

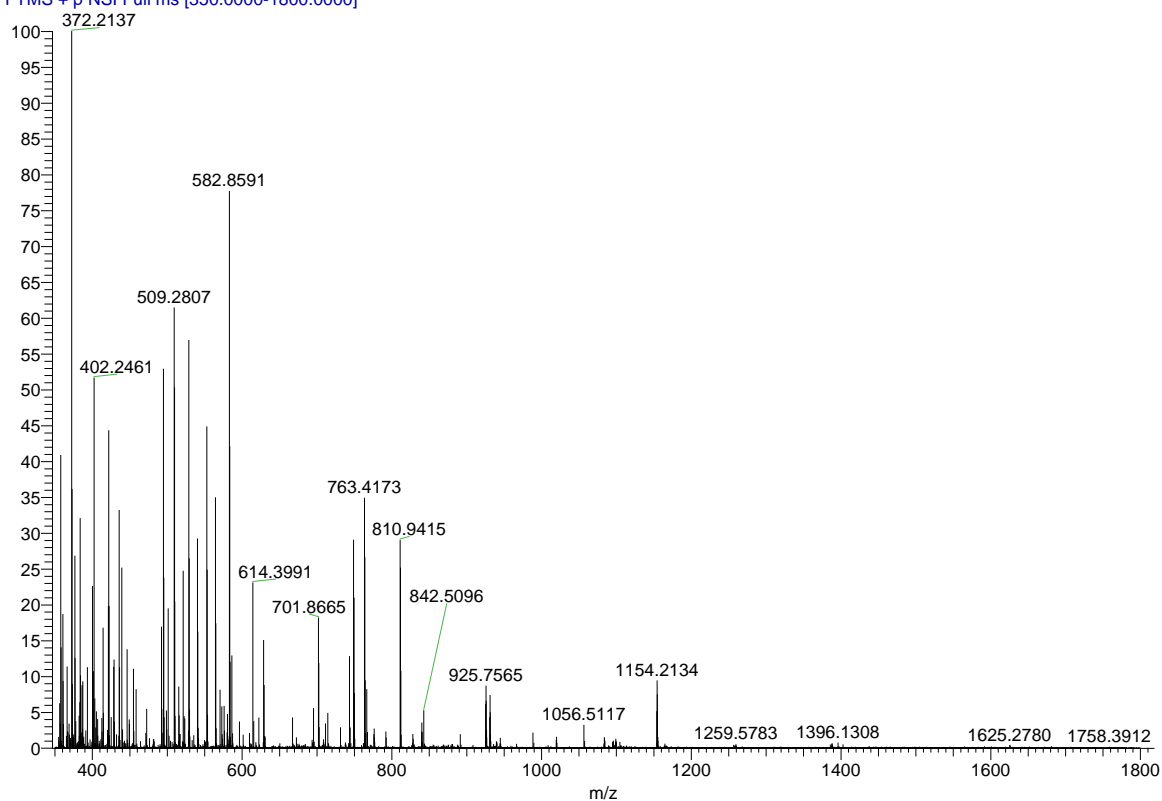
Supplementary material for the article:

Nikolić, J.; Nešić, A.; Kull, S.; Schocker, F.; Jappe, U.; Gavrović-Jankulović, M. Employment of Proteomic and Immunological Based Methods for the Identification of Catalase as Novel Allergen from Banana. *Journal of Proteomics* **2018**, *175*, 87–94. <https://doi.org/10.1016/j.jprot.2018.01.007>

