

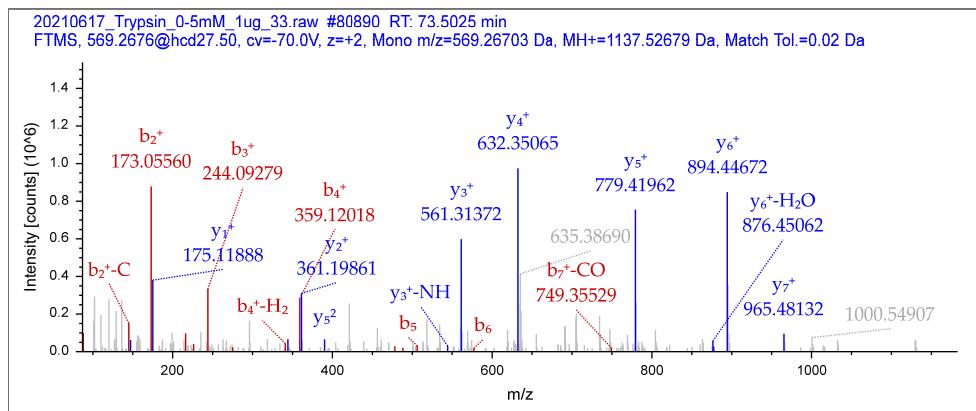
Supplementary S3. MS/MS spectra of all modifications identified on glycolytic enzymes

Fructose bisphosphate aldolase A (K147)

Sequence: DGADFAKWR, K7-Carboxyethyl (72.02113 Da)

Charge: +2, Monoisotopic m/z: 569.26703 Da (-2.78 mmu/-4.88 ppm), MH+: 1137.52679 Da, RT: 73.5025 min,

Identified with: Sequest HT (v1.17); XCorr:3.04, Percolator q-Value:1.9e-3, Percolator PEP:2.4e-2,



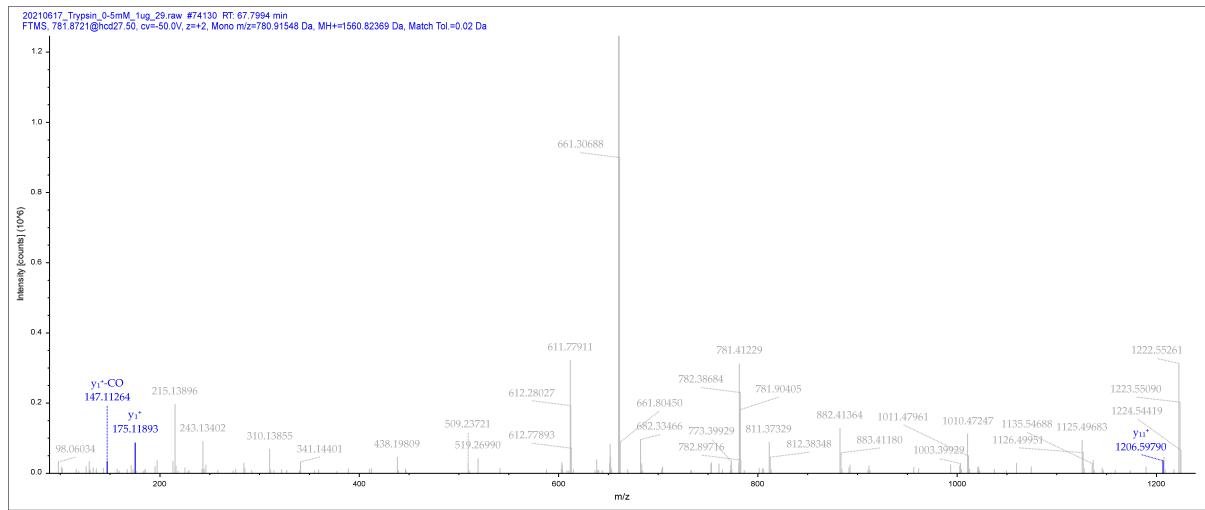
#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	116.03422	58.52075	D			9
2	173.05568	87.03148	G	1022.505...	511.75634	8
3	244.09280	122.55004	A	965.48394	483.24561	7
4	359.11974	180.06351	D	894.44683	447.72705	6
5	506.18815	253.59772	F	779.41988	390.21358	5
6	577.22527	289.11627	A	632.35147	316.67937	4
7	777.34136	389.17432	K-Carb...	561.31436	281.16082	3
8	963.42067	482.21397	W	361.19827	181.10277	2
9			R	175.11895	88.06311	1

