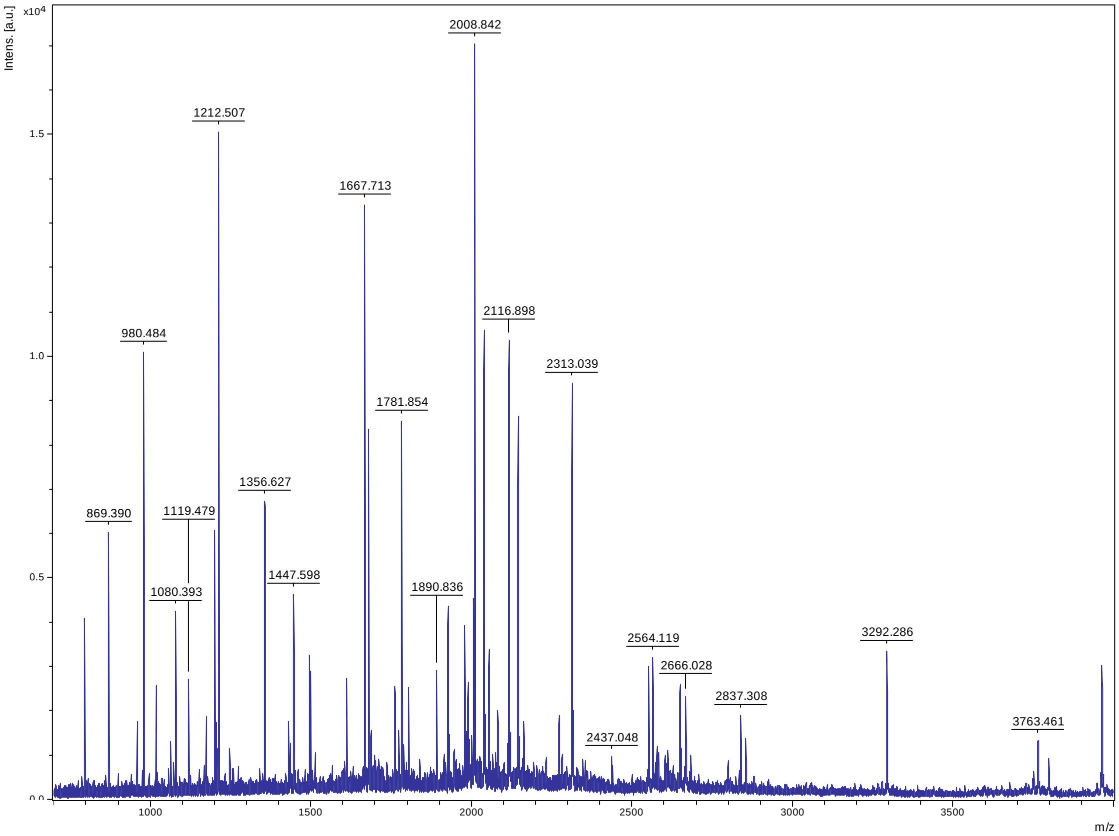
Supplementary Figure S2

PMF-based identifications: The MS spectra were created on Ultroflex Ⅱ MALDI TOF/TOF mass spectrometer (Bruker Daltonics, Germany) with flexanalysis 2.4 software. The external calibration of the Ultroflex spectrometer itself and a two-point internal calibration for each spectrum were performed as described previously (Dai et al. 2007). PMFs were searched against the NCBInr (http://www.ncbi.nlm.nih.gov/) and MSDB (ftp://ftp.ncbi.nih.gov/repository/MSDB) protein database using the MASCOT v.2.1 (www.matrixscience.com; Matrix Science, London, UK) search engine. Oryza sativa (66,973 sequence entries in NCBI in February 2006; 66,430 sequence entries in MSDB in December 2006) was chosen as the taxonomic category. All peptide masses were supposed as mono-isotopic and $[M+H]^+$ (protonated molecularions). Searches involved use of mass accuracy of ±200 ppm and one missing cleavage site was allowed for each search. Carbamidomethyl (C) was set as a fixed modification, and oxidation (M), pyro-glu (N-term Q) and Acetyl (N-term) were set as variable modifications.

Spot 1193

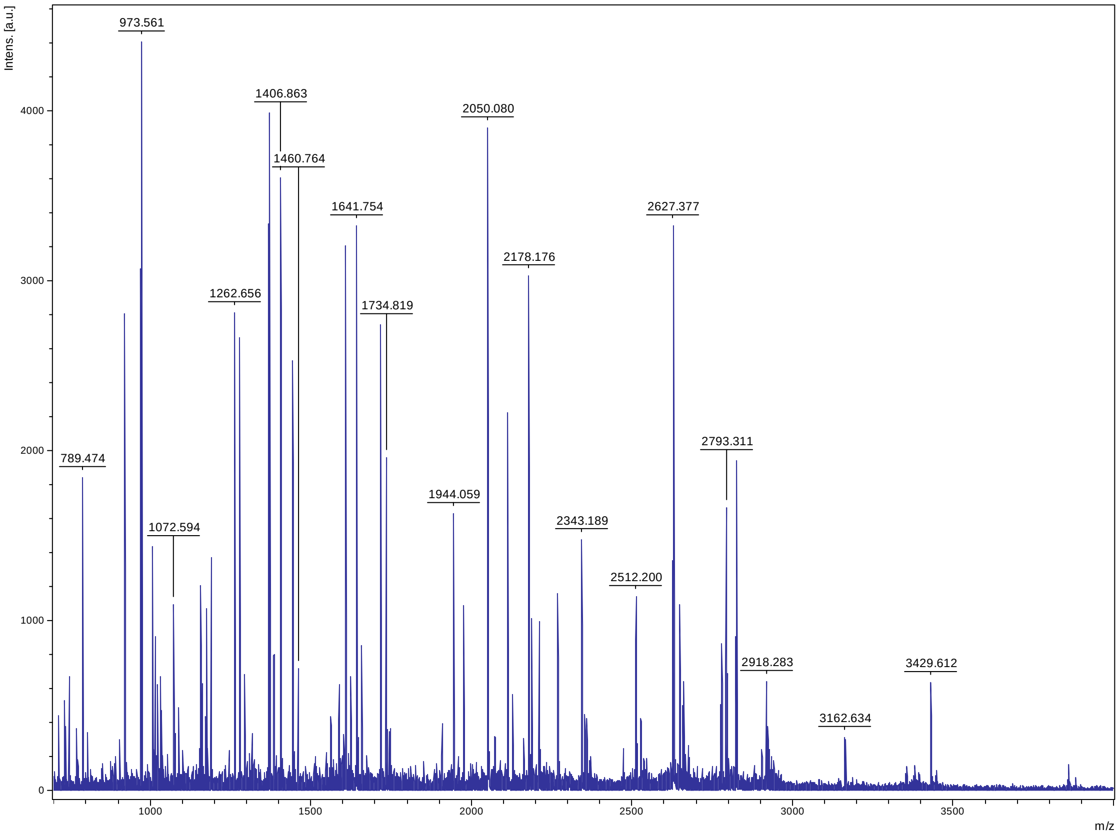


Match to: gi|50930099 Score: 177 Expect: 1.3e-13

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
19 - 38	2132.1197	2131.1124	2131.1465	-0.0341	0	R.WLAAAFFSSVDVAIVAGLPR.V	Acetyl (N-term)
45 - 58	1513.7661	1512.7588	1512.6602	0.0987	0	R.DAPTCGMWGPHVSR.C	
87 - 106	2313.1862	2312.1789	2312.1437	0.0353	0	R.SLIAWNVNDQDTSLFLYASR.D	
107 - 123	1803.8428	1802.8355	1802.7893	0.0462	0	R.DATMHVSDGAIHGYDSK.I	
124 - 140	1890.9597	1889.9524	1889.9370	0.0154	0	K.IELEPEHASLPDNVAEK.F	
124 - 145	2551.3464	2550.3391	2550.3118	0.0274	1	K.IELEPEHASLPDNVAEKFPFIR.S	
164 - 176	1447.7058	1446.6985	1446.6674	0.0312	0	K.CQLAVASYDAHGR.H	Carbamidomethyl (C)
207 - 221	1761.9167	1760.9094	1760.8733	0.0361	0	K.DVDLYLWAPTAQDVR.V	
222 - 239	1991.0162	1990.0089	1990.0233	-0.0144	0	R.VCFYDGPAGPLLQTVQLK.E	Acetyl (N-term)
240 - 251	1356.7150	1355.7077	1355.7197	-0.0120	0	K.ELNGVWSVTVPR.Y	
252 - 263	1667.8285	1666.8212	1666.7991	0.0222	1	R.YRENQYYLYEVK.V	
275 - 283	1080.4097	1079.4024	1079.4706	-0.0682	0	K.CLADDPYAR.G	Carbamidomethyl (C)
332 - 345	1610.6838	1609.6765	1609.6427	0.0338	0	R.DFSAHDSTVDCNSR.G	Carbamidomethyl (C)
350 - 360	1212.5682	1211.5609	1211.5934	-0.0325	0	R.AFTFQDSAGIR.H	
402 - 435	3796.8977	3795.8904	3795.8420	0.0485	0	K.LPPGSDEQQAAIVSIQQEDPYNWGYDPVLWGVPK.G	
436 - 447	1207.4965	1206.4892	1206.5265	-0.0373	0	K.GSYASNPDGPSR.I	
453 - 460	959.4373	958.4300	958.5018	-0.0718	0	R.QMVQALNR.I	
489 - 496	980.4796	979.4723	979.5491	-0.0767	0	K.IVPGYYLR.R	
498 - 521	2649.2210	2648.2137	2648.1707	0.0431	0	R.NVNGQIENSAAMNNTASEHFMVDR.L	
498 - 521	2665.1912	2664.1839	2664.1656	0.0184	0	R.NVNGQIENSAAMNNTASEHFMVDR.L	Oxidation (M)
574 - 590	1988.9830	1987.9757	1987.9315	0.0442	0	K.IYLYGEGWDFGEVAQNK.R	
574 - 591	2145.0954	2144.0881	2144.0326	0.0555	1	K.IYLYGEGWDFGEVAQNKR.G	
592 - 611	2039.0040	2037.9967	2037.9537	0.0430	0	R.GINASQINMSGTGIGSFNDR.I	
592 - 611	2055.0172	2054.0099	2053.9486	0.0613	0	R.GINASQINMSGTGIGSFNDR.I	Oxidation (M)
614 - 650	3960.8727	3959.8654	3959.7985	0.0669	0	R.DSVNGGNPFGNPLQQGFSTGLFLEPNGYYQGNEADTR.R	
651 - 669	2083.1583	2082.1510	2082.1221	0.0289	1	R.RELATYADHIQIGLAGNLK.D	
652 - 669	1927.0475	1926.0402	1926.0210	0.0192	0	R.ELATYADHIQIGLAGNLK.D	
723 - 732	1072.5482	1071.5409	1071.5812	-0.0402	0	K.TPIGLSIDEK.C	
723 - 734	1430.6544	1429.6471	1429.7235	-0.0764	1	K.TPIGLSIDEKCR.I	Acetyl (N-term); Carbamidomethyl (C)
735 - 760	2853.5111	2852.5038	2852.4642	0.0396	0	R.INHLASSMIALSQGIPFFHAGDEILR.S	Oxidation (M)
767 - 794	3292.5288	3291.5215	3291.4897	0.0319	1	R.DSYNSGDWFNKLDFTYETNNWGVGLPPR.D	
778 - 794	1978.9854	1977.9781	1977.9584	0.0197	0	K.LDFTYETNNWGVGLPPR.D	
795 - 807	1678.8997	1677.8924	1677.8587	0.0338	1	R.DKNEENWHLIKPR.L	
797 - 807	1435.7536	1434.7463	1434.7368	0.0096	0	K.NEENWHLIKPR.L	
808 - 817	1200.6450	1199.6377	1199.6662	-0.0285	0	R.LENPSFRPLK.N	
818 - 832	1773.9633	1772.9560	1772.9461	0.0100	0	K.NHILSVFDNFVDILK.I	
842 - 851	1119.5175	1118.5102	1118.5567	-0.0465	0	R.LSTASDIEQR.V	
854 - 871	1971.9996	1970.9923	1970.9957	-0.0034	0	R.FHNTGPSMVPGVIVMSIK.D	Acetyl (N-term); Oxidation (M)
944 - 953	1174.6285	1173.6212	1173.6618	-0.0406	1	R.RTTAVFVQPR.C	
945 - 953	1018.5084	1017.5011	1017.5607	-0.0596	0	R.TTAVFVQPR.C	

Spot 1196

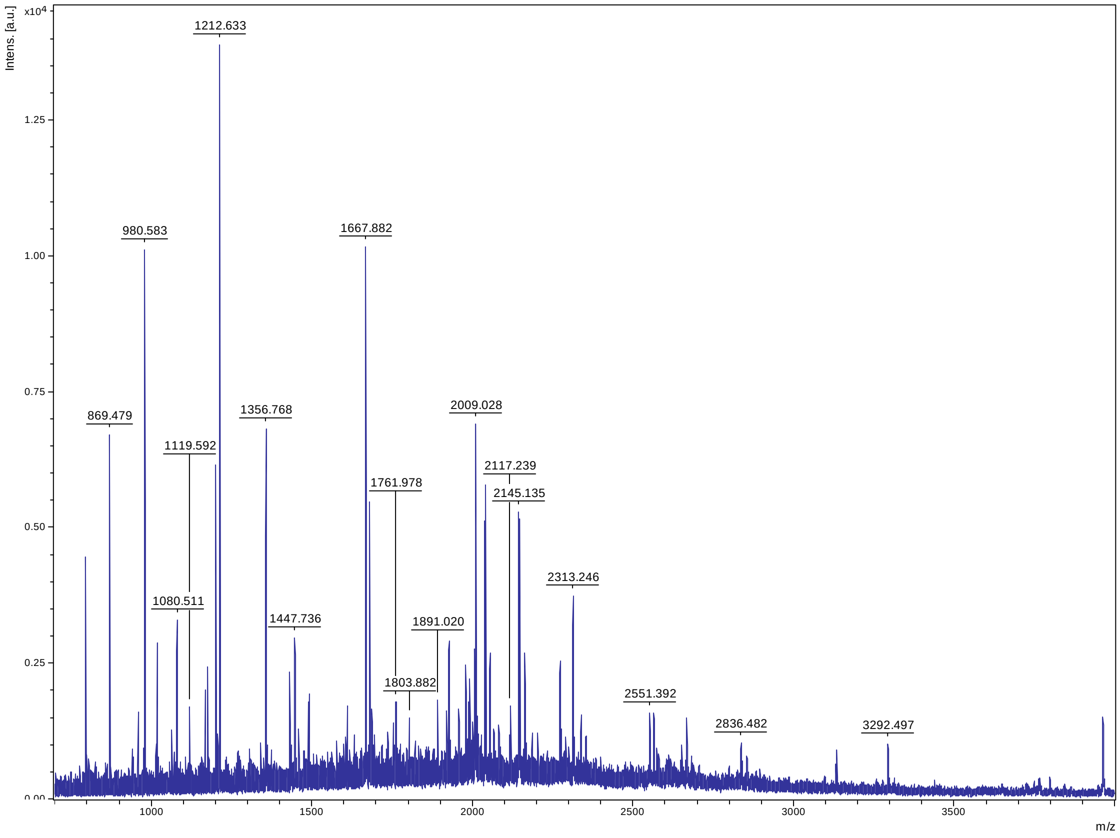


Match to: gi|50878307 Score: 165 Expect: 2.1e-12

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 6	734.2758	733.2685	733.3428	-0.0743	0	-.MPSVSR.A	Acetyl (N-term); Oxidation (M)
49 - 64	1527.7592	1526.7519	1526.7007	0.0512	1	R.SGSGGSARGGHCSPLR.A	Acetyl (N-term)
156 - 168	1406.8801	1405.8728	1405.8405	0.0323	0	R.LGDPARPLLLSVR.S	
169 - 198	2903.3825	2902.3752	2902.4237	-0.0485	0	R.SGAAVSMPGMMDTVLNLGLNDEVAAGLAAK.S	
203 - 209	921.3396	920.3323	920.4028	-0.0705	0	R.FAYDSYR.R	
211 - 230	2352.1493	2351.1420	2351.1329	0.0091	0	R.FLDMFGNVVMDIPHALFEEK.L	
211 - 235	2924.4480	2923.4407	2923.4321	0.0086	1	R.FLDMFGNVVMDIPHALFEEKLEAMK.A	
276 - 293	2072.1409	2071.1336	2071.1214	0.0122	1	K.KQLQLAVLAVFNSWDSPR.A	
277 - 293	1944.0712	1943.0639	1943.0264	0.0375	0	K.QLQLAVLAVFNSWDSPR.A	
308 - 333	2659.3088	2658.3015	2658.2893	0.0122	0	K.GTAVNVQTMVFGNMGNTSGTGVLFTR.N	
308 - 333	2675.3030	2674.2957	2674.2842	0.0115	0	K.GTAVNVQTMVFGNMGNTSGTGVLFTR.N	Oxidation (M)
341 - 360	2178.1880	2177.1807	2177.1479	0.0328	1	K.KLYGEFLVNAQGEDVVAGIR.T	
342 - 360	2050.0821	2049.0748	2049.0530	0.0218	0	K.LYGEFLVNAQGEDVVAGIR.T	
361 - 384	2918.2739	2917.2666	2917.2568	0.0098	1	R.TPEDLDAMRDHMPEPYEELVENCK.I	Carbamidomethyl (C)
361 - 384	2934.2204	2933.2131	2933.2517	-0.0386	1	R.TPEDLDAMRDHMPEPYEELVENCK.I	Carbamidomethyl (C); Oxidation (M)
385 - 404	2512.1881	2511.1808	2511.1773	0.0035	1	K.ILESHYKEMMDIEFTVQENR.L	
385 - 404	2528.1973	2527.1900	2527.1722	0.0178	1	K.ILESHYKEMMDIEFTVQENR.L	Oxidation (M)
385 - 404	2544.1588	2543.1515	2543.1672	-0.0156	1	K.ILESHYKEMMDIEFTVQENR.L	2 Oxidation (M)
392 - 404	1641.7666	1640.7593	1640.7174	0.0419	0	K.EMMDIEFTVQENR.L	
392 - 404	1673.7776	1672.7703	1672.7072	0.0631	0	K.EMMDIEFTVQENR.L	2 Oxidation (M)
405 - 411	1006.4495	1005.4422	1005.4888	-0.0466	0	R.LWMLQCR.T	Carbamidomethyl (C)
405 - 411	1022.4581	1021.4508	1021.4837	-0.0329	0	R.LWMLQCR.T	Carbamidomethyl (C); Oxidation (M)
423 - 435	1444.7677	1443.7604	1443.7391	0.0213	0	K.IAVDMVNEGLVER.R	
423 - 435	1460.7675	1459.7602	1459.7340	0.0262	0	K.IAVDMVNEGLVER.R	Oxidation (M)
423 - 436	1600.8816	1599.8743	1599.8402	0.0341	1	K.IAVDMVNEGLVERR.T	
441 - 462	2536.1773	2535.1700	2535.2216	-0.0515	0	K.MVEPGHLDQLLHPQFENPSGYK.D	
503 - 523	2112.0684	2111.0611	2111.0316	0.0295	0	R.TETSPEDVGGMHAAVGILTAR.G	
503 - 523	2128.0312	2127.0239	2127.0266	-0.0026	0	R.TETSPEDVGGMHAAVGILTAR.G	Oxidation (M)
584 - 606	2647.2596	2646.2523	2646.2458	0.0066	0	K.QPLCPPALSGDLETFMSWVDEVR.K	Carbamidomethyl (C)
610 - 624	1562.7393	1561.7320	1561.7042	0.0278	0	K.VMANADTPEDATTAR.Q	
625 - 635	1174.5646	1173.5573	1173.5560	0.0013	0	R.QNGAEGIGLCR.T	Carbamidomethyl (C)
636 - 646	1385.6002	1384.5929	1384.5717	0.0212	0	R.TEHMFFASDER.I	Oxidation (M)
652 - 662	1294.6495	1293.6422	1293.6421	0.0002	0	R.QMIMASSLELR.Q	Oxidation (M)
683 - 692	1072.5575	1071.5502	1071.5746	-0.0244	0	R.AMDGLPVTIR.L	
693 - 712	2343.1911	2342.1838	2342.1728	0.0110	0	R.LLDPPLHEFLPEGHVEDMVR.E	
693 - 712	2359.1763	2358.1690	2358.1678	0.0013	0	R.LLDPPLHEFLPEGHVEDMVR.E	Oxidation (M)
713 - 728	1734.8443	1733.8370	1733.7890	0.0480	0	R.ELCSETGAAQDDVLAR.V	Carbamidomethyl (C)
732 - 742	1262.6650	1261.6577	1261.6488	0.0089	0	K.LSEVNPMLGFR.G	
746 - 759	1607.8611	1606.8538	1606.8024	0.0514	0	R.LGISYPELTEMQAR.A	
816 - 824	1015.5289	1014.5216	1014.5532	-0.0315	0	K.VGTMIEIPR.A	
904 - 922	1974.9979	1973.9906	1973.9668	0.0238	0	K.VGICGEHGGEPLSVAFFAK.A	Carbamidomethyl (C)
923 - 939	1907.9746	1906.9673	1906.9723	-0.0050	1	K.AGLDYVSCSPFRVPIAR.L	Carbamidomethyl (C)

Spot 1197

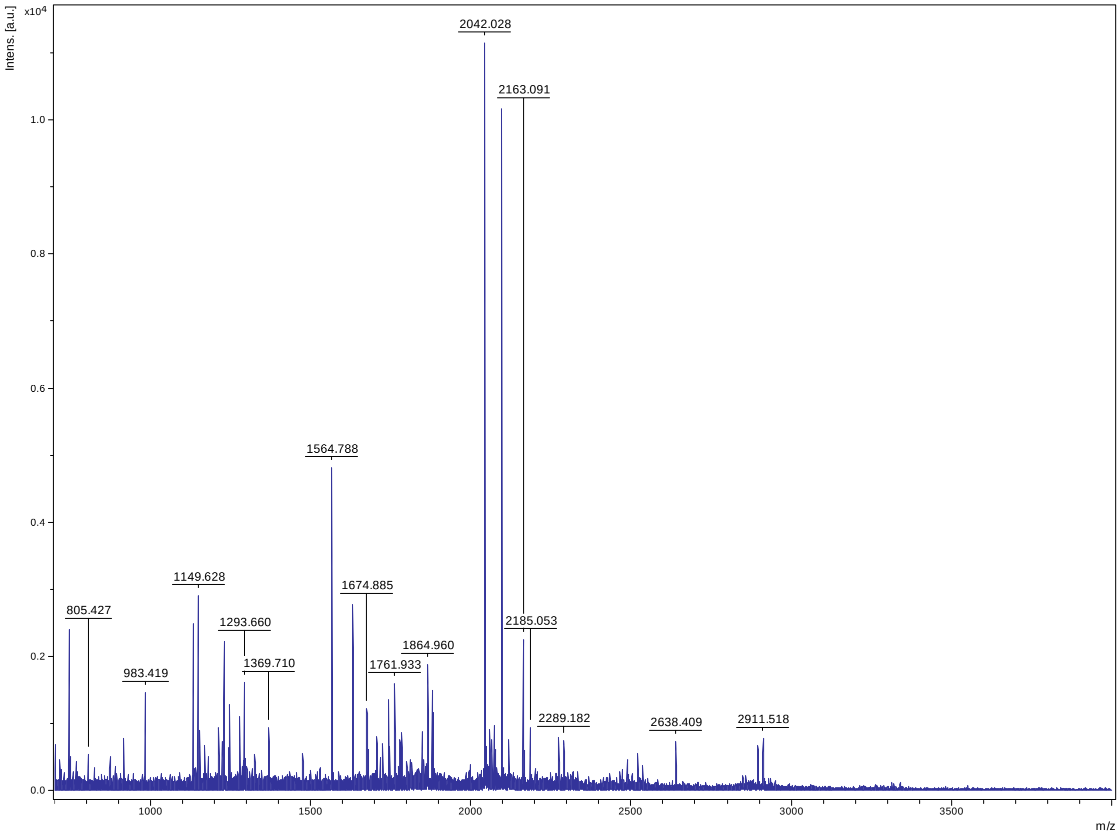


Match to: gi|50930099 Score: 150 Expect: 6.7e-11

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
87 - 106	2313.2456	2312.2383	2312.1437	0.0947	0	R.SLIAWNVNDQDTSLFLYASR.D	
124 - 140	1891.0195	1890.0123	1889.9370	0.0752	0	K.IELEPEHASLPDNVAEK.F	
124 - 145	2551.3921	2550.3848	2550.3118	0.0731	1	K.IELEPEHASLPDNVAEKFPFIR.S	
152 - 163	1200.6992	1199.6919	1199.6761	0.0158	0	R.VPSSVDVASLVK.C	
164 - 176	1447.7360	1446.7287	1446.6674	0.0613	0	K.CQLAVASYDAHGR.H	Carbamidomethyl (C)
207 - 221	1761.9781	1760.9709	1760.8733	0.0976	0	K.DVDLYLWAPTAQDVR.V	
207 - 221	1803.8820	1802.8747	1802.8839	-0.0092	0	K.DVDLYLWAPTAQDVR.V	Acetyl (N-term)
222 - 239	2006.1146	2005.1073	2005.0342	0.0731	0	R.VCFYDGPAGPLLQTVQLK.E	Carbamidomethyl (C)
240 - 251	1356.7678	1355.7605	1355.7197	0.0408	0	K.ELNGVWSVTVPR.Y	
252 - 263	1667.8822	1666.8749	1666.7991	0.0759	1	R.YRENQYYLYEVK.V	
275 - 283	1080.5106	1079.5033	1079.4706	0.0328	0	K.CLADDPYAR.G	Carbamidomethyl (C)
332 - 345	1610.7153	1609.7081	1609.6427	0.0654	0	R.DFSAHDSTVDCNSR.G	Carbamidomethyl (C)
350 - 360	1212.6326	1211.6253	1211.5934	0.0318	0	R.AFTFQDSAGIR.H	
436 - 447	1207.5654	1206.5582	1206.5265	0.0317	0	K.GSYASNPDGPSR.I	
453 - 460	959.5280	958.5207	958.5018	0.0189	0	R.QMVQALNR.I	
453 - 460	975.5393	974.5320	974.4967	0.0353	0	R.QMVQALNR.I	Oxidation (M)
489 - 496	980.5827	979.5754	979.5491	0.0264	0	K.IVPGYYLR.R	
574 - 590	1989.0208	1988.0135	1987.9315	0.0820	0	K.IYLYGEGWDFGEVAQNK.R	
574 - 591	2145.1353	2144.1280	2144.0326	0.0954	1	K.IYLYGEGWDFGEVAQNKR.G	
652 - 669	1927.0967	1926.0894	1926.0210	0.0684	0	R.ELATYADHIQIGLAGNLK.D	
723 - 732	1072.6217	1071.6144	1071.5812	0.0333	0	K.TPIGLSIDEK.C	
723 - 734	1430.7051	1429.6978	1429.7235	-0.0257	1	K.TPIGLSIDEKCR.I	Acetyl (N-term); Carbamidomethyl (C)
767 - 794	3292.4973	3291.4900	3291.4897	0.0004	1	R.DSYNSGDWFNKLDFTYETNNWGVGLPPR.D	
778 - 794	1979.0348	1978.0275	1977.9584	0.0691	0	K.LDFTYETNNWGVGLPPR.D	
795 - 807	1678.9416	1677.9344	1677.8587	0.0757	1	R.DKNEENWHLIKPR.L	
835 - 841	869.4790	868.4717	868.4443	0.0275	0	R.YSSPLFR.L	
842 - 851	1119.5917	1118.5844	1118.5567	0.0277	0	R.LSTASDIEQR.V	
944 - 953	1174.6990	1173.6917	1173.6618	0.0299	1	R.RTTAVFVQPR.C	
945 - 953	1018.5923	1017.5850	1017.5607	0.0243	0	R.TTAVFVQPR.C	

Spot 1198

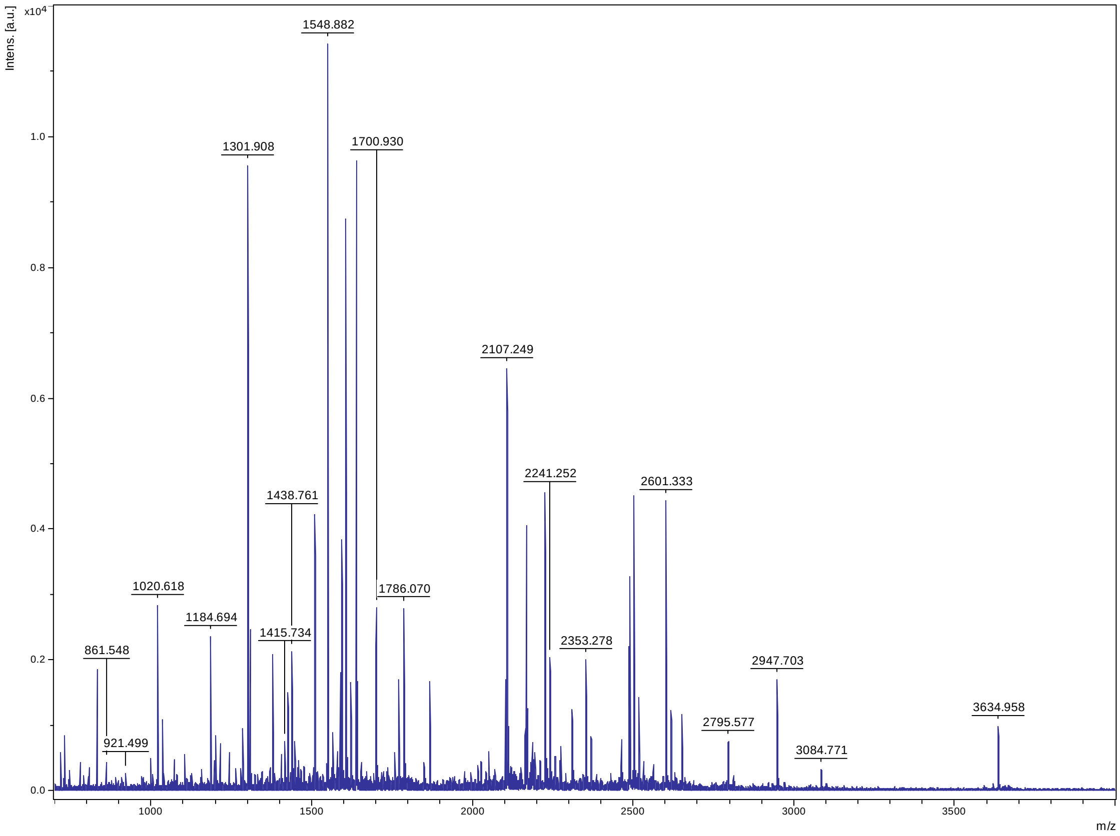


Match to: gi|51090952 Score: 269 Expect: 1.3e-23

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
51 - 72	2488.2319	2487.2247	2487.1964	0.0282	0	R.HSDGLPHLNQAEEATWMGLLPR.R	Oxidation (M)
74 - 87	1674.8853	1673.8780	1673.8525	0.0255	1	R.AGPRDELDWLALYR.S	
78 - 87	1293.6597	1292.6524	1292.6401	0.0123	0	R.DELDWLALYR.S	
92 - 113	2095.0576	2094.0503	2094.0129	0.0374	0	R.GGGDVGGEPAGFLSPASLHDVR.V	
151 - 169	2042.0276	2041.0203	2040.9904	0.0299	0	K.LPTVGEPYGGWEAPDGQLR.G	
199 - 208	1224.6372	1223.6299	1223.6220	0.0080	0	K.VVDILYSCQK.K	Carbamidomethyl (C)
242 - 257	1761.9335	1760.9262	1760.9131	0.0131	0	K.IMQGLLDQYTLAGNPK.G	
242 - 257	1777.9369	1776.9296	1776.9080	0.0216	0	K.IMQGLLDQYTLAGNPK.G	Oxidation (M)
275 - 284	1277.7172	1276.7099	1276.7139	-0.0040	1	K.KLIQEYSIQR.H	
276 - 284	1149.6276	1148.6203	1148.6189	0.0013	0	K.LIQEYSIQR.H	
353 - 363	1369.7101	1368.7028	1368.7037	-0.0009	1	K.RYEVVGDQLYK.E	
354 - 363	1213.6185	1212.6113	1212.6026	0.0087	0	R.YEVVGDQLYK.E	
402 - 416	1742.8546	1741.8473	1741.8192	0.0281	0	K.ISSNEETCATYNLLK.V	Carbamidomethyl (C)
430 - 436	983.4193	982.4120	982.4144	-0.0025	0	K.YTDHYER.L	
437 - 447	1228.6736	1227.6663	1227.6757	-0.0094	0	R.LLINGIMGNQR.G	
437 - 447	1244.6730	1243.6657	1243.6706	-0.0049	0	R.LLINGIMGNQR.G	Oxidation (M)
448 - 464	1848.9689	1847.9616	1847.9425	0.0191	1	R.GKEPGVMIYFLPMGPGR.S	
448 - 464	1864.9600	1863.9527	1863.9375	0.0152	1	R.GKEPGVMIYFLPMGPGR.S	Oxidation (M)
448 - 464	1880.9478	1879.9405	1879.9324	0.0081	1	R.GKEPGVMIYFLPMGPGR.S	2 Oxidation (M)
563 - 573	1168.6213	1167.6141	1167.6108	0.0033	0	K.GDARPANVNVR.I	
606 - 615	1147.5936	1146.5864	1146.5921	-0.0057	0	K.LWGDDTLSLK.F	
743 - 759	1631.7963	1630.7890	1630.7699	0.0191	0	R.AYHSPSGASAIDAATGR.L	
764 - 791	2895.5188	2894.5115	2894.4708	0.0407	0	R.DVALEPFDRPGMAVTDALSVGRPGPATR.F	
764 - 791	2911.5178	2910.5105	2910.4657	0.0448	0	R.DVALEPFDRPGMAVTDALSVGRPGPATR.F	Oxidation (M)
836 - 852	1722.7678	1721.7605	1721.7492	0.0113	0	R.KPTAAGGGEDDDDTAFR.R	
836 - 853	1878.8820	1877.8747	1877.8503	0.0244	1	R.KPTAAGGGEDDDDTAFRR.A	
853 - 864	1288.6746	1287.6673	1287.7047	-0.0374	1	R.RAASFTQAAPLR.L	
854 - 864	1132.6162	1131.6089	1131.6036	0.0053	0	R.AASFTQAAPLR.L	
865 - 878	1564.7880	1563.7807	1563.7681	0.0126	0	R.LYHPLSFSATGTDR.N	

Spot 1202

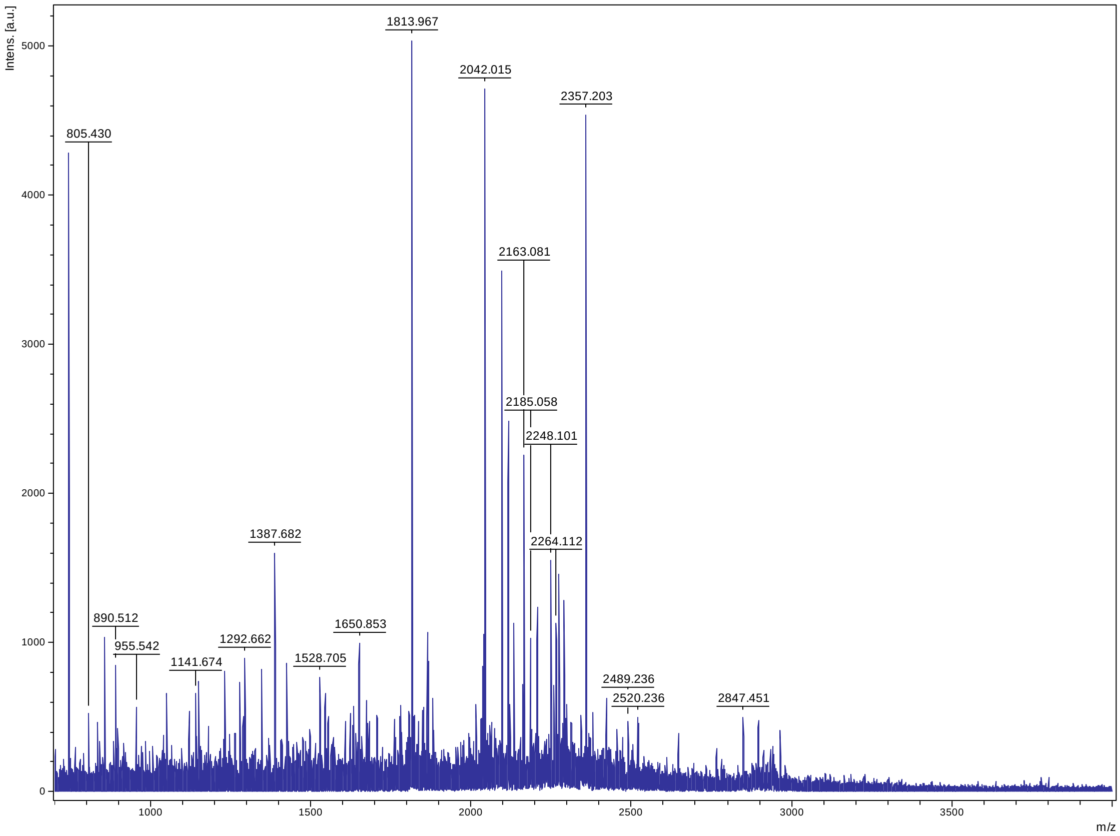


Match to: gi|13195430 Score: 304 Expect: 5.3e-26

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
8 - 36	2947.7031	2946.6959	2946.4669	78	0	R.GVQGSVSPEEEISSVLNSIDSSTIASNIK.H	
62 - 80	2353.2780	2352.2707	2352.0732	84	0	K.SVLDTLIMNWNATYDYYDR.T	
62 - 84	2795.5773	2794.5700	2794.3272	87	1	K.SVLDTLIMNWNATYDYYDRTNVK.Q	
85 - 97	1588.8879	1587.8806	1587.7392	89	0	K.QAYYLSMEFLQGR.A	Gln->pyro-Glu (N-term Q)
85 - 97	1605.9169	1604.9096	1604.7657	90	0	K.QAYYLSMEFLQGR.A	
167 - 176	1184.6940	1183.6867	1183.7077	-18	1	K.HGLFKQIITK.D	
172 - 197	3084.7708	3083.7635	3083.5022	85	1	K.QIITKDGQEEVAENWLEMGNPWEIVR.T	
177 - 197	2501.3504	2500.3431	2500.1329	84	0	K.DGQEEVAENWLEMGNPWEIVR.T	
242 - 247	718.4656	717.4583	717.3769	113	0	K.TTNNLR.L	
248 - 280	3634.9582	3633.9509	3633.6648	79	0	R.LWSTTVPSQDFDLEAFNAGDHASAYEAHLNAEK.I	
299 - 316	2109.3048	2108.2975	2108.0936	97	1	R.LKQQYTLCSASLQDIIAR.F	Carboxymethyl (C)
301 - 319	2225.2689	2224.2616	2224.0946	75	1	K.QQYTLCSASLQDIIARFER.R	Gln->pyro-Glu (N-term Q)
321 - 333	1438.7610	1437.7538	1437.6412	78	0	R.AGDSLSWEDFPSK.V	
359 - 371	1548.8824	1547.8751	1547.7368	89	0	K.GLSWNEAWSITER.T	
372 - 387	1786.0697	1785.0624	1784.9308	74	0	R.TVAYTNHTVLPEALEK.W	
388 - 395	1020.6175	1019.6103	1019.5110	97	0	K.WSLDIMQK.L	
436 - 448	1426.8910	1425.8838	1425.7715	79	0	R.ILDNIDLPDSIAK.L	
471 - 481	1215.7430	1214.7357	1214.6394	79	0	K.SLEPSVVVEEK.T	
595 - 612	2103.2271	2102.2198	2102.0684	72	1	K.WIGSDDWVLNTDKLAELK.K	
613 - 625	1638.8885	1637.8812	1637.7321	91	1	K.KFADDEDLQSEWR.A	
614 - 625	1510.7778	1509.7705	1509.6372	88	0	K.FADDEDLQSEWR.A	
641 - 658	2027.1710	2026.1637	2026.0081	77	1	R.EKTGYIVSPDAMFDVQVK.R	
643 - 658	1770.0192	1769.0119	1768.8706	80	0	K.TGYIVSPDAMFDVQVK.R	
666 - 676	1284.8866	1283.8793	1283.7601	93	0	R.QLLNILGIVYR.Y	Gln->pyro-Glu (N-term Q)
666 - 676	1301.9077	1300.9004	1300.7867	87	0	R.QLLNILGIVYR.Y	
687 - 695	1103.7009	1102.6936	1102.5883	95	1	K.DRINSFVPR.V	
689 - 695	832.5579	831.5506	831.4603	109	0	R.INSFVPR.V	
689 - 702	1594.8916	1593.8843	1593.8337	32	1	R.INSFVPRVCIFGGK.A	Carboxymethyl (C)
703 - 711	998.6255	997.6183	997.5233	95	0	K.AFATYVQAK.R	
716 - 735	2168.2822	2167.2749	2167.1161	73	0	K.FITDVAATVNHDPEIGDLLK.V	
775 - 794	2107.2493	2106.2421	2106.0602	86	0	K.FAMNGCILIGTLDGANVEIR.E	
795 - 816	2464.3854	2463.3781	2463.1706	84	0	R.EEVGEENFFLFGAEAHEIAGLR.K	
824 - 829	730.4733	729.4660	729.3810	117	0	K.FVPDPR.F	
830 - 835	807.5248	806.5176	806.4286	110	1	R.FEEVKR.F	
839 - 862	2601.3331	2600.3258	2600.1125	82	0	R.SGVFGTYNYDDLMGSLEGNEGYGR.A	
871 - 884	1700.9304	1699.9232	1699.7763	86	1	K.DFPSYIECQEKVDK.A	
895 - 910	1757.9279	1756.9207	1756.8414	45	1	R.MSILNTASSSKFNSDR.T	
911 - 917	861.5482	860.5409	860.4392	118	0	R.TIHEYAK.D	
918 - 928	1308.8492	1307.8420	1307.7489	71	0	K.DIWDIKPVILP.-	

Spot 1203

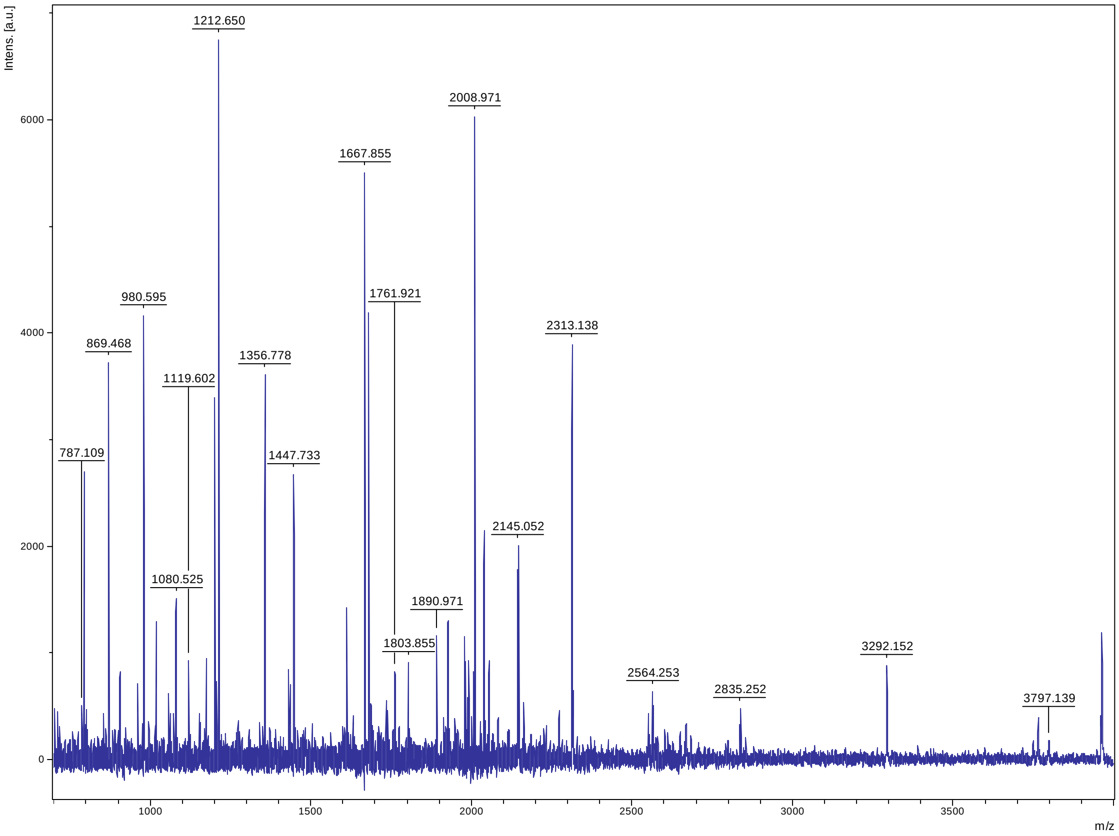


Match to: gi|38344860; Score: 163 Expect: 2.4e-11

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 10	1120.63	1119.62	1119.63	-0.00	1	VKFTVEELR
4 - 11	1049.58	1048.58	1048.57	0.01	1	FTVEELRR
33 - 55	2257.18	2256.18	2256.20	-0.02	0	STLTDSLVAAAGIIAQEVAGDVR
151 - 159	1039.64	1038.64	1038.65	-0.02	0	IRPVLTVNK
163 - 180	2206.04	2205.03	2205.00	0.03	0	CFLELQVEGEEAYQTFSR
244 - 255	1424.69	1423.69	1423.68	0.01	0	LWGENFFDPATK
244 - 256	1552.78	1551.78	1551.77	0.01	1	LWGENFFDPATKK
269 - 280	1543.78	1542.78	1542.77	0.02	1	RGFVQFCYEPIK
270 - 280	1387.68	1386.68	1386.66	0.02	0	GFVQFCYEPIK
349 - 368	2357.20	2356.20	2356.17	0.03	1	YRVENLYEGPLDDVYATAIR
351 - 368	2038.03	2037.03	2037.01	0.03	0	VENLYEGPLDDVYATAIR
432 - 438	834.46	833.46	833.45	0.01	0	TVIWMGK
472 - 482	1277.72	1276.71	1276.59	0.12	1	EADACPIRAMK Oxidation (M)
483 - 490	890.51	889.51	889.50	0.01	0	FSVSPVVR
544 - 565	2422.20	2421.19	2421.19	0.00	0	DLQEDFMGGAEIIVSPPVVSFR Oxidation (M)
587 - 606	2248.10	2247.10	2247.08	0.01	0	LYMEARPLEEGLAEAIDDGR
587 - 606	2264.11	2263.11	2263.08	0.03	0	LYMEARPLEEGLAEAIDDGR Oxidation (M)
619 - 632	1650.85	1649.85	1649.83	0.02	1	ILSEEFGWDKDLAK
662 - 673	1294.66	1293.65	1293.64	0.02	0	DSVVAGFQWASK
702 - 711	955.54	954.54	954.52	0.02	0	GGGQVIPTAR
713 - 724	1346.78	1345.78	1345.77	0.01	0	VIYASQLTAKPR
753 - 770	2116.08	2115.08	2115.06	0.03	0	GHVFEEMQRPGTPLYNIK
753 - 770	2132.07	2131.07	2131.05	0.02	0	GHVFEEMQRPGTPLYNIK Oxidation (M)
771 - 786	1813.97	1812.96	1812.94	0.02	0	AYLPVIESFGFSSQLR

Spot 1213

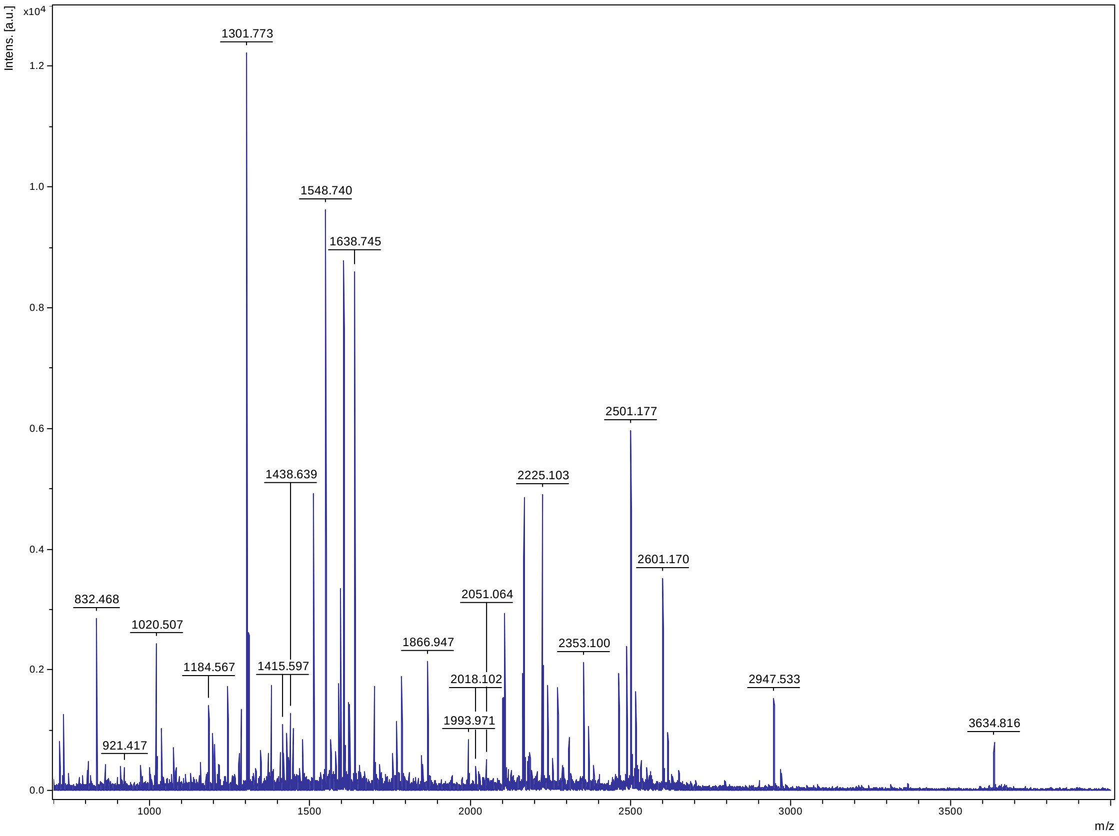


Match to: gi|50930099 Score: 181 Expect: 5.3e-14

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
81 - 86	795.3319	794.3246	794.4075	-0.0829	0	R.AYWVTR.S	
87 - 106	2313.1133	2312.1060	2312.1437	-0.0376	0	R.SLIAWNVNDQDTSLFLYASR.D	
107 - 123	1803.8219	1802.8146	1802.7893	0.0253	0	R.DATMHVSDGAIHGYDSK.I	
124 - 140	1890.9245	1889.9172	1889.9370	-0.0198	0	K.IELEPEHASLPDNVAEK.F	
152 - 163	1200.6940	1199.6867	1199.6761	0.0106	0	R.VPSSVDVASLVK.C	
207 - 221	1761.9006	1760.8933	1760.8733	0.0200	0	K.DVDLYLWAPTAQDVR.V	
240 - 251	1356.7431	1355.7358	1355.7197	0.0161	0	K.ELNGVWSVTVPR.Y	
252 - 263	1667.8212	1666.8139	1666.7991	0.0149	1	R.YRENQYYLYEVK.V	
275 - 283	1080.4622	1079.4549	1079.4706	-0.0157	0	K.CLADDPYAR.G	Carbamidomethyl (C)
332 - 345	1610.6633	1609.6560	1609.6427	0.0133	0	R.DFSAHDSTVDCNSR.G	Carbamidomethyl (C)
350 - 360	1212.6135	1211.6062	1211.5934	0.0128	0	R.AFTFQDSAGIR.H	
436 - 447	1207.5627	1206.5554	1206.5265	0.0289	0	K.GSYASNPDGPSR.I	
489 - 496	980.5409	979.5336	979.5491	-0.0154	0	K.IVPGYYLR.R	
574 - 590	1988.9319	1987.9246	1987.9315	-0.0069	0	K.IYLYGEGWDFGEVAQNK.R	
574 - 591	2145.0246	2144.0173	2144.0326	-0.0153	1	K.IYLYGEGWDFGEVAQNKR.G	
592 - 611	2038.9471	2037.9398	2037.9537	-0.0139	0	R.GINASQINMSGTGIGSFNDR.I	
592 - 611	2054.9882	2053.9809	2053.9486	0.0323	0	R.GINASQINMSGTGIGSFNDR.I	Oxidation (M)
652 - 669	1927.0072	1925.9999	1926.0210	-0.0211	0	R.ELATYADHIQIGLAGNLK.D	
723 - 734	1430.6764	1429.6691	1429.7235	-0.0544	1	K.TPIGLSIDEKCR.I	Acetyl (N-term); Carbamidomethyl (C)
778 - 794	1978.9676	1977.9603	1977.9584	0.0019	0	K.LDFTYETNNWGVGLPPR.D	
795 - 807	1678.8929	1677.8856	1677.8587	0.0270	1	R.DKNEENWHLIKPR.L	
835 - 841	869.3900	868.3827	868.4443	-0.0616	0	R.YSSPLFR.L	
842 - 851	1119.5702	1118.5629	1118.5567	0.0062	0	R.LSTASDIEQR.V	
944 - 953	1174.6768	1173.6695	1173.6618	0.0077	1	R.RTTAVFVQPR.C	
945 - 953	1018.5455	1017.5382	1017.5607	-0.0225	0	R.TTAVFVQPR.C	

Spot 1214

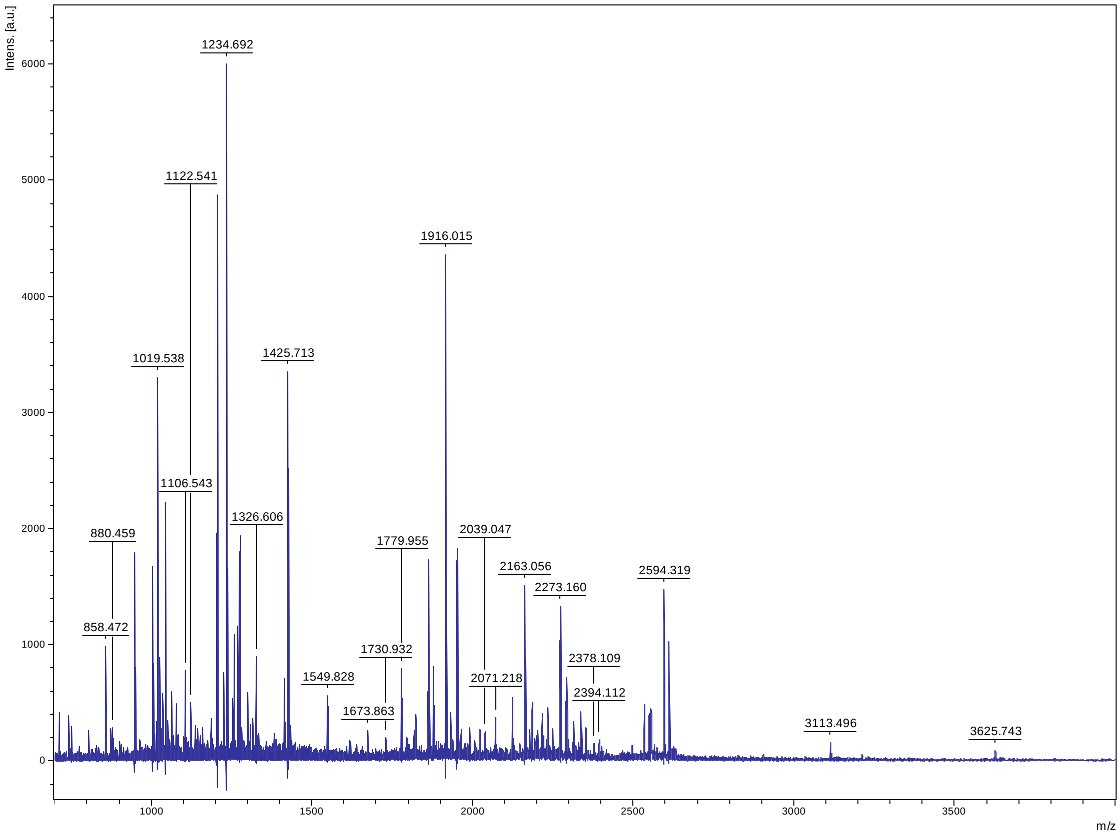


Match to: gi|13195430 Score: 327 Expect: 1.1e-27

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
8 - 36	2947.5564	2946.5491	2946.4669	28	0	R.GVQGSVSPEEEISSVLNSIDSSTIASNIK.H	
62 - 80	2353.1202	2352.1130	2352.0732	17	0	K.SVLDTLIMNWNATYDYYDR.T	
62 - 80	2369.1036	2368.0964	2368.0681	12	0	K.SVLDTLIMNWNATYDYYDR.T	Oxidation (M)
85 - 97	1588.7571	1587.7498	1587.7392	7	0	K.QAYYLSMEFLQGR.A	Gln->pyro-Glu (N-term Q)
85 - 97	1605.7850	1604.7777	1604.7657	8	0	K.QAYYLSMEFLQGR.A	
85 - 97	1621.7712	1620.7639	1620.7606	2	0	K.QAYYLSMEFLQGR.A	Oxidation (M)
143 - 164	2488.2812	2487.2739	2487.2256	19	0	R.LASCFLDSLATLNYPAWGYGLR.Y	
177 - 197	2501.1952	2500.1880	2500.1329	22	0	K.DGQEEVAENWLEMGNPWEIVR.T	
177 - 197	2517.1904	2516.1831	2516.1278	22	0	K.DGQEEVAENWLEMGNPWEIVR.T	Oxidation (M)
198 - 205	908.4795	907.4722	907.4651	8	0	R.TDVSYPVK.F	
218 - 227	1184.5745	1183.5673	1183.5808	-11	0	R.MHWIGGENIK.V	
218 - 227	1200.5740	1199.5667	1199.5757	-7	0	R.MHWIGGENIK.V	Oxidation (M)
228 - 239	1308.7293	1307.7221	1307.7238	-1	0	K.VVAHDIPIPGYK.T	
242 - 247	718.3831	717.3759	717.3769	-1	0	K.TTNNLR.L	
248 - 280	3634.8371	3633.8299	3633.6648	45	0	R.LWSTTVPSQDFDLEAFNAGDHASAYEAHLNAEK.I	
281 - 295	1700.7976	1699.7903	1699.7876	2	0	K.ICHVLYPGDESPEGK.V	
301 - 316	1849.9292	1848.9220	1848.9040	10	0	K.QQYTLCSASLQDIIAR.F	Gln->pyro-Glu (N-term Q)
301 - 316	1866.9588	1865.9515	1865.9305	11	0	K.QQYTLCSASLQDIIAR.F	
320 - 333	1594.7571	1593.7498	1593.7423	5	1	R.RAGDSLSWEDFPSK.V	
321 - 333	1438.6505	1437.6432	1437.6412	1	0	R.AGDSLSWEDFPSK.V	
334 - 352	2225.1213	2224.1140	2224.0803	15	0	K.VAVQMNDTHPTLCIPELMR.I	
334 - 352	2241.1043	2240.0970	2240.0752	10	0	K.VAVQMNDTHPTLCIPELMR.I	Oxidation (M)
359 - 371	1548.7519	1547.7446	1547.7368	5	0	K.GLSWNEAWSITER.T	
372 - 387	1785.9334	1784.9262	1784.9308	-3	0	R.TVAYTNHTVLPEALEK.W	
388 - 395	1020.5154	1019.5082	1019.5110	-3	0	K.WSLDIMQK.L	
388 - 395	1036.5063	1035.4990	1035.5059	-7	0	K.WSLDIMQK.L	Oxidation (M)
407 - 418	1345.7134	1344.7061	1344.7323	-19	0	K.IDGELMNIIISK.Y	
419 - 428	1126.5627	1125.5554	1125.5554	0	0	K.YGTEDTSLLK.K	
436 - 448	1426.7635	1425.7562	1425.7715	-11	0	R.ILDNIDLPDSIAK.L	
471 - 481	1215.6166	1214.6094	1214.6394	-25	0	K.SLEPSVVVEEK.T	
583 - 594	1378.6889	1377.6817	1377.6962	-11	0	R.FCNPELSAIISK.W	
595 - 612	2103.0933	2102.0860	2102.0684	8	1	K.WIGSDDWVLNTDKLAELK.K	
613 - 625	1638.7576	1637.7503	1637.7321	11	1	K.KFADDEDLQSEWR.A	
614 - 625	1510.6495	1509.6423	1509.6372	3	0	K.FADDEDLQSEWR.A	
641 - 658	2027.0166	2026.0093	2026.0081	1	1	R.EKTGYIVSPDAMFDVQVK.R	
643 - 658	1769.8833	1768.8761	1768.8706	3	0	K.TGYIVSPDAMFDVQVK.R	
666 - 676	1284.7567	1283.7495	1283.7601	-8	0	R.QLLNILGIVYR.Y	Gln->pyro-Glu (N-term Q)
666 - 676	1301.7870	1300.7797	1300.7867	-5	0	R.QLLNILGIVYR.Y	
687 - 695	1103.5811	1102.5738	1102.5883	-13	1	K.DRINSFVPR.V	
689 - 695	832.4719	831.4646	831.4603	5	0	R.INSFVPR.V	
703 - 711	998.5367	997.5294	997.5233	6	0	K.AFATYVQAK.R	
716 - 735	2168.1380	2167.1307	2167.1161	7	0	K.FITDVAATVNHDPEIGDLLK.V	
795 - 816	2464.2349	2463.2276	2463.1706	23	0	R.EEVGEENFFLFGAEAHEIAGLR.K	
830 - 835	807.4338	806.4265	806.4286	-3	1	R.FEEVKR.F	
839 - 862	2601.1863	2600.1790	2600.1125	26	0	R.SGVFGTYNYDDLMGSLEGNEGYGR.A	
839 - 862	2617.1785	2616.1712	2616.1075	24	0	R.SGVFGTYNYDDLMGSLEGNEGYGR.A	Oxidation (M)
863 - 881	2309.1102	2308.1029	2308.0722	13	1	R.ADYFLVGKDFPSYIECQEK.V	
871 - 881	1415.6058	1414.5985	1414.6075	-6	0	K.DFPSYIECQEK.V	
871 - 884	1757.8217	1756.8144	1756.7978	9	1	K.DFPSYIECQEKVDK.A	
911 - 917	861.4490	860.4418	860.4392	3	0	R.TIHEYAK.D	

Spot 1216

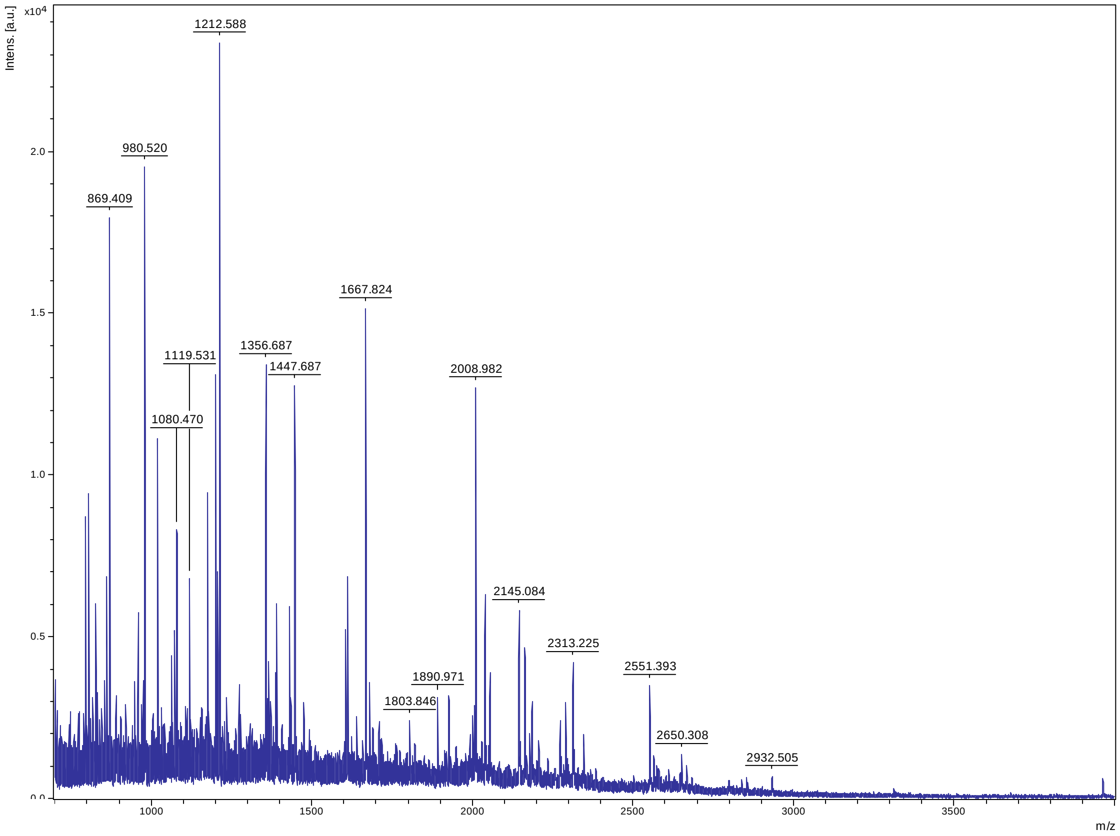


Match to: gi|1196837 Score: 370 Expect: 5.4e-32

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
1 - 12	1334.7006	1333.6933	1333.6408	39	1	-.MGETTGERALNR.L	
18 - 37	2201.0735	2200.0662	2200.1236	-26	1	R.ERIGDSLSAHTNELVAVFSR.L	
20 - 37	1916.0150	1915.0077	1914.9799	15	0	R.IGDSLSAHTNELVAVFSR.L	
20 - 43	2555.5325	2554.5252	2554.3503	68	1	R.IGDSLSAHTNELVAVFSRLVNQGK.G	
44 - 64	2337.1904	2336.1832	2336.1583	11	0	K.GMLQPHQIIAEYNAAIPEGER.E	
44 - 66	2594.3186	2593.3113	2593.2958	6	1	K.GMLQPHQIIAEYNAAIPEGEREK.L	
67 - 77	1258.7086	1257.7013	1257.6928	7	1	K.LKDSALEDVLR.G	
105 - 124	2292.2023	2291.1950	2291.2049	-4	0	R.INVSQLGVEELSVPEYLQFK.E	
125 - 156	3625.7433	3624.7360	3624.7736	-10	0	K.EQLVDGSTQNNFVLELDFEPFNASFPRPSLSK.S	
157 - 167	1204.6533	1203.6460	1203.6360	8	0	K.SIGNGVQFLNR.H	
173 - 188	2023.0541	2022.0468	2022.0397	4	1	K.LFHDKESMYPLLNFLR.A	
178 - 188	1382.7210	1381.7137	1381.7064	5	0	K.ESMYPLLNFLR.A	
194 - 202	1068.4778	1067.4705	1067.4562	13	0	K.GMTMMLNDR.I	
205 - 214	1043.5969	1042.5897	1042.5771	12	0	R.SLDALQGALR.K	
219 - 235	1951.9628	1950.9556	1950.9337	11	0	K.HLAGITADTPYSEFHHR.F	
236 - 243	963.4761	962.4689	962.5073	-40	0	R.FQELGLEK.G	
244 - 251	949.4062	948.3989	948.3872	12	0	K.GWGDCAQR.V	Carbamidomethyl (C)
317 - 325	1106.5435	1105.5362	1105.5260	9	0	R.AMENEMLLR.I	
326 - 336	1267.7576	1266.7504	1266.7408	8	1	R.IKQQGLNITPR.I	
328 - 336	1009.5550	1008.5477	1008.5352	12	0	K.QQGLNITPR.I	Gln->pyro-Glu (N-term Q)
328 - 336	1026.5778	1025.5706	1025.5618	9	0	K.QQGLNITPR.I	
337 - 342	714.4877	713.4804	713.4800	1	0	R.ILIVTR.L	
343 - 355	1425.7130	1424.7057	1424.6831	16	0	R.LLPDAHGTTCGQR.L	Carbamidomethyl (C)
343 - 358	1795.9303	1794.9230	1794.9047	10	1	R.LLPDAHGTTCGQRLEK.V	Carbamidomethyl (C)
359 - 369	1275.7169	1274.7096	1274.7095	0	0	K.VLGTEHTHILR.V	
432 - 445	1549.8285	1548.8212	1548.8082	8	0	K.LGVTHCTIAHALEK.T	Carbamidomethyl (C)
446 - 456	1414.7059	1413.6986	1413.6928	4	1	K.TKYPNSDLYWK.K	
494 - 512	2217.0133	2216.0060	2216.0031	1	0	K.ETVGQYESHMAFTMPGLYR.V	
513 - 523	1225.6539	1224.6466	1224.6503	-3	0	R.VVHGIDVFDPK.F	
524 - 544	2378.1091	2377.1018	2377.1300	-12	0	K.FNIVSPGADMSIYFPFTESQK.R	
524 - 545	2534.2469	2533.2396	2533.2311	3	1	K.FNIVSPGADMSIYFPFTESQKR.L	
575 - 583	1062.6210	1061.6137	1061.6055	8	0	K.KPIIFSMAR.L	
589 - 599	1234.6923	1233.6851	1233.6717	11	0	K.NLTGLVELYGR.N	
603 - 618	1779.9546	1778.9474	1778.9349	7	0	R.LQELVNLVVVCGDHGK.E	Carbamidomethyl (C)
603 - 621	2124.1252	2123.1179	2123.1045	6	1	R.LQELVNLVVVCGDHGKESK.D	Carbamidomethyl (C)
632 - 646	1861.9605	1860.9533	1860.9305	12	0	K.MFNLIEQYNLNGHIR.W	
647 - 654	1005.5070	1004.4997	1004.4862	13	0	R.WISAQMNR.V	
657 - 662	751.3733	750.3660	750.3660	-0	0	R.NGELYR.Y	
663 - 668	857.3801	856.3728	856.3571	18	0	R.YICDMR.G	Carbamidomethyl (C)
723 - 733	1253.6775	1252.6702	1252.6703	-0	0	K.ASALLVEFFEK.C	
734 - 743	1326.6060	1325.5987	1325.5823	12	0	K.CQEDPNHWIK.I	Carbamidomethyl (C)
744 - 751	858.4715	857.4643	857.4719	-9	0	K.ISQGGLQR.I	
777 - 783	880.4585	879.4513	879.4450	7	0	K.YVTNLDR.R	
777 - 784	1036.5448	1035.5375	1035.5461	-8	1	K.YVTNLDRR.E	
788 - 797	1299.7248	1298.7175	1298.7056	9	1	R.RYLEMLYALK.Y	
789 - 797	1143.6068	1142.5995	1142.6045	-4	0	R.YLEMLYALK.Y	
801 - 816	1618.8553	1617.8481	1617.8284	12	0	K.MATTVPLAIEGEASTK.-	

Spot 1218

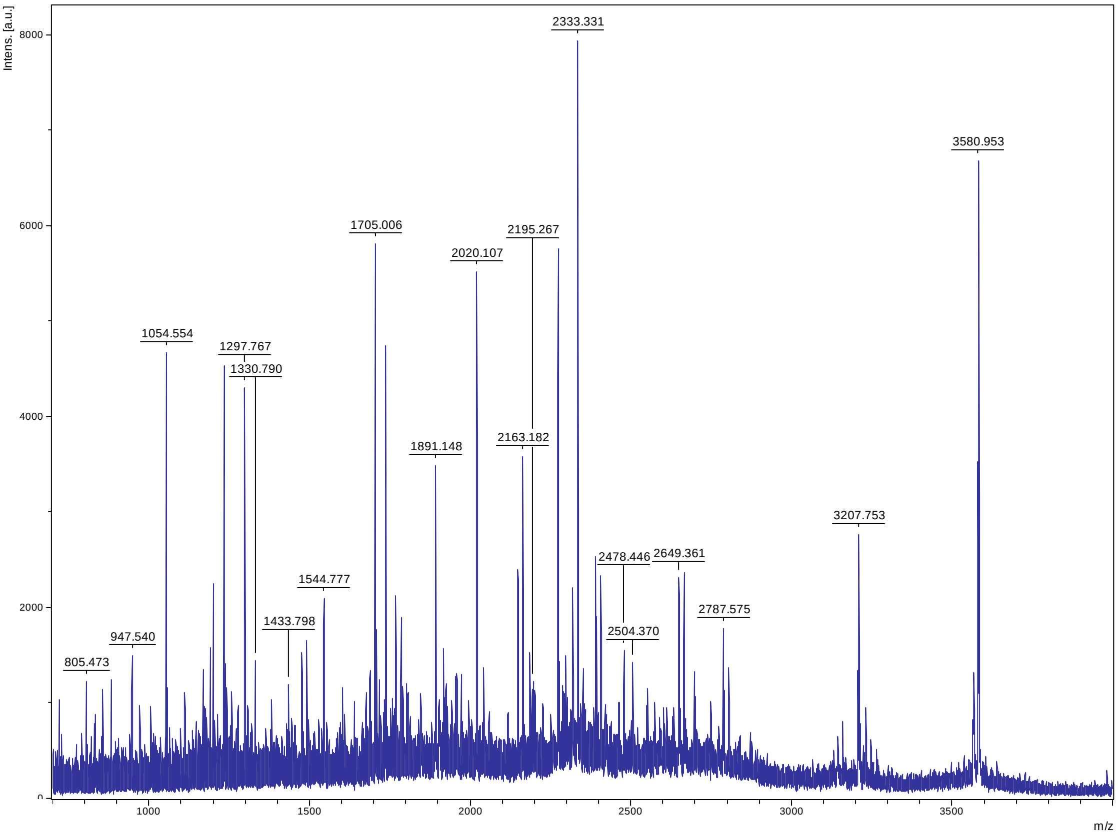


Match to: gi|38346454; Score: 287

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
87 - 106	2313.23	2312.22	2312.14	0.08	0	SLIAWNVNDQDTSLFLYASR
107 - 123	1803.85	1802.84	1802.79	0.05	0	DATMHVSDGAIHGYDSK
124 - 140	1890.97	1889.97	1889.94	0.03	0	IELEPEHASLPDNVAEK
124 - 145	2551.39	2550.39	2550.31	0.08	1	IELEPEHASLPDNVAEKFPFIR
149 - 163	1604.89	1603.88	1603.89	-0.01	1	TFRVPSSVDVASLVK
164 - 176	1447.69	1446.68	1446.67	0.02	0	CQLAVASYDAHGR
222 - 239	2006.08	2005.08	2005.03	0.04	0	VCFYDGPAGPLLQTVQLK
240 - 251	1356.69	1355.68	1355.72	-0.04	0	ELNGVWSVTVPR
252 - 263	1667.82	1666.82	1666.80	0.02	1	YRENQYYLYEVK
264 - 274	1274.64	1273.64	1273.63	0.01	0	VYHPSTSQVEK
275 - 283	1080.47	1079.47	1079.47	-0.00	0	CLADDPYAR
332 - 345	1610.69	1609.69	1609.64	0.04	0	DFSAHDSTVDCNSR
332 - 349	2028.06	2027.06	2026.86	0.20	1	DFSAHDSTVDCNSRGGFR
350 - 360	1212.59	1211.59	1211.59	-0.01	0	AFTFQDSAGIR
393 - 401	1020.48	1019.48	1019.53	-0.05	0	FVDEAQLAK
436 - 447	1207.53	1206.53	1206.53	0.00	0	GSYASNPDGPSR
453 - 460	958.49	957.49	957.47	0.02	0	QMVQALNR Oxidation (M); Pyro-glu (N-term Q)
453 - 460	959.47	958.47	958.50	-0.04	0	QMVQALNR
453 - 460	975.48	974.47	974.50	-0.02	0	QMVQALNR Oxidation (M)
489 - 496	980.52	979.52	979.55	-0.03	0	IVPGYYLR
498 - 521	2665.26	2664.25	2664.17	0.09	0	NVNGQIENSAAMNNTASEHFMVDR Oxidation (M)
522 - 535	1689.83	1688.83	1688.91	-0.08	0	LIVDDLLNWAINYK
574 - 591	2145.08	2144.08	2144.03	0.05	1	IYLYGEGWDFGEVAQNKR
592 - 611	2039.01	2038.01	2037.95	0.05	0	GINASQINMSGTGIGSFNDR
592 - 611	2055.01	2054.01	2053.95	0.06	0	GINASQINMSGTGIGSFNDR Oxidation (M)
652 - 669	1927.03	1926.03	1926.02	0.01	0	ELATYADHIQIGLAGNLK
723 - 732	1072.55	1071.55	1071.58	-0.03	0	TPIGLSIDEK
723 - 734	1388.69	1387.69	1387.71	-0.02	1	TPIGLSIDEKCR
795 - 807	1678.89	1677.89	1677.86	0.03	1	DKNEENWHLIKPR
808 - 817	1200.66	1199.65	1199.67	-0.01	0	LENPSFRPLK
835 - 841	869.41	868.41	868.44	-0.04	0	YSSPLFR
842 - 851	1119.53	1118.53	1118.56	-0.03	0	LSTASDIEQR
852 - 871	2185.13	2184.12	2184.15	-0.03	1	VRFHNTGPSMVPGVIVMSIK Oxidation (M)
944 - 953	1174.64	1173.64	1173.66	-0.02	1	RTTAVFVQPR
945 - 953	1018.53	1017.52	1017.56	-0.04	0	TTAVFVQPR

Spot 1221



Match to: gi|51090745 Score: 117 Expect: 6.7e-07

Matched peptides:

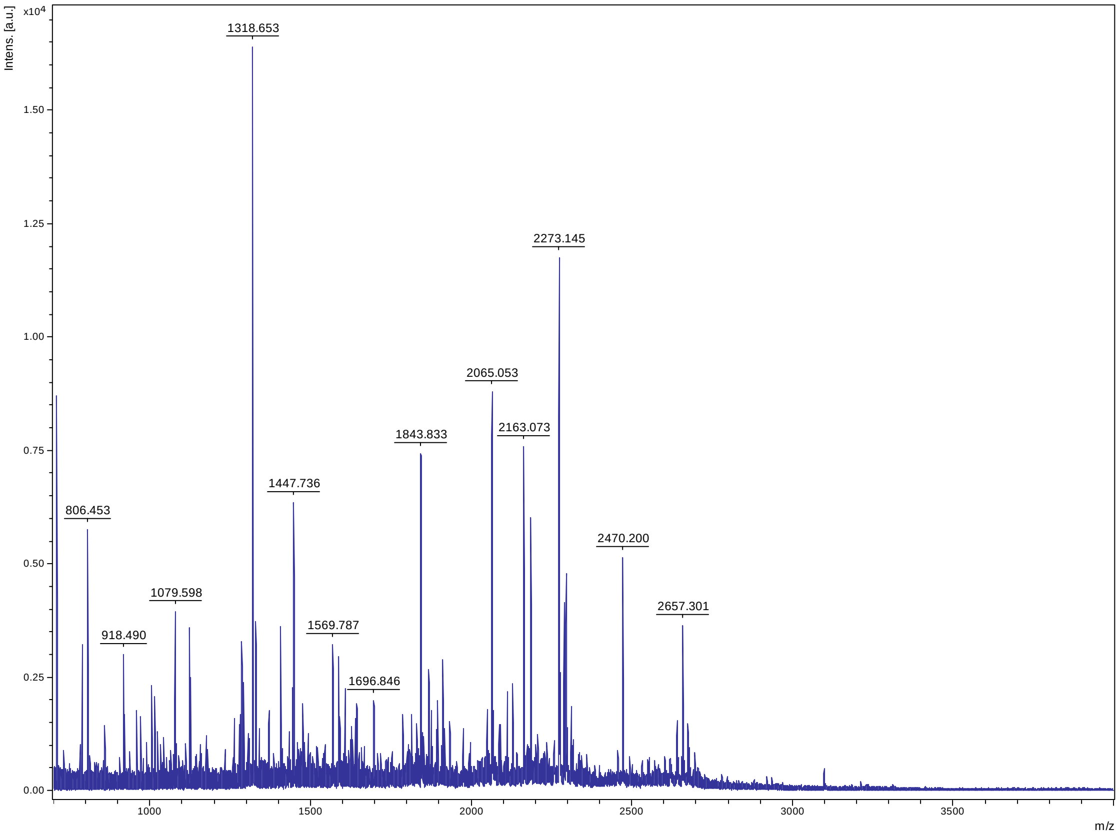
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
34 - 44	971.5848	970.5775	970.5195	0.0580	0	R.ASASAAAVAPR.R	
53 - 74	2390.2993	2389.2920	2389.1623	0.1297	0	R.VVITGMGLVSVFGNDVDAYYDR.L	
53 - 74	2406.3242	2405.3169	2405.1572	0.1597	0	R.VVITGMGLVSVFGNDVDAYYDR.L	Oxidation (M)
75 - 87	1297.7675	1296.7602	1296.7037	0.0565	0	R.LLAGESGIGPIDR.F	
75 - 96	2333.3313	2332.3240	2332.1811	0.1429	1	R.LLAGESGIGPIDRFDASNFPTR.F	
88 - 96	1054.5543	1053.5470	1053.4879	0.0591	0	R.FDASNFPTR.F	
103 - 116	1544.7770	1543.7697	1543.6902	0.0795	1	R.GFSSEGYIDGKNDR.R	
117 - 123	947.5402	946.5329	946.4654	0.0674	1	R.RLDDCLR.Y	Carbamidomethyl (C)
153 - 177	2478.4465	2477.4393	2477.2834	0.1558	0	R.AGVLVGTGMGGLTVFSDGVQNLIEK.G	Oxidation (M)
232 - 259	2787.5750	2786.5677	2786.4206	0.1471	1	R.RGEADVMIAGGTEAAIIPIGVGGFVACR.A	Carbamidomethyl (C)
232 - 259	2803.5833	2802.5760	2802.4155	0.1604	1	R.RGEADVMIAGGTEAAIIPIGVGGFVACR.A	Carbamidomethyl (C); Oxidation (M)
270 - 279	1231.6448	1230.6375	1230.5741	0.0634	0	K.TASRPWDQDR.D	
303 - 326	2649.3608	2648.3536	2648.1999	0.1537	0	R.DAPIIAEYLGGAVNCDAYHMTDPR.S	Carbamidomethyl (C)
303 - 326	2665.3779	2664.3707	2664.1948	0.1759	0	R.DAPIIAEYLGGAVNCDAYHMTDPR.S	Carbamidomethyl (C); Oxidation (M)
338 - 372	3580.9531	3579.9458	3579.7804	0.1655	0	K.QSLADAGVAPEEVNYINAHATSTLAGDLAEVNAIR.Q	
373 - 382	1190.6935	1189.6862	1189.6342	0.0520	1	R.QVFKDPSEIK.I	
388 - 407	1956.1024	1955.0951	1954.9968	0.0984	0	K.SMIGHCLGAAGGLEAIATVK.A	Carbamidomethyl (C)
408 - 436	3207.7529	3206.7457	3206.6036	0.1421	0	K.AITTGWVHPSINQFNPEPAVEFDTVPNVK.K	

Match to: gi|108706457 Score: 75 Expect: 0.002

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 21	1735.9635	1734.9562	1734.9012	0.0550	0	M.SLSTVNHAAAAAAAAAGPGK.S	
22 - 34	1231.6448	1230.6375	1230.6356	0.0019	0	K.SFSAAAPAAPSVR.L	
82 - 89	882.6025	881.5952	881.5334	0.0618	0	K.LVDVLAPR.F	
167 - 181	1705.0062	1703.9989	1703.9107	0.0883	0	R.AHLLFDLHQAVDGLR.E	
236 - 243	1006.5324	1005.5251	1005.4443	0.0808	0	R.FEGFEYSK.S	
256 - 278	2698.5857	2697.5784	2697.4125	0.1659	1	R.FAERLEPFIADTVHLLNESIQQK.K	
260 - 278	2195.2673	2194.2601	2194.1633	0.0967	0	R.LEPFIADTVHLLNESIQQK.K	
336 - 354	2020.1068	2019.0995	2018.9948	0.1047	0	R.VGSGPFPTELFGEEGDLLR.K	
336 - 355	2148.2021	2147.1949	2147.0898	0.1051	1	R.VGSGPFPTELFGEEGDLLRK.S	
369 - 379	1330.7900	1329.7828	1329.7227	0.0601	1	R.RCGWLDIVALK.Y	Carbamidomethyl (C)
418 - 434	1917.1075	1916.1003	1915.9891	0.1112	0	K.LQSFPGDLDTLEQVQVK.Y	
465 - 482	1891.1482	1890.1409	1890.0362	0.1047	0	R.IEELVGVPVHYIGVGPGR.D	

Spot 1222

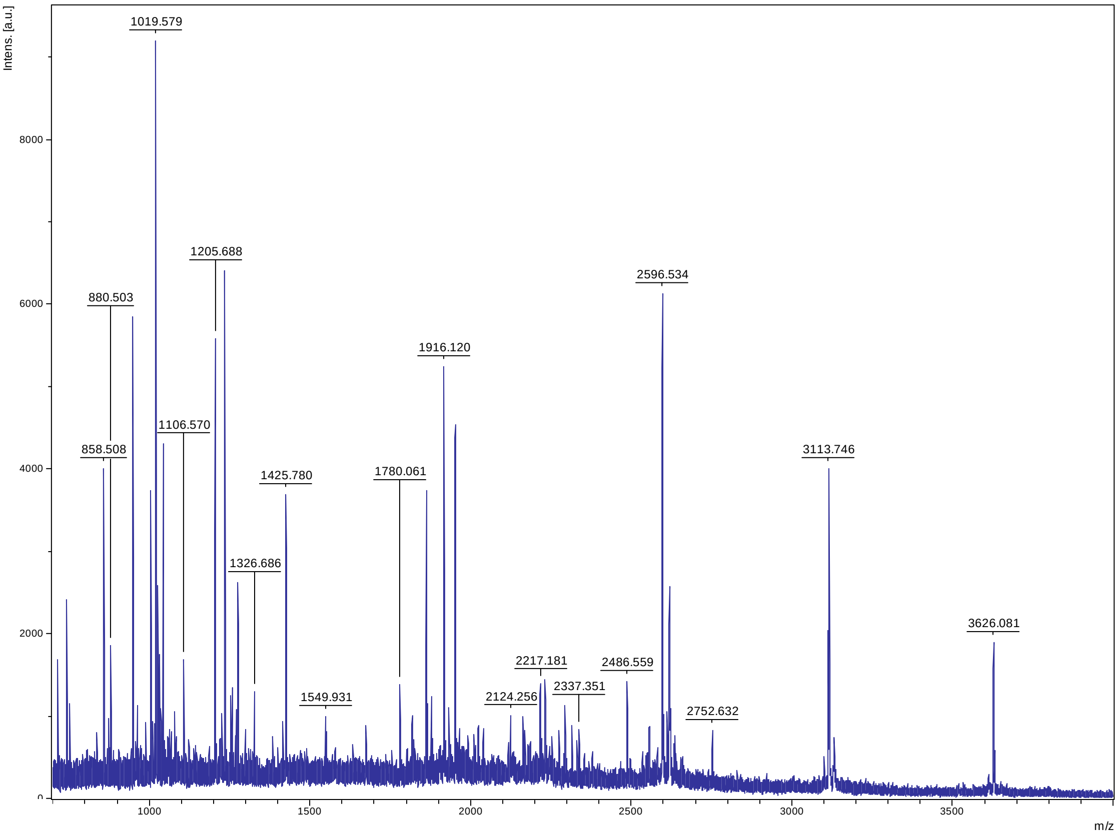


Match to: gi|77548284; Score: 222

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
38 - 48	1281.63	1280.62	1280.60	0.02	0	APEIDEDLHSR
49 - 55	806.45	805.45	805.44	0.01	0	QLAVYGR
49 - 59	1278.67	1277.67	1277.64	0.02	1	QLAVYGRETMK Pyro-glu (N-term Q)
163 - 181	2273.13	2272.13	2272.07	0.06	0	AVEFDSYCHNHQPPIAFIK
262 - 282	2470.19	2469.19	2469.14	0.04	0	NARPYSFTLEEDTTSYGTYVR
302 - 317	1813.90	1812.89	1812.86	0.03	1	DAIKEPGEFLMSDFSK
302 - 317	1829.88	1828.88	1828.86	0.02	1	DAIKEPGEFLMSDFSK Oxidation (M)
340 - 352	1447.73	1446.73	1446.72	0.01	1	RFPIAGSSDDVQR
341 - 352	1291.63	1290.63	1290.62	0.01	0	FPIAGSSDDVQR
376 - 385	1124.60	1123.59	1123.59	0.01	0	LLHHFASGSR
386 - 405	2063.09	2062.09	2062.06	0.03	0	AVLNPMAAMFGGIVGQEVVK 2 Oxidation (M)
443 - 456	1569.78	1568.78	1568.78	-0.01	0	YDAQISVFGSNLQK
463 - 477	1628.83	1627.83	1627.81	0.02	0	IFMVGSGALGCEFLK
463 - 477	1644.81	1643.81	1643.81	0.01	0	IFMVGSGALGCEFLK Oxidation (M)
478 - 491	1519.78	1518.78	1518.73	0.05	0	NLALMGISCNQNGK
513 - 520	957.49	956.49	956.47	0.02	0	DWNIGQPK
535 - 543	1079.60	1078.59	1078.59	0.01	0	LHVEALQNR
580 - 596	1911.00	1910.00	1910.00	0.00	0	CVYFQKPLLESGTLGAK
597 - 619	2657.29	2656.29	2656.24	0.05	1	CNTQMVIPHLTENYGASRDPPEK
597 - 619	2673.29	2672.29	2672.23	0.06	1	CNTQMVIPHLTENYGASRDPPEK Oxidation (M)
651 - 670	2065.04	2064.04	2064.03	0.01	0	TPTEVNAFLSNPGGYATVAR
684 - 690	918.49	917.49	917.46	0.02	0	VIECLER
691 - 704	1843.82	1842.82	1842.80	0.02	1	EKCETFQDCITWAR
693 - 704	1586.69	1585.69	1585.67	0.03	0	CETFQDCITWAR
705 - 714	1318.65	1317.65	1317.64	0.01	1	LKFEDYFSNR
707 - 714	1077.52	1076.52	1076.46	0.06	0	FEDYFSNR
783 - 798	1786.92	1785.92	1785.93	-0.02	1	MAEAVDKVIVPDFQPK
790 - 798	1042.60	1041.60	1041.59	0.01	0	VIVPDFQPK
871 - 881	1305.69	1304.69	1304.70	-0.01	1	NYSIPEVDKLK
911 - 922	1329.70	1328.70	1328.68	0.02	1	VLGGGHKVEDYR
946 - 956	1444.75	1443.75	1443.64	0.11	0	HQDMAWTVWDR
1011 - 1021	1286.71	1285.71	1285.70	0.01	1	EVAKVEVPPYR
1015 - 1021	859.48	858.48	858.46	0.02	0	VEVPPYR
1015 - 1022	1015.57	1014.56	1014.56	0.00	1	VEVPPYRR

Spot 1224

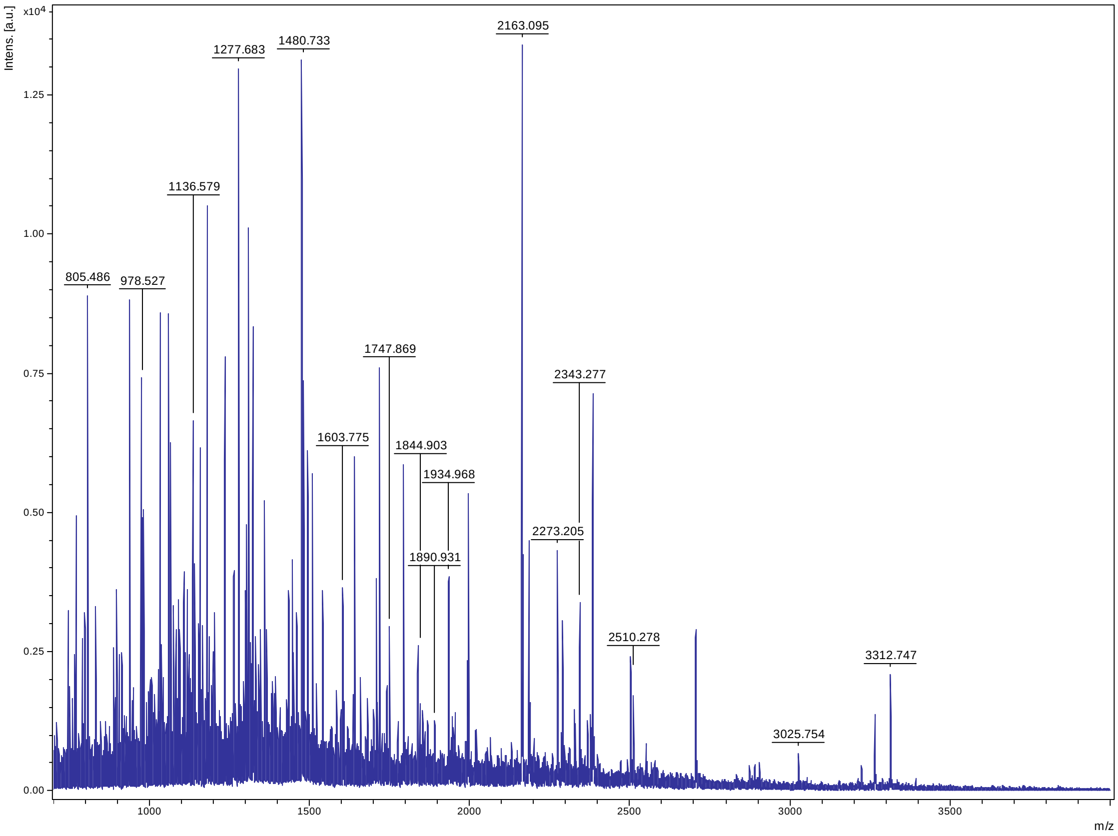


Match to: gi|3915054 Score: 187 Expect: 5.3e-13

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
20 - 37	1916.0487	1915.0414	1914.9799	0.0616	0	R.IGDSLSAHTNELVAVFSR.L	
44 - 64	2337.2121	2336.2048	2336.1582	0.0466	0	K.GMLQPHQIIAEYNAAIPEGER.E	
44 - 66	2594.3190	2593.3117	2593.2958	0.0159	1	K.GMLQPHQIIAEYNAAIPEGEREK.L	
44 - 66	2610.2902	2609.2829	2609.2907	-0.0078	1	K.GMLQPHQIIAEYNAAIPEGEREK.L	Oxidation (M)
67 - 77	1258.7382	1257.7309	1257.6928	0.0381	1	K.LKDSALEDVLR.G	
105 - 124	2292.2294	2291.2221	2291.2048	0.0173	0	R.INVSQLGVEELSVPEYLQFK.E	
125 - 156	3625.7175	3624.7102	3624.7735	-0.0633	0	K.EQLVDGSTQNNFVLELDFEPFNASFPRPSLSK.S	
205 - 214	1043.6029	1042.5956	1042.5771	0.0186	0	R.SLDALQGALR.K	
219 - 235	1951.9959	1950.9886	1950.9336	0.0550	0	K.HLAGITADTPYSEFHHR.F	
244 - 251	949.3867	948.3794	948.3872	-0.0078	0	K.GWGDCAQR.V	Carbamidomethyl (C)
252 - 273	2486.3733	2485.3660	2485.3791	-0.0131	1	R.VRETIHLLLDLLEAPEPSALEK.F	
254 - 273	2231.2418	2230.2345	2230.2096	0.0249	0	R.ETIHLLLDLLEAPEPSALEK.F	
317 - 325	1106.5509	1105.5436	1105.5260	0.0177	0	R.AMENEMLLR.I	
317 - 325	1122.5657	1121.5584	1121.5209	0.0376	0	R.AMENEMLLR.I	Oxidation (M)
328 - 336	1026.5789	1025.5716	1025.5618	0.0099	0	K.QQGLNITPR.I	
337 - 342	714.4091	713.4018	713.4799	-0.0781	0	R.ILIVTR.L	
343 - 355	1425.7487	1424.7414	1424.6830	0.0584	0	R.LLPDAHGTTCGQR.L	Carbamidomethyl (C)
359 - 369	1275.7641	1274.7568	1274.7095	0.0473	0	K.VLGTEHTHILR.V	
426 - 445	2314.2212	2313.2139	2313.2085	0.0054	1	R.CLLAHKLGVTHCTIAHALEK.T	Acetyl (N-term); 2 Carbamidomethyl (C)
432 - 445	1549.9031	1548.8958	1548.8082	0.0876	0	K.LGVTHCTIAHALEK.T	Carbamidomethyl (C)
446 - 456	1414.7806	1413.7733	1413.6928	0.0805	1	K.TKYPNSDLYWK.K	
494 - 512	2217.0741	2216.0668	2216.0030	0.0638	0	K.ETVGQYESHMAFTMPGLYR.V	
513 - 523	1225.7351	1224.7278	1224.6502	0.0776	0	R.VVHGIDVFDPK.F	
545 - 567	2752.4151	2751.4078	2751.4079	-0.0000	1	K.RLTSLHLEIEELLFSDVENTEHK.F	
546 - 567	2596.3033	2595.2960	2595.3067	-0.0107	0	R.LTSLHLEIEELLFSDVENTEHK.F	
575 - 583	1062.6139	1061.6066	1061.6055	0.0011	0	K.KPIIFSMAR.L	
575 - 583	1078.6134	1077.6061	1077.6004	0.0057	0	K.KPIIFSMAR.L	Oxidation (M)
603 - 618	1780.0201	1779.0128	1778.9348	0.0780	0	R.LQELVNLVVVCGDHGK.E	Carbamidomethyl (C)
603 - 621	2124.1458	2123.1385	2123.1044	0.0341	1	R.LQELVNLVVVCGDHGKESK.D	Carbamidomethyl (C)
632 - 646	1861.9936	1860.9863	1860.9304	0.0559	0	K.MFNLIEQYNLNGHIR.W	
647 - 654	1005.5055	1004.4982	1004.4862	0.0121	0	R.WISAQMNR.V	
657 - 662	751.3134	750.3061	750.3660	-0.0599	0	R.NGELYR.Y	
723 - 733	1253.7306	1252.7233	1252.6703	0.0531	0	K.ASALLVEFFEK.C	
734 - 743	1326.6604	1325.6531	1325.5823	0.0709	0	K.CQEDPNHWIK.I	Carbamidomethyl (C)
744 - 751	858.4166	857.4093	857.4719	-0.0626	0	K.ISQGGLQR.I	
777 - 783	880.4339	879.4266	879.4450	-0.0184	0	K.YVTNLDR.R	
788 - 797	1299.7795	1298.7722	1298.7056	0.0666	1	R.RYLEMLYALK.Y	

Spot 1229

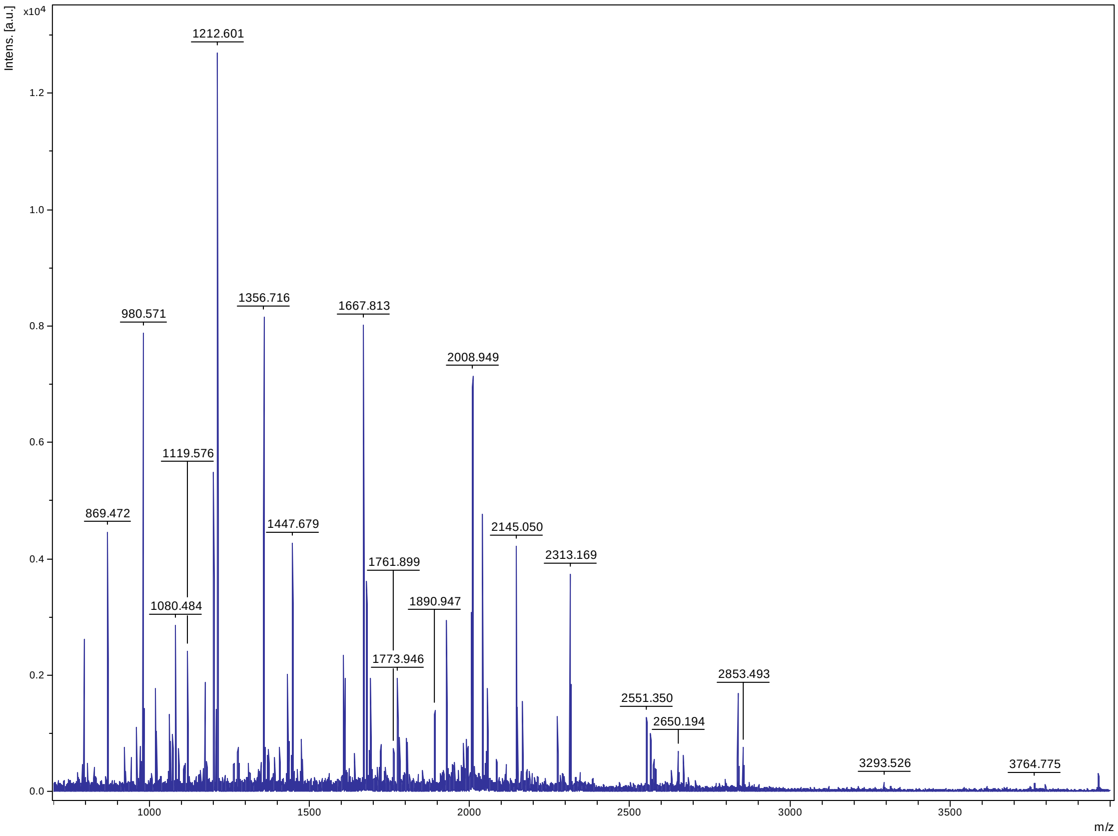


Match to: gi|34906196; Score: 114

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
22 - 33	1358.69	1357.69	1357.72	-0.03	1	GIDVVLNEESKR
34 - 46	1520.74	1519.74	1519.75	-0.00	1	ETPAIVCFGDKQR
74 - 82	1135.56	1134.56	1134.57	-0.01	1	KYSDPELQR
75 - 82	1007.53	1006.53	1006.47	0.06	0	YSDPELQR
83 - 90	936.53	935.53	935.49	0.04	0	DIAAFPFR
91 - 104	1480.73	1479.73	1479.75	-0.02	0	VSEGPDGFPLVHAR
127 - 153	3025.75	3024.75	3024.47	0.28	0	GIAESNLNTAVVDCCIGIPVYFTDLQR
155 - 169	1540.82	1539.82	1539.84	-0.02	0	AVLDAATIAGLCPLR
220 - 227	974.52	973.52	973.50	0.02	0	ILSHAYDR
252 - 259	978.53	977.52	977.49	0.03	0	IDVYQNAR
306 - 313	888.56	887.56	887.51	0.05	0	ISASILER
321 - 343	2343.28	2342.28	2342.19	0.09	0	ALAEAGLTTENVHFVEVVGSGSR
350 - 360	1322.66	1321.66	1321.70	-0.05	1	ILTDFFGKEPR
435 - 455	2327.19	2326.19	2326.13	0.06	0	SNTFQVDVTYVDTGDLQISPK
456 - 471	1680.84	1679.84	1679.85	-0.02	1	ISTYTVGPFNPGKGDK
597 - 609	1597.74	1596.74	1596.75	-0.01	1	AVEKEYEMALQDR Oxidation (M)
619 - 629	1346.62	1345.62	1345.60	0.02	0	NAVESYVYDMR
636 - 645	1201.63	1200.63	1200.53	0.10	0	YNDFVTAEDK
689 - 695	1043.53	1042.53	1042.45	0.07	1	YKEWMDR Oxidation (M)
696 - 710	1740.82	1739.82	1739.83	-0.01	0	GPSIDQLAYCINSFR
731 - 743	1603.78	1602.77	1602.78	-0.01	0	VINQCSEAEVWLR

Spot 1230

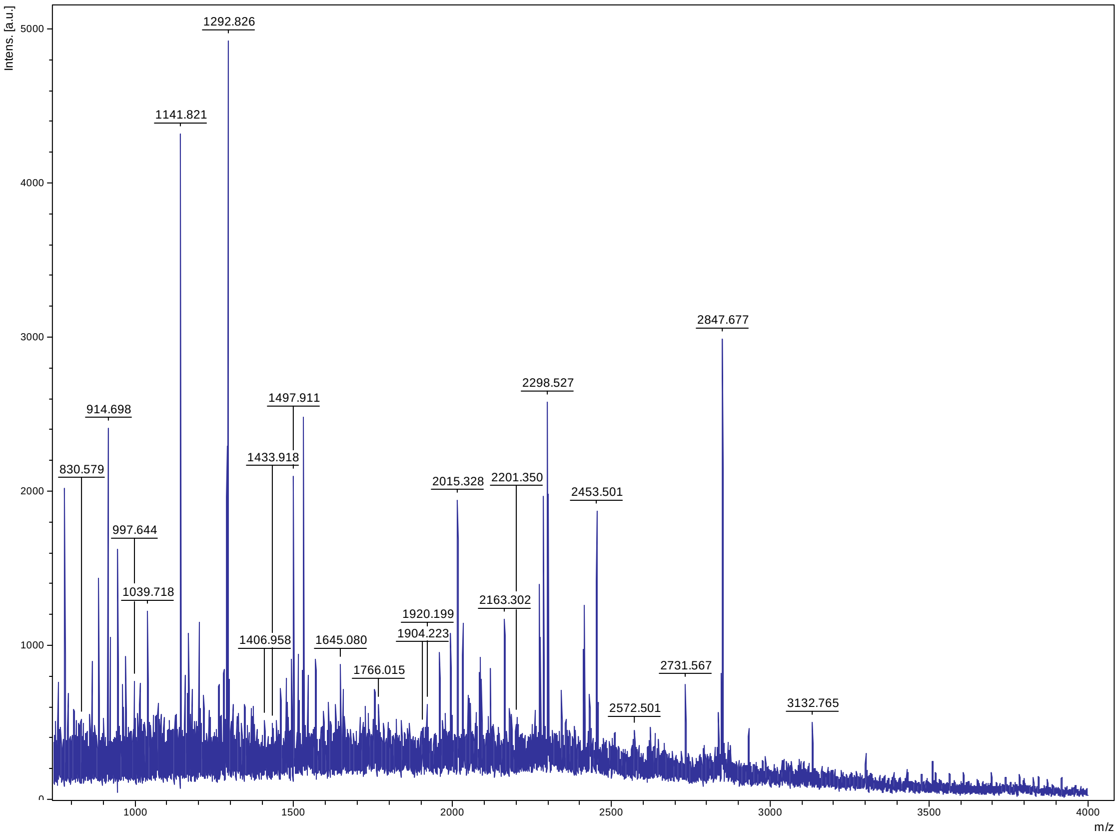


Match to: gi|3172048 Score: 292 Expect: 3.7e-26

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
93 - 112	2313.1690	2312.1617	2312.1437	8	0	R.SLIAWNVNDQDTSLFLYASR.D	
113 - 129	1803.8086	1802.8013	1802.7894	7	0	R.DATMHVSDGAIHGYDSK.I	
130 - 146	1890.9470	1889.9398	1889.9370	1	0	K.IELEPEHASLPDNVAEK.F	
130 - 151	2551.3501	2550.3428	2550.3118	12	1	K.IELEPEHASLPDNVAEKFPFIR.S	
155 - 169	1604.9071	1603.8998	1603.8934	4	1	R.TFRVPSSVDVASLVK.C	
170 - 182	1447.6789	1446.6716	1446.6674	3	0	K.CQLAVASYDAHGR.H	
213 - 227	1761.8993	1760.8920	1760.8734	11	0	K.DVDLYLWAPTAQDVR.V	
228 - 245	2006.0313	2005.0240	2005.0343	-5	0	R.VCFYDGPAGPLLQTVQLK.E	
246 - 257	1356.7161	1355.7088	1355.7198	-8	0	K.ELNGVWSVTVPR.Y	
270 - 280	1274.6296	1273.6223	1273.6303	-6	0	K.VYHPSTSQVEK.C	
281 - 289	1080.4844	1079.4771	1079.4706	6	0	K.CLADDPYAR.G	
338 - 351	1610.6567	1609.6494	1609.6427	4	0	R.DFSAHDSTVDCNSR.G	
399 - 422	2576.3531	2575.3458	2575.3183	11	0	K.LSAAGLTHVHLLPSFHFASVDDNK.S	
427 - 435	1020.5406	1019.5333	1019.5287	4	0	K.FVDEAQLAK.L	
470 - 481	1207.5367	1206.5294	1206.5265	2	0	K.GSYASNPDGPSR.I	
487 - 494	942.4976	941.4903	941.4753	16	0	R.QMVQALNR.I	Gln->pyro-Glu (N-term Q)
487 - 494	959.5282	958.5209	958.5018	20	0	R.QMVQALNR.I	
487 - 494	975.5249	974.5177	974.4967	21	0	R.QMVQALNR.I	Oxidation (M)
523 - 530	980.5711	979.5639	979.5491	15	0	K.IVPGYYLR.R	
575 - 583	1091.5533	1090.5460	1090.5303	14	0	R.FDLMGHIMK.S	
608 - 624	1988.9387	1987.9314	1987.9316	-0	0	K.IYLYGEGWDFGEVAQNK.R	
608 - 625	2145.0500	2144.0427	2144.0327	5	1	K.IYLYGEGWDFGEVAQNKR.G	
626 - 645	2038.9687	2037.9615	2037.9538	4	0	R.GINASQINMSGTGIGSFNDR.I	
626 - 645	2054.9575	2053.9503	2053.9487	1	0	R.GINASQINMSGTGIGSFNDR.I	Oxidation (M)
648 - 684	3960.8674	3959.8601	3959.7987	16	0	R.DSVNGGNPFGNPLQQGFSTGLFLEPNGYYQGNEADTR.R	
686 - 703	1927.0272	1926.0199	1926.0210	-1	0	R.ELATYADHIQIGLAGNLK.D	
686 - 708	2573.3844	2572.3771	2572.3649	5	1	R.ELATYADHIQIGLAGNLKDYVLR.T	
757 - 766	1072.5890	1071.5817	1071.5812	1	0	K.TPIGLSIDEK.C	
769 - 794	2853.4928	2852.4856	2852.4643	7	0	R.INHLASSMIALSQGIPFFHAGDEILR.S	Oxidation (M)
812 - 828	1978.9619	1977.9546	1977.9585	-2	0	K.LDFTYETNNWGVGLPPR.D	
829 - 841	1678.8770	1677.8697	1677.8587	7	1	R.DKNEENWHLIKPR.L	
831 - 841	1435.7463	1434.7390	1434.7368	2	0	K.NEENWHLIKPR.L	
842 - 851	1200.6719	1199.6647	1199.6662	-1	0	R.LENPSFRPLK.N	
869 - 875	869.4722	868.4649	868.4443	24	0	R.YSSPLFR.L	
876 - 885	1119.5758	1118.5685	1118.5567	10	0	R.LSTASDIEQR.V	
978 - 987	1174.6750	1173.6678	1173.6618	5	1	R.RTTAVFVQPR.C	
979 - 987	1018.5780	1017.5707	1017.5607	10	0	R.TTAVFVQPR.C	

Spot 1236

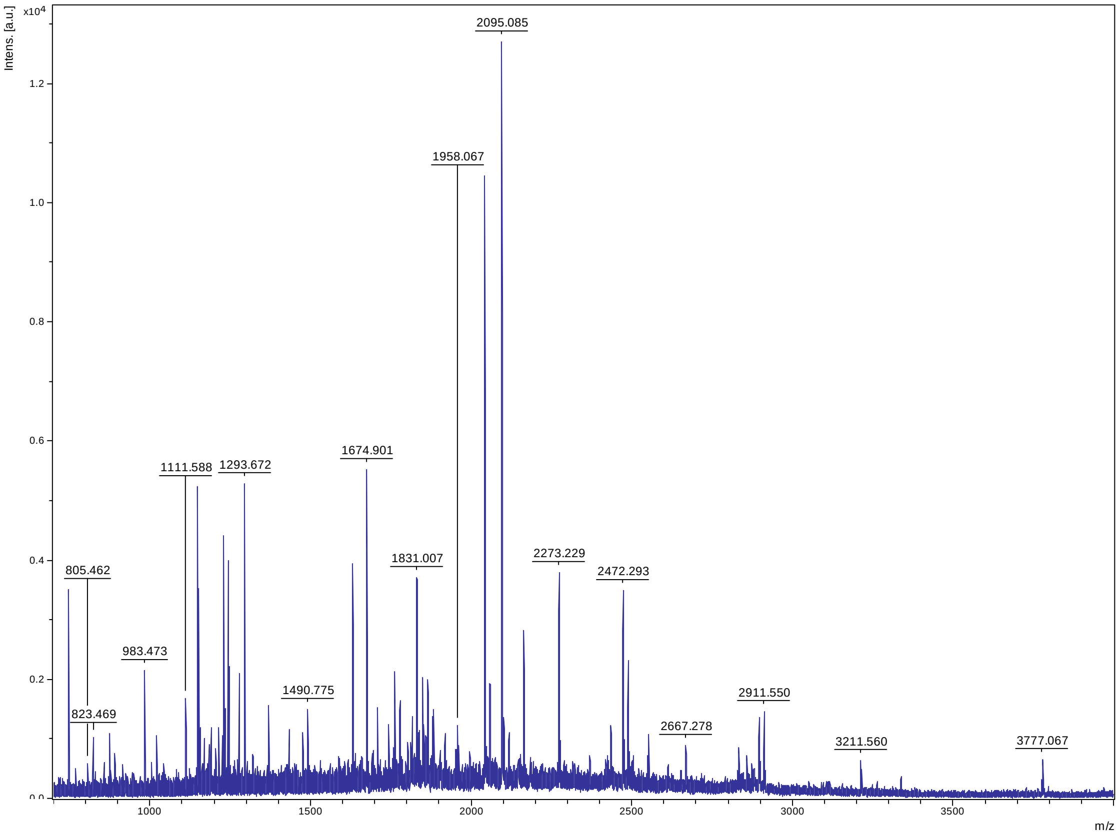


Match to: gi|50941891 Score: 97 Expect: 1.3e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
9 - 24	1644.9900	1643.9827	1643.8882	0.0945	0	K.NILTTLPKPGGGEYGK.F	
25 - 35	1292.7432	1291.7359	1291.6561	0.0799	0	K.FYSLPALNDPR.I	
45 - 52	914.5031	913.4958	913.5596	-0.0638	0	R.ILLESAIR.N	
67 - 76	1202.6741	1201.6668	1201.5979	0.0689	0	K.IIDWENTSPK.L	
77 - 86	1141.7130	1140.7057	1140.6655	0.0402	0	K.LAEIPFKPAR.V	
87 - 105	2015.1483	2014.1410	2014.0921	0.0490	0	R.VLLQDFTGVPAVVDLAAMR.D	
87 - 105	2031.1256	2030.1183	2030.0870	0.0313	0	R.VLLQDFTGVPAVVDLAAMR.D	Oxidation (M)
118 - 138	2298.2832	2297.2759	2297.2743	0.0017	0	K.INPLVPVDLVIDHSVQVDVAR.S	
358 - 378	2412.1174	2411.1101	2411.1566	-0.0464	0	R.VYSSYLELDLNEVEPCISGPK.R	Carbamidomethyl (C)
405 - 415	1288.7118	1287.7045	1287.6459	0.0587	1	K.GFAVPKEQQDK.V	Acetyl (N-term)
460 - 472	1513.8593	1512.8520	1512.8010	0.0511	0	K.ACELGLEVKPWVK.T	Acetyl (N-term)
485 - 497	1568.9251	1567.9178	1567.8246	0.0933	0	K.YLLQSGLQEYLNK.Q	
709 - 716	945.3566	944.3493	944.3988	-0.0494	0	K.DFNSYGSR.R	
755 - 763	1039.5814	1038.5741	1038.5749	-0.0008	0	K.LYVFDAALK.Y	
764 - 785	2284.0657	2283.0584	2283.0767	-0.0182	1	K.YKSEGHDTIVLAGAEYGSGSSR.D	
766 - 785	1993.0156	1992.0083	1991.9184	0.0899	0	K.SEGHDTIVLAGAEYGSGSSR.D	
866 - 872	884.3386	883.3313	883.4222	-0.0909	0	K.SFTCTLR.F	Carbamidomethyl (C)
873 - 893	2453.1524	2452.1451	2452.2426	-0.0975	0	R.FDTEVELAYFNHGGILPYVIR.N	

Spot 1242

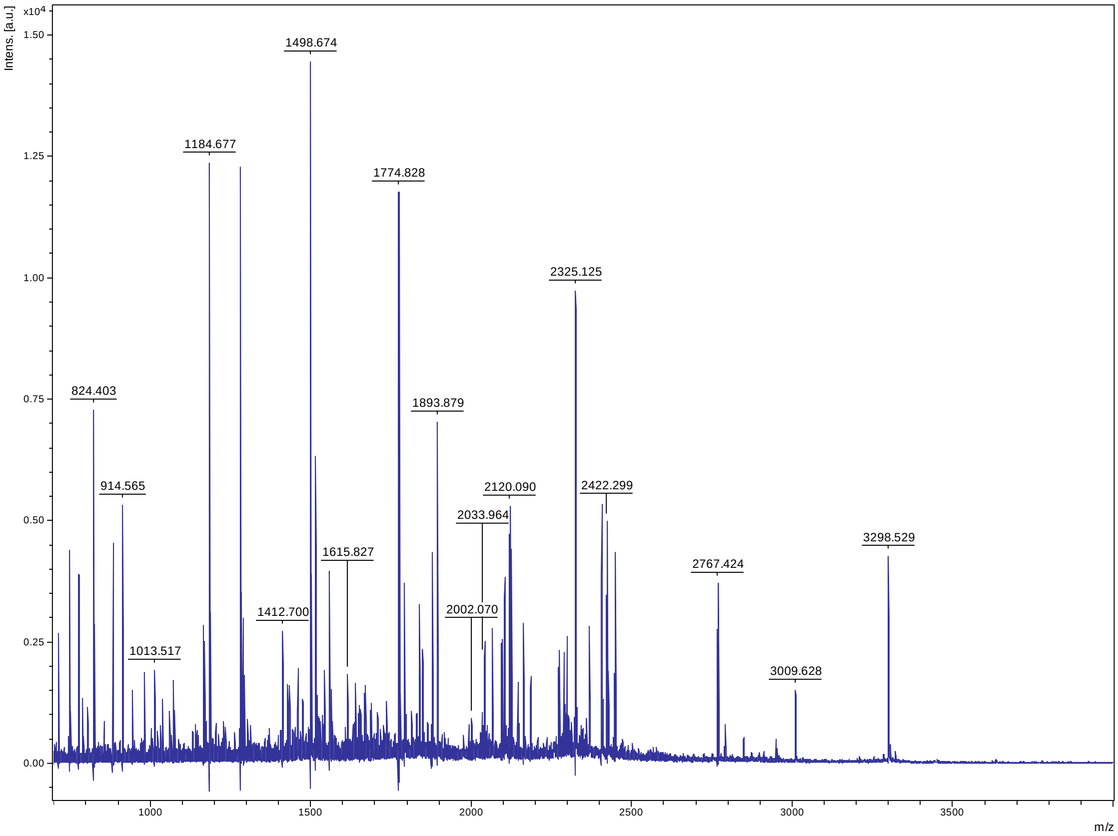


Match to: gi|51090952 Score: 167 Expect: 1.3e-12

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
51 - 72	2472.2026	2471.1953	2471.2015	-0.0062	0	R.HSDGLPHLNQAEEATWMGLLPR.R	
51 - 72	2488.1874	2487.1801	2487.1964	-0.0163	0	R.HSDGLPHLNQAEEATWMGLLPR.R	Oxidation (M)
74 - 87	1674.8680	1673.8607	1673.8525	0.0082	1	R.AGPRDELDWLALYR.S	
78 - 87	1293.6550	1292.6477	1292.6401	0.0076	0	R.DELDWLALYR.S	
92 - 113	2095.0155	2094.0082	2094.0129	-0.0047	0	R.GGGDVGGEPAGFLSPASLHDVR.V	
151 - 169	2042.0095	2041.0022	2040.9904	0.0118	0	K.LPTVGEPYGGWEAPDGQLR.G	
170 - 193	2667.1900	2666.1827	2666.2196	-0.0369	0	R.GHFTGHYLSAAAHMWASTHNDALR.E	Oxidation (M)
199 - 208	1224.6263	1223.6190	1223.6220	-0.0030	0	K.VVDILYSCQK.K	Carbamidomethyl (C)
242 - 257	1761.9343	1760.9270	1760.9131	0.0140	0	K.IMQGLLDQYTLAGNPK.G	
242 - 257	1777.9079	1776.9006	1776.9080	-0.0073	0	K.IMQGLLDQYTLAGNPK.G	Oxidation (M)
258 - 272	1816.8941	1815.8868	1815.8865	0.0003	0	K.GLEIVVWMTDYFSTR.V	
276 - 284	1149.6308	1148.6235	1148.6189	0.0046	0	K.LIQEYSIQR.H	
353 - 363	1369.7260	1368.7187	1368.7037	0.0150	1	K.RYEVVGDQLYK.E	
354 - 363	1213.6131	1212.6058	1212.6026	0.0032	0	R.YEVVGDQLYK.E	
402 - 416	1742.8422	1741.8349	1741.8192	0.0157	0	K.ISSNEETCATYNLLK.V	Carbamidomethyl (C)
430 - 436	983.4090	982.4017	982.4144	-0.0127	0	K.YTDHYER.L	
437 - 447	1228.6945	1227.6872	1227.6757	0.0115	0	R.LLINGIMGNQR.G	
448 - 464	1848.9430	1847.9357	1847.9425	-0.0068	1	R.GKEPGVMIYFLPMGPGR.S	
448 - 464	1864.9586	1863.9513	1863.9375	0.0139	1	R.GKEPGVMIYFLPMGPGR.S	Oxidation (M)
448 - 464	1880.9624	1879.9551	1879.9324	0.0228	1	R.GKEPGVMIYFLPMGPGR.S	2 Oxidation (M)
563 - 573	1168.6155	1167.6082	1167.6108	-0.0026	0	K.GDARPANVNVR.I	
606 - 615	1147.5968	1146.5895	1146.5921	-0.0025	0	K.LWGDDTLSLK.F	
616 - 621	746.3849	745.3776	745.4486	-0.0710	0	K.FPITLR.T	
743 - 759	1631.7917	1630.7844	1630.7699	0.0145	0	R.AYHSPSGASAIDAATGR.L	
764 - 791	2895.4196	2894.4123	2894.4708	-0.0585	0	R.DVALEPFDRPGMAVTDALSVGRPGPATR.F	
764 - 791	2911.4043	2910.3970	2910.4657	-0.0687	0	R.DVALEPFDRPGMAVTDALSVGRPGPATR.F	Oxidation (M)

Spot 1248

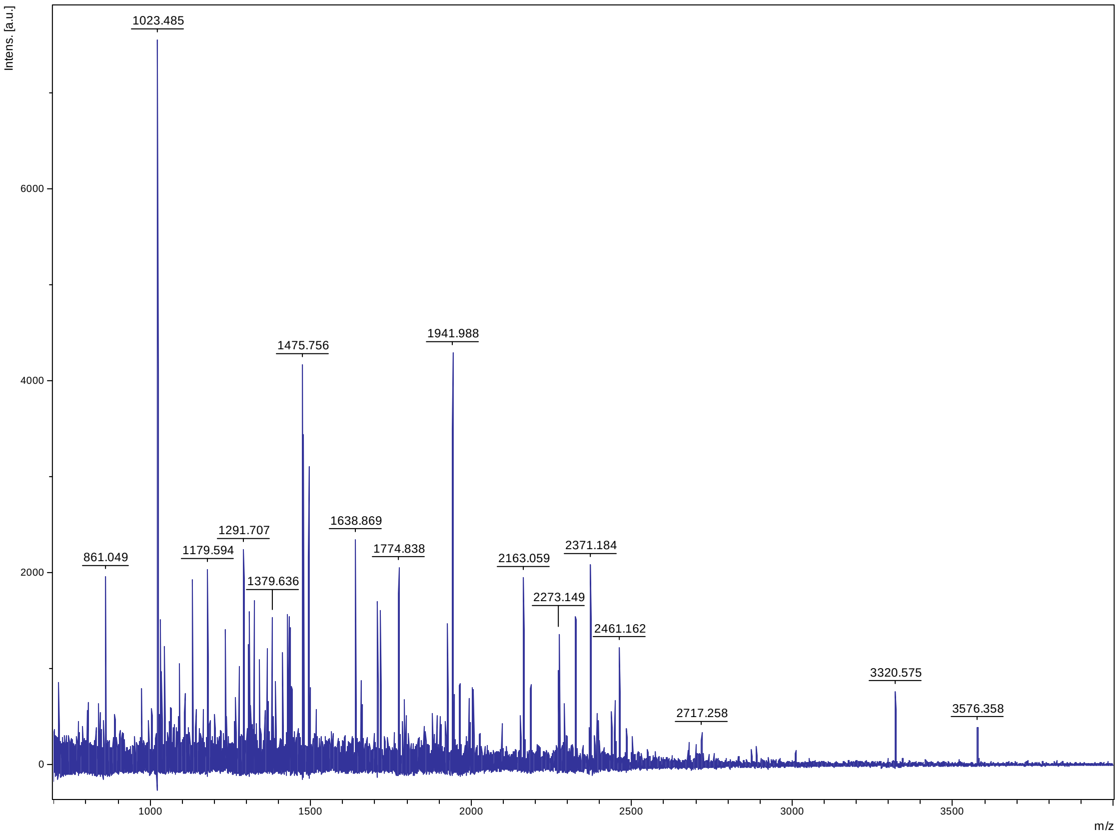


Match to: gi|115468938 Score: 304 Expect: 1.3e-26

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
92 - 112	2124.0670	2123.0597	2123.0535	3	0	K.NSYDEILTGLAKPGGGAEFGK.Y	
113 - 123	1281.6463	1280.6390	1280.6401	-1	0	K.YYSLPALSDPR.I	
127 - 132	748.4230	747.4157	747.4279	-16	0	R.LPYSIR.I	
133 - 140	914.5653	913.5581	913.5596	-2	0	R.ILLESAIR.N	
155 - 164	1172.5918	1171.5845	1171.5873	-2	0	K.ILDWENSAPK.Q	
165 - 174	1167.6468	1166.6396	1166.6448	-4	0	K.QVEIPFKPAR.V	Gln->pyro-Glu (N-term Q)
165 - 174	1184.6771	1183.6698	1183.6713	-1	0	K.QVEIPFKPAR.V	
175 - 193	2104.0903	2103.0831	2103.0857	-1	0	R.VLLQDFTGVPAVVDLACMR.D	
175 - 193	2120.0902	2119.0830	2119.0806	1	0	R.VLLQDFTGVPAVVDLACMR.D	Oxidation (M)
199 - 226	3009.6281	3008.6208	3008.6295	-3	1	K.LGSDPNKINPLVPVDLVIDHSVQVDVAR.S	
206 - 226	2298.2776	2297.2703	2297.2744	-2	0	K.INPLVPVDLVIDHSVQVDVAR.S	
227 - 241	1774.8278	1773.8205	1773.8104	6	0	R.SENAVQANMELEFHR.N	
227 - 241	1790.8240	1789.8167	1789.8053	6	0	R.SENAVQANMELEFHR.N	Oxidation (M)
251 - 257	824.4033	823.3960	823.3977	-2	0	K.WGSTAFR.N	
258 - 279	2406.3029	2405.2956	2405.2889	3	0	R.NMLVVPPGSGIVHQVNLEYLAR.V	
258 - 279	2422.2993	2421.2920	2421.2838	3	0	R.NMLVVPPGSGIVHQVNLEYLAR.V	Oxidation (M)
369 - 385	1877.8872	1876.8799	1876.8665	7	0	K.FVEFYGGGMSELSLADR.A	
369 - 385	1893.8793	1892.8720	1892.8615	6	0	K.FVEFYGGGMSELSLADR.A	Oxidation (M)
408 - 413	752.4171	751.4099	751.4116	-2	0	K.TLDYLK.L	
418 - 430	1515.7164	1514.7091	1514.6923	11	0	R.SDDTVAMIESYLR.A	Oxidation (M)
434 - 445	1498.6738	1497.6666	1497.6558	7	0	K.MFVDYNQPEAER.V	
434 - 445	1514.6787	1513.6714	1513.6507	14	0	K.MFVDYNQPEAER.V	Oxidation (M)
446 - 466	2426.1937	2425.1864	2425.1723	6	0	R.VYSSYLELNLEEVEPCLSGPK.R	
504 - 515	1290.6445	1289.6372	1289.6404	-3	0	K.VAEFSFHGTPAK.L	
548 - 560	1542.8118	1541.8045	1541.8276	-15	0	K.ACELGLEVKPWIK.T	
561 - 571	1015.5814	1014.5741	1014.5710	3	0	K.TSLAPGSGVVK.K	
672 - 679	1013.5172	1012.5099	1012.4978	12	1	K.DGKEVYFR.D	
675 - 679	713.3517	712.3445	712.3544	-14	0	K.EVYFR.D	
680 - 693	1615.8271	1614.8198	1614.8141	4	0	R.DIWPSTEEIAEVVK.S	
743 - 755	1412.7000	1411.6927	1411.6952	-2	0	K.DMTMSPPGPRPVK.D	
743 - 755	1428.6819	1427.6747	1427.6901	-11	0	K.DMTMSPPGPRPVK.D	Oxidation (M)
756 - 786	3298.5287	3297.5214	3297.5361	-4	0	K.DAYCLLNFGDSITTDHISPAGSIHPDSPAAR.Y	
796 - 804	1073.5150	1072.5078	1072.4938	13	1	R.KDFNSYGSR.R	
797 - 804	945.4125	944.4052	944.3988	7	0	K.DFNSYGSR.R	
805 - 813	1061.5267	1060.5194	1060.5083	10	1	R.RGNDEIMAR.G	
814 - 820	778.4158	777.4085	777.4133	-6	0	R.GTFANIR.L	
834 - 842	981.5403	980.5330	980.5291	4	0	K.TIHIPSGEK.L	
852 - 873	2325.1253	2324.1180	2324.1033	6	1	K.YKNEGHDTIILAGAEYGSGSSR.D	
854 - 873	2033.9636	2032.9563	2032.9450	6	0	K.NEGHDTIILAGAEYGSGSSR.D	
913 - 927	1557.7328	1556.7255	1556.7067	12	0	K.SGEDADTLGLTGHER.F	
928 - 953	2767.4237	2766.4164	2766.4189	-1	0	R.FTVHLPANVSEIKPGQDVTVTTDNGK.S	
954 - 960	884.4314	883.4241	883.4222	2	0	K.SFTCTLR.F	
961 - 981	2447.2194	2446.2121	2446.2056	3	0	R.FDTEVELAYYDNGGILPYVIR.K	

Spot 1252

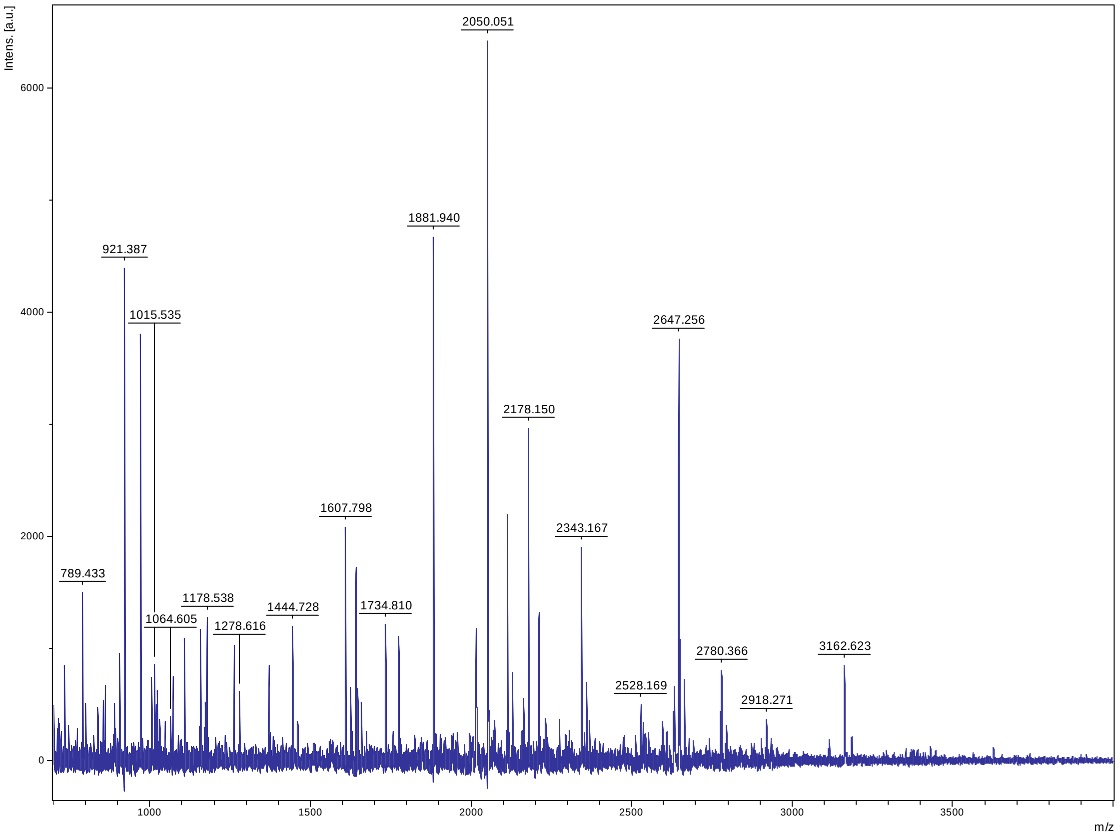


Match to: gi|38344900; Score: 111

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
133 - 143	1131.63	1130.63	1130.59	0.04	0	AIGEVVSTEAR
171 - 184	1441.72	1440.72	1440.71	0.01	0	GQETPGEDPLLASK
185 - 204	1942.00	1940.99	1940.95	0.05	0	YAVGYVTGLQDAGGGSDALK
211 - 221	1411.65	1410.65	1410.62	0.03	0	HYTAYDVDNWK
226 - 246	2461.20	2460.20	2460.15	0.05	0	YTFDAVVSQQDLDDTFQPPFK
320 - 342	2371.21	2370.21	2370.17	0.03	0	SGLDLNCGNFLAQHTVAAVQAGK
351 - 361	1291.74	1290.74	1290.71	0.02	0	AITNNFIVLMR
362 - 370	1023.53	1022.53	1022.48	0.05	0	LGFFDGDPR
371 - 380	1043.66	1042.65	1042.62	0.04	1	KLPFGSLGPK
381 - 392	1379.65	1378.65	1378.61	0.03	0	DVCTSSNQELAR
579 - 591	1494.78	1493.78	1493.76	0.02	0	LPVTWYPASFADK
599 - 610	1339.65	1338.65	1338.60	0.05	0	MRPDSSTGYPGR Oxidation (M)
614 - 631	2004.94	2003.94	2003.92	0.02	0	FYTGDTVYAFGDGLSYTK

Spot 1257

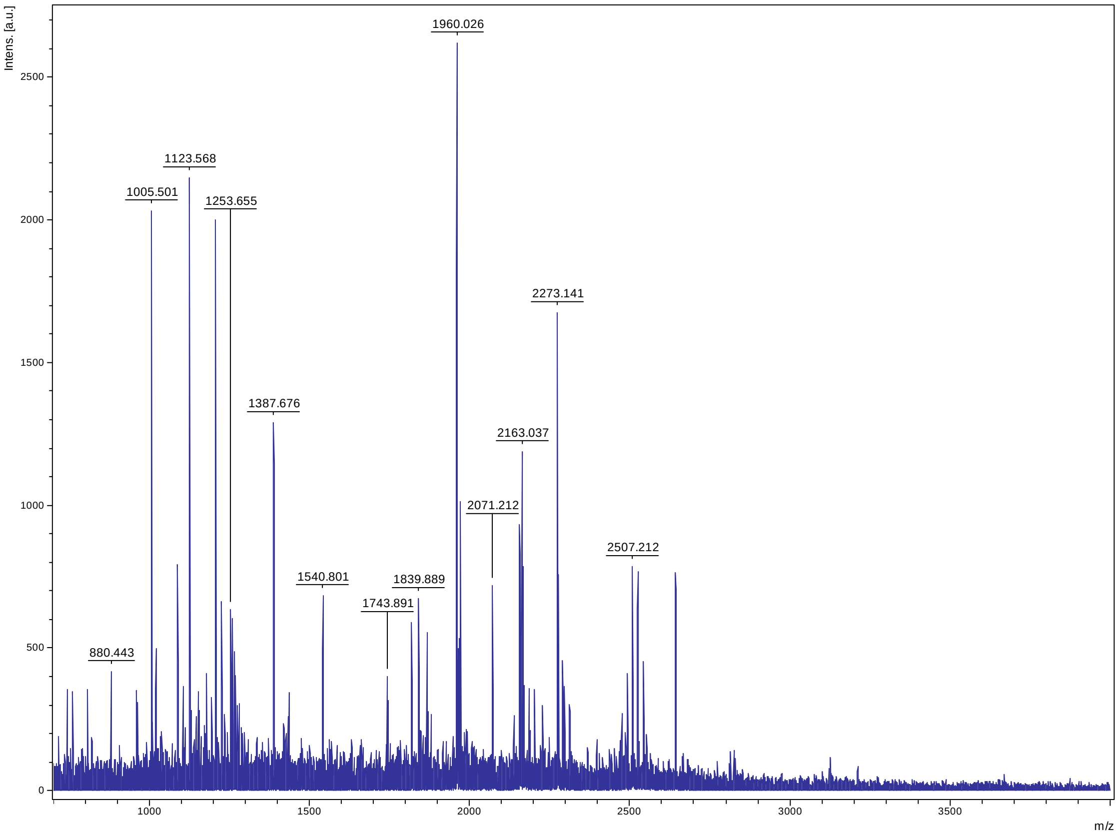


Match to: gi|50878307 Score: 141 Expect: 5.3e-10

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
40 - 48	1006.5658	1005.5585	1005.5719	-0.0134	0	R.HGKPEVAIR.S	
77 - 82	734.3956	733.3883	733.3911	-0.0028	0	R.VFHFGK.G	
203 - 209	921.4596	920.4523	920.4028	0.0495	0	R.FAYDSYR.R	
211 - 230	2352.1075	2351.1002	2351.1329	-0.0327	0	R.FLDMFGNVVMDIPHALFEEK.L	
211 - 230	2368.1440	2367.1367	2367.1278	0.0089	0	R.FLDMFGNVVMDIPHALFEEK.L	Oxidation (M)
299 - 307	1015.6322	1014.6249	1014.6073	0.0176	1	R.SINKITGLK.G	Acetyl (N-term)
341 - 360	2178.2035	2177.1962	2177.1479	0.0483	1	K.KLYGEFLVNAQGEDVVAGIR.T	
342 - 360	2050.1120	2049.1047	2049.0530	0.0517	0	K.LYGEFLVNAQGEDVVAGIR.T	
361 - 384	2919.1574	2918.1501	2918.2408	-0.0907	1	R.TPEDLDAMRDHMPEPYEELVENCK.I	Acetyl (N-term); Oxidation (M)
385 - 404	2512.2067	2511.1994	2511.1773	0.0221	1	K.ILESHYKEMMDIEFTVQENR.L	
385 - 404	2528.1213	2527.1140	2527.1722	-0.0582	1	K.ILESHYKEMMDIEFTVQENR.L	Oxidation (M)
385 - 404	2544.1795	2543.1722	2543.1672	0.0051	1	K.ILESHYKEMMDIEFTVQENR.L	2 Oxidation (M)
392 - 404	1641.8431	1640.8358	1640.7174	0.1184	0	K.EMMDIEFTVQENR.L	
423 - 435	1444.8628	1443.8555	1443.7391	0.1164	0	K.IAVDMVNEGLVER.R	
441 - 462	2536.2293	2535.2220	2535.2216	0.0005	0	K.MVEPGHLDQLLHPQFENPSGYK.D	
441 - 464	2779.2836	2778.2763	2778.3435	-0.0672	1	K.MVEPGHLDQLLHPQFENPSGYKDK.V	
441 - 464	2795.1870	2794.1797	2794.3384	-0.1587	1	K.MVEPGHLDQLLHPQFENPSGYKDK.V	Oxidation (M)
465 - 496	3162.4904	3161.4831	3161.6144	-0.1313	0	K.VIATGLPASPGAAVGQIVFTAEDAEAWHAQGK.D	
503 - 523	2112.0915	2111.0842	2111.0316	0.0526	0	R.TETSPEDVGGMHAAVGILTAR.G	
503 - 523	2128.0521	2127.0448	2127.0266	0.0183	0	R.TETSPEDVGGMHAAVGILTAR.G	Oxidation (M)
563 - 583	2210.1825	2209.1752	2209.1378	0.0374	0	K.ALHEGEWLSLNGSTGEVIIGK.Q	
584 - 606	2647.1994	2646.1921	2646.2458	-0.0536	0	K.QPLCPPALSGDLETFMSWVDEVR.K	Carbamidomethyl (C)
584 - 606	2663.2260	2662.2187	2662.2407	-0.0220	0	K.QPLCPPALSGDLETFMSWVDEVR.K	Carbamidomethyl (C); Oxidation (M)
625 - 635	1174.6815	1173.6742	1173.5560	0.1182	0	R.QNGAEGIGLCR.T	Carbamidomethyl (C)
669 - 674	789.4631	788.4558	788.4545	0.0014	0	R.LLPYQR.S	
675 - 682	970.5376	969.5303	969.4556	0.0748	0	R.SDFEGIFR.A	
683 - 692	1072.6790	1071.6717	1071.5746	0.0971	0	R.AMDGLPVTIR.L	
693 - 712	2343.1799	2342.1726	2342.1728	-0.0002	0	R.LLDPPLHEFLPEGHVEDMVR.E	
693 - 712	2359.1600	2358.1527	2358.1678	-0.0150	0	R.LLDPPLHEFLPEGHVEDMVR.E	Oxidation (M)
713 - 728	1734.9171	1733.9098	1733.7890	0.1208	0	R.ELCSETGAAQDDVLAR.V	Carbamidomethyl (C)
732 - 742	1262.7604	1261.7531	1261.6488	0.1043	0	K.LSEVNPMLGFR.G	
746 - 759	1607.9234	1606.9161	1606.8024	0.1137	0	R.LGISYPELTEMQAR.A	

Spot 1262

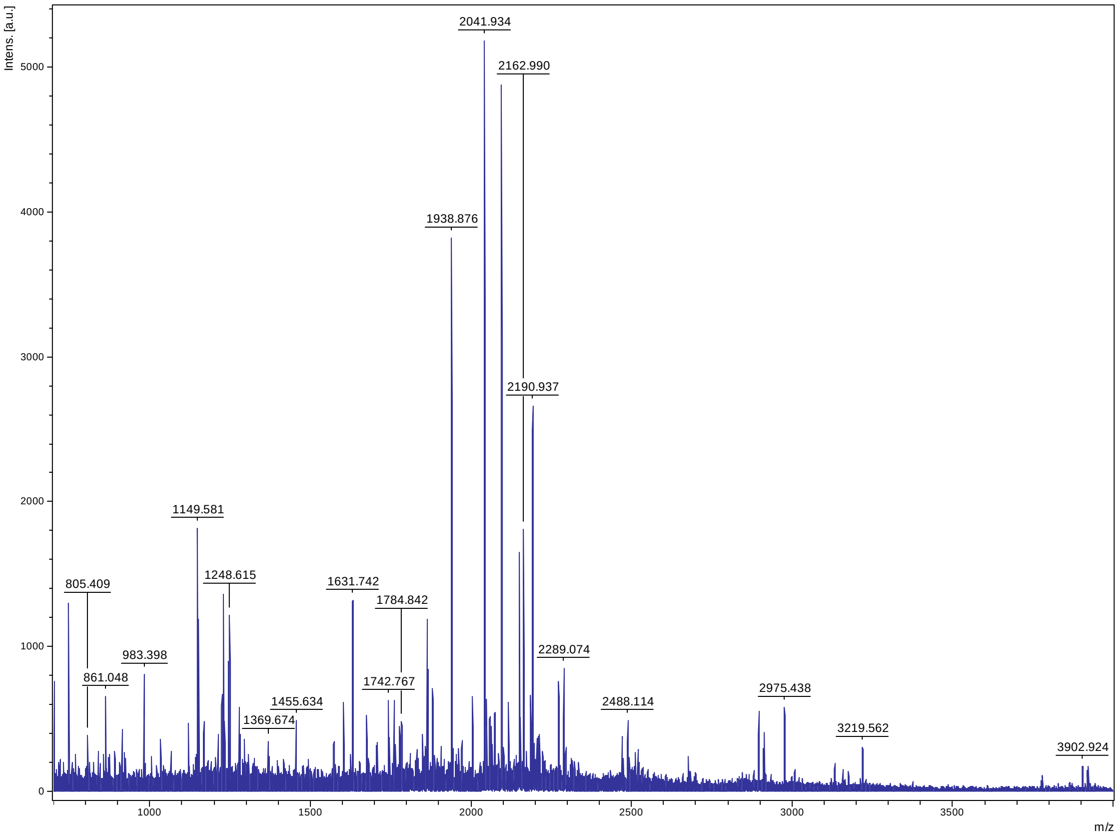


Match to: gi|267056 Score: 263 Expect: 2.3e-22

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
15 - 32	1960.0262	1959.0190	1959.0213	-0.0024	0	R.LGATFSSHPNELIALFSR.Y	
44 - 60	1970.0137	1969.0064	1969.0156	-0.0092	1	R.HQLLAEFDALIEADKEK.Y	
61 - 69	1123.5679	1122.5606	1122.5709	-0.0103	0	K.YAPFEDILR.A	
149 - 159	1204.5968	1203.5895	1203.6360	-0.0464	0	K.SIGNGVQFLNR.H	
165 - 180	1968.0729	1967.0656	1967.0767	-0.0111	1	K.LFQDKESLYPLLNFLK.A	
207 - 227	2525.2046	2524.1973	2524.1692	0.0281	1	R.KAEEYLMGIPQDTPYSEFNHR.F	
207 - 227	2541.1785	2540.1712	2540.1641	0.0071	1	R.KAEEYLMGIPQDTPYSEFNHR.F	Oxidation (M)
228 - 235	963.4988	962.4915	962.5072	-0.0157	0	R.FQELGLEK.G	
309 - 317	1088.5616	1087.5544	1087.5695	-0.0152	0	R.ALENEMLLR.I	
309 - 317	1104.5411	1103.5339	1103.5645	-0.0306	0	R.ALENEMLLR.I	Oxidation (M)
335 - 347	1387.6761	1386.6689	1386.6925	-0.0236	0	R.LLPDAVGTTCGQR.V	Carbamidomethyl (C)
335 - 350	1743.8906	1742.8833	1742.8985	-0.0151	1	R.LLPDAVGTTCGQRVEK.V	Carbamidomethyl (C)
351 - 361	1253.6548	1252.6475	1252.6775	-0.0300	0	K.VIGTEHTDILR.V	
424 - 437	1540.8009	1539.7936	1539.8079	-0.0143	0	K.LGVTQCTIAHALEK.T	Carbamidomethyl (C)
486 - 504	2167.0789	2166.0716	2166.0745	-0.0029	0	K.DTVGQYESHIAFTLPGLYR.V	
505 - 515	1225.6279	1224.6207	1224.6502	-0.0296	0	R.VVHGIDVFDPK.F	
516 - 537	2507.2119	2506.2046	2506.1838	0.0209	1	K.FNIVSPGADMSVYFPYTEADKR.L	
516 - 537	2523.1831	2522.1758	2522.1787	-0.0029	1	K.FNIVSPGADMSVYFPYTEADKR.L	Oxidation (M)
538 - 559	2642.2847	2641.2774	2641.2547	0.0227	0	R.LTAFHPEIEELLYSEVENDEHK.F	
564 - 575	1435.7449	1434.7376	1434.7653	-0.0277	1	K.DKNKPIIFSMAR.L	Oxidation (M)
566 - 575	1176.6176	1175.6103	1175.6485	-0.0382	0	K.NKPIIFSMAR.L	
597 - 613	1839.8892	1838.8819	1838.8944	-0.0126	0	R.DLANLVIVCGDHGNQSK.D	Carbamidomethyl (C)
614 - 622	1151.5184	1150.5112	1150.5254	-0.0143	1	K.DREEQAEFK.K	
623 - 632	1258.6254	1257.6181	1257.6427	-0.0246	1	K.KMYGLIDQYK.L	
639 - 646	1005.5012	1004.4939	1004.4862	0.0077	0	R.WISAQMNR.V	
639 - 646	1021.4901	1020.4828	1020.4811	0.0018	0	R.WISAQMNR.V	Oxidation (M)
715 - 725	1266.6328	1265.6255	1265.6655	-0.0400	0	K.AADILVNFFEK.C	
726 - 743	2155.9683	2154.9610	2154.9752	-0.0142	1	K.CKQDSTYWDNISQGGLQR.I	Carbamidomethyl (C)
769 - 775	880.4427	879.4354	879.4450	-0.0096	0	K.YVSNLER.R	

Spot 1264



Match to: gi|51090952; Score: 178

Matched peptides:

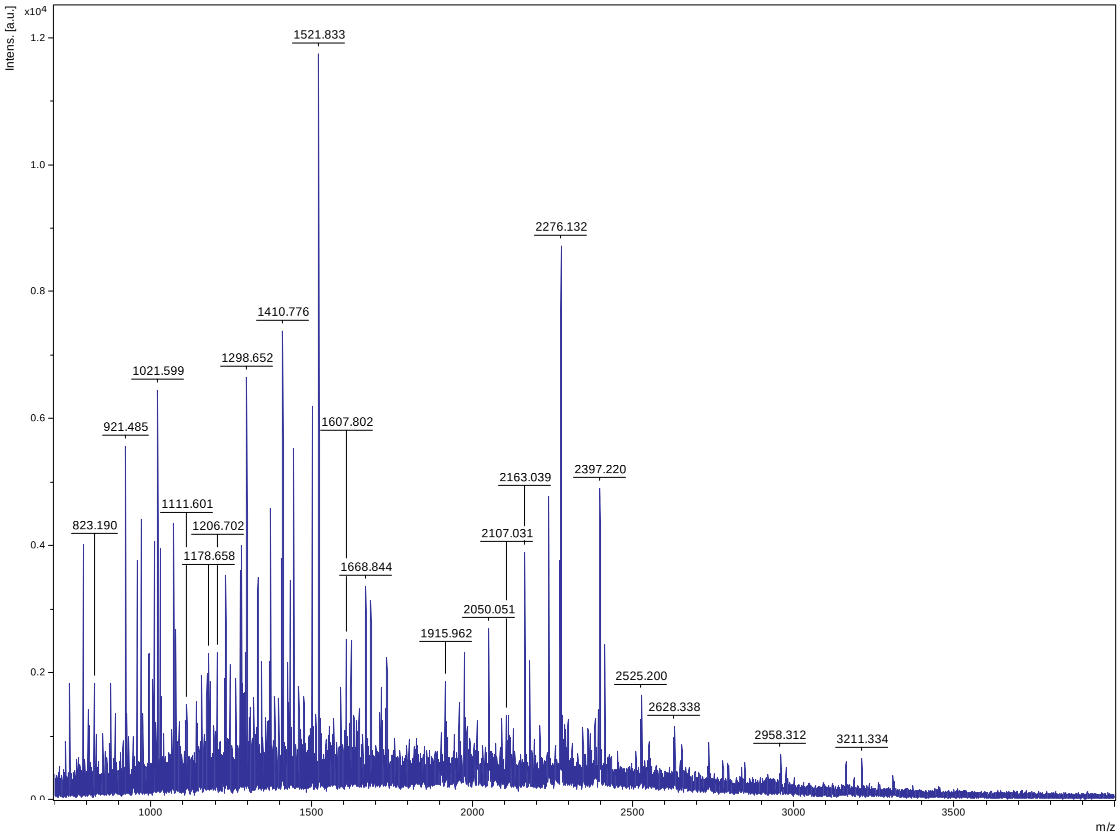
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
51 - 72	2472.12	2471.12	2471.20	-0.08	0	HSDGLPHLNQAEEATWMGLLPR
51 - 72	2488.11	2487.11	2487.20	-0.09	0	HSDGLPHLNQAEEATWMGLLPR Oxidation (M)
74 - 87	1674.79	1673.79	1673.85	-0.06	1	AGPRDELDWLALYR
78 - 87	1293.60	1292.60	1292.64	-0.04	0	DELDWLALYR
92 - 113	2094.96	2093.96	2094.01	-0.05	0	GGGDVGGEPAGFLSPASLHDVR
151 - 169	2041.93	2040.93	2040.99	-0.06	0	LPTVGEPYGGWEAPDGQLR
199 - 208	1224.57	1223.57	1223.62	-0.06	0	VVDILYSCQK
242 - 257	1761.85	1760.85	1760.91	-0.07	0	IMQGLLDQYTLAGNPK
242 - 257	1777.84	1776.84	1776.91	-0.07	0	IMQGLLDQYTLAGNPK Oxidation (M)
275 - 284	1277.66	1276.66	1276.71	-0.06	1	KLIQEYSIQR
276 - 284	1149.58	1148.58	1148.62	-0.04	0	LIQEYSIQR
353 - 363	1369.67	1368.67	1368.70	-0.03	1	RYEVVGDQLYK
354 - 363	1213.59	1212.59	1212.60	-0.02	0	YEVVGDQLYK
402 - 416	1742.77	1741.76	1741.82	-0.05	0	ISSNEETCATYNLLK
430 - 436	983.40	982.40	982.41	-0.02	0	YTDHYER
430 - 447	2192.92	2191.91	2192.08	-0.17	1	YTDHYERLLINGIMGNQR
437 - 447	1228.64	1227.63	1227.68	-0.04	0	LLINGIMGNQR
437 - 447	1244.62	1243.62	1243.67	-0.05	0	LLINGIMGNQR Oxidation (M)
448 - 464	1864.86	1863.86	1863.94	-0.08	1	GKEPGVMIYFLPMGPGR Oxidation (M)
448 - 464	1880.85	1879.84	1879.93	-0.09	1	GKEPGVMIYFLPMGPGR 2 Oxidation (M)
563 - 573	1168.56	1167.56	1167.61	-0.05	0	GDARPANVNVR
606 - 615	1147.55	1146.55	1146.59	-0.04	0	LWGDDTLSLK
743 - 759	1631.74	1630.74	1630.77	-0.03	0	AYHSPSGASAIDAATGR
764 - 791	2895.39	2894.39	2894.47	-0.08	0	DVALEPFDRPGMAVTDALSVGRPGPATR
764 - 791	2911.39	2910.39	2910.47	-0.08	0	DVALEPFDRPGMAVTDALSVGRPGPATR Oxidation (M)

Match to: gi|1346109; Score: 123

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
42 - 69	2975.44	2974.44	2974.48	-0.05	0	SLLVWDLTNPVQNVGEGAGASEYGVPFR
101 - 111	1248.61	1247.61	1247.65	-0.04	0	LWDLSTGVTTR
113 - 130	2004.95	2003.94	2004.01	-0.06	1	FVGHDKDVLSVAFSVDNR
143 - 151	1120.50	1119.50	1119.54	-0.04	0	LWNTLGECK
152 - 172	2190.94	2189.93	2189.99	-0.06	0	YTIGGDLGGGEGHNGWVSCVR
173 - 189	1938.88	1937.87	1937.93	-0.05	0	FSPNTFQPTIVSGSWDR
193 - 200	1034.47	1033.46	1033.50	-0.04	0	VWNLTNCK
230 - 243	1572.76	1571.76	1571.83	-0.07	1	DGVTLLWDLAEGKR
244 - 262	2150.00	2149.00	2149.06	-0.06	0	LYSLDAGSIIHSLCFSPNR
263 - 274	1455.63	1454.63	1454.69	-0.06	0	YWLCAATQDSIK
275 - 281	890.45	889.45	889.45	-0.00	0	IWDLESK
282 - 295	1602.85	1601.85	1601.91	-0.07	0	HIVQDLKPEIPVSK

Spot 1265



Match to: gi|50916753 Score: 274 Expect: 2.7e-23

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
84 - 105	2525.2002	2524.1929	2524.2155	-0.0226	0	R.ITQQEFTEMAWQSIVSSPEVAK.E	Oxidation (M)
157 - 168	1246.6561	1245.6489	1245.6023	0.0466	0	K.VLGEDPGSMLGR.D	Oxidation (M)
169 - 176	957.6039	956.5966	956.5291	0.0675	0	R.DLEALIQR.A	
183 - 203	2397.2205	2396.2132	2396.1647	0.0484	1	K.EYGDSFVSVEHLVLGFAEDKR.F	
211 - 220	1178.6582	1177.6509	1177.6343	0.0167	0	K.DFQITVQSLK.T	
273 - 279	889.5727	888.5654	888.4851	0.0803	0	R.CIQILSR.R	Carbamidomethyl (C)
296 - 305	1029.6262	1028.6189	1028.5614	0.0575	0	K.TAIAEGLAQR.I	
306 - 318	1410.7760	1409.7687	1409.7626	0.0061	0	R.IVQGDVPQALTNR.R	
334 - 341	1071.5447	1070.5374	1070.4781	0.0593	1	K.YRGEFEDR.L	
393 - 404	1369.6010	1368.5937	1368.6707	-0.0770	1	R.CIGATTLDEYRK.Y	
393 - 404	1426.7064	1425.6991	1425.6922	0.0070	1	R.CIGATTLDEYRK.Y	Carbamidomethyl (C)
405 - 414	1233.6768	1232.6695	1232.6401	0.0294	1	K.YIEKDPALER.R	
415 - 434	2393.2324	2392.2251	2392.2386	-0.0135	1	R.RFQQVYVDQPSVEDTISILR.G	
416 - 434	2237.1372	2236.1299	2236.1375	-0.0076	0	R.FQQVYVDQPSVEDTISILR.G	
438 - 447	1295.6823	1294.6750	1294.6530	0.0220	1	R.ERYELHHGVR.I	
440 - 447	1010.5863	1009.5790	1009.5093	0.0697	0	R.YELHHGVR.I	
448 - 462	1501.8265	1500.8193	1500.8147	0.0045	0	R.ISDSALVAAALLSDR.Y	
468 - 483	1731.9137	1730.9064	1730.9090	-0.0026	1	R.FLPDKAIDLVDESAAK.L	
486 - 500	1718.8616	1717.8543	1717.8556	-0.0013	0	K.MEITSKPTALDEIDR.A	
486 - 500	1734.8177	1733.8105	1733.8505	-0.0401	0	K.MEITSKPTALDEIDR.A	Oxidation (M)
501 - 509	1088.6338	1087.6265	1087.6059	0.0206	1	R.AVIKLEMER.L	
510 - 518	1006.5696	1005.5623	1005.4978	0.0645	0	R.LSLTNDTDK.A	
538 - 547	1332.6710	1331.6637	1331.6470	0.0168	1	K.QKDLTEQWER.E	
540 - 547	1076.5653	1075.5580	1075.4934	0.0646	0	K.DLTEQWER.E	
555 - 564	1230.6705	1229.6633	1229.6615	0.0017	1	K.IQSIKEEIDR.V	
565 - 574	1185.6646	1184.6573	1184.6149	0.0424	0	R.VNVEIQQAER.E	
586 - 594	1021.5993	1020.5920	1020.5352	0.0568	0	K.YGSLNALQR.Q	
612 - 629	2091.0288	2090.0215	2090.0313	-0.0098	1	K.SMLREEVTQDDIAEIVSR.W	
612 - 629	2107.0315	2106.0242	2106.0262	-0.0020	1	K.SMLREEVTQDDIAEIVSR.W	Oxidation (M)
646 - 655	1286.7136	1285.7063	1285.6918	0.0146	0	K.LLYLEEELHK.R	
646 - 656	1442.8040	1441.7967	1441.7929	0.0038	1	K.LLYLEEELHKR.V	
666 - 673	873.5546	872.5473	872.4715	0.0757	0	K.AVSEAIQR.S	
704 - 718	1668.8440	1667.8367	1667.8340	0.0027	0	K.ALAAFMFNTEEAVVR.I	
704 - 718	1684.8395	1683.8322	1683.8290	0.0032	0	K.ALAAFMFNTEEAVVR.I	Oxidation (M)
719 - 732	1711.8865	1710.8792	1710.7705	0.1087	1	R.IDMSEYMEKHSVSR.L	
733 - 754	2276.1323	2275.1250	2275.1483	-0.0233	0	R.LIGAPPGYVGYEEGGQLTEAVR.R	
756 - 768	1622.8555	1621.8482	1621.8715	-0.0233	0	R.RPYSIILFDEIEK.A	
769 - 785	1915.9625	1914.9552	1914.9587	-0.0035	0	K.AHGDVFNVFLQILDDGR.V	
833 - 848	1958.0095	1957.0022	1956.9298	0.0725	1	R.VMDAARSVFRPEFMNR.I	2 Oxidation (M)
839 - 848	1282.6558	1281.6485	1281.6288	0.0197	0	R.SVFRPEFMNR.I	
839 - 848	1298.6517	1297.6445	1297.6237	0.0208	0	R.SVFRPEFMNR.I	Oxidation (M)
849 - 860	1521.8333	1520.8260	1520.8238	0.0022	0	R.IDEYIVFKPLER.E	
885 - 910	2735.3271	2734.3199	2734.3965	-0.0766	0	K.LEVSPGAVEFLGSLGYDPNYGARPVK.R	
911 - 923	1589.8221	1588.8149	1588.8572	-0.0424	1	K.RVIQQYVENELAK.G	
912 - 923	1433.7596	1432.7524	1432.7561	-0.0038	0	R.VIQQYVENELAK.G	
928 - 954	2958.3118	2957.3045	2957.4617	-0.1573	1	R.GDFKDEDSILVDTQVTVPSNGQLPQQK.L	

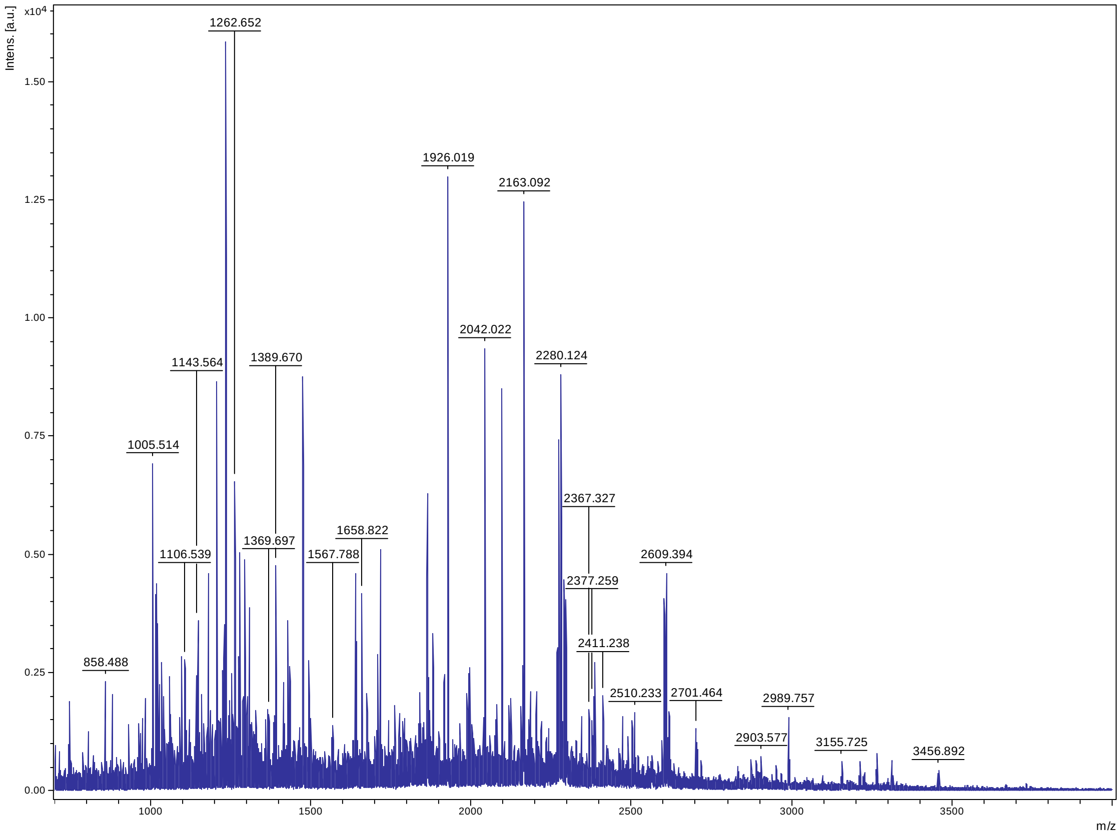
Match to: gi|50878307 Score: 102 Expect: 4.2e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 12	1332.6710	1331.6637	1331.6802	-0.0164	1	-.MPSVSRAVCVQR.A
38 - 48	1233.6768	1232.6695	1232.7101	-0.0406	1	R.ARHGKPEVAIR.S
40 - 48	1006.5696	1005.5623	1005.5719	-0.0096	0	R.HGKPEVAIR.S
156 - 168	1406.8496	1405.8423	1405.8405	0.0018	0	R.LGDPARPLLLSVR.S

203 - 209	921.4850	920.4778	920.4028	0.0750	0	R.FAYDSYR.R	
231 - 238	889.5727	888.5654	888.5102	0.0552	1	K.LEAMKAVK.G	
341 - 360	2178.1418	2177.1346	2177.1479	-0.0134	1	K.KLYGEFLVNAQGEDVVAGIR.T	
342 - 360	2050.0508	2049.0435	2049.0530	-0.0095	0	K.LYGEFLVNAQGEDVVAGIR.T	
405 - 414	1292.7023	1291.6950	1291.6529	0.0421	1	R.LWMLQCRTGK.R	Carbamidomethyl (C)
423 - 435	1444.7501	1443.7428	1443.7391	0.0038	0	K.IAVDMVNEGLVER.R	
423 - 435	1460.7687	1459.7614	1459.7340	0.0274	0	K.IAVDMVNEGLVER.R	Oxidation (M)
503 - 523	2112.0435	2111.0362	2111.0316	0.0045	0	R.TETSPEDVGGMHAAVGILTAR.G	
625 - 635	1174.6139	1173.6066	1173.5560	0.0506	0	R.QNGAEGIGLCR.T	Carbamidomethyl (C)
625 - 646	2525.2002	2524.1929	2524.1223	0.0707	1	R.QNGAEGIGLCRTEHMFFASDER.I	Carbamidomethyl (C)
636 - 646	1369.6010	1368.5937	1368.5768	0.0169	0	R.TEHMFFASDER.I	
636 - 646	1385.6030	1384.5958	1384.5717	0.0240	0	R.TEHMFFASDER.I	Oxidation (M)
652 - 662	1278.6826	1277.6753	1277.6471	0.0282	0	R.QMIMASSLELR.Q	
675 - 682	970.5406	969.5333	969.4556	0.0778	0	R.SDFEGIFR.A	
683 - 692	1088.6338	1087.6265	1087.5695	0.0570	0	R.AMDGLPVTIR.L	Oxidation (M)
713 - 728	1734.8177	1733.8105	1733.7890	0.0215	0	R.ELCSETGAAQDDVLAR.V	Carbamidomethyl (C)
713 - 731	2091.0288	2090.0215	2089.9949	0.0266	1	R.ELCSETGAAQDDVLARVEK.L	Carbamidomethyl (C)
732 - 742	1262.6857	1261.6784	1261.6488	0.0296	0	K.LSEVNPMLGFR.G	
746 - 759	1607.8025	1606.7952	1606.8024	-0.0072	0	R.LGISYPELTEMQAR.A	
861 - 882	2628.3384	2627.3311	2627.3747	-0.0436	0	K.FLPIYLSQGILQHDPFEVLDQR.G	
904 - 922	1974.9910	1973.9837	1973.9668	0.0169	0	K.VGICGEHGGEPLSVAFFAK.A	Carbamidomethyl (C)
923 - 934	1371.6462	1370.6390	1370.6288	0.0101	0	K.AGLDYVSCSPFR.V	Carbamidomethyl (C)

Spot 1270



Match to: gi|401140; Score: 202

Matched peptides:

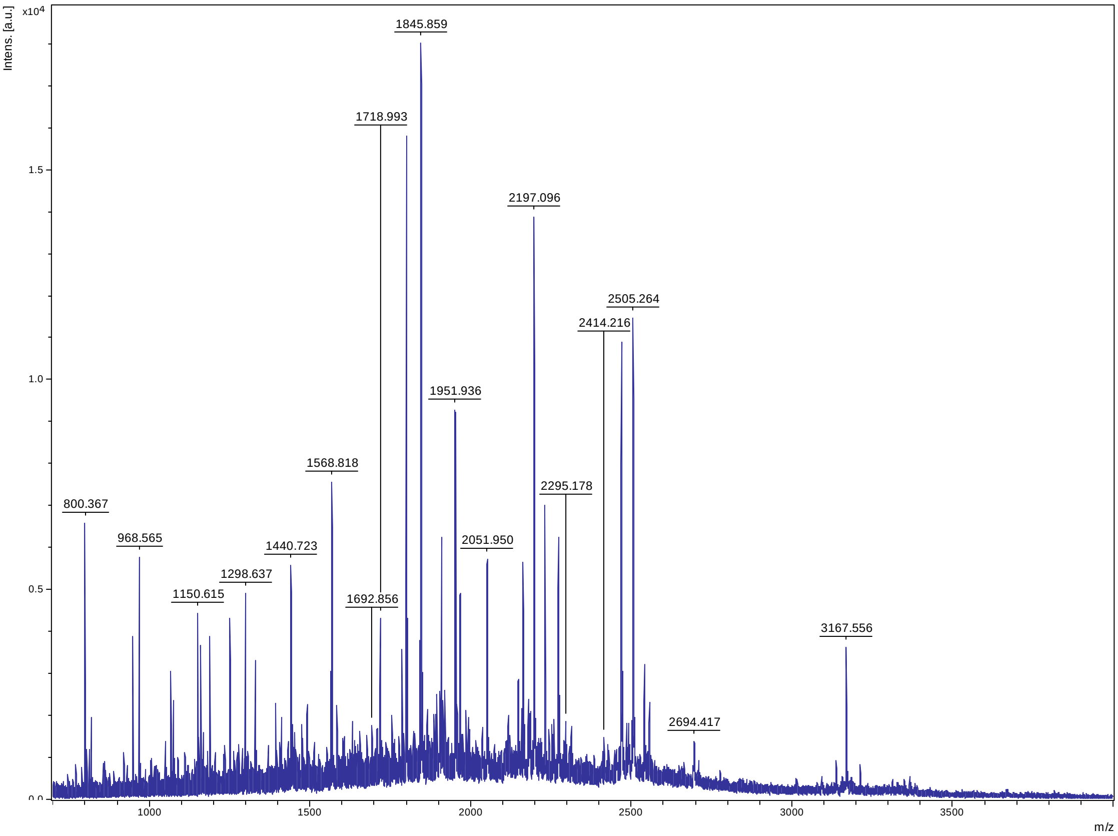
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 12	1277.69	1276.69	1276.62	0.07	1	MGEAAGDRVLSR Oxidation (M)
20 - 37	1926.02	1925.02	1925.00	0.02	0	IGDSLSAHPNELVAVFTR
44 - 66	2601.40	2600.39	2600.27	0.13	1	GMLQAHQIIAEYNNAISEADREK
44 - 66	2617.39	2616.38	2616.26	0.12	1	GMLQAHQIIAEYNNAISEADREK Oxidation (M)
67 - 77	1262.65	1261.65	1261.67	-0.02	1	LKDGAFEDVLR
69 - 77	1021.51	1020.50	1020.49	0.02	0	DGAFEDVLR
157 - 167	1204.62	1203.62	1203.64	-0.01	0	SIGNGVQFLNR
173 - 188	2039.04	2038.04	2038.03	0.01	1	LFHDKESMYPLLNFLR Oxidation (M)
194 - 204	1369.70	1368.69	1368.63	0.06	1	GMTMMLNDRIR 2 Oxidation (M)
205 - 214	1015.59	1014.59	1014.58	0.01	0	SLSALQGALR
215 - 235	2411.24	2410.24	2410.13	0.11	1	KAEEHLSGLSADTPYSEFHHR
236 - 243	963.51	962.51	962.51	0.00	0	FQELGLEK
317 - 325	1106.54	1105.54	1105.53	0.01	0	AMENEMLLR
328 - 336	1026.57	1025.57	1025.56	0.01	0	QQGLNITPR
343 - 355	1389.67	1388.67	1388.67	-0.00	0	LLPDATGTTCGQR
359 - 369	1275.69	1274.69	1274.71	-0.02	0	VLGTEHTHILR
432 - 445	1567.79	1566.79	1566.76	0.02	0	MGVTHCTIAHALEK
446 - 456	1414.70	1413.70	1413.69	0.01	1	TKYPNSDLYWK
494 - 512	2203.05	2202.05	2201.99	0.06	0	DTVGQYESHMAFTMPGLYR
524 - 543	2280.12	2279.12	2279.06	0.06	0	FNIVSPGADMSIYFPYSESR
524 - 543	2296.18	2295.18	2295.05	0.12	0	FNIVSPGADMSIYFPYSESR Oxidation (M)
546 - 567	2609.39	2608.39	2608.27	0.13	0	LTSLHPEIEELLYSEVDNNEHK
603 - 621	2078.08	2077.08	2077.06	0.02	0	LQELVNLVVVCGDHGNPSK
632 - 646	1862.92	1861.92	1861.91	0.00	0	MFDLIEQYNLNGHIR
632 - 646	1878.93	1877.92	1877.91	0.01	0	MFDLIEQYNLNGHIR Oxidation (M)
647 - 654	1005.51	1004.51	1004.49	0.03	0	WISAQMNR
723 - 733	1253.65	1252.64	1252.67	-0.03	0	ASALLVEFFEK
744 - 751	858.49	857.49	857.47	0.01	0	ISQGGLQR
752 - 759	1096.58	1095.58	1095.56	0.02	1	IEEKYTWK
777 - 783	880.48	879.47	879.44	0.03	0	YVSNLER
789 - 797	1143.56	1142.56	1142.60	-0.04	0	YLEMLYALK

Match to: gi|51090952; Score: 89

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
51 - 72	2472.29	2471.29	2471.20	0.09	0	HSDGLPHLNQAEEATWMGLLPR
51 - 72	2488.30	2487.29	2487.20	0.10	0	HSDGLPHLNQAEEATWMGLLPR Oxidation (M)
74 - 87	1674.84	1673.84	1673.85	-0.02	1	AGPRDELDWLALYR
92 - 113	2095.06	2094.06	2094.01	0.05	0	GGGDVGGEPAGFLSPASLHDVR
151 - 169	2042.02	2041.02	2040.99	0.03	0	LPTVGEPYGGWEAPDGQLR
242 - 257	1761.90	1760.89	1760.91	-0.02	0	IMQGLLDQYTLAGNPK
275 - 284	1277.69	1276.69	1276.71	-0.03	1	KLIQEYSIQR
276 - 284	1149.61	1148.60	1148.62	-0.01	0	LIQEYSIQR
353 - 363	1369.70	1368.69	1368.70	-0.01	1	RYEVVGDQLYK
354 - 363	1213.63	1212.63	1212.60	0.03	0	YEVVGDQLYK
402 - 416	1742.82	1741.81	1741.82	-0.00	0	ISSNEETCATYNLLK
430 - 436	983.43	982.43	982.41	0.02	0	YTDHYER
448 - 464	1864.92	1863.92	1863.94	-0.02	1	GKEPGVMIYFLPMGPGR Oxidation (M)
448 - 464	1880.95	1879.95	1879.93	0.02	1	GKEPGVMIYFLPMGPGR 2 Oxidation (M)
450 - 466	1878.93	1877.92	1877.95	-0.03	1	EPGVMIYFLPMGPGRSK
592 - 615	2594.40	2593.40	2593.36	0.03	1	LNLTSAGDFLSVTKLWGDDTLSLK
606 - 615	1147.55	1146.54	1146.59	-0.05	0	LWGDDTLSLK
865 - 878	1564.78	1563.78	1563.77	0.01	0	LYHPLSFSATGTDR

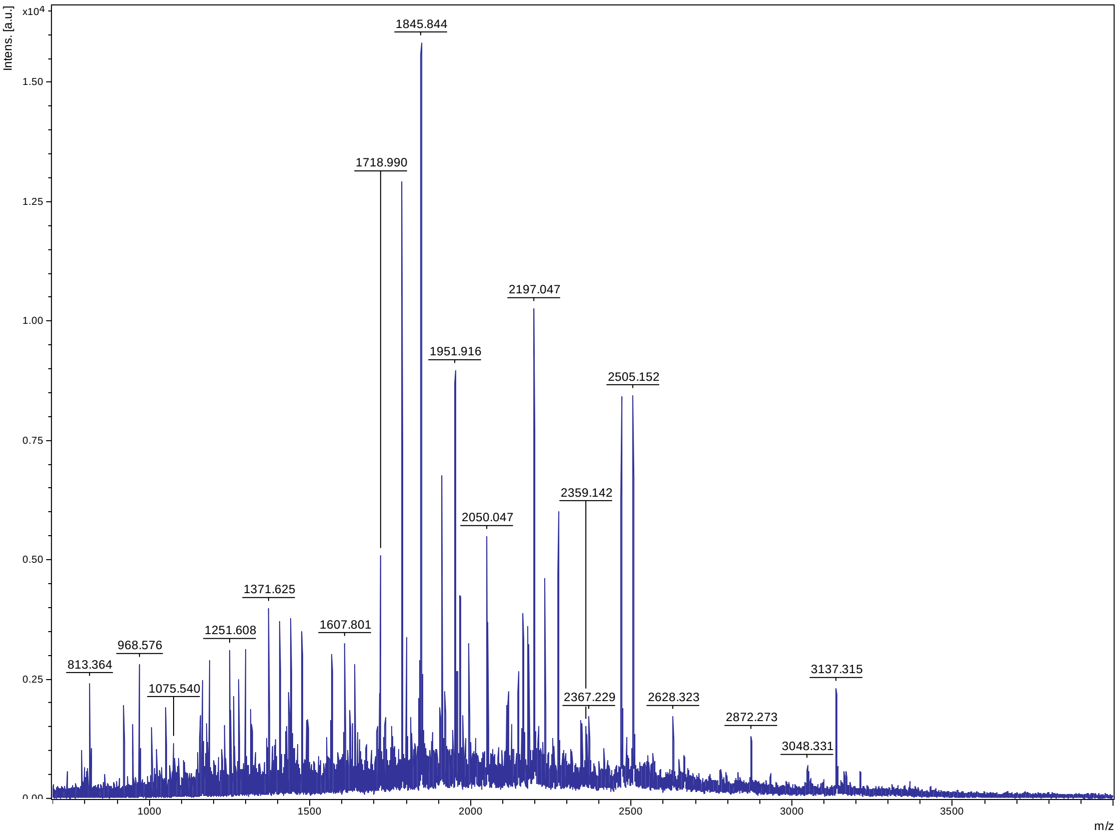
Spot 1275



Match to: gi|37534770 Score: 176 Expect: 1.7e-13

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
18 - 26	1067.5426	1066.5353	1066.5295	0.0059	0	K.DYSTAILER.K	
33 - 55	2540.2029	2539.1956	2539.1860	0.0096	0	R.LVVDEATNDDNSVVALHPDTMER.L	
33 - 55	2556.2386	2555.2313	2555.1809	0.0504	0	R.LVVDEATNDDNSVVALHPDTMER.L	Oxidation (M)
73 - 88	1892.8714	1891.8641	1891.8543	0.0098	0	K.DTICIVLADETCEEPK.I	2 Carbamidomethyl (C)
103 - 116	1583.8277	1582.8204	1582.7773	0.0431	0	R.LGDVVSVHQCQDVK.Y	Carbamidomethyl (C)
155 - 162	947.5618	946.5545	946.5600	-0.0054	1	R.KGDLFLVR.G	
172 - 198	3167.4236	3166.4163	3166.4838	-0.0675	1	K.VIETDPTEYCIVAPDTEIFCDGEPIKR.E	2 Carbamidomethyl (C)
199 - 216	2051.9363	2050.9290	2050.9079	0.0212	1	R.EDEERLDEVGYDDVGGVR.K	
224 - 231	968.5748	967.5675	967.5702	-0.0027	0	R.ELVELPLR.H	
224 - 237	1719.0162	1718.0089	1717.9879	0.0211	1	R.ELVELPLRHPQLFK.S	
246 - 257	1158.6798	1157.6725	1157.6444	0.0281	0	K.GILLYGPPGSGK.T	
263 - 283	2256.1264	2255.1191	2255.1295	-0.0104	0	R.AVANETGAFFFLINGPEIMSK.L	
284 - 293	1075.5567	1074.5494	1074.5305	0.0189	0	K.LAGESESNLR.K	
330 - 342	1446.8457	1445.8384	1445.8163	0.0221	0	R.IVSQLLTLMDGLK.A	Oxidation (M)
366 - 371	797.3653	796.3580	796.3980	-0.0400	1	R.FGRFDR.E	
372 - 383	1298.6977	1297.6904	1297.6513	0.0391	0	R.EIDIGVPDEVGR.L	
372 - 388	1909.0488	1908.0415	1908.0316	0.0100	1	R.EIDIGVPDEVGRLEVLR.I	
408 - 430	2448.1864	2447.1791	2447.1573	0.0219	0	K.DTHGYVGADLAALCTEAALQCIR.E	Carbamidomethyl (C)
408 - 430	2505.1751	2504.1678	2504.1787	-0.0109	0	K.DTHGYVGADLAALCTEAALQCIR.E	2 Carbamidomethyl (C)
460 - 471	1187.6532	1186.6459	1186.6306	0.0154	0	K.TALGTSNPSALR.E	
472 - 492	2313.1296	2312.1223	2312.1535	-0.0312	0	R.ETVVEVPNVSWEDIGGLENVK.R	
472 - 493	2469.2422	2468.2349	2468.2546	-0.0197	1	R.ETVVEVPNVSWEDIGGLENVKR.E	
528 - 539	1251.6447	1250.6374	1250.6117	0.0257	0	K.GVLFYGPPGCGK.T	Carbamidomethyl (C)
545 - 558	1564.8151	1563.8078	1563.7715	0.0364	0	K.AIANECQANFISVK.G	Carbamidomethyl (C)
559 - 575	1951.9213	1950.9140	1950.9145	-0.0005	0	K.GPELLTMWFGESEANVR.E	Oxidation (M)
583 - 601	2180.0650	2179.0577	2179.0255	0.0322	0	R.QSAPCVLFFDELDSIATQR.G	Carbamidomethyl (C); Pyro-glu (N-term Q)
583 - 601	2197.0541	2196.0468	2196.0521	-0.0053	0	R.QSAPCVLFFDELDSIATQR.G	Carbamidomethyl (C)
615 - 629	1676.8616	1675.8543	1675.8273	0.0271	0	R.VLNQLLTEMDGMNAK.K	
615 - 629	1692.8698	1691.8625	1691.8222	0.0403	0	R.VLNQLLTEMDGMNAK.K	Oxidation (M)
615 - 629	1708.8518	1707.8445	1707.8171	0.0274	0	R.VLNQLLTEMDGMNAK.K	2 Oxidation (M)
654 - 668	1799.9754	1798.9681	1798.9465	0.0216	0	R.LDQLIYIPLPDEQSR.L	
679 - 692	1440.7753	1439.7680	1439.7983	-0.0303	1	K.SPVAKDVDLNALAK.Y	
693 - 708	1845.8625	1844.8552	1844.8363	0.0190	0	K.YTQGFSGADITEICQR.A	Carbamidomethyl (C)
769 - 781	1568.8633	1567.8560	1567.8107	0.0454	1	R.KYQAFAQTLQQSR.G	
782 - 788	799.3377	798.3304	798.3660	-0.0356	0	R.GFGSEFR.F	

Spot 1276



Match to: gi|37534770 Score: 112 Expect: 4.2e-07

Matched peptides:

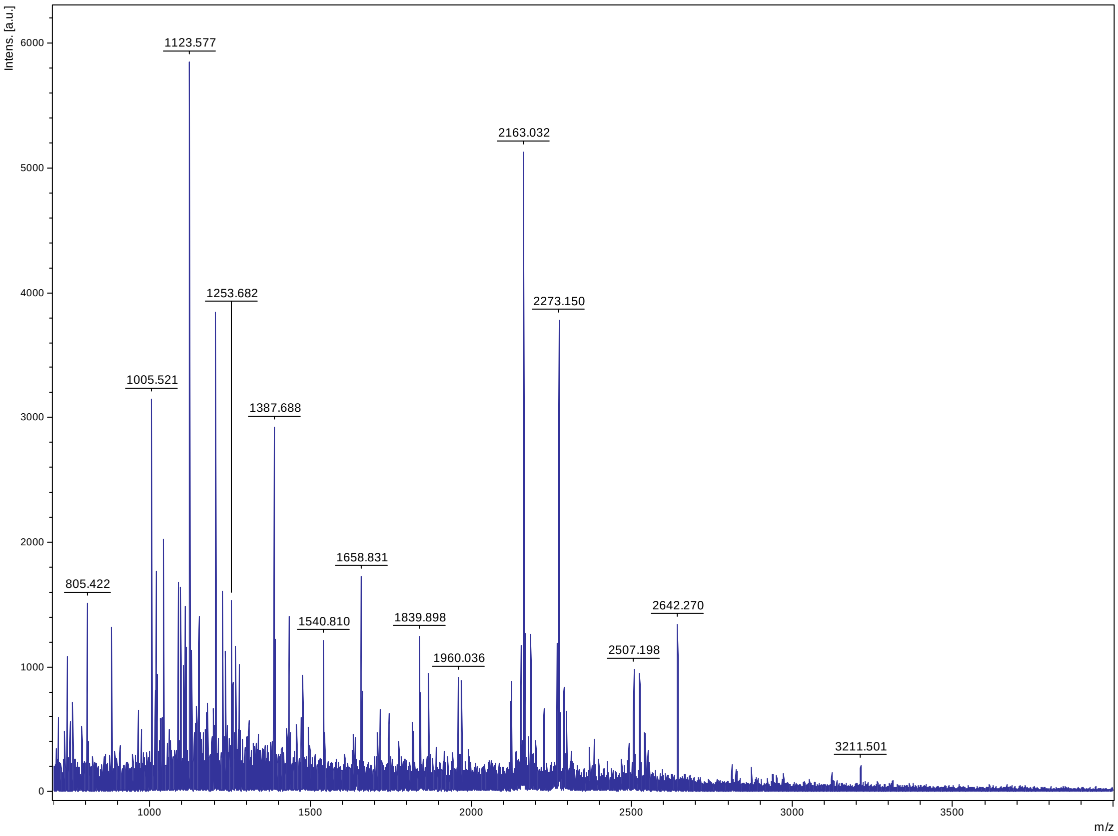
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
101 - 116	1839.0117	1838.0044	1837.9468	0.0576	1	R.VRLGDVVSVHQCQDVK.Y	Carbamidomethyl (C)
224 - 237	1719.0326	1718.0253	1717.9879	0.0375	1	R.ELVELPLRHPQLFK.S	
263 - 283	2256.2251	2255.2178	2255.1295	0.0883	0	R.AVANETGAFFFLINGPEIMSK.L	
345 - 364	2148.2288	2147.2215	2147.1269	0.0946	0	R.SHVIVMGATNRPNSIDPALR.R	
372 - 383	1298.6249	1297.6176	1297.6513	-0.0337	0	R.EIDIGVPDEVGR.L	
372 - 388	1909.0977	1908.0904	1908.0316	0.0589	1	R.EIDIGVPDEVGRLEVLR.I	
408 - 430	2505.2969	2504.2896	2504.1787	0.1109	0	K.DTHGYVGADLAALCTEAALQCIR.E	2 Carbamidomethyl (C)
460 - 471	1187.5745	1186.5672	1186.6306	-0.0633	0	K.TALGTSNPSALR.E	
472 - 493	2469.3623	2468.3550	2468.2546	0.1004	1	R.ETVVEVPNVSWEDIGGLENVKR.E	
559 - 575	1952.0021	1950.9948	1950.9145	0.0803	0	K.GPELLTMWFGESEANVR.E	Oxidation (M)
581 - 601	2367.3536	2366.3463	2366.1688	0.1775	1	K.ARQSAPCVLFFDELDSIATQR.G	
583 - 601	2197.1446	2196.1373	2196.0521	0.0852	0	R.QSAPCVLFFDELDSIATQR.G	Carbamidomethyl (C)
615 - 629	1708.8931	1707.8858	1707.8171	0.0687	0	R.VLNQLLTEMDGMNAK.K	2 Oxidation (M)
654 - 668	1800.0062	1798.9989	1798.9465	0.0524	0	R.LDQLIYIPLPDEQSR.L	
693 - 708	1845.9017	1844.8944	1844.8363	0.0582	0	K.YTQGFSGADITEICQR.A	Carbamidomethyl (C)
769 - 781	1568.8479	1567.8406	1567.8107	0.0300	1	R.KYQAFAQTLQQSR.G	
770 - 781	1440.7296	1439.7223	1439.7157	0.0066	0	K.YQAFAQTLQQSR.G	

Match to: gi|50878307 Score: 75 Expect: 0.002

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
21 - 30	947.4144	946.4071	946.4402	-0.0331	1	R.CRDGAAAAGR.R	
156 - 168	1406.8348	1405.8275	1405.8405	-0.0130	0	R.LGDPARPLLLSVR.S	
277 - 293	1944.1064	1943.0991	1943.0264	0.0727	0	K.QLQLAVLAVFNSWDSPR.A	
277 - 296	2256.2251	2255.2178	2255.2426	-0.0247	1	K.QLQLAVLAVFNSWDSPRAIK.Y	
341 - 360	2178.2403	2177.2330	2177.1479	0.0851	1	K.KLYGEFLVNAQGEDVVAGIR.T	
342 - 360	2050.1498	2049.1425	2049.0530	0.0895	0	K.LYGEFLVNAQGEDVVAGIR.T	
419 - 435	1800.0062	1798.9989	1798.9610	0.0379	1	K.GAVKIAVDMVNEGLVER.R	
423 - 435	1444.7446	1443.7373	1443.7391	-0.0018	0	K.IAVDMVNEGLVER.R	
503 - 523	2112.1177	2111.1104	2111.0316	0.0788	0	R.TETSPEDVGGMHAAVGILTAR.G	
503 - 523	2128.1392	2127.1319	2127.0266	0.1054	0	R.TETSPEDVGGMHAAVGILTAR.G	Oxidation (M)
693 - 712	2359.2656	2358.2583	2358.1678	0.0906	0	R.LLDPPLHEFLPEGHVEDMVR.E	Oxidation (M)
713 - 728	1734.8894	1733.8821	1733.7890	0.0931	0	R.ELCSETGAAQDDVLAR.V	Carbamidomethyl (C)
732 - 742	1262.6251	1261.6178	1261.6488	-0.0310	0	K.LSEVNPMLGFR.G	
746 - 759	1607.8385	1606.8312	1606.8024	0.0288	0	R.LGISYPELTEMQAR.A	
861 - 882	2628.4992	2627.4919	2627.3747	0.1172	0	K.FLPIYLSQGILQHDPFEVLDQR.G	
904 - 922	1975.0577	1974.0504	1973.9668	0.0836	0	K.VGICGEHGGEPLSVAFFAK.A	Carbamidomethyl (C)

Spot 1287

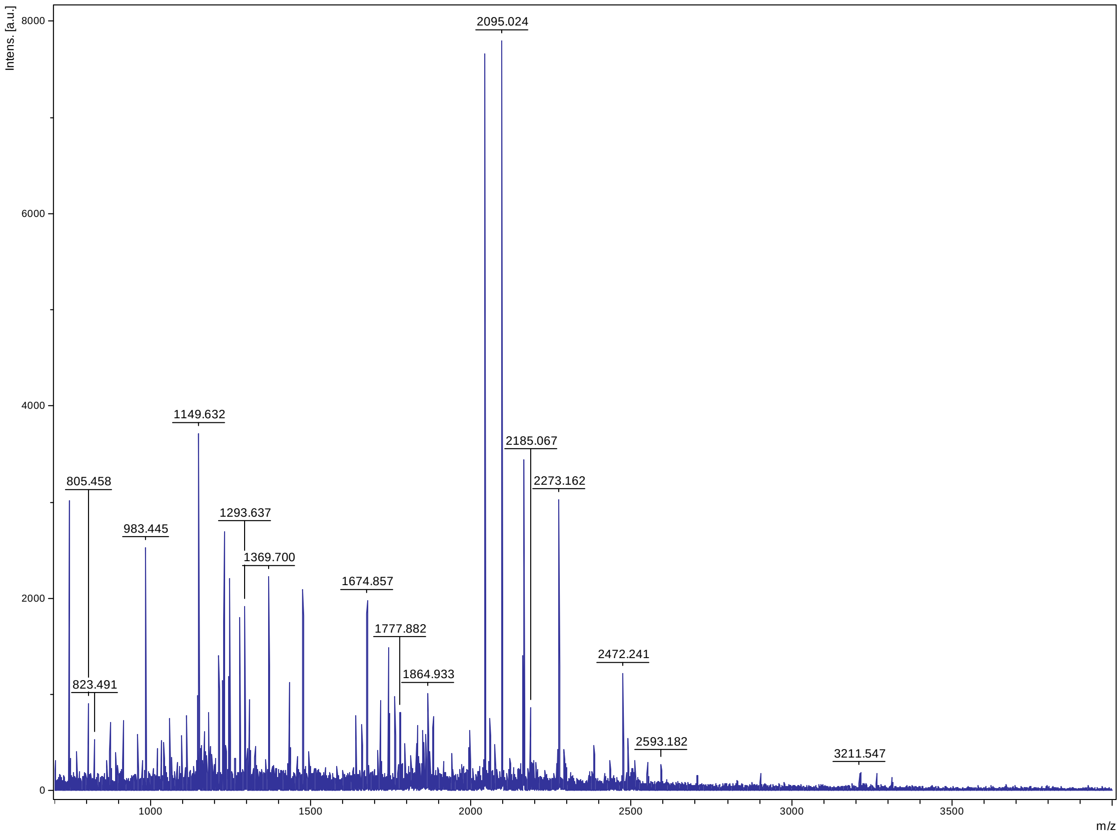


Match to: gi|267056 Score: 218 Expect: 2.3e-17

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
15 - 32	1960.0361	1959.0289	1959.0213	0.0075	0	R.LGATFSSHPNELIALFSR.Y	
44 - 60	1970.0144	1969.0071	1969.0156	-0.0085	1	R.HQLLAEFDALIEADKEK.Y	
61 - 69	1123.5771	1122.5699	1122.5709	-0.0011	0	K.YAPFEDILR.A	
97 - 116	2226.1362	2225.1290	2225.1466	-0.0177	0	R.VNVSELAVEELSVSEYLAFK.E	
149 - 159	1204.6433	1203.6360	1203.6360	0.0001	0	K.SIGNGVQFLNR.H	
228 - 235	963.5202	962.5129	962.5072	0.0057	0	R.FQELGLEK.G	
309 - 317	1088.5782	1087.5710	1087.5695	0.0014	0	R.ALENEMLLR.I	
309 - 317	1104.5696	1103.5623	1103.5645	-0.0021	0	R.ALENEMLLR.I	Oxidation (M)
335 - 347	1387.6880	1386.6807	1386.6925	-0.0118	0	R.LLPDAVGTTCGQR.V	Carbamidomethyl (C)
335 - 350	1743.8873	1742.8801	1742.8985	-0.0184	1	R.LLPDAVGTTCGQRVEK.V	Carbamidomethyl (C)
351 - 361	1253.6820	1252.6747	1252.6775	-0.0028	0	K.VIGTEHTDILR.V	
424 - 437	1540.8097	1539.8024	1539.8079	-0.0055	0	K.LGVTQCTIAHALEK.T	Carbamidomethyl (C)
486 - 504	2167.0735	2166.0662	2166.0745	-0.0083	0	K.DTVGQYESHIAFTLPGLYR.V	
505 - 515	1225.6534	1224.6462	1224.6502	-0.0041	0	R.VVHGIDVFDPK.F	
516 - 537	2507.1982	2506.1910	2506.1838	0.0072	1	K.FNIVSPGADMSVYFPYTEADKR.L	
516 - 537	2523.1770	2522.1697	2522.1787	-0.0090	1	K.FNIVSPGADMSVYFPYTEADKR.L	Oxidation (M)
538 - 559	2642.2705	2641.2632	2641.2547	0.0085	0	R.LTAFHPEIEELLYSEVENDEHK.F	
597 - 613	1839.8981	1838.8908	1838.8944	-0.0036	0	R.DLANLVIVCGDHGNQSK.D	Carbamidomethyl (C)
614 - 622	1151.5328	1150.5256	1150.5254	0.0001	1	K.DREEQAEFK.K	
623 - 632	1258.6372	1257.6299	1257.6427	-0.0128	1	K.KMYGLIDQYK.L	
624 - 632	1130.5684	1129.5611	1129.5477	0.0133	0	K.MYGLIDQYK.L	
624 - 632	1146.5569	1145.5496	1145.5427	0.0069	0	K.MYGLIDQYK.L	Oxidation (M)
639 - 646	1005.5211	1004.5138	1004.4862	0.0277	0	R.WISAQMNR.V	
639 - 646	1021.5137	1020.5065	1020.4811	0.0254	0	R.WISAQMNR.V	Oxidation (M)
715 - 725	1266.6573	1265.6501	1265.6655	-0.0155	0	K.AADILVNFFEK.C	
726 - 743	2155.9849	2154.9776	2154.9752	0.0024	1	K.CKQDSTYWDNISQGGLQR.I	Carbamidomethyl (C)
769 - 775	880.4605	879.4532	879.4450	0.0082	0	K.YVSNLER.R	
781 - 789	1177.5996	1176.5923	1176.5889	0.0035	0	R.YIEMFYALK.Y	

Spot 1310

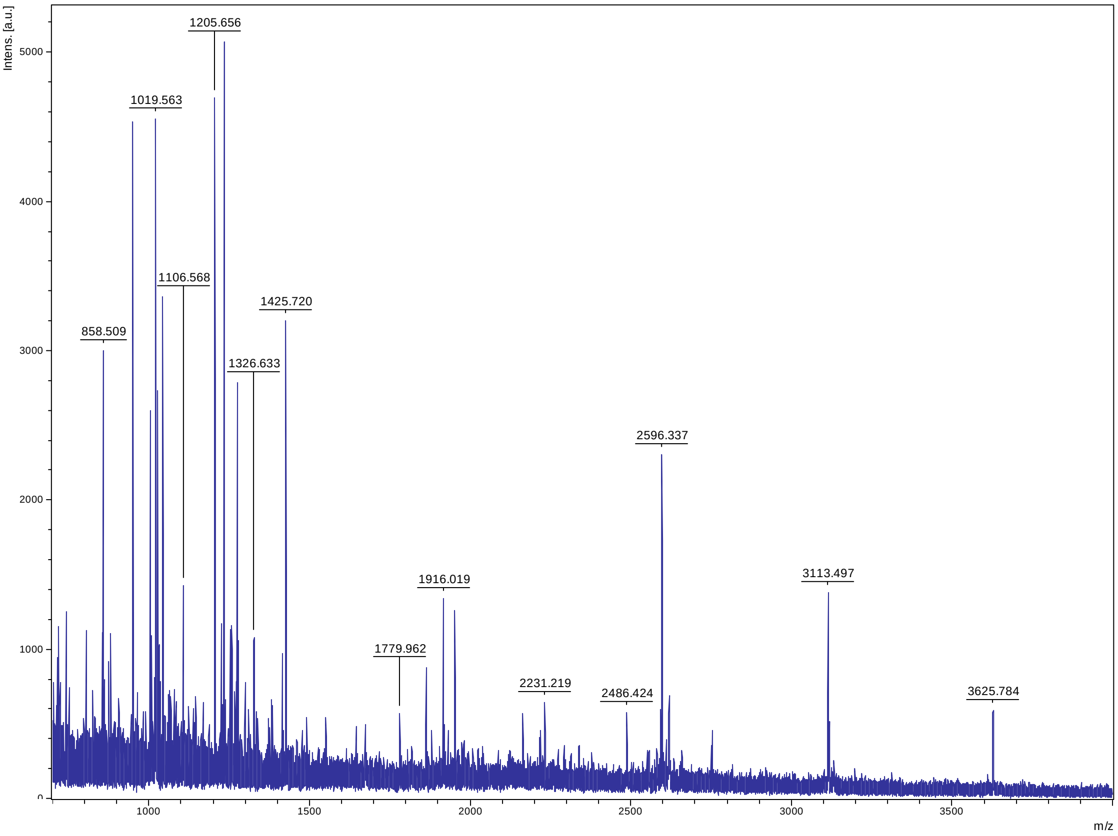


Match to: gi|51090952 Score: 181 Expect: 1.3e-13

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
51 - 72	2472.2410	2471.2337	2471.2015	0.0322	0	R.HSDGLPHLNQAEEATWMGLLPR.R	
51 - 72	2488.2148	2487.2076	2487.1964	0.0111	0	R.HSDGLPHLNQAEEATWMGLLPR.R	Oxidation (M)
74 - 87	1674.8568	1673.8495	1673.8525	-0.0030	1	R.AGPRDELDWLALYR.S	
78 - 87	1293.6373	1292.6301	1292.6401	-0.0100	0	R.DELDWLALYR.S	
92 - 113	2095.0237	2094.0164	2094.0129	0.0035	0	R.GGGDVGGEPAGFLSPASLHDVR.V	
141 - 146	823.4913	822.4841	822.4388	0.0452	0	R.LTWTFR.Q	
151 - 169	2042.0001	2040.9928	2040.9904	0.0024	0	K.LPTVGEPYGGWEAPDGQLR.G	
199 - 208	1224.6259	1223.6186	1223.6220	-0.0034	0	K.VVDILYSCQK.K	Carbamidomethyl (C)
242 - 257	1761.8981	1760.8908	1760.9131	-0.0223	0	K.IMQGLLDQYTLAGNPK.G	
242 - 257	1777.8816	1776.8743	1776.9080	-0.0337	0	K.IMQGLLDQYTLAGNPK.G	Oxidation (M)
275 - 284	1277.7021	1276.6949	1276.7139	-0.0190	1	K.KLIQEYSIQR.H	
276 - 284	1149.6324	1148.6252	1148.6189	0.0062	0	K.LIQEYSIQR.H	
353 - 363	1369.7001	1368.6928	1368.7037	-0.0109	1	K.RYEVVGDQLYK.E	
354 - 363	1213.6138	1212.6065	1212.6026	0.0039	0	R.YEVVGDQLYK.E	
395 - 401	872.5528	871.5455	871.5127	0.0328	1	K.RLVDEIK.I	
402 - 416	1742.8068	1741.7995	1741.8192	-0.0197	0	K.ISSNEETCATYNLLK.V	Carbamidomethyl (C)
430 - 436	983.4451	982.4379	982.4144	0.0234	0	K.YTDHYER.L	
437 - 447	1228.6804	1227.6731	1227.6757	-0.0026	0	R.LLINGIMGNQR.G	
437 - 447	1244.6782	1243.6709	1243.6706	0.0003	0	R.LLINGIMGNQR.G	Oxidation (M)
448 - 464	1848.9315	1847.9242	1847.9425	-0.0183	1	R.GKEPGVMIYFLPMGPGR.S	
448 - 464	1864.9329	1863.9256	1863.9375	-0.0119	1	R.GKEPGVMIYFLPMGPGR.S	Oxidation (M)
448 - 464	1880.9325	1879.9252	1879.9324	-0.0072	1	R.GKEPGVMIYFLPMGPGR.S	2 Oxidation (M)
563 - 573	1168.6174	1167.6102	1167.6108	-0.0007	0	K.GDARPANVNVR.I	
574 - 591	1857.9474	1856.9401	1856.9632	-0.0231	0	R.IPSWTSVDGAIATLNGQK.L	
606 - 615	1147.6045	1146.5972	1146.5921	0.0051	0	K.LWGDDTLSLK.F	

Spot 1311

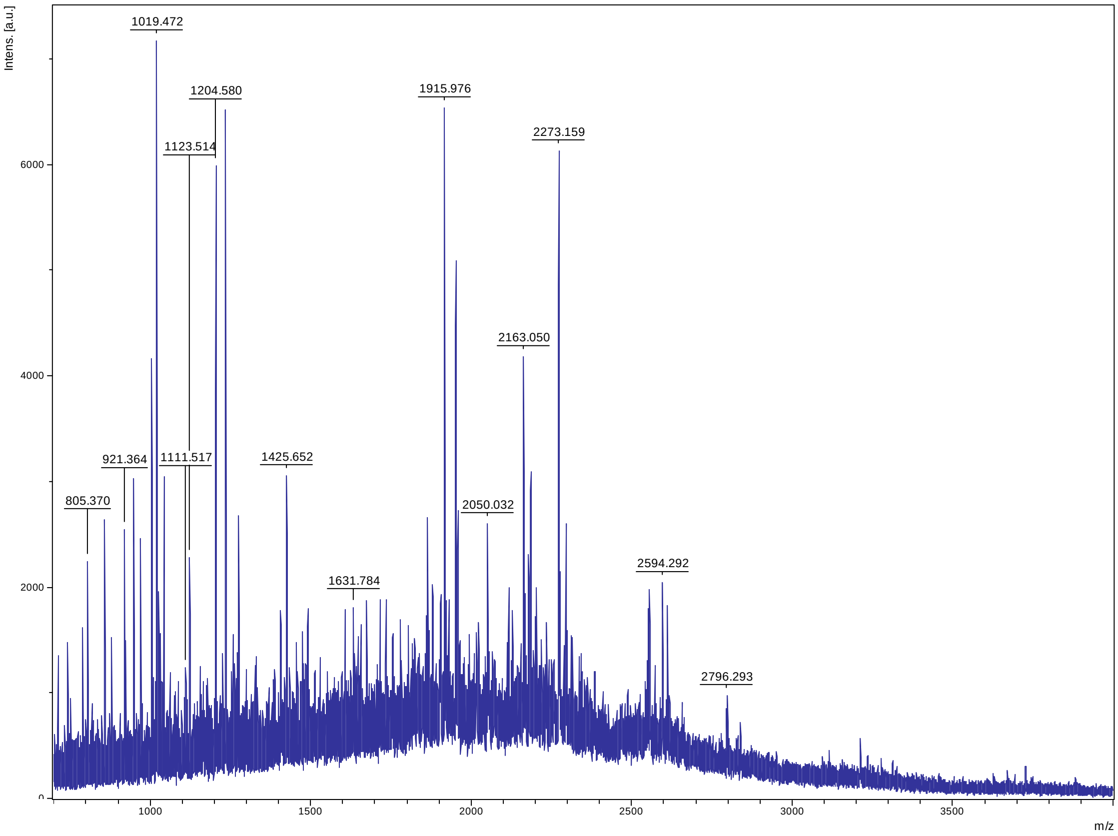


Match to: gi|3915054 Score: 151 Expect: 5.3e-11

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 12	1334.7058	1333.6985	1333.6408	0.0577	1	-.MGETTGERALNR.L	
20 - 37	1915.9126	1914.9053	1914.9799	-0.0746	0	R.IGDSLSAHTNELVAVFSR.L	
67 - 77	1258.7425	1257.7352	1257.6928	0.0424	1	K.LKDSALEDVLR.G	
69 - 77	1017.5543	1016.5470	1016.5138	0.0332	0	K.DSALEDVLR.G	
178 - 188	1382.7172	1381.7099	1381.7064	0.0036	0	K.ESMYPLLNFLR.A	
194 - 202	1068.5146	1067.5073	1067.4562	0.0511	0	K.GMTMMLNDR.I	
205 - 214	1043.6232	1042.6159	1042.5771	0.0389	0	R.SLDALQGALR.K	
236 - 243	963.5340	962.5267	962.5072	0.0195	0	R.FQELGLEK.G	
236 - 243	1005.5305	1004.5232	1004.5178	0.0054	0	R.FQELGLEK.G	Acetyl (N-term)
244 - 251	949.4139	948.4066	948.3872	0.0194	0	K.GWGDCAQR.V	Carbamidomethyl (C)
317 - 325	1106.5671	1105.5598	1105.5260	0.0339	0	R.AMENEMLLR.I	
317 - 325	1122.6034	1121.5961	1121.5209	0.0752	0	R.AMENEMLLR.I	Oxidation (M)
326 - 336	1267.7732	1266.7659	1266.7408	0.0251	1	R.IKQQGLNITPR.I	
328 - 336	1026.6010	1025.5937	1025.5618	0.0320	0	K.QQGLNITPR.I	
337 - 342	714.4695	713.4622	713.4799	-0.0177	0	R.ILIVTR.L	
343 - 355	1425.6956	1424.6883	1424.6830	0.0053	0	R.LLPDAHGTTCGQR.L	Carbamidomethyl (C)
359 - 369	1275.7472	1274.7399	1274.7095	0.0304	0	K.VLGTEHTHILR.V	
432 - 445	1549.8078	1548.8005	1548.8082	-0.0077	0	K.LGVTHCTIAHALEK.T	Carbamidomethyl (C)
446 - 456	1414.7253	1413.7180	1413.6928	0.0252	1	K.TKYPNSDLYWK.K	
513 - 523	1225.6754	1224.6681	1224.6502	0.0179	0	R.VVHGIDVFDPK.F	
575 - 583	1062.6375	1061.6302	1061.6055	0.0247	0	K.KPIIFSMAR.L	
575 - 583	1078.6322	1077.6249	1077.6004	0.0245	0	K.KPIIFSMAR.L	Oxidation (M)
603 - 618	1779.9033	1778.8960	1778.9348	-0.0388	0	R.LQELVNLVVVCGDHGK.E	Carbamidomethyl (C)
657 - 662	751.3552	750.3479	750.3660	-0.0181	0	R.NGELYR.Y	
663 - 668	857.3678	856.3605	856.3571	0.0034	0	R.YICDMR.G	Carbamidomethyl (C)
723 - 733	1253.6933	1252.6860	1252.6703	0.0158	0	K.ASALLVEFFEK.C	
734 - 743	1326.6164	1325.6091	1325.5823	0.0269	0	K.CQEDPNHWIK.I	Carbamidomethyl (C)
788 - 797	1299.7359	1298.7286	1298.7056	0.0230	1	R.RYLEMLYALK.Y	