Mass spectrometry of banana catalase – Full MS

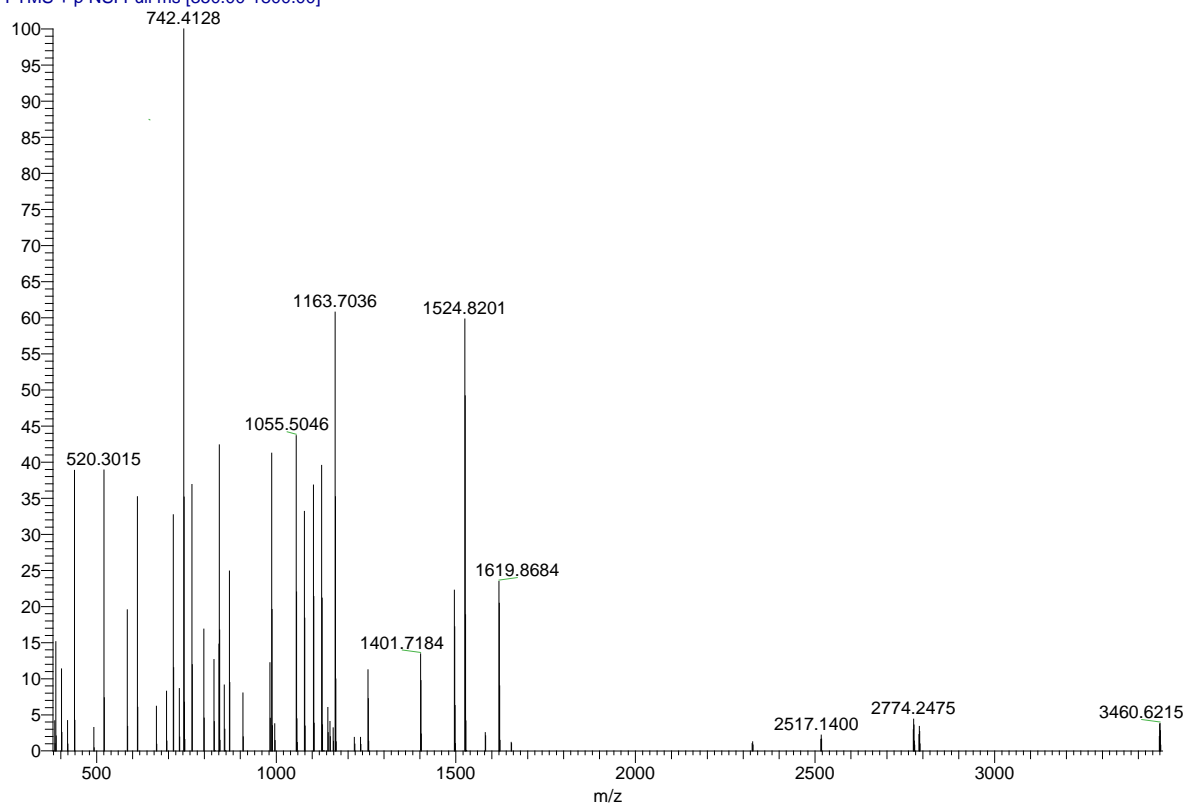
Full MS (original)

170907_Skadi_peptide_35451 #1-778 RT: 0.00-4.96 AV: 100 NL: 1.10E7
T: FTMS + p NSI Full ms [350.0000-1800.0000]



Full MS (deconvoluted)

170907_Skadi_peptide_35451_XT_00001_M_#1 RT: 1.00 AV: 1 NL: 6.69E6
T: FTMS + p NSI Full ms [350.00-1800.00]

