

Quantitative Persulfide Side Identification (qPerS-SID) Reveals Protein Targets of H₂S Releasing Donors in Mammalian Cells

Sebastian Longen*^{§1}, Florian Richter*², Yvette Köhler¹, Ilka Wittig², Karl-Friedrich Beck¹ and Josef Pfeilschifter¹

SUPPLEMENTARY INFORMATION

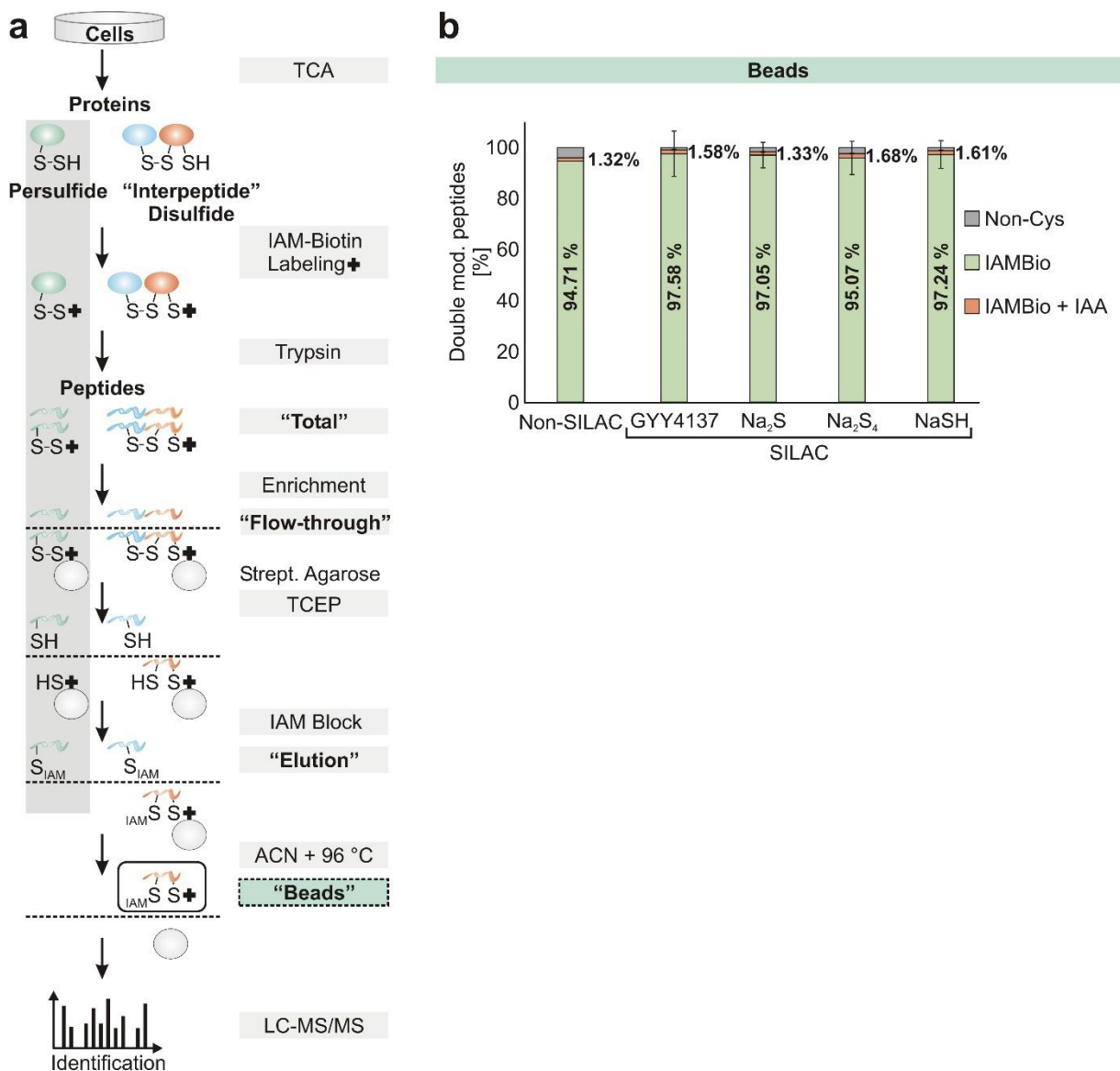


Fig S1: Evaluation of possible false positive persulfides. a) Scheme showing a special case, which might lead to the detection of false positive peptides. After digestion, two peptides connected by a disulfide bond might occur (“interpeptide disulfide”; orange and blue peptide). If in addition one of

these peptides contains at least an additional cysteine previously labelled with IAMBio (orange peptide, +), this interconnected peptide would be susceptible to TCEP treatment resulting in an elution of a non-persulfide peptide and thus, resulting in detection of a false positive peptide (blue peptide). As an indirect marker of such a case, peptides with at least two cysteines that contain both an IAMBio and IAM label can be measured in the beads fraction. **b)** Mean values of double modified peptides in the beads fraction of the experiment as described in Fig 1 (Non-SILAC, two independent experiments) and as described in Fig 2 using the H₂S donors GYY4137, Na₂S, NASH and Na₂S₄ (SILAC, four independent experiments). Error bars indicate the standard deviation in the SILAC samples. IAMBio: iodoacetyl-PEG2-Biotin; IAM: iodoacetamide. Note that the actual value of false positive peptides might be lower because the double labelling can also appear when a persulfide or another reversible thiol oxidation is present instead of an “interpeptide disulfide bond”.

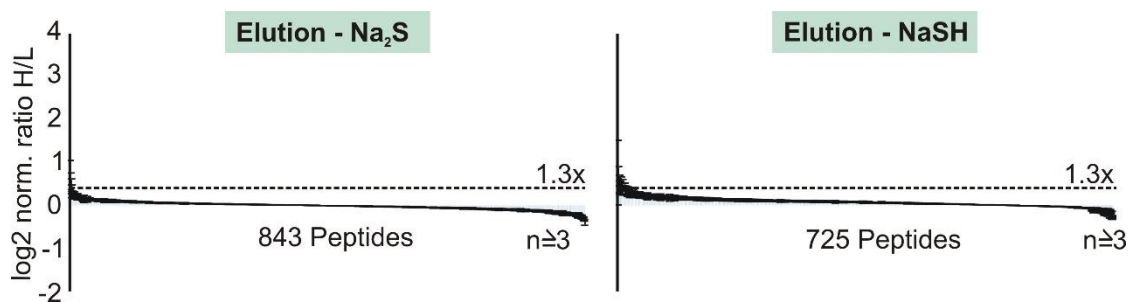


Fig S2: Quantitative changes of persulfides after treatment with 200 μ M NaSH and Na₂S. The experiment was performed as described in Fig 2A, except that NaSH and Na₂S were used instead of GYY4137 and Na₂S₄. The experiment was done four times (two times forward, two times reversed) and the mean values and error bars of peptides appearing in at least 3 of 4 experiments are plotted as the log₂ value. For normalisation the median of the heavy to light ratio (H/L) of non-cysteine peptides in the total fraction were used and multiplied with the measured H/L ratios. Dashed line: threshold of peptides that were at least 30 % induced (1.3x). The cells were grown in heavy or light SILAC medium allowing the quantification of induced persulfides.

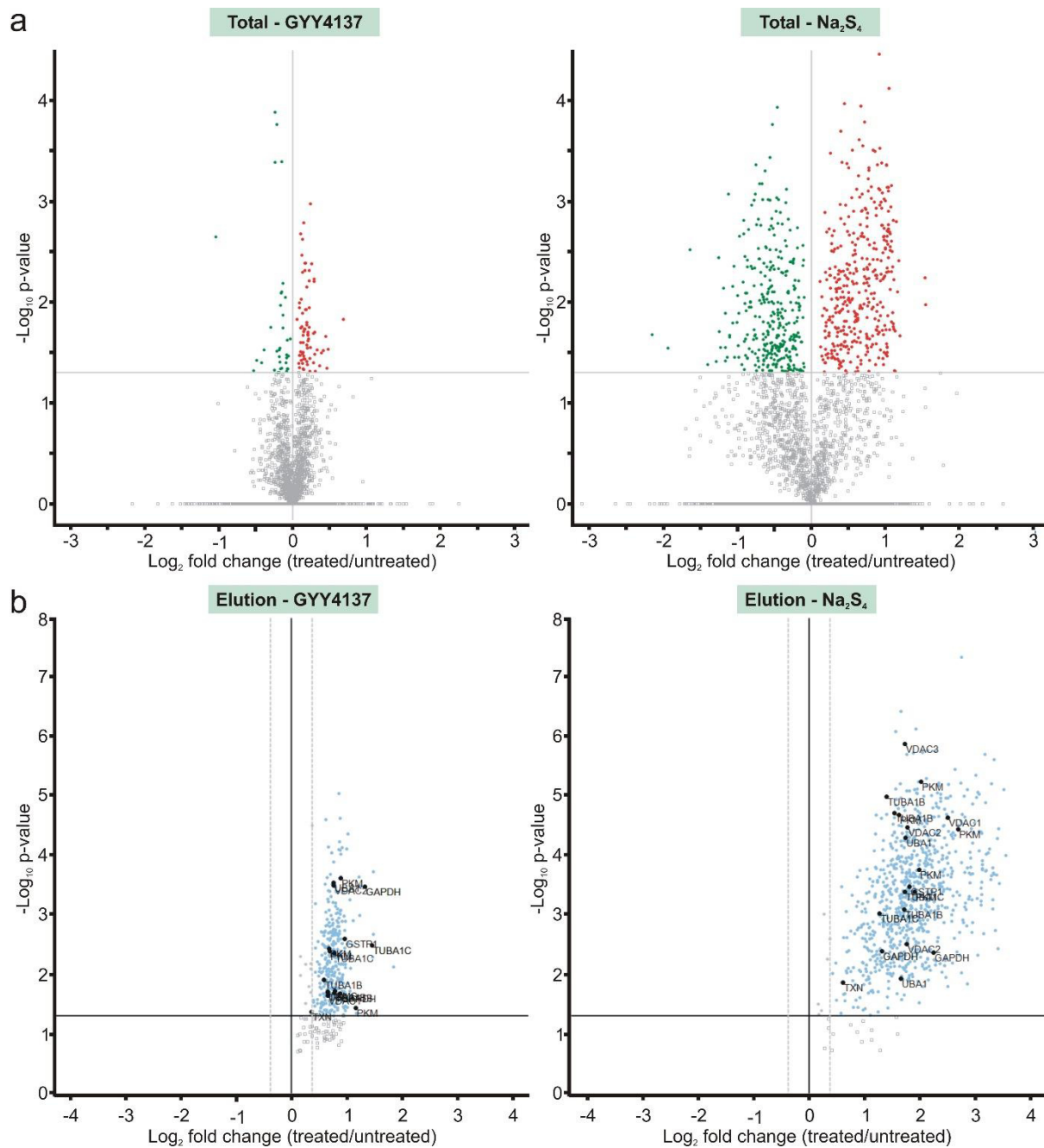


Fig S3: Statistical evaluation of the peptides identified in the total and elution fraction of GYY4137 and Na₂S₄ treated cells. One sample students *t*-test of the log₂-normalised ratios containing all peptides identified in the total fraction excluding cysteine containing peptides (a) and the TCEP elution fraction (b). The -log₁₀ p-values were plotted against the log₂ mean treated/untreated ratio. Red/green dots: Peptides significantly changed in the total fraction; blue: Peptides in samples of the elution fraction identified in at least 3 of 4 experiments and significantly enriched at least 1.3 fold; grey dashed line: log₂ change of +/- 1.3; black: Peptides/proteins that were further discussed in the

paper. Note that the significant peptides in volcano plots of the elution fraction have a clear orientation to the right side because this fraction is highly enriched by our qPerS-SID strategy.

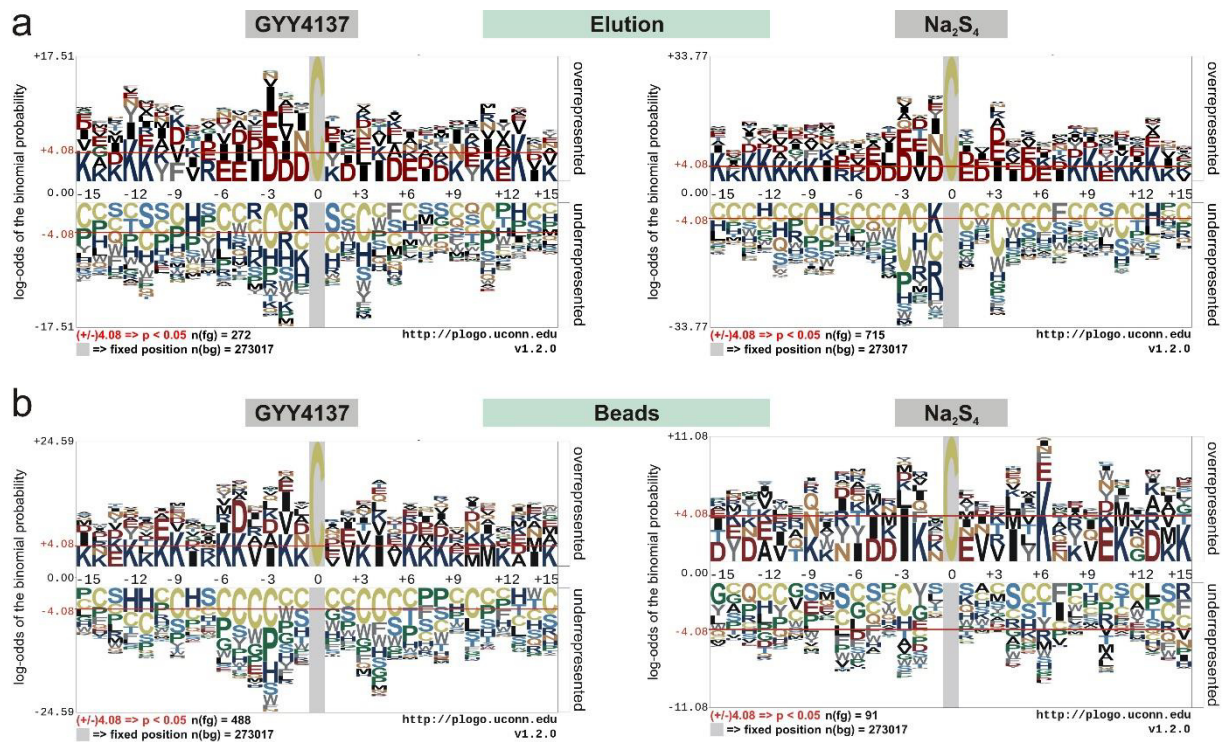


Fig S4: Amino acid enrichment analysis of persulfide containing peptides induced by GYY4137 and Na₂S₄. **a)** pLogo²⁴ analysis of enriched amino acids 15 positions before or after the reactive cysteine. Red: negative charged amino acids, blue: positive charged amino acids, black: hydrophobic amino acids. **b)** pLogo analysis of enriched amino acids 15 positions before or after cysteines not affected by H₂S stimulation found at the beads fraction. Red: negative charged amino acids, blue: positive charged amino acids, black: hydrophobic amino acids.

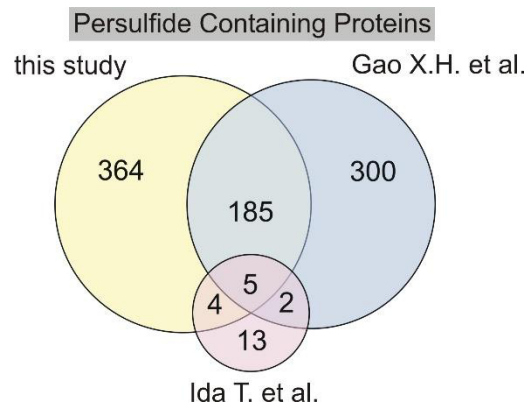
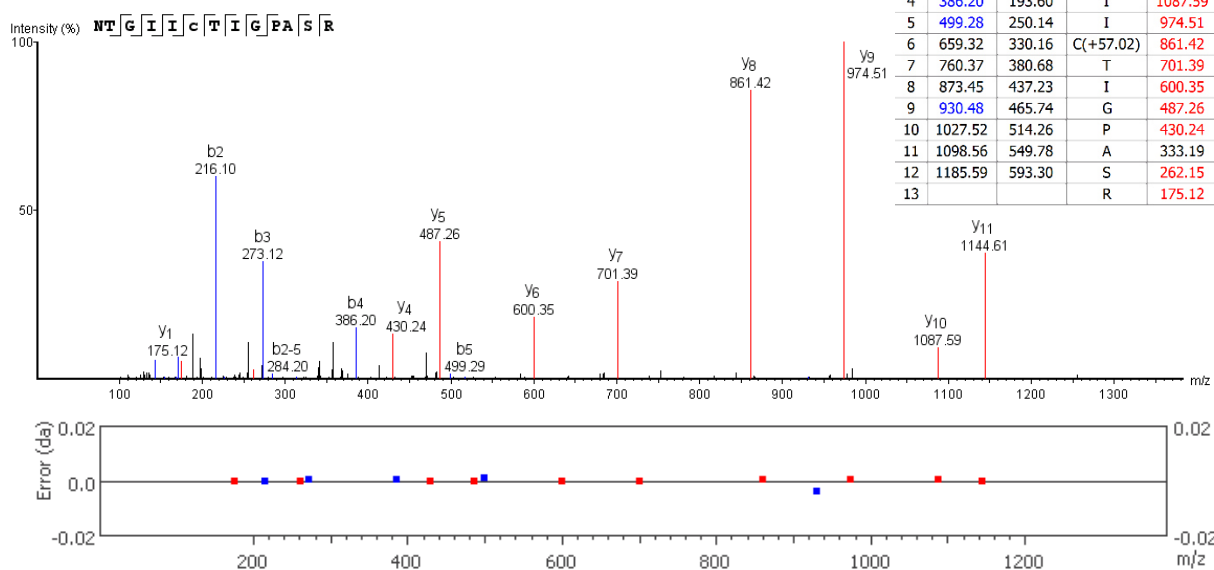


Fig S5: Comparison of different persulfide proteomes. Venn diagram comparing proteins that form persulfides identified to by our approach, a similar strategy invented by Gao X.H. et al. and the tag-switch method applied by Ida T. et al. Note that for the study of Gao X.H. et al. and our study proteins were considered forming persulfides, if the respective peptides were enriched 1.3 fold or more.

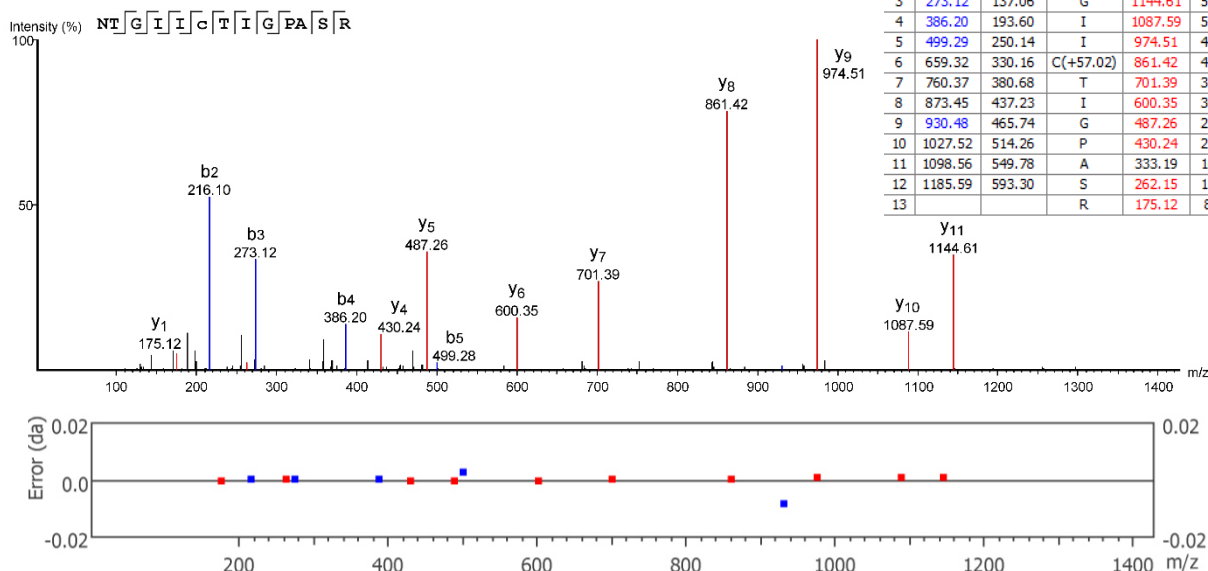
[Fig S6 a] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, GYY4137)

NTGIIC⁴⁹(+57.02)TIGPASR



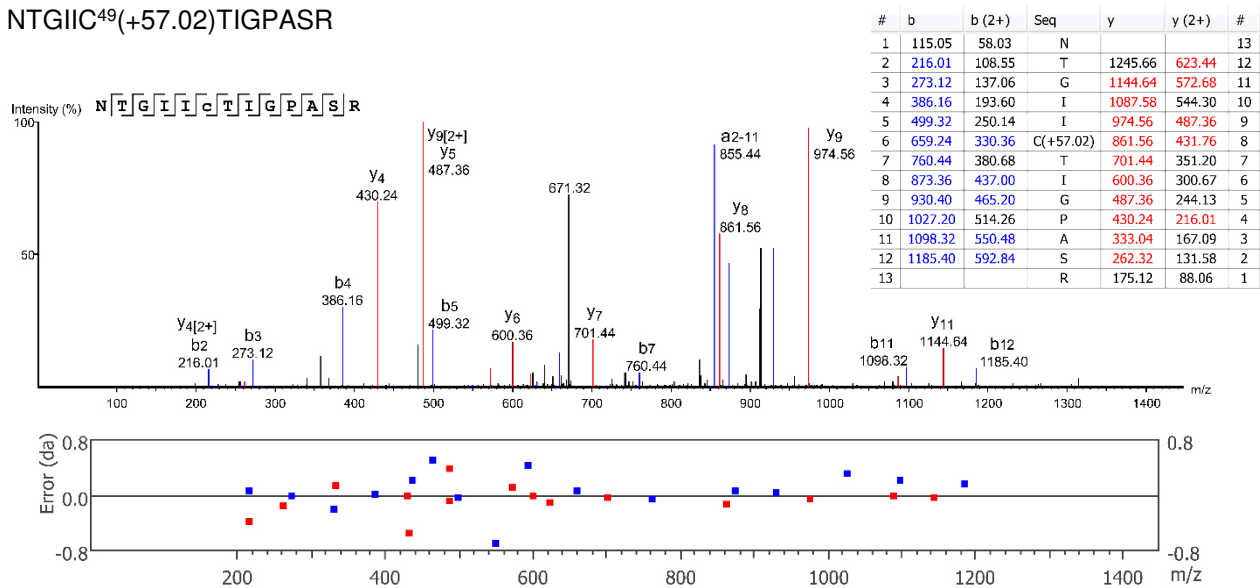
[Fig S6 b] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, Na₂S₄)

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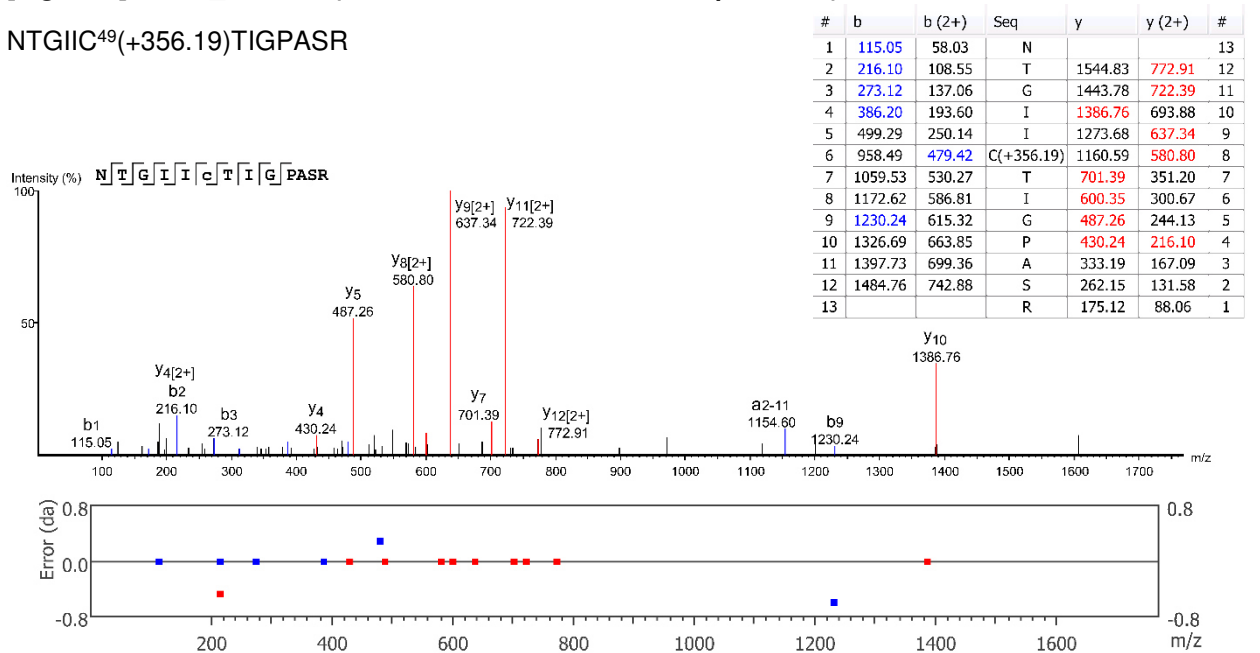
[Fig S6 c] PKM2_RABBIT (Carbamidomethyl, TCEP Elution, 500 μ M Na₂S₄)

NTGIIC⁴⁹(+57.02)TIGPASR



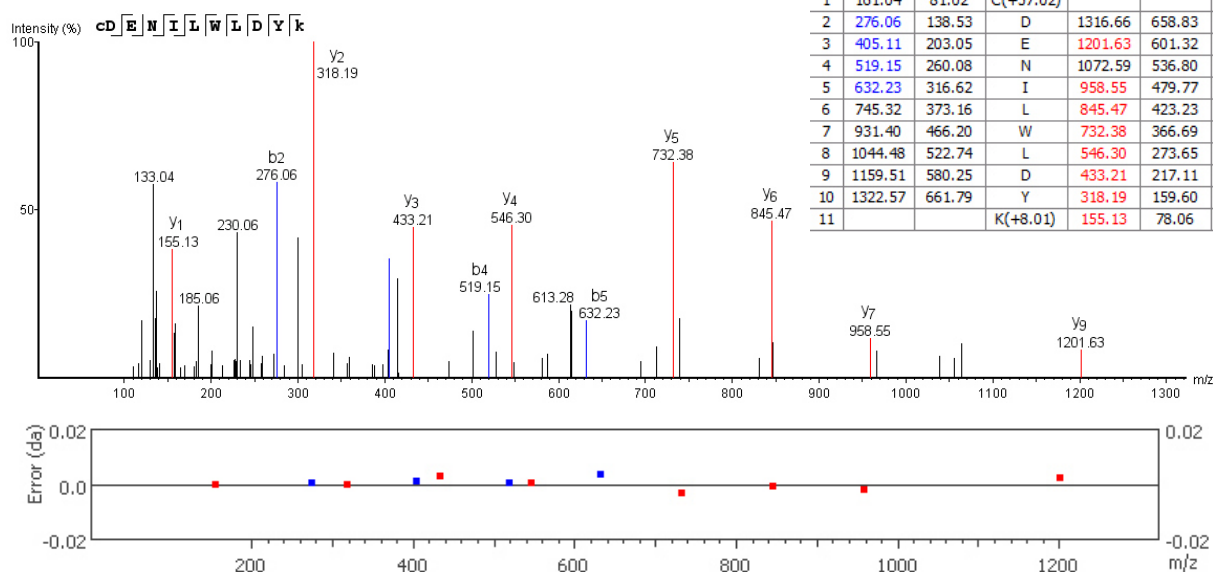
[Fig S6 d] PKM2_RABBIT (S-iodoTMT, TMT-Elution, 500 μ M Na₂S₄)

