Supporting Information

Naive Pluripotent and Trophoblastic Stem Cell Lines as a Model for Detecting Missing Proteins in the Context of the Chromosome-Centric Human Proteome Project

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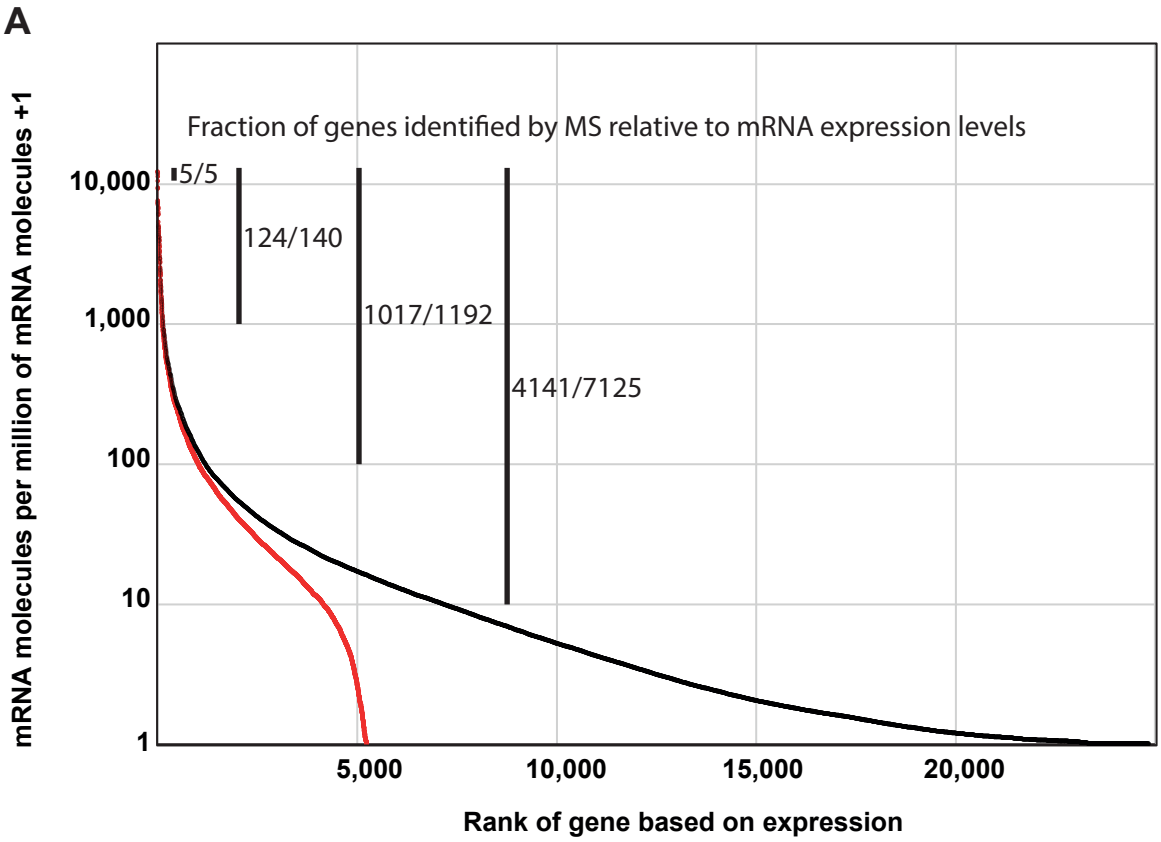
Supplementary Figure 1: Transcriptomic expression levels of missing proteins and all genes in hNPSCs and hTSCs. Distribution of average transcriptomic expression levels (mRNA molecules per million of mRNA molecules+1) for all genes (black) (**A, B**), corresponding to all proteins identified in hNPSCs (red) (**A**) or in hTSCs (blue) (**B**).

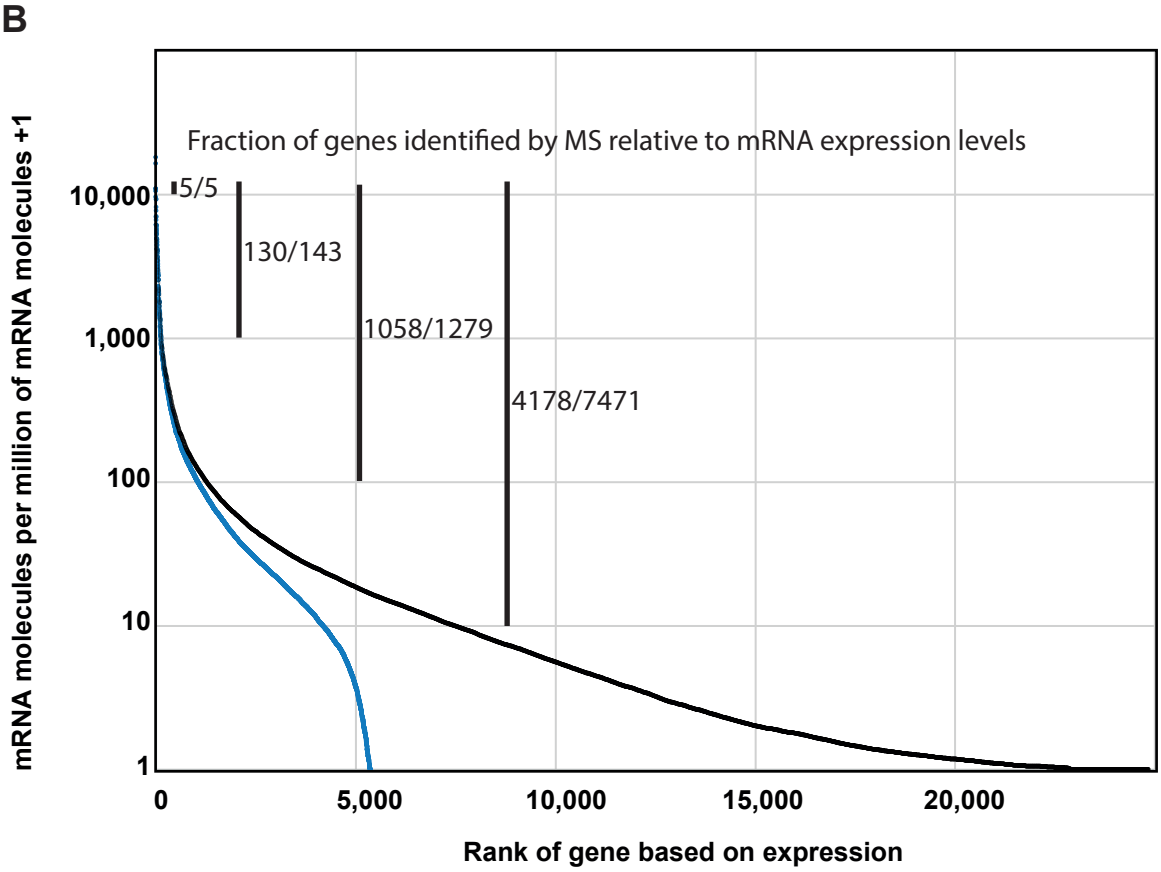
Supplementary Table 1: List of Missing proteins (PE2-PE4) with mRNA expressed at more than 20 upm in the 3'SRP datasets

Supplementary Table 2: Proteins identified after using Mascot and Proline for hNPSCs and hTSCs (lysis buffer, trypsin and merge) (Excel file)

Supplementary Table 3: Peptides identified using PaSER for hNPSCs and hTSCs (lysis buffer and trypsin) (Excel file)

Supplementary Material 1: Spectra of peptides of interest identified with the PaSER search engine.





Distribution of transcriptomic expression levels for genes detected by MS in hTSCs

Distribution of transcriptomic expression levels for genes detected by MS in hNPSCs

Distribution of transcriptomic expression levels for all genes

Girard et al, Supplementary Figure 1

Supplementary table 1. List of Missing proteins (PE2-PE4) with more 20 upm in the 3'SRP datasets

hNPSCs	hTSCs
ESRG	CBDW5
TRIM61	SMIM30
CBWD5	RTL8C
ZNF676	MTRNR2L10
ZNF208	C19orf48
ZNF880	C12orf56
C19orf48	ESRG
SMIM30	ERVV-1
ZNF492	ZNF429
ARGFX	
ZNF728	
ZNF781	
ZNF793	
ZNF429	

- hNPSCs

Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Tampon_Lyse_Slot1_11_1_4632
Created date: 2022-06-16 17:30:20.0
Search name:
Activation type: CID

Peptide sequence: K.DFNQSSHLTTHK.R
Scan number: 13664
Calculated M+H: 1414.671
Measured M+H: 1414.6743
Charge state: 2
File name: 0e085448-f297-46bb-9d2a-30bd2c0d9586_1655400612
search type: light

Protein: P0DKX0

Medium/low Quality

Ions:
a ☐1+ ☐2+ ☐3+
b ☑1+ ☐2+ ☐3+
c ☐1+ ☐2+ ☐3+
x ☐1+ ☐2+ ☐3+
y ☑1+ ☐2+ ☐3+
z ☐1+ ☐2+ ☐3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)
☐ H_3PO_4 (^)
☑ Precursor (#)
☐ Precursor with reduced charges

Mass Type:
◉Mono ○Avg

Mass Tol: 30
○Dalton ◉PPM

Update

Peak Assignment:
◉Most Intense
○Nearest Match
☐Peak Detect
☐Precursor Removal

Peak Labels:
◉Ion ○m/z
○None

Width: 750

Height: 450

Precursor Neutral Losses
707.8425 [M+2H]

