Supplemental Tables

Supplemental Table 1. Primers used for RT- or QRT-PCR and other analyses

Genes	Sequences	Annealing Temp. (°C)	Length of amplified fragments (bp)
	I[a]		
Gh *UER1*	5'-CACTTGAGTCCGACATAGCCAAC	58.4	247
	5'-TCCTTAAACCCGATACCCGTTC		
Gh *UGP1*	5'-GTCGGTTCAAGACAATCCCAAG	59.2	300
	5'-TCCGCAAGACCACAAAGCAG		
Gh *UGP2*	5'-CAATTTGTGGGTCAACCTGAATGC	62.6	572
	5'-CAACACACCAAAATCGGGGAAAC		
Gh *UGD1*	5'-GACCCGCAGGTGACCGAAGA	63.2	400
	5'-TGAATCAAACTGACCCGGACTCC		
Gh *RHM1*	5’-ATGGCTAAAAGGAACTTGAACG	56.6	479
	5’-CAGACTAGGATACTGCTTGGTGC		
Gh *RHM2*	5’-ATCTCACAAAACAGAAACAATTCGTG	57.1	209
	5’-GAAATCTTGGTGATGAAGTTGCGT		
Gh *RHM3*	5’-GGAAGAACAAGCCAAGGTGATC	58.4	286
	5’-TGAAACTAAACAGATGCGGAGG		
Gh *RHM4*	5’-GTGTTGTGAGCCACAATGAGATACTG	59.5	315
	5’-AACAAACAACACCACCTGGATGAG		
Gh *GAE1*	5'-ACGCCAGGGAAGTTCAAGGTCG	65.0	386
	5'-GCCGTGGCTGTTAAGCAGGGAT		
Gh *GAE2*	5'-TAGCCAAAGCAGCCAATCCTC	57.8	443
	5'-GAAGAAATAAGCCATGTCGGGTC		
Gh *GAE3*	5'-TGAAAGGTTGTTTAGGAGCGTTAGAC	58.6	279
	5'-ACCCAGAAGATAAATCCGTGGTG		
Gh *GAE4*	5'-TAGCTGCATTGGATACTGCTGAG	58.2	185
	5'-CCCGTTCCGTGGTAACTTCATA		
Gh *GAE5*	5'-GGGATATTATGAAGTTGCCACGAA	57.3	159
	5'-TCTTCCCACCATTATAGTAACCAAGA		
Gh *UBQ7*	5'-GAAGGCATTCCACCTGACCAAC	57.2	198
	5'-CTTGACCTTCTTCTTCTTGTGCTTG		
At *UER1*	5'-CTCGGTATGAGAAAGTTGTGGACA	58.0	334
	5'-TTCTTGTTGGGCTCAAACACGAAC		
At *GAE6*	5’-CAATCCTCAACAGCCAAACGAC	60.0	480
	5’-ACTCGCTGGTTGGTCTGTTCG		
At *UBQ5*	5'-GGTGCTAAGAAGAGGAAGAAT	58.1	237
	5'-CTCCTTCTTTCTGGTAAACGT		
	II		
Gh *UER1*	5'-GGATCCATGGGGTTTCCGGCAAATG	63.1	913

	5'-TCGACCTGATCAAGCTCCACCAGTCTTC		
Gh *UGP1*	5'-GATCCATGGAGAAACTCGATCATATCAAATCTC	62.3	1413
	5'-CTCGAGGCTGGATAAGTCTCCGGGGCCATT		
Gh *UGP2*	5'-GGATCCATGGAAAAGCTGGAACACCTCAA	63.1	1407
	5'-CTCGAGGATGTCTTCGGGGACATTAATTTC		
Gh *UGD1*	5'-GCTAGCATGAAGATCTGTTGCATTGGAGC	61.3	1452
	5'-GAGCTCTTATGCTACTGCAGGCATGTCC		
Gh *GAE3*	5’- GGATCCATGCCAACAGATACAAGCAAA	56.1	1391
	5’- GAATTCCATGGAAATGAAAATATGAAAGC		
	III		
At *UER1g*	5'-GCCTGCAGCATACTAATTACACTGCTAAGACA	61.7	5028
	5'- GCGAATTCAGCTTAATTAAACACATGAAAGA		
Gh *UER1c*	5'- GCAAGCTTCATACTAATTACACTGCTAAGACA	61.8	2935
	5'- GCGTCGACTCAAGCTCCACCAGTCTTCT		
At *GAE6g*	5’-GCCGAATTCTGTTTAACTTATTCGCATTTTTGTCG	58.0	4717
	5’-GCCCTGCAGTTACATGATTCGGTATGAGATAGTTTG		
Gh *GAE3c*	5’-GCGGTACCATGCCAACAGATACAAGCAAA	56.1	1391
	5’-GCTCTAGACATGGAAATGAAAATATGAAAGC		
	IV		
FP	5'-TTGTGTGAATTGTTGAGGTTTTG	59.1	
RP	5'-TGGAAACTCTGGCAATGTTTC	58.5	
LBb1	5'-GCGTGGACCGCTTGCTGCAACT	58.0	
	V		
FP’	5’-CATAGGCCTAATTTGGGGATC	59.7	
RP’	5’-TTGGTCTGTTCGGTGTTCTTC	60.1	
LBb1.3	5’-ATTTTGCCGATTTCGGAAC	56.0	
[b]*NPT-II*	5'-GTTGTCACTGAAGCGGGAAGGGA	65.0	533
	5'-AGAAGGCGATAGAAGGCGATGCG		

[a] I, primers for QRT-PCR. Primers named At *UER1* and At *GAE6* were also used for RT-PCR analysis. II, primers used for protein expression. III, primers for plant genetic transformation. IV, primers for identification of SALK_100812. V, primers for identification of SALK_104454C.

[b] *NPT-II* primers were used in Southern blotting experiments for probe synthesis.

Supplemental Table 2. Detailed information regarding all identified peptides

Spot no.	Protein name	Accession no.	Start	End	Observed	MW(Exp.)[a]	MW(Theo.)[b]	ppm	Miss	Sequence	Modification
1	profilin	ABO43717	48	73	2762.54	2761.54	2761.375	59	1	EITDIMKDFDEPGHLAPTGLHLGGAK	
			48	73	2778.55	2777.54	2777.369	61	1	EITDIMKDFDEPGHLAPTGLHLGGAK	Oxidation (M)
			55	73	1932.09	1931.08	1930.954	68	0	DFDEPGHLAPTGLHLGGAK	
			74	86	1416.87	1415.86	1415.76	73	0	FMVIQGEPGAVIR	
			74	86	1432.9	1431.89	1431.754	93	0	FMVIQGEPGAVIR	Oxidation (M)
			98	123	2936.66	2935.65	2935.457	67	1	KTAQALVFGIYEEPVTPGQCNMVVER	
			98	123	2952.68	2951.67	2951.452	75	1	KTAQALVFGIYEEPVTPGQCNMVVER	Oxidation (M)
			99	123	2808.55	2807.55	2807.362	65	0	TAQALVFGIYEEPVTPGQCNMVVER	
			99	123	2824.58	2823.57	2823.357	75	0	TAQALVFGIYEEPVTPGQCNMVVER	Oxidation (M)
			124	133	1078.6	1077.59	1077.534	54	0	LGDYLAEQGL	
2	major latex-like protein	FJ415202	26	40	1722.91	1721.91	1721.83	46	0	DSTTIFPQALSHDYK	
			41	56	1612.96	1611.95	1611.86	55	1	SIQVLEGDGKAPGSVR	
			57	68	1303.81	1302.8	1302.72	61	0	LINYAEGSPIVK	

			83	95	1526.92	1525.91	1525.84	45	1	KYVYSIIDGDLLK	
			84	95	1398.83	1397.82	1397.74	57	0	YVYSIIDGDLLK	
			117	123	985.49	984.48	984.4	81	0	WSCEFEK	
			124	135	1284.75	1283.74	1283.66	62	0	ASEEIPDPSVIK	
			124	140	1859.05	1858.04	1857.97	37	1	ASEEIPDPSVIKEFAVK	
			141	152	1478.8	1477.79	1477.72	47	1	NFKEIDDYLHGK	
			144	153	1160.65	1159.64	1159.55	77	1	EIDDYLHGKA	
3	annexin 1	AAR13288	6	22	1844.05	1843.04	1842.959	47	1	VPAHVPAPSEDAEQLRK	
			22	41	2311.29	2310.28	2310.212	30	1	KAFEGWGTNEQLIIDILAHR	
			23	41	2183.2	2182.19	2182.117	33	0	AFEGWGTNEQLIIDILAHR	
			23	46	2723.5	2722.49	2722.394	36	1	AFEGWGTNEQLIIDILAHRNAAQR	
			52	63	1457.81	1456.81	1456.72	60	1	TYREAYGEDLLK	
			55	75	2445.22	2444.21	2444.123	35	1	EAYGEDLLKSLDEELSSDFER	
			76	87	1330.81	1329.81	1329.729	58	0	AVVLFTLDPAER	
			76	97	2414.35	2413.34	2413.264	32	1	AVVLFTLDPAERDAFLAHEATK	
			88	98	1258.72	1257.71	1257.647	53	1	DAFLAHEATKR	
			98	113	1994.06	1993.05	1992.966	41	1	RFTSSHWVLMEIACTR	
			98	113	2010.01	2009	2008.961	21	1	RFTSSHWVLMEIACTR	Oxidation (M)
			99	113	1837.96	1836.95	1836.865	47	0	FTSSHWVLMEIAC	

										TR	
			99	113	1853.95	1852.94	1852.86	44	0	FTSSHWVLMEIACTR	Oxidation (M)
			114	123	1216.71	1215.7	1215.636	52	1	SSHELFNVRK	
			124	131	1037.56	1036.55	1036.534	19	1	AYHDLYKK	
			132	142	1265.68	1264.67	1264.605	51	0	SLEEDVAHHTK	
			132	146	1756.91	1755.9	1755.818	49	1	SLEEDVAHHTKGDYR	
			158	169	1426.71	1425.71	1425.656	36	0	YQGEEVNMTLAR	Oxidation (M)
			252	266	1715.95	1714.95	1714.9	27	1	QAINKLGTDEWALTR	
			306	316	1088.59	1087.58	1087.595	-9	0	MLLALIGAGDV	Oxidation (M)
6	annexin	AAB67993	21	40	2184.26	2183.25	2183.149	46	1	KAFSGWGTNEGLIIDILGHR	
			22	40	2056.18	2055.17	2055.054	57	0	AFSGWGTNEGLIIDILGHR	
			22	45	2654.49	2653.48	2653.336	53	1	AFSGWGTNEGLIIDILGHRNAEQR	
			50	62	1530.91	1529.9	1529.761	92	1	KTYAETYGEDLLK	
			51	62	1402.8	1401.79	1401.666	91	0	TYAETYGEDLLK	
			63	74	1436.83	1435.82	1435.694	88	1	ALDKELSNDFER	
			75	86	1395.92	1394.91	1394.792	85	0	LVLLWALDPAER	
			75	96	2422.45	2421.44	2421.327	48	1	LVLLWALDPAERDALLANEATK	
			98	112	1795.98	1794.97	1794.839	75	0	WTSSNQVLMEIACTR	
			98	112	1811.98	1810.97	1810.834	77	0	WTSSNQVLMEIACTR	Oxidation (M)

			113	121	1009.62	1008.61	1008.546	61	0	SANQLLHAR
			130	146	1951.05	1950.04	1949.923	61	1	KSLEEDVAHHTTGDFHK
			131	146	1822.97	1821.96	1821.828	74	0	SLEEDVAHHTTGDFHK
18	annexin	FJ415173	25	40	1738.98	1737.97	1737.92	34	1	GWGTDEKAIISVLGHR
			32	40	965.6	964.59	964.58	10	0	AIISVLGHR
			50	62	1612.89	1611.89	1611.8	49	0	LAYEDLYQEDLIK
			50	63	1768.99	1767.98	1767.9	45	1	LAYEDLYQEDLIKR
			63	74	1409.76	1408.75	1408.68	49	1	RLESELSGDFEK
			79	96	1980.15	1979.14	1979.08	30	1	WILDPADRDAVLANVAIK
			87	96	1013.59	1012.58	1012.59	-9	0	DAVLANVAIK
			97	112	1891.06	1890.05	1889.98	37	1	KLSPDHHVIVEISCTR
			98	112	1762.97	1761.96	1761.88	45	0	LSPDHHVIVEISCTR
			98	121	2757.51	2756.5	2756.43	25	1	LSPDHHVIVEISCTRSPEELLAVR
			113	122	1169.71	1168.71	1168.66	42	1	SPEELLAVRR
			128	141	1627.9	1626.89	1626.8	55	1	YKHSLEEDVAAHTK
			147	156	1088.71	1087.7	1087.68	27	0	LLVALVSAFR
			180	190	1429.77	1428.76	1428.7	48	1	DKEFNHEEIIR
5	fiber annexin	AAC33305	22	41	2184.21	2183.2	2183.149	23	1	KAFSGWGTNEGLIIDILGHR

			23	41	2056.11	2055.11	2055.054	25	0	AFSGWGTNEGLIIDILGHR	
			51	63	1530.83	1529.83	1529.761	42	1	KTYAETYGEDLLK	
			52	63	1402.75	1401.74	1401.666	55	0	TYAETYGEDLLK	
			64	75	1436.75	1435.75	1435.694	37	1	ALDKELSNDFER	
			76	87	1395.87	1394.86	1394.792	47	0	LVLLWALDPAER	
			76	97	2422.38	2421.37	2421.327	18	1	LVLLWALDPAERDALLANEATK	
			98	113	1952.01	1951	1950.94	31	1	RWTSSNQVLMEIACTR	
			98	113	1967.98	1966.98	1966.935	21	1	RWTSSNQVLMEIACTR	Oxidation (M)
			99	113	1795.92	1794.91	1794.839	40	0	WTSSNQVLMEIACTR	
			99	113	1811.92	1810.91	1810.834	43	0	WTSSNQVLMEIACTR	Oxidation (M)
			114	122	1009.56	1008.55	1008.546	1	0	SANQLLHAR	
			132	146	1713.85	1712.85	1712.775	41	0	SLEEDVAHHTTGDFR	
			132	147	1841.96	1840.95	1840.87	46	1	SLEEDVAHHTTGDFRK	
			294	305	1375.81	1374.8	1374.678	87	1	AIVKDTHGDYEK	
4	copper/zinc superoxide dismutase	FJ415203	4	38	3425.82	3424.81	3424.7	32	0	AVAVLSSNEGVSGTVFFSQEGDGPTTVTGNLSGLK	
			39	68	3100.52	3099.51	3099.46	16	0	AGLHGFHVHALGDITNGCMSTGPHFNPAGK	

			39	68	3116.53	3115.52	3115.45	22	0	AGLHGFHVHALGDITNGCMSTGPHFNPAGK	Oxidation (M)
			69	78	1153.52	1152.51	1152.48	26	0	EHGAPEDENR	
			69	101	3470.63	3469.63	3469.51	34	1	EHGAPEDENRHAGDLGNVTVGDDGCASFSITDK	
			79	101	2336.07	2335.07	2335.04	12	0	HAGDLGNVTVGDDGCASFSITDK	
			102	114	1365.81	1364.8	1364.78	21	0	QIPLTGPNSIIGR	
			115	127	1335.72	1334.71	1334.68	14	0	AVVVHADPDDLGK	
			115	134	2044.05	2043.05	2043.04	4	1	AVVVHADPDDLGKGGHELSK	
			143	152	987.56	986.55	986.52	30	0	VACGIIGLQG	
7	copper/zinc superoxide dismutase	FJ415203	4	38	3425.75	3424.74	3424.7	11	0	AVAVLSSNEGVSGTVFFSQEGDGPTTVTGNLSGLK	
			39	68	3100.46	3099.46	3099.46	0	0	AGLHGFHVHALGDITNGCMSTGPHFNPAGK	
			39	68	3116.47	3115.46	3115.45	3	0	AGLHGFHVHALGDITNGCMSTGPHFNPAGK	Oxidation (M)
			69	78	1153.5	1152.49	1152.48	8	0	EHGAPEDENR	
			69	101	3470.57	3469.56	3469.51	14	1	EHGAPEDENRHAGDLGNVTVGDDGCASFSITDK	

			79	101	2336.05	2335.04	2335.04	0	0	HAGDLGNVTVGDDGCASFSITDK
			102	114	1365.8	1364.79	1364.78	7	0	QIPLTGPNSIIGR
			115	127	1335.7	1334.69	1334.68	7	0	AVVVHADPDDLGK
			115	134	2044.04	2043.03	2043.04	-4	1	AVVVHADPDDLGKGGHELSK
			143	152	987.55	986.54	986.52	20	0	VACGIIGLQG
8	peroxiredoxin	FJ415174	2	36	3598.12	3597.11	3596.84	75	1	APIAVGDVLPDGTLSYFDADDKLQQVSVHSLAAGK
			37	54	1935.13	1934.12	1934.07	25	1	KVIIFGVPGAFTPTCSLK
			38	54	1807.05	1806.04	1805.97	33	0	VIIFGVPGAFTPTCSLK
			55	62	926.51	925.5	925.5	0	0	HVPGFIEK
			100	121	2306.21	2305.21	2305.16	21	0	FLADGSATYTHALGLELNLGDK
			100	126	2790.52	2789.51	2789.43	28	1	FLADGSATYTHALGLELNLGDKGLGTR
			129	138	1189.75	1188.75	1188.69	50	1	RFALLVDDLK
			130	138	1033.61	1032.6	1032.59	19	0	FALLVDDLK
			130	140	1260.81	1259.8	1259.75	39	1	FALLVDDLKVK
			141	160	2010.04	2009.03	2008.96	34	0	AANVESGGEFTVSSADDILK
9	dimethylmenaquinone	FJ415179	24	34	1305.8	1304.79	1304.72	53	0	ALQPIFQIYGR

	methyltransferase									
			35	46	1313.88	1312.88	1312.79	68	0	RPVFSGPIVTLK
			47	55	1104.65	1103.65	1103.6	45	0	VFEDNVLIR
			66	76	1071.65	1070.64	1070.61	28	0	VLVVDGGGSLR
			104	116	1461.76	1460.75	1460.66	61	0	DVDEINGCDIGVR
			134	143	1064.66	1063.65	1063.61	37	0	HVPITIAGTR
			144	161	2055.04	2054.03	2053.97	34	0	ICDGEWLYADTDGILVSK
10	benzoquinone reductase	ABN12321	5	18	1750.84	1749.83	1749.844	-6	0	VYIVYYSMYGHVEK
			58	81	2564.27	2563.26	2563.26	2	0	SDVPVITPNDLAEADGFVFGFPTR
			91	101	1206.63	1205.63	1205.619	6	0	AFLDATGGLWR
			160	175	1472.65	1471.65	1471.633	10	0	GGSPYGAGTYAGDGSR
			176	190	1685.81	1684.81	1684.824	-11	0	MPSELELAQAFHQGK
13	benzoquinone reductase	ABN12321	37	51	1717.94	1716.93	1716.893	22	0	LWQVSETLSEEVLGK
			58	81	2564.34	2563.33	2563.26	28	0	SDVPVITPNDLAEADGFVFGFPTR
			91	101	1206.67	1205.66	1205.619	34	0	AFLDATGGLWR
			160	175	1472.7	1471.69	1471.633	42	0	GGSPYGAGTYAGDGSR
			176	190	1685.88	1684.88	1684.824	31	0	MPSELELAQAFHQGK
14	benzoquinone reductase	ABN12320	5	18	1750.79	1749.78	1749.844	-37	0	VYIVYYSMYGHVEK

			37	51	1727.86	1726.85	1726.914	-35	0	LWQVPETLSDEILGK	
			82	90	1046.51	1045.5	1045.473	26	0	FGMMSAQFK	
			91	101	1224.54	1223.53	1223.576	-35	0	AFMDATGGLWR	
			176	190	1719.75	1718.75	1718.809	-36	0	MPSELEFAQAFHQGK	
88	benzoquinone reductase	FJ415183	5	18	1764.87	1763.86	1763.86	0	0	LYIVYYSMYGHVEK	
			5	18	1780.87	1779.87	1779.85	0	0	LYIVYYSMYGHVEK	Oxidation (M)
			37	51	1727.94	1726.93	1726.91	5	0	LWQVPETLSDEILGK	
			58	81	2615.35	2614.34	2614.31	-86	0	SDVPIITPHDLAEADGFIFGFPTR	
			82	90	1046.49	1045.48	1045.47	11	0	FGMMSAQFK	
			82	90	1062.48	1061.47	1061.47	9	0	FGMMSAQFK	Oxidation (M)
			82	90	1078.47	1077.47	1077.46	0	0	FGMMSAQFK	2 Oxidation (M)
			82	101	2300.16	2299.15	2299.02	0	1	FGMMSAQFKAFMDATGGLWR	3 Oxidation (M)
			91	101	1224.6	1223.59	1223.58	56	0	AFMDATGGLWR	
			91	101	1240.59	1239.58	1239.57	8	0	AFMDATGGLWR	Oxidation (M)
			160	175	1486.67	1485.66	1485.65	8	0	GGSPYGAGTYAGDGTR	
			182	190	999.54	998.53	998.53	6	0	LAQAFHQGK	
11	ascorbate peroxidase	ABR18607	39	50	1331.76	1330.75	1330.667	0	0	LAWHSAGTFDVK	
			39	52	1560.92	1559.91	1559.81	63	1	LAWHSAGTFDVKTK	

			62	79	1869.03	1868.02	1867.965	28	0	HPAELAHAANNGLDIAVR	
			120	130	1258.68	1257.67	1257.61	50	0	EDKPHPPPEGR	
			131	142	1309.76	1308.75	1308.679	54	1	LPDATKGSDHLR	
			143	167	2625.33	2624.32	2624.313	4	0	QVFSAQMGLSDQHIVALSGGHTLGR	Oxidation (M)
			173	192	2320.16	2319.16	2319.085	31	0	SGFEGPWTTNPLIFDNSYFK	
			210	223	1612.02	1611.01	1610.94	47	0	VLLSDPVFRPLVEK	
			224	241	2076.98	2075.97	2075.911	30	0	YAADEDAFFADYTEAHLK	
12	ascorbate peroxidase	ABR18607	53	61	895.471	894.464	894.427	42	0	TGGPFGTMK	
			62	79	1869.02	1868.01	1867.965	25	0	HPAELAHAANNGLDIAVR	
			120	130	1258.67	1257.66	1257.61	38	0	EDKPHPPPEGR	
			143	167	2609.42	2608.41	2608.318	37	0	QVFSAQMGLSDQHIVALSGGHTLGR	
			173	192	2320.17	2319.16	2319.085	33	0	SGFEGPWTTNPLIFDNSYFK	
			200	209	1113.65	1112.64	1112.608	28	0	EGLLQLPTDK	
			224	241	2076.98	2075.97	2075.911	28	0	YAADEDAFFADYTEAHLK	
15	ascorbate peroxidase	ABR18607	53	61	895.481	894.474	894.427	53	0	TGGPFGTMK	
			86	119	3733.04	3732.03	3731.862	46	0	EQFPNLTYADFYQLAGVVAVEITGGP	

										EIPFHPGR	
			120	130	1258.68	1257.68	1257.61	53	0	EDKPHPPPEGR	
			143	167	2609.43	2608.42	2608.318	39	0	QVFSAQMGLSDQHIVALSGGHTLGR	
			173	192	2320.18	2319.17	2319.085	37	0	SGFEGPWTTNPLIFDNSYFK	
			224	241	2076.99	2075.98	2075.911	34	0	YAADEDAFFADYTEAHLK	
16	ascorbate peroxidase	ABR18607	39	50	1331.66	1330.65	1330.67	-7	0	LAWHSAGTFDVK	
			53	79	2761.33	2760.32	2760.38	-18	1	TGGPFGTMKHPAELAHAANNGLDIAVR	Oxidation (M)
			62	79	1868.95	1867.94	1867.97	-10	0	HPAELAHAANNGLDIAVR	
			120	130	1258.62	1257.61	1257.61	0	0	EDKPHPPPEGR	
			173	192	2320.06	2319.06	2319.08	-12	0	SGFEGPWTTNPLIFDNSYFK	
			193	209	1869.97	1868.97	1869.01	-21	1	ELLSGEKEGLLQLPTDK	
			200	209	1113.62	1112.62	1112.61	8	0	EGLLQLPTDK	
			210	223	1611.95	1610.94	1610.94	0	0	VLLSDPVFRPLVEK	
			224	241	2076.9	2075.89	2075.91	-9	0	YAADEDAFFADYTEAHLK	
19	ascorbate peroxidase	ABR18607	39	50	1331.71	1330.7	1330.667	27	0	LAWHSAGTFDVK	
			53	79	2761.41	2760.4	2760.377	9	1	TGGPFGTMKHPA	Oxidation (M)

										ELAHAANNGLDIAVR	
			62	79	1869.02	1868.01	1867.965	25	0	HPAELAHAANNGLDIAVR	
			120	130	1258.66	1257.65	1257.61	34	0	EDKPHPPPEGR	
			131	142	1309.73	1308.72	1308.679	34	1	LPDATKGSDHLR	
			173	192	2320.1	2319.09	2319.085	3	0	SGFEGPWTTNPLIFDNSYFK	
			200	223	2706.63	2705.62	2705.537	32	1	EGLLQLPTDKVLLSDPVFRPLVEK	
			210	223	1612	1610.99	1610.94	33	0	VLLSDPVFRPLVEK	
			224	241	2076.96	2075.95	2075.911	20	0	YAADEDAFFADYTEAHLK	
20	ascorbate peroxidase	ABR18607	25	38	1585.89	1584.88	1584.848	22	1	GLIAEKNCAPLMLR	
			39	50	1331.71	1330.7	1330.667	27	0	LAWHSAGTFDVK	
			53	79	2745.42	2744.41	2744.382	11	1	TGGPFGTMKHPAELAHAANNGLDIAVR	
			53	79	2761.41	2760.4	2760.377	9	1	TGGPFGTMKHPAELAHAANNGLDIAVR	Oxidation (M)
			62	79	1869.02	1868.01	1867.965	25	0	HPAELAHAANNGLDIAVR	
			120	130	1258.64	1257.63	1257.61	18	0	EDKPHPPPEGR	
			131	142	1309.73	1308.72	1308.679	34	1	LPDATKGSDHLR	
			137	167	3274.73	3273.72	3273.643	24	1	GSDHLRQVFSAQ	

										MGLSDQHIVALSGGHTLGR	
			137	167	3290.72	3289.71	3289.638	23	1	GSDHLRQVFSAQMGLSDQHIVALSGGHTLGR	Oxidation (M)
			143	167	2609.31	2608.3	2608.318	-6	0	QVFSAQMGLSDQHIVALSGGHTLGR	
			143	167	2625.33	2624.32	2624.313	4	0	QVFSAQMGLSDQHIVALSGGHTLGR	Oxidation (M)
			173	192	2320.1	2319.09	2319.085	3	0	SGFEGPWTTNPLIFDNSYFK	
			210	223	1612	1610.99	1610.94	33	0	VLLSDPVFRPLVEK	
			224	241	2076.96	2075.95	2075.911	20	0	YAADEDAFFADYTEAHLK	
			224	250	2980.44	2979.43	2979.345	29	1	YAADEDAFFADYTEAHLKLSELGFADA	
21	ascorbate peroxidase	ABR18607	39	50	1331.73	1330.72	1330.667	43	0	LAWHSAGTFDVK	
			39	52	1560.86	1559.85	1559.81	29	1	LAWHSAGTFDVKTK	
			53	79	2736.42	2735.41	2735.381	10	1	TGGPFGTMKQPAELAHAANNGLDIAVR	
			53	79	2752.43	2751.42	2751.376	17	1	TGGPFGTMKQPAELAHAANNGLDIAVR	Oxidation (M)

			62	79	1860.01	1859	1858.965	20	0	QPAELAHAANNGLDIAVR	
			120	130	1258.67	1257.66	1257.61	41	0	EDKPHPPPEGR	
			131	142	1293.7	1292.7	1292.647	38	0	LPNATEGADHLR	
			143	167	2630.32	2629.31	2629.292	8	0	QVFSNQMGLSDQDIVALSGGHTLGR	
			143	167	2646.34	2645.33	2645.287	17	0	QVFSNQMGLSDQDIVALSGGHTLGR	Oxidation (M)
			173	192	2320.13	2319.12	2319.085	16	0	SGFEGPWTTNPLIFDNSYFK	
			210	241	3655.97	3654.96	3654.825	38	1	VLLSDPVFRPLVDKYAADEDAFFADYTEAHLK	
			224	241	2076.95	2075.95	2075.911	17	0	YAADEDAFFADYTEAHLK	
			242	250	922.438	921.431	921.4444	-14	0	LSELGFADA	
17	ascorbate peroxidase	FJ415185	86	119	3683.56	3682.55	3682.9	-95	0	EQLPILSYADFYQLAGVVAVEITGGPEIPFHPGR	
			120	130	1258.54	1257.53	1257.61	-63	0	EDKPHPPPEGR	
			131	142	1293.58	1292.57	1292.65	-61	0	LPNATEGADHLR	
			173	192	2319.92	2318.91	2319.08	-73	0	SGFEGPWTTNPLIFDNSYFK	
			224	241	2076.77	2075.77	2075.91	-72	0	YAADEDAFFADYTEAHLK	
38	stromal ascorbate peroxidase	FJ415186	131	138	1613.77	1612.76	1612.74	12	0	FCHPILVR	TMPP[c]
			139	149	1261.54	1260.54	1260.59	-39	0	LGWHDAGTYNK	

			150	156	1515.66	1514.65	1514.64	6	0	NIEEWPR	TMPP
			166	171	1336.63	1335.62	1335.59	22	0	FEVELK	TMPP
			192	216	3131.36	3130.35	3130.43	-25	0	YSGVTYADLFQLASATAIEEAGGPK	TMPP
			238	251	1970.94	1969.93	1969.92	5	0	LPAAGPPSPADHLR	TMPP
			252	256	1285.57	1284.56	1284.53	23	0	EVFYR	TMPP
			293	309	2356.03	2355.02	2355.05	-12	0	DGPGAPGGQSWTVQWLK	TMPP
			323	342	2835.27	2834.26	2834.31	-17	0	DEDLLVLPTDAVLFEDPSFK	TMPP
			343	347	1181.4	1180.39	1180.5	-93	0	VYAEK	TMPP
			348	357	1277.54	1276.53	1276.56	-23	0	YAEDQETFFK	
			348	357	1849.75	1848.74	1848.74	0	0	YAEDQETFFK	TMPP
			366	372	1274.62	1273.61	1273.59	23	0	LSNLGAK	TMPP
40	stromal ascorbate peroxidase	FJ415186	2	15	1448.83	1447.82	1447.84	-13	0	ADPVVASHLSLVLK	
			131	138	1041.6	1040.59	1040.56	28	0	FCHPILVR	
			139	149	1261.64	1260.63	1260.59	31	0	LGWHDAGTYNK	
			150	156	943.49	942.48	942.46	21	0	NIEEWPR	
			224	237	1544.72	1543.71	1543.66	38	0	VDVSGPNECPEEGR	
			238	251	1398.79	1397.78	1397.74	28	0	LPAAGPPSPADHLR	
			323	342	2263.19	2262.18	2262.13	22	0	DEDLLVLPTDAVLFEDPSFK	
			348	357	1277.61	1276.61	1276.56	39	0	YAEDQETFFK	
			358	365	904.44	903.43	903.41	22	0	DYAEAHAK	

22	α-1,4 glucan phosphorylase	FJ415211	153	176	2807.39	2806.38	2806.39	-3	1	LASCFLDSLATLNYPAWGYGLRYR
			216	227	1329.76	1328.75	1328.66	67	1	FYGKVLTDSDGK
			344	362	2225.22	2224.21	2224.08	58	0	VAVQMNDTHPTLCIPELMR
			578	588	1261.59	1260.58	1260.66	-63	1	FQNKTNGVTPR
			713	721	998.53	997.52	997.52	0	0	AFATYVQAK
			713	722	1154.65	1153.64	1153.62	17	1	AFATYVQAKR
			726	745	2140.15	2139.14	2139.08	28	0	FITDVGATVNHDPDIGDLLK
			805	818	1615.82	1614.81	1614.76	37	0	EEVGEENFFLFGAK
			805	826	2463.22	2462.21	2462.22	-4	1	EEVGEENFFLFGAKAHEIAGLR
			819	827	994.59	993.58	993.57	10	1	AHEIAGLRK
			834	845	1462.83	1461.83	1461.75	54	1	FVPDPQFEEVKK
			849	872	2490.23	2489.22	2489.15	28	0	SGVFGSSNYNELLGSLEGNEGFGR
			873	880	912.49	911.48	911.48	0	0	ADYFLVGK
			873	891	2309.13	2308.13	2308.07	21	1	ADYFLVGKDFPSYIECQEK
			881	891	1415.68	1414.68	1414.61	49	0	DFPSYIECQEK
			881	897	2151.16	2150.15	2149.95	93	1	DFPSYIECQEKVDETYK
			905	920	1780.84	1779.83	1779.76	39	0	MSIMNTAGSYNFSSDR
			921	927	889.45	888.44	888.45	0	0	TIHEYAR
			928	938	1337.82	1336.82	1336.74	59	0	EIWNIKPVELP

23	s-formylglutathione hydrolase	FJ415188	73	89	1625.84	1624.84	1624.84	-6	0	AASAEGVALIAPDTSPR
			119	128	1373.58	1372.57	1372.66	-65	1	NWRMYDYVVK
			133	145	1491.72	1490.72	1490.76	-33	0	LLSENFPQLDTSK
			171	189	2028.91	2027.9	2027.99	-44	0	SASAFAPIANPINCPWGQK
			200	212	1569.67	1568.66	1568.72	-31	0	AAWEEYDATCLIK
			214	230	1901.85	1900.85	1900.92	-36	0	FHNVSATILIDQGEDDK
			231	240	1212.63	1211.63	1211.67	-33	0	FLHDQLLAQK
			241	255	1802.86	1801.85	1801.95	-55	1	FEEACRSVNVPLLLR
			247	255	1010.6	1009.59	1009.63	-29	0	SVNVPLLLR
			256	276	2571.09	2570.08	2570.22	-54	0	LQPGYDHSYFFISTFIDDHIR
24	triosephosphate isomerase	FJ415177	4	12	1082.59	1081.58	1081.57	9	1	KFFVGGNWK
			5	12	954.51	953.5	953.48	31	0	FFVGGNWK
			23	53	3278.89	3277.88	3277.82	18	0	IVSTLNAGEVPSQDVVEVVVSPPFVFLPLVK
			54	70	2028.96	2027.95	2028	-24	0	TSLRPDFHVAAQNCWVK
			71	99	3097.67	3096.66	3096.61	19	1	KGGAFTGEVSAEMLVNLSIPWVIIGHSER
			105	123	2053.03	2052.02	2052.05	-14	1	ESNEFVADKVAYALAQGLK

			114	123	1033.63	1032.62	1032.6	29	0	VAYALAQGLK
			124	135	1388.73	1387.72	1387.71	7	0	VIACIGETLEQR
			155	175	2319.17	2318.16	2318.19	-12	0	ISNWTDVVLAYEPVWAIGTGK
			176	190	1708.84	1707.83	1707.84	0	0	VATPAQAQEVHCELR
			176	191	1836.91	1835.9	1835.93	-16	1	VATPAQAQEVHCELRK
			191	206	1756.92	1755.91	1755.93	-5	1	KWLQANVSPEVAASTR
			192	206	1628.82	1627.81	1627.83	-12	0	WLQANVSPEVAASTR
			207	219	1353.69	1352.68	1352.68	7	0	IIYGGSVTAANCK
			220	246	2842.45	2841.44	2841.52	-24	0	ELAAQPDVDGFLVGGASLKPEFIDIIK
25	20S proteasome subunit α-1	FJ415181	4	21	1905.96	1904.95	1904.91	20	1	GSGGGYDRHITIFSPEGR
			12	21	1156.64	1155.63	1155.6	25	0	HITIFSPEGR
			22	30	1144.62	1143.61	1143.6	17	0	LFQVEYAFK
			22	33	1442.86	1441.85	1441.8	41	1	LFQVEYAFKAVK
			75	88	1436.82	1435.81	1435.75	41	0	FLGLLATGMTADAR
			89	102	1632.9	1631.89	1631.84	30	1	TLVQQARNEAAEFR
			96	104	1139.59	1138.58	1138.55	26	1	NEAAEFRFR
			103	116	1703.9	1702.89	1702.84	29	1	FRYGYEMPVDVLSK
			154	164	1288.6	1287.59	1287.55	38	0	CDPAGHFYGHK

			165	181	1822.96	1821.95	1821.91	21	1	ATSAGSKEQEAINFLEK
			229	246	2057.05	2056.04	2056	24	1	VLSTEEIDEHLTAISERD
26	heat shock protein 70	FJ415196	5	28	2588.28	2587.27	2587.21	23	0	GEGPAIGIDLGTTYSCVGVWQHDR
			29	39	1228.68	1227.67	1227.62	40	0	VEIIANDQGNR
			40	52	1473.74	1472.74	1472.68	40	0	TTPSYVGFTDTER
			117	130	1565.88	1564.87	1564.82	31	0	QFAAEEISSMVLIK
			133	144	1340.72	1339.72	1339.7	7	0	EIAEAYLGFTVK
			145	159	1680.89	1679.89	1679.83	35	0	NAVVTVPAYFNDSQR
			164	175	1215.7	1214.69	1214.64	41	0	DAGVIAGLNVMR
			227	242	1675.79	1674.78	1674.72	29	0	ATAGDTHLGGEDFDNR
			243	252	1278.71	1277.71	1277.62	62	0	MVNHFVQEFK
68	heat shock protein 70	FJ415196	243	253	1434.74	1433.73	1433.72	6	1	MVNHFVQEFKR
			258	267	1098.62	1097.61	1097.59	18	1	DISGNPRALR
			278	305	3195.7	3194.69	3194.6	28	1	RTLSSTAQTTIEIDSLYEGIDFYTTITR
			279	305	3039.57	3038.56	3038.5	23	0	TLSSTAQTTIEIDSLYEGIDFYTTITR
			306	317	1540.79	1539.78	1539.75	19	1	ARFEELNMDLFR
			308	317	1313.64	1312.63	1312.61	15	0	FEELNMDLFR
			308	318	1441.74	1440.74	1440.71	20	1	FEELNMDLFRK
			332	348	1786.94	1785.93	1785.9	16	1	MDKSSVHDVVLVGGSTR

			335	348	1412.77	1411.76	1411.74	14	0	SSVHDVVLVGGSTR
			352	363	1436.78	1435.77	1435.75	13	0	VQQLLQDFFNGK
			431	453	2658.27	2657.27	2657.26	0	0	EQVFSTYSDNQPGVLIQVYEGER
			476	499	2575.37	2574.36	2574.26	38	0	GVPQITVCFDIDANGILNVSAEDK
			507	515	1017.58	1016.57	1016.56	9	1	ITITNDKGR
			546	556	1374.63	1373.62	1373.6	14	0	NSLENYAYNMR
			604	615	1386.74	1385.73	1385.72	7	0	ELESICNPIIAK
63	heat shock protein 70	FJ415199	308	317	1313.68	1312.67	1312.61	45	0	FEELNMDLFR
			335	348	1412.8	1411.79	1411.74	35	0	SSVHDVVLVGGSTR
			368	393	2574.33	2573.32	2573.26	23	0	SINPDEAVAYGAAVQAAILSGEGNEK
			394	422	3033.5	3032.5	3032.72	-72	0	VQDLLLLDVTPLSLGLETAGGVMTVLIPR
			431	453	2658.34	2657.33	2657.26	26	0	EQVFSTYSDNQPGVLIQVYEGER
			546	556	1358.66	1357.65	1357.61	29	0	NALENYAYNMR
			576	601	2905.4	2904.39	2904.33	20	0	IEDAIDGAIQWLDGNQLAEADEFEDK
			604	615	1386.79	1385.78	1385.72	43	0	ELESICNPIIAK
			616	643	2612.14	2611.13	2611.06	26	0	MYQGAGADMGGGMDEDAPPTGGSSAGPK

67	heat shock protein 70	FJ415194	306	317	1540.83	1539.82	1539.75	45	1	ARFEELNMDLFR
			308	318	1441.78	1440.77	1440.71	41	1	FEELNMDLFRK
			335	348	1426.83	1425.82	1425.76	49	0	STVHDVVLVGGSTR
			352	367	1967.09	1966.08	1966	40	1	VQQLLQDFFNGKELCK
			368	393	2571.3	2570.29	2570.23	23	0	SINPDEAVACGAAVQAAILSGEGNEK
			394	422	3007.77	3006.76	3006.67	29	0	VQDLLLLDVTPLSSGLETAGGVMTVLIPR
			431	453	2658.33	2657.33	2657.26	22	0	EQVFSTYSDNQPGVLIQVYEGER
			431	455	2915.51	2914.51	2914.41	34	1	EQVFSTYSDNQPGVLIQVYEGERTR
			546	556	1358.68	1357.67	1357.61	44	0	NALENYAYNMR
90	heat shock protein 70	FJ415194	5	28	2588.14	2587.13	2587.21	-30	0	GEGPAIGIDLGTTYSCVGVWQHDR
			29	39	1228.6	1227.59	1227.62	-24	0	VEIIANDQGNR
			40	52	1473.67	1472.66	1472.68	-13	0	TTPSYVGFTDTER
			60	74	1661.82	1660.81	1660.82	-6	0	NQVAMNPINTVFDAK
			97	112	1718.78	1717.78	1717.89	-64	0	VIAGPGDKPMICVAYK
			145	159	1680.81	1679.81	1679.83	-11	0	NAVVTVPAYFNDSQR
			164	175	1215.62	1214.61	1214.64	-24	0	DAGVIAGLNVMR

			227	242	1675.71	1674.7	1674.72	-11	0	ATAGDTHLGGEDFDNR
			243	252	1278.66	1277.66	1277.62	31	0	MVNHFVQEFK
73	heat shock protein 70	FJ415195	306	317	1540.81	1539.8	1539.75	32	1	ARFEELNMDLFR
			335	348	1412.76	1411.76	1411.74	7	0	SSVHDVVLVGGSTR
			352	367	1967.06	1966.05	1966	25	1	VQQLLQDFFNGKELCK
			431	453	2658.3	2657.29	2657.26	11	0	EQVFSTYSDNQPGVLIQVYEGER
			431	455	2915.48	2914.47	2914.41	20	1	EQVFSTYSDNQPGVLIQVYEGERTR
			507	515	1017.56	1016.55	1016.56	-9	1	ITITNDKGR
			546	556	1358.66	1357.65	1357.61	29	0	NALENYAYNMR
			546	560	1800.99	1799.98	1799.86	66	1	NALENYAYNMRNTVK
27	catalase	FJ415187	92	102	1150.7	1149.69	1149.69	0	0	APGVQTPVILR
			118	129	1456.81	1455.8	1455.76	27	2	DPRGFAVKFYTR
			151	163	1493.88	1492.88	1492.79	60	0	FPDMVHALKPNPK
			292	305	1620.99	1619.99	1619.87	74	0	TWPEDILPLQPVGR
			340	353	1712.06	1711.05	1710.91	81	1	LLQTRIFSYADTQR
			356	369	1495.95	1494.94	1494.82	80	0	LGPNYLQLPANAPK
			387	396	1269.65	1268.64	1268.57	55	0	DEEINYFPSR
			387	401	1900.05	1899.05	1898.88	89	1	DEEINYFPSRYDP

										VR	
			397	416	2329.31	2328.31	2328.11	81	1	YDPVRHAEMFPIPPAVCTGR	Oxidation (M)
			402	416	1682.95	1681.94	1681.81	77	0	HAEMFPIPPAVCTGR	
			402	416	1698.95	1697.94	1697.8	82	0	HAEMFPIPPAVCTGR	Oxidation (M)
			420	434	1862.04	1861.03	1860.92	64	2	CIIEKENNFKQPGER	
			435	445	1437.83	1436.82	1436.69	90	2	YRSWAADRQER	
			437	445	1118.62	1117.61	1117.53	80	1	SWAADRQER	
			450	458	1072.65	1071.64	1071.53	93	0	WVEALSDPR	
			450	464	1808.07	1807.06	1806.94	66	1	WVEALSDPRVTHEIR	
28	serine hydroxymethyltransferase	FJ415180	59	67	1010.46	1009.45	1009.43	19	0	YSEGMPGNR	
			68	83	1991.98	1990.98	1990.87	50	0	YYGGNEFIDEIENLCR	
			86	96	1240.75	1239.74	1239.66	64	0	AIQAFHLDPTK	
			97	123	2945.58	2944.57	2944.43	50	0	WGVNVQPYSGSPANFAAYTAVLQPHDR	
			124	145	2261.19	2260.18	2260.09	39	0	IMGLDLPSGGHLTHGYYTSGGK	
			147	160	1618.92	1617.91	1617.83	49	0	ISATSIYFESLPYK	
			177	183	846.48	845.48	845.48	0	0	ALDFRPK	
			184	194	1206.7	1205.69	1205.62	58	0	LIICGGSAYPR	

			195	200	825.34	824.34	824.35	-12	0	DWDYAR	
31	serine hydroxymethyltransferase	FJ415180	59	67	1010.43	1009.42	1009.43	-9	0	YSEGMPGNR	
			68	83	1991.86	1990.86	1990.87	-10	0	YYGGNEFIDEIENLCR	
			86	96	1240.64	1239.63	1239.66	-24	0	AIQAFHLDPTK	
			97	123	2945.42	2944.41	2944.43	-3	0	WGVNVQPYSGSPANFAAYTAVLQPHDR	
			124	145	2261.08	2260.08	2260.09	-8	0	IMGLDLPSGGHLTHGYYTSGGK	
			124	145	2277.07	2276.07	2276.09	-8	0	IMGLDLPSGGHLTHGYYTSGGK	Oxidation (M)
			147	160	1618.84	1617.83	1617.83	0	0	ISATSIYFESLPYK	
			161	176	1874.89	1873.88	1873.89	-5	1	VNSTTGYIDYDKLEEK	
			184	194	1206.63	1205.63	1205.62	0	0	LIICGGSAYPR	
			195	200	825.34	824.33	824.35	-12	0	DWDYAR	
			265	278	1640.81	1639.81	1639.74	42	1	KGQPEDAVYDFEDK	
			333	359	2951.44	2950.43	2950.57	-47	0	GYQLVTGGTENHLVLWDLRPLGLTGNK	
29	lactoylglutathione lyase	FJ415204	40	48	1182.48	1181.48	1181.49	-8	0	FYTECFGMK	
			40	48	1198.48	1197.47	1197.48	-16	0	FYTECFGMK	Oxidation (M)
			126	147	2411.22	2410.22	2410.25	-16	1	GGSSVIAFVKDPD	

										GYIFELIQR	
			136	147	1465.72	1464.72	1464.72	-6	0	DPDGYIFELIQR	
			148	160	1501.74	1500.73	1500.74	-6	0	ASTPEPLCQVMLR	
			148	160	1517.75	1516.74	1516.74	6	0	ASTPEPLCQVMLR	Oxidation (M)
			220	235	1714.82	1713.81	1713.82	-5	0	GNAYAQVAISTDDVYK	
			236	250	1580.82	1579.81	1579.82	-6	0	SGEVVEHVIQELGGK	
			265	275	1278.63	1277.63	1277.63	0	0	ITSFLDPDGWK	
			276	286	1292.68	1291.67	1291.67	7	0	TVLVDNEDFLK	
			276	289	1662.89	1661.88	1661.89	-6	1	TVLVDNEDFLKELK	
30	alpha-soluble NSF attachment protein	FJ415171	29	44	1877.9	1876.89	1876.83	31	1	YEDAADLFDKAANCFK	
			90	107	2094.04	2093.03	2093	14	0	EAISCLQQAVNLFCDIGR	
			138	155	2017.9	2016.89	2016.85	19	0	AADFFQNEDVSSSANQCK	
			156	170	1779.97	1778.96	1778.93	16	1	QKVAQFAAQIEQYQK	
			158	170	1523.83	1522.82	1522.78	26	0	VAQFAAQIEQYQK	
			171	180	1206.66	1205.65	1205.63	16	0	AIEIYEEIAR	
			194	206	1483.78	1482.77	1482.74	20	0	GHLLNAGICQLCK	
			207	218	1257.7	1256.69	1256.67	15	0	GDVVAITNALER	
			219	230	1399.68	1398.67	1398.64	21	0	YQDLDPTFSGTR	
32	UER1	FJ415167	21	30	1001.54	1000.53	1000.57	-39	0	TGWIGGLLGK	
			31	45	1733.75	1732.74	1732.74	5	0	LCESQGIDYEYGSGR	

			50	83	3748.79	3747.78	3747.84	-16	0	ISLESDIANVKPTHVFNAAGVTGRPNVDWCESHK
			89	102	1518.81	1517.8	1517.79	6	0	TNVVGTLTLADVCR
			89	104	1761.92	1760.91	1760.91	5	1	TNVVGTLTLADVCRDK
			133	146	1633.8	1632.79	1632.73	36	0	EEDTPNFIGSFYSK
			149	156	932.45	931.44	931.5	-64	0	AMVEELLK
			157	165	1168.51	1167.5	1167.53	-25	0	NYENVCTLR
			166	178	1455.78	1454.77	1454.77	6	1	VRMPISSDLANPR
			168	178	1200.58	1199.57	1199.6	-25	0	MPISSDLANPR
			214	237	2804.31	2803.3	2803.38	-24	0	NLTGIWNFTNPGVVSHNEILEMYR
			238	247	1298.61	1297.6	1297.6	7	0	DYIDPNFTWK
			248	256	1092.49	1091.49	1091.52	-36	0	NFNLEEQAK
			248	262	1727.98	1726.98	1726.94	23	1	NFNLEEQAKVIVAPR
			272	283	1417.84	1416.83	1416.82	0	1	LKTEFPELLSIK
			274	283	1176.64	1175.63	1175.64	-17	0	TEFPELLSIK
			289	295	896.42	895.41	895.44	-44	0	YVFEPNK
			289	296	1024.49	1023.49	1023.54	-48	1	YVFEPNKK
33	UER1	FJ415167	21	30	1001.55	1000.54	1000.57	-29	0	TGWIGGLLGK
			31	45	1733.79	1732.79	1732.74	28	0	LCESQGIDYEYGSGR
			50	83	3748.88	3747.87	3747.84	8	0	ISLESDIANVKPTHVFNAAGVTGRPN

										VDWCESHK
			89	102	1518.85	1517.84	1517.79	39	0	TNVVGTLTLADVCR
			89	104	1761.94	1760.93	1760.91	11	1	TNVVGTLTLADVCRDK
			149	156	932.48	931.47	931.5	-32	0	AMVEELLK
			157	165	1168.56	1167.55	1167.53	17	0	NYENVCTLR
			166	178	1455.81	1454.8	1454.77	20	1	VRMPISSDLANPR
			168	178	1200.63	1199.62	1199.6	16	0	MPISSDLANPR
			190	213	2682.44	2681.43	2681.45	-7	1	VVNIPNSMTILDELLPISIEMGKR
			214	237	2804.36	2803.35	2803.38	-7	0	NLTGIWNFTNPGVVSHNEILEMYR
			238	247	1298.64	1297.63	1297.6	23	0	DYIDPNFTWK
			248	256	1092.53	1091.52	1091.52	0	0	NFNLEEQAK
			272	283	1417.87	1416.86	1416.82	28	1	LKTEFPELLSIK
			289	296	1024.54	1023.54	1023.54	0	1	YVFEPNKK
34	fructokinase	FJ415169	41	55	1334.78	1333.78	1333.75	22	0	APGGAPANVAIAVAR
			41	59	1689.86	1688.85	1688.97	-71	1	APGGAPANVAIAVARLGGK
			81	96	1633.84	1632.83	1632.79	24	0	QNGVSGDGILFDQGAR
			97	105	991.59	990.58	990.59	0	0	TALAFVTLR
			106	116	1420.67	1419.66	1419.62	21	1	ADGEREFMFYR
			139	153	1776.95	1775.94	1775.9	22	0	VFHYGSISLIVEPCR
			165	177	1346.74	1345.74	1345.7	29	0	GAGALLSYDPNLR

			178	188	1254.68	1253.67	1253.64	23	0	LPLWPSADEAR
			178	189	1382.78	1381.78	1381.74	28	1	LPLWPSADEARK
			190	202	1528.9	1527.89	1527.87	13	1	QILSIWDKADIVK
			203	216	1537.8	1536.8	1536.77	19	0	VSDVELEFLTGSNK
			217	224	908.38	907.37	907.4	-33	0	VDDETAMK
			225	240	1900.16	1899.15	1899.1	26	0	LWRPNFTLLLVTLGEK
			248	277	3139.74	3138.74	3138.52	70	1	NFRGAVDAFHVNTVDTTGAGDSFVGALLCK
			251	277	2722.33	2721.32	2721.31	7	0	GAVDAFHVNTVDTTGAGDSFVGALLCK
			278	292	1740	1738.99	1738.95	23	1	IVENPTILEDEAKLR
35	enolase	ABW21688	206	227	2323.92	2322.91	2323.035	-54	0	YGQDATNVGDEGGFAPNIQENK
			246	262	1801.8	1800.79	1800.86	-37	0	VVIGMDVAASEFYGTDK
			290	314	3016.2	3015.2	3015.345	-49	0	SFVAEYPIVSIEDPFDQDDWEHYSK
			323	336	1510.8	1509.8	1509.84	-30	0	VQIVGDDLLVTNPK
			354	368	1573.8	1572.79	1572.836	-29	0	VNQIGSVTESIEAVK
			383	404	2252.02	2251.01	2251.122	-48	0	SGETEDTFIADLSVGLATGQIK

			423	439	1811.81	1810.81	1810.874	-38	0	IEEELGAEAVYAGASFR	
36	actin	AAP73454	21	30	976.47	975.463	975.441	22	0	AGFAGDDAPR	
			42	52	1176.55	1175.54	1175.543	0	0	HTGVMVGMGQK	2 Oxidation (M)
			87	97	1515.76	1514.75	1514.742	7	0	IWHHTFYNELR	
			98	115	1954.07	1953.06	1953.057	3	0	VAPEEHPVLLTEAPLNPK	
			150	179	3151.68	3150.67	3150.635	12	0	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	
			194	208	1804.96	1803.95	1803.883	39	1	ILTERGYMFTTTAER	Oxidation (M)
			199	208	1192.57	1191.56	1191.523	33	0	GYMFTTTAER	Oxidation (M)
			218	233	1855.91	1854.9	1854.925	-12	0	LAYVALDYEQELETAK	
			234	256	2479.2	2478.19	2478.224	-13	1	SSSSVEKNYELPDGQVITIGAER	
			241	256	1774.9	1773.89	1773.89	2	0	NYELPDGQVITIGAER	
			287	314	3014.59	3013.58	3013.453	43	1	CDVDITKDLYGNIVLSGGSTMFPGIADR	
			362	374	1445.68	1444.67	1444.658	10	0	GEYDESGPSIVHR	
52	actin	AAP73452	71	86	1932.81	1931.81	1931.87	-36	0	YPIEHGIVSNWDDMEK	
			87	97	1515.73	1514.73	1514.74	-13	0	IWHHTFYNELR	
			98	115	1954.01	1953	1953.06	-25	0	VAPEEHPVLLTEAPLNPK	

			218	233	1855.9	1854.89	1854.93	-16	0	LAYVALDYEQELETAK	
			241	256	1774.87	1773.86	1773.89	-16	0	NYELPDGQVITIGAER	
			294	314	2183.02	2182.01	2182.07	-27	0	DLYGNIVLSGGSTMFPGIADR	
			362	374	1445.65	1444.64	1444.66	-6	0	GEYDESGPSIVHR	
53	actin	AAP73457	42	52	1176.56	1175.55	1175.543	8	0	HTGVMVGMGQK	2 Oxidation (M)
			53	64	1338.66	1337.65	1337.621	24	1	DAYVGDEAQSKR	
			71	86	1932.89	1931.88	1931.872	5	0	YPIEHGIVSNWDDMEK	
			71	86	1948.9	1947.89	1947.867	13	0	YPIEHGIVSNWDDMEK	Oxidation (M)
			71	97	3445.53	3444.52	3444.599	-22	1	YPIEHGIVSNWDDMEKIWHHTFYNELR	Oxidation (M)
			87	97	1515.78	1514.77	1514.742	20	0	IWHHTFYNELR	
			98	115	1954.08	1953.07	1953.057	8	0	VAPEEHPVLLTEAPLNPK	
			150	179	3151.61	3150.6	3150.635	-10	0	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	
			180	193	1547.78	1546.77	1546.803	-19	1	LDLAGRDLTDSLMK	
			180	193	1563.83	1562.82	1562.797	16	1	LDLAGRDLTDSLMK	Oxidation (M)
			186	193	922.5	921.493	921.4477	49	0	DLTDSLMK	
			199	208	1192.57	1191.56	1191.523	33	0	GYMFTTTAER	Oxidation (M)

			199	212	1673.9	1672.89	1672.824	41	1	GYMFTTTAEREIVR	
			199	212	1689.85	1688.84	1688.819	14	1	GYMFTTTAEREIVR	Oxidation (M)
			218	233	1855.94	1854.93	1854.925	4	0	LAYVALDYEQELETAK	
			234	256	2479.22	2478.21	2478.224	-4	1	SSSSVEKNYELPDGQVITIGAER	
			241	256	1774.9	1773.89	1773.89	2	0	NYELPDGQVITIGAER	
			287	293	905.5	904.493	904.4436	54	1	CDVDIRK	
			293	314	2311.16	2310.15	2310.168	-7	1	KDLYGNIVLSGGSTMFPGIADR	
			293	314	2327.15	2326.14	2326.163	-9	1	KDLYGNIVLSGGSTMFPGIADR	Oxidation (M)
			294	314	2183.08	2182.07	2182.073	0	0	DLYGNIVLSGGSTMFPGIADR	
			294	314	2199.08	2198.07	2198.068	2	0	DLYGNIVLSGGSTMFPGIADR	Oxidation (M)
			318	328	1147.63	1146.62	1146.595	24	0	EITALAPSSMK	
			318	328	1163.63	1162.62	1162.59	28	0	EITALAPSSMK	Oxidation (M)
			329	337	1008.64	1007.63	1007.613	20	1	IKVVAPPER	
			331	338	895.54	894.533	894.5287	5	1	VVAPPERK	
			362	374	1445.69	1444.68	1444.658	17	0	GEYDESGPSIVHR	
			362	375	1573.8	1572.79	1572.753	25	1	GEYDESGPSIVHRK	
71	actin	AAP73460	21	30	976.5	975.493	975.441	53	0	AGFAGDDAPR	
			31	41	1198.79	1197.78	1197.698	71	0	AVFPSIVGRPR	

42	52	1144.62	1143.61	1143.553	52	0	HTGVMVGMGQK	
42	52	1160.64	1159.63	1159.548	73	0	HTGVMVGMGQK	Oxidation (M)
42	52	1176.6	1175.59	1175.543	43	0	HTGVMVGMGQK	2 Oxidation (M)
53	64	1338.71	1337.7	1337.621	61	1	DAYVGDEAQSKR	
87	97	1515.83	1514.82	1514.742	53	0	IWHHTFYNELR	
98	115	1954.16	1953.15	1953.057	49	0	VAPEEHPVLLTEAPLNPK	
150	179	3151.76	3150.75	3150.635	37	0	TTGIVLDSGDGVSHTVPIYEGYALPHAILR	
180	193	1531.88	1530.87	1530.808	43	1	LDLAGRDLTDALMK	
180	193	1547.89	1546.88	1546.803	52	1	LDLAGRDLTDALMK	Oxidation (M)
199	208	1192.61	1191.6	1191.523	67	0	GYMFTTTAER	Oxidation (M)
199	212	1673.91	1672.9	1672.824	47	1	GYMFTTTAEREIVR	
218	233	1856.02	1855.01	1854.925	47	0	LAYVALDYEQELETAK	
234	256	2479.3	2478.29	2478.224	28	1	SSSSVEKNYELPDGQVITIGAER	
241	256	1774.98	1773.97	1773.89	47	0	NYELPDGQVITIGAER	
241	258	2077.88	2076.87	2077.059	-90	1	NYELPDGQVITIGAERFR	
294	314	2183.16	2182.15	2182.073	37	0	DLYGNIVLSGGSTMFPGIADR	
294	314	2199.16	2198.15	2198.068	39	0	DLYGNIVLSGGST	Oxidation (M)

										MFPGIADR
			329	337	1008.67	1007.66	1007.613	50	1	IKVVAPPER
			362	374	1445.75	1444.74	1444.658	58	0	GEYDESGPSIVHR
			362	375	1573.86	1572.85	1572.753	63	1	GEYDESGPSIVHRK
37	granule bound starch synthase	FJ415189	336	344	1028.57	1027.57	1027.57	0	0	K.GVELDNIIR.K
			386	398	1443.67	1442.66	1442.68	-13	0	K.EAIQGEVGLPCDR.D
			399	408	1086.62	1085.61	1085.62	-9	0	R.DVPLIGFIGR.L
			414	424	1113.59	1112.59	1112.61	-17	0	K.GSDILAEAIPK.L
			425	439	1572.78	1571.77	1571.83	-38	0	K.LAAENCQIVVLGTGK.K
			441	458	2205.97	2204.96	2205.04	-36	0	K.AMENQIEQLEIQYPDNVR.A
			463	483	2313.14	2312.13	2312.24	-43	0	K.FNVPLAHMIIAGADYILVPSR.F
			497	514	1776.93	1775.92	1775.97	-28	0	R.YGTVPIVASTGGLVDTVK.E
39	granule bound starch synthase	FJ415205	131	142	1361.82	1360.81	1360.69	95	0	DAWDTSVLVDLK
			318	335	1998.04	1997.03	1997	15	0	VLTVSPYYAQELVSGEDK
			336	344	1028.59	1027.59	1027.57	19	0	GVELDNIIR
			346	366	2232.07	2231.06	2231.05	4	0	TGITGIVNGMDVQEWNPASDK
			372	379	928.49	927.49	927.44	53	0	YDATTVMK
			386	408	2426.28	2425.27	2425.23	16	0	EALQAEVGLPCD

										GDVPLIGFIGR
			414	424	1113.62	1112.62	1112.61	8	0	GSDILAEAIPK
			445	458	1744.92	1743.91	1743.88	17	0	QIEQLEIQYPDNVR
			463	483	2297.28	2296.28	2296.24	17	0	FNVPLAHMIIAGADYILVPSR
			497	514	1777.01	1776	1775.97	16	0	YGTVPIVASTGGLVDTVK
			515	539	2791.27	2790.27	2790.22	17	0	EGFTGFQMGAFNVECDEVDPSDVIK
			558	571	1787.78	1786.78	1786.75	16	0	EMIQNCMAQDFSWK
			580	603	2367.26	2366.25	2366.24	4	0	MLLSLGVAGSEPGIEGEEVAPLAK
41	glutamine synthase	FJ415178	39	52	1449.85	1448.84	1448.82	13	1	TLPGPVTDPSKLPK
			53	83	3530.89	3529.88	3529.64	67	1	WNYDGSSTNQAPGDDSEVILYPQAIFKDPFR
			85	107	2531.27	2530.26	2530.23	11	1	GNNILVMCDAYTPAGEPIPTNKR
			113	137	2991.63	2990.62	2990.47	50	0	IFSHPDVVAEEPWYGIEQEYTLLQK
			113	140	3335.64	3334.63	3334.64	-2	1	IFSHPDVVAEEPWYGIEQEYTLLQKDTK
			138	165	3006.51	3005.5	3005.42	29	1	DTKWPLGWPVGGFPGPQGPYYCGV

										GADK
			141	165	2662.29	2661.28	2661.25	15	0	WPLGWPVGGFPGPQGPYYCGVGADK
			166	177	1423.74	1422.73	1422.69	28	1	SFGRDIVDSHYK
			269	276	899.58	898.57	898.56	11	1	AIEKLGLR
			277	290	1610.8	1609.79	1609.76	18	1	HKEHIAAYGEGNER
42	malate dehydrogenase	FJ415192	56	67	1918.89	1917.88	1917.91	-15	0	MELVDAAFPLLK
			101	105	1151.36	1150.35	1150.45	-86	0	DVMSK
			106	111	1295.64	1294.63	1294.58	46	0	NVSIYK
			143	151	1531.69	1530.69	1530.69	-6	0	EFAPSIPAK
			164	171	1417.64	1416.63	1416.65	-14	0	ALGQISEK
			172	180	1573.74	1572.73	1572.74	0	0	LNVQVSDVK
			216	231	2465.13	2464.12	2464.09	12	0	DDAWLNGEFITTVQQR
			232	237	1144.57	1143.56	1143.55	8	0	GAAIIK
			313	324	1947.84	1946.84	1946.87	-15	0	LDLTGQELTEEK
			325	332	1514.61	1513.6	1513.6	0	0	ELAYSCLS
56	malate dehydrogenase	FJ415192	56	67	1346.72	1345.71	1345.73	-14	0	MELVDAAFPLLK
			68	93	2605.2	2604.19	2604.3	-42	0	GVVATTDVVEACTGVNVAVMVGGFPR
			127	142	1649.97	1648.96	1648.99	-18	0	VLVVANPANTNALILK
			143	151	959.53	958.52	958.51	10	0	EFAPSIPAK

			181	211	3420.49	3419.49	3419.67	-52	0	NVIIWGNHSSSQYPDVNHATVMTPSGEKPVR	
			216	231	1892.85	1891.84	1891.91	-31	0	DDAWLNGEFITTVQQR	
			241	256	1629.77	1628.76	1628.79	-18	0	LSSALSAASAACDHIR	
			294	310	1934.9	1933.89	1933.95	-31	0	NGEWTIVQGLAIDEFSR	
43	phenylcoumaran benzylic ether reductase-like protein	ABN12322	19	36	2034.14	2033.13	2033.074	27	1	FIVEASAKEGHPTFVFVR	
			27	36	1188.65	1187.65	1187.609	31	0	EGHPTFVFVR	
			48	72	2885.57	2884.56	2884.479	29	1	LVDNFKNLGVHLLLGDMYDHESLVK	Oxidation (M)
			54	72	2169.13	2168.12	2168.094	13	0	NLGVHLLLGDMYDHESLVK	Oxidation (M)
			73	94	2368.21	2367.2	2367.32	-49	1	AIKQVDVVISVVGQMQLADQVK	
			108	119	1434.67	1433.66	1433.617	31	0	FFPSEFGMDVDK	Oxidation (M)
			108	127	2242.1	2241.09	2241.041	23	1	FFPSEFGMDVDKNNAVEPAK	
			108	127	2258.08	2257.07	2257.036	14	1	FFPSEFGMDVDKNNAVEPAK	Oxidation (M)
			120	127	842.474	841.467	841.4294	44	0	NNAVEPAK	
			219	232	1727.95	1726.94	1726.857	48	0	NTYSFNELIALWEK	

			241	250	1205.69	1204.68	1204.634	41	0	TYVPEDQLLK	
51	phenylcoumaran benzylic ether reductase-like protein	ABN12322	19	26	864.43	863.423	863.4752	-61	0	FIVEASAK	
			19	36	2034.06	2033.05	2033.074	-10	1	FIVEASAKEGHPTFVFVR	
			27	36	1188.61	1187.6	1187.609	-5	0	EGHPTFVFVR	
			54	72	2153.07	2152.06	2152.099	-17	0	NLGVHLLLGDMYDHESLVK	
			54	72	2169.07	2168.06	2168.094	-14	0	NLGVHLLLGDMYDHESLVK	Oxidation (M)
			76	94	2056.06	2055.05	2055.104	-25	0	QVDVVISVVGQMQLADQVK	
			76	94	2072.07	2071.06	2071.098	-17	0	QVDVVISVVGQMQLADQVK	Oxidation (M)
			108	119	1434.65	1433.64	1433.617	18	0	FFPSEFGMDVDK	Oxidation (M)
			108	127	2242.01	2241	2241.041	-17	1	FFPSEFGMDVDKNNAVEPAK	
			120	127	842.44	841.433	841.4294	4	0	NNAVEPAK	
			138	173	3897.91	3896.9	3896.92	-4	1	RAVEAEGIPYTYVPANCFAGYFLPTLSQPGATSPPR	
			139	173	3741.73	3740.72	3740.819	-26	0	AVEAEGIPYTYVPANCFAGYFLPTLSQPGATSPPR	
			176	185	1011.55	1010.54	1010.576	-33	0	VVILGDGNPK	
			186	200	1678.85	1677.84	1677.836	4	0	AVFNHEADIGTYTI	

										K	
			211	218	943.56	942.553	942.5902	-40	0	TLFIKPPK	
			219	232	1727.87	1726.86	1726.857	4	0	NTYSFNELIALWEK	
			241	250	1205.64	1204.63	1204.634	-1	0	TYVPEDQLLK	
			297	308	1381.67	1380.66	1380.656	5	0	YTTVEEGLSHFV	
45	β-tubulin 19	ABY86665	1	19	2110.1	2109.09	2109.057	16	1	MREILHIQGGQCGNQIGAK	
			1	19	2126.11	2125.1	2125.052	21	1	MREILHIQGGQCGNQIGAK	Oxidation (M)
			20	35	1888.91	1887.9	1887.857	25	0	FWEVVCSEHGIDPTGR	
			36	46	1349.71	1348.7	1348.662	31	0	YQGDLDLQLER	
			47	58	1445.7	1444.69	1444.641	33	0	INVYYNEASCGR	
			63	77	1647.85	1646.84	1646.801	25	0	AVLMDLEPGTMDSIR	
			63	77	1663.84	1662.84	1662.796	24	0	AVLMDLEPGTMDSIR	Oxidation (M)
			63	77	1679.91	1678.9	1678.791	67	0	AVLMDLEPGTMDSIR	2 Oxidation (M)
			78	103	2750.39	2749.39	2749.336	18	0	SGPVGQIFRPDNFVFGQSGAGNNWAK	
			104	121	1973.04	1972.03	1971.99	20	0	GHYTEGAELIDSVLDVVR	
			104	122	2101.14	2100.13	2100.085	21	1	GHYTEGAELIDSVLDVVRK	
			123	154	3383.6	3382.59	3382.505	25	0	EAENCDCLQGFQ	

										VCHSLGGGTGSGMGTLLISK	
			123	154	3399.58	3398.58	3398.5	22	0	EAENCDCLQGFQVCHSLGGGTGSGMGTLLISK	Oxidation (M)
			155	162	1077.53	1076.53	1076.525	1	1	IREEYPDR	
			163	174	1384.76	1383.75	1383.693	39	0	MMLTFSVFPSPK	
			163	174	1400.74	1399.74	1399.688	34	0	MMLTFSVFPSPK	Oxidation (M)
			214	241	3093.59	3092.58	3092.546	13	1	TLKLTTPSFGDLNHLISATMSGVTCCLR	
			242	251	1146.62	1145.61	1145.583	23	0	FPGQLNSDLR	
			242	252	1274.73	1273.72	1273.678	32	1	FPGQLNSDLRK	
			252	262	1267.82	1266.81	1266.781	21	1	KLAVNLIPFPR	
			253	262	1139.73	1138.72	1138.686	30	0	LAVNLIPFPR	
			263	276	1622.89	1621.88	1621.844	23	0	LHFFMVGFAPLTSR	
			263	276	1638.89	1637.89	1637.839	29	0	LHFFMVGFAPLTSR	Oxidation (M)
			283	297	1730.92	1729.92	1729.871	26	0	ALTVPELTQQMWDAK	
			283	297	1746.91	1745.9	1745.866	19	0	ALTVPELTQQMWDAK	Oxidation (M)
			298	309	1431.66	1430.66	1430.597	41	1	NMMCAADPRHGR	Oxidation (M)
46	α-tubulin 4	AAN33000	41	60	1977.93	1976.92	1976.875	21	0	TVGGGDDAFNTFFSETGAGK	
			41	64	2467.2	2466.19	2466.156	14	1	TVGGGDDAFNTFFSETGAGKHVPR	

65	79	1701.96	1700.95	1700.899	33	0	AVFVDLEPTVIDEVR	
85	96	1396.8	1395.79	1395.751	28	0	QLFHPEQLISGK	
85	105	2385.22	2384.21	2384.187	9	1	QLFHPEQLISGKEDAANNFAR	
106	121	1889	1887.99	1887.951	22	1	GHYTIGKEIVDLCLDR	
113	121	1132.59	1131.58	1131.559	17	0	EIVDLCLDR	
113	123	1401.79	1400.78	1400.745	27	1	EIVDLCLDRIR	
124	156	3321.85	3320.84	3320.719	36	1	KLADNCTGLQGFLVFNAVGGGTGSGLGSLLLER	
125	156	3193.73	3192.72	3192.624	32	0	LADNCTGLQGFLVFNAVGGGTGSGLGSLLLER	
215	229	1848.01	1847	1846.965	18	1	RSLDIERPTYTNLNR	
216	229	1691.92	1690.91	1690.864	27	0	SLDIERPTYTNLNR	
230	243	1473.91	1472.9	1472.856	32	0	LVSQVISSLTASLR	
244	264	2395.22	2394.21	2394.186	10	0	FDGALNVDVTEFQTNLVPYPR	
265	280	1792.95	1791.95	1791.923	13	0	IHFMLSSYAPVISAEK	
265	280	1808.97	1807.96	1807.918	25	0	IHFMLSSYAPVISAEK	Oxidation (M)
281	304	2641.26	2640.26	2640.22	14	0	AYHEQLSVAEITNSAFEPSSMMAK	

			281	304	2657.28	2656.27	2656.215	22	0	AYHEQLSVAEITNSAFEPSSMMAK	Oxidation (M)
			281	304	2673.35	2672.35	2672.21	51	0	AYHEQLSVAEITNSAFEPSSMMAK	2 Oxidation (M)
49	α-tubulin 4	AAN33000	65	79	1702.01	1701	1700.899	61	0	AVFVDLEPTVIDEVR	
			85	96	1396.84	1395.83	1395.751	59	0	QLFHPEQLISGK	
			85	105	2385.33	2384.32	2384.187	57	1	QLFHPEQLISGKEDAANNFAR	
			106	121	1889.06	1888.05	1887.951	54	1	GHYTIGKEIVDLCLDR	
			113	121	1132.62	1131.61	1131.559	47	0	EIVDLCLDR	
			124	156	3321.9	3320.89	3320.719	52	1	KLADNCTGLQGFLVFNAVGGGTGSGLGSLLLER	
			125	156	3193.87	3192.86	3192.624	75	0	LADNCTGLQGFLVFNAVGGGTGSGLGSLLLER	
			215	229	1848.07	1847.06	1846.965	53	1	RSLDIERPTYTNLNR	
			216	229	1691.96	1690.95	1690.864	53	0	SLDIERPTYTNLNR	
			244	264	2395.33	2394.32	2394.186	57	0	FDGALNVDVTEFQTNLVPYPR	
			265	280	1793.03	1792.02	1791.923	56	0	IHFMLSSYAPVISAEK	
			265	280	1809.04	1808.03	1807.918	64	0	IHFMLSSYAPVISAEK	Oxidation (M)

48	α-tubulin	ABO47738	65	79	1701.98	1700.97	1700.899	41	0	AVFVDLEPTVIDEVR	
			85	96	1396.81	1395.8	1395.751	38	0	QLFHPEQLISGK	
			85	105	2385.26	2384.25	2384.187	28	1	QLFHPEQLISGKEDAANNFAR	
			106	121	1889	1888	1887.951	24	1	GHYTIGKEIVDLCLDR	
			113	121	1132.62	1131.61	1131.559	44	0	EIVDLCLDR	
			124	156	3339.83	3338.83	3338.675	45	1	KLADNCTGLQGFMVFNAVGGGTGSGLGSLLLER	
			124	156	3355.79	3354.78	3354.67	34	1	KLADNCTGLQGFMVFNAVGGGTGSGLGSLLLER	Oxidation (M)
			125	156	3211.69	3210.68	3210.58	31	0	LADNCTGLQGFMVFNAVGGGTGSGLGSLLLER	
			125	156	3227.7	3226.7	3226.575	37	0	LADNCTGLQGFMVFNAVGGGTGSGLGSLLLER	Oxidation (M)
			215	229	1848.02	1847.01	1846.965	24	1	RSLDIERPTYTNLNR	
			216	229	1691.93	1690.92	1690.864	35	0	SLDIERPTYTNLNR	
			230	243	1519.9	1518.9	1518.862	22	0	LISQTISSLTTSLR	
			244	264	2409.25	2408.25	2408.201	19	0	FDGAINVDITEFQTNLVPYPR	
			265	280	1792.99	1791.98	1791.923	31	0	IHFMLSSYAPVISA	

										EK	
			265	280	1809	1807.99	1807.918	39	0	IHFMLSSYAPVISAEK	Oxidation (M)
			281	304	2679.35	2678.34	2678.272	26	0	AYHEQISVPEITNAVFEPSSMMAK	
			281	304	2695.34	2694.33	2694.267	24	0	AYHEQISVPEITNAVFEPSSMMAK	Oxidation (M)
			281	304	2711.34	2710.33	2710.262	26	0	AYHEQISVPEITNAVFEPSSMMAK	2 Oxidation (M)
			353	373	2239.19	2238.18	2238.158	11	1	CGINYQPPAVVPGGDLAKVQR	
50	glyceraldehyde-3-phosphate dehydrogenase C subunit	FJ415206	49	57	1119.56	1118.55	1118.51	35	0	YDSVHGQWK	
			83	107	2738.37	2737.36	2737.28	29	0	NPEEIPWAEAGAEYVVESTGVFTDK	
			129	140	1305.7	1304.69	1304.64	30	0	DAPMFVVGVNEK	
			170	188	2033.14	2032.13	2032.07	34	0	FGIVEGLMTTVHSITATQK	
			237	250	1498.91	1497.91	1497.84	46	0	VPTVDVSVVDLTVR	
			274	293	2198.12	2197.11	2197.05	27	0	GILGYVDEDLVSTDFIGDNR	
			312	325	1775.86	1774.85	1774.8	33	0	LVTWYDNEWGYSSR	
54	2-nitropropane dioxygenase	FJ415176	60	77	1994.16	1993.15	1993.1	25	0	ELTDKPFGVGVLLPFPHK	

60	81	2478.44	2477.44	2477.37	28	1	ELTDKPFGVGVLLPFPHKENIK
88	100	1446.81	1445.8	1445.73	48	0	VAVLQVAWGECSK
101	125	2647.45	2646.44	2646.4	15	1	ELVLEAHNAGVMVVPQVGSLEEAKK
125	157	3347.98	3346.98	3346.84	41	1	KVIDAGVDAIIVQGHEAGGHVLGQDGLISLLPR
126	157	3219.9	3218.9	3218.74	46	0	VIDAGVDAIIVQGHEAGGHVLGQDGLISLLPR
158	179	2173.22	2172.21	2172.15	27	0	VVDAVADHDIPVIAAGGIVDAR
180	190	1033.62	1032.62	1032.6	19	0	GYVAALALGAK
203	211	1095.55	1094.54	1094.5	36	0	ESYAHPTYK
212	228	2094.07	2093.06	2093.01	28	1	QKLIEHDETEYTDIFGR
214	228	1837.92	1836.91	1836.85	32	0	LIEHDETEYTDIFGR
229	237	995.58	994.57	994.53	30	0	ALWPGAPQR
241	248	1052.53	1051.52	1051.48	38	0	TPFVCDWK
265	276	1413.78	1412.77	1412.71	42	0	SLIHGMETEIQR
277	305	3011.55	3010.55	3010.46	29	0	FSASDPNPTTTGEIENMALYAGQSVGLIK
306	316	1210.77	1209.76	1209.71	41	1	EILPAGEVVKR
316	326	1291.81	1290.8	1290.75	38	1	RLVEGAQHLIR

			317	326	1135.69	1134.68	1134.65	26	0	LVEGAQHLIR
55	quinone oxidoreductase	FJ415175	14	22	1114.56	1113.56	1113.51	35	0	AWTYPEYGK
			29	39	1237.77	1236.76	1236.68	64	0	LQSDVVVPQPR
			40	58	2055.18	2054.18	2054.1	34	0	DDQVLLQVVAAGINPIDFK
			40	59	2211.27	2210.26	2210.21	27	1	DDQVLLQVVAAGINPIDFKR
			66	85	2066.21	2065.2	2065.15	24	0	NIDSPLPIIPGYDVAGVVVK
			93	106	1641.85	1640.85	1640.77	48	1	FKEGDQVYGDINEK
			95	106	1366.74	1365.73	1365.6	87	0	EGDQVYGDINEK
			107	126	2160.17	2159.16	2159.09	32	0	AVDHPTQFGTIAEFTVVAEK
			107	133	2923.71	2922.7	2922.62	27	1	AVDHPTQFGTIAEFTVVAEKLLALKPK
			134	156	2521.39	2520.38	2520.31	27	0	NLSFVEAASLPLVIETAYEGLER
			157	163	806.37	805.36	805.35	12	0	CHFSAGK
			164	183	1898.16	1897.15	1897.11	21	0	SILVLGGAGGVGTMIIQLAK
			200	225	2961.57	2960.56	2960.5	20	1	LDLLKSLGADLPIDYTNQNFEDLPEK
			205	238	3918.1	3917.09	3916.81	71	1	SLGADLPIDYTNQNFEDLPEKFDVVYDAVGQCER

			226	238	1557.78	1556.77	1556.69	44	0	FDVVYDAVGQCER	
			284	310	3025.61	3024.6	3024.51	33	0	VKPMIDPNGIFPFSETPQAFAYLETGR	
57	gibberellin 20-oxidase 1	ABA01482	14	28	1790.96	1789.95	1789.896	32	1	TLQASFVRDEDERPK	
			29	52	2550.31	2549.3	2549.265	15	0	VAYNQFSNDIPVISLAGIDDVDGK	
			59	80	2531.25	2530.24	2530.216	9	1	KIVEACEDWGVFQVVDHGVDTK	
			60	80	2403.17	2402.16	2402.121	16	0	IVEACEDWGVFQVVDHGVDTK	
			91	100	1180.63	1179.63	1179.581	39	0	EFFALPAEEK	
			91	102	1449.84	1448.83	1448.766	42	1	EFFALPAEEKLR	
			111	128	1986.01	1985	1984.976	13	0	GGFIVSSHLQGEAVQDWR	
			129	139	1387.78	1386.77	1386.718	38	0	EIVTYFSYPLR	
			142	158	2092.05	2091.04	2091.006	18	1	DYSRWPDKPEGWVEVTK	
			146	158	1570.84	1569.83	1569.783	31	0	WPDKPEGWVEVTK	
			146	163	2207.1	2206.09	2206.058	17	1	WPDKPEGWVEVTKEYSEK	
			164	183	2221.15	2220.15	2220.157	-5	1	LMGLACKLLEVLSEAMGLEK	Oxidation (M)
			171	183	1431.8	1430.79	1430.769	16	0	LLEVLSEAMGLEK	
			171	183	1447.84	1446.83	1446.764	44	0	LLEVLSEAMGLEK	Oxidation (M)
			171	188	1990.11	1989.11	1989.07	18	1	LLEVLSEAMGLEK	Oxidation (M)

										EALTK	
			197	204	965.563	964.556	964.5382	18	0	VVVNFYPK	
			205	215	1241.71	1240.71	1240.649	46	0	CPQPDLTLGLK	
			205	216	1397.81	1396.8	1396.75	37	1	CPQPDLTLGLKR	
			216	238	2490.38	2489.37	2489.335	15	1	RHTDPGTITLLLQDQVGGLQATR	
			217	238	2334.28	2333.28	2333.234	18	0	HTDPGTITLLLQDQVGGLQATR	
			270	285	1847.89	1846.88	1846.838	23	1	FKNADHQAVVNSDCSR	
			272	304	3599.89	3598.89	3598.747	38	1	NADHQAVVNSDCSRLSIATFQNPAPDATVYPLK	
			286	304	2046.12	2045.11	2045.083	13	0	LSIATFQNPAPDATVYPLK	
			358	368	1225.72	1224.71	1224.697	10	0	LEAKPLEEILA	
58	flavanone-3-hydroxylase	ABM64799	2	13	1230.68	1229.67	1229.65	18	0	APSTLTALAEEK	
			14	21	921.5	920.493	920.508	-17	0	TLQASFVR	
			14	28	1790.9	1789.89	1789.896	-2	1	TLQASFVRDEDERPK	
			60	80	2403.13	2402.12	2402.121	1	0	IVEACEDWGVFQVVDHGVDTK	
			81	87	835.41	834.403	834.4269	-29	0	LVSEMTR	
			81	87	851.4	850.393	850.4218	-34	0	LVSEMTR	Oxidation (M)
			91	100	1180.59	1179.58	1179.581	1	0	EFFALPAEEK	
			101	109	1026.5	1025.49	1025.496	-4	1	LRFDMSGGK	Oxidation (M)
			111	128	1985.95	1984.94	1984.976	-17	0	GGFIVSSHLQGEA	

							VQDWR	
129	139	1359.74	1358.73	1358.712	15	0	EIVTYFSYPLK	
129	141	1602.86	1601.85	1601.845	5	1	EIVTYFSYPLKSR	
142	158	2106.01	2105	2105.022	-9	1	DYSRWPDKPEGWIEVTK	
146	158	1584.83	1583.82	1583.798	15	0	WPDKPEGWIEVTK	
164	170	808.37	807.363	807.3983	-44	0	LMGLACK	Oxidation (M)
171	183	1431.79	1430.78	1430.769	10	0	LLEVLSEAMGLEK	
197	204	965.54	964.533	964.5382	-6	0	VVVNFYPK	
205	215	1241.67	1240.66	1240.649	11	0	CPQPDLTLGLK	
205	216	1397.77	1396.76	1396.75	9	1	CPQPDLTLGLKR	
216	238	2490.34	2489.33	2489.335	-1	1	RHTDPGTITLLLQDQVGGLQATR	
217	238	2334.22	2333.21	2333.234	-9	0	HTDPGTITLLLQDQVGGLQATR	
272	285	1571.78	1570.77	1570.691	52	0	NADHQAVVNSNCSR	
272	304	3599.02	3598.01	3597.763	69	1	NADHQAVVNSNCSRLSIATFQNPAPDATVYPLK	
286	304	2046.09	2045.08	2045.083	0	0	LSIATFQNPAPDATVYPLK	
307	324	2152.07	2151.06	2151.056	3	0	EGEKPILEEPITFAEMYR	
307	324	2168.06	2167.05	2167.051	1	0	EGEKPILEEPITFAEMYR	Oxidation (M)
358	368	1225.7	1224.69	1224.697	-3	0	LEAKPLEEILA	

59	mannitol dehydrogenase	FJ415191	13	32	2158.06	2157.05	2157.03	9	0	AFGWAATDNSGILSPFNFSR	
			44	58	1843.92	1842.91	1842.89	10	0	ILYCGVCHSDLHTLR	
			59	80	2435.25	2434.24	2434.2	16	0	NDWGFSFYPVVPGHEISGVVTK	
			94	104	1074.62	1073.61	1073.59	18	0	VGVGVLVGSCK	
			105	119	2033.76	2032.76	2032.74	9	0	TCECCEQDLENYCPR	
			120	133	1632.8	1631.8	1631.78	6	0	IIFTYNSYNPDGTK	
			134	147	1616.77	1615.76	1615.73	18	0	NYGGYSDMIVVDQR	
			152	176	2676.42	2675.41	2675.33	29	0	FPDNLPLDAGAPLLCAGITVYSPMK	Oxidation (M)
			186	201	1500.9	1499.89	1499.86	20	0	HLGVSGLGGLGHVAVK	
			227	240	1491.77	1490.76	1490.73	20	0	LGADSFLVSNDPEK	
			274	295	2389.42	2388.42	2388.4	8	0	LVTVGLPNKPLELPVFPLVMGR	
			274	295	2405.44	2404.43	2404.39	16	0	LVTVGLPNKPLELPVFPLVMGR	Oxidation (M)
			308	318	1371.62	1370.61	1370.58	21	0	ETQEMLDFCAK	
			308	318	1387.62	1386.61	1386.58	21	0	ETQEMLDFCAK	Oxidation (M)
			319	329	1294.74	1293.73	1293.7	23	0	HNITADIELIR	
			349	359	1192.64	1191.64	1191.61	16	0	FVIDVANSLSQ	
60	adenosine kinase	FJ415170	43	69	2977.49	2976.48	2976.45	13	0	HLPMYQEMASKPNVEYIAGGATQNS	