Fructose bisphosphate aldolase A K41 (uniprot K42)

Sequence: GILAADESTGSIAKR, K14-Carboxyethyl (72.02113 Da)

Charge: +2, Monoisotopic m/z: 780.91548 Da (+0.46 mmu/+0.59 ppm), MH⁺: 1560.82369 Da, RT: 67.7994 min,

Identified with: Sequest HT (v1.17); **XCorr:1.18**, Percolator q-Value:4.9e-5, Percolator PEP:2.7e-4,



#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	58.02874	29.51801	G			15
2	171.11280	86.06004	I	1503.801...	752.40429	14
3	284.19687	142.60207	L	1390.717...	695.86226	13
4	355.23398	178.12063	A	1277.633...	639.32023	12
5	426.27110	213.63919	A	1206.596...	603.80167	11
6	541.29804	271.15266	D	1135.558...	568.28312	10
7	670.34063	335.67395	E	1020.532...	510.76965	9
8	757.37266	379.18997	S	891.48942	446.24835	8
9	858.42034	429.71381	T	804.45739	402.73233	7
10	915.44180	458.22454	G	703.40971	352.20850	6
11	1002.473...	501.74055	S	646.38825	323.69776	5
12	1115.557...	558.28259	I	559.35622	280.18175	4
13	1186.595...	593.80114	A	446.27216	223.63972	3
14	1386.711...	693.85919	K-Carb...	375.23504	188.12116	2
15			R	175.11895	88.06311	1

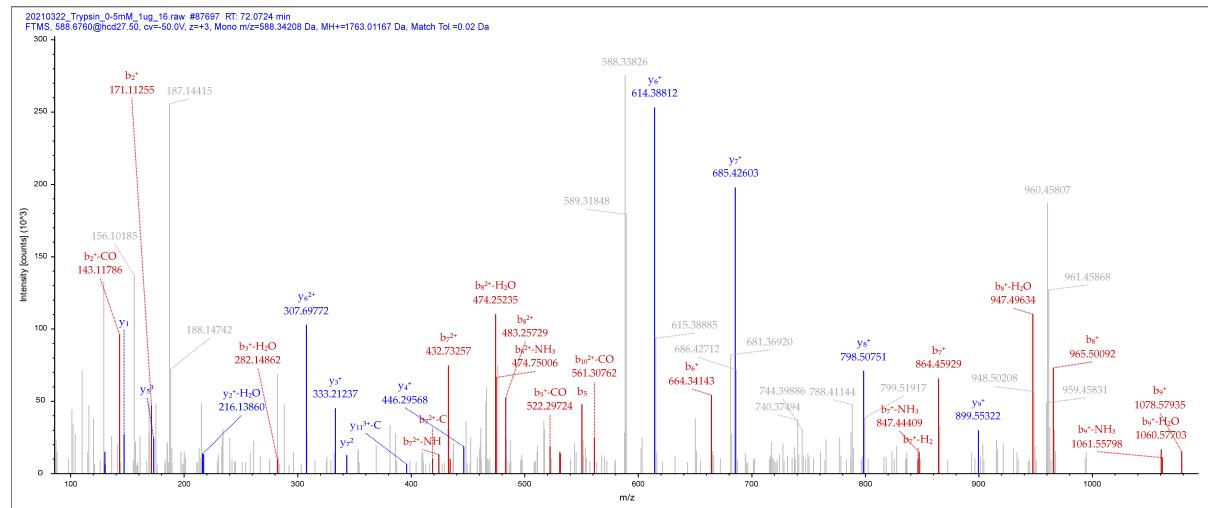
Alpha enolase (K71)

Sequence: AVEHINKTIAPALVSK, K7-Carboxyethyl (72.02113 Da)