DFNQSSHLTTHK, MH+ 1414.6710, m/z 707.8391
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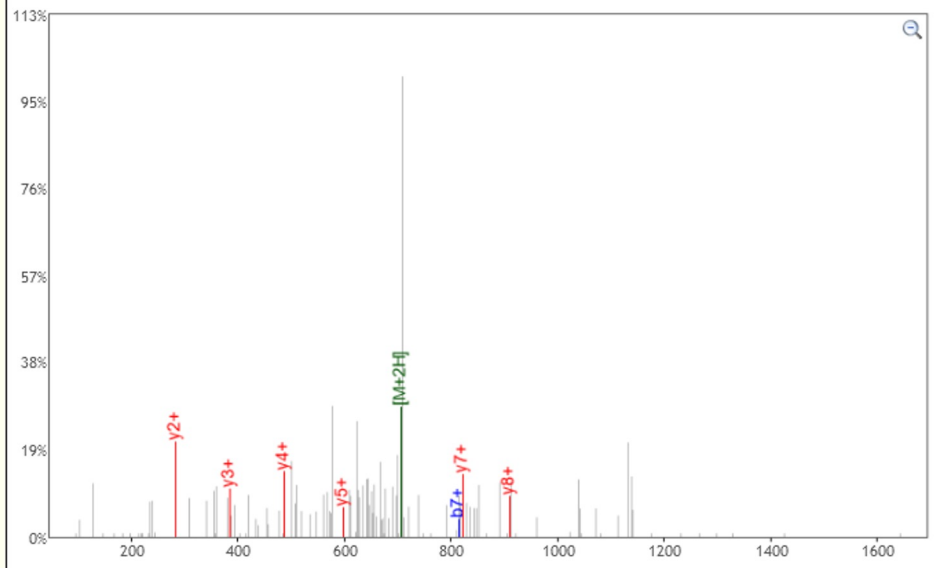

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐Enable tooltip

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377.1456	3	N	10	1152.5756
505.2041	4	Q	9	1038.5327
592.2362	5	S	8	910.4741
679.2682	6	S	7	823.4421
816.3271	7	H	6	736.4100
929.4112	8	L	5	599.3511
1030.4588	9	T	4	486.2671
1131.5065	10	T	3	385.2194
1268.5654	11	H	2	284.1717
	12	K	1	147.1128

[Click] to move table

Static Modifications:
C: 57.02146

Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.DFNQSSHLTTHK.R	0	1414.67096	0.0	1.5917	0.8108	707.8408	1.02805	0.9874	NA	7	22	64.258
2	R.GQTEALEECLHK.H	0	1414.66308	0.8481	0.2418	0.838	707.8408	1.02805	0.9945	NA	2	20	9.51
3	K.KEEEATEWQHK.A	0	1414.6597	0.8681	0.21	0.1929	707.8408	1.02805	0.9705	NA	3	20	8.221
4	K.HTTLHSSQNFDK.G	0	1414.67096	0.8749	0.1991	0.6373	707.8408	1.02805	0.9837	NA	3	22	7.777

Fragment Ion View

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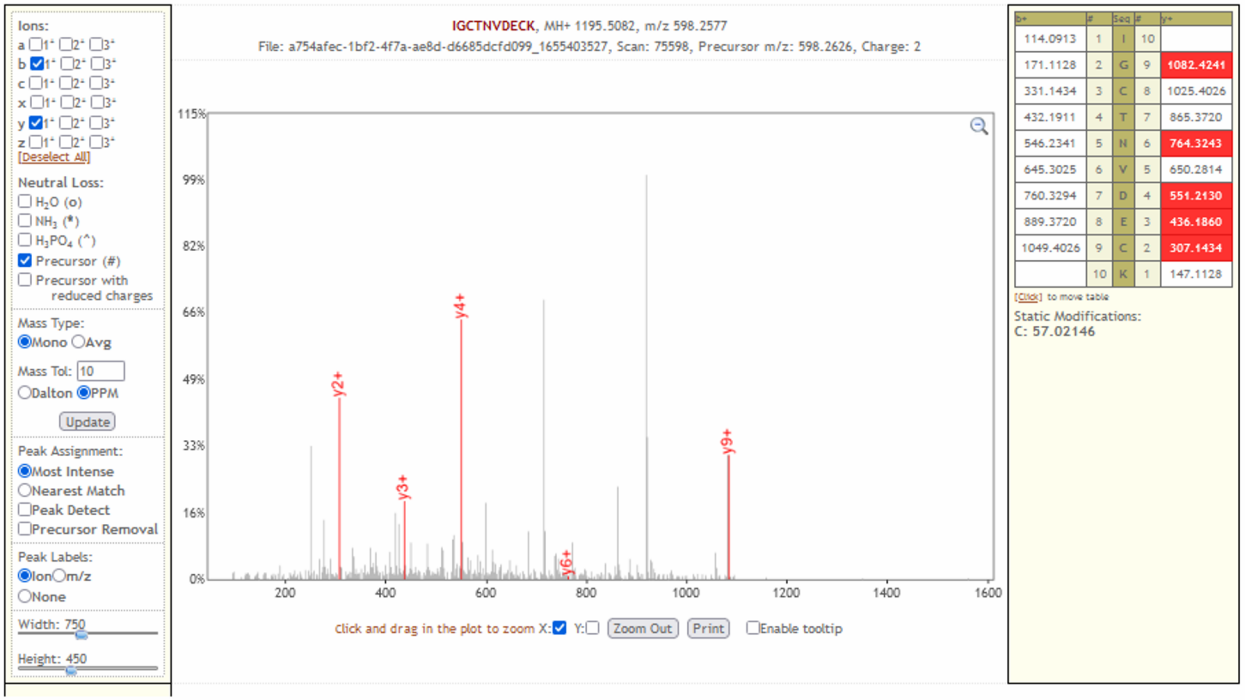
Protein: P0DKX0

High Quality



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Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.IGCTNVDECK.V	0	1195.50816	0.0	0.2536	0.494	598.2626	0.94138	0.8918	NA	4	18	499.0
2	K.(42.010565)SIGTFSDPCK(42.010565).D	0	1195.52996	1.0	0.0	NA	598.2626	0.94138	NA	NA	0	18	-1.0
3	K.SM(15.994915)LEEMNVGK(42.010565).P	0	1195.53331	1.0	0.0	NA	598.2626	0.94138	NA	NA	0	16	-1.0
4	K.(42.010565)K(42.010565)SECFSSPK(42.010565).T	0	1195.52995	1.0	0.0	NA	598.2626	0.94138	NA	NA	0	16	-1.0

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Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Trypsine_Slot1_10_1_4630
Created date: 2022-06-16 18:18:54.0
Search name:
Activation type: CID

Peptide sequence: K.(42.010565)AFIWSSRLSEHK(42.010565).R
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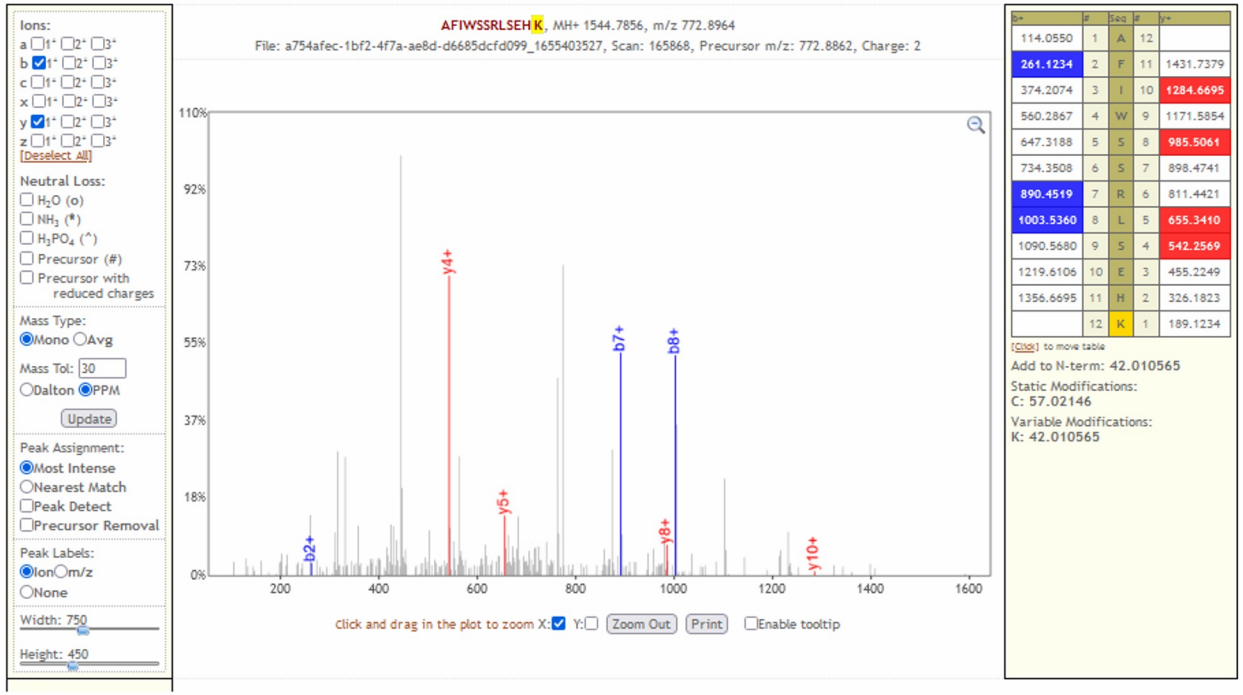
search type: light

Protein: P0DKX0

Medium Quality



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Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.(42.010565)AFIWSSRLSEHK(42.010565).R	0	1544.78559	0.0	1.205	0.7573	772.8862	1.1015	1.0671	NA	7	21	11.994
2	K.(42.010565)QGK(42.010565)DIYTIDHTK(42.010565).P	0	1544.75908	0.2364	0.9201	0.7877	772.8862	1.1015	1.0664	NA	4	22	9.104
3	R.(42.010565)FHQSLNETNSRK(42.010565).K	0	1544.74519	0.2955	0.8489	0.6215	772.8862	1.1015	1.0534	NA	4	22	8.382
4	K.AENARMVVNIDNAK.L	0	1544.78494	0.3856	0.7403	0.1298	772.8862	1.1015	1.036	NA	9	23	7.281