										IK
			70	89	2163.16	2162.15	2162.1	23	0	VAQWMLQIPGATGYIGCIGK
			102	129	2923.4	2922.39	2922.35	13	0	AAGVNVQYLEDETAPTGTCAVCVVGGER
			130	142	1424.77	1423.76	1423.71	35	0	SLIANLSAANCYK
			186	203	2179.12	2178.11	2178.06	22	1	NKVFSMNLSAPFICEFFK
			188	203	1936.97	1935.96	1935.93	20	0	VFSMNLSAPFICEFFK
			188	208	2508.2	2507.19	2507.19	3	1	VFSMNLSAPFICEFFKDAQEK
			209	224	1859.92	1858.91	1858.86	32	0	ALPYMDFVFGNETEAR
			229	243	1682.89	1681.88	1681.83	29	0	VHGWETDDVAEIALK
			275	285	1281.87	1280.86	1280.82	31	1	VKQFPVILLPK
			277	285	1054.69	1053.68	1053.66	18	0	QFPVILLPK
			286	310	2550.32	2549.31	2549.31	0	1	EKLVDTNGAGDAFVGGFLSQLVQGK
			288	310	2293.19	2292.18	2292.17	4	0	LVDTNGAGDAFVGGFLSQLVQGK
			318	329	1351.73	1350.72	1350.67	37	0	AGCYASNVIIQR
			330	341	1442.69	1441.68	1441.65	20	0	SGCTYPEKPEFK
61	adenosine kinase	FJ415170	43	69	2977.46	2976.45	2976.45	0	0	HLPMYQEMASKPNVEYIAGGATQNSIK

43	69	2993.46	2992.45	2992.44	3	0	HLPMYQEMASKPNVEYIAGGATQNSIK	Oxidation (M)
43	69	3009.44	3008.44	3008.44	0	0	HLPMYQEMASKPNVEYIAGGATQNSIK	2 Oxidation (M)
70	89	2163.11	2162.11	2162.1	0	0	VAQWMLQIPGATGYIGCIGK	
70	89	2179.12	2178.11	2178.1	4	0	VAQWMLQIPGATGYIGCIGK	Oxidation (M)
102	129	2923.36	2922.36	2922.35	3	0	AAGVNVQYLEDETAPTGTCAVCVVGGER	
130	142	1424.74	1423.73	1423.71	14	0	SLIANLSAANCYK	
148	157	1213.66	1212.66	1212.65	0	0	KPENWALVEK	
209	224	1859.88	1858.87	1858.86	5	0	ALPYMDFVFGNETEAR	
209	224	1875.88	1874.87	1874.85	10	0	ALPYMDFVFGNETEAR	Oxidation (M)
229	243	1682.86	1681.85	1681.83	11	0	VHGWETDDVAEIALK	
257	274	1813.96	1812.96	1812.95	5	0	TTVITQGADPVIVAEDGK	
257	276	2041.12	2040.11	2040.11	0	1	TTVITQGADPVIVAEDGKVK	
275	285	1281.83	1280.82	1280.82	0	1	VKQFPVILLPK	
277	285	1054.68	1053.67	1053.66	9	0	QFPVILLPK	
311	329	2211.1	2210.09	2210.06	18	1	SIEDCVRAGCYAS	

										NVIIQR
			318	329	1351.7	1350.7	1350.67	14	0	AGCYASNVIIQR
			330	341	1442.69	1441.68	1441.65	20	0	SGCTYPEKPEFK
62	phosphoglycerate dehydrogenase	FJ415190	270	278	1068.53	1067.52	1067.5	28	0	MLNDETFAK
			291	301	1157.66	1156.66	1156.61	43	0	GGVIDEEALVR
			333	363	3091.71	3090.7	3090.63	25	0	VTVTPHLGASTMEAQEGVAIEIAEAVVGALK
			364	393	3153.75	3152.74	3152.67	22	0	GELAATAVNAPMVPAEVLTELKPYVELAEK
			491	502	1256.64	1255.63	1255.58	47	0	FASAMSESGEIK
			517	534	1980.1	1979.09	1979	45	0	VGSFEVDVSLEGSIILCR
			535	563	3020.55	3019.54	3019.47	23	0	QVDQPGMIGTVGSILGEENVNVSFMSVGR
65	phosphoglycerate dehydrogenase	FJ415190	270	278	1068.57	1067.56	1067.5	65	0	MLNDETFAK
			291	301	1157.68	1156.68	1156.61	60	0	GGVIDEEALVR
			333	363	3091.78	3090.77	3090.63	48	0	VTVTPHLGASTMEAQEGVAIEIAEAVVGALK
			364	393	3153.84	3152.83	3152.67	53	0	GELAATAVNAPMVPAEVLTELKPYVELAEK
			467	490	2566.48	2565.47	2565.35	46	0	ILLDGSPESPLESI

										QVQIANVESK
			491	502	1256.66	1255.65	1255.58	63	0	FASAMSESGEIK
			517	534	1980.12	1979.12	1979	55	0	VGSFEVDVSLEGSIILCR
			535	563	3020.63	3019.62	3019.47	49	0	QVDQPGMIGTVGSILGEENVNVSFMSVGR
64	pyruvate dehydrogenase α subunit	FJ415197	63	69	925.53	924.52	924.51	10	0	ELLTFFR
			92	113	2367.06	2366.05	2366.1	-21	0	GFCHLYDGQEAVAVGMEAAITK
			115	122	1011.5	1010.49	1010.49	0	0	DCIITAYR
			123	130	1021.46	1020.45	1020.44	9	0	DHCTFVSR
			131	144	1492.76	1491.76	1491.78	-13	0	GGTLLEVFAELMGR
			162	187	2663.21	2662.2	2662.3	-33	0	DSNFYGGHGIVGAQVPLGCGLAFAQK
			281	292	1421.7	1420.69	1420.7	-7	0	NGPIILEMDTYR
			293	306	1594.65	1593.64	1593.66	-12	0	YHGHSMSDPGSTYR
			376	386	1107.54	1106.54	1106.54	0	0	GLGVESFGADR
66	anthocyanidin reductase	ABM64802	10	26	1719.95	1718.94	1718.95	-4	1	RACVVGGSGFVASLLVK
			32	40	980.5	979.493	979.5087	-16	0	GYAVNTTVR
			32	46	1677.82	1676.81	1676.812	1	1	GYAVNTTVRDPDNQK

			47	61	1693.98	1692.97	1692.977	-3	1	KISHLVTLQELGDLK
			48	61	1565.89	1564.88	1564.882	0	0	ISHLVTLQELGDLK
			125	149	2535.31	2534.3	2534.315	-5	0	VVLTSSAAAVSINTLDGTDLVMTEK
			150	171	2496.24	2495.23	2495.201	13	0	DWTDIEFLSSAKPPTWGYPASK
			248	255	914.5	913.493	913.5021	-10	0	AHVFLAEK
			248	261	1501.77	1500.76	1500.769	-4	1	AHVFLAEKESASGR
			256	276	2239.15	2238.14	2238.095	21	1	ESASGRYICSAVNTSVPELAK
			262	276	1651.85	1650.84	1650.829	9	0	YICSAVNTSVPELAK
			281	286	825.41	824.403	824.4181	-19	1	RYPDFK
			282	299	2085.03	2084.02	2084.026	-1	1	YPDFKVPTDFGDFPSKPK
			287	299	1434.72	1433.71	1433.719	-4	0	VPTDFGDFPSKPK
			307	315	1027.54	1026.53	1026.539	-6	0	LISEGFSFK
			316	330	1862.91	1861.9	1861.899	2	0	YGIEEIYDQTVEYLK
69	luminal binding protein	FJ415200	314	331	2052.96	2051.96	2052.01	-24	0	VEIESLFDGVDFSEPLTR
			332	343	1523.74	1522.73	1522.75	-13	1	ARFEELNNDLFR
			334	343	1296.6	1295.6	1295.61	-15	0	FEELNNDLFR
			361	374	1473.77	1472.77	1472.78	-13	0	SQIDEIVLVGGSTR
			384	393	1212.54	1211.53	1211.55	-8	1	DYFDGKEPNK
			394	421	2661.2	2660.2	2660.26	-22	0	GVNPDEAVAYGA

										AVQGGILSGEGGDETK	
			456	479	2819.34	2818.33	2818.38	-17	1	KSQVFTTYQDQQTTVSIQVFEGER	
			457	479	2691.24	2690.24	2690.28	-18	0	SQVFTTYQDQQTTVSIQVFEGER	
			487	501	1594.91	1593.91	1593.92	-12	1	LLGKFDLTGIPPAPR	
			491	501	1183.63	1182.62	1182.64	-16	0	FDLTGIPPAPR	
			542	549	1003.47	1002.46	1002.5	-29	0	LSQEEIER	
			553	563	1324.57	1323.56	1323.58	-15	1	EAEEFAEEDKK	
			572	582	1391.63	1390.62	1390.64	-14	0	NSLETYIYNMK	Oxidation (M)
			609	628	2441.01	2440.01	2440.06	-20	1	EALEWLDDNQSAEKEDYEEK	
			629	646	2103.08	2102.08	2102.12	-19	1	LKEVEAVCNPIITAVYQR	
			631	646	1861.91	1860.9	1860.94	-21	0	EVEAVCNPIITAVYQR	
			647	666	1931.85	1930.84	1930.73	56	0	SGGAPGGGSTEEDDDSHDEL	
70	luminal binding protein	FJ415200	314	331	2053.1	2052.09	2052.01	43	0	VEIESLFDGVDFSEPLTR	
			334	343	1296.71	1295.7	1295.61	69	0	FEELNNDLFR	
			361	374	1473.88	1472.88	1472.78	61	0	SQIDEIVLVGGSTR	
			394	421	2661.36	2660.35	2660.26	33	0	GVNPDEAVAYGAAVQGGILSGEGGDETK	
			457	479	2691.41	2690.4	2690.28	44	0	SQVFTTYQDQQT	

										TVSIQVFEGER
			502	521	2144.2	2143.2	2143.12	37	0	GTPQIEVTFEVDANGILNVK
			542	549	1003.58	1002.57	1002.5	79	0	LSQEEIER
			631	646	1862.02	1861.02	1860.94	42	0	EVEAVCNPIITAVYQR
			647	666	1931.84	1930.84	1930.73	56	0	SGGAPGGGSTEEDDDSHDEL
72	luminal binding protein	FJ415200	314	331	2053.05	2052.05	2052.01	19	0	VEIESLFDGVDFSEPLTR
			334	343	1296.67	1295.66	1295.61	38	0	FEELNNDLFR
			361	374	1473.84	1472.83	1472.78	33	0	SQIDEIVLVGGSTR
			394	421	2661.31	2660.31	2660.26	18	0	GVNPDEAVAYGAAVQGGILSGEGGDETK
			457	479	2691.36	2690.35	2690.28	26	0	SQVFTTYQDQQTTVSIQVFEGER
			502	521	2144.14	2143.13	2143.12	9	0	GTPQIEVTFEVDANGILNVK
			542	549	1003.54	1002.53	1002.5	29	0	LSQEEIER
			609	622	1647.8	1646.79	1646.74	30	0	EALEWLDDNQSAEK
			631	646	1861.98	1860.98	1860.94	21	0	EVEAVCNPIITAVYQR
			647	666	1931.77	1930.77	1930.73	20	0	SGGAPGGGSTEEDDDSHDEL
74	phosphoglycerate kinase	FJ415172	20	41	2577.38	2576.37	2576.29	31	1	VFVRVDLNVPLDDNFNITDDTR

			24	41	2076.06	2075.05	2074.98	33	0	VDLNVPLDDNFNITDDTR
			51	69	2080.2	2079.19	2079.14	24	1	YLMGHGSKVILSSHLGRPK
			59	69	1206.8	1205.79	1205.72	58	0	VILSSHLGRPK
			75	83	1072.71	1071.7	1071.64	46	0	YSLKPLVPR
			75	93	2140.34	2139.34	2139.27	32	1	YSLKPLVPRLSELLGVEVK
			84	93	1086.66	1085.65	1085.63	18	0	LSELLGVEVK
			106	122	1767.07	1766.06	1765.98	50	0	MVAALPDGGVLLLENVR
			137	155	2062.15	2061.14	2061.06	38	1	KLASLADLYVNDAFGTAHR
			138	155	1934.04	1933.04	1932.97	36	0	LASLADLYVNDAFGTAHR
			138	165	2885.57	2884.56	2884.45	38	1	LASLADLYVNDAFGTAHRAHASTEGVAK
			233	257	2610.45	2609.45	2609.35	34	1	AQGHAVGSSLVEEDKLDLATSLLEK
			262	284	2316.33	2315.32	2315.24	38	1	GVSLLLPSDVVVADKFAADANSK
			343	366	2272.3	2271.29	2271.23	26	1	LAELSGKGVTTIIGGGDSVAAVEK
75	chloroplast biotin carboxylase	ABP98813	12	25	1473.87	1472.86	1472.81	33	1	SVTSPPGLFLGRSR
			72	83	1310.89	1309.88	1309.783	75	1	ILVANRGEIAVR
			167	178	1342.81	1341.8	1341.704	70	0	INFIGPNPDSIR

			214	225	1370.86	1369.85	1369.743	80	0	LAHEIGFPVMIK	Oxidation (M)
			247	268	2323.32	2322.31	2322.186	54	1	LLQQAKSEAAAAFGNDGVYLEK	
			253	268	1641.89	1640.88	1640.768	67	0	SEAAAAFGNDGVYLEK	
			305	319	1636	1635	1634.888	67	0	LLEEAPSPALTPELR	
			305	320	1764.11	1763.11	1762.983	70	1	LLEEAPSPALTPELRK	
			349	359	1414.66	1413.66	1413.569	62	0	GSFYFMEMNTR	2 Oxidation (M)
			360	381	2565.43	2564.43	2564.316	43	0	IQVEHPVTEMISSVDLIEEQIR	
			360	381	2581.41	2580.4	2580.311	34	0	IQVEHPVTEMISSVDLIEEQIR	Oxidation (M)
			390	398	1163.73	1162.72	1162.635	71	1	YKQEDIVLR	
			399	405	858.412	857.405	857.3814	27	0	GHSIECR	
			406	421	1732.01	1731	1730.885	66	1	INAEDAFKGFRPGPGR	
			414	421	843.484	842.477	842.4511	30	0	GFRPGPGR	
			422	434	1393.85	1392.85	1392.74	77	0	ITSYLPSGGPFVR	
			456	463	955.623	954.616	954.5651	53	0	LIVWAPTR	
			456	465	1212.83	1211.82	1211.703	99	1	LIVWAPTREK	
			491	499	1133.7	1132.69	1132.613	72	0	LILDIEDFR	
77	chloroplast biotin carboxylase	ABP98813	72	83	1310.79	1309.79	1309.783	2	1	ILVANRGEIAVR	
			87	110	2655.32	2654.31	2654.32	-4	1	TAHEMGIPCVAVYSTIDKDALHVK	
			87	110	2671.37	2670.37	2670.315	19	1	TAHEMGIPCVAVY	Oxidation (M)

							STIDKDALHVK	
111	140	3160.73	3159.72	3159.612	34	0	LADESVCIGEAPSSQSYLLIPNVLSAAISR	
141	163	2732.27	2731.26	2731.202	22	0	NCTMLHPGYGFLSENAVFVEMCR	
167	178	1342.71	1341.7	1341.704	-3	0	INFIGPNPDSIR	
192	213	2183.13	2182.12	2182.112	5	0	NAGVPTVPGSDGLLQSTEEAIK	
214	225	1354.75	1353.74	1353.748	-2	0	LAHEIGFPVMIK	
214	225	1370.76	1369.75	1369.743	8	0	LAHEIGFPVMIK	Oxidation (M)
253	268	1641.79	1640.78	1640.768	6	0	SEAAAAFGNDGVYLEK	
285	294	1177.59	1176.59	1176.568	15	0	YGNVVHFGER	
285	300	1936.92	1935.91	1935.901	6	1	YGNVVHFGERDCSIQR	
305	319	1635.9	1634.89	1634.888	4	0	LLEEAPSPALTPELR	
305	320	1764.01	1763	1762.983	11	1	LLEEAPSPALTPELRK	
320	348	2911.64	2910.63	2910.48	52	1	KAMGDAAVAAAASIGYIGVGTVEFLLDER	Oxidation (M)
349	359	1382.59	1381.59	1381.58	5	0	GSFYFMEMNTR	
349	359	1398.6	1397.59	1397.574	13	0	GSFYFMEMNTR	Oxidation (M)
349	359	1414.6	1413.59	1413.569	13	0	GSFYFMEMNTR	2 Oxidation (M)
360	381	2581.33	2580.33	2580.311	6	0	IQVEHPVTEMISSVDLIEEQIR	Oxidation (M)

			390	398	1163.65	1162.65	1162.635	10	1	YKQEDIVLR
			414	421	843.463	842.456	842.4511	5	0	GFRPGPGR
			422	434	1393.76	1392.75	1392.74	9	0	ITSYLPSGGPFVR
			435	455	2372.14	2371.13	2371.104	12	0	MDSHVYSDYVVPPSYDSLLGK
			456	463	955.57	954.563	954.5651	-2	0	LIVWAPTR
			491	499	1133.63	1132.62	1132.613	9	0	LILDIEDFR
			503	520	2023.08	2022.07	2022.042	16	1	VDTAFIPKHEEELAAPQK
76	dihydrolipoamide dehydrogenase	FJ415193	116	130	1666.86	1665.85	1665.81	24	0	FSSVEIDLPAMMAQK
			159	178	2051.09	2050.08	2050.05	19	0	FISPSEVSVDTIEGGSTVVK
			238	260	2474.3	2473.29	2473.24	20	0	LGSEVTVVEFAPDIVPSMDAEIR
			292	316	2469.32	2468.32	2468.28	16	0	LTVEPAAGGDQTTLEADVVLVSAGR
			317	327	1105.61	1104.6	1104.58	18	0	SPFTAGLGLDK
			367	381	1594.79	1593.78	1593.73	31	0	AEEDGVACVEFIAGK
			422	429	951.53	950.52	950.5	31	0	FPFLANSR
			497	509	1459.76	1458.75	1458.72	27	0	EAAMATYDKPIHI
78	UGP2	FJ415165	9	22	1447.77	1446.76	1446.72	27	0	SAVAALSEISENEK
			23	31	1019.55	1018.55	1018.56	-9	0	NGFINLVSR
			32	44	1547.8	1546.79	1546.74	32	0	YLSGEAQHIEWSK
			45	70	2814.34	2813.33	2813.35	-7	0	IQTPTDEVVVPYDTLSPSPDDPAETK

			45	71	2942.42	2941.41	2941.44	-10	1	IQTPTDEVVVPYDTLSPSPDDPAETKK
			121	141	2438.16	2437.16	2437.14	8	0	YGCNVPLVLMNSFNTHDDTLK
			142	163	2653.27	2652.27	2652.29	-11	1	IVDKYSNSNIEIHTFNQSQYPR
			146	163	2198	2197	2197.02	-9	0	YSNSNIEIHTFNQSQYPR
			181	200	2161.01	2160	2159.97	13	0	DGWYPPGHGDVFPSLMNSGK
			228	236	1078.66	1077.66	1077.63	27	0	ILNHLVQNK
			228	246	2330.15	2329.14	2329.16	-4	1	ILNHLVQNKNEYCMEVTPK
			263	280	2108.11	2107.1	2107.09	4	0	VQLLEIAQVPDEHVNEFK
			325	337	1312.78	1311.77	1311.75	15	0	VLQLETAAGAAIR
			338	349	1385.77	1384.76	1384.73	28	0	FFDHAIGINVPR
			383	397	1613.86	1612.86	1612.81	31	0	ANPTNPSIELGPEFK
			383	398	1741.94	1740.94	1740.9	17	1	ANPTNPSIELGPEFKK
			408	419	1314.78	1313.78	1313.74	22	0	SIPSIIELDSLK
			420	433	1461.68	1460.67	1460.8	-88	0	VTGDVWFGAGIVLK
79	UGP1	FJ415164	9	22	1526.77	1525.77	1525.77	-6	0	SHLATLSQIGENEK
			23	31	1019.54	1018.53	1018.56	-19	0	NGFINLVSR

			45	71	2942.47	2941.47	2941.48	-3	1	IQTPTDEVVVPYDTLAPLSDDPAETKK	
			102	119	2106.05	2105.05	2105.12	-33	0	NGFTFLDLIVQQIENLNK	
			121	141	2438.1	2437.09	2437.14	-20	0	YGCNVPLVLMNSFNTHDDTLK	
			121	141	2454.08	2453.08	2453.14	-24	0	YGCNVPLVLMNSFNTHDDTLK	Oxidation (M)
			146	163	2181.01	2180	2180.04	-18	0	YANSNIQIHTFNQSQYPR	
			164	175	1423.69	1422.68	1422.69	0	0	LVAEDFTPFPCK	
			210	227	1938.91	1937.91	1937.97	-36	0	EYAFVANSDNLGAIVDLK	
			235	246	1512.66	1511.66	1511.67	-13	1	NKNEYCMEVTPK	
			253	262	1024.5	1023.49	1023.52	-29	0	GGTLISYEGK	
			263	280	2050.06	2049.05	2049.09	-19	0	VQLLEIAQVPDAHVNEFK	
			311	318	957.49	956.48	956.5	-20	0	MEIIPNPK	Oxidation (M)
			325	337	1312.76	1311.76	1311.75	0	0	VLQLETAAGAAIR	
			338	349	1399.73	1398.73	1398.74	-7	0	FFEHAIGINVPR	
			357	378	2412.21	2411.21	2411.26	-20	0	ATSDLLLVQSDLYTLVDGFVSR	
			446	457	1339.73	1338.73	1338.74	-7	0	LEIPDGIVIENK	
80	UGP1	FJ415164	9	22	1526.9	1525.89	1525.77	78	0	SHLATLSQIGENEK	
			23	31	1019.62	1018.62	1018.56	58	0	NGFINLVSR	
			32	44	1547.88	1546.88	1546.74	90	0	YLSGEAQHIEWSK	

81	95	1463.81	1462.8	1462.69	75	0	LNGGLGTTMGCTGPK	
96	119	2789.79	2788.79	2788.51	100	1	SVIEVRNGFTFLDLIVQQIENLNK	
102	120	2234.29	2233.29	2233.21	35	1	NGFTFLDLIVQQIENLNKK	
121	141	2438.31	2437.3	2437.14	65	0	YGCNVPLVLMNSFNTHDDTLK	
121	141	2454.31	2453.3	2453.14	69	0	YGCNVPLVLMNSFNTHDDTLK	Oxidation (M)
142	163	2636.52	2635.51	2635.31	75	1	IVDKYANSNIQIHTFNQSQYPR	
146	163	2181.19	2180.19	2180.04	68	0	YANSNIQIHTFNQSQYPR	
164	175	1423.82	1422.81	1422.69	84	0	LVAEDFTPFPCK	
181	200	2145.13	2144.12	2143.98	65	0	DGWYPPGHGDVFPALMNSGK	
181	200	2161.13	2160.12	2159.97	64	0	DGWYPPGHGDVFPALMNSGK	Oxidation (M)
201	227	2942.68	2941.67	2941.51	54	1	LATFLSQDKEYAFVANSDNLGAIVDLK	
235	246	1512.82	1511.81	1511.67	92	1	NKNEYCMEVTPK	
263	280	2050.23	2049.22	2049.09	63	0	VQLLEIAQVPDAHVNEFK	
287	301	1774.06	1773.05	1772.96	56	0	IFNTNNLWLNLNAVK	
325	337	1312.88	1311.87	1311.75	91	0	VLQLETAAGAAIR	

			338	349	1399.87	1398.87	1398.74	92	0	FFEHAIGINVPR
			357	378	2412.44	2411.43	2411.26	70	0	ATSDLLLVQSDLYTLVDGFVSR
			383	397	1699.96	1698.96	1698.81	88	0	ENPENPSIELGPEFK
			383	398	1828.05	1827.05	1826.9	76	1	ENPENPSIELGPEFKK
81	UGD1	FJ415166	23	37	1668.94	1667.93	1667.86	47	0	CPDIEVAVVDISVPR
			38	58	2285.24	2284.24	2284.17	26	0	IAAWNSDQLPIYEPGLDGVVK
			64	73	1199.65	1198.64	1198.59	41	0	NLFFSTDVEK
			77	90	1519.87	1518.86	1518.79	46	0	EADIVFVSVNTPTK
			99	110	1353.72	1352.72	1352.64	59	0	AADLTYWESAAR
			146	172	3033.67	3032.66	3032.56	32	1	GIKFQILSNPEFLAEGTAIQDLFNPDR
			149	172	2735.46	2734.45	2734.36	32	0	FQILSNPEFLAEGTAIQDLFNPDR
			186	202	2025.12	2024.11	2024.05	34	1	AVQALKEVYAHWVPEER
			192	202	1414.75	1413.75	1413.67	56	0	EVYAHWVPEER
			203	215	1475.87	1474.86	1474.8	40	0	ILTTNLWSAELSK
			203	225	2531.46	2530.45	2530.39	23	1	ILTTNLWSAELSKLAANAFLAQR
			216	225	1074.66	1073.65	1073.6	46	0	LAANAFLAQR
			260	274	1618.86	1617.85	1617.76	55	0	FLNASVGFGGSCFQK

			275	300	3166.74	3165.73	3165.59	44	1	DILNLVYICECNGLPEVAEYWKQVIK
			326	334	979.61	978.6	978.59	10	0	IAILGFAFK
			326	335	1107.73	1106.73	1106.69	36	1	IAILGFAFKK
			359	373	1790.97	1789.96	1789.88	44	0	LSIYDPQVTEDQVQR
			374	397	2837.48	2836.47	2836.37	38	1	DLSMNKFDWDHPLHLQPMSPTTVK
			411	425	1833.91	1832.9	1832.84	32	0	DAHGICILTEWDEFK
			411	426	1962.01	1961	1960.94	35	1	DAHGICILTEWDEFKK
			432	446	1800.95	1799.94	1799.87	38	0	IYDNMQKPAFVFDGR
			447	455	1043.57	1042.56	1042.54	19	0	NIVNADELR
			456	473	2075.22	2074.22	2074.15	33	0	EIGFIVYSIGKPLDPWLK
83	UGD1	FJ415166	3	22	2050.97	2049.96	2050.04	-39	0	ICCIGAGYVGGPTMAVIALK
			23	37	1668.82	1667.81	1667.86	-23	0	CPDIEVAVVDISVPR
			38	58	2285.11	2284.1	2284.17	-35	0	IAAWNSDQLPIYEPGLDGVVK
			64	73	1199.56	1198.55	1198.59	-25	0	NLFFSTDVEK
			99	110	1353.62	1352.61	1352.64	-22	0	AADLTYWESAAR
			149	172	2735.32	2734.31	2734.36	-18	0	FQILSNPEFLAEGTAIQDLFNPDR
			192	202	1414.66	1413.65	1413.67	-14	0	EVYAHWVPEER

			203	215	1475.78	1474.77	1474.8	-20	0	ILTTNLWSAELSK
			216	225	1074.58	1073.57	1073.6	-27	0	LAANAFLAQR
			260	274	1618.73	1617.72	1617.76	-24	0	FLNASVGFGGSCFQK
			275	296	2698.22	2697.21	2697.28	-25	0	DILNLVYICECNGLPEVAEYWK
			326	334	979.56	978.55	978.59	-40	0	IAILGFAFK
			359	373	1790.85	1789.84	1789.88	-27	0	LSIYDPQVTEDQVQR
			380	397	2148.98	2147.98	2148.05	-32	0	FDWDHPLHLQPMSPTTVK
			411	425	1833.79	1832.78	1832.84	-32	0	DAHGICILTEWDEFK
			411	426	1961.88	1960.88	1960.94	-30	1	DAHGICILTEWDEFKK
			432	446	1800.83	1799.82	1799.87	-22	0	IYDNMQKPAFVFDGR
			447	455	1043.53	1042.52	1042.54	-19	0	NIVNADELR
82	myo-inositol-1-phosphate synthase	FJ415168	1	7	928.46	927.45	927.45	0	0	MFIENFK
			1	14	1681.85	1680.84	1680.85	-5	1	MFIENFKVESPNVK
			48	54	914.48	913.47	913.49	-21	1	TVKYEFK
			51	61	1376.72	1375.71	1375.71	0	1	YEFKTDIHVPK
			62	85	2315.17	2314.16	2314.21	-21	0	LGVMLVGWGGNNGSTLTGGVIANK
			86	93	891.44	890.43	890.45	-22	0	EGISWATK
			94	112	2127.07	2126.06	2126.08	-9	1	DKVQQANYFGSL

							TQASTIR
96	112	1883.96	1882.95	1882.95	0	0	VQQANYFGSLTQASTIR
113	126	1587.76	1586.75	1586.76	-6	0	IGSYNGEEIYAPFK
156	165	1176.65	1175.64	1175.65	-8	1	AKVFDIDLQK
166	193	3207.49	3206.49	3206.55	-21	0	QLRPYMESMVPLPGIYDPDFIAANQGER
204	214	1327.74	1326.73	1326.75	-15	1	EQVQQVIKDIK
225	235	1287.71	1286.7	1286.7	0	0	VVVLWTANTER
299	308	1138.51	1137.5	1137.51	-8	0	NCLIGGDDFK
299	313	1639.79	1638.78	1638.77	6	1	NCLIGGDDFKSGQTK
388	396	1027.5	1026.49	1026.5	-9	0	YVPYVGDSK
388	397	1183.61	1182.6	1182.6	0	1	YVPYVGDSKR
397	411	1734.78	1733.77	1733.78	0	1	RAMDEYTSEIFMGGK
398	411	1578.68	1577.68	1577.67	0	0	AMDEYTSEIFMGGK
412	442	3417.97	3416.96	3416.86	29	0	NTIVLHNTCEDSLLAAPIILDLVLLAELSTR
453	468	1860.97	1859.97	1859.99	-16	0	FHSFHPVATILSYLTK
469	484	1559.91	1558.9	1558.91	-6	0	APLVPPGTPVVNALSK
487	494	959.51	958.5	958.53	-31	0	AMLENILR
495	510	1762.91	1761.9	1761.9	0	0	ASIGLAPENNMILE

										YK	
84	acyltransferase-like protein	AAL67994	40	52	1423.65	1422.64	1422.626	12	1	NDGGGEFEDKVEK	
			59	70	1381.75	1380.74	1380.729	10	0	VVLEEFYQLGGK	
			71	80	1087.59	1086.58	1086.567	15	1	LGKDDDGVLR	
			213	221	1012.5	1011.49	1011.492	1	0	QGQPAPQMR	
			213	221	1028.52	1027.51	1027.487	25	0	QGQPAPQMR	Oxidation (M)
			227	236	1107.62	1106.61	1106.597	14	1	FSEAAVDKIK	
			239	264	2855.43	2854.42	2854.44	-6	0	VNSTPPPSDGSKPFSTFQSLAVHIWR	
			271	287	2074.99	2073.98	2073.983	0	0	NLKPEDYTVFTVFADCR	
			271	288	2203.08	2202.07	2202.078	-2	1	NLKPEDYTVFTVFADCRK	
			330	337	870.45	869.443	869.4243	21	0	AIESHDAK	
			352	370	2052.07	2051.06	2051.026	18	1	IFQFKDAGVNCVAVGSSPR	
			357	370	1388.67	1387.66	1387.651	8	0	DAGVNCVAVGSSPR	
			371	387	1983.02	1982.01	1982.041	-14	1	FKVYEVDFGWGKPVGVR	
			373	387	1707.87	1706.86	1706.878	-9	0	VYEVDFGWGKPVGVR	
			388	404	1935.89	1934.88	1934.895	-6	1	SGSNNRFDGMVYLYQGK	
			388	404	1951.89	1950.88	1950.889	-3	1	SGSNNRFDGMVYLYQGK	Oxidation (M)
			394	404	1320.65	1319.64	1319.622	16	0	FDGMVYLYQGK	

			394	404	1336.63	1335.62	1335.617	4	0	FDGMVYLYQGK	Oxidation (M)
			409	423	1694.8	1693.79	1693.79	1	0	SIDVEITMEAQAMEK	
			409	423	1726.81	1725.8	1725.78	13	0	SIDVEITMEAQAMEK	2 Oxidation (M)
			409	426	2065.03	2064.02	2064.012	5	1	SIDVEITMEAQAMEKLEK	
			409	426	2097.01	2096	2096.002	0	1	SIDVEITMEAQAMEKLEK	2 Oxidation (M)
85	acyltransferase-like protein	AAL67994	59	70	1381.77	1380.76	1380.729	24	0	VVLEEFYQLGGK	
			116	140	2814.56	2813.55	2813.617	-23	0	ELIPFNGVLNLEGLHRPLLSIQLTK	
			213	221	1012.53	1011.52	1011.492	30	0	QGQPAPQMR	
			213	221	1028.54	1027.53	1027.487	45	0	QGQPAPQMR	Oxidation (M)
			227	236	1107.62	1106.61	1106.597	14	1	FSEAAVDKIK	
			237	264	3098.85	3097.84	3097.573	87	1	SRVNSTPPPSDGSKPFSTFQSLAVHIWR	
			239	264	2855.4	2854.39	2854.44	-17	0	VNSTPPPSDGSKPFSTFQSLAVHIWR	
			271	287	2074.97	2073.96	2073.983	-10	0	NLKPEDYTVFTVFADCR	
			271	288	2203.08	2202.07	2202.078	-2	1	NLKPEDYTVFTVFADCRK	
			357	370	1388.7	1387.69	1387.651	30	0	DAGVNCVAVGSSPR	
			371	387	1983.03	1982.02	1982.041	-9	1	FKVYEVDFGWGK	

										PVGVR	
			373	387	1707.85	1706.84	1706.878	-21	0	VYEVDFGWGKPVGVR	
			388	404	1935.88	1934.87	1934.895	-11	1	SGSNNRFDGMVYLYQGK	
			388	404	1951.89	1950.88	1950.889	-3	1	SGSNNRFDGMVYLYQGK	Oxidation (M)
			405	423	2052	2050.99	2050.966	13	1	SGGRSIDVEITMEAQAMEK	
86	pyruvate decarboxylase	FJ415201	111	127	1951.05	1950.04	1949.97	35	0	GDFQELDQIEAVKPFSK	
			137	144	959.51	958.5	958.45	52	0	EIPDCVAR	
			236	247	1258.75	1257.74	1257.68	47	0	TGIPFLPTPMGK	
			248	262	1538.83	1537.82	1537.75	45	0	GLVNDDHELAASAAR	
			269	278	1059.62	1058.61	1058.55	56	0	CDVALVVGAR	
			297	308	1420.83	1419.82	1419.75	49	0	FILVDVSEEEIK	
			381	405	2411.31	2410.3	2410.22	33	0	DAILGVGSPAPVVVSEGANTMDVGR	
			468	485	1875.08	1874.08	1874	37	0	LPVVVIVFNNGGVYGGDR	
			497	520	2461.3	2460.29	2460.2	40	0	DDPAPTSFVPGAAYHTLIEAFGGK	
			532	541	1054.57	1053.56	1053.51	47	0	SALSESFSAR	
			542	560	1982.18	1981.18	1981.1	40	0	KPVVINVIIDPFAGAESGR	
87	glycine-rich RNA-binding protein	FJ415184	10	22	1467.69	1466.68	1466.66	13	0	CFVGGLAWATDDR	

			39	47	1073.58	1072.57	1072.56	9	1	IINDRETGR	
			50	57	930.5	929.5	929.48	21	0	GFGFVTFR	
			50	60	1302.67	1301.66	1301.64	15	1	GFGFVTFRDEK	
			64	77	1489.69	1488.68	1488.66	13	0	DAIEGMNGQNLDGR	
			64	77	1505.68	1504.67	1504.66	13	0	DAIEGMNGQNLDGR	Oxidation (M)
			78	87	1131.6	1130.59	1130.57	17	0	NITVNEAQSR	
			89	105	1400.63	1399.62	1399.59	21	0	SGGGGGGFGGGNGGYSR	
			116	124	907.46	906.46	906.44	11	1	QGGYGGGRR	
			144	154	1110.52	1109.51	1109.48	27	1	REGGYGDGGSR	
			145	154	954.4	953.4	953.38	10	0	EGGYGDGGSR	
			158	167	990.44	989.44	989.43	0	0	GGGASEGNWR	
			158	168	1077.48	1076.48	1076.46	9	1	GGGASEGNWRS	
89	manganese superoxide dismutase	AAC78469	26	36	1418.81	1417.81	1417.674	93	0	HHQTYITNYNK	
			26	47	2679.56	2678.55	2678.356	73	1	HHQTYITNYNKALEQLHEAIQK	
			37	47	1279.82	1278.81	1278.693	92	0	ALEQLHEAIQK	
			37	55	2053.25	2052.25	2052.085	78	1	ALEQLHEAIQKGDSSTVVK	
			56	75	2240.32	2239.32	2239.165	68	1	LQSAIKFNGGGHVNHSIFWK	
			62	75	1599.9	1598.89	1598.774	74	0	FNGGGHVNHSIFWK	
			62	81	2264.3	2263.29	2263.176	52	1	FNGGGHVNHSIF	

										WKNLAPIR	
			76	89	1434.89	1433.89	1433.763	86	1	NLAPIREGGGEPPK	
			82	109	2924.73	2923.72	2923.472	85	1	EGGGEPPKASLGWAIDTHFGSLESLIQK	
			133	148	1796.17	1795.16	1795.009	83	1	KLVIETTPNQDPLVTK	
			134	148	1668.07	1667.06	1666.914	89	0	LVIETTPNQDPLVTK	
			149	170	2611.48	2610.47	2610.364	41	0	GPHLVPLLGIDVWEHAYYLQYK	
			149	178	3597.08	3596.07	3595.898	49	1	GPHLVPLLGIDVWEHAYYLQYKNVRPDYLK	
			171	182	1545.97	1544.96	1544.846	75	1	NVRPDYLKNIWK	
			179	187	1200.78	1199.77	1199.682	77	1	NIWKVINWK	
			188	198	1348.7	1347.69	1347.565	94	1	YASEVYEKECA	
91	glyceraldehyde-3-phosphate dehydrogenase	FJ415182	6	13	833.52	832.52	832.46	72	0	IGINGFGR	
			49	57	1119.61	1118.6	1118.51	80	0	YDSVHGQWK	
			68	82	1677.06	1676.06	1675.97	53	0	TLLFGEKPVTVFGIR	
			121	140	2165.19	2164.19	2164.09	46	1	VIISAPSKDAPMFVMGVNEK	2 Oxidation (M)
			129	140	1337.72	1336.71	1336.62	74	0	DAPMFVMGVNEK	
			129	140	1353.72	1352.71	1352.61	73	0	DAPMFVMGVNEK	Oxidation (M)

			141	164	2744.42	2743.41	2743.28	47	0	DYKPEYDIISNASCTTNCLAPLAK	
			165	188	2655.51	2654.51	2654.41	37	1	VIHDKFGIIEGLMTTVHSITATQK	Oxidation (M)
			189	199	1307.71	1306.71	1306.6	84	1	TVDGPSMKDWR	Oxidation (M)
			203	217	1434.84	1433.83	1433.75	55	0	AASFNIIPSSTGAAK	
			222	236	1603.93	1602.92	1602.89	18	1	VLPALNGKLTGMAFR	Oxidation (M)
			237	250	1498.92	1497.91	1497.84	46	0	VPTVDVSVVDLTVR	
			274	293	2159.11	2158.1	2158.01	41	0	GILGYTDEDLVSTDFVGDSR	
			301	311	1147.69	1146.68	1146.6	69	0	AGIALNENFAK	
			312	325	1775.9	1774.89	1774.8	50	0	LVSWYDNEWGYSTR	
92	isocitrate dehydrogenase	FJ415198	8	22	1676.78	1675.78	1675.75	11	0	VANPIVEMDGDEMTR	
			8	22	1692.78	1691.77	1691.75	11	0	VANPIVEMDGDEMTR	Oxidation (M)
			8	22	1708.77	1707.76	1707.74	11	0	VANPIVEMDGDEMTR	2 Oxidation (M)
			32	42	1299.82	1298.81	1298.78	23	0	LILPFVELDIK	
			43	51	1117.6	1116.59	1116.57	17	0	YFDLGLPHR	
			52	68	1806.92	1805.91	1805.89	11	1	DATDDKVTIESAEATLK	
			103	111	1033.59	1032.59	1032.57	19	0	NILNGTVFR	
			103	117	1773.98	1772.98	1772.96	11	1	NILNGTVFREPIIC	

							K	
135	142	993.47	992.46	992.45	10	0	HAFGDQYR	
156	166	1202.66	1201.65	1201.63	16	0	LVFVPEGQGEK	
167	192	2945.4	2944.39	2944.31	30	0	TEYEVFNFTGEGGVSLAMYNTDESIR	Oxidation (M)
193	205	1431.68	1430.67	1430.65	13	0	AFAEASMNTAYQK	
207	214	1007.57	1006.56	1006.55	9	0	WPLYLSTK	
225	238	1816.92	1815.91	1815.88	16	1	FKDIFQEVYEANWK	
227	238	1541.78	1540.77	1540.72	32	0	DIFQEVYEANWK	
239	251	1609.8	1608.8	1608.77	18	1	SKYEAAGIWYEHR	
241	251	1394.68	1393.67	1393.64	21	0	YEAAGIWYEHR	
252	262	1251.69	1250.68	1250.66	15	0	LIDDMVAYALK	
252	262	1267.69	1266.68	1266.65	23	0	LIDDMVAYALK	Oxidation (M)
263	272	1156.53	1155.52	1155.5	17	0	SEGGYVWACK	
304	316	1355.72	1354.71	1354.68	22	0	TIEAEAAHGTVTR	
324	340	1797.91	1796.9	1796.87	16	0	GGETSTNSIASIFAWTR	
354	360	877.52	876.51	876.5	22	0	LLDFIEK	
354	373	2207.2	2206.2	2206.16	18	1	LLDFIEKLEAACIATVESGK	
374	386	1426.67	1425.67	1425.8	-91	1	MTKDLALIIHGSK	
377	386	1066.65	1065.64	1065.62	28	0	DLALIIHGSK	
390	407	2055.08	2054.07	2054.02	24	1	DKYLNTEEFIDAVAADLK	
392	407	1811.93	1810.92	1810.9	11	0	YLNTEEFIDAVAADLK	

93	isocitrate dehydrogenase	FJ415198	8	22	1676.79	1675.78	1675.75	17	0	VANPIVEMDGDEMTR	
			8	22	1692.79	1691.78	1691.75	17	0	VANPIVEMDGDEMTR	Oxidation (M)
			32	42	1299.83	1298.83	1298.78	30	0	LILPFVELDIK	
			43	51	1117.62	1116.61	1116.57	35	0	YFDLGLPHR	
			52	68	1806.92	1805.92	1805.89	16	1	DATDDKVTIESAEATLK	
			58	74	1849.89	1848.88	1849.02	-75	1	VTIESAEATLKYNVAIK	
			96	111	1758.96	1757.95	1757.95	0	1	SPNGTIRNILNGTVFR	
			103	111	1033.62	1032.62	1032.57	38	0	NILNGTVFR	
			118	134	1935.07	1934.06	1934.06	5	0	NVPQLVPGWTKPICIGR	
			135	142	993.5	992.49	992.45	40	0	HAFGDQYR	
			156	166	1202.67	1201.67	1201.63	24	0	LVFVPEGQGEK	
			167	192	2929.28	2928.27	2928.31	-13	0	TEYEVFNFTGEGGVSLAMYNTDESIR	
			167	192	2945.29	2944.28	2944.31	-10	0	TEYEVFNFTGEGGVSLAMYNTDESIR	Oxidation (M)
			207	214	1007.59	1006.58	1006.55	39	0	WPLYLSTK	
			227	238	1541.77	1540.76	1540.72	25	0	DIFQEVYEANWK	
			239	251	1609.82	1608.81	1608.77	24	1	SKYEAAGIWYEHR	
			241	251	1394.69	1393.68	1393.64	28	0	YEAAGIWYEHR	
			263	272	1156.55	1155.55	1155.5	34	0	SEGGYVWACK	
			304	316	1355.72	1354.72	1354.68	22	0	TIEAEAAHGTVTR	
			324	340	1797.89	1796.89	1796.87	11	0	GGETSTNSIASIFA	

										WTR	
			374	386	1426.68	1425.67	1425.8	-91	1	MTKDLALIIHGSK	
			377	386	1066.67	1065.67	1065.62	46	0	DLALIIHGSK	
			392	407	1811.94	1810.93	1810.9	16	0	YLNTEEFIDAVAA DLK	
94	eukaryotic translation initiation factor 5A	GU295062	19	29	1262.77	1261.76	1261.68	63	1	TYPQQAGTIRK	
			42	52	1134.65	1133.64	1133.63	8	1	VVEVSTSKTGK	
			58	69	1407.83	1406.82	1406.7	85	0	CHFVGIDIFTAK	
			58	70	1535.91	1534.9	1534.8	65	1	CHFVGIDIFTAKK	
			70	88	2216.21	2215.2	2215.08	54	1	KLEDIVPSSHNCD VPHVNR	
			71	88	2088.08	2087.07	2086.99	43	0	LEDIVPSSHNCDV PHVNR	
			129	154	2816.47	2815.46	2815.31	56	1	DGFAEGKDLVVSV MSAMGEEQICALK	2 Oxidation (M)
			136	154	2112.09	2111.09	2110.99	42	0	DLVVSVMSAMGE EQICALK	2 Oxidation (M)
			136	159	2622.4	2621.39	2621.27	41	1	DLVVSVMSAMGE EQICALKDIGPK	2 Oxidation (M)
95	chalcone isomerase	GU295063	42	61	2314.26	2313.25	2313.22	12	0	FTAIGVYLEPEVV GHLQQWK	
			62	85	2588.33	2587.32	2587.28	15	0	GKPGNVLAEDDD FFEALINAPVEK	
			94	109	1763.98	1762.97	1762.92	28	1	EIKGSQYGVQLES AVR	
			97	109	1393.76	1392.75	1392.7	35	0	GSQYGVQLESAV	

										R
			97	111	1664.89	1663.88	1663.83	30	1	GSQYGVQLESAVRDR
			112	128	2010.93	2009.92	2009.9	14	1	LAADDKYEEEEEEALEK
			129	136	983.51	982.51	982.51	0	0	VVEFFQSK
			141	168	3027.52	3026.51	3026.45	19	1	DSVITYHFPANSATAEIAFTTEGKEEAK
			183	189	852.41	851.4	851.43	-35	0	WYLGGTR
			190	209	2023.07	2022.06	2022.03	14	0	GVSATTISSLANTLSAELCK
96	Triosephosphate isomerase	GU295064	44	57	1433.76	1432.75	1432.73	13	1	KPCRAVTAMAGSGK
			66	75	1123.59	1122.58	1122.53	44	1	CNGTKDSITK
			123	136	1435.78	1434.77	1434.74	20	0	GGAFTGEISVEQLK
			123	141	2009.05	2008.04	2007.99	24	1	GGAFTGEISVEQLKDIGCK
			142	150	1096.63	1095.62	1095.58	36	0	WVILGHSER
			142	151	1252.74	1251.73	1251.68	39	1	WVILGHSERR
			152	163	1371.73	1370.72	1370.68	29	0	HIIGEDDQFIGK
			152	164	1499.83	1498.82	1498.78	26	1	HIIGEDDQFIGKK
			165	186	2361.22	2360.21	2360.2	4	0	AAYALNEGLGVIACIGELLEER
			187	197	1329.67	1328.66	1328.62	30	1	EAGKTFDVCFR
			191	197	944.43	943.42	943.42	0	0	TFDVCFR
			227	245	2156.09	2155.08	2155.12	-18	0	VATPQQAQEVHV

										AVHDWLK	
			258	274	1752.88	1751.88	1751.85	17	0	IIYGGSVNGSNCAELAK	
			258	289	3282.57	3281.56	3281.62	-18	1	IIYGGSVNGSNCAELAKQEDIDGFLVGGASLK	
			290	303	1449.81	1448.8	1448.75	34	0	GPEFATIVNSVTSK	
			290	304	1577.79	1576.78	1576.85	-38	1	GPEFATIVNSVTSKK	
97	thiazole biosynthetic enzyme	GU295068	2	17	1682.87	1681.86	1681.87	-5	1	ASSIATTLTSSSKLCR	
			66	76	1290.72	1289.71	1289.7	7	1	FDPIKESIVSR	
			81	112	3521.72	3520.72	3520.59	36	1	RYMMDMITYADTDVVVVGAGSAGLSCAYELSK	3 Oxidation (M)
			82	112	3365.56	3364.55	3364.49	17	0	YMMDMITYADTDVVVVGAGSAGLSCAYELSK	3 Oxidation (M)
			150	168	2317.12	2316.11	2316.1	4	0	FLDELAIEYDEQDDYVVIK	
			169	180	1322.7	1321.69	1321.67	15	0	HAALFTSTIMSK	Oxidation (M)
			181	188	910.56	909.55	909.58	-32	0	LLARPNVK	
			189	201	1402.81	1401.8	1401.79	14	0	LFNAVAAEDLIVK	
			189	204	1744.97	1743.96	1743.95	5	1	LFNAVAAEDLIVKEGR	
			234	251	1773.9	1772.89	1772.85	22	0	VVVSSCGHDGPFGATGVK	

			234	252	1929.98	1928.97	1928.95	10	1	VVVSSCGHDGPFGATGVKR	
			253	266	1475.79	1474.78	1474.79	-6	1	LKSIGMIDSVPGMK	
			267	279	1434.73	1433.72	1433.68	27	0	ALDMNTAEDAIVR	Oxidation (M)
			283	303	2216.08	2215.07	2215.09	-4	0	EIVPGMIVTGMEVAEIDGSPR	Oxidation (M)
			283	303	2232.09	2231.08	2231.08	0	0	EIVPGMIVTGMEVAEIDGSPR	2 Oxidation (M)
			304	317	1503.7	1502.69	1502.66	19	0	MGPTFGAMMISGQK	3 Oxidation (M)
			325	357	3252.68	3251.67	3251.62	15	0	SLGLPNAIDGTYVGSIHPELILAAADSAETADA	
98	transaldolase	GU295065	109	129	2305.08	2304.07	2304.04	17	0	NAVDMALADSTCSPLDNPELR	Oxidation (M)
			161	170	1158.65	1157.65	1157.62	25	0	LAYDTHGIIR	
			161	171	1314.78	1313.77	1313.72	38	1	LAYDTHGIIRR	
			171	177	908.53	907.52	907.54	-11	1	RVHDLLR	
			178	188	1301.72	1300.71	1300.67	38	0	LYDEIAVPPER	
			193	204	1344.72	1343.72	1343.68	22	0	IPSTWQGIEASR	
			248	261	1509.78	1508.77	1508.72	33	0	SHSGDPEIEAAIQR	
			296	311	1777.07	1776.06	1776.01	28	0	DIFSLLGVDYIIAPLK	
			341	350	1216.61	1215.61	1215.57	32	0	YDFTAEELTK	
			351	380	3091.55	3090.54	3090.53	3	0	WDQLSLASAMGPASVELLAAGLDGY	Oxidation (M)

										VNQAK
100	transaldolase	GU295065	2	19	1862.1	1861.09	1861.02	37	1	SVTLKSPPSSFLSSSLPK
			161	170	1158.67	1157.66	1157.62	34	0	LAYDTHGIIR
			161	171	1314.79	1313.78	1313.72	45	1	LAYDTHGIIRR
			171	177	908.53	907.52	907.54	-11	1	RVHDLLR
			178	188	1301.74	1300.73	1300.67	53	0	LYDEIAVPPER
			189	204	1846.11	1845.1	1845.01	48	1	LLFKIPSTWQGIEASR
			193	204	1344.74	1343.73	1343.68	37	0	IPSTWQGIEASR
			248	261	1509.8	1508.79	1508.72	46	0	SHSGDPEIEAAIQR
			296	311	1777.06	1776.05	1776.01	28	0	DIFSLLGVDYIIAPLK
			327	332	859.4	858.39	858.4	-11	1	YSYDRR
			332	340	985.57	984.56	984.55	20	1	RLSPQSAAR
			341	350	1216.66	1215.65	1215.57	74	0	YDFTAEELTK
99	U2 small nuclear ribonucleoprotein A	GU295066	2	11	1186.74	1185.73	1185.71	16	1	VKLTADLIWK
			12	20	1133.59	1132.58	1132.55	26	0	CPHFFNALK
			12	22	1418.78	1417.77	1417.69	56	1	CPHFFNALKER
			31	56	2862.47	2861.46	2861.42	13	0	IAVIENLGATEDQFDTIDLSDNEIVK
			57	64	1009.55	1008.54	1008.53	9	0	LDNFPYLK
			57	65	1165.66	1164.65	1164.63	17	1	LDNFPYLKR
			65	75	1283.8	1282.79	1282.75	38	1	RLGTLLINNNR
			66	75	1127.69	1126.68	1126.65	35	0	LGTLLINNNR
			79	99	2389.34	2388.33	2388.29	16	0	INPNIGEFLPNLHT

										LVLTNNR	
			100	114	1637	1635.99	1635.94	30	0	LVNLVEIDPLSSLPK	
			115	127	1518.9	1517.89	1517.85	32	0	LQFLSLLDNNITK	
			154	165	1406.77	1405.76	1405.72	28	1	ERLEAENLFASK	
			156	165	1121.59	1120.58	1120.58	8	0	LEAENLFASK	
			183	198	1830.88	1829.87	1829.84	21	0	EVPNVSEVAEEEQMPK	Oxidation (M)
			199	211	1378.87	1377.86	1377.82	29	0	VVAPTPEQILAIK	
			212	225	1500.84	1499.83	1499.79	26	0	AAIVNSQTLEEVAR	
			212	228	1871.06	1870.05	1870.02	21	1	AAIVNSQTLEEVARLEK	
			229	250	2237.2	2236.19	2236.17	8	1	ALQTGQLPADLKIPGDDTNAAK	
101	chalcone synthase	ABS52573	69	94	3181.52	3180.51	3180.445	21	1	YMYLTEEILKENPNVCEYMAPSLDAR	2 Oxidation (M)
			124	146	2570.27	2569.26	2569.219	15	0	ITHLVFCTTSGVDMPGADYQLTK	Oxidation (M)
			147	155	982.617	981.61	981.6335	-24	0	LLGLRPSVK	
			156	172	2019.96	2018.95	2018.949	1	1	RLMMYQQGCFAGGTVLR	2 Oxidation (M)
			157	172	1863.88	1862.88	1862.848	15	0	LMMYQQGCFAGGTVLR	2 Oxidation (M)
			176	185	1087.55	1086.54	1086.542	-1	1	DLAENNKGAR	
			186	199	1593.9	1592.89	1592.86	21	0	VLVVCSEITAVTFR	
			260	269	1156.68	1155.67	1155.665	6	0	EVGLTFHLLK	

			260	277	1966.14	1965.13	1965.13	-1	1	EVGLTFHLLKDVPGLISK	
			329	350	2587.24	2586.24	2586.192	17	0	HVLSEYGNMSSACVLFILDEMR	Oxidation (M)
			329	350	2603.2	2602.19	2602.187	2	0	HVLSEYGNMSSACVLFILDEMR	2 Oxidation (M)
102	protein disulfide isomerase	ABO41843	48	64	2179.04	2178.03	2177.982	22	0	HDFIVLEFYAPWCGHCK	
			65	72	986.49	985.483	985.4869	-4	0	HLAPEYEK	
			80	88	1037.58	1036.58	1036.571	6	0	HDPPIFLAK	
			89	106	1995.97	1994.96	1994.907	26	1	VDADDEANKDLASQYDVK	
			129	138	1136.61	1135.6	1135.576	22	0	EADGIVEYLK	
			129	139	1264.69	1263.68	1263.671	6	1	EADGIVEYLKK	
			150	162	1461.77	1460.77	1460.736	21	1	LTEDASNLIDDKK	
			172	186	1753.81	1752.8	1752.755	24	0	FSGEEFESYMALAEK	Oxidation (M)
			187	200	1637.84	1636.83	1636.785	31	1	LRSDYDFGHTLDAK	
			189	200	1368.64	1367.63	1367.599	26	0	SDYDFGHTLDAK	
			205	215	1099.63	1098.62	1098.603	13	0	GESSVVGPLVR	
			216	228	1596.91	1595.9	1595.86	25	0	LFKPFDELVVDFK	
			229	237	1076.58	1075.57	1075.555	13	0	DFKPEALEK	
			238	262	2815.45	2814.45	2814.423	8	0	FIEESSIPLVTLFNNDPSNHPFVAK	
			271	288	1961.01	1960	1959.95	24	0	AMLFADLSTEGFDSLLSK	Oxidation (M)
			289	297	1185.61	1184.61	1184.583	20	1	YREVAEQYK	

			379	391	1480.81	1479.8	1479.764	27	0	VVVADTLQDMVFK	Oxidation (M)
			395	409	1893.91	1892.9	1892.87	16	0	NVLLEFYAPWCGHCK	
			410	424	1724.99	1723.98	1723.951	16	1	KLAPILDEVAVHYEK	
			433	448	1870.88	1869.87	1869.838	19	0	FDATSNDILDENFDVR	
			449	456	1002.51	1001.5	1001.497	7	0	GYPTVYFR	
			457	471	1605.78	1604.77	1604.827	-33	1	SANGNITPYLGNRTK	
			470	479	1207.69	1206.69	1206.65	30	1	TKEDIVDFIK	
			483	495	1537.82	1536.81	1536.778	24	1	DKPVHQESLKDEL	
103	RNA helicase -like protein	GU295067	73	83	1306.67	1305.66	1305.61	38	0	FLDEPEDSNIK	
			84	109	2828.48	2827.47	2827.42	21	0	AVTAGETPYTSAFTFEELNLSPELLK	
			123	149	2851.59	2850.58	2850.54	14	0	IQAISLPMILTPPHLDLIAQAHNGSGK	Oxidation (M)
			150	160	1302.68	1301.67	1301.61	46	0	TTCFTLGMLSR	Oxidation (M)
			161	177	1953.07	1952.06	1952	35	1	VDPNLKAPQALCICPTR	
			178	189	1425.91	1424.9	1424.84	49	1	ELAIQNLEVLRK	
			215	231	1734.12	1733.11	1733.06	34	1	RAPIIAQVVIGTPGTIK	
			333	339	842.48	841.47	841.54	-83	1	VLVIKDR	
			340	346	863.43	862.42	862.45	-34	0	ILEFGER	
			340	355	1891.13	1890.12	1890.07	26	1	ILEFGERLGQTIIFVR	

			347	355	1046.66	1045.65	1045.63	19	0	LGQTIIFVR	
			366	386	2295.21	2294.2	2294.15	21	0	ALVEFGYDVTTIQGALNQAER	
			366	388	2538.27	2537.26	2537.28	-3	1	ALVEFGYDVTTIQGALNQAERDK	
			392	409	2019.16	2018.15	2018.1	24	1	EFKDGLTQVLISTDLLAR	
			395	409	1614.98	1613.97	1613.9	43	0	DGLTQVLISTDLLAR	
			410	427	2090.15	2089.14	2089.08	28	0	GFDQQQVNLVINYDLPVK	
			428	442	1938.94	1937.93	1937.88	25	1	HDNRVEPDCEVYLHR	
104	Betaine-aldehyde dehydrogenase	AAR23816	9	17	1163.61	1162.6	1162.577	22	0	QLFIDGEWR	
			9	22	1743.99	1742.98	1742.936	28	1	QLFIDGEWREPILK	
			25	56	3286.8	3285.8	3285.757	12	1	LPTINPATEEIIGNIPAATAEDVELAVAAARR	
			63	74	1228.68	1227.68	1227.636	33	1	GKDWATAPGAVR	
			65	74	1043.54	1042.53	1042.52	13	0	DWATAPGAVR	
			132	144	1475.79	1474.78	1474.785	-5	1	QKAPVSLPMETFK	
			246	264	1929.91	1928.91	1929.043	-71	0	IMAAAAQMVKPVSLELGGK	Oxidation (M)
			246	264	1946.07	1945.06	1945.038	13	0	IMAAAAQMVKPVSLELGGK	2 Oxidation (M)

265	277	1489.83	1488.82	1488.771	35	0	SPIIVFEDVDLDK	
300	308	1064.64	1063.63	1063.614	18	0	LIVHENIAR	
323	332	1209.55	1208.54	1208.513	23	0	ISDPFEEGCR	
333	344	1233.69	1232.68	1232.64	34	0	LGPVVSGGQYEK	
354	370	1751	1749.99	1749.937	31	0	SEGATILSGGVRPEHLK	
371	391	2485.3	2484.29	2484.272	8	1	KGFFVEPTIITDVTTSMQIWR	Oxidation (M)
372	391	2341.2	2340.19	2340.182	4	0	GFFVEPTIITDVTTSMQIWR	
372	391	2357.24	2356.23	2356.177	22	0	GFFVEPTIITDVTTSMQIWR	Oxidation (M)
392	402	1276.7	1275.69	1275.653	32	0	EEVFGPVLCVK	
470	483	1622.85	1621.84	1621.799	25	0	ELGEWGLDNYLSVK	
484	498	1913.94	1912.93	1912.874	28	0	QVTQYVSDEPWGWYR	

[a] Exp., experimental molecular weight (MW).

[b] Theo., theoretical molecular weight (MW).

[c] These peptides were identified after derivatization by a positively charged tag, N-Tris (2,4,6-trimethoxyphenyl) phosphonium-acetyl (TMPP-Ac), that enhanced the rate of peptide ionization. A custom monoisotopic modification titled TMPP-Ac (N-term) (m/z 573.18841) was set in the modifications file of Mascot to accommodate TMPP derivatization. Variable modification, TMPP-Ac (N-term).

Supplemental Table 3. Most significantly up-regulated metabolic pathways during cotton ovule development as identified by KOBAS[a]

Serial No.	KEGG pathway(s)	No. of *Arabidopsis* proteins located in various pathways	No. of up-regulated proteins in wild-type cotton	p-value	FDR-corrected p-value (<0.001)
	Total	3001	81	—	—
1	Nucleotide sugar metabolism	14	7	1.24×10^{-7}	1.46×10^{-6}
2	Ascorbate & aldarate metabolism	20	7	1.32×10^{-6}	3.82×10^{-6}
3	Cytoskeleton proteins	40	9	1.46×10^{-6}	3.82×10^{-6}
4	Glycolysis & gluconeogenesis	55	9	1.85×10^{-5}	3.11×10^{-5}
5	Pyruvate metabolism	37	7	6.78×10^{-5}	9.98×10^{-5}
6	Starch & sucrose metabolism	69	9	0.0001	0.0001
7	Gly, Ser, & Thr metabolism	28	6	0.0001	0.0001
8	Chaperones & folding catalysts	30	6	0.0002	0.0002
9	Amyotrophic lateral sclerosis	6	3	0.0006	0.0005

[a] Pathways were manually curated for plant specificity and accuracy. The web site for the KEGG pathway database is http://www.genome.jp/kegg/pathway.html.

Supplemental Table 4. Comparisons of proteins commonly identified in four different cotton proteomes

Spot No.	Protein name	NCBI acc. No.	pI/MW (exp.)	pI/MW (theo.)	Spot No. in ref. 18	NCBI acc. no.	Spot No. in ref. 40	NCBI acc. No.	Spot No. in ref. 39	NCBI acc. No.
1	profilin	ABO43717	5.33/13.01	5.38/14.41	36	AAO92742			4	EV489411
2	major latex-like protein	FJ415202	5.44/14.83	5.46/17.16						
3	annexin 1	AAR13288	6.31/15.81	6.19/36.15	27	AAR13288	93	AAR13288	13	ES793672
4	copper/zinc superoxide dismutase	FJ415203	5.83/15.98	5.47/15.36						
5	fiber annexin	AAC33305	6.11/16.04	6.34/36.21	26	AAC33305	27	AAC33305	10	CO129429
6	annexin	AAB67993	6.08/16.10	6.41/36.03	25	AAB67993	28	AAB67993	9	ES795476
7	copper/zinc superoxide dismutase	FJ415203	5.83/16.35	5.47/15.36						
8	peroxiredoxin	FJ415174	5.35/17.41	5.58/17.30	37	BF274296				
9	dimethylmenaquinone methyltransferase	FJ415179	5.41/18.54	5.60/18.05	46	CO099125	108	AAM61756		
10	benzoquinone reductase	ABN12321	6.09/21.65	6.09/21.65			103	AAM78225		
11	ascorbate peroxidase	ABR18607	5.13/27.49	5.93/27.74	1	CO096528				
12	cytosolic ascorbate peroxidase	ABR18607	5.43/27.51	5.93/27.74						

13	benzoquinone reductase	ABN12321	6.27/27.60	6.09/21.65				
14	benzoquinone reductase	ABN12320	6.47/27.83	6.20/21.79				
15	cytosolic ascorbate peroxidase	ABR18607	5.68/27.84	5.93/27.74				
16	ascorbate peroxidase	ABR18607	5.29/27.87	5.93/27.74				
17	ascorbate peroxidase	FJ415185	4.96/27.89	5.62/27.58				
18	annexin	FJ415173	6.52/28.49	6.74/35.98	24	CO496267	95	AAB67994
19	ascorbate peroxidase	ABR18607	5.32/28.70	5.93/27.74	2	CO096528		
20	ascorbate peroxidase	ABR18607	5.64/28.75	5.93/27.74	3	CO107707		
21	ascorbate peroxidase	ABR18607	5.15/29.28	5.93/27.74	4	CO096528	102	AAC08576
22	α-1,4 glucan phosphorylase	FJ415211	4.94/30.21	5.32/10.67	18	DT457191		
23	s-formylglutathione hydrolase	FJ415188	6.59/30.65	6.82/32.18				
24	triosephosphate isomerase	FJ415177	6.53/31.54	6.00/27.47	40	DT460335		
25	20S proteasome subunit α-1	FJ415181	6.44/31.80	5.91/27.39	49	CO121697	151	O24362
26	heat shock cognate 70	FJ415196	6.27/32.83	5.07/71.57				
27	catalase	FJ415187	6.30/33.59	6.68/57.25			13	CAA36380

28	serine hydroxymethyltransferase	FJ415180	5.54/34.18	7.57/52.38	47	AI731061		
29	lactoylglutathione lyase	FJ415204	5.71/34.38	5.69/32.61				
30	alpha-soluble NSF attachment protein	FJ415171	5.08/34.75	5.11/33.05	17	CO099225		
31	serine hydroxymethyltransferase	FJ415180	5.83/34.82	7.57/52.38				
32	UER1	FJ415167	5.94/34.94	5.73/33.95	11	CO122899		
33	UER1	FJ415167	6.22/34.97	5.73/33.95	12	CO122899		
34	fructokinase	FJ415169	5.05/36.08	5.28/35.20	15	CO106532		
35	enolase	ABW21688	5.21/36.28	5.49/47.98			117	CAA41115
36	actin	AAP73454	5.43/36.64	5.23/41.90	29	AAP73454	79	AAP73455
37	granule bound starch synthase	FJ415189	4.97/36.64	8.79/63.84				
38	stromal ascorbate peroxidase	FJ415186	6.24/36.78	8.89/41.05				
39	granule bound starch synthase	FJ415205	4.91/36.78	8.59/67.73				
40	chloroplast stromal ascorbate peroxidase	FJ415186	6.10/37.04	8.89/41.05				
41	glutamine synthase	FJ415178	5.64/37.12	5.77/39.36	41	BG447133	212	CAA42689
42	malate dehydrogenase	FJ415192	6.14/38.50	6.10/36.87				

43	phenylcoumaran benzylic ether reductase-like protein	ABN12322	5.58/38.89	5.76/33.89					16	DW226959
44	glyceraldehyde-3-phosphate dehydrogenase C subunit	FJ415206	6.35/39.17	7.70/36.65			91	CAD79700		
45	β-tubulin 19	ABY86665	5.75/39.76	4.76/50.65	34	AAL92118	69	AAL92118	34	DT544715
46	α-tubulin 4	AAN33000	5.57/39.90	5.36/34.41	32	AAN33000			41	ES807127
47	serine hydroxymethyltransferase	FJ415180	6.31/40.17	7.57/52.38	48	CX023265	12	CAB10172		
48	α-tubulin	ABO47738	5.72/40.45	4.97/50.29	35	BAC24799			37	EE592712
49	α-tubulin 4	AAN33000	5.43/40.90	5.36/34.41	31	AAN33000			38	DT571427
50	glyceraldehyde-3-phosphate dehydrogenase C subunit	FJ415206	6.61/41.24	7.70/36.65			23	P34921		
51	phenylcoumaran benzylic ether reductase-like protein	ABN12322	5.87/41.46	5.76/33.89	42	CO109185				
52	actin	AAP73452	5.62/42.35	5.44/41.94			92	AAP73453		
53	actin	AAP73457	5.56/43.29	5.31/41.91	28	AAP73460	140	AAB62881		
54	2-nitropropane dioxygenase	FJ415176	5.43/43.73	5.32/36.17	39	DT456206				
55	quinone oxidoreductase	FJ415175	5.21/45.90	5.28/34.39	38	CO088730				
56	malate dehydrogenase	FJ415192	6.67/46.15	6.10/35.87						
57	gibberellin 20-oxidase 1	ABA01482	5.23/48.01	5.35/41.72	44	CAC26951				

58	flavanone-3-hydroxylase	ABM64799	5.33/48.10	5.43/41.75	45	AAO63022		
59	mannitol dehydrogenase	FJ415191	5.93/49.11	5.85/39.57				
60	adenosine kinase	FJ415170	5.46/49.66	5.47/37.81	16	BF272730	211	AAU14831
61	adenosine kinase	FJ415170	5.46/49.66	5.47/37.81				
62	phosphoglycerate dehydrogenase	FJ415190	5.20/49.84	7.14/64.06				
63	heat shock protein 70	FJ415199	4.59/49.92	5.10/71.35				
64	pyruvate dehydrogenase α subunit	FJ415197	6.74/50.17	7.16/43.69				
65	phosphoglycerate dehydrogenase	FJ415190	5.13/50.35	7.14/64.06				
66	anthocyanidin reductase	ABM64802	5.53/51.74	5.54/36.54	43	CAD91910		
67	heat shock protein 70	FJ415194	4.69/52.90	5.14/71.28			180	CAA47345
68	heat shock protein 70	FJ415196	4.75/52.95	5.10/71.37			177	CAA52149
69	luminal binding protein	FJ415200	4.57/53.09	5.13/73.57				
70	luminal binding protein	FJ415200	4.50/53.55	5.13/73.57				
71	actin	AAP73460	5.45/53.58	5.37/41.94	30	AAP73460	76	AAP73460
72	luminal binding protein	FJ415200	4.55/53.94	5.13/73.57				

73	heat shock protein 70	FJ415195	4.75/54.07	5.07/71.57			50	AAL59960		
74	phosphoglycerate kinase	FJ415172	6.14/56.40	5.97/42.29	21	BAA33802	82	BAA33802		
75	chloroplast biotin carboxylase	ABP98813	6.30/57.92	7.57/59.17	23	AAF80469				
76	dihydrolipoamide dehydrogenase	FJ415193	6.62/59.37	6.93/54.13						
77	chloroplast biotin carboxylase	ABP98813	6.31/59.64	7.57/59.17	22	AAC23573				
78	UGP2	FJ415165	5.54/60.41	5.62/51.45	7	CO091798				
79	UGP1	FJ415164	6.07/61.70	5.81/51.74	5	CO109042				
80	UGP1	FJ415164	6.10/61.70	5.81/51.74	6	CO109042			14	EV482616
81	UGD1	FJ415166	6.11/62.84	5.84/53.64	9	Q96558				
82	myo-inositol-1-phosphate synthase	FJ415168	5.69/63.53	5.46/56.54	14	Q9LW96				
83	UGD1	FJ415166	6.30/64.12	5.84/53.64	8	AAB58398				
84	acyltransferase-like protein	AAL67994	5.67/64.47	5.67/48.29	19	AAL67994	61	AAL67994		
85	acyltransferase-like protein	AAL67994	5.56/64.82	5.67/48.29	20	AAL67994				
86	pyruvate decarboxylase	FJ415201	6.57/69.52	6.13/60.77						
87	glycine-rich RNA-binding protein	FJ415184	7.82/15.01	7.82/17.08					5	DW231397

88	benzoquinone reductase	FJ415183	7.68/24.72	6.97/21.74						
89	manganese superoxide dismutase	AAC78469	7.49/25.40	8.54/22.14						
90	heat shock cognate protein 70	FJ415194	7.52/33.12	5.14/71.28						
91	glyceraldehyde-3-phosphate dehydrogenase	FJ415182	7.74/43.72	7.06/37.04			143	AAM65189		
92	isocitrate dehydrogenase	FJ415198	7.32/53.15	6.29/46.41			209	CAD24779		
93	isocitrate dehydrogenase	FJ415198	7.07/53.29	6.29/46.41			208	AAM13090		
94	eukaryotic translation initiation factor 5A	GU295062	5.55/18.88	5.61/17.63	60	CAA45104	109	CAA45104		
95	chalcone isomerase	GU295063	4.84/29.85	4.85/23.42	52	BQ411585				
96	triosephosphate isomerase	GU295064	5.52/30.18	6.66/33.50	53	BAC92722				
97	thiazole biosynthetic enzyme	GU295068	5.03/36.81	5.64/38.24	54	AAW66657				
98	transaldolase	GU295065	4.91/45.56	5.78/43.06	50	CAA31366				
99	U2 small nuclear ribonucleoprotein A	GU295066	5.06/45.90	4.97/32.19	57	CO130432				
100	transaldolase	GU295065	5.09/46.62	5.78/43.06	58	BQ401915				
101	chalcone synthase	ABS52573	6.11/54.17	6.12/42.98	51	CAA64366				
102	protein disulfide isomerase	ABO41843	5.01/65.30	5.07/55.89	55	CO080059			55	ES791121

103	RNA helicase -like protein	GU295067	5.91/69.24	5.65/56.15	59	CO098559		
104	betaine-aldehyde dehydrogenase	AAR23816	5.44/69.43	5.60/55.37	61	AAR23816	55	AAR23816

Supplemental Figure Legends

Supplemental Fig. 1. Comparative proteomic analysis of wild-type and *fl* mutant cotton ovules. Silver-stained 2-DE analyses using proteins (100 µg) extracted from wild-type ovules with fibers attached (WT-10, upper panel) and *fl* mutant (FL-10, lower panel) ovules. Triplicate protein samples obtained from different cotton ovule collections were separated on 12.5% SDS-PAGE gels with pH ranging from 4 to 7 (for best resolution, only pH 4–6.8 is shown) and 3 to 10 (only pH 6.7–9 is shown) using 24-cm Immobiline DryStrip gels and scanned after silver staining. One representative gel is shown. The protein spots numbered 1–93 (labeled in black) were present in significantly higher levels in wild-type samples and spots 94–104 (labeled in red) were preferentially accumulated in the mutant. Open arrows indicate eight protein spots present in higher levels in wild-type samples that could not be identified, and circles indicate two protein spots present in higher levels after silver staining, but were not found after Coomassie Blue R-350 staining prior to MALDI-TOF analysis.

Supplemental Fig. 2. Deduced amino acid sequences of UER1, UGD1, UGP1, and UGP2 from upland cotton materials. Peptide sequences obtained from Nano-LC-FTICR-MS for each of the protein spots that matched sequences in the NCBI “EST others” database are shown in RED, and peptide sequences obtained from MALDI-TOF-TOF MS/MS are shown in BLUE.

Supplemental Fig. 3. Functional characterization of cotton UER1, UGD1, UGP1,

and UGP2. *A*, UER1 enzyme activity analysis. Top panel, expression and purification of recombinant UER1 (37.2 kDa) after IPTG induction. Middle panel, analysis of UDP-Rha production from UDP-4K6DG by UER1 expressed *in vitro*. The substrate and coenzyme are shown in the upper HPLC trace, and the lower trace shows the products after incubation with the purified enzyme. Bottom panel, mass spectrum identification of L-Rha from the HPLC eluant after cleavage of UDP and alditol acetate derivatization. *B*, UGP1 and UGP2 enzyme activity analysis. Top panel, expression and purification of recombinant UGP1 (56.3 kDa) and UGP2 (55.9 kDa). Middle panel, both UGP1 and UGP2 enzymatically synthesized UDP-D-glucose from D-glucose. Bottom panel, mass spectrum identification of D-Glc from the HPLC eluant after cleavage of UDP and alditol acetate derivatization. *C*, UGD1 enzyme activity analysis. Top panel, expression and purification of recombinant UGD1 (55.5 kDa). Middle panel, synthesis of UDP-GlcA from UDP-Glc and NAD^+ by UGD1. Bottom panel, mass spectrum identification of D-GlcA from the HPLC eluant after cleavage of UDP and trimethylsilyl methoxime derivatization. *D*, GAE3 enzyme activity analysis. Top panel, expression and purification of recombinant GAE3 (53.9 kDa). Middle panel, *in vitro*–expressed GAE3 synthesized UDP-GalA from UDP-GlcA. Bottom panel, mass spectrum identification of UDP-GalA from the HPLC eluant after cleavage of UDP and trimethylsilyl methoxime derivatization.

Supplemental Fig. 4. Two-DE analysis of proteomes obtained from 1-dpa wild-type or *fl* mutant ovules treated with exogenous ethylene or C24:0 for 24 h.

Comparative proteomic analysis was carried out as in Supplemental Fig. 1. WT-Air-24, proteome obtained from 1-dpa wild-type cotton ovules cultured in air for 24 h; WT-Eth-24, proteome from 1-dpa ovules cultured in 0.1 μM ethylene for 24 h; WT-C:24:0-24, proteome from 1-dpa ovules cultured in 5 μM C24:0 for 24 h; FL-Air-24, proteome from 1-dpa *fl* mutant ovules cultured in air for 24 h; FL-Eth-24, proteome from 1-dpa mutant ovules cultured in 0.1 μM ethylene for 24 h; FL-C24:0-24, proteome from 1-dpa mutant ovules cultured in 5 μM C24:0 for 24 h. Gels of pH 3 to 10 were not performed in this experiment because all polypeptides of interest appeared in gels of pH 4 to 7.

Supplemental Fig. 5. QRT-PCR analysis of different UDP-L-rhamnose synthase *(RHM)* isoforms in different cotton samples. *A.* None of the *RHM* transcripts were preferentially expressed in fiber cells. *B*, *RHM* transcription was not activated by exogenous Eth treatment. RNA samples were extracted from WT ovules cultured for 24 h in the presence of 0.1 μM Eth. Air, no ethylene was added to the culture. GenBank Accession Numbers: *RHM1*, FJ415210; *RHM2,* GQ292791; *RHM3*, GQ292792; *RHM4*, GQ292793.

Supplemental Fig. 6. Major metabolic pathways leading from Glc-1-P or sucrose to various cell wall components. Modified from Seifert (34). UGP, UDP-D-glucose pyrophosphorylase; UER, UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase 4-reductase; UGD, UDP-D-glucose dehydrogenase; GAE, UDP-D-glucuronic acid 4-epimerase;

Sus, sucrose synthase. RHM, UDP-L-rhamnose synthase. Enzymes in bold were identified from the 2-D gels (Supplemental Fig. 1).

Supplemental Fig. 7. QRT-PCR analysis of different *GAE* transcripts in developing cotton ovules. Black bars (with scales on the left side) indicate the increase relative to that obtained from 0-dpa wild-type ovules (which was set to 1) of the same gene to show whether it is preferentially expressed in fiber cells. Open bars (with scales on the right side) indicate the increase for the individual gene relative to cotton *UBQ7*. See legend to Fig. 1 for experimental details and nomenclature. ***, significant at $p \leq 0.001$. GenBank Accession Numbers: *GAE1*, FJ415208; *GAE2*, GQ292788; *GAE3*, GQ292789; *GAE4*, GQ292790; *GAE5*, no complete CDS was obtained.

Supplemental Fig. 8. Characterization of the *uer1-1 Arabidopsis* mutant. *A*, schematic of *uer1-1* genomic organization. The T-DNA was inserted between nucleotides 23347178 and 23347179 as determined by sequencing of a genomic clone amplified from the mutant using the reverse primer (RP) and forward primer (FP). *B*, identification of T-DNA insertion by genomic PCR. WT, wild-type (Col); *uer1-1*, homozygous mutant plants. RP, complementary to the region downstream of the T-DNA; FP, complementary to the region upstream of the T-DNA; LBb1, complementary to the left-most region of the T-DNA. *C*, Southern blot analysis. *D*, RT-PCR analysis of *UER1* transcripts in WT and *uer1-1* plants. No *UER1* transcript was observed in *uer1-1* plants after either 28 or 32 PCR cycles.

Supplemental Fig. 9. Characterization of the *gae6-1 Arabidopsis* mutant. A, schematic of *gae6-1* genomic organization. The T-DNA was inserted between nucleotides 8603876 and 8603877 as determined by sequencing of a genomic clone amplified from the mutant using RP' and FP' as primers. B, identification of T-DNA insertion by genomic PCR. WT, wild-type (Col); *gae6-1*, homozygous mutant plants. LBb1.3, complementary to the left-most region of the T-DNA. C, Southern blot analysis. D, RT-PCR analysis of *GAE6* transcripts in WT and gae6-1 plants. No *GAE6* transcript was observed in *gae6-1* plants after either 28 or 32 PCR cycles.