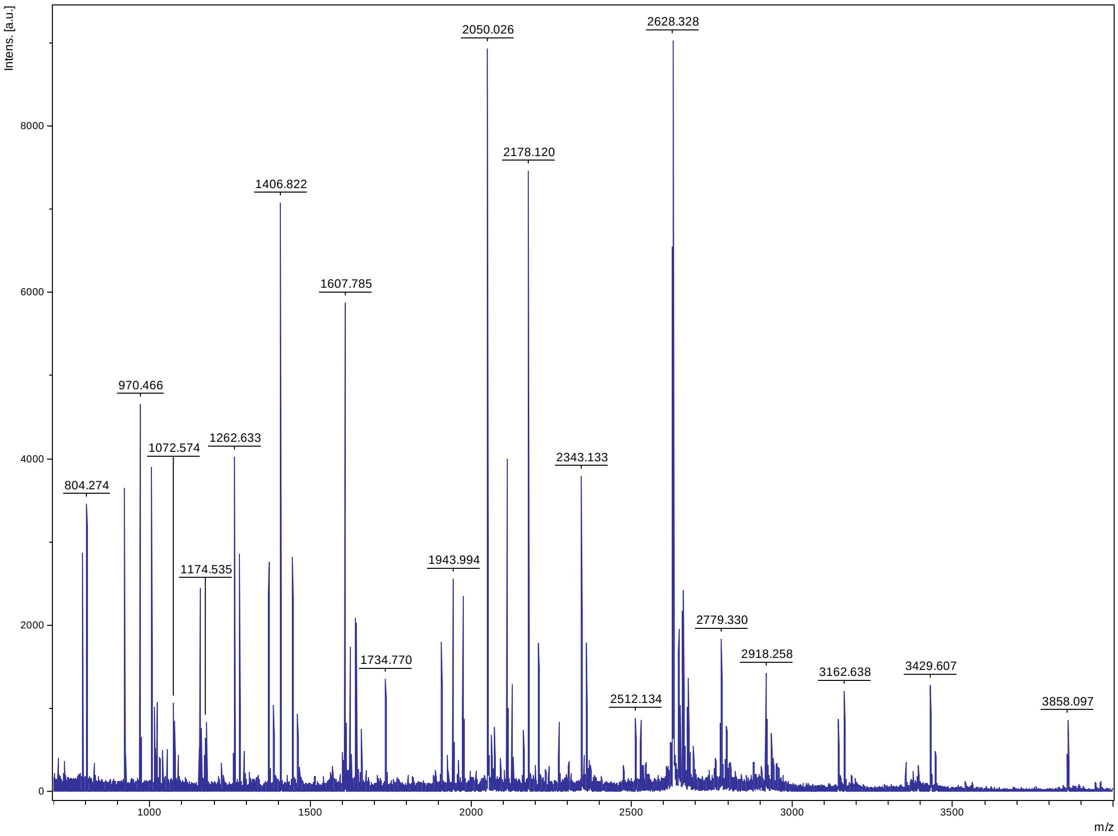
Spot 1319



Match to: gi|3915054 Score: 109 Expect: 8.4e-07

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
20 - 37	1916.0162	1915.0089	1914.9799	0.0290	0	R.IGDSLSAHTNELVAVFSR.L	
20 - 43	2555.5048	2554.4975	2554.3502	0.1473	1	R.IGDSLSAHTNELVAVFSRLVNQGK.G	
44 - 66	2594.3115	2593.3042	2593.2958	0.0084	1	K.GMLQPHQIIAEYNAAIPEGEREK.L	
44 - 66	2610.2812	2609.2739	2609.2907	-0.0168	1	K.GMLQPHQIIAEYNAAIPEGEREK.L	Oxidation (M)
157 - 167	1204.6285	1203.6212	1203.6360	-0.0147	0	K.SIGNGVQFLNR.H	
205 - 214	1043.5485	1042.5412	1042.5771	-0.0358	0	R.SLDALQGALR.K	
219 - 235	1951.9900	1950.9827	1950.9336	0.0491	0	K.HLAGITADTPYSEFHHR.F	
343 - 355	1425.7122	1424.7049	1424.6830	0.0219	0	R.LLPDAHGTTCGQR.L	Carbamidomethyl (C)
359 - 369	1275.7083	1274.7010	1274.7095	-0.0085	0	K.VLGTEHTHILR.V	
524 - 545	2550.2335	2549.2262	2549.2260	0.0002	1	K.FNIVSPGADMSIYFPFTESQKR.L	Oxidation (M)
622 - 630	1123.5294	1122.5221	1122.5193	0.0029	1	K.DKEEQAEFK.K	
647 - 654	1005.4563	1004.4490	1004.4862	-0.0371	0	R.WISAQMNR.V	
760 - 776	2050.0629	2049.0556	2049.0393	0.0163	1	K.LYSERLMTLSGVYGFWK.Y	

Spot 1322

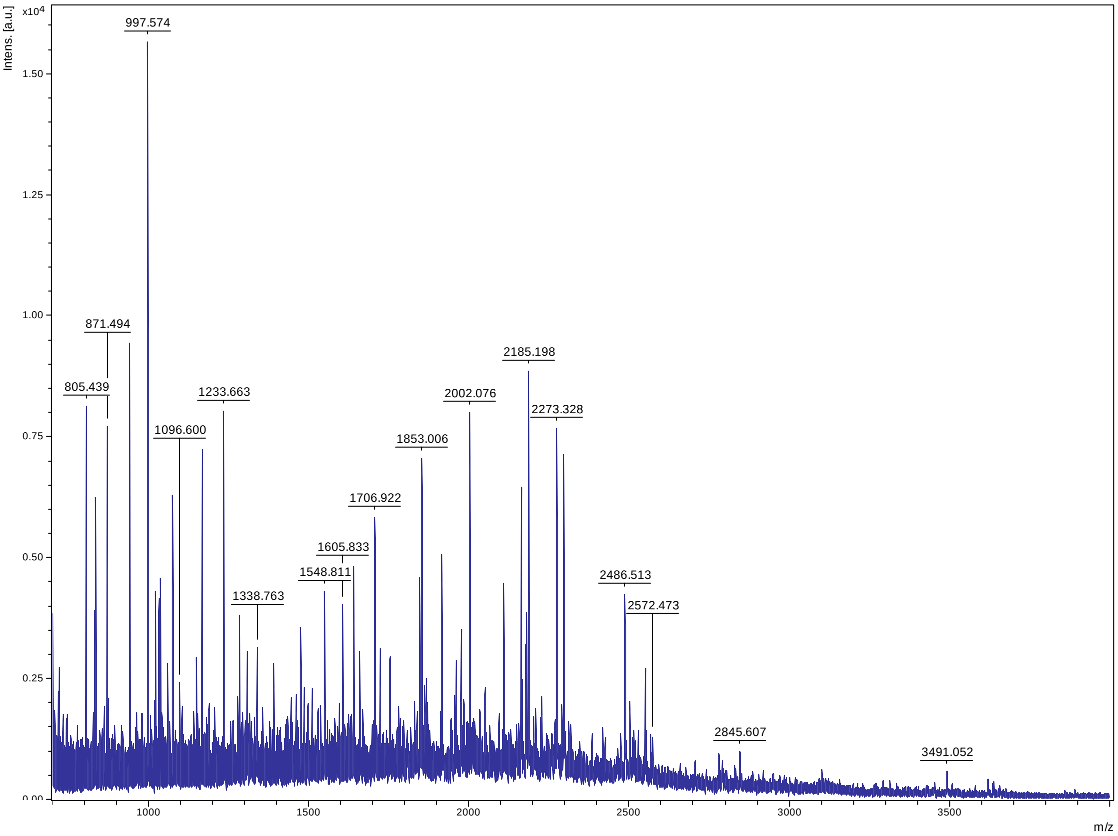


Match to: gi|50878307; Score: 421

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
156 - 168	1406.82	1405.82	1405.84	-0.02	0	LGDPARPLLLSVR
203 - 209	921.41	920.41	920.40	0.01	0	FAYDSYR
203 - 210	1077.50	1076.50	1076.50	-0.00	1	FAYDSYRR
211 - 230	2352.08	2351.08	2351.13	-0.05	0	FLDMFGNVVMDIPHALFEEK
211 - 230	2368.12	2367.11	2367.13	-0.01	0	FLDMFGNVVMDIPHALFEEK Oxidation (M)
276 - 293	2072.05	2071.05	2071.12	-0.07	1	KQLQLAVLAVFNSWDSPR
277 - 293	1943.99	1942.99	1943.03	-0.04	0	QLQLAVLAVFNSWDSPR
308 - 333	2659.26	2658.26	2658.29	-0.03	0	GTAVNVQTMVFGNMGNTSGTGVLFTR
308 - 333	2675.28	2674.27	2674.28	-0.01	0	GTAVNVQTMVFGNMGNTSGTGVLFTR Oxidation (M)
341 - 360	2178.12	2177.12	2177.15	-0.03	1	KLYGEFLVNAQGEDVVAGIR
342 - 360	2050.03	2049.02	2049.05	-0.03	0	LYGEFLVNAQGEDVVAGIR
361 - 384	2918.26	2917.26	2917.26	-0.00	1	TPEDLDAMRDHMPEPYEELVENCK
361 - 384	2934.25	2933.25	2933.25	-0.01	1	TPEDLDAMRDHMPEPYEELVENCK Oxidation (M)
385 - 404	2512.13	2511.13	2511.18	-0.05	1	ILESHYKEMMDIEFTVQENR
385 - 404	2528.14	2527.14	2527.17	-0.04	1	ILESHYKEMMDIEFTVQENR Oxidation (M)
392 - 404	1641.70	1640.70	1640.72	-0.02	0	EMMDIEFTVQENR
405 - 411	1006.49	1005.49	1005.49	-0.00	0	LWMLQCR
405 - 411	1022.48	1021.48	1021.48	-0.00	0	LWMLQCR Oxidation (M)
423 - 435	1444.73	1443.73	1443.74	-0.01	0	IAVDMVNEGLVER
423 - 435	1460.71	1459.71	1459.73	-0.03	0	IAVDMVNEGLVER Oxidation (M)
441 - 464	2779.33	2778.33	2778.34	-0.02	1	MVEPGHLDQLLHPQFENPSGYKDK
441 - 464	2795.33	2794.33	2794.34	-0.01	1	MVEPGHLDQLLHPQFENPSGYKDK Oxidation (M)
465 - 496	3162.64	3161.64	3161.61	0.02	0	VIATGLPASPGAAVGQIVFTAEDAEAWHAQGK
465 - 502	3858.10	3857.10	3857.05	0.05	1	VIATGLPASPGAAVGQIVFTAEDAEAWHAQGKDVILVR
503 - 523	2112.01	2111.00	2111.03	-0.03	0	TETSPEDVGGMHAAVGILTAR
503 - 523	2127.99	2126.99	2127.03	-0.04	0	TETSPEDVGGMHAAVGILTAR Oxidation (M)
524 - 539	1600.82	1599.81	1599.79	0.02	1	GGMTSHAAVVARGWGK Oxidation (M)
540 - 549	1171.44	1170.44	1170.46	-0.02	0	CCVSGCSSVR
563 - 583	2210.11	2209.10	2209.14	-0.03	0	ALHEGEWLSLNGSTGEVIIGK
584 - 606	2647.22	2646.22	2646.25	-0.03	0	QPLCPPALSGDLETFMSWVDEVR
584 - 606	2663.23	2662.23	2662.24	-0.01	0	QPLCPPALSGDLETFMSWVDEVR Oxidation (M)
584 - 607	2775.31	2774.31	2774.34	-0.03	1	QPLCPPALSGDLETFMSWVDEVRK
625 - 635	1174.53	1173.53	1173.56	-0.02	0	QNGAEGIGLCR
636 - 646	1369.57	1368.57	1368.58	-0.01	0	TEHMFFASDER
636 - 646	1385.56	1384.55	1384.57	-0.02	0	TEHMFFASDER Oxidation (M)
652 - 662	1261.60	1260.60	1260.62	-0.02	0	QMIMASSLELR Pyro-glu (N-term Q)
652 - 662	1294.62	1293.62	1293.64	-0.02	0	QMIMASSLELR Oxidation (M)
675 - 682	970.47	969.46	969.46	0.01	0	SDFEGIFR
683 - 692	1072.57	1071.57	1071.57	-0.00	0	AMDGLPVTIR
683 - 692	1088.56	1087.56	1087.57	-0.01	0	AMDGLPVTIR Oxidation (M)
693 - 712	2343.13	2342.13	2342.17	-0.04	0	LLDPPLHEFLPEGHVEDMVR
693 - 712	2359.14	2358.14	2358.17	-0.03	0	LLDPPLHEFLPEGHVEDMVR Oxidation (M)
713 - 728	1734.77	1733.77	1733.79	-0.02	0	ELCSETGAAQDDVLAR
732 - 742	1262.63	1261.63	1261.65	-0.02	0	LSEVNPMLGFR
732 - 742	1278.64	1277.63	1277.64	-0.01	0	LSEVNPMLGFR Oxidation (M)
746 - 759	1607.78	1606.78	1606.80	-0.02	0	LGISYPELTEMQAR
746 - 759	1623.78	1622.77	1622.80	-0.02	0	LGISYPELTEMQAR Oxidation (M)
816 - 824	1015.55	1014.54	1014.55	-0.01	0	VGTMIEIPR
825 - 855	3429.61	3428.60	3428.59	0.02	0	AALVADEIAEQAEFFSFGTNDLTQMTFGYSR
825 - 855	3445.61	3444.61	3444.58	0.03	0	AALVADEIAEQAEFFSFGTNDLTQMTFGYSR Oxidation (M)
856 - 882	3142.60	3141.60	3141.61	-0.01	1	DDVGKFLPIYLSQGILQHDPFEVLDQR
861 - 882	2628.33	2627.33	2627.37	-0.05	0	FLPIYLSQGILQHDPFEVLDQR
904 - 922	1974.95	1973.95	1973.97	-0.02	0	VGICGEHGGEPLSVAFFAK
923 - 934	1371.61	1370.61	1370.63	-0.02	0	AGLDYVSCSPFR
923 - 939	1907.95	1906.94	1906.97	-0.03	1	AGLDYVSCSPFRVPIAR

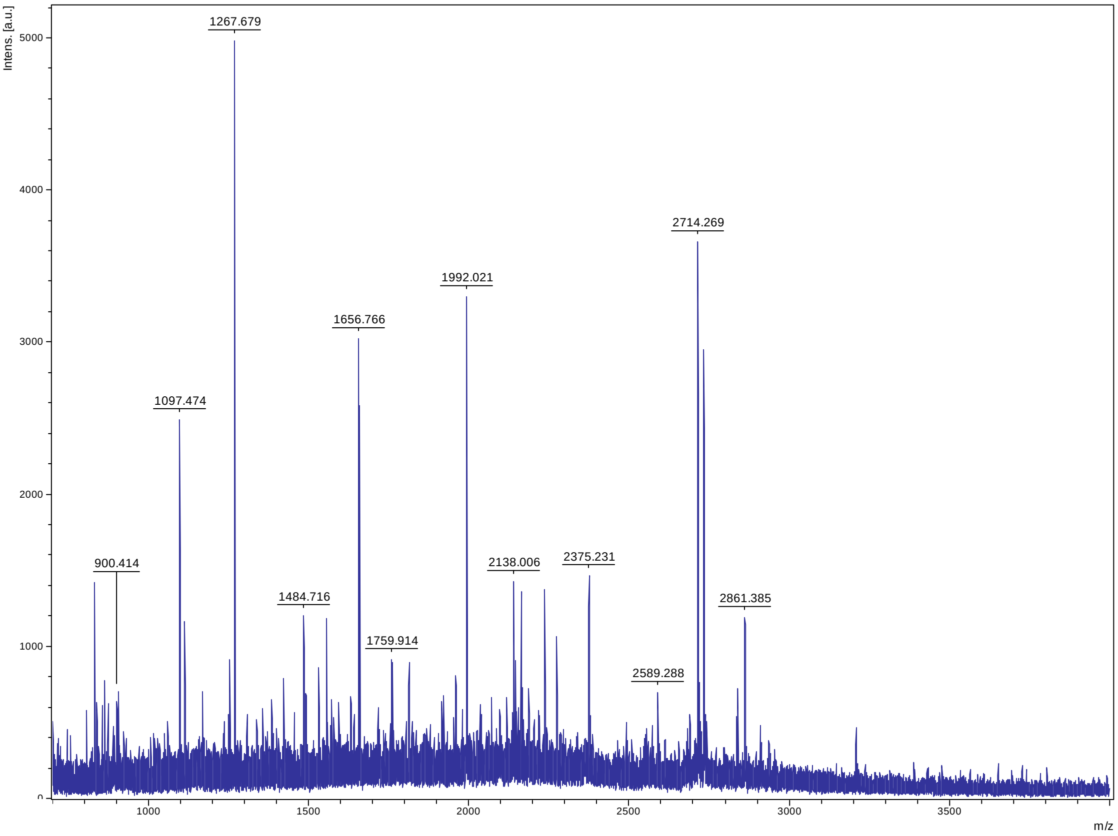
Spot 1324



Match to: gi|14091865; Score: 121

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
61 - 67	979.50	978.50	978.43	0.06	1	WRESMDR
88 - 94	871.49	870.49	870.46	0.03	0	VLYYTGR
95 - 102	1032.58	1031.58	1031.55	0.03	0	IHEIHEVR
159 - 182	2486.51	2485.51	2485.32	0.19	0	VLDGAILVLCSVGGVQSQSITVDR
186 - 191	833.48	832.48	832.46	0.02	1	RYEIPR
192 - 200	1075.66	1074.66	1074.62	0.04	1	VAFINKLDR
198 - 207	1188.62	1187.62	1187.58	0.04	1	LDRMGADPWK
198 - 207	1204.62	1203.62	1203.57	0.05	1	LDRMGADPWK Oxidation (M)
201 - 207	804.33	803.33	803.36	-0.04	0	MGADPWK
372 - 393	2294.42	2293.42	2293.30	0.12	1	VLLAGTPAEPLVALAFKLEEGR
394 - 401	997.57	996.57	996.54	0.03	0	FGQLTYLR
402 - 408	835.50	834.50	834.46	0.04	0	IYDGVIR
402 - 409	963.62	962.62	962.55	0.06	1	IYDGVIRK
501 - 509	1167.61	1166.61	1166.57	0.04	1	FQKEDPTFR
510 - 535	2845.61	2844.61	2844.39	0.22	0	VGLDPESGETIISGMGELHLDIYVER Oxidation (M)
570 - 579	1037.51	1036.51	1036.47	0.04	0	QSGGQGQYGR
617 - 636	2185.20	2184.20	2184.07	0.12	1	GFKEACNSGSLIGHPVENIR
620 - 636	1853.01	1852.00	1851.89	0.11	0	EACNSGSLIGHPVENIR
637 - 655	1960.10	1959.10	1958.99	0.10	0	IVLTDGASHAVDSSELAFK
656 - 663	940.55	939.55	939.52	0.03	0	LASIYAFR
664 - 679	1829.02	1828.01	1827.94	0.08	0	QCYAAARPVILEPVMK Pyro-glu (N-term Q)
664 - 679	1846.06	1845.05	1844.96	0.09	0	QCYAAARPVILEPVMK
664 - 679	1862.08	1861.08	1860.96	0.12	0	QCYAAARPVILEPVMK Oxidation (M)
684 - 699	1779.97	1778.96	1778.86	0.10	1	VPTEFQGTVTGDMNKR

Spot 1327

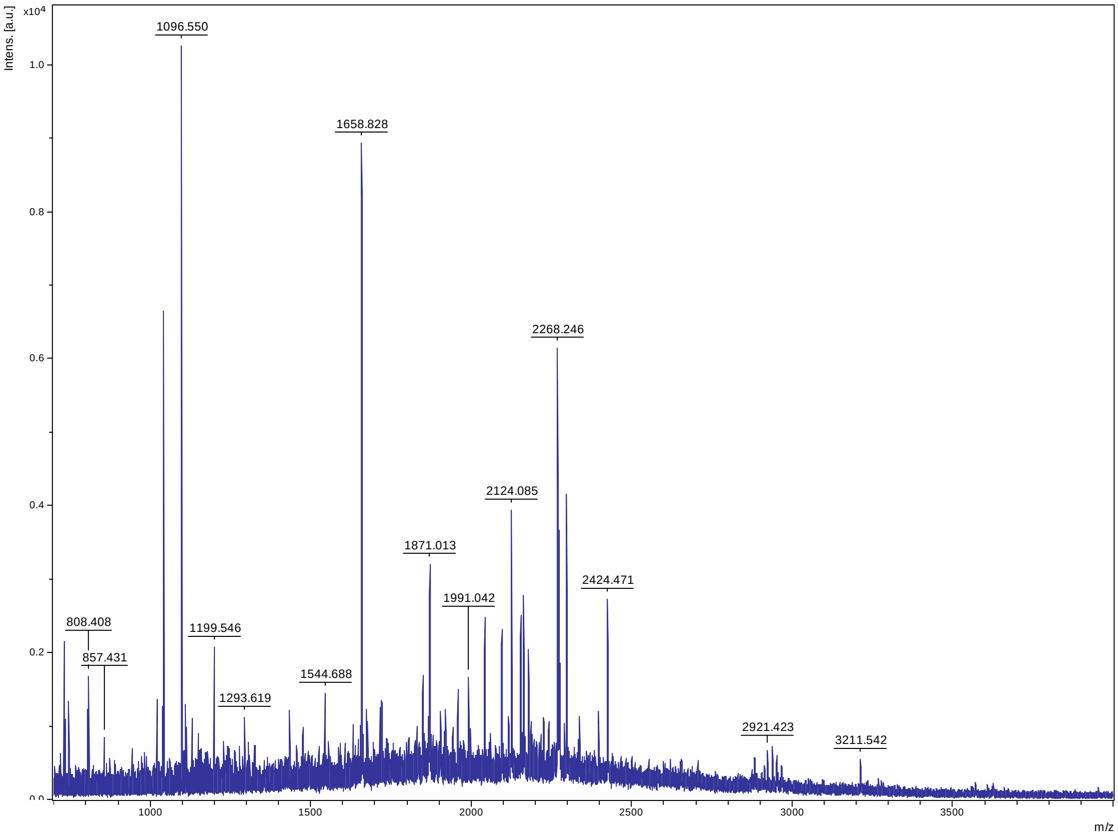


Match to: gi|50947075 Score: 108 Expect: 1.1e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
69 - 86	2144.9679	2143.9606	2143.9545	0.0061	1	K.AEETAEEEKFEYQAEVSR.L	
105 - 118	1530.8297	1529.8224	1529.8049	0.0175	1	R.ELVSNASDALDKLR.F	
119 - 137	1992.0611	1991.0538	1991.0211	0.0328	0	R.FLGVTDSSLLADGGELEIR.I	
249 - 269	2375.2077	2374.2004	2374.2280	-0.0276	1	R.GTQITLVLRPDDKFEFADPGR.I	
324 - 339	2138.0311	2137.0238	2137.0091	0.0147	0	K.YWDWELANETKPIWMR.S	
324 - 342	2492.1543	2491.1470	2491.1994	-0.0524	1	K.YWDWELANETKPIWMRSPK.E	Acetyl (N-term)
340 - 346	830.5155	829.5082	829.4545	0.0537	1	R.SPKEIEK.T	
355 - 378	2861.2877	2860.2804	2860.3707	-0.0903	1	K.KAFNEFLDPLAYTHFTTEGEVEFR.S	
356 - 378	2733.2252	2732.2179	2732.2758	-0.0578	0	K.AFNEFLDPLAYTHFTTEGEVEFR.S	
408 - 422	1812.9298	1811.9225	1811.8842	0.0383	1	K.RVFISDDFDGELFPR.Y	
409 - 422	1656.8324	1655.8251	1655.7831	0.0420	0	R.VFISDDFDGELFPR.Y	
429 - 442	1484.8027	1483.7954	1483.7630	0.0324	0	K.GVVDSNDLPLNVSR.E	
488 - 501	1631.8370	1630.8297	1630.8137	0.0160	1	K.FIKLGCIEDTGNHK.R	Carbamidomethyl (C)
491 - 502	1384.7555	1383.7482	1383.6564	0.0918	1	K.LGCIEDTGNHKR.L	Acetyl (N-term)
645 - 653	1097.5594	1096.5521	1096.4760	0.0762	0	K.FGWSANMER.L	
645 - 653	1113.5667	1112.5594	1112.4709	0.0885	0	K.FGWSANMER.L	Oxidation (M)
657 - 670	1555.7703	1554.7630	1554.7348	0.0283	0	K.AQTLGDTSSLEFMR.G	
657 - 670	1571.7680	1570.7607	1570.7297	0.0310	0	K.AQTLGDTSSLEFMR.G	Oxidation (M)
674 - 685	1421.8128	1420.8055	1420.7714	0.0341	0	R.IFEINPDHPIVK.D	

Spot 1329

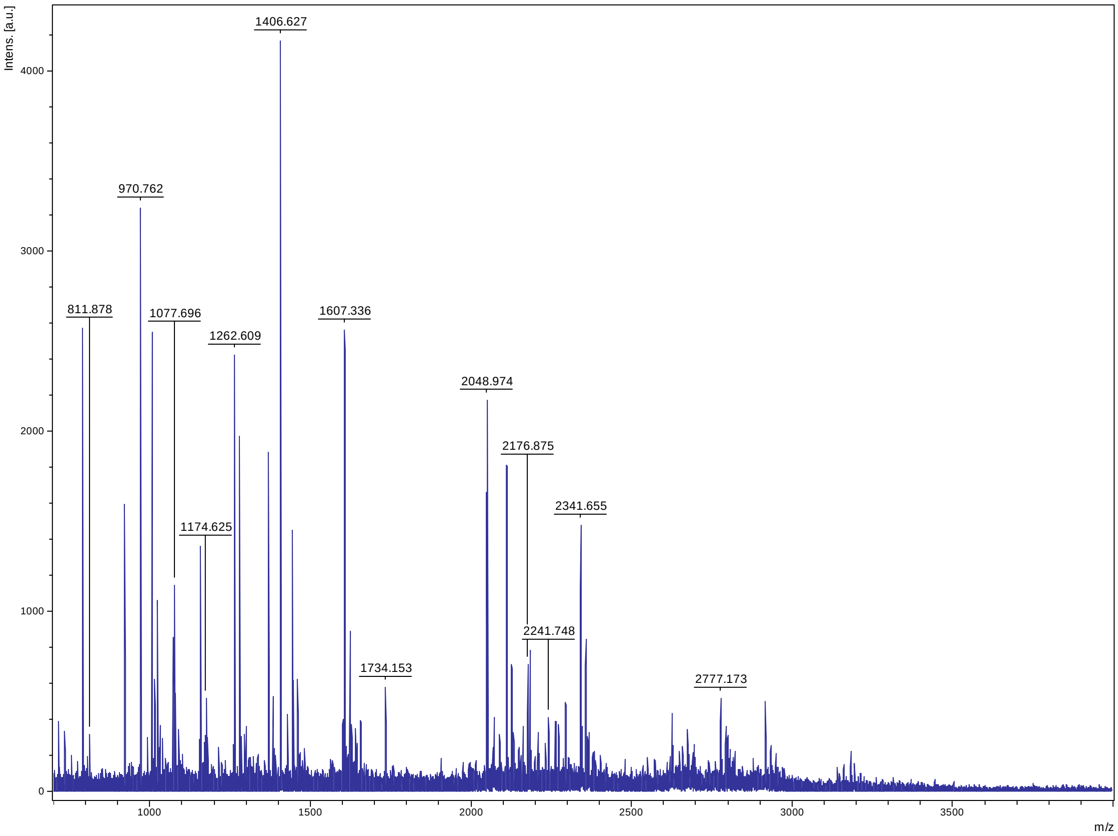


Match to: gi|77556631 Score: 113 Expect: 3.4e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
19 - 28	1199.5044	1198.4971	1198.5658	-0.0687	0	K.FALESFWDGK.S
112 - 129	2178.0287	2177.0214	2177.0581	-0.0367	0	K.WFDTNYHFIVPELGPNTK.F
254 - 270	1870.9858	1869.9785	1869.9836	-0.0051	0	K.TLTSLNSVTAYGFDLIR.G
288 - 297	1096.5045	1095.4972	1095.5712	-0.0740	0	K.YLFAGVVDGR.N
350 - 358	1021.4544	1020.4471	1020.5392	-0.0921	0	K.SWLAFAAQK.V
368 - 388	2124.0396	2123.0323	2123.0395	-0.0072	1	K.ALAGQKDEAYFAANAAAQASR.R
427 - 448	2424.3936	2423.3863	2423.3787	0.0076	1	K.KLNLPVLPTTTIGSFPQTVELR.R
428 - 448	2296.2966	2295.2893	2295.2838	0.0055	0	K.LNLPVLPTTTIGSFPQTVELR.R
478 - 494	1991.0225	1990.0152	1990.0007	0.0146	0	K.IQEELDIDVLVHGEPER.N
591 - 611	2268.1895	2267.1822	2267.1644	0.0178	0	K.EVEDLEAGGIQVIQIDEAALR.E
619 - 633	1848.8378	1847.8305	1847.8743	-0.0438	0	K.AEHAFYLDWAVHSFR.I
690 - 705	1658.7868	1657.7795	1657.8212	-0.0417	0	K.YGAGIGPGVYDIHSPR.I

Spot 1331

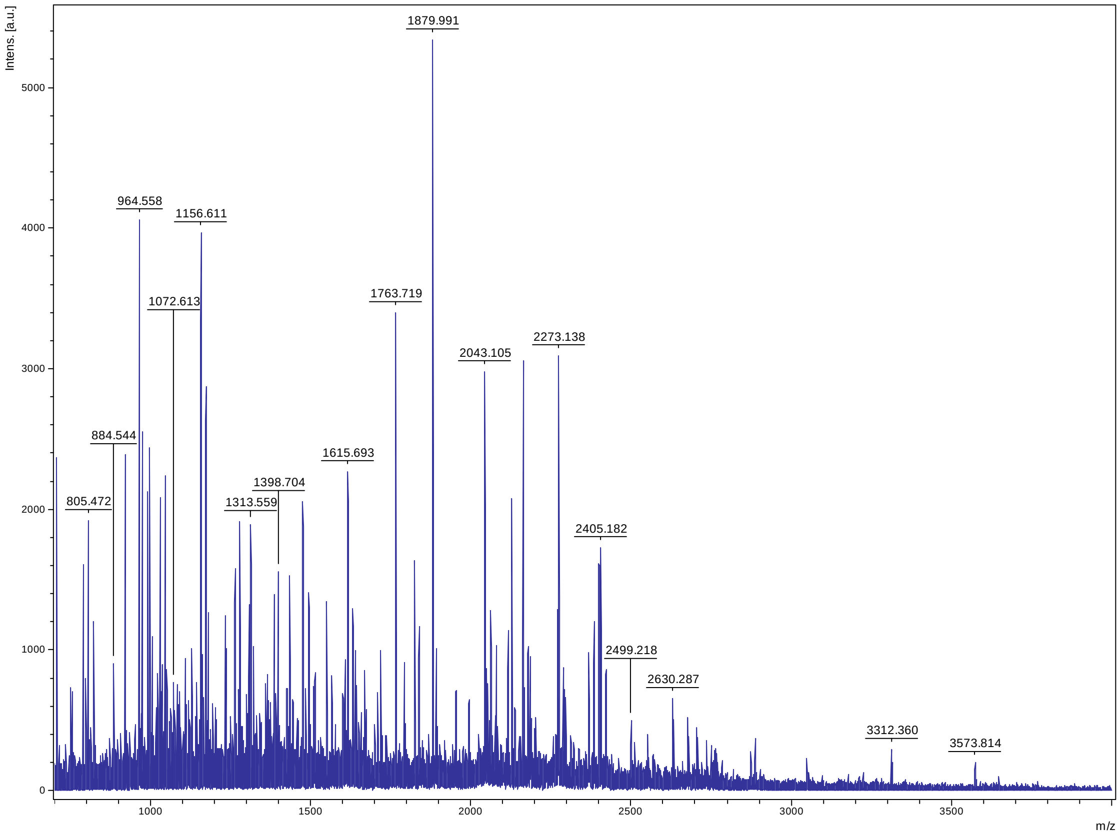


Match to: gi|50878307 Score: 160 Expect: 7.1e-12

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
40 - 48	1006.5109	1005.5036	1005.5719	-0.0683	0	R.HGKPEVAIR.S	
156 - 168	1406.9474	1405.9401	1405.8405	0.0996	0	R.LGDPARPLLLSVR.S	
203 - 209	921.3823	920.3750	920.4028	-0.0278	0	R.FAYDSYR.R	
203 - 210	1077.5439	1076.5366	1076.5039	0.0327	1	R.FAYDSYRR.F	
341 - 360	2178.1897	2177.1824	2177.1479	0.0345	1	K.KLYGEFLVNAQGEDVVAGIR.T	
342 - 360	2050.1268	2049.1195	2049.0530	0.0665	0	K.LYGEFLVNAQGEDVVAGIR.T	
423 - 435	1444.8328	1443.8255	1443.7391	0.0864	0	K.IAVDMVNEGLVER.R	
423 - 435	1460.8343	1459.8270	1459.7340	0.0930	0	K.IAVDMVNEGLVER.R	Oxidation (M)
423 - 436	1600.9215	1599.9142	1599.8402	0.0740	1	K.IAVDMVNEGLVERR.T	
441 - 464	2779.2978	2778.2905	2778.3435	-0.0530	1	K.MVEPGHLDQLLHPQFENPSGYKDK.V	
441 - 464	2795.2764	2794.2691	2794.3384	-0.0693	1	K.MVEPGHLDQLLHPQFENPSGYKDK.V	Oxidation (M)
503 - 523	2112.0820	2111.0747	2111.0316	0.0431	0	R.TETSPEDVGGMHAAVGILTAR.G	
503 - 523	2128.0735	2127.0662	2127.0266	0.0397	0	R.TETSPEDVGGMHAAVGILTAR.G	Oxidation (M)
636 - 646	1369.6697	1368.6624	1368.5768	0.0856	0	R.TEHMFFASDER.I	
636 - 646	1385.6685	1384.6612	1384.5717	0.0895	0	R.TEHMFFASDER.I	Oxidation (M)
652 - 662	1278.7340	1277.7267	1277.6471	0.0796	0	R.QMIMASSLELR.Q	
669 - 674	789.3599	788.3526	788.4545	-0.1018	0	R.LLPYQR.S	
675 - 682	970.4547	969.4474	969.4556	-0.0081	0	R.SDFEGIFR.A	
683 - 692	1072.6100	1071.6027	1071.5746	0.0281	0	R.AMDGLPVTIR.L	
683 - 692	1088.6039	1087.5966	1087.5695	0.0271	0	R.AMDGLPVTIR.L	Oxidation (M)
693 - 712	2343.1998	2342.1925	2342.1728	0.0197	0	R.LLDPPLHEFLPEGHVEDMVR.E	
693 - 712	2359.1730	2358.1657	2358.1678	-0.0020	0	R.LLDPPLHEFLPEGHVEDMVR.E	Oxidation (M)
732 - 742	1262.7150	1261.7077	1261.6488	0.0589	0	K.LSEVNPMLGFR.G	
746 - 759	1607.9010	1606.8937	1606.8024	0.0913	0	R.LGISYPELTEMQAR.A	
816 - 824	1015.5591	1014.5518	1014.5532	-0.0013	0	K.VGTMIEIPR.A	
861 - 882	2628.3226	2627.3153	2627.3747	-0.0594	0	K.FLPIYLSQGILQHDPFEVLDQR.G	

Spot 1341

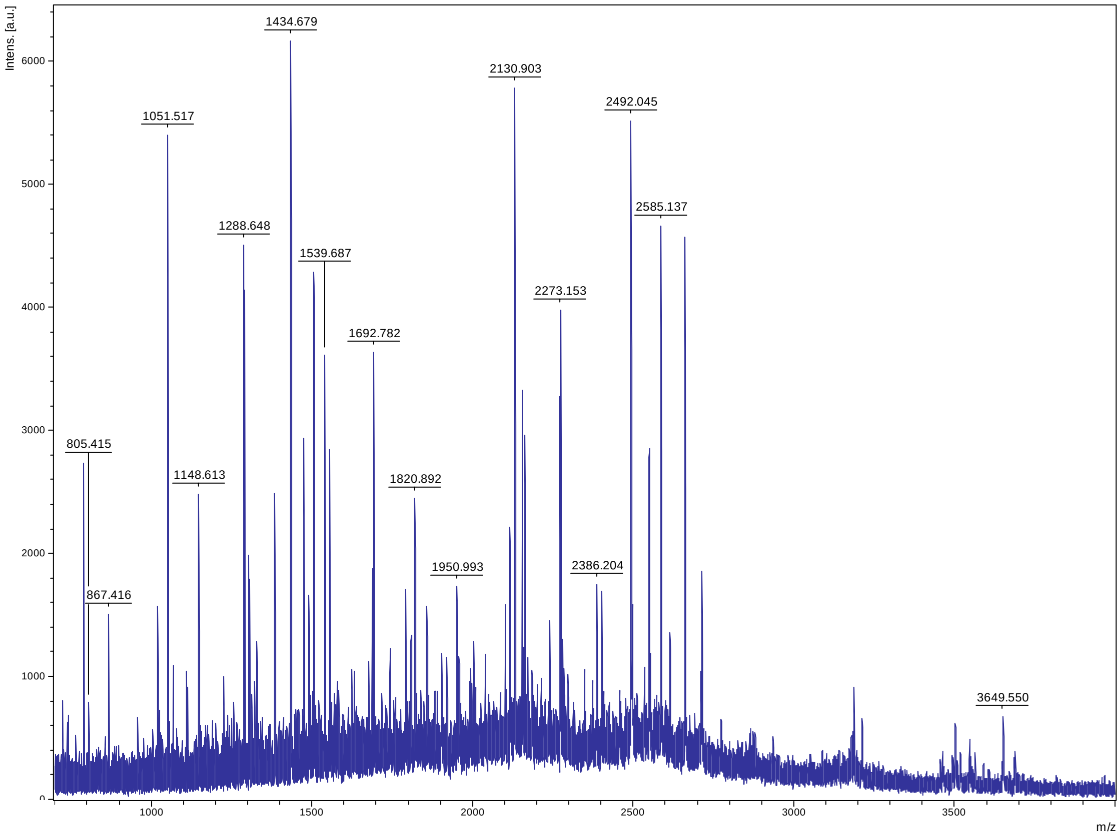


Match to: gi|50948547 Score: 262 Expect: 2.6e-21

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
39 - 57	1879.9910	1878.9837	1878.9799	0.0038	0	K.IAVSPGTEGTSSPLTLHGR.D	
115 - 129	1763.7189	1762.7116	1762.7039	0.0077	0	K.STGNFCTQCEAEGFR.K	2 Carbamidomethyl (C)
115 - 130	1891.8176	1890.8104	1890.7988	0.0115	1	K.STGNFCTQCEAEGFRK.I	2 Carbamidomethyl (C)
175 - 184	1305.6412	1304.6340	1304.6189	0.0150	0	K.HYALWEDPFK.K	
201 - 210	1159.5195	1158.5123	1158.4611	0.0511	0	R.EDSFTTCSGR.K	Carbamidomethyl (C)
216 - 225	1128.6283	1127.6210	1127.5975	0.0235	0	R.IWTPGQDLAK.T	
226 - 234	1037.5549	1036.5477	1036.5011	0.0465	0	K.TAHAMYSLK.A	Oxidation (M)
270 - 277	964.5582	963.5509	963.5137	0.0371	0	K.SLNIFQSR.L	
278 - 310	3573.8145	3572.8072	3572.7323	0.0748	0	R.LVLASPETATDGDYAAILGVVGHEYFHNWTGNR.V	
311 - 322	1509.7468	1508.7396	1508.7809	-0.0414	1	R.VTCRDWFQLTLK.E	
315 - 322	1050.5858	1049.5785	1049.5546	0.0240	0	R.DWFQLTLK.E	
323 - 329	821.4901	820.4828	820.4443	0.0386	0	K.EGLTVFR.D	
323 - 340	2115.9709	2114.9637	2114.9691	-0.0054	1	K.EGLTVFRDQEFSSDLGCR.T	Carbamidomethyl (C)
330 - 340	1313.5594	1312.5522	1312.5354	0.0168	0	R.DQEFSSDLGCR.T	Carbamidomethyl (C)
330 - 343	1641.7600	1640.7527	1640.7464	0.0063	1	R.DQEFSSDLGCRTVK.R	Carbamidomethyl (C)
384 - 392	989.4876	988.4803	988.4436	0.0367	0	K.TMFGASGFR.K	Oxidation (M)
393 - 401	1173.5983	1172.5910	1172.5648	0.0262	1	R.KGMDLYFQR.H	Oxidation (M)
394 - 401	1029.5143	1028.5070	1028.4749	0.0321	0	K.GMDLYFQR.H	
441 - 455	1606.8018	1605.7945	1605.7522	0.0423	0	K.VSSSYDASSQTFSLK.F	
519 - 538	2399.2910	2398.2837	2398.2896	-0.0058	1	K.KEEEFIFNNIPEKPVPSLLR.G	
520 - 538	2271.1707	2270.1634	2270.1946	-0.0312	0	K.EEEFIFNNIPEKPVPSLLR.G	
546 - 568	2676.2512	2675.2439	2675.2238	0.0201	0	R.LDSDLTESDLFFLLANDSDEFNR.W	
651 - 668	2043.1047	2042.0975	2042.1007	-0.0033	1	K.ELALQLKDDLLSTVTNNR.S	
669 - 682	1615.6929	1614.6856	1614.6732	0.0124	0	R.SSEAYTFNHDSMAR.R	
669 - 682	1631.6608	1630.6535	1630.6682	-0.0147	0	R.SSEAYTFNHDSMAR.R	Oxidation (M)
711 - 733	2405.1821	2404.1749	2404.1804	-0.0056	0	K.SATNMTEQFAALAALSQNPGQVR.D	
711 - 733	2421.1726	2420.1653	2420.1754	-0.0100	0	K.SATNMTEQFAALAALSQNPGQVR.D	Oxidation (M)
734 - 753	2499.2180	2498.2107	2498.2117	-0.0010	1	R.DDTLLDFYNKWQHDYLVVSK.W	
744 - 753	1274.6738	1273.6666	1273.6455	0.0211	0	K.WQHDYLVVSK.W	
773 - 782	1156.6115	1155.6042	1155.5859	0.0183	0	K.LLGHPAFDMR.N	
773 - 782	1172.6039	1171.5966	1171.5808	0.0158	0	K.LLGHPAFDMR.N	Oxidation (M)
787 - 804	1952.9691	1951.9618	1951.9614	0.0005	0	K.VYSLIGGFCGSPVNFHAK.D	Carbamidomethyl (C)
811 - 829	2126.1992	2125.1919	2125.1895	0.0025	1	K.FLGEVVLQLDKINPQVASR.M	
822 - 829	884.5440	883.5367	883.4875	0.0492	0	K.INPQVASR.M	
850 - 871	2366.2495	2365.2422	2365.1834	0.0588	0	K.AQLEMIVSANGLSENVYEIASK.S	

Spot 1345

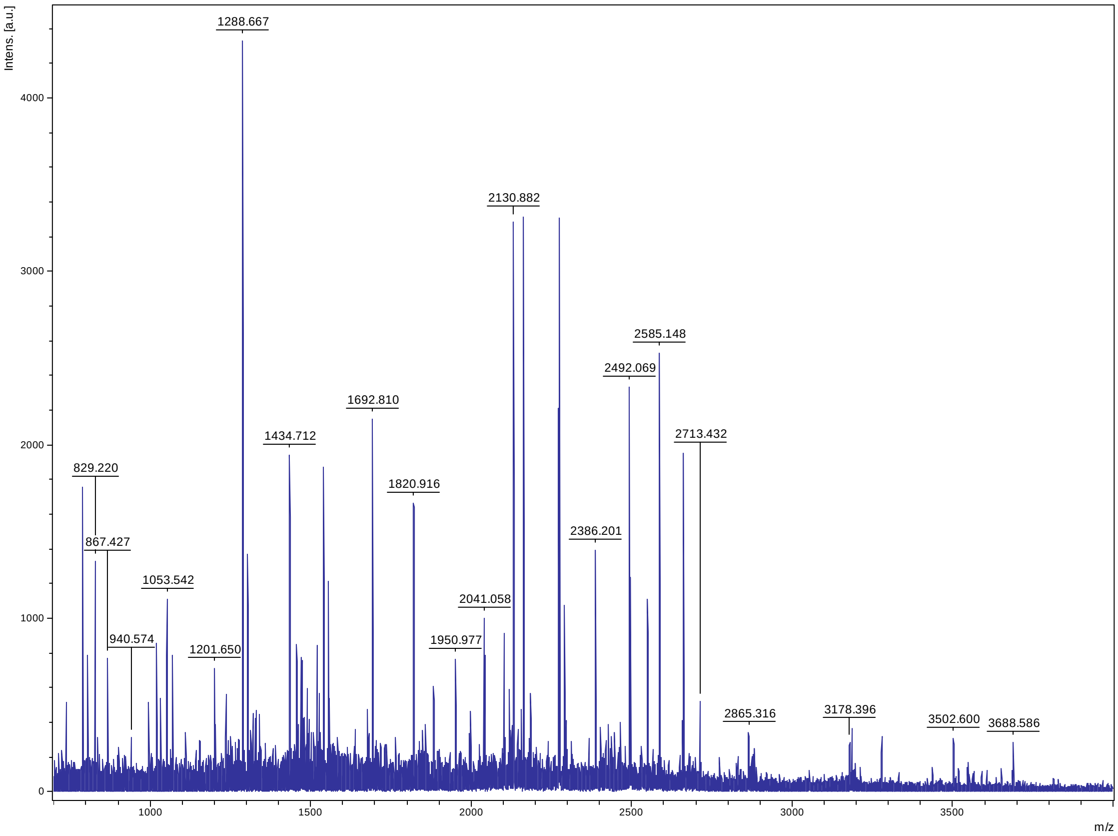


Match to: gi|3252794 Score: 135 Expect: 2.1e-09

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 17	1820.9150	1819.9077	1819.9072	0.0005	1	-.VEAVVMPERYALGGACR.V
10 - 17	867.3774	866.3701	866.4068	-0.0367	0	R.YALGGACR.V Carbamidomethyl (C)
75 - 95	2535.2187	2534.2114	2534.2164	-0.0050	0	R.TGNVWHVFIEGELHNMLYGYR.F
166 - 175	1288.6832	1287.6759	1287.6645	0.0114	0	K.DLVIYEMHLR.G
166 - 175	1304.6751	1303.6678	1303.6594	0.0084	0	K.DLVIYEMHLR.G Oxidation (M)
273 - 291	2102.0786	2101.0713	2101.0149	0.0564	0	R.GIEVIMDVVFNHTAEGNEK.G
292 - 298	789.3996	788.3923	788.4544	-0.0621	0	K.GPILSFR.G
333 - 340	1051.5161	1050.5088	1050.5168	-0.0080	0	R.EFIVDCLR.Y Carbamidomethyl (C)
341 - 352	1555.7229	1554.7156	1554.6925	0.0231	0	R.YWVTEMHVDGFR.F Oxidation (M)
407 - 427	2386.2119	2385.2046	2385.1905	0.0141	0	K.LIAEAWDAGGLYQVGQFPHWK.I
428 - 435	1019.4748	1018.4675	1018.4872	-0.0197	0	K.IWSEWNGK.Y
446 - 470	2585.1076	2584.1003	2584.1222	-0.0219	0	K.GTDGFAGGFAECLCGSPHLYQAGGR.K 2 Carbamidomethyl (C)
507 - 529	2492.0744	2491.0671	2491.0709	-0.0038	0	R.DGENHNLSWNCGEEGEFAGLSVK.R
563 - 579	2130.9066	2129.8993	2129.8762	0.0232	0	K.GGNNNTYCHDHYVNYFR.W Carbamidomethyl (C)
592 - 600	1148.6349	1147.6276	1147.5518	0.0758	1	R.FCSLMTKFR.K Oxidation (M)
602 - 616	1692.8256	1691.8183	1691.7937	0.0246	0	K.QCESLGLADFPTAQR.L Carbamidomethyl (C)
617 - 634	2155.0526	2154.0453	2154.0143	0.0310	0	R.LHWHGHQPGKPDWSETSR.F
671 - 693	2660.2579	2659.2506	2659.2806	-0.0299	0	R.WEPLVDTGKPAPYDFLTDDLPDR.V

Spot 1347

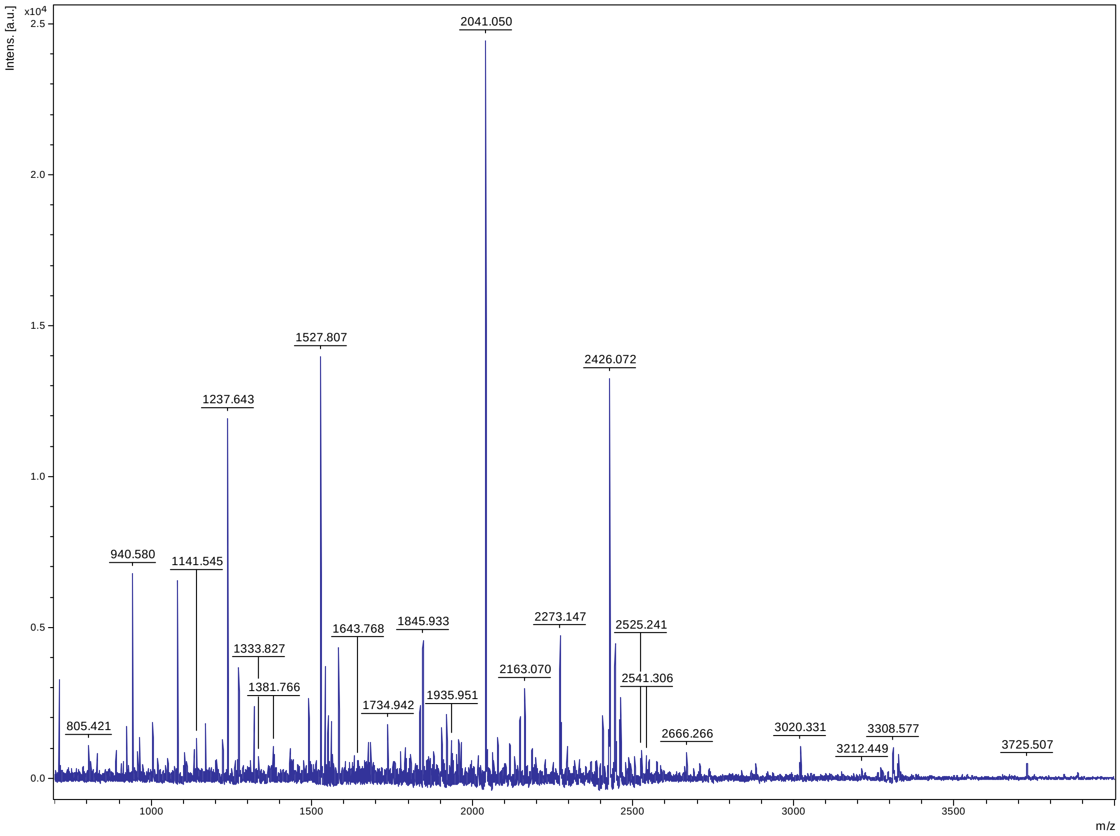


Match to: gi|3252794 Score: 165 Expect: 2.6e-11

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 17	1820.9155	1819.9083	1819.9072	0.0010	1	-.VEAVVMPERYALGGACR.V	
10 - 17	867.4271	866.4198	866.4068	0.0130	0	R.YALGGACR.V	Carbamidomethyl (C)
166 - 175	1288.6675	1287.6602	1287.6645	-0.0043	0	K.DLVIYEMHLR.G	
166 - 175	1304.6552	1303.6479	1303.6594	-0.0115	0	K.DLVIYEMHLR.G	Oxidation (M)
180 - 197	1883.9283	1882.9211	1882.9173	0.0038	0	K.HSSSNVEHPGTYIGAISK.L	
203 - 228	3178.3955	3177.3882	3177.3551	0.0331	0	K.ELGVNCVELMPCHEFNELEYFSCSSK.M	3 Carbamidomethyl (C)
273 - 291	2102.0161	2101.0088	2101.0149	-0.0061	0	R.GIEVIMDVVFNHTAEGNEK.G	
273 - 291	2118.0071	2116.9998	2117.0098	-0.0100	0	R.GIEVIMDVVFNHTAEGNEK.G	Oxidation (M)
299 - 311	1472.7346	1471.7273	1471.7017	0.0257	0	R.GIDNSTYYMLAPK.G	
299 - 311	1488.7196	1487.7123	1487.6966	0.0157	0	R.GIDNSTYYMLAPK.G	Oxidation (M)
333 - 340	994.5085	993.5013	993.4953	0.0060	0	R.EFIVDCLR.Y	
333 - 340	1051.5215	1050.5142	1050.5168	-0.0026	0	R.EFIVDCLR.Y	Carbamidomethyl (C)
341 - 352	1555.7190	1554.7117	1554.6925	0.0192	0	R.YWVTEMHVDGFR.F	Oxidation (M)
353 - 361	1053.5421	1052.5348	1052.5324	0.0024	0	R.FDLASIMTR.G	
353 - 361	1069.5303	1068.5230	1068.5274	-0.0044	0	R.FDLASIMTR.G	Oxidation (M)
407 - 427	2386.2009	2385.1937	2385.1905	0.0031	0	K.LIAEAWDAGGLYQVGQFPHWK.I	
428 - 435	1019.4866	1018.4793	1018.4872	-0.0079	0	K.IWSEWNGK.Y	
446 - 470	2585.1484	2584.1412	2584.1222	0.0189	0	K.GTDGFAGGFAECLCGSPHLYQAGGR.K	2 Carbamidomethyl (C)
507 - 529	2492.0688	2491.0616	2491.0709	-0.0093	0	R.DGENHNLSWNCGEEGEFAGLSVK.R	
507 - 529	2549.1130	2548.1058	2548.0924	0.0134	0	R.DGENHNLSWNCGEEGEFAGLSVK.R	Carbamidomethyl (C)
563 - 579	2130.8816	2129.8743	2129.8762	-0.0018	0	K.GGNNNTYCHDHYVNYFR.W	Carbamidomethyl (C)
602 - 616	1675.7693	1674.7620	1674.7672	-0.0051	0	K.QCESLGLADFPTAQR.L	Carbamidomethyl (C); Pyro-glu (N-term Q)
602 - 616	1692.8097	1691.8024	1691.7937	0.0087	0	K.QCESLGLADFPTAQR.L	Carbamidomethyl (C)
671 - 693	2660.3103	2659.3030	2659.2806	0.0225	0	R.WEPLVDTGKPAPYDFLTDDLPDR.V	

Spot 1355

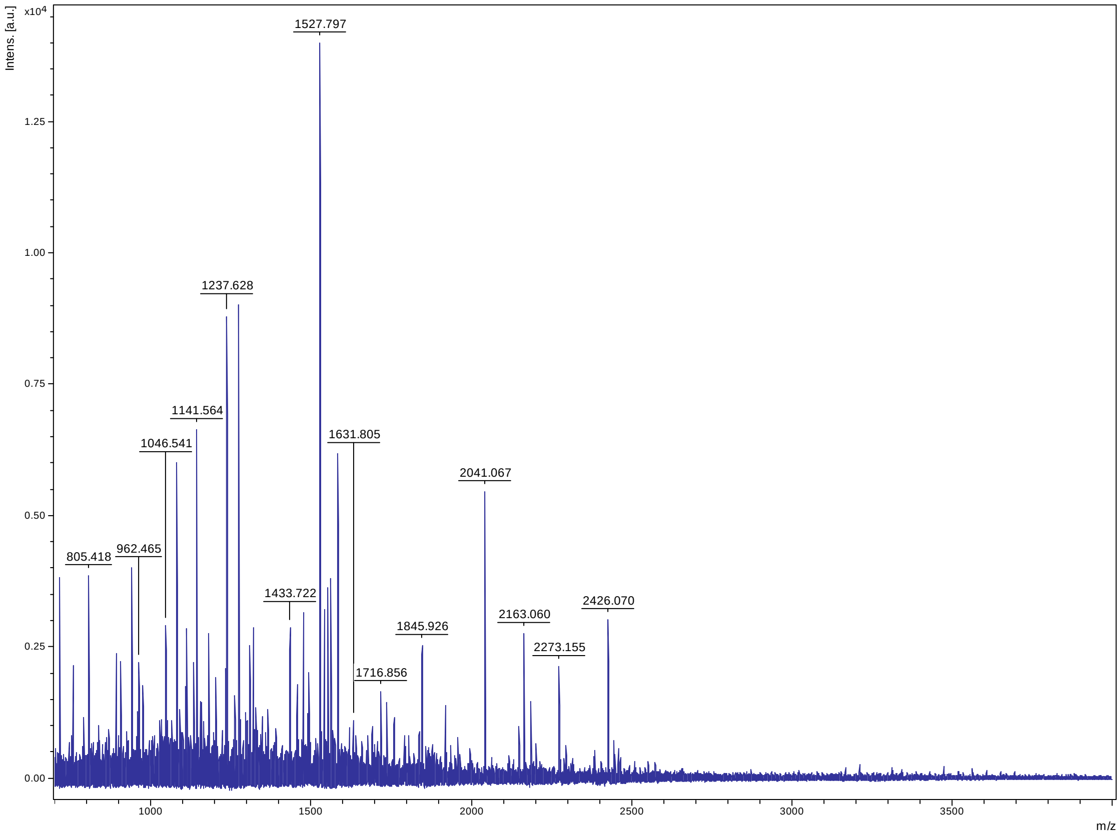


Match to: gi|50725880 Score: 128 Expect: 1.1e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
35 - 48	1560.8069	1559.7996	1559.8155	-0.0158	1	R.ELISNSSDALDKIR.F	
58 - 72	1734.9464	1733.9391	1733.9352	0.0039	0	K.LDAQPELFIHIVPDK.A	
89 - 100	1272.6619	1271.6546	1271.6833	-0.0287	0	K.SDLVNNLGTIAR.S	
142 - 162	2426.0606	2425.0533	2425.0570	-0.0037	0	K.HNDDEQYVWESQAGGSFTVTR.D	
175 - 190	2041.0391	2040.0318	2040.0415	-0.0097	1	K.ITLYLKDDQLEYLEER.R	
198 - 213	1965.0413	1964.0340	1964.0043	0.0297	1	K.KHSEFISYPISLWTEK.T	
199 - 213	1836.9068	1835.8995	1835.9094	-0.0098	0	K.HSEFISYPISLWTEK.T	
236 - 243	962.3447	961.3374	961.4240	-0.0866	0	K.VEDVDEEK.E	
255 - 272	2294.1565	2293.1492	2293.1789	-0.0297	1	K.EVSHEWNVMNKQKPIWLR.K	
273 - 287	1845.9165	1844.9092	1844.9196	-0.0103	1	R.KPEEITKEEYAAFYK.S	
288 - 300	1541.7523	1540.7450	1540.7521	-0.0071	0	K.SLTNDWEEHLAVK.H	
301 - 311	1320.6178	1319.6105	1319.6509	-0.0404	0	K.HFSVEGQLEFK.A	
319 - 328	1237.6156	1236.6083	1236.6251	-0.0168	1	K.RAPFDLFDTR.K	
360 - 373	1527.7883	1526.7810	1526.7940	-0.0130	0	K.GIVDSEDLPLNISR.E	
393 - 404	1441.7318	1440.7245	1440.6958	0.0287	0	K.CVELFFEIAENK.E	
443 - 456	1583.7864	1582.7791	1582.7838	-0.0047	1	K.SGDELTSLKDYVTR.M	
457 - 472	1862.9171	1861.9098	1861.8767	0.0331	1	R.MKEGQSEIYYITGESK.K	
457 - 472	1878.9087	1877.9014	1877.8716	0.0298	1	R.MKEGQSEIYYITGESK.K	Oxidation (M)
473 - 483	1261.5991	1260.5918	1260.6713	-0.0795	1	K.KAVENSPFLEK.L	
474 - 483	1133.5077	1132.5004	1132.5764	-0.0760	0	K.AVENSPFLEK.L	
487 - 507	2420.2406	2419.2333	2419.1980	0.0353	1	K.KGYEVLYMVDAIDEYAVGQLK.E	Oxidation (M)
488 - 512	2882.4523	2881.4450	2881.3730	0.0720	1	K.GYEVLYMVDAIDEYAVGQLKEFEGK.K	Oxidation (M)
606 - 620	1775.8000	1774.7927	1774.8229	-0.0302	0	K.TMEINPENAIMDELR.K	
606 - 620	1807.8523	1806.8450	1806.8128	0.0323	0	K.TMEINPENAIMDELR.K	2 Oxidation (M)
606 - 621	1919.9672	1918.9599	1918.9128	0.0471	1	K.TMEINPENAIMDELRK.R	Oxidation (M)
606 - 621	1935.9417	1934.9344	1934.9077	0.0267	1	K.TMEINPENAIMDELRK.R	2 Oxidation (M)

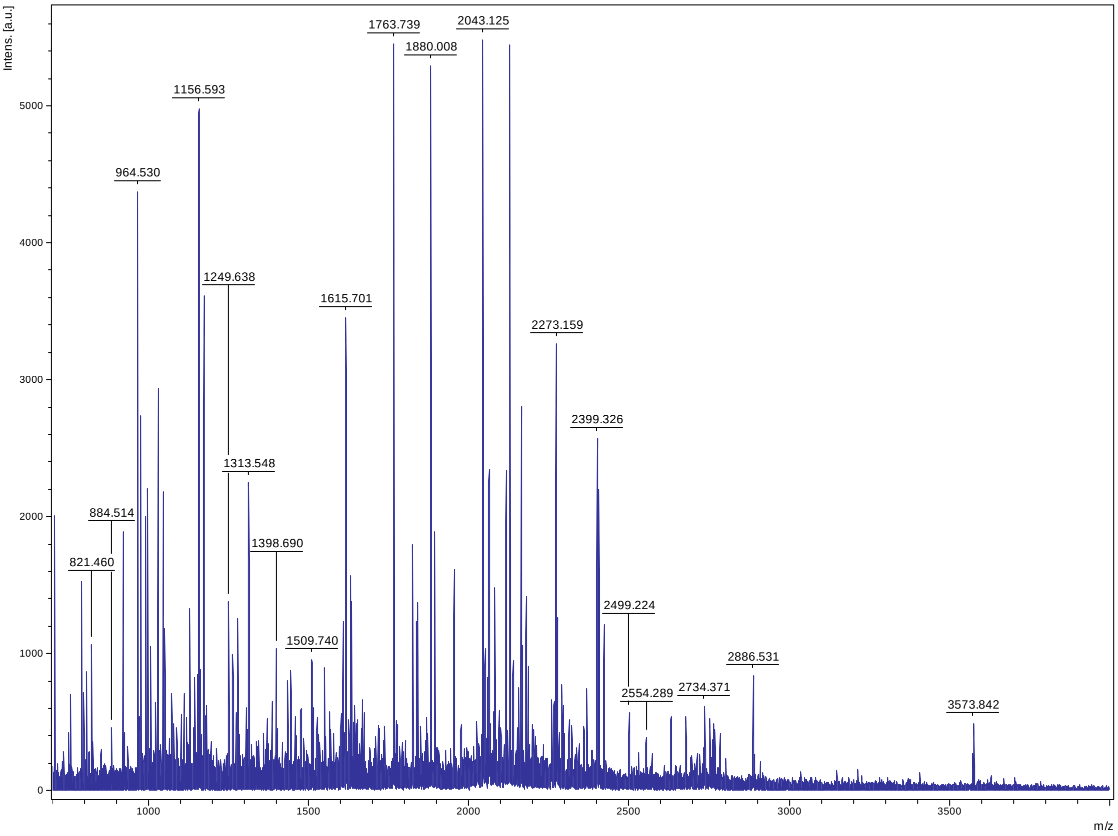
Spot 1356



Match to: gi|39104468 Score: 161 Expect: 5.3e-12

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
35 - 48	1560.8469	1559.8396	1559.8155	0.0242	1	R.ELISNSSDALDKIR.F	
47 - 55	1108.5609	1107.5536	1107.5924	-0.0388	1	K.IRFESLTDK.S	
58 - 72	1734.9459	1733.9386	1733.9352	0.0034	0	K.LDAQPELFIHIVPDK.A	
89 - 100	1272.6907	1271.6834	1271.6833	0.0001	0	K.SDLVNNLGTIAR.S	
142 - 162	2426.0342	2425.0269	2425.0570	-0.0301	0	K.HNDDEQYVWESQAGGSFTVTR.D	
163 - 171	962.3974	961.3901	961.4465	-0.0563	0	R.DTSGEQLGR.G	
175 - 190	2041.0699	2040.0626	2040.0415	0.0211	1	K.ITLYLKDDQLEYLEER.R	
199 - 213	1836.9336	1835.9263	1835.9094	0.0170	0	K.HSEFISYPISLWTEK.T	
255 - 265	1388.6880	1387.6807	1387.6190	0.0617	0	K.EVSHEWNVMNK.Q	Oxidation (M)
266 - 272	940.5159	939.5086	939.5654	-0.0568	0	K.QKPIWLR.K	
273 - 287	1845.9440	1844.9367	1844.9196	0.0172	1	R.KPEEITKEEYAAFYK.S	
288 - 300	1541.7681	1540.7608	1540.7521	0.0087	0	K.SLTNDWEEHLAVK.H	
301 - 311	1320.6492	1319.6419	1319.6509	-0.0090	0	K.HFSVEGQLEFK.A	
319 - 328	1237.6403	1236.6330	1236.6251	0.0079	1	K.RAPFDLFDTR.K	
360 - 373	1527.8250	1526.8177	1526.7940	0.0237	0	K.GIVDSEDLPLNISR.E	
393 - 409	2148.0080	2147.0007	2146.9880	0.0127	1	K.CVELFFEIAENKEDYNK.F	Carbamidomethyl (C)
410 - 416	891.3585	890.3512	890.4174	-0.0662	0	K.FYEAFSK.N	
443 - 456	1583.8074	1582.8001	1582.7838	0.0163	1	K.SGDELTSLKDYVTR.M	
457 - 472	1878.8794	1877.8721	1877.8716	0.0005	1	R.MKEGQSEIYYITGESK.K	Oxidation (M)
473 - 483	1261.6735	1260.6662	1260.6713	-0.0051	1	K.KAVENSPFLEK.L	
474 - 483	1133.5496	1132.5423	1132.5764	-0.0341	0	K.AVENSPFLEK.L	
565 - 585	2444.0207	2443.0134	2443.0606	-0.0472	0	R.VVDSPCCLVTGEYGWTANMER.I	2 Carbamidomethyl (C)
565 - 585	2460.0469	2459.0396	2459.0555	-0.0159	0	R.VVDSPCCLVTGEYGWTANMER.I	2 Carbamidomethyl (C); Oxidation (M)

Spot 1360

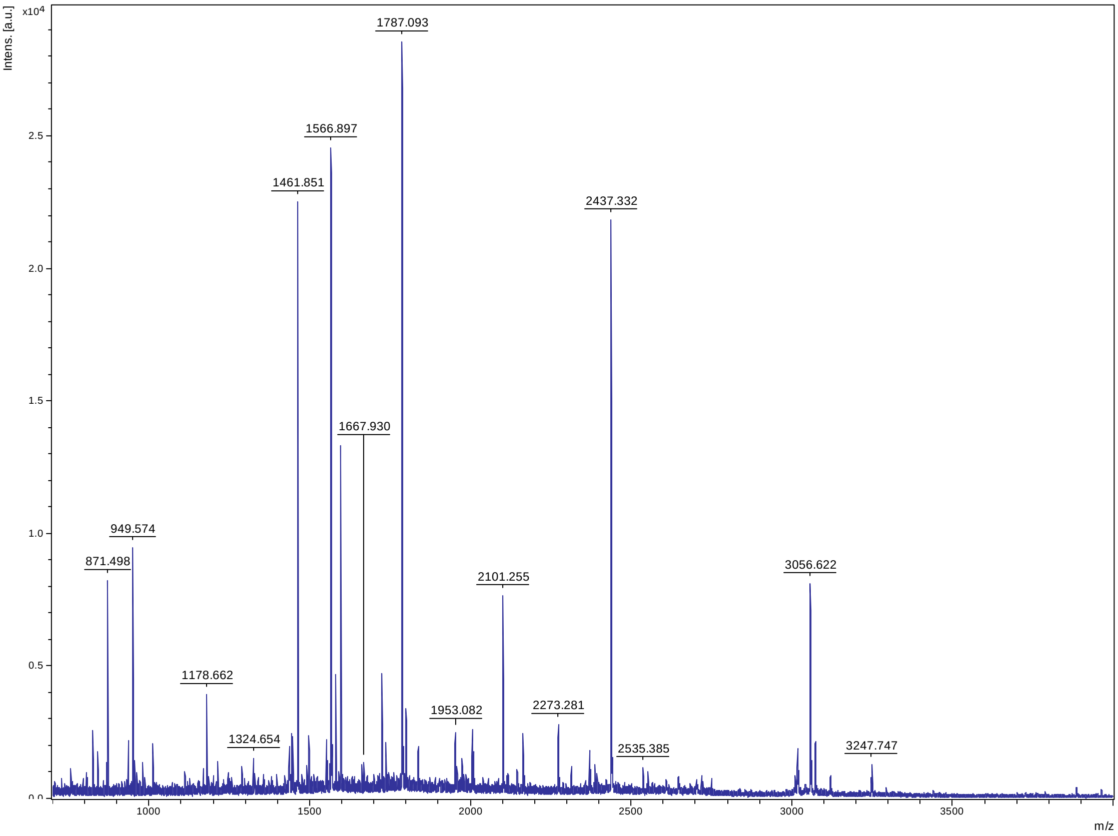


Match to: gi|42408435 Score: 391 Expect: 1.1e-34

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
1 - 10	1249.6378	1248.6306	1248.6788	-39	1	-.MDLPKEIFLK.E	Oxidation (M)
39 - 57	1880.0075	1879.0003	1878.9799	11	0	K.IAVSPGTEGTSSPLTLHGR.D	
70 - 81	1457.6839	1456.6766	1456.6504	18	1	K.DLKSEDYMVDSR.H	
73 - 81	1101.4787	1100.4715	1100.4444	25	0	K.SEDYMVDSR.H	
115 - 129	1763.7385	1762.7312	1762.7039	15	0	K.STGNFCTQCEAEGFR.K	
115 - 130	1891.8307	1890.8234	1890.7989	13	1	K.STGNFCTQCEAEGFRK.I	
130 - 147	2265.0895	2264.0822	2264.0718	5	1	R.KITYFQDRPDVMATYTCR.I	
131 - 147	2137.0038	2135.9965	2135.9769	9	0	K.ITYFQDRPDVMATYTCR.I	
148 - 174	2886.5315	2885.5242	2885.5022	8	1	R.IEADKTLYPVLLSNGNLIEQGDLEGGK.H	
175 - 184	1305.6383	1304.6310	1304.6190	9	0	K.HYALWEDPFK.K	
201 - 210	1159.4969	1158.4896	1158.4612	25	0	R.EDSFTTCSGR.K	
216 - 225	1128.5891	1127.5819	1127.5975	-14	0	R.IWTPGQDLAK.T	
270 - 277	964.5296	963.5223	963.5138	9	0	K.SLNIFQSR.L	
278 - 310	3573.8416	3572.8343	3572.7325	29	0	R.LVLASPETATDGDYAAILGVVGHEYFHNWTGNR.V	
315 - 322	1050.5562	1049.5490	1049.5546	-5	0	R.DWFQLTLK.E	
323 - 329	821.4596	820.4523	820.4443	10	0	K.EGLTVFR.D	
323 - 340	2115.9948	2114.9875	2114.9691	9	1	K.EGLTVFRDQEFSSDLGCR.T	
330 - 340	1313.5480	1312.5407	1312.5354	4	0	R.DQEFSSDLGCR.T	
330 - 343	1641.7554	1640.7482	1640.7464	1	1	R.DQEFSSDLGCRTVK.R	
353 - 374	2554.2894	2553.2821	2553.2587	9	0	R.TYQFPQDAGPMAHPIRPHSYIK.G	
384 - 392	989.4559	988.4486	988.4437	5	0	K.TMFGASGFR.K	Oxidation (M)
393 - 401	1173.5870	1172.5797	1172.5648	13	1	R.KGMDLYFQR.H	Oxidation (M)
394 - 401	1029.4909	1028.4836	1028.4749	8	0	K.GMDLYFQR.H	
441 - 455	1606.7752	1605.7679	1605.7522	10	0	K.VSSSYDASSQTFSLK.F	
519 - 538	2399.3255	2398.3182	2398.2896	12	1	K.KEEEFIFNNIPEKPVPSLLR.G	
520 - 538	2271.2089	2270.2016	2270.1946	3	0	K.EEEFIFNNIPEKPVPSLLR.G	
546 - 568	2676.2775	2675.2702	2675.2239	17	0	R.LDSDLTESDLFFLLANDSDEFNR.W	
609 - 619	1265.6700	1264.6627	1264.6663	-3	1	R.NTSLDKEFIAK.A	
620 - 645	2734.3712	2733.3639	2733.3288	13	0	K.AITLPGQGEIMDMMPVADPDAVHAVR.T	
620 - 645	2750.3628	2749.3555	2749.3237	12	0	K.AITLPGQGEIMDMMPVADPDAVHAVR.T	Oxidation (M)
620 - 645	2766.3332	2765.3259	2765.3187	3	0	K.AITLPGQGEIMDMMPVADPDAVHAVR.T	2 Oxidation (M)
651 - 668	2043.1254	2042.1181	2042.1008	9	1	K.ELALQLKDDLLSTVTNNR.S	
669 - 682	1615.7014	1614.6941	1614.6732	13	0	R.SSEAYTFNHDSMAR.R	
669 - 682	1631.6880	1630.6807	1630.6682	8	0	R.SSEAYTFNHDSMAR.R	Oxidation (M)
687 - 710	2762.3551	2761.3478	2761.3156	12	0	K.NTCLAYLASLNEPDTTELAFVEYK.S	
711 - 733	2405.2237	2404.2165	2404.1805	15	0	K.SATNMTEQFAALAALSQNPGQVR.D	
711 - 733	2421.2013	2420.1940	2420.1754	8	0	K.SATNMTEQFAALAALSQNPGQVR.D	Oxidation (M)
734 - 753	2499.2242	2498.2169	2498.2118	2	1	R.DDTLLDFYNKWQHDYLVVSK.W	
744 - 753	1274.6495	1273.6422	1273.6455	-3	0	K.WQHDYLVVSK.W	
754 - 772	2059.0509	2058.0436	2058.0534	-5	0	K.WFALQATSDIPGNVANVQK.L	
773 - 782	1156.5935	1155.5862	1155.5859	0	0	K.LLGHPAFDMR.N	
773 - 782	1172.5760	1171.5687	1171.5808	-10	0	K.LLGHPAFDMR.N	Oxidation (M)
787 - 804	1952.9710	1951.9637	1951.9615	1	0	K.VYSLIGGFCGSPVNFHAK.D	
811 - 821	1260.7173	1259.7101	1259.7125	-2	0	K.FLGEVVLQLDK.I	
811 - 829	2126.2213	2125.2140	2125.1895	12	1	K.FLGEVVLQLDKINPQVASR.M	
822 - 829	884.5142	883.5069	883.4875	22	0	K.INPQVASR.M	
839 - 844	825.4153	824.4080	824.3777	37	1	R.RYDESR.Q	
850 - 871	2366.2150	2365.2077	2365.1835	10	0	K.AQLEMIVSANGLSENVYEIASK.S	

Spot 1370

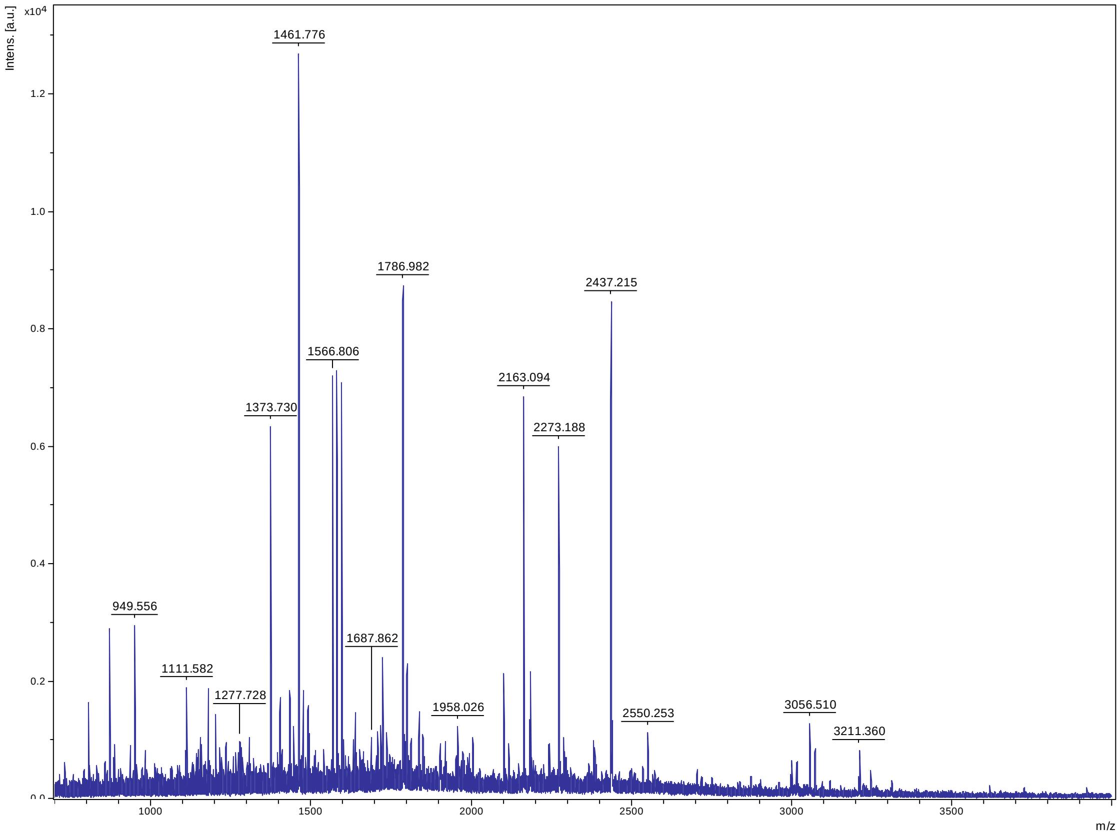


Match to: gi|77554415 Score: 97 Expect: 1.3e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
63 - 93	3056.4708	3055.4635	3055.5607	-0.0972	0	K.VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR.T	
63 - 93	3072.4877	3071.4804	3071.5556	-0.0752	0	K.VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR.T	Oxidation (M)
116 - 129	1579.8854	1578.8781	1578.8041	0.0740	0	R.QAVVNPENTFFSVK.R	
116 - 130	1735.9719	1734.9646	1734.9052	0.0594	1	R.QAVVNPENTFFSVKR.F	
168 - 180	1461.8320	1460.8247	1460.7623	0.0624	0	K.QFAAEEISAQVLR.K	
197 - 210	1566.8702	1565.8629	1565.7838	0.0792	0	K.AVVTVPAYFNDSQR.T	
227 - 242	1723.9748	1722.9675	1722.8828	0.0847	0	R.IINEPTAASLAYGFEK.K	
290 - 299	1178.6327	1177.6254	1177.6131	0.0123	0	K.VVDWLASNFK.K	
323 - 348	2750.3328	2749.3255	2749.4207	-0.0952	1	K.AKMELSTLSQTNISLPFITATADGPK.H	Oxidation (M)
325 - 348	2535.2987	2534.2914	2534.2938	-0.0023	0	K.MELSTLSQTNISLPFITATADGPK.H	
325 - 348	2551.2494	2550.2421	2550.2887	-0.0466	0	K.MELSTLSQTNISLPFITATADGPK.H	Oxidation (M)
380 - 399	2101.1636	2100.1563	2100.1062	0.0501	1	R.DAKLSVDNLDEVILVGGSTR.I	
383 - 399	1787.0353	1786.0280	1785.9472	0.0809	0	K.LSVDNLDEVILVGGSTR.I	
400 - 408	1012.5807	1011.5734	1011.5964	-0.0230	0	R.IPSVQELVK.K	
442 - 464	2370.3540	2369.3467	2369.3127	0.0341	0	K.DVVLLDVTPLSLGLETLGGVMTK.I	
442 - 464	2386.2950	2385.2877	2385.3076	-0.0199	0	K.DVVLLDVTPLSLGLETLGGVMTK.I	Oxidation (M)
477 - 499	2437.2111	2436.2038	2436.1768	0.0271	0	K.SEVFSTAADGQTSVEINVLQGER.E	
500 - 506	949.5155	948.5082	948.4664	0.0418	1	R.EFVRDNK.S	Acetyl (N-term)
513 - 521	935.4963	934.4890	934.5236	-0.0346	0	R.LDGIPPAPR.G	
530 - 545	1661.9423	1660.9350	1660.8671	0.0679	0	K.FDIDANGILSVAAIDK.G	
530 - 549	2005.1378	2004.1305	2004.0527	0.0778	1	K.FDIDANGILSVAAIDKGTGK.K	
551 - 568	1973.1006	1972.0933	1972.0113	0.0821	1	K.QDITITGASTLPKDEVER.M	

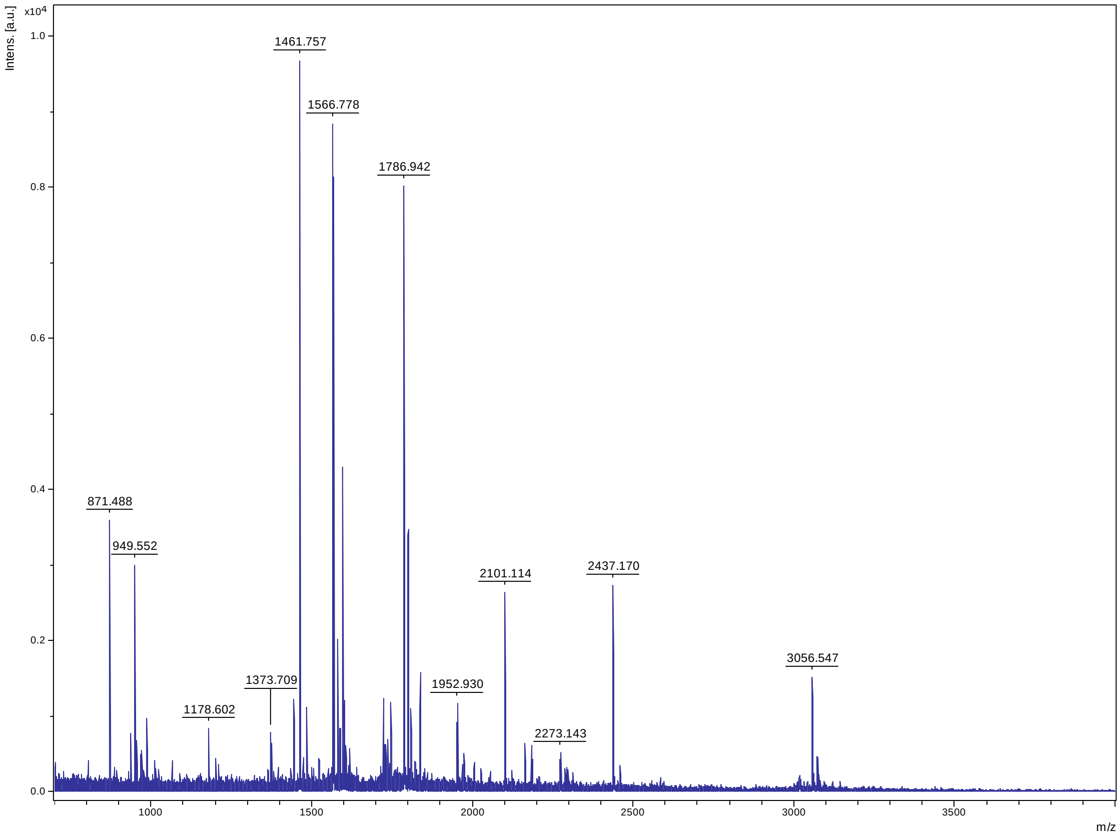
Spot 1376



Match to: Q2QV45_ORYSA Score: 108 Expect: 1.1e-06

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
63 - 93	3056.5103	3055.5030	3055.5607	-0.0577	0	K.VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR.T	
63 - 93	3072.4741	3071.4668	3071.5556	-0.0888	0	K.VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR.T	Oxidation (M)
116 - 129	1579.8207	1578.8134	1578.8041	0.0093	0	R.QAVVNPENTFFSVK.R	
116 - 130	1735.9246	1734.9173	1734.9052	0.0120	1	R.QAVVNPENTFFSVKR.F	
168 - 180	1444.7540	1443.7468	1443.7357	0.0110	0	K.QFAAEEISAQVLR.K	Pyro-glu (N-term Q)
168 - 180	1461.7760	1460.7687	1460.7623	0.0064	0	K.QFAAEEISAQVLR.K	
197 - 210	1566.8060	1565.7988	1565.7838	0.0150	0	K.AVVTVPAYFNDSQR.T	
227 - 242	1723.9067	1722.8995	1722.8828	0.0167	0	R.IINEPTAASLAYGFEK.K	
290 - 299	1178.6359	1177.6286	1177.6131	0.0155	0	K.VVDWLASNFK.K	
357 - 369	1595.7975	1594.7902	1594.7661	0.0241	1	R.AKFEELCSDLIDR.L	Carbamidomethyl (C)
359 - 371	1580.8241	1579.8168	1579.7915	0.0253	1	K.FEELCSDLIDRLK.T	
372 - 379	871.4940	870.4867	870.4923	-0.0056	0	K.TPVTNALR.D	
380 - 399	2101.1575	2100.1502	2100.1062	0.0440	1	R.DAKLSVDNLDEVILVGGSTR.I	
383 - 399	1786.9817	1785.9744	1785.9472	0.0272	0	K.LSVDNLDEVILVGGSTR.I	
477 - 499	2437.2146	2436.2073	2436.1768	0.0306	0	K.SEVFSTAADGQTSVEINVLQGER.E	
513 - 521	935.5417	934.5345	934.5236	0.0109	0	R.LDGIPPAPR.G	
530 - 549	2005.0630	2004.0557	2004.0527	0.0030	1	K.FDIDANGILSVAAIDKGTGK.K	

Spot 1382

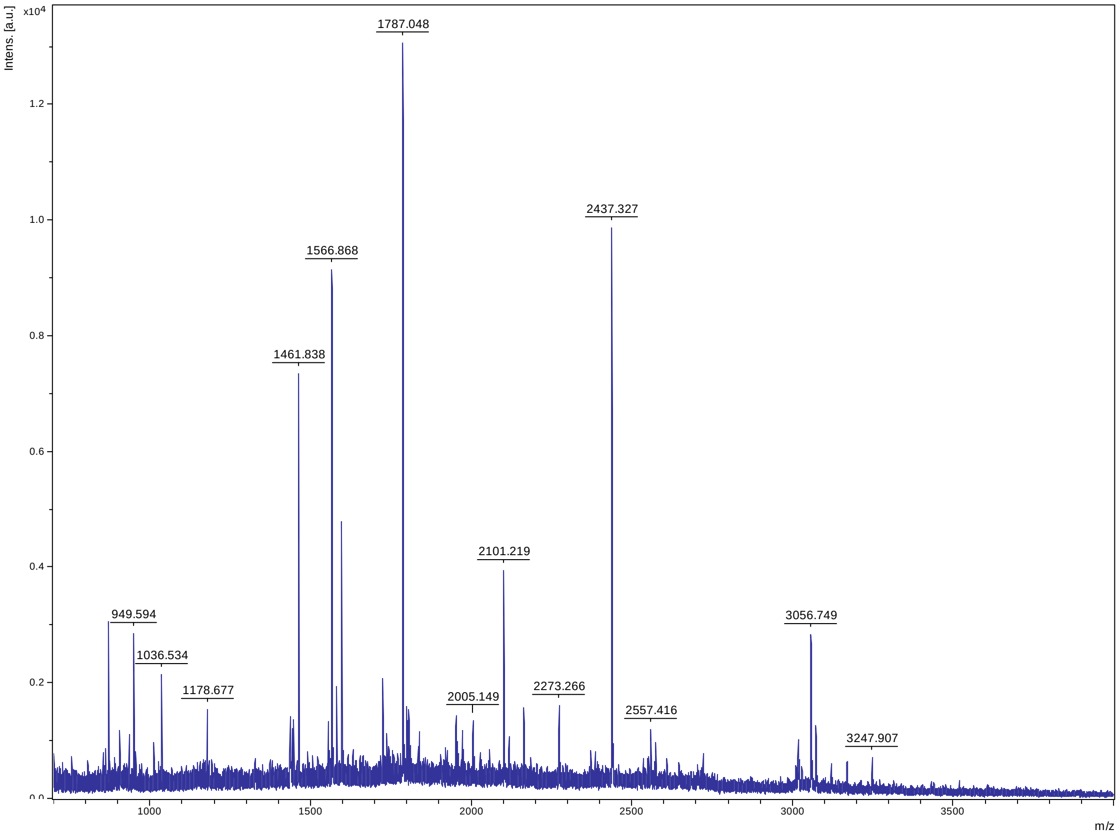


Match to: gi|77554415; Score: 157

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
63 - 93	3056.55	3055.55	3055.56	-0.02	0	VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR
63 - 93	3072.55	3071.54	3071.56	-0.01	0	VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR Oxidation (M)
94 - 103	1066.56	1065.56	1065.57	-0.01	0	TTPSVVAYTK
116 - 129	1579.80	1578.80	1578.80	-0.01	0	QAVVNPENTFFSVK
116 - 130	1735.91	1734.91	1734.91	0.00	1	QAVVNPENTFFSVKR
145 - 152	987.53	986.53	986.53	-0.00	0	QVSYHVVR
168 - 180	1444.73	1443.73	1443.74	-0.01	0	QFAAEEISAQVLR Pyro-glu (N-term Q)
168 - 180	1461.76	1460.76	1460.76	-0.01	0	QFAAEEISAQVLR
197 - 210	1566.78	1565.78	1565.78	-0.01	0	AVVTVPAYFNDSQR
227 - 242	1723.88	1722.87	1722.88	-0.01	0	IINEPTAASLAYGFEK
290 - 299	1178.60	1177.60	1177.61	-0.01	0	VVDWLASNFK
349 - 356	956.51	955.51	955.51	-0.00	0	HIETTLSR
357 - 369	1595.77	1594.76	1594.77	-0.00	1	AKFEELCSDLIDR
372 - 379	871.49	870.49	870.49	-0.01	0	TPVTNALR
380 - 399	2101.11	2100.11	2100.11	0.01	1	DAKLSVDNLDEVILVGGSTR
383 - 399	1786.94	1785.94	1785.95	-0.01	0	LSVDNLDEVILVGGSTR
400 - 408	1012.57	1011.57	1011.60	-0.03	0	IPSVQELVK
477 - 499	2437.17	2436.17	2436.18	-0.01	0	SEVFSTAADGQTSVEINVLQGER
513 - 521	935.54	934.54	934.52	0.01	0	LDGIPPAPR
551 - 568	1973.00	1971.99	1972.01	-0.02	1	QDITITGASTLPKDEVER

Spot 1385

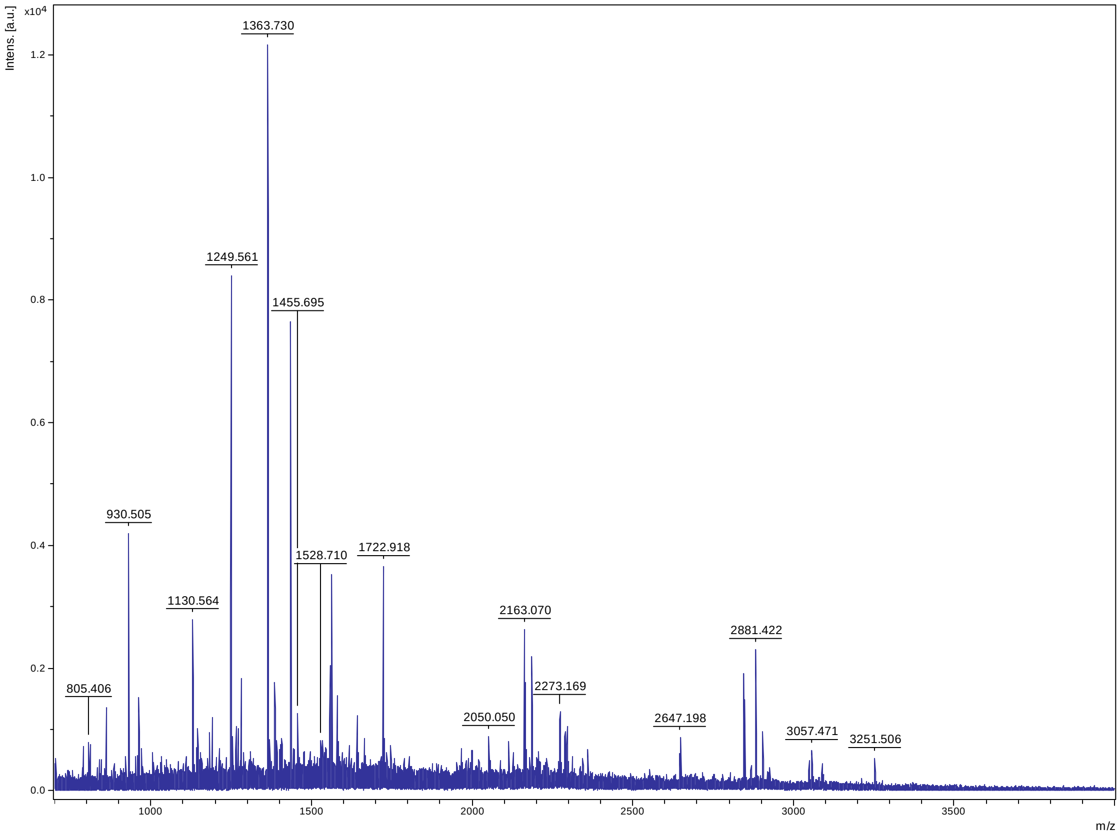


Match to: gi|77554415 Score: 104 Expect: 2.7e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
116 - 129	1579.8912	1578.8839	1578.8041	0.0798	0	R.QAVVNPENTFFSVK.R	
116 - 130	1735.9495	1734.9422	1734.9052	0.0370	1	R.QAVVNPENTFFSVKR.F	
168 - 180	1461.8457	1460.8384	1460.7623	0.0761	0	K.QFAAEEISAQVLR.K	
168 - 181	1631.8933	1630.8860	1630.8678	0.0182	1	K.QFAAEEISAQVLRK.L	Acetyl (N-term)
197 - 210	1566.8551	1565.8478	1565.7838	0.0641	0	K.AVVTVPAYFNDSQR.T	
227 - 242	1723.9497	1722.9424	1722.8828	0.0596	0	R.IINEPTAASLAYGFEK.K	
290 - 299	1178.6909	1177.6836	1177.6131	0.0705	0	K.VVDWLASNFK.K	
325 - 348	2535.3342	2534.3269	2534.2938	0.0332	0	K.MELSTLSQTNISLPFITATADGPK.H	
357 - 369	1595.8556	1594.8483	1594.7661	0.0823	1	R.AKFEELCSDLIDR.L	Carbamidomethyl (C)
380 - 399	2101.1531	2100.1458	2100.1062	0.0396	1	R.DAKLSVDNLDEVILVGGSTR.I	
383 - 399	1787.0077	1786.0004	1785.9472	0.0532	0	K.LSVDNLDEVILVGGSTR.I	
442 - 464	2370.2899	2369.2826	2369.3127	-0.0300	0	K.DVVLLDVTPLSLGLETLGGVMTK.I	
442 - 464	2386.2942	2385.2869	2385.3076	-0.0207	0	K.DVVLLDVTPLSLGLETLGGVMTK.I	Oxidation (M)
477 - 499	2437.1792	2436.1719	2436.1768	-0.0048	0	K.SEVFSTAADGQTSVEINVLQGER.E	
500 - 506	949.5734	948.5661	948.4664	0.0997	1	R.EFVRDNK.S	Acetyl (N-term)
530 - 549	2005.0995	2004.0922	2004.0527	0.0395	1	K.FDIDANGILSVAAIDKGTGK.K	
551 - 568	1973.0659	1972.0586	1972.0113	0.0474	1	K.QDITITGASTLPKDEVER.M	

Spot 1386

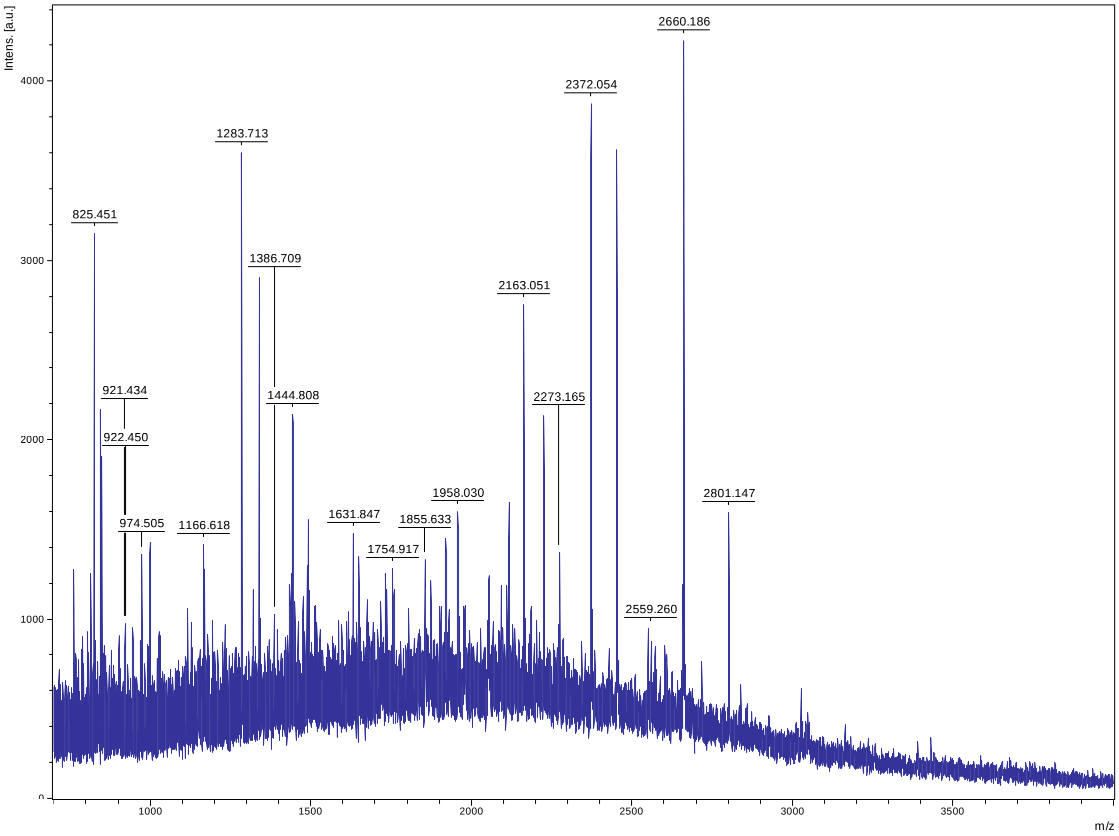


Match to: gi|77551210; Score: 101

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
93 - 104	1561.81	1560.81	1560.81	0.00	1	KFVYVEQAFFQR
94 - 104	1433.72	1432.72	1432.71	0.00	0	FVYVEQAFFQR
156 - 166	1363.73	1362.73	1362.73	-0.00	1	FIKEEFGQIPR
198 - 206	1181.55	1180.55	1180.55	-0.00	1	IDYQDRDTR
211 - 217	930.51	929.50	929.50	0.01	0	ELEVVWR
221 - 235	1557.79	1556.79	1556.79	-0.00	0	TFGSSADIFAGIFPK
286 - 298	1528.71	1527.71	1527.68	0.02	0	TNHVMFTMGTDFK
299 - 307	1249.56	1248.56	1248.56	0.00	0	YQYAESWFR
322 - 336	1642.84	1641.84	1641.82	0.01	0	VNALYSTPSIYTDAK
337 - 346	1190.62	1189.62	1189.62	-0.01	0	HAENVPWPLK
377 - 386	1130.56	1129.56	1129.56	0.00	0	VMSGYYLAAR
377 - 386	1146.55	1145.55	1145.55	-0.00	0	VMSGYYLAAR Oxidation (M)
387 - 392	811.41	810.40	810.43	-0.02	0	QLEFFK
395 - 422	2881.42	2880.42	2880.37	0.05	0	SNSDLTTDSLADALALAQHHDAVTGTEK
432 - 442	1265.64	1264.64	1264.68	-0.04	1	RLSIGYTQAEK
509 - 524	1722.92	1721.92	1721.89	0.02	0	IPVISDSIVVHDSEGR

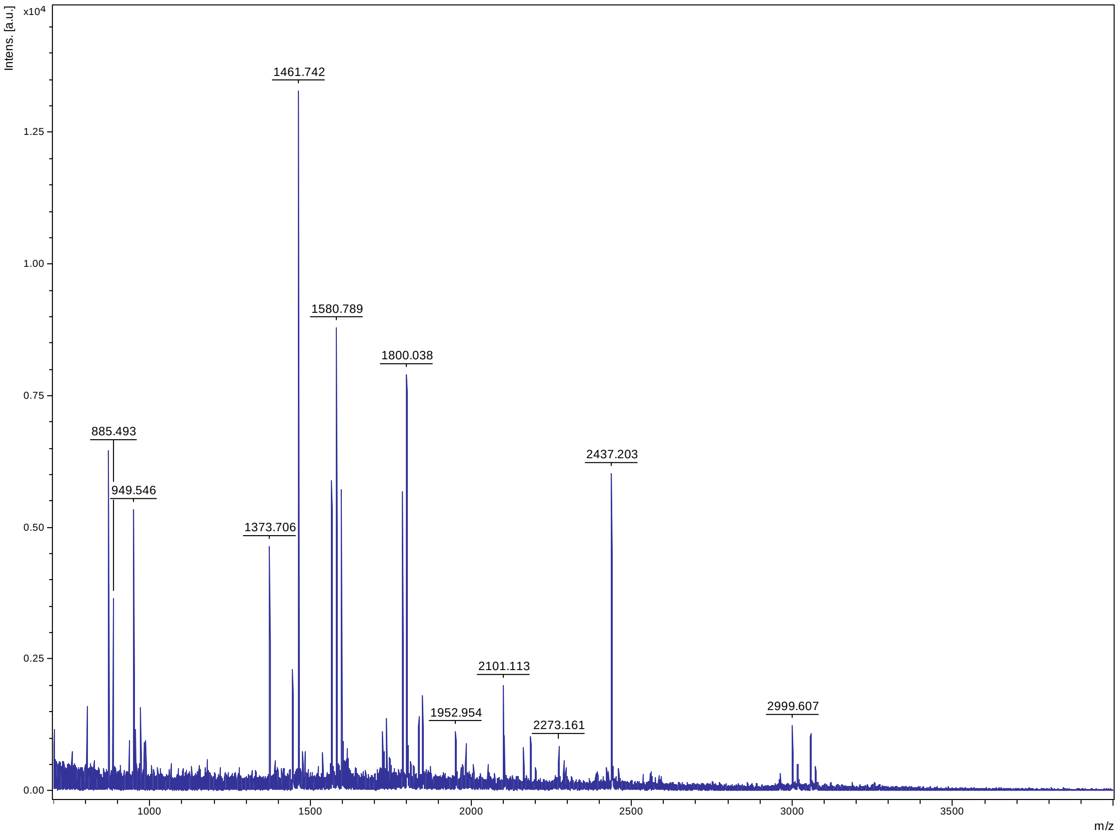
Spot 1389



Match to: gi|51854277 Score: 68 Expect: 0.01

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
56 - 68	1166.5387	1165.5314	1165.6203	-0.0889	0	R.NPAGPAALAAASR.D	
69 - 91	2452.0676	2451.0603	2451.0713	-0.0110	0	R.DSVFDFTSVDDSLAAAAEDSSFR.L	
110 - 119	1283.6632	1282.6559	1282.6894	-0.0335	0	R.FNQRPQLPQR.R	
163 - 174	1434.7101	1433.7028	1433.6609	0.0419	0	K.SSVDIQPDWTMR.E	
266 - 276	1339.6889	1338.6816	1338.7044	-0.0228	0	R.SIHSWDIVVQR.V	
336 - 361	2801.1879	2800.1806	2800.2463	-0.0657	1	R.DGEKVTFDEPNPFASEGEEAASVGYR.Y	
340 - 361	2372.0886	2371.0813	2371.0603	0.0210	0	K.VTFDEPNPFASEGEEAASVGYR.Y	
365 - 376	1444.8000	1443.7927	1443.7721	0.0206	1	R.WKLDDEISIVAR.C	
377 - 390	1438.6615	1437.6542	1437.6418	0.0124	0	R.CEVHAVNADPGGGR.Q	Carbamidomethyl (C)
507 - 519	1512.8737	1511.8664	1511.8823	-0.0159	1	K.YVLVKDPAKPQVR.I	

Spot 1390

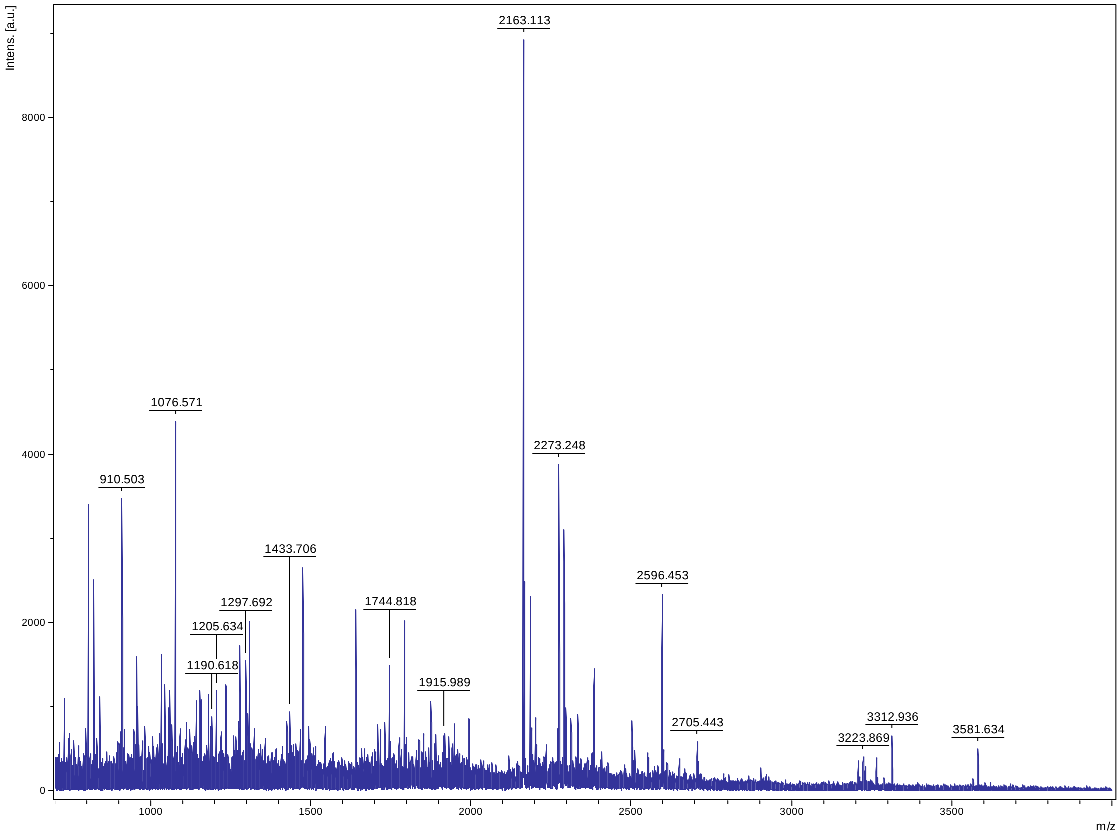


Match to: gi|77554415; Score: 100

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
63 - 93	3056.65	3055.64	3055.56	0.08	0	VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR
63 - 93	3072.64	3071.64	3071.56	0.08	0	VVGIDLGTTNSAVAAMEGGKPTVITNAEGQR Oxidation (M)
116 - 130	1735.91	1734.91	1734.91	0.00	1	QAVVNPENTFFSVKR
145 - 152	970.53	969.52	969.50	0.02	0	QVSYHVVR Pyro-glu (N-term Q)
145 - 152	987.53	986.52	986.53	-0.01	0	QVSYHVVR
168 - 180	1444.71	1443.71	1443.74	-0.02	0	QFAAEEISAQVLR Pyro-glu (N-term Q)
168 - 180	1461.74	1460.74	1460.76	-0.02	0	QFAAEEISAQVLR
197 - 210	1566.78	1565.77	1565.78	-0.01	0	AVVTVPAYFNDSQR
227 - 242	1723.89	1722.88	1722.88	0.00	0	IINEPTAASLAYGFEK
349 - 356	956.54	955.53	955.51	0.03	0	HIETTLSR
357 - 369	1595.76	1594.76	1594.77	-0.00	1	AKFEELCSDLIDR
372 - 379	871.48	870.48	870.49	-0.01	0	TPVTNALR
380 - 399	2101.11	2100.11	2100.11	0.00	1	DAKLSVDNLDEVILVGGSTR
383 - 399	1786.95	1785.95	1785.95	0.00	0	LSVDNLDEVILVGGSTR
477 - 499	2437.20	2436.20	2436.18	0.02	0	SEVFSTAADGQTSVEINVLQGER
513 - 521	935.56	934.55	934.52	0.03	0	LDGIPPAPR

Spot 1394

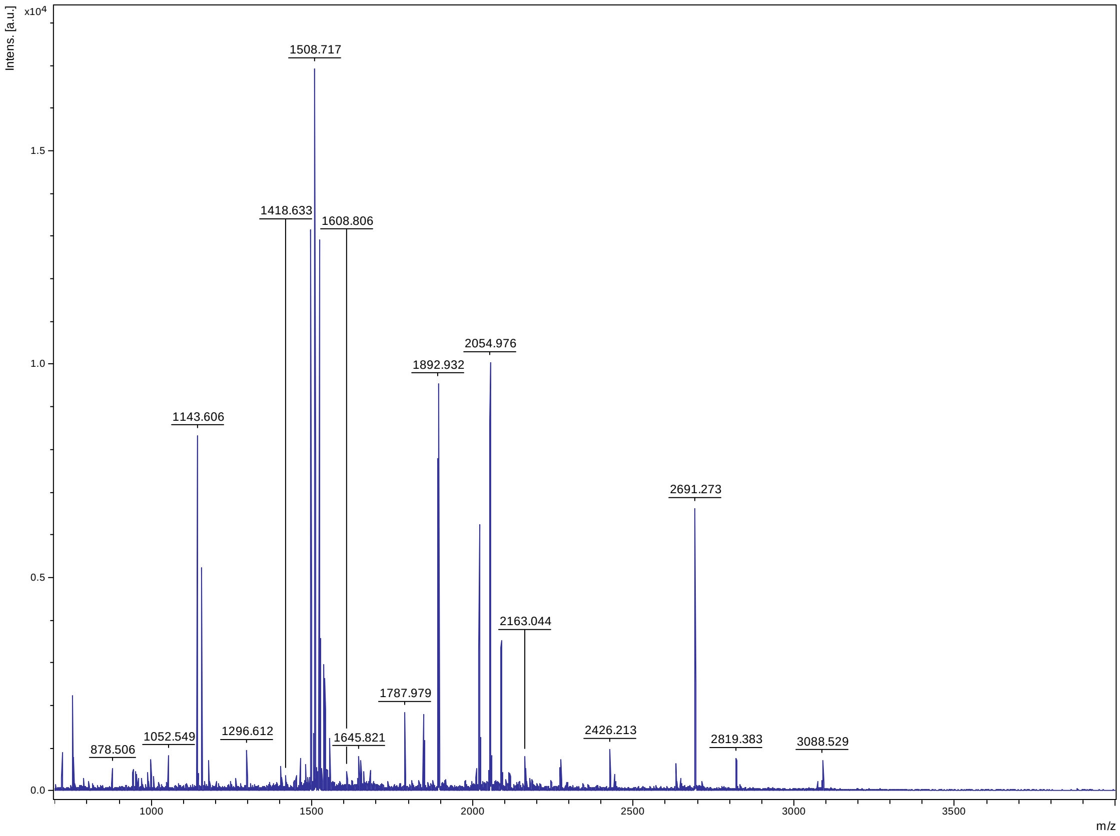


Match to: gi|51964830; Score: 79

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
10 - 18	957.56	956.55	956.50	0.05	0	DLAGGLQQR
37 - 60	2596.45	2595.45	2595.23	0.22	0	VEYGDATTTIDPTCANVVAQAFPR
86 - 93	820.54	819.54	819.46	0.08	0	VGVVFSGR
133 - 145	1467.73	1466.73	1466.75	-0.02	0	TIEITDDVLASYK
222 - 236	1744.82	1743.82	1743.81	0.00	0	NQFVETTVGFDTVCK
237 - 254	1874.97	1873.96	1873.96	0.01	0	VNSQLVSNVCLDAISAGK
255 - 260	910.50	909.50	909.44	0.06	0	YYYFVR
293 - 301	1076.57	1075.57	1075.59	-0.03	0	LTLMEVINK Oxidation (M)
474 - 488	1708.77	1707.77	1707.83	-0.06	1	WRCAAAPLTAMMSVK Oxidation (M)
493 - 514	2163.11	2162.11	2162.26	-0.15	1	GPGAIPIGKPAIHPSPIDLKGK

Spot 1399

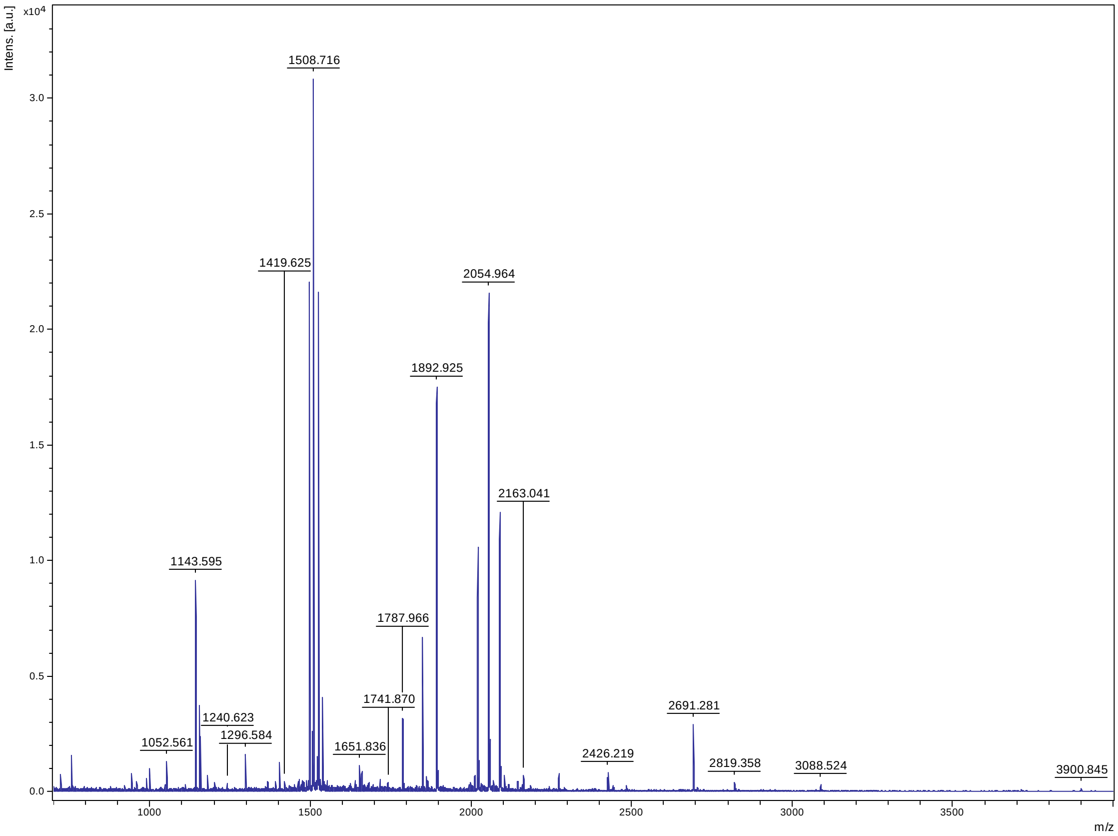


Match to: gi|41052822; Score: 298

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
32 - 51	2116.07	2115.07	2115.09	-0.03	0	LGTVIGIDLGTTYSCVGVYK
52 - 65	1536.74	1535.73	1535.74	-0.01	0	NGHVEIIANDQGNR
66 - 78	1508.72	1507.71	1507.73	-0.02	0	ITPSWVAFTDSER
86 - 94	998.50	997.50	997.49	0.00	0	NQAAVNPER
95 - 101	878.51	877.50	877.50	0.00	1	TIFDVKR
143 - 156	1506.75	1505.75	1505.78	-0.03	0	VFSPEEVSAMILGK
168 - 185	2021.02	2020.02	2020.04	-0.02	1	KINDAVVTVPAYFNDAQR
169 - 185	1892.93	1891.93	1891.94	-0.01	0	INDAVVTVPAYFNDAQR
190 - 201	1155.63	1154.63	1154.64	-0.01	0	DAGVIAGLNVAR
202 - 217	1659.86	1658.86	1658.89	-0.03	0	IINEPTAAAIAYGLDK
202 - 218	1787.98	1786.98	1786.98	-0.01	1	IINEPTAAAIAYGLDKK
266 - 272	943.48	942.48	942.49	-0.01	0	IMEYFIK
266 - 272	959.49	958.48	958.48	0.00	0	IMEYFIK Oxidation (M)
302 - 310	1052.55	1051.55	1051.55	-0.01	0	ALSNQHQVR
302 - 328	3088.53	3087.53	3087.53	0.00	1	ALSNQHQVRVEIESLFDGTDFSEPLTR
311 - 328	2054.98	2053.97	2053.98	-0.01	0	VEIESLFDGTDFSEPLTR
331 - 340	1296.61	1295.61	1295.61	-0.00	0	FEELNNDLFR
349 - 371	2426.21	2425.21	2425.23	-0.02	1	AMDDAGLEKSQIHEIVLVGGSTR
349 - 371	2442.22	2441.21	2441.22	-0.01	1	AMDDAGLEKSQIHEIVLVGGSTR Oxidation (M)
375 - 386	1495.80	1494.80	1494.78	0.01	1	VQQLLRDYFEGK
391 - 418	2691.27	2690.27	2690.27	0.00	0	GVNPDEAVAYGAAVQGSILSGEGGDETK
453 - 476	2819.38	2818.38	2818.38	0.00	1	KSQVFTTYQDQQTTVSIQVFEGER
484 - 498	1554.88	1553.88	1553.89	-0.01	1	LLGKFDLSGIPAAPR
488 - 498	1143.61	1142.60	1142.61	-0.00	0	FDLSGIPAAPR
539 - 546	989.49	988.49	988.48	0.01	0	LSQEEIDR
569 - 579	1402.63	1401.63	1401.66	-0.03	0	NQLETYVYNMK
569 - 579	1418.63	1417.63	1417.65	-0.02	0	NQLETYVYNMK Oxidation (M)
626 - 643	2089.10	2088.09	2088.10	-0.01	1	LKEVEAVCNPIISAVYQR
628 - 643	1847.92	1846.92	1846.92	-0.01	0	EVEAVCNPIISAVYQR
644 - 665	2011.89	2010.89	2010.80	0.08	0	TGGAPGGGADGEGGVDDEHDEL

Spot 1400

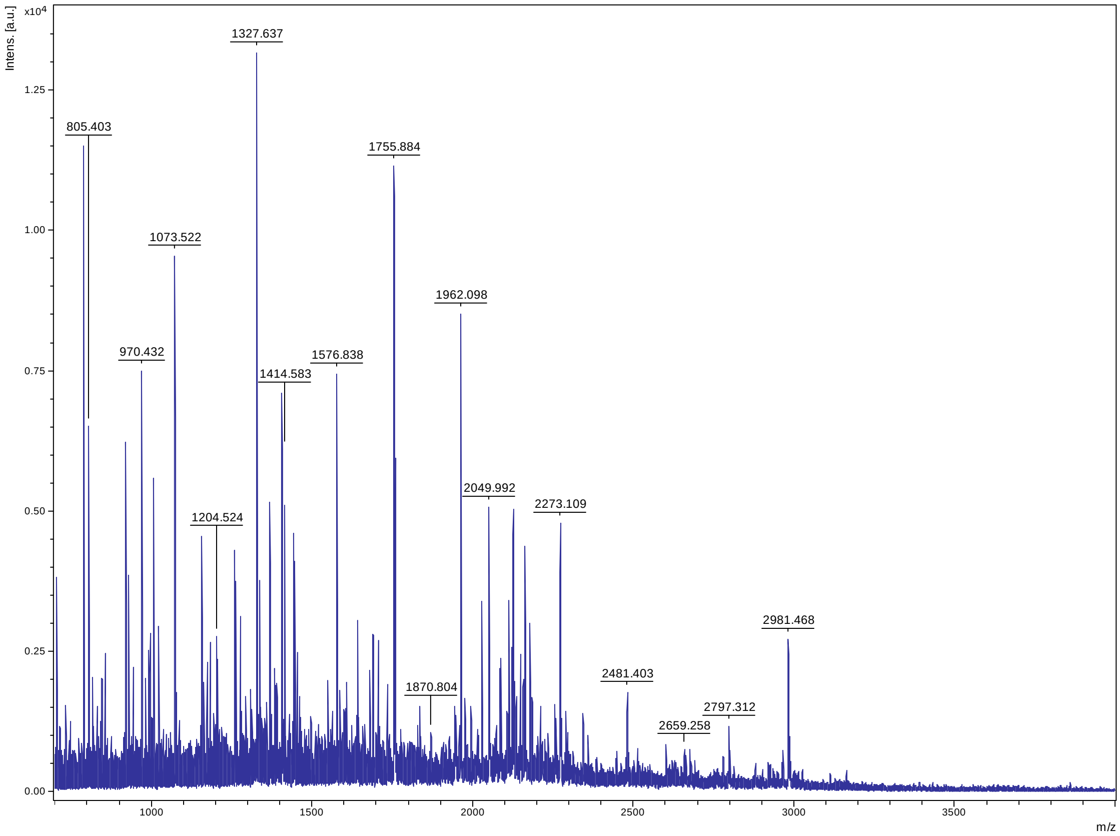


Match to: gi|41052822 Score: 304 Expect: 8.4e-26

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
52 - 65	1536.7428	1535.7355	1535.7440	-0.0085	0	K.NGHVEIIANDQGNR.I
66 - 78	1508.7164	1507.7092	1507.7307	-0.0215	0	R.ITPSWVAFTDSER.L
86 - 94	998.4786	997.4714	997.4941	-0.0227	0	K.NQAAVNPER.T
143 - 156	1506.7424	1505.7352	1505.7799	-0.0447	0	K.VFSPEEVSAMILGK.M
157 - 167	1240.6230	1239.6158	1239.6169	-0.0011	1	K.MKETAEAYLGK.K
168 - 185	2021.0142	2020.0069	2020.0377	-0.0308	1	K.KINDAVVTVPAYFNDAQR.Q
169 - 185	1892.9254	1891.9181	1891.9428	-0.0246	0	K.INDAVVTVPAYFNDAQR.Q
190 - 201	1155.6263	1154.6191	1154.6407	-0.0216	0	K.DAGVIAGLNVAR.I
202 - 217	1659.8799	1658.8726	1658.8879	-0.0153	0	R.IINEPTAAAIAYGLDK.K
202 - 218	1787.9655	1786.9582	1786.9828	-0.0247	1	R.IINEPTAAAIAYGLDKK.G
266 - 272	943.4786	942.4714	942.4884	-0.0171	0	R.IMEYFIK.L
266 - 272	959.4891	958.4819	958.4834	-0.0015	0	R.IMEYFIK.L Oxidation (M)
302 - 310	1052.5614	1051.5541	1051.5523	0.0019	0	R.ALSNQHQVR.V
302 - 328	3088.5239	3087.5167	3087.5261	-0.0094	1	R.ALSNQHQVRVEIESLFDGTDFSEPLTR.A
311 - 328	2054.9644	2053.9571	2053.9844	-0.0273	0	R.VEIESLFDGTDFSEPLTR.A
331 - 340	1296.5836	1295.5763	1295.6146	-0.0382	0	R.FEELNNDLFR.K
349 - 371	2426.2188	2425.2115	2425.2270	-0.0156	1	K.AMDDAGLEKSQIHEIVLVGGSTR.I
349 - 371	2442.1826	2441.1753	2441.2220	-0.0466	1	K.AMDDAGLEKSQIHEIVLVGGSTR.I Oxidation (M)
375 - 386	1495.7931	1494.7858	1494.7830	0.0028	1	K.VQQLLRDYFEGK.E
391 - 418	2691.2815	2690.2742	2690.2670	0.0072	0	K.GVNPDEAVAYGAAVQGSILSGEGGDETK.D
453 - 476	2819.3579	2818.3506	2818.3773	-0.0267	1	K.KSQVFTTYQDQQTTVSIQVFEGER.S
488 - 498	1143.5950	1142.5877	1142.6084	-0.0207	0	K.FDLSGIPAAPR.G
537 - 546	1202.6057	1201.5984	1201.6051	-0.0066	1	K.GRLSQEEIDR.M
539 - 546	989.4940	988.4867	988.4825	0.0042	0	R.LSQEEIDR.M
569 - 579	1402.6382	1401.6309	1401.6598	-0.0289	0	R.NQLETYVYNMK.N
606 - 625	2483.1001	2482.0928	2482.1023	-0.0095	1	K.EALEWLDENQTAEKEEYEEK.L
626 - 643	2089.0950	2088.0877	2088.1037	-0.0160	1	K.LKEVEAVCNPIISAVYQR.T Carbamidomethyl (C)
628 - 643	1847.9100	1846.9028	1846.9247	-0.0219	0	K.EVEAVCNPIISAVYQR.T Carbamidomethyl (C)
644 - 665	2011.7867	2010.7795	2010.8038	-0.0243	0	R.TGGAPGGGADGEGGVDDEHDEL.-

Spot 1401



Match to: gi|27261082; Score: 140

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
74 - 81	999.46	998.46	998.47	-0.01	0	CRPGPEQR
82 - 100	2121.06	2120.06	2120.10	-0.04	0	AEPLPTVEGSLFHDRPTVR
104 - 118	1758.85	1757.85	1757.89	-0.04	0	LYFVSAHEQPPAPFR
171 - 180	1162.60	1161.60	1161.64	-0.04	0	VLETEVAVFR
194 - 209	1870.80	1869.80	1869.87	-0.07	0	GGWPTWHGEGTVFFHR
210 - 220	1337.57	1336.57	1336.62	-0.05	0	VADDGWWSVFR
221 - 235	1585.73	1584.73	1584.76	-0.03	0	VDVSPETLEPTGGER
236 - 252	1835.92	1834.91	1834.96	-0.05	1	RVTPPGLHCFTPAAVGR
237 - 252	1679.81	1678.81	1678.86	-0.05	0	VTPPGLHCFTPAAVGR
272 - 289	2148.99	2147.99	2148.04	-0.05	0	HVELFDLETESFSPLTER
320 - 338	2028.01	2027.01	2027.07	-0.06	0	GDSVVPYLQPVQSPVSSLR
420 - 439	2136.03	2135.03	2135.07	-0.04	1	LEFDAGELTTGRDEVAATLK
432 - 439	846.42	845.41	845.45	-0.03	0	DEVAATLK
440 - 459	2086.01	2085.01	2085.03	-0.02	0	VLTRPEAGNDAFPAVSPCGK
460 - 467	1006.47	1005.47	1005.55	-0.08	1	WVVFRSGR
472 - 492	2157.02	2156.02	2156.05	-0.03	0	NLYIVDAAHGEDVGAGEGTIR
543 - 556	1278.60	1277.60	1277.65	-0.05	0	VHVAGPAGSAAADR
559 - 569	1331.56	1330.56	1330.61	-0.05	0	INHVCFSPDSR
602 - 609	816.44	815.44	815.45	-0.01	0	LDGSGLVR

Match to: gi|55741328; Score: 125

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
41 - 56	1576.84	1575.84	1575.87	-0.04	0	DGGSAQRPLAPAPLVK
109 - 130	2481.40	2480.40	2480.21	0.19	1	TIFVASEQESEIMDVKEQAQAK
134 - 147	1454.71	1453.71	1453.75	-0.04	0	SVVFVTGEASPYAK
148 - 165	1755.88	1754.88	1754.93	-0.05	0	SGGLGDVCGSLPIALALR
169 - 175	831.45	830.45	830.45	-0.00	0	VMVVMPR
169 - 175	847.44	846.44	846.45	-0.01	0	VMVVMPR Oxidation (M)
176 - 193	2111.99	2110.99	2110.98	0.01	1	YMNGALNKNFANAFYTEK Oxidation (M)
184 - 193	1204.52	1203.52	1203.56	-0.03	0	NFANAFYTEK
197 - 213	2124.91	2123.91	2123.95	-0.04	0	IPCFGGEHEVTFFHEYR
292 - 299	1073.52	1072.52	1072.55	-0.03	0	YRPYGVYR
366 - 393	2981.47	2980.47	2980.48	-0.01	0	IVTVSQGYSWEVTTAEGGQGLNELLSSR
439 - 456	1962.10	1961.10	1961.15	-0.05	0	ELGLPIRPDVPLIGFIGR
468 - 475	928.50	927.50	927.52	-0.02	0	LAIPDLMR
468 - 475	944.50	943.50	943.52	-0.02	0	LAIPDLMR Oxidation (M)
476 - 495	2255.97	2254.97	2255.01	-0.05	0	DNIQFVMLGSGDPGFEGWMR
507 - 518	1327.64	1326.63	1326.68	-0.05	0	GWVGFSVPVSHR
519 - 531	1446.70	1445.69	1445.74	-0.04	0	ITAGCDILLMPSR
532 - 558	2964.41	2963.41	2963.44	-0.03	0	FEPCGLNQLYAMQYGTVPVVHGTGGLR
587 - 592	805.40	804.40	804.43	-0.03	0	MLWALR Oxidation (M)
593 - 599	841.40	840.40	840.42	-0.02	0	MAISTYR
600 - 610	1331.56	1330.56	1330.63	-0.07	1	EHKSSWEGLMK

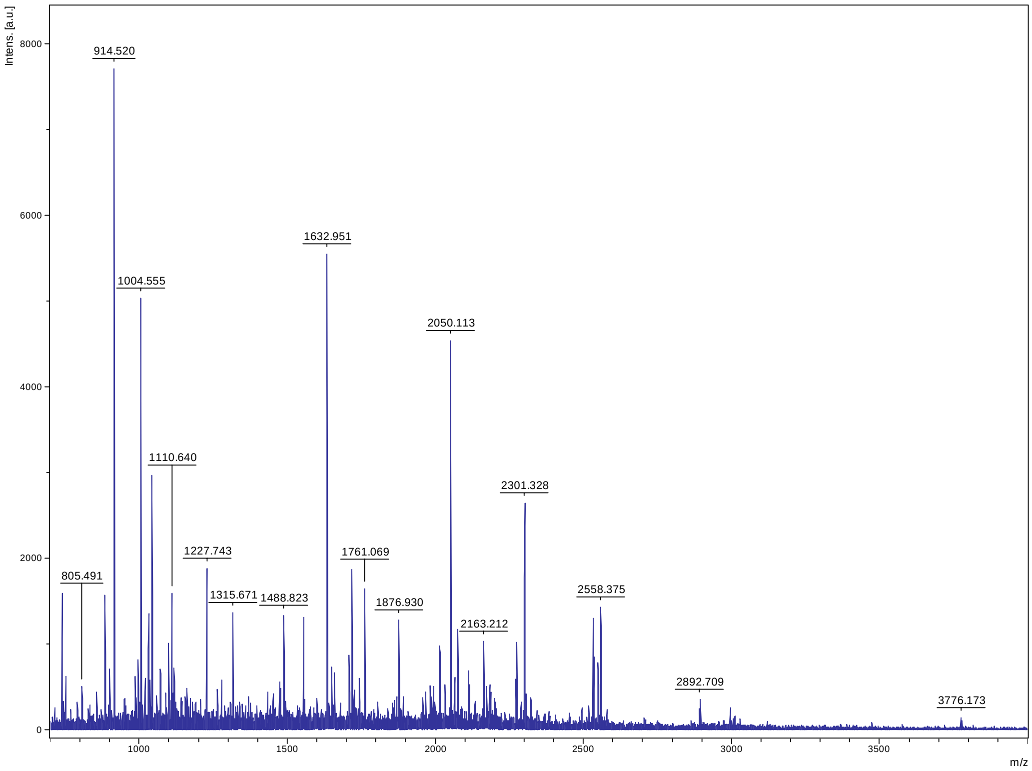
Match to: gi|50878307; Score: 111

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
13 - 20	831.45	830.45	830.41	0.04	1	ASGNNGRR
156 - 168	1406.80	1405.80	1405.84	-0.04	0	LGDPARPLLLSVR
203 - 209	921.38	920.38	920.40	-0.02	0	FAYDSYR
203 - 210	1077.49	1076.48	1076.50	-0.02	1	FAYDSYRR
277 - 293	1943.95	1942.95	1943.03	-0.08	0	QLQLAVLAVFNSWDSPR
308 - 333	2659.26	2658.26	2658.29	-0.03	0	GTAVNVQTMVFGNMGNTSGTGVLFTR
308 - 333	2675.25	2674.25	2674.28	-0.03	0	GTAVNVQTMVFGNMGNTSGTGVLFTR Oxidation (M)

341 - 360	2178.11	2177.11	2177.15	-0.04	1	KLYGEFLVNAQGEDVVAGIR
342 - 360	2049.99	2048.99	2049.05	-0.06	0	LYGEFLVNAQGEDVVAGIR
392 - 404	1641.68	1640.68	1640.72	-0.04	0	EMMDIEFTVQENR
405 - 411	1006.47	1005.47	1005.49	-0.02	0	LWMLQCR
405 - 411	1022.47	1021.47	1021.48	-0.02	0	LWMLQCR Oxidation (M)
423 - 435	1444.71	1443.70	1443.74	-0.04	0	IAVDMVNEGLVER
423 - 435	1460.70	1459.70	1459.73	-0.04	0	IAVDMVNEGLVER Oxidation (M)
441 - 464	2779.31	2778.31	2778.34	-0.03	1	MVEPGHLDQLLHPQFENPSGYKDK
503 - 523	2111.99	2110.99	2111.03	-0.04	0	TETSPEDVGGMHAAVGILTAR
503 - 523	2127.98	2126.98	2127.03	-0.05	0	TETSPEDVGGMHAAVGILTAR Oxidation (M)
625 - 635	1174.53	1173.53	1173.56	-0.03	0	QNGAEGIGLCR
636 - 646	1369.54	1368.54	1368.58	-0.04	0	TEHMFFASDER
636 - 646	1385.56	1384.56	1384.57	-0.01	0	TEHMFFASDER Oxidation (M)
652 - 662	1294.60	1293.60	1293.64	-0.04	0	QMIMASSLELR Oxidation (M)
652 - 662	1310.63	1309.63	1309.64	-0.01	0	QMIMASSLELR 2 Oxidation (M)
675 - 682	970.43	969.43	969.46	-0.03	0	SDFEGIFR
683 - 692	1072.53	1071.53	1071.57	-0.05	0	AMDGLPVTIR
683 - 692	1088.55	1087.55	1087.57	-0.02	0	AMDGLPVTIR Oxidation (M)
693 - 712	2343.15	2342.15	2342.17	-0.02	0	LLDPPLHEFLPEGHVEDMVR
713 - 728	1734.78	1733.77	1733.79	-0.01	0	ELCSETGAAQDDVLAR
732 - 742	1262.60	1261.60	1261.65	-0.05	0	LSEVNPMLGFR
732 - 742	1278.60	1277.60	1277.64	-0.04	0	LSEVNPMLGFR Oxidation (M)
746 - 759	1607.74	1606.74	1606.80	-0.06	0	LGISYPELTEMQAR
804 - 815	1359.65	1358.65	1358.69	-0.05	1	VFTDMGKTIGYK

Spot 1403

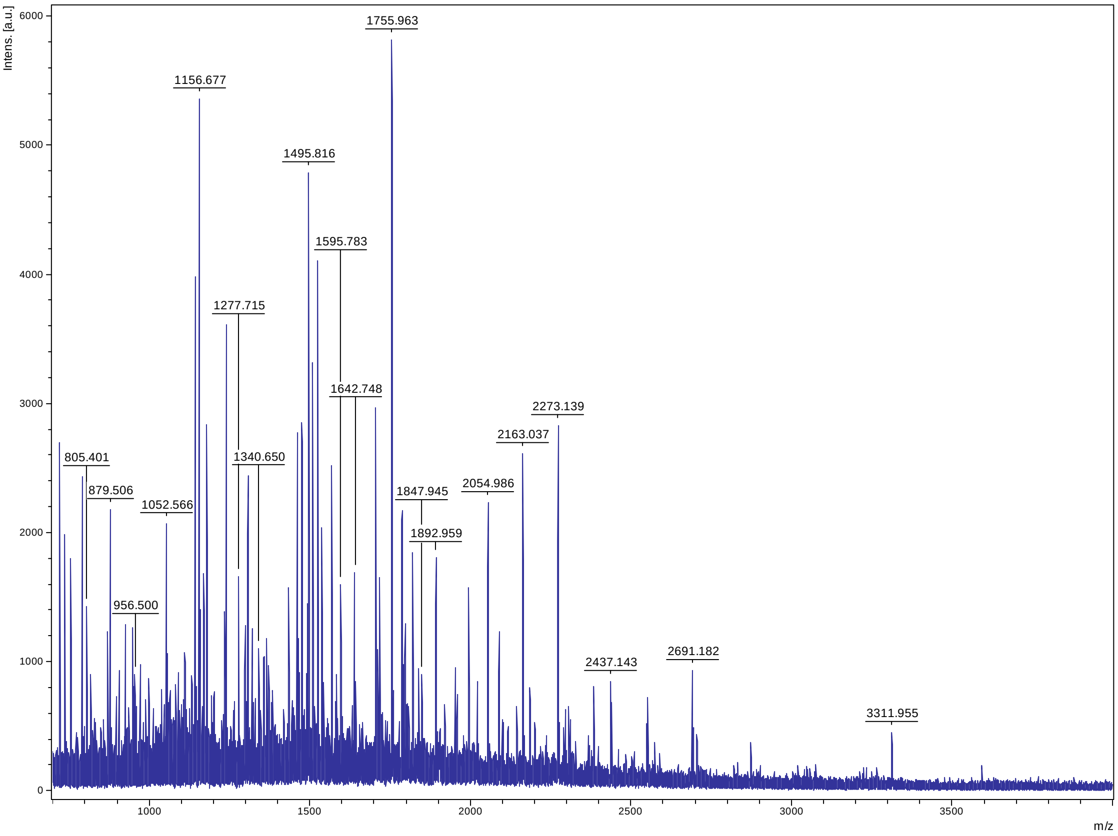


Match to: gi|17981609 Score: 297 Expect: 1.1e-25

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
10 - 25	1632.9514	1631.9441	1631.8267	0.1174	0	K.ATTPFDGQKPGTSGLR.K
10 - 26	1761.0691	1760.0618	1759.9216	0.1402	1	K.ATTPFDGQKPGTSGLRK.K
70 - 85	1658.0153	1657.0080	1656.8981	0.1099	1	K.DAVQIITKMAAANGVR.R
78 - 85	805.4906	804.4833	804.3912	0.0922	0	K.MAAANGVR.R Oxidation (M)
86 - 105	2171.3477	2170.3404	2170.1680	0.1724	1	R.RVWVGQNSLMSTPAVSAVIR.E
86 - 105	2187.3267	2186.3194	2186.1629	0.1565	1	R.RVWVGQNSLMSTPAVSAVIR.E Oxidation (M)
87 - 105	2015.2288	2014.2215	2014.0669	0.1546	0	R.VWVGQNSLMSTPAVSAVIR.E
115 - 137	2301.3281	2300.3208	2300.1436	0.1772	0	K.ATGAFILTASHNPGGPTEDFGIK.Y
138 - 153	1708.8563	1707.8490	1707.7410	0.1081	0	K.YNMENGGPAPESVTDK.I
207 - 215	1099.6448	1098.6375	1098.5597	0.0778	0	K.TIFDFESIK.K
207 - 216	1227.7433	1226.7360	1226.6546	0.0814	1	K.TIFDFESIKK.L
223 - 240	2050.1128	2049.1055	2048.9414	0.1641	0	K.FTFCYDALHGVAGTYATR.I Carbamidomethyl (C)
241 - 259	2076.2139	2075.2066	2075.0608	0.1458	0	R.IFVEELGAAESSLLNCVPK.E Carbamidomethyl (C)
260 - 275	1717.9203	1716.9130	1716.7743	0.1387	0	K.EDFGGGHPDPNLTYAK.E
286 - 304	1876.9296	1875.9223	1875.7870	0.1352	0	K.SSNAEPPEFGAAADGDADR.N
362 - 370	1110.6404	1109.6331	1109.5545	0.0786	0	K.FFEVPTGWK.F
418 - 433	1743.0333	1742.0260	1741.9210	0.1051	1	K.DNLGGDKLVTVEDIVR.Q
425 - 433	1043.6927	1042.6855	1042.6022	0.0833	0	K.LVTVEDIVR.Q
434 - 441	987.5173	986.5100	986.4359	0.0741	0	R.QHWGTYGR.H Pyro-glu (N-term Q)
434 - 441	1004.5551	1003.5478	1003.4624	0.0854	0	R.QHWGTYGR.H
447 - 458	1315.6705	1314.6633	1314.5728	0.0905	0	R.YDYENVDAGAAK.E
483 - 506	2558.3750	2557.3677	2557.1707	0.1970	1	R.SDVSDVVAADEFEYKDPVDGSVSK.H
512 - 519	914.5196	913.5123	913.4293	0.0830	0	R.YLFGDGSR.L
524 - 535	1118.6978	1117.6905	1117.6091	0.0814	0	R.LSGTGSVGATIR.V
536 - 543	1071.6217	1070.6144	1070.5284	0.0860	0	R.VYIEQYEK.D
536 - 547	1488.8232	1487.8160	1487.7143	0.1016	1	R.VYIEQYEKDSSK.T
551 - 565	1554.9380	1553.9307	1553.8300	0.1007	0	R.DSQDALAPLVDVALK.L
569 - 575	884.4803	883.4731	883.3858	0.0873	0	K.MQEYTGR.S
569 - 575	900.4612	899.4539	899.3807	0.0732	0	K.MQEYTGR.S Oxidation (M)

Spot 1405

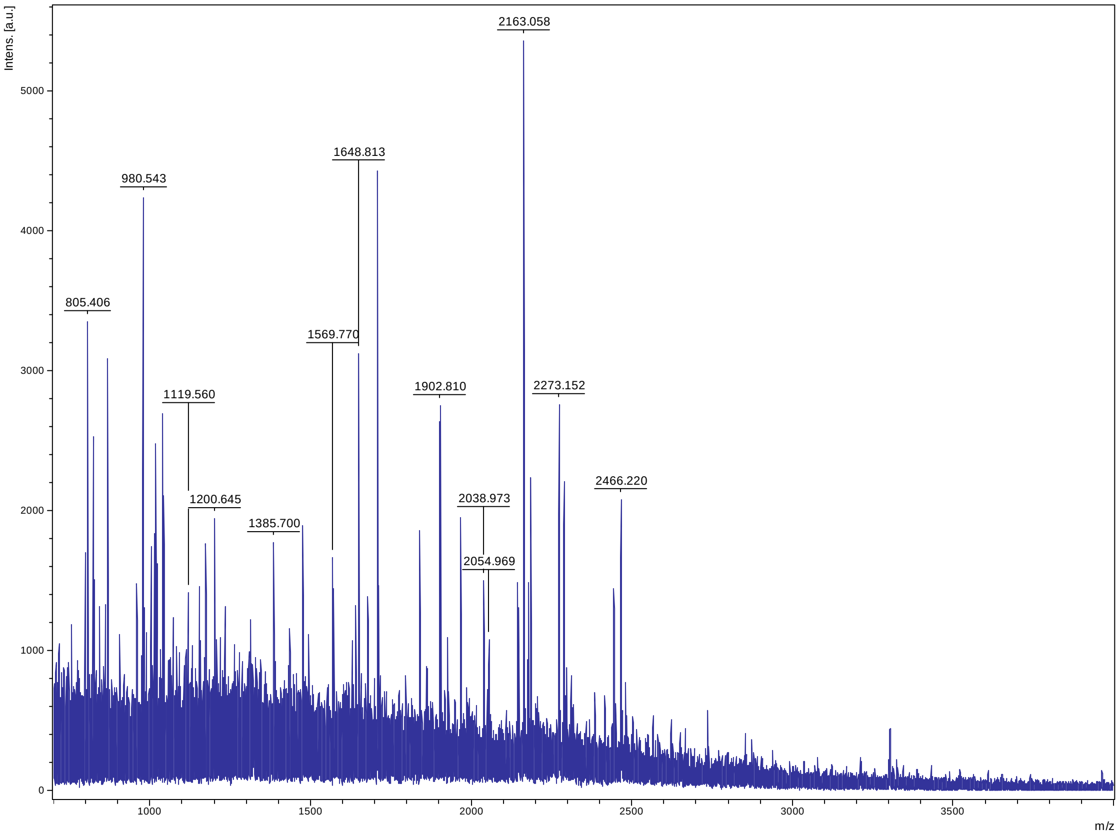


Match to: gi|2267006 Score: 67 Expect: 0.012

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
32 - 51	2101.1355	2100.1282	2100.0812	0.0470	0	K.LGTVIGIDLGTTYSCVGVYK.N	Acetyl (N-term)
52 - 65	1536.7662	1535.7589	1535.7440	0.0149	0	K.NGHVEIIANDQGNR.I	
66 - 78	1508.7673	1507.7600	1507.7307	0.0293	0	R.ITPSWVAFTDSER.L	
86 - 94	998.4262	997.4189	997.4941	-0.0751	0	K.NQAAVNPER.T	
168 - 185	2021.0755	2020.0682	2020.0377	0.0305	1	K.KINDAVVTVPAYFNDAQR.Q	
169 - 185	1892.9882	1891.9809	1891.9428	0.0382	0	K.INDAVVTVPAYFNDAQR.Q	
190 - 201	1197.5958	1196.5885	1196.6513	-0.0627	0	K.DAGVIAGLNVAR.I	Acetyl (N-term)
302 - 310	1052.5195	1051.5122	1051.5523	-0.0400	0	R.ALSNQHQVR.V	
302 - 310	1094.4888	1093.4815	1093.5628	-0.0813	0	R.ALSNQHQVR.V	Acetyl (N-term)
311 - 328	2055.0237	2054.0164	2053.9844	0.0321	0	R.VEIESLFDGTDFSEPLTR.A	
331 - 340	1296.6384	1295.6311	1295.6146	0.0166	0	R.FEELNNDLFR.K	
331 - 341	1466.7819	1465.7746	1465.7201	0.0545	1	R.FEELNNDLFRK.T	Acetyl (N-term)
349 - 357	949.4380	948.4307	948.4222	0.0085	0	K.AMDDAGLEK.S	
358 - 371	1495.8433	1494.8360	1494.8154	0.0206	0	K.SQIHEIVLVGGSTR.I	
381 - 390	1226.5498	1225.5425	1225.5615	-0.0189	1	R.DYFEGKEPNK.G	
391 - 418	2691.2558	2690.2485	2690.2670	-0.0185	0	K.GVNPDEAVAYGAAVQGSILSGEGGDETK.D	
488 - 498	1143.5880	1142.5807	1142.6084	-0.0276	0	K.FDLSGIPAAPR.G	
626 - 643	2089.1373	2088.1300	2088.1037	0.0263	1	K.LKEVEAVCNPIISAVYQR.T	Carbamidomethyl (C)
628 - 643	1847.9637	1846.9564	1846.9247	0.0318	0	K.EVEAVCNPIISAVYQR.T	Carbamidomethyl (C)
656 - 663	1027.5141	1026.5068	1026.4142	0.0927	0	R.LDDEHDEL.-	Acetyl (N-term)

Spot 1407



Match to: gi|38346454; Score: 122

Matched peptides:

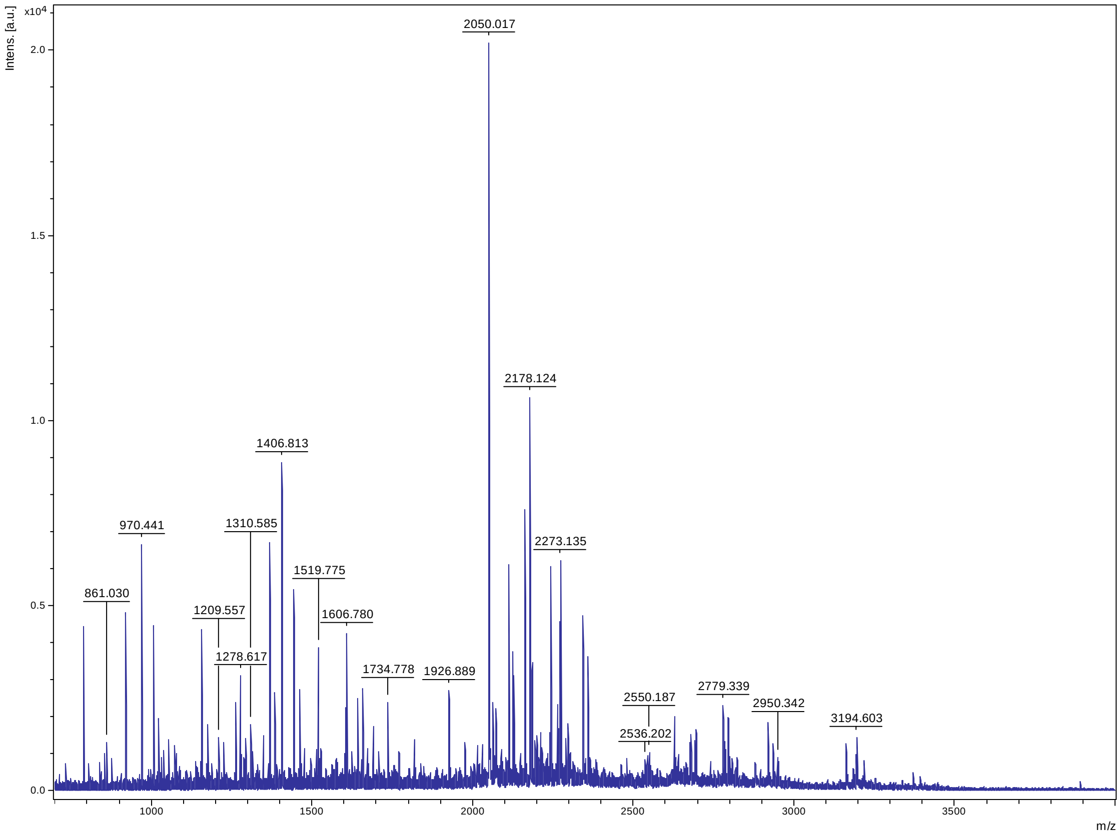
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 16	1648.81	1647.81	1647.77	0.04	0	MAVGEECAAAVASQVR
393 - 401	1020.49	1019.49	1019.53	-0.04	0	FVDEAQLAK
453 - 460	959.51	958.51	958.50	0.01	0	QMVQALNR
489 - 496	980.54	979.54	979.55	-0.01	0	IVPGYYLR
574 - 591	2145.04	2144.04	2144.03	0.01	1	IYLYGEGWDFGEVAQNKR
592 - 611	2038.97	2037.97	2037.95	0.02	0	GINASQINMSGTGIGSFNDR
592 - 611	2054.97	2053.97	2053.95	0.02	0	GINASQINMSGTGIGSFNDR Oxidation (M)
652 - 669	1927.02	1926.01	1926.02	-0.01	0	ELATYADHIQIGLAGNLK
723 - 732	1072.58	1071.57	1071.58	-0.01	0	TPIGLSIDEK
795 - 807	1678.87	1677.87	1677.86	0.01	1	DKNEENWHLIKPR
797 - 807	1435.74	1434.74	1434.74	0.01	0	NEENWHLIKPR
808 - 817	1200.65	1199.64	1199.67	-0.02	0	LENPSFRPLK
835 - 841	869.44	868.44	868.44	-0.00	0	YSSPLFR
842 - 851	1119.56	1118.56	1118.56	0.00	0	LSTASDIEQR
852 - 871	2185.04	2184.04	2184.15	-0.11	1	VRFHNTGPSMVPGVIVMSIK Oxidation (M)
944 - 953	1174.65	1173.65	1173.66	-0.01	1	RTTAVFVQPR
945 - 953	1018.54	1017.54	1017.56	-0.02	0	TTAVFVQPR

Match to: gi|37535166; Score: 78

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
43 - 49	843.50	842.50	842.52	-0.02	0	TILELVR
50 - 64	1902.81	1901.81	1901.78	0.03	0	SYDGDHICYDHFAFR
75 - 88	1648.81	1647.81	1647.79	0.02	0	SLAEFFTDFGYVPR
75 - 92	2176.10	2175.10	2175.06	0.03	1	SLAEFFTDFGYVPREELR
100 - 122	2466.22	2465.22	2465.20	0.02	0	ALWFSPPTNDGYTGTGVYGPLPR
265 - 272	1014.49	1013.49	1013.48	0.01	0	SYIEFAER
265 - 279	1839.93	1838.93	1838.99	-0.07	1	SYIEFAERLVLPQFK
293 - 314	2443.15	2442.15	2442.13	0.02	1	DGFEVGNADKIFESTSNDQLTR

Spot 1408



Match to: gi|50878307; Score: 205

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
156 - 168	1406.81	1405.81	1405.84	-0.03	0	LGDPARPLLLSVR
203 - 209	921.39	920.39	920.40	-0.02	0	FAYDSYR
203 - 210	1077.49	1076.49	1076.50	-0.01	1	FAYDSYRR
239 - 252	1513.70	1512.70	1512.74	-0.05	0	GLHNDTDLTATDLK
276 - 293	2072.03	2071.03	2071.12	-0.09	1	KQLQLAVLAVFNSWDSPR
277 - 293	1926.89	1925.89	1926.00	-0.11	0	QLQLAVLAVFNSWDSPR Pyro-glu (N-term Q)
308 - 333	2691.27	2690.26	2690.28	-0.02	0	GTAVNVQTMVFGNMGNTSGTGVLFTR 2 Oxidation (M)
341 - 360	2178.12	2177.12	2177.15	-0.03	1	KLYGEFLVNAQGEDVVAGIR
342 - 360	2050.02	2049.01	2049.05	-0.04	0	LYGEFLVNAQGEDVVAGIR
361 - 384	2918.25	2917.25	2917.26	-0.00	1	TPEDLDAMRDHMPEPYEELVENCK
361 - 384	2934.27	2933.26	2933.25	0.01	1	TPEDLDAMRDHMPEPYEELVENCK Oxidation (M)
361 - 384	2950.34	2949.34	2949.25	0.09	1	TPEDLDAMRDHMPEPYEELVENCK 2 Oxidation (M)
385 - 404	2544.14	2543.14	2543.17	-0.02	1	ILESHYKEMMDIEFTVQENR 2 Oxidation (M)
392 - 404	1641.70	1640.70	1640.72	-0.02	0	EMMDIEFTVQENR
392 - 404	1673.71	1672.71	1672.71	0.01	0	EMMDIEFTVQENR 2 Oxidation (M)
405 - 411	1006.48	1005.47	1005.49	-0.01	0	LWMLQCR
405 - 411	1022.47	1021.47	1021.48	-0.02	0	LWMLQCR Oxidation (M)
405 - 414	1292.64	1291.64	1291.65	-0.02	1	LWMLQCRTGK
423 - 435	1444.72	1443.72	1443.74	-0.02	0	IAVDMVNEGLVER
423 - 435	1460.71	1459.71	1459.73	-0.03	0	IAVDMVNEGLVER Oxidation (M)
441 - 462	2536.20	2535.20	2535.22	-0.02	0	MVEPGHLDQLLHPQFENPSGYK
441 - 464	2779.34	2778.34	2778.34	-0.01	1	MVEPGHLDQLLHPQFENPSGYKDK
441 - 464	2795.33	2794.33	2794.34	-0.01	1	MVEPGHLDQLLHPQFENPSGYKDK Oxidation (M)
465 - 496	3162.62	3161.61	3161.61	-0.00	0	VIATGLPASPGAAVGQIVFTAEDAEAWHAQGK
497 - 523	2823.31	2822.31	2822.46	-0.15	1	DVILVRTETSPEDVGGMHAAVGILTAR Oxidation (M)
503 - 523	2112.00	2111.00	2111.03	-0.03	0	TETSPEDVGGMHAAVGILTAR
503 - 523	2128.00	2127.00	2127.03	-0.02	0	TETSPEDVGGMHAAVGILTAR Oxidation (M)
625 - 635	1174.54	1173.54	1173.56	-0.02	0	QNGAEGIGLCR
636 - 646	1369.56	1368.55	1368.58	-0.02	0	TEHMFFASDER
636 - 646	1385.55	1384.55	1384.57	-0.02	0	TEHMFFASDER Oxidation (M)
652 - 662	1261.60	1260.59	1260.62	-0.03	0	QMIMASSLELR Pyro-glu (N-term Q)
652 - 662	1294.62	1293.62	1293.64	-0.02	0	QMIMASSLELR Oxidation (M)
652 - 662	1310.59	1309.58	1309.64	-0.05	0	QMIMASSLELR 2 Oxidation (M)
675 - 682	970.44	969.44	969.46	-0.02	0	SDFEGIFR
683 - 692	1072.56	1071.56	1071.57	-0.02	0	AMDGLPVTIR
693 - 712	2343.16	2342.16	2342.17	-0.02	0	LLDPPLHEFLPEGHVEDMVR
693 - 712	2359.17	2358.17	2358.17	-0.00	0	LLDPPLHEFLPEGHVEDMVR Oxidation (M)
713 - 728	1734.78	1733.78	1733.79	-0.01	0	ELCSETGAAQDDVLAR
732 - 742	1262.62	1261.62	1261.65	-0.03	0	LSEVNPMLGFR
732 - 742	1278.62	1277.61	1277.64	-0.03	0	LSEVNPMLGFR Oxidation (M)
746 - 759	1623.77	1622.77	1622.80	-0.03	0	LGISYPELTEMQAR Oxidation (M)
861 - 882	2628.35	2627.34	2627.37	-0.03	0	FLPIYLSQGILQHDPFEVLDQR

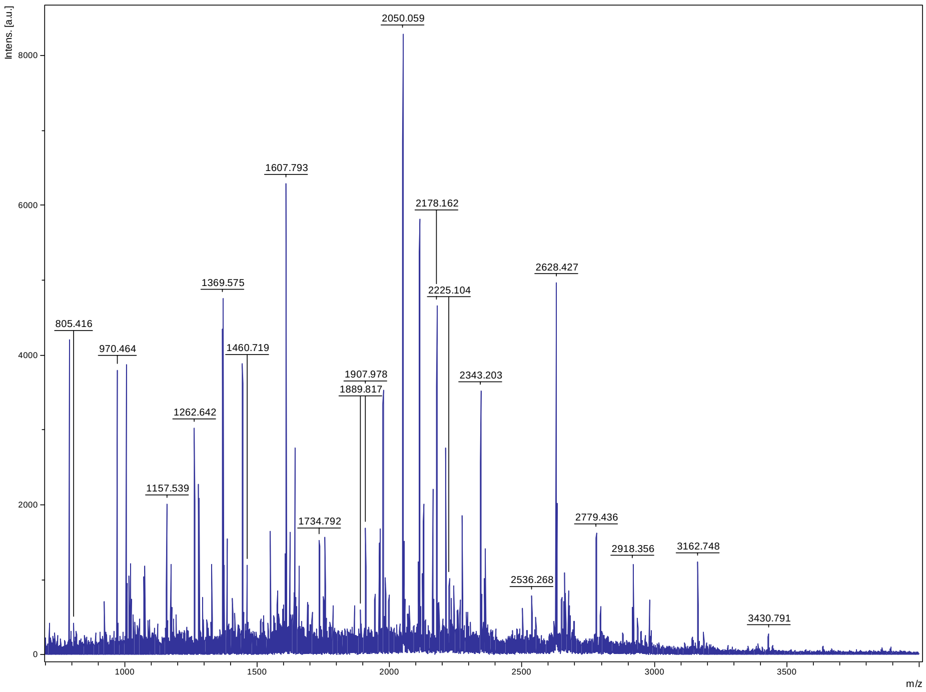
Match to: gi|51964146; Score: 119

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
15 - 24	1077.49	1076.49	1076.57	-0.08	1	VRDGGIGFTR
76 - 86	1476.66	1475.66	1475.67	-0.01	1	QKYCESIYETR
92 - 107	1691.84	1690.84	1690.88	-0.05	0	TVMVGNVPLGSDHPIR
118 - 128	1292.64	1291.64	1291.64	-0.01	1	DVAKTVEEVMR Oxidation (M)
161 - 179	2124.12	2123.11	2123.15	-0.04	0	NYNIPLVADIHFAPTVALR
180 - 188	1137.54	1136.54	1136.56	-0.03	1	VAECFDKIR
199 - 220	2785.25	2784.25	2784.28	-0.02	1	AQFEQLEYTEDDYQKELEHIEK
259 - 269	1209.56	1208.55	1208.59	-0.03	0	GMVESALEFAR

273 - 284	1528.69	1527.69	1527.75	-0.06	1	KLDFHNFVFSMK Oxidation (M)
285 - 296	1348.67	1347.67	1347.70	-0.03	0	ASNPVIMVQAYR
328 - 345	1818.92	1817.92	1817.96	-0.03	0	SAIGIGTLLMDGLGDTIR Oxidation (M)
346 - 360	1770.79	1769.78	1769.81	-0.03	0	VSLTEPPEEEIDPCR
346 - 361	1926.89	1925.89	1925.92	-0.03	1	VSLTEPPEEEIDPCRR
386 - 391	875.39	874.39	874.40	-0.01	0	YFDFQR
428 - 434	861.47	860.47	860.48	-0.00	0	APELLYR
459 - 469	1224.57	1223.57	1223.61	-0.05	0	ELPPVEDAQAR
520 - 537	2063.06	2062.05	2062.09	-0.04	1	LAVTLRGDESYEQLDLLK
627 - 637	1310.59	1309.58	1309.61	-0.03	0	DTSFNLLQGCR
643 - 653	1315.54	1314.54	1314.53	0.01	0	TEYVSCPSCGR
654 - 666	1519.78	1518.77	1518.80	-0.03	0	TLFDLQEVSAQIR
712 - 732	2243.10	2242.10	2242.24	-0.14	1	TVVQRGIAMEGATDALIQLIK Oxidation (M)
737 - 744	970.44	969.44	969.44	-0.01	0	WVDPPVEE

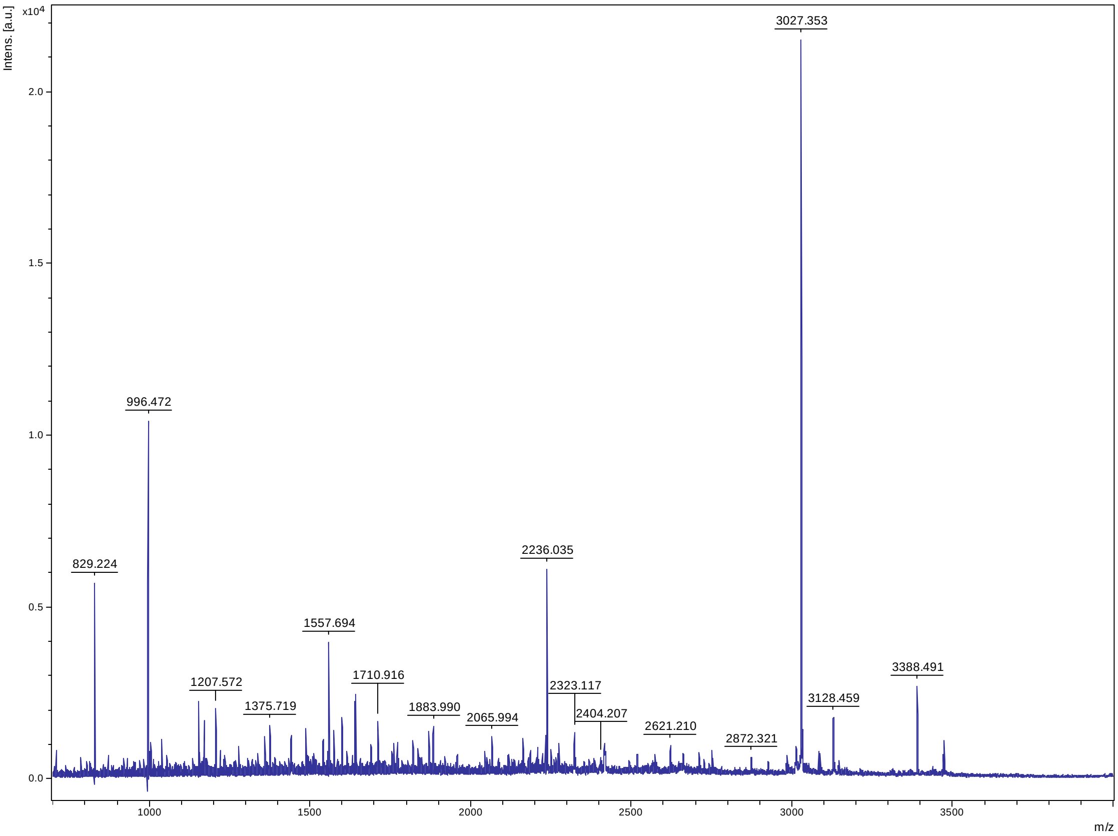
Spot 1411



Match to: gi|50878307 Score: 156

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
60 - 66	921.4184	920.4112	920.4028	9	0	R.FAYDSYR.R	
134 - 150	1944.0150	1943.0077	1943.0265	-10	0	K.QLQLAVLAVFNSWDSPR.A	
165 - 190	2659.3700	2658.3627	2658.2895	28	0	K.GTAVNVQTMVFGNMGNTSGTGVLFTR.N	
165 - 190	2675.3808	2674.3735	2674.2844	33	0	K.GTAVNVQTMVFGNMGNTSGTGVLFTR.N	Oxidation (M)
198 - 217	2178.1620	2177.1548	2177.1481	3	1	K.KLYGEFLVNAQGEDVVAGIR.T	
199 - 217	2050.0588	2049.0516	2049.0531	-1	0	K.LYGEFLVNAQGEDVVAGIR.T	
218 - 241	2918.3563	2917.3490	2917.2568	32	1	R.TPEDLDAMRDHMPEPYEELVENCK.I	
227 - 241	1889.8169	1888.8097	1888.7971	7	0	R.DHMPEPYEELVENCK.I	
249 - 261	1641.7202	1640.7130	1640.7174	-3	0	K.EMMDIEFTVQENR.L	
249 - 261	1657.7210	1656.7137	1656.7123	1	0	K.EMMDIEFTVQENR.L	Oxidation (M)
262 - 268	1006.5018	1005.4945	1005.4888	6	0	R.LWMLQCR.T	
262 - 268	1022.4906	1021.4833	1021.4837	-0	0	R.LWMLQCR.T	Oxidation (M)
280 - 292	1444.7326	1443.7253	1443.7392	-10	0	K.IAVDMVNEGLVER.R	
280 - 292	1460.7189	1459.7117	1459.7341	-15	0	K.IAVDMVNEGLVER.R	Oxidation (M)
298 - 319	2536.2682	2535.2609	2535.2216	16	0	K.MVEPGHLDQLLHPQFENPSGYK.D	
298 - 321	2779.4364	2778.4291	2778.3435	31	1	K.MVEPGHLDQLLHPQFENPSGYKDK.V	
298 - 321	2795.4087	2794.4014	2794.3385	23	1	K.MVEPGHLDQLLHPQFENPSGYKDK.V	Oxidation (M)
322 - 353	3162.7481	3161.7408	3161.6146	40	0	K.VIATGLPASPGAAVGQIVFTAEDAEAWHAQGK.D	
360 - 380	2112.0457	2111.0385	2111.0317	3	0	R.TETSPEDVGGMHAAVGILTAR.G	
360 - 380	2128.0307	2127.0235	2127.0266	-1	0	R.TETSPEDVGGMHAAVGILTAR.G	Oxidation (M)
381 - 392	1156.5847	1155.5774	1155.5819	-4	0	R.GGMTSHAAVVAR.G	
397 - 406	1171.4784	1170.4711	1170.4580	11	0	K.CCVSGCSSVR.V	
397 - 412	1785.9160	1784.9087	1784.7604	83	1	K.CCVSGCSSVRVNDASK.I	
441 - 463	2647.3006	2646.2934	2646.2458	18	0	K.QPLCPPALSGDLETFMSWVDEVR.K	
441 - 463	2663.3170	2662.3097	2662.2407	26	0	K.QPLCPPALSGDLETFMSWVDEVR.K	Oxidation (M)
482 - 492	1157.5395	1156.5322	1156.5295	2	0	R.QNGAEGIGLCR.T	Gln->pyro-Glu (N-term Q)
482 - 492	1174.5511	1173.5438	1173.5560	-10	0	R.QNGAEGIGLCR.T	
493 - 503	1369.5751	1368.5678	1368.5768	-7	0	R.TEHMFFASDER.I	
493 - 503	1385.5720	1384.5647	1384.5718	-5	0	R.TEHMFFASDER.I	Oxidation (M)
509 - 519	1294.6266	1293.6193	1293.6421	-18	0	R.QMIMASSLELR.Q	Oxidation (M)
532 - 539	970.4644	969.4571	969.4556	2	0	R.SDFEGIFR.A	
540 - 549	1072.5754	1071.5682	1071.5747	-6	0	R.AMDGLPVTIR.L	
550 - 569	2343.2028	2342.1955	2342.1729	10	0	R.LLDPPLHEFLPEGHVEDMVR.E	
550 - 569	2359.1996	2358.1924	2358.1678	10	0	R.LLDPPLHEFLPEGHVEDMVR.E	Oxidation (M)
570 - 585	1734.7920	1733.7848	1733.7890	-2	0	R.ELCSETGAAQDDVLAR.V	
589 - 599	1262.6421	1261.6349	1261.6489	-11	0	K.LSEVNPMLGFR.G	
589 - 599	1278.6358	1277.6286	1277.6438	-12	0	K.LSEVNPMLGFR.G	Oxidation (M)
600 - 616	1996.9729	1995.9657	1995.9506	8	1	R.GCRLGISYPELTEMQAR.A	Oxidation (M)
603 - 616	1607.7930	1606.7857	1606.8025	-10	0	R.LGISYPELTEMQAR.A	
603 - 616	1623.7810	1622.7737	1622.7974	-15	0	R.LGISYPELTEMQAR.A	Oxidation (M)
673 - 681	1015.5533	1014.5461	1014.5532	-7	0	K.VGTMIEIPR.A	
673 - 681	1031.5458	1030.5386	1030.5481	-9	0	K.VGTMIEIPR.A	Oxidation (M)
718 - 739	2628.4271	2627.4199	2627.3748	17	0	K.FLPIYLSQGILQHDPFEVLDQR.G	
761 - 779	1974.9678	1973.9605	1973.9669	-3	0	K.VGICGEHGGEPLSVAFFAK.A	
780 - 791	1371.6220	1370.6147	1370.6289	-10	0	K.AGLDYVSCSPFR.V	
780 - 796	1907.9782	1906.9710	1906.9724	-1	1	K.AGLDYVSCSPFRVPIAR.L	

Spot 1412

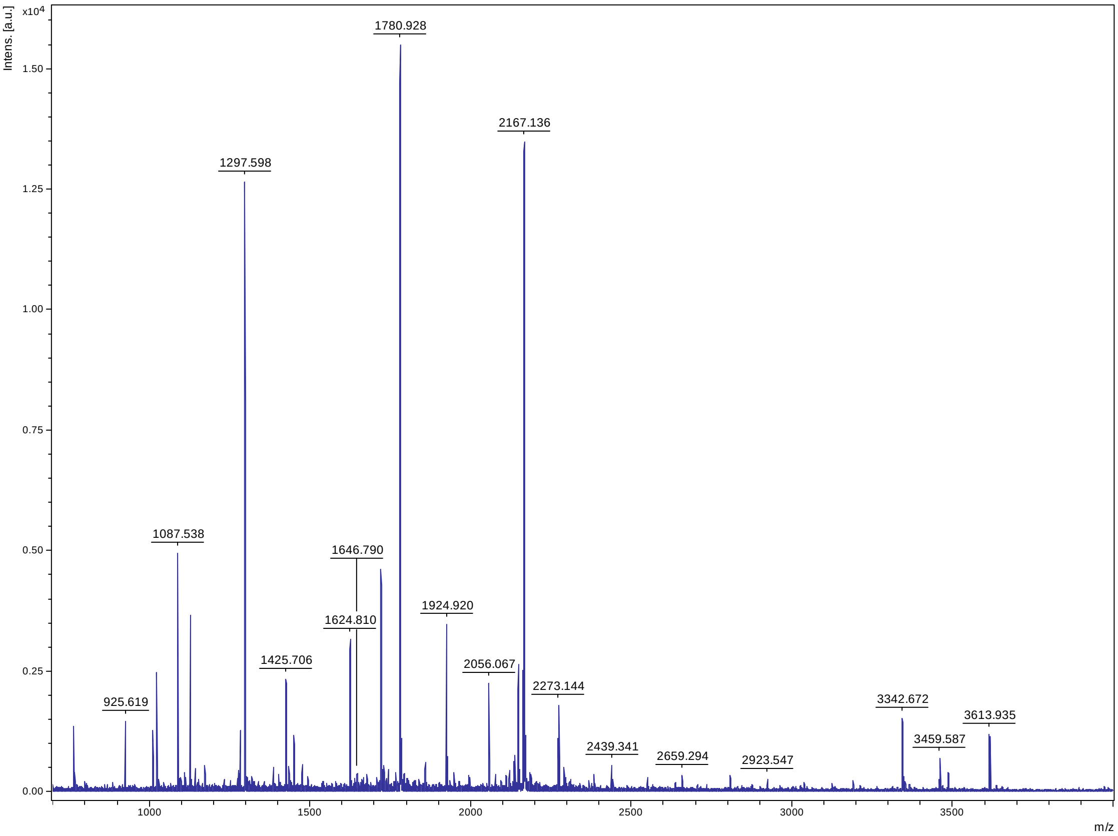


Match to: gi|55775372 Score: 75

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
21 - 27	996.4722	995.4649	995.4613	4	0	K.NPYWFNR.D	
21 - 29	1267.6637	1266.6564	1266.5894	53	1	K.NPYWFNRDR.F	
68 - 102	3471.6061	3470.5988	3470.7682	-49	0	K.TPGHPENFETPGVEVTTGPLGQGIANAVGLALAEK.H	
149 - 175	3027.3530	3026.3458	3026.4145	-23	0	K.LIAFYDDNHISIDGDTEIAFTEDVSAR.F	
188 - 197	1152.4897	1151.4824	1151.4843	-2	0	K.NGNDGYDEIR.A	
227 - 240	1391.6962	1390.6889	1390.6841	3	0	K.ANSYSVHGSALGTK.E	
241 - 263	2751.2862	2750.2790	2750.3228	-16	1	K.EVEATRENLGWPYEPFFVPEDVK.S	
247 - 263	2065.9941	2064.9868	2064.9833	2	0	R.ENLGWPYEPFFVPEDVK.S	
300 - 316	1710.9158	1709.9085	1709.8988	6	0	K.SIVSGELPAGWADALPK.Y	
317 - 327	1207.5722	1206.5649	1206.5517	11	0	K.YTPESPADATR.N	
328 - 339	1359.7033	1358.6960	1358.6976	-1	0	R.NLSQQCLNALAK.V	
340 - 360	2059.0861	2058.0789	2058.1031	-12	0	K.VVPGLLGGSADLASSNMTLLK.M	Oxidation (M)
455 - 475	2233.1045	2232.0972	2232.1031	-3	0	R.AMPNILMLRPADGNETAGAYK.I	
494 - 507	1441.7868	1440.7795	1440.7824	-2	0	K.LAQLPGTSIEGVEK.G	
508 - 537	3128.4588	3127.4515	3127.5383	-28	0	K.GGYIVSDNSTGNKPDFIVMSTGSELEIVAK.A	
551 - 568	2236.0352	2235.0279	2235.0194	4	0	R.VVSFVCWELFDEQSAEYK.E	
551 - 579	3388.4915	3387.4842	3387.6333	-44	1	R.VVSFVCWELFDEQSAEYKESVLPEAVTAR.V	
569 - 579	1171.6381	1170.6309	1170.6244	5	0	K.ESVLPEAVTAR.V	
615 - 631	1883.9905	1882.9832	1882.9676	8	0	K.IYQEYGITAENVIATAK.S	

Spot 1429

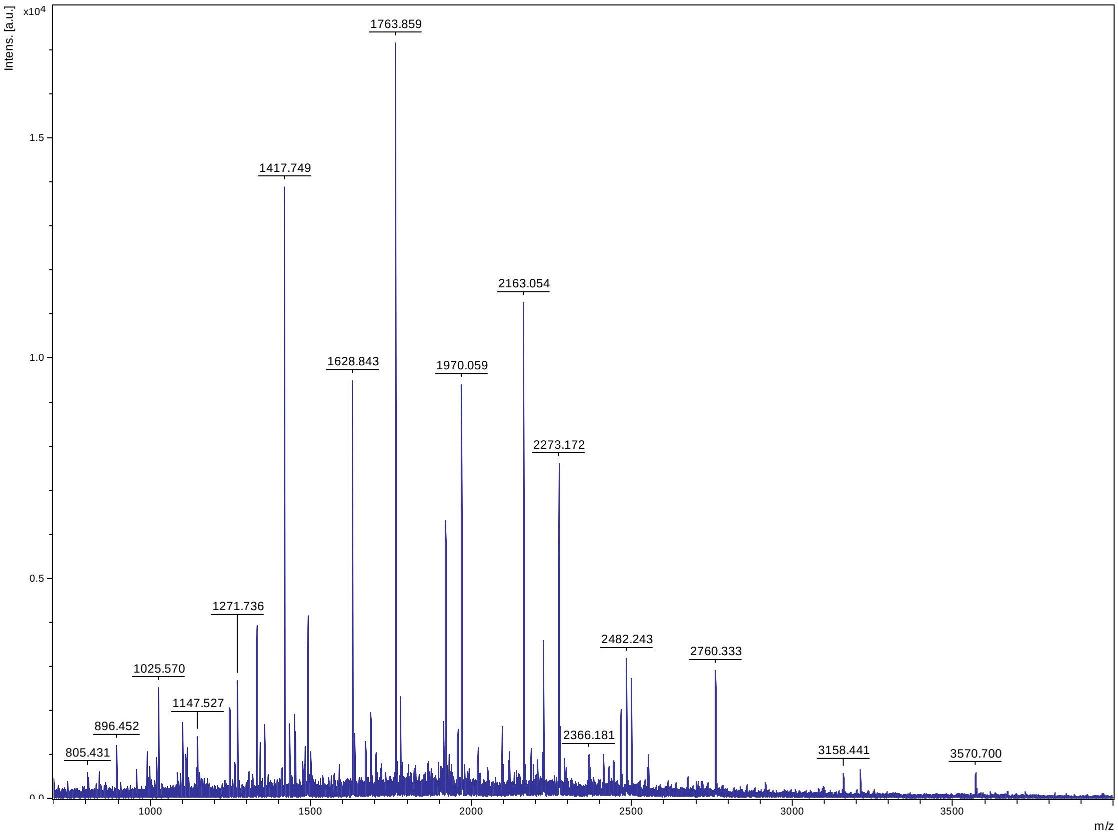


Match to: gi|51535304 Score: 348 Expect: 2.1e-29

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
131 - 160	3342.6716	3341.6644	3341.6707	-0.0063	1	K.VDATEDTDLAQKYDVQGFPTILFFIDGVPK.D
143 - 160	2056.0667	2055.0594	2055.0716	-0.0123	0	K.YDVQGFPTILFFIDGVPK.D
169 - 178	1173.6552	1172.6479	1172.6553	-0.0074	1	K.EAIVSWVNKK.L
195 - 223	2923.5474	2922.5401	2922.5297	0.0103	1	K.ILTGEDKAILAVLDSLSGAHSDEIAAASR.L
202 - 223	2167.1355	2166.1282	2166.1280	0.0002	0	K.AILAVLDSLSGAHSDEIAAASR.L
224 - 240	1924.9200	1923.9128	1923.9214	-0.0086	0	R.LEDAINFYQTSNPDVAK.L
241 - 249	1011.5546	1010.5473	1010.5549	-0.0076	0	K.LFHLDPAAK.R
250 - 257	925.6193	924.6120	924.6120	0.0000	0	K.RPSLVLLK.K
259 - 272	1730.8350	1729.8277	1729.8199	0.0078	1	K.QEEEKLTFYDGPFK.A
264 - 272	1087.5380	1086.5307	1086.5386	-0.0079	0	K.LTFYDGPFK.A
273 - 305	3485.8262	3484.8189	3484.8453	-0.0264	1	K.ASAIADFVSANKLPLVNTLTQETAPSIFDNPIK.K
285 - 306	2439.3406	2438.3333	2438.3420	-0.0087	1	K.LPLVNTLTQETAPSIFDNPIKK.Q
335 - 342	1022.6003	1021.5930	1021.5960	-0.0030	0	K.LLFVFVER.D
343 - 374	3459.5874	3458.5801	3458.5749	0.0053	0	R.DNEEVGEPVANYFGITGQETTVLAYTGNEDAR.N
375 - 388	1624.8099	1623.8027	1623.8144	-0.0117	0	R.NFFLDGEISVENIK.R
375 - 389	1780.9277	1779.9205	1779.9155	0.0050	1	R.NFFLDGEISVENIKR.F
389 - 398	1283.6082	1282.6009	1282.6193	-0.0184	1	K.RFAEDFLEEK.L
390 - 398	1127.5142	1126.5069	1126.5182	-0.0113	0	R.FAEDFLEEK.L
399 - 417	2136.0339	2135.0267	2135.0422	-0.0155	1	K.LTPFYKSEPVPESNEGDVK.I
405 - 417	1386.6282	1385.6209	1385.6310	-0.0101	0	K.SEPVPESNEGDVK.I
472 - 481	1143.4675	1142.4603	1142.4774	-0.0172	0	K.MDGTANEHPR.A Oxidation (M)
482 - 497	1721.9221	1720.9148	1720.9188	-0.0039	0	R.AKPDGFPTILFYPAGK.K
498 - 509	1425.7057	1424.6984	1424.6935	0.0049	1	K.KSFEPITFEGDR.T
499 - 509	1297.5979	1296.5906	1296.5986	-0.0080	0	K.SFEPITFEGDR.T
499 - 516	2148.0354	2147.0281	2147.0244	0.0037	1	K.SFEPITFEGDRTVVEMYK.F
538 - 550	1450.7084	1449.7011	1449.7059	-0.0048	1	K.TEKDQSTASTNLR.G
541 - 550	1092.5237	1091.5164	1091.5207	-0.0043	0	K.DQSTASTNLR.G

Spot 1439

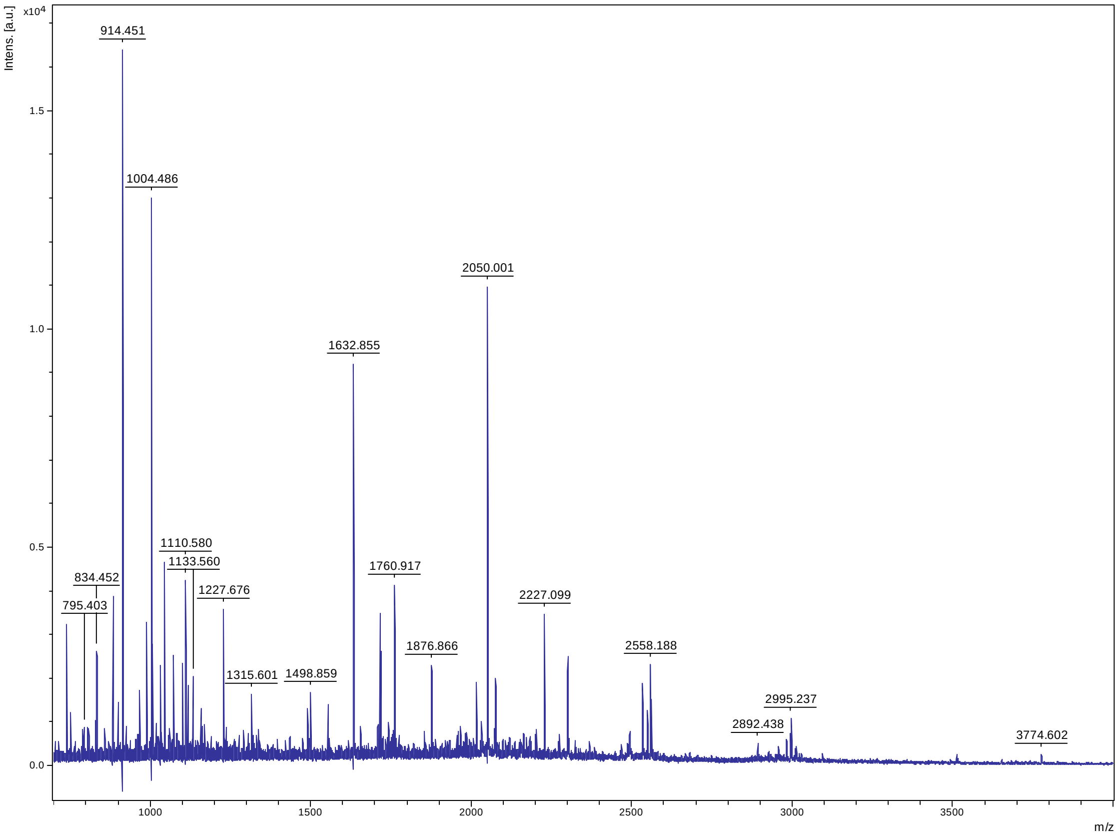


Match to: gi|50901676 Score: 116 Expect: 1.7e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
30 - 45	1670.8570	1669.8497	1669.8973	-0.0476	0	R.HMFGVVGIPVTSLASR.A	
30 - 45	1686.8691	1685.8618	1685.8922	-0.0304	0	R.HMFGVVGIPVTSLASR.A	Oxidation (M)
119 - 135	1920.9681	1919.9608	1919.9992	-0.0384	0	R.GDFQELDQIAATKPFIK.I	
220 - 230	1271.7514	1270.7441	1270.7509	-0.0068	1	R.RAERPLVVFGK.G	
221 - 230	1115.6499	1114.6426	1114.6498	-0.0072	0	R.AERPLVVFGK.G	
244 - 259	1702.8744	1701.8671	1701.9011	-0.0340	0	K.LVDTTGIPFLPTPMGK.G	Oxidation (M)
275 - 290	1571.7603	1570.7530	1570.8500	-0.0970	0	R.SLAIGQCDVALVVGAR.L	
275 - 290	1628.8433	1627.8360	1627.8715	-0.0355	0	R.SLAIGQCDVALVVGAR.L	Carbamidomethyl (C)
291 - 302	1450.7594	1449.7521	1449.7768	-0.0247	0	R.LNWLLHFGEPPK.W	
309 - 322	1763.8527	1762.8454	1762.8811	-0.0356	0	K.FILVDVCEEEIELR.K	Carbamidomethyl (C)
323 - 333	1120.6165	1119.6092	1119.6400	-0.0308	0	R.KPHVGIVGDAK.R	
342 - 362	2466.1556	2465.1483	2465.2413	-0.0929	1	R.EIKDQPFCLAPSHPWVEAITK.K	Carbamidomethyl (C)
345 - 362	2095.9737	2094.9664	2095.0197	-0.0532	0	K.DQPFCLAPSHPWVEAITK.K	Carbamidomethyl (C)
345 - 363	2224.0859	2223.0786	2223.1146	-0.0360	1	K.DQPFCLAPSHPWVEAITKK.A	Carbamidomethyl (C)
378 - 389	1417.7665	1416.7592	1416.7765	-0.0173	0	K.DVVPFNFLTPLR.I	
393 - 417	2482.1484	2481.1411	2481.2168	-0.0757	0	R.DAILAEGNPAPVVVSEGANTMDVGR.A	
393 - 417	2498.1323	2497.1250	2497.2118	-0.0867	0	R.DAILAEGNPAPVVVSEGANTMDVGR.A	Oxidation (M)
418 - 426	1025.5628	1024.5555	1024.5665	-0.0110	0	R.AVLVQNEPR.T	
455 - 477	2428.1252	2427.1179	2427.1991	-0.0811	0	R.LVVAVEGDSGFGFSAMEVETLVR.Y	Oxidation (M)
499 - 524	2760.2014	2759.1941	2759.3078	-0.1137	1	R.SPDEITGPYKDDPAPTSFVPAAGYHK.M	
533 - 543	1263.6411	1262.6338	1262.6394	-0.0056	0	K.GYLVETPDELK.S	
544 - 551	896.4262	895.4189	895.4399	-0.0210	0	K.SALSESFR.A	
554 - 572	1970.0345	1969.0272	1969.0632	-0.0360	0	R.KPAVINVIIDPYAGAESGR.M	

Spot 1446

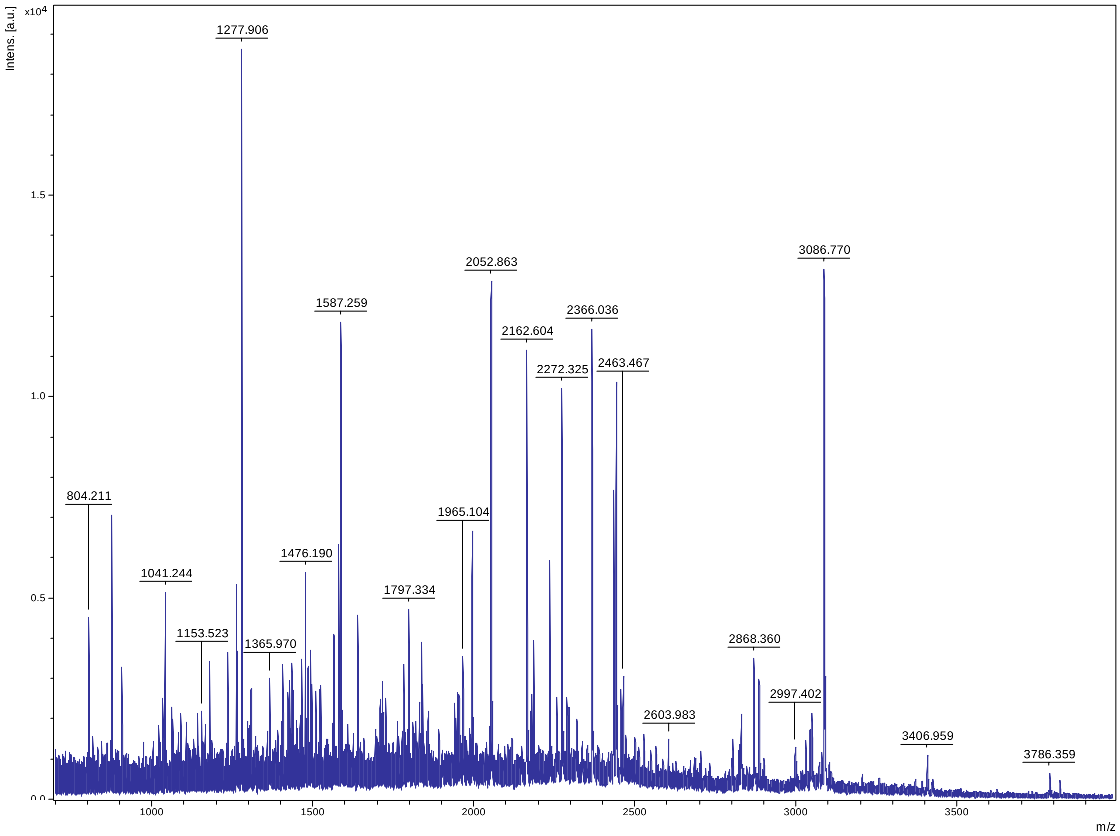


Match to: gi|50918261 Score: 207 Expect: 1.3e-16

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 9	1110.6317	1109.6244	1109.6154	0.0090	1	-.MVLFSVTKK.A	Acetyl (N-term); Oxidation (M)
10 - 25	1632.9206	1631.9133	1631.8267	0.0866	0	K.ATTPFDGQKPGTSGLR.K	
10 - 26	1761.0033	1759.9960	1759.9216	0.0744	1	K.ATTPFDGQKPGTSGLRK.K	
78 - 86	987.5061	986.4988	986.5079	-0.0091	1	K.MAAANGVRR.V	Acetyl (N-term)
87 - 105	2015.1309	2014.1236	2014.0669	0.0567	0	R.VWVGQNSLMSTPAVSAVIR.E	
87 - 105	2031.1096	2030.1023	2030.0618	0.0405	0	R.VWVGQNSLMSTPAVSAVIR.E	Oxidation (M)
115 - 137	2301.1919	2300.1846	2300.1436	0.0410	0	K.ATGAFILTASHNPGGPTEDFGIK.Y	
207 - 215	1099.6401	1098.6328	1098.5597	0.0731	0	K.TIFDFESIK.K	
207 - 216	1227.7425	1226.7352	1226.6546	0.0806	1	K.TIFDFESIKK.L	
223 - 240	1993.0266	1992.0193	1991.9199	0.0994	0	K.FTFCYDALHGVAGTYATR.I	
223 - 240	2050.0160	2049.0087	2048.9414	0.0673	0	K.FTFCYDALHGVAGTYATR.I	Carbamidomethyl (C)
241 - 259	2076.1102	2075.1029	2075.0608	0.0421	0	R.IFVEELGAAESSLLNCVPK.E	Carbamidomethyl (C)
260 - 275	1717.8656	1716.8583	1716.7743	0.0840	0	K.EDFGGGHPDPNLTYAK.E	
276 - 285	1133.6190	1132.6117	1132.5910	0.0207	1	K.ELVDRMGLGK.S	Oxidation (M)
286 - 304	1876.8729	1875.8656	1875.7870	0.0786	0	K.SSNAEPPEFGAAADGDADR.N	
286 - 310	2533.1636	2532.1563	2532.1550	0.0013	1	K.SSNAEPPEFGAAADGDADRNMILGK.R	
286 - 310	2549.1478	2548.1405	2548.1499	-0.0094	1	K.SSNAEPPEFGAAADGDADRNMILGK.R	Oxidation (M)
371 - 397	2995.1588	2994.1515	2994.2404	-0.0889	0	K.FFGNLMDAGMCSICGEESFGTGSDHIR.E	2 Carbamidomethyl (C)
371 - 397	3012.2595	3011.2522	3011.2193	0.0329	0	K.FFGNLMDAGMCSICGEESFGTGSDHIR.E	Acetyl (N-term); Carbamidomethyl (C); 2 Oxidation (M)
418 - 433	1743.0126	1742.0053	1741.9210	0.0844	1	K.DNLGGDKLVTVEDIVR.Q	
425 - 433	1043.6797	1042.6724	1042.6022	0.0702	0	K.LVTVEDIVR.Q	
434 - 441	1004.5355	1003.5282	1003.4624	0.0658	0	R.QHWGTYGR.H	
442 - 446	739.3509	738.3436	738.3449	-0.0013	0	R.HYYTR.Y	
447 - 458	1315.6704	1314.6631	1314.5728	0.0904	0	R.YDYENVDAGAAK.E	
483 - 506	2558.1609	2557.1536	2557.1707	-0.0171	1	R.SDVSDVVAADEFEYKDPVDGSVSK.H	
512 - 519	914.4780	913.4707	913.4293	0.0414	0	R.YLFGDGSR.L	
524 - 535	1118.6745	1117.6672	1117.6091	0.0581	0	R.LSGTGSVGATIR.V	
536 - 547	1488.8062	1487.7989	1487.7143	0.0846	1	R.VYIEQYEKDSSK.T	
551 - 565	1554.9032	1553.8959	1553.8300	0.0659	0	R.DSQDALAPLVDVALK.L	
569 - 575	884.4081	883.4008	883.3858	0.0151	0	K.MQEYTGR.S	

Spot 1449

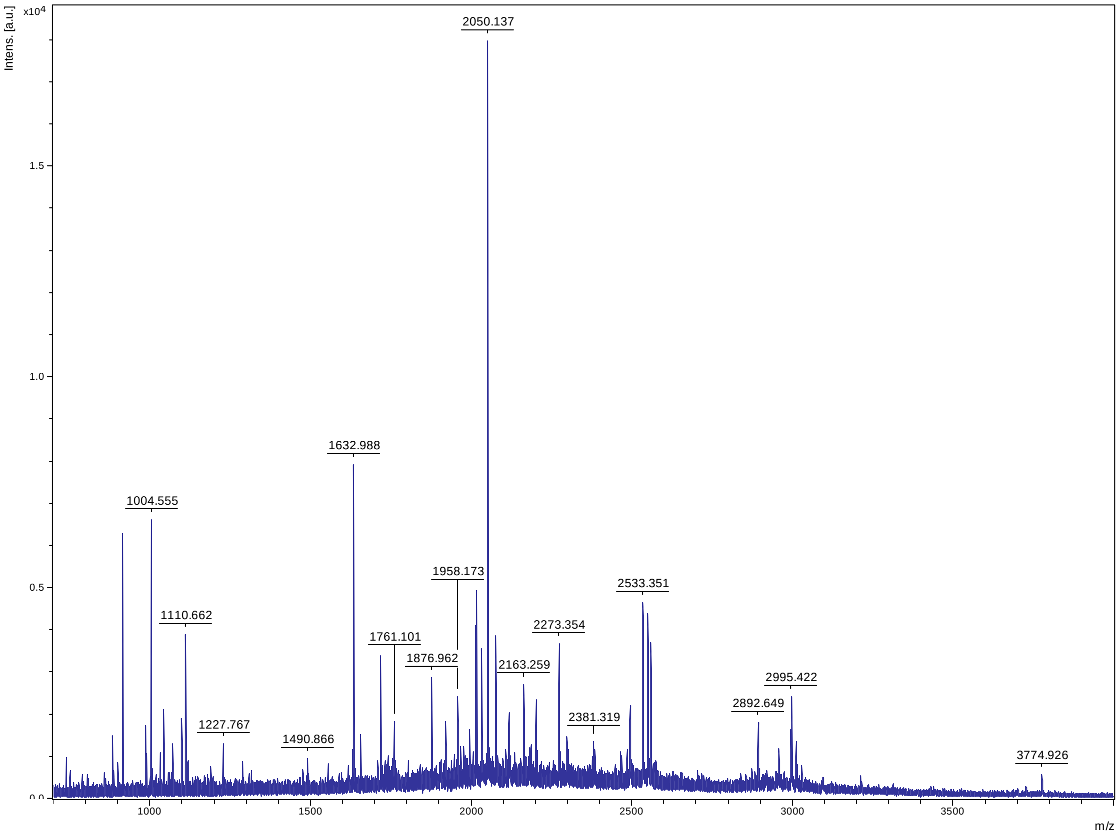


Match to: gi|50921137 Score: 69 Expect: 0.0096

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 23	2184.1452	2183.1379	2183.0276	0.1103	0	-.MADATHAAADGGVATILASADGR.D	Acetyl (N-term)
2 - 23	2053.0627	2052.0554	2051.9871	0.0683	0	M.ADATHAAADGGVATILASADGR.D	Acetyl (N-term)
36 - 57	2501.2514	2500.2441	2500.2242	0.0199	1	K.ISSIKASTVALYFSASWCPPCR.R	2 Carbamidomethyl (C)
36 - 57	2543.0984	2542.0911	2542.2348	-0.1437	1	K.ISSIKASTVALYFSASWCPPCR.R	Acetyl (N-term); 2 Carbamidomethyl (C)
41 - 57	1901.0267	1900.0194	1899.8647	0.1547	0	K.ASTVALYFSASWCPPCR.R	Acetyl (N-term)
41 - 58	2015.1568	2014.1495	2013.9553	0.1942	1	K.ASTVALYFSASWCPPCRR.F	
63 - 75	1463.7515	1462.7442	1462.7667	-0.0225	0	K.LIEAYNELVSQGK.S	
76 - 97	2443.1480	2442.1407	2442.1015	0.0393	0	K.SFEVVFVSGDSDQDAFNAYFAK.M	
120 - 132	1405.7372	1404.7299	1404.8162	-0.0863	0	K.VMGIPHLVILDAK.S	
133 - 159	3092.2011	3091.1938	3091.3934	-0.1995	0	K.SGEIYTEDGVELVHEYGTEAYPFTTER.I	
169 - 185	1856.9855	1855.9782	1855.9540	0.0242	1	K.AAKDNQTIHSLFGTPTR.D	
172 - 185	1586.7955	1585.7882	1585.7849	0.0034	0	K.DNQTIHSLFGTPTR.D	
193 - 204	1299.5958	1298.5885	1298.6717	-0.0832	1	K.GDKVPISDLEGK.Y	Acetyl (N-term)
278 - 295	1949.1108	1948.1035	1948.0379	0.0656	0	R.YFELSGLPMLVLIGPDGK.T	
296 - 322	3002.2128	3001.2055	3001.3617	-0.1562	0	K.TLNDDIADIIDEHGPDAWEGFPFSAEK.L	
332 - 354	2434.3450	2433.3377	2433.3002	0.0375	1	K.AKAESQTLESLLVTGDLDFVLGK.D	
334 - 354	2235.2244	2234.2171	2234.1681	0.0490	0	K.AESQTLESLLVTGDLDFVLGK.D	
334 - 358	2606.3468	2605.3395	2605.3486	-0.0091	1	K.AESQTLESLLVTGDLDFVLGKDGAK.V	
397 - 411	1835.9638	1834.9565	1834.8849	0.0716	1	K.EKHNDFEIVFISSDR.E	
399 - 411	1578.7577	1577.7504	1577.7474	0.0030	0	K.HNDFEIVFISSDR.E	
444 - 458	1437.7750	1436.7677	1436.8238	-0.0561	0	K.ITGIPSLVAIGPDGK.T	
507 - 518	1484.7410	1483.7337	1483.7532	-0.0194	0	K.HDLHDHELVLTR.C	
538 - 548	1448.6589	1447.6516	1447.6224	0.0292	1	R.CKECDFDLHPK.C	2 Carbamidomethyl (C)
540 - 548	1160.4150	1159.4077	1159.4968	-0.0891	0	K.ECDFDLHPK.C	Carbamidomethyl (C)
540 - 554	1890.9945	1889.9872	1889.8288	0.1585	1	K.ECDFDLHPKCALEEK.G	2 Carbamidomethyl (C)
555 - 579	2628.2328	2627.2255	2627.0573	0.1682	0	K.GDVEMGEENAEAAPAGYVCEGDVCR.K	Carbamidomethyl (C)

