

Supplementary Table 1. PLS-DA VIP top 30 scores peptides. The table shows the top 30 peptides that contribute to the separation between the 4 groups (SCM-D2, SCM-D21, H-D2, H-D21), their deriving proteins, their position in the deriving protein, and variations between the groups.

VIP rank	P.N *	P.F* + Mod*	DERIVING PROTEIN	P.P*	SCM-D2/H-D2	SCM-D21/H-D21	SCM-D21/SCM-D2	H-D21/H-D2
1	119	[R].SNVQSPDATEED	Osteopontin	170-192	Up	Down	Up	Up
2	396	FTSHIESEEMH.[D] [A].ILNKPEDETHLE AQPTDASAQFIR.[N]	GLYCAM1	19-42	Down	Down	Down	Down
3	108	[E].KFQSEEQQTED	β -casein	47-71	Up	Down	Up	Up
4	773	ELQDKIHPPAQTQ.[S] [K].TKVIPYVRYL.[-]	α_{S2} -casein	213-222	Down	Down	Down	Down
5	383	[V].IPYVRYL.[-]	α_{S2} -casein	216-222	Down	Down	Down	Down
6	238	[-].MLPLSLLK.[T] <i>1xMet-loss [N-Term]</i>	U6 snRNA-associated Sm-like protein LSm4	1-8	Down	Down	Down	Down
7	102	[N].TLPTKETIEQEK QAK.[-]	Thymosin beta-10	28-42	Up	Down	Up	Up
8	771	[P].HQPLPTV.[M]	β -casein	163-170	Up	Up	Up	Up
9	214	[K].VKEAMAPK.[H]	β -casein	113-120	Down	Down	Down	Down
10	119	[R].SNVQSPDATEED	Osteopontin	170-192	Up	Down	Up	Up
11	480	FTSHIESEEMH.[D] <i>1xOxidation [M22]</i> [A].ILNKPEDETHLE AQPTDASAQF.[I]	GLYCAM1	19-40	Down	Down	Down	Down
12	649	[T].KVIPYVRYL.[-]	α_{S2} -casein	214-222	Down	Down	Down	Down
13	552	[K].ASADESLALGKP GKEPR.[S]	Fibroblast growth factor-binding protein 1	35-51	Down	Down	Down	Down
14	931	[P].LPPTVMFPPQS.[V]	β -casein	166-176	Down	Up	Up	Up
15	106	[A].ILNKPEDETH.[L]	GLYCAM1	19-28	Down	Down	Down	Down
16	740	[K].VIPYVRYL.[-]	α_{S2} -casein	215-222	Down	Down	Down	Down
17	455	[K].FALPQYL.[K]	α_{S2} -casein	189-195	Up	Down	Down	Down
18	37	[K].AMKPWIQPK.[T]	α_{S2} -casein	204-212	Down	Down	Down	Down
19	441	[V].APFPEVF.[G]	α_{S1} -casein	41-47	Down	Down	Down	Down
20	484	[K].TKVIPYVR.[Y]	α_{S2} -casein	213-220	Down	Down	Down	Down
21	678	[K].AMKPWIQPK.[K] <i>1xOxidation [M2]</i>	α_{S2} -casein	204-211	Down	Down	Down	Down
22	12	[R].QPQSQNPKLPLSL L.[K]	GLYCAM1	75-88	Down	Down	Down	Down

23	258	[H].KEMPPF.[K]	β -casein	122-127	Up	Down	Down	Down
24	372	[K].AMKPWIQP.[K]	α_{S2} -casein	204-211	Up	Down	Down	Down
25	505	[K].TTMPLW.[-]	α_{S1} -casein	209-214	Down	Down	Down	Down
26	1074	[K].GLDIQKV.[A]	β -lactoglobulin	25-31	Up	Up	Up	Up
27	185	[K].TKVIPYV.[R]	α_{S2} -casein	213-219	Up	Up	Down	Down
28	116	[A].ILNKPEDETHLE AQPTDASAQ.[F]	GLYCAM1	19-39	Down	Down	Down	Down
29	100	[K].FALPQYLK.[T]	α_{S2} -casein	189-196	Down	Down	Down	Down
30	764	[M].KPWIQP.[K]	α_{S2} -casein	206-211	Down	Down	Down	Down

P.N*- Peptide number

P.F* + Mod*- Peptide fragment + Modification

P.P*- Peptide position

Supplementary Table 2. PLS-DA VIP top 30 scores peptides. The table shows the top 30 peptides that contribute the most to the separation between SCM-D2 and H-D2 groups, their deriving proteins, their position in the deriving protein, and variations between the groups.

VIP rank	P.N*	P.F* + Mod*	Deriving Protein	P. P*	SCM-D2/H-D2
1	599	[Y].PVEPFOTESQL.[T]	β -casein	130-140	Up
2	940	[K].YFLQPEVLHKYSVD.[P]	Neutral cholesterol ester hydrolase 1	168-181	Down
3	136	[R].SSRQPQSQNPKLPLSILKEKHL.[R]	GLYCAM1	72-93	Down
4	861	[F].LKEAGQGAKD.[M]	SAA-3 protein	25-34	Up
5	788	[Y].PVEPFOTESQS.[L]	β -casein	130-139	Up
6	1003	[V].VVPFLQPEVMGV.[S]	β -casein	98-110	Up
		<i>1xOxidation [M11]</i>			
7	704	[K].GMTRDQVRED.[S]	SAA-3 protein	93-102	Up
8	242	[P].VEPFOTESQ.[S]	β -casein	131-138	Up
9	217	[D].SVAYGLKS.[R]	Osteopontin	155-162	Down
10	103	[F].SDIPNPIGSENSEKTTMPL.[W]	α_{S1} -casein	195-213	Up
11	1004	[D].APSFSDIPNPIGSENSE.[K]	α_{S1} -casein	191-207	Up
12	1060	[I].KQMEAESISSSEEIVPNSVEQK.[H]	α_{S1} -casein	73-94	Up
13	850	[I].VFVVDSDVVERMEEAKT.[E]	ADP-ribosylation factor-like protein 4A	97-113	Down
14	1147	[P].KYPVEPFOTESQ.[S]	β -casein	128-138	Up
15	961	[K].ALLDPSFF.[A]	Polymeric immunoglobulin receptor	594-601	Up
16	789	[R].NAVPIITPL.[N]	α_{S2} -casein	130-138	Up
17	715	[F].LLYQEPVLGPV.[R]	β -casein	206-216	Up
18	41	[V].VPPFLQPEVMGV.[S]	β -casein	99-110	Up
19	630	[K].EGIHAQQKEPMIGV.[N]	α_{S1} -casein	140-153	Up
20	15	[V].KRNAVPIITPT.[L]	α_{S2} -casein	128-137	Up
21	479	[I].NKKIEKFQSEEQQQTEDELQDKIH PFAQTQ.[S]	β -casein	42-71	Down
22	813	[-].MAMVSEFLK.[Q]	Annexin A1	1-9	Up
		<i>1xMet-loss+Acetyl [N-Term]</i>			
23	453	[E].TIQGITDPLF.[K]	SAA-3 protein	82-91	Up
24	962	[Y].YVPLGTQYTDAPSF.[S]	α_{S1} -casein	181-194	Up
25	342	[P].SFSDIPNPIGSENSEKTTMP.[L]	α_{S1} -casein	193-212	Down
		<i>1xOxidation [M19]</i>			
26	787	[F].QSEEQQQTEDELQDKIH PFAQTQ.[S]	β -casein	49-71	Up
27	500	[A].LPIIQKLEPQIA.[V]	Perilipin-2	66-77	Down
28	42	[K].HIQKEDVPSELYL.[G]	α_{S1} -casein	95-107	Up
29	33	[T].FLKEAGQGAKD.[M]	SAA-3 protein	24-34	Up
30	561	[T].WLKPDPSQKQT.[F]	Osteopontin	43-53	Up

P.N* - Peptide number

P.F* + Mod* - Peptide fragment + Modification

P.P* - Peptide position

Supplementary Table 3. Comparison of the 'SCM-D2' group vs. 'H-D2' group (P<0.05). The table shows peptides that have changed significantly in the comparison between the two groups, displaying the fold change and the corresponding p-value.

P.N*	Peptide fragment+Modification	FC*	log2(FC)	raw. pval*
1004	[D].APSFSDIPNPIGSENSE.[K]	12.381	3.6301	5.73E-12
961	[K].ALLDPSFF.[A]	13.602	3.7657	1.19E-06
1018	[L].INNQFLPYYPYAKPAA.[V]	7.5343	2.9135	1.79E-05
788	[Y].PVEPFOTESQS.[L]	7.9609	2.9929	2.44E-05
242	[P].VEPFOTESQ.[S]	14.112	3.8188	4.03E-05
861	[F].LKEAGQGAKD.[M]	27.644	4.7889	9.29E-05
569	[V].RGPFPIL.[V]	6.9686	2.8009	0.00010429
217	[D].SVAYGLKS.[R]	0.12733	-2.9733	0.00028116
132	[K].AMKPWIQPK.[T]	0.13796	-2.8577	0.00036738
	<i>1xOxidation [M2]</i>			
480	[A].ILNKPEDETHLEAQPTDASAQF.[I]	0.34614	-1.5306	0.00040317
599	[Y].PVEPFOTESQSL.[T]	23.957	4.5824	0.00043633
136	[R].SSRQPQSQNPQLPLSILKEKHL.[R]	0.20289	-2.3012	0.00050149
228	[E].MPFPKYPVEPFOTESQSL.[T]	4.4708	2.1605	0.00055967
500	[A].LPPIQKLEPQIA.[V]	0.1554	-2.6859	0.00061046
716	[E].MPFPKYPVEPFOTESQ.[S]	2.2854	1.1925	0.000622
656	[M].PEPAKSAPAP.[K]	8.5629	3.0981	0.00062994
443	[K].AAPAGAAIQR.[A]	0.2522	-1.9874	0.00082646
453	[E].TIQGTDPLF.[K]	10.809	3.4341	0.0011595
963	[V].LSLSQSKVLPVP.[Q]	13.101	3.7116	0.0013167
383	[V].IPYVRYL.[-]	0.31404	-1.671	0.001393
387	[E].IPLSPMGEDSASGDIETLH.[S]	0.14257	-2.8103	0.0014416
715	[F].LLYQEPVLGPV.[R]	22.088	4.4652	0.0014499
1147	[P].KYPVEPFOTESQ.[S]	21.525	4.4279	0.0015509
603	[Q].EVLNENLL.[R]	0.43172	-1.2118	0.0016413
643	[K].HKEMPFKYPVEPFOTESQSL.[T]	4.0136	2.0049	0.001651
813	[-].MAMVSEFLK.[Q]	20.06	4.3262	0.0017225
	<i>1xMet-loss+Acetyl [N-Term]</i>			
646	[L].EQLLRLK.[K]	0.47207	-1.0829	0.001731
802	[Y].FYPELF.[R]	4.3811	2.1313	0.0018713
412	[H].KEMPFKYPVEPFOTESQSL.[T]	4.4831	2.1645	0.001872
704	[K].GMTRDQVRED.[S]	11.188	3.4839	0.0019266
318	[K].YPVEPFOTESQSL.[T]	6.1086	2.6108	0.0021431
765	[L].LYQEPVLGPVRGPFPII.[V]	11.957	3.5798	0.0021699
257	[K].EMPFPKYPVEPFOTESQSL.[T]	4.6845	2.2279	0.002264
1003	[V].VVPPFLQPEVMGV.[S]	62.936	5.9758	0.002343
	<i>1xOxidation [M11]</i>			
269	[K].EMPFPKYPVEPFOTESQSL.[T]	3.9087	1.9667	0.0024337
	<i>1xOxidation [M2]</i>			
577	[P].FLQPEVM.[G]	4.84	2.275	0.0030584
755	[D].GRGDSVAYGLKS.[R]	0.38868	-1.3634	0.003435
488	[Y].QEPVLGPV.[R]	2.4995	1.3216	0.0037911

226	[I].QGITDPLF.[K]	5.4468	2.4454	0.0038538
724	[D].GRGDSVAYGL.[K]	0.38595	-1.3735	0.0038789
414	[N].IPPLTQTPVVVPPF.[L]	0.25684	-1.9611	0.0039634
515	[R].NAVPIITP.[T]	2.3498	1.2325	0.0042847
490	[V].VVPPFLQPEVMGVSKVK.[E]	2.3238	1.2165	0.0042888
559	[V].VVPPFLQPEVMGVVS.[K]	4.2522	2.0882	0.0043483
251	[Q].TPVVVPPFLQPE.[V]	0.30465	-1.7148	0.0045001
418	[V].RGPFIIV.[-]	3.2803	1.7138	0.0045018
940	[K].YFLQPEVLHKYSVD.[P]	0.0045922	-7.7666	0.0046541
709	[D].GRGDSVAYGLK.[S]	0.33897	-1.5608	0.0048029
396	[A].ILNKPEDETHLEAQPTDASAQFIR.[N]	0.34564	-1.5327	0.0048234
1060	[I].KQMEAESISSEEIVPNSVEQK.[H]	28.14	4.8145	0.0049487
582	[K].HKEMPFKYPVEPFTESQSL.[T]	3.3967	1.7641	0.0049724
	<i>1xOxidation [M4]</i>			
936	[P].LPPTVMF.[P]	0.16274	-2.6194	0.0050162
456	[A].QQKEPMIGV.[N]	4.9985	2.3215	0.0050361
404	[A].IPPKKNQDKTEIPTINT.[I]	0.34075	-1.5532	0.0053683
904	[F].VAPFPEVFGKEKVNELSKDIGSESTEDQAMED. [I]	5.2761	2.3995	0.0054144
363	[K].VKEAMAPKHKEMPFPK.[Y]	0.38153	-1.3901	0.0057568
377	[K].YPVEPFT.[E]	0.29041	-1.7838	0.0058195
949	[S].ISSSEEIVPNSVEQK.[H]	9.5169	3.2505	0.0059732
326	[R].NAVPIPTLNR.[E]	0.34815	-1.5222	0.0059876
560	[S].DIPNPIG.[S]	0.46263	-1.1121	0.0062591
718	[L].YQEPVLGPV.[R]	4.5145	2.1746	0.0062851
990	[E].DGSDDPPSGDFLTEGGGVR.[G]	0.15921	-2.651	0.0067138
19	[P].FPKYPVEPFT.[E]	0.0995	-3.3292	0.006865
654	[E].GIHAQQKEPMIG.[V]	2.5207	1.3338	0.006956
293	[T].EDGSDDPPSGDFLTEGGGVR.[G]	0.2882	-1.7948	0.0071643
41	[V].VPPFLQPEVMGV.[S]	9.1085	3.1872	0.0071961
521	[L].GYLEQLL.[R]	2.0687	1.0487	0.0072404
630	[K].EGIHAQQKEPMIGV.[N]	4.1988	2.07	0.0073383
103	[F].SDIPNPIGSENSEKTTMPL.[W]	5.6244	2.4917	0.0076722
474	[Q].TPVVVPPF.[L]	0.44342	-1.1733	0.0076928
850	[I].VFVVDSDVERMEEAKT.[E]	0.030185	-5.05	0.0078178
1161	[R].TLNPEHLGQGGVQ.[R]	11.601	3.5362	0.0081447
18	[E].MPFPKYPVEPFT.[E]	0.079407	-3.6546	0.0083009
417	[T].IQGITDPLF.[K]	3.9209	1.9712	0.0083717
70	[F].SDIPNPIGSENSEKTTMPLW.[-]	6.2861	2.6522	0.008423
782	[L].TQTPVVVPP.[F]	2.7233	1.4453	0.0085255
537	[R].RGSKASADESLALGKPGKEPR.[S]	0.44481	-1.1687	0.0096637
155	[P].VEPFTESQSL.[T]	5.3466	2.4186	0.0098312
477	[D].SVAYGLK.[S]	0.28498	-1.8111	0.010022
286	[R].SSRQPQSQNPKLPLSILKEK.[H]	0.35761	-1.4835	0.010778
180	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPL. [W]	3.4813	1.7996	0.011524

263	[Y].TDAPSFSDIPNPIGSENSEKTTMPL.[W]	4.3263	2.1131	0.012332
	<i>1xOxidation [M23]</i>			
496	[K].EGIHAQQKEPMIGVNQ.[E]	2.1289	1.0901	0.012369
	<i>1xOxidation [M11]</i>			
342	[P].SFSDIPNPIGSENSEKTTMP.[L]	0.34896	-1.5189	0.012921
	<i>1xOxidation [M19]</i>			
437	[V].VVPPFLQPEVMGVSKV.[K]	5.748	2.5231	0.012938
290	[V].LSLSQSKVLPVPQK.[A]	2.2146	1.1471	0.013289
778	[K].AVPYPQRDMPIQAF.[L]	2.8493	1.5106	0.013379
167	[F].SDIPNPIGSENSEK.[T]	2.9036	1.5378	0.014256
33	[T].FLKEAGQGAKD.[M]	8.1371	3.0245	0.014472
15	[V].KRNAVPIPT.[L]	9.6143	3.2652	0.014485
962	[Y].YVPLGTQYTDAPSF.[S]	56.523	5.8208	0.015188
693	[L].YQEPVLGPVRGPFPII.[V]	7.0062	2.8086	0.015464
547	[R].ELEELNVPGEIVE.[S]	0.49334	-1.0194	0.016135
50	[K].LPLSILKEK.[H]	0.18376	-2.4441	0.016357
183	[LG].ITDPLF.[SK]	3.6883	1.883	0.016841
272	[V].VPPFLQPEVMG.[V]	3.0451	1.6065	0.016923
37	[K].AMKPWIQPK.[T]	0.12283	-3.0252	0.017038
201	[R].ISHELDSASSEVN.[-]	0.25254	-1.9854	0.017309
406	[E].GIHAQQKEPMIGVNQ.[E]	2.7535	1.4613	0.017613
237	[P].FPKYPVEPFTESQSL.[T]	3.6135	1.8534	0.018104
543	[R].ELEELNVPGE.[I]	0.44723	-1.1609	0.018164
54	[V].VVPPFLQPEVMGV.[S]	11.827	3.564	0.018565
513	[F].SDIPNPIGSENSEKTT.[M]	15.215	3.9274	0.019979
45	[M].KPWIQPK.[T]	0.15817	-2.6605	0.02033
542	[Y].QEPVLGPVR.[G]	0.46355	-1.1092	0.020834
463	[N].AVPITPT.[L]	2.1567	1.1088	0.020835
863	[E].DSPEVIESPPEINTVQVTST.[A]	0.21335	-2.2287	0.021054
976	[P].VPQKAVPYP.[Q]	0.18798	-2.4113	0.021214
516	[E].SPPEINTVQVTST.[A]	0.27637	-1.8553	0.022103
309	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPL W.[-]	3.1134	1.6385	0.022203
1125	[F].RPAGLPDKY.[-]	18.215	4.1871	0.022374
216	[K].EGIHAQQKEPMIGVNQELAY.[F]	2.4053	1.2662	0.02315
322	[E].SPPEINTVQVTSTAV.[-]	0.49508	-1.0143	0.023176
334	[A].LIVTQTMK.[G]	0.40649	-1.2987	0.023463
628	[A].RELEELNVPGEIV.[E]	4.611	2.2051	0.023535
971	[S].ISSSEEIVPNSVEQ.[K]	5.9135	2.564	0.023766
130	[D].IPNPIGSENSEKT.[T]	3.485	1.8012	0.02422
519	[T].DAPSFSDIPNPIGSENSEKTTMPLW.[-]	2.1469	1.1023	0.024748
689	[L].SLSQSKVLPVP.[Q]	2.9235	1.5477	0.024751
245	[Y].TDAPSFSDIPNPIGSENSEKTTMPL.[W]	3.29	1.7181	0.025094
232	[F].SDIPNPIGSENSEKTTMPLW.[-]	3.6273	1.8589	0.025614
	<i>1xOxidation [M17]</i>			
358	[T].QYTDAPSFSDIPNPIGSENSEKTTMPLW.[-]	2.6926	1.429	0.02577
619	[R].SSRQPQSQNPKLPLSILK.[E]	0.48678	-1.0386	0.025791

117	[Y].TDAPSFSDIPNPIGSENSEKTTMPLW.[-]	3.275	1.7115	0.026415
884	[E].LEELNVPGEIVESLSSEESIT.[R]	5.9541	2.5739	0.026487
107	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	2.9257	1.5488	0.026592
390	[P].SFSDIPNPIGSENSEKTTMP.[L]	0.45713	-1.1293	0.026843
90	[F].SDIPNPIGSENSEKT.[T]	5.4587	2.4485	0.028497
1230	[K].KTVDMESTEVEFTK.[K]	10.938	3.4513	0.028516
230	[K].TVDMESTEVEFTKK.[T]	0.36089	-1.4704	0.028549
409	[L].LYQEPVLGPV.[R]	5.7899	2.5335	0.028649
1138	[Y].TDAPSFSDIPNPIGSENSEKTT.[M]	7.036	2.8148	0.028858
419	[P].FPKYPVEPFTESEQ.[S]	2.1792	1.1238	0.029331
719	[S].LPQNIPPLTQTPVVVPP.[F]	0.4632	-1.1103	0.029478
392	[A].VPITPTLN.[R]	0.4303	-1.2166	0.030515
540	[G].ITDPLFK.[G]	2.625	1.3923	0.030745
260	[V].VPPFLQPEVM.[G]	2.8868	1.5295	0.031818
42	[K].HIQKEDVPSELYL.[G]	4.1055	2.0375	0.032012
214	[K].VKEAMAPK.[H]	0.3414	-1.5505	0.033106
25	[L].TLTDVENL.[H]	18.194	4.1854	0.034899
238	[-].MLPLSLLK.[T]	0.37348	-1.4209	0.035012
	<i>1xMet-loss [N-Term]</i>			
137	[F].SDIPNPIGSENSEKTTMP.[L]	2.9698	1.5703	0.0352
561	[T].WLKPDPSQKQT.[F]	19.129	4.2577	0.035909
706	[T].QTPVVVPPFL.[Q]	3.7538	1.9083	0.036689
172	[L].GTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	5.0112	2.3252	0.03792
213	[I].SHELDSASSEVN.[-]	0.14462	-2.7897	0.039912
711	[L].SSLTETIEGVDAEDGHSPGEQQK.[R]	3.0758	1.6209	0.040047
713	[L].EELNVPGE.[I]	0.43834	-1.1899	0.040379
471	[T].WLKPDPSQK.[Q]	2.3501	1.2327	0.041232
666	[L].EELNVPGEIVESLSSEESITRIN.[K]	5.7195	2.5159	0.041905
208	[D].IPNPIGSENSEKTTMPLW.[-]	2.4635	1.3007	0.04278
673	[V].DMESTEVEFTKK.[T]	0.042579	-4.5537	0.044737
371	[F].LLYQEPVLGPVRGPFPIIV.[-]	4.9406	2.3047	0.046981
550	[K].KIEKFQSEEQQQTEDELQDKIHPFAQTQ.[S]	0.33465	-1.5793	0.047618
552	[K].ASADESLALGKPGKEPR.[S]	0.4067	-1.298	0.047686
38	[P].EVIESPPEINTVQVTSTAV.[-]	0.22183	-2.1725	0.048781
732	[I].KHQGLPQEV.[L]	3.6631	1.8731	0.049489
283	[Y].VPLGTQYTDAPSF.[S]	14.121	3.8197	0.049569

P.N*- Peptide number

FC*- Fold change

raw. pval* - Raw p-value

Supplementary Table 4. PLS-DA VIP top 30 scores peptides. The table shows the top 30 peptides that contribute the most to the separation between SCM-D21 and H-D21 groups, their deriving proteins, their position in the deriving protein, and variations between the groups.