Supplemental Figures

Fig. S1

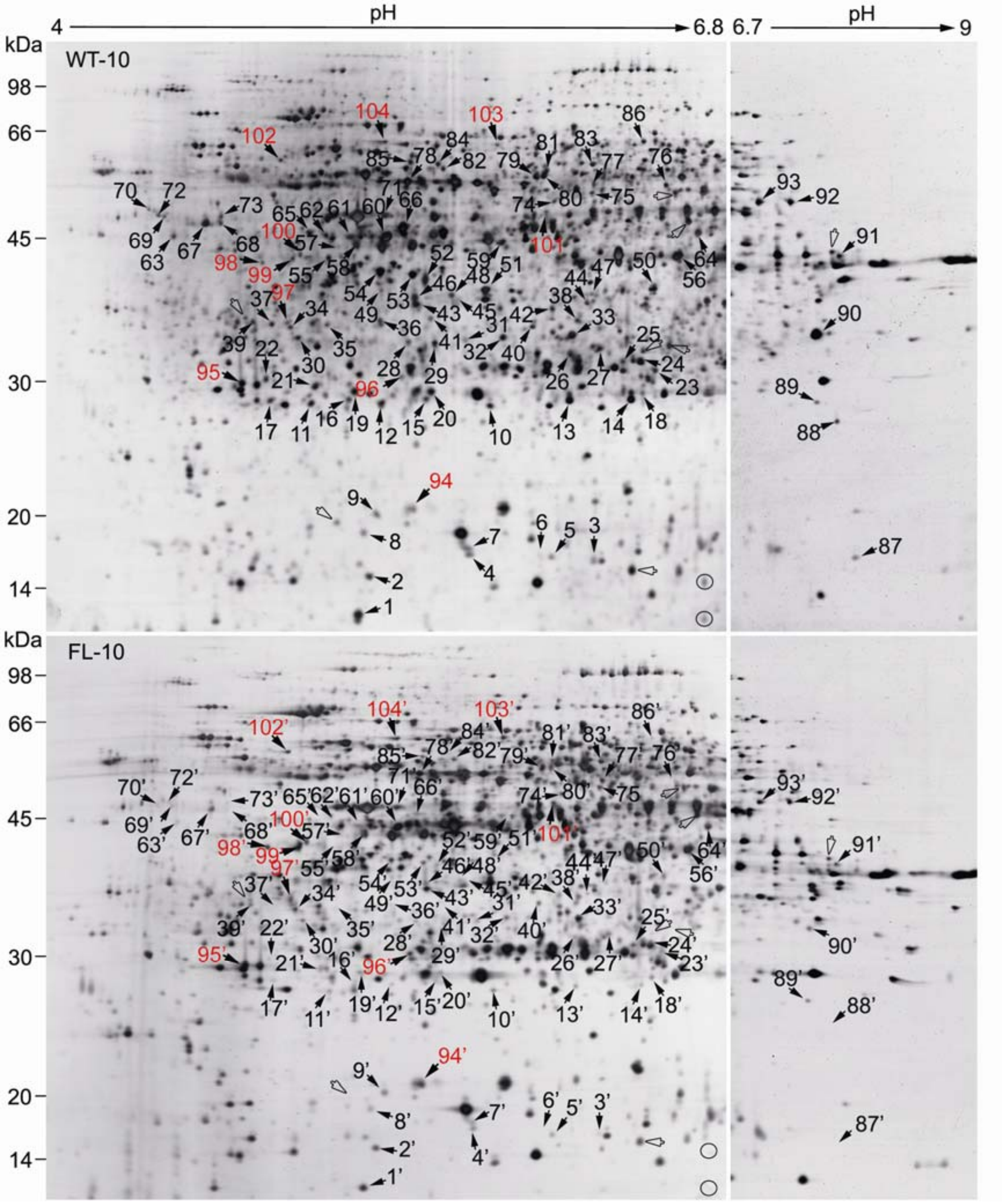


Fig. S2

UER1 (spot 32, 33)

MGFPANGSSD KPLKFLIYGR **TGWIGGLLGK** LCESQGIDYE YGSGRLESRI SLESDIANVK PTHVFNAAGV
TGRPNVDWCE SHKVETIR**TN VVGTLTLADV CR**DKGLILIN YATGCIFEYD EAHQIGTGIG FKEEDTPNFT
GSFYSKTKAM VEELLK NYEN VCTLRVR**MPI SSDLANPR**NF ITKITRYDKV VNIPNSMTIL DELLPISIEM
GKRNLTGIWN FTNPGVVSHN EILEMYR**DYI DPNFTWKNFN LEEQAK**VIVA PR**SNNELDAT K**LK**TEFPELL**
SIKESLVKYV FEPNKKTGGA

UGP1 (spot 79, 80)

MEKLDHIKSH LATLSQIGEN EKNGFINLVS RYLSGEAQHI EWSKIQTPTD EVVVPYDTLA PLSDDPAETK
KLLDKLVVLK LNGGLGTTMG CTGPKSVIEV RNGFTFLDLI VQQIENLNKK YGCNVPLVLM NSFNTHDDTL
KIVDKYANSN IQIHTFNQSQ YPR**LVAEDFT PFPCK**GQPGK DGWYPPGHGD VFPALMNSGK LATFLSQDKE
YAFVANSDNL GAIVDLKILN HLVKNKNEYC MEVTPKTLAD VKGGTLISYE GKVQLLEIAQ VPDAHVNEFK
SIEKFKIFNT NNLWLNLNAV KRLVEADALK **MEIIPNPK**EV EGTK**VLQLET AAGAAIRFFE HAIGINVPR**S
RFLPVKATSD LLLVQSDLYT LVDGFVSRNS ARENPENPSI ELGPEFKK**VS NFLSR**FKTIP SIINLDSLTV
TGDVWFGAGI VLKGKVKIAA KPGEKLEIPD GIVIENKEIN GPGDLSS

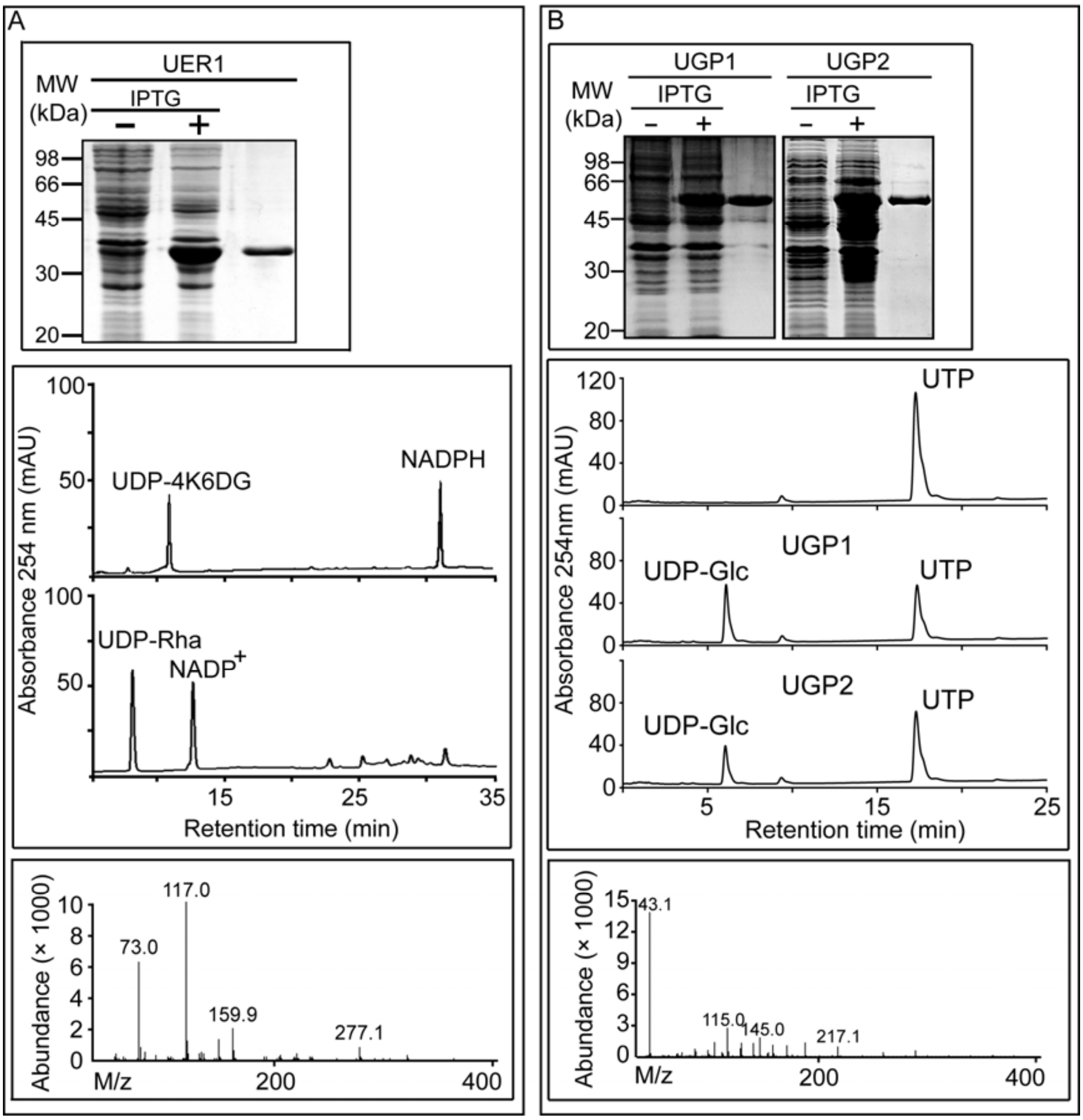
UGP2 (spot 78)

MEKLEHLKSA VAALSEISEN EKNGFINLVS RYLSGEAQHI EWSKIQTPTD EVVVPYDTLS PSPDDPAETK
KLLDKLVVLK LNGGLGTTMG CTGPKSVIEV RNGLTFLDLI VIQIENLNSK YGCNVPLVLM NSFNTHDDTL
KIVDKYSNSN IEIHTFNQSQ YPRLVVEDFA PLPSKGQHGK DGWYPPGHGD VFPSLMNSGK LDAFLSQGKE
YVFVANSDNL GAIVDMKILN HLVQNKNEYC MEVTPKTLAD VKGGTLISYE GK**VQLLEIAQ VPDEHVNEFK**
SIEKFK**IFNT NNLWVNLNAI K**RLVEADALK MEIIPNPKEV NGIK**VLQLET AAGAAIR**FFD HAIGINVPRS
RFLPVKATSD LLLVQSDLYT LVDGFVIRNK DRANPTNPSI ELGPEFKKVG NFLSRFKSIP SIIELDSLKV
TGDVWFGAGI VLKGKVSIAA KPGVKLEIPD GAVIEKKEIN VPEDI

UGD1 (spot 81, 83)

MKICCIGAGY VGGPTMAVIA LKCPDIEVAV VDISVPRIAA WNSDQLPIYE PGLDGVVKEC RGRNLFFSTD
VEKHVREADI VFVSVNTPTK TRGLGAGK**AA DLTYWESAAR** MIADVSKSDK IVVEKSTVPV KTAEAIEKIL
THNSKGIKFQ ILSNPEFLAE GTAIQDLFNP DRVLIGGRET PEGNKAVQAL K**EVYAHWVPE ER**ILTTNLWS
AELSK**LAANA FLAQR**ISSVN AMSALCEATG ADVTQVSYAV GKDTRIGPK**F LNASVGFGGS CFQK**DILNLV
YICECNGLPE VAEYWKQVIK INDYQKNRFV NRVVSSMFNT VSNKK**IAILG FAFK**KDTGDT RETPAIDVCK
GLLGDKARLS IYDPQVTEDQ VQRDLSMNKF DWDHPLHLQP MSPTTVKQVS CVWDAYEATK DAHGICILTE
WDEFKKLDFK RIYDNMQKPA FVFDGRNIVN ADELREIGFI VYSIGKPLDP WLKDMPAVA

Fig. S3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+
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30
20
100
50
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NADPH
UDP-Rha
NADP$^+$
15
25
35
Retention time (min)
Abundance (× 1000)
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8
6
4
2
0
117.0
73.0
159.9
277.1
M/z
200
400
B
UGP1
UGP2
MW (kDa)
IPTG
−
+
98
66
45
30
20
120
80
40
0
UTP
Absorbance 254nm (mAU)
UGP1
UDP-Glc
UTP
UGP2
UDP-Glc
UTP
5
15
25
Retention time (min)
Abundance (× 1000)
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217.1
M/z
200
400

Fig. S3 (continued…)

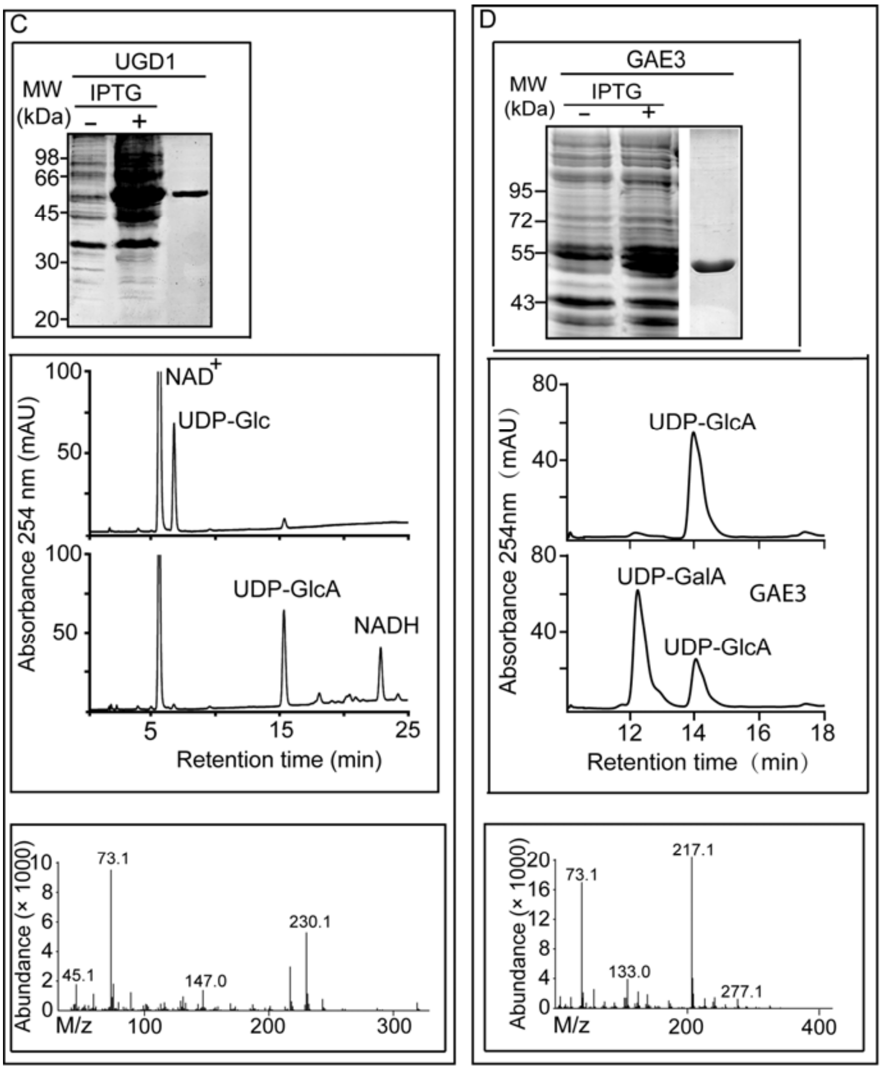
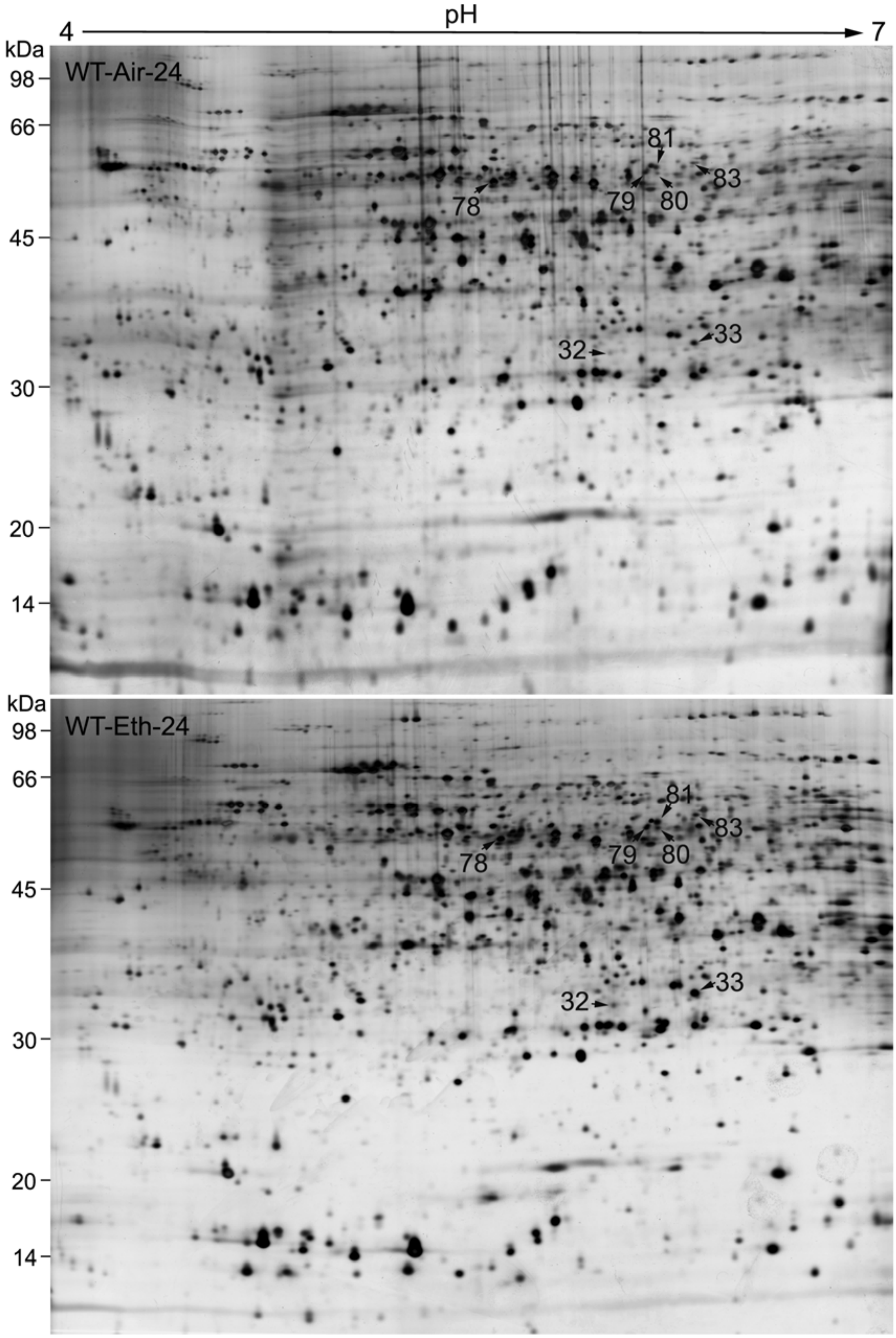


Fig. S4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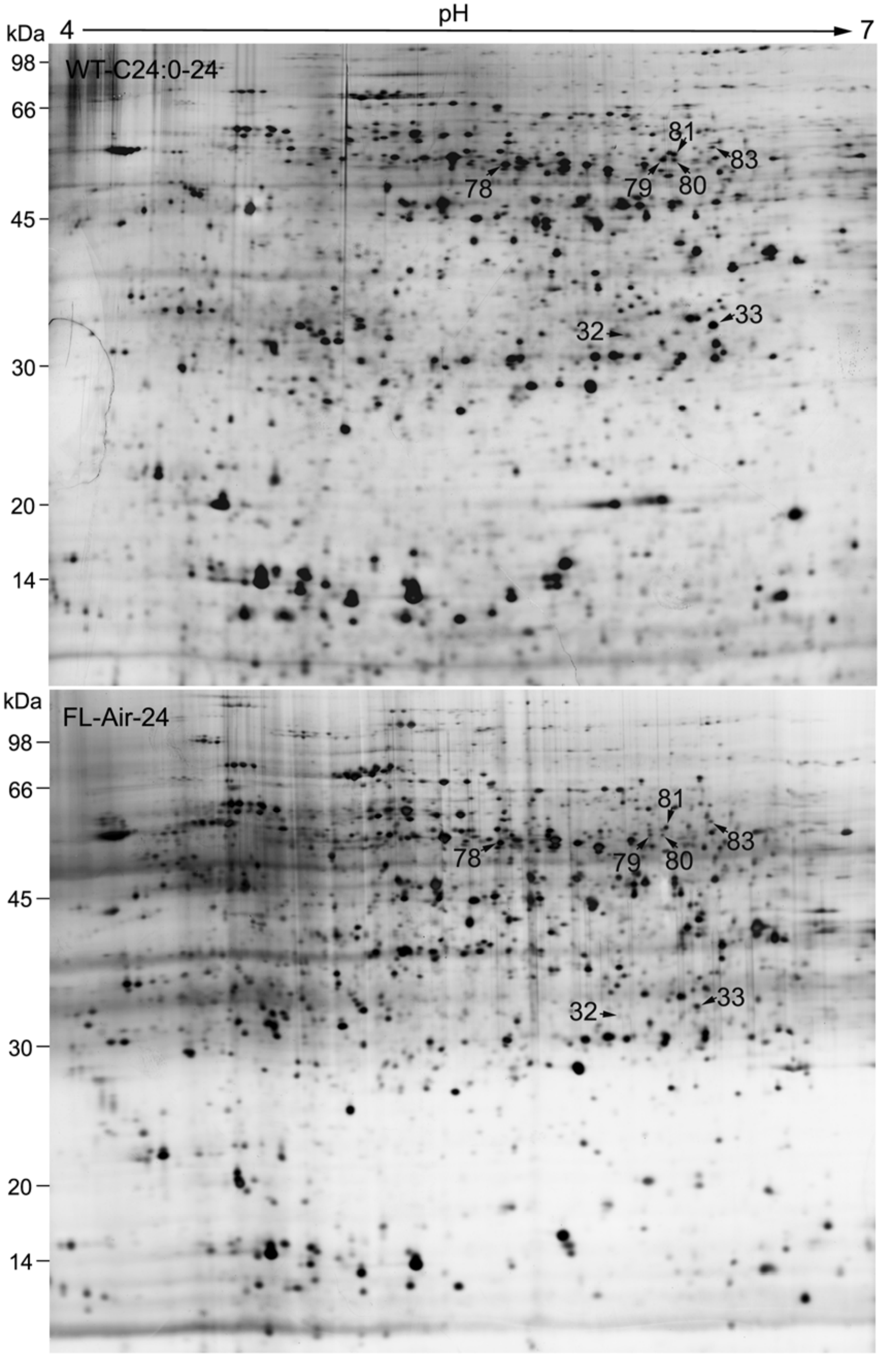
33
32

Fig. S4 (continued…)



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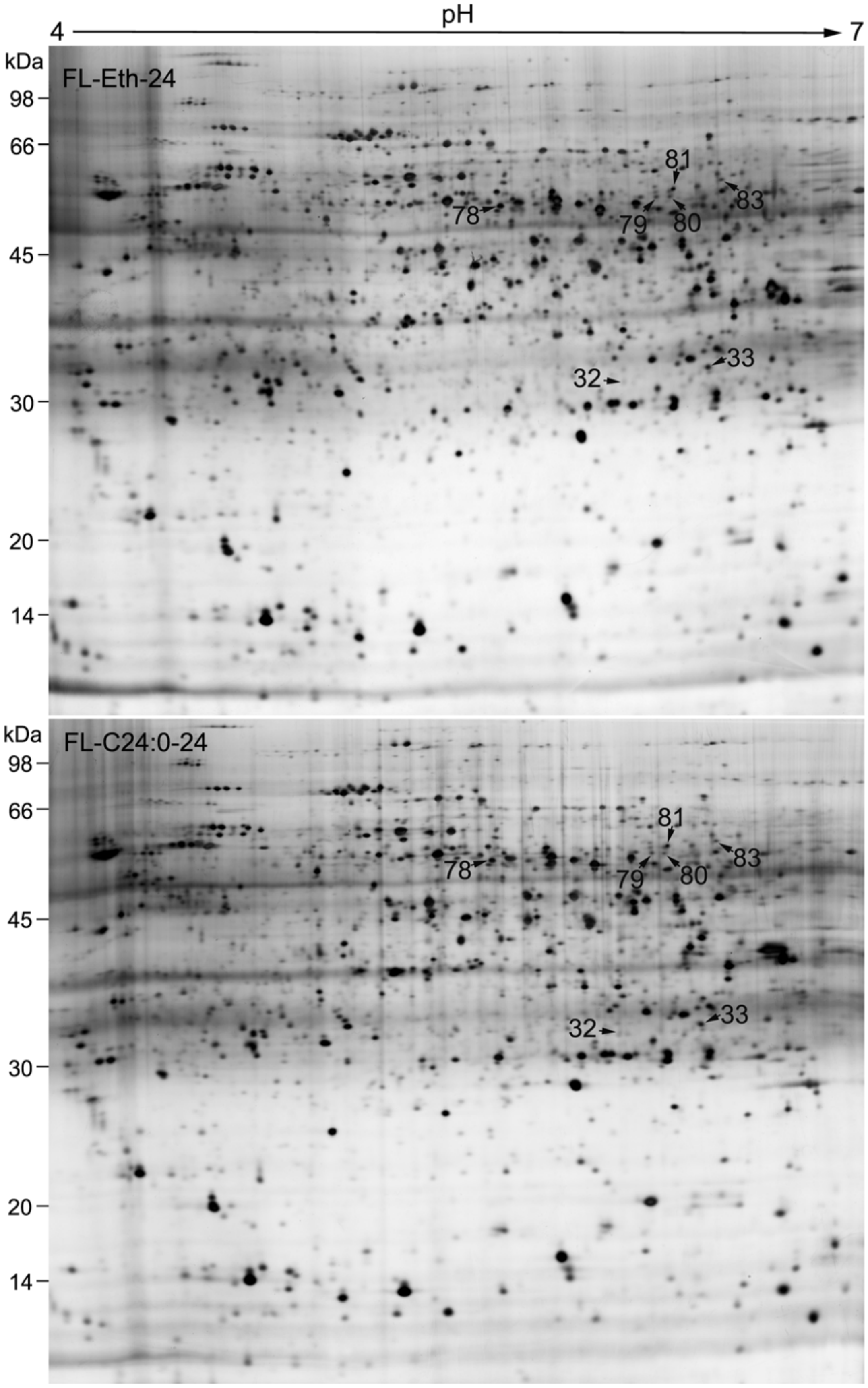


Fig. S5

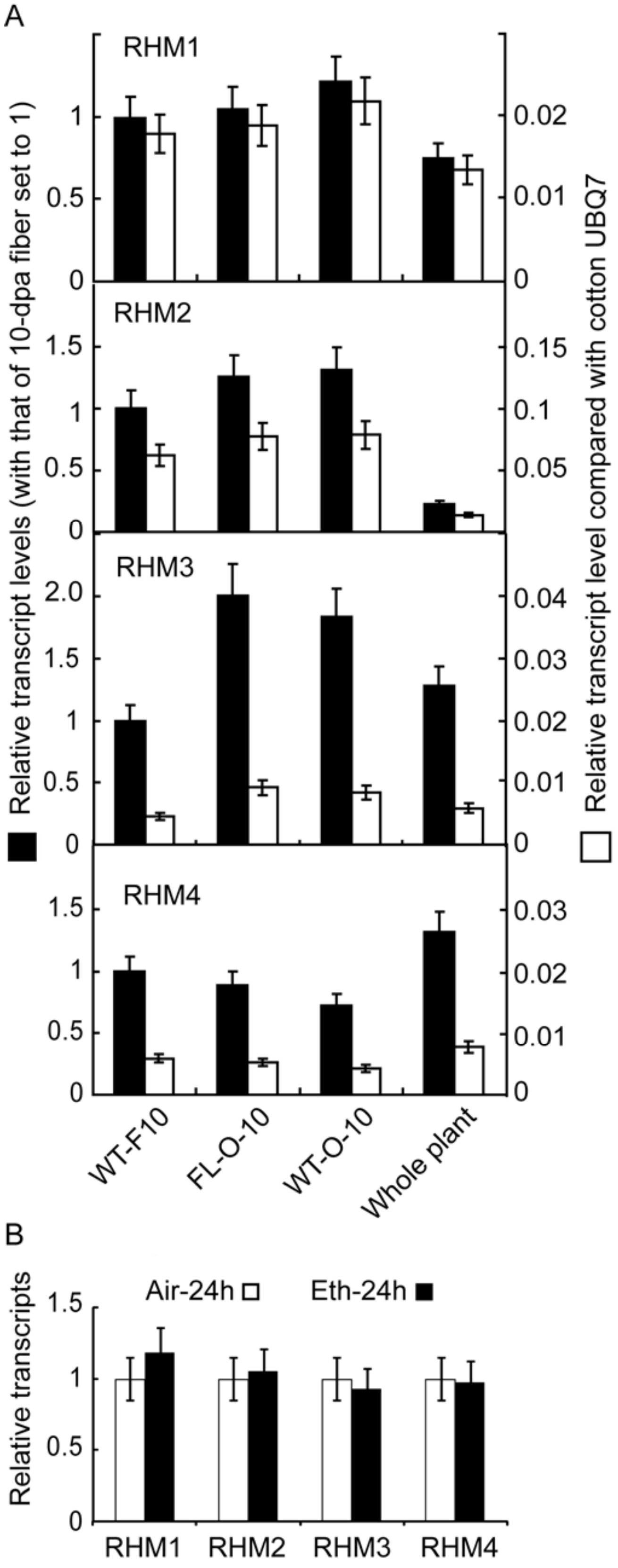
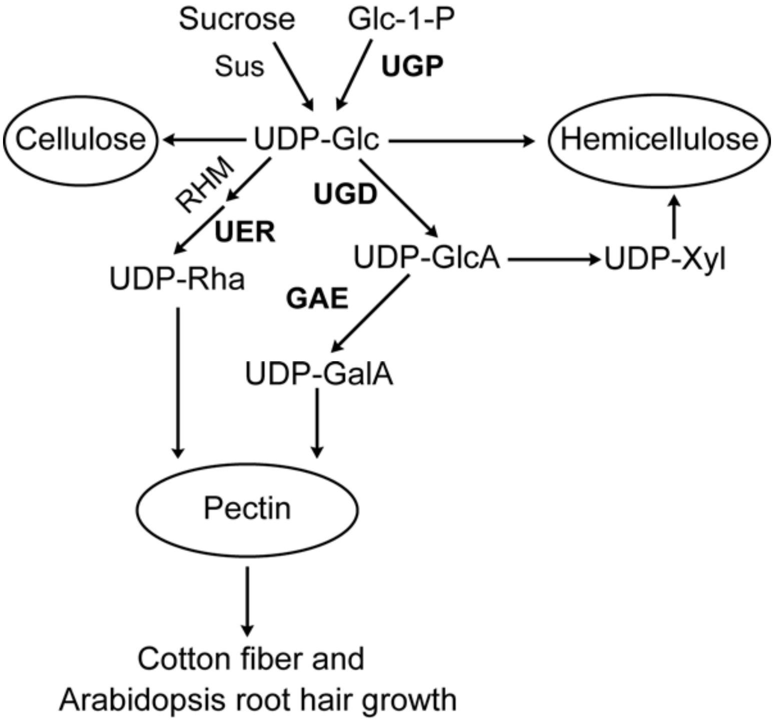

A
RHM1
RHM2
RHM3
RHM4
Relative transcript levels (with that of 10-dpa fiber set to 1)
Relative transcript level compared with cotton UBQ7
0
0.5
1
1.5
2.0
0.01
0.02
0.03
0.04
0.05
0.1
0.15
WT-F10
FL-O-10
WT-O-10
Whole plant
B
Relative transcripts
Air-24h
Eth-24h
RHM1
RHM2
RHM3
RHM4

Fig. S6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Sus
UGP
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RHM
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UGD
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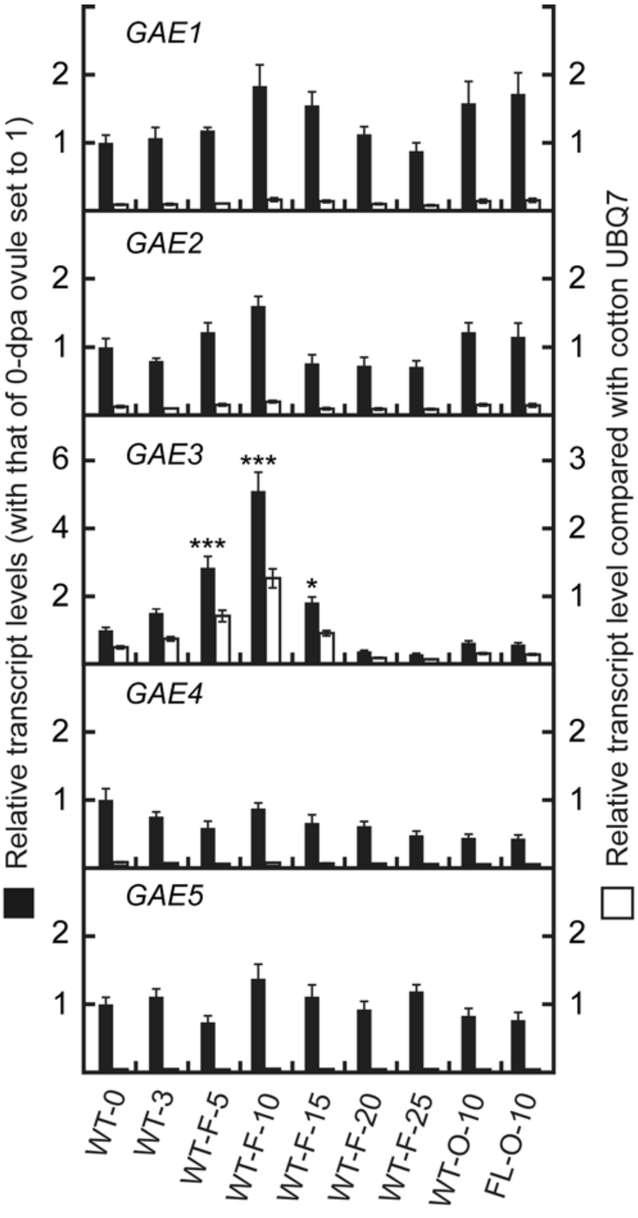
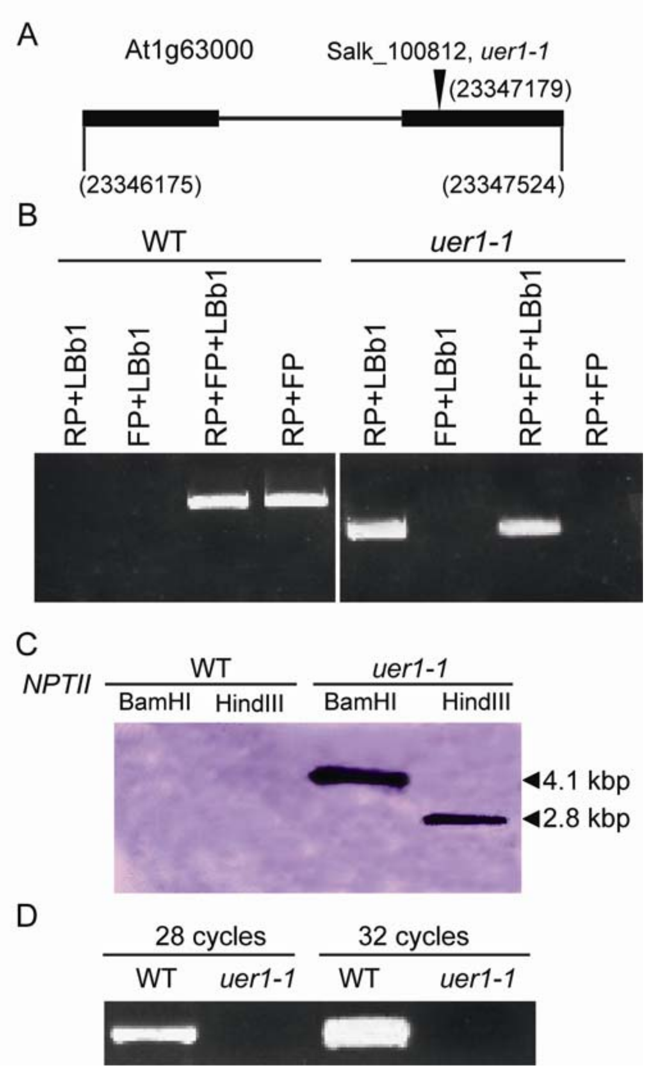
UDP-Xyl
GAE
UDP-GalA
Pectin
Cotton fiber and
Arabidopsis root hair growth

Fig. S7



GAE1
GAE2
GAE3
GAE4
GAE5
***
***
*
2
1
6
4
3
WT-0
WT-3
WT-F-5
WT-F-10
WT-F-15
WT-F-20
WT-F-25
WT-O-10
FL-O-10
■ Relative transcript levels (with that of 0-dpa ovule set to 1)
□ Relative transcript level compared with cotton UBQ7

Fig. S8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(23346175)
(23347524)
B
WT
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FP+LBb1
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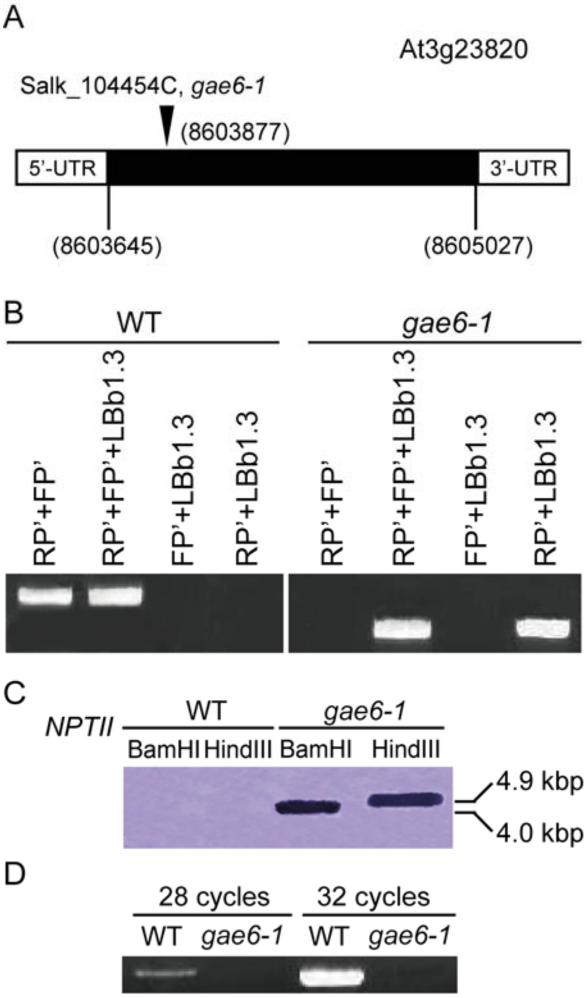
RP+FP
C
NPTII
WT
uer1-1
BamHI
HindIII
BamHI
HindIII
4.1 kbp
2.8 kbp
D
28 cycles
32 cycles
WT
uer1-1
WT
uer1-1

Fig. S9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3'-UTR
(8603645)
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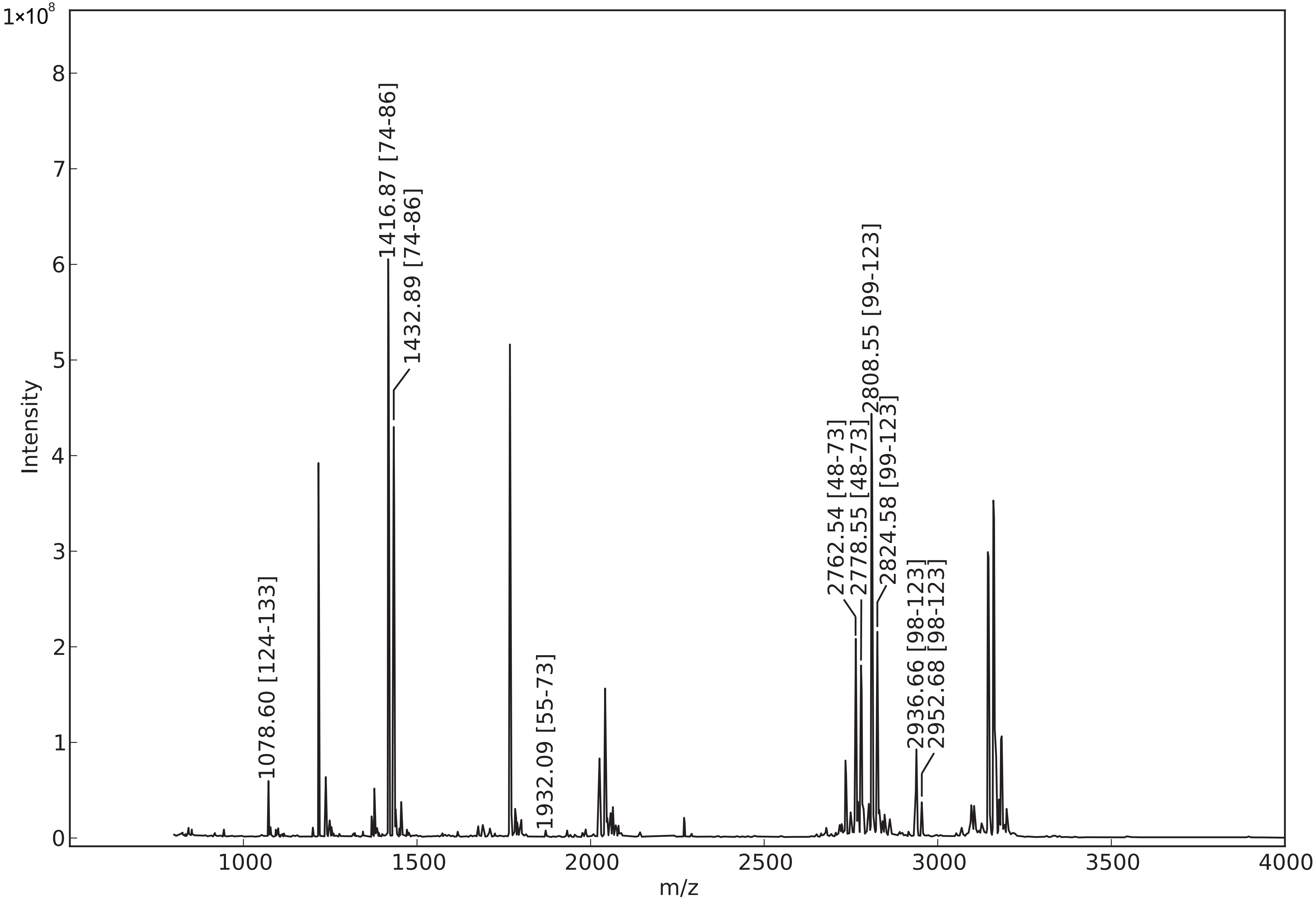
B
WT
gae6-1
RP'+FP'
RP'+FP'+LBb1.3
FP'+LBb1.3
RP'+LBb1.3
RP'+FP'
RP'+FP'+LBb1.3
FP'+LBb1.3
RP'+LBb1.3
C
NPTII
WT
gae6-1
BamHI
HindIII
BamHI
HindIII
4.9 kbp
4.0 kbp
D
28 cycles
32 cycles
WT
gae6-1
WT
gae6-1

Supplemental spectra 1 for Table I

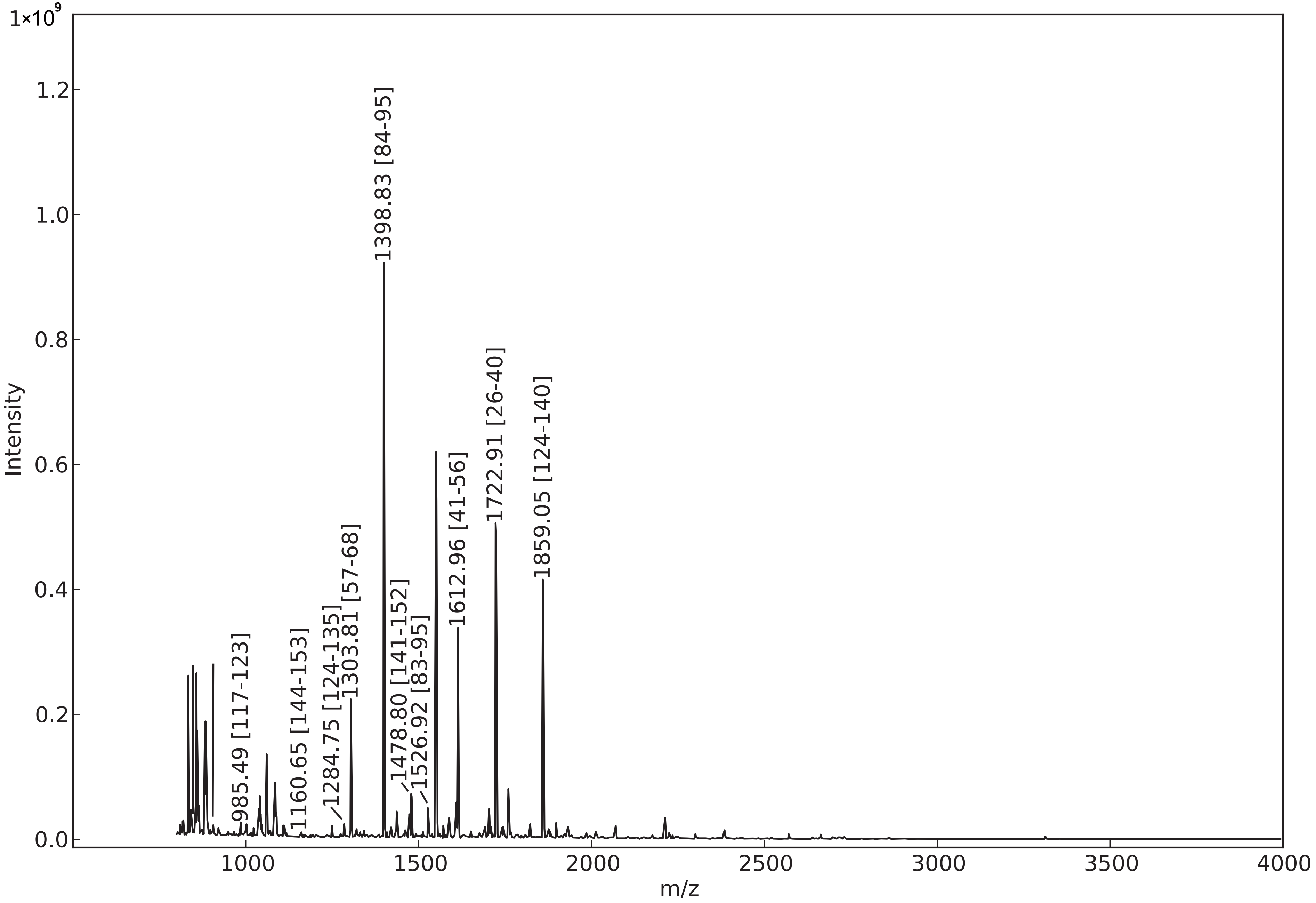
Annotated spectra for Table I: 104 differentially expressed proteins identified by PMF

Spot numbers of the 104 proteins correspond to the proteins that list in Table I

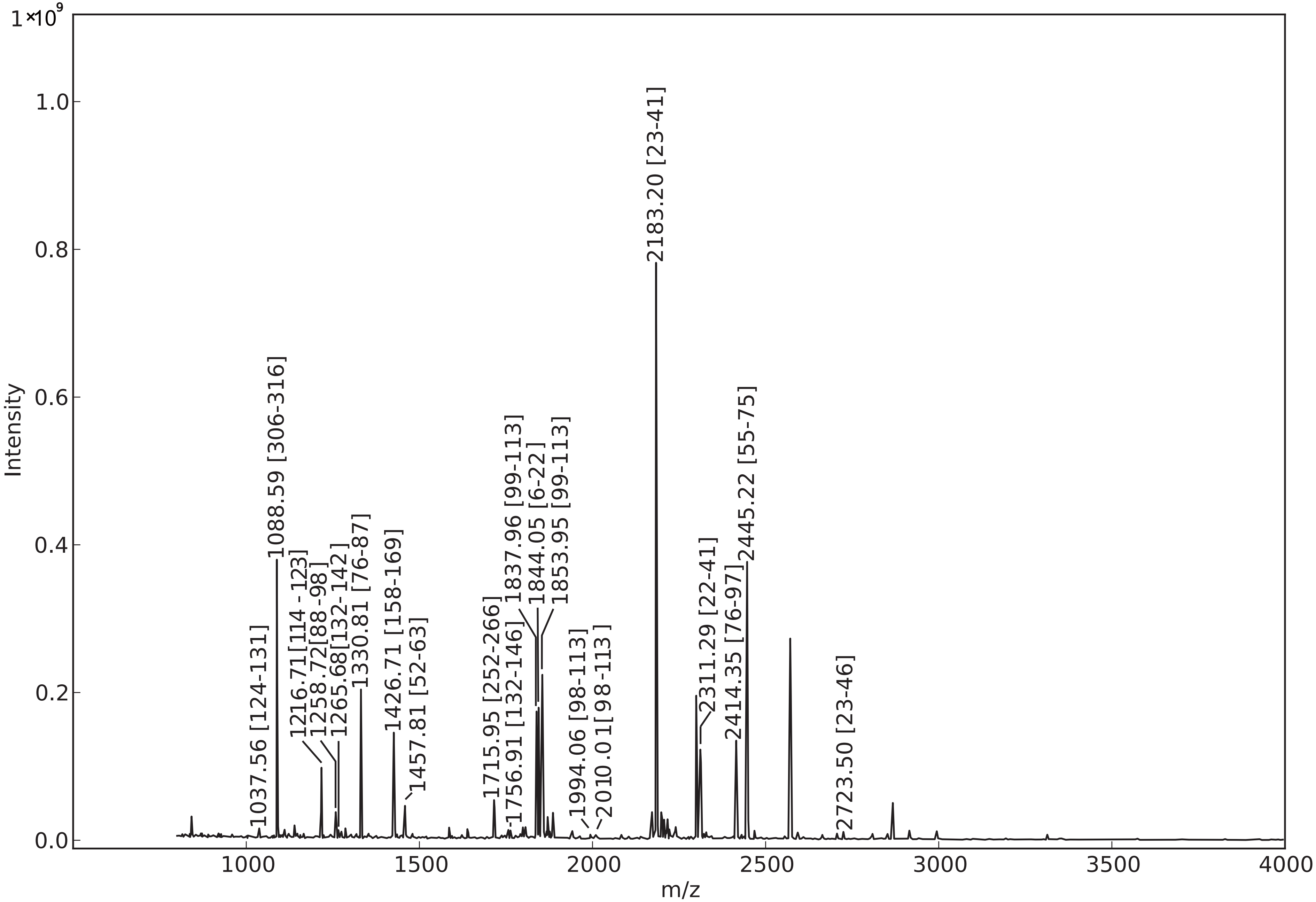
Spot No. 01


1×10^8
8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1078.60 [124-133]
1416.87 [74-86]
1432.89 [74-86]
1932.09 [55-73]
2762.54 [48-73]
2778.55 [48-73]
2808.55 [99-123]
2824.58 [99-123]
2936.66 [98-123]
2952.68 [98-123]

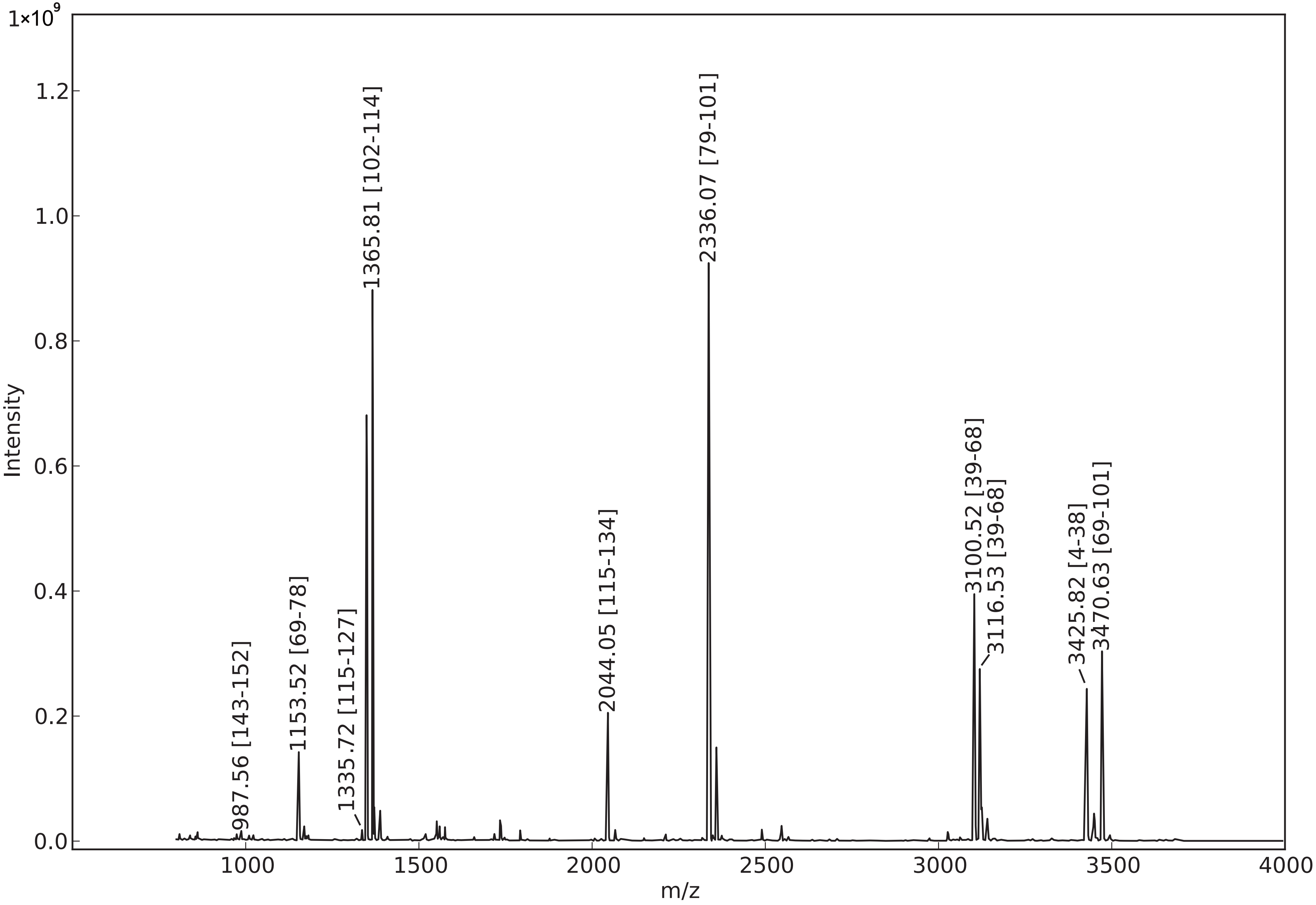
Spot No. 02


1×10^9
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
985.49 [117-123]
1160.65 [144-153]
1284.75 [124-135]
1303.81 [57-68]
1398.83 [84-95]
1478.80 [141-152]
1526.92 [83-95]
1612.96 [41-56]
1722.91 [26-40]
1859.05 [124-140]

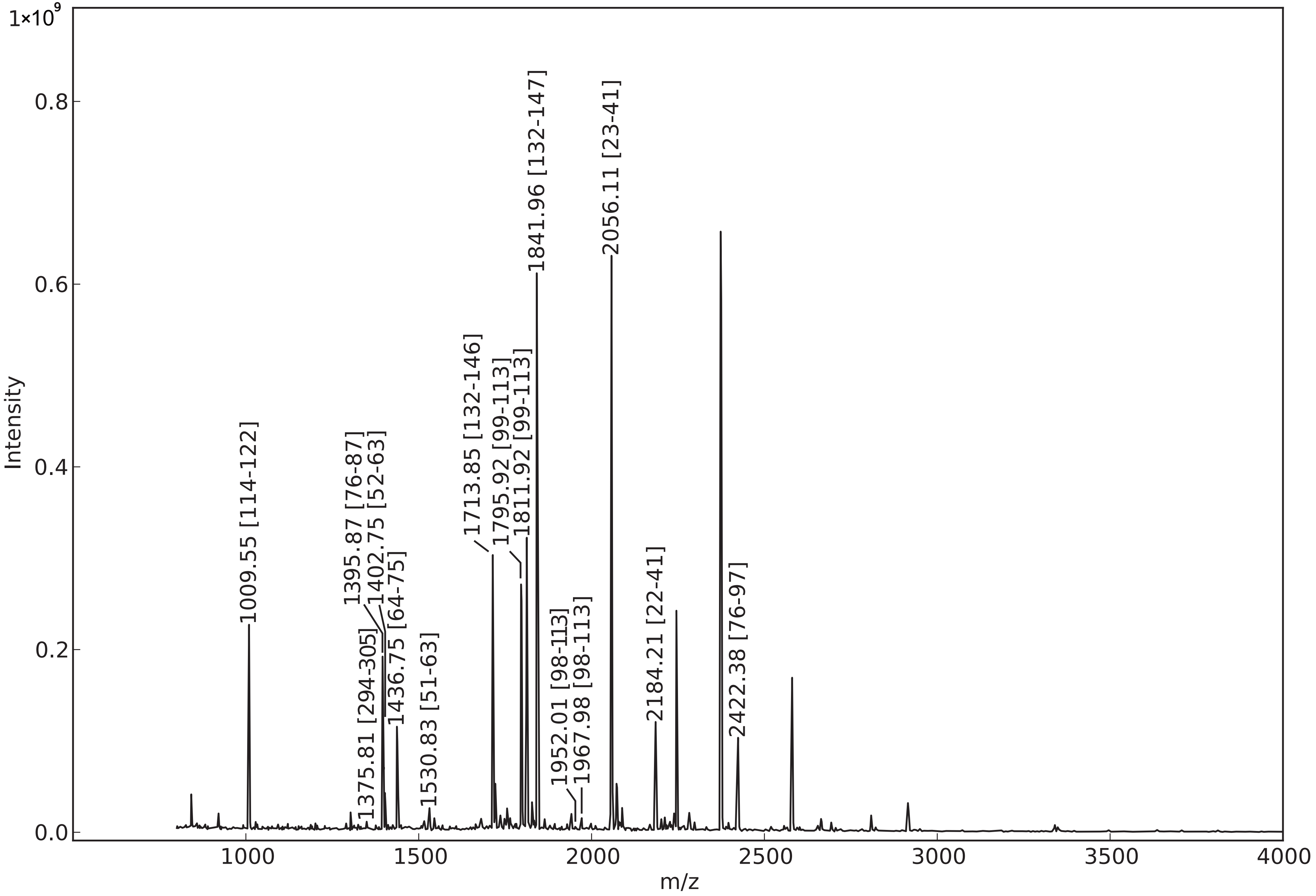
Spot No. 03


1×10^9
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1037.56 [124-131]
1088.59 [306-316]
1216.71 [114 -123]
1258.72[88-98]
1265.68[132-142]
1330.81 [76-87]
1426.71 [158-169]
1457.81 [52-63]
1715.95 [252-266]
1756.91 [132-146]
1837.96 [99-113]
1844.05 [6-22]
1853.95 [99-113]
1994.06 [98-113]
2010.01[98-113]
2183.20 [23-41]
2311.29 [22-41]
2414.35 [76-97]
2445.22 [55-75]
2723.50 [23-46]

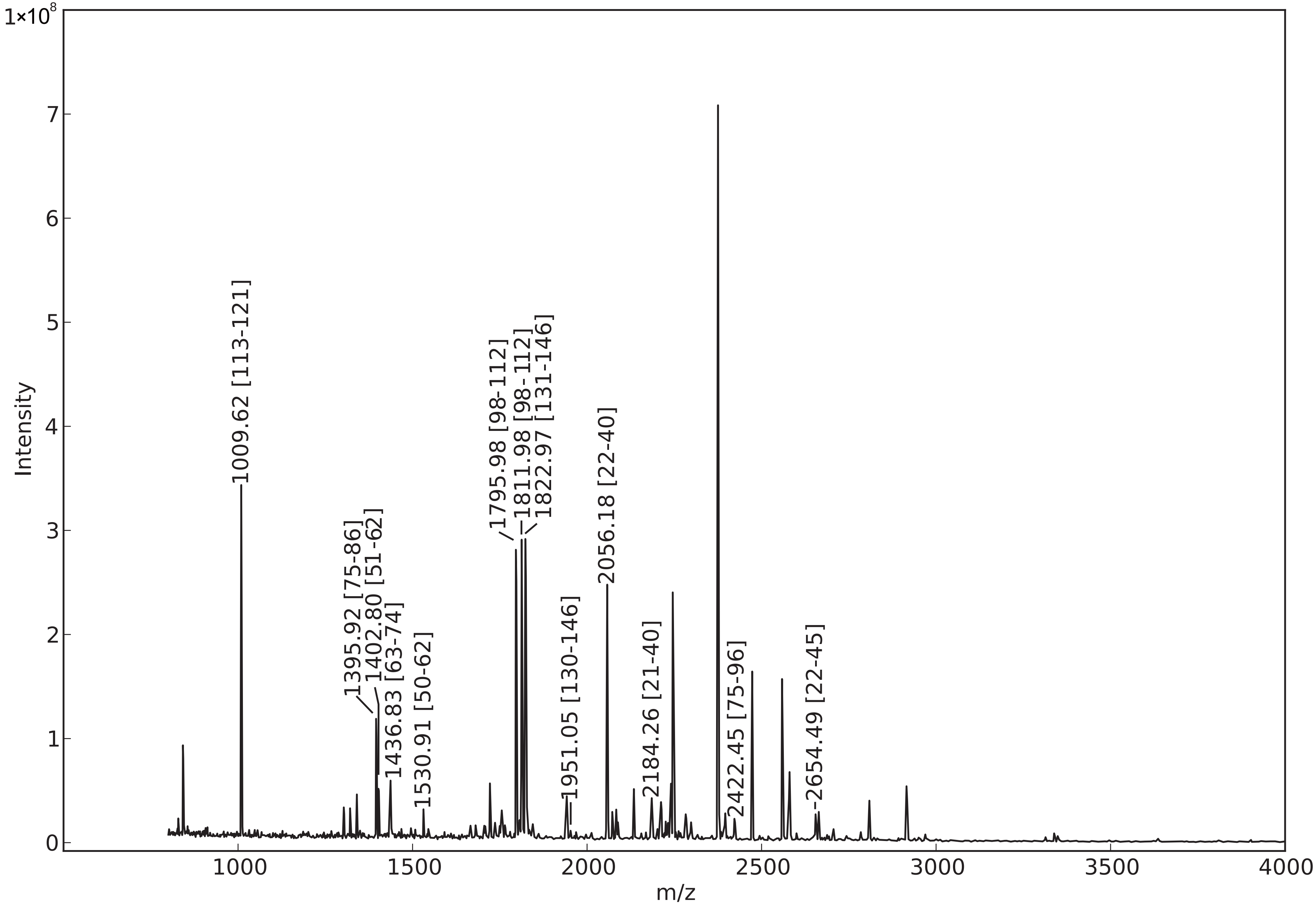
Spot No. 04


1×10^9
Intensity
1.2
1.0
0.8
0.6
0.4
0.2
0.0
1000
1500
2000
2500
3000
3500
4000
m/z
987.56 [143-152]
1153.52 [69-78]
1335.72 [115-127]
1365.81 [102-114]
2044.05 [115-134]
2336.07 [79-101]
3100.52 [39-68]
3116.53 [39-68]
3425.82 [4-38]
3470.63 [69-101]

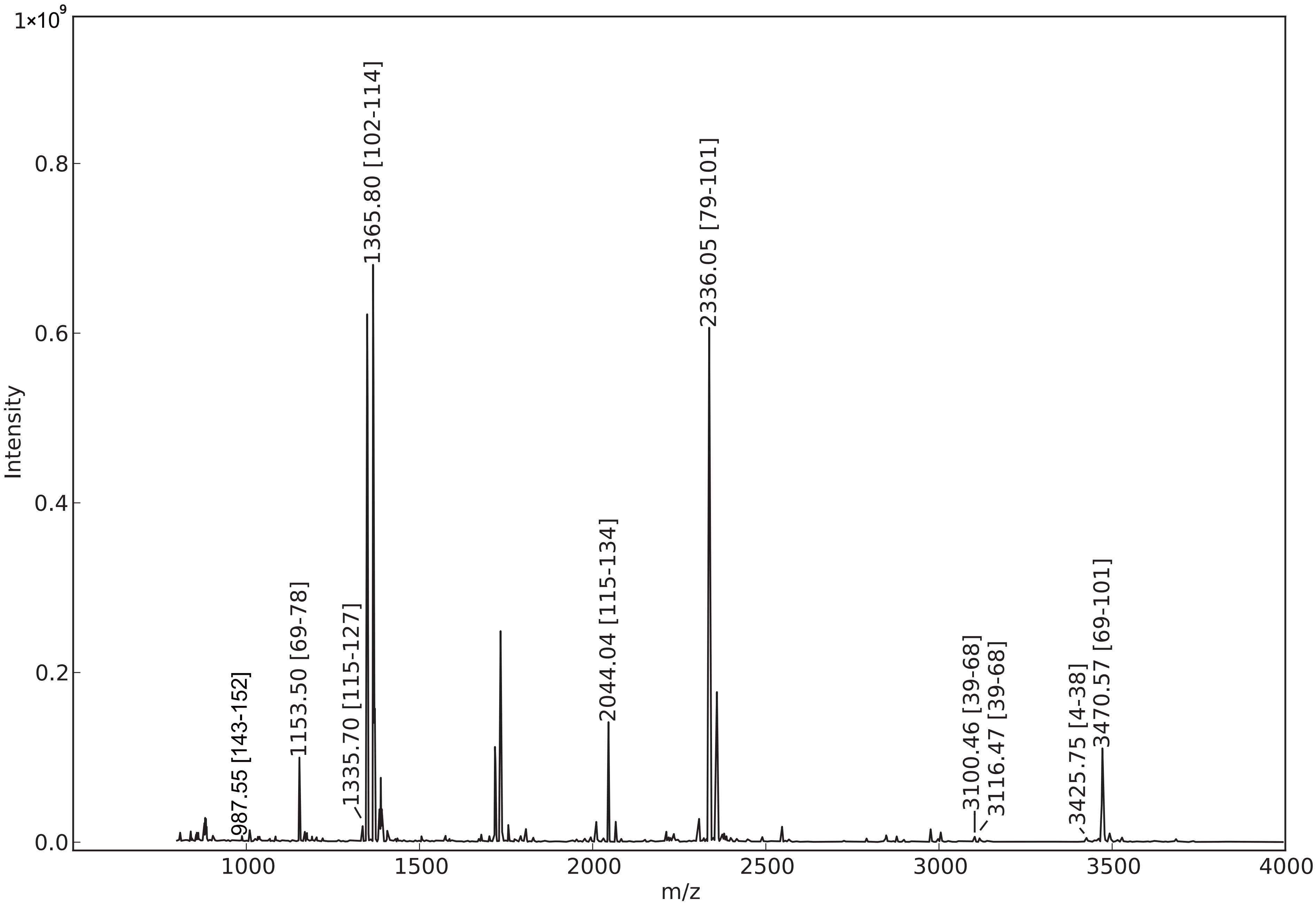
Spot No. 05


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1009.55 [114-122]
1375.81 [294-305]
1395.87 [76-87]
1402.75 [52-63]
1436.75 [64-75]
1530.83 [51-63]
1713.85 [132-146]
1795.92 [99-113]
1811.92 [99-113]
1841.96 [132-147]
1952.01 [98-113]
1967.98 [98-113]
2056.11 [23-41]
2184.21 [22-41]
2422.38 [76-97]

Spot No. 06

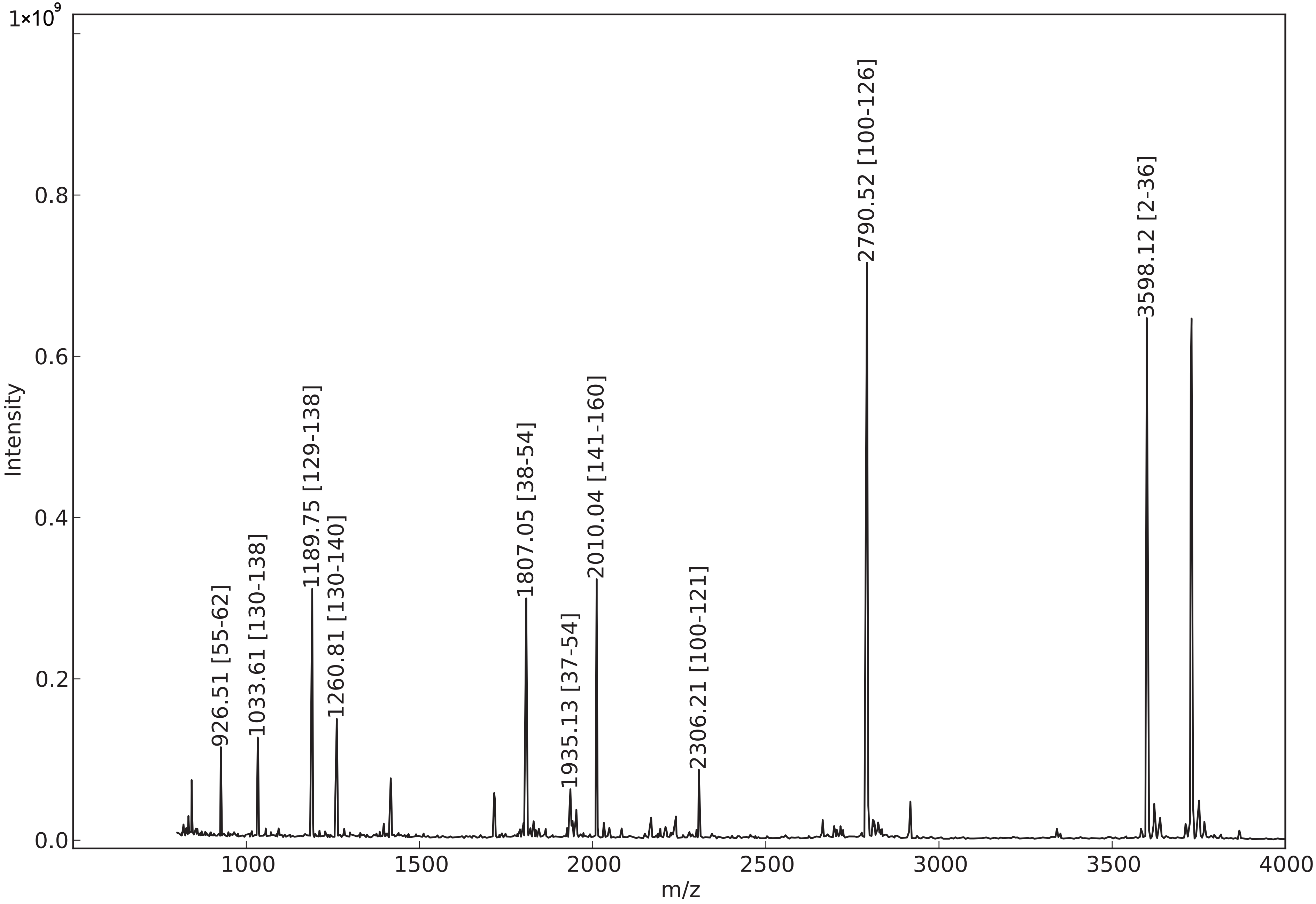

1×10^8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1009.62 [113-121]
1395.92 [75-86]
1402.80 [51-62]
1436.83 [63-74]
1530.91 [50-62]
1795.98 [98-112]
1811.98 [98-112]
1822.97 [131-146]
1951.05 [130-146]
2056.18 [22-40]
2184.26 [21-40]
2422.45 [75-96]
2654.49 [22-45]

Spot No. 07



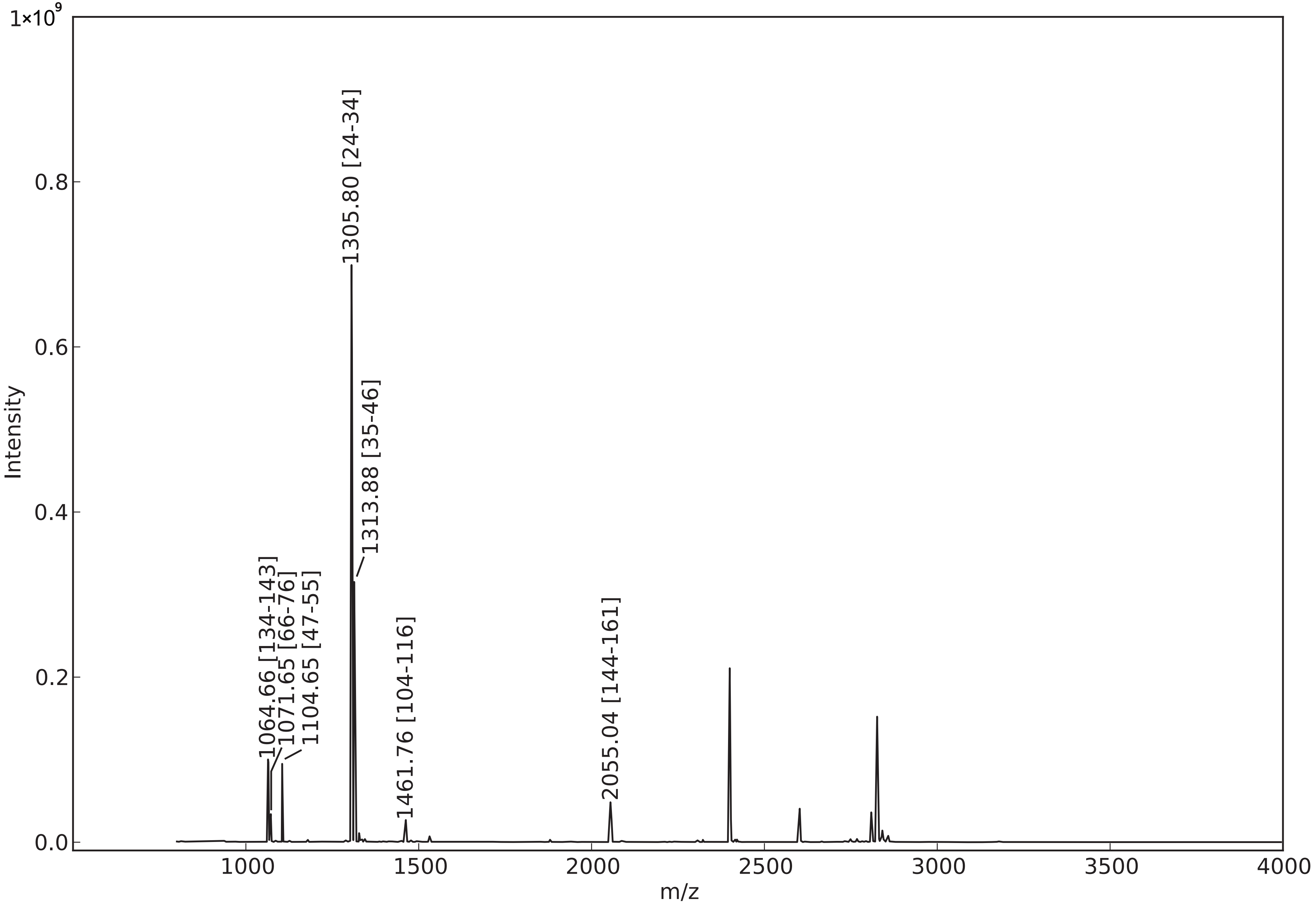
1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
987.55 [143-152]
1153.50 [69-78]
1335.70 [115-127]
1365.80 [102-114]
2044.04 [115-134]
2336.05 [79-101]
3100.46 [39-68]
3116.47 [39-68]
3425.75 [4-38]
3470.57 [69-101]

Spot No. 08

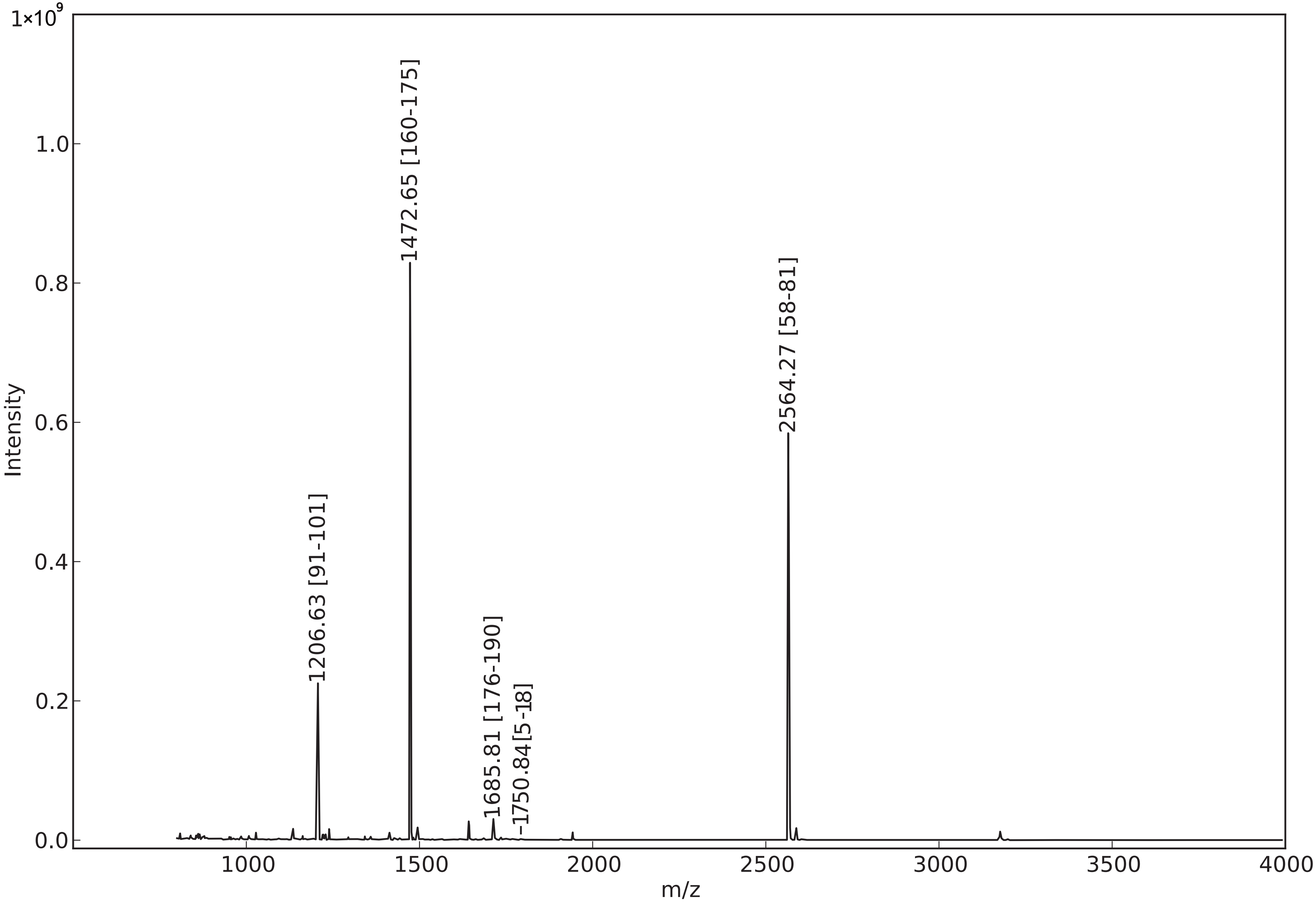


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
926.51 [55-62]
1033.61 [130-138]
1189.75 [129-138]
1260.81 [130-140]
1807.05 [38-54]
1935.13 [37-54]
2010.04 [141-160]
2306.21 [100-121]
2790.52 [100-126]
3598.12 [2-36]

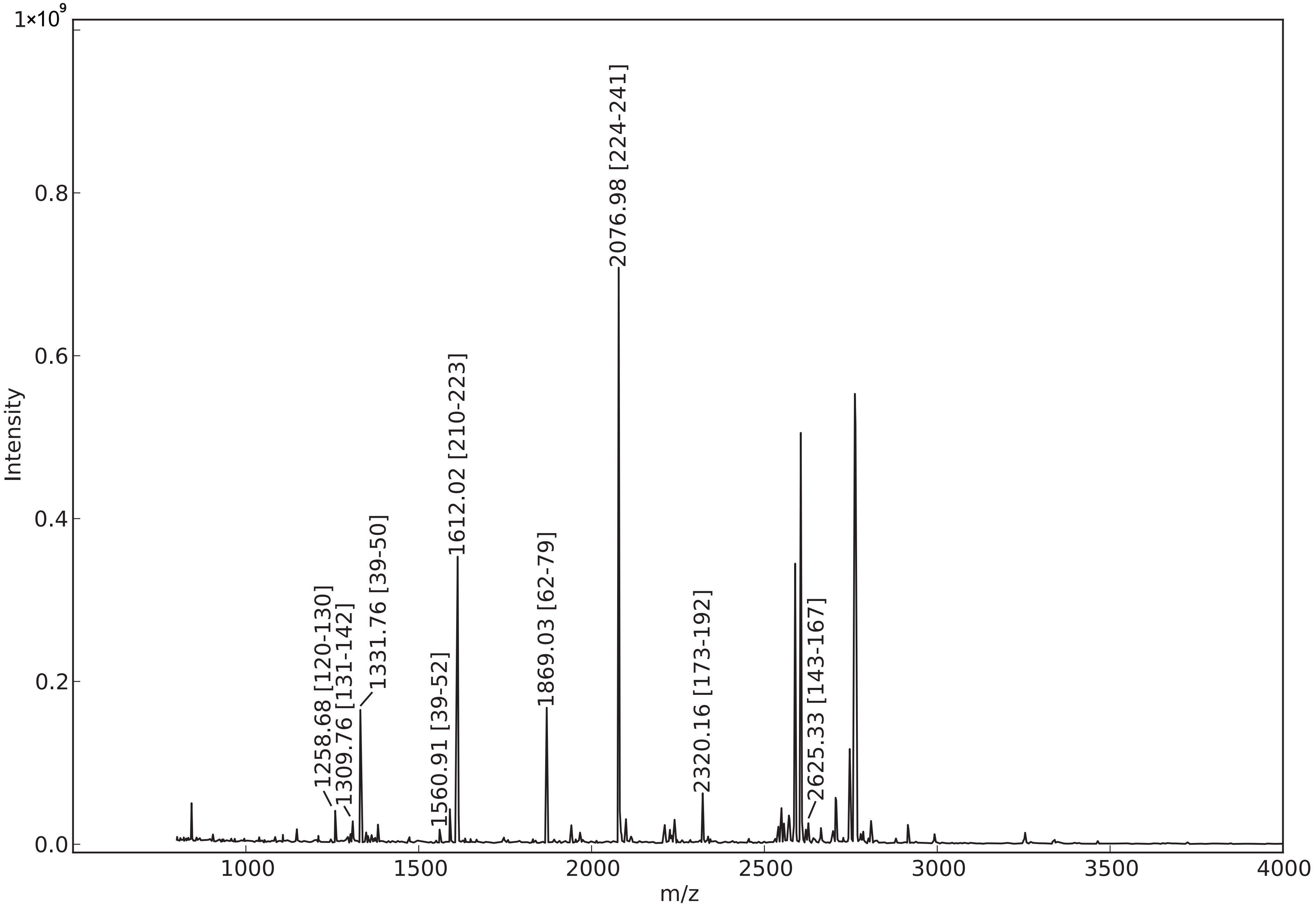
Spot No. 09


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1305.80 [24-34]
1313.88 [35-46]
1064.66 [134-143]
1071.65 [66-76]
1104.65 [47-55]
1461.76 [104-116]
2055.04 [144-161]

Spot No. 10

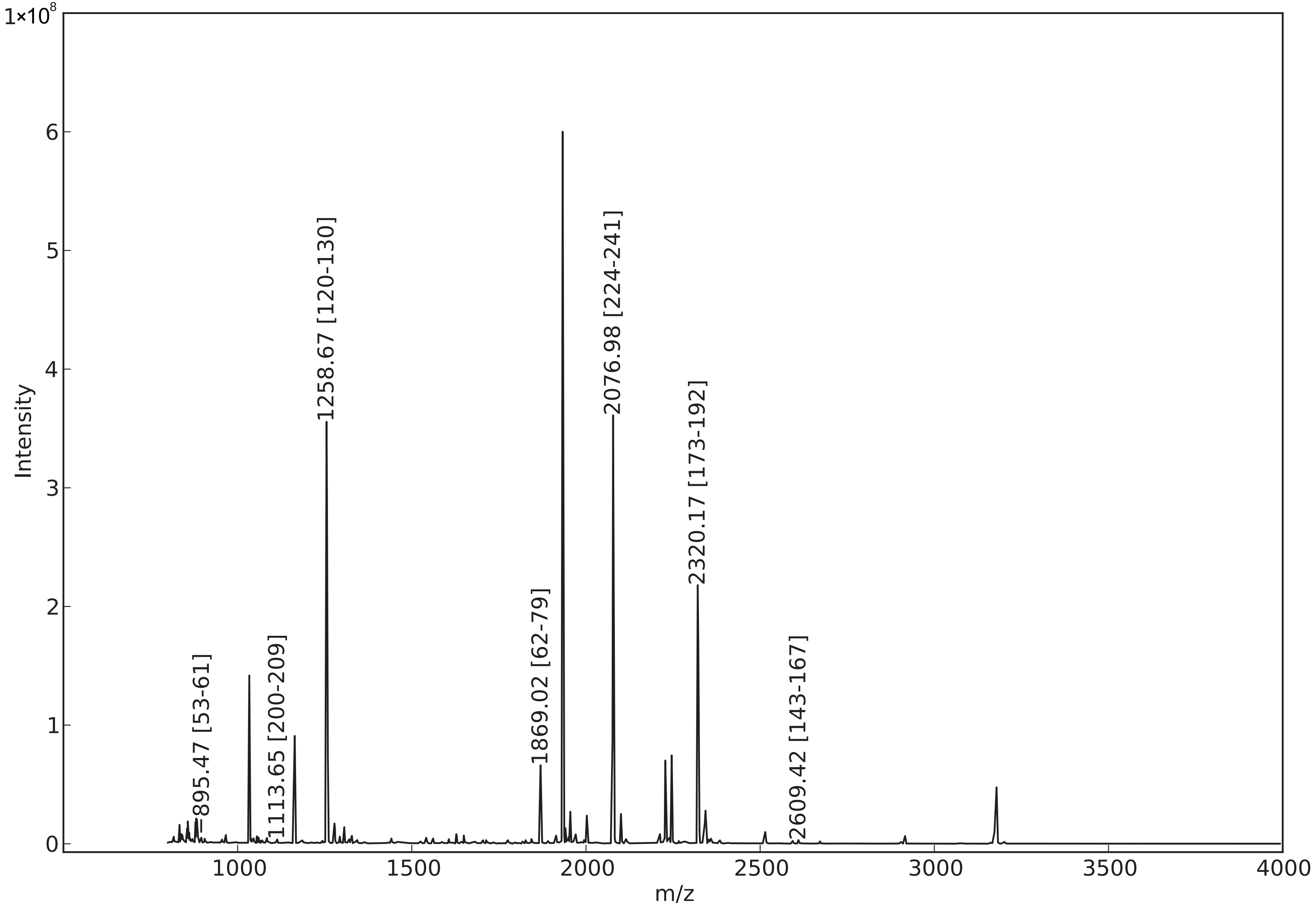

1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1206.63 [91-101]
1472.65 [160-175]
1685.81 [176-190]
1750.84[5-18]
2564.27 [58-81]

Spot No. 11

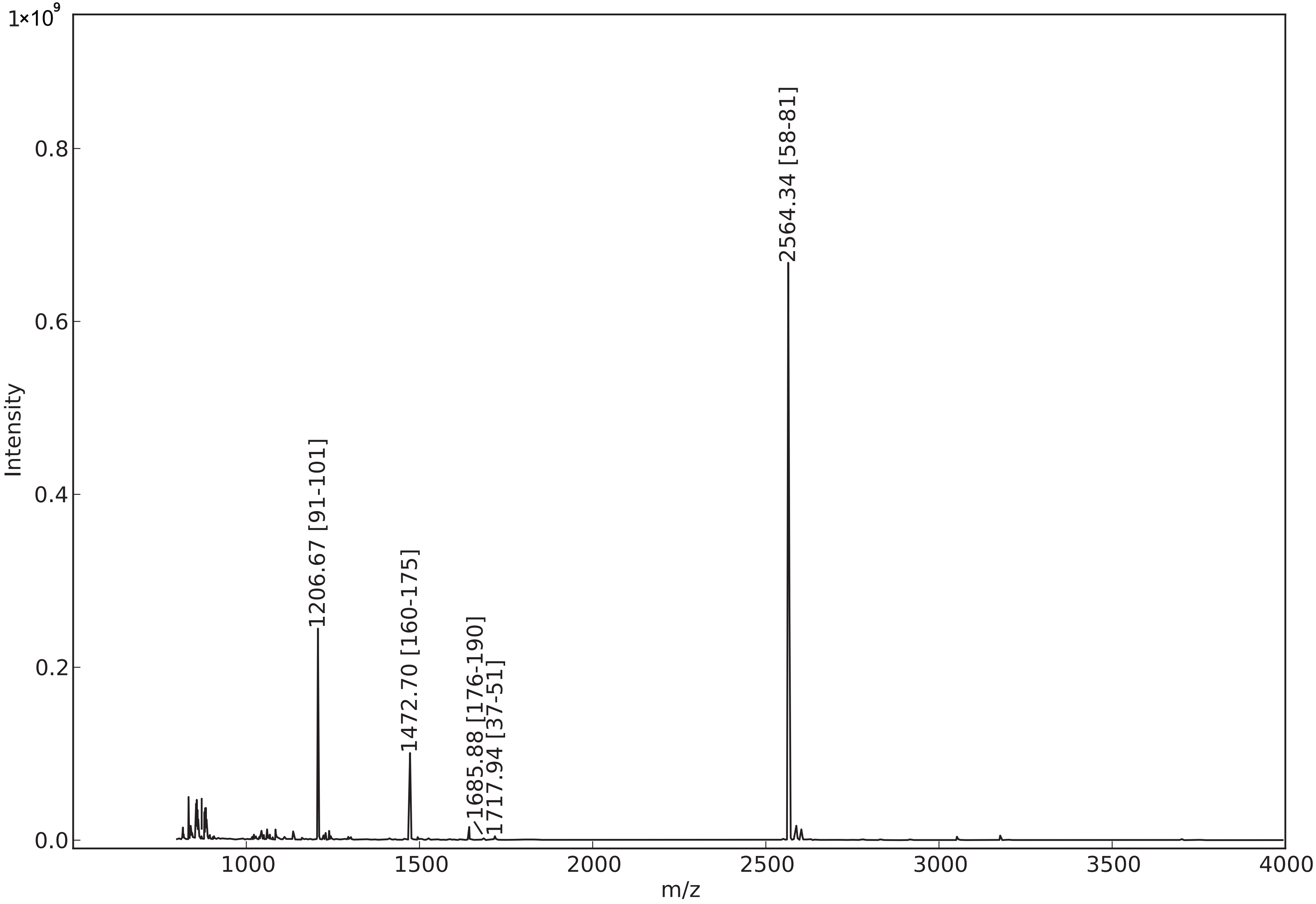


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1258.68 [120-130]
1309.76 [131-142]
1331.76 [39-50]
1560.91 [39-52]
1612.02 [210-223]
1869.03 [62-79]
2076.98 [224-241]
2320.16 [173-192]
2625.33 [143-167]

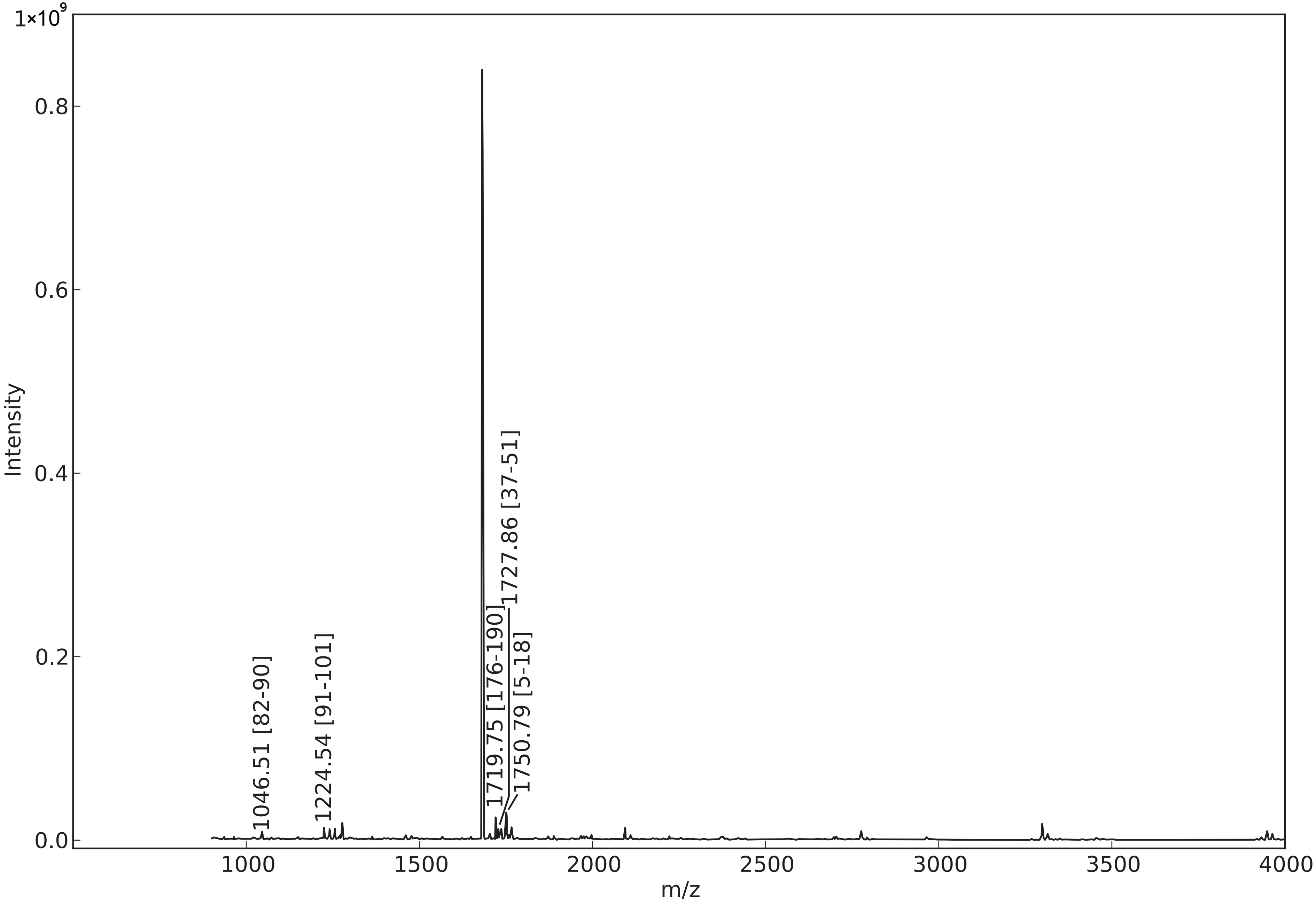
Spot No. 12


1×10^8
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
895.47 [53-61]
1113.65 [200-209]
1258.67 [120-130]
1869.02 [62-79]
2076.98 [224-241]
2320.17 [173-192]
2609.42 [143-167]