Charge: +3, Monoisotopic m/z: 588.34208 Da (+1.84 mmu/+3.13 ppm), MH⁺: 1763.01167 Da, RT: 72.0724 min,

Identified with: Sequest HT (v1.17); XCorr:3.57, Percolator q-Value:1.0e-4, Percolator PEP:6.5e-4,

#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	72.04439	36.52583	24.68631	A				16
2	171.11280	86.06004	57.70912	V	1691.969...	846.48816	564.66120	15
3	300.15540	150.58134	100.72332	E	1592.900...	796.95395	531.63840	14
4	437.21431	219.11079	146.40962	H	1463.858...	732.43266	488.62420	13
5	550.29837	275.65282	184.10431	I	1326.799...	663.90320	442.93789	12
6	664.34130	332.67429	222.11862	N	1213.715...	607.36117	405.24321	11
7	864.45739	432.73233	288.82398	K-Carb...	1099.672...	550.33971	367.22890	10
8	965.50507	483.25617	322.50654	T	899.55604	450.28166	300.52353	9
9	1078.589...	539.79821	360.20123	I	798.50837	399.75782	266.84097	8
10	1149.626...	575.31676	383.88027	A	685.42430	343.21579	229.14628	7
11	1246.679...	623.84314	416.23119	P	614.38719	307.69723	205.46725	6
12	1317.716...	659.36170	439.91023	A	517.33442	259.17085	173.11633	5
13	1430.800...	715.90373	477.60491	L	446.29731	223.65229	149.43729	4
14	1529.868...	765.43794	510.62772	V	333.21325	167.11026	111.74260	3
15	1616.900...	808.95395	539.63840	S	234.14483	117.57605	78.71980	2
16				K	147.11280	74.06004	49.70912	1



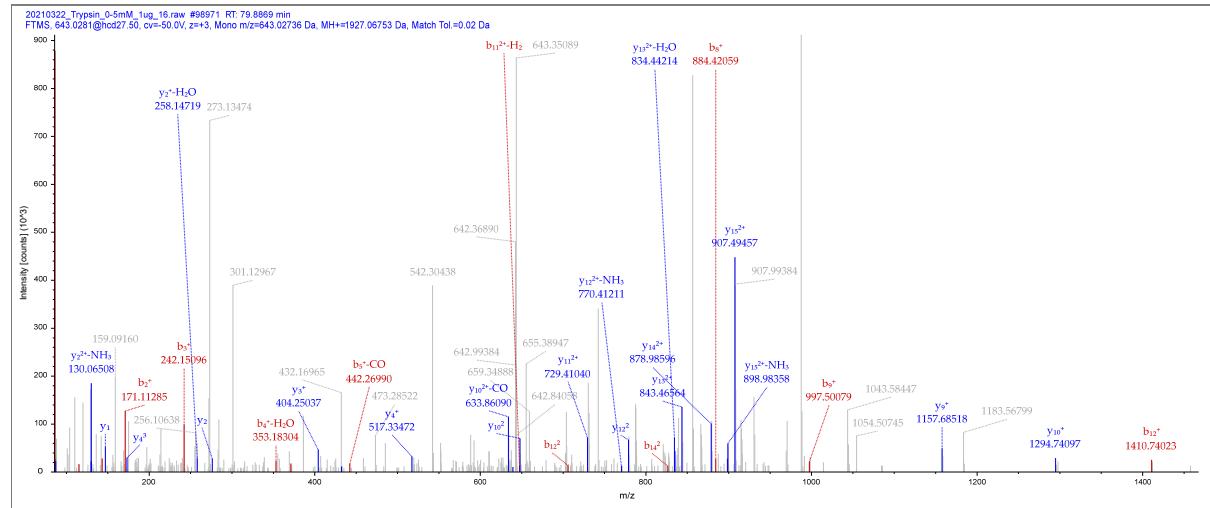
Alpha enolase (K193)

Sequence: IGAEVYHNLKNVIKEK, K10-Carboxyethyl (72.02113 Da)

Charge: +3, Monoisotopic m/z: 643.02736 Da (+0.93 mmu/+1.45 ppm), MH+: 1927.06753 Da, RT: 79.8869 min,