Fragment Ion View

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search type: light

Protein: P0DKX0

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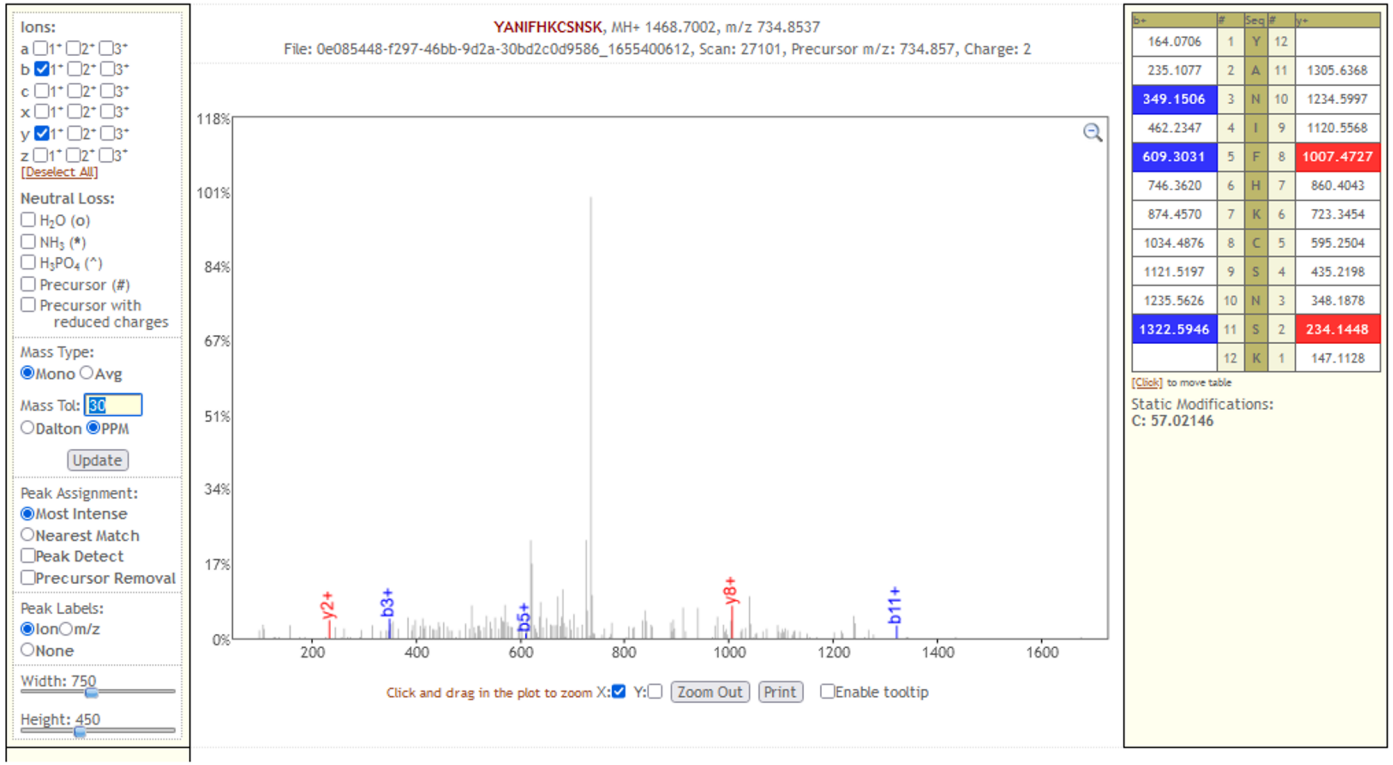

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Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
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2	R.DISDKLQEMDFK.L	0	1468.69879	0.2872	0.309	0.0253	734.857	1.02478	1.0234	NA	4	21	10.578
3	K.ISDFGTSK(42.010565)ELSDK.S	0	1468.71655	0.3377	0.2872	6.0E-4	734.857	1.02478	1.0426	NA	6	23	9.814
4	R.IDSLM(15.994915)DEISFLK(42.010565).K	0	1468.72394	0.4786	0.2261	0.0514	734.857	1.02478	1.0188	NA	4	21	7.679

Fragment Ion View

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Search name:
Activation type: CID

Peptide sequence: K.FISNPQLGSLTEIAK.Q
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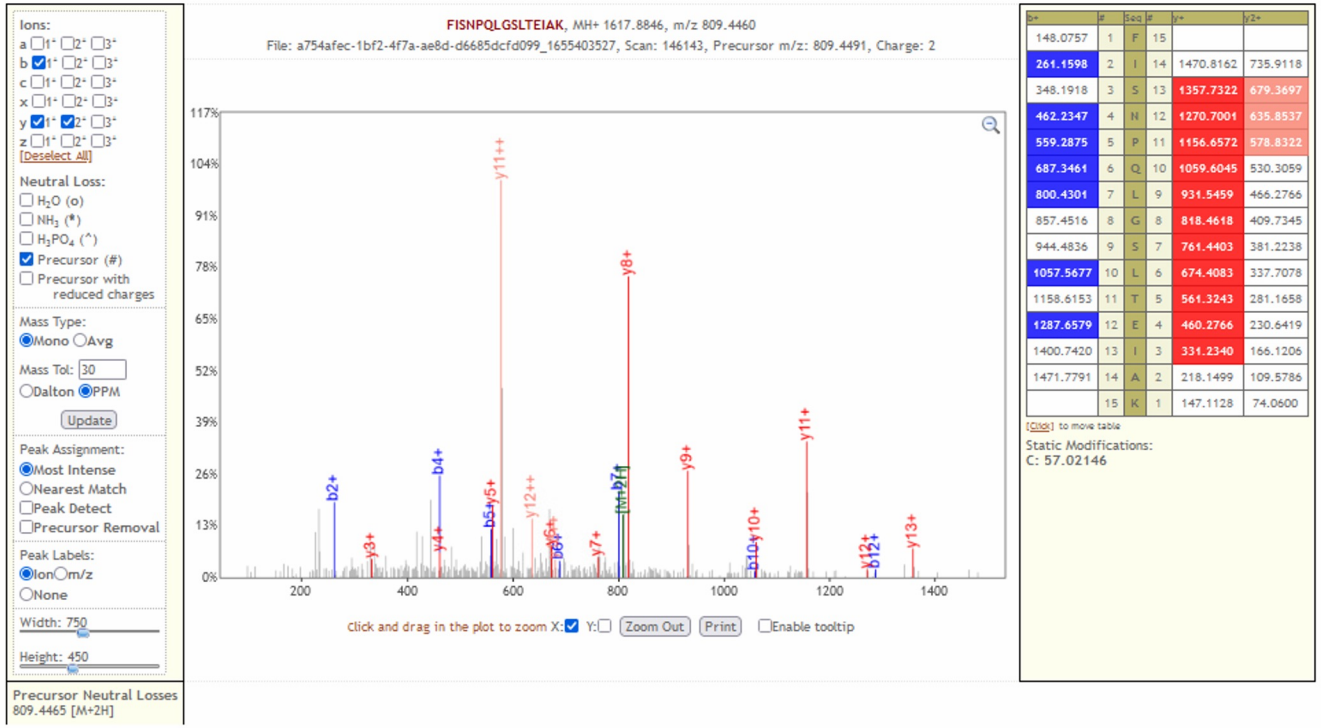
Protein: Q5EBN2

High Quality



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687.3461	6	Q	10	1059.6045	530.3059
800.4301	7	L	9	931.5459	466.2766
857.4516	8	G	8	818.4618	409.7345
944.4836	9	S	7	761.4403	381.2238
1057.5677	10	L	6	674.4083	337.7078
1158.6153	11	T	5	561.3243	281.1658
1287.6579	12	E	4	460.2766	230.6419
1400.7420	13	I	3	331.2340	166.1206
1471.7791	14	A	2	218.1499	109.5786
	15	K	1	147.1128	74.0600

Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.FISNPQLGSLTEIAK.Q	0	1617.88464	0.0	3.158	0.1003	809.4491	1.13703	1.0684	NA	15	25	40.732
2	K.IYSVNLQKQPWNK.M	0	1617.87474	0.6426	1.1285	0.6969	809.4491	1.13703	1.0905	NA	5	22	14.412
3	K.FNLSPPSICKVLDK.P	0	1617.86687	0.7767	0.7052	0.4298	809.4491	1.13703	1.0834	NA	4	24	8.921
4	R.PQVHINMLYYVIK.S	0	1617.88212	0.813	0.5906	0.9939	809.4491	1.13703	1.0972	NA	6	21	7.436

