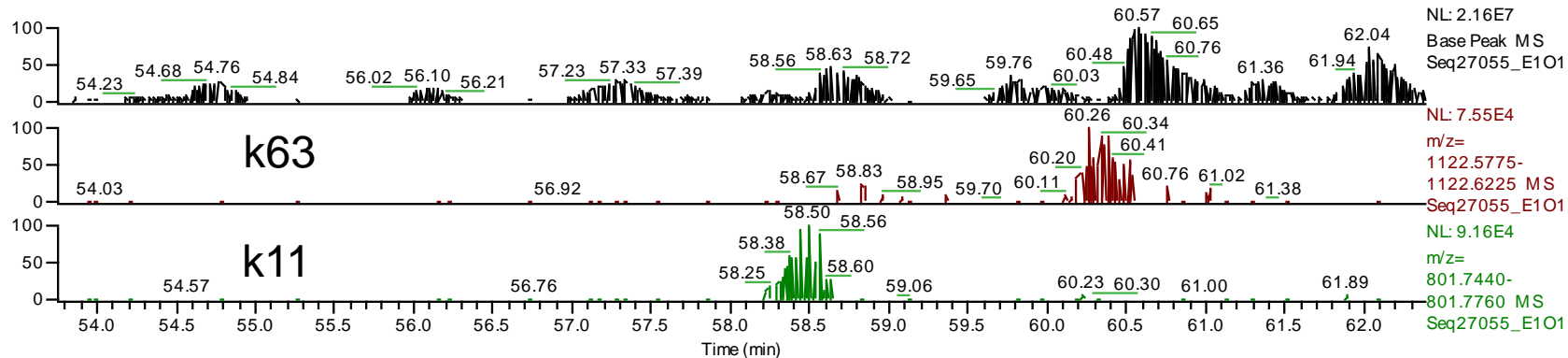
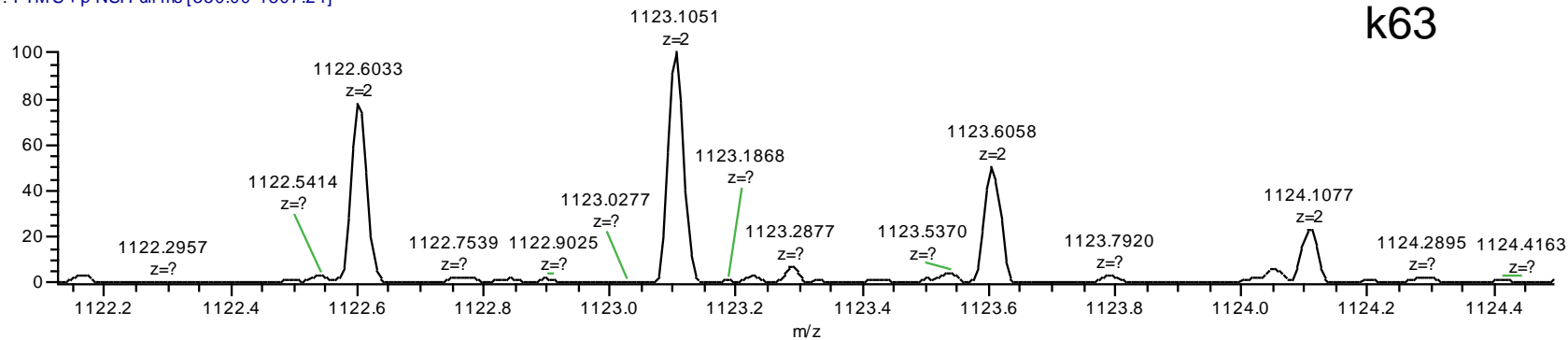