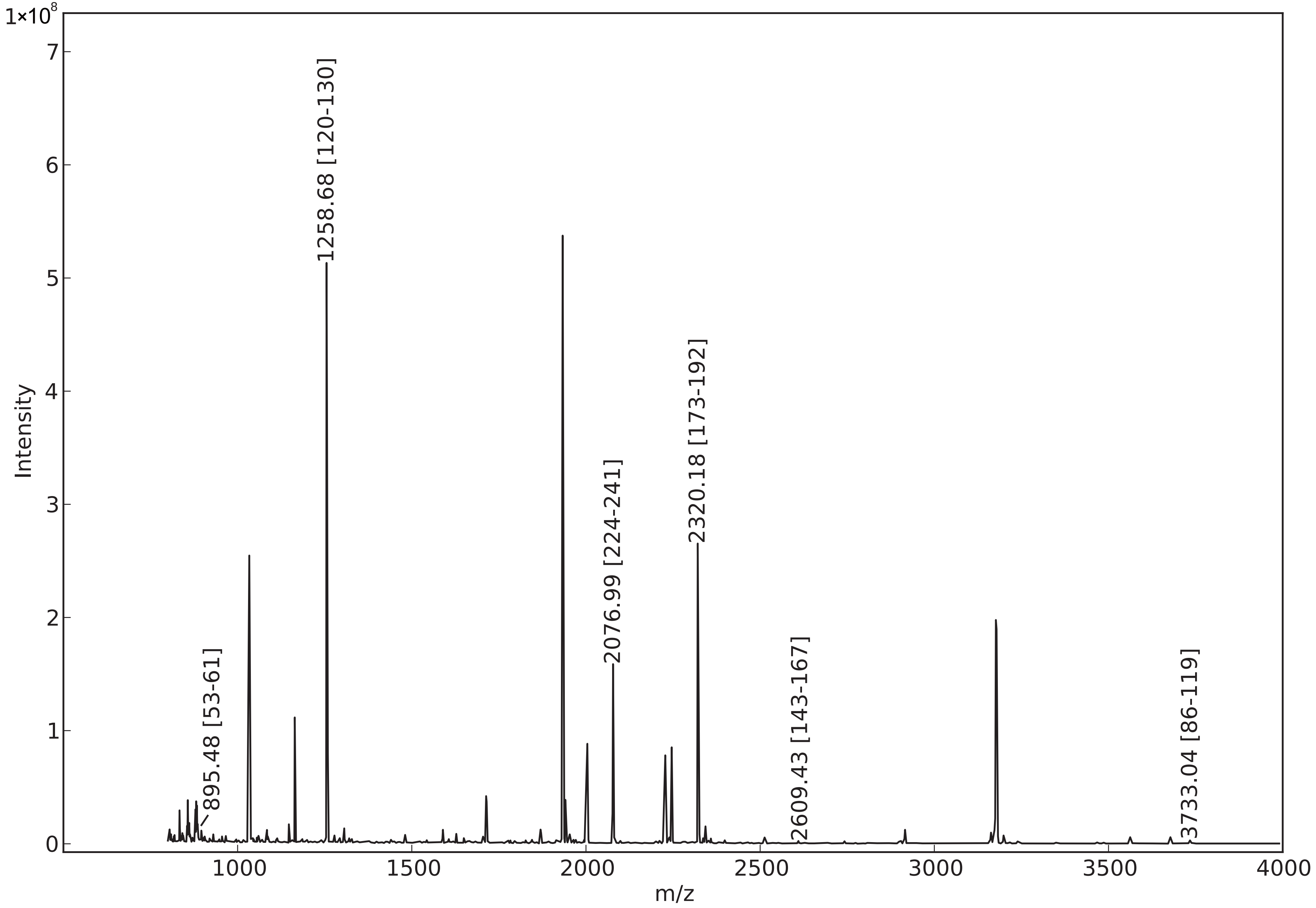
Spot No. 13


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1206.67 [91-101]
1472.70 [160-175]
1685.88 [176-190]
1717.94 [37-51]
2564.34 [58-81]

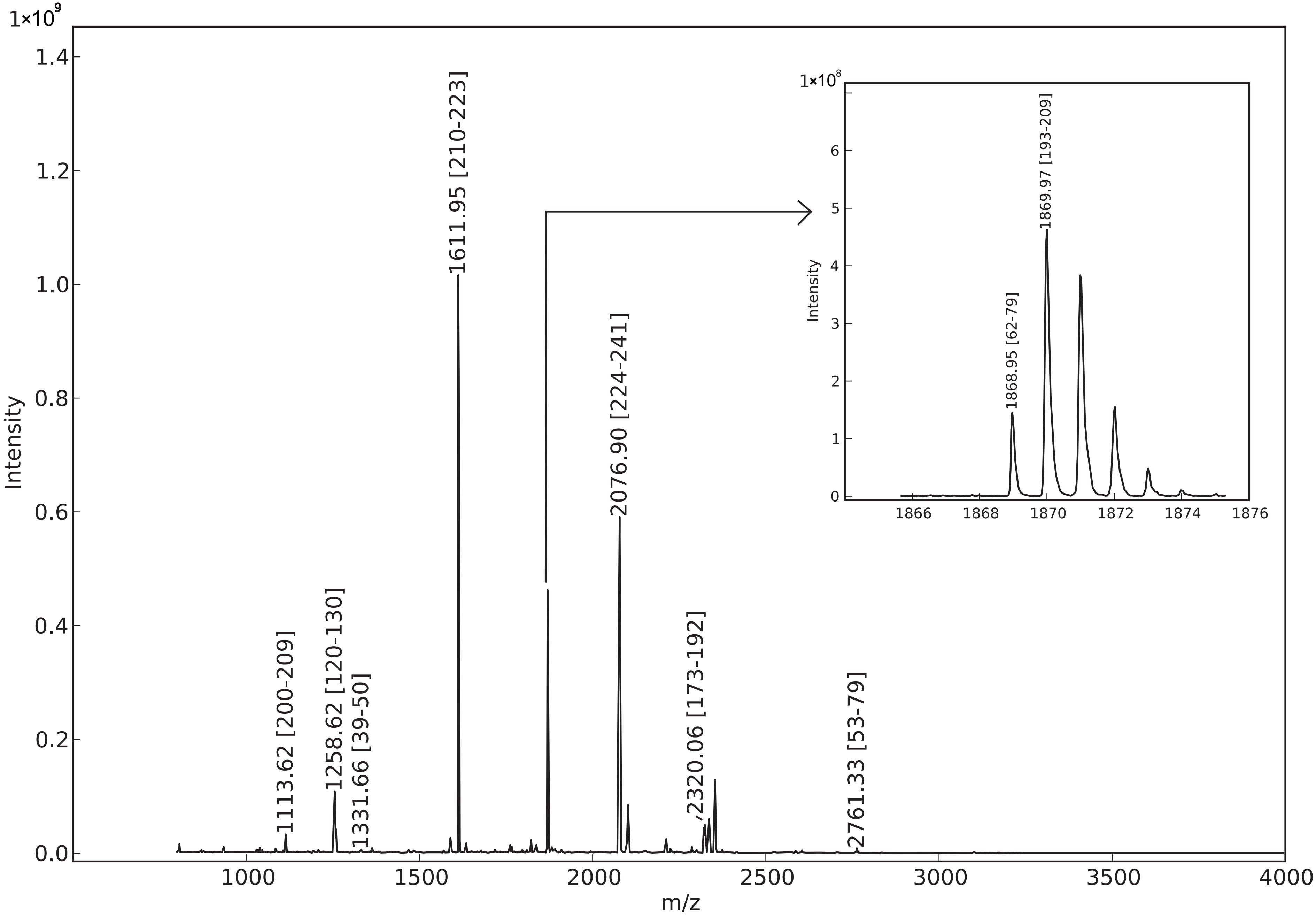
Spot No. 14


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1046.51 [82-90]
1224.54 [91-101]
1719.75 [176-190]
1727.86 [37-51]
1750.79 [5-18]

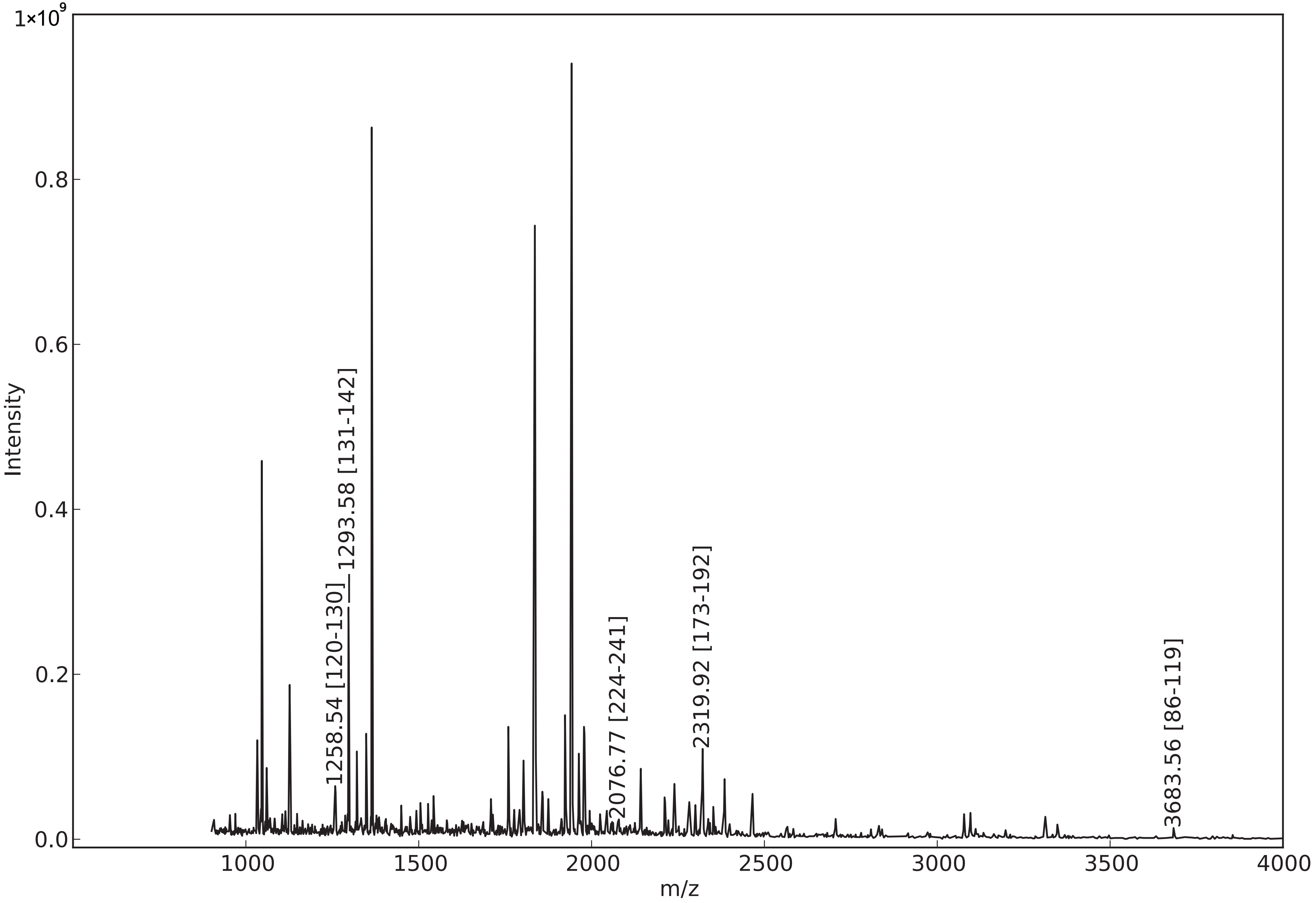
Spot No. 15


1×10⁸
Intensity
0
1
2
3
4
5
6
7
m/z
1000
1500
2000
2500
3000
3500
4000
895.48 [53-61]
1258.68 [120-130]
2076.99 [224-241]
2320.18 [173-192]
2609.43 [143-167]
3733.04 [86-119]

Spot No. 16

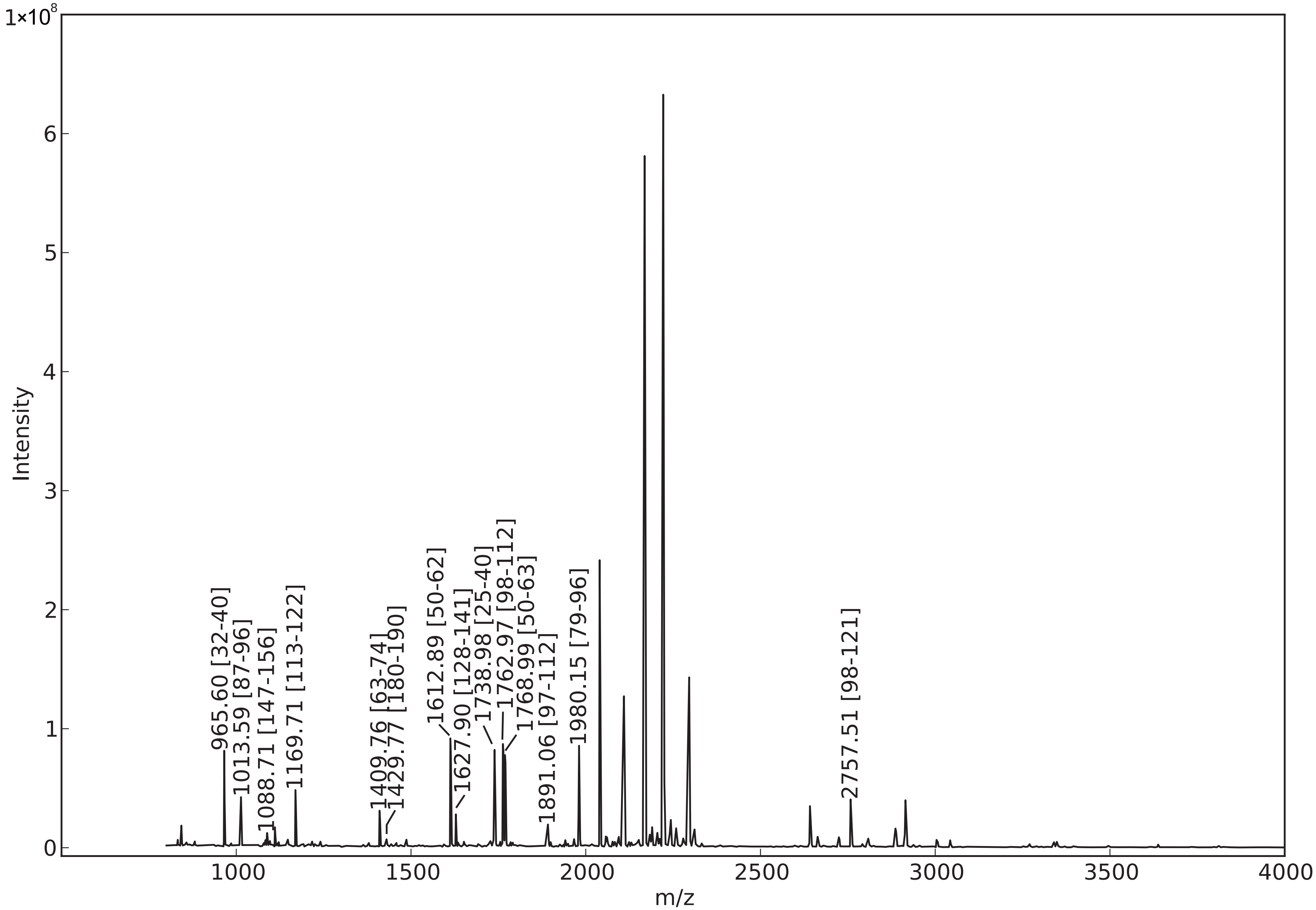

1×10^9
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1113.62 [200-209]
1258.62 [120-130]
1331.66 [39-50]
1611.95 [210-223]
2076.90 [224-241]
2320.06 [173-192]
2761.33 [53-79]
1×10^8
6
5
4
3
2
1
0
Intensity
1866
1868
1870
1872
1874
1876
1869.97 [193-209]
1868.95 [62-79]

Spot No. 17

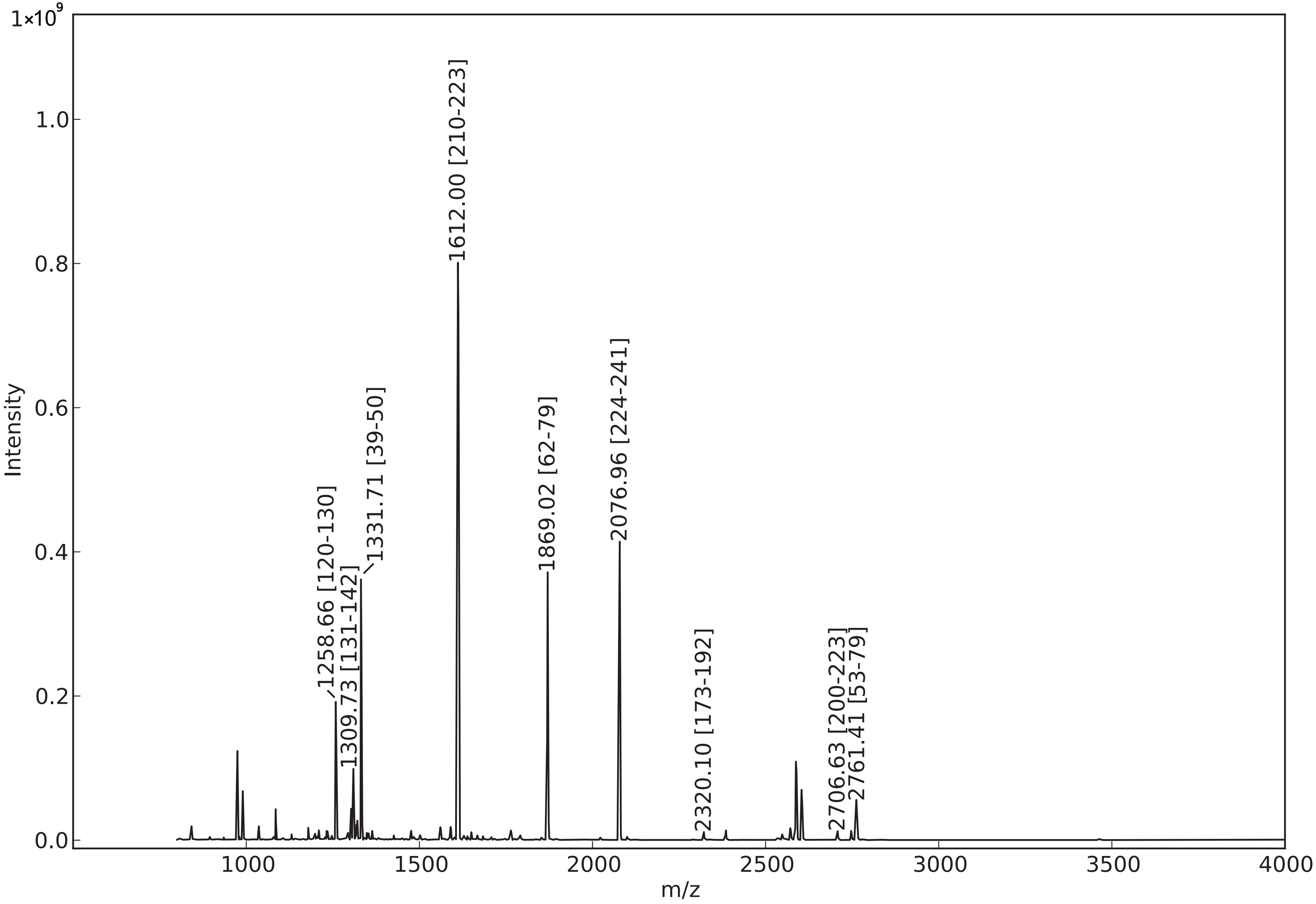


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1258.54 [120-130]
1293.58 [131-142]
2076.77 [224-241]
2319.92 [173-192]
3683.56 [86-119]

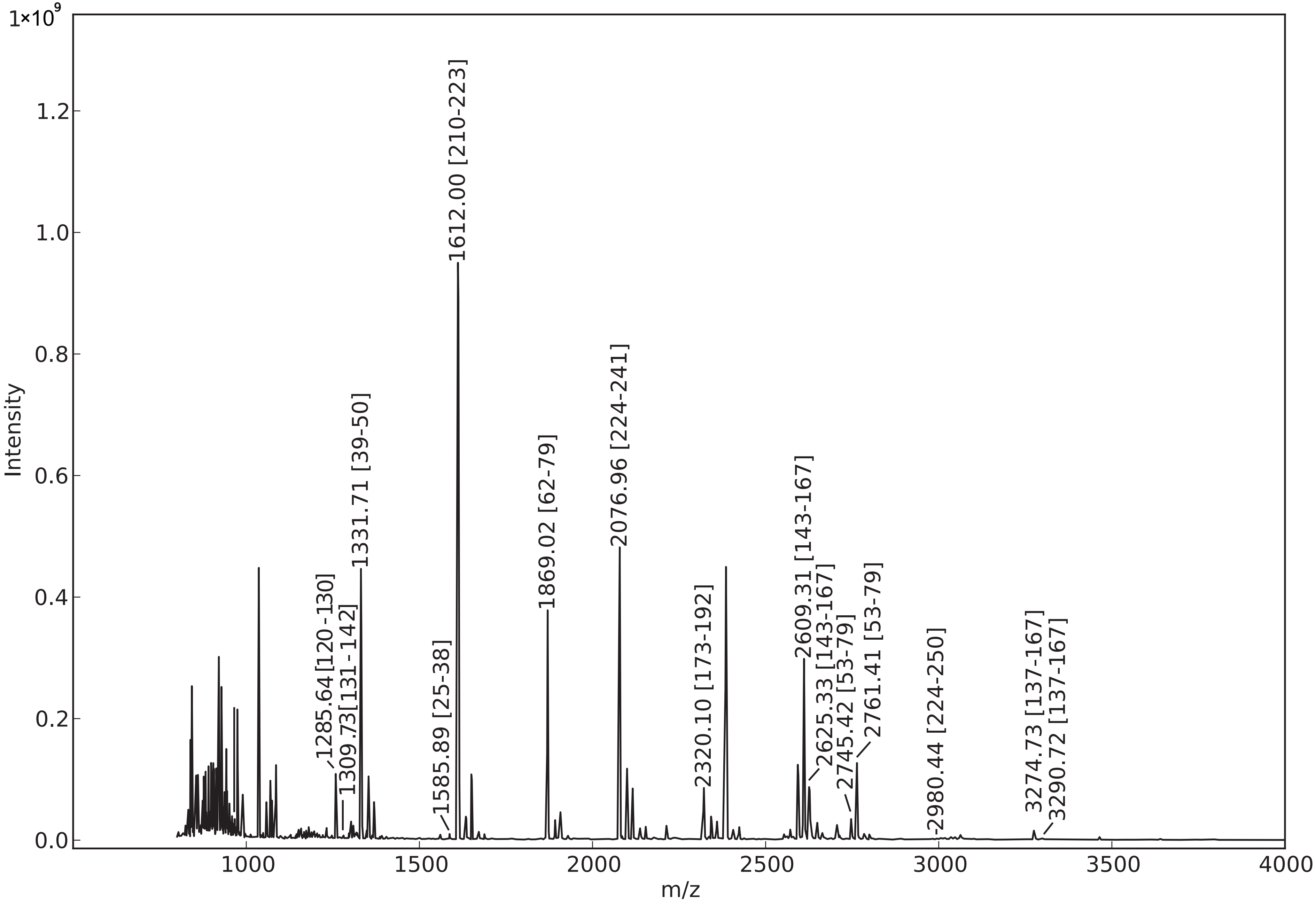
Spot No. 18


1×10^8
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
965.60 [32-40]
1013.59 [87-96]
1088.71 [147-156]
1169.71 [113-122]
1409.76 [63-74]
1429.77 [180-190]
1612.89 [50-62]
1627.90 [128-141]
1738.98 [25-40]
1762.97 [98-112]
1768.99 [50-63]
1891.06 [97-112]
1980.15 [79-96]
2757.51 [98-121]

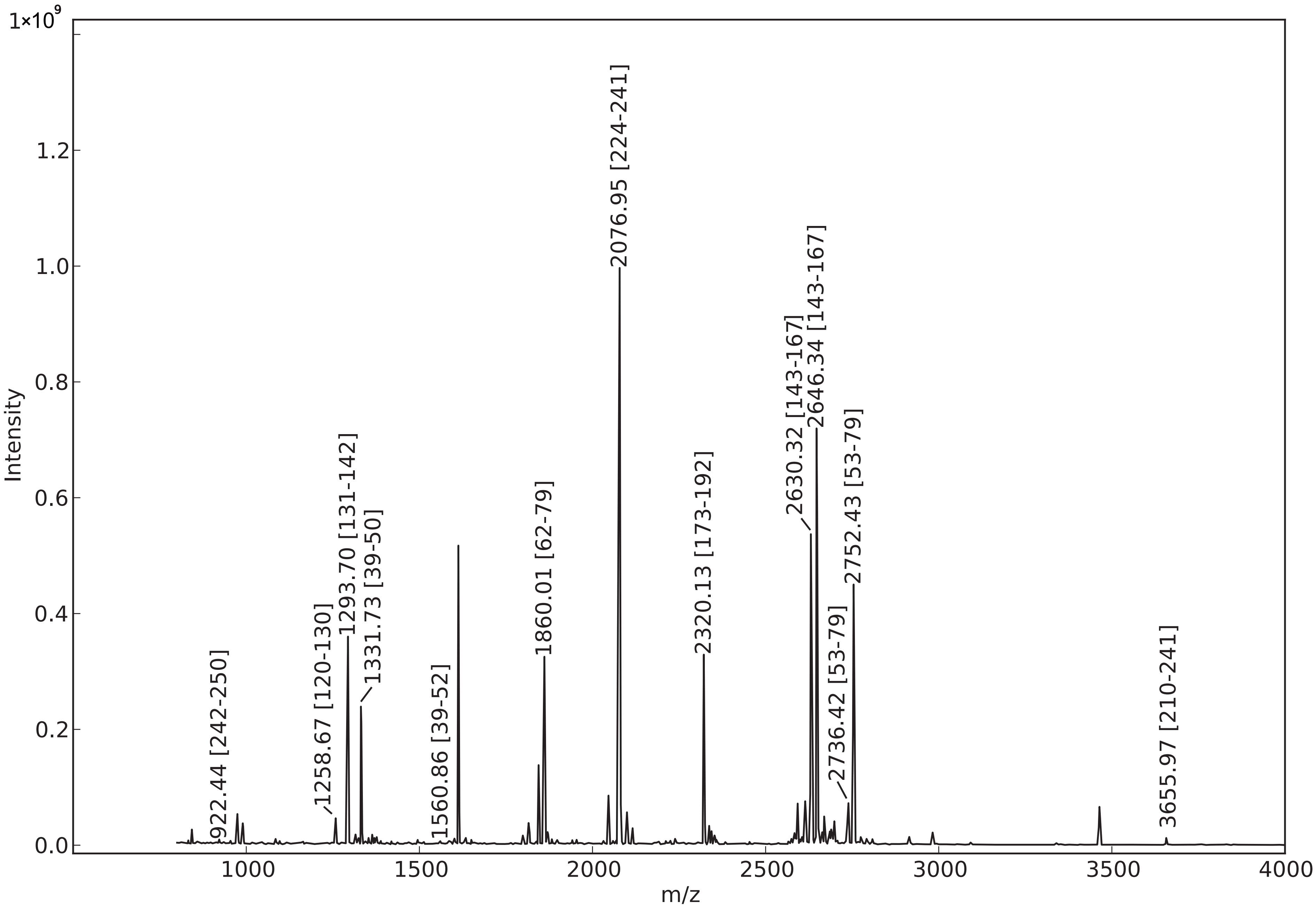
Spot No. 19


1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1258.66 [120-130]
1309.73 [131-142]
1331.71 [39-50]
1612.00 [210-223]
1869.02 [62-79]
2076.96 [224-241]
2320.10 [173-192]
2706.63 [200-223]
2761.41 [53-79]

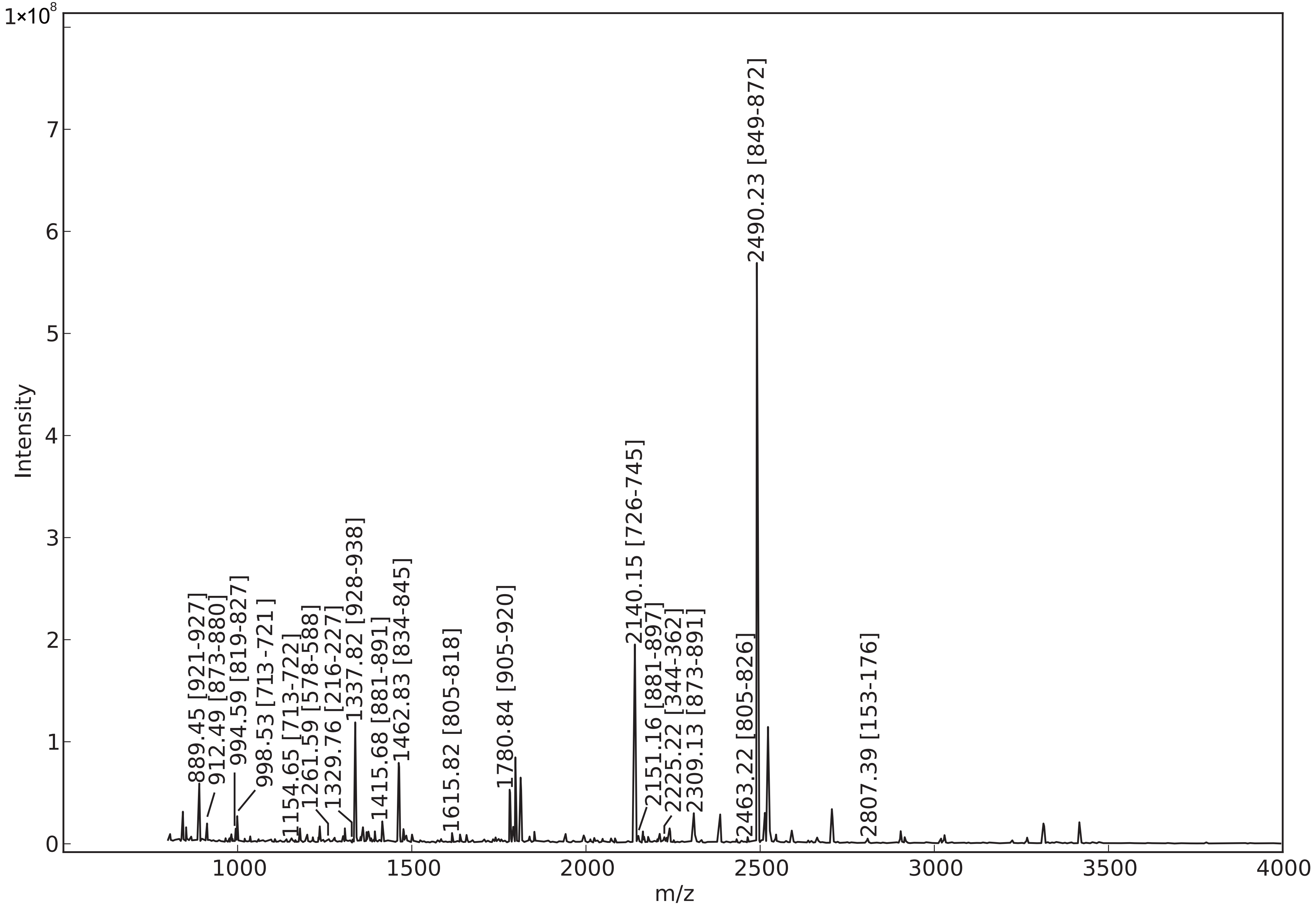
Spot No. 20


1×10^9
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1285.64[120-130]
1309.73[131-142]
1331.71 [39-50]
1585.89 [25-38]
1612.00 [210-223]
1869.02 [62-79]
2076.96 [224-241]
2320.10 [173-192]
2609.31 [143-167]
2625.33 [143-167]
2745.42 [53-79]
2761.41 [53-79]
2980.44 [224-250]
3274.73 [137-167]
3290.72 [137-167]

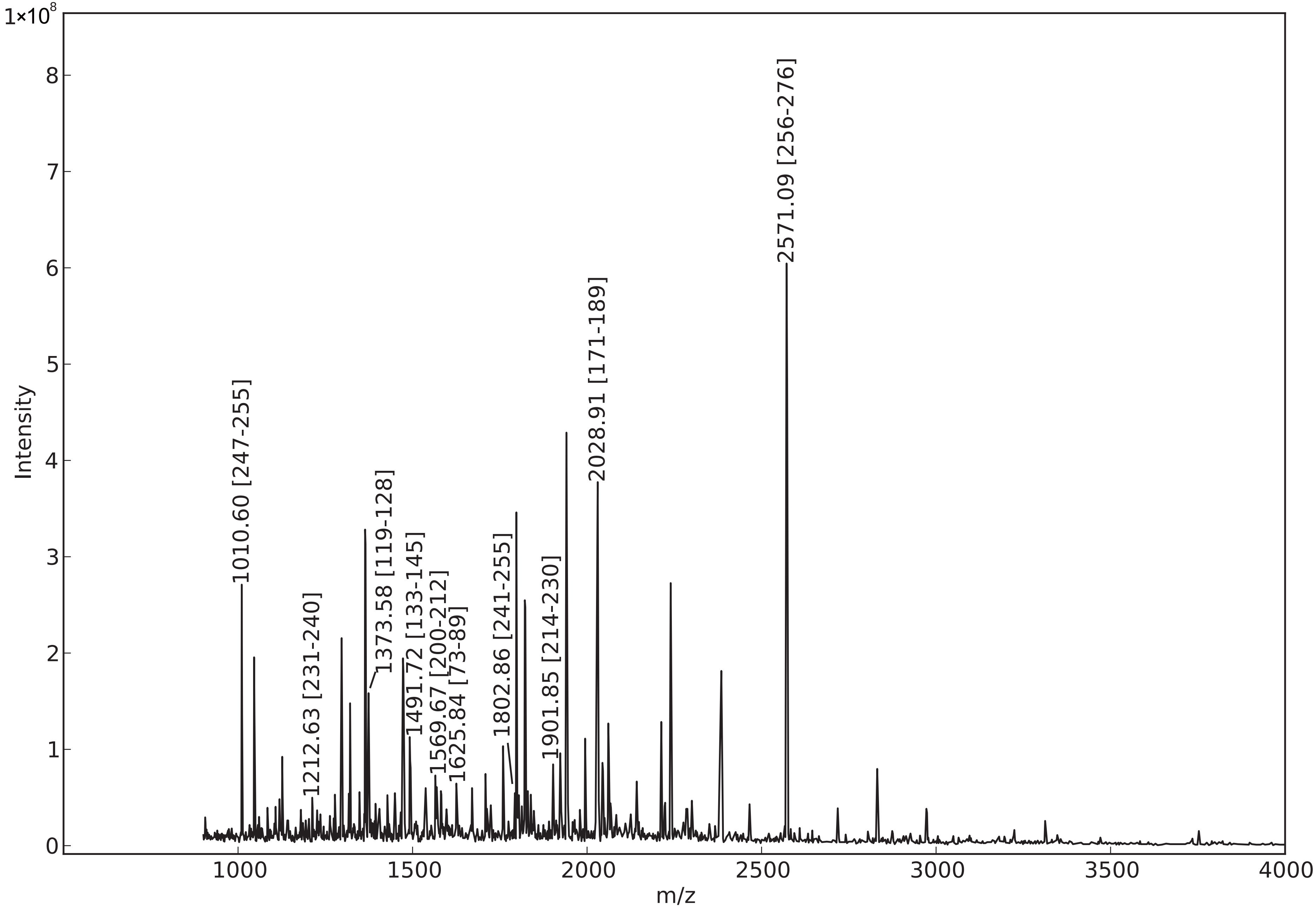
Spot No. 21


1×10^9
Intensity
1.2
1.0
0.8
0.6
0.4
0.2
0.0
m/z
1000
1500
2000
2500
3000
3500
4000
922.44 [242-250]
1258.67 [120-130]
1293.70 [131-142]
1331.73 [39-50]
1560.86 [39-52]
1860.01 [62-79]
2076.95 [224-241]
2320.13 [173-192]
2630.32 [143-167]
2646.34 [143-167]
2736.42 [53-79]
2752.43 [53-79]
3655.97 [210-241]

Spot No. 22

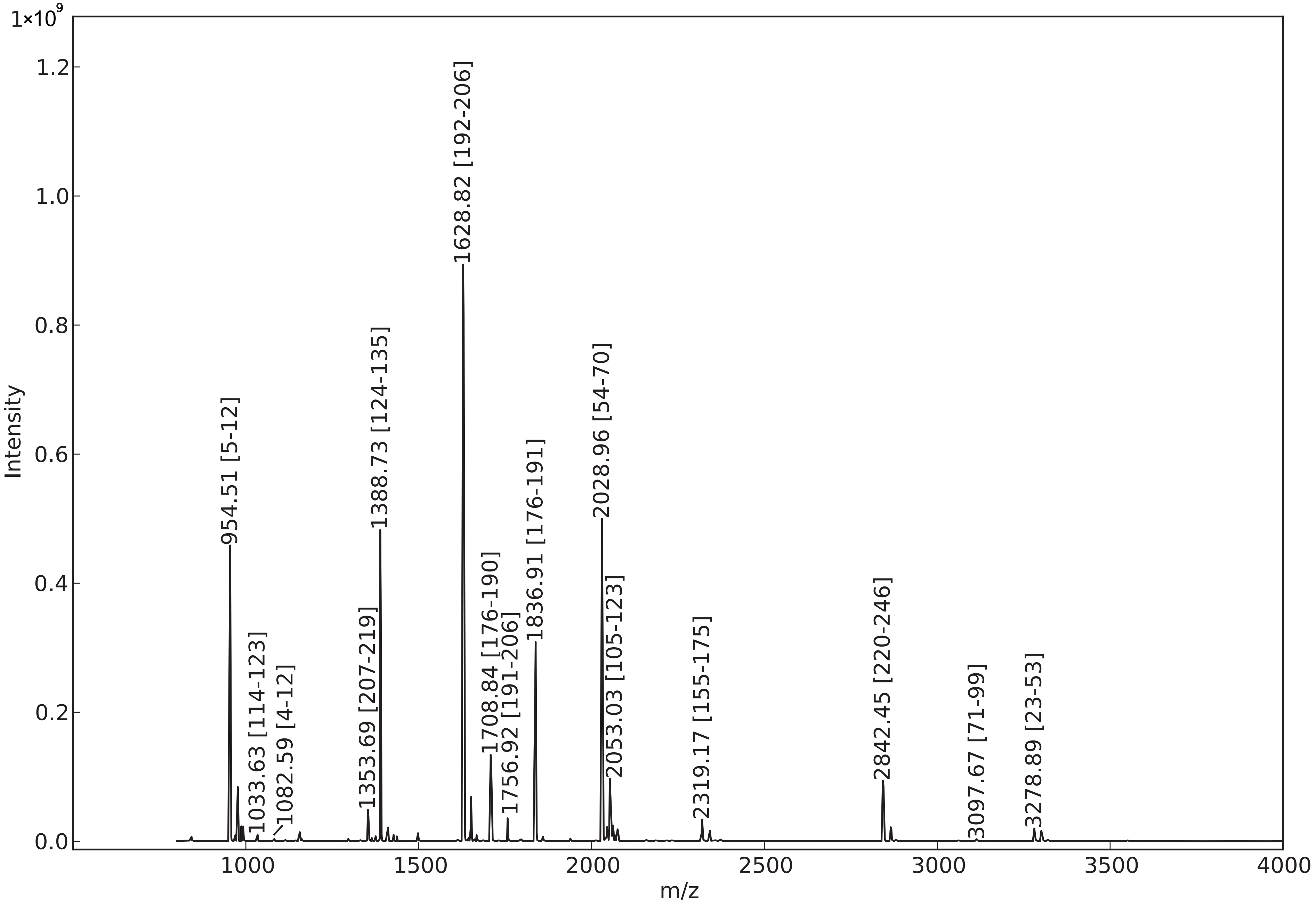

1×10^8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
889.45 [921-927]
912.49 [873-880]
994.59 [819-827]
998.53 [713-721]
1154.65 [713-722]
1261.59 [578-588]
1329.76 [216-227]
1337.82 [928-938]
1415.68 [881-891]
1462.83 [834-845]
1615.82 [805-818]
1780.84 [905-920]
2140.15 [726-745]
2151.16 [881-897]
2225.22 [344-362]
2309.13 [873-891]
2463.22 [805-826]
2490.23 [849-872]
2807.39 [153-176]

Spot No. 23



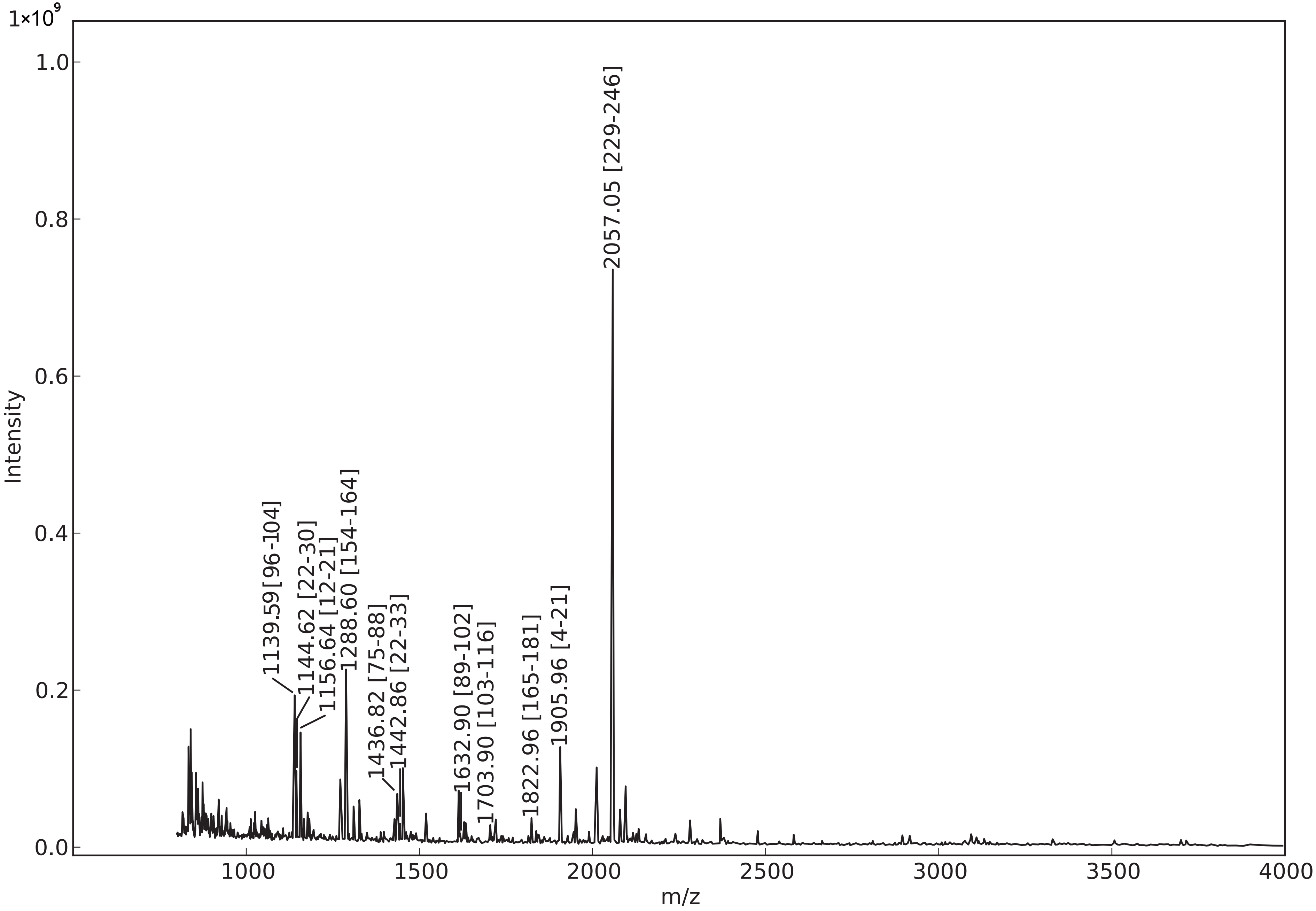
1×10^8
8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1010.60 [247-255]
1212.63 [231-240]
1373.58 [119-128]
1491.72 [133-145]
1569.67 [200-212]
1625.84 [73-89]
1802.86 [241-255]
1901.85 [214-230]
2028.91 [171-189]
2571.09 [256-276]

Spot No. 24



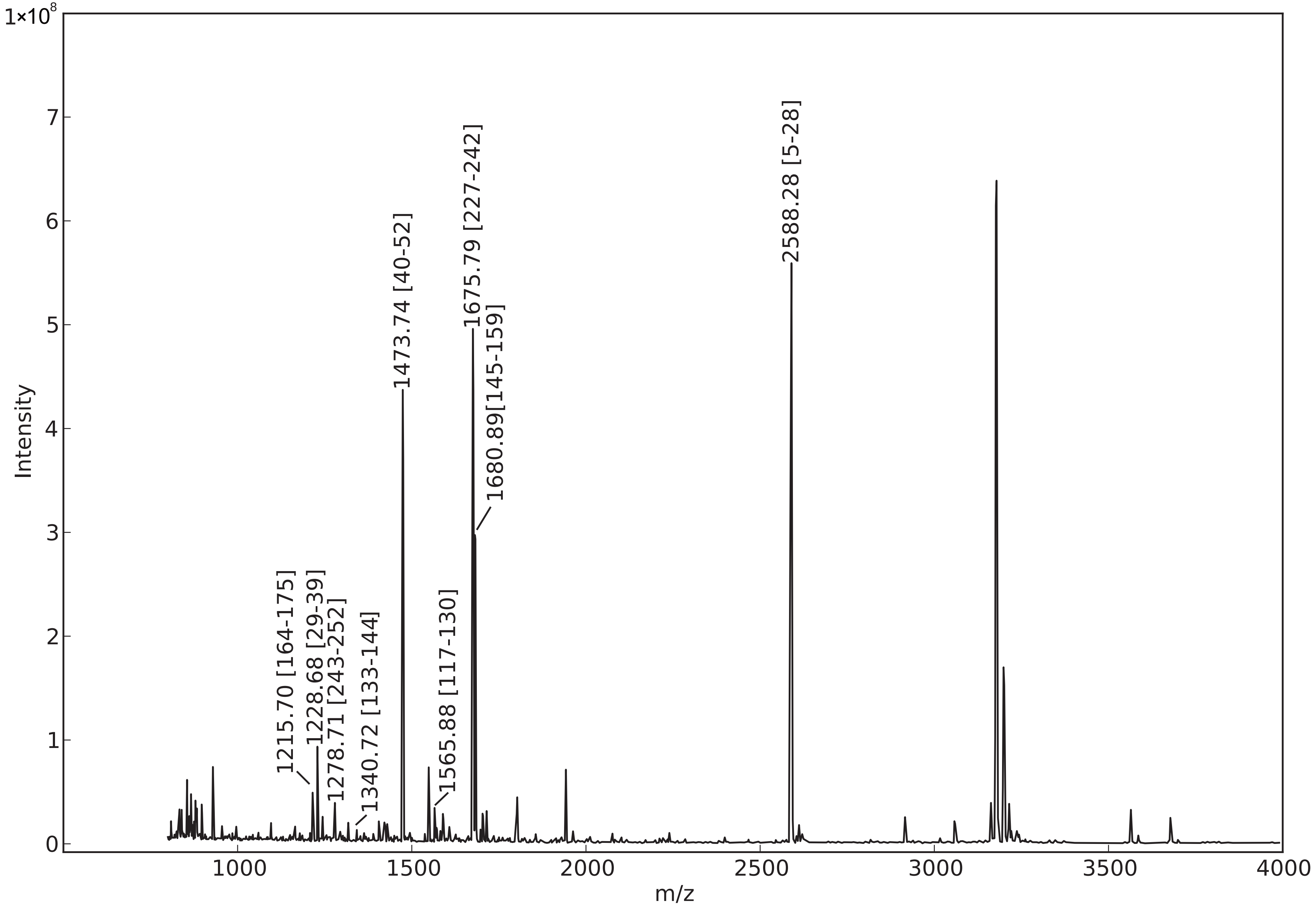
1×10⁹
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
954.51 [5-12]
1033.63 [114-123]
1082.59 [4-12]
1353.69 [207-219]
1388.73 [124-135]
1628.82 [192-206]
1708.84 [176-190]
1756.92 [191-206]
1836.91 [176-191]
2028.96 [54-70]
2053.03 [105-123]
2319.17 [155-175]
2842.45 [220-246]
3097.67 [71-99]
3278.89 [23-53]

Spot No. 25

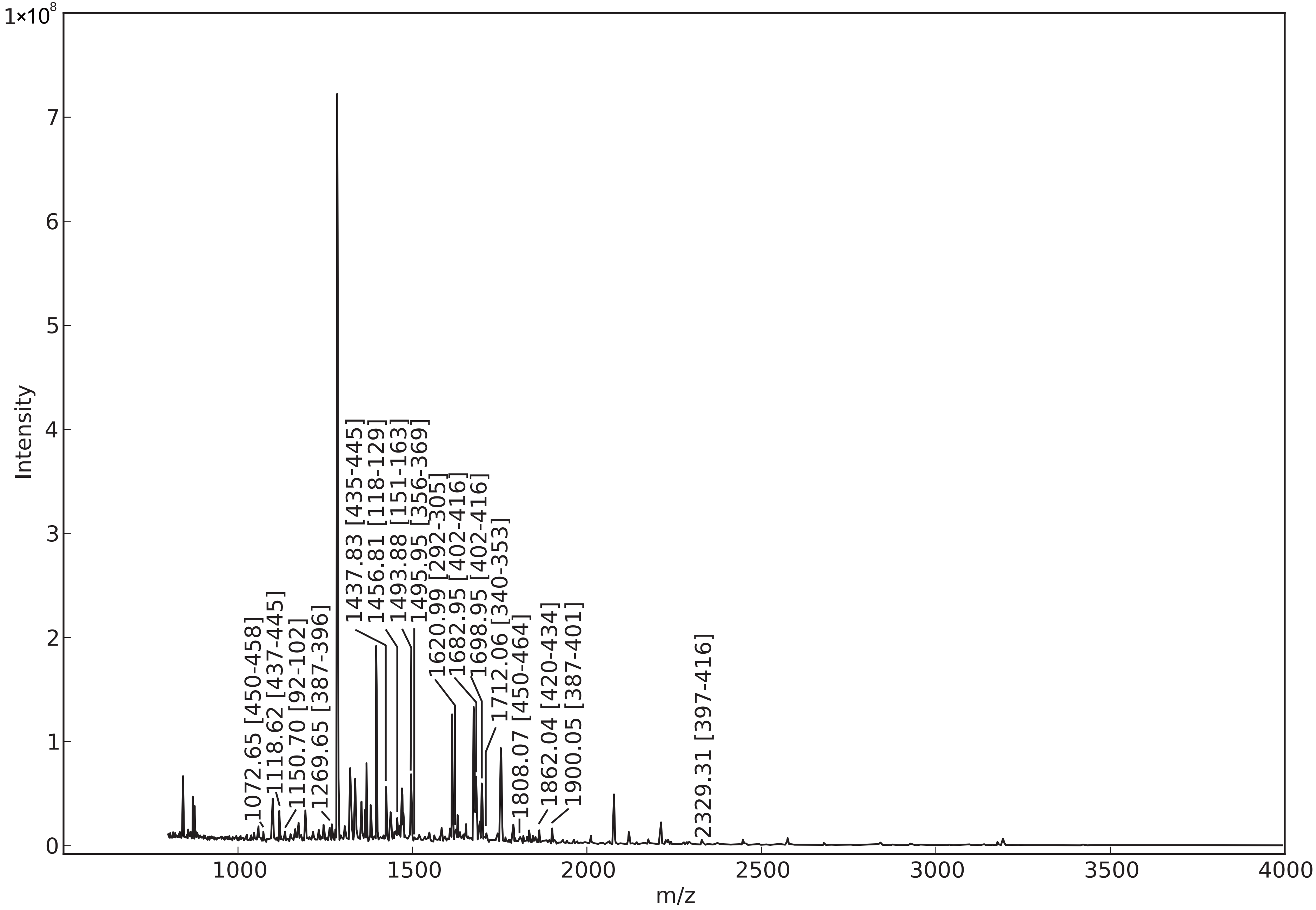


1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1139.59 [96-104]
1144.62 [22-30]
1156.64 [12-21]
1288.60 [154-164]
1436.82 [75-88]
1442.86 [22-33]
1632.90 [89-102]
1703.90 [103-116]
1822.96 [165-181]
1905.96 [4-21]
2057.05 [229-246]

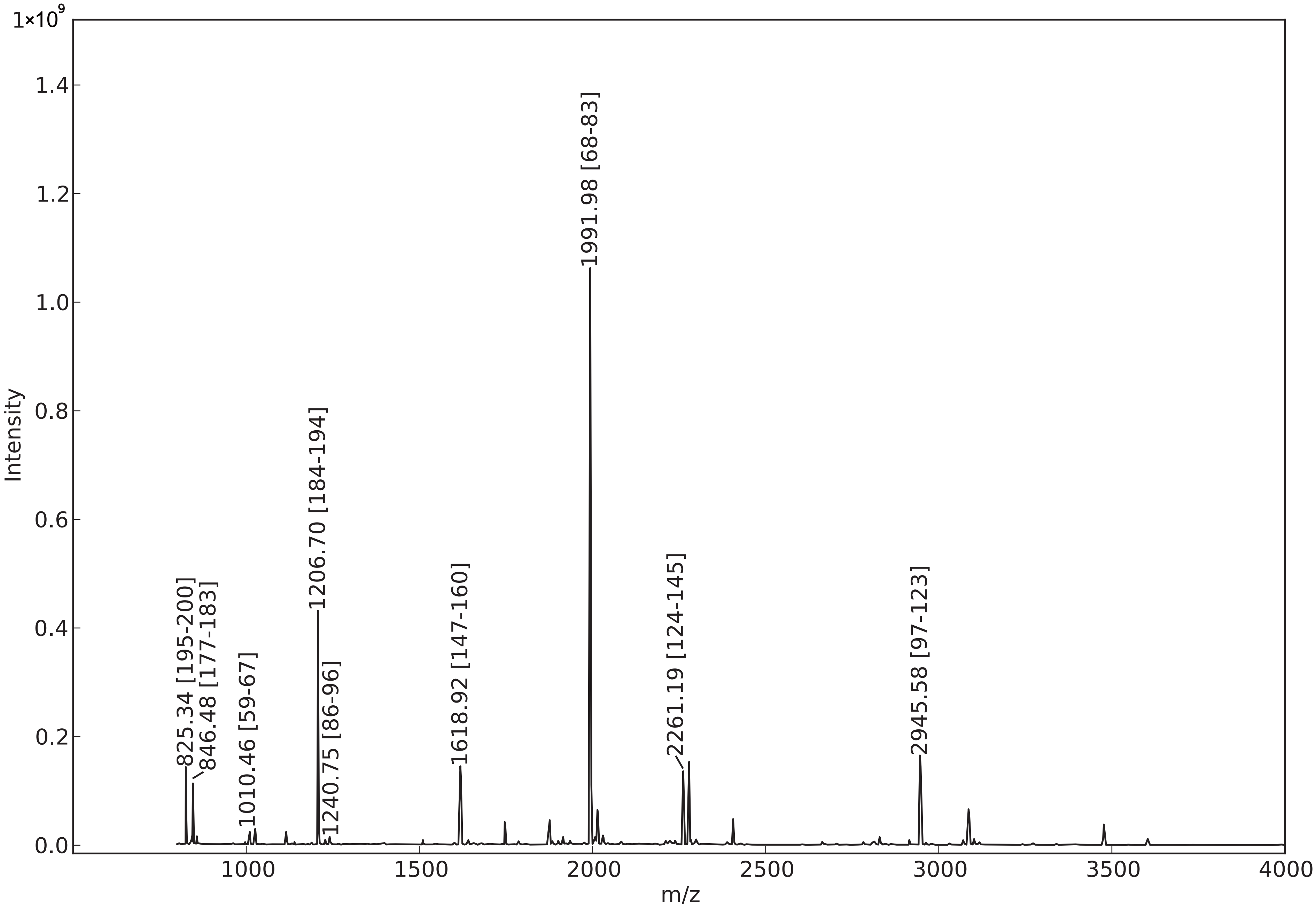
Spot No. 26


1×10^8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1215.70 [164-175]
1228.68 [29-39]
1278.71 [243-252]
1340.72 [133-144]
1473.74 [40-52]
1565.88 [117-130]
1675.79 [227-242]
1680.89[145-159]
2588.28 [5-28]

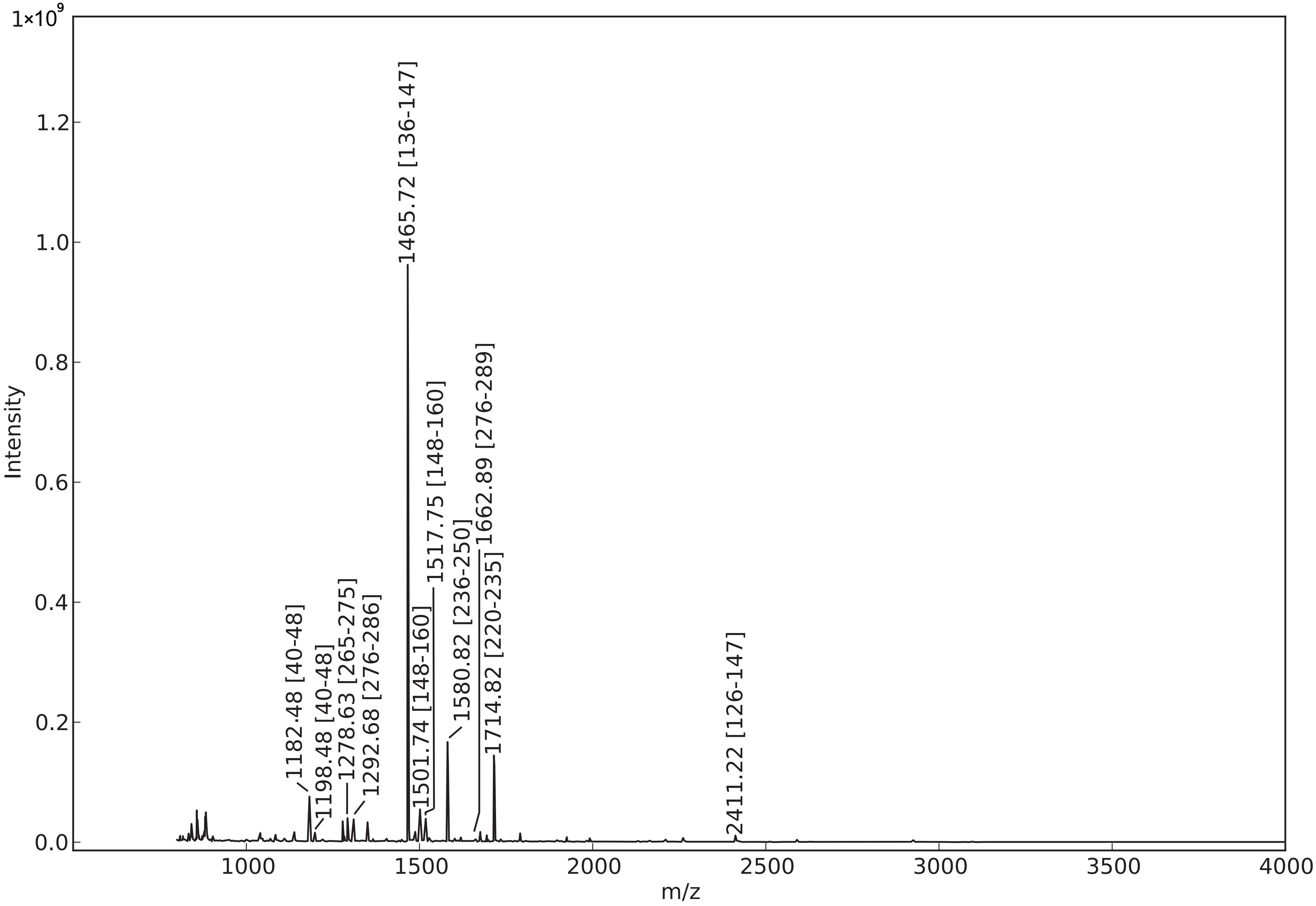
Spot No. 27


1×10^8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1072.65 [450-458]
1118.62 [437-445]
1150.70 [92-102]
1269.65 [387-396]
1437.83 [435-445]
1456.81 [118-129]
1493.88 [151-163]
1495.95 [356-369]
1620.99 [292-305]
1682.95 [402-416]
1698.95 [402-416]
1712.06 [340-353]
1808.07 [450-464]
1862.04 [420-434]
1900.05 [387-401]
2329.31 [397-416]

Spot No. 28


1×10^9
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
825.34 [195-200]
846.48 [177-183]
1010.46 [59-67]
1206.70 [184-194]
1240.75 [86-96]
1618.92 [147-160]
1991.98 [68-83]
2261.19 [124-145]
2945.58 [97-123]

Spot No. 29


1×10^9
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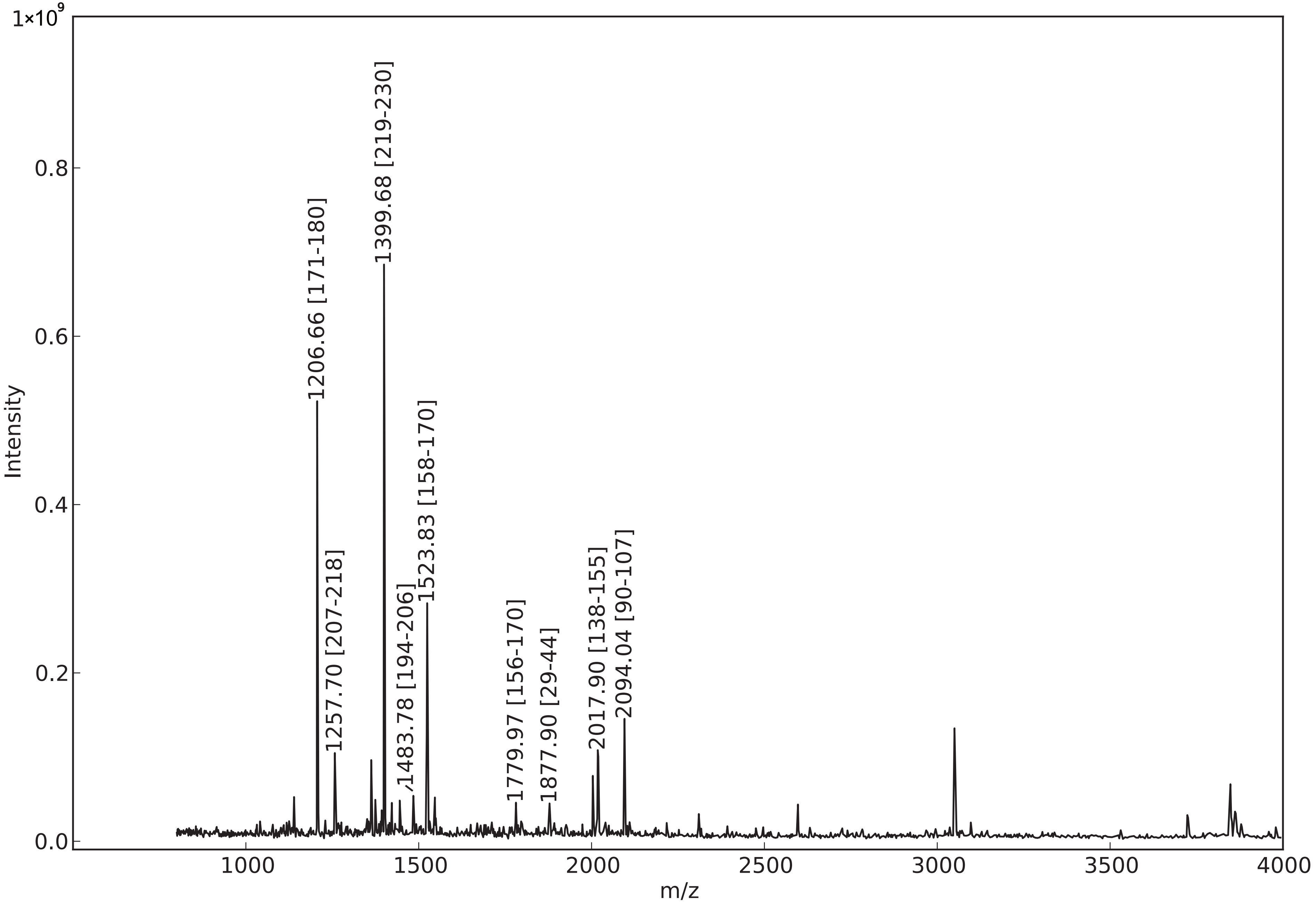
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1182.48 [40-48]
1198.48 [40-48]
1278.63 [265-275]
1292.68 [276-286]
1465.72 [136-147]
1501.74 [148-160]
1517.75 [148-160]
1580.82 [236-250]
1662.89 [276-289]
1714.82 [220-235]
2411.22 [126-147]

Spot No. 30


1×10^9
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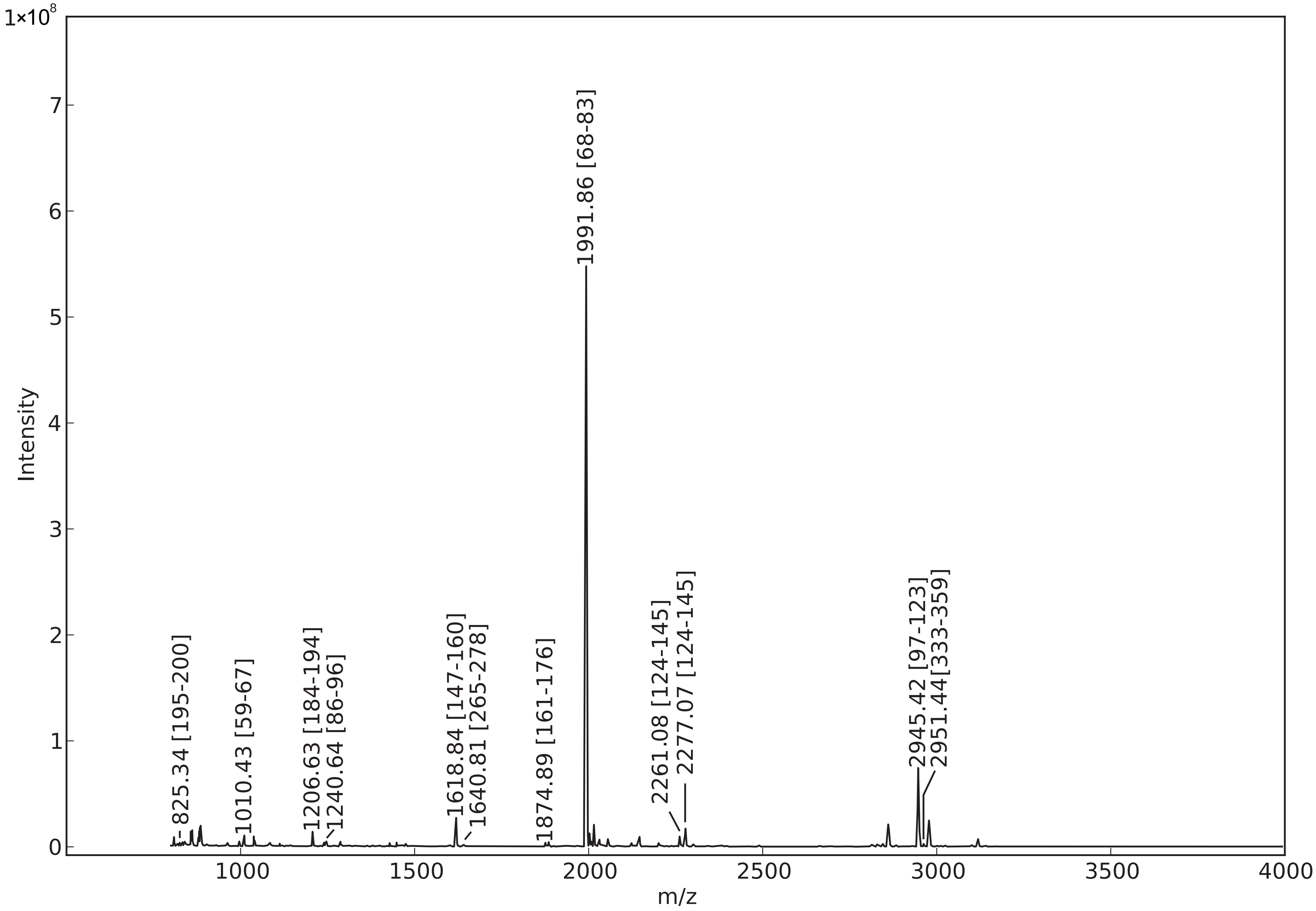
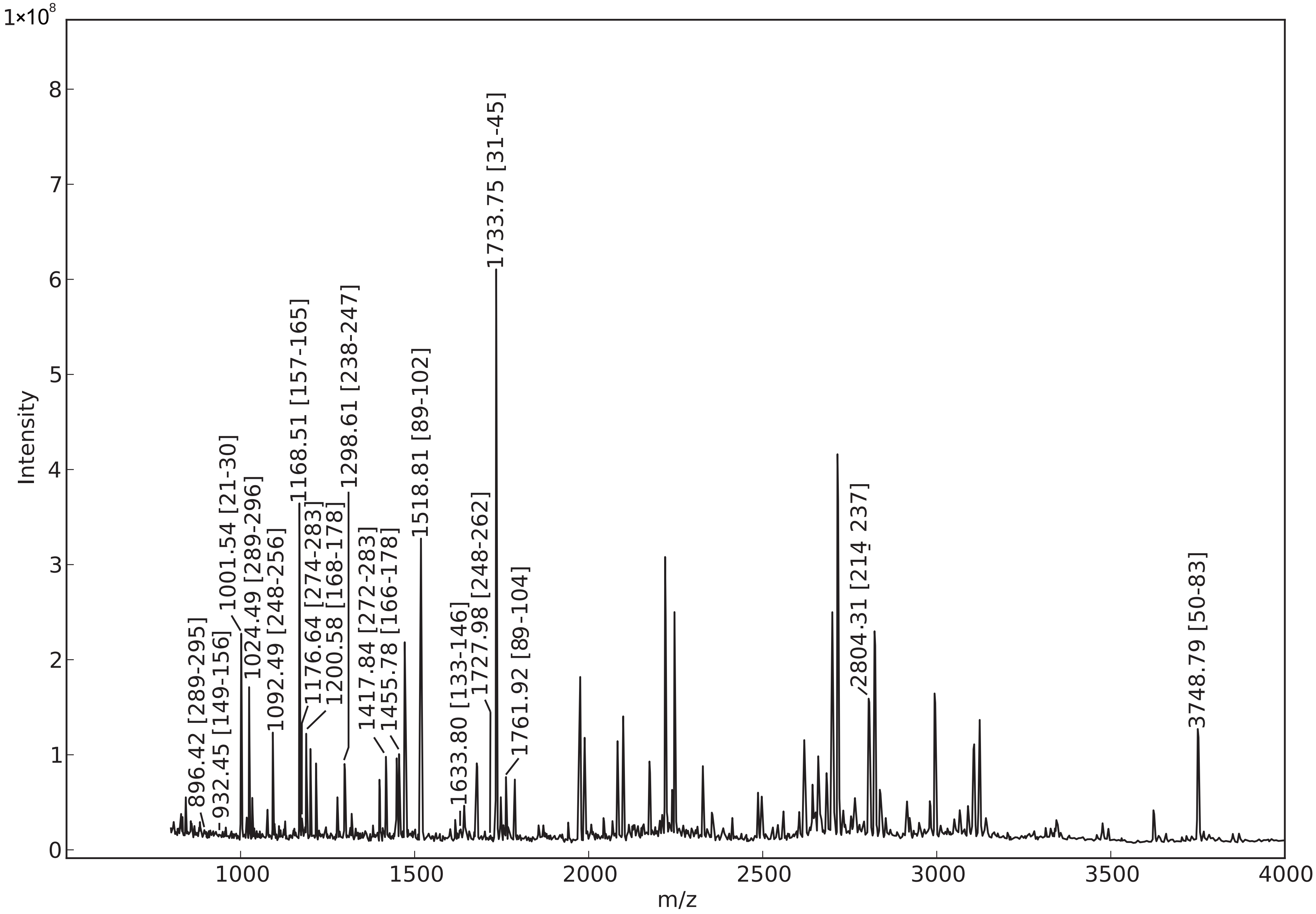
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1206.66 [171-180]
1257.70 [207-218]
1399.68 [219-230]
1483.78 [194-206]
1523.83 [158-170]
1779.97 [156-170]
1877.90 [29-44]
2017.90 [138-155]
2094.04 [90-107]

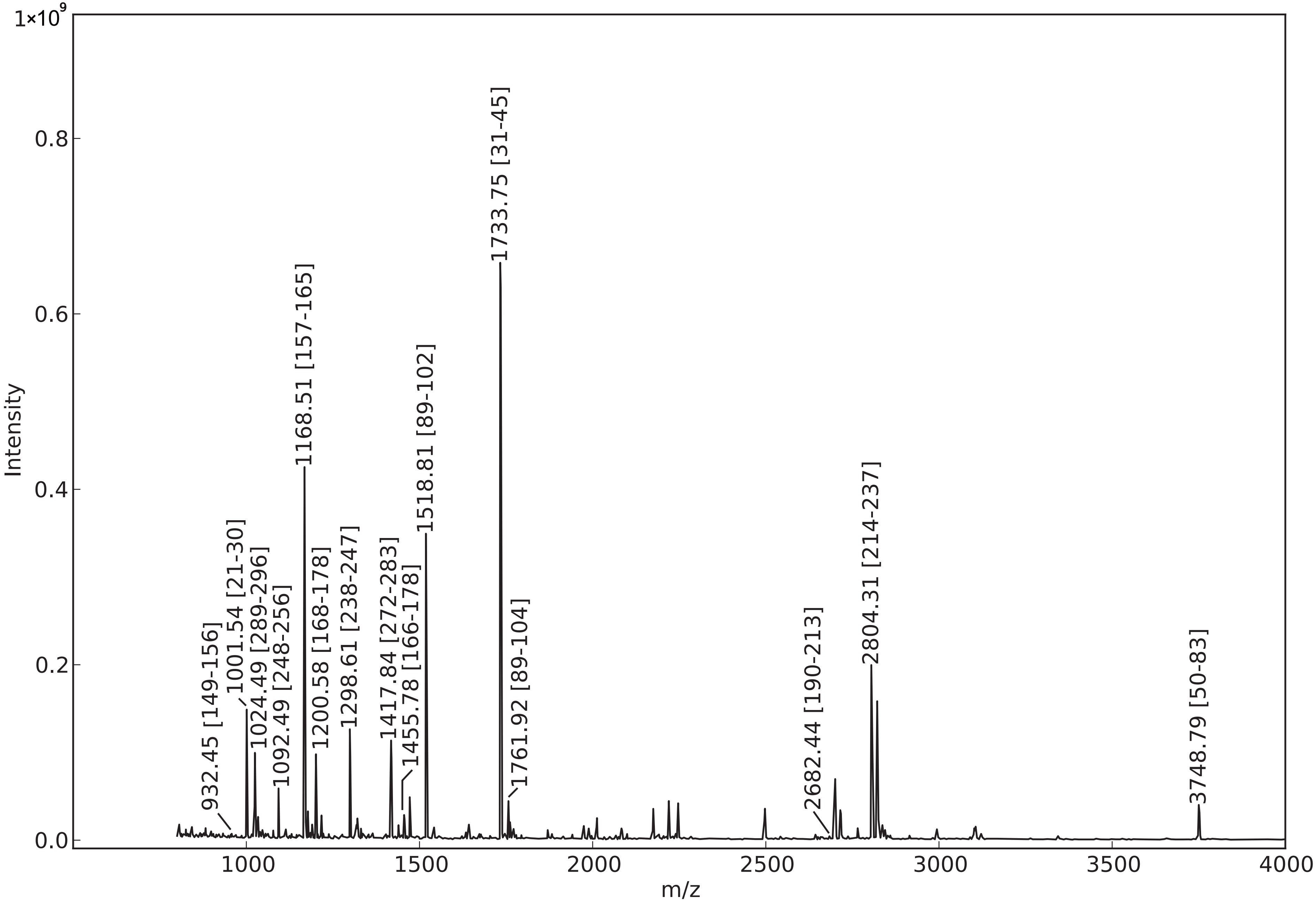
Spot No. 31


1×10⁸
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
825.34 [195-200]
1010.43 [59-67]
1206.63 [184-194]
1240.64 [86-96]
1618.84 [147-160]
1640.81 [265-278]
1874.89 [161-176]
1991.86 [68-83]
2261.08 [124-145]
2277.07 [124-145]
2945.42 [97-123]
2951.44[333-359]

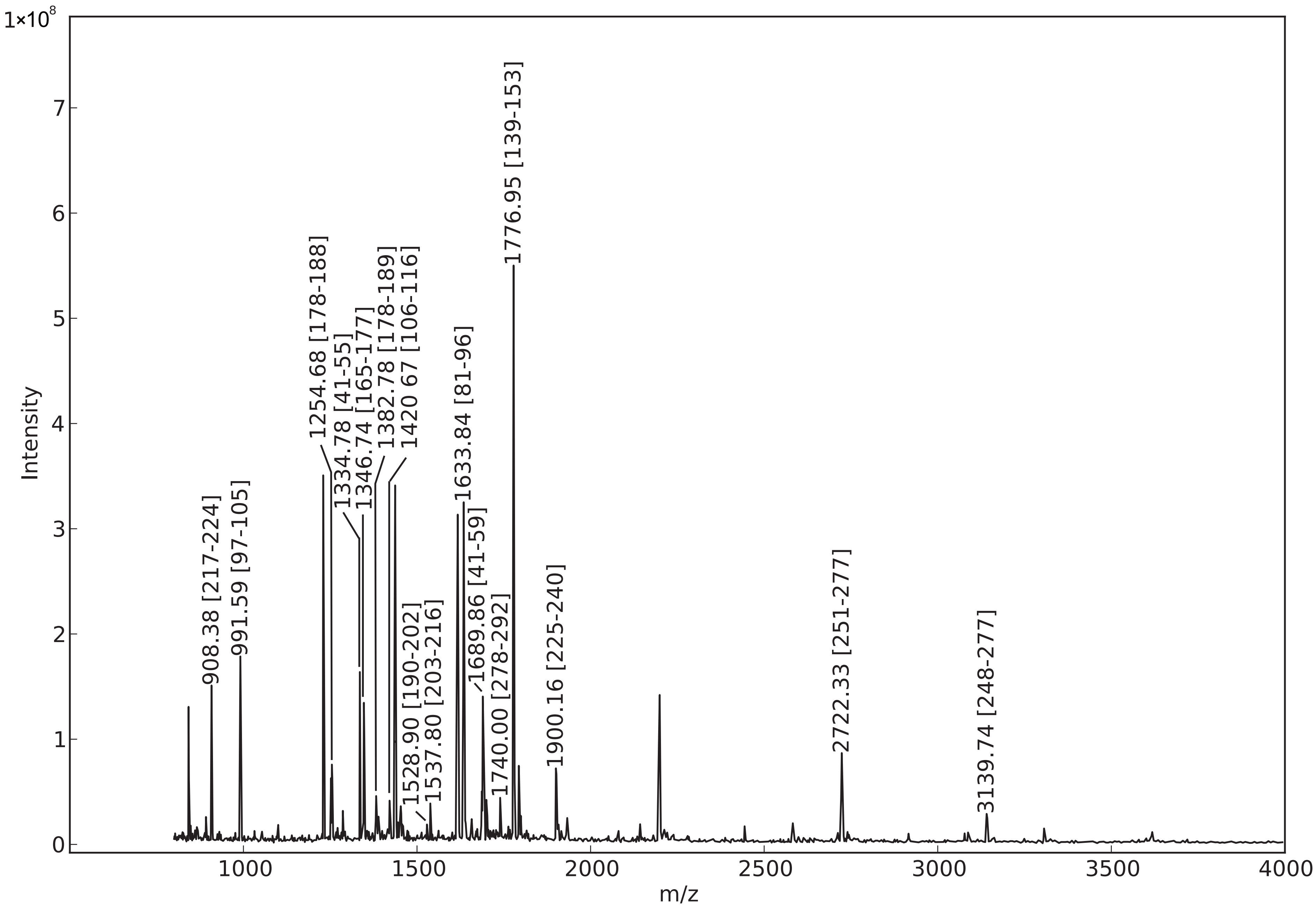
Spot No. 32


1×10^8
8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
896.42 [289-295]
932.45 [149-156]
1001.54 [21-30]
1024.49 [289-296]
1092.49 [248-256]
1168.51 [157-165]
1176.64 [274-283]
1200.58 [168-178]
1298.61 [238-247]
1417.84 [272-283]
1455.78 [166-178]
1518.81 [89-102]
1633.80 [133-146]
1727.98 [248-262]
1733.75 [31-45]
1761.92 [89-104]
2804.31 [214-237]
3748.79 [50-83]

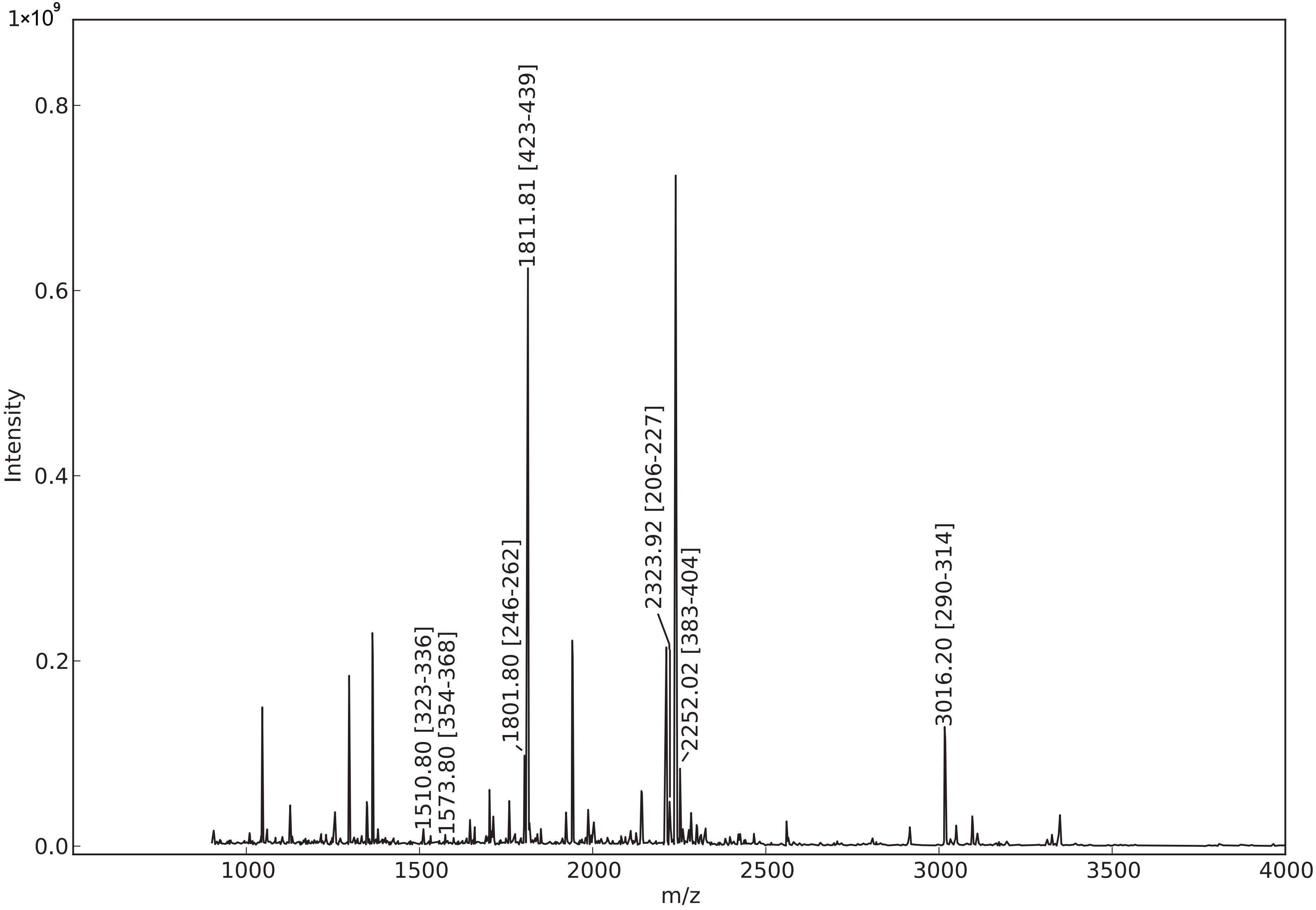
Spot No. 33


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
932.45 [149-156]
1001.54 [21-30]
1024.49 [289-296]
1092.49 [248-256]
1168.51 [157-165]
1200.58 [168-178]
1298.61 [238-247]
1417.84 [272-283]
1455.78 [166-178]
1518.81 [89-102]
1733.75 [31-45]
1761.92 [89-104]
2682.44 [190-213]
2804.31 [214-237]
3748.79 [50-83]