VIP rank	P.N*	P.F* + Mod*	Deriving Protein	P.P*	SCM-D21/H-D21
1	94	[E].VIESPPEINTVQVTSTAV.[-]	K-casein	173-190	Up
2	359	[R].ELEELNVPGEIVESLSSEESITR.[I]	β -casein	17-40	Down
3	482	[A].LPVKPTSSGSSEEKQ.[L]	Osteopontin	17-31	Down
4	1108	[D].PPSGDFLTEGGGV.R.[G]	Fibrinogen alpha chain	25-38	Up
5	251	[Q].TPVVVPFLQPE.[V]	β -casein	95-106	Down
6	872	[E].VFGKEKVNEL.[S]	α_{S1} -casein	46-55	Up
7	526	[-].MASVAVEPQLSVVTR.[V] <i>1xMet-loss+Acetyl [N-Term]</i>	Perilipin-2	1-15	Down
8	620	[Y].VPLGTQYTDAPSFSDIPNPIGSENSEKTT MP.[L]	α_{S1} -casein	182-212	Down
9	1200	[Q].SLVYPFGPIPN.[S]	β -casein	72-83	Down
10	826	[R].ELEELNVPGEIVESLSSEESIT.[R]	β -casein	17-39	Down
11	776	[V].YFPFGPIPN.[S]	β -casein	75-83	Down
12	1	[P].KKTSQLTDHSKETNSSELSKELTPKA.[K]	Osteopontin	196-221	Up
13	968	[Y].YQQKPVA.[L]	K-casein	64-70	Up
14	690	[V].YFPFGPIP.[N]	β -casein	75-82	Down
15	353	[M].APKHKEMPFKYP.[V]	β -casein	118-130	Down
16	1161	[R].TLNPEHLGQGGVQ.[R]	Complement C3	945-957	Up
17	1143	[L].TDHSKETNSSELSKELTPK.[A]	Osteopontin	202-220	Up
18	788	[Y].PVEPFTEQS.[L]	β -casein	130-13	Up
19	1128	[P].HPHLSF.[M]	K-casein	121-126	Up
20	347	[R].TLNPEHLGQGGVQR.[E]	Complement C3	945-958	Up
21	519	[T].DAPSFSDIPNPIGSENSEKTTMPLW.[-]	α_{S1} -casein	190-214	Down
22	992	[L].DLDHKSEEDKHL.[K]	Osteopontin	251-262	Up
23	329	[P].KKTSQLTDHSKETNSSELSKELTPK.[A]	Osteopontin	196-220	Up
24	656	[M].PEPAKSAPAP.[K]	Histone H2B type 1	2-11	Up
25	704	[K].GMTRDQVRED.[S]	SAA-3 protein	93-102	Up
26	527	[V].APFPEVFGKEK.[V]	α_{S1} -casein	41-51	Down
27	451	[K].HKEMPFKYP.[P]	β -casein	121-129	Up
28	1171	[I].TGPVPREF.[K]	Fibrinogen alpha chain	233-240	Up
29	754	[H].QPLPPTV.[M]	β -casein	164-170	Down
30	85	[H].QPHQPLPP.[T]	β -casein	161-168	Down

P.N*- Peptide number

P.F* + Mod*-Peptide fragment + Modification

P.P*- Peptide position

Supplementary Table 5. Comparison of the 'SCM-D21' group vs. 'H-D21' group (P<0.05). The table shows peptides that have changed significantly in the comparison between the two groups, displaying the fold change and the corresponding p-value.

P.N*	Peptide fragment+Modification	FC*	log2(FC)	raw. pval*
690	[V].YFPFGPIP.[N]	0.081478	-3.6174	2.02E-08
776	[V].YFPFGPIP.[S]	0.081969	-3.6088	2.09E-06
1200	[Q].SLVYFPFGPIP.[S]	0.040234	-4.6355	5.75E-06
629	[R].QPQSQNPQLP.[L]	0.17292	-2.5318	0.000276
440	[I].LNKPEDETHLEAQPTDASAQ.[F]	0.25157	-1.9909	0.000466
251	[Q].TPVVVPPFLQPE.[V]	0.15586	-2.6817	0.000576
292	[E].MPFPKYPV.[E]	0.31324	-1.6747	0.00089
620	[Y].VPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	0.23931	-2.0631	0.000979
94	[E].VIESPPEINTVQVTSTAV.[-]	52.288	5.7084	0.001703
359	[R].ELEELNVPGEIVESLSSEESITR.[I]	0.059935	-4.0605	0.002249
1108	[D].PPSGDFLTEGGGVR.[G]	54.071	5.7568	0.003255
1098	[P].HQPLPPTVM.[F]	19.833	4.3099	0.003576
610	[P].QRDMPIQA.[F]	4.986	2.3179	0.003592
526	[-].MASVAVEPQLSVVTR.[V] <i>1xMet-loss+Acetyl [N-Term]</i>	0.013119	-6.2522	0.003912
968	[Y].YQQKPVA.[L]	64.826	6.0185	0.004057
1143	[L].TDHSKETNSSELSKELTPK.[A]	13.694	3.7754	0.005029
1074	[K].GLDIQKV.[A]	5.4122	2.4362	0.005285
587	[D].APSFSDIPNPIGSENSEKTTMPLW.[-]	0.29798	-1.7467	0.005299
879	[K].IEKFQSEEQQTEDELQDKIHFAQ.[T]	0.1674	-2.5787	0.005768
734	[G].LPQEVLN.[E]	0.28038	-1.8346	0.005769
353	[M].APKHKEMPFKYP.[V]	0.1223	-3.0315	0.006033
492	[R].QPQSQNPQLPLS.[I]	0.16027	-2.6414	0.006578
136	[R].SSRQPQSQNPQLPLSILKEKHL.[R]	0.25682	-1.9612	0.006693
727	[Q].SWMHQPHQPLPPTVMFPPQSV.[L]	0.37281	-1.4235	0.006928
725	[F].SDIPNPIGSENSEKTTM.[P]	2.6463	1.404	0.006971
206	[E].MPFPKYP.[V]	0.31967	-1.6454	0.007123
241	[Q].EPVLGPVRGPFPIIV.[-]	0.36113	-1.4694	0.007532
826	[R].ELEELNVPGEIVESLSSEESIT.[R]	0.063824	-3.9698	0.007626
571	[T].QTPVVVPPFLQPE.[V]	0.2946	-1.7632	0.007897
1161	[R].TLNPEHLGQGGVQ.[R]	4.7159	2.2375	0.008022
249	[K].KTVDMESTEVFTEKK.[T]	0.11237	-3.1537	0.008225
872	[E].VFGKEKVNEL.[S]	142.44	7.1542	0.008839
1136	[P].KYPVEPFTESQSLT.[L]	3.4185	1.7734	0.009351
660	[Q].TPVVVPPFLQPEV.[M]	0.25971	-1.945	0.009463
1174	[N].ELSKDIGSESTEDQAMED.[I]	4.1328	2.0471	0.009473
739	[K].NQDKTEIPTINT.[I]	15.619	3.9652	0.009883
1061	[D].FTSHIESEEMH.[D]	17.921	4.1636	0.00995
1128	[P].HPHLSF.[M]	24.819	4.6334	0.010912
788	[Y].PVEPFTESQS.[L]	28.655	4.8407	0.010954

366	[R].SGKDPNHFRPAGLPDKY.[-]	3.5103	1.8116	0.01146
719	[S].LPQNIPPLTQTPVVVPP.[F]	0.33365	-1.5836	0.011802
1114	[I].SDKELQEMSTEGSKYVNKEIK.[N]	6.0496	2.5968	0.012277
320	[E].MPFPKYVPVEPFTE.[S]	0.17221	-2.5378	0.012307
860	[P].IKHQGLPQE.[V]	11.283	3.4961	0.013013
527	[V].APFPEVFGKEK.[V]	0.14479	-2.788	0.013352
548	[K].KTETQEKNPLPSKETIEQEKQ.[A]	0.39508	-1.3398	0.013661
568	[N].YDAAQRGPGGA.[W]	5.5736	2.4786	0.013751
1047	[L].SDQVPDTESETKILLQGTPVAQ.[M]	7.8976	2.9814	0.013809
275	[D].IPNPIGSENSEK.[T]	0.14508	-2.7851	0.014563
547	[R].ELEELNVPGEIVE.[S]	0.4528	-1.143	0.014807
253	[RSGQAH].PPPPPPPP.[PAH]	0.17854	-2.4857	0.015238
1214	[S].SSEEIVPNSVEQKHQI.[K]	15.966	3.997	0.015622
451	[K].HKEMPFPHY.[P]	23.78	4.5717	0.016402
387	[E].IPLSPMGEDSASGDIETLH.[S]	0.067346	-3.8923	0.017467
329	[P].KKTSQSLTDHSKETNSSELSKELTPK.[A]	159.7	7.3192	0.017482
122	[K].ALLDPSFFAKESVKDAAGGPGAPADPGRPTGYSGSSK A.[L]	0.44273	-1.1755	0.017825
104	[N].VPGEIVES.[L]	0.067083	-3.8979	0.018221
371	[F].LLYQEPVLGPVRGPFPIIV.[-]	0.1588	-2.6547	0.018719
111	[K].TVYQHQAAMKPWIQPK.[T]	0.37551	-1.4131	0.018913
30	[A].RELEELNVPGEIVESLSSEES.[I]	0.3095	-1.692	0.019168
697	[V].APFPEVFGKEKV.[N]	0.2135	-2.2277	0.01932
344	[L].GPVRGPFPIIV.[-]	0.43716	-1.1938	0.019421
865	[E].VIESPPEINTVQVTSTA.[V]	47.563	5.5718	0.01977
301	[K].VKEAMAPKH.[K]	31.04	4.956	0.020108
	<i>1xOxidation [M5]</i>			
336	[K].KYKVPQL.[E]	7.535	2.9136	0.020719
618	[Q].TPVVVPPFL.[Q]	0.3556	-1.4917	0.020977
1116	[D].GSDPPSGDFLTEGGGVR.[G]	26.232	4.7132	0.021475
701	[A].RPKHPIK.[H]	0.35643	-1.4883	0.021727
732	[I].KHQGLPQEV.[L]	2.9358	1.5537	0.021737
684	[Q].EPVLGPV.[R]	0.4597	-1.1212	0.021981
322	[E].SPPEINTVQVTSTAV.[-]	2.5377	1.3435	0.022053
1134	[P].KYPVEPFTEQSLTLTDVEN.[L]	14.689	3.8767	0.022056
163	[K].KIEKFQSEEQQQTEDELQDKIHQFAQ.[T]	0.13949	-2.8418	0.023523
347	[R].TLNPEHLGQGGVQR.[E]	4.5928	2.1994	0.024413
361	[Y].SIGSSSESAEVATEEVK.[I]	3.3711	1.7532	0.0245
209	[K].KIEKFQSEEQQQTEDELQDKIHQF.[A]	0.36385	-1.4586	0.025058
365	[K].IEKFQSEEQQQTEDELQDK.[I]	0.44363	-1.1726	0.025141
934	[K].AIQISYNPDQPSKPNN.[I]	39.489	5.3034	0.025746
1100	[P].HQPLPPTVMFPPQSVL.[S]	21.074	4.3974	0.025974
608	[Q].EPVLGPVRGPFPII.[V]	0.31582	-1.6628	0.026805
1217	[L].SRYPSYGLN.[Y]	25.271	4.6594	0.028013
114	[I].VESLSSSEESITRIN.[K]	37.472	5.2277	0.028037

838	[P].SFSDIPNPIGSENSE.[K]	2.5735	1.3637	0.028114
704	[K].GMTRDQVRED.[S]	32.521	5.0233	0.028138
762	[Q].TPVVVPPFLQPEVM.[G]	0.30257	-1.7247	0.028626
942	[N].YDAAQRGPGG.[A]	3.6719	1.8765	0.029198
1201	[Q].SLTLTDVENLHLPLLLQ.[S]	0.098714	-3.3406	0.029203
1036	[Y].GLNYYQKQKPA.[L]	10.955	3.4535	0.029783
717	[Q].EPVLGPVRGFPF.[I]	0.39908	-1.3252	0.030001
307	[D].IPNPIGSENSEKTT.[M]	0.17234	-2.5367	0.030248
254	[R].FFVAPFPEVFGKEK.[V]	0.27658	-1.8542	0.030351
1106	[F].PPSDTPIKF.[D]	20.214	4.3373	0.031067
588	[T].QTPVVVPPFLQPEVMGVSKVKE.[A]	0.44553	-1.1664	0.031183
1070	[Q].SKVLPVPQ.[K]	125.71	6.9739	0.031472
181	[K].VPQLEIVPNSAE.[E]	0.062785	-3.9934	0.032053
295	[M].PEPAKSAPAPKKGS.[K]	7.2116	2.8503	0.032107
289	[P].FPEVFGKEK.[V]	0.27357	-1.87	0.034194
799	[P].ITPTLNREQLSTSEENS.[K]	23.533	4.5566	0.034673
1	[P].KKTSQLTDHSKETNSSELSKELTPKA.[K]	483.27	8.9167	0.035042
857	[P].IKHQGLPQEVLN.[E]	29.27	4.8714	0.035059
800	[Q].TPVVVPPFLQPEVMG.[V]	0.38747	-1.3679	0.03567
1099	[P].HQPLPTVMFPPQSV.[L]	3.1137	1.6386	0.036043
1109	[L].PQNIPPLTQTPVVVPPF.[L]	3.1981	1.6772	0.036338
861	[F].LKEAGQGAKD.[M]	8.0354	3.0064	0.037352
314	[E].SLSSSEESITRIN.[K]	16.875	4.0768	0.038375
648	[E].LSKDIGSESTEDQAMED.[I]	3.3384	1.7392	0.038478
497	[K].TKLTEEEKNRLNFLK.[K]	0.42429	-1.2369	0.038881
965	[Q].YTDAPSFSDIPNPIGSENSEKTT.[M]	0.48911	-1.0318	0.039005
992	[L].DLDHKSEEDKHL.[K]	40.264	5.3314	0.039518
247	[R].GPFPIIV.[-]	0.43438	-1.203	0.039748
920	[P].IKHQGLPQEVLNENL.[L]	4.0896	2.032	0.040138
955	[E].LSKDIGSESTEDQAMEDIKQMEAES.[I]	4.1857	2.0655	0.040368
132	[K].AMKPWIQPK.[T]	0.27101	-1.8836	0.040438
	<i>1xOxidation [M2]</i>			
812	[K].YPVEPFTE.[S]	0.28724	-1.7996	0.040742
759	[G].LPQEVLNENLLR.[F]	0.21513	-2.2167	0.041223
315	[N].SVEQKHIQKEDVPSE.[Y]	7.3003	2.868	0.041522
441	[V].APFPEVF.[G]	0.16582	-2.5923	0.041607
656	[M].PEPAKSAPAP.[K]	12.042	3.59	0.041961
1046	[S].SEEIVPNSVEQKHIQ.[K]	4.8164	2.268	0.042018
957	[I].AEKTKIPAVFK.[I]	4.3146	2.1092	0.042516
680	[-].MADKPDGE.[I]	5.9734	2.5785	0.044165
	<i>1xMet-loss+Acetyl [N-Term]</i>			
824	[T].QYTDAPSFSDIPNPIGSENSEKTT.[M]	0.37984	-1.3965	0.044655
469	[G].TQYTDAPSFSDIPNPIGSENSEKTTMPL.[W]	5.7739	2.5296	0.045158
500	[A].LPIIQKLEPQIA.[V]	0.08001	-3.6437	0.045178
850	[I].VFVVDSDVERMEEAKT.[E]	0.16885	-2.5662	0.045381

794	[P].IKHQGLPQEVLENEN.[L]	13.915	3.7986	0.045401
1022	[N].AVPITPTLNREQL.[S]	5.7257	2.5175	0.045981
134	[K].KIEKFQSEEQQTDELQDKIHPFAQTQSL.[V]	0.21604	-2.2106	0.046036
585	[M].APKHKEMPFP.[K]	0.24157	-2.0495	0.046532
369	[P].FPKYPVEPFTE.[S]	0.18842	-2.408	0.046887
120	[P].IKHQGLPQEVLENENLL.[R]	109.01	6.7684	0.046949
1211	[S].SSEEIVPNSVEQKHIQKEDVPSERYLGY.[L]	8.9978	3.1696	0.047514
769	[L].VYPFPGPIPN.[S]	0.035852	-4.8018	0.047567
1126	[I].RNLQISNEDLSKEPSISRED.[L]	8.8383	3.1438	0.047795
976	[P].VPQKAVPYP.[Q]	2.9564	1.5639	0.047846
435	[P].VEPFTESQSLTLTDVEN.[L]	5.436	2.4425	0.048435
705	[R].NAVPTPTLNREQLSTSEENSKKT.[V]	0.044019	-4.5057	0.04865
378	[E].MPFPKYPVER.[F]	0.36454	-1.4559	0.049032

P.N* - Peptide number

FC*- Fold change

raw. pval* - Raw p-value

Supplementary Table 6. PLS-DA VIP top 30 scores peptides. The table shows the top 30 peptides that contribute the most to the separation between SCM-D2 and SCM-D21 groups, their deriving proteins, their position in the deriving protein, and variations between the groups.

VIP rank	P.N*	P.F* + Mod*	Deriving Protein	P.P*	SCM-D21/SCM-D2
1	1193	[R].SNVQSPDATEEDFTSHIESEEMH.[D]	Osteopontin	170-192	Up
2	931	[P].LPPTVMFPPQS.[V]	β -casein	166-176	Up
3	1084	[E].KFQSEEQQQTEDELQDKIHPFAQTQ.[S]	β -casein	47-71	Up
4	396	[A].ILNKPEDETHLEAQPTDASAQFIR.[N]	GLYCAM1	19-42	Down
5	455	[K].FALPQYL.[K]	α_{S2} -casein	189-195	Down
6	771	[P].HQPLPPTV.[M]	β -casein	163-170	Up
7	773	[K].TKVIPYVRYL.[-]	α_{S2} -casein	213-222	Down
8	238	[-].MLPLSLLK.[T] <i>1xMet-loss [N-Term]</i>	U6 snRNA-associated Sm-like protein LSm4	1-8	Down
9	441	[V].APFPEVF.[G]	α_{S1} -casein	41-47	Down
10	258	[H].KEMPPF.[K]	β -casein	122-127	Down
11	936	[P].LPPTVMF.[P]	β -casein	166-172	Up
12	383	[V].IPYVRYL.[-]	α_{S2} -casein	216-222	Down
13	1025	[N].TLPTKETIEQEKQAK.[-]	Thymosin beta-10	28-42	Up
14	1192	[R].SNVQSPDATEEDFTSHIESEEMH.[D] <i>1xOxidation [M22]</i>	Osteopontin	170-192	Up
15	214	[K].VKEAMAPK.[H]	β -casein	113-120	Down
16	649	[T].KVIPYVRYL.[-]	α_{S2} -casein	214-222	Down
17	552	[K].ASADESLALGKPGKEPR.[S]	Fibroblast growth factor-binding protein 1	35-51	Down
18	527	[V].APFPEVFGKEK.[V]	α_{S1} -casein	41-51	Down
19	678	[K].AMKPWIQP.[K] <i>1xOxidation [M2]</i>	α_{S2} -casein	204-211	Down
20	339	[Y].LEQLLRL.[K]	α_{S1} -casein	110-116	Down
21	372	[K].AMKPWIQP.[K]	α_{S2} -casein	204-211	Down
22	434	[V].APFPEVFG.[K]	α_{S1} -casein	41-48	Down
23	1074	[K].GLDIQKV.[A]	Beta-lactoglobulin	25-31	Up
24	764	[M].KPWIQP.[K]	α_{S2} -casein	206-211	Down
25	185	[K].TKVIPYV.[R]	α_{S2} -casein	213-219	Down
26	106	[A].ILNKPEDETH.[L]	GLYCAM1	19-28	Down
27	1154	[P].EVFGKEKVNELSKDIGSESTEDQAME D.[I]	α_{S1} -casein	45-71	Up
28	740	[K].VIPYVRYL.[-]	α_{S2} -casein	215-222	Down
29	425	[V].APFPEV.[F]	α_{S1} -casein	41-46	Down
30	484	[K].TKVIPYVR.[Y]	α_{S2} -casein	213-220	Down

P.N* - Peptide number

P.F* + Mod*- Peptide fragment + Modification

P.P* - Peptide position

Supplementary Table 7. Comparison of the 'SCM-D21' group vs. 'SCM-D2' group (P<0.05). The table shows peptides that have changed significantly in the comparison between the two groups, displaying the fold change and the corresponding p-value.