NTGIIC⁴⁹(+356.19)TIGPASR



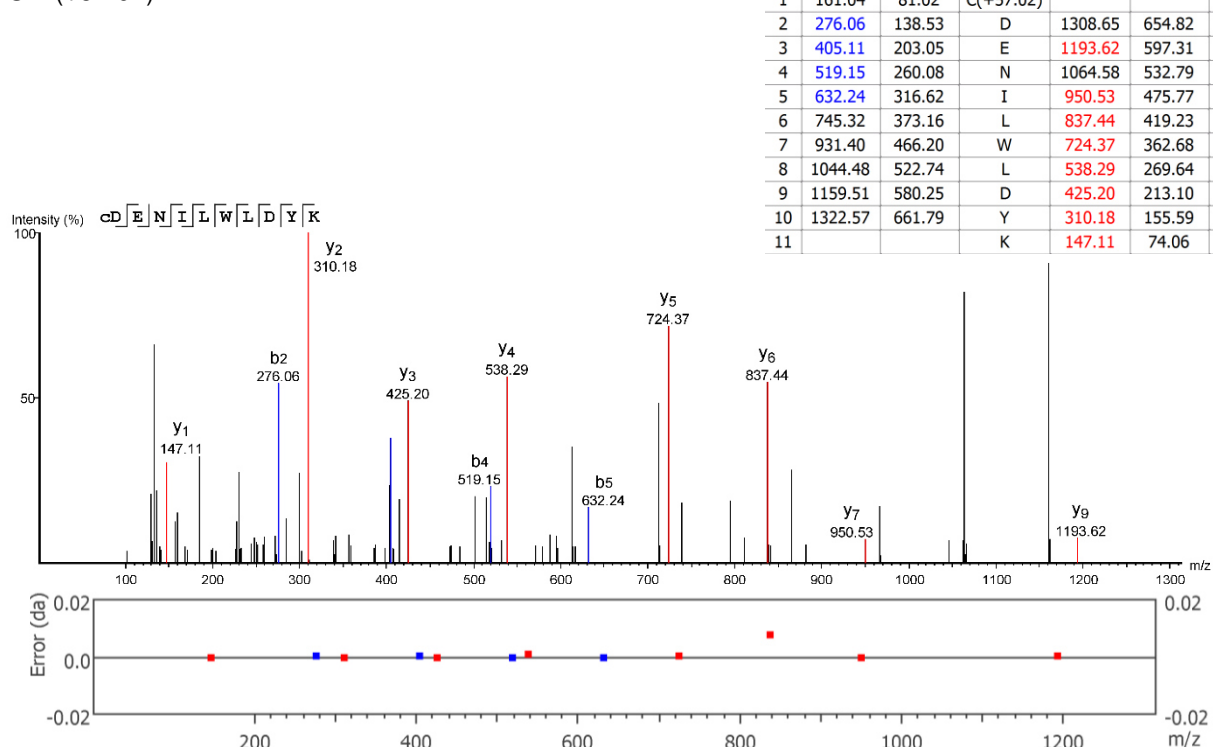
[Fig S6 e] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, GYY4137)

C¹⁵²(+57.02)DENILWL^YDK



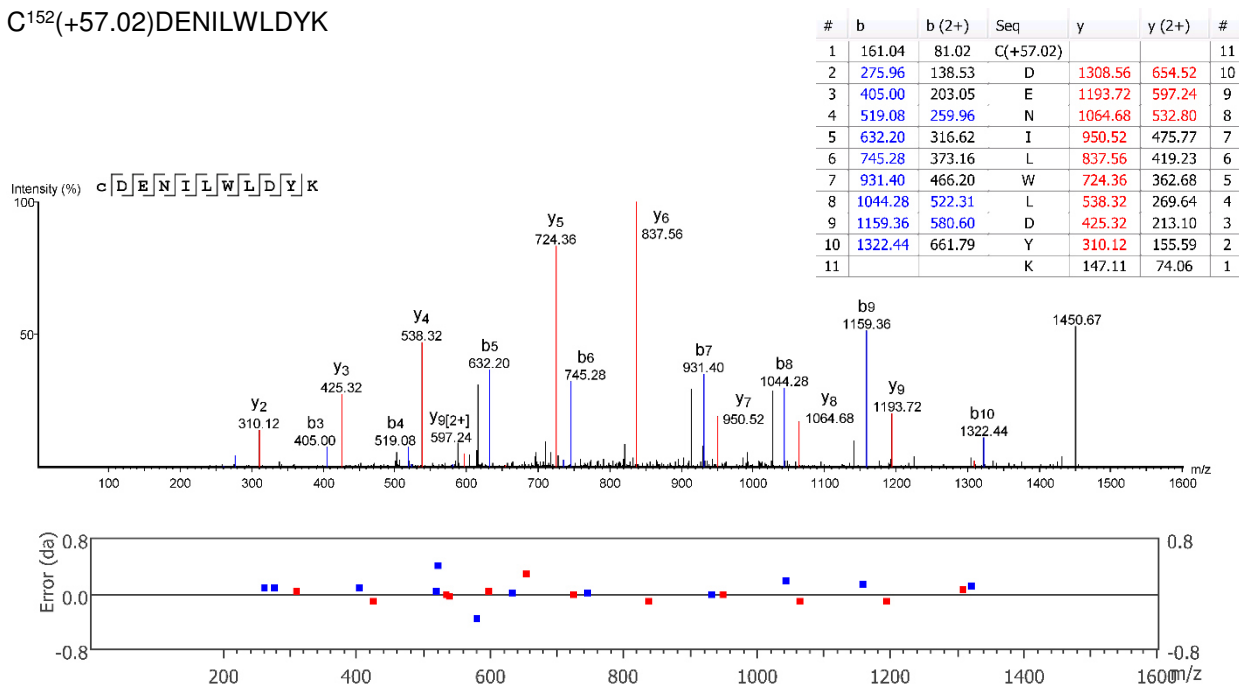
[Fig S6 f] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, Na₂S₄)

C¹⁵²(+57.02)DENILWL^YDK



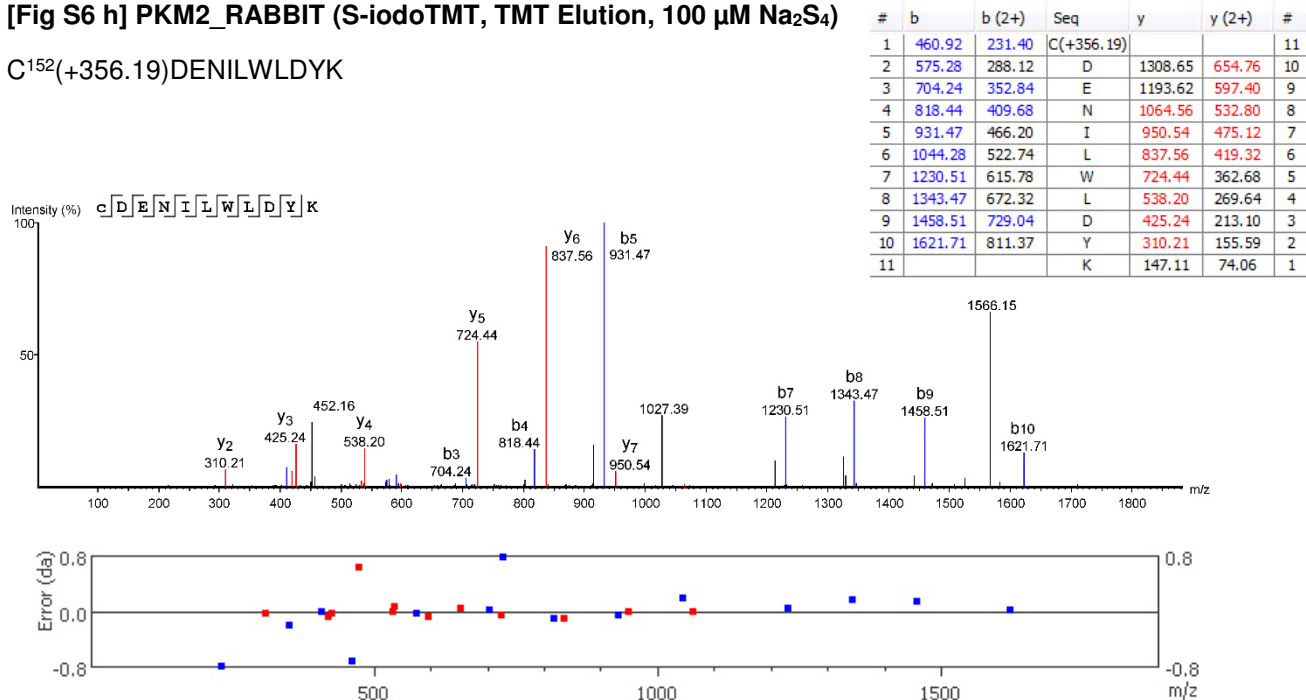
[Fig S6 g] PKM2_RABBIT (Carbamidomethyl, TCEP Elution, 500 μ M Na₂S₄)

C¹⁵²(+57.02)DENILWLDYK



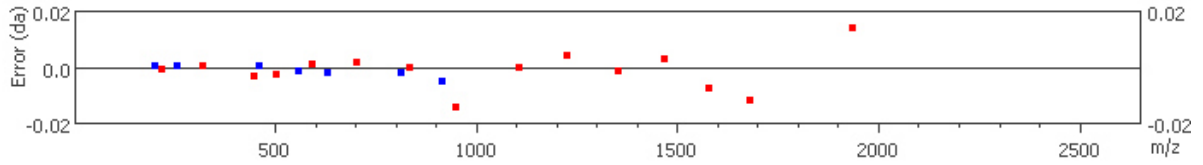
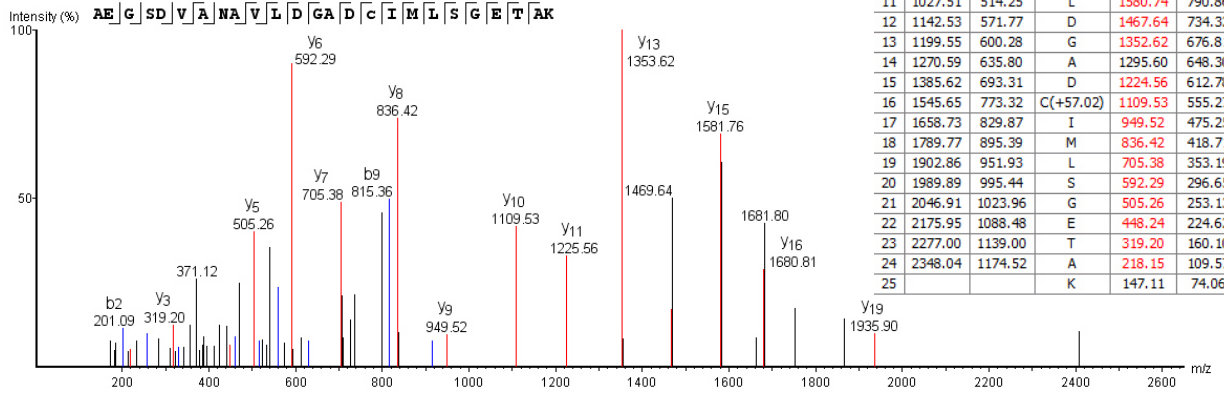
[Fig S6 h] PKM2_RABBIT (S-iodoTMT, TMT Elution, 100 μ M Na₂S₄)

C¹⁵²(+356.19)DENILWLDYK



[Fig S6 i] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, GYY4137)

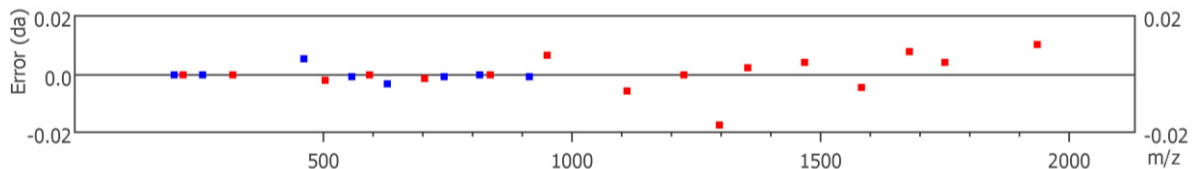
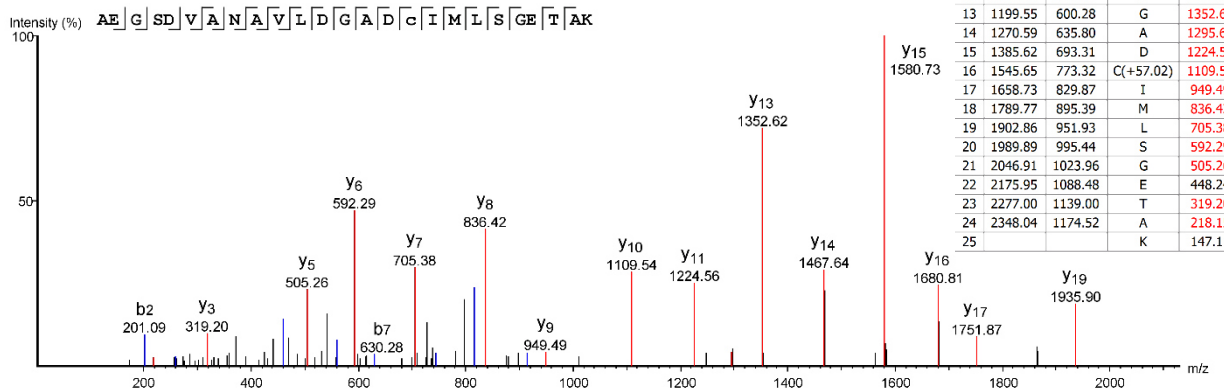
AEGSDVANAVLDGADC³⁵⁸(+57.02)IMLSGETAK



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2	201.09	101.04	E	2423.11	1212.05	24
3	258.11	129.55	G	2294.06	1147.53	23
4	345.14	173.07	S	2237.04	1119.02	22
5	460.17	230.58	D	2150.01	1075.51	21
6	559.24	280.12	V	2034.98	1017.99	20
7	630.28	315.64	A	1935.90	968.46	19
8	744.32	372.66	N	1864.88	932.94	18
9	815.36	408.18	A	1750.83	875.92	17
10	914.43	457.71	V	1679.81	840.40	16
11	1027.51	514.25	L	1580.74	790.86	15
12	1142.53	571.77	D	1467.64	734.32	14
13	1199.55	600.28	G	1352.62	676.81	13
14	1270.59	635.80	A	1295.60	648.30	12
15	1385.62	693.31	D	1224.56	612.78	11
16	1545.65	773.32	C(+57.02)	1109.53	555.27	10
17	1658.73	829.87	I	949.52	475.25	9
18	1789.77	895.39	M	836.42	418.71	8
19	1902.86	951.93	L	705.38	353.19	7
20	1989.89	995.44	S	592.29	296.65	6
21	2046.91	1023.96	G	505.26	253.13	5
22	2175.95	1088.48	E	448.24	224.62	4
23	2277.00	1139.00	T	319.20	160.10	3
24	2348.04	1174.52	A	218.15	109.57	2
25			K	147.11	74.06	1

[Fig S6 j] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, Na₂S₄)

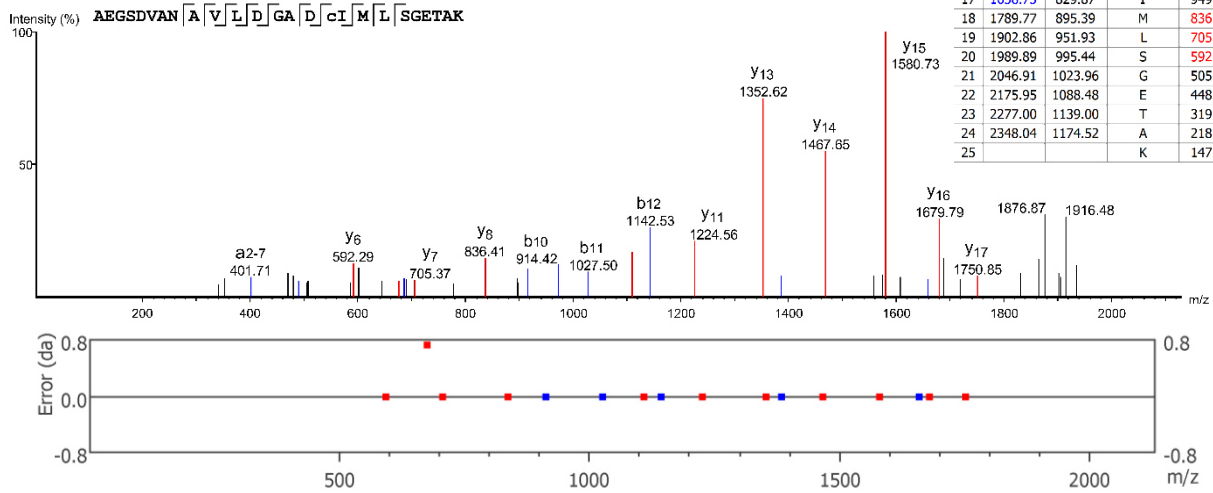
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2	201.09	101.04	E	2423.11	1212.05	24
3	258.11	129.55	G	2294.06	1147.53	23
4	345.14	173.07	S	2237.04	1119.02	22
5	460.16	230.58	D	2150.01	1075.51	21
6	559.24	280.12	V	2034.98	1017.99	20
7	630.28	315.64	A	1935.90	968.46	19
8	744.32	372.66	N	1864.88	932.94	18
9	815.35	408.18	A	1750.83	875.92	17
10	914.42	457.71	V	1679.79	840.40	16
11	1027.51	514.25	L	1580.73	790.86	15
12	1142.53	571.77	D	1467.64	734.32	14
13	1199.55	600.28	G	1352.62	676.81	13
14	1270.59	635.80	A	1295.61	648.30	12
15	1385.62	693.31	D	1224.56	612.78	11
16	1545.65	773.32	C(+57.02)	1109.54	555.27	10
17	1658.73	829.87	I	949.49	475.25	9
18	1789.77	895.39	M	836.42	418.71	8
19	1902.86	951.93	L	705.38	353.19	7
20	1989.89	995.44	S	592.29	296.65	6
21	2046.91	1023.96	G	505.26	253.13	5
22	2175.95	1088.48	E	448.24	224.62	4
23	2277.00	1139.00	T	319.20	160.10	3
24	2348.04	1174.52	A	218.15	109.57	2
25			K	147.11	74.06	1

[Fig S6 k] PKM2_RABBIT (Carbamidomethyl, TCEP Elution, 500 μ M Na₂S₄)

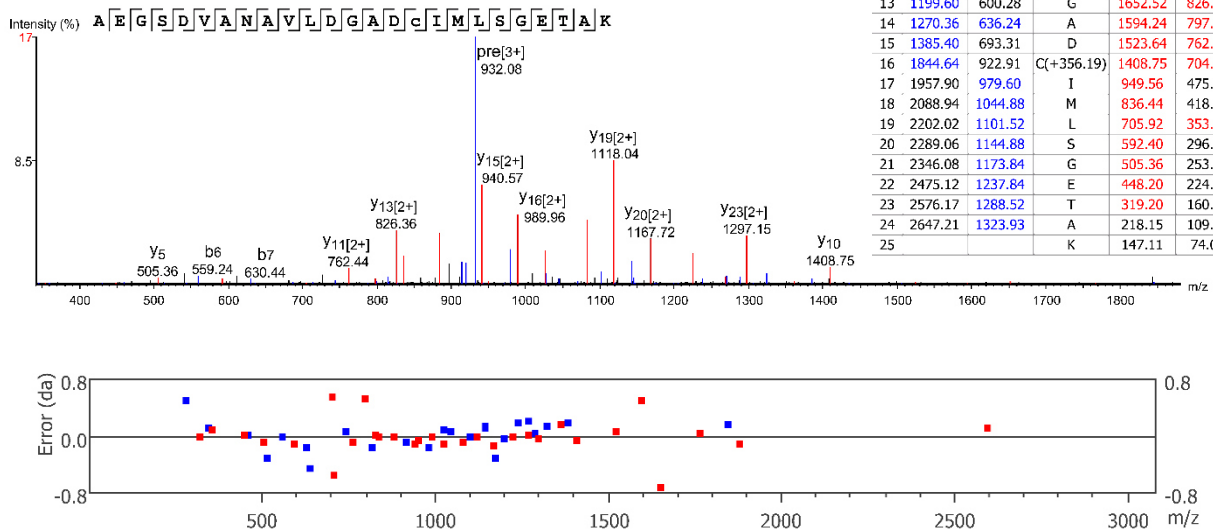
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2	201.09	101.04	E	2423.11	1212.05	24
3	258.11	129.55	G	2294.06	1147.53	23
4	345.14	173.07	S	2237.04	1119.02	22
5	460.17	230.58	D	2150.01	1075.51	21
6	559.24	280.12	V	2034.98	1017.99	20
7	630.27	315.64	A	1935.92	968.46	19
8	744.32	372.66	N	1864.88	932.94	18
9	815.35	408.18	A	1750.85	875.92	17
10	914.42	457.71	V	1679.79	840.40	16
11	1027.50	514.25	L	1580.73	790.86	15
12	1142.53	571.77	D	1467.65	734.32	14
13	1199.55	600.28	G	1352.62	676.05	13
14	1270.59	635.80	A	1295.60	648.30	12
15	1385.62	693.31	D	1224.56	612.78	11
16	1545.65	773.32	C(+57.02)	1109.53	555.27	10
17	1658.73	829.87	I	949.50	475.25	9
18	1789.77	895.39	M	836.41	418.71	8
19	1902.86	951.93	L	705.37	353.19	7
20	1989.89	995.44	S	592.29	296.65	6
21	2046.91	1023.96	G	505.26	253.13	5
22	2175.95	1088.48	E	448.24	224.62	4
23	2277.00	1139.00	T	319.20	160.10	3
24	2348.04	1174.52	A	218.15	109.57	2
25			K	147.11	74.06	1

[Fig S6 l] PKM2_RABBIT (S-iodoTMT, TMT Elution, 100 μ M Na₂S₄)

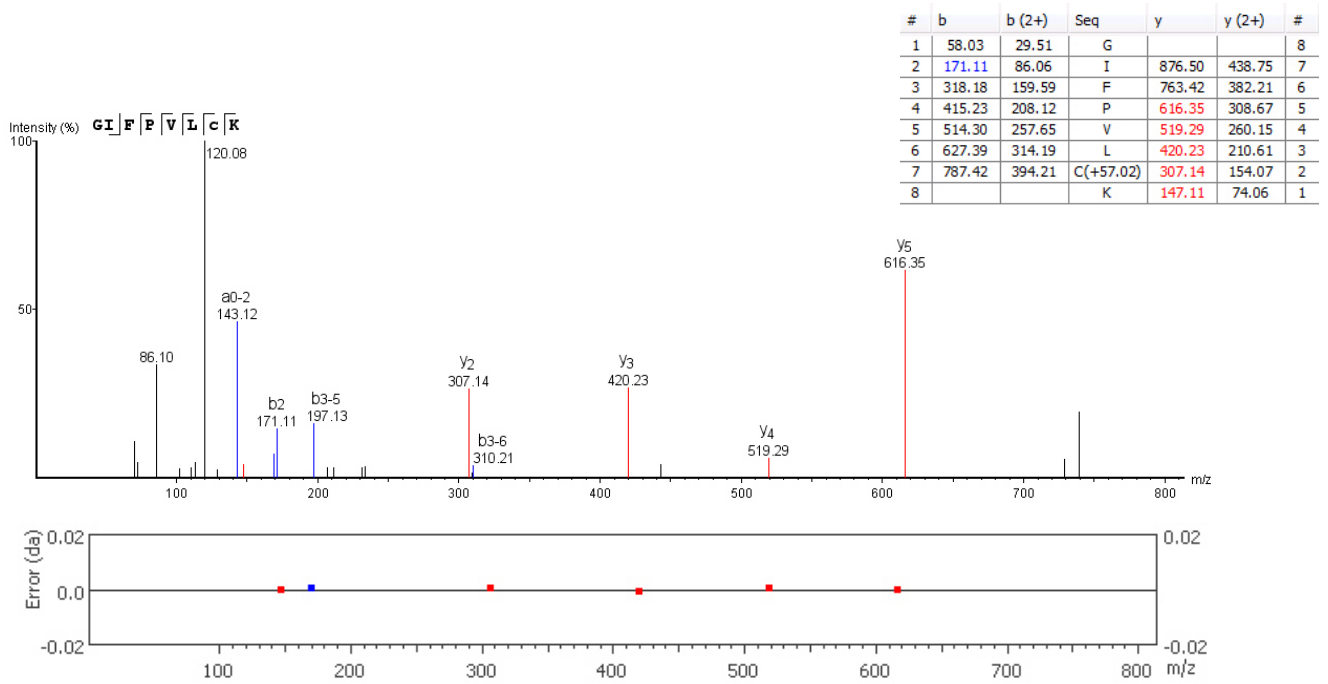
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3	258.11	129.55	G	2593.11	1297.15	23
4	345.00	173.07	S	2536.21	1268.56	22
5	460.12	230.58	D	2449.18	1225.08	21
6	559.24	279.60	V	2334.15	1167.72	20
7	630.44	315.64	A	2235.08	1118.04	19
8	744.24	372.66	N	2164.04	1082.60	18
9	815.52	408.18	A	2050.00	1025.60	17
10	914.52	457.71	V	1978.96	989.96	16
11	1027.40	514.56	L	1880.00	940.57	15
12	1142.40	571.77	D	1766.76	883.92	14
13	1199.60	600.28	G	1652.52	826.36	13
14	1270.36	636.24	A	1594.24	797.32	12
15	1385.40	693.31	D	1523.64	762.44	11
16	1844.64	922.91	C(+356.19)	1408.75	704.28	10
17	1957.90	979.60	I	949.56	475.25	9
18	2088.94	1044.88	M	836.44	418.71	8
19	2202.02	1101.52	L	705.92	353.08	7
20	2289.06	1144.88	S	592.40	296.65	6
21	2346.08	1173.84	G	505.36	253.13	5
22	2475.12	1237.84	E	448.20	224.62	4
23	2576.17	1288.52	T	319.20	160.10	3
24	2647.21	1323.93	A	218.15	109.57	2
25			K	147.11	74.06	1

