 2 203.10263491337102 203.06613159179688

y5++ 2 288.155399136671 288.1654357910156

y6++ 2 323.673956216421 324.10052490234375

y3+ 1 405.19799335997106 405.1404113769531

b9++ 2 528.753467067321 529.203125

y5+ 1 575.303521806571 575.2425537109375

y6+ 1 646.340635966071 646.2567138671875

y14++ 2 794.8781146415212 794.42041015625

y8+ 1 904.4258244126711 904.3262329101562

===================================

Peptide ID m/z: 909.025940946774

Peptide ID rt: 1872.81594

Peptide scan index: 6759

Peptide ID score type: hyperscore

- Peptide hit sequence: TGLLIIVLGMILMEGSR

- Peptide hit monoisotopic m/z: 908.5253795254708

comparsion score = 0.9994493430838929

Spectrum 1 of TGLLIIVLGMILMEGSR has 62 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

b8++ 2 412.286216147071 411.9189680484324

b9++ 2 440.796948194921 440.76801145195816

y4+ 1 448.21504039187107 448.21566739952095

y8++ 2 468.7357077973209 468.73570501714863

y9++ 2 497.2464398451709 497.2602735027682

b5+ 1 498.32861283847103 498.306640451699

b10++ 2 506.317190703471 506.2927098283694

y10++ 2 553.7884720206209 553.8375504205185

y5+ 1 579.2555254089709 578.8342913048089

b6+ 1 611.412677189371 611.49780209775

y12++ 2 659.864711339621 659.8444467670449

y6+ 1 692.3395897598709 692.3376464903297

b7+ 1 710.4810914764711 710.5065076134562

b14++ 2 749.4427946745709 749.4135524356741

y14++ 2 772.948775690521 773.3180674944591

b15++ 2 777.9535267224209 777.9565544899589

b16++ 2 821.4695413021709 821.0170621763637

b8+ 1 823.5651558273711 823.6564940114906

y16++ 2 858.0015399138209 858.4843099105291

y9+ 1 993.4856032235709 993.0140845327334

===================================

Peptide ID m/z: 606.351539343898

Peptide ID rt: 1874.87958

Peptide scan index: 6777

Peptide ID score type: hyperscore

- Peptide hit sequence: TGLLIIVLGMILMEGSR

- Peptide hit monoisotopic m/z: 606.019345172571

comparsion score = 0.9994521426107262

Spectrum 1 of TGLLIIVLGMILMEGSR has 62 peaks.

Number of matched peaks: 21

ion theo. m/z observed m/z

b3++ 2 136.583880301721 137.05982971191406

b2+ 1 159.076419785771 159.07615661621094

y1+ 1 175.118952913371 175.1194305419922

b3+ 1 272.160484136671 272.1622009277344

y5++ 2 290.1314009378709 290.16400146484375

b7++ 2 355.744183971621 356.2054138183594

b8++ 2 412.286216147071 412.1568298339844

b9++ 2 440.796948194921 441.198974609375

y4+ 1 448.21504039187107 448.2342224121094

y8++ 2 468.7357077973209 468.7426452636719

y10++ 2 553.7884720206209 553.303466796875

y5+ 1 579.2555254089709 579.3079223632812

b13++ 2 684.9214975629209 685.3327026367188

b7+ 1 710.4810914764711 710.3397827148438

y13++ 2 716.406743515071 716.359375

y14++ 2 772.948775690521 773.4456176757812

b16++ 2 821.4695413021709 821.4111328125

b8+ 1 823.5651558273711 823.4219970703125

y15++ 2 829.490807865971 829.4111938476562

y16++ 2 858.0015399138209 858.4358520507812

y8+ 1 936.4641391278709 936.477294921875

===================================

Peptide ID m/z: 916.520080566406

Peptide ID rt: 1876.23504

Peptide scan index: 6789

Peptide ID score type: hyperscore

- Peptide hit sequence: TGLLIIVLGMILM(Oxidation)EGSR

- Peptide hit monoisotopic m/z: 916.522837025471

comparsion score = 1.0000030075271926

Spectrum 1 of TGLLIIVLGMILM(Oxidation)EGSR has 62 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

b9++ 2 440.796948194921 441.17608642578125

b7+ 1 710.4810914764711 710.237548828125

b14++ 2 757.440252174571 757.239501953125

b8+ 1 823.5651558273711 823.3194580078125

b10+ 1 1011.6271049401711 1011.4210815429688

===================================

Peptide ID m/z: 463.734252929688

Peptide ID rt: 1957.0961399999999

Peptide scan index: 7433

Peptide ID score type: hyperscore

- Peptide hit sequence: QAPGSDPVR

- Peptide hit monoisotopic m/z: 463.738150971621

comparsion score = 1.000008405766683

Spectrum 1 of QAPGSDPVR has 30 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