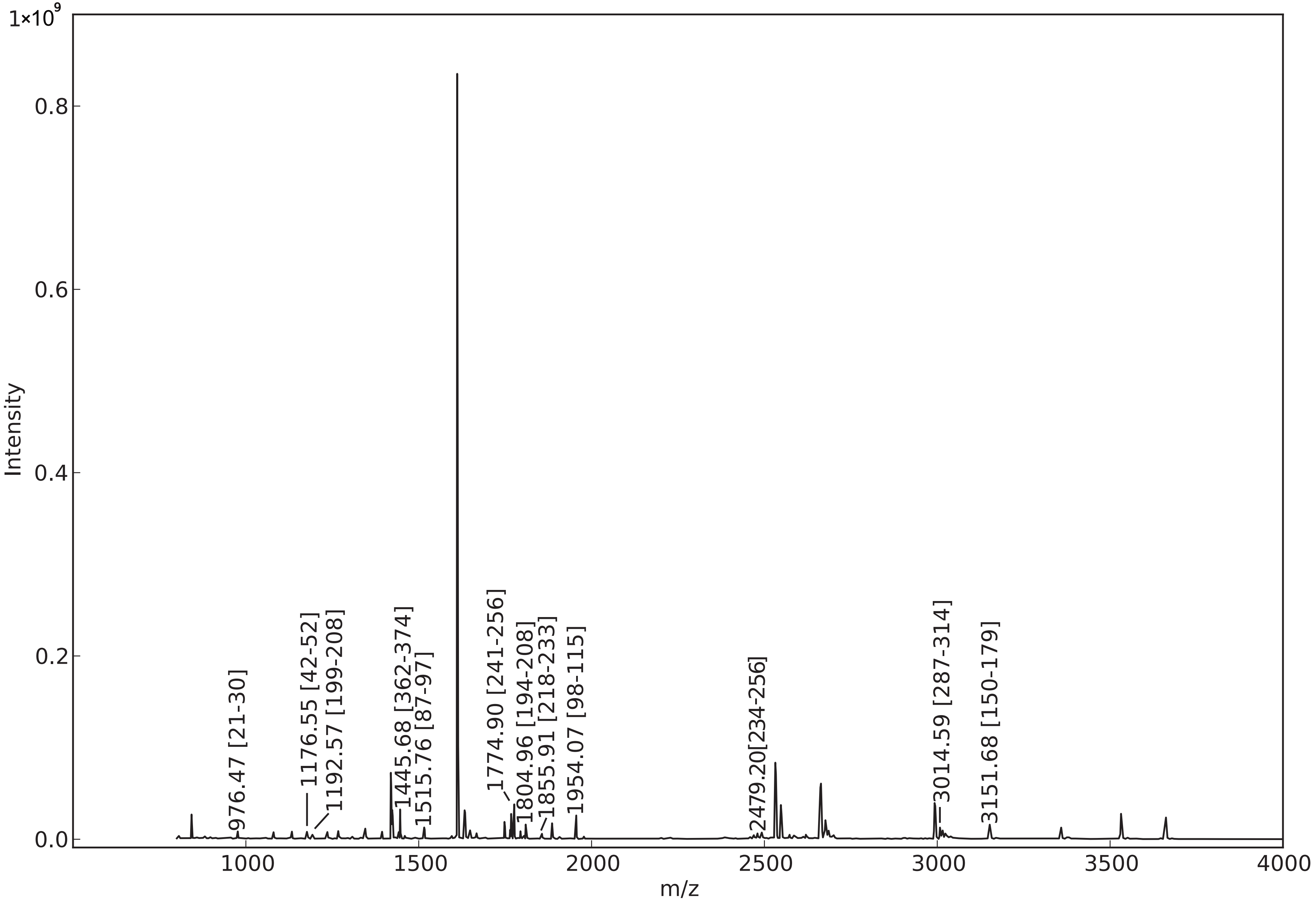
Spot No. 34


1×10⁸
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
908.38 [217-224]
991.59 [97-105]
1254.68 [178-188]
1334.78 [41-55]
1346.74 [165-177]
1382.78 [178-189]
1420 67 [106-116]
1528.90 [190-202]
1537.80 [203-216]
1633.84 [81-96]
1689.86 [41-59]
1740.00 [278-292]
1776.95 [139-153]
1900.16 [225-240]
2722.33 [251-277]
3139.74 [248-277]

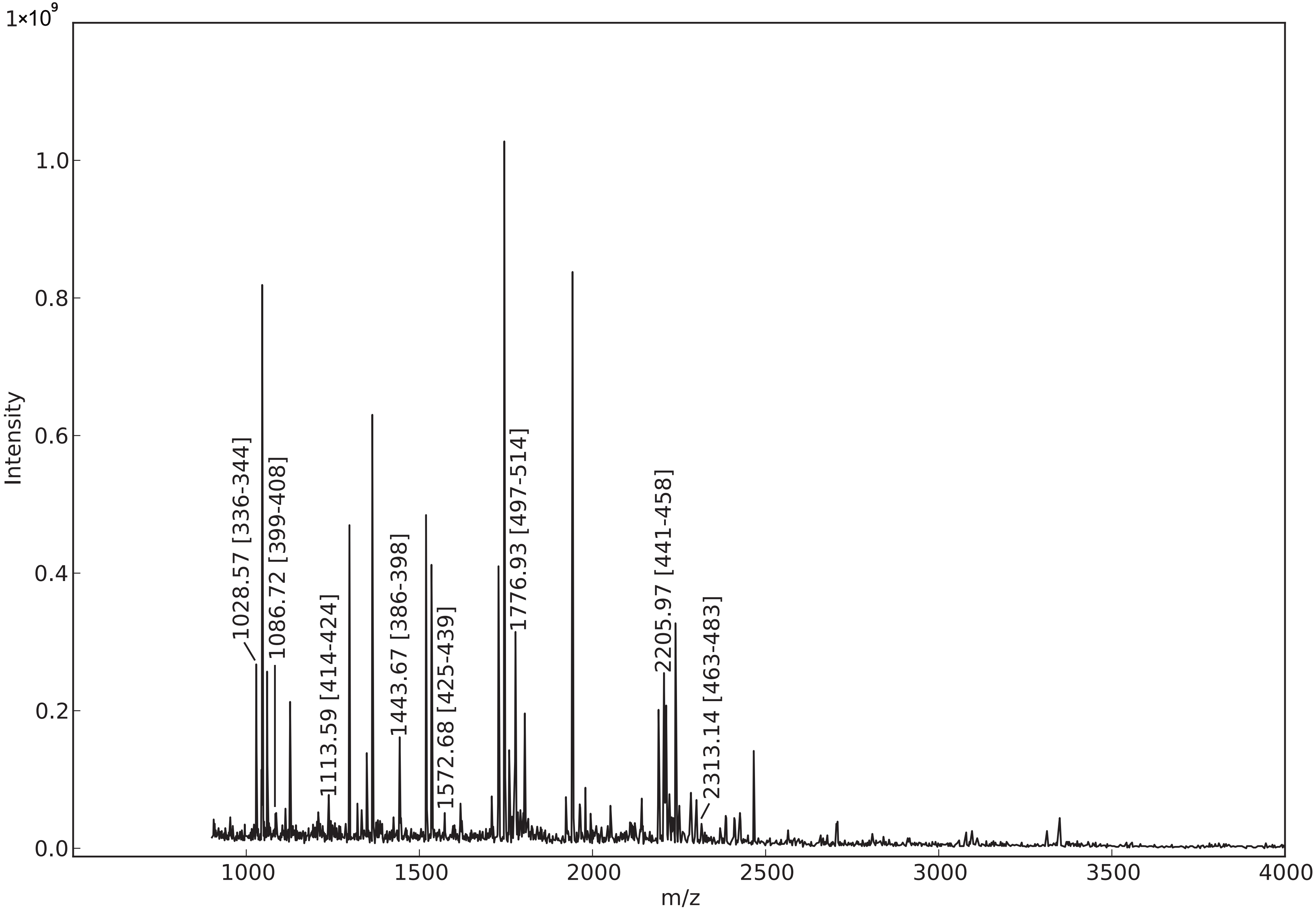
Spot No. 35


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1510.80 [323-336]
1573.80 [354-368]
1801.80 [246-262]
1811.81 [423-439]
2323.92 [206-227]
2252.02 [383-404]
3016.20 [290-314]

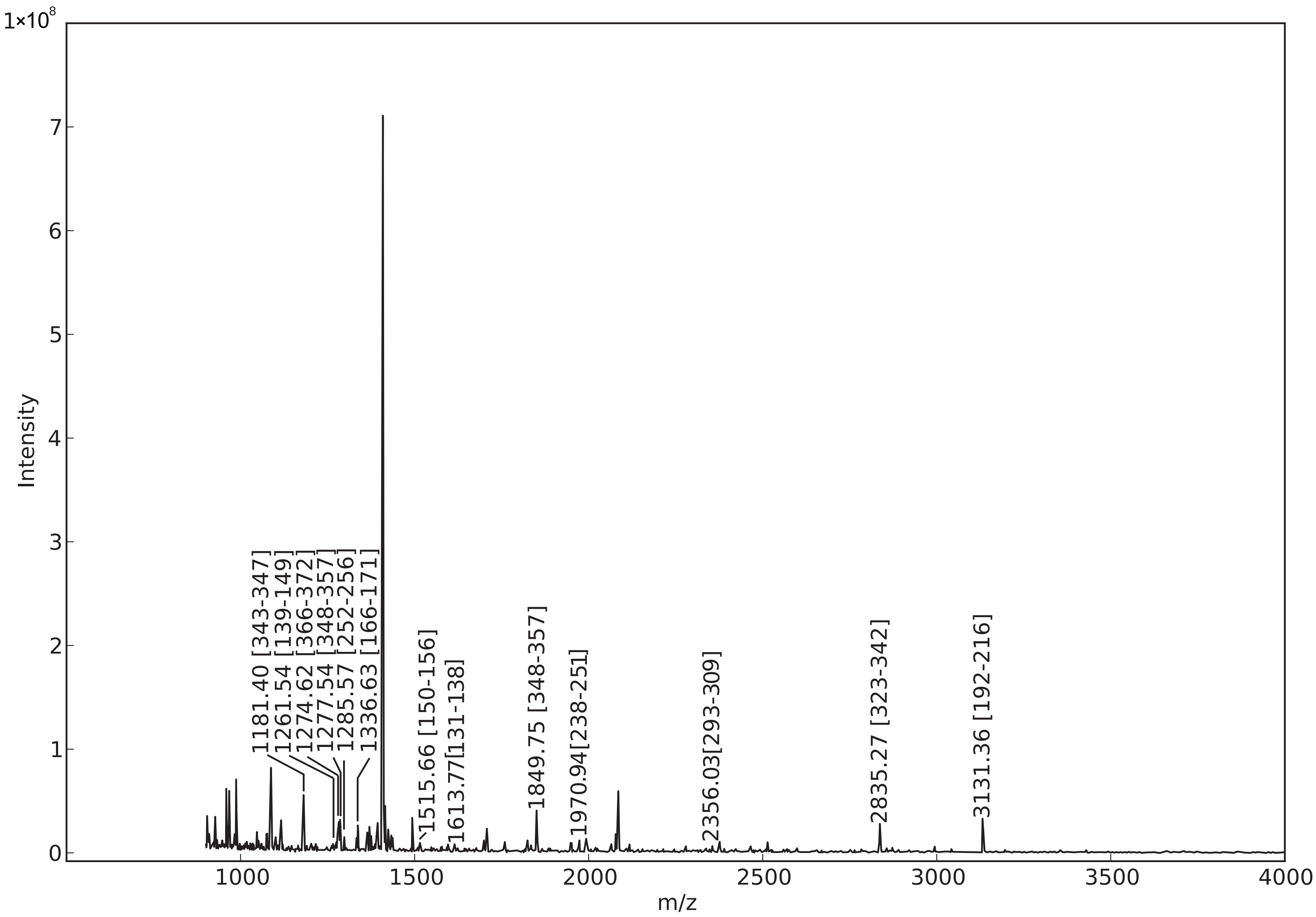
Spot No. 36


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
976.47 [21-30]
1176.55 [42-52]
1192.57 [199-208]
1445.68 [362-374]
1515.76 [87-97]
1774.90 [241-256]
1804.96 [194-208]
1855.91 [218-233]
1954.07 [98-115]
2479.20[234-256]
3014.59 [287-314]
3151.68 [150-179]

Spot No. 37

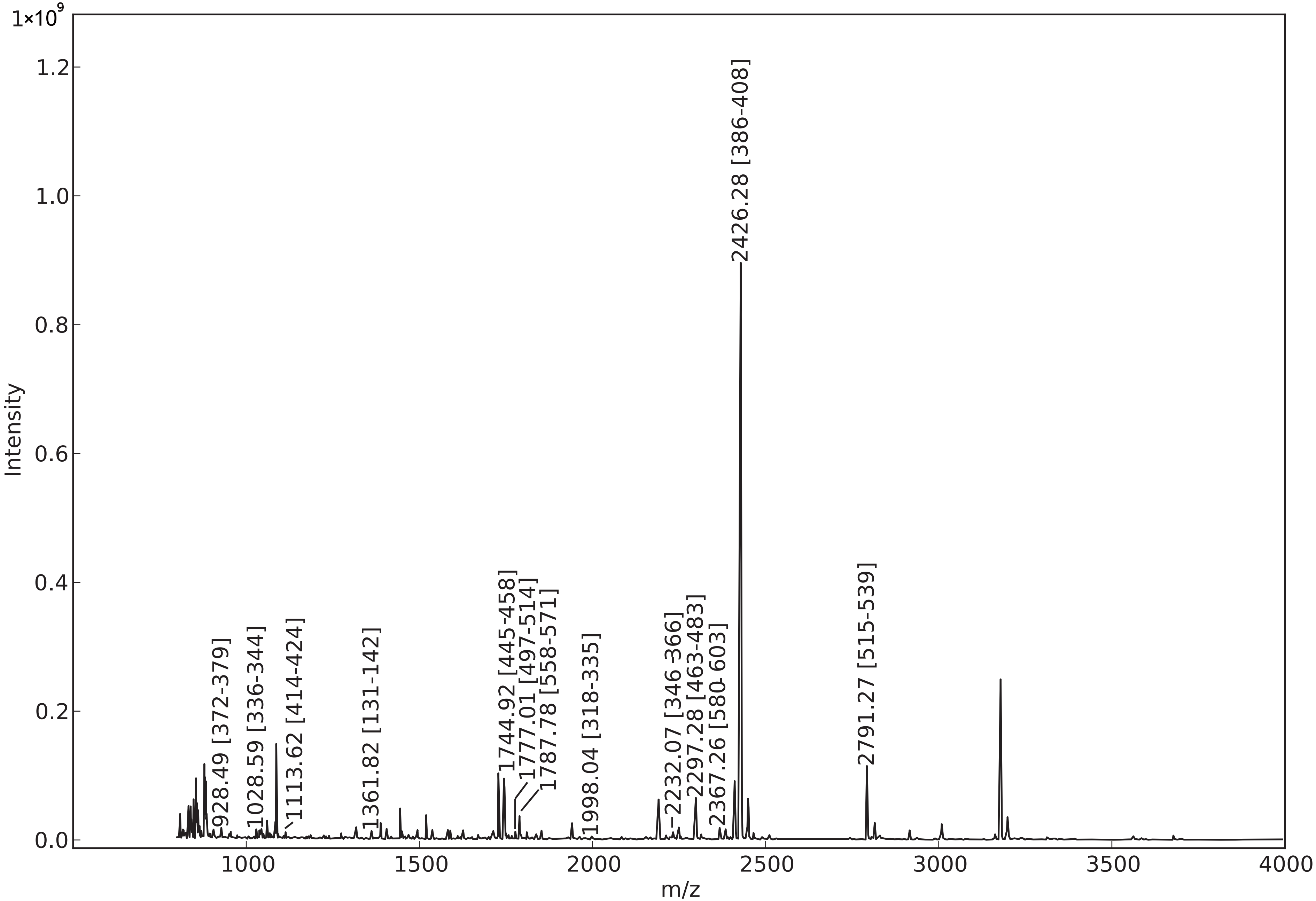

1×10^9
Intensity
1.0
0.8
0.6
0.4
0.2
0.0
1000
1500
2000
2500
3000
3500
4000
m/z
1028.57 [336-344]
1086.72 [399-408]
1113.59 [414-424]
1443.67 [386-398]
1572.68 [425-439]
1776.93 [497-514]
2205.97 [441-458]
2313.14 [463-483]

Spot No. 38

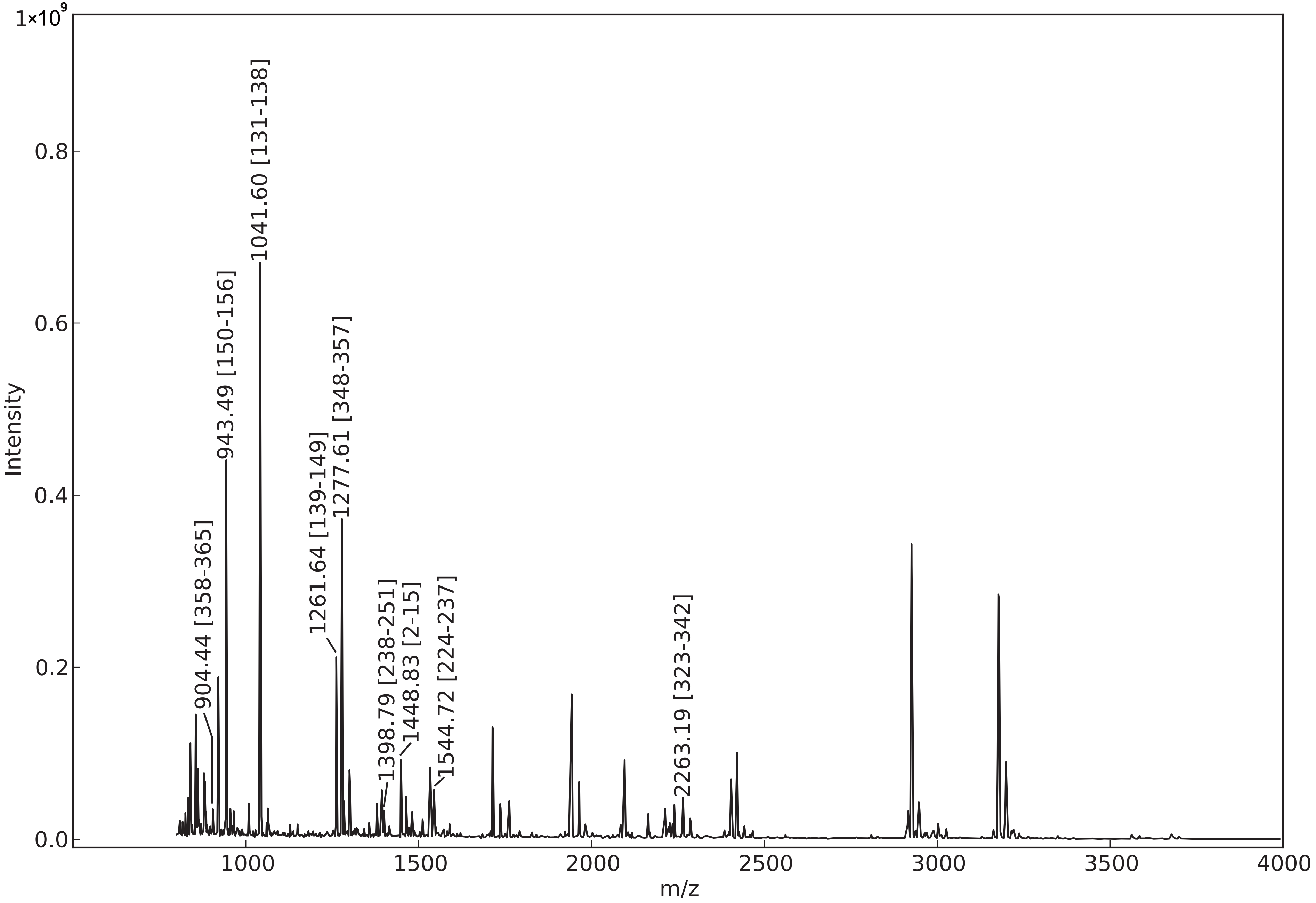


1×10⁸
Intensity
7
6
5
4
3
2
1
0
1181.40 [343-347]
1261.54 [139-149]
1274.62 [366-372]
1277.54 [348-357]
1285.57 [252-256]
1336.63 [166-171]
1515.66 [150-156]
1613.77[131-138]
1849.75 [348-357]
1970.94[238-251]
2356.03[293-309]
2835.27 [323-342]
3131.36 [192-216]
1000
1500
2000
2500
3000
3500
4000
m/z

Spot No. 39

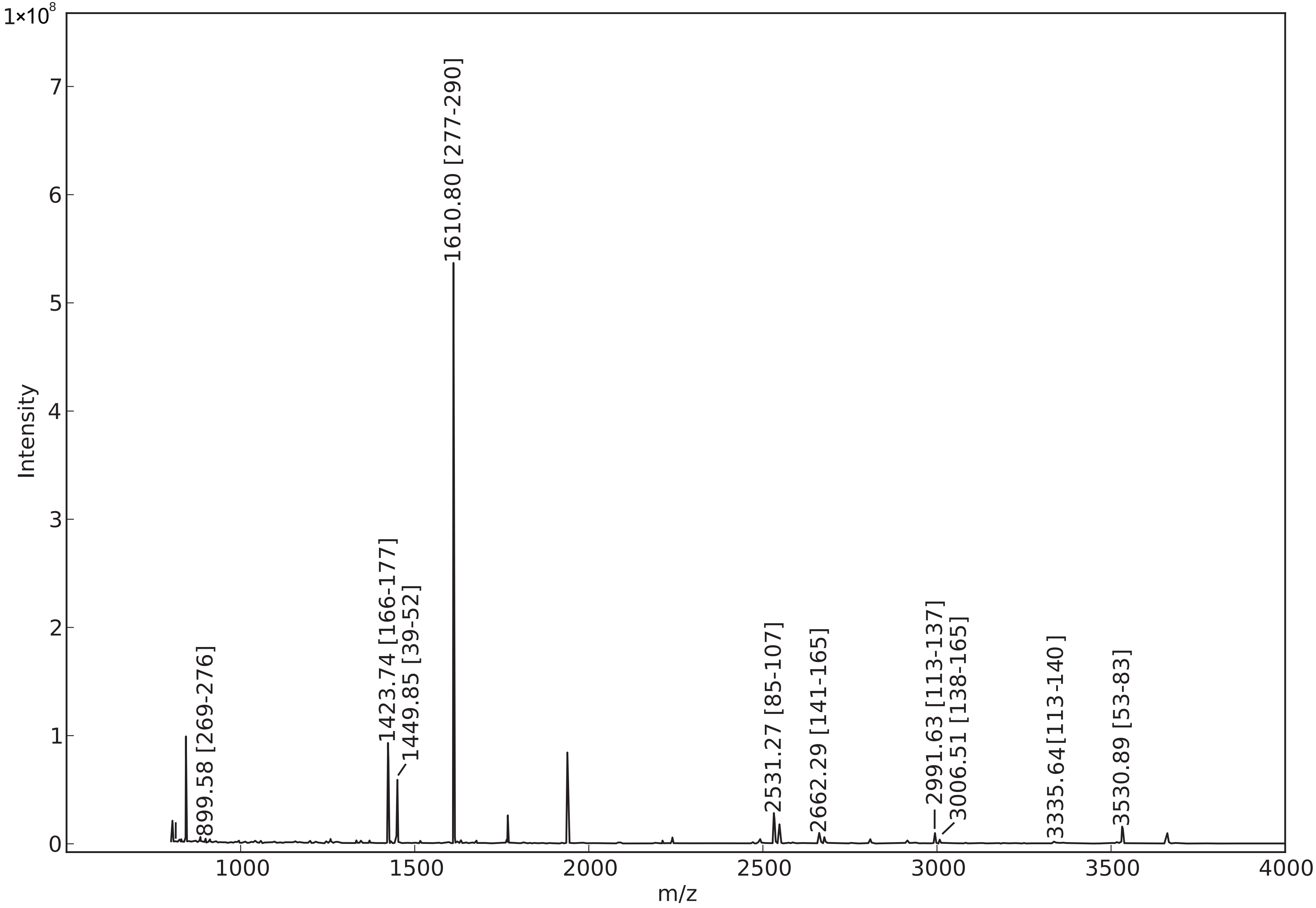

1×10^9
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
928.49 [372-379]
1028.59 [336-344]
1113.62 [414-424]
1361.82 [131-142]
1744.92 [445-458]
1777.01 [497-514]
1787.78 [558-571]
1998.04 [318-335]
2232.07 [346-366]
2297.28 [463-483]
2367.26 [580-603]
2426.28 [386-408]
2791.27 [515-539]

Spot No. 40



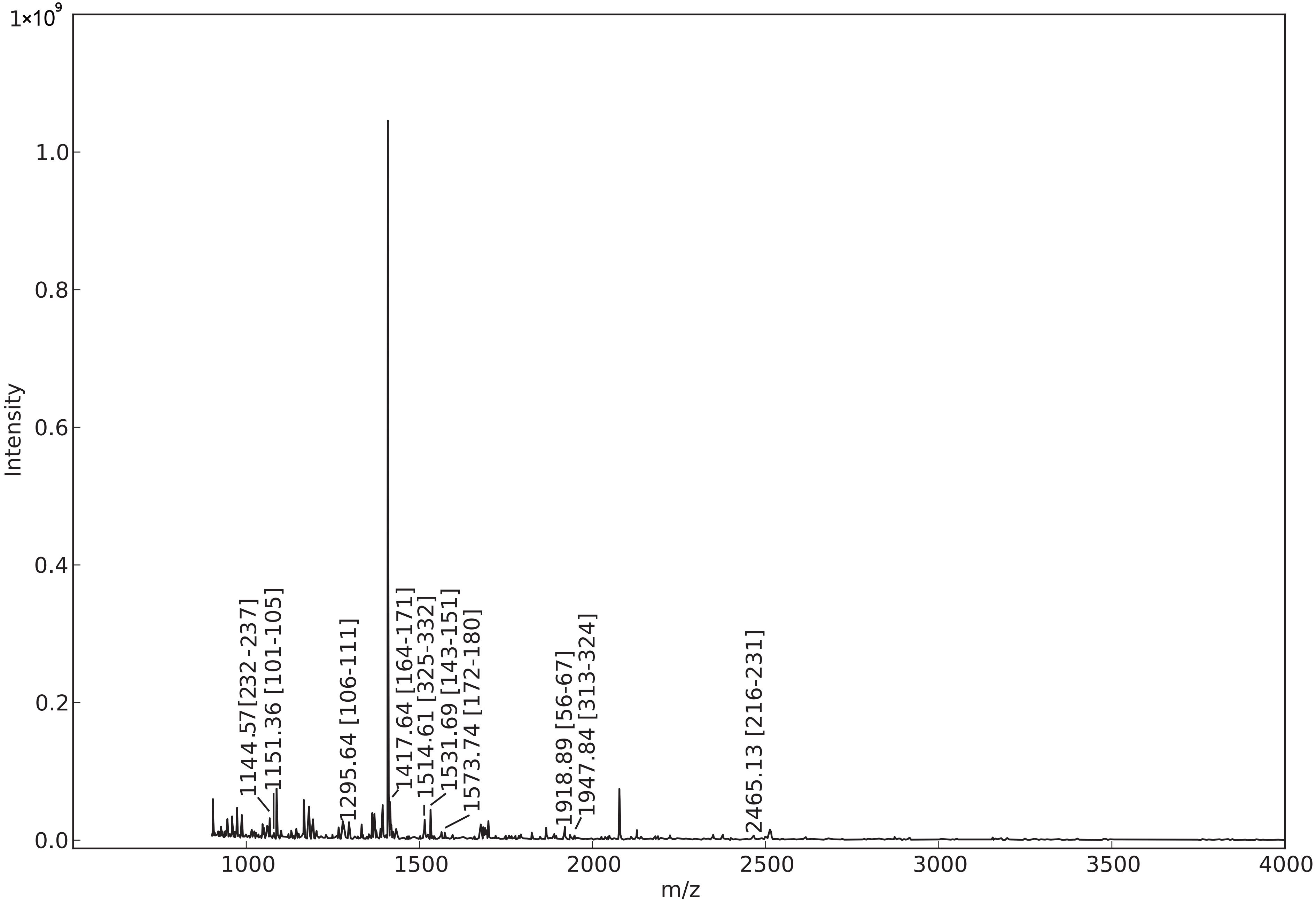
1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
904.44 [358-365]
943.49 [150-156]
1041.60 [131-138]
1261.64 [139-149]
1277.61 [348-357]
1398.79 [238-251]
1448.83 [2-15]
1544.72 [224-237]
2263.19 [323-342]

Spot No. 41

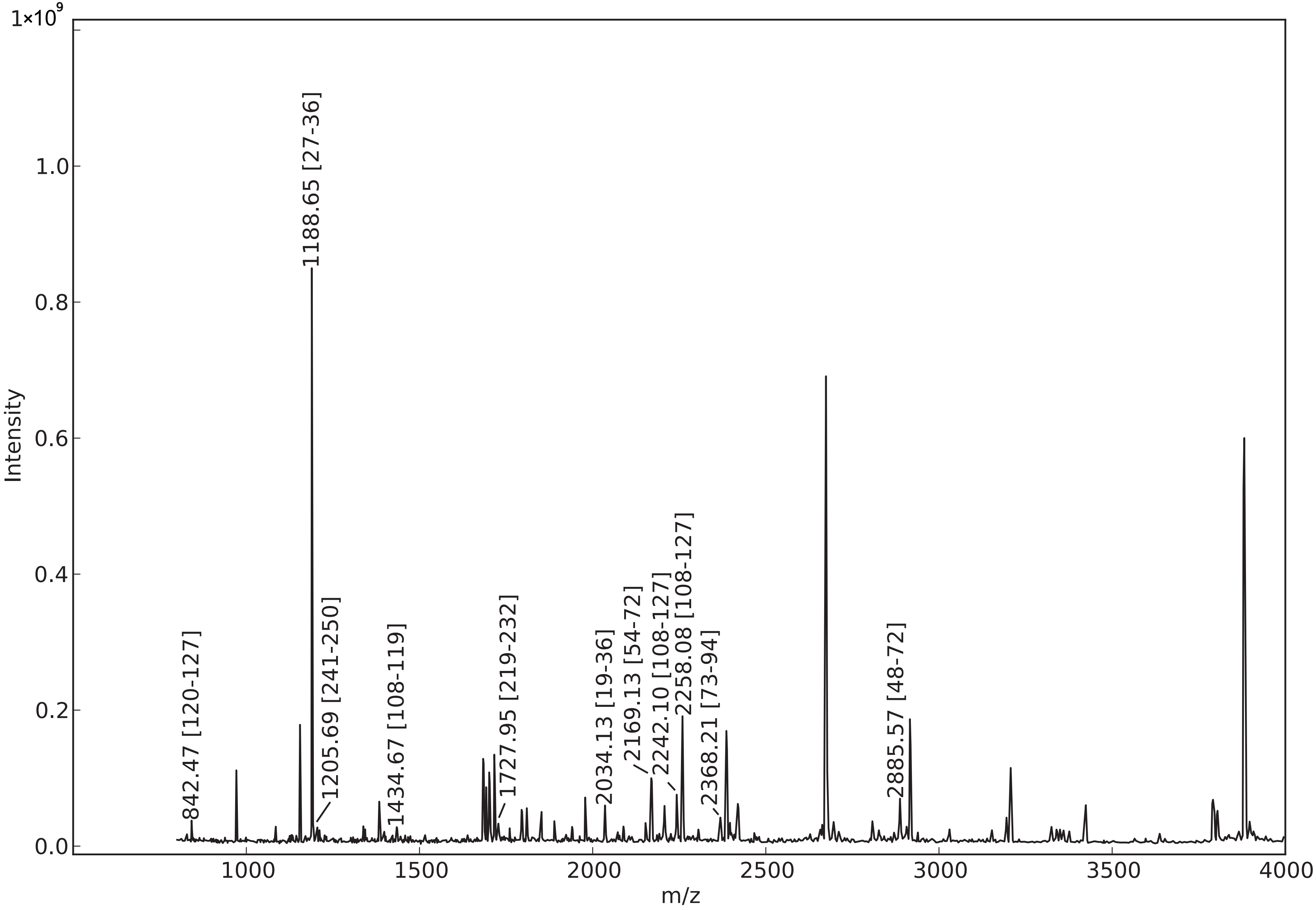


1×10⁸
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
899.58 [269-276]
1423.74 [166-177]
1449.85 [39-52]
1610.80 [277-290]
2531.27 [85-107]
2662.29 [141-165]
2991.63 [113-137]
3006.51 [138-165]
3335.64[113-140]
3530.89 [53-83]

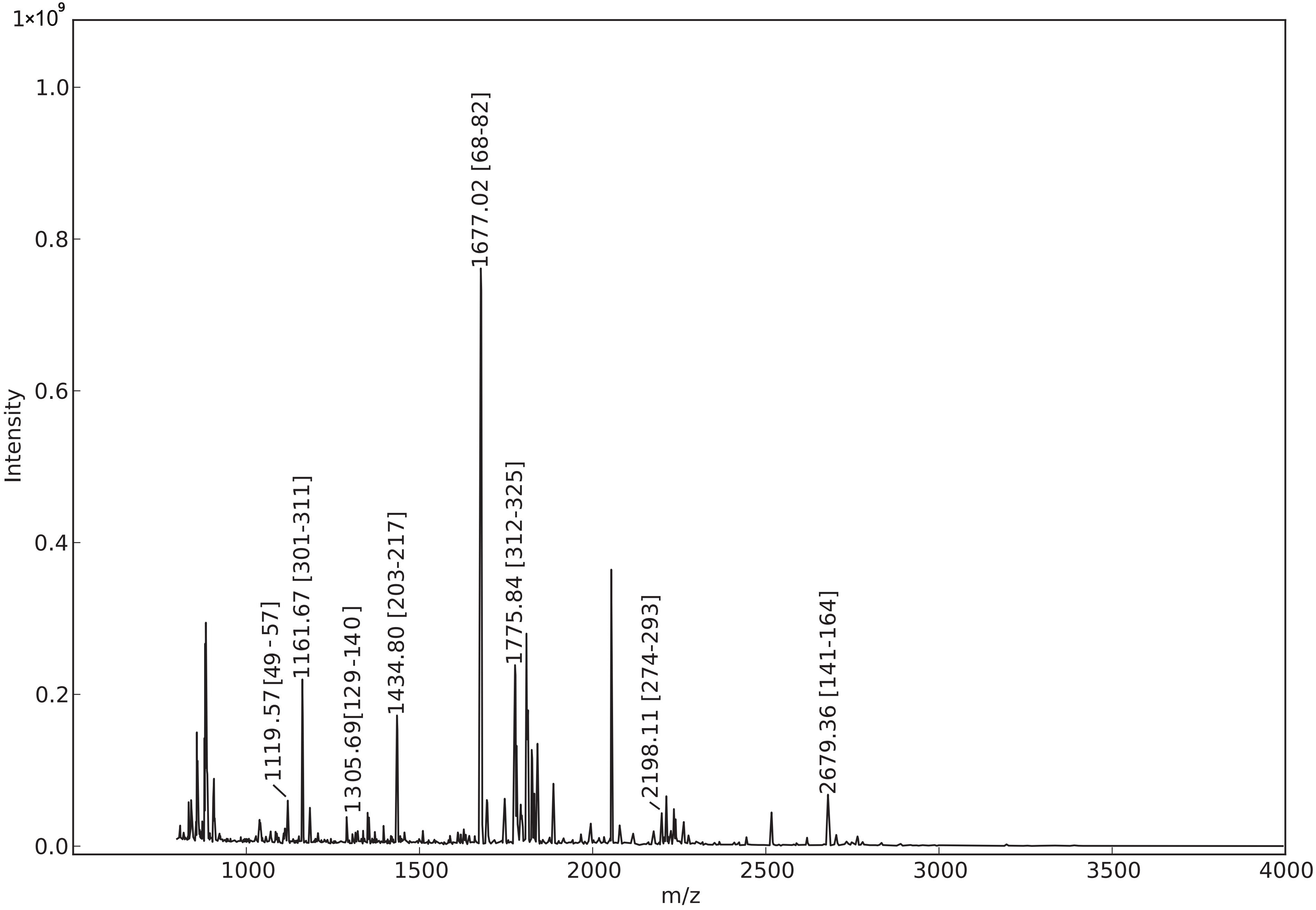
Spot No. 42


1×10^9
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1144.57[232 -2237]
1151.36 [101-105]
1295.64 [106-111]
1417.64 [164-171]
1514.61 [325-332]
1531.69 [143-151]
1573.74 [172-180]
1918.89 [56-67]
1947.84 [313-324]
2465.13 [216-231]

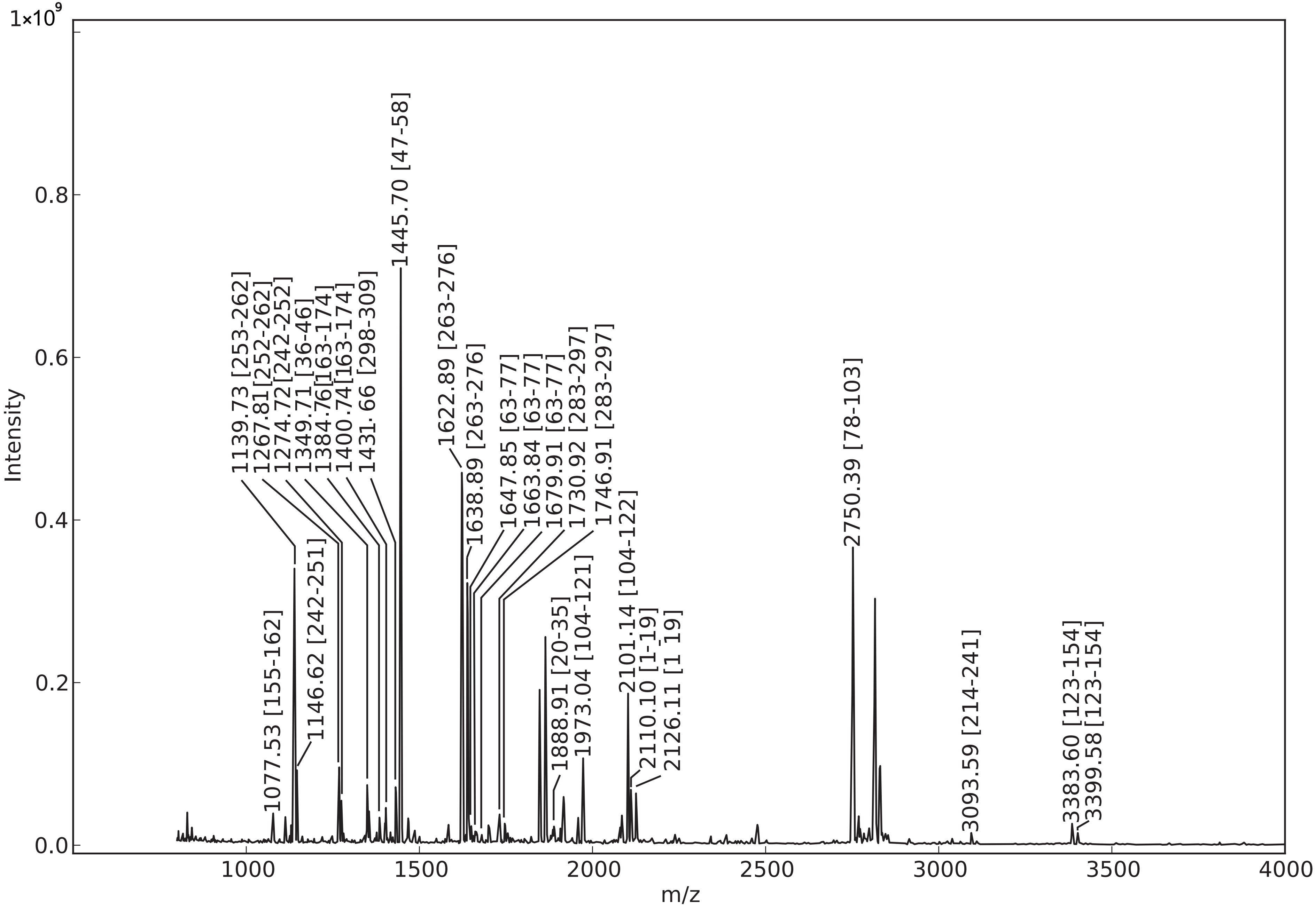
Spot No. 43


1×10^9
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
842.47 [120-127]
1188.65 [27-36]
1205.69 [241-250]
1434.67 [108-119]
1727.95 [219-232]
2034.13 [19-36]
2169.13 [54-72]
2242.10 [108-127]
2258.08 [108-127]
2368.21 [73-94]
2885.57 [48-72]

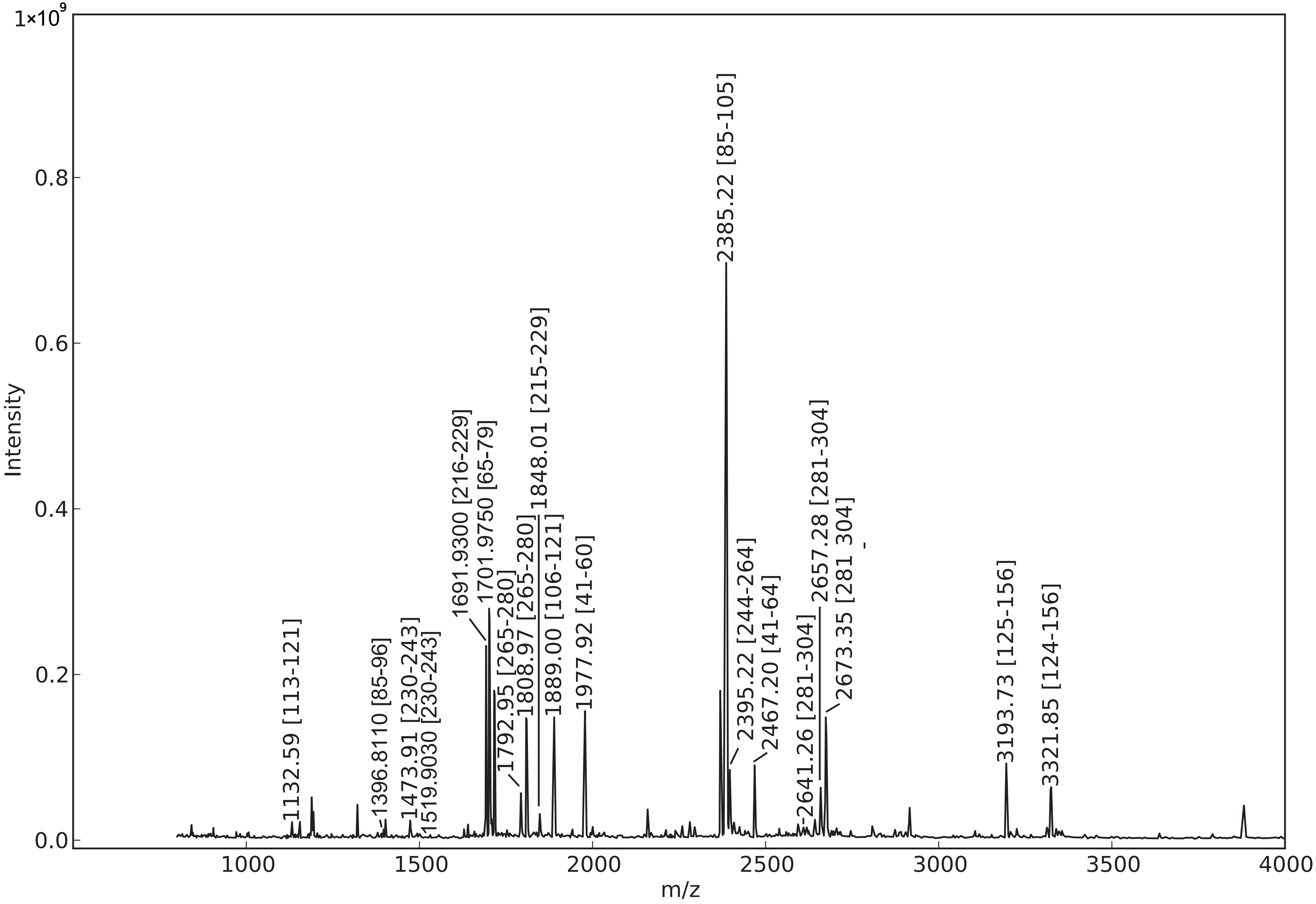
Spot No. 44


1×10⁹
Intensity
1.0
0.8
0.6
0.4
0.2
0.0
1000
1500
2000
2500
3000
3500
4000
m/z
1119.57 [49 - 57]
1161.67 [301-311]
1305.69[129-140]
1434.80 [203-217]
1677.02 [68-82]
1775.84 [312-325]
2198.11 [274-293]
2679.36 [141-164]

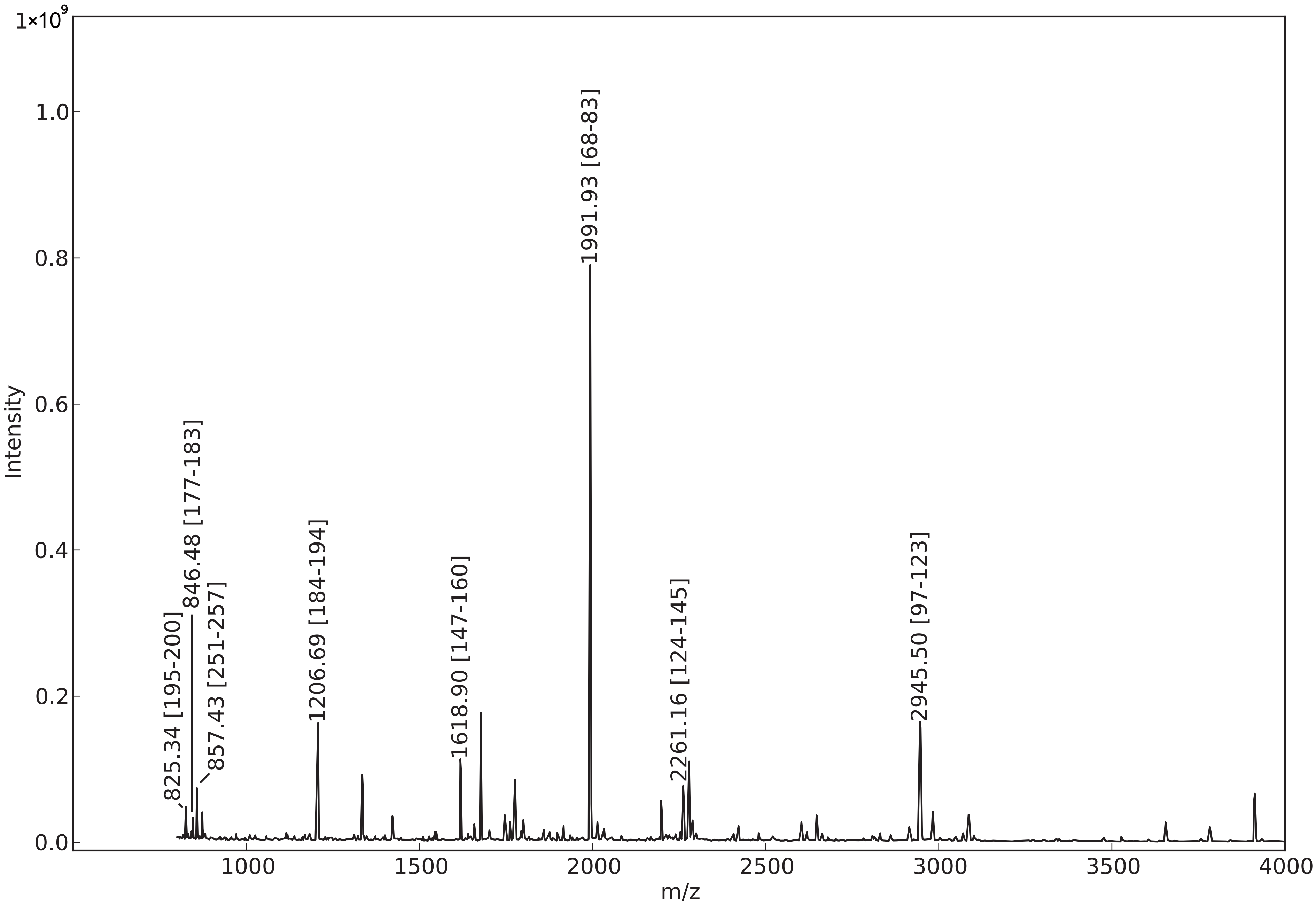
Spot No. 45


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1077.53 [155-162]
1139.73 [253-262]
1146.62 [242-251]
1267.81[252-262]
1274.72[242-252]
1349.71 [36-46]
1384.76[163-174]
1400.74[163-174]
1431.66 [298-309]
1445.70 [47-58]
1622.89 [263-276]
1638.89 [263-276]
1647.85 [63-77]
1663.84 [63-77]
1679.91 [63-77]
1730.92 [283-297]
1746.91 [283-297]
1888.91 [20-35]
1973.04 [104-121]
2101.14 [104-122]
2110.10 [1-19]
2126.11 [1 19]
2750.39 [78-103]
3093.59 [214-241]
3383.60 [123-154]
3399.58 [123-154]

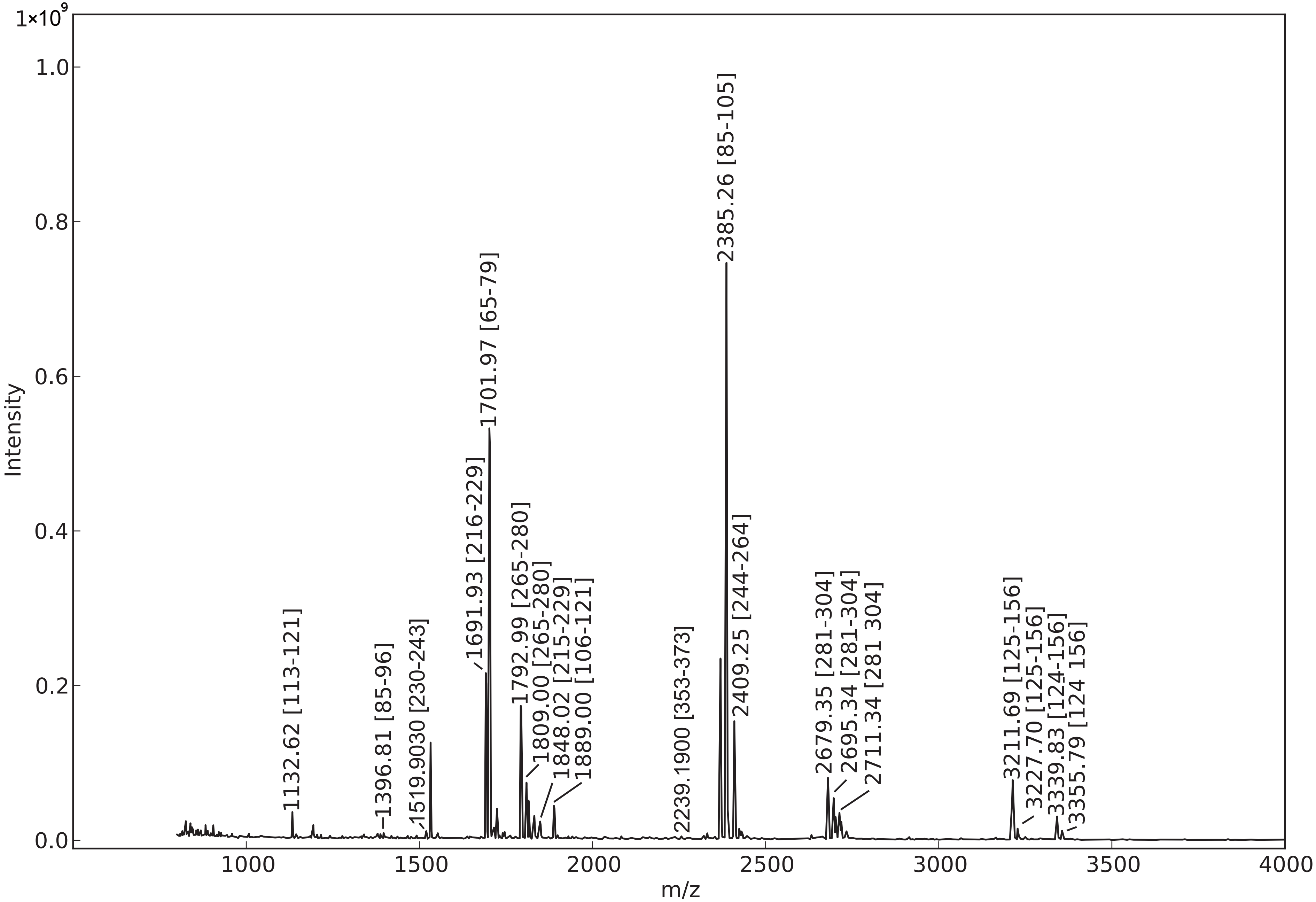
Spot No. 46


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1132.59 [113-121]
1396.8110 [85-96]
1473.91 [230-243]
1519.9030 [230-243]
1691.9300 [216-229]
1701.9750 [65-79]
1792.95 [265-280]
1808.97 [265-280]
1848.01 [215-229]
1889.00 [106-121]
1977.92 [41-60]
2385.22 [85-105]
2395.22 [244-264]
2467.20 [41-64]
2641.26 [281-304]
2657.28 [281-304]
2673.35 [281-304]
3193.73 [125-156]
3321.85 [124-156]

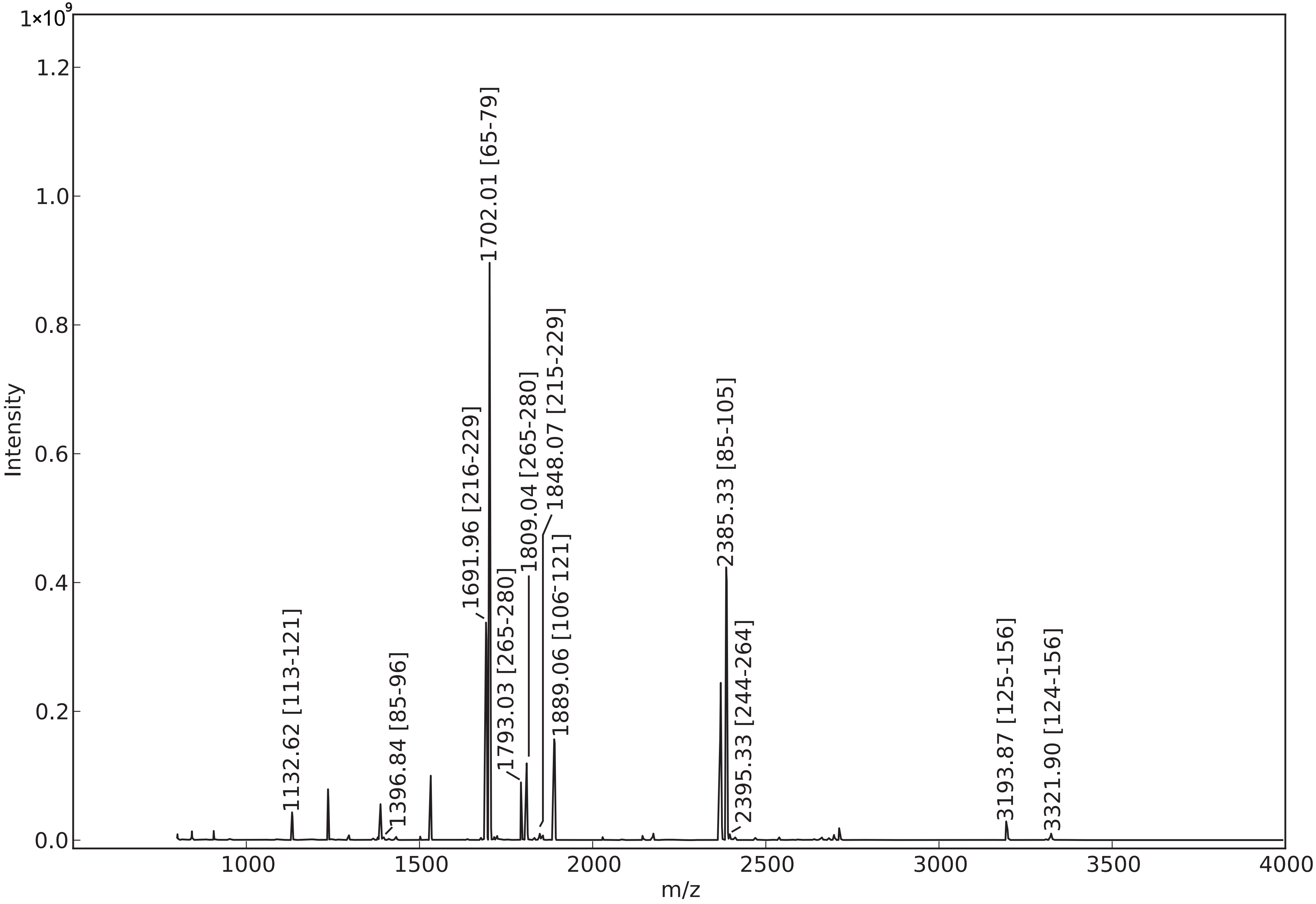
Spot No. 47


1×10^9
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
825.34 [195-200]
846.48 [177-183]
857.43 [251-257]
1206.69 [184-194]
1618.90 [147-160]
1991.93 [68-83]
2261.16 [124-145]
2945.50 [97-123]

Spot No. 48

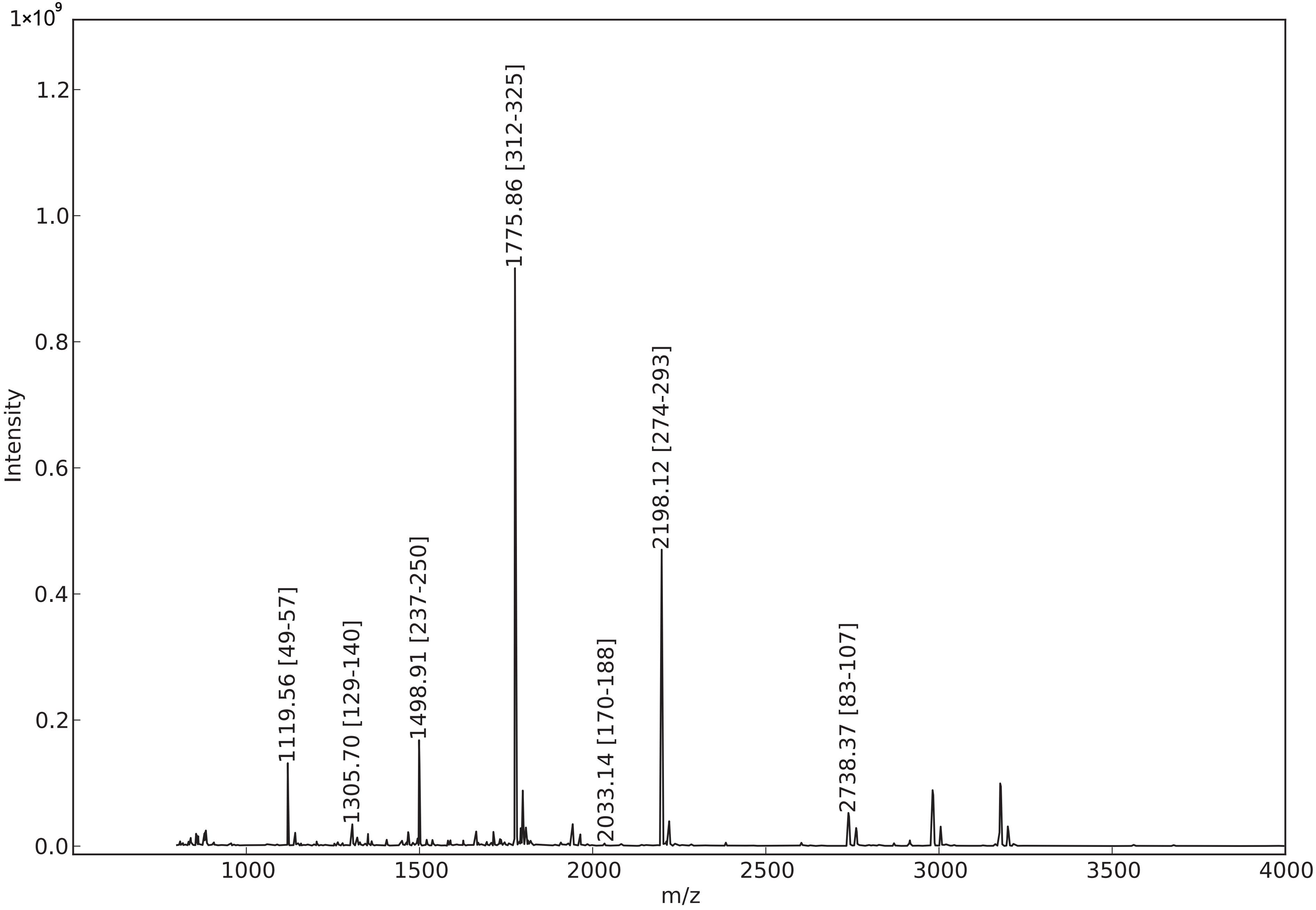

1×10^9
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1132.62 [113-121]
1396.81 [85-96]
1519.9030 [230-243]
1691.93 [216-229]
1701.97 [65-79]
1792.99 [265-280]
1809.00 [265-280]
1848.02 [215-229]
1889.00 [106-121]
2239.1900 [353-373]
2385.26 [85-105]
2409.25 [244-264]
2679.35 [281-304]
2695.34 [281-304]
2711.34 [281 304]
3211.69 [125-156]
3227.70 [125-156]
3339.83 [124-156]
3355.79 [124 156]

Spot No. 49



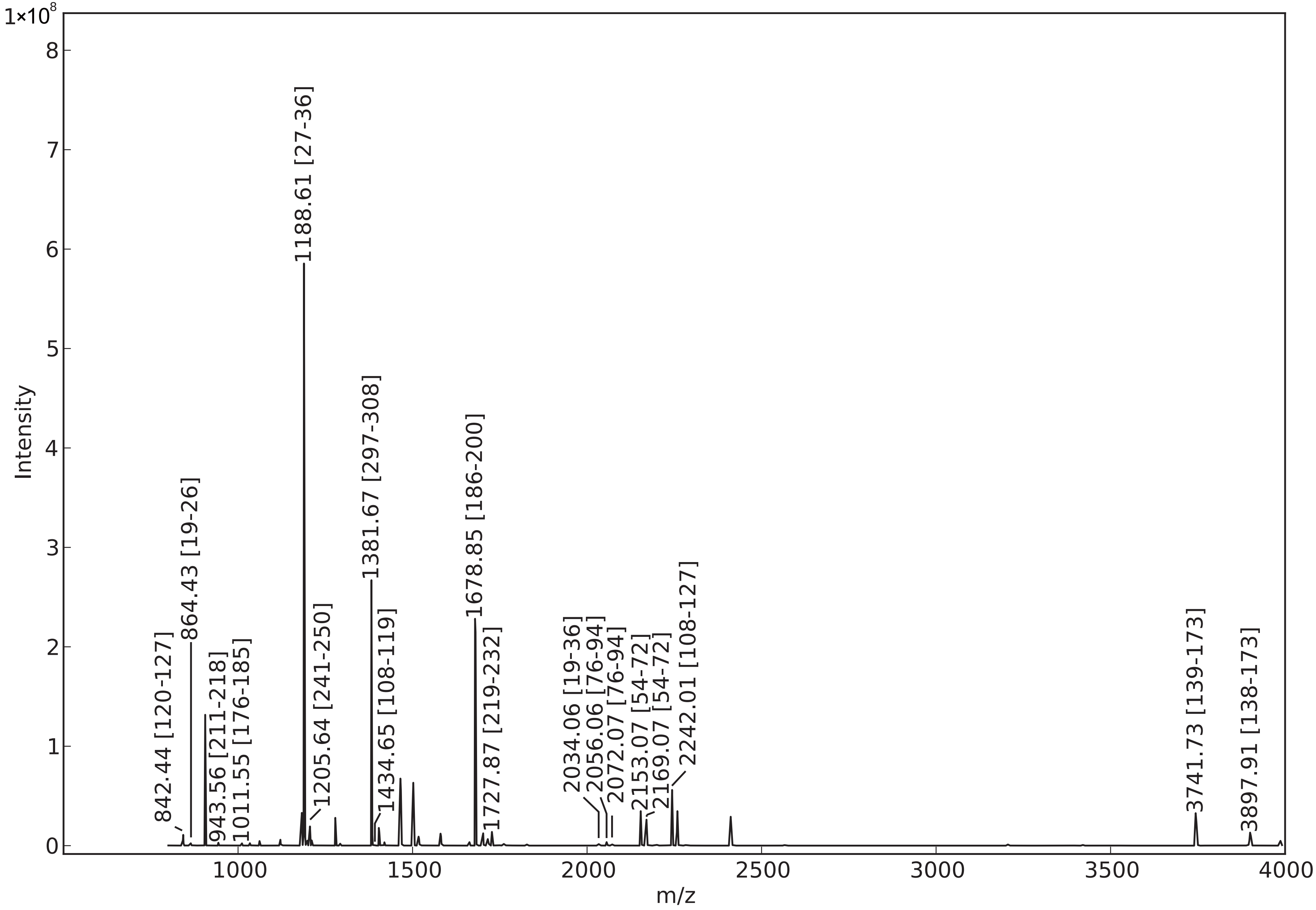
1×10^9
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1132.62 [113-121]
1396.84 [85-96]
1691.96 [216-229]
1702.01 [65-79]
1793.03 [265-280]
1809.04 [265-280]
1848.07 [215-229]
1889.06 [106-121]
2385.33 [85-105]
2395.33 [244-264]
3193.87 [125-156]
3321.90 [124-156]

Spot No. 50

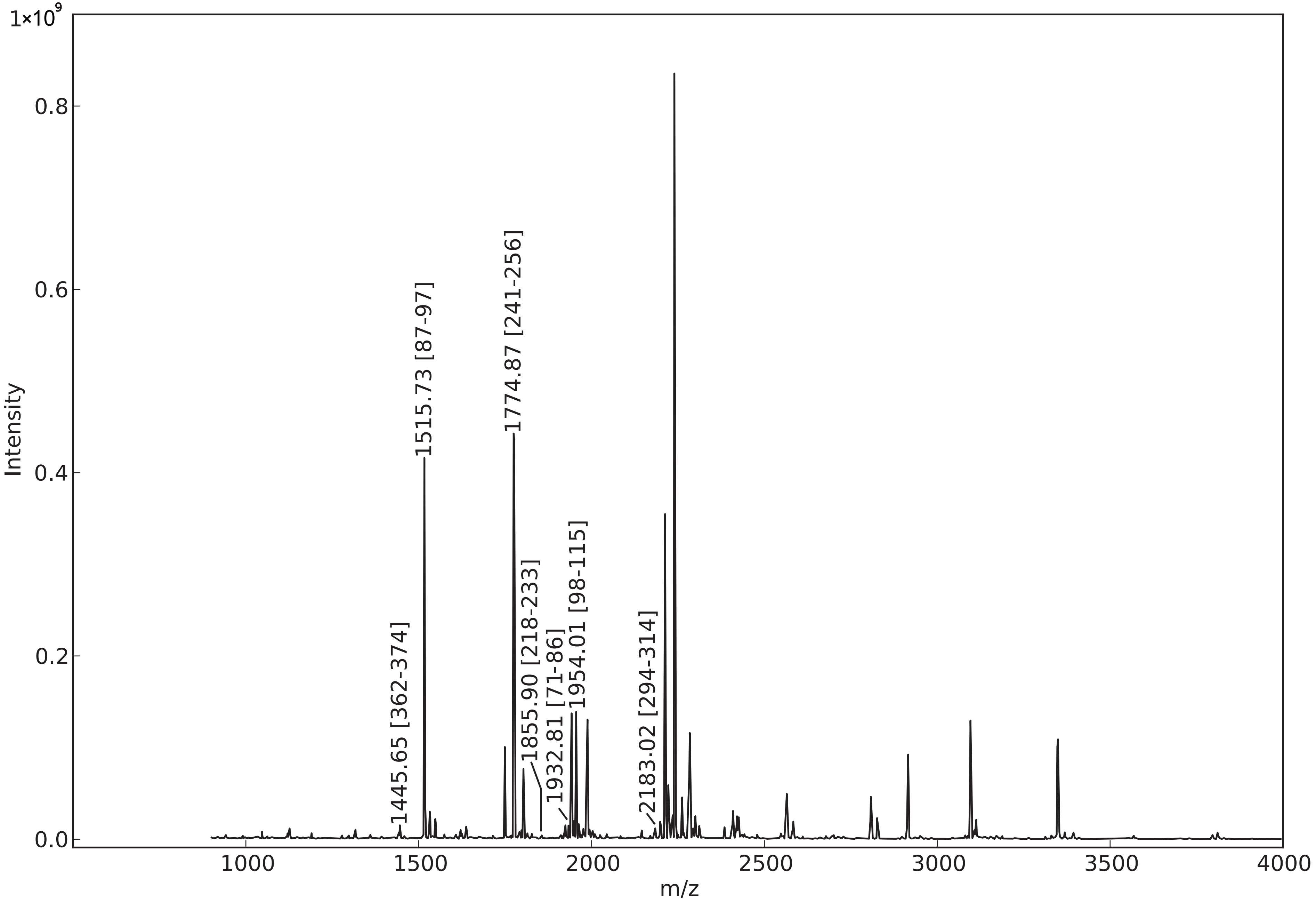


1×10⁹
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1119.56 [49-57]
1305.70 [129-140]
1498.91 [237-250]
1775.86 [312-325]
2033.14 [170-188]
2198.12 [274-293]
2738.37 [83-107]

Spot No. 51

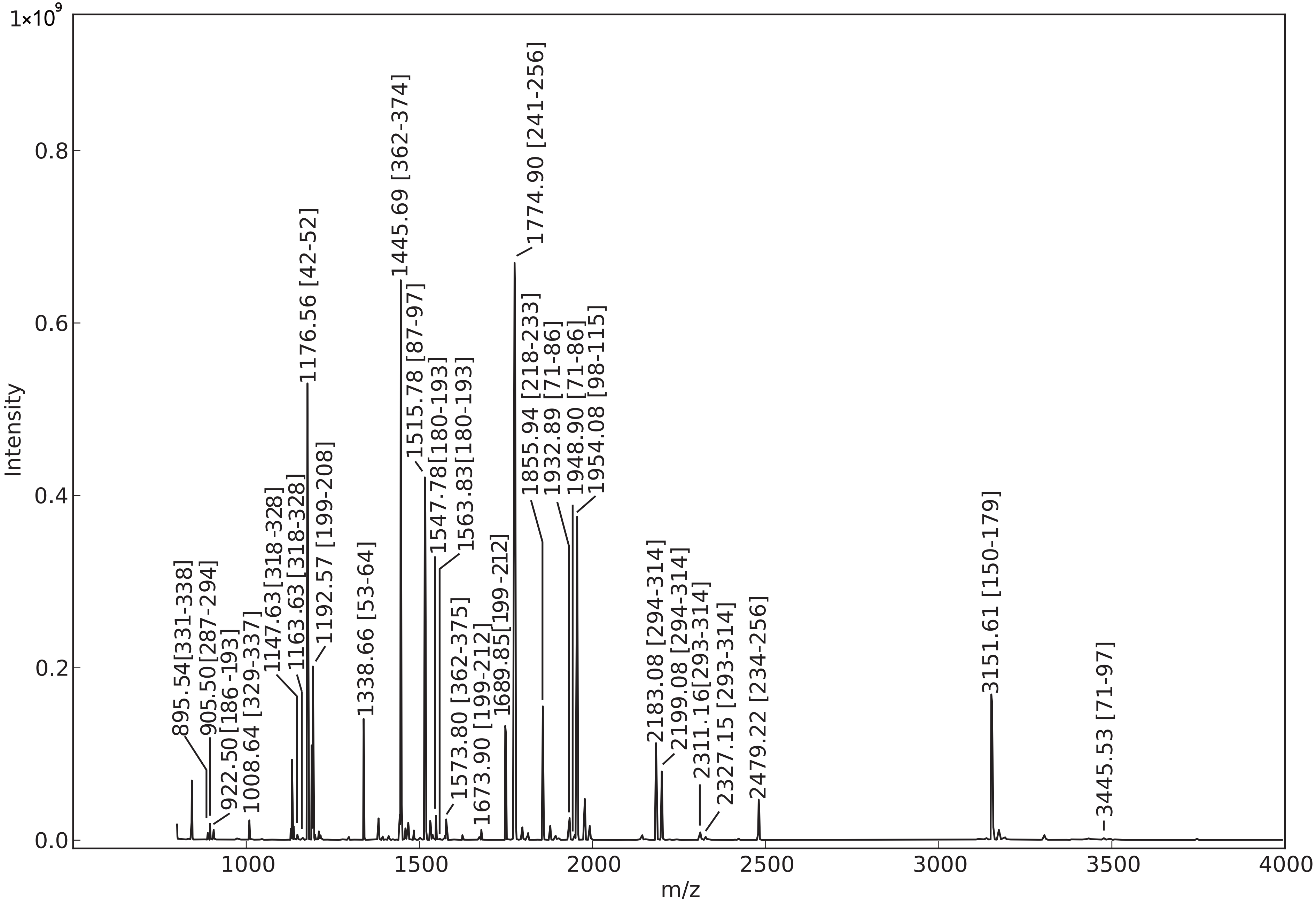

1×10^8
8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
842.44 [120-127]
864.43 [19-26]
943.56 [211-218]
1011.55 [176-185]
1188.61 [27-36]
1205.64 [241-250]
1381.67 [297-308]
1434.65 [108-119]
1678.85 [186-200]
1727.87 [219-232]
2034.06 [19-36]
2056.06 [76-94]
2072.07 [76-94]
2153.07 [54-72]
2169.07 [54-72]
2242.01 [108-127]
3741.73 [139-173]
3897.91 [138-173]

Spot No. 52

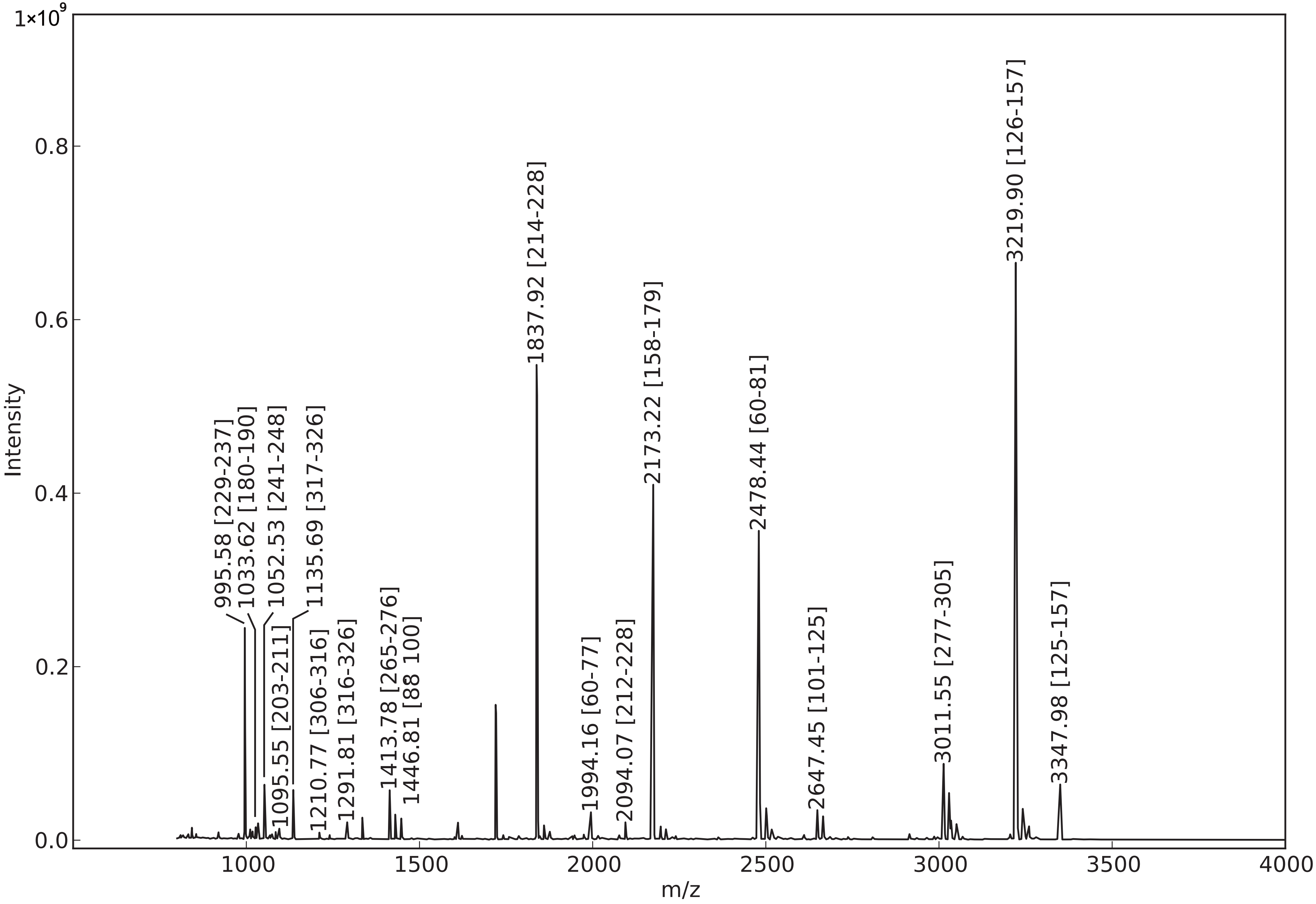


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1445.65 [362-374]
1515.73 [87-97]
1774.87 [241-256]
1855.90 [218-233]
1932.81 [71-86]
1954.01 [98-115]
2183.02 [294-314]

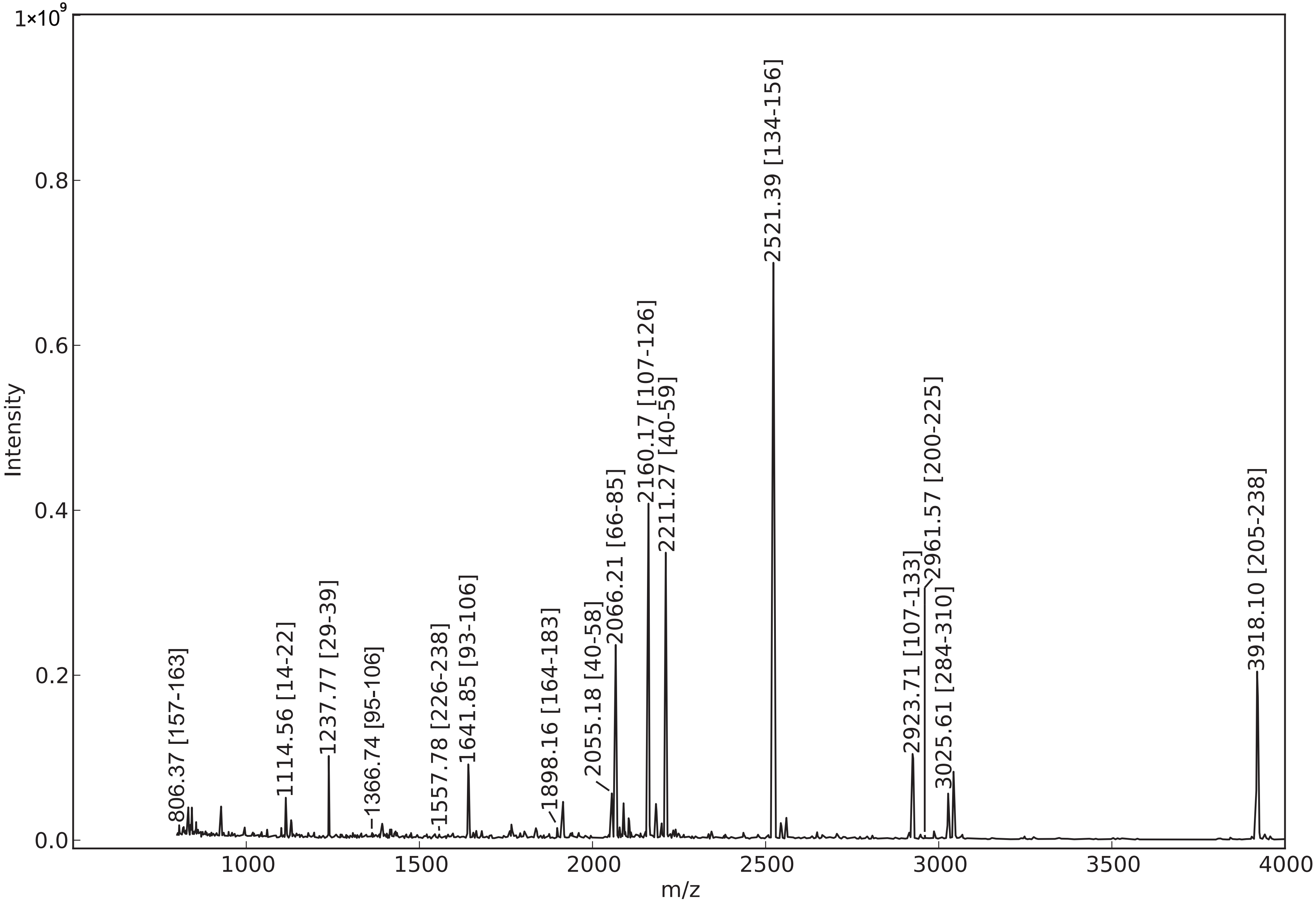
Spot No. 53


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
895.54[331-338]
905.50[287-294]
922.50[186-193]
1008.64 [329-337]
1147.63[318-328]
1163.63 [318-328]
1176.56 [42-52]
1192.57 [199-208]
1338.66 [53-64]
1445.69 [362-374]
1515.78 [87-97]
1547.78[180-193]
1563.83[180-193]
1573.80 [362-375]
1673.90 [199-212]
1689.85[199-212]
1774.90 [241-256]
1855.94 [218-233]
1932.89 [71-86]
1948.90 [71-86]
1954.08 [98-115]
2183.08 [294-314]
2199.08 [294-314]
2311.16[293-314]
2327.15 [293-314]
2479.22 [234-256]
3151.61 [150-179]
3445.53 [71-97]

Spot No. 54


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
995.58 [229-237]
1033.62 [180-190]
1052.53 [241-248]
1135.69 [317-326]
1095.55 [203-211]
1210.77 [306-316]
1291.81 [316-326]
1413.78 [265-276]
1446.81 [88 100]
1837.92 [214-228]
1994.16 [60-77]
2094.07 [212-228]
2173.22 [158-179]
2478.44 [60-81]
2647.45 [101-125]
3011.55 [277-305]
3219.90 [126-157]
3347.98 [125-157]

Spot No. 55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0.6
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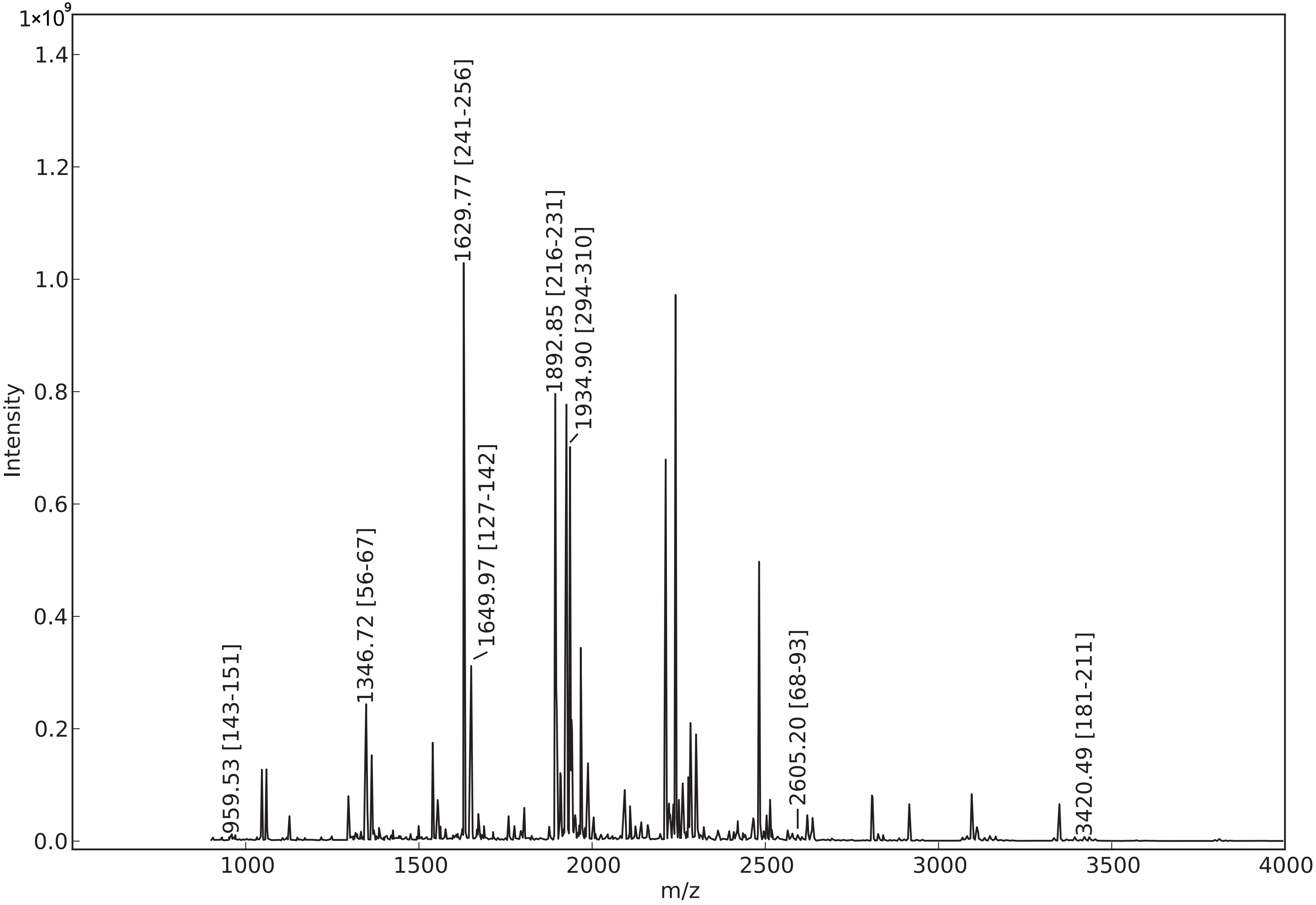
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
806.37 [157-163]
1114.56 [14-22]
1237.77 [29-39]
1366.74 [95-106]
1557.78 [226-238]
1641.85 [93-106]
1898.16 [164-183]
2055.18 [40-58]
2066.21 [66-85]
2160.17 [107-126]
2211.27 [40-59]
2521.39 [134-156]
2923.71 [107-133]
2961.57 [200-225]
3025.61 [284-310]
3918.10 [205-238]