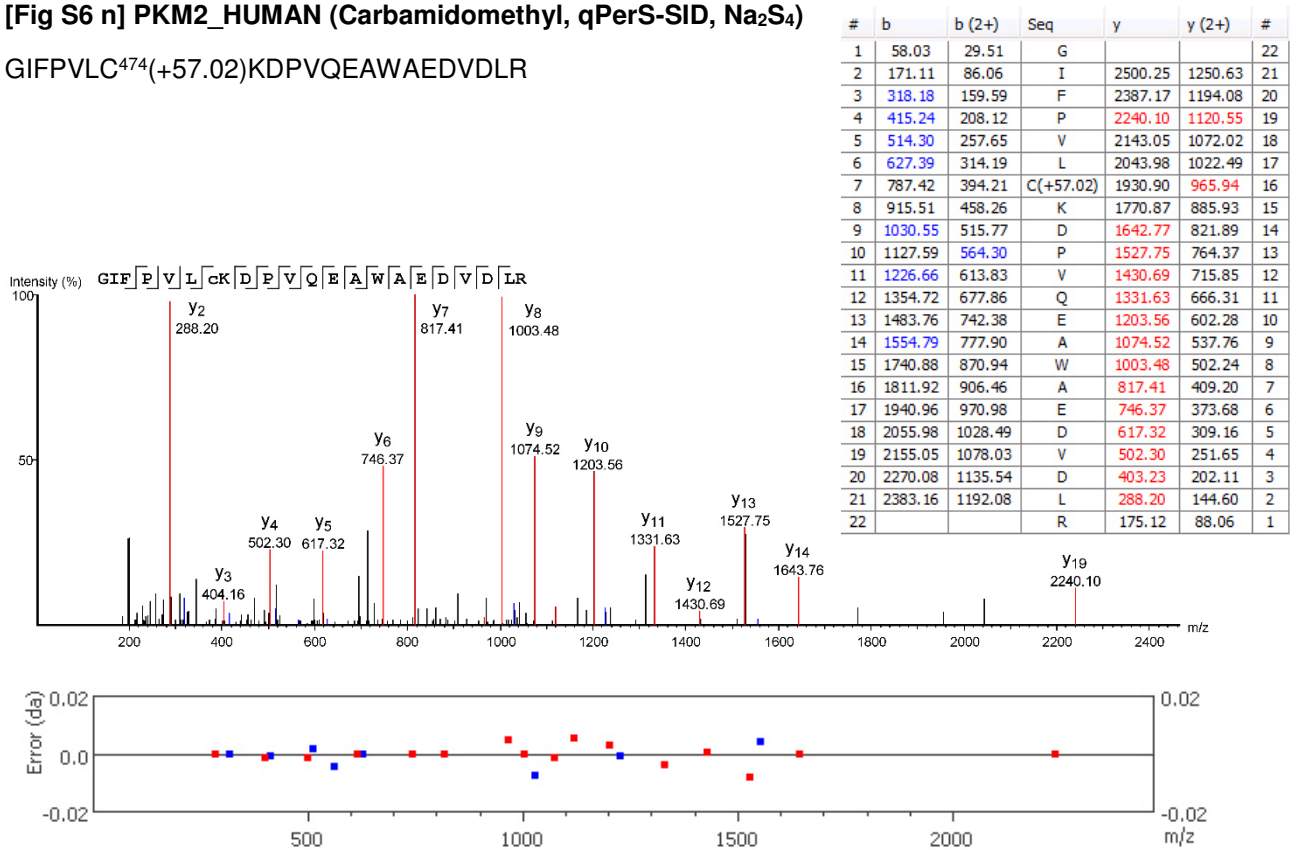
[Fig S6 m] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, GYY4137)

GIFPVL⁴⁷⁴(+57.02)K



[Fig S6 n] PKM2_HUMAN (Carbamidomethyl, qPerS-SID, Na₂S₄)

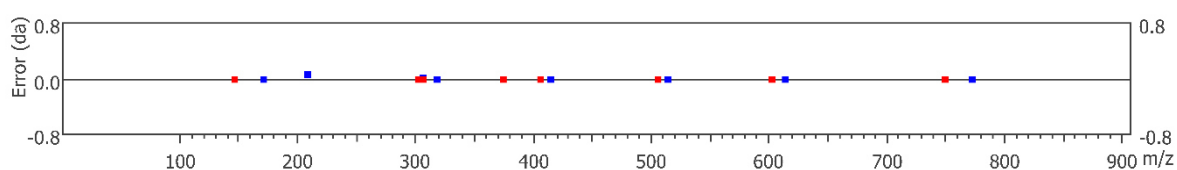
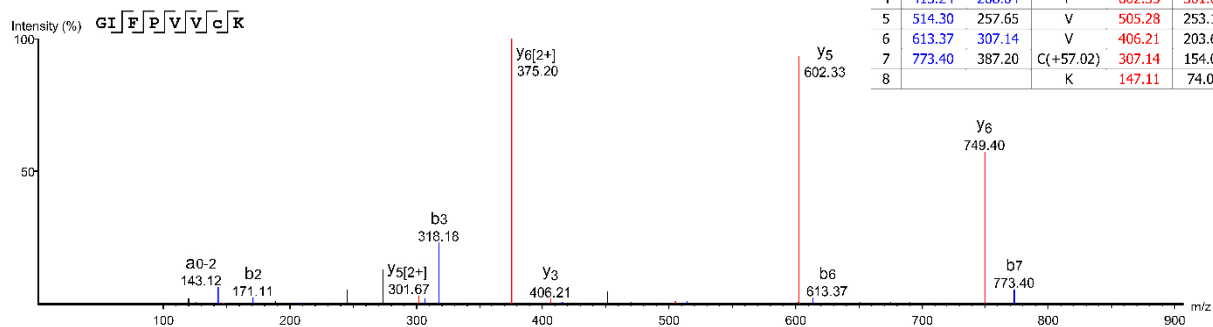
GIFPVL⁴⁷⁴(+57.02)KDPVQEAWAEDVDLR



[Fig S6 o] PKM2_RABBIT (Carbamidomethyl, TCEP Elution, 500 μ M Na₂S₄)

GIFPVVC⁴⁷⁴(+57.02)K

#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			8
2	171.11	86.06	I	862.49	431.74	7
3	318.18	159.59	F	749.40	375.20	6
4	415.24	208.04	P	602.33	301.67	5
5	514.30	257.65	V	505.28	253.14	4
6	613.37	307.14	V	406.21	203.61	3
7	773.40	387.20	C(+57.02)	307.14	154.07	2
8			K	147.11	74.06	1



[Fig S6 p] PKM2_RABBIT (S-iodoTMT, TMT Elution, 100 μ M Na₂S₄)

GIFPVVC⁴⁷⁴(+356.19)K

#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			8
2	171.11	86.06	I	1161.65	581.33	7
3	318.18	159.59	F	1048.56	524.71	6
4	415.27	208.12	P	901.49	451.25	5
5	514.30	257.66	V	804.45	402.86	4
6	613.37	307.19	V	705.38	353.19	3
7	1072.57	536.78	C(+356.19)	606.31	303.66	2
8			K	147.11	74.06	1

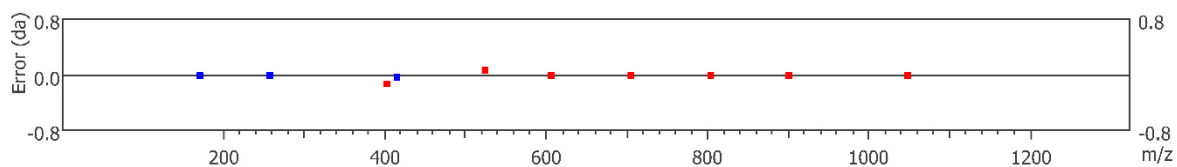
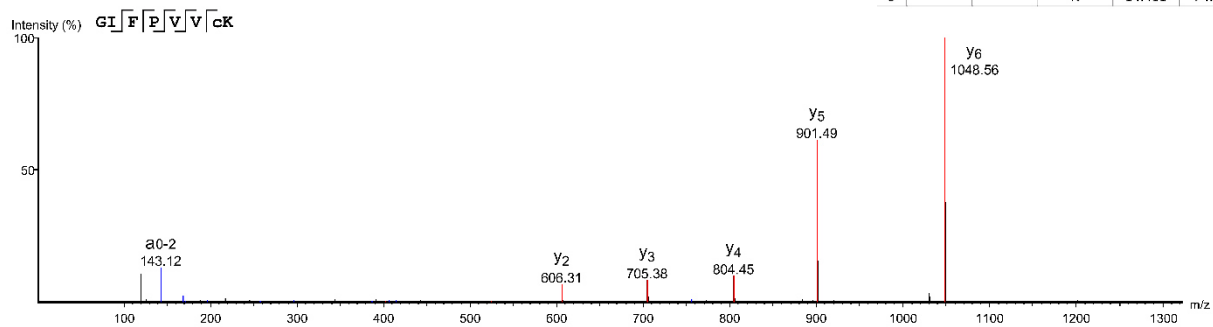


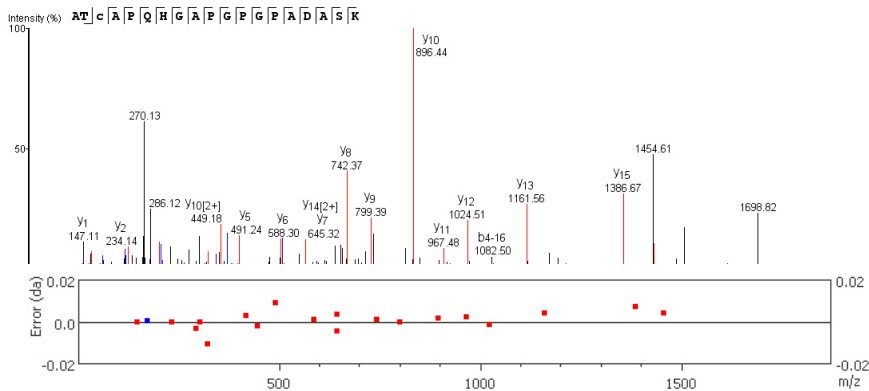
Fig S6: MS spectra of PKM2 persulfide peptides. a-p) The MS/MS fragment ions of the four identified PKM2 persulfide peptides identified in the proteomic approach (qPerS-SID, +57.02 Da) and rabbit PKM2 in the in vitro experiment (TCEP elution +57.02 Da, TMT elution +356.19 Da) are depicted in red and blue, respectively. The inset shows the sequence coverage of the peptides by b, b²⁺, y and y²⁺ ions. Lower panels indicate the mass error.

Supplementary Figure S7

[S7.1] FilaminA

ATC(+446.17)APQHGAPGPGPADASK

m/z=727.0016 z=3

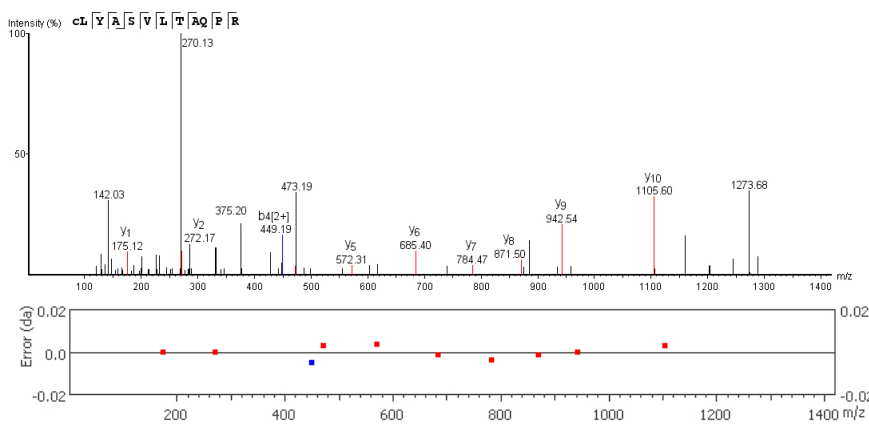


#	b	b (2+)	Seq	y	y (2+)	#
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3	722.27	361.63	C(+446.17)	2006.89	1003.94	17
4	793.30	397.15	A	1457.71	729.36	16
5	890.36	445.68	P	1386.67	693.84	15
6	1018.42	509.71	Q	1289.62	645.32	14
7	1155.47	578.24	H	1161.56	581.28	13
8	1212.50	606.75	G	1024.51	512.75	12
9	1283.53	642.27	A	967.48	484.24	11
10	1380.59	690.79	P	896.44	448.73	10
11	1437.61	719.30	G	799.39	400.20	9
12	1534.66	767.83	P	742.37	371.69	8
13	1591.68	796.34	G	645.32	323.17	7
14	1688.73	844.87	P	588.30	294.65	6
15	1759.77	880.39	A	491.24	246.12	5
16	1874.80	937.90	D	420.21	210.60	4
17	1945.84	973.42	A	305.18	153.09	3
18	2032.87	1016.93	S	234.14	117.57	2
19			K	147.11	74.06	1

[S7.2] ElongationFactor2

C(+446.17)LYASVLTAQPR

m/z=884.4415 z=2

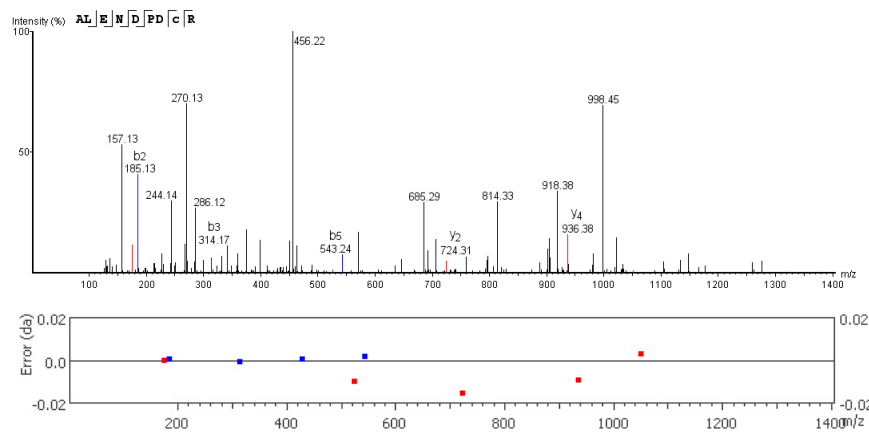


#	b	b (2+)	Seq	y	y (2+)	#
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2	663.27	332.13	L	1218.68	609.84	11
3	826.33	413.67	Y	1105.60	553.30	10
4	897.37	449.19	A	942.54	471.77	9
5	984.40	492.70	S	871.50	436.25	8
6	1083.47	542.23	V	784.47	392.73	7
7	1196.55	598.78	L	685.40	343.20	6
8	1297.60	649.30	T	572.31	286.66	5
9	1368.64	684.82	A	471.26	236.13	4
10	1496.70	748.85	Q	400.23	200.62	3
11	1593.75	797.37	P	272.17	136.59	2
12			R	175.12	88.06	1

[S7.3] Plastin-3

ALENDPDC(+446.17)R

m/z=739.8156 z=2



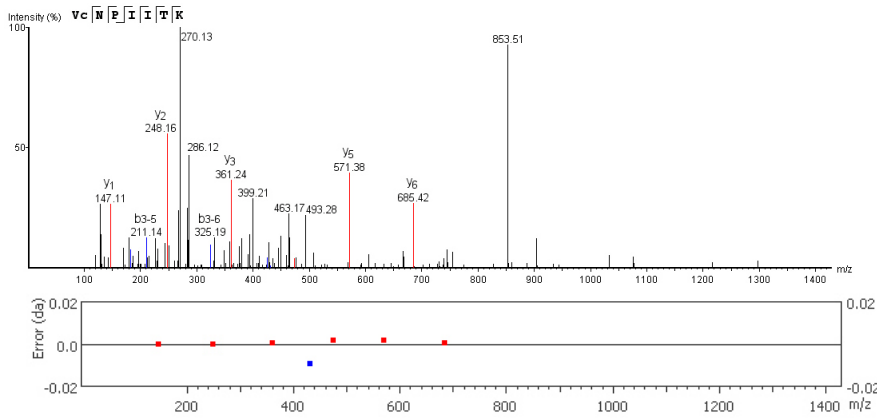
#	b	b (2+)	Seq	y	y (2+)	#
1	72.04	36.52	A			9
2	185.13	93.06	L	1407.57	704.29	8
3	314.17	157.59	E	1294.49	647.74	7
4	428.21	214.61	N	1165.44	583.22	6
5	543.24	272.12	D	1051.40	526.21	5
6	640.29	320.65	P	936.38	468.69	4
7	755.32	378.16	D	839.32	420.16	3
8	1304.50	652.75	C(+446.17)	724.31	362.65	2
9			R	175.12	88.06	1

Supplementary Figure S7

[S7.4] Heat shock cognate 71 kDa protein

VC(+446.17)NPIITK

m/z=667.3468 z=2

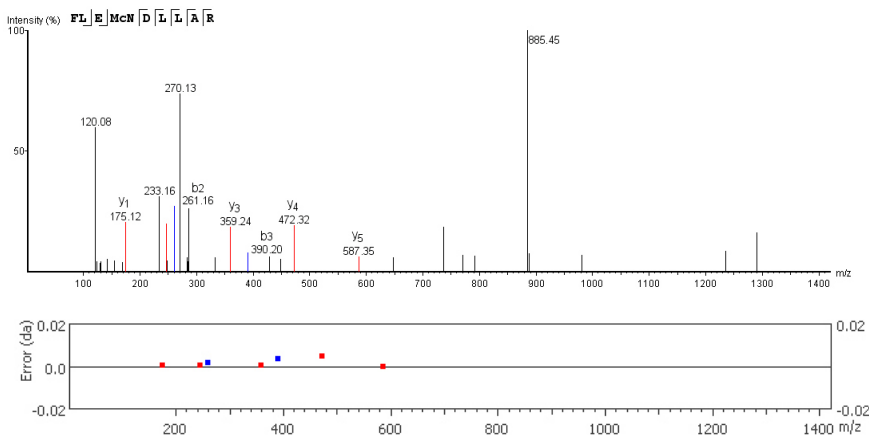


#	b	b (2+)	Seq	y	y (2+)	#
1	100.08	50.54	V			8
2	649.25	325.13	C(+446.17)	1234.60	617.80	7
3	763.29	382.15	N	685.42	343.21	6
4	860.35	430.68	P	571.38	286.19	5
5	973.43	487.22	I	474.33	237.66	4
6	1086.52	543.76	I	361.24	181.12	3
7	1187.56	594.28	T	248.16	124.58	2
8			K	147.11	74.06	1

[S7.5] Heat shock 70 kDa protein 4

FLEMC(+446.17)NDLLAR

m/z=885.91425 z=2

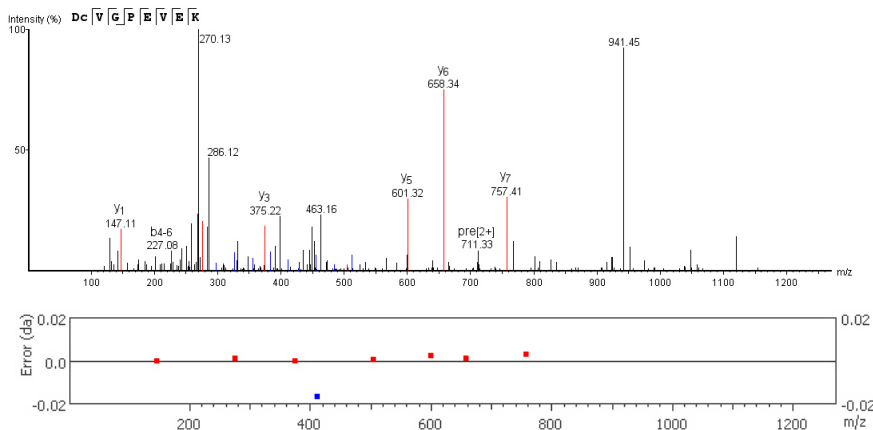


#	b	b (2+)	Seq	y	y (2+)	#
1	148.08	74.54	F			11
2	261.16	131.08	L	1623.74	812.37	10
3	390.20	195.60	E	1510.65	755.83	9
4	521.24	261.12	M	1381.61	691.30	8
5	1070.42	535.71	C(+446.17)	1250.57	625.78	7
6	1184.46	592.73	N	701.39	351.20	6
7	1299.49	650.24	D	587.35	294.18	5
8	1412.57	706.79	L	472.32	236.66	4
9	1525.66	763.33	L	359.24	180.12	3
10	1596.69	798.85	A	246.15	123.58	2
11			R	175.12	88.06	1

[S7.6] Phosphoglycerate kinase 1

DC(+446.17)VGPEVEK

m/z=711.3179 z=2



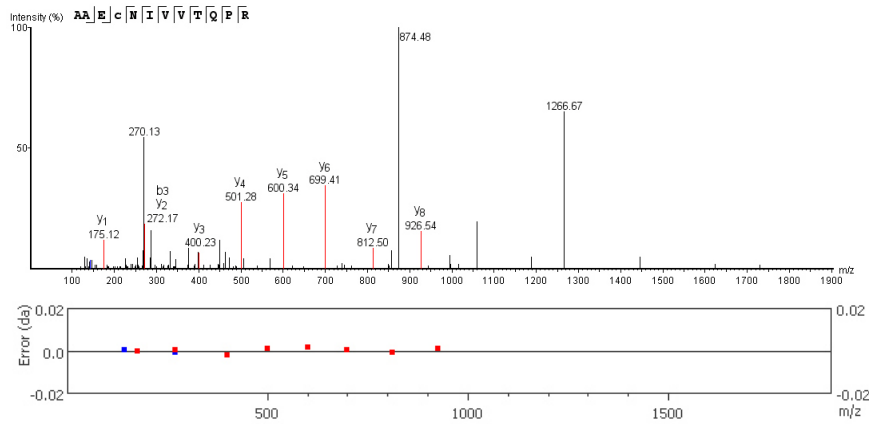
#	b	b (2+)	Seq	y	y (2+)	#
1	116.03	58.52	D			9
2	665.21	333.10	C(+446.17)	1306.58	653.79	8
3	764.28	382.64	V	757.41	379.20	7
4	821.30	411.17	G	658.34	329.67	6
5	918.35	459.68	P	601.32	301.16	5
6	1047.40	524.20	E	504.27	252.63	4
7	1146.46	573.73	V	375.22	188.11	3
8	1275.51	638.25	E	276.15	138.58	2
9			K	147.11	74.06	1

Supplementary Figure S7

[S7.7] ATP-dependent RNA helicase A

AAEC(+446.17)NIVVTQPR

m/z=873.9295 z=2

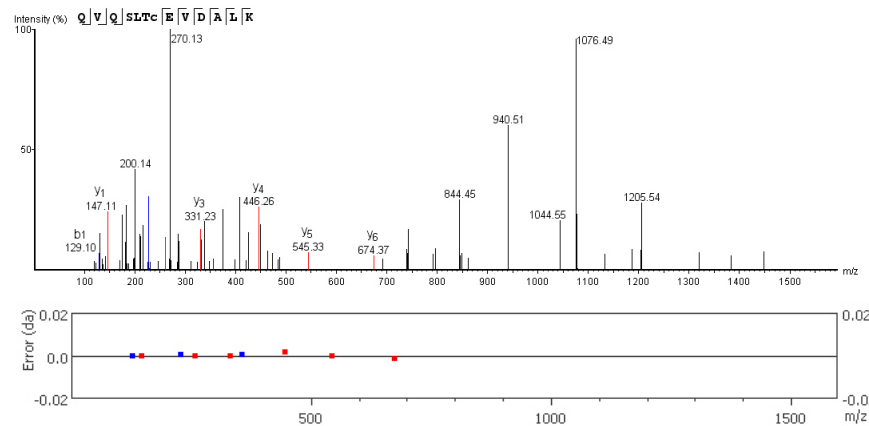


#	b	b (2+)	Seq	y	y (2+)	#
1	72.04	36.52	A			12
2	143.08	72.04	A	1675.80	838.40	11
3	272.13	136.56	E	1604.76	802.88	10
4	821.30	411.15	C(+446.17)	1475.72	738.36	9
5	935.34	468.17	N	926.54	463.77	8
6	1048.43	524.71	I	812.50	406.75	7
7	1147.49	574.25	V	699.41	350.21	6
8	1246.56	623.78	V	600.34	300.67	5
9	1347.61	674.31	T	501.28	251.14	4
10	1475.67	738.33	Q	400.23	200.62	3
11	1572.72	786.86	P	272.17	136.59	2
12			R	175.12	88.06	1

[S7.8] Vimentin

QVQSLTC(+446.17)EVDALK

m/z=940.4598 z=2

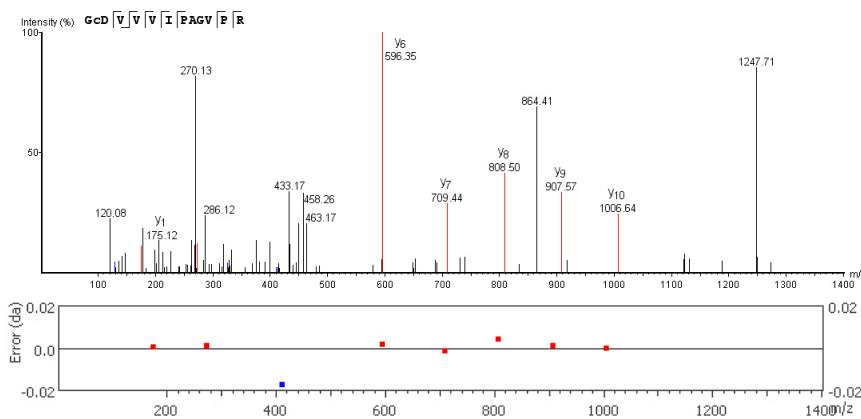


#	b	b (2+)	Seq	y	y (2+)	#
1	129.07	65.03	Q			13
2	228.13	114.57	V	1751.84	876.42	12
3	356.19	178.60	Q	1652.77	826.88	11
4	443.23	222.11	S	1524.71	762.86	10
5	556.31	278.65	L	1437.68	719.34	9
6	657.36	329.18	T	1324.59	662.80	8
7	1206.53	603.77	C(+446.17)	1223.55	612.27	7
8	1335.57	668.29	E	674.37	337.69	6
9	1434.64	717.82	V	545.33	273.16	5
10	1549.67	775.34	D	446.26	223.63	4
11	1620.71	810.85	A	331.23	166.12	3
12	1733.79	867.40	L	260.20	130.60	2
13			K	147.11	74.06	1

[S7.9] Malate dehydrogenase, mitochondrial

GC(+446.17)DVVVIPAGVPR

m/z=864.4452 z= 2



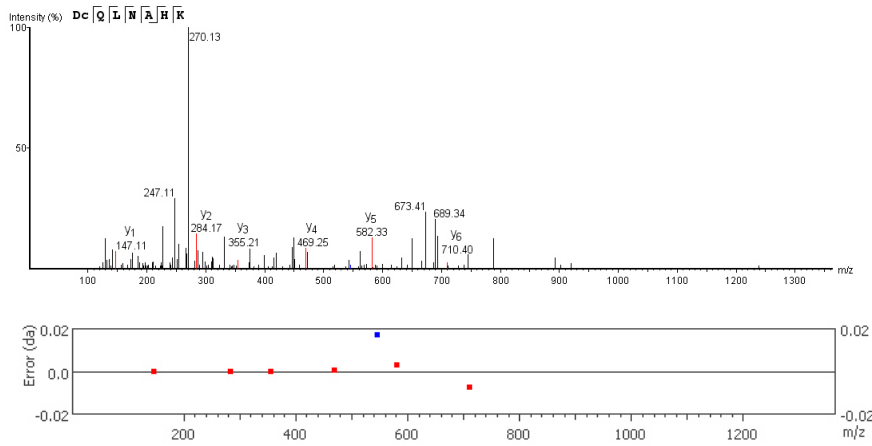
#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			13
2	607.20	304.10	C(+446.17)	1670.84	835.92	12
3	722.23	361.62	D	1121.67	561.33	11
4	821.30	411.17	V	1006.64	503.82	10
5	920.37	460.68	V	907.57	454.29	9
6	1019.44	510.22	V	808.50	404.75	8
7	1132.52	566.76	I	709.44	355.22	7
8	1229.57	615.29	P	596.35	298.68	6
9	1300.61	650.81	A	499.30	250.15	5
10	1357.63	679.32	G	428.26	214.63	4
11	1456.70	728.85	V	371.24	186.12	3
12	1553.75	777.38	P	272.17	136.59	2
13			R	175.12	88.06	1