b5+ 1 441.209226359971 441.230339144388

y4+ 1 486.26707558327104 486.28428155572925

b6+ 1 556.236170519471 556.234710376505

y5+ 1 573.299104742771 573.2973012779531

y6+ 1 630.320568838471 630.3196013574296

b7+ 1 653.288934742771 653.2877674248589

y7+ 1 727.373333061771 727.3741040311609

b8+ 1 752.357349029871 751.9083639493871

===================================

Peptide ID m/z: 799.396911621094

Peptide ID rt: 2140.6108200000003

Peptide scan index: 8796

Peptide ID score type: hyperscore

- Peptide hit sequence: ASEC(Carbamidomethyl)MQVIFGIDVK

- Peptide hit monoisotopic m/z: 798.891655499121

comparsion score = 0.9993679533725639

Spectrum 1 of ASEC(Carbamidomethyl)MQVIFGIDVK has 50 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b2+ 1 159.076419785771 159.07916259765625

y9++ 2 509.80021972682096 510.2602844238281

y5+ 1 531.313691806571 531.7381591796875

b10++ 2 562.249179877071 561.7705688476562

b9+ 1 1066.469619191671 1066.552001953125

b10+ 1 1123.4910832873709 1123.5267333984375

b11+ 1 1236.575147638271 1236.6214599609375

===================================

Peptide ID m/z: 992.998657226563

Peptide ID rt: 2360.0544

Peptide scan index: 10582

Peptide ID score type: hyperscore

- Peptide hit sequence: LLTQEWVQENYLEYR

- Peptide hit monoisotopic m/z: 992.4941776040711

comparsion score = 0.9994919634394059

Spectrum 1 of LLTQEWVQENYLEYR has 54 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

y2++ 2 169.594779333621 169.150146484375

y1+ 1 175.118952913371 175.11903381347656

b2+ 1 227.175405168571 227.1024932861328

b4++ 2 228.64446955692102 229.12550354003906

b3+ 1 328.223084391871 328.2010803222656

y6++ 2 429.21123735997094 429.1883239746094

b8++ 2 499.768919599221 500.2621765136719

y8++ 2 557.761823599221 557.2969970703125

y4+ 1 580.3089407746709 580.265869140625

b10++ 2 621.3116808065711 621.3292236328125

y10++ 2 700.335687402271 700.3782348632812

y12++ 2 828.886273641521 828.4574584960938

<Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!> occurred 19 times

Process finished with exit code 0

**Mzml #2 Beshoy Atef**

C:\Users\besho\PycharmProjects\pythonProject1\venv\Scripts\python.exe C:/Users/besho/PycharmProjects/pythonProject1/main.py

Proteins: 1

Peptides: 14

Processed peptides: 14

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 3 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 3 hits for 3 of 3 peptides.

Peptide hits passing enzyme filter: 3

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 3 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 3

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 703.339111328125

Peptide ID rt: 1928.6962291039797

Peptide scan index: 2907

Peptide ID score type: hyperscore

- Peptide hit sequence: APEEAIWEALSVMGLYDGR

- Peptide hit monoisotopic m/z: 703.0103438973377

comparsion score = 0.9995325619953561

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of APEEAIWEALSVMGLYDGR has 70 peaks.

Number of matched peaks: 0

ion theo. m/z observed m/z

===================================

Peptide ID m/z: 606.022155761719

Peptide ID rt: 3487.02412724802

Peptide scan index: 6664

Peptide ID score type: hyperscore

- Peptide hit sequence: TGLLIIVLGMILMEGSR

- Peptide hit monoisotopic m/z: 606.019345172571

comparsion score = 0.999995362233672

Spectrum 1 of TGLLIIVLGMILMEGSR has 62 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

y2++ 2 131.579129269821 131.14369201660156

b3++ 2 136.583880301721 137.02304077148438

b2+ 1 159.076419785771 159.12466430664062

y1+ 1 175.118952913371 175.15603637695312

y4++ 2 224.611158429321 224.1388397216797

b5++ 2 249.667944652621 250.16555786132812

y2+ 1 262.15098207287105 262.15557861328125

===================================

Peptide ID m/z: 611.683715820313

Peptide ID rt: 4821.05549832

Peptide scan index: 9468

Peptide ID score type: hyperscore

- Peptide hit sequence: TGLLIIVLGM(Oxidation)ILMEGSR

- Peptide hit monoisotopic m/z: 611.3509835059043

comparsion score = 0.9994560386261674

Spectrum 1 of TGLLIIVLGM(Oxidation)ILMEGSR has 62 peaks.