RT: 53.75 - 62.39



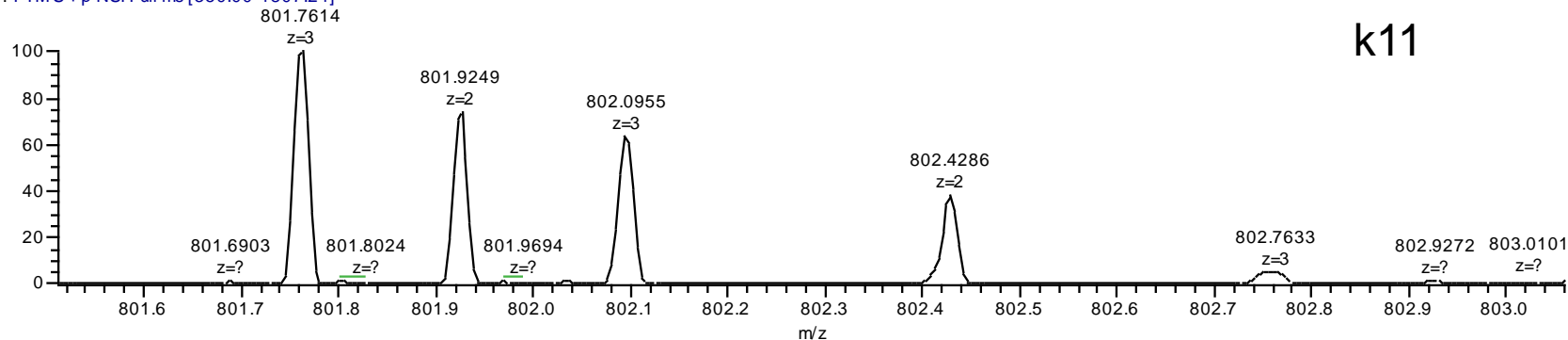
Seq27055\_E101 # 7609-7940 RT: 59.00-61.21 AV: 106 NL: 9.18E3

T: FTMS +p NSI Full ms [350.00-1807.24]