Supplementary Figure S7

[S7.10] Transcription intermediary factor 1-beta

DC(+446.17)QLNAHK

m/z=458.8761 z=3

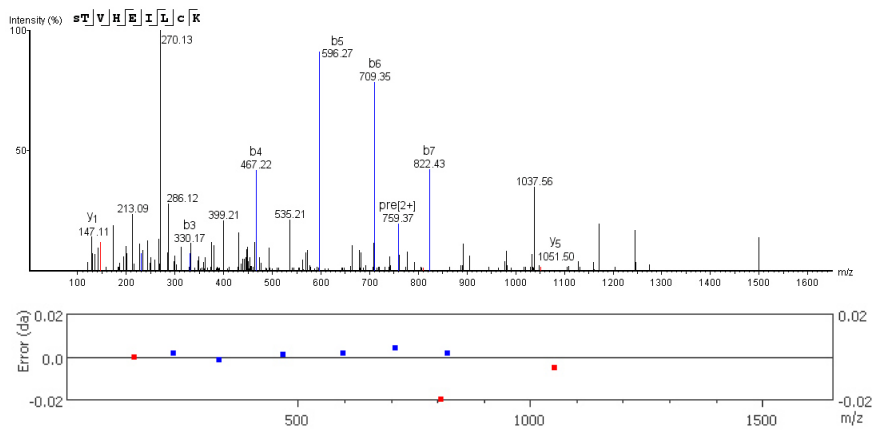


#	b	b (2+)	Seq	y	y (2+)	#
1	116.03	58.52	D			8
2	665.21	333.10	C(+446.17)	1259.57	630.28	7
3	793.27	397.13	Q	710.40	355.70	6
4	906.35	453.68	L	582.33	291.67	5
5	1020.40	510.70	N	469.25	235.13	4
6	1091.43	546.20	A	355.21	178.10	3
7	1228.49	614.75	H	284.17	142.59	2
8			K	147.11	74.06	1

[S7.11] Annexin A2

S(+42.01)TVHEILC(+446.17)K

m/z=759.3701 z=2

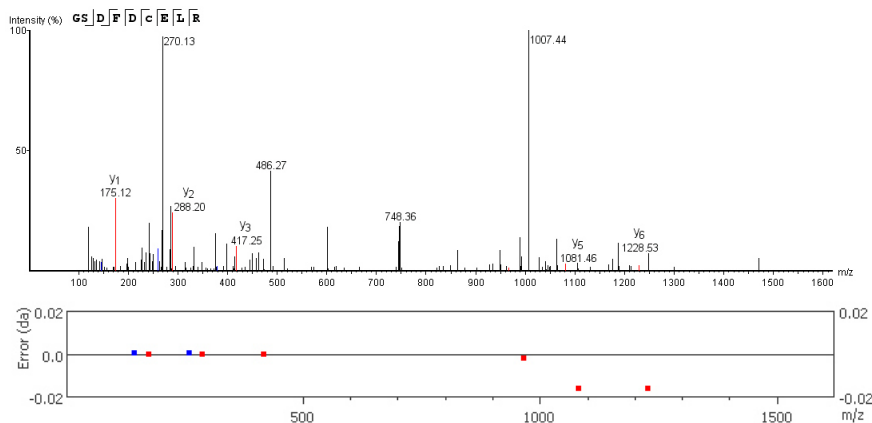


#	b	b (2+)	Seq	y	y (2+)	#
1	130.05	65.53	S(+42.01)			9
2	231.10	116.05	T	1388.67	694.84	8
3	330.17	165.58	V	1287.63	644.31	7
4	467.22	234.11	H	1188.56	594.78	6
5	596.27	298.63	E	1051.50	526.25	5
6	709.35	355.18	I	922.46	461.73	4
7	822.43	411.72	L	809.39	405.19	3
8	1371.61	686.31	C(+446.17)	696.29	348.64	2
9			K	147.11	74.06	1

[S7.12] Heterogeneous nuclear ribonucleoprotein K

GSDFDC(+446.17)ELR

m/z=744.31067 z=2



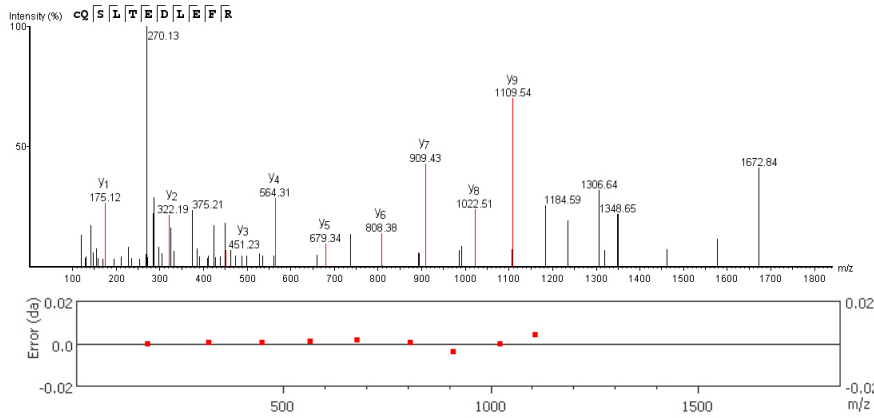
#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			9
2	145.06	73.03	S	1430.57	715.79	8
3	260.09	130.54	D	1343.54	672.27	7
4	407.16	204.08	F	1228.53	614.76	6
5	522.18	261.59	D	1081.46	541.22	5
6	1071.36	536.18	C(+446.17)	966.42	483.71	4
7	1200.40	600.70	E	417.25	209.12	3
8	1313.49	657.24	L	288.20	144.60	2
9			R	175.12	88.06	1

Supplementary Figure S7

[S7.13] Lamin-B1

C(+446.17)QSLTEDLEFR

m/z=893.90204 z=2

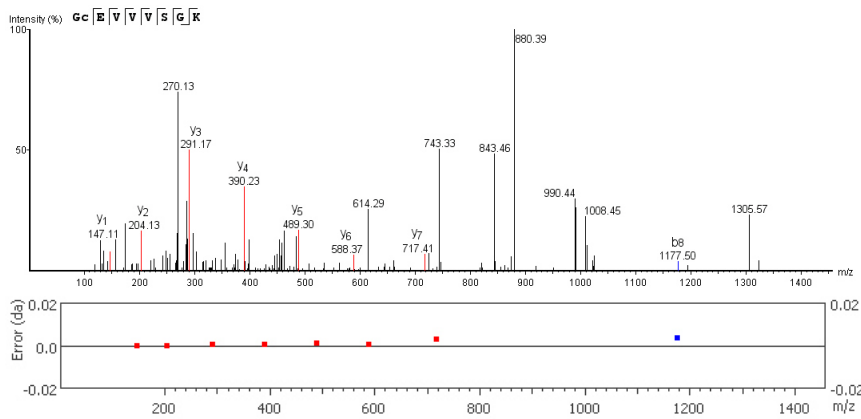


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			11
2	678.24	339.62	Q	1237.61	619.30	10
3	765.27	383.14	S	1109.54	555.27	9
4	878.36	439.68	L	1022.51	511.76	8
5	979.41	490.20	T	909.43	455.22	7
6	1108.45	554.72	E	808.38	404.69	6
7	1223.47	612.24	D	679.34	340.17	5
8	1336.56	668.78	L	564.31	282.66	4
9	1465.60	733.30	E	451.23	226.11	3
10	1612.67	806.83	F	322.19	161.59	2
11			R	175.12	88.06	1

[S7.14] 40S ribosomal protein S3

GC(+446.17)EVVVSQK

m/z=662.3185 z=2

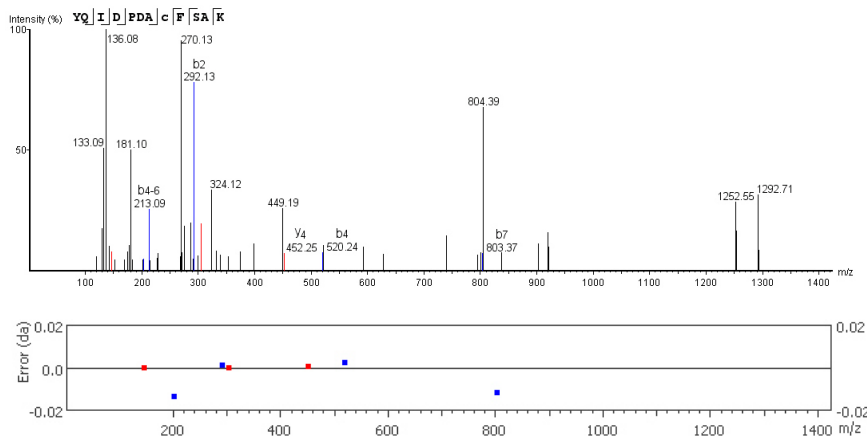


#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			9
2	607.20	304.10	C(+446.17)	1266.59	633.79	8
3	736.25	368.62	E	717.41	359.21	7
4	835.32	418.16	V	588.37	294.69	6
5	934.38	467.69	V	489.30	245.15	5
6	1033.45	517.23	V	390.23	195.62	4
7	1120.48	560.74	S	291.17	146.08	3
8	1177.50	589.25	G	204.13	102.57	2
9			K	147.11	74.06	1

[S7.15] Voltage-dependent anion-selective channel protein 1

YQIDPDAC(+446.17)FSAK

m/z=902.39935 z=2



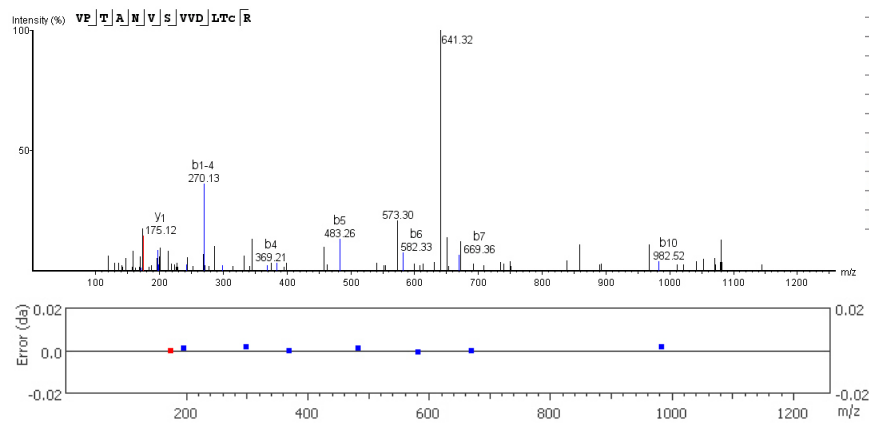
#	b	b (2+)	Seq	y	y (2+)	#
1	164.07	82.54	Y			12
2	292.13	146.56	Q	1640.71	820.86	11
3	405.21	203.12	I	1512.65	756.83	10
4	520.24	260.62	D	1399.57	700.28	9
5	617.29	309.15	P	1284.54	642.77	8
6	732.32	366.66	D	1187.49	594.24	7
7	803.37	402.18	A	1072.46	536.73	6
8	1352.53	676.77	C(+446.17)	1001.43	501.21	5
9	1499.60	750.30	F	452.25	226.63	4
10	1586.63	793.82	S	305.18	153.09	3
11	1657.67	829.34	A	218.15	109.57	2
12			K	147.11	74.06	1

Supplementary Figure S7

[S7.16] Glyceraldehyd-3-Phosphat Dehydrogenase

VPTANVSVVDLTC(+446.17)R

m/z=640.6566 z=3

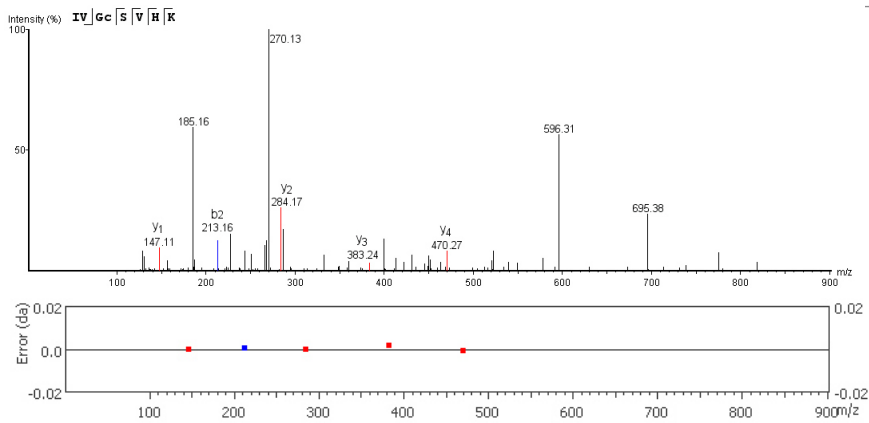


#	b	b (2+)	Seq	y	y (2+)	#
1	100.08	50.54	V			14
2	197.13	99.06	P	1820.87	910.94	13
3	298.17	149.59	T	1723.82	862.41	12
4	369.21	185.11	A	1622.77	811.88	11
5	483.26	242.13	N	1551.73	776.37	10
6	582.33	291.66	V	1437.69	719.34	9
7	669.36	335.18	S	1338.62	669.81	8
8	768.43	384.71	V	1251.59	626.29	7
9	867.49	434.25	V	1152.52	576.76	6
10	982.52	491.76	D	1053.45	527.23	5
11	1095.60	548.30	L	938.43	469.71	4
12	1196.65	598.83	T	825.34	413.17	3
13	1745.83	873.41	C(+446.17)	724.29	362.65	2
14			R	175.12	88.06	1

[S7.17] Heterogeneous nuclear ribonucleoproteins C1/C2

IVGC(+446.17)SVHK

m/z=430.2179 z=3

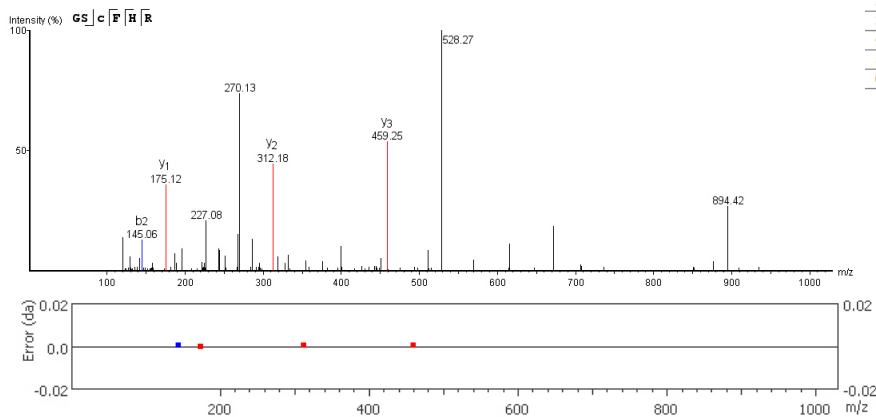


#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	I			8
2	213.16	107.08	V	1175.54	588.27	7
3	270.18	135.59	G	1076.47	538.73	6
4	319.36	159.68	C(+446.17)	1019.45	510.22	5
5	406.39	203.19	S	470.27	235.64	4
6	1005.46	502.73	V	383.24	192.12	3
7	1142.52	571.26	H	284.17	142.59	2
8			K	147.11	74.06	1

[S7.18] Peptidyl-prolyl cis-trans isomerase A

GSC(+446.17)FHR

m/z=384.83542 z=3



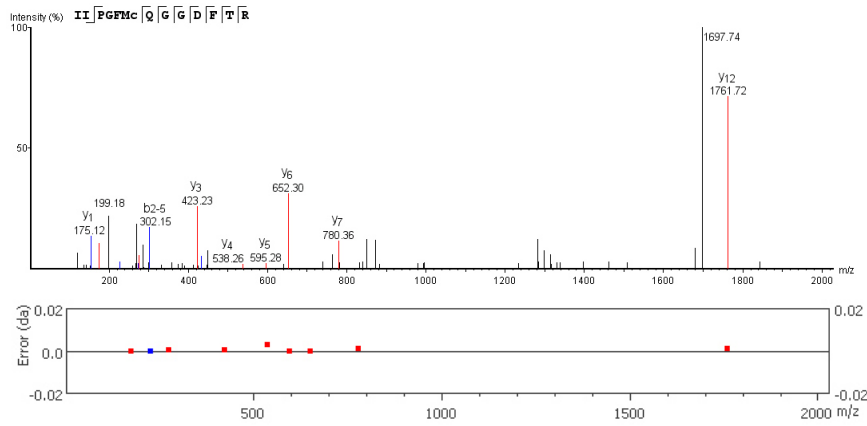
#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			6
2	145.06	73.03	S	1095.45	548.23	5
3	694.24	347.62	C(+446.17)	1008.42	504.71	4
4	841.30	421.15	F	459.25	230.12	3
5	978.36	489.68	H	312.18	156.59	2
6			R	175.12	88.06	1

Supplementary Figure S7

[S7.19] PeptidylProlylCisTransIsomerase

IIPGFMC(+446.17)QGDFTR

m/z=994.4574 z=2

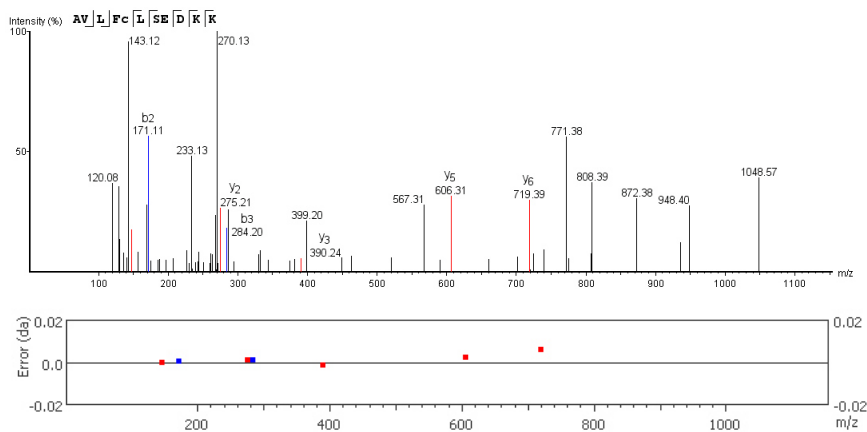


#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	I			14
2	227.18	114.09	I	1874.81	937.90	13
3	324.23	162.61	P	1761.72	881.36	12
4	381.25	191.13	G	1664.67	832.83	11
5	528.32	264.66	F	1607.65	804.32	10
6	659.36	330.18	M	1460.58	730.79	9
7	1208.53	604.77	C(+446.17)	1329.54	665.27	8
8	1336.59	668.80	Q	780.36	390.68	7
9	1393.61	697.31	G	652.30	326.65	6
10	1450.64	725.82	G	595.28	298.14	5
11	1565.66	783.33	D	538.26	269.63	4
12	1712.73	856.87	F	423.23	212.12	3
13	1813.78	907.39	T	276.17	138.58	2
14			R	175.12	88.06	1

[S7.20] Colfin-1

AVLFC(+446.17)LSDEKK

m/z=566.95306 z=3

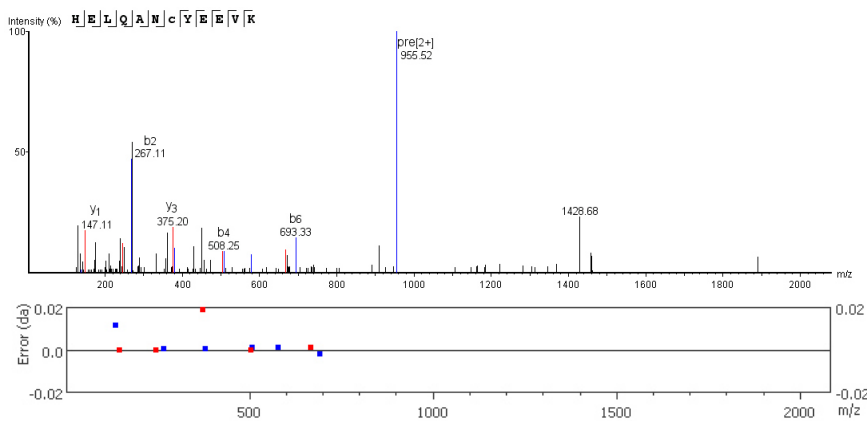


#	b	b (2+)	Seq	y	y (2+)	#
1	72.04	36.52	A			11
2	171.11	86.06	V	1627.79	814.39	10
3	284.20	142.60	L	1528.72	764.86	9
4	431.27	216.13	F	1415.64	708.32	8
5	980.44	490.72	C(+446.17)	1268.57	634.78	7
6	1093.52	547.26	L	719.39	360.20	6
7	1180.56	590.78	S	606.31	303.65	5
8	1309.60	655.30	E	519.28	260.14	4
9	1424.63	712.81	D	390.24	195.62	3
10	1552.72	776.86	K	275.21	138.10	2
11			K	147.11	74.06	1

[S7.21] Colfin-1

HELQANC(+446.17)YEEVK

m/z=954.9251 z=2



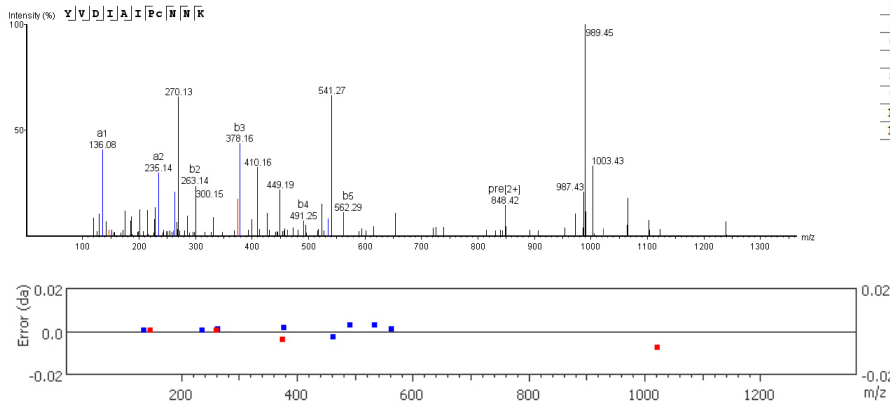
#	b	b (2+)	Seq	y	y (2+)	#
1	138.05	69.53	H			12
2	267.11	134.05	E	1771.77	886.38	11
3	380.19	190.60	L	1642.73	821.86	10
4	508.25	254.63	Q	1529.64	765.32	9
5	579.29	290.14	A	1401.58	701.29	8
6	693.33	347.17	N	1330.55	665.77	7
7	1242.51	621.75	C(+446.17)	1216.50	608.75	6
8	1405.57	703.29	Y	667.33	334.16	5
9	1534.61	767.81	E	504.27	252.63	4
10	1663.66	832.33	E	375.20	188.11	3
11	1762.72	881.86	V	246.18	123.59	2
12			K	147.11	74.06	1

Supplementary Figure S7

[S7.22] 40S ribosomal protein SA

YVDIAIPC(+446.17)NNK

m/z=848.4052 z=2

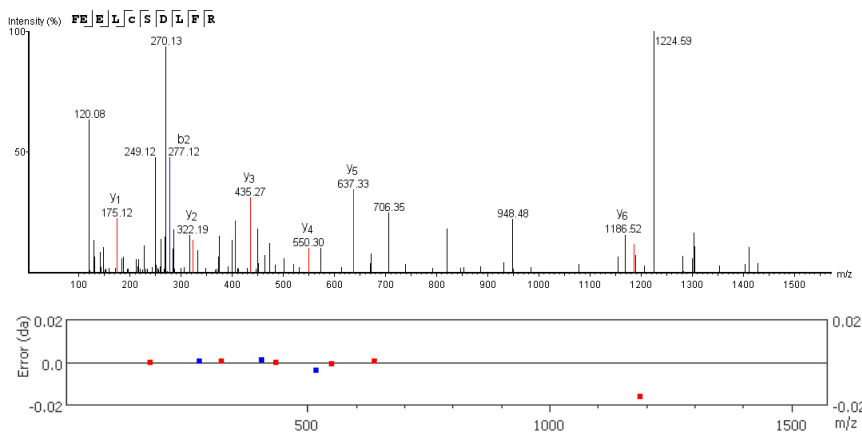


#	b	a	b (2+)	Seq	y	y (2+)	#
1	164.07	136.08	82.54	Y			11
2	263.14	235.14	132.07	V	1532.73	766.86	10
3	378.16	350.17	189.58	D	1433.66	717.33	9
4	491.25	463.26	246.13	I	1318.63	659.82	8
5	562.29	534.29	281.64	A	1205.55	603.27	7
6	675.37	647.38	338.19	I	1134.51	567.76	6
7	772.42	744.43	386.71	P	1021.43	511.21	5
8	1321.60	1293.60	661.30	C(+446.17)	924.37	462.69	4
9	1435.64	1407.65	718.32	N	375.20	188.10	3
10	1549.69	1521.69	775.34	N	261.15	131.08	2
11				K	147.11	74.06	1

[S7.23] Heat shock protein HSP 90-alpha

FEELC(+446.17)SDLFR

m/z=852.884 z=2

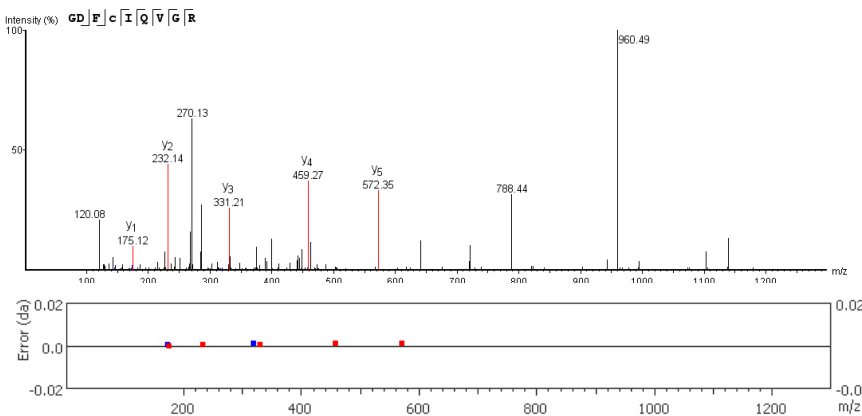


#	b	b (2+)	Seq	y	y (2+)	#
1	148.08	74.54	F			10
2	277.12	139.06	E	1557.67	779.34	9
3	406.16	203.58	E	1428.63	714.82	8
4	519.25	260.12	L	1299.59	650.29	7
5	1068.42	534.71	C(+446.17)	1186.52	593.75	6
6	1155.45	578.23	S	637.33	319.17	5
7	1270.48	635.74	D	550.30	275.65	4
8	1383.56	692.28	L	435.27	218.14	3
9	1530.63	765.82	F	322.19	161.59	2
10			R	175.12	88.06	1