P.N*	Peptide fragment+Modification	FC*	log2(FC)	raw.pval*
697	[V].APFPEVFGKEKV.[N]	0.0267	-5.2271	3.76E-14
238	[-].MLPLSLLK.[T] <i>IxMet-loss [N-Term]</i>	0.00389	-8.0052	4.01E-13
683	[K].FALPQYLKTVYQH.Q.[K]	0.01199	-6.382	2.12E-11
936	[P].LPPTVMF.[P]	262.96	8.0387	3.38E-11
387	[E].IPLSPMGEDSASGDIETLH.[S]	0.11024	-3.1813	4.30E-11
12	[R].QPQSQNPKLPLSIL.[K]	0.00896	-6.8019	6.59E-11
297	[Q].EPVLGPVRGPFPI.[I]	0.01666	-5.9076	7.76E-11
288	[V].VPPFLQPEVMGVSK.[V]	0.05113	-4.2898	8.49E-11
931	[P].LPPTVMFPPQS.[V]	568.18	9.1502	8.94E-11
231	[-].MAVPQFP.[S] <i>IxMet-loss [N-Term]</i>	0.01162	-6.427	1.25E-10
682	[E].MPFPKYVPEPFTESQSLTL.[T]	0.08023	-3.6397	2.65E-10
343	[K].HIQKEDVP.[S]	0.03876	-4.6894	3.03E-10
638	[R].FFVAPFPEVFGKE.[K]	0.02567	-5.2839	4.87E-10
338	[A].ILNKPEDETHLEAQPTDASAQFI.[R]	0.01647	-5.924	6.11E-10
649	[T].KVIPYVRYL.[-]	0.00688	-7.1838	8.64E-10
663	[A].LPQYLKTVYQ.[H]	0.04465	-4.4852	9.52E-10
455	[K].FALPQYL.[K]	0.00364	-8.1012	1.49E-09
635	[R].FFVAPFPEVFG.[K]	0.02785	-5.1662	1.74E-09
258	[H].KEMPFP.[K]	0.00355	-8.1361	1.91E-09
325	[R].FFVAPFPEVFGK.[E]	0.00867	-6.849	2.12E-09
515	[R].NAVPITP.[T]	0.01513	-6.0463	3.18E-09
254	[R].FFVAPFPEVFGKEK.[V]	0.01144	-6.4505	3.37E-09
838	[P].SFSDIPNPIGSENSE.[K]	92.015	6.5238	3.38E-09
221	[K].TVDMESTEFT.[K]	0.00904	-6.7897	3.69E-09
667	[G].YLEQLLRL.[K]	0.02224	-5.4909	4.02E-09
396	[A].ILNKPEDETHLEAQPTDASAQFIR.[N]	0.00481	-7.7008	4.79E-09
250	[P].QPAAAAIQ.[R]	0.02698	-5.2122	6.99E-09
339	[Y].LEQLLRL.[K]	0.0095	-6.718	8.31E-09
1074	[K].GLDIQKV.[A]	202.39	7.661	2.17E-08
541	[R].YQKFALPQYL.[K]	0.01532	-6.0281	2.30E-08
71	[F].FVAPFP.[E]	0.00781	-6.9997	2.35E-08
771	[P].HQPLPPTV.[M]	319.44	8.3194	2.36E-08
185	[K].TKVIPYV.[R]	0.00952	-6.7154	3.61E-08
214	[K].VKEAMAPK.[H]	0.01003	-6.6402	3.73E-08
939	[L].LYQEPVLGPVRGP.[F]	39.707	5.3113	6.10E-08
480	[A].ILNKPEDETHLEAQPTDASAQF.[I]	0.01422	-6.1355	6.10E-08
779	[A].LPQYLKTV.[Y]	0.01765	-5.8244	6.38E-08
425	[V].APFPEV.[F]	0.01504	-6.0549	7.02E-08
535	[G].LPQEVLENENLLRF.[F]	0.06942	-3.8485	7.74E-08

326	[R].NAVITPTLNR.[E]	0.03478	-4.8457	8.23E-08
14	[R].SSRQPQSQNPKLPLSILKE.[K]	0.01931	-5.6944	8.92E-08
161	[K].HKEMPPF.[K]	0.01893	-5.723	1.09E-07
1114	[I].SDKELQEMSTEGSKYVNKEIK.[N]	177.53	7.4719	1.12E-07
181	[K].VPQLEIVPNSAE.[E]	0.02393	-5.385	1.45E-07
615	[FGY].YLEQLI.[GRL]	0.03401	-4.878	1.65E-07
764	[M].KPWIQP.[K]	0.01602	-5.9641	1.79E-07
552	[K].ASADESLALGKPGKEPR.[S]	0.0241	-5.3746	1.96E-07
678	[K].AMKPWIQP.[K]	0.01727	-5.8559	2.03E-07
	<i>1xOxidation [M2]</i>			
450	[Q].KAMKPWIQP.[K]	0.0169	-5.8869	2.41E-07
400	[T].KVIPIYVR.[Y]	0.02984	-5.0669	3.14E-07
263	[Y].TDAPSFSDIPNPIGSENSEKTTMPL.[W]	0.02562	-5.2868	3.31E-07
	<i>1xOxidation [M23]</i>			
1099	[P].HQPLPPTVMFPPQSV.[L]	32.273	5.0123	3.43E-07
616	[F].FVAPFPEVFGK.[E]	0.02797	-5.1599	4.06E-07
606	[Q].KFALPQYL.[K]	0.03235	-4.9502	4.09E-07
619	[R].SSRQPQSQNPKLPLSILK.[E]	0.02759	-5.1798	4.19E-07
158	[P].FPEVFGKE.[K]	0.02838	-5.1392	5.65E-07
740	[K].VIPYVRYL.[-]	0.01849	-5.7568	5.69E-07
593	[F].VAPFPEVFGKE.[K]	0.10438	-3.2601	6.60E-07
546	[F].FVAPFPEVFG.[K]	0.03189	-4.9708	7.21E-07
267	[I].PPKKNQDKTEIPTI.[N]	17.079	4.0942	7.71E-07
462	[F].VAPFPEVFG.[K]	0.03841	-4.7023	8.12E-07
470	[Y].QKFALPQYL.[K]	0.0324	-4.9481	9.40E-07
37	[K].AMKPWIQPK.[T]	0.03666	-4.7695	9.61E-07
39	[F].FVAPFPEVF.[G]	0.01215	-6.3626	9.70E-07
804	[G].LPQEVNLNENLL.[R]	0.06297	-3.9891	1.01E-06
67	[H].QKAMKPWIQP.[K]	0.02693	-5.2147	1.13E-06
193	[F].VAPFPEVF.[G]	0.04093	-4.6105	1.15E-06
361	[Y].SIGSSSEESAEEVATEEVK.[I]	41.929	5.3899	1.17E-06
521	[L].GYLEQLL.[R]	0.04715	-4.4065	1.20E-06
816	[Q].GPIVLNPWDQVK.[R]	0.05626	-4.1518	1.22E-06
188	[F].FVAPFPEV.[F]	0.01251	-6.3214	1.39E-06
262	[R].FFVAPFP.[E]	0.02941	-5.0876	1.72E-06
208	[D].IPNPIGSENSEKTTMPLW.[-]	0.0246	-5.3454	1.76E-06
527	[V].APFPEVFGKEK.[V]	0.02409	-5.3753	1.81E-06
652	[A].MKPWIQP.[K]	0.03681	-4.7637	1.92E-06
490	[V].VVPPFLQPEVMGVSKVK.[E]	0.09283	-3.4293	2.07E-06
434	[V].APFPEVFG.[K]	0.02288	-5.4495	2.10E-06
50	[K].LPLSILKEK.[H]	0.02266	-5.4635	2.16E-06
658	[F].FVAPFPEVFGKEK.[V]	0.04111	-4.6046	2.25E-06
100	[K].FALPQYLK.[T]	0.01381	-6.178	2.33E-06
492	[R].QPQSQNPKLPLS.[I]	0.01489	-6.0692	2.40E-06
753	[A].IPPKKNQDKTEIPT.[I]	22.204	4.4727	2.41E-06

484	[K].TKVIPYVR.[Y]	0.02051	-5.6078	2.41E-06
773	[K].TKVIPYVRYL.[-]	0.00976	-6.6793	3.00E-06
441	[V].APFPEVF.[G]	0.01425	-6.1331	3.07E-06
407	[V].APFPEVFGKE.[K]	0.0271	-5.2057	3.22E-06
570	[F].ALPQYL.[K]	0.03901	-4.6801	3.26E-06
505	[K].TTMPLW.[-]	0.01431	-6.1268	3.29E-06
285	[YGN].LEQILR.[LTG]	0.04952	-4.336	3.40E-06
124	[F].VAPFPEV.[F]	0.03052	-5.0342	3.69E-06
629	[R].QPQSQNPQLP.[L]	0.02474	-5.3368	3.79E-06
281	[V].VPPFLQPEVMGVSKVKE.[A]	0.06484	-3.9471	3.86E-06
60	[R].SSRQPQSQNP.[K]	0.02271	-5.4605	3.97E-06
228	[E].MPFPKYPVEPFTESQSL.[T]	0.03248	-4.9444	4.09E-06
373	[P].FPEVFG.[K]	0.0384	-4.7028	4.13E-06
46	[A].ILNKPEDETHLEAQPTDA.[S]	0.01557	-6.0049	5.01E-06
383	[V].IPYVRYL.[-]	0.0166	-5.9125	5.32E-06
1154	[P].EVFGKEKVNELSKDIGSESTEDQAMED.[I]	469.46	8.8748	5.32E-06
412	[H].KEMPFKYPVEPFTESQSL.[T]	0.04267	-4.5508	5.59E-06
489	[I].QPLVELLSSPHMTVCEQA.[V]	0.05719	-4.1282	5.83E-06
	<i>1xOxidation [M12]</i>			
116	[A].ILNKPEDETHLEAQPTDASAQ.[F]	0.02039	-5.6163	6.08E-06
200	[K].VPQLEIVPNSAEERLHSM.[K]	0.02537	-5.3006	6.09E-06
	<i>1xOxidation [M18]</i>			
372	[K].AMKPWIQP.[K]	0.01355	-6.2058	6.87E-06
1008	[N].VQSPDATEEDFTSHIESEEMHDAPK.[K]	27.884	4.8014	6.90E-06
291	[K].TKVIPYVRY.[L]	0.03528	-4.825	7.18E-06
98	[R].SSRQPQSQNPQLPLSIL.[K]	0.07782	-3.6837	7.30E-06
526	[-].MASVAVEPQLSVVTR.[V]	0.02422	-5.3679	7.74E-06
	<i>1xMet-loss+Acetyl [N-Term]</i>			
1221	[L].SQSKVLPVPQKAVPYPQRDMPIQA.[F]	37.155	5.2155	8.46E-06
	<i>1xOxidation [M20]</i>			
721	[F].VAPFPEVFGK.[E]	0.05271	-4.2457	9.31E-06
821	[L].TDVENLHLP.[L]	9.4415	3.239	9.66E-06
1161	[R].TLNPEHLGQGGVQ.[R]	33.015	5.0451	1.03E-05
106	[A].ILNKPEDETH.[L]	0.01998	-5.6451	1.04E-05
346	[V].APFPEVFGK.[E]	0.04335	-4.528	1.04E-05
1121	[S].HELDSASSEVN.[-]	21.597	4.4328	1.13E-05
1141	[I].NNQFLPYPPYAKPAAVRSPAQ.[I]	37.316	5.2217	1.16E-05
483	[K].FALPQYLKT.[V]	0.05659	-4.1433	1.28E-05
378	[E].MPFPKYPVEP.[F]	0.09385	-3.4135	1.28E-05
759	[G].LPQEVLNENLLR.[F]	0.10296	-3.2798	1.35E-05
555	[V].VPPFLQPEVMGVVS.[K]	0.05732	-4.1249	1.36E-05
423	[M].KPWIQPKT.[K]	0.04239	-4.5603	1.49E-05
1140	[I].NNQFLPYPPYAKPAAVRSPA.[Q]	31.385	4.972	1.52E-05
610	[P].QRDMPIQA.[F]	18.148	4.1817	1.55E-05
1084	[E].KFQSEEQQQTEDELQDKIHFAQTQ.[S]	783.27	9.6134	1.61E-05
444	[R].FFVAPFPE.[V]	0.1199	-3.0601	1.67E-05

1190	[R].SNVQSPDATEEDFTSHIESEEMHDAPKTSQ.[L]	88.494	6.4675	1.75E-05
1192	[R].SNVQSPDATEEDFTSHIESEEMH.[D] <i>1xOxidation [M22]</i>	386.97	8.5961	1.95E-05
1193	[R].SNVQSPDATEEDFTSHIESEEMH.[D]	1659.6	10.697	2.06E-05
1068	[Q].SKVLPVPQKAVPYPQRDMPIQA.[F]	39.729	5.3121	2.08E-05
109	[H].KEMPFPK.[Y]	0.0423	-4.5631	2.10E-05
475	[F].ALPQYLK.[T]	0.08891	-3.4915	2.16E-05
1071	[I].PPKKNQDKTEIPT.[I]	130.77	7.0308	2.18E-05
613	[F].FVAPFPE.[V]	0.10728	-3.2205	2.35E-05
140	[K].TVDMESTEVEFTK.[K]	0.0413	-4.5979	2.36E-05
720	[K].AMKPWIQPKTK.[V]	0.08317	-3.5878	2.41E-05
636	[F].ALPQYLKT.[V]	0.07515	-3.7341	2.45E-05
844	[L].SRYPSYGLNYYQKQKPA.[L]	139.55	7.1246	2.61E-05
661	[V].VVPPFLQPEVMGVSKVKE.[A]	0.08087	-3.6283	2.66E-05
102	[D].IPNPIGSENSEKTTMPL.[W]	0.02919	-5.0983	2.71E-05
1012	[N].AVPITPTLNREQLSTSEENSKKT.[V]	112.16	6.8094	2.87E-05
815	[L].SQSKVLPVPQKAVPYPQR.[D]	48.732	5.6068	2.95E-05
1065	[V].PLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	46.846	5.5499	3.47E-05
512	[V].ENLHLPLPLLQ.[S]	22.944	4.52	3.60E-05
732	[I].KHQGLPQEV.[L]	15.578	3.9614	4.11E-05
1142	[Q].SWMHQPHQPLPPTVMFPPQS.[V]	44.627	5.4798	4.19E-05
438	[M].KPWIQPKTK.[V]	0.10085	-3.3097	4.23E-05
735	[F].FVAPFPEVFGKE.[K]	0.11032	-3.1802	4.27E-05
731	[P].TVMFPPQS.[V]	39.426	5.3011	4.33E-05
286	[R].SSRQPQSQNPKLPLSILKEK.[H]	0.07483	-3.7402	4.34E-05
841	[L].NREQLSTSEENSKKT.[V]	126.43	6.9821	4.39E-05
1105	[L].PVPQKAVPYPQRD.[M]	131.16	7.0352	4.49E-05
121	[V].APFPEVFGKEKVNELS.[K]	0.06171	-4.0184	4.91E-05
334	[A].LIVTQTMK.[G]	0.07519	-3.7333	4.94E-05
876	[I].EKFQSEEQQQTEDELQDKIHP.[F]	22.469	4.4898	5.00E-05
1196	[R].SNVQSPDATEEDFTSH.[I]	71.962	6.1692	5.00E-05
289	[P].FPEVFGKEK.[V]	0.07743	-3.691	5.07E-05
912	[S].EETKENERFTVK.[A]	90.967	6.5073	5.16E-05
401	[K].HIQKEDVPSEK.[Y]	0.12266	-3.0273	5.39E-05
964	[S].LSQSKVLPVPQ.[K]	34.688	5.1164	5.47E-05
662	[P].HQPLPPT.[V]	26.372	4.7209	5.67E-05
199	[P].NPIGSENSEKTTMPLW.[-]	0.08041	-3.6364	5.85E-05
592	[I].VPNSAEERLHSM.[K]	0.1176	-3.088	5.93E-05
1206	[L].SLSQSKVLPVPQKAVPYPQRDMPIQA.[F] <i>1xOxidation [M22]</i>	23.606	4.5611	6.03E-05
574	[R].FFVAPFPEVFGKEKV.[N]	0.18694	-2.4194	6.09E-05
1175	[Q].KAVPYPQRDMPIQA.[F]	18.989	4.2471	6.24E-05
61	[K].VPQLEIVPNSAEERLHSM.[K]	0.02168	-5.5273	6.24E-05
465	[K].YPVEPFTEQSLLTLDVEN.[L]	0.13898	-2.847	6.24E-05
823	[L].SQSKVLPVPQKAVPYPQRDMP.[I]	112.2	6.8099	6.38E-05

272	[V].VPPFLQPEVMG.[V]	0.11843	-3.0779	6.70E-05
431	[G].LPQEVLENEN.[L]	0.08549	-3.5481	7.23E-05
165	[K].VPQLEIVPNS.[A]	0.03401	-4.878	7.40E-05
578	[K].VKEAMAP.[K]	0.12338	-3.0188	7.77E-05
169	[A].LPQYLKT.[V]	0.04046	-4.6273	8.01E-05
44	[K].TVYQHQBK.[A]	0.04479	-4.4807	8.06E-05
1226	[L].SQSKVLPVPQKAVP.[Y]	114.03	6.8333	8.27E-05
1223	[L].SQSKVLPVPQKAVPYPQRDMPIQ.[A]	51.665	5.6911	8.36E-05
264	[K].VPQLEIVPNSAEER.[L]	0.05803	-4.1071	8.43E-05
608	[Q].EPVLGPVRGPFPII.[V]	0.15226	-2.7154	8.44E-05
647	[K].AMKPWIQPKT.[K]	0.04126	-4.5992	8.70E-05
468	[K].TKLTEEEKNRLNFL.[K]	0.06791	-3.8802	8.80E-05
1225	[L].SQSKVLPVPQKAVPYP.[Q]	34.73	5.1181	8.84E-05
603	[Q].EVLNENLL.[R]	0.21938	-2.1885	8.96E-05
1083	[E].KFQSEEQQTEDELQDKIHPFAQTS.[L]	73.468	6.199	9.32E-05
742	[Y].LEQLRLK.[K]	0.14085	-2.8278	9.54E-05
351	[Q].LTDHSKETNSSELSKELTPK.[A]	348.98	8.447	9.85E-05
707	[Y].TDAPSFSDIPNPIGSENSE.[K]	11.804	3.5611	0.000102
1194	[R].SNVQSPDATEEDFTSHIESEE.[M]	31.681	4.9855	0.000104
1228	[S].NVQSPDATEEDFTSHIESEEMH.[D]	76.918	6.2652	0.000105
976	[P].VPQKAVPYP.[Q]	27.679	4.7907	0.000108
508	[L].SLSQSKVLPVPQKAVPYPQRD.[M]	70.244	6.1343	0.000108
449	[K].KTKLTEEEKNRLNFL.[K]	0.12675	-2.98	0.000109
695	[S].LEDKLDLDHKSEEDKHL.[K]	210.7	7.7191	0.000111
1010	[N].VQSPDATEEDFTSHIESEEMH.[D]	23.546	4.5574	0.000112
1009	[N].VQSPDATEEDFTSHIESEEMH.[D]	19.772	4.3054	0.000118
	<i>1xOxidation [M20]</i>			
1234	[L].SLSQSKVLPVPQKAVPYPQRDMPIQ.[A]	53.168	5.7325	0.000128
957	[I].AEKTKIPAVFK.[I]	119.16	6.8968	0.000129
572	[L].SQSKVLPVPQKAVPYPQRD.[M]	191.4	7.5805	0.000131
937	[N].ANEEEYSIGSSSEESAEEVATEEVK.[I]	89.848	6.4894	0.000136
1191	[Q].FLPYYPYAKPAAVRSPAQ.[I]	77.34	6.2731	0.000137
1219	[L].SQSKVLPVPQKAVPYPQRDMPIQAFL.[L]	97.402	6.6059	0.000142
308	[R].GSKASADESLALGKPGKEPR.[S]	0.11113	-3.1697	0.000146
1039	[I].PPKKNQDKTEIPTINTIA.[S]	69.041	6.1094	0.000147
447	[K].EGIHAQQKEPMIGVNQEL.[A]	0.22445	-2.1555	0.000153
111	[K].TVYQHQBKAMKPWIQPK.[T]	0.08925	-3.4861	0.000154
1098	[P].HQPLPPTVM.[F]	71.568	6.1613	0.000158
8	[E].EQQTEDELQDKIHP.[F]	32.047	5.0021	0.000159
1108	[D].PPSGDFLTEGGGVR.[G]	350.13	8.4517	0.000159
237	[P].FPKYPVEPFTESQSL.[T]	0.06732	-3.8928	0.000164
1137	[I].NNQFLPYYPYAKPAAV.[R]	55.367	5.791	0.000169
149	[P].QLEIVPNSAEERLHSM.[K]	0.06699	-3.8998	0.000169
734	[G].LPQEVLEN.[E]	0.1135	-3.1393	0.00017
763	[S].KVLVPVPQK.[A]	14.404	3.8484	0.000184