Spot No. 56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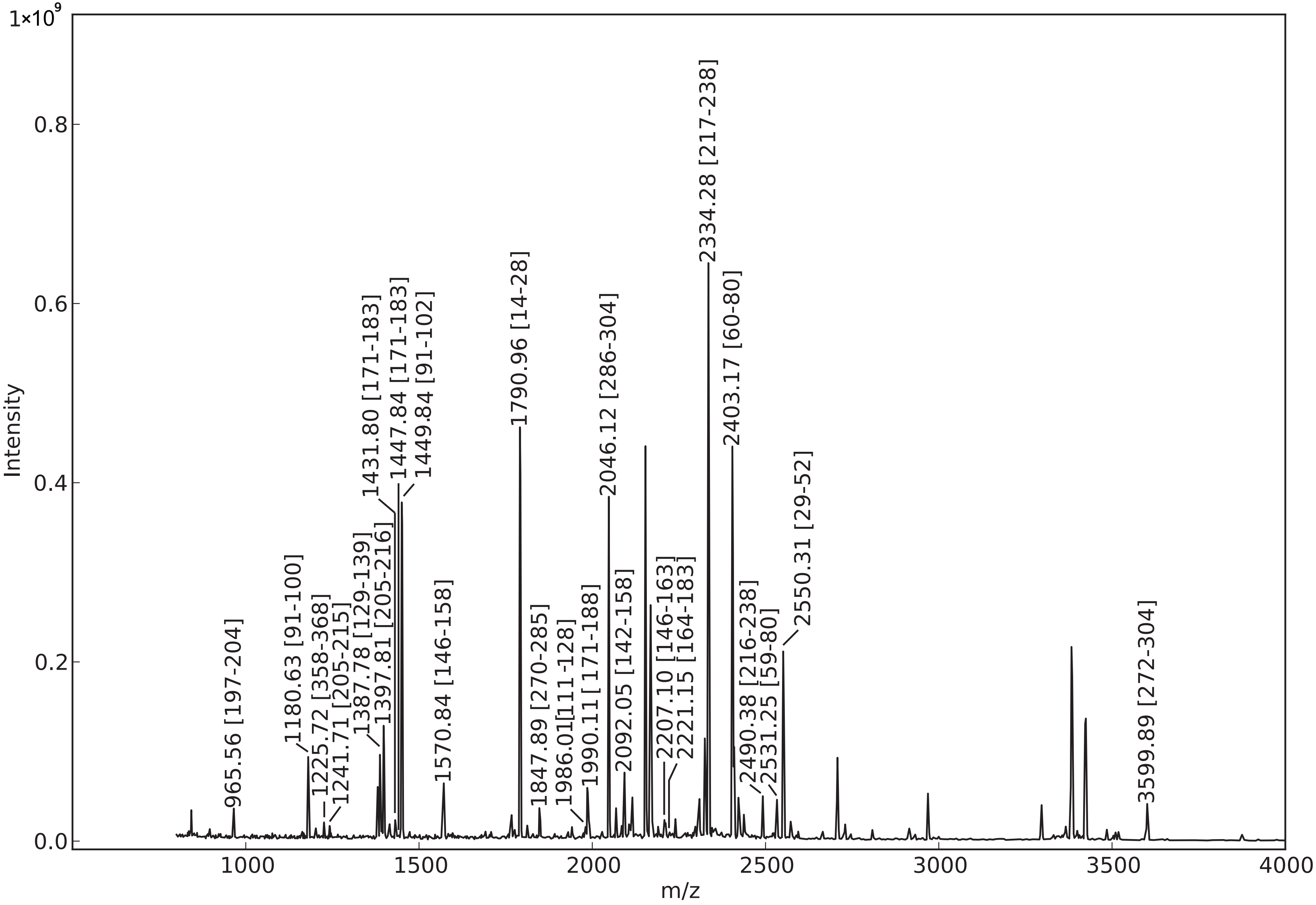
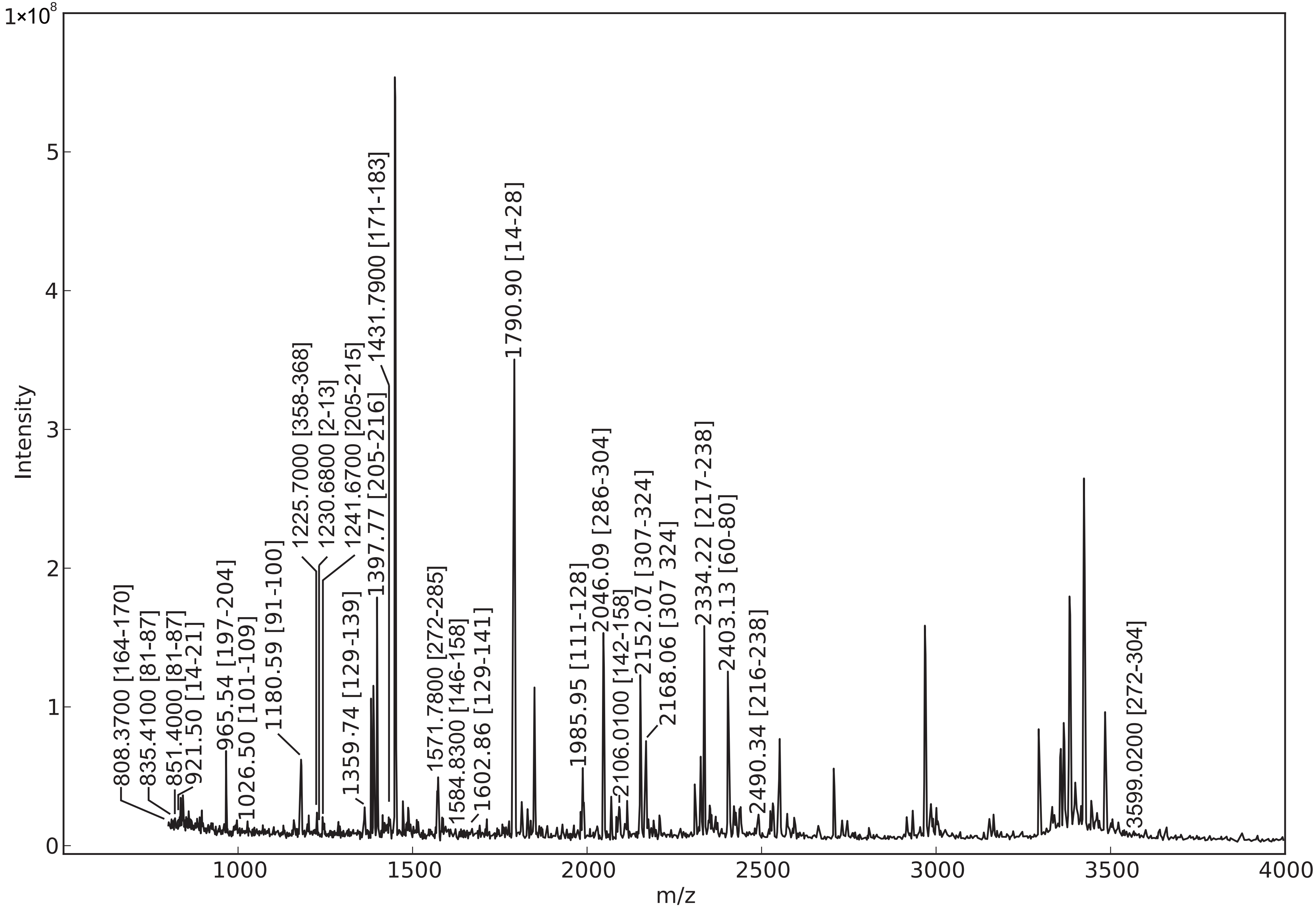
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
959.53 [143-151]
1346.72 [56-67]
1629.77 [241-256]
1649.97 [127-142]
1892.85 [216-231]
1934.90 [294-310]
2605.20 [68-93]
3420.49 [181-211]

Spot No. 57

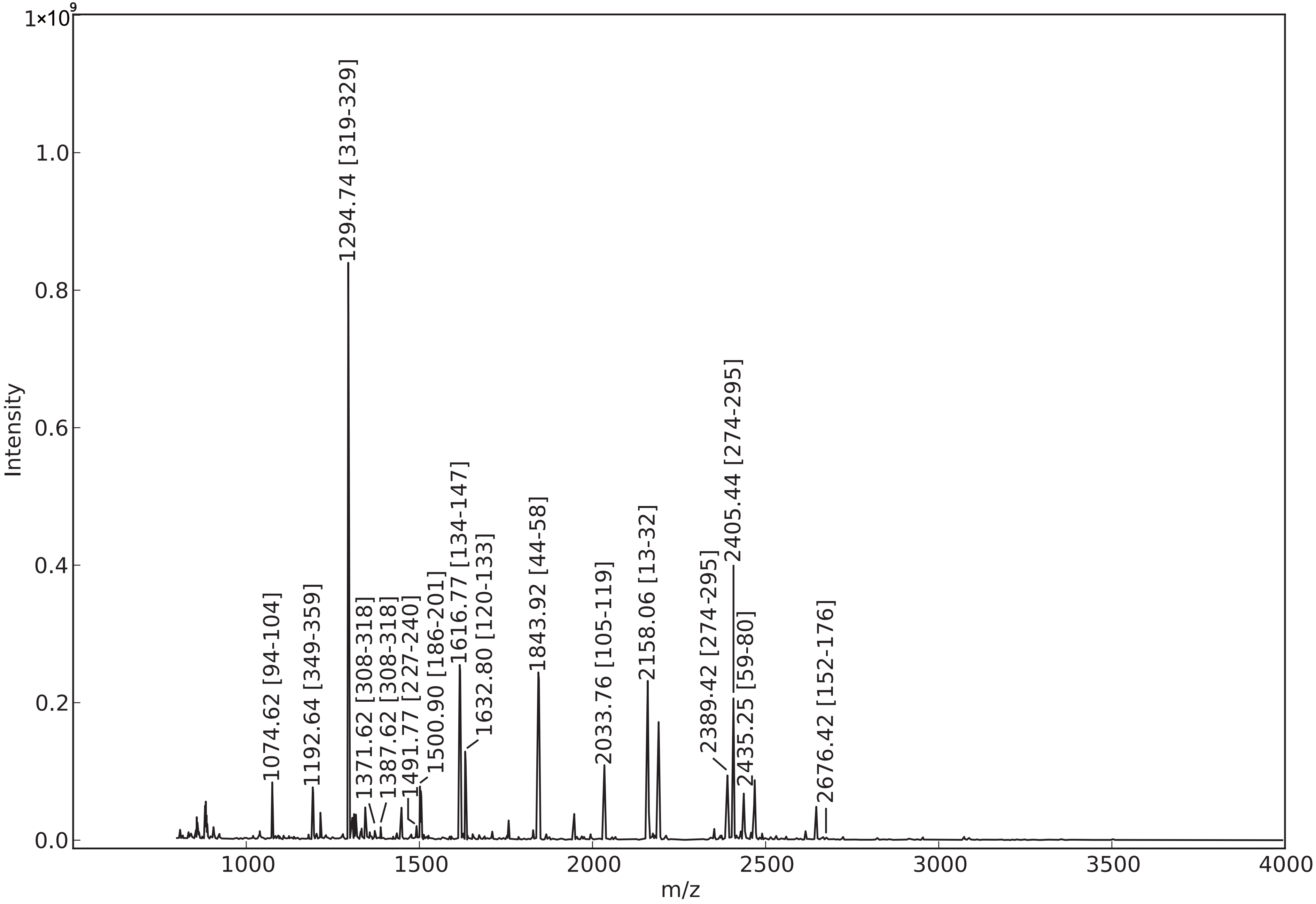


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
965.56 [197-204]
1180.63 [91-100]
1225.72 [358-368]
1241.71 [205-215]
1387.78 [129-139]
1397.81 [205-216]
1431.80 [171-183]
1447.84 [171-183]
1449.84 [91-102]
1570.84 [146-158]
1790.96 [14-28]
1847.89 [270-285]
1986.01[111-128]
1990.11 [171-188]
2046.12 [286-304]
2092.05 [142-158]
2207.10 [146-163]
2221.15 [164-183]
2334.28 [217-238]
2403.17 [60-80]
2490.38 [216-238]
2531.25 [59-80]
2550.31 [29-52]
3599.89 [272-304]

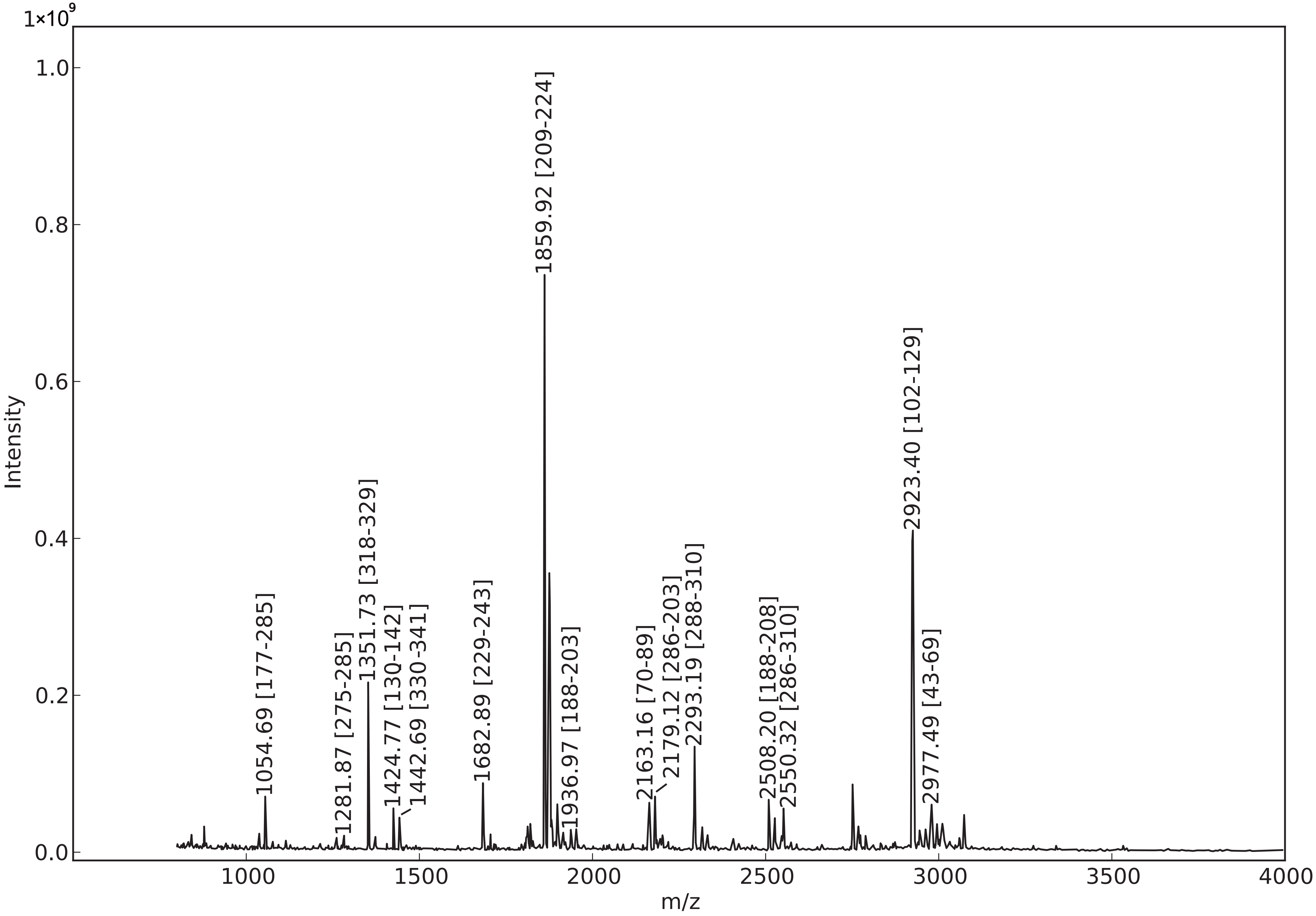
Spot No. 58


1×10⁸
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
808.3700 [164-170]
835.4100 [81-87]
851.4000 [81-87]
921.50 [14-21]
965.54 [197-204]
1026.50 [101-109]
1180.59 [91-100]
1225.7000 [358-368]
1230.6800 [2-13]
1241.6700 [205-215]
1359.74 [129-139]
1397.77 [205-216]
1431.7900 [171-183]
1571.7800 [272-285]
1584.8300 [146-158]
1602.86 [129-141]
1790.90 [14-28]
1985.95 [111-128]
2046.09 [286-304]
2106.0100 [142-158]
2152.07 [307-324]
2168.06 [307 324]
2334.22 [217-238]
2403.13 [60-80]
2490.34 [216-238]
3599.0200 [272-304]

Spot No. 59

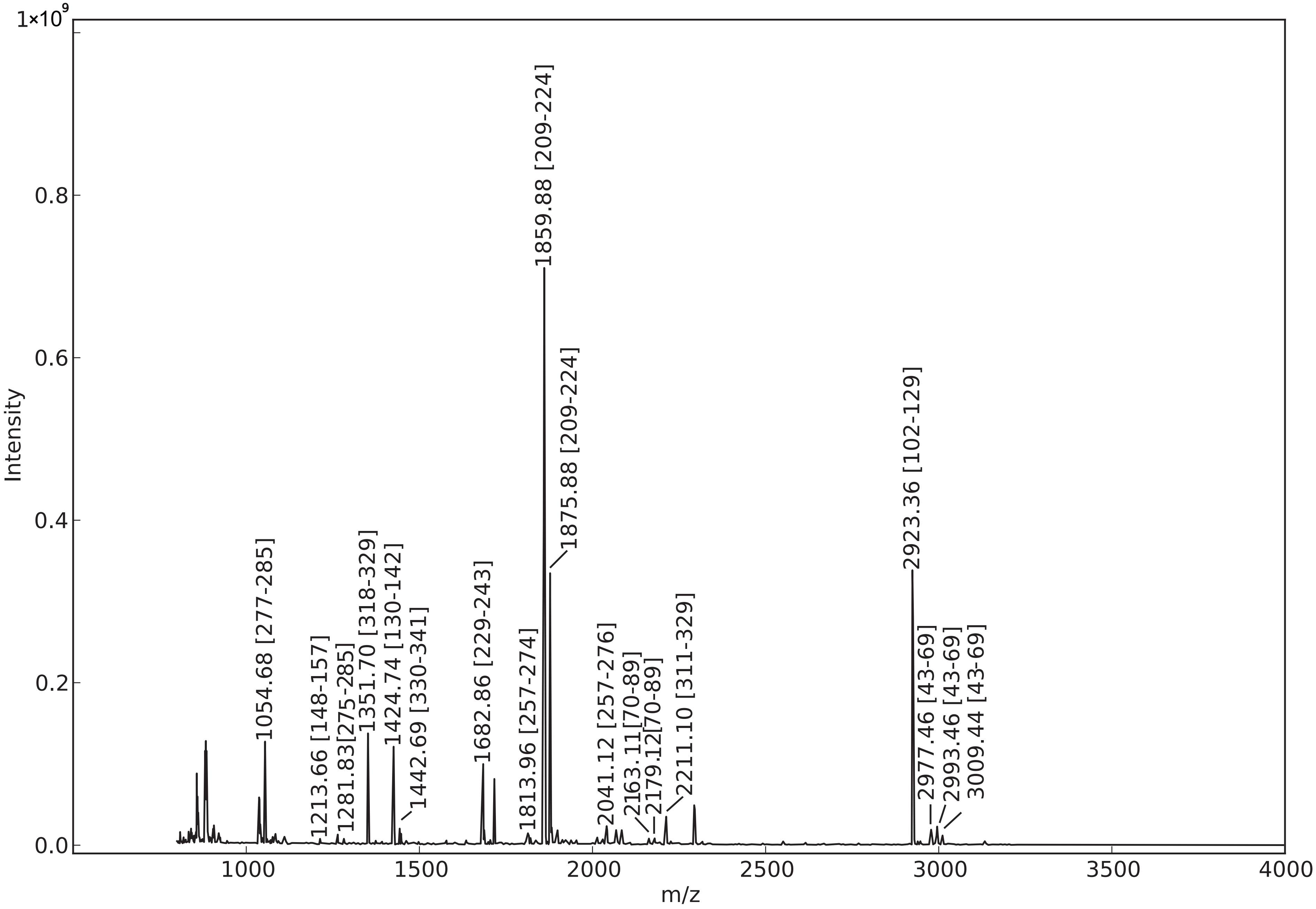

1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1074.62 [94-104]
1192.64 [349-359]
1294.74 [319-329]
1371.62 [308-318]
1387.62 [308-318]
1491.77 [227-240]
1500.90 [186-201]
1616.77 [134-147]
1632.80 [120-133]
1843.92 [44-58]
2033.76 [105-119]
2158.06 [13-32]
2389.42 [274-295]
2405.44 [274-295]
2435.25 [59-80]
2676.42 [152-176]

Spot No. 60

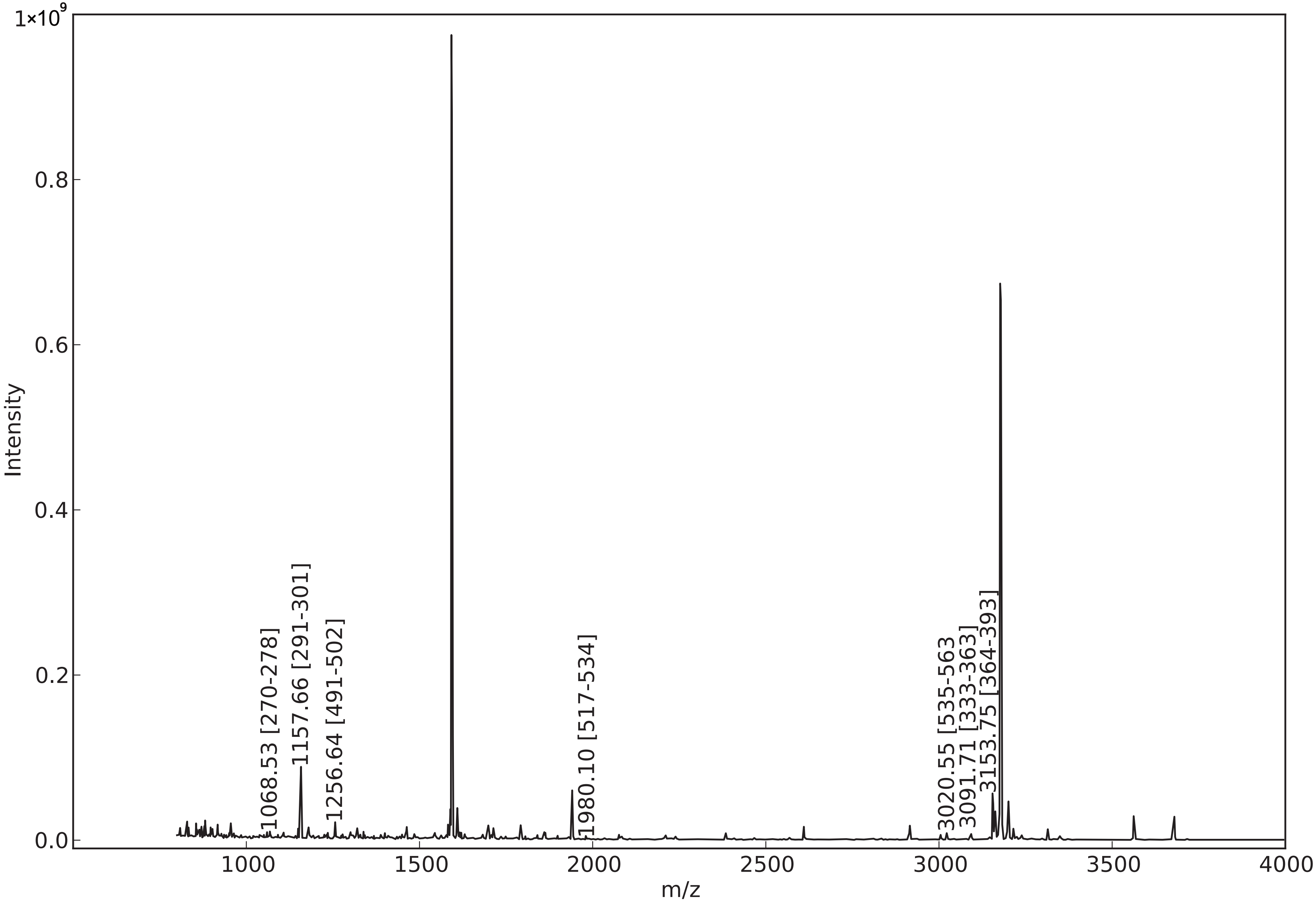


1×10^9
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1054.69 [177-285]
1281.87 [275-285]
1351.73 [318-329]
1424.77 [130-142]
1442.69 [330-341]
1682.89 [229-243]
1859.92 [209-224]
1936.97 [188-203]
2163.16 [70-89]
2179.12 [286-203]
2293.19 [288-310]
2508.20 [188-208]
2550.32 [286-310]
2923.40 [102-129]
2977.49 [43-69]
1000
1500
2000
2500
3000
3500
4000
m/z

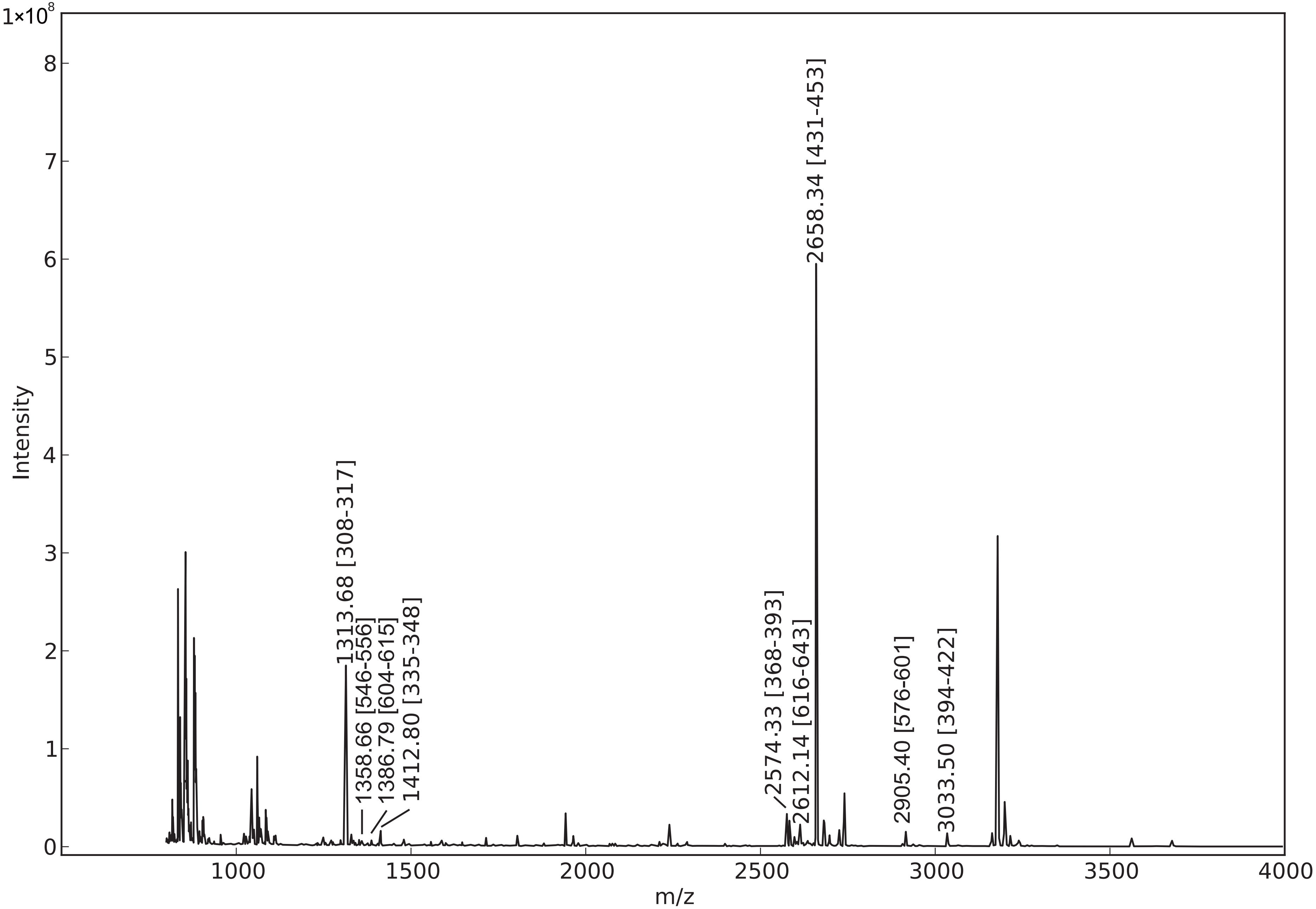
Spot No. 61


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1054.68 [277-285]
1213.66 [148-157]
1281.83[275-285]
1351.70 [318-329]
1424.74 [130-142]
1442.69 [330-341]
1682.86 [229-243]
1813.96 [257-274]
1859.88 [209-224]
1875.88 [209-224]
2041.12 [257-276]
2163.11[70-89]
2179.12[70-89]
2211.10 [311-329]
2923.36 [102-129]
2977.46 [43-69]
2993.46 [43-69]
3009.44 [43-69]

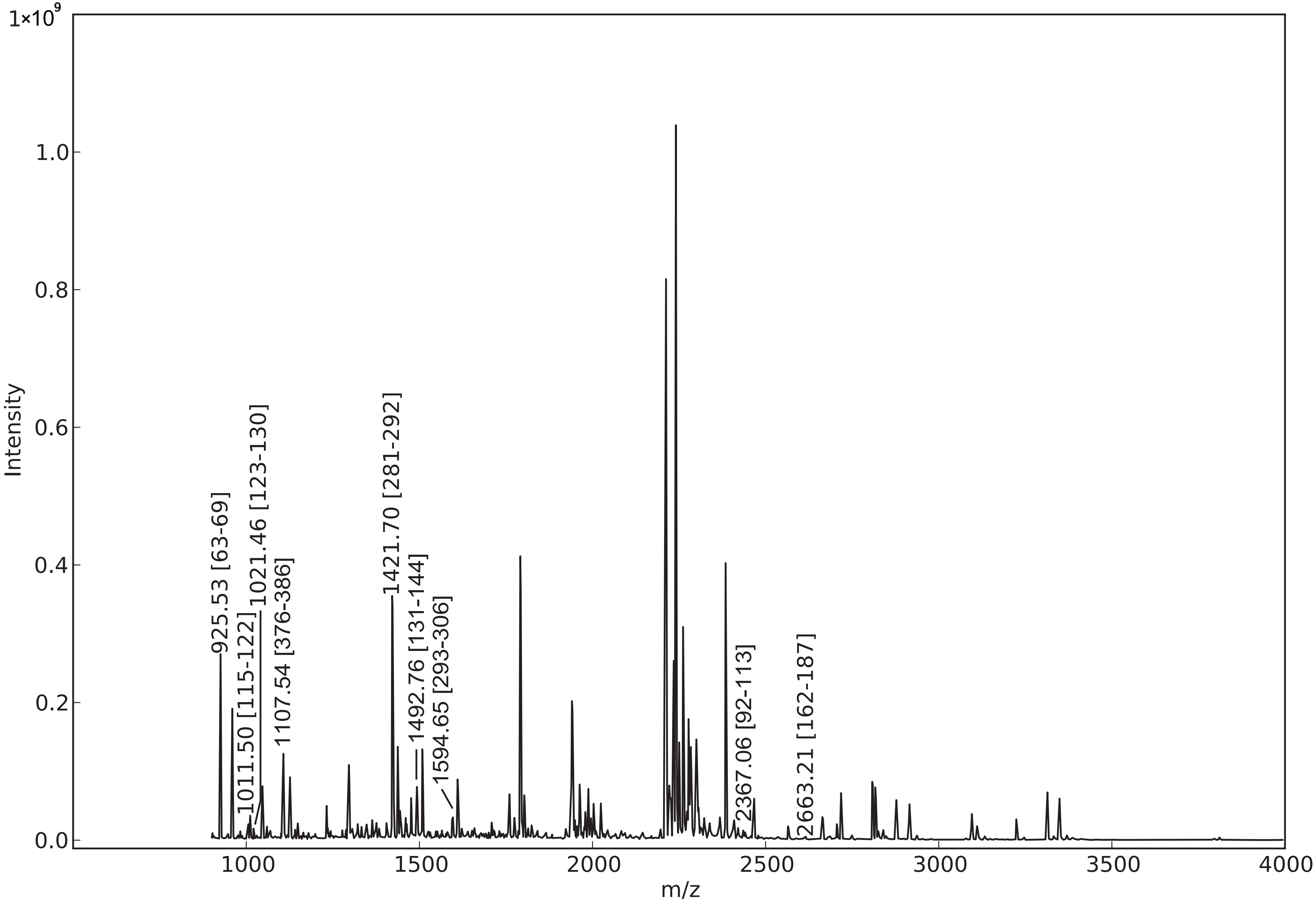
Spot No. 62


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1068.53 [270-278]
1157.66 [291-301]
1256.64 [491-502]
1980.10 [517-534]
3020.55 [535-563]
3091.71 [333-363]
3153.75 [364-393]

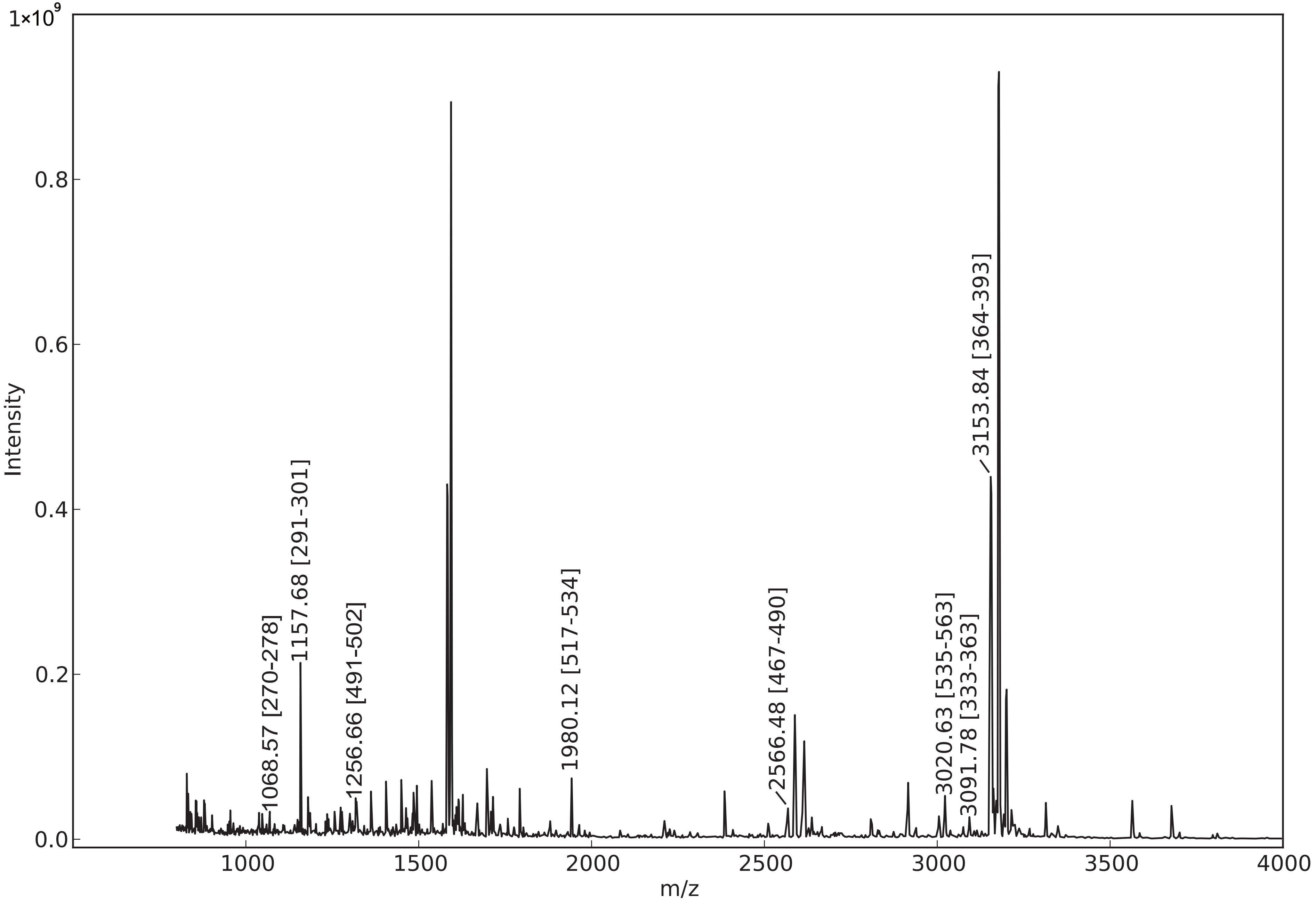
Spot No. 63


1×10⁸
8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1313.68 [308-317]
1358.66 [546-556]
1386.79 [604-615]
1412.80 [335-348]
2574.33 [368-393]
2612.14 [616-643]
2658.34 [431-453]
2905.40 [576-601]
3033.50 [394-422]

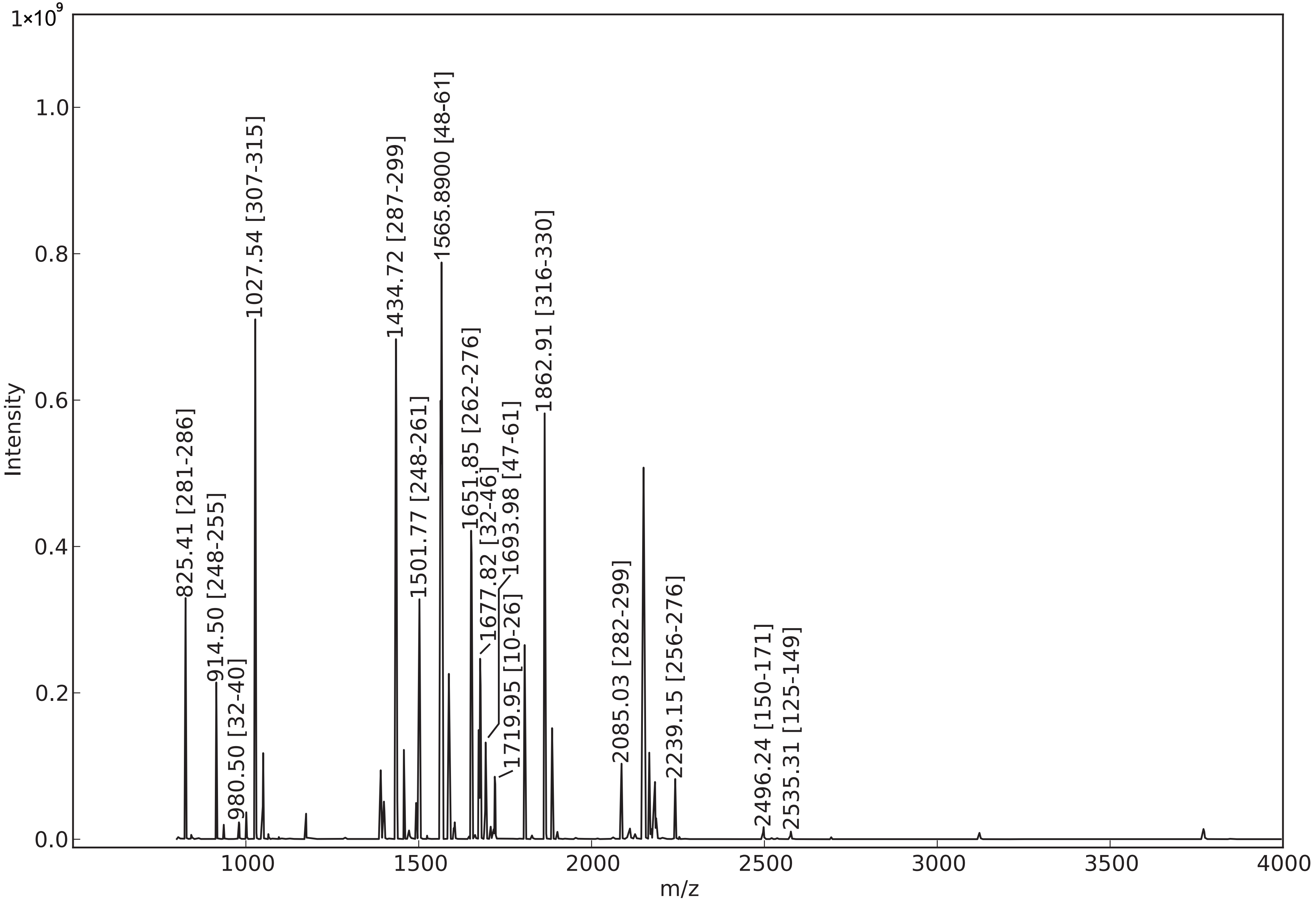
Spot No. 64


1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
925.53 [63-69]
1011.50 [115-122]
1021.46 [123-130]
1107.54 [376-386]
1421.70 [281-292]
1492.76 [131-144]
1594.65 [293-306]
2367.06 [92-113]
2663.21 [162-187]

Spot No. 65

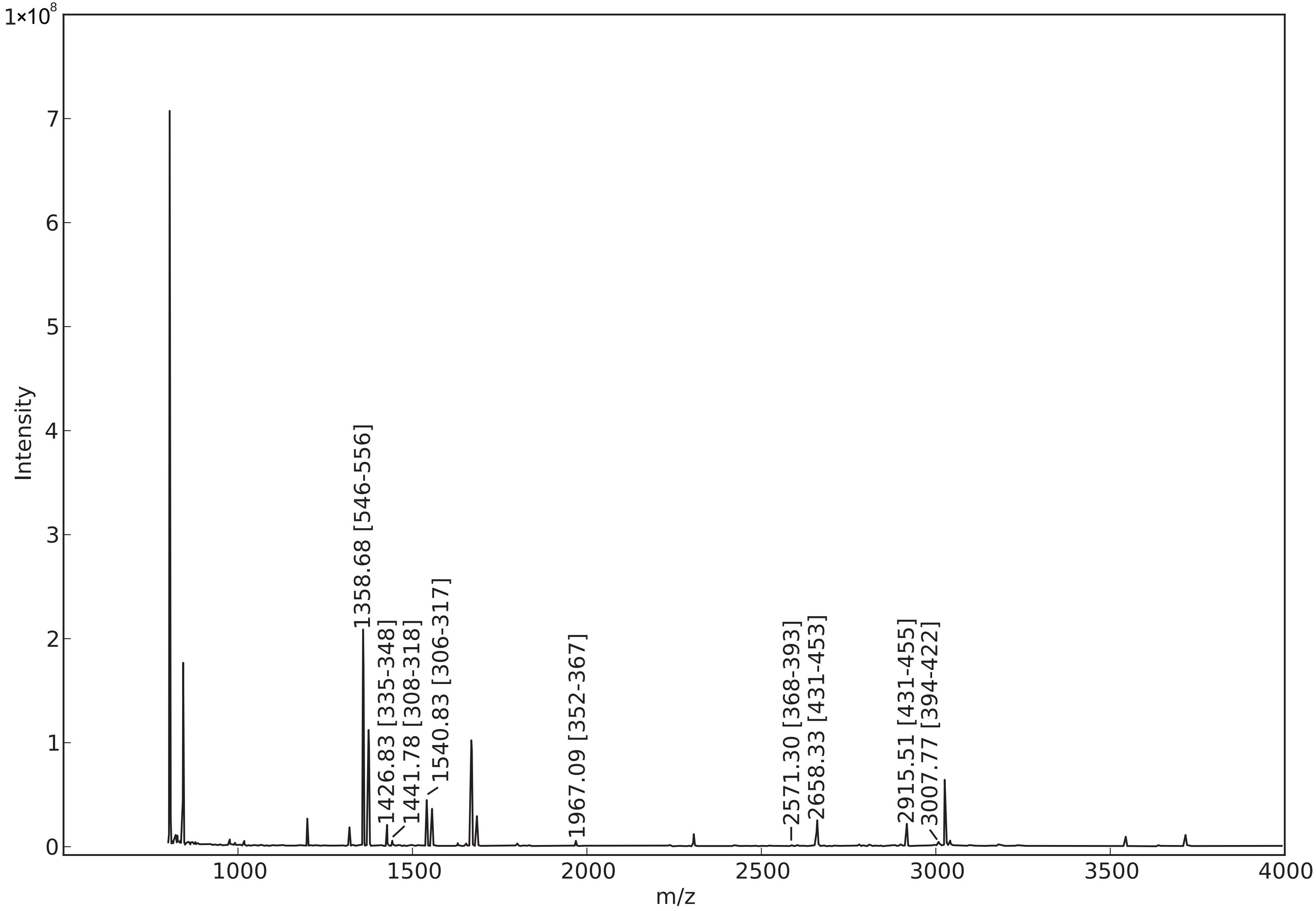

1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1068.57 [270-278]
1157.68 [291-301]
1256.66 [491-502]
1980.12 [517-534]
2566.48 [467-490]
3020.63 [535-563]
3091.78 [333-363]
3153.84 [364-393]

Spot No. 66



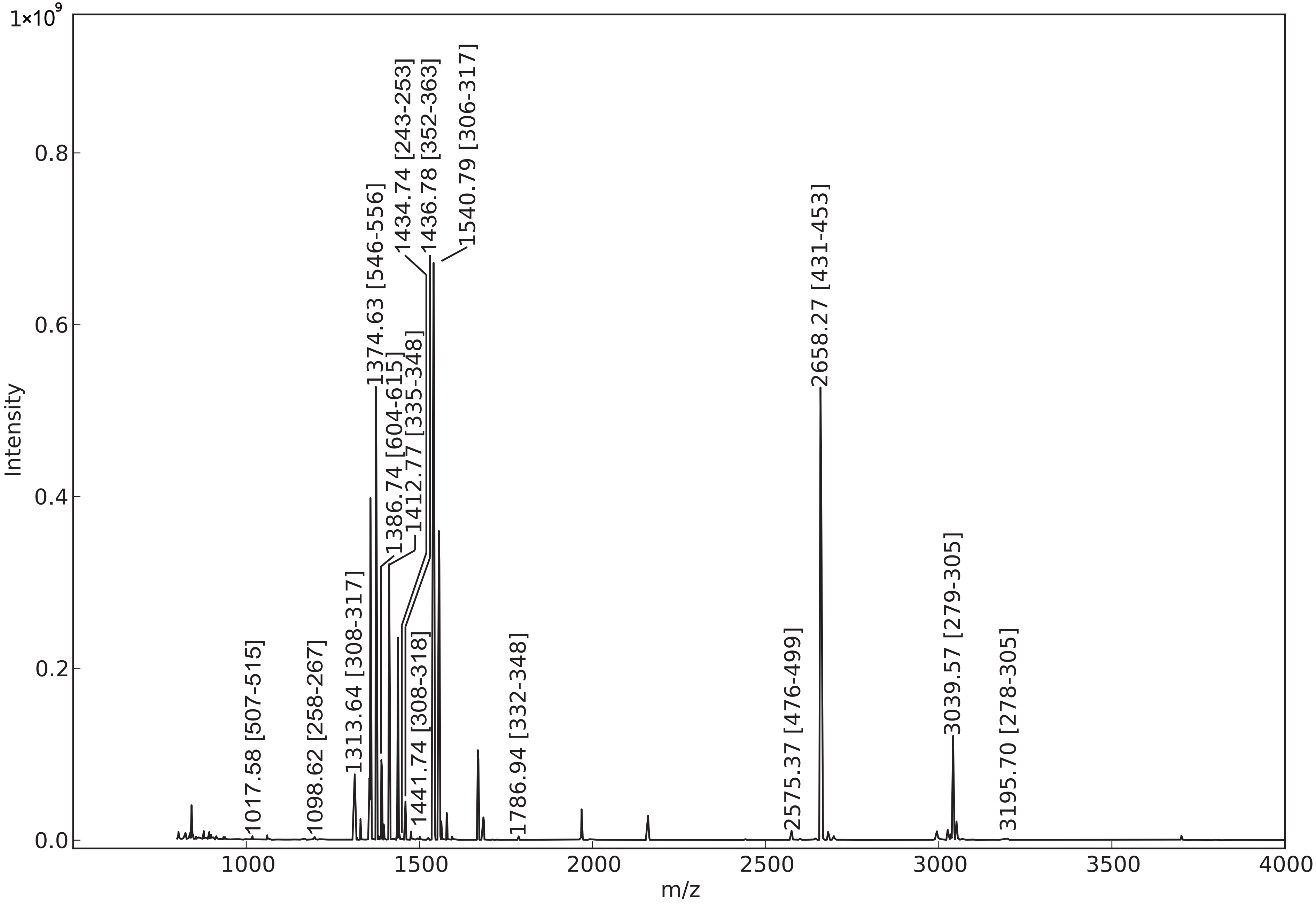
1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
825.41 [281-286]
914.50 [248-255]
980.50 [32-40]
1027.54 [307-315]
1434.72 [287-299]
1501.77 [248-261]
1565.8900 [48-61]
1651.85 [262-276]
1677.82 [32-46]
1693.98 [47-61]
1719.95 [10-26]
1862.91 [316-330]
2085.03 [282-299]
2239.15 [256-276]
2496.24 [150-171]
2535.31 [125-149]

Spot No. 67

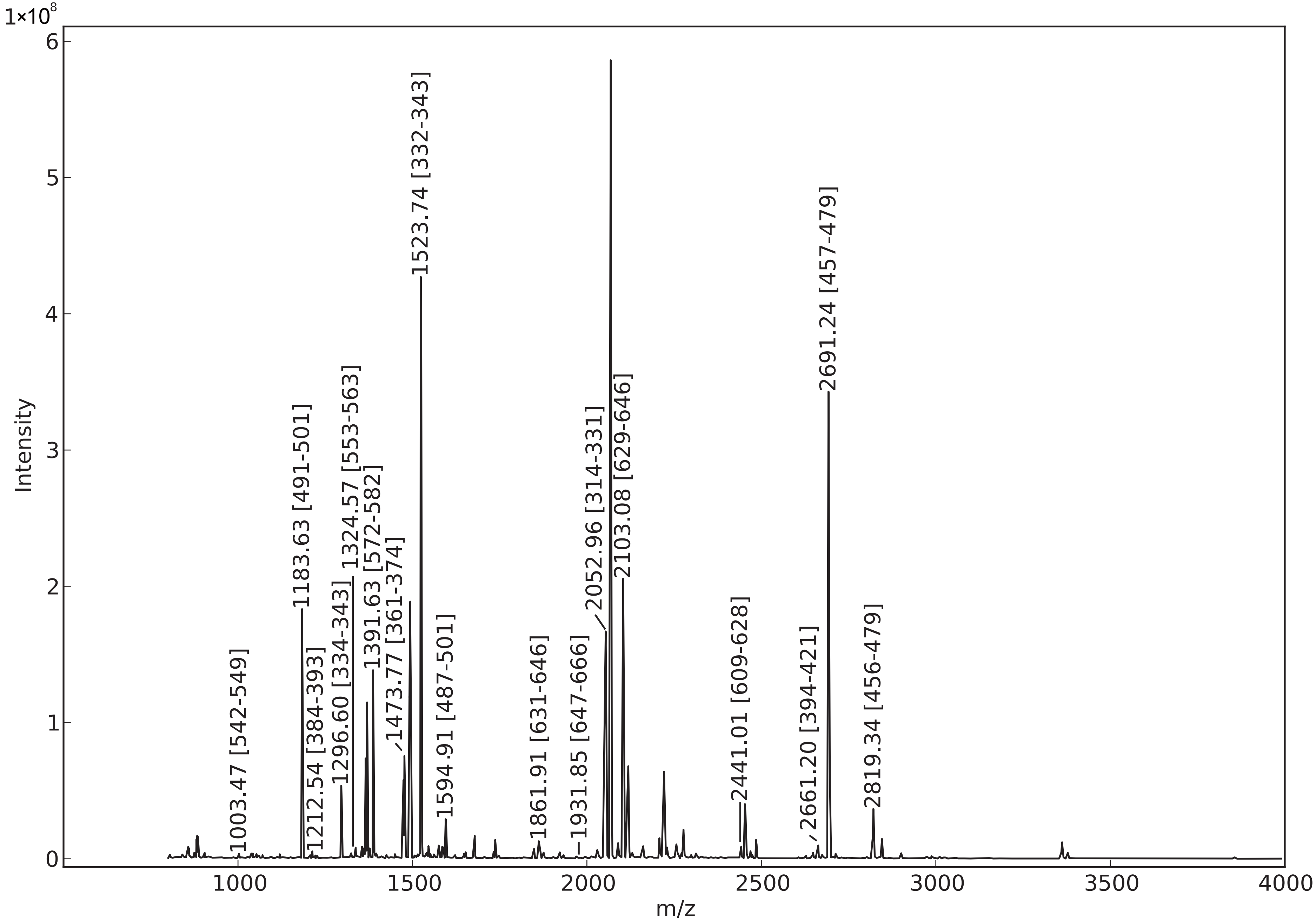


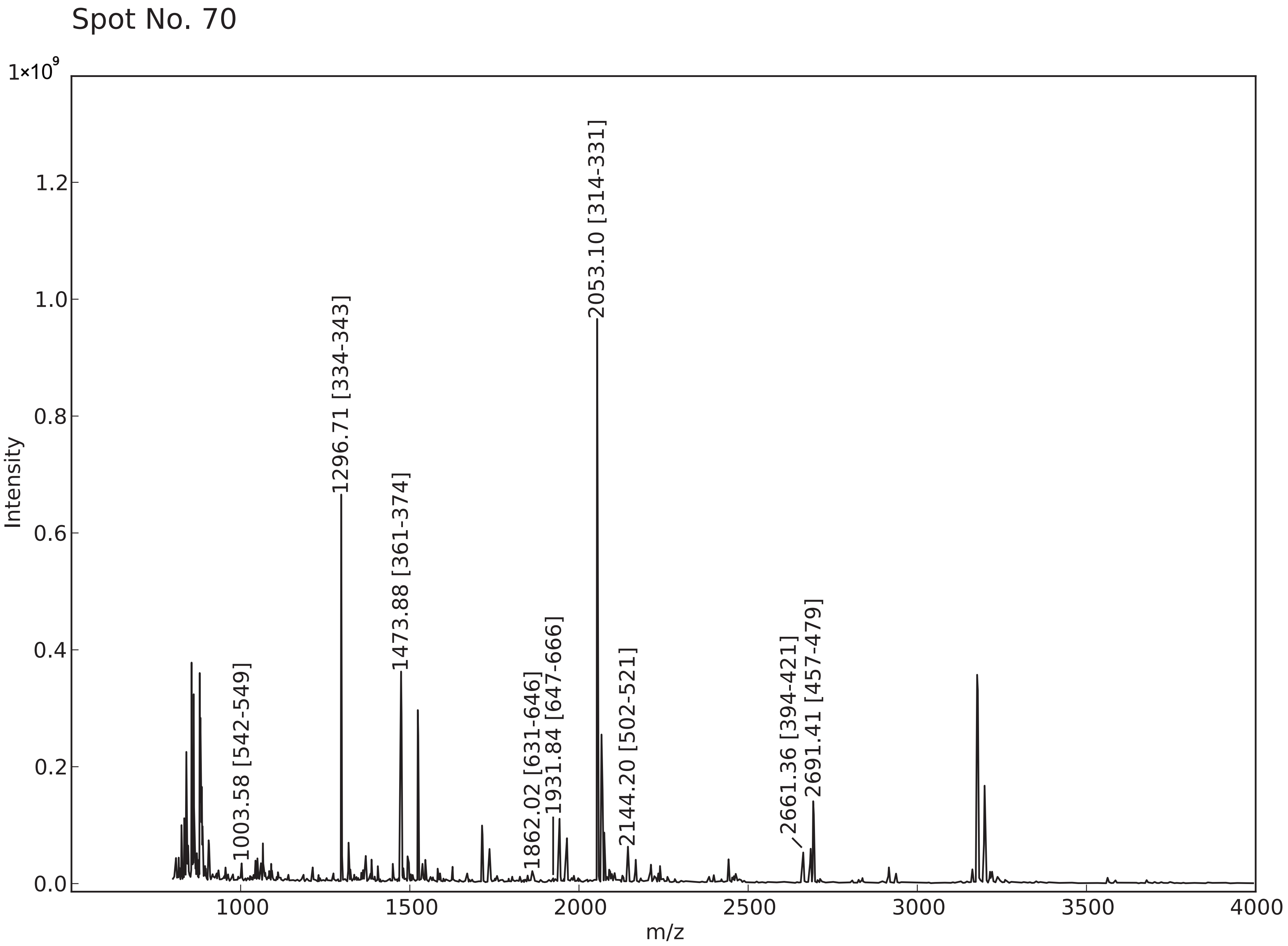
1×10^8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1358.68 [546-556]
1426.83 [335-348]
1441.78 [308-318]
1540.83 [306-317]
1967.09 [352-367]
2571.30 [368-393]
2658.33 [431-453]
2915.51 [431-455]
3007.77 [394-422]

Spot No. 68


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1017.58 [507-515]
1098.62 [258-267]
1313.64 [308-317]
1374.63 [546-556]
1386.74 [604-615]
1412.77 [335-348]
1434.74 [243-253]
1436.78 [352-363]
1441.74 [308-318]
1540.79 [306-317]
1786.94 [332-348]
2575.37 [476-499]
2658.27 [431-453]
3039.57 [279-305]
3195.70 [278-305]

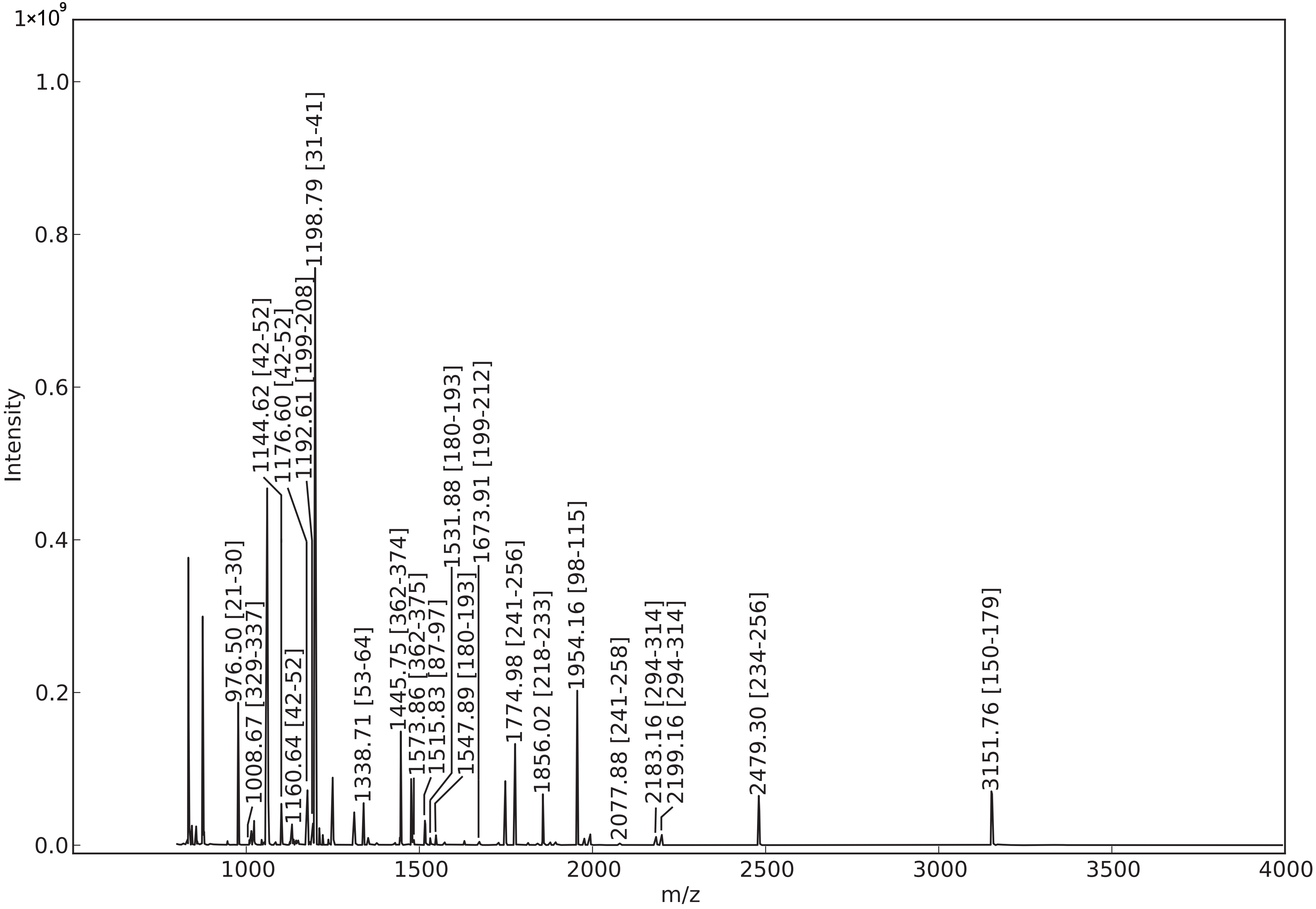
Spot No. 69


1×10^8
Intensity
6
5
4
3
2
1
0
m/z
1000
1500
2000
2500
3000
3500
4000
1003.47 [542-549]
1183.63 [491-501]
1212.54 [384-393]
1296.60 [334-343]
1324.57 [553-563]
1391.63 [572-582]
1473.77 [361-374]
1523.74 [332-343]
1594.91 [487-501]
1861.91 [631-646]
1931.85 [647-666]
2052.96 [314-331]
2103.08 [629-646]
2441.01 [609-628]
2661.20 [394-421]
2691.24 [457-479]
2819.34 [456-479]

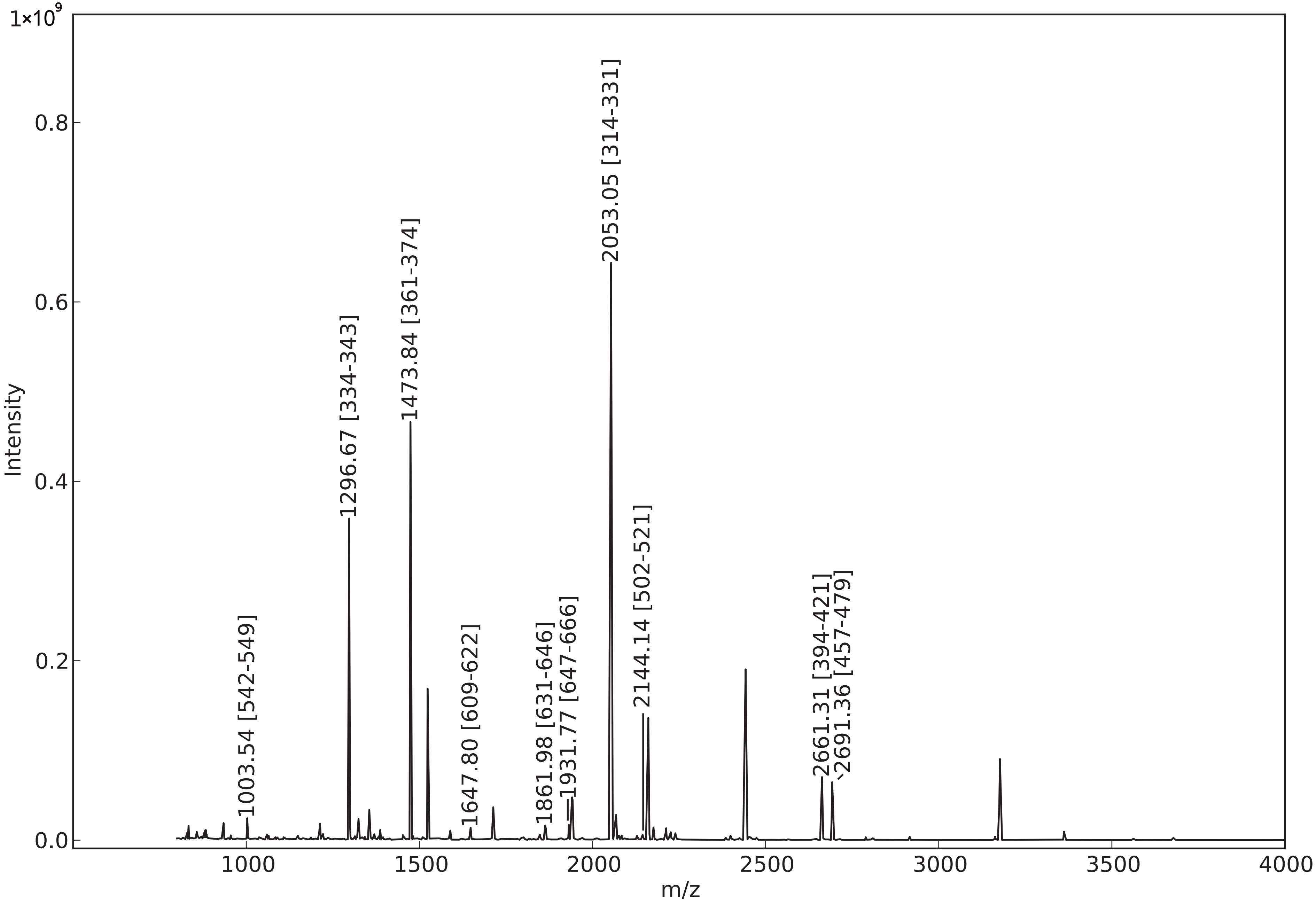


Spot No. 70
1×10⁹
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1003.58 [542-549]
1296.71 [334-343]
1473.88 [361-374]
1862.02 [631-646]
1931.84 [647-666]
2053.10 [314-331]
2144.20 [502-521]
2661.36 [394-421]
2691.41 [457-479]

Spot No. 71

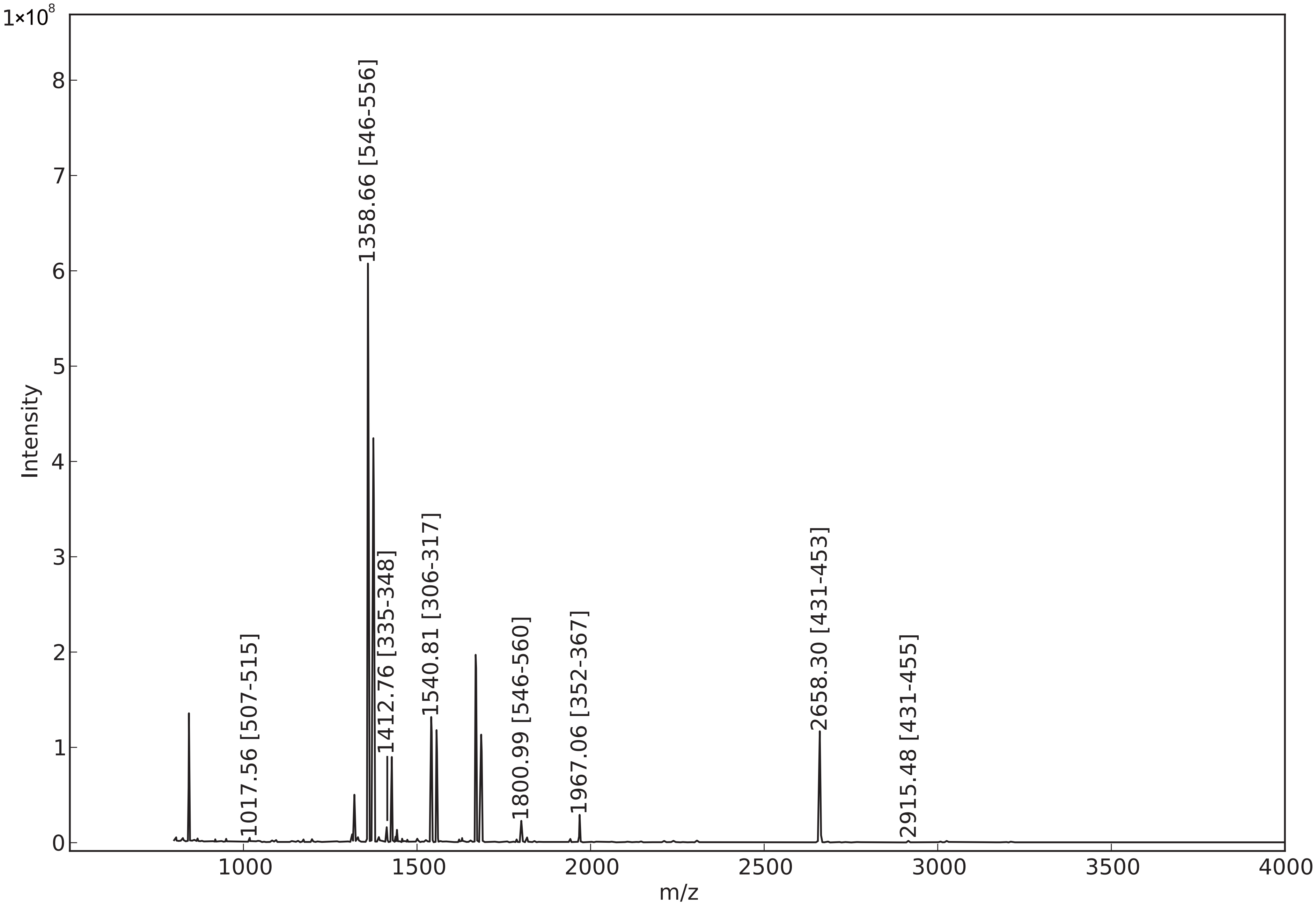

1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
976.50 [21-30]
1008.67 [329-337]
1144.62 [42-52]
1160.64 [42-52]
1176.60 [42-52]
1192.61 [199-208]
1198.79 [31-41]
1338.71 [53-64]
1445.75 [362-374]
1573.86 [362-375]
1515.83 [87-97]
1531.88 [180-193]
1547.89 [180-193]
1673.91 [199-212]
1774.98 [241-256]
1856.02 [218-233]
1954.16 [98-115]
2077.88 [241-258]
2183.16 [294-314]
2199.16 [294-314]
2479.30 [234-256]
3151.76 [150-179]

Spot No. 72

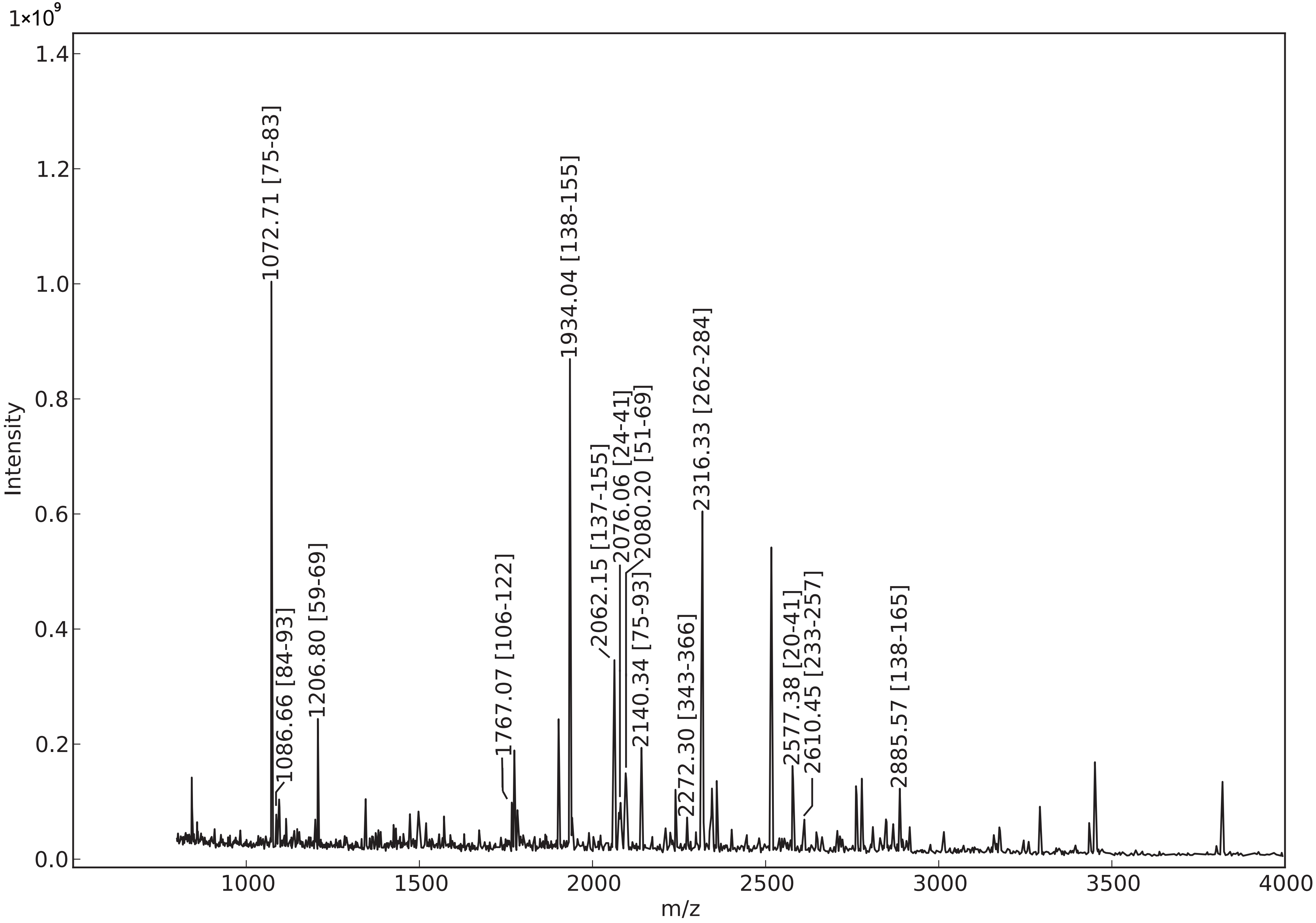


1×10^9
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1003.54 [542-549]
1296.67 [334-343]
1473.84 [361-374]
1647.80 [609-622]
1861.98 [631-646]
1931.77 [647-666]
2053.05 [314-331]
2144.14 [502-521]
2661.31 [394-421]
2691.36 [457-479]

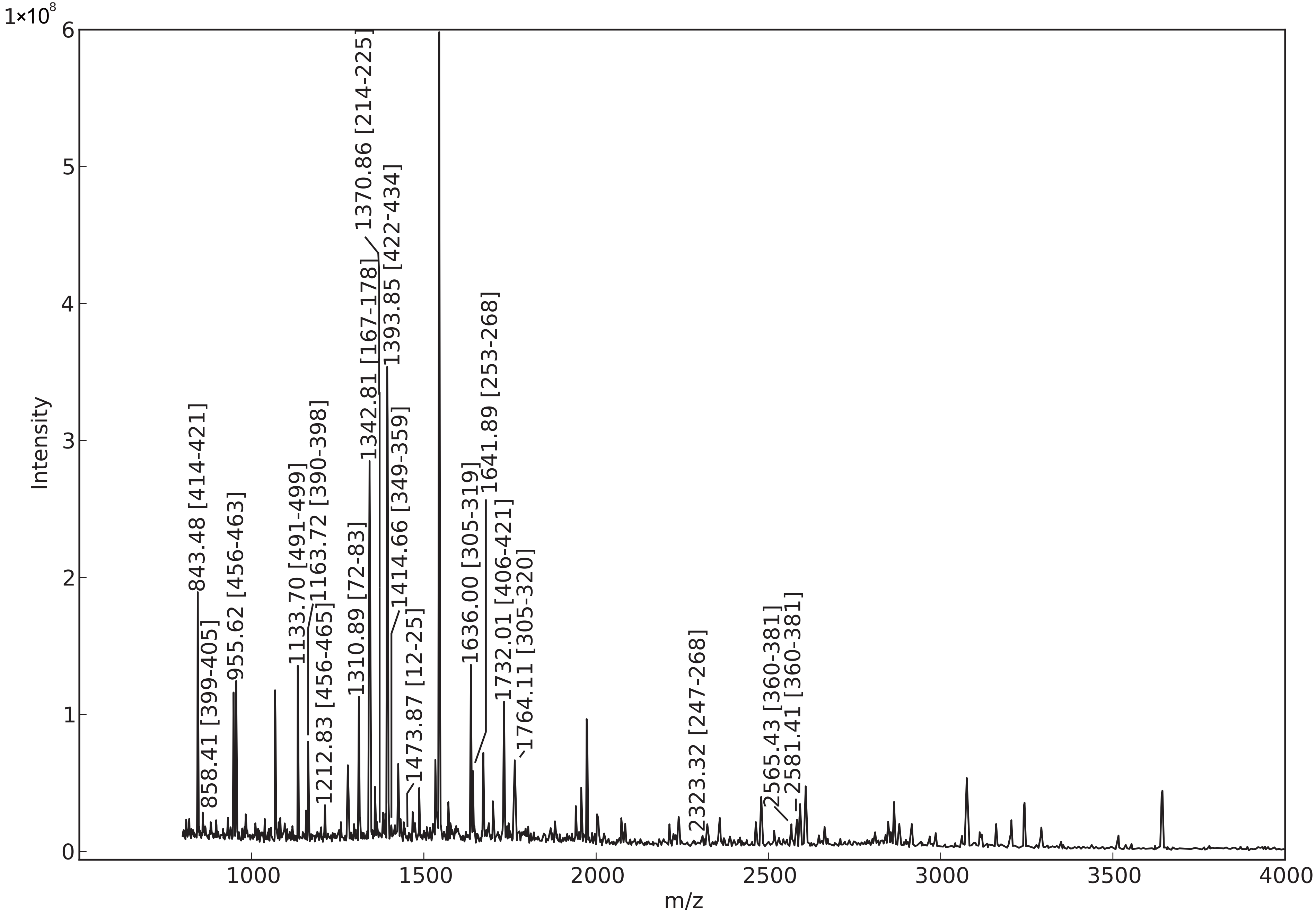
Spot No. 73


1×10^8
8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1358.66 [546-556]
1017.56 [507-515]
1412.76 [335-348]
1540.81 [306-317]
1800.99 [546-560]
1967.06 [352-367]
2658.30 [431-453]
2915.48 [431-455]

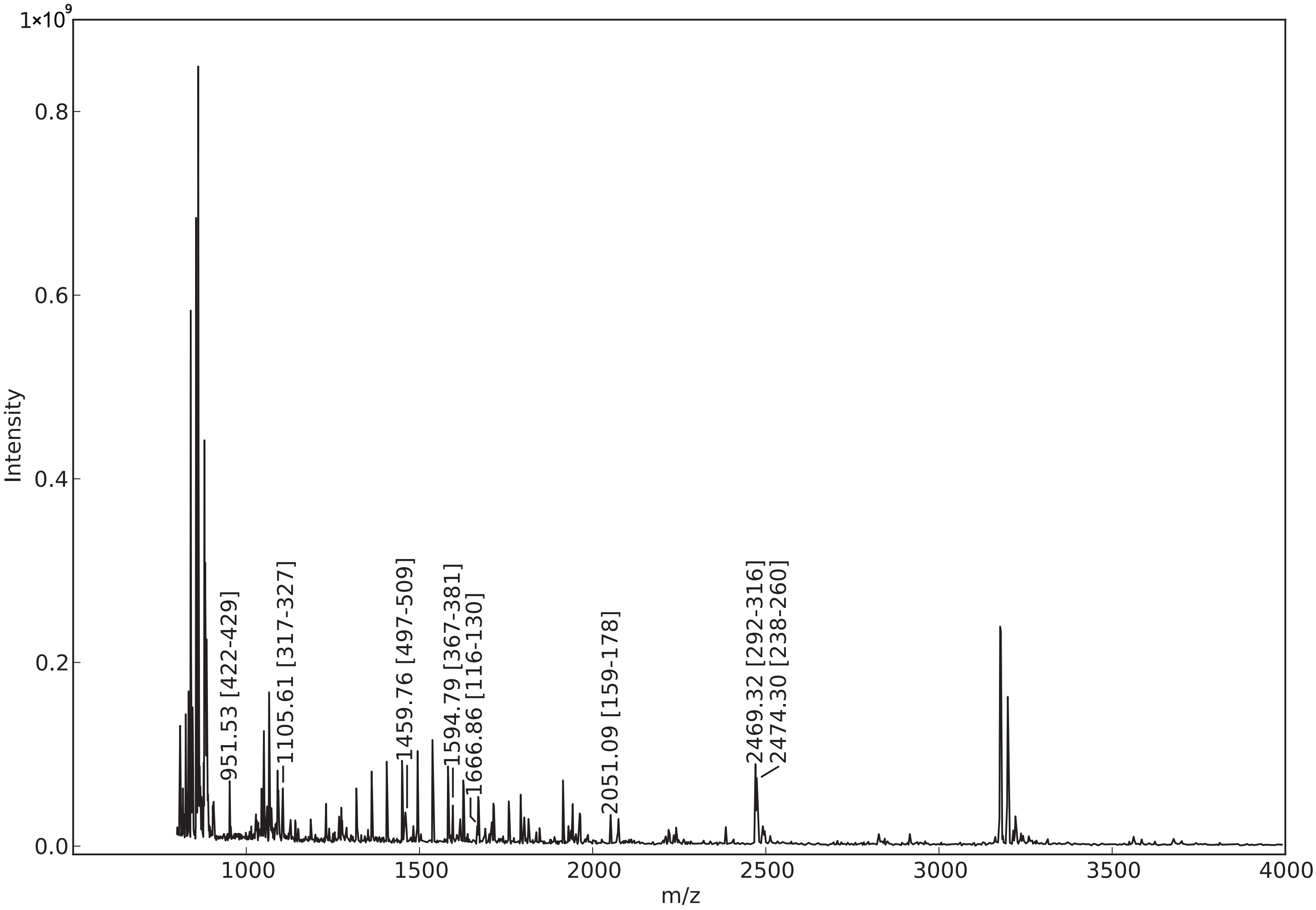
Spot No. 74


1×10⁹
Intensity
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
m/z
1000
1500
2000
2500
3000
3500
4000
1072.71 [75-83]
1086.66 [84-93]
1206.80 [59-69]
1767.07 [106-122]
1934.04 [138-155]
2062.15 [137-155]
2076.06 [24-41]
2080.20 [51-69]
2140.34 [75-93]
2272.30 [343-366]
2316.33 [262-284]
2577.38 [20-41]
2610.45 [233-257]
2885.57 [138-165]

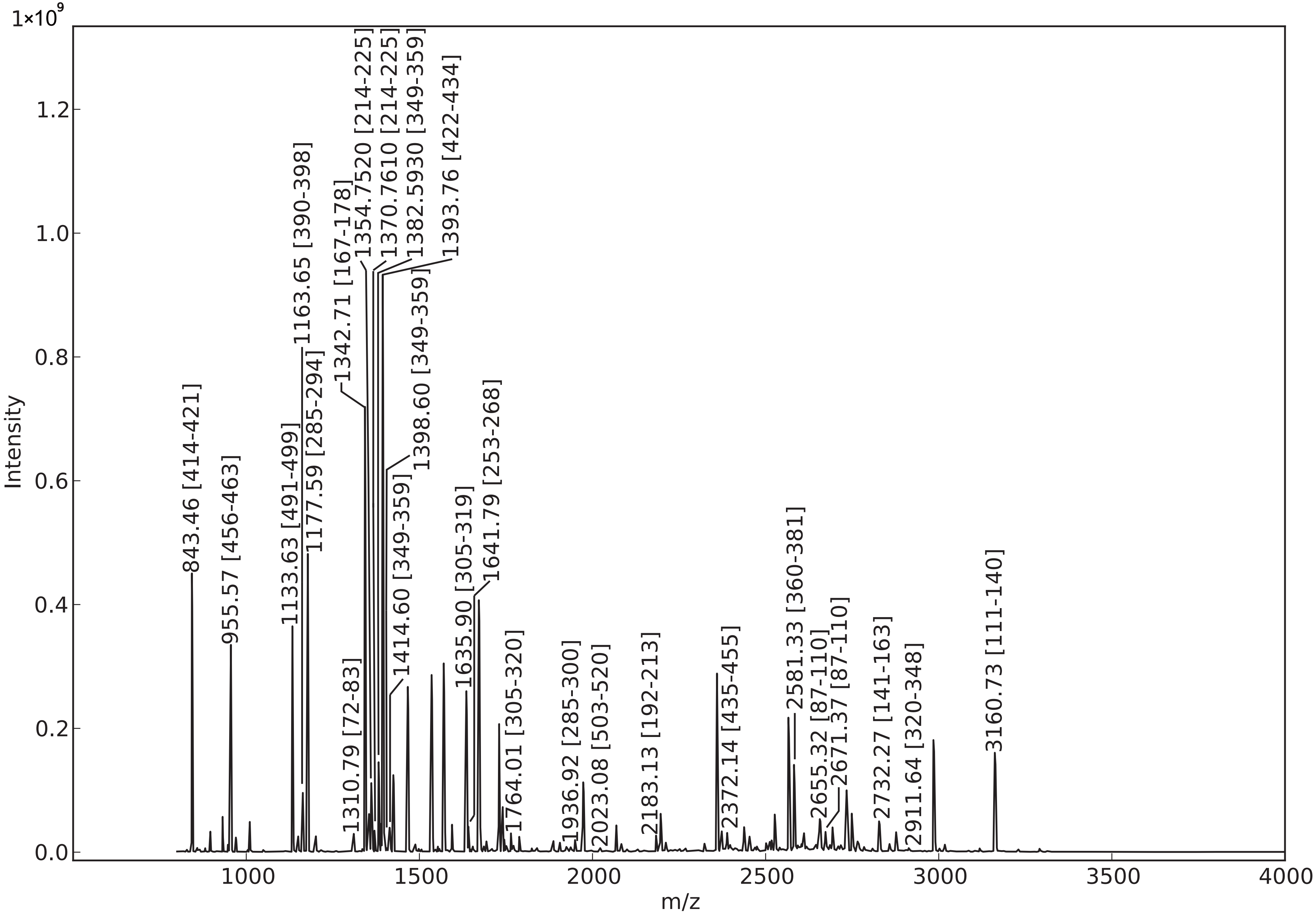
Spot No. 75


1×10^8
6
5
4
3
2
1
0
Intensity
843.48 [414-421]
858.41 [399-405]
955.62 [456-463]
1133.70 [491-499]
1163.72 [390-398]
1212.83 [456-465]
1310.89 [72-83]
1342.81 [167-178]
1370.86 [214-225]
1393.85 [422-434]
1414.66 [349-359]
1473.87 [12-25]
1636.00 [305-319]
1641.89 [253-268]
1732.01 [406-421]
1764.11 [305-320]
2323.32 [247-268]
2565.43 [360-381]
2581.41 [360-381]
1000
1500
2000
2500
3000
3500
4000
m/z

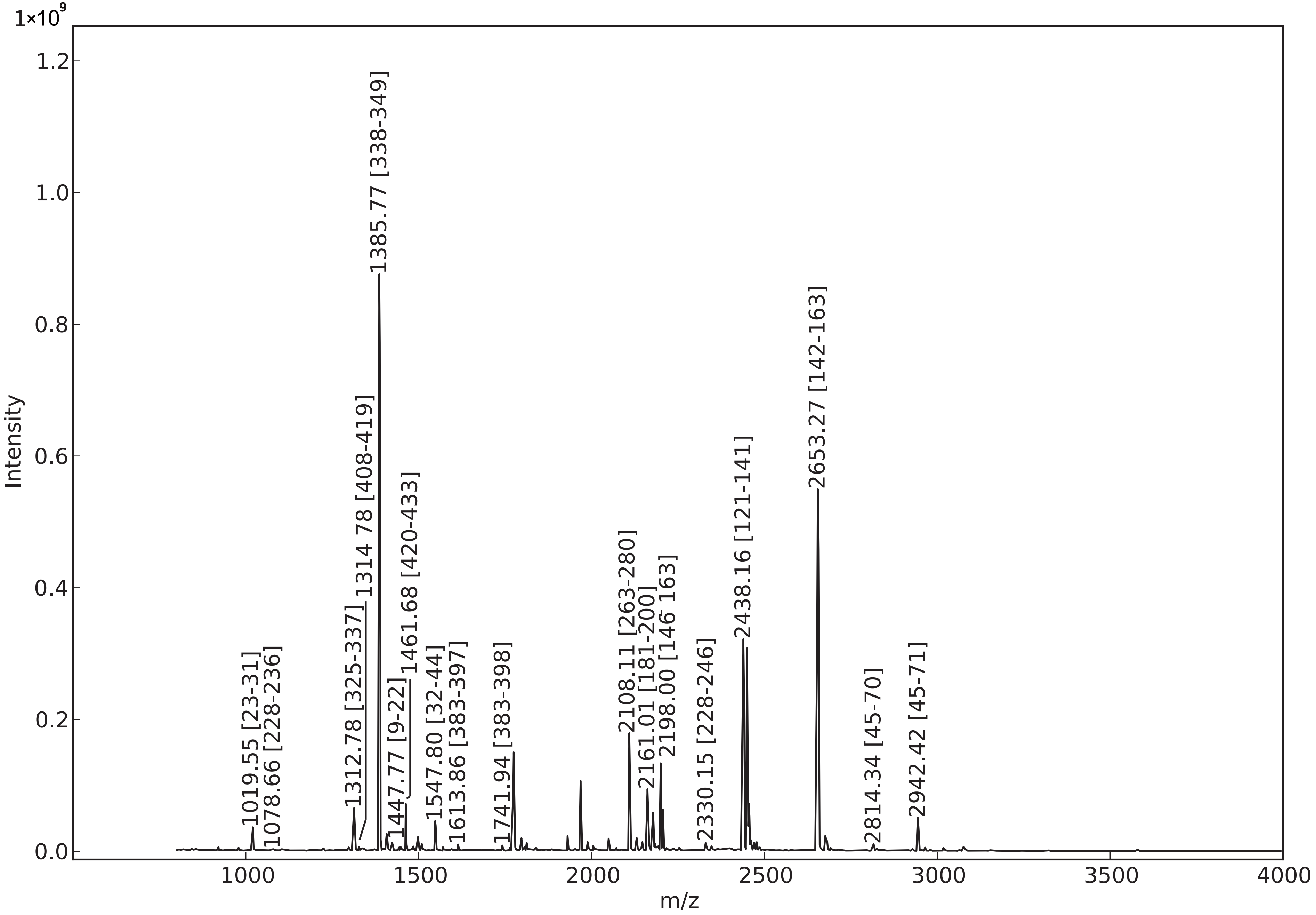
Spot No. 76


1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
951.53 [422-429]
1105.61 [317-327]
1459.76 [497-509]
1594.79 [367-381]
1666.86 [116-130]
2051.09 [159-178]
2469.32 [292-316]
2474.30 [238-260]