[S7.24] Nucleoside diphosphate kinase A

GDFC(+446.17)IQVGR

m/z=720.83356 z=2



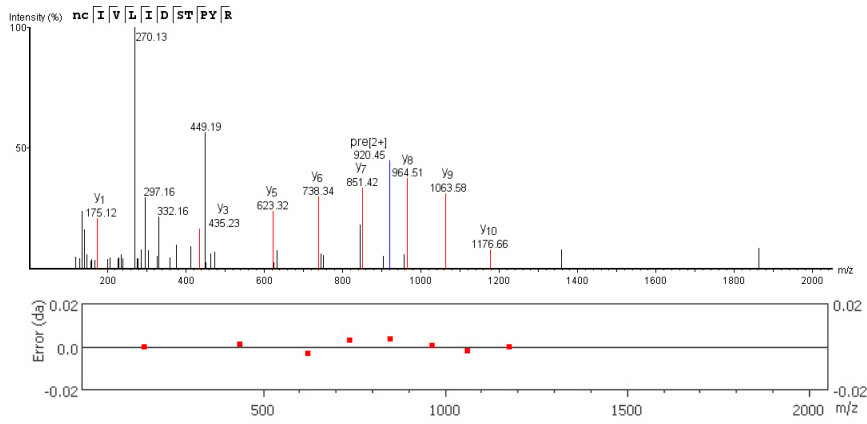
#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			9
2	173.06	87.03	D	1383.62	692.31	8
3	320.12	160.56	F	1268.59	634.80	7
4	869.30	435.15	C(+446.17)	1121.53	561.26	6
5	982.38	491.69	I	572.35	286.68	5
6	1110.44	555.72	Q	459.27	230.13	4
7	1209.51	605.26	V	331.21	166.10	3
8	1266.53	633.77	G	232.14	116.57	2
9			R	175.12	88.06	1

Supplementary Figure S7

[S7.25] 40S ribosomal protein S8

NC(+446.17)IVLIDSTPYR

m/z=920.4532 z=2

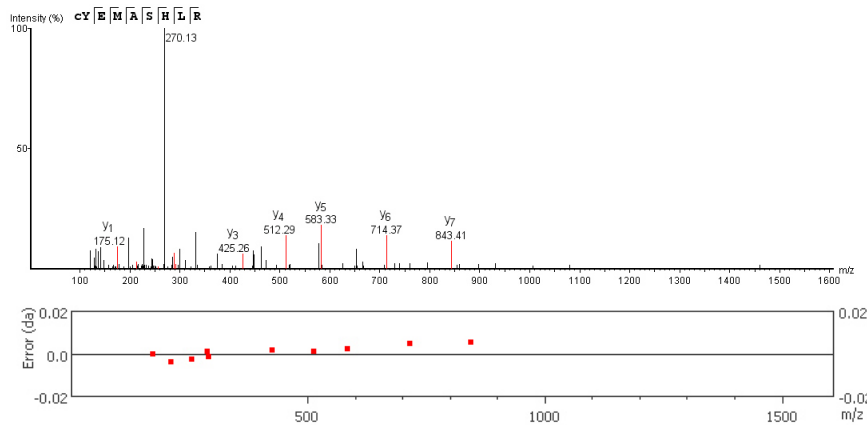


#	b	b (2+)	Seq	y	y (2+)	#
1	115.05	58.03	N			12
2	664.23	332.61	C(+446.17)	1725.84	863.42	11
3	777.31	389.15	I	1176.66	588.83	10
4	876.38	438.69	V	1063.58	532.29	9
5	989.46	495.23	L	964.51	482.75	8
6	1102.55	551.77	I	851.42	426.21	7
7	1217.57	609.29	D	738.34	369.67	6
8	1304.61	652.80	S	623.32	312.16	5
9	1405.65	703.33	T	536.28	268.64	4
10	1502.71	751.85	P	435.23	218.12	3
11	1665.77	833.38	Y	338.18	169.59	2
12			R	175.12	88.06	1

[S7.26] Profilin-1

C(+446.17)YEMASHLR

m/z=519.228 z=3

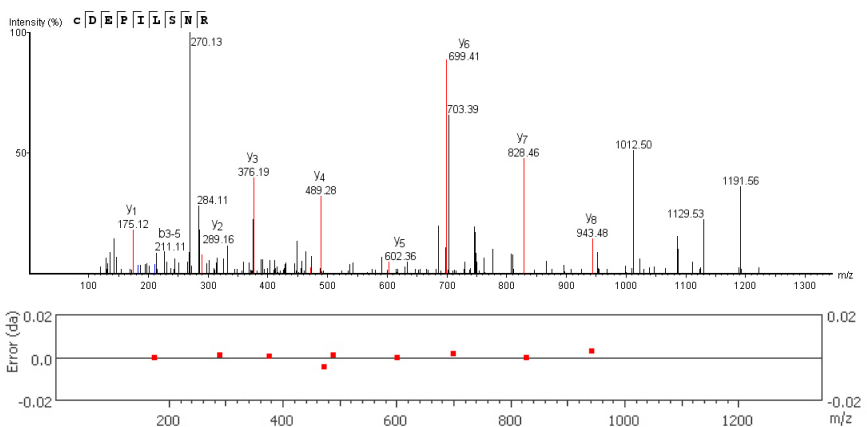


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			9
2	713.25	357.12	Y	1006.48	503.74	8
3	842.29	421.64	E	843.41	422.21	7
4	973.33	487.16	M	714.37	357.69	6
5	1044.37	522.68	A	583.33	292.17	5
6	1131.40	566.20	S	512.29	256.65	4
7	1268.46	634.73	H	425.26	213.13	3
8	1381.54	691.27	L	288.20	144.60	2
9			R	175.12	88.06	1

[S7.27] Phosphatidylethanolamine-binding protein 1

C(+446.17)DEPILSNR

m/z=746.8427 z=2



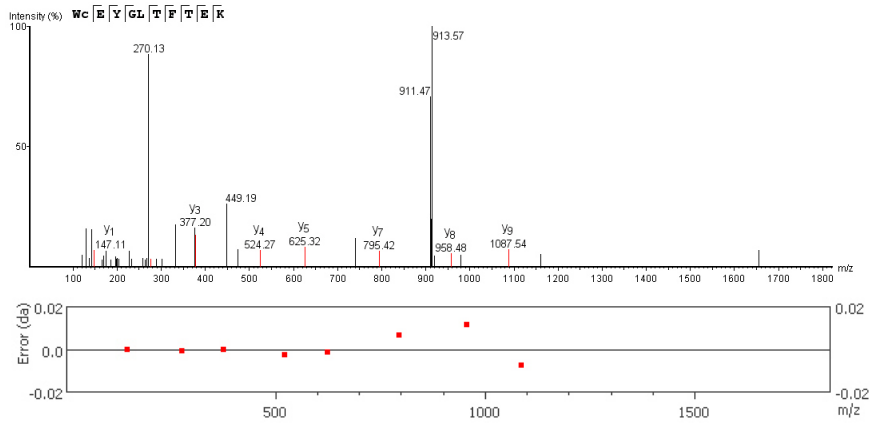
#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			9
2	665.21	333.10	D	943.48	472.25	8
3	794.25	397.63	E	828.46	414.73	7
4	891.31	446.15	P	699.41	350.21	6
5	1004.39	502.69	I	602.36	301.68	5
6	1117.47	559.24	L	489.28	245.14	4
7	1204.51	602.75	S	376.19	188.60	3
8	1318.55	659.77	N	289.16	145.08	2
9			R	175.12	88.06	1

Supplementary Figure S7

[S7.28] Voltage-dependent anion-selective channel protein 2

WC(+446.17)EYGLTFTEK

m/z=911.90094 z=2

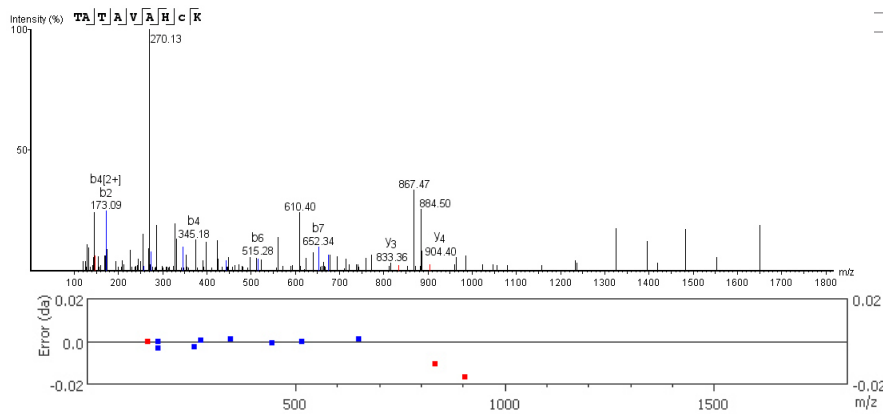


#	b	b (2+)	Seq	y	y (2+)	#
1	187.09	94.04	W			11
2	736.26	368.63	C(+446.17)	1636.71	818.85	10
3	865.30	433.15	E	1087.54	544.27	9
4	1028.37	514.68	Y	958.48	479.74	8
5	1085.39	543.19	G	795.42	398.21	7
6	1198.47	599.74	L	738.40	369.70	6
7	1299.52	650.26	T	625.32	313.16	5
8	1446.59	723.79	F	524.27	262.64	4
9	1547.64	774.32	T	377.20	189.10	3
10	1676.68	838.84	E	276.16	138.58	2
11			K	147.11	74.06	1

[S7.29] 40S ribosomal protein S16

TATAVAHC(+446.17)K

m/z=674.3229 z=2

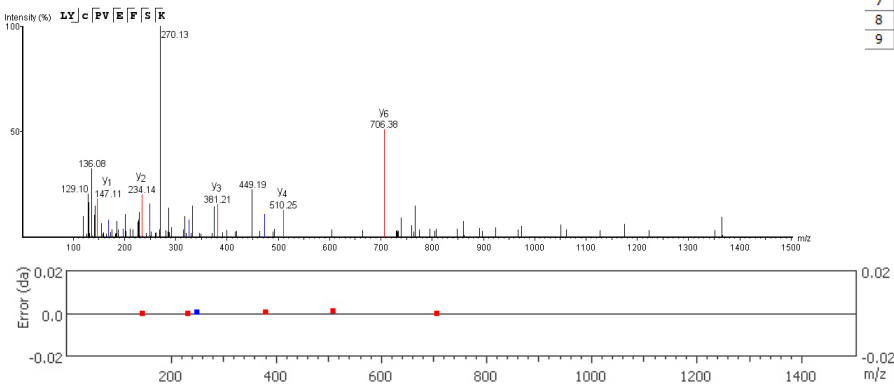


#	b	b (2+)	Seq	y	y (2+)	#
1	102.06	51.53	T			9
2	173.09	87.05	A	1246.57	623.79	8
3	274.14	137.57	T	1175.54	588.27	7
4	345.18	173.09	A	1074.49	537.74	6
5	444.25	222.62	V	1003.45	502.23	5
6	515.28	258.14	A	904.40	452.69	4
7	652.34	326.67	H	833.36	417.17	3
8	1201.52	601.26	C(+446.17)	696.29	348.64	2
9			K	147.11	74.06	1

[S7.30] Spermine Synthase

LYC(+446.17)PVEFSK

m/z=766.3578 z=2



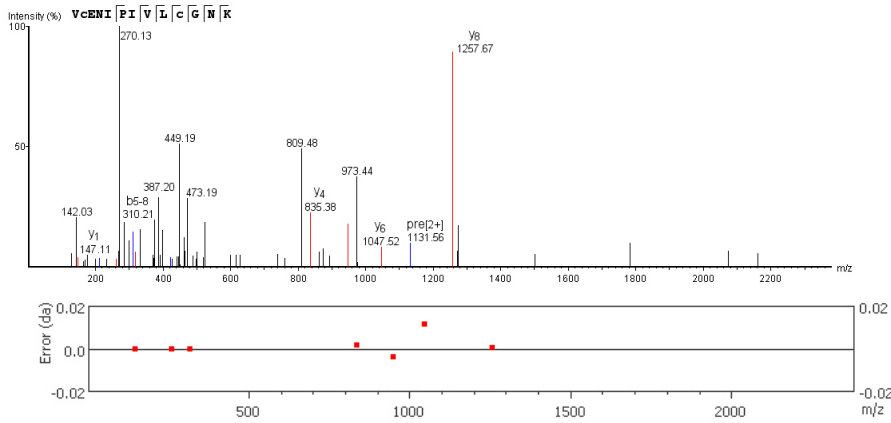
#	b	a	b (2+)	Seq	y	y (2+)	#
1	114.09	86.10	57.55	L			9
2	277.16	249.16	139.08	Y	1418.62	709.81	8
3	826.33	798.34	413.67	C(+446.17)	1255.55	628.28	7
4	923.38	895.39	462.19	P	706.38	353.69	6
5	1022.45	994.46	511.73	V	609.32	305.16	5
6	1151.49	1123.50	576.25	E	510.25	255.63	4
7	1298.56	1270.57	649.78	F	381.21	191.11	3
8	1385.59	1357.60	693.30	S	234.14	117.57	2
9				K	147.11	74.06	1

Supplementary Figure S7

[S7.31] GTP-binding nuclear protein Ran

VC(+446.17)ENIPIVLC(+414.19)GNK

m/z=1131.553 z=2

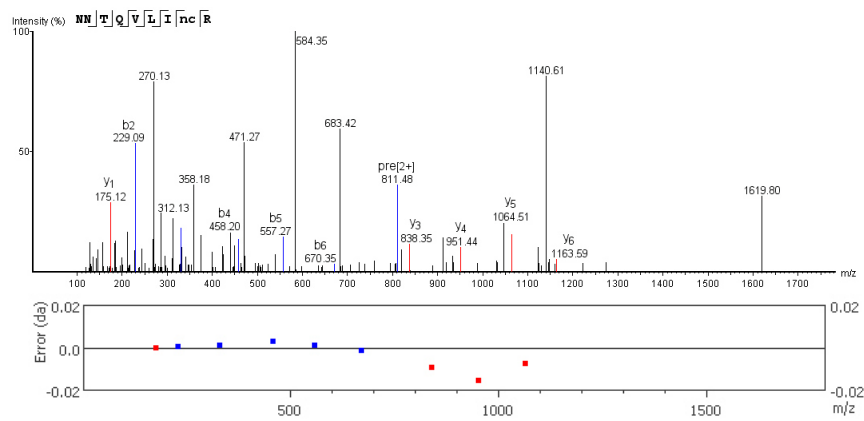


#	b	b (2+)	Seq	y	y (2+)	#
1	100.08	50.54	V			13
2	649.25	325.13	C(+446.17)	2163.01	1082.01	12
3	778.29	389.65	E	1613.84	807.42	11
4	892.34	446.67	N	1484.80	742.90	10
5	1005.42	503.21	I	1370.75	685.88	9
6	1102.47	551.74	P	1257.67	629.33	8
7	1215.56	608.28	I	1160.62	580.81	7
8	1314.63	657.81	V	1047.52	524.27	6
9	1427.71	714.36	L	948.47	474.73	5
10	1944.91	972.96	C(+414.19)	835.38	418.19	4
11	2001.93	1001.47	G	318.18	159.59	3
12	2115.98	1058.49	N	261.16	131.08	2
13			K	147.11	74.06	1

[S7.32] Small nuclear ribonucleoprotein Sm D2

NNTQVLINC(+446.17)R

m/z=810.89215 z=2

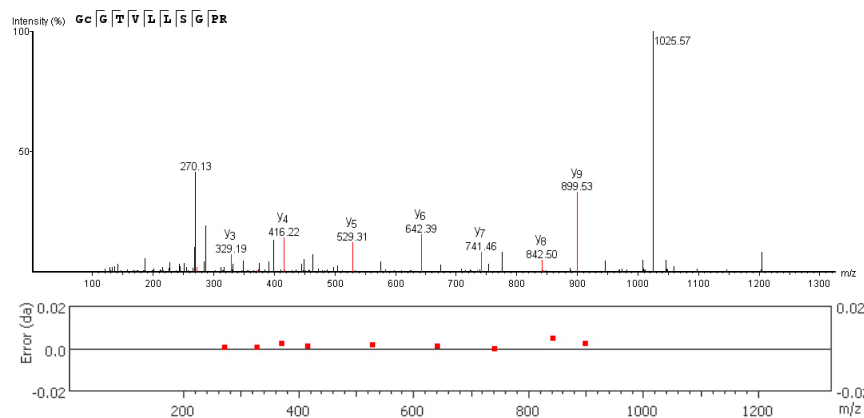


#	b	b (2+)	Seq	y	y (2+)	#
1	115.05	58.03	N			10
2	229.09	115.05	N	1506.72	753.86	9
3	330.14	165.57	T	1392.68	696.84	8
4	458.20	229.60	Q	1291.63	646.32	7
5	557.27	279.13	V	1163.57	582.29	6
6	670.35	335.68	L	1064.51	532.75	5
7	783.44	392.22	I	951.44	476.21	4
8	897.48	449.24	N	838.35	419.67	3
9	1446.65	723.83	C(+446.17)	724.29	362.65	2
10			R	175.12	88.06	1

[S7.33] 60S ribosomal protein L18

GC(+446.17)GTVLLSGPR

m/z=753.37744 z=2



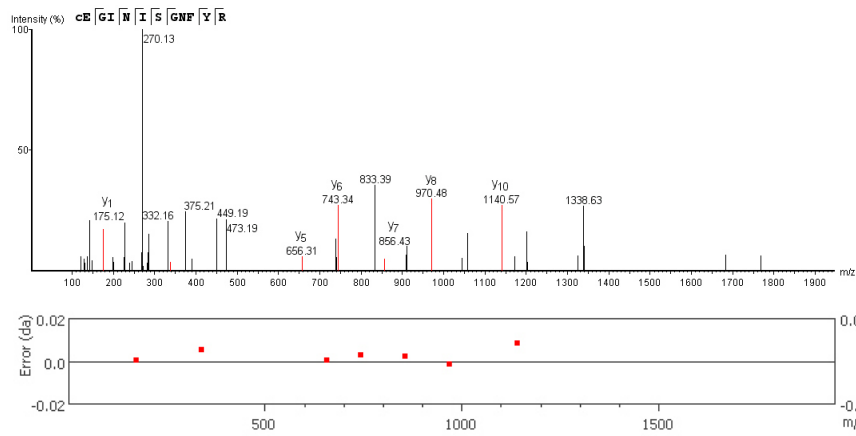
#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			11
2	607.20	304.10	C(+446.17)	1448.71	724.85	10
3	664.23	332.61	G	899.53	450.27	9
4	765.27	383.14	T	842.50	421.75	8
5	864.34	432.67	V	741.46	371.23	7
6	977.43	489.21	L	642.39	321.70	6
7	1090.51	545.75	L	529.31	265.15	5
8	1177.54	589.27	S	416.22	208.61	4
9	1234.56	617.78	G	329.19	165.10	3
10	1331.62	666.31	P	272.17	136.59	2
11			R	175.12	88.06	1

Supplementary Figure S7

[S7.34] 60S ribosomal protein L13a

C(+446.17)EGINISGNFYR

m/z=909.9098 z=2

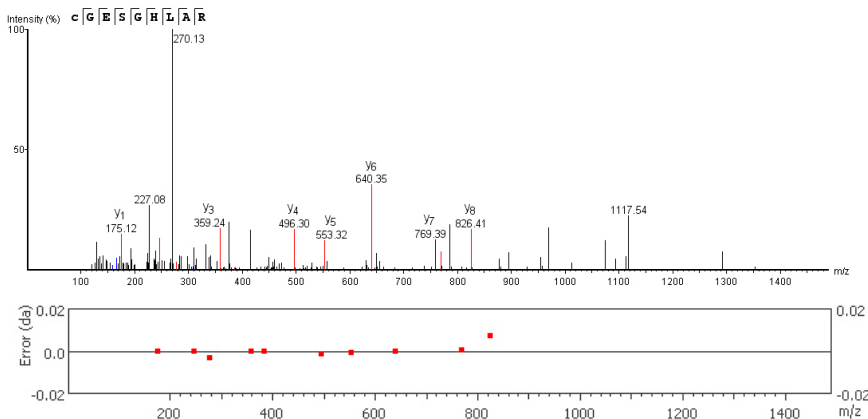


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			12
2	679.23	340.11	E	1269.62	635.31	11
3	736.25	368.62	G	1140.57	570.79	10
4	849.33	425.17	I	1083.56	542.28	9
5	963.37	482.19	N	970.48	485.74	8
6	1076.46	538.73	I	856.43	428.72	7
7	1163.49	582.24	S	743.34	372.17	6
8	1220.51	610.76	G	656.31	328.66	5
9	1334.55	667.78	N	599.29	300.15	4
10	1481.62	741.31	F	485.25	243.13	3
11	1644.69	822.84	Y	338.18	169.59	2
12			R	175.12	88.06	1

[S7.35] Cellular nucleic acid-binding protein

C(+446.17)GESGHLAR

m/z=459.20724 z=3

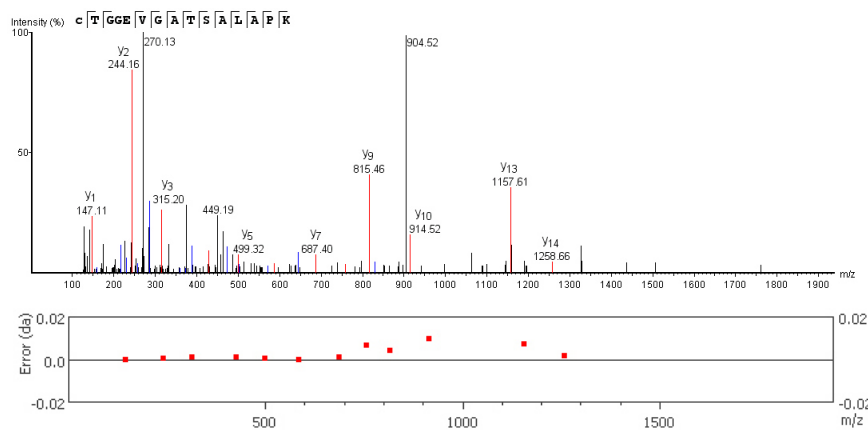


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			9
2	607.20	304.10	G	826.41	413.71	8
3	736.25	368.62	E	769.39	385.20	7
4	823.28	412.14	S	640.35	320.68	6
5	880.30	440.65	G	553.32	277.16	5
6	1017.36	509.18	H	496.30	248.65	4
7	1130.44	565.72	L	359.24	180.12	3
8	1201.48	601.24	A	246.16	123.58	2
9			R	175.12	88.06	1

[S7.36] 60S ribosomal Protein L12

C(+446.17)TGGEVGATSALAPK

m/z=904.43085 z=2



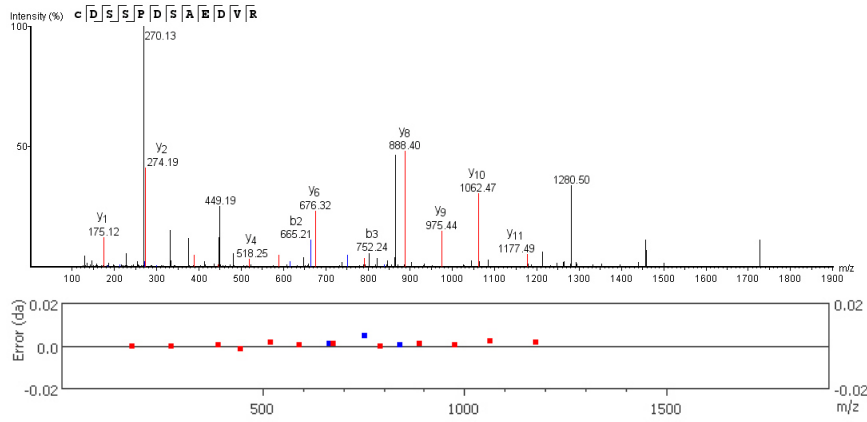
#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			15
2	651.23	326.12	T	1258.66	629.83	14
3	708.25	354.63	G	1157.61	579.31	13
4	765.27	383.14	G	1100.59	550.80	12
5	894.32	447.66	E	1043.57	522.29	11
6	993.38	497.19	V	914.52	457.77	10
7	1050.41	525.70	G	815.46	408.23	9
8	1121.44	561.22	A	758.43	379.72	8
9	1222.49	611.75	T	687.40	344.20	7
10	1309.52	655.26	S	586.36	293.68	6
11	1380.56	690.78	A	499.32	250.16	5
12	1493.64	747.32	L	428.29	214.64	4
13	1564.68	782.84	A	315.20	158.10	3
14	1661.73	831.37	P	244.16	122.58	2
15			K	147.11	74.06	1

Supplementary Figure S7

[S7.37] Alpha-2-HS-glycoprotein

C(+446.17)DSSPDSAEDVR

m/z=863.83984 z=2

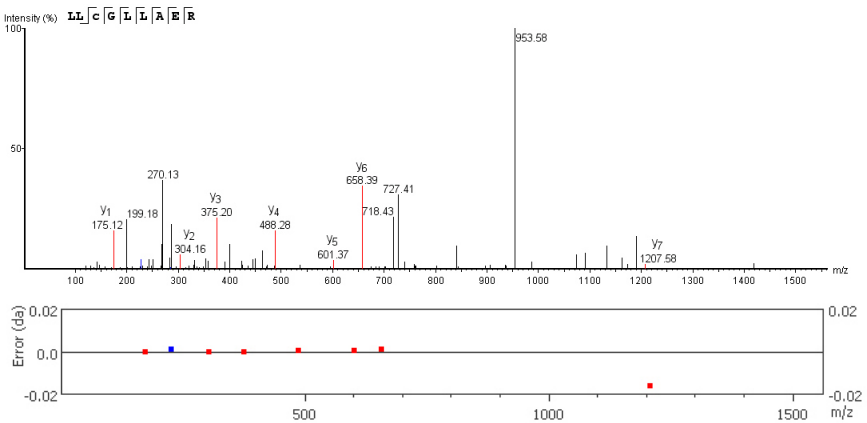


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			12
2	665.21	333.10	D	1177.49	589.25	11
3	752.24	376.62	S	1062.47	531.73	10
4	839.27	420.14	S	975.44	488.22	9
5	936.33	468.66	P	888.40	444.70	8
6	1051.35	526.18	D	791.35	396.18	7
7	1138.39	569.69	S	676.32	338.66	6
8	1209.42	605.21	A	589.29	295.15	5
9	1338.47	669.73	E	518.25	259.63	4
10	1453.49	727.25	D	389.21	195.11	3
11	1552.56	776.78	V	274.19	137.99	2
12			R	175.12	88.06	1