733	[M].KPWIQPKTKVIP.[Y]	0.15175	-2.7202	0.000193
1025	[N].TLPTKETIEQEKQAK.[-]	111.63	6.8026	0.000194
324	[P].QLEIVPNS.[A]	0.1475	-2.7612	0.000195
811	[H].QPLPPTVMFPPQS.[V]	28.5	4.8329	0.000197
744	[Y].QGPIVLNPWDQVK.[R]	0.13473	-2.8919	0.0002
125	[T].QYTDAPSFSDIPNPIGSENSEKTTMPLW.[-]	0.1683	-2.5709	0.000212
	<i>1xOxidation [M25]</i>			
942	[N].YDAAQRGPGG.[A]	20.476	4.3559	0.000215
388	[K].IHPFAQT.[Q]	0.08314	-3.5883	0.000215
1148	[E].EQQQTEDELQDKIHPFAQTQ.[S]	45.755	5.5159	0.000219
621	[S].SRQPQSQNPKLPLS.[I]	0.07443	-3.7481	0.000232
534	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSE.[K]	25.101	4.6497	0.000234
1128	[P].HPHLSF.[M]	230.5	7.8486	0.000235
817	[H].QPLPPTVMFPPQSV.[L]	43.55	5.4446	0.000242
292	[E].MPFPKYPV.[E]	0.20121	-2.3132	0.000244
1062	[N].SLPQNIPPLT.[Q]	19.024	4.2498	0.000244
467	[R].SEETKENERFTVK.[A]	35.413	5.1462	0.000258
217	[D].SVAYGLKS.[R]	59.683	5.8992	0.00026
65	[L].TDVENLHLPLP.[L]	13.622	3.7679	0.000262
445	[S].DIPNPIGSENSEKTTMPL.[W]	0.09087	-3.46	0.000278
203	[D].IPNPIGSENSEKTTMP.[L]	0.0765	-3.7083	0.000283
440	[I].LNKPEDETHLEAQPTDASAQ.[F]	0.19173	-2.3828	0.000301
443	[K].AAPAGAAIQSR.[A]	0.22808	-2.1324	0.000305
1129	[L].SLSQSKVLPVPQKAVPYP.[Q]	26.979	4.7538	0.000305
236	[S].RQPQSQNPKLPL.[L]	0.10432	-3.261	0.000312
45	[M].KPWIQPK.[T]	0.18004	-2.4736	0.000315
580	[N].FLKKISQ.[R]	0.18504	-2.4341	0.000316
510	[R].SSRQPQSQNPKLPLS.[I]	0.09759	-3.3571	0.000316
168	[Q].GLPQEVNEN.[L]	0.12425	-3.0086	0.000319
1131	[L].SLSQSKVLPVPQKAVPYPQRDMP.[I]	39.737	5.3124	0.000321
643	[K].HKEMPFPKYVPEPFTESQSL.[T]	0.14933	-2.7435	0.000333
261	[L].EIVPNSAEERLHSM.[K]	0.11948	-3.0652	0.000342
839	[L].SLSQSKVLPVPQKAVPYPQ.[R]	14.317	3.8397	0.000347
833	[L].SKDIGSESTEDQAMED.[I]	359.75	8.4909	0.00037
309	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW.[-]	0.12566	-2.9924	0.000393
28	[A].APAGAAIQS.[R]	0.14684	-2.7677	0.000404
363	[K].VKEAMAPKHKEMPFPK.[Y]	0.15614	-2.6791	0.000416
537	[R].RGSKASADESLALGKPGKEPR.[S]	0.22862	-2.129	0.000425
522	[V].VPPFLQPEV.[M]	0.25384	-1.978	0.000428
743	[T].LTDVENLHLPLLLQ.[S]	56.973	5.8322	0.000459
366	[R].SGKDPNHFRPAGLPDKY.[-]	6.2465	2.643	0.000481
275	[D].IPNPIGSENSEK.[T]	0.14942	-2.7425	0.000483
206	[E].MPFPKYV.[V]	0.12546	-2.9947	0.000484
408	[R].NAVPIPT.[L]	0.14555	-2.7804	0.000493
175	[Q].SQNPKLPL.[L]	0.12177	-3.0378	0.000511

878	[I].EKFQSEEQQQTEDELQDKIHFAQTQ.[S]	49.888	5.6406	0.000515
209	[K].KIEKFQSEEQQQTEDELQDKIHFP.[A]	0.13589	-2.8795	0.000517
725	[F].SDIPNPIGSENSEKTTM.[P]	6.4507	2.6894	0.000519
575	[F].VAPFPE.[V]	0.19609	-2.3504	0.00052
877	[V].IESPPEINTVQVTST.[A]	17.483	4.1279	0.000532
219	[P].QSQNPCLP.[L]	0.08814	-3.5041	0.000535
9	[K].EMPFPK.[Y]	0.14759	-2.7603	0.000537
637	[S].EEQQQTEDELQDKIHFP.[F]	58.024	5.8586	0.000541
218	[K].HKEMPFPK.[Y]	0.13039	-2.9391	0.000565
1116	[D].GSDPPSGDFLTGGGVR.[G]	256.75	8.0042	0.000577
310	[L].NENLLRF.[F]	0.25323	-1.9815	0.000581
32	[V].SKVKEAMAPK.[H]	0.11367	-3.1371	0.000628
918	[R].EEVPAADLSDQVPDTESETKILLQGTPVAQ.[M]	34.342	5.1019	0.000632
1143	[L].TDHSKETNSSELSKELTPK.[A]	67.257	6.0716	0.000651
355	[T].PVVVPFL.[Q]	16.443	4.0394	0.000652
316	[L].SQSKVLPVPQKA.[V]	82.374	6.3641	0.000661
1042	[Q].SEEQQQTEDELQDKIHFAQTQ.[T]	45.731	5.5151	0.000676
1041	[Q].SEEQQQTEDELQDKIHFAQTQ.[S]	49.845	5.6394	0.000678
273	[P].VPQKAVPYPQRD.[M]	23.346	4.5451	0.000714
812	[K].YPVEPFTE.[S]	0.3166	-1.6592	0.000716
429	[K].AVPYPQRD.[M]	5.2186	2.3837	0.000728
17	[K].KTETQEKNPLPSKETIEQEKAQES.[-]	25.659	4.6814	0.000746
717	[Q].EPVLGPVRGPPF.[I]	0.14853	-2.7512	0.000752
525	[Q].GPVLPNPWDQV.[K]	0.23532	-2.0873	0.0008
509	[P].QLEIVPNSAEER.[L]	0.16269	-2.6198	0.000884
428	[P].FPEVFGKEKV.[N]	0.12331	-3.0196	0.000885
1144	[Q].SWMHQPHQPLPPT.[V]	11.375	3.5078	0.000892
55	[K].EMPFPKYP.[V]	0.22637	-2.1433	0.000915
680	[-].MADKPDLE.[I]	20.332	4.3457	0.000921
	<i>1xMet-loss+Acetyl [N-Term]</i>			
564	[E].VLNENLLRF.[F]	0.20911	-2.2577	0.00094
144	[D].IPNPIGSENSEKTTMP.[L]	0.08712	-3.5208	0.000943
	<i>1xOxidation [M15]</i>			
255	[V].KEAMAPKH.[K]	0.11803	-3.0828	0.000963
395	[K].TVYQHQAAMKPWIQF.[K]	0.1353	-2.8858	0.000973
958	[E].AESISSSEEIVPNSVEQ.[K]	36.859	5.2039	0.00104
1205	[P].FPEVFGKEKVNELSKDIGSESTEDQAMED.[I]	19.878	4.3131	0.001066
828	[L].LYQEPVL.[G]	11.2	3.4854	0.001068
1197	[R].SNVQSPDATEED.[F]	401.25	8.6484	0.001078
367	[R].YLGYLEQL.[L]	0.1586	-2.6565	0.001132
127	[E].MPFPKYP.[V]	0.13996	-2.8369	0.001136
	<i>1xOxidation [M1]</i>			
430	[L].YQEPVLGPVR.[G]	11.849	3.5667	0.001142
566	[L].EELNVPGEIVES.[L]	3.5719	1.8367	0.001199
868	[P].VKPTSSGSSEKQLNNKYPDAVATWLKPDPSQ.[K]	17.431	4.1236	0.001221
669	[R].NAVPTPTLN.[R]	0.21192	-2.2384	0.001235

1130	[N].TLPTKETIEQEKQA.[K]	40.472	5.3388	0.001248
722	[Q].SEEQQQTEDELQDKIHP.[F]	34.869	5.1239	0.001283
1027	[N].TLPTKETIEQEKQ.[A]	60.295	5.914	0.001286
553	[L].GPVRGPFP.[I]	0.20266	-2.3029	0.001292
257	[K].EMPFKYPVEPFTESQSL.[T]	0.15956	-2.6478	0.001295
358	[T].QYTDAPSFSDIPNPIGSENSEKTTMPLW.[-]	0.16526	-2.5972	0.001341
866	[E].VIESPPEINTVQVTST.[A]	22.842	4.5136	0.001353
1207	[R].SNVQSPDATEEDF.[T]	31.392	4.9723	0.001391
212	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMPLW.[-] <i>1xOxidation [M31]</i>	0.05975	-4.0649	0.001426
586	[V].NELSKDIGSESTEDQAMED.[I]	26.55	4.7306	0.001427
557	[S].EEQQQTEDELQDKIHPFAQTQ.[S]	45.955	5.5222	0.001445
952	[N].YYQKQPVALI.[N]	31.904	4.9957	0.001471
301	[K].VKEAMAPKH.[K] <i>1xOxidation [M5]</i>	0.13154	-2.9264	0.001472
104	[N].VPGEIVES.[L]	0.08556	-3.5469	0.001476
883	[V].TQTMKGLDIQKV.[A]	52.565	5.716	0.001478
576	[K].RNAVPITPT.[L]	0.2785	-1.8443	0.001485
371	[F].LLYQEPVLGPVRGPFPIIV.[-]	0.0722	-3.7919	0.00152
86	[E].KFQSEEQQQTEDELQDKIHP.[F]	57.44	5.844	0.001522
584	[K].AVPYPQRDMPIQA.[F]	4.8245	2.2704	0.001534
631	[P].VPQKAVPYPQRDMPIQA.[F]	17.626	4.1396	0.001547
688	[K].KIEKFQSEEQQQTEDELQ.[D]	11.785	3.5589	0.001549
64	[I].RISHELDSASSEVN.[-]	21.884	4.4518	0.001564
493	[P].IVLNPWDQVK.[R]	0.22673	-2.1409	0.001568
781	[P].HQPLPP.[T]	40.536	5.3411	0.00157
1089	[M].HQP HQPLPPTV.[M]	106.89	6.74	0.001582
919	[Q].LGGPEAGKSEQPENK.[-]	111.05	6.795	0.001584
159	[S].DIPNPIGSENSEKTTMP.[L]	0.21426	-2.2226	0.001708
1036	[Y].GLNYYQQKPVA.[L]	74.097	6.2114	0.001733
172	[L].GTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	26.71	4.7393	0.001806
1092	[T].QTPVVVPPFLQPEVM.[G]	52.559	5.7159	0.001834
307	[D].IPNPIGSENSEKTT.[M]	0.16996	-2.5567	0.001878
626	[V].PPFLQPEVM.[G]	0.12535	-2.996	0.00188
398	[L].YQGPIVLNPWDQVK.[R]	0.26096	-1.9381	0.001889
320	[E].MPFPKYPVEPFTESQSL.[S]	0.30218	-1.7265	0.001918
582	[K].HKEMPFPKYPVEPFTESQSL.[T] <i>1xOxidation [M4]</i>	0.23494	-2.0896	0.001967
530	[Q].GLPQEV LN.[E]	0.21646	-2.2078	0.001991
948	[Q].LTDHSKETNSSELSKELTPKA.[K]	52.02	5.701	0.002013
151	[P].NPIGSENSEKTTMPL.[W]	0.05894	-4.0847	0.00206
786	[L].SLSQSKVLPVPQKAVPYPQR.[D]	13.783	3.7848	0.002064
971	[S].ISSSEEIVPNSVEQ.[K]	23.535	4.5567	0.002149
1115	[R].RSNVQSPDATEEDFTSHIESEMH.[D]	18.753	4.229	0.002214
497	[K].TKLTEEEKNRLNFLK.[K]	0.14372	-2.7987	0.002248
968	[Y].YQQKPVA.[L]	151.04	7.2388	0.002323

807	[S].LSQSKVLP.[V]	24.08	4.5897	0.002324
134	[K].KIEKFQSEEQQQTEDELQDKIHFAQTQSL.[V]	10.588	3.4043	0.002343
726	[K].IEKFQSEEQQQTEDELQDKIHFP.[F]	23.979	4.5837	0.002355
797	[Q].SEEQQQTEDELQDKIHFAQTQS.[L]	22.608	4.4988	0.002395
1132	[M].FPPQSVLS.[L]	41.214	5.3651	0.002396
460	[I].LNKPEDETHLEAQPTDASAQF.[I]	0.16417	-2.6068	0.002493
757	[V].APFPEVFGKEKVNE.[L]	0.29576	-1.7575	0.002528
1186	[Q].FLPYPPYAKPAA.[V]	37.73	5.2377	0.002613
95	[R].FFVAPFPEVFGKEKVNE.[L]	0.19673	-2.3457	0.00266
568	[N].YDAAQRGPGGA.[W]	11.91	3.5741	0.002746
293	[T].EDGSDPPSGDFLTEGGGVR.[G]	145.92	7.189	0.002749
684	[Q].EPVLGPV.[R]	0.32504	-1.6213	0.002798
34	[R].GSKASADESLALGKPGKEP.[R]	0.25907	-1.9486	0.002829
248	[R].NAVITPTLNREQ.[L]	0.22259	-2.1676	0.002906
729	[R].YPSYGLNYYQKPVA.[L]	22.792	4.5105	0.002974
224	[L].HLPLLLQ.[S]	7.8746	2.9772	0.002976
692	[Y].QEPVLGPVRGPFPI.[I]	0.31775	-1.654	0.002986
1069	[N].PLPSKETIEQEKQAGES.[-]	85.041	6.4101	0.003012
420	[L].SLSQSKVLP.[V]	16.717	4.0633	0.003041
29	[K].KYKVPQLEIVPNSAEERLHSM.[K]	0.07643	-3.7097	0.003041
1101	[Q].KAVPYPQRDMPIQ.[A]	34.764	5.1195	0.003042
517	[K].AAPAGAAIQSRAGEIQN.[K]	0.39973	-1.3229	0.003144
83	[K].VPQLEIVPNSAEERLHS.[M]	0.12637	-2.9843	0.003158
196	[T].QYTDAPSFSDIPNPIGSENSEKTTMPL.[W]	0.14822	-2.7542	0.003165
1011	[N].VQSPDATEEDFTSH.[I]	76.347	6.2545	0.003241
1204	[L].SLSQSKVLPVPQKAVPYPQRDMPIQAFL.[L]	9.5388	3.2538	0.00326
724	[D].GRGDSVAYGL.[K]	13.578	3.7632	0.003267
798	[I].NNQFLPYPPYAKPAA.[V]	52.353	5.7102	0.003283
499	[L].LYQEPVLGPVR.[G]	21.262	4.4102	0.003336
777	[K].FQSEEQQQTEDELQDKIHFAQ.[T]	12.985	3.6988	0.003346
785	[D].VENLHLPLLLQ.[S]	36.33	5.1831	0.00335
117	[Y].TDAPSFSDIPNPIGSENSEKTTMPLW.[-]	0.18662	-2.4218	0.003442
290	[V].LSLSQSKVLPVPQK.[A]	0.41812	-1.258	0.003454
822	[Q].SKVLPVPQKAVPYP.[Q]	37.528	5.2299	0.003567
1171	[I].TGPVPREF.[K]	1481.2	10.533	0.00362
24	[L].TLTDVENLHLPLLLQ.[S]	9.9307	3.3119	0.003691
318	[K].YPVEPFTESQSL.[T]	0.2884	-1.7939	0.003718
411	[K].HIQKEDVPSELYLGYLEQ.[L]	0.21497	-2.2178	0.003744
1064	[L].SKDIGSESTEDQAMEDIKQMEAES.[I]	283.62	8.1478	0.003774
129	[Q].LEIVPNSAEERLHSM.[K]	0.1483	-2.7534	0.003793
132	[K].AMKPWIQPK.[T]	0.32566	-1.6186	0.003918
	<i>1xOxidation [M2]</i>			
463	[N].AVPITPT.[L]	0.31885	-1.649	0.003993
1217	[L].SRYPSYGLN.[Y]	163.44	7.3526	0.004133
66	[K].YKVPQLEIVPNSAEER.[L]	0.12091	-3.048	0.004185

739	[K].NQDKTEIPTINT.[I]	29.19	4.8674	0.004219
900	[-].MSDKPDMAEIEKFDK.[S] <i>1xMet-loss+Acetyl [N-Term]</i>	92.358	6.5292	0.004287
646	[L].EQLLRLK.[K]	0.34819	-1.5221	0.004316
997	[S].VLSLSQSKVLPVPQKAVPYPQRDMPIQA.[F]	14.38	3.846	0.004344
139	[P].NPIGSENSEKTTMP.[L]	0.12119	-3.0447	0.004399
340	[K].NMAINPSKEN.[L]	0.3689	-1.4387	0.00441
1053	[L].SKDIGSESTEDQAMEDIKQMEAESISSSEEIVPNSV EQ.[K]	184.78	7.5297	0.00441
426	[K].EMPFPKYPVEPFTESQS.[L] <i>1xOxidation [M2]</i>	0.32992	-1.5998	0.004435
1187	[I].KQMEAESISSSEEIVPNSVEQKHIQKEDVPSEK.[Y]	21.881	4.4516	0.004435
1189	[R].SNVQSPDATEEDFTSHIESEEMHDAPKKTSQL.[T]	43.633	5.4474	0.00444
1087	[K].KEEAPSLRPVPPPISGGGY.[R]	140.53	7.1348	0.004614
1061	[D].FTSHIESEEMH.[D]	41.536	5.3763	0.004666
666	[L].EELNVPGEIVESLSSEESITRIN.[K]	0.07662	-3.7061	0.00468
992	[L].DLDHKSEEDKHL.[K]	332.64	8.3778	0.004701
157	[P].NSAEERLH.[S]	0.29912	-1.7412	0.004753
1168	[E].ELNVPGEIVESLSSEES.[I]	9.2946	3.2164	0.004777
1022	[N].AVPITPTLNREQL.[S]	20.815	4.3796	0.00483
648	[E].LSKDIGSESTEDQAMED.[I]	13.816	3.7882	0.004832
192	[S].LPQNIPPLTQTPV.[V]	0.27907	-1.8413	0.004961
487	[E].IVPNSAEERLHSM.[K]	0.26894	-1.8946	0.004996
294	[R].SNVQSPDATEEDFTSHIESEEMHDAPK.[K]	38.133	5.253	0.005075
500	[A].LPPIQKLEPQIA.[V]	0.20119	-2.3134	0.005176
138	[F].FVAPFPEVFGKEKV.[N]	0.35888	-1.4784	0.00521
889	[V].NELSKDIGSESTEDQAMEDIKQMEAESISSSEEIVP NSVEQ.[K]	38.543	5.2684	0.005305
1122	[L].PQNIPPLTQTPVVPPFLQPEVM.[G]	37.364	5.2236	0.005541
1203	[E].SISSSEEIVPNSVEQ.[K]	59.371	5.8917	0.005645
738	[N].PIGSENSEKTTMPLW.[-]	0.36929	-1.4372	0.005652
1102	[T].QTPVVVPPFLQPEVMG.[V]	36.362	5.1843	0.005661
225	[P].FPKYPVEP.[F]	0.24744	-2.0148	0.005675
947	[V].APFPEVFGKEKVNELSKDIGSESTEDQAMED.[I]	12.112	3.5984	0.005677
315	[N].SVEQKHIQKEDVPSEK.[Y]	23.477	4.5532	0.005796
887	[V].NELSKDIGSESTEDQAMEDIKQMEAES.[I]	94.913	6.5685	0.006028
679	[L].EIVPNSAEERLHSM.[K] <i>1xOxidation [M14]</i>	0.35613	-1.4895	0.006048
791	[S].VPESMTVSDLRQAIVAMMNRKDELEENRS.[L] <i>3xOxidation [M5; M17; M18]</i>	27.559	4.7844	0.006081
730	[K].AAPAGAAIQSRAGEIQNK.[A]	0.34803	-1.5227	0.006132
536	[Q].GLPQEVLENLL.[R]	0.27141	-1.8815	0.006149
163	[K].KIEKFQSEEQQTDELQDKIHPFAQ.[T]	10.548	3.3989	0.006193
946	[P].LPPTVMFPPQ.[S]	26.429	4.7241	0.006275
938	[A].IPPKKNQDKTEIPTIN.[T]	67.234	6.0711	0.006564
216	[K].EGIHAQQKEPMIGVNQELAY.[F]	0.25937	-1.9469	0.00662
820	[L].YQEPVLGPVRGP.[F]	35.177	5.1366	0.006722

502	[K].VKEAMAPKH.[K]	0.1602	-2.6421	0.006784
48	[H].LPLPLLQ.[S]	23.482	4.5535	0.006799
364	[L].SQSKVLP.[V]	24.15	4.5939	0.0068
115	[L].SLSQSKVLPVPQKAVPYPQRDMPIQA.[F]	31.79	4.9905	0.006814
321	[E].ELNVPGEIVES.[L]	3.0283	1.5985	0.006838
1151	[I].SSSEEIVPNSVEQKHIQKEDVPSE.[Y]	165.6	7.3715	0.00694
561	[T].WLKPDPSQKQT.[F]	13.112	3.7129	0.006975
131	[P].NPIGSENSEKTTMP.[L]	0.11298	-3.1459	0.006976
	<i>1xOxidation [M13]</i>			
130	[D].IPNPIGSENSEKT.[T]	0.20679	-2.2738	0.007096
1023	[N].AVPITPTLNREQLSTSEEN.[S]	27.077	4.759	0.007297
1180	[N].ELSKDIGSESTEDQAMEDIKQMEAESISSSEEIVPN SVEQ.[K]	48.805	5.6089	0.007328
873	[I].VESLSSSEESITRINK.[K]	58.834	5.8786	0.007333
352	[L].TEEEKNRLNFL.[K]	0.24901	-2.0057	0.007352
569	[V].RGPFPIL.[V]	0.26367	-1.9232	0.007517
280	[E].KFQSEEQQTDELQDK.[I]	31.746	4.9885	0.007542
1112	[F].SDKIAKYIPIQYV.[L]	22.814	4.5119	0.007571
477	[D].SVAYGLK.[S]	40.11	5.3259	0.007641
755	[D].GRGDSVAYGLKS.[R]	12.946	3.6945	0.007685
164	[D].APSFSDIPNPIG.[S]	0.1182	-3.0807	0.007955
243	[Y].TDAPSFSDIPNPIGSENSEKTTMPLW.[-]	0.23392	-2.0959	0.008199
	<i>1xOxidation [M23]</i>			
360	[M].HQPHQPLPP.[T]	14.17	3.8248	0.008347
1178	[N].ELSKDIGSESTEDQAMEDIKQMEAES.[I]	33.665	5.0732	0.008453
332	[Q].LEIVPNSAEER.[L]	0.38036	-1.3946	0.00846
63	[K].VPQLEIVPNSAEERLH.[S]	0.23894	-2.0653	0.008577
93	[K].LTEEEKNR.[L]	0.45613	-1.1325	0.008742
1213	[S].SSEEIVPNSVEQKHIQKEDVPSE.[R]	2047.8	11	0.008794
190	[E].HVSSEESIISQETYKQEK.[N]	13.322	3.7358	0.008809
1113	[F].SDKIAKYIPIQY.[V]	16.901	4.0791	0.008896
313	[Q].EPVLGPVRGP.[F]	0.25407	-1.9767	0.009047
337	[L].LYQEPVLGPVRGPFPIIV.[-]	0.39596	-1.3366	0.009155
627	[K].TVYQHQQAMKPWIQPKT.[K]	0.30152	-1.7297	0.009222
186	[R].NAVITPTLNREQLSTSEENSK.[K]	0.13889	-2.848	0.009237
784	[E].MPFPKYPVEPFTES.[Q]	0.44798	-1.1585	0.009454
1212	[S].SSEEIVPNSVEQKHIQKEDVPSE.[Y]	197.25	7.6239	0.009538
642	[K].VKEAMAPKHK.[E]	0.26092	-1.9383	0.009756
967	[Y].YQQKPVALI.[N]	53.981	5.7544	0.010138
790	[P].IKHQGLPQEV.[L]	15.73	3.9754	0.010585
806	[K].FQSEEQQTDELQDKIHP.[F]	15.038	3.9106	0.010588
256	[R].NAVITPTLNREQLSTSEENS.[K]	0.27508	-1.8621	0.010704
573	[S].LSQSKVLPVP.[Q]	10.613	3.4077	0.010966
558	[K].AAPAGAAIQS.[R]	0.32204	-1.6347	0.010978
133	[L].TDVENLHLPLPLLQ.[S]	25.294	4.6607	0.011001
954	[N].YYQQKPVA.[L]	317.81	8.312	0.011106