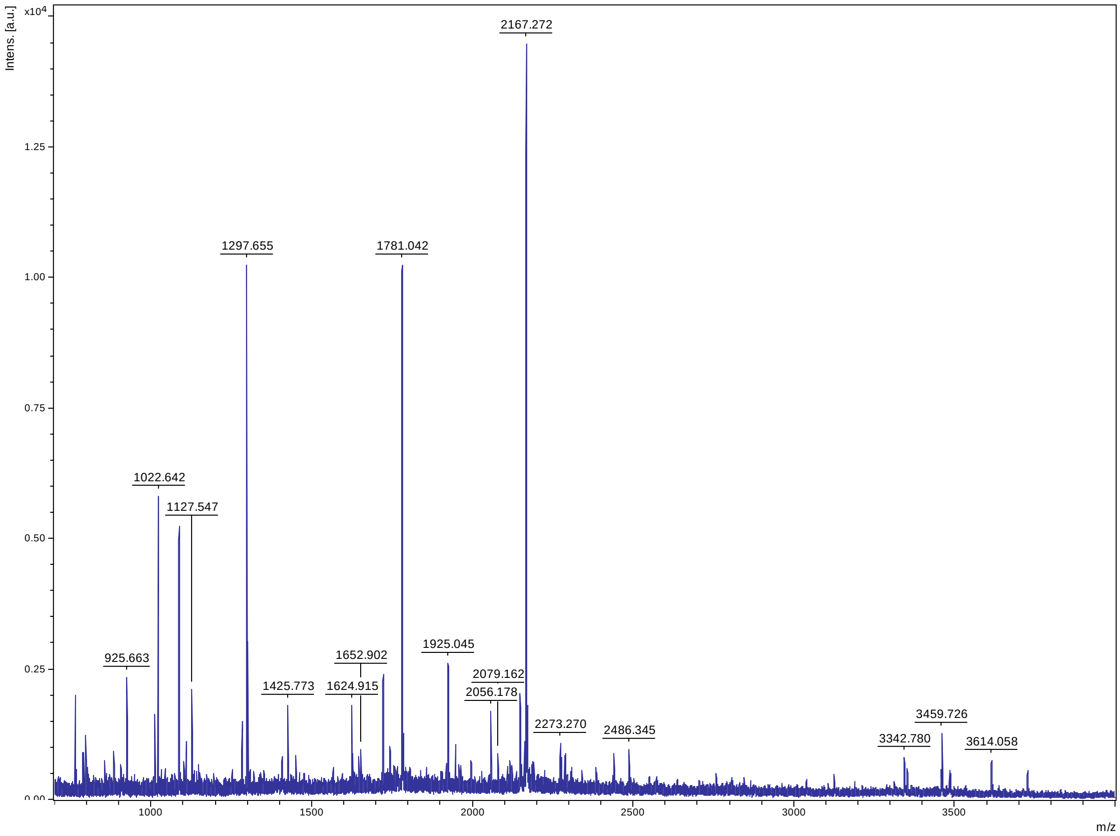
Spot 1450



Match to: gi|50918261 Score: 120 Expect: 6.7e-08

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
10 - 25	1632.8721	1631.8648	1631.8267	0.0381	0	K.ATTPFDGQKPGTSGLR.K	
10 - 26	1760.9784	1759.9711	1759.9216	0.0495	1	K.ATTPFDGQKPGTSGLRK.K	
87 - 105	2015.0790	2014.0717	2014.0669	0.0048	0	R.VWVGQNSLMSTPAVSAVIR.E	
87 - 105	2031.0833	2030.0760	2030.0618	0.0142	0	R.VWVGQNSLMSTPAVSAVIR.E	Oxidation (M)
207 - 215	1099.5678	1098.5605	1098.5597	0.0008	0	K.TIFDFESIK.K	
207 - 216	1227.6689	1226.6616	1226.6546	0.0070	1	K.TIFDFESIKK.L	
223 - 240	2049.9648	2048.9575	2048.9414	0.0161	0	K.FTFCYDALHGVAGTYATR.I	Carbamidomethyl (C)
241 - 259	2076.1122	2075.1049	2075.0608	0.0441	0	R.IFVEELGAAESSLLNCVPK.E	Carbamidomethyl (C)
260 - 275	1717.8378	1716.8305	1716.7743	0.0562	0	K.EDFGGGHPDPNLTYAK.E	
286 - 304	1876.8227	1875.8154	1875.7870	0.0284	0	K.SSNAEPPEFGAAADGDADR.N	
286 - 310	2533.1391	2532.1318	2532.1550	-0.0232	1	K.SSNAEPPEFGAAADGDADRNMILGK.R	
286 - 310	2549.1526	2548.1453	2548.1499	-0.0046	1	K.SSNAEPPEFGAAADGDADRNMILGK.R	Oxidation (M)
362 - 370	1110.5606	1109.5533	1109.5545	-0.0012	0	K.FFEVPTGWK.F	
425 - 433	1043.5910	1042.5837	1042.6022	-0.0185	0	K.LVTVEDIVR.Q	
434 - 441	1004.4467	1003.4394	1003.4624	-0.0230	0	R.QHWGTYGR.H	
483 - 506	2558.1622	2557.1549	2557.1707	-0.0158	1	R.SDVSDVVAADEFEYKDPVDGSVSK.H	
512 - 519	914.3887	913.3814	913.4293	-0.0479	0	R.YLFGDGSR.L	
536 - 543	1071.5473	1070.5400	1070.5284	0.0116	0	R.VYIEQYEK.D	

Spot 1453

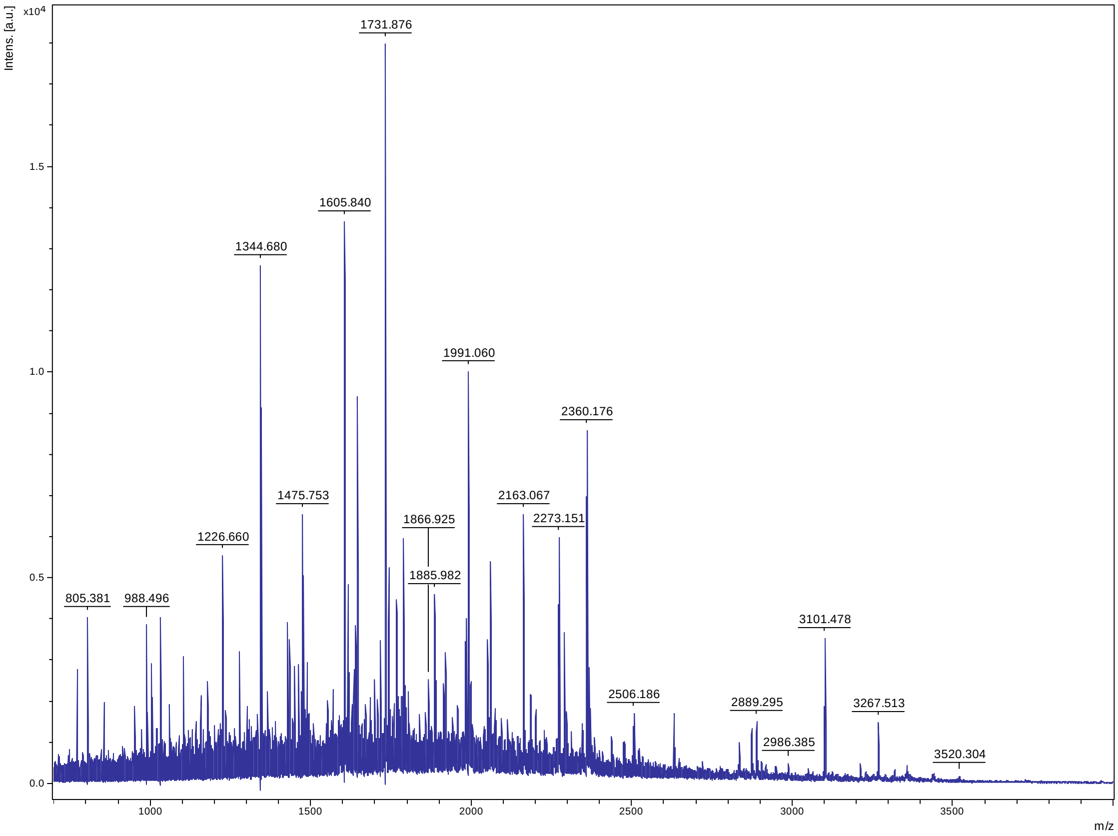


Match to: gi|51535304 Score: 130 Expect: 6.7e-09

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
131 - 160	3342.6192	3341.6119	3341.6707	-0.0587	1	K.VDATEDTDLAQKYDVQGFPTILFFIDGVPK.D	
143 - 160	2056.0903	2055.0830	2055.0716	0.0114	0	K.YDVQGFPTILFFIDGVPK.D	
202 - 223	2167.1699	2166.1626	2166.1280	0.0346	0	K.AILAVLDSLSGAHSDEIAAASR.L	
241 - 249	1011.5063	1010.4990	1010.5549	-0.0559	0	K.LFHLDPAAK.R	
250 - 257	925.5345	924.5272	924.6120	-0.0848	0	K.RPSLVLLK.K	
264 - 272	1087.5092	1086.5019	1086.5386	-0.0366	0	K.LTFYDGPFK.A	
285 - 306	2439.2982	2438.2909	2438.3420	-0.0511	1	K.LPLVNTLTQETAPSIFDNPIKK.Q	
335 - 342	1022.5358	1021.5285	1021.5960	-0.0675	0	K.LLFVFVER.D	
343 - 374	3459.5244	3458.5171	3458.5749	-0.0578	0	R.DNEEVGEPVANYFGITGQETTVLAYTGNEDAR.N	
375 - 388	1624.8445	1623.8372	1623.8144	0.0229	0	R.NFFLDGEISVENIK.R	
375 - 389	1780.9581	1779.9508	1779.9155	0.0354	1	R.NFFLDGEISVENIKR.F	
405 - 422	1924.9595	1923.9522	1923.9788	-0.0266	1	K.SEPVPESNEGDVKIVVGK.N	Acetyl (N-term)
472 - 481	1127.4747	1126.4674	1126.4825	-0.0151	0	K.MDGTANEHPR.A	
482 - 497	1721.9439	1720.9366	1720.9188	0.0178	0	R.AKPDGFPTILFYPAGK.K	
498 - 509	1425.7029	1424.6956	1424.6935	0.0021	1	K.KSFEPITFEGDR.T	
499 - 509	1297.6044	1296.5971	1296.5986	-0.0015	0	K.SFEPITFEGDR.T	
499 - 516	2148.0603	2147.0530	2147.0244	0.0286	1	K.SFEPITFEGDRTVVEMYK.F	
538 - 550	1450.7600	1449.7527	1449.7059	0.0468	1	K.TEKDQSTASTNLR.G	

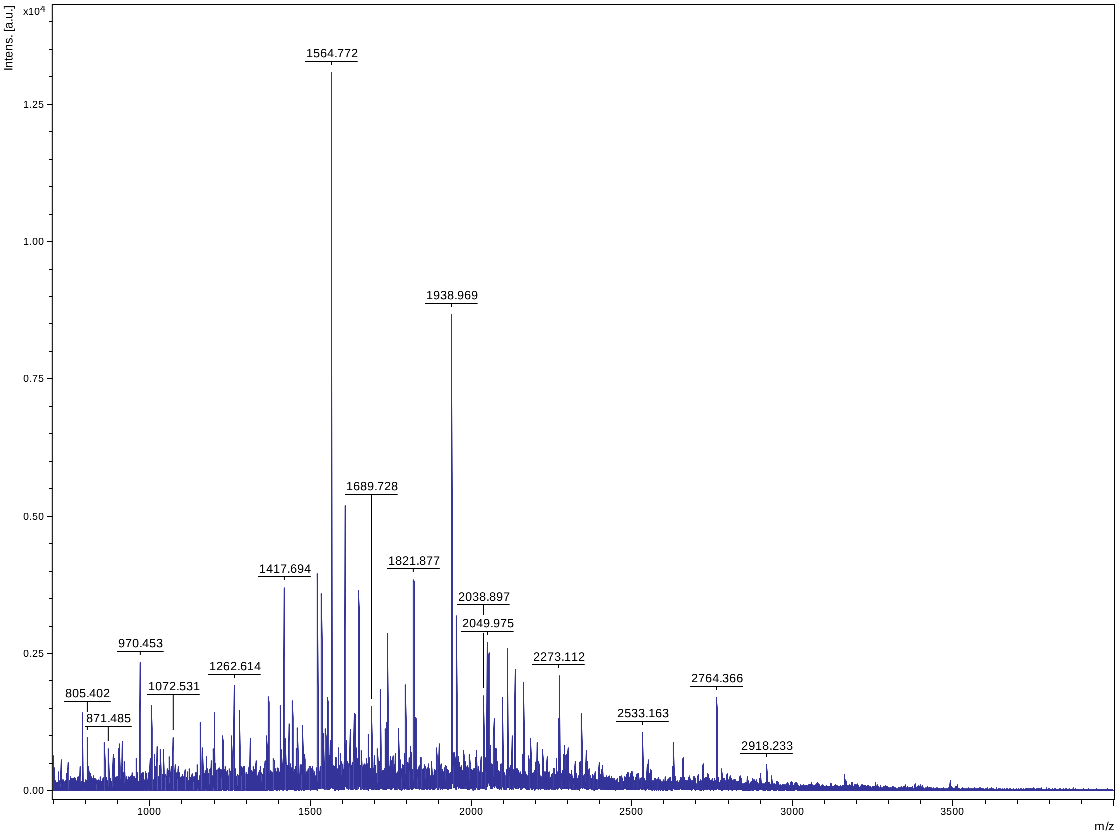
Spot 1459



Match to: gi|75142638 Score: 75 Expect: 1.7e-12

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
1 - 15	1553.7805	1552.7732	1552.7589	9	0	-.MAVMTDVSTTGTALR.T
32 - 46	1767.8420	1766.8347	1766.8145	11	0	R.FIDEMTTNVDAVQER.V
77 - 93	1991.0600	1990.0527	1990.0524	0	1	R.AKVPVVSYDDLQPYIQR.I
79 - 93	1791.9068	1790.8995	1790.9203	-12	0	K.VPVVSYDDLQPYIQR.I
94 - 122	2986.3846	2985.3774	2985.4792	-34	1	R.IANGDRSPILSTHPVSEFLTSSGTSAGER.K
123 - 134	1461.7454	1460.7382	1460.7367	1	1	R.KLMPTIMDELDR.R
233 - 243	1103.6308	1102.6235	1102.6499	-24	0	R.LGAVFASGLLR.A
298 - 306	988.4964	987.4892	987.5138	-25	0	K.GDWAGIITR.V
403 - 416	1641.8277	1640.8204	1640.8410	-13	0	R.EYELVITTYAGLNR.Y
425 - 436	1344.6795	1343.6723	1343.6735	-1	0	R.VTGFHNAAPQFR.F
487 - 500	1731.8763	1730.8690	1730.9396	-41	0	R.IPGHYVIYWELLTK.G
501 - 514	1302.6745	1301.6672	1301.6576	7	0	K.GAGATVVDADTLGR.C
532 - 543	1226.6604	1225.6532	1225.6666	-11	0	R.VADGSIGPLEIR.V
544 - 560	1982.9958	1981.9886	1981.9931	-2	0	R.VVRPGTFEELMDYAISR.G

Spot 1461



Match to: gi|52075907; Score: 125

Matched peptides:

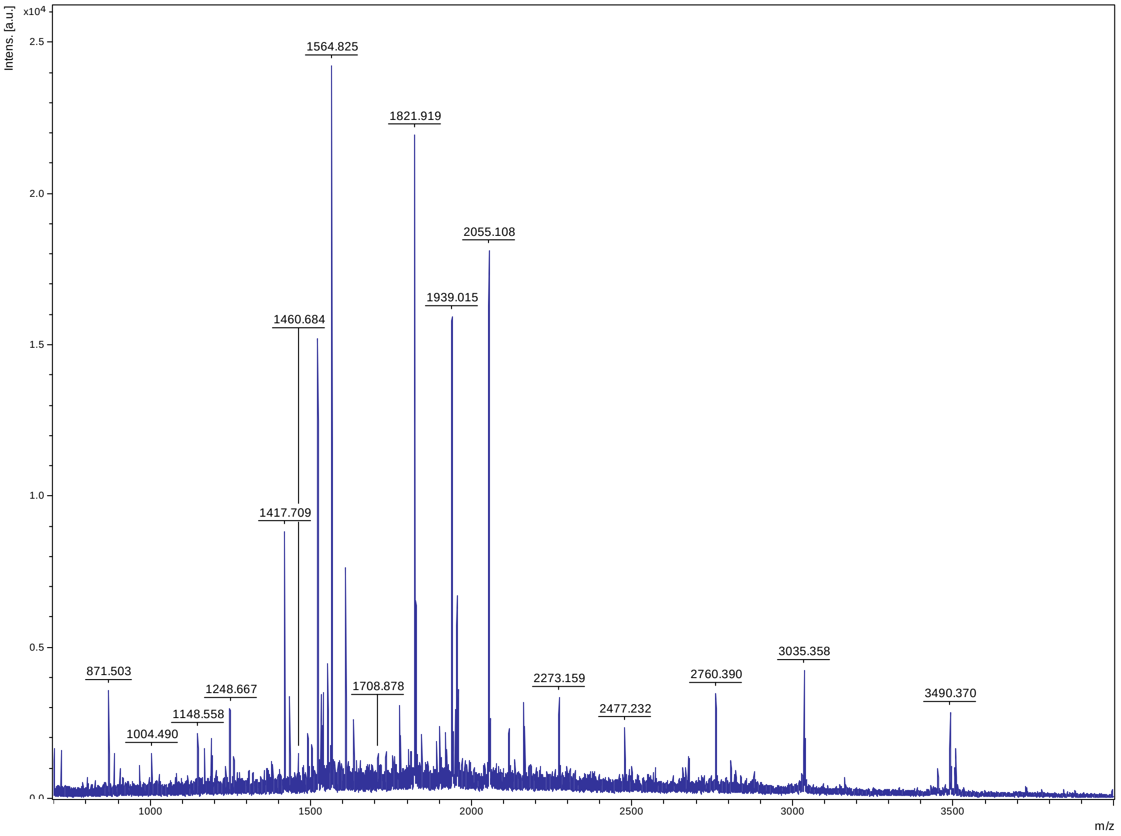
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
6 - 22	2038.90	2037.89	2037.92	-0.02	1	VTTFEDSEKESEYGYVR
23 - 44	2206.10	2205.09	2205.13	-0.03	1	KVSGPVVVADGMGGAAMYELVR
45 - 56	1312.69	1311.69	1311.71	-0.02	0	VGNDNLIGEIIR
113 - 120	906.45	905.45	905.46	-0.01	0	SGDVYIPR
201 - 211	1406.69	1405.69	1405.72	-0.03	0	QFTMLQTWPVR
201 - 211	1422.69	1421.69	1421.71	-0.03	0	QFTMLQTWPVR Oxidation (M)
220 - 231	1255.65	1254.65	1254.69	-0.04	0	LAADTPLLTGQR
265 - 279	1689.73	1688.73	1688.75	-0.02	0	YSNSEAVVYVGCGER
309 - 323	1545.75	1544.75	1544.80	-0.05	0	TTLVANTSNMPVAAR
309 - 323	1561.75	1560.75	1560.79	-0.05	0	TTLVANTSNMPVAAR Oxidation (M)
324 - 338	1733.83	1732.82	1732.87	-0.04	0	EASIYTGITIAEYFR
339 - 353	1680.79	1679.79	1679.66	0.13	0	DMGYNVSMMADSTSR Oxidation (M)
365 - 381	1795.84	1794.84	1794.86	-0.02	0	LAEMPADSGYPAYLAAR
382 - 388	885.45	884.45	884.44	0.01	0	LASFYER
460 - 476	2135.99	2134.99	2135.02	-0.03	1	ALESFYEKFDQDFIDIR
479 - 485	871.49	870.48	870.50	-0.02	1	AREVLQR
481 - 498	2097.07	2096.07	2096.11	-0.04	1	EVLQREDDLNEIVQLVGK
486 - 506	2301.13	2300.13	2300.14	-0.01	1	EDDLNEIVQLVGKDALAESDK
537 - 542	809.37	808.37	808.37	-0.01	0	SVWMMR
543 - 557	1739.88	1738.88	1738.91	-0.03	0	NIIHFNTLANQAVER
575 - 581	901.40	900.40	900.42	-0.02	0	MGDLFYR
604 - 613	1200.57	1199.57	1199.58	-0.01	0	LYDDLTTGFR

Match to: gi|50878307; Score: 68

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
21 - 30	1004.46	1003.46	1003.46	-0.00	1	CRDGAAAAGR
203 - 209	921.42	920.42	920.40	0.02	0	FAYDSYR
342 - 360	2049.98	2048.97	2049.05	-0.08	0	LYGEFLVNAQGEDVVAGIR
361 - 384	2918.23	2917.23	2917.26	-0.03	1	TPEDLDAMRDHMPEPYEELVENCK
405 - 411	1006.49	1005.48	1005.49	-0.01	0	LWMLQCR
405 - 411	1022.47	1021.47	1021.48	-0.01	0	LWMLQCR Oxidation (M)
423 - 435	1444.71	1443.71	1443.74	-0.03	0	IAVDMVNEGLVER
503 - 523	2111.99	2110.99	2111.03	-0.04	0	TETSPEDVGGMHAAVGILTAR
503 - 523	2128.01	2127.01	2127.03	-0.02	0	TETSPEDVGGMHAAVGILTAR Oxidation (M)
636 - 646	1369.56	1368.56	1368.58	-0.02	0	TEHMFFASDER
649 - 662	1636.84	1635.84	1635.84	-0.01	1	AVRQMIMASSLELR 2 Oxidation (M)
675 - 682	970.45	969.45	969.46	-0.00	0	SDFEGIFR
683 - 692	1072.53	1071.53	1071.57	-0.05	0	AMDGLPVTIR
693 - 712	2343.14	2342.14	2342.17	-0.03	0	LLDPPLHEFLPEGHVEDMVR
693 - 712	2359.13	2358.13	2358.17	-0.04	0	LLDPPLHEFLPEGHVEDMVR Oxidation (M)
732 - 742	1262.61	1261.61	1261.65	-0.04	0	LSEVNPMLGFR
732 - 742	1278.61	1277.61	1277.64	-0.04	0	LSEVNPMLGFR Oxidation (M)
746 - 759	1607.85	1606.84	1606.80	0.04	0	LGISYPELTEMQAR
746 - 759	1623.78	1622.78	1622.80	-0.02	0	LGISYPELTEMQAR Oxidation (M)
816 - 824	1015.55	1014.54	1014.55	-0.01	0	VGTMIEIPR
861 - 882	2628.32	2627.31	2627.37	-0.06	0	FLPIYLSQGILQHDPFEVLDQR
923 - 934	1371.64	1370.63	1370.63	0.00	0	AGLDYVSCSPFR

Spot 1474

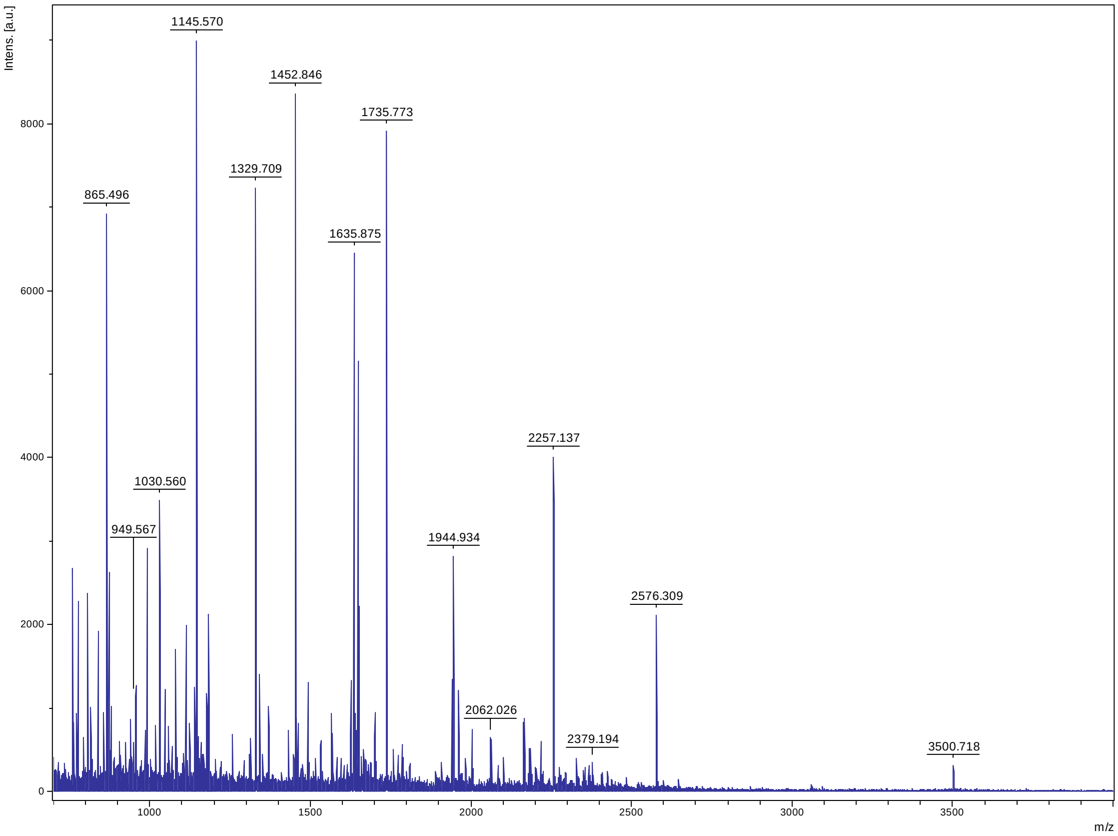


Match to: gi|50913271 Score: 131 Expect: 5.3e-09

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
85 - 95	1191.5527	1190.5454	1190.6295	-0.0841	0	R.TTPSVVAFNQK.G	
85 - 98	1533.7953	1532.7880	1532.7946	-0.0066	1	R.TTPSVVAFNQKGER.L	
107 - 120	1552.7776	1551.7703	1551.7681	0.0022	0	R.QAVTNPQNTFFGTK.R	
126 - 134	1148.5035	1147.4962	1147.5622	-0.0659	1	R.RFEDPQTQK.E	
146 - 159	1460.6778	1459.6705	1459.6579	0.0126	0	K.APNGDAWVETTDGK.Q	
160 - 173	1538.8150	1537.8077	1537.8140	-0.0063	0	K.QYSPSQIGAFVLTK.M	
189 - 202	1564.8188	1563.8115	1563.8045	0.0070	0	K.AVITVPAYFNDAQR.Q	
219 - 235	1776.9185	1775.9112	1775.9053	0.0059	0	R.IINEPTAAALSYGTNNK.E	
265 - 291	3035.4071	3034.3998	3034.4559	-0.0561	1	K.ATNGDTFLGGEDFDNTLLEFLVSEFKR.S	
314 - 339	2676.3721	2675.3648	2675.4017	-0.0369	1	K.AKIELSSTAQTEINLPFITADASGAK.H	
316 - 339	2477.2307	2476.2234	2476.2696	-0.0462	0	K.IELSSTAQTEINLPFITADASGAK.H	
348 - 360	1521.8010	1520.7937	1520.8198	-0.0261	1	R.SKFESLVNSLIER.T	
378 - 390	1417.7080	1416.7007	1416.7282	-0.0275	0	K.EVDEVLLVGGMTR.V	
378 - 390	1433.7094	1432.7021	1432.7231	-0.0210	0	K.EVDEVLLVGGMTR.V	Oxidation (M)
394 - 404	1248.6235	1247.6162	1247.6761	-0.0599	0	K.VQEIVSEIFGK.S	
409 - 428	1939.0283	1938.0210	1937.9992	0.0218	0	K.GVNPDEAVAMGAAIQGGILR.G	
467 - 484	1950.0341	1949.0268	1948.9966	0.0302	1	K.KSQVFSTAADNQTQVGIR.V	
468 - 484	1821.9191	1820.9118	1820.9016	0.0102	0	K.SQVFSTAADNQTQVGIR.V	
485 - 497	1490.6988	1489.6915	1489.7194	-0.0279	1	R.VLQGEREMATDNK.L	
560 - 574	1827.8962	1826.8889	1826.8581	0.0309	1	K.MVQEAELHSQKDQER.K	
560 - 574	1843.9094	1842.9021	1842.8530	0.0491	1	K.MVQEAELHSQKDQER.K	Oxidation (M)
600 - 618	2055.1235	2054.1162	2054.0895	0.0267	1	R.DKIPAEVATEIETAIADLR.S	

Spot 1477

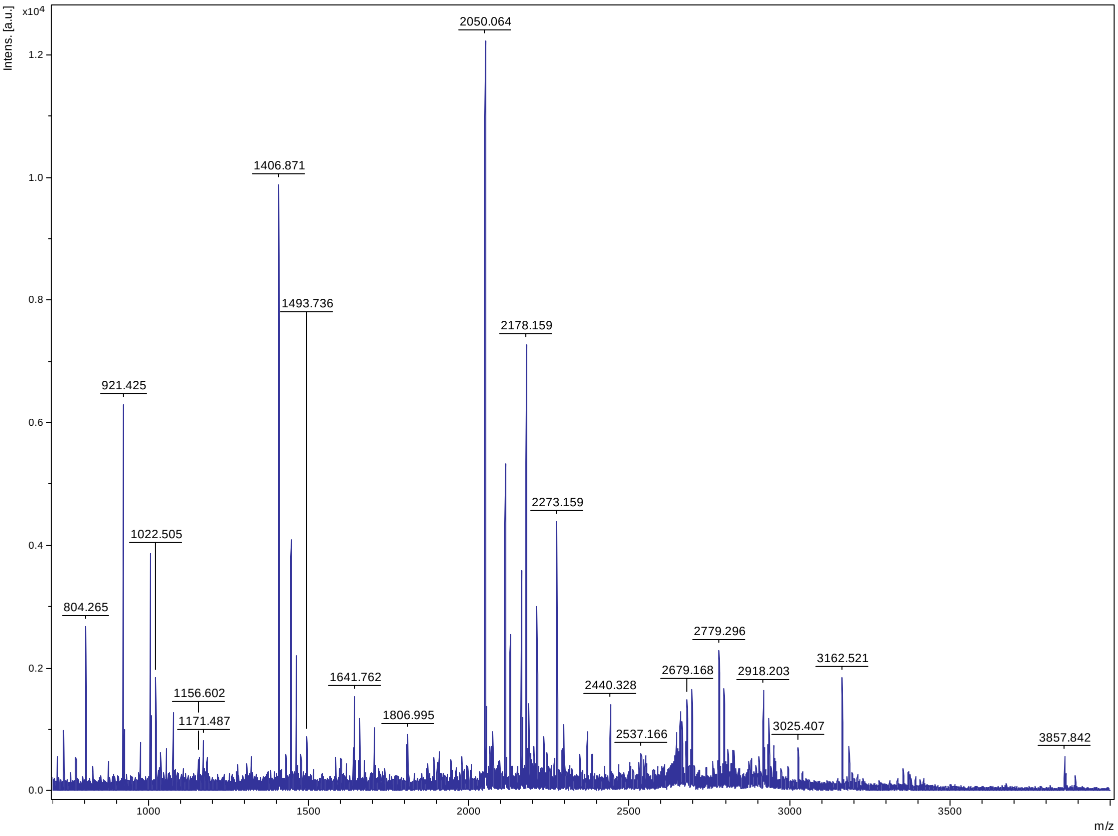


Match to: gi|77548611; Score: 297

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
63 - 69	816.50	815.50	815.48	0.02	0	AFARPVR
77 - 84	1030.56	1029.56	1029.54	0.02	0	RPEYVPNR
77 - 92	2003.01	2002.01	2002.00	0.01	1	RPEYVPNRIDDPNYVR
85 - 92	991.50	990.50	990.48	0.02	0	IDDPNYVR
93 - 99	865.50	864.49	864.47	0.02	0	IFDTTLR
124 - 145	2257.14	2256.14	2256.13	0.01	0	LGVDIIEAGFPASSPDDLDAVR
146 - 170	2576.31	2575.31	2575.31	-0.00	0	SIAIEVGNTPVGEDGHVPVICGLSR
175 - 184	1145.57	1144.57	1144.55	0.02	0	DIDAAWEAVR
208 - 218	1183.70	1182.70	1182.70	0.00	1	KTPEQVVAIAK
219 - 225	839.43	838.42	838.40	0.02	0	EMVAYAR
219 - 225	855.42	854.42	854.40	0.02	0	EMVAYAR Oxidation (M)
226 - 241	1735.77	1734.77	1734.75	0.02	0	SLGCPDVEFSPEDAGR
245 - 256	1532.81	1531.81	1531.83	-0.02	0	EFLYHILEEVIK
257 - 278	2328.17	2327.17	2327.17	0.00	0	AGATTLNIPDTVGYTLPYEFGK
285 - 319	3500.72	3499.72	3499.72	-0.01	0	ANTPGIENAIISTHCQNDLGLATANTLAGAHAGAR
320 - 331	1311.69	1310.69	1310.68	0.01	0	QLEVTINGIGER Pyro-glu (N-term Q)
320 - 331	1328.73	1327.72	1327.71	0.01	0	QLEVTINGIGER
332 - 345	1431.74	1430.74	1430.74	-0.00	0	AGNASLEEVVMAIK
332 - 345	1447.74	1446.74	1446.74	-0.00	0	AGNASLEEVVMAIK Oxidation (M)
349 - 368	2163.08	2162.08	2162.10	-0.03	0	ELLGGLYTGINTQHITMSSK
369 - 382	1642.80	1641.80	1641.80	-0.00	0	MVQEHSGLHVQPHK Oxidation (M)
383 - 403	2166.07	2165.07	2165.07	-0.00	0	AIVGANAFAHESGIHQDGMLK
383 - 403	2182.07	2181.07	2181.06	0.00	0	AIVGANAFAHESGIHQDGMLK Oxidation (M)
406 - 420	1649.85	1648.84	1648.83	0.01	0	GTYEIISPDDIGLTR
421 - 430	1047.59	1046.59	1046.58	0.01	0	ANEFGIVLGK
469 - 487	2218.12	2217.12	2217.12	0.00	1	RVTDEDIEALLSDEIFQPK
470 - 487	2062.03	2061.02	2061.02	0.01	0	VTDEDIEALLSDEIFQPK
520 - 534	1492.75	1491.74	1491.74	0.00	0	IACAVGTGPVDAAYK
535 - 547	1452.85	1451.84	1451.83	0.01	0	AVDDIIQIPTVLR
548 - 565	1944.93	1943.93	1943.91	0.02	0	EYSMTSVTEGIDAIATTR
548 - 565	1960.92	1959.92	1959.91	0.01	0	EYSMTSVTEGIDAIATTR Oxidation (M)
577 - 586	1112.57	1111.57	1111.55	0.02	0	HALTGHSFSR
587 - 603	1635.88	1634.87	1634.86	0.01	0	AFSGSGAALDIVVSSVR
604 - 611	879.50	878.50	878.49	0.02	0	AYLSALNK
612 - 620	939.51	938.51	938.49	0.02	0	MSSFVGAIK
612 - 620	955.52	954.51	954.48	0.03	0	MSSFVGAIK Oxidation (M)
621 - 630	1079.51	1078.51	1078.49	0.02	0	ASSEVSESQR

Spot 1480

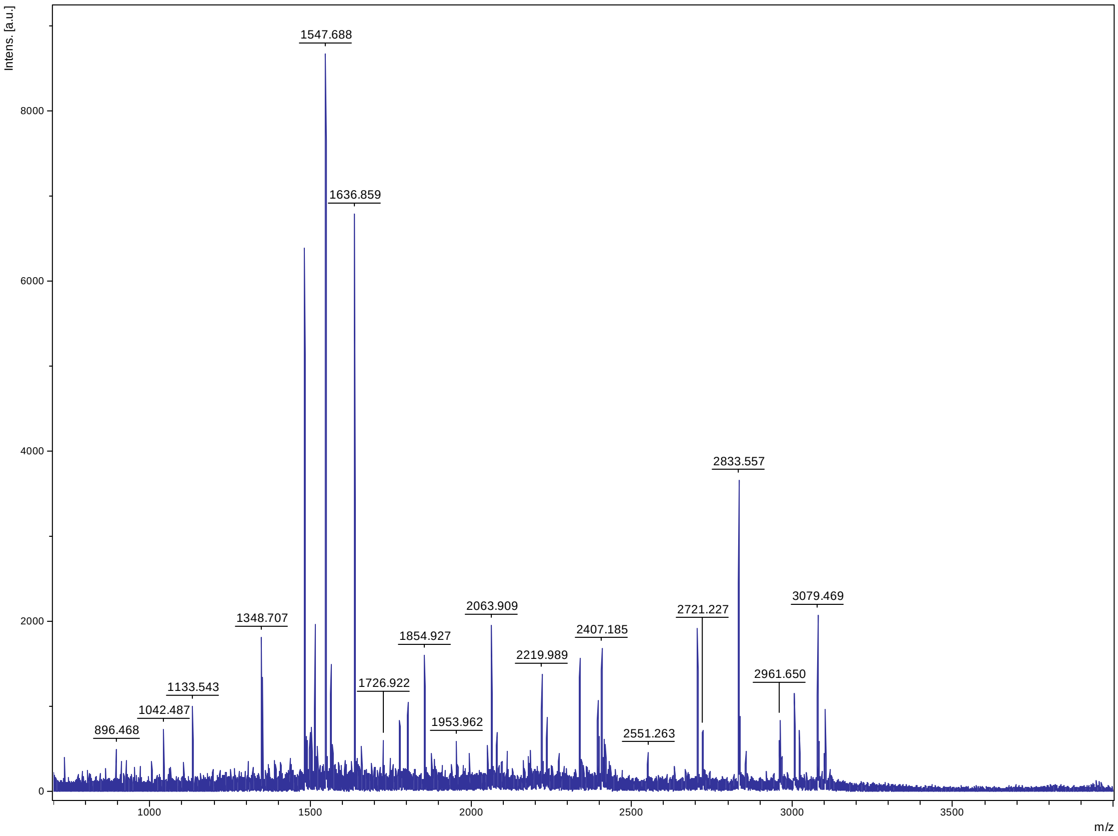


Match to: gi|50878307 Score: 74 Expect: 0.0031

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
99 - 131	3353.4960	3352.4887	3352.6067	-0.1179	0	K.GANLAEMASIGLSVPPGFTVSTEACQQYQAAGK.T	Carbamidomethyl (C)
156 - 168	1406.8897	1405.8824	1405.8405	0.0419	0	R.LGDPARPLLLSVR.S	
203 - 209	921.2885	920.2812	920.4028	-0.1216	0	R.FAYDSYR.R	
203 - 210	1077.4730	1076.4657	1076.5039	-0.0382	1	R.FAYDSYRR.F	
210 - 230	2550.1689	2549.1616	2549.2446	-0.0830	1	R.RFLDMFGNVVMDIPHALFEEK.L	Acetyl (N-term)
239 - 259	2345.1521	2344.1448	2344.1910	-0.0462	1	K.GLHNDTDLTATDLKELVAQYK.D	
276 - 293	2072.0629	2071.0556	2071.1214	-0.0658	1	K.KQLQLAVLAVFNSWDSPR.A	
277 - 296	2256.1277	2255.1204	2255.2426	-0.1221	1	K.QLQLAVLAVFNSWDSPRAIK.Y	
341 - 360	2178.1563	2177.1490	2177.1479	0.0011	1	K.KLYGEFLVNAQGEDVVAGIR.T	
342 - 360	2050.0649	2049.0576	2049.0530	0.0046	0	K.LYGEFLVNAQGEDVVAGIR.T	
361 - 384	2918.1655	2917.1582	2917.2568	-0.0986	1	R.TPEDLDAMRDHMPEPYEELVENCK.I	Carbamidomethyl (C)
392 - 404	1641.7774	1640.7701	1640.7174	0.0527	0	K.EMMDIEFTVQENR.L	
405 - 411	1006.4196	1005.4123	1005.4888	-0.0765	0	R.LWMLQCR.T	Carbamidomethyl (C)
423 - 435	1444.7982	1443.7909	1443.7391	0.0518	0	K.IAVDMVNEGLVER.R	
441 - 462	2536.1598	2535.1525	2535.2216	-0.0690	0	K.MVEPGHLDQLLHPQFENPSGYK.D	
465 - 496	3162.4566	3161.4493	3161.6144	-0.1651	0	K.VIATGLPASPGAAVGQIVFTAEDAEAWHAQGK.D	
503 - 523	2112.0468	2111.0395	2111.0316	0.0079	0	R.TETSPEDVGGMHAAVGILTAR.G	
540 - 549	1171.4466	1170.4393	1170.4580	-0.0187	0	K.CCVSGCSSVR.V	3 Carbamidomethyl (C)
563 - 583	2210.1390	2209.1317	2209.1378	-0.0061	0	K.ALHEGEWLSLNGSTGEVIIGK.Q	
584 - 606	2573.1735	2572.1662	2572.1978	-0.0315	0	K.QPLCPPALSGDLETFMSWVDEVR.K	Pyro-glu (N-term Q)
584 - 606	2647.1969	2646.1896	2646.2458	-0.0561	0	K.QPLCPPALSGDLETFMSWVDEVR.K	Carbamidomethyl (C)
713 - 731	2133.0329	2132.0256	2132.0055	0.0201	1	R.ELCSETGAAQDDVLARVEK.L	Acetyl (N-term); Carbamidomethyl (C)
856 - 882	3184.4548	3183.4475	3183.6240	-0.1765	1	R.DDVGKFLPIYLSQGILQHDPFEVLDQR.G	Acetyl (N-term)
904 - 934	3369.4697	3368.4624	3368.5957	-0.1332	1	K.VGICGEHGGEPLSVAFFAKAGLDYVSCSPFR.V	Acetyl (N-term); 2 Carbamidomethyl (C)

Spot 1489

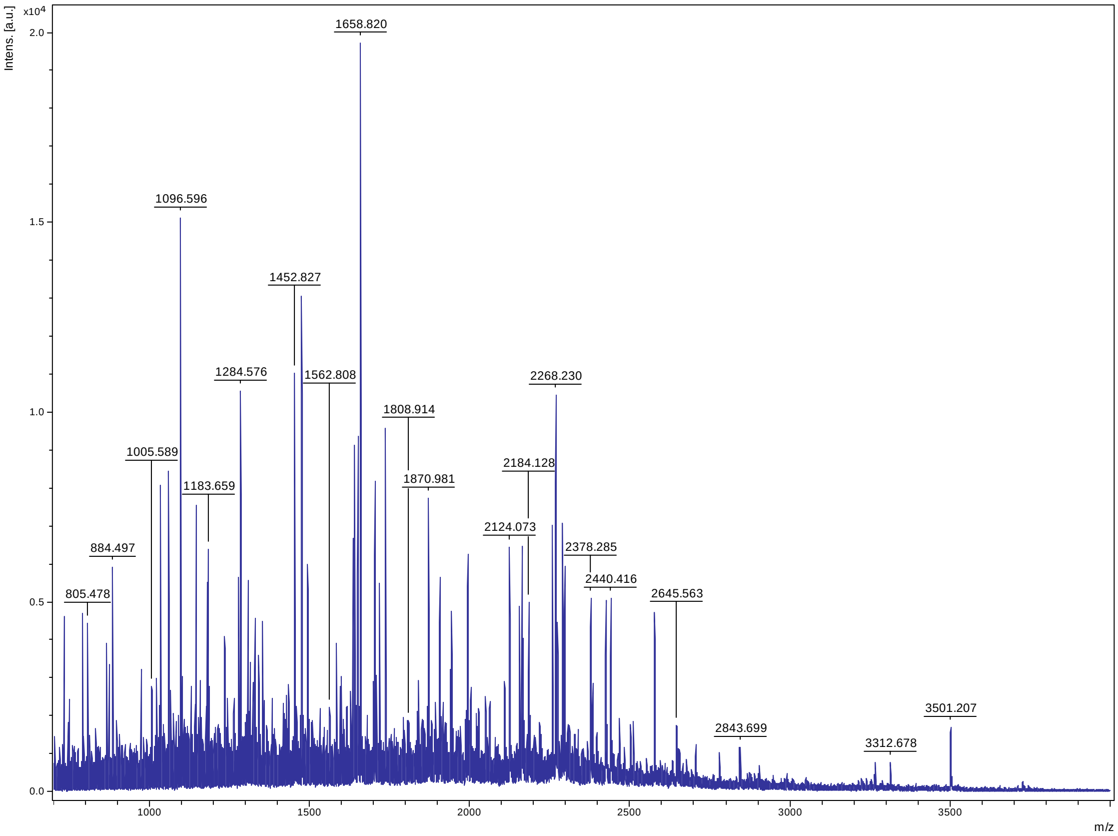


Match to: gi|57863824; Score: 264

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
65 - 92	2721.23	2720.22	2720.22	0.00	0	AHGTAVGLPSDDDMGNSEVGHNALGAGR Oxidation (M)
110 - 117	926.48	925.48	925.45	0.03	0	IFEGEGFK
121 - 142	2338.15	2337.15	2337.17	-0.02	0	ESFDQGTLHLIGLLSDGGVHSR
163 - 170	910.52	909.51	909.50	0.01	0	VHILTDGR
171 - 192	2407.18	2406.18	2406.19	-0.01	0	DVLDGTSVGFVETLENDLSQLR
195 - 206	1133.54	1132.54	1132.53	0.01	0	GIDACIASGGGR
207 - 222	2063.91	2062.91	2062.91	-0.01	1	MYVTMDRYENDWDVVK
207 - 222	2079.92	2078.91	2078.91	0.01	1	MYVTMDRYENDWDVVK Oxidation (M)
223 - 236	1563.80	1562.80	1562.80	0.00	1	RGWDAQVLGEAPHK
224 - 245	2394.18	2393.18	2393.21	-0.03	1	GWDAQVLGEAPHKFQNAVEAVK
270 - 286	1776.91	1775.90	1775.92	-0.02	0	AVGPIVDGDAVVTFNFR
290 - 304	1802.86	1801.86	1801.86	-0.01	1	MVMIAKALEYEDFDK
296 - 307	1547.69	1546.69	1546.69	-0.01	1	ALEYEDFDKFDR
315 - 340	3005.50	3004.50	3004.50	0.00	1	YAGMLQYDGELKLPSHYLVSPPEIER
315 - 340	3021.50	3020.50	3020.50	-0.00	1	YAGMLQYDGELKLPSHYLVSPPEIER Oxidation (M)
327 - 340	1636.86	1635.86	1635.86	-0.01	0	LPSHYLVSPPEIER
341 - 348	896.47	895.47	895.47	0.00	0	TSGEYLVK
349 - 361	1482.68	1481.68	1481.73	-0.05	1	NGIRTFACSETVK
353 - 361	1042.49	1041.48	1041.48	0.00	0	TFACSETVK
362 - 373	1481.67	1480.67	1480.70	-0.03	0	FGHVTFFWNGNR
374 - 400	3079.47	3078.47	3078.47	-0.00	1	SGYFDETKEEYVEIPSDSGITFNVKPK
412 - 423	1348.71	1347.71	1347.71	-0.01	1	DAILSGKFDQVR
424 - 446	2397.13	2396.13	2396.15	-0.02	0	VNLPNGDMVGHTGDIEATVVACK
492 - 520	2961.65	2960.65	2960.66	-0.01	1	KGEIQILTSHTLQPVPVAIGGPGLHSGVR
493 - 520	2833.56	2832.55	2832.56	-0.01	0	GEIQILTSHTLQPVPVAIGGPGLHSGVR

Spot 1490



Match to: gi|77548611; Score: 104

Matched peptides:

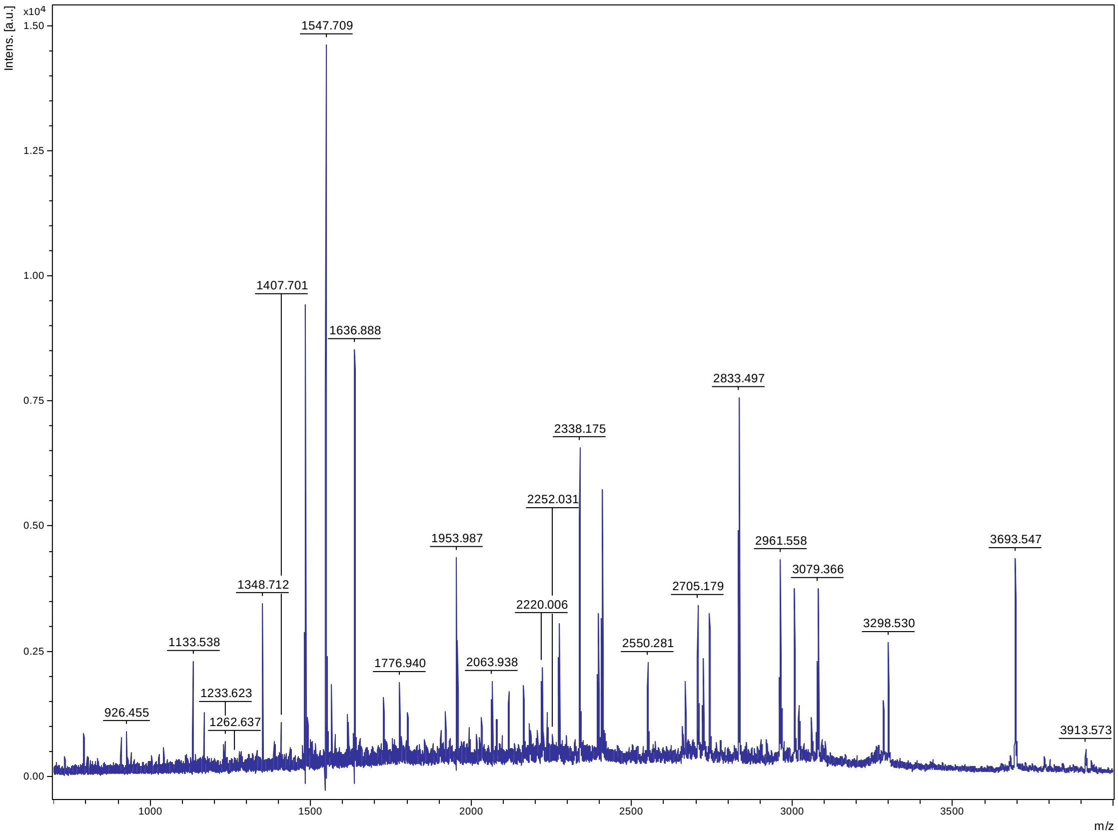
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
77 - 92	2003.02	2002.02	2002.00	0.02	1	RPEYVPNRIDDPNYVR
93 - 99	865.53	864.53	864.47	0.06	0	IFDTTLR
124 - 145	2257.19	2256.18	2256.13	0.06	0	LGVDIIEAGFPASSPDDLDAVR
146 - 170	2576.46	2575.46	2575.31	0.15	0	SIAIEVGNTPVGEDGHVPVICGLSR
175 - 184	1145.56	1144.56	1144.55	0.01	0	DIDAAWEAVR
191 - 205	1808.91	1807.91	1807.90	0.01	0	IHTFIATSEIHMQHK Oxidation (M)
191 - 207	2062.07	2061.07	2061.09	-0.03	1	IHTFIATSEIHMQHKLR
208 - 218	1183.66	1182.66	1182.70	-0.04	1	KTPEQVVAIAK
226 - 241	1735.77	1734.76	1734.75	0.01	0	SLGCPDVEFSPEDAGR
245 - 256	1532.81	1531.81	1531.83	-0.02	0	EFLYHILEEVIK
349 - 368	2163.10	2162.10	2162.10	-0.00	0	ELLGGLYTGINTQHITMSSK
383 - 403	2166.09	2165.09	2165.07	0.02	0	AIVGANAFAHESGIHQDGMLK
406 - 420	1649.80	1648.79	1648.83	-0.04	0	GTYEIISPDDIGLTR
535 - 547	1452.83	1451.82	1451.83	-0.01	0	AVDDIIQIPTVLR
548 - 565	1944.95	1943.94	1943.91	0.03	0	EYSMTSVTEGIDAIATTR
587 - 603	1635.85	1634.85	1634.86	-0.02	0	AFSGSGAALDIVVSSVR

Match to: gi|52076758; Score: 91

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
40 - 49	1102.68	1101.68	1101.67	0.01	0	HALPLPSVLR
50 - 71	2028.02	2027.02	2027.00	0.02	0	SPFALADGPASSAAGNPGEIAK
72 - 97	2778.67	2777.66	2777.51	0.15	0	LFPNLFGQPSVSLVPSPEPASTRPLK
145 - 157	1651.80	1650.80	1650.79	0.00	0	YVELTADYVYPYR
158 - 169	1341.57	1340.57	1340.56	0.01	0	NQGGFDMICSGR
249 - 262	1599.76	1598.76	1598.74	0.01	0	IYSEMIGNVMTDAR
249 - 262	1615.77	1614.77	1614.74	0.03	0	IYSEMIGNVMTDAR Oxidation (M)
267 - 272	884.50	883.49	883.43	0.06	0	YYHFVR
277 - 303	2843.70	2842.70	2842.46	0.23	0	AASHITLECALQTHPNVALIGEEVAAK
376 - 383	1007.58	1006.58	1006.55	0.03	0	QLFDFLPK
384 - 393	1242.68	1241.68	1241.70	-0.02	0	TIQEQLLLER
384 - 403	2288.28	2287.27	2287.23	0.05	1	TIQEQLLLERDPHGNVQVAK
409 - 421	1562.81	1561.81	1561.82	-0.02	1	MLIAMVETELEKR
409 - 421	1594.83	1593.83	1593.81	0.02	1	MLIAMVETELEKR 2 Oxidation (M)
433 - 443	1284.58	1283.57	1283.57	0.01	0	GQSHFFGYEGR
526 - 536	1351.69	1350.69	1350.69	-0.00	1	FASLRDEWSLK

Spot 1496

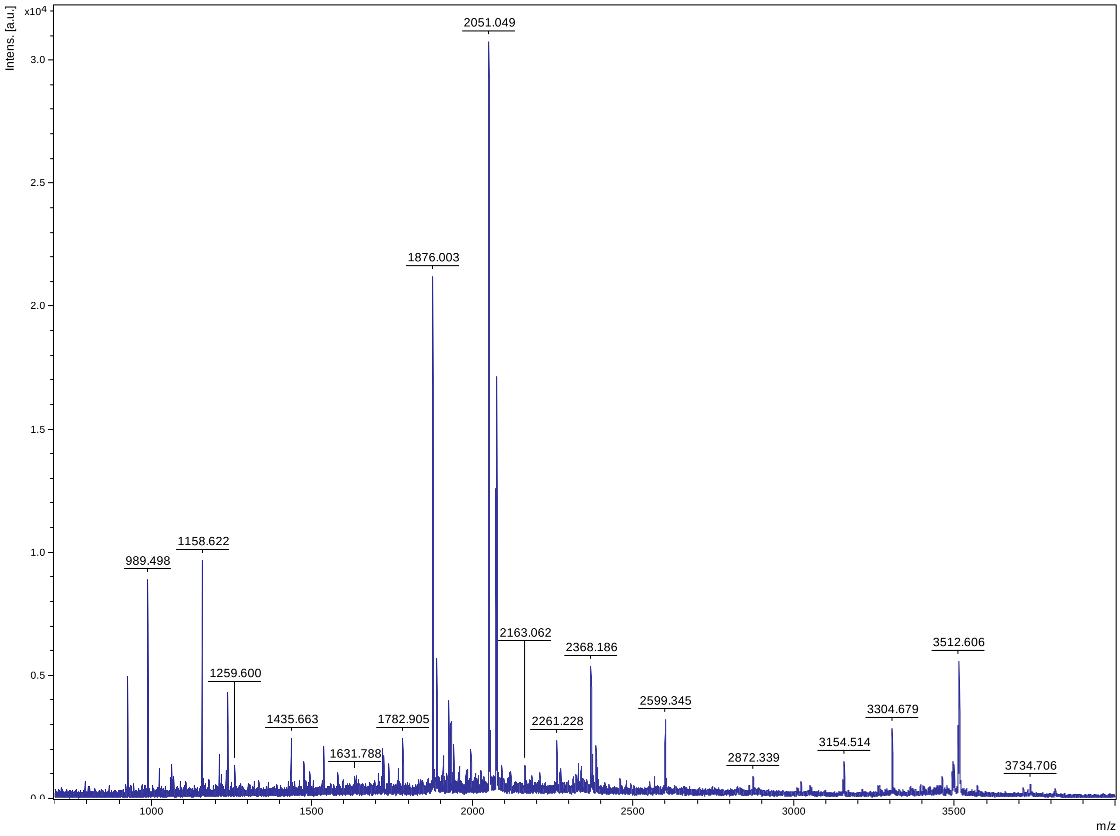


Match to: Q5KQH5_ORYSA Score: 183 Expect: 1.2e-12

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 15	1615.7979	1614.7906	1614.7314	0.0592	0	M.GSSDFSWTLPDHPK.L	Acetyl (N-term)
2 - 18	1954.0224	1953.0151	1952.9632	0.0519	1	M.GSSDFSWTLPDHPKLPK.G	Acetyl (N-term)
65 - 92	2721.1801	2720.1728	2720.2208	-0.0479	0	K.AHGTAVGLPSDDDMGNSEVGHNALGAGR.I	Oxidation (M)
110 - 117	926.4596	925.4523	925.4545	-0.0021	0	K.IFEGEGFK.Y	
118 - 142	2742.3772	2741.3699	2741.4136	-0.0437	1	K.YIKESFDQGTLHLIGLLSDGGVHSR.L	
121 - 142	2338.1867	2337.1794	2337.1712	0.0082	0	K.ESFDQGTLHLIGLLSDGGVHSR.L	
163 - 192	3298.5954	3297.5881	3297.6840	-0.0959	1	R.VHILTDGRDVLDGTSVGFVETLENDLSQLR.A	
171 - 192	2407.2138	2406.2065	2406.1914	0.0151	0	R.DVLDGTSVGFVETLENDLSQLR.A	
195 - 206	1133.5757	1132.5684	1132.5294	0.0390	0	K.GIDACIASGGGR.M	Carbamidomethyl (C)
207 - 222	2079.9407	2078.9334	2078.9077	0.0257	1	R.MYVTMDRYENDWDVVK.R	Oxidation (M)
223 - 236	1563.8731	1562.8658	1562.7953	0.0705	1	K.RGWDAQVLGEAPHK.F	
224 - 236	1407.7683	1406.7610	1406.6942	0.0668	0	R.GWDAQVLGEAPHK.F	
224 - 245	2394.2365	2393.2292	2393.2127	0.0165	1	R.GWDAQVLGEAPHKFQNAVEAVK.T	
270 - 286	1776.9792	1775.9719	1775.9205	0.0514	0	K.AVGPIVDGDAVVTFNFR.A	
290 - 304	1802.9502	1801.9429	1801.8630	0.0799	1	R.MVMIAKALEYEDFDK.F	
296 - 307	1547.7591	1546.7518	1546.6939	0.0579	1	K.ALEYEDFDKFDR.V	
315 - 340	3005.4314	3004.4241	3004.5004	-0.0762	1	R.YAGMLQYDGELKLPSHYLVSPPEIER.T	
327 - 340	1636.9353	1635.9280	1635.8620	0.0660	0	K.LPSHYLVSPPEIER.T	
349 - 361	1482.7588	1481.7515	1481.7296	0.0219	1	K.NGIRTFACSETVK.F	Carbamidomethyl (C)
374 - 400	3079.3901	3078.3828	3078.4709	-0.0880	1	R.SGYFDETKEEYVEIPSDSGITFNVKPK.M	
412 - 423	1348.7724	1347.7651	1347.7146	0.0505	1	R.DAILSGKFDQVR.V	
492 - 520	2961.5939	2960.5866	2960.6559	-0.0692	1	K.KGEIQILTSHTLQPVPVAIGGPGLHSGVR.F	
493 - 520	2833.5329	2832.5256	2832.5609	-0.0353	0	K.GEIQILTSHTLQPVPVAIGGPGLHSGVR.F	

Spot 1497

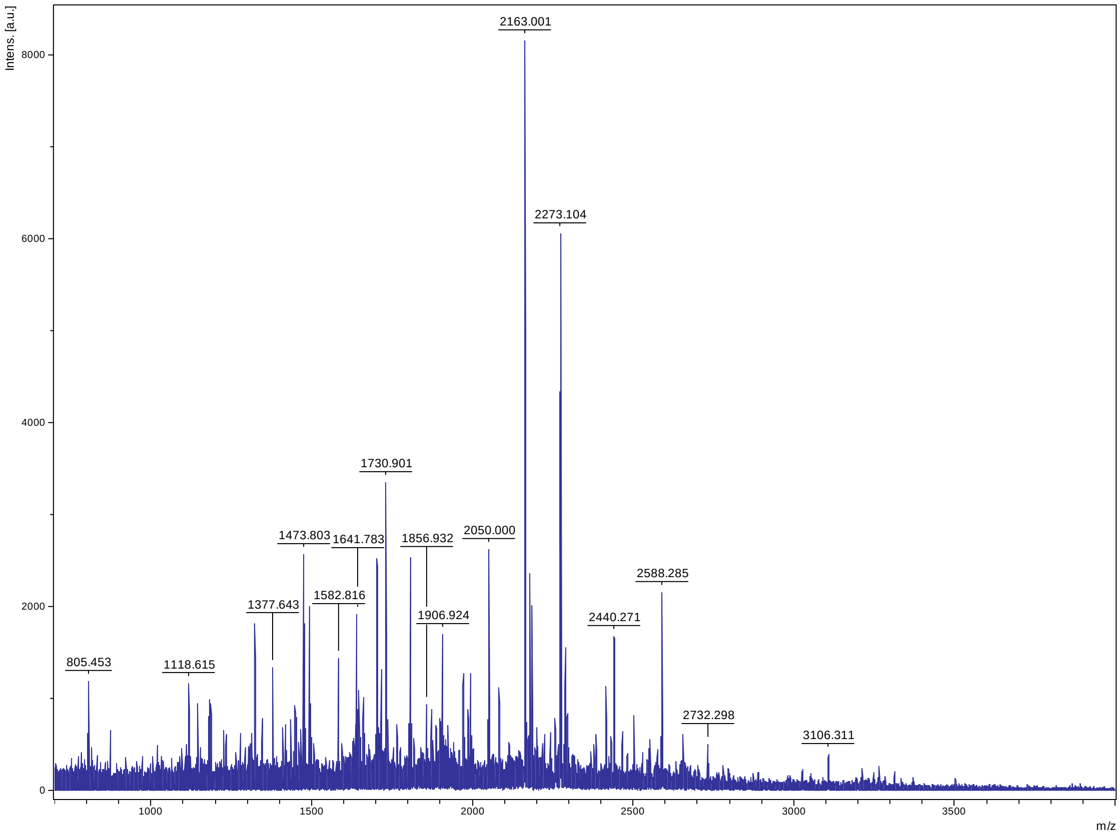


Match to: gi|1706328 Score: 82 Expect: 0.0004

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
150 - 165	1876.0029	1874.9957	1875.0002	-0.0046	0	R.ILHHTIGLPDFSQELR.C	
197 - 219	2599.3450	2598.3377	2598.3264	0.0113	0	R.ESKPVYLSISCNLPGLPHPTFSR.D	Carbamidomethyl (C)
220 - 229	1158.6221	1157.6148	1157.6233	-0.0085	0	R.DPVPFFLAPR.L	
234 - 249	1721.8801	1720.8729	1720.8705	0.0024	0	K.MGLEAAVEATVEFLNK.A	
234 - 249	1737.8738	1736.8665	1736.8654	0.0011	0	K.MGLEAAVEATVEFLNK.A	Oxidation (M)
345 - 352	925.5389	924.5316	924.5392	-0.0076	0	K.AIIVQPER.V	
353 - 367	1579.7740	1578.7668	1578.7720	-0.0052	0	R.VIVGNGPAFGCVMMK.E	Carbamidomethyl (C)
380 - 389	1259.5996	1258.5923	1258.5942	-0.0018	1	K.NTTAYENYKR.I	
417 - 437	2373.0776	2372.0704	2372.0412	0.0291	0	K.MLNSDSAVIAETGDSWFNCQK.L	Carbamidomethyl (C)
417 - 437	2389.0603	2388.0530	2388.0362	0.0169	0	K.MLNSDSAVIAETGDSWFNCQK.L	Carbamidomethyl (C); Oxidation (M)
474 - 495	2368.1865	2367.1792	2367.1562	0.0230	0	R.VIACIGDGSFQVTAQDVSTMIR.C	Carbamidomethyl (C)
526 - 542	1887.8978	1886.8906	1886.8911	-0.0005	0	K.NWNYTGLVDAIHNGEGK.C	
550 - 566	1908.9257	1907.9184	1907.8855	0.0328	1	K.CEEELTEAIGMALGEKK.D	Acetyl (N-term); Oxidation (M)
567 - 583	2051.0486	2050.0413	2049.9499	0.0914	1	K.DCLCFIEVIAHKDDTSK.E	2 Carbamidomethyl (C)
579 - 591	1535.7267	1534.7194	1534.7263	-0.0069	1	K.DDTSKELLEWGSR.V	
584 - 591	989.4977	988.4905	988.4978	-0.0073	0	K.ELLEWGSR.V	
592 - 603	1237.6239	1236.6166	1236.6211	-0.0044	0	R.VSAANSRPPNPQ.-	

Spot 1498

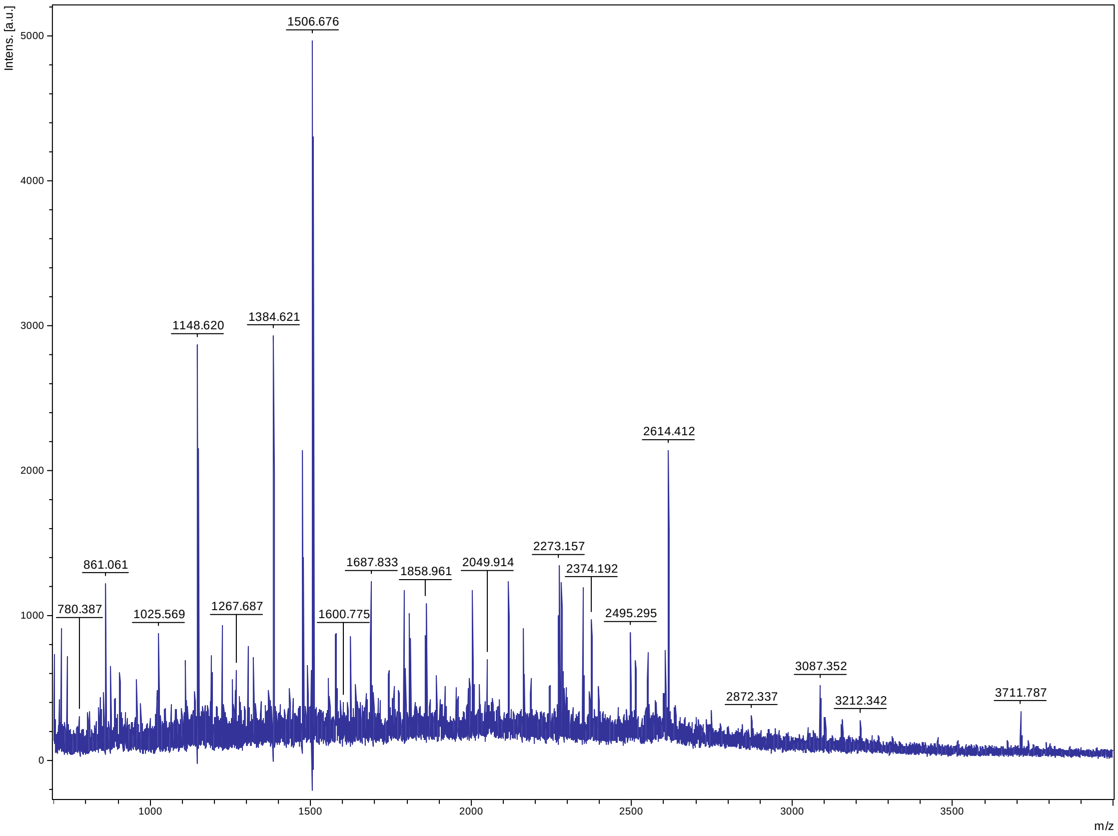


Match to: gi|77557138; Score: 88

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
50 - 65	1802.82	1801.82	1801.91	-0.10	1	LLPRSPSSFTPCLDGR
66 - 82	1898.96	1897.95	1897.98	-0.02	0	YLLLGPDAELNHSEISK
66 - 93	3106.31	3105.31	3105.50	-0.20	1	YLLLGPDAELNHSEISKFSENDAGAYPR
83 - 93	1226.57	1225.57	1225.54	0.03	0	FSENDAGAYPR
104 - 117	1646.80	1645.80	1645.78	0.01	0	LMDFVIDSPPPEMR
104 - 117	1662.80	1661.79	1661.78	0.01	0	LMDFVIDSPPPEMR Oxidation (M)
167 - 178	1447.76	1446.76	1446.75	0.01	0	ILNNWFEGDVLK
260 - 284	2588.29	2587.28	2587.39	-0.10	0	VQGVVLADGTEVLTSVVLSNATPYR
315 - 329	1806.89	1805.89	1805.89	-0.00	1	INVAVDRLPQFSCCK
402 - 413	1377.64	1376.64	1376.63	0.01	0	LSEGSWQDSNVR
485 - 505	1970.92	1969.92	1969.92	-0.01	0	GLYLCGSGAHPGGGVMGAPGR
485 - 505	1986.90	1985.90	1985.92	-0.02	0	GLYLCGSGAHPGGGVMGAPGR Oxidation (M)
506 - 516	1186.67	1185.66	1185.64	0.03	0	NAASVVLEDLR

Spot 1499

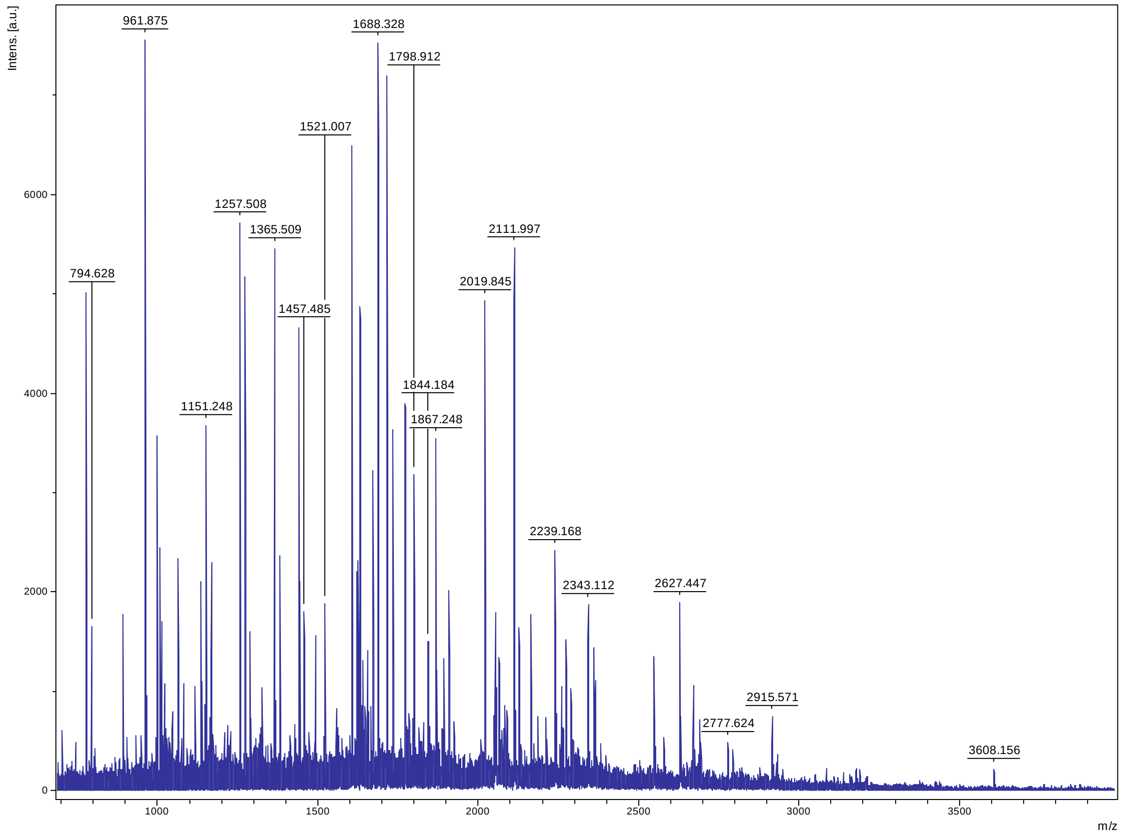


Match to: Q5JK78_ORYSA Score: 71 Expect: 0.0055

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
11 - 28	2004.1287	2003.1214	2003.0251	0.0963	0	K.ETFPGIEIDTSQPPVVFK.T	
29 - 41	1474.7961	1473.7888	1473.7827	0.0061	0	K.TQLYTLTGVPPER.Q	
130 - 140	1224.5345	1223.5272	1223.6146	-0.0874	0	K.SALLSYSDNVR.G	
157 - 179	2614.2566	2613.2493	2613.4278	-0.1785	0	R.NTFGELDQSVRPVAPLLFLQTLR.K	
227 - 236	1148.5172	1147.5099	1147.6237	-0.1137	0	K.ELFGIDLVSR.V	
303 - 310	1025.3794	1024.3721	1024.5705	-0.1984	0	R.YLTVQFVR.F	
326 - 344	2348.0618	2347.0545	2347.0929	-0.0384	1	R.KVDYPLELDVYDFCSDELK.Q	Carbamidomethyl (C)
352 - 361	1191.5183	1190.5110	1190.5713	-0.0603	1	R.QMLRDAENAK.F	Oxidation (M)
419 - 430	1305.5743	1304.5670	1304.6149	-0.0479	0	R.SADSGHYVGWVK.Q	
436 - 447	1506.6919	1505.6846	1505.6787	0.0060	0	K.WIEFDDDNPSIR.K	

Spot 1503

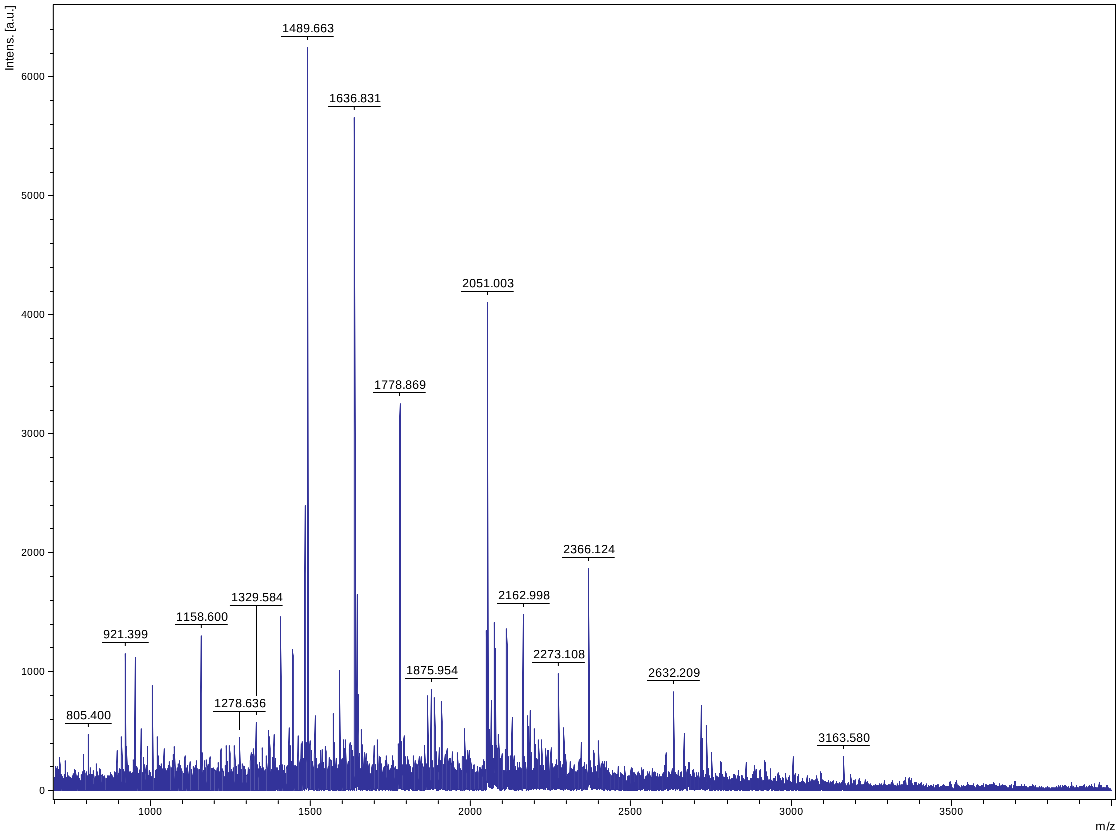


Match to: gi|108710781 Score: 78 Expect: 0.0012

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
150 - 163	1689.9638	1688.9565	1688.9097	0.0468	0	K.QILSQETQYLPITR.G	
189 - 203	1672.9376	1671.9303	1671.8831	0.0472	0	K.AVPELQLEYGIAVDR.V	
233 - 254	2259.1796	2258.1723	2258.1807	-0.0084	1	R.LDAPTKAPAWPVGSEGNRPPAK.I	
239 - 254	1633.8902	1632.8829	1632.8372	0.0458	0	K.APAWPVGSEGNRPPAK.I	
255 - 266	1174.6016	1173.5943	1173.6757	-0.0814	0	K.IPVPVPPSPSGK.D	
255 - 279	2672.3395	2671.3322	2671.3956	-0.0633	1	K.IPVPVPPSPSGKDDEILTEPQELSK.Q	
333 - 350	1908.9465	1907.9392	1907.9047	0.0346	0	R.YPMNDAAGTINEIGSTVR.R	
333 - 351	2065.0337	2064.0264	2064.0058	0.0207	1	R.YPMNDAAGTINEIGSTVRR.V	
333 - 351	2080.9974	2079.9901	2080.0007	-0.0106	1	R.YPMNDAAGTINEIGSTVRR.V	Oxidation (M)
397 - 405	901.3647	900.3574	900.4089	-0.0515	0	K.YGGASAGYR.T	
456 - 480	2547.2543	2546.2470	2546.2805	-0.0334	0	R.SSYIAPDLVASVPDPGAVAAAAWYR.A	

Spot 1506

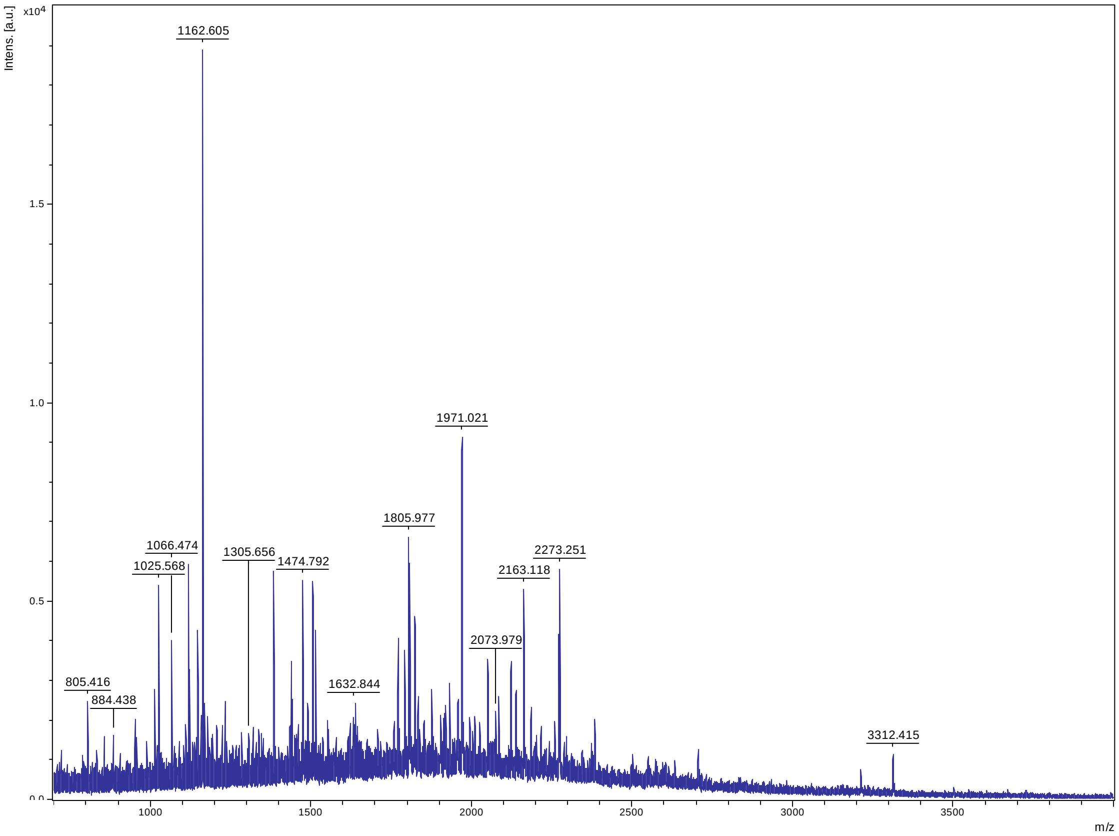


Match to: gi|56785335; Score: 109

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
38 - 53	1875.95	1874.95	1874.90	0.05	0	YNCIHVAQTPVMDSLK
65 - 92	2719.19	2718.18	2718.24	-0.06	0	AHGTAVGLPSEDDMGNSEVGHNALGAGR
65 - 92	2735.18	2734.17	2734.24	-0.06	0	AHGTAVGLPSEDDMGNSEVGHNALGAGR Oxidation (M)
163 - 170	910.50	909.49	909.50	-0.01	0	VHILTDGR
171 - 192	2366.12	2365.12	2365.16	-0.04	0	DVLDGSSVGFVETLESDLSQLR
207 - 222	2063.90	2062.90	2062.91	-0.01	1	MYVTMDRYENDWDVVK
223 - 236	1589.77	1588.76	1588.80	-0.04	1	RGWDAQVLGEAPYK
237 - 245	1005.53	1004.52	1004.53	-0.01	0	FQNAVEAVK
253 - 269	1864.88	1863.88	1863.93	-0.05	0	ASDQYLPPFVIVDESGK
270 - 286	1778.87	1777.87	1777.90	-0.03	0	SVGPVVDGDAVVTFNFR
296 - 307	1489.66	1488.66	1488.69	-0.03	1	ALEYADFDKFDR
315 - 326	1387.64	1386.64	1386.65	-0.01	0	YAGMLQYDGELK
327 - 340	1636.83	1635.83	1635.86	-0.03	0	LPSHYLVSPPEIER
341 - 348	896.46	895.46	895.47	-0.00	0	TSGEYLVK
362 - 373	1481.65	1480.65	1480.70	-0.05	0	FGHVTFFWNGNR

Spot 1508

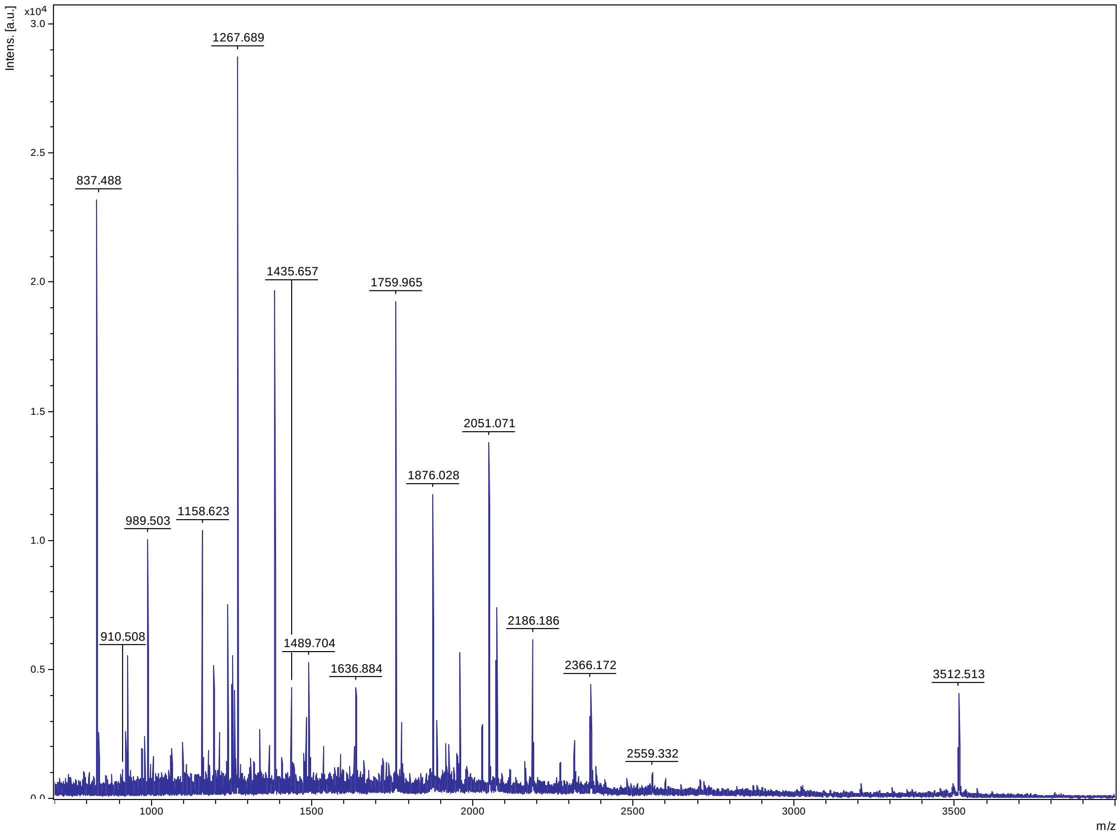


Match to: gi|57900359 Score: 82 Expect: 0.00039

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
4 - 12	1148.5921	1147.5848	1147.6250	-0.0402	1	K.FSVRGIWQR.W	
24 - 40	1914.9092	1913.9019	1913.9193	-0.0173	0	K.NDEAITVFTGVPTMYTR.L	
24 - 40	1930.9176	1929.9103	1929.9142	-0.0039	0	K.NDEAITVFTGVPTMYTR.L	Oxidation (M)
41 - 61	2243.0518	2242.0445	2242.0211	0.0234	0	R.LLQGYDGMDPEQQSASSFAAK.Q	
62 - 79	1946.0034	1944.9961	1944.9657	0.0304	1	K.QLRLMMCGSSALPSPLMK.R	Pyro-glu (N-term Q)
62 - 79	1961.9378	1960.9305	1960.9606	-0.0301	1	K.QLRLMMCGSSALPSPLMK.R	Oxidation (M); Pyro-glu (N-term Q)
62 - 79	2003.1492	2002.1419	2001.9872	0.1547	1	K.QLRLMMCGSSALPSPLMK.R	Carbamidomethyl (C); Pyro-glu (N-term Q)
62 - 79	2051.0028	2049.9955	2049.9719	0.0236	1	K.QLRLMMCGSSALPSPLMK.R	Carbamidomethyl (C); 3 Oxidation (M); Pyro-glu (N-term Q)
65 - 79	1654.8317	1653.8244	1653.7598	0.0646	0	R.LMMCGSSALPSPLMK.R	Carbamidomethyl (C); 2 Oxidation (M)
81 - 88	1013.4459	1012.4386	1012.4726	-0.0340	0	R.WEEVTGHR.L	
93 - 110	2009.9777	2008.9704	2008.9498	0.0206	0	R.YGMTEFVMALSNPLHGAR.K	Oxidation (M)
93 - 110	2025.9648	2024.9575	2024.9447	0.0128	0	R.YGMTEFVMALSNPLHGAR.K	2 Oxidation (M)
126 - 144	2122.9958	2121.9885	2121.9922	-0.0036	0	K.IIMEDGAETTSEVGELCIR.S	Carbamidomethyl (C)
126 - 144	2138.9672	2137.9599	2137.9871	-0.0272	0	K.IIMEDGAETTSEVGELCIR.S	Carbamidomethyl (C); Oxidation (M)
155 - 170	1771.8642	1770.8569	1770.8828	-0.0258	0	R.KPEVTAESFIDGGFFK.T	
171 - 188	1970.9530	1969.9457	1969.9632	-0.0175	0	K.TGDTVTVDDEGYFIILGR.T	
246 - 265	2216.1755	2215.1682	2215.1848	-0.0166	1	K.RAELDSKPALTLEALTSWSK.D	
247 - 265	2060.0730	2059.0657	2059.0837	-0.0180	0	R.AELDSKPALTLEALTSWSK.D	
277 - 285	1162.6078	1161.6005	1161.6182	-0.0177	0	R.LYLWDSLPR.N	

Spot 1511

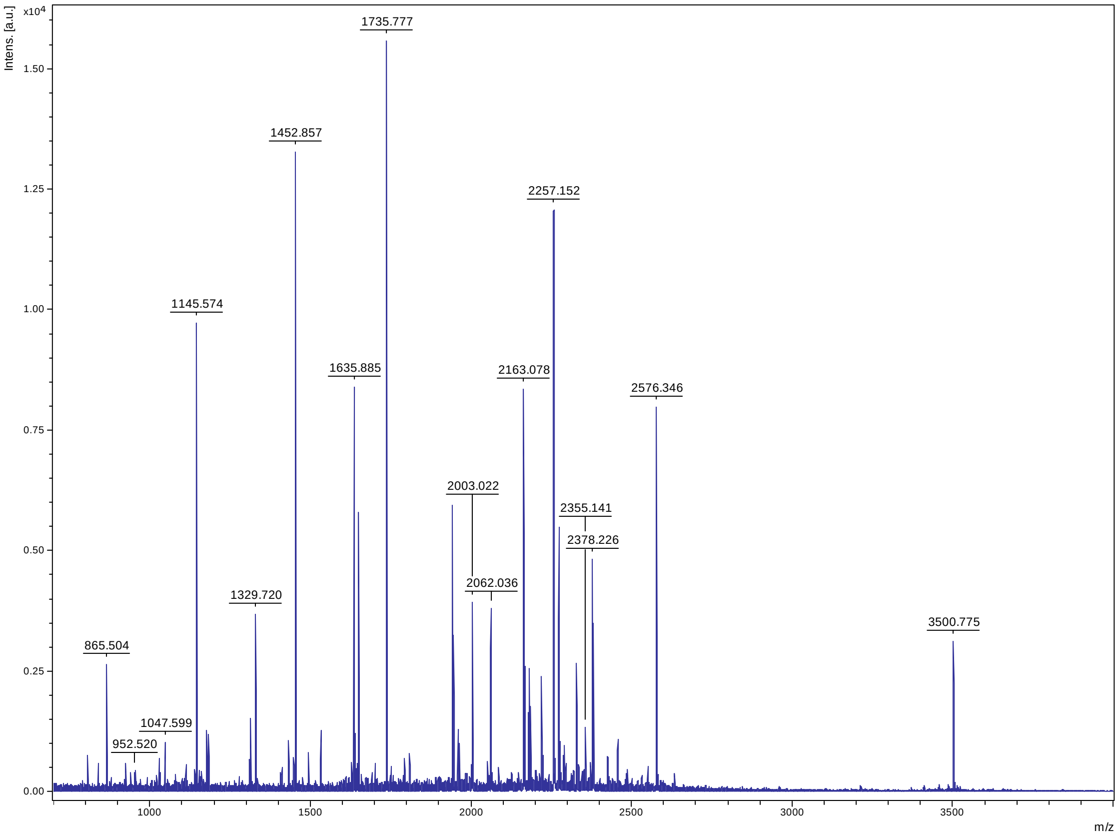


Match to: gi|110815966 Score: 66 Expect: 0.018

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
85 - 103	2073.9465	2072.9393	2072.9043	0.0349	0	R.LVGCCNELNAGYAADGYAR.A	2 Carbamidomethyl (C)
152 - 167	1876.0276	1875.0203	1875.0002	0.0201	0	R.ILHHTIGLPDFSQELR.C	
222 - 231	1158.6228	1157.6155	1157.6233	-0.0078	0	R.DPVPFFLAPR.L	
236 - 251	1721.9014	1720.8941	1720.8705	0.0236	0	K.MGLEAAVEATVEFLNK.A	
347 - 354	925.5385	924.5312	924.5392	-0.0081	0	K.AIIVQPER.V	
382 - 391	1259.5875	1258.5802	1258.5942	-0.0139	1	K.NTTAYENYKR.I	
392 - 409	2051.0706	2050.0633	2050.0370	0.0262	0	R.IFVPEGQPLESEPNEPLR.V	
410 - 419	1211.6281	1210.6208	1210.7186	-0.0978	1	R.VNVLFKHVQK.M	
529 - 545	1887.9186	1886.9113	1886.8911	0.0203	0	K.NWNYTGLVDAIHNGEGK.C	
581 - 593	1535.7467	1534.7394	1534.7263	0.0131	1	K.DDTSKELLEWGSR.V	
586 - 593	989.5029	988.4957	988.4978	-0.0021	0	K.ELLEWGSR.V	
594 - 605	1237.6135	1236.6062	1236.6211	-0.0148	0	R.VSAANSRPPNPQ.-	

Spot 1512

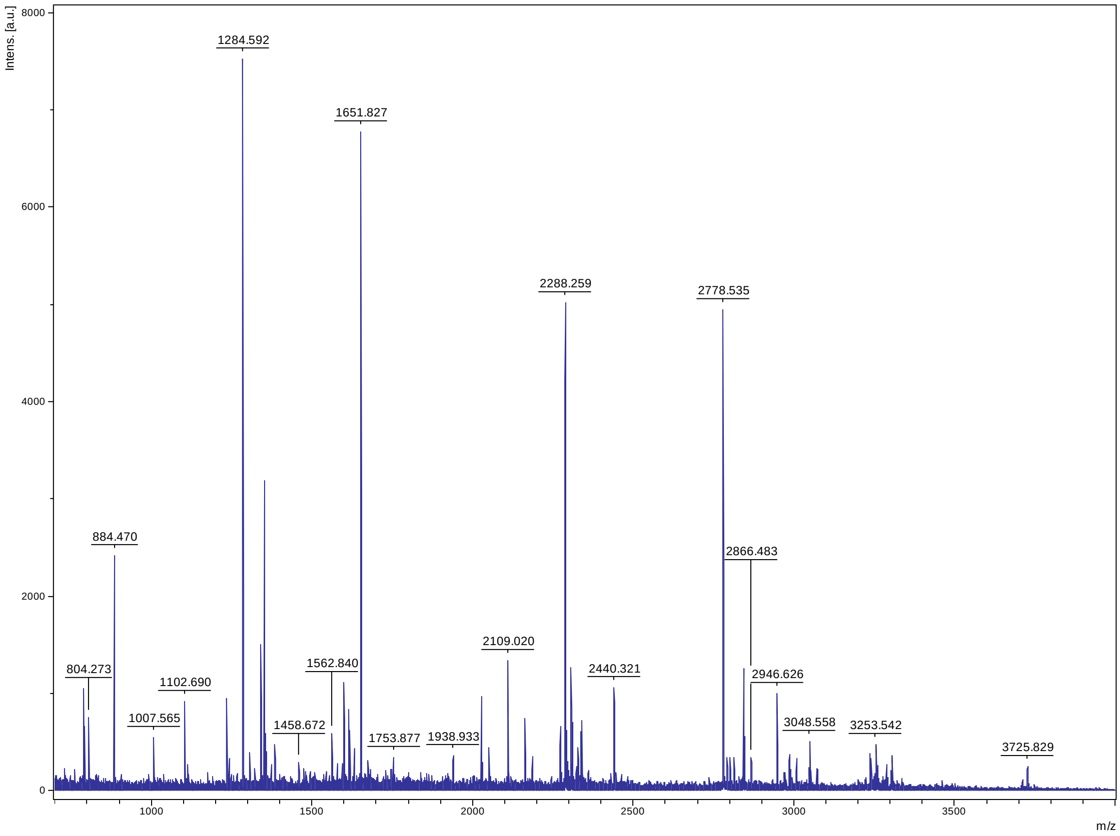


Match to: gi|77548611; Score: 419

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
35 - 57	2166.09	2165.09	2165.11	-0.02	1	AAAPRFSHGLATAAAAANPSASR
77 - 84	1030.56	1029.56	1029.54	0.03	0	RPEYVPNR
77 - 92	2003.02	2002.02	2002.00	0.02	1	RPEYVPNRIDDPNYVR
85 - 92	991.52	990.52	990.48	0.04	0	IDDPNYVR
93 - 99	865.50	864.50	864.47	0.03	0	IFDTTLR
93 - 114	2355.14	2354.14	2354.11	0.03	1	IFDTTLRDGEQSPGATMTSAEK
93 - 114	2371.14	2370.14	2370.10	0.04	1	IFDTTLRDGEQSPGATMTSAEK Oxidation (M)
124 - 145	2257.15	2256.15	2256.13	0.02	0	LGVDIIEAGFPASSPDDLDAVR
146 - 170	2576.35	2575.34	2575.31	0.04	0	SIAIEVGNTPVGEDGHVPVICGLSR
175 - 184	1145.57	1144.57	1144.55	0.02	0	DIDAAWEAVR
191 - 205	1792.94	1791.94	1791.91	0.03	0	IHTFIATSEIHMQHK
191 - 205	1808.92	1807.92	1807.90	0.01	0	IHTFIATSEIHMQHK Oxidation (M)
208 - 218	1183.72	1182.72	1182.70	0.02	1	KTPEQVVAIAK
219 - 225	839.43	838.43	838.40	0.02	0	EMVAYAR
226 - 241	1735.78	1734.77	1734.75	0.02	0	SLGCPDVEFSPEDAGR
245 - 256	1532.85	1531.85	1531.83	0.02	0	EFLYHILEEVIK
257 - 278	2328.19	2327.19	2327.17	0.02	0	AGATTLNIPDTVGYTLPYEFGK
285 - 319	3500.78	3499.77	3499.72	0.05	0	ANTPGIENAIISTHCQNDLGLATANTLAGAHAGAR
320 - 331	1311.70	1310.70	1310.68	0.01	0	QLEVTINGIGER Pyro-glu (N-term Q)
320 - 331	1328.73	1327.73	1327.71	0.02	0	QLEVTINGIGER
332 - 345	1431.76	1430.76	1430.74	0.02	0	AGNASLEEVVMAIK
332 - 345	1447.77	1446.76	1446.74	0.03	0	AGNASLEEVVMAIK Oxidation (M)
349 - 368	2163.08	2162.08	2162.10	-0.03	0	ELLGGLYTGINTQHITMSSK
349 - 368	2179.14	2178.14	2178.10	0.04	0	ELLGGLYTGINTQHITMSSK Oxidation (M)
369 - 382	1626.84	1625.83	1625.81	0.02	0	MVQEHSGLHVQPHK
383 - 403	2182.09	2181.09	2181.06	0.02	0	AIVGANAFAHESGIHQDGMLK Oxidation (M)
383 - 405	2457.26	2456.26	2456.23	0.03	1	AIVGANAFAHESGIHQDGMLKYK
406 - 420	1649.85	1648.85	1648.83	0.02	0	GTYEIISPDDIGLTR
421 - 430	1047.60	1046.60	1046.58	0.02	0	ANEFGIVLGK
441 - 458	2222.08	2221.08	2221.08	-0.00	1	LVELGYEITDKEFEDFFK
469 - 487	2218.13	2217.13	2217.12	0.01	1	RVTDEDIEALLSDEIFQPK
470 - 487	2062.04	2061.03	2061.02	0.02	0	VTDEDIEALLSDEIFQPK
488 - 510	2425.27	2424.27	2424.24	0.03	0	VFWSLADVQATCGTLGLSTATVK
520 - 534	1492.76	1491.76	1491.74	0.02	0	IACAVGTGPVDAAYK
535 - 547	1452.86	1451.85	1451.83	0.02	0	AVDDIIQIPTVLR
548 - 565	1944.94	1943.94	1943.91	0.03	0	EYSMTSVTEGIDAIATTR
548 - 565	1960.94	1959.94	1959.91	0.03	0	EYSMTSVTEGIDAIATTR Oxidation (M)
577 - 586	1112.59	1111.58	1111.55	0.03	0	HALTGHSFSR
587 - 603	1635.89	1634.88	1634.86	0.02	0	AFSGSGAALDIVVSSVR
612 - 620	939.53	938.52	938.49	0.03	0	MSSFVGAIK
612 - 620	955.52	954.51	954.48	0.03	0	MSSFVGAIK Oxidation (M)
621 - 630	1079.52	1078.52	1078.49	0.03	0	ASSEVSESQR

Spot 1518

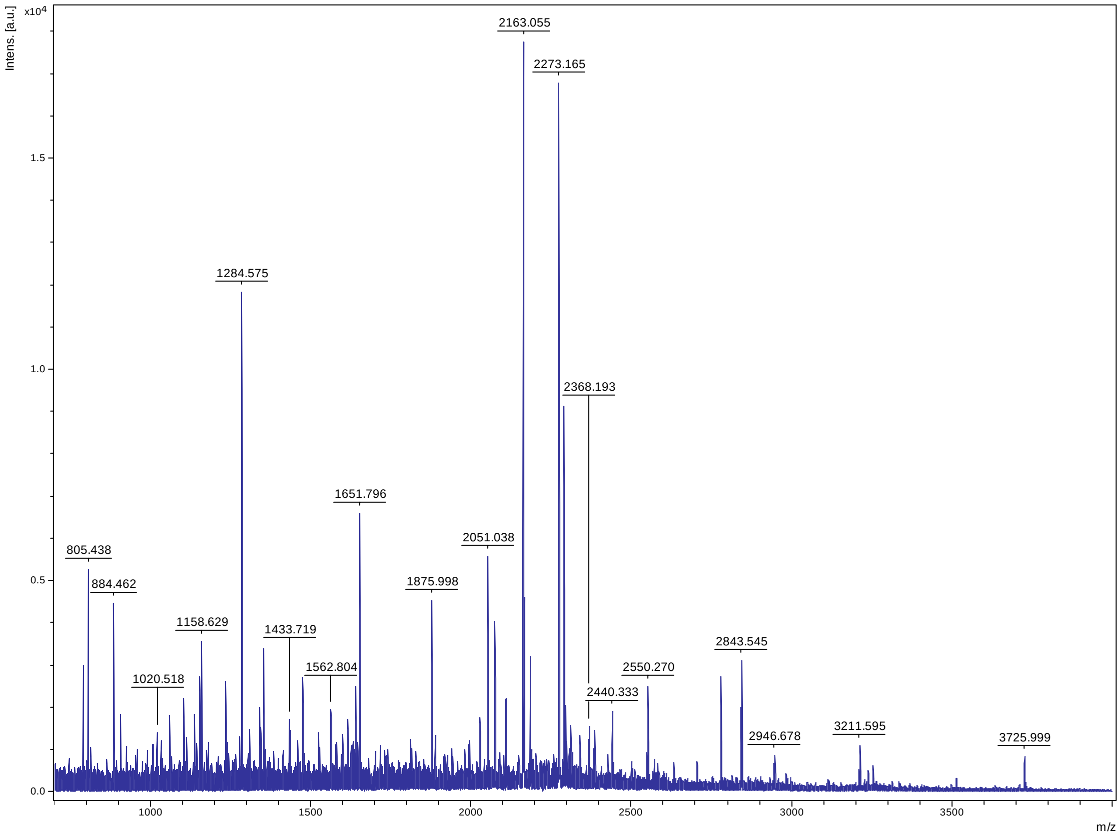


Match to: gi|52076758; Score: 276

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
26 - 37	1339.69	1338.69	1338.68	0.01	0	LASVYSEVQTSR
40 - 49	1102.69	1101.69	1101.67	0.02	0	HALPLPSVLR
50 - 71	2028.03	2027.03	2027.00	0.03	0	SPFALADGPASSAAGNPGEIAK
72 - 97	2778.54	2777.53	2777.51	0.02	0	LFPNLFGQPSVSLVPSPEPASTRPLK
98 - 126	3048.56	3047.56	3047.52	0.04	0	VGVVLSGGQAPGGHNVICGIFDYLQEYAK
145 - 157	1651.83	1650.82	1650.79	0.03	0	YVELTADYVYPYR
158 - 169	1341.59	1340.59	1340.56	0.03	0	NQGGFDMICSGR
180 - 213	3725.83	3724.83	3724.79	0.04	1	QAEDTVNKLDLDGLVVIGGDDSNTNACLLAEYFR
236 - 248	1458.67	1457.67	1457.65	0.02	0	EVPTSFGFDTACK
249 - 262	1599.78	1598.77	1598.74	0.03	0	IYSEMIGNVMTDAR
249 - 262	1615.76	1614.76	1614.74	0.02	0	IYSEMIGNVMTDAR Oxidation (M)
249 - 262	1631.77	1630.76	1630.73	0.03	0	IYSEMIGNVMTDAR 2 Oxidation (M)
267 - 272	884.47	883.47	883.43	0.03	0	YYHFVR
277 - 303	2843.50	2842.50	2842.46	0.04	0	AASHITLECALQTHPNVALIGEEVAAK
321 - 346	2946.63	2945.62	2945.59	0.03	1	RAELGYNYGVILIPEGLIDFIPEVQK
322 - 346	2790.48	2789.48	2789.49	-0.01	0	AELGYNYGVILIPEGLIDFIPEVQK
347 - 367	2306.22	2305.22	2305.20	0.02	0	LIAELNEILAHDVVDEAGAWK
376 - 383	1007.57	1006.56	1006.55	0.01	0	QLFDFLPK
384 - 393	1242.71	1241.70	1241.70	0.01	0	TIQEQLLLER
384 - 403	2288.26	2287.26	2287.23	0.03	1	TIQEQLLLERDPHGNVQVAK
409 - 421	1562.84	1561.84	1561.82	0.02	1	MLIAMVETELEKR
433 - 443	1284.59	1283.59	1283.57	0.02	0	GQSHFFGYEGR
444 - 470	2985.39	2984.39	2984.35	0.04	0	CGLPTIFDSNYCYALGYGSGALLQCGK
526 - 536	1351.72	1350.72	1350.69	0.02	1	FASLRDEWSLK
537 - 567	3253.54	3252.54	3252.51	0.03	0	NHYISPGPIQFSGPGSNDANHTLMLELGAEA Oxidation (M)

Spot 1523

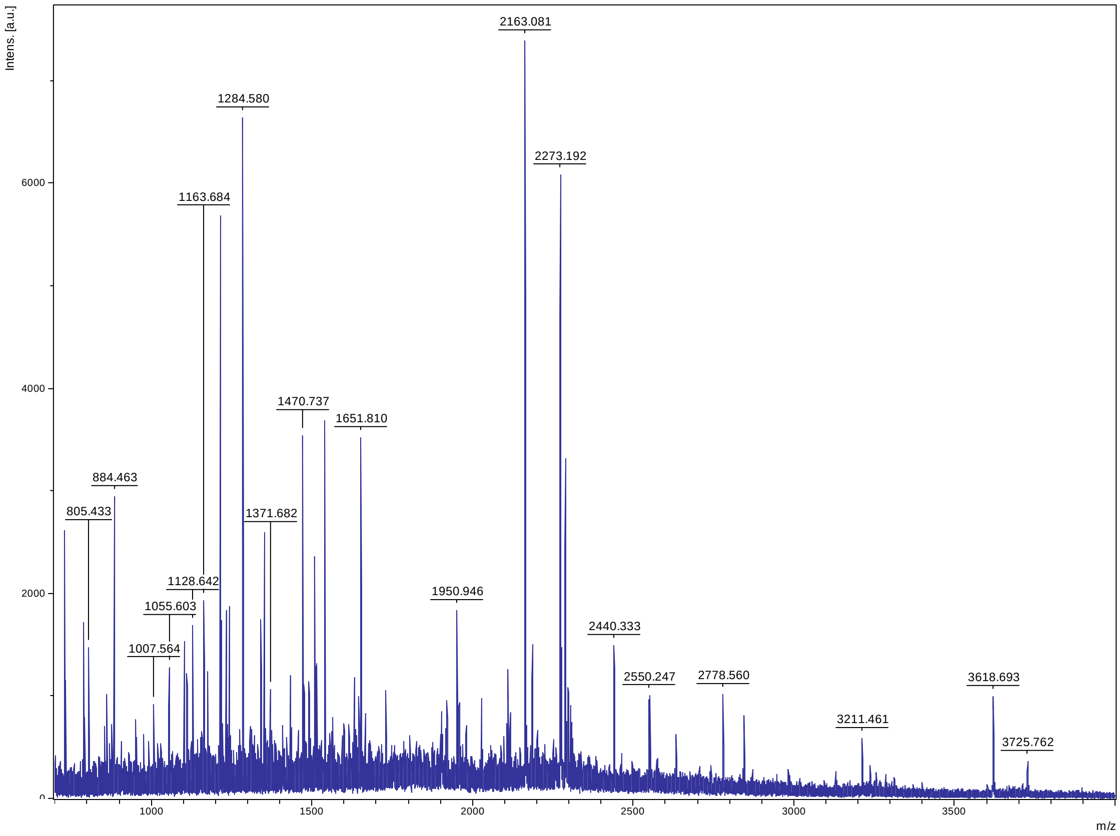


Match to: gi|50931897; Score: 108

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
131 - 144	1431.73	1430.72	1430.74	-0.01	1	SVGDLTAADLEGKR
149 - 166	2028.94	2027.93	2027.94	-0.01	0	ADLNVPLDDNQNITDDTR
169 - 179	1230.73	1229.72	1229.74	-0.01	0	AAIPTIQYLIK
194 - 221	3004.59	3003.59	3003.61	-0.03	1	AEDVIGPDVEKLVSELPNGSVLLLENVR
236 - 254	2062.06	2061.06	2061.06	-0.00	1	KLASLADLYVNDAFGTAHR
237 - 254	1933.97	1932.96	1932.97	-0.01	0	LASLADLYVNDAFGTAHR
265 - 277	1447.84	1446.84	1446.86	-0.02	0	FLKPSVAGFLLQK
278 - 290	1377.69	1376.69	1376.72	-0.03	0	ELDYLVGAVSSPK
291 - 301	1102.62	1101.62	1101.63	-0.01	0	RPFAAIVGGSK

Spot 1526

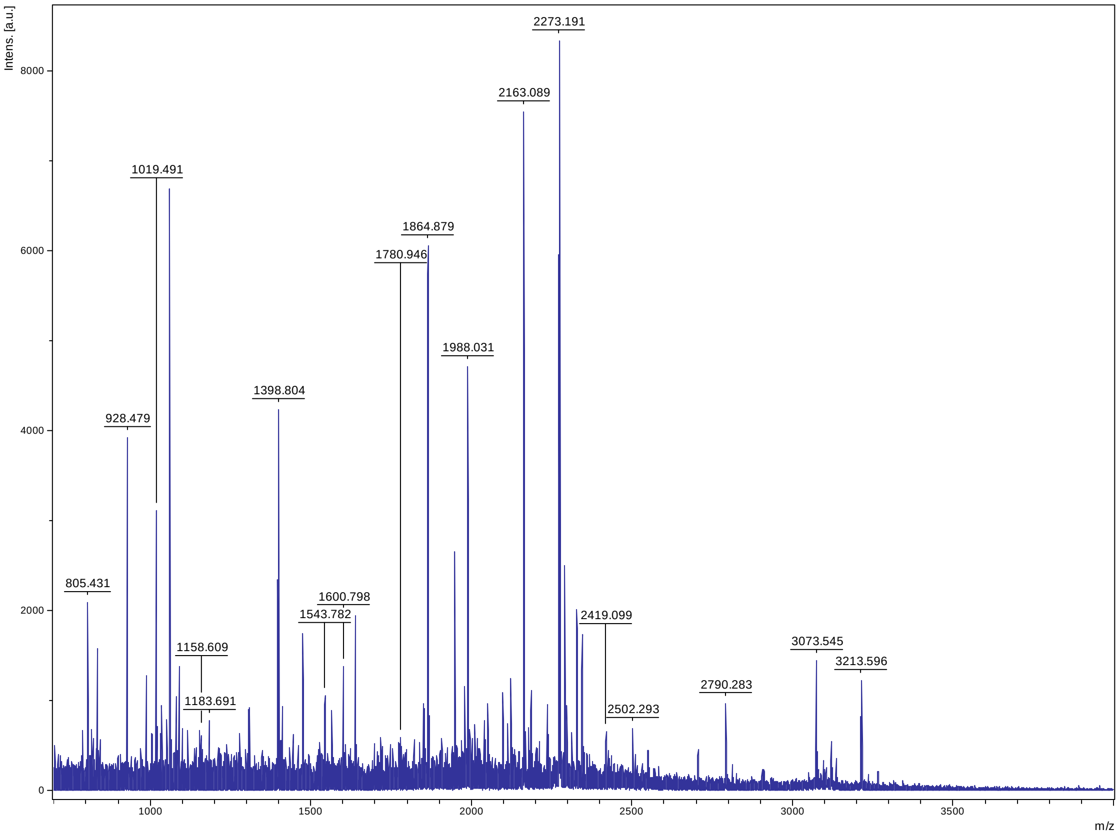


Match to: gi|52076758 Score: 114 Expect: 2.7e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 25	2108.0235	2107.0162	2107.0042	0.0121	0	M.AAAAVAANGGGDGAQASNAPAPTR.L	Acetyl (N-term)
40 - 49	1102.6748	1101.6675	1101.6658	0.0017	0	K.HALPLPSVLR.S	
50 - 71	2028.0031	2026.9958	2026.9959	-0.0001	0	R.SPFALADGPASSAAGNPGEIAK.L	
72 - 97	2778.4979	2777.4906	2777.5115	-0.0209	0	K.LFPNLFGQPSVSLVPSPEPASTRPLK.V	
145 - 157	1651.8121	1650.8048	1650.7929	0.0119	0	K.YVELTADYVYPYR.N	
158 - 169	1341.5992	1340.5919	1340.5601	0.0318	0	R.NQGGFDMICSGR.D	Carbamidomethyl (C)
180 - 213	3725.6721	3724.6648	3724.7889	-0.1241	1	K.QAEDTVNKLDLDGLVVIGGDDSNTNACLLAEYFR.G	Carbamidomethyl (C)
249 - 262	1599.7838	1598.7765	1598.7432	0.0333	0	K.IYSEMIGNVMTDAR.S	
249 - 262	1615.7659	1614.7586	1614.7381	0.0205	0	K.IYSEMIGNVMTDAR.S	Oxidation (M)
249 - 262	1631.8066	1630.7993	1630.7330	0.0663	0	K.IYSEMIGNVMTDAR.S	2 Oxidation (M)
267 - 272	884.4143	883.4070	883.4340	-0.0270	0	K.YYHFVR.L	
277 - 303	2843.3957	2842.3884	2842.4646	-0.0762	0	R.AASHITLECALQTHPNVALIGEEVAAK.K	Carbamidomethyl (C)
309 - 321	1554.7717	1553.7644	1553.7759	-0.0115	1	K.SVTDYITDIVCKR.A	Acetyl (N-term)
347 - 367	2306.2024	2305.1951	2305.1953	-0.0002	0	K.LIAELNEILAHDVVDEAGAWK.S	
376 - 383	1007.5414	1006.5341	1006.5487	-0.0146	0	R.QLFDFLPK.T	
384 - 393	1242.7159	1241.7086	1241.6979	0.0107	0	K.TIQEQLLLER.D	
384 - 403	2288.2566	2287.2493	2287.2284	0.0209	1	K.TIQEQLLLERDPHGNVQVAK.I	
409 - 421	1636.8758	1635.8685	1635.8211	0.0474	1	K.MLIAMVETELEKR.K	Acetyl (N-term); 2 Oxidation (M)
427 - 432	790.3408	789.3335	789.3922	-0.0587	0	K.YPAHFR.G	
433 - 443	1284.5917	1283.5844	1283.5683	0.0162	0	R.GQSHFFGYEGR.C	
504 - 512	1111.5692	1110.5619	1110.6549	-0.0930	1	R.HGKYKPVIK.K	Acetyl (N-term)
526 - 536	1351.7204	1350.7131	1350.6932	0.0200	1	K.FASLRDEWSLK.N	

Spot 1532

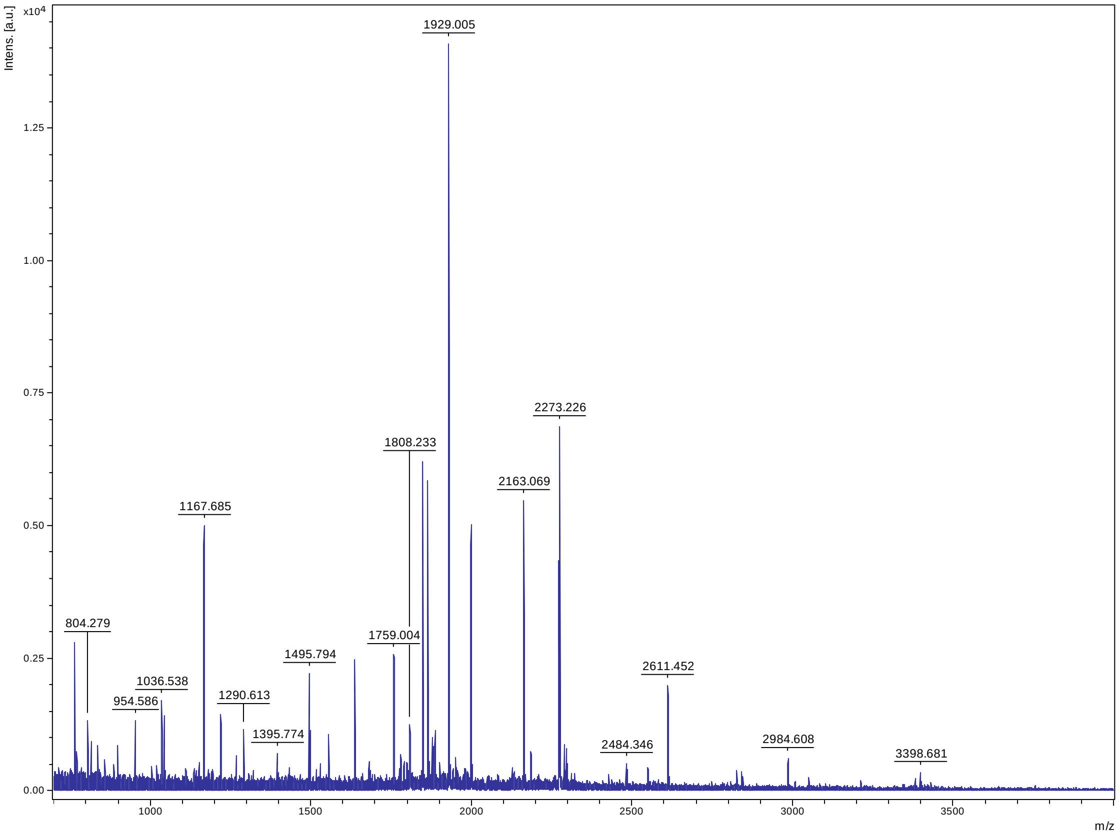


Match to: gi|78708007; Score: 181

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
57 - 67	1183.69	1182.69	1182.66	0.03	0	SIPTKPVEGQK
115 - 126	1411.78	1410.77	1410.75	0.02	1	YFNKDAAQIITK
141 - 154	1397.82	1396.82	1396.80	0.01	0	NGLLSTPAVSAVIR
181 - 208	3073.54	3072.54	3072.49	0.05	0	FNYSSGQPAPETITDQIYGNTLSISEIK
263 - 283	2328.17	2327.17	2327.13	0.04	0	FVFDAMHAVTGAYADPIFVEK
263 - 283	2344.18	2343.18	2343.12	0.06	0	FVFDAMHAVTGAYADPIFVEK Oxidation (M)
314 - 337	2419.10	2418.10	2418.04	0.05	0	ELVFTMFGSGAPDFGAASDGDGDR
314 - 343	3119.47	3118.47	3118.41	0.05	1	ELVFTMFGSGAPDFGAASDGDGDRNMILGR Oxidation (M)
377 - 386	1034.52	1033.52	1033.49	0.03	0	SMPTSGALDR
377 - 386	1050.50	1049.50	1049.48	0.02	0	SMPTSGALDR Oxidation (M)
387 - 403	1947.06	1946.05	1946.03	0.02	1	VADKLNVPFFEVPTGWK
404 - 413	1099.55	1098.55	1098.52	0.03	0	FFGNLMDAGK
404 - 413	1115.55	1114.54	1114.51	0.03	0	FFGNLMDAGK Oxidation (M)
414 - 430	1864.88	1863.88	1863.84	0.03	0	LSICGEESFGTGSDHIR
414 - 432	2122.03	2121.03	2120.98	0.05	1	LSICGEESFGTGSDHIREK
458 - 466	987.57	986.57	986.54	0.03	0	LVSVEDVAR
458 - 474	1988.03	1987.03	1986.99	0.04	1	LVSVEDVAREHWATYGR
467 - 474	1019.49	1018.49	1018.46	0.03	0	EHWATYGR
493 - 498	816.41	815.41	815.38	0.03	0	MMEHLR
510 - 534	2790.28	2789.28	2789.23	0.05	0	YGNYTLQFADDFSYTDPVDGSTVSK
539 - 546	928.48	927.48	927.44	0.03	0	FVFTDGSR
596 - 602	836.48	835.47	835.46	0.02	1	LKDFTGR

Spot 1536

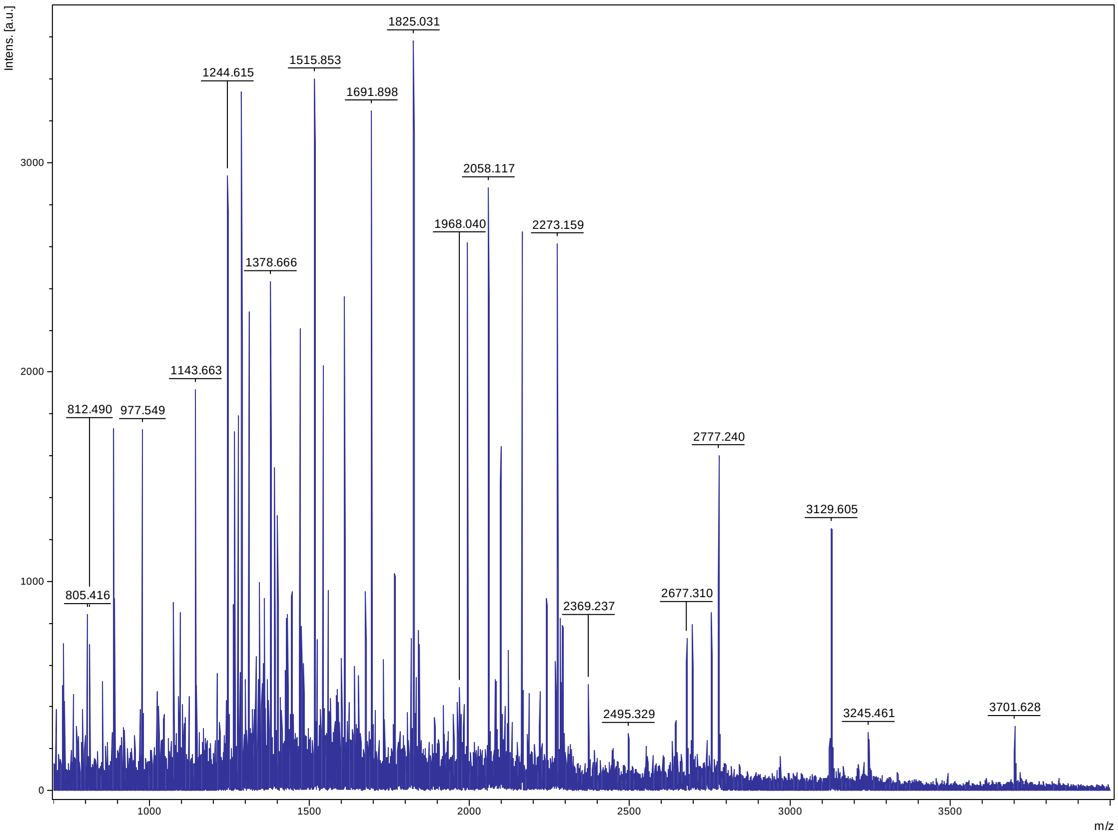


Match to: gi|77554291; Score: 256

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
41 - 47	836.42	835.42	835.41	0.01	0	DIAFDQK
59 - 70	1167.69	1166.68	1166.68	0.01	0	LANAVGVTLGPR
73 - 83	1220.61	1219.61	1219.61	-0.00	0	NVVLDEYGSPK
84 - 93	1043.59	1042.59	1042.58	0.01	0	VVNDGVTIAR
94 - 110	1846.94	1845.94	1845.93	0.01	0	AIELYDPMENAGAALIR
94 - 110	1862.94	1861.93	1861.92	0.01	0	AIELYDPMENAGAALIR Oxidation (M)
116 - 132	1636.78	1635.77	1635.77	0.00	0	TNDSAGDGTTTASVLAR
137 - 152	1555.90	1554.90	1554.90	0.00	0	LGLLSVTSGANPVSLK
158 - 168	1267.67	1266.67	1266.68	-0.01	0	TVHGLIEELEK
158 - 169	1395.77	1394.77	1394.78	-0.01	1	TVHGLIEELEKK
233 - 245	1495.79	1494.79	1494.77	0.02	0	GYISPQFVTNLEK
246 - 254	1036.54	1035.54	1035.52	0.01	0	SIVEFENAK
255 - 261	816.48	815.48	815.48	0.01	0	VLITDQK
267 - 274	954.59	953.58	953.58	0.00	0	EILPILEK
304 - 312	898.57	897.57	897.56	0.00	0	GILNVAAIK
321 - 338	1887.10	1886.10	1886.09	0.01	1	KAVLQDIAIVTGAEFLAK
322 - 338	1759.00	1758.00	1757.99	0.01	0	AVLQDIAIVTGAEFLAK
339 - 356	1929.01	1928.00	1927.99	0.02	0	DLGLLVENATEEQLGTAR
387 - 403	1998.97	1997.97	1997.94	0.03	1	ELSETDSIYDTEKLAER
416 - 427	1290.61	1289.61	1289.61	0.00	0	VGAATETELEDR
436 - 465	2984.61	2983.61	2983.57	0.04	0	NATFAAIEEGIVPGGGTAYVHLSTTVPAIK
475 - 482	857.52	856.52	856.50	0.02	0	LGADIIQK
483 - 505	2273.23	2272.22	2272.24	-0.02	0	ALVAPASLIAHNAGVEGEVVVEK

Spot 1537



Match to: gi|5360657 Score: 90 Expect: 5.9e-05

Matched peptides:

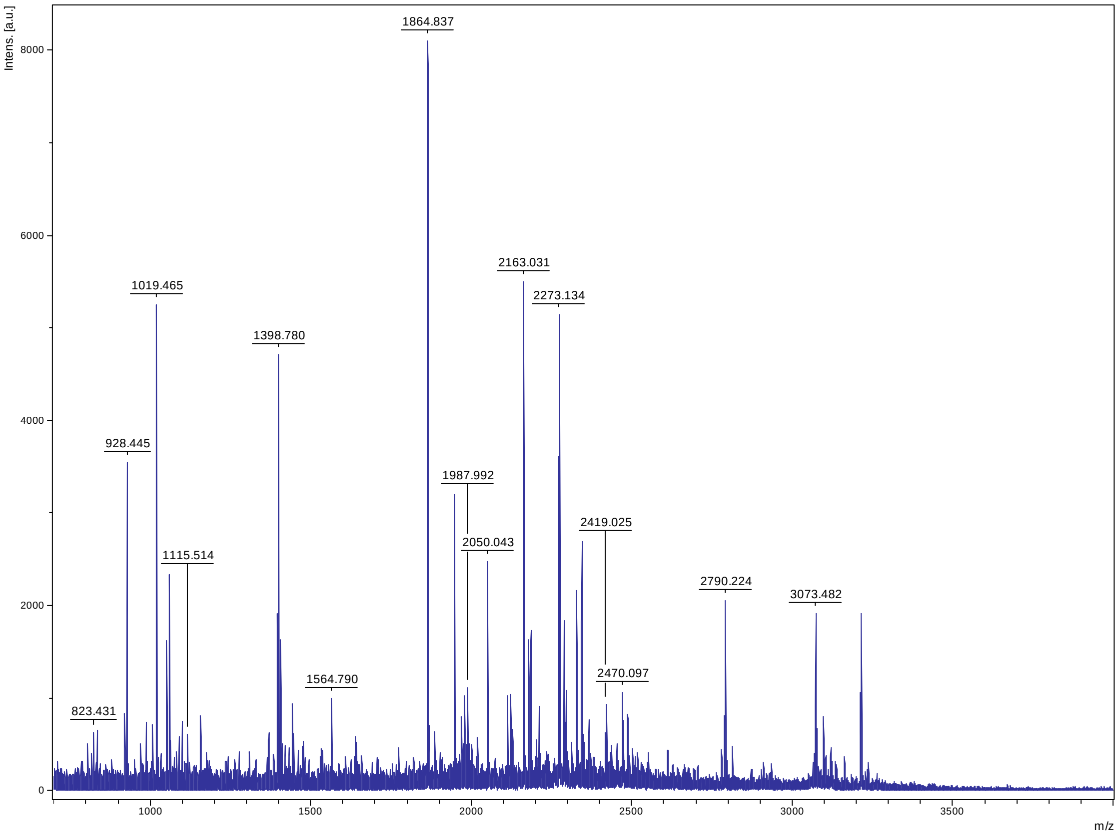
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 12	1198.7181	1197.7108	1197.7557	-0.0449	1	M.ASLVLSLRIAR.S
28 - 34	732.3433	731.3360	731.3860	-0.0500	1	R.RGAVACR.A
35 - 47	1389.7133	1388.7060	1388.7412	-0.0351	0	R.AATFQQLDAVAVR.E
35 - 52	1991.9445	1990.9372	1990.9959	-0.0587	1	R.AATFQQLDAVAVREEESK.F
68 - 82	1790.8191	1789.8118	1789.9297	-0.1179	1	K.RCIFSDHLTPVLAYR.C
91 - 111	2239.9262	2238.9189	2239.0392	-0.1203	0	R.EAPSFLFESVEQGSEGTNVGR.Y
112 - 126	1562.8145	1561.8072	1561.8173	-0.0101	0	R.YSVVGAQPAMEIVAK.A
141 - 150	1218.5583	1217.5510	1217.5863	-0.0352	1	R.REQFAPDPMK.I
142 - 153	1428.7105	1427.7032	1427.7231	-0.0199	1	R.EQFAPDPMKIPR.S
203 - 223	2450.1308	2449.1235	2449.2641	-0.1406	0	R.NLPDIHLGLYNDIVVFDHVEK.K
248 - 256	1043.5618	1042.5545	1042.5771	-0.0225	0	K.NQLEALLSR.L
257 - 271	1522.8421	1521.8348	1521.8514	-0.0166	0	R.LHSVNVPTLTAGSVK.L
284 - 292	1102.6484	1101.6411	1101.4760	0.1651	1	K.SSMSREDYK.K
300 - 315	1824.9466	1823.9393	1823.9893	-0.0500	0	K.EHILAGDIFQVVLSQR.F
319 - 329	1400.6816	1399.6743	1399.6884	-0.0141	1	R.RTFADPFEVYR.A
320 - 329	1244.5831	1243.5758	1243.5873	-0.0115	0	R.TFADPFEVYR.A
333 - 346	1622.8411	1621.8338	1621.8286	0.0052	0	R.IVNPSPYMAYLQAR.G
365 - 376	1310.7866	1309.7793	1309.7830	-0.0037	0	R.TIVNRPLAGTIR.R
458 - 470	1167.6587	1166.6514	1166.6659	-0.0144	0	R.AALPVGTVSGAPK.V
473 - 483	1264.5646	1263.5573	1263.5839	-0.0265	0	R.AMELIDQMEGK.M
486 - 498	1287.5983	1286.5910	1286.6043	-0.0133	0	R.GPYSGGFGGVSFR.G
499 - 508	1074.5408	1073.5335	1073.5539	-0.0204	0	R.GDMDIALALR.T
509 - 517	977.5206	976.5133	976.5341	-0.0208	0	R.TIVFPTGSR.F
518 - 527	1270.5105	1269.5032	1269.5223	-0.0191	0	R.FDTMYSYTDK.N

Match to: gi|11995457 Score: 73 Expect: 0.0033

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
7 - 20	1608.8631	1607.8558	1607.8783	-0.0225	1	R.KEHQFLAELGLAPR.N
8 - 20	1480.7596	1479.7523	1479.7834	-0.0310	0	K.EHQFLAELGLAPR.N
72 - 80	1014.5434	1013.5361	1013.5368	-0.0007	0	K.TWMAIPAPK.R
82 - 93	1326.6974	1325.6901	1325.7415	-0.0514	1	R.GEIVRQIGDALR.A
96 - 101	732.3433	731.3360	731.4191	-0.0830	0	K.LHHLGR.L
204 - 211	886.4993	885.4920	885.5283	-0.0363	0	K.IVASVLER.N
212 - 237	2638.2718	2637.2645	2637.2856	-0.0211	0	R.NNLPGSIFTAFCGGADIGQAISLDTR.I
238 - 248	1149.6268	1148.6195	1148.6441	-0.0246	0	R.IPLVSFTGSTK.V
249 - 260	1342.7113	1341.7040	1341.7186	-0.0146	0	K.VGLMVQQQVNAR.F
249 - 263	1674.8170	1673.8097	1673.9035	-0.0937	1	K.VGLMVQQQVNARFGK.C
288 - 300	1276.7035	1275.6962	1275.6935	0.0028	0	R.SVLFAAVGTAGQR.C
288 - 305	1840.7754	1839.7681	1839.9083	-0.1402	1	R.SVLFAAVGTAGQRCTTCR.R
306 - 315	1299.7478	1298.7405	1298.7459	-0.0053	1	R.RLLLHESIYR.T
307 - 315	1143.6391	1142.6318	1142.6448	-0.0129	0	R.LLLHESIYR.T
316 - 326	1354.7116	1353.7043	1353.7180	-0.0136	0	R.TFLDQLVEVYK.Q
330 - 349	2058.0232	2057.0159	2057.0905	-0.0746	0	R.IGDPLENGTLLGPLHTPASR.D
433 - 439	888.4869	887.4796	887.5229	-0.0432	0	K.RPDIIFK.W
471 - 484	1378.6393	1377.6320	1377.6272	0.0048	1	K.ATGGGREAGSDSWK.Q

Spot 1540

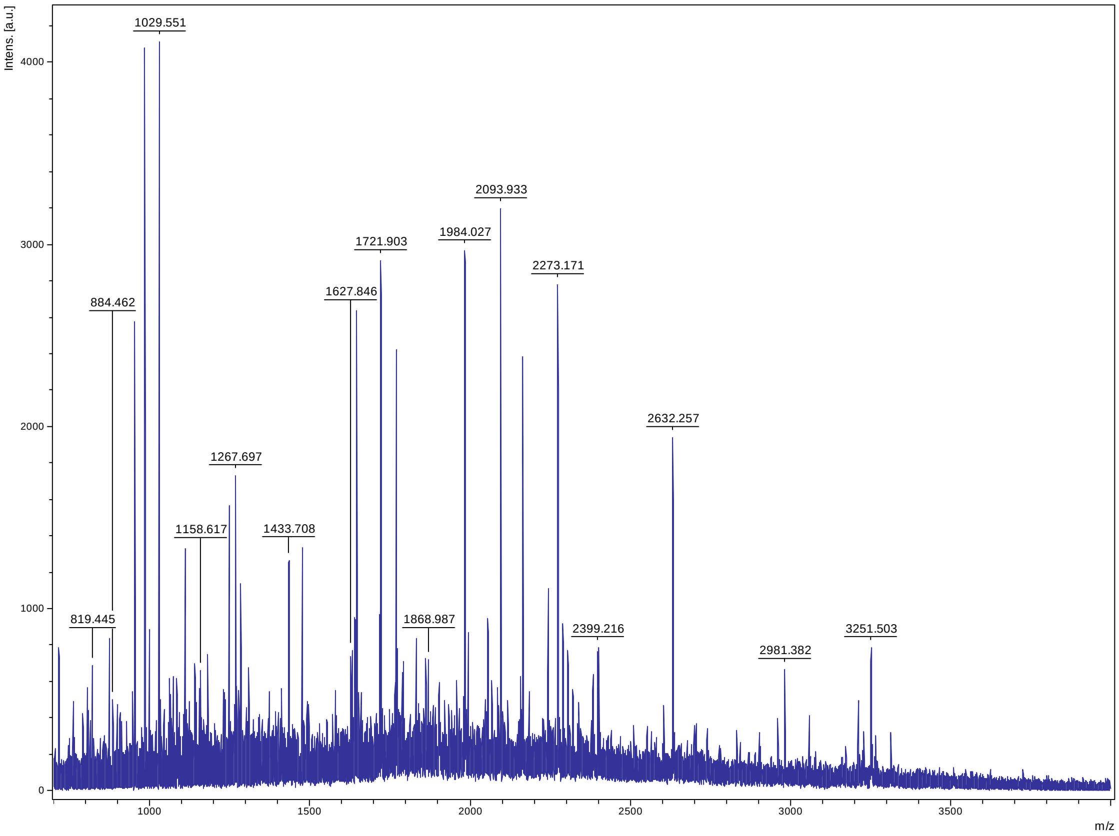


Match to: gi|78708007; Score: 138

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
141 - 154	1397.79	1396.78	1396.80	-0.02	0	NGLLSTPAVSAVIR
157 - 180	2470.10	2469.09	2469.11	-0.02	0	QANGGFIMSASHNPGGPDNDWGIK
181 - 208	3073.48	3072.48	3072.49	-0.01	0	FNYSSGQPAPETITDQIYGNTLSISEIK
263 - 283	2328.11	2327.11	2327.13	-0.02	0	FVFDAMHAVTGAYADPIFVEK
263 - 283	2344.12	2343.11	2343.12	-0.01	0	FVFDAMHAVTGAYADPIFVEK Oxidation (M)
314 - 337	2419.03	2418.02	2418.04	-0.02	0	ELVFTMFGSGAPDFGAASDGDGDR
387 - 403	1947.02	1946.02	1946.03	-0.01	1	VADKLNVPFFEVPTGWK
404 - 413	1099.51	1098.51	1098.52	-0.01	0	FFGNLMDAGK
404 - 413	1115.51	1114.51	1114.51	0.00	0	FFGNLMDAGK Oxidation (M)
414 - 430	1864.84	1863.83	1863.84	-0.01	0	LSICGEESFGTGSDHIR
414 - 432	2121.97	2120.97	2120.98	-0.01	1	LSICGEESFGTGSDHIREK
458 - 466	987.54	986.54	986.54	0.00	0	LVSVEDVAR
458 - 474	1987.99	1986.99	1986.99	-0.00	1	LVSVEDVAREHWATYGR
467 - 474	1019.46	1018.46	1018.46	0.00	0	EHWATYGR
475 - 492	2274.88	2273.88	2273.92	-0.04	1	NFFSRYDYEECESESANK
510 - 534	2790.22	2789.22	2789.23	-0.01	0	YGNYTLQFADDFSYTDPVDGSTVSK
539 - 546	928.45	927.44	927.44	-0.00	0	FVFTDGSR
596 - 602	836.46	835.46	835.46	0.00	1	LKDFTGR

Spot 1545

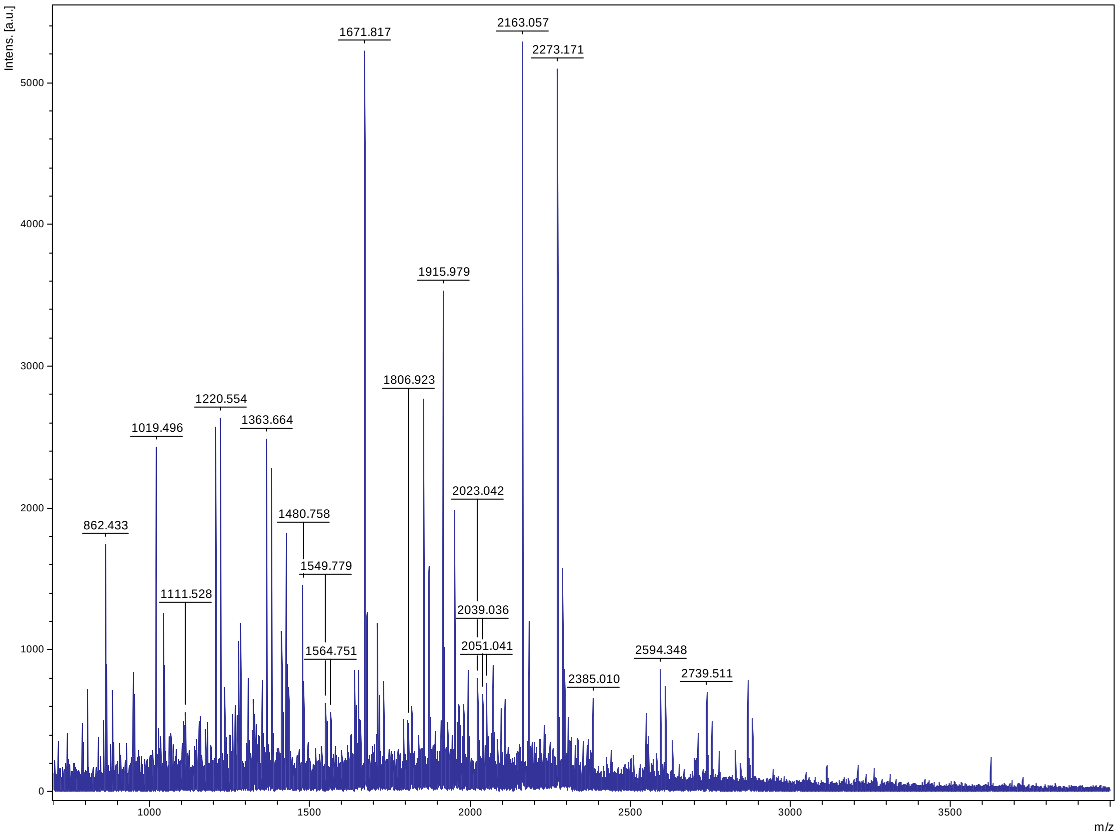


Match to: gi|34907404 Score: 68 Expect: 0.011

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
188 - 194	873.3210	872.3137	872.3664	-0.0527	0	R.YGDDTFR.W	
195 - 202	984.4523	983.4450	983.4825	-0.0374	0	R.WAPPQTER.D	
203 - 224	2157.9910	2156.9837	2157.0014	-0.0177	0	R.DGYWPPAAAGSAADEDALGVPK.G	
241 - 262	2321.0765	2320.0692	2320.1044	-0.0352	0	K.TVGEAVAAAPDYGDEMFVVHVK.E	Oxidation (M)
268 - 288	2185.0642	2184.0569	2184.1459	-0.0890	1	K.ETVNVPLEKTNVVVVGDGMGK.T	
268 - 288	2243.0709	2242.0636	2242.1514	-0.0878	1	K.ETVNVPLEKTNVVVVGDGMGK.T	Acetyl (N-term); Oxidation (M)
321 - 339	1983.9964	1982.9891	1982.9810	0.0082	0	R.DLTISNTAGPDAHQAVAFR.S	
345 - 365	2383.1357	2382.1284	2382.2001	-0.0717	0	R.TVLDTVELLGHQDTLYAHAMR.Q	
345 - 365	2399.1509	2398.1436	2398.1951	-0.0514	0	R.TVLDTVELLGHQDTLYAHAMR.Q	Oxidation (M)
373 - 389	1768.9483	1767.9410	1767.9155	0.0256	0	R.VSGTVDFVFGNSATVLR.D	
390 - 398	997.5777	996.5704	996.5968	-0.0263	0	R.DTALIVLPR.Q	
399 - 415	1869.0026	1867.9953	1867.9500	0.0454	1	R.QLRPEKGENDAVTAQGR.T	
416 - 427	1267.7174	1266.7101	1266.6932	0.0169	0	R.TDPAQPTGIVLR.G	
443 - 457	1860.9622	1859.9549	1859.9794	-0.0245	0	R.EKPDVHHVYLGRPWK.E	
462 - 476	1721.9011	1720.8938	1720.8818	0.0121	0	R.TVYVGCTLSEIVQPR.G	Carbamidomethyl (C)
477 - 488	1411.6875	1410.6802	1410.6390	0.0412	0	R.GWMAWNGDFALK.T	Oxidation (M)
489 - 509	2093.9069	2092.8996	2092.8973	0.0023	0	K.TLYYGEYESAGPGGDGASGSR.I	
519 - 538	2304.1489	2303.1416	2303.1586	-0.0169	1	R.DHVDVYSVASFIQGDKWIPK.I	

Spot 1547

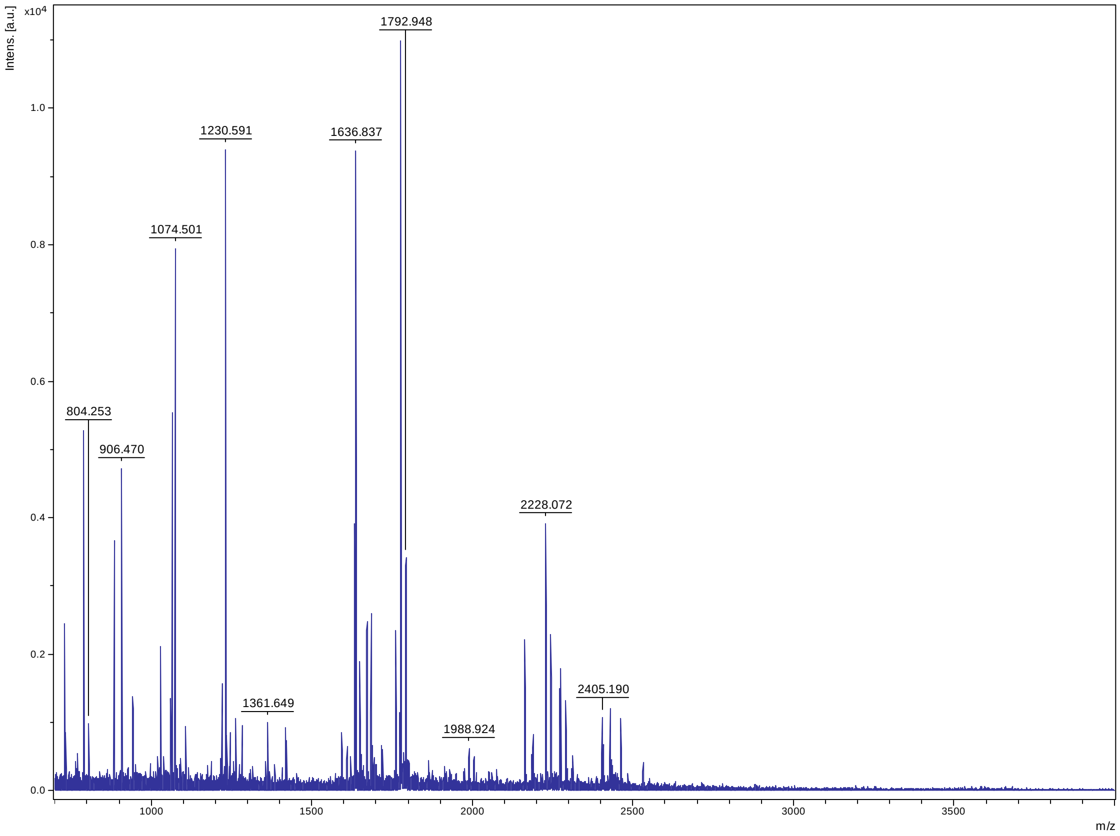


Match to: gi|3915054 Score: 97 Expect: 6.5e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
20 - 37	1915.9790	1914.9717	1914.9799	-0.0081	0	R.IGDSLSAHTNELVAVFSR.L	
44 - 66	2594.3477	2593.3404	2593.2958	0.0446	1	K.GMLQPHQIIAEYNAAIPEGEREK.L	
44 - 66	2610.3430	2609.3357	2609.2907	0.0450	1	K.GMLQPHQIIAEYNAAIPEGEREK.L	Oxidation (M)
157 - 167	1204.6123	1203.6050	1203.6360	-0.0309	0	K.SIGNGVQFLNR.H	
173 - 188	2023.0420	2022.0347	2022.0396	-0.0049	1	K.LFHDKESMYPLLNFLR.A	
173 - 188	2039.0365	2038.0292	2038.0346	-0.0053	1	K.LFHDKESMYPLLNFLR.A	Oxidation (M)
189 - 202	1729.7999	1728.7927	1728.7382	0.0545	1	R.AHNYKGMTMMLNDR.I	3 Oxidation (M)
205 - 214	1043.5397	1042.5324	1042.5771	-0.0447	0	R.SLDALQGALR.K	
219 - 235	1951.9346	1950.9273	1950.9336	-0.0063	0	K.HLAGITADTPYSEFHHR.F	
244 - 251	949.3570	948.3497	948.3872	-0.0375	0	K.GWGDCAQR.V	Carbamidomethyl (C)
317 - 325	1106.4968	1105.4896	1105.5260	-0.0364	0	R.AMENEMLLR.I	
317 - 327	1363.6644	1362.6572	1362.6999	-0.0427	1	R.AMENEMLLRIK.Q	Oxidation (M)
317 - 327	1379.6639	1378.6567	1378.6948	-0.0381	1	R.AMENEMLLRIK.Q	2 Oxidation (M)
326 - 336	1267.6914	1266.6841	1266.7408	-0.0567	1	R.IKQQGLNITPR.I	
328 - 336	1026.5394	1025.5322	1025.5618	-0.0296	0	K.QQGLNITPR.I	
343 - 355	1425.6653	1424.6580	1424.6830	-0.0250	0	R.LLPDAHGTTCGQR.L	Carbamidomethyl (C)
370 - 380	1275.6719	1274.6646	1274.6731	-0.0085	1	R.VPFRTENGTVR.K	
432 - 445	1549.7791	1548.7718	1548.8082	-0.0364	0	K.LGVTHCTIAHALEK.T	Carbamidomethyl (C)
446 - 456	1414.6581	1413.6508	1413.6928	-0.0420	1	K.TKYPNSDLYWK.K	
524 - 545	2550.2578	2549.2505	2549.2260	0.0246	1	K.FNIVSPGADMSIYFPFTESQKR.L	Oxidation (M)

Spot 1549

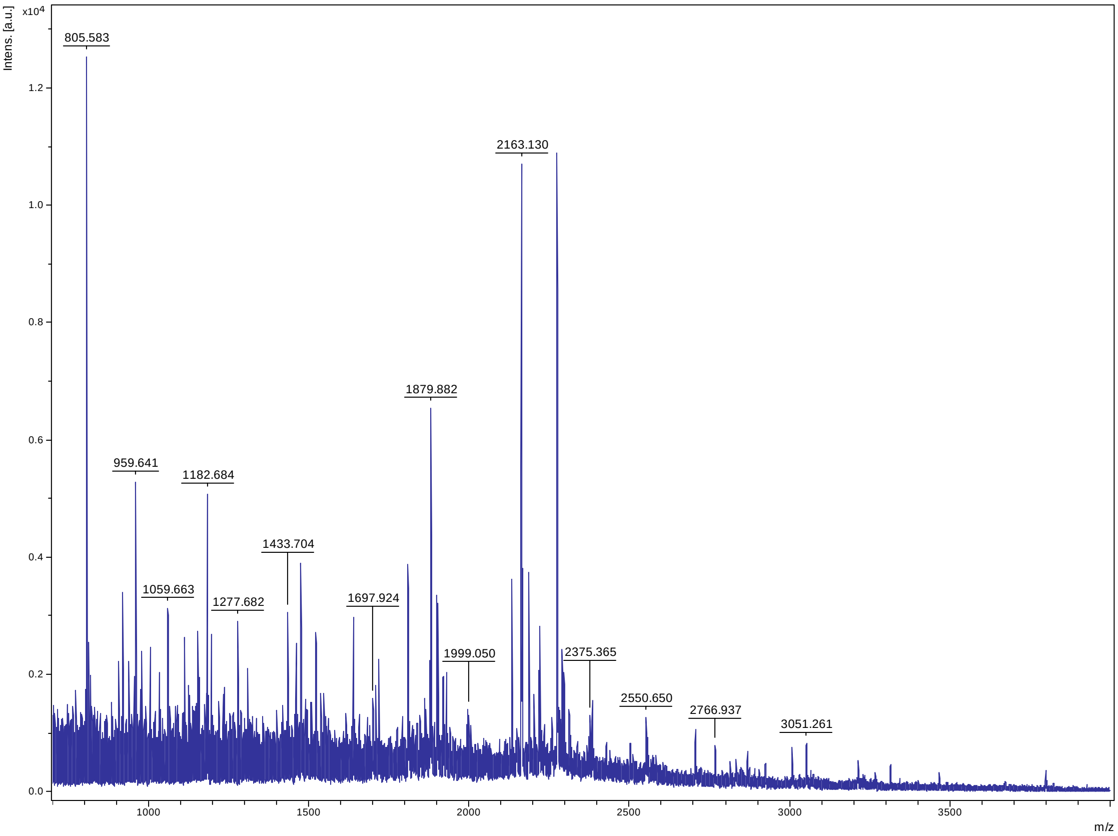


Match to: gi|50912399 Score: 124 Expect: 2.8e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
104 - 114	1174.4371	1173.4298	1173.5261	-0.0963	0	R.VAEGDAEDVNR.A	
121 - 130	1230.4641	1229.4568	1229.5941	-0.1373	1	R.RAFDEGPWPR.M	
122 - 130	1074.3184	1073.3111	1073.4930	-0.1819	0	R.AFDEGPWPR.M	
143 - 164	2429.1844	2428.1771	2428.1546	0.0225	0	R.FADLIEQHADEIAALETWDGGK.T	
325 - 344	2228.0772	2227.0699	2227.0579	0.0120	0	K.SPFIVMDDADVDQAVELAHR.A	
345 - 359	1775.7239	1774.7166	1774.7337	-0.0171	0	R.ALFFNQGQCCCAGSR.T	3 Carbamidomethyl (C)
382 - 403	2403.2159	2402.2086	2402.1865	0.0221	1	R.VVGDPFRTGVEQGPQIDGEQFK.K	
389 - 403	1632.7534	1631.7461	1631.7791	-0.0329	0	R.TGVEQGPQIDGEQFK.K	
389 - 404	1760.8471	1759.8398	1759.8740	-0.0342	1	R.TGVEQGPQIDGEQFKK.I	
411 - 425	1361.5653	1360.5580	1360.6582	-0.1002	0	K.SGVDSGATLVAGGDR.A	
430 - 446	1988.8822	1987.8749	1987.9237	-0.0487	0	R.GFYIQPTVFADVEDEMK.I	
447 - 461	1671.8812	1670.8739	1670.9243	-0.0503	0	K.IAQEEIFGPVQSILK.F	
462 - 470	1065.3614	1064.3541	1064.5502	-0.1960	0	K.FSTVEEVVR.R	
462 - 471	1221.5187	1220.5114	1220.6513	-0.1399	1	K.FSTVEEVVRR.A	
471 - 487	1792.9086	1791.9013	1791.9379	-0.0366	1	R.RANATPYGLAAGVFTQR.L	
472 - 487	1636.8066	1635.7993	1635.8368	-0.0375	0	R.ANATPYGLAAGVFTQR.L	
500 - 521	2405.2238	2404.2165	2404.1738	0.0427	0	R.VGTVWVNTYDVFDAAVPFGGYK.M	
542 - 553	1283.6251	1282.6178	1282.7285	-0.1107	1	K.AVVTPIKDAAWL.-	

Spot 1554

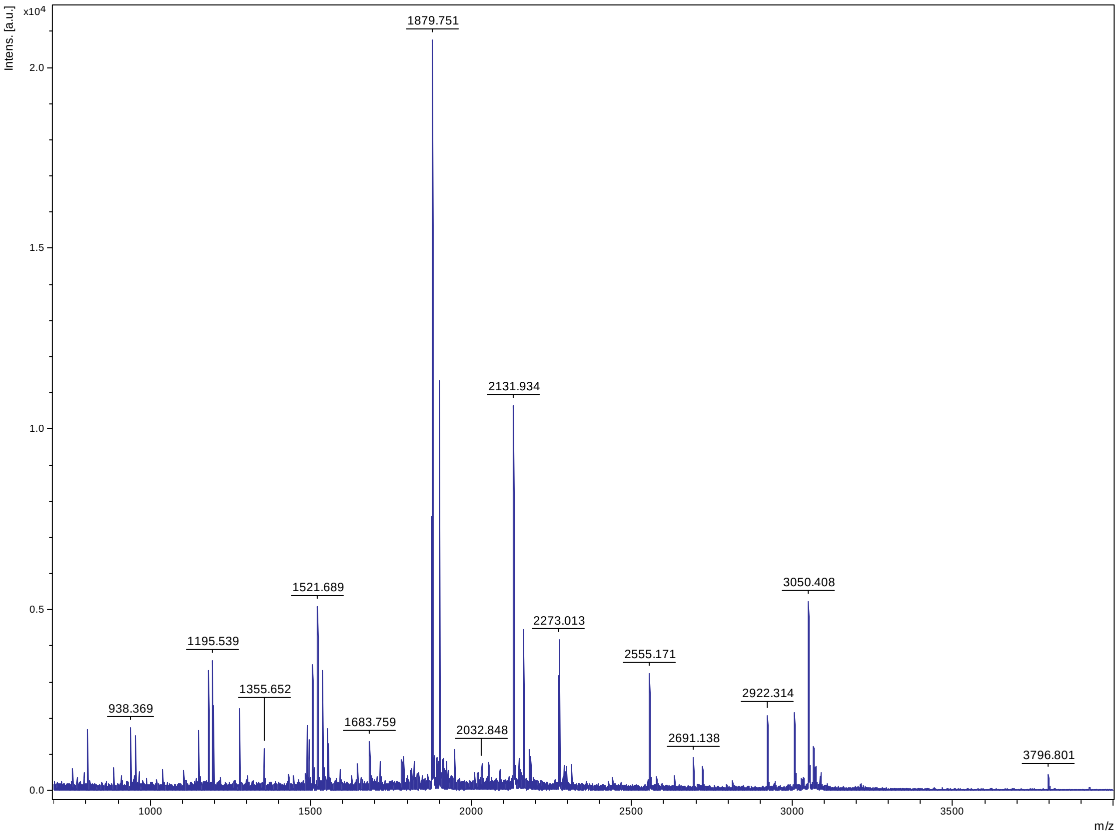


Match to: Q5WA72_ORYSA Score: 99 Expect: 8.4e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
66 - 79	1545.7335	1544.7262	1544.7616	-0.0354	0	R.AQSMVLVLDNDNAR.R
80 - 99	2375.3650	2374.3577	2374.1739	0.1838	1	R.RAVEENAEVLLLGYAPWCER.S Carbamidomethyl (C)
81 - 99	2219.1189	2218.1116	2218.0728	0.0389	0	R.AVEENAEVLLLGYAPWCER.S Carbamidomethyl (C)
100 - 106	802.6110	801.6037	801.4167	0.1871	0	R.SAQLMPR.F
100 - 106	818.6188	817.6116	817.4116	0.2000	0	R.SAQLMPR.F Oxidation (M)
107 - 115	919.6151	918.6078	918.4923	0.1156	0	R.FAEAAAALR.A
126 - 133	977.6146	976.6073	976.4978	0.1095	1	K.LDGERYPK.A
164 - 171	959.6409	958.6337	958.5236	0.1101	0	K.DAIVTWVR.K
185 - 192	938.5643	937.5570	937.4392	0.1178	0	K.DSAEEFLK.K
194 - 203	1125.6254	1124.6181	1124.5866	0.0315	0	K.DQTFAVGLFK.N
204 - 215	1461.6598	1460.6525	1460.6459	0.0066	0	K.NFEGAEYEEFVK.A
216 - 231	1809.8267	1808.8194	1808.8176	0.0018	0	K.AATSENEVQFVETNDR.N
232 - 252	2273.3000	2272.2928	2272.2830	0.0098	1	R.NVAKILFPGIASEEQFLGLVK.S
406 - 414	954.5800	953.5727	953.5657	0.0070	1	K.GPIEKVVGR.T
502 - 509	906.6449	905.6376	905.4640	0.1736	1	K.SNLKDMAK.F
515 - 533	1999.0503	1998.0430	1998.0520	-0.0090	1	K.LQIADVETVAAGDIVKDEL.-

Spot 1557

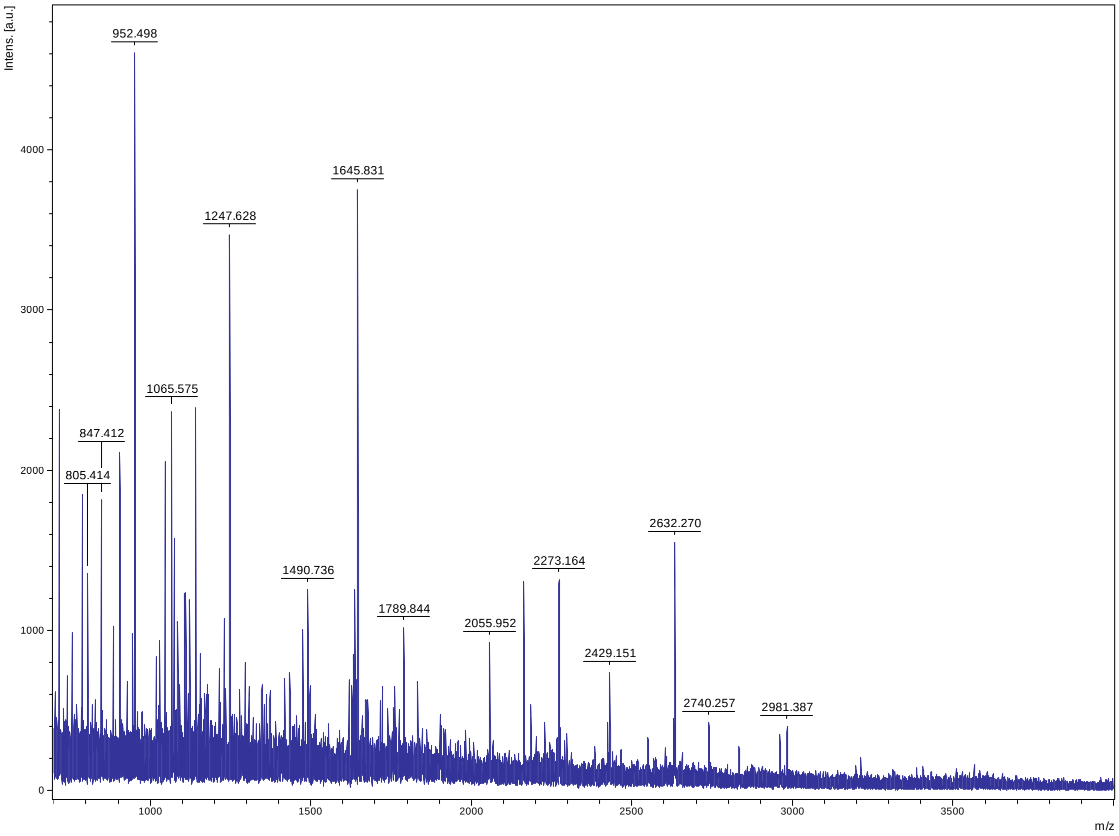


Match to: gi|62546209; Score: 285

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
57 - 73	2180.83	2179.83	2179.94	-0.11	0	HPFMVVEFYAPWCGHCK Oxidation (M)
57 - 74	2292.95	2291.95	2292.04	-0.10	1	HPFMVVEFYAPWCGHCKK
105 - 121	1947.95	1946.95	1947.08	-0.13	1	NKPLATKYEIQGFPTLK
112 - 121	1195.54	1194.54	1194.63	-0.09	0	YEIQGFPTLK
129 - 137	1104.47	1103.47	1103.57	-0.10	1	NIQEYKGPR
138 - 147	1150.50	1149.50	1149.59	-0.09	0	EAEGIVEYLK
138 - 148	1278.59	1277.59	1277.69	-0.10	1	EAEGIVEYLKK
196 - 213	2148.91	2147.90	2148.06	-0.16	1	LRSDYDFGHTLHANHLPR
214 - 224	1182.58	1181.58	1181.65	-0.08	0	GDAAVERPLVR
225 - 237	1536.71	1535.71	1535.82	-0.11	0	LFKPFDELVVDSK
225 - 246	2555.17	2554.17	2554.32	-0.15	1	LFKPFDELVVDSKDFDVTALEK
238 - 246	1037.45	1036.44	1036.51	-0.06	0	DFDVTALEK
247 - 255	965.40	964.40	964.49	-0.09	0	FIDASSTPK
256 - 271	1899.88	1898.87	1898.99	-0.12	1	VVTFDKNPDNHPYLLK
272 - 279	885.40	884.40	884.44	-0.04	0	FFQSSAAK
296 - 308	1506.60	1505.59	1505.70	-0.11	1	SVYYGAAEEFKDK
312 - 330	2131.93	2130.93	2131.07	-0.14	0	FLIGDIEASQGAFQYFGLR
312 - 345	3796.80	3795.80	3795.94	-0.14	1	FLIGDIEASQGAFQYFGLREDQVPLIIIQDGESK
331 - 345	1683.76	1682.76	1682.87	-0.12	0	EDQVPLIIIQDGESK
350 - 362	1521.69	1520.69	1520.80	-0.11	0	AHVEPDQIVSWLK
375 - 400	2922.31	2921.31	2921.48	-0.17	1	SEPIPEVNDEPVKVVVADNVHDFVFK
388 - 400	1488.67	1487.67	1487.78	-0.11	0	VVVADNVHDFVFK
404 - 418	1879.75	1878.75	1878.85	-0.11	0	NVLVEFYAPWCGHCK
420 - 432	1355.65	1354.65	1354.77	-0.12	0	LAPILDEAATTLK
442 - 469	3065.28	3064.28	3064.40	-0.12	0	MDATANDVPSEFDVQGYPTLYFVTPSGK Oxidation (M)
470 - 477	938.37	937.37	937.43	-0.07	0	MVPYESGR
470 - 477	954.37	953.37	953.43	-0.06	0	MVPYESGR Oxidation (M)

Spot 1559

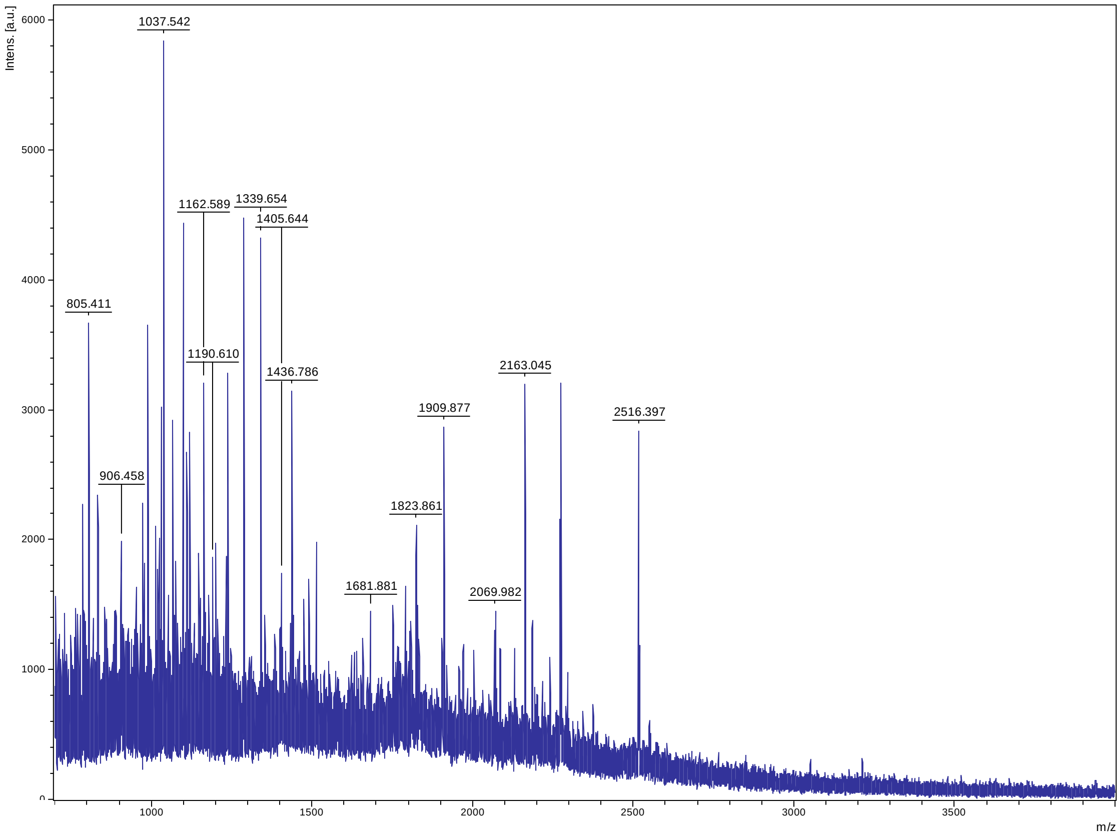


Match to: gi|55296000 Score: 120 Expect: 6.7e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
15 - 23	847.3172	846.3099	846.3831	-0.0732	0	R.AGEGAGTER.L	
54 - 68	1789.8382	1788.8309	1788.8213	0.0096	1	R.CVFTSDADRDTPHLR.T	Carbamidomethyl (C)
103 - 114	1247.6360	1246.6287	1246.6128	0.0159	0	R.ATPAVPVGGCYR.L	Carbamidomethyl (C)
224 - 242	2055.9745	2054.9672	2054.9327	0.0345	0	K.HVDDNADITISCAPIDGSR.A	Carbamidomethyl (C)
313 - 326	1645.8597	1644.8524	1644.8260	0.0265	0	K.YAHLQDFGSEILPR.A	
372 - 379	952.4464	951.4391	951.4814	-0.0423	0	K.TPFFTSPR.Y	
380 - 388	1086.6065	1085.5992	1085.6233	-0.0241	1	R.YLPPARLEK.C	
391 - 417	2981.4385	2980.4312	2980.4270	0.0043	1	K.IKDAIISDGCSFSECTIEHSVIGISSR.V	2 Carbamidomethyl (C)
393 - 417	2740.2893	2739.2820	2739.2479	0.0341	0	K.DAIISDGCSFSECTIEHSVIGISSR.V	2 Carbamidomethyl (C)
418 - 425	905.4147	904.4074	904.4688	-0.0613	0	R.VSIGCELK.D	Carbamidomethyl (C)
450 - 459	1027.5461	1026.5388	1026.5709	-0.0321	0	K.VPIGIGENTK.I	
462 - 470	1106.5103	1105.5030	1105.5008	0.0022	0	R.NCIIDMNAR.I	Carbamidomethyl (C)
462 - 470	1122.4855	1121.4782	1121.4957	-0.0175	0	R.NCIIDMNAR.I	Carbamidomethyl (C); Oxidation (M)
474 - 496	2632.2884	2631.2811	2631.2564	0.0247	0	R.NVIIANTQGVQESDHPEEGYYIR.S	

Spot 1565

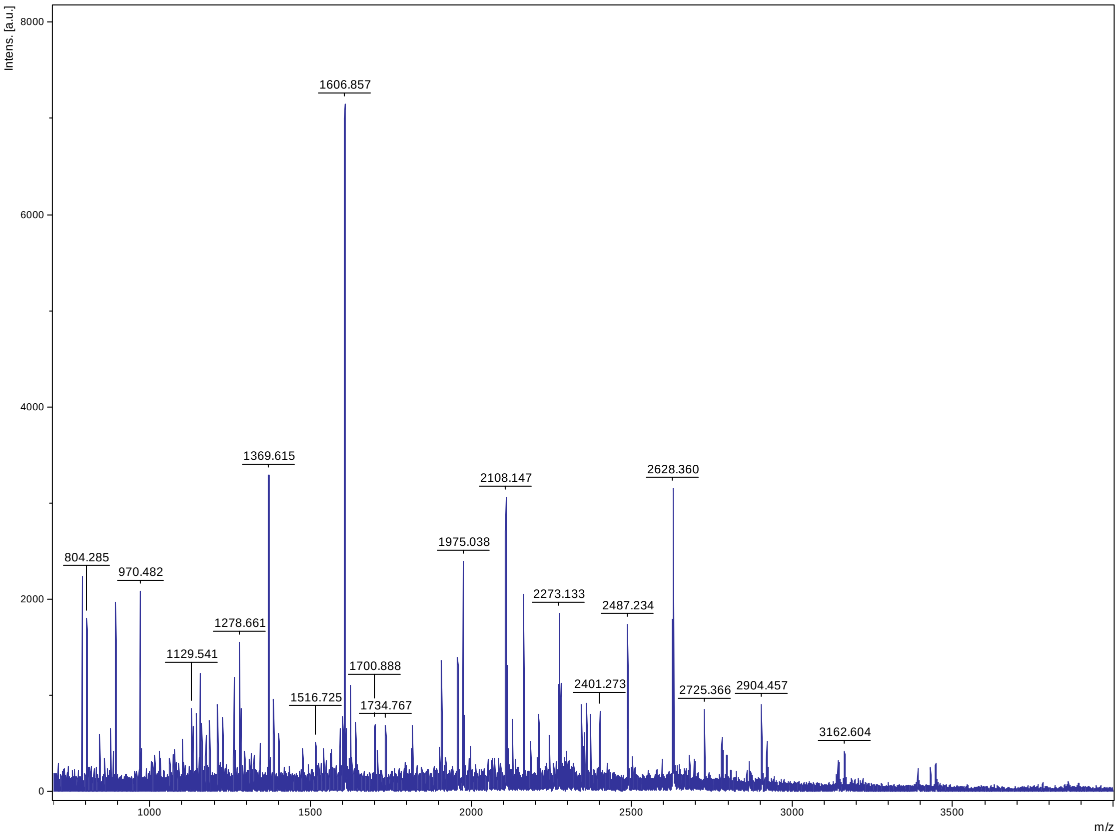


Match to: gi|34898202 Score: 86 Expect: 0.00016

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 19	1790.9509	1789.9436	1789.7835	0.1601	1	-.MGQGTPGGMGKQGGAPGDR.K	2 Oxidation (M)
31 - 40	1099.6259	1098.6186	1098.5822	0.0365	1	R.KFEPPAAPSR.V	
32 - 40	1013.5191	1012.5118	1012.4978	0.0141	0	K.FEPPAAPSR.V	Acetyl (N-term)
76 - 92	2070.0307	2069.0234	2069.0139	0.0096	1	R.VKDYLLMEEEFVAAQER.L	
76 - 92	2086.0727	2085.0654	2085.0088	0.0566	1	R.VKDYLLMEEEFVAAQER.L	Oxidation (M)
207 - 228	2516.3467	2515.3394	2515.3322	0.0073	0	K.EAVELPLTHPELYEDIGIRPPK.G	
229 - 240	1190.6831	1189.6758	1189.6342	0.0416	0	K.GVILYGEPGTGK.T	
246 - 257	1237.7019	1236.6946	1236.6462	0.0484	0	K.AVANSTSATFLR.V	
258 - 266	972.5047	971.4974	971.5651	-0.0677	0	R.VVGSELIQK.Y	
302 - 311	1147.6162	1146.6089	1146.5166	0.0923	1	K.RYDAHSGGER.E	
316 - 330	1751.8888	1750.8815	1750.8559	0.0256	0	R.TMLELLNQLDGFDSR.G	
342 - 354	1436.8701	1435.8628	1435.8147	0.0482	0	R.IESLDPALLRPGR.I	
358 - 367	1199.7420	1198.7347	1198.6961	0.0386	1	R.KIEFPLPDIK.T	
405 - 416	1287.7603	1286.7530	1286.7016	0.0514	0	K.AICTEAGLLALR.E	Carbamidomethyl (C)

Spot 1566



Match to: gi|62900380; Score: 181

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 8	844.48	843.48	843.46	0.02	0	SLRPSER
29 - 37	1161.66	1160.65	1160.56	0.09	1	REDNMVEIR
51 - 76	2401.27	2400.27	2400.28	-0.01	0	DGLPAAAAAAAAASPLLAHSSALQQK
77 - 103	2904.46	2903.45	2903.43	0.02	0	LEGLPAMVQAVQSDDSAVQLEATTQFR
77 - 103	2920.40	2919.40	2919.43	-0.03	0	LEGLPAMVQAVQSDDSAVQLEATTQFR Oxidation (M)
111 - 125	1606.86	1605.85	1605.87	-0.02	0	SPPIEEVINTGVVPR
126 - 132	894.54	893.54	893.51	0.02	0	FIAFLQR
159 - 171	1343.77	1342.77	1342.79	-0.02	0	VVVESGAVPIFVK
172 - 181	1102.57	1101.57	1101.57	0.01	0	LLSSPSEDVR
172 - 197	2725.37	2724.36	2724.37	-0.01	1	LLSSPSEDVREQAVWALGNVAGDSPK
182 - 197	1641.79	1640.79	1640.82	-0.03	0	EQAVWALGNVAGDSPK
200 - 220	2279.20	2278.20	2278.23	-0.03	0	DLVLASGGLYPLLQQLNEHAK
226 - 236	1369.62	1368.61	1368.62	-0.01	0	NATWTLSNFCR
237 - 255	2108.15	2107.14	2107.15	-0.01	0	GKPQPNFEQVKPALSALQR
295 - 312	1959.13	1958.13	1958.14	-0.01	0	LVELLMHPSASVLIPALR
295 - 312	1975.04	1974.04	1974.13	-0.10	0	LVELLMHPSASVLIPALR Oxidation (M)
352 - 365	1592.73	1591.73	1591.74	-0.01	0	EACWTISNITAGNR
394 - 412	1957.01	1956.01	1955.93	0.08	0	EAAWAISNATSGGTHDQIK
413 - 433	2487.23	2486.23	2486.25	-0.02	0	YLVAQGCIKPLCDLLVCPDPR
434 - 447	1600.88	1599.87	1599.89	-0.02	0	IVTVCLEGLENILK

Match to: gi|2443405; Score: 128

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
23 - 31	844.48	843.48	843.43	0.05	1	DGAAAAGRR
32 - 39	886.47	885.46	885.51	-0.05	1	SVVAQRAR
203 - 210	1077.58	1076.57	1076.50	0.07	1	FAYDSYRR
392 - 404	1641.79	1640.79	1640.72	0.07	0	EMMDIEFTVQENR
465 - 496	3162.60	3161.60	3161.61	-0.01	0	VIATGLPASPGAAVGQIVFTAEDAEAWHAQGK
503 - 523	2112.02	2111.02	2111.03	-0.02	0	TETSPEDVGGMHAAVGILTAR
503 - 523	2128.04	2127.03	2127.03	0.01	0	TETSPEDVGGMHAAVGILTAR Oxidation (M)
524 - 539	1600.88	1599.87	1599.79	0.08	1	GGMTSHAAVVARGWGK Oxidation (M)
636 - 646	1369.62	1368.61	1368.58	0.04	0	TEHMFFASDER
636 - 646	1385.58	1384.58	1384.57	0.01	0	TEHMFFASDER Oxidation (M)
652 - 662	1278.66	1277.66	1277.65	0.01	0	QMIMASSLELR
675 - 682	970.48	969.48	969.46	0.02	0	SDFEGIFR
693 - 712	2343.16	2342.16	2342.17	-0.02	0	LLDPPLHEFLPEGHVEDMVR
693 - 712	2359.16	2358.16	2358.17	-0.01	0	LLDPPLHEFLPEGHVEDMVR Oxidation (M)
713 - 728	1734.77	1733.76	1733.79	-0.02	0	ELCSETGAAQDDVLAR
732 - 742	1262.65	1261.65	1261.65	0.00	0	LSEVNPMLGFR
746 - 759	1623.79	1622.79	1622.80	-0.01	0	LGISYPELTEMQAR Oxidation (M)
816 - 824	1015.56	1014.56	1014.55	0.00	0	VGTMIEIPR
856 - 882	3142.62	3141.62	3141.61	0.01	1	DDVGKFLPIYLSQGILQHDPFEVLDQR
861 - 882	2628.36	2627.36	2627.37	-0.02	0	FLPIYLSQGILQHDPFEVLDQR
904 - 922	1975.04	1974.04	1973.97	0.07	0	VGICGEHGGEPLSVAFFAK
923 - 934	1371.64	1370.63	1370.63	0.00	0	AGLDYVSCSPFR
923 - 939	1907.97	1906.97	1906.97	-0.00	1	AGLDYVSCSPFRVPIAR

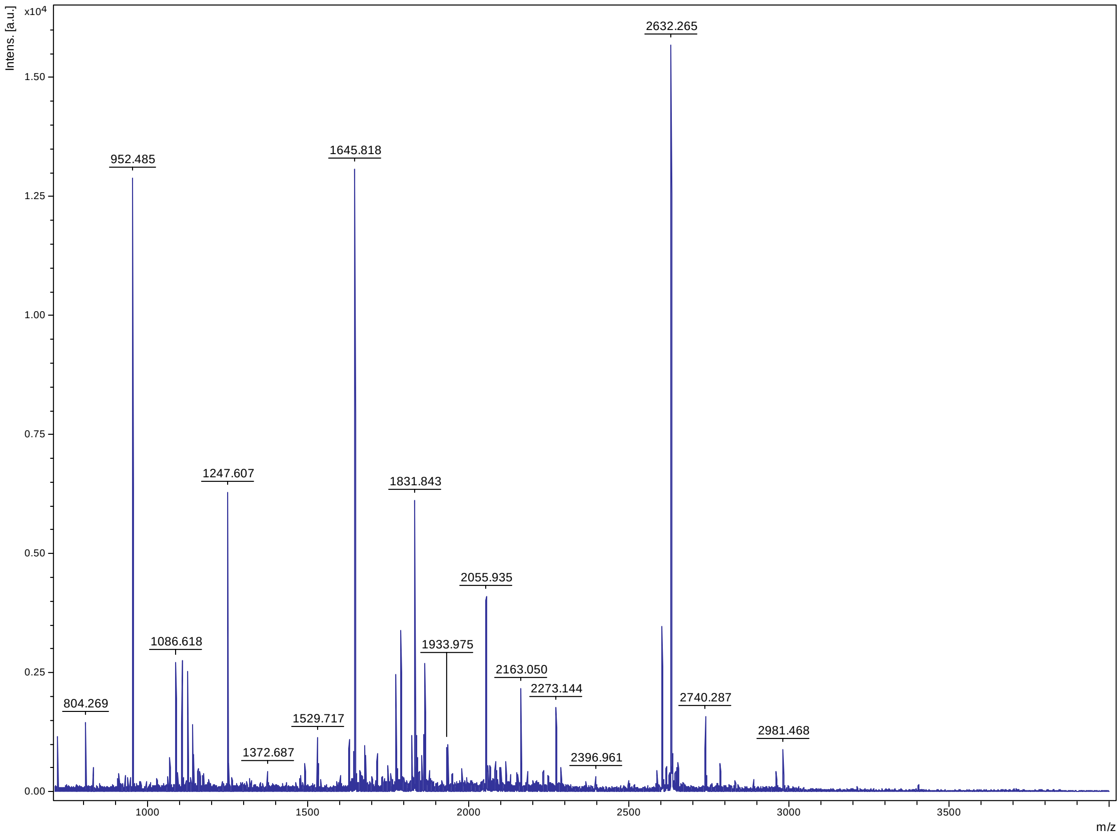
Match to: gi|50900276; Score: 92

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
97 - 106	1134.64	1133.63	1133.61	0.03	0	ELGLFVDVSR

107 - 115	1129.54	1128.54	1128.53	0.01	0	MGFTEEFLR
107 - 115	1145.52	1144.52	1144.52	-0.01	0	MGFTEEFLR Oxidation (M)
144 - 151	1077.58	1076.57	1076.52	0.05	0	MVGHYWLR Oxidation (M)
152 - 162	1186.62	1185.62	1185.61	0.00	0	DPGLAPNSFLR
285 - 301	1815.89	1814.88	1814.91	-0.03	0	QGVAVTQENSLLDNTAR
302 - 308	844.48	843.48	843.46	0.02	0	IEGWLAR
309 - 318	1211.56	1210.56	1210.56	-0.00	0	FPMFDWVGGR
309 - 318	1227.55	1226.55	1226.55	-0.01	0	FPMFDWVGGR Oxidation (M)
353 - 378	2904.46	2903.45	2903.46	-0.01	1	NTVVKENPAALLALCWYWASEGIGNK
426 - 438	1516.72	1515.72	1515.74	-0.02	0	GSTDQHAYIQQLR
482 - 502	2351.19	2350.19	2350.18	0.02	1	SALYSNDRESISVTVQEVTPR
503 - 513	1161.66	1160.65	1160.66	-0.00	0	AVGALVALYER
514 - 536	2371.20	2370.20	2370.23	-0.03	0	AVGIYASLVNINAYHQPGVEAGK
549 - 573	2782.40	2781.40	2781.42	-0.03	1	VLTVLNEASCKDPAEPLTLDQIAER

Spot 1571

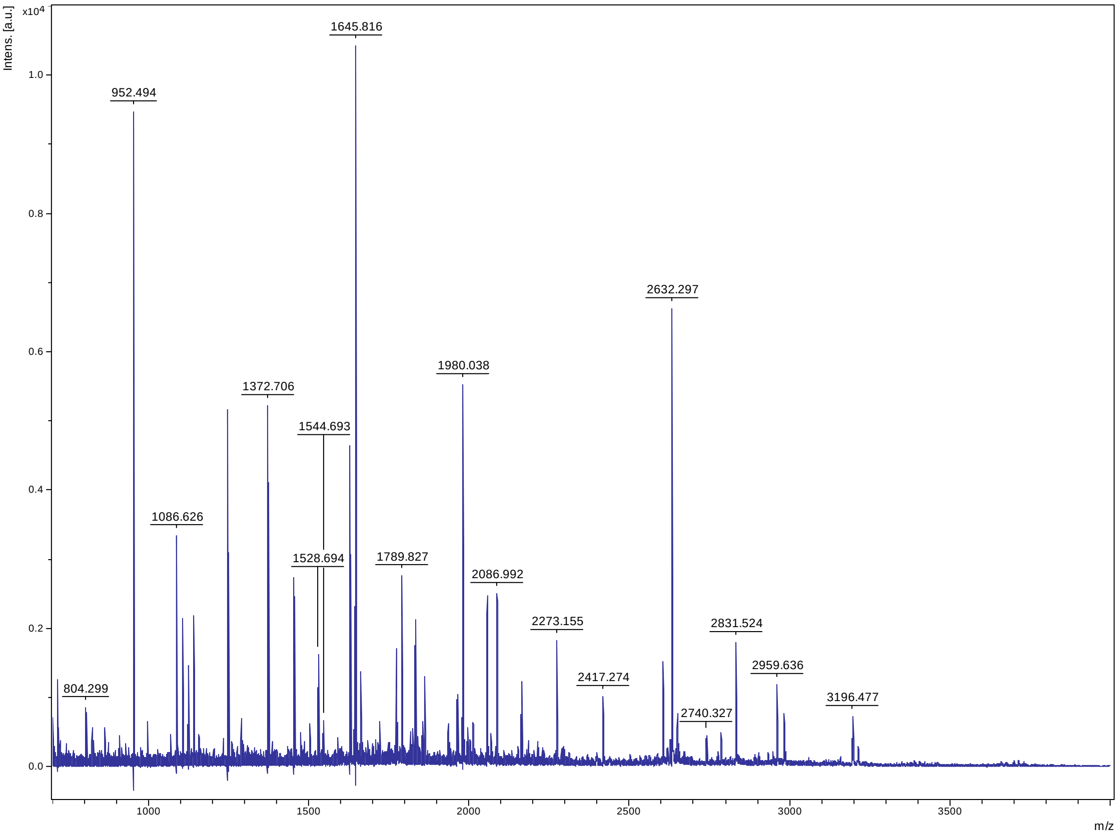


Match to: gi|34912986 Score: 100 Expect: 7.1e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 17	2083.8789	2082.8716	2082.8817	-0.0101	0	-.MQFMMPLDTNACAQPMR.R Acetyl (N-term); Carbamidomethyl (C)
2 - 17	1853.8463	1852.8390	1852.8092	0.0298	0	M.QFMMPLDTNACAQPMR.R
28 - 41	1661.7774	1660.7701	1660.8276	-0.0575	1	R.LMERLNIGGMTQEK.A Acetyl (N-term)
32 - 41	1090.7003	1089.6930	1089.5488	0.1442	0	R.LNIGGMTQEK.A
58 - 72	1789.8032	1788.7959	1788.8213	-0.0254	1	R.CVFTSDADRDTPHLR.T Carbamidomethyl (C)
58 - 72	1831.8273	1830.8200	1830.8319	-0.0119	1	R.CVFTSDADRDTPHLR.T Acetyl (N-term); Carbamidomethyl (C)
107 - 118	1247.7274	1246.7201	1246.6128	0.1073	0	R.ATPAVPVGGCYR.L Carbamidomethyl (C)
119 - 134	1822.8548	1821.8475	1821.8753	-0.0278	0	R.LIDIPMSNCFNSGINK.I Carbamidomethyl (C)
135 - 148	1627.8118	1626.8045	1626.8188	-0.0142	0	K.IFVMTQFNSASLNR.H
219 - 227	1155.6748	1154.6675	1154.5464	0.1212	0	R.MNYMELVQK.H
228 - 246	1998.9453	1997.9380	1997.9112	0.0268	0	K.HVDDNADITISCAPIDGSR.A
228 - 246	2055.9108	2054.9035	2054.9327	-0.0292	0	K.HVDDNADITISCAPIDGSR.A Carbamidomethyl (C)
247 - 260	1529.7521	1528.7448	1528.7157	0.0291	1	R.ASDYGLVKFDDSGR.V
261 - 277	1933.9473	1932.9400	1932.9866	-0.0466	0	R.VIQFLEKPEGADLESMK.V
317 - 330	1645.8308	1644.8235	1644.8260	-0.0024	0	K.YAHLQDFGSEILPR.A
354 - 368	1677.8195	1676.8122	1676.8409	-0.0287	0	K.SFFDANLALTEQPPK.F
354 - 375	2604.4211	2603.4138	2603.2583	0.1555	1	K.SFFDANLALTEQPPKFEFYDPK.T
354 - 375	2646.4395	2645.4322	2645.2689	0.1633	1	K.SFFDANLALTEQPPKFEFYDPK.T Acetyl (N-term)
376 - 383	952.6650	951.6577	951.4814	0.1763	0	K.TPFFTSPR.Y
384 - 392	1086.7625	1085.7552	1085.6233	0.1319	1	R.YLPPARLEK.C
448 - 463	1714.9515	1713.9442	1713.9664	-0.0222	1	K.LLFEGKVPIGIGENTK.I
466 - 474	1106.6793	1105.6720	1105.5008	0.1712	0	R.NCIIDMNAR.I Carbamidomethyl (C)
478 - 500	2632.4234	2631.4161	2631.2564	0.1597	0	R.NVIIANTQGVQESDHPEEGYYIR.S

Spot 1573

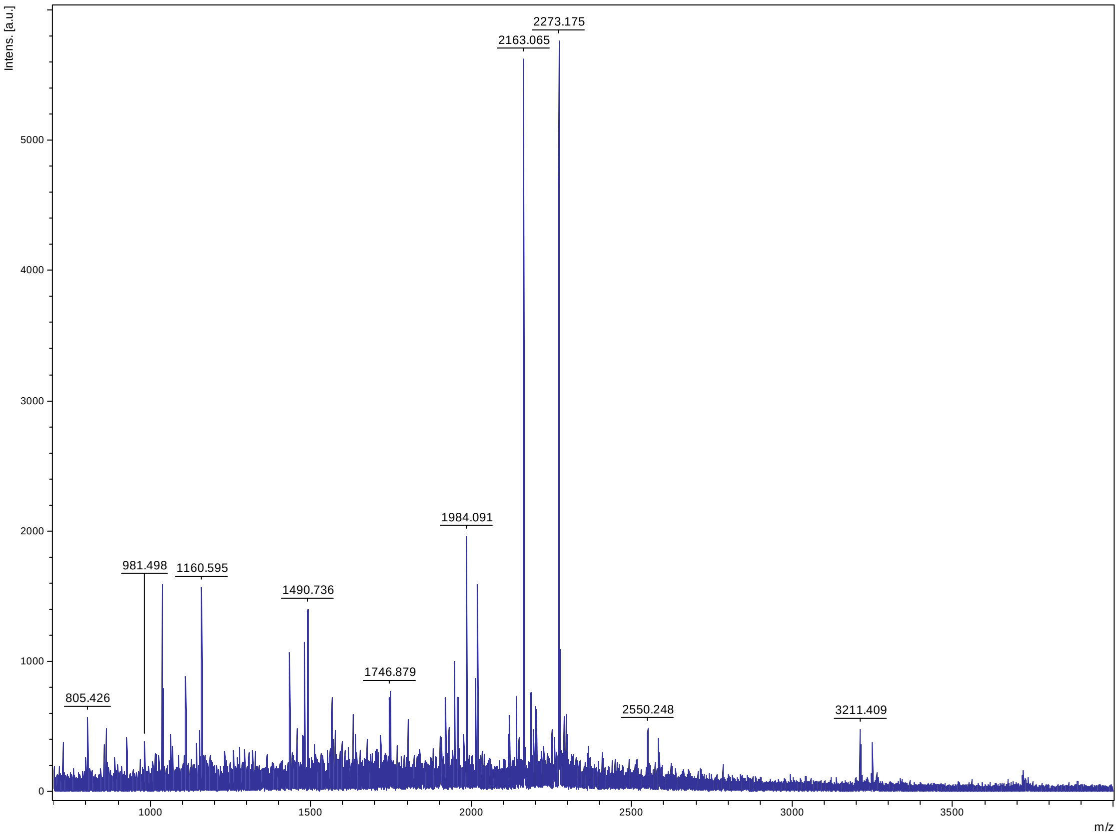


Match to: gi|13540812 Score: 109 Expect: 8.9e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 17	2001.9952	2000.9879	2000.8286	0.1593	0	-.MEFMMPLDTNACAQPMR.R	Oxidation (M)
2 - 18	2067.9705	2066.9632	2066.9158	0.0474	1	M.EFMMPLDTNACAQPMRR.A	Carbamidomethyl (C)
28 - 41	1661.7842	1660.7769	1660.8276	-0.0507	1	R.LMERLNIGGMTQEK.A	Acetyl (N-term)
58 - 72	1789.8381	1788.8308	1788.8213	0.0095	1	R.CVFTSDADRDTPHLR.T	Carbamidomethyl (C)
78 - 106	2959.6211	2958.6138	2958.5562	0.0576	1	R.KNYADASHVSAVILGGGTGVQLFPLTSTR.A	
79 - 106	2831.5496	2830.5423	2830.4613	0.0811	0	K.NYADASHVSAVILGGGTGVQLFPLTSTR.A	
107 - 118	1247.5629	1246.5556	1246.6128	-0.0572	0	R.ATPAVPVGGCYR.L	Carbamidomethyl (C)
119 - 134	1838.9340	1837.9267	1837.8702	0.0565	0	R.LIDIPMSNCFNSGINK.I	Carbamidomethyl (C); Oxidation (M)
135 - 148	1627.8096	1626.8023	1626.8188	-0.0164	0	K.IFVMTQFNSASLNR.H	
135 - 148	1643.8033	1642.7960	1642.8137	-0.0177	0	K.IFVMTQFNSASLNR.H	Oxidation (M)
228 - 246	2055.9475	2054.9402	2054.9327	0.0075	0	K.HVDDNADITISCAPIDGSR.A	Carbamidomethyl (C)
315 - 330	1860.9438	1859.9365	1859.9529	-0.0164	1	K.SKYAHLQDFGSEILPR.A	
317 - 330	1645.8105	1644.8032	1644.8260	-0.0227	0	K.YAHLQDFGSEILPR.A	
339 - 353	1831.8648	1830.8575	1830.8498	0.0077	0	K.ACVFTEYWEDIGTIK.S	Carbamidomethyl (C)
354 - 375	2604.2845	2603.2772	2603.2583	0.0189	1	K.SFFDANLALTEQPPKFEFYDPK.T	
376 - 383	952.3478	951.3405	951.4814	-0.1409	0	K.TPFFTSPR.Y	
384 - 392	1086.5316	1085.5243	1085.6233	-0.0990	1	R.YLPPARLEK.C	
395 - 421	2981.4792	2980.4719	2980.4270	0.0450	1	K.IKDAIISDGCSFSECTIEHSVIGISSR.V	2 Carbamidomethyl (C)
397 - 421	2740.3095	2739.3022	2739.2479	0.0543	0	K.DAIISDGCSFSECTIEHSVIGISSR.V	2 Carbamidomethyl (C)
466 - 474	1106.4372	1105.4299	1105.5008	-0.0709	0	R.NCIIDMNAR.I	Carbamidomethyl (C)
478 - 500	2632.3022	2631.2949	2631.2564	0.0385	0	R.NVIIANTQGVQESDHPEEGYYIR.S	

Spot 1576

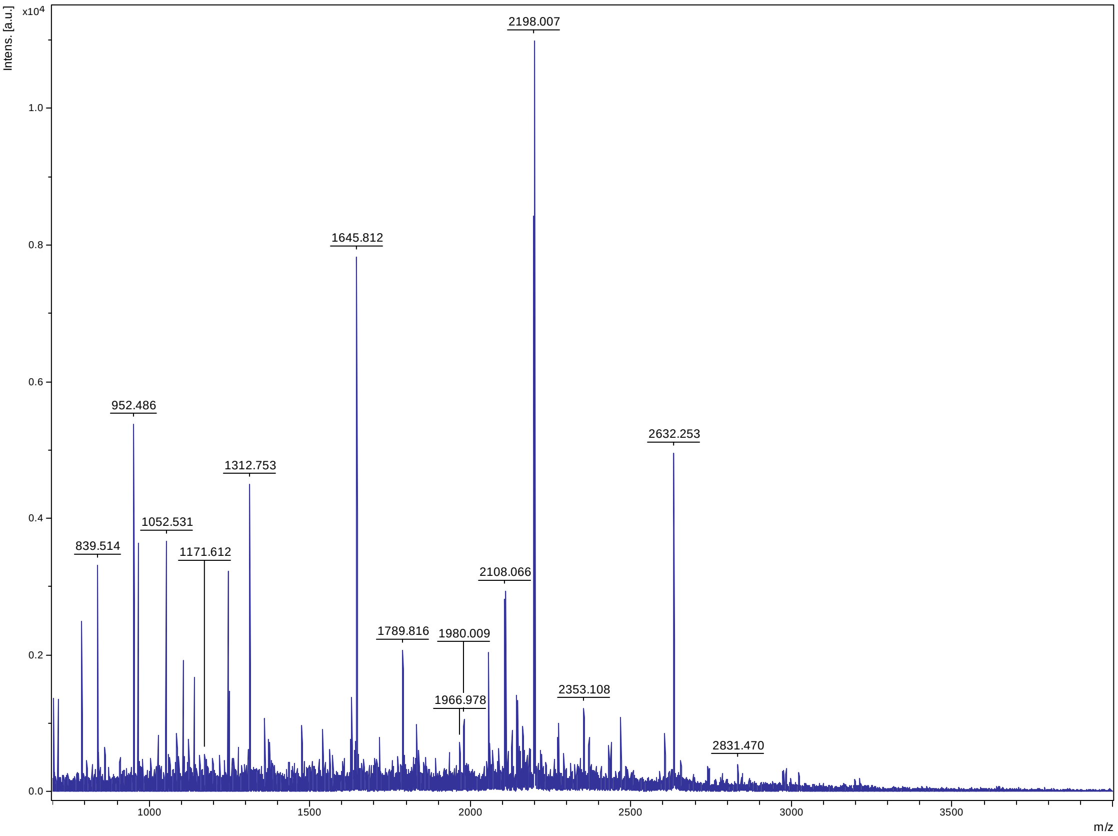


Match to: gi|50919601 Score: 74 Expect: 0.0029

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
33 - 40	1039.4207	1038.4134	1038.4043	0.0091	0	K.FDDGWEDR.W	
63 - 79	2018.8977	2017.8904	2017.8653	0.0251	1	K.WYGDADDKGIQTSEDYR.F	
105 - 117	1433.7167	1432.7094	1432.6768	0.0326	1	K.HEQKLDCGGGYVK.L	
105 - 117	1490.7361	1489.7288	1489.6983	0.0305	1	K.HEQKLDCGGGYVK.L	Carbamidomethyl (C)
166 - 187	2583.3513	2582.3440	2582.3526	-0.0086	1	K.DVPCKTDQLTHVYTLIIRPDAK.Y	Carbamidomethyl (C)
171 - 187	1984.0909	1983.0837	1983.0789	0.0048	0	K.TDQLTHVYTLIIRPDAK.Y	
198 - 212	1746.8789	1745.8716	1745.8624	0.0092	0	K.QTGSIYDDWNIIPPK.N	
221 - 247	3247.4163	3246.4090	3246.4516	-0.0427	1	K.KPEDWDDNEYIPDPEDKKPEGYDDIPK.E	
330 - 347	2011.9586	2010.9513	2010.9786	-0.0272	0	K.SGTLFDNILITDDPEYAK.K	
349 - 356	981.4978	980.4905	980.4603	0.0302	0	K.FAEETWAK.H	

Spot 1577



Match to: gi|15823775; Score: 195

Matched peptides:

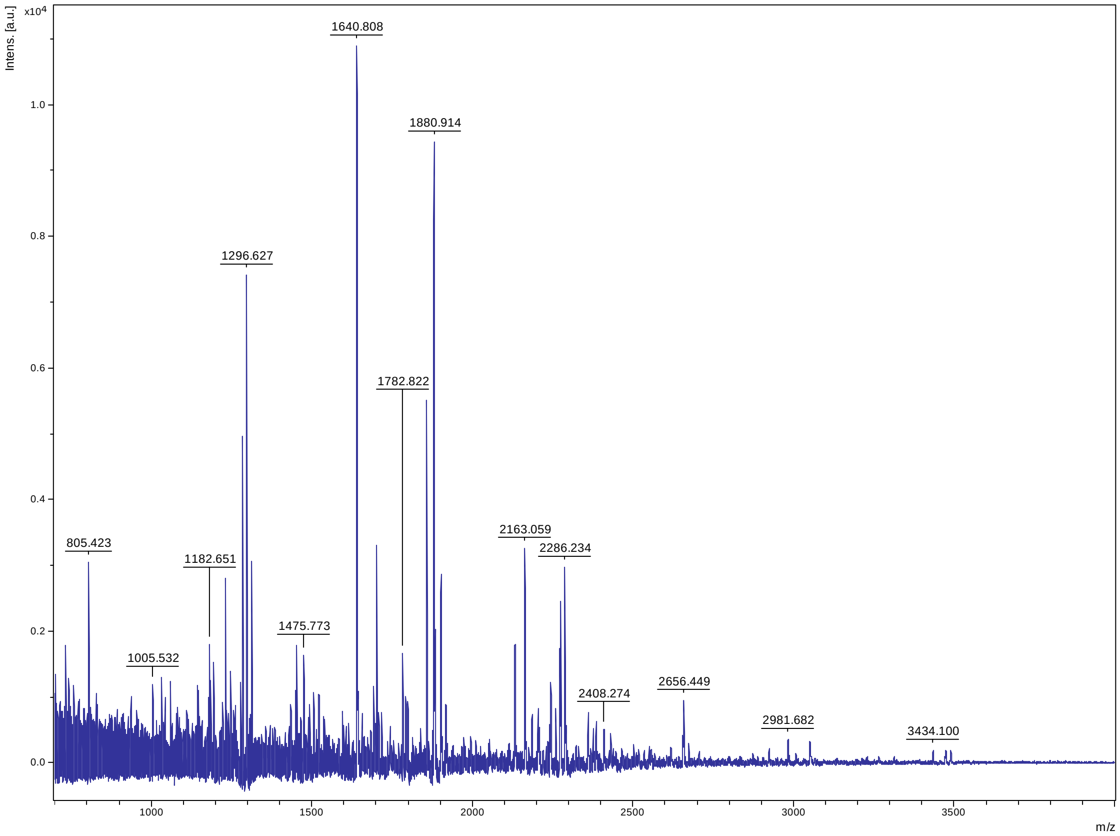
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
14 - 27	1561.74	1560.74	1560.76	-0.02	1	AATDKLDQISENEK
28 - 36	965.54	964.54	964.53	0.01	0	SGFISLVSR
50 - 76	2973.48	2972.48	2972.49	-0.01	1	IQTPTDEVVVPYDTLSAAPEDLNETKK
86 - 106	2163.04	2162.03	2162.08	-0.05	1	LNGGLGTTMGCTGPKSVIEVR Oxidation (M)
126 - 146	2467.11	2466.11	2466.13	-0.02	0	YGCNVPLLLMNSFNTHDDTQK
151 - 168	2198.01	2197.01	2197.02	-0.01	0	YSNSNIEIHTFNQSQYPR
169 - 180	1358.73	1357.73	1357.75	-0.02	0	IVTEDFLPLPSK
183 - 205	2430.13	2429.13	2429.14	-0.01	1	TGKDGWYPPGHGDVFPSLNNSGK
186 - 205	2143.96	2142.96	2142.98	-0.02	0	DGWYPPGHGDVFPSLNNSGK
215 - 232	1966.98	1965.98	1966.00	-0.03	0	EYVFVANSDNLGAIVDIK
233 - 251	2353.11	2352.11	2352.14	-0.03	0	ILNHLIHNQNEYCMEVTPK
233 - 251	2369.11	2368.11	2368.13	-0.02	0	ILNHLIHNQNEYCMEVTPK Oxidation (M)
258 - 267	1052.53	1051.53	1051.53	-0.00	0	GGTLISYEGR
268 - 285	2108.07	2107.06	2107.09	-0.03	0	VQLLEIAQVPDEHVNEFK
307 - 315	1028.58	1027.58	1027.60	-0.03	1	RLVEAEALK
330 - 342	1312.75	1311.75	1311.75	-0.00	0	VLQLETAAGAAIR
347 - 354	839.51	838.51	838.50	0.01	0	AIGINVPR
362 - 383	2438.28	2437.27	2437.31	-0.04	0	ATSDLLLVQSDLYTLVDGFVIR
388 - 402	1629.79	1628.79	1628.80	-0.02	0	TNPSNPSIELGPEFK

Match to: gi|55296000; Score: 155

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
54 - 68	1789.82	1788.81	1788.82	-0.01	1	CVFTSDADRDTPHLR
75 - 102	2831.47	2830.47	2830.46	0.01	0	NYADASHVSAVILGGGTGVQLFPLTSTR
103 - 114	1247.62	1246.61	1246.61	0.00	0	ATPAVPVGGCYR
131 - 144	1627.80	1626.79	1626.82	-0.03	0	IFVMTQFNSASLNR
131 - 144	1643.80	1642.80	1642.81	-0.02	0	IFVMTQFNSASLNR Oxidation (M)
215 - 223	1171.61	1170.61	1170.54	0.07	0	MNYMELVQK Oxidation (M)
224 - 242	2055.93	2054.93	2054.93	-0.00	0	HVDDNADITISCAPIDGSR
257 - 273	1933.96	1932.95	1932.99	-0.03	0	VIQFLEKPEGADLESMK
313 - 326	1645.81	1644.81	1644.83	-0.02	0	YAHLQDFGSEILPR
327 - 334	909.52	908.52	908.51	0.01	0	AVLEHNVK
335 - 349	1831.83	1830.83	1830.85	-0.02	0	ACVFTEYWEDIGTIK
350 - 371	2604.26	2603.26	2603.26	0.00	1	SFFDANLALTEQPPKFEFYDPK
372 - 379	952.49	951.48	951.48	0.00	0	TPFFTSPR
380 - 388	1086.61	1085.61	1085.62	-0.01	1	YLPPARLEK
393 - 417	2740.21	2739.21	2739.25	-0.04	0	DAIISDGCSFSECTIEHSVIGISSR
426 - 443	2143.96	2142.96	2142.79	0.17	0	DTMMMGADQYETEEETSK 3 Oxidation (M)
462 - 470	1106.52	1105.52	1105.50	0.02	0	NCIIDMNAR
474 - 496	2632.25	2631.25	2631.26	-0.01	0	NVIIANTQGVQESDHPEEGYYIR