[S7.38] Macrophage migration inhibitory factor

LLC(+446.17)GLLAER

m/z=717.3777 z=2

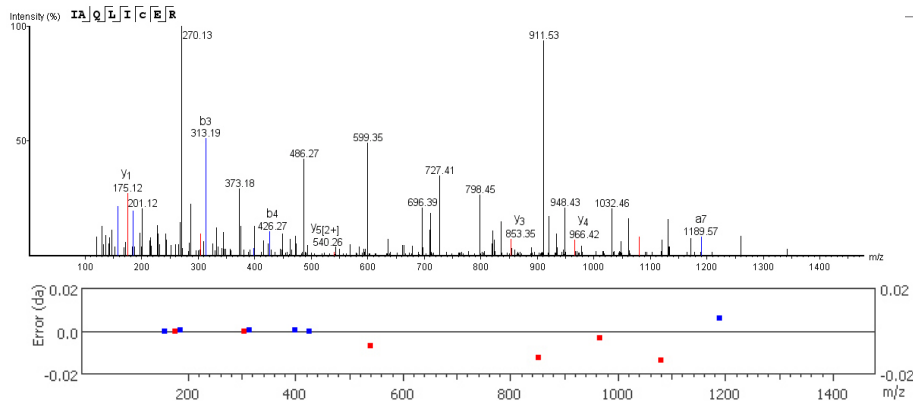


#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	L			9
2	227.17	114.09	L	1320.65	660.82	8
3	776.35	388.68	C(+446.17)	1207.58	604.28	7
4	833.37	417.19	G	658.39	329.69	6
5	946.46	473.73	L	601.37	301.18	5
6	1059.54	530.27	L	488.28	244.64	4
7	1130.58	565.79	A	375.20	188.10	3
8	1259.62	630.31	E	304.16	152.58	2
9			R	175.12	88.06	1

[S7.39] DUTP pyrophosphatase, isoform CRA_c

IAQLIC(+446.17)ER

m/z=696.35547 z=2



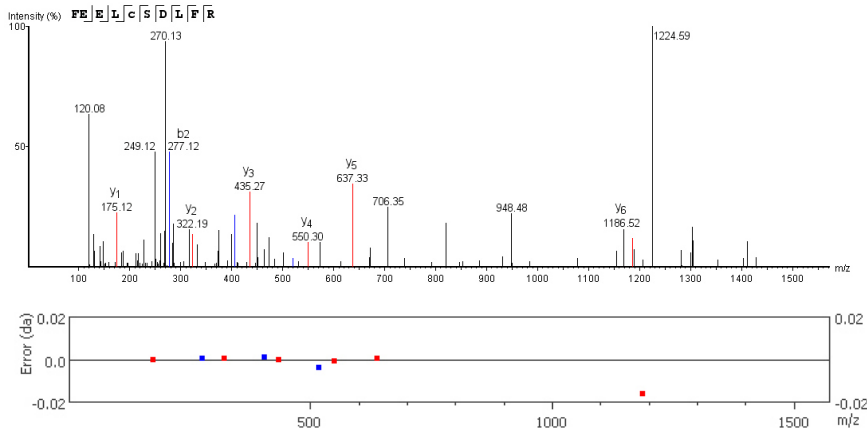
#	b	a	b (2+)	Seq	y	y (2+)	#
1	114.09	86.10	57.55	I			8
2	185.13	157.13	93.06	A	1278.60	639.80	7
3	313.19	285.19	157.09	Q	1207.56	604.28	6
4	426.27	398.28	213.64	L	1079.52	540.26	5
5	539.36	511.36	270.18	I	966.42	483.71	4
6	1088.53	1060.54	544.77	C(+446.17)	853.35	427.17	3
7	1217.57	1189.57	609.29	E	304.16	152.58	2
8				R	175.12	88.06	1

Supplementary Figure S7

[S7.40] Heat shock 70 kDa protein 1A/1B

FEELC(+446.17)SDLFR

m/z=852.8824 z=2

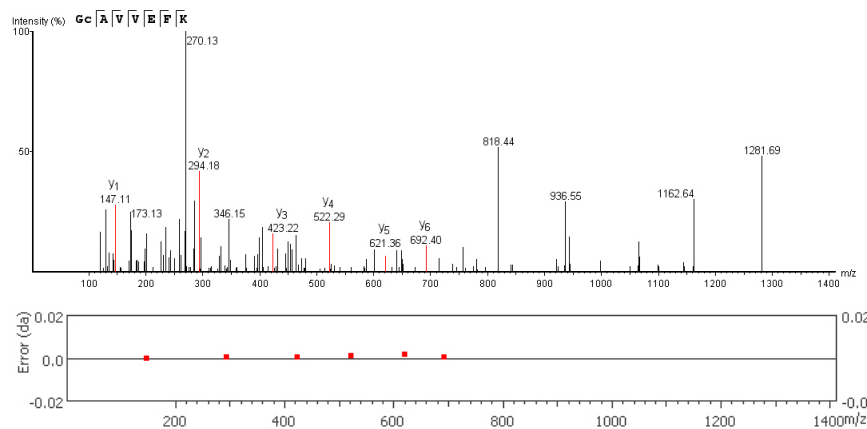


#	b	b (2+)	Seq	y	y (2+)	#
1	148.08	74.54	F			10
2	277.12	139.06	E	1557.67	779.34	9
3	406.16	203.58	E	1428.63	714.82	8
4	519.25	260.12	L	1299.59	650.29	7
5	1068.42	534.71	C(+446.17)	1186.52	593.75	6
6	1155.45	578.23	S	637.33	319.17	5
7	1270.48	635.74	D	550.30	275.65	4
8	1383.56	692.28	L	435.27	218.14	3
9	1530.63	765.82	F	322.19	161.59	2
10			R	175.12	88.06	1

[S7.41] Heterogeneous nuclear ribonucleoprotein M

GC(+446.17)AVVEFK

m/z=649.8092 z=2

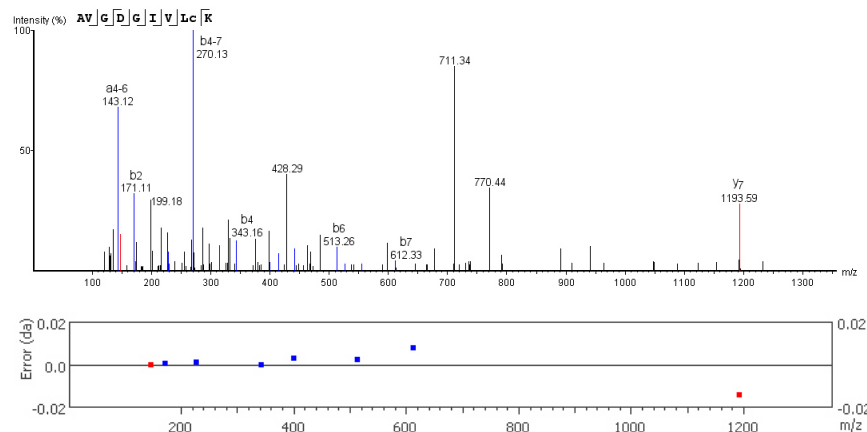


#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			8
2	607.20	304.10	C(+446.17)	1241.57	621.29	7
3	678.24	339.62	A	692.40	346.70	6
4	777.31	389.15	V	621.36	311.18	5
5	876.38	438.69	V	522.29	261.65	4
6	1005.42	503.21	E	423.22	212.11	3
7	1152.49	576.74	F	294.18	147.59	2
8			K	147.11	74.06	1

[S7.42] Plastin-3

AVGDGIVLC(+446.17)K

m/z=710.8606 z=2

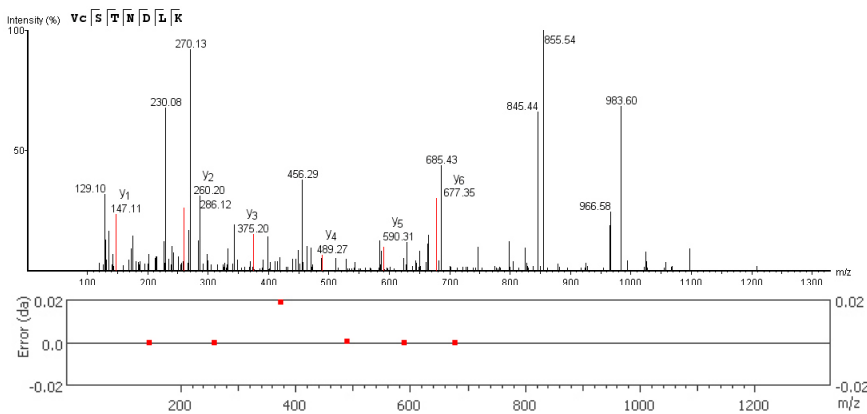


#	b	b (2+)	Seq	y	y (2+)	#
1	72.04	36.52	A			10
2	171.11	86.06	V	1349.66	675.33	9
3	228.13	114.57	G	1250.59	625.80	8
4	343.16	172.08	D	1193.59	597.29	7
5	400.18	200.59	G	1078.55	539.77	6
6	513.26	257.13	I	1021.52	511.26	5
7	612.33	306.67	V	908.44	454.72	4
8	725.42	363.21	L	809.37	405.19	3
9	1274.59	637.80	C(+446.17)	696.29	348.64	2
10			K	147.11	74.06	1

Supplementary Figure S7

[S7.43] Poly [ADP-ribose] polymerase 1

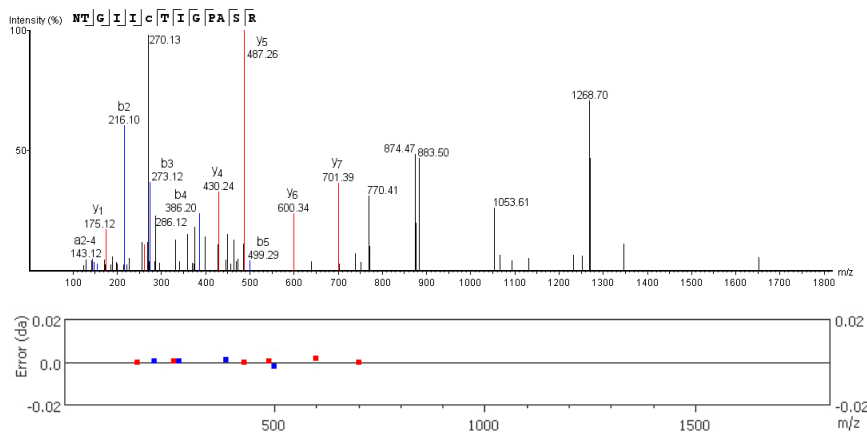
VC(+446.17)STNDLK
m/z=663.3062 z=2



#	b	b (2+)	Seq	y	y (2+)	#
1	100.08	50.54	V			8
2	649.25	325.13	C(+446.17)	1226.52	613.76	7
3	736.28	368.64	S	677.35	339.17	6
4	837.33	419.17	T	590.31	295.66	5
5	951.37	476.19	N	489.27	245.13	4
6	1066.40	533.70	D	375.20	188.11	3
7	1179.48	590.24	L	260.20	130.60	2
8			K	147.11	74.06	1

[S7.44] Pyruvate kinase PKM

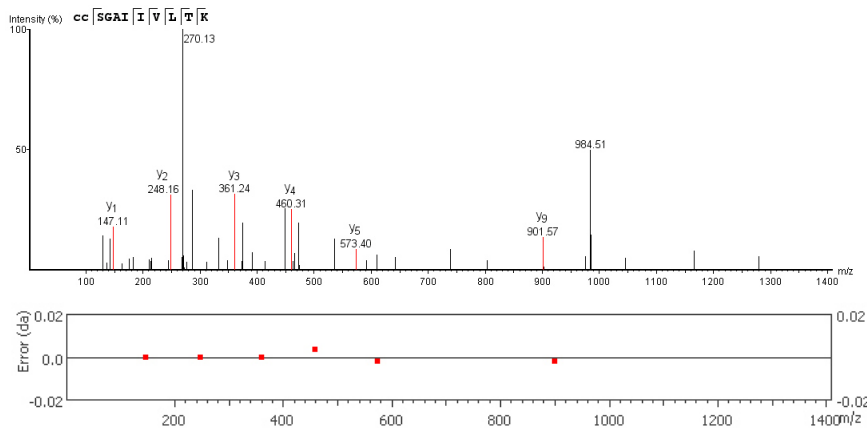
NTGIIC(+446.17)TIGPASR
m/z=874.9383 z=2



#	b	b (2+)	Seq	y	y (2+)	#
1	115.05	58.03	N			13
2	216.10	108.55	T	1634.81	817.90	12
3	273.12	137.06	G	1533.76	767.38	11
4	386.20	193.60	I	1476.74	738.87	10
5	499.29	250.14	I	1363.65	682.33	9
6	1048.46	524.73	C(+446.17)	1250.57	625.78	8
7	1149.51	575.26	T	701.39	351.20	7
8	1262.59	631.80	I	600.34	300.67	6
9	1319.62	660.31	G	487.26	244.13	5
10	1416.67	708.83	P	430.24	215.62	4
11	1487.71	744.35	A	333.19	167.09	3
12	1574.74	787.87	S	262.15	131.58	2
13			R	175.12	88.06	1

[S7.45] Pyruvate Kinase PKM

C(+446.17)C(+414.19)SGAIIVLTK
m/z=984.4862 z=2



#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			11
2	1067.39	534.19	C(+414.19)	1418.77	709.89	10
3	1154.42	577.71	S	901.57	451.29	9
4	1211.44	606.22	G	814.54	407.77	8
5	1282.48	641.74	A	757.52	379.26	7
6	1395.56	698.28	I	686.48	343.74	6
7	1508.64	754.82	I	573.40	287.20	5
8	1607.71	804.36	V	460.31	230.66	4
9	1720.80	860.90	L	361.24	181.12	3
10	1821.84	911.42	T	248.16	124.58	2
11			K	147.11	74.06	1

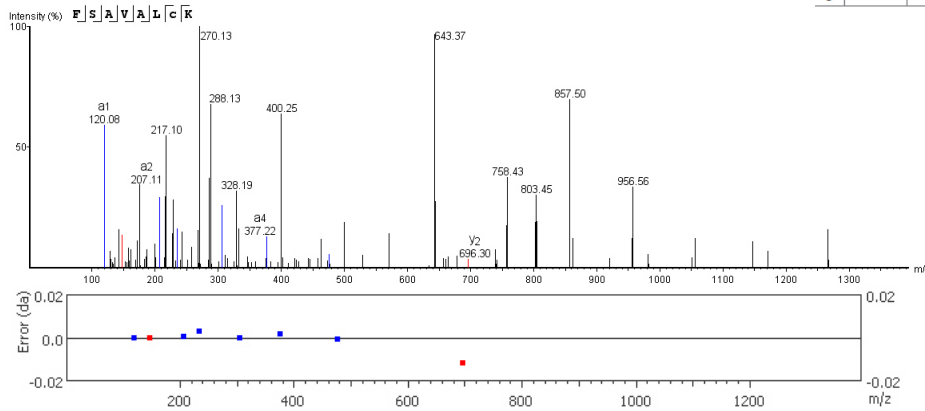
Supplementary Figure S7

[S7.46] Ubiquitin carboxyl-terminal hydrolase isozyme L1

FSAVALC(+446.17)K

m/z=642.81976 z=2

#	b	a	b (2+)	Seq	y	y (2+)	#
1	148.08	120.08	74.54	F			8
2	235.10	207.11	118.05	S	1137.55	569.27	7
3	306.14	278.15	153.57	A	1050.51	525.76	6
4	405.21	377.22	203.11	V	979.48	490.24	5
5	476.25	448.26	238.63	A	880.41	440.70	4
6	589.33	561.34	295.17	L	809.37	405.19	3
7	1138.51	1110.51	569.75	C(+446.17)	696.30	348.64	2
8				K	147.11	74.06	1

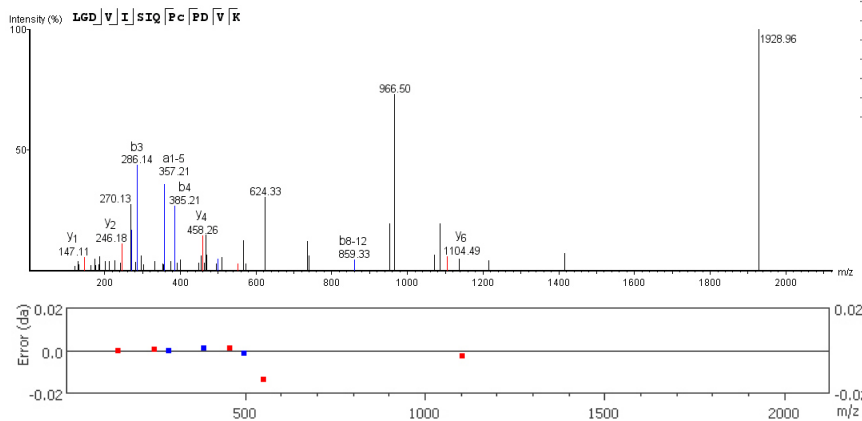


[S7.47] Transitional endoplasmic reticulum ATPase

LGDVISIQPC(+446.17)PDVK

m/z=965.4863 z=2

#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	L			14
2	171.11	86.06	G	1816.86	908.93	13
3	286.14	143.57	D	1759.84	880.42	12
4	385.21	193.10	V	1644.82	822.91	11
5	498.29	249.65	I	1545.75	773.37	10
6	585.32	293.16	S	1432.66	716.83	9
7	698.41	349.70	I	1345.63	673.32	8
8	826.47	413.73	Q	1232.55	616.77	7
9	923.52	462.26	P	1104.49	552.76	6
10	1472.70	736.85	C(+446.17)	1007.44	504.22	5
11	1569.75	785.37	P	458.26	229.63	4
12	1684.77	842.89	D	361.21	181.10	3
13	1783.84	892.42	V	246.18	123.59	2
14			K	147.11	74.06	1

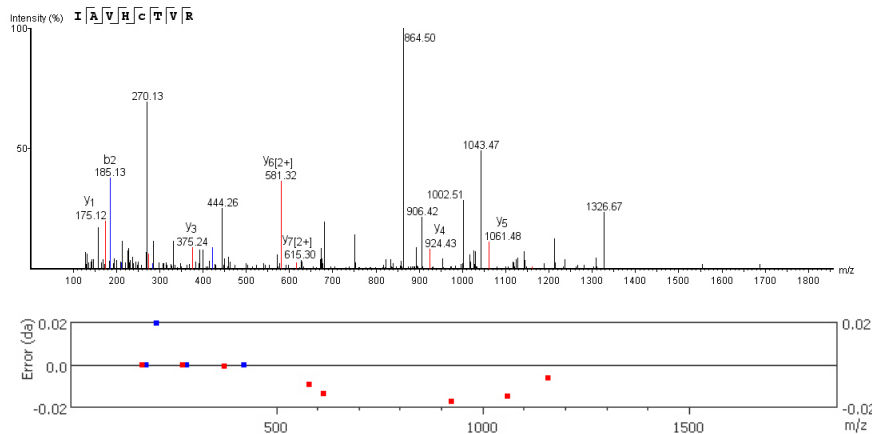


[S7.48] 60S ribosomal Protein L11

IAVHC(+446.17)TVR

m/z=672.8422 z=2

#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	I			8
2	185.13	93.06	A	1231.57	616.30	7
3	284.20	142.60	V	1160.54	580.78	6
4	421.26	211.11	H	1061.48	531.23	5
5	970.43	485.72	C(+446.17)	924.43	462.71	4
6	1071.48	536.24	T	375.24	188.12	3
7	1170.55	585.77	V	274.19	137.59	2
8			R	175.12	88.06	1

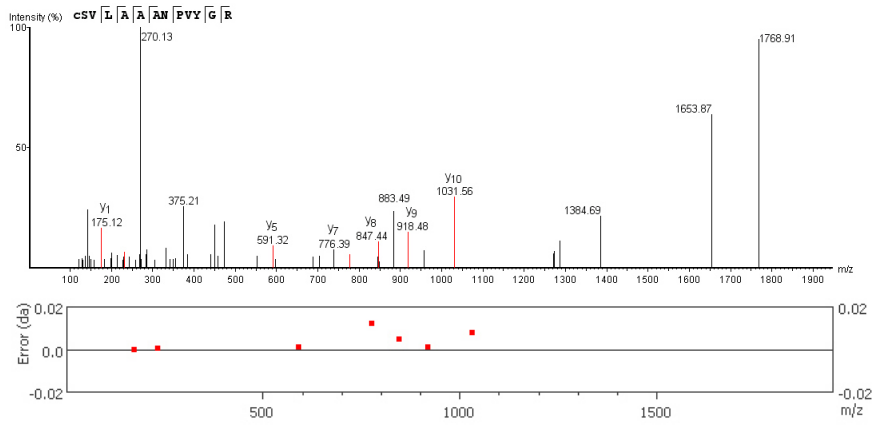


Supplementary Figure S7

[S7.49] DNA replication licensing factor MCM3

C(+446.17)SVLAAANPVYGR

m/z=883.93005 z=2

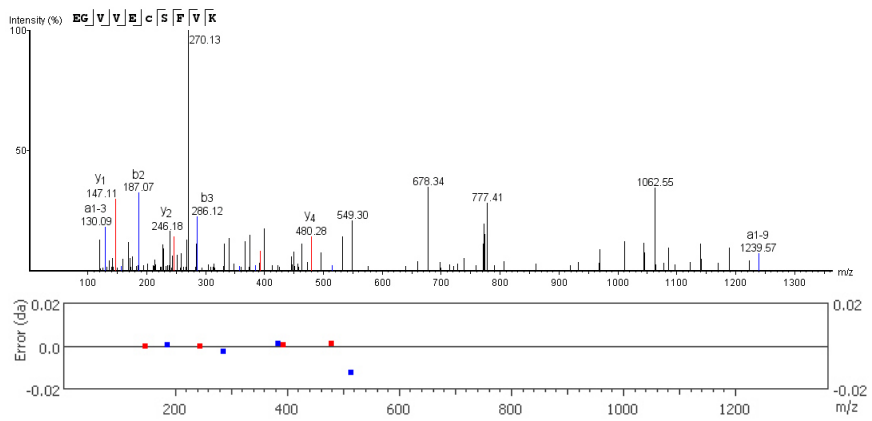


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			13
2	637.21	319.11	S	1217.66	609.33	12
3	736.28	368.64	V	1130.63	565.82	11
4	849.37	425.18	L	1031.56	516.28	10
5	920.40	460.70	A	918.48	459.74	9
6	991.44	496.22	A	847.44	424.22	8
7	1062.48	531.74	A	776.39	388.70	7
8	1176.52	588.76	N	705.37	353.18	6
9	1273.57	637.29	P	591.32	296.16	5
10	1372.64	686.82	V	494.27	247.64	4
11	1535.71	768.35	Y	395.20	198.10	3
12	1592.73	796.86	G	232.14	116.57	2
13			R	175.12	88.06	1

[S7.50] Malate dehydrogenase, mitochondrial

EGVVEC(+446.17)SFVK

m/z=771.8625 z=2

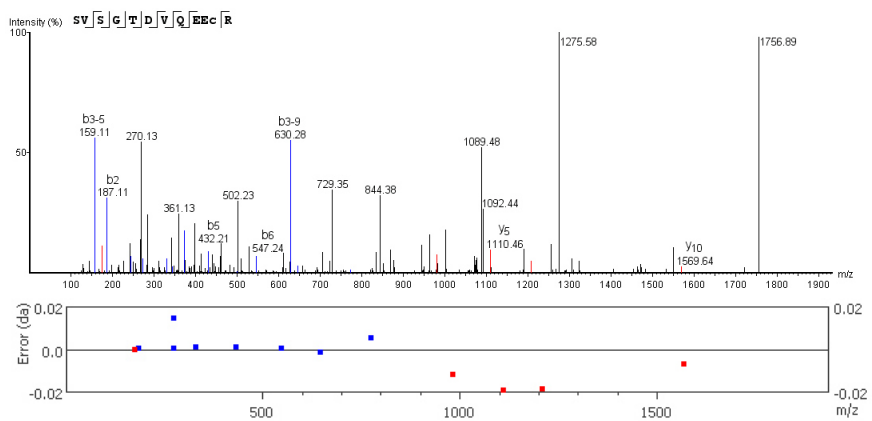


#	b	b (2+)	Seq	y	y (2+)	#
1	130.05	65.53	E			10
2	187.07	94.04	G	1413.66	707.33	9
3	286.14	143.57	V	1356.64	678.82	8
4	385.21	193.10	V	1257.57	629.28	7
5	514.26	257.63	E	1158.50	579.75	6
6	1063.43	532.21	C(+446.17)	1029.46	515.23	5
7	1150.46	575.73	S	480.28	240.64	4
8	1297.53	649.26	F	393.25	197.12	3
9	1396.60	698.80	V	246.18	123.59	2
10			K	147.11	74.06	1

[S7.51] Nuclear autoantigenic sperm protein

SVSGTDVQEEC(+446.17)R

m/z=878.3794 z=2



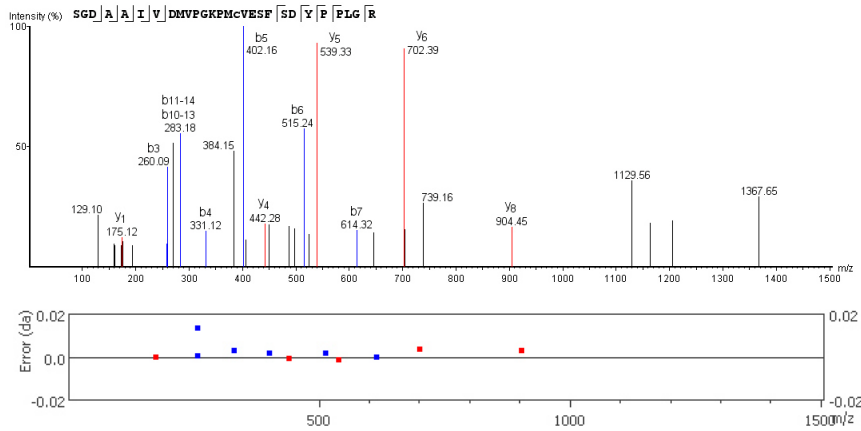
#	b	b (2+)	Seq	y	y (2+)	#
1	88.04	44.52	S			12
2	187.11	94.05	V	1668.70	834.85	11
3	274.14	137.57	S	1569.64	785.32	10
4	331.16	166.08	G	1482.60	741.80	9
5	432.21	216.60	T	1425.58	713.29	8
6	547.24	274.10	D	1324.53	662.77	7
7	646.31	323.65	V	1209.52	605.25	6
8	774.36	387.68	Q	1110.46	555.72	5
9	903.41	452.20	E	982.39	491.69	4
10	1032.45	516.72	E	853.34	427.17	3
11	1581.62	791.31	C(+446.17)	724.29	362.65	2
12			R	175.12	88.06	1