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Peptide sequence: K.FISNPQLGSLTEIAK.Q
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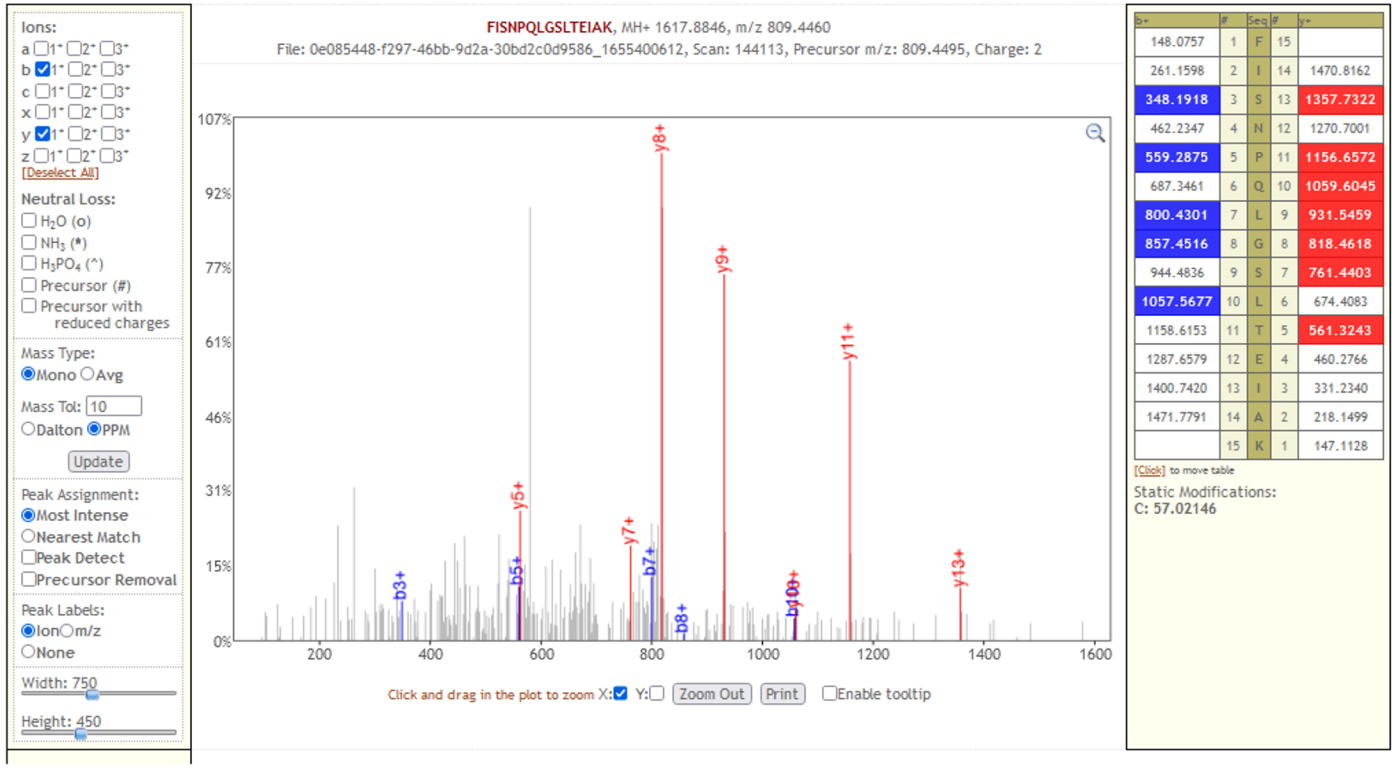
Protein: Q5EBN2

High Quality



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348.1918	3	S	13	1357.7322
462.2347	4	N	12	1270.7001
559.2875	5	P	11	1156.6572
687.3461	6	Q	10	1059.6045
800.4301	7	L	9	931.5459
857.4516	8	G	8	818.4618
944.4836	9	S	7	761.4403
1057.5677	10	L	6	674.4083
1158.6153	11	T	5	561.3243
1287.6579	12	E	4	460.2766
1400.7420	13	I	3	331.2340
1471.7791	14	A	2	218.1499
	15	K	1	147.1128

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Static Modifications:
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Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.FISNPQLGSLTEIAK.Q	0	1617.88464	0.0	2.8581	0.1258	809.4495	1.13213	1.0684	NA	14	25	55.064
2	K.FNLSPPSICKVLDK.P	0	1617.86687	0.7676	0.6642	0.4994	809.4495	1.13213	1.0834	NA	4	24	12.622
3	K.IYSVNLQKQPWNK.M	0	1617.87474	0.7961	0.5827	0.7837	809.4495	1.13213	1.0905	NA	5	22	11.046
4	R.PQVHINMLYYVIK.S	0	1617.88212	0.8166	0.5241	0.914	809.4495	1.13213	1.0972	NA	5	20	9.913

Fragment Ion View

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Peptide sequence: K.LEEYNAPWK.E
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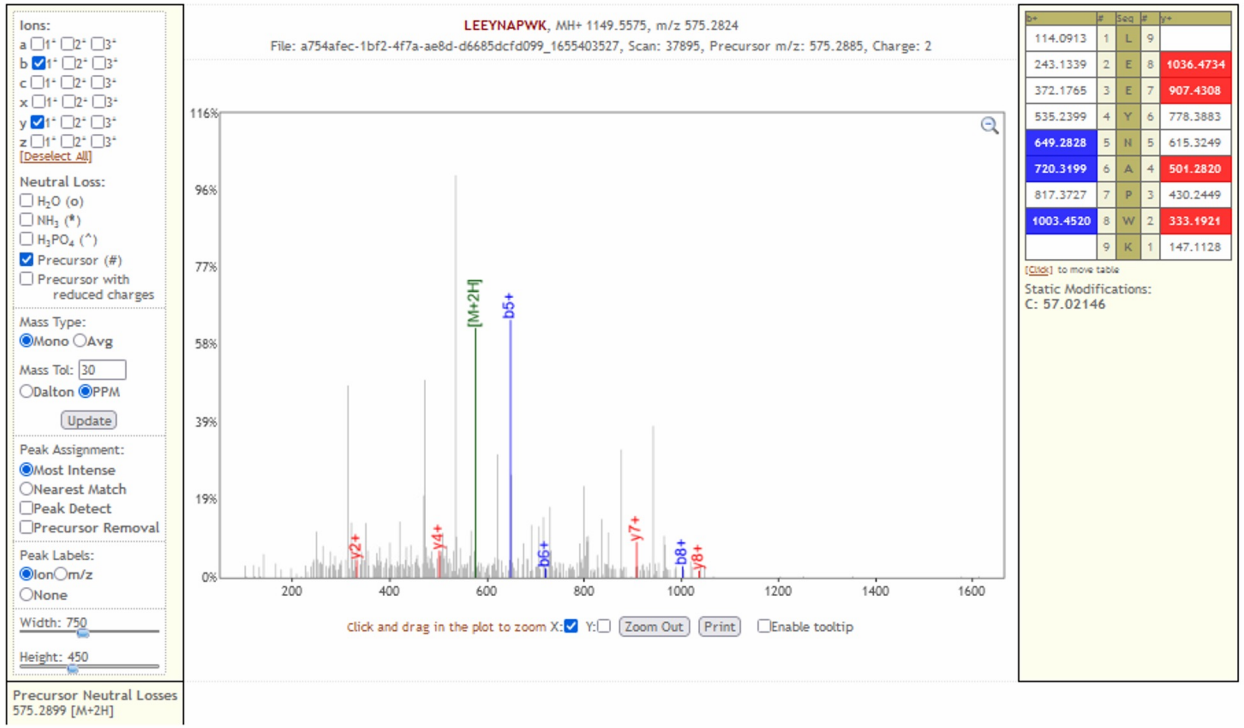
search type: light

Protein: Q5EBN2

Medium/low Quality



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Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.LEEYNAPWK.E	0	1149.55748	0.0	0.2372	0.3796	575.2885	0.90525	0.8778	NA	4	14	51.092
2	-.PSASSVLSNCK.T	0	1149.55684	0.6828	0.0752	0.5127	575.2885	0.90525	0.8746	NA	5	18	16.094
3	K.(42.010565)VFEETK(42.010565)GQK.Y	0	1149.57861	0.7032	0.0704	0.0033	575.2885	0.90525	0.9063	NA	3	16	15.046
4	K.(42.010565)EIM(15.994915)LKNDTK.V	0	1149.58197	1.0	0.0	NA	575.2885	0.90525	NA	NA	2	16	-0.165

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Fragment Ion View

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Sample name: HPP_CSnaives_Trypsine_Slot1_10_1_4630
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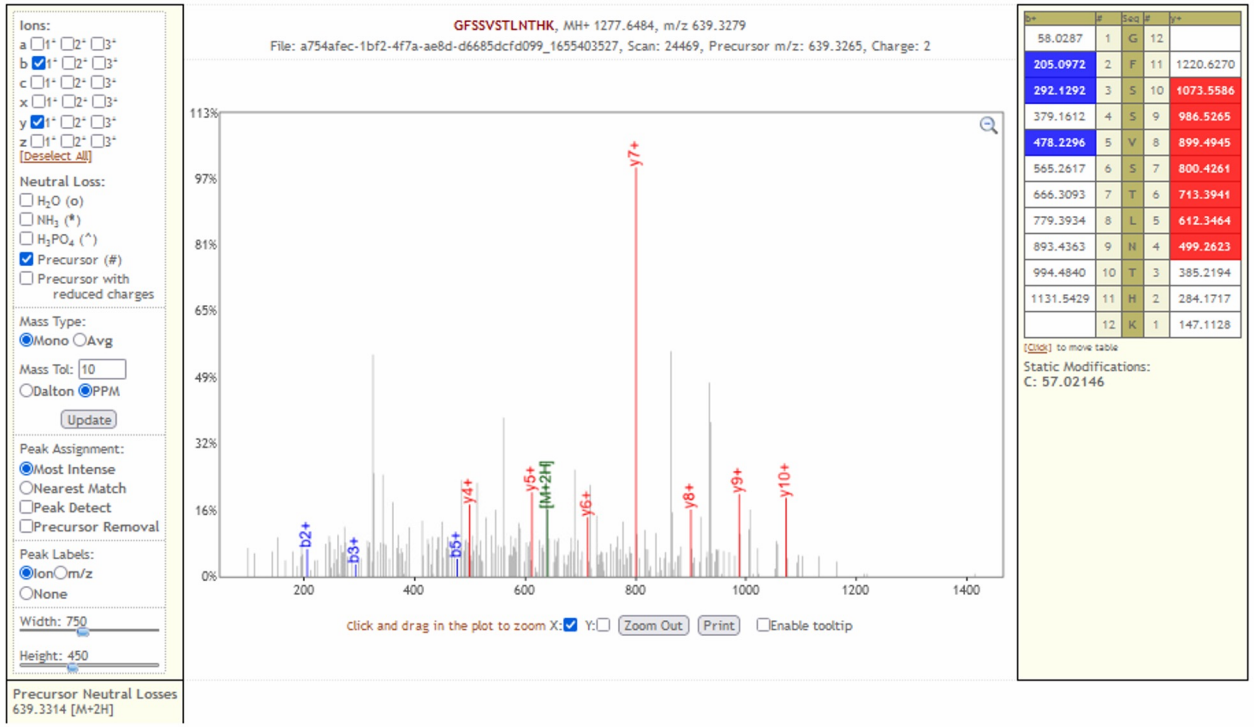
search type: light