170	[K].VLPVPQKAVPYPQRD.[M]	14.906	3.8978	0.01114
1152	[I].SSSEEIVPNSVEQKHIQKEDVPSE.[R]	65.515	6.0338	0.011304
405	[S].FSDIPNP.[I]	0.40814	-1.2929	0.011371
783	[I].NNQFLPYYPYAKPAAVR.[S]	9.2734	3.2131	0.011388
960	[S].ISSSEEIVPNSVEQKHIQKEDVPSE.[R]	28.485	4.8321	0.011416
768	[S].LSQSKVLPVPQKAVPYPQRDMPIQA.[F]	15.151	3.9213	0.011499
849	[E].VFGKEKVNELSKDIGSESTEDQAMED.[I]	1415.7	10.467	0.011617
397	[L].TDVENLHLPLPLL.[Q]	20.583	4.3634	0.011856
559	[V].VVPFLQPEVMGVSKV.[K]	0.40346	-1.3095	0.011929
448	[Q].SKVLPVPQK.[A]	23.539	4.557	0.011968
950	[T].LPTKETIEQEK.[Q]	552.76	9.1105	0.011971
949	[S].ISSSEEIVPNSVEQK.[H]	10.631	3.4102	0.012001
418	[V].RGPFPPIV.[-]	0.31284	-1.6765	0.012004
415	[Q].GLPQEVLENL.[L]	0.3957	-1.3375	0.012172
403	[K].AMKPWQPKTKVIP.[Y]	0.35075	-1.5115	0.012266
840	[N].KKIEKFQSEEQQQTEDELQDKIHFAQTQ.[S]	27.65	4.7892	0.012316
587	[D].APSFSDIPNPIGSENSEKTTMPLW.[-]	0.4196	-1.2529	0.012349
244	[S].DIPNPIGSENSEK.[T]	0.38954	-1.3602	0.012471
766	[Q].EPVLGPVR.[G]	0.36999	-1.4345	0.012473
533	[K].IEKFQSEEQQQTEDELQDKIHFAQTQ.[S]	10.559	3.4004	0.012553
990	[E].DGSDPPSGDFLTEGGGVR.[G]	224.58	7.8111	0.012772
714	[Q].YTDAPSFSDIPNPIGSENSE.[K]	59.265	5.8891	0.01279
1110	[L].PQNIPPLTQTPVVVPFL.[Q]	23.741	4.5693	0.012874
495	[T].QYTDAPSFSDIPNPIGSENSEK.[T]	0.47524	-1.0733	0.012886
701	[A].RPKHPIK.[H]	0.39523	-1.3392	0.013174
1218	[E].KVNELSKDIGSESTEDQAMEDIKQMEAES.[I]	79.297	6.3092	0.013204
853	[L].EDKLDLDHKSEEDKHL.[K]	88.26	6.4637	0.013303
1001	[N].AVPITPTLNREQLSTSEENSKK.[T]	42.242	5.4006	0.013323
215	[V].KEVNEL.[E]	0.34093	-1.5525	0.01353
690	[V].YPFPGPIP.[N]	0.09038	-3.4678	0.013583
404	[A].IPPKKNQDKTEIPTINT.[I]	89.155	6.4782	0.013771
21	[K].YKVPQLEIVPNSAEERLHSM.[K]	0.11443	-3.1275	0.013783
668	[P].QEVLENLL.[R]	0.32512	-1.621	0.013796
585	[M].APKHKEMPFP.[K]	0.06465	-3.9513	0.013934
348	[K].FQSEEQQQTEDELQDKIHFAQTQ.[S]	19.564	4.2901	0.014519
369	[P].FPKYPVEPFTE.[S]	0.39386	-1.3442	0.014592
1157	[L].NKPEDETHLEAQPTDASAQFIRN.[L]	41.387	5.3711	0.014712
716	[E].MPFPKYPVEPFTEsq.[S]	0.40927	-1.2889	0.014971
625	[T].PVVVPPFLQPEVMGVSKVKE.[A]	24.701	4.6265	0.0151
1216	[L].SRYPsyGLNYYQKPV.[A]	32.205	5.0092	0.015181
1019	[R].ARPATATVGQK.[K]	84.707	6.4044	0.015367
204	[I].VPNSAEERLH.[S]	0.21365	-2.2267	0.015687
520	[K].HIQKEDVPS.[E]	0.35897	-1.4781	0.015881
511	[K].VNELSKDIGSESTEDQAMED.[I]	9.6891	3.2764	0.015979
70	[F].SDIPNPIGSENSEKTTMPLW.[-]	0.28221	-1.8252	0.015981

875	[-].MSDKPDMAEIEKF.[D] <i>1xMet-loss+Acetyl [N-Term]</i>	76.321	6.254	0.017165
808	[E].NLHLPLPLLQ.[S]	10.481	3.3897	0.017226
92	[T].MEHVSSEESIISQETYKQEK.[N]	7.2258	2.8532	0.017509
624	[E].MPFPKYPVEPFTESQS.[L]	0.41504	-1.2687	0.017802
705	[R].NAVPIPTLNREQLSTSEENSKKT.[V]	6.3526	2.6674	0.018166
213	[I].SHELDSASSEVN.[-]	8.1213	3.0217	0.018375
435	[P].VEPFTESQSLTLTDVEN.[L]	11.94	3.5777	0.018541
674	[K].KIEKFQSEEQQQTEDELQDKIHP.[F]	7.8743	2.9771	0.018879
43	[Y].KVPQLEIVPNSAEERLHSM.[K]	0.14127	-2.8235	0.019254
787	[F].QSEEQQQTEDELQDKIHPFAQTQ.[S]	18.254	4.1902	0.019266
554	[E].VLNENLL.[R]	0.36114	-1.4694	0.019272
230	[K].TVDMESTEVEFTKK.[T]	0.10572	-3.2417	0.019579
892	[K].EKVNELSKDIGSESTEDQAMEDIKQMEAES.[I]	5.7625	2.5267	0.019641
399	[S].DIPNPIGSENSEKTTMPLW.[-]	0.00892	-6.8081	0.019686
1018	[L].INNQFLPYYPYAKPAA.[V]	7.0035	2.8081	0.019744
1052	[L].SKDIGSESTEDQAMED.[I] <i>1xOxidation [M14]</i>	87.249	6.4471	0.019856
222	[K].KTSQLTDHSKETNSSELSKELTPK.[A]	77.528	6.2766	0.020154
1136	[P].KYPVEPFTESQSLT.[L]	3.4185	1.7734	0.020154
706	[T].QTPVVVPFL.[Q]	30.562	4.9337	0.020196
664	[N].IPPLTQTPVVVPP.[F]	7.1585	2.8397	0.020217
1174	[N].ELSKDIGSESTEDQAMED.[I]	4.1328	2.0471	0.020372
1188	[R].SNVQSPDATEEDFTSHIESEEMHDAPKKTSQLTDH SKETN.[S]	4.0767	2.0274	0.020703
927	[R].YPSYGLNYYQQKPVALI.[N]	8.1697	3.0303	0.021278
994	[K].VNELSKDIGSESTEDQAMEDIKQMEAES.[I]	86.653	6.4372	0.021475
386	[K].EMPFPKYPVEPFTESQS.[L]	0.40078	-1.3191	0.021585
80	[K].IHPFAQTQS.[L]	0.4371	-1.1939	0.021649
774	[K].FQSEEQQQTEDELQDKIHPFAQTQSL.[V]	4.6557	2.219	0.021686
1134	[P].KYPVEPFTESQSLTLTDVEN.[L]	20.565	4.3621	0.021713
984	[T].DAPSFSDIPNPIGSENSE.[K]	41.705	5.3821	0.02184
392	[A].VPITPTLN.[R]	0.43433	-1.2031	0.021919
87	[K].KYKVPQLEIVPNSAEER.[L]	0.21902	-2.1909	0.021985
922	[H].QPLPPTVMFPPQSVL.[S]	6.7361	2.7519	0.022117
656	[M].PEPAKSAPAP.[K]	35.156	5.1357	0.02215
249	[K].KTVDMESTEVEFTKK.[T]	0.04554	-4.4567	0.02224
1055	[I].KQMEAESISSSEEIVPNSVEQKHQKEDVPSE.[R]	93.335	6.5443	0.022251
830	[E].EQQQTEDELQDKIHPFAQTQS.[L]	14.529	3.8609	0.022413
926	[P].LPPTVMFPPQSVLS.[L]	39.21	5.2932	0.022539
1033	[I].PPKKNQDKTEIPTINTI.[A]	162.93	7.3481	0.022852
1156	[K].NPLPSKETIEQEKGAGES.[-]	69.261	6.114	0.023034
479	[I].NKKIEKFQSEEQQQTEDELQDKIHPFAQTQ.[S]	27.732	4.7935	0.023046
327	[M].PEPAKSAPAPKKGSK.[K]	21.909	4.4534	0.023319
865	[E].VIESPPEINTVQVTSTA.[V]	66.588	6.0572	0.023628
951	[W].YYVPLGTQYTDAPSFSDIPNPIGSENSE.[K]	11.722	3.5511	0.023862

341	[V].LGPVRGPF.[I]	0.38722	-1.3688	0.024026
1120	[L].PQNIPPLTQTPVVPPFLQPEV.[M]	9.6198	3.266	0.024053
745	[E].MPFPKYPVEPFTESQSLT.[L]	0.47425	-1.0763	0.024063
276	[L].SQSKVLPVPQK.[A]	12.755	3.673	0.02423
232	[F].SDIPNPIGSENSEKTTMPLW.[-]	0.4077	-1.2944	0.024299
	<i>1xOxidation [M17]</i>			
761	[-].MSETAPAAPAAPPAEKTVPVK.[K]	223.09	7.8015	0.024314
	<i>1xMet-loss+Acetyl [N-Term]</i>			
173	[F].VAPFPEVFGKEKV.[N]	0.33528	-1.5765	0.024403
501	[I].VLNPWDQVK.[R]	0.44217	-1.1773	0.024414
155	[P].VEPFTESQSL.[T]	0.29032	-1.7843	0.024536
1146	[L].NPEHLGQGGVQ.[R]	13.874	3.7943	0.025143
1170	[T].LEDSPEVIESPPEINTVQVTST.[A]	9.8544	3.3008	0.025852
247	[R].GPFPIIV.[-]	0.49493	-1.0147	0.026057
1045	[S].SEEIVPNSVEQKHIQKEDVPSE.[R]	34.809	5.1214	0.026106
269	[K].EMPFPKYPVEPFTESQSL.[T]	0.41389	-1.2727	0.026127
	<i>1xOxidation [M2]</i>			
860	[P].IKHQGLPQE.[V]	11.283	3.4961	0.026518
1100	[P].HQPLPPTVMFPPQSVL.[S]	29.504	4.8828	0.026961
1075	[L].SKDIGSESTEDQAMEDIKQMEAESISSSEEIVPNSV EQK.[H]	6.4872	2.6976	0.027065
609	[G].YLEQLLR.[L]	0.09384	-3.4137	0.02762
503	[K].LTEEEKNRLN.[F]	0.43985	-1.1849	0.027654
914	[D].IGSESTEDQAMEDIKQMEAESISSSEEIVPNSVEQ.[K]	10.634	3.4106	0.027676
81	[Q].KEDVPSEY.[L]	0.4374	-1.193	0.027839
1047	[L].SDQVPDTESETKILLQGTPVAQ.[M]	7.8976	2.9814	0.027858
1185	[Q].FLPYPPYAKPA.[A]	36.941	5.2072	0.028146
1230	[K].KTVDMESTEVEFTK.[K]	0.09142	-3.4513	0.028516
1231	[V].FGKEKVNELSKDIGSESTEDQAMED.[I]	166.82	7.3822	0.028548
928	[R].YPSYGLNYYQKPVAL.[I]	7.0666	2.821	0.028651
965	[Q].YTDAPSFSDIPNPIGSENSEKTT.[M]	13.979	3.8052	0.028714
1117	[I].GSESTEDQAMEDIKQMEAES.[I]	21.709	4.4403	0.029289
311	[L].SQSKVLPVPQ.[K]	18.584	4.216	0.029293
969	[M].AIPPKKNQDKTEIPTINTIASGEPTSTPTTEAVESTV ATLE.[D]	7.774	2.9586	0.029516
195	[H].DAPKKTSQLTDHSEKTNSSSELSKELTPKA.[K]	14.703	3.878	0.029538
872	[E].VFGKEKVNEL.[S]	94.959	6.5692	0.030086
1214	[S].SSEEIVPNSVEQKHIQ.[K]	15.966	3.997	0.03086
657	[W].YYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	10.117	3.3387	0.031479
1057	[N].SLPQNIPPLTQTPVVPPFLQPEVMGVSKVKE.[A]	26.14	4.7082	0.031924
975	[-].MADKPDLEINSFDKAKLK.[K]	51.712	5.6924	0.032117
	<i>1xMet-loss+Acetyl [N-Term]</i>			
79	[V].KEAMAPK.[H]	0.08246	-3.6002	0.032524
147	[K].IHPFAQTQ.[S]	0.48702	-1.0379	0.032538
864	[P].EDETHLEAQPTDASAQFIRN.[L]	43.336	5.4375	0.033217
274	[RF].RPPIRPP.[FI]	1336.1	10.384	0.033556

402	[S].LTLTDVENL.[H]	0.24126	-2.0513	0.034698
727	[Q].SWMHQPHQPLPPTVMFPPQSV.[L]	16.182	4.0163	0.034965
6	[A].KNTMEHVSSEESIISQETY.[K]	0.07896	-3.6627	0.035012
	<i>1xOxidation [M4]</i>			
1044	[Q].GITDPLFK.[G]	59.532	5.8956	0.035156
75	[K].EKVNELSKDIGSESTEDQAMEDIK.[Q]	0.2229	-2.1655	0.03531
52	[V].SKVKEAMAP.[K]	0.38333	-1.3834	0.035452
279	[L].TDVENLHLPLPL.[L]	27.121	4.7613	0.035495
1037	[Y].GLNYYQQKPVALI.[N]	19.72	4.3016	0.03583
855	[S].DPPSGDFLTEGGGVR.[G]	52.499	5.7142	0.035867
902	[-].MSDKPDMAEIEKFDDSK.[L]	32.753	5.0336	0.036031
	<i>1xMet-loss+Acetyl [N-Term]</i>			
930	[R].YPSYGLNYYQQKPV.[A]	22.563	4.4959	0.036524
842	[Q].TPVVVPPFLQPEVM.[G]	26.608	4.7338	0.036625
	<i>1xOxidation [M14]</i>			
246	[L].GPVRGPFPII.[V]	0.47989	-1.0592	0.036821
845	[N].SLPQNIPPLTQTPVVVPPFLQPEVMG.[V]	44.006	5.4596	0.037418
105	[R].NAVPIPTLNREQLSTSEENSKK.[T]	0.20803	-2.2651	0.037564
550	[K].KIEKFQSEEQQQTEDELQDKIHPFAQTQ.[S]	15.166	3.9227	0.037922
518	[R].EEVPAADLSDQVPDTESETK.[I]	10.936	3.451	0.038018
545	[R].ELEELNVPGEIVESLSSEES.[I]	5.1579	2.3668	0.038615
51	[V].VPPFLQPE.[V]	0.34961	-1.5162	0.039016
528	[N].AVPIPTLNREQLSTSEENSK.[K]	12.312	3.622	0.039644
751	[L].YQEPVLGPVRGPFPII.[I]	8.5475	3.0955	0.040032
689	[L].SLSQSKVLPVP.[Q]	10.376	3.3752	0.040048
437	[V].VPPFLQPEVMGVSKV.[K]	0.4526	-1.1437	0.040065
848	[T].ETQEKNPLPSKETIEQEKGAGES.[-]	34.922	5.1261	0.040564
685	[M].GVSKVKEAMAP.[K]	6.5365	2.7085	0.040688
322	[E].SPPEINTVQVTSTAV.[-]	2.3483	1.2316	0.041074
394	[H].KEMPFKYP.[V]	0.37089	-1.4309	0.041197
245	[Y].TDAPSFSDIPNPIGSENSEKTTMPL.[W]	0.33909	-1.5603	0.041492
410	[E].LEELNVPGEIVES.[L]	4.9224	2.2994	0.045583
347	[R].TLNPEHLGQGGVQR.[E]	8.3312	3.0585	0.045741
89	[D].APSFSDIPNPIGSEN.[S]	0.43918	-1.1871	0.046169
205	[M].FPPQSV.[L]	42.955	5.4248	0.046324
934	[K].AIQISYNPDQPSKPNN.[I]	39.489	5.3034	0.046695
260	[V].VPPFLQPEVM.[G]	0.36067	-1.4713	0.046823
782	[L].TQTPVVVPP.[F]	5.2945	2.4045	0.047163
118	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEK.[T]	2.2039	1.1401	0.048728
847	[AD].ERFFSDK.[EI]	70.701	6.1437	0.049325
792	[M].HQPHQPLPPT.[V]	6.307	2.6569	0.049429

P.N*- Peptide number

FC*- Fold change

raw. pval* - Raw p-value

Supplementary Table 8. PLS-DA VIP top 30 scores peptides. The table shows the top 30 peptides that contribute the most to the separation between H-D2 and H-D21 groups, their deriving proteins, their position in the deriving protein, and variations between the groups.

VIP rank	P.N*	P.F* + Mod*	Deriving Protein	P.P*	H-D21/H-D2
1	1193	[R].SNVQSPDATEEDFTSHIESEEMH.[D]	Osteopontin	170-192	Up
2	1084	[E].KFQSEEQQQTDELQDKIHFAQTQ.[S]	β -casein	47-71	Up
3	773	[K].TKVIPYVRYL.[-]	α_{S2} -casein	213-222	Down
4	1025	[N].TLPTKETIEQEKAQ.[-]	Thymosin beta-10	28-42	Up
5	1192	[R].SNVQSPDATEEDFTSHIESEEMH.[D]	Osteopontin	170-192	Up
6	238	<i>1xOxidation [M22]</i> [-].MLPLSLLK.[T] <i>1xMet-loss [N-Term]</i>	U6 snRNA-associated Sm-like protein LSm4	1-8	Down
7	301	[K].VKEAMAPKH.[K] <i>1xOxidation [M5]</i>	β -casein	113-121	Down
8	950	[T].LPTKETIEQEKAQ.[Q]	Thymosin beta-10	29-39	Up
9	396	[A].ILNKPEDETHLEAQPTDASAQFIR.[N]	GLYCAM1	19-42	Down
10	771	[P].HQPLPPTV.[M]	β -casein	163-170	Up
11	993	[K].VNELSKDIGSESTEDQAMEDIKQMEAES ISSSEEIVPNSVEQ.[K]	α_{S1} -casein	52-93	Up
12	383	[V].IPYVRYL.[-]	α_{S2} -casein	216-222	Down
13	214	[K].VKEAMAPK.[H]	β -casein	113-120	Down
14	115	[L].SLSQSKVLPVPQKAVPYPQRDMPIQA.[F]	β -casein	179-204	Up
15	480	[A].ILNKPEDETHLEAQPTDASAQF.[I]	GLYCAM1	19-40	Down
16	86	[E].KFQSEEQQQTDELQDKIHFAQTQ.[F]	β -casein	47-66	Up
17	502	[K].VKEAMAPKH.[K]	β -casein	113-121	Down
18	727	[Q].SWMHQPHQPLPPTVMFPQSV.[L]	β -casein	157-177	Up
19	1089	[M].HQPHQPLPPTV.[M]	β -casein	160-170	Up
20	185	[K].TKVIPYV.[R]	α_{S2} -casein	213-219	Down
21	37	[K].AMKPWIQPK.[T]	α_{S2} -casein	204-212	Down
22	484	[K].TKVIPYVR.[Y]	α_{S2} -casein	213-220	Down
23	740	[K].VIPYVRYL.[-]	α_{S2} -casein	215-222	Down
24	649	[T].KVIPYVRYL.[-]	α_{S2} -casein	214-222	Down
25	50	[K].LPLSILKEK.[H]	GLYCAM1	83-91	Down
26	106	[A].ILNKPEDETH.[L]	GLYCAM1	19-28	Down
27	786	[L].SLSQSKVLPVPQKAVPYPQR.[D]	β -casein	179-198	Up
28	12	[R].QPQSQNPKLPLSIL.[K]	GLYCAM1	75-88	Down
29	98	[R].SSRQPQSQNPKLPLSIL.[K]	GLYCAM1	72-88	Down
30	557	[S].EEQQQTDELQDKIHFAQTQ.[S]	β -casein	51-71	Up

P.N* - Peptide number

P.F* + Mod*-Peptide fragment + Modification

P.P* - Peptide position

Supplementary Table 9. Comparison of the 'H-D21' group Vs. 'H-D2' group (P <0.05). The table shows peptides that have changed significantly in the comparison between the two groups, displaying the fold change and the corresponding p-value.