Number of matched peaks: 30

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.17001342773438

b4++ 2 193.125912477171 193.52700805664062

y5++ 2 290.1314009378709 290.5580139160156

y7++ 2 403.21546528877093 403.2740173339844

b9++ 2 440.796948194921 440.87200927734375

y4+ 1 448.21504039187107 448.3890686035156

y8++ 2 476.7331652973209 476.40203857421875

b5+ 1 498.32861283847103 498.373046875

y9++ 2 505.2438973451709 505.45306396484375

b10++ 2 514.314648203471 514.2630004882812

y10++ 2 561.7859295206209 562.1610107421875

b11++ 2 570.856680378921 570.9230346679688

y5+ 1 579.2555254089709 579.2230834960938

b12++ 2 627.3987125543711 627.863037109375

y6+ 1 692.3395897598709 691.9929809570312

b13++ 2 692.918955062921 693.1930541992188

b7+ 1 710.4810914764711 710.4840087890625

y13++ 2 724.404201015071 724.6620483398438

b14++ 2 757.440252174571 757.510986328125

y14++ 2 780.946233190521 781.3729858398438

b15++ 2 785.950984222421 786.302001953125

y7+ 1 805.4236541107709 805.5140380859375

b8+ 1 823.5651558273711 823.9090576171875

b16++ 2 829.466998802171 829.8469848632812

y15++ 2 837.488265365971 837.2870483398438

y16++ 2 865.9989974138209 865.5960083007812

y8+ 1 952.4590541278709 952.5110473632812

y9+ 1 1009.4805182235709 1009.3750610351562

b10+ 1 1027.622019940171 1027.18603515625

b11+ 1 1140.706084291071 1140.455078125

<Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!> occurred 3 times

Process finished with exit code 0

**Mzml #1 John Osama**

C:\Users\ZeyadaNet\PycharmProjects\pythonProject\venv\Scripts\python.exe C:/Users/ZeyadaNet/Desktop/3wdy/mzml1/main.py

Proteins: 1

Peptides: 25

Processed peptides: 25

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 5 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 5 hits for 5 of 5 peptides.

Peptide hits passing enzyme filter: 5

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 5 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 5

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 533.2861328125

Peptide ID rt: 2461.0784087029797

Peptide scan index: 4223

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDMGVAGFR

- Peptide hit monodists m/z: 532.7815040599211

comparison score = 0.9990537373437454

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_getinfo'!

Spectrum 1 of LVDMGVAGFR has 34 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b2++ 2 107.083515785771 107.06007385253906

y2++ 2 161.59732183362104 162.06581115722656

b3++ 2 164.596987865521 164.6768798828125

y1+ 1 175.118952913371 175.11846923828125

b4++ 2 230.117230374071 230.1368408203125

y6++ 2 303.671550152621 303.1771545410156

b3+ 1 328.186699264271 328.2367248535156

===================================

Peptide ID m/z: 533.28662109375

Peptide ID rt: 2524.0847360479797

Peptide scan index: 4373

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDMGVAGFR

- Peptide hit monodists m/z: 532.7815040599211

comparison score = 0.999052822602613

Spectrum 1 of LVDMGVAGFR has 34 peaks.

Number of matched peaks: 8

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.11849975585938

b2+ 1 213.159755104771 213.06898498535156

b4++ 2 230.117230374071 230.09539794921875

b5++ 2 258.627962421921 259.07489013671875

y5++ 2 275.160818104771 275.1170654296875

y6++ 2 303.671550152621 303.222412109375

b6++ 2 308.162169565471 308.1429748535156

b8++ 2 372.191458693071 372.1776428222656

===================================

Peptide ID m/z: 497.241363525391

Peptide ID rt: 3380.7294139360197

Peptide scan index: 6400

Peptide ID score type: hyperscore

- Peptide hit sequence: HMWPGDLSAVYGR

- Peptide hit monodists m/z: 496.9066014082043

comparison score = 0.9993267613240916

Spectrum 1 of HMWPGDLSAVYGR has 46 peaks.

Number of matched peaks: 19

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.18002319335938

y3++ 2 198.10551138147102 198.510009765625

y2+ 1 232.14041700907103 232.27403259277344

y6++ 2 326.674290184521 326.2170104980469

b6++ 2 362.647217985721 362.1900634765625

y7++ 2 383.216322359971 383.06207275390625

y3+ 1 395.20374629617106 395.4470520019531

b7++ 2 419.189250161171 419.24700927734375

y8++ 2 440.729794439721 441.11407470703125

b8++ 2 462.705264740921 462.4700012207031

y9++ 2 469.240526487571 469.16400146484375

y4+ 1 494.27216058327105 494.3910217285156

b9++ 2 498.223821820671 497.8000183105469

b10++ 2 547.758028964221 547.791015625

b4+ 1 552.238751249471 552.6170043945312

y11++ 2 610.806565258721 610.968017578125

b11++ 2 629.289693607771 629.2930297851562

b12++ 2 657.800425655621 658.0620727539062

b6+ 1 724.287159504671 724.384033203125

===================================

Peptide ID m/z: 644.851440429688

Peptide ID rt: 5378.407072959

Peptide scan index: 10482

Peptide ID score type: hyperscore

- Peptide hit sequence: TSIVHLFEWR

- Peptide hit monodists m/z: 644.345857402271

comparison score = 0.9992159697633922

Spectrum 1 of TSIVHLFEWR has 34 peaks.