Spot No. 77


1×10⁹
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
843.46 [414-421]
955.57 [456-463]
1133.63 [491-499]
1163.65 [390-398]
1177.59 [285-294]
1310.79 [72-83]
1342.71 [167-178]
1354.7520 [214-225]
1370.7610 [214-225]
1382.5930 [349-359]
1393.76 [422-434]
1398.60 [349-359]
1414.60 [349-359]
1635.90 [305-319]
1641.79 [253-268]
1764.01 [305-320]
1936.92 [285-300]
2023.08 [503-520]
2183.13 [192-213]
2372.14 [435-455]
2581.33 [360-381]
2655.32 [87-110]
2671.37 [87-110]
2732.27 [141-163]
2911.64 [320-348]
3160.73 [111-140]

Spot No. 78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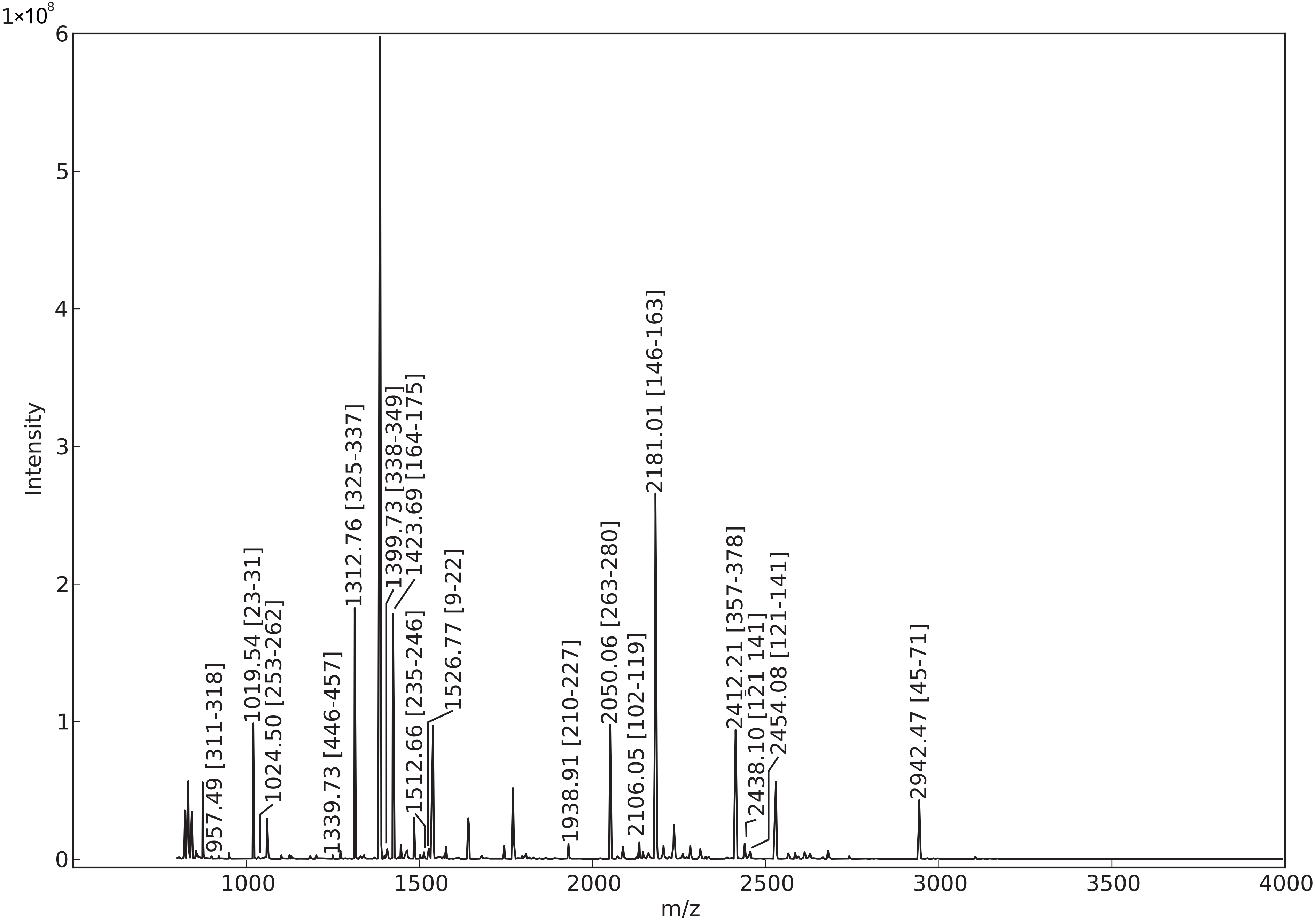
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1019.55 [23-31]
1078.66 [228-236]
1312.78 [325-337]
1314 78 [408-419]
1385.77 [338-349]
1447.77 [9-22]
1461.68 [420-433]
1547.80 [32-44]
1613.86 [383-397]
1741.94 [383-398]
2108.11 [263-280]
2161.01 [181-200]
2198.00 [146 163]
2330.15 [228-246]
2438.16 [121-141]
2653.27 [142-163]
2814.34 [45-70]
2942.42 [45-71]

Spot No. 79


1×10^8
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Intensity
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3000
3500
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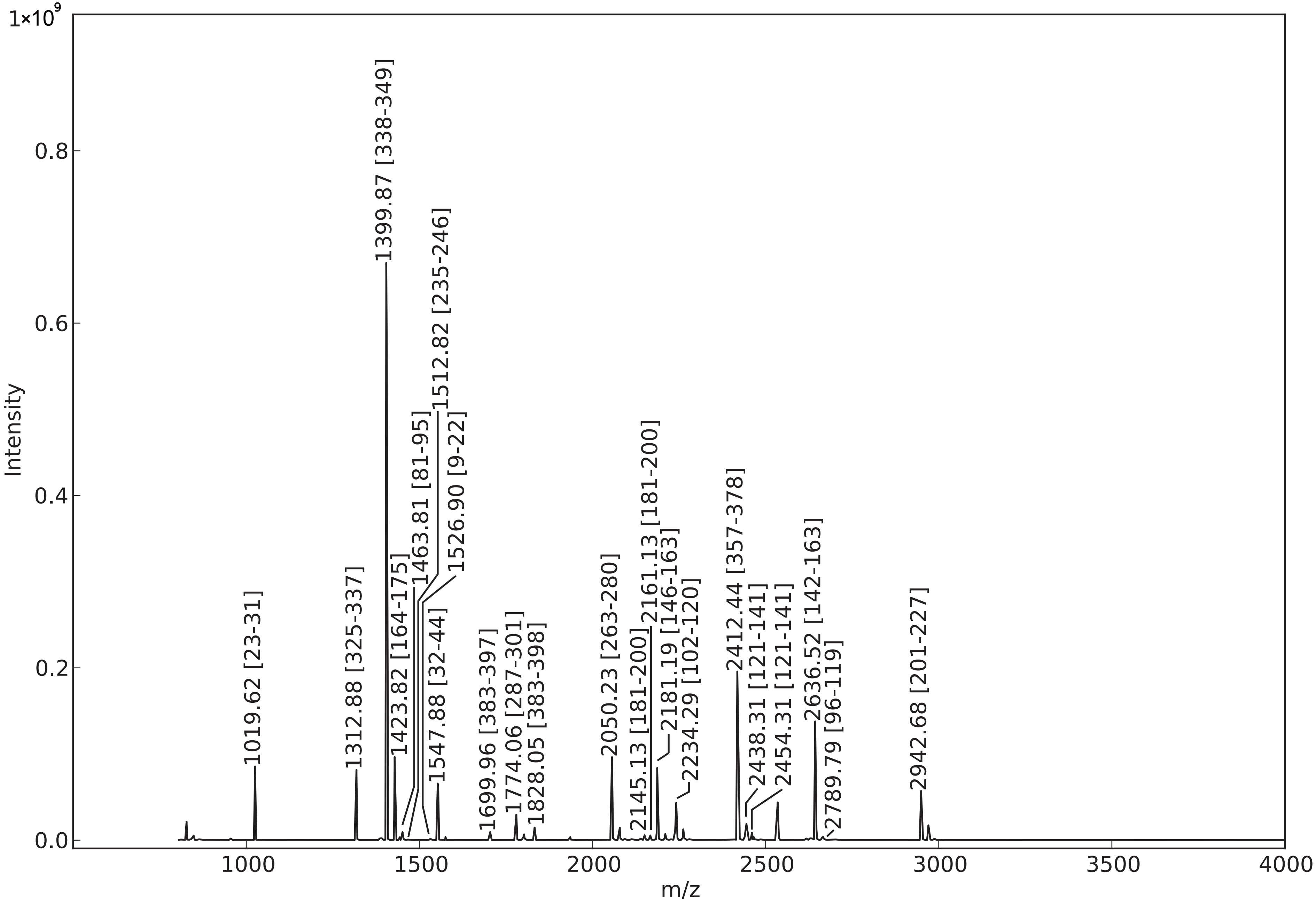
m/z
957.49 [311-318]
1019.54 [23-31]
1024.50 [253-262]
1339.73 [446-457]
1312.76 [325-337]
1399.73 [338-349]
1423.69 [164-175]
1512.66 [235-246]
1526.77 [9-22]
1938.91 [210-227]
2050.06 [263-280]
2106.05 [102-119]
2181.01 [146-163]
2412.21 [357-378]
2438.10 [121-141]
2454.08 [121-141]
2942.47 [45-71]

Spot No. 80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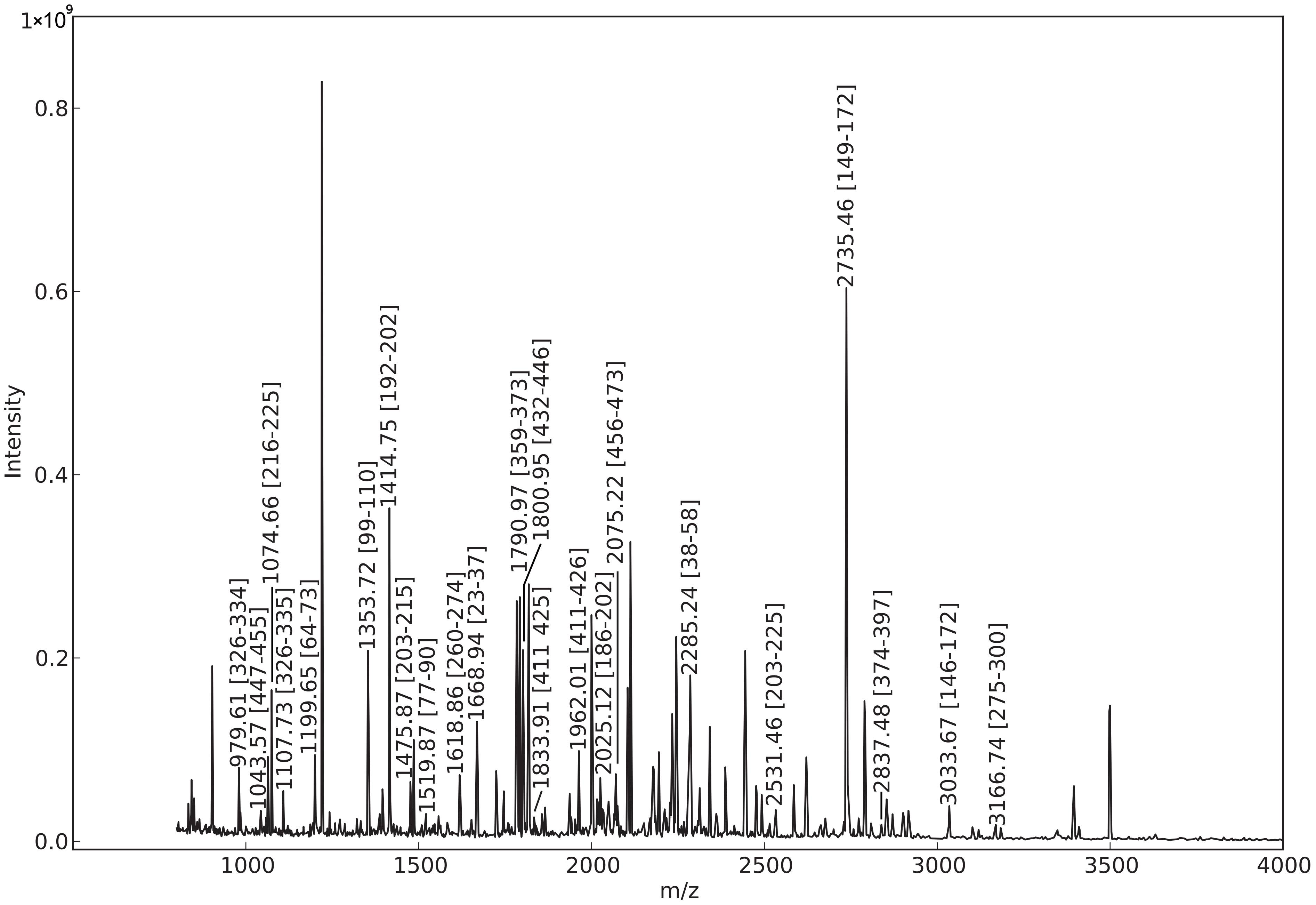
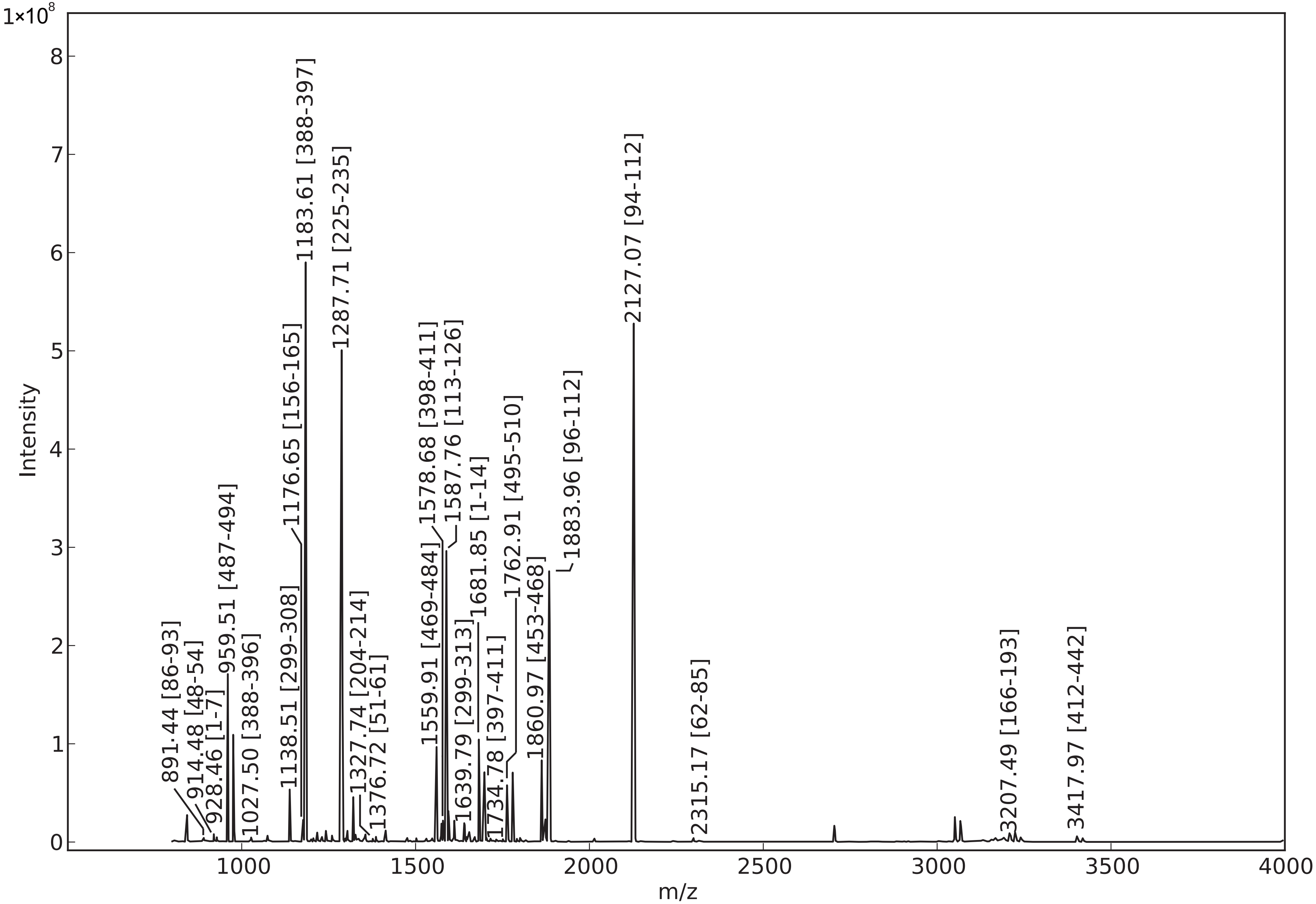
2500
3000
3500
4000
m/z
1019.62 [23-31]
1312.88 [325-337]
1399.87 [338-349]
1423.82 [164-175]
1463.81 [81-95]
1512.82 [235-246]
1526.90 [9-22]
1547.88 [32-44]
1699.96 [383-397]
1774.06 [287-301]
1828.05 [383-398]
2050.23 [263-280]
2145.13 [181-200]
2161.13 [181-200]
2181.19 [146-163]
2234.29 [102-120]
2412.44 [357-378]
2438.31 [121-141]
2454.31 [121-141]
2636.52 [142-163]
2789.79 [96-119]
2942.68 [201-227]

Spot No. 81



1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
979.61 [326-334]
1043.57 [447-455]
1074.66 [216-225]
1107.73 [326-335]
1199.65 [64-73]
1353.72 [99-110]
1414.75 [192-202]
1475.87 [203-215]
1519.87 [77-90]
1618.86 [260-274]
1668.94 [23-37]
1790.97 [359-373]
1800.95 [432-446]
1833.91 [411 425]
1962.01 [411-426]
2025.12 [186-202]
2075.22 [456-473]
2285.24 [38-58]
2531.46 [203-225]
2735.46 [149-172]
2837.48 [374-397]
3033.67 [146-172]
3166.74 [275-300]

Spot No. 82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7
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1
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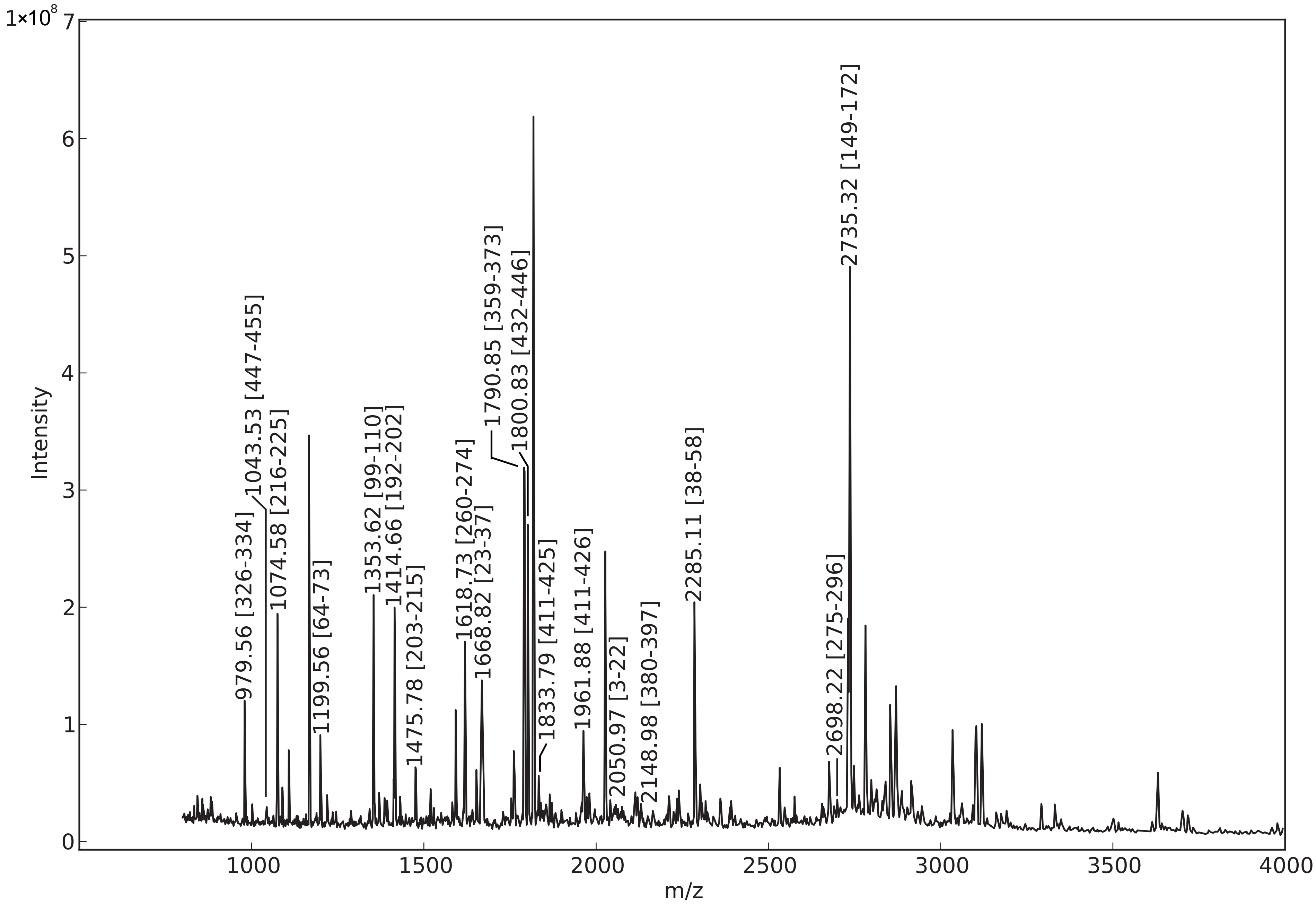
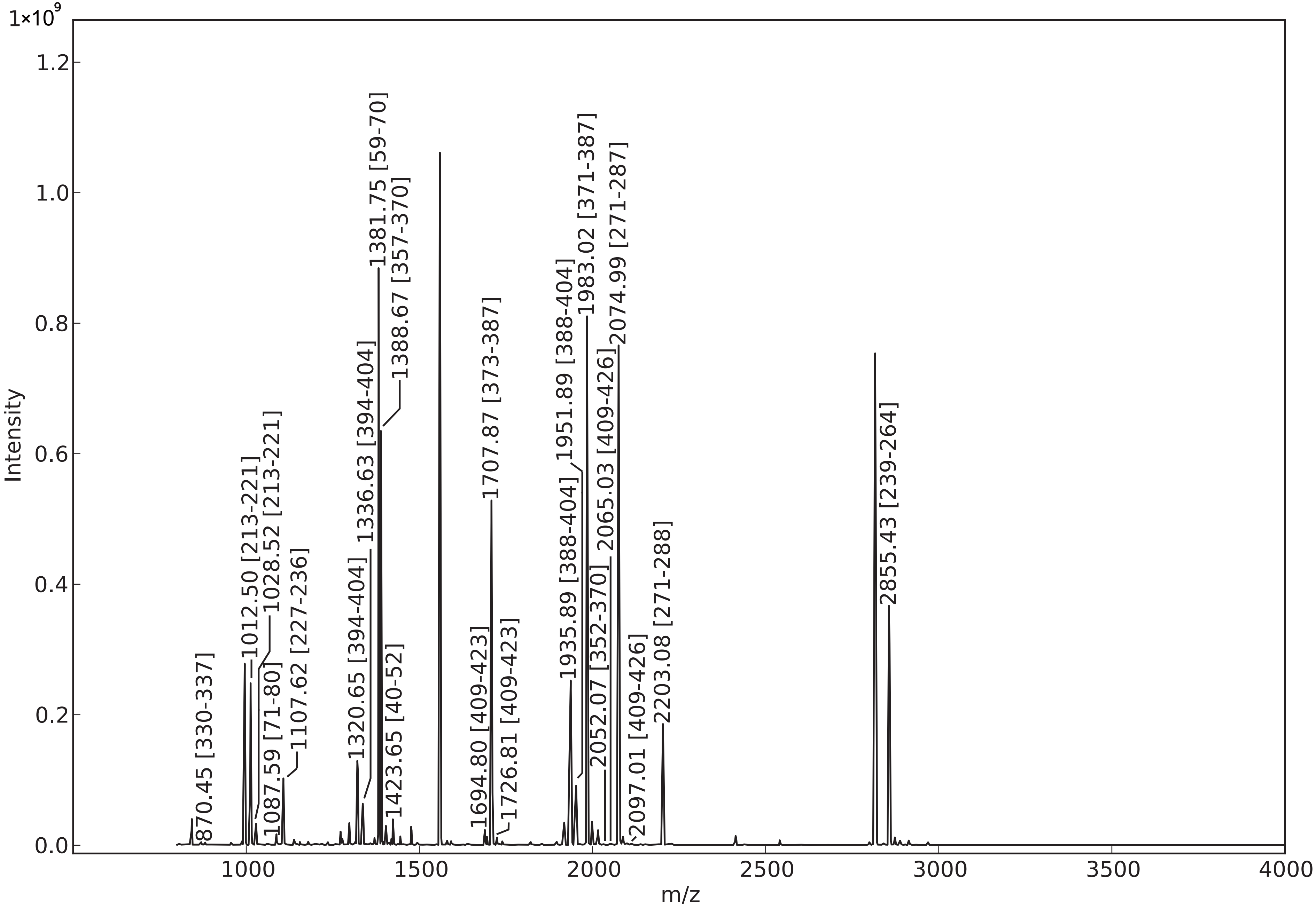
2000
2500
3000
3500
4000
m/z
891.44 [86-93]
914.48 [48-54]
928.46 [1-7]
959.51 [487-494]
1027.50 [388-396]
1138.51 [299-308]
1176.65 [156-165]
1183.61 [388-397]
1287.71 [225-235]
1327.74 [204-214]
1376.72 [51-61]
1559.91 [469-484]
1578.68 [398-411]
1587.76 [113-126]
1639.79 [299-313]
1681.85 [1-14]
1734.78 [397-411]
1762.91 [495-510]
1860.97 [453-468]
1883.96 [96-112]
2127.07 [94-112]
2315.17 [62-85]
3207.49 [166-193]
3417.97 [412-442]

Spot No. 83


1×10^8
7
6
5
4
3
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
979.56 [326-334]
1043.53 [447-455]
1074.58 [216-225]
1199.56 [64-73]
1353.62 [99-110]
1414.66 [192-202]
1475.78 [203-215]
1618.73 [260-274]
1668.82 [23-37]
1790.85 [359-373]
1800.83 [432-446]
1833.79 [411-425]
1961.88 [411-426]
2050.97 [3-22]
2148.98 [380-397]
2285.11 [38-58]
2698.22 [275-296]
2735.32 [149-172]

Spot No. 84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Intensity
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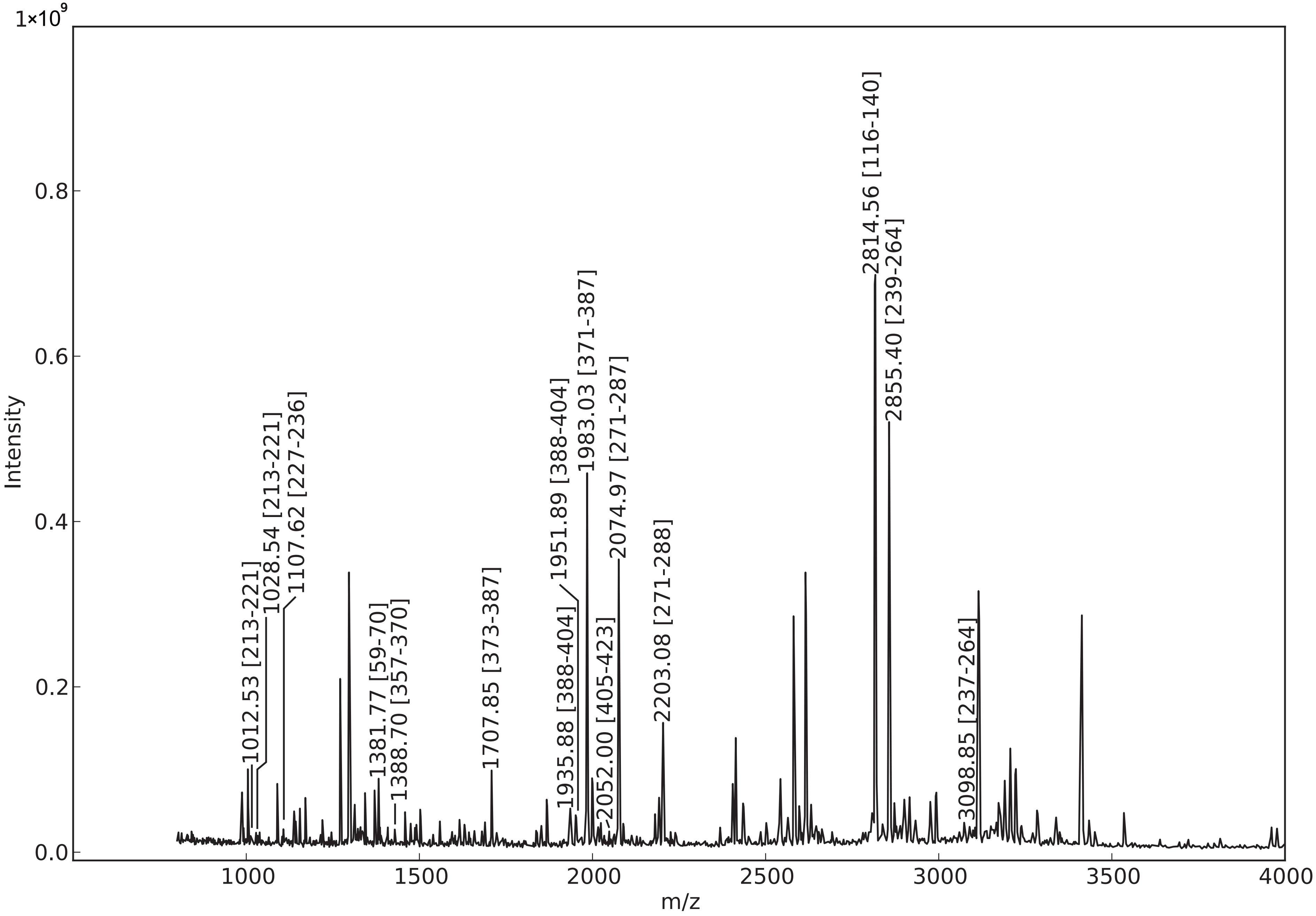
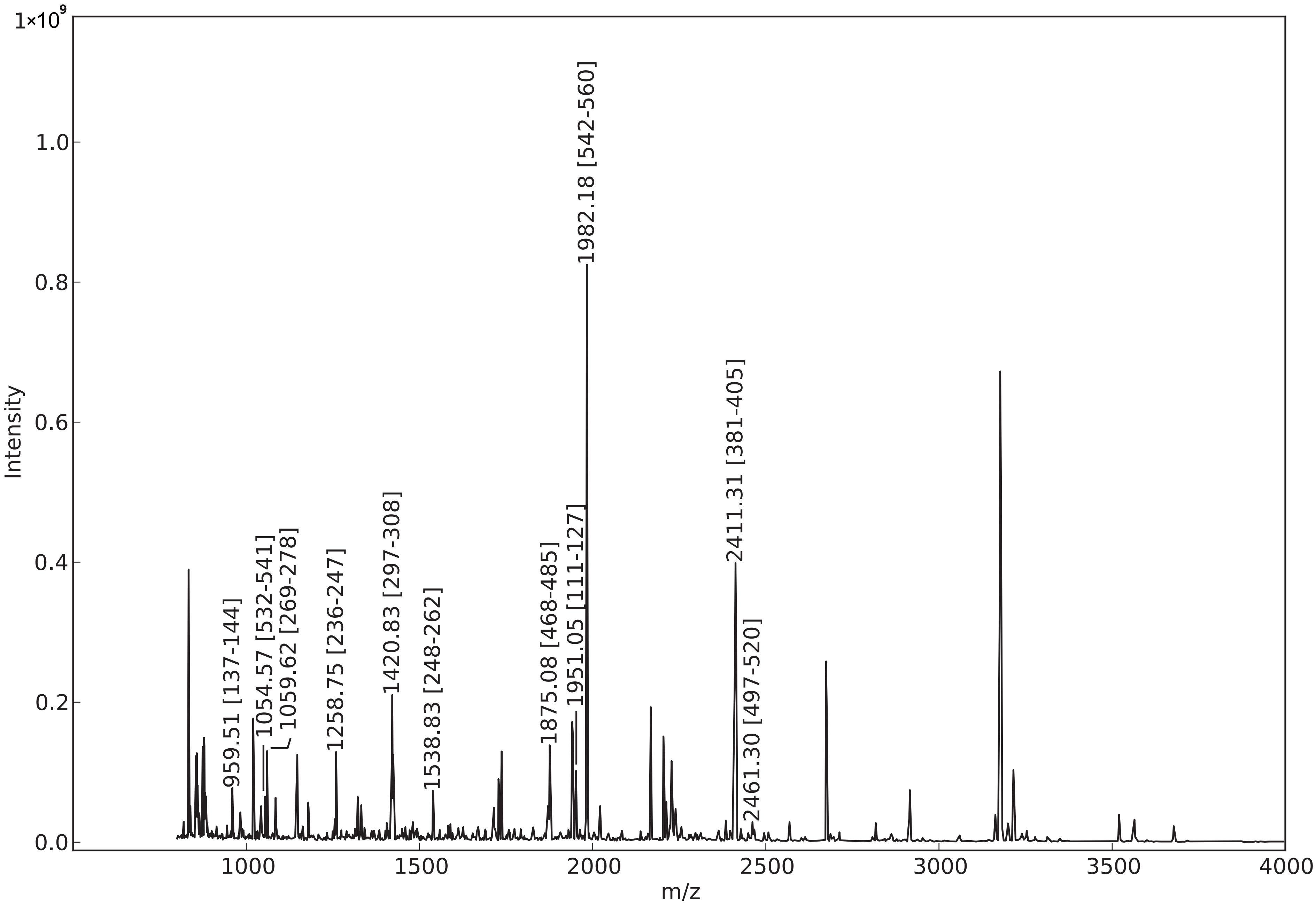
0.6
0.4
0.2
0.0
1000
1500
2000
2500
3000
3500
4000
m/z
870.45 [330-337]
1012.50 [213-221]
1028.52 [213-221]
1087.59 [71-80]
1107.62 [227-236]
1320.65 [394-404]
1336.63 [394-404]
1381.75 [59-70]
1388.67 [357-370]
1423.65 [40-52]
1694.80 [409-423]
1707.87 [373-387]
1726.81 [409-423]
1935.89 [388-404]
1951.89 [388-404]
1983.02 [371-387]
2052.07 [352-370]
2065.03 [409-426]
2074.99 [271-287]
2097.01 [409-426]
2203.08 [271-288]
2855.43 [239-264]

Spot No. 85

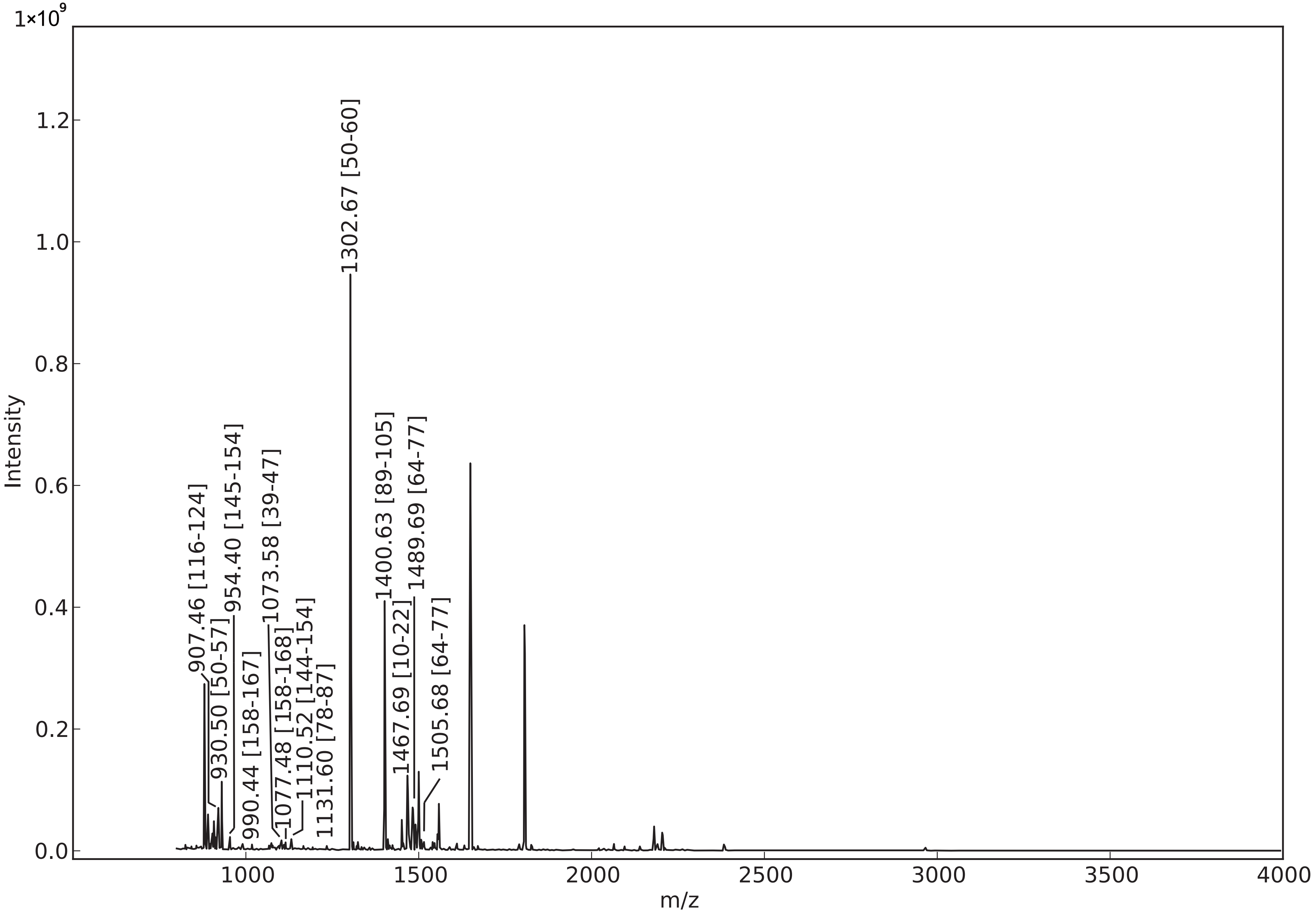

1×10⁹
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1012.53 [213-221]
1028.54 [213-221]
1107.62 [227-236]
1381.77 [59-70]
1388.70 [357-370]
1707.85 [373-387]
1935.88 [388-404]
1951.89 [388-404]
1983.03 [371-387]
2052.00 [405-423]
2074.97 [271-287]
2203.08 [271-288]
2814.56 [116-140]
2855.40 [239-264]
3098.85 [237-264]

Spot No. 86



1×10⁹
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
959.51 [137-144]
1054.57 [532-541]
1059.62 [269-278]
1258.75 [236-247]
1420.83 [297-308]
1538.83 [248-262]
1875.08 [468-485]
1951.05 [111-127]
1982.18 [542-560]
2411.31 [381-405]
2461.30 [497-520]

Spot No. 87


1×10^9
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1.0
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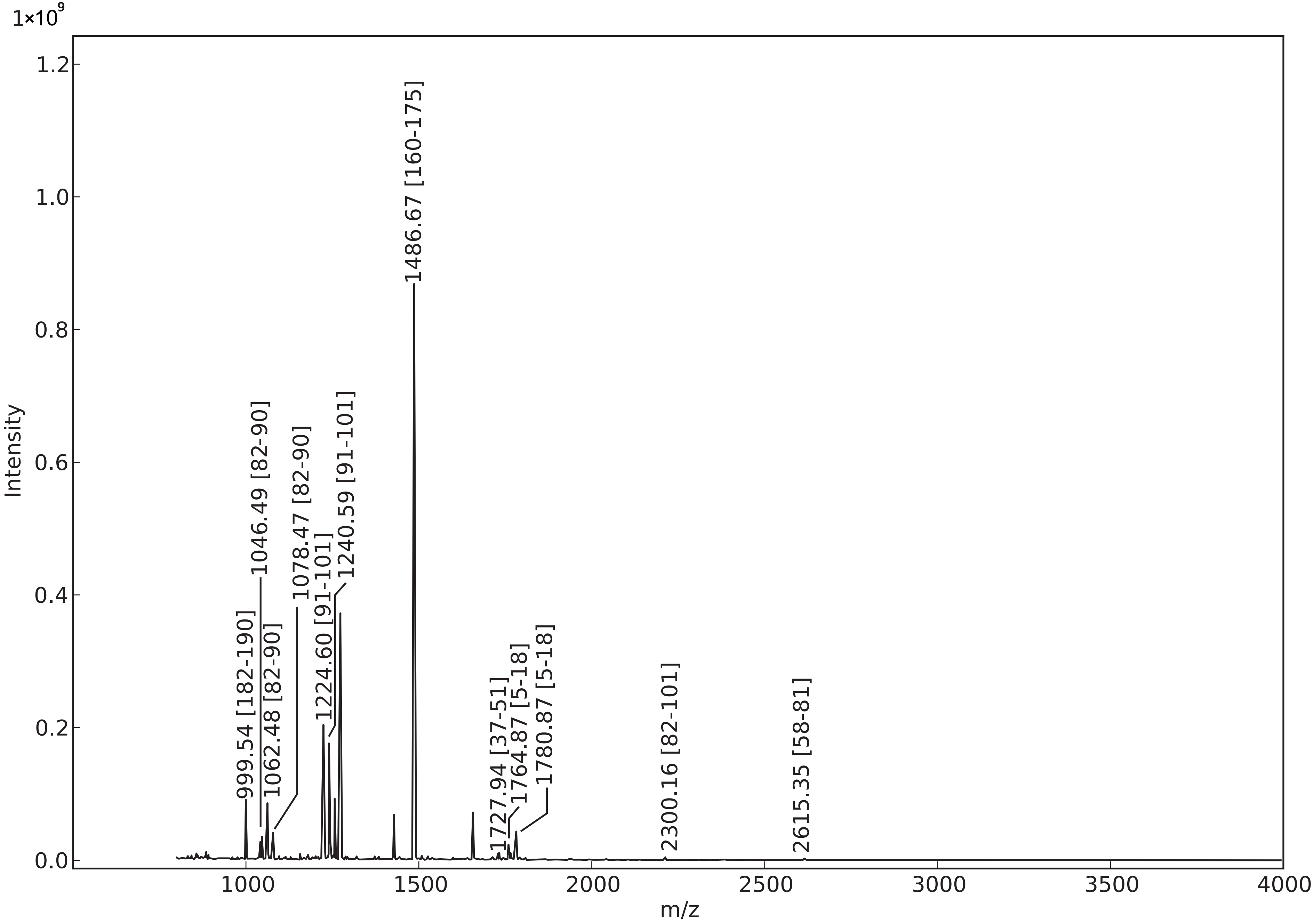
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
907.46 [116-124]
930.50 [50-57]
954.40 [145-154]
990.44 [158-167]
1073.58 [39-47]
1077.48 [158-168]
1110.52 [144-154]
1131.60 [78-87]
1302.67 [50-60]
1400.63 [89-105]
1467.69 [10-22]
1489.69 [64-77]
1505.68 [64-77]

Spot No. 88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Intensity
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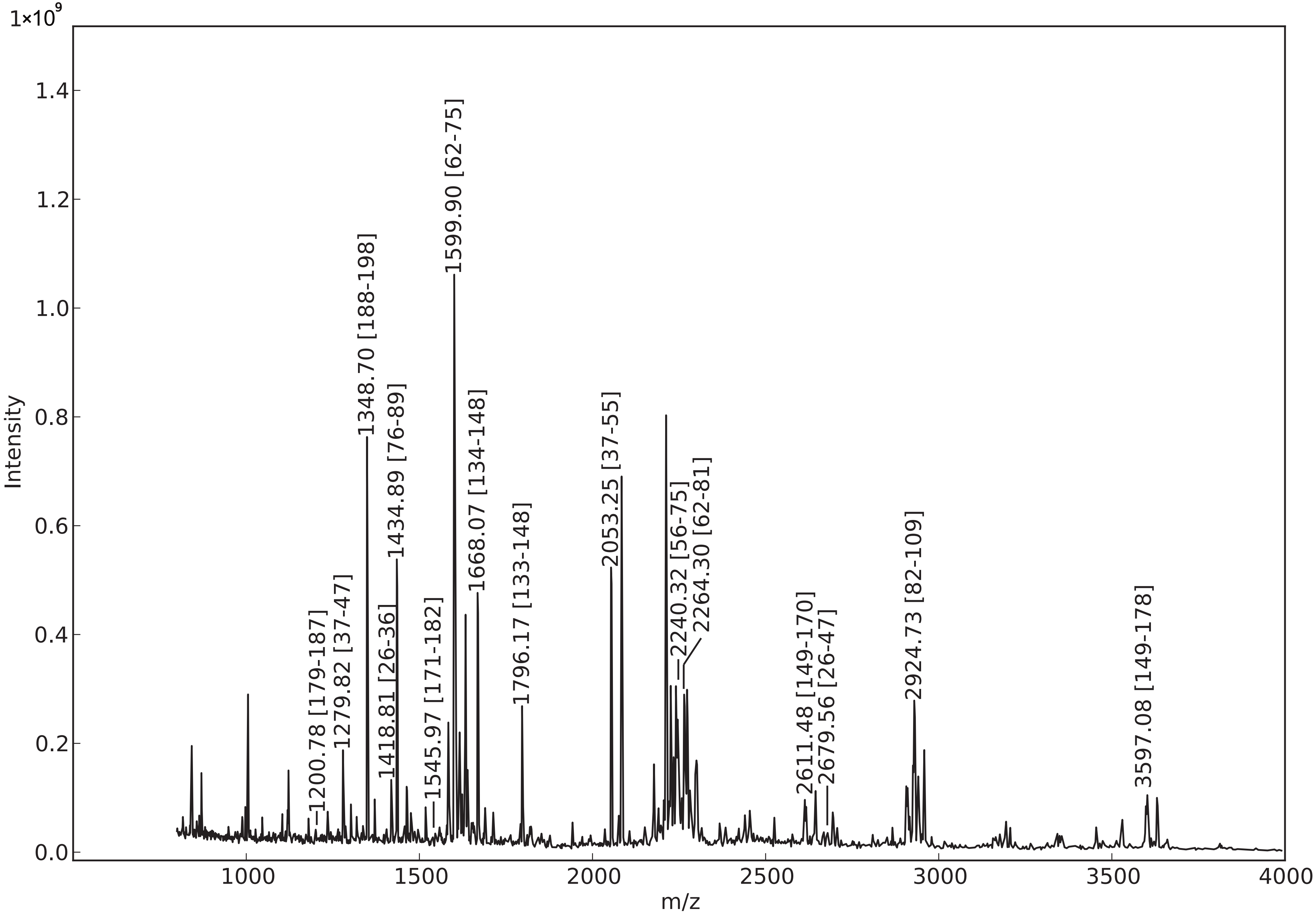
0.6
0.4
0.2
0.0
m/z
1000
1500
2000
2500
3000
3500
4000
999.54 [182-190]
1046.49 [82-90]
1062.48 [82-90]
1078.47 [82-90]
1224.60 [91-101]
1240.59 [91-101]
1486.67 [160-175]
1727.94 [37-51]
1764.87 [5-18]
1780.87 [5-18]
2300.16 [82-101]
2615.35 [58-81]

Spot No. 89


1×10^9
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1.2
1.0
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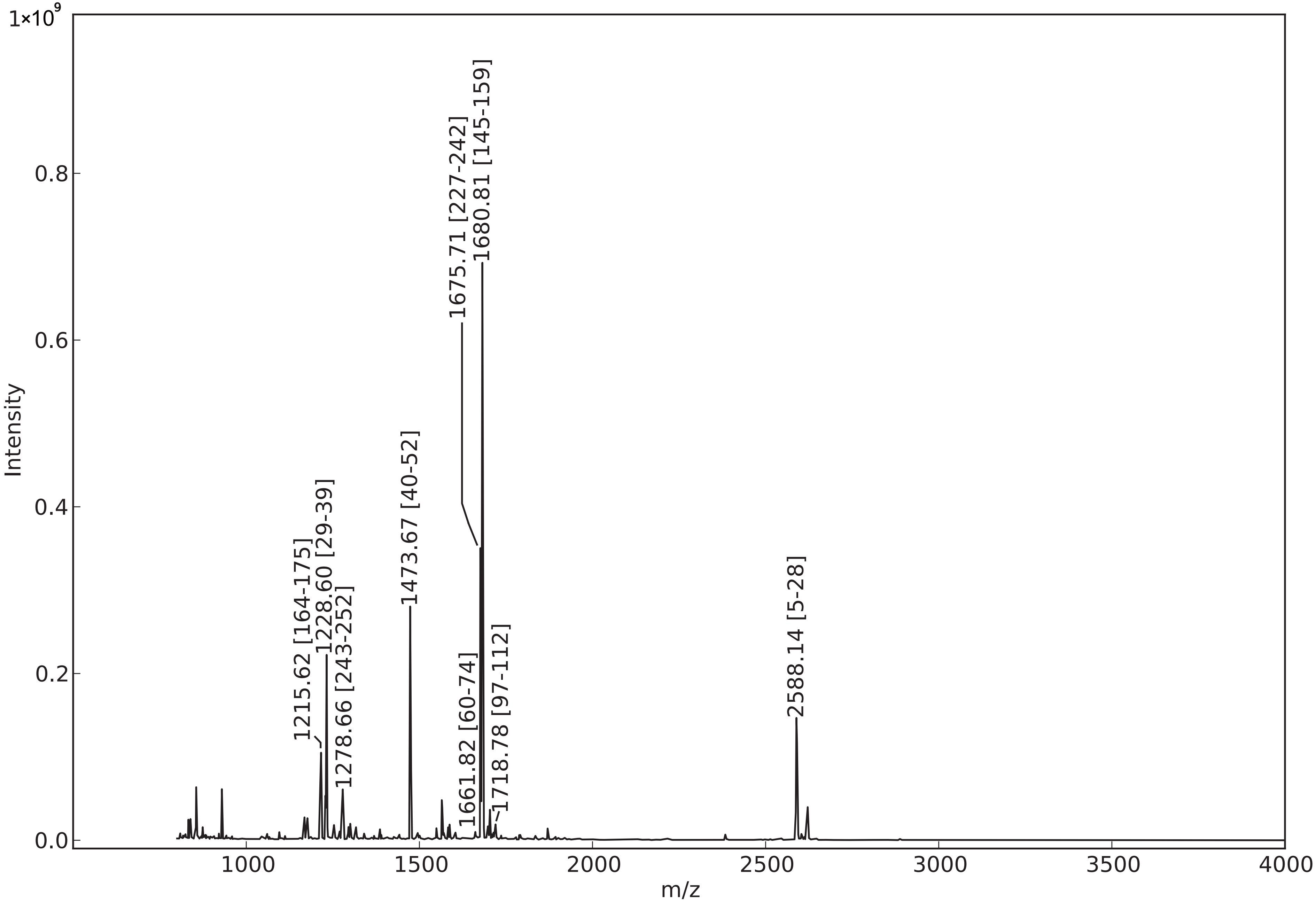
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1200.78 [179-187]
1279.82 [37-47]
1348.70 [188-198]
1418.81 [26-36]
1434.89 [76-89]
1545.97 [171-182]
1599.90 [62-75]
1668.07 [134-148]
1796.17 [133-148]
2053.25 [37-55]
2240.32 [56-75]
2264.30 [62-81]
2611.48 [149-170]
2679.56 [26-47]
2924.73 [82-109]
3597.08 [149-178]

Spot No. 90


1×10^9
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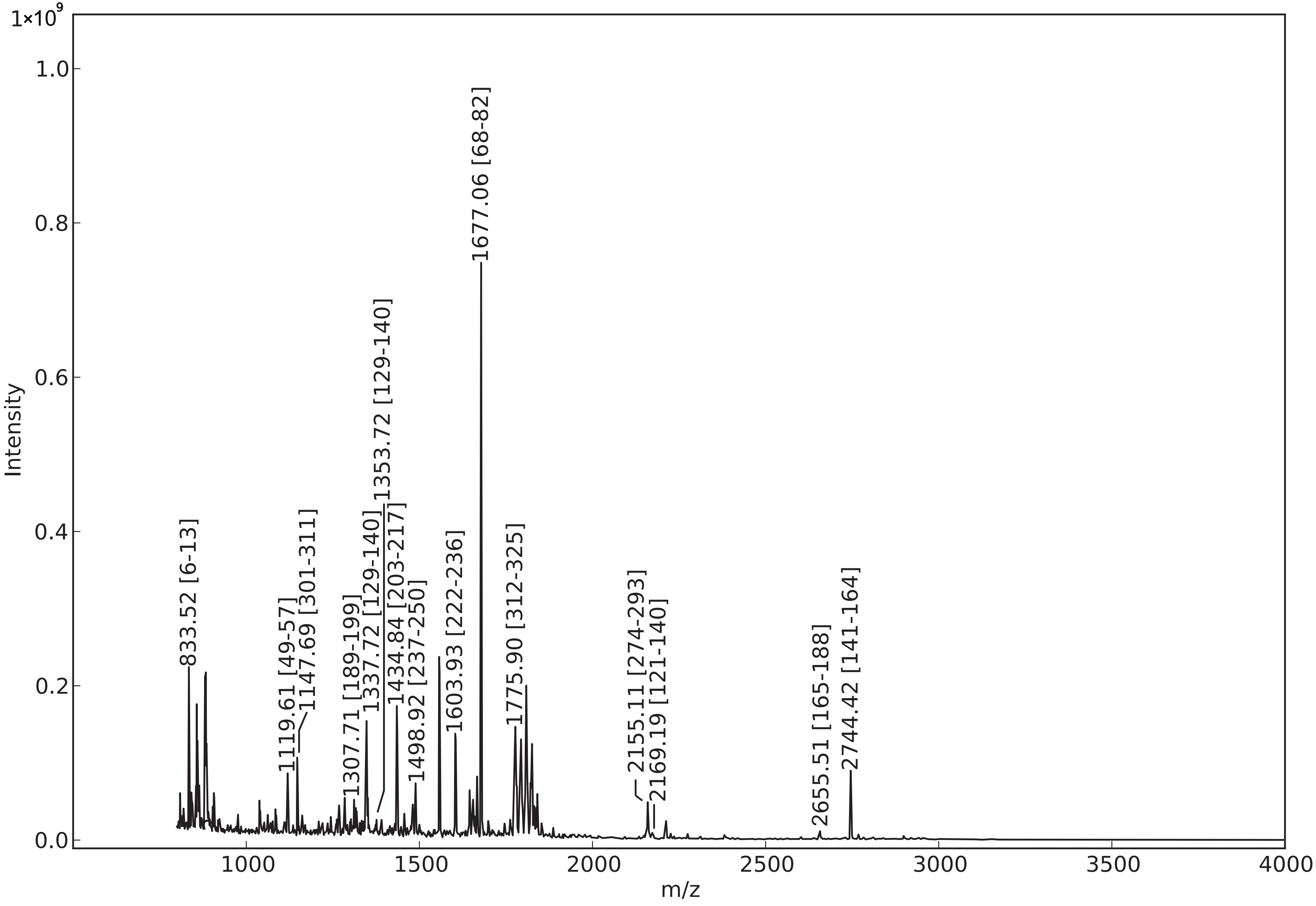
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1215.62 [164-175]
1228.60 [29-39]
1278.66 [243-252]
1473.67 [40-52]
1661.82 [60-74]
1675.71 [227-242]
1680.81 [145-159]
1718.78 [97-112]
2588.14 [5-28]

Spot No. 91


1×10⁹
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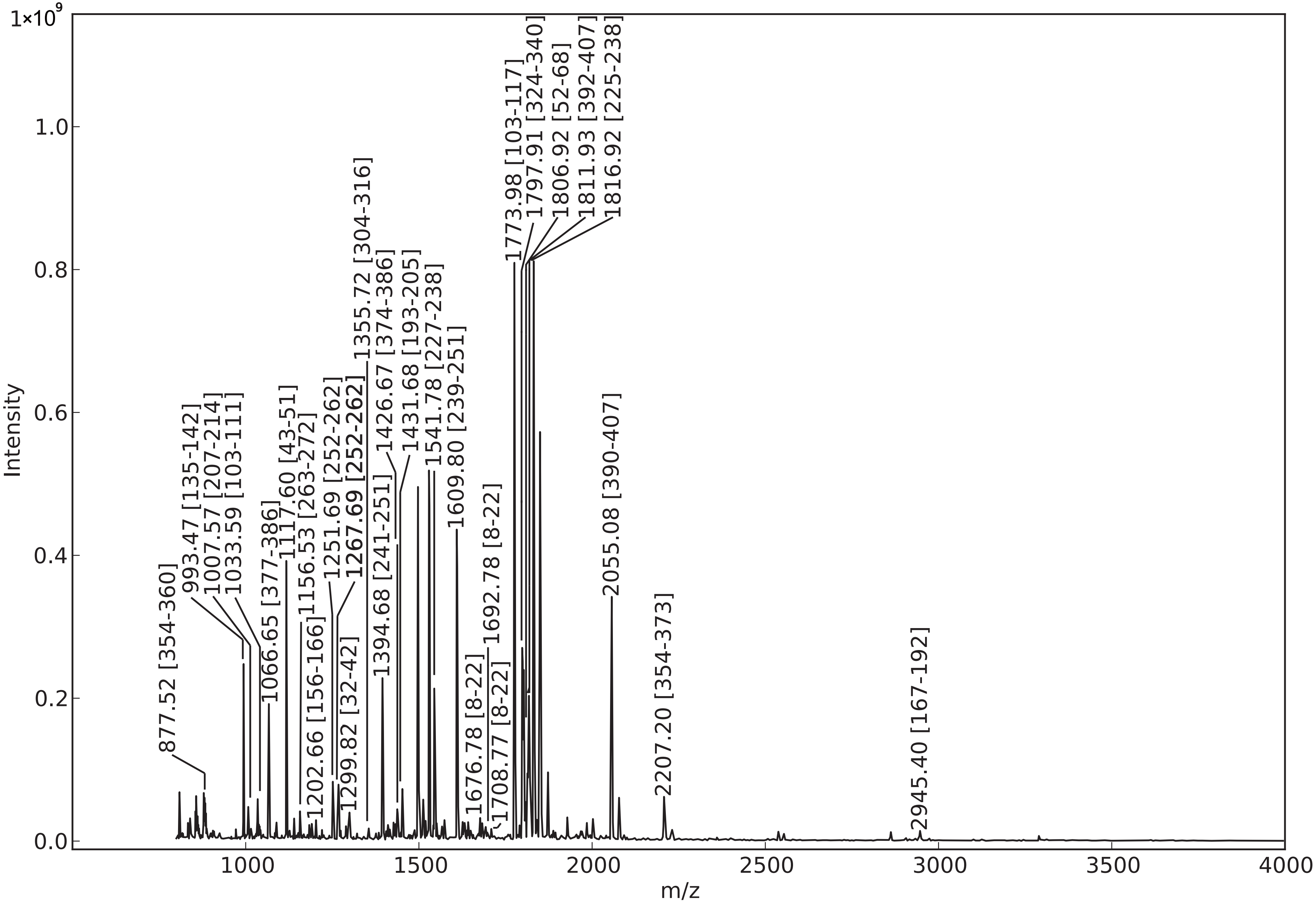
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
833.52 [6-13]
1119.61 [49-57]
1147.69 [301-311]
1307.71 [189-199]
1337.72 [129-140]
1353.72 [129-140]
1434.84 [203-217]
1498.92 [237-250]
1603.93 [222-236]
1677.06 [68-82]
1775.90 [312-325]
2155.11 [274-293]
2169.19 [121-140]
2655.51 [165-188]
2744.42 [141-164]

Spot No. 92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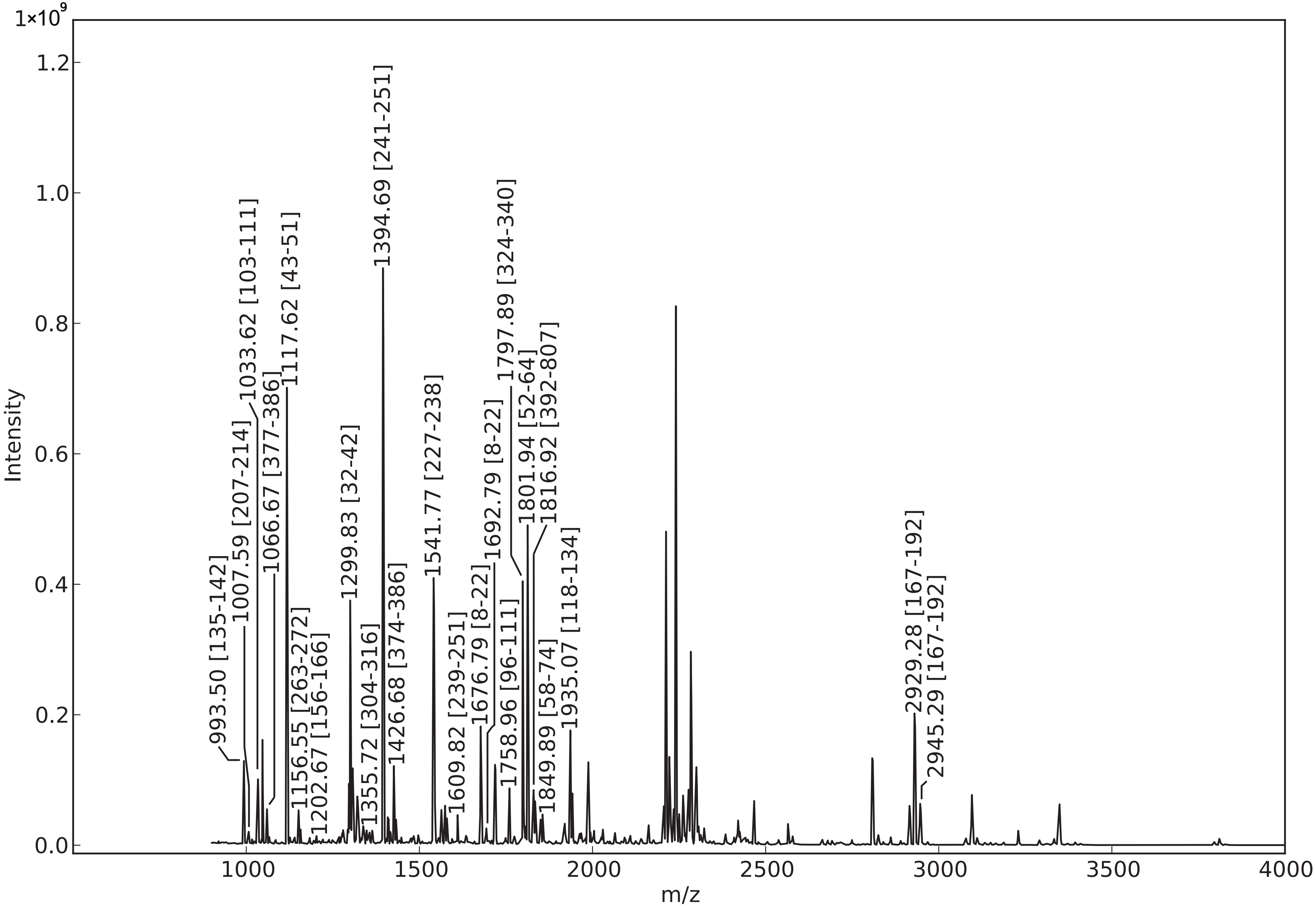
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
877.52 [354-360]
993.47 [135-142]
1007.57 [207-214]
1033.59 [103-111]
1066.65 [377-386]
1117.60 [43-51]
1156.53 [263-272]
1202.66 [156-166]
1251.69 [252-262]
1267.69 [252-262]
1299.82 [32-42]
1355.72 [304-316]
1394.68 [241-251]
1426.67 [374-386]
1431.68 [193-205]
1541.78 [227-238]
1609.80 [239-251]
1676.78 [8-22]
1692.78 [8-22]
1708.77 [8-22]
1773.98 [103-117]
1797.91 [324-340]
1806.92 [52-68]
1811.93 [392-407]
1816.92 [225-238]
2055.08 [390-407]
2207.20 [354-373]
2945.40 [167-192]

Spot No. 93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0.6
0.4
0.2
0.0
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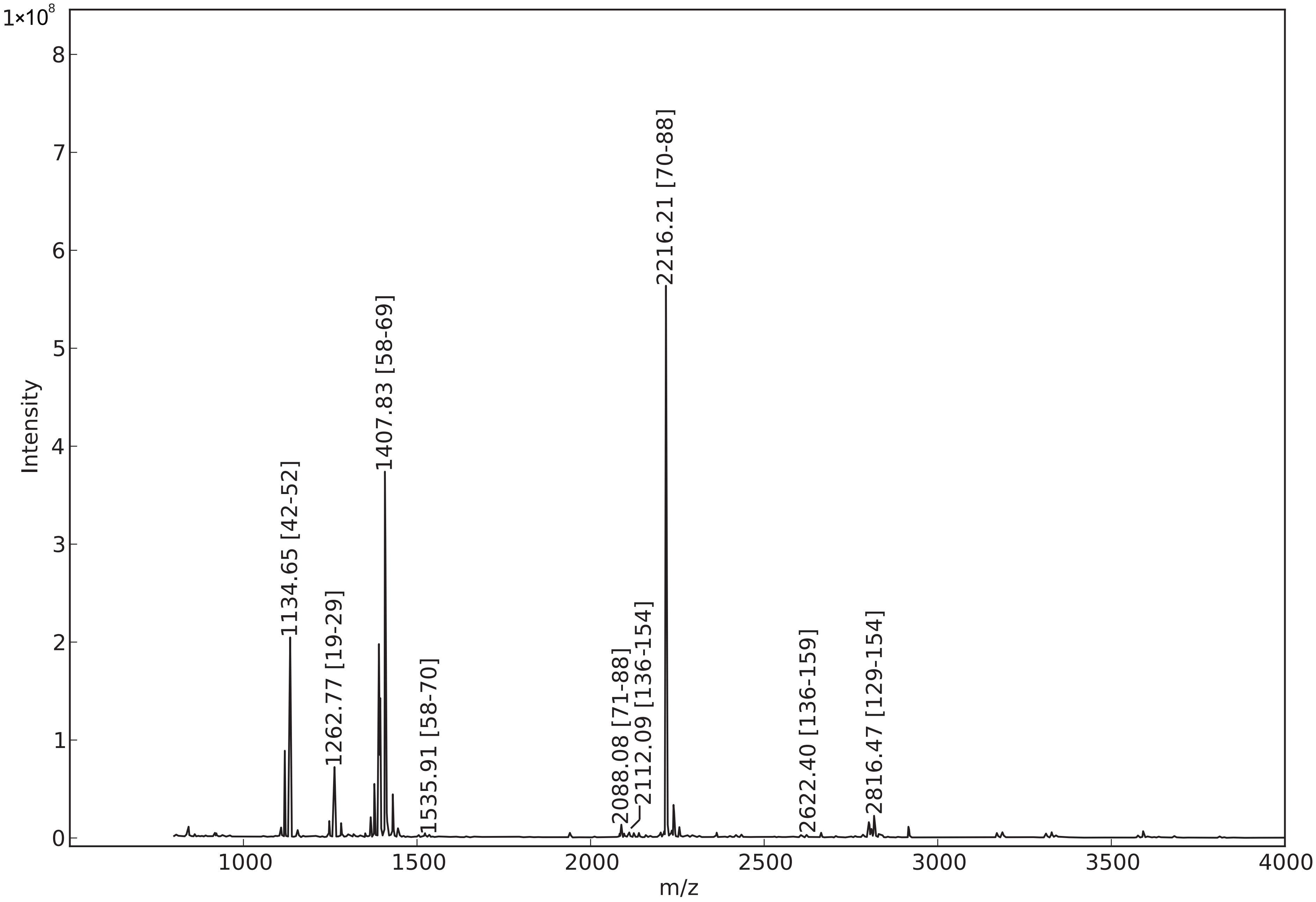
1000
1500
2000
2500
3000
3500
4000
m/z
993.50 [135-142]
1007.59 [207-214]
1033.62 [103-111]
1066.67 [377-386]
1117.62 [43-51]
1156.55 [263-272]
1202.67 [156-166]
1299.83 [32-42]
1355.72 [304-316]
1394.69 [241-251]
1426.68 [374-386]
1541.77 [227-238]
1609.82 [239-251]
1676.79 [8-22]
1692.79 [8-22]
1758.96 [96-111]
1797.89 [324-340]
1801.94 [52-64]
1816.92 [392-807]
1849.89 [58-74]
1935.07 [118-134]
2929.28 [167-192]
2945.29 [167-192]

Spot No. 94


1×10^8
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7
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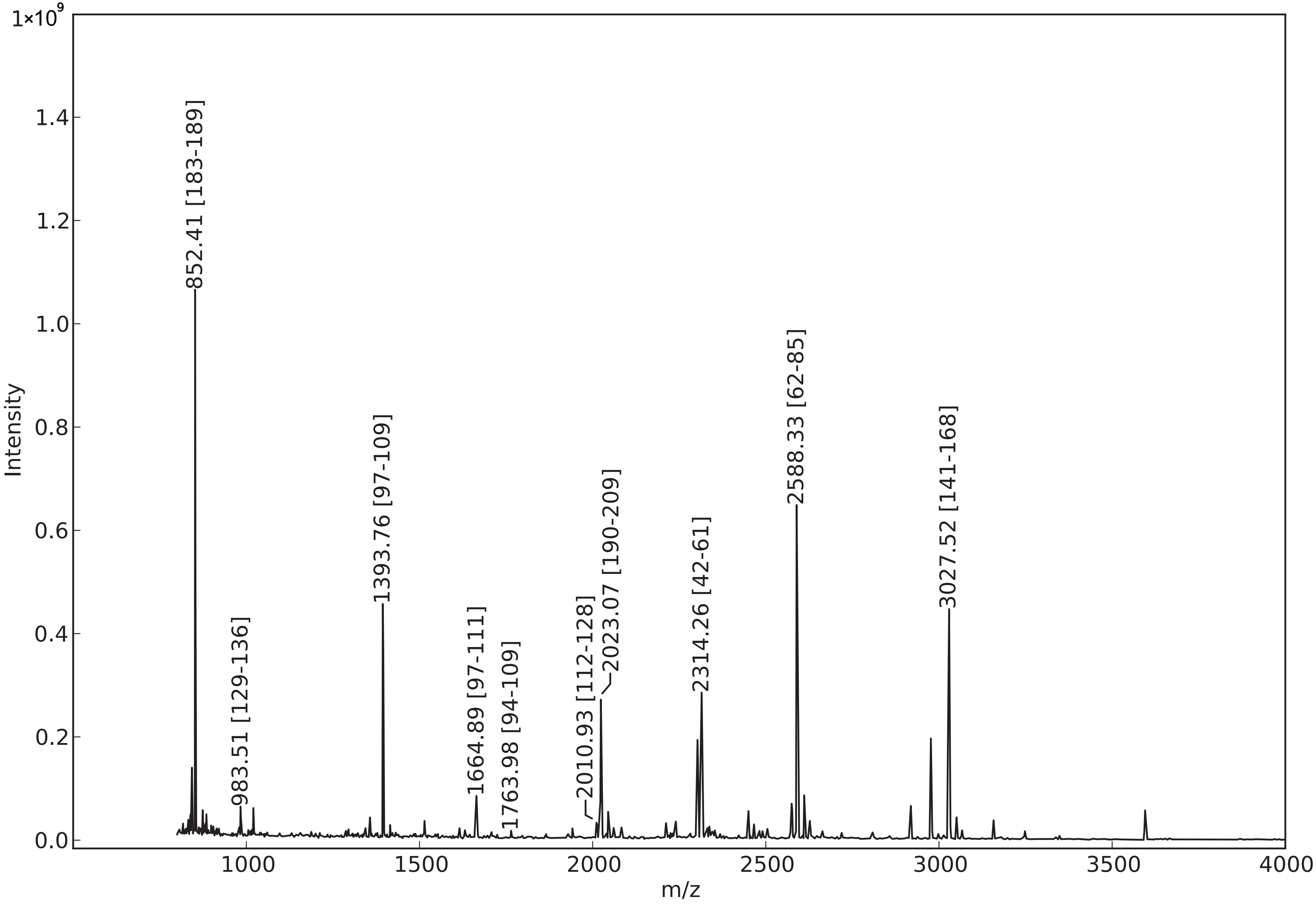
2
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1134.65 [42-52]
1262.77 [19-29]
1407.83 [58-69]
1535.91 [58-70]
2088.08 [71-88]
2112.09 [136-154]
2216.21 [70-88]
2622.40 [136-159]
2816.47 [129-154]

Spot No. 95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0.6
0.4
0.2
0.0
Intensity
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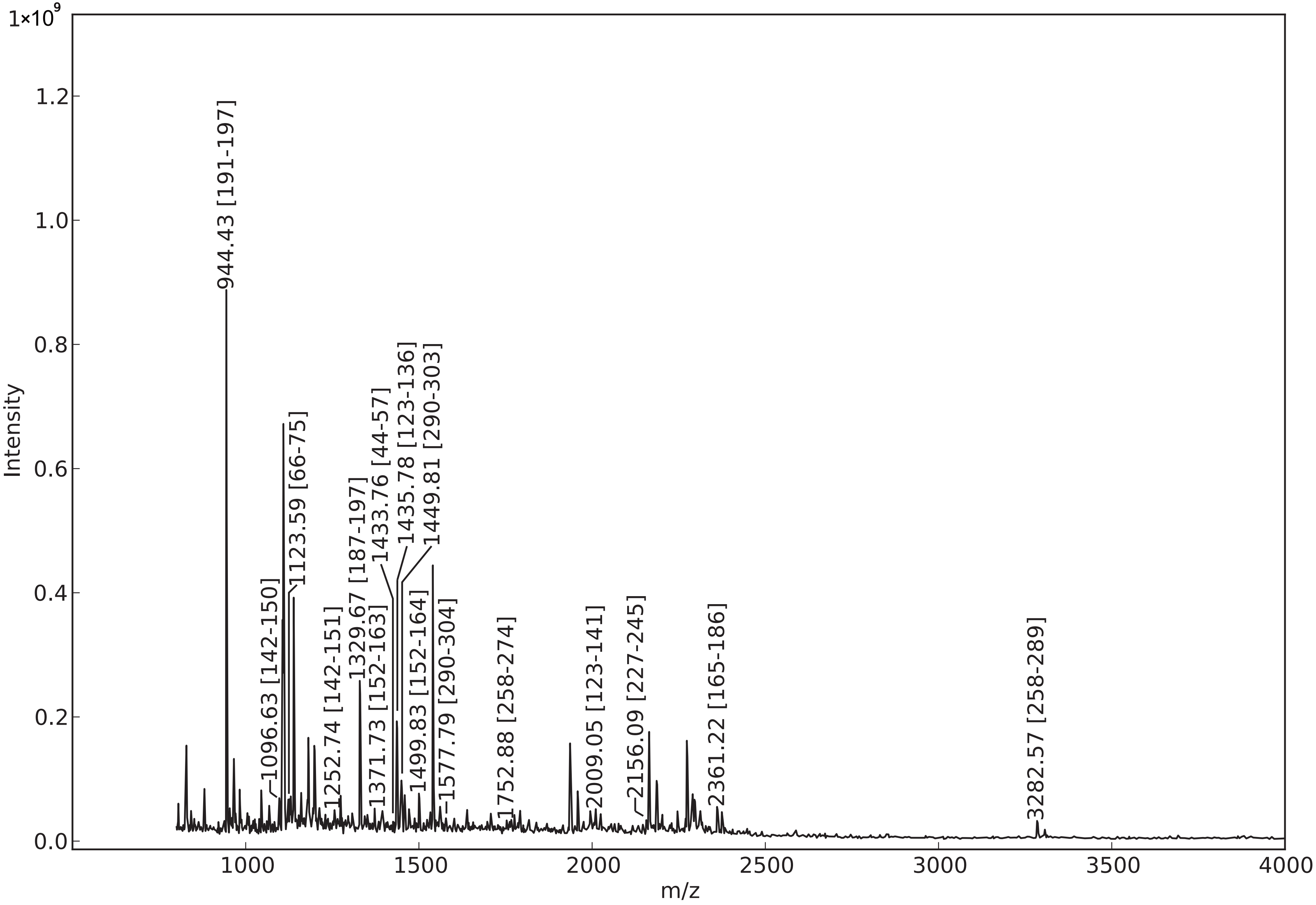
1500
2000
2500
3000
3500
4000
m/z
852.41 [183-189]
983.51 [129-136]
1393.76 [97-109]
1664.89 [97-111]
1763.98 [94-109]
2010.93 [112-128]
2023.07 [190-209]
2314.26 [42-61]
2588.33 [62-85]
3027.52 [141-168]

Spot No. 96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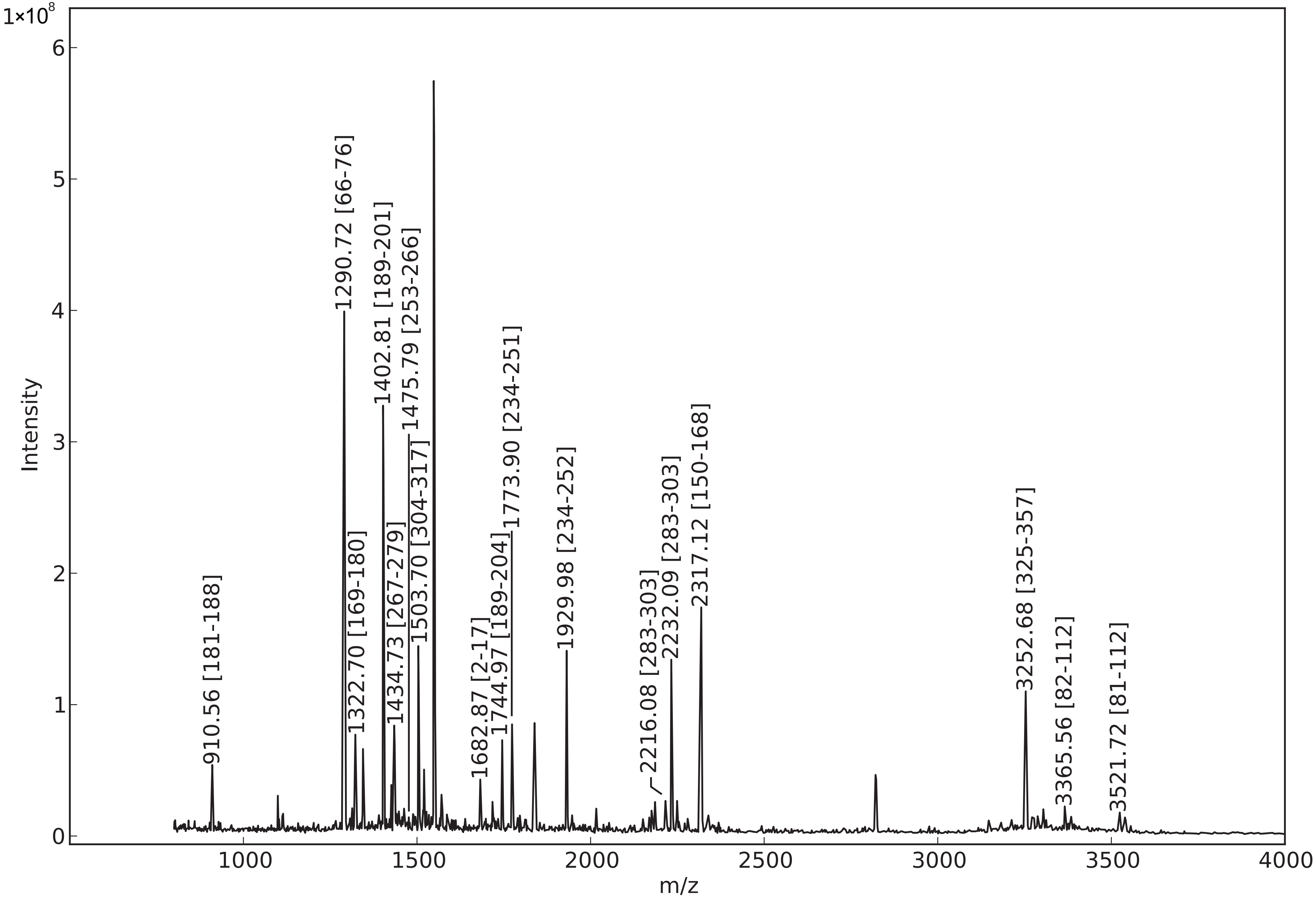
1500
2000
2500
3000
3500
4000
m/z
944.43 [191-197]
1096.63 [142-150]
1123.59 [66-75]
1252.74 [142-151]
1329.67 [187-197]
1371.73 [152-163]
1433.76 [44-57]
1435.78 [123-136]
1449.81 [290-303]
1499.83 [152-164]
1577.79 [290-304]
1752.88 [258-274]
2009.05 [123-141]
2156.09 [227-245]
2361.22 [165-186]
3282.57 [258-289]

Spot No. 97


1×10^8
6
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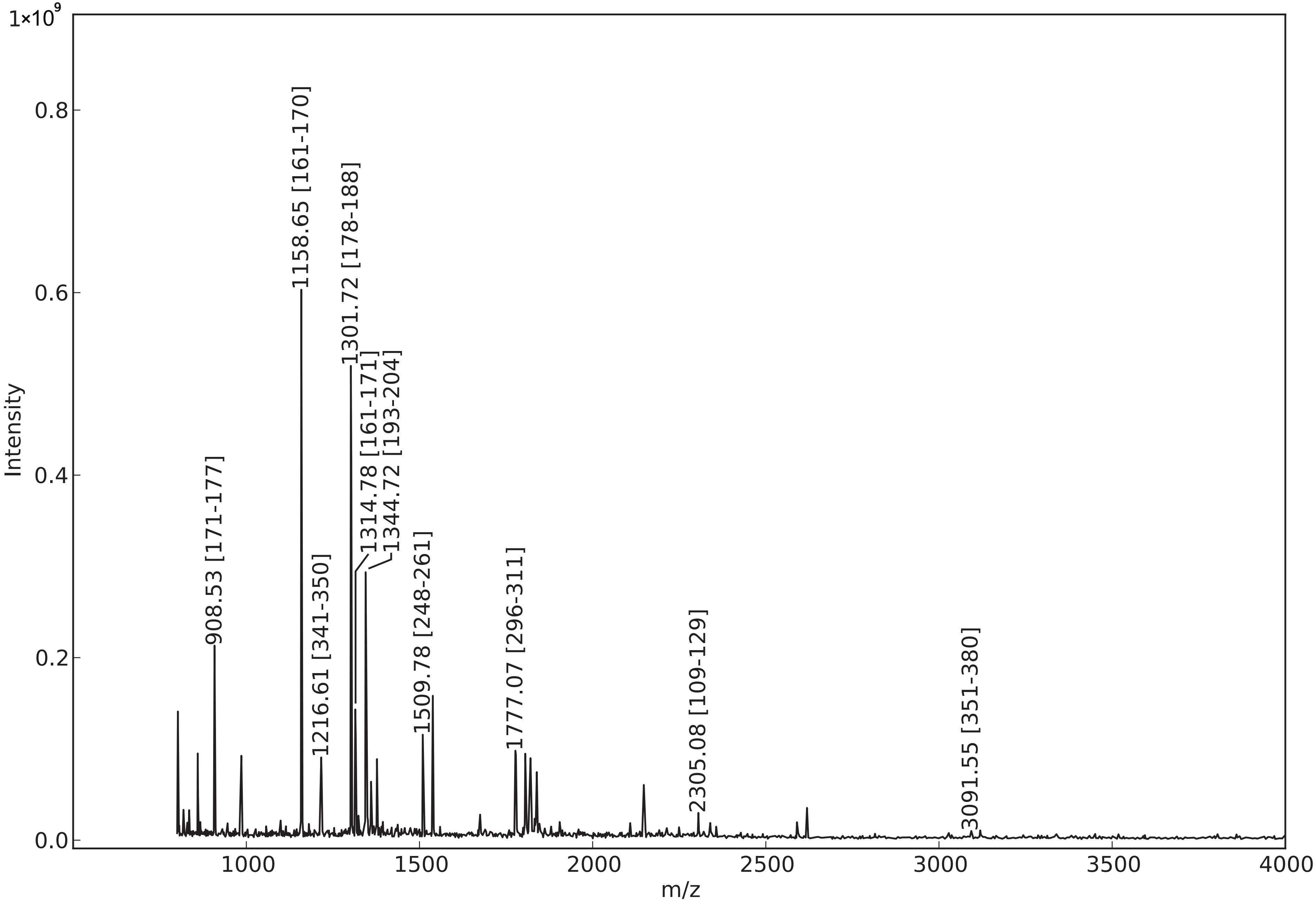
1
0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
910.56 [181-188]
1290.72 [66-76]
1322.70 [169-180]
1402.81 [189-201]
1434.73 [267-279]
1475.79 [253-266]
1503.70 [304-317]
1682.87 [2-17]
1744.97 [189-204]
1773.90 [234-251]
1929.98 [234-252]
2216.08 [283-303]
2232.09 [283-303]
2317.12 [150-168]
3252.68 [325-357]
3365.56 [82-112]
3521.72 [81-112]