Supplementary Figure S7

[S7.52] Putative elongation factor 1-alpha-like 3

SGDAAIVDMVPGKPMC(+446.17)VESFSDYPPLGR

m/z=1128.852 z=3

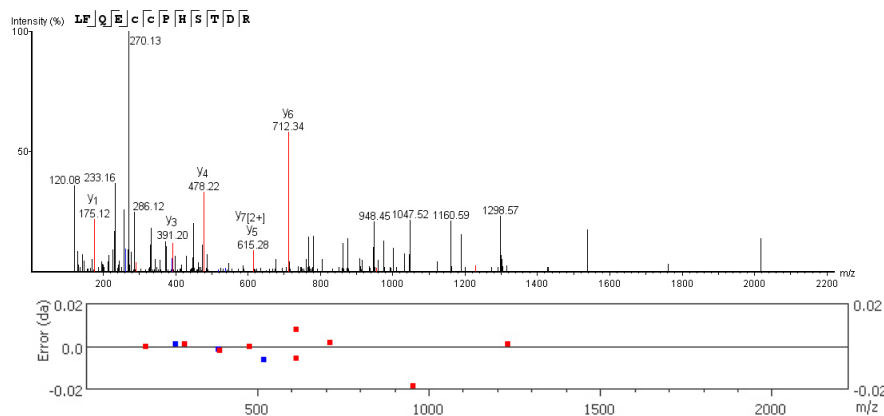


#	b	b (2+)	Seq	y	y (2+)	#
1	88.04	44.52	S			28
2	145.06	73.03	G	3297.51	1649.26	27
3	260.09	130.54	D	3240.49	1620.75	26
4	331.12	166.06	A	3125.46	1563.23	25
5	402.16	201.58	A	3054.43	1527.71	24
6	515.24	258.11	I	2983.39	1492.19	23
7	614.32	307.66	V	2870.31	1435.65	22
8	729.34	365.17	D	2771.24	1386.12	21
9	860.38	430.69	M	2656.21	1328.60	20
10	959.45	480.23	V	2525.17	1263.08	19
11	1056.50	528.75	P	2426.10	1213.55	18
12	1113.53	557.26	G	2329.05	1165.02	17
13	1241.62	621.31	K	2272.03	1136.51	16
14	1338.67	669.84	P	2143.93	1072.47	15
15	1469.71	735.36	M	2046.88	1023.94	14
16	2018.89	1009.94	C(+446.17)	1915.84	958.42	13
17	2117.96	1059.48	V	1366.66	683.83	12
18	2247.00	1124.00	E	1267.60	634.30	11
19	2334.03	1167.52	S	1138.55	569.78	10
20	2481.10	1241.05	F	1051.52	526.26	9
21	2568.13	1284.57	S	904.45	452.73	8
22	2683.16	1342.08	D	817.42	409.21	7
23	2846.22	1423.61	Y	702.39	351.70	6
24	2943.27	1472.14	P	539.33	270.16	5
25	3040.33	1520.66	P	442.28	221.64	4
26	3153.41	1577.21	L	345.22	173.11	3
27	3210.43	1605.72	G	232.14	116.57	2
28			R	175.12	88.06	1

[S7.53] Heterogeneous nuclear ribonucleoprotein K

LFQEC(+446.17)C(+414.19)PHSTDR

m/z=766.0003 z=3

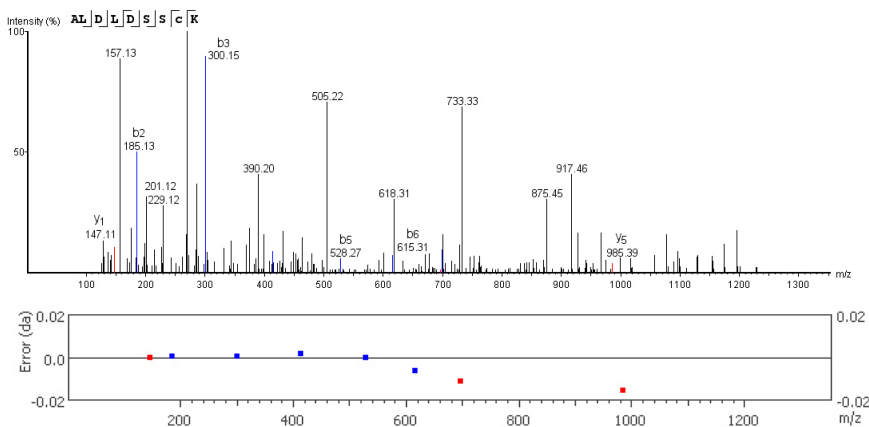


#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	L			12
2	261.16	131.08	F	2182.88	1091.94	11
3	389.22	195.11	Q	2035.82	1018.41	10
4	518.27	259.63	E	1907.76	954.40	9
5	1067.44	534.22	C(+446.17)	1778.72	889.86	8
6	1584.64	792.82	C(+414.19)	1229.54	615.28	7
7	1681.69	841.35	P	712.34	356.67	6
8	1818.75	909.88	H	615.28	308.14	5
9	1905.78	953.39	S	478.22	239.61	4
10	2006.83	1003.92	T	391.20	196.10	3
11	2121.86	1061.43	D	290.14	145.57	2
12			R	175.12	88.06	1

[S7.54] Stress-induced-phosphoprotein 1

ALDLSSC(+446.17)K

m/z=699.3172 z=2



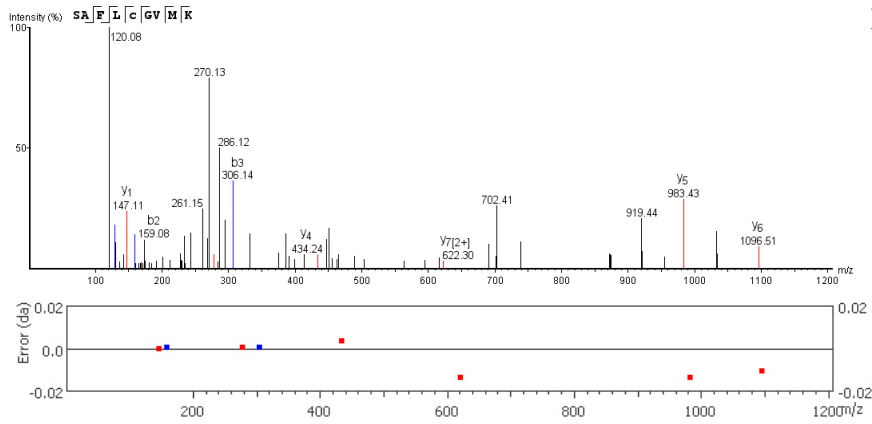
#	b	b (2+)	Seq	y	y (2+)	#
1	72.04	36.52	A			9
2	185.13	93.06	L	1326.57	663.79	8
3	300.15	150.58	D	1213.49	607.24	7
4	413.24	207.12	L	1098.46	549.73	6
5	528.27	264.63	D	985.39	493.19	5
6	615.31	308.15	S	870.35	435.68	4
7	702.33	351.67	S	783.32	392.16	3
8	1251.51	626.25	C(+446.17)	696.30	348.64	2
9			K	147.11	74.06	1

Supplementary Figure S7

[S7.55] Heterogeneous nuclear ribonucleoprotein R

SAFLC(+446.17)GVMK

m/z=701.3325 z=2

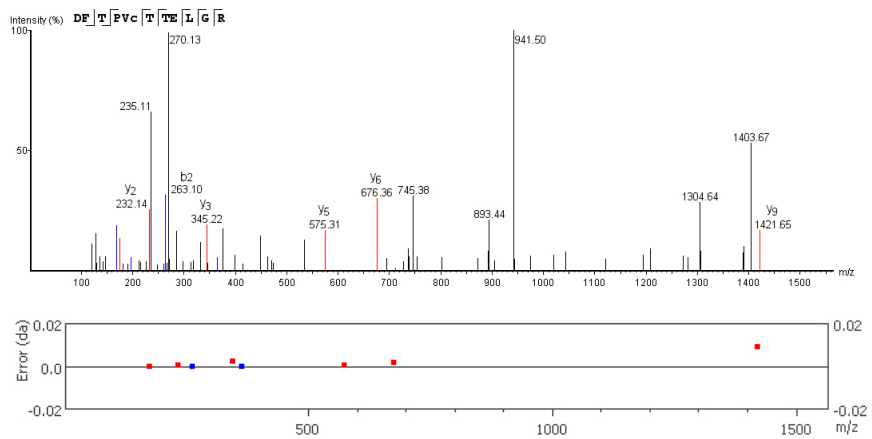


#	b	b (2+)	Seq	y	y (2+)	#
1	88.04	44.52	S			9
2	159.08	80.04	A	1314.61	657.80	8
3	306.14	153.57	F	1243.57	622.30	7
4	419.23	210.11	L	1096.51	548.75	6
5	968.40	484.70	C(+446.17)	983.43	492.21	5
6	1025.43	513.21	G	434.24	217.62	4
7	1124.49	562.75	V	377.22	189.11	3
8	1255.53	628.27	M	278.15	139.58	2
9			K	147.11	74.06	1

[S7.56] Peridoxin-6

DFTPVC(+446.17)TTELGR

m/z=892.9135 z=2

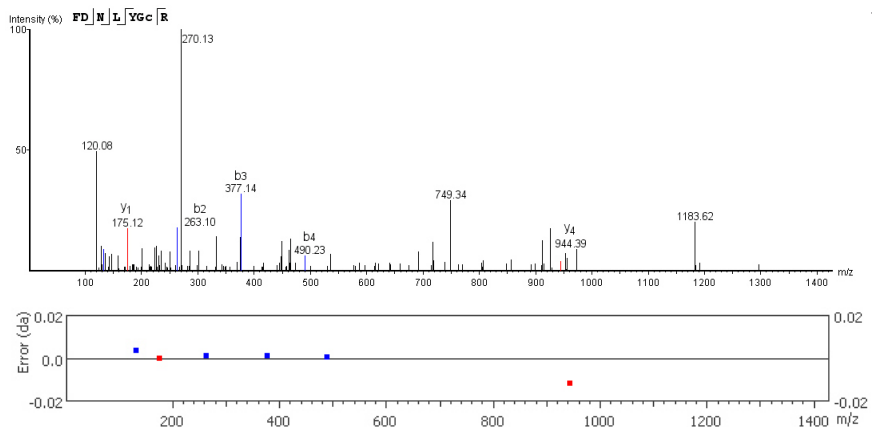


#	b	b (2+)	Seq	y	y (2+)	#
1	116.03	58.52	D			12
2	263.10	132.05	F	1669.77	835.39	11
3	364.15	182.58	T	1522.71	761.85	10
4	461.20	231.10	P	1421.65	711.33	9
5	560.27	280.64	V	1324.61	662.80	8
6	1109.45	555.22	C(+446.17)	1225.54	613.27	7
7	1210.49	605.75	T	676.36	338.68	6
8	1311.54	656.27	T	575.31	288.16	5
9	1440.58	720.79	E	474.27	237.63	4
10	1553.67	777.33	L	345.22	173.11	3
11	1610.69	805.85	G	232.14	116.57	2
12			R	175.12	88.06	1

[S7.57] Adenosylhomocysteinase

FDNLYGC(+446.17)R

m/z=717.3129 z=2



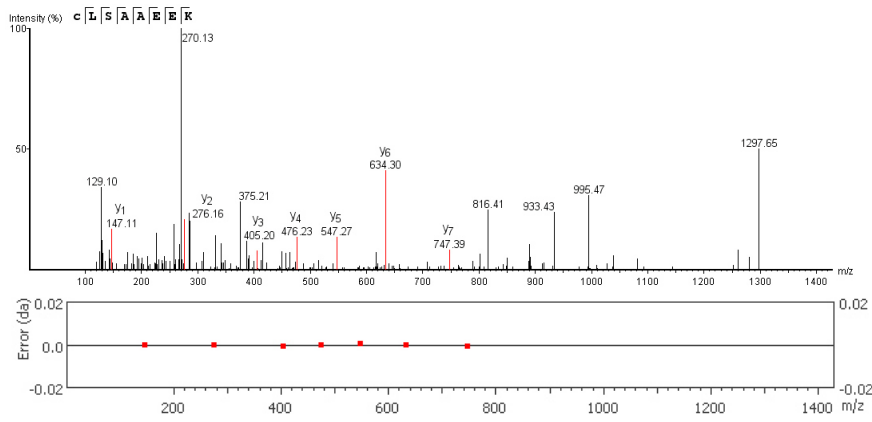
#	b	b (2+)	Seq	y	y (2+)	#
1	148.08	74.54	F			8
2	263.10	132.05	D	1286.53	643.77	7
3	377.14	189.07	N	1171.51	586.25	6
4	490.23	245.62	L	1057.46	529.23	5
5	653.29	327.15	Y	944.39	472.69	4
6	710.31	355.66	G	781.32	391.16	3
7	1259.49	630.24	C(+446.17)	724.29	362.65	2
8			R	175.12	88.06	1

Supplementary Figure S7

[S7.58] Tropomyosin alpha-3 chain

C(+446.17)LSAAEEK

m/z=648.79333 z=2

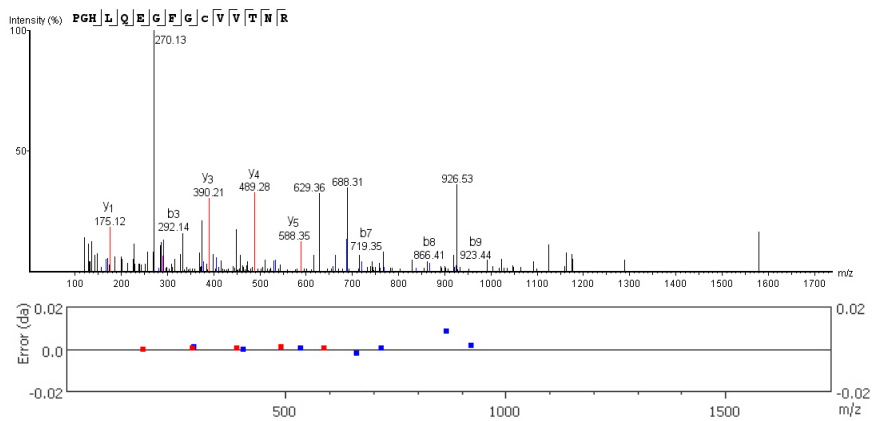


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			8
2	663.27	332.13	L	747.39	374.19	7
3	750.30	375.65	S	634.30	317.65	6
4	821.34	411.17	A	547.27	274.14	5
5	892.37	446.69	A	476.23	238.62	4
6	1021.42	511.21	E	405.20	203.10	3
7	1150.46	575.73	E	276.16	138.58	2
8			K	147.11	74.06	1

[S7.59] Plasminogen activator inhibitor 1 RNA-binding protein

PGHLQEGFGC(+446.17)VVTNR

m/z=687.326 z=3

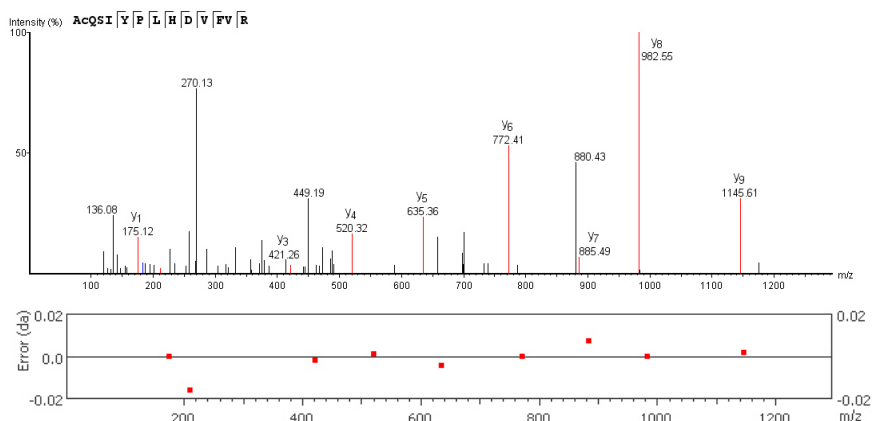


#	b	b (2+)	Seq	y	y (2+)	#
1	98.06	49.53	P			15
2	155.08	78.04	G	1962.90	981.95	14
3	292.14	146.57	H	1905.88	953.44	13
4	405.22	203.11	L	1768.82	884.91	12
5	533.28	267.14	Q	1655.73	828.37	11
6	662.33	331.66	E	1527.68	764.34	10
7	719.35	360.17	G	1398.63	699.82	9
8	866.41	433.71	F	1341.61	671.31	8
9	923.44	462.22	G	1194.54	597.77	7
10	1472.61	736.81	C(+446.17)	1137.52	569.26	6
11	1571.68	786.34	V	588.35	294.67	5
12	1670.75	835.87	V	489.28	245.14	4
13	1771.80	886.40	T	390.21	195.60	3
14	1885.84	943.42	N	289.16	145.08	2
15			R	175.12	88.06	1

[S7.60] 40S ribosomal protein S3a

AC(+446.17)QSIYPLHDFVFR

m/z=698.67615 z=3



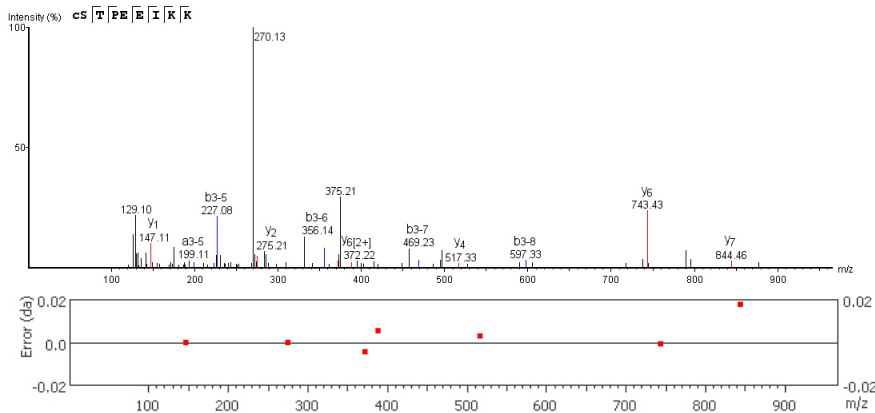
#	b	b (2+)	Seq	y	y (2+)	#
1	72.04	36.52	A			14
2	621.22	311.11	C(+446.17)	2022.96	1011.98	13
3	749.28	375.14	Q	1473.78	737.39	12
4	836.31	418.66	S	1345.73	673.36	11
5	949.39	475.20	I	1258.69	629.85	10
6	1112.46	556.73	Y	1145.61	573.31	9
7	1209.51	605.26	P	982.55	491.77	8
8	1322.59	661.80	L	885.49	443.25	7
9	1459.65	730.33	H	772.41	386.71	6
10	1574.68	787.84	D	635.36	318.18	5
11	1673.75	837.37	V	520.32	260.66	4
12	1820.82	910.91	F	421.26	211.14	3
13	1919.89	960.44	V	274.19	137.59	2
14			R	175.12	88.06	1

Supplementary Figure S7

[S7.61] Dextrin

C(+446.17)STPEEIKK

m/z=494.2378 z=3

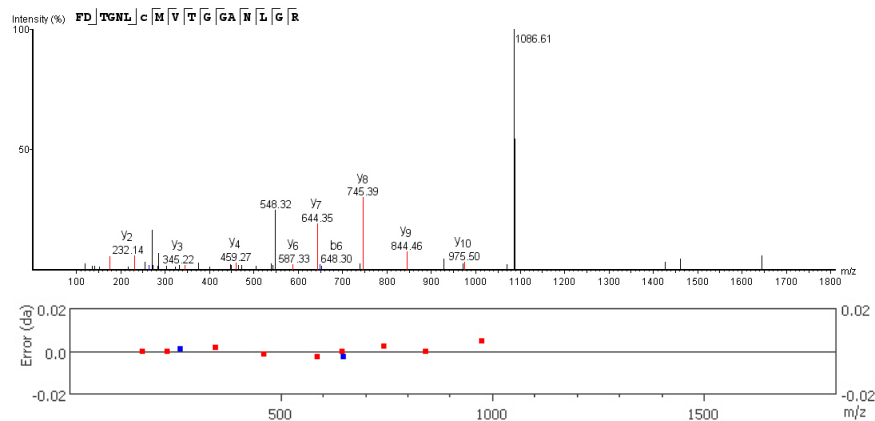


#	b	b (2+)	Seq	y	y (2+)	#
1	550.18	275.59	C(+446.17)			9
2	637.21	319.11	S	931.51	466.25	8
3	738.26	369.63	T	844.46	422.74	7
4	835.32	418.16	P	743.43	372.22	6
5	964.36	482.68	E	646.38	323.69	5
6	1093.40	547.20	E	517.33	259.17	4
7	1206.48	603.74	I	388.29	194.65	3
8	1334.58	667.79	K	275.21	138.10	2
9			K	147.11	74.06	1

[S7.62] 40S ribosomal protein S4, X isoform

FDTGNLC(+446.17)MVTGGANLGR

m/z=1086.4978 z=2

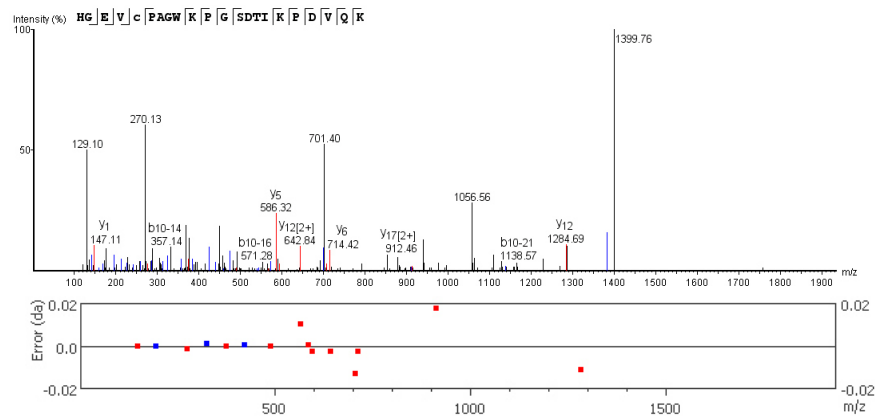


#	b	b (2+)	Seq	y	y (2+)	#
1	148.08	74.54	F			17
2	263.10	132.05	D	2024.90	1012.95	16
3	364.15	182.58	T	1909.88	955.44	15
4	421.17	211.09	G	1808.83	904.91	14
5	535.22	268.11	N	1751.81	876.40	13
6	648.30	324.65	L	1637.76	819.38	12
7	1197.47	599.24	C(+446.17)	1524.68	762.84	11
8	1328.51	664.76	M	975.50	488.25	10
9	1427.58	714.29	V	844.46	422.73	9
10	1528.63	764.82	T	745.39	373.20	8
11	1585.65	793.33	G	644.35	322.67	7
12	1642.67	821.84	G	587.33	294.16	6
13	1713.71	857.36	A	530.30	265.65	5
14	1827.75	914.38	N	459.27	230.13	4
15	1940.84	970.92	L	345.22	173.11	3
16	1997.86	999.43	G	232.14	116.57	2
17			R	175.12	88.06	1

[S7.63] Peredoxin-1

HGEVC(+446.17)PAGWKPGSDTIKPDVQK

m/z=699.5911 z=4



#	b	b (2+)	Seq	y	y (2+)	#
1	138.07	69.53	H			22
2	195.09	98.04	G	2658.27	1329.64	21
3	324.13	162.57	E	2601.25	1301.13	20
4	423.20	212.10	V	2472.21	1236.60	19
5	972.37	486.69	C(+446.17)	2373.14	1187.07	18
6	1069.43	535.21	P	1823.96	912.46	17
7	1140.46	570.73	A	1726.91	863.96	16
8	1197.49	599.24	G	1655.88	828.44	15
9	1383.56	692.28	W	1598.85	799.93	14
10	1511.66	756.33	K	1412.77	706.90	13
11	1608.71	804.86	P	1284.69	642.84	12
12	1665.73	833.37	G	1187.63	594.32	11
13	1752.77	876.88	S	1130.61	565.79	10
14	1867.79	934.40	D	1043.57	522.29	9
15	1968.84	984.92	T	928.55	464.77	8
16	2081.92	1041.46	I	827.50	414.25	7
17	2210.02	1105.51	K	714.42	357.71	6
18	2307.07	1154.04	P	596.32	293.66	5
19	2422.10	1211.55	D	489.27	245.13	4
20	2521.17	1261.08	V	374.24	187.62	3
21	2649.23	1325.11	Q	275.17	138.09	2
22			K	147.11	74.06	1

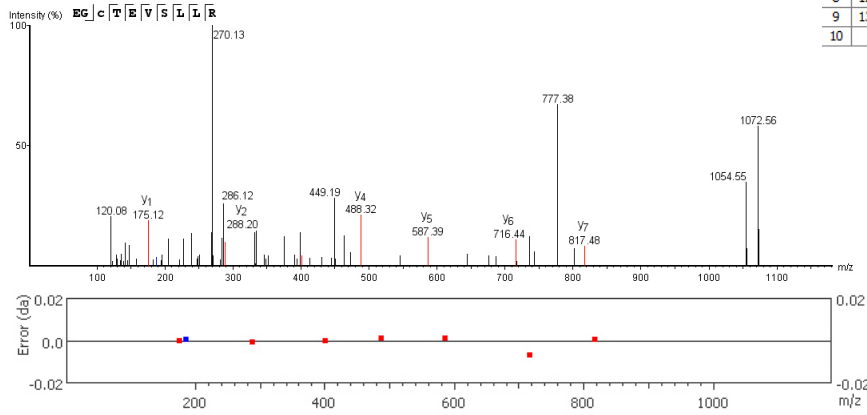
Supplementary Figure S7

[S7.64] Heterogeneous nuclear ribonucleoprotein U

EGC(+446.17)TEVSLLR

m/z=776.8697 z=2

#	b	b (2+)	Seq	y	y (2+)	#
1	130.05	65.53	E			10
2	187.07	94.04	G	1423.67	712.34	9
3	736.25	368.62	C(+446.17)	1366.65	683.83	8
4	837.29	419.15	T	817.48	409.24	7
5	966.34	483.67	E	716.44	358.72	6
6	1065.41	533.20	V	587.39	294.19	5
7	1152.44	576.72	S	488.32	244.66	4
8	1265.52	633.26	L	401.29	201.14	3
9	1378.61	689.80	L	288.20	144.60	2
10			R	175.12	88.06	1

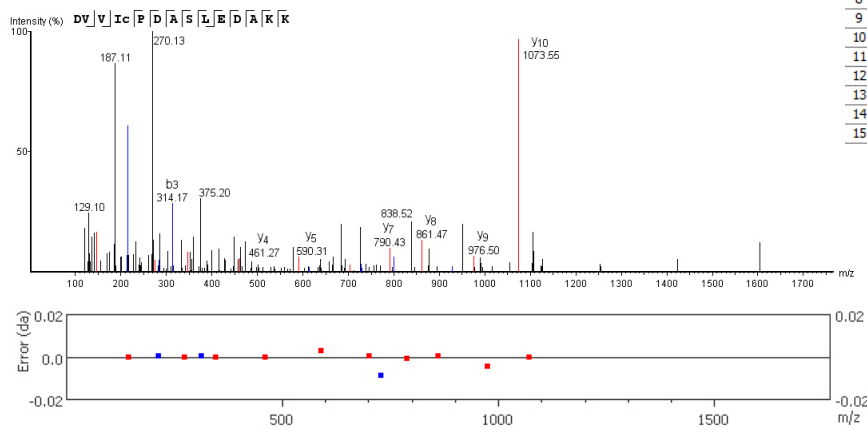


[S7.65] Protein deglycase DJ-1

DVVIC(+446.17)PDASLEDAKK

m/z=683.6673 z=3

#	b	b (2+)	Seq	y	y (2+)	#
1	116.03	58.52	D			15
2	215.10	108.05	V	1933.94	967.47	14
3	314.17	157.59	V	1834.87	917.94	13
4	427.26	214.13	I	1735.81	868.40	12
5	976.43	488.72	C(+446.17)	1622.72	811.86	11
6	1073.48	537.24	P	1073.55	537.27	10
7	1188.51	594.76	D	976.50	488.75	9
8	1259.55	630.27	A	861.47	431.23	8
9	1346.58	673.79	S	790.43	395.72	7
10	1459.66	730.34	L	703.40	352.20	6
11	1588.71	794.85	E	590.31	295.66	5
12	1703.73	852.37	D	461.27	231.14	4
13	1774.77	887.89	A	346.25	173.62	3
14	1902.87	951.93	K	275.21	138.10	2
15			K	147.11	74.06	1