Number of matched peaks: 19

ion theo. m/z observed m/z

y1+ 1 175.118952913371 175.22305297851562

b4++ 2 201.123369977171 200.8710174560547

b3+ 1 302.171049200471 301.9560241699219

y2+ 1 361.19826623237105 361.5550231933594

y5++ 2 375.700307780221 375.4790344238281

b7++ 2 399.72906540782105 400.0750732421875

b4+ 1 401.23946348757096 400.8140563964844

y6++ 2 444.229763891871 444.4600524902344

b8++ 2 464.2503625194711 463.9049987792969

y3+ 1 490.24086045567105 490.2570495605469

y7++ 2 493.76397103542104 493.3520202636719

b5+ 1 538.2983757108709 538.5330200195312

y8++ 2 550.306003210871 550.446044921875

y9++ 2 593.8220177906211 593.47998046875

y4+ 1 637.3092747427711 637.2760009765625

b6+ 1 651.3824400617709 651.31201171875

y5+ 1 750.3933390936711 750.3380737304688

b7+ 1 798.450854348871 798.2039794921875

y6+ 1 887.4522513169711 887.623046875

===================================

Peptide ID m/z: 533.285339355469

Peptide ID rt: 6264.77506031898

Peptide scan index: 12146

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDMGVAGFR

- Peptide hit monodists m/z: 532.7815040599211

comparison score = 0.9990552238016578

Spectrum 1 of LVDMGVAGFR has 34 peaks.

Number of matched peaks: 5

ion theo. m/z observed m/z

b3++ 2 164.596987865521 165.0765838623047

y1+ 1 175.118952913371 175.1180877685547

b4++ 2 230.117230374071 230.1695556640625

y6++ 2 303.671550152621 304.1396179199219

b7++ 2 343.680726645221 343.2533874511719

<Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!> occurred 5 times

<Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_getinfo'!> occurred 5 times

Process finished with exit code 0

**Mzml #2 John Osama**

C:\Users\ZeyadaNet\PycharmProjects\pythonProject\venv\Scripts\python.exe C:/Users/ZeyadaNet/Desktop/3wdy/mzml2/main.py

Proteins: 1

Peptides: 25

Processed peptides: 25

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 61 peptides to 1 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 61 hits for 61 of 61 peptides.

Peptide hits passing enzyme filter: 61

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 61 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 61

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 1

matched proteins : 1 (1 new)

matched target proteins: 1 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

-----------------------------------

===================================

Peptide ID m/z: 635.86975

Peptide ID rt: 1012.806725551002

Peptide scan index: 847

Peptide ID score type: hyperscore

- Peptide hit sequence: LENLLDLALEK

- Peptide hit monodists m/z: 635.866289045821

comparison score = 0.9999945571334712

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_getinfo'!

Spectrum 1 of LENLLDLALEK has 38 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

b7++ 2 406.231638455671 406.2243

b9++ 2 498.292227710871 498.28421

b7+ 1 811.4560004445709 811.41522

===================================

Peptide ID m/z: 476.74832

Peptide ID rt: 1969.2468624940018

Peptide scan index: 7225

Peptide ID score type: hyperscore

- Peptide hit sequence: QIHVGADGR

- Peptide hit monodists m/z: 476.751592503521

comparison score = 1.000006864216157

Spectrum 1 of QIHVGADGR has 30 peaks.

Number of matched peaks: 21

ion theo. m/z observed m/z

b2++ 2 121.57859776982102 121.08384

y1+ 1 175.118952913371 175.11818

y4++ 2 209.60587589742101 209.13914

y5++ 2 238.116607945271 238.11839

b4++ 2 239.642261025021 240.09721

b2+ 1 242.149919072871 242.14957

b5++ 2 268.152993072871 268.12894

y6++ 2 287.650815088821 287.1702

y3+ 1 347.167361168571 347.20529

y7++ 2 356.180271200471 356.19333

b7++ 2 361.185022232371 360.71548

b3+ 1 379.208831296171 379.20694

b8++ 2 389.695754280221 389.2019

y4+ 1 418.204475328071 418.21518

y5+ 1 475.22593942377097 475.58109

b5+ 1 535.298709678971 535.31378

y6+ 1 574.294353710871 574.35547

b6+ 1 606.335823838471 606.35876

y7+ 1 711.353265934171 711.32916

b7+ 1 721.362767997971 721.3598

y8+ 1 824.437330285071 824.42688

===================================

Peptide ID m/z: 533.28027

Peptide ID rt: 2078.393011902

Peptide scan index: 8085

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDMGVAGFR

- Peptide hit monodists m/z: 532.7815040599211

comparison score = 0.999064720807918

Spectrum 1 of LVDMGVAGFR has 34 peaks.