Spot No. 98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0.6
0.4
0.2
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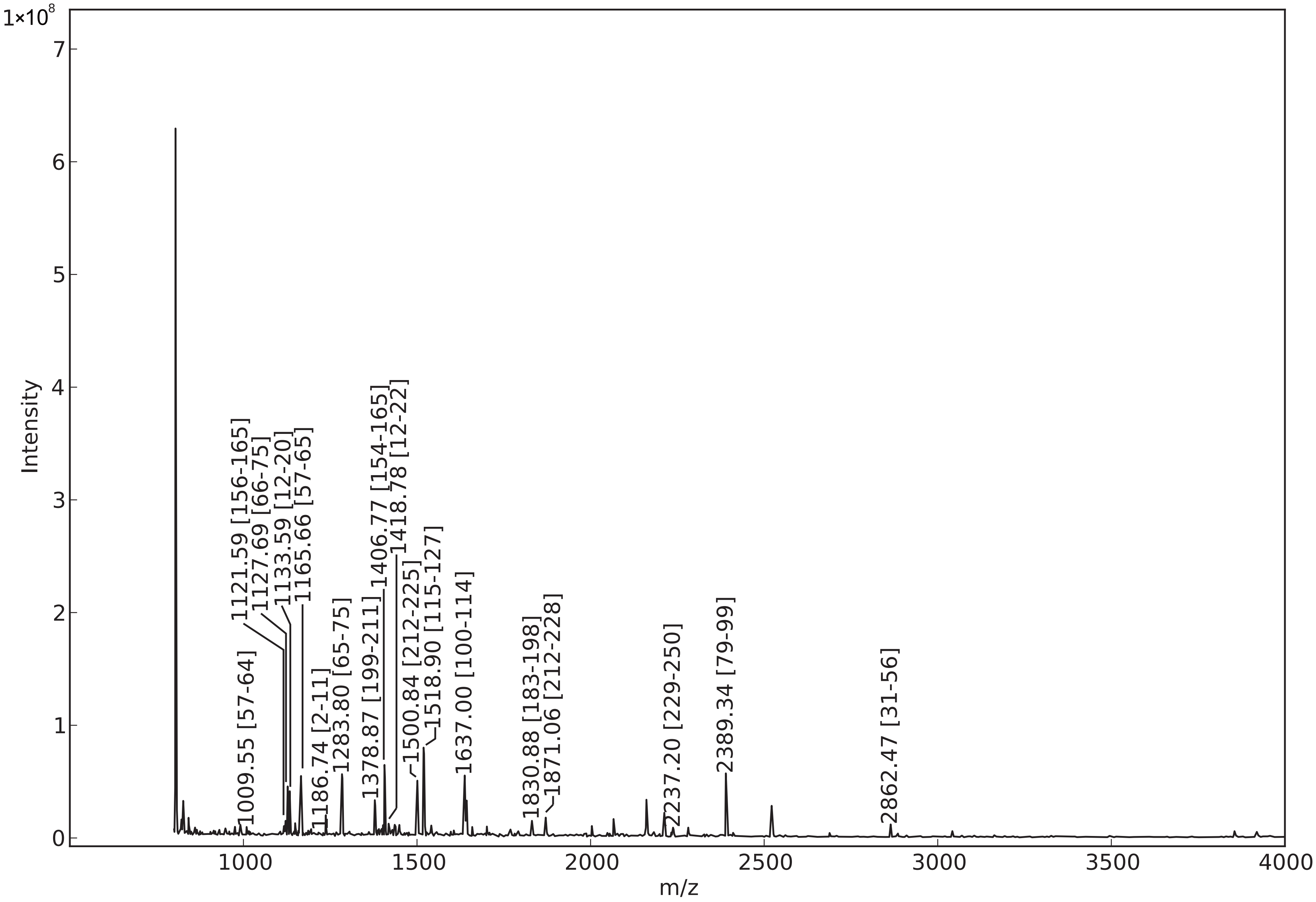
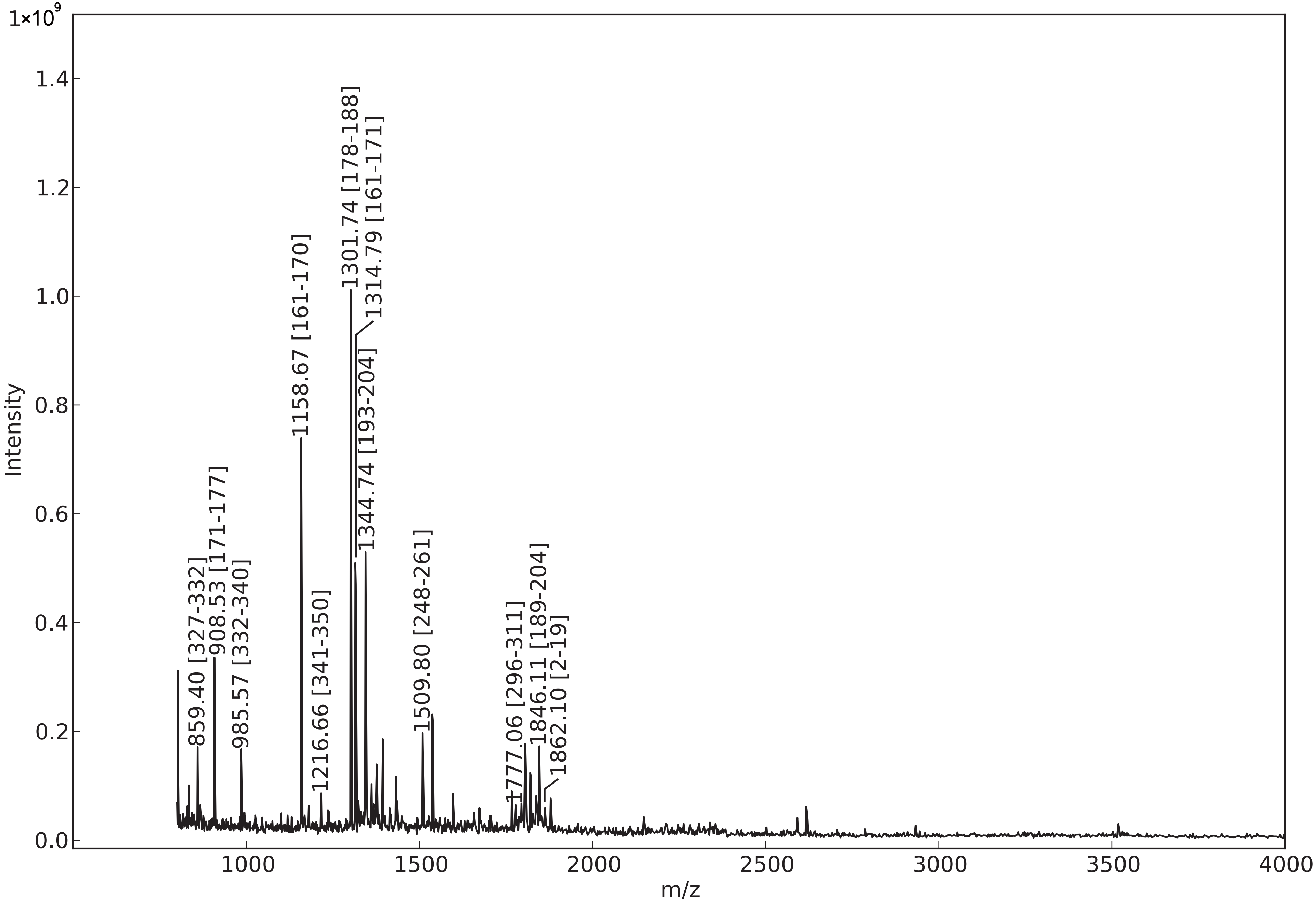
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
908.53 [171-177]
1158.65 [161-170]
1216.61 [341-350]
1301.72 [178-188]
1314.78 [161-171]
1344.72 [193-204]
1509.78 [248-261]
1777.07 [296-311]
2305.08 [109-129]
3091.55 [351-380]

Spot No. 99


1×10⁸
0
1
2
3
4
5
6
7
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1009.55 [57-64]
1121.59 [156-165]
1127.69 [66-75]
1133.59 [12-20]
1165.66 [57-65]
1186.74 [2-11]
1283.80 [65-75]
1378.87 [199-211]
1406.77 [154-165]
1418.78 [12-22]
1500.84 [212-225]
1518.90 [115-127]
1637.00 [100-114]
1830.88 [183-198]
1871.06 [212-228]
2237.20 [229-250]
2389.34 [79-99]
2862.47 [31-56]

Spot No. 100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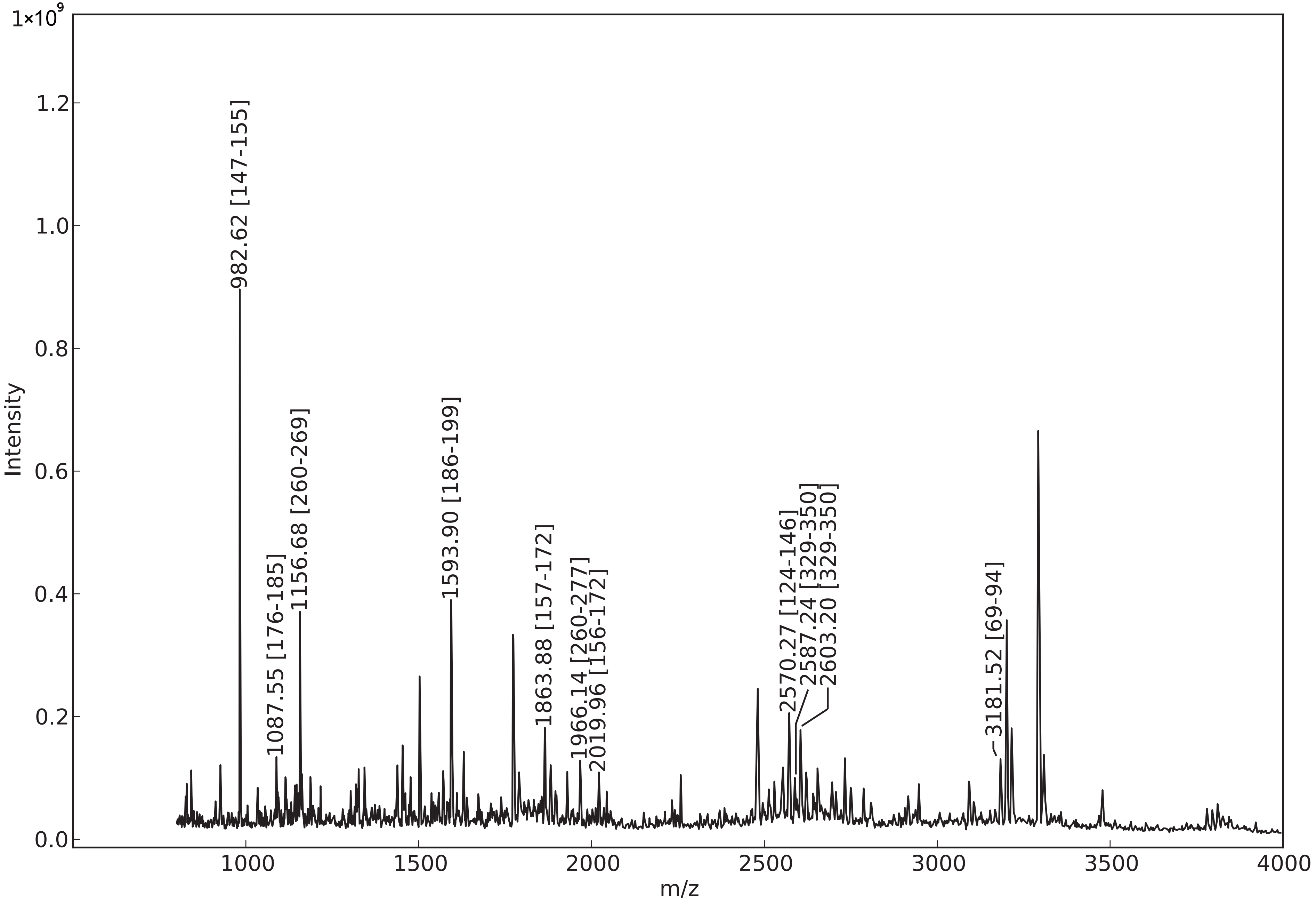
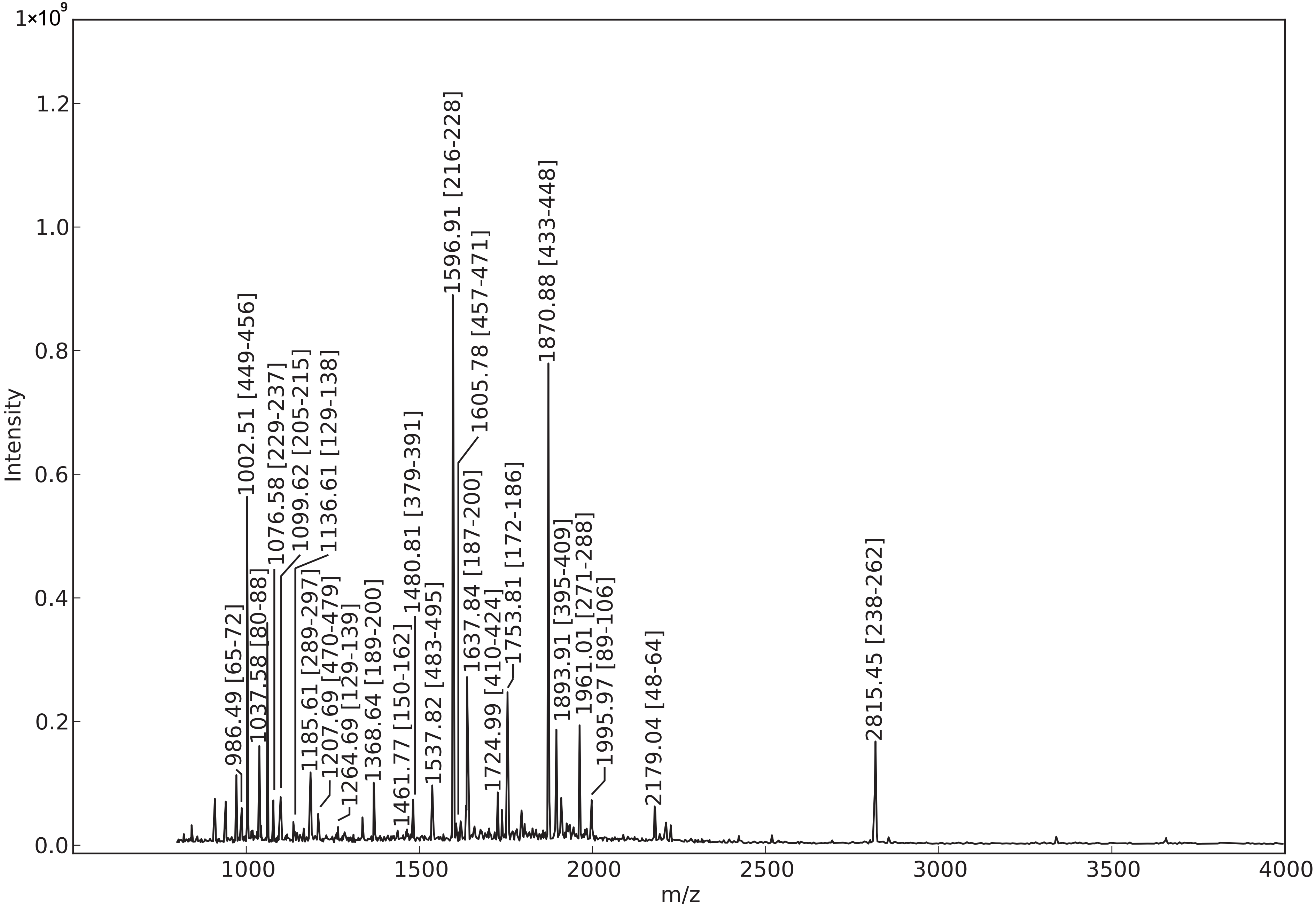
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
859.40 [327-332]
908.53 [171-177]
985.57 [332-340]
1158.67 [161-170]
1216.66 [341-350]
1301.74 [178-188]
1314.79 [161-171]
1344.74 [193-204]
1509.80 [248-261]
1777.06 [296-311]
1846.11 [189-204]
1862.10 [2-19]

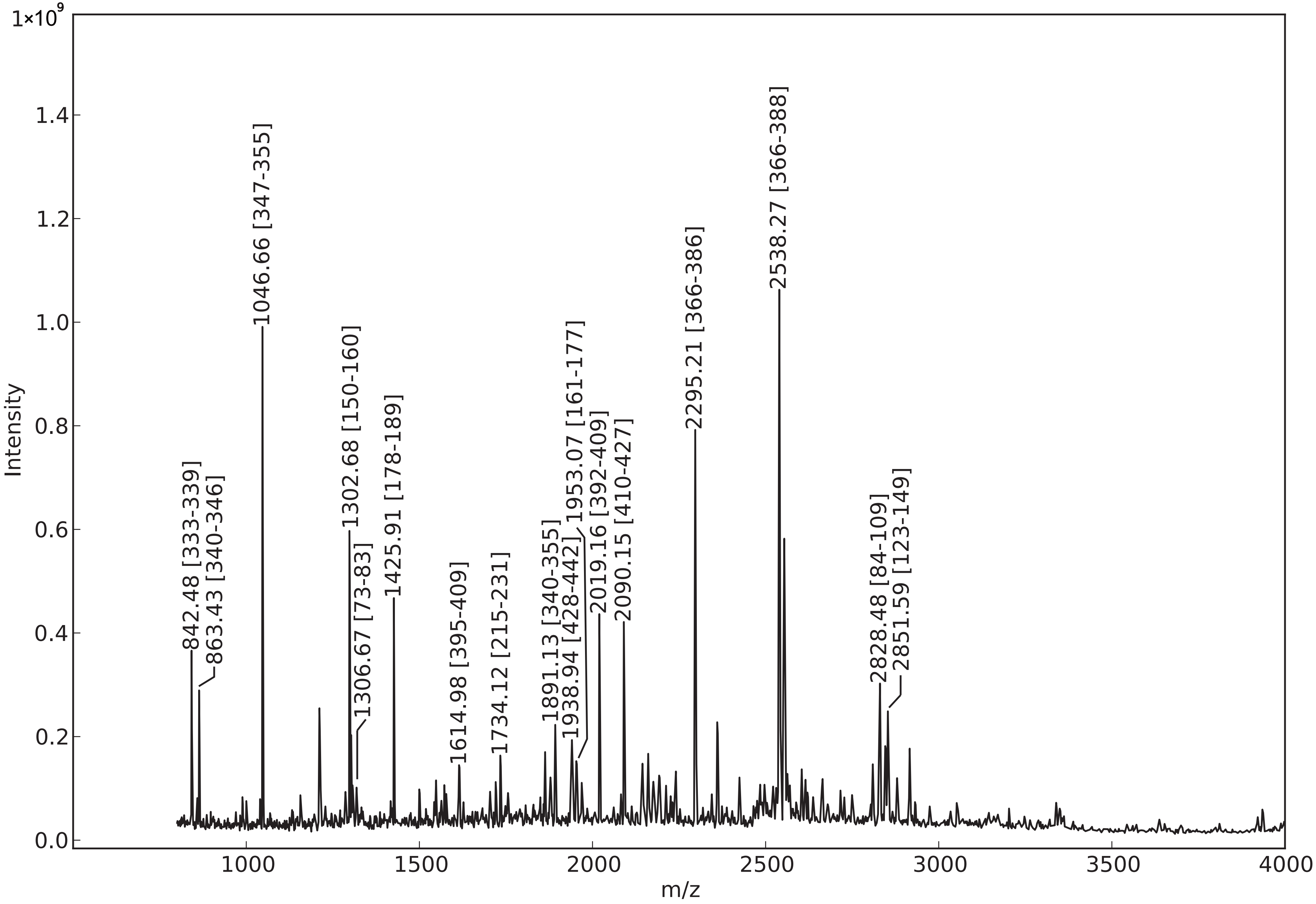
Spot No. 101


1×10^9
Intensity
0.0
0.2
0.4
0.6
0.8
1.0
1.2
m/z
1000
1500
2000
2500
3000
3500
4000
982.62 [147-155]
1087.55 [176-185]
1156.68 [260-269]
1593.90 [186-199]
1863.88 [157-172]
1966.14 [260-277]
2019.96 [156-172]
2570.27 [124-146]
2587.24 [329-350]
2603.20 [329-350]
3181.52 [69-94]

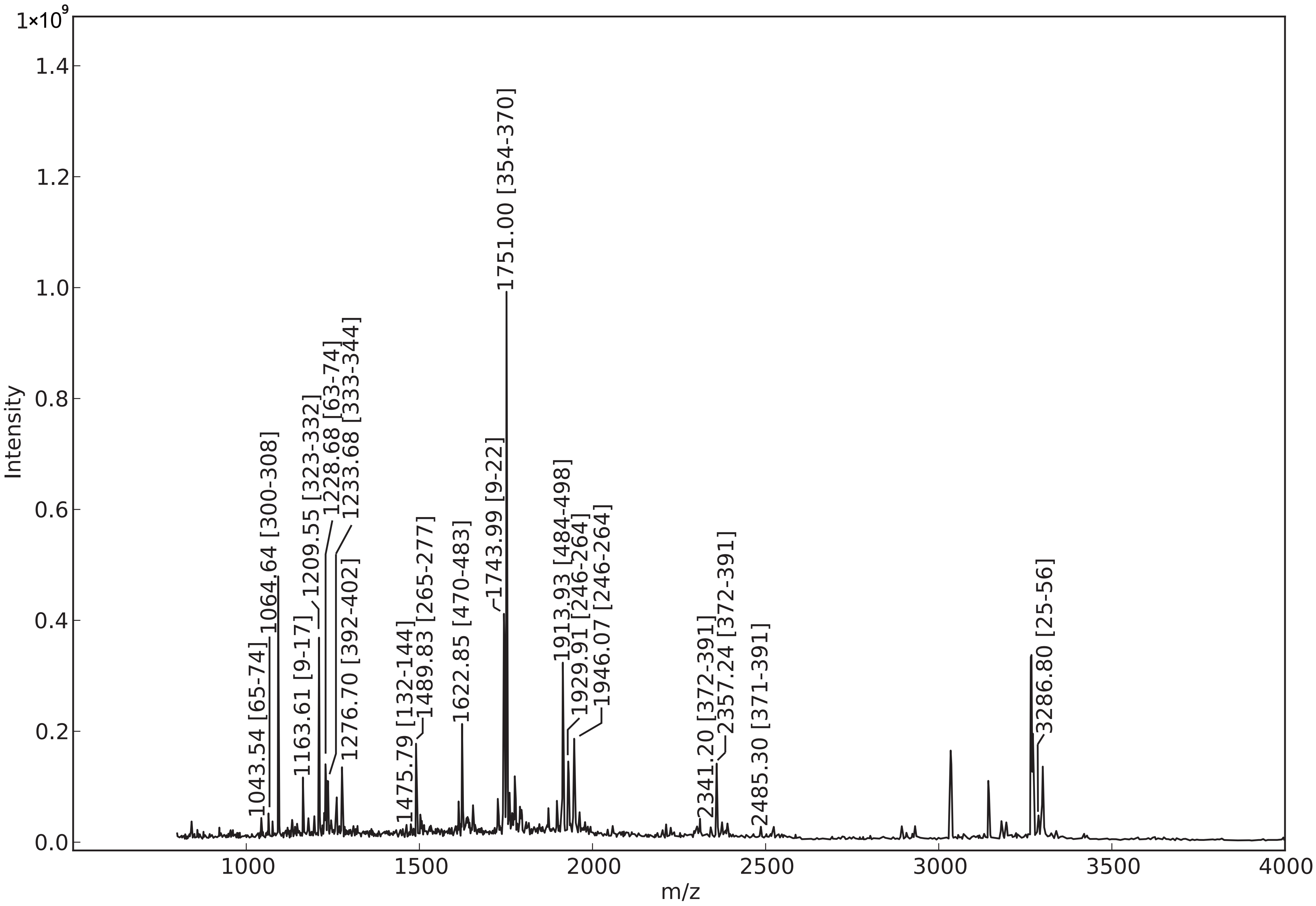
Spot No. 102


1×10⁹
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
986.49 [65-72]
1002.51 [449-456]
1037.58 [80-88]
1076.58 [229-237]
1099.62 [205-215]
1136.61 [129-138]
1185.61 [289-297]
1207.69 [470-479]
1264.69 [129-139]
1368.64 [189-200]
1461.77 [150-162]
1480.81 [379-391]
1537.82 [483-495]
1596.91 [216-228]
1605.78 [457-471]
1637.84 [187-200]
1724.99 [410-424]
1753.81 [172-186]
1870.88 [433-448]
1893.91 [395-409]
1961.01 [271-288]
1995.97 [89-106]
2179.04 [48-64]
2815.45 [238-262]

Spot No. 103


1×10⁹
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
842.48 [333-339]
863.43 [340-346]
1046.66 [347-355]
1302.68 [150-160]
1306.67 [73-83]
1425.91 [178-189]
1614.98 [395-409]
1734.12 [215-231]
1891.13 [340-355]
1938.94 [428-442]
1953.07 [161-177]
2019.16 [392-409]
2090.15 [410-427]
2295.21 [366-386]
2538.27 [366-388]
2828.48 [84-109]
2851.59 [123-149]

Spot No. 104

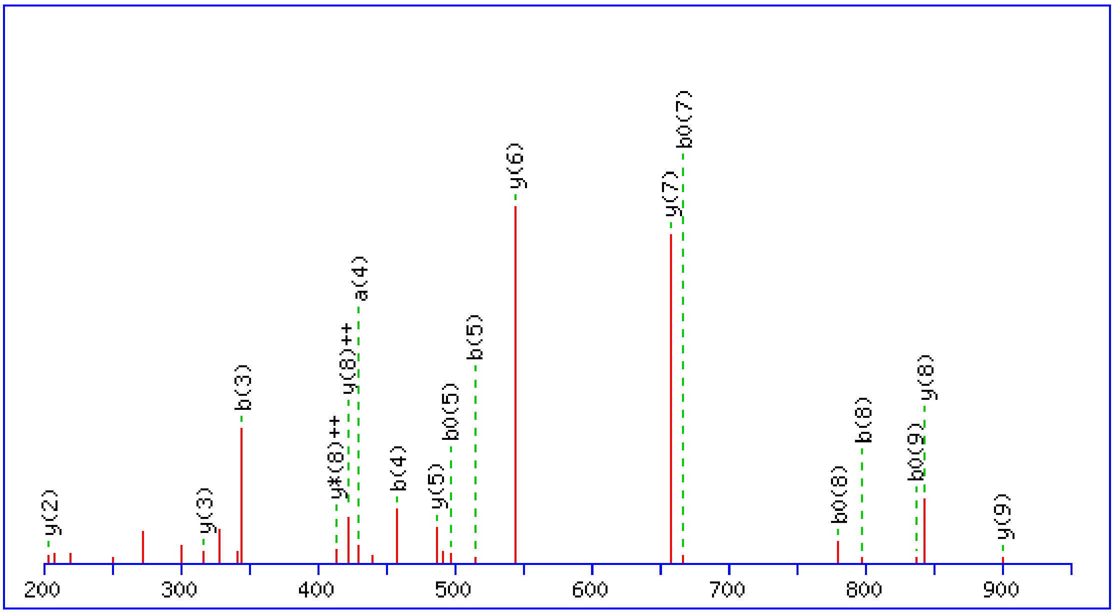

1×10^9
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Intensity
1000
1500
2000
2500
3000
3500
4000
m/z
1043.54 [65-74]
1064.64 [300-308]
1163.61 [9-17]
1209.55 [323-332]
1228.68 [63-74]
1233.68 [333-344]
1276.70 [392-402]
1475.79 [132-144]
1489.83 [265-277]
1622.85 [470-483]
1743.99 [9-22]
1751.00 [354-370]
1913.93 [484-498]
1929.91 [246-264]
1946.07 [246-264]
2341.20 [372-391]
2357.24 [372-391]
2485.30 [371-391]
3286.80 [25-56]

Supplemental Spectra 2. All spectra from spot 32, 33, 79, 80, 78 and 83 were obtained by ESI-FTICR MS. All spectra from spot 81 were obtained by MALDI-TOF-TOF MS/MS.

Gh UER1

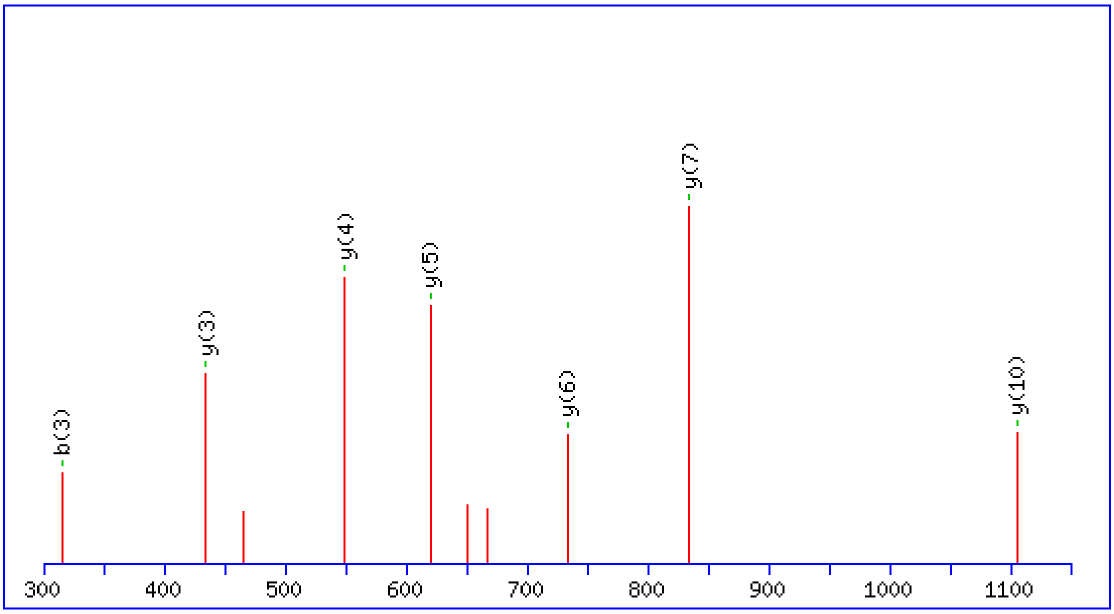
Spot 32:

MS/MS Fragmentation of TGWIGGLLGK
Found in DT545676



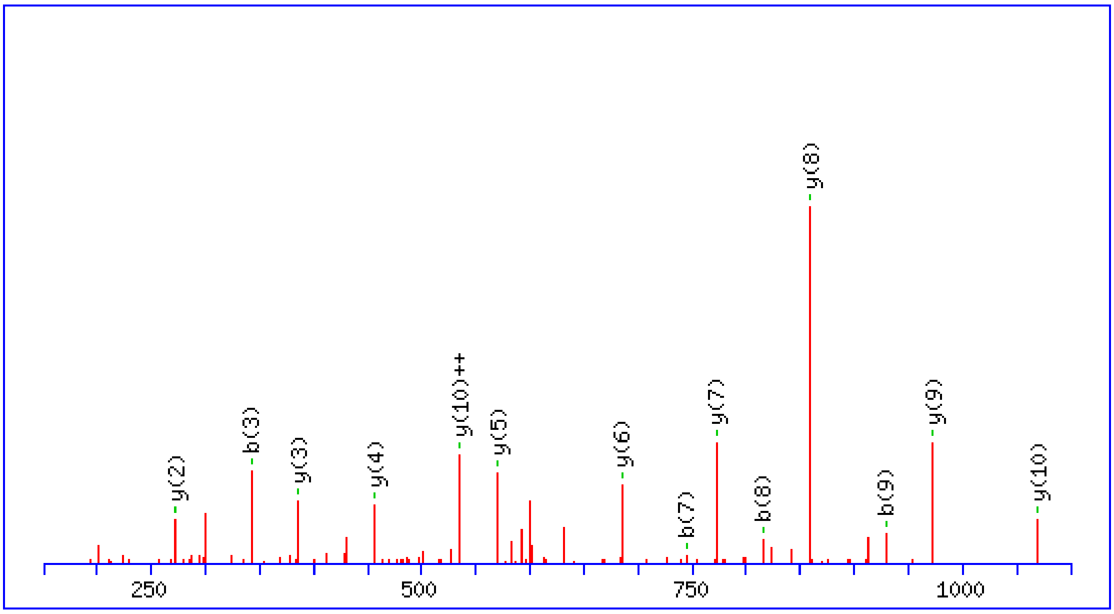
Precursor charge: 2+
Precursor m/z: 501.294986
Monoisotopic mass of neutral peptide Mr(calc): 1000.57
Fixed modifications: Carbamidomethyl (C)
Ions Score: 60 Expect: 0.00014
Matches (Bold Red): 18/108 fragment ions using 25 most intense peaks

MS/MS Fragmentation of TNVVGTLTLADVCR
Found in DT545676



Precursor charge: 2+
Precursor m/z: 759.903082
Monoisotopic mass of neutral peptide Mr(calc): 1517.79
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 Expect: 0.00012
Matches (**Bold Red**): 7/200 fragment ions using 7 most intense peaks

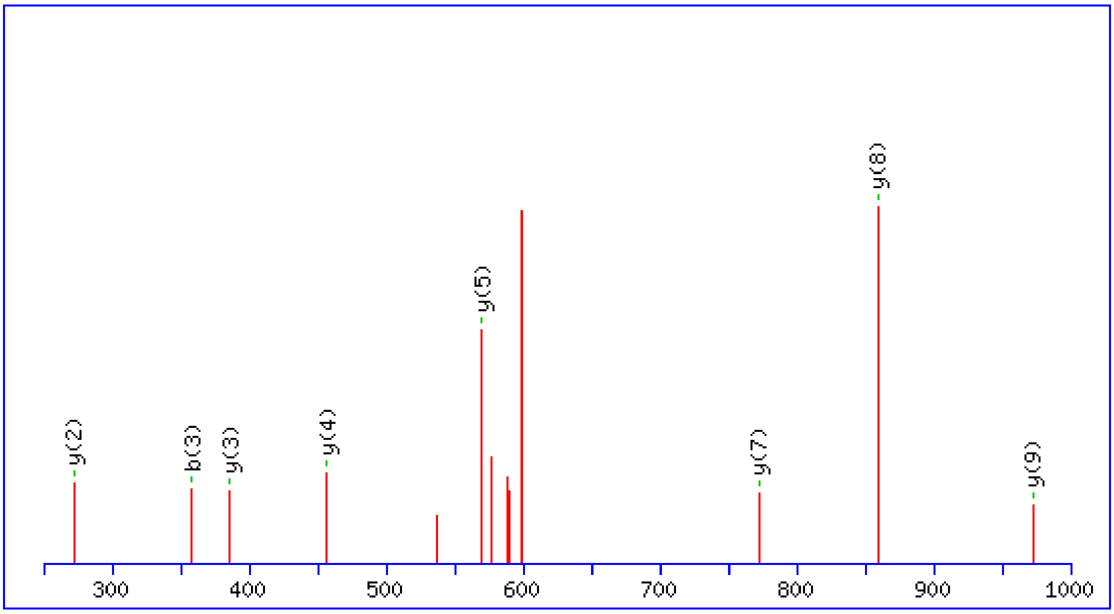
MS/MS Fragmentation of **MPISSDLANPR**
Found in **DT545676**



Precursor charge: 2+
Precursor m/z: 600.802804
Monoisotopic mass of neutral peptide Mr(calc): 1199.60
Fixed modifications: Carbamidomethyl (C)
Ions Score: 92 Expect: 1.1e-007

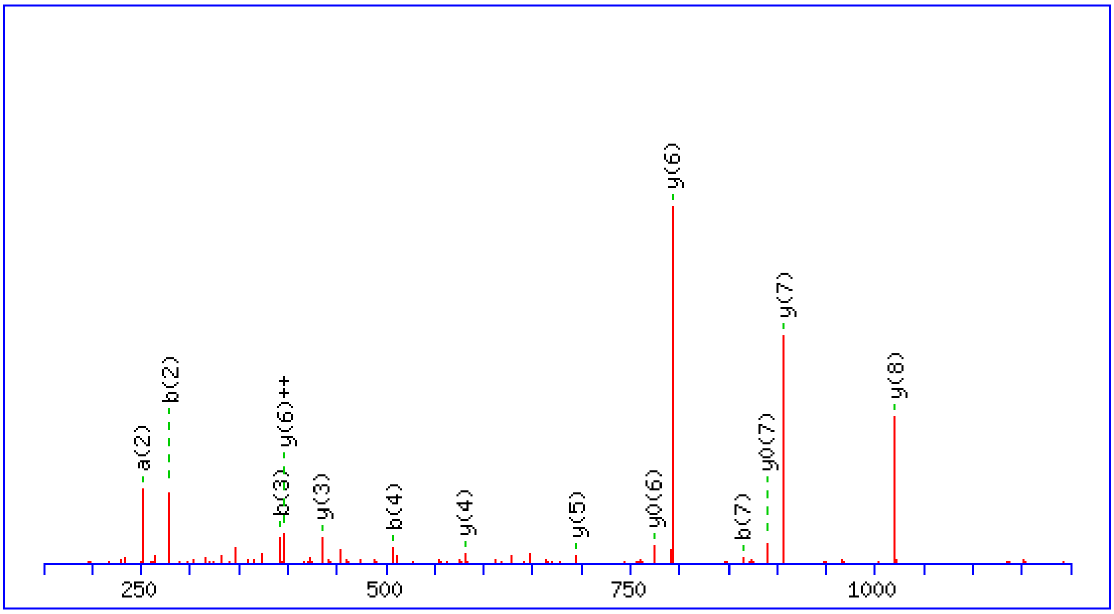
Matches (Bold Red): 14/128 fragment ions using 18 most intense peaks

MS/MS Fragmentation of MPISSDLANPR
Found in DT545676



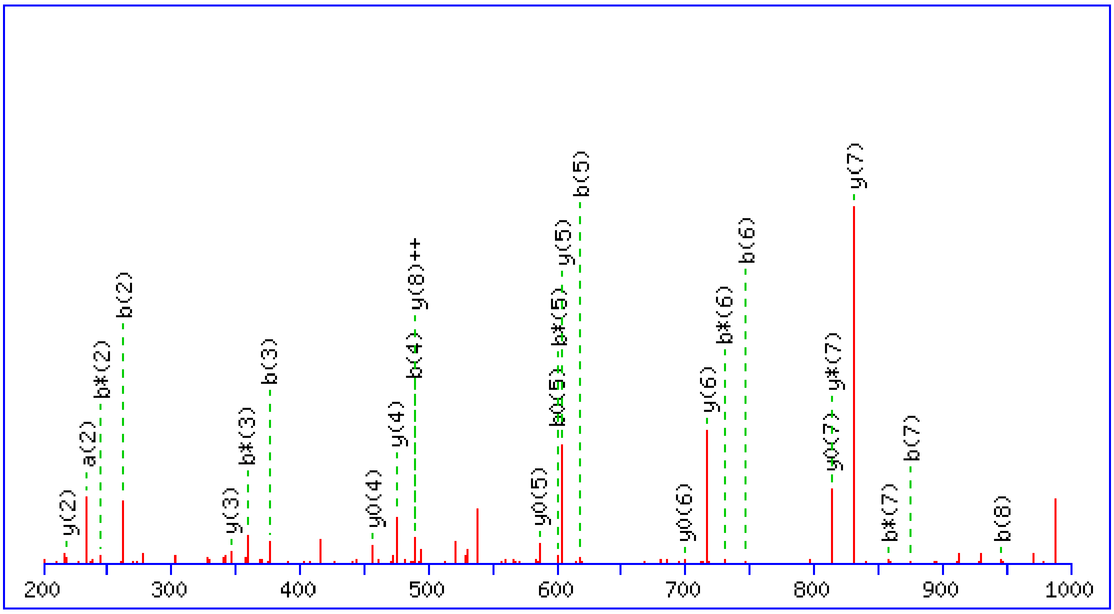
Precursor charge: 2+
Precursor m/z: 608.803327
Monoisotopic mass of neutral peptide Mr(calc): 1215.59
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
M1 : Oxidation (M)
Ions Score: 67 **Expect:** 2.5e-005
Matches (Bold Red): 8/128 fragment ions using 11 most intense peaks

MS/MS Fragmentation of DYIDPNFTWK
Found in DT545676



Precursor charge: 2+
Precursor m/z: 649.806700
Monoisotopic mass of neutral peptide Mr(calc): 1297.60
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect:** 0.0041
Matches (Bold Red): 14/130 fragment ions using 21 most intense peaks

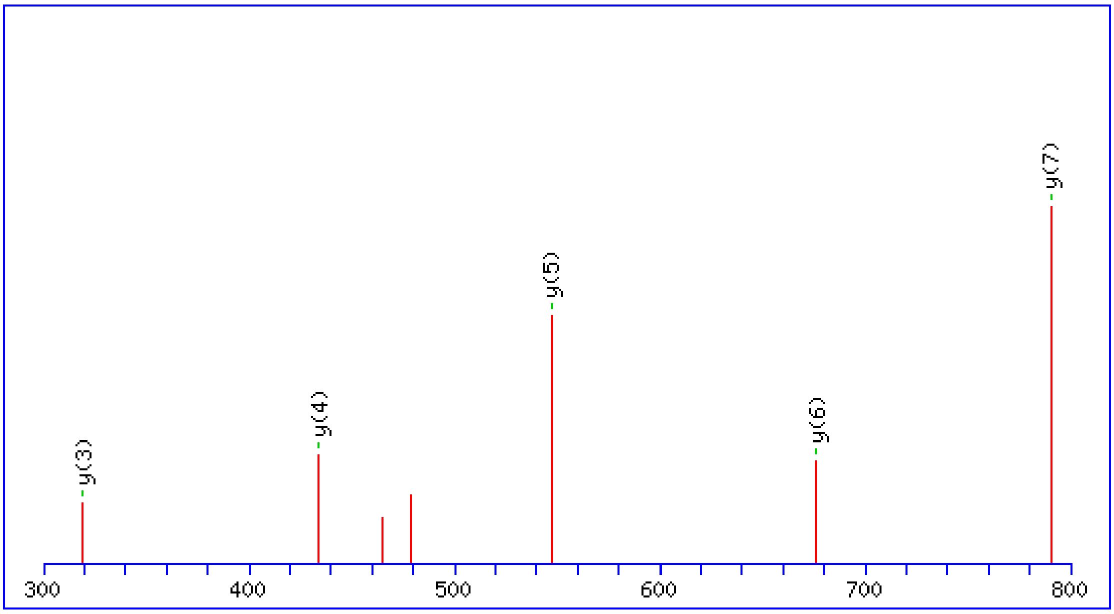
MS/MS Fragmentation of NFNLEEQAK
Found in DT545676



Precursor charge: 2+
Precursor m/z: 546.767838
Monoisotopic mass of neutral peptide Mr(calc): 1091.52
Fixed modifications: Carbamidomethyl (C)
Ions Score: 46 **Expect:** 0.0051

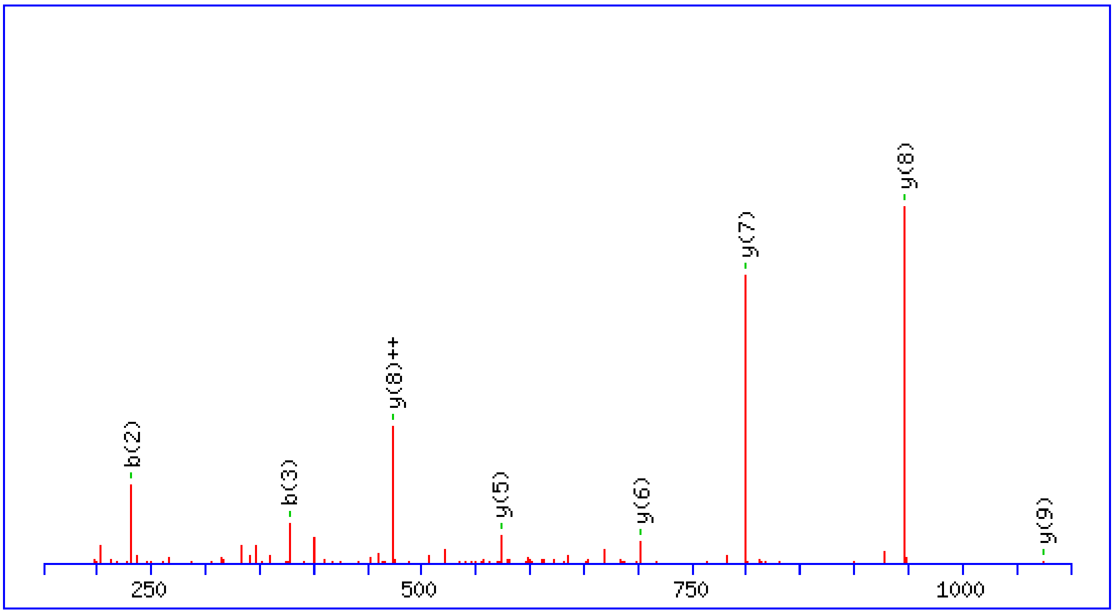
Matches (Bold Red): 26/114 fragment ions using 48 most intense peaks

MS/MS Fragmentation of SNNELDATK
Found in DT545676



Precursor charge: 2+
Precursor m/z: 496.240565
Monoisotopic mass of neutral peptide Mr(calc): 990.46
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00071
Matches (Bold Red): 5/124 fragment ions using 5 most intense peaks

MS/MS Fragmentation of TEFPELLSIK
Found in DT545676

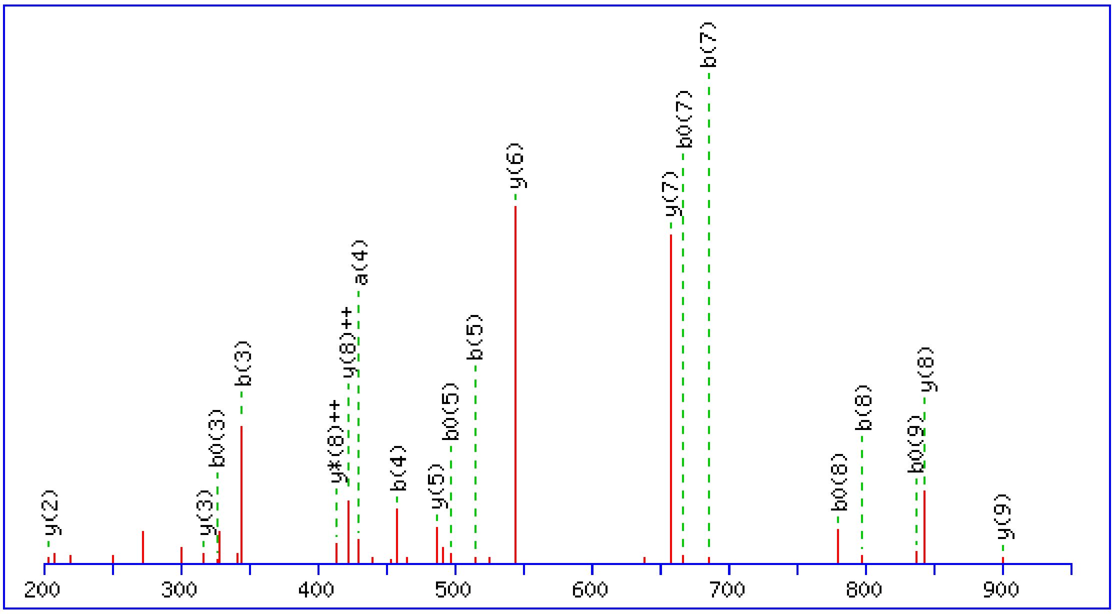


Precursor charge: 2+

Precursor m/z: 588.828849
Monoisotopic mass of neutral peptide Mr(calc): 1175.64
Fixed modifications: Carbamidomethyl (C)
Ions Score: 46 Expect: 0.0041
Matches (Bold Red): 8/122 fragment ions using 12 most intense peaks

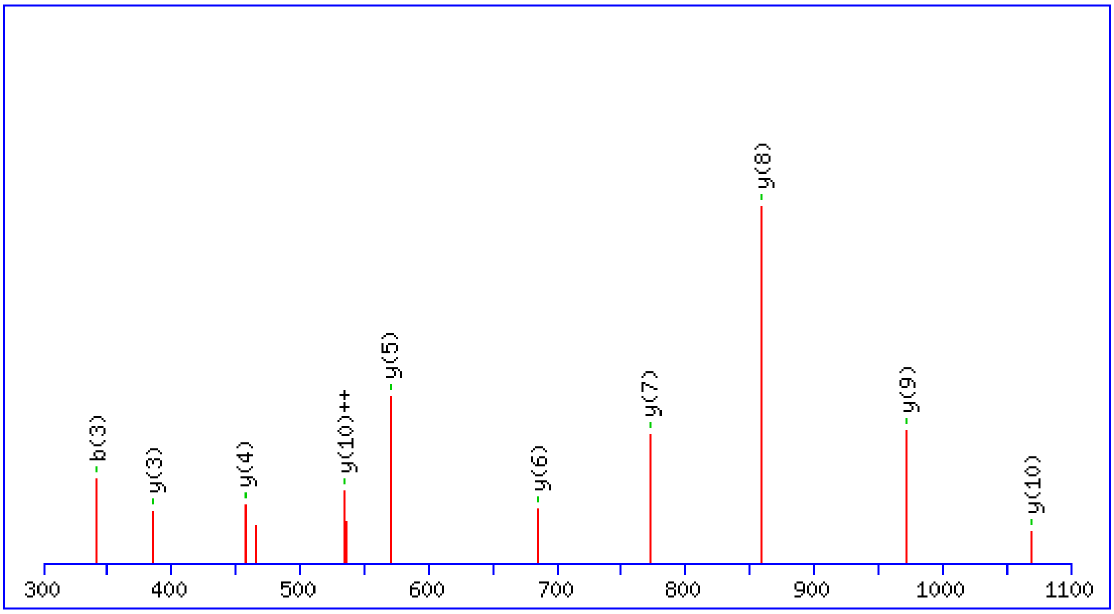
Spot 33

MS/MS Fragmentation of TGWIGGLLGK
Found in DT545676



Precursor charge: 2+
Precursor m/z: 501.294476
Monoisotopic mass of neutral peptide Mr(calc): 1000.57
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 Expect: 0.00052
Matches (Bold Red): 20/108 fragment ions using 31 most intense peaks

MS/MS Fragmentation of MPISSDLANPR
Found in DT545676



Precursor charge: 2+

Precursor m/z: 600.808537

Monoisotopic mass of neutral peptide Mr(calc): 1199.60

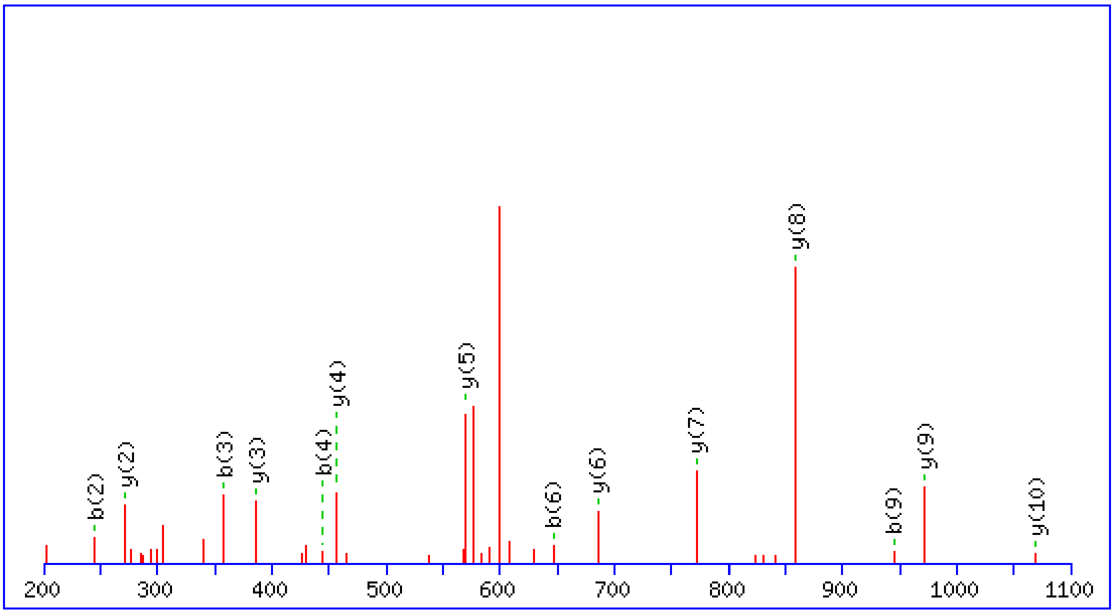
Fixed modifications: Carbamidomethyl (C)

Ions Score: 93   Expect: 9.7e-008

Matches (Bold Red): 10/128 fragment ions using 10 most intense peaks

MS/MS Fragmentation of MPISSDLANPR

Found in DT545676



Precursor charge: 2+

Precursor m/z: 608.803613

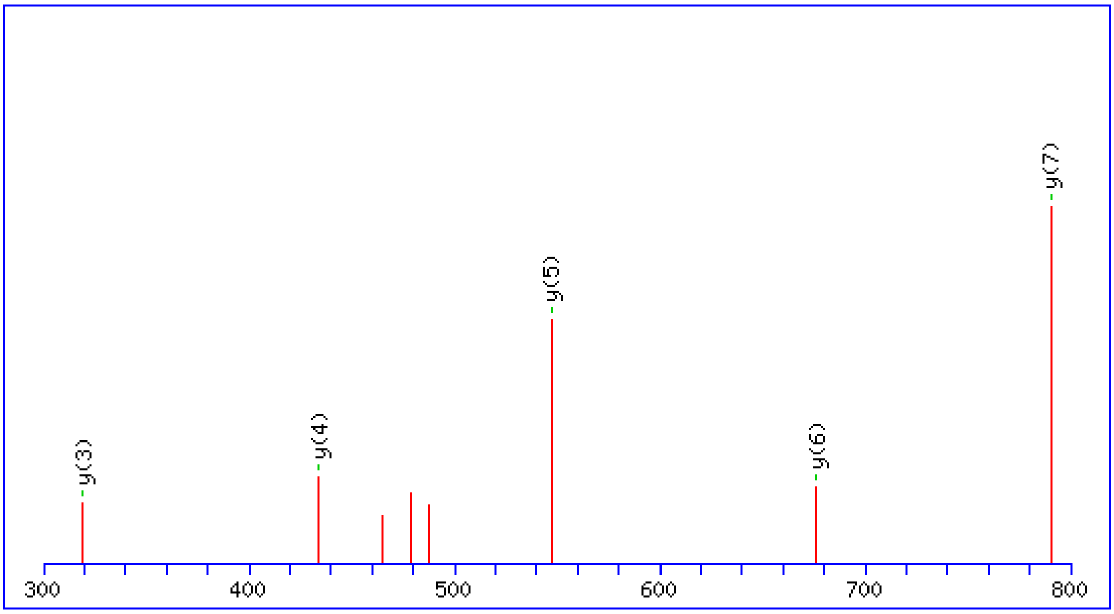
Monoisotopic mass of neutral peptide Mr(calc): 1215.59

Fixed modifications: Carbamidomethyl (C)

Variable modifications:

M1 : Oxidation (M)
Ions Score: 80 **Expect:** 1.3e-006
Matches (Bold Red): 14/128 fragment ions using 22 most intense peaks

MS/MS Fragmentation of SNNELDATK
Found in DT545676

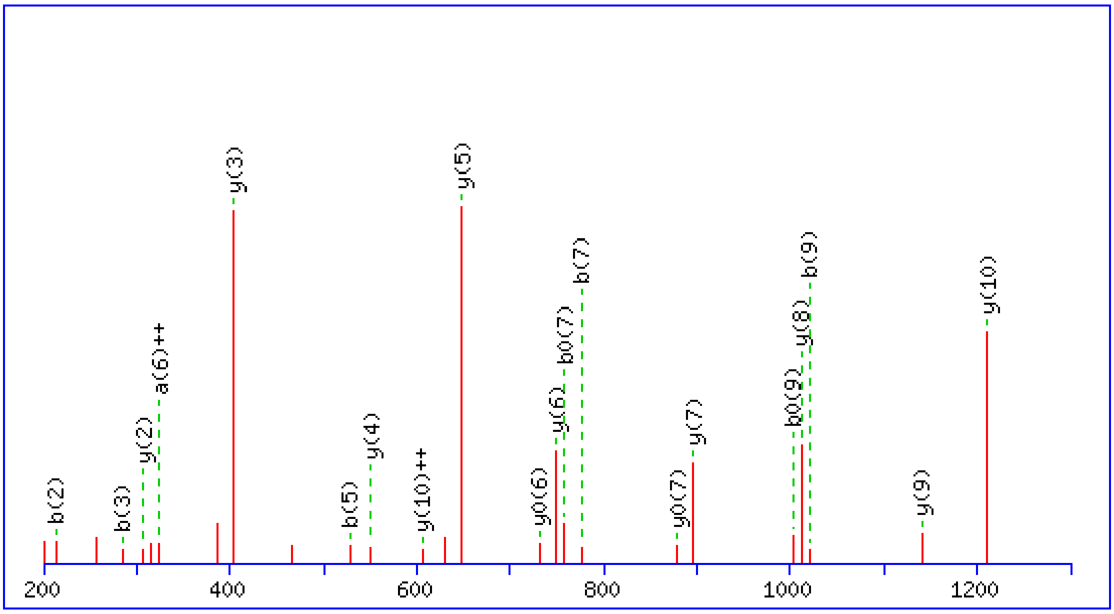


Precursor charge: 2+
Precursor m/z: 496.239682
Monoisotopic mass of neutral peptide Mr(calc): 990.46
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.0006
Matches (Bold Red): 5/124 fragment ions using 5 most intense peaks

Gh UGP1

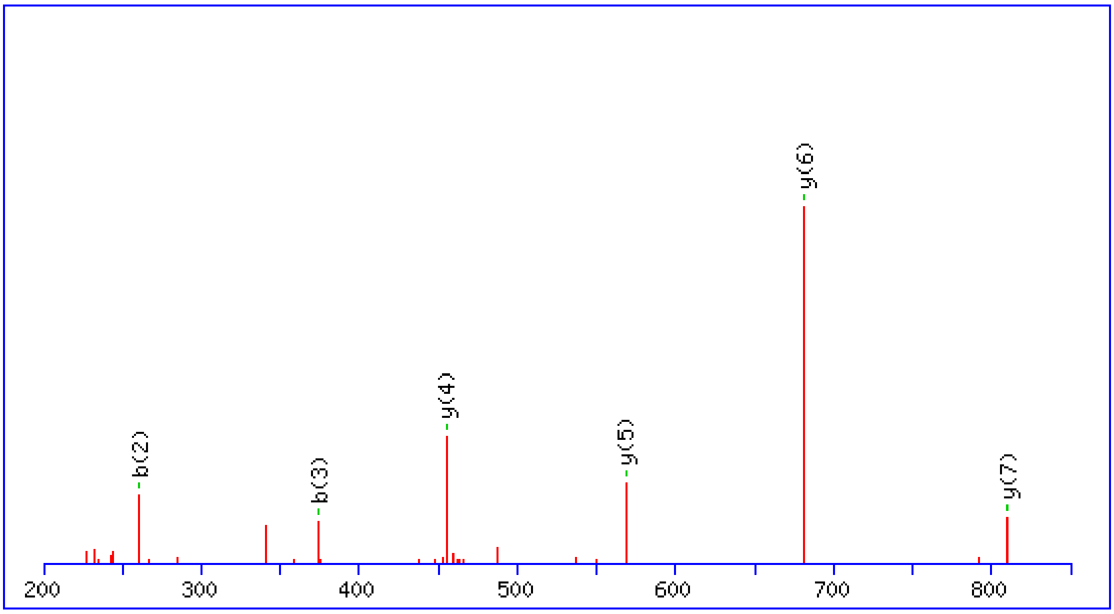
Spot79

MS/MS Fragmentation of LVAEDFTPFPCK
Found in CO109041



Precursor charge: 2+
Precursor m/z: 712.352879
Monoisotopic mass of neutral peptide Mr(calc): 1422.69
Fixed modifications: Carbamidomethyl (C)
Ions Score: 75 Expect: 4.7e-006
Matches (Bold Red): 20/138 fragment ions using 28 most intense peaks

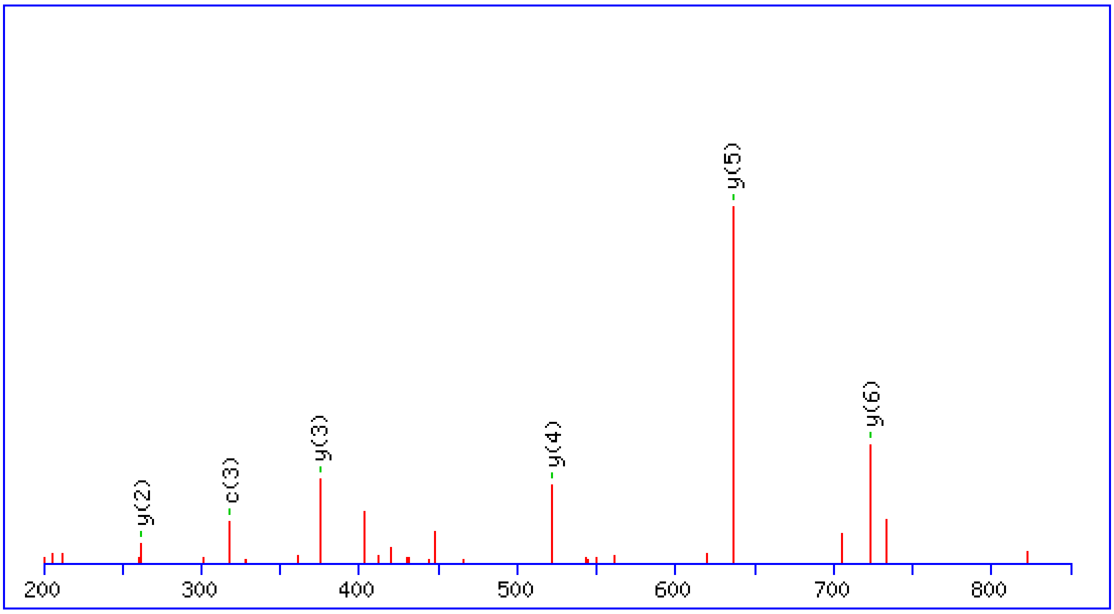
MS/MS Fragmentation of MEIIPNPK
Found in C0109041



Precursor charge: 2+
Precursor m/z: 471.260945
Monoisotopic mass of neutral peptide Mr(calc): 940.51
Fixed modifications: Carbamidomethyl (C)
Ions Score: 41 Expect: 0.0077

Matches (**Bold Red**): 6/88 fragment ions using 6 most intense peaks

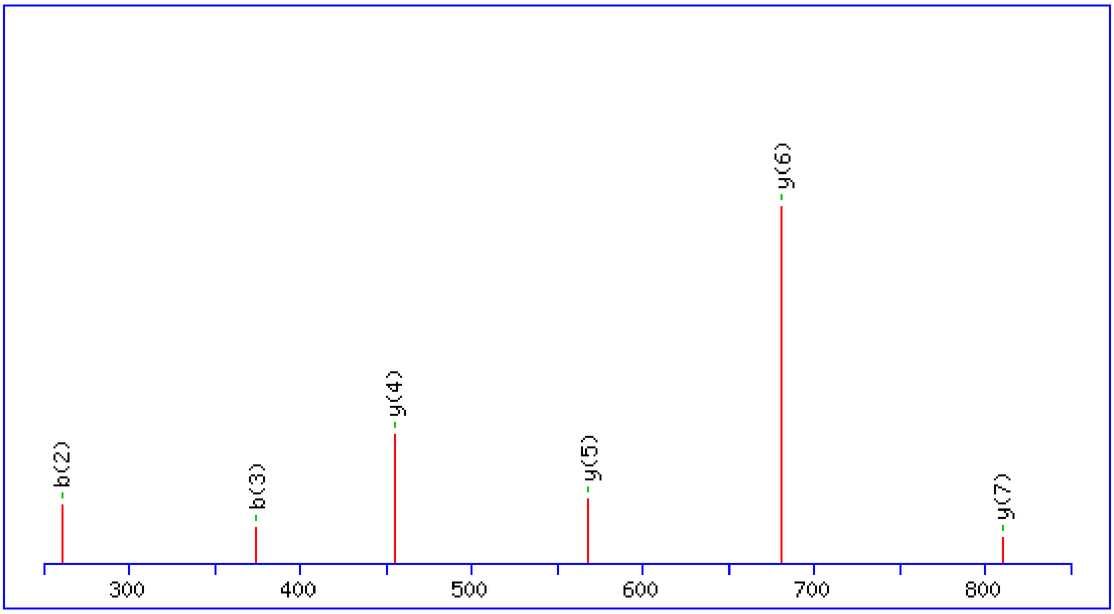
MS/MS Fragmentation of **VSNFLSR**
Found in **C0109041**



Precursor charge: 2+
Precursor m/z: 411.728469
Monoisotopic mass of neutral peptide Mr(calc): 821.44
Fixed modifications: Carbamidomethyl (C)
Ions Score: 55 **Expect:** 0.00094
Matches (**Bold Red**): 6/88 fragment ions using 7 most intense peaks

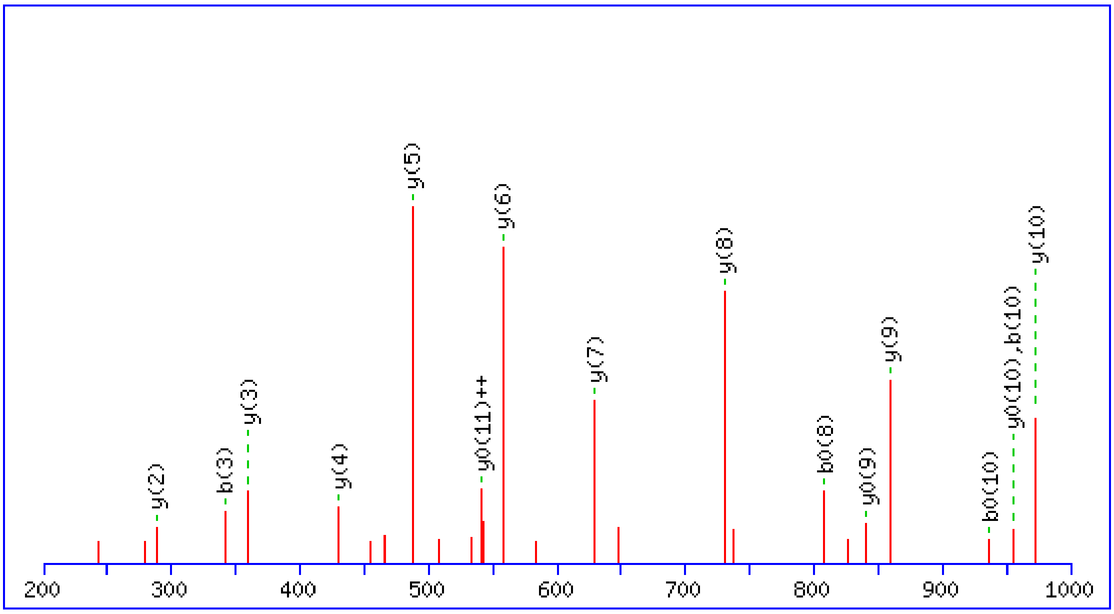
Spot 80

MS/MS Fragmentation of **MEIIPNPK**
Found in **ES824132**



Precursor charge: 2+
Precursor m/z: 471.261061
Monoisotopic mass of neutral peptide Mr(calc): 940.51
Fixed modifications: Carbamidomethyl (C)
Ions Score: 42 Expect: 0.0063
Matches (**Bold Red**): 6/88 fragment ions using 6 most intense peaks

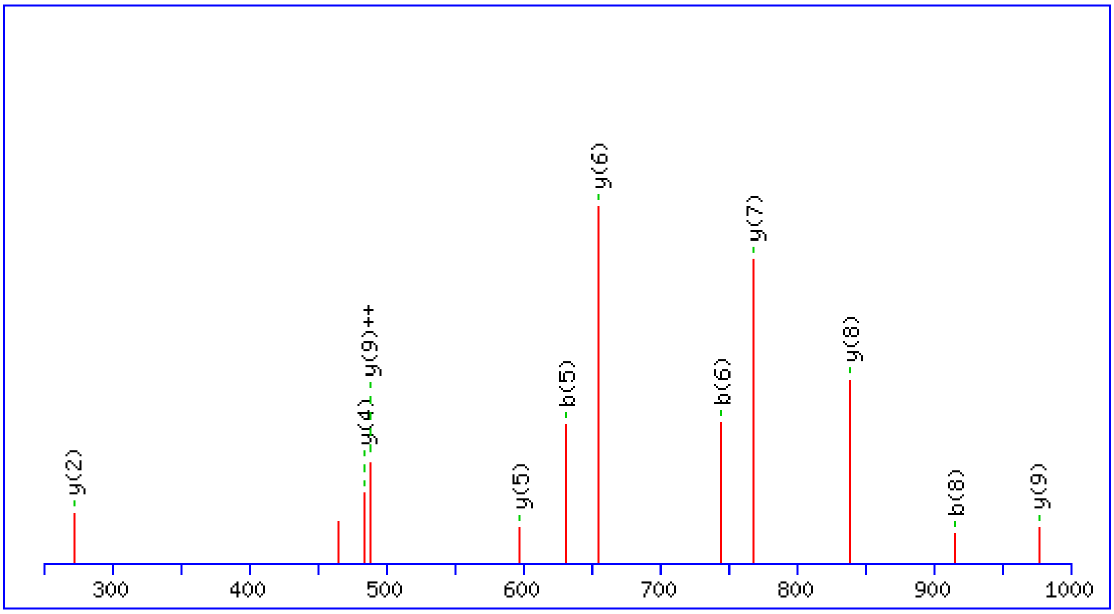
MS/MS Fragmentation of VLQLETAAGAAIR
Found in ES824132



Precursor charge: 2+
Precursor m/z: 656.885979
Monoisotopic mass of neutral peptide Mr(calc): 1311.75
Fixed modifications: Carbamidomethyl (C)
Ions Score: 103 Expect: 4.8e-009

Matches (Bold Red): 16/166 fragment ions using 16 most intense peaks

MS/MS Fragmentation of FFEHAIGINVPR
Found in EV482616

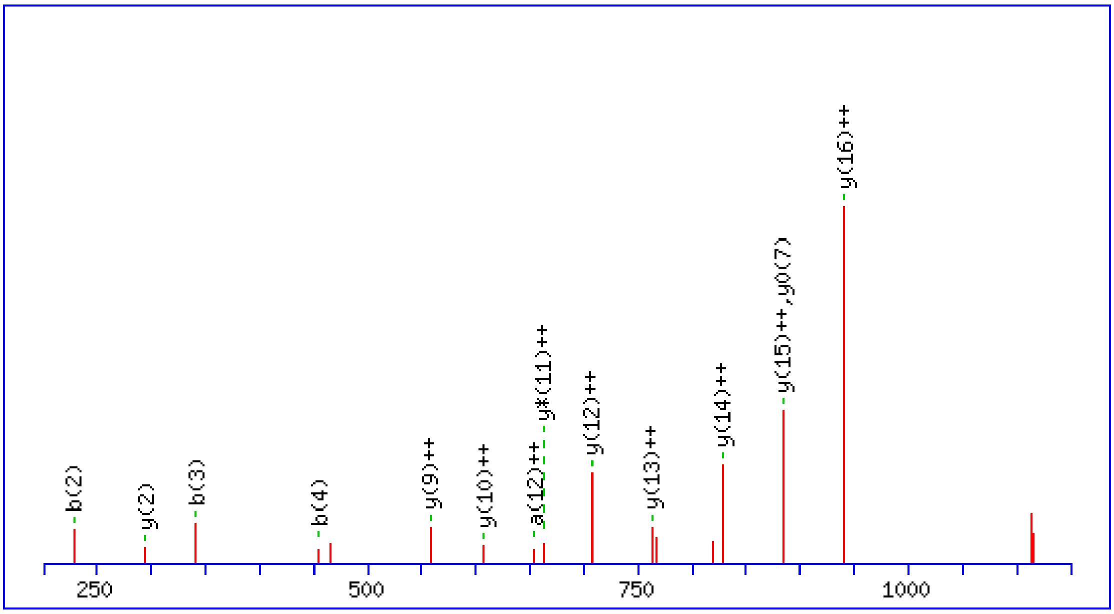


Precursor charge: 2+
Precursor m/z: 700.379610
Monoisotopic mass of neutral peptide Mr(calc): 1398.74
Fixed modifications: Carbamidomethyl (C)
Ions Score: 70 **Expect:** 1.4e-005
Matches (Bold Red): 11/138 fragment ions using 12 most intense peaks

Gh UGP2

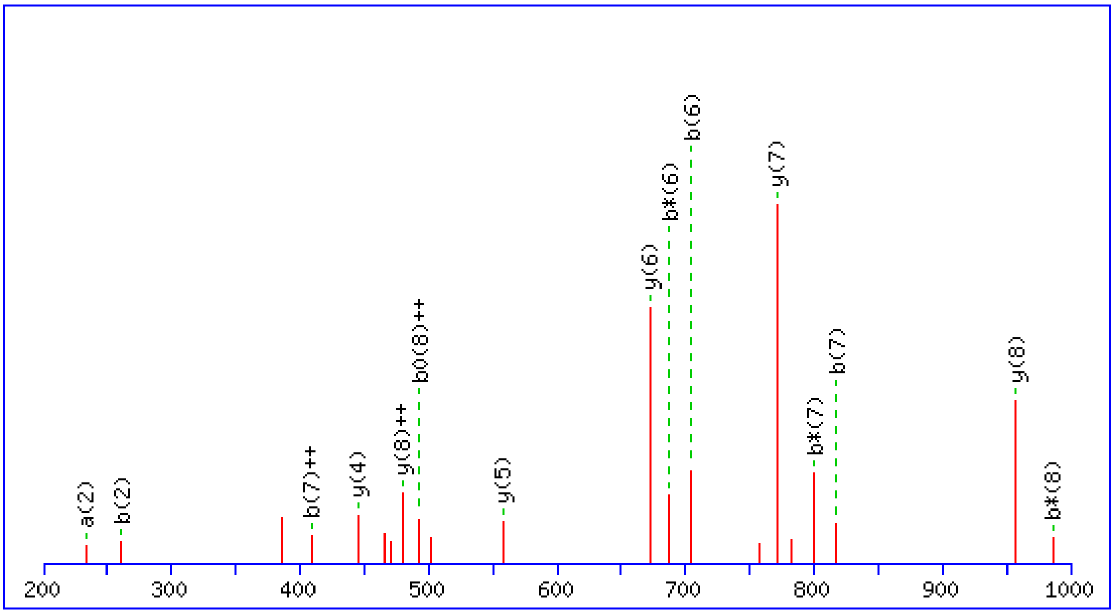
Spot 78

MS/MS Fragmentation of VQLLEIAQVPDEHVNEFK
Found in EX172531



Precursor charge: 3+
Precursor m/z: 703.368945
Monoisotopic mass of neutral peptide Mr(calc): 2107.09
Fixed modifications: Carboxymethyl (C)
Ions Score: 50 Expect: 0.00081
Matches (Bold Red): 14/258 fragment ions using 19 most intense peaks

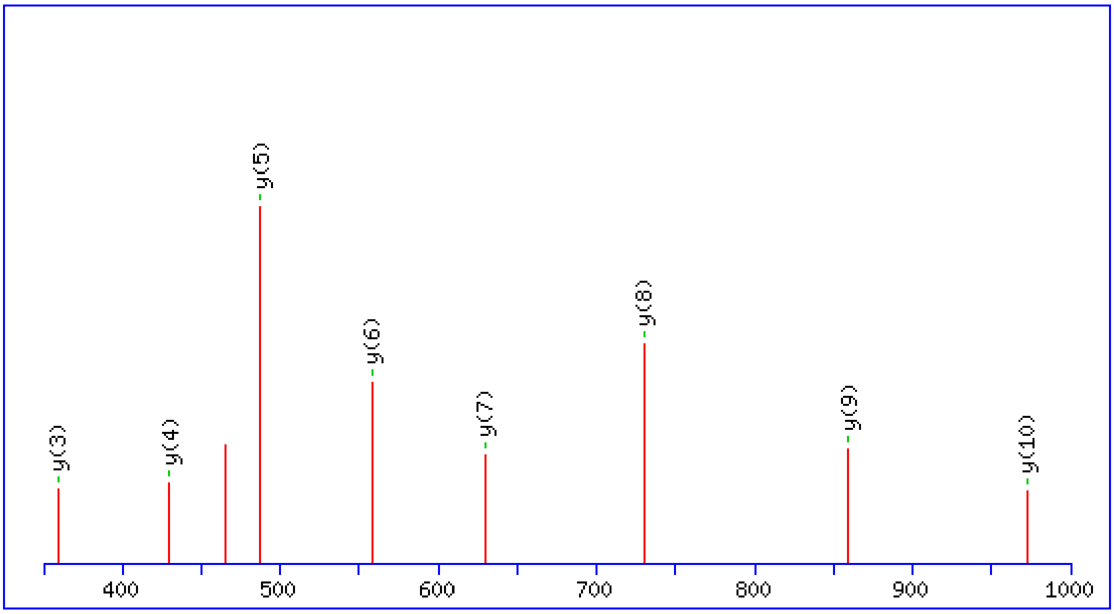
MS/MS Fragmentation of IFNTNNLWVNLNAIK
Found in EX172531



Precursor charge: 3+
Precursor m/z: 591.991483
Monoisotopic mass of neutral peptide Mr(calc): 1772.96
Fixed modifications: Carboxymethyl (C)
Ions Score: 46 Expect: 0.0028

Matches (Bold Red): 15/192 fragment ions using 16 most intense peaks

MS/MS Fragmentation of VLQLETAAGAAIR
Found in EX172531

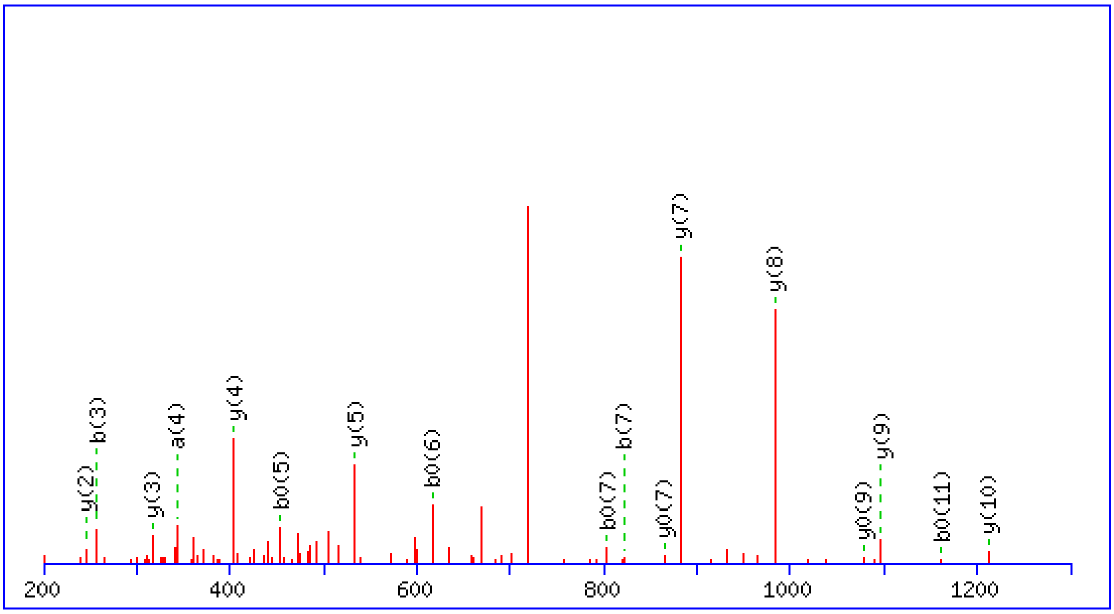


Precursor charge: 2+
Precursor m/z: 656.879840
Monoisotopic mass of neutral peptide Mr(calc): 1311.75
Fixed modifications: Carboxymethyl (C)
Ions Score: 89 **Expect:** 1.6e-007
Matches (Bold Red): 8/166 fragment ions using 9 most intense peaks

Gh UGD1

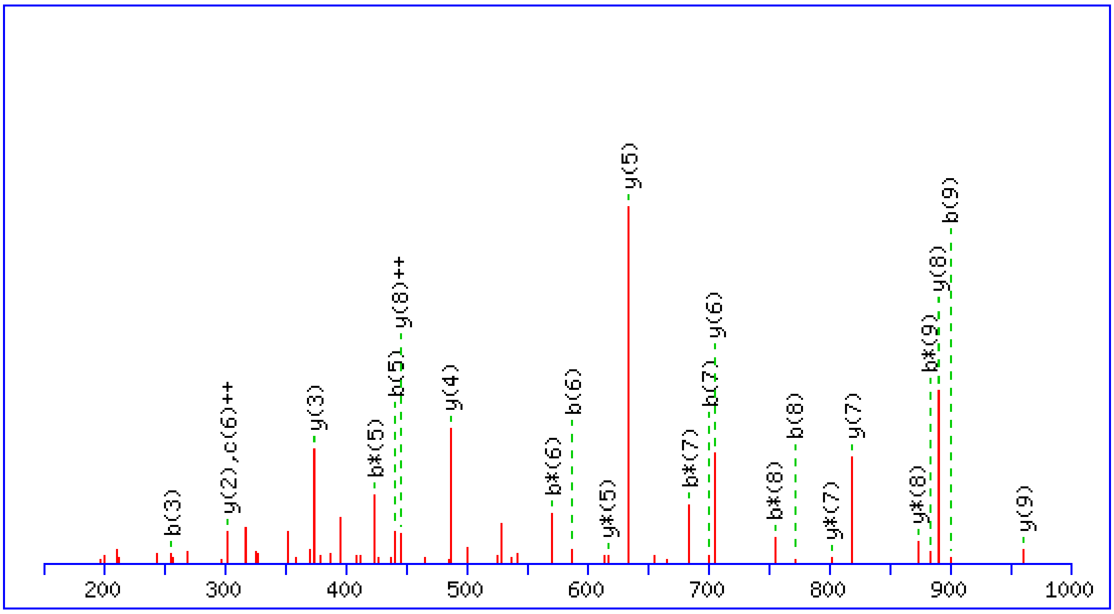
Spot 83

MS/MS Fragmentation of AADLTYWESAAR
Found in BQ408827



Precursor charge: 2+
Precursor m/z: 677.325629
Monoisotopic mass of neutral peptide Mr(calc): 1352.64
Fixed modifications: Carbamidomethyl (C)
Ions Score: 64 Expect: 5.4e-005
Matches (**Bold Red**): 17/144 fragment ions using 24 most intense peaks

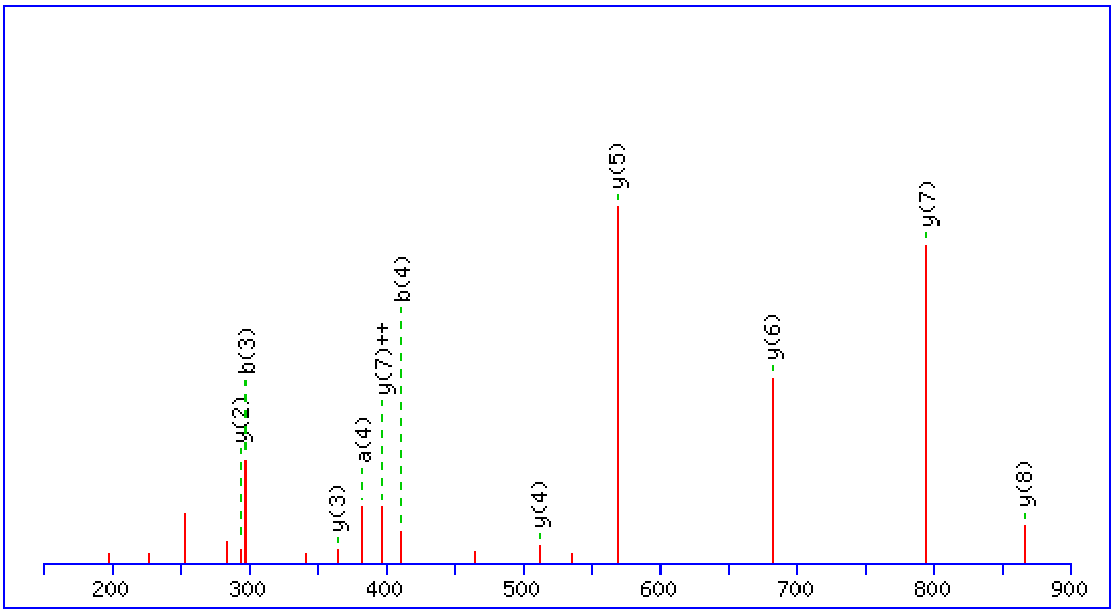
MS/MS Fragmentation of **LAANAFLAQR**
Found in **EY197769**



Precursor charge: 2+
Precursor m/z: 537.807238
Monoisotopic mass of neutral peptide Mr(calc): 1073.60
Fixed modifications: Carbamidomethyl (C)
Ions Score: 72 Expect: 8.9e-006

Matches (Bold Red): 24/102 fragment ions using 32 most intense peaks

MS/MS Fragmentation of IAILGFAFK
Found in EY197769

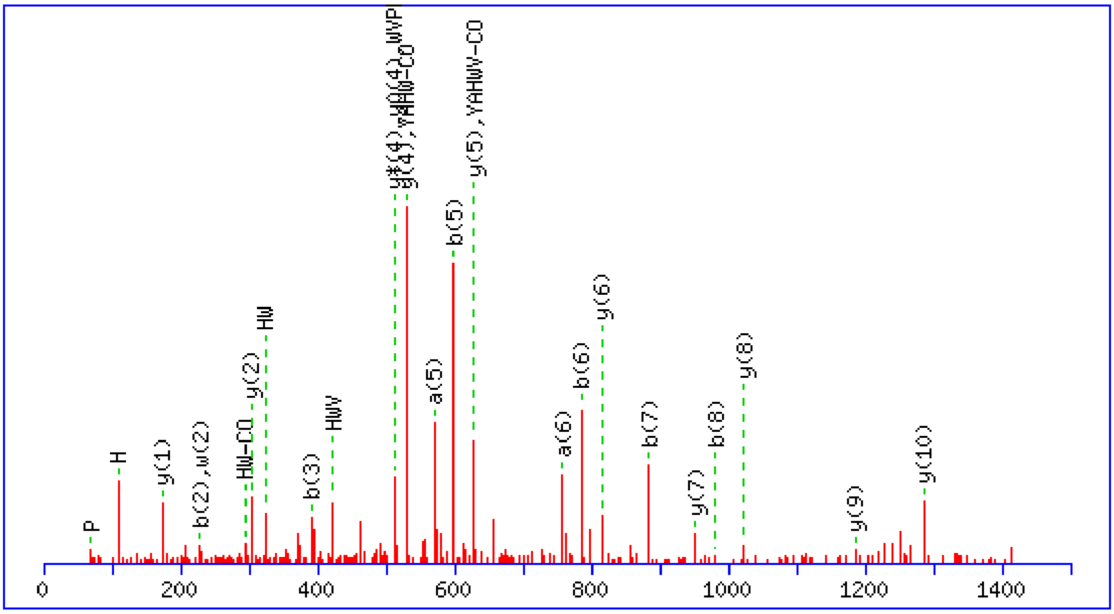


Precursor charge: 2+
Precursor m/z: 490.304020
Monoisotopic mass of neutral peptide Mr(calc): 978.59
Fixed modifications: Carboxymethyl (C)
Ions Score: 63 **Expect:** 3.1e-005
Matches (Bold Red): 11/80 fragment ions using 16 most intense peaks

Spot 81

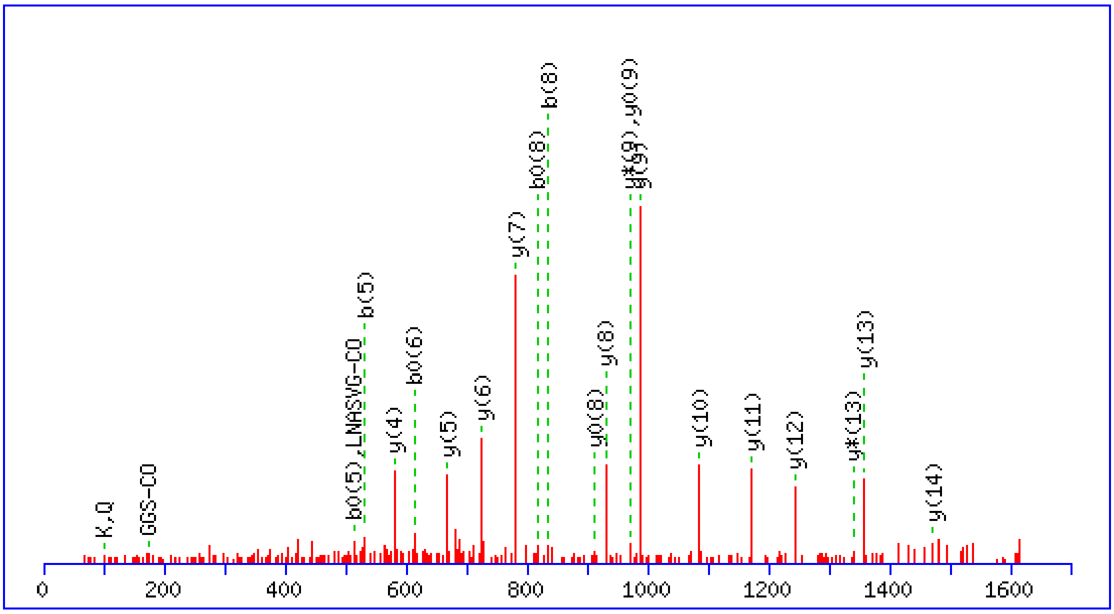
MALDI-TOF-TOF MS/MS spectra of ions and the detailed information of mascot search results

MS/MS Fragmentation of EVYAHWVPEER
Found in AI730020



Precursor charge: 1+
Precursor m/z: 1414.697000
Monoisotopic mass of neutral peptide Mr(calc): 1413.67
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 **Expect:** 0.0018
Matches (Bold Red): 29/149 fragment ions using 35 most intense peaks

MS/MS Fragmentation of FLNASVGFGGSCFQK
Found in AI727145



Precursor charge: 1+
Precursor m/z: 1618.781000
Monoisotopic mass of neutral peptide Mr(calc): 1617.76
Fixed modifications: Carbamidomethyl (C)
Ions Score: 76 **Expect:** 3.7e-005

Matches (Bold Red): 24/240 fragment ions using 42 most intense peaks