Spot 1578

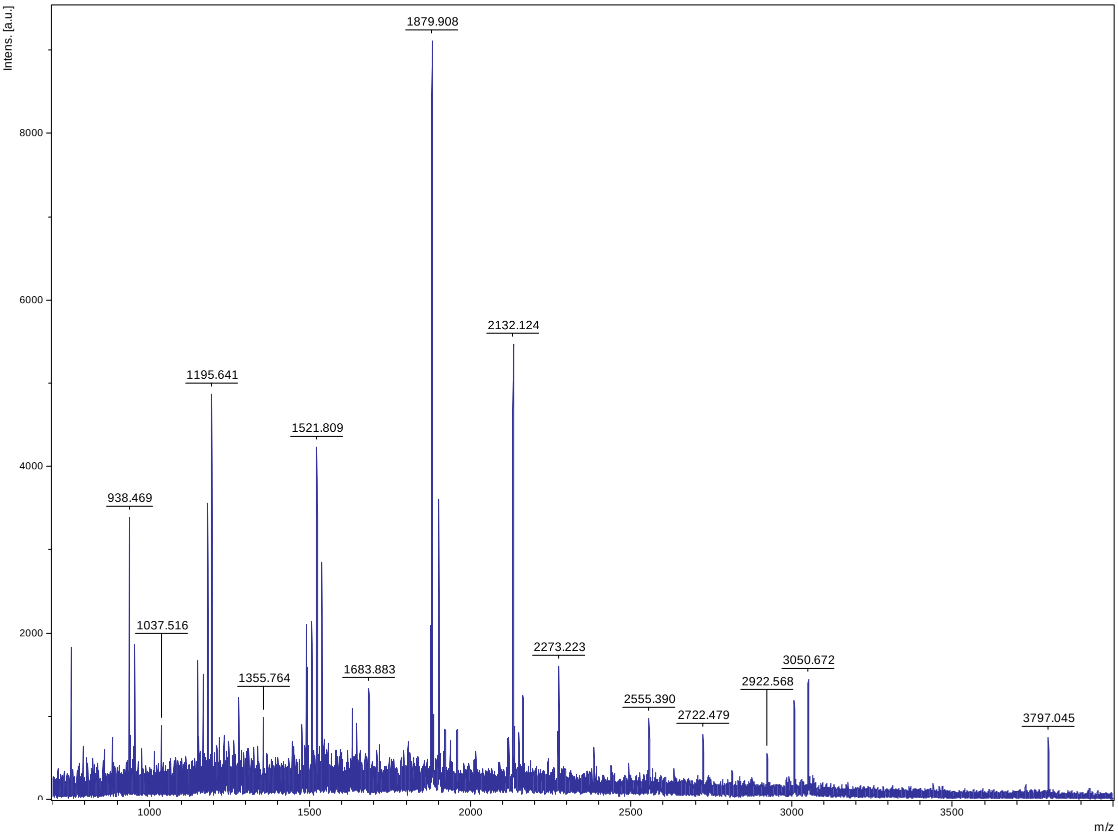


Match to: gi|50919629; Score: 83

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
43 - 57	1640.79	1639.79	1639.80	-0.01	0	AIVAESCDVPAPQQR
64 - 86	2656.37	2655.37	2655.33	0.04	1	ILKDEQTLASYGVETDHTIHMVR
164 - 182	2242.23	2241.23	2241.13	0.10	0	EIMNMPLMQNILNSPDLIR
164 - 182	2258.25	2257.24	2257.13	0.12	0	EIMNMPLMQNILNSPDLIR Oxidation (M)
164 - 182	2290.22	2289.21	2289.12	0.10	0	EIMNMPLMQNILNSPDLIR 3 Oxidation (M)
183 - 192	1230.60	1229.60	1229.60	0.00	0	NIIMNNPQMR
183 - 192	1246.62	1245.61	1245.60	0.02	0	NIIMNNPQMR Oxidation (M)
193 - 212	2286.17	2285.16	2285.21	-0.05	1	EIVDRNPDLAHVLNDPSILR
234 - 249	1782.79	1781.79	1781.81	-0.02	0	AMSNIESSPEGFNMLR
234 - 249	1798.80	1797.79	1797.80	-0.01	0	AMSNIESSPEGFNMLR Oxidation (M)
251 - 271	2360.24	2359.23	2359.05	0.19	0	MYETVQEPFLNATTMAGEGDR
272 - 289	1856.89	1855.88	1855.89	-0.01	0	SSNPFSALLGNHGSNQAR
411 - 420	1296.63	1295.62	1295.60	0.03	0	EMFQNPEFVR
411 - 420	1312.65	1311.65	1311.59	0.06	0	EMFQNPEFVR Oxidation (M)

Spot 1582

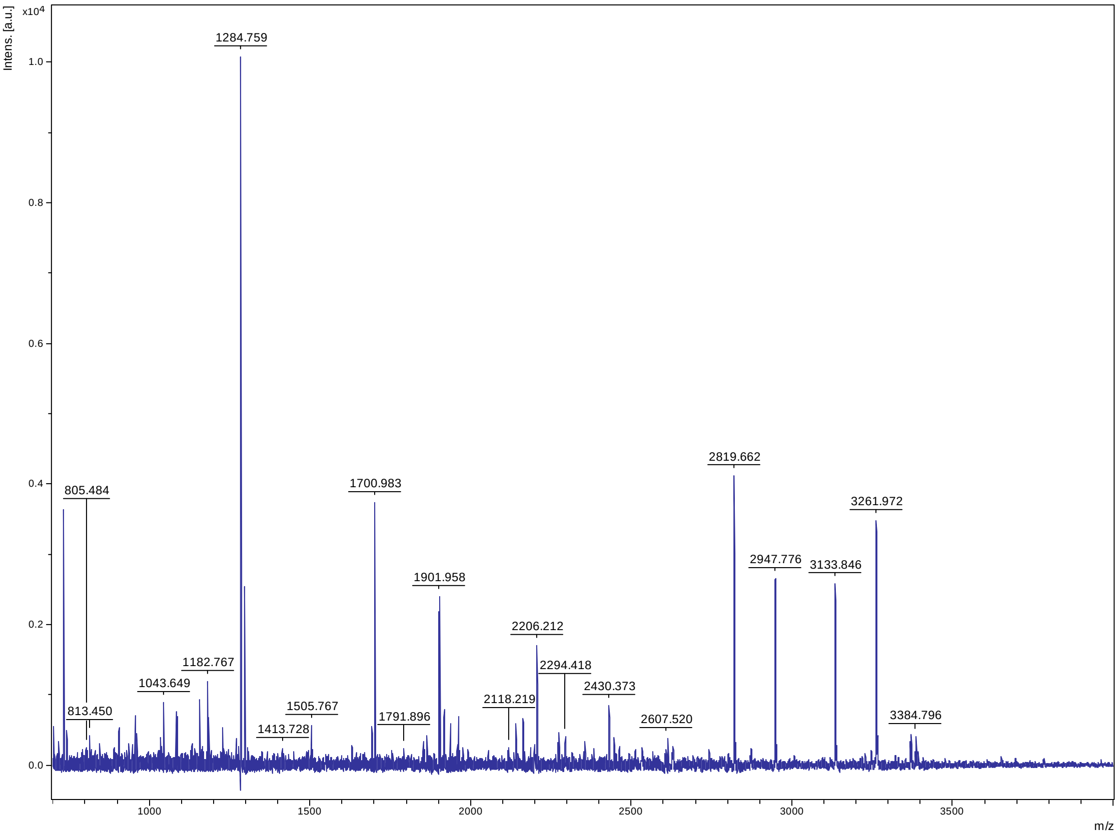


Match to: gi|62734634 Score: 87 Expect: 0.00013

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
112 - 121	1195.6064	1194.5991	1194.6284	-0.0293	0	K.YEIQGFPTLK.I	
138 - 147	1150.5634	1149.5561	1149.5917	-0.0356	0	R.EAEGIVEYLK.K	
138 - 148	1278.6623	1277.6550	1277.6866	-0.0316	1	R.EAEGIVEYLKK.Q	
159 - 171	1445.6741	1444.6668	1444.7045	-0.0377	1	K.SPEDATNLIDDKK.I	
172 - 195	2722.3547	2721.3474	2721.3788	-0.0314	0	K.IYIVGIFSELSGTEYTNFIEVAEK.L	
196 - 213	2149.0312	2148.0239	2148.0613	-0.0374	1	K.LRSDYDFGHTLHANHLPR.G	
214 - 224	1182.6317	1181.6244	1181.6516	-0.0272	0	R.GDAAVERPLVR.L	
225 - 237	1536.8042	1535.7969	1535.8235	-0.0266	0	R.LFKPFDELVVDSK.D	
225 - 246	2555.2728	2554.2655	2554.3206	-0.0551	1	R.LFKPFDELVVDSKDFDVTALEK.F	
238 - 246	1037.4670	1036.4597	1036.5077	-0.0479	0	K.DFDVTALEK.F	
247 - 261	1654.7833	1653.7760	1653.8613	-0.0853	1	K.FIDASSTPKVVTFDK.N	
256 - 271	1899.9646	1898.9573	1898.9890	-0.0317	1	K.VVTFDKNPDNHPYLLK.F	
272 - 279	885.3964	884.3891	884.4392	-0.0501	0	K.FFQSSAAK.A	
296 - 306	1263.5781	1262.5708	1262.5818	-0.0110	0	K.SVYYGAAEEFK.D	
296 - 308	1506.6787	1505.6714	1505.7038	-0.0323	1	K.SVYYGAAEEFKDK.E	
312 - 330	2132.0459	2131.0386	2131.0737	-0.0351	0	K.FLIGDIEASQGAFQYFGLR.E	
331 - 345	1683.8287	1682.8214	1682.8726	-0.0512	0	R.EDQVPLIIIQDGESK.K	
331 - 346	1811.9414	1810.9341	1810.9676	-0.0335	1	R.EDQVPLIIIQDGESKK.F	
350 - 362	1521.7805	1520.7732	1520.7987	-0.0255	0	K.AHVEPDQIVSWLK.E	
363 - 368	758.2465	757.2392	757.3282	-0.0890	0	K.EYFDGK.L	
375 - 400	2922.4203	2921.4130	2921.4810	-0.0679	1	K.SEPIPEVNDEPVKVVVADNVHDFVFK.S	
388 - 400	1488.7486	1487.7413	1487.7772	-0.0359	0	K.VVVADNVHDFVFK.S	
404 - 418	1822.8669	1821.8596	1821.8330	0.0266	0	K.NVLVEFYAPWCGHCK.K	Carbamidomethyl (C)
404 - 418	1879.8442	1878.8369	1878.8545	-0.0176	0	K.NVLVEFYAPWCGHCK.K	2 Carbamidomethyl (C)
404 - 419	1992.9934	1991.9861	1991.9385	0.0476	1	K.NVLVEFYAPWCGHCKK.L	Acetyl (N-term); Carbamidomethyl (C)
420 - 432	1355.7282	1354.7209	1354.7708	-0.0498	0	K.LAPILDEAATTLK.S	
470 - 477	938.3990	937.3917	937.4327	-0.0410	0	K.MVPYESGR.T	
470 - 477	954.3929	953.3856	953.4276	-0.0420	0	K.MVPYESGR.T	Oxidation (M)

Spot 1584

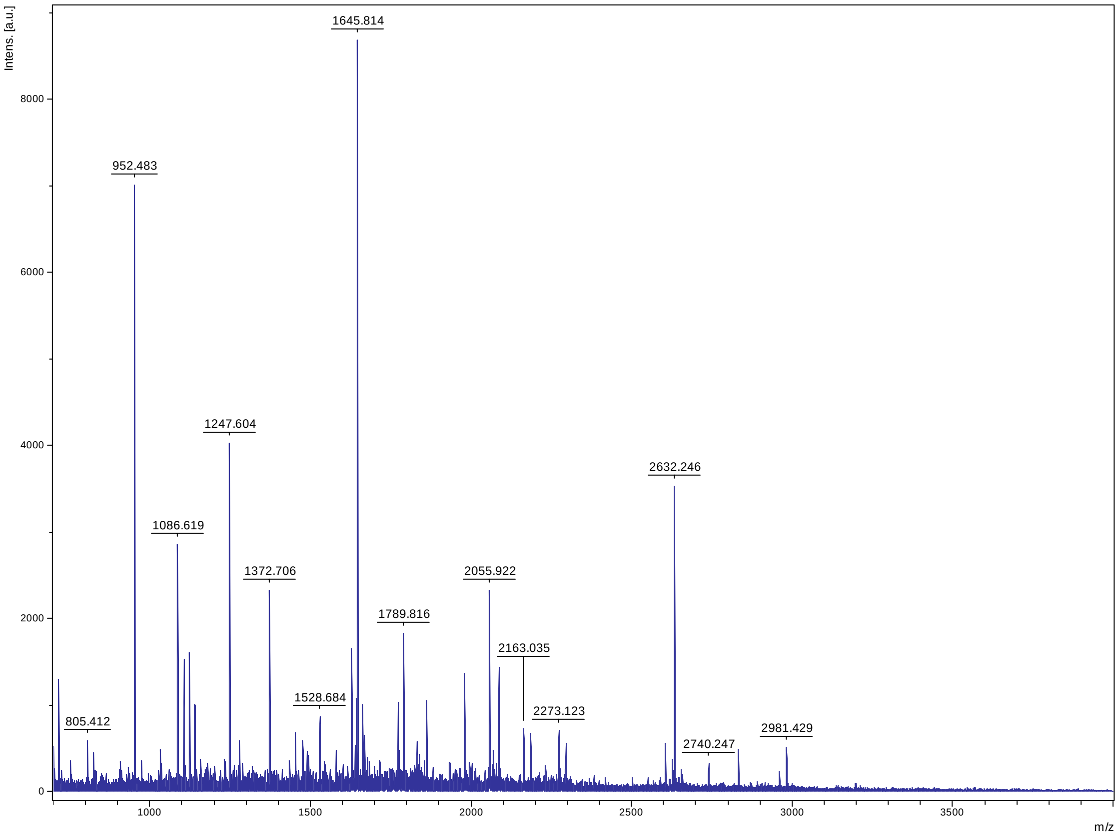


Match to: gi|34897924 Score: 166 Expect: 1.7e-12

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 24	2355.2125	2354.2052	2354.1497	0.0555	0	-.MASTFGATSTVGLMAAPTGIVSDK.K	Acetyl (N-term)
79 - 90	1182.7687	1181.7614	1181.7019	0.0595	0	K.LADLVGVTLGPK.G	
105 - 114	1043.6466	1042.6393	1042.5771	0.0623	0	R.IVNDGVTVAR.E	
137 - 161	2430.2476	2429.2403	2429.2649	-0.0245	0	K.TNDLAGDGTTTSVVLAQGLIAEGVK.V	
162 - 174	1295.8140	1294.8067	1294.7357	0.0711	0	K.VVAAGANPVQITR.G	
227 - 236	1087.6666	1086.6593	1086.6033	0.0561	1	R.KGVVTLEEGR.S	
237 - 252	1901.9087	1900.9014	1900.8624	0.0390	0	R.SSENNLYVVEGMQFER.G	
237 - 252	1917.9202	1916.9129	1916.8574	0.0556	0	R.SSENNLYVVEGMQFER.G	Oxidation (M)
253 - 265	1505.7872	1504.7799	1504.7085	0.0714	0	R.GYISPYFVTDSEK.M	
287 - 297	1284.7699	1283.7626	1283.7085	0.0542	0	R.DLINVLEEAIR.G	
333 - 339	733.3615	732.3542	732.3554	-0.0012	0	K.APGFGER.K	
341 - 357	1863.0694	1862.0621	1862.0149	0.0472	0	K.TQYLDDIAILTGATVIR.D	
341 - 366	2819.4547	2818.4474	2818.4963	-0.0489	1	K.TQYLDDIAILTGATVIRDEVGLSLDK.A	
383 - 400	1936.9637	1935.9564	1935.9385	0.0179	1	K.ESTTIVGDGSTQEEVTKR.V	
406 - 419	1693.8851	1692.8778	1692.8206	0.0573	1	K.NLIEAAEQEYEKEK.L	
427 - 447	2141.1805	2140.1732	2140.1738	-0.0006	1	K.LAGGVAVIQVGAQTETELKEK.K	
460 - 476	1700.9559	1699.9486	1699.8926	0.0560	0	K.AAVEEGIVVGGGCTLLR.L	Carbamidomethyl (C)
477 - 485	956.5011	955.4938	955.5814	-0.0876	1	R.LAARVDAIK.D	
534 - 556	2446.1295	2445.1222	2445.1521	-0.0299	0	K.FGYNAATGQYEDLMAAGIIDPTK.V	
571 - 601	3384.6155	3383.6082	3383.6118	-0.0036	1	K.TFLTSDVVVVEIKEPEPAPVTNPMDNSGYGY.-	Oxidation (M)

Spot 1585

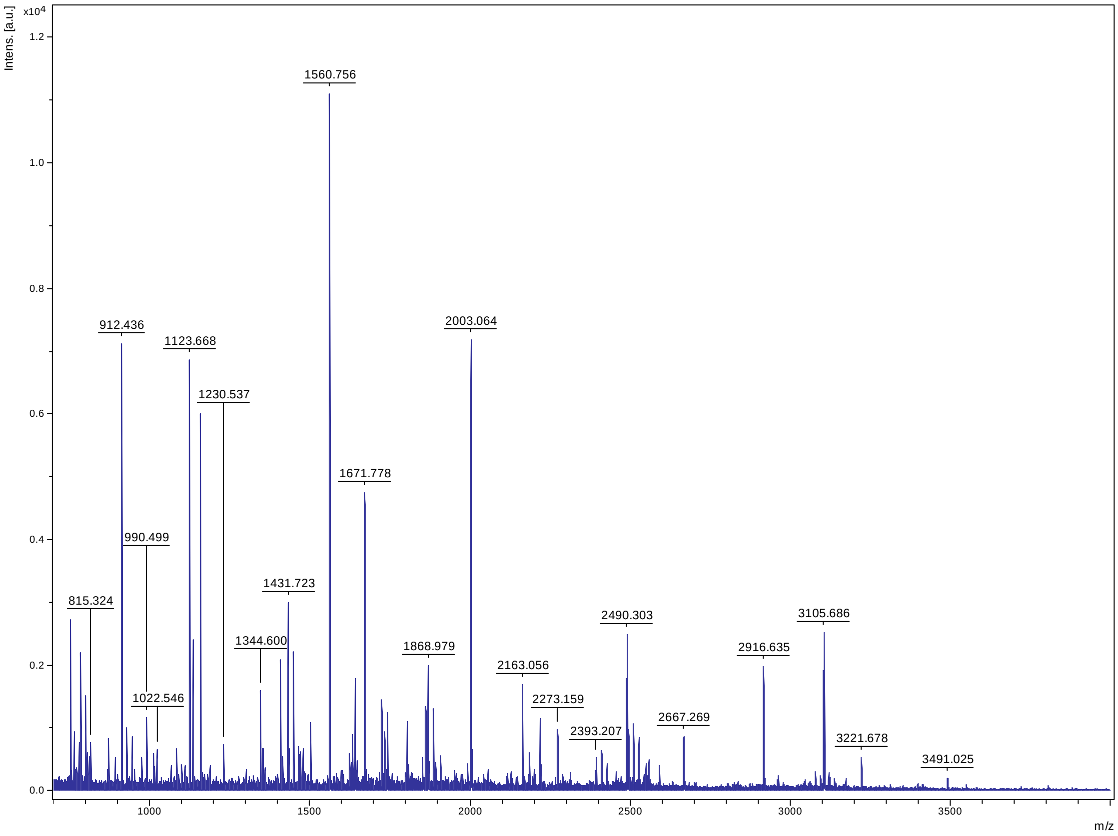


Match to: gi|55296000; Score: 157

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
54 - 68	1789.82	1788.81	1788.82	-0.01	1	CVFTSDADRDTPHLR
75 - 102	2831.45	2830.45	2830.46	-0.01	0	NYADASHVSAVILGGGTGVQLFPLTSTR
103 - 114	1247.60	1246.60	1246.61	-0.01	0	ATPAVPVGGCYR
131 - 144	1627.80	1626.80	1626.82	-0.02	0	IFVMTQFNSASLNR
131 - 144	1643.81	1642.80	1642.81	-0.01	0	IFVMTQFNSASLNR Oxidation (M)
224 - 242	2055.92	2054.92	2054.93	-0.01	0	HVDDNADITISCAPIDGSR
287 - 301	1772.78	1771.78	1771.92	-0.14	1	QKYPYIASMGIYVLK Oxidation (M); Pyro-glu (N-term Q)
289 - 302	1661.78	1660.78	1660.89	-0.11	1	YPYIASMGIYVLKK Oxidation (M)
311 - 326	1860.95	1859.94	1859.95	-0.01	1	SKYAHLQDFGSEILPR
313 - 326	1645.81	1644.81	1644.83	-0.01	0	YAHLQDFGSEILPR
350 - 371	2604.22	2603.22	2603.26	-0.04	1	SFFDANLALTEQPPKFEFYDPK
372 - 379	952.48	951.48	951.48	-0.00	0	TPFFTSPR
380 - 388	1086.62	1085.62	1085.62	-0.01	1	YLPPARLEK
391 - 417	2981.43	2980.43	2980.43	-0.00	1	IKDAIISDGCSFSECTIEHSVIGISSR
393 - 417	2740.25	2739.25	2739.25	-0.00	0	DAIISDGCSFSECTIEHSVIGISSR
462 - 470	1106.51	1105.51	1105.50	0.01	0	NCIIDMNAR
462 - 470	1122.48	1121.47	1121.50	-0.02	0	NCIIDMNAR Oxidation (M)
474 - 496	2632.25	2631.24	2631.26	-0.01	0	NVIIANTQGVQESDHPEEGYYIR

Spot 1590

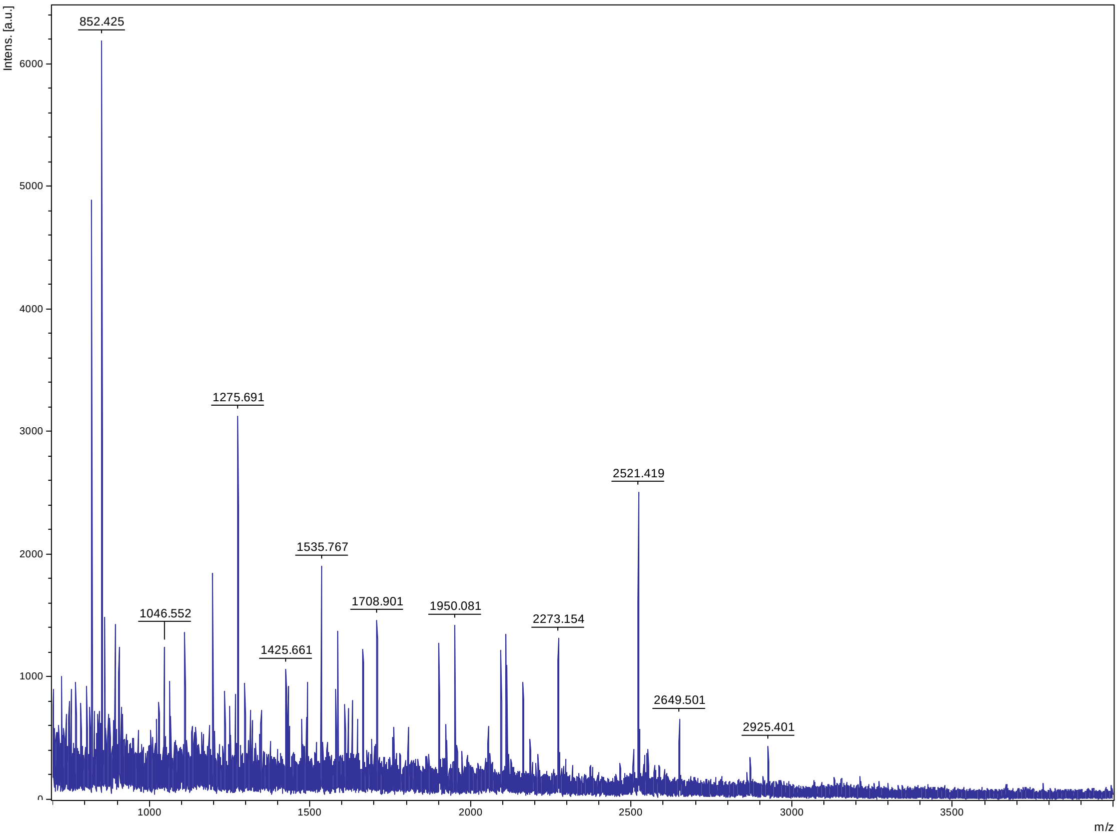


Match to: gi|115465273 Score: 179 Expect: 1.7e-13

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
53 - 64	1344.6004	1343.5931	1343.6429	-37	1	R.AADENIREEAAR.H
67 - 90	2667.2689	2666.2617	2666.1938	25	0	R.APNHNFSAWYAPFPPAPNGDPDER.Y
91 - 99	1157.5551	1156.5478	1156.5764	-25	0	R.YSLDEIVYR.S
100 - 109	990.4992	989.4919	989.5142	-23	0	R.SSSGGLLDVR.H
110 - 117	928.4156	927.4083	927.4232	-16	0	R.HDMDALAR.F
110 - 117	944.4156	943.4083	943.4182	-10	0	R.HDMDALAR.F Oxidation (M)
118 - 124	912.4357	911.4285	911.4290	-1	0	R.FPGSYWR.D
134 - 145	1352.6109	1351.6036	1351.6561	-39	0	R.TTWPFGSGVWSK.K
174 - 188	1724.8503	1723.8430	1723.8828	-23	1	R.LGRDHLAGMNDLWVK.H
174 - 188	1740.8518	1739.8446	1739.8777	-19	1	R.LGRDHLAGMNDLWVK.H Oxidation (M)
177 - 188	1414.5938	1413.5865	1413.6711	-60	0	R.DHLAGMNDLWVK.H Oxidation (M)
189 - 199	1230.5366	1229.5293	1229.5612	-26	0	K.HCGISHTGSFK.D
200 - 212	1431.7226	1430.7153	1430.7552	-28	0	K.DLGMTVLVSQVNR.L
200 - 212	1447.7121	1446.7048	1446.7501	-31	0	K.DLGMTVLVSQVNR.L Oxidation (M)
288 - 305	2003.0640	2002.0568	2002.0735	-8	0	R.EVTAELPIYLANSLNSLR.L
288 - 310	2558.4376	2557.4303	2557.3751	22	1	R.EVTAELPIYLANSLNSLRLEGQK.T
344 - 349	815.3242	814.3169	814.3102	8	0	K.GFEMCR.V Oxidation (M)
350 - 359	1123.6679	1122.6606	1122.6873	-24	1	R.VLGLVDRVPR.L
360 - 373	1560.7557	1559.7484	1559.7878	-25	0	R.LVCAQAANANPLYR.Y
377 - 405	3105.6864	3104.6791	3104.5091	55	0	K.SGWTEFTPQVAEPTFASAIQIGDPVSVDR.A
412 - 434	2495.1718	2494.1646	2494.1203	18	0	K.ATDGIVEEATEEELMNAMSLADR.T
412 - 434	2511.1625	2510.1552	2510.1152	16	0	K.ATDGIVEEATEEELMNAMSLADR.T Oxidation (M)
412 - 434	2527.1638	2526.1566	2526.1101	18	0	K.ATDGIVEEATEEELMNAMSLADR.T 2 Oxidation (M)
435 - 452	1907.9182	1906.9109	1906.9434	-17	0	R.TGMFACPHTGVALAALFK.L Oxidation (M)
488 - 494	866.4421	865.4348	865.3674	78	0	K.IEDMACK.Y
495 - 503	974.5186	973.5113	973.5233	-12	0	K.YANPPVSVK.A

Spot 1599

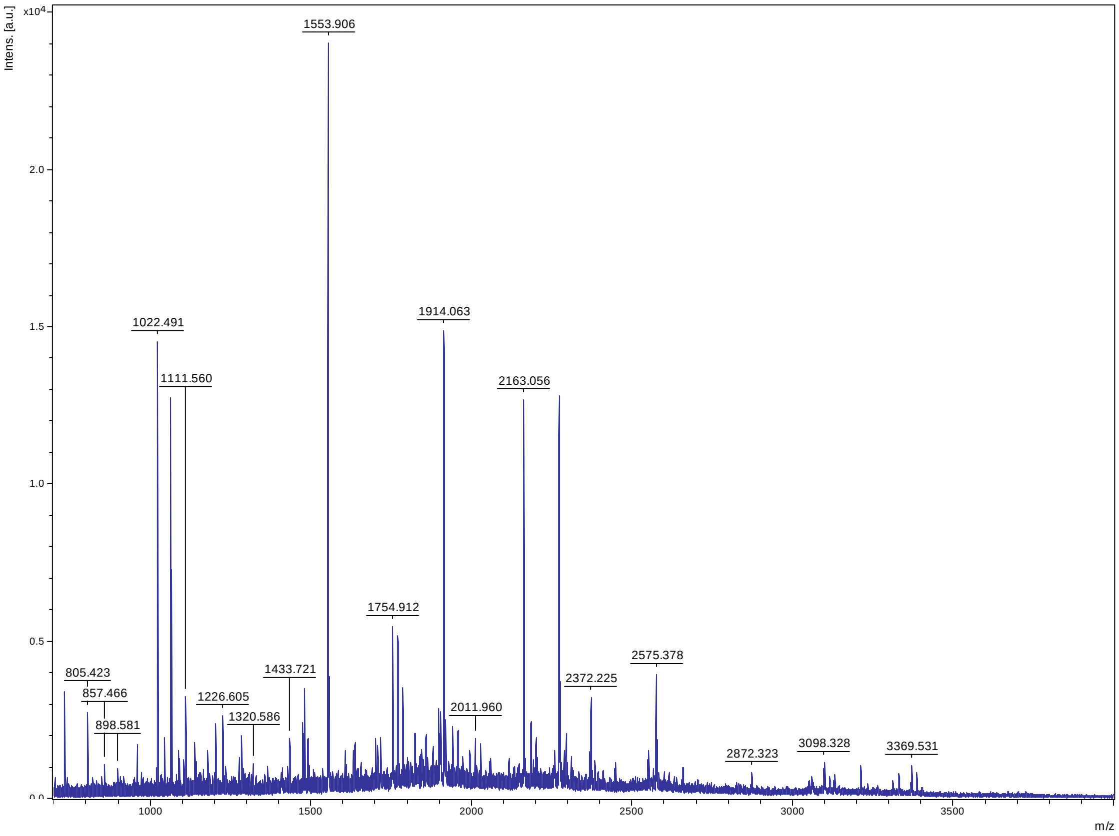


Match to: gi|37535140 Score: 111 Expect: 5.3e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
50 - 59	1030.5398	1029.5325	1029.5342	-0.0017	0	R.GVEELADAVK.V	
137 - 148	1235.5787	1234.5714	1234.5798	-0.0083	0	K.SVAAGMNAMDLR.R	
137 - 148	1267.6092	1266.6019	1266.5696	0.0323	0	K.SVAAGMNAMDLR.R	2 Oxidation (M)
150 - 163	1433.7358	1432.7285	1432.7595	-0.0310	0	R.GISMAVDAVVTNLK.G	Oxidation (M)
168 - 187	2093.0461	2092.0388	2092.0106	0.0283	0	R.MISTSEEIAQVGTISANGER.E	
168 - 187	2109.0518	2108.0445	2108.0055	0.0390	0	R.MISTSEEIAQVGTISANGER.E	Oxidation (M)
188 - 199	1347.7413	1346.7340	1346.7115	0.0225	1	R.EIGELIAKAMEK.V	Oxidation (M)
244 - 256	1580.8133	1579.8060	1579.7916	0.0144	0	K.CELDDPLILIHDK.K	Carbamidomethyl (C)
244 - 257	1708.8985	1707.8912	1707.8865	0.0047	1	K.CELDDPLILIHDKK.V	Carbamidomethyl (C)
274 - 297	2649.4764	2648.4691	2648.5112	-0.0420	1	K.KQRPLLIVAEDVESEALGTLIINK.L	
275 - 297	2521.4372	2520.4299	2520.4162	0.0137	0	K.QRPLLIVAEDVESEALGTLIINK.L	
382 - 395	1585.7763	1584.7690	1584.7519	0.0172	1	R.SAIELSTSDYDKEK.L	
436 - 455	1901.0427	1900.0354	1900.0305	0.0050	0	K.AAVEEGIVPGGGVALLYASK.E	
469 - 479	1196.7303	1195.7230	1195.7288	-0.0058	0	K.IGVQIIQNALK.T	
500 - 514	1665.8102	1664.8029	1664.7893	0.0136	0	K.LLEQDNTDLGYDAAK.G	

Spot 1602

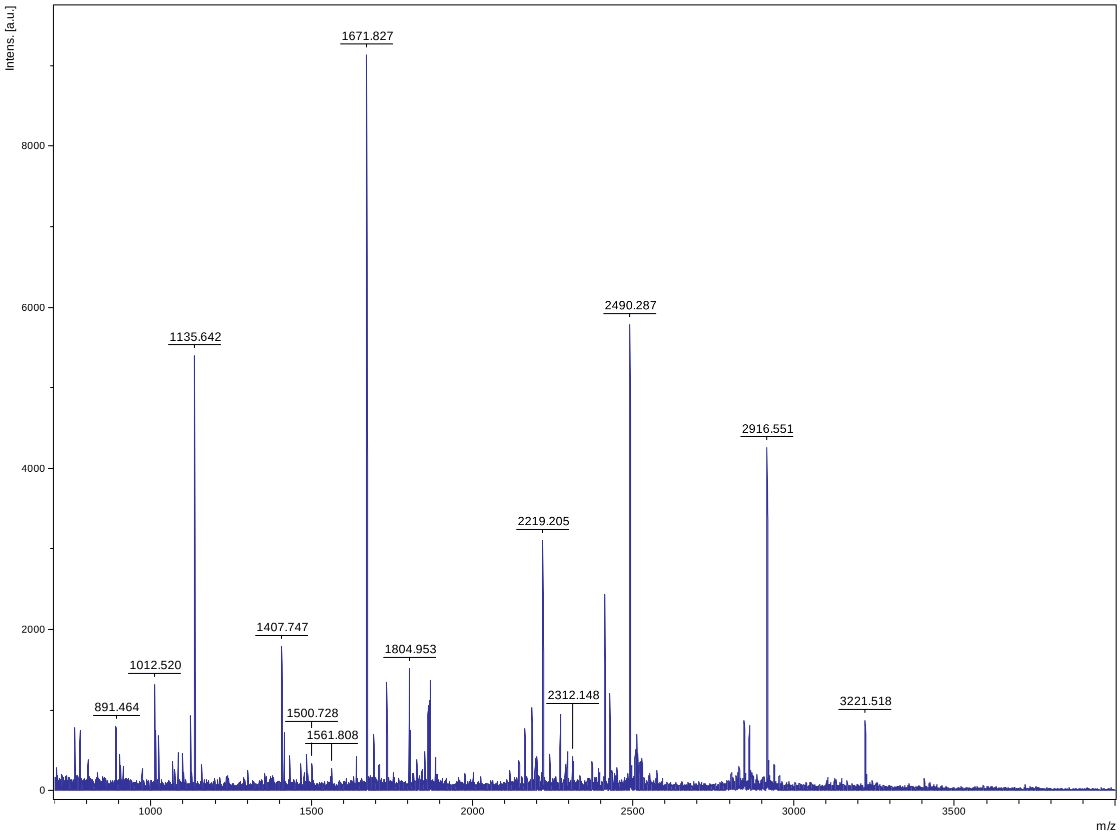


Match to: gi|50920285 Score: 101 Expect: 5.3e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 19	1958.0010	1956.9937	1956.9649	0.0289	0	M.ATMPSTCASSSSLFLLLR.R	Carbamidomethyl (C); Oxidation (M)
46 - 54	1022.4643	1021.4570	1021.4828	-0.0258	0	K.EIAFDQGSR.S	
64 - 75	1138.6966	1137.6893	1137.6869	0.0024	0	K.LAAAVAVTLGPR.G	
78 - 88	1204.6398	1203.6325	1203.6135	0.0190	0	R.NVVLDEFGSPK.V	
89 - 98	1043.5608	1042.5535	1042.5771	-0.0235	0	K.VVNDGVTIAR.A	
99 - 115	1754.9142	1753.9069	1753.9032	0.0037	0	R.AIELADPMENAGAALIR.E	
99 - 115	1770.9308	1769.9235	1769.8981	0.0254	0	R.AIELADPMENAGAALIR.E	Oxidation (M)
121 - 137	1636.8267	1635.8194	1635.7700	0.0495	0	K.TNDSAGDGTTTASVLAR.E	
175 - 185	1143.5770	1142.5697	1142.6407	-0.0710	1	K.SRPVKGSGDIK.A	
238 - 250	1479.7733	1478.7660	1478.7405	0.0255	0	R.GYISPQFVTNPEK.S	
272 - 284	1553.9252	1552.9179	1552.8824	0.0355	0	K.EIIPLLEQTTQLR.A	
363 - 385	2447.1587	2446.1514	2446.2915	-0.1400	1	K.VTISQSSTTIIADVATKDEIQAR.I	
380 - 390	1284.7164	1283.7091	1283.7197	-0.0106	1	K.DEIQARIAQLK.R	
421 - 432	1290.6571	1289.6498	1289.6099	0.0399	0	K.VGAATETELEDR.K	
441 - 464	2372.1584	2371.1511	2371.2171	-0.0660	0	K.NATFAAIEEGIVPGGGAAYVHLSK.F	
488 - 510	2271.2169	2270.2096	2270.2633	-0.0537	0	K.ALVAPAALIAHNAGVEGEVIVEK.I	
527 - 540	1490.7881	1489.7808	1489.7888	-0.0080	0	R.HENLVQAGVIDPAK.V	

Spot 1603

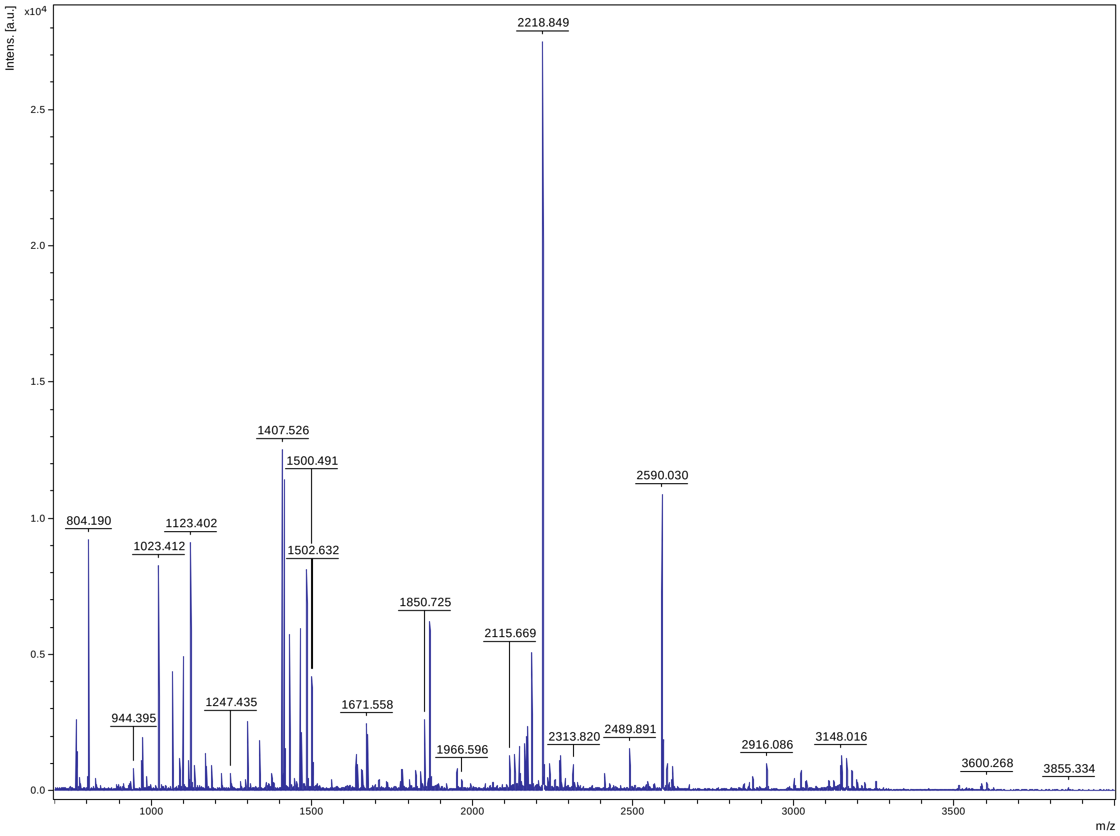


Match to: gi|56784135; Score: 131

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
42 - 48	891.46	890.46	890.43	0.03	0	WGPQFEK
57 - 82	2916.55	2915.55	2915.51	0.04	0	LYLSEQTDGTVPNTLVIANCEVVKPR
83 - 97	1671.83	1670.82	1670.80	0.02	0	VAAAEHISQFNEEAR
106 - 115	1135.64	1134.64	1134.61	0.03	0	TIIHPGEVNR
116 - 124	1084.63	1083.63	1083.60	0.03	1	IRELPQNSK
125 - 146	2490.29	2489.28	2489.26	0.03	0	IIATHTDSPDVLIWDVEAQPNR
147 - 162	1885.00	1884.00	1883.99	0.01	0	QAQLAQMESRPDLILR Oxidation (M)
283 - 311	3221.52	3220.52	3220.47	0.04	0	AHGGDVHCVDWNLHDVNYILTGSADNSVR
317 - 334	1804.95	1803.95	1803.94	0.01	1	NLGSGGAGIPVHKFEGHK
371 - 387	1861.98	1860.97	1860.95	0.02	1	KNPNAPAGLFFQHAGHR
372 - 387	1733.88	1732.88	1732.85	0.02	0	NPNAPAGLFFQHAGHR
424 - 443	2411.21	2410.20	2410.17	0.03	0	MSDLIYRPEDEVLAELENFK
424 - 443	2427.18	2426.18	2426.17	0.01	0	MSDLIYRPEDEVLAELENFK Oxidation (M)
444 - 452	1012.52	1011.52	1011.49	0.03	0	THLASCAPR

Spot 1605

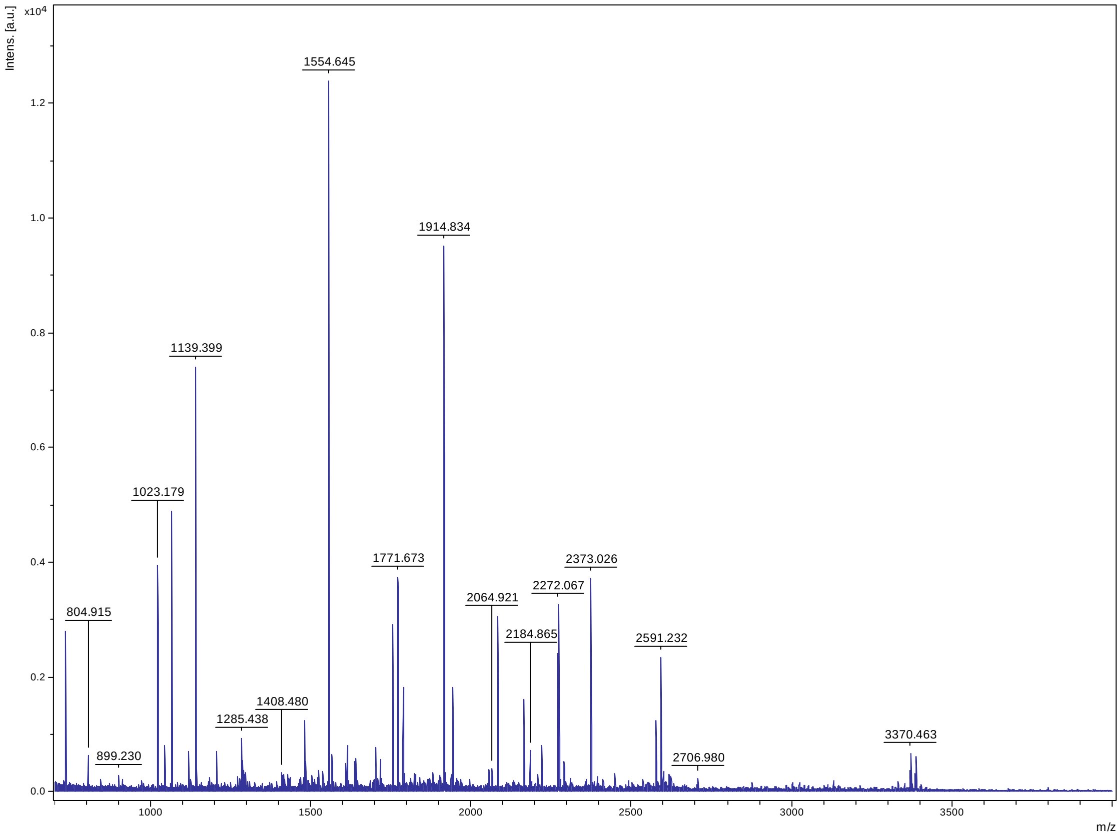


Match to: Q338N8_ORYSA Score: 99 Expect: 8.2e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 23	2489.9024	2488.8951	2489.2406	-0.3454	1	-.MAAPSVAVDNLNPKVLNCEYAVR.G	Oxidation (M)
2 - 14	1337.5185	1336.5112	1336.6986	-0.1874	0	M.AAPSVAVDNLNPK.V	Acetyl (N-term)
15 - 23	1066.4208	1065.4135	1065.5277	-0.1141	0	K.VLNCEYAVR.G	
15 - 23	1123.4185	1122.4112	1122.5491	-0.1379	0	K.VLNCEYAVR.G	Carbamidomethyl (C)
24 - 32	1022.4561	1021.4488	1021.5668	-0.1180	0	R.GEIVIHAQR.L	
70 - 87	2183.7423	2182.7350	2183.0602	-0.3252	1	R.EVIALCDHPCLLEKEETK.S	2 Carbamidomethyl (C)
98 - 108	1099.5092	1098.5019	1098.6397	-0.1378	0	R.ATTILASIPGR.A	
109 - 120	1219.4448	1218.4375	1218.5993	-0.1617	0	R.ATGAYSHSQGIK.G	
124 - 133	944.3948	943.3875	943.5087	-0.1211	0	R.DAIAAGIASR.D	
223 - 243	2218.8690	2217.8617	2218.1705	-0.3088	0	R.ALVVINPGNPTGQVLAEENQR.D	
282 - 300	2115.6812	2114.6739	2114.9830	-0.3090	0	R.SMGYNEDDLPLVSFQSVSK.G	
282 - 300	2131.6871	2130.6798	2130.9779	-0.2981	0	R.SMGYNEDDLPLVSFQSVSK.G	Oxidation (M)
301 - 309	1089.3402	1088.3329	1088.4709	-0.1379	1	K.GYYGECGKR.G	Carbamidomethyl (C)
309 - 323	1640.5814	1639.5741	1639.8140	-0.2399	1	K.RGGYMEITGFSAPVR.E	
309 - 323	1656.5713	1655.5640	1655.8089	-0.2449	1	K.RGGYMEITGFSAPVR.E	Oxidation (M)
310 - 323	1484.5151	1483.5078	1483.7129	-0.2051	0	R.GGYMEITGFSAPVR.E	
310 - 323	1500.5107	1499.5034	1499.7078	-0.2044	0	R.GGYMEITGFSAPVR.E	Oxidation (M)
310 - 328	2145.7497	2144.7424	2145.0564	-0.3140	1	R.GGYMEITGFSAPVREQIYK.V	
363 - 374	1300.5439	1299.5366	1299.7146	-0.1780	1	K.AEKDGILQSLAR.R	
366 - 375	1170.4850	1169.4777	1169.6516	-0.1739	1	K.DGILQSLARR.A	Acetyl (N-term)
378 - 393	1780.5959	1779.5886	1779.8461	-0.2575	0	K.ALENAFNSLEGITCNK.T	Carbamidomethyl (C)
394 - 409	1838.6543	1837.6470	1837.9284	-0.2814	0	K.TEGAMYLFPQLSLPQK.A	Oxidation (M)
410 - 419	972.4299	971.4227	971.5399	-0.1173	1	K.AIDAAKAANK.A	
416 - 428	1407.5415	1406.5342	1406.7306	-0.1964	1	K.AANKAPDAFYALR.L	
420 - 428	1023.4223	1022.4150	1022.5185	-0.1035	0	K.APDAFYALR.L	
429 - 453	2590.3127	2589.3054	2589.4066	-0.1012	0	R.LLEATGIVVVPGSGFGQVPGTWHIR.C	
454 - 469	1867.7593	1866.7520	1867.0237	-0.2717	1	R.CTILPQEEKIPAIISR.F	Carbamidomethyl (C)
463 - 469	769.4154	768.4081	768.4857	-0.0776	0	K.IPAIISR.F	
472 - 483	1414.4291	1413.4218	1413.6135	-0.1917	1	K.AFHEGFMAAYRD.-	
472 - 483	1430.4200	1429.4127	1429.6084	-0.1957	1	K.AFHEGFMAAYRD.-	Oxidation (M)

Spot 1608

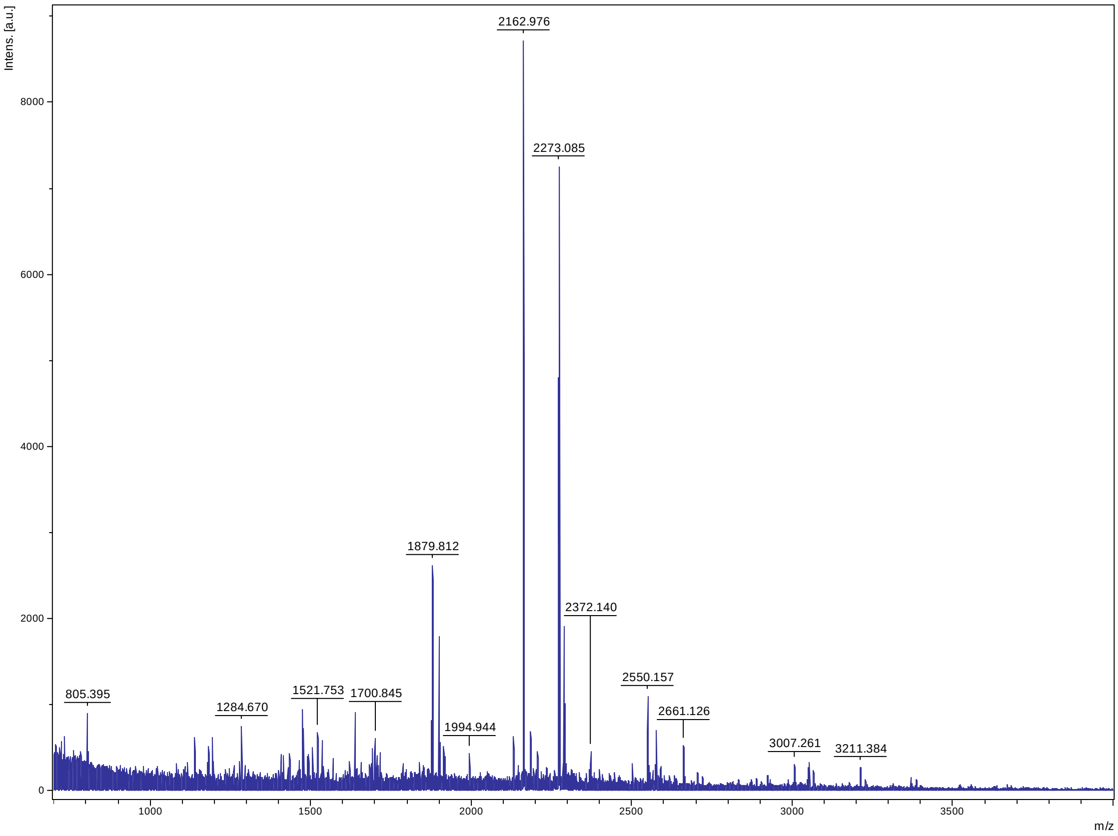


Match to: Q7X9A7_ORYSA Score: 76 Expect: 0.0015

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
46 - 54	1022.7796	1021.7723	1021.4828	0.2895	0	K.EIAFDQGSR.S	
64 - 75	1138.9837	1137.9764	1137.6869	0.2895	0	K.LAAAVAVTLGPR.G	
78 - 88	1204.8981	1203.8908	1203.6135	0.2773	0	R.NVVLDEFGSPK.V	
89 - 98	1043.8761	1042.8688	1042.5771	0.2918	0	K.VVNDGVTIAR.A	
99 - 115	1754.9139	1753.9066	1753.9032	0.0034	0	R.AIELADPMENAGAALIR.E	
99 - 115	1770.9127	1769.9054	1769.8981	0.0073	0	R.AIELADPMENAGAALIR.E	Oxidation (M)
238 - 250	1479.9217	1478.9144	1478.7405	0.1739	0	R.GYISPQFVTNPEK.S	
267 - 284	2081.9621	2080.9548	2081.2096	-0.2547	1	K.ISSIKEIIPLLEQTTQLR.A	
272 - 284	1554.0299	1553.0226	1552.8824	0.1402	0	K.EIIPLLEQTTQLR.A	
309 - 324	1613.0365	1612.0292	1611.9096	0.1196	1	R.GILNVAAIKAPGFGER.R	
318 - 324	733.5913	732.5840	732.3554	0.2286	0	K.APGFGER.R	
327 - 343	1787.9763	1786.9690	1786.9828	-0.0138	0	K.ALLQDIAIVTGAEFQAK.D	
380 - 390	1284.9830	1283.9757	1283.7197	0.2560	1	K.DEIQARIAQLK.R	
421 - 432	1290.8829	1289.8756	1289.6099	0.2657	0	K.VGAATETELEDR.K	

Spot 1611

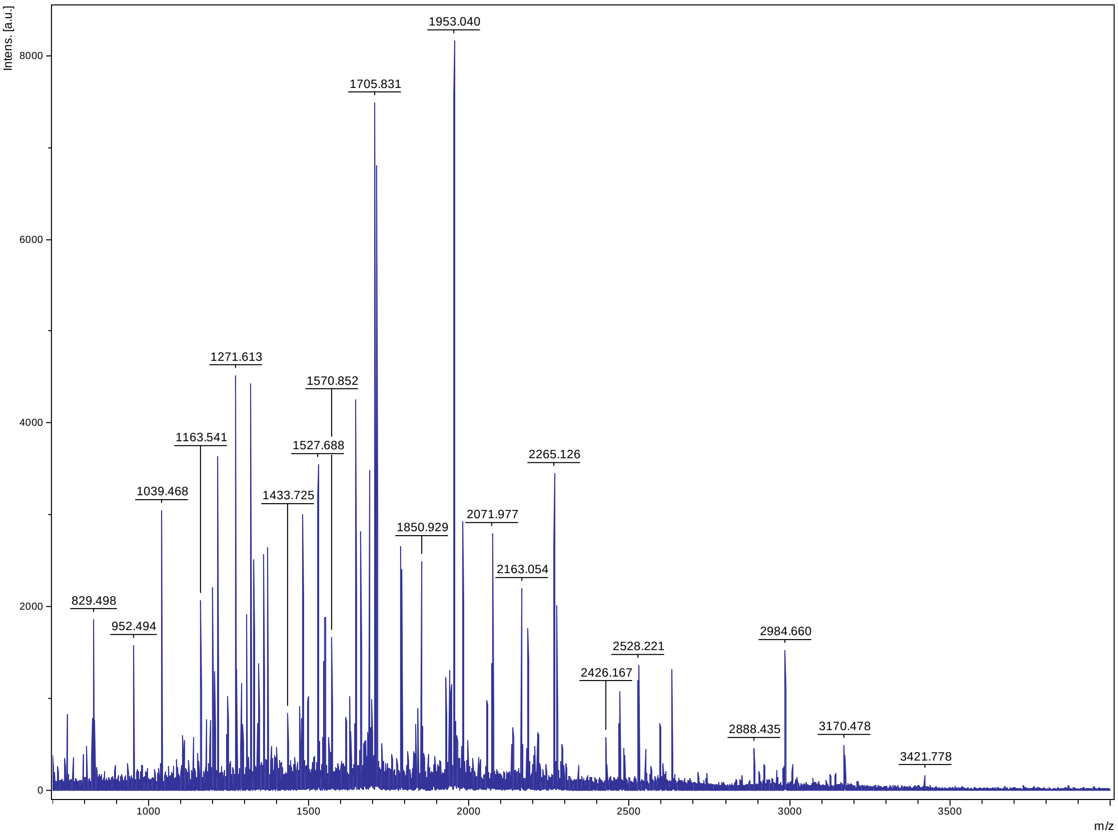


Match to: gi|77549143; Score: 85

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
112 - 121	1195.60	1194.60	1194.63	-0.03	0	YEIQGFPTLK
214 - 224	1182.62	1181.61	1181.65	-0.04	0	GDAAVERPLVR
225 - 237	1536.76	1535.76	1535.82	-0.06	0	LFKPFDELVVDSK
256 - 271	1899.93	1898.93	1898.99	-0.06	1	VVTFDKNPDNHPYLLK
296 - 308	1506.67	1505.67	1505.70	-0.04	1	SVYYGAAEEFKDK
312 - 330	2132.02	2131.02	2131.07	-0.05	0	FLIGDIEASQGAFQYFGLR
350 - 362	1521.75	1520.75	1520.80	-0.05	0	AHVEPDQIVSWLK
404 - 418	1879.81	1878.81	1878.85	-0.04	0	NVLVEFYAPWCGHCK
442 - 469	3065.35	3064.35	3064.40	-0.05	0	MDATANDVPSEFDVQGYPTLYFVTPSGK Oxidation (M)

Spot 1613



Match to: gi|75261364 Score: 161 Expect: 1.1e-11

Matched peptides:

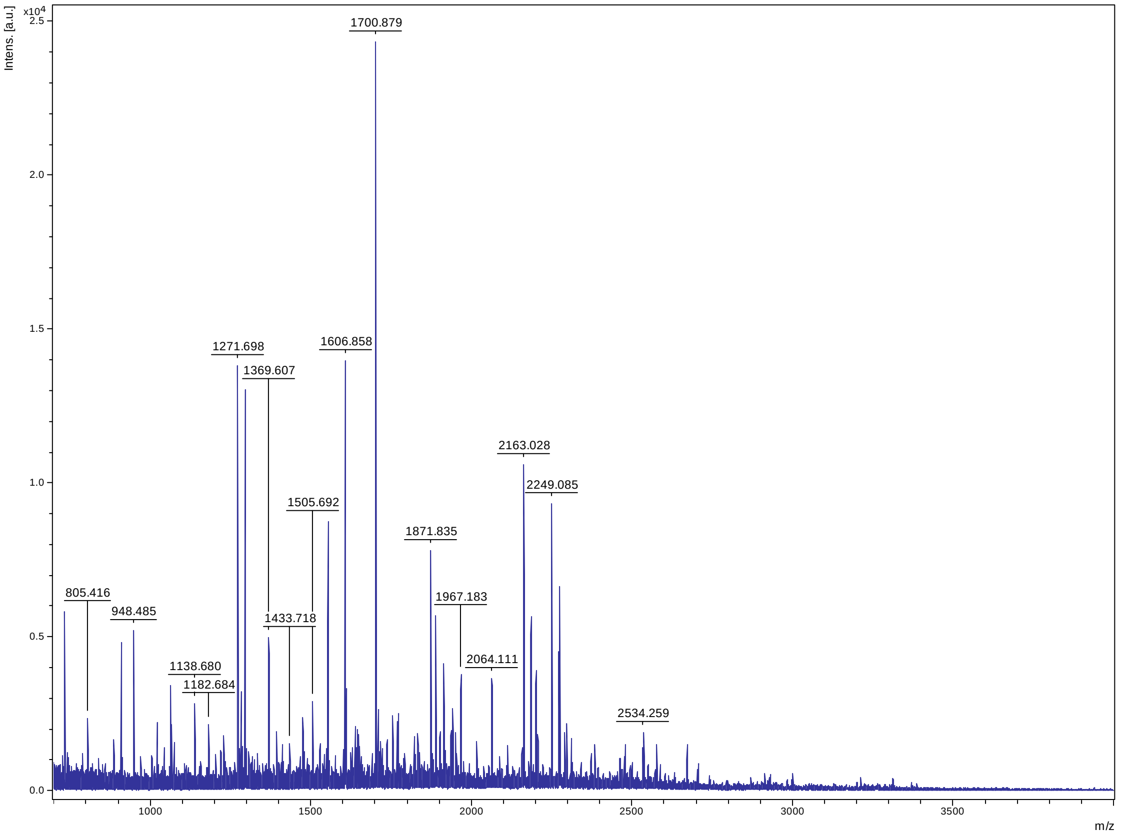
Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
100 - 107	1039.4685	1038.4612	1038.4658	-4	0	K.DVEFSEWK.G	
108 - 122	1570.8516	1569.8443	1569.8614	-11	0	K.GDILAIAVTENDLVK.G	
123 - 134	1294.6443	1293.6371	1293.6565	-15	1	K.GSDSKFENAVLK.K	
135 - 156	2265.1260	2264.1187	2264.1172	1	1	K.KLDGQLGGLLSEASAEEDFTGK.A	
136 - 156	2137.0261	2136.0188	2136.0222	-2	0	K.LDGQLGGLLSEASAEEDFTGK.A	
157 - 164	829.4979	828.4906	828.4818	11	0	K.AGQSVVLR.L	
173 - 190	1787.9185	1786.9112	1786.9247	-8	0	R.VGLIGLGQNAPSTTTACK.G	
202 - 223	2183.0921	2182.0848	2182.0906	-3	0	K.SAQASSAAIVFASVGGIQEDFK.L	
224 - 243	1953.0398	1952.0325	1952.0327	-0	0	K.LTAAAAIASGTVLGLHEDSR.Y	
255 - 270	1688.8346	1687.8273	1687.8417	-9	0	K.QVDLIGFGSGPEVDQK.L	
273 - 285	1370.6841	1369.6768	1369.6878	-8	0	K.YANDLSSGVIFGK.E	
368 - 379	1271.6135	1270.6062	1270.6194	-10	0	K.GLTFDSGGYNIK.T	
380 - 390	1192.5774	1191.5701	1191.5628	6	0	K.TGPGCSIELMK.F	
380 - 390	1208.5572	1207.5499	1207.5577	-6	0	K.TGPGCSIELMK.F	Oxidation (M)
391 - 404	1328.6227	1327.6155	1327.6231	-6	0	K.FDMGGSAAVFGAAK.A	
391 - 404	1344.6078	1343.6005	1343.6180	-13	0	K.FDMGGSAAVFGAAK.A	Oxidation (M)
445 - 456	1318.6133	1317.6060	1317.6161	-8	0	K.TIEVNNTDAEGR.L	
457 - 473	1850.9287	1849.9214	1849.9244	-2	0	R.LTLADALVYACNQGVDK.I	
505 - 516	1190.6029	1189.5957	1189.5826	11	0	K.EVAAASEISGEK.F	
520 - 531	1529.6660	1528.6587	1528.6578	1	0	R.MPLEESYWESMK.S	
520 - 531	1545.6619	1544.6546	1544.6527	1	0	R.MPLEESYWESMK.S	Oxidation (M)
532 - 543	1163.5411	1162.5338	1162.5401	-5	0	K.SGVADMVNTGGR.Q	
544 - 555	1205.6722	1204.6649	1204.6816	-14	0	R.QGGSITAALFLK.Q	
562 - 577	1926.8937	1925.8865	1925.8917	-3	0	K.VQWMHIDMAGPVWNDK.K	
562 - 577	1942.9452	1941.9380	1941.8866	26	0	K.VQWMHIDMAGPVWNDK.K	Oxidation (M)

Match to: gi|13560275 Score: 137 Expect: 2.7e-09

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
46 - 74	3170.4781	3169.4708	3169.3843	27	0	R.LPVTHVGDELHHSGWNACSSCHGDPSASR.R	
76 - 86	1215.7386	1214.7314	1214.7387	-6	0	R.FLILPSLLSGR.V	
87 - 97	1304.6996	1303.6924	1303.7136	-16	1	R.VYVVDTLKDPR.A	
160 - 178	2426.1673	2425.1600	2425.1280	13	0	R.WEKPGHSPLFGYDYWYQPR.H	
181 - 194	1481.7150	1480.7077	1480.7133	-4	0	K.TMISSSWGAPAAFR.T	
181 - 194	1497.7209	1496.7137	1496.7082	4	0	K.TMISSSWGAPAAFR.T	Oxidation (M)
195 - 209	1705.8308	1704.8235	1704.8220	1	0	R.TGFDLQHVQDGLYGR.H	
210 - 222	1550.7713	1549.7640	1549.7678	-2	0	R.HLHVYDWPGGELK.Q	
223 - 238	1694.9110	1693.9038	1693.9251	-13	0	K.QTLDLGSTGLLPLEVR.F	Gln->pyro-Glu (N-term Q)
223 - 238	1711.9627	1710.9554	1710.9516	2	0	K.QTLDLGSTGLLPLEVR.F	
239 - 260	2468.2111	2467.2039	2467.1624	17	1	R.FLHDPSKDTGYVGCALTSNMVR.F	
239 - 260	2484.1878	2483.1806	2483.1573	9	1	R.FLHDPSKDTGYVGCALTSNMVR.F	Oxidation (M)
246 - 260	1643.7819	1642.7747	1642.7443	18	0	K.DTGYVGCALTSNMVR.F	
264 - 281	1939.0206	1938.0134	1938.0211	-4	0	K.TADGSWSHEVAISIKPLK.V	
305 - 317	1661.8540	1660.8467	1660.8725	-16	0	R.YLYLVNWLHGDIR.Q	
318 - 341	2595.4144	2594.4072	2594.3857	8	0	R.QYNIEDPAKPVLAGQVWAGGLLQK.G	
342 - 363	2528.2214	2527.2141	2527.1966	7	1	K.GSEVVYVTEDDKEEQYSVPQVK.G	
369 - 381	1343.6550	1342.6477	1342.6915	-33	0	R.GGPQMIQLSLDGK.R	
383 - 392	1199.6332	1198.6259	1198.6346	-7	0	R.IYVTNSLFSR.W	
393 - 404	1527.6878	1526.6805	1526.7042	-15	0	R.WDEQFYGQDLVK.K	
419 - 445	2888.4349	2887.4276	2887.3599	23	0	K.GGLSINPNFFVDFGAEPEGPSLAHEMR.Y	

Spot 1616

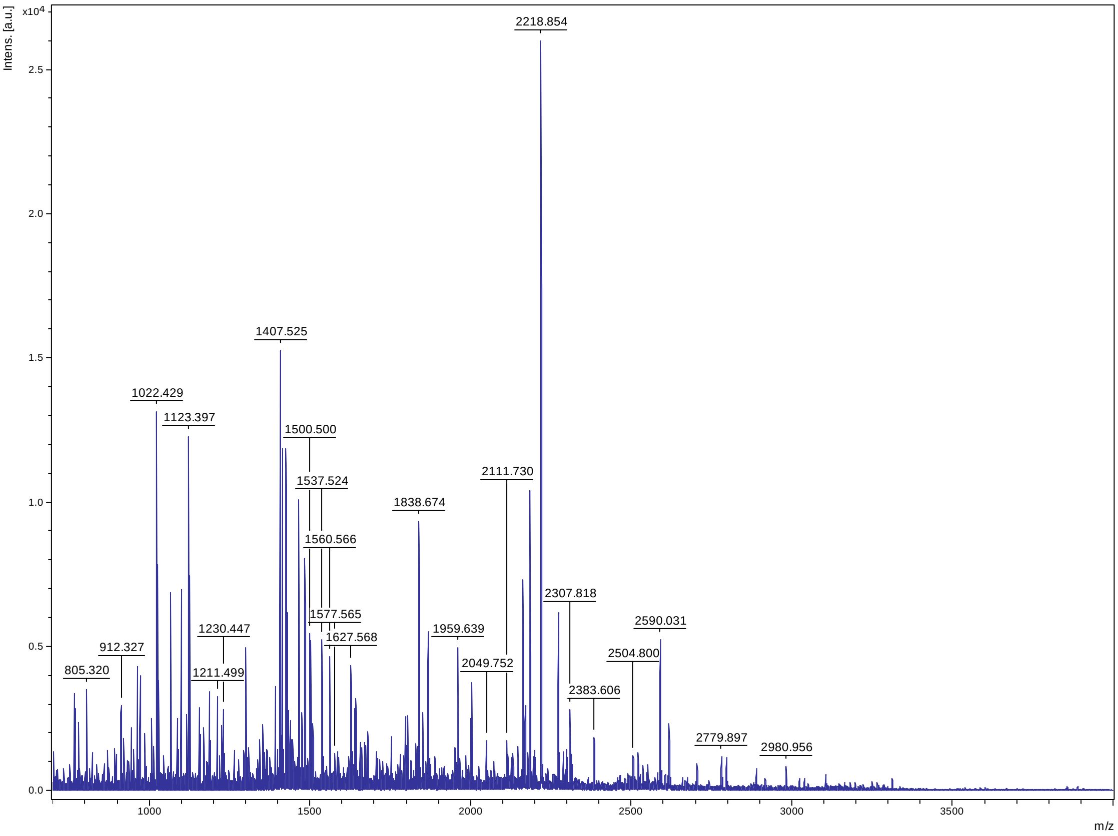


Match to: gi|51963782; Score: 130

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
55 - 66	1410.74	1409.73	1409.76	-0.02	1	ELYFNKDGLAIK
75 - 86	1182.68	1181.68	1181.70	-0.02	0	LADLVGVTLGPK
158 - 170	1295.72	1294.72	1294.74	-0.02	0	VVAAGANPVQITR
233 - 248	1871.83	1870.83	1870.85	-0.02	0	SAENNLYVVEGMQFDR
233 - 248	1887.83	1886.83	1886.85	-0.02	0	SAENNLYVVEGMQFDR Oxidation (M)
249 - 261	1505.69	1504.69	1504.71	-0.02	0	GYISPYFVTDSEK
283 - 293	1271.70	1270.70	1270.71	-0.02	0	DLITILEDAIR
336 - 353	1951.03	1950.03	1950.04	-0.01	1	KSQYLDDIATLTGGTVIR
337 - 353	1822.93	1821.93	1821.95	-0.02	0	SQYLDDIATLTGGTVIR
379 - 396	1935.94	1934.94	1934.92	0.02	1	DSTTIVGDGTTQDEVNKR
402 - 413	1479.73	1478.72	1478.69	0.03	0	NQIEVAEQEYEK
402 - 415	1736.83	1735.83	1735.83	0.00	1	NQIEVAEQEYEKEK
423 - 441	1899.96	1898.96	1899.03	-0.07	0	LSGGVAVIQVGAQTETELK
423 - 443	2157.15	2156.15	2156.17	-0.02	1	LSGGVAVIQVGAQTETELKEK
445 - 455	1229.67	1228.67	1228.68	-0.01	1	LRVEDALNATK
456 - 472	1700.88	1699.88	1699.89	-0.02	0	AAVEEGIVVGGGCTLLR
473 - 490	2016.01	2015.01	2015.04	-0.03	1	LASKVDAIIETLENDEQK
522 - 529	948.48	947.48	947.48	0.00	0	VLANDNFR
530 - 552	2478.18	2477.18	2477.18	-0.00	1	YGYNAATGKYEDLMAAGIIDPTK Oxidation (M)
539 - 555	1890.97	1889.97	1889.99	-0.02	1	YEDLMAAGIIDPTKVVR

Spot 1619

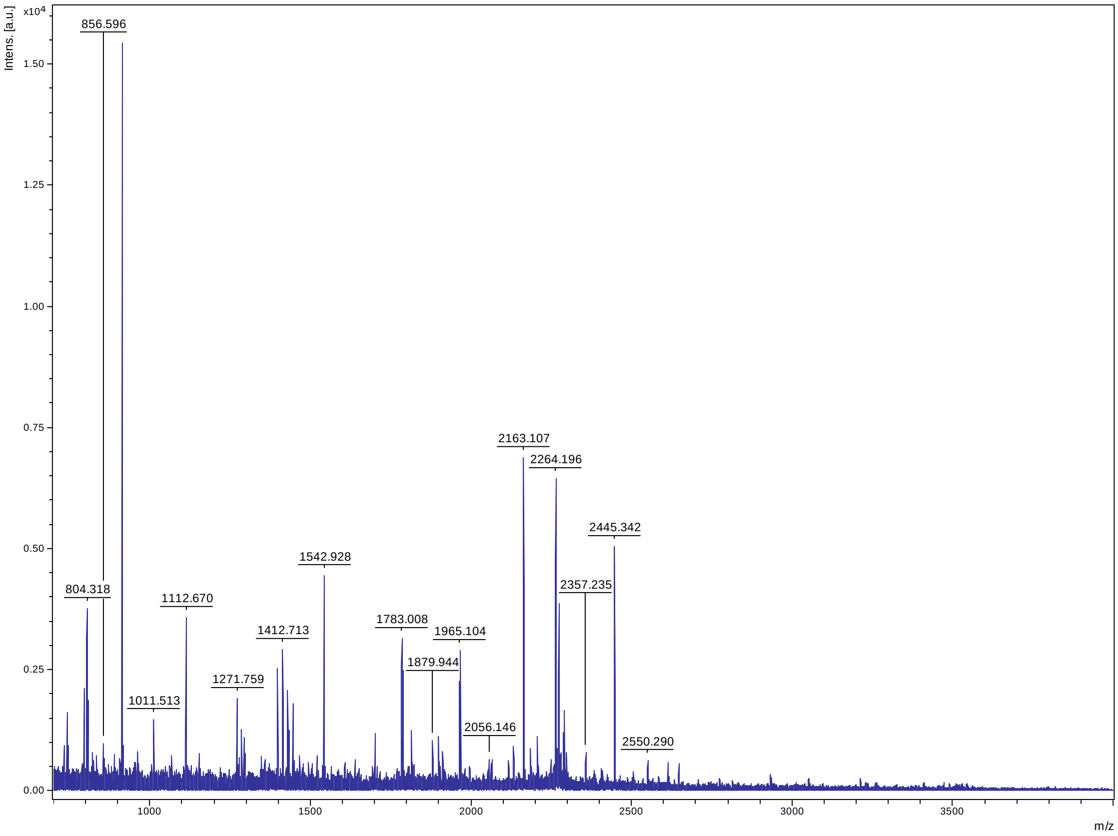


Match to: Q338N8_ORYSA Score: 79 Expect: 0.0009

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
15 - 23	1066.4169	1065.4096	1065.5277	-0.1180	0	K.VLNCEYAVR.G	
15 - 23	1123.4404	1122.4331	1122.5491	-0.1160	0	K.VLNCEYAVR.G	Carbamidomethyl (C)
24 - 32	1022.4370	1021.4297	1021.5668	-0.1371	0	R.GEIVIHAQR.L	
70 - 87	2183.7712	2182.7639	2183.0602	-0.2963	1	R.EVIALCDHPCLLEKEETK.S	2 Carbamidomethyl (C)
98 - 108	1099.5075	1098.5002	1098.6397	-0.1395	0	R.ATTILASIPGR.A	
124 - 133	944.3999	943.3926	943.5087	-0.1161	0	R.DAIAAGIASR.D	
282 - 300	2131.7347	2130.7274	2130.9779	-0.2505	0	R.SMGYNEDDLPLVSFQSVSK.G	Oxidation (M)
301 - 309	1089.3541	1088.3468	1088.4709	-0.1240	1	K.GYYGECGKR.G	Carbamidomethyl (C)
309 - 323	1640.6230	1639.6157	1639.8140	-0.1983	1	K.RGGYMEITGFSAPVR.E	
310 - 323	1484.5191	1483.5118	1483.7129	-0.2011	0	R.GGYMEITGFSAPVR.E	
310 - 323	1500.5371	1499.5298	1499.7078	-0.1780	0	R.GGYMEITGFSAPVR.E	Oxidation (M)
363 - 374	1300.5450	1299.5377	1299.7146	-0.1769	1	K.AEKDGILQSLAR.R	
410 - 419	972.4243	971.4170	971.5399	-0.1230	1	K.AIDAAKAANK.A	
416 - 428	1407.5557	1406.5484	1406.7306	-0.1822	1	K.AANKAPDAFYALR.L	
420 - 428	1023.3955	1022.3882	1022.5185	-0.1303	0	K.APDAFYALR.L	
454 - 469	1867.7608	1866.7535	1867.0237	-0.2702	1	R.CTILPQEEKIPAIISR.F	Carbamidomethyl (C)
463 - 469	769.4082	768.4010	768.4857	-0.0848	0	K.IPAIISR.F	
472 - 483	1414.4279	1413.4206	1413.6135	-0.1929	1	K.AFHEGFMAAYRD.-	
472 - 483	1430.4553	1429.4480	1429.6084	-0.1604	1	K.AFHEGFMAAYRD.-	Oxidation (M)

Spot 1626

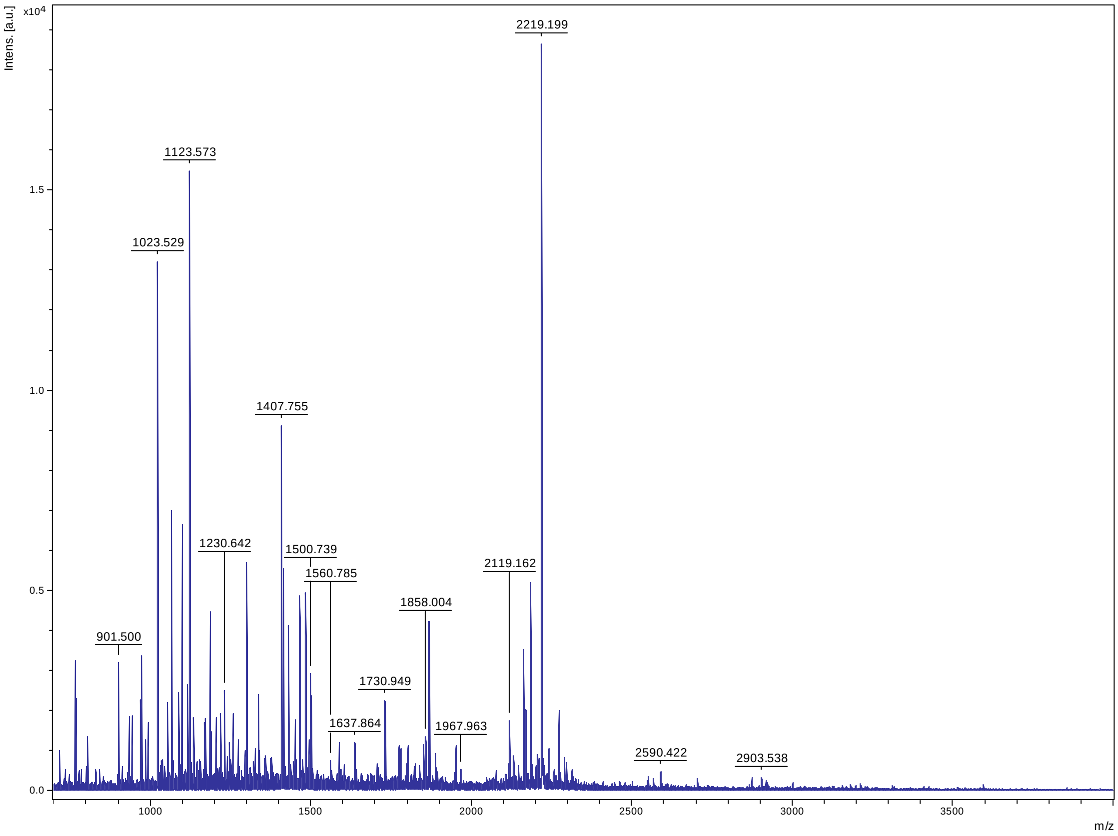


Match to: gi|49388150; Score: 142

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
11 - 32	2445.34	2444.34	2444.26	0.08	0	SFVEVAPGSHFPIQNLPFGVFR
77 - 92	1911.10	1910.09	1909.92	0.18	0	QETLNMFLGMGRPAWK 2 Oxidation (M)
101 - 110	1112.67	1111.67	1111.62	0.04	0	ILSADEPVLR
101 - 116	1783.01	1782.01	1781.95	0.05	1	ILSADEPVLRDNEALK
156 - 175	2264.20	2263.19	2263.13	0.06	0	GPQTPVNPNWFQLPVGYHGR
176 - 190	1542.93	1541.93	1541.88	0.05	0	ASSVIVSGTDIIRPK
191 - 207	1787.90	1786.90	1786.84	0.06	0	GQGHPTGDSRPYFGPSK
251 - 266	1784.99	1783.99	1783.95	0.04	0	DIQAWETIPLGPFLGK
292 - 303	1396.71	1395.71	1395.69	0.02	0	QEPEPLPYLAEK Pyro-glu (N-term Q)
304 - 319	1965.10	1964.10	1964.05	0.05	0	NHVNYDIPLEVWIKPK
385 - 393	962.55	961.55	961.48	0.07	0	EISVGNSTR
394 - 409	1897.95	1896.95	1896.90	0.05	1	KFLEDGDEVILTACCK
410 - 423	1446.68	1445.67	1445.62	0.05	0	GEGYNVGFGTCTGK

Spot 1628

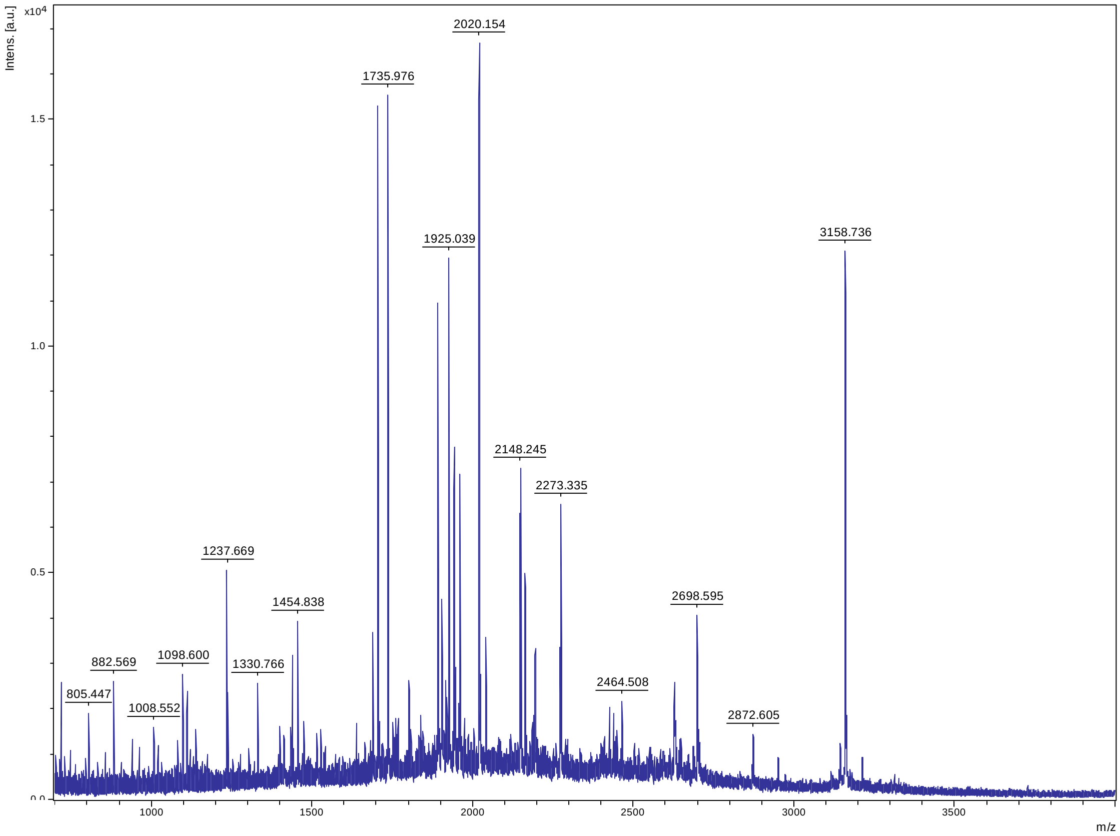


Match to: gi|78708519 Score: 89 Expect: 8.4e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 14	1295.4161	1294.4088	1294.6881	-0.2792	0	M.AAPSVAVDNLNPK.V	
15 - 23	1066.4247	1065.4174	1065.5277	-0.1102	0	K.VLNCEYAVR.G	
15 - 23	1123.4091	1122.4018	1122.5491	-0.1473	0	K.VLNCEYAVR.G	Carbamidomethyl (C)
24 - 32	1022.4422	1021.4349	1021.5668	-0.1319	0	R.GEIVIHAQR.L	
70 - 83	1696.7585	1695.7512	1695.8324	-0.0812	0	R.EVIALCDHPCLLEK.E	2 Carbamidomethyl (C)
98 - 108	1099.5044	1098.4971	1098.6397	-0.1426	0	R.ATTILASIPGR.A	
109 - 120	1219.4282	1218.4209	1218.5993	-0.1783	0	R.ATGAYSHSQGIK.G	
124 - 133	944.4407	943.4334	943.5087	-0.0752	0	R.DAIAAGIASR.D	
210 - 215	747.4429	746.4356	746.3559	0.0797	0	K.QLEDSR.L	
210 - 217	971.3037	970.2965	970.5083	-0.2119	1	K.QLEDSRLK.G	Gln->pyro-Glu (N-term Q)
216 - 222	800.5216	799.5144	799.4915	0.0228	1	R.LKGIDVR.A	
282 - 300	2116.2325	2115.2252	2114.9830	0.2423	0	R.SMGYNEDDLPLVSFQSVSK.G	
282 - 300	2132.2669	2131.2596	2130.9779	0.2817	0	R.SMGYNEDDLPLVSFQSVSK.G	Oxidation (M)
301 - 308	933.3170	932.3098	932.3698	-0.0600	0	K.GYYGECGK.R	Carbamidomethyl (C)
301 - 309	1089.3464	1088.3391	1088.4709	-0.1317	1	K.GYYGECGKR.G	Carbamidomethyl (C)
309 - 323	1640.7048	1639.6975	1639.8140	-0.1165	1	K.RGGYMEITGFSAPVR.E	
310 - 323	1484.5548	1483.5475	1483.7129	-0.1654	0	R.GGYMEITGFSAPVR.E	
310 - 323	1500.5468	1499.5395	1499.7078	-0.1683	0	R.GGYMEITGFSAPVR.E	Oxidation (M)
310 - 328	2146.3540	2145.3467	2145.0564	0.2903	1	R.GGYMEITGFSAPVREQIYK.V	
363 - 374	1300.5390	1299.5317	1299.7146	-0.1829	1	K.AEKDGILQSLAR.R	
378 - 393	1780.7956	1779.7883	1779.8461	-0.0578	0	K.ALENAFNSLEGITCNK.T	Carbamidomethyl (C)
394 - 409	1822.9359	1821.9286	1821.9335	-0.0048	0	K.TEGAMYLFPQLSLPQK.A	
394 - 409	1838.9176	1837.9103	1837.9284	-0.0181	0	K.TEGAMYLFPQLSLPQK.A	Oxidation (M)
410 - 419	972.4347	971.4274	971.5399	-0.1126	1	K.AIDAAKAANK.A	
416 - 428	1407.5517	1406.5444	1406.7306	-0.1862	1	K.AANKAPDAFYALR.L	
420 - 428	1023.4077	1022.4004	1022.5185	-0.1181	0	K.APDAFYALR.L	
454 - 469	1868.0548	1867.0475	1867.0237	0.0238	1	R.CTILPQEEKIPAIISR.F	Carbamidomethyl (C)
463 - 469	769.5429	768.5356	768.4857	0.0499	0	K.IPAIISR.F	
463 - 471	1044.4044	1043.3971	1043.6491	-0.2520	1	K.IPAIISRFK.A	
472 - 483	1414.4495	1413.4422	1413.6135	-0.1713	1	K.AFHEGFMAAYRD.-	
472 - 483	1430.4442	1429.4369	1429.6084	-0.1715	1	K.AFHEGFMAAYRD.-	Oxidation (M)

Spot 1635

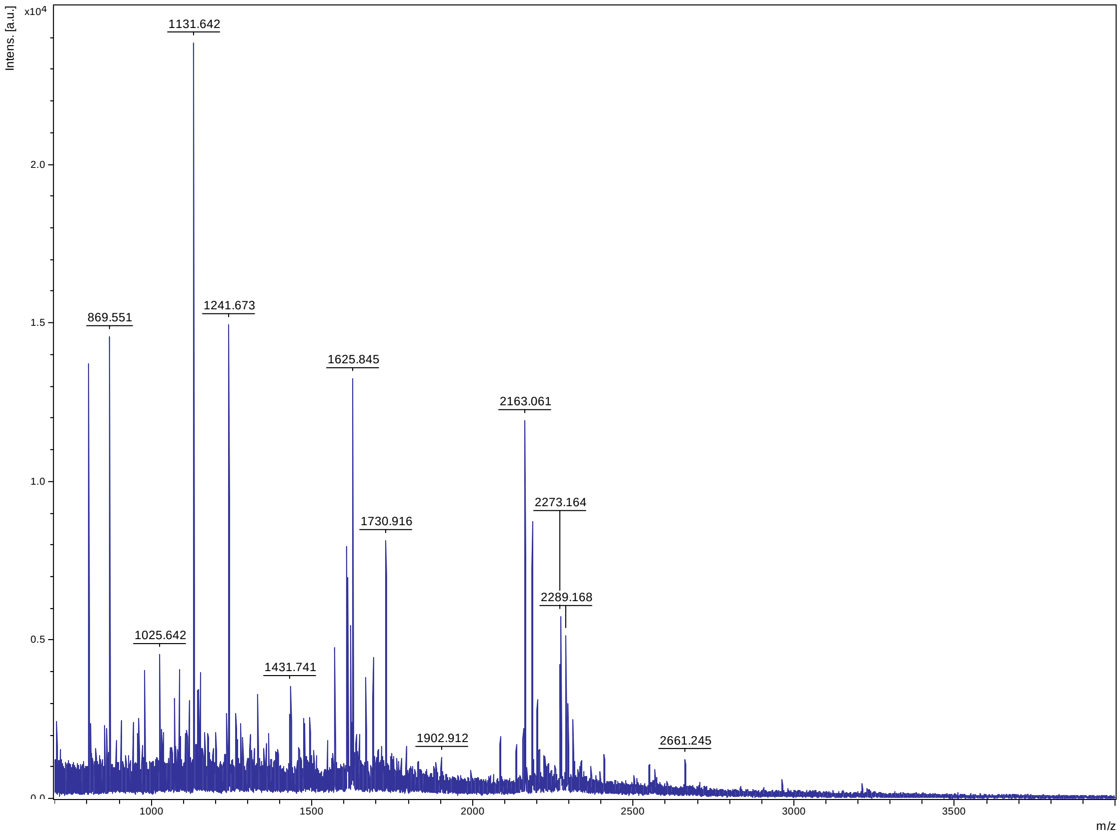


Match to: gi|50908803 Score: 75 Expect: 0.0022

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
18 - 27	1138.6327	1137.6254	1137.5891	0.0364	0	K.QRPDPAAIDR.D	
18 - 41	2704.3921	2703.3848	2703.2194	0.1654	1	K.QRPDPAAIDRDMSSEVVDSNPYSR.L	Oxidation (M); Pyro-glu (N-term Q)
48 - 56	1096.5413	1095.5340	1095.5018	0.0321	0	R.MGIVDNYER.I	
57 - 80	2464.5083	2463.5010	2463.3154	0.1856	1	R.IRDYSIAIVGIGGVGSVAAEMLTR.C	Oxidation (M)
59 - 80	2195.3379	2194.3306	2194.1303	0.2004	0	R.DYSIAIVGIGGVGSVAAEMLTR.C	Oxidation (M)
86 - 101	1943.0924	1942.0851	1941.9506	0.1346	0	R.LLLYDYDTVELANMNR.L	
86 - 101	1959.1100	1958.1027	1957.9455	0.1572	0	R.LLLYDYDTVELANMNR.L	Oxidation (M)
102 - 113	1438.8102	1437.8029	1437.7438	0.0591	0	R.LFFRPDQVGMTK.T	
102 - 113	1454.8378	1453.8305	1453.7387	0.0918	0	R.LFFRPDQVGMTK.T	Oxidation (M)
142 - 151	1098.6005	1097.5932	1097.5757	0.0175	0	K.GFETFLGSLK.A	
159 - 175	1925.0391	1924.0318	1923.8996	0.1322	0	R.NTGVDLVLSCVDNYEAR.M	Carbamidomethyl (C)
365 - 393	3158.7356	3157.7283	3157.4938	0.2345	0	R.ELPTADSYQEPVAPVTSGAIDDDLEELQR.Q	

Spot 1643

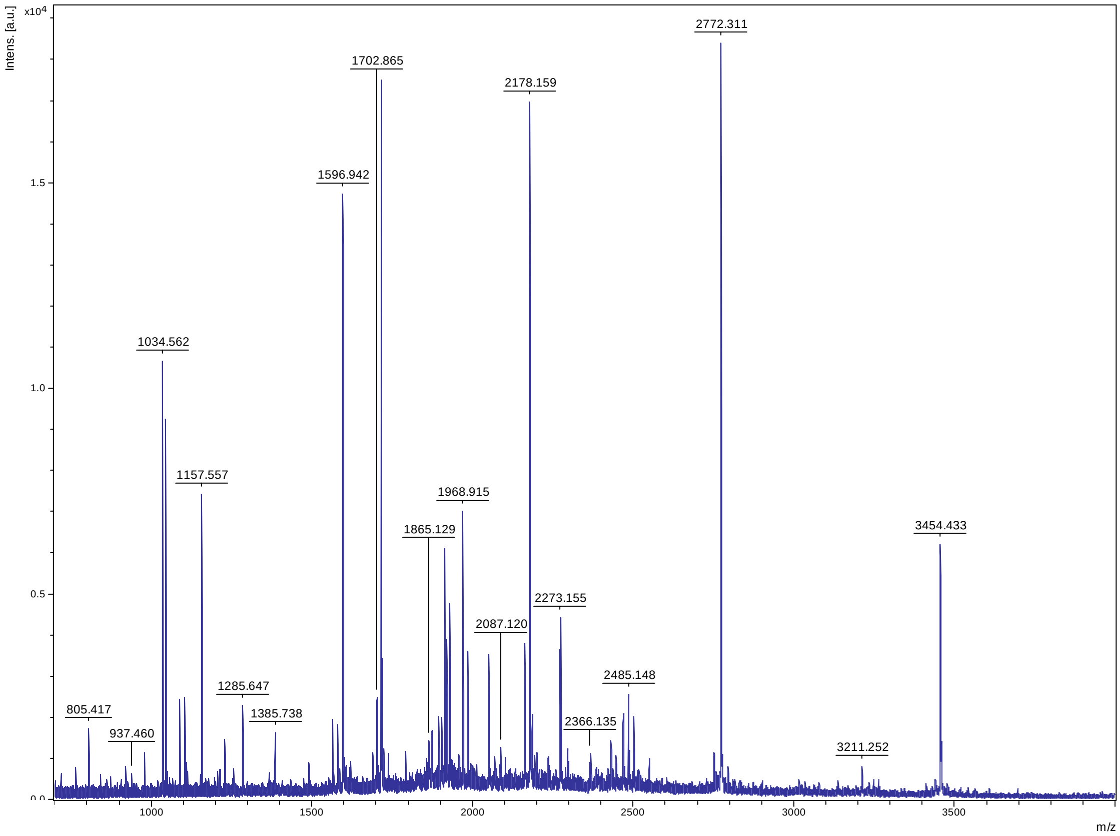


Match to: gi|55773816; Score: 97

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
94 - 103	961.44	960.44	960.42	0.02	0	GANQAACGGR
104 - 114	1131.64	1130.64	1130.64	-0.01	0	LAAGPTYLVAR
123 - 135	1241.67	1240.67	1240.68	-0.01	0	LLEGALADAGGVR
123 - 138	1625.84	1624.84	1624.89	-0.05	1	LLEGALADAGGVRLDR
187 - 195	1025.64	1024.64	1024.65	-0.01	1	RAGVLLLQR
188 - 195	869.55	868.55	868.55	-0.00	0	AGVLLLQR
196 - 210	1667.87	1666.87	1666.87	0.00	0	EIPDWVNVQVAQAAK
248 - 261	1609.78	1608.78	1608.78	-0.00	0	LTGMPTETFEQISR
278 - 294	1730.92	1729.91	1729.90	0.01	0	LGSQGSALFIEGGEPIR
346 - 355	1071.56	1070.56	1070.55	0.00	1	GAIPSMPDRK
346 - 355	1087.56	1086.56	1086.55	0.01	1	GAIPSMPDRK Oxidation (M)

Spot 1649

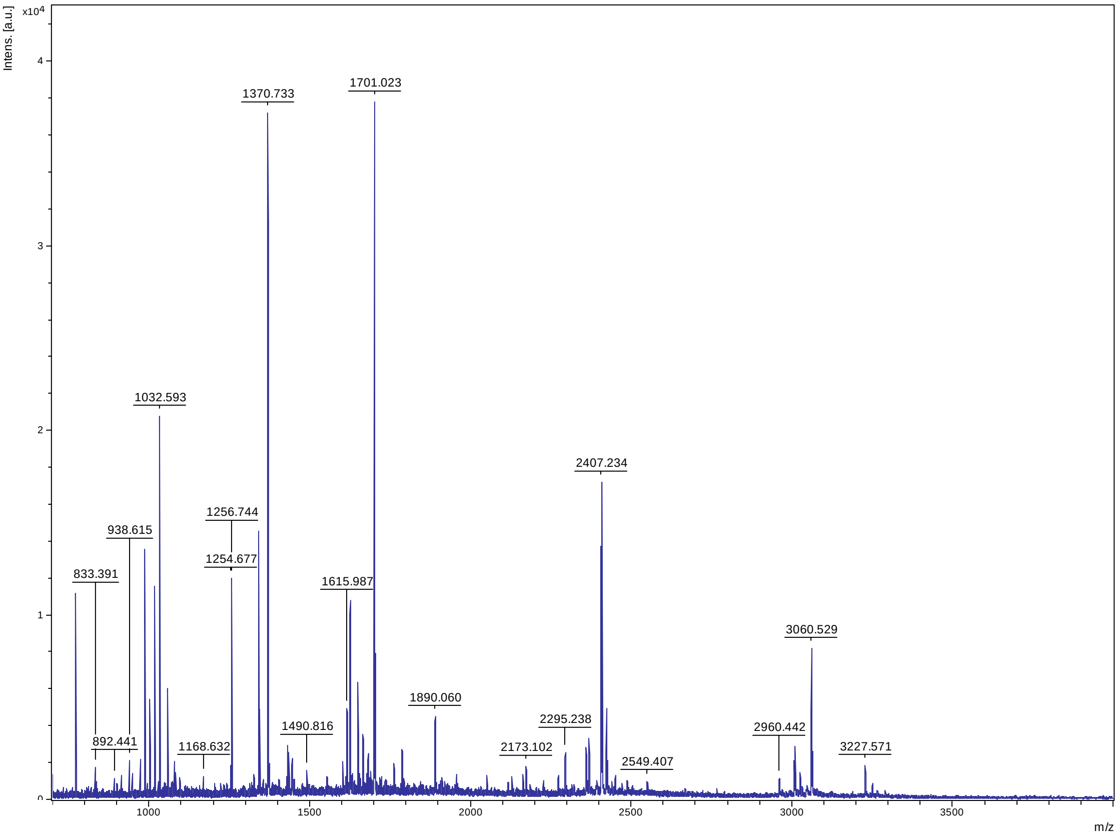


Match to: gi|14150751 Score: 202 Expect: 4.2e-16

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
6 - 23	1968.9437	1967.9364	1967.8782	0.0583	0	K.DGAADLEEGTLEIGMEYR.T	
43 - 50	1034.6044	1033.5971	1033.5556	0.0415	0	K.YQEIVNIR.L	
58 - 68	1229.7005	1228.6932	1228.6411	0.0521	1	R.RGQVLEVDGEK.A	
69 - 83	1563.8855	1562.8782	1562.7940	0.0843	0	K.AVVQVFEGTSGIDNK.Y	
84 - 95	1385.7938	1384.7865	1384.7238	0.0627	0	K.YTTVQFTGEVLK.T	
96 - 105	1088.6232	1087.6159	1087.5695	0.0464	0	K.TPVSLDMLGR.I	
96 - 105	1104.6193	1103.6120	1103.5645	0.0476	0	K.TPVSLDMLGR.I	Oxidation (M)
106 - 138	3454.4399	3453.4326	3453.7415	-0.3089	0	R.IFNGSGKPIDNGPPILPEAYLDISGSSINPSER.T	
139 - 160	2469.1626	2468.1553	2468.1927	-0.0373	0	R.TYPEEMIQTGISTIDVMNSIAR.G	
139 - 160	2485.1345	2484.1272	2484.1876	-0.0604	0	R.TYPEEMIQTGISTIDVMNSIAR.G	Oxidation (M)
164 - 183	2178.1721	2177.1648	2177.1415	0.0233	0	K.IPLFSAAGLPHNEIAAQICR.Q	Carbamidomethyl (C)
235 - 249	1716.0109	1715.0036	1714.9253	0.0783	0	R.VTLFLNLANDPTIER.I	
255 - 269	1702.9095	1701.9022	1701.8283	0.0739	0	R.IALTTAEYLAYECGK.H	Carbamidomethyl (C)
270 - 286	1904.0197	1903.0124	1902.9873	0.0251	0	K.HVLVILTDMSSYADALR.E	
270 - 286	1920.0411	1919.0338	1918.9822	0.0516	0	K.HVLVILTDMSSYADALR.E	Oxidation (M)
300 - 315	1912.9299	1911.9226	1911.8712	0.0514	0	R.GYPGYMYTDLATIYER.A	
300 - 315	1928.9315	1927.9242	1927.8662	0.0581	0	R.GYPGYMYTDLATIYER.A	Oxidation (M)
365 - 378	1579.9498	1578.9425	1578.8770	0.0656	0	R.QIYPPINVLPSLSR.L	Pyro-glu (N-term Q)
365 - 378	1596.9960	1595.9887	1595.9035	0.0852	0	R.QIYPPINVLPSLSR.L	
391 - 408	2051.0415	2050.0342	2049.9868	0.0475	1	R.RDHSDVSNQLYANYAIGK.D	
392 - 408	1894.9555	1893.9482	1893.8857	0.0626	0	R.DHSDVSNQLYANYAIGK.D	
415 - 438	2772.2803	2771.2730	2771.3904	-0.1174	1	K.AVVGEEALSSEDLLYLEFLDKFER.K	
439 - 449	1285.7188	1284.7115	1284.6462	0.0653	1	R.KFVTQGAYDTR.N	

Spot 1665

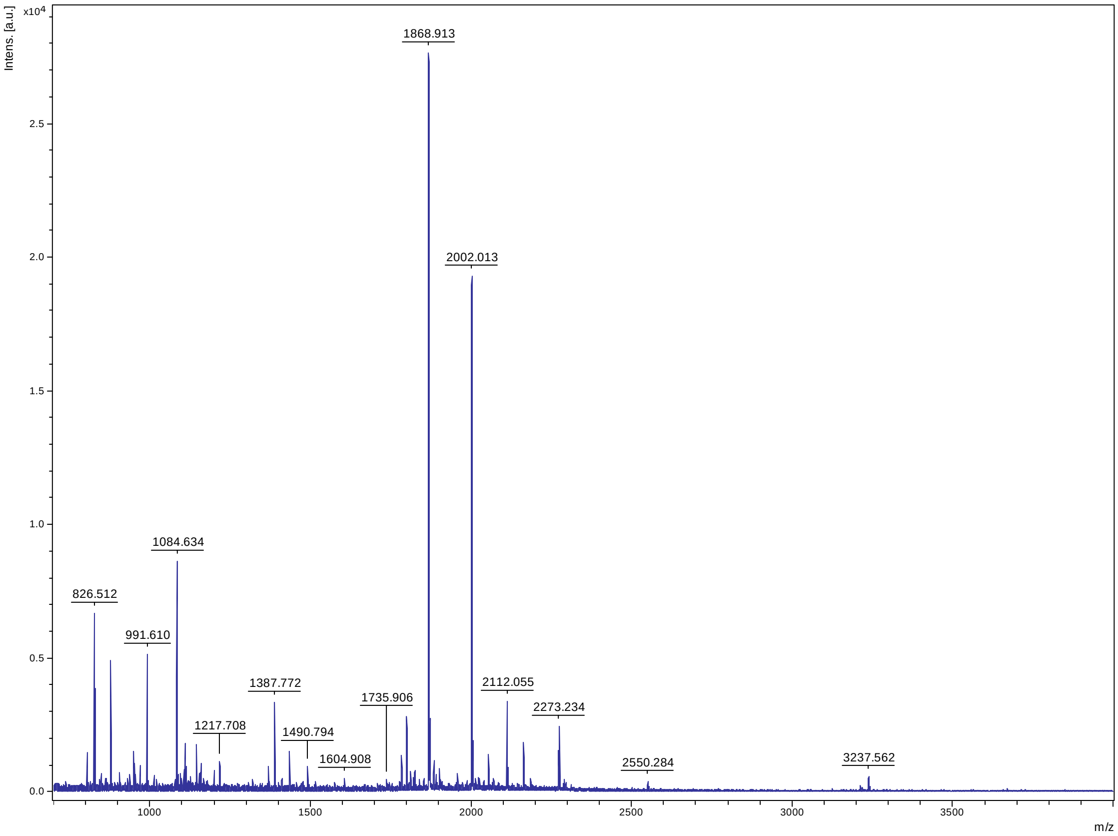


Match to: gi|50944557 Score: 113 Expect: 3.4e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
70 - 81	1256.7437	1255.7364	1255.7036	0.0327	0	R.AKPAVPLGANYR.L	
98 - 111	1625.9459	1624.9386	1624.8573	0.0814	0	K.IYVLTQFNSASLNR.H	
116 - 125	1056.5662	1055.5589	1055.5035	0.0553	0	R.AYGNNIGGYK.N	
126 - 153	3060.5293	3059.5220	3059.4372	0.0848	0	K.NEGFVEVLAAQQSPDNPNWFQGTADAVR.Q	
206 - 219	1553.8539	1552.8466	1552.7555	0.0911	1	R.ATAFGLMKIDEEGR.I	Oxidation (M)
220 - 233	1615.9867	1614.9794	1614.8980	0.0814	1	R.IVEFAEKPKGEQLK.A	
234 - 248	1649.9156	1648.9084	1648.8164	0.0920	0	K.AMMVDTTILGLDDVR.A	
234 - 248	1665.9111	1664.9039	1664.8113	0.0925	0	K.AMMVDTTILGLDDVR.A	Oxidation (M)
266 - 273	986.6204	985.6131	985.5742	0.0389	0	K.NVMLQLLR.E	
266 - 273	1002.6187	1001.6114	1001.5692	0.0423	0	K.NVMLQLLR.E	Oxidation (M)
274 - 296	2407.2339	2406.2266	2406.1273	0.0993	0	R.EQFPGANDFGSEVIPGATNIGMR.V	
297 - 324	3227.5708	3226.5635	3226.5498	0.0137	0	R.VQAYLYDGYWEDIGTIEAFYNANLGITK.K	
325 - 335	1370.7332	1369.7259	1369.6666	0.0593	0	K.KPVPDFSFYDR.S	
336 - 344	1032.5933	1031.5860	1031.5400	0.0460	0	R.SAPIYTQPR.H	
345 - 368	2549.4067	2548.3995	2548.3206	0.0788	1	R.HLPPSKVLDADVTDSVIGEGCVIK.N	Carbamidomethyl (C)
372 - 380	1017.6371	1016.6298	1016.5879	0.0419	0	K.IHHSVVGLR.S	
381 - 407	3008.4255	3007.4183	3007.3678	0.0505	1	R.SCISEGAIIEDSLLMGADYYETEADKK.L	Carbamidomethyl (C)
381 - 407	3024.4282	3023.4209	3023.3627	0.0583	1	R.SCISEGAIIEDSLLMGADYYETEADKK.L	Carbamidomethyl (C); Oxidation (M)
428 - 435	900.5635	899.5562	899.5188	0.0374	1	R.AIIDKNAR.I	
442 - 453	1341.7533	1340.7460	1340.7048	0.0412	0	K.IINVDNVQEAAR.E	
442 - 461	2295.2383	2294.2310	2294.1542	0.0768	1	K.IINVDNVQEAARETDGYFIK.S	
454 - 461	972.5197	971.5124	971.4600	0.0524	0	R.ETDGYFIK.S	

Spot 1663

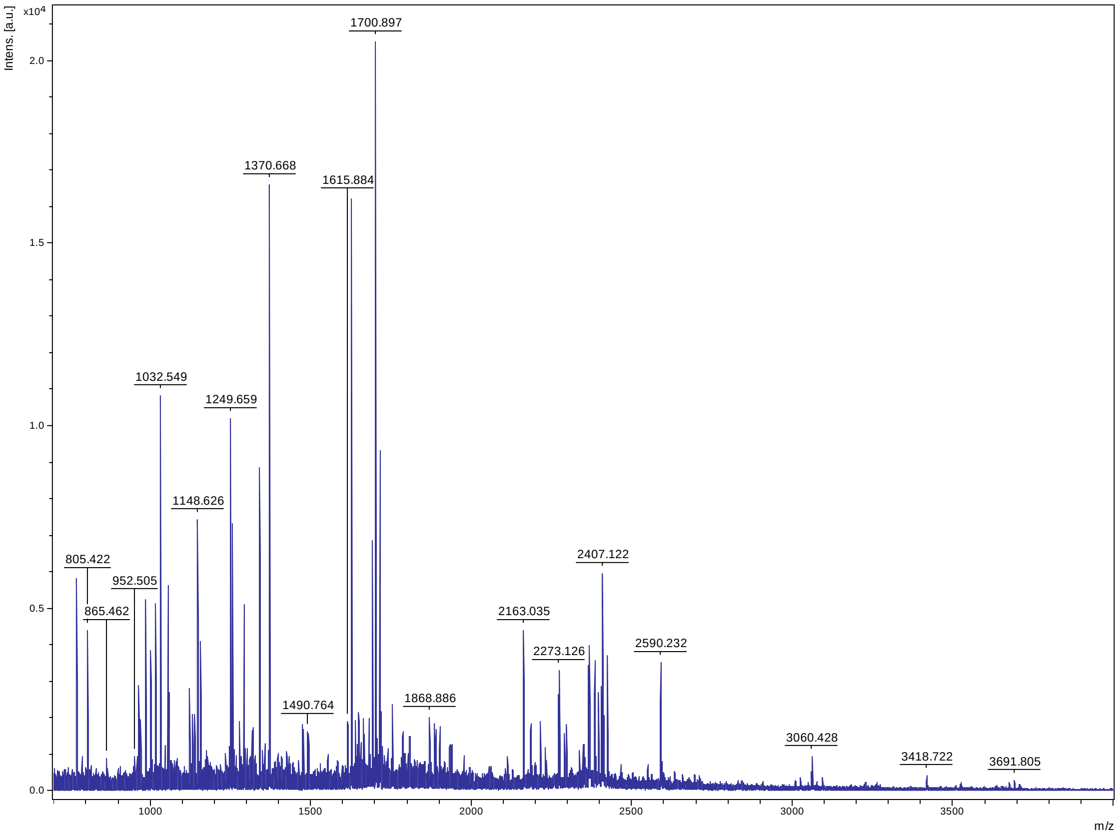


Match to: gi|34909168 Score: 164 Expect: 2.7e-12

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
21 - 29	1084.6340	1083.6268	1083.5600	0.0667	0	R.VFQVEYATK.A	
30 - 41	1159.6857	1158.6784	1158.6244	0.0540	0	K.AVDNSGTVVGIK.C	
42 - 52	1217.7081	1216.7009	1216.6485	0.0524	1	K.CKDGIVLGVEK.L	Carbamidomethyl (C)
58 - 65	937.4857	936.4784	936.4157	0.0628	0	K.MMLEGSNR.R	
58 - 65	953.4823	952.4750	952.4106	0.0644	0	K.MMLEGSNR.R	Oxidation (M)
58 - 65	969.4708	968.4635	968.4055	0.0580	0	K.MMLEGSNR.R	2 Oxidation (M)
67 - 86	2054.1504	2053.1431	2053.0605	0.0826	0	R.IHSVHWHSGLAVAGLAADGR.Q	
102 - 110	991.6100	990.6027	990.5385	0.0642	0	K.VYGEPISVK.E	
144 - 159	1783.9054	1782.8981	1782.8498	0.0483	0	R.DGPQLYMIEPSGVSYK.Y	
144 - 159	1799.9088	1798.9015	1798.8447	0.0568	0	R.DGPQLYMIEPSGVSYK.Y	Oxidation (M)
160 - 167	826.5120	825.5047	825.4384	0.0663	0	K.YFGAALGK.G	
181 - 187	878.5057	877.4985	877.4327	0.0657	0	K.LSELTCR.E	Carbamidomethyl (C)
196 - 205	1144.6542	1143.6469	1143.5924	0.0545	0	K.IIYGVHDEAK.D	
196 - 207	1387.7725	1386.7652	1386.7143	0.0509	1	K.IIYGVHDEAKDK.A	
206 - 222	2112.0547	2111.0474	2110.9629	0.0845	1	K.DKAFELELSWICDESNR.Q	Carbamidomethyl (C)
208 - 222	1811.8727	1810.8654	1810.8195	0.0459	0	K.AFELELSWICDESNR.Q	
208 - 222	1868.9128	1867.9056	1867.8410	0.0645	0	K.AFELELSWICDESNR.Q	Carbamidomethyl (C)
223 - 236	1604.9080	1603.9007	1603.8682	0.0325	1	R.QHQKVPADLLEQAK.V	
227 - 236	1083.6642	1082.6569	1082.5971	0.0598	0	K.VPADLLEQAK.V	

Spot 1666



Match to: gi|50944557; Score: 137

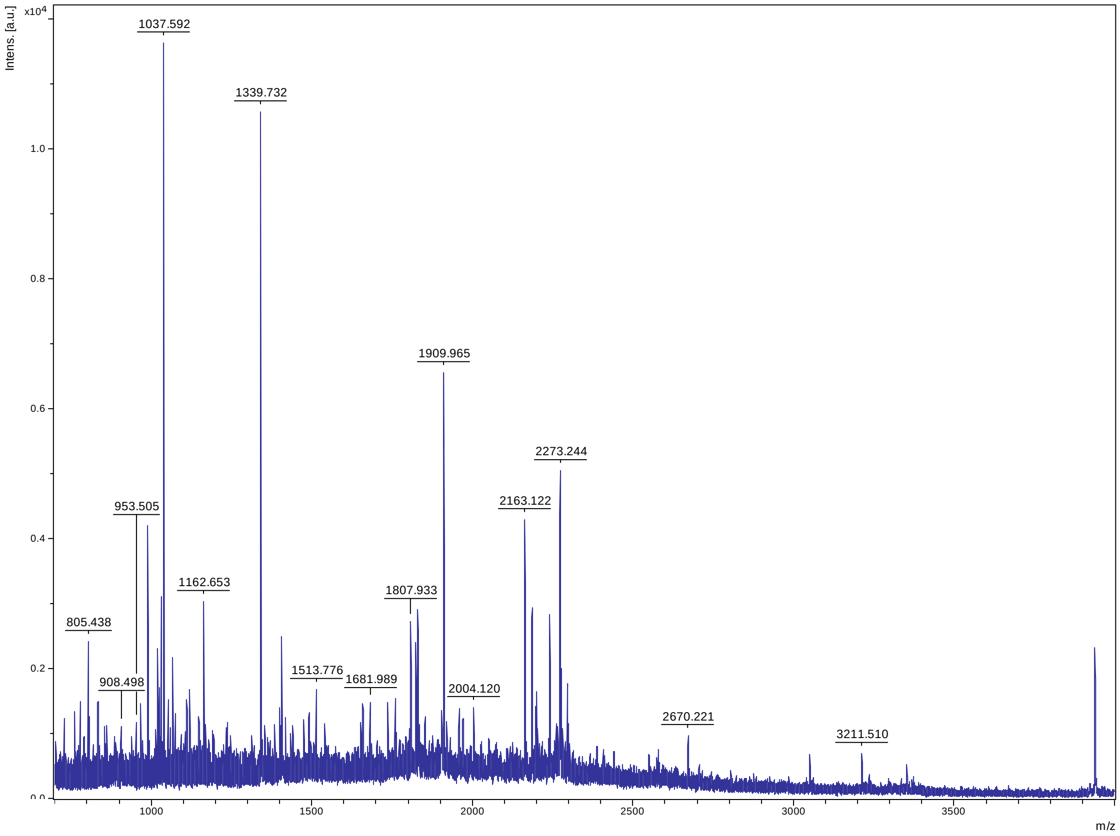
Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
44 - 61	1700.90	1699.89	1699.91	-0.02	0	SVDESVLGIILGGGAGTR
70 - 81	1256.71	1255.70	1255.70	-0.00	0	AKPAVPLGANYR
82 - 97	1786.93	1785.92	1785.93	-0.00	0	LIDIPVSNCLNSNISK
98 - 111	1625.85	1624.84	1624.86	-0.01	0	IYVLTQFNSASLNR
126 - 153	3060.43	3059.43	3059.44	-0.01	0	NEGFVEVLAAQQSPDNPNWFQGTADAVR
206 - 219	1553.83	1552.83	1552.76	0.07	1	ATAFGLMKIDEEGR Oxidation (M)
220 - 233	1615.88	1614.88	1614.90	-0.02	1	IVEFAEKPKGEQLK
234 - 248	1649.81	1648.81	1648.82	-0.01	0	AMMVDTTILGLDDVR
234 - 248	1665.81	1664.81	1664.81	-0.00	0	AMMVDTTILGLDDVR Oxidation (M)
234 - 248	1681.81	1680.81	1680.81	0.00	0	AMMVDTTILGLDDVR 2 Oxidation (M)
249 - 265	1932.97	1931.97	1931.97	-0.01	1	AKEMPYIASMGIYVISK 2 Oxidation (M)
266 - 273	986.58	985.58	985.57	0.00	0	NVMLQLLR
266 - 273	1002.58	1001.58	1001.57	0.01	0	NVMLQLLR Oxidation (M)
274 - 296	2407.12	2406.12	2406.13	-0.01	0	EQFPGANDFGSEVIPGATNIGMR
274 - 296	2423.12	2422.11	2422.12	-0.01	0	EQFPGANDFGSEVIPGATNIGMR Oxidation (M)
325 - 335	1370.67	1369.67	1369.67	-0.00	0	KPVPDFSFYDR
336 - 344	1032.55	1031.55	1031.54	0.01	0	SAPIYTQPR
336 - 350	1691.85	1690.85	1690.92	-0.06	1	SAPIYTQPRHLPPSK
351 - 368	1889.93	1888.93	1888.95	-0.02	0	VLDADVTDSVIGEGCVIK
372 - 380	1017.59	1016.59	1016.59	-0.00	0	IHHSVVGLR
442 - 453	1341.71	1340.70	1340.70	0.00	0	IINVDNVQEAAR
442 - 461	2295.13	2294.13	2294.15	-0.03	1	IINVDNVQEAARETDGYFIK

Match to: **gi|54290767**; Score: **121**

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
12 - 34	2215.08	2214.07	2214.09	-0.02	0	TVEAMQADAAAAAAAGADLVEIR
12 - 34	2231.08	2230.07	2230.09	-0.02	0	TVEAMQADAAAAAAAGADLVEIR Oxidation (M)
35 - 44	1249.66	1248.66	1248.66	-0.00	0	LDFIEGFRPR
45 - 52	964.56	963.55	963.55	0.00	0	EHLPSLLR
117 - 139	2590.23	2589.23	2589.24	-0.01	0	LIVSSHNYESTPSCEELADLVAR
150 - 162	1319.67	1318.67	1318.67	-0.00	0	IATTASDIADVSR
193 - 206	1490.76	1489.76	1489.75	0.02	0	FGGYLTFGTLDATK
217 - 225	1148.63	1147.62	1147.62	0.00	0	ELLDIYNIR
253 - 273	2365.17	2364.16	2364.21	-0.05	0	CLQSIGYNAVYLPLLADDLAR
309 - 318	1057.63	1056.63	1056.63	-0.00	0	SIGAINTIIR
324 - 358	3418.72	3417.72	3417.74	-0.02	1	LVGYNTDYIGAISAIEDGIGGPGSKDAAISPLAGR
349 - 358	970.51	969.51	969.52	-0.01	0	DAAISPLAGR
359 - 377	1700.90	1699.89	1700.00	-0.10	1	LVVVVGAGGAGKAIAYGAK
393 - 406	1292.73	1291.73	1291.74	-0.01	0	AVSLAAAVGGHALR
441 - 457	1932.97	1931.97	1932.00	-0.04	1	KALSFYDVVFDAVYAPK
472 - 481	1122.60	1121.59	1121.59	0.00	0	VVSGVEMFVR
472 - 481	1138.60	1137.60	1137.59	0.01	0	VVSGVEMFVR Oxidation (M)
482 - 502	2352.03	2351.03	2351.07	-0.04	0	QAMGQFEHFTGGIEAPESLMR Oxidation (M)
482 - 502	2368.19	2367.19	2367.06	0.13	0	QAMGQFEHFTGGIEAPESLMR 2 Oxidation (M)

Spot 1670

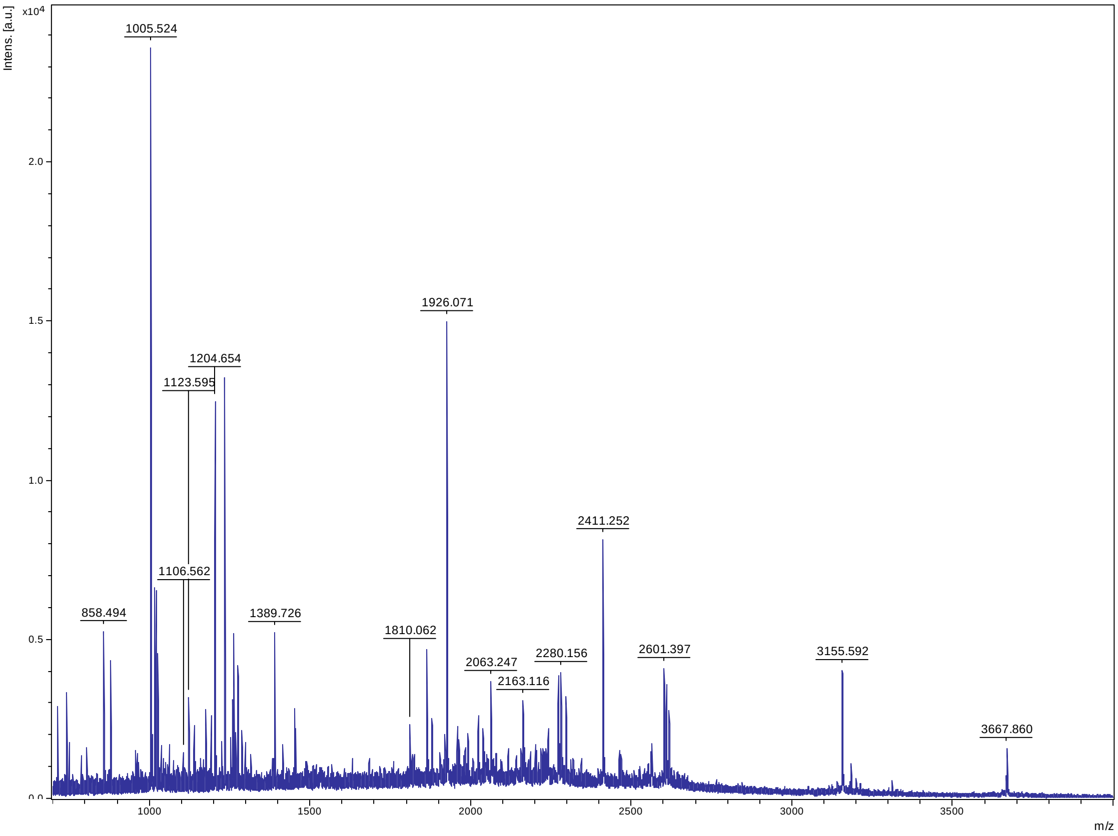


Match to: gi|77550894 Score: 107 Expect: 1.3e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
9 - 27	1909.9325	1908.9252	1908.8700	0.0552	0	R.GEGAAATESEAYLEGEAVR.E	
57 - 78	2280.2166	2279.2093	2279.1831	0.0262	0	K.ANDPALPLADQLIVMSPSGVQK.E	Oxidation (M)
121 - 149	3049.4187	3048.4114	3048.4289	-0.0174	1	K.AYLMRGAGAVIHSHGMETCIATMLDPGAK.E	3 Oxidation (M)
126 - 149	2440.2495	2439.2422	2439.1344	0.1078	0	R.GAGAVIHSHGMETCIATMLDPGAK.E	Carbamidomethyl (C); Oxidation (M)
206 - 220	1759.9161	1758.9088	1758.8477	0.0611	0	R.NHGIYVWGDSWINAK.T	
221 - 235	1829.8904	1828.8831	1828.8454	0.0377	0	K.TQAECYHYLFDAAIK.L	Carbamidomethyl (C)
236 - 255	2240.1247	2239.1174	2239.1273	-0.0099	0	K.LYQLGIDWTTPEHGPINSAK.R	
259 - 273	1490.7840	1489.7767	1489.7082	0.0685	0	R.SVLSSSIPNGCPDSK.S	
376 - 383	1020.5198	1019.5125	1019.5301	-0.0176	0	K.QLQGHIWR.T	Pyro-glu (N-term Q)
390 - 404	1658.9159	1657.9086	1657.8562	0.0524	0	K.ELQGVVFDDVPEALK.H	
405 - 412	953.4377	952.4304	952.4337	-0.0033	0	K.HWHASGMK.V	
422 - 437	1823.9095	1822.9022	1822.9325	-0.0303	1	R.EAQRLLFGNTAYGDLR.Q	
426 - 437	1339.7279	1338.7206	1338.6931	0.0275	0	R.LLFGNTAYGDLR.Q	
438 - 451	1651.8252	1650.8179	1650.7348	0.0832	0	R.QYLCGFFDTTTGNK.R	Carbamidomethyl (C)
438 - 452	1790.9027	1789.8954	1789.8093	0.0861	1	R.QYLCGFFDTTTGNKR.E	Carbamidomethyl (C); Pyro-glu (N-term Q)
487 - 510	2578.3571	2577.3498	2577.3451	0.0047	0	K.SAGFEVIISIRPGNAPLPENHGFR.T	

Spot 1672

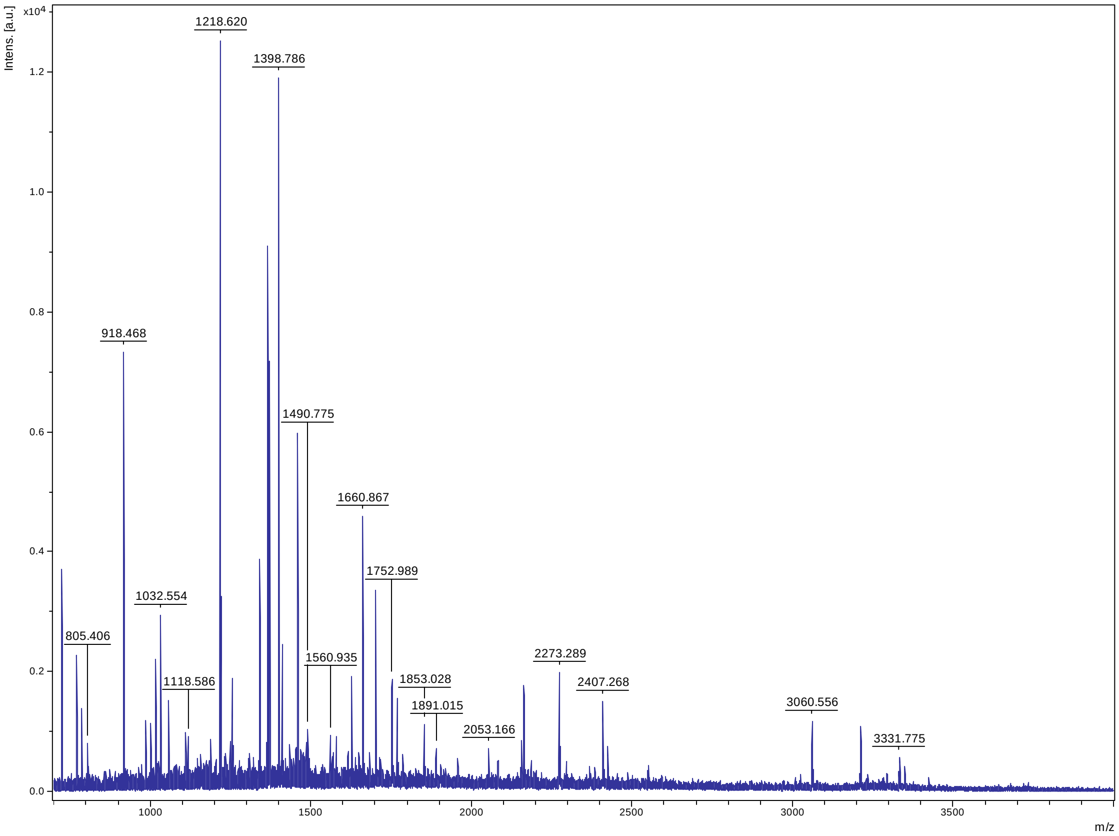


Match to: gi|14018066 Score: 227 Expect: 1.3e-18

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
20 - 37	1926.0418	1925.0345	1925.0006	0.0339	0	R.IGDSLSAHPNELVAVFTR.L	
44 - 64	2344.1993	2343.1920	2343.1277	0.0644	0	K.GMLQAHQIIAEYNNAISEADR.E	
44 - 66	2601.2816	2600.2743	2600.2652	0.0091	1	K.GMLQAHQIIAEYNNAISEADREK.L	
44 - 66	2617.2725	2616.2652	2616.2601	0.0051	1	K.GMLQAHQIIAEYNNAISEADREK.L	Oxidation (M)
67 - 77	1262.7125	1261.7052	1261.6666	0.0386	1	K.LKDGAFEDVLR.S	
157 - 167	1204.6559	1203.6486	1203.6360	0.0127	0	K.SIGNGVQFLNR.H	
173 - 188	2023.0850	2022.0777	2022.0396	0.0381	1	K.LFHDKESMYPLLNFLR.A	
173 - 188	2039.0631	2038.0558	2038.0346	0.0213	1	K.LFHDKESMYPLLNFLR.A	Oxidation (M)
205 - 214	1015.5863	1014.5790	1014.5822	-0.0031	0	R.SLSALQGALR.K	
215 - 235	2411.1745	2410.1672	2410.1301	0.0371	1	R.KAEEHLSGLSADTPYSEFHHR.F	
252 - 273	2462.3233	2461.3160	2461.2952	0.0209	0	R.SQETIHLLLDLLEAPDPSTLEK.F	
326 - 336	1267.7833	1266.7760	1266.7408	0.0352	1	R.IKQQGLNITPR.I	
328 - 336	1026.5701	1025.5628	1025.5618	0.0011	0	K.QQGLNITPR.I	
343 - 355	1389.7392	1388.7319	1388.6718	0.0601	0	R.LLPDATGTTCGQR.L	Carbamidomethyl (C)
343 - 358	1759.9514	1758.9441	1758.8934	0.0507	1	R.LLPDATGTTCGQRLEK.V	Carbamidomethyl (C)
359 - 369	1275.7612	1274.7539	1274.7095	0.0444	0	K.VLGTEHTHILR.V	
370 - 380	1287.7863	1286.7790	1286.7095	0.0696	1	R.VPFRTENGIVR.K	
446 - 456	1414.7532	1413.7459	1413.6928	0.0531	1	K.TKYPNSDLYWK.K	
494 - 512	2203.0301	2202.0228	2201.9873	0.0355	0	K.DTVGQYESHMAFTMPGLYR.V	
494 - 512	2219.0504	2218.0431	2217.9823	0.0609	0	K.DTVGQYESHMAFTMPGLYR.V	Oxidation (M)
524 - 543	2280.0917	2279.0844	2279.0568	0.0276	0	K.FNIVSPGADMSIYFPYSESR.K	
524 - 543	2296.1045	2295.0972	2295.0517	0.0455	0	K.FNIVSPGADMSIYFPYSESR.K	Oxidation (M)
546 - 567	2609.3048	2608.2975	2608.2656	0.0319	0	R.LTSLHPEIEELLYSEVDNNEHK.F	
574 - 583	1176.6710	1175.6637	1175.6485	0.0153	0	R.NKPIIFSMAR.L	
574 - 583	1192.6841	1191.6768	1191.6434	0.0335	0	R.NKPIIFSMAR.L	Oxidation (M)
603 - 621	2078.1265	2077.1192	2077.0625	0.0567	0	R.LQELVNLVVVCGDHGNPSK.D	Carbamidomethyl (C)
622 - 630	1123.5758	1122.5685	1122.5193	0.0493	1	K.DKEEQAEFK.K	
624 - 630	880.4092	879.4019	879.3974	0.0046	0	K.EEQAEFK.K	
631 - 646	1991.0206	1990.0133	1990.0094	0.0039	1	K.KMFDLIEQYNLNGHIR.W	
632 - 646	1862.9697	1861.9624	1861.9144	0.0480	0	K.MFDLIEQYNLNGHIR.W	
632 - 646	1878.9614	1877.9541	1877.9094	0.0448	0	K.MFDLIEQYNLNGHIR.W	Oxidation (M)
647 - 654	1005.4984	1004.4911	1004.4862	0.0050	0	R.WISAQMNR.V	
723 - 733	1253.7256	1252.7183	1252.6703	0.0481	0	K.ASALLVEFFEK.C	
744 - 751	858.4303	857.4230	857.4719	-0.0489	0	K.ISQGGLQR.I	
788 - 797	1299.7509	1298.7436	1298.7056	0.0380	1	R.RYLEMLYALK.Y	

Spot 1676



Match to: gi|34894958 Score: 111 Expect: 5.3e-07

Matched peptides:

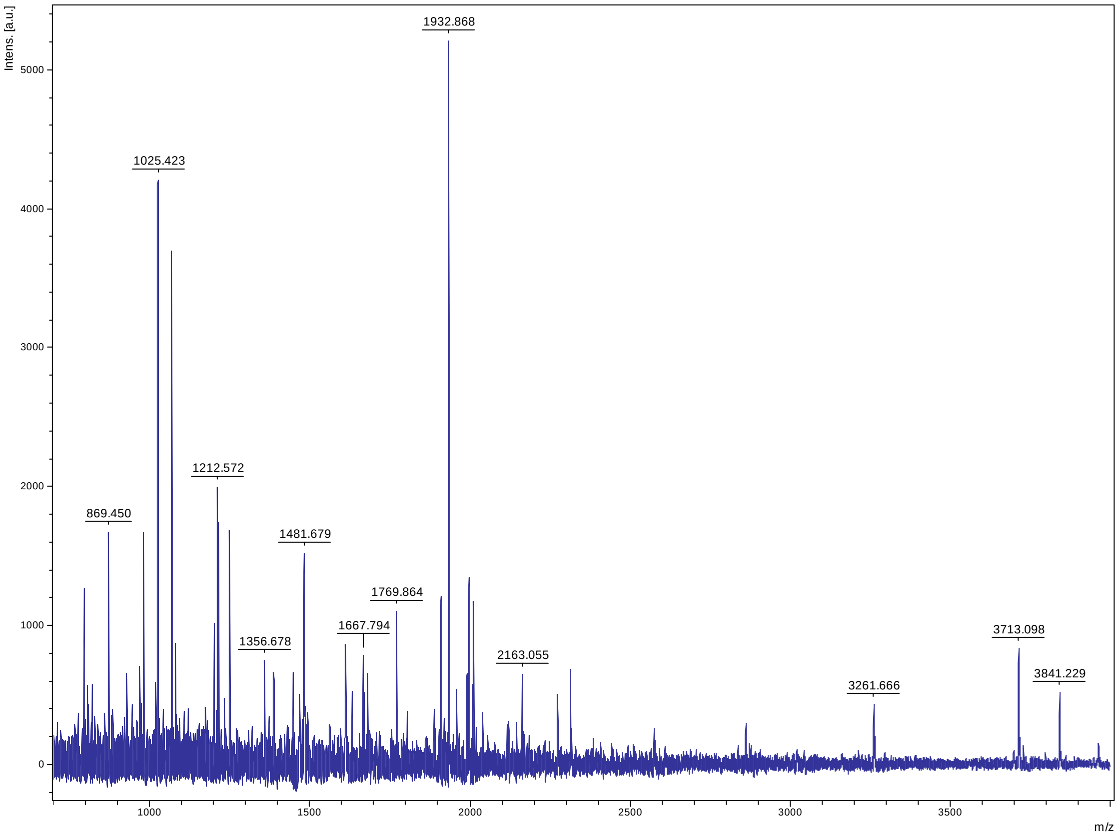
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
100 - 115	1660.8396	1659.8323	1659.8250	0.0074	0	K.TAIIEGDVVGGTCVNR.G	Carbamidomethyl (C)
122 - 129	786.4196	785.4123	785.4759	-0.0636	0	K.ALLAVSGR.M	
130 - 140	1469.7053	1468.6980	1468.6551	0.0429	1	R.MRELQDEHHMK.S	Oxidation (M)
130 - 140	1485.7142	1484.7069	1484.6500	0.0569	1	R.MRELQDEHHMK.S	2 Oxidation (M)
141 - 153	1366.7245	1365.7172	1365.6888	0.0284	0	K.SLGLQVSTAGYDR.Q	
177 - 192	1560.9250	1559.9177	1559.8922	0.0255	0	K.ALGVDILTGFGTIVGK.Q	
200 - 210	1218.6220	1217.6147	1217.6040	0.0107	0	K.VGFPDNEITAR.N	
232 - 241	1118.5821	1117.5748	1117.5768	-0.0019	0	K.TVFTSDHALK.L	
319 - 331	1410.8461	1409.8388	1409.8129	0.0259	0	K.DGKPVLIELIDAK.T	
334 - 350	1852.9564	1851.9491	1851.9690	-0.0199	1	K.EHKETLEVDAALIATGR.A	
337 - 350	1458.7978	1457.7905	1457.7725	0.0180	0	K.ETLEVDAALIATGR.A	
356 - 368	1398.7983	1397.7910	1397.7626	0.0284	0	K.GLGLENVNVVTQR.G	
369 - 376	918.4486	917.4413	917.4606	-0.0193	0	R.GFVPVDER.M	
400 - 416	1752.9525	1751.9452	1751.9352	0.0101	0	K.LMLAHAASAQGISVVER.I	
400 - 416	1768.9635	1767.9562	1767.9301	0.0261	0	K.LMLAHAASAQGISVVER.I	Oxidation (M)
473 - 484	1187.6314	1186.6241	1186.5829	0.0412	0	K.ALAENEGDGLAK.M	
526 - 543	2053.0578	2052.0505	2052.0680	-0.0174	0	K.FAVHAHPTLSEVLDELFK.A	

Match to: gi|50944557 Score: 75 Expect: 0.0022

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
44 - 61	1700.9194	1699.9121	1699.9104	0.0018	0	R.SVDESVLGIILGGGAGTR.L	
70 - 81	1256.7346	1255.7273	1255.7036	0.0237	0	R.AKPAVPLGANYR.L	
98 - 111	1625.8699	1624.8626	1624.8573	0.0054	0	K.IYVLTQFNSASLNR.H	
220 - 233	1615.9266	1614.9193	1614.8980	0.0213	1	R.IVEFAEKPKGEQLK.A	
266 - 273	986.5691	985.5618	985.5742	-0.0124	0	K.NVMLQLLR.E	
266 - 273	1002.5706	1001.5633	1001.5692	-0.0058	0	K.NVMLQLLR.E	Oxidation (M)
274 - 296	2407.1113	2406.1040	2406.1273	-0.0233	0	R.EQFPGANDFGSEVIPGATNIGMR.V	
274 - 296	2423.0827	2422.0754	2422.1222	-0.0468	0	R.EQFPGANDFGSEVIPGATNIGMR.V	Oxidation (M)
325 - 335	1370.7056	1369.6983	1369.6666	0.0317	0	K.KPVPDFSFYDR.S	
336 - 344	1032.5407	1031.5334	1031.5400	-0.0066	0	R.SAPIYTQPR.H	
351 - 368	1889.9657	1888.9584	1888.9451	0.0133	0	K.VLDADVTDSVIGEGCVIK.N	Carbamidomethyl (C)
372 - 380	1017.5843	1016.5770	1016.5879	-0.0109	0	K.IHHSVVGLR.S	
442 - 453	1341.7362	1340.7289	1340.7048	0.0242	0	K.IINVDNVQEAAR.E	

Spot 1677

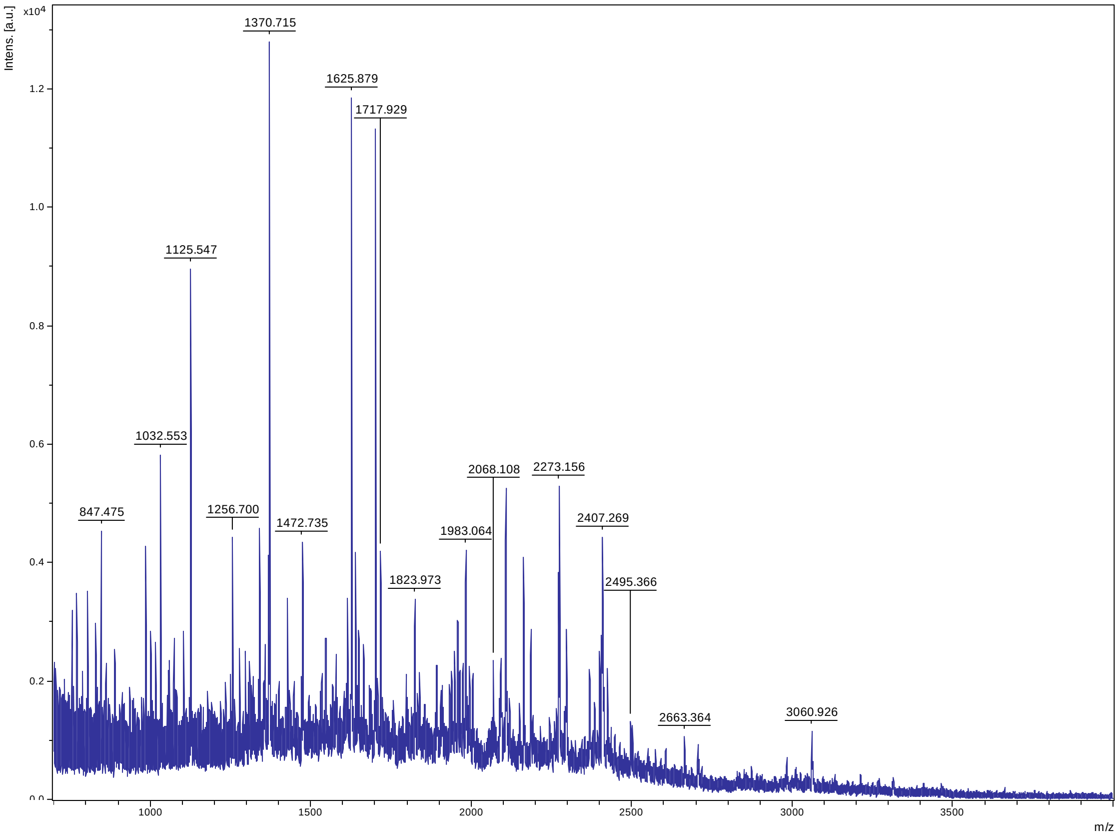


Match to: BAC82932 Score: 111 Expect: 5.3e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
37 - 44	1025.5213	1024.5140	1024.4250	0.0890	0	K.FEDGWESR.W
84 - 99	1909.0634	1908.0561	1907.8941	0.1621	1	R.FYAISAEYPEFSNKDK.T
113 - 121	968.5460	967.5388	967.4433	0.0955	0	K.LDCGGGYVK.L Carbamidomethyl (C)
132 - 153	2441.3348	2440.3275	2440.1078	0.2197	1	K.FGGDTPYSIMFGPDICGYSTKK.V Carbamidomethyl (C)
169 - 201	3841.1385	3840.1312	3839.9291	0.2021	1	K.KDVPCETDQLSHVYTLIIHPDATYTILIDNVEK.Q Carbamidomethyl (C)
170 - 201	3713.0494	3712.0421	3711.8342	0.2080	0	K.DVPCETDQLSHVYTLIIHPDATYTILIDNVEK.Q Carbamidomethyl (C)
202 - 216	1770.0445	1769.0372	1768.8784	0.1588	0	K.QSGSIYEHWDILPPK.Q
252 - 259	884.5161	883.5088	883.4287	0.0801	0	K.EIPDPDAK.K
260 - 283	2861.4629	2860.4556	2860.2351	0.2205	0	K.KPEDWDDEEDGEWTAPTIPNPEYK.G
293 - 299	820.4938	819.4865	819.3875	0.0990	0	K.NPNYQGK.W
302 - 323	2575.4298	2574.4225	2574.1988	0.2237	1	K.APMIDNPDFKDDPYIYAFDSLK.Y
324 - 333	1248.7968	1247.7895	1247.6914	0.0982	0	K.YIGIELWQVK.S
334 - 351	1996.1770	1995.1697	1994.9836	0.1861	0	K.SGTLFDNFLITDDPELAK.T
352 - 360	1068.5898	1067.5825	1067.4923	0.0902	0	K.TFAEETWGK.H
377 - 383	805.4655	804.4582	804.3501	0.1081	0	K.EEEEAAK.A

Spot 1681



Match to: gi|50944557; Score: 90

Matched peptides:

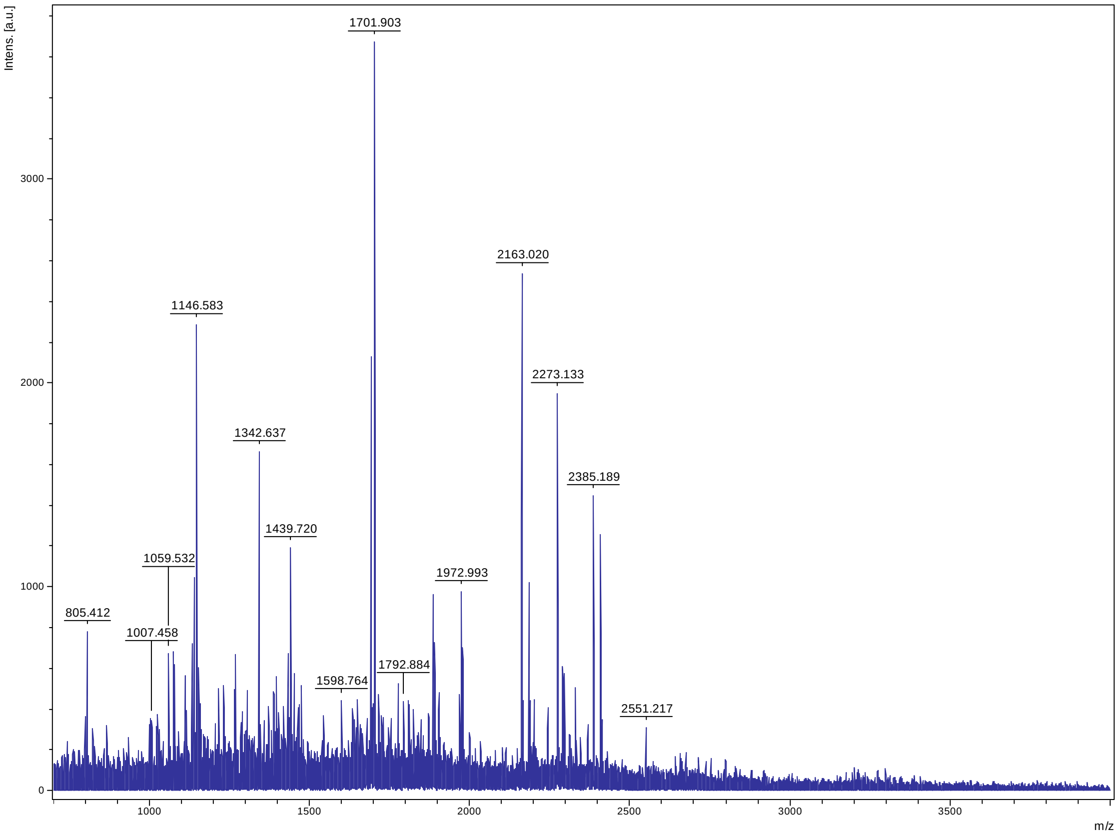
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
44 - 61	1700.93	1699.93	1699.91	0.02	0	SVDESVLGIILGGGAGTR
70 - 81	1256.70	1255.70	1255.70	-0.01	0	AKPAVPLGANYR
98 - 111	1625.88	1624.88	1624.86	0.02	0	IYVLTQFNSASLNR
234 - 248	1649.90	1648.90	1648.82	0.08	0	AMMVDTTILGLDDVR
234 - 248	1665.88	1664.88	1664.81	0.06	0	AMMVDTTILGLDDVR Oxidation (M)
251 - 265	1717.93	1716.93	1716.85	0.08	0	EMPYIASMGIYVISK Oxidation (M)
266 - 273	986.58	985.58	985.57	0.00	0	NVMLQLLR
266 - 273	1002.57	1001.57	1001.57	-0.00	0	NVMLQLLR Oxidation (M)
274 - 296	2407.27	2406.27	2406.13	0.14	0	EQFPGANDFGSEVIPGATNIGMR
274 - 296	2423.20	2422.20	2422.12	0.07	0	EQFPGANDFGSEVIPGATNIGMR Oxidation (M)
325 - 335	1370.71	1369.71	1369.67	0.05	0	KPVPDFSFYDR
336 - 344	1032.55	1031.55	1031.54	0.01	0	SAPIYTQPR
372 - 380	1017.59	1016.59	1016.59	-0.00	0	IHHSVVGLR
442 - 453	1341.71	1340.71	1340.70	0.00	0	IINVDNVQEAAR
442 - 461	2295.22	2294.22	2294.15	0.06	1	IINVDNVQEAARETDGYFIK

Match to: gi|50940893; Score: 85

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
129 - 137	1125.55	1124.54	1124.55	-0.01	0	ETPLYFAER
145 - 156	1321.63	1320.63	1320.69	-0.05	1	ADGTGPMIYLKR
156 - 166	1277.69	1276.69	1276.63	0.06	1	REDLNHTGAHK
185 - 204	1983.06	1982.06	1982.00	0.06	0	IIAETGAGQHGVATATVCAR
205 - 220	1947.86	1946.86	1946.87	-0.01	0	FGLQCIIYMGAQDMER Oxidation (M)
221 - 227	847.47	846.47	846.47	0.00	0	QALNVFR
228 - 236	1032.55	1031.55	1031.58	-0.03	1	MKLLGAEVR Oxidation (M)
401 - 417	1958.03	1957.03	1956.91	0.12	1	AEYDSVTDQEALDAFKR
421 - 439	2068.11	2067.11	2067.13	-0.02	0	LEGIIPALETSHALAYLEK
440 - 449	1127.60	1126.60	1126.58	0.02	0	LCPTLPDGVR
450 - 457	890.45	889.45	889.44	0.01	0	VVVNCSGR
458 - 467	1057.56	1056.56	1056.52	0.04	1	GDKDVHTASK

Spot 1693

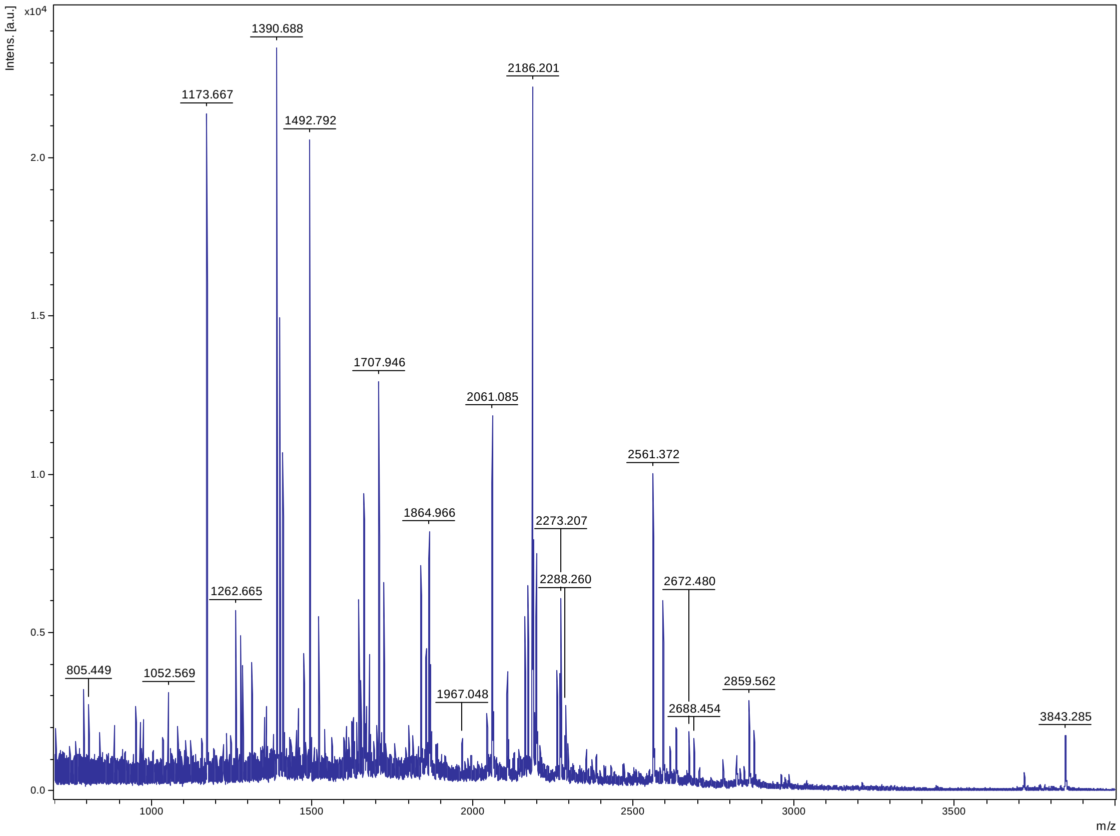


Match to: gi|77549556 Score: 113 Expect: 8.4e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
41 - 60	1977.8444	1976.8371	1976.8751	-0.0380	0	K.TVGGGDDAFNTFFSETGAGK.H	
65 - 79	1701.9028	1700.8956	1700.8984	-0.0029	0	R.AVFVDLEPTVIDEVR.T	
85 - 96	1396.7256	1395.7183	1395.7510	-0.0327	0	R.QLFHPEQLISGK.E	
85 - 105	2385.1890	2384.1817	2384.1872	-0.0055	1	R.QLFHPEQLISGKEDAANNFAR.G	
97 - 105	1007.4576	1006.4504	1006.4468	0.0036	0	K.EDAANNFAR.G	
113 - 121	1132.5645	1131.5572	1131.5594	-0.0022	0	K.EIVDLCLDR.I	Carbamidomethyl (C)
216 - 229	1691.8582	1690.8509	1690.8638	-0.0129	0	R.SLDIERPTYTNLNR.L	
230 - 243	1473.8472	1472.8399	1472.8562	-0.0163	0	R.LVSQVISSLTASLR.F	
265 - 280	1792.8840	1791.8768	1791.9229	-0.0461	0	R.IHFMLSSYAPVISAEK.A	
312 - 320	1153.5559	1152.5486	1152.4588	0.0898	0	K.YMACCLMYR.G	
340 - 352	1598.7642	1597.7569	1597.7599	-0.0030	0	R.TIQFVDWCPTGFK.C	Carbamidomethyl (C)
374 - 390	1885.9169	1884.9096	1884.9073	0.0023	0	R.AVCMISNSTSVVEVFSR.I	Carbamidomethyl (C)
395 - 402	1059.5323	1058.5251	1058.5219	0.0032	1	K.FDLMYSKR.A	
395 - 402	1075.5177	1074.5104	1074.5168	-0.0064	1	K.FDLMYSKR.A	Oxidation (M)

Spot 1694



Match to: gi|84028177; Score: 235

Matched peptides:

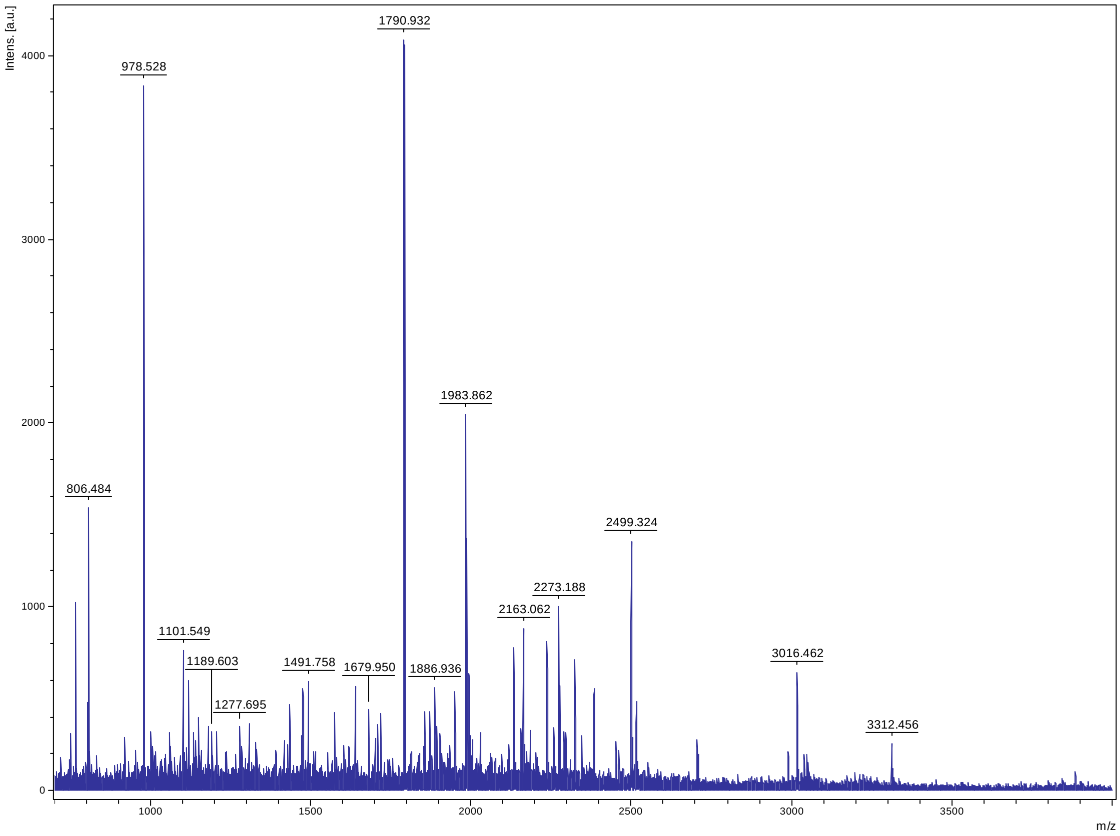
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
71 - 95	2561.37	2560.37	2560.30	0.07	0	ITDEFTGAGAVGQVCQVIGAVVDVR
96 - 115	2262.25	2261.25	2261.21	0.04	0	FDEGLPPILTALEVLDHNIR
116 - 130	1707.95	1706.94	1706.91	0.03	0	LVLEVAQHLGENMVR
116 - 130	1723.95	1722.95	1722.91	0.04	0	LVLEVAQHLGENMVR Oxidation (M)
131 - 142	1262.66	1261.66	1261.63	0.03	0	TIAMDGTEGLVR
131 - 142	1278.67	1277.66	1277.63	0.03	0	TIAMDGTEGLVR Oxidation (M)
146 - 159	1409.83	1408.82	1408.80	0.02	0	VLNTGSPITVPVGR
165 - 189	2859.56	2858.56	2858.47	0.08	1	IMNVIGEPIDEKGDITTNHFLPIHR
165 - 189	2875.59	2874.59	2874.47	0.12	1	IMNVIGEPIDEKGDITTNHFLPIHR Oxidation (M)
177 - 189	1520.82	1519.81	1519.79	0.02	0	GDITTNHFLPIHR
190 - 209	2172.21	2171.20	2171.15	0.06	0	EAPAFVEQATEQQILVTGIK
210 - 219	1173.67	1172.66	1172.66	0.01	0	VVDLLAPYQR
223 - 233	975.58	974.57	974.55	0.02	0	IGLFGGAGVGK
234 - 246	1457.83	1456.83	1456.83	-0.01	0	TVLIMELINNVAK
234 - 246	1473.86	1472.86	1472.83	0.03	0	TVLIMELINNVAK Oxidation (M)
247 - 260	1390.69	1389.69	1389.68	0.01	0	AHGGFSVFAGVGER
261 - 269	1123.58	1122.58	1122.54	0.03	1	TREGNDLYR
263 - 278	1852.91	1851.91	1851.90	0.01	1	EGNDLYREMIESGVIK
263 - 278	1868.95	1867.94	1867.90	0.04	1	EGNDLYREMIESGVIK Oxidation (M)
288 - 302	1662.80	1661.79	1661.77	0.03	0	CALVYGQMNEPPGAR
288 - 302	1678.81	1677.81	1677.76	0.05	0	CALVYGQMNEPPGAR Oxidation (M)
305 - 317	1399.79	1398.79	1398.76	0.03	0	VGLTGLTVAEHFR
318 - 333	1864.97	1863.96	1863.94	0.03	0	DAEGQDVLLFIDNIFR
334 - 347	1492.79	1491.79	1491.77	0.02	0	FTQANSEVSALLGR
348 - 368	2186.20	2185.20	2185.14	0.06	0	IPSAVGYQPTLATDLGGLQER
374 - 410	3843.29	3842.28	3841.97	0.31	1	KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR
411 - 429	2044.05	2043.05	2043.02	0.03	0	QISELGIYPAVDPLDSTSR Pyro-glu (N-term Q)
411 - 429	2061.08	2060.08	2060.04	0.04	0	QISELGIYPAVDPLDSTSR
430 - 445	1839.91	1838.91	1838.87	0.03	0	MLSPHVLGEDHYNTAR
430 - 445	1855.91	1854.91	1854.87	0.04	0	MLSPHVLGEDHYNTAR Oxidation (M)
456 - 479	2672.48	2671.48	2671.37	0.10	1	NLQDIIAILGMDELSEDDKLTVAR
456 - 479	2688.45	2687.45	2687.37	0.08	1	NLQDIIAILGMDELSEDDKLTVAR Oxidation (M)

Match to: gi|15823775; Score: 94

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
28 - 36	965.56	964.56	964.53	0.02	0	SGFISLVSR
86 - 106	2163.09	2162.09	2162.08	0.01	1	LNGGLGTTMGCTGPKSVIEVR Oxidation (M)
151 - 168	2198.08	2197.08	2197.02	0.06	0	YSNSNIEIHTFNQSQYPR
169 - 180	1358.75	1357.75	1357.75	-0.00	0	IVTEDFLPLPSK
215 - 232	1967.05	1966.05	1966.00	0.04	0	EYVFVANSDNLGAIVDIK
233 - 251	2353.22	2352.21	2352.14	0.08	0	ILNHLIHNQNEYCMEVTPK
258 - 267	1052.57	1051.57	1051.53	0.04	0	GGTLISYEGR
268 - 285	2108.12	2107.12	2107.09	0.03	0	VQLLEIAQVPDEHVNEFK
330 - 342	1312.76	1311.76	1311.75	0.01	0	VLQLETAAGAAIR
343 - 354	1390.69	1389.69	1389.78	-0.09	1	FFEKAIGINVPR
347 - 354	839.50	838.50	838.50	-0.00	0	AIGINVPR
347 - 356	1082.60	1081.60	1081.64	-0.03	1	AIGINVPRSR
425 - 438	1451.75	1450.75	1450.75	0.00	0	VSGDVWFGSGVTLK

Spot 1695

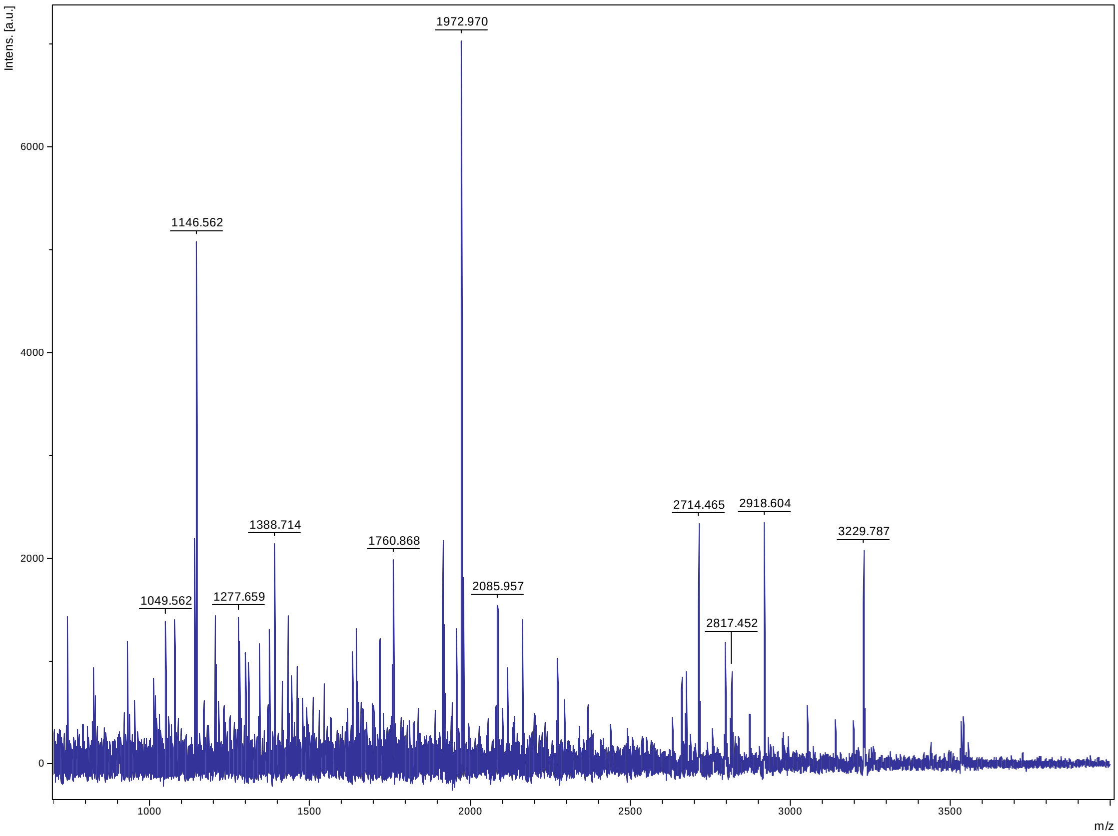


Match to: gi|33113259; Score: 183

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
18 - 35	1983.86	1982.86	1982.85	0.01	0	GNPTVEVDVCCSDGTFAR
36 - 53	1790.93	1789.93	1789.92	0.01	0	AAVPSGASTGVYEALELR
133 - 147	1679.95	1678.95	1678.95	-0.00	1	KIPLYQHIANLAGNK
169 - 185	1854.94	1853.93	1853.94	-0.01	0	LAMQEFMILPTGAASFK
169 - 185	1870.95	1869.94	1869.94	0.01	0	LAMQEFMILPTGAASFK Oxidation (M)
169 - 185	1886.94	1885.93	1885.93	0.00	0	LAMQEFMILPTGAASFK 2 Oxidation (M)
190 - 199	1189.60	1188.60	1188.60	0.00	0	MGVEVYHNLK
206 - 227	2324.06	2323.06	2323.04	0.02	0	YGQDATNVGDEGGFAPNIQENK
291 - 315	3016.46	3015.46	3015.34	0.11	0	SFVSEYPIVSIEDPFDQDDWEHYAK
316 - 338	2499.32	2498.32	2498.27	0.05	0	MTAEIGEQVQIVGDDLLVTNPTR
316 - 338	2515.31	2514.31	2514.26	0.04	0	MTAEIGEQVQIVGDDLLVTNPTR Oxidation (M)
347 - 354	918.53	917.52	917.50	0.02	0	SCNALLLK
355 - 369	1573.84	1572.84	1572.84	0.00	0	VNQIGSVTESIEAVK
374 - 383	1101.55	1100.55	1100.52	0.03	0	AGWGVMTSHR
374 - 383	1117.52	1116.52	1116.51	0.01	0	AGWGVMTSHR Oxidation (M)
384 - 405	2236.15	2235.15	2235.13	0.02	0	SGETEDTFIADLAVGLATGQIK
418 - 423	806.48	805.48	805.44	0.04	0	YNQLLR
424 - 438	1491.76	1490.76	1490.76	-0.01	0	IEEELGAAAVYAGAK
439 - 446	978.53	977.53	977.50	0.03	1	FRAPVEPY

Spot 1700

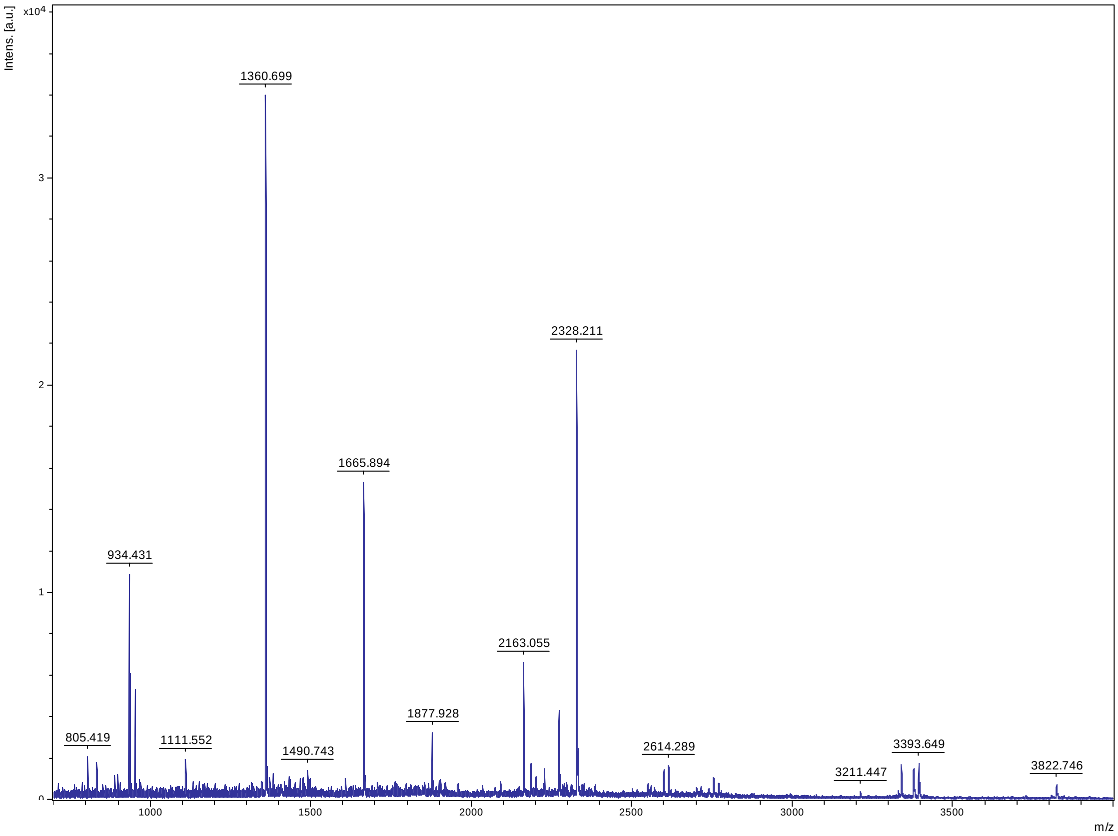


Match to: gi|34897076 Score: 66 Expect: 0.019

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 19	1979.0532	1978.0459	1978.0166	0.0293	1	M.REILHIQGGQCGNQIGAK.F	Carbamidomethyl (C)
20 - 35	1890.8779	1889.8706	1889.8366	0.0340	0	K.FWEVICDEHGVDATGR.Y	Carbamidomethyl (C)
36 - 46	1308.6135	1307.6062	1307.5993	0.0069	0	R.YAGDSDLQLER.I	Acetyl (N-term)
36 - 58	2632.2865	2631.2792	2631.2200	0.0592	1	R.YAGDSDLQLERINVYYNEASGGR.Y	Acetyl (N-term)
47 - 58	1342.5925	1341.5852	1341.6313	-0.0460	0	R.INVYYNEASGGR.Y	
63 - 77	1633.7871	1632.7798	1632.7851	-0.0053	0	R.AVLMDLEPGTMDSVR.S	
104 - 121	1973.0054	1971.9981	1971.9901	0.0080	0	K.GHYTEGAELIDSVLDVVR.K	
104 - 122	2101.0853	2100.0780	2100.0851	-0.0070	1	K.GHYTEGAELIDSVLDVVRK.E	
155 - 162	1077.4453	1076.4380	1076.5250	-0.0870	1	K.IREEYPDR.M	
242 - 251	1146.5367	1145.5294	1145.5829	-0.0535	0	R.FPGQLNSDLR.K	
263 - 276	1664.8084	1663.8011	1663.8544	-0.0533	0	R.LHFFMVGFAPLTSR.G	Acetyl (N-term)
277 - 297	2492.2418	2491.2345	2491.2165	0.0180	1	R.GSQQYRALTVPELTQQMWDAK.N	Acetyl (N-term)
283 - 297	1730.8512	1729.8439	1729.8709	-0.0270	0	R.ALTVPELTQQMWDAK.N	
298 - 309	1431.6198	1430.6125	1430.5965	0.0160	1	K.NMMCAADPRHGR.Y	Carbamidomethyl (C); Oxidation (M)
325 - 350	3140.5162	3139.5089	3139.4920	0.0170	1	K.EVDEQMLNVQNKNSSYFVEWIPNNVK.S	Oxidation (M)
337 - 350	1696.8526	1695.8453	1695.8256	0.0197	0	K.NSSYFVEWIPNNVK.S	
381 - 390	1215.5453	1214.5380	1214.5753	-0.0373	0	R.VSEQFTAMFR.R	
381 - 390	1231.5906	1230.5833	1230.5703	0.0131	0	R.VSEQFTAMFR.R	Oxidation (M)

Spot 1701

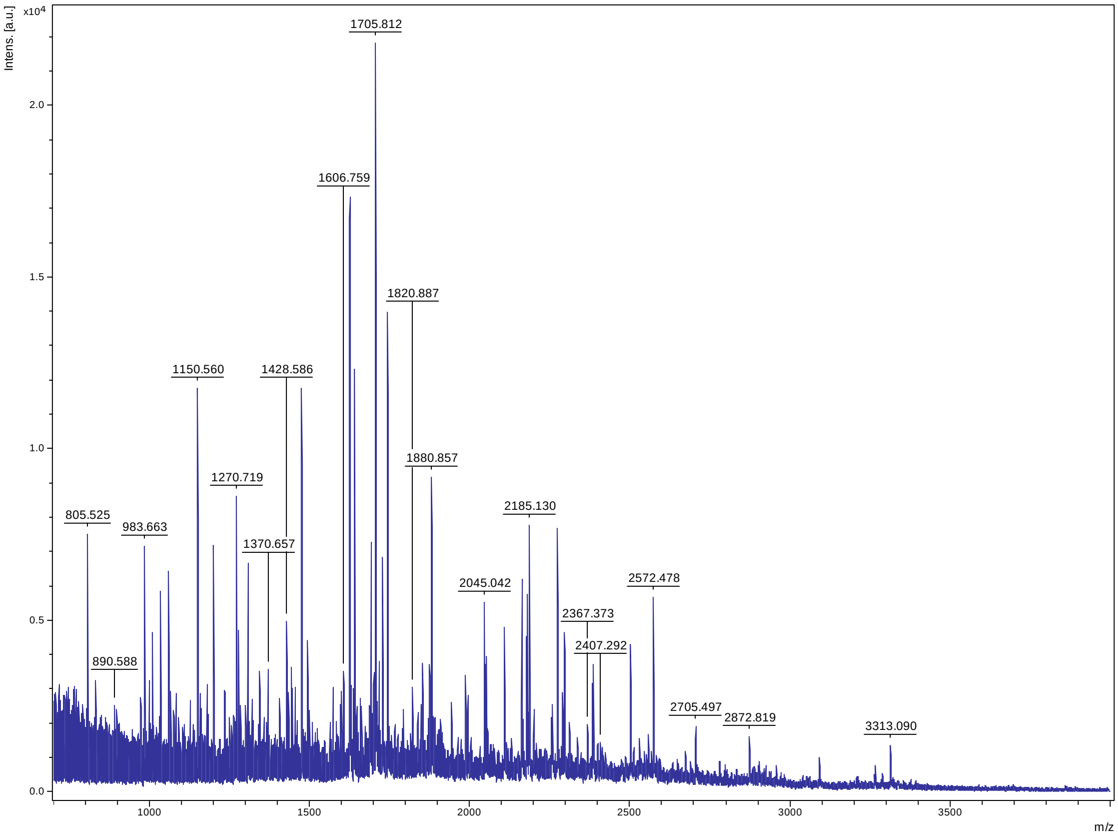


Match to: gi|53793163 Score: 107 Expect: 1.3e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
10 - 27	1877.9001	1876.8928	1876.9053	-0.0125	0	K.GTNFEIEASPEASVAEVK.R	
10 - 28	2033.9920	2032.9847	2033.0065	-0.0217	1	K.GTNFEIEASPEASVAEVKR.I	
28 - 51	2754.2751	2753.2678	2753.3918	-0.1240	1	K.RIIESTQGQNVYPADQQMLIHQGK.I	
28 - 51	2770.2070	2769.1997	2769.3867	-0.1870	1	K.RIIESTQGQNVYPADQQMLIHQGK.I	Oxidation (M)
29 - 51	2598.1612	2597.1539	2597.2907	-0.1368	0	R.IIESTQGQNVYPADQQMLIHQGK.I	
29 - 51	2614.1747	2613.1674	2613.2856	-0.1182	0	R.IIESTQGQNVYPADQQMLIHQGK.I	Oxidation (M)
52 - 63	1346.6896	1345.6823	1345.7089	-0.0266	1	K.ILKDDTTLEGNK.V	
64 - 76	1466.7883	1465.7810	1465.7850	-0.0040	0	K.VAENSFLVIMLSK.A	Oxidation (M)
191 - 198	934.3620	933.3547	933.4304	-0.0757	0	R.AAYNNPER.A	
199 - 219	2328.1149	2327.1076	2327.1797	-0.0721	0	R.AIDYLYSGIPENVEPPQPVAR.A	
317 - 334	2192.9802	2191.9729	2192.1702	-0.1972	1	K.QNPQILRLIQENQAEFLR.L	Pyro-glu (N-term Q)
324 - 334	1360.6975	1359.6902	1359.7146	-0.0244	0	R.LIQENQAEFLR.L	
335 - 368	3377.4028	3376.3955	3376.6932	-0.2976	0	R.LVNESPDSGAAGGNILGQLAAAMPQALTVTPEER.E	
335 - 368	3393.3914	3392.3841	3392.6881	-0.3040	0	R.LVNESPDSGAAGGNILGQLAAAMPQALTVTPEER.E	Oxidation (M)
374 - 381	937.3896	936.3823	936.4487	-0.0664	0	R.LEAMGFNR.E	
374 - 381	953.3958	952.3885	952.4436	-0.0551	0	R.LEAMGFNR.E	Oxidation (M)
382 - 413	3822.5404	3821.5331	3821.7518	-0.2187	1	R.ELVLEVFFACNKDEELAANYLLDHGHEFEDQQ.-	Carbamidomethyl (C)

Spot 1703

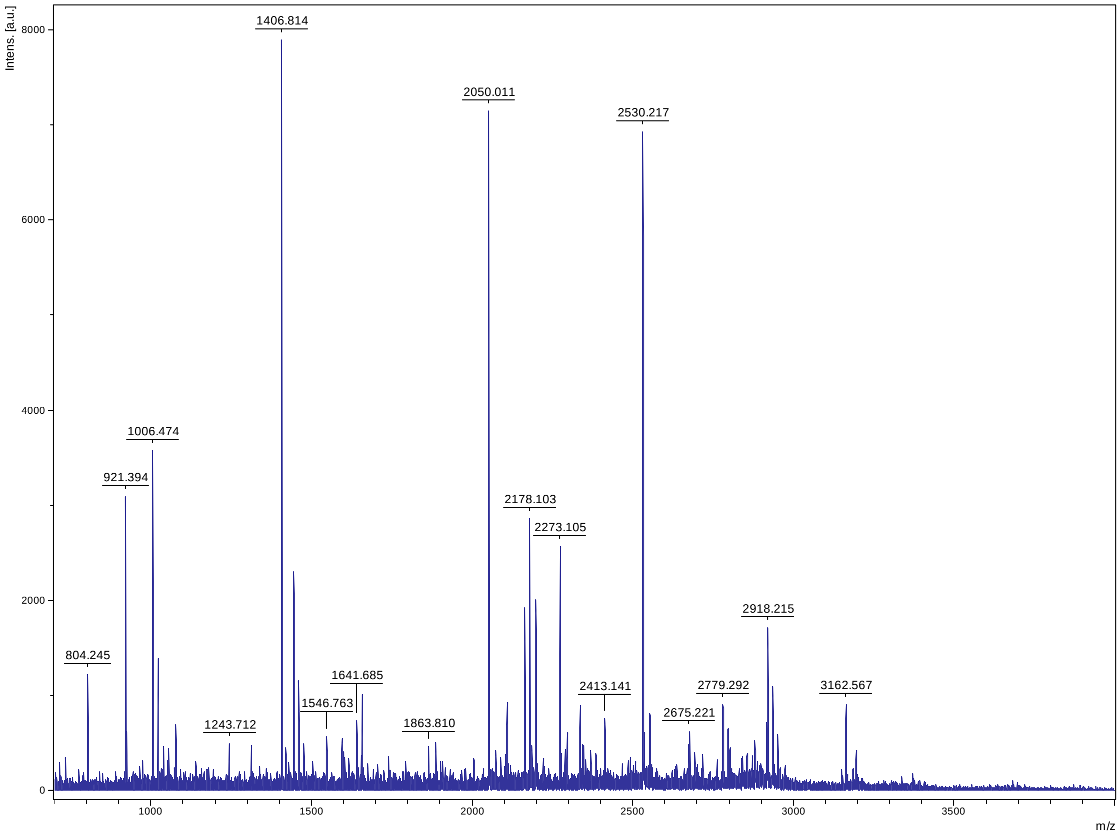


Match to: gi|50582723; Score: 180

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
8 - 31	2407.29	2406.29	2406.27	0.02	1	VAAPASVAAAARCGTSLARPWPAR
77 - 90	1270.72	1269.72	1269.74	-0.02	0	TVVAVILGGGAGTR
99 - 110	1199.68	1198.67	1198.68	-0.01	0	AKPAVPIGGAYR
127 - 140	1625.82	1624.81	1624.86	-0.04	0	VYILTQFNSASLNR
175 - 184	1150.56	1149.56	1149.56	0.00	0	WFQGTADAVR
185 - 194	1284.60	1283.60	1283.58	0.02	0	QFDWLFDDAK
195 - 211	1943.01	1942.01	1942.02	-0.01	1	AKDIDDVLILSGDHLYR
197 - 211	1743.85	1742.85	1742.88	-0.03	0	DIDDVLILSGDHLYR
212 - 222	1428.59	1427.58	1427.60	-0.01	0	MDYMDFVQSHR
212 - 222	1444.60	1443.60	1443.59	0.01	0	MDYMDFVQSHR Oxidation (M)
212 - 222	1460.64	1459.63	1459.59	0.05	0	MDYMDFVQSHR 2 Oxidation (M)
225 - 239	1691.75	1690.75	1690.77	-0.01	0	GADISICCLPIDDSR
300 - 307	983.66	982.66	982.62	0.04	0	EILLNLLR
308 - 326	2107.09	2106.09	2106.05	0.03	1	WRFPTANDFGSEIIPASAK
332 - 346	1847.88	1846.88	1846.88	0.00	0	AYLFNDYWEDIGTIK
347 - 361	1705.81	1704.81	1704.85	-0.04	0	SFFEANLSLAEQPPR
362 - 375	1726.76	1725.76	1725.78	-0.03	0	FSFYDANKPMYTSR
362 - 375	1742.78	1741.78	1741.78	0.00	0	FSFYDANKPMYTSR Oxidation (M)
376 - 387	1370.66	1369.66	1369.71	-0.06	1	RNLPPSMINNSK
388 - 403	1880.86	1879.85	1879.86	-0.00	0	ITDSIISHGCFLDSCR
404 - 412	1009.60	1008.60	1008.57	0.03	0	IEHSVVGIR
423 - 438	1874.90	1873.89	1873.84	0.05	0	DTVMLGADFYETDLER
457 - 467	1344.67	1343.67	1343.70	-0.03	1	IQNCIIDKNAR
471 - 493	2572.48	2571.48	2571.22	0.26	1	NVTISNSEGVQEADRTSEGFYIR
486 - 493	972.56	971.55	971.47	0.08	0	TSEGFYIR

Spot 1707

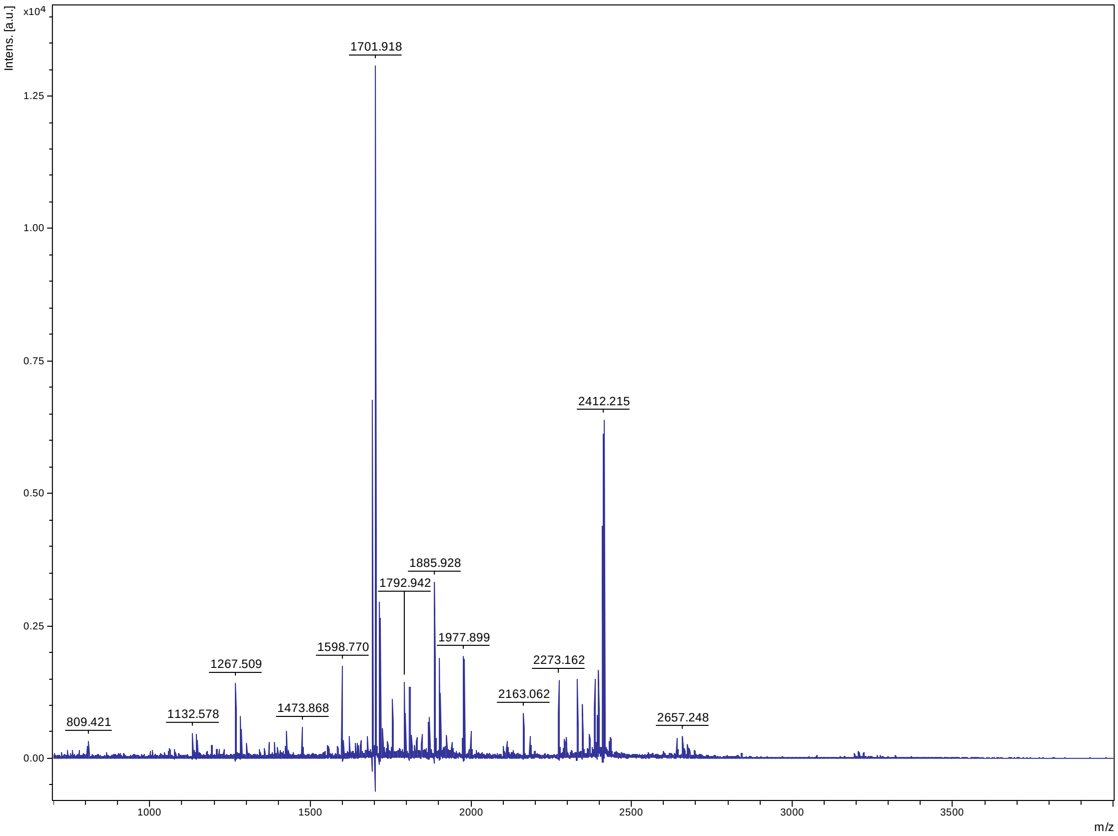


Match to: gi|50878307; Score: 123

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
156 - 168	1406.81	1405.81	1405.84	-0.03	0	LGDPARPLLLSVR
203 - 209	921.39	920.39	920.40	-0.01	0	FAYDSYR
203 - 210	1077.50	1076.50	1076.50	-0.01	1	FAYDSYRR
239 - 259	2345.15	2344.15	2344.19	-0.04	1	GLHNDTDLTATDLKELVAQYK
276 - 293	2071.98	2070.97	2071.12	-0.15	1	KQLQLAVLAVFNSWDSPR
308 - 333	2675.22	2674.22	2674.28	-0.07	0	GTAVNVQTMVFGNMGNTSGTGVLFTR Oxidation (M)
341 - 360	2178.10	2177.10	2177.15	-0.05	1	KLYGEFLVNAQGEDVVAGIR
342 - 360	2050.01	2049.01	2049.05	-0.04	0	LYGEFLVNAQGEDVVAGIR
361 - 384	2918.22	2917.21	2917.26	-0.04	1	TPEDLDAMRDHMPEPYEELVENCK
361 - 384	2934.21	2933.21	2933.25	-0.04	1	TPEDLDAMRDHMPEPYEELVENCK Oxidation (M)
361 - 384	2950.25	2949.25	2949.25	-0.00	1	TPEDLDAMRDHMPEPYEELVENCK 2 Oxidation (M)
392 - 404	1641.69	1640.68	1640.72	-0.03	0	EMMDIEFTVQENR
405 - 411	1006.47	1005.47	1005.49	-0.02	0	LWMLQCR
405 - 411	1022.47	1021.47	1021.48	-0.01	0	LWMLQCR Oxidation (M)
423 - 435	1444.71	1443.70	1443.74	-0.03	0	IAVDMVNEGLVER
423 - 435	1460.72	1459.72	1459.73	-0.02	0	IAVDMVNEGLVER Oxidation (M)
441 - 462	2552.17	2551.17	2551.22	-0.05	0	MVEPGHLDQLLHPQFENPSGYK Oxidation (M)
441 - 464	2779.29	2778.29	2778.34	-0.05	1	MVEPGHLDQLLHPQFENPSGYKDK
441 - 464	2795.29	2794.28	2794.34	-0.05	1	MVEPGHLDQLLHPQFENPSGYKDK Oxidation (M)
465 - 496	3162.57	3161.56	3161.61	-0.05	0	VIATGLPASPGAAVGQIVFTAEDAEAWHAQGK
524 - 539	1600.81	1599.80	1599.79	0.01	1	GGMTSHAAVVARGWGK Oxidation (M)

Spot 1709

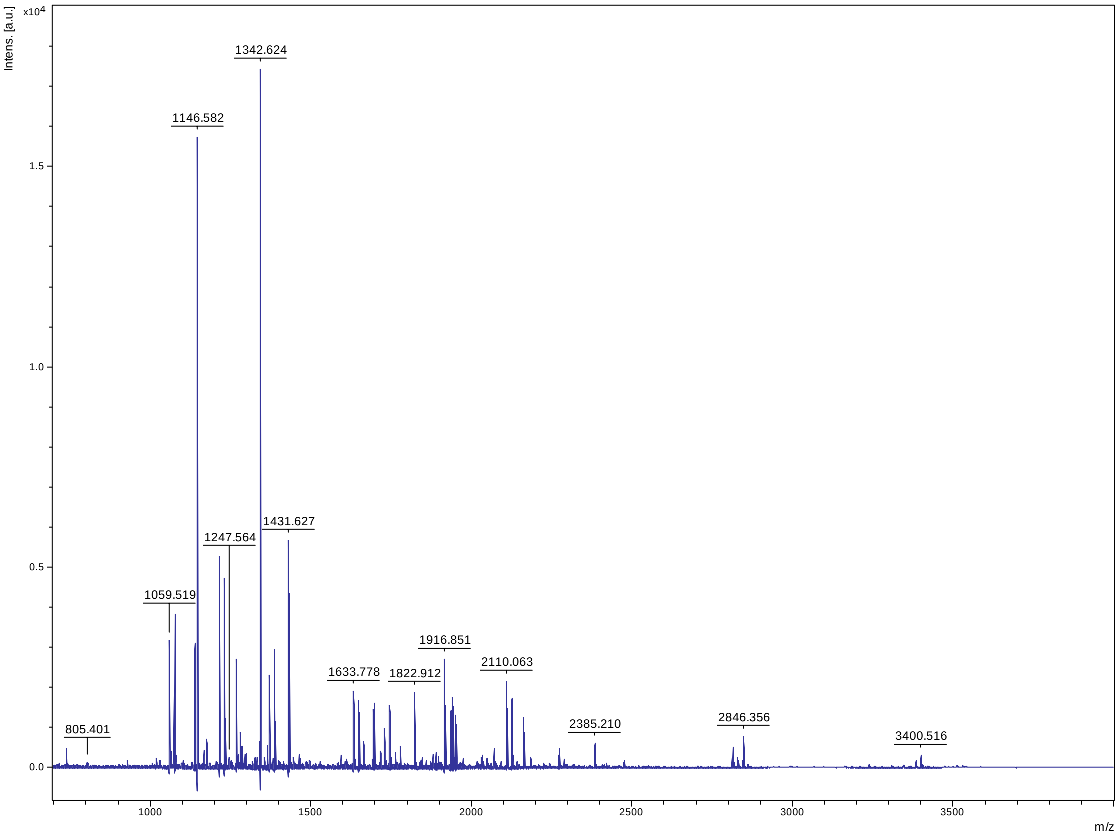


Match to: gi|10441016; Score: 172

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
41 - 60	1977.89	1976.88	1976.88	0.01	0	TVGGGDDAFNTFFSETGAGK
65 - 79	1701.91	1700.90	1700.90	0.00	0	AVFVDLEPTVIDEVR
85 - 105	2412.19	2411.19	2411.20	-0.01	1	QLFHPEQLINGKEDAANNFAR
113 - 121	1132.57	1131.57	1131.56	0.01	0	EIVDLCLDR
215 - 229	1847.96	1846.95	1846.96	-0.01	1	RSLDIERPTYTNLNR
216 - 229	1691.87	1690.87	1690.86	0.00	0	SLDIERPTYTNLNR
230 - 243	1473.87	1472.87	1472.86	0.01	0	LVSQVISSLTASLR
265 - 280	1792.93	1791.93	1791.92	0.00	0	IHFMLSSYAPVISAEK
265 - 280	1808.92	1807.91	1807.92	-0.00	0	IHFMLSSYAPVISAEK Oxidation (M)
281 - 304	2641.21	2640.20	2640.22	-0.02	0	AYHEQLSVAEITNSAFEPSSMMAK
281 - 304	2657.23	2656.22	2656.21	0.01	0	AYHEQLSVAEITNSAFEPSSMMAK Oxidation (M)
281 - 304	2673.21	2672.21	2672.21	-0.00	0	AYHEQLSVAEITNSAFEPSSMMAK 2 Oxidation (M)
312 - 320	1267.51	1266.50	1266.50	0.00	0	YMACCLMYR
312 - 320	1283.50	1282.50	1282.50	0.00	0	YMACCLMYR Oxidation (M)
312 - 320	1299.50	1298.50	1298.49	0.01	0	YMACCLMYR 2 Oxidation (M)
339 - 352	1754.87	1753.86	1753.86	0.00	1	RTIQFVDWCPTGFK
340 - 352	1598.76	1597.75	1597.76	-0.01	0	TIQFVDWCPTGFK
353 - 370	1901.92	1900.92	1900.94	-0.01	0	CGINYQPPSVVPSGDLAK
374 - 390	1885.92	1884.91	1884.91	0.01	0	AVCMISNSTSVVEVFSR
374 - 394	2395.15	2394.15	2394.17	-0.02	1	AVCMISNSTSVVEVFSRIDHK Oxidation (M)
403 - 422	2330.01	2329.00	2329.01	-0.01	0	AFVHWYVGEGMEEGEFSEAR
403 - 422	2346.01	2345.01	2345.01	0.00	0	AFVHWYVGEGMEEGEFSEAR Oxidation (M)

Spot 1710

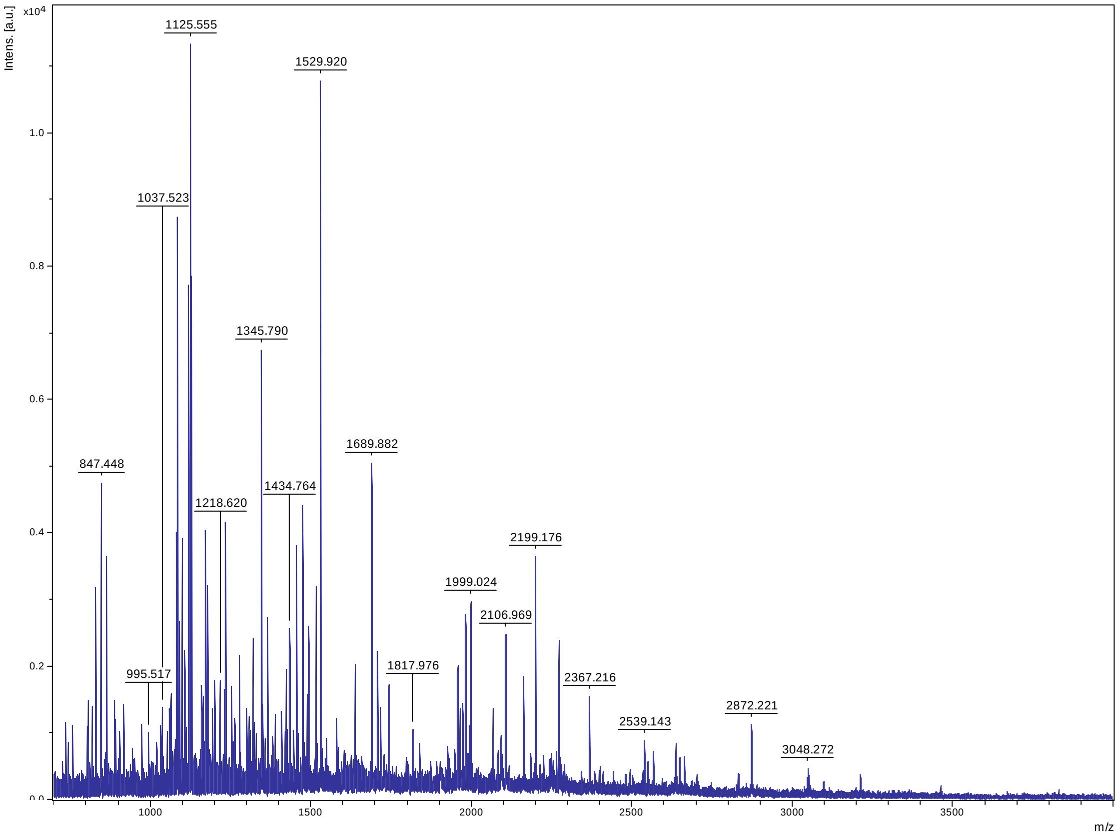


Match to: gi|74053562; Score: 224

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 19	2110.06	2109.05	2109.06	-0.00	1	MREILHIQGGQCGNQIGAK
1 - 19	2126.05	2125.04	2125.05	-0.01	1	MREILHIQGGQCGNQIGAK Oxidation (M)
3 - 19	1822.91	1821.90	1821.92	-0.01	0	EILHIQGGQCGNQIGAK
20 - 35	1942.86	1941.86	1941.87	-0.01	0	FWEVICDEHGIDHTGK
36 - 46	1282.59	1281.59	1281.58	0.00	0	YSGDSDLQLER
47 - 58	1342.62	1341.61	1341.63	-0.02	0	INVYYNEASGGR
63 - 77	1633.77	1632.77	1632.79	-0.02	0	AVLMDLEPGTMDSVR
63 - 77	1649.76	1648.76	1648.78	-0.02	0	AVLMDLEPGTMDSVR Oxidation (M)
63 - 77	1665.77	1664.77	1664.77	-0.00	0	AVLMDLEPGTMDSVR 2 Oxidation (M)
78 - 103	2814.33	2813.33	2813.33	0.00	0	SGPYGQIFRPDNFVFGQSGAGNNWAK
155 - 162	1077.51	1076.51	1076.53	-0.02	1	IREEYPDR
242 - 251	1146.57	1145.57	1145.58	-0.01	0	FPGQLNSDLR
242 - 252	1274.63	1273.63	1273.68	-0.05	1	FPGQLNSDLRK
252 - 262	1267.76	1266.76	1266.78	-0.02	1	KLAVNLIPFPR
253 - 262	1139.67	1138.67	1138.69	-0.01	0	LAVNLIPFPR
283 - 297	1730.86	1729.86	1729.87	-0.01	0	ALTVPELTQQMWDAK
283 - 297	1746.86	1745.85	1745.87	-0.01	0	ALTVPELTQQMWDAK Oxidation (M)
298 - 306	1065.39	1064.39	1064.42	-0.03	0	NMMCAADPR
298 - 309	1431.62	1430.61	1430.60	0.02	1	NMMCAADPRHGR Oxidation (M)
310 - 318	1059.51	1058.51	1058.52	-0.01	0	YLTASAMFR
310 - 318	1075.51	1074.50	1074.52	-0.01	0	YLTASAMFR Oxidation (M)
337 - 350	1696.80	1695.80	1695.83	-0.02	0	NSSYFVEWIPNNVK
351 - 362	1285.64	1284.63	1284.67	-0.04	0	SSVCDIPPIGLK
363 - 379	1935.88	1934.87	1934.89	-0.01	0	MASTFIGNSTSIQEMFR Oxidation (M)
363 - 379	1951.87	1950.87	1950.88	-0.02	0	MASTFIGNSTSIQEMFR 2 Oxidation (M)
381 - 390	1215.56	1214.56	1214.58	-0.01	0	VSEQFTAMFR
381 - 390	1231.56	1230.55	1230.57	-0.02	0	VSEQFTAMFR Oxidation (M)
381 - 391	1371.67	1370.66	1370.68	-0.01	1	VSEQFTAMFRR
381 - 391	1387.66	1386.66	1386.67	-0.01	1	VSEQFTAMFRR Oxidation (M)

Spot 1712

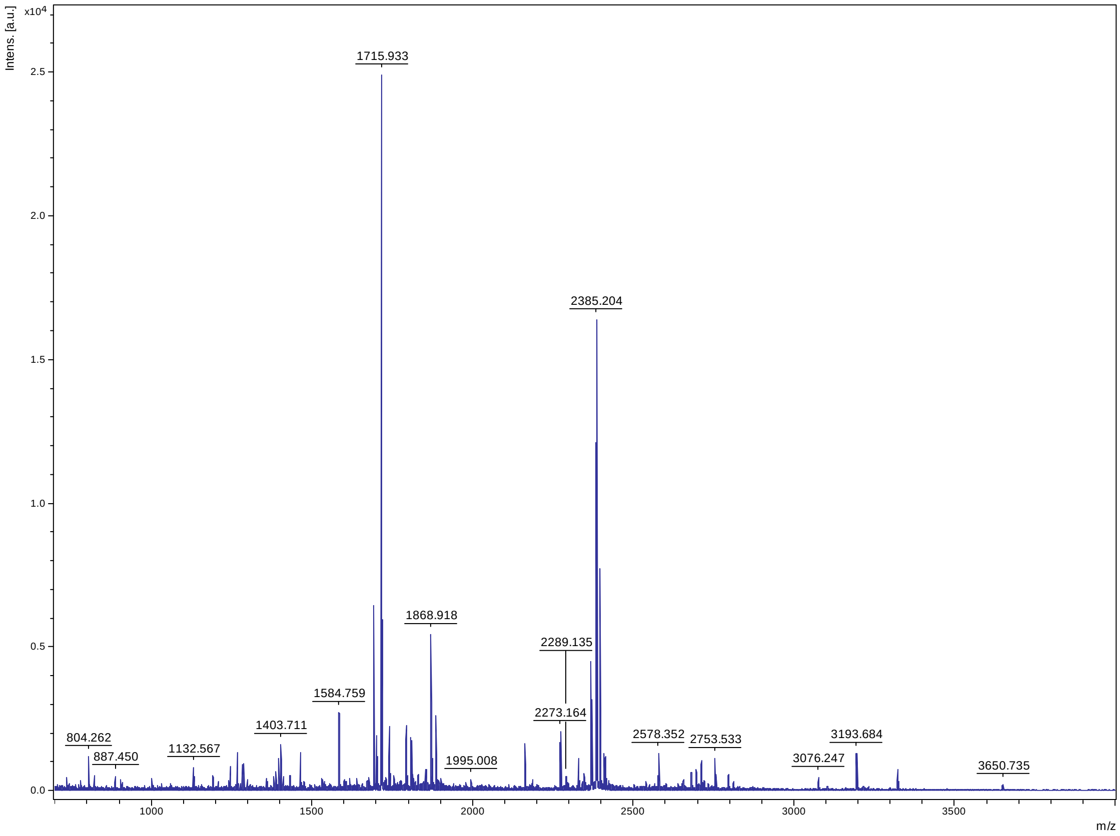


Match to: gi|55296661 Score: 95 Expect: 2.2e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 16	1421.7898	1420.7825	1420.7674	0.0152	0	M.APPPAVLSSGELGAR.G	
80 - 102	2637.3185	2636.3112	2636.3274	-0.0162	1	R.RLDFDLLPFDASEFPGGDPFLLR.W	
109 - 123	1529.9473	1528.9400	1528.9089	0.0311	0	R.SLHLLGPVIAGVTPR.V	
124 - 142	1965.1490	1964.1417	1964.0942	0.0475	0	R.VTATVTDVTLVSHVNPIAK.D	
173 - 187	1455.7357	1454.7284	1454.7001	0.0284	0	K.DAGADVGDVDIPGVR.R	
191 - 203	1579.9435	1578.9362	1578.8882	0.0480	1	K.RSWLPQPLLDLNK.L	
192 - 203	1423.8269	1422.8196	1422.7871	0.0325	0	R.SWLPQPLLDLNK.L	
208 - 218	1350.7433	1349.7360	1349.6761	0.0599	1	K.QFIENGREMVK.T	
219 - 239	2199.2385	2198.2312	2198.1946	0.0366	0	K.TDGVLINTFDALEPVALAALR.D	
246 - 265	1999.0699	1998.0626	1998.0210	0.0416	0	R.GFPPVFAVGPHSSLASEATK.G	
266 - 285	2083.0910	2082.0837	2082.0064	0.0773	1	K.GAAADAEGSPMAWLRQQPAR.S	
286 - 295	1084.5307	1083.5234	1083.5712	-0.0478	0	R.SVVYVAFGSR.C	
296 - 304	1099.4878	1098.4805	1098.5240	-0.0435	0	R.CAVSHEQIR.E	Carbamidomethyl (C)
305 - 316	1160.5789	1159.5716	1159.5833	-0.0116	0	R.EIAAGLEASGSR.F	
336 - 345	1120.5303	1119.5230	1119.5560	-0.0330	0	R.DVLGDGFLER.V	
355 - 364	1172.5951	1171.5878	1171.5985	-0.0107	0	K.AWVDQDAVLR.D	
459 - 476	1742.9845	1741.9772	1741.9362	0.0410	0	K.AVAVGGTSHTGILDFVAK.L	

Spot 1715



Match to: gi|135399; Score: 271

Matched peptides:

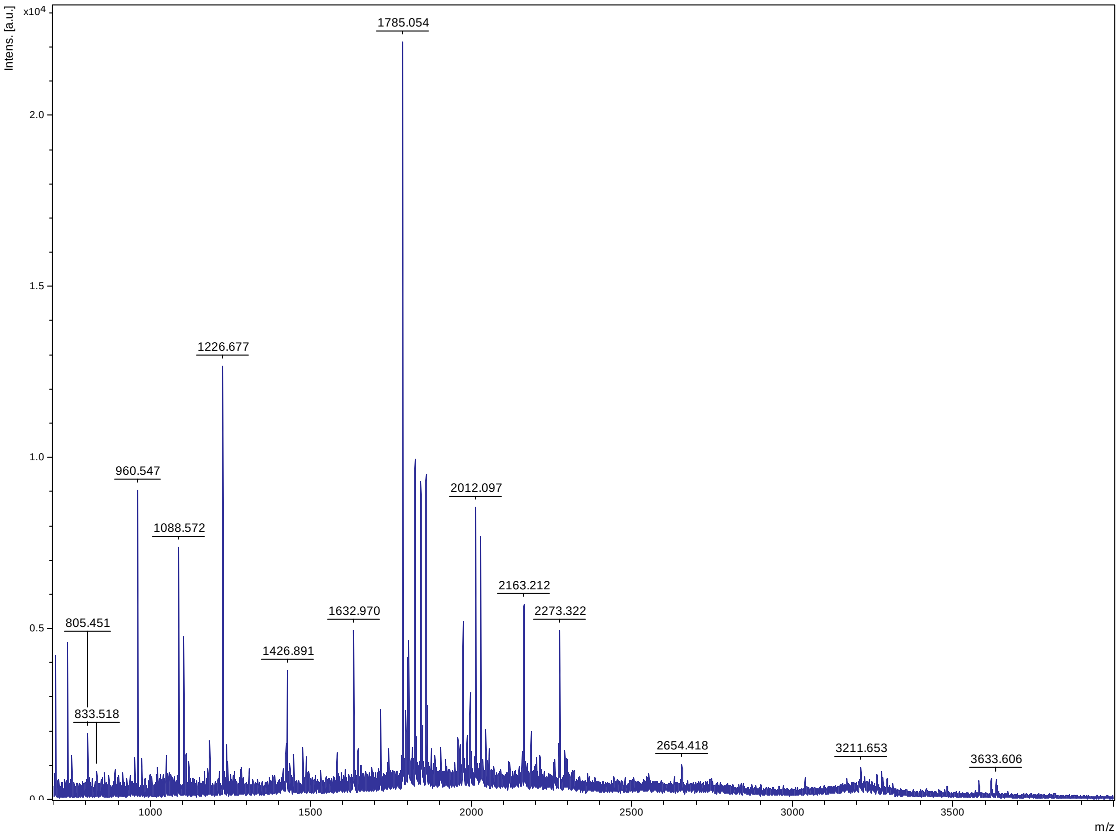
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
65 - 79	1715.93	1714.93	1714.91	0.02	0	AIFVDLEPTVIDEVR
85 - 96	1396.74	1395.74	1395.75	-0.01	0	QLFHPEQLISGK
85 - 105	2368.17	2367.17	2367.16	0.01	1	QLFHPEQLISGKEDAANNFAR Pyro-glu (N-term Q)
85 - 105	2385.20	2384.20	2384.19	0.01	1	QLFHPEQLISGKEDAANNFAR
106 - 121	1874.95	1873.95	1873.94	0.02	1	GHYTVGKEIVDLCLDR
113 - 121	1132.57	1131.56	1131.56	0.00	0	EIVDLCLDR
113 - 123	1387.74	1386.74	1386.73	0.01	1	EIVDLCLDRVR
124 - 156	3321.76	3320.76	3320.72	0.04	1	KLADNCTGLQGFLVFNAVGGGTGSGLGSLLLER
125 - 156	3193.68	3192.68	3192.62	0.06	0	LADNCTGLQGFLVFNAVGGGTGSGLGSLLLER
216 - 229	1691.88	1690.88	1690.86	0.02	0	SLDIERPTYTNLNR
230 - 243	1531.89	1530.88	1530.90	-0.01	0	LISQIISSLTTSLR
244 - 264	2395.21	2394.21	2394.19	0.03	0	FDGAINVDVTEFQTNLVPYPR
265 - 280	1792.93	1791.93	1791.92	0.01	0	IHFMLSSYAPVISAEK
265 - 280	1808.94	1807.93	1807.92	0.02	0	IHFMLSSYAPVISAEK Oxidation (M)
281 - 304	2679.29	2678.29	2678.27	0.02	0	AYHEQLSVPEITNAVFEPSSMMAK
281 - 304	2695.29	2694.28	2694.27	0.02	0	AYHEQLSVPEITNAVFEPSSMMAK Oxidation (M)
281 - 304	2711.30	2710.30	2710.26	0.03	0	AYHEQLSVPEITNAVFEPSSMMAK 2 Oxidation (M)
312 - 320	1267.51	1266.50	1266.50	0.00	0	YMACCLMYR
312 - 320	1283.50	1282.49	1282.50	-0.00	0	YMACCLMYR Oxidation (M)
312 - 320	1299.48	1298.48	1298.49	-0.01	0	YMACCLMYR 2 Oxidation (M)
327 - 336	1001.57	1000.57	1000.56	0.02	0	DVNAAVATIK
339 - 352	1740.87	1739.87	1739.85	0.02	1	RTVQFVDWCPTGFK
340 - 352	1584.76	1583.76	1583.74	0.01	0	TVQFVDWCPTGFK
353 - 370	1871.95	1870.95	1870.92	0.02	0	CGINYQPPSVVPGGDLAK
374 - 390	1868.92	1867.92	1867.89	0.02	0	AVCMISNNTAVAEVFSR
374 - 390	1884.91	1883.91	1883.89	0.02	0	AVCMISNNTAVAEVFSR Oxidation (M)
391 - 401	1380.70	1379.70	1379.69	0.01	1	IDHKFDLMYAK
395 - 401	887.45	886.45	886.43	0.02	0	FDLMYAK
395 - 401	903.42	902.42	902.42	-0.00	0	FDLMYAK Oxidation (M)
403 - 422	2330.02	2329.02	2329.01	0.00	0	AFVHWYVGEGMEEGEFSEAR
403 - 422	2346.02	2345.02	2345.01	0.01	0	AFVHWYVGEGMEEGEFSEAR Oxidation (M)
423 - 450	3076.25	3075.24	3075.21	0.03	1	EDLAALEKDYEEVGAEGADDENDDGEDY

Match to: gi|34912654; Score: 102

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
9 - 37	2753.53	2752.53	2752.51	0.02	1	SPPALVPPAGPTPGGSLPLSSIDKTAAVR
38 - 64	2795.43	2794.43	2794.40	0.03	1	VSVDFIQVFPSSAEAAKDQAASVAAMR
70 - 80	1245.68	1244.68	1244.67	0.01	0	ALVHYYPVAGR
124 - 135	1431.79	1430.79	1430.79	-0.00	0	EELLPRPPPEVR
182 - 194	1463.84	1462.84	1462.83	0.01	0	GLPEPSLKPIWAR
195 - 218	2578.35	2577.35	2577.33	0.02	0	DAIPNPPKPPLGPPPSFTAFNFEK
219 - 230	1359.77	1358.76	1358.78	-0.01	1	SVIEISLDSIKR
258 - 270	1403.71	1402.71	1402.71	-0.00	0	TLAIDFAPDADVR
271 - 278	822.45	821.45	821.44	0.01	0	LGFAASTR
310 - 321	1286.73	1285.73	1285.72	0.01	0	DASLVEIVTAIR
403 - 414	1411.73	1410.73	1410.73	0.00	0	LVLQCVEAQHSK

Spot 1718

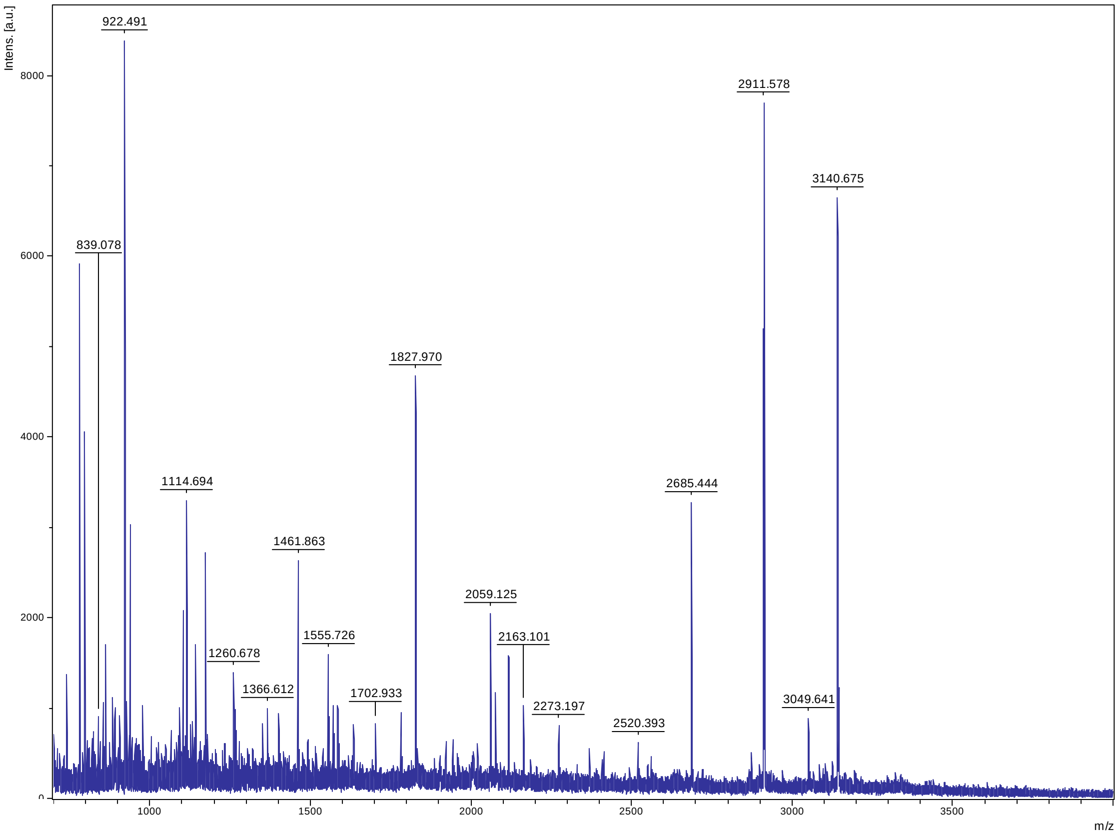


Match to: gi|34900784 Score: 115 Expect: 2.1e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
45 - 53	1088.5407	1087.5334	1087.5120	0.0214	0	R.EPGMAEWLR.G	
45 - 53	1104.5369	1103.5296	1103.5069	0.0227	0	R.EPGMAEWLR.G	Oxidation (M)
59 - 71	1632.8987	1631.8914	1631.8532	0.0383	1	R.IHRHPELAFEEVR.T	
62 - 71	1226.6356	1225.6283	1225.6091	0.0192	0	R.HPELAFEEVR.T	
72 - 77	704.3243	703.3170	703.3864	-0.0694	0	R.TSELVR.A	
78 - 93	1784.9557	1783.9484	1783.9257	0.0228	0	R.AELDAIGVPYQWPVAR.T	
94 - 114	1824.0163	1823.0090	1822.9900	0.0190	0	R.TGVVATIAGGGGGDGPVVALR.A	
115 - 131	1995.9501	1994.9428	1994.9407	0.0021	0	R.ADMDALPVQELVDWEHK.S	
263 - 278	1715.9723	1714.9650	1714.9505	0.0146	0	R.EIDPLQGAVVSITFVK.G	
279 - 297	2011.9656	2010.9583	2010.9468	0.0115	0	K.GGEAYNVIPQSVEFGGTMR.S	
279 - 297	2027.9596	2026.9523	2026.9417	0.0106	0	K.GGEAYNVIPQSVEFGGTMR.S	Oxidation (M)
322 - 350	3277.1772	3276.1699	3276.3732	-0.2032	0	R.CGGGVDFMEESMRPYPAVVNDEGMYAHAR.A	Carbamidomethyl (C); 2 Oxidation (M)
356 - 363	742.3911	741.3838	741.4497	-0.0658	0	R.LLGAGGVR.V	
364 - 380	1842.8969	1841.8896	1841.8770	0.0127	0	R.VAPQLMGAEDFGFYAAR.M	
364 - 380	1858.9146	1857.9073	1857.8719	0.0354	0	R.VAPQLMGAEDFGFYAAR.M	Oxidation (M)

Spot 1720

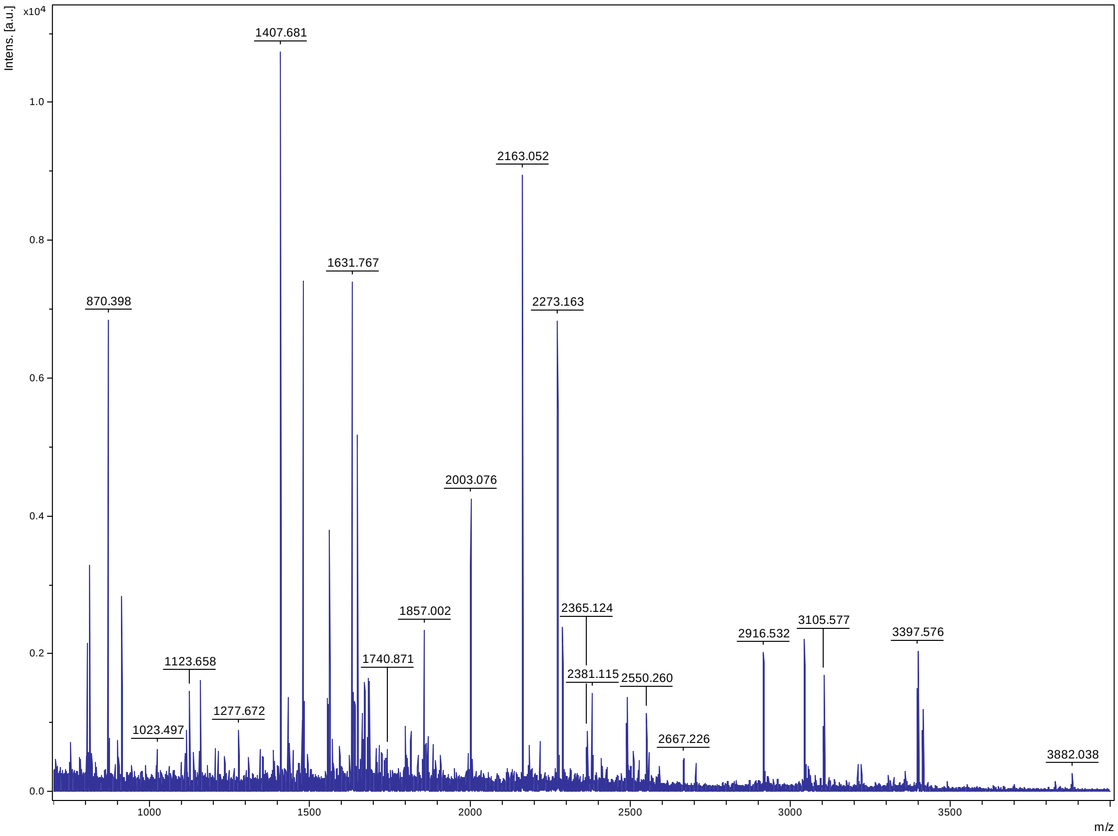


Match to: gi|50905315 Score: 146 Expect: 1.7e-10

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 14	1366.6057	1365.5984	1365.5870	0.0114	0	M.AGMAPEGSQFDAK.H	Acetyl (N-term); Oxidation (M)
55 - 70	1827.9457	1826.9384	1826.9315	0.0070	0	R.GIYAYGFEKPSAIQQR.G	
92 - 119	3140.5814	3139.5741	3139.5681	0.0060	0	K.TATFCSGILQQLDYGLVECQSLVLAPTR.E	2 Carbamidomethyl (C)
140 - 150	1142.5398	1141.5325	1141.5662	-0.0337	0	K.VHACVGGTSVR.E	Carbamidomethyl (C)
155 - 169	1461.8534	1460.8461	1460.8463	-0.0001	0	R.ILASGVHVVVGTPGR.V	
186 - 198	1555.7116	1554.7043	1554.7058	-0.0014	0	K.MFVLDEADEMLSR.G	
186 - 198	1571.7339	1570.7266	1570.7007	0.0259	0	K.MFVLDEADEMLSR.G	Oxidation (M)
215 - 233	2059.1032	2058.0959	2058.0819	0.0140	0	K.IQVGVFSATMPPEALEITR.K	
215 - 233	2075.1034	2074.0961	2074.0768	0.0193	0	K.IQVGVFSATMPPEALEITR.K	Oxidation (M)
215 - 233	2117.0344	2116.0271	2116.0874	-0.0602	0	K.IQVGVFSATMPPEALEITR.K	Acetyl (N-term); Oxidation (M)
246 - 255	1173.6189	1172.6116	1172.6401	-0.0284	1	K.RDELTLEGIK.Q	
256 - 267	1584.7721	1583.7648	1583.7619	0.0029	1	K.QFYVNVEKEDWK.L	
268 - 290	2685.3790	2684.3717	2684.3731	-0.0014	0	K.LDTLCDLYETLAITQSVIFVNTR.R	Carbamidomethyl (C)
333 - 342	1114.6513	1113.6440	1113.6757	-0.0317	0	R.VLITTDLLAR.G	
343 - 367	2911.5238	2910.5165	2910.4875	0.0290	0	R.GIDVQQVSLVINYDLPTQPENYLHR.I	
377 - 386	1104.6075	1103.6002	1103.6451	-0.0448	1	R.KGVAINFVTR.D	
391 - 397	922.3966	921.3893	921.4742	-0.0849	0	R.MLFDIQR.F	
391 - 397	938.3986	937.3913	937.4691	-0.0778	0	R.MLFDIQR.F	Oxidation (M)

Spot 1724

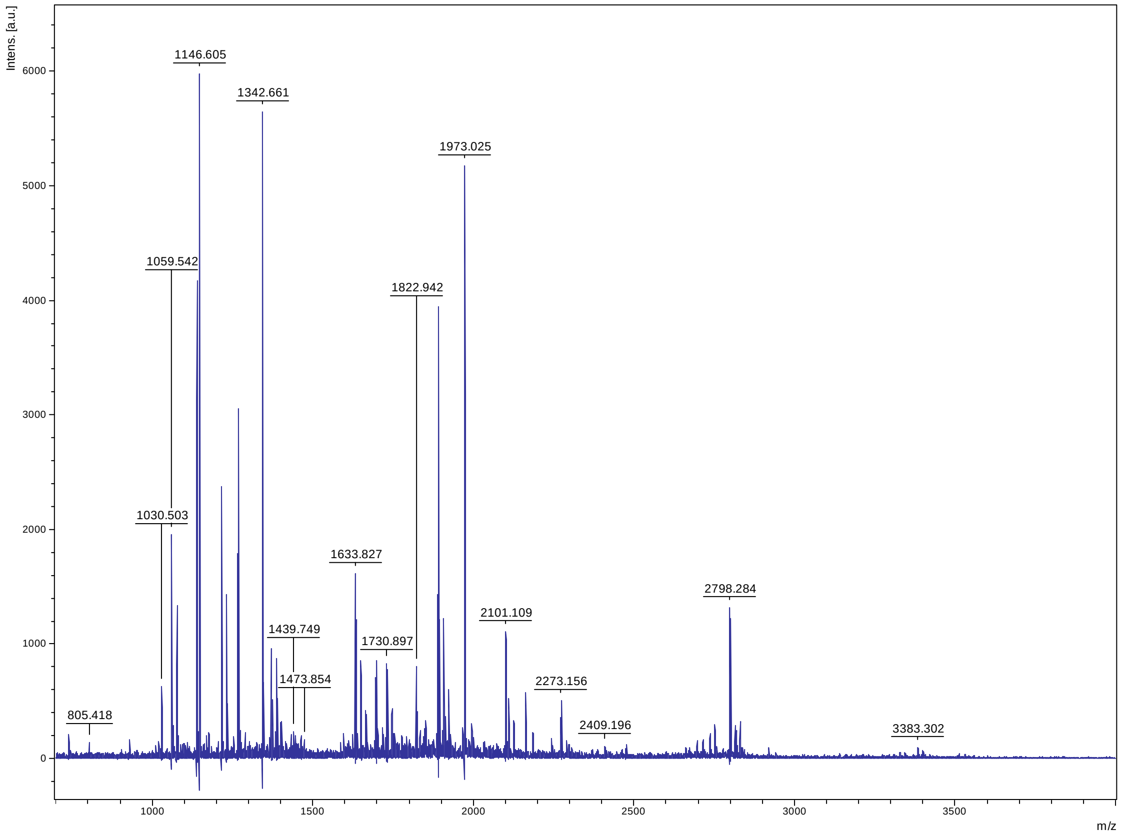


Match to: gi|50252009; Score: 171

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
74 - 81	818.41	817.41	817.43	-0.02	0	EISLSGGR
82 - 87	810.36	809.36	809.39	-0.03	0	FQSCLR
146 - 161	1798.91	1797.91	1797.90	0.00	1	LMNVKEDHGELSSIAR
146 - 161	1814.90	1813.90	1813.90	0.00	1	LMNVKEDHGELSSIAR Oxidation (M)
151 - 161	1213.55	1212.55	1212.57	-0.03	0	EDHGELSSIAR
162 - 169	805.39	804.39	804.32	0.07	0	QGSGSACR Pyro-glu (N-term Q)
225 - 236	1407.68	1406.68	1406.70	-0.03	0	DSVETSPLLQYR
237 - 244	899.48	898.48	898.49	-0.01	0	AQTVVPER
254 - 262	1113.60	1112.59	1112.54	0.06	1	SRNFESFAR
256 - 262	870.40	869.40	869.40	-0.01	0	NFESFAR
263 - 291	3397.58	3396.57	3396.50	0.08	0	LTCADSNQFHAVCLDTSPPIFYMNDTSHR
263 - 291	3413.58	3412.58	3412.49	0.08	0	LTCADSNQFHAVCLDTSPPIFYMNDTSHR Oxidation (M)
299 - 325	2916.53	2915.53	2915.42	0.11	0	WNQSEGTPQVAYTFDAGPNAVLIAPNR
299 - 326	3044.58	3043.58	3043.52	0.06	1	WNQSEGTPQVAYTFDAGPNAVLIAPNRK
335 - 354	2365.12	2364.12	2364.10	0.02	0	LLYYFPPQDNDLSSYMVGDK
335 - 354	2381.11	2380.11	2380.09	0.02	0	LLYYFPPQDNDLSSYMVGDK Oxidation (M)
355 - 363	903.49	902.48	902.51	-0.02	0	SILSDAGLK
364 - 378	1569.76	1568.76	1568.79	-0.03	0	SIEDVEALPAPAETK
384 - 395	1478.68	1477.68	1477.70	-0.02	1	FKGDVSYFICSR
386 - 395	1203.51	1202.51	1202.54	-0.03	0	GDVSYFICSR
402 - 419	1857.00	1856.00	1856.01	-0.01	0	VVTDESLALIDSVTGLPK

Spot 1727

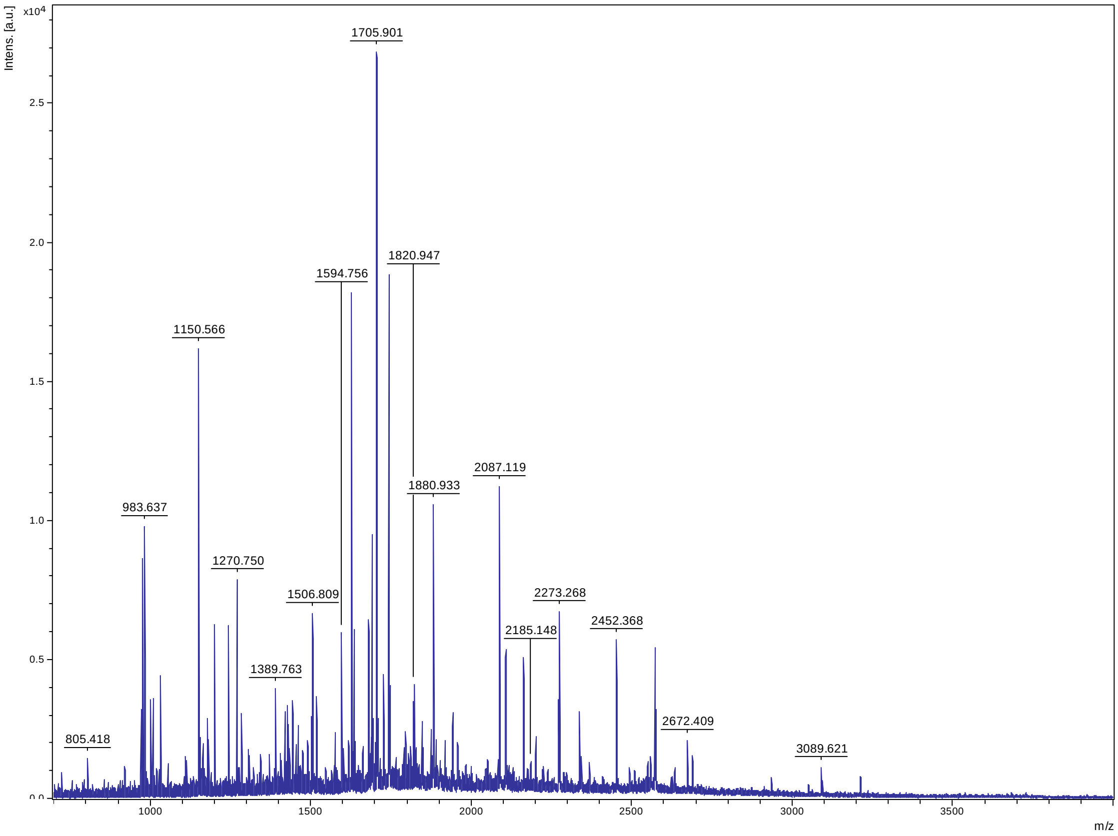


Match to: gi|34897076 Score: 137 Expect: 1.3e-09

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
20 - 35	1833.8619	1832.8546	1832.8151	0.0395	0	K.FWEVICDEHGVDATGR.Y
47 - 58	1342.6762	1341.6689	1341.6313	0.0377	0	R.INVYYNEASGGR.Y
63 - 77	1633.8539	1632.8466	1632.7851	0.0615	0	R.AVLMDLEPGTMDSVR.S
78 - 103	2798.3373	2797.3300	2797.3360	-0.0059	0	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
104 - 121	1973.0257	1972.0184	1971.9901	0.0283	0	K.GHYTEGAELIDSVLDVVR.K
104 - 122	2101.1222	2100.1149	2100.0851	0.0299	1	K.GHYTEGAELIDSVLDVVRK.E
155 - 162	1077.5431	1076.5358	1076.5250	0.0108	1	K.IREEYPDR.M
242 - 251	1146.6067	1145.5994	1145.5829	0.0165	0	R.FPGQLNSDLR.K
242 - 252	1274.6900	1273.6827	1273.6778	0.0049	1	R.FPGQLNSDLRK.L
252 - 262	1267.8170	1266.8097	1266.7812	0.0285	1	R.KLAVNLIPFPR.L
253 - 262	1139.7131	1138.7058	1138.6862	0.0196	0	K.LAVNLIPFPR.L
263 - 276	1622.8772	1621.8699	1621.8438	0.0261	0	R.LHFFMVGFAPLTSR.G
277 - 282	738.2532	737.2459	737.3456	-0.0997	0	R.GSQQYR.A
283 - 297	1730.9124	1729.9051	1729.8709	0.0342	0	R.ALTVPELTQQMWDAK.N
310 - 318	1059.5329	1058.5256	1058.5219	0.0038	0	R.YLTASAMFR.G
325 - 336	1446.7001	1445.6928	1445.6820	0.0108	0	K.EVDEQMLNVQNK.N
337 - 350	1696.8599	1695.8526	1695.8256	0.0270	0	K.NSSYFVEWIPNNVK.S
363 - 379	1889.9244	1888.9171	1888.8811	0.0360	0	K.MAATFVGNSTSIQEMFR.R
381 - 390	1215.6110	1214.6037	1214.5753	0.0284	0	R.VSEQFTAMFR.R

Spot 1730

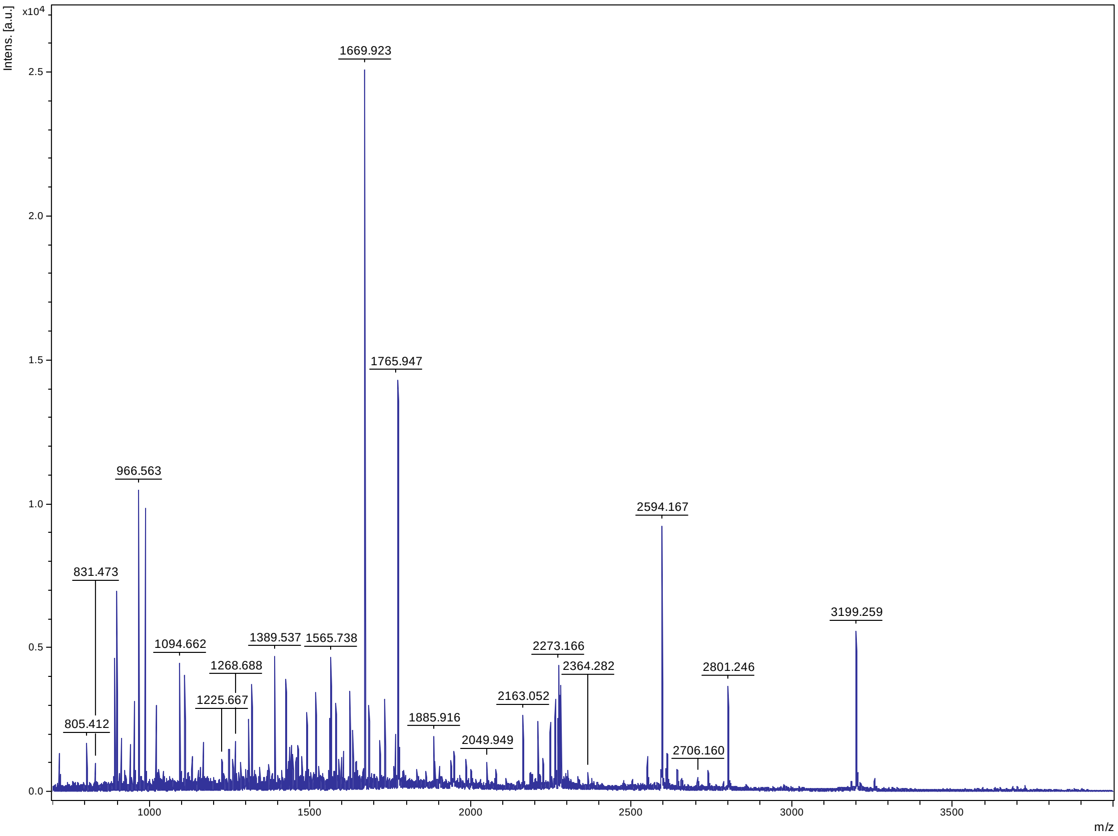


Match to: gi|50582723 Score: 192 Expect: 1.7e-14

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 19	1874.9437	1873.9364	1873.9502	-0.0137	1	-.MAAMDLRVAAPASVAAAAR.C	2 Oxidation (M)
46 - 73	2688.3911	2687.3838	2687.3725	0.0113	1	R.LSVRTSVATTEAAAAAVGASEDAALEAR.D	
77 - 90	1270.7504	1269.7431	1269.7404	0.0027	0	K.TVVAVILGGGAGTR.L	
99 - 110	1199.6957	1198.6884	1198.6822	0.0062	0	R.AKPAVPIGGAYR.L	
111 - 126	1790.9194	1789.9122	1789.8702	0.0419	0	R.LIDVPMSNCINSGINK.V	Carbamidomethyl (C); Oxidation (M)
127 - 140	1625.8896	1624.8824	1624.8573	0.0251	0	K.VYILTQFNSASLNR.H	
175 - 184	1150.5665	1149.5593	1149.5567	0.0026	0	R.WFQGTADAVR.Q	
185 - 194	1284.5967	1283.5894	1283.5822	0.0072	0	R.QFDWLFDDAK.A	
195 - 211	1943.0857	1942.0784	1942.0159	0.0625	1	K.AKDIDDVLILSGDHLYR.M	
197 - 211	1743.9406	1742.9333	1742.8839	0.0494	0	K.DIDDVLILSGDHLYR.M	
212 - 222	1428.6112	1427.6039	1427.5962	0.0078	0	R.MDYMDFVQSHR.Q	
212 - 222	1444.6128	1443.6055	1443.5911	0.0144	0	R.MDYMDFVQSHR.Q	Oxidation (M)
212 - 222	1460.6019	1459.5947	1459.5860	0.0086	0	R.MDYMDFVQSHR.Q	2 Oxidation (M)
223 - 239	1919.0067	1917.9994	1917.9037	0.0958	1	R.QRGADISICCLPIDDSR.A	Carbamidomethyl (C)
225 - 239	1691.8157	1690.8084	1690.7654	0.0430	0	R.GADISICCLPIDDSR.A	2 Carbamidomethyl (C)
300 - 307	983.6373	982.6301	982.6175	0.0126	0	K.EILLNLLR.W	
308 - 326	2107.1604	2106.1531	2106.0534	0.0997	1	R.WRFPTANDFGSEIIPASAK.E	
332 - 346	1847.9493	1846.9421	1846.8777	0.0643	0	K.AYLFNDYWEDIGTIK.S	
347 - 361	1705.9009	1704.8936	1704.8471	0.0465	0	K.SFFEANLSLAEQPPR.F	
362 - 375	1726.8424	1725.8351	1725.7820	0.0531	0	R.FSFYDANKPMYTSR.R	
362 - 375	1742.8411	1741.8338	1741.7770	0.0568	0	R.FSFYDANKPMYTSR.R	Oxidation (M)
376 - 387	1370.7021	1369.6949	1369.7136	-0.0187	1	R.RNLPPSMINNSK.I	
388 - 403	1880.9330	1879.9257	1879.8557	0.0701	0	K.ITDSIISHGCFLDSCR.I	2 Carbamidomethyl (C)
404 - 412	1009.5890	1008.5817	1008.5716	0.0101	0	R.IEHSVVGIR.S	
447 - 456	1027.5999	1026.5926	1026.5709	0.0217	0	K.VPIGIGENTK.I	
457 - 467	1344.7148	1343.7076	1343.6979	0.0096	1	K.IQNCIIDKNAR.I	Carbamidomethyl (C)
471 - 485	1618.7993	1617.7920	1617.7594	0.0327	0	K.NVTISNSEGVQEADR.T	
486 - 493	972.4952	971.4879	971.4712	0.0167	0	R.TSEGFYIR.S	

Spot 1732



Match to: gi|50919439 Score: 134 Expect: 2.7e-09

Matched peptides:

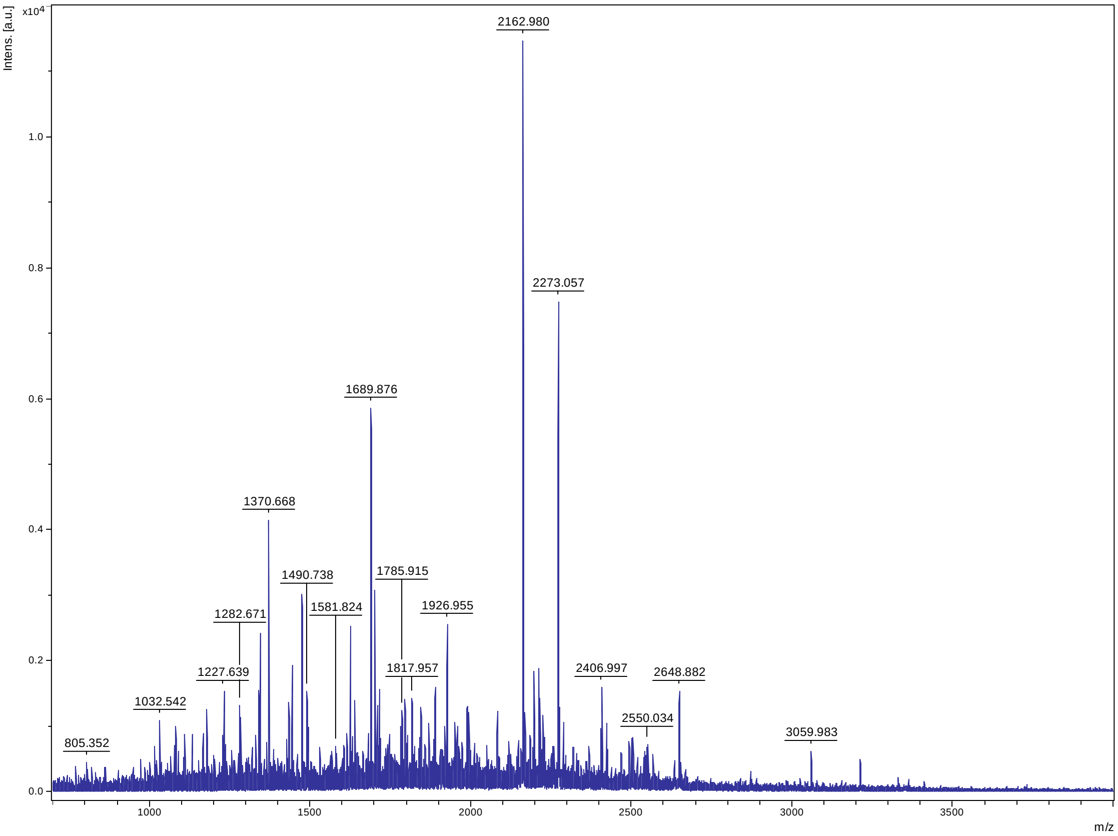
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
31 - 48	1938.8925	1937.8852	1938.0322	-0.1470	1	R.LLARGYSVHAAVLNPDDK.A	
35 - 48	1485.7642	1484.7569	1484.7259	0.0310	0	R.GYSVHAAVLNPDDK.A	
35 - 66	3199.4639	3198.4566	3198.5441	-0.0875	1	R.GYSVHAAVLNPDDKAETDHLHALAAAGGGEGR.R	
49 - 66	1732.8683	1731.8610	1731.8288	0.0322	0	K.AETDHLHALAAAGGGEGR.R	
70 - 86	1669.9496	1668.9423	1668.9198	0.0225	0	R.VFPGDLLDGAALLAAAR.G	
87 - 102	1717.8443	1716.8370	1716.8075	0.0295	0	R.GCSGVFHLASPCIVDR.V	Carbamidomethyl (C)
103 - 123	2263.2899	2262.2826	2262.2405	0.0421	0	R.VLDPQAQLMVPAVEGTLNVLR.A	
103 - 123	2279.2752	2278.2679	2278.2354	0.0325	0	R.VLDPQAQLMVPAVEGTLNVLR.A	Oxidation (M)
133 - 155	2364.3209	2363.3136	2363.2960	0.0176	1	R.RVVVTSSISAIVPSPGWPAGEVR.D	
134 - 155	2208.2162	2207.2089	2207.1949	0.0140	0	R.VVVTSSISAIVPSPGWPAGEVR.D	
156 - 168	1789.8850	1788.8777	1788.7083	0.1694	1	R.DERCWTDLDYCEK.N	2 Carbamidomethyl (C)
159 - 168	1389.5613	1388.5540	1388.5377	0.0163	0	R.CWTDLDYCEK.N	2 Carbamidomethyl (C)
260 - 275	1885.9328	1884.9255	1884.8941	0.0315	0	R.HLCVQSIAHWSDFASK.V	Carbamidomethyl (C)
276 - 284	1111.5741	1110.5668	1110.5597	0.0071	0	K.VAELYPEYK.V	
276 - 287	1435.7960	1434.7887	1434.7758	0.0129	1	K.VAELYPEYKVPK.L	
291 - 298	899.4783	898.4710	898.4872	-0.0162	0	K.ETQPGLVR.A	
291 - 304	1456.7274	1455.7201	1455.7681	-0.0480	1	K.ETQPGLVRAEAASK.K	
305 - 318	1574.8867	1573.8794	1573.8901	-0.0107	1	K.KLIALGLQFSPMEK.I	
305 - 318	1590.9039	1589.8966	1589.8850	0.0116	1	K.KLIALGLQFSPMEK.I	Oxidation (M)
306 - 318	1446.8214	1445.8141	1445.7952	0.0190	0	K.LIALGLQFSPMEK.I	
306 - 318	1462.8064	1461.7991	1461.7901	0.0090	0	K.LIALGLQFSPMEK.I	Oxidation (M)

Match to: gi|77556476 Score: 77 Expect: 0.0015

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
7 - 31	2801.3383	2800.3310	2800.3820	-0.0509	0	R.NPLQEYQVAHIPGALFFDVDGISDR.T	
32 - 43	1326.6945	1325.6872	1325.6649	0.0223	0	R.TSSLPHMLPSEK.A	
67 - 79	1642.7913	1641.7840	1641.8238	-0.0398	1	K.GLFSAARVWWMFR.V	Oxidation (M)
74 - 79	940.4370	939.4297	939.4425	-0.0128	0	R.VWWMFR.V	Oxidation (M)
86 - 97	1425.7835	1424.7762	1424.7564	0.0198	0	K.VWVLDGGLPQWR.A	
98 - 114	1699.8109	1698.8036	1698.7948	0.0089	0	R.ASGYDVESSASSDAILK.A	
140 - 152	1603.9103	1602.9030	1602.8882	0.0148	0	K.LQPHLIWNLDQVK.E	
159 - 166	953.5096	952.5023	952.5090	-0.0067	0	K.THQLIDAR.G	
171 - 179	987.4836	986.4763	986.4821	-0.0058	0	R.FDGAVPEPR.K	
205 - 212	966.5513	965.5440	965.5545	-0.0105	0	K.LLPPEELR.K	
205 - 213	1094.6569	1093.6496	1093.6495	0.0001	1	K.LLPPEELRK.R	
249 - 273	2643.2141	2642.2068	2642.1925	0.0143	0	K.TDVPVYDGSWTEWGAHPDTPVATAA.-	

Spot 1736

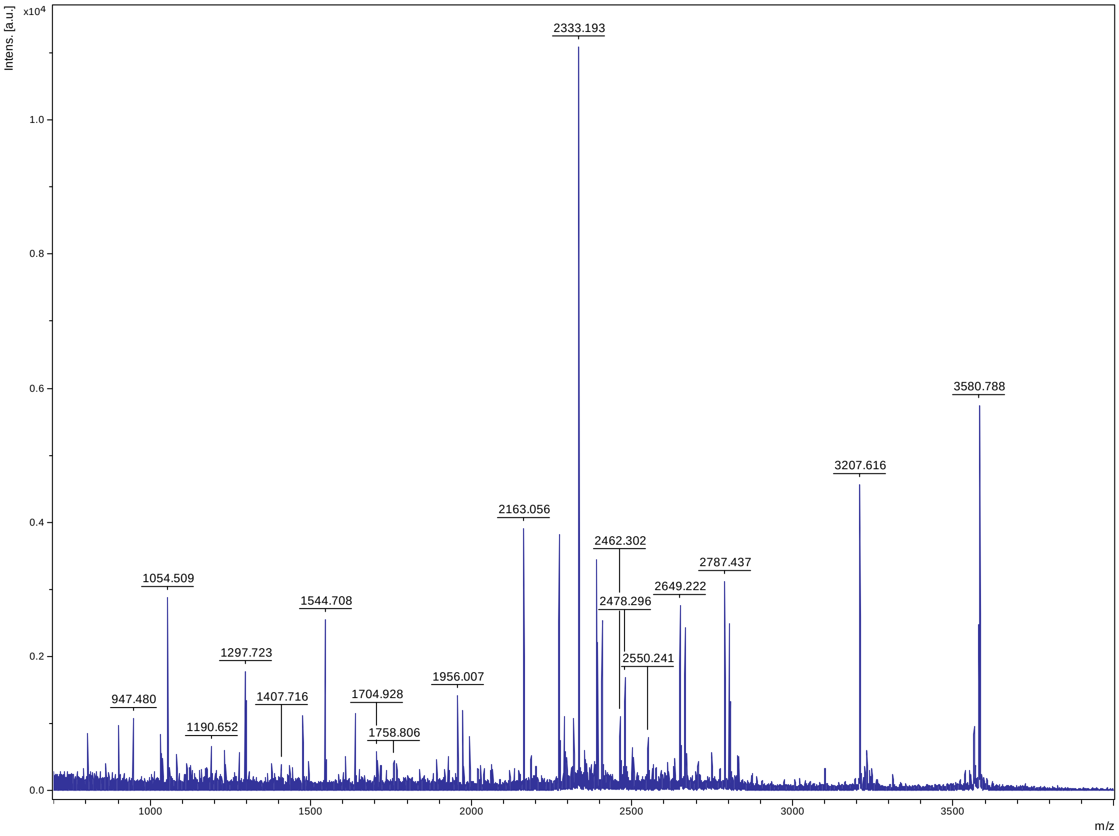


Match to: gi|51978958 Score: 76 Expect: 0.0018

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
13 - 33	2196.9697	2195.9625	2196.0368	-0.0743	0	K.ALEGDMATDNSSSLALAEVFR.A	
13 - 33	2212.9758	2211.9686	2212.0317	-0.0632	0	K.ALEGDMATDNSSSLALAEVFR.A	Oxidation (M)
34 - 42	1022.5729	1021.5657	1021.6032	-0.0376	0	R.APLRPDVVR.F	
62 - 75	1444.6365	1443.6292	1443.6491	-0.0199	0	R.AGHQTSAESWGTGR.A	
91 - 101	1111.5464	1110.5391	1110.4698	0.0693	0	R.AGQGAFGNMCR.G	
91 - 101	1168.5619	1167.5546	1167.4913	0.0633	0	R.AGQGAFGNMCR.G	Carbamidomethyl (C)
126 - 144	1796.0535	1795.0462	1795.0567	-0.0105	0	R.VAVASALAATSVPSLVLAR.G	
148 - 167	2169.0737	2168.0665	2168.1463	-0.0799	0	R.IETVPELPLVISDSAESIEK.T	
228 - 239	1282.6714	1281.6641	1281.6676	-0.0035	0	R.NLPGVDVANVER.L	
240 - 253	1445.8086	1444.8013	1444.8150	-0.0137	0	R.LNLLDLAPGGHLGR.F	
254 - 263	1227.6394	1226.6321	1226.6335	-0.0014	0	R.FVIWTESAFK.K	
265 - 279	1710.8865	1709.8792	1709.8875	-0.0083	1	K.LEEVYGTFEAPSLKK.K	
297 - 312	1782.9641	1781.9568	1781.9886	-0.0318	0	R.IINSDEVQSVVKPLNK.E	
342 - 351	1077.5846	1076.5773	1076.5648	0.0125	1	R.KMATLAEAAR.I	Oxidation (M)

Spot 1742

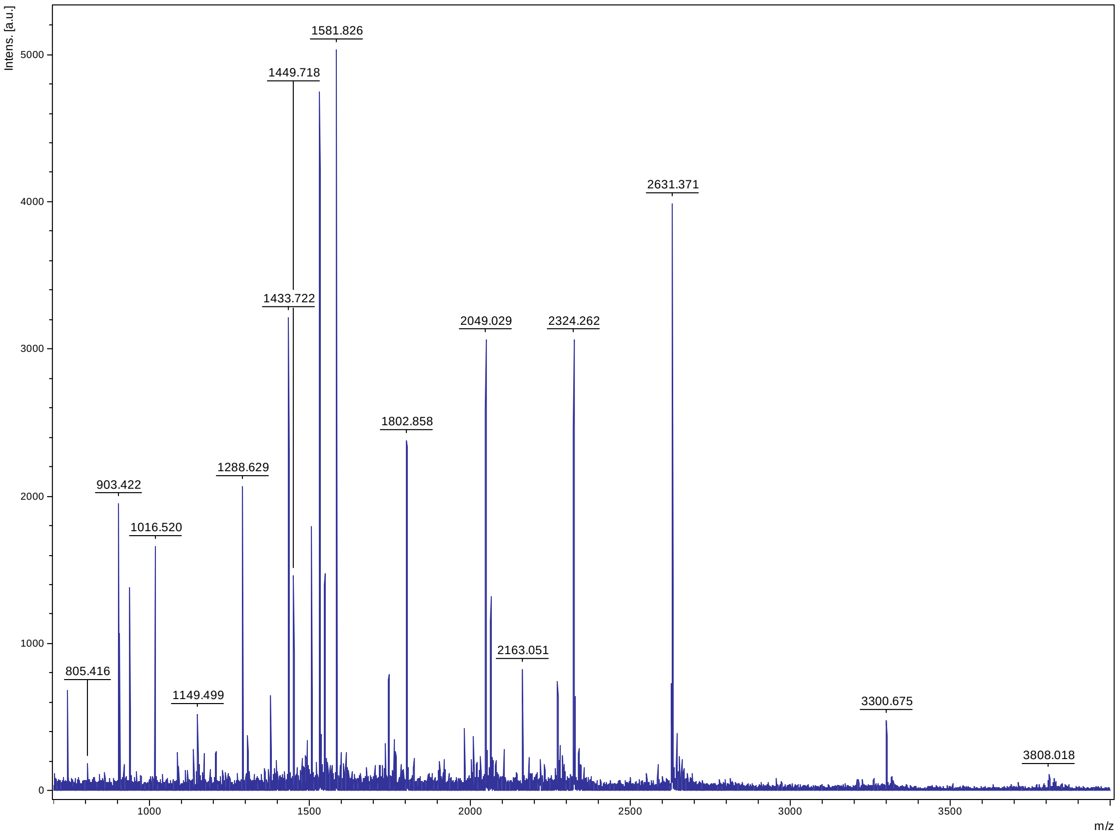


Match to: gi|51090745; Score: 141

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
53 - 74	2390.18	2389.18	2389.16	0.01	0	VVITGMGLVSVFGNDVDAYYDR
53 - 74	2406.17	2405.17	2405.16	0.01	0	VVITGMGLVSVFGNDVDAYYDR Oxidation (M)
75 - 87	1297.72	1296.72	1296.70	0.02	0	LLAGESGIGPIDR
75 - 96	2333.19	2332.19	2332.18	0.01	1	LLAGESGIGPIDRFDASNFPTR
88 - 96	1054.51	1053.51	1053.49	0.02	0	FDASNFPTR
103 - 116	1544.71	1543.71	1543.69	0.02	1	GFSSEGYIDGKNDR
117 - 123	947.48	946.48	946.47	0.01	1	RLDDCLR
153 - 177	2462.30	2461.30	2461.29	0.01	0	AGVLVGTGMGGLTVFSDGVQNLIEK
153 - 177	2478.30	2477.29	2477.28	0.01	0	AGVLVGTGMGGLTVFSDGVQNLIEK Oxidation (M)
232 - 259	2787.44	2786.44	2786.42	0.01	1	RGEADVMIAGGTEAAIIPIGVGGFVACR
232 - 259	2803.43	2802.43	2802.42	0.01	1	RGEADVMIAGGTEAAIIPIGVGGFVACR Oxidation (M)
270 - 279	1231.58	1230.58	1230.57	0.01	0	TASRPWDQDR
303 - 326	2649.22	2648.22	2648.20	0.02	0	DAPIIAEYLGGAVNCDAYHMTDPR
303 - 326	2665.22	2664.21	2664.19	0.02	0	DAPIIAEYLGGAVNCDAYHMTDPR Oxidation (M)
338 - 372	3563.74	3562.74	3562.75	-0.02	0	QSLADAGVAPEEVNYINAHATSTLAGDLAEVNAIR Pyro-glu (N-term Q)
338 - 372	3580.79	3579.79	3579.78	0.01	0	QSLADAGVAPEEVNYINAHATSTLAGDLAEVNAIR
373 - 382	1190.65	1189.65	1189.63	0.02	1	QVFKDPSEIK
388 - 407	1956.01	1955.01	1955.00	0.01	0	SMIGHCLGAAGGLEAIATVK
388 - 407	1972.00	1971.00	1970.99	0.01	0	SMIGHCLGAAGGLEAIATVK Oxidation (M)
408 - 436	3207.62	3206.61	3206.60	0.01	0	AITTGWVHPSINQFNPEPAVEFDTVPNVK

Spot 1744

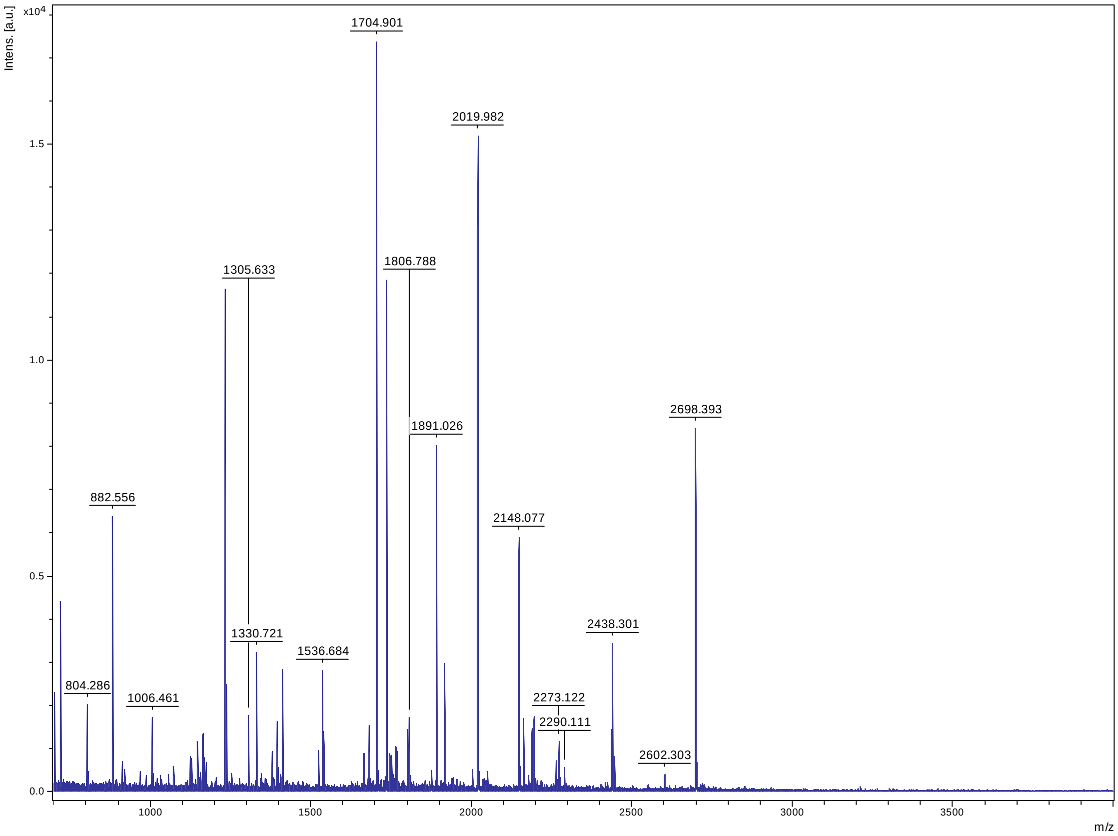


Match to: gi|115479945 Score: 247 Expect: 2.7e-20

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
47 - 53	937.4870	936.4797	936.4930	-14	0	R.FDLLHHR.G	
47 - 61	1734.9627	1733.9555	1733.8346	70	1	R.FDLLHHRGSSHGESR.T	
65 - 77	1530.7347	1529.7274	1529.7449	-11	0	R.ATYPQAHYPPMVR.L	
65 - 77	1546.7208	1545.7135	1545.7398	-17	0	R.ATYPQAHYPPMVR.L	Oxidation (M)
82 - 88	903.4223	902.4150	902.4246	-11	0	R.LWDDAQR.D	
94 - 106	1433.7216	1432.7143	1432.7497	-25	0	R.VLTPTPHLDMGPR.A	
94 - 106	1449.7175	1448.7103	1448.7446	-24	0	R.VLTPTPHLDMGPR.A	Oxidation (M)
139 - 155	1746.8540	1745.8467	1745.8658	-11	0	R.LPEGWTAATSEIGGVMK.A	
139 - 155	1762.8412	1761.8340	1761.8607	-15	0	R.LPEGWTAATSEIGGVMK.A	Oxidation (M)
159 - 169	1136.5684	1135.5612	1135.6059	-39	0	K.AVAMFQSLAAK.N	
176 - 185	1087.5784	1086.5711	1086.6033	-30	1	R.DRTEVVGIAK.Q	
195 - 205	1149.4990	1148.4917	1148.5098	-16	0	K.TSSGEEFHGAK.C	
206 - 216	1205.5913	1204.5840	1204.6274	-36	0	K.CIITVGAWASK.L	
220 - 239	2324.2618	2323.2546	2323.2147	17	0	R.SVAGVDLPVQPLHTLICYWR.A	
245 - 278	3808.0182	3807.0109	3806.7702	63	0	R.EHELTPESGFPTFASYGDPYIYSTPSMEFPGLIK.V	
279 - 292	1504.6830	1503.6757	1503.7001	-16	1	K.VAAHGGPPCDPDRR.D	
293 - 308	1581.8259	1580.8186	1580.8311	-8	0	R.DWLAGAGAGLVEPVAR.W	
309 - 327	2049.0291	2048.0218	2048.0150	3	0	R.WIDEVMPGHVDTAGGPVIR.Q	
309 - 327	2065.0159	2064.0086	2064.0099	-1	0	R.WIDEVMPGHVDTAGGPVIR.Q	Oxidation (M)
352 - 365	1376.6564	1375.6491	1375.6885	-29	0	K.DVVVGAGFSGHGFK.M	
373 - 384	1288.6286	1287.6213	1287.6492	-22	0	R.ILAEMALDGEAR.T	
373 - 384	1304.6058	1303.5985	1303.6442	-35	0	R.ILAEMALDGEAR.T	Oxidation (M)
385 - 394	1016.5205	1015.5132	1015.5298	-16	0	R.TAAEAGVELR.H	
398 - 413	1802.8580	1801.8507	1801.8595	-5	1	R.IGRFEDNPEGNLAENK.V	

Spot 1749

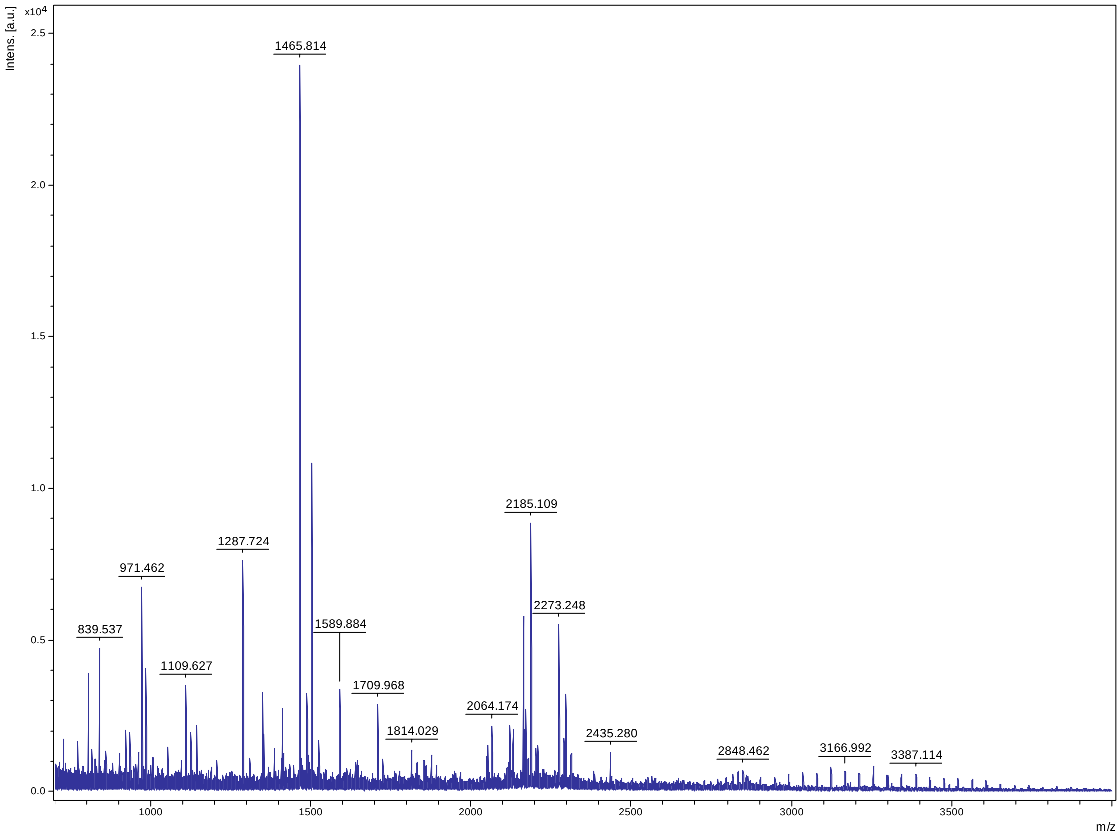


Match to: gi|115451055 Score: 228 Expect: 1.2e-18

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 21	1735.9221	1734.9148	1734.9012	0.0136	0	M.SLSTVNHAAAAAAAAAGPGK.S	
60 - 79	2004.0212	2003.0139	2002.9959	0.0180	0	R.VSALSQVSGVLGSQWGDEGK.G	
60 - 81	2189.1303	2188.1230	2188.1123	0.0107	1	R.VSALSQVSGVLGSQWGDEGKGK.L	
82 - 89	882.4573	881.4500	881.5334	-0.0834	0	K.LVDVLAPR.F	
96 - 112	1763.8210	1762.8137	1762.7692	0.0445	0	R.CQGGANAGHTIYNSEGK.K	Carbamidomethyl (C)
167 - 181	1704.9756	1703.9683	1703.9107	0.0576	0	R.AHLLFDLHQAVDGLR.E	
167 - 181	1746.8045	1745.7972	1745.9212	-0.1240	0	R.AHLLFDLHQAVDGLR.E	Acetyl (N-term)
182 - 194	1380.7347	1379.7274	1379.6932	0.0342	0	R.EAELANSFIGTTK.R	
182 - 195	1536.7610	1535.7537	1535.7943	-0.0406	1	R.EAELANSFIGTTKR.G	
195 - 204	1124.5610	1123.5537	1123.5444	0.0093	1	K.RGIGPCYSSK.V	Carbamidomethyl (C)
217 - 230	1681.8618	1680.8545	1680.8181	0.0364	1	R.HMDTFGDKLDVLFK.D	Oxidation (M)
236 - 243	1006.4167	1005.4094	1005.4443	-0.0349	0	R.FEGFEYSK.S	
244 - 252	1148.5750	1147.5677	1147.5655	0.0022	1	K.SMLREEVER.Y	
244 - 252	1164.5766	1163.5693	1163.5604	0.0089	1	K.SMLREEVER.Y	Oxidation (M)
256 - 278	2698.3672	2697.3599	2697.4125	-0.0526	1	R.FAERLEPFIADTVHLLNESIQQK.K	
260 - 278	2195.1901	2194.1828	2194.1633	0.0195	0	R.LEPFIADTVHLLNESIQQK.K	
321 - 330	1073.5842	1072.5769	1072.5950	-0.0181	0	R.CIGDLIGVVK.A	Carbamidomethyl (C)
321 - 335	1665.8727	1664.8654	1664.8919	-0.0265	1	R.CIGDLIGVVKAYTTR.V	Carbamidomethyl (C)
336 - 354	2020.0408	2019.0335	2018.9948	0.0387	0	R.VGSGPFPTELFGEEGDLLR.K	
336 - 355	2148.1161	2147.1088	2147.0898	0.0190	1	R.VGSGPFPTELFGEEGDLLRK.S	
355 - 368	1524.8111	1523.8038	1523.7514	0.0524	1	R.KSGMEFGTTTGRPR.R	
355 - 368	1540.8053	1539.7980	1539.7463	0.0517	1	R.KSGMEFGTTTGRPR.R	Oxidation (M)
356 - 368	1396.7182	1395.7109	1395.6564	0.0545	0	K.SGMEFGTTTGRPR.R	
356 - 368	1412.7050	1411.6977	1411.6514	0.0464	0	K.SGMEFGTTTGRPR.R	Oxidation (M)
369 - 379	1330.7673	1329.7600	1329.7227	0.0373	1	R.RCGWLDIVALK.Y	Carbamidomethyl (C)
370 - 379	1174.6391	1173.6318	1173.6216	0.0102	0	R.CGWLDIVALK.Y	Carbamidomethyl (C)
395 - 405	1169.6902	1168.6829	1168.6703	0.0126	0	K.LDVLSGLPEVK.L	
406 - 417	1305.6760	1304.6687	1304.6360	0.0327	0	K.LGVSYNQPDGQK.L	
418 - 434	1917.0439	1916.0366	1915.9891	0.0476	0	K.LQSFPGDLDTLEQVQVK.Y	
461 - 482	2438.3077	2437.3004	2437.3116	-0.0112	1	R.YVERIEELVGVPVHYIGVGPGR.D	
465 - 482	1891.0881	1890.0808	1890.0362	0.0446	0	R.IEELVGVPVHYIGVGPGR.D	

Spot 1755

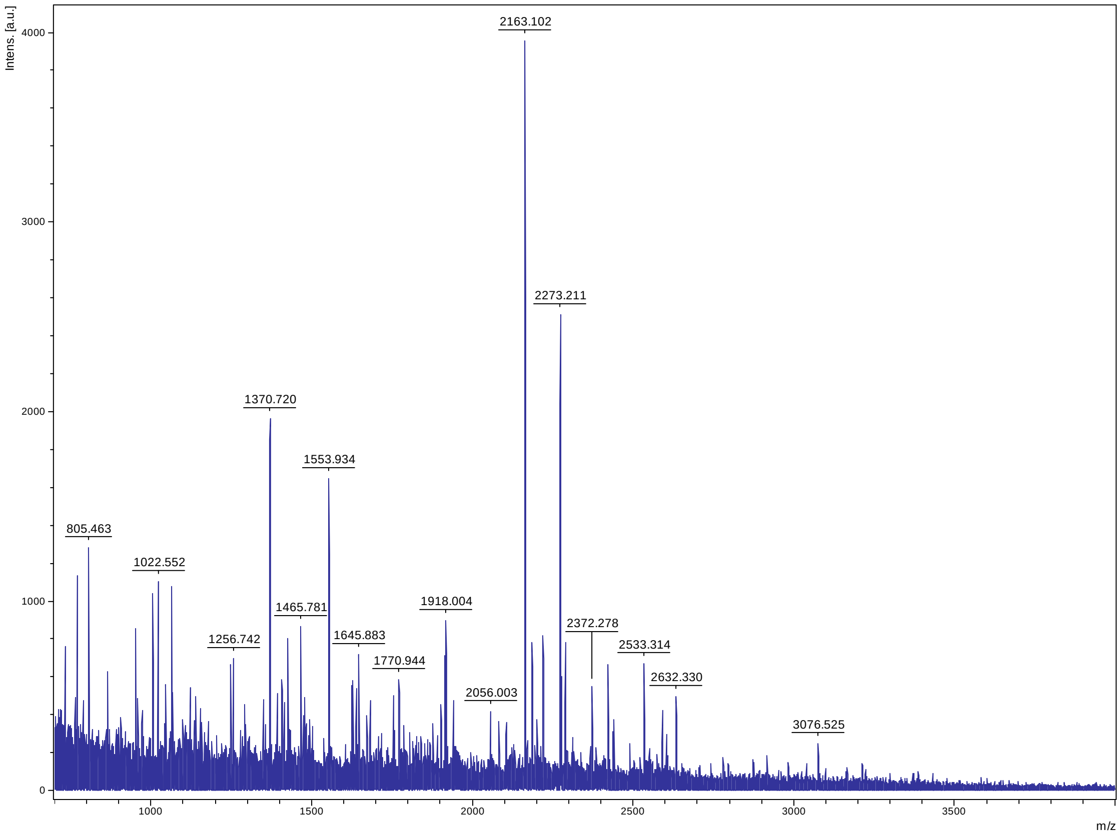


Match to: gi|57283874; Score: 67

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 8	921.47	920.46	920.43	0.04	0	MSPQTETK
19 - 32	1814.03	1813.03	1812.85	0.18	1	DYKLTYYTPEYETK
22 - 32	1407.78	1406.78	1406.66	0.11	0	LTYYTPEYETK
132 - 139	985.63	984.63	984.57	0.06	1	ALRLEDLR
140 - 146	805.48	804.48	804.44	0.04	0	IPPTYSK
147 - 159	1465.81	1464.81	1464.75	0.06	0	TFQGPPHGIQVER
165 - 177	1502.92	1501.91	1501.84	0.07	0	YGRPLLGCTIKPK
188 - 194	971.46	970.46	970.40	0.06	0	ACYECLR
195 - 213	2170.07	2169.07	2168.98	0.09	1	GGLDFTKDDENVNSQPFMR
306 - 316	1309.71	1308.71	1308.69	0.02	1	NHGMHFRVLAK
320 - 339	2050.14	2049.14	2049.01	0.13	1	MSGGDHIHAGTVVGKLEGER

Spot 1760

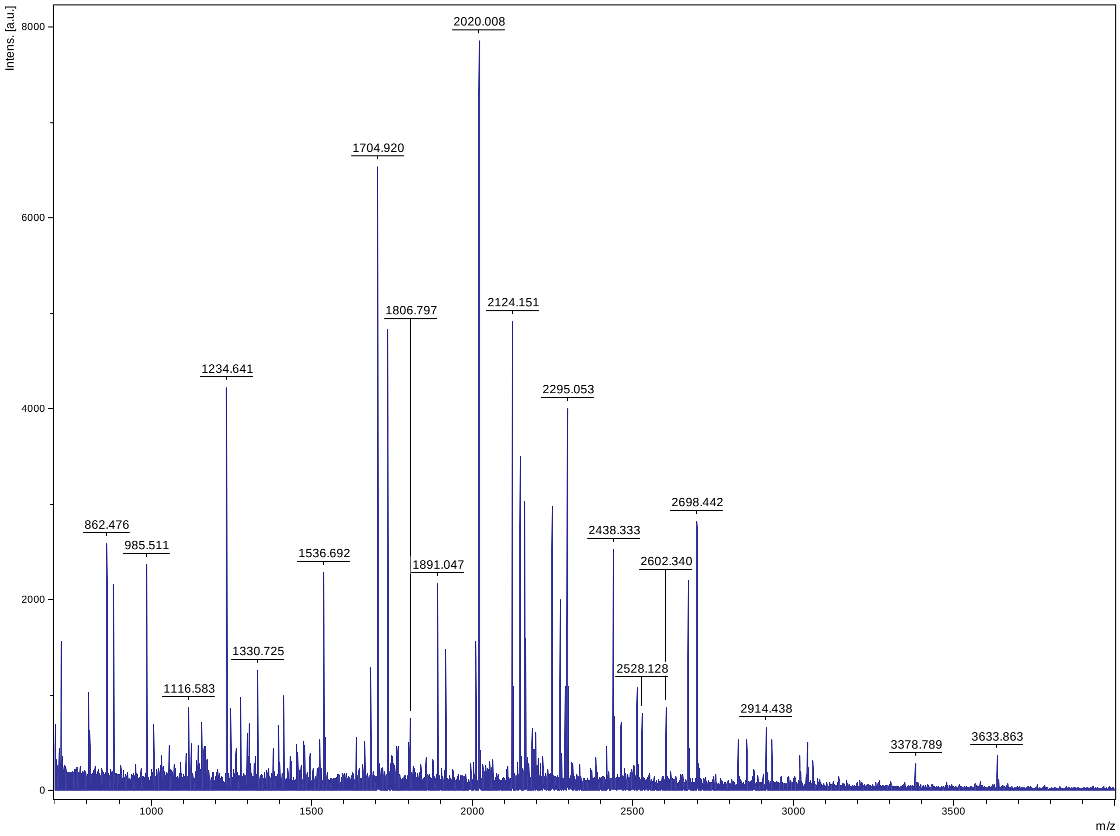


Match to: Q7X9A7_ORYSA Score: 83 Expect: 0.00036

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
46 - 54	1022.5666	1021.5593	1021.4828	0.0765	0	K.EIAFDQGSR.S
64 - 75	1138.7123	1137.7050	1137.6869	0.0181	0	K.LAAAVAVTLGPR.G
78 - 88	1204.6652	1203.6579	1203.6135	0.0444	0	R.NVVLDEFGSPK.V
89 - 98	1043.5980	1042.5907	1042.5771	0.0137	0	K.VVNDGVTIAR.A
99 - 115	1754.9560	1753.9487	1753.9032	0.0455	0	R.AIELADPMENAGAALIR.E
238 - 250	1479.7947	1478.7874	1478.7405	0.0469	0	R.GYISPQFVTNPEK.S
251 - 259	1064.5944	1063.5871	1063.5298	0.0574	0	K.SLVEFENAR.I
267 - 284	2082.2668	2081.2595	2081.2096	0.0500	1	K.ISSIKEIIPLLEQTTQLR.A
272 - 284	1553.9327	1552.9254	1552.8824	0.0430	0	K.EIIPLLEQTTQLR.A
285 - 308	2489.3152	2488.3079	2488.4628	-0.1548	1	R.APLLIIAEDVAGEALATLVVNKLR.G
318 - 324	733.4283	732.4210	732.3554	0.0655	0	K.APGFGER.R
344 - 361	1914.1097	1913.1024	1913.0469	0.0555	0	K.DLGLLVESTTVEQLGIAR.K
392 - 408	1941.9719	1940.9646	1940.8963	0.0683	1	R.ELSQTDSAYDSEKLAER.I
441 - 464	2372.2862	2371.2789	2371.2171	0.0618	0	K.NATFAAIEEGIVPGGGAAYVHLSK.F

Spot 1763

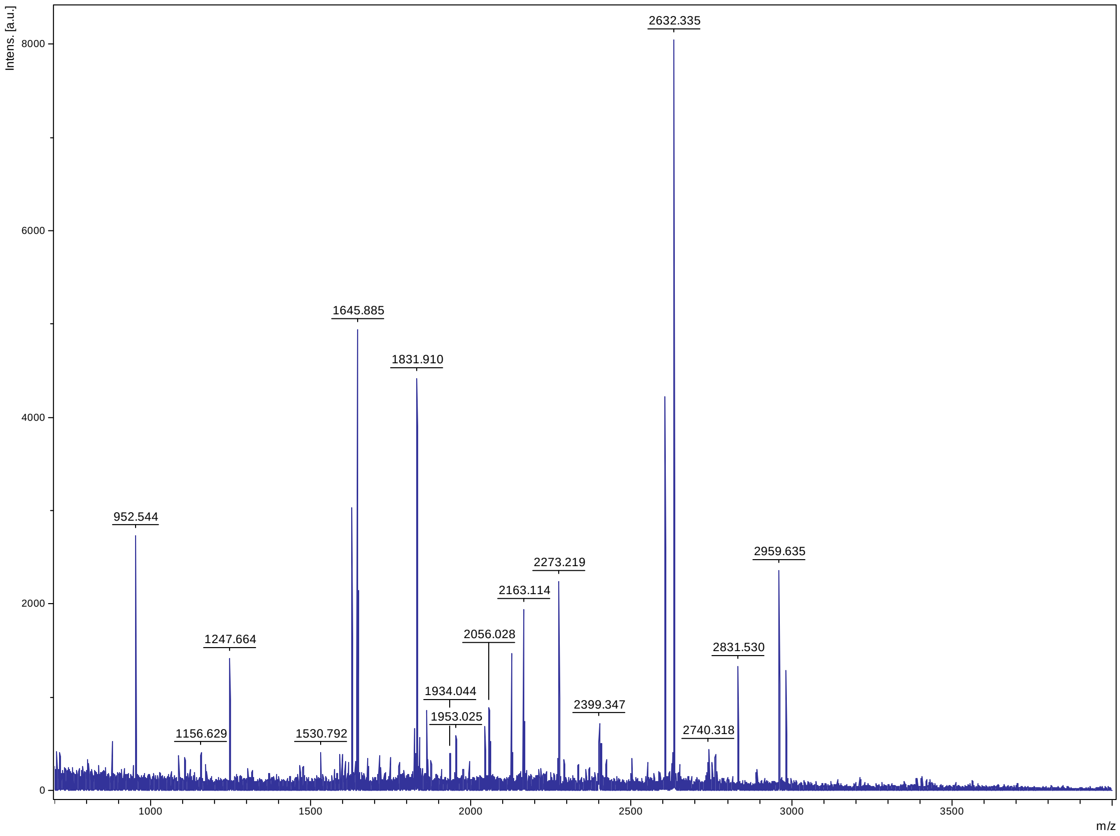


Match to: gi|115451055 Score: 144 Expect: 3.1e-10

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
56 - 79	2417.2204	2416.2131	2416.1982	0.0150	1	R.AADRVSALSQVSGVLGSQWGDEGK.G
60 - 81	2189.0986	2188.0913	2188.1123	-0.0210	1	R.VSALSQVSGVLGSQWGDEGKGK.L
82 - 89	882.4774	881.4701	881.5334	-0.0633	0	K.LVDVLAPR.F
96 - 112	1763.7729	1762.7656	1762.7692	-0.0036	0	R.CQGGANAGHTIYNSEGK.K Carbamidomethyl (C)
167 - 181	1704.9057	1703.8984	1703.9107	-0.0123	0	R.AHLLFDLHQAVDGLR.E
167 - 181	1746.7558	1745.7485	1745.9212	-0.1727	0	R.AHLLFDLHQAVDGLR.E Acetyl (N-term)
195 - 204	1124.5273	1123.5200	1123.5444	-0.0244	1	K.RGIGPCYSSK.V Carbamidomethyl (C)
212 - 224	1536.6884	1535.6811	1535.6861	-0.0049	1	R.VCDLRHMDTFGDK.L
217 - 230	1665.8207	1664.8134	1664.8232	-0.0098	1	R.HMDTFGDKLDVLFK.D
217 - 230	1681.8049	1680.7976	1680.8181	-0.0205	1	R.HMDTFGDKLDVLFK.D Oxidation (M)
244 - 252	1148.5546	1147.5473	1147.5655	-0.0182	1	K.SMLREEVER.Y
255 - 259	720.3166	719.3093	719.3714	-0.0621	1	K.RFAER.L Acetyl (N-term)
256 - 278	2698.4546	2697.4473	2697.4125	0.0348	1	R.FAERLEPFIADTVHLLNESIQQK.K
260 - 278	2195.1600	2194.1527	2194.1633	-0.0106	0	R.LEPFIADTVHLLNESIQQK.K
336 - 354	2020.0096	2019.0023	2018.9948	0.0075	0	R.VGSGPFPTELFGEEGDLLR.K
336 - 355	2148.0992	2147.0919	2147.0898	0.0021	1	R.VGSGPFPTELFGEEGDLLRK.S
355 - 368	1524.7564	1523.7491	1523.7514	-0.0023	1	R.KSGMEFGTTTGRPR.R
356 - 368	1396.6473	1395.6400	1395.6564	-0.0164	0	K.SGMEFGTTTGRPR.R
356 - 368	1412.6354	1411.6281	1411.6514	-0.0232	0	K.SGMEFGTTTGRPR.R Oxidation (M)
369 - 379	1330.7224	1329.7151	1329.7227	-0.0076	1	R.RCGWLDIVALK.Y Carbamidomethyl (C)
406 - 417	1305.6352	1304.6279	1304.6360	-0.0081	0	K.LGVSYNQPDGQK.L
418 - 434	1916.9824	1915.9751	1915.9891	-0.0139	0	K.LQSFPGDLDTLEQVQVK.Y
418 - 449	3634.0278	3633.0205	3632.8362	0.1844	1	K.LQSFPGDLDTLEQVQVKYEVLPGWQSDISSVR.S
435 - 449	1735.8514	1734.8441	1734.8577	-0.0135	0	K.YEVLPGWQSDISSVR.S
461 - 482	2438.3385	2437.3312	2437.3116	0.0196	1	R.YVERIEELVGVPVHYIGVGPGR.D
465 - 482	1891.0450	1890.0377	1890.0362	0.0015	0	R.IEELVGVPVHYIGVGPGR.D

Spot 1767

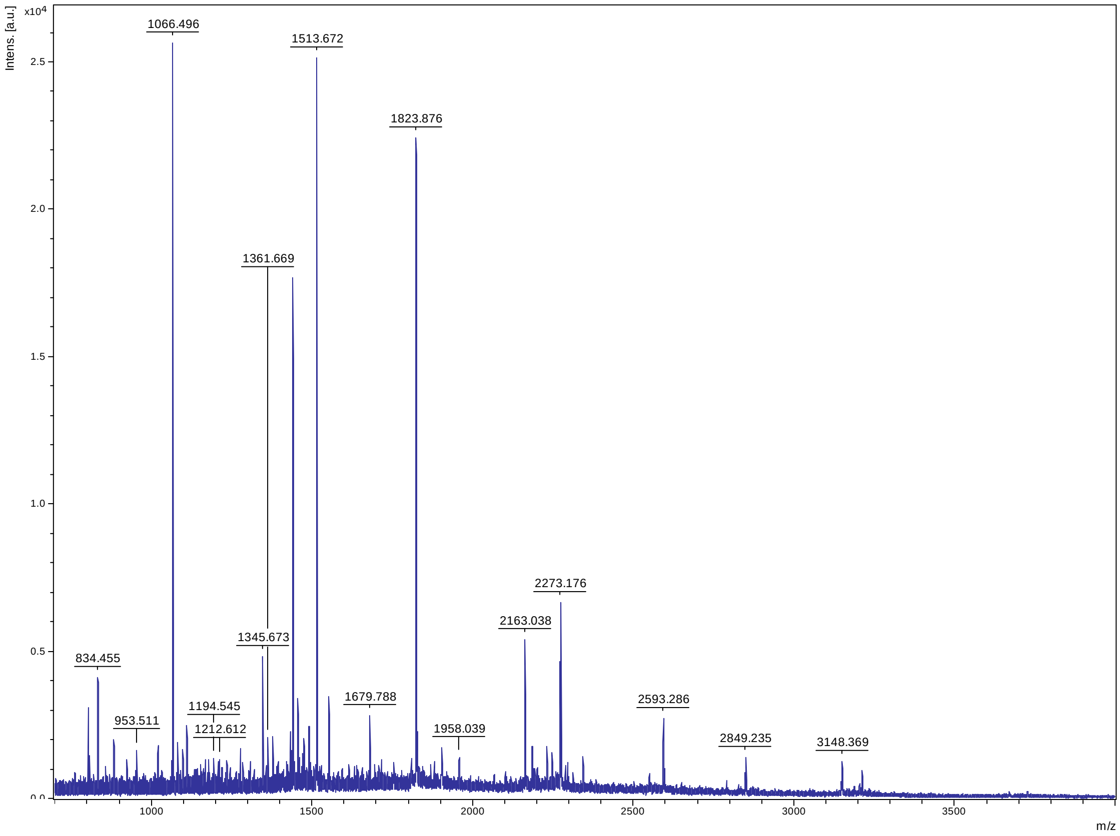


Match to: gi|55296000; Score: 198

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
28 - 37	1106.56	1105.56	1105.54	0.01	0	LNIGGMTQEK Oxidation (M)
74 - 102	2959.63	2958.63	2958.56	0.08	1	KNYADASHVSAVILGGGTGVQLFPLTSTR
75 - 102	2831.53	2830.53	2830.46	0.07	0	NYADASHVSAVILGGGTGVQLFPLTSTR
103 - 114	1247.66	1246.66	1246.61	0.05	0	ATPAVPVGGCYR
115 - 130	1822.94	1821.94	1821.88	0.06	0	LIDIPMSNCFNSGINK
131 - 144	1627.88	1626.88	1626.82	0.06	0	IFVMTQFNSASLNR
131 - 144	1643.87	1642.86	1642.81	0.05	0	IFVMTQFNSASLNR Oxidation (M)
224 - 242	2056.03	2055.03	2054.93	0.09	0	HVDDNADITISCAPIDGSR
257 - 273	1934.04	1933.04	1932.99	0.05	0	VIQFLEKPEGADLESMK
289 - 302	1645.89	1644.88	1644.89	-0.01	1	YPYIASMGIYVLKK
311 - 326	1861.02	1860.02	1859.95	0.07	1	SKYAHLQDFGSEILPR
335 - 349	1831.91	1830.91	1830.85	0.06	0	ACVFTEYWEDIGTIK
350 - 371	2604.31	2603.31	2603.26	0.05	1	SFFDANLALTEQPPKFEFYDPK
372 - 379	952.54	951.54	951.48	0.06	0	TPFFTSPR
380 - 388	1086.67	1085.66	1085.62	0.04	1	YLPPARLEK
391 - 417	2981.51	2980.50	2980.43	0.08	1	IKDAIISDGCSFSECTIEHSVIGISSR
393 - 417	2740.32	2739.32	2739.25	0.07	0	DAIISDGCSFSECTIEHSVIGISSR
474 - 496	2632.34	2631.33	2631.26	0.08	0	NVIIANTQGVQESDHPEEGYYIR

Spot 1768

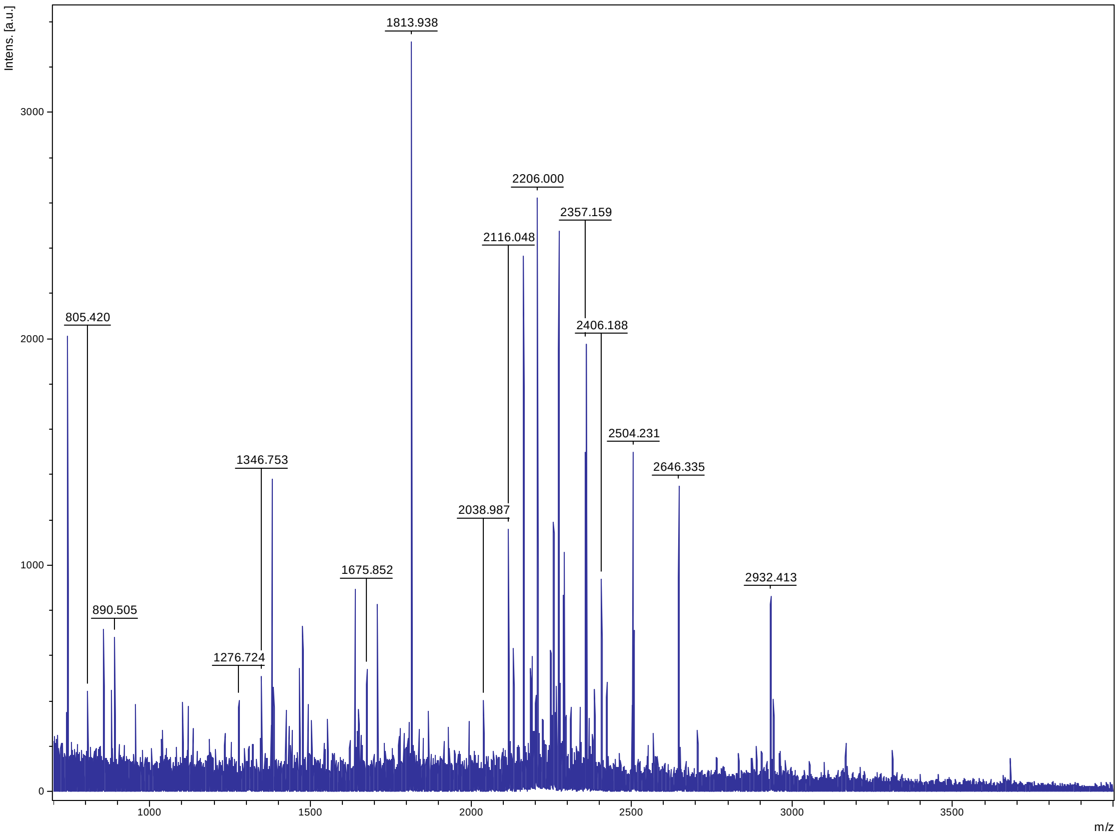


Match to: gi|56202334 Score: 74 Expect: 0.0027

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
40 - 50	1361.6966	1360.6893	1360.6200	0.0693	0	K.QGGWYNFLHEK.V	Pyro-glu (N-term Q)
40 - 50	1378.6771	1377.6698	1377.6465	0.0233	0	K.QGGWYNFLHEK.V	
97 - 118	2593.2654	2592.2581	2592.3118	-0.0537	1	K.SLIEAFHDKNVECLADIVINHR.C	Carbamidomethyl (C)
106 - 118	1552.8188	1551.8115	1551.7827	0.0288	0	K.NVECLADIVINHR.C	Carbamidomethyl (C)
127 - 140	1456.7959	1455.7886	1455.6452	0.1434	0	R.GVYCVFEGGTPDGR.L	
127 - 140	1513.6918	1512.6845	1512.6667	0.0179	0	R.GVYCVFEGGTPDGR.L	Carbamidomethyl (C)
141 - 159	2229.8986	2228.8913	2228.9103	-0.0189	0	R.LDWGPDMICSDDTQYSNGR.G	Carbamidomethyl (C)
141 - 159	2245.8951	2244.8878	2244.9052	-0.0174	0	R.LDWGPDMICSDDTQYSNGR.G	Carbamidomethyl (C); Oxidation (M)
163 - 180	1823.8787	1822.8714	1822.8598	0.0117	0	R.DTGAGFGAAPDIDHLNPR.V	
184 - 193	1345.6953	1344.6880	1344.6826	0.0054	0	R.ELTDWLNWLR.T	
208 - 215	834.3981	833.3908	833.4395	-0.0487	0	K.GYSAPLAR.I	
242 - 254	1490.7466	1489.7393	1489.8517	-0.1124	1	R.HRLDPVALAVPFR.Q	

Spot 1771

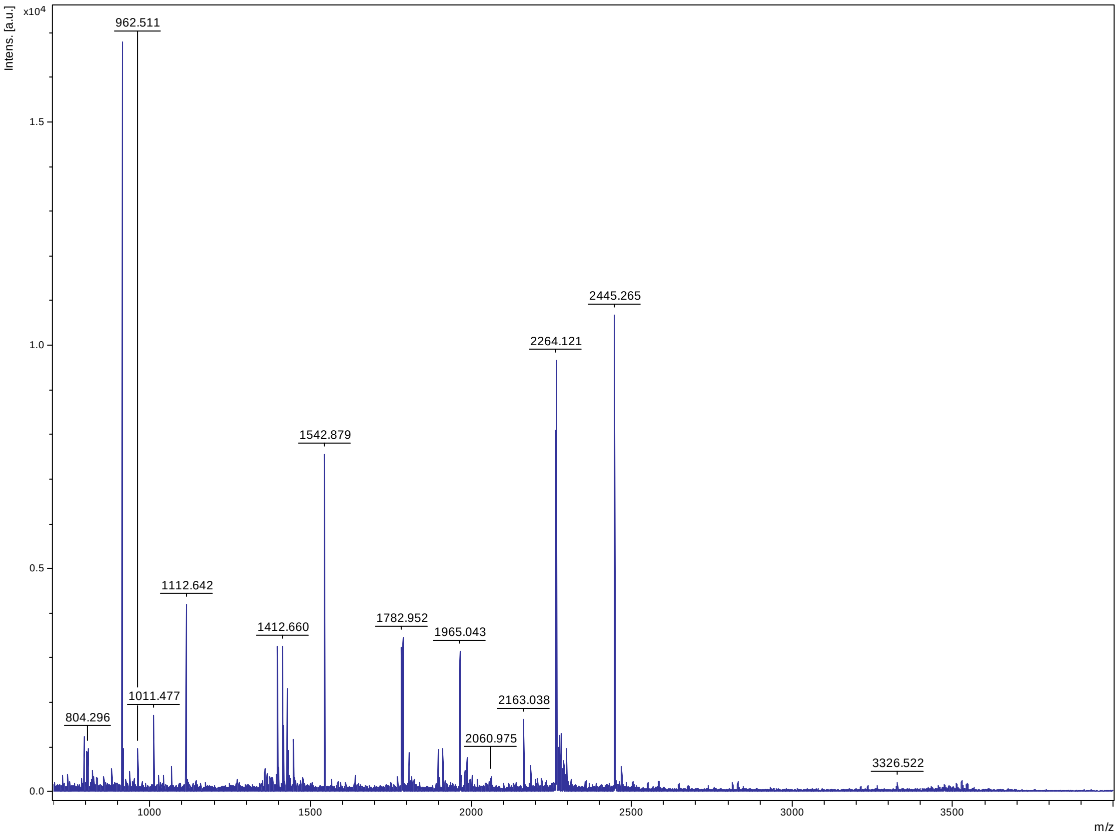


Match to: gi|38344860; Score: 119

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
33 - 55	2257.19	2256.18	2256.20	-0.01	0	STLTDSLVAAAGIIAQEVAGDVR
94 - 120	2932.41	2931.41	2931.42	-0.01	0	DGNEYLINLIDSPGHVDFSSEVTAALR
121 - 144	2646.33	2645.33	2645.34	-0.01	0	ITDGALVVVDCIEGVCVQTETVLR
163 - 180	2206.00	2205.00	2205.00	-0.01	0	CFLELQVEGEEAYQTFSR
270 - 280	1387.65	1386.64	1386.66	-0.02	0	GFVQFCYEPIK
349 - 368	2357.16	2356.16	2356.17	-0.01	1	YRVENLYEGPLDDVYATAIR
483 - 490	890.51	889.50	889.50	0.00	0	FSVSPVVR
544 - 565	2406.19	2405.19	2405.19	-0.01	0	DLQEDFMGGAEIIVSPPVVSFR
544 - 565	2422.18	2421.17	2421.19	-0.01	0	DLQEDFMGGAEIIVSPPVVSFR Oxidation (M)
587 - 606	2248.08	2247.08	2247.08	-0.01	0	LYMEARPLEEGLAEAIDDGR
713 - 724	1346.75	1345.75	1345.77	-0.02	0	VIYASQLTAKPR
725 - 751	2940.57	2939.57	2939.60	-0.03	0	LLEPVYLVEIQAPENALGGIYGVLNQK
753 - 770	2116.05	2115.05	2115.06	-0.01	0	GHVFEEMQRPGTPLYNIK
753 - 770	2132.03	2131.03	2131.05	-0.02	0	GHVFEEMQRPGTPLYNIK Oxidation (M)
771 - 786	1813.94	1812.94	1812.94	-0.01	0	AYLPVIESFGFSSQLR

Spot 1775

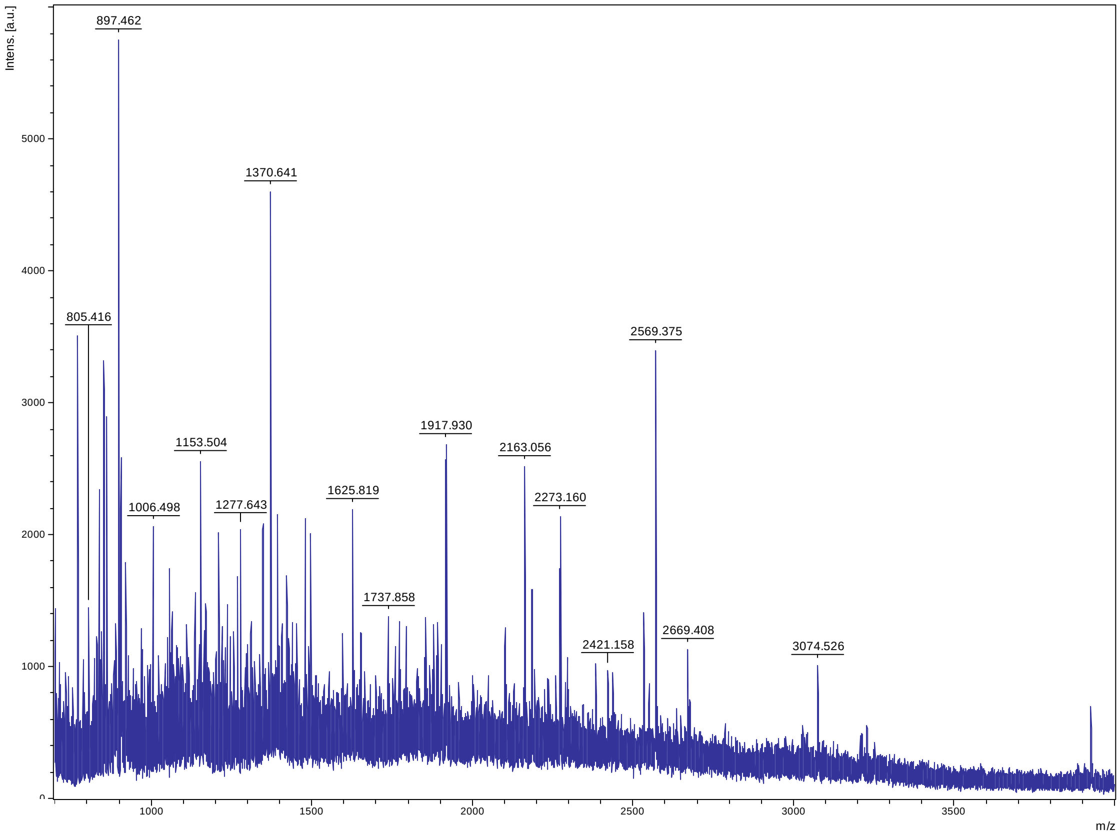


Match to: gi|49388150; Score: 155

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
11 - 32	2445.26	2444.26	2444.26	-0.00	0	SFVEVAPGSHFPIQNLPFGVFR
77 - 92	1911.04	1910.04	1909.92	0.12	0	QETLNMFLGMGRPAWK 2 Oxidation (M)
101 - 110	1112.64	1111.64	1111.62	0.02	0	ILSADEPVLR
101 - 116	1782.95	1781.95	1781.95	-0.00	1	ILSADEPVLRDNEALK
156 - 175	2264.12	2263.12	2263.13	-0.01	0	GPQTPVNPNWFQLPVGYHGR
176 - 190	1542.88	1541.88	1541.88	-0.00	0	ASSVIVSGTDIIRPK
191 - 207	1787.85	1786.85	1786.84	0.01	0	GQGHPTGDSRPYFGPSK
251 - 266	1784.94	1783.94	1783.95	-0.01	0	DIQAWETIPLGPFLGK
292 - 303	1396.66	1395.66	1395.69	-0.03	0	QEPEPLPYLAEK Pyro-glu (N-term Q)
304 - 319	1965.04	1964.04	1964.05	-0.01	0	NHVNYDIPLEVWIKPK
385 - 393	962.51	961.51	961.48	0.03	0	EISVGNSTR
394 - 409	1897.89	1896.89	1896.90	-0.01	1	KFLEDGDEVILTACCK
410 - 423	1446.63	1445.62	1445.62	-0.00	0	GEGYNVGFGTCTGK

Spot 1778

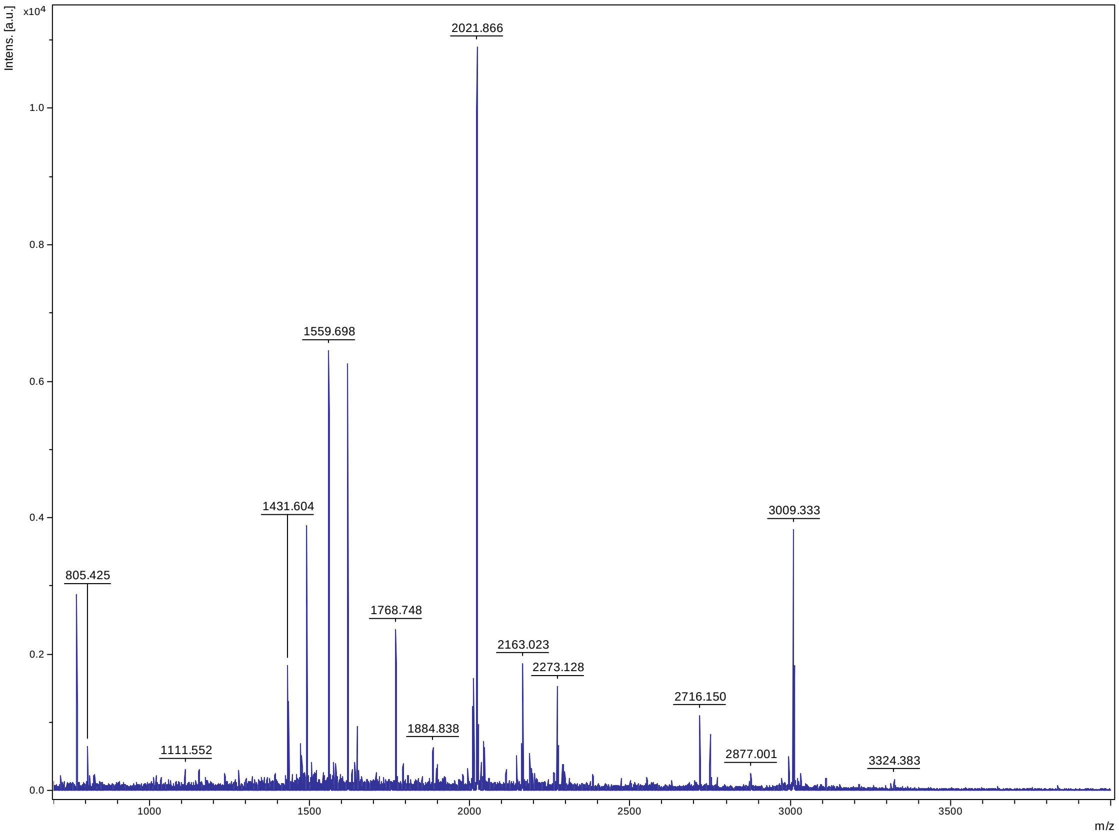


Match to: gi|50944557 Score: 70 Expect: 0.0075

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 12	1231.6114	1230.6041	1230.7084	-0.1043	1	M.NVLASKIFPSR.S	
27 - 37	1149.5924	1148.5851	1148.5673	0.0178	1	K.ATIDDAKNSSK.N	
70 - 81	1256.7247	1255.7174	1255.7036	0.0138	0	R.AKPAVPLGANYR.L	
98 - 111	1625.8655	1624.8582	1624.8573	0.0010	0	K.IYVLTQFNSASLNR.H	
183 - 188	771.3576	770.3503	770.4187	-0.0684	0	K.FIQAHR.E	
189 - 205	1890.9534	1889.9461	1889.9040	0.0421	1	R.ETDSDITVAALPMDEKR.A	
214 - 228	1759.9430	1758.9357	1758.9151	0.0206	1	K.IDEEGRIVEFAEKPK.G	
251 - 273	2669.2151	2668.2078	2668.4154	-0.2075	1	K.EMPYIASMGIYVISKNVMLQLLR.E	
325 - 335	1370.6889	1369.6816	1369.6666	0.0150	0	K.KPVPDFSFYDR.S	
351 - 371	2235.1357	2234.1284	2234.0922	0.0362	1	K.VLDADVTDSVIGEGCVIKNCK.I	Carbamidomethyl (C)
413 - 426	1434.7989	1433.7916	1433.7925	-0.0008	1	K.GGIPIGIGKNCHIR.R	
442 - 461	2295.0614	2294.0541	2294.1542	-0.1001	1	K.IINVDNVQEAARETDGYFIK.S	

Spot 1784

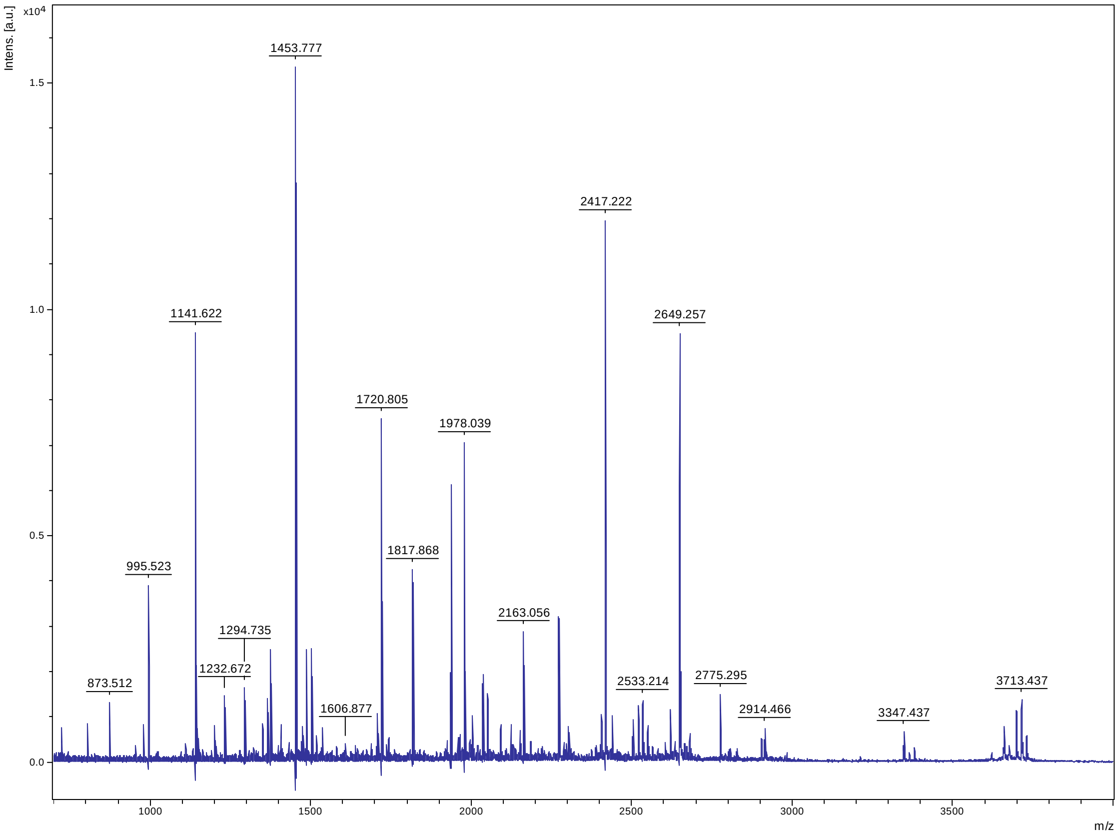


Match to: gi|32352182 Score: 82

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
152 - 165	1617.7024	1616.6951	1616.7066	-0.0115	1	R.KQQEEESYGSGYGR.K	
153 - 165	1472.5752	1471.5679	1471.5851	-0.0172	0	K.QQEEESYGSGYGR.K	Pyro-glu (N-term Q)
153 - 165	1489.6071	1488.5998	1488.6116	-0.0119	0	K.QQEEESYGSGYGR.K	
212 - 229	2021.8662	2020.8589	2020.8762	-0.0172	0	R.KPQQEESYGSEYGSGYGR.K	
230 - 258	3009.3328	3008.3255	3008.3284	-0.0029	0	R.KPQAESYGSGYGSRPQQGGEEYGSGGYGR.K	
260 - 273	1431.6042	1430.5970	1430.6062	-0.0092	0	K.AQEESYGSAGYGGR.K	
260 - 274	1559.6984	1558.6911	1558.7011	-0.0100	1	K.AQEESYGSAGYGGRK.T	
275 - 291	1768.7482	1767.7409	1767.7587	-0.0178	1	K.TEEESYGGGSGYGYGKK.A	
376 - 381	825.3593	824.3520	824.3300	0.0219	1	R.RQEYDD.-	

Spot 1790

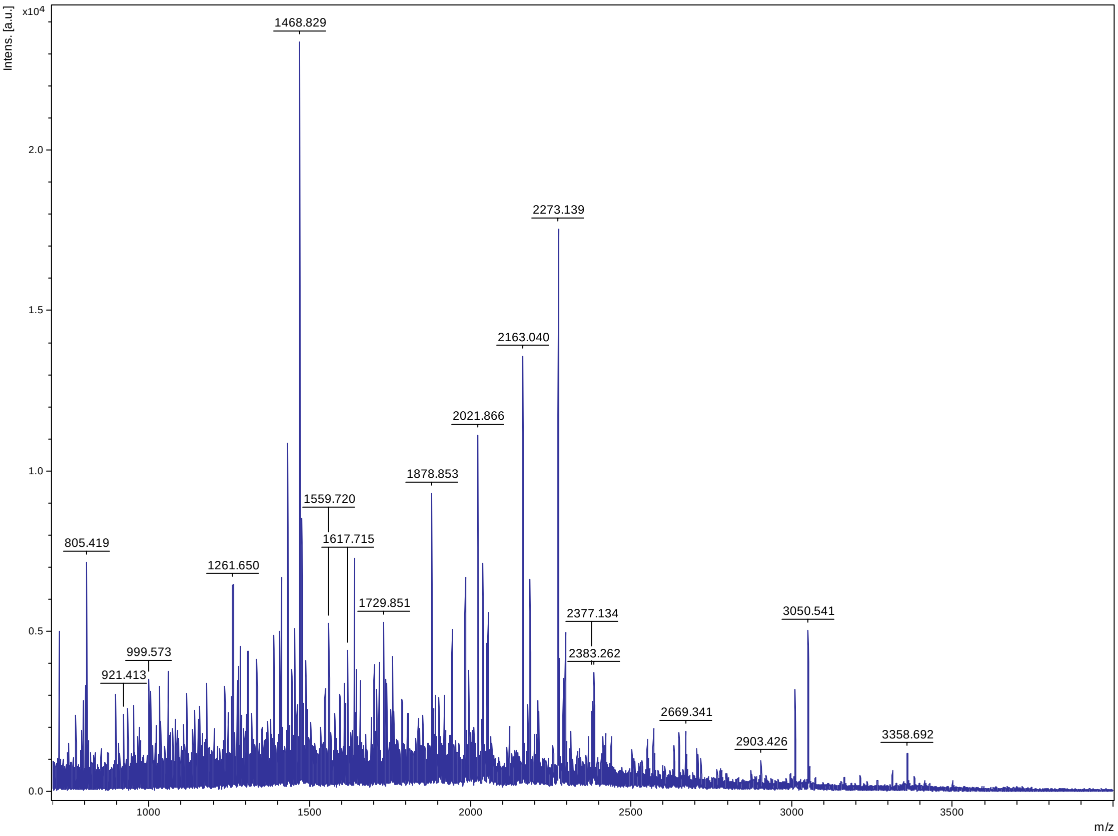


Match to: gi|3024122; Score: 139

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
50 - 62	1470.73	1469.73	1469.73	0.00	0	TNMVMVFGEITTK
77 - 91	1535.73	1534.73	1534.73	0.00	0	GIGFVSDDVGLDADR
94 - 115	2417.28	2416.27	2416.25	0.02	0	VLVNIEQQSPDIAQGVHGHFTK
116 - 149	3697.85	3696.85	3696.76	0.09	0	RPEEIGAGDQGHMFGYATDETPELMPLSHVLATK
116 - 149	3713.84	3712.84	3712.75	0.09	0	RPEEIGAGDQGHMFGYATDETPELMPLSHVLATK Oxidation (M)
116 - 149	3729.86	3728.86	3728.74	0.11	0	RPEEIGAGDQGHMFGYATDETPELMPLSHVLATK 2 Oxidation (M)
159 - 171	1502.75	1501.75	1501.75	0.00	1	KNGTCAWLRPDGK
160 - 171	1374.66	1373.66	1373.65	0.01	0	NGTCAWLRPDGK
190 - 213	2649.35	2648.35	2648.33	0.02	0	VHTVLISTQHDETVTNDEIAADLK
240 - 254	1453.76	1452.76	1452.75	0.01	0	FVIGGPHGDAGLTGR
240 - 255	1581.82	1580.82	1580.84	-0.02	1	FVIGGPHGDAGLTGRK
255 - 275	2092.06	2091.06	2091.05	0.01	1	KIIIDTYGGWGAHGGGAFSGK
256 - 275	1963.99	1962.99	1962.96	0.03	0	IIIDTYGGWGAHGGGAFSGK
256 - 279	2405.18	2404.18	2404.18	-0.00	1	IIIDTYGGWGAHGGGAFSGKDPTK
294 - 302	873.54	872.54	872.51	0.03	0	SIVASGLAR
330 - 337	955.60	954.60	954.57	0.02	1	IPDKEILK
366 - 374	979.49	978.49	978.47	0.02	0	TAAYGHFGR

Spot 1799

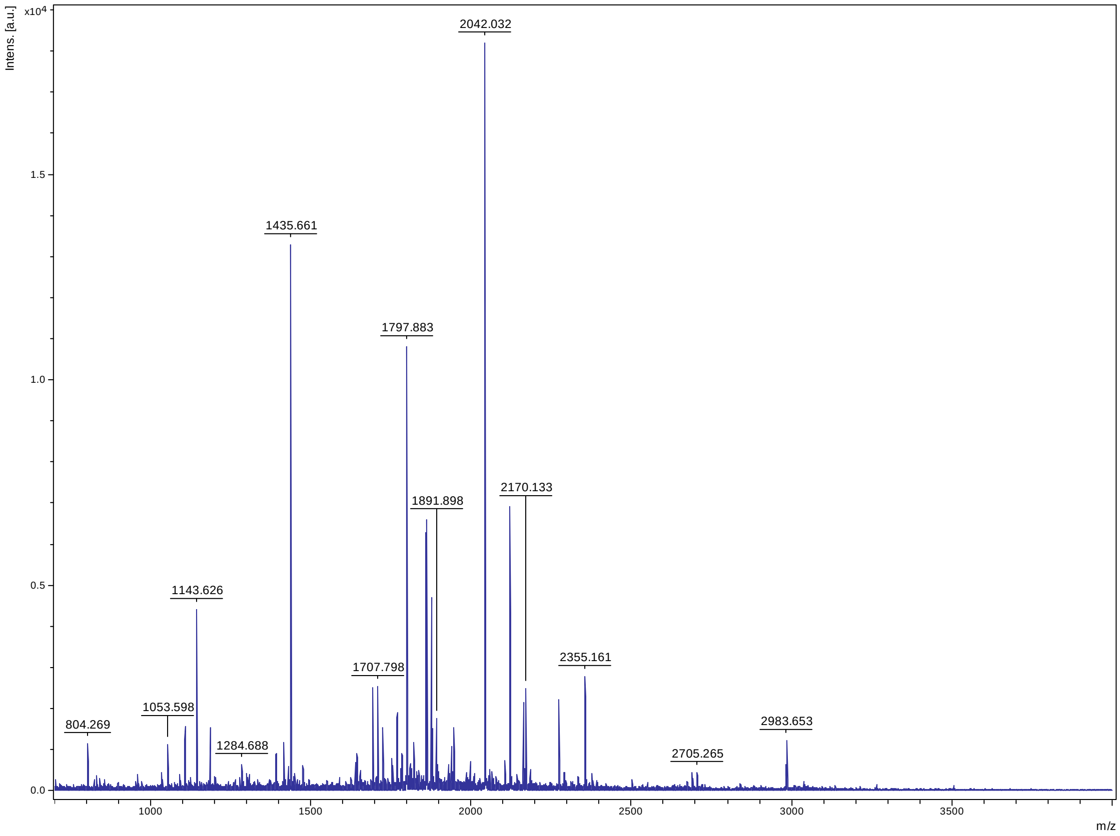


Match to: gi|108706593 Score: 73 Expect: 0.0035

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
18 - 34	1805.9696	1804.9623	1804.9822	-0.0198	0	R.AASEPLIVEEIVVDPPK.A	
18 - 39	2438.2839	2437.2767	2437.3103	-0.0337	1	R.AASEPLIVEEIVVDPPKAYEIR.I	
42 - 57	1983.9303	1982.9230	1982.9706	-0.0476	0	K.IICTSLCHTDVTLWHK.V	2 Carbamidomethyl (C)
58 - 64	801.4258	800.4185	800.4181	0.0004	0	K.VDPAFPR.I	
170 - 187	1878.8535	1877.8462	1877.8698	-0.0236	0	K.IACLLGCCGGTGVGAAWR.L	3 Carbamidomethyl (C)
221 - 230	1082.5773	1081.5700	1081.6131	-0.0431	0	K.IIGVDLNPNK.E	
231 - 251	2295.1306	2294.1233	2294.1066	0.0168	1	K.EEVGKEFGVTDFVNPSQLGDK.S	
236 - 251	1752.8323	1751.8250	1751.8366	-0.0116	0	K.EFGVTDFVNPSQLGDK.S	
300 - 315	1884.9032	1883.8959	1883.9127	-0.0168	0	K.DSQPLCLPSFEFLFGK.C	Carbamidomethyl (C)
329 - 337	999.5734	998.5661	998.5648	0.0013	0	K.TDIPILAEK.C	
338 - 347	1236.5903	1235.5831	1235.5889	-0.0059	1	K.CMNKELELEK.L	
373 - 379	965.4847	964.4775	964.4510	0.0264	0	R.CIIWMDK.-	Carbamidomethyl (C)

Spot 1800

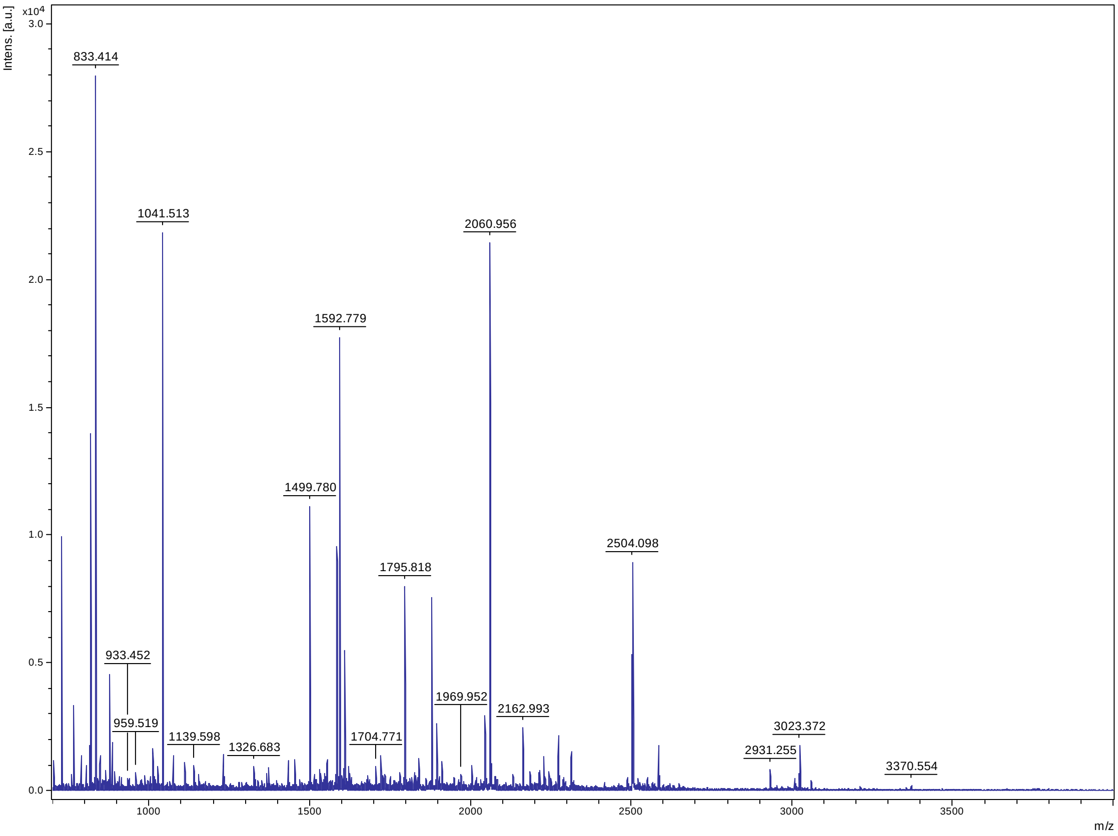


Match to: gi|50910077 Score: 101 Expect: 5.6e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 23	2289.1068	2288.0995	2288.1318	-0.0323	0	-.MASLASASASTSLVFSTSSSKPR.L	Oxidation (M)
67 - 83	1810.0168	1809.0095	1808.9645	0.0450	0	R.TKPHVNIGTIGHVDHGK.T	
104 - 115	1435.5929	1434.5856	1434.6626	-0.0770	1	K.KYDEIDAAPEER.A	
105 - 115	1307.4281	1306.4208	1306.5677	-0.1469	0	K.YDEIDAAPEER.A	
118 - 133	1797.9544	1796.9471	1796.8792	0.0679	0	R.GITINTATVEYETETR.H	
134 - 148	1753.9112	1752.9039	1752.7678	0.1361	0	R.HYAHVDCPGHADYVK.N	Acetyl (N-term)
134 - 148	1768.8706	1767.8633	1767.7787	0.0846	0	R.HYAHVDCPGHADYVK.N	Carbamidomethyl (C)
196 - 213	2170.1282	2169.1209	2169.1164	0.0045	1	K.KDQVDDEELLQLVELEVR.E	
197 - 213	2042.0929	2041.0856	2041.0215	0.0642	0	K.DQVDDEELLQLVELEVR.E	
214 - 235	2355.0670	2354.0597	2354.1528	-0.0931	0	R.ELLSSYEYDGDEVPIVAGSALK.A	
274 - 292	2121.1489	2120.1416	2120.1153	0.0263	0	R.QTDLPFLLAVEDVFSITGR.G	
318 - 332	1784.9598	1783.9525	1783.8232	0.1293	1	R.ETRNCTVTGVEMFQK.T	Acetyl (N-term)
333 - 348	1691.8634	1690.8561	1690.8018	0.0543	0	K.TMDDAMAGDNVGLLLR.G	
333 - 348	1723.8479	1722.8406	1722.7916	0.0490	0	K.TMDDAMAGDNVGLLLR.G	2 Oxidation (M)
388 - 402	1929.9890	1928.9817	1928.9144	0.0673	0	R.HSPFFPGYRPQFYMR.T	
388 - 402	1945.9754	1944.9681	1944.9093	0.0588	0	R.HSPFFPGYRPQFYMR.T	Oxidation (M)
418 - 429	1413.5555	1412.5482	1412.5370	0.0112	1	K.DEEAKMCMPGDR.V	2 Oxidation (M)
430 - 447	2104.0980	2103.0907	2103.0526	0.0382	1	R.VKMVVELIQPVACEQGMR.F	Acetyl (N-term); 2 Oxidation (M)
432 - 447	1844.9762	1843.9689	1843.8994	0.0696	0	K.MVVELIQPVACEQGMR.F	Acetyl (N-term)
432 - 447	1859.9857	1858.9784	1858.9103	0.0681	0	K.MVVELIQPVACEQGMR.F	Carbamidomethyl (C)
432 - 447	1875.9903	1874.9830	1874.9052	0.0778	0	K.MVVELIQPVACEQGMR.F	Carbamidomethyl (C); Oxidation (M)
432 - 447	1891.9808	1890.9735	1890.9001	0.0734	0	K.MVVELIQPVACEQGMR.F	Carbamidomethyl (C); 2 Oxidation (M)

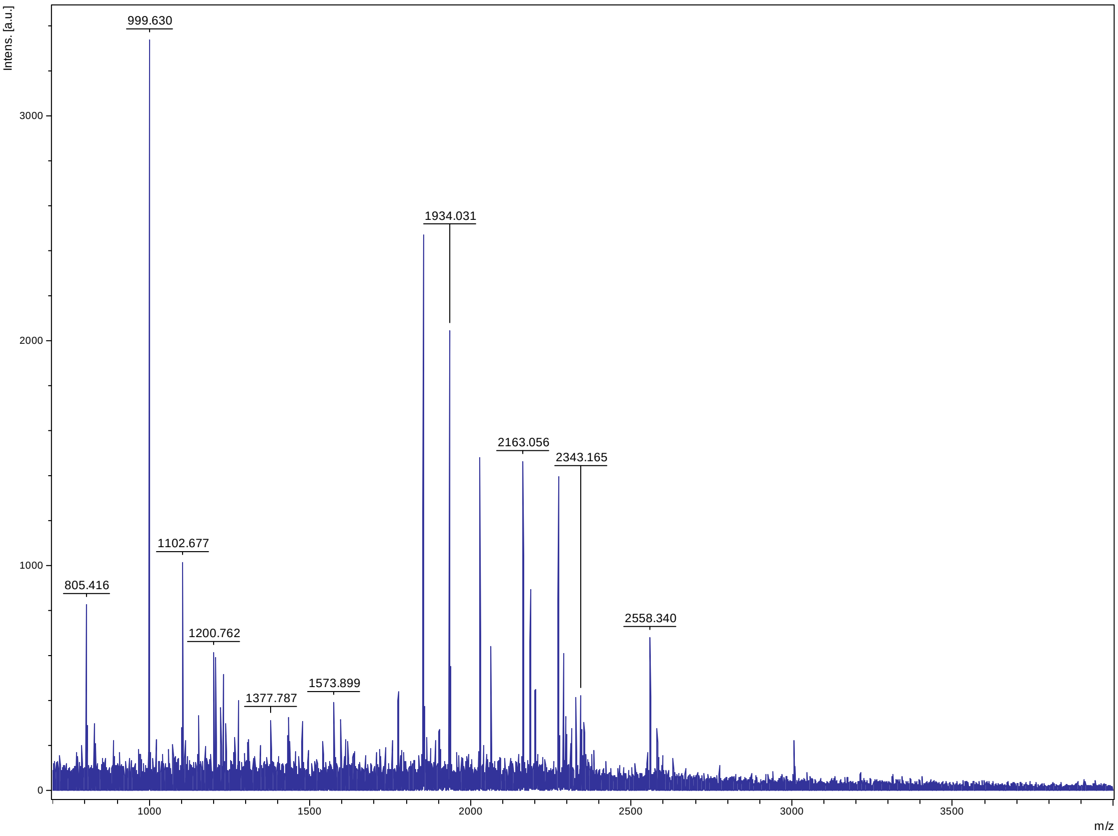
Spot 1805



Match to: gi|77554103 Score: 231 Expect: 1.1e-18

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
86 - 104	2045.0961	2044.0888	2044.1356	-0.0468	0	K.VVLAYSGGLDTSVIVPWLR.E	
105 - 130	2931.2551	2930.2479	2930.2949	-0.0470	0	R.ENYGCEVVCFTADVGQGDIELEGLEK.K	2 Carbamidomethyl (C)
105 - 131	3059.3782	3058.3709	3058.3898	-0.0189	1	R.ENYGCEVVCFTADVGQGDIELEGLEKK.A	2 Carbamidomethyl (C)
134 - 143	959.5191	958.5118	958.5447	-0.0329	0	K.ASGASQLVVK.D	
144 - 159	2003.9525	2002.9452	2002.9709	-0.0257	1	K.DLKEEFVSEYIYPCLR.A	
144 - 159	2060.9561	2059.9488	2059.9924	-0.0436	1	K.DLKEEFVSEYIYPCLR.A	Carbamidomethyl (C)
147 - 159	1704.7709	1703.7636	1703.7865	-0.0229	0	K.EEFVSEYIYPCLR.A	Carbamidomethyl (C)
189 - 202	1371.6025	1370.5953	1370.6248	-0.0295	0	K.EVGADAVAHGCTGK.G	Carbamidomethyl (C)
222 - 234	1584.7806	1583.7734	1583.8208	-0.0475	1	K.VVAPWREWDITGR.E	
228 - 234	876.4035	875.3962	875.4137	-0.0175	0	R.EWDITGR.E	
228 - 242	1795.8179	1794.8106	1794.8424	-0.0318	1	R.EWDITGREDAIEYAK.K	
235 - 242	938.4367	937.4294	937.4392	-0.0098	0	R.EDAIEYAK.K	
244 - 252	1004.5121	1003.5049	1003.5814	-0.0766	0	K.HNVPIPVTK.K	
259 - 280	2585.2092	2584.2020	2584.2306	-0.0286	1	R.DRNLWHLSHEGDILEDPANEPK.E	
261 - 280	2314.0518	2313.0445	2313.1025	-0.0580	0	R.NLWHLSHEGDILEDPANEPK.E	
316 - 325	1014.5588	1013.5516	1013.5757	-0.0241	0	K.DLSPASLLAK.L	
338 - 344	892.4171	891.4098	891.4120	-0.0022	0	R.IDMVENR.L	Oxidation (M)
352 - 367	1592.7792	1591.7719	1591.8028	-0.0309	0	R.GVYETPGGTIMAAAVR.E	
352 - 367	1608.7700	1607.7627	1607.7977	-0.0349	0	R.GVYETPGGTIMAAAVR.E	Oxidation (M)
368 - 376	1075.5216	1074.5143	1074.5557	-0.0413	0	R.ELESLTLDR.E	
368 - 382	1878.8875	1877.8802	1877.9193	-0.0391	1	R.ELESLTLDRETMQWK.D	
368 - 382	1894.8695	1893.8622	1893.9142	-0.0520	1	R.ELESLTLDRETMQWK.D	Oxidation (M)
389 - 397	1041.5128	1040.5055	1040.5290	-0.0235	0	K.YAELVYAGR.W	
398 - 403	833.4144	832.4072	832.4232	-0.0160	0	R.WFDPLR.Q	
404 - 424	2228.0479	2227.0406	2227.1042	-0.0636	0	R.QSIDAFMENITATTTGSVTLK.L	
404 - 424	2244.0371	2243.0298	2243.0991	-0.0693	0	R.QSIDAFMENITATTTGSVTLK.L	Oxidation (M)
437 - 443	885.4340	884.4267	884.4392	-0.0125	0	K.SPYSLYR.E	
437 - 465	3370.5542	3369.5469	3369.5425	0.0045	1	K.SPYSLYREDISSFENGEIYNQADAEGFIR.L	
444 - 465	2504.0981	2503.0909	2503.1138	-0.0230	0	R.EDISSFENGEIYNQADAEGFIR.L	
466 - 472	819.4535	818.4462	818.4650	-0.0188	0	R.LYGLPTR.V	

Spot 1811

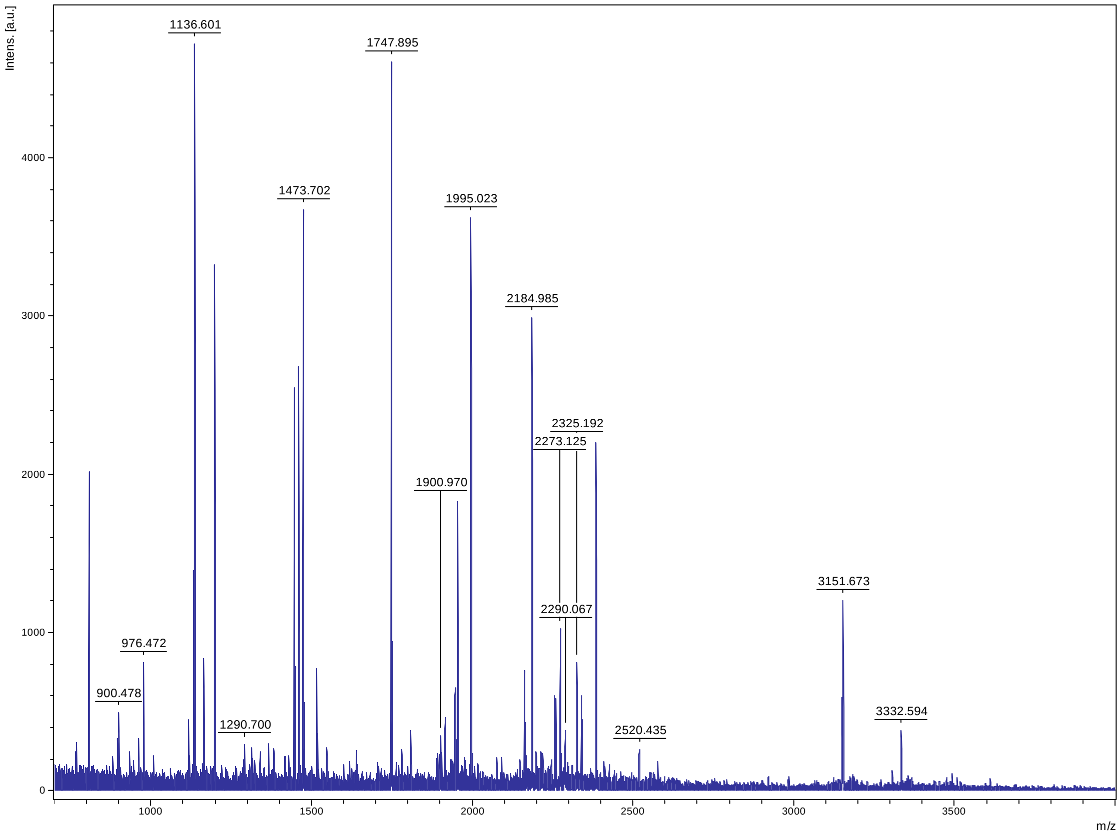


Match to: gi|50931897 Score: 78

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
131 - 144	1431.7039	1430.6966	1430.7365	-0.0399	1	K.SVGDLTAADLEGKR.V
149 - 166	2028.9032	2027.8959	2027.9396	-0.0437	0	R.ADLNVPLDDNQNITDDTR.V
169 - 179	1230.7242	1229.7170	1229.7383	-0.0214	0	R.AAIPTIQYLIK.N
236 - 254	2062.0137	2061.0064	2061.0643	-0.0579	1	K.KLASLADLYVNDAFGTAHR.A
237 - 254	1933.9398	1932.9325	1932.9693	-0.0368	0	K.LASLADLYVNDAFGTAHR.A
278 - 290	1377.7064	1376.6991	1376.7187	-0.0195	0	K.ELDYLVGAVSSPK.R
291 - 301	1102.6284	1101.6211	1101.6294	-0.0083	0	K.RPFAAIVGGSK.V

Spot 1812



Match to: gi|50948447; Score: 134

Matched peptides:

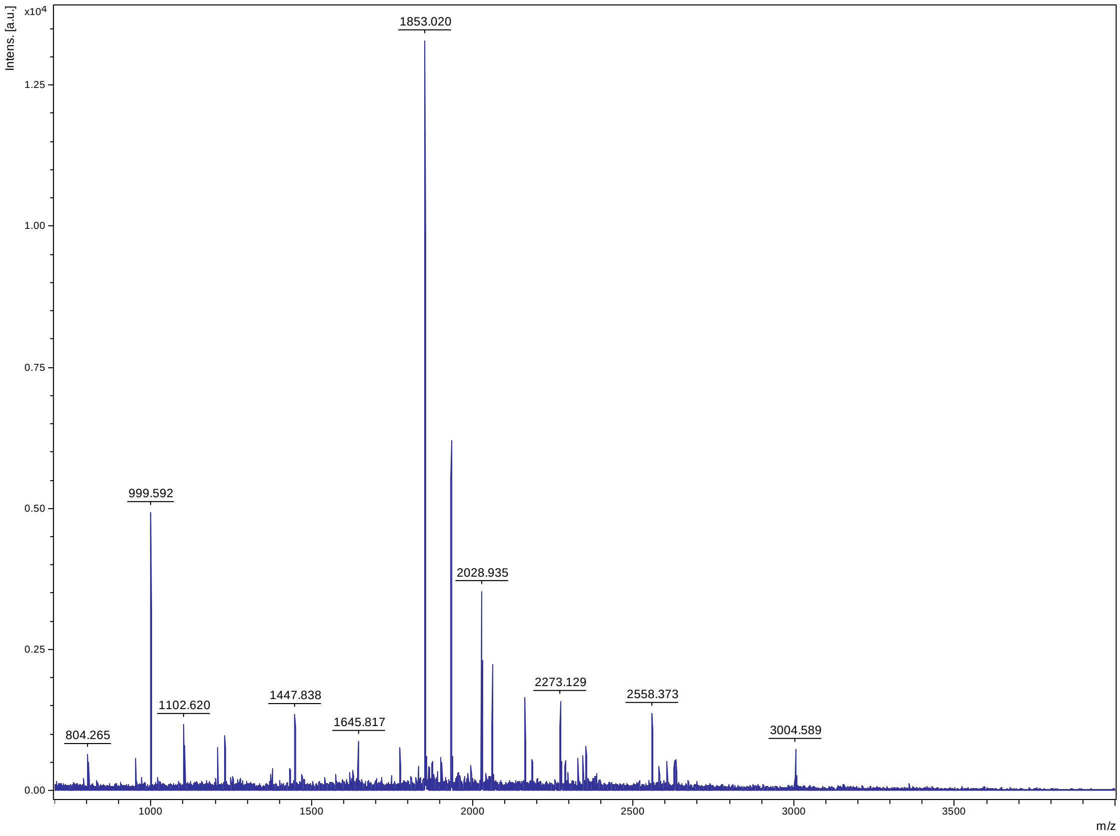
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
41 - 53	1446.76	1445.76	1445.75	0.01	0	ESVAPYERPALSK
54 - 63	1136.60	1135.60	1135.58	0.02	0	GYLFPQNAAR
64 - 77	1473.70	1472.70	1472.68	0.02	0	LPGFHTCVGSGGER
78 - 86	1164.59	1163.59	1163.59	0.00	0	LLPEWYSEK
130 - 147	1995.02	1994.02	1994.01	0.01	0	LTDFGVQGAEANDILYLR
185 - 202	2256.99	2255.99	2255.98	0.01	0	TNNFDVTMVYPEPWCMPR
185 - 202	2273.12	2272.12	2271.98	0.15	0	TNNFDVTMVYPEPWCMPR Oxidation (M)
203 - 219	1914.92	1913.91	1913.92	-0.01	0	LFTSGLAAFYEGYYANK
312 - 320	1118.61	1117.60	1117.57	0.03	1	RVEHVDHAR
334 - 351	2184.98	2183.98	2183.97	0.01	0	EAGESVPEYDYLPYFYSR
352 - 381	3332.59	3331.59	3331.53	0.06	0	SFDLSWQFYGDNVGEDVLFGDNDPTAAKPK
382 - 388	900.48	899.48	899.45	0.02	0	FGSYWIK
392 - 410	1946.01	1945.01	1945.02	-0.01	0	VVGVFLEGGSAEENQVIAK

Match to: gi|76800642; Score: 109

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
21 - 30	976.47	975.47	975.44	0.03	0	AGFAGDDAPR
31 - 41	1198.73	1197.72	1197.70	0.02	0	AVFPSIVGRPR
87 - 97	1515.75	1514.75	1514.74	0.01	0	IWHHTFYNELR
98 - 115	1954.07	1953.06	1953.06	0.01	0	VAPEEHPVLLTEAPLNPK
150 - 179	3151.67	3150.67	3150.63	0.04	0	TTGIVLDSGDGVSHTVPIYEGYALPHAILR
199 - 208	1132.54	1131.53	1131.52	0.01	0	GYSFTTTAER
216 - 233	2163.05	2162.05	2162.01	0.04	1	EKLSYIALDYDQEMETAK Oxidation (M)
241 - 256	1747.90	1746.89	1746.88	0.01	0	SYELPDGQVITIGAER
293 - 314	2325.19	2324.19	2324.18	0.01	1	KDLYGNIVLSGGTTMFPGIADR
293 - 314	2341.19	2340.19	2340.18	0.01	1	KDLYGNIVLSGGTTMFPGIADR Oxidation (M)
331 - 338	895.56	894.55	894.53	0.02	1	VVAPPERK
362 - 374	1459.68	1458.68	1458.67	0.00	0	AEYDESGPSIVHR

Spot 1816

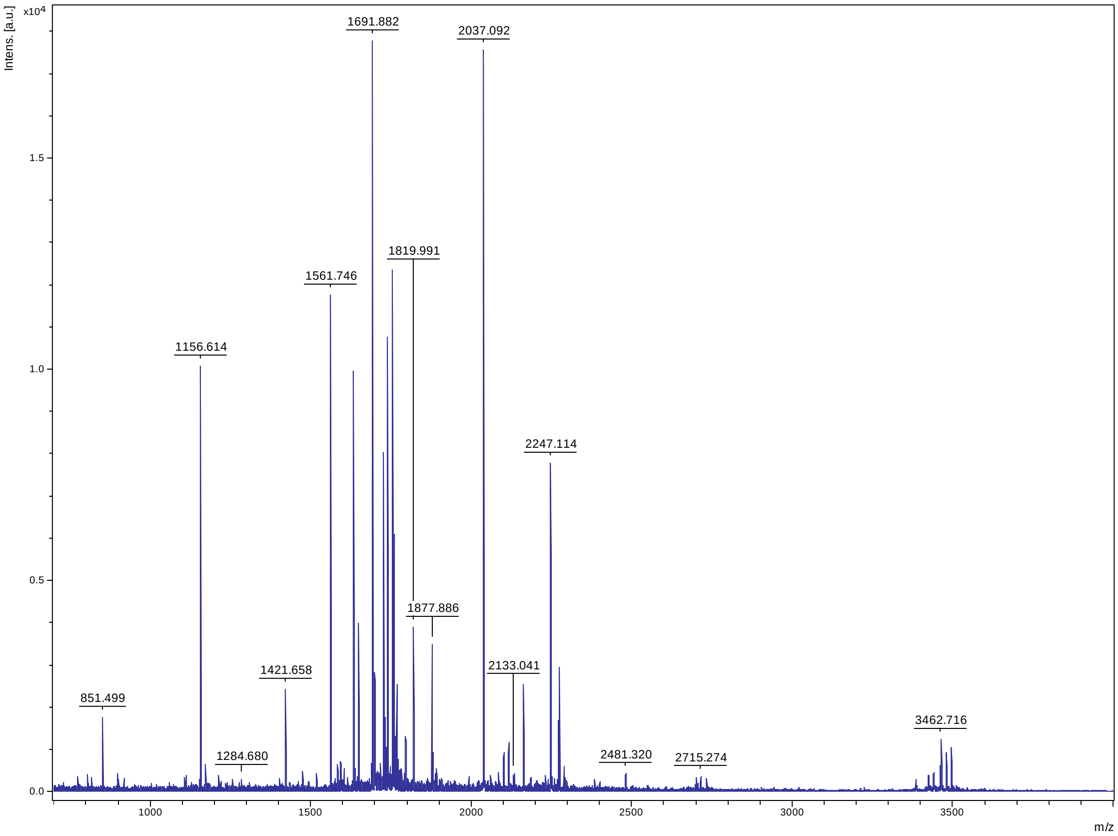


Match to: gi|50931897; Score: 108

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
131 - 144	1431.73	1430.72	1430.74	-0.01	1	SVGDLTAADLEGKR
149 - 166	2028.94	2027.93	2027.94	-0.01	0	ADLNVPLDDNQNITDDTR
169 - 179	1230.73	1229.72	1229.74	-0.01	0	AAIPTIQYLIK
194 - 221	3004.59	3003.59	3003.61	-0.03	1	AEDVIGPDVEKLVSELPNGSVLLLENVR
236 - 254	2062.06	2061.06	2061.06	-0.00	1	KLASLADLYVNDAFGTAHR
237 - 254	1933.97	1932.96	1932.97	-0.01	0	LASLADLYVNDAFGTAHR
265 - 277	1447.84	1446.84	1446.86	-0.02	0	FLKPSVAGFLLQK
278 - 290	1377.69	1376.69	1376.72	-0.03	0	ELDYLVGAVSSPK
291 - 301	1102.62	1101.62	1101.63	-0.01	0	RPFAAIVGGSK

Spot 1825

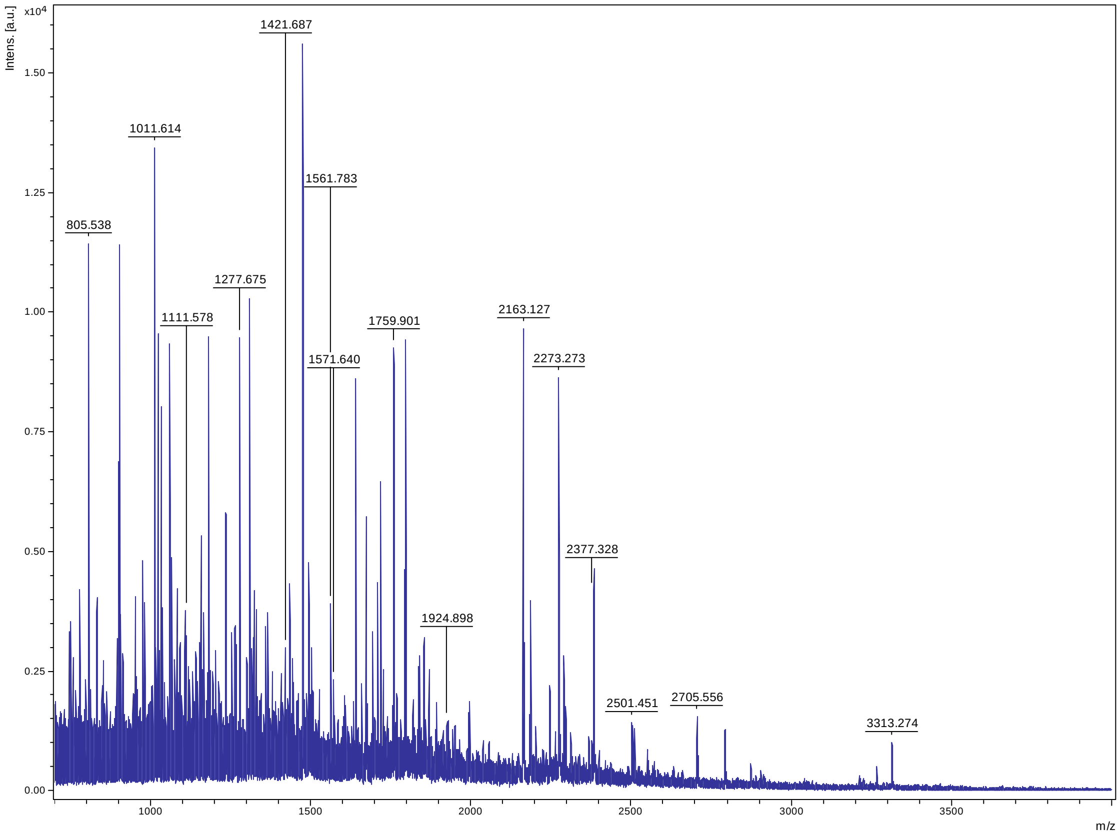


Match to: gi|21685576; Score: 358

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
64 - 80	1795.94	1794.94	1794.95	-0.01	0	TKPHVNVGTIGHVDHGK
81 - 89	919.54	918.53	918.54	-0.01	0	TTLTAAITK
99 - 112	1561.75	1560.74	1560.77	-0.02	1	AVAFDEIDKAPEEK
115 - 129	1603.79	1602.78	1602.83	-0.04	0	GITIATAHVEYETAK
115 - 130	1759.92	1758.92	1758.93	-0.00	1	GITIATAHVEYETAKR
131 - 145	1768.79	1767.79	1767.78	0.01	0	HYAHVDCPGHADYVK
146 - 172	2715.27	2714.27	2714.31	-0.04	0	NMITGAAQMDGGILVVSAPDGPMPQTK Oxidation (M)
146 - 172	2731.25	2730.25	2730.30	-0.05	0	NMITGAAQMDGGILVVSAPDGPMPQTK 2 Oxidation (M)
173 - 179	851.50	850.50	850.50	-0.01	0	EHILLAR
211 - 217	899.48	898.48	898.48	0.00	0	ELLSFYK
211 - 227	2037.09	2036.09	2036.10	-0.01	1	ELLSFYKFPGDEIPIIR
218 - 227	1156.61	1155.61	1155.63	-0.02	0	FPGDEIPIIR
228 - 248	2100.08	2099.07	2099.12	-0.05	1	GSALSALQGTNDEIGKNAILK
249 - 262	1632.76	1631.76	1631.79	-0.02	0	LMDAVDEYIPDPVR
249 - 262	1648.76	1647.76	1647.78	-0.02	0	LMDAVDEYIPDPVR Oxidation (M)
249 - 266	2117.04	2116.03	2116.05	-0.02	1	LMDAVDEYIPDPVRQLDK
249 - 266	2133.04	2132.04	2132.05	-0.01	1	LMDAVDEYIPDPVRQLDK Oxidation (M)
267 - 281	1738.87	1737.86	1737.88	-0.01	0	SFLMPIEDVFSIQGR
267 - 281	1754.87	1753.86	1753.87	-0.01	0	SFLMPIEDVFSIQGR Oxidation (M)
289 - 312	2481.32	2480.32	2480.34	-0.02	1	VEQGTIKTGEDVEILGLTPSGPLK
296 - 312	1725.88	1724.88	1724.92	-0.04	0	TGEDVEILGLTPSGPLK
313 - 322	1112.55	1111.55	1111.56	-0.01	0	TTVTGVEMFK
313 - 323	1256.64	1255.64	1255.65	-0.01	1	TTVTGVEMFKK Oxidation (M)
323 - 339	1819.99	1818.99	1819.00	-0.01	1	KILDHGEAGDNVGLLLR
324 - 339	1691.88	1690.88	1690.90	-0.02	0	ILDHGEAGDNVGLLLR
344 - 359	1727.83	1726.83	1726.91	-0.09	1	GDVQRGQVVCKPGTVK
349 - 359	1172.62	1171.62	1171.64	-0.02	0	GQVVCKPGTVK
360 - 373	1732.89	1731.89	1731.91	-0.02	1	TYQKFEAEIYVLTK
364 - 373	1212.63	1211.63	1211.64	-0.02	0	FEAEIYVLTK
379 - 393	1877.89	1876.88	1876.89	-0.01	0	HTAFLSNYSPQFYFR
401 - 433	3462.72	3461.71	3461.76	-0.04	0	VVLPDGVEMVMPGDNVTAGFELISPVPLEPGQR
401 - 433	3478.73	3477.73	3477.75	-0.03	0	VVLPDGVEMVMPGDNVTAGFELISPVPLEPGQR Oxidation (M)
401 - 433	3494.73	3493.72	3493.75	-0.02	0	VVLPDGVEMVMPGDNVTAGFELISPVPLEPGQR 2 Oxidation (M)
442 - 450	817.46	816.46	816.47	-0.01	0	TVGAGVVSK

Spot 1836

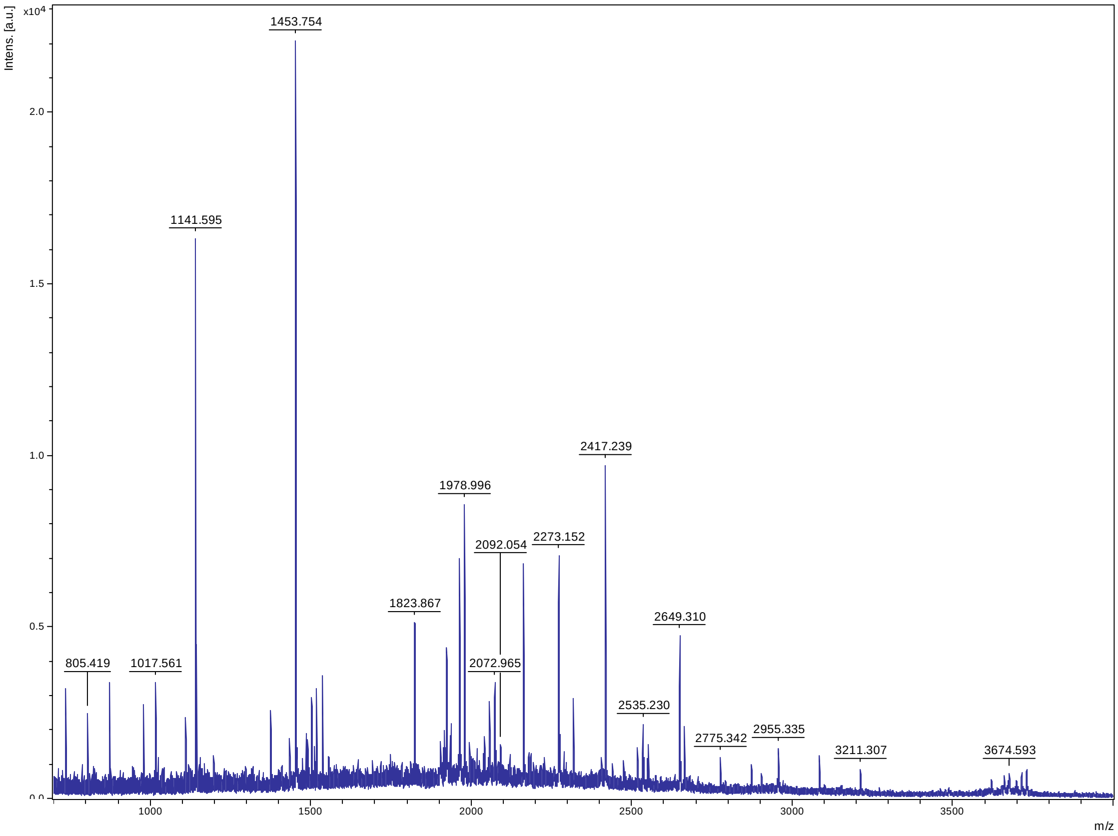


Match to: gi|14209591; Score: 69

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
87 - 101	1672.91	1671.91	1671.96	-0.04	0	LEKPVVILISSDGFR
108 - 115	902.58	901.58	901.49	0.09	0	AATPHIHR
206 - 216	1443.56	1442.56	1442.57	-0.01	1	GSWDCPDKYCR
281 - 288	900.60	899.60	899.51	0.09	0	LIAGLEER
289 - 310	2377.33	2376.33	2376.11	0.22	0	GVFEDVNVILVGDHGMVGTCDK Oxidation (M)
289 - 311	2505.32	2504.32	2504.20	0.12	1	GVFEDVNVILVGDHGMVGTCDKK Oxidation (M)
370 - 379	1251.61	1250.61	1250.63	-0.03	1	MYLKEDLPSR
380 - 387	1024.53	1023.53	1023.48	0.05	0	LHYADSYR
388 - 404	1929.00	1928.00	1928.03	-0.03	1	IPPIIGLPEEGYKVEMK Oxidation (M)
426 - 434	1011.61	1010.61	1010.57	0.05	0	TIFIAHGPR

Spot 1841

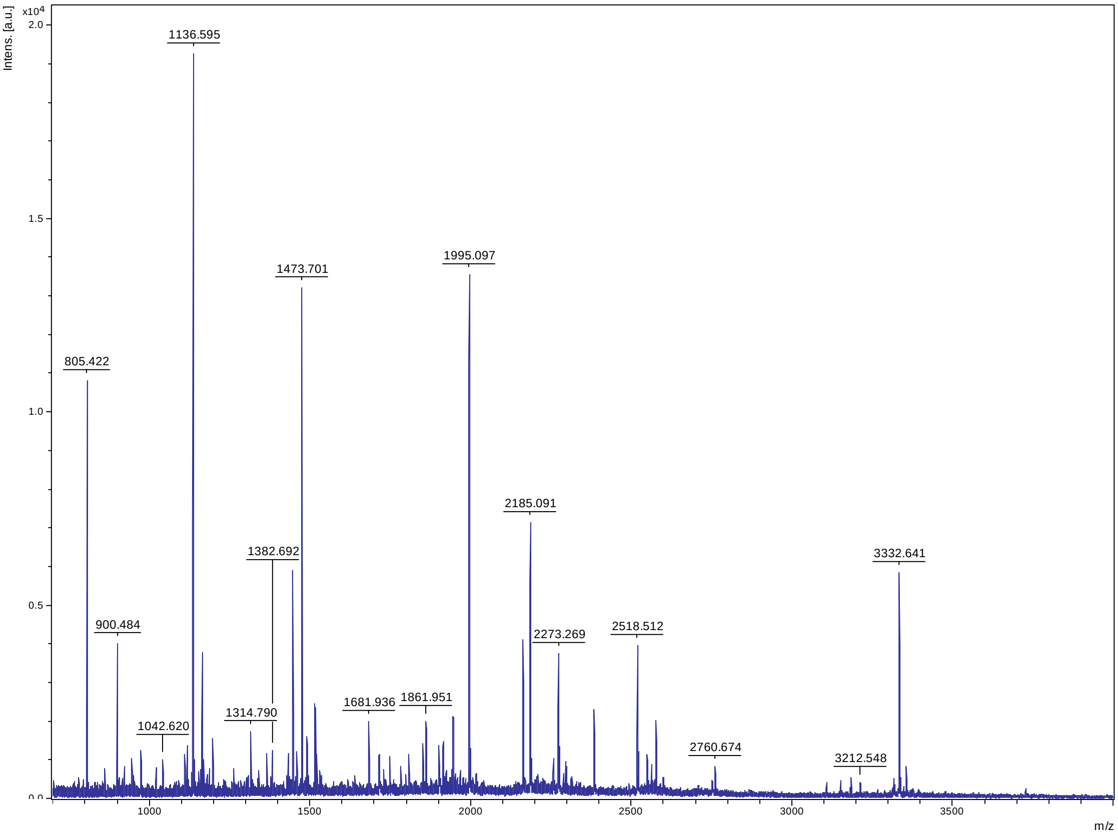


Match to: gi|34894718 Score: 127 Expect: 1.3e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
77 - 91	1535.8561	1534.8488	1534.7263	0.1225	0	R.GIGFVSDDVGLDADR.C	
77 - 93	1824.0117	1823.0044	1822.8519	0.1525	1	R.GIGFVSDDVGLDADRCK.V	Carbamidomethyl (C)
94 - 115	2417.4661	2416.4588	2416.2498	0.2090	0	K.VLVNIEQQSPDIAQGVHGHFTK.R	
160 - 171	1374.7307	1373.7234	1373.6510	0.0725	0	K.NGTCAWLRPDGK.T	Carbamidomethyl (C)
172 - 189	1963.1409	1962.1336	1961.9880	0.1456	0	K.TQVTVEYLNDAGAMVPVR.V	
172 - 189	1979.1595	1978.1523	1977.9829	0.1694	0	K.TQVTVEYLNDAGAMVPVR.V	Oxidation (M)
190 - 213	2649.5750	2648.5677	2648.3293	0.2384	0	R.VHTVLISTQHDETVTNDEIAADLK.E	
214 - 229	1923.2107	1922.2034	1922.0513	0.1522	1	K.EHVIKPVIPDKYLDEK.T	
230 - 239	1141.6710	1140.6637	1140.6040	0.0598	0	K.TIFHLNPSGR.F	
240 - 254	1453.8579	1452.8506	1452.7473	0.1033	0	R.FVIGGPHGDAGLTGR.K	
255 - 275	2092.2332	2091.2259	2091.0537	0.1722	1	R.KIIIDTYGGWGAHGGGAFSGK.D	
294 - 302	873.5706	872.5633	872.5079	0.0554	0	K.SIVASGLAR.R	
341 - 357	2041.1553	2040.1480	2039.9808	0.1672	0	K.ENFDFRPGMMTINLDLK.R	
341 - 357	2057.1504	2056.1431	2055.9757	0.1674	0	K.ENFDFRPGMMTINLDLK.R	Oxidation (M)
341 - 357	2073.1416	2072.1343	2071.9706	0.1637	0	K.ENFDFRPGMMTINLDLK.R	2 Oxidation (M)
366 - 374	979.5375	978.5303	978.4671	0.0631	0	K.TAAYGHFGR.E	
366 - 388	2663.5430	2662.5357	2662.3179	0.2178	1	K.TAAYGHFGREDPDFTWEVVKPLK.Y	

Spot 1842

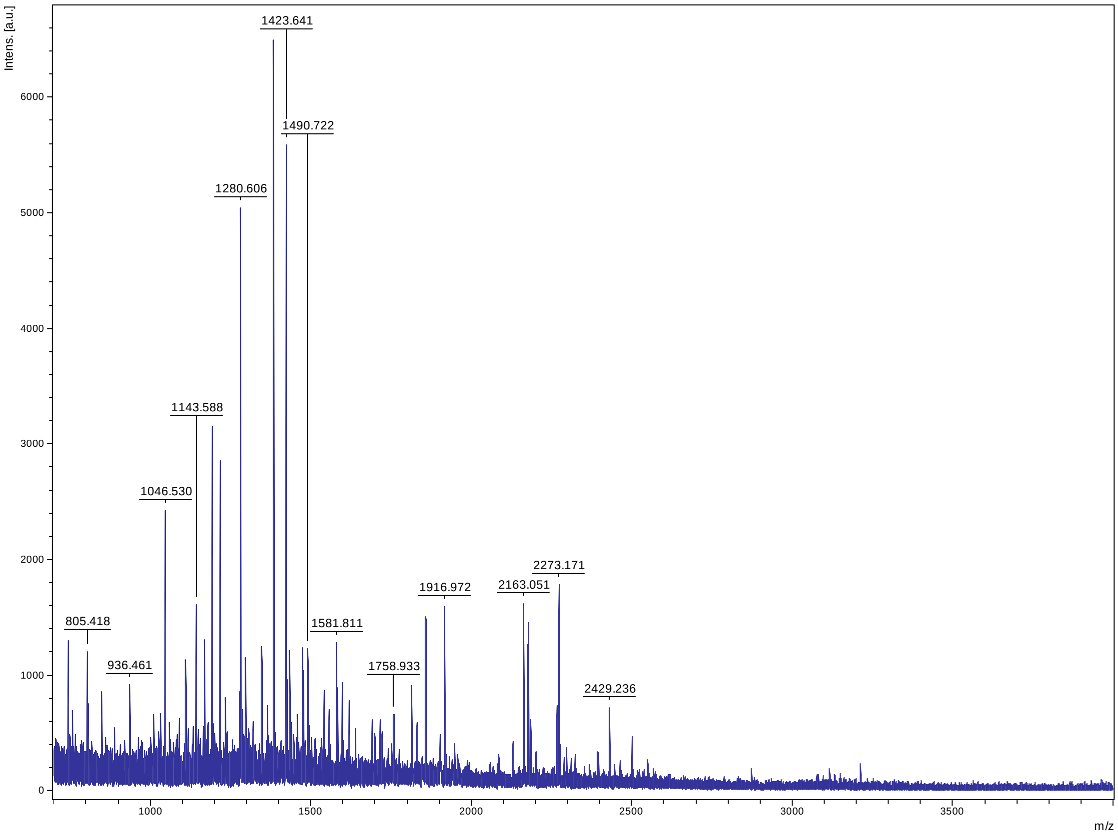


Match to: gi|50948447 Score: 121 Expect: 5.3e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 23	2295.1113	2294.1040	2294.1993	-0.0952	1	-.MAAAKHFTYVILGGGVAAGYAAR.E	
28 - 40	1339.7931	1338.7858	1338.7870	-0.0012	0	K.QGVKPGELAIISK.E	
41 - 53	1446.7503	1445.7430	1445.7514	-0.0084	0	K.ESVAPYERPALSK.G	
54 - 63	1136.5869	1135.5796	1135.5774	0.0022	0	K.GYLFPQNAAR.L	
54 - 77	2576.2124	2575.2051	2575.2389	-0.0338	1	K.GYLFPQNAARLPGFHTCVGSGGER.L	Acetyl (N-term)
64 - 77	1473.6833	1472.6760	1472.6830	-0.0070	0	R.LPGFHTCVGSGGER.L	Carbamidomethyl (C)
64 - 77	1515.7349	1514.7276	1514.6935	0.0341	0	R.LPGFHTCVGSGGER.L	Acetyl (N-term); Carbamidomethyl (C)
78 - 86	1164.6051	1163.5978	1163.5862	0.0116	0	R.LLPEWYSEK.G	
87 - 98	1314.7840	1313.7767	1313.7806	-0.0038	0	K.GIELILSTEIVK.A	
130 - 147	1994.9858	1993.9785	1994.0108	-0.0323	0	K.LTDFGVQGAEANDILYLR.D	
167 - 184	1730.9621	1729.9548	1729.9977	-0.0429	0	K.AVIVGGGYIGLELSAALK.T	
185 - 202	2257.9686	2256.9613	2256.9642	-0.0029	0	K.TNNFDVTMVYPEPWCMPR.L	Acetyl (N-term); Oxidation (M)
185 - 202	2288.9498	2287.9425	2287.9700	-0.0275	0	K.TNNFDVTMVYPEPWCMPR.L	Carbamidomethyl (C); 2 Oxidation (M)
203 - 219	1914.8656	1913.8583	1913.9199	-0.0616	0	R.LFTSGLAAFYEGYYANK.G	
226 - 244	1806.8631	1805.8558	1805.8795	-0.0236	0	K.GTVAVGFDADANGDVTAVK.L	
247 - 270	2518.3166	2517.3093	2517.4066	-0.0973	0	K.NGNVLEADIVIVGVGGRPLTHLFK.G	
282 - 305	2563.1549	2562.1476	2562.2351	-0.0875	0	K.TDAFFETSVPGVYAIADVAAFPMK.L	Oxidation (M)
312 - 320	1118.5769	1117.5696	1117.5741	-0.0044	1	R.RVEHVDHAR.K	
313 - 321	1132.5190	1131.5117	1131.5785	-0.0667	1	R.VEHVDHARK.S	Acetyl (N-term)
334 - 351	2184.9623	2183.9550	2183.9687	-0.0137	0	K.EAGESVPEYDYLPYFYSR.S	
382 - 388	900.4347	899.4274	899.4541	-0.0267	0	K.FGSYWIK.D	
392 - 410	1945.9866	1944.9793	1945.0155	-0.0362	0	K.VVGVFLEGGSAEENQVIAK.V	

Spot 1844

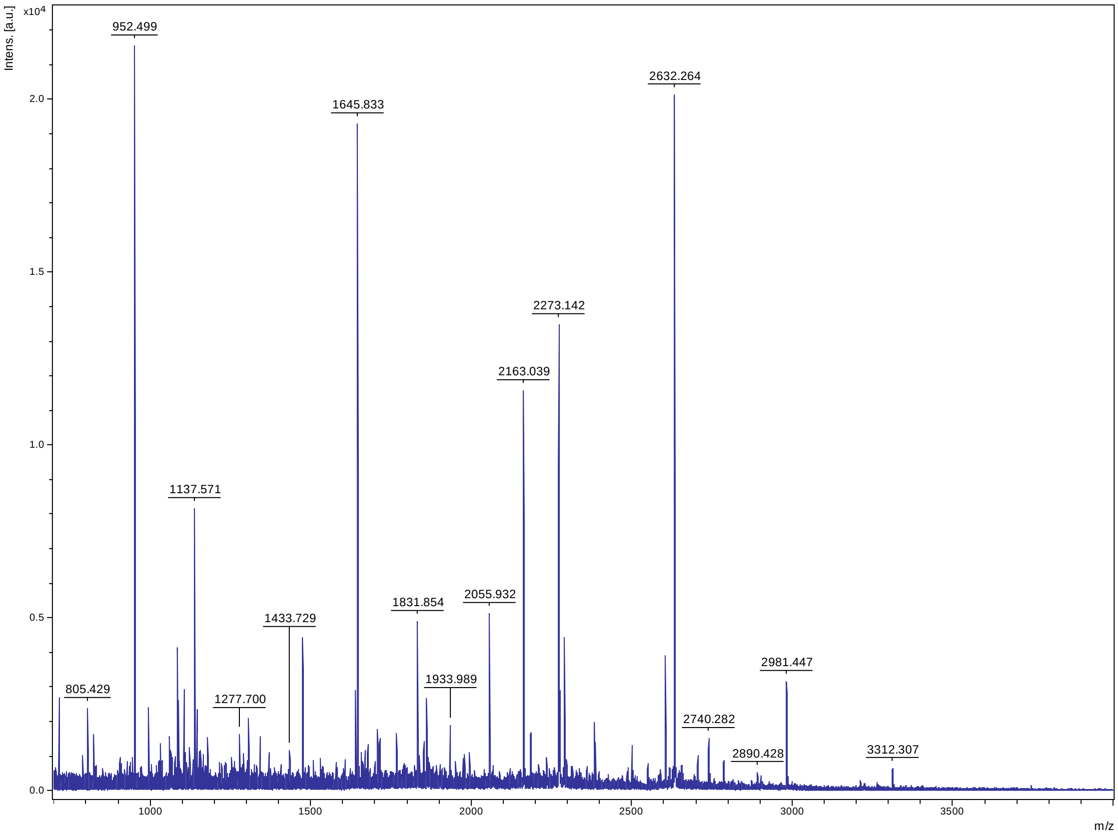


Match to: Q7XK23_ORYSA Score: 89 Expect: 8.4e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
48 - 62	1581.8109	1580.8036	1580.8232	-0.0195	0	R.GDMPTVPPAVIESIR.R	
48 - 62	1597.8011	1596.7939	1596.8181	-0.0242	0	R.GDMPTVPPAVIESIR.R	Oxidation (M)
66 - 88	2273.1707	2272.1634	2272.2030	-0.0397	1	K.VCLKGGLATPVGGGVSSLNMQLR.K	Oxidation (M)
70 - 88	1813.9427	1812.9355	1812.9515	-0.0160	0	K.GGLATPVGGGVSSLNMQLR.K	
90 - 109	2266.1196	2265.1124	2265.1099	0.0024	0	K.ELDLYASLVNCSNFPGLPTR.H	Carbamidomethyl (C)
147 - 154	1010.5125	1009.5052	1009.5015	0.0038	1	K.FCSERIAK.Y	Carbamidomethyl (C)
155 - 165	1423.6406	1422.6333	1422.6568	-0.0234	0	K.YAFEYAYLNNR.K	
179 - 189	1280.6060	1279.5987	1279.6230	-0.0244	0	K.LADGLFLESCR.E	Carbamidomethyl (C)
293 - 302	1217.5918	1216.5845	1216.5989	-0.0144	0	R.HLQFPSFADR.L	
293 - 308	1858.9755	1857.9682	1857.9737	-0.0055	1	R.HLQFPSFADRLETAVK.R	

Spot 1850

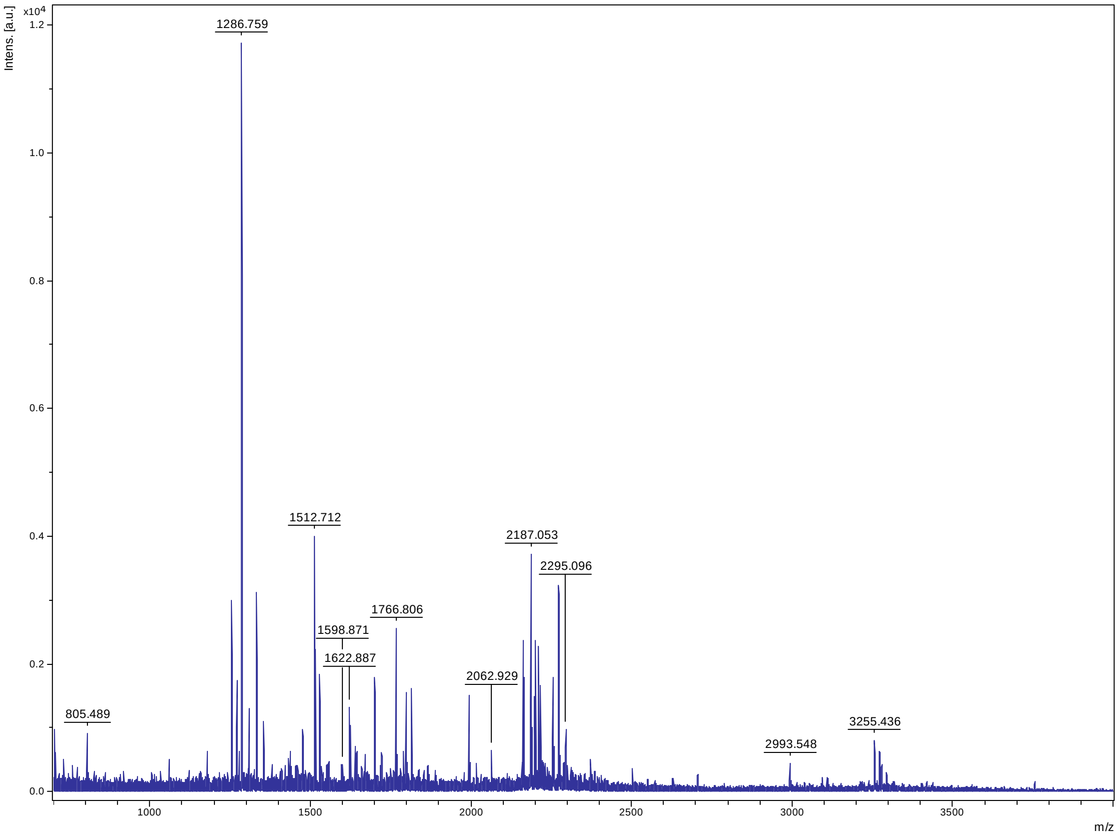


Match to: gi|13540812; Score: 164

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
228 - 246	2055.93	2054.93	2054.93	-0.00	0	HVDDNADITISCAPIDGSR
247 - 260	1529.72	1528.72	1528.72	0.01	1	ASDYGLVKFDDSGR
261 - 277	1933.99	1932.99	1932.99	-0.00	0	VIQFLEKPEGADLESMK
307 - 314	928.57	927.57	927.56	0.00	0	DVLLDILK
315 - 330	1860.97	1859.96	1859.95	0.01	1	SKYAHLQDFGSEILPR
317 - 330	1645.83	1644.83	1644.83	0.00	0	YAHLQDFGSEILPR
339 - 353	1831.85	1830.85	1830.85	0.00	0	ACVFTEYWEDIGTIK
354 - 368	1677.84	1676.84	1676.84	-0.00	0	SFFDANLALTEQPPK
354 - 375	2604.25	2603.24	2603.26	-0.02	1	SFFDANLALTEQPPKFEFYDPK
369 - 375	945.47	944.46	944.43	0.04	0	FEFYDPK
376 - 383	952.50	951.50	951.48	0.01	0	TPFFTSPR
384 - 392	1086.64	1085.64	1085.62	0.01	1	YLPPARLEK
395 - 421	2981.45	2980.44	2980.43	0.02	1	IKDAIISDGCSFSECTIEHSVIGISSR
397 - 421	2740.28	2739.28	2739.25	0.03	0	DAIISDGCSFSECTIEHSVIGISSR
448 - 463	1714.95	1713.95	1713.97	-0.02	1	LLFEGKVPIGIGENTK
454 - 463	1027.57	1026.57	1026.57	-0.00	0	VPIGIGENTK
466 - 474	1106.52	1105.52	1105.50	0.02	0	NCIIDMNAR
466 - 474	1122.52	1121.52	1121.50	0.03	0	NCIIDMNAR Oxidation (M)
478 - 500	2632.26	2631.26	2631.26	0.00	0	NVIIANTQGVQESDHPEEGYYIR

Spot 1853

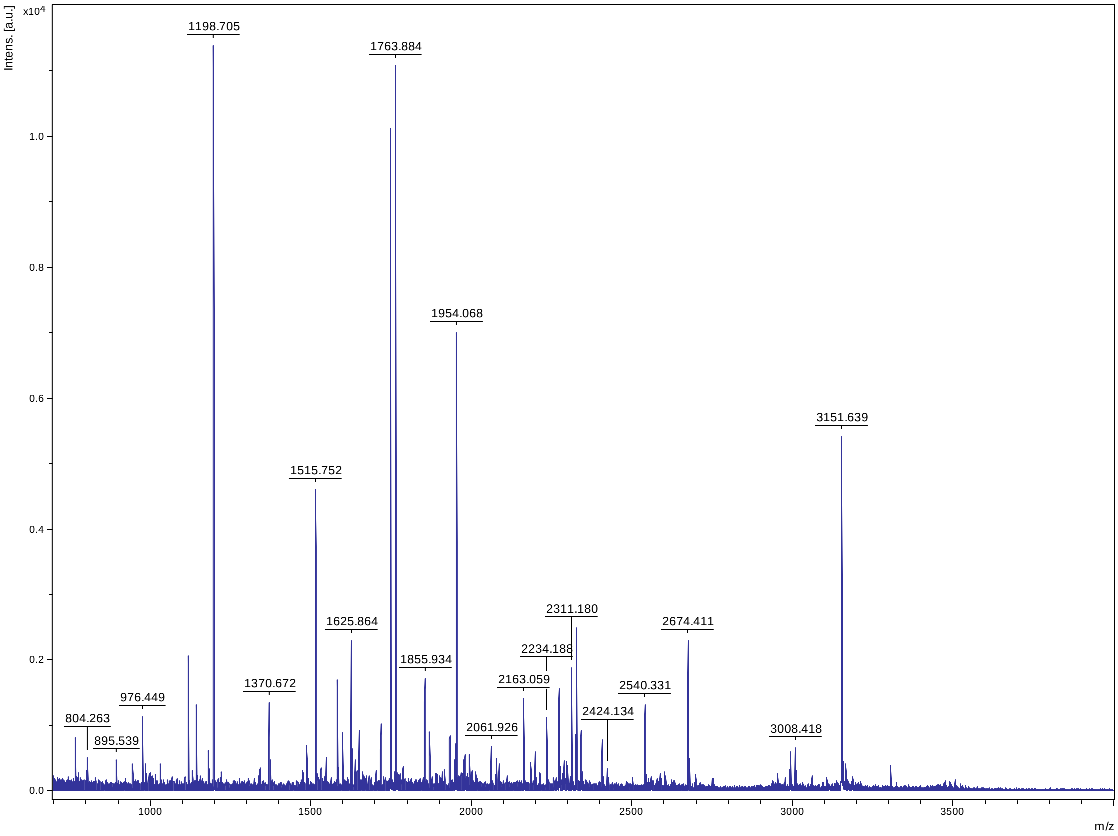


Match to: gi|51965038; Score: 150

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
51 - 65	1699.86	1698.85	1698.85	0.01	1	AYTVEKSEEIFNAAK
66 - 77	1255.68	1254.68	1254.64	0.04	0	ELMPGGVNSPVR
66 - 77	1271.66	1270.66	1270.63	0.02	0	ELMPGGVNSPVR Oxidation (M)
81 - 93	1332.74	1331.74	1331.71	0.03	0	SVGGQPIVFDSVK
164 - 177	1512.71	1511.71	1511.69	0.02	0	FVNSGTEACMGALR
164 - 177	1528.70	1527.70	1527.68	0.02	0	FVNSGTEACMGALR Oxidation (M)
191 - 205	1766.81	1765.80	1765.79	0.02	0	FEGCYHGHADSFLVK
206 - 223	1622.89	1621.89	1621.87	0.02	0	AGSGVATLGLPDSPGVPK
278 - 297	2255.10	2254.10	2254.13	-0.03	1	DLTKQDGALLVFDEVMTGFR
278 - 297	2271.10	2270.10	2270.13	-0.03	1	DLTKQDGALLVFDEVMTGFR Oxidation (M)
282 - 297	1797.88	1796.88	1796.88	0.00	0	QDGALLVFDEVMTGFR
282 - 297	1813.89	1812.88	1812.87	0.01	0	QDGALLVFDEVMTGFR Oxidation (M)
298 - 318	2187.05	2186.05	2186.09	-0.04	0	LAYGGAQEYFGITPDVSTLGK
319 - 332	1286.76	1285.76	1285.71	0.04	0	IIGGGLPVGAYGGR
368 - 386	2199.06	2198.06	2198.09	-0.03	1	LMEPGTYDYLDKITGDLVR
368 - 386	2215.05	2214.04	2214.09	-0.04	1	LMEPGTYDYLDKITGDLVR Oxidation (M)
395 - 405	1254.63	1253.63	1253.54	0.09	0	TGHEMCGGHIR
395 - 405	1270.56	1269.56	1269.53	0.02	0	TGHEMCGGHIR Oxidation (M)
406 - 424	2062.93	2061.93	2061.94	-0.01	0	GMFGFFFTAGPVHNFGDAK Oxidation (M)
437 - 466	3255.44	3254.43	3254.54	-0.11	0	GMLEEGVYLAPSQFEAGFTSLAHTSQDIEK
437 - 466	3271.43	3270.43	3270.54	-0.11	0	GMLEEGVYLAPSQFEAGFTSLAHTSQDIEK Oxidation (M)

Spot 1863

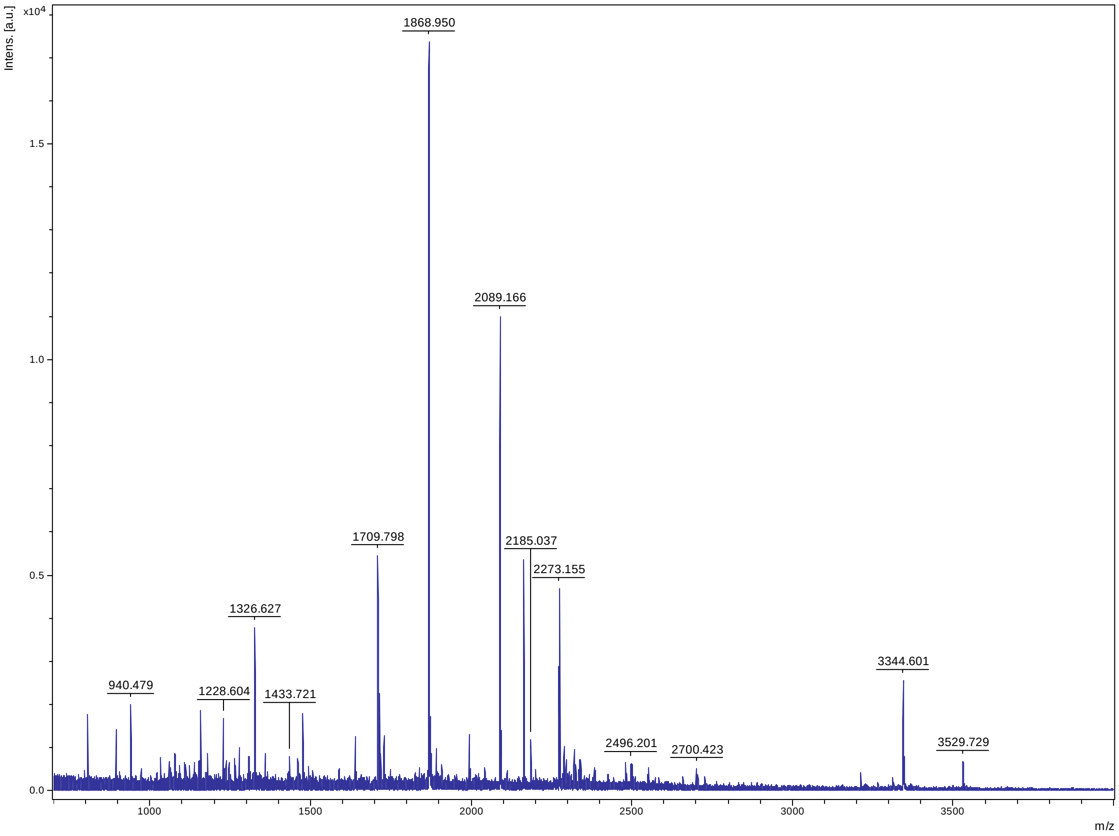


Match to: gi|15289940; Score: 140

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 30	2992.43	2991.43	2991.33	0.09	1	ADGEDIQPLVCDNGTGMVKAGFAGDDAPR Oxidation (M)
21 - 30	976.45	975.45	975.44	0.01	0	AGFAGDDAPR
31 - 41	1198.70	1197.70	1197.70	0.00	0	AVFPSIVGRPR
71 - 86	1932.89	1931.89	1931.87	0.02	0	YPIEHGIVSNWDDMEK
71 - 86	1948.88	1947.88	1947.87	0.01	0	YPIEHGIVSNWDDMEK Oxidation (M)
87 - 97	1515.75	1514.75	1514.74	0.01	0	IWHHTFYNELR
98 - 115	1954.07	1953.07	1953.06	0.01	0	VAPEEHPVLLTEAPLNPK
150 - 179	3151.64	3150.64	3150.63	0.00	0	TTGIVLDSGDGVSHTVPIYEGYALPHAILR
180 - 193	1547.75	1546.75	1546.80	-0.05	1	LDLAGRDLTDSLMK
199 - 208	1118.52	1117.51	1117.50	0.01	0	GYSFTTSAER
218 - 233	1855.93	1854.93	1854.93	0.01	0	LAYVALDYEQELETAK
241 - 256	1763.88	1762.88	1762.87	0.01	0	SYELPDGQVITIGSER
293 - 314	2311.18	2310.18	2310.17	0.01	1	KDLYGNVVLSGGTTMFPGIADR
293 - 314	2327.18	2326.18	2326.16	0.01	1	KDLYGNVVLSGGTTMFPGIADR Oxidation (M)
294 - 314	2183.07	2182.07	2182.07	-0.00	0	DLYGNVVLSGGTTMFPGIADR
294 - 314	2199.08	2198.08	2198.07	0.01	0	DLYGNVVLSGGTTMFPGIADR Oxidation (M)
331 - 338	895.54	894.54	894.53	0.01	1	VVAPPERK
362 - 374	1487.67	1486.66	1486.67	-0.00	0	DEYDESGPAIVHR

Spot 1873

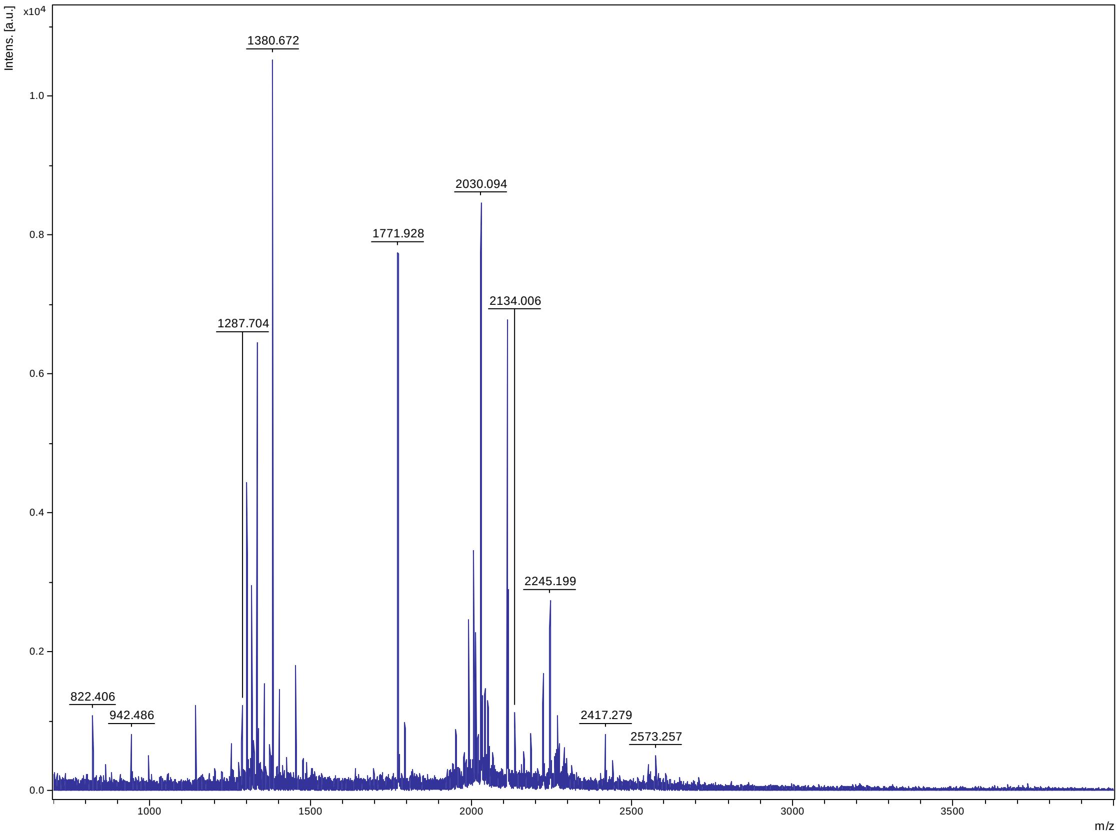


Match to: gi|77552725; Score: 238

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
50 - 61	1433.72	1432.72	1432.64	0.08	1	ELDEGKQTDQDR
56 - 63	1076.53	1075.53	1075.50	0.02	1	QTDQDRWK
64 - 78	1709.80	1708.80	1708.79	0.01	0	GLAYDISDDQQDITR
79 - 111	3529.73	3528.73	3528.72	0.01	1	GKGFVDSLFQAPTGDGTHEAVLSSYEYLSQGLR
81 - 111	3344.60	3343.60	3343.60	-0.00	0	GFVDSLFQAPTGDGTHEAVLSSYEYLSQGLR
139 - 147	1093.56	1092.56	1092.56	-0.01	0	NFMTLPNIK Oxidation (M)
148 - 158	1152.69	1151.68	1151.71	-0.02	0	VPLILGIWGGK
163 - 172	1228.60	1227.60	1227.60	0.01	0	SFQCELVFAK
173 - 195	2320.05	2319.05	2319.05	-0.01	0	MGINPIMMSAGELESGNAGEPAK Oxidation (M)
173 - 195	2336.06	2335.06	2335.05	0.01	0	MGINPIMMSAGELESGNAGEPAK 2 Oxidation (M)
201 - 209	1078.60	1077.60	1077.58	0.01	1	YREAADIIK
213 - 227	1712.74	1711.74	1711.75	-0.01	0	MCCLFINDLDAGAGR
213 - 227	1728.77	1727.76	1727.74	0.02	0	MCCLFINDLDAGAGR Oxidation (M)
264 - 287	2700.42	2699.42	2699.43	-0.01	1	EDNPRVPIIVTGNDFSTLYAPLIR
269 - 287	2089.17	2088.16	2088.16	0.00	0	VPIIVTGNDFSTLYAPLIR
294 - 300	940.48	939.48	939.46	0.02	0	FYWAPTR
294 - 303	1326.63	1325.62	1325.62	0.01	1	FYWAPTRDDR
309 - 323	1717.87	1716.87	1716.87	-0.00	1	GIFRTDNVPDEDIVK
324 - 340	1868.95	1867.95	1867.95	0.00	0	IVDSFPGQSIDFFGALR
343 - 349	895.42	894.42	894.41	0.01	0	VYDDEVR
351 - 363	1460.74	1459.74	1459.74	-0.00	1	WVSDTGVENIGKR
400 - 422	2496.20	2495.20	2495.20	0.00	1	RVQLAEQYLSEAALGDANSDAMK Oxidation (M)

Spot 1882

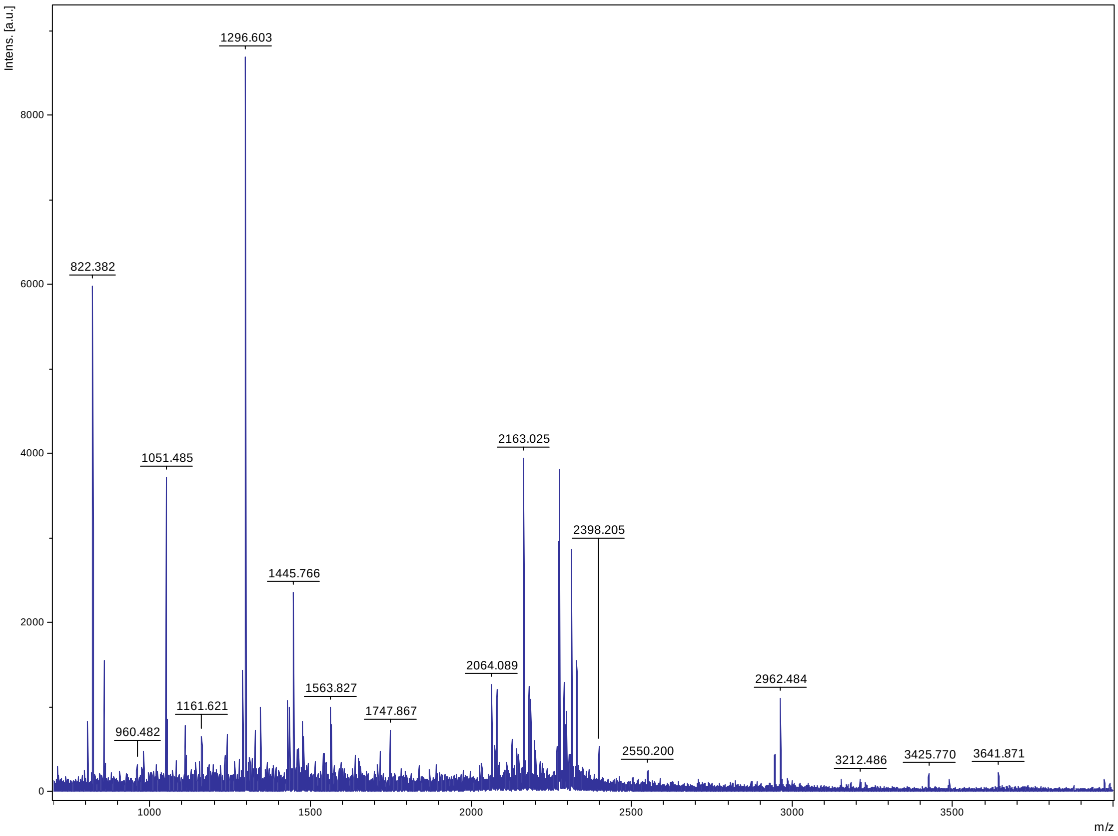


Match to: gi|38347227; Score: 128

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
5 - 16	1380.67	1379.67	1379.67	-0.00	0	SPYFVPESEGIR
17 - 26	942.49	941.48	941.49	-0.01	0	AGESPAAALR
28 - 47	2112.02	2111.01	2111.00	0.01	0	ILASPGAHQAPCCFDALGAR
69 - 87	1990.97	1989.97	1989.98	-0.02	0	LGLPDAGLISYGEMVDQGR
69 - 87	2006.98	2005.98	2005.98	-0.00	0	LGLPDAGLISYGEMVDQGR Oxidation (M)
163 - 174	1287.70	1286.70	1286.72	-0.02	1	KESGSDIVIIAR
179 - 189	1284.66	1283.65	1283.65	0.00	0	QAISIDEALWR Pyro-glu (N-term Q)
179 - 189	1301.67	1300.67	1300.68	-0.01	0	QAISIDEALWR
274 - 290	1771.93	1770.93	1770.93	-0.00	0	STGAPRPGSLPSFQEIK
291 - 297	822.41	821.40	821.40	0.00	0	DTLGFNR
304 - 321	2013.05	2012.04	2012.07	-0.03	0	QYATVQQAQPLSTNIVLR Pyro-glu (N-term Q)
304 - 321	2030.09	2029.09	2029.10	-0.00	0	QYATVQQAQPLSTNIVLR
333 - 344	1253.70	1252.70	1252.70	-0.01	0	INEGIPAGILEK
348 - 369	2223.23	2222.23	2222.19	0.04	0	AIPGLAGVNLTEILQGADQSQK
372 - 383	1373.69	1372.69	1372.69	-0.01	1	LLLDREDATGDR

Spot 1886

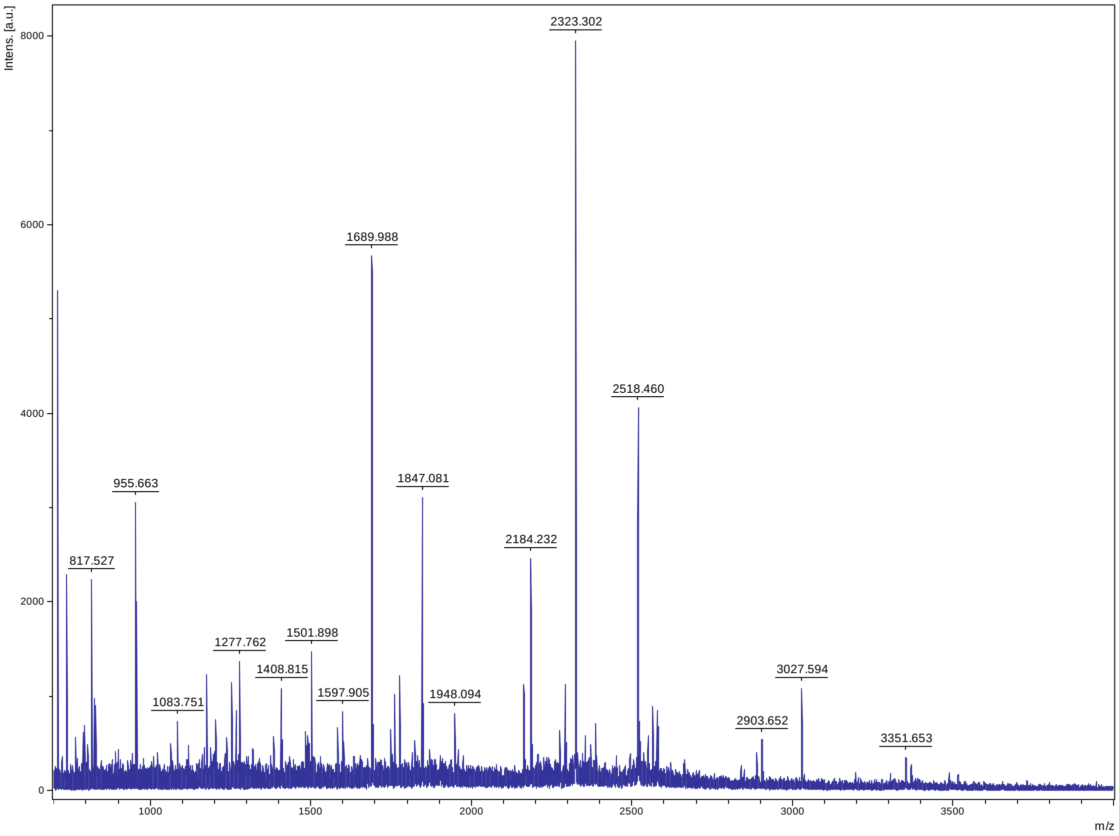


Match to: gi|78708994 Score: 137 Expect: 3.3e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
58 - 77	2064.0886	2063.0813	2063.1058	-0.0244	0	R.AAVLNRPGHLNALTTTMGAR.L	
58 - 77	2080.0872	2079.0799	2079.1007	-0.0208	0	R.AAVLNRPGHLNALTTTMGAR.L	Oxidation (M)
81 - 97	2125.9382	2124.9310	2124.8994	0.0315	0	K.FYMSWEDNPDIGFVMMK.G	Oxidation (M)
102 - 111	1051.4851	1050.4778	1050.4916	-0.0138	0	R.AFCAGGDVVR.L	Carbamidomethyl (C)
212 - 231	2180.0278	2179.0206	2179.0401	-0.0196	0	K.LNGVDMIALGLATHYSMSDR.L	Oxidation (M)
212 - 231	2196.0122	2195.0049	2195.0350	-0.0301	0	K.LNGVDMIALGLATHYSMSDR.L	2 Oxidation (M)
232 - 238	858.4661	857.4588	857.4606	-0.0018	0	R.LNLVDER.L	
239 - 265	2962.4836	2961.4764	2961.4859	-0.0095	0	R.LATLLTDDPSVIDTSLTHYGDLVYPDK.S	
239 - 271	3641.8708	3640.8636	3640.8624	0.0012	1	R.LATLLTDDPSVIDTSLTHYGDLVYPDKSSIVHR.L	
278 - 297	2312.0664	2311.0591	2311.0711	-0.0120	0	K.CFSLETVEEIVDAMEIEAAR.L	Carbamidomethyl (C)
278 - 297	2328.0559	2327.0486	2327.0660	-0.0174	0	K.CFSLETVEEIVDAMEIEAAR.L	Carbamidomethyl (C); Oxidation (M)
298 - 308	1289.6448	1288.6375	1288.6663	-0.0288	0	R.LNEDWSTLALK.R	
298 - 309	1445.7664	1444.7591	1444.7674	-0.0083	1	R.LNEDWSTLALKR.L	
330 - 339	1296.6030	1295.5958	1295.6180	-0.0222	0	R.YQTLDECLVR.E	Carbamidomethyl (C)
352 - 357	822.3820	821.3747	821.3820	-0.0073	0	K.FSHEFR.E	

Spot 1898

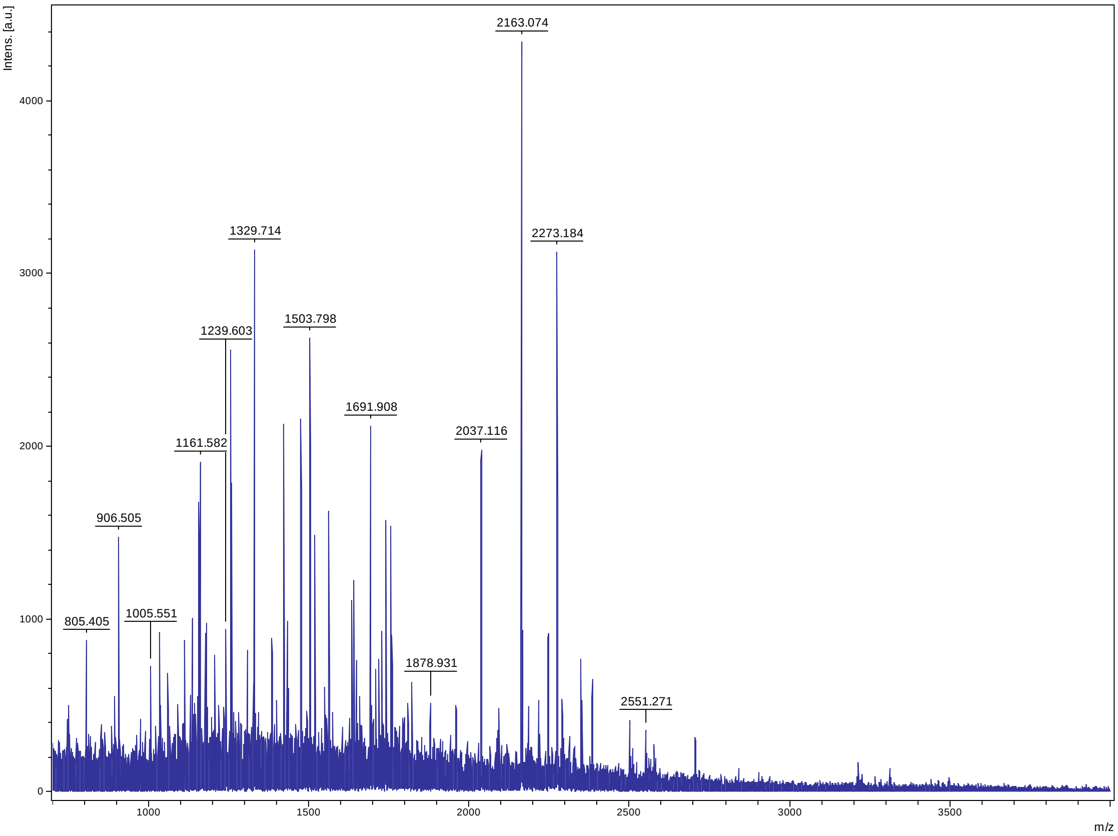


Match to: gi|21263611 Score: 78 Expect: 0.00097

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 14	1598.8328	1597.8255	1597.7969	0.0286	1	-.MAMWRAAAGHLLGR.A	Acetyl (N-term); Oxidation (M)
37 - 58	2308.1272	2307.1199	2307.0952	0.0247	1	K.GGEYADKNPNFVGCVEGALGIR.E	Acetyl (N-term)
37 - 58	2323.1269	2322.1196	2322.1062	0.0135	1	K.GGEYADKNPNFVGCVEGALGIR.E	Carbamidomethyl (C)
44 - 58	1602.7962	1601.7889	1601.7983	-0.0094	0	K.NPNFVGCVEGALGIR.E	Carbamidomethyl (C)
65 - 83	2184.0622	2183.0549	2183.0494	0.0055	1	K.GHHYIVTDDKEGLNSELEK.H	
84 - 105	2563.2269	2562.2196	2562.2689	-0.0493	0	K.HIEDMHVLITTPFHPAYVSAER.I	
162 - 183	2518.2542	2517.2469	2517.2552	-0.0083	0	R.NFLPGYQQVVHGEWNVAGIAYR.A	
208 - 220	1689.8906	1688.8833	1688.8457	0.0377	0	R.LKPFNCNLLYHDR.L	Carbamidomethyl (C)
223 - 234	1383.8295	1382.8222	1382.7292	0.0930	1	K.IDPELEKEIGAK.Y	Acetyl (N-term)
230 - 245	1821.9570	1820.9497	1820.8866	0.0632	1	K.EIGAKYEEDLDAMLPK.C	
246 - 258	1501.8194	1500.8121	1500.7858	0.0264	0	K.CDVIVINTPLTEK.T	Carbamidomethyl (C)
273 - 282	1083.6317	1082.6244	1082.6560	-0.0315	1	K.KGVIIVNNAR.G	
274 - 282	955.5155	954.5082	954.5610	-0.0528	0	K.GVIIVNNAR.G	
321 - 341	2354.1638	2353.1565	2353.1307	0.0258	0	R.YMPNHAMTPHISGTTIDAQLR.Y	
321 - 341	2386.0924	2385.0851	2385.1205	-0.0354	0	R.YMPNHAMTPHISGTTIDAQLR.Y	2 Oxidation (M)
342 - 352	1238.6466	1237.6393	1237.6125	0.0269	1	R.YAAGVKDMLDR.Y	
342 - 352	1254.6144	1253.6071	1253.6074	-0.0003	1	R.YAAGVKDMLDR.Y	Oxidation (M)
353 - 367	1846.9783	1845.9710	1845.9301	0.0410	1	R.YFKGEDFPVQNYIVK.E	
356 - 367	1408.7394	1407.7321	1407.7034	0.0288	0	K.GEDFPVQNYIVK.E	
368 - 376	1023.4459	1022.4386	1022.4669	-0.0282	0	K.EGQLASQYQ.-	

Spot 1908



Match to: gi|37700305; Score: 167

Matched peptides:

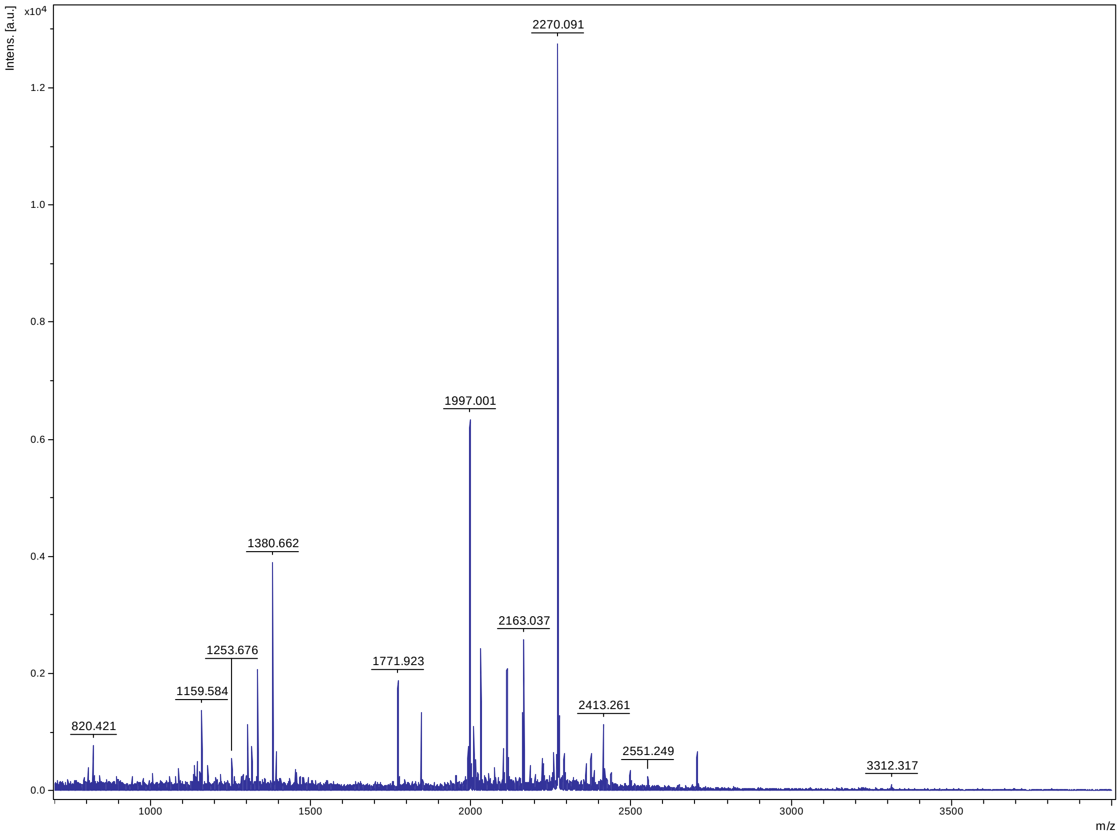
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
7 - 18	1329.71	1328.71	1328.72	-0.01	0	VSIAHQTSFALR
19 - 35	1503.80	1502.80	1502.80	0.00	0	LAAALSSPAHPAGGAGR
138 - 151	1517.75	1516.75	1516.75	-0.00	0	AAEVASQVNSWVEK
159 - 171	1421.72	1420.72	1420.73	-0.01	0	EILPPGSVDHTTR
172 - 181	1137.65	1136.64	1136.66	-0.02	0	LVLGNALYFK
182 - 192	1239.60	1238.60	1238.59	0.01	1	GAWTEKFDASK
195 - 204	1130.55	1129.54	1129.54	0.00	0	DGEFHLLDGK
216 - 226	1384.74	1383.74	1383.74	-0.00	1	KQYILSYDNLK
217 - 226	1256.64	1255.64	1255.64	-0.01	0	QYILSYDNLK
230 - 238	1005.55	1004.55	1004.49	0.06	0	LPYQQGGDK
230 - 239	1161.58	1160.58	1160.59	-0.01	1	LPYQQGGDKR
261 - 270	1205.59	1204.59	1204.60	-0.01	0	LNSEPEFLEK
276 - 283	906.51	905.50	905.50	0.01	0	QVTVGQFK
325 - 334	1177.60	1176.60	1176.63	-0.03	0	NLFVSSVFHK
335 - 357	2349.22	2348.22	2348.19	0.03	0	SFVEVNEEGTEAAAATAAVITLR

Match to: gi|21685576; Score: 73

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
99 - 112	1561.77	1560.76	1560.77	-0.00	1	AVAFDEIDKAPEEK
115 - 130	1759.91	1758.91	1758.93	-0.02	1	GITIATAHVEYETAKR
211 - 227	2037.12	2036.11	2036.10	0.02	1	ELLSFYKFPGDEIPIIR
218 - 227	1156.62	1155.62	1155.63	-0.01	0	FPGDEIPIIR
249 - 262	1632.79	1631.78	1631.79	-0.00	0	LMDAVDEYIPDPVR
249 - 262	1648.78	1647.78	1647.78	-0.00	0	LMDAVDEYIPDPVR Oxidation (M)
267 - 281	1738.88	1737.88	1737.88	0.00	0	SFLMPIEDVFSIQGR
267 - 281	1754.89	1753.88	1753.87	0.01	0	SFLMPIEDVFSIQGR Oxidation (M)
296 - 312	1725.91	1724.91	1724.92	-0.01	0	TGEDVEILGLTPSGPLK
313 - 323	1256.64	1255.64	1255.65	-0.01	1	TTVTGVEMFKK Oxidation (M)
324 - 339	1691.91	1690.91	1690.90	0.01	0	ILDHGEAGDNVGLLLR

Spot 1913



Match to: gi|38347227; Score: 126

Matched peptides:

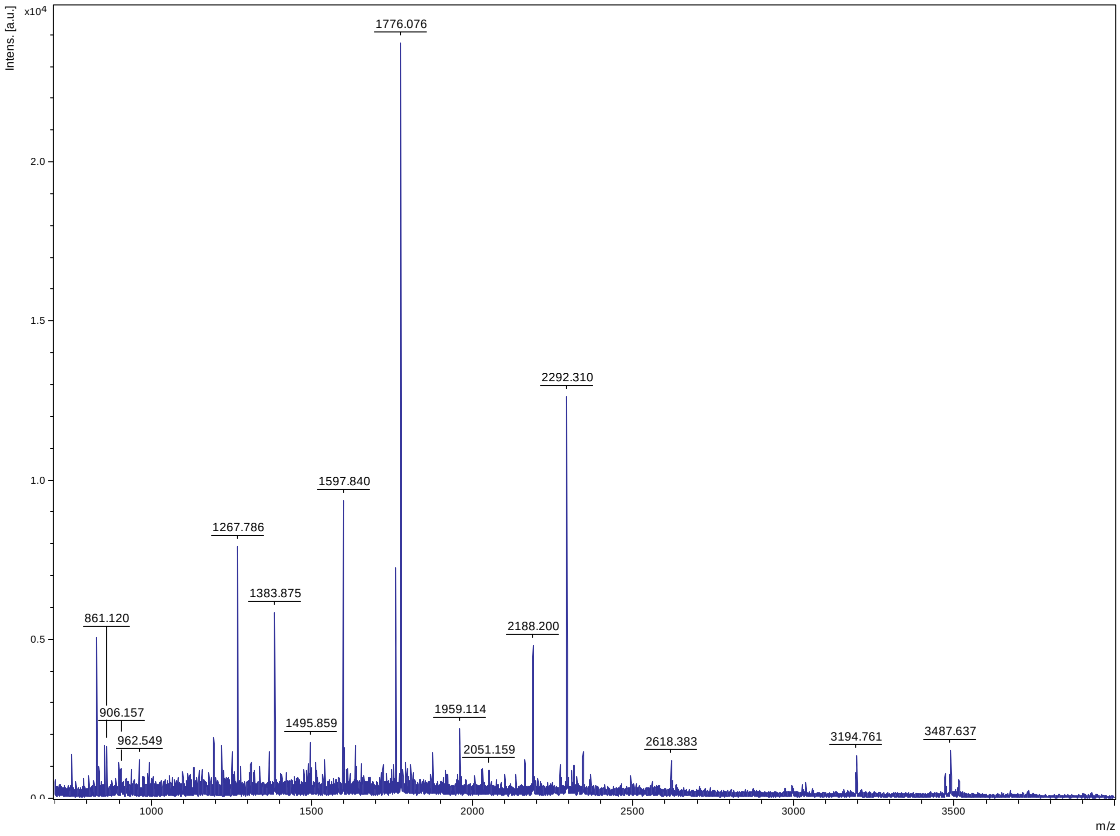
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
5 - 16	1380.66	1379.66	1379.67	-0.01	0	SPYFVPESEGIR
28 - 47	2112.00	2111.00	2111.00	-0.01	0	ILASPGAHQAPCCFDALGAR
69 - 87	1990.96	1989.96	1989.98	-0.02	0	LGLPDAGLISYGEMVDQGR
69 - 87	2006.96	2005.96	2005.98	-0.02	0	LGLPDAGLISYGEMVDQGR Oxidation (M)
117 - 135	2009.99	2008.99	2008.99	-0.00	0	GYINAGFAGIMLEDQVAPK Oxidation (M)
164 - 174	1159.58	1158.58	1158.62	-0.04	0	ESGSDIVIIAR
179 - 189	1301.66	1300.66	1300.68	-0.02	0	QAISIDEALWR
274 - 290	1771.92	1770.92	1770.93	-0.01	0	STGAPRPGSLPSFQEIK
291 - 297	822.38	821.38	821.40	-0.02	0	DTLGFNR
304 - 321	2013.02	2012.02	2012.07	-0.05	0	QYATVQQAQPLSTNIVLR Pyro-glu (N-term Q)
304 - 321	2030.07	2029.07	2029.10	-0.03	0	QYATVQQAQPLSTNIVLR
333 - 344	1253.68	1252.67	1252.70	-0.03	0	INEGIPAGILEK
345 - 369	2551.25	2550.25	2550.40	-0.16	1	ISKAIPGLAGVNLTEILQGADQSQK
348 - 369	2223.18	2222.18	2222.19	-0.01	0	AIPGLAGVNLTEILQGADQSQK

Match to: gi|50918915; Score: 83

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
116 - 136	1997.00	1996.00	1996.01	-0.01	0	AHAPAAVASGAVVVDNSSAFR
137 - 157	2375.15	2374.15	2374.17	-0.02	0	MDPEVPLVIPEVNPEAMAHVR 2 Oxidation (M)
190 - 210	2100.98	2099.98	2099.99	-0.01	0	MVVSTYQAASGAGAAAMEELK Oxidation (M)
190 - 210	2116.97	2115.96	2115.98	-0.02	0	MVVSTYQAASGAGAAAMEELK 2 Oxidation (M)
211 - 220	1086.59	1085.58	1085.61	-0.02	0	LQTQEVLAGK
269 - 275	820.42	819.42	819.43	-0.01	0	VTATCIR
281 - 300	2270.09	2269.09	2269.10	-0.01	0	AHAESVNLQFEKPLDEDTAR
305 - 315	1159.58	1158.58	1158.59	-0.01	0	AAEGVTIIDDR
320 - 336	1844.92	1843.92	1843.93	-0.01	1	FPTPLEVSDKDDVAVGR
348 - 359	1392.69	1391.69	1391.69	-0.00	0	GLDIFVCGDQIR

Spot 1914

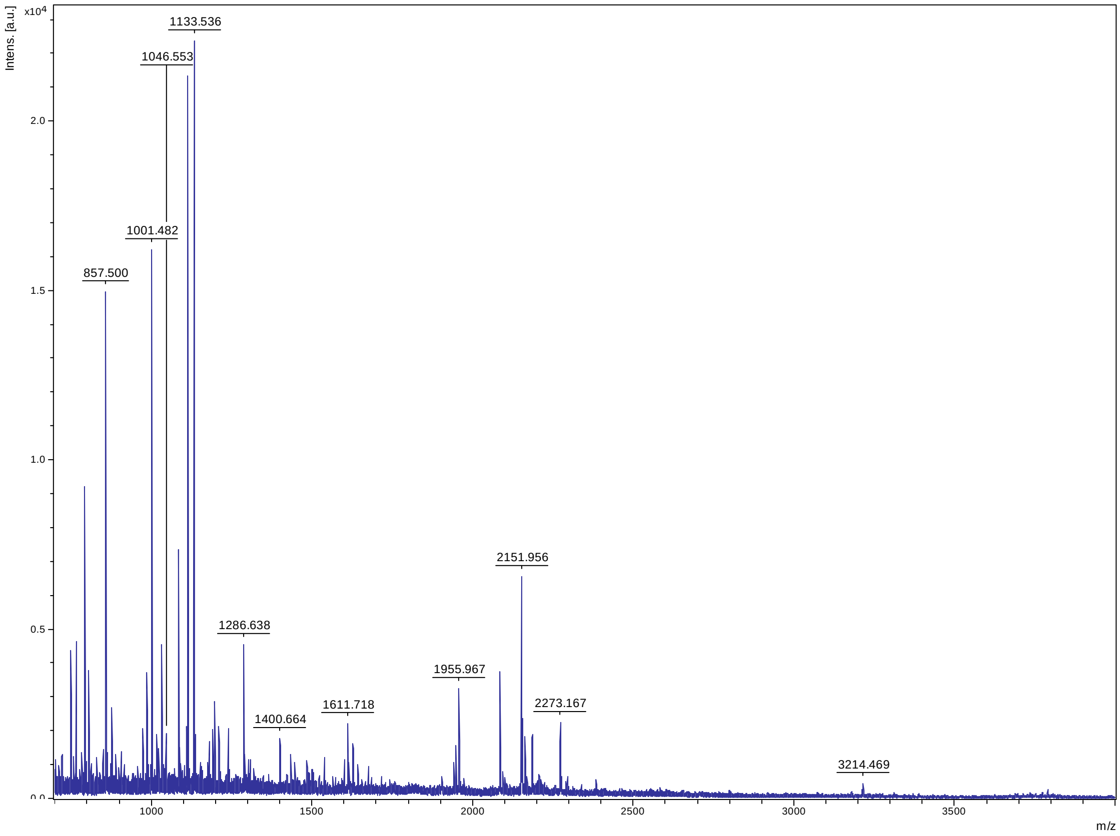


Match to: gi|19387272 Score: 82 Expect: 0.00044

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
75 - 90	1776.0762	1775.0689	1774.9617	0.1072	0	K.IIAEYIWVGGTGIDLR.S	
109 - 139	3487.6372	3486.6299	3486.6367	-0.0068	1	K.WNYDGSSTGQAPGEDSEVILYPQAIFKDPFR.G	
140 - 163	2618.3826	2617.3753	2617.2628	0.1125	1	R.GGNNILVMCDTYTPAGEPIPTNKR.N	Carbamidomethyl (C)
166 - 174	962.5491	961.5418	961.4869	0.0549	0	R.AAQVFSDPK.V	
175 - 193	2292.3103	2291.3030	2291.1949	0.1081	0	K.VVSQVPWFGIEQEYTLLQR.D	
280 - 308	3194.7610	3193.7537	3193.7896	-0.0359	1	R.ITEQAGVVLTLDPKPIQADSVICFVIRLR.L	
309 - 318	1218.8131	1217.8058	1217.7166	0.0893	1	R.LILQITKSMR.E	Oxidation (M)
316 - 327	1367.7574	1366.7502	1366.6550	0.0951	1	K.SMREDGGFEVIK.K	
319 - 327	993.6176	992.6103	992.4814	0.1289	0	R.EDGGFEVIK.K	
329 - 336	899.6486	898.6413	898.5600	0.0814	0	K.AILNLSLR.H	
337 - 350	1597.8398	1596.8326	1596.7280	0.1045	0	R.HDLHISAYGEGNER.R	
337 - 351	1753.9487	1752.9415	1752.8291	0.1123	1	R.HDLHISAYGEGNERR.L	
351 - 371	2344.2766	2343.2693	2343.1719	0.0974	1	R.RLTGLHETASIDNFSWGVANR.G	
352 - 371	2188.2000	2187.1927	2187.0708	0.1219	0	R.LTGLHETASIDNFSWGVANR.G	
385 - 392	937.5633	936.5560	936.4664	0.0896	1	K.GKGYLEDR.R	

Spot 1932

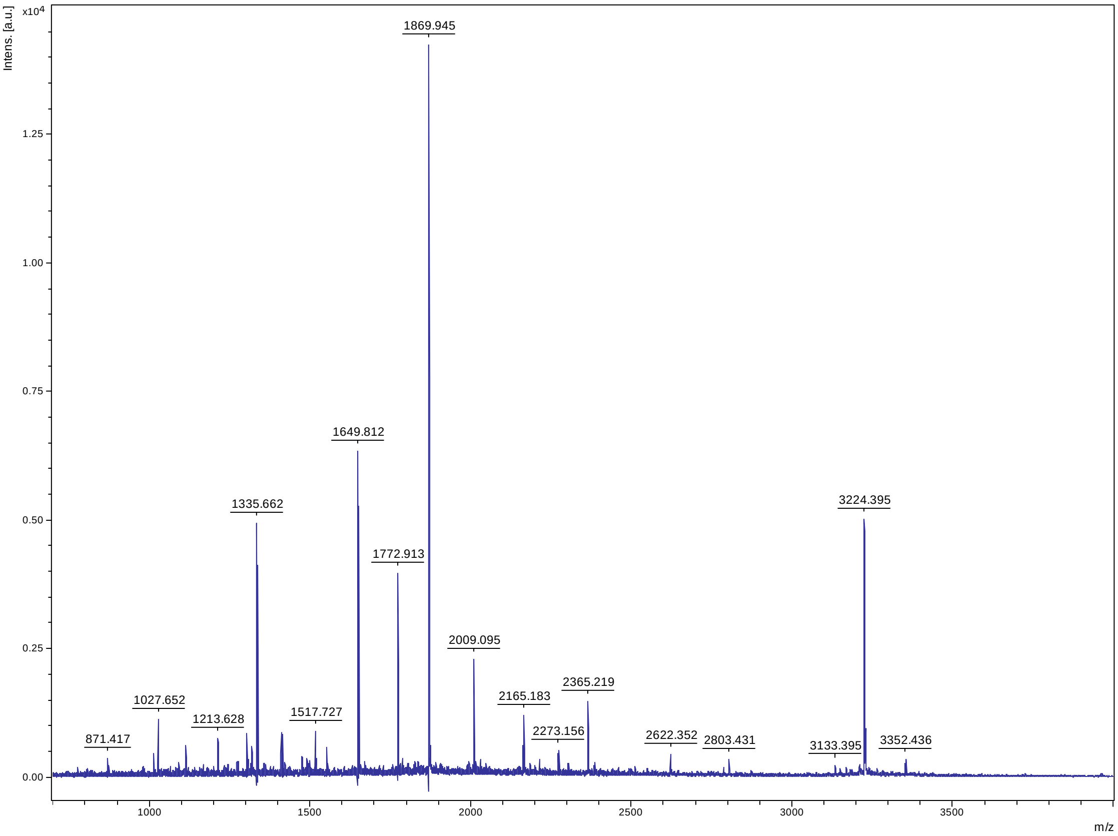


Match to: gi|37535646 Score: 164 Expect: 2.7e-12

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 14	1433.6928	1432.6855	1432.6729	0.0127	1	-.MARASSSSSPPSPR.L	Oxidation (M)
85 - 97	1302.6374	1301.6301	1301.6826	-0.0525	0	R.ETADALVNTGLAK.L	
98 - 114	2151.9112	2150.9039	2150.9367	-0.0328	0	K.LGYQYVNIDDCWAEYSR.D	Carbamidomethyl (C)
145 - 159	1600.6897	1599.6824	1599.7198	-0.0374	0	K.LGIYSDAGSQTCSNK.M	Carbamidomethyl (C)
160 - 172	1484.6451	1483.6378	1483.6613	-0.0234	0	K.MPGSLDHEEQDVK.T	
173 - 183	1286.6078	1285.6005	1285.6342	-0.0337	0	K.TFASWGVDYLK.Y	
173 - 192	2295.1205	2294.1132	2294.0062	0.1071	1	K.TFASWGVDYLKYDNCNDAGR.S	
184 - 192	1084.3681	1083.3608	1083.4039	-0.0431	0	K.YDNCNDAGR.S	Carbamidomethyl (C)
198 - 206	1133.4997	1132.4924	1132.5005	-0.0081	1	R.YTRMSNAMK.T	2 Oxidation (M)
211 - 221	1400.6243	1399.6170	1399.6594	-0.0424	0	K.NIFFSLCEWGK.E	Carbamidomethyl (C)
222 - 230	1001.4109	1000.4036	1000.4726	-0.0690	0	K.ENPATWAGR.M	
237 - 251	1611.6698	1610.6625	1610.6995	-0.0369	0	R.TTGDIADNWGSMTSR.A	
237 - 251	1627.6868	1626.6795	1626.6944	-0.0149	0	R.TTGDIADNWGSMTSR.A	Oxidation (M)
297 - 306	1113.5511	1112.5438	1112.6012	-0.0574	0	K.APLLIGCDVR.S	Carbamidomethyl (C)
314 - 334	2185.0564	2184.0491	2184.1385	-0.0894	0	K.NILSNSEVIAVNQDSLGVQGK.K	
336 - 353	1955.9392	1954.9319	1954.9496	-0.0177	0	K.VQSDNGLEVWAGPLSNNR.K	
336 - 354	2084.0252	2083.0179	2083.0446	-0.0267	1	K.VQSDNGLEVWAGPLSNNRK.A	
354 - 361	985.5223	984.5150	984.5868	-0.0718	1	R.KAVVLWNR.Q	

Spot 1939

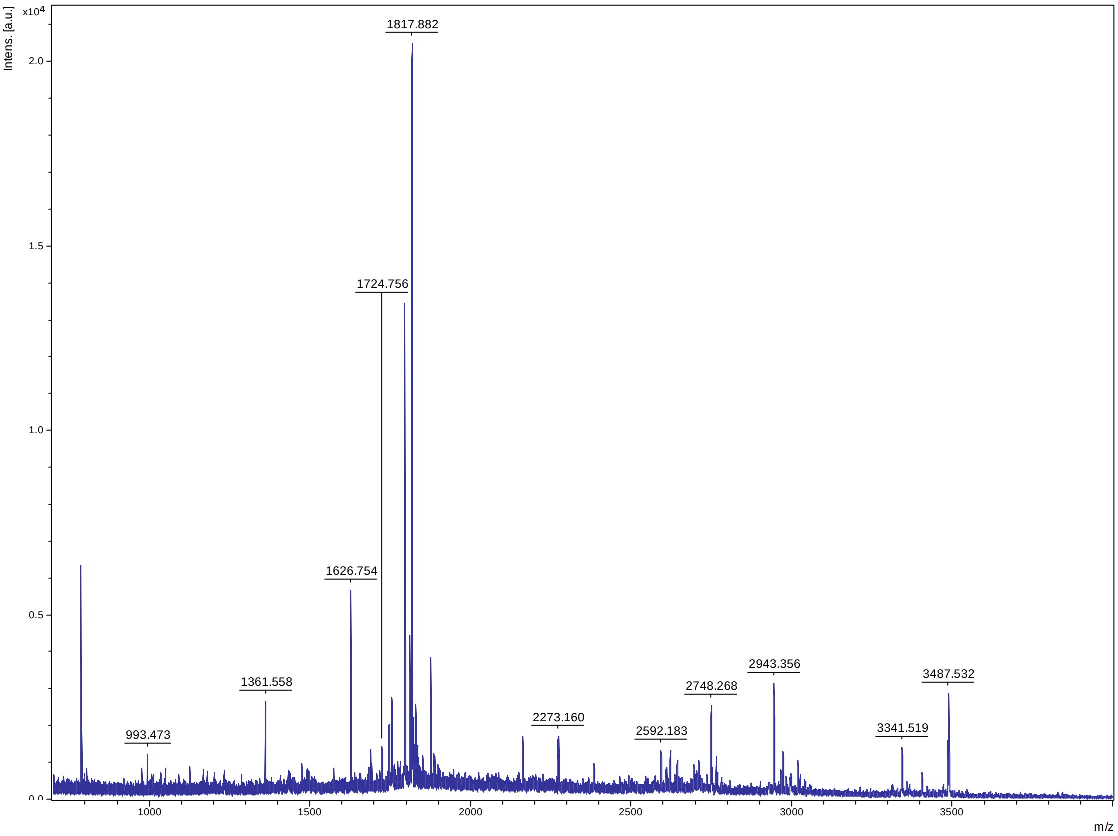


Match to: gi|51964178 Score: 182 Expect: 4.2e-14

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
33 - 42	1114.5796	1113.5723	1113.6029	-0.0306	0	K.LNNAILAEEK.H	
43 - 53	1303.6129	1302.6056	1302.6278	-0.0222	0	K.HLPMYDELASK.G	
43 - 53	1319.6297	1318.6224	1318.6227	-0.0003	0	K.HLPMYDELASK.G	Oxidation (M)
54 - 69	1649.8290	1648.8217	1648.8168	0.0049	0	K.GNVEYIAGGATQNSIR.V	
70 - 89	2215.0569	2214.0496	2214.0271	0.0225	0	R.VAQWMLQTPGATSYMGCIGK.D	Carbamidomethyl (C); Oxidation (M)
130 - 142	1410.6760	1409.6687	1409.6972	-0.0285	0	R.SLVANLSAANCYK.S	Carbamidomethyl (C)
148 - 157	1213.6213	1212.6140	1212.6502	-0.0362	0	K.KPENWALVEK.A	
209 - 224	1869.9531	1868.9458	1868.9308	0.0150	0	K.VLPFVDYIFGNETEAR.I	
229 - 243	1772.9227	1771.9154	1771.9104	0.0050	1	K.VRGWETENVEEIALK.I	
231 - 243	1517.7443	1516.7370	1516.7409	-0.0039	0	R.GWETENVEEIALK.I	
244 - 253	1013.5438	1012.5365	1012.5917	-0.0551	0	K.ISQLPLASGK.Q	
256 - 276	2165.1754	2164.1681	2164.1851	-0.0170	1	K.RIAVITQGADPVVVAEDGQVK.T	
257 - 276	2009.0947	2008.0874	2008.0840	0.0034	0	R.IAVITQGADPVVVAEDGQVK.T	
277 - 285	1027.6067	1026.5994	1026.6477	-0.0483	0	K.TFPVILLPK.E	
286 - 310	2621.2833	2620.2760	2620.3496	-0.0735	1	K.EKLVDTNGAGDAFVGGFLSQLVQQK.S	
288 - 310	2364.2089	2363.2016	2363.2120	-0.0104	0	K.LVDTNGAGDAFVGGFLSQLVQQK.S	
318 - 329	1335.6697	1334.6624	1334.6765	-0.0140	0	K.AGCYAANVIIQR.S	Carbamidomethyl (C)
330 - 341	1414.5732	1413.5659	1413.5871	-0.0211	0	R.SGCTYPEKPDFN.-	Carbamidomethyl (C)

Spot 1942

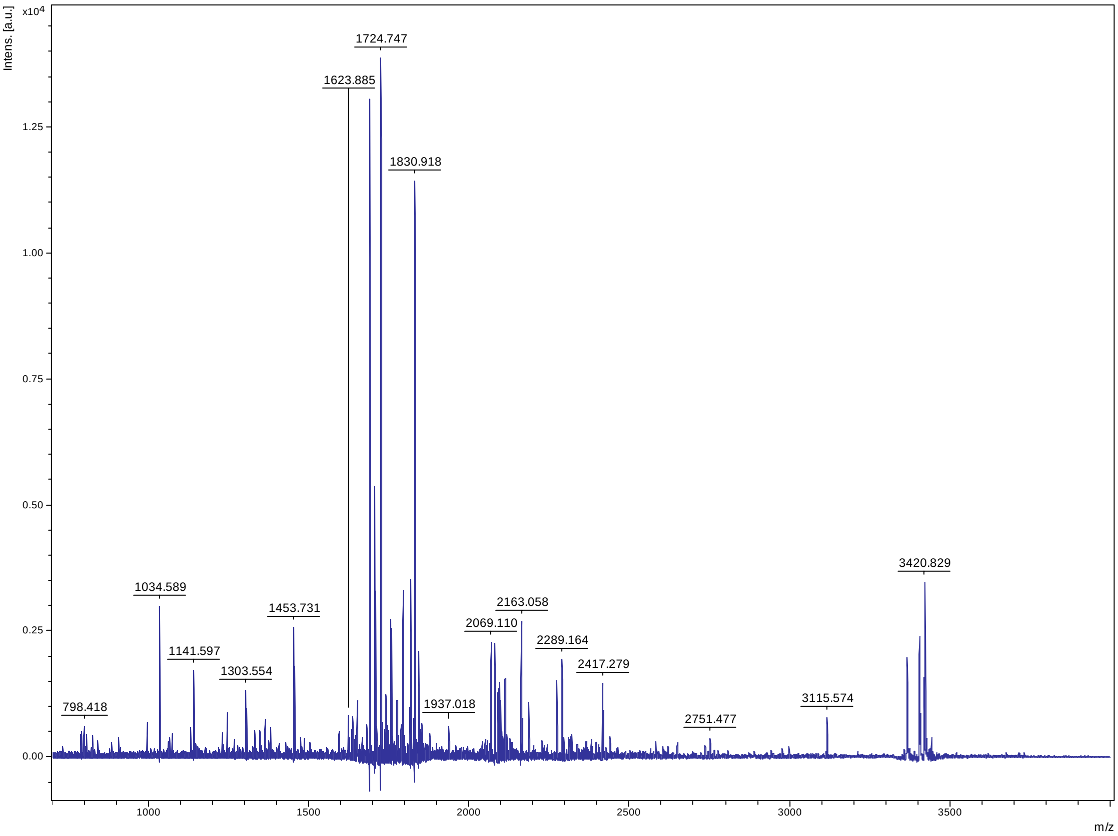


Match to: gi|50912511 Score: 80 Expect: 0.00069

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 18	1875.9110	1874.9037	1874.9473	-0.0435	0	M.ASLTDLVNLNLSDTTEK.I	Acetyl (N-term)
19 - 34	1793.8319	1792.8246	1792.9181	-0.0935	0	K.IIAEYIWIGGSGMDLR.S	
19 - 34	1809.8631	1808.8558	1808.9130	-0.0572	0	K.IIAEYIWIGGSGMDLR.S	Oxidation (M)
53 - 79	2972.4615	2971.4542	2971.3875	0.0667	0	K.WNYDGSSTGQAPGEDSEVILYPQAIFK.D	
84 - 106	2592.2012	2591.1939	2591.2182	-0.0242	1	R.KGNNILVMCDCYTPAGEPIPTNK.R	2 Carbamidomethyl (C)
84 - 106	2608.2008	2607.1935	2607.2131	-0.0196	1	R.KGNNILVMCDCYTPAGEPIPTNK.R	2 Carbamidomethyl (C); Oxidation (M)
85 - 106	2465.1243	2464.1170	2464.1072	0.0098	0	K.GNNILVMCDCYTPAGEPIPTNK.R	Acetyl (N-term); Carbamidomethyl (C); Oxidation (M)
85 - 107	2620.2580	2619.2507	2619.2243	0.0264	1	K.GNNILVMCDCYTPAGEPIPTNKR.H	2 Carbamidomethyl (C)
85 - 107	2636.2410	2635.2337	2635.2192	0.0145	1	K.GNNILVMCDCYTPAGEPIPTNKR.H	2 Carbamidomethyl (C); Oxidation (M)
113 - 137	2943.4646	2942.4573	2942.4225	0.0348	0	K.IFSSPEVASEEPWYGIEQEYTLLQK.D	
224 - 255	3341.6921	3340.6848	3340.6727	0.0121	0	R.ITEIAGVVVSFDPKPIPGDWNGAGAHTNYSTK.S	
296 - 311	1817.7951	1816.7878	1816.8492	-0.0614	0	R.HETADINTFSWGVANR.G	
333 - 356	2766.3921	2765.3848	2765.3768	0.0080	0	R.RPASNMDPYIVTSMIAETTIIWKP.-	2 Oxidation (M)

Spot 1944

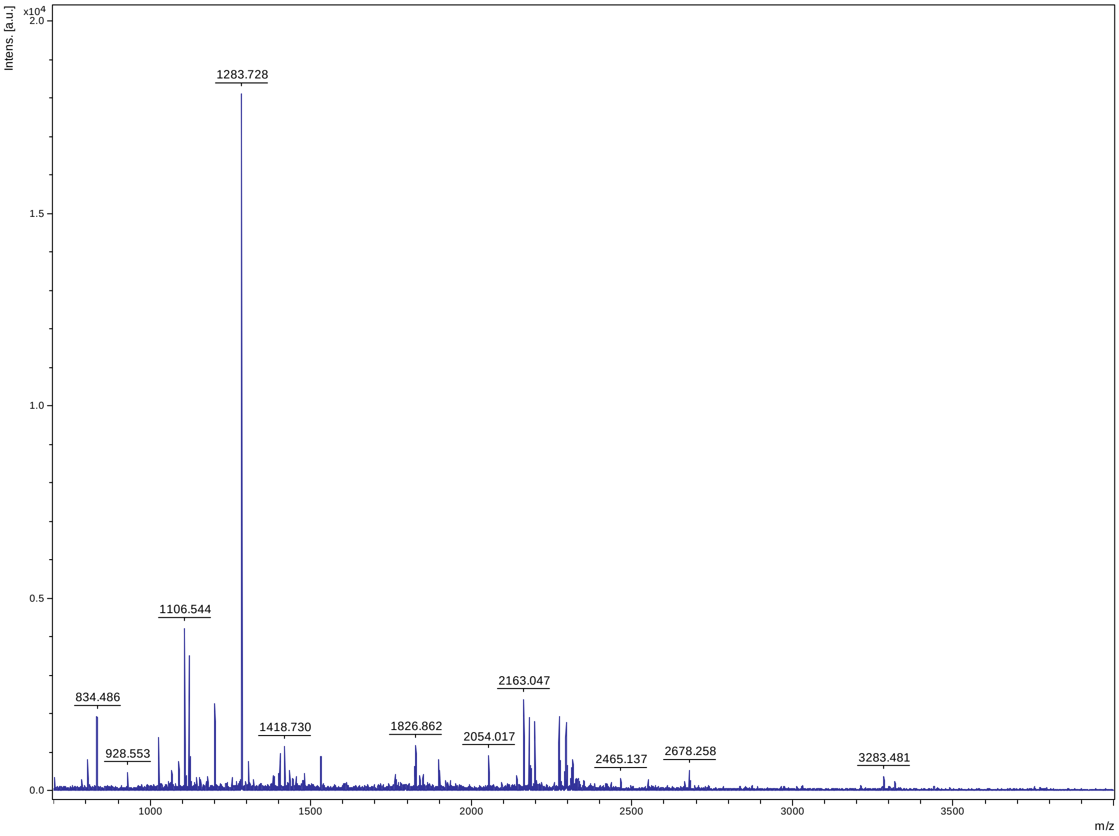


Match to: gi|50941315 Score: 83 Expect: 0.00036

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 34	3404.5669	3403.5596	3403.5655	-0.0059	0	M.GSTAADMAAAADEEACMYALQLASSSILPMTLK.N Carbamidomethyl (C); Oxidation (M)
35 - 56	2069.1256	2068.1183	2068.1163	0.0020	0	K.NAIELGLLETLQSAAVAGGGGK.A
87 - 95	1034.4477	1033.4404	1033.5920	-0.1516	0	R.LLASYNVVR.C
139 - 148	1331.6117	1330.6044	1330.6631	-0.0587	0	K.VLMESWYYLK.D
139 - 148	1347.6334	1346.6261	1346.6580	-0.0319	0	K.VLMESWYYLK.D Oxidation (M)
149 - 160	1245.5716	1244.5643	1244.6400	-0.0757	0	K.DAVLDGGIPFNK.A
161 - 175	1689.7427	1688.7354	1688.7252	0.0102	0	K.AYGMTAFEYHGTDAR.F
161 - 175	1705.7362	1704.7289	1704.7202	0.0088	0	K.AYGMTAFEYHGTDAR.F Oxidation (M)
231 - 262	3420.6189	3419.6116	3419.6607	-0.0491	0	R.GINYDLPHVISEAPPFPGVEHVGGDMFASVPR.G Oxidation (M)
271 - 283	1724.7904	1723.7831	1723.7525	0.0306	0	K.WILHDWSDEHCAR.L Carbamidomethyl (C)
287 - 297	1303.5343	1302.5270	1302.5663	-0.0392	0	K.NCYDALPEHGK.V Carbamidomethyl (C)
287 - 314	3115.4101	3114.4028	3114.4749	-0.0721	1	K.NCYDALPEHGKVVVVECVLPESSDATAR.E 2 Carbamidomethyl (C)
298 - 314	1773.8005	1772.7932	1772.8978	-0.1046	0	K.VVVVECVLPESSDATAR.E
298 - 314	1815.8950	1814.8877	1814.9083	-0.0206	0	K.VVVVECVLPESSDATAR.E Acetyl (N-term)
298 - 314	1830.9491	1829.9418	1829.9192	0.0226	0	K.VVVVECVLPESSDATAR.E Carbamidomethyl (C)
315 - 333	2080.0409	2079.0336	2079.0029	0.0307	0	R.EQGVFHVDMIMLAHNPGGK.E
315 - 333	2096.0041	2094.9968	2094.9978	-0.0010	0	R.EQGVFHVDMIMLAHNPGGK.E Oxidation (M)
315 - 333	2112.0246	2111.0173	2110.9928	0.0246	0	R.EQGVFHVDMIMLAHNPGGK.E 2 Oxidation (M)
315 - 335	2365.1686	2364.1613	2364.1466	0.0147	1	R.EQGVFHVDMIMLAHNPGGKER.Y
315 - 335	2439.2253	2438.2180	2438.1470	0.0710	1	R.EQGVFHVDMIMLAHNPGGKER.Y Acetyl (N-term); 2 Oxidation (M)

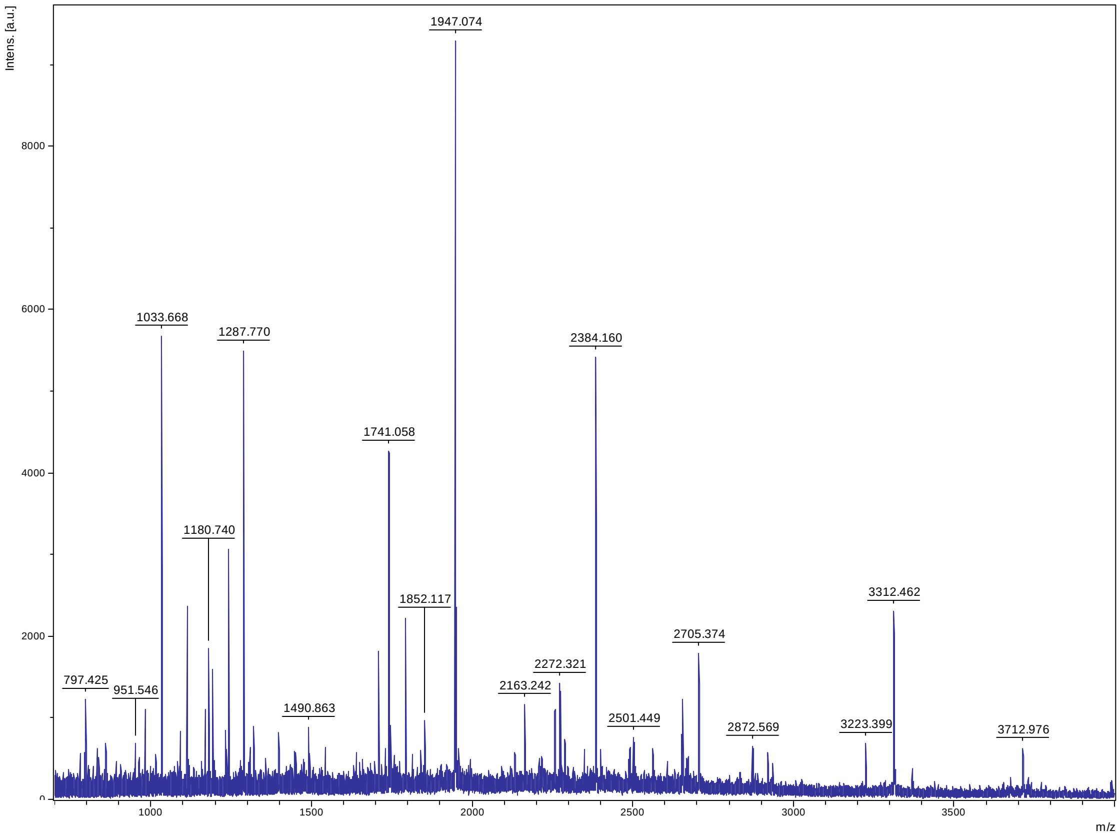
Spot 1948



Match to: gi|108885236 Score: 170 Expect: 1.3e-12

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
18 - 37	2295.1836	2294.1763	2294.1477	12	0	K.EHAMDPRPEAIIQSYKPANK.L	
18 - 37	2311.1554	2310.1481	2310.1426	2	0	K.EHAMDPRPEAIIQSYKPANK.L	Oxidation (M)
40 - 54	1444.7782	1443.7709	1443.7682	2	1	K.DKVAIVTGGDSGIGR.A	
42 - 54	1201.6617	1200.6544	1200.6463	7	0	K.VAIVTGGDSGIGR.A	
74 - 85	1404.6630	1403.6557	1403.6528	2	1	K.GQEEKDAEETLR.A	
94 - 113	2179.9760	2178.9688	2178.9674	1	1	R.TGAKDPMAIPADLGYDDNCR.K	
94 - 113	2195.9714	2194.9642	2194.9623	1	1	R.TGAKDPMAIPADLGYDDNCR.K	Oxidation (M)
98 - 113	1822.7679	1821.7606	1821.7662	-3	0	K.DPMAIPADLGYDDNCR.K	
157 - 167	1384.7369	1383.7296	1383.6533	55	0	R.TNIFSYFFMSK.H	
157 - 167	1400.6604	1399.6531	1399.6482	3	0	R.TNIFSYFFMSK.H	Oxidation (M)
177 - 197	2054.0170	2053.0097	2053.0011	4	1	R.RGGAGAGGCSIINTSSINAYK.G	
178 - 197	1897.9043	1896.8970	1896.9000	-2	0	R.GGAGAGGCSIINTSSINAYK.G	
201 - 209	1025.5511	1024.5438	1024.5441	-0	0	K.TLLDYTATK.G	
210 - 217	834.4861	833.4789	833.4759	4	0	K.GAIVAFTR.A	
218 - 229	1283.7278	1282.7206	1282.7245	-3	0	R.ALALQLAEEGIR.V	
230 - 251	2293.1960	2292.1887	2292.2154	-12	0	R.VNGVAPGPIWTPLIPASFAEEK.V	
254 - 263	1089.5242	1088.5169	1088.5073	9	0	R.QFGSQVPMGR.A	Gln->pyro-Glu (N-term Q)
254 - 263	1105.5208	1104.5135	1104.5023	10	0	R.QFGSQVPMGR.A	Gln->pyro-Glu (N-term Q); Oxidation (M)
254 - 263	1106.5439	1105.5367	1105.5339	3	0	R.QFGSQVPMGR.A	
254 - 263	1122.5358	1121.5285	1121.5288	-0	0	R.QFGSQVPMGR.A	Oxidation (M)

Spot 1953

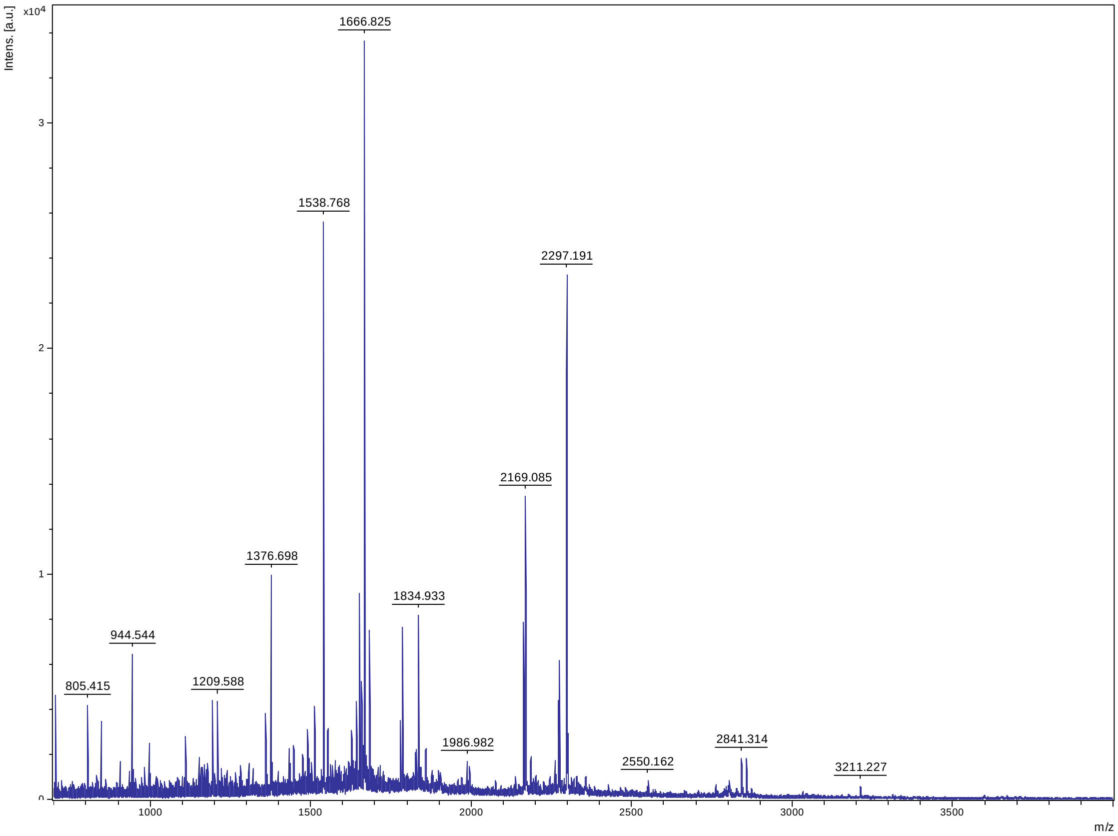


Match to: gi|51965068 Score: 93 Expect: 3.3e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
7 - 35	2872.4136	2871.4063	2871.4071	-0.0008	1	K.GAEAAAAAVAGAGEEENMAAWLVAKNTLK.I	Acetyl (N-term); Oxidation (M)
41 - 50	1112.5586	1111.5513	1111.6026	-0.0512	0	K.LPPVGPYDVR.V	
78 - 105	2918.4428	2917.4355	2917.4061	0.0294	0	K.EPMVIGHECAGVIEEVGSGVTHLAVGDR.V	Carbamidomethyl (C)
106 - 116	1287.6223	1286.6150	1286.6441	-0.0291	0	R.VALEPGISCWR.C	Carbamidomethyl (C)
133 - 156	2652.3518	2651.3445	2651.3318	0.0127	0	K.FFATPPVHGSLANQIVHPGDLCFK.L	Carbamidomethyl (C)
182 - 207	2491.4632	2490.4559	2490.3879	0.0681	0	R.ADVGPETGVLIMGAGPIGLVTLLAAR.A	
214 - 223	1180.5802	1179.5729	1179.6247	-0.0518	0	R.VVIVDVDEHR.L	
286 - 306	2256.1983	2255.1910	2255.1224	0.0686	0	K.VCLVGMGHNEMTVPLTSAAIR.E	Carbamidomethyl (C)
286 - 306	2272.1284	2271.1211	2271.1173	0.0038	0	K.VCLVGMGHNEMTVPLTSAAIR.E	Carbamidomethyl (C); Oxidation (M)
332 - 341	1191.6895	1190.6822	1190.7135	-0.0313	0	K.IDVKPLITHR.F	
342 - 358	1946.9219	1945.9146	1945.8693	0.0453	0	R.FGFSQEDVEEAFEVSAR.G	

Spot 1956

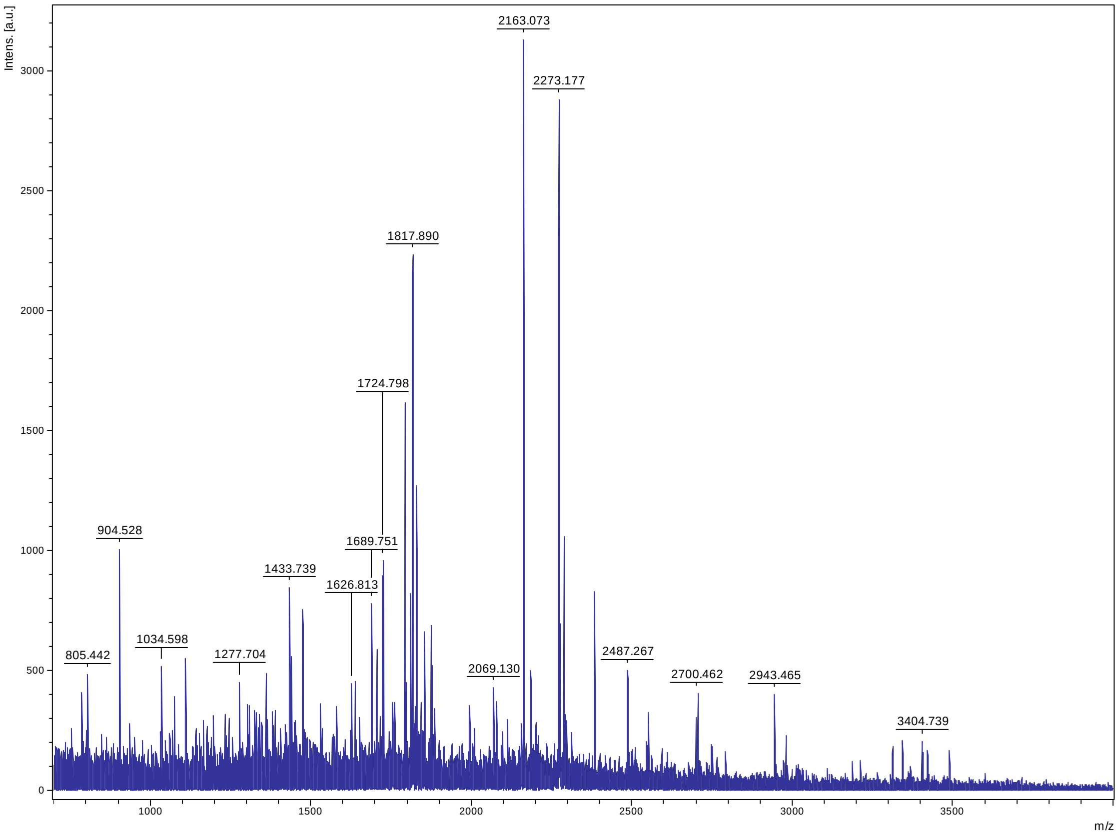


Match to: gi|50921411 Score: 125 Expect: 2.1e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
63 - 89	2841.2914	2840.2841	2840.4126	-0.1285	1	K.AAPAAAAHSAVTREEALELYEDMVLGR.I	
63 - 89	2857.2953	2856.2880	2856.4075	-0.1195	1	K.AAPAAAAHSAVTREEALELYEDMVLGR.I	Oxidation (M)
76 - 89	1666.8141	1665.8068	1665.7919	0.0149	0	R.EEALELYEDMVLGR.I	
76 - 89	1682.8340	1681.8267	1681.7868	0.0399	0	R.EEALELYEDMVLGR.I	Oxidation (M)
90 - 101	1626.6635	1625.6562	1625.6676	-0.0114	0	R.IFEDMCAQMYYR.G	Carbamidomethyl (C)
90 - 101	1642.6735	1641.6662	1641.6625	0.0037	0	R.IFEDMCAQMYYR.G	Carbamidomethyl (C); Oxidation (M)
90 - 101	1658.6846	1657.6773	1657.6575	0.0199	0	R.IFEDMCAQMYYR.G	Carbamidomethyl (C); 2 Oxidation (M)
90 - 103	1827.8682	1826.8609	1826.7789	0.0820	1	R.IFEDMCAQMYYRGK.M	Carbamidomethyl (C); Oxidation (M)
104 - 123	2245.0410	2244.0337	2244.1037	-0.0699	0	K.MFGFVHLYNGQEAVSTGFIK.L	
104 - 123	2261.0879	2260.0806	2260.0986	-0.0179	0	K.MFGFVHLYNGQEAVSTGFIK.L	Oxidation (M)
124 - 136	1481.7118	1480.7045	1480.7344	-0.0299	0	K.LLNQADCVVSTYR.D	
124 - 136	1538.7543	1537.7470	1537.7558	-0.0088	0	K.LLNQADCVVSTYR.D	Carbamidomethyl (C)
150 - 158	981.4629	980.4556	980.5000	-0.0444	0	R.SVMAELFGK.A	
150 - 158	997.4629	996.4556	996.4950	-0.0393	0	R.SVMAELFGK.A	Oxidation (M)
202 - 208	944.4873	943.4800	943.5239	-0.0439	1	K.YRHEVLK.Q	
264 - 273	1151.5589	1150.5516	1150.5870	-0.0354	1	R.ATSDPEIYKK.G	
273 - 291	1970.9606	1969.9533	1969.9753	-0.0220	1	K.KGPAFGMPGVHVDGMDVLK.V	Oxidation (M)
274 - 291	1842.8856	1841.8783	1841.8803	-0.0020	0	K.GPAFGMPGVHVDGMDVLK.V	Oxidation (M)
274 - 291	1858.8793	1857.8720	1857.8753	-0.0032	0	K.GPAFGMPGVHVDGMDVLK.V	2 Oxidation (M)
306 - 318	1510.6856	1509.6783	1509.6769	0.0014	0	R.GEGPTLVECETYR.F	Carbamidomethyl (C)
321 - 331	1209.5773	1208.5700	1208.5785	-0.0085	0	R.GHSLADPDELR.R	
321 - 336	1834.9041	1833.8968	1833.8969	-0.0001	1	R.GHSLADPDELRRPDEK.S	
350 - 364	1778.9764	1777.9691	1777.9461	0.0230	1	K.KYIIEQNLATESELK.S	
351 - 364	1650.8472	1649.8399	1649.8512	-0.0112	0	K.YIIEQNLATESELK.S	
370 - 389	2169.0450	2168.0377	2168.0637	-0.0259	0	K.IDDVVEEAVEFADASPLPPR.S	
390 - 401	1376.6844	1375.6771	1375.6983	-0.0212	0	R.SQLLENVFSDPK.G	
402 - 410	847.3635	846.3562	846.4235	-0.0673	0	K.GFGIGPDGK.Y	
411 - 425	1784.8298	1783.8225	1783.8199	0.0026	1	K.YRCEDPLFTQGTAQV.-	Carbamidomethyl (C)

Spot 1962

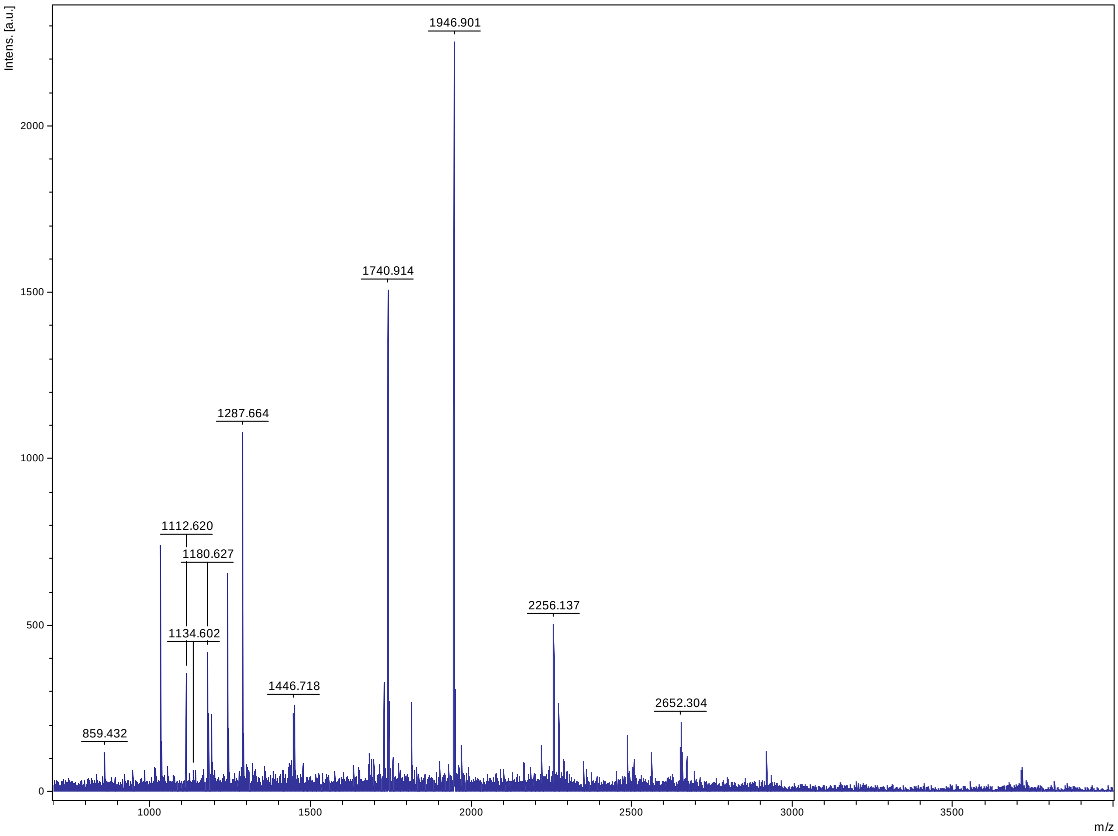


Match to: Q19BJ6_ORYSA Score: 103 Expect: 3.3e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
35 - 56	2069.1252	2068.1179	2068.1163	0.0016	0	K.NAIELGLLETLQSAAVAGGGGK.A	
57 - 72	1623.8887	1622.8814	1622.9243	-0.0428	1	K.AALLTPAEVADKLPSK.A	
73 - 86	1530.8115	1529.8042	1529.7442	0.0600	1	K.ANPAAADMVDRMLR.L	
87 - 95	1034.5945	1033.5872	1033.5920	-0.0048	0	R.LLASYNVVR.C	
139 - 148	1331.6808	1330.6735	1330.6631	0.0104	0	K.VLMESWYYLK.D	
139 - 148	1347.6758	1346.6685	1346.6580	0.0105	0	K.VLMESWYYLK.D	Oxidation (M)
149 - 160	1245.6565	1244.6492	1244.6400	0.0092	0	K.DAVLDGGIPFNK.A	
161 - 175	1689.7664	1688.7591	1688.7252	0.0339	0	K.AYGMTAFEYHGTDAR.F	
161 - 175	1705.7751	1704.7678	1704.7202	0.0477	0	K.AYGMTAFEYHGTDAR.F	Oxidation (M)
179 - 193	1716.8672	1715.8599	1715.9028	-0.0429	1	R.VFNEGMKNHSVIITK.K	
195 - 225	2980.6261	2979.6188	2979.5552	0.0636	0	K.LLDLYTGFDAASTVVDVGGGVGATVAAVVSR.H	
231 - 262	3404.7515	3403.7442	3403.6658	0.0784	0	R.GINYDLPHVISEAPPFPGVEHVGGDMFASVPR.G	
231 - 262	3420.7335	3419.7262	3419.6607	0.0655	0	R.GINYDLPHVISEAPPFPGVEHVGGDMFASVPR.G	Oxidation (M)
271 - 283	1724.8022	1723.7949	1723.7525	0.0424	0	K.WILHDWSDEHCAR.L	Carbamidomethyl (C)
287 - 297	1303.6130	1302.6057	1302.5663	0.0395	0	K.NCYDALPEHGK.V	Carbamidomethyl (C)
298 - 314	1830.9515	1829.9442	1829.9192	0.0250	0	K.VVVVECVLPESSDATAR.E	Carbamidomethyl (C)
315 - 333	2080.0374	2079.0301	2079.0029	0.0272	0	R.EQGVFHVDMIMLAHNPGGK.E	
315 - 333	2096.0439	2095.0366	2094.9978	0.0388	0	R.EQGVFHVDMIMLAHNPGGK.E	Oxidation (M)
315 - 333	2112.0241	2111.0168	2110.9928	0.0241	0	R.EQGVFHVDMIMLAHNPGGK.E	2 Oxidation (M)
354 - 368	1761.9037	1760.8964	1760.8773	0.0191	0	K.ATYIYANAWAIEFTK.-	

Spot 1967

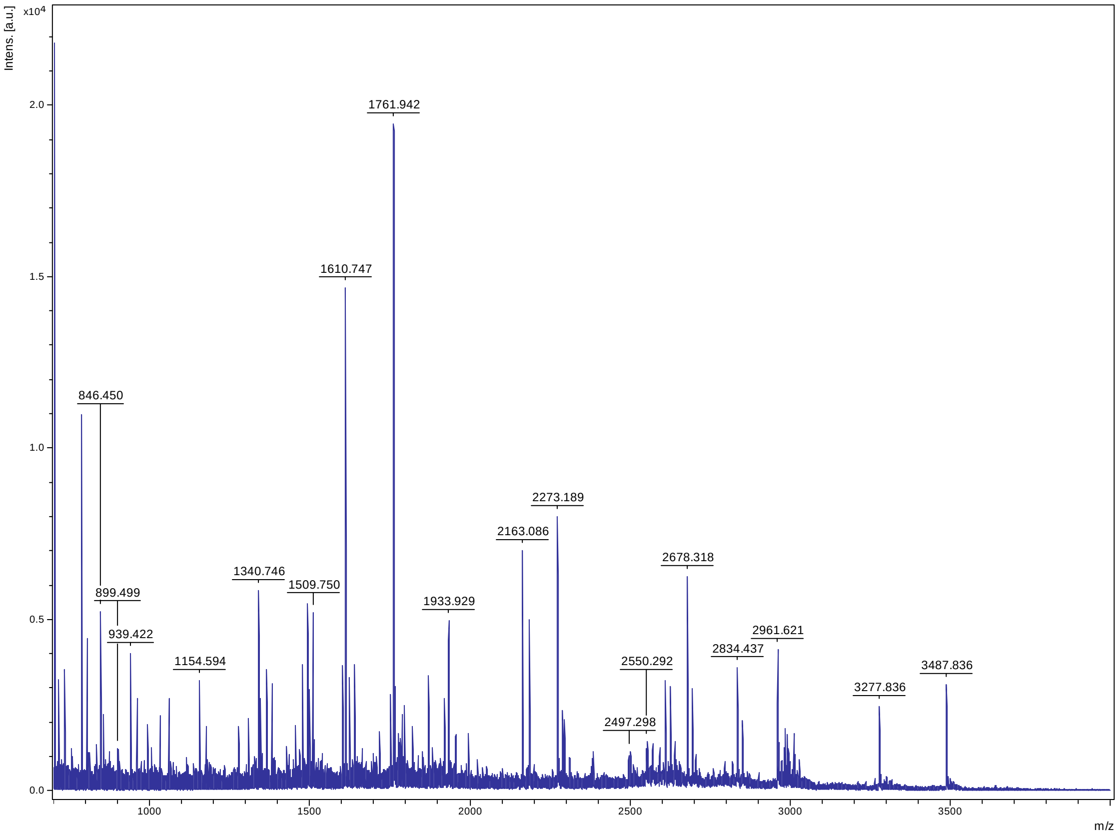


Match to: gi|51965068 Score: 204

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
36 - 50	1728.9697	1727.9625	1727.9432	0.0192	1	K.IMPFKLPPVGPYDVR.V	
36 - 50	1744.9536	1743.9463	1743.9381	0.0082	1	K.IMPFKLPPVGPYDVR.V	Oxidation (M)
41 - 50	1112.6201	1111.6128	1111.6026	0.0103	0	K.LPPVGPYDVR.V	
55 - 67	1446.7179	1445.7106	1445.7085	0.0021	0	K.AVGICGSDVHYLR.E	Carbamidomethyl (C)
106 - 116	1287.6644	1286.6572	1286.6441	0.0130	0	R.VALEPGISCWR.C	Carbamidomethyl (C)
133 - 156	2652.3035	2651.2962	2651.3318	-0.0356	0	K.FFATPPVHGSLANQIVHPGDLCFK.L	Carbamidomethyl (C)
157 - 180	2654.2512	2653.2439	2653.2298	0.0142	0	K.LPENVSLEEGAMCEPLSVGVHACR.R	2 Carbamidomethyl (C)
214 - 223	1180.6270	1179.6197	1179.6247	-0.0051	0	R.VVIVDVDEHR.L	
229 - 237	859.4323	858.4250	858.4559	-0.0309	0	R.SLGADAAVR.V	
254 - 271	1813.8152	1812.8079	1812.8022	0.0057	0	R.AAMGGDIDVSLDCAGFSK.T	Carbamidomethyl (C)
272 - 281	1032.5730	1031.5657	1031.5611	0.0046	0	K.TVATALEATR.G	
286 - 306	2256.1370	2255.1297	2255.1224	0.0073	0	K.VCLVGMGHNEMTVPLTSAAIR.E	Carbamidomethyl (C)
286 - 306	2272.1233	2271.1160	2271.1173	-0.0013	0	K.VCLVGMGHNEMTVPLTSAAIR.E	Carbamidomethyl (C); Oxidation (M)
316 - 328	1740.9142	1739.9069	1739.8705	0.0364	1	R.YKDTWPLCIEFLR.S	Carbamidomethyl (C)
318 - 328	1449.7550	1448.7477	1448.7122	0.0355	0	K.DTWPLCIEFLR.S	Carbamidomethyl (C)
332 - 341	1191.7332	1190.7259	1190.7135	0.0124	0	K.IDVKPLITHR.F	
342 - 358	1946.9014	1945.8941	1945.8693	0.0248	0	R.FGFSQEDVEEAFEVSAR.G	

Spot 1973

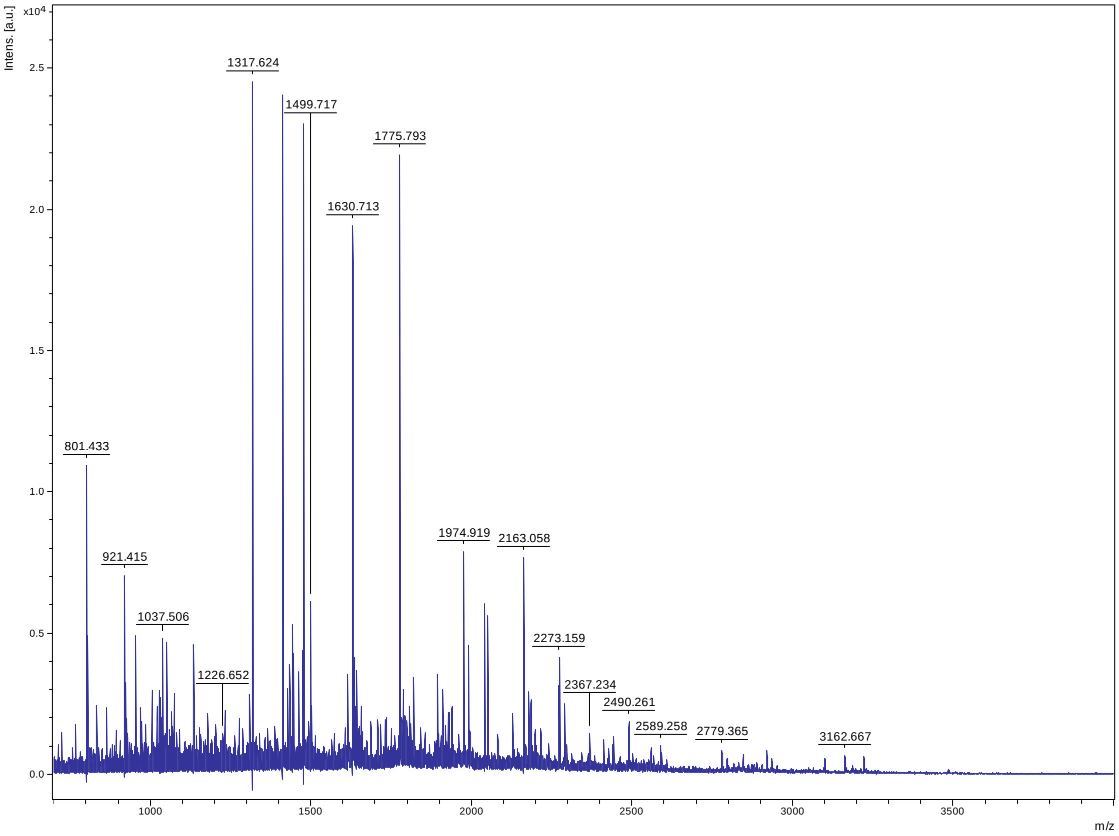


Match to: gi|121332; Score: 108

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
19 - 34	1761.94	1760.94	1760.95	-0.01	0	IIAEYIWVGGSGIDLR
42 - 52	1154.59	1153.59	1153.63	-0.04	0	GPITDVSQLPK
53 - 83	3487.84	3486.83	3486.64	0.20	1	WNYDGSSTGQAPGEDSEVILYPQAIFKDPFR
85 - 107	2678.32	2677.32	2677.23	0.09	1	GDNILVMCDCYTPQGEPIPTNKR
85 - 107	2694.32	2693.31	2693.22	0.09	1	GDNILVMCDCYTPQGEPIPTNKR Oxidation (M)
113 - 137	2961.62	2960.62	2960.50	0.12	0	IFSHPDVVAEVPWYGIEQEYTLLQK
138 - 165	2990.52	2989.52	2989.39	0.13	0	DVNWPLGWPVGGFPGPQGPYYCAAGAEK
170 - 177	960.44	959.44	959.47	-0.03	0	DIVDAHYK
224 - 255	3277.84	3276.83	3276.68	0.16	0	VTEVAGVVLSLDPKPIPGDWNGAGAHTNFSTK
269 - 276	899.50	898.50	898.56	-0.06	1	AIDKLALR
277 - 290	1610.75	1609.74	1609.76	-0.02	1	HKEHIAAYGEGNER
279 - 290	1345.57	1344.57	1344.61	-0.03	0	EHIAAYGEGNER
333 - 355	2609.38	2608.37	2608.30	0.07	0	RPASNMDPYVVTGMIAETTLLWK Oxidation (M)
333 - 355	2625.38	2624.38	2624.30	0.08	0	RPASNMDPYVVTGMIAETTLLWK 2 Oxidation (M)

Spot 1980

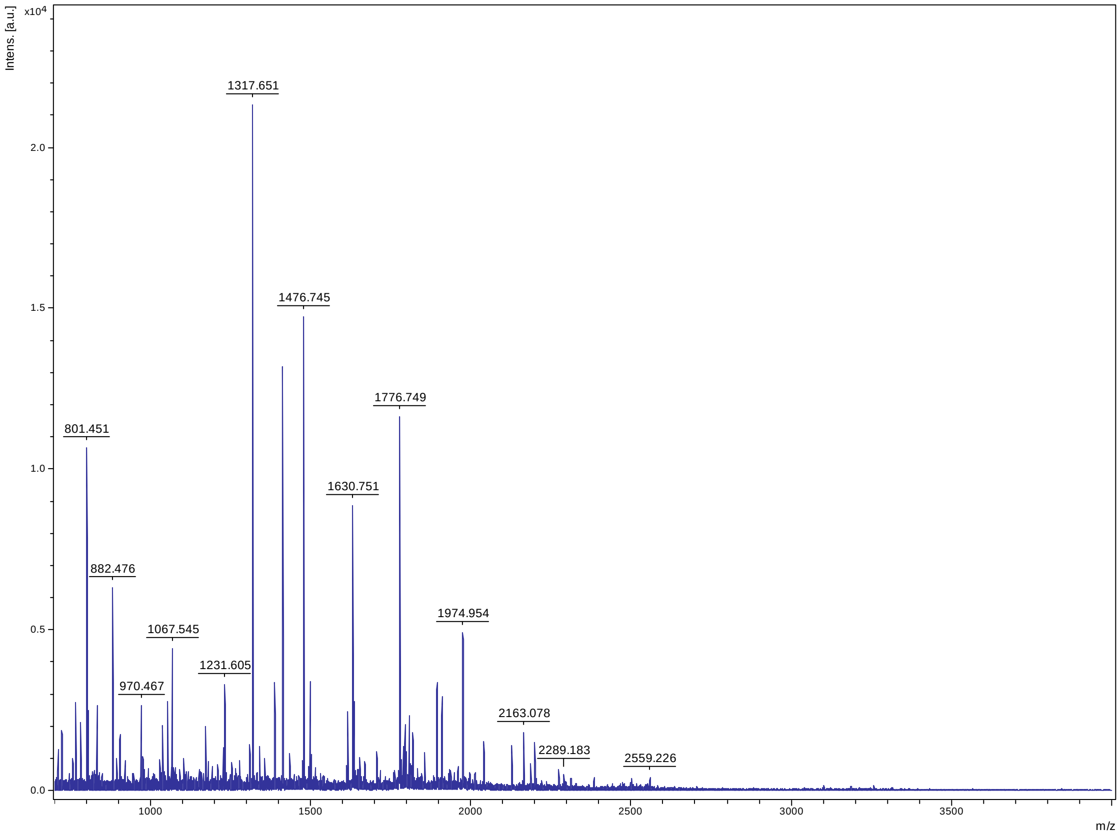


Match to: gi|38345797 Score: 192 Expect: 8.4e-15

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence	
53 - 72	2198.1055	2197.0982	2197.1266	-13	1	R.ASVAIEKETPESEPPPTFLR.E	
60 - 72	1499.7173	1498.7100	1498.7304	-14	0	K.ETPESEPPPTFLR.E	
60 - 84	2559.2460	2558.2387	2558.1885	20	1	K.ETPESEPPPTFLREDGSGAGSGSVR.E	
85 - 92	1051.5274	1050.5201	1050.5280	-8	1	R.ERFEAMIR.R	
85 - 92	1067.5257	1066.5185	1066.5229	-4	1	R.ERFEAMIR.R	Oxidation (M)
87 - 92	766.3882	765.3809	765.3843	-4	0	R.FEAMIR.R	
93 - 111	1974.9195	1973.9122	1973.9225	-5	1	R.RVQGEVCAALEEADGSGAR.F	
94 - 111	1818.8352	1817.8279	1817.8214	4	0	R.VQGEVCAALEEADGSGAR.F	
112 - 128	1775.7930	1774.7857	1774.8751	-50	0	R.FVEDVWSRPGGGGGISR.V	
139 - 156	1893.9254	1892.9181	1892.9455	-14	0	K.AGVNVSVVYGVMPPDAYR.A	
139 - 156	1909.9253	1908.9180	1908.9404	-12	0	K.AGVNVSVVYGVMPPDAYR.A	Oxidation (M)
192 - 203	1476.7164	1475.7091	1475.7310	-15	0	K.NPFAPTLHFNYR.Y	
204 - 211	970.4744	969.4671	969.4444	23	0	R.YFETDAPK.D	
204 - 218	1634.7602	1633.7529	1633.7736	-13	1	R.YFETDAPKDAPGAPR.Q	
219 - 239	2441.1922	2440.1849	2440.1587	11	0	R.QWWFGGGTDLTPSYIIEEDVK.H	
247 - 259	1613.6878	1612.6805	1612.6980	-11	1	K.QACDKFDPSFYPR.F	Gln->pyro-Glu (N-term Q)
247 - 259	1630.7131	1629.7059	1629.7246	-11	1	K.QACDKFDPSFYPR.F	
252 - 259	1028.4945	1027.4872	1027.4763	11	0	K.FDPSFYPR.F	
263 - 271	1309.5686	1308.5614	1308.5485	10	0	K.WCDDYFYIK.H	
328 - 333	801.4329	800.4256	800.4293	-5	0	K.AWQQLR.R	
337 - 346	1317.6237	1316.6164	1316.6401	-18	0	R.YVEFNLVYDR.G	
347 - 353	723.4015	722.3943	722.3963	-3	0	R.GTTFGLK.T	
358 - 370	1411.8206	1410.8134	1410.8446	-22	0	R.IESILVSLPLTAR.W	

Spot 1981

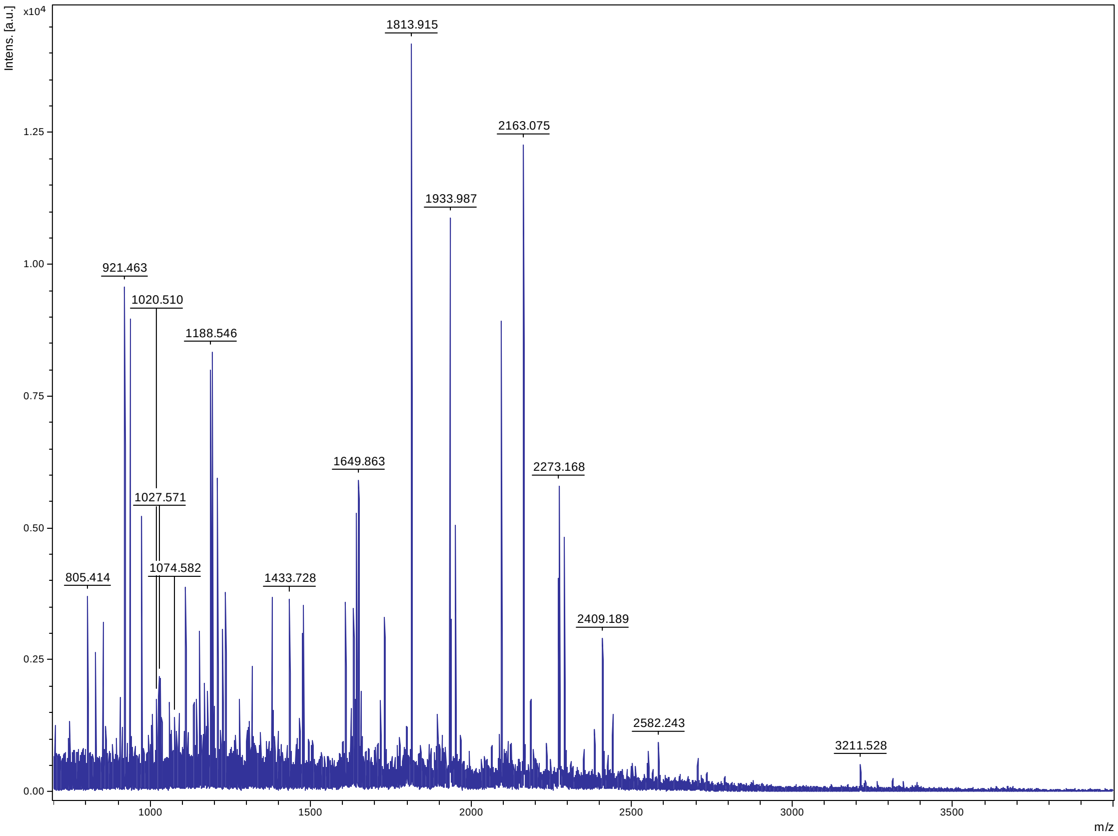


Match to: gi|38345797; Score: 257

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
53 - 72	2198.16	2197.16	2197.13	0.03	1	ASVAIEKETPESEPPPTFLR
60 - 72	1499.76	1498.75	1498.73	0.02	0	ETPESEPPPTFLR
60 - 84	2559.23	2558.22	2558.19	0.04	1	ETPESEPPPTFLREDGSGAGSGSVR
73 - 84	1078.49	1077.49	1077.47	0.02	0	EDGSGAGSGSVR
85 - 92	1051.55	1050.55	1050.53	0.02	1	ERFEAMIR
85 - 92	1067.55	1066.54	1066.52	0.02	1	ERFEAMIR Oxidation (M)
93 - 111	1974.95	1973.95	1973.92	0.03	1	RVQGEVCAALEEADGSGAR
94 - 111	1818.86	1817.86	1817.82	0.04	0	VQGEVCAALEEADGSGAR
112 - 128	1775.81	1774.81	1774.87	-0.06	0	FVEDVWSRPGGGGGISR
139 - 156	1893.98	1892.98	1892.95	0.04	0	AGVNVSVVYGVMPPDAYR
139 - 156	1909.98	1908.97	1908.94	0.03	0	AGVNVSVVYGVMPPDAYR Oxidation (M)
174 - 191	1795.00	1794.00	1793.98	0.01	0	AGPVPFFAAGISSVLHPK
192 - 203	1476.75	1475.74	1475.73	0.01	0	NPFAPTLHFNYR
204 - 211	970.47	969.46	969.44	0.02	0	YFETDAPK
204 - 218	1634.79	1633.79	1633.77	0.02	1	YFETDAPKDAPGAPR
240 - 246	882.48	881.47	881.45	0.02	0	HFHSVQK
247 - 259	1613.72	1612.72	1612.70	0.02	1	QACDKFDPSFYPR Pyro-glu (N-term Q)
247 - 259	1630.75	1629.75	1629.72	0.02	1	QACDKFDPSFYPR
252 - 259	1028.48	1027.48	1027.48	0.00	0	FDPSFYPR
263 - 271	1309.59	1308.58	1308.55	0.04	0	WCDDYFYIK
318 - 327	1231.60	1230.60	1230.59	0.01	1	KDTPFTEEHK
319 - 327	1103.52	1102.52	1102.49	0.02	0	DTPFTEEHK
328 - 333	801.45	800.45	800.43	0.02	0	AWQQLR
337 - 346	1317.65	1316.65	1316.64	0.01	0	YVEFNLVYDR
354 - 370	1783.05	1782.05	1782.04	0.01	1	TGGRIESILVSLPLTAR
358 - 370	1411.86	1410.86	1410.84	0.01	0	IESILVSLPLTAR
371 - 384	1776.75	1775.75	1775.74	0.01	0	WQYDHTPEEGTEER
385 - 394	1171.66	1170.65	1170.64	0.01	1	KLLDACINPK

Spot 1989

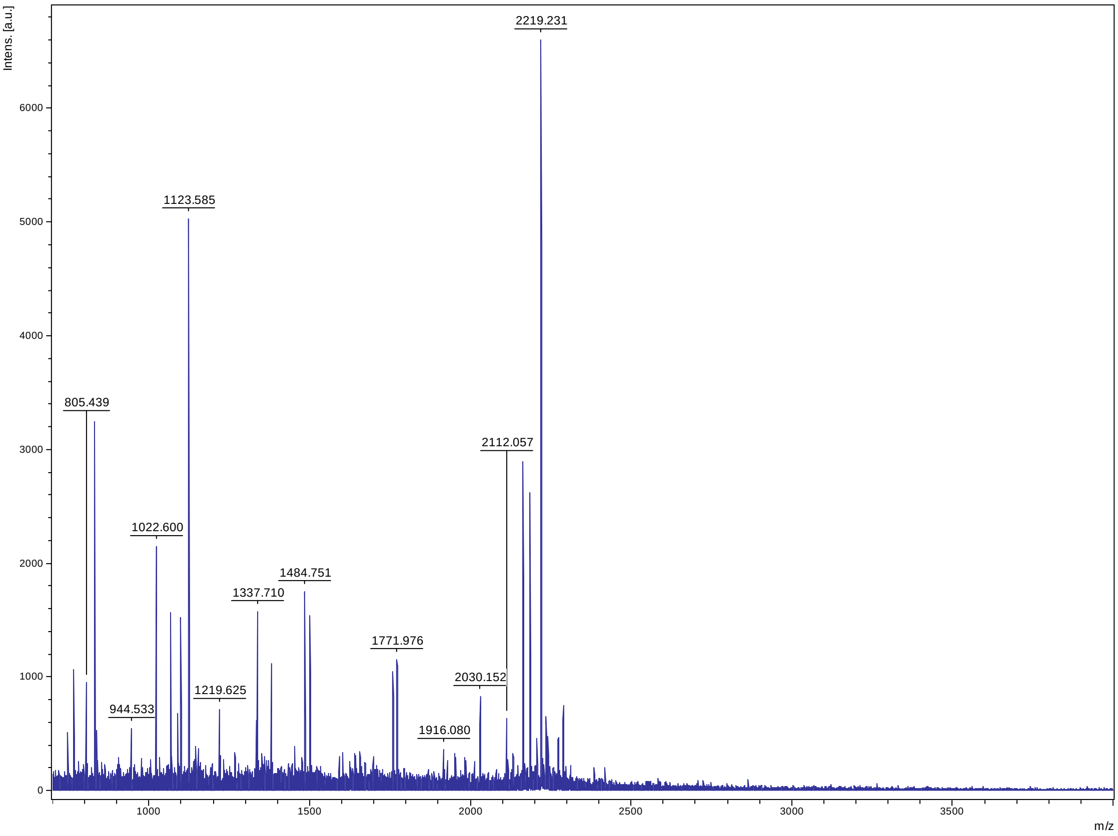


Match to: gi|27804772; Score: 187

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 11	1199.55	1198.55	1198.57	-0.02	0	METVAAASYTR
85 - 93	1027.57	1026.57	1026.58	-0.01	1	ATPDKNLIR
94 - 103	1209.58	1208.58	1208.57	0.01	0	LLICMGEAMR Oxidation (M)
94 - 103	1225.59	1224.59	1224.57	0.02	0	LLICMGEAMR 2 Oxidation (M)
137 - 149	1608.81	1607.81	1607.80	0.00	0	LLFEALEYSHVCK
201 - 220	1933.99	1932.98	1932.97	0.01	0	LTGVTGGDQVAAAMGIYGPR
201 - 220	1949.98	1948.98	1948.97	0.01	0	LTGVTGGDQVAAAMGIYGPR Oxidation (M)
221 - 228	922.56	921.56	921.55	0.00	0	TTYIIALK
229 - 243	1730.82	1729.81	1729.80	0.02	0	DCPGTHEFLLLDEGK
229 - 248	2409.19	2408.19	2408.16	0.03	1	DCPGTHEFLLLDEGKWQHVK
258 - 265	921.46	920.46	920.45	0.01	0	MFSPGNLR
258 - 265	937.45	936.45	936.45	0.00	0	MFSPGNLR Oxidation (M)
266 - 282	2093.04	2092.03	2092.02	0.02	1	ATFDNPEYDKLINYYVK
276 - 282	912.51	911.51	911.51	-0.00	0	LINYYVK
289 - 303	1633.86	1632.86	1632.85	0.00	0	YTGGMVPDVNQIIVK
289 - 303	1649.86	1648.86	1648.85	0.01	0	YTGGMVPDVNQIIVK Oxidation (M)
306 - 317	1235.66	1234.66	1234.66	-0.00	0	GIFTNVTSPTAK
345 - 358	1625.84	1624.84	1624.84	-0.00	1	QSVLDKVINNLDER Pyro-glu (N-term Q)
345 - 358	1642.88	1641.88	1641.87	0.01	1	QSVLDKVINNLDER
351 - 358	972.50	971.50	971.50	-0.00	0	VINNLDER
359 - 366	853.43	852.43	852.43	-0.01	0	TQVAYGSK
359 - 371	1478.78	1477.78	1477.79	-0.01	1	TQVAYGSKNEIIR
367 - 381	1813.91	1812.91	1812.90	0.01	1	NEIIRFEETLYGSSR
372 - 381	1188.55	1187.54	1187.55	-0.00	0	FEETLYGSSR

Spot 1991

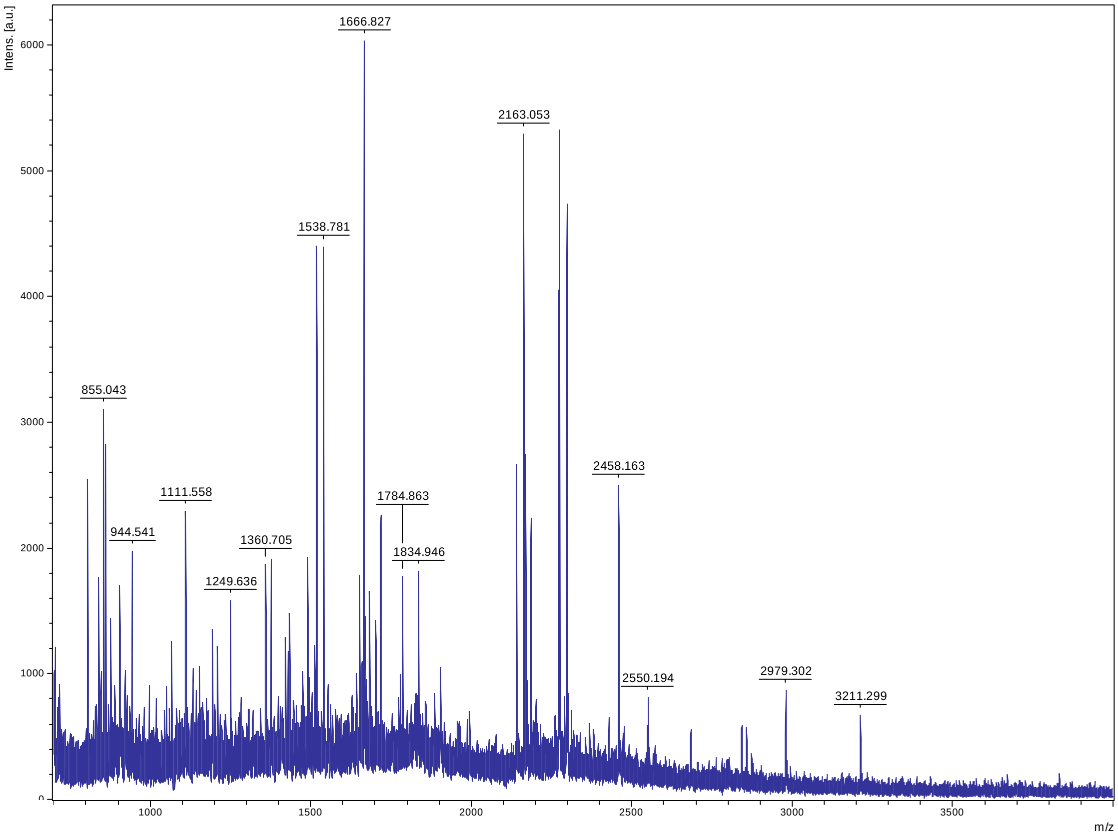


Match to: gi|4730886; Score: 98

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
15 - 23	1123.59	1122.58	1122.55	0.03	0	VLNCEYAVR
24 - 32	1022.60	1021.60	1021.57	0.03	0	GEIVIHAQR
70 - 87	2184.11	2183.11	2183.06	0.05	1	EVIALCDHPCLLEKEETK
88 - 97	1066.58	1065.57	1065.55	0.03	0	SLFSADAISR
98 - 108	1099.67	1098.66	1098.64	0.02	0	ATTILASIPGR
109 - 120	1219.62	1218.62	1218.60	0.02	0	ATGAYSHSQGIK
124 - 133	944.53	943.53	943.51	0.02	0	DAIAAGIASR
223 - 243	2219.23	2218.23	2218.17	0.06	0	ALVVINPGNPTGQVLAEENQR
301 - 309	1089.51	1088.51	1088.47	0.04	1	GYYGECGKR
310 - 323	1484.75	1483.75	1483.71	0.04	0	GGYMEITGFSAPVR
310 - 323	1500.74	1499.74	1499.71	0.03	0	GGYMEITGFSAPVR Oxidation (M)

Spot 1996

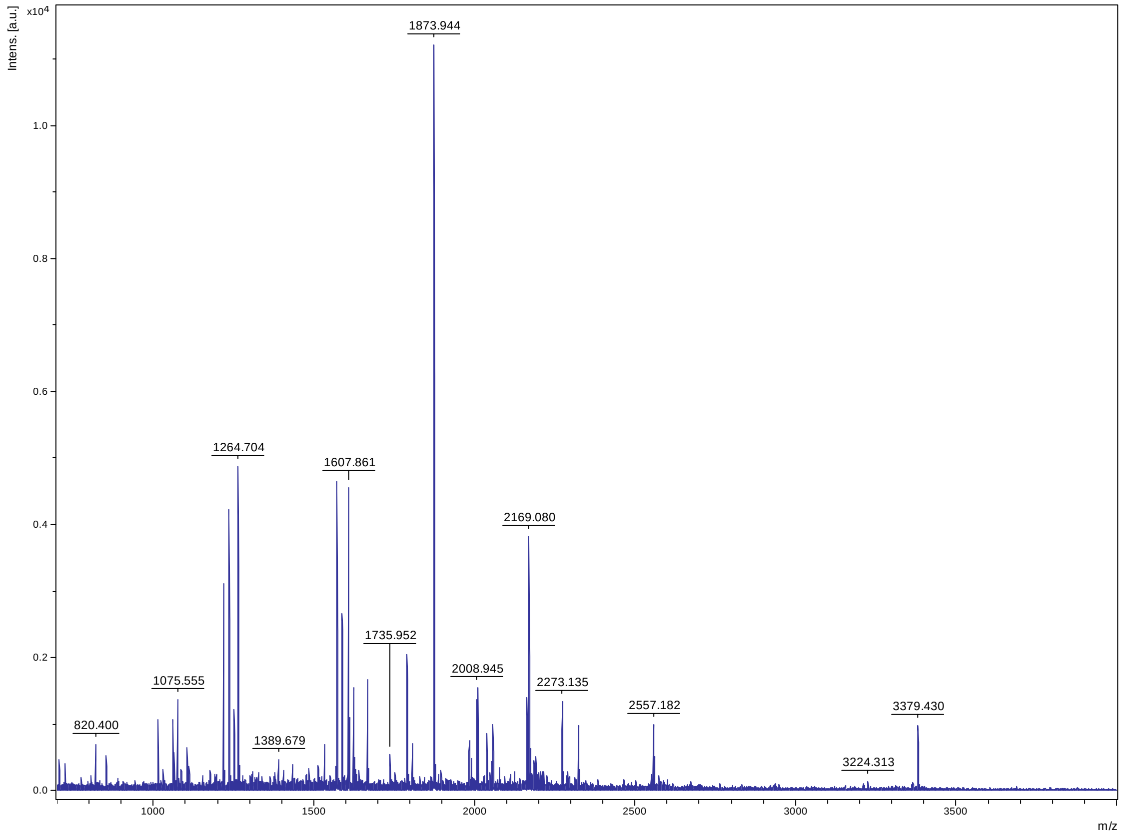


Match to: gi|50921411 Score: 99 Expect: 8.4e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
63 - 89	2857.4246	2856.4173	2856.4075	0.0098	1	K.AAPAAAAHSAVTREEALELYEDMVLGR.I	Oxidation (M)
76 - 89	1666.8134	1665.8061	1665.7919	0.0142	0	R.EEALELYEDMVLGR.I	
76 - 89	1682.8318	1681.8245	1681.7868	0.0377	0	R.EEALELYEDMVLGR.I	Oxidation (M)
124 - 136	1538.7746	1537.7673	1537.7558	0.0115	0	K.LLNQADCVVSTYR.D	Carbamidomethyl (C)
150 - 164	1702.9037	1701.8964	1701.7636	0.1328	1	R.SVMAELFGKATGCCR.G	2 Carbamidomethyl (C); Oxidation (M)
202 - 208	944.5153	943.5080	943.5239	-0.0159	1	K.YRHEVLK.Q	
321 - 336	1834.9080	1833.9007	1833.8969	0.0038	1	R.GHSLADPDELRRPDEK.S	
350 - 364	1778.9502	1777.9429	1777.9461	-0.0032	1	K.KYIIEQNLATESELK.S	
351 - 364	1650.8698	1649.8625	1649.8512	0.0114	0	K.YIIEQNLATESELK.S	
370 - 389	2169.0633	2168.0560	2168.0637	-0.0076	0	K.IDDVVEEAVEFADASPLPPR.S	
390 - 401	1376.7029	1375.6956	1375.6983	-0.0027	0	R.SQLLENVFSDPK.G	
411 - 425	1784.8584	1783.8511	1783.8199	0.0312	1	K.YRCEDPLFTQGTAQV.-	Carbamidomethyl (C)

Spot 2002



Match to: gi|54291764 Score: 142

Matched peptides:

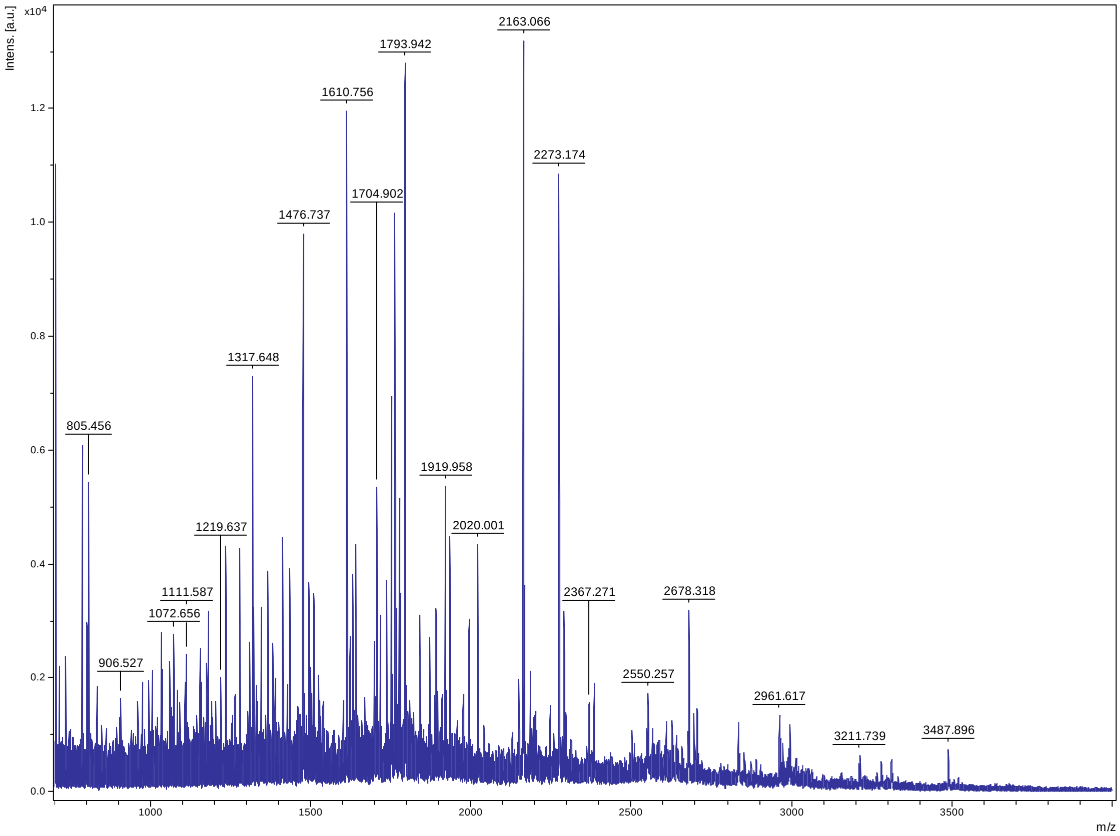
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
16 - 30	1873.9436	1872.9363	1872.9370	-0.0006	0	R.FHPTDEELVINYLQR.R	
76 - 84	1075.5551	1074.5478	1074.5570	-0.0092	0	R.YPNSVRPSR.S	
85 - 92	853.4321	852.4248	852.4130	0.0118	0	R.SAASGFWK.A	
93 - 113	2174.0618	2173.0545	2173.0871	-0.0326	0	K.ATGTDKPVQVANMQSTPVAMK.K	
93 - 113	2190.0540	2189.0467	2189.0820	-0.0353	0	K.ATGTDKPVQVANMQSTPVAMK.K	Oxidation (M)
114 - 128	1735.9515	1734.9443	1734.9490	-0.0048	1	K.KALVFYVGRPPMETK.T	
115 - 128	1607.8611	1606.8538	1606.8541	-0.0003	0	K.ALVFYVGRPPMETK.T	
115 - 128	1623.8507	1622.8434	1622.8490	-0.0056	0	K.ALVFYVGRPPMETK.T	Oxidation (M)
129 - 137	1236.5714	1235.5641	1235.5757	-0.0116	0	K.TTWIMHEYR.L	
129 - 137	1252.5620	1251.5547	1251.5706	-0.0159	0	K.TTWIMHEYR.L	Oxidation (M)
138 - 161	2324.1289	2323.1216	2323.1404	-0.0188	0	R.LTNTGGSTASHPSLSSSTAHPSVK.L	
162 - 169	1062.5222	1061.5149	1061.5215	-0.0066	0	K.LDEWVLCK.I	Carbamidomethyl (C)
170 - 189	2169.0801	2168.0728	2168.0861	-0.0133	1	K.IFNKSPEPDNTAPPSNVVSR.L	
174 - 189	1666.8076	1665.8003	1665.7958	0.0045	0	K.SPEPDNTAPPSNVVSR.L	

Match to: gi|34897838 Score: 107

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
35 - 49	1513.7434	1512.7361	1512.7460	-0.0098	0	K.SLLDGSYAGAFDGLK.D	
35 - 53	2008.9449	2007.9377	2007.9537	-0.0160	1	K.SLLDGSYAGAFDGLKDHDK.S	
134 - 145	1433.7052	1432.6979	1432.7860	-0.0881	1	K.GLEKILDHHMIK.V	
146 - 167	2557.1816	2556.1744	2556.1921	-0.0177	1	K.VWNDLYSATDKYTDGWLSSAHK.L	
184 - 202	1984.0209	1983.0136	1983.0459	-0.0323	0	K.HSSINCIVTSGSLIPSLAK.C	Carbamidomethyl (C)
208 - 225	2056.9702	2055.9629	2055.9789	-0.0159	0	R.LDDVVAFENVYSSWEVGK.L	
234 - 242	1105.5219	1104.5146	1104.5312	-0.0166	1	K.ERYDGPNVR.F	
236 - 242	820.4002	819.3929	819.3875	0.0054	0	R.YDGPNVR.F	
243 - 260	2037.8689	2036.8616	2036.8754	-0.0137	0	R.FCAIGDGHEECTAAQIMK.W	2 Carbamidomethyl (C)
243 - 260	2053.8523	2052.8450	2052.8703	-0.0253	0	R.FCAIGDGHEECTAAQIMK.W	2 Carbamidomethyl (C); Oxidation (M)
266 - 275	1218.5923	1217.5850	1217.5941	-0.0091	0	K.IEFHPDAPHR.F	
276 - 286	1264.7037	1263.6965	1263.7088	-0.0123	0	R.FPGLNLPTIHR.I	

Spot 2003



Match to: gi|38345797; Score: 78

Matched peptides:

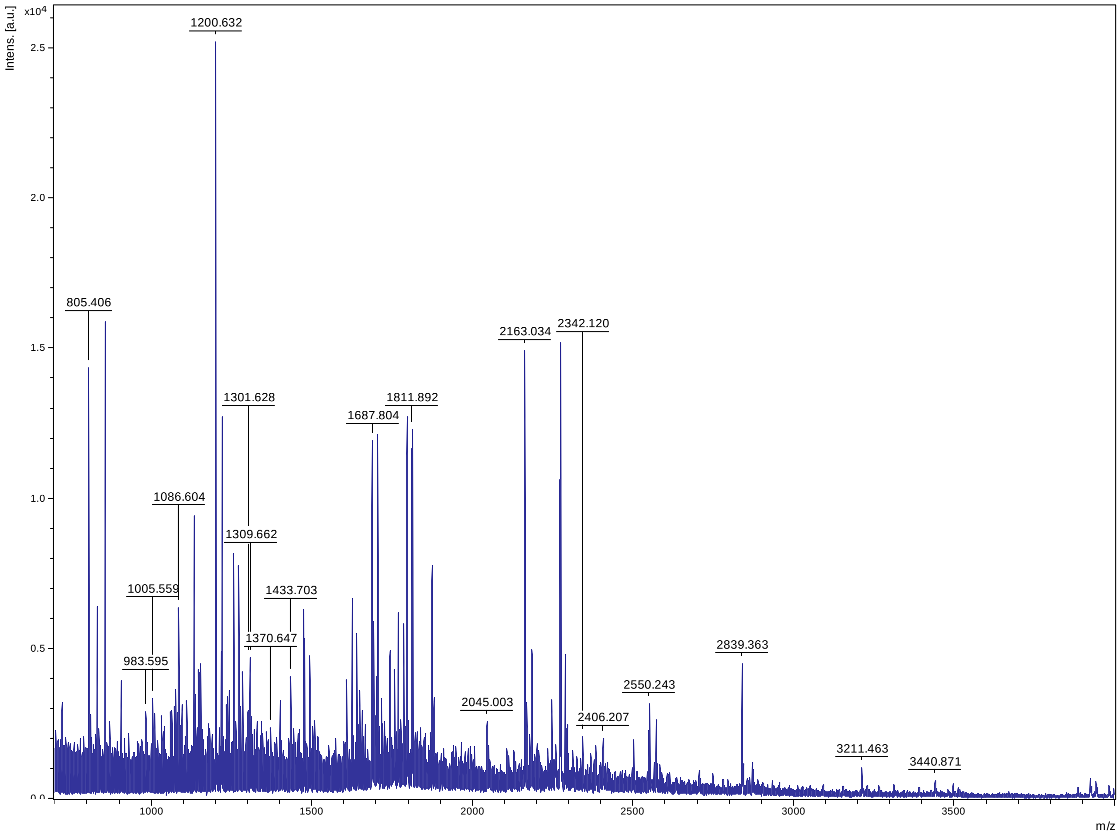
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
53 - 72	2198.12	2197.12	2197.13	-0.01	1	ASVAIEKETPESEPPPTFLR
60 - 72	1499.75	1498.75	1498.73	0.02	0	ETPESEPPPTFLR
93 - 111	1974.93	1973.93	1973.92	0.01	1	RVQGEVCAALEEADGSGAR
112 - 128	1775.82	1774.81	1774.87	-0.06	0	FVEDVWSRPGGGGGISR
129 - 138	1190.72	1189.72	1189.65	0.07	1	VLQDGRVFEK
139 - 156	1893.94	1892.94	1892.95	-0.01	0	AGVNVSVVYGVMPPDAYR
192 - 203	1476.74	1475.74	1475.73	0.00	0	NPFAPTLHFNYR
204 - 218	1634.77	1633.77	1633.77	-0.00	1	YFETDAPKDAPGAPR
247 - 259	1630.74	1629.74	1629.72	0.02	1	QACDKFDPSFYPR
328 - 333	801.48	800.47	800.43	0.04	0	AWQQLR
337 - 346	1317.65	1316.65	1316.64	0.01	0	YVEFNLVYDR
358 - 370	1411.83	1410.83	1410.84	-0.02	0	IESILVSLPLTAR

Match to: gi|34902480; Score: 71

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
19 - 34	1761.94	1760.94	1760.95	-0.00	0	IIAEYIWVGGSGIDLR
42 - 52	1154.66	1153.66	1153.63	0.02	0	GPITDVSQLPK
53 - 83	3487.90	3486.89	3486.64	0.26	1	WNYDGSSTGQAPGEDSEVILYPQAIFKDPFR
85 - 107	2678.32	2677.32	2677.23	0.09	1	GDNILVMCDCYTPQGEPIPTNKR
85 - 107	2694.28	2693.28	2693.22	0.06	1	GDNILVMCDCYTPQGEPIPTNKR Oxidation (M)
113 - 137	2961.62	2960.61	2960.50	0.12	0	IFSHPDVVAEVPWYGIEQEYTLLQK
162 - 169	960.51	959.50	959.47	0.03	0	DIVDAHYK
269 - 282	1610.76	1609.75	1609.76	-0.01	1	HKEHIAAYGEGNER
271 - 282	1345.63	1344.63	1344.61	0.02	0	EHIAAYGEGNER
325 - 347	2625.34	2624.33	2624.30	0.04	0	RPASNMDPYVVTGMIAETTLLWK 2 Oxidation (M)

Spot 2011



Match to: gi|50582723; Score: 100

Matched peptides:

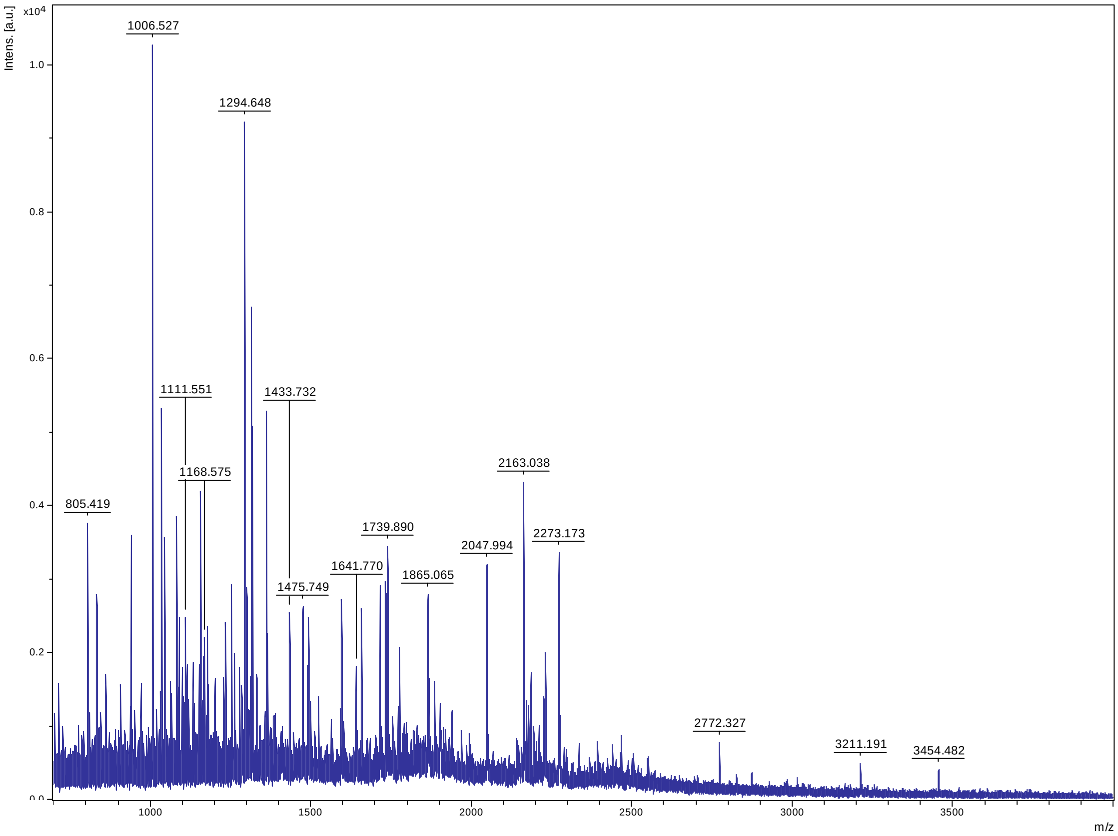
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
77 - 90	1270.70	1269.70	1269.74	-0.04	0	TVVAVILGGGAGTR
99 - 110	1199.64	1198.64	1198.68	-0.04	0	AKPAVPIGGAYR
127 - 140	1625.83	1624.83	1624.86	-0.03	0	VYILTQFNSASLNR
175 - 184	1150.56	1149.56	1149.56	0.00	0	WFQGTADAVR
185 - 194	1284.67	1283.67	1283.58	0.08	0	QFDWLFDDAK
197 - 211	1743.85	1742.85	1742.88	-0.04	0	DIDDVLILSGDHLYR
225 - 239	1691.81	1690.81	1690.77	0.05	0	GADISICCLPIDDSR
285 - 298	1645.79	1644.78	1644.86	-0.08	0	EKPYIASMGVYIFK
300 - 307	983.60	982.59	982.62	-0.02	0	EILLNLLR
308 - 326	2107.03	2106.03	2106.05	-0.02	1	WRFPTANDFGSEIIPASAK
347 - 361	1705.82	1704.82	1704.85	-0.02	0	SFFEANLSLAEQPPR
376 - 387	1370.65	1369.64	1369.71	-0.07	1	RNLPPSMINNSK
388 - 403	1880.85	1879.85	1879.86	-0.01	0	ITDSIISHGCFLDSCR
404 - 412	1009.57	1008.56	1008.57	-0.01	0	IEHSVVGIR
457 - 467	1344.68	1343.68	1343.70	-0.02	1	IQNCIIDKNAR
471 - 493	2572.24	2571.23	2571.22	0.01	1	NVTISNSEGVQEADRTSEGFYIR

Match to: gi|130190; Score: 67

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
38 - 60	1645.82	1644.81	1644.74	0.07	0	AGGGGGGGGGGGGAAAAESVSK
330 - 340	1256.66	1255.66	1255.58	0.08	0	MIADCHAAPVR Oxidation (M)
452 - 466	1811.92	1810.91	1810.99	-0.08	1	HILRTGTLLCDMLLR
456 - 466	1308.67	1307.67	1307.66	0.01	0	TGTLLCDMLLR Oxidation (M)
485 - 495	1254.62	1253.62	1253.55	0.07	0	CDGAALYYHGK
583 - 591	1111.55	1110.55	1110.50	0.05	1	DDGQRMHPR
707 - 723	1965.02	1964.02	1964.01	0.01	1	SLVNDLIFKESEETVNK
731 - 740	1146.58	1145.58	1145.56	0.02	1	GDEDKNVEIK
751 - 763	1433.74	1432.74	1432.75	-0.01	0	GPIFVIVNACSTR
957 - 968	1427.78	1426.77	1426.70	0.07	0	FTNSLLEMTDLK Oxidation (M)
991 - 1006	1703.85	1702.85	1702.86	-0.01	0	DASLQSIEDGSLVLEK
1007 - 1029	2550.20	2549.20	2549.31	-0.11	1	GEFSLGSVMNAVVSQVMIQLRER
1099 - 1119	2367.26	2366.26	2366.07	0.19	0	FACPGEGLPPEIVQDMFSNSR Oxidation (M)

Spot 2015

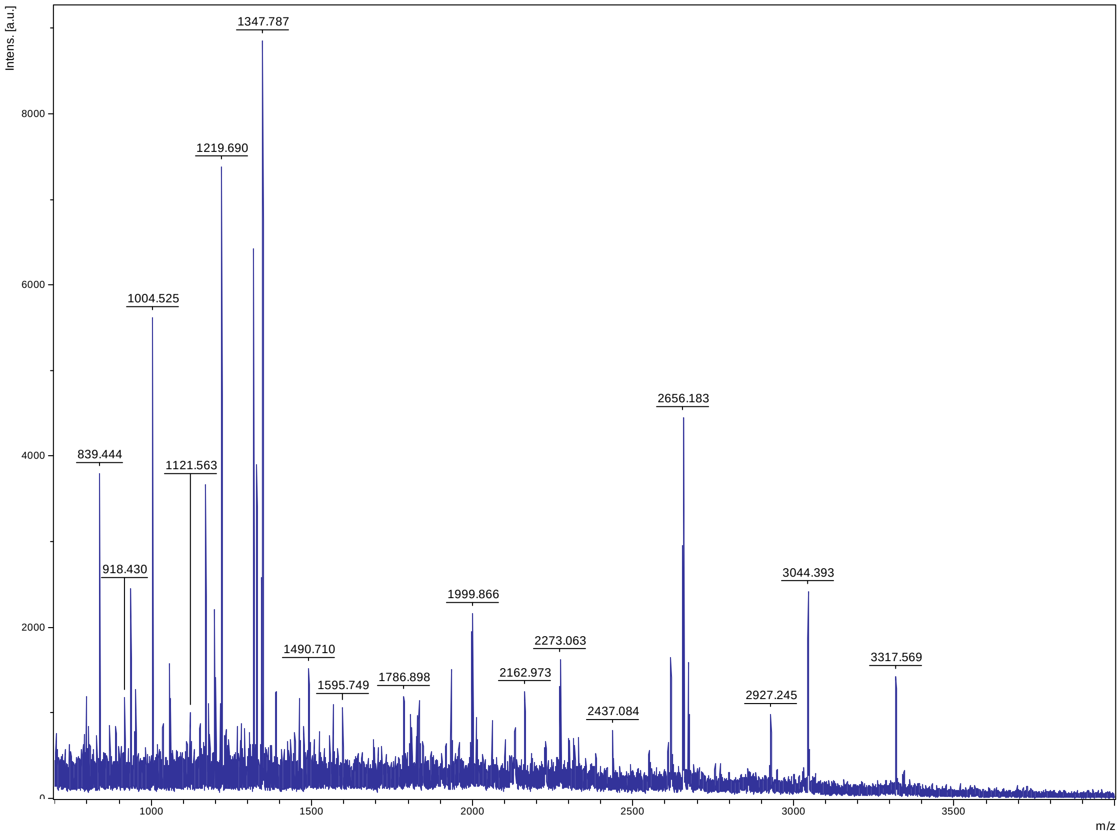


Match to: gi|77556798 Score: 70 Expect: 0.0064

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
54 - 63	1006.5114	1005.5041	1005.5243	-0.0202	0	R.SAAAAAFLER.R	
75 - 88	1641.7701	1640.7628	1640.7616	0.0012	0	K.YQGLGNDFIMVDNR.D	
131 - 147	1884.7951	1883.7878	1883.7777	0.0101	0	R.IFNSDGSEPEMCGNGVR.C	Carbamidomethyl (C); Oxidation (M)
152 - 166	1733.9062	1732.8989	1732.8784	0.0206	0	R.FIAELENLQGTHSFK.I	
167 - 183	1775.9641	1774.9568	1774.9577	-0.0009	0	K.IHTGAGLIIPEIQNDGK.V	
186 - 206	2210.1297	2209.1224	2209.1664	-0.0440	1	K.VDMGQPILSGPDIPTKLPSTK.N	Oxidation (M)
269 - 279	1294.6641	1293.6568	1293.6564	0.0004	0	R.TNTEFVEVLSR.S	
290 - 313	2231.0702	2230.0629	2230.1197	-0.0568	0	R.GAGATLACGTGACAVVVAAVLEGR.A	2 Carbamidomethyl (C)
318 - 332	1739.8774	1738.8701	1738.8712	-0.0011	0	K.CVVDLPGGPLEIEWR.E	Carbamidomethyl (C)
333 - 354	2439.0208	2438.0135	2438.0484	-0.0349	0	R.EDDNHIYMTGPAEAVFYGSAVH.-	Oxidation (M)

Spot 2020

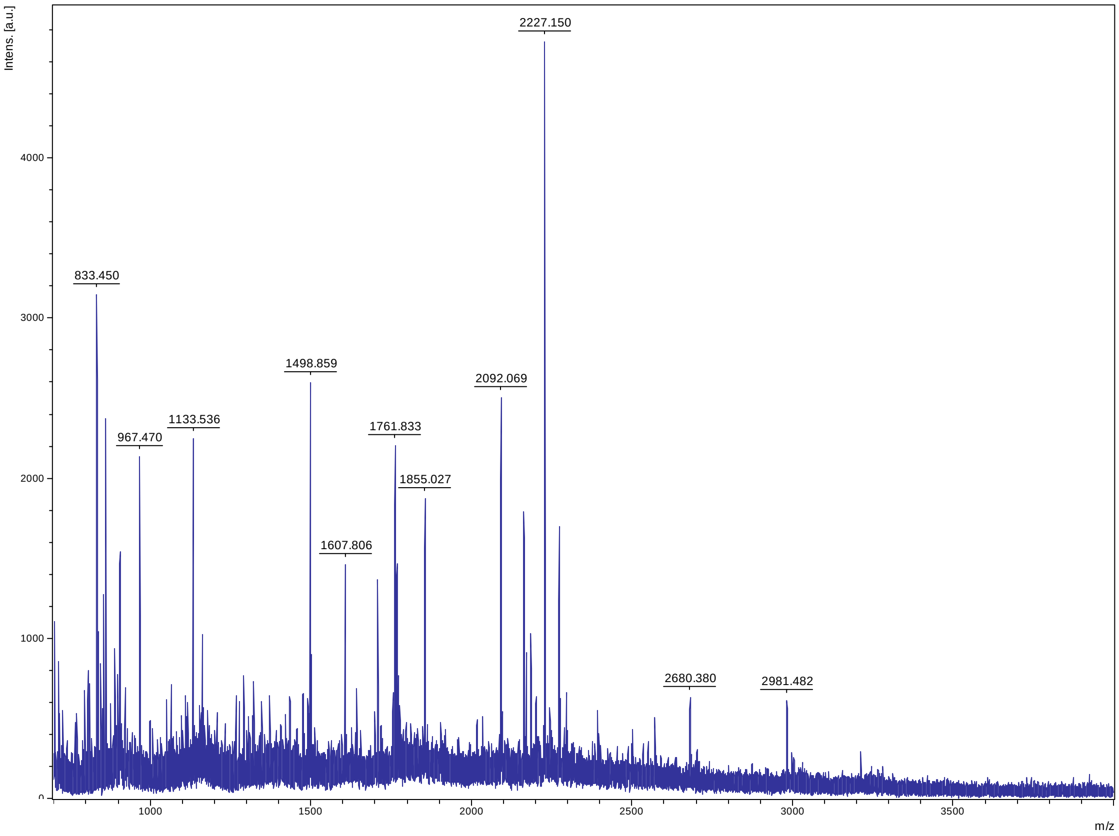


Match to: Q7FAY6_ORYSA Score: 109 Expect: 8.4e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
63 - 81	1996.8213	1995.8140	1995.8778	-0.0638	0	K.SDMGVLGATSIDFSGHSCR.Y Carbamidomethyl (C)
63 - 81	2012.8235	2011.8162	2011.8727	-0.0565	0	K.SDMGVLGATSIDFSGHSCR.Y Carbamidomethyl (C); Oxidation (M)
82 - 89	1004.5251	1003.5178	1003.5127	0.0051	0	R.YFGYLVSR.K
92 - 122	3317.5691	3316.5618	3316.6067	-0.0449	1	K.YVISIDDNCLPAKDNGGLTVDAVAQHMSNLK.T Oxidation (M)
123 - 138	1933.8698	1932.8625	1932.9410	-0.0785	0	K.TPATPFFFNTLYDPFR.K
123 - 139	2061.9634	2060.9561	2061.0359	-0.0798	1	K.TPATPFFFNTLYDPFRK.G
146 - 152	839.4441	838.4368	838.4337	0.0031	0	R.GYPFSLR.E
211 - 222	1328.7219	1327.7146	1327.7322	-0.0175	0	R.EVLGPVMFPALR.L
211 - 222	1344.7236	1343.7164	1343.7271	-0.0107	0	R.EVLGPVMFPALR.L Oxidation (M)
229 - 244	1999.8663	1998.8591	1998.9370	-0.0779	1	K.HRWDTLEDVWNGLCAK.V Carbamidomethyl (C)
256 - 263	936.4880	935.4807	935.4898	-0.0091	0	K.TGLPYVMR.S
256 - 263	952.4990	951.4917	951.4848	0.0069	0	K.TGLPYVMR.S Oxidation (M)
264 - 276	1318.6916	1317.6844	1317.6776	0.0068	1	R.SDAEAGKALESLK.E
271 - 282	1388.7286	1387.7214	1387.7347	-0.0133	1	K.ALESLKEWEGVK.V
318 - 327	1058.6010	1057.5937	1057.5920	0.0017	0	K.LGPQNAIFAK.A

Spot 2031

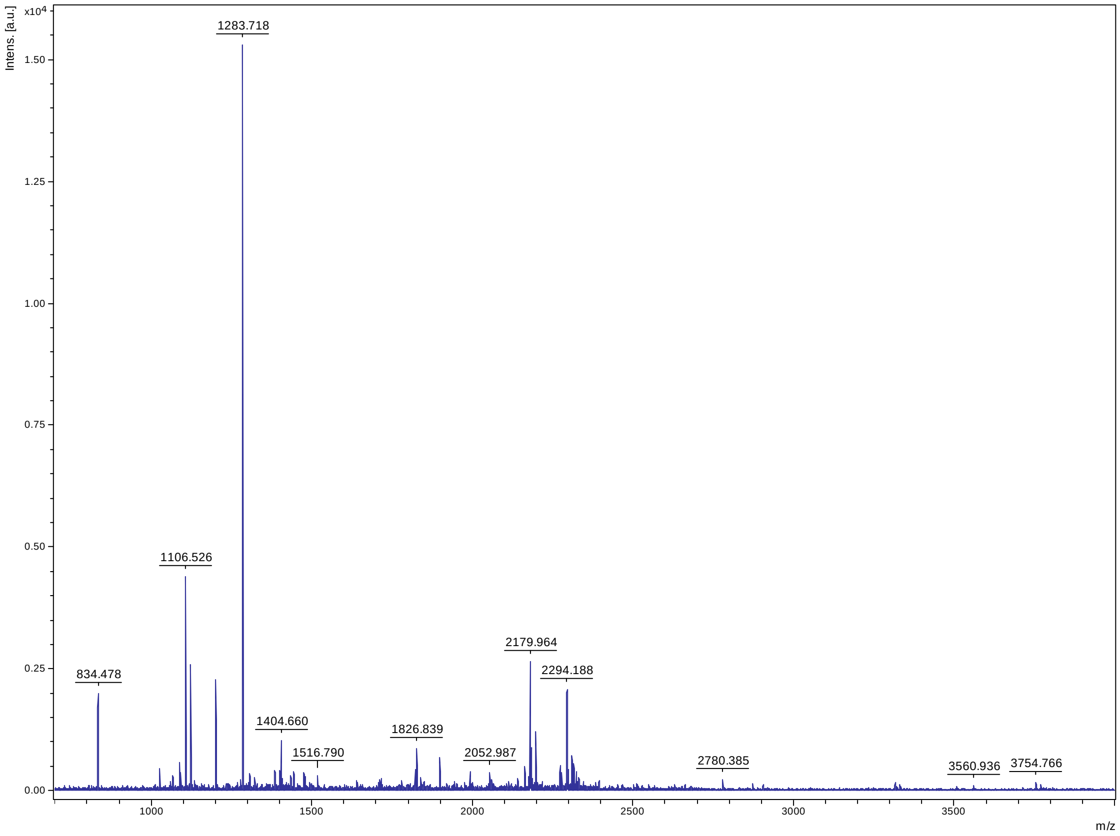


Match to: gi|50925303 Score: 115 Expect: 2.1e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
6 - 13	833.3891	832.3818	832.4555	-0.0737	0	K.IGINGFGR.I	
49 - 57	1133.5369	1132.5296	1132.5301	-0.0005	0	K.YDTVHGQWK.H	
68 - 82	1755.9266	1754.9193	1754.9025	0.0169	1	K.TLLFGEKEVTVFGCR.N	Carbamidomethyl (C)
75 - 82	967.4388	966.4315	966.4593	-0.0277	0	K.EVTVFGCR.N	Carbamidomethyl (C)
83 - 109	2981.3074	2980.3001	2980.3977	-0.0976	1	R.NPEEIPWGETGAEFVVESTGVFTDKDK.A	
141 - 164	2680.2516	2679.2443	2679.2884	-0.0440	0	K.EYKPDIDIVSNASCTTNCLAPLAK.V	2 Carbamidomethyl (C)
203 - 217	1434.7515	1433.7442	1433.7514	-0.0072	0	R.AASFNIIPSSTGAAK.A	
237 - 250	1498.8534	1497.8461	1497.8402	0.0059	0	R.VPTVDVSVVDLTVR.L	
251 - 261	1291.6901	1290.6828	1290.6819	0.0009	0	R.LEKPASYDQIK.A	
274 - 293	2227.0631	2226.0558	2226.0440	0.0118	0	K.GILGYVEEDLVSTDFQGDNR.S	
301 - 311	1161.6158	1160.6085	1160.6189	-0.0104	0	K.AGIALNDNFVK.L	
312 - 325	1761.7992	1760.7919	1760.7794	0.0125	0	K.LVSWYDNEWGYSSR.V	

Spot 2033

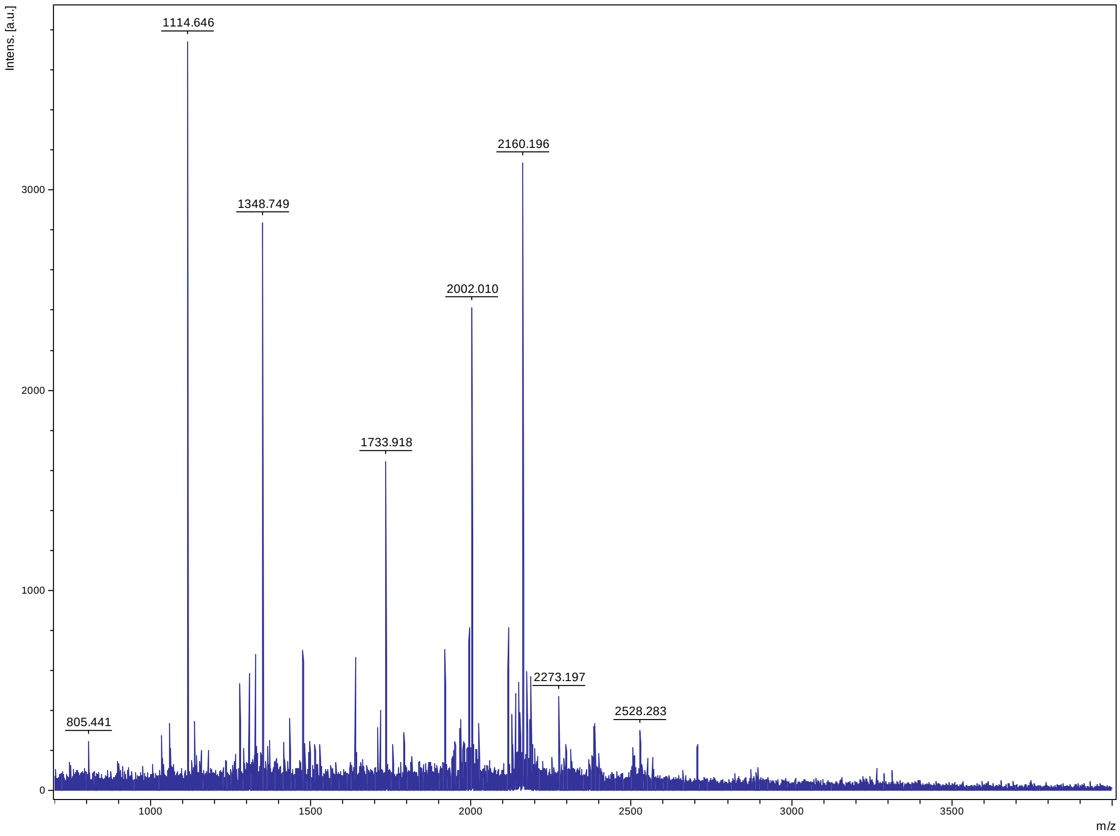


Match to: gi|46391111 Score: 145 Expect: 1.3e-10

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
18 - 37	2311.1462	2310.1390	2310.1426	-0.0036	0	K.EHAMDPRPEAIIQSYKPANK.L	Oxidation (M)
40 - 54	1444.7657	1443.7585	1443.7681	-0.0096	1	K.DKVAIVTGGDSGIGR.A	
42 - 54	1201.6489	1200.6417	1200.6462	-0.0045	0	K.VAIVTGGDSGIGR.A	
74 - 85	1404.6595	1403.6523	1403.6528	-0.0005	1	K.GQEEKDAEETLR.A	
79 - 85	833.3946	832.3873	832.3926	-0.0053	0	K.DAEETLR.A	
94 - 113	2179.9636	2178.9563	2178.9674	-0.0110	1	R.TGAKDPMAIPADLGYDDNCR.K	Carbamidomethyl (C)
94 - 113	2195.9617	2194.9544	2194.9623	-0.0079	1	R.TGAKDPMAIPADLGYDDNCR.K	Carbamidomethyl (C); Oxidation (M)
98 - 113	1822.7638	1821.7565	1821.7662	-0.0096	0	K.DPMAIPADLGYDDNCR.K	Carbamidomethyl (C)
157 - 167	1384.7124	1383.7051	1383.6533	0.0519	0	R.TNIFSYFFMSK.H	
157 - 167	1400.6390	1399.6318	1399.6482	-0.0164	0	R.TNIFSYFFMSK.H	Oxidation (M)
178 - 197	1897.8949	1896.8876	1896.8999	-0.0123	0	R.GGAGAGGCSIINTSSINAYK.G	Carbamidomethyl (C)
201 - 209	1025.5416	1024.5344	1024.5441	-0.0097	0	K.TLLDYTATK.G	
210 - 217	834.4776	833.4703	833.4759	-0.0056	0	K.GAIVAFTR.A	
218 - 229	1283.7180	1282.7107	1282.7244	-0.0137	0	R.ALALQLAEEGIR.V	
254 - 263	1089.5077	1088.5004	1088.5073	-0.0069	0	R.QFGSQVPMGR.A	Pyro-glu (N-term Q)
254 - 263	1105.4729	1104.4656	1104.5022	-0.0366	0	R.QFGSQVPMGR.A	Oxidation (M); Pyro-glu (N-term Q)
254 - 263	1106.5264	1105.5191	1105.5338	-0.0147	0	R.QFGSQVPMGR.A	
254 - 263	1122.5227	1121.5154	1121.5287	-0.0133	0	R.QFGSQVPMGR.A	Oxidation (M)

Spot 2035

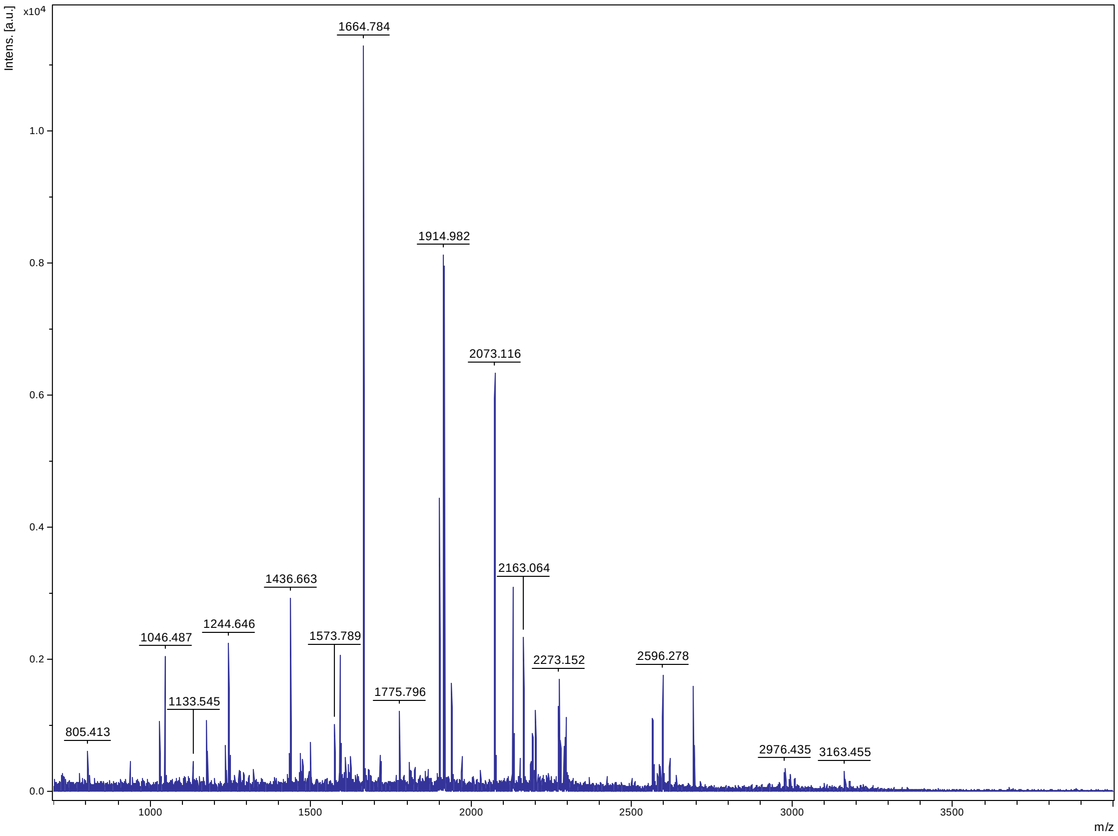


Match to: gi|57899533; Score: 127

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
140 - 161	2160.20	2159.19	2159.16	0.04	0	SVLVEPTSGNTGIGLAFIAASR
196 - 203	805.44	804.44	804.42	0.02	1	GMKGAVDK
228 - 242	1790.80	1789.79	1789.82	-0.02	0	VHYETTGPEIWEDSK
243 - 263	1919.04	1918.03	1918.03	0.01	1	GKVDVFIGGIGTGGTISGAGR
245 - 263	1733.92	1732.92	1732.91	0.01	0	VDVFIGGIGTGGTISGAGR
274 - 294	2116.18	2115.17	2115.13	0.04	0	VIGIEPSESNILSGGKPGPHK
295 - 305	1114.65	1113.64	1113.63	0.01	0	IQGIGAGFVPR
362 - 373	1348.75	1347.75	1347.75	-0.01	0	LVVVVFPSFGER
374 - 384	1326.72	1325.72	1325.73	-0.01	0	YLSSILFQSIR
374 - 389	2002.01	2001.01	2000.99	0.02	1	YLSSILFQSIREECEK

Spot 2046

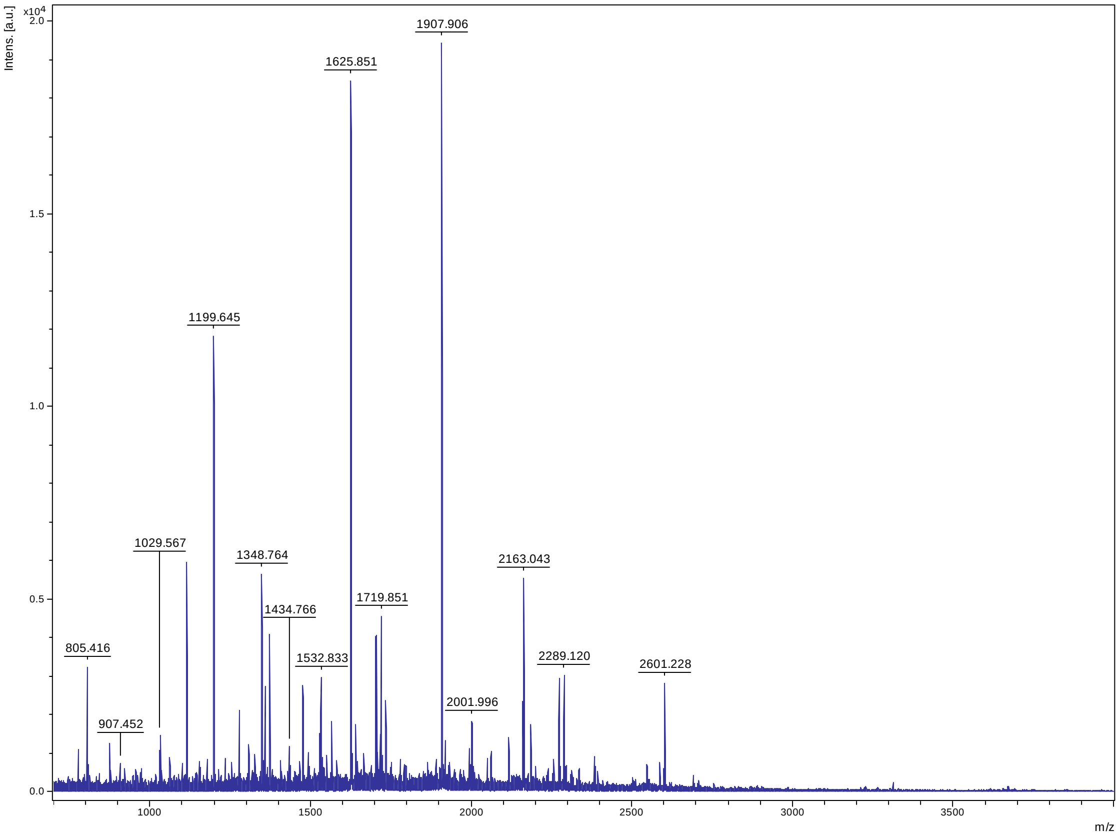


Match to: gi|51964302; Score: 113

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
13 - 31	1914.98	1913.98	1913.98	0.00	0	VCIIGSGPSAHTAAIYAAR
106 - 127	2073.12	2072.11	2072.11	0.00	0	VASDSTTVLADAVVVATGAVAR
128 - 140	1592.76	1591.76	1591.76	-0.00	1	RLHFAGSDAYWNR
129 - 140	1436.66	1435.66	1435.66	-0.00	0	LHFAGSDAYWNR
141 - 156	1664.78	1663.78	1663.78	0.00	0	GISACAVCDGAAPIFR
157 - 178	2278.13	2277.12	2277.13	-0.01	0	NKPIAVIGGGDSAMEESNFLTK
157 - 178	2294.14	2293.14	2293.13	0.01	0	NKPIAVIGGGDSAMEESNFLTK Oxidation (M)
179 - 188	1244.65	1243.64	1243.65	-0.00	0	YGSHVYIIHR
241 - 260	2130.12	2129.11	2129.12	-0.00	0	ISDLQVSGLFFAIGHEPATK
261 - 286	2691.38	2690.37	2690.36	0.02	0	FLGGQLELDADGYVATKPGSTHTSVK
301 - 329	2976.44	2975.43	2975.38	0.06	0	QAITAAGSGCMAALDAEHYLQEVGAQEGK
301 - 329	2992.38	2991.38	2991.37	0.01	0	QAITAAGSGCMAALDAEHYLQEVGAQEGK Oxidation (M)

Spot 2049



Match to: gi|34897250; Score: 92

Matched peptides:

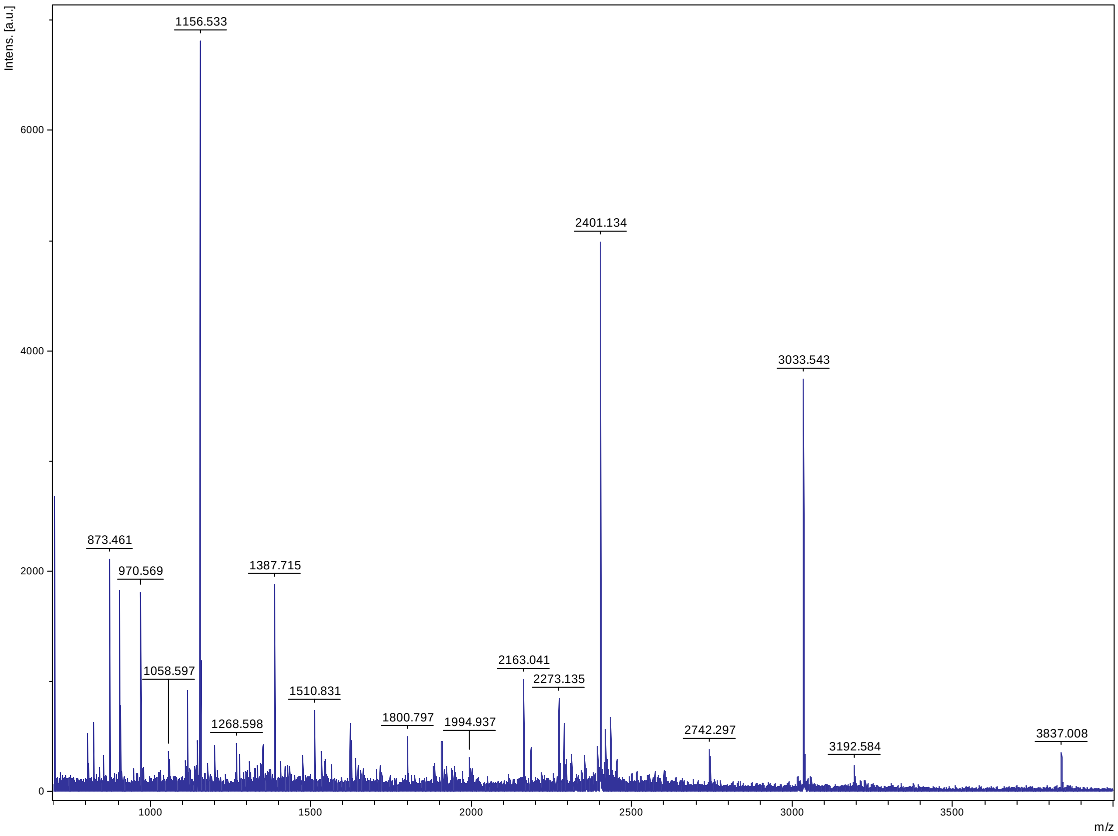
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
77 - 90	1372.72	1371.72	1371.70	0.02	0	GAGVDIDAGTELVR
77 - 91	1528.81	1527.81	1527.80	0.01	1	GAGVDIDAGTELVRR
257 - 267	1199.64	1198.64	1198.63	0.01	0	SGLSLNDQLPR
268 - 288	2255.08	2254.08	2254.12	-0.04	0	NDGMITTVGEALMAPTVIYVK 2 Oxidation (M)
289 - 296	956.57	955.57	955.57	0.00	0	QVLEIINK
301 - 316	1625.85	1624.85	1624.83	0.02	0	GIAHITGGGFTDNIPR
317 - 325	875.50	874.49	874.49	0.00	0	VFPSGLGAK
326 - 338	1532.83	1531.83	1531.82	0.01	0	IFTAAWEVPPVFR
339 - 352	1703.86	1702.86	1702.83	0.03	1	WIQEVGKIEDAEMR
339 - 352	1719.85	1718.85	1718.83	0.02	1	WIQEVGKIEDAEMR Oxidation (M)
368 - 385	1907.91	1906.90	1906.89	0.01	0	EAADGILEGTHGPNHAYR
386 - 398	1358.71	1357.71	1357.69	0.02	0	IGEVISGEGVHYV

Match to: gi|57899533; Score: 82

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
121 - 132	1358.71	1357.71	1357.61	0.10	0	IGYSMISDAEEK Oxidation (M)
140 - 161	2160.15	2159.15	2159.16	-0.01	0	SVLVEPTSGNTGIGLAFIAASR
196 - 203	805.42	804.41	804.42	-0.00	1	GMKGAVDK
243 - 263	1919.02	1918.01	1918.03	-0.01	1	GKVDVFIGGIGTGGTISGAGR
245 - 263	1733.93	1732.92	1732.91	0.01	0	VDVFIGGIGTGGTISGAGR
274 - 294	2116.12	2115.12	2115.13	-0.02	0	VIGIEPSESNILSGGKPGPHK
295 - 305	1114.64	1113.64	1113.63	0.01	0	IQGIGAGFVPR
362 - 373	1348.76	1347.76	1347.75	0.01	0	LVVVVFPSFGER
374 - 384	1326.73	1325.73	1325.73	-0.01	0	YLSSILFQSIR
374 - 389	2002.00	2000.99	2000.99	0.01	1	YLSSILFQSIREECEK

Spot 2052

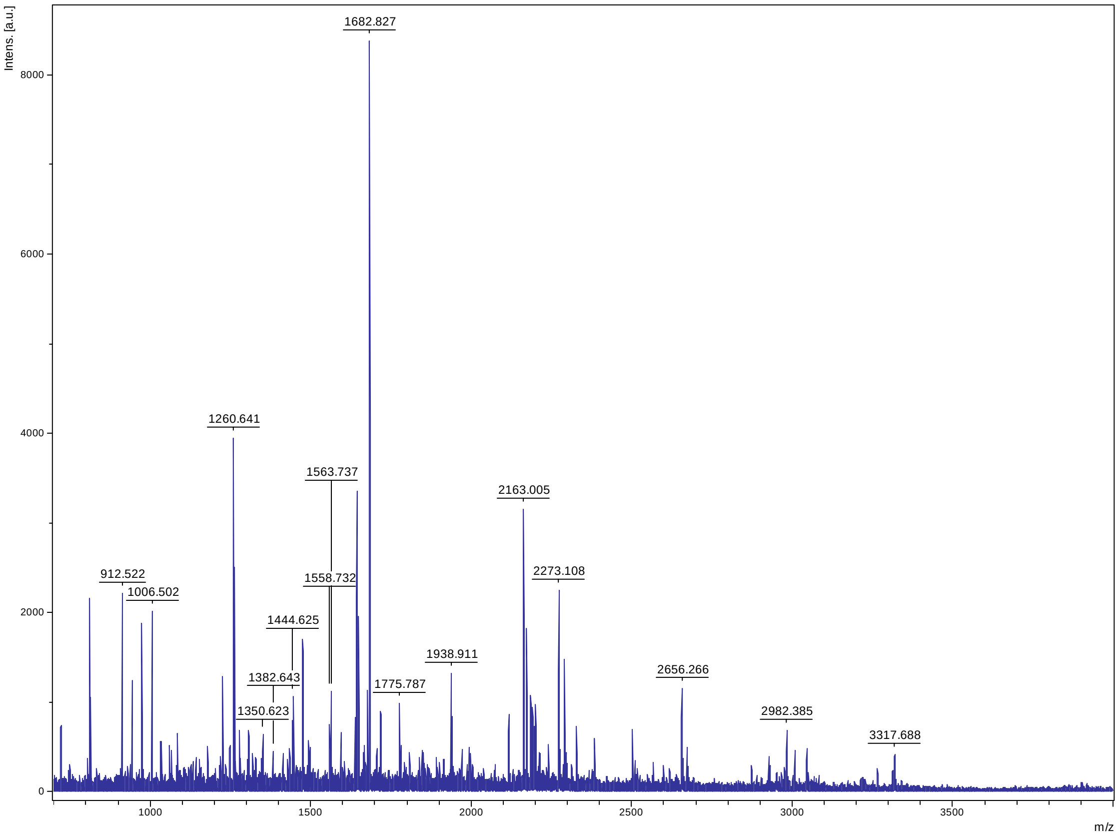


Match to: gi|108864048 Score: 69 Expect: 0.0098

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
68 - 81	1543.8978	1542.8905	1542.8114	0.0792	1	K.RLASIGLENTEANR.Q	
69 - 81	1387.7927	1386.7854	1386.7103	0.0752	0	R.LASIGLENTEANR.Q	
118 - 126	1058.6197	1057.6124	1057.6019	0.0105	0	K.IVDILTEQK.I	
136 - 158	2401.1367	2400.1294	2400.1491	-0.0197	0	K.GLVPLAGSNNESWCQGLDGLASR.E	Carbamidomethyl (C)
159 - 168	1156.5822	1155.5749	1155.5308	0.0441	0	R.EAAYYQQGAR.F	
174 - 188	1510.9050	1509.8977	1509.8402	0.0575	0	R.TVVSIPNGPSELAVK.E	
189 - 196	873.4026	872.3953	872.4504	-0.0551	0	K.EAAWGLAR.Y	
197 - 224	3033.4248	3032.4175	3032.5454	-0.1279	0	R.YAAISQDNGLVPIVEPEILLDGEHGIDR.T	
265 - 278	1622.8371	1621.8298	1621.7947	0.0351	1	K.DRATPEQVSDYTLK.L	
267 - 278	1351.7398	1350.7325	1350.6667	0.0658	0	R.ATPEQVSDYTLK.L	
334 - 343	1115.5905	1114.5832	1114.5407	0.0425	0	K.TWGGQPENVK.A	
344 - 352	970.5548	969.5475	969.5607	-0.0132	0	K.AAQDALLLR.A	

Spot 2053

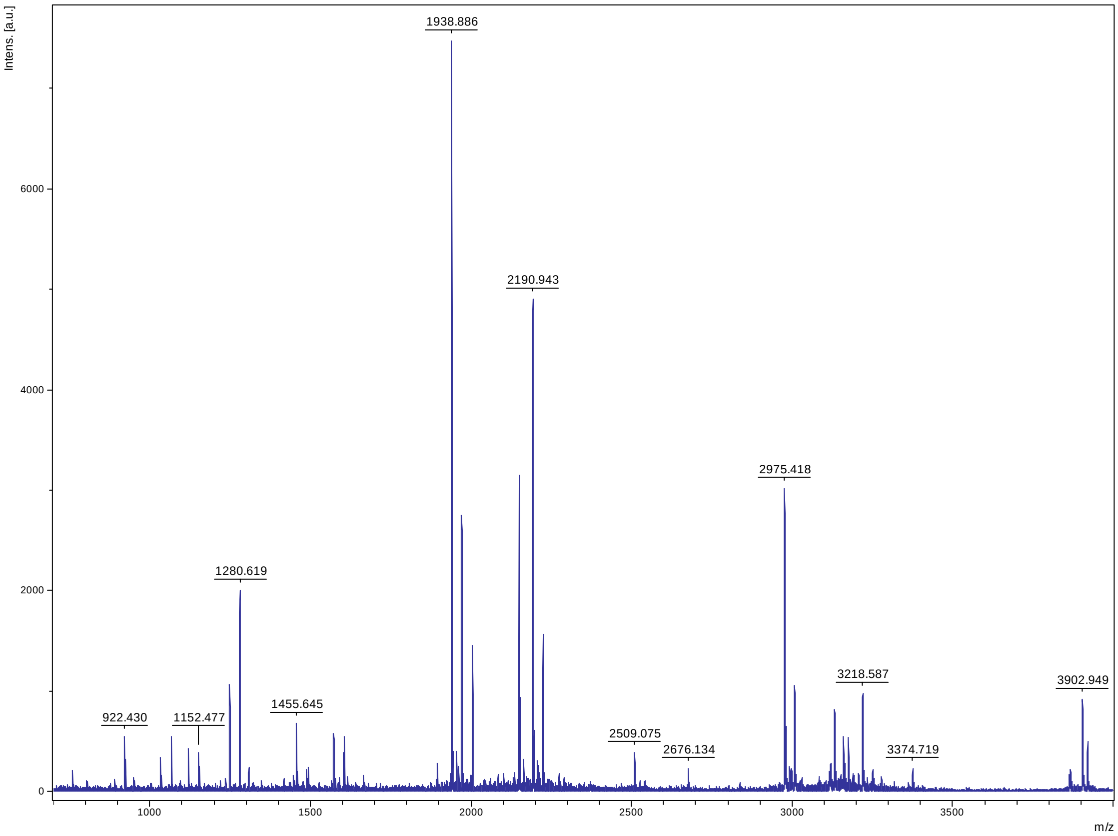


Match to: gi|34015231; Score: 181

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
8 - 17	1225.67	1224.67	1224.67	-0.00	0	GHERPLTFLR
18 - 30	1558.73	1557.73	1557.72	0.00	1	YNRDGDLLFSCAK
31 - 44	1643.71	1642.70	1642.71	-0.01	0	DHTPNVWFADNGDR
50 - 62	1444.63	1443.62	1443.63	-0.01	0	GHNGAVWSCDVSR
78 - 85	974.52	973.52	973.50	0.02	0	LWDVQTGR
86 - 91	812.44	811.44	811.42	0.02	0	ELFTFR
98 - 125	2982.38	2981.38	2981.47	-0.09	0	SVEFAIGDGLAVITTDNFMENVPTAQVK Oxidation (M)
126 - 146	2328.13	2327.13	2327.19	-0.05	1	RIAEDPDDQSEESLLVITGIK
127 - 146	2172.04	2171.04	2171.08	-0.04	0	IAEDPDDQSEESLLVITGIK
152 - 159	912.52	911.52	911.50	0.02	0	AVWGPLNR
160 - 171	1260.64	1259.64	1259.67	-0.03	0	TIITAGEDATIR
172 - 182	1350.62	1349.62	1349.63	-0.01	0	IWDTETGQCLK
200 - 213	1563.74	1562.74	1562.74	-0.00	0	SADWSHFLTGSLDK
276 - 285	1085.62	1084.62	1084.61	0.01	0	ILQEEIGGVK
286 - 301	1682.83	1681.83	1681.83	-0.01	0	GHFGPINALAFNPDGR
314 - 326	1648.79	1647.79	1647.80	-0.02	1	LHHFDSDYFNIKI

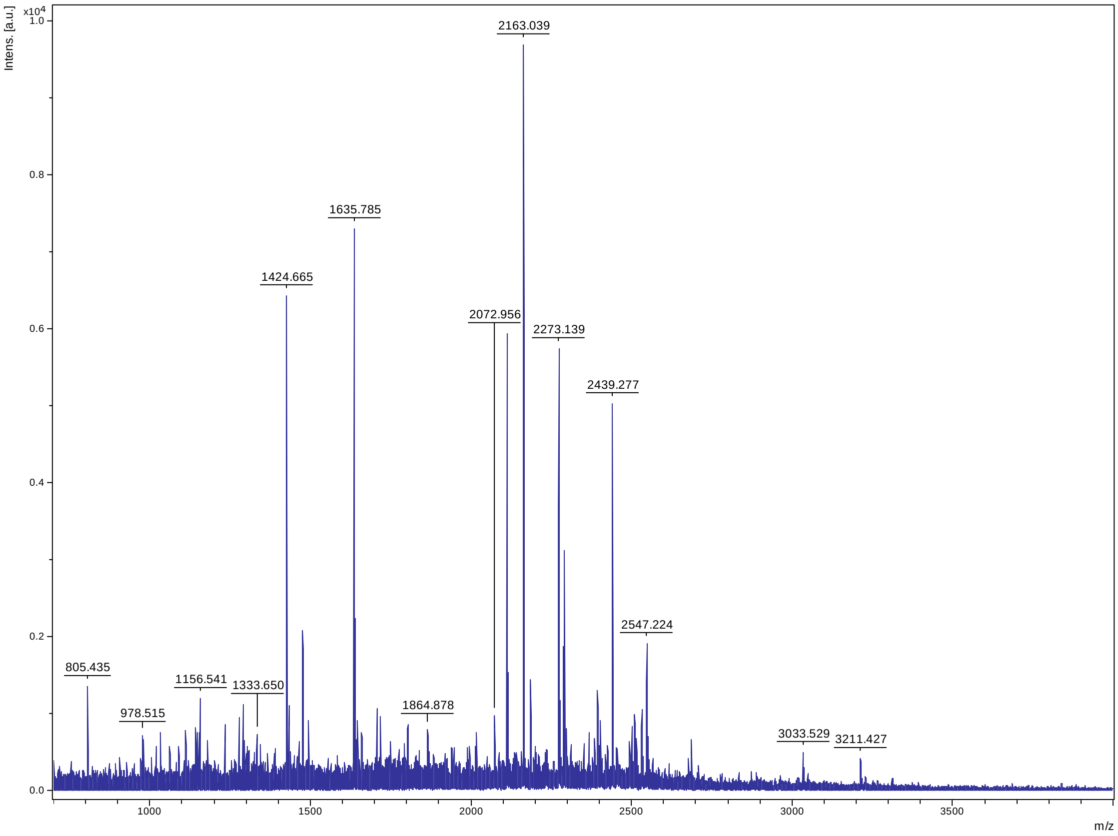
Spot 2057



Match to: gi|1346109; Score: 230

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
40 - 69	3218.59	3217.59	3217.60	-0.02	1	DKSLLVWDLTNPVQNVGEGAGASEYGVPFR
42 - 69	2975.42	2974.42	2974.48	-0.07	0	SLLVWDLTNPVQNVGEGAGASEYGVPFR
42 - 70	3131.53	3130.53	3130.58	-0.05	1	SLLVWDLTNPVQNVGEGAGASEYGVPFRR
101 - 111	1248.63	1247.63	1247.65	-0.02	0	LWDLSTGVTTR
113 - 130	2004.97	2003.97	2004.01	-0.04	1	FVGHDKDVLSVAFSVDNR
143 - 151	1120.52	1119.52	1119.54	-0.02	0	LWNTLGECK
152 - 172	2190.94	2189.94	2189.99	-0.05	0	YTIGGDLGGGEGHNGWVSCVR
173 - 189	1938.89	1937.88	1937.93	-0.04	0	FSPNTFQPTIVSGSWDR
193 - 200	1034.48	1033.47	1033.50	-0.03	0	VWNLTNCK
203 - 229	2676.13	2675.13	2675.21	-0.08	0	CNLEGHGGYVNAVAVSPDGSLCASGGK
230 - 243	1572.79	1571.79	1571.83	-0.04	1	DGVTLLWDLAEGKR
244 - 262	2150.02	2149.02	2149.06	-0.04	0	LYSLDAGSIIHSLCFSPNR
263 - 274	1455.64	1454.64	1454.69	-0.04	0	YWLCAATQDSIK
275 - 281	890.42	889.42	889.45	-0.04	0	IWDLESK
282 - 295	1602.86	1601.86	1601.91	-0.05	0	HIVQDLKPEIPVSK
296 - 323	3158.38	3157.38	3157.41	-0.03	0	NQMLYCTSLNWSADGSTLYAGYTDGTIR
296 - 323	3174.40	3173.40	3173.41	-0.00	0	NQMLYCTSLNWSADGSTLYAGYTDGTIR Oxidation (M)

Spot 2060

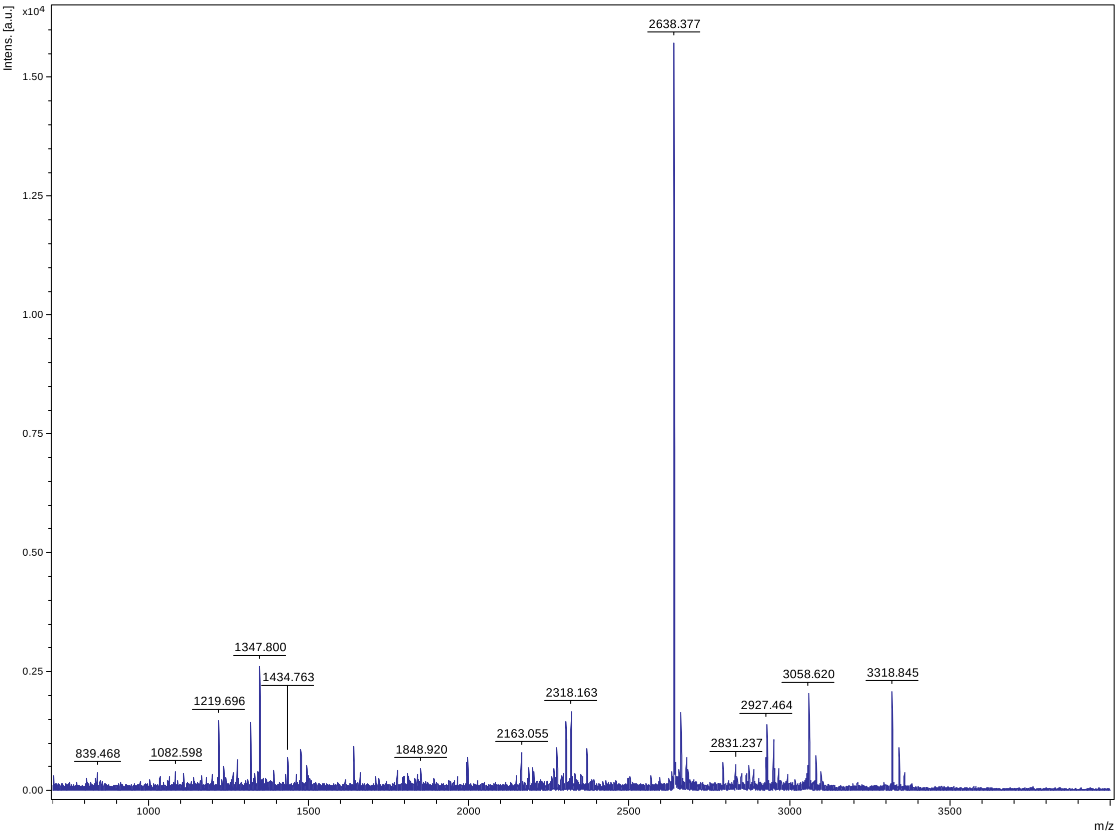


Match to: gi|51963288; Score: 81

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
70 - 84	1635.79	1634.78	1634.77	0.01	0	SYVFGEDVGFGGVFR
98 - 121	2509.19	2508.18	2508.23	-0.04	0	VFNTPLCEQGIAGFAVGLAAMGNR Oxidation (M)
150 - 162	1424.67	1423.66	1423.65	0.01	0	SGNEFNCGGLTIR
202 - 220	2112.16	2111.16	2111.18	-0.02	1	GLLLASIRDPNPVVFFEPK
225 - 246	2531.24	2530.24	2530.25	-0.01	0	LAVEEVPEEDYMLPLSEAEVIR
225 - 246	2547.22	2546.22	2546.25	-0.02	0	LAVEEVPEEDYMLPLSEAEVIR Oxidation (M)
273 - 283	1290.64	1289.64	1289.63	0.01	0	DGISCELIDLR
284 - 299	1802.93	1801.92	1801.95	-0.02	1	TLIPWDKETVEASVSK
303 - 326	2439.28	2438.27	2438.28	-0.01	0	LLVSHEAPITGGFGAEIAASITER

Spot 2072

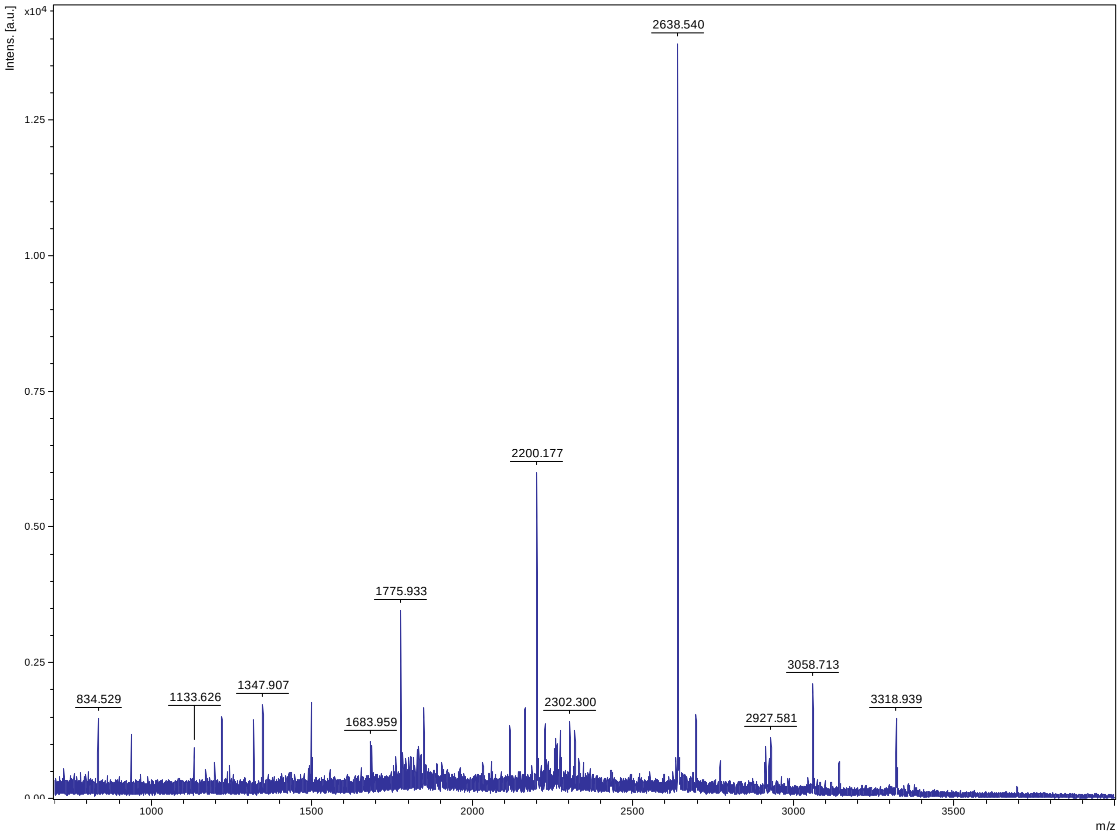


Match to: gi|50932771; Score: 74

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
29 - 47	1809.06	1808.06	1808.06	-0.00	0	VAILGAAGGIGQPLALLMK Oxidation (M)
48 - 80	3318.84	3317.84	3317.79	0.06	0	LNPLVSSLSLYDIAGTPGVAADVSHINSPALVK
81 - 106	2638.38	2637.37	2637.36	0.01	0	GFVGEEQLGEALEGSDVVIIPAGVPR
113 - 124	1318.70	1317.69	1317.69	0.00	0	DDLFNINAGIVK
167 - 178	1347.80	1346.80	1346.79	0.01	1	KLFGVTTLDVVR
168 - 178	1219.70	1218.69	1218.70	-0.00	0	LFGVTTLDVVR
268 - 294	2927.46	2926.46	2926.44	0.02	0	GLNGVPDVVECSFVQSTVTELPFFASK

Spot 2074

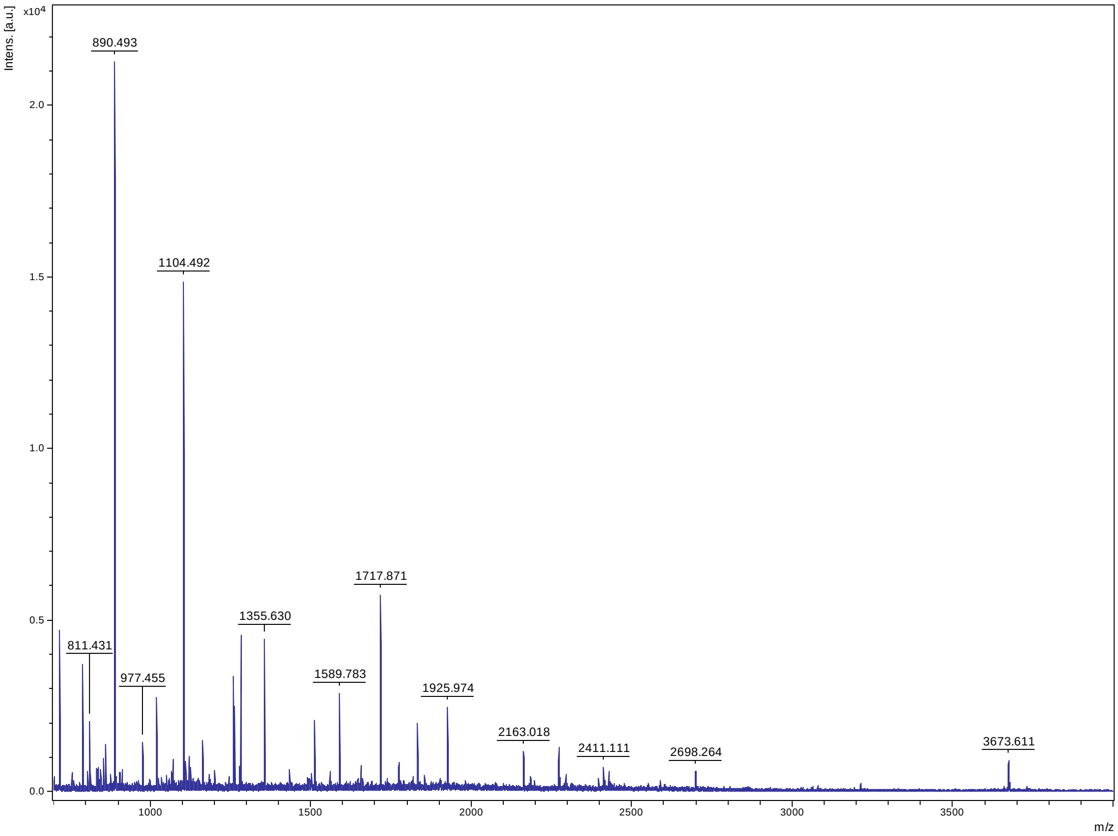


Match to: Q6K5G8_ORYSA Score: 72 Expect: 0.0045

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
6 - 13	833.5287	832.5215	832.4555	0.0660	0	K.IGINGFGR.I	
49 - 57	1133.6263	1132.6191	1132.5301	0.0889	0	K.YDTVHGQWK.H	
75 - 82	937.5724	936.5651	936.4487	0.1164	0	K.EVAVFGCR.N	Carbamidomethyl (C)
83 - 109	2923.5662	2922.5589	2922.3922	0.1667	1	R.NPEEIPWAAAGAEYVVESTGVFTDKDK.A	
189 - 196	834.5287	833.5215	833.3953	0.1262	0	K.TVDGPSMK.D	
237 - 250	1498.9606	1497.9533	1497.8402	0.1131	0	R.VPTVDVSVVDLTVR.L	
274 - 293	2200.1772	2199.1700	2199.0331	0.1369	0	K.GILGYVEEDLVSTDFQGDSR.S	
312 - 325	1775.9330	1774.9257	1774.7951	0.1306	0	K.LVSWYDNEWGYSTR.V	

Spot 2076

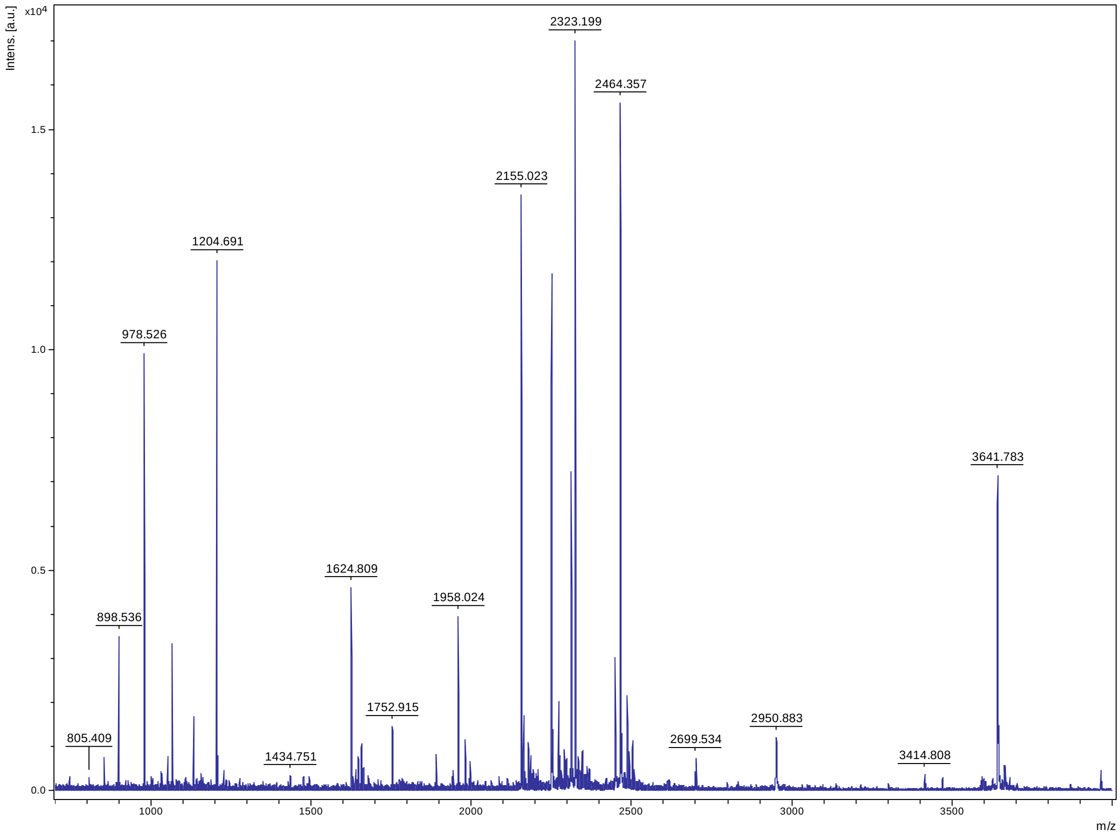


Match to: gi|55733795 Score: 72 Expect: 0.0039

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
19 - 30	1355.6299	1354.6226	1354.6517	-0.0291	1	R.GEDDKFSLAFAR.I	
24 - 30	811.4308	810.4236	810.4388	-0.0152	0	K.FSLAFAR.I	
31 - 39	1163.5579	1162.5506	1162.5771	-0.0265	0	R.IENHYFVNK.G	
40 - 54	1656.7761	1655.7688	1655.8155	-0.0466	0	K.GFLPSDSHLLDNVDK.I	
40 - 56	1925.9736	1924.9664	1925.0006	-0.0343	1	K.GFLPSDSHLLDNVDKIR.H	
82 - 89	977.4546	976.4473	976.4654	-0.0181	0	K.AWPEAEFK.M	
90 - 113	2411.1108	2410.1036	2410.1433	-0.0398	0	K.MVPDAGHSANEVGVAAELVSANEK.L	Oxidation (M)

Spot 2078

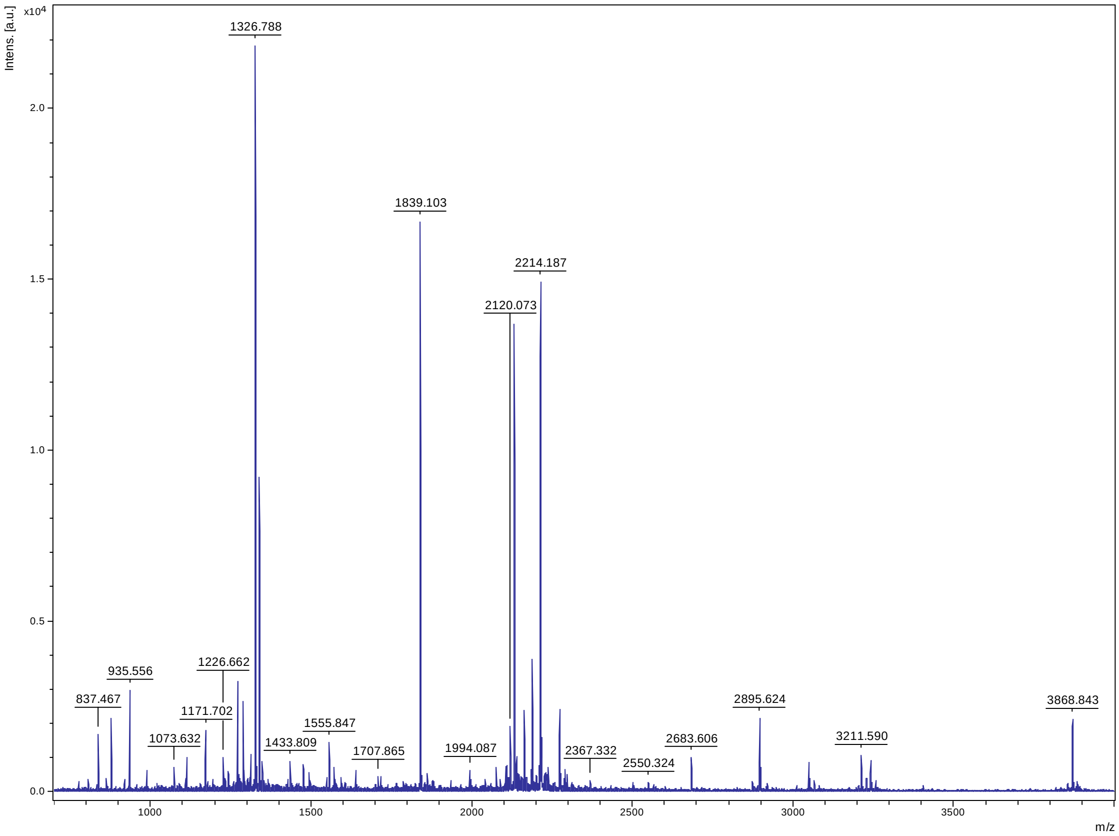


Match to: gi|34894098; Score: 205

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 9	805.41	804.41	804.40	0.01	1	ASGGEEKK
12 - 23	1204.69	1203.69	1203.70	-0.01	0	ILVVGGTGYIGR
24 - 31	852.49	851.48	851.50	-0.01	0	HVVLASAR
42 - 58	1888.97	1887.97	1887.97	-0.00	1	DLSPSDPAKSQLLQSFR
51 - 58	978.53	977.52	977.53	-0.01	0	SQLLQSFR
59 - 80	2323.20	2322.20	2322.20	0.00	0	DAGVTLLHGDLYDHASLLSAVR
81 - 99	1958.02	1957.02	1957.04	-0.02	0	DADVVISTLGALQIADQTK
114 - 134	2311.13	2310.13	2310.14	-0.01	1	RFLPSEFGLDPDHTGAVEPAR
115 - 134	2155.02	2154.02	2154.04	-0.02	0	FLPSEFGLDPDHTGAVEPAR
193 - 213	2250.15	2249.15	2249.16	-0.01	0	VVFVEEGDIGTYTVLAAVDPR
218 - 225	898.54	897.53	897.54	-0.01	0	TVNIRPAK
226 - 239	1624.81	1623.81	1623.83	-0.02	0	NAVSHEELVALWEK
226 - 240	1752.91	1751.91	1751.92	-0.01	1	NAVSHEELVALWEKK
248 - 257	1132.62	1131.62	1131.62	-0.00	0	VYVPEDAVLK
258 - 279	2447.30	2446.30	2446.32	-0.02	0	QIQESEIPLNIVLSIAHAGYIR Pyro-glu (N-term Q)
258 - 279	2464.36	2463.35	2463.35	0.01	0	QIQESEIPLNIVLSIAHAGYIR
280 - 312	3641.78	3640.78	3640.74	0.04	0	GETTTPLDPATAVEATQLFPDVQYTTVDDYLNR

Spot 2080

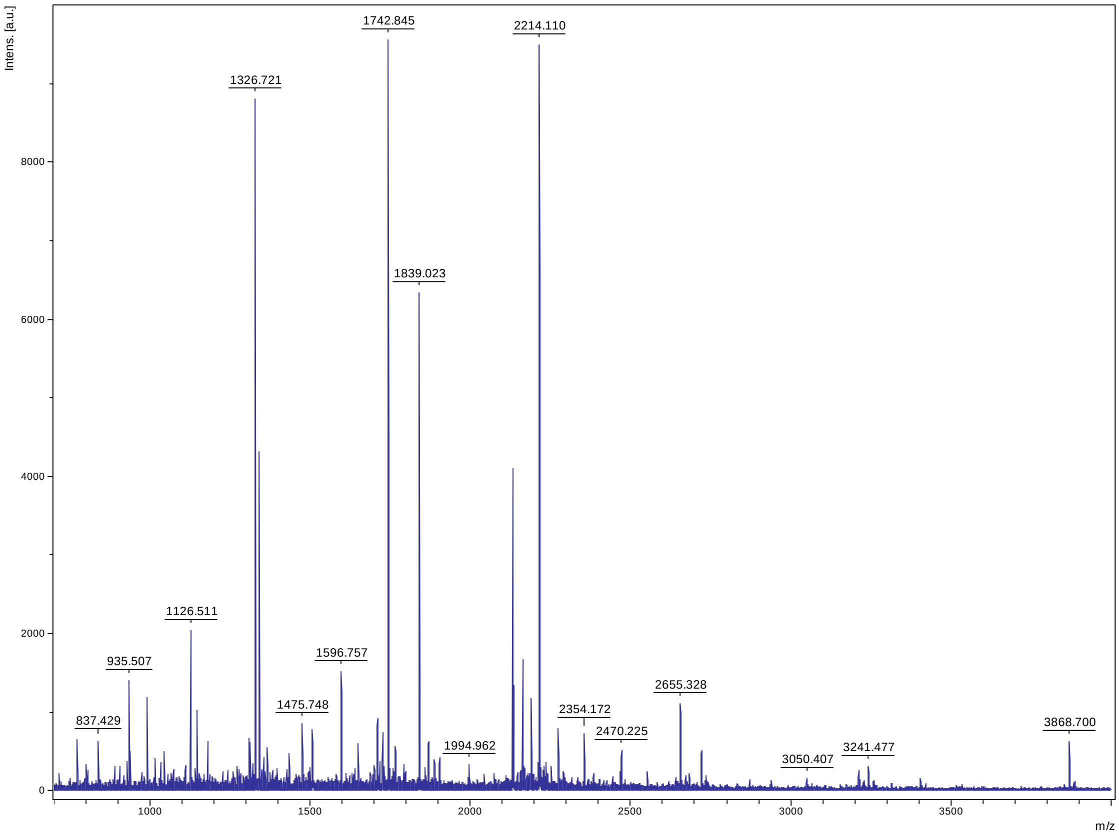


Match to: gi|50899346 Score: 76 Expect: 0.0018

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
29 - 48	2041.0172	2040.0099	2040.0210	-0.0111	1	R.AALPSFGRALSTQTGFASCR.K	
68 - 79	1271.6571	1270.6498	1270.6703	-0.0205	0	R.AMSAQGLPIDLR.G	
68 - 79	1287.6590	1286.6517	1286.6652	-0.0135	0	R.AMSAQGLPIDLR.G	Oxidation (M)
83 - 100	1839.0321	1838.0248	1837.8998	0.1250	0	R.AFIAGVADDNGYGWAIAK.A	
101 - 126	2683.4990	2682.4917	2682.4744	0.0173	0	K.ALAAAGAEILVGTWVPALNIFETSLR.R	
170 - 179	1112.4958	1111.4885	1111.5298	-0.0413	0	R.YAGSSNWTVK.E	
180 - 206	2895.5190	2894.5117	2894.5024	0.0093	1	K.EVAETVKNDFGTIDILVHSLANGPEVK.N	
187 - 206	2139.1274	2138.1201	2138.1007	0.0194	0	K.NDFGTIDILVHSLANGPEVK.N	
256 - 268	1225.5741	1224.5668	1224.5808	-0.0140	0	R.TIPGYGGGMSSAK.A	
277 - 284	878.3488	877.3415	877.4657	-0.1242	0	R.VLAYEAGR.K	
290 - 301	1171.6105	1170.6032	1170.6356	-0.0324	0	R.VNTISAGPLGSR.A	
312 - 324	1555.7819	1554.7746	1554.7752	-0.0005	0	K.MIEYSYVNAPLQK.E	
312 - 324	1571.7803	1570.7730	1570.7701	0.0029	0	K.MIEYSYVNAPLQK.E	Oxidation (M)

Spot 2084

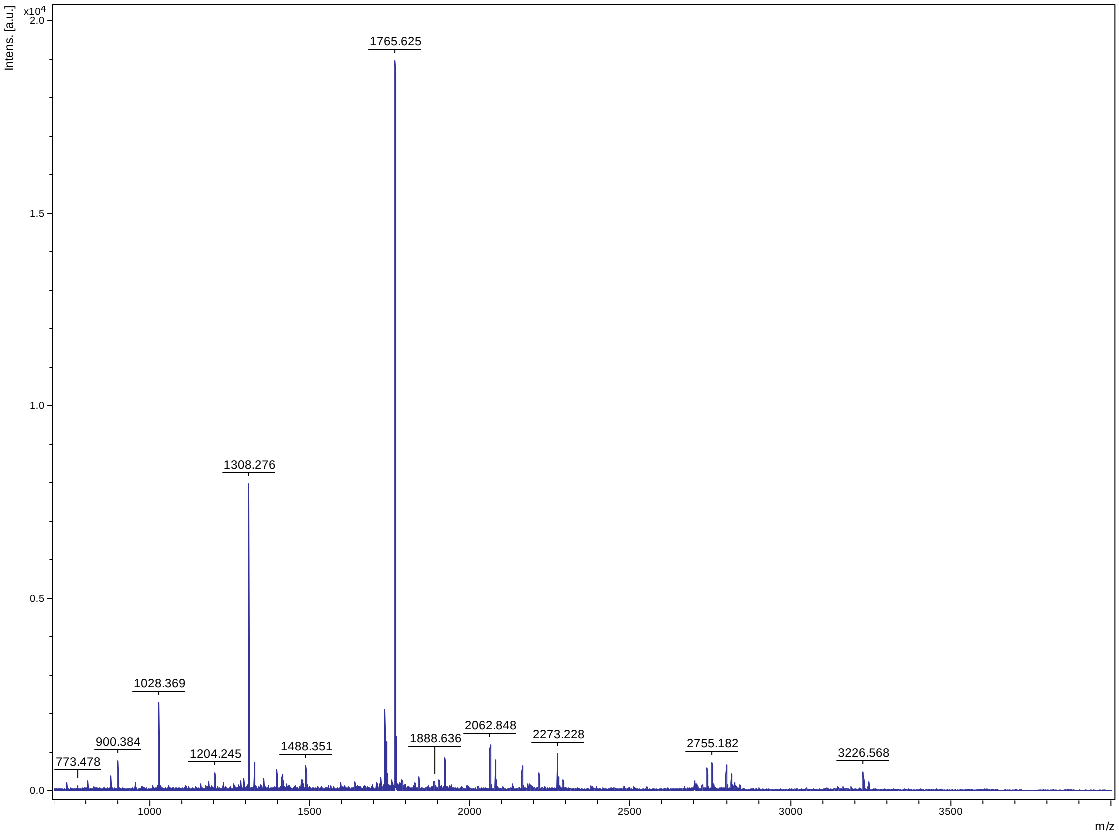


Match to: gi|55733910 Score: 73 Expect: 0.0033

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 24	2551.2448	2550.2375	2550.3515	-0.1140	0	M.LFNLGLTAYLIGNMTNLVVEGTR.R Acetyl (N-term)
63 - 77	1742.8688	1741.8615	1741.8669	-0.0053	0	R.AESLNQQQLMDQLPK.S
78 - 93	1868.9327	1867.9254	1867.9939	-0.0685	1	K.SICKGICEYLFLPVVK.D Carbamidomethyl (C)
82 - 99	2188.1031	2187.0958	2187.1689	-0.0731	1	K.GICEYLFLPVVKDVYLFK.G Acetyl (N-term)
182 - 190	1145.6222	1144.6149	1144.6386	-0.0237	1	R.TRTLCQLLR.L Acetyl (N-term)
287 - 297	1308.6766	1307.6693	1307.6795	-0.0101	0	K.GYEDCVLVLLK.Q Carbamidomethyl (C)
287 - 305	2236.1008	2235.0935	2235.1391	-0.0456	1	K.GYEDCVLVLLKQACNVNIK.D 2 Carbamidomethyl (C)
324 - 350	3049.4696	3048.4623	3048.5868	-0.1244	1	K.IFNILYHFARVSSPHHAAGDLLCLAAR.R Carbamidomethyl (C)
352 - 362	1272.6624	1271.6551	1271.7085	-0.0534	1	R.GDLDTLRELLK.H
426 - 449	2470.2381	2469.2308	2469.3703	-0.1395	1	K.TRELAHPVTIVVDSPSPAAAAVIR.E
450 - 458	935.4346	934.4273	934.3992	0.0282	0	R.EVGSSGDSR.N Acetyl (N-term)
518 - 536	2132.0103	2131.0030	2131.0830	-0.0800	1	R.KTLIMNDEGAEIDSIDVIR.D
537 - 561	2683.3599	2682.3526	2682.2152	0.1374	1	R.DNDKLFIVTEEHMTAVASMDSVSGS.-

Spot 2087

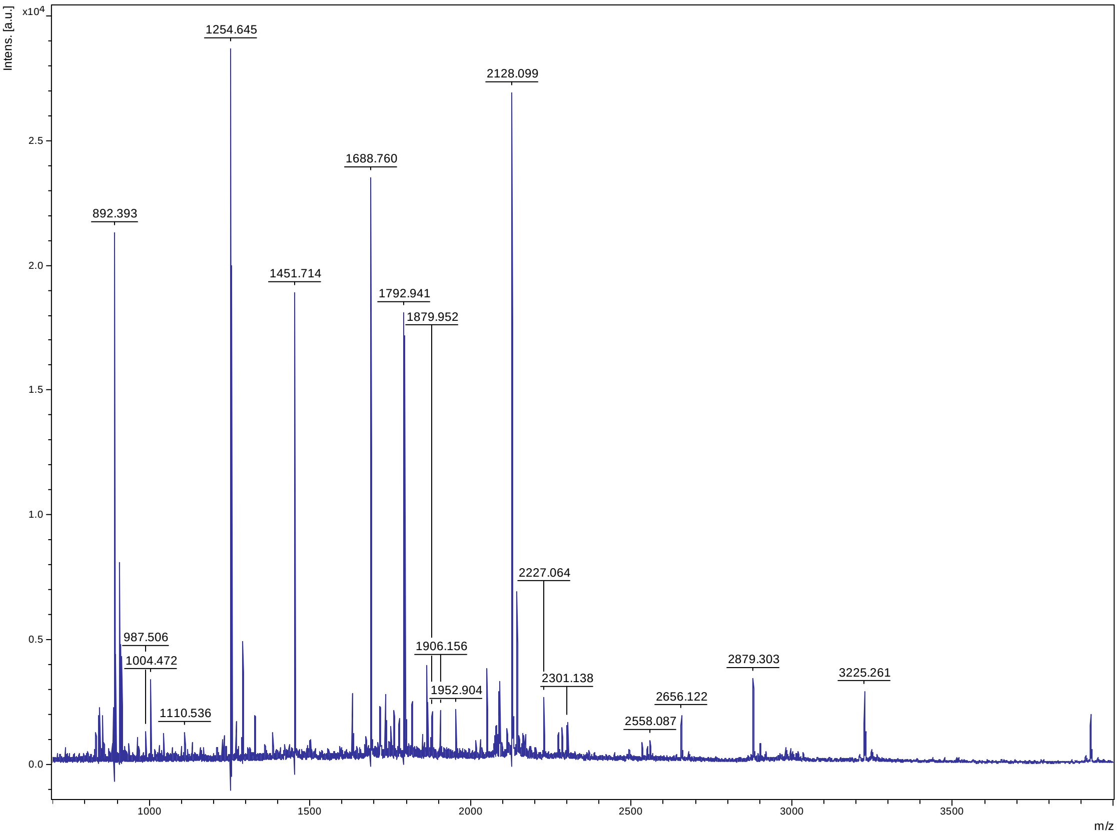


Match to: gi|55168333 Score: 78 Expect: 0.00096

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
43 - 60	1733.8308	1732.8235	1732.8995	-0.0760	0	K.LSLNAGGLALPSFSDSGK.V
126 - 151	2738.4335	2737.4262	2737.3169	0.1093	0	K.AGQFTNMQLTGATGIFTGFSTEFVGR.A
177 - 189	1355.5036	1354.4963	1354.6841	-0.1877	1	K.SGQKLPEPSAADR.E
211 - 223	1397.6378	1396.6305	1396.8111	-0.1806	0	R.VVVLNTANLPMVK.E
258 - 270	1229.4708	1228.4635	1228.6523	-0.1888	1	R.GSGRVQVVGADGK.R
271 - 287	1922.0039	1920.9966	1921.0533	-0.0567	1	K.RVLDTHVEGGNLFIVPR.F
325 - 343	2062.9803	2061.9730	2061.9928	-0.0198	0	K.AISPEVLEASFNATPEMEK.L
349 - 359	1308.4754	1307.4681	1307.6510	-0.1828	1	K.RIDSEIFFAPN.-

Spot 2088

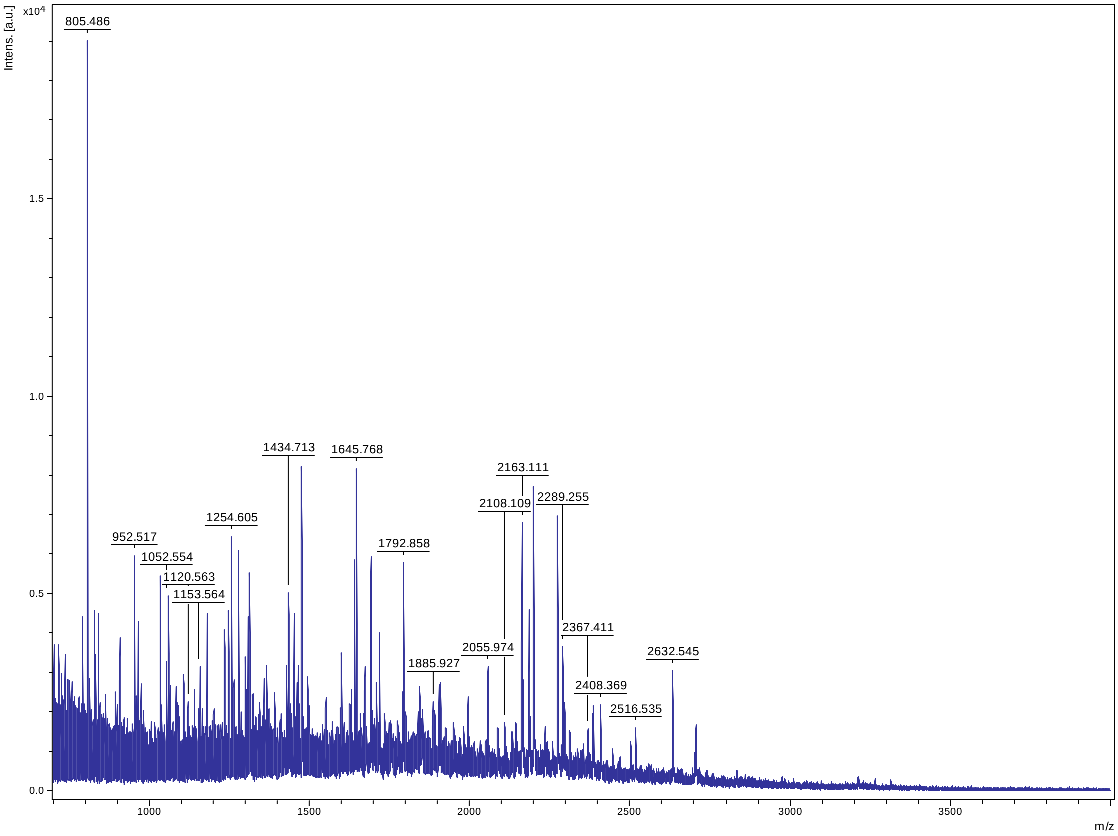


Match to: gi|50940457 Score: 68 Expect: 0.01

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
62 - 71	922.4042	921.3969	921.4919	-0.0950	0	K.LGGSSAFVGK.F	
103 - 111	963.5481	962.5408	962.5800	-0.0392	0	R.TALAFVTLK.S	
117 - 122	892.3440	891.3367	891.3949	-0.0581	0	R.EFMFYR.N	
117 - 141	3033.4700	3032.4627	3032.4623	0.0005	1	R.EFMFYRNPSADMLLTEAELNLDLIR.R	2 Oxidation (M)
123 - 142	2300.2743	2299.2670	2299.1841	0.0829	1	R.NPSADMLLTEAELNLDLIRR.A	Oxidation (M)
145 - 159	1735.9686	1734.9613	1734.8763	0.0850	0	K.IFHYGSISLITEPCR.S	
160 - 167	858.3421	857.3348	857.4177	-0.0829	0	R.SAHVAAMR.A	Oxidation (M)
171 - 183	1394.7604	1393.7531	1393.6660	0.0872	0	K.SAGILCSYDPNVR.L	
171 - 183	1436.7087	1435.7014	1435.6765	0.0249	0	K.SAGILCSYDPNVR.L	Acetyl (N-term)
171 - 183	1451.7828	1450.7755	1450.6874	0.0881	0	K.SAGILCSYDPNVR.L	Carbamidomethyl (C)
195 - 202	887.4470	886.4397	886.5276	-0.0879	0	R.AGILSIWK.E	
195 - 208	1632.9163	1631.9090	1631.8922	0.0168	1	R.AGILSIWKEADFIK.V	Acetyl (N-term)
203 - 226	2656.2962	2655.2889	2655.2187	0.0702	1	K.EADFIKVSDDEVAFLTQGDANDEK.N	
209 - 237	3225.5380	3224.5307	3224.5513	-0.0205	1	K.VSDDEVAFLTQGDANDEKNVLSLWFDGLK.L	
227 - 237	1291.7535	1290.7462	1290.6972	0.0491	0	K.NVLSLWFDGLK.L	
238 - 246	987.5222	986.5149	986.5648	-0.0498	0	K.LLIVTDGEK.G	
238 - 249	1360.7566	1359.7493	1359.7180	0.0313	1	K.LLIVTDGEKGCR.Y	Carbamidomethyl (C)
257 - 286	2879.5135	2878.5062	2878.4711	0.0351	0	K.GSVPGFSVNTVDTTGAGDAFVGSLLVNVAK.D	
316 - 336	2034.1340	2033.1267	2033.1520	-0.0253	1	K.GAIPALPTVAVAQELISKAAN.-	

Spot 2090

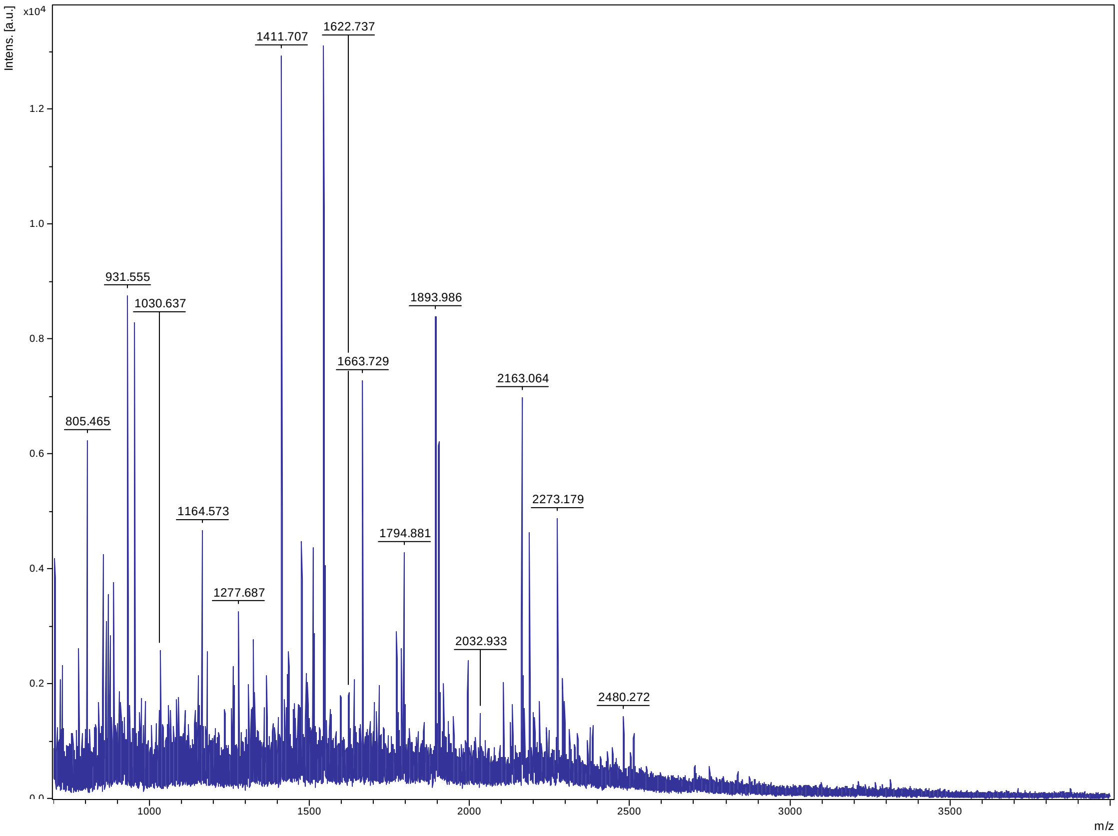


Match to: gi|15823775; Score: 97

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
28 - 36	965.56	964.56	964.53	0.02	0	SGFISLVSR
86 - 106	2163.11	2162.11	2162.08	0.03	1	LNGGLGTTMGCTGPKSVIEVR Oxidation (M)
151 - 168	2198.08	2197.08	2197.02	0.06	0	YSNSNIEIHTFNQSQYPR
186 - 205	2144.04	2143.04	2142.98	0.06	0	DGWYPPGHGDVFPSLNNSGK
206 - 214	958.57	957.57	957.55	0.02	0	LDTLLAQGK
258 - 267	1052.55	1051.55	1051.53	0.02	0	GGTLISYEGR
268 - 285	2108.11	2107.11	2107.09	0.01	0	VQLLEIAQVPDEHVNEFK
330 - 342	1312.69	1311.69	1311.75	-0.06	0	VLQLETAAGAAIR
343 - 354	1390.66	1389.66	1389.78	-0.12	1	FFEKAIGINVPR
347 - 354	839.56	838.56	838.50	0.06	0	AIGINVPR
347 - 356	1082.59	1081.59	1081.64	-0.05	1	AIGINVPRSR
388 - 402	1629.74	1628.74	1628.80	-0.07	0	TNPSNPSIELGPEFK
425 - 438	1451.64	1450.64	1450.75	-0.10	0	VSGDVWFGSGVTLK

Spot 2093

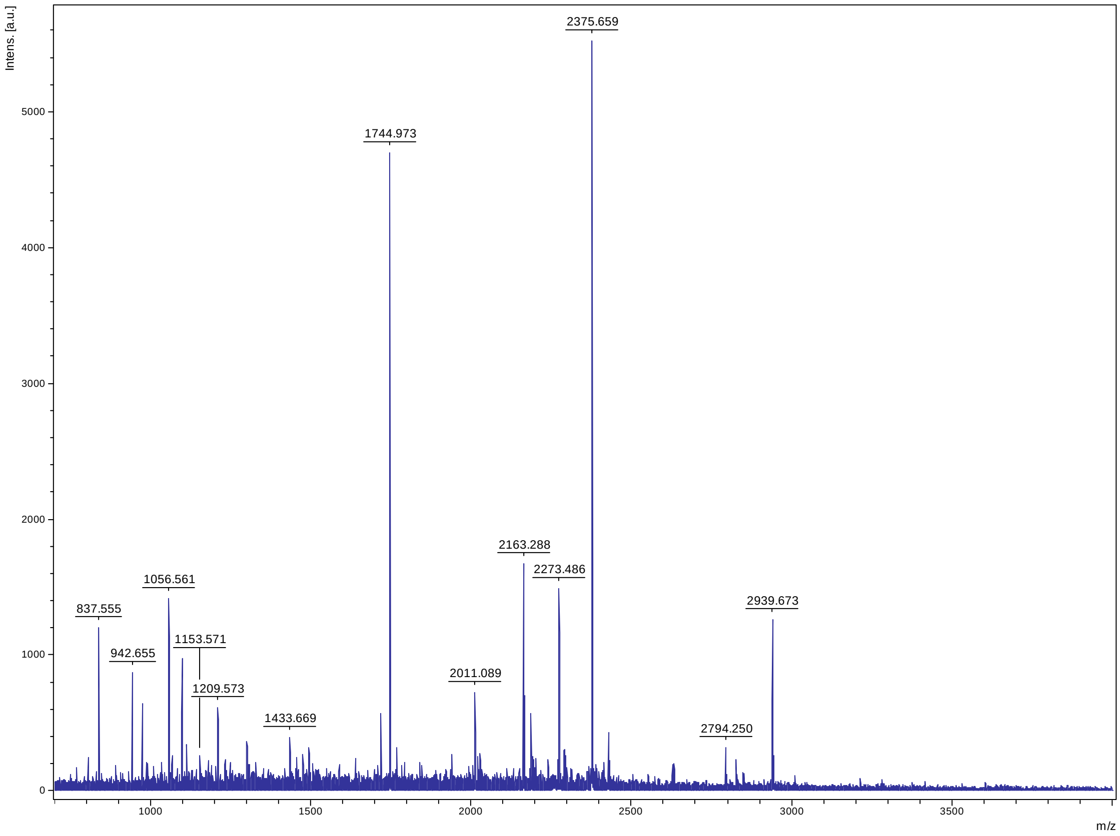


Match to: gi|34899936; Score: 92

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
6 - 12	876.48	875.47	875.42	0.06	0	VVVDECR
13 - 25	1411.71	1410.70	1410.71	-0.01	0	GVLFVYSDGAVER
27 - 36	986.57	985.57	985.53	0.03	0	AAPGFATPVR
27 - 44	1902.93	1901.93	1901.93	0.00	1	AAPGFATPVRDDGSVEWK
45 - 52	864.47	863.46	863.41	0.05	0	DAVFDAAR
86 - 96	1511.66	1510.65	1510.64	0.01	0	TWPNCQNYCLR
97 - 111	1543.83	1542.83	1542.84	-0.01	0	LAAELGAVVVAPDYR
153 - 171	1893.99	1892.98	1892.99	-0.00	0	VFVSGDSAGGTIAHHLAVR
186 - 201	1769.89	1768.89	1768.90	-0.01	0	VAGYVQLMPFFGGVER
186 - 201	1785.88	1784.87	1784.89	-0.02	0	VAGYVQLMPFFGGVER Oxidation (M)
202 - 216	1663.73	1662.73	1662.73	-0.00	0	TPSEAACPDDAFLNR
316 - 327	1164.57	1163.57	1163.56	0.01	0	LFVDTDGGGAR

Spot 2095

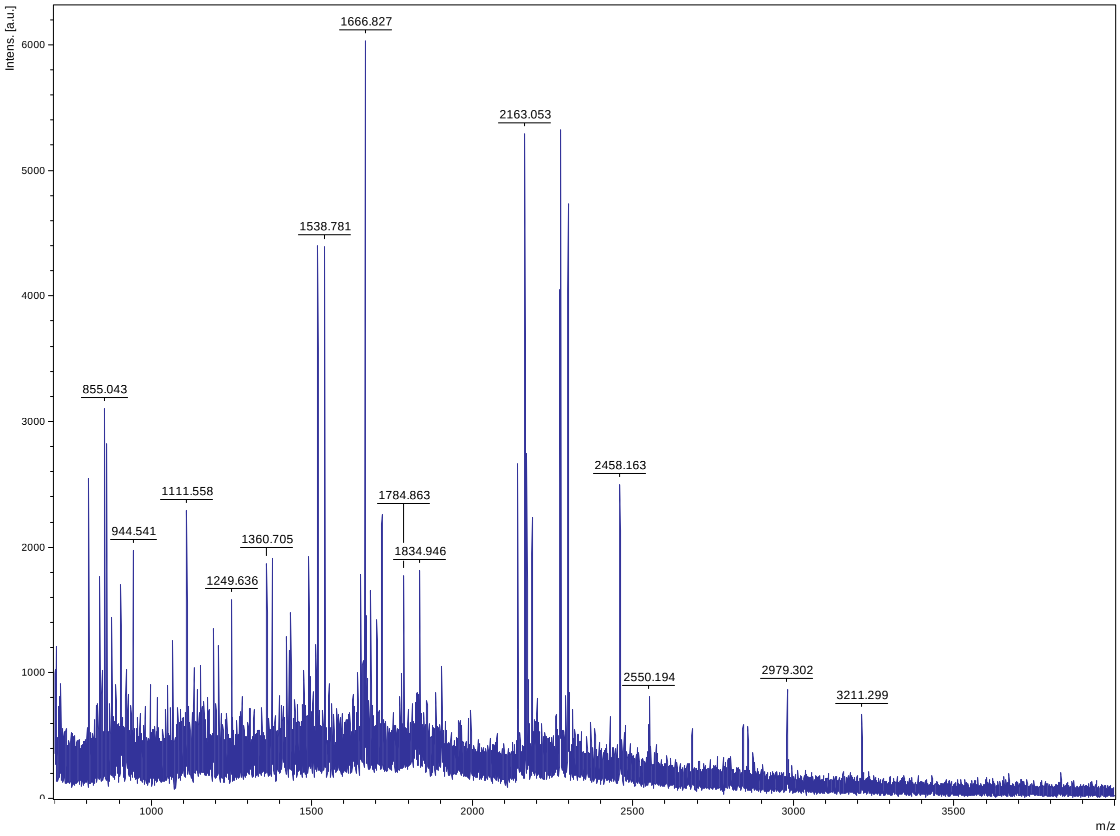


Match to: gi|51979438 Score: 106

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
9 - 18	1056.5612	1055.5539	1055.5247	0.0292	0	R.AGGPEVLEER.D	
185 - 195	1209.5729	1208.5656	1208.5859	-0.0203	0	K.GLGADVCINYK.T	Carbamidomethyl (C)
211 - 226	1744.9725	1743.9653	1743.9519	0.0134	0	K.GVDVILDNIGGLYLQR.N	
227 - 236	1058.5854	1057.5782	1057.5516	0.0266	0	R.NLNSLAVDGR.L	
259 - 268	1098.6499	1097.6426	1097.6669	-0.0243	1	R.RLTIQAAGLR.N	
260 - 268	942.6548	941.6476	941.5658	0.0818	0	R.LTIQAAGLR.N	
276 - 284	987.6197	986.6124	986.5648	0.0477	0	K.ALIVSEVEK.N	
285 - 294	1097.6067	1096.5994	1096.6029	-0.0035	0	K.NVWPAVVQGK.V	

Spot 2098



Match to: gi|62732953 Score: 127 Expect: 1.3e-08

Matched peptides:

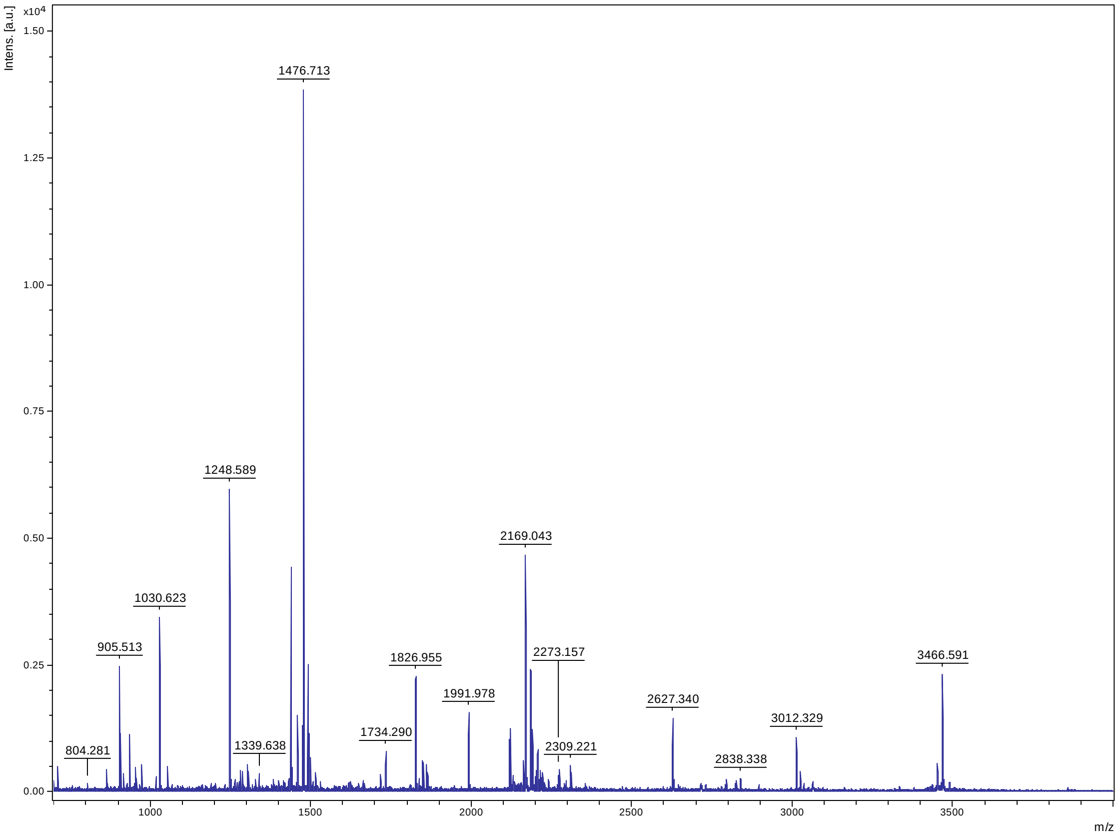
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
48 - 57	1001.5607	1000.5534	1000.5665	-0.0131	1	K.TAKTIASPGR.G	
72 - 85	1543.8335	1542.8262	1542.8114	0.0149	1	K.RLASIGLENTEANR.Q	
73 - 85	1387.7412	1386.7339	1386.7103	0.0237	0	R.LASIGLENTEANR.Q	
122 - 130	1058.6017	1057.5944	1057.6019	-0.0075	0	K.IVDILTEQK.I	
137 - 162	2743.2471	2742.2398	2742.3394	-0.0996	1	K.VDKGLVPLAGSNNESWCQGLDGLASR.E	Carbamidomethyl (C)
140 - 162	2401.1066	2400.0993	2400.1491	-0.0498	0	K.GLVPLAGSNNESWCQGLDGLASR.E	Carbamidomethyl (C)
163 - 172	1156.5537	1155.5464	1155.5308	0.0156	0	R.EAAYYQQGAR.F	
178 - 192	1510.8670	1509.8597	1509.8402	0.0195	0	R.TVVSIPNGPSELAVK.E	
193 - 200	873.4478	872.4405	872.4504	-0.0099	0	K.EAAWGLAR.Y	
201 - 228	3033.4121	3032.4048	3032.5454	-0.1406	0	R.YAAISQDNGLVPIVEPEILLDGEHGIDR.T	
229 - 235	822.3985	821.3912	821.4283	-0.0371	0	R.TFEVAQK.V	
271 - 282	1351.6951	1350.6878	1350.6667	0.0211	0	R.ATPEQVSDYTLK.L	
338 - 347	1115.5672	1114.5599	1114.5407	0.0192	0	K.TWGGQPENVK.A	
348 - 356	970.5682	969.5609	969.5607	0.0002	0	K.AAQDALLLR.A	

Match to: gi|50944223 Score: 106 Expect: 1.7e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
68 - 83	1673.8475	1672.8402	1672.8090	0.0312	0	R.AMSSESGPQGLPIDLR.G	Oxidation (M)
86 - 104	1995.0362	1994.0289	1994.0009	0.0280	1	K.RAFIAGVADDNGYGWAIAK.A	
87 - 104	1838.9297	1837.9224	1837.8998	0.0226	0	R.AFIAGVADDNGYGWAIAK.A	
105 - 130	2683.3891	2682.3818	2682.4744	-0.0926	0	K.ALAAAGAEILVGTWVPALNIFETSLR.R	
139 - 150	1345.7561	1344.7488	1344.7322	0.0166	1	R.KLPDGSLMEIVK.V	Oxidation (M)
151 - 169	2150.0388	2149.0315	2149.0102	0.0213	0	K.VYPLDAVYDSPEDVPEDVK.G	
151 - 172	2449.1673	2448.1600	2448.1696	-0.0095	1	K.VYPLDAVYDSPEDVPEDVKGNK.R	
174 - 183	1112.5711	1111.5638	1111.5298	0.0340	0	R.YAGSSNWTVK.E	
191 - 218	3022.4000	3021.3927	3021.5770	-0.1843	0	K.NDFGSIDILVHSLANGPEVTKPLLETSR.R	
281 - 288	862.4511	861.4438	861.4708	-0.0270	0	K.VLAFEAGR.K	
294 - 305	1171.6602	1170.6529	1170.6356	0.0173	0	R.VNTISAGPLGSR.A	
316 - 328	1555.7901	1554.7828	1554.7752	0.0077	0	K.MIEYSYVNAPLQK.E	
316 - 328	1571.7881	1570.7808	1570.7701	0.0107	0	K.MIEYSYVNAPLQK.E	Oxidation (M)

Spot 2099

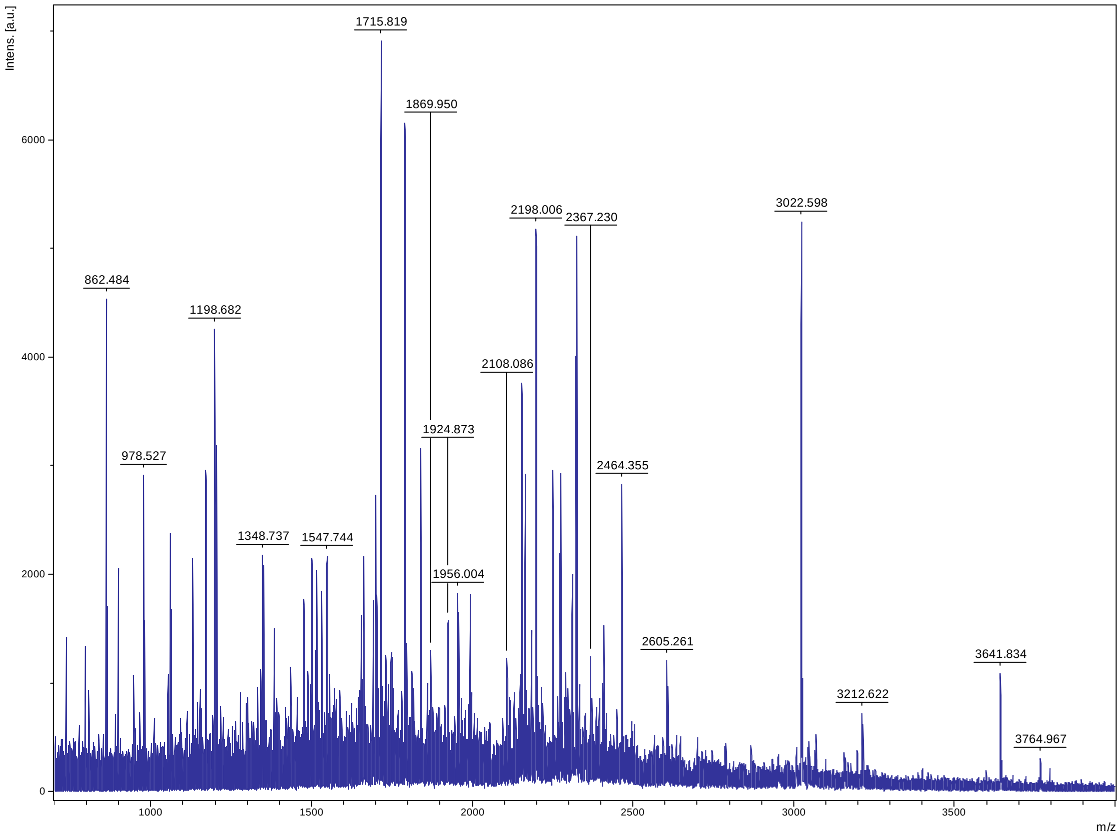


Match to: gi|62733213 Score: 96 Expect: 1.5e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
54 - 69	1859.9749	1858.9676	1858.9366	0.0311	0	R.YTTVIITFYNAFGHGR.Y
70 - 87	1826.9766	1825.9693	1825.9574	0.0120	0	R.YSLDISGHPLAAVGADIK.H
132 - 164	3466.4602	3465.4529	3465.5861	-0.1331	0	R.AGVARPFGDDAAVDGIDFFIDQGGADHYDDLAR.R
177 - 186	1030.5871	1029.5798	1029.6182	-0.0384	0	R.VGVLLTATTR.C
197 - 205	905.4267	904.4194	904.5130	-0.0936	0	K.ALATGVFAR.I
222 - 226	712.1562	711.1489	711.3228	-0.1738	0	R.YSWEK.W
227 - 235	934.4008	933.3935	933.4708	-0.0773	0	K.WAAAFPGSK.V
236 - 254	2169.0368	2168.0295	2168.0612	-0.0316	0	K.VYIGLVASPEQDSAWMFQK.D
255 - 265	1476.7410	1475.7337	1475.7118	0.0219	0	K.DLYYEMLQFVR.S
266 - 282	1991.9900	1990.9827	1990.9788	0.0039	1	R.SLPNYGGLAIYDRYFDK.K

Spot 2101

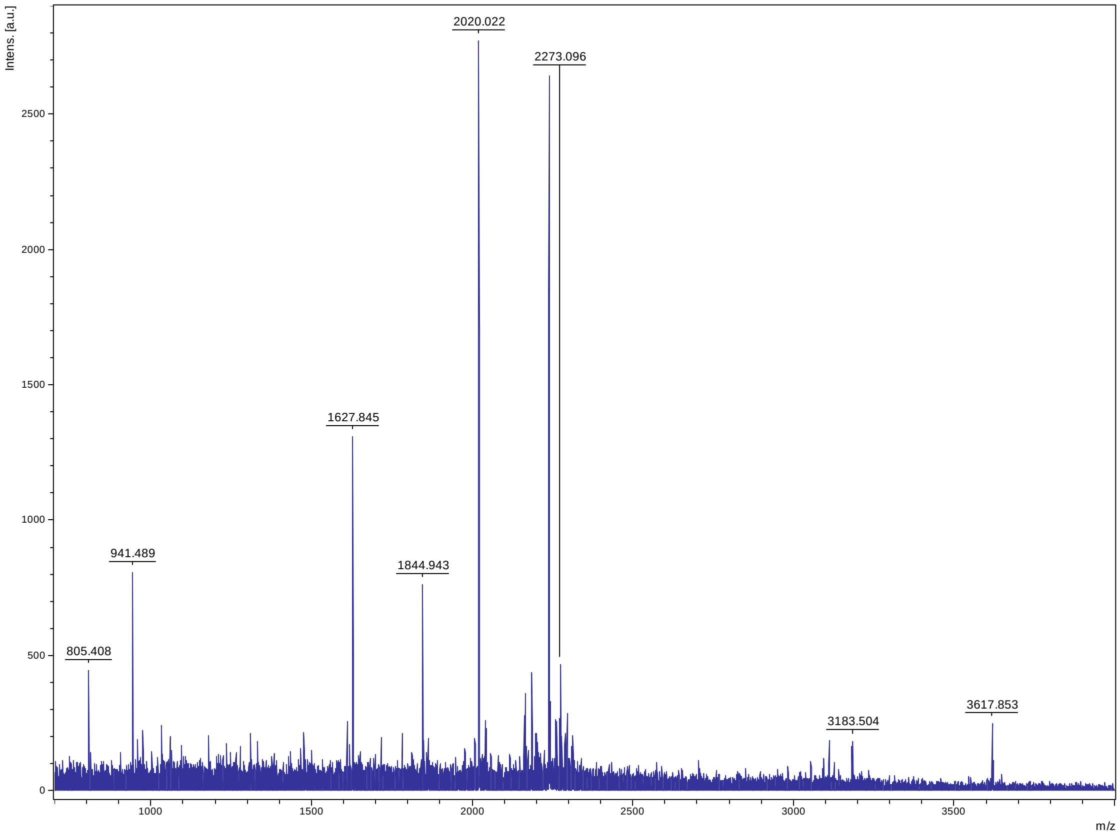


Match to: gi|34894098; Score: 105

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 9	805.43	804.42	804.40	0.03	1	ASGGEEKK
12 - 23	1204.69	1203.69	1203.70	-0.01	0	ILVVGGTGYIGR
51 - 58	978.53	977.52	977.53	-0.01	0	SQLLQSFR
59 - 80	2323.19	2322.18	2322.20	-0.01	0	DAGVTLLHGDLYDHASLLSAVR
114 - 134	2311.12	2310.11	2310.14	-0.03	1	RFLPSEFGLDPDHTGAVEPAR
115 - 134	2155.03	2154.03	2154.04	-0.01	0	FLPSEFGLDPDHTGAVEPAR
193 - 213	2250.15	2249.15	2249.16	-0.01	0	VVFVEEGDIGTYTVLAAVDPR
218 - 225	898.55	897.54	897.54	0.00	0	TVNIRPAK
245 - 257	1530.76	1529.76	1529.85	-0.09	1	LERVYVPEDAVLK
258 - 279	2464.35	2463.35	2463.35	0.00	0	QIQESEIPLNIVLSIAHAGYIR
280 - 312	3641.83	3640.83	3640.74	0.09	0	GETTTPLDPATAVEATQLFPDVQYTTVDDYLNR

Spot 2102

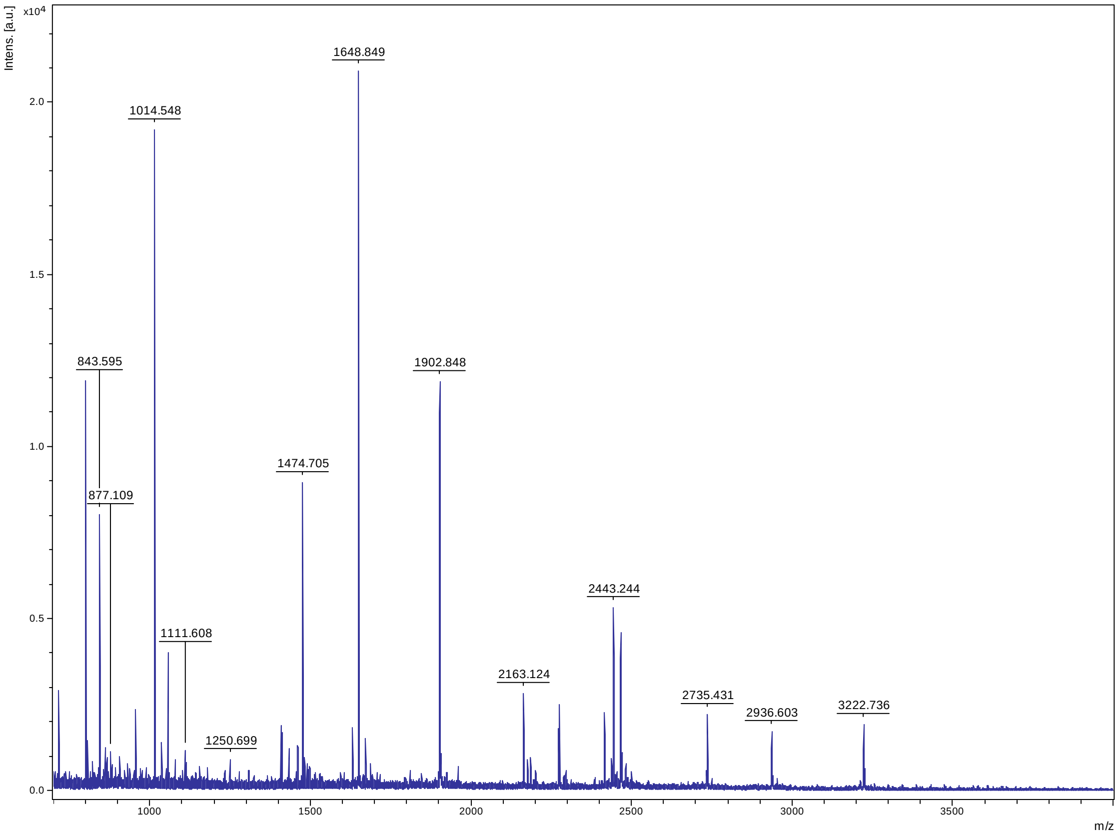


Match to: gi|51963422; Score: 72

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
54 - 72	2020.02	2019.02	2019.05	-0.03	0	ATNPTLAPAHLQDLPGFTR
169 - 184	1844.94	1843.94	1843.97	-0.03	0	HSVISDEVTTLVIFER
186 - 217	3617.85	3616.85	3616.83	0.02	1	YTTIEGYHPDLIVGSTDKQPLLETPGEVFELR
204 - 217	1610.77	1609.76	1609.84	-0.07	0	QPLLETPGEVFELR Pyro-glu (N-term Q)
204 - 217	1627.84	1626.84	1626.86	-0.02	0	QPLLETPGEVFELR
302 - 309	941.49	940.49	940.50	-0.01	1	DVNRDPLI

Spot 2105

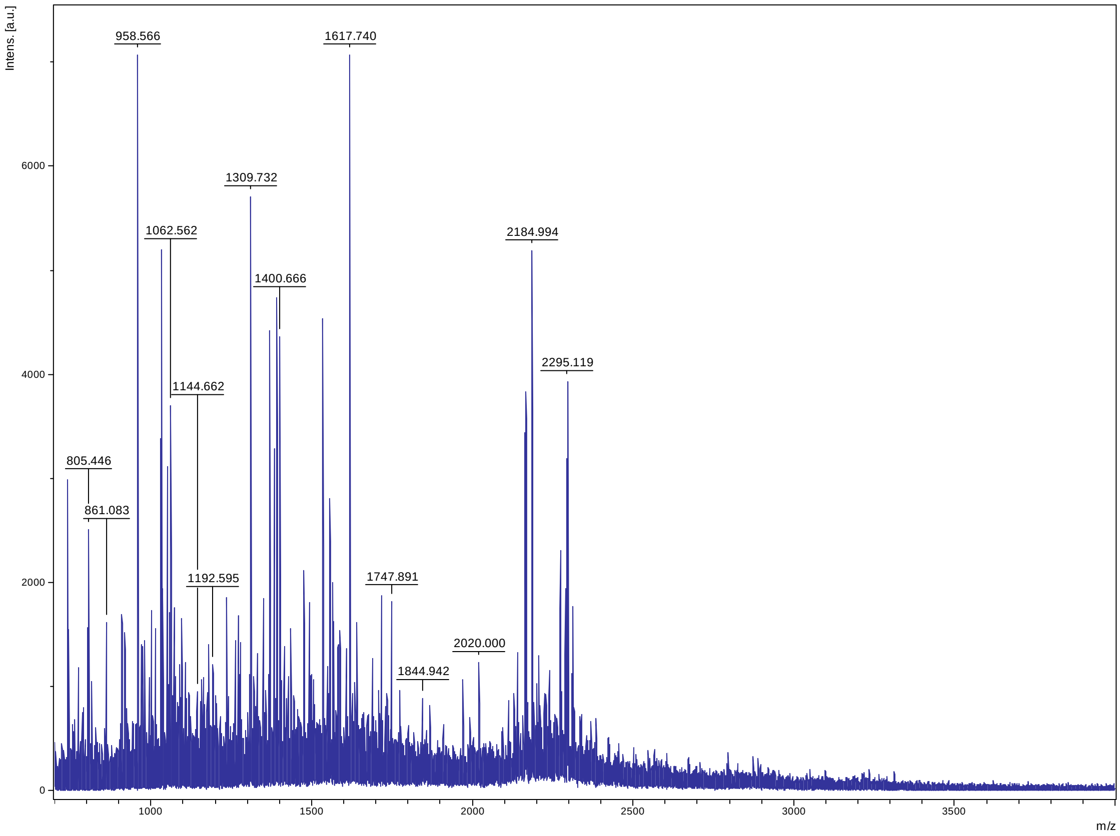


Match to: gi|37535166 Score: 214 Expect: 2.7e-17

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
18 - 24	799.3763	798.3690	798.3660	0.0030	0	K.GADSFFR.T	
43 - 49	843.5381	842.5308	842.5225	0.0083	0	K.TILELVR.S	
50 - 64	1902.8361	1901.8288	1901.7791	0.0497	0	R.SYDGDHICYDHFAFR.T	Carbamidomethyl (C)
65 - 74	1056.5882	1055.5809	1055.5287	0.0522	0	R.TFGVDGYGIK.S	
75 - 88	1648.8456	1647.8383	1647.7932	0.0451	0	K.SLAEFFTDFGYVPR.E	
75 - 92	2176.0842	2175.0769	2175.0636	0.0133	1	K.SLAEFFTDFGYVPREELR.F	
98 - 122	2735.3304	2734.3231	2734.3867	-0.0635	1	K.LRALWFSPPTNDGYTGTGVYGPLPR.I	
100 - 122	2466.2574	2465.2501	2465.2015	0.0486	0	R.ALWFSPPTNDGYTGTGVYGPLPR.I	
123 - 143	2415.2959	2414.2886	2414.2944	-0.0058	0	R.IFISELLVDELSPQSQDIIQK.Y	
154 - 179	2936.4758	2935.4685	2935.4715	-0.0030	0	K.HATLASTSGELTWEKPIYSDFQVLSR.E	
204 - 209	716.4079	715.4006	715.4228	-0.0222	0	R.LISDIR.S	
217 - 224	955.4879	954.4806	954.4446	0.0360	0	K.FVEDNGFK.L	
265 - 272	1014.5323	1013.5250	1013.4818	0.0433	0	R.SYIEFAER.L	
280 - 291	1474.7173	1473.7100	1473.6596	0.0504	0	K.DLPNDEVNEHHR.R	
280 - 292	1630.8279	1629.8206	1629.7607	0.0599	1	K.DLPNDEVNEHHRR.D	
293 - 314	2443.1592	2442.1519	2442.1298	0.0221	1	R.DGFEVGNADKIFESTSNDQLTR.R	
303 - 314	1410.7268	1409.7195	1409.6787	0.0409	0	K.IFESTSNDQLTR.R	

Spot 2108

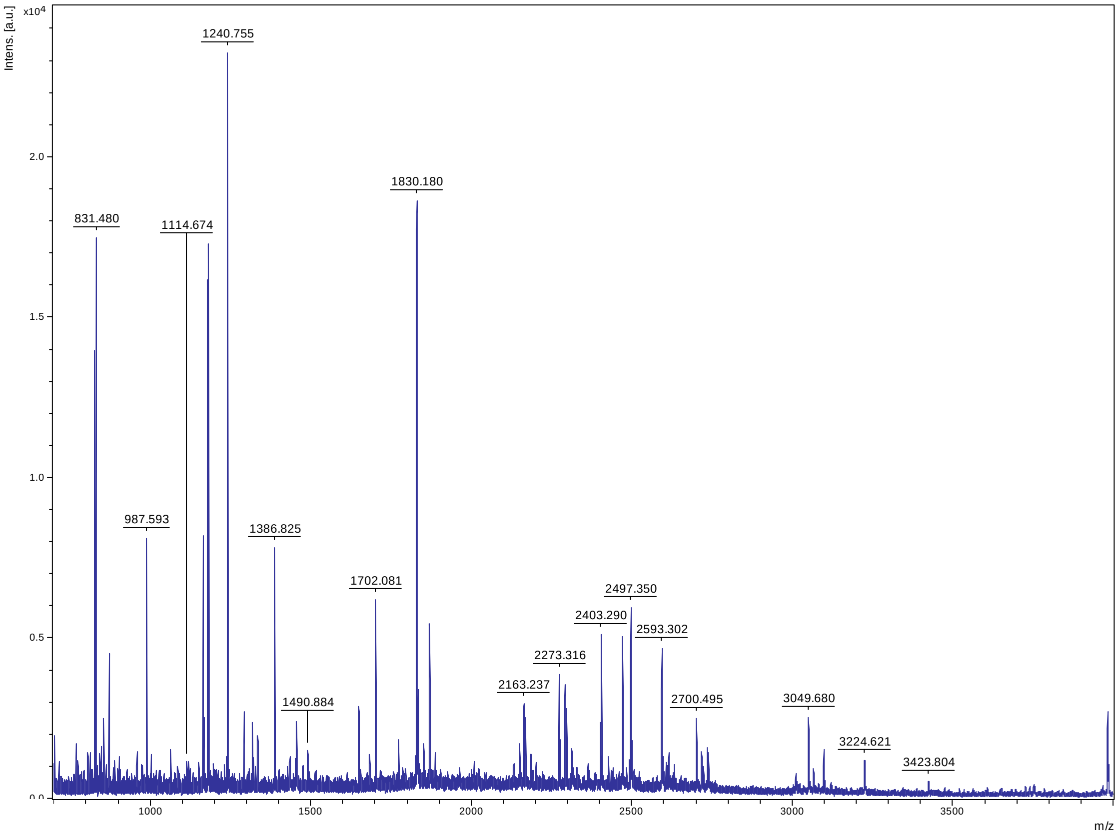


Match to: gi|51535089; Score: 186

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
51 - 63	1556.77	1555.77	1555.76	0.01	1	RAYADTYGEELLR
52 - 63	1400.67	1399.66	1399.66	0.00	0	AYADTYGEELLR
64 - 75	1368.61	1367.61	1367.62	-0.01	0	SITDEISGDFER
88 - 97	1057.58	1056.58	1056.56	0.03	0	DAVLANEVAR
98 - 106	1037.53	1036.53	1036.51	0.02	1	KWYPGSGSR
99 - 106	909.46	908.46	908.41	0.04	0	WYPGSGSR
107 - 115	1030.58	1029.58	1029.56	0.01	0	VLVEIACAR
116 - 124	958.57	957.56	957.54	0.02	0	GPAQLFAVR
125 - 130	803.41	802.41	802.37	0.03	0	QAYHER
133 - 148	1773.87	1772.87	1772.84	0.02	1	RSLEEDVAAHATGDFR
134 - 148	1617.74	1616.74	1616.74	-0.01	0	SLEEDVAAHATGDFR
150 - 159	1144.66	1143.66	1143.70	-0.04	0	LLVPLISAYR
185 - 193	1051.52	1050.52	1050.50	0.02	0	AYGDDEIIR
210 - 220	1349.61	1348.61	1348.60	0.01	0	YNDEYGHPINK
224 - 235	1391.70	1390.70	1390.71	-0.01	1	ADPKDEFLSTLR
228 - 235	980.52	979.52	979.50	0.02	0	DEFLSTLR
240 - 246	1014.37	1013.37	1013.35	0.02	0	CFCCPDR
240 - 250	1581.61	1580.61	1580.62	-0.01	1	CFCCPDRYFEK
254 - 268	1548.76	1547.76	1547.76	-0.00	0	LAIAGMGTDENSLTR
254 - 268	1564.77	1563.77	1563.76	0.02	0	LAIAGMGTDENSLTR Oxidation (M)
288 - 295	970.50	969.50	969.54	-0.04	1	RNSVPLER
289 - 295	814.48	813.47	813.43	0.04	0	NSVPLER

Spot 2114



Match to: gi|50253039 Score: 86 Expect: 0.00016

Matched peptides:

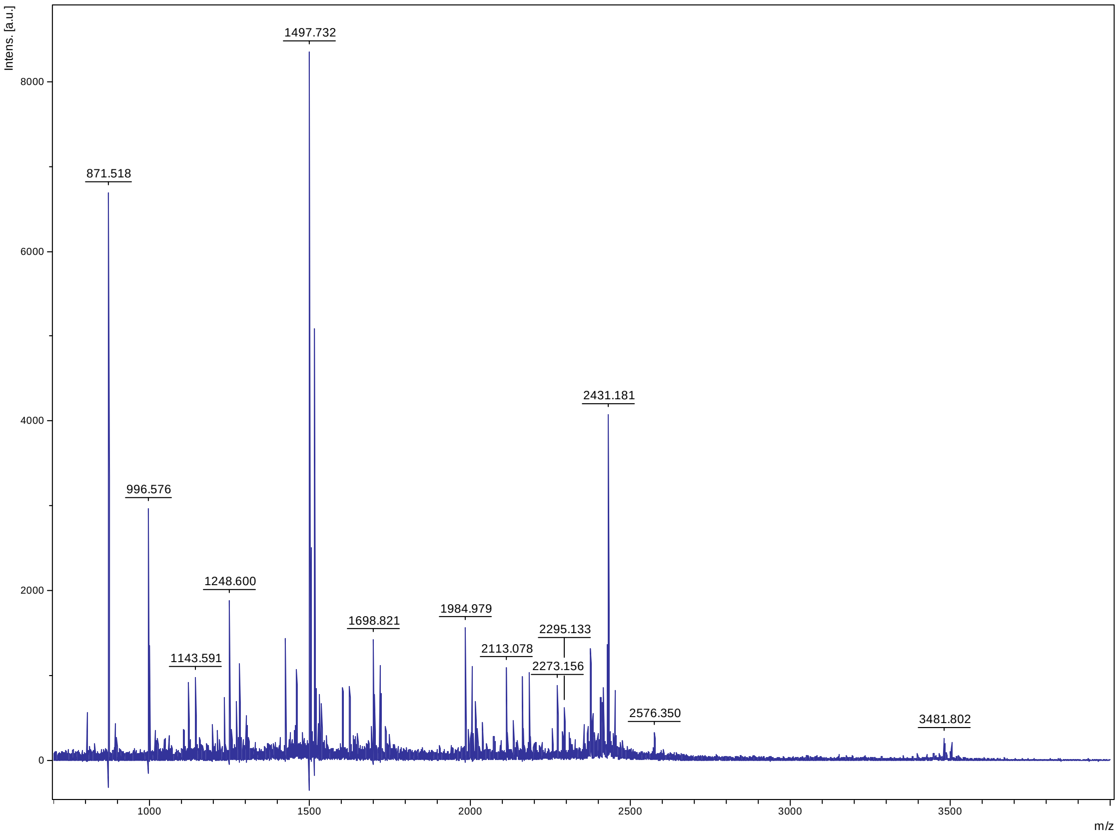
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
11 - 33	2497.3496	2496.3423	2496.1438	0.1986	0	K.VSVAAVQFACTDVESENVDTAER.L	Carbamidomethyl (C)
42 - 62	2470.4053	2469.3980	2469.2110	0.1870	0	K.GANIVLVQELFEGQYFCQAQR.L	Carbamidomethyl (C)
63 - 68	825.4935	824.4862	824.4181	0.0681	0	R.LDFFQR.A	
87 - 122	3981.0291	3980.0218	3979.9478	0.0739	0	K.ELEVVIPVSFFEEANNAHYNSVAIIDADGTDLGLYR.K	
123 - 135	1455.7124	1454.7051	1454.7153	-0.0102	1	R.KSHIPDGPGYQEK.F	
136 - 146	1292.7198	1291.7126	1291.5873	0.1253	0	K.FYFNPGDTGFK.A	
171 - 198	3049.6799	3048.6727	3048.4862	0.1865	0	R.AMVLQGAEILFYPTAIGSEPQDNNLDSR.E	
204 - 221	1834.1740	1833.1667	1832.9678	0.1988	0	R.VMQGHAGANLVPLVASNR.I	
204 - 221	1850.1320	1849.1247	1848.9628	0.1619	0	R.VMQGHAGANLVPLVASNR.I	Oxidation (M)
222 - 253	3423.8037	3422.7964	3422.6993	0.0972	1	R.IGRETVETEHGESTITFFGNSFIAGPTGEIVK.L	
225 - 253	3097.6748	3096.6675	3096.4927	0.1749	0	R.ETVETEHGESTITFFGNSFIAGPTGEIVK.L	
254 - 273	2291.3044	2290.2972	2290.1216	0.1756	1	K.LANDKDEDVLVAEFDLDEIK.S	
277 - 283	872.5273	871.5200	871.4453	0.0747	0	R.HGWGIFR.D	
284 - 291	1062.6594	1061.6521	1061.5618	0.0904	1	R.DRRPDLYK.V	
292 - 300	987.5934	986.5861	986.5648	0.0213	0	K.VLLTLDGEK.S	

Match to: gi|77556463 Score: 76 Expect: 0.0018

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
5 - 20	1386.8254	1385.8182	1385.6898	0.1284	0	K.SGVAEEGGAAAAAAVR.R	
21 - 29	987.5934	986.5861	986.5045	0.0816	1	R.RWVEAGGGR.L	
22 - 29	831.4799	830.4726	830.4034	0.0691	0	R.WVEAGGGR.L	
30 - 55	2700.4956	2699.4883	2699.3112	0.1772	0	R.LVMDGGLATELEANGADLNDPLWSAK.C	
30 - 55	2716.4858	2715.4786	2715.3061	0.1725	0	R.LVMDGGLATELEANGADLNDPLWSAK.C	Oxidation (M)
56 - 65	1181.7459	1180.7386	1180.6386	0.0999	0	K.CLLSSPHLVR.K	Carbamidomethyl (C)
95 - 107	1451.8721	1450.8648	1450.7303	0.1345	1	K.GFSKEQSEDLLAK.S	
171 - 191	2296.4270	2295.4197	2295.2474	0.1724	1	R.RLEVLAEAGPDLIAFETIPNK.L	
218 - 240	2403.2900	2402.2828	2402.1205	0.1622	0	K.DGVHIVSGDSLIECATIANGCSK.V	2 Carbamidomethyl (C)
241 - 252	1240.7551	1239.7479	1239.6393	0.1085	0	K.VGAVGINCTPPR.F	Carbamidomethyl (C)
253 - 262	1168.7032	1167.6960	1167.7128	-0.0168	0	R.FIHGLILSIR.K	
263 - 278	1830.1804	1829.1731	1829.0046	0.1685	1	R.KVTDKPILIYPNSGER.Y	
264 - 278	1702.0806	1701.0733	1700.9097	0.1636	0	K.VTDKPILIYPNSGER.Y	
285 - 306	2593.3020	2592.2947	2592.1114	0.1833	0	K.EWVESTGVSDGDFVSYVNEWCK.D	Carbamidomethyl (C)
307 - 317	1120.6464	1119.6391	1119.5164	0.1226	0	K.DGAVLIGGCCR.T	Carbamidomethyl (C)
307 - 317	1177.6385	1176.6313	1176.5379	0.0934	0	K.DGAVLIGGCCR.T	2 Carbamidomethyl (C)
334 - 342	960.6090	959.6017	959.5188	0.0829	0	R.HSSLHLPVA.-	

Spot 2118

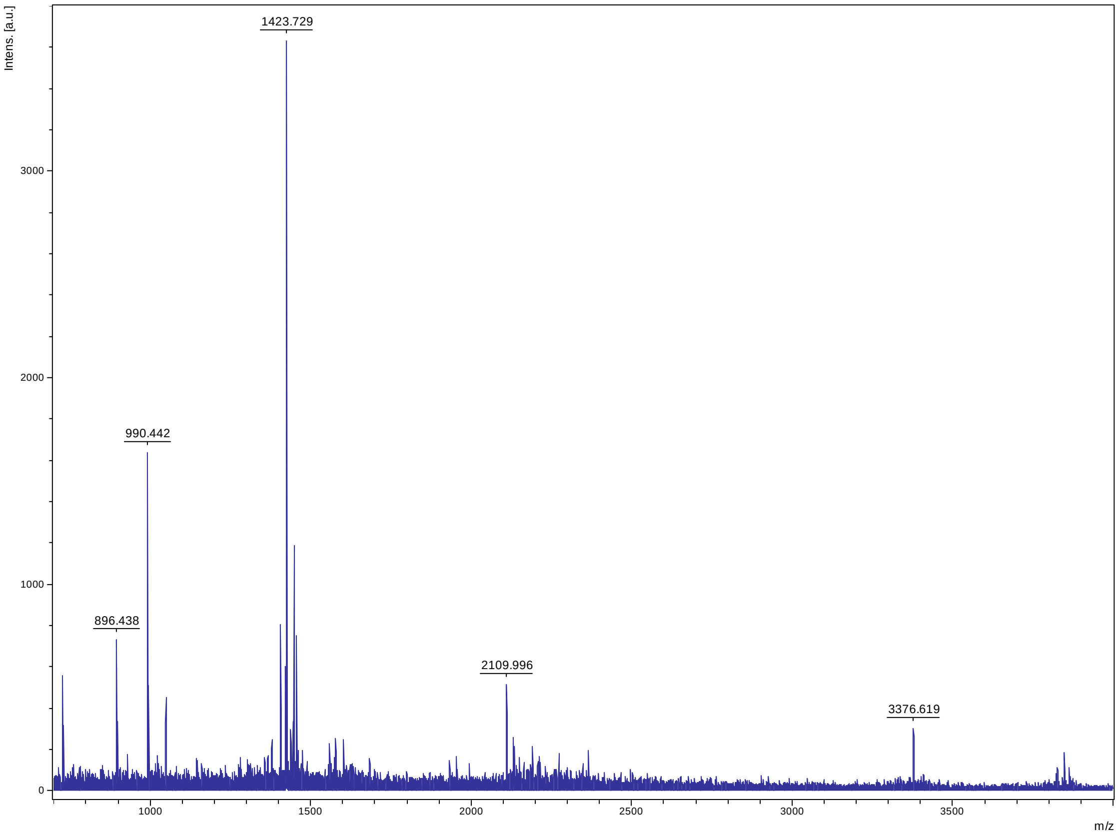


Match to: gi|84029333; Score: 82

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
25 - 31	871.51	870.51	870.51	-0.00	0	LLHAVYR
41 - 49	1195.41	1194.41	1194.45	-0.04	0	CYTECFGMK
41 - 49	1211.42	1210.42	1210.45	-0.03	0	CYTECFGMK Oxidation (M)
119 - 127	996.57	995.56	995.58	-0.01	1	ITREPGPVK
128 - 149	2415.10	2414.10	2414.16	-0.06	0	GGSTVIAFAQDPDGYMFELIQR
128 - 149	2431.12	2430.12	2430.15	-0.03	0	GGSTVIAFAQDPDGYMFELIQR Oxidation (M)
150 - 162	1497.71	1496.71	1496.75	-0.04	0	GPTPEPLCQVMLR
150 - 162	1513.72	1512.71	1512.74	-0.03	0	GPTPEPLCQVMLR Oxidation (M)
222 - 237	1698.80	1697.80	1697.83	-0.03	0	GNAYAQVAIGTEDVYK
253 - 266	1503.85	1502.85	1502.89	-0.05	1	ILRQPGPLPGLNTK
256 - 266	1104.58	1103.58	1103.60	-0.02	0	QPGPLPGLNTK Pyro-glu (N-term Q)
256 - 266	1121.61	1120.61	1120.62	-0.02	0	QPGPLPGLNTK
267 - 277	1248.59	1247.59	1247.62	-0.03	0	IASFLDPDGWK
278 - 291	1602.84	1601.84	1601.87	-0.02	1	VVLVDNADFLKELQ

Spot 2119

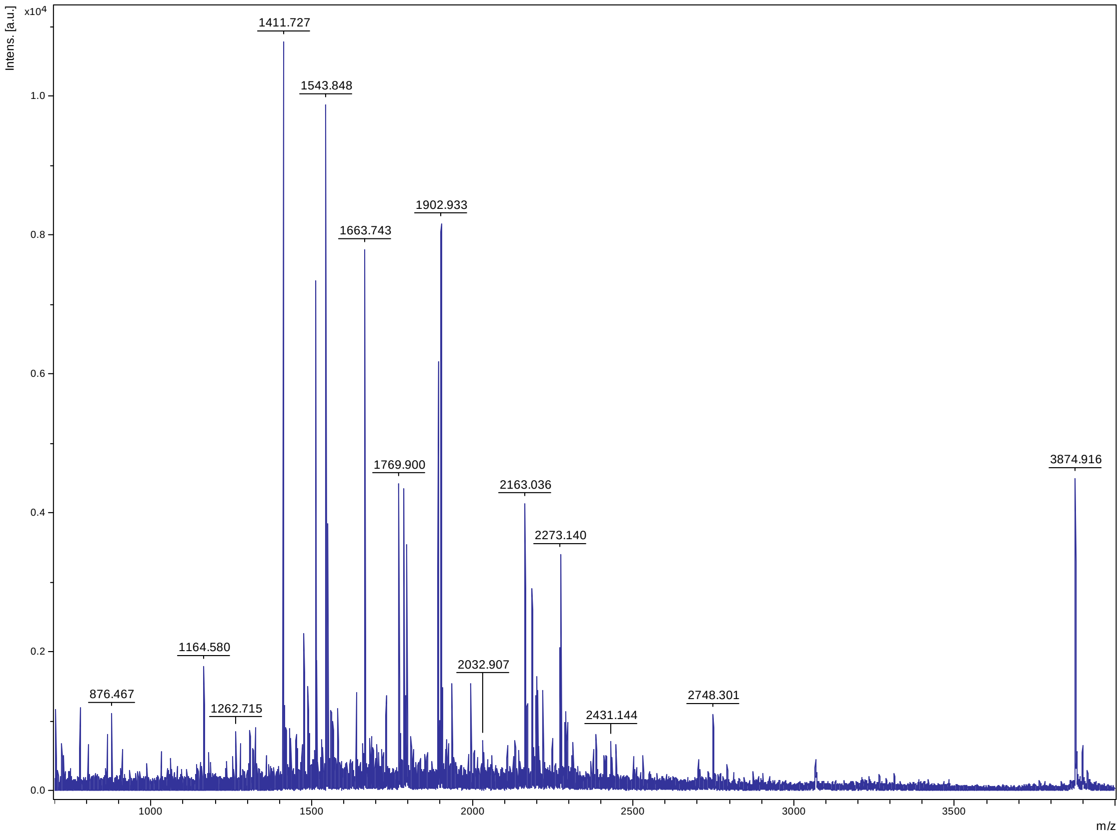


Match to: gi|18147582; Score: 118

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
68 - 80	1448.66	1447.65	1447.64	0.01	0	YGSLLASCSYDGR
86 - 103	2110.00	2108.99	2108.99	0.00	0	EGSKPDEWAQAHTFIEHK
104 - 135	3376.62	3375.62	3375.60	0.02	0	SSVNSIAWAPHELGLCLACGSSDGNISVFTAR
136 - 144	994.45	993.45	993.42	0.03	0	SDGGWDTTR
196 - 202	895.45	894.45	894.43	0.01	0	LYNGSWR
203 - 213	1405.62	1404.62	1404.61	0.01	0	MDCFPALQMHR
203 - 213	1421.62	1420.61	1420.60	0.01	0	MDCFPALQMHR Oxidation (M)
249 - 256	990.44	989.44	989.42	0.02	0	EGEQWEGR
257 - 267	1423.73	1422.73	1422.73	-0.00	0	VLYDFQTPVWR

Spot 2120

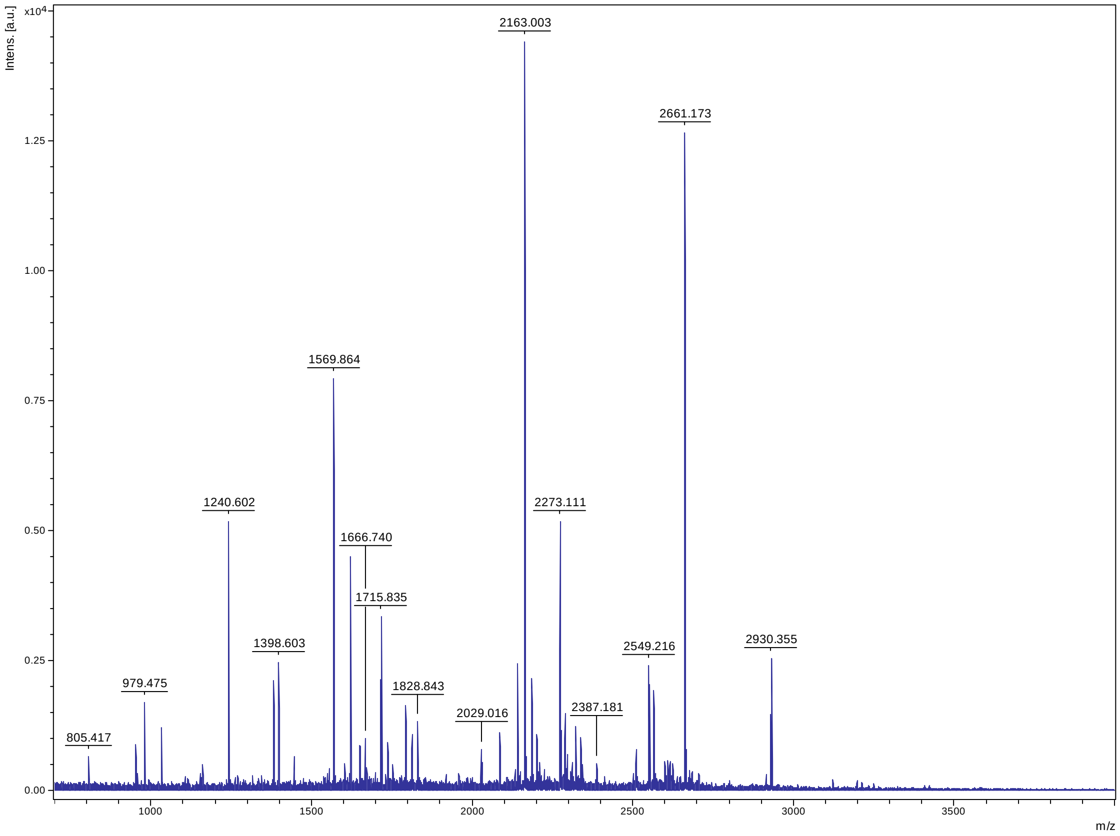


Match to: gi|34899936; Score: 108

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
6 - 12	876.47	875.46	875.42	0.05	0	VVVDECR
13 - 25	1411.73	1410.72	1410.71	0.01	0	GVLFVYSDGAVER
27 - 44	1902.93	1901.93	1901.93	0.00	1	AAPGFATPVRDDGSVEWK
45 - 52	864.45	863.45	863.41	0.04	0	DAVFDAAR
86 - 96	1511.65	1510.65	1510.64	0.01	0	TWPNCQNYCLR
97 - 111	1543.85	1542.85	1542.84	0.01	0	LAAELGAVVVAPDYR
153 - 171	1893.99	1892.99	1892.99	0.00	0	VFVSGDSAGGTIAHHLAVR
186 - 201	1769.90	1768.90	1768.90	0.00	0	VAGYVQLMPFFGGVER
186 - 201	1785.90	1784.90	1784.89	0.01	0	VAGYVQLMPFFGGVER Oxidation (M)
202 - 216	1663.74	1662.74	1662.73	0.01	0	TPSEAACPDDAFLNR
225 - 264	3874.92	3873.91	3873.97	-0.06	0	LSLPAGGATADHPFSNPFGPASPDLAAAEFAPTLVVVGGR
316 - 327	1164.58	1163.58	1163.56	0.02	0	LFVDTDGGGGAR

Spot 2121

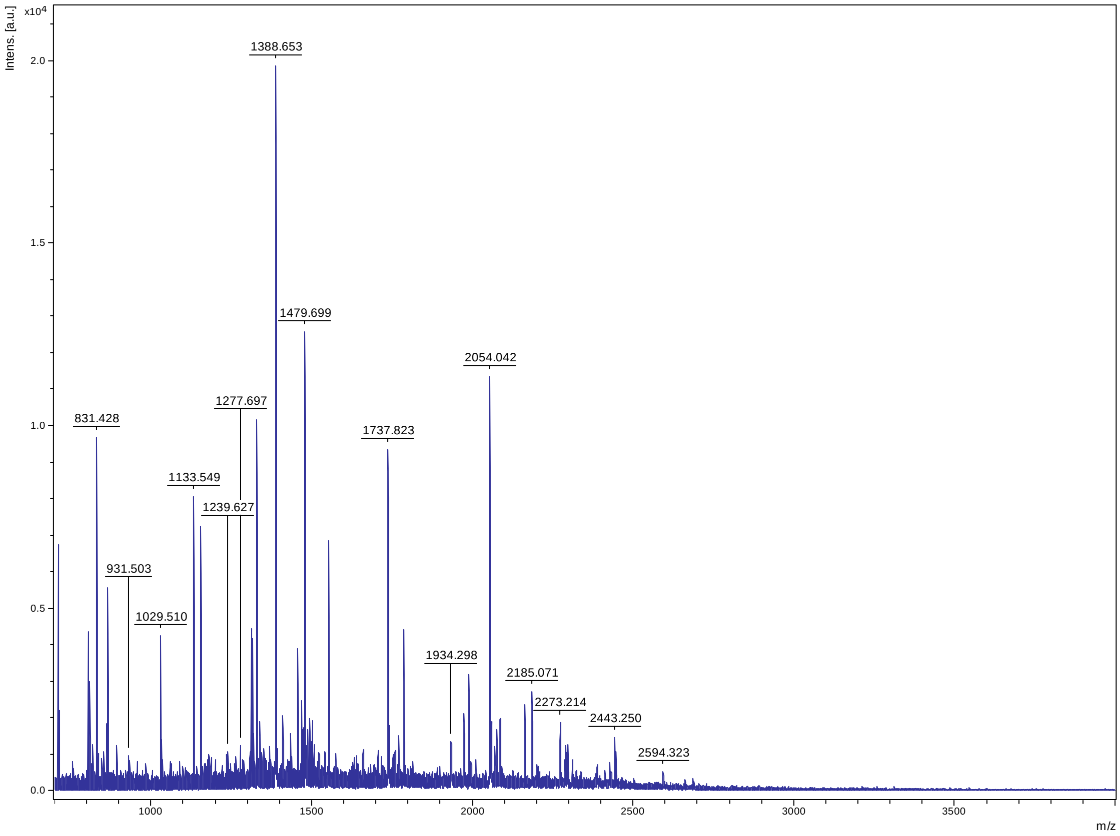


Match to: gi|50540752; Score: 139

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
20 - 36	1569.86	1568.86	1568.89	-0.03	0	VALVTGGASGIGEAIVR
37 - 44	957.53	956.53	956.52	0.01	1	LFREHGAK
45 - 57	1446.66	1445.66	1445.68	-0.02	0	VCIADIQDEAGQK
45 - 59	1715.84	1714.83	1714.87	-0.03	1	VCIADIQDEAGQKLR
58 - 83	2930.36	2929.35	2929.39	-0.03	1	LRDSLGGDQDVLFVHCDVSVEEDVAR
60 - 83	2661.17	2660.17	2660.20	-0.03	0	DSLGGDQDVLFVHCDVSVEEDVAR
84 - 108	2614.23	2613.23	2613.27	-0.05	1	AVDATAEKFGTLDIMVNNAGFTGQK Oxidation (M)
92 - 108	1812.85	1811.85	1811.89	-0.04	0	FGTLDIMVNNAGFTGQK
92 - 108	1828.84	1827.84	1827.88	-0.04	0	FGTLDIMVNNAGFTGQK Oxidation (M)
114 - 121	979.47	978.47	978.48	-0.00	0	NIDFSEVR
193 - 215	2549.22	2548.21	2548.25	-0.03	0	VNCVSPYAVPTALSMPYLPQGER
193 - 215	2565.20	2564.20	2564.24	-0.04	0	VNCVSPYAVPTALSMPYLPQGER Oxidation (M)
242 - 256	1620.79	1619.79	1619.82	-0.03	0	DVAQAVLYLASDEAR
257 - 277	2321.14	2320.13	2320.16	-0.03	0	YISALNLMVDGGFTSVNHNLR
257 - 277	2337.12	2336.12	2336.16	-0.04	0	YISALNLMVDGGFTSVNHNLR Oxidation (M)

Spot 2124

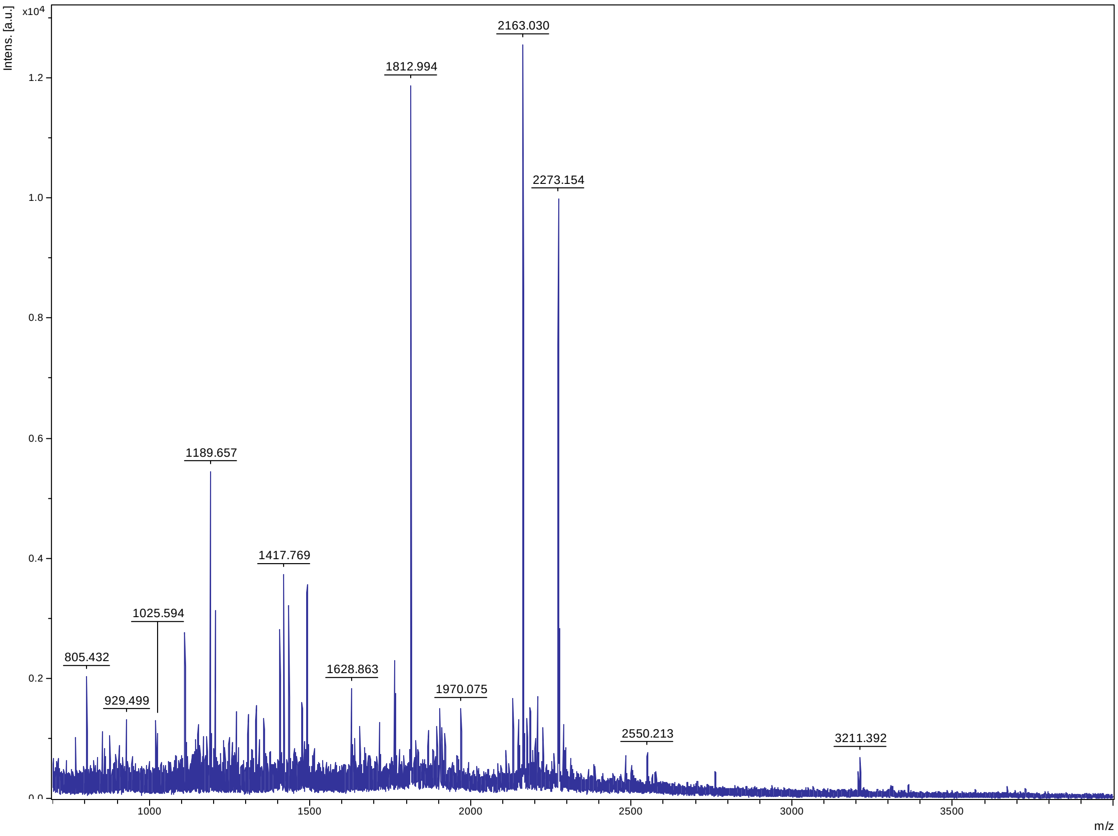


Match to: gi|51091938; Score: 195

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
26 - 41	1552.79	1551.79	1551.79	-0.00	0	LGGDPTVPAGTDPVTR
46 - 53	810.43	809.42	809.41	0.01	0	DIHAGAAR
101 - 111	1155.60	1154.60	1154.61	-0.01	0	AGAIGVSVYYR
112 - 130	2054.04	2053.04	2053.03	0.01	0	LAPENPLPAAYEDAWAAVR
136 - 151	1737.82	1736.82	1736.81	0.01	0	GDGADPWLLDHADLSR
152 - 170	1972.99	1971.98	1971.98	0.01	0	LFLAGCSAGANIAHNMAVR
152 - 170	1989.00	1988.00	1987.97	0.03	0	LFLAGCSAGANIAHNMAVR Oxidation (M)
171 - 184	1329.64	1328.63	1328.65	-0.02	0	CGGGGALPDGVTLR
185 - 196	1316.72	1315.72	1315.73	-0.01	0	GLVVVHPYFTGK
197 - 210	1388.65	1387.65	1387.67	-0.02	0	EAVGAEAAFGPDVR
219 - 231	1479.70	1478.70	1478.70	-0.01	0	FVFPETSGLDDPR
219 - 241	2594.32	2593.32	2593.24	0.08	1	FVFPETSGLDDPRVNPFVDDATR
232 - 241	1133.55	1132.55	1132.55	-0.01	0	VNPFVDDATR
242 - 251	1029.51	1028.51	1028.51	0.00	0	AAAAAIPCER
252 - 266	1785.95	1784.95	1784.95	0.01	1	VQVCVAEQDVLLKER
267 - 272	831.43	830.43	830.42	0.01	0	GLWYHR
267 - 275	1201.62	1200.62	1200.64	-0.02	1	GLWYHRELK
276 - 289	1472.70	1471.70	1471.68	0.01	0	ASGYGGEVELFESK
290 - 312	2427.22	2426.22	2426.18	0.04	0	GVGHAFHFVGMAGSDQAVELLER
290 - 312	2443.25	2442.25	2442.17	0.07	0	GVGHAFHFVGMAGSDQAVELLER Oxidation (M)

Spot 2130

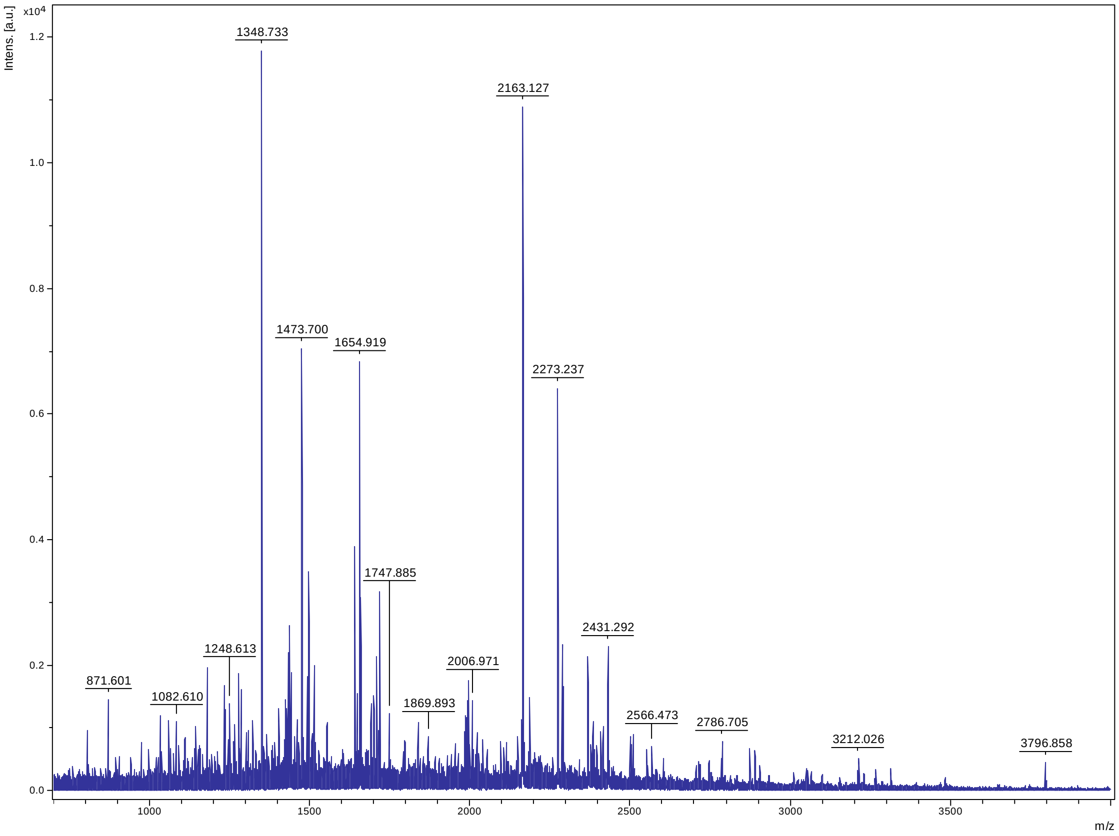


Match to: gi|50924834 Score: 94 Expect: 2.7e-05

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
18 - 34	2131.9680	2130.9607	2130.9601	0.0006	1	K.LAEQAERYEEMVEFMEK.V	
18 - 34	2147.9413	2146.9340	2146.9550	-0.0210	1	K.LAEQAERYEEMVEFMEK.V	Oxidation (M)
38 - 49	1406.6562	1405.6489	1405.6572	-0.0083	0	K.TVDSEELTVEER.N	
38 - 57	2295.1707	2294.1634	2294.1641	-0.0007	1	K.TVDSEELTVEERNLLSVAYK.N	
65 - 76	1417.7921	1416.7848	1416.7725	0.0123	1	R.ASWRIISSIEQK.E	
161 - 177	1813.0052	1811.9979	1811.9893	0.0086	0	K.AAQDIALAELPPTHPIR.L	
204 - 222	2175.0193	2174.0120	2173.9902	0.0218	0	K.QAFDEAISELDTLSEESYK.D	
223 - 232	1189.6301	1188.6228	1188.6536	-0.0308	0	K.DSTLIMQLLR.D	
223 - 232	1205.6398	1204.6325	1204.6485	-0.0160	0	K.DSTLIMQLLR.D	Oxidation (M)
233 - 251	2208.0363	2207.0290	2207.0230	0.0061	0	R.DNLTLWTSDISEDTAEEIR.E	

Spot 2131

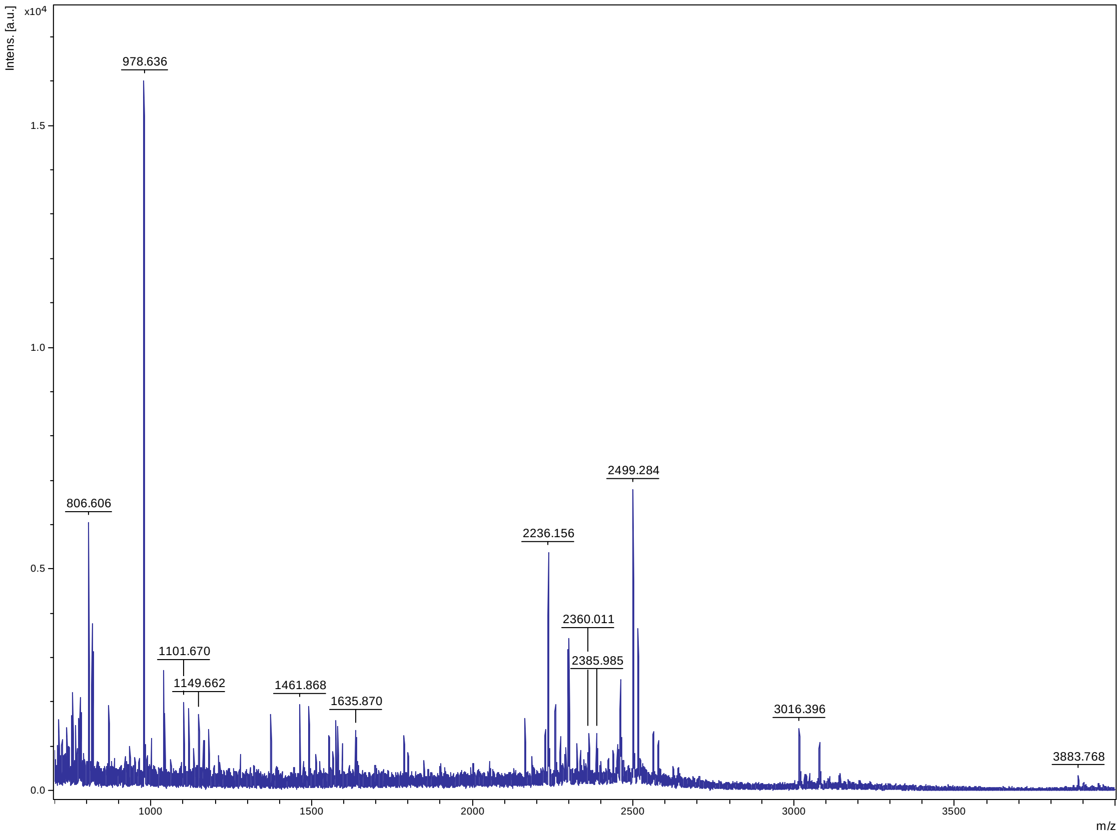


Match to: gi|11131901; Score: 105

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
27 - 49	2550.41	2549.41	2549.22	0.19	1	VVDGCEAQIAAKLEIMEPCSSVK Oxidation (M)
52 - 70	2039.04	2038.04	2038.03	0.01	1	IGYSMITDAEEKGLITPGK Oxidation (M)
71 - 92	2148.13	2147.13	2147.13	0.00	0	SVLIEPTSGNTGIGLAFMAAAK
114 - 129	1690.87	1689.86	1689.90	-0.04	0	AFGAELVLTDPLLGMK Oxidation (M)
142 - 158	1990.98	1989.98	1989.96	0.02	0	MPNSYILQQFENPANPK
142 - 158	2006.97	2005.97	2005.96	0.01	0	MPNSYILQQFENPANPK Oxidation (M)
159 - 170	1473.70	1472.70	1472.73	-0.03	0	IHYETTGPEIWK
205 - 225	2165.19	2164.19	2164.13	0.06	0	IYGVEPTESAILSGGRPGPHK
265 - 282	1654.92	1653.92	1653.94	-0.02	0	EGLLVGISSGAAAVAAIR
283 - 290	941.58	940.58	940.51	0.07	0	VAQRPENK
293 - 304	1348.73	1347.73	1347.75	-0.02	0	LVVVVFPSFGER
305 - 315	1285.67	1284.67	1284.70	-0.02	0	YLSSVLFESIK
305 - 316	1441.77	1440.77	1440.80	-0.03	1	YLSSVLFESIKR

Spot 2136

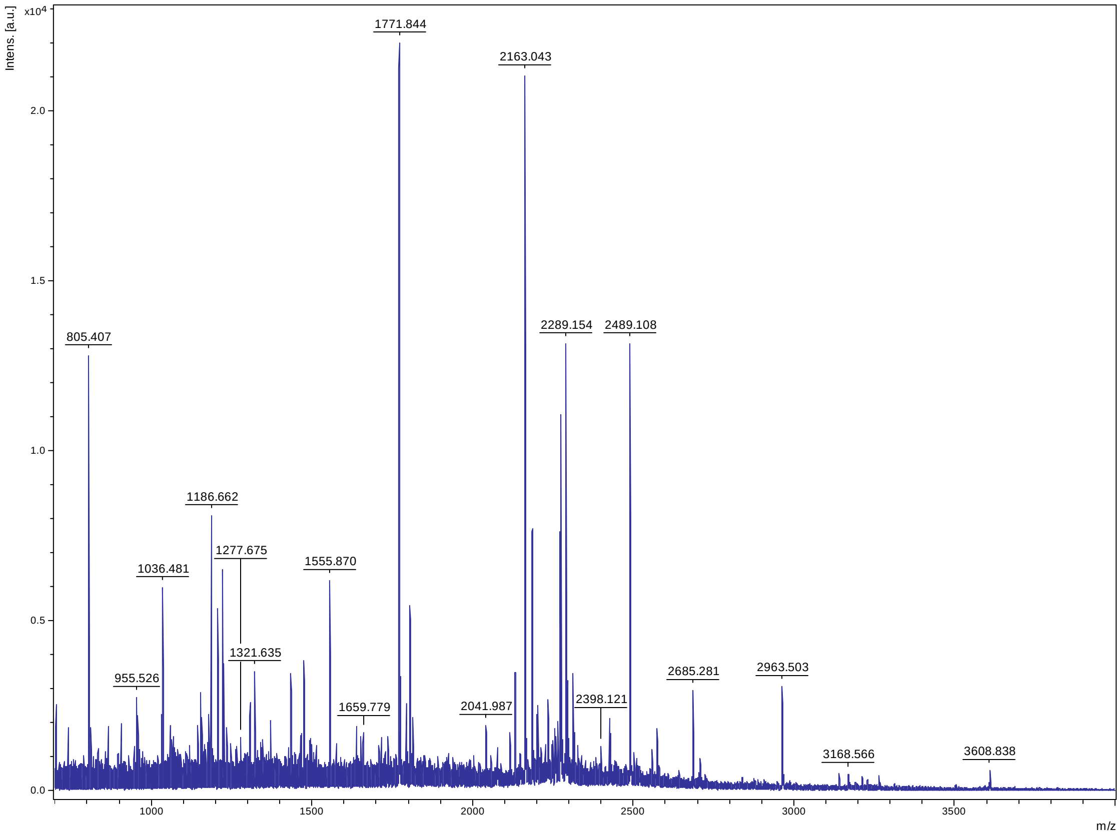


Match to: AAP94211 Score: 80 Expect: 0.00063

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
67 - 82	1580.9207	1579.9134	1579.8933	0.0201	0	K.AVDNVNSVIAPALIGK.D	
112 - 126	1513.8391	1512.8318	1512.8697	-0.0379	0	K.LGANAILAVSLAICK.A	Carbamidomethyl (C)
206 - 227	2324.0825	2323.0752	2323.0352	0.0401	0	K.YGQDATNVGDEGGFAPNIQENK.E	
291 - 315	3016.3960	3015.3887	3015.3450	0.0437	0	K.SFVSEYPIVSIEDPFDQDDWEHYAK.M	
316 - 338	2499.2837	2498.2764	2498.2686	0.0078	0	K.MTAEIGEQVQIVGDDLLVTNPTR.V	
316 - 338	2515.3215	2514.3143	2514.2635	0.0508	0	K.MTAEIGEQVQIVGDDLLVTNPTR.V	Oxidation (M)
355 - 369	1573.9353	1572.9280	1572.8358	0.0922	0	K.VNQIGSVTESIEAVK.M	
374 - 383	1101.6703	1100.6630	1100.5185	0.1445	0	R.AGWGVMTSHR.S	
374 - 383	1117.6632	1116.6559	1116.5134	0.1425	0	R.AGWGVMTSHR.S	Oxidation (M)
384 - 405	2236.1558	2235.1485	2235.1270	0.0215	0	R.SGETEDTFIADLAVGLATGQIK.T	
418 - 423	806.6063	805.5990	805.4446	0.1544	0	K.YNQLLR.I	
424 - 438	1491.8649	1490.8576	1490.7616	0.0960	0	R.IEEELGAAAVYAGAK.F	
439 - 446	978.6363	977.6290	977.4970	0.1320	1	K.FRAPVEPY.-	

Spot 2139

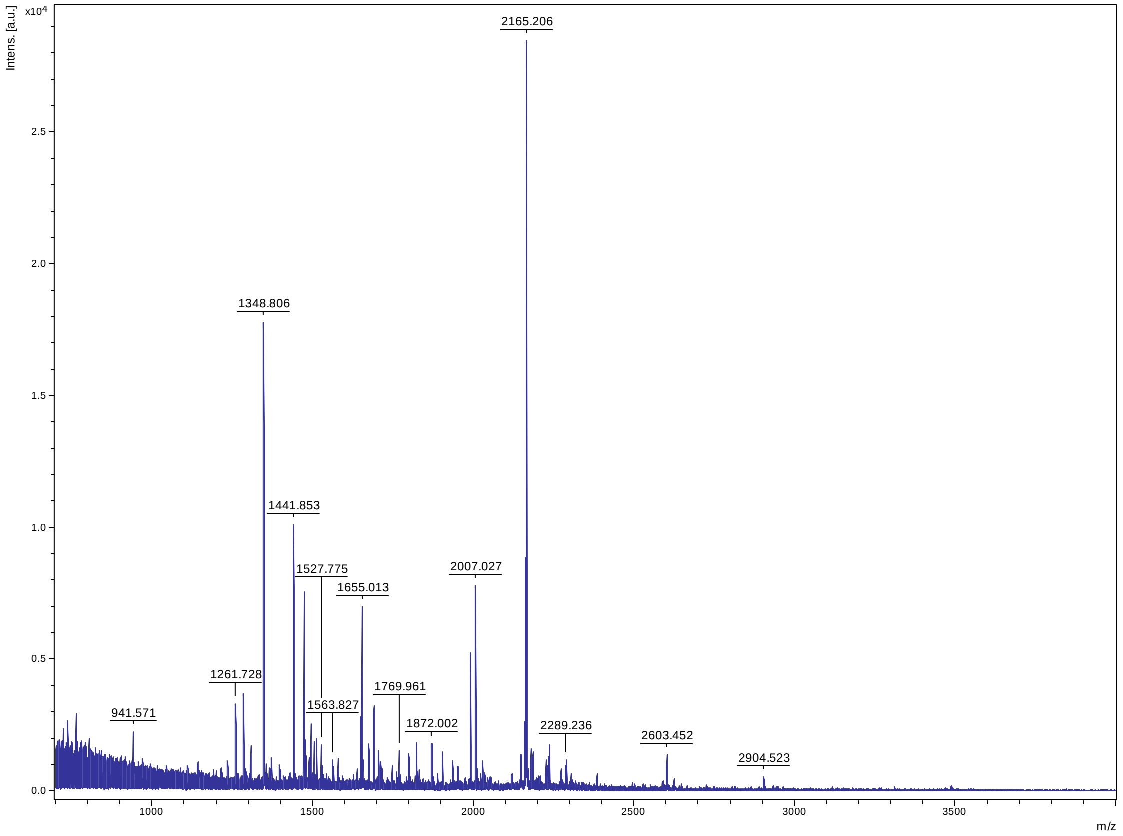


Match to: gi|75220444; Score: 80

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
31 - 38	947.51	946.51	946.47	0.03	0	SCAPLMLR
31 - 38	963.49	962.48	962.47	0.02	0	SCAPLMLR Oxidation (M)
39 - 61	2398.12	2397.12	2397.14	-0.02	1	LAWHSAGTFDVSSKTGGPFGTMK Oxidation (M)
62 - 79	1805.94	1804.94	1804.94	-0.01	0	TPAELSHAANAGLDIAVR
143 - 167	2557.28	2556.28	2556.28	0.00	0	QVFGAQMGLSDQDIVALSGGHTLGR
143 - 167	2573.28	2572.28	2572.27	0.01	0	QVFGAQMGLSDQDIVALSGGHTLGR Oxidation (M)
171 - 181	1321.64	1320.63	1320.62	0.01	1	ERSGFEGPWTR
173 - 181	1036.48	1035.48	1035.48	0.00	0	SGFEGPWTR
182 - 209	3168.57	3167.56	3167.57	-0.00	1	NPLQFDNSYFTELLSGDKEGLLQLPSDK
210 - 223	1555.87	1554.87	1554.88	-0.01	0	ALLSDPAFRPLVEK
230 - 241	1497.74	1496.74	1496.73	0.01	1	AFFEDYKEAHLK

Spot 2144

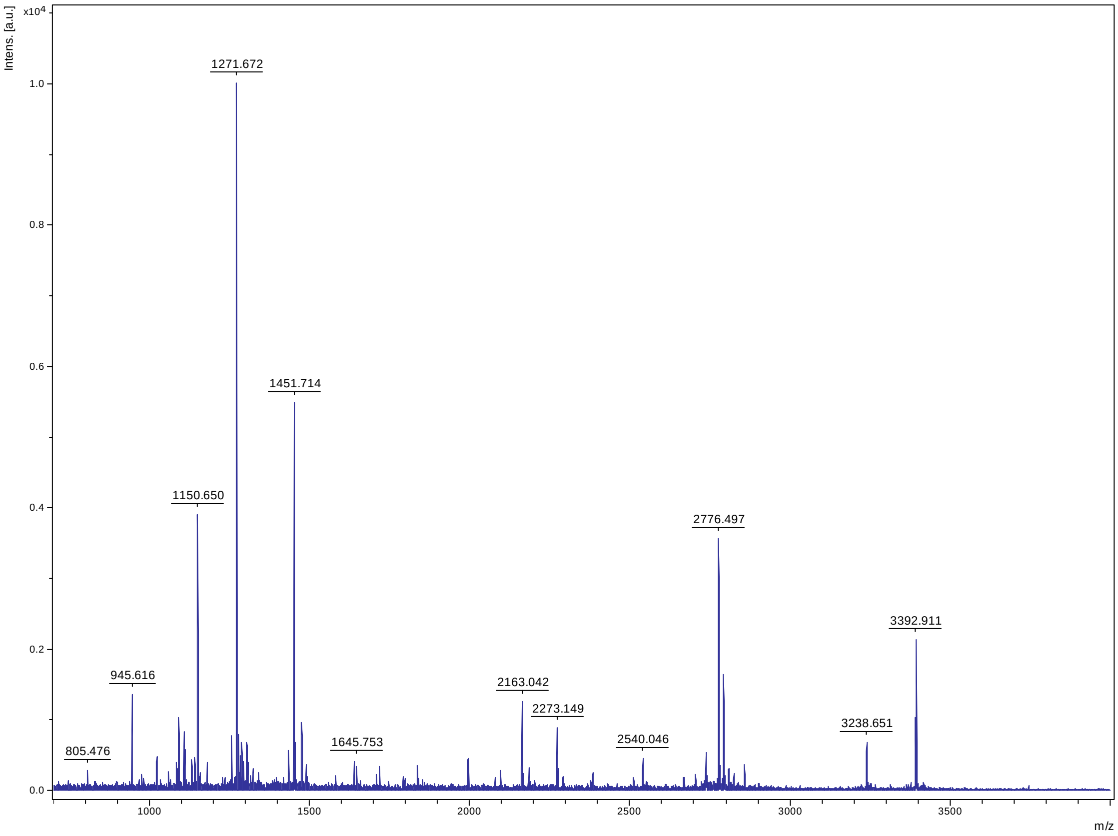


Match to: gi|11131901; Score: 198

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
27 - 38	1260.69	1259.69	1259.62	0.07	0	VVDGCEAQIAAK
39 - 49	1308.69	1307.69	1307.61	0.08	0	LEIMEPCSSVK Oxidation (M)
39 - 51	1563.83	1562.83	1562.74	0.08	1	LEIMEPCSSVKDR
39 - 51	1579.80	1578.79	1578.74	0.06	1	LEIMEPCSSVKDR Oxidation (M)
52 - 63	1356.69	1355.69	1355.63	0.06	0	IGYSMITDAEEK
52 - 63	1372.70	1371.70	1371.62	0.07	0	IGYSMITDAEEK Oxidation (M)
71 - 92	2148.18	2147.18	2147.13	0.05	0	SVLIEPTSGNTGIGLAFMAAAK
96 - 108	1479.79	1478.79	1478.73	0.06	0	LILTMPASMSMER
96 - 108	1495.79	1494.78	1494.72	0.06	0	LILTMPASMSMER Oxidation (M)
96 - 108	1511.79	1510.78	1510.72	0.06	0	LILTMPASMSMER 2 Oxidation (M)
96 - 108	1527.78	1526.77	1526.71	0.06	0	LILTMPASMSMER 3 Oxidation (M)
114 - 129	1674.97	1673.97	1673.91	0.06	0	AFGAELVLTDPLLGMK
114 - 129	1690.96	1689.96	1689.90	0.06	0	AFGAELVLTDPLLGMK Oxidation (M)
142 - 158	1991.03	1990.03	1989.96	0.07	0	MPNSYILQQFENPANPK
142 - 158	2007.03	2006.03	2005.96	0.07	0	MPNSYILQQFENPANPK Oxidation (M)
159 - 170	1473.79	1472.79	1472.73	0.06	0	IHYETTGPEIWK
171 - 194	2160.24	2159.24	2159.18	0.06	1	ATAGKVDILVSGIGTGGTVTGTGK
195 - 204	1261.73	1260.73	1260.67	0.05	1	YLKEQNPEIK
205 - 225	2165.21	2164.20	2164.13	0.08	0	IYGVEPTESAILSGGRPGPHK
265 - 282	1655.01	1654.01	1653.94	0.07	0	EGLLVGISSGAAAVAAIR
283 - 290	941.57	940.57	940.51	0.06	0	VAQRPENK
293 - 304	1348.81	1347.80	1347.75	0.05	0	LVVVVFPSFGER
305 - 315	1285.75	1284.75	1284.70	0.05	0	YLSSVLFESIK
305 - 316	1441.85	1440.85	1440.80	0.05	1	YLSSVLFESIKR

Spot 2145

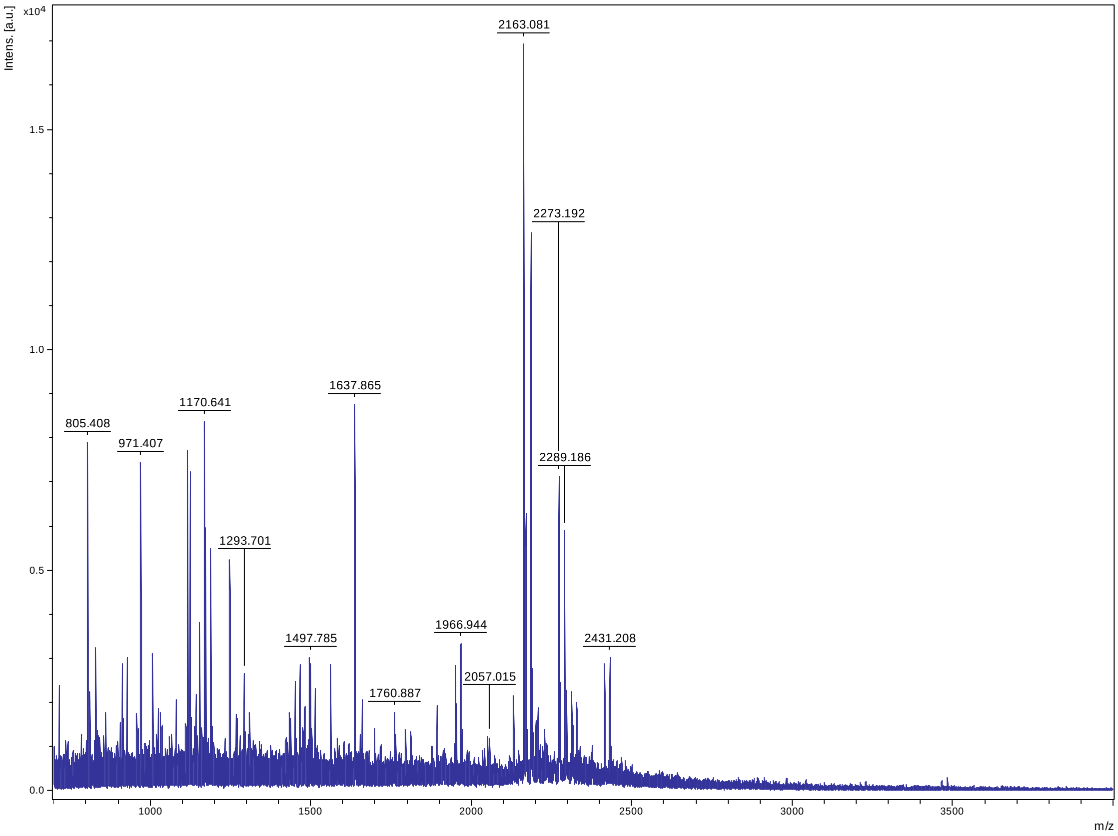


Match to: gi|6166140 Score: 120

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
15 - 23	1150.6504	1149.6431	1149.6393	0.0038	1	K.KLDEYLLTR.S
16 - 23	1022.5751	1021.5678	1021.5444	0.0234	0	K.LDEYLLTR.S
56 - 65	1271.6719	1270.6646	1270.6822	-0.0176	0	R.WFTHIDALLR.L
66 - 77	1131.6021	1130.5948	1130.5931	0.0017	0	R.LSGVTADGQGVK.V
96 - 118	2540.0461	2539.0389	2538.9881	0.0507	0	K.APAADDDDDDDVDLFGEETEEEK.K
140 - 157	2094.9529	2093.9456	2093.9827	-0.0371	0	K.SSVLLDVKPWDDETDMTK.L Oxidation (M)
167 - 176	1091.5631	1090.5558	1090.5481	0.0078	0	K.MEGLLWGASK.L
177 - 185	945.6155	944.6083	944.5694	0.0388	0	K.LVPVGYGIK.K

Spot 2146

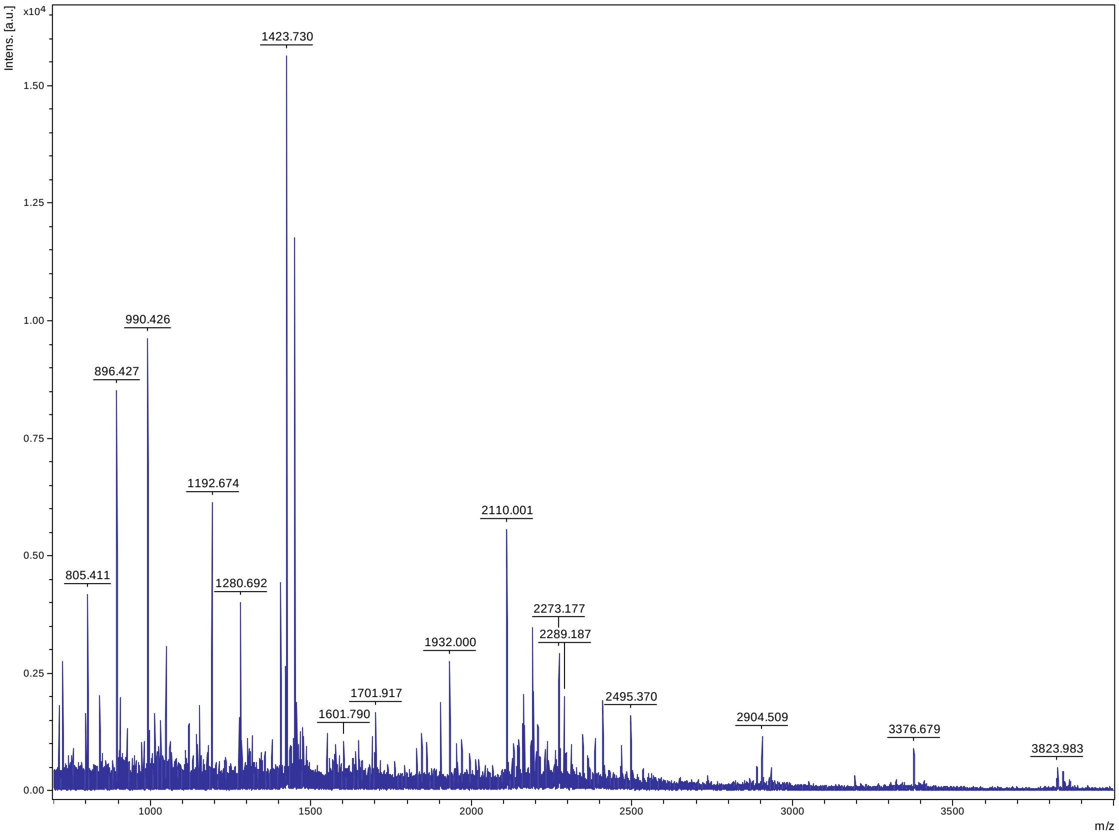


Match to: gi|57283874; Score: 181

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
140 - 146	805.41	804.41	804.44	-0.03	0	IPPTYSK
188 - 194	971.41	970.40	970.40	0.00	0	ACYECLR
195 - 213	2170.02	2169.02	2168.98	0.04	1	GGLDFTKDDENVNSQPFMR
202 - 213	1451.67	1450.66	1450.61	0.05	0	DDENVNSQPFMR
202 - 213	1467.64	1466.64	1466.61	0.03	0	DDENVNSQPFMR Oxidation (M)
218 - 227	1247.63	1246.62	1246.61	0.02	0	FVFCAEAIYK
228 - 236	962.48	961.48	961.47	0.01	0	SQAETGEIK
237 - 252	1794.86	1793.86	1793.81	0.05	0	GHYLNATAGTCEEMIK
237 - 252	1810.85	1809.85	1809.80	0.05	0	GHYLNATAGTCEEMIK Oxidation (M)
237 - 253	1950.95	1949.95	1949.91	0.04	1	GHYLNATAGTCEEMIKR
237 - 253	1966.94	1965.94	1965.90	0.04	1	GHYLNATAGTCEEMIKR Oxidation (M)
286 - 295	1187.67	1186.67	1186.66	0.01	0	DNGLLLHIHR
296 - 303	912.47	911.47	911.46	0.00	0	AMHAVIDR
296 - 303	928.48	927.48	927.46	0.02	0	AMHAVIDR Oxidation (M)
304 - 312	1153.58	1152.58	1152.52	0.05	1	QKNHGMHFR Oxidation (M); Pyro-glu (N-term Q)
304 - 312	1170.64	1169.64	1169.55	0.09	1	QKNHGMHFR Oxidation (M)
306 - 312	914.42	913.42	913.40	0.02	0	NHGMHFR Oxidation (M)
306 - 316	1309.70	1308.70	1308.69	0.01	1	NHGMHFRVLAK
320 - 334	1465.72	1464.71	1464.71	-0.00	0	MSGGDHIHAGTVVGK
320 - 334	1481.74	1480.74	1480.71	0.03	0	MSGGDHIHAGTVVGK Oxidation (M)
320 - 339	2050.01	2049.01	2049.01	0.00	1	MSGGDHIHAGTVVGKLEGER
335 - 350	1893.99	1892.98	1892.97	0.02	1	LEGEREMTLGFVDLLR Oxidation (M)
340 - 350	1293.70	1292.70	1292.68	0.02	0	EMTLGFVDLLR
340 - 356	2057.02	2056.01	2056.02	-0.01	1	EMTLGFVDLLRDDFIEK Oxidation (M)
351 - 358	1037.49	1036.49	1036.48	0.01	1	DDFIEKDR
422 - 431	1116.59	1115.59	1115.58	0.01	0	VALEACVQAR
451 - 463	1560.80	1559.80	1559.74	0.05	0	WSPELAAACEIWK

Spot 2147



Match to: gi|18147582; Score: 160

Matched peptides:

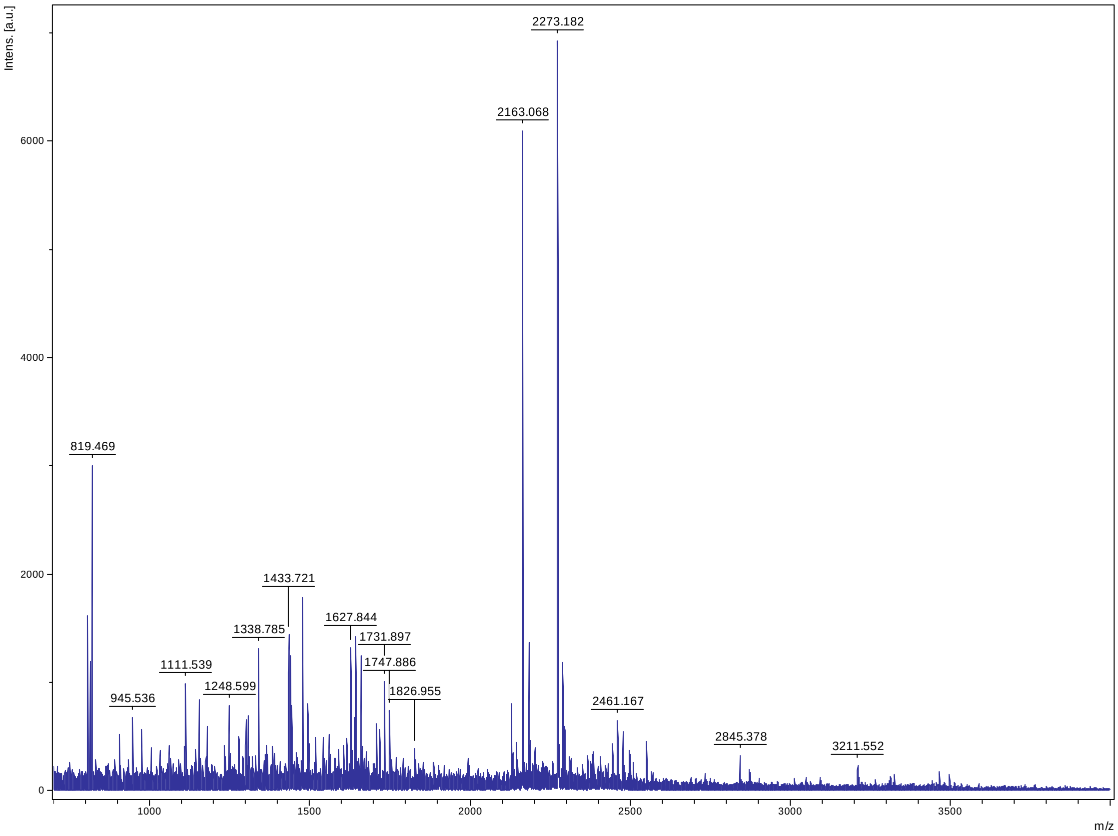
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
6 - 24	2191.03	2190.03	2190.01	0.02	0	IETGHQDVVHDIAMDYYGK
6 - 24	2207.02	2206.02	2206.00	0.02	0	IETGHQDVVHDIAMDYYGK Oxidation (M)
6 - 25	2347.16	2346.15	2346.11	0.05	1	IETGHQDVVHDIAMDYYGKR
26 - 36	1120.57	1119.56	1119.58	-0.01	0	IATASSDNTIK
68 - 80	1448.66	1447.65	1447.64	0.01	0	YGSLLASCSYDGR
86 - 103	2110.00	2109.00	2108.99	0.01	0	EGSKPDEWAQAHTFIEHK
104 - 135	3376.68	3375.68	3375.60	0.08	0	SSVNSIAWAPHELGLCLACGSSDGNISVFTAR
136 - 144	994.42	993.42	993.42	0.01	0	SDGGWDTTR
145 - 181	3823.98	3822.98	3822.90	0.08	0	IDQAHPVGVTSVSWAPAMAPGALINTGPSGQFEYVQK
196 - 202	895.44	894.44	894.43	0.00	0	LYNGSWR
203 - 213	1405.62	1404.62	1404.61	0.01	0	MDCFPALQMHR
203 - 213	1421.62	1420.62	1420.60	0.01	0	MDCFPALQMHR Oxidation (M)
218 - 229	1280.69	1279.69	1279.69	-0.00	0	DVAWAPNLGLPK
230 - 248	1932.00	1931.00	1931.00	-0.00	0	STIASASQDGTVVIWTAPK
249 - 256	990.43	989.42	989.42	0.00	0	EGEQWEGR
257 - 267	1423.73	1422.73	1422.73	-0.00	0	VLYDFQTPVWR

Match to: gi|30089728; Score: 113

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
7 - 27	2273.18	2272.18	2272.21	-0.04	1	KLVIDTDPGIDDAMAIFVALR
7 - 27	2289.19	2288.18	2288.21	-0.02	1	KLVIDTDPGIDDAMAIFVALR Oxidation (M)
8 - 27	2145.09	2144.09	2144.12	-0.03	0	LVIDTDPGIDDAMAIFVALR
8 - 27	2161.11	2160.11	2160.11	-0.01	0	LVIDTDPGIDDAMAIFVALR Oxidation (M)
28 - 50	2495.37	2494.37	2494.33	0.04	0	SPEVELLGLTTIFGNVYTTLATR
51 - 61	1192.67	1191.67	1191.67	-0.00	0	NALHLLEAVGR
62 - 75	1466.76	1465.76	1465.78	-0.02	0	TDIPVAEGSHVTIK
225 - 234	1284.67	1283.67	1283.65	0.01	0	ILGLYYDYHK
241 - 267	2888.51	2887.51	2887.48	0.03	0	GVYLHDPATLIAAVDPSLMTYTEGVVR
241 - 267	2904.51	2903.51	2903.47	0.03	0	GVYLHDPATLIAAVDPSLMTYTEGVVR Oxidation (M)
276 - 284	981.52	980.52	980.52	-0.00	0	GLTVFDTTK
287 - 300	1550.81	1549.80	1549.81	-0.01	0	YGEITAWTGKPTVK
287 - 317	3376.68	3375.68	3375.76	-0.08	1	YGEITAWTGKPTVKVAVTVDAPAVVEMIMQR Oxidation (M)
301 - 317	1828.95	1827.95	1827.96	-0.01	0	VAVTVDAPAVVEMIMQR
301 - 317	1844.95	1843.95	1843.95	-0.00	0	VAVTVDAPAVVEMIMQR Oxidation (M)
301 - 317	1860.95	1859.95	1859.95	-0.00	0	VAVTVDAPAVVEMIMQR 2 Oxidation (M)

Spot 2164

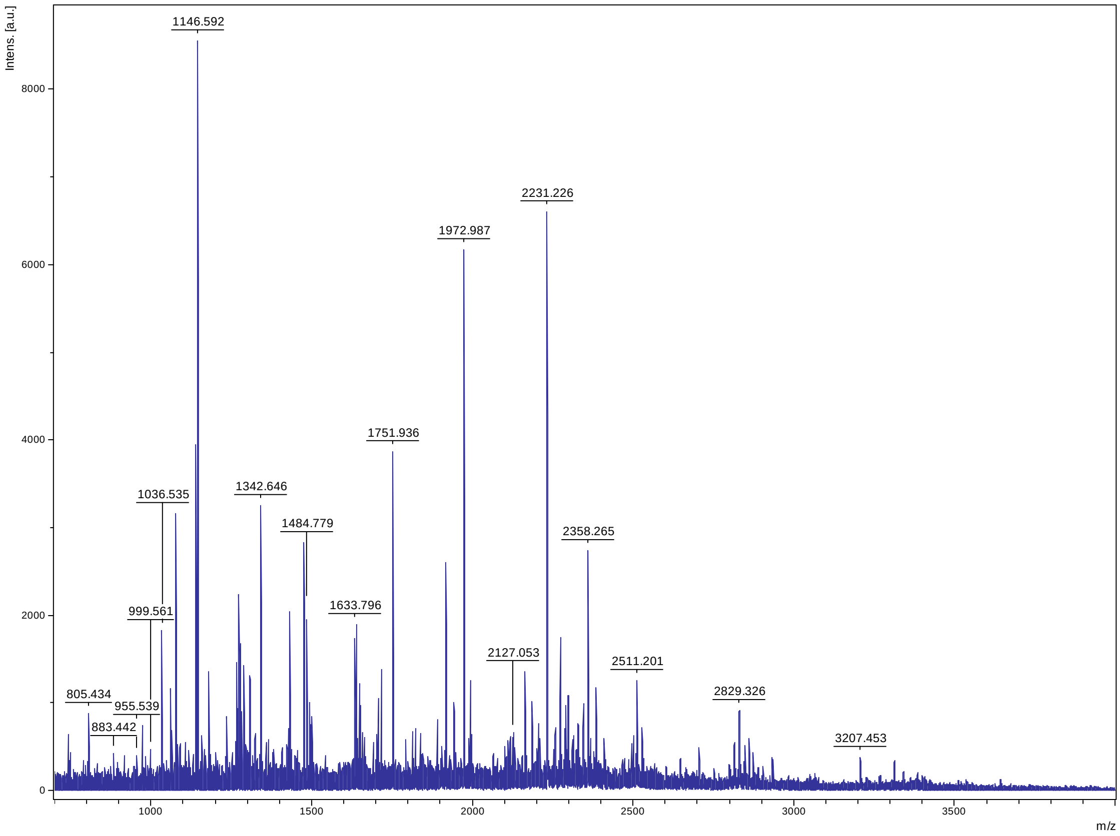


Match to: gi|6630689 Score: 91

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
45 - 66	2461.1672	2460.1600	2460.1374	0.0226	0	R.AGVPMEVMGLMLGEFVDDYTVR.V	2 Oxidation (M)
138 - 150	1338.7845	1337.7773	1337.7918	-0.0145	0	R.AVAVVIDPIQSVK.G	
151 - 159	1004.5686	1003.5613	1003.5814	-0.0201	1	K.GKVVIDAFR.L	
153 - 159	819.4692	818.4620	818.4650	-0.0030	0	K.VVIDAFR.L	
160 - 173	1627.8438	1626.8365	1626.8221	0.0143	0	R.LINPQTMMLGQEPR.Q	
160 - 173	1643.8348	1642.8276	1642.8171	0.0105	0	R.LINPQTMMLGQEPR.Q	Oxidation (M)
160 - 173	1659.8196	1658.8123	1658.8120	0.0003	0	R.LINPQTMMLGQEPR.Q	2 Oxidation (M)
197 - 206	1299.6332	1298.6259	1298.6407	-0.0148	0	R.HYYSIAINYR.K	
223 - 230	945.5360	944.5287	944.5331	-0.0044	0	K.WTDGLILK.S	
231 - 252	2550.2844	2549.2771	2549.2431	0.0340	1	K.SFDTHSKTNEQTVQEMLNLAIK.Y	Oxidation (M)
238 - 252	1731.8971	1730.8898	1730.8872	0.0026	0	K.TNEQTVQEMLNLAIK.Y	
238 - 252	1747.8864	1746.8791	1746.8822	-0.0031	0	K.TNEQTVQEMLNLAIK.Y	Oxidation (M)
268 - 275	813.4933	812.4860	812.4868	-0.0008	0	K.LAIANVGR.Q	

Spot 2165

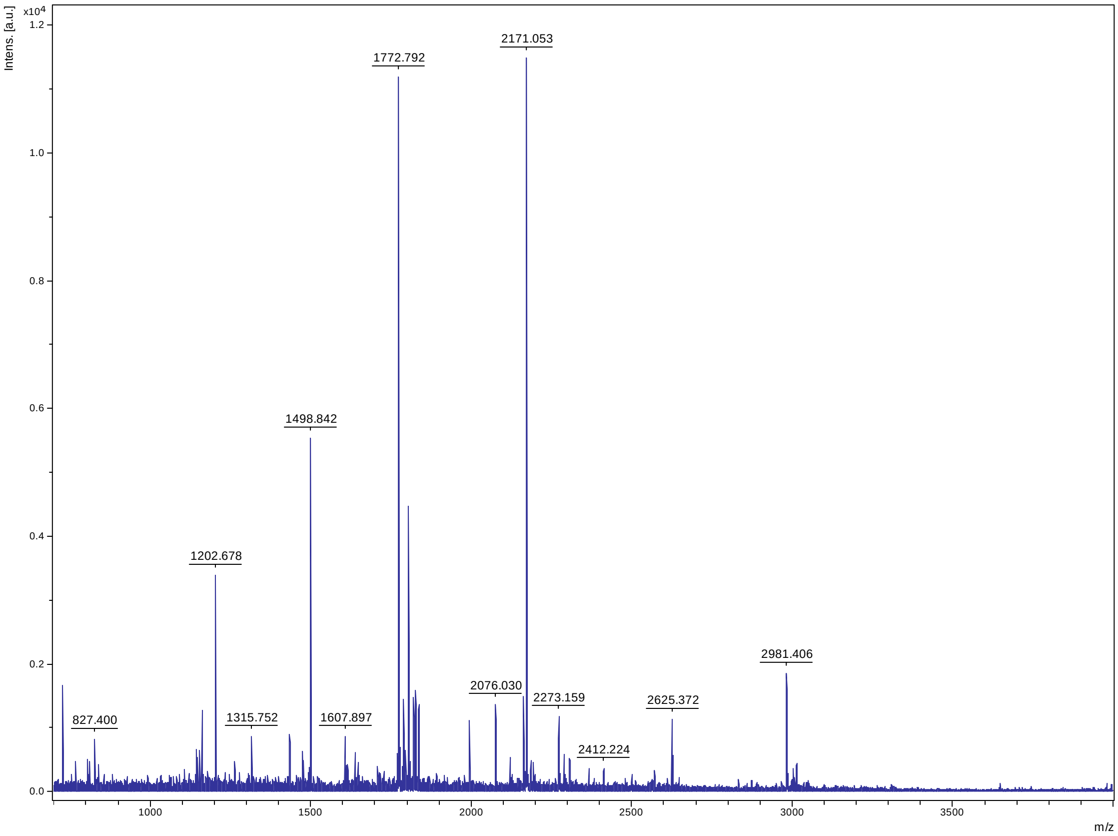


Match to: gi|74053562; Score: 103

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
3 - 19	1822.93	1821.93	1821.92	0.01	0	EILHIQGGQCGNQIGAK
20 - 35	1942.89	1941.89	1941.87	0.02	0	FWEVICDEHGIDHTGK
36 - 46	1282.62	1281.61	1281.58	0.03	0	YSGDSDLQLER
47 - 58	1342.65	1341.64	1341.63	0.01	0	INVYYNEASGGR
63 - 77	1633.80	1632.79	1632.79	0.01	0	AVLMDLEPGTMDSVR
63 - 77	1649.80	1648.80	1648.78	0.02	0	AVLMDLEPGTMDSVR Oxidation (M)
78 - 103	2814.31	2813.31	2813.33	-0.02	0	SGPYGQIFRPDNFVFGQSGAGNNWAK
104 - 121	1972.99	1971.99	1971.99	-0.00	0	GHYTEGAELIDSVLDVVR
155 - 162	1077.54	1076.54	1076.53	0.02	1	IREEYPDR
242 - 251	1146.59	1145.59	1145.58	0.01	0	FPGQLNSDLR
252 - 262	1267.78	1266.78	1266.78	-0.00	1	KLAVNLIPFPR
253 - 262	1139.69	1138.69	1138.69	0.00	0	LAVNLIPFPR
263 - 282	2358.27	2357.26	2357.17	0.09	1	LHFFMVGFAPLTSRGSQQYR Oxidation (M)
298 - 309	1431.64	1430.64	1430.60	0.04	1	NMMCAADPRHGR Oxidation (M)

Spot 2166

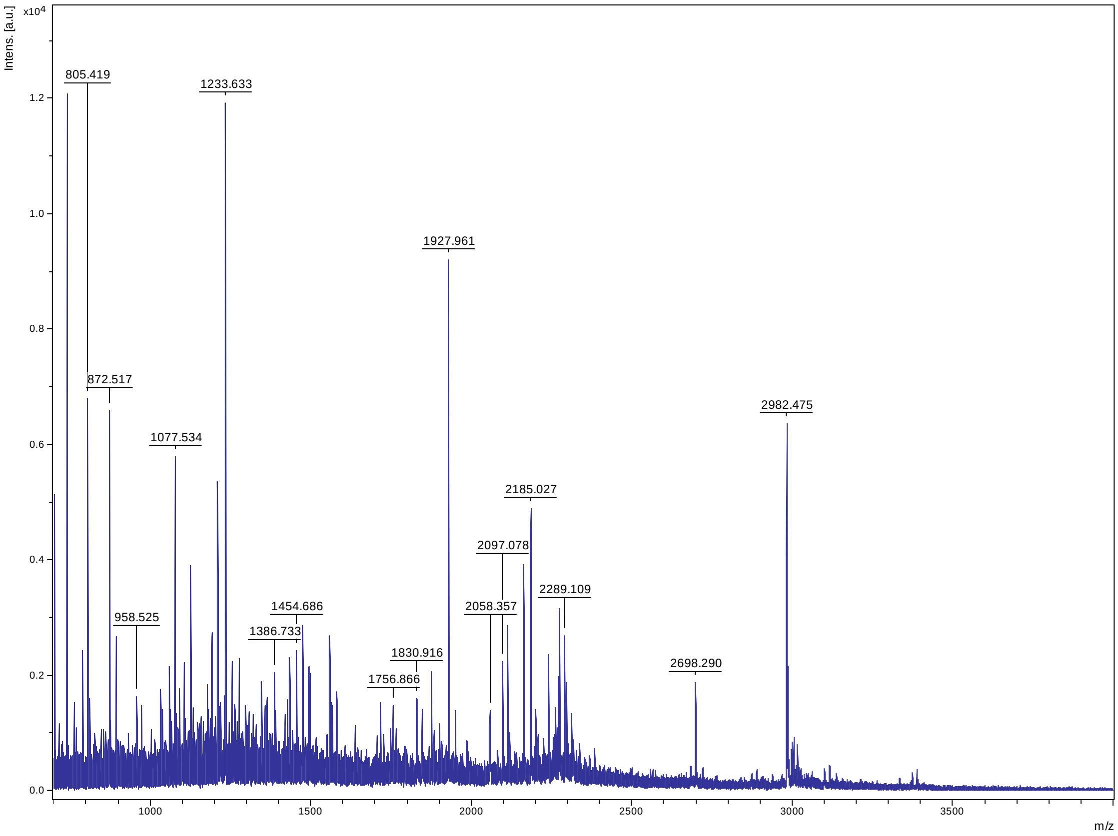


Match to: gi|84028207; Score: 136

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
83 - 109	2981.41	2980.40	2980.40	0.01	1	NPDEIPWAEAGAEYVVESTGVFTDKEK
165 - 188	2625.37	2624.37	2624.36	0.01	0	VIHDNFGIIEGLMTTVHAITATQK Oxidation (M)
203 - 217	1434.75	1433.75	1433.75	-0.00	0	AASFNIIPSSTGAAK
222 - 236	1647.85	1646.85	1646.88	-0.03	1	VLPDLNGKLTGMSFR
230 - 236	811.40	810.40	810.41	-0.00	0	LTGMSFR
230 - 236	827.40	826.40	826.40	-0.00	0	LTGMSFR Oxidation (M)
230 - 250	2307.22	2306.22	2306.23	-0.01	1	LTGMSFRVPTVDVSVVDLTVR Oxidation (M)
237 - 250	1498.84	1497.84	1497.84	-0.00	0	VPTVDVSVVDLTVR
254 - 261	838.43	837.43	837.42	0.01	0	AASYDAIK
272 - 293	2412.22	2411.22	2411.22	-0.00	1	LKGIIGYVEEDLVSTDFVGDSR
274 - 293	2171.05	2170.05	2170.04	0.01	0	GIIGYVEEDLVSTDFVGDSR
301 - 311	1161.61	1160.61	1160.62	-0.01	0	AGIALNDNFVK
312 - 325	1772.79	1771.79	1771.80	-0.01	0	LVAWYDNEWGYSNR

Spot 2171

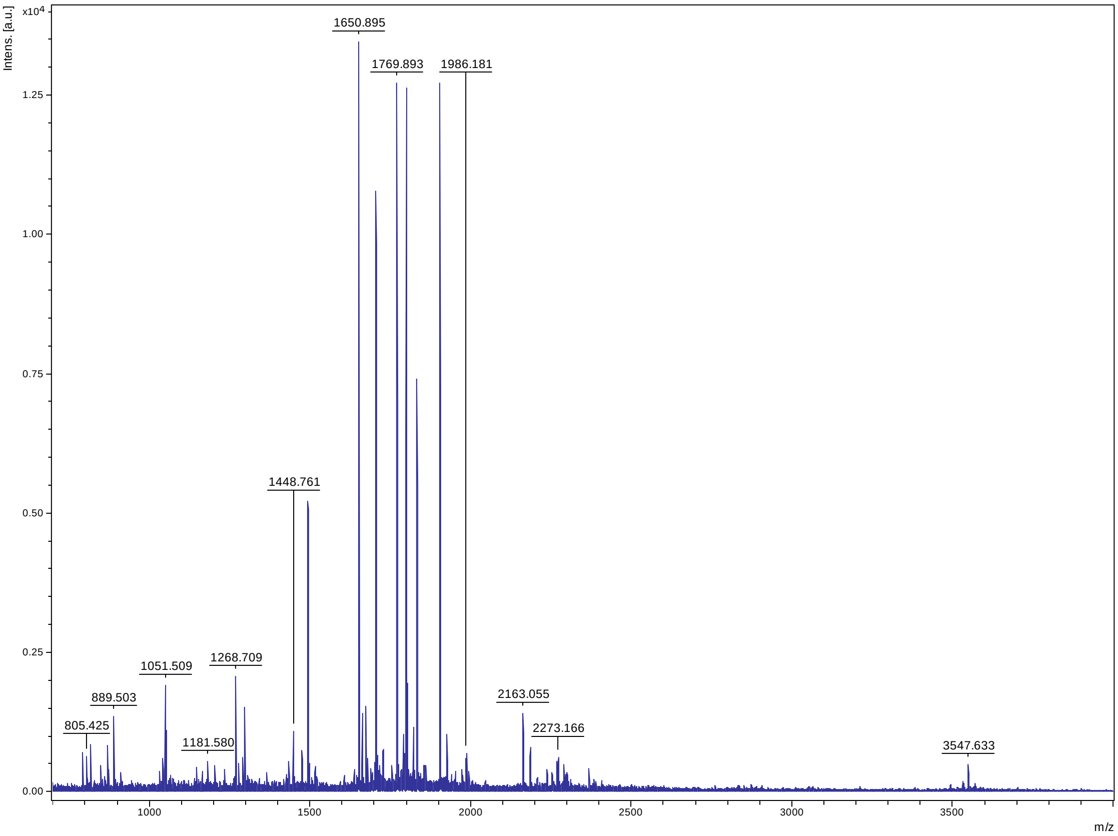


Match to: gi|52077303; Score: 121

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
32 - 47	1927.96	1926.96	1926.97	-0.01	0	SEPLYQYVLESTVFPR
32 - 53	2698.29	2697.29	2697.31	-0.02	1	SEPLYQYVLESTVFPREPDCLR
113 - 120	872.52	871.51	871.51	0.00	0	IVAIDVSR
113 - 133	2275.16	2274.16	2274.17	-0.02	1	IVAIDVSRESYDEVGAPVIDK
121 - 133	1421.67	1420.67	1420.67	-0.00	0	ESYDEVGAPVIDK
144 - 161	1899.94	1898.94	1898.97	-0.03	0	VGLAMPVLDELVAEEGNK Oxidation (M)
144 - 163	2097.08	2096.08	2096.09	-0.02	1	VGLAMPVLDELVAEEGNKGR
144 - 163	2113.07	2112.07	2112.09	-0.02	1	VGLAMPVLDELVAEEGNKGR Oxidation (M)
174 - 182	1134.55	1133.55	1133.56	-0.01	0	VNFLGYHER
189 - 219	2982.48	2981.47	2981.49	-0.02	0	VGGLIAYDNTLWGGSVAAPPAAADEAVPSGR
229 - 238	1077.53	1076.53	1076.53	0.01	0	EFNAAIAADR
229 - 239	1233.63	1232.63	1232.63	0.00	1	EFNAAIAADRR
240 - 255	1830.92	1829.91	1829.93	-0.02	0	VKPCQLAIADGVMLCR
240 - 255	1846.92	1845.92	1845.93	-0.00	0	VKPCQLAIADGVMLCR Oxidation (M)

Spot 2178

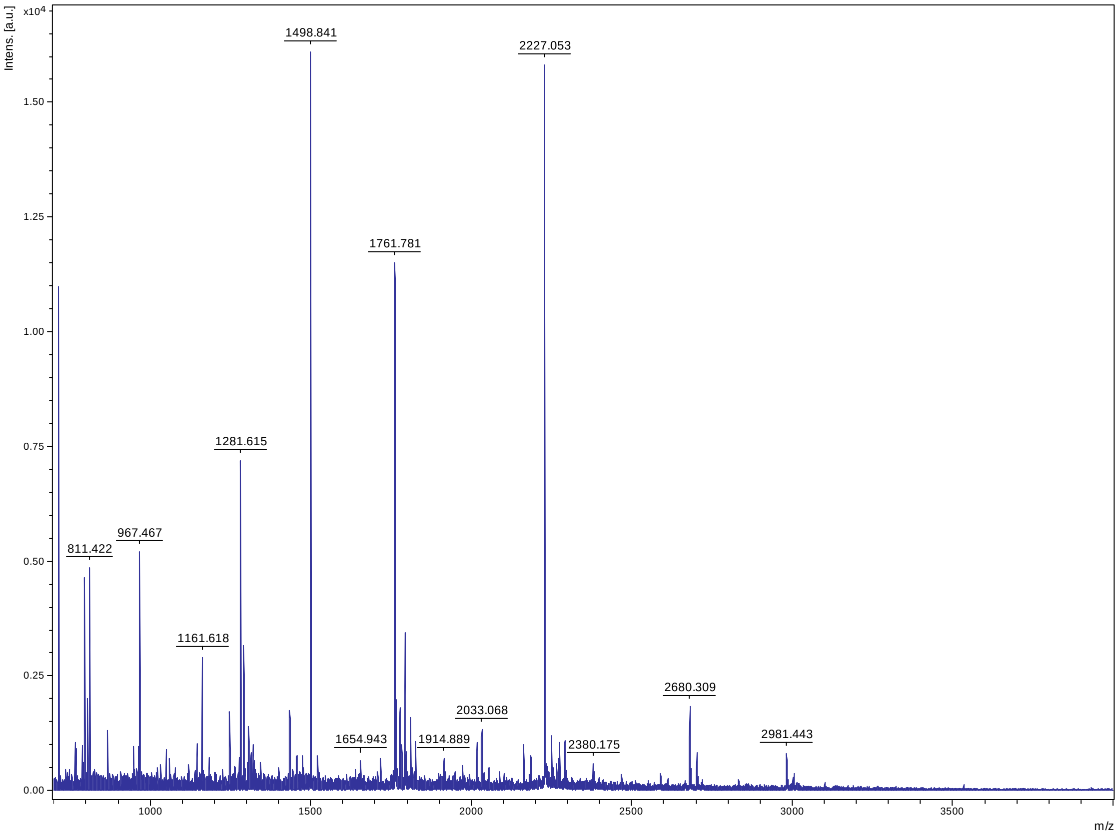


Match to: gi|46359906; Score: 186

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
21 - 35	1769.89	1768.89	1768.88	0.01	0	VEAVVVFNICDSYVR
36 - 42	871.44	870.44	870.43	0.01	0	RPDQAER
43 - 60	1833.07	1832.07	1832.05	0.01	0	VIGTLLGSVLPDGTVHVR
61 - 90	3547.63	3546.63	3546.60	0.03	0	NSYVVPHNESPDQVALDIEYHHNMYASHHK Oxidation (M)
121 - 136	1799.94	1798.93	1798.92	0.01	0	EVQSPIHLTVDTGFTR
143 - 154	1295.67	1294.67	1294.65	0.02	0	AYISSNLSLGDR
155 - 168	1650.89	1649.89	1649.89	0.00	0	HLAAQFQEIPLDLR
175 - 187	1448.76	1447.76	1447.83	-0.07	1	VGFDILKSTIVEK
182 - 201	2237.09	2236.08	2236.06	0.02	1	STIVEKLPNDLEGMESSMEK
182 - 201	2269.05	2268.05	2268.05	-0.00	1	STIVEKLPNDLEGMESSMEK 2 Oxidation (M)
202 - 211	1268.71	1267.71	1267.71	0.00	0	LYVLIDEIYK
212 - 220	1051.51	1050.51	1050.50	0.01	0	YVDDVVEGR
230 - 240	1181.58	1180.58	1180.58	-0.00	0	FISDAVASMPK Oxidation (M)
241 - 248	848.47	847.47	847.44	0.02	0	LSPAAFDK
254 - 268	1705.95	1704.95	1704.94	0.01	0	IQDNLALVYLSSITR
269 - 276	889.50	888.50	888.49	0.01	0	TQISIAEK

Spot 2189

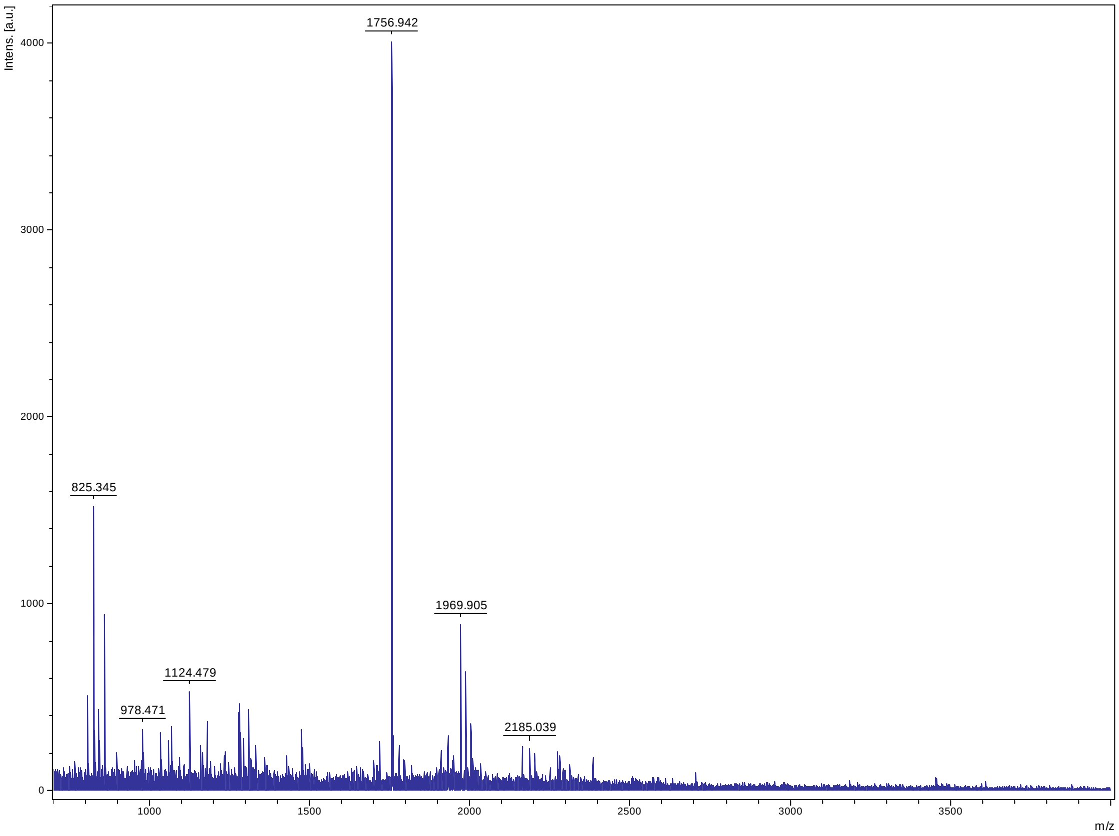


Match to: gi|38346061; Score: 160

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
75 - 82	967.47	966.47	966.46	0.01	0	EVTVFGCR
83 - 109	2981.44	2980.44	2980.40	0.04	1	NPEEIPWGETGAEFVVESTGVFTDKDK
129 - 140	1305.66	1304.65	1304.64	0.01	0	DAPMFVVGVNEK
129 - 140	1321.65	1320.65	1320.64	0.01	0	DAPMFVVGVNEK Oxidation (M)
141 - 164	2680.31	2679.31	2679.29	0.02	0	EYKPDIDIVSNASCTTNCLAPLAK
170 - 188	2017.08	2016.08	2016.07	0.01	0	FGIVEGLMTTVHAITATQK
170 - 188	2033.07	2032.07	2032.07	-0.00	0	FGIVEGLMTTVHAITATQK Oxidation (M)
189 - 199	1247.60	1246.60	1246.59	0.00	1	TVDGPSSKDWR
203 - 217	1434.75	1433.75	1433.75	-0.01	0	AASFNIIPSSTGAAK
230 - 236	811.42	810.42	810.41	0.01	0	LTGMAFR Oxidation (M)
230 - 250	2291.24	2290.24	2290.24	0.01	1	LTGMAFRVPTVDVSVVDLTVR Oxidation (M)
237 - 250	1498.84	1497.84	1497.84	-0.00	0	VPTVDVSVVDLTVR
251 - 261	1291.68	1290.68	1290.68	-0.01	0	LEKPASYDQIK
274 - 293	2227.05	2226.05	2226.04	0.01	0	GILGYVEEDLVSTDFQGDNR
301 - 311	1161.62	1160.62	1160.62	-0.00	0	AGIALNDNFVK
312 - 325	1761.78	1760.78	1760.78	-0.00	0	LVSWYDNEWGYSSR
332 - 337	809.32	808.32	808.32	0.00	0	HMYNTQ Oxidation (M)

Spot 2190

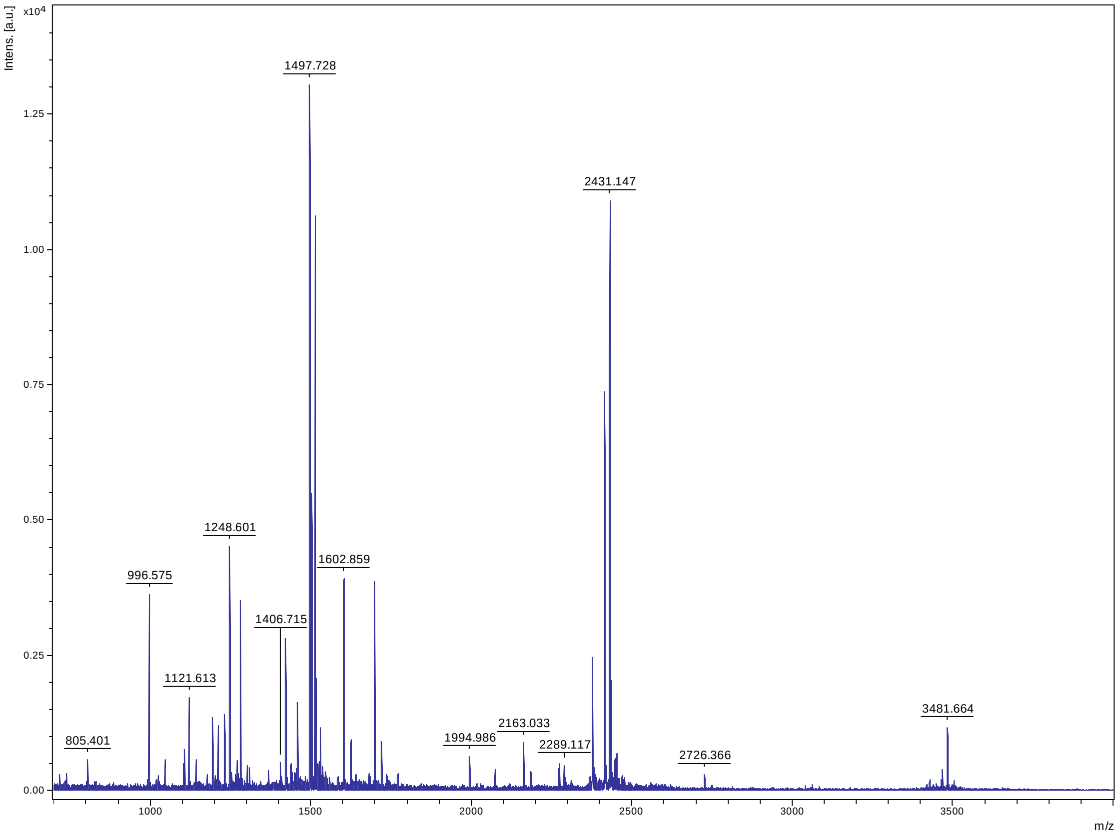


Match to: gi|50947283; Score: 78

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
57 - 66	1069.51	1068.51	1068.52	-0.01	0	TAIHSNDSPK
71 - 86	1969.90	1968.90	1968.91	-0.00	0	SESLHEYMLNTMVYPR
71 - 86	1985.90	1984.90	1984.90	-0.01	0	SESLHEYMLNTMVYPR Oxidation (M)
87 - 92	825.35	824.34	824.35	-0.01	0	ENEFMR
87 - 92	841.35	840.34	840.34	0.00	0	ENEFMR Oxidation (M)
152 - 159	858.49	857.49	857.50	-0.01	0	VVAIDVSR
212 - 220	1124.48	1123.48	1123.47	0.01	0	GNYGEYHER
274 - 289	1756.94	1755.94	1755.92	0.02	0	VEAVQLPVSDGITLCR

Spot 2193

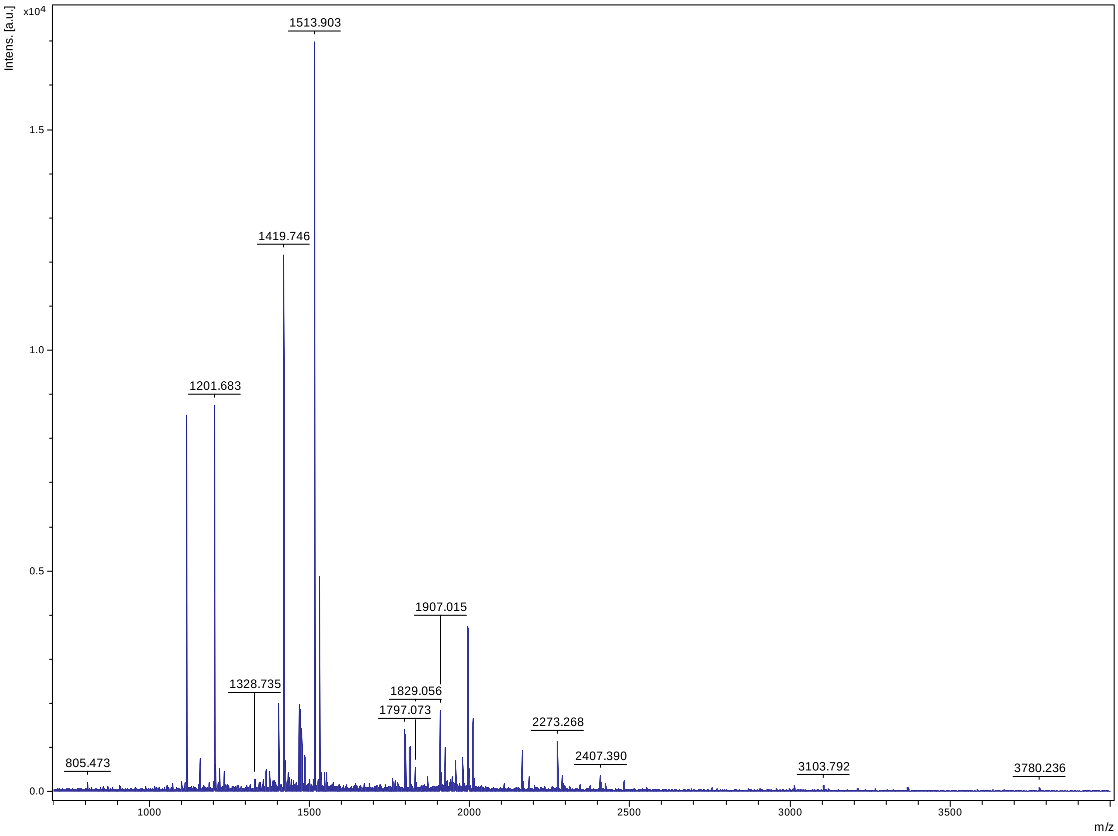


Match to: gi|84029333; Score: 157

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
41 - 49	1195.44	1194.44	1194.45	-0.01	0	CYTECFGMK
41 - 49	1211.44	1210.44	1210.45	-0.01	0	CYTECFGMK Oxidation (M)
88 - 106	2073.96	2072.96	2072.98	-0.03	0	YDIGAGFGHFAIATEDVYK
119 - 127	996.57	995.57	995.58	-0.00	1	ITREPGPVK
128 - 149	2415.14	2414.14	2414.16	-0.02	0	GGSTVIAFAQDPDGYMFELIQR
128 - 149	2431.15	2430.15	2430.15	-0.01	0	GGSTVIAFAQDPDGYMFELIQR Oxidation (M)
150 - 162	1497.73	1496.73	1496.75	-0.02	0	GPTPEPLCQVMLR
150 - 162	1513.73	1512.73	1512.74	-0.02	0	GPTPEPLCQVMLR Oxidation (M)
192 - 221	3465.65	3464.65	3464.66	-0.01	1	YTIAMLGYADEDKTTVIELTYNYGVTEYTK
192 - 221	3481.66	3480.66	3480.65	0.01	1	YTIAMLGYADEDKTTVIELTYNYGVTEYTK Oxidation (M)
205 - 221	1994.99	1993.98	1993.99	-0.00	0	TTVIELTYNYGVTEYTK
222 - 237	1698.82	1697.81	1697.83	-0.01	0	GNAYAQVAIGTEDVYK
222 - 247	2726.37	2725.36	2725.38	-0.02	1	GNAYAQVAIGTEDVYKSAEAVELVTK
238 - 247	1046.56	1045.55	1045.57	-0.01	0	SAEAVELVTK
253 - 266	1503.87	1502.87	1502.89	-0.02	1	ILRQPGPLPGLNTK
256 - 266	1104.58	1103.58	1103.60	-0.02	0	QPGPLPGLNTK Pyro-glu (N-term Q)
256 - 266	1121.61	1120.61	1120.62	-0.01	0	QPGPLPGLNTK
267 - 277	1248.60	1247.60	1247.62	-0.02	0	IASFLDPDGWK
278 - 291	1602.86	1601.86	1601.87	-0.01	1	VVLVDNADFLKELQ

Spot 2195

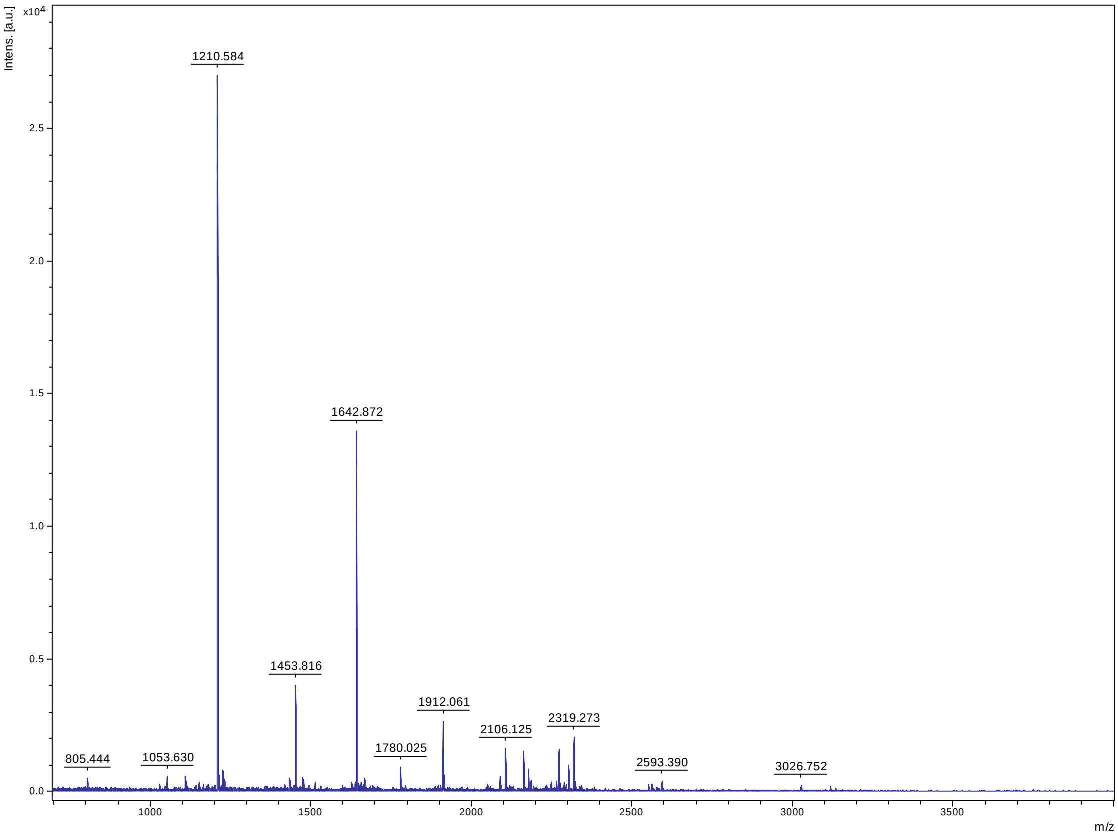


Match to: gi|4105683 Score: 98

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
55 - 70	2009.9651	2008.9578	2008.8632	0.0946	0	R.QVEAHHFCAHLNEDMR.Q	Carbamidomethyl (C); Oxidation (M)
71 - 83	1362.7078	1361.7005	1361.6397	0.0607	0	R.QCLIFDGPDAGAR.L	
71 - 83	1402.7122	1401.7049	1401.6347	0.0702	0	R.QCLIFDGPDAGAR.L	Carbamidomethyl (C); Pyro-glu (N-term Q)
71 - 83	1419.7456	1418.7383	1418.6612	0.0771	0	R.QCLIFDGPDAGAR.L	Carbamidomethyl (C)
116 - 130	1513.9025	1512.8952	1512.8122	0.0830	0	K.GGVLFMPGVPGVVER.R	
116 - 130	1529.9010	1528.8937	1528.8071	0.0866	0	K.GGVLFMPGVPGVVER.R	Oxidation (M)
143 - 151	1201.6826	1200.6753	1200.6040	0.0714	0	K.TIHFWQVDR.G	
152 - 168	1797.0734	1796.0661	1795.9688	0.0973	0	R.GDALPLGLPQIMMALTR.D	
152 - 168	1813.0580	1812.0507	1811.9637	0.0870	0	R.GDALPLGLPQIMMALTR.D	Oxidation (M)
152 - 168	1829.0562	1828.0489	1827.9586	0.0902	0	R.GDALPLGLPQIMMALTR.D	2 Oxidation (M)
174 - 183	1233.6860	1232.6788	1232.6070	0.0717	1	R.QELAKCVEEK.F	Carbamidomethyl (C)
184 - 192	1114.6202	1113.6130	1113.5454	0.0675	1	K.FSVSFDKER.E	
196 - 214	1907.0154	1906.0081	1905.9155	0.0926	0	R.AYMSGPDHGIHPLANAAGK.G	
196 - 214	1923.0076	1922.0003	1921.9104	0.0899	0	R.AYMSGPDHGIHPLANAAGK.G	Oxidation (M)
222 - 235	1468.8084	1467.8011	1467.7140	0.0871	0	R.EVDLPAMTTAHAGR.V	
222 - 235	1484.7988	1483.7916	1483.7089	0.0827	0	R.EVDLPAMTTAHAGR.V	Oxidation (M)

Spot 2200

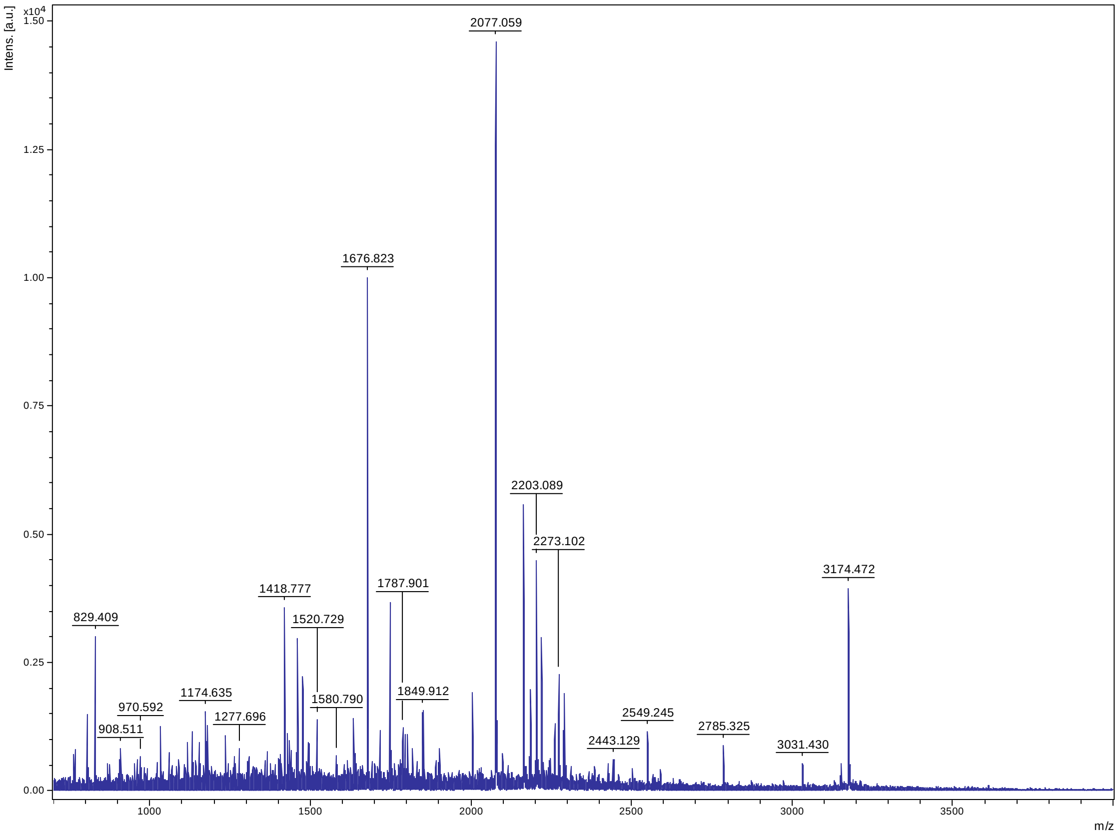


Match to: gi|14192878 Score: 88

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
95 - 112	1912.0607	1911.0534	1911.0438	0.0096	1	R.LRSPAAEALGPTHVLHSR.Y
97 - 112	1642.8718	1641.8646	1641.8587	0.0059	0	R.SPAAEALGPTHVLHSR.Y
171 - 183	1453.8158	1452.8085	1452.8187	-0.0102	1	K.VKEGVEVPQLVEK.V
173 - 183	1226.6516	1225.6443	1225.6553	-0.0110	0	K.EGVEVPQLVEK.V
184 - 195	1030.5475	1029.5402	1029.5454	-0.0052	0	K.VAAATAAAGEAK.G
199 - 209	1210.5836	1209.5763	1209.5778	-0.0014	0	R.VSFGENFSPAR.A
212 - 235	2562.1711	2561.1639	2561.1631	0.0008	0	K.GYQFGMVAVFDSVEELDAVEGDGK.V
241 - 270	3026.7522	3025.7449	3025.6851	0.0598	0	K.AAVRPLLDEVLVLDFVVGPAAVEAPAPANL.-

Spot 2201

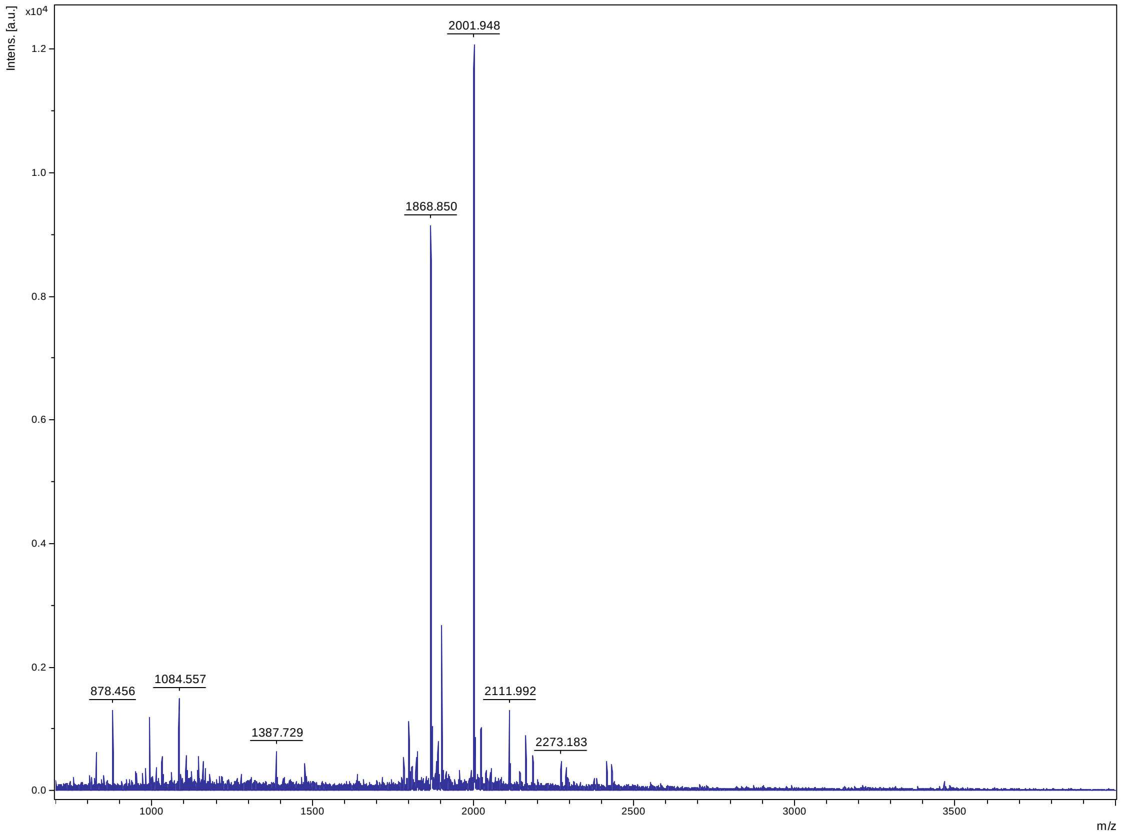


Match to: gi|78099751; Score: 91

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
8 - 14	908.51	907.51	907.50	0.01	1	YKDELIK
40 - 52	1520.73	1519.73	1519.73	0.00	0	FASINVENVEENR
40 - 53	1676.82	1675.82	1675.83	-0.01	1	FASINVENVEENRR
85 - 94	1117.63	1116.63	1116.62	0.01	0	DGKPFVDVLK
95 - 103	869.52	868.52	868.50	0.01	0	EGGVLPGIK
117 - 129	1457.71	1456.71	1456.69	0.02	1	ETTTQGHDDLGKR
133 - 139	829.41	828.41	828.38	0.03	0	YYEAGAR
149 - 168	2077.06	2076.06	2076.10	-0.04	0	IGPNEPSQLAIDLNAQGLAR
169 - 196	3174.47	3173.47	3173.61	-0.14	0	YAIICQENGLVPIVEPEILVDGPHDIDR
197 - 210	1632.78	1631.78	1631.77	0.01	0	CAYVSEVVLAACYK
318 - 325	905.48	904.48	904.52	-0.05	1	ARAAFLTR

Spot 2204

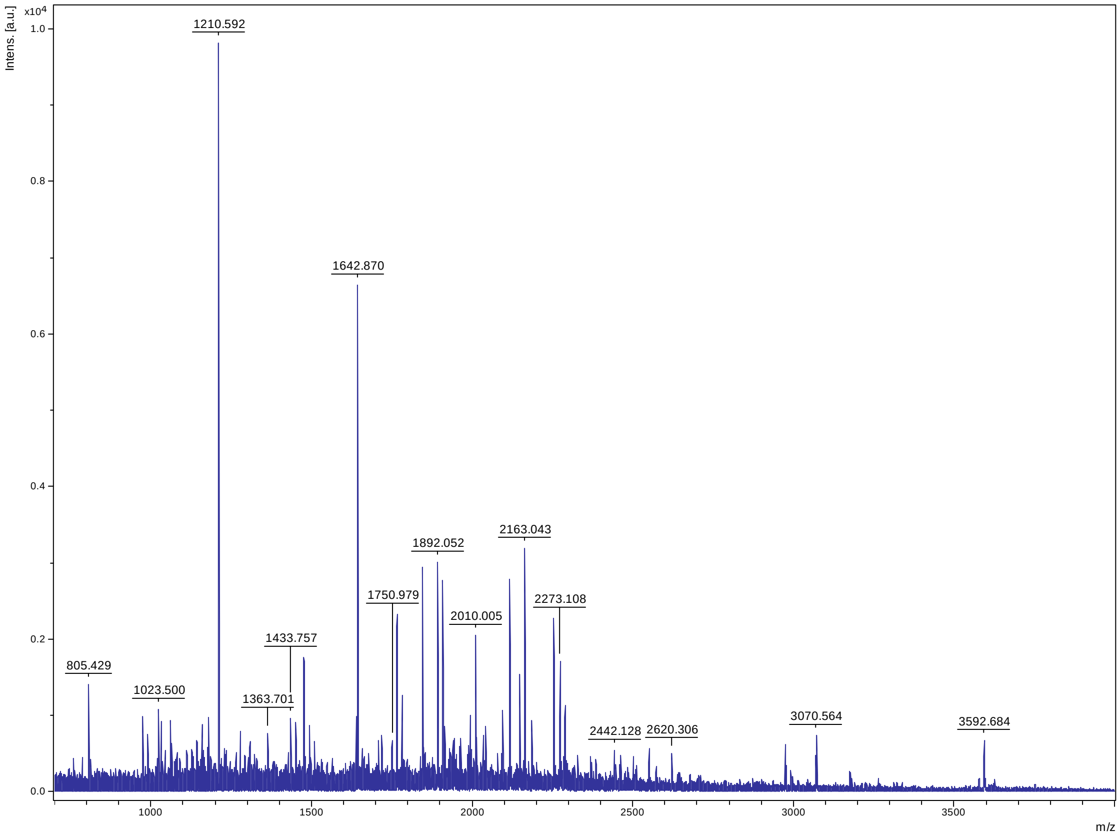


Match to: gi|12229919; Score: 133

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
21 - 29	1084.56	1083.55	1083.56	-0.01	0	VFQVEYATK
30 - 41	1159.65	1158.64	1158.62	0.02	0	AVDNSGTVVGIK
102 - 110	991.57	990.57	990.54	0.03	0	VYGEPISVK
144 - 159	1783.87	1782.87	1782.85	0.02	0	DGPQLYMIEPSGVSYK
144 - 159	1799.87	1798.87	1798.84	0.02	0	DGPQLYMIEPSGVSYK Oxidation (M)
160 - 167	826.47	825.47	825.44	0.03	0	YFGAALGK
181 - 187	878.46	877.45	877.43	0.02	0	LSELTCR
196 - 205	1144.61	1143.61	1143.59	0.02	0	IIYGVHDEAK
196 - 207	1387.73	1386.73	1386.71	0.01	1	IIYGVHDEAKDK
206 - 222	2111.99	2110.99	2110.96	0.03	1	DKAFELELSWICDESNR
208 - 222	1868.85	1867.85	1867.84	0.01	0	AFELELSWICDESNR
227 - 236	1083.60	1082.59	1082.60	-0.00	0	VPADLLEQAK

Spot 2206

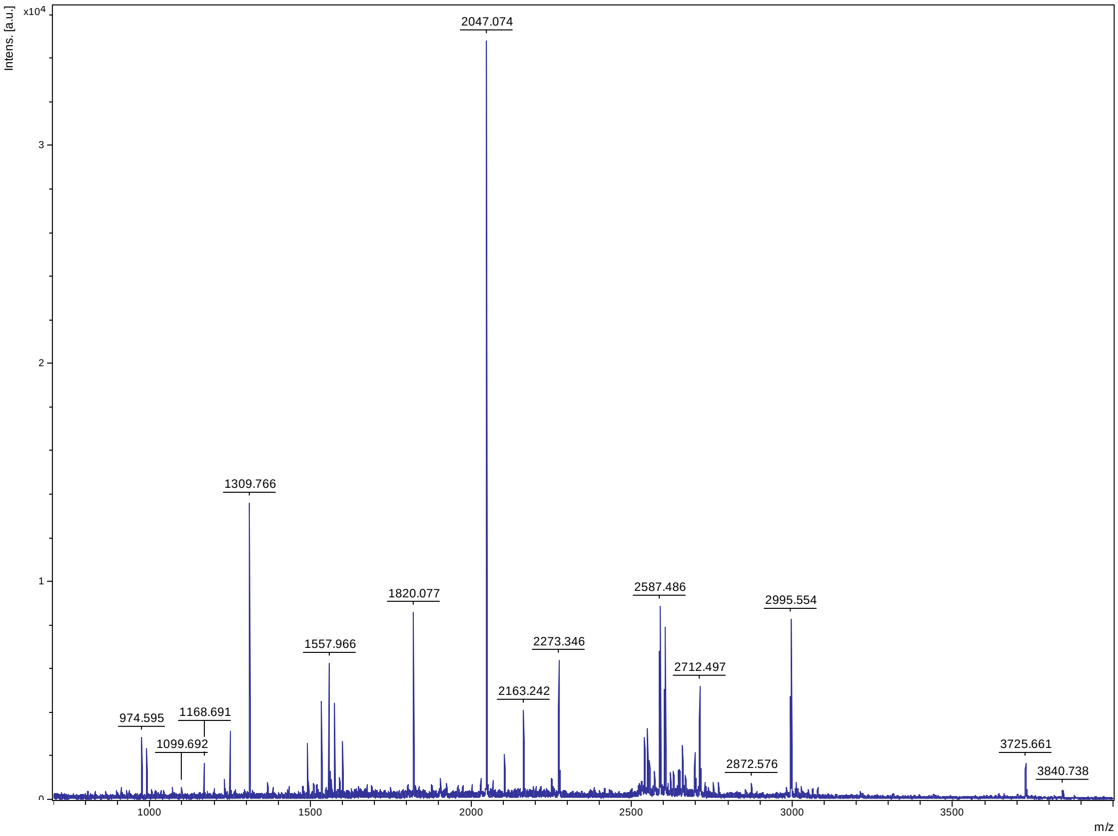


Match to: gi|51965092; Score: 80

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
16 - 23	974.53	973.52	973.50	0.02	0	AMVEQLQR
16 - 23	990.52	989.52	989.50	0.02	0	AMVEQLQR Oxidation (M)
32 - 41	1161.60	1160.60	1160.59	0.01	0	VAQVMETIDR
88 - 111	2442.13	2441.13	2441.17	-0.05	0	ALDVGSGTGYLTACFAIMVGPEGR
112 - 130	2035.08	2034.08	2034.10	-0.02	0	AVGVEHIPELVTSSIENIK
112 - 131	2163.04	2162.04	2162.19	-0.15	1	AVGVEHIPELVTSSIENIKK
132 - 151	2010.00	2009.00	2009.02	-0.02	0	SAAAPQLTDGSLSIHITDGR
152 - 185	3592.68	3591.68	3591.88	-0.20	0	EGWPELAPYDAIHVGAAAPQIPQALIEQLKPGGR
208 - 217	1145.63	1144.62	1144.62	0.00	1	VSIRDETAVR

Spot 2209

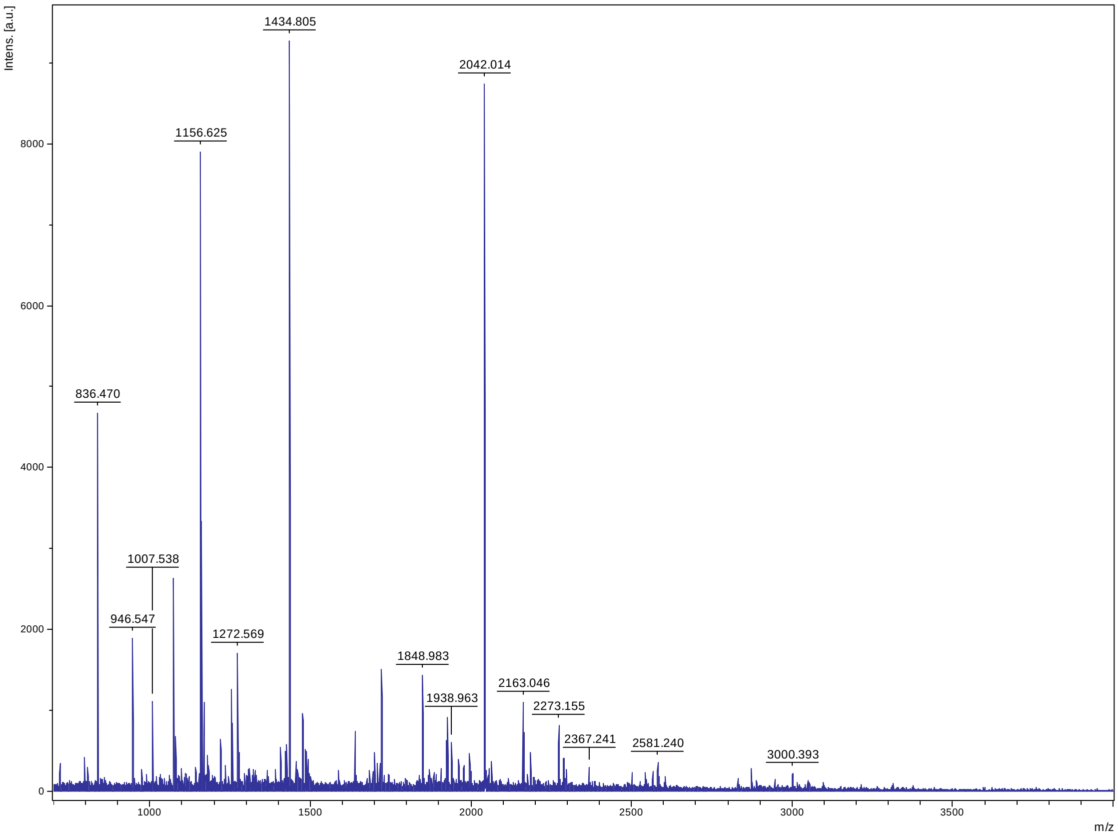


Match to: gi|50940199 Score: 86

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
5 - 19	1599.9307	1598.9234	1598.7827	0.1406	0	K.SYPTVSDEYLAAVGK.A	
32 - 39	974.5952	973.5879	973.4837	0.1042	0	K.NCAPLMLR.L	Carbamidomethyl (C)
40 - 53	1533.8700	1532.8627	1532.7372	0.1256	0	R.LAWHSAGTFDVSSR.T	
54 - 62	911.5243	910.5170	910.4218	0.0952	0	R.TGGPFGTMK.N	Oxidation (M)
63 - 80	1820.0775	1819.0702	1818.8972	0.1730	0	K.NPGEQSHAANAGLDIAVR.L	
132 - 143	1309.7659	1308.7586	1308.6422	0.1164	0	R.LPDATQGSDHLR.Q	
144 - 168	2587.4866	2586.4793	2586.3223	0.1570	1	R.QVFSAQMGLSDKDIVALSGGHTLGR.C	
144 - 168	2603.4866	2602.4793	2602.3172	0.1621	1	R.QVFSAQMGLSDKDIVALSGGHTLGR.C	Oxidation (M)
174 - 200	2995.5540	2994.5467	2994.3922	0.1545	0	R.SGFEGAWTSNPLIFDNSYFTELVSGEK.E	
201 - 210	1099.6918	1098.6845	1098.5921	0.0924	0	K.EGLLQLPSDK.A	
211 - 224	1557.9661	1556.9588	1556.8384	0.1204	0	K.ALMADPAFRPLVEK.Y	
225 - 242	2047.0745	2046.0672	2045.9006	0.1666	0	K.YAADEDAFFADYAEAHLK.L	

Spot 2215

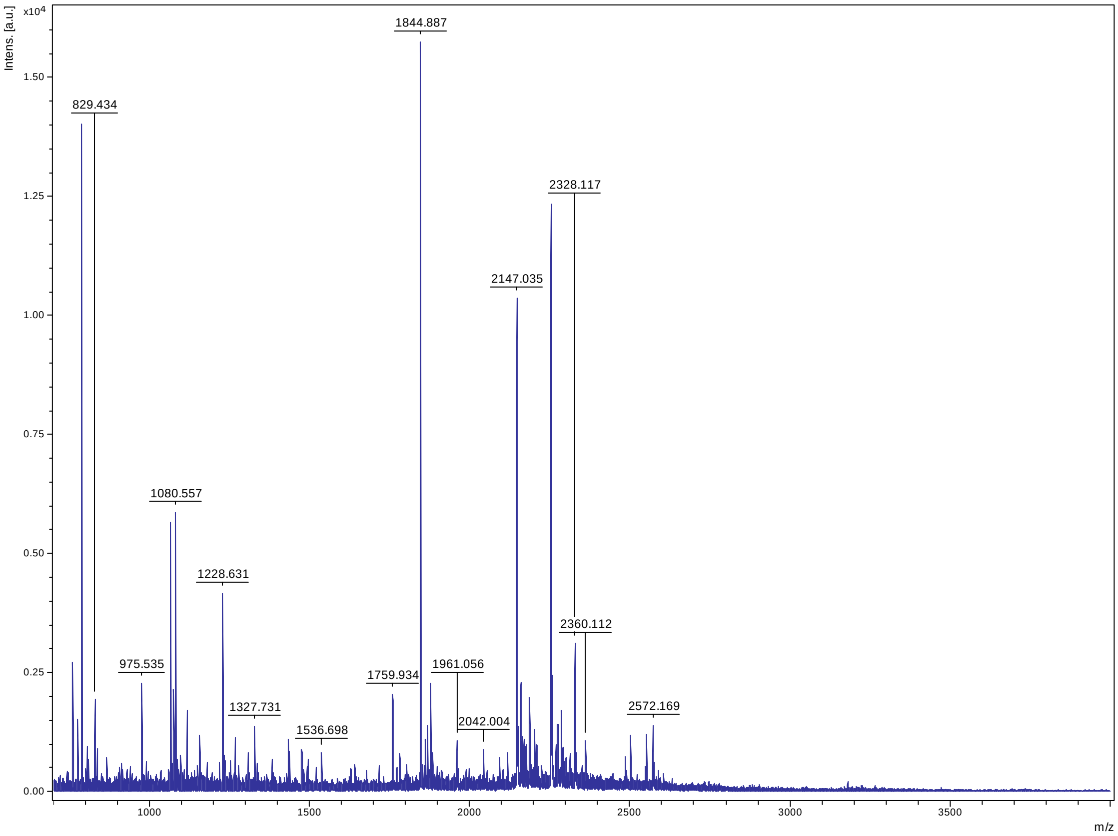


Match to: gi|12229922; Score: 192

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
12 - 21	1156.62	1155.62	1155.60	0.02	0	HITIFSPEGR
22 - 30	1160.61	1159.61	1159.59	0.02	0	LYQVEYAFK
34 - 43	946.55	945.54	945.52	0.02	0	SAGVTSIGVR
44 - 54	1220.63	1219.63	1219.62	0.00	1	GKDSVCVVTQK
60 - 74	1721.97	1720.96	1720.95	0.01	0	LLDHTSVTHLFPITK
75 - 88	1434.81	1433.80	1433.79	0.02	0	YIGLLATGLTADAR
89 - 95	836.47	835.47	835.46	0.01	0	SLVYQAR
103 - 116	1698.87	1697.87	1697.85	0.02	1	FKWGYEMPVDVLAK Oxidation (M)
105 - 116	1407.71	1406.71	1406.69	0.02	0	WGYEMPVDVLAK
105 - 116	1423.71	1422.71	1422.69	0.02	0	WGYEMPVDVLAK Oxidation (M)
122 - 147	3000.39	2999.39	2999.45	-0.06	0	AQVYTQHAYMRPLGVVAMVLGYDEEK 2 Oxidation (M)
154 - 164	1272.57	1271.57	1271.55	0.02	0	CDPAGHFFGHK
165 - 181	1848.98	1847.98	1847.96	0.02	1	ATSAGLKEQEAINFLEK
212 - 221	1072.62	1071.61	1071.59	0.02	0	ATEIEVGVVR
229 - 245	1926.98	1925.98	1925.97	0.01	0	ALTTEEIDQHLTAISER
229 - 246	2042.01	2041.01	2041.00	0.02	1	ALTTEEIDQHLTAISERD

Spot 2217

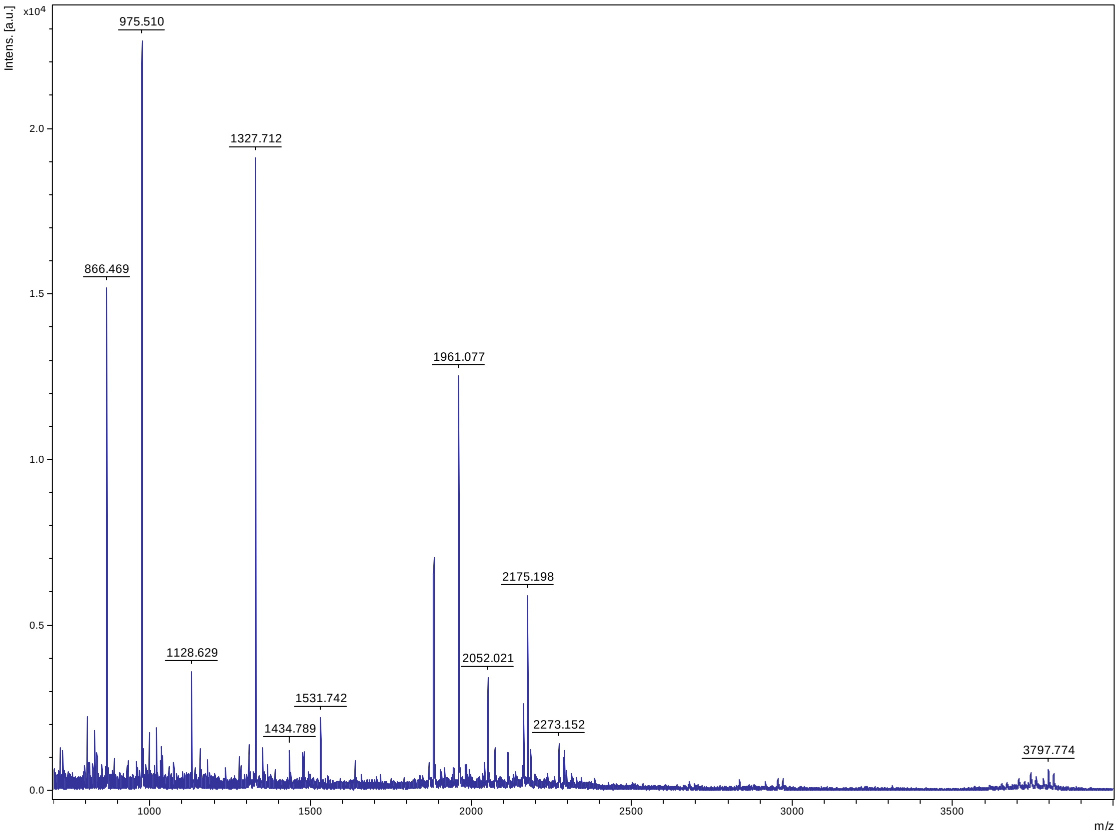


Match to: gi|1296955; Score: 153

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
106 - 128	2550.21	2549.20	2549.20	0.01	0	LAPFNPEYPDESVLWTESGDVGK
169 - 175	907.41	906.40	906.37	0.04	0	GDNQCWK
176 - 193	1844.89	1843.89	1843.89	-0.00	0	ILPWGDEAYAGGSANAPR
194 - 201	829.43	828.43	828.41	0.02	0	GGNEPTVR
202 - 215	1628.84	1627.83	1627.80	0.03	1	IFCKADEGFSVTVR
206 - 215	1080.56	1079.56	1079.52	0.03	0	ADEGFSVTVR
216 - 227	1228.63	1227.63	1227.60	0.03	0	GGSVCLAPTNPR
216 - 235	2328.12	2327.12	2327.11	0.00	1	GGSVCLAPTNPRDEYQHWIK
228 - 235	1118.53	1117.53	1117.52	0.01	0	DEYQHWIK
228 - 238	1520.71	1519.70	1519.69	0.02	1	DEYQHWIKDMR
228 - 238	1536.70	1535.70	1535.68	0.01	1	DEYQHWIKDMR Oxidation (M)
236 - 244	1087.54	1086.54	1086.52	0.02	1	DMRHSNSIK
239 - 257	2147.04	2146.03	2146.04	-0.01	1	HSNSIKDEEGYPAFALVNR
245 - 257	1480.73	1479.73	1479.70	0.03	0	DEEGYPAFALVNR
265 - 274	1075.54	1074.54	1074.52	0.02	0	HSQGEGHPVK
326 - 334	990.55	989.55	989.52	0.03	0	DGTTVALWK
335 - 342	1064.44	1063.44	1063.41	0.02	0	WCEGDNQR

Spot 2222

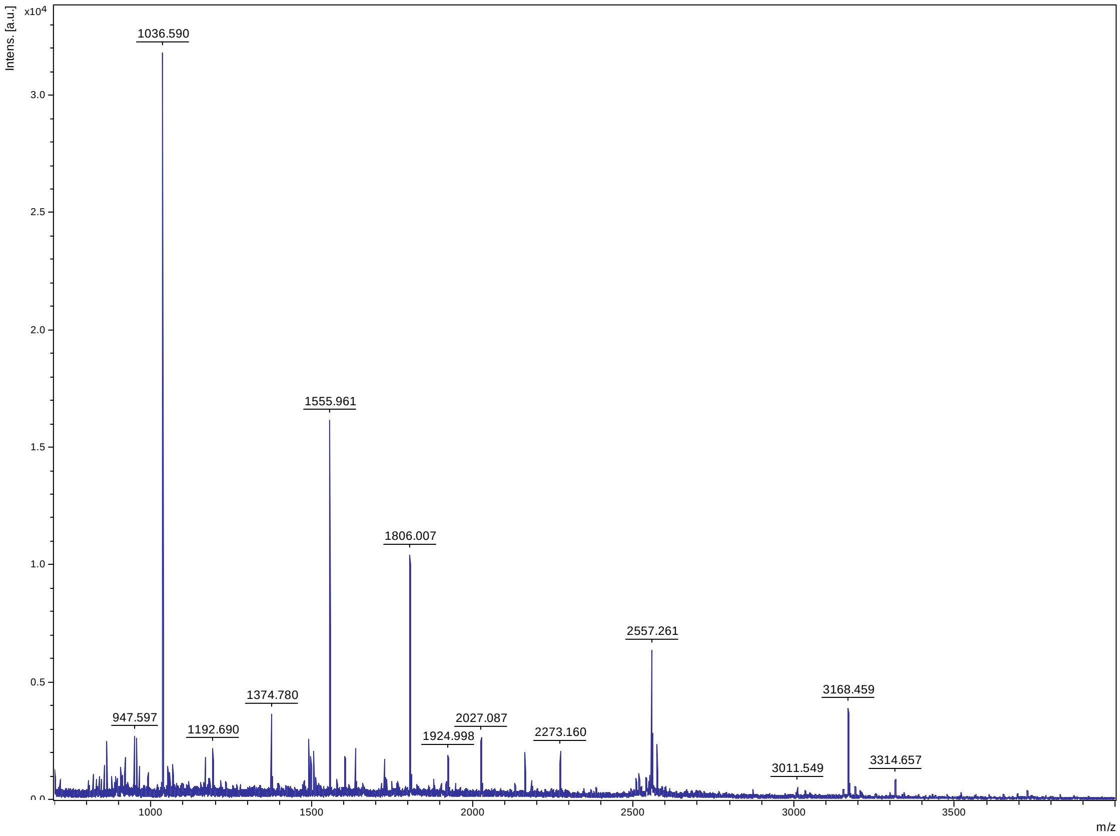


Match to: gi|46275847; Score: 72

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
21 - 27	820.49	819.49	819.42	0.07	0	NAMLVEK Oxidation (M)
58 - 71	1531.74	1530.74	1530.73	0.01	1	ATEGPIVADKNCEK
182 - 198	1884.04	1883.04	1883.01	0.02	1	EGLTREEGIQLVAEAIR
187 - 198	1327.71	1326.71	1326.71	-0.00	0	EEGIQLVAEAIR
199 - 218	2052.02	2051.02	2051.00	0.02	0	GGIFNDLGSGSNVDVCVITK
219 - 225	866.47	865.47	865.47	0.00	1	GKTEYLR
226 - 233	975.51	974.51	974.50	0.00	0	NHQLPNPR
255 - 261	827.54	826.54	826.53	0.01	0	ITQLKPK

Spot 2234

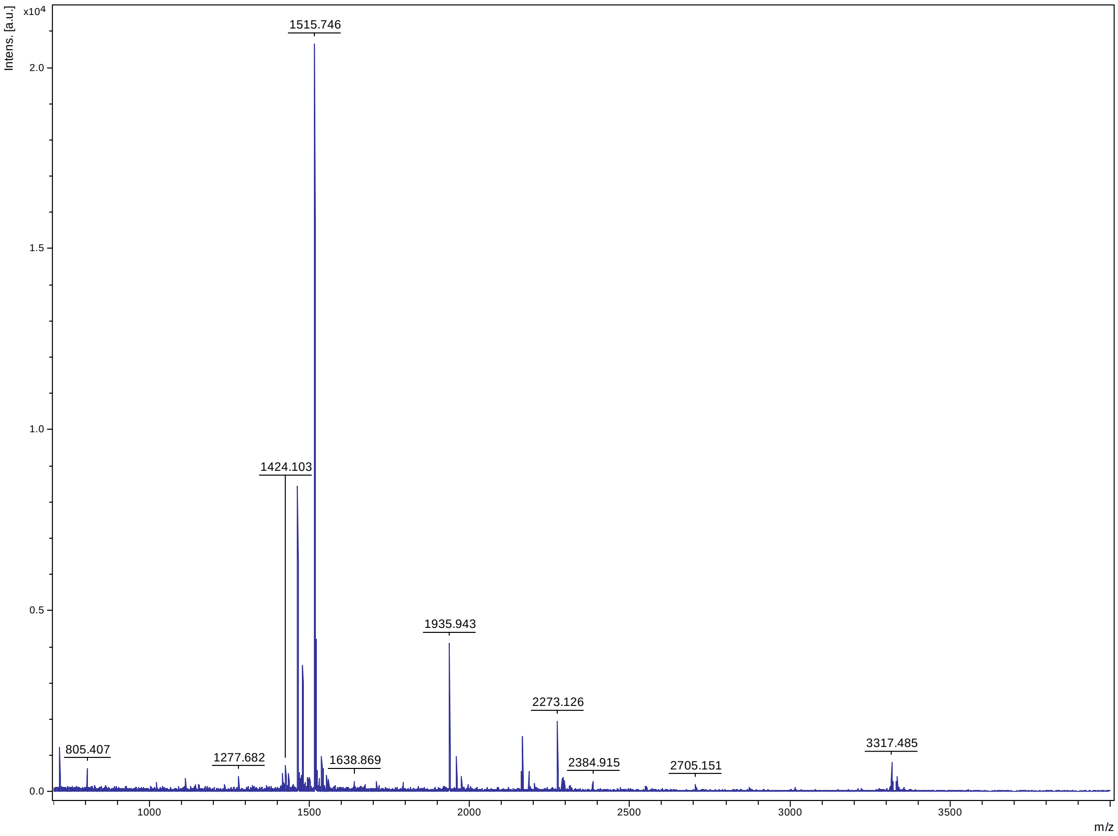


Match to: gi|50920595 Score: 81 Expect: 0.00056

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 18	1924.9723	1923.9650	1923.9577	0.0073	1	M.AKNYPVVSAEYQEAVEK.A	
4 - 18	1725.8813	1724.8740	1724.8257	0.0484	0	K.NYPVVSAEYQEAVEK.A	
31 - 38	947.4759	946.4686	946.4728	-0.0042	0	K.SCAPLMLR.L	Carbamidomethyl (C)
39 - 52	1505.7820	1504.7747	1504.7310	0.0437	0	R.LAWHSAGTFDVSSK.T	
62 - 79	1805.9912	1804.9839	1804.9431	0.0408	0	K.TPAELSHAANAGLDIAVR.M	
120 - 130	1192.6266	1191.6193	1191.5884	0.0310	0	R.EDKPAPPPEGR.L	
143 - 167	2557.2538	2556.2465	2556.2754	-0.0289	0	R.QVFGAQMGLSDQDIVALSGGHTLGR.C	
143 - 167	2573.2409	2572.2336	2572.2703	-0.0367	0	R.QVFGAQMGLSDQDIVALSGGHTLGR.C	Oxidation (M)
182 - 209	3168.4856	3167.4783	3167.5662	-0.0879	1	R.NPLQFDNSYFTELLSGDKEGLLQLPSDK.A	
210 - 223	1555.9303	1554.9230	1554.8769	0.0461	0	K.ALLSDPAFRPLVEK.Y	
230 - 236	919.4170	918.4097	918.4123	-0.0026	0	K.AFFEDYK.E	
230 - 241	1497.7750	1496.7677	1496.7299	0.0378	1	K.AFFEDYKEAHLK.L	

Spot 2237

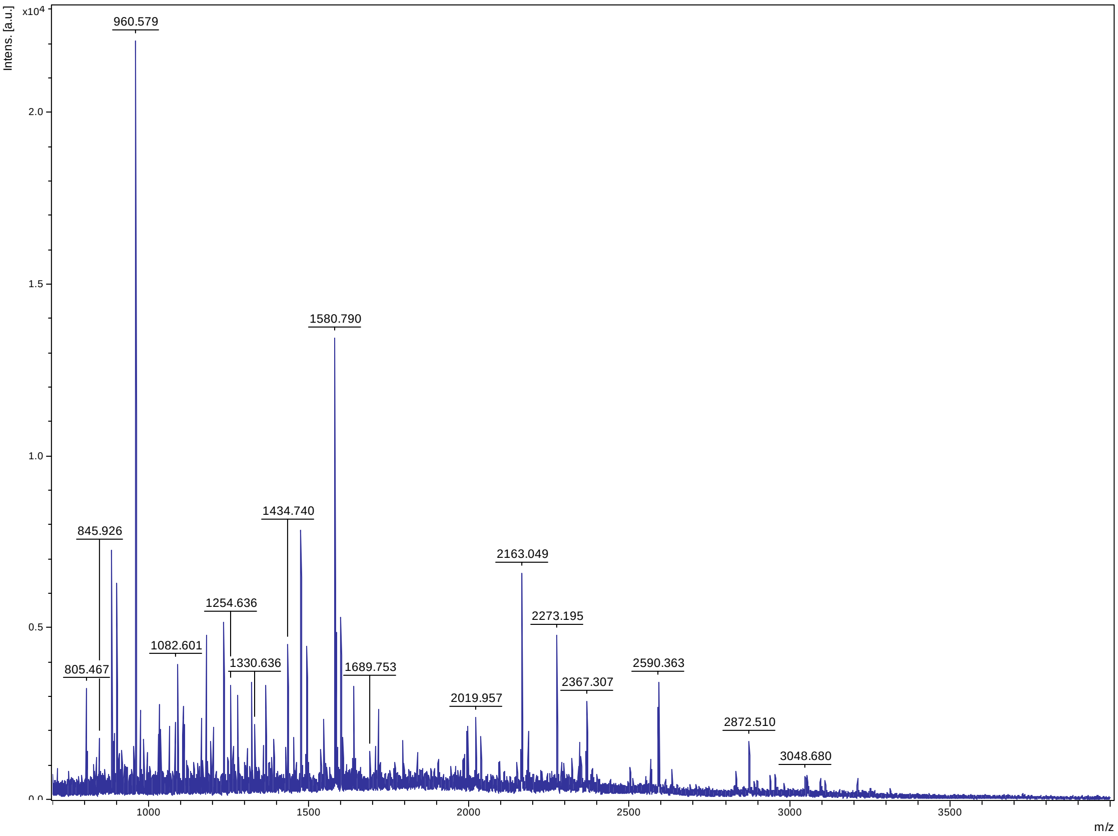


Match to: gi|46575976 Score: 68

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
17 - 29	1519.8730	1518.8658	1518.8809	-0.0152	0	K.NILFVISKPDVFK.S	
30 - 43	1514.7104	1513.7032	1513.7300	-0.0268	0	K.SPTSDTYVIFGEAK.I	
44 - 60	1935.9425	1934.9352	1934.9585	-0.0233	0	K.IEDLSSQLQTQAAEQFK.A	
61 - 92	3317.4849	3316.4776	3316.5140	-0.0364	0	K.APDLSSMLSKPEASTAAQEDDEAVDETGVEPK.D	
61 - 92	3333.4817	3332.4744	3332.5089	-0.0345	0	K.APDLSSMLSKPEASTAAQEDDEAVDETGVEPK.D	Oxidation (M)
93 - 105	1462.7407	1461.7334	1461.7497	-0.0162	0	K.DIELVMTQATVSR.S	
93 - 105	1478.7288	1477.7215	1477.7446	-0.0231	0	K.DIELVMTQATVSR.S	Oxidation (M)

Spot 2239

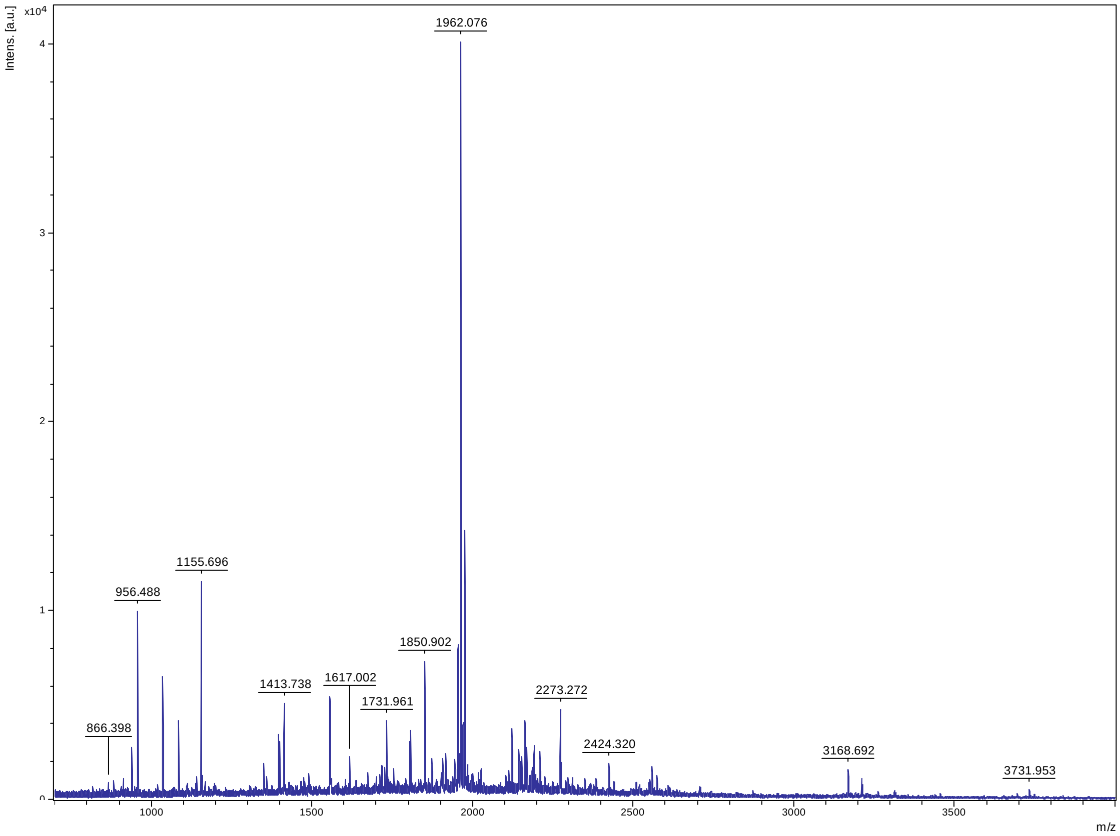


Match to: gi|34913460 Score: 72 Expect: 0.0047

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
54 - 65	1330.6360	1329.6287	1329.6088	0.0199	0	R.DDTTFDAYVVGK.E	
66 - 85	2345.2009	2344.1937	2344.1739	0.0198	0	K.ENAPGIVVLQEWWGVDYEIK.N	
86 - 99	1580.7902	1579.7829	1579.7855	-0.0026	0	K.NHAVHISQIGEGYR.A	
100 - 107	960.5787	959.5714	959.5440	0.0274	0	R.ALIPDLYR.G	
110 - 131	2365.2397	2364.2325	2364.1783	0.0542	0	K.VALDVAEAQHLMEGLDWPGAVK.D	Oxidation (M)
190 - 214	2590.3625	2589.3553	2589.2863	0.0690	0	K.AQAPIQAHFGELDSFVGFADVTAAK.S	
222 - 248	2954.4729	2953.4656	2953.3486	0.1170	0	K.SSGVPHEVHIYPGCSHAFMNTSPEAVK.R	Carbamidomethyl (C); Oxidation (M)
252 - 269	2019.9570	2018.9498	2018.9367	0.0130	0	K.EMGLTDENQAAIDLAWSR.F	
252 - 269	2035.9434	2034.9361	2034.9316	0.0045	0	K.EMGLTDENQAAIDLAWSR.F	Oxidation (M)
270 - 276	884.4525	883.4452	883.4010	0.0442	0	R.FSTWMGR.F	
270 - 276	900.4548	899.4475	899.3959	0.0515	0	R.FSTWMGR.F	Oxidation (M)

Spot 2240

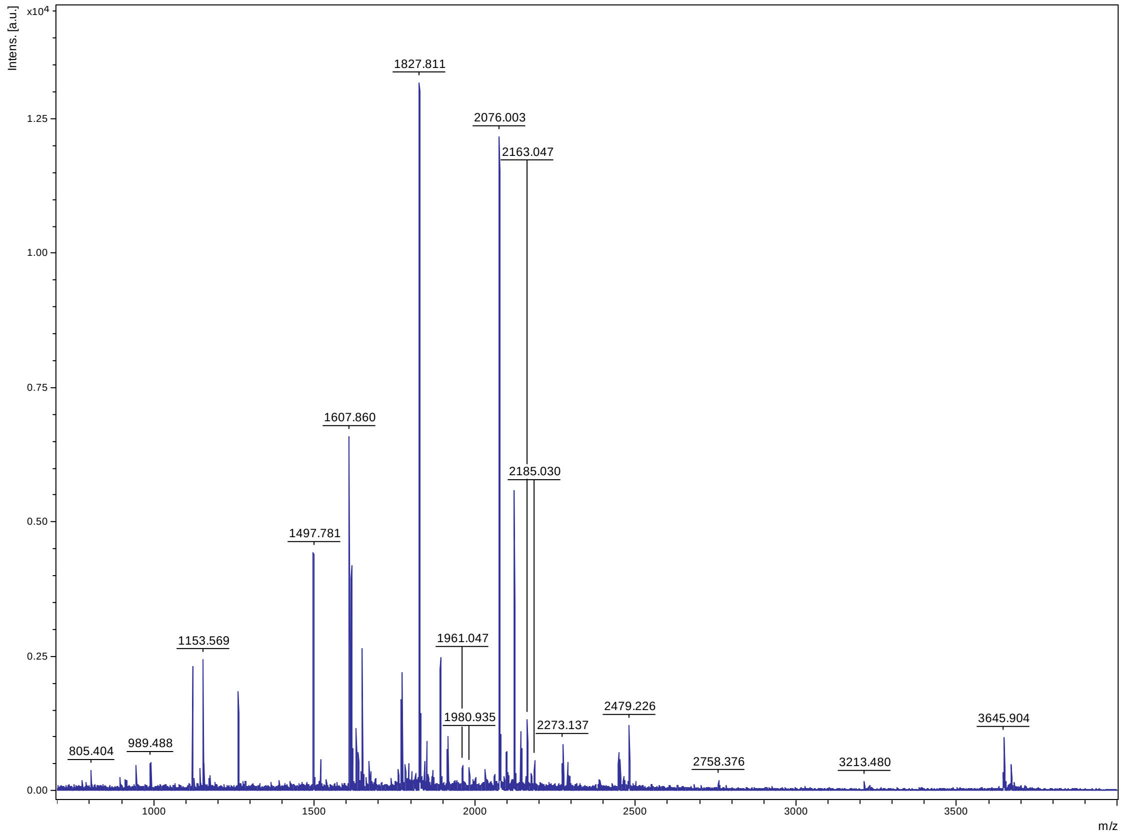


Match to: gi|51979316 Score: 78 Expect: 0.0011

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 18	1850.7952	1849.7879	1849.8370	-0.0491	0	M.GDSQYSFSLTTFSPSGK.L	Acetyl (N-term)
19 - 39	2122.1792	2121.1719	2121.1793	-0.0074	0	K.LVQIEHALTAVGSGQTSLGIK.A	
52 - 64	1428.7554	1427.7481	1427.7871	-0.0390	0	K.LPSILVDETSVQK.I	
92 - 99	1084.4329	1083.4256	1083.5461	-0.1205	1	R.KQAQQYYR.L	
93 - 99	939.3026	938.2953	938.4246	-0.1293	0	K.QAQQYYR.L	Pyro-glu (N-term Q)
93 - 99	956.3248	955.3175	955.4512	-0.1336	0	K.QAQQYYR.L	
103 - 112	1155.5765	1154.5692	1154.6659	-0.0967	0	K.ETIPVTQLVR.E	
177 - 196	2348.1846	2347.1773	2347.1729	0.0044	1	K.RYTEDMELDDAIHTAILTLK.E	
178 - 196	2192.0749	2191.0676	2191.0718	-0.0042	0	R.YTEDMELDDAIHTAILTLK.E	
197 - 214	1961.9739	1960.9666	1960.9853	-0.0187	0	K.EGYEGQISANNIEIGVIR.S	
221 - 235	1731.8600	1730.8527	1730.8978	-0.0450	1	K.VLTPAEIKDFLEEVE.-	

Spot 2245

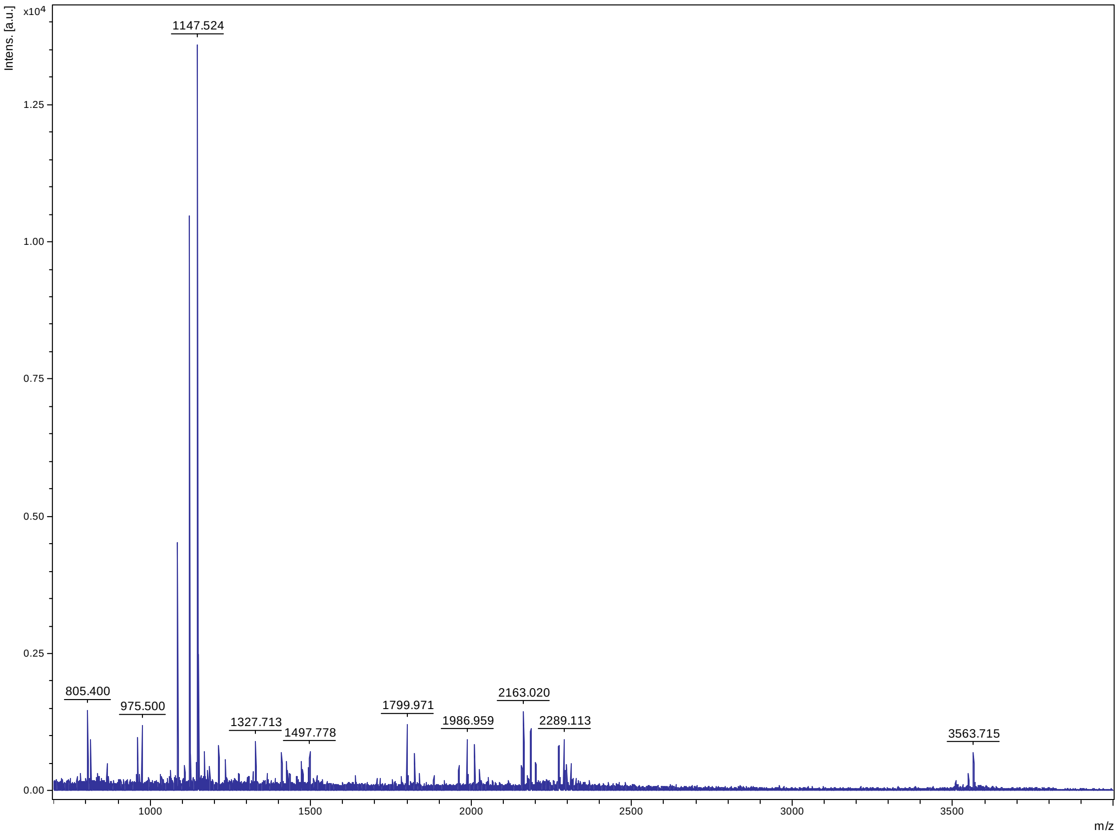


Match to: gi|28192425; Score: 170

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
9 - 25	1827.81	1826.81	1826.84	-0.03	0	AAVGHPDTLGDCPFSQR
26 - 33	944.56	943.55	943.56	-0.00	0	VLLTLEEK
34 - 40	894.45	893.45	893.47	-0.02	1	KVPYEMK
41 - 53	1615.84	1614.84	1614.88	-0.04	0	LIDVQNKPDWFLK
60 - 69	989.49	988.49	988.50	-0.01	0	VPVFNGGDGK
70 - 84	1771.86	1770.86	1770.90	-0.04	0	WIPDSDVITQVIEEK
70 - 102	3645.90	3644.90	3644.85	0.05	1	WIPDSDVITQVIEEKYPTPSLVTPPEYASVGSK
85 - 102	1892.94	1891.93	1891.96	-0.02	0	YPTPSLVTPPEYASVGSK
123 - 136	1607.86	1606.86	1606.89	-0.04	0	ALLTELQALEEHLK
158 - 169	1497.78	1496.78	1496.81	-0.04	0	LYHLQVALEHFK
170 - 190	2447.23	2446.23	2446.23	0.00	1	GWKIPEDLTNVHAYTEALFSR
173 - 190	2076.00	2075.00	2075.03	-0.03	0	IPEDLTNVHAYTEALFSR
201 - 210	1121.58	1120.58	1120.60	-0.02	0	EHLIAGWAPK

Spot 2246

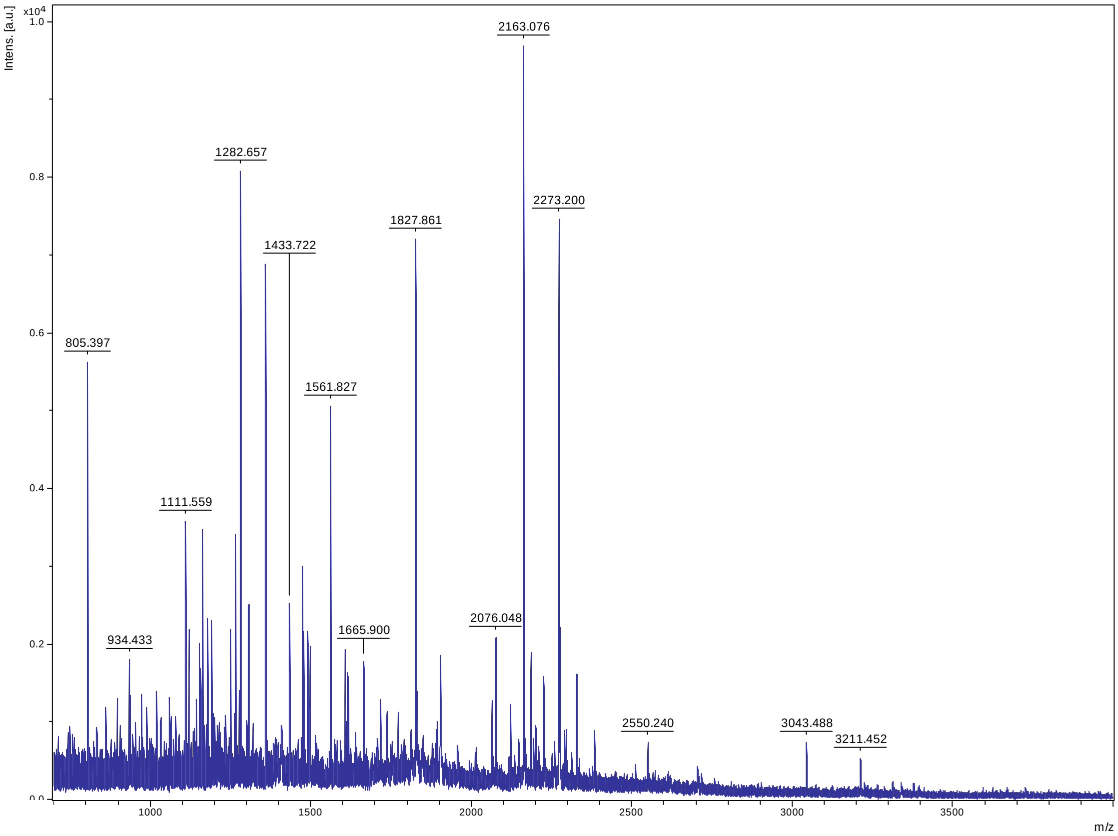


Match to: gi|77556961; Score: 89

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
104 - 112	1121.56	1120.56	1120.58	-0.02	0	DTIELFVER
117 - 127	1085.61	1084.60	1084.62	-0.02	0	GITVIAGVEAR
128 - 142	1471.83	1470.83	1470.86	-0.03	0	GFIFGPPIALALGAK
151 - 169	2157.02	2156.02	2156.05	-0.03	1	KLPGEVISEEYSLEYGTDK
183 - 201	1799.97	1798.97	1799.00	-0.04	0	AVVVDDLIATGGTLSAAVK
183 - 205	2311.09	2310.09	2310.32	-0.22	1	AVVVDDLIATGGTLSAAVKLIER
206 - 223	1986.96	1985.96	1985.98	-0.02	0	AGAEVVECACVIELPELK
228 - 238	1213.72	1212.71	1212.76	-0.05	0	LGNKPVFVLVK

Spot 2248



Match to: gi|55168334 Score: 86 Expect: 0.00018

Matched peptides:

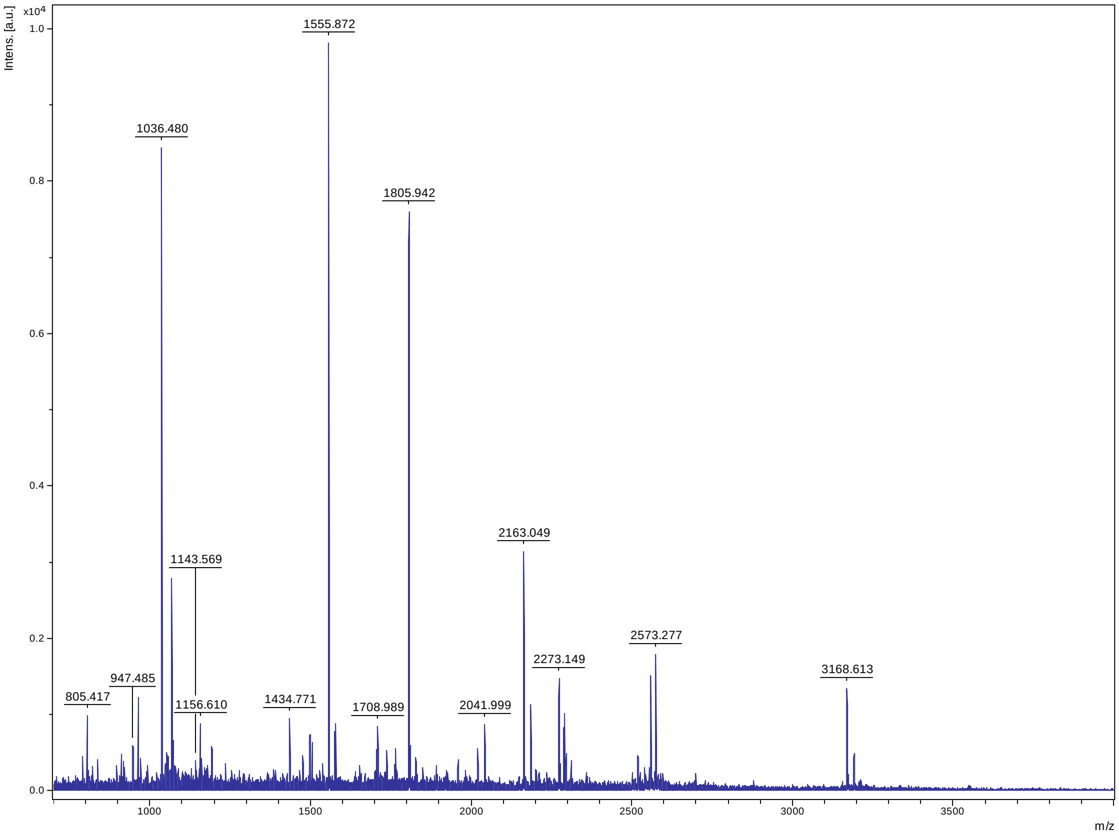
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
1 - 8	937.4038	936.3965	936.4408	-0.0443	0	-.MGVEVCVK.A Carbamidomethyl (C); Oxidation (M)
9 - 25	1827.8698	1826.8625	1826.8369	0.0256	0	K.AAVGHPDTLGDCPFSQR.V Carbamidomethyl (C)
41 - 53	1615.9221	1614.9148	1614.8769	0.0379	0	K.LIDVQNKPDWFLK.I
70 - 84	1771.9406	1770.9333	1770.9039	0.0294	0	K.WIPDSDVITQVIEEK.Y
85 - 102	1892.9678	1891.9605	1891.9567	0.0038	0	K.YPTPSLVTPPEYASVGSK.I
103 - 112	1263.6611	1262.6538	1262.6369	0.0169	0	K.IFSCFTTFLK.S Carbamidomethyl (C)
123 - 136	1607.9173	1606.9100	1606.8930	0.0170	0	K.ALLTELQALEEHLK.A
137 - 157	2121.1039	2120.0966	2120.1014	-0.0048	0	K.AHGPFINGQNISAADLSLAPK.L
158 - 169	1497.8537	1496.8464	1496.8139	0.0325	0	K.LYHLQVALEHFK.G
173 - 190	2076.0375	2075.0302	2075.0323	-0.0021	0	K.IPEDLTNVHAYTEALFSR.E

Match to: gi|50939487 Score: 82 Expect: 0.00038

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
67 - 79	1471.7604	1470.7531	1470.7137	0.0395	0	K.LLGISCDDVQSHK.D Carbamidomethyl (C)
67 - 83	2013.9906	2012.9833	2012.9989	-0.0156	1	K.LLGISCDDVQSHKDWIK.D Carbamidomethyl (C)
84 - 93	1162.5906	1161.5833	1161.5778	0.0055	0	K.DIEAYKPGNR.V
94 - 104	1249.6232	1248.6159	1248.6172	-0.0013	0	R.VTYPIMADPSR.E
141 - 151	1282.6641	1281.6568	1281.6539	0.0029	0	K.LSFLYPACVGR.N Carbamidomethyl (C)
152 - 158	862.3514	861.3441	861.4014	-0.0573	0	R.NMDEVVR.A
159 - 168	987.4697	986.4624	986.5396	-0.0772	0	R.AVDALQTAAK.H
169 - 182	1561.8504	1560.8431	1560.8161	0.0271	0	K.HAVATPVNWKPGER.V
196 - 211	1736.9080	1735.9007	1735.8417	0.0591	1	K.EKFPQGFDTADLPSGK.G
198 - 211	1479.7486	1478.7413	1478.7041	0.0372	0	K.FPQGFDTADLPSGK.G

Spot 2251

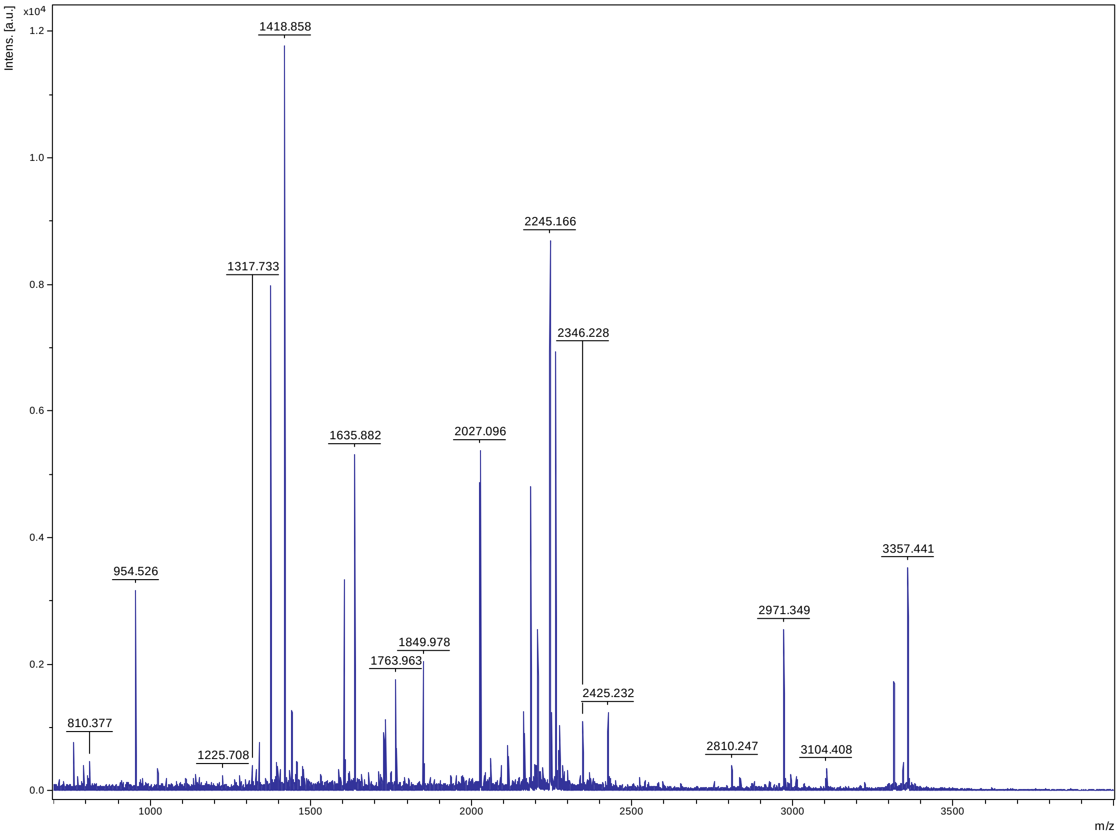


Match to: gi|75220444; Score: 122

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
31 - 38	947.48	946.48	946.47	0.01	0	SCAPLMLR
31 - 38	963.47	962.47	962.47	0.00	0	SCAPLMLR Oxidation (M)
39 - 52	1505.73	1504.73	1504.73	-0.00	0	LAWHSAGTFDVSSK
53 - 61	895.45	894.45	894.43	0.02	0	TGGPFGTMK
53 - 61	911.43	910.42	910.42	0.00	0	TGGPFGTMK Oxidation (M)
62 - 79	1805.94	1804.94	1804.94	-0.00	0	TPAELSHAANAGLDIAVR
120 - 130	1192.59	1191.59	1191.59	0.00	0	EDKPAPPPEGR
143 - 167	2557.27	2556.26	2556.28	-0.01	0	QVFGAQMGLSDQDIVALSGGHTLGR
143 - 167	2573.28	2572.27	2572.27	0.00	0	QVFGAQMGLSDQDIVALSGGHTLGR Oxidation (M)
173 - 181	1036.48	1035.48	1035.48	0.00	0	SGFEGPWTR
182 - 209	3168.61	3167.61	3167.57	0.04	1	NPLQFDNSYFTELLSGDKEGLLQLPSDK
210 - 223	1555.87	1554.87	1554.88	-0.01	0	ALLSDPAFRPLVEK
230 - 236	919.41	918.41	918.41	-0.00	0	AFFEDYK
230 - 241	1497.73	1496.73	1496.73	-0.00	1	AFFEDYKEAHLK

Spot 2254

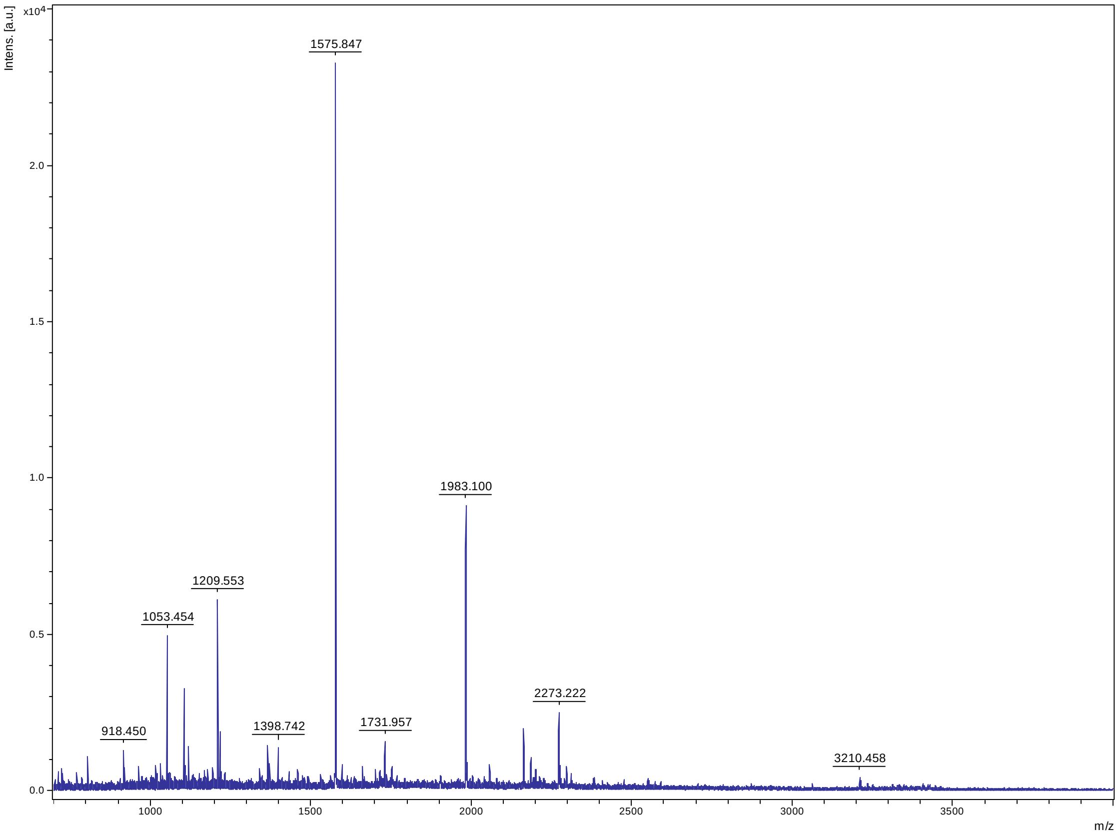


Match to: gi|115434516 Score: 151 Expect: 1.1e-10

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Sequence
5 - 12	954.5261	953.5188	953.4760	45	0	K.FFVGGNWK.C
26 - 53	3011.4299	3010.4226	3010.6631	-80	0	K.ILNEGQIASTDVVEVVVSPPYVFLPVVK.S
54 - 70	2027.0962	2026.0889	2026.0418	23	0	K.SQLRPEIQVAAQNCWVK.K
101 - 113	1394.7527	1393.7454	1393.6725	52	0	R.SLLGESNEFVGDK.V
101 - 123	2425.2321	2424.2248	2424.2536	-12	1	R.SLLGESNEFVGDKVAYALSQGLK.V
124 - 135	1374.7731	1373.7658	1373.6973	50	0	K.VIACVGETLEQR.E
155 - 175	2346.2285	2345.2212	2345.2420	-9	1	R.IKDWTNVVVAYEPVWAIGTGK.V
176 - 190	1635.8815	1634.8742	1634.8013	45	0	K.VATPDQAQEVHDGLR.K
176 - 191	1763.9627	1762.9554	1762.8962	34	1	K.VATPDQAQEVHDGLRK.W
191 - 206	1731.9699	1730.9626	1730.8951	39	1	R.KWLAANVSAEVAESTR.I
192 - 206	1603.8876	1602.8803	1602.8002	50	0	K.WLAANVSAEVAESTR.I
207 - 219	1339.7437	1338.7364	1338.6602	57	0	R.IIYGGSVTGANCK.E