Number of matched peaks: 19

ion theo. m/z observed m/z

b2++ 2 107.083515785771 107.04909

b3++ 2 164.596987865521 165.0542

y1+ 1 175.118952913371 175.08632

y3++ 2 190.10805388147102 190.08583

b2+ 1 213.159755104771 213.15924

y4++ 2 225.62661096122102 226.11826

b4++ 2 230.11723037407097 230.07645

b5++ 2 258.627962421921 259.07425

y6++ 2 303.671550152621 303.17575

b3+ 1 328.186699264271 328.18607

b7++ 2 343.680726645221 344.14481

y3+ 1 379.208831296171 379.24472

y4+ 1 450.245945455671 450.24808

b4+ 1 459.22718428137097 459.26108

b5+ 1 516.2486483770709 516.28461

y5+ 1 549.314359742771 549.79889

y6+ 1 606.335823838471 606.33105

b6+ 1 615.317062664171 615.3512

b7+ 1 686.354176823671 686.37109

===================================

Peptide ID m/z: 532.78027

Peptide ID rt: 2196.858840991002

Peptide scan index: 9037

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDMGVAGFR

- Peptide hit monodists m/z: 532.7815040599211

comparison score = 1.0000023162643037

Spectrum 1 of LVDMGVAGFR has 34 peaks.

Number of matched peaks: 17

ion theo. m/z observed m/z

b2++ 2 107.083515785771 107.04899

b3++ 2 164.596987865521 165.05386

y1+ 1 175.118952913371 175.11877

y3++ 2 190.10805388147102 190.12579

b2+ 1 213.159755104771 213.15894

y4++ 2 225.62661096122102 225.17001

b4++ 2 230.11723037407097 230.11189

b5++ 2 258.627962421921 259.09146

b6++ 2 308.162169565471 308.12305

b3+ 1 328.186699264271 328.14859

b7++ 2 343.680726645221 343.23264

b8++ 2 372.191458693071 372.19791

y4+ 1 450.245945455671 450.26208

b4+ 1 459.22718428137097 459.25513

y9++ 2 476.239471884471 476.2655

y6+ 1 606.335823838471 606.36499

b6+ 1 615.317062664171 615.32825

===================================

Peptide ID m/z: 533.28027

Peptide ID rt: 2199.071742574002

Peptide scan index: 9060

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDMGVAGFR

- Peptide hit monodists m/z: 532.7815040599211

comparison score = 0.999064720807918

Spectrum 1 of LVDMGVAGFR has 34 peaks.

Number of matched peaks: 19

ion theo. m/z observed m/z

b2++ 2 107.083515785771 107.05309

y2++ 2 161.597321833621 162.09068

b3++ 2 164.596987865521 165.05418

y1+ 1 175.118952913371 175.11896

b2+ 1 213.159755104771 213.15929

y4++ 2 225.62661096122102 226.08189

b4++ 2 230.11723037407097 230.11334

b5++ 2 258.627962421921 259.09167

y5++ 2 275.160818104771 275.13971

y6++ 2 303.671550152621 303.70172

b6++ 2 308.162169565471 308.17255

y2+ 1 322.187367200471 322.18597

b7++ 2 343.680726645221 343.23187

b8++ 2 372.191458693071 372.23273

y3+ 1 379.208831296171 379.20255

y9++ 2 476.239471884471 476.2446

y5+ 1 549.314359742771 549.3067

y6+ 1 606.335823838471 606.39838

b8+ 1 743.375640919371 743.44183

===================================

Peptide ID m/z: 626.2785

Peptide ID rt: 2202.831741550002

Peptide scan index: 9096

Peptide ID score type: hyperscore

- Peptide hit sequence: WTDIAAEC(Carbamidomethyl)ER

- Peptide hit monodists m/z: 625.777148091821

comparison score = 0.9991994745018725

Spectrum 1 of WTDIAAEC(Carbamidomethyl)ER has 34 peaks.