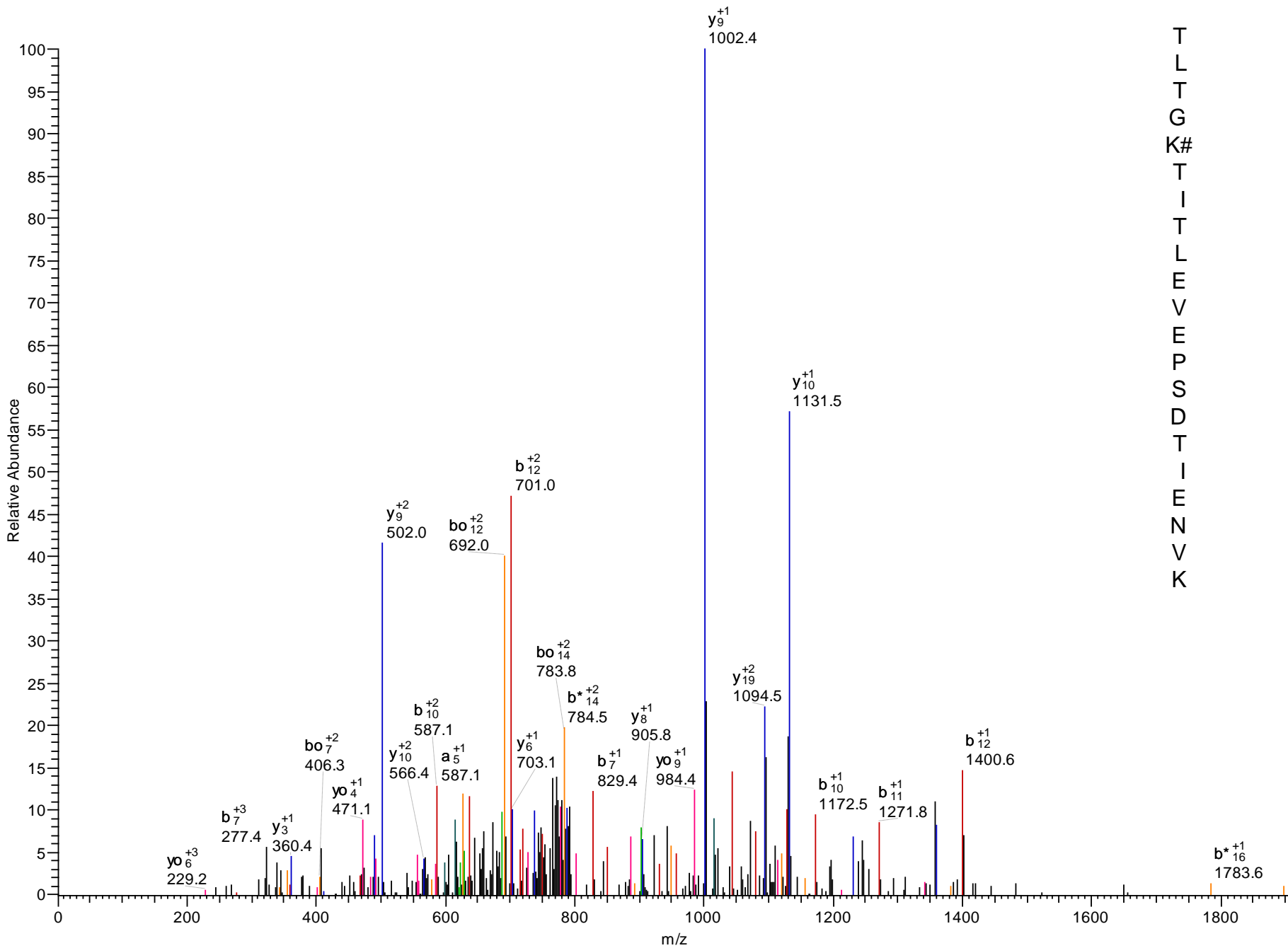


Seq27055\_E101 # 7490-7546 RT: 58.26-58.60 AV: 17 NL: 4.08E4

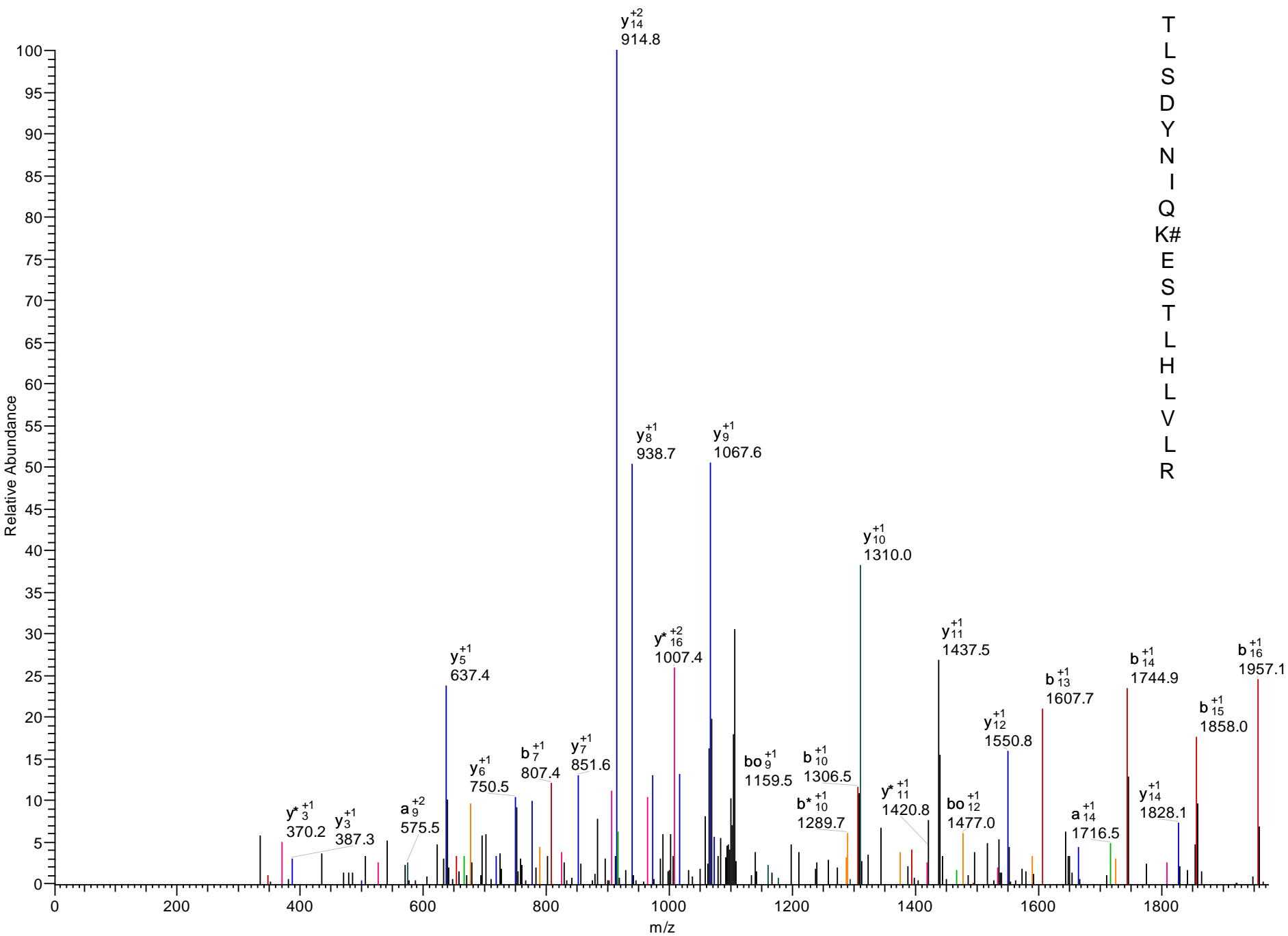
T: FTMS +p NSI Full ms [350.00-1807.24]