P.N*	Peptide fragment+Modification	FC*	log2(FC)	raw. pval*
1193	[R].SNVQSPDATEEDFTSHIESEEMH.[D]	1170.6	10.193	5.11E-20
1192	[R].SNVQSPDATEEDFTSHIESEEMH.[D]	378.66	8.5648	5.96E-19
	<i>1xOxidation [M22]</i>			
1129	[L].SLSQSKVLPVPQKAVPYP.[Q]	88.733	6.4714	2.48E-14
1074	[K].GLDIQKV.[A]	56.092	5.8097	7.66E-14
326	[R].NAVPIPTLNR.[E]	0.012108	-6.3679	2.06E-13
948	[Q].LTDHSKETNSSELSKELTPKA.[K]	14.444	3.8524	4.23E-13
1025	[N].TLPTKETIEQEKQAK.[-]	566.12	9.145	6.60E-13
1084	[E].KFQSEEQQTDELQDKIHFAQTQ.[S]	878.68	9.7792	1.48E-12
1009	[N].VQSPDATEEDFTSHIESEEMH.[D]	10.461	3.387	2.02E-12
	<i>1xOxidation [M20]</i>			
727	[Q].SWMHQPHQPLPPTVMFPQSV.[L]	117.78	6.8799	2.37E-12
1089	[M].HQPHQPLPPTV.[M]	192.28	7.587	4.65E-12
1010	[N].VQSPDATEEDFTSHIESEEMH.[D]	11.934	3.577	5.58E-12
1004	[D].APSFSDIPNPIGSENSE.[K]	47.628	5.5737	6.06E-12
1027	[N].TLPTKETIEQEKQ.[A]	66.28	6.0505	6.85E-12
771	[P].HQPLPPTV.[M]	243.08	7.9253	9.97E-12
1069	[N].PLPSKETIEQEKQAGES.[-]	24.66	4.6241	1.05E-11
844	[L].SRYPYGLNYYQKQKPA.[L]	58.403	5.868	3.22E-11
1137	[I].NNQFLPYPYAKPAAV.[R]	90.642	6.5021	7.54E-11
950	[T].LPTKETIEQEK.[Q]	424.16	8.7285	1.49E-10
301	[K].VKEAMAPKH.[K]	0.003884	-8.0084	1.77E-10
	<i>1xOxidation [M5]</i>			
238	[-].MLPLSLLK.[T]	0.003751	-8.0584	1.94E-10
	<i>1xMet-loss [N-Term]</i>			
1157	[L].NKPEDETHLEAQPTDASAQFIRN.[L]	91.563	6.5167	2.13E-10
1092	[T].QTPVVVPFLQPEVM.[G]	135.32	7.0802	2.70E-10
1130	[N].TLPTKETIEQEKQA.[K]	137.95	7.108	2.78E-10
919	[Q].LGGPEAGKSEQPENK.[-]	122.53	6.937	3.00E-10
786	[L].SLSQSKVLPVPQKAVPYPQR.[D]	86.7	6.438	4.03E-10
50	[K].LPLSILKEK.[H]	0.004164	-7.9077	4.90E-10
1175	[Q].KAVPYPQRDMPIQA.[F]	14.093	3.8169	5.15E-10
1083	[E].KFQSEEQQTDELQDKIHFAQTQS.[L]	72.7	6.1839	6.41E-10
185	[K].TKVIPYV.[R]	0.011339	-6.4626	1.21E-09
1131	[L].SLSQSKVLPVPQKAVPYPQRDMP.[I]	155.14	7.2774	4.96E-09
900	[-].MSDKPDMAEIEKFDK.[S]	105.02	6.7145	5.27E-09
	<i>1xMet-loss+Acetyl [N-Term]</i>			
902	[-].MSDKPDMAEIEKFDKSK.[L]	43.528	5.4439	5.63E-09
	<i>1xMet-loss+Acetyl [N-Term]</i>			
798	[I].NNQFLPYPYAKPAA.[V]	48.827	5.6096	9.44E-09
763	[S].KVLVPVPQK.[A]	4.4363	2.1493	9.80E-09
258	[H].KEMPPF.[K]	0.007221	-7.1135	1.13E-08

1228	[S].NVQSPDATEEDFTSHIESEEMH.[D]	31.818	4.9918	1.28E-08
649	[T].KVIPIVRYL.[-]	0.012684	-6.3009	1.38E-08
557	[S].EEQQQTEDELQDKIHPFAQTQ.[S]	61.196	5.9354	1.48E-08
98	[R].SSRQPQSQNPCLPLSIL.[K]	0.004769	-7.7122	1.61E-08
1225	[L].SQSKVLPVPQKAVPYP.[Q]	14.326	3.8406	1.73E-08
964	[S].LSQSKVLPVPQ.[K]	17.201	4.1044	1.80E-08
1206	[L].SLSQSKVLPVPQKAVPYPQRDMPIQA.[F]	56.369	5.8168	1.87E-08
	<i>1xOxidation [M22]</i>			
1234	[L].SLSQSKVLPVPQKAVPYPQRDMPIQ.[A]	80.044	6.3227	2.21E-08
1216	[L].SRYPSYGLNYYQQKP.V.[A]	53.671	5.7461	5.65E-08
470	[Y].QKFALPQYL.[K]	0.026476	-5.2392	7.09E-08
1226	[L].SQSKVLPVPQKAVP.[Y]	26.013	4.7012	1.04E-07
86	[E].KFQSEEQQTEDELQDKIHP.[F]	75.122	6.2312	1.05E-07
448	[Q].SKVLPVPQK.[A]	6.0939	2.6074	1.29E-07
815	[L].SQSKVLPVPQKAVPYPQR.[D]	22.228	4.4743	1.34E-07
396	[A].ILNKPEDETHLEAQPTDASAQFIR.[N]	0.009157	-6.771	1.61E-07
671	[L].SQSKVLPVP.[Q]	4.9947	2.3204	1.90E-07
115	[L].SLSQSKVLPVPQKAVPYPQRDMPIQA.[F]	172.14	7.4275	2.02E-07
519	[T].DAPSFSDIPNPIGSENSEKTTMPLW.[-]	6.8257	2.771	2.27E-07
351	[Q].LTDHSEKTNSSSELSKELTPK.[A]	18.13	4.1803	2.30E-07
67	[H].QKAMKPWIQP.[K]	0.028524	-5.1317	2.34E-07
234	[L].SLSQSKVLPVPQ.[K]	10.744	3.4254	2.36E-07
822	[Q].SKVLPVPQKAVPYP.[Q]	12.526	3.6469	2.48E-07
754	[H].QPLPPTV.[M]	38.967	5.2842	2.59E-07
619	[R].SSRQPQSQNPCLPLSILK.[E]	0.027935	-5.1618	2.74E-07
839	[L].SLSQSKVLPVPQKAVPYPQ.[R]	15.482	3.9525	2.76E-07
606	[Q].KFALPQYL.[K]	0.036839	-4.7626	2.80E-07
1008	[N].VQSPDATEEDFTSHIESEEMHDAPK.[K]	66.291	6.0507	2.80E-07
1196	[R].SNVQSPDATEEDFTSH.[I]	33.329	5.0587	3.23E-07
60	[R].SSRQPQSQNP.[K]	0.026612	-5.2318	3.36E-07
1042	[Q].SEEQQQTEDELQDKIHPFAQ.[T]	68.45	6.097	3.81E-07
480	[A].ILNKPEDETHLEAQPTDASAQF.[I]	0.02123	-5.5578	3.91E-07
743	[T].LTDVENLHLPLLLQ.[S]	29.639	4.8894	4.09E-07
443	[K].AAPAGAAIQR.[A]	0.035296	-4.8244	4.54E-07
695	[S].LEDKLDLDHKSEEDKHL.[K]	33.261	5.0558	4.60E-07
14	[R].SSRQPQSQNPCLPLSILKE.[K]	0.00855	-6.8698	4.97E-07
420	[L].SLSQSKVLP.[V]	16.741	4.0653	5.69E-07
116	[A].ILNKPEDETHLEAQPTDASAQ.[F]	0.03205	-4.9635	5.77E-07
740	[K].VIPIVRYL.[-]	0.019866	-5.6536	5.93E-07
773	[K].TKVIPIVRYL.[-]	0.007351	-7.0878	6.77E-07
936	[P].LPPTVMF.[P]	24.107	4.5914	7.59E-07
94	[E].VIESPPEINTVQVTSTAV.[-]	0.12093	-3.0478	8.47E-07
689	[L].SLSQSKVLPVP.[Q]	23.707	4.5672	9.29E-07
294	[R].SNVQSPDATEEDFTSHIESEEMHDAPK.[K]	60.09	5.909	9.55E-07
12	[R].QPQSQNPCLPLSIL.[K]	0.005899	-7.4053	9.90E-07

629	[R].QPQSQNPQLP.[L]	0.12976	-2.946	1.06E-06
693	[L].YQEPVLGPVRGPFPII.[V]	14.589	3.8668	1.11E-06
548	[K].KTETQEKNPLPSKETIEQEKQ.[A]	25.252	4.6583	1.14E-06
393	[K].KTETQEKNPLPSKETIEQEK.[Q]	19.393	4.2775	1.18E-06
297	[Q].EPVLGPVRGPFPI.[I]	0.052124	-4.2619	1.22E-06
339	[Y].LEQLLRL.[K]	0.029827	-5.0673	1.23E-06
250	[P].QPAAAAIQ.[R]	0.040445	-4.6279	1.28E-06
455	[K].FALPQYL.[K]	0.022435	-5.4781	1.31E-06
637	[S].EEQQQTEDELQDKIHP.[F]	27.815	4.7978	1.32E-06
975	[-].MADKPDIGEINSFDKAKLK.[K]	49.222	5.6212	1.32E-06
	<i>1xMet-loss+Acetyl [N-Term]</i>			
499	[L].LYQEPVLGPVR.[G]	17.332	4.1154	1.37E-06
613	[F].FVAPFPE.[V]	0.076686	-3.7049	1.40E-06
1062	[N].SLPQNIPPLT.[Q]	18.205	4.1863	1.43E-06
473	[T].DAPSFSDIPNPIGSENSEKTTMP.[L]	7.9073	2.9832	1.44E-06
541	[R].YQKFALPQYL.[K]	0.035599	-4.812	1.52E-06
146	[-].MSDKPDMAEIEKFDKSKLK.[K]	13.744	3.7808	1.53E-06
	<i>1xMet-loss+Acetyl [N-Term]</i>			
502	[K].VKEAMAPKH.[K]	0.018316	-5.7708	1.61E-06
1102	[T].QTPVVVPPFLQPEVMG.[V]	92.613	6.5331	1.62E-06
1097	[H].QPHQPLPPTVMFPPQSV.[L]	171.6	7.4229	1.75E-06
821	[L].TDVENLHLP.[L]	3.6834	1.881	1.83E-06
1140	[I].NNQFLPYYPYAKPAAVRSPA.[Q]	16.201	4.018	2.02E-06
468	[K].TKLTEEEKNRLNFL.[K]	0.039712	-4.6543	2.10E-06
876	[I].EKFAQSEEQQQTEDELQDKIHP.[F]	43.433	5.4407	2.73E-06
683	[K].FALPQYLKTVYQH.[K]	0.020488	-5.6091	2.95E-06
505	[K].TTMPLW.[-]	0.012943	-6.2716	3.08E-06
828	[L].LYQEPVL.[G]	25.668	4.6819	3.12E-06
663	[A].LPQYLKTVYQ.[H]	0.095205	-3.3928	3.24E-06
797	[Q].SEEQQQTEDELQDKIHPFAQTQS.[L]	16.628	4.0556	3.52E-06
777	[K].FQSEEQQQTEDELQDKIHPFAQ.[T]	35.847	5.1638	3.59E-06
774	[K].FQSEEQQQTEDELQDKIHPFAQTQSL.[V]	11.094	3.4717	3.59E-06
221	[K].TVDMESTEVEFT.[K]	0.049973	-4.3227	3.75E-06
722	[Q].SEEQQQTEDELQDKIHP.[F]	14.244	3.8323	3.92E-06
1101	[Q].KAVPYPQRDMPIQ.[A]	14.176	3.8254	3.97E-06
450	[Q].KAMKPWIQ.[K]	0.034318	-4.8649	3.97E-06
357	[L].SLSQSKVLPVPQK.[A]	6.5873	2.7197	4.10E-06
732	[I].KHQGLPQEV.[L]	19.437	4.2807	4.35E-06
161	[K].HKEMPFP.[K]	0.036046	-4.794	4.59E-06
1060	[I].KQMEAESISSSEEIVPNSVEQK.[H]	84.496	6.4008	4.68E-06
678	[K].AMKPWIQ.[K]	0.039439	-4.6642	4.80E-06
	<i>1xOxidation [M2]</i>			
823	[L].SQSKVLPVPQKAVPYPQRDMPI.[I]	44.832	5.4865	5.12E-06
1105	[L].PVPQKAVPYPQRD.[M]	12.057	3.5918	5.15E-06
706	[T].QTPVVVPPFL.[Q]	103.52	6.6937	5.26E-06
1200	[Q].SLVYPPFGPIPN.[S]	24.855	4.6355	5.75E-06

383	[V].IPYVRYL.[-]	0.017415	-5.8436	5.97E-06
214	[K].VKEAMAPK.[H]	0.019187	-5.7037	6.12E-06
832	[H].QPHQPLPPTV.[M]	91.579	6.5169	6.12E-06
930	[R].YPSYGLNYYQQKPV.[A]	81.447	6.3478	6.20E-06
791	[S].VPESMTVSDLRQAIVAMMNRKDELEENRS.[L] <i>3xOxidation [M5; M17; M18]</i>	81.488	6.3485	6.22E-06
48	[H].LPLPLLQ.[S]	19.277	4.2688	6.65E-06
1223	[L].SQSKVLPVPQKAVPYPQRDMPIQ.[A]	63.527	5.9893	6.99E-06
580	[N].FLKKISQ.[R]	0.10397	-3.2658	7.05E-06
274	[RF].RPPIRPP.[FI]	13.904	3.7975	7.33E-06
172	[L].GTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	123.61	6.9497	7.66E-06
325	[R].FFVAPFPEVFGK.[E]	0.04148	-4.5914	7.90E-06
578	[K].VKEAMAP.[K]	0.031968	-4.9672	8.12E-06
285	[YGN].LEQILR.[LTG]	0.044412	-4.4929	8.22E-06
348	[K].FQSEEQQTEDELQDKIHPFAQTQ.[S]	18.261	4.1907	8.27E-06
653	[K].HQGLPQEV.[L]	8.2282	3.0406	8.59E-06
1141	[I].NNQFLPYYPYAKPAAVRSPAQ.[I]	35.326	5.1427	8.63E-06
1194	[R].SNVQSPDATEEDFTSHIESEE.[M]	12.414	3.6339	8.72E-06
939	[L].LYQEPVLGPVRGP.[F]	17.879	4.1602	8.74E-06
533	[K].IEKFQSEEQQTEDELQDKIHPFAQTQ.[S]	10.106	3.3372	9.12E-06
376	[I].NKKIEKFQSEEQQTEDELQDK.[I]	7.3992	2.8874	1.00E-05
785	[D].VENLHLPLPLLQ.[S]	24.238	4.5992	1.04E-05
37	[K].AMKPWIQPK.[T]	0.014144	-6.1436	1.04E-05
333	[S].QSKVLPVPQK.[A]	11.633	3.5401	1.06E-05
397	[L].TDVENLHLPLPLL.[Q]	20.475	4.3558	1.07E-05
1138	[Y].TDAPSFSDIPNPIGSENSEKTT.[M]	37.844	5.242	1.08E-05
400	[T].KVIPIYVR.[Y]	0.076241	-3.7133	1.10E-05
878	[I].EKFQSEEQQTEDELQDKIHPFAQTQ.[S]	67.606	6.0791	1.10E-05
779	[A].LPQYLKTV.[Y]	0.049337	-4.3412	1.14E-05
1012	[N].AVPITPTLNREQLSTSEENSKKT.[V]	147.08	7.2004	1.20E-05
1185	[Q].FLPYYPYAKPA.[A]	12.739	3.6712	1.30E-05
492	[R].QPQSQNPKLPLS.[I]	0.071182	-3.8124	1.36E-05
1190	[R].SNVQSPDATEEDFTSHIESEEMHDAPKKTSQ.[L]	160.96	7.3306	1.39E-05
343	[K].HIQKEDVP.[S]	0.069213	-3.8528	1.39E-05
952	[N].YYQQKPVALI.[N]	11.518	3.5258	1.46E-05
410	[E].LEELNVPGEIVES.[L]	6.3608	2.6692	1.56E-05
552	[K].ASADESLALGKPGKEPR.[S]	0.030924	-5.0151	1.56E-05
842	[Q].TPVVVPPFLQPEVM.[G] <i>1xOxidation [M14]</i>	47.872	5.5811	1.63E-05
352	[L].TEEEKNRLNFL.[K]	0.077917	-3.6819	1.67E-05
997	[S].VLSLSQSKVLPVPQKAVPYPQRDMPIQA.[F]	25.06	4.6473	1.74E-05
725	[F].SDIPNPIGSENSEKTTM.[P]	7.452	2.8976	1.85E-05
558	[K].AAPAGAAIQS.[R]	0.20557	-2.2823	1.89E-05
254	[R].FFVAPFPEVFGKEK.[V]	0.040364	-4.6308	2.05E-05
662	[P].HQPLPPT.[V]	11.358	3.5056	2.26E-05

833	[L].SKDIGSESTEDQAMED.[I]	10.82	3.4356	2.29E-05
17	[K].KTETQEKNPLPSKETIEQEKQAGES.[-]	9.9444	3.3139	2.33E-05
729	[R].YPSYGLNYYQQKPVA.[L]	38.789	5.2776	2.33E-05
1221	[L].SQSKVLPVPQKAVPYPQRDMPIQA.[F]	75.459	6.2376	2.36E-05
	<i>1xOxidation [M20]</i>			
512	[V].ENLHLPLPLLQ.[S]	13.288	3.732	2.42E-05
667	[G].YLEQLLRL.[K]	0.04112	-4.604	2.61E-05
931	[P].LPPTVMFPPQS.[V]	61.043	5.9318	2.65E-05
1219	[L].SQSKVLPVPQKAVPYPQRDMPIQAFL.[L]	37.112	5.2138	2.71E-05
140	[K].TVDMESTEVEFTK.[K]	0.049736	-4.3296	2.72E-05
316	[L].SQSKVLPVPQKA.[V]	13.08	3.7093	2.75E-05
163	[K].KIEKFQSEEQQQTEDELQDKIHFAQ.[T]	50.553	5.6597	2.84E-05
707	[Y].TDAPSFSDIPNPIGSENSE.[K]	6.5557	2.7127	2.89E-05
59	[T].EEEKNRLNFL.[K]	0.037916	-4.721	2.89E-05
1159	[N].TLPTKETIEQEK.[Q]	25.101	4.6497	2.90E-05
286	[R].SSRQPQSQNPKLPLSILKEK.[H]	0.059482	-4.0714	3.06E-05
638	[R].FFVAPFPEVFGKE.[K]	0.060124	-4.0559	3.08E-05
508	[L].SLSQSKVLPVPQKAVPYPQRD.[M]	21.093	4.3987	3.10E-05
635	[R].FFVAPFPEVFG.[K]	0.072698	-3.7819	3.18E-05
360	[M].HQPHQPLPP.[T]	14.07	3.8145	3.19E-05
1068	[Q].SKVLPVPQKAVPYPQRDMPIQA.[F]	37.133	5.2146	3.32E-05
884	[E].LEELNVPGEIVESLSSEESIT.[R]	211.54	7.7248	3.33E-05
109	[H].KEMPFK.[Y]	0.047651	-4.3913	3.50E-05
642	[K].VKEAMAPKHK.[E]	0.11019	-3.1819	3.53E-05
276	[L].SQSKVLPVPQK.[A]	4.8829	2.2877	3.55E-05
781	[P].HQPLPP.[T]	20.498	4.3574	3.57E-05
338	[A].ILNKPEDETHLEAQPTDASAQFI.[R]	0.11333	-3.1414	3.69E-05
1142	[Q].SWMHQPHQPLPPTVMFPPQS.[V]	165.55	7.3711	3.86E-05
757	[V].APFPEVFGKEKVNE.[L]	0.28222	-1.8251	3.91E-05
782	[L].TQTPVVVPP.[F]	20.434	4.3529	3.93E-05
39	[F].FVAPFPEVF.[G]	0.050284	-4.3138	4.05E-05
764	[M].KPWIQP.[K]	0.058544	-4.0943	4.09E-05
255	[V].KEAMAPKH.[K]	0.098254	-3.3473	4.15E-05
100	[K].FALPQYLK.[T]	0.023717	-5.3979	4.35E-05
484	[K].TKVIPYVR.[Y]	0.062784	-3.9935	4.54E-05
688	[K].KIEKFQSEEQQQTEDELQ.[D]	10.691	3.4184	4.57E-05
24	[L].TLTDVENLHLPLPLLQ.[S]	14.138	3.8216	4.61E-05
311	[L].SQSKVLPVPQ.[K]	3.9963	1.9986	4.93E-05
467	[R].SEETKENERFTVK.[A]	39.679	5.3103	4.94E-05
720	[K].AMKPWIQPKTK.[V]	0.10952	-3.1908	5.21E-05
577	[P].FLQPEVM.[G]	6.1526	2.6212	5.51E-05
610	[P].QRDMPIQA.[F]	2.8423	1.507	5.60E-05
787	[F].QSEEQQQTEDELQDKIHFAQTQ.[S]	2.784	1.4771	5.74E-05
364	[L].SQSKVLP.[V]	10.191	3.3492	6.67E-05
965	[Q].YTDAPSFSDIPNPIGSENSEKTT.[M]	13.654	3.7712	6.78E-05