Protein: Q8N7Q3

High Quality



Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.GFSSVSTLNTHK.A	0	1277.64844	0.0	1.4448	0.3124	639.3265	0.99354	0.9693	NA	8	19	80.497
2	R.GFHFTVDGNKR.A	0	1277.63855	0.7665	0.3374	0.6378	639.3265	0.99354	0.961	NA	3	17	18.616
3	R.LAPPAPEESNPR.G	0	1277.64843	0.8694	0.1887	0.0401	639.3265	0.99354	0.9224	NA	4	20	10.306
4	K.THFIITNMMK(42.010565).G	0	1277.63806	0.9504	0.0716	0.7957	639.3265	0.99354	0.9578	NA	4	17	3.764

Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Trypsine_Slot1_10_1_4630
Created date: 2022-06-16 18:18:54.0
Search name:
Activation type: CID

Peptide sequence: K.(42.010565)AFSWSSILTEHK(42.010565)IIHTGEK(42.010565).P
Scan number: 190964
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Measured M+H: 2310.147
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search type: light

Protein: Q8N7Q3

Low Quality

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534.2347	4	W	16	1963.0284
621.2667	5	S	15	1776.9490
708.2988	6	S	14	1689.9170
821.3828	7	I	13	1602.8850
934.4669	8	L	12	1489.8009
1035.5146	9	T	11	1376.7169
1164.5572	10	E	10	1275.6692
1301.6161	11	H	9	1146.6266
1471.7216	12	K	8	1009.5677
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1834.9486	15	H	5	613.2940
1935.9963	16	T	4	476.2351
1993.0178	17	G	3	375.1874
2122.0604	18	E	2	318.1660
	19	K	1	189.1234

Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.(42.010565)AFSWSSILTEHK(42.010565)IIHTGEK(42.010565).P	0	2310.17645	0.0	0.2967	0.0014	1155.5771	1.31729	1.3432	NA	5	23	27.983
2	K.DAFDRNPELQNLLLDDFFK.S	0	2310.14007	0.2162	0.2326	0.7649	1155.5771	1.31729	1.2837	NA	5	23	21.909
3	K.(42.010565)MFSGTANLK(42.010565)IHQNIHSEEK(42.010565).P	0	2310.11829	0.8777	0.0363	0.0221	1155.5771	1.31729	1.3245	NA	5	24	3.325
4	R.(42.010565)SAGVIDSIFTPWHKPWEQK(42.010565).L	0	2310.15533	0.9465	0.0159	0.0136	1155.5771	1.31729	1.3282	NA	4	23	1.393

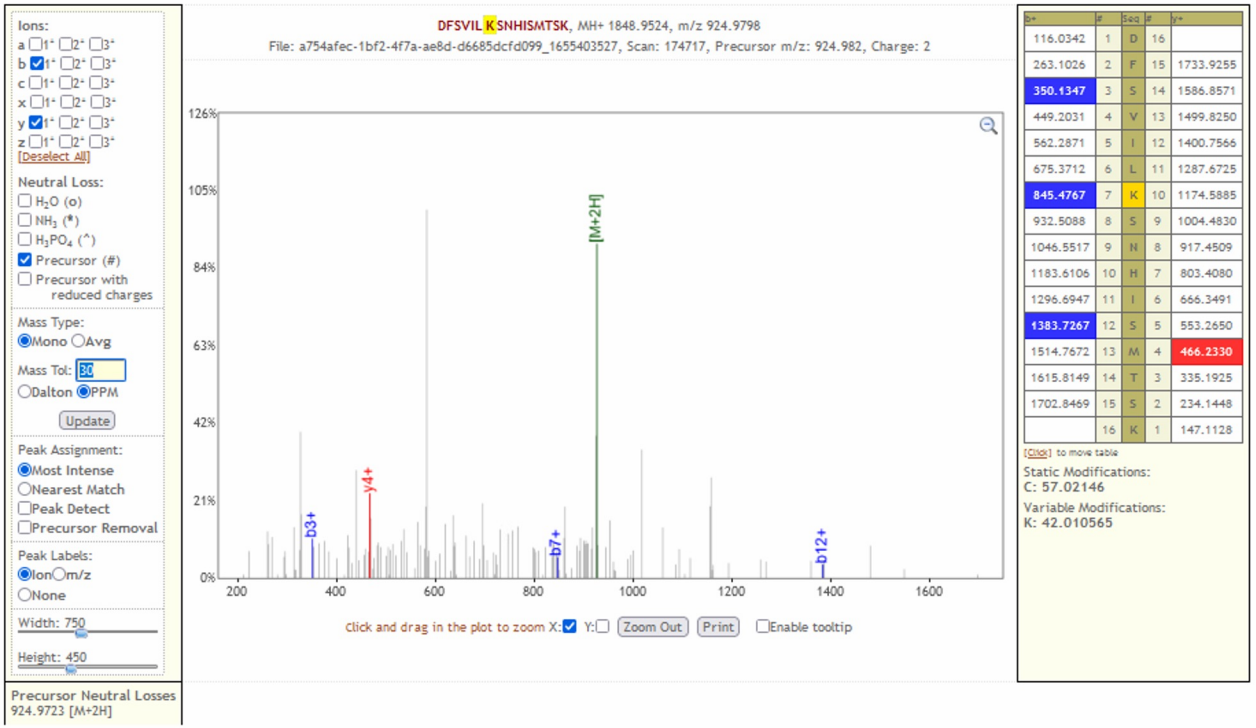
Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Trypsine_Slot1_10_1_4630
Created date: 2022-06-16 18:18:54.0
Search name:
Activation type: CID

Peptide sequence: K.DFSVILK(42.010565)SNHISMTSK.V
Scan number: 174717
Calculated M+H: 1848.9524
Measured M+H: 1848.9567
Charge state: 2
File name: a754afec-1bf2-4f7a-ae8d-d6685dcfd099_1655403527
search type: light

Protein: A4D1E1

Low Quality



Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.DFSVILK(42.010565)SNHISMTSK.V	0	1848.95239	0.0	0.4648	0.2566	924.982	1.22315	1.205	NA	4	26	17.912
2	R.GFTEFLVCRPGLDAPK(42.010565).T	0	1848.93127	0.403	0.2775	0.751	924.982	1.22315	1.1774	NA	3	26	10.615
3	R.(42.010565)PIDSFETIPLIPSAHK(42.010565).F	0	1848.97417	0.4388	0.2608	0.719	924.982	1.22315	1.1766	NA	3	27	9.966
4	R.IENTLPAMSVLLTYNK(42.010565).N	0	1848.97753	0.6226	0.1754	0.2689	924.982	1.22315	1.1625	NA	2	27	6.639

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Fragment Ion View

Project name: 224001
Sample name: HPP_CSnaives_Trypsine_Slot1_10_1_4630
Created date: 2022-06-16 18:18:54.0
Search name:
Activation type: CID

Peptide sequence: K.CQEQSSNVEISSNSCK(42.010565).S
Scan number: 21309
Calculated M+H: 1898.7854
Measured M+H: 1898.7878
Charge state: 2
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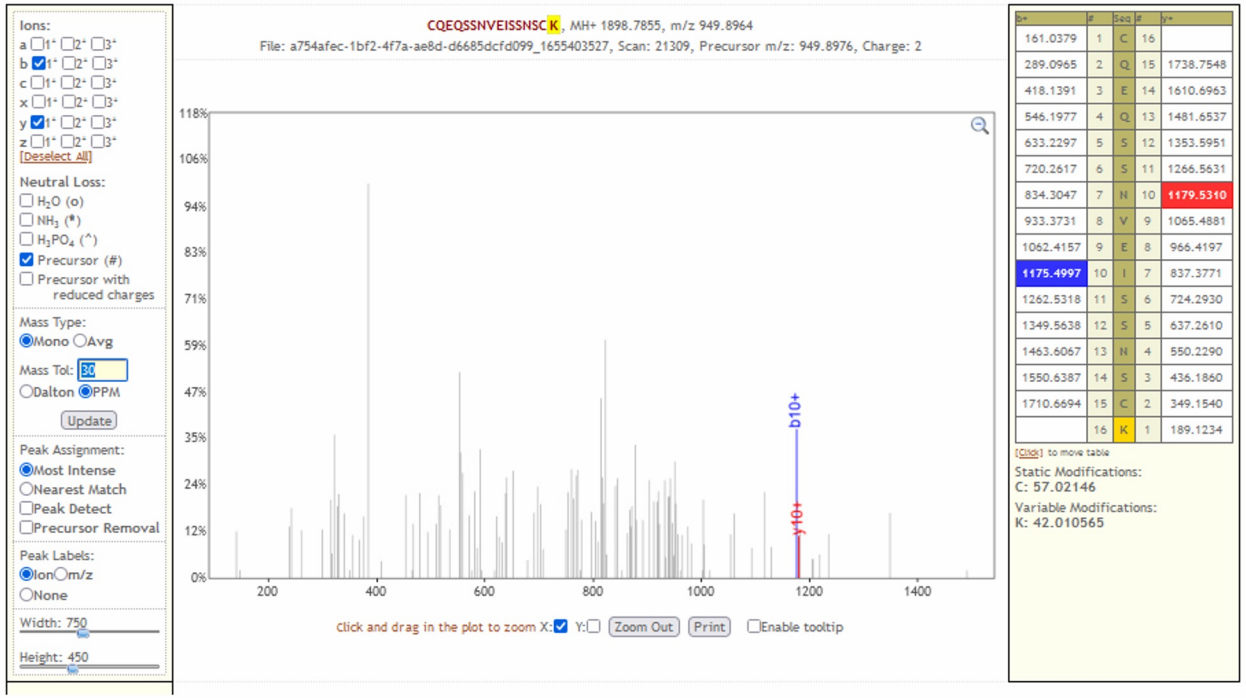
search type: light