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Referer #1 P53 N/V1 MDM2 MDMX				P (pro)	Sf	Score	Coverage	MW	Acsn	Peptide (Hits)	Count	
Scan(s)	Peptide	MH+	DeltaM	z	Type	P (pep)	Sf	XC	DeltaCn	Sp	RSp	Ions
1	gij260080636 gb ACX31156.1 MDM2 [Homo sapiens]		(ppm)			4.11E-14	20.38	242.28	41.80	52436.5	260080636	26 (22 2 0 1 1)
3487	R.AISETTEENSDELSEGER.Q	1765.77226	0.62633	2	CID	4.55E-08	0.87	2.83	0.54	613.8	1	16/30
3303	R.AISETTEEN@SDELSEGER.Q	1766.75627	-3.10912	2	CID	4.51E-08	0.96	4.23	0.65	1086.1	1	18/30
4171	K.AKLENSTQAEEGFDVPDCKK.T	2266.06564	0.32690	3	CID	6.24E-10	0.90	4.48	0.07	1156.7	1	32/76
4208	K.AKLENSTQAEEGFDVPD^CKK.T	2280.08129	0.55485	3	CID	9.26E-04	0.73	3.78	0.26	382.0	1	21/76
4439	K.AKLEN@STQAEEGFDVPDCKK.T	2267.04965	-0.40333	3	CID	6.53E-07	0.89	5.30	0.05	822.6	1	28/76
6890	K.DLVQELQEEKPSSSHLVS.R	2181.11460	-0.58959	3	CID	7.66E-09	0.88	3.84	0.06	1423.6	1	33/72
5261	R.ENWLPEDK.G	1030.48400	-0.18363	2	CID	3.37E-01	0.66	2.23	0.49	217.8	1	8/14
3845	R.ENWLPEDK.GK.D	1215.60043	-0.13234	2	CID	2.17E-04	0.72	2.04	0.49	154.4	1	12/18
8053	L.FYLGQYIM*TK.R	1279.63912	-1.36412	2	CID	1.05E-05	0.96	3.42	0.73	1021.1	1	14/18
4052	K.IYTM*IYR.N	975.49682	-0.00251	2	CID	2.67E-04	0.85	2.27	0.51	238.1	1	10/12
5695	K.IYTM.IYR.N	959.50190	-0.02244	2	CID	2.89E-03	0.78	2.17	0.49	147.0	1	9/12
3393	R.KIYTM*IYR.N	1103.59178	1.12635	3	CID	9.80E-04	0.89	2.65	0.60	667.3	1	17/28
4789	R.KIYTM.IYR.N	1087.59686	-0.01272	2	CID	2.15E-01	0.69	2.06	0.55	279.7	1	8/14
5339	K.LENSTQAEEGFDVPDCK.K	1938.83860	1.42218	2	CID	5.67E-05	0.60	2.87	0.18	436.2	1	14/32
4446	K.LENSTQAEEGFDVPDCKK.T	2066.93356	1.21966	2	CID	1.01E-04	0.37	2.75	0.12	293.9	1	12/34
8998	D.PEISLADYWK.C	1221.61502	-1.58062	2	CID	3.79E-04	0.87	2.77	0.59	547.5	1	11/18
3749	R.SSSSESTGTPSNPDL DAGVSEHSGD.W	2419.99679	0.33717	2	CID	3.54E-07	0.80	3.54	0.25	517.9	1	20/48
3321	K.TGHLM*ACFTCAK.K	1412.61201	0.15541	2	CID	1.77E-07	0.94	2.61	0.68	909.1	1	16/22
2	His-RFP-p53					6.17E-12	21.73	260.24	42.10	70829.9		26 (26 0 0 0 0)
5150	R.CSDSDGLAPPQH.LIR.V	1665.80137	0.92336	2	CID	1.74E-03	0.68	2.56	0.58	230.9	1	11/28
1058	K.DGGHYDAEVK.T	1090.47998	0.26912	2	CID	2.89E-03	0.65	2.28	0.35	322.0	1	11/18
4646	R.ELNEALELKDAQAGKEPGGSR.A	2212.12042	0.73612	3	CID	2.33E-08	0.84	3.84	0.14	1101.3	1	26/80
3320	R.GTNFSPDGPVM*QK.K	1393.64164	-0.08208	2	CID	8.33E-07	0.95	3.84	0.59	804.2	1	17/24
5309	K.HPADIPDY.LK.L	1168.59970	-0.03675	2	CID	5.51E-07	0.93	2.40	0.81	344.9	1	15/18
7804	R.HSTGAENLYFQGLEEE.PQ.S	2048.91959	1.01930	2	CID	3.72E-08	0.93	3.71	0.52	781.4	1	18/34
7703	R.HSTGAENLYFQGLEEE.PQSDPS.V	2435.06335	0.57132	2	CID	1.67E-07	0.73	3.20	0.35	377.5	1	15/42
3233	K.KPVQLPGAYK.T	1100.64626	-0.96941	2	CID	1.54E-02	0.90	2.64	0.59	447.8	1	14/18
7501	K.LDITSHNEDY.TIVEQYER.A	2225.03568	1.21136	2	CID	6.17E-12	0.93	4.75	0.07	1095.6	1	19/34
3761	R.LGFLHSGTAK.S	1030.56801	-0.20305	2	CID	2.84E-05	0.92	2.78	0.61	539.4	1	14/18
1279	K.LKDGGHYDAEVK.T	1331.65901	-0.20027	2	CID	4.52E-08	0.96	3.41	0.52	1583.1	1	18/22
3498	K.LRGTNFSPDGPVM*QK.K	1662.82682	-0.07346	3	CID	2.48E-02	0.77	3.13	0.37	578.3	1	21/56
8445	K.LSFPEGFKWER.V	1395.70556	0.47460	2	CID	1.26E-06	0.42	2.12	0.28	216.9	1	10/20
5166	R.M*EGSVNGHEFEIEGEGEGR.PYEGTQTA	3054.33815	-0.91699	4	CID	2.54E-04	0.90	4.42	0.64	402.2	1	29/162
5652	R.MEGSVNGHEFEIEGEGEGR.PYEGTQTA	3038.34323	0.85976	4	CID	3.13E-03	0.80	3.47	0.44	483.6	1	31/162