372	[K].AMKPWIQP.[K]	0.039372	-4.6667	6.79E-05
133	[L].TDVENLHLPLLLQ.[S]	20.628	4.3666	6.84E-05
106	[A].ILNKPEDETH.[L]	0.10314	-3.2774	6.84E-05
841	[L].NREQLSTSEENSKKT.[V]	66.792	6.0616	6.87E-05
121	[V].APFPEVFGKEKVNELS.[K]	0.036264	-4.7853	6.96E-05
664	[N].IPPLTQTPVVVPP.[F]	4.1325	2.047	7.02E-05
820	[L].YQEPVLGPVRGP.[F]	5.9328	2.5687	7.04E-05
291	[K].TKVIPYVRY.[L]	0.014648	-6.0932	7.38E-05
817	[H].QPLPPTVMFPPQSV.[L]	30.83	4.9463	7.44E-05
1189	[R].SNVQSPDATEEDFTSHIESEEMHDAPKKTSQL.[T]	59.123	5.8856	7.75E-05
349	[L].SLSQSKVLPVPQKAVPYPQRDMPIQAF.[L]	16.388	4.0345	7.88E-05
750	[F].VAPFPEVFGKEKVNE.[L]	0.2831	-1.8206	7.93E-05
1148	[E].EQQQTEDELQDKIHFAQTQ.[S]	26.771	4.7426	8.87E-05
883	[V].TQTMKGLDIQKV.[A]	40.847	5.3522	8.98E-05
1110	[L].PQNIPPLTQTPVVVPPFL.[Q]	28.429	4.8293	9.09E-05
949	[S].ISSSEEIVPNSVEQK.[H]	21.73	4.4416	9.38E-05
806	[K].FQSEEQQQTEDELQDKIHP.[F]	22.151	4.4693	9.43E-05
636	[F].ALPQYLKT.[V]	0.14057	-2.8306	9.69E-05
1168	[E].ELNVPGEIVESLSSEES.[I]	59.734	5.9005	9.90E-05
218	[K].HKEMPFPK.[Y]	0.073984	-3.7567	9.97E-05
1204	[L].SLSQSKVLPVPQKAVPYPQRDMPIQAF.[L]	28.028	4.8088	0.000102
266	[K].KIEKFQSEEQQQTEDELQDKIHFA.[Q]	3.4374	1.7813	0.000102
303	[S].EEQQQTEDELQDK.[I]	12.22	3.6111	0.000103
441	[V].APFPEVF.[G]	0.062775	-3.9937	0.000108
1001	[N].AVPITPTLNREQLSTSEENSKK.[T]	20.738	4.3742	0.00011
497	[K].TKLTEEEKNRLNFLK.[K]	0.20896	-2.2587	0.000114
482	[A].LPVKPTSSGSSEEKQ.[L]	8.8675	3.1485	0.000115
280	[E].KFQSEEQQQTEDELQDK.[I]	16.376	4.0335	0.000117
71	[F].FVAPFP.[E]	0.026129	-5.2582	0.00012
573	[S].LSQSKVLPVP.[Q]	9.033	3.1752	0.000122
1191	[Q].FLPYPYAKPAAVRSPAQ.[I]	58.247	5.8641	0.000123
572	[L].SQSKVLPVPQKAVPYPQRD.[M]	20.046	4.3252	0.000125
1197	[R].SNVQSPDATEED.[F]	55.269	5.7884	0.000129
1112	[F].SDKIAKYIPIQYV.[L]	69.815	6.1255	0.000133
733	[M].KPWIQPKTKVIP.[Y]	0.25246	-1.9859	0.000134
588	[T].QTPVVVPPFLQPEVMGVSKVKE.[A]	6.7707	2.7593	0.000138
621	[S].SRQPQSQNPKLPLS.[I]	0.088357	-3.5005	0.000143
728	[R].SPAQILQ.[W]	9.1854	3.1993	0.000143
1095	[H].QPHQPLPPTVM.[F]	8.6303	3.1094	0.000148
151	[P].NPIGSENSEKTTMPL.[W]	0.13561	-2.8825	0.000148
679	[L].EIVPNSAEERLHSM.[K]	0.12114	-3.0452	0.00015
	<i>1xOxidation [M14]</i>			
762	[Q].TPVVVPPFLQPEVM.[G]	14.923	3.8995	0.000151
824	[T].QYTDAPSFSDIPNPIGSENSEKTT.[M]	9.0748	3.1819	0.000152
811	[H].QPLPPTVMFPPQS.[V]	18.869	4.238	0.000155

515	[R].NAVPIPT.[T]	0.15809	-2.6612	0.000159
310	[L].NENLLRF.[F]	0.21714	-2.2033	0.00016
193	[F].VAPFPEVF.[G]	0.081882	-3.6103	0.000164
993	[K].VNELSKDIGSESTEDQAMEDIKQMEAESISSSEEIV PNSVEQ.[K]	1226.7	10.261	0.000172
262	[R].FFVAPFP.[E]	0.051449	-4.2807	0.000176
188	[F].FVAPFPEV.[F]	0.073543	-3.7653	0.000177
537	[R].RGSKASADESLALGKPGKEPR.[S]	0.1461	-2.7749	0.000186
475	[F].ALPQYLK.[T]	0.10211	-3.2918	0.000196
120	[P].IKHQGLPQEVLNENLL.[R]	0.05411	-4.208	0.000196
647	[K].AMKPWIQPKT.[K]	0.068781	-3.8618	0.000197
205	[M].FPPQSV.[L]	47.127	5.5585	0.000207
1144	[Q].SWMHQPHQPLPPT.[V]	22.734	4.5068	0.000221
623	[R].HPHPLS.[F]	7.579	2.922	0.000225
457	[S].LPQNIPPLT.[Q]	7.4249	2.8924	0.000225
134	[K].KIEKFQSEEQQQTEDELQDKIHFAQTQSL.[V]	19.876	4.313	0.000225
224	[L].HLPLPLLQ.[S]	7.2411	2.8562	0.000233
1113	[F].SDKIAKYIPIQY.[V]	23.659	4.5643	0.000252
719	[S].LPQNIPPLTQTPVVVPP.[F]	6.7779	2.7608	0.000259
553	[L].GPVRGPFPI.[I]	0.33141	-1.5933	0.000267
889	[V].NELSKDIGSESTEDQAMEDIKQMEAESISSSEEIVP NSVEQ.[K]	275.7	8.1069	0.000271
240	[K].FQSEEQQQTEDELQDKIHFAQTQS.[L]	3.6439	1.8655	0.000272
699	[H].QPHQPLPPT.[V]	4.352	2.1217	0.000275
620	[Y].VPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	8.0563	3.0101	0.000278
697	[V].APFPEVFGKEKV.[N]	0.21884	-2.1921	0.000289
963	[V].LSLSQSKVLPVP.[Q]	118.38	6.8873	0.000298
561	[T].WLKPDPSQKQT.[F]	190.88	7.5765	0.000303
407	[V].APFPEVFGKE.[K]	0.090431	-3.467	0.000305
868	[P].VKPTSSGSSEKQLNNKYPDAVATWLKPDPSQ.[K]	10.222	3.3536	0.000307
692	[Y].QEPVLGPVRGPFPI.[I]	0.19908	-2.3286	0.000312
374	[K].KIEKFQSEEQQQTEDELQDKIHFAQTQS.[L]	4.3382	2.1171	0.000322
741	[F].VAPFPEVFGKEKVNELS.[K]	0.20726	-2.2705	0.000323
1039	[I].PPKKNQDKTEIPTINTIA.[S]	11.671	3.5449	0.000336
425	[V].APFPEV.[F]	0.1065	-3.2311	0.000337
367	[R].YLGYLEQL.[L]	0.10451	-3.2583	0.00035
361	[Y].SIGSSSEESAEEVATEEVK.[I]	10.969	3.4554	0.000352
984	[T].DAPSFSDIPNPIGSENSE.[K]	17.915	4.1631	0.000353
838	[P].SFSDIPNPIGSENSE.[K]	5.011	2.3251	0.000356
633	[K].FQSEEQQQTEDELQDKIHFAQT.[Q]	3.5166	1.8142	0.000359
85	[H].QPHQPLPP.[T]	14.229	3.8307	0.000366
813	[-].MAMVSEFLK.[Q]	92.646	6.5337	0.000379
	<i>1xMet-loss+Acetyl [N-Term]</i>			
550	[K].KIEKFQSEEQQQTEDELQDKIHFAQTQ.[S]	11.425	3.5141	0.000382
1155	[Q].SWMHQPHQPLPP.[T]	34.546	5.1104	0.000385
518	[R].EEVPAADLSDQVPDTESETK.[I]	8.7392	3.1275	0.000386

877	[V].IESPPEINTVQVTST.[A]	18.869	4.238	0.00039
783	[I].NNQFLPYYPYAKPA AVR.[S]	8.7357	3.1269	0.000393
658	[F].FVAPFPEVFGKEK.[V]	0.10906	-3.1968	0.000395
164	[D].APSFSDIPNPIG.[S]	0.041621	-4.5866	0.0004
355	[T].PVVVPPFL.[Q]	12.023	3.5877	0.000408
259	[I].NNQFLPYYPYAKPA.[A]	3.2554	1.7029	0.00041
313	[Q].EPVLGPVRGP.[F]	0.1801	-2.4732	0.000414
175	[Q].SQNP KLP.[L]	0.15717	-2.6696	0.00042
546	[F].FVAPFPEVFG.[K]	0.096751	-3.3696	0.000422
845	[N].SLPQNIPPLTQTPVVPPFLQPEVMG.[V]	35.956	5.1682	0.000423
904	[F].VAPFPEVFGKEKVNELSKDIGSESTEDQAMED.[I]	90.686	6.5028	0.000433
705	[R].NAVPIPTLNREQLSTSEENSKKT.[V]	160.07	7.3226	0.000438
527	[V].APFPEVFGKEK.[V]	0.10696	-3.2249	0.000445
570	[F].ALPQYL.[K]	0.11596	-3.1083	0.000461
65	[L].TDVENLHLPLP.[L]	4.8865	2.2888	0.000466
308	[R].GSKASADESLALGKPGKEPR.[S]	0.16421	-2.6064	0.000471
392	[A].VPITPTLN.[R]	0.14949	-2.7419	0.000472
46	[A].ILNKPEDETHLEAQPTDA.[S]	0.284	-1.8161	0.000475
510	[R].SSRQPQSQNPKLPLS.[I]	0.20039	-2.3191	0.000476
8	[E].EQQQTEDELQDKIHP.[F]	9.2163	3.2042	0.000482
44	[K].TVYQH QK.[A]	0.032448	-4.9457	0.000496
305	[L].TLTDVENLHLPLP.[L]	5.8247	2.5422	0.000497
356	[K].KIEKFQSEEQQQTEDELQDKIHPFAQT.[Q]	4.3141	2.1091	0.000505
9	[K].EMPFPK.[Y]	0.038107	-4.7138	0.000535
807	[S].LSQSKVLP.[V]	14.692	3.8769	0.000538
158	[P].FPEVFGKE.[K]	0.21214	-2.2369	0.000553
334	[A].LIVTQTMK.[G]	0.10653	-3.2307	0.000556
652	[A].MKPWIQP.[K]	0.14389	-2.797	0.000567
1187	[I].KQMEAESISSSEEIVPNSVEQKHIQKEDVP SER.[Y]	38.899	5.2817	0.000569
1053	[L].SKDIGSESTEDQAMEDIKQMEAESISSSEEIVPNSVE Q.[K]	839.29	9.713	0.000572
616	[F].FVAPFPEVFGK.[E]	0.089029	-3.4896	0.000578
513	[F].SDIPNPIGSENSEKTT.[M]	49.393	5.6262	0.000595
416	[A].LPVKPTSSGSSEEKQLNNKYPDAVAT.[W]	13.763	3.7828	0.000598
170	[K].VLPVPQKAVPYPQRD.[M]	5.6944	2.5095	0.000617
826	[R].ELEELNVPGEIVESLSSEESIT.[R]	55.085	5.7836	0.000618
477	[D].SVAYGLK.[S]	5.5108	2.4623	0.000658
289	[P].FPEVFGKEK.[V]	0.21387	-2.2252	0.00066
72	[L].TEAPLNPK.[A]	0.0525	-4.2515	0.000673
230	[K].TVDMESTE VFTKK.[T]	0.1374	-2.8635	0.000687
363	[K].VKEAMAPKHKEMPFPK.[Y]	0.15318	-2.7067	0.000695
375	[P].SFSDIPNPIGSENSEKTTMPL.[W]	0.28729	-1.7994	0.000716
937	[N].ANEE EYSIGSSSEESA EVATEEVK.[I]	87.246	6.447	0.000717
808	[E].NLHLPLPLLQ.[S]	7.5384	2.9143	0.000733
447	[K].EGIHAAQQKEPMIGVNQEL.[A]	0.20354	-2.2966	0.000766

766	[Q].EPVLGPVR.[G]	0.38311	-1.3842	0.000767
169	[A].LPQYLKT.[V]	0.10676	-3.2276	0.000814
645	[K].HPIKHQGLPQEV.[L]	4.9307	2.3018	0.000816
947	[V].APFPEVFGKEKVNELSKDIGSESTEDQAMED.[I]	155.36	7.2795	0.000832
323	[K].FQSEEQQTDELQDKIHPFA.[Q]	4.3396	2.1176	0.000835
403	[K].AMKPWIQPKTKVIP.[Y]	0.18973	-2.3979	0.000854
102	[D].IPNPIGSENSEKTTMPL.[W]	0.12892	-2.9554	0.000957
174	[S].FSDIPNPIGSENSEKTTMP.[L]	2.8666	1.5193	0.000959
528	[N].AVPITPTLNREQLSTSEENSK.[K]	3.885	1.9579	0.000992
219	[P].QSQNPGLP.[L]	0.16225	-2.6238	0.000995
483	[K].FALPQYLKT.[V]	0.17034	-2.5535	0.001012
717	[Q].EPVLGPVRGPPF.[I]	0.34932	-1.5174	0.001018
946	[P].LPPTVMFPPQ.[S]	14.847	3.8921	0.00103
346	[V].APFPEVFGK.[E]	0.13378	-2.9021	0.001032
434	[V].APFPEVFG.[K]	0.11969	-3.0627	0.001068
735	[F].FVAPFPEVFGKE.[K]	0.16507	-2.5988	0.00114
535	[G].LPQEVLNENLLRF.[F]	0.2532	-1.9817	0.001141
111	[K].TVYQHQAAMKPWIQPK.[T]	0.10382	-3.2678	0.001147
581	[E].IVPNSAEERLHSM.[K]	0.25985	-1.9442	0.001183
	<i>1xOxidation [M13]</i>			
724	[D].GRGDSVAYGL.[K]	4.6804	2.2266	0.00119
66	[K].YKVPQLEIVPNSAEER.[L]	0.2707	-1.8852	0.001202
816	[Q].GPIVLNPWDQVK.[R]	0.22654	-2.1421	0.001209
674	[K].KIEKFQSEEQQTDELQDKIHP.[F]	11.287	3.4966	0.00123
615	[FGY].YLEQLI.[GRL]	0.15961	-2.6474	0.001254
614	[N].SLPQNIPPLTQTPVVPPFLQPE.[V]	5.9922	2.5831	0.001261
423	[M].KPWIQPK.[K]	0.19843	-2.3333	0.001262
1186	[Q].FLPYPYAKPAA.[V]	17.93	4.1643	0.001292
971	[S].ISSSEEIVPNSVEQ.[K]	32.646	5.0288	0.001304
45	[M].KPWIQPK.[T]	0.13028	-2.9403	0.001324
1115	[R].RSNVQSPDATEEDFTSHIESEEMH.[D]	9.4057	3.2335	0.001361
830	[E].EQQQTDELQDKIHPFAQTQS.[L]	7.5663	2.9196	0.001363
288	[V].VPPFLQPEVMGVSK.[V]	0.32294	-1.6307	0.001388
345	[F].LPYPYAA.[K]	8.4855	3.085	0.001393
236	[S].RQPQSQNPGLP.[L]	0.2372	-2.0758	0.001403
261	[L].EIVPNSAEERLHSM.[K]	0.20366	-2.2958	0.001434
21	[K].YKVPQLEIVPNSAEERLHSM.[K]	0.17699	-2.4983	0.001435
1161	[R].TLNPEHLGQGGVQ.[R]	81.216	6.3437	0.001461
747	[V].LSLSQSKVLPVPQ.[K]	15.919	3.9927	0.0015
1132	[M].FPPQSVLS.[L]	12.11	3.5981	0.001515
996	[K].DIGSESTEDQAMEDIKQMEAESISSSEEIVPNSVEQ. [K]	46.53	5.5401	0.001543
1099	[P].HQPLPTVMFPPQSV.[L]	10.365	3.3736	0.001544
560	[S].DIPNPIG.[S]	0.22664	-2.1415	0.001591
359	[R].ELEELNVPGEIVESLSSEESITR.[I]	39.844	5.3163	0.001601

124	[F].VAPFPEV.[F]	0.12502	-2.9998	0.001619
566	[L].EELNVPGEIVES.[L]	3.2876	1.717	0.001628
444	[R].FFVAPFPE.[V]	0.11308	-3.1445	0.001646
804	[G].LPQEVLENENLL.[R]	0.27786	-1.8476	0.001708
776	[V].YFPFGPIPN.[S]	4.3701	2.1277	0.00172
1005	[V].VVPPFLQPEVM.[G]	89.909	6.4904	0.001752
1147	[P].KYPVEPFTESQ.[S]	24.664	4.6243	0.001755
564	[E].VLNENLLRF.[F]	0.14291	-2.8068	0.00177
901	[-].MSDKPDMAEIEKFDD.[S]	9.9035	3.3079	0.001817
	<i>1xOxidation [M7]; 1xMet-loss+Acetyl [N-Term]</i>			
584	[K].AVPYPQRDMPIQA.[F]	3.4843	1.8009	0.00184
28	[A].APAGAAIQS.[R]	0.058474	-4.0961	0.001897
597	[K].HPIKHQGLPQEVLENENLL.[R]	0.35289	-1.5027	0.001916
1114	[I].SDKELQEMSTEGSKYVNKEIK.[N]	19.104	4.2558	0.001919
523	[K].VLPVPQKAVPYPQRDMPIQA.[F]	2.7017	1.4339	0.001942
755	[D].GRGDSVAYGLKS.[R]	6.0623	2.5999	0.00195
231	[-].MAVPQFPF.[S]	0.1155	-3.114	0.001984
	<i>1xMet-loss [N-Term]</i>			
1104	[T].QEKNPLPSKETIEQEKQAGES.[-]	10.159	3.3447	0.001986
792	[M].HQPHQPLPPT.[V]	7.2129	2.8506	0.002016
1122	[L].PQNIPPLTQTPVVPPFLQPEVM.[G]	29.434	4.8794	0.002022
503	[K].LTEEEKNRLN.[F]	0.28538	-1.809	0.002049
1041	[Q].SEEQQQTEDELQDKIHPPAQTQ.[S]	24.718	4.6275	0.00205
983	[L].ELDPPPKDV.[E]	33.113	5.0493	0.002133
1180	[N].ELSKDIGSESTEDQAMEDIKQMEAESISSEEIVPNS VEQ.[K]	231.65	7.8558	0.002216
7	[A].KNTMEHVSSSEESIISQETY.[K]	0.061613	-4.0206	0.002228
401	[K].HIQKEDVPSE.[Y]	0.2323	-2.1059	0.002248
793	[N].NQFLPYPPYAKPA.[A]	8.2652	3.0471	0.002292
107	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	7.8094	2.9652	0.002302
132	[K].AMKPWIQPK.[T]	0.16578	-2.5927	0.002305
	<i>1xOxidation [M2]</i>			
445	[S].DIPNPIGSENSEKTTMPL.[W]	0.070296	-3.8304	0.002307
593	[F].VAPFPEVFGKE.[K]	0.18923	-2.4018	0.002351
803	[K].HPIKHQGLPQEVLENENLL.[L]	0.36653	-1.448	0.002356
40	[E].LEELNVPGEIVESLSSEES.[I]	10.978	3.4565	0.002365
545	[R].ELEELNVPGEIVESLSSEES.[I]	30.611	4.936	0.002403
223	[Q].SEEQQQTEDELQDK.[I]	7.0033	2.808	0.002426
487	[E].IVPNSAEERLHSM.[K]	0.35528	-1.493	0.002442
759	[G].LPQEVLENENLLR.[F]	0.25356	-1.9796	0.002512
1058	[N].SLPQNIPPLTQTPVVPPFLQPEVM.[G]	12.884	3.6875	0.002596
217	[D].SVAYGLKS.[R]	8.487	3.0853	0.002622
95	[R].FFVAPFPEVFGKEKVNE.[L]	0.07549	-3.7276	0.002633
592	[I].VPNSAEERLHSM.[K]	0.3548	-1.4949	0.002663
1120	[L].PQNIPPLTQTPVVPPFLQPEV.[M]	13.383	3.7423	0.002725
462	[F].VAPFPEVFG.[K]	0.18247	-2.4542	0.002746