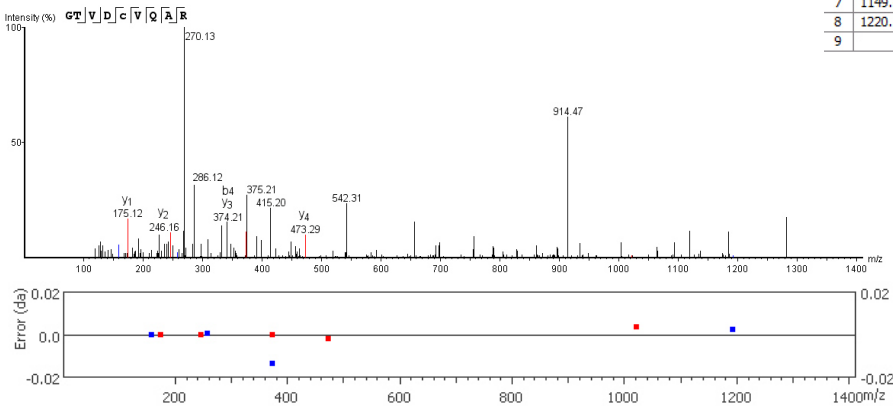


[S7.66] Programmed cell death protein 4

GTVDC(+446.17)VQAR

m/z=697.8236 z=2

#	b	a	b (2+)	Seq	y	y (2+)	#
1	58.03	30.03	29.51	G			9
2	159.08	131.08	80.04	T	1337.60	669.30	8
3	258.14	230.15	129.57	V	1236.55	618.78	7
4	373.19	345.18	187.09	D	1137.48	569.24	6
5	922.35	894.35	461.67	C(+446.17)	1022.45	511.73	5
6	1021.42	993.42	511.21	V	473.29	237.14	4
7	1149.47	1121.48	575.24	Q	374.21	187.61	3
8	1220.51	1192.51	610.76	A	246.16	123.58	2
9				R	175.12	88.06	1

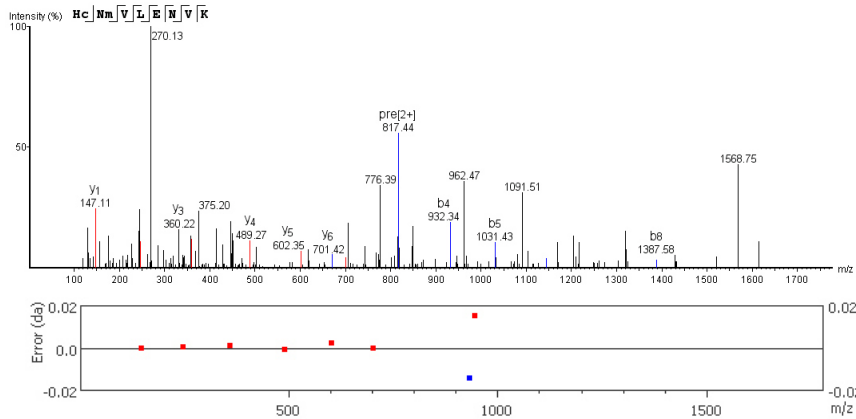


Supplementary Figure S7

[S7.67] Small nuclear ribonucleoprotein Sm D2

HC(+446.17)NMVLENVK

m/z=816.8777 z=2

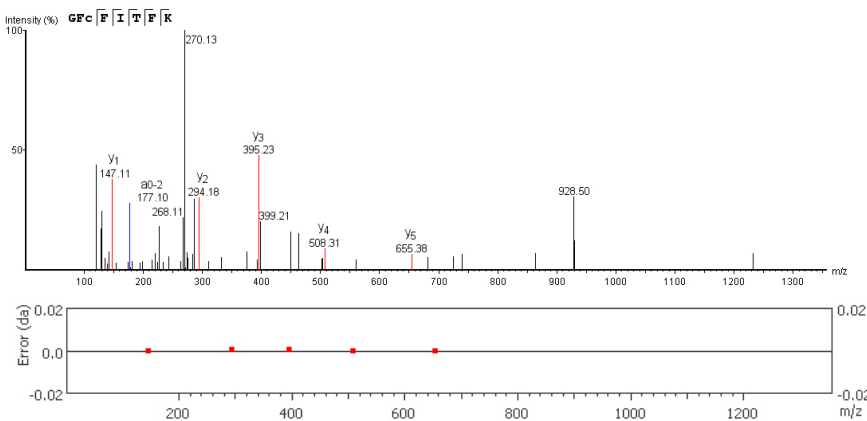


#	b	b (2+)	Seq	y	y (2+)	#
1	138.07	69.53	H			10
2	687.24	344.12	C(+446.17)	1495.68	748.34	9
3	801.28	401.14	N	946.49	473.75	8
4	932.34	466.66	M	832.46	416.73	7
5	1031.39	516.20	V	701.42	351.21	6
6	1144.48	572.74	L	602.35	301.68	5
7	1273.52	637.26	E	489.27	245.13	4
8	1387.56	694.28	N	360.22	180.61	3
9	1486.63	743.82	V	246.18	123.59	2
10			K	147.11	74.06	1

[S7.68] Heterogeneous nuclear ribonucleoprotein D0

GFC(+446.17)FITFK

m/z=704.8352 z=2

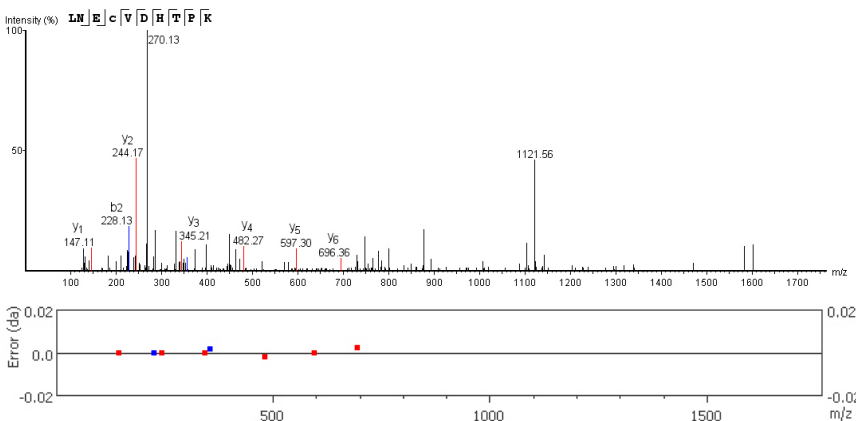


#	b	b (2+)	Seq	y	y (2+)	#
1	58.03	29.51	G			8
2	205.10	103.05	F	1351.62	676.31	7
3	754.27	377.64	C(+446.17)	1204.56	602.78	6
4	901.34	451.17	F	655.38	328.19	5
5	1014.43	507.71	I	508.31	254.66	4
6	1115.47	558.24	T	395.23	198.11	3
7	1262.54	631.77	F	294.18	147.59	2
8			K	147.11	74.06	1

[S7.69] Glutathione S-transferase omega-1

LNEC(+446.17)VDHTPK

m/z=801.36676 z=2



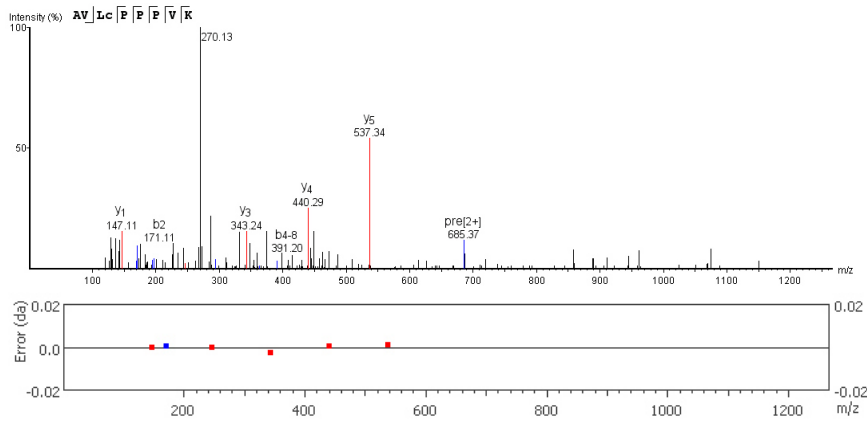
#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	L			10
2	228.13	114.57	N	1488.63	744.81	9
3	357.18	179.09	E	1374.59	687.79	8
4	906.35	453.68	C(+446.17)	1245.54	623.27	7
5	1005.42	503.21	V	696.36	348.68	6
6	1120.45	560.72	D	597.30	299.15	5
7	1257.51	629.25	H	482.27	241.64	4
8	1358.55	679.78	T	345.21	173.11	3
9	1455.61	728.30	P	244.17	122.58	2
10			K	147.11	74.06	1

Supplementary Figure S7

[S7.70] Ras-related C3 botulinum toxin substrate 1

AVLC(+446.17)PPPVK

m/z=685.3553 z=2

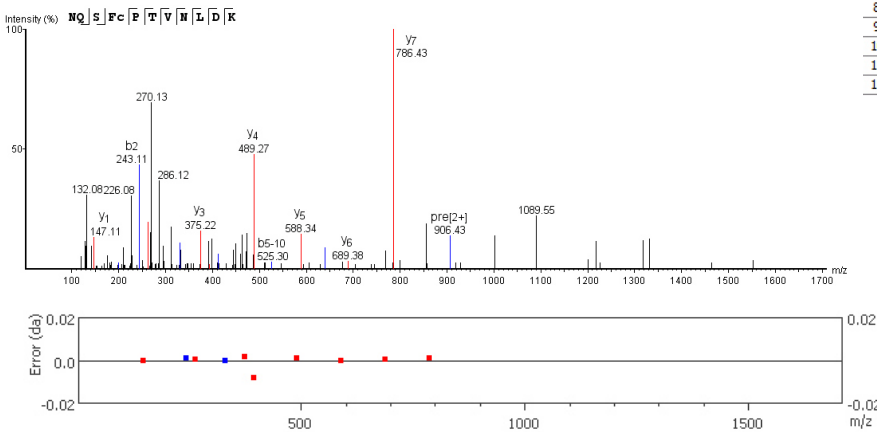


#	b	b (2+)	Seq	y	y (2+)	#
1	72.04	36.52	A			9
2	171.11	86.06	V	1298.67	649.83	8
3	284.20	142.60	L	1199.60	600.30	7
4	833.37	417.19	C(+446.17)	1086.51	543.76	6
5	930.43	465.71	P	537.34	269.17	5
6	1027.48	514.24	P	440.29	220.64	4
7	1124.53	562.77	P	343.24	172.12	3
8	1223.60	612.30	V	246.18	123.59	2
9			K	147.11	74.06	1

[S7.71] 60S ribosomal protein L27a

NQSFC(+446.17)PTVNLDK

m/z=906.4186 z=2

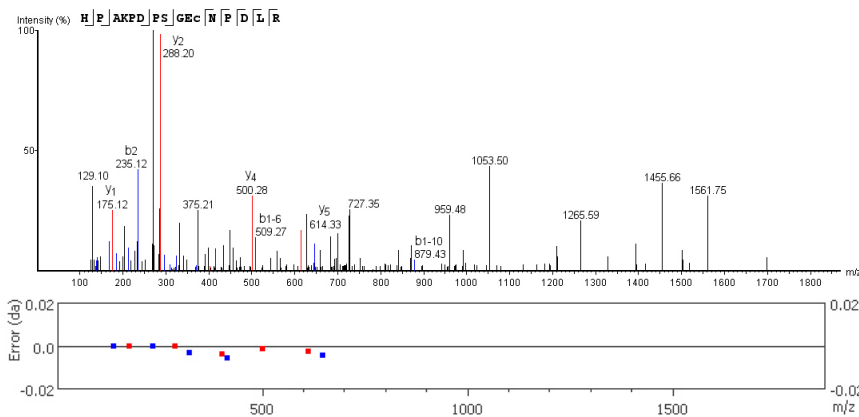


#	b	b (2+)	Seq	y	y (2+)	#
1	115.05	58.03	N			12
2	243.11	122.05	Q	1697.77	849.38	11
3	330.14	165.57	S	1569.71	785.36	10
4	477.21	239.10	F	1482.68	741.84	9
5	1026.38	513.69	C(+446.17)	1335.61	668.31	8
6	1123.44	562.22	P	786.43	393.73	7
7	1224.49	612.74	T	689.38	345.19	6
8	1323.55	662.28	V	588.34	294.67	5
9	1437.60	719.30	N	489.27	245.13	4
10	1550.68	775.84	L	375.22	188.11	3
11	1665.71	833.35	D	262.14	131.57	2
12			K	147.11	74.06	1

[S7.72] Histone-binding protein RBBP7

HPAKPDPSGEC(+446.17)NPDLR

m/z=727.0025 z=3



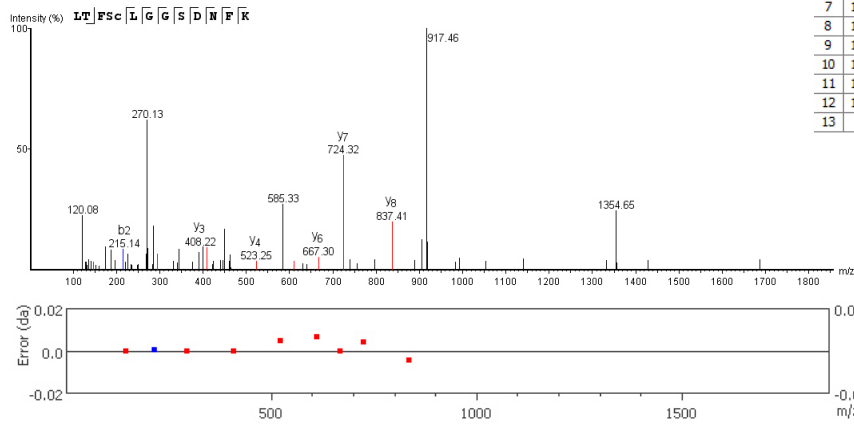
#	b	b (2+)	Seq	y	y (2+)	#
1	138.07	69.53	H			16
2	235.12	118.06	P	2041.91	1021.46	15
3	306.16	153.58	A	1944.86	972.93	14
4	434.25	217.63	K	1873.82	937.41	13
5	531.30	266.15	P	1745.73	873.36	12
6	646.34	323.67	D	1648.68	824.84	11
7	743.38	372.19	P	1533.65	767.32	10
8	830.42	415.71	S	1436.60	718.80	9
9	887.44	444.22	G	1349.56	675.28	8
10	1016.48	508.74	E	1292.54	646.77	7
11	1565.66	783.33	C(+446.17)	1163.50	582.25	6
12	1679.70	840.35	N	614.33	307.66	5
13	1776.75	888.88	P	500.28	250.64	4
14	1891.78	946.39	D	403.23	202.11	3
15	2004.86	1002.93	L	288.20	144.60	2
16			R	175.12	88.06	1

Supplementary Figure S7

[S7.73] Prostaglandin E synthase 3

LTFSC(+446.17)LGGSDNFK

m/z=917.9189 z=2

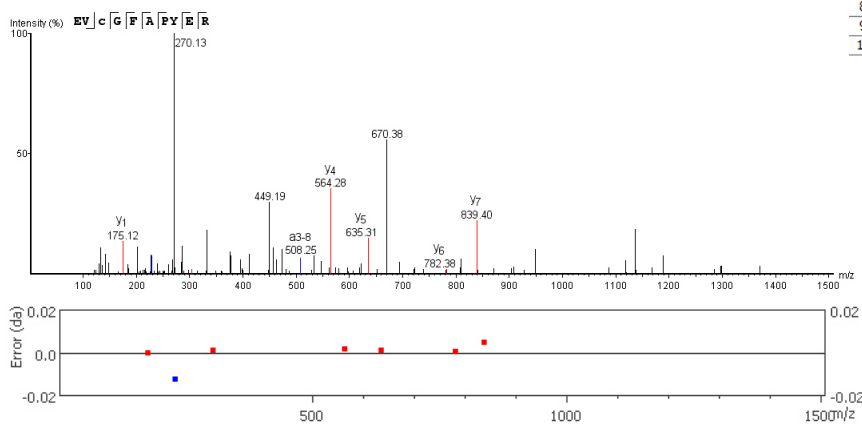


#	b	b (2+)	Seq	y	y (2+)	#
1	114.09	57.55	L			13
2	215.14	108.07	T	1721.73	861.37	12
3	362.21	181.60	F	1620.69	810.84	11
4	449.24	225.12	S	1473.62	737.31	10
5	998.41	499.71	C(+446.17)	1386.59	693.79	9
6	1111.50	556.25	L	837.41	419.21	8
7	1168.52	584.76	G	724.32	362.66	7
8	1225.54	613.27	G	667.30	334.15	6
9	1312.57	656.79	S	610.28	305.64	5
10	1427.60	714.30	D	523.25	262.13	4
11	1541.64	771.32	N	408.22	204.61	3
12	1688.71	844.86	F	294.18	147.59	2
13			K	147.11	74.06	1

[S7.74] 60S ribosomal protein L36

EVC(+446.17)GFAPYER

m/z=808.8582 z=2

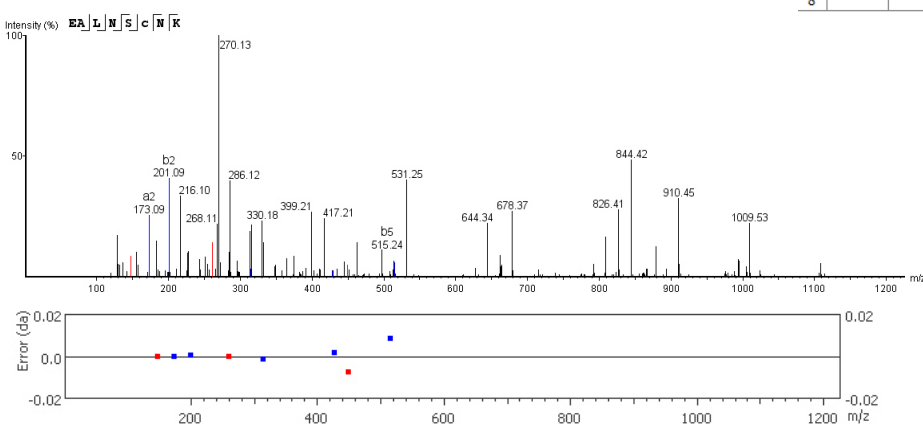


#	b	b (2+)	Seq	y	y (2+)	#
1	130.05	65.53	E			10
2	229.13	115.06	V	1487.65	744.32	9
3	778.29	389.65	C(+446.17)	1388.58	694.79	8
4	835.32	418.16	G	839.40	420.20	7
5	982.38	491.69	F	782.38	391.69	6
6	1053.42	527.21	A	635.31	318.16	5
7	1150.47	575.74	P	564.28	282.64	4
8	1313.54	657.27	Y	467.22	234.11	3
9	1442.58	721.79	E	304.16	152.58	2
10			R	175.12	88.06	1

[S7.75] Nucleolin

EALNSC(+446.17)NK

m/z=662.7971 z=2



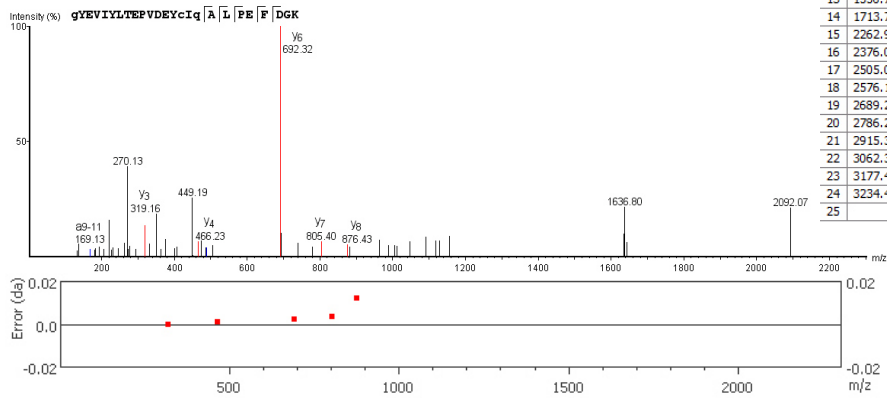
#	b	a	b (2+)	Seq	y	y (2+)	#
1	130.05	102.06	65.53	E			8
2	201.09	173.09	101.04	A	1195.53	598.26	7
3	314.17	286.18	157.59	L	1124.49	562.74	6
4	428.21	400.22	214.61	N	1011.41	506.20	5
5	515.24	487.25	258.12	S	897.36	449.19	4
6	1064.42	1036.43	532.71	C(+446.17)	810.33	405.67	3
7	1178.46	1150.47	589.73	N	261.16	131.08	2
8				K	147.11	74.06	1

Supplementary Figure S7

[S7.76] Endoplasmic

G(+42.01)YEVIYLTEPVDEYC(+446.17)IQ(+.98)ALPEFDGK

m/z=1127.5282 z=3

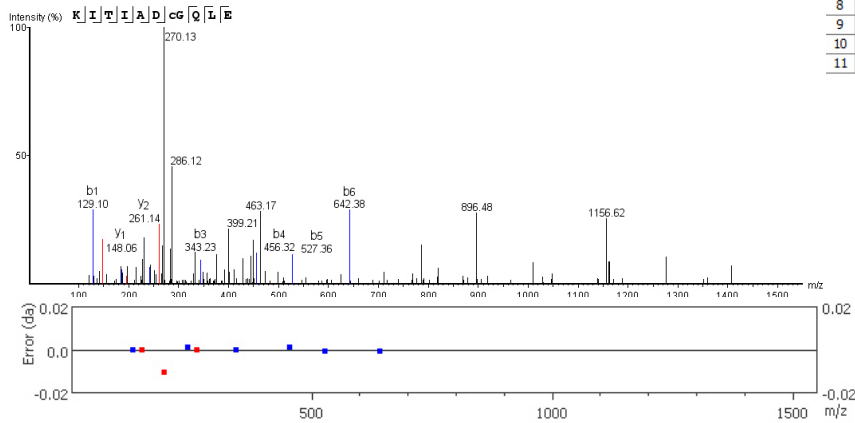


#	b	a	b (2+)	Seq	y	y (2+)	#
1	100.04	72.04	50.52	G(+42.01)			25
2	263.10	235.11	132.05	Y	3281.50	1641.25	24
3	392.15	364.15	196.57	E	3118.43	1559.72	23
4	491.21	463.22	246.11	V	2989.39	1495.20	22
5	604.30	576.30	302.65	I	2890.32	1445.66	21
6	767.36	739.37	384.18	Y	2777.24	1389.12	20
7	880.45	852.45	440.72	L	2614.18	1307.59	19
8	981.49	953.50	491.25	T	2501.09	1251.05	18
9	1110.54	1082.54	555.77	E	2400.04	1200.52	17
10	1207.59	1179.59	604.29	P	2271.00	1136.00	16
11	1306.66	1278.66	653.83	V	2173.95	1087.47	15
12	1421.68	1393.69	711.34	D	2074.88	1037.94	14
13	1550.73	1522.73	775.86	E	1959.85	980.43	13
14	1713.79	1685.79	857.39	Y	1830.81	915.91	12
15	2262.96	2234.97	1131.98	C(+446.17)	1667.75	834.37	11
16	2376.05	2348.05	1188.52	I	1118.57	559.79	10
17	2505.09	2477.10	1253.05	Q(+.98)	1005.49	503.24	9
18	2576.13	2548.13	1288.56	A	876.43	438.72	8
19	2689.21	2661.22	1345.11	L	805.40	403.20	7
20	2786.27	2758.27	1393.63	P	692.32	346.66	6
21	2915.31	2887.31	1458.15	E	595.27	298.14	5
22	3062.38	3034.38	1531.69	F	466.23	233.61	4
23	3177.40	3149.41	1589.20	D	319.16	160.08	3
24	3234.42	3206.43	1617.71	G	204.13	102.57	2
25				K	147.11	74.06	1

[S7.77] Peptidyl-prolyl cis-trans isomerase A

KITIADC(+446.17)GQLE

m/z=818.9002 z=2

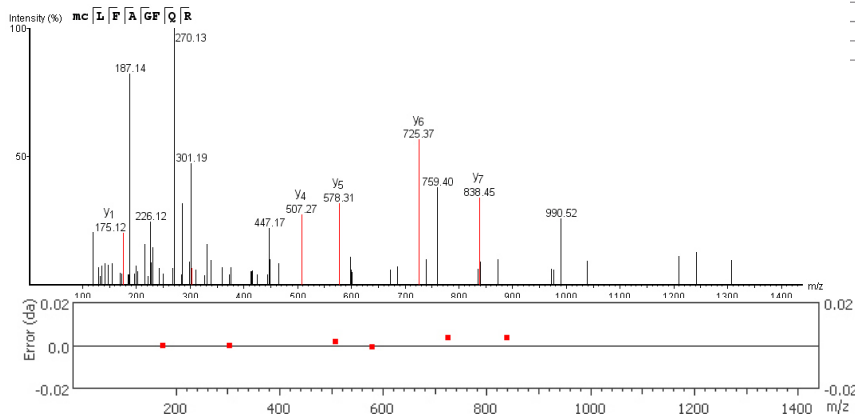


#	b	b (2+)	Seq	y	y (2+)	#
1	129.10	65.05	K			11
2	242.19	121.59	I	1508.68	754.84	10
3	343.23	172.12	T	1395.60	698.30	9
4	456.32	228.66	I	1294.55	647.77	8
5	527.36	264.18	A	1181.46	591.23	7
6	642.38	321.69	D	1110.43	555.71	6
7	1191.56	596.28	C(+446.17)	995.40	498.20	5
8	1248.58	624.79	G	446.22	223.61	4
9	1376.64	688.82	Q	389.20	195.11	3
10	1489.72	745.36	L	261.14	131.07	2
11			E	148.06	74.53	1

[S7.78] Heterogeneous nuclear ribonucleoprotein U

MC(+446.17)LFAGFQR

m/z=759.8464 z=2



#	b	b (2+)	Seq	y	y (2+)	#
1	132.05	66.52	M			9
2	681.22	341.11	C(+446.17)	1387.63	694.32	8
3	794.31	397.65	L	838.45	419.73	7
4	941.38	471.19	F	725.37	363.19	6
5	1012.41	506.71	A	578.31	289.65	5
6	1069.43	535.22	G	507.27	254.13	4
7	1216.50	608.75	F	450.25	225.62	3
8	1344.56	672.78	Q	303.18	152.09	2
9			R	175.12	88.06	1

Fig S7: MS spectra of persulfide peptides (S-IAMBio, +446.17 Da) found in the total fraction of non-stimulated cells. MS/MS fragment ions of persulfide peptides identified in the total fraction of the initial proteomic approach (Fig 1) are depicted in red and blue, respectively. The inset shows the sequence coverage of the peptides by b, b²⁺, y and y²⁺ ions. Lower panels indicate the mass error.