Protein: A4D1E1

Low Quality



Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.CQEQSSNVEISSNSCK(42.010565).S	0	1898.78546	0.0	0.2166	0.1992	949.8976	1.13201	1.1148	NA	2	26	70.928
2	K.ICEQGMNAWSNGSMWK.R	0	1898.79823	0.8241	0.0381	0.2945	949.8976	1.13201	1.1107	NA	1	24	12.097
3	K.(42.010565)NHAGSPGCEESDAGK(42.010565)EK(42.010565).L	0	1898.78209	1.0	0.0	NA	949.8976	1.13201	NA	NA	0	27	-0.454
4	K.(42.010565)GNECFQK(42.010565)GDYPQAMK(42.010565).H	0	1898.80475	1.0	0.0	NA	949.8976	1.13201	NA	NA	0	21	-0.454

Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Tampon_Lyse_Slot1_11_1_4632
Created date: 2022-06-16 17:30:20.0
Search name:
Activation type: CID

Peptide sequence: -.M(15.994915)NVM(15.994915)GFNTDR.L
Scan number: 4556
Calculated M+H: 1216.5085
Measured M+H: 1216.5121
Charge state: 2
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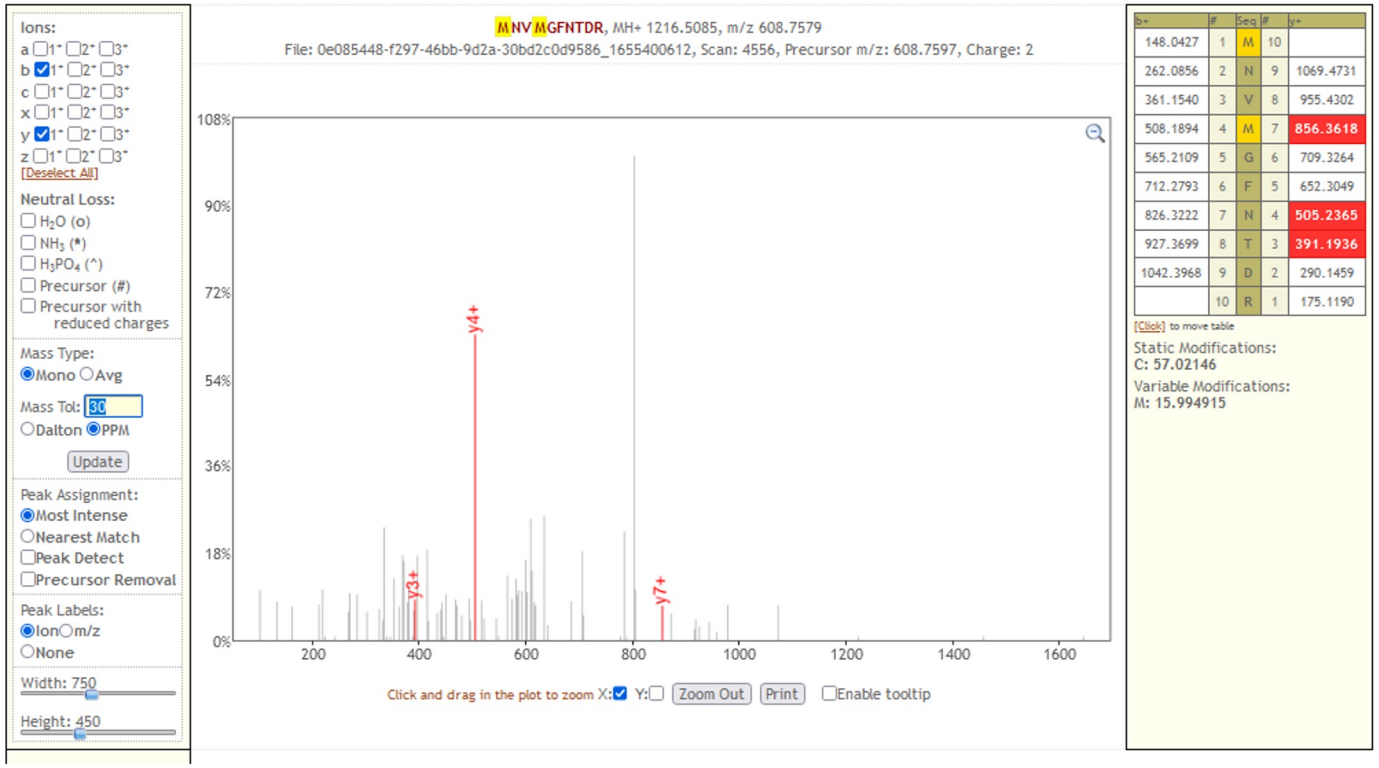
search type: light

Protein: P0DJD0

Low Quality



Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	-.M(15.994915)NVM(15.994915)GFNTDR.L	0	1216.50851	0.0	0.4447	0.0096	608.7597	0.89008	0.8887	NA	3	18	13.57
2	K.(42.010565)EGWK(42.010565)CHCR.N	0	1216.49861	0.1536	0.3764	0.0	608.7597	0.89008	0.9129	NA	2	14	11.458
3	R.SM(15.994915)RNESM(15.994915)SSR.L	0	1216.50447	0.2721	0.3237	0.0018	608.7597	0.89008	0.8959	NA	4	16	9.829
4	R.AYGAMTCTDGK(42.010565).L	0	1216.49727	0.6895	0.1381	0.0	608.7597	0.89008	0.9123	NA	3	18	4.09

Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Tampon_Lyse_Slot1_11_1_4632
Created date: 2022-06-16 17:30:20.0
Search name:
Activation type: CID

Peptide sequence: R.ERLELYDEHVSSR.S
Scan number: 127401
Calculated M+H: 1632.7976
Measured M+H: 1632.816
Charge state: 2
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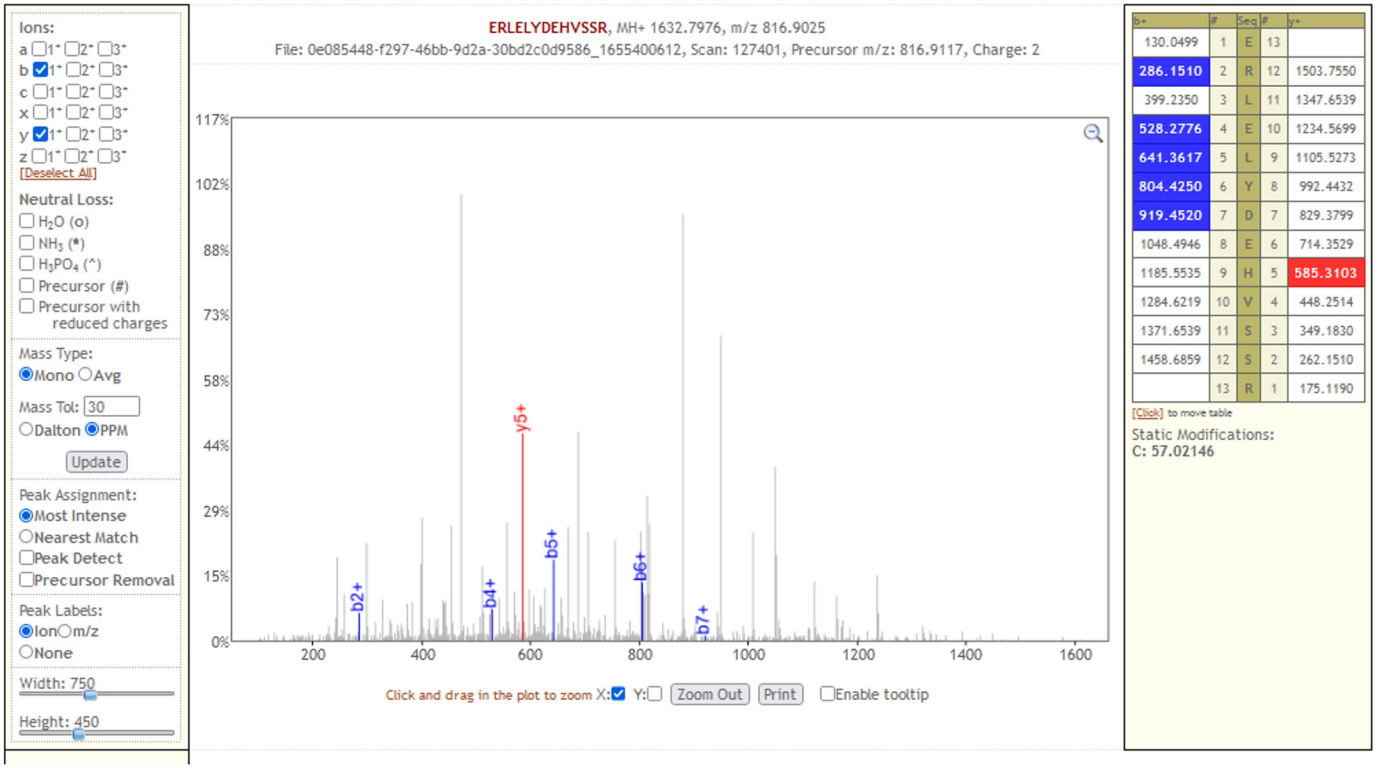
search type: light