Identified with: Sequest HT (v1.17); XCorr:2.06, Percolator q-Value:4.6e-5, Percolator PEP:2.2e-4,

#1	b ⁺	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	114.09134	57.54931	38.70196	I				16
2	171.11280	86.06004	57.70912	G	1813.980...	907.49397	605.33174	15
3	242.14992	121.57860	81.38816	A	1756.959...	878.98324	586.32459	14
4	371.19251	186.09989	124.40235	E	1685.922...	843.46469	582.64555	13
5	470.26092	235.63410	157.42516	V	1556.879...	778.94339	519.63135	12
6	633.32425	317.16576	211.77960	Y	1457.811...	729.40918	486.60855	11
7	770.38317	385.69522	257.46591	H	1294.747...	647.87752	432.25410	10
8	884.42609	442.71668	295.48022	N	1157.688...	579.34806	386.56780	9
9	997.51016	499.25872	333.17490	L	1043.645...	522.32660	348.55349	8
10	1197.626...	599.31676	399.88027	K-Carb...	930.56186	465.78457	310.85880	7
11	1311.669...	656.33823	437.89458	N	730.44577	365.72652	244.15344	6
12	1410.737...	705.87243	470.91738	V	616.40284	308.70506	206.13913	5
13	1523.821...	762.41447	508.61207	I	517.33442	259.17085	173.11633	4
14	1651.916...	826.46195	551.31039	K	404.25036	202.62882	135.42164	3
15	1780.959...	890.98324	594.32459	E	276.15540	138.58134	92.72332	2
16				K	147.11280	74.06004	49.70912	1



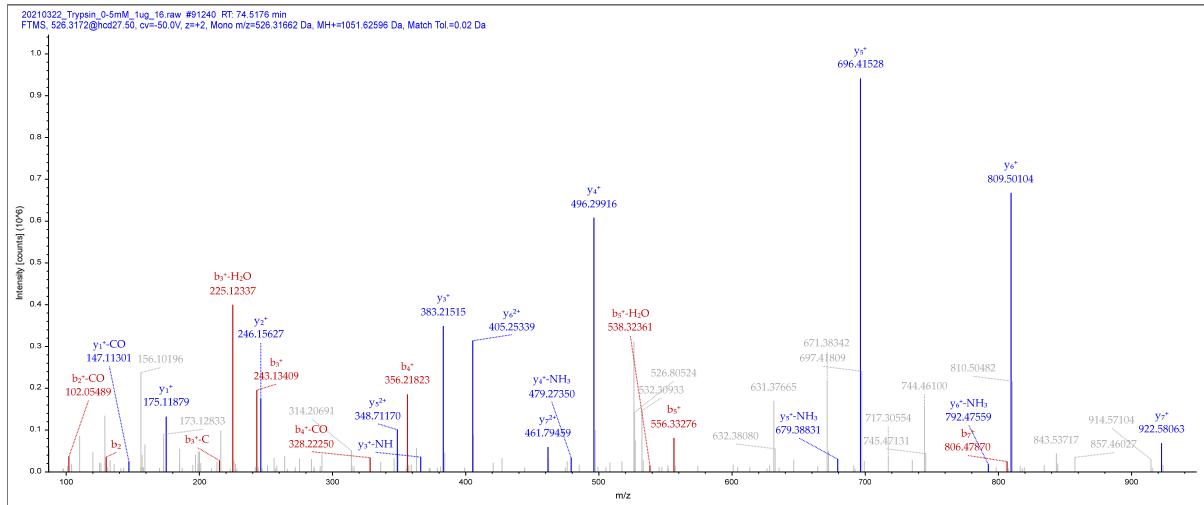
Alpha enolase (K5)

Sequence: MSILKIHAR, K5-Carboxyethyl (72.02113 Da), M1-Met-loss+Acetyl (-89.02992 Da)

Charge: +2, Monoisotopic m/z: 526.31662 Da (+0.05 mmu/+0.1 ppm), MH+: 1051.62596 Da, RT: 74.5176 min,

Identified with: Sequest HT (v1.17); **XCorr:2.76**, Percolator q-Value:2.0e-4, Percolator PEP:1.5e-3,