Number of matched peaks: 18

ion theo. m/z observed m/z

b2++ 2 144.570772737921 144.12103

y2++ 2 152.58441180172102 152.1431

y1+ 1 175.118952913371 175.11841

b3++ 2 202.084244817671 202.08226

y3++ 2 232.59973629432102 232.15236

b4++ 2 258.626276993121 258.14426

b2+ 1 288.134269009071 288.08243

b5++ 2 294.144834072871 294.13126

y4++ 2 297.121033405971 297.15536

b6++ 2 329.663391152621 329.81937

y5++ 2 332.639590485721 332.67902

y6++ 2 368.158147565471 368.15723

b3+ 1 403.16121316857095 403.22919

y3+ 1 464.192196121871 464.28366

b8++ 2 474.20001275687105 474.23755

y8++ 2 482.213651820671 482.34451

b4+ 1 516.245277519471 516.25964

b6+ 1 658.319505838471 658.29907

===================================

Peptide ID m/z: 533.27991

Peptide ID rt: 2203.510759981998

Peptide scan index: 9104

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDMGVAGFR

- Peptide hit monodists m/z: 532.7815040599211

comparison score = 0.9990653952441619

Spectrum 1 of LVDMGVAGFR has 34 peaks.

Number of matched peaks: 12

ion theo. m/z observed m/z

b2++ 2 107.083515785771 107.0526

b3++ 2 164.596987865521 165.05385

y3++ 2 190.10805388147102 190.09692

b5++ 2 258.627962421921 258.14612

b6++ 2 308.162169565471 308.16043

y2+ 1 322.187367200471 322.15848

b3+ 1 328.186699264271 328.13675

b7++ 2 343.680726645221 344.17065

y3+ 1 379.208831296171 379.20847

b9++ 2 445.72566583662103 446.1839

b5+ 1 516.2486483770709 516.26593

b6+ 1 615.317062664171 615.31354

===================================

Peptide ID m/z: 540.78009

Peptide ID rt: 2483.838907486002

Peptide scan index: 11513

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDM(Oxidation)GVAGFR

- Peptide hit monodists m/z: 540.778961559921

comparison score = 0.9999979133106046

Spectrum 1 of LVDM(Oxidation)GVAGFR has 34 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

y2++ 2 161.597321833621 162.09068

b3++ 2 164.596987865521 165.05399

y1+ 1 175.118952913371 175.11772

b2+ 1 213.159755104771 213.15843

y4++ 2 225.62661096122102 226.08064

b4++ 2 238.114687874071 238.1265

y6++ 2 303.671550152621 304.12741

b6++ 2 316.159627065471 316.14804

y2+ 1 322.187367200471 322.18701

b3+ 1 328.186699264271 328.14841

b7++ 2 351.678184145221 352.15967

y3+ 1 379.208831296171 379.15918

b8++ 2 380.188916193071 380.18893

b4+ 1 475.222099281371 475.19064

y9++ 2 484.236929384471 484.24188

b5+ 1 532.243563377071 532.2547

y5+ 1 549.314359742771 549.2641

y6+ 1 606.335823838471 606.28912

b7+ 1 702.3490918236711 702.35779

y9+ 1 967.4665823021711 967.43304

===================================

Peptide ID m/z: 540.78253

Peptide ID rt: 2516.101511902998

Peptide scan index: 11791

Peptide ID score type: hyperscore

- Peptide hit sequence: LVDM(Oxidation)GVAGFR

- Peptide hit monodists m/z: 540.778961559921

comparison score = 0.9999934013399453

Spectrum 1 of LVDM(Oxidation)GVAGFR has 34 peaks.

Number of matched peaks: 11

ion theo. m/z observed m/z

b3++ 2 164.596987865521 165.05405

b2+ 1 213.159755104771 213.159

y4++ 2 225.62661096122102 226.11763

b5++ 2 266.625419921921 266.1608

y6++ 2 303.671550152621 303.67456

b6++ 2 316.159627065471 316.16483

y2+ 1 322.187367200471 321.70264

y3+ 1 379.208831296171 379.24445

y6+ 1 606.335823838471 606.40387

b6+ 1 631.3119776641711 631.32172

y7+ 1 753.3712238555711 753.38678

===================================

Peptide ID m/z: 644.35199

Peptide ID rt: 2538.866620318998

Peptide scan index: 11997

Peptide ID score type: hyperscore

- Peptide hit sequence: TSIVHLFEWR

- Peptide hit monodists m/z: 644.345857402271

comparison score = 0.999990482534664

Spectrum 1 of TSIVHLFEWR has 34 peaks.