279	[L].TDVENLHLPLPL.[L]	14.505	3.8585	0.002796
836	[E].KVNELSKDIGSESTEDQAMEDIKQMEAEISISSEEI VPNSVEQ.[K]	320.08	8.3223	0.002811
284	[F].FVAPFPEVFGKEKVNE.[L]	0.18835	-2.4085	0.00286
153	[S].LSSSEESITR.[I]	0.20469	-2.2885	0.002883
30	[A].RELEELNVPGEIVESLSSEES.[I]	5.3855	2.4291	0.003008
74	[K].NTMEHVSSEESIISQETY.[K]	0.039821	-4.6503	0.003117
430	[L].YQEPVLPVVR.[G]	3.29	1.7181	0.003129
438	[M].KPWIQPKTK.[V]	0.18684	-2.4201	0.003198
200	[K].VPQLEIVPNSAEERLHSM.[K]	0.22946	-2.1237	0.003221
	<i>1xOxidation [M18]</i>			
6	[A].KNTMEHVSSEESIISQETY.[K]	0.020904	-5.5801	0.00326
	<i>1xOxidation [M4]</i>			
571	[T].QTPVVVPPFLQPE.[V]	4.0233	2.0084	0.00329
1213	[S].SSEEIVPNSVEQKHIQKEDVPSE.[R]	100.91	6.657	0.003293
609	[G].YLEQLLR.[L]	0.13693	-2.8685	0.003388
726	[K].IEKFQSEEQQQTEDELQDKIHP.[F]	36.665	5.1963	0.003476
197	[S].FSDIPNPIGSENSEKTTMP.[L]	3.2538	1.7021	0.003501
	<i>1xOxidation [M18]</i>			
1033	[I].PPKKNQDKTEIPTINTI.[A]	8.9333	3.1592	0.003606
112	[K].VNELSKDIGSESTEDQAMEDIK.[Q]	0.3397	-1.5577	0.003609
721	[F].VAPFPEVFGK.[E]	0.19453	-2.3619	0.003634
605	[L].YQEPVLPVVRGPFPIIV.[-]	2.8369	1.5043	0.003729
544	[F].SDIPNPIG.[S]	3.3731	1.7541	0.003741
738	[N].PIGSENSEKTTMPLW.[-]	0.30314	-1.7219	0.003831
362	[K].IEKFQSEEQQQTEDELQDKIHPFAQTQS.[L]	2.3864	1.2548	0.003899
181	[K].VPQLEIVPNSAE.[E]	0.35487	-1.4946	0.004062
211	[S].VLSLSQSKVLPVPQ.[K]	3.5237	1.8171	0.004152
1011	[N].VQSPDATEEDFTSH.[I]	21.392	4.419	0.004176
1055	[I].KQMEAEISISSEIIVPNSVEQKHIQKEDVPSE.[R]	138.56	7.1143	0.004241
282	[P].VLGPVRGPF.[I]	0.33618	-1.5727	0.004342
669	[R].NAVPIPTLN.[R]	0.26621	-1.9094	0.004361
590	[L].TDVENLHLPLPLLQS.[W]	3.1154	1.6394	0.004397
38	[P].EVIESPPEINTVQVTSTAV.[-]	0.13754	-2.8621	0.004424
627	[K].TVYQHQAAMKPWIQPKT.[K]	0.27385	-1.8685	0.004429
2	[A].KNTMEHVSSEESIISQETYKQE.[K]	0.002754	-8.5045	0.004446
	<i>1xOxidation [M4]</i>			
186	[R].NAVPIPTLNREQLSTSEENSK.[K]	0.3035	-1.7203	0.004614
646	[L].EQLLRLK.[K]	0.29699	-1.7515	0.004775
770	[A].RELEELNVPGE.[I]	0.49744	-1.0074	0.00478
660	[Q].TPVVVPPFLQPEV.[M]	4.2156	2.0758	0.00485
668	[P].QEVLENENLL.[R]	0.39622	-1.3356	0.005059
267	[I].PPKKNQDKTEIPTI.[N]	11.708	3.5495	0.005068
520	[K].HIQKEDVPS.[E]	0.31611	-1.6615	0.005073
1145	[Q].SVLSLSQSKVLPVPQ.[K]	21.136	4.4017	0.005103
583	[L].EIVPNSAEER.[L]	0.32956	-1.6014	0.005166
575	[F].VAPFPE.[V]	0.31715	-1.6568	0.005215

61	[K].VPQLEIVPNSAEERLHSM.[K]	0.40611	-1.3001	0.00524
336	[K].KYKVPQL.[E]	0.20804	-2.2651	0.005487
853	[L].EDKLDLDHKSEEDKHL.[K]	26.159	4.7092	0.005536
800	[Q].TPVVVPPFLQPEVMG.[V]	4.3239	2.1123	0.005648
1205	[P].FPEVFGKEKVNELSKDIGSESTEDQAMED.[I]	166.59	7.3802	0.005666
534	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSE.[K]	15.045	3.9112	0.005677
879	[K].IEKFQSEEQQQTEDELQDKIHFAQ.[T]	5.9739	2.5787	0.005768
449	[K].KTKLTEEEKNRLNFL.[K]	0.093198	-3.4236	0.00577
742	[Y].LEQLRLK.[K]	0.28466	-1.8127	0.006111
761	[-].MSETAPAAPAAPAEKTPVKK.[K]	37.945	5.2458	0.006121
	<i>1xMet-loss+Acetyl [N-Term]</i>			
136	[R].SSRQPQSQNPKLPLSILKEKHL.[R]	0.27624	-1.856	0.006216
875	[-].MSDKPDMAEIEKF.[D]	28.732	4.8446	0.006236
	<i>1xMet-loss+Acetyl [N-Term]</i>			
958	[E].AESISSSEEIVPNSVEQ.[K]	5.7479	2.523	0.006359
567	[R].SGKDPNHFRPA.[G]	4.6422	2.2148	0.006597
893	[K].EKNELSKDIGSESTEDQAMEDIKQMEAESISSSEE IVPNSVEQ.[K]	69.116	6.1109	0.006655
540	[G].ITDPLFK.[G]	16.146	4.0131	0.006716
1018	[L].INNQFLPYPYAKPAA.[V]	37.317	5.2218	0.006914
928	[R].YPSYGLNYYQQKPVAL.[I]	11.668	3.5444	0.006926
62	[S].FIDPKKQPAT.[R]	0.36167	-1.4673	0.007021
1151	[I].SSSEEIVPNSVEQKHIQKEDVPSEK.[Y]	18.043	4.1733	0.007267
517	[K].AAPAGAAIQSRAGEIQN.[K]	0.41939	-1.2536	0.007587
273	[P].VPQKAVPYPQRD.[M]	11.541	3.5286	0.007671
967	[Y].YQQKPVALI.[N]	8.5288	3.0923	0.007811
283	[Y].VPLGTQYTDAPSF.[S]	10.339	3.3701	0.00784
942	[N].YDAAQRGPGG.[A]	28.378	4.8267	0.007852
110	[TGSQRVAHLFE].PPPPPP.[APQYHTDGSMLEK]	0.34965	-1.516	0.008038
278	[T].DVENLHLPLLLQ.[S]	3.6338	1.8615	0.008201
1179	[L].NKPETHLEAQPTDASAQFI.[R]	28.96	4.856	0.008229
607	[N].AVPITPTLN.[R]	0.4715	-1.0847	0.008303
994	[K].VNELSKDIGSESTEDQAMEDIKQMEAES.[I]	27.718	4.7928	0.008477
195	[H].DAPKKTSQLTDHSEKTNSELSKELTPKA.[K]	2.826	1.4987	0.008482
1209	[T].FLKEAGQGAKDM.[W]	16.054	4.0048	0.008539
16	[A].KNTMEHVSSSEESIISQETYKQE.[K]	0.028241	-5.1461	0.008855
918	[R].EEVPAADLSDQVPDTESETKILLQGTQVAQ.[M]	10.524	3.3955	0.008867
767	[A].VPYPQRD.[M]	2.8199	1.4956	0.009019
887	[V].NELSKDIGSESTEDQAMEDIKQMEAES.[I]	47.462	5.5687	0.009295
655	[Y].TDAPSFSDIPNPIGSENSEK.[T]	2.6527	1.4075	0.009877
906	[-].MSETAPAAPA.[A]	16.449	4.0399	0.01002
	<i>1xMet-loss+Acetyl [N-Term]</i>			
600	[Y].FEKTQEELTPFF.[K]	0.18927	-2.4015	0.010162
1201	[Q].SLTLTDVENLHLPLLLQ.[S]	16.951	4.0833	0.010285
411	[K].HIQKEDVPSEKLYGYLEQ.[L]	0.23075	-2.1156	0.010292
1154	[P].EVFGKEKVNELSKDIGSESTEDQAMED.[I]	325.97	8.3486	0.010349

90	[F].SDIPNPIGSENSEKT.[T]	5.6172	2.4899	0.010423
57	[H].IQKEDVPSEK.[Y]	0.331	-1.5951	0.010501
586	[V].NELSKDIGSESTEDQAMED.[I]	8.7334	3.1265	0.010503
1071	[I].PPKKNQDKTEIPT.[I]	245.82	7.9414	0.010544
108	[Y].TDAPSFSDIPNPIGSENSEKTTMP.[L]	2.7631	1.4663	0.010705
943	[A].WYYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	32.844	5.0375	0.01116
248	[R].NAVPIPTLNREQ.[L]	0.31377	-1.6722	0.011335
556	[L].EELNVPGEIVESLSSEES.[I]	11.375	3.5078	0.011343
322	[E].SPPEINTVQVTSTAV.[-]	0.45814	-1.1261	0.011522
809	[L].TQTPVVVPFLQPE.[V]	2.3252	1.2173	0.01153
387	[E].IPLSPMGEDSASGDIETLH.[S]	0.23338	-2.0993	0.011708
938	[A].IPPKKNQDKTEIPTIN.[T]	27.264	4.7689	0.012091
493	[P].IVLNPWDQVK.[R]	0.37737	-1.4059	0.012132
378	[E].MPFPKYPVEP.[F]	0.3394	-1.559	0.012166
439	[N].PIGSENSEKTTMP.[L]	0.42594	-1.2313	0.012186
469	[G].TQYTDAPSFSDIPNPIGSENSEKTTMPL.[W]	0.41282	-1.2764	0.012284
500	[A].LPPIQKLEPQIA.[V]	0.39078	-1.3556	0.013138
256	[R].NAVPIPTLNREQSLSTSEENS.[K]	0.27961	-1.8385	0.013476
29	[K].KYKVPQLEIVPNSAEERLHSM.[K]	0.40235	-1.3135	0.014139
478	[F].FAKESVKDAAGGPGAPADPGRPTGYSGSSKA.[L]	2.3297	1.2202	0.014274
165	[K].VPQLEIVPNS.[A]	0.36516	-1.4534	0.014461
818	[A].RETIQGITDPLF.[K]	21.074	4.3974	0.014778
591	[Q].GLPQEVLENE.[N]	0.39782	-1.3298	0.01485
618	[Q].TPVVVPFL.[Q]	3.1016	1.633	0.01497
264	[K].VPQLEIVPNSAEER.[L]	0.42869	-1.222	0.015066
168	[Q].GLPQEVLENNEN.[L]	0.24325	-2.0395	0.015315
805	[L].TLTDVENLHLPLLLQS.[W]	3.1784	1.6683	0.015766
1156	[K].NPLPSKETIEQEKQAGES.[-]	7.9134	2.9843	0.015984
554	[E].VLNENLL.[R]	0.42158	-1.2461	0.016193
196	[T].QYTDAPSFSDIPNPIGSENSEKTTMPL.[W]	0.35574	-1.4911	0.016361
1065	[V].PLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	17.951	4.166	0.016588
914	[D].IGSESTEDQAMEDIKQMEAESSSEEIVPNSVEQ.[K]	30.88	4.9486	0.016952
1188	[R].SNVQSPDATEEDFTSHIESEEMHDAPKKTSQLTDH SKETN.[S]	9.1023	3.1862	0.017087
1178	[N].ELSKDIGSESTEDQAMEDIKQMEAES.[I]	16.196	4.0175	0.017087
549	[L].EELNVPGEIVESLSSEESIT.[R]	18.325	4.1958	0.017191
849	[E].VFGKEKVNELSKDIGSESTEDQAMED.[I]	281.91	8.1391	0.017354
105	[R].NAVPIPTLNREQSLSTSEENSKK.[T]	0.40356	-1.3091	0.017461
1057	[N].SLPQNIPPLTQTPVVVPFLQPEVMGVSKVKE.[A]	286.84	8.1641	0.017518
340	[K].NMAINPSKEN.[L]	0.20568	-2.2815	0.01758
330	[E].LEELNVPGEIVESLSSEESITR.[I]	16.914	4.0801	0.017625
608	[Q].EPVLGPVRGPFPII.[V]	0.45992	-1.1206	0.017712
1119	[I].GSESTEDQAMEDIKQMEAESSSEEIVPNSVEQ.[K]	174.08	7.4436	0.017713
1098	[P].HQPLPPTVM.[F]	3.6085	1.8514	0.017867

907	[-].MSETAPAAPAAAPPAEKTTPVK.[K] <i>1xMet-loss+Acetyl [N-Term]</i>	16.335	4.0299	0.01816
1064	[L].SKDIGSESTEDQAMEDIKQMEAES.[I]	33.046	5.0464	0.018544
204	[I].VPNSAEERLH.[S]	0.4235	-1.2396	0.018991
960	[S].ISSSEEIVPNSVEQKHIQKEDVPSE.[R]	12.932	3.6928	0.019039
395	[K].TVYQHQAAMKPWIQP.[K]	0.11215	-3.1564	0.019045
974	[-].MADKPDLGEINSFDK.[A] <i>1xMet-loss+Acetyl [N-Term]</i>	4.9047	2.2942	0.019419
1087	[K].KEEAPSLRPVPPISGGGY.[R]	4.7419	2.2455	0.019556
765	[L].LYQEPVLGPVRGPFPII.[V]	10.732	3.4238	0.019827
961	[K].ALLDPSFF.[A]	12.528	3.6471	0.020188
399	[S].DIPNPIGSENSEKTTMPLW.[-]	0.051524	-4.2786	0.020231
892	[K].EKNELSKDIGSESTEDQAMEDIKQMEAES.[I]	4.3097	2.1076	0.020429
1218	[E].KVNELSKDIGSESTEDQAMEDIKQMEAES.[I]	33.416	5.0625	0.020554
1007	[-].MAMVSEFLKQA.[W] <i>1xMet-loss+Acetyl [N-Term]</i>	19.34	4.2735	0.020621
866	[E].VIESPPEINTVQVTST.[A]	4.3385	2.1172	0.020723
1003	[V].VVPFLQPEVMGV.[S] <i>1xOxidation [M11]</i>	154.74	7.2737	0.020732
144	[D].IPNPIGSENSEKTTMP.[L] <i>1xOxidation [M15]</i>	0.38171	-1.3894	0.020976
622	[L].NVPGEIVESLSSEESIT.[R]	10.73	3.4235	0.021068
734	[G].LPQEVLN.[E]	0.44707	-1.1614	0.021198
327	[M].PEPAKSAPAPKKGSK.[K]	4.7557	2.2497	0.02154
1054	[F].LPYPYAKPAAV.[R]	5.8373	2.5453	0.021597
187	[K].EKNELSKDIGSESTEDQAMEDIK.[Q] <i>1xOxidation [M20]</i>	0.18822	-2.4095	0.021706
861	[F].LKEAGQGAKD.[M]	10.229	3.3546	0.022161
536	[Q].GLPQEVNLNENLL.[R]	0.35596	-1.4902	0.022659
1207	[R].SNVQSPDATEEDF.[T]	82.041	6.3583	0.022716
718	[L].YQEPVLGPV.[R]	6.2863	2.6522	0.022898
1212	[S].SSEEIVPNSVEQKHIQKEDVPSE.[Y]	8.2899	3.0514	0.022911
1056	[M].PFPKYPVEPFTESQSL.[T]	7.0164	2.8107	0.022917
227	[T].DAPSFSDIPNPIGSENSEKTTMP.[L] <i>1xOxidation [M22]</i>	8.9304	3.1587	0.023277
350	[K].FQSEEQQTEDELQDK.[I]	7.6621	2.9377	0.023487
1072	[S].GAWYYVPLGTQYTDAPSFSDIPNPIGSENSEKTTM P.[L]	16.644	4.0569	0.023691
1128	[P].HPHLSF.[M]	9.287	3.2152	0.023956
466	[K].VLPVPQK.[A]	2.1142	1.0801	0.024165
831	[Q].TEDELQDKIHQAFTQS.[L]	4.9808	2.3164	0.024478
428	[P].FPEVFGKEKV.[N]	0.46838	-1.0942	0.024779
20	[A].KNTMEHVSSEESIISQETYS.[Q]	0.11248	-3.1523	0.024837
1146	[L].NPEHLGQGGVQ.[R]	99.501	6.6366	0.02508
1152	[I].SSEEIVPNSVEQKHIQKEDVPSE.[R]	11.826	3.5639	0.025198
940	[K].YFLQPEVLHKYSVD.[P]	0.026127	-5.2583	0.025209
957	[I].AEKTKIPAVFK.[I]	41.427	5.3725	0.025318
834	[L].INNQFLPYPYAKPAAV.[R]	10.934	3.4507	0.025326

744	[Y].QGPIVLNPWDQVK.[R]	0.47729	-1.0671	0.025431
292	[E].MPFPKYPV.[E]	0.42096	-1.2483	0.025502
731	[P].TVMFPPQS.[V]	8.8947	3.1529	0.025725
489	[I].QPLVELLSSPHMTVCEQA.[V]	0.18924	-2.4017	0.026053
	<i>1xOxidation [M12]</i>			
84	[H].DAPKKTSQLTDHSKETNSSELSKELTPK.[A]	3.0887	1.627	0.026443
1116	[D].GSDPPSGDFLTEGGGVR.[G]	9.7875	3.2909	0.026483
96	[A].KNTMEHVSSEESIISQETYK.[Q]	0.026715	-5.2262	0.026749
	<i>1xOxidation [M4]</i>			
698	[Q].YTDAPSFSDIPNPIGSENSEKTTMP.[L]	5.5966	2.4845	0.02697
1231	[V].FGKEKVNELSKDIGSESTEDQAMED.[I]	15.583	3.9619	0.027385
80	[K].IHPFAQTQS.[L]	0.28301	-1.8211	0.027428
945	[-].MADKPDGEINSF.[D]	8.7466	3.1287	0.027616
	<i>1xMet-loss+Acetyl [N-Term]</i>			
927	[R].YPSYGLNYYQKQPVALL.[N]	15.48	3.9523	0.027723
249	[K].KTVDMESTEVEFTKK.[T]	0.18605	-2.4263	0.028437
207	[Y].QEPVLGPVRGPFPII.[V]	2.3434	1.2286	0.028852
751	[L].YQEPVLGPVRGPFPII.[I]	2.9848	1.5776	0.0289
82	[K].KTKLTEEEKNRNLFLK.[K]	0.23371	-2.0972	0.029396
730	[K].AAPAGAAIQSRAGEIQNK.[A]	0.4867	-1.0389	0.030203
75	[K].EKNELSKDIGSESTEDQAMEDIK.[Q]	0.47057	-1.0875	0.030911
825	[P].YPQRDMPIQA.[F]	2.3962	1.2608	0.031827
656	[M].PEPAKSAPAP.[K]	25	4.6438	0.032491
488	[Y].QEPVLGPV.[R]	5.1613	2.3677	0.032745
565	[G].VSKVKEAMAP.[K]	4.8877	2.2892	0.033596
429	[K].AVPYPQRD.[M]	2.9075	1.5398	0.034213
1006	[-].MAMVSEFLKQ.[A]	22.389	4.4847	0.035679
	<i>1xMet-loss+Acetyl [N-Term]</i>			
951	[W].YYVPLGTQYTDAPSFSDIPNPIGSENSE.[K]	22.692	4.5041	0.035696
529	[E].VLNENLLR.[F]	0.33123	-1.5941	0.036148
353	[M].APKHKEMPFKYP.[V]	8.7107	3.1228	0.037048
159	[S].DIPNPIGSENSEKTTMP.[L]	0.3606	-1.4715	0.03744
673	[V].DMESTEVFTKK.[T]	0.050947	-4.2949	0.037991
542	[Y].QEPVLGPVR.[G]	2.447	1.291	0.038755
775	[V].LPVPQKAVPYPQRDMPIQA.[F]	2.2342	1.1598	0.040486
222	[K].KTSQTLTDHSKETNSSELSKELTPK.[A]	3.5434	1.8251	0.041561
568	[N].YDAAQRGPGGA.[W]	14.264	3.8343	0.041912
485	[A].VPYPQRDMPII.[I]	0.48578	-1.0416	0.042051
511	[K].VNELSKDIGSESTEDQAMED.[I]	3.6915	1.8842	0.042074
324	[P].QLEIVPNS.[A]	0.47507	-1.0738	0.042247
398	[L].YQGPIVLNPWDQVK.[R]	0.49967	-1.0009	0.044494
1086	[M].KEGIHAQQKEPMIGVNQE.[L]	2.6899	1.4275	0.044967
917	[R].EEVPAADLSDQVPDTESETKIL.[L]	2.9569	1.5641	0.045283
142	[K].EKNELSKDIGSESTEDQAMED.[I]	5.036	2.3323	0.045349
1125	[F].RPAGLPDKY.[-]	38.488	5.2663	0.045372
1013	[-].MASGVAVSDGVIK.[V]	15.688	3.9716	0.045594
	<i>1xMet-loss+Acetyl [N-Term]</i>			

1171	[I].TGPVPREF.[K]	19.352	4.2744	0.046173
657	[W].YYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	36.12	5.1747	0.046624
915	[R].VAPEEHPVLLTEAPLNPK.[A]	12.522	3.6464	0.046645
1036	[Y].GLNYYQKPVA.[L]	10.145	3.3428	0.046762
1035	[P].SGAWYYVPLGTQYTDAPSFSDIPNPIGSENSEKTTMP.[L]	3.7144	1.8931	0.048033
1044	[Q].GITDPLFK.[G]	3.6671	1.8746	0.048086
962	[Y].YVPLGTQYTDAPSF.[S]	60.443	5.9175	0.048684
926	[P].LPPTVMFPPQSVLS.[L]	4.0387	2.0139	0.049032
714	[Q].YTDAPSFSDIPNPIGSENSE.[K]	8.4949	3.0866	0.049078
796	[F].LLYQEPVL.[G]	14.757	3.8833	0.049168
190	[E].HVSSSEESIISQETYKQEK.[N]	3.829	1.937	0.049199
599	[Y].PVEPFTESQSL.[T]	5.8831	2.5566	0.049271
846	[Y].YVPLGTQYTDAPSFSDIPNPIGSENSEKTT.[M]	29.743	4.8945	0.049516
1021	[-].MDDIAALVV.[D] <i>1xMet-loss+Acetyl [N-Term]</i>	3.6073	1.8509	0.049579
1210	[L].SQEFHSLEDKLDLDHKSEEDKHL.[K]	4.7542	2.2492	0.04967
953	[N].YYQKPVAL.[I]	4.0885	2.0316	0.04993

P.N*- Peptide number

FC*- Fold change

raw. pval* - Raw p-value