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	43.01784	22.01256	M-Met...			9
2	130.04987	65.52857	S	1009.615...	505.31128	8
3	243.13393	122.07061	I	922.58326	461.79527	7
4	356.21800	178.61264	L	809.49920	405.25324	6
5	556.33409	278.67068	K-Carb...	696.41513	348.71121	5
6	669.41815	335.21271	I	496.29904	248.65316	4
7	806.47707	403.74217	H	383.21498	192.11113	3
8	877.51418	439.26073	A	246.15607	123.58167	2
9			R	175.11895	88.06311	1



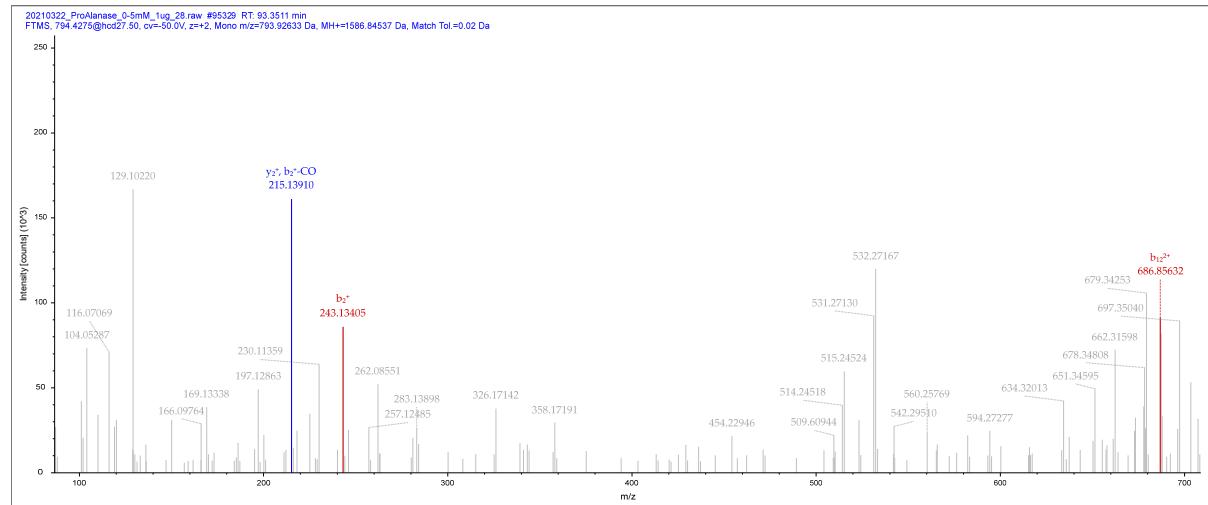
Glyceraldehyde-3-phosphate dehydrogenase (R234)

Sequence: ELNGKLTGMAFRVP, R12-MG-H1 (54.01057 Da)

Charge: +2, Monoisotopic m/z: 793.92633 Da (+4.73 mmu/+5.95 ppm), MH⁺: 1586.84537 Da, RT: 93.3511 min,

Identified with: Sequest HT (v1.17); **XCorr:1.71**, Percolator q-Value:2.9e-3, Percolator PEP:1.2e-2,

#1	b ⁺	b ²⁺	Seq.	y ⁺	y ²⁺	#2
1	130.04987	65.52857	E			14
2	243.13393	122.07061	L	1457.793...	729.40030	13
3	357.17686	179.09207	N	1344.709...	672.85827	12
4	414.19832	207.60280	G	1230.666...	615.83681	11
5	542.29329	271.65028	K	1173.644...	587.32608	10
6	655.37735	328.19231	L	1045.549...	523.27859	9
7	756.42503	378.71615	T	932.46585	466.73656	8
8	813.44649	407.22689	G	831.41817	416.21272	7
9	944.48698	472.74713	M	774.39671	387.70199	6
10	1015.524...	508.26568	A	643.35622	322.18175	5
11	1162.592...	581.79989	F	572.31911	286.66319	4
12	1372.704...	686.85573	R-MG-...	425.25069	213.12899	3
13	1471.772...	736.38994	V	215.13902	108.07315	2
14			P	116.07061	58.53894	1