Number of matched peaks: 20

ion theo. m/z observed m/z

b3++ 2 151.589162833621 152.05664

y1+ 1 175.118952913371 175.11855

y2++ 2 181.10277134957101 181.10858

b2+ 1 189.086984849571 189.08644

b4++ 2 201.123369977171 201.12277

y3++ 2 245.62406846122101 246.12311

b5++ 2 269.65282608882103 270.14926

b3+ 1 302.171049200471 302.13321

y4++ 2 319.158275604771 319.1489

b6++ 2 326.19485826427103 326.24213

y2+ 1 361.19826623237105 361.151

y5++ 2 375.700307780221 375.70404

b7++ 2 399.72906540782105 400.21915

b8++ 2 464.2503625194711 464.25873

y7++ 2 493.76397103542104 494.26315

b5+ 1 538.2983757108709 538.3078

b9++ 2 557.2900191789711 557.3028

y9++ 2 593.8220177906211 594.30304

y4+ 1 637.309274742771 637.30139

b8+ 1 927.493448572171 927.4292

===================================

Peptide ID m/z: 644.35168

Peptide ID rt: 2543.363395167

Peptide scan index: 12037

Peptide ID score type: hyperscore

- Peptide hit sequence: TSIVHLFEWR

- Peptide hit monodists m/z: 644.345857402271

comparison score = 0.9999909636338203

Spectrum 1 of TSIVHLFEWR has 34 peaks.

Number of matched peaks: 18

ion theo. m/z observed m/z

b3++ 2 151.589162833621 152.05597

y1+ 1 175.118952913371 175.08604

y2++ 2 181.10277134957101 181.09659

b2+ 1 189.086984849571 189.08632

b4++ 2 201.123369977171 201.12268

b5++ 2 269.65282608882103 270.14426

b3+ 1 302.171049200471 302.16956

y4++ 2 319.158275604771 319.1445

b6++ 2 326.19485826427103 326.16965

y5++ 2 375.700307780221 375.69763

b4+ 1 401.23946348757096 401.28543

y6++ 2 444.229763891871 444.207

b8++ 2 464.2503625194711 464.23669

y7++ 2 493.76397103542104 494.26093

b5+ 1 538.2983757108709 538.27167

y5+ 1 750.393339093671 750.38666

b7+ 1 798.450854348871 797.99188

b8+ 1 927.493448572171 927.46564

Process finished with exit code 0

**Mzml #1 Kerolos Ramses**

Proteins: 4

Peptides: 81

Processed peptides: 81

Peptide identification engine: SIMPLESEARCHENGINE

Enzyme: Trypsin

Mapping 6 peptides to 4 proteins.

Searching with up to 3 ambiguous amino acid(s) and 0 mismatch(es)!

Building trie ... done (0s)

Merge took: 0.00 s (wall), 0.00 s (CPU), 0.00 s (system), 0.00 s (user)

Memory usage (Aho-Corasick): 0 MB (working set delta), 0 MB (peak working set delta)

Aho-Corasick done:

found 6 hits for 6 of 6 peptides.

Peptide hits passing enzyme filter: 6

... rejected by enzyme filter: 0

-----------------------------------

Peptide statistics

unmatched : 0 (0 %)

target/decoy:

match to target DB only: 6 (100 %)

match to decoy DB only : 0 (0 %)

match to both : 0 (0 %)

mapping to proteins:

no match (to 0 protein) : 0

unique match (to 1 protein) : 6

non-unique match (to >1 protein): 0

-----------------------------------

Protein statistics

total proteins searched: 4

matched proteins : 3 (3 new)

matched target proteins: 3 (100 %)

matched decoy proteins : 0 (0 %)

orphaned proteins : 0 (all removed)

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===================================

Peptide ID m/z: 524.276000976563

Peptide ID rt: 624.638453745

Peptide scan index: 134

Peptide ID score type: hyperscore

- Peptide hit sequence: YGEIPAELR

- Peptide hit monoisotopic m/z: 524.277109147071

comparsion score = 1.0000021137158785

Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!

Spectrum 1 of YGEIPAELR has 30 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

y6++ 2 349.713415344021 350.0963428106187

b3+ 1 350.13466407287103 350.1182901294447

b6+ 1 631.308606806571 631.3078184912123

===================================

Peptide ID m/z: 479.235626220703

Peptide ID rt: 2392.58823638502

Peptide scan index: 4042

Peptide ID score type: hyperscore

- Peptide hit sequence: SDGIGAFYK

- Peptide hit monoisotopic m/z: 479.237452487571

comparsion score = 1.0000038107911182

Spectrum 1 of SDGIGAFYK has 30 peaks.