Protein:
A0A096LP55

Medium Quality



b+	#	Seq	#	y+
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286.1510	2	R	12	1503.7550
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528.2776	4	E	10	1234.5699
641.3617	5	L	9	1105.5273
804.4250	6	Y	8	992.4432
919.4520	7	D	7	829.3799
1048.4946	8	E	6	714.3529
1185.5535	9	H	5	585.3103
1284.6219	10	V	4	448.2514
1371.6539	11	S	3	349.1830
1458.6859	12	S	2	262.1510
	13	R	1	175.1190

[Click] to move table

Static Modifications:
C: 57.02146

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Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	R.ERLELYDEHVSSR.S	0	1632.79758	0.0	0.39	0.9119	816.9117	1.09206	1.0534	NA	6	18	14.387
2	R.(42.010565)VGADVTFFK(42.010565)QATHK.L	0	1632.83803	0.1098	0.3472	0.0	816.9117	1.09206	1.1453	NA	4	18	12.793
3	K.LEVGADNLSIEESTR.S	0	1632.80749	0.1601	0.3276	0.665	816.9117	1.09206	1.0479	NA	3	22	12.062
4	R.(42.010565)SLTLTKM(15.994915)NTHICR.A	0	1632.81959	0.2352	0.2983	0.0047	816.9117	1.09206	1.1031	NA	5	19	10.972

Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Trypsine_Slot1_10_1_4630
Created date: 2022-06-16 18:18:54.0
Search name:
Activation type: CID

Peptide sequence: K.WSSTLSYHK.K
Scan number: 14846
Calculated M+H: 1108.5421
Measured M+H: 1108.5559
Charge state: 2
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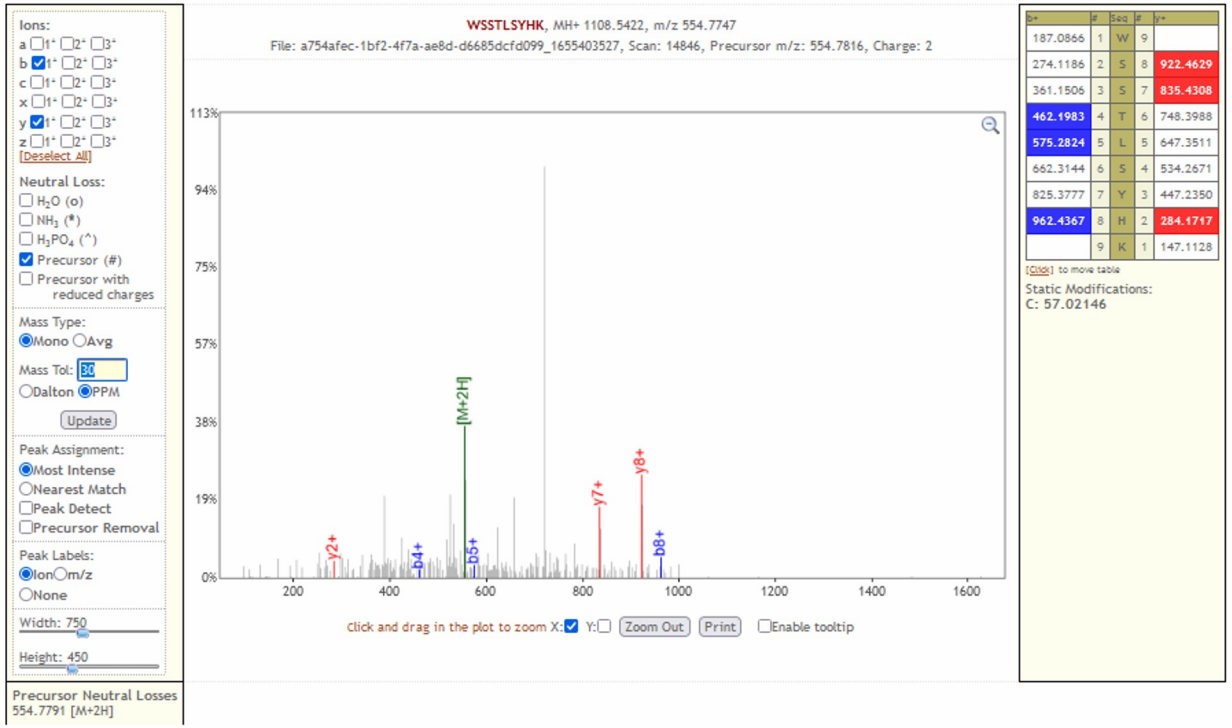
search type: light

Protein: O43345

Medium Quality



Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.WSSTLSYHK.K	0	1108.54217	0.0	0.3989	0.3293	554.7816	0.89762	0.8714	NA	7	16	33.732
2	K.WMADK(42.010565)LFR.A	0	1108.5608	0.3646	0.2535	0.0	554.7816	0.89762	0.9185	NA	4	14	21.388
3	K.SVSENETSKK.N	0	1108.54803	0.828	0.0686	0.8217	554.7816	0.89762	0.861	NA	3	16	5.699
4	K.SWNNSLLM(15.994915)K.I	0	1108.54555	0.9624	0.015	0.6716	554.7816	0.89762	0.8638	NA	3	14	1.147

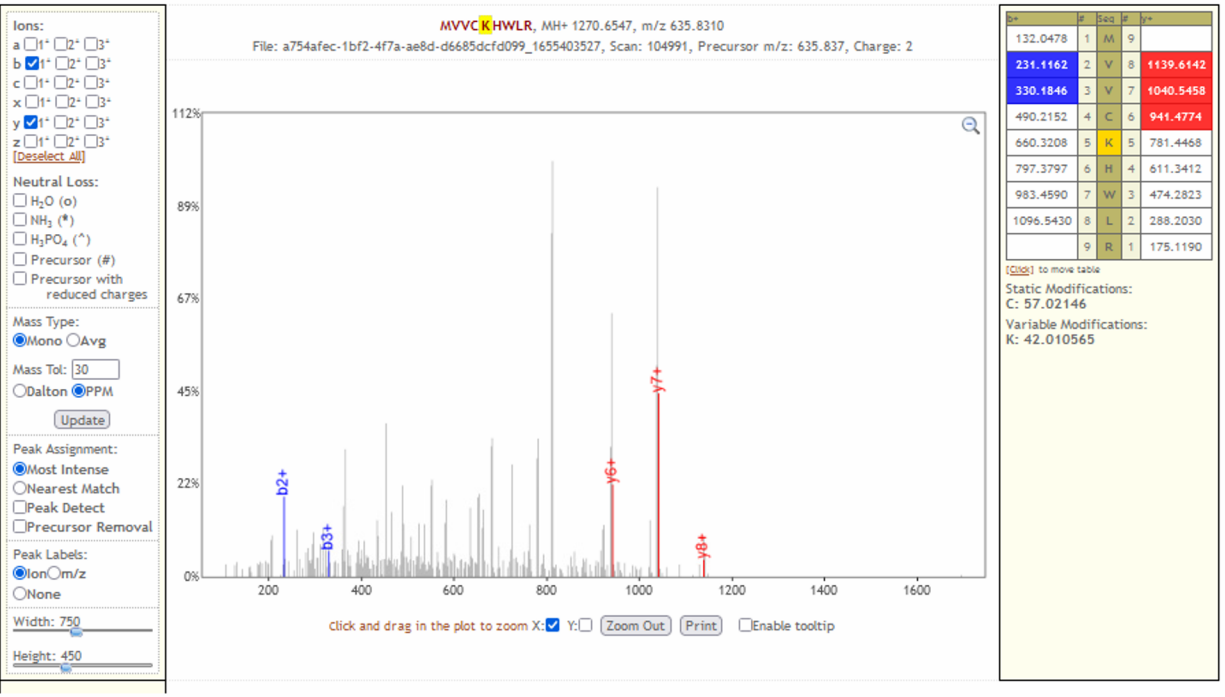
Fragment Ion View

Project name: 2224001
Sample name: HPP_CSnaives_Trypsine_Slot1_10_1_4630
Created date: 2022-06-16 18:18:54.0
Search name:
Activation type: CID

Peptide sequence: K.MVVCK(42.010565)HWLR.G
Scan number: 104991
Calculated M+H: 1270.6547
Measured M+H: 1270.6666
Charge state: 2
File name: a754afec-1bf2-4f7a-ae8d-d6685dcfd099_1655403527
search type: light

Protein: A6NMK7

Medium Quality



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Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.MVVCK(42.010565)HWLR.G	0	1270.65471	0.0	0.2426	0.0338	635.837	0.99199	0.9847	NA	5	14	36.256
2	R.QLRVSHGCVSK.I	0	1270.66845	0.3868	0.1487	0.5223	635.837	0.99199	0.9425	NA	4	17	22.184
3	R.QNQREAHFIK.R	0	1270.66509	1.0	0.0	0.4681	635.837	0.99199	0.9412	NA	1	15	-0.117
4	R.LQHEM(15.994915)ELKAR.L	0	1270.6572	1.0	0.0	NA	635.837	0.99199	NA	NA	1	15	-0.117

- hTSCs

Fragment Ion View

Project name: 2224001
Sample name: 364_C_HPP_SCT_TamponLyse_Slot1_10_1_4751
Created date: 2022-06-16 16:12:07.0
Search name:
Activation type: CID