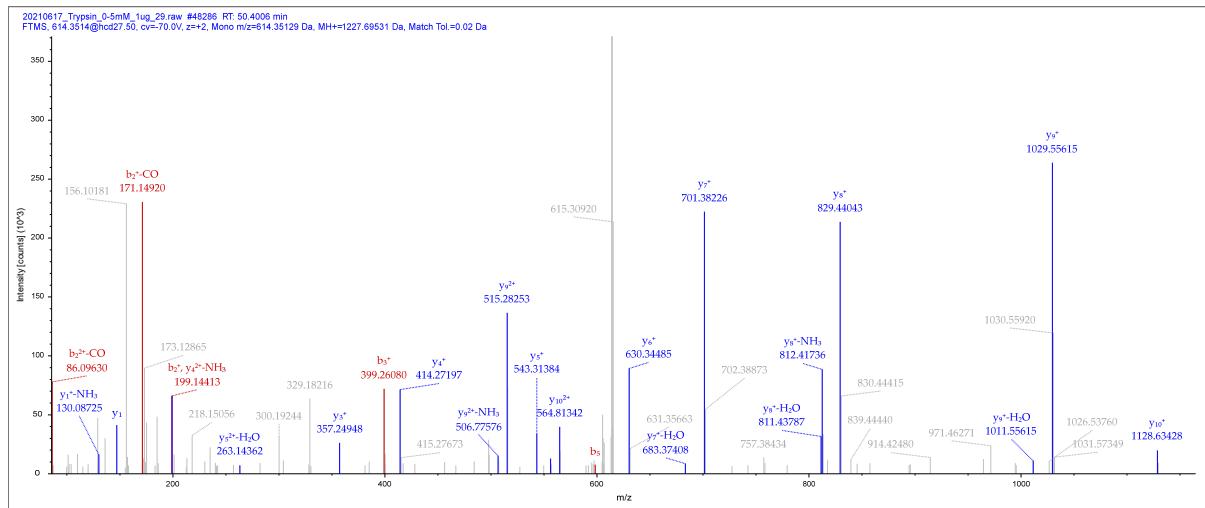
Glyceraldehyde-3-phosphate dehydrogenase (R263)

Sequence: VKVKQASEGPLK, K3-Carboxyethyl (72.02113 Da)

Charge: +2, Monoisotopic m/z: 614.35129 Da (+0.49 mmu/+0.8 ppm), MH⁺: 1227.69531 Da, RT: 50.4006 min,

Identified with: Sequest HT (v1.17); XCorr:2.39, Percolator q-Value:2.6e-5, Percolator PEP:9.2e-5,

#1	b*	b ²⁺	Seq.	y*	y ²⁺	#2
1	100.07569	50.54148	V			11
2	199.14410	100.07569	V	1128.625...	564.81660	10
3	399.26020	200.13374	K-Carb...	1029.557...	515.28239	9
4	527.31877	264.16303	Q	829.44141	415.22434	8
5	598.35589	299.68158	A	701.38283	351.19505	7
6	685.38792	343.19760	S	630.34572	315.67650	6
7	814.43051	407.71889	E	543.31369	272.16048	5
8	871.45197	436.22962	G	414.27110	207.63919	4
9	968.50474	484.75601	P	357.24963	179.12845	3
10	1081.588...	541.29804	L	260.19687	130.60207	2
11			K	147.11280	74.06004	1