5421	R.M*EGSVN@GHEFEIEGEGEGRPYEGTQ`	3055.32216	1.67791	4	CID	1.03E-08	0.86	3.52	0.57	545.2	1	34/162	1
6349	H.PADIPDYLK.L	1031.54079	0.38509	2	CID	8.95E-03	0.69	2.20	0.40	356.5	1	10/16	1
708	R.RTEENLR.K	1046.52251	0.11309	2	CID	6.13E-06	0.88	2.70	0.49	385.2	1	11/14	
6147	D.SSLQDGEFIYK.V	1286.62631	0.25333	2	CID	8.92E-05	0.87	2.36	0.64	630.0	1	12/20	1
3583	K.SVTCTYSPALNK.M	1340.65151	0.65458	2	CID	9.16E-06	0.95	3.25	0.65	915.2	1	16/22	
8194	K.TCPVQLWVDSTPPPGTR.V	1910.94294	1.00845	2	CID	1.47E-06	0.85	3.27	0.59	322.2	1	14/32	
2574	K.TM*GWEASTER.M	1183.50481	0.09863	2	CID	1.94E-03	0.93	2.59	0.67	836.4	1	13/18	2
4037	K.TYQGSYGFR.L	1078.49523	0.38775	2	CID	5.46E-05	0.77	2.43	0.61	249.1	1	9/16	
3141	R.VEYLDDR.N	909.43124	0.09278	2	CID	2.30E-04	0.92	2.30	0.63	508.5	1	11/12	
4866	R.VEYLDDRNTFR.H	1427.69137	0.31632	2	CID	2.90E-07	0.84	2.48	0.60	342.8	1	12/20	
3	gj 51703339 sp P62988.1 UBIQ_HUMAN Ubiquitin					1.05E-09	5.32	60.22	68.40	8559.6	51703339	6 (6 0 0 0 0)	
5849	K.ESTLHLVLR.L	1067.62077	-0.22360	2	CID	2.41E-07	0.89	2.41	0.76	191.9	1	12/16	
1628	K.IQDKEGIPDQQR.L	1523.78125	0.59458	2	CID	1.05E-09	0.95	3.58	0.66	667.5	1	18/24	
7633	K.TITLEVEPSDTIENVK.A	1787.92730	0.40550	2	CID	5.33E-06	0.92	3.07	0.55	709.3	1	19/30	
3564	R.TLSDYNIQK.E	1081.55242	-0.33824	2	CID	8.79E-03	0.88	2.08	0.60	444.5	1	13/16	
7800	R.TLSDYNIQK#ESTLHLVLR.L	2244.19724	1.77146	2	CID	4.91E-08	0.78	3.56	0.04	728.7	1	17/34	
7517	K.TLTGK#TITLEVEPSDTIENVK.A	2402.26505	0.20329	3	CID	4.05E-03	0.89	4.47	0.03	1250.9	1	31/80	

Modifications:

M\* Oxidized Met

K# glygly Lys