Peptide sequence: K.FMVYLQKENIIDESGMPK.E
Scan number: 97332
Calculated M+H: 2142.061
Measured M+H: 2142.0664
Charge state: 2
File name: ff00a868-2948-43ed-b802-aecc062f79f7_1655395920
search type: light

Protein: A0A087X0M5

Low Quality

Ions:
a ☐1+ ☐2+ ☐3+
b ☑1+ ☐2+ ☐3+
c ☐1+ ☐2+ ☐3+
x ☐1+ ☐2+ ☐3+
y ☑1+ ☐2+ ☐3+
z ☐1+ ☐2+ ☐3+
[Deselect All]

Neutral Loss:
☐ H_2O (o)
☐ NH_3 (*)
☐ H_3PO_4 (^)
☑ Precursor (#)
☐ Precursor with reduced charges

Mass Type:
◉Mono ○Avg

Mass Tol: 30
○Dalton ◉PPM

Update

Peak Assignment:
◉Most Intense
○Nearest Match
☐Peak Detect
☐Precursor Removal

Peak Labels:
◉Ion ○m/z
○None

Width: 750

Height: 450

Precursor Neutral Losses
1071.5322 [M+2H]

FMVYLQKENIIDESGMPK, MH+ 2142.0610, m/z 1071.5341
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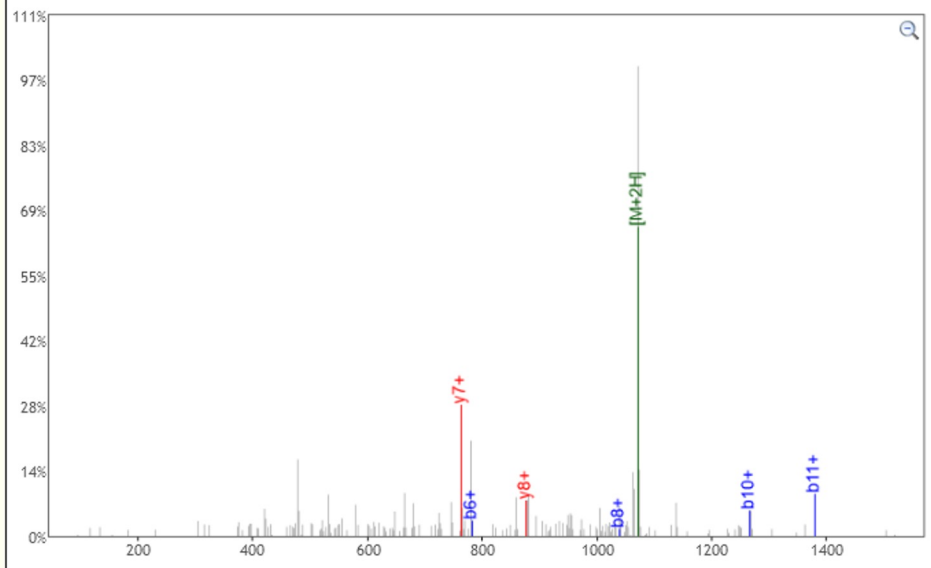

Click and drag in the plot to zoom X:☑ Y:☐ Zoom Out Print ☐Enable tooltip

b+	#	Seq	#	y+
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279.1162	2	M	17	1994.9926
378.1846	3	V	16	1863.9521
541.2479	4	Y	15	1764.8837
654.3320	5	L	14	1601.8203
782.3906	6	Q	13	1488.7363
910.4855	7	K	12	1360.6777
1039.5281	8	E	11	1232.5827
1153.5710	9	N	10	1103.5401
1266.6551	10	I	9	989.4972
1379.7392	11	I	8	876.4131
1494.7661	12	D	7	763.3291
1623.8087	13	E	6	648.3021
1710.8407	14	S	5	519.2595
1767.8622	15	G	4	432.2275
1898.9027	16	M	3	375.2061
1995.9554	17	P	2	244.1656
	18	K	1	147.1128

[Click] to move table

Static Modifications:
C: 57.02146

Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.FMVYLQKENIIDESGMPK.E	0	2142.06094	0.0	1.2034	0.0014	1071.5369	1.24594	1.2762	NA	6	25	41.772
2	K.PSMSPQAKIAQQIAANMADK(42.010565).D	0	2142.06818	0.6269	0.449	0.0081	1071.5369	1.24594	1.2655	NA	5	26	15.45
3	R.VDPWYQSNVNTLCPAIHK.L	0	2142.04367	0.7693	0.2776	0.2313	1071.5369	1.24594	1.2372	NA	3	24	9.471
4	R.(42.010565)DAIEELYLETQVDVHK(42.010565)R.G	0	2142.07129	0.8474	0.1836	0.0	1071.5369	1.24594	1.2984	NA	2	23	6.189

Fragment Ion View

Project name: 2224001
Sample name: 364_C_HPP_TSC_Trypsine_Slot1_12_1_4682
Created date: 2022-06-16 16:54:37.0
Search name:
Activation type: CID

Peptide sequence: K.ELSMK(42.010565)IYFS.-
Scan number: 151347
Calculated M+H: 1159.5703
Measured M+H: 1159.5876
Charge state: 1
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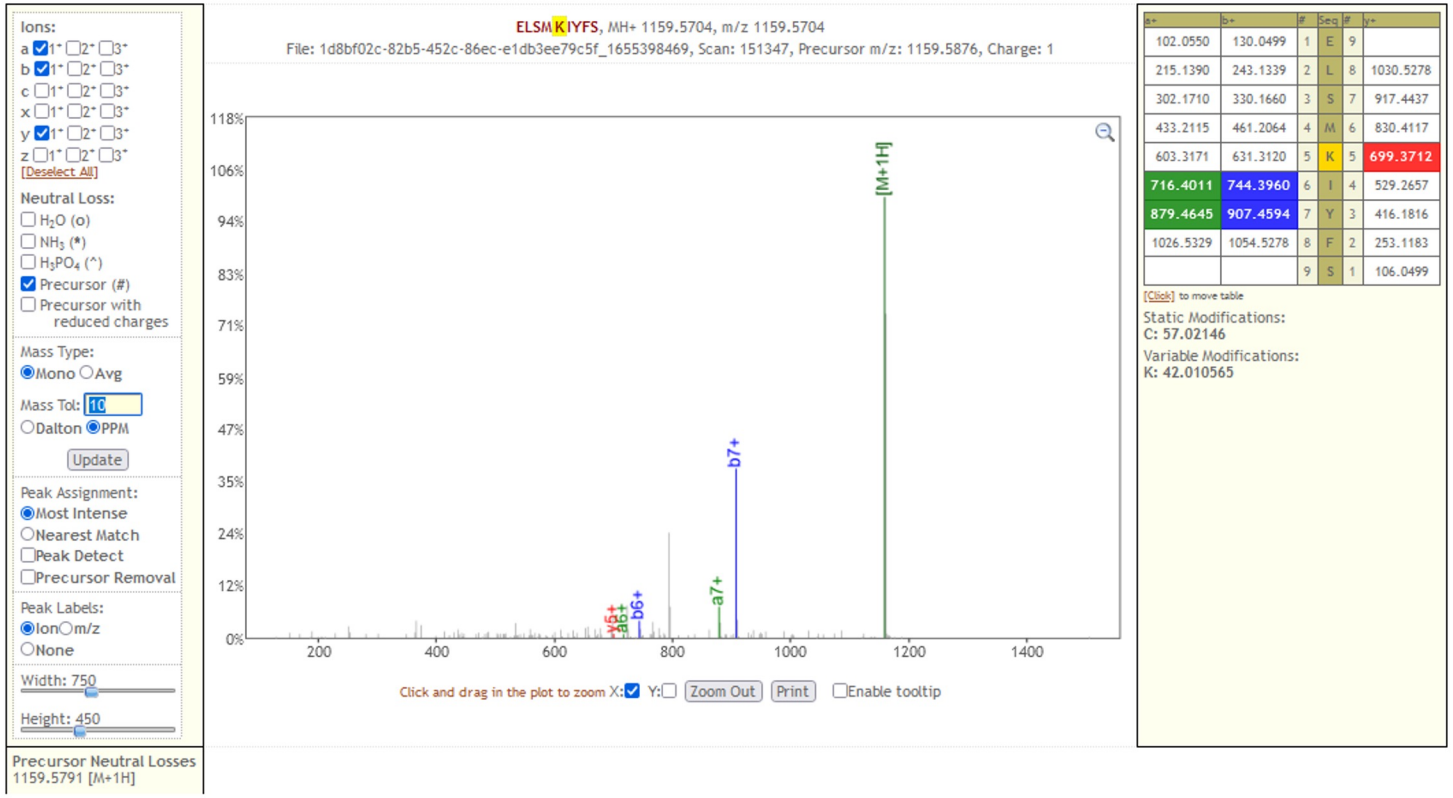
search type: light

Protein: Q8NGP6

Low Quality



Show FullScreen

Rank By Corer	Sequence	Rank By Sp	Calculated Mass	DeltaCN	XCorr	TIMScore	Measured m/z	Measured 1/K0	Predicted 1/K0	Corrected 1/K0	Matched Ions	Expected Ions	SP
1	K.ELSMK(42.010565)IYFS.-	0	1159.57035	0.0	0.7881	NA	1159.5876	1.40785	NA	NA	5	14	12.047
2	K.SNTSK(42.010565)PNTVK(42.010565).S	0	1159.59533	0.2788	0.5683	NA	1159.5876	1.40785	NA	NA	4	17	8.609
3	R.PLYDPDANVR.G	0	1159.5742	0.3794	0.4891	NA	1159.5876	1.40785	NA	NA	6	17	7.369
4	R.PISKCQAEAR.R	0	1159.5888	0.4162	0.46	NA	1159.5876	1.40785	NA	NA	6	17	6.914