Number of matched peaks: 7

ion theo. m/z observed m/z

b2++ 2 102.036763126271 102.03916931152344

b3++ 2 130.547495174121 130.14051818847656

y1+ 1 147.112804913371 147.08816528320312

y2++ 2 155.59170533362104 155.13870239257812

b4++ 2 187.089527349571 187.09039306640625

b2+ 1 203.066249785771 203.1116180419922

y3++ 2 229.12591247717103 229.129150390625

===================================

Peptide ID m/z: 609.83740234375

Peptide ID rt: 3444.372813201

Peptide scan index: 6548

Peptide ID score type: hyperscore

- Peptide hit sequence: YLEATGQLPVK

- Peptide hit monoisotopic m/z: 609.8400739182209

comparsion score = 1.0000043807979975

Spectrum 1 of YLEATGQLPVK has 38 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

b6++ 2 318.155399136671 318.4029846191406

y4+ 1 456.318047774671 456.5086364746094

y9++ 2 471.766377099221 471.3490295410156

===================================

Peptide ID m/z: 711.351013183594

Peptide ID rt: 3466.4976788980202

Peptide scan index: 6604

Peptide ID score type: hyperscore

- Peptide hit sequence: LNHNAAFMQIPMGLEGNFK

- Peptide hit monoisotopic m/z: 711.3520465059045

comparsion score = 1.00000145261944

Spectrum 1 of LNHNAAFMQIPMGLEGNFK has 70 peaks.

Number of matched peaks: 3

ion theo. m/z observed m/z

y2++ 2 147.594247833621 147.6368865966797

y3++ 2 204.615711929321 204.72850036621094

y4+ 1 465.245611487571 465.27301025390625

===================================

Peptide ID m/z: 627.013610839844

Peptide ID rt: 3749.47081854498

Peptide scan index: 7265

Peptide ID score type: hyperscore

- Peptide hit sequence: LGSWNVIMFLTLEQVK

- Peptide hit monoisotopic m/z: 626.6779765321044

comparsion score = 0.9994647096937975

Spectrum 1 of LGSWNVIMFLTLEQVK has 58 peaks.

Number of matched peaks: 18

ion theo. m/z observed m/z

b4++ 2 222.61571192932098 222.16700744628906

y2+ 1 246.18121920047105 246.11500549316406

b3+ 1 258.144834072871 258.26300048828125

b6++ 2 329.171383168571 329.4130554199219

y6++ 2 359.210705859971 359.5690612792969

b4+ 1 444.224147391871 444.2130126953125

b8++ 2 451.233657852571 451.44000244140625

y9++ 2 554.8071876875209 554.489013671875

b5+ 1 558.267075583271 558.291015625

b10++ 2 581.309897171571 581.3980102539062

y10++ 2 611.3492198629709 611.2620239257812

b11++ 2 631.8337367832211 632.2250366210938

y11++ 2 660.883427006521 661.0599975585938

b13++ 2 752.8970660703211 753.2550048828125

y13++ 2 810.944547761721 810.988037109375

b14++ 2 816.9263551979211 817.2650146484375

y7+ 1 830.4981996040709 830.3049926757812

b8+ 1 901.460039238371 901.56005859375

===================================

Peptide ID m/z: 567.820434570313

Peptide ID rt: 4421.189246961

Peptide scan index: 8681

Peptide ID score type: hyperscore

- Peptide hit sequence: NIGVTAVAFNK

- Peptide hit monoisotopic m/z: 567.319308306571

comparsion score = 0.9991174564470875

Spectrum 1 of NIGVTAVAFNK has 38 peaks.

Number of matched peaks: 22

ion theo. m/z observed m/z

y3++ 2 204.615711929321 204.26901245117188

y2+ 1 261.15573310477106 260.8570251464844

b6++ 2 278.658108620721 278.5370178222656

b3+ 1 285.155733104771 285.487060546875

b7++ 2 328.19231576427103 328.24200439453125

b8++ 2 363.710872844021 364.0039978027344

y7++ 2 375.71087284402097 375.62506103515625

b4+ 1 384.224147391871 384.1050109863281

y8++ 2 425.245079987571 425.0150146484375

b9++ 2 437.245079987571 437.49005126953125

y4+ 1 479.26126155137104 479.06903076171875

b5+ 1 485.271826615171 485.37506103515625

b10++ 2 494.266544083271 494.0090026855469

b6+ 1 556.308940774671 555.9720458984375

y5+ 1 578.329675838471 578.2369995117188

y6+ 1 649.366789997971 649.2540283203125

b7+ 1 655.377355061771 654.885986328125

b8+ 1 726.414469221271 726.5750732421875

y7+ 1 750.4144692212709 750.2930297851562

y8+ 1 849.482883508371 849.3380126953125

b9+ 1 873.4828835083711 873.10400390625

y9+ 1 906.504347604071 906.2470092773438

<Warning: TheoreticalSpectrumGenerator received the unknown parameter 'add\_b\_ion'!> occurred 6 times

Process finished with exit code 0