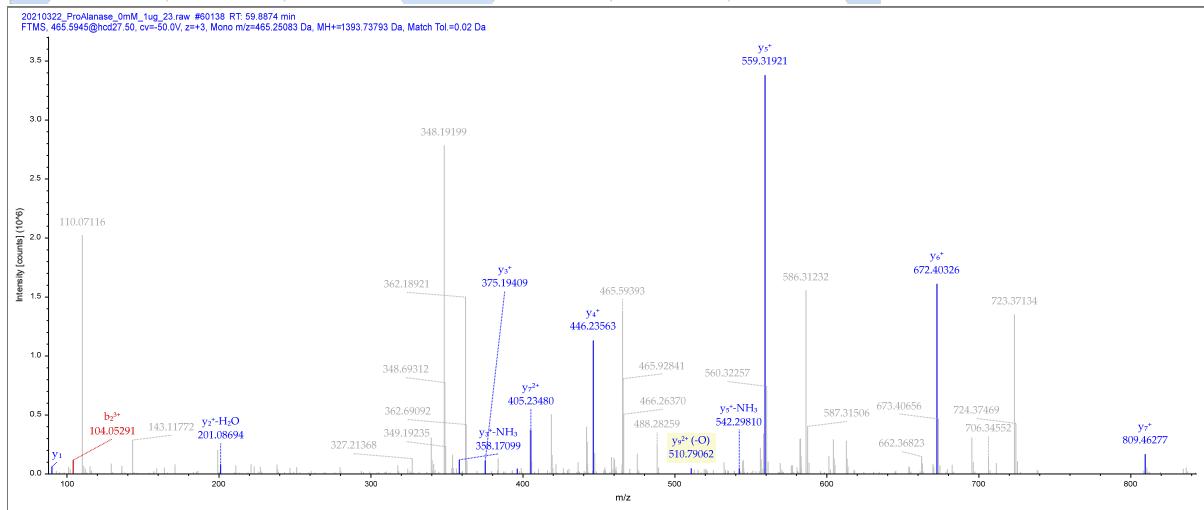
Pyruvate Kinase (R376)

Sequence: VRMQHLIAREA, M3-Oxidation (15.99492 Da), R2-MG-H1 (54.01057 Da)

Charge: +3, Monoisotopic m/z: 465.25083 Da (+0.35 mmu/+0.75 ppm), MH+: 1393.73793 Da, RT: 59.8874 min,

Identified with: Sequest HT (v1.17); XCorr:1.93, Percolator q-Value:2.0e-3, Percolator PEP:8.1e-3,

#1	b+	b ²⁺	b ³⁺	Seq.	y ⁺	y ²⁺	y ³⁺	#2
1	100.07569	50.54148	34.03008	V				11
2	310.18737	155.59732	104.06731	R-MG...	1294.668...	647.83787	432.22767	10
3	457.22277	229.11502	153.07911	M-Oxi...	1084.556...	542.78203	362.19045	9
4	585.28134	293.14431	195.76530	Q	937.52139	469.26433	313.17865	8
5	722.34026	361.67377	241.45160	H	809.46281	405.23504	270.49246	7
6	835.42432	418.21580	279.14629	L	672.40390	336.70559	224.80615	6
7	948.50838	474.75783	316.84098	I	559.31984	280.16356	187.11146	5
8	1019.545...	510.27639	340.52002	A	446.23577	223.62152	149.41678	4
9	1175.646...	588.32694	392.55372	R	375.19866	188.10297	125.73774	3
10	1304.689...	652.84824	435.56792	E	219.09755	110.05241	73.70403	2
11				A	90.05496	45.53112	30.68984	1



Glucose-6-phosphate isomerase (R6)

Sequence: MAALTRDPQFQK, R6-Carboxyethyl (72.02113 Da), M1-Met-loss+Acetyl (-89.02992 Da)

Charge: +2, Monoisotopic m/z: 694.86454 Da (+2.48 mmu/+3.57 ppm), MH+: 1388.72181 Da, RT: 68.9469 min,

Identified with: Sequest HT (v1.17); XCorr:2.02, Percolator q-Value:6.1e-4, Percolator PEP:5.3e-3,

#1	b*	b ²⁺	Seq.	y*	y ²⁺	#2
1	43.01784	22.01256	M-Met...			12
2	114.05495	57.53112	A	1346.706...	673.85678	11
3	185.09207	93.04967	A	1275.669...	638.33823	10
4	298.17613	149.59170	L	1204.632...	602.81967	9
5	399.22381	200.11554	T	1091.548...	546.27764	8
6	627.34605	314.17666	R-Car...	990.50032	495.75380	7
7	742.37299	371.69014	D	762.37808	381.69268	6
8	839.42576	420.21652	P	647.35114	324.17921	5
9	967.48434	484.24581	Q	550.29837	275.65282	4
10	1114.552...	557.78001	F	422.23980	211.62354	3
11	1242.611...	621.80930	Q	275.17138	138.08933	2
12			K	147.11280	74.06004	1