Spot 2257

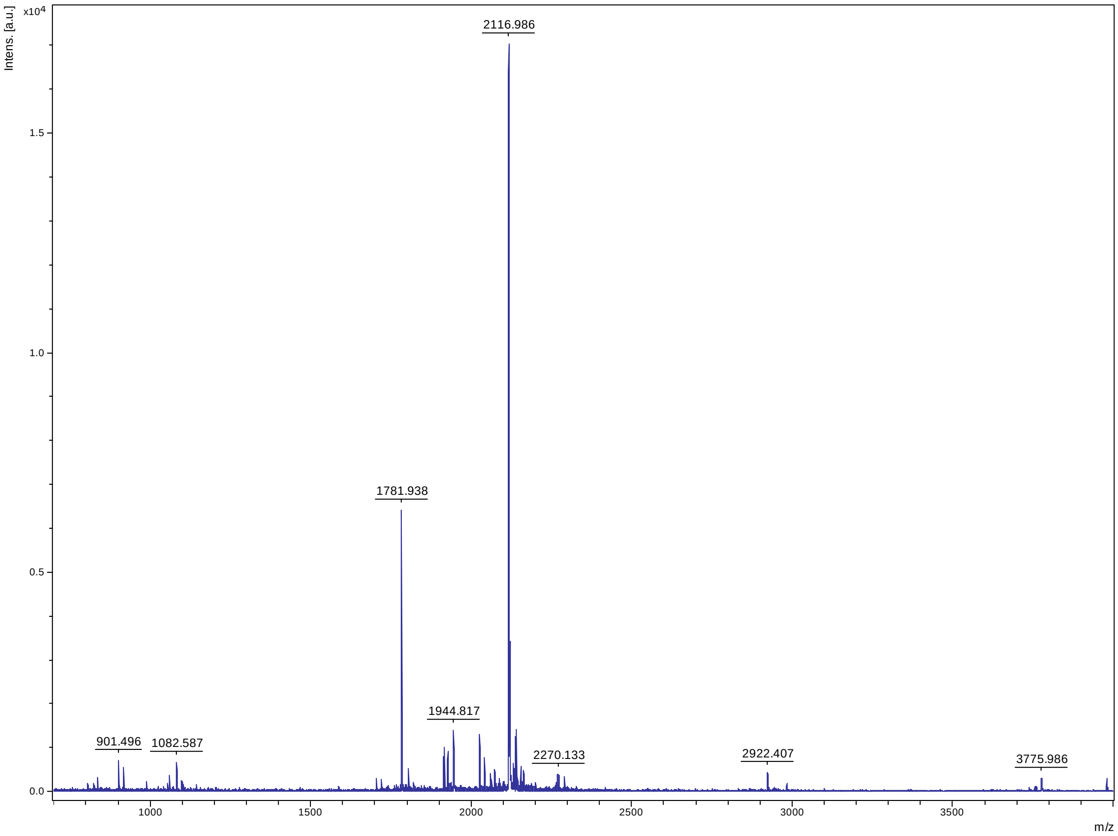


Match to: gi|51535468 Score: 84 Expect: 0.00027

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
18 - 26	1053.4582	1052.4509	1052.4709	-0.0200	0	K.NCFAIASDR.R	Carbamidomethyl (C)
18 - 27	1209.5675	1208.5602	1208.5720	-0.0118	1	K.NCFAIASDRR.L	Carbamidomethyl (C)
28 - 41	1575.8608	1574.8535	1574.8416	0.0119	0	R.LGVQLQTVATDFQR.V	
45 - 66	2476.3451	2475.3378	2475.3121	0.0257	1	K.IHDKLYIGLSGLATDAQTLYQR.L	
49 - 66	1983.0796	1982.0723	1982.0472	0.0251	0	K.LYIGLSGLATDAQTLYQR.L	
73 - 80	1106.5823	1105.5750	1105.5880	-0.0129	1	K.LYQLREER.D	
81 - 98	2041.0974	2040.0901	2040.0601	0.0300	0	R.DMKPQTFASLVSALLYEK.R	
81 - 98	2057.1166	2056.1093	2056.0550	0.0543	0	R.DMKPQTFASLVSALLYEK.R	Oxidation (M)
81 - 99	2213.2083	2212.2010	2212.1561	0.0449	1	R.DMKPQTFASLVSALLYEKR.F	Oxidation (M)
177 - 195	2078.0390	2077.0317	2077.0553	-0.0236	0	R.DCLSGWGGFVLLVTPTEVK.E	Carbamidomethyl (C)

Spot 2269

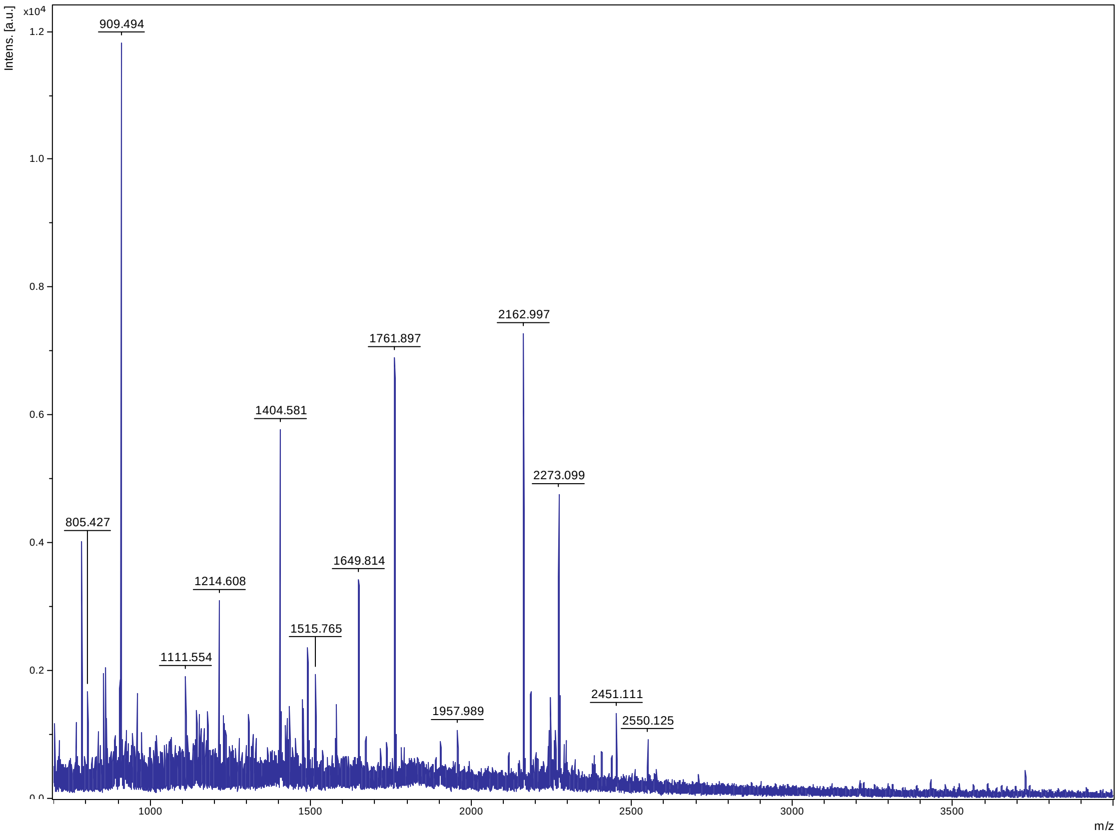


Match to: gi|77548365 Score: 67 Expect: 0.013

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
34 - 53	2199.0118	2198.0045	2198.0412	-0.0367	1	K.TTEIGEDASPMYKEQIASTK.I	
63 - 89	2981.5373	2980.5300	2980.3906	0.1395	1	K.HSSLCSACENITSEAVNFLSEKQIQDK.I	
85 - 91	900.3527	899.3454	899.5188	-0.1734	1	K.QIQDKIR.T	
90 - 107	2153.9575	2152.9502	2153.0575	-0.1073	1	K.IRTILHDTCSQTFSFEQK.C	
123 - 139	2024.9648	2023.9575	2024.0335	-0.0760	1	K.IAEIKPAAFCKQYGLCR.D	2 Carbamidomethyl (C)
149 - 166	2162.0581	2161.0508	2160.9820	0.0689	0	K.SESTCLFCHHIIDEITSK.L	Acetyl (N-term); Carbamidomethyl (C)
169 - 186	2160.0279	2159.0206	2159.0820	-0.0613	1	K.DPDAEFEIIQLLLKECNK.I	Acetyl (N-term)
197 - 215	2261.0721	2260.0648	2260.2540	-0.1892	1	R.MVLQYVPLVLVNGEKFLEK.N	Acetyl (N-term)
212 - 229	2069.9152	2068.9079	2068.9380	-0.0300	1	K.FLEKNDVCAMIQACDAGK.R	2 Carbamidomethyl (C)

Spot 2275

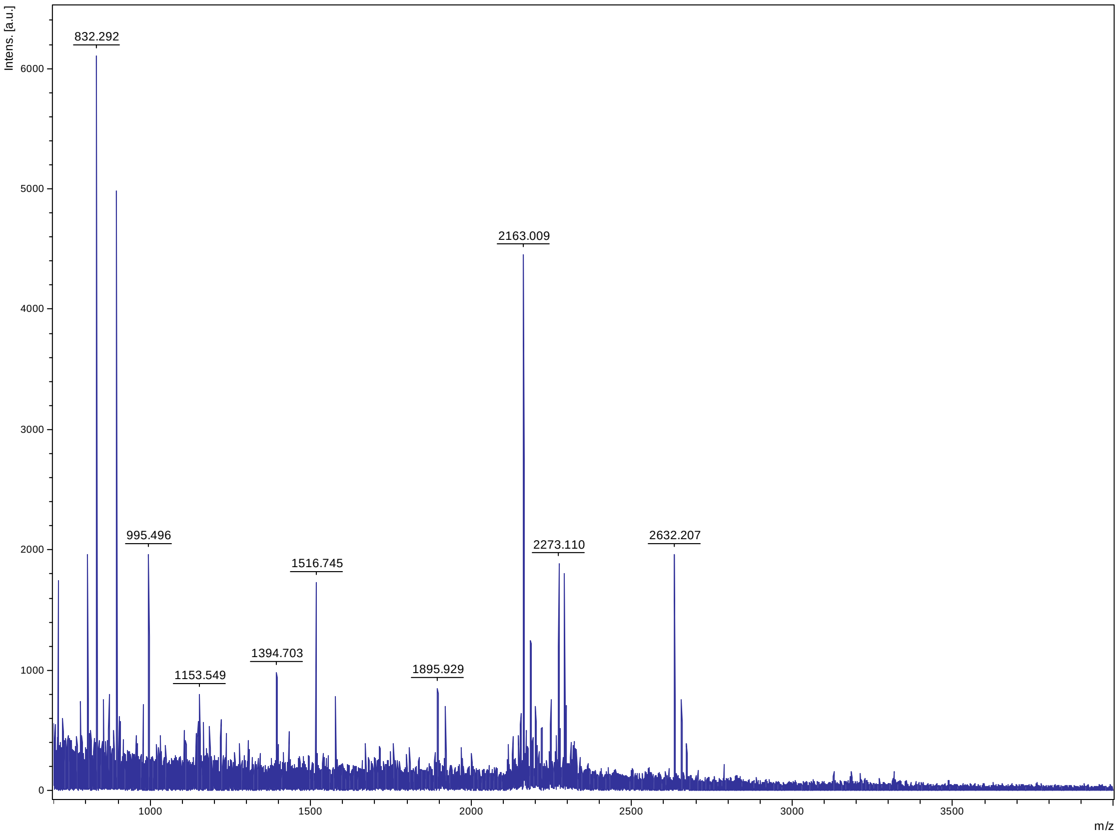


Match to: gi|34912576 Score: 76 Expect: 0.0015

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 15	1649.8138	1648.8066	1648.8096	-0.0031	0	M.ALPNQQTVDYPSFK.L Acetyl (N-term)
33 - 40	960.4857	959.4784	959.4712	0.0072	0	R.HLTGEFEK.K
41 - 61	2451.1106	2450.1033	2450.1940	-0.0906	1	K.KYEPTIGVEVHPLDFFTNCGK.I Carbamidomethyl (C)
64 - 74	1404.5811	1403.5738	1403.5816	-0.0078	0	R.FYCWDTAGQEK.F Carbamidomethyl (C)
80 - 98	2245.9670	2244.9598	2245.0296	-0.0698	0	R.DGYYIHGQCAIIMFDVTSR.L Carbamidomethyl (C)
103 - 109	909.4938	908.4866	908.4617	0.0249	0	K.NVPTWHR.D
114 - 126	1515.7649	1514.7576	1514.7585	-0.0009	0	R.VCENIPIVLCGNK.V 2 Carbamidomethyl (C)
146 - 155	1214.6080	1213.6008	1213.5979	0.0029	0	K.NLQYYEVSAK.S
156 - 169	1761.8966	1760.8893	1760.8885	0.0008	0	K.SNYNFEKPFLYLAR.K

Spot 2283

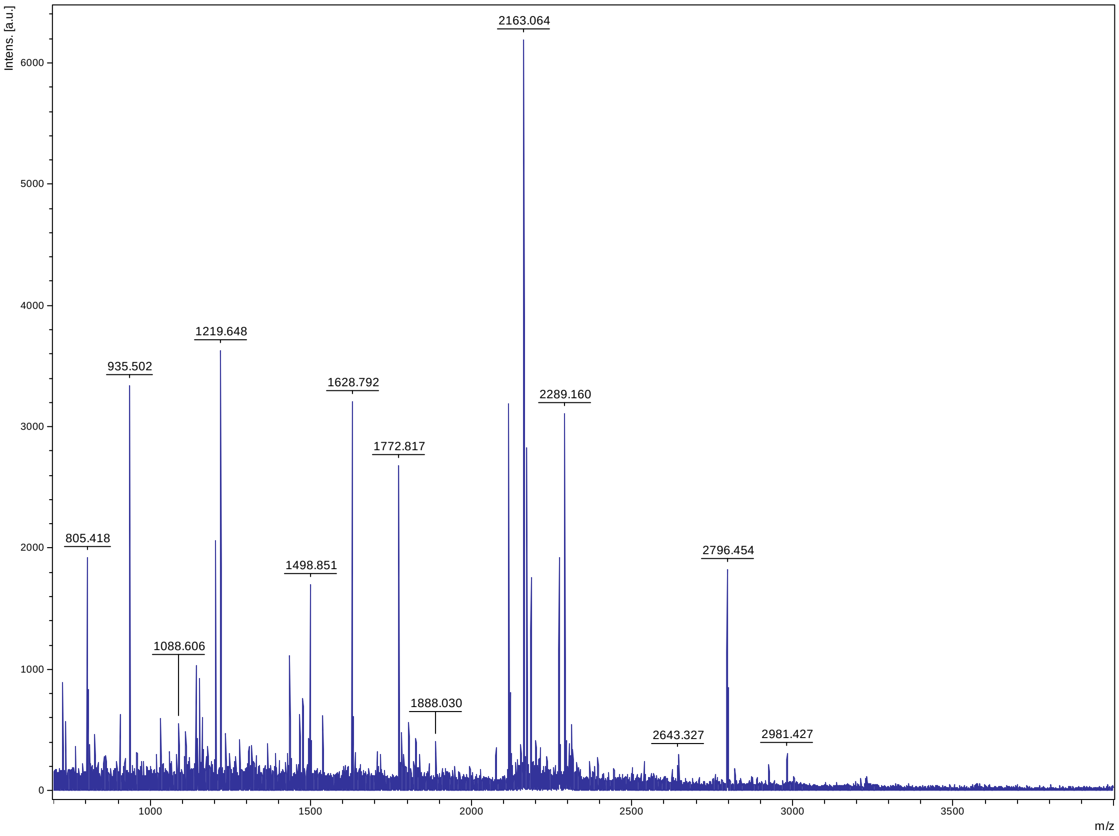


Match to: gi|51964836; Score: 74

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
13 - 26	1576.85	1575.85	1575.89	-0.04	1	IDKVYITVQLADAK
16 - 26	1220.64	1219.64	1219.68	-0.04	0	VYITVQLADAK
30 - 54	2632.21	2631.20	2631.23	-0.03	0	VNLEPEGVFSFSATAGTDGNLYESK
55 - 67	1516.74	1515.74	1515.78	-0.04	1	LELNDKVNVEESK
74 - 81	995.50	994.49	994.52	-0.02	0	SIFCIVEK
74 - 85	1394.70	1393.70	1393.73	-0.03	1	SIFCIVEKAEAK
90 - 96	873.47	872.47	872.47	-0.00	1	LVRDDQK
93 - 102	1184.58	1183.58	1183.60	-0.02	1	DDQKAPHFVK

Spot 2289

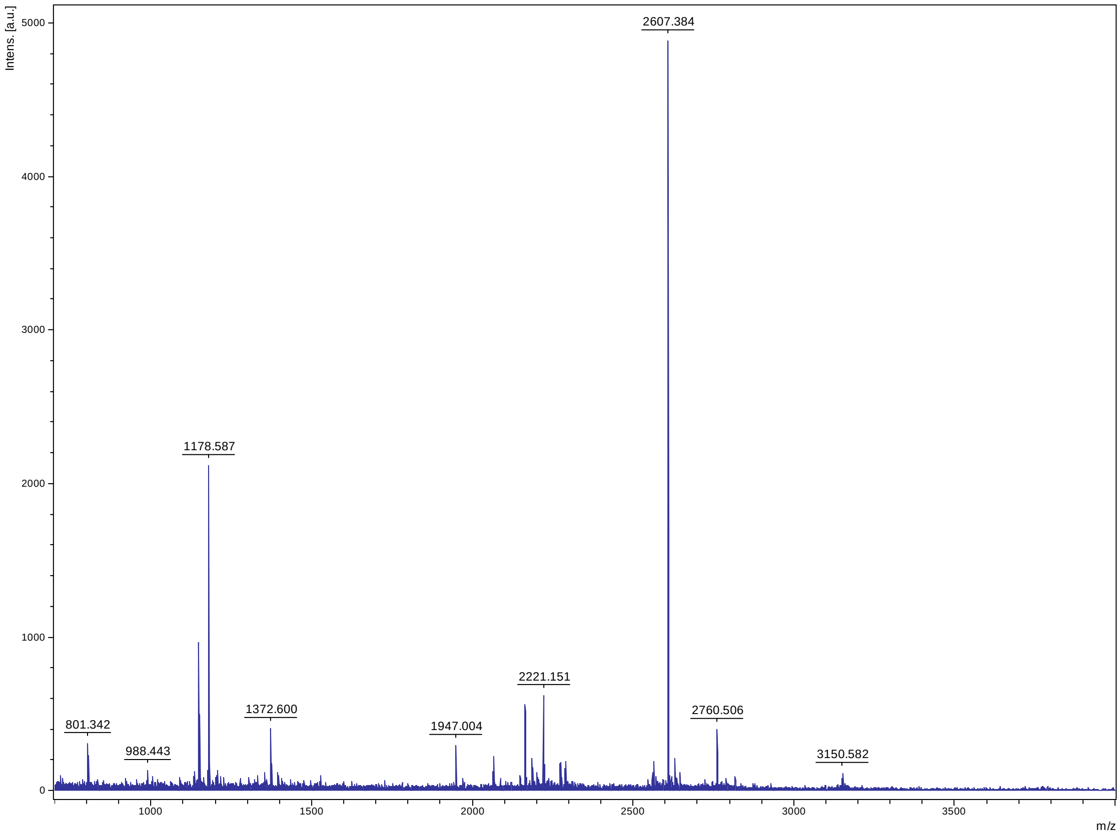


Match to: gi|14140144; Score: 92

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
111 - 137	2796.45	2795.45	2795.42	0.03	0	LGSFAFVGLPTAAYPTPFVAPGEETTR
138 - 153	1628.79	1627.79	1627.78	0.01	0	YAVIIGGANFGCGSSR
154 - 166	1219.65	1218.65	1218.65	-0.00	0	EHAPVALGAAGAR
167 - 175	935.50	934.50	934.49	0.01	0	AVVAEGYAR
167 - 179	1498.85	1497.85	1497.81	0.04	1	AVVAEGYARIFFR
180 - 199	2121.06	2120.05	2120.04	0.01	0	NSVATGEVYPLELADTGAWK
203 - 223	2289.16	2288.16	2288.08	0.08	0	TGDVVTVELDNCVMINHTSGK
227 - 247	2115.17	2114.17	2114.15	0.02	0	LKPIGDAGPVIEAGGIFAYAR

Spot 2291

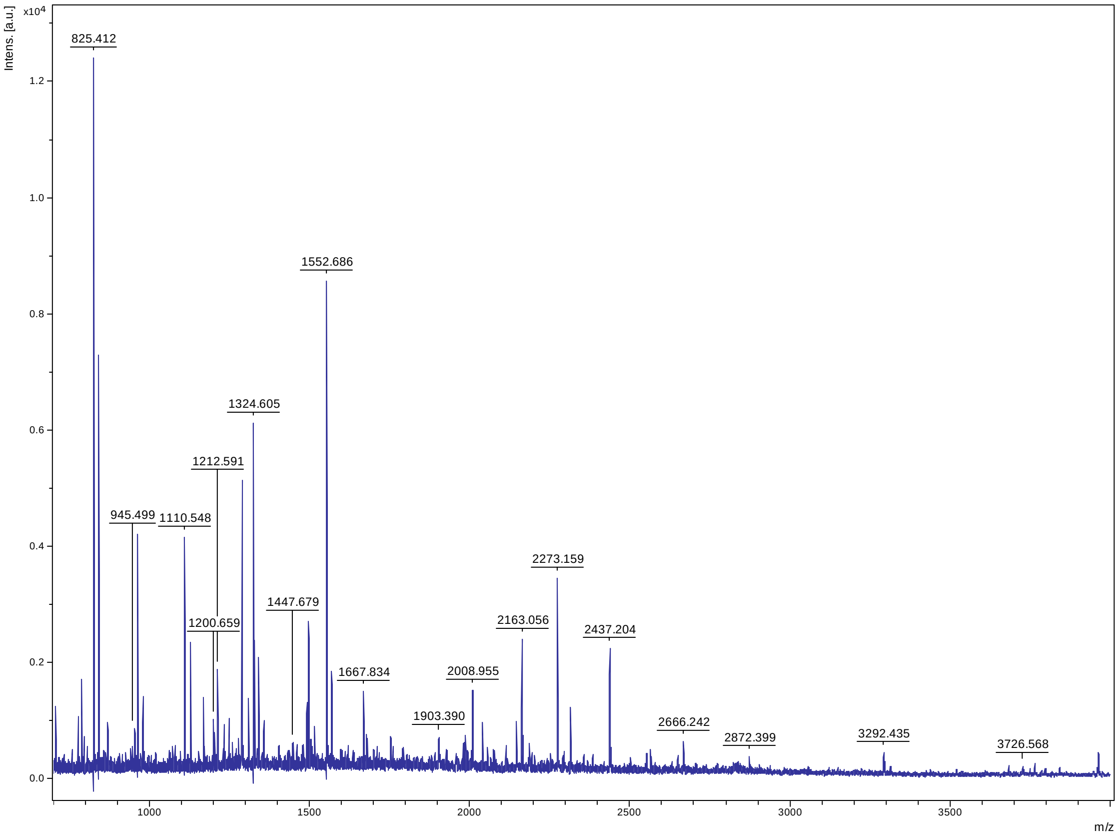


Match to: gi|51090748; Score: 130

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
58 - 67	1149.60	1148.59	1148.62	-0.03	0	YTSLKPLGDR
79 - 105	2607.38	2606.38	2606.40	-0.02	0	TVGGILLPSTAQSKPQGGEVVAVGEGR
127 - 138	1372.60	1371.60	1371.63	-0.03	0	YAGTEVQFNDTK
158 - 165	988.44	987.44	987.48	-0.04	0	DMKPLNDR
170 - 188	1947.00	1946.00	1946.02	-0.02	1	VAEAEDKTAGGLILTETTK
189 - 209	2065.03	2064.03	2064.07	-0.04	0	EKPSIGTVVAVGPGPLDDEGK
189 - 210	2221.15	2220.15	2220.17	-0.03	1	EKPSIGTVVAVGPGPLDDEGKR
226 - 232	801.34	800.34	800.37	-0.03	0	YAGSEFK
233 - 243	1178.59	1177.58	1177.61	-0.02	0	GADGTNYIVLR

Spot 2296

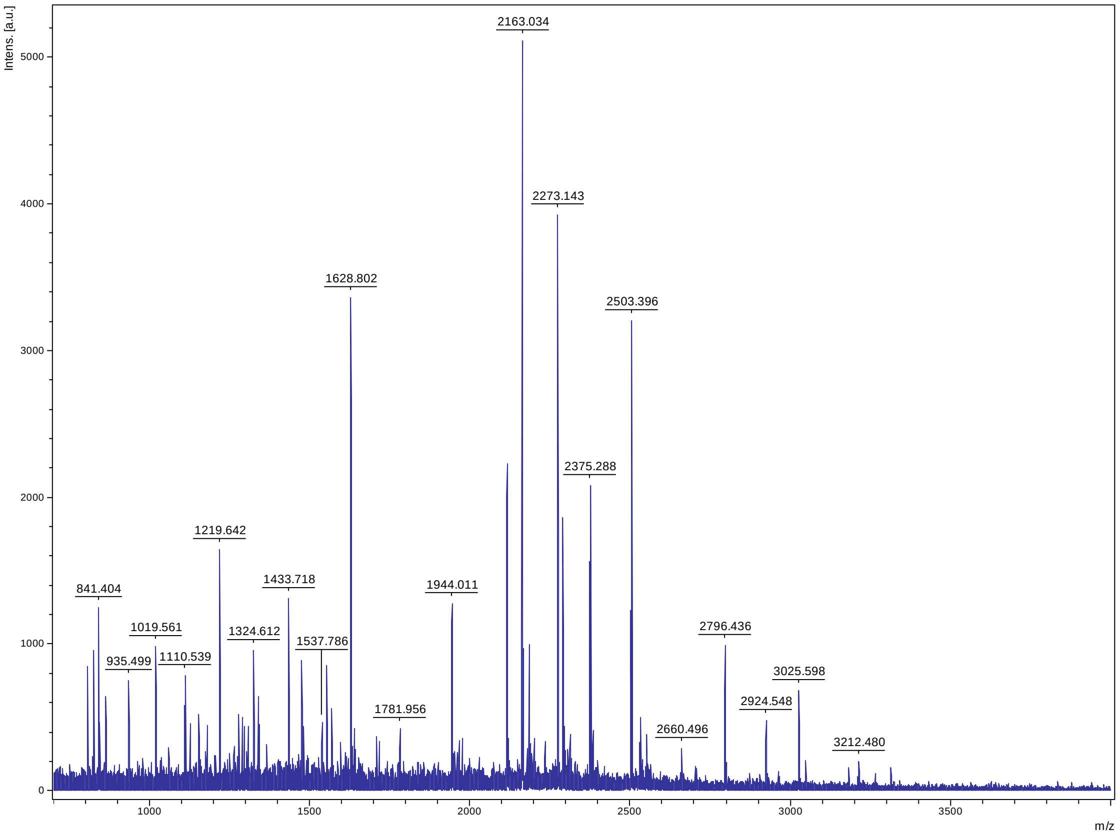


Match to: gi|169805 Score: 79 Expect: 0.0016

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
27 - 37	1289.6223	1288.6150	1288.5718	0.0433	0	R.EVQDSPLDACR.Q	
38 - 47	1168.6125	1167.6053	1167.6360	-0.0308	1	R.QVLDRQLTGR.E	Gln->pyro-Glu (N-term Q)
48 - 55	1110.5720	1109.5647	1109.5440	0.0207	1	R.ERFQPMFR.R	
50 - 55	825.4010	824.3937	824.4003	-0.0066	0	R.FQPMFR.R	
50 - 55	841.4099	840.4026	840.3952	0.0073	0	R.FQPMFR.R	Oxidation (M)
56 - 63	839.5231	838.5158	838.5137	0.0021	0	R.RPGALGLR.M	
64 - 75	1552.7600	1551.7527	1551.6592	0.0935	0	R.MQCCQQLQDVSR.E	
150 - 160	1324.6550	1323.6478	1323.6064	0.0414	0	R.QYAAQLPSMCR.V	
150 - 160	1340.6763	1339.6690	1339.6013	0.0677	0	R.QYAAQLPSMCR.V	Oxidation (M)

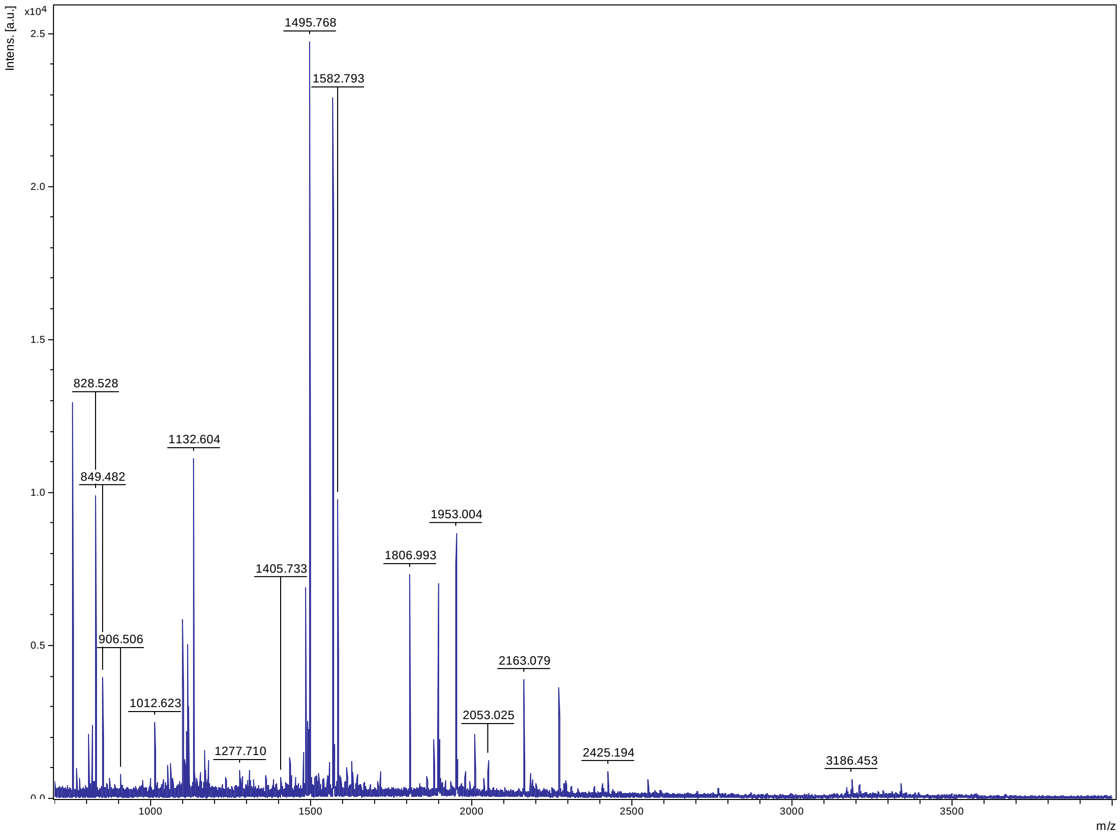
Spot 2299



Match to: gi|29367567 Score: 79

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 7	863.4642	862.4570	862.4582	-0.0012	1	-.MNVDKLK.K	Oxidation (M)
46 - 72	3025.5977	3024.5904	3024.5919	-0.0015	1	R.VGVNNIPGIEEVNIFKDDVVIQFQNPK.V	
73 - 91	1944.0111	1943.0038	1943.0112	-0.0074	0	K.VQASIGANTWVVSGTPQTK.K	
92 - 113	2503.3965	2502.3892	2502.3805	0.0087	1	K.KLQDLLPTIINQLGPDNLDNLR.R	
93 - 113	2375.2876	2374.2803	2374.2856	-0.0053	0	K.LQDLLPTIINQLGPDNLDNLR.R	
93 - 114	2531.3901	2530.3829	2530.3867	-0.0038	1	K.LQDLLPTIINQLGPDNLDNLRR.L	
114 - 121	1019.5607	1018.5535	1018.5559	-0.0025	1	R.RLAEQFQK.Q	

Spot 2302

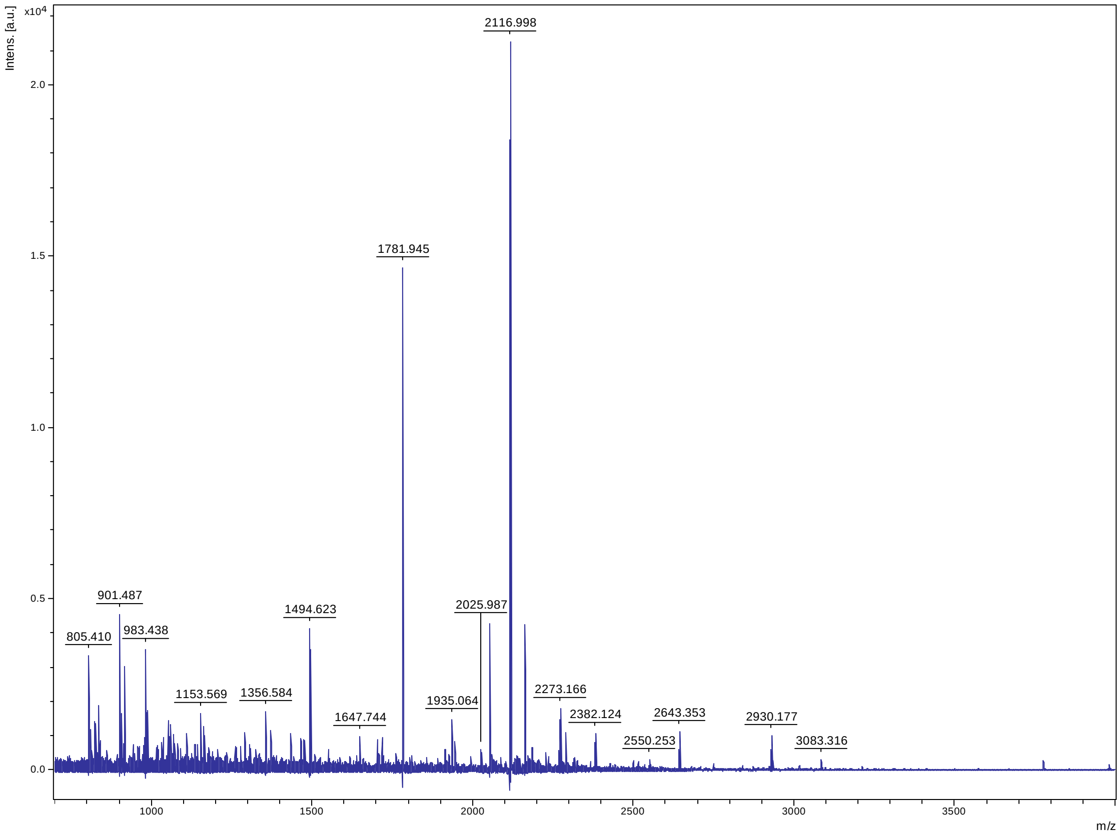


Match to: gi|51979378 Score: 146 Expect: 1.7e-10

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
45 - 54	1099.5261	1098.5188	1098.5128	0.0061	0	R.TSTGMYVANR.A	
45 - 54	1115.5155	1114.5082	1114.5077	0.0005	0	R.TSTGMYVANR.A	Oxidation (M)
55 - 70	1896.9638	1895.9565	1895.9411	0.0154	1	R.ASDKITQLTDNVYICR.S	Carbamidomethyl (C)
59 - 70	1495.7886	1494.7813	1494.7500	0.0313	0	K.ITQLTDNVYICR.S	Carbamidomethyl (C)
71 - 85	1568.7800	1567.7727	1567.7478	0.0250	0	R.SGSAADTQVISDYVR.Y	
86 - 102	1981.0668	1980.0595	1980.0581	0.0014	0	R.YFLHQHTIQLGQPATVK.V	
110 - 116	849.4221	848.4148	848.4756	-0.0607	0	R.LLAYQNK.N	
117 - 130	1535.7750	1534.7677	1534.7272	0.0406	0	K.NMLQAGMIVGGWDK.Y	Oxidation (M)
117 - 130	1551.7530	1550.7457	1550.7221	0.0236	0	K.NMLQAGMIVGGWDK.Y	2 Oxidation (M)
117 - 147	3339.4382	3338.4309	3338.6790	-0.2481	1	K.NMLQAGMIVGGWDKYEGGQIFSVPLGGTILR.Q	2 Oxidation (M)
131 - 147	1806.9914	1805.9841	1805.9675	0.0166	0	K.YEGGQIFSVPLGGTILR.Q	
148 - 169	2425.1666	2424.1593	2424.1749	-0.0156	0	R.QPFAIGGSGSSYLYGLLDHEWK.E	
170 - 179	1153.5692	1152.5619	1152.4604	0.1015	0	K.EGMSQEEAEK.F	Oxidation (M)
170 - 183	1610.8113	1609.8040	1609.7657	0.0383	1	K.EGMSQEEAEKFVVK.V	
170 - 183	1626.7970	1625.7897	1625.7606	0.0291	1	K.EGMSQEEAEKFVVK.V	Oxidation (M)
192 - 200	817.3495	816.3422	816.4089	-0.0667	0	R.DGASGGVVR.T	
201 - 211	1132.5966	1131.5893	1131.5884	0.0010	0	R.TVTINADGVSR.K	
212 - 218	828.4614	827.4541	827.4290	0.0252	1	R.KFHPGDK.L	
219 - 246	3186.3833	3185.3760	3185.5703	-0.1942	0	K.LQLWHEELEPQNSLLDILAAGNPDPMVQ.-	Oxidation (M)

Spot 2307

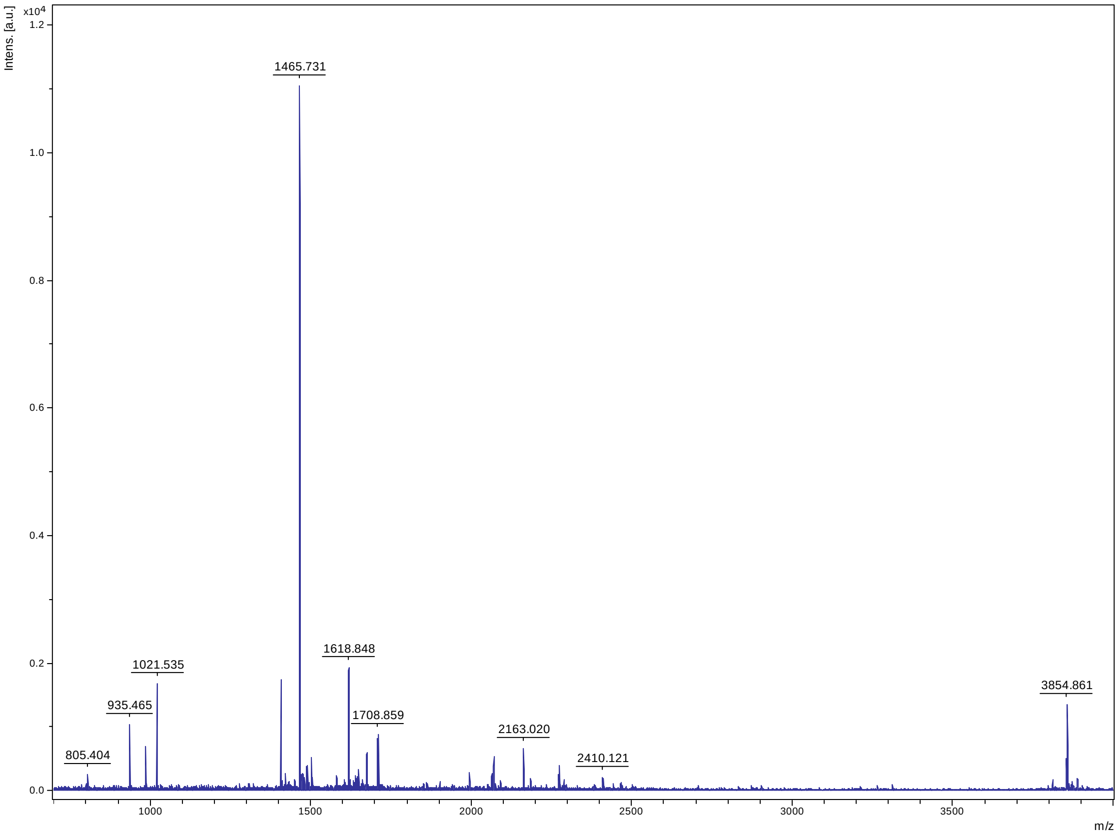


Match to: gi|41052743; Score: 72

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
19 - 40	2382.13	2381.13	2381.12	0.01	0	GFGFISPDDGSEDLFVHQSSIK
46 - 64	2052.93	2051.93	2051.93	0.00	0	SLAEGEQVEFAISESEDGR
67 - 79	1291.64	1290.64	1290.65	-0.00	0	AVDVTGPDGSFVK
80 - 95	1164.53	1163.53	1163.51	0.02	0	GGAGGGGGGGGGFGSR
106 - 115	983.44	982.43	982.43	0.01	0	SYGGSWGGGR
117 - 128	1037.48	1036.48	1036.44	0.04	0	SGGGGPGGGCFK
173 - 204	2930.17	2929.16	2929.13	0.03	0	DCFNSGGGGGGGGGGGGGGACYNCGETGHLAR
225 - 237	1494.62	1493.62	1493.61	0.00	0	SCYNCGEAGHIAR

Spot 2315

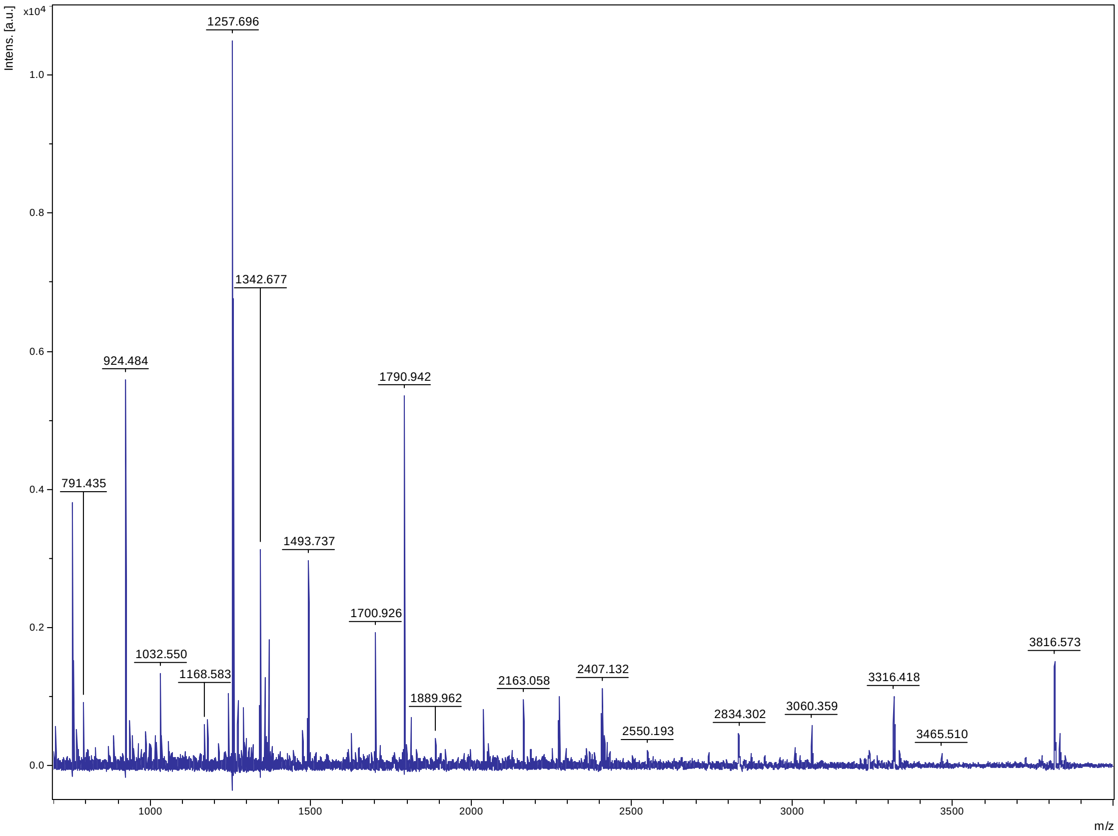


Match to: gi|1583954; Score: 101

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
22 - 32	1407.64	1406.63	1406.66	-0.03	0	LTYYTPEYETK
22 - 41	2410.12	2409.12	2409.17	-0.06	1	LTYYTPEYETKDTDILAAFR
33 - 41	1021.54	1020.53	1020.52	0.01	0	DTDILAAFR
42 - 79	3854.86	3853.86	3853.86	-0.01	0	VTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDR
132 - 139	985.57	984.57	984.57	0.00	1	ALRLEDLR
140 - 146	805.40	804.40	804.44	-0.04	0	IPPTYSK
147 - 161	1708.86	1707.86	1707.87	-0.01	1	TFQGPPHGIQVERDK
165 - 177	1502.82	1501.82	1501.84	-0.02	0	YGRPLLGCTIKPK
320 - 334	1465.73	1464.73	1464.71	0.01	0	MSGGDHIHAGTVVGK

Spot 2317

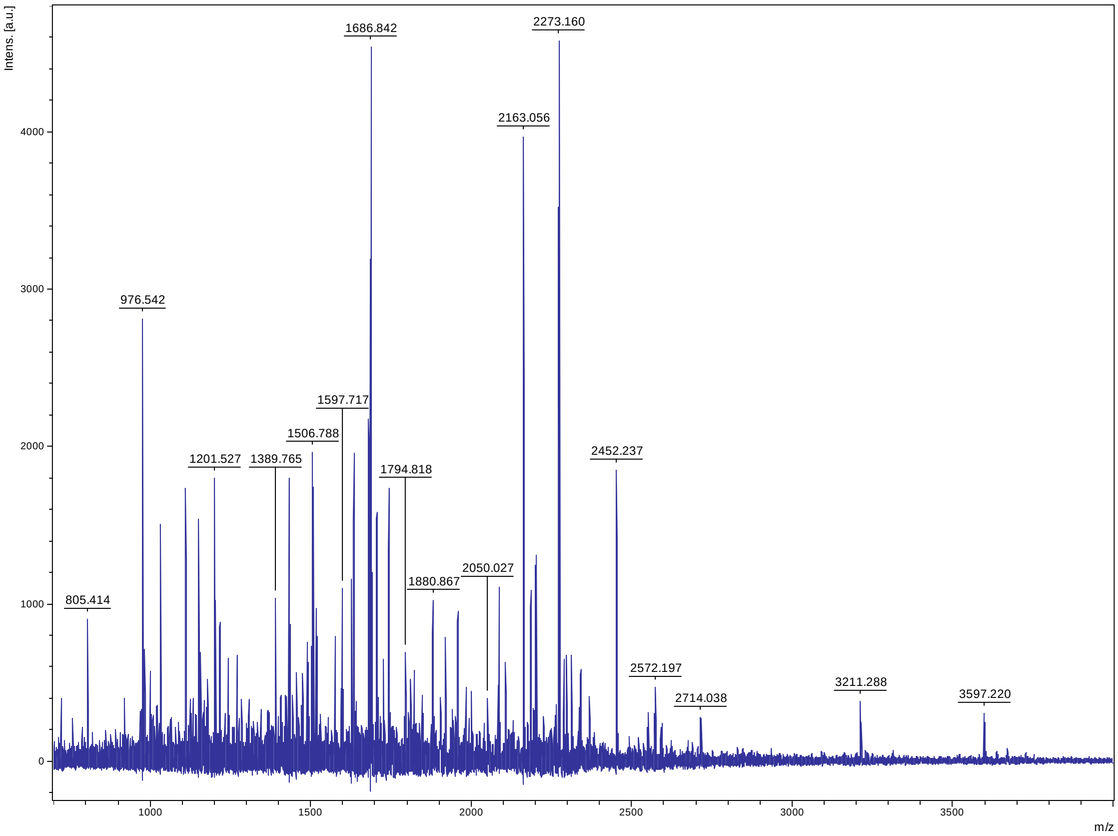


Match to: gi|50924894 Score: 85 Expect: 0.00022

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 12	1242.6735	1241.6662	1241.7230	-0.0568	1	M.ASKVELVVEVK.S	Acetyl (N-term)
13 - 23	1257.6541	1256.6468	1256.6877	-0.0409	1	K.SPADKLWTALR.D	
24 - 31	936.3169	935.3096	935.4600	-0.1504	0	R.DSTELFPK.I	
32 - 38	924.3201	923.3128	923.4752	-0.1624	0	K.IFPEQYK.S	
58 - 69	1342.6407	1341.6334	1341.6638	-0.0304	0	K.YTEGVPMVTFAK.E	
58 - 69	1358.6492	1357.6419	1357.6587	-0.0168	0	K.YTEGVPMVTFAK.E	Oxidation (M)
72 - 80	1032.4416	1031.4343	1031.5135	-0.0791	1	K.VEVADDEKK.V	
81 - 96	1790.9734	1789.9661	1789.9137	0.0524	0	K.VVSYSVVDGELVSFYK.N	
108 - 128	2037.0288	2036.0215	2035.9309	0.0907	0	K.GGAAAPAADGAVVSWTMDFDK.A	
108 - 140	3316.6663	3315.6590	3315.5604	0.0986	1	K.GGAAAPAADGAVVSWTMDFDKASEEVPDPDVIK.E	
129 - 140	1298.6207	1297.6134	1297.6401	-0.0267	0	K.ASEEVPDPDVIK.E	

Spot 2322



Match to: gi|50923963 Score: 181 Expect: 5.3e-14

Matched peptides:

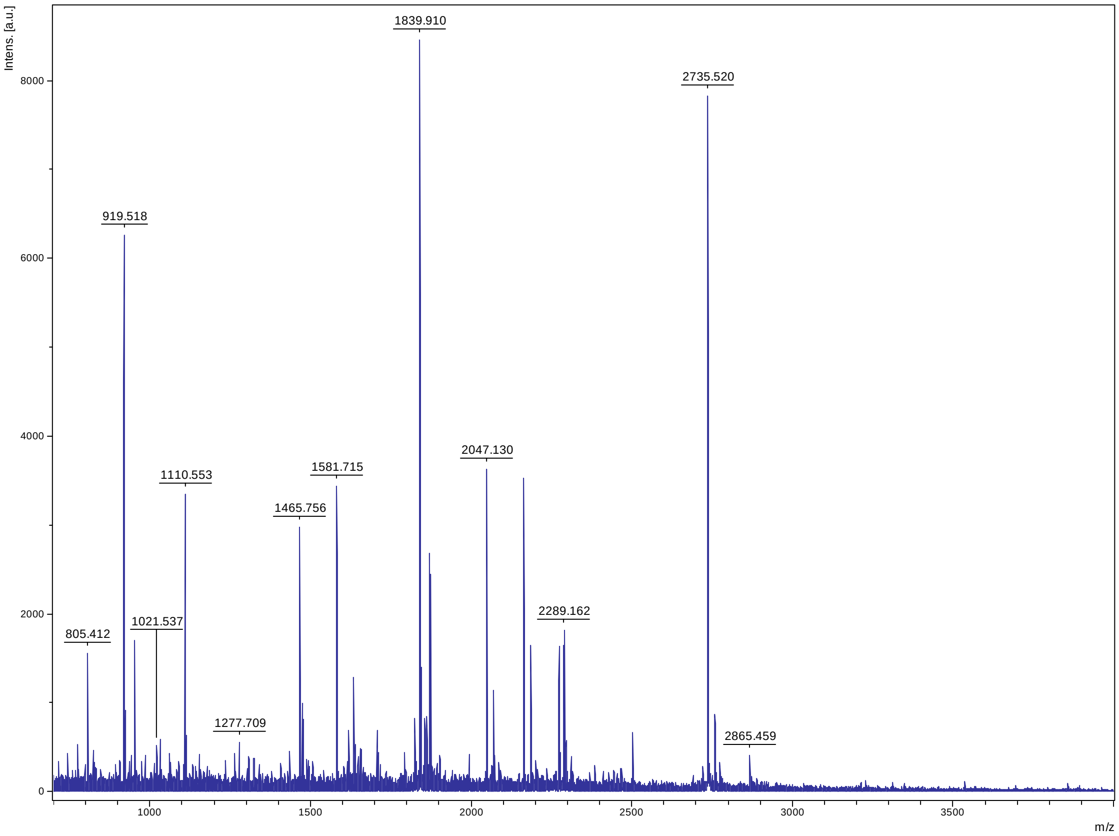
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
65 - 73	1156.6166	1155.6093	1155.6440	-0.0347	1	R.RLFYVPSFK.I	
66 - 73	1000.4940	999.4867	999.5429	-0.0562	0	R.LFYVPSFK.I	
74 - 92	1956.9385	1955.9312	1955.9450	-0.0138	0	K.IYGGVAGLYDYGPPGCAVK.A	Carbamidomethyl (C)
93 - 100	976.4757	975.4684	975.5290	-0.0606	0	K.ANVLAFWR.Q	
101 - 124	2714.0695	2713.0622	2713.3164	-0.2542	0	R.QHFVLEEGMLEVDCPCVTPEVVLK.A	
171 - 192	2341.2216	2340.2143	2340.1961	0.0183	0	K.TAEFNHVLAVLDDLSAEQLGAK.I	
193 - 204	1333.7196	1332.7123	1332.7289	-0.0165	1	K.IKEYGIVAPDTK.N	
254 - 266	1389.7602	1388.7529	1388.7564	-0.0035	0	K.LPFAAAQIGQAFR.N	
254 - 272	2086.0929	2085.0856	2085.1119	-0.0263	1	K.LPFAAAQIGQAFRNEISPR.Q	
280 - 295	1918.8930	1917.8857	1917.8996	-0.0138	0	R.EFTLAEIEHFVDPEDK.S	
280 - 299	2368.1740	2367.1667	2367.1382	0.0285	1	R.EFTLAEIEHFVDPEDKSHPK.F	
300 - 313	1821.8797	1820.8724	1820.8555	0.0169	1	K.FRDVSDLEFFMFPR.E	Oxidation (M)
302 - 313	1502.6904	1501.6831	1501.6911	-0.0080	0	R.DVSDLEFFMFPR.E	
302 - 313	1518.6781	1517.6708	1517.6860	-0.0152	0	R.DVSDLEFFMFPR.E	Oxidation (M)
302 - 320	2287.1834	2286.1761	2286.0990	0.0771	1	R.DVSDLEFFMFPREQQLTGK.S	
325 - 347	2452.2494	2451.2421	2451.2393	0.0028	0	K.LNIGQAVSEGTVNNETLGYFIGR.V	
348 - 359	1409.8146	1408.8073	1408.7966	0.0108	0	R.VYLFLTQLGIDK.D	
348 - 361	1680.9184	1679.9111	1679.9246	-0.0135	1	R.VYLFLTQLGIDKDR.L	
473 - 484	1366.6522	1365.6449	1365.6962	-0.0512	1	K.GEVEFKVCTLGK.D	Carbamidomethyl (C)
506 - 520	1634.8753	1633.8680	1633.8827	-0.0147	1	R.KFTPSVIEPSFGIGR.I	
507 - 520	1506.7874	1505.7801	1505.7878	-0.0076	0	K.FTPSVIEPSFGIGR.I	
521 - 536	2131.0579	2130.0506	2130.0179	0.0328	0	R.IIYCLFEHCFYQRPGK.A	2 Carbamidomethyl (C)
577 - 596	1984.0506	1983.0433	1983.0459	-0.0025	0	K.ALTAAGISHIIDMTGNTIGK.R	
577 - 596	2000.0291	1999.0218	1999.0408	-0.0189	0	K.ALTAAGISHIIDMTGNTIGK.R	Oxidation (M)
598 - 621	2591.2378	2590.2305	2590.3602	-0.1297	1	R.YARTDEIGVPLAITVDNTTSVTVR.D	
601 - 621	2201.1289	2200.1216	2200.1586	-0.0370	0	R.TDEIGVPLAITVDNTTSVTVR.D	
627 - 641	1685.8797	1684.8724	1684.8995	-0.0271	1	K.DQIRVEVDEVASVVK.E	
642 - 656	1810.7697	1809.7624	1809.7992	-0.0368	0	K.EVTDGQSTWADIMWR.Y	Oxidation (M)
657 - 673	1792.7412	1791.7339	1791.7435	-0.0095	0	R.YPAHTASAAEEEEASET.-	

Match to: gi|50582723 Score: 90

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
77 - 90	1270.7390	1269.7317	1269.7404	-0.0087	0	K.TVVAVILGGGAGTR.L	
99 - 110	1199.6921	1198.6849	1198.6822	0.0027	0	R.AKPAVPIGGAYR.L	
127 - 140	1625.8523	1624.8450	1624.8573	-0.0122	0	K.VYILTQFNSASLNR.H	
175 - 184	1150.5699	1149.5627	1149.5567	0.0060	0	R.WFQGTADAVR.Q	
223 - 239	1918.9264	1917.9191	1917.9037	0.0155	1	R.QRGADISICCLPIDDSR.A	Carbamidomethyl (C)
225 - 239	1691.7745	1690.7673	1690.7654	0.0018	0	R.GADISICCLPIDDSR.A	2 Carbamidomethyl (C)
300 - 307	983.6340	982.6268	982.6175	0.0093	0	K.EILLNLLR.W	
308 - 326	2107.0684	2106.0611	2106.0534	0.0077	1	R.WRFPTANDFGSEIIPASAK.E	
347 - 361	1705.8552	1704.8479	1704.8471	0.0009	0	K.SFFEANLSLAEQPPR.F	
362 - 375	1726.7863	1725.7790	1725.7820	-0.0031	0	R.FSFYDANKPMYTSR.R	
362 - 375	1742.8529	1741.8456	1741.7770	0.0687	0	R.FSFYDANKPMYTSR.R	Oxidation (M)
388 - 403	1880.8669	1879.8597	1879.8557	0.0040	0	K.ITDSIISHGCFLDSCR.I	2 Carbamidomethyl (C)
471 - 493	2572.2383	2571.2310	2571.2200	0.0110	1	K.NVTISNSEGVQEADRTSEGFYIR.S	

Spot 2328

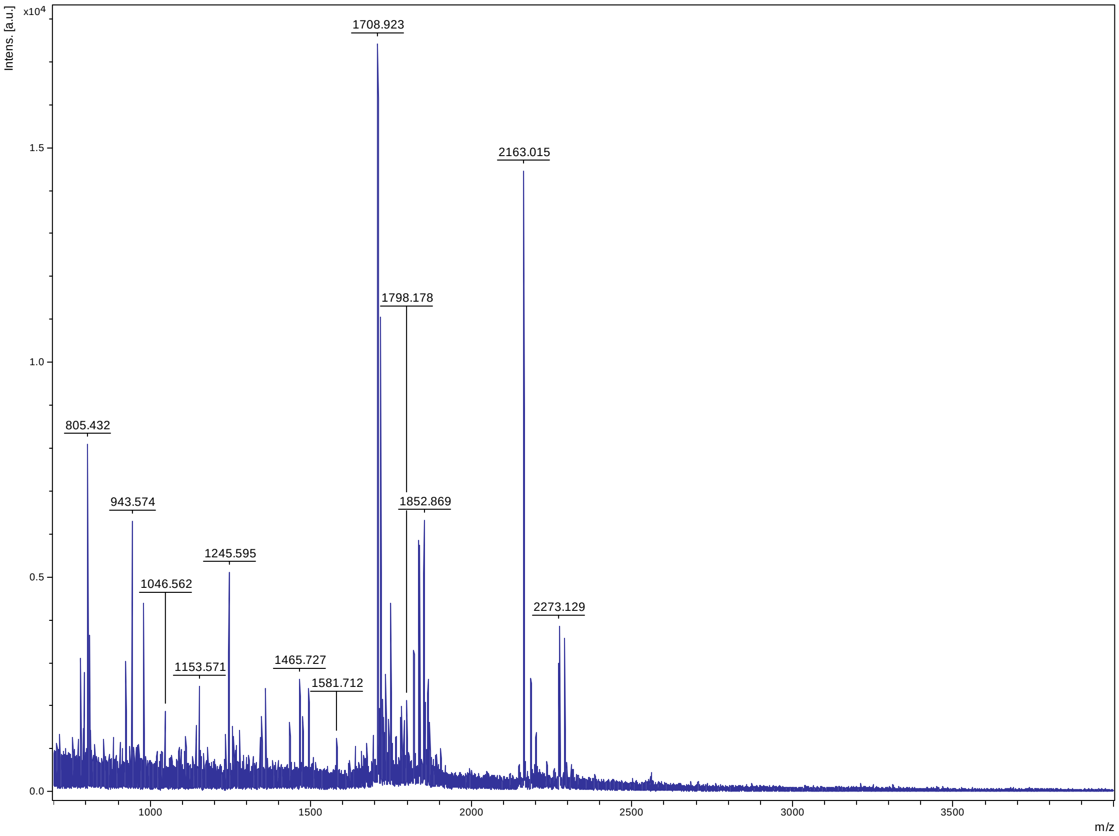


Match to: gi|53793125; Score: 69

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
11 - 24	1581.72	1580.71	1580.70	0.01	0	SGAEVHTGHELCER
28 - 52	2735.52	2734.52	2734.48	0.04	0	ELLVELGLPDGLLPLPSLEEVGYNR
53 - 60	919.52	918.52	918.51	0.01	0	AAGFVWLR
61 - 76	1632.79	1631.79	1631.79	0.00	0	QTQAGGATHTFDTIGK
77 - 92	1822.87	1821.87	1821.87	0.00	0	QVWYAGEVTAFVEQGR Pyro-glu (N-term Q)
77 - 92	1839.91	1838.91	1838.90	0.01	0	QVWYAGEVTAFVEQGR
133 - 151	2047.13	2046.13	2046.11	0.01	1	ALPVTAFQLNPAPPEPEKK

Spot 2330

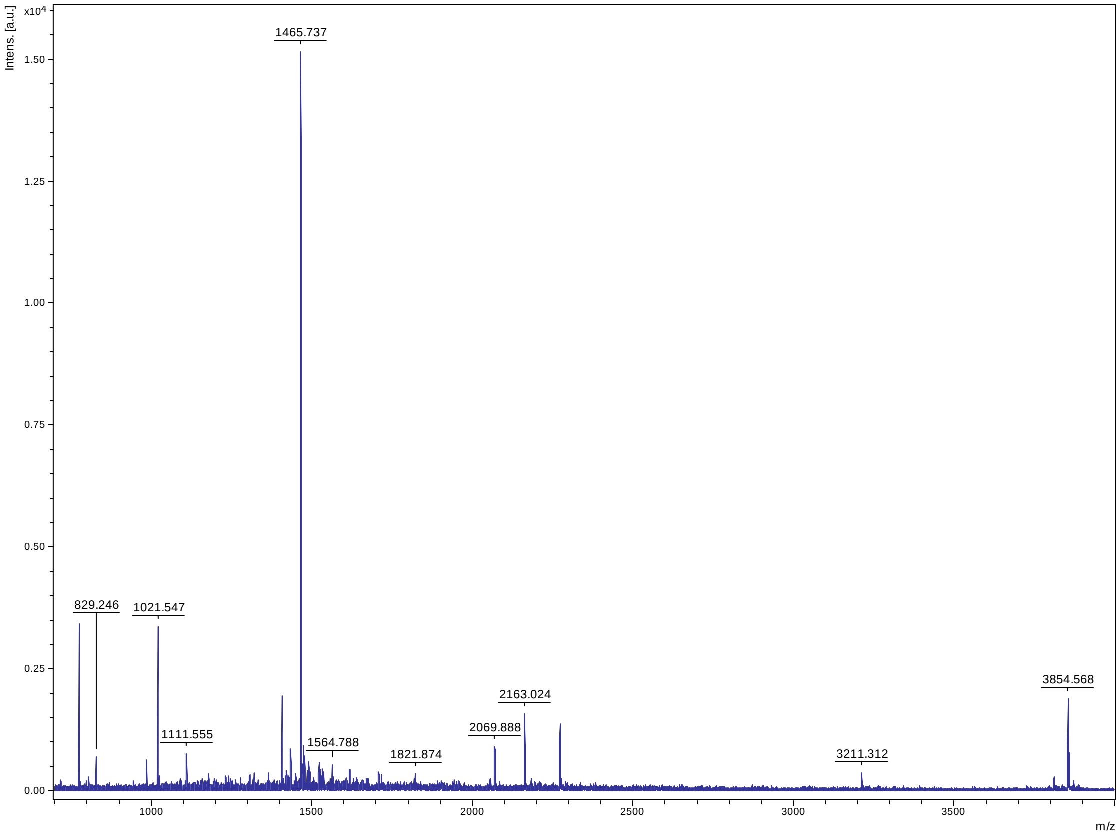


Match to: gi|50096951; Score: 92

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
16 - 24	943.57	942.57	942.55	0.02	0	GLIGDIISR
16 - 27	1347.74	1346.74	1346.76	-0.01	1	GLIGDIISRFEK
34 - 42	1111.58	1110.58	1110.53	0.05	1	GMKFMNVER
34 - 42	1143.58	1142.58	1142.52	0.06	1	GMKFMNVER 2 Oxidation (M)
37 - 42	811.41	810.41	810.37	0.04	0	FMNVER Oxidation (M)
86 - 102	1865.02	1864.02	1864.04	-0.02	1	RIIGATRPWEAAPGTIR
87 - 102	1708.92	1707.92	1707.94	-0.02	0	IIGATRPWEAAPGTIR
103 - 111	979.50	978.50	978.48	0.02	0	ADYAVEVGR
140 - 149	1245.59	1244.59	1244.58	0.01	0	SNLHPWIYES

Spot 2331

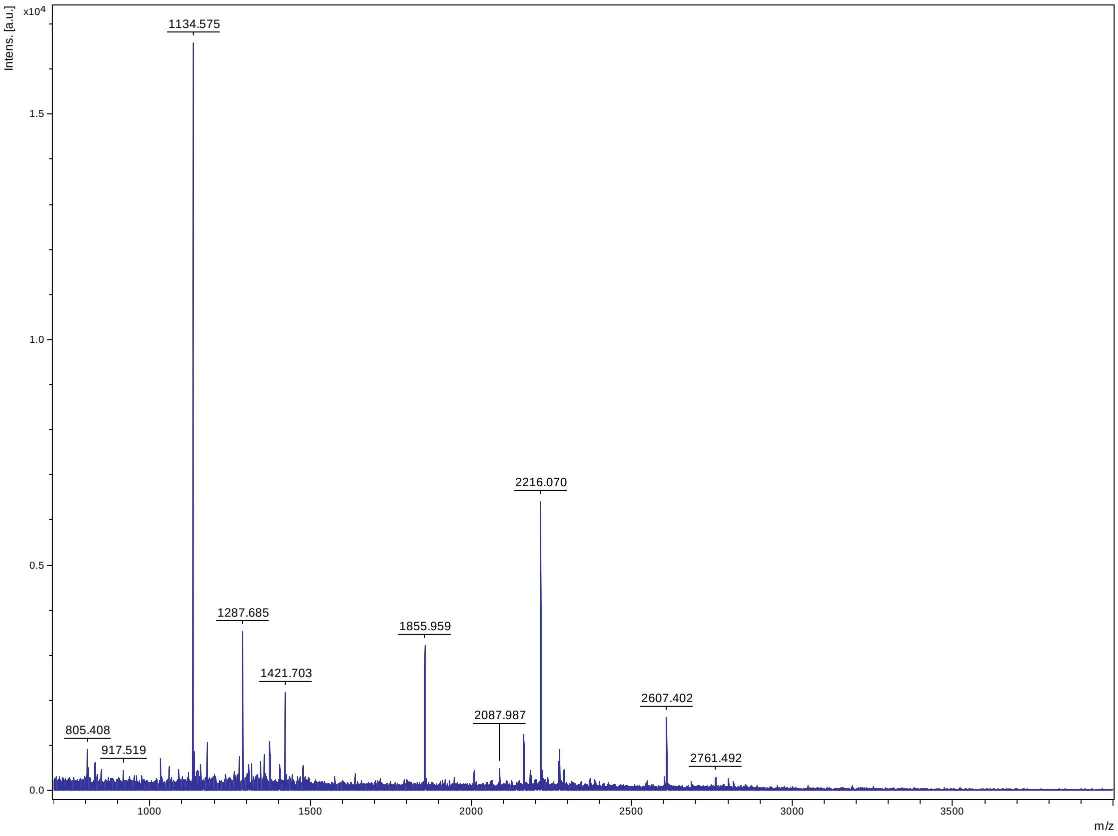


Match to: gi|113534025 Score: 84 Expect: 0.00037

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
22 - 32	1407.6569	1406.6496	1406.6605	-0.0110	0	K.LTYYTPEYETK.D	
33 - 41	1021.5474	1020.5401	1020.5240	0.0162	0	K.DTDILAAFR.V	
132 - 139	985.5954	984.5881	984.5716	0.0165	1	R.ALRLEDLR.I	
140 - 146	805.4400	804.4327	804.4381	-0.0054	0	R.IPPTYSK.T	
147 - 159	1465.7366	1464.7293	1464.7473	-0.0180	0	K.TFQGPPHGIQVER.D	
147 - 161	1708.8309	1707.8237	1707.8692	-0.0456	1	K.TFQGPPHGIQVERDK.L	
188 - 196	1111.5553	1110.5480	1110.5128	0.0352	0	R.ACYDSINLR.S	Carbamidomethyl (C)

Spot 2336

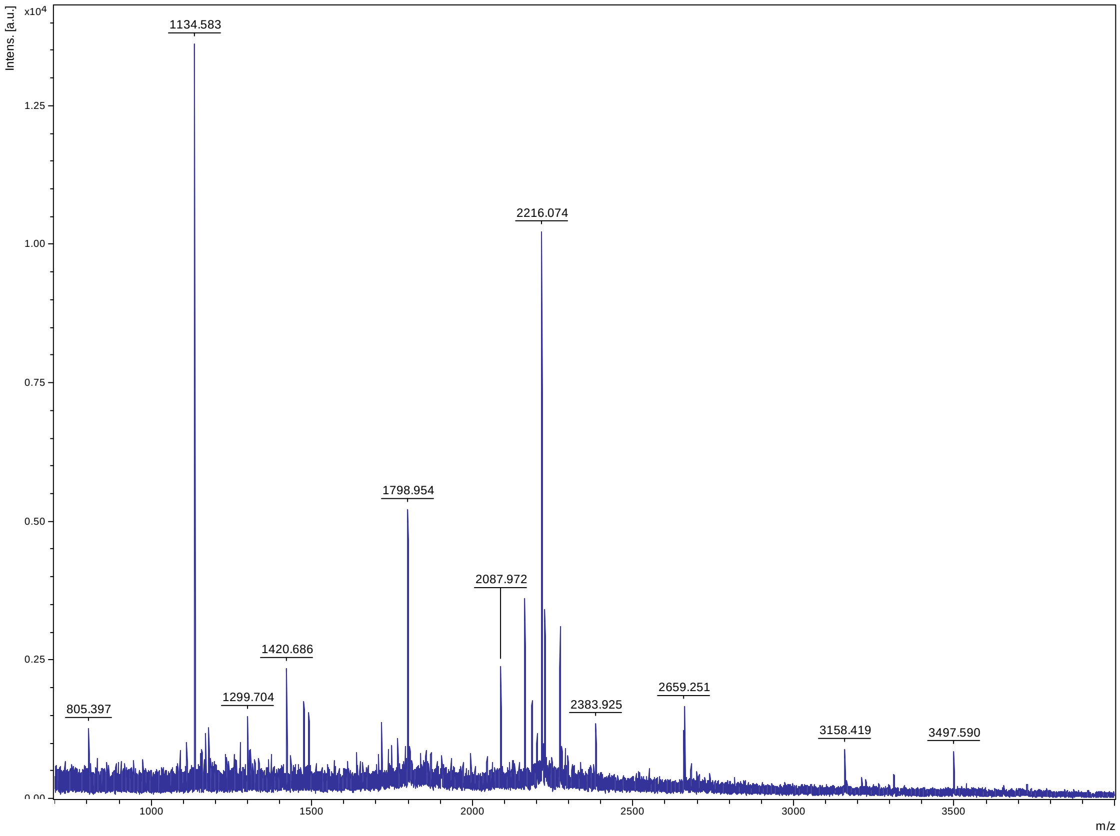


Match to: gi|77555893; Score: 78

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
20 - 29	1134.58	1133.57	1133.58	-0.01	0	TYPQQAGTIR
59 - 70	1421.70	1420.70	1420.72	-0.02	0	CHFVAIDIFTAK
71 - 89	2216.07	2215.07	2215.08	-0.01	1	KLEDIVPSSHNCDVPHVNR
72 - 89	2087.99	2086.98	2086.99	-0.00	0	LEDIVPSSHNCDVPHVNR
114 - 129	1855.96	1854.96	1854.97	-0.01	1	DDLRLPTDDNLLSQIK
118 - 129	1356.70	1355.70	1355.73	-0.03	0	LPTDDNLLSQIK

Spot 2337

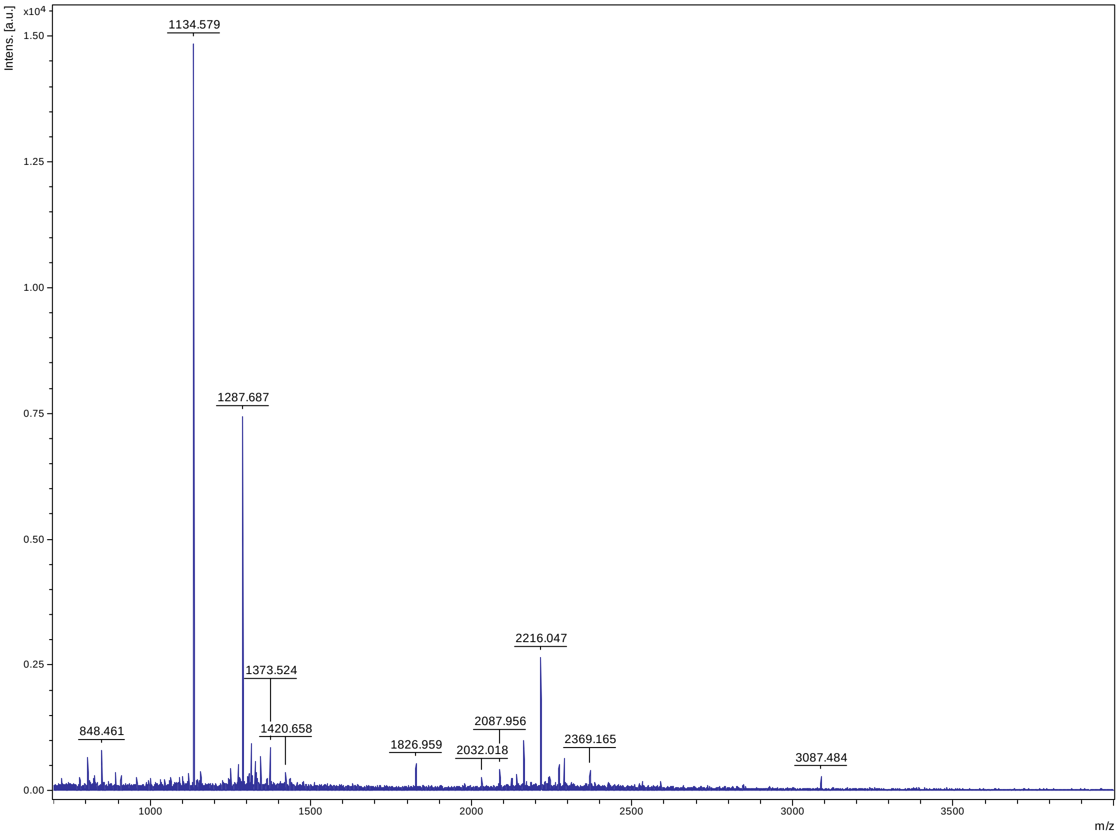


Match to: gi|50938957 Score: 80 Expect: 0.00061

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
20 - 29	1134.5830	1133.5757	1133.5829	-0.0072	0	K.TYPQQAGTIR.K
59 - 70	1420.6862	1419.6789	1419.6969	-0.0180	0	K.CHFVAIDIFNGK.K Carbamidomethyl (C)
71 - 89	2216.0737	2215.0665	2215.0804	-0.0139	1	K.KLEDIVPSSHNCDVPHVNR.T Carbamidomethyl (C)
72 - 89	2087.9719	2086.9646	2086.9854	-0.0207	0	K.LEDIVPSSHNCDVPHVNR.T Carbamidomethyl (C)
90 - 113	2659.2512	2658.2439	2658.2912	-0.0472	0	R.TEYQLIDISEDGFVSLLTESGNTK.D
114 - 129	1798.9541	1797.9468	1797.9472	-0.0004	1	K.DDLRLPTDDSLLGQIK.T
118 - 129	1299.7045	1298.6972	1298.7082	-0.0110	0	R.LPTDDSLLGQIK.T

Spot 2338

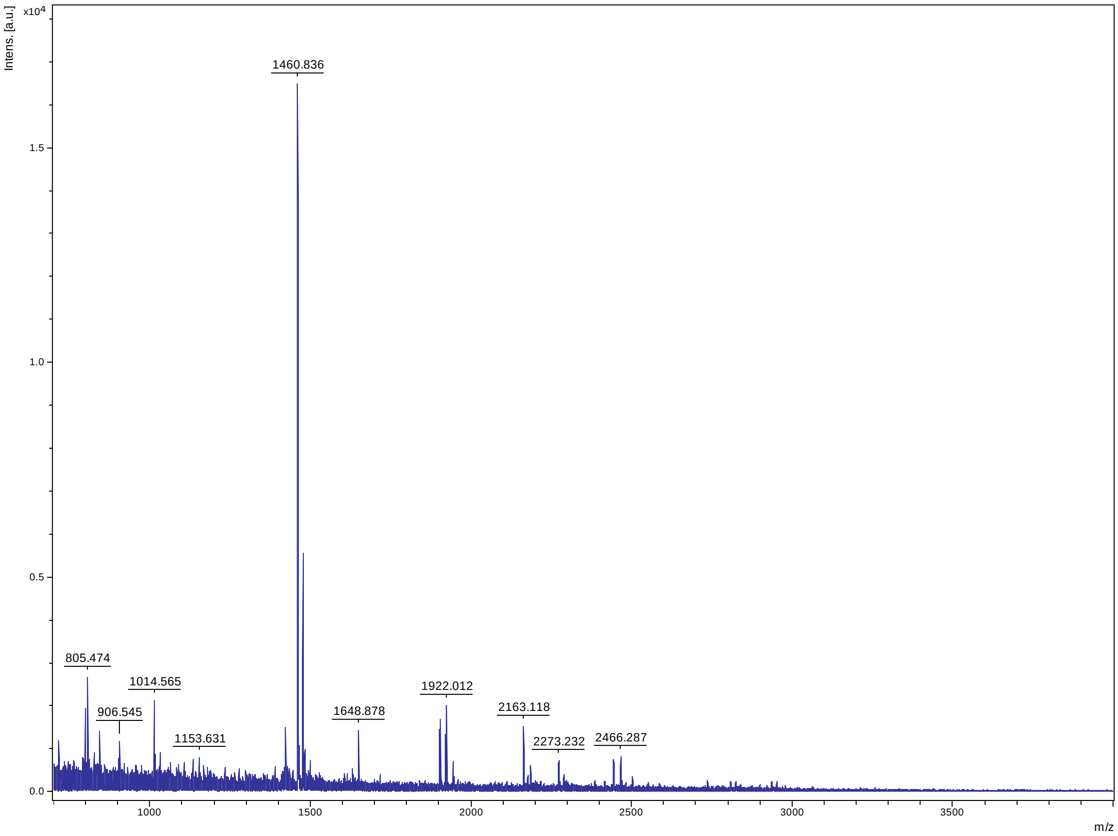


Match to: gi|20429034; Score: 135

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
20 - 29	1134.58	1133.58	1133.58	-0.01	0	TYPQQAGTIR
43 - 50	848.46	847.46	847.47	-0.01	0	VVEVSTSK
59 - 70	1420.66	1419.66	1419.70	-0.04	0	CHFVAIDIFNGK
71 - 89	2216.05	2215.04	2215.08	-0.04	1	KLEDIVPSSHNCDVPHVNR
72 - 89	2087.96	2086.95	2086.99	-0.03	0	LEDIVPSSHNCDVPHVNR
90 - 117	3087.48	3086.48	3086.49	-0.01	1	TDYQLIDISEDGFVSLLTESGGTKDDLR
114 - 129	1826.96	1825.96	1825.98	-0.02	1	DDLRLPSDEALLTQIK
118 - 129	1327.71	1326.71	1326.74	-0.03	0	LPSDEALLTQIK
118 - 136	2032.02	2031.02	2031.05	-0.04	1	LPSDEALLTQIKDGFAEGK

Spot 2341

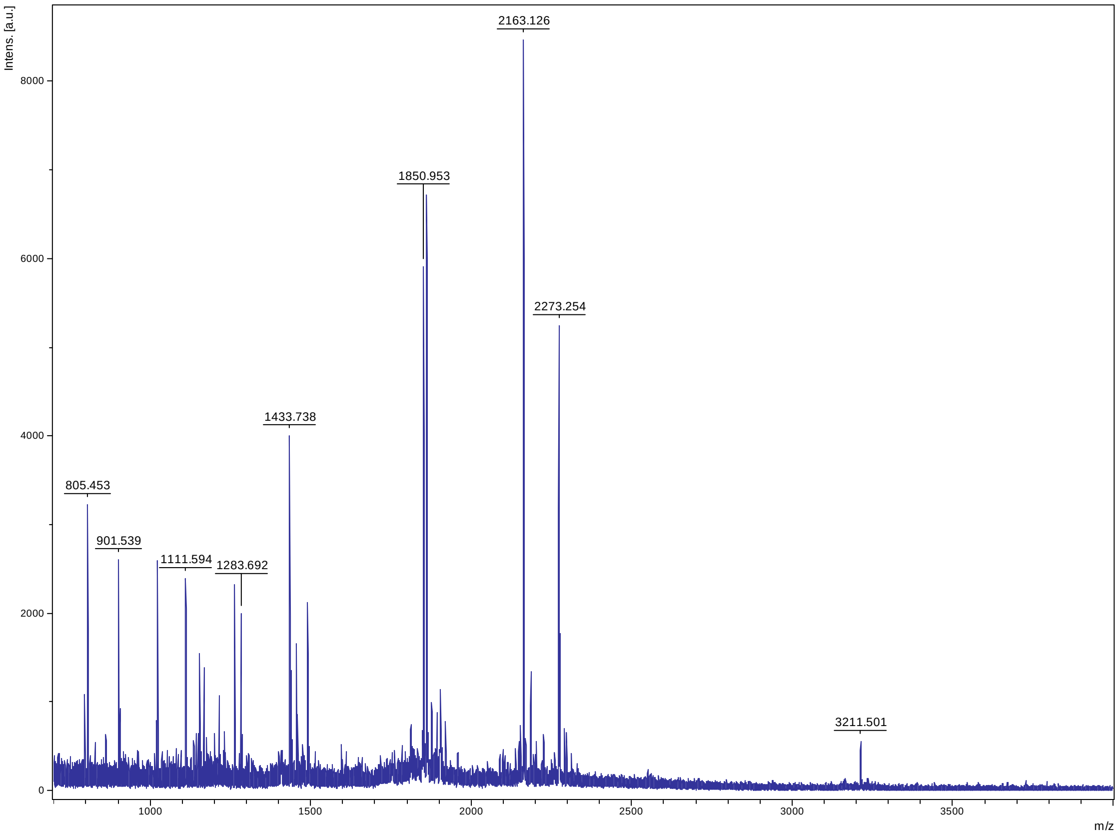


Match to: gi|37535166; Score: 91

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
43 - 49	843.58	842.58	842.52	0.05	0	TILELVR
50 - 64	1902.87	1901.87	1901.78	0.09	0	SYDGDHICYDHFAFR
75 - 88	1648.88	1647.88	1647.79	0.08	0	SLAEFFTDFGYVPR
100 - 122	2466.29	2465.28	2465.20	0.08	0	ALWFSPPTNDGYTGTGVYGPLPR
265 - 272	1014.56	1013.56	1013.48	0.08	0	SYIEFAER
280 - 291	1474.78	1473.78	1473.66	0.12	0	DLPNDEVNEHHR
280 - 292	1630.86	1629.86	1629.76	0.10	1	DLPNDEVNEHHRR
293 - 314	2443.22	2442.22	2442.13	0.09	1	DGFEVGNADKIFESTSNDQLTR

Spot 2343

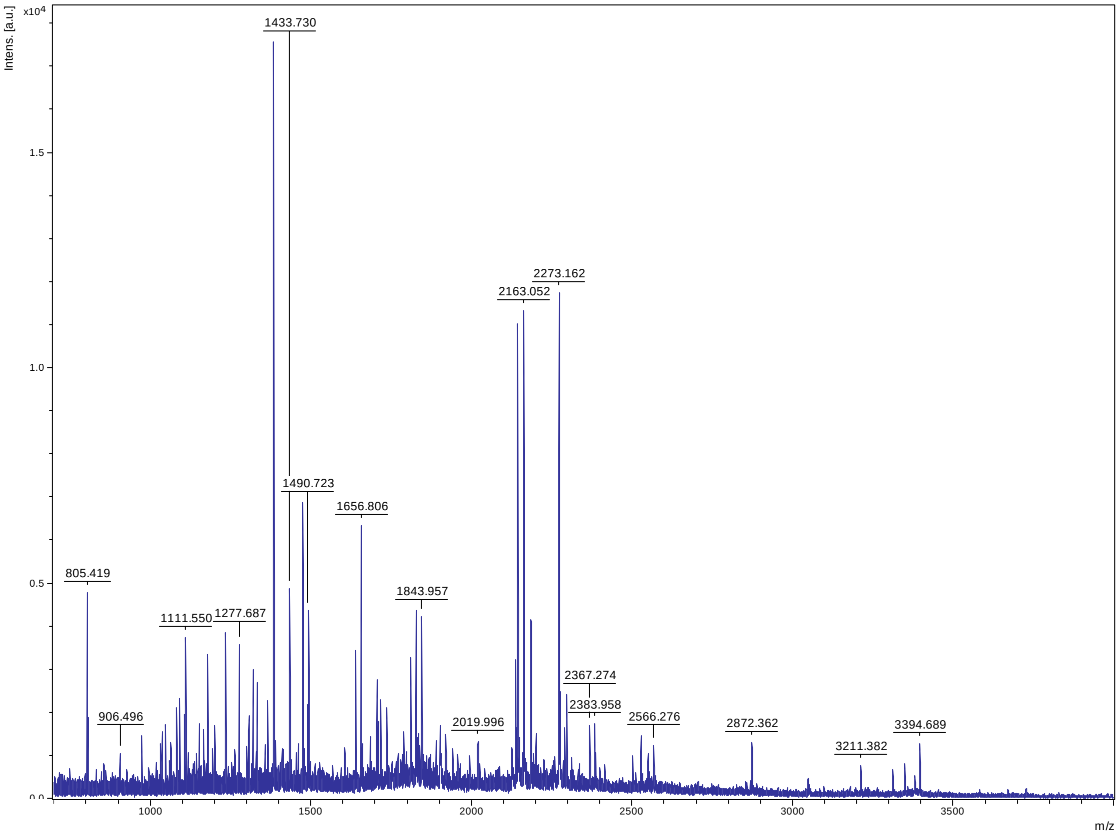


Match to: gi|77557031 Score: 107 Expect: 1.3e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 14	1283.7052	1282.6979	1282.6517	0.0463	0	M.ASSGDPSAVVVPR.N	Acetyl (N-term)
18 - 24	901.5040	900.4967	900.4916	0.0051	0	R.LLEELER.G	
18 - 27	1215.6925	1214.6852	1214.6506	0.0346	1	R.LLEELERGEK.G	
28 - 47	2136.8286	2135.8213	2135.8775	-0.0562	0	K.GIGDGSVSYGMDDADDIYMR.S	
28 - 47	2152.8815	2151.8742	2151.8724	0.0018	0	K.GIGDGSVSYGMDDADDIYMR.S	Oxidation (M)
48 - 64	1861.9409	1860.9336	1860.9231	0.0106	0	R.SWTGTIIGPHNTVHEGR.I	
48 - 64	1903.9383	1902.9310	1902.9336	-0.0026	0	R.SWTGTIIGPHNTVHEGR.I	Acetyl (N-term)
70 - 84	1850.9058	1849.8985	1849.9032	-0.0047	1	K.LFCDKDYPDRPPTVK.F	Carbamidomethyl (C)
89 - 104	1875.8950	1874.8877	1874.8614	0.0263	0	R.INMTCVNPENGLVDQR.K	Carbamidomethyl (C); Oxidation (M)
106 - 113	1022.5559	1021.5486	1021.5345	0.0141	0	K.FSLLSNWR.R	
115 - 126	1439.7649	1438.7576	1438.7377	0.0199	0	R.EYTMEAILTQLK.K	
115 - 126	1455.7618	1454.7545	1454.7327	0.0219	0	R.EYTMEAILTQLK.K	Oxidation (M)
136 - 146	1262.7031	1261.6958	1261.6706	0.0252	1	R.KLVQPPEGTFF.-	

Spot 2344

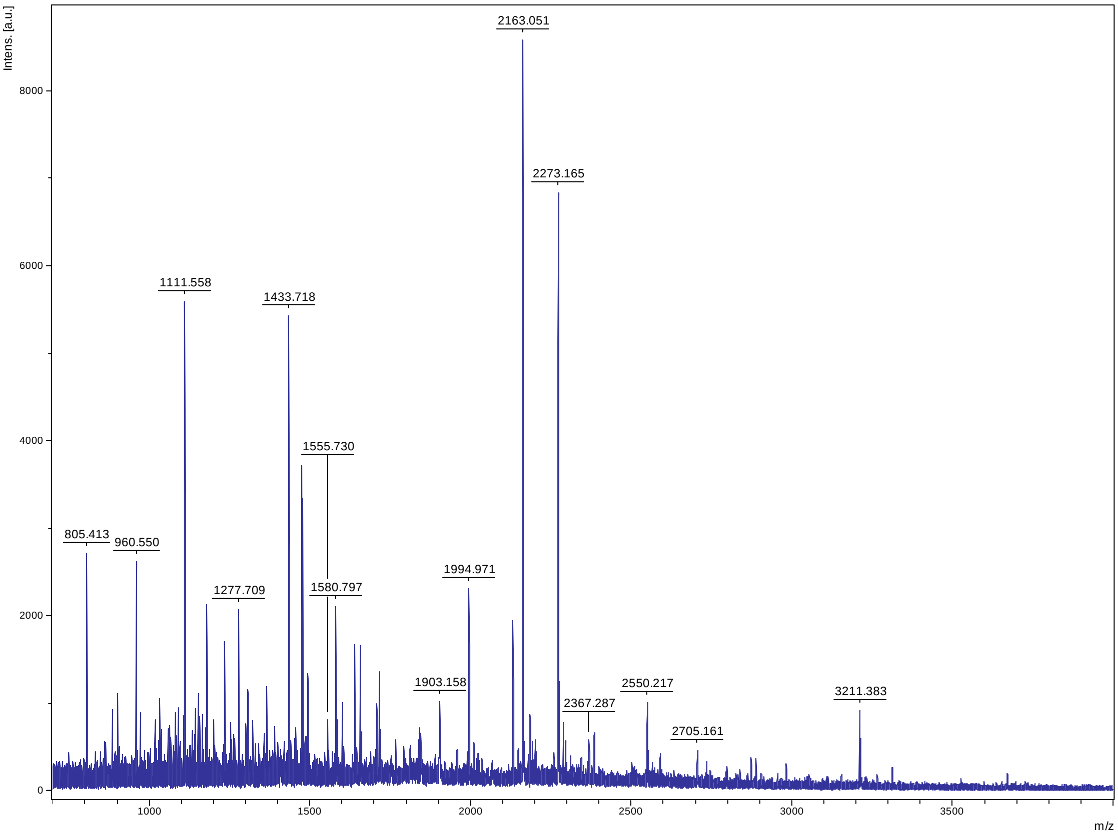


Match to: gi|51535721 Score: 82 Expect: 0.00043

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
40 - 49	1165.5744	1164.5671	1164.6549	-0.0878	1	R.GRIAVMPHLR.A	Oxidation (M)
106 - 122	1835.9920	1834.9847	1834.9651	0.0196	0	K.VVLFAVPGAFTPTCTQK.H	Carbamidomethyl (C)
138 - 154	1809.8923	1808.8850	1808.8549	0.0302	0	K.GVDAVACVSVNDAFVMR.A	Carbamidomethyl (C)
155 - 178	2528.2296	2527.2223	2527.2917	-0.0694	1	R.AWKESLGVGDEVLLLSDGNGELAR.A	
158 - 178	2143.0606	2142.0533	2142.0803	-0.0270	0	K.ESLGVGDEVLLLSDGNGELAR.A	
179 - 196	1827.9956	1826.9883	1826.9559	0.0324	0	R.AMGVELDLSDKPAGLGVR.S	
179 - 196	1843.9786	1842.9713	1842.9509	0.0205	0	R.AMGVELDLSDKPAGLGVR.S	Oxidation (M)
199 - 210	1333.7648	1332.7575	1332.7401	0.0174	1	R.RYALLAEDGVVK.V	
200 - 210	1177.6153	1176.6080	1176.6390	-0.0310	0	R.YALLAEDGVVK.V	
211 - 230	2126.0377	2125.0304	2125.0248	0.0056	0	K.VLNLEEGGAFTTSSAEEMLK.A	

Spot 2351

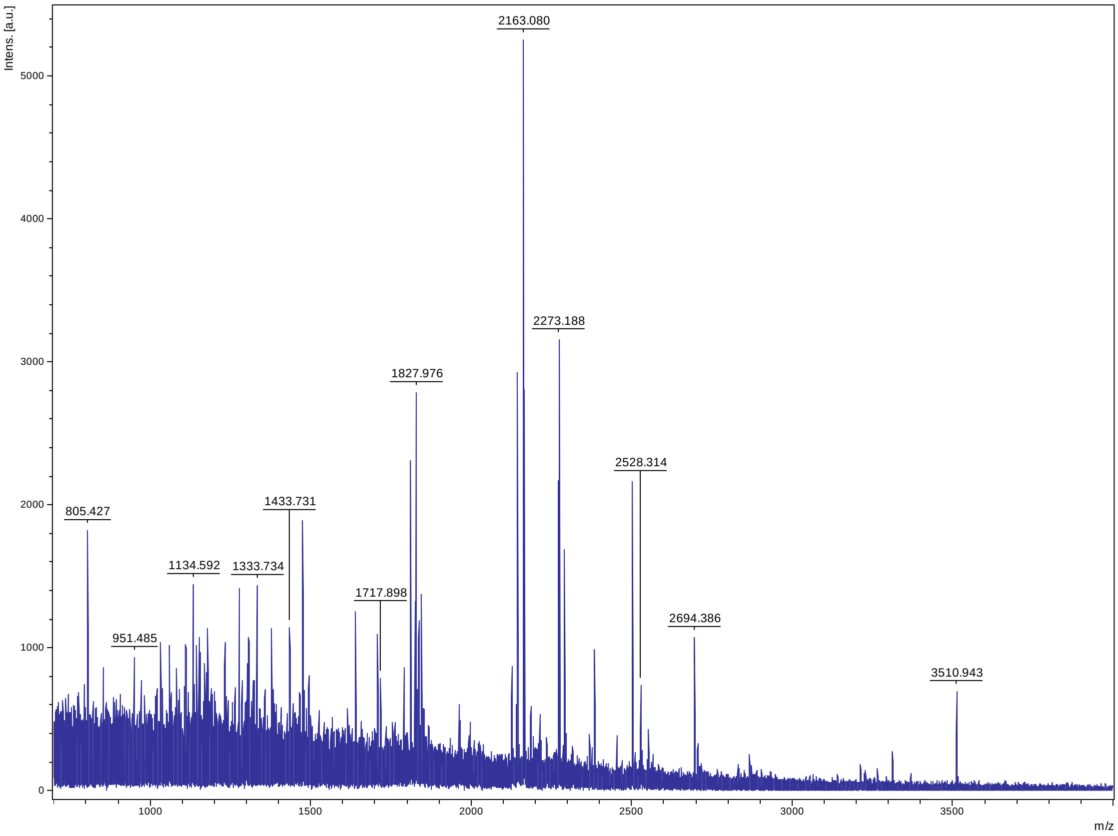


Match to: gi|18539471 Score: 68 Expect: 0.011

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
35 - 56	2131.0178	2130.0105	2130.0817	-0.0712	0	K.IASHIVASAHPVDGDGSVGSVR.Q	
57 - 70	1688.6033	1687.5960	1687.7486	-0.1526	0	R.QFNFTSAMPFSHMK.E	Oxidation (M)
57 - 72	1957.9004	1956.8931	1956.8974	-0.0043	1	R.QFNFTSAMPFSHMKER.L	
71 - 80	1263.6297	1262.6224	1262.6506	-0.0282	1	K.ERLEFLDVDK.C	
73 - 84	1555.6031	1554.5958	1554.7058	-0.1100	1	R.LEFLDVDKCECK.S	2 Carbamidomethyl (C)
85 - 95	1017.6062	1016.5989	1016.5502	0.0488	0	K.STLVEGGGIGK.A	
96 - 117	2179.1047	2178.0974	2178.1644	-0.0669	1	K.AIETATSHIKVEPAANGGSVVK.V	
124 - 136	1440.7300	1439.7227	1439.8235	-0.1008	1	K.LLPGVEVKDEITK.A	
137 - 146	1093.5823	1092.5750	1092.6179	-0.0428	1	K.AKESLTGIFK.T	

Spot 2354

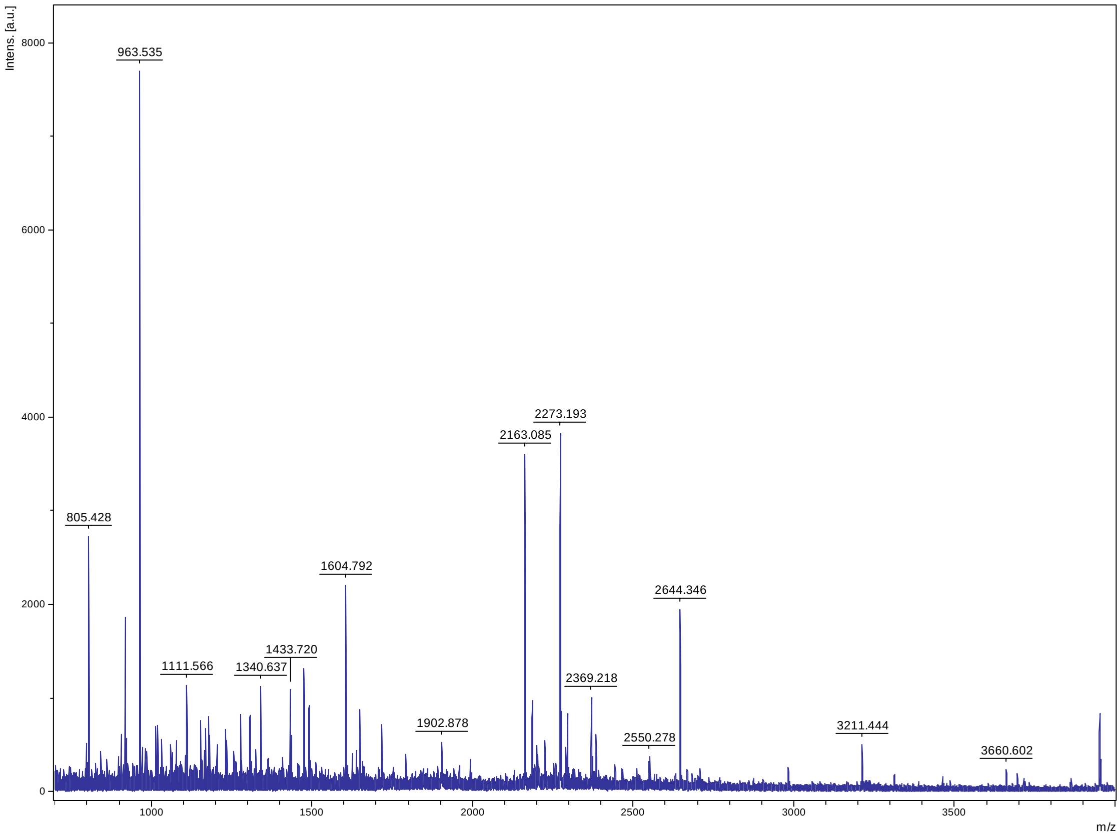


Match to: gi|51535721; Score: 102

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
106 - 122	1835.98	1834.98	1834.97	0.01	0	VVLFAVPGAFTPTCTQK
123 - 130	854.47	853.47	853.48	-0.01	0	HVPGFVAK
138 - 154	1809.89	1808.89	1808.85	0.03	0	GVDAVACVSVNDAFVMR
138 - 154	1825.87	1824.87	1824.85	0.02	0	GVDAVACVSVNDAFVMR Oxidation (M)
155 - 178	2528.31	2527.31	2527.29	0.02	1	AWKESLGVGDEVLLLSDGNGELAR
158 - 178	2143.10	2142.10	2142.08	0.02	0	ESLGVGDEVLLLSDGNGELAR
179 - 196	1827.98	1826.97	1826.96	0.02	0	AMGVELDLSDKPAGLGVR
179 - 196	1843.97	1842.97	1842.95	0.02	0	AMGVELDLSDKPAGLGVR Oxidation (M)
199 - 210	1333.73	1332.73	1332.74	-0.01	1	RYALLAEDGVVK
211 - 230	2126.04	2125.04	2125.02	0.02	0	VLNLEEGGAFTTSSAEEMLK

Spot 2355

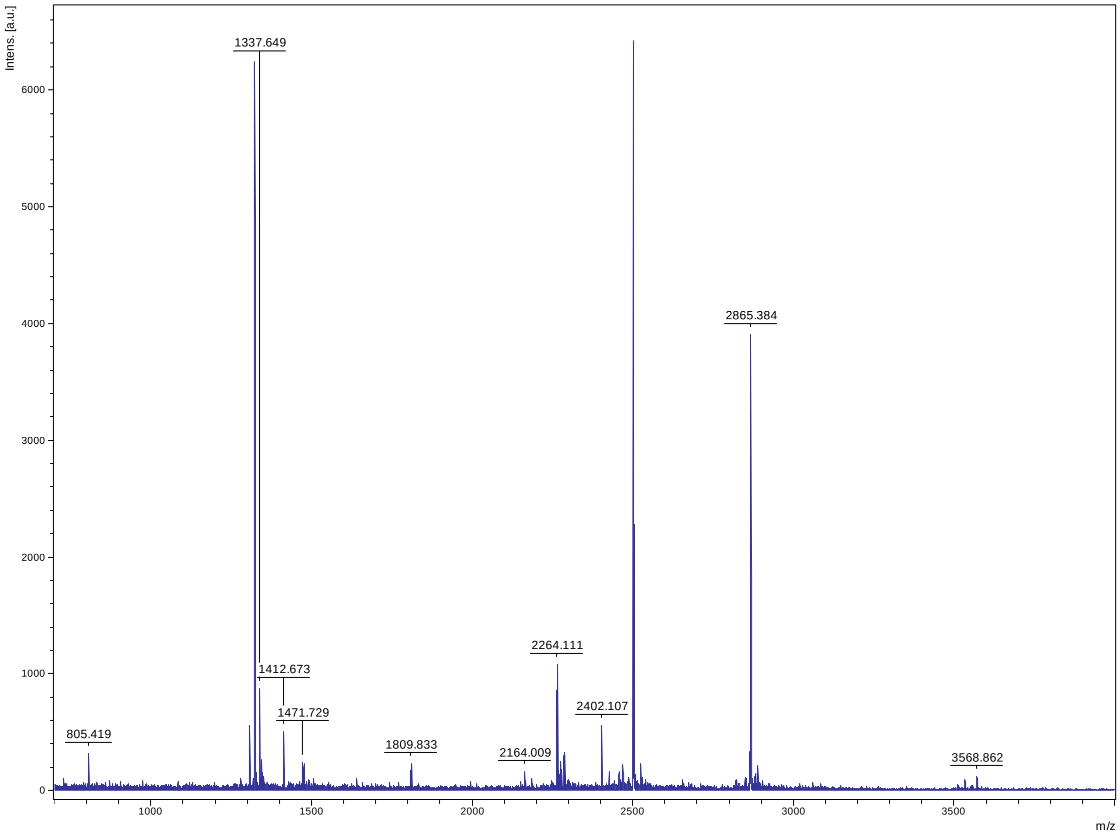


Match to: gi|50251353 Score: 83 Expect: 0.00031

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
39 - 49	1111.5617	1110.5544	1110.6298	-0.0754	0	R.AIPVGAPHPPR.V	
129 - 162	3950.6663	3949.6590	3949.8038	-0.1448	1	K.YKDQGFEILAFPCNQFGGQEPGTNEEIVQFACTR.F	2 Carbamidomethyl (C)
131 - 162	3659.4581	3658.4508	3658.6456	-0.1947	0	K.DQGFEILAFPCNQFGGQEPGTNEEIVQFACTR.F	2 Carbamidomethyl (C)
165 - 185	2369.2037	2368.1964	2368.1586	0.0378	1	K.AEYPIFDKVDVNGDNTAPIYK.F	
192 - 200	920.4437	919.4364	919.4763	-0.0398	0	K.GGLFGDNIK.W	
206 - 213	963.4911	962.4838	962.5185	-0.0347	1	K.FLVDKEGR.V	
218 - 229	1340.6457	1339.6384	1339.6329	0.0055	0	R.YAPTTSPLSMEK.D	Oxidation (M)

Spot 2361

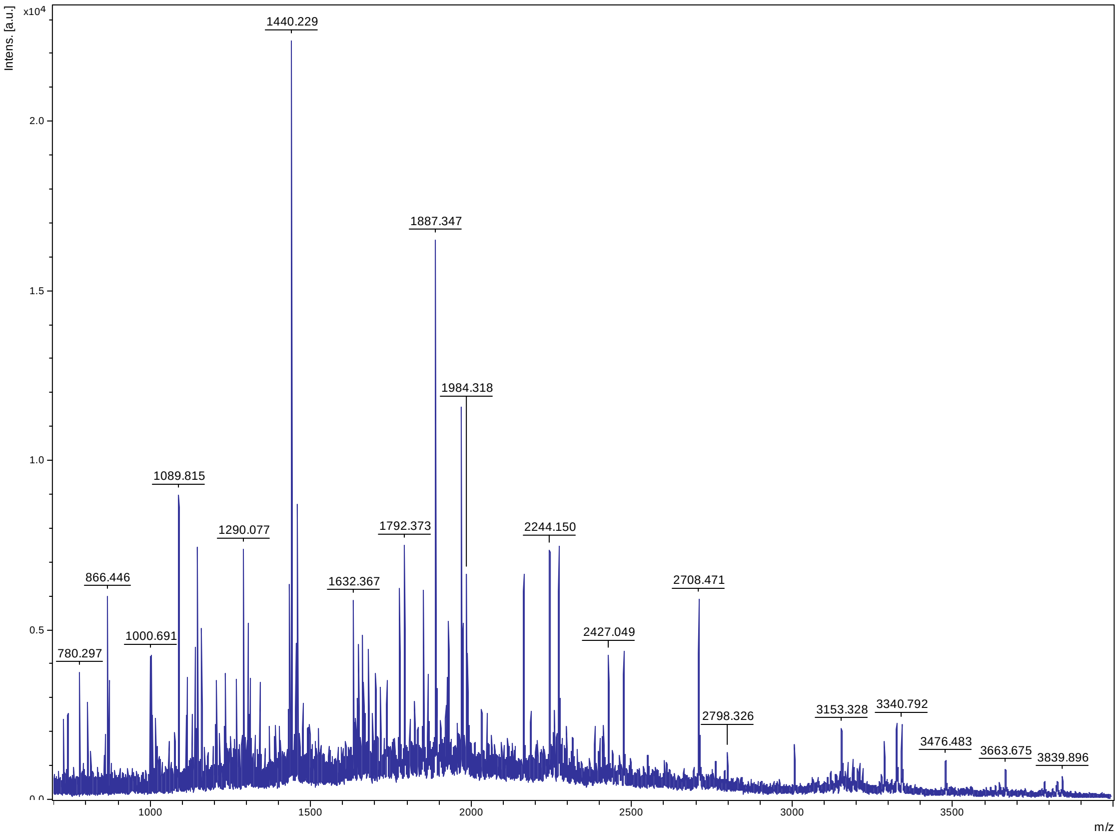


Match to: gi|50948527; Score: 89

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
129 - 151	2264.11	2263.11	2263.14	-0.04	0	HAGDLGNIVANAEGVAEATIVDK
129 - 164	3568.86	3567.86	3567.86	-0.00	1	HAGDLGNIVANAEGVAEATIVDKQIPLSGPNSVVGR
152 - 164	1306.70	1305.69	1305.70	-0.01	0	QIPLSGPNSVVGR Pyro-glu (N-term Q)
165 - 177	1471.73	1470.73	1470.74	-0.01	0	AFVVHELEDDLGK
165 - 192	2865.38	2864.38	2864.41	-0.02	1	AFVVHELEDDLGKGGHELSLSTGNAGGR
178 - 192	1412.67	1411.67	1411.68	-0.01	0	GGHELSLSTGNAGGR

Spot 2364

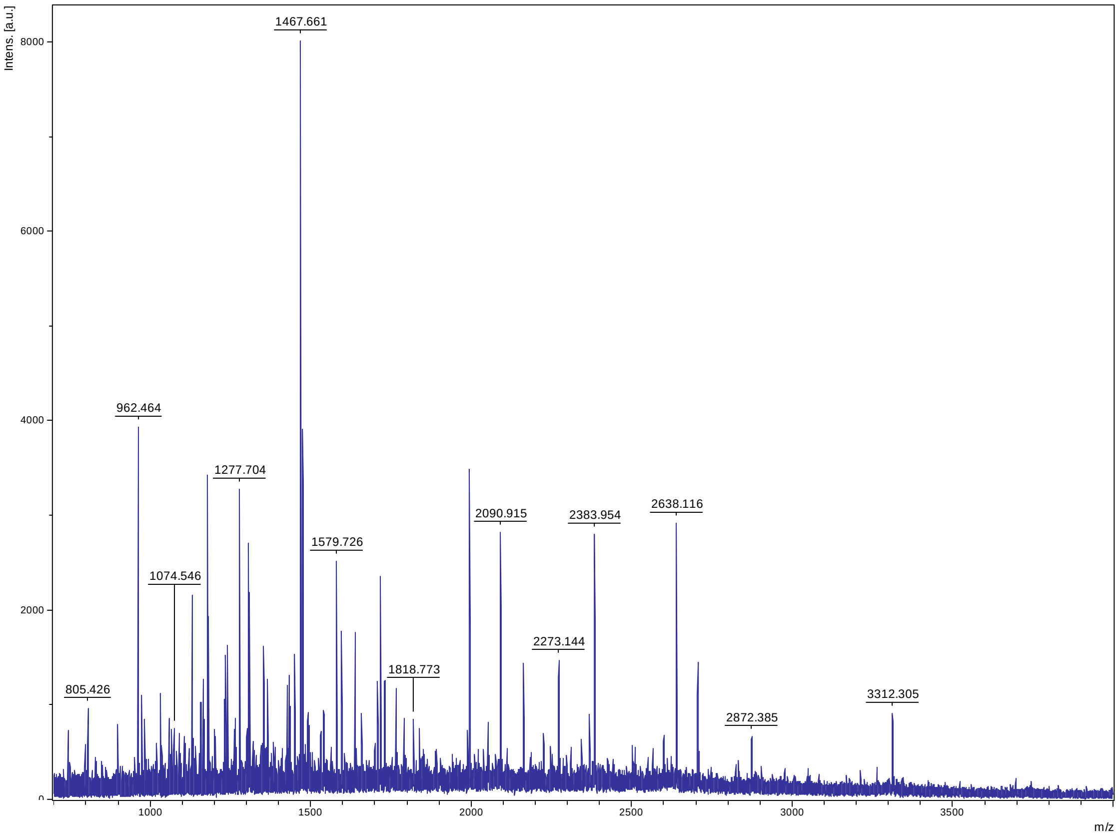


Match to: gi|51090590 Score: 100 Expect: 6.9e-06

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 32	3175.2464	3174.2391	3174.3969	-0.1577	0	M.SSPPPAAAAAMAVDDADDDQLASMSTEDIVR.A	Acetyl (N-term); Oxidation (M)
2 - 32	3191.2760	3190.2687	3190.3918	-0.1230	0	M.SSPPPAAAAAMAVDDADDDQLASMSTEDIVR.A	Acetyl (N-term); 2 Oxidation (M)
43 - 50	1000.5053	999.4980	999.5713	-0.0732	1	R.VLKDELQR.T	
120 - 134	1668.9603	1667.9530	1667.9498	0.0033	0	R.QTIFLPVIGLVDPEK.L	
135 - 145	1139.6502	1138.6429	1138.6709	-0.0280	0	K.LKPGDLVGVNK.D	
135 - 161	3007.5081	3006.5008	3006.5549	-0.0541	1	K.LKPGDLVGVNKDSYLILDTLPSEYDSR.V	
146 - 161	1886.8980	1885.8907	1885.8945	-0.0038	0	K.DSYLILDTLPSEYDSR.V	
184 - 199	1831.9275	1830.9202	1830.9913	-0.0711	0	K.QIQELVEAIVLPMTHK.D	Pyro-glu (N-term Q)
184 - 199	1848.9776	1847.9703	1848.0179	-0.0475	0	K.QIQELVEAIVLPMTHK.D	
184 - 199	1864.9932	1863.9859	1864.0128	-0.0268	0	K.QIQELVEAIVLPMTHK.D	Oxidation (M)
184 - 201	2136.1137	2135.1064	2135.1408	-0.0344	1	K.QIQELVEAIVLPMTHKDR.F	Oxidation (M)
205 - 223	1919.9654	1918.9581	1919.1356	-0.1774	1	K.LGIRPPKGVLLYGPPGTGK.T	
212 - 223	1158.6166	1157.6093	1157.6444	-0.0351	0	K.GVLLYGPPGTGK.T	
241 - 256	1660.8513	1659.8440	1659.8654	-0.0213	0	K.LAGPQLVQMFIGDGAK.L	Oxidation (M)
241 - 259	2055.0821	2054.0748	2054.1346	-0.0597	1	K.LAGPQLVQMFIGDGAKLVR.D	Acetyl (N-term)
267 - 284	2049.0387	2048.0314	2048.0499	-0.0185	1	K.EKSPCIIFIDEIDAIGTK.R	Carbamidomethyl (C)
299 - 315	1967.9360	1966.9287	1966.9306	-0.0018	0	R.TMLELLNQLDGFSSDER.I	
299 - 315	1983.9308	1982.9235	1982.9255	-0.0020	0	R.TMLELLNQLDGFSSDER.I	Oxidation (M)
325 - 334	1114.5506	1113.5433	1113.5852	-0.0419	0	R.ADILDPALMR.S	
325 - 334	1130.5777	1129.5704	1129.5801	-0.0097	0	R.ADILDPALMR.S	Oxidation (M)
341 - 352	1439.7230	1438.7157	1438.7204	-0.0047	1	R.KIEFPHPSEEAR.A	
342 - 352	1311.6133	1310.6060	1310.6255	-0.0194	0	K.IEFPHPSEEAR.A	
362 - 376	1775.8774	1774.8701	1774.8671	0.0030	1	R.KMNVNPDVNFEELAR.S	
377 - 387	1195.5654	1194.5581	1194.5517	0.0065	0	R.STDDFNGAQLK.A	
377 - 399	2409.1457	2408.1384	2408.1827	-0.0443	1	R.STDDFNGAQLKAVCVEAGMLALR.R	
388 - 399	1289.6446	1288.6373	1288.6631	-0.0258	0	K.AVCVEAGMLALR.R	Carbamidomethyl (C)
388 - 399	1305.6668	1304.6595	1304.6580	0.0015	0	K.AVCVEAGMLALR.R	Carbamidomethyl (C); Oxidation (M)
400 - 420	2400.1127	2399.1054	2399.1716	-0.0662	1	R.RDATEVTHEDFNEGIIQVQAK.K	
401 - 420	2244.0479	2243.0406	2243.0705	-0.0299	0	R.DATEVTHEDFNEGIIQVQAK.K	

Spot 2367

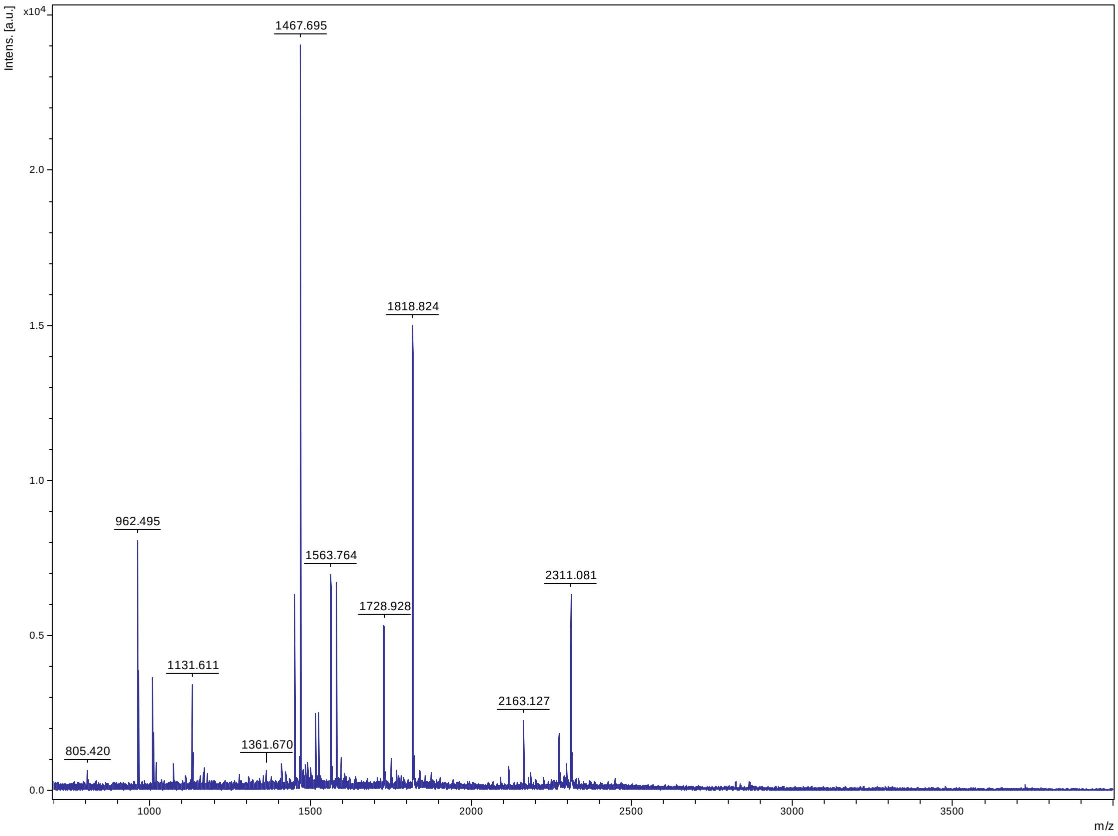


Match to: gi|50881454 Score: 69 Expect: 0.009

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 9	962.4064	961.3991	961.4505	-0.0513	0	M.AAPDVEYR.C	Acetyl (N-term)
10 - 22	1467.6794	1466.6721	1466.6612	0.0109	0	R.CFVGGLAWATDDR.S	Carbamidomethyl (C)
23 - 38	1730.8578	1729.8505	1729.8410	0.0095	0	R.SLEAAFSTYGEILDSK.I	
39 - 47	1073.5377	1072.5304	1072.5625	-0.0321	1	K.IINDRETGR.S	
50 - 63	1579.7414	1578.7341	1578.7136	0.0205	0	R.GFGFVTFSSEQSMR.D	
50 - 63	1595.7362	1594.7289	1594.7085	0.0204	0	R.GFGFVTFSSEQSMR.D	Oxidation (M)
78 - 87	1131.5708	1130.5635	1130.5680	-0.0044	0	R.NITVNEAQSR.R	
149 - 161	1239.4954	1238.4881	1238.5064	-0.0183	0	R.GGGYGGDSGGNWR.N	
149 - 162	1353.5745	1352.5672	1352.5493	0.0179	1	R.GGGYGGDSGGNWRN.-	

Spot 2368

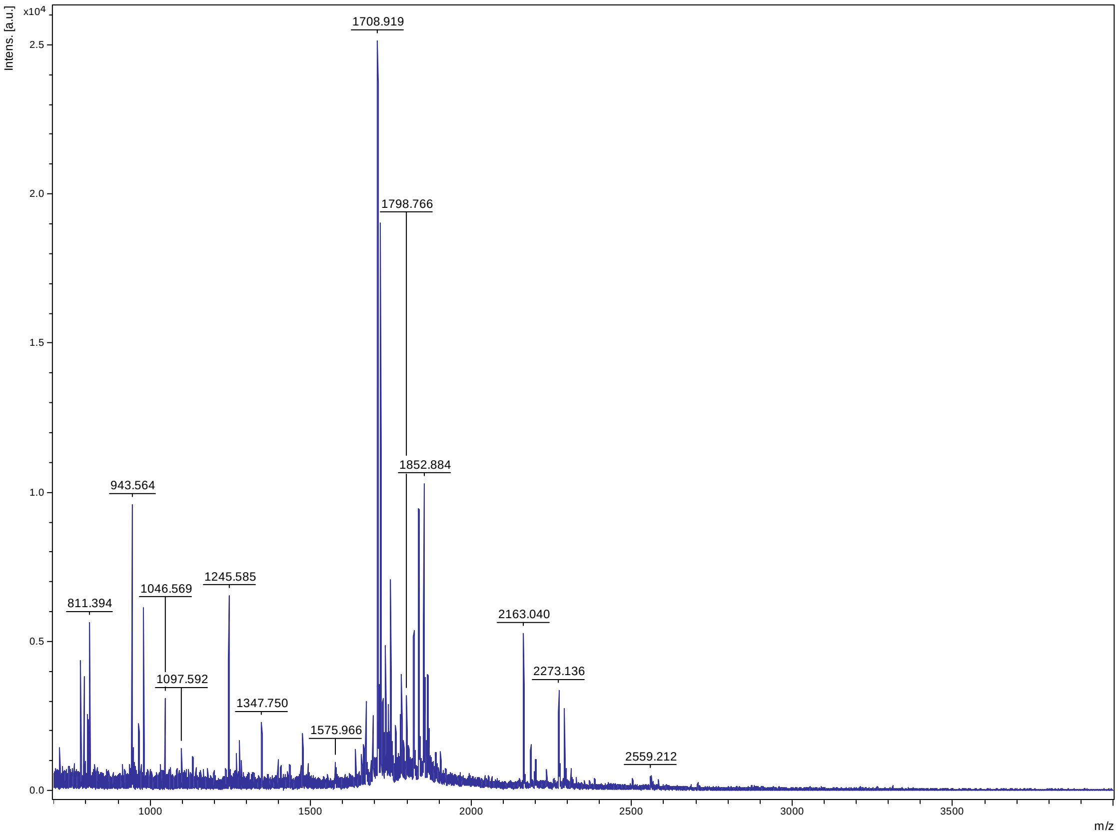


Match to: gi|2624326 Score: 67 Expect: 0.013

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
2 - 9	962.4329	961.4256	961.4505	-0.0248	0	M.AAPDVEYR.C	Acetyl (N-term)
10 - 22	1410.6620	1409.6547	1409.6397	0.0150	0	R.CFVGGLAWATDDR.S	
10 - 22	1467.6733	1466.6660	1466.6612	0.0048	0	R.CFVGGLAWATDDR.S	Carbamidomethyl (C)
23 - 38	1728.8917	1727.8844	1727.8617	0.0227	0	R.SLEAAFSTFGEILESK.I	
39 - 47	1073.5478	1072.5405	1072.5625	-0.0220	1	K.IINDRETGR.S	
50 - 63	1563.7430	1562.7357	1562.7187	0.0170	0	R.GFGFVTFSSEQAMR.D	
50 - 63	1579.7344	1578.7271	1578.7136	0.0135	0	R.GFGFVTFSSEQAMR.D	Oxidation (M)
78 - 87	1131.5845	1130.5772	1130.5680	0.0093	0	R.NITVNEAQSR.R	
88 - 100	1165.5567	1164.5494	1164.5383	0.0111	1	R.RSGGGGGGGYGQR.G	
89 - 100	1009.4170	1008.4097	1008.4372	-0.0275	0	R.SGGGGGGGYGQR.G	
89 - 123	2824.0961	2823.0888	2823.1727	-0.0839	1	R.SGGGGGGGYGQRGGGGGYGGGGGYGGGGGGGYASR.E	Acetyl (N-term)
150 - 159	1019.4186	1018.4113	1018.4216	-0.0103	0	R.GGGNSDGNWR.N	

Spot 2373

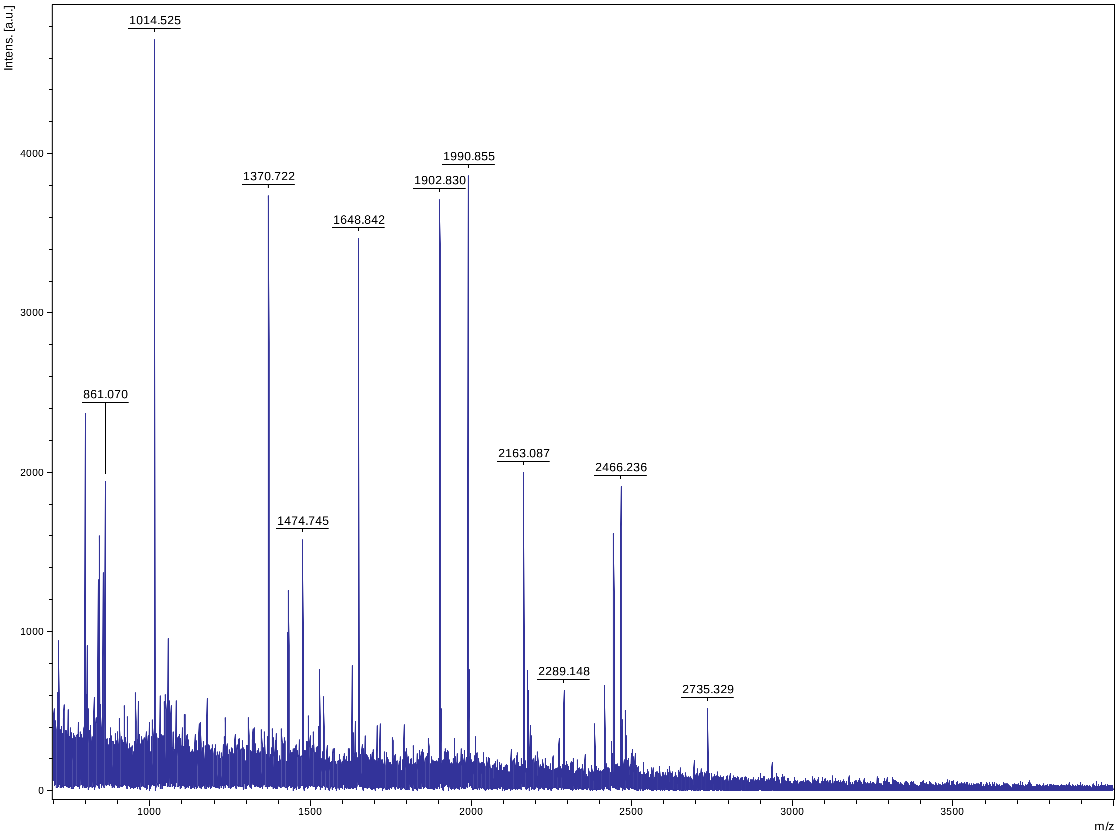


Match to: gi|50096951; Score: 73

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
16 - 24	943.56	942.56	942.55	0.01	0	GLIGDIISR
16 - 27	1347.75	1346.75	1346.76	-0.01	1	GLIGDIISRFEK
37 - 42	811.39	810.39	810.37	0.02	0	FMNVER Oxidation (M)
86 - 102	1865.05	1864.05	1864.04	0.00	1	RIIGATRPWEAAPGTIR
87 - 102	1708.92	1707.92	1707.94	-0.03	0	IIGATRPWEAAPGTIR
103 - 111	979.49	978.49	978.48	0.01	0	ADYAVEVGR
140 - 149	1245.59	1244.58	1244.58	0.00	0	SNLHPWIYES

Spot 2379

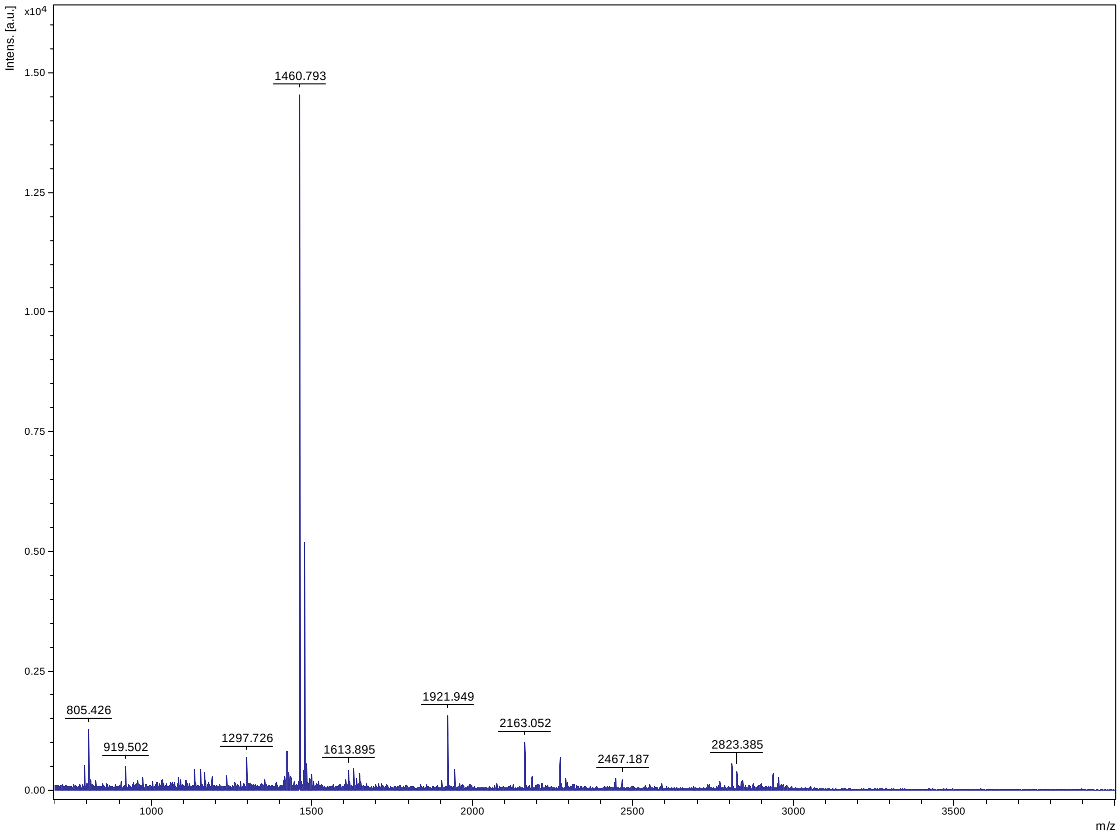


Match to: gi|37535166; Score: 178

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
43 - 49	843.56	842.55	842.52	0.03	0	TILELVR
50 - 64	1902.83	1901.83	1901.78	0.05	0	SYDGDHICYDHFAFR
65 - 74	1056.55	1055.55	1055.53	0.02	0	TFGVDGYGIK
75 - 88	1648.84	1647.84	1647.79	0.05	0	SLAEFFTDFGYVPR
75 - 92	2176.11	2175.11	2175.06	0.04	1	SLAEFFTDFGYVPREELR
98 - 122	2735.33	2734.33	2734.39	-0.06	1	LRALWFSPPTNDGYTGTGVYGPLPR
100 - 122	2466.24	2465.23	2465.20	0.03	0	ALWFSPPTNDGYTGTGVYGPLPR
123 - 143	2415.32	2414.32	2414.29	0.02	0	IFISELLVDELSPQSQDIIQK
217 - 224	955.49	954.49	954.44	0.05	0	FVEDNGFK
265 - 272	1014.52	1013.52	1013.48	0.04	0	SYIEFAER
280 - 291	1474.74	1473.74	1473.66	0.08	0	DLPNDEVNEHHR
280 - 292	1630.80	1629.80	1629.76	0.03	1	DLPNDEVNEHHRR
293 - 314	2443.18	2442.18	2442.13	0.05	1	DGFEVGNADKIFESTSNDQLTR

Spot 2381

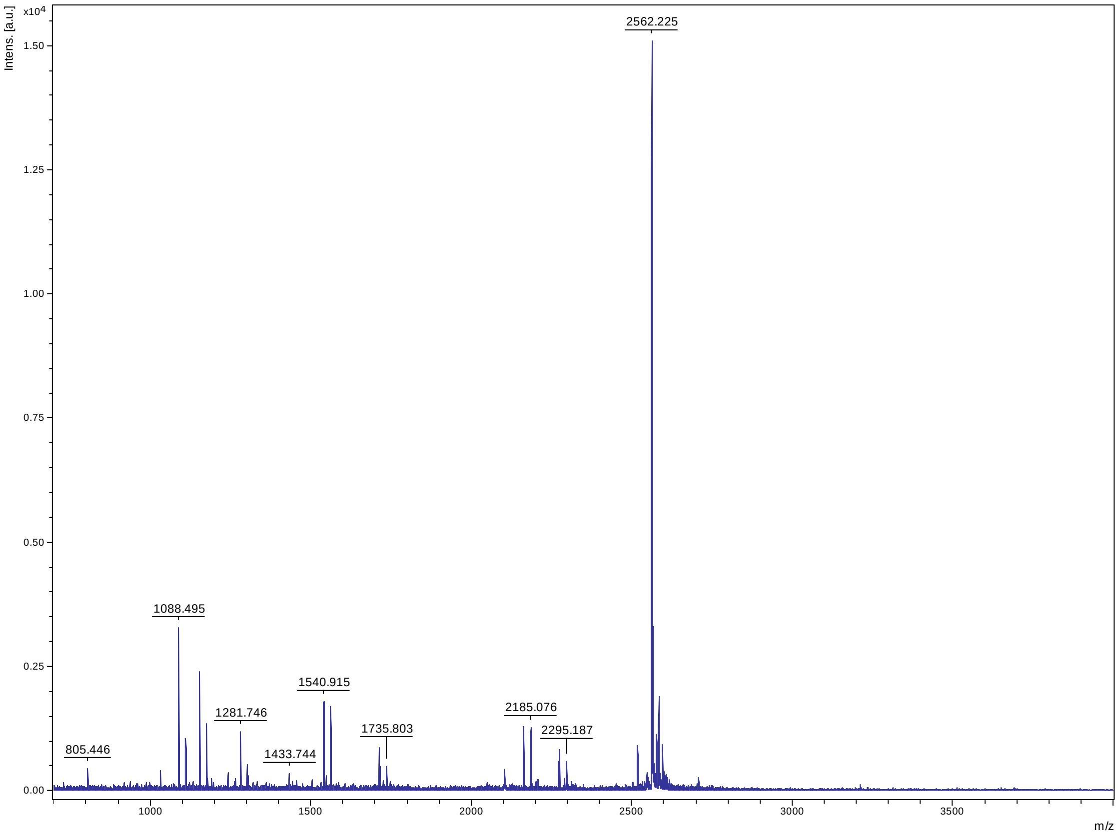


Match to: gi|55775452; Score: 77

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
53 - 71	1921.95	1920.95	1920.95	0.00	0	DFDEPGSLAPTGLFLGGTK
72 - 84	1460.79	1459.79	1459.79	0.00	0	YMVIQGEPGVVIR
72 - 84	1476.79	1475.79	1475.78	0.01	0	YMVIQGEPGVVIR Oxidation (M)
88 - 96	919.50	918.50	918.50	0.00	1	GTGGICVKK
96 - 121	2935.47	2934.47	2934.47	-0.00	1	KTGLSLILGIYDEPMTPGQCNMIVER
96 - 121	2951.44	2950.43	2950.46	-0.03	1	KTGLSLILGIYDEPMTPGQCNMIVER Oxidation (M)
97 - 121	2823.39	2822.38	2822.37	0.02	0	TGLSLILGIYDEPMTPGQCNMIVER Oxidation (M)
122 - 131	1167.51	1166.51	1166.53	-0.02	0	LGDYLIEQGC

Spot 2384

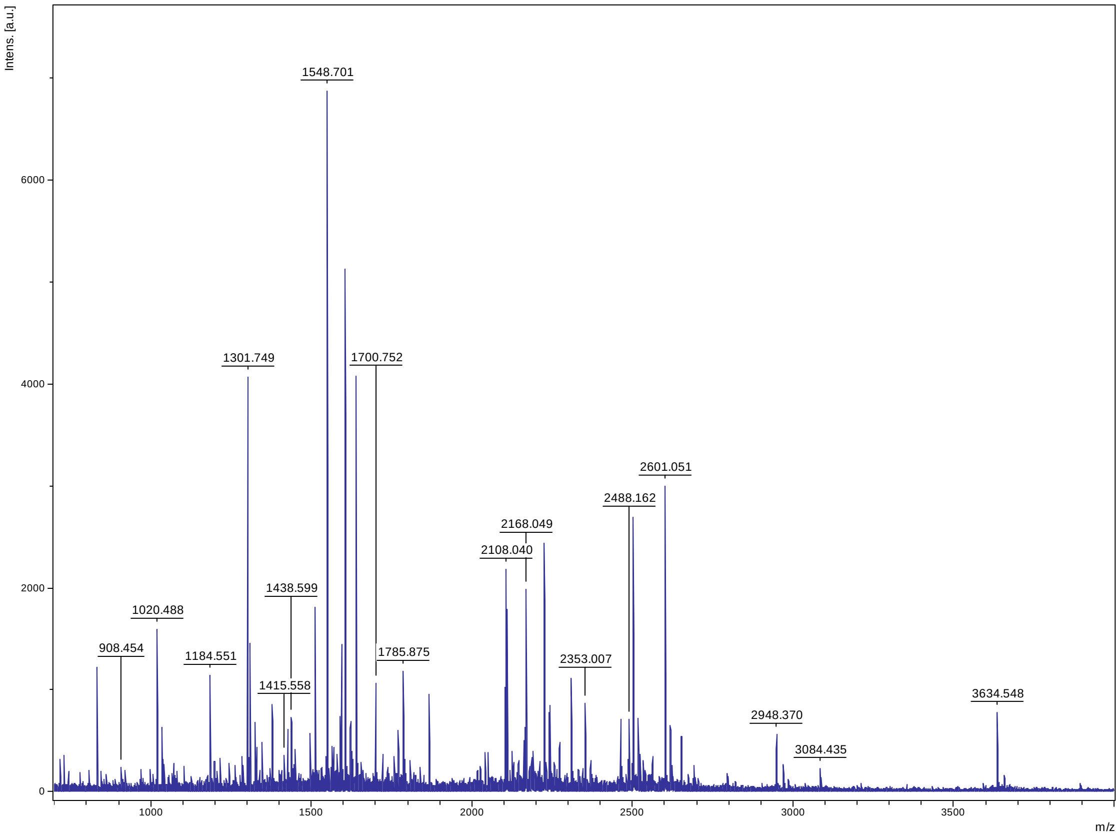


Match to: gi|55584168 Score: 85

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
6 - 20	1548.8784	1547.8711	1547.8558	0.0153	1	K.AKETVASAPVVVYSK.S	
21 - 28	1031.4713	1030.4640	1030.4364	0.0276	0	K.SYCPFCVR.V	Carbamidomethyl (C)
21 - 28	1088.4950	1087.4877	1087.4579	0.0298	0	K.SYCPFCVR.V	2 Carbamidomethyl (C)
31 - 41	1281.7460	1280.7387	1280.7128	0.0259	1	K.KLFEQLGATFK.A	
32 - 41	1153.6469	1152.6396	1152.6179	0.0217	0	K.LFEQLGATFK.A	
42 - 65	2562.2251	2561.2178	2561.1881	0.0297	0	K.AIELDGESDGSELQSALAEWTGQR.T	
92 - 107	1540.9153	1539.9080	1539.8871	0.0209	0	K.LVPLLTEAGAIASSAK.T	

Spot 2461

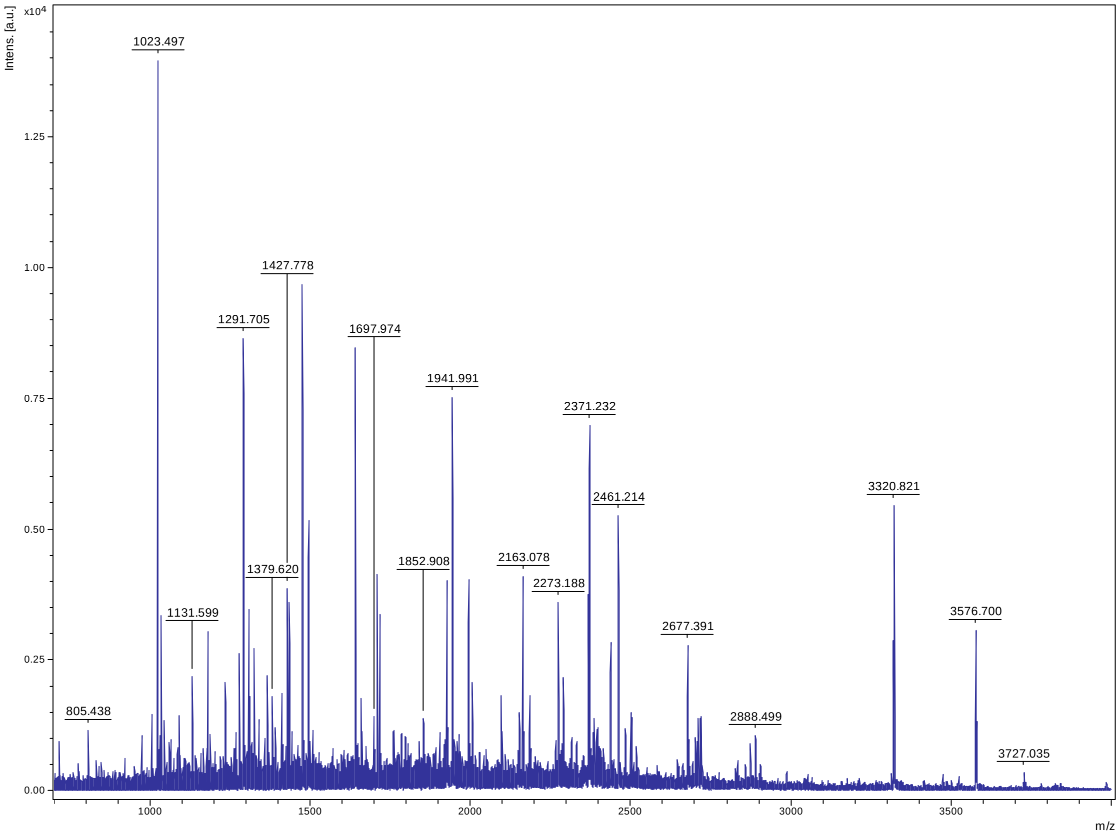


Match to: gi|13195430 Score: 321

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
37 - 54	2106.9888	2105.9815	2106.0323	-0.0508	0	K.HHAEFTPVFSPEHFSPLK.A	
62 - 80	2353.0066	2351.9993	2352.0732	-0.0739	0	K.SVLDTLIMNWNATYDYYDR.T	
85 - 97	1588.7003	1587.6930	1587.7391	-0.0461	0	K.QAYYLSMEFLQGR.A	Pyro-glu (N-term Q)
85 - 97	1605.7289	1604.7216	1604.7657	-0.0440	0	K.QAYYLSMEFLQGR.A	
85 - 97	1621.7211	1620.7138	1620.7606	-0.0468	0	K.QAYYLSMEFLQGR.A	Oxidation (M)
143 - 164	2488.1619	2487.1546	2487.2256	-0.0710	0	R.LASCFLDSLATLNYPAWGYGLR.Y	Carbamidomethyl (C)
172 - 197	3084.4348	3083.4275	3083.5021	-0.0746	1	K.QIITKDGQEEVAENWLEMGNPWEIVR.T	
177 - 197	2517.0654	2516.0582	2516.1277	-0.0696	0	K.DGQEEVAENWLEMGNPWEIVR.T	Oxidation (M)
198 - 205	908.4542	907.4469	907.4651	-0.0182	0	R.TDVSYPVK.F	
218 - 227	1184.5507	1183.5434	1183.5808	-0.0374	0	R.MHWIGGENIK.V	
218 - 227	1200.5476	1199.5403	1199.5757	-0.0354	0	R.MHWIGGENIK.V	Oxidation (M)
228 - 239	1308.7019	1307.6946	1307.7237	-0.0291	0	K.VVAHDIPIPGYK.T	
299 - 316	2108.0400	2107.0328	2107.1095	-0.0768	1	R.LKQQYTLCSASLQDIIAR.F	Carbamidomethyl (C)
301 - 316	1866.8832	1865.8759	1865.9305	-0.0546	0	K.QQYTLCSASLQDIIAR.F	Carbamidomethyl (C)
320 - 333	1594.7045	1593.6972	1593.7423	-0.0451	1	R.RAGDSLSWEDFPSK.V	
321 - 333	1438.5989	1437.5916	1437.6412	-0.0496	0	R.AGDSLSWEDFPSK.V	
334 - 352	2168.0496	2167.0423	2167.0588	-0.0165	0	K.VAVQMNDTHPTLCIPELMR.I	
334 - 352	2241.0095	2240.0022	2240.0752	-0.0729	0	K.VAVQMNDTHPTLCIPELMR.I	Carbamidomethyl (C); Oxidation (M)
388 - 395	1020.4877	1019.4804	1019.5110	-0.0306	0	K.WSLDIMQK.L	
388 - 395	1036.4835	1035.4762	1035.5059	-0.0297	0	K.WSLDIMQK.L	Oxidation (M)
407 - 418	1345.7050	1344.6977	1344.7322	-0.0346	0	K.IDGELMNIIISK.Y	
436 - 448	1426.7238	1425.7165	1425.7715	-0.0550	0	R.ILDNIDLPDSIAK.L	
471 - 481	1215.6161	1214.6088	1214.6394	-0.0306	0	K.SLEPSVVVEEK.T	
583 - 594	1378.6548	1377.6475	1377.6962	-0.0487	0	R.FCNPELSAIISK.W	Carbamidomethyl (C)
595 - 607	1548.7009	1547.6937	1547.7256	-0.0319	0	K.WIGSDDWVLNTDK.L	
595 - 612	2103.0129	2102.0057	2102.0684	-0.0627	1	K.WIGSDDWVLNTDKLAELK.K	
614 - 625	1510.6050	1509.5977	1509.6372	-0.0395	0	K.FADDEDLQSEWR.A	
643 - 658	1769.8175	1768.8102	1768.8705	-0.0603	0	K.TGYIVSPDAMFDVQVK.R	
643 - 658	1785.8749	1784.8676	1784.8654	0.0022	0	K.TGYIVSPDAMFDVQVK.R	Oxidation (M)
666 - 676	1284.7318	1283.7245	1283.7601	-0.0356	0	R.QLLNILGIVYR.Y	Pyro-glu (N-term Q)
666 - 676	1301.7491	1300.7419	1300.7867	-0.0448	0	R.QLLNILGIVYR.Y	
687 - 695	1103.5643	1102.5571	1102.5883	-0.0312	1	K.DRINSFVPR.V	
703 - 711	998.5068	997.4996	997.5232	-0.0237	0	K.AFATYVQAK.R	
795 - 816	2464.1106	2463.1033	2463.1705	-0.0672	0	R.EEVGEENFFLFGAEAHEIAGLR.K	
839 - 862	2601.0510	2600.0437	2600.1124	-0.0687	0	R.SGVFGTYNYDDLMGSLEGNEGYGR.A	
839 - 862	2617.0234	2616.0162	2616.1073	-0.0912	0	R.SGVFGTYNYDDLMGSLEGNEGYGR.A	Oxidation (M)
863 - 881	2309.0015	2307.9942	2308.0721	-0.0779	1	R.ADYFLVGKDFPSYIECQEK.V	Carbamidomethyl (C)
871 - 881	1415.5584	1414.5511	1414.6075	-0.0564	0	K.DFPSYIECQEK.V	Carbamidomethyl (C)
871 - 884	1700.7524	1699.7452	1699.7763	-0.0311	1	K.DFPSYIECQEKVDK.A	

Spot 2477

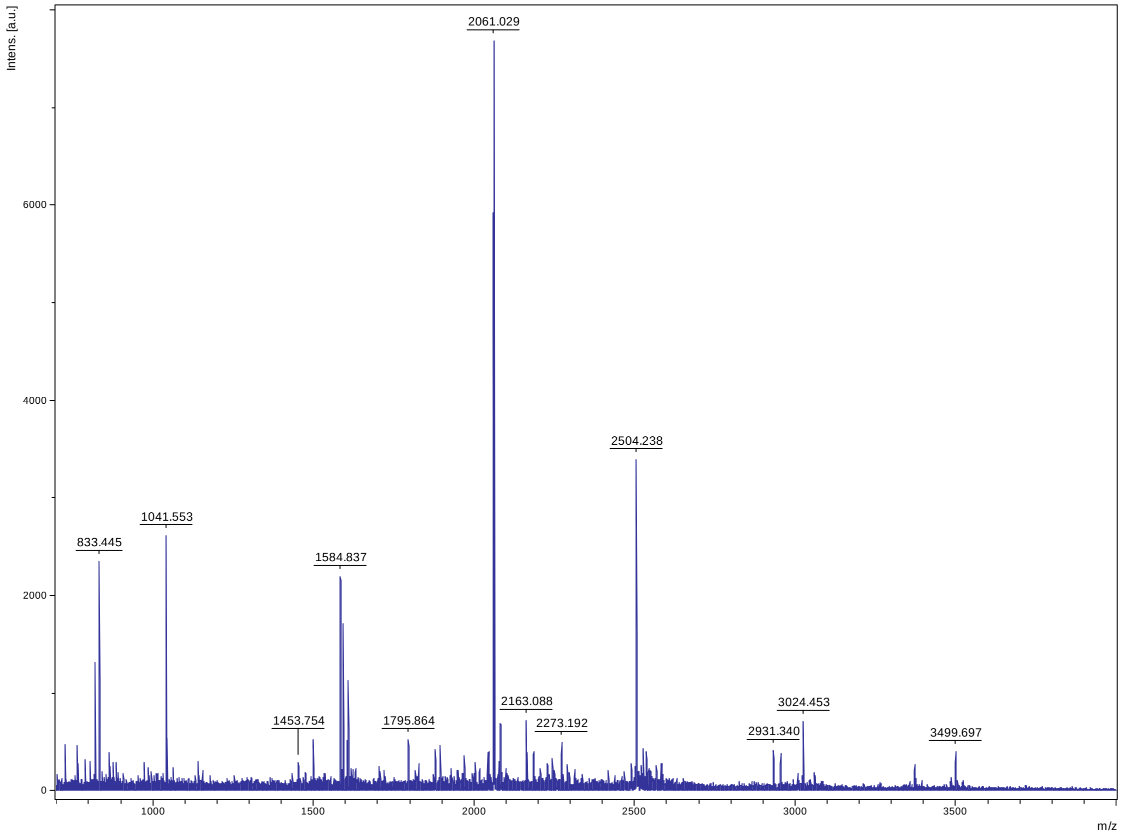


Match to: gi|38344900; Score: 150

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
133 - 143	1131.60	1130.60	1130.59	0.00	0	AIGEVVSTEAR
171 - 184	1441.71	1440.71	1440.71	-0.00	0	GQETPGEDPLLASK
185 - 204	1941.99	1940.99	1940.95	0.04	0	YAVGYVTGLQDAGGGSDALK
211 - 221	1411.63	1410.63	1410.62	0.01	0	HYTAYDVDNWK
211 - 225	1852.91	1851.91	1851.85	0.05	1	HYTAYDVDNWKGVER
226 - 246	2461.21	2460.21	2460.15	0.06	0	YTFDAVVSQQDLDDTFQPPFK
247 - 263	1903.86	1902.86	1902.83	0.03	0	SCVIDGNVASVMCSYNK
320 - 342	2371.23	2370.23	2370.17	0.05	0	SGLDLNCGNFLAQHTVAAVQAGK
343 - 350	920.44	919.44	919.42	0.01	0	LSESDVDR
351 - 361	1291.70	1290.70	1290.71	-0.01	0	AITNNFIVLMR
362 - 370	1023.50	1022.49	1022.48	0.01	0	LGFFDGDPR
371 - 380	1043.61	1042.61	1042.62	-0.01	1	KLPFGSLGPK
381 - 392	1379.62	1378.62	1378.61	0.00	0	DVCTSSNQELAR
525 - 547	2367.29	2366.29	2366.22	0.07	1	GPVILVVMSGGPFDISFAKSSDK Oxidation (M)
579 - 591	1494.77	1493.77	1493.76	0.02	0	LPVTWYPASFADK
599 - 610	1339.62	1338.62	1338.60	0.02	0	MRPDSSTGYPGR Oxidation (M)
599 - 613	1759.92	1758.92	1758.81	0.11	1	MRPDSSTGYPGRTYR Oxidation (M)
614 - 631	2004.96	2003.96	2003.92	0.04	0	FYTGDTVYAFGDGLSYTK

Spot 2483

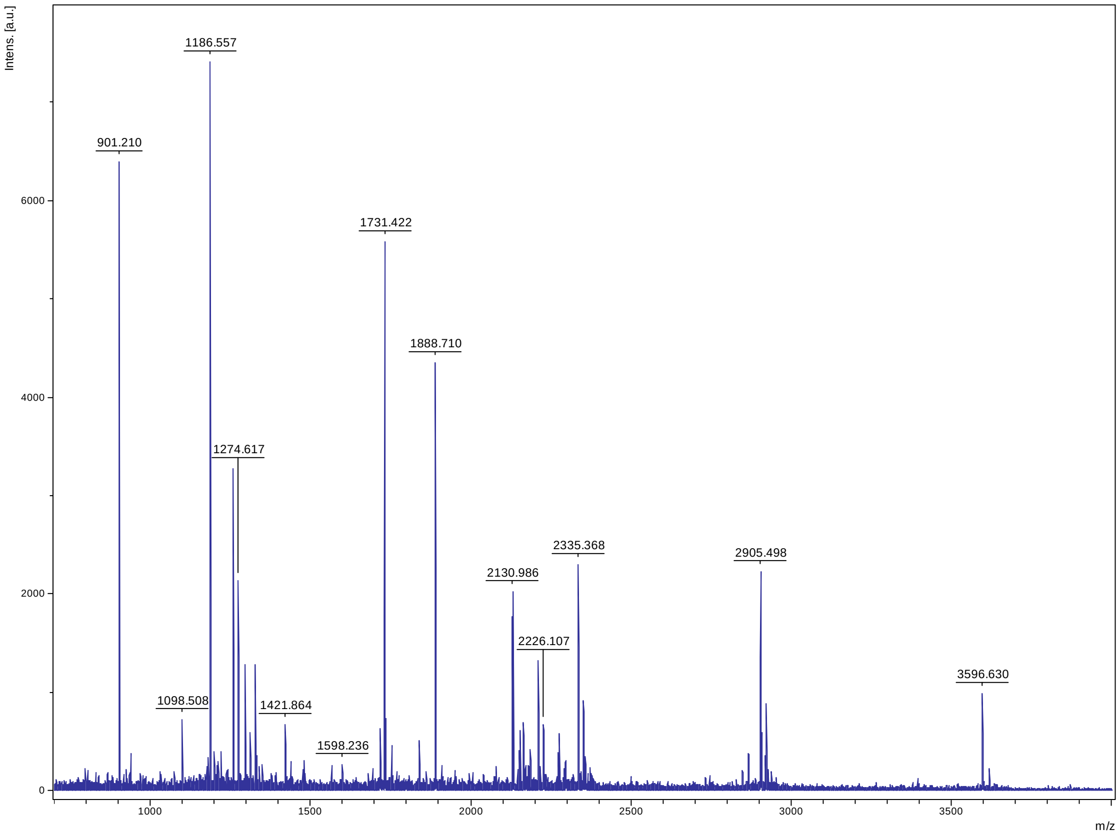


Match to: gi|77554103; Score: 132

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
86 - 104	2045.13	2044.13	2044.14	-0.01	0	VVLAYSGGLDTSVIVPWLR
105 - 130	2931.34	2930.34	2930.29	0.04	0	ENYGCEVVCFTADVGQGDIELEGLEK
144 - 159	2061.03	2060.03	2059.99	0.03	1	DLKEEFVSEYIYPCLR
209 - 221	1584.84	1583.84	1583.82	0.01	0	FELTFYALNPELK
228 - 242	1795.86	1794.86	1794.84	0.02	1	EWDITGREDAIEYAK
338 - 344	876.45	875.45	875.42	0.03	0	IDMVENR
352 - 367	1592.83	1591.83	1591.80	0.03	0	GVYETPGGTIMAAAVR
352 - 367	1608.82	1607.82	1607.80	0.02	0	GVYETPGGTIMAAAVR Oxidation (M)
368 - 382	1878.95	1877.95	1877.92	0.03	1	ELESLTLDRETMQWK
368 - 382	1894.93	1893.93	1893.91	0.02	1	ELESLTLDRETMQWK Oxidation (M)
389 - 397	1041.55	1040.55	1040.53	0.02	0	YAELVYAGR
398 - 403	833.44	832.44	832.42	0.02	0	WFDPLR
444 - 465	2504.24	2503.24	2503.11	0.12	0	EDISSFENGEIYNQADAEGFIR
466 - 472	819.48	818.47	818.46	0.01	0	LYGLPTR

Spot 20d pick

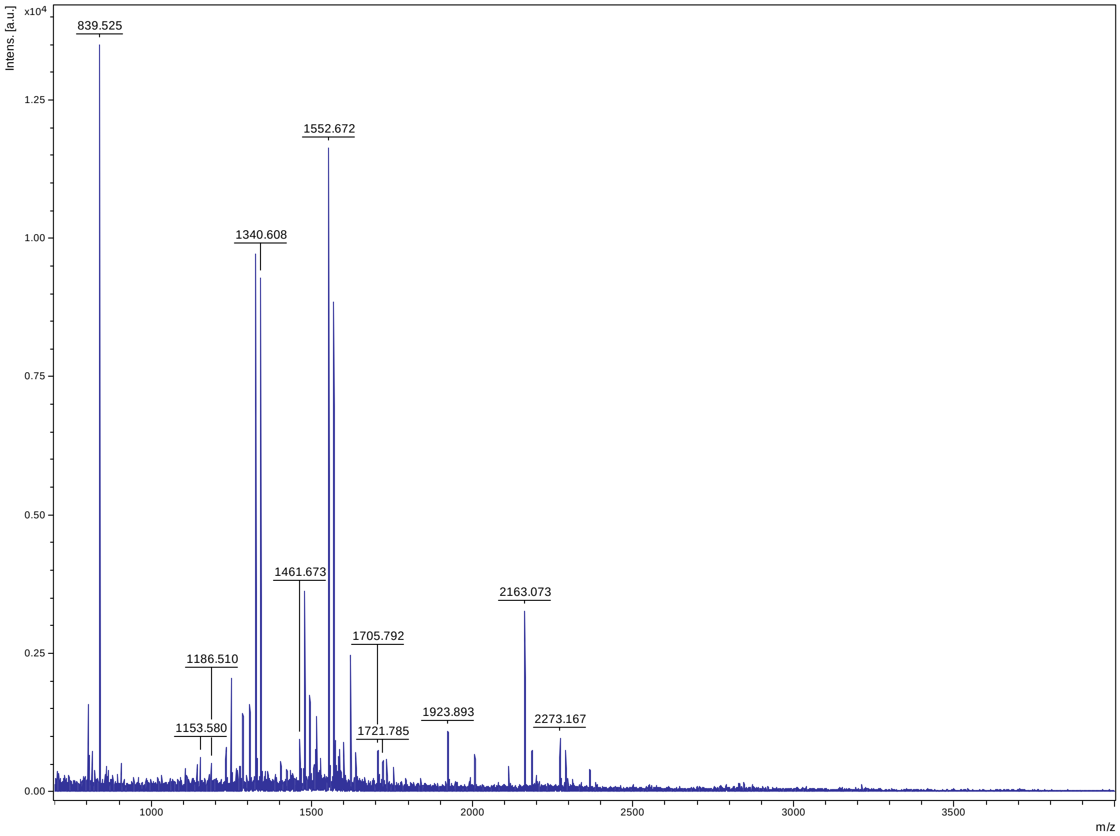


Match to: gi|6979321 Score: 109

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
37 - 55	2357.4236	2356.4163	2356.1925	0.2238	1	R.VKILFTSLCHTDVYFWEAK.G	Carbamidomethyl (C)
56 - 63	901.2103	900.2031	900.4817	-0.2787	0	K.GQTPVFPR.I	
105 - 115	1295.6360	1294.6287	1294.5645	0.0642	0	K.SAESNMCDLLR.I	Carbamidomethyl (C)
105 - 115	1311.6370	1310.6297	1310.5595	0.0702	0	K.SAESNMCDLLR.I	Carbamidomethyl (C); Oxidation (M)
161 - 169	938.2363	937.2290	937.5233	-0.2943	0	K.INPAAPLDK.V	
170 - 191	2130.9858	2129.9786	2130.1540	-0.1754	0	K.VCVLSCGISTGLGATINVAKPK.G	
219 - 228	1098.5083	1097.5010	1097.6193	-0.1182	0	R.IIGIDLNANR.F	
234 - 244	1326.7611	1325.7538	1325.6438	0.1101	1	R.KFGCTEFVNPK.D	Carbamidomethyl (C)
235 - 244	1198.5245	1197.5173	1197.5488	-0.0315	0	K.FGCTEFVNPK.D	Carbamidomethyl (C)
303 - 312	1258.6267	1257.6194	1257.5924	0.0270	0	K.THPMNFLNER.T	
303 - 312	1274.6171	1273.6098	1273.5873	0.0225	0	K.THPMNFLNER.T	Oxidation (M)
316 - 325	1186.5570	1185.5497	1185.5930	-0.0433	0	K.GTFFGNYKPR.T	
326 - 337	1421.8635	1420.8562	1420.7272	0.1291	0	R.TDLPNVVELYMK.K	
326 - 337	1437.9139	1436.9067	1436.7221	0.1846	0	R.TDLPNVVELYMK.K	Oxidation (M)

6d12

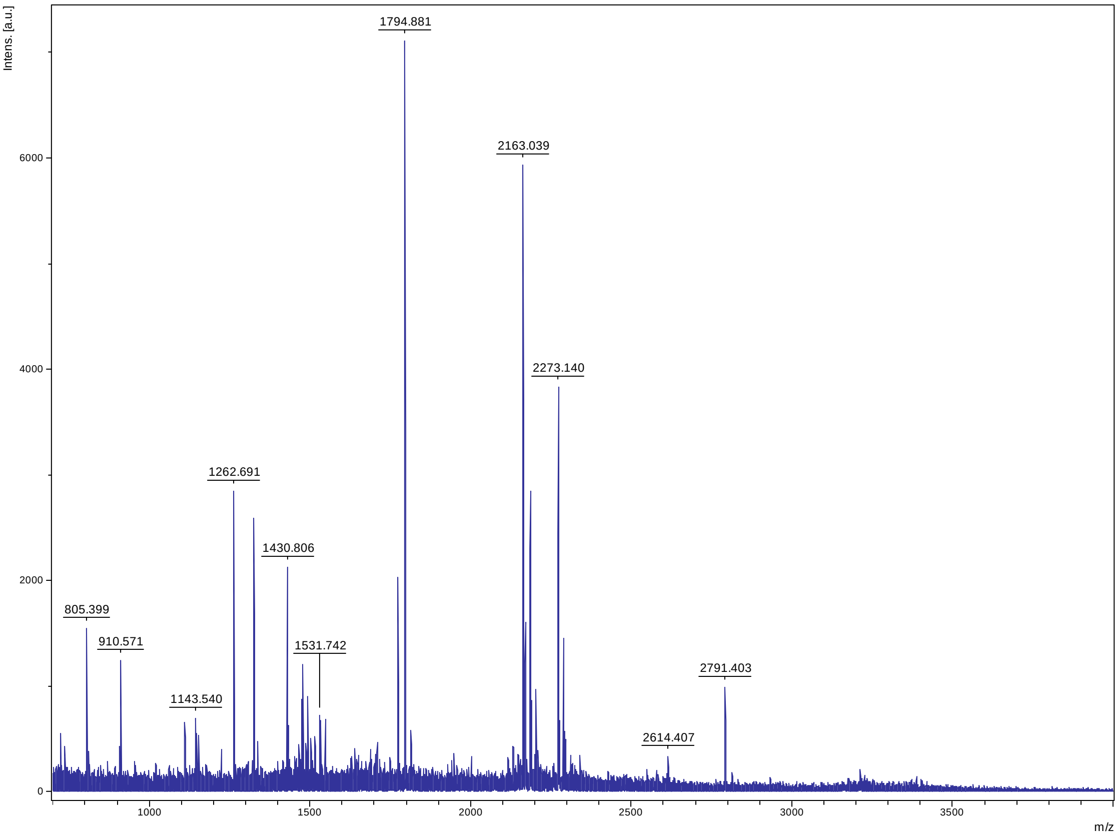


Match to: gi|51964662; Score: 95

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
18 - 39	2366.15	2365.15	2365.12	0.03	0	GFGFITPDDGGEDLFVHQSSLK
45 - 63	1923.89	1922.89	1922.86	0.03	0	SLNDGDVVEFSVGSGNDGR
66 - 89	2112.07	2111.07	2111.04	0.03	0	AVDVTAPGGGALTGGSRPSGGGDR
105 - 118	1186.51	1185.51	1185.48	0.03	0	GYGGGGGGYGGGDR
119 - 135	1329.57	1328.57	1328.55	0.02	0	GYGGGGGYGGGGGGGSR
136 - 148	1568.68	1567.67	1567.63	0.04	1	ACYKCGEEGHMAR
149 - 168	1732.70	1731.70	1731.67	0.03	0	DCSQGGGGGGGYGGGGGGYR
169 - 190	2007.84	2006.83	2006.81	0.03	0	GGGGGGGGGGCYNCGETGHIAR

Spot 6d15

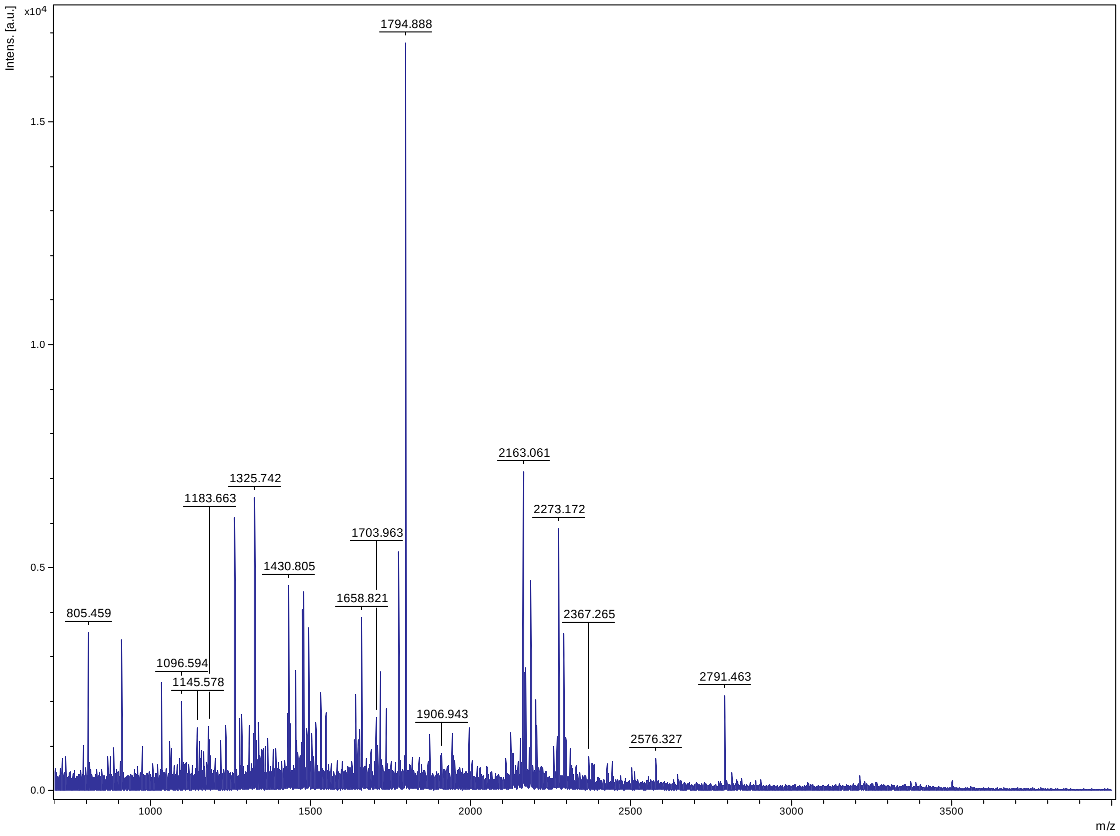


Match to: Q8GVQ3_ORYSA Score: 122 Expect: 4.2e-08

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
57 - 67	1262.6914	1261.6841	1261.7030	-0.0189	1	R.FSPIKESIVSR.E	
136 - 159	2791.4036	2790.3963	2790.4115	-0.0152	0	R.KPAHLFLDELGVAYDEQEDYVVIK.H	
160 - 171	1336.6368	1335.6296	1335.6605	-0.0309	0	K.HAALFTSTVMSR.L	Oxidation (M)
172 - 179	910.5715	909.5642	909.5759	-0.0117	0	R.LLARPNVK.L	
180 - 192	1430.8058	1429.7985	1429.8180	-0.0195	0	K.LFNAVAVEDLIVK.E	
225 - 242	1773.8628	1772.8555	1772.8515	0.0040	0	R.VVVSSCGHDGPFGATGVK.R	Carbamidomethyl (C)
244 - 257	1515.7468	1514.7396	1514.7585	-0.0189	0	R.LQDIGMIDAVPGMR.A	
244 - 257	1531.7419	1530.7347	1530.7534	-0.0187	0	R.LQDIGMIDAVPGMR.A	Oxidation (M)
244 - 257	1547.7393	1546.7320	1546.7483	-0.0163	0	R.LQDIGMIDAVPGMR.A	2 Oxidation (M)
258 - 270	1476.6973	1475.6900	1475.6926	-0.0026	0	R.ALDMNTAEDEIVR.L	
258 - 270	1492.6879	1491.6806	1491.6875	-0.0069	0	R.ALDMNTAEDEIVR.L	Oxidation (M)
274 - 294	2170.0674	2169.0601	2169.0809	-0.0208	0	R.EVVPGMIVTGMEVAEIDGAPR.M	
274 - 294	2186.0654	2185.0582	2185.0758	-0.0176	0	R.EVVPGMIVTGMEVAEIDGAPR.M	Oxidation (M)
274 - 294	2202.0483	2201.0411	2201.0707	-0.0296	0	R.EVVPGMIVTGMEVAEIDGAPR.M	2 Oxidation (M)
295 - 308	1503.6415	1502.6342	1502.6567	-0.0225	0	R.MGPTFGAMMISGQK.A	3 Oxidation (M)
316 - 328	1325.7357	1324.7284	1324.7462	-0.0178	0	K.ALGRPNAIDGTIK.K	

Spot 6d16



Match to: gi|32352138; Score: 126

Matched peptides:

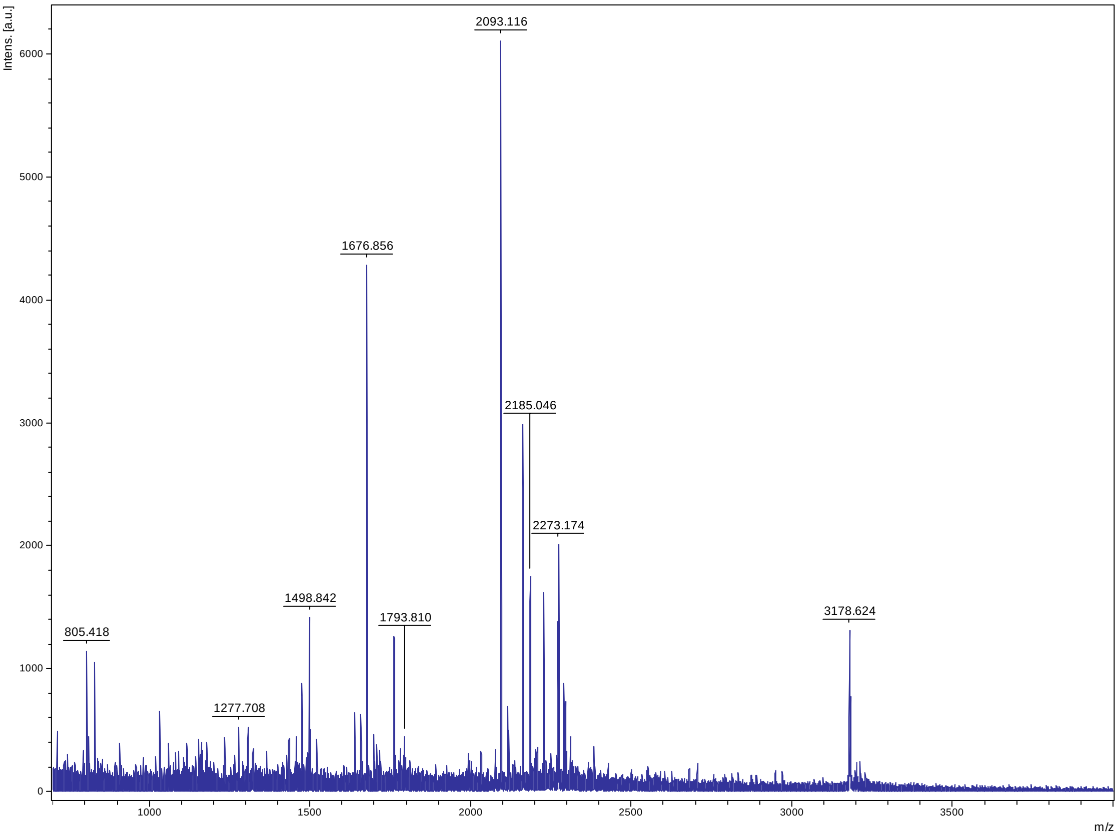
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
2 - 20	1870.99	1869.99	1869.96	0.03	1	AAMATTASSLLKTSFAGAR Oxidation (M)
60 - 70	1262.70	1261.70	1261.70	-0.01	1	FSPIKESIVSR
139 - 162	2791.46	2790.46	2790.41	0.05	0	KPAHLFLDELGVAYDEQEDYVVIK
163 - 174	1336.66	1335.66	1335.66	-0.00	0	HAALFTSTVMSR Oxidation (M)
175 - 182	910.61	909.61	909.58	0.04	0	LLARPNVK
183 - 195	1430.80	1429.80	1429.82	-0.02	0	LFNAVAVEDLIVK
228 - 245	1773.86	1772.86	1772.85	0.00	0	VVVSSCGHDGPFGATGVK
246 - 260	1703.96	1702.96	1702.85	0.11	1	RLQDIGMIDAVPGMR 2 Oxidation (M)
247 - 260	1515.75	1514.75	1514.76	-0.01	0	LQDIGMIDAVPGMR
247 - 260	1531.76	1530.76	1530.75	0.00	0	LQDIGMIDAVPGMR Oxidation (M)
247 - 260	1547.76	1546.76	1546.75	0.01	0	LQDIGMIDAVPGMR 2 Oxidation (M)
261 - 273	1492.70	1491.70	1491.69	0.01	0	ALDMNTAEDEIVR Oxidation (M)
277 - 297	2170.09	2169.08	2169.08	0.00	0	EVVPGMIVTGMEVAEIDGAPR
277 - 297	2202.08	2201.08	2201.07	0.01	0	EVVPGMIVTGMEVAEIDGAPR 2 Oxidation (M)
298 - 311	1487.69	1486.69	1486.66	0.03	0	MGPTFGAMMISGQK 2 Oxidation (M)
298 - 311	1503.67	1502.67	1502.66	0.01	0	MGPTFGAMMISGQK 3 Oxidation (M)
319 - 331	1325.74	1324.74	1324.75	-0.01	0	ALGRPNAIDGTIK

Match to: gi|77548611; Score: 89

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
93 - 99	865.53	864.52	864.47	0.05	0	IFDTTLR
124 - 145	2257.14	2256.14	2256.13	0.01	0	LGVDIIEAGFPASSPDDLDAVR
146 - 170	2576.33	2575.32	2575.31	0.02	0	SIAIEVGNTPVGEDGHVPVICGLSR
175 - 184	1145.58	1144.58	1144.55	0.02	0	DIDAAWEAVR
188 - 205	2202.08	2201.08	2201.16	-0.08	1	RPRIHTFIATSEIHMQHK
208 - 218	1183.66	1182.66	1182.70	-0.04	1	KTPEQVVAIAK
226 - 241	1735.77	1734.77	1734.75	0.02	0	SLGCPDVEFSPEDAGR
320 - 331	1328.70	1327.69	1327.71	-0.02	0	QLEVTINGIGER
349 - 368	2163.06	2162.06	2162.10	-0.05	0	ELLGGLYTGINTQHITMSSK
406 - 420	1649.83	1648.83	1648.83	-0.00	0	GTYEIISPDDIGLTR
520 - 534	1492.70	1491.70	1491.74	-0.04	0	IACAVGTGPVDAAYK
535 - 547	1452.81	1451.81	1451.83	-0.02	0	AVDDIIQIPTVLR
587 - 603	1635.85	1634.85	1634.86	-0.01	0	AFSGSGAALDIVVSSVR

Spot 6d17

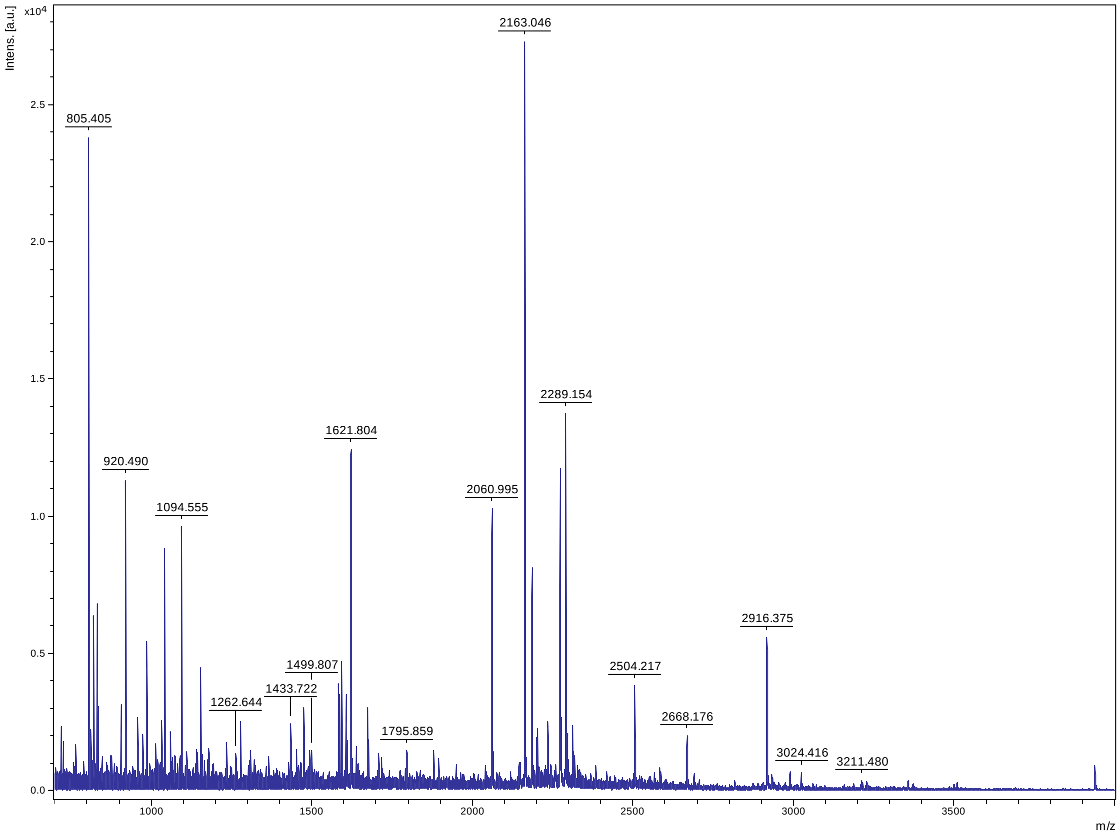


Match to: gi|786178; Score: 71

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
40 - 52	1520.76	1519.76	1519.73	0.03	0	FASINVENVEENR
40 - 53	1676.86	1675.85	1675.83	0.03	1	FASINVENVEENRR
85 - 94	1117.63	1116.63	1116.62	0.01	0	DGKPFVDVLK
117 - 129	1457.71	1456.71	1456.69	0.02	1	ETTTQGHDDLGKR
133 - 139	829.39	828.39	828.38	0.01	0	YYEAGAR
149 - 168	2093.12	2092.11	2092.09	0.02	0	IGPNEPSQLSIDLNAQGLAR
169 - 196	3178.62	3177.62	3177.60	0.02	0	YAIICQENGLVPIVEPEILVDGSHDIER

Spot 6d22

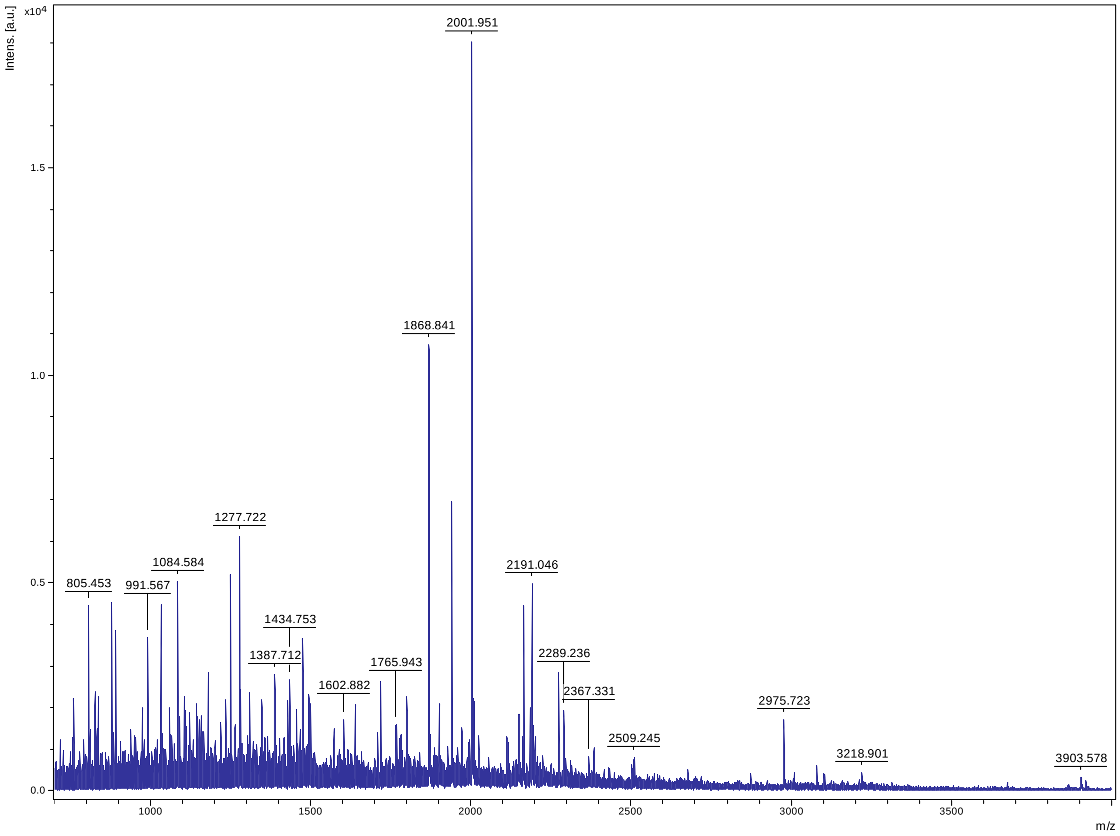


Match to: gi|77554103; Score: 97

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
105 - 130	2931.33	2930.33	2930.29	0.03	0	ENYGCEVVCFTADVGQGDIELEGLEK
144 - 159	2060.99	2059.99	2059.99	-0.00	1	DLKEEFVSEYIYPCLR
168 - 188	2234.41	2233.41	2233.23	0.18	1	YLLGTSMARPVIAKAMVDVAK
222 - 234	1584.82	1583.82	1583.82	-0.00	1	VVAPWREWDITGR
228 - 242	1795.86	1794.86	1794.84	0.01	1	EWDITGREDAIEYAK
316 - 325	1014.56	1013.56	1013.58	-0.02	0	DLSPASLLAK
338 - 344	876.43	875.42	875.42	0.01	0	IDMVENR
352 - 367	1592.81	1591.80	1591.80	0.00	0	GVYETPGGTIMAAAVR
352 - 367	1608.79	1607.79	1607.80	-0.01	0	GVYETPGGTIMAAAVR Oxidation (M)
368 - 382	1878.93	1877.93	1877.92	0.01	1	ELESLTLDRETMQWK
368 - 382	1894.93	1893.93	1893.91	0.01	1	ELESLTLDRETMQWK Oxidation (M)
389 - 397	1041.53	1040.53	1040.53	-0.00	0	YAELVYAGR
398 - 403	833.43	832.43	832.42	0.01	0	WFDPLR
437 - 443	885.45	884.44	884.44	0.00	0	SPYSLYR
444 - 465	2504.22	2503.21	2503.11	0.10	0	EDISSFENGEIYNQADAEGFIR
466 - 472	819.47	818.47	818.46	0.00	0	LYGLPTR

Spot 6d23



Match to: **gi|12229919**; Score: **118**

Matched peptides:

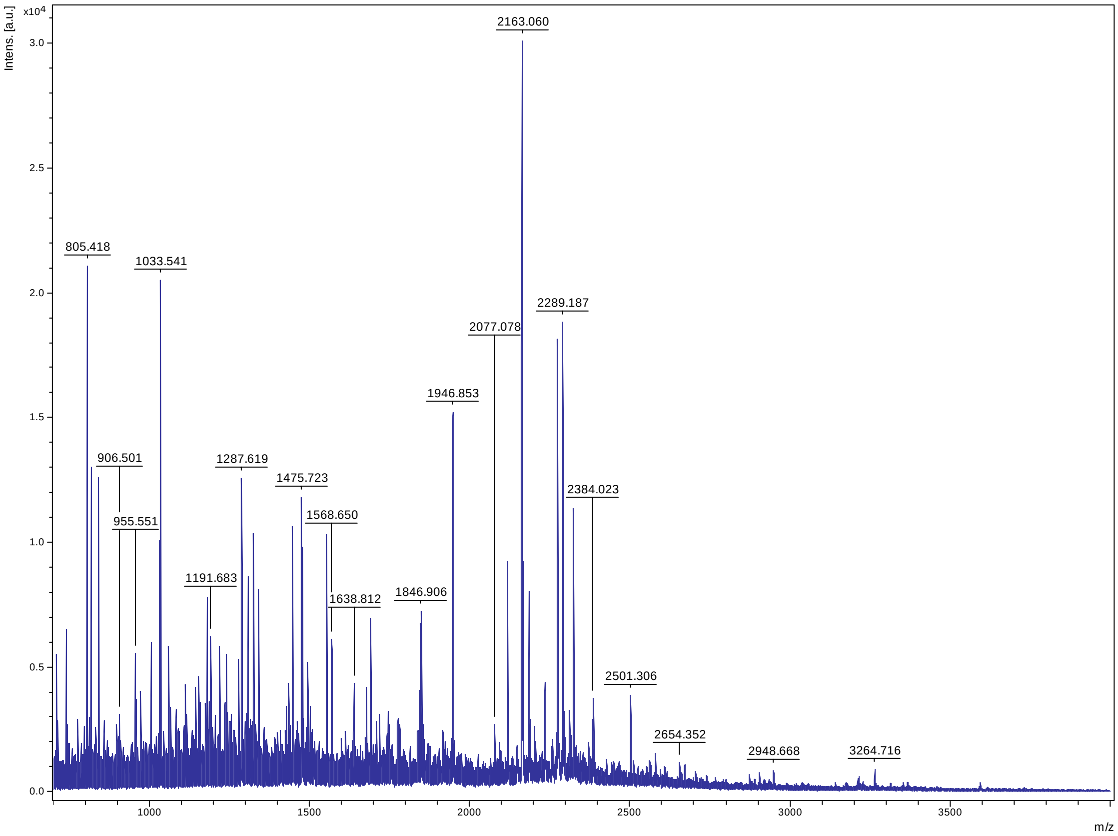
Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
21 - 29	1084.58	1083.58	1083.56	0.02	0	VFQVEYATK
30 - 41	1159.64	1158.63	1158.62	0.01	0	AVDNSGTVVGIK
58 - 65	937.47	936.47	936.42	0.06	0	MMLEGSNR
58 - 65	953.48	952.48	952.41	0.07	0	MMLEGSNR Oxidation (M)
94 - 101	884.47	883.47	883.39	0.07	0	SEAASYEK
102 - 110	991.57	990.56	990.54	0.03	0	VYGEPISVK
144 - 159	1783.86	1782.86	1782.85	0.01	0	DGPQLYMIEPSGVSYK
144 - 159	1799.84	1798.84	1798.84	-0.00	0	DGPQLYMIEPSGVSYK Oxidation (M)
160 - 167	826.49	825.49	825.44	0.05	0	YFGAALGK
181 - 187	878.47	877.47	877.43	0.04	0	LSELTCR
196 - 205	1144.60	1143.60	1143.59	0.00	0	IIYGVHDEAK
196 - 207	1387.71	1386.71	1386.71	-0.00	1	IIYGVHDEAKDK
206 - 222	2112.01	2111.00	2110.96	0.04	1	DKAFELELSWICDESNR
208 - 222	1868.84	1867.84	1867.84	-0.00	0	AFELELSWICDESNR
227 - 236	1083.61	1082.61	1082.60	0.01	0	VPADLLEQAK

Match to: gi|1346109; Score: 101

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence
40 - 69	3218.90	3217.90	3217.60	0.29	1	DKSLLVWDLTNPVQNVGEGAGASEYGVPFR
42 - 69	2975.72	2974.72	2974.48	0.24	0	SLLVWDLTNPVQNVGEGAGASEYGVPFR
101 - 111	1248.64	1247.64	1247.65	-0.01	0	LWDLSTGVTTR
143 - 151	1120.56	1119.56	1119.54	0.02	0	LWNTLGECK
152 - 172	2191.05	2190.04	2189.99	0.05	0	YTIGGDLGGGEGHNGWVSCVR
173 - 189	1938.94	1937.94	1937.93	0.01	0	FSPNTFQPTIVSGSWDR
230 - 243	1572.83	1571.83	1571.83	-0.00	1	DGVTLLWDLAEGKR
244 - 262	2150.10	2149.10	2149.06	0.03	0	LYSLDAGSIIHSLCFSPNR
263 - 274	1455.70	1454.70	1454.69	0.01	0	YWLCAATQDSIK
275 - 281	890.53	889.52	889.45	0.07	0	IWDLESK
282 - 295	1602.88	1601.88	1601.91	-0.03	0	HIVQDLKPEIPVSK

Spot 6d24



Match to: gi|108710002 Score: 115 Expect: 2.2e-07

Matched peptides:

Start - End	Observed	Mr (expt)	Mr (calc)	Delta	Miss	Sequence	
1 - 10	1227.6206	1226.6133	1226.4907	0.1226	0	-.MEETSPTNMR.R	2 Oxidation (M)
1 - 11	1393.7316	1392.7243	1392.6125	0.1118	1	-.MEETSPTNMRR.K	Acetyl (N-term)
2 - 11	1262.6369	1261.6296	1261.5721	0.0576	1	M.EETSPTNMRR.K	Acetyl (N-term)
12 - 24	1734.8344	1733.8271	1733.8136	0.0135	1	R.KYSWWWNSHICPK.N	
12 - 24	1791.7412	1790.7339	1790.8351	-0.1012	1	R.KYSWWWNSHICPK.N	Carbamidomethyl (C)
25 - 39	1850.9291	1849.9218	1849.8516	0.0702	1	K.NSKWLQENLTDMDSK.I	Acetyl (N-term)
28 - 41	1720.8418	1719.8345	1719.8501	-0.0156	1	K.WLQENLTDMDSKIK.M	
46 - 57	1407.7105	1406.7032	1406.7041	-0.0009	1	K.IIEEDAESFAKR.A	
65 - 80	2038.9943	2037.9870	2038.0669	-0.0799	1	R.RPELMALLEELYRAYR.A	Oxidation (M)
86 - 94	1073.5625	1072.5552	1072.4937	0.0615	0	R.YDHAAGELR.Q	Acetyl (N-term)
148 - 157	1217.6095	1216.6022	1216.5432	0.0590	1	K.QAKDNQDNER.L	
151 - 157	932.5184	931.5111	931.3631	0.1480	0	K.DNQDNER.L	Acetyl (N-term)
151 - 160	1259.6850	1258.6777	1258.5902	0.0876	1	K.DNQDNERLQK.E	
158 - 170	1546.7985	1545.7912	1545.7886	0.0027	1	R.LQKELESLSEENK.D	
161 - 170	1219.6343	1218.6270	1218.5615	0.0655	0	K.ELESLSEENK.D	Acetyl (N-term)
176 - 185	1174.6445	1173.6372	1173.6241	0.0131	0	R.ISSLLEQTNK.A	Acetyl (N-term)
176 - 194	2116.9771	2115.9698	2116.1449	-0.1751	1	R.ISSLLEQTNKAELEVVCLK.E	
176 - 194	2216.0937	2215.0864	2215.1769	-0.0905	1	R.ISSLLEQTNKAELEVVCLK.E	Acetyl (N-term); Carbamidomethyl (C)
186 - 194	1060.5868	1059.5795	1059.5634	0.0161	0	K.AELEVVCLK.E	Carbamidomethyl (C)
205 - 217	1446.7256	1445.7183	1445.7296	-0.0113	0	K.EAIVLQCQQSTAR.L	
205 - 217	1503.8072	1502.7999	1502.7511	0.0488	0	K.EAIVLQCQQSTAR.L	Carbamidomethyl (C)
223 - 234	1501.7846	1500.7773	1500.7684	0.0089	1	K.SEILHTQEKFNR.L	
237 - 252	1914.8953	1913.8880	1913.8101	0.0779	0	K.EEMQSGFQPFTTADER.S	Acetyl (N-term)
253 - 269	1972.9637	1971.9564	1972.0298	-0.0734	1	R.SVLLEKANQEMNLELNK.L	
259 - 269	1319.6552	1318.6479	1318.6187	0.0293	0	K.ANQEMNLELNK.L	Oxidation (M)
259 - 269	1361.6942	1360.6869	1360.6292	0.0577	0	K.ANQEMNLELNK.L	Acetyl (N-term); Oxidation (M)
276 - 284	1196.6344	1195.6271	1195.5833	0.0439	1	K.QKHEELNEK.Q	Acetyl (N-term)
302 - 314	1538.7352	1537.7279	1537.6938	0.0341	0	K.CMQAEMAQLSLEK.Q	Carbamidomethyl (C)
302 - 322	2465.1628	2464.1555	2464.2011	-0.0456	1	K.CMQAEMAQLSLEKQLILAQDK.M	Acetyl (N-term); 2 Oxidation (M)
315 - 322	970.5673	969.5600	969.5495	0.0106	0	K.QLILAQDK.M	Acetyl (N-term)
331 - 336	745.3927	744.3854	744.4017	-0.0163	0	K.QIEVSK.A	Acetyl (N-term)
331 - 338	944.5236	943.5163	943.5338	-0.0175	1	K.QIEVSKAK.D	Acetyl (N-term)
375 - 383	1132.5407	1131.5334	1131.5845	-0.0511	0	R.LQDEIITMK.N	Acetyl (N-term)
375 - 387	1617.7862	1616.7789	1616.8192	-0.0402	1	R.LQDEIITMKNAQR.R	Acetyl (N-term); Oxidation (M)
389 - 400	1471.7558	1470.7485	1470.6772	0.0713	1	R.LEEDVCRHVDEK.K	
389 - 400	1513.8804	1512.8731	1512.6878	0.1853	1	R.LEEDVCRHVDEK.K	Acetyl (N-term)
401 - 411	1383.7238	1382.7165	1382.7340	-0.0175	1	K.KTLQNELCHLK.E	Carbamidomethyl (C)
402 - 411	1240.7176	1239.7103	1239.6281	0.0822	0	K.TLQNELCHLK.E	Acetyl (N-term)
402 - 414	1655.8341	1654.8268	1654.8097	0.0171	1	K.TLQNELCHLKEDR.S	Carbamidomethyl (C)
420 - 425	741.4721	740.4648	740.4181	0.0468	1	K.KHSSIK.E	Acetyl (N-term)
447 - 457	1213.6979	1212.6906	1212.6826	0.0081	1	K.DGNVELKGIIR.N	
458 - 472	1846.9258	1845.9185	1845.9445	-0.0260	1	R.NHESTEVLHIENLRR.L	
486 - 498	1459.7311	1458.7238	1458.7929	-0.0691	0	K.SLSAVTTELEVLR.E	Acetyl (N-term)
543 - 561	2163.0402	2162.0329	2162.0491	-0.0161	0	K.NVFLENSLSDANAELESLR.G	Acetyl (N-term)
564 - 585	2533.2193	2532.2120	2532.2343	-0.0223	1	K.LKELEESSEALYSQNSALQHEK.S	
586 - 594	1049.5529	1048.5456	1048.4971	0.0485	0	K.STLACQVDR.I	Carbamidomethyl (C)
612 - 620	1141.5724	1140.5651	1140.5523	0.0128	1	K.RHSDLQEEK.G	
630 - 635	786.3490	785.3417	785.4395	-0.0978	0	K.LQEQIR.F	
640 - 648	1136.6078	1135.6005	1135.5006	0.0999	0	K.EHNDLEHSR.K	
640 - 649	1264.6549	1263.6476	1263.5956	0.0520	1	K.EHNDLEHSRK.S	
650 - 658	1082.5951	1081.5878	1081.5404	0.0475	0	K.SQLDALHEK.I	Acetyl (N-term)
650 - 669	2337.1799	2336.1726	2336.1872	-0.0146	1	K.SQLDALHEKINVLSQEGWNR.E	
692 - 709	2093.0756	2092.0683	2091.9782	0.0901	0	K.QCLEDIADANSDFLAQLK.M	Acetyl (N-term); Carbamidomethyl (C)
692 - 711	2310.1175	2309.1102	2309.1031	0.0071	1	K.QCLEDIADANSDFLAQLKMK.Q	Carbamidomethyl (C)
710 - 721	1505.7531	1504.7458	1504.7265	0.0193	1	K.MKQEVCQVLEEK.M	Acetyl (N-term)
712 - 721	1204.6159	1203.6086	1203.5805	0.0281	0	K.QEVCQVLEEK.M	
712 - 731	2540.2372	2539.2299	2539.1570	0.0730	1	K.QEVCQVLEEKMEYLSENNQK.L	Acetyl (N-term); Carbamidomethyl (C)

732 - 741	1103.5756	1102.5683	1102.6420	-0.0736	1	K.LTKCIGSVLK.V	Acetyl (N-term)
735 - 748	1609.8286	1608.8213	1608.8908	-0.0695	1	K.CIGSVLKVLHLEEK.Y	Acetyl (N-term)
790 - 807	2025.9271	2024.9198	2025.0894	-0.1696	0	K.SLVVTLLEHFGQEVADLR.S	
821 - 829	1157.6113	1156.6040	1156.6088	-0.0047	0	K.SEELLQLQR.E	Acetyl (N-term)
821 - 831	1372.7223	1371.7150	1371.7357	-0.0207	1	K.SEELLQLQREK.Q	
832 - 850	2449.1874	2448.1801	2448.1557	0.0245	1	K.QELVNITDEFWEEVETRNR.K	Acetyl (N-term)
861 - 873	1475.7620	1474.7547	1474.7779	-0.0232	0	K.FLVGQLSELQGSR.R	Acetyl (N-term)
874 - 882	1115.6407	1114.6334	1114.6346	-0.0012	1	R.RSLQSEIIK.L	Acetyl (N-term)
883 - 898	1967.9293	1966.9220	1966.8612	0.0608	0	K.LIQENSMLSDELCDSR.E	Acetyl (N-term); Carbamidomethyl (C); Oxidation (M)
883 - 900	2225.0877	2224.0804	2223.9987	0.0817	1	K.LIQENSMLSDELCDSREK.E	Acetyl (N-term); Carbamidomethyl (C); Oxidation (M)
903 - 918	1874.9198	1873.9125	1873.9019	0.0107	0	R.VFEDDFSILISEVMSK.D	Oxidation (M)
919 - 926	948.5001	947.4928	947.5440	-0.0512	0	K.DILSVVFR.S	
959 - 969	1399.7492	1398.7419	1398.6193	0.1227	1	K.MMNMKLGDLEK.E	Acetyl (N-term); 3 Oxidation (M)
981 - 1011	3264.6933	3263.6860	3263.5112	0.1748	1	R.TISICNSTSTENAIGSGYPVGRDTDHLNSGR.S	Acetyl (N-term)
1046 - 1056	1314.6497	1313.6424	1313.5843	0.0582	0	K.MQSEMEVLTSK.E	2 Oxidation (M)
1046 - 1056	1324.6446	1323.6373	1323.6050	0.0323	0	K.MQSEMEVLTSK.E	Acetyl (N-term)
1046 - 1056	1340.6401	1339.6328	1339.5999	0.0329	0	K.MQSEMEVLTSK.E	Acetyl (N-term); Oxidation (M)
1046 - 1056	1356.7315	1355.7242	1355.5948	0.1294	0	K.MQSEMEVLTSK.E	Acetyl (N-term); 2 Oxidation (M)
1046 - 1064	2185.0547	2184.0474	2184.0289	0.0185	1	K.MQSEMEVLTSKENSAIDIK.S	2 Oxidation (M)
1057 - 1071	1679.8497	1678.8424	1678.7719	0.0705	1	K.ENSAIDIKSCDEDIK.R	
1091 - 1113	2654.3187	2653.3114	2653.3957	-0.0843	1	K.VLELIITCESFEISSMVQKEVLK.E	Oxidation (M)
1164 - 1177	1633.8046	1632.7973	1632.7777	0.0196	0	K.QTLSLANDCLQSNK.L	Acetyl (N-term); Carbamidomethyl (C)
1178 - 1191	1689.8501	1688.8428	1688.8767	-0.0338	1	K.LRMEENALSTQVLK.T	Acetyl (N-term); Oxidation (M)
1180 - 1195	1922.9334	1921.9261	1921.9237	0.0024	1	R.MEENALSTQVLKTNMR.S	Acetyl (N-term); Oxidation (M)
1192 - 1204	1465.7376	1464.7303	1464.6739	0.0564	1	K.TNMRSSGDQNTVR.T	
1196 - 1204	1005.5695	1004.5622	1004.4523	0.1100	0	R.SSGDQNTVR.T	Acetyl (N-term)
1205 - 1213	1091.5775	1090.5702	1090.5692	0.0010	1	R.TVKDMELQK.L	
1205 - 1213	1107.5474	1106.5401	1106.5641	-0.0240	1	R.TVKDMELQK.L	Oxidation (M)
1208 - 1213	805.3653	804.3580	804.3687	-0.0107	0	K.DMELQK.L	Acetyl (N-term)
1208 - 1219	1412.7172	1411.7099	1411.7493	-0.0394	1	K.DMELQKLHGTIK.A	
1214 - 1219	710.2701	709.2628	709.4122	-0.1494	0	K.LHGTIK.A	Acetyl (N-term)
1224 - 1236	1500.7880	1499.7807	1499.7831	-0.0024	0	K.VVTDTAVLLDQER.L	Acetyl (N-term)
1237 - 1248	1418.7481	1417.7408	1417.7313	0.0095	1	R.LDFNANLQEARK.Q	
1255 - 1273	2353.1692	2352.1619	2352.1592	0.0027	1	K.LKEILDDDLIEMNYEQMLK.D	
1255 - 1273	2427.2689	2426.2616	2426.1596	0.1020	1	K.LKEILDDDLIEMNYEQMLK.D	Acetyl (N-term); 2 Oxidation (M)
1274 - 1296	2442.2944	2441.2871	2441.2761	0.0110	1	K.DIQLDLIQISSGNKTGSLGQANK.T	Acetyl (N-term)
1288 - 1304	1716.8487	1715.8414	1715.8802	-0.0387	1	K.TGSLGQANKTVAQANEK.M	
1297 - 1320	2510.1954	2509.1881	2509.2343	-0.0461	1	K.TVAQANEKMLDSHGIVGASSSHVR.N	Oxidation (M)
1321 - 1337	2095.0386	2094.0313	2093.9766	0.0547	1	R.NDLRPPQSESFERDNYK.R	
1334 - 1347	1675.7952	1674.7879	1674.8763	-0.0883	1	R.DNYKRPPSELMVVK.E	
1359 - 1371	1597.8282	1596.8209	1596.7896	0.0313	1	R.SITTEPHQEWKNK.V	
1376 - 1382	760.3954	759.3881	759.3875	0.0006	0	R.LASDAQR.L	
1414 - 1428	1663.8228	1662.8155	1662.8100	0.0055	0	R.EAEGFITQLIDSNGK.L	Acetyl (N-term)
1457 - 1462	775.3824	774.3751	774.4170	-0.0419	1	K.IMERAR.K	
1457 - 1462	817.4086	816.4013	816.4276	-0.0262	1	K.IMERAR.K	Acetyl (N-term)
1471 - 1484	1657.8236	1656.8163	1656.9120	-0.0956	1	R.LEVEMQKVQEALLK.Y	
1485 - 1495	1329.6687	1328.6614	1328.6208	0.0406	1	K.YEEQTSTRTSK.T	
1496 - 1500	758.3775	757.3702	757.3653	0.0049	1	K.TMHRR.S	Acetyl (N-term); Oxidation (M)
1503 - 1513	1365.7149	1364.7076	1364.7564	-0.0488	1	K.VQLVDFLYGRR.R	
1522 - 1529	942.5164	941.5091	941.3227	0.1864	0	R.CSPCGCMK.A	2 Carbamidomethyl (C)
1522 - 1529	958.5235	957.5162	957.3177	0.1986	0	R.CSPCGCMK.A	2 Carbamidomethyl (C); Oxidation (M)

1. Dai S, Chen T, Chong K, Xue Y, Liu S, Wang T (2007) Proteomics Identification of Differentially Expressed Proteins Associated with Pollen Germination and Tube Growth Reveals Characteristics of Germinated Oryza sativa Pollen. Molecular & Cellular Proteomics 6: 207