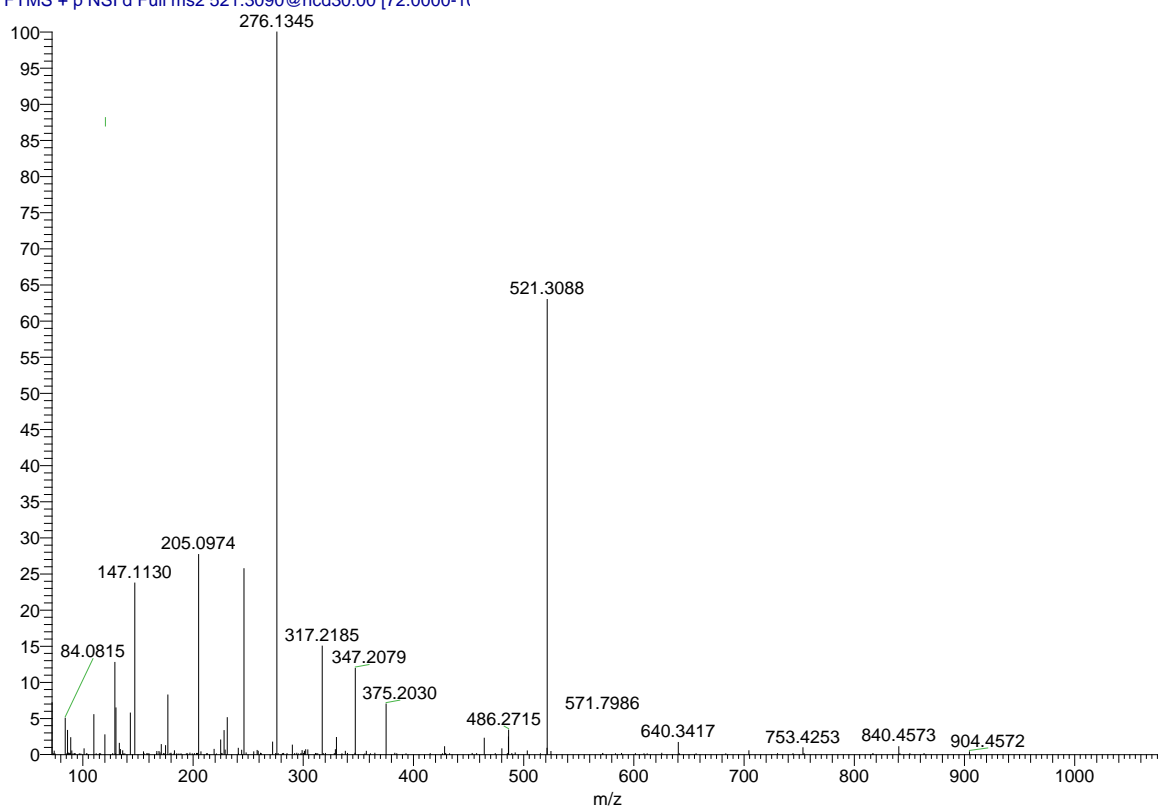


sequence coverage (bold ~58 %):	<pre> >ABV55108.1 catalase 2 [Musa acuminata AAA Group] MDPYKFRPSSSFDTNFTTTNAGAPVWNDQALTVGSRGPILLEDYHLVEKIAHFARERI PERVVHARGASAKGFFECTHDVTHLTCADFLRAPGVQTPIILRFSTVIHERGSPETIRD PRGFAVKFYTREGNWDLGNNFPVFFIIRGDIKFPDVIHAFKPNPKSHVQYWRVFDFLS HHPESLHTFFFLFDDVGVPSPDYRHMEGFGVNTYTFVSKEGKVNYVKFHWKPTCGVKCLL EDEAIVVGGKNHSHATQDLYDSIAAGNYPEWKLFVQVMDPDTEDRYDFDPLDDTKTWPE DLLPLQPVGRLVLRNNIDNFFSENEQLAFGPGLVVPGIYYSDDKMLQCRVFAYGDTQRY RLGPNYLTLPVNAPKCAHHNNHYDGLMNMVHRDEVDYFPSRHASLRHAERFPIPNRVV TGKREKNVIPKQNDFKQGERYRSWAPDRQERFVRRWAEQLAHPKVSYELRSIWISFLS KCDTSLGQKVANRLNMRANI </pre>
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Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **GFAVK**

170907_Skadi_peptide_35451 #43 RT: 0.63 AV: 1 NL: 1.13E6
 T: FTMS + p NSI d Full ms2 521.3090@hcd30.00 [72.0000-1(

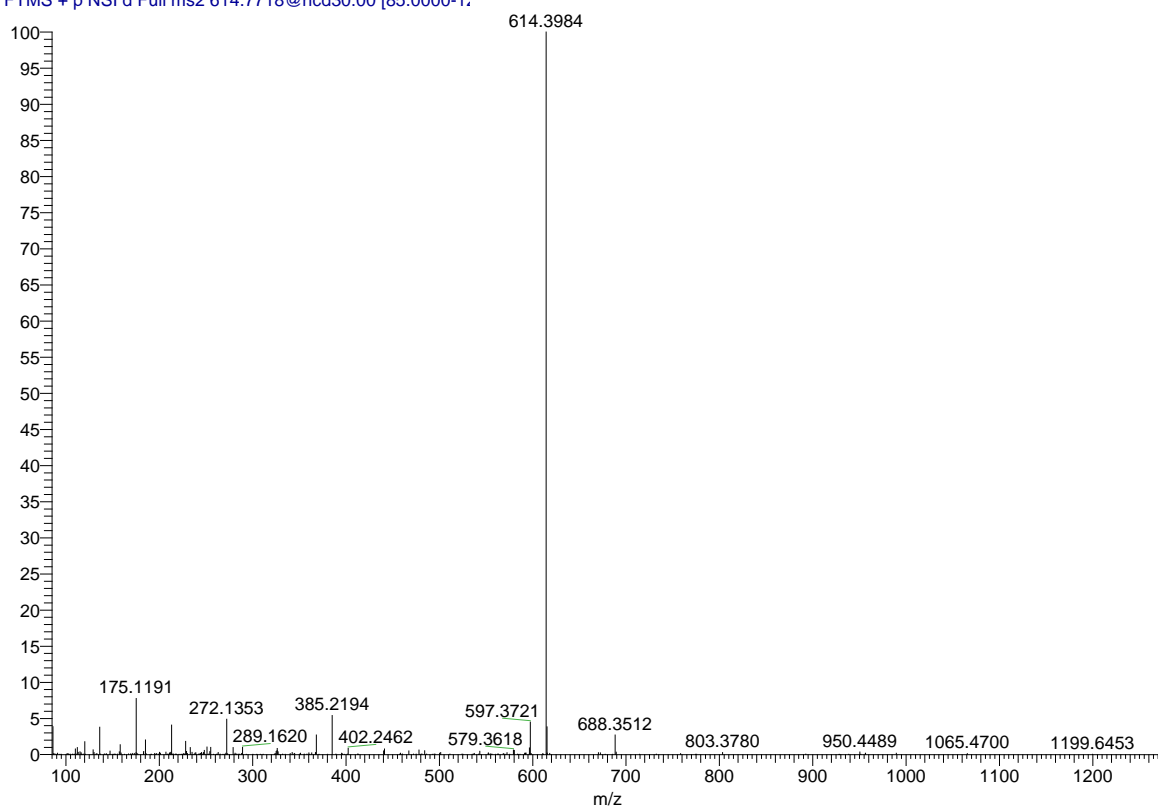


MS/MS mass 521.3090 m/z [M+H] ⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	G	---	---
	205.0974	205.0972	F	464.2873	464.2867
	276.1345	276.1343	A	317.2185	317.2183
	375.2030	375.2027	V	246.1814	246.1812
	---	---	K	147.1130	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **LVLNR**

170907_Skadi_peptide_35451 #656 RT: 4.28 AV: 1 NL: 2.09E6
 T: FTMS + p NSI d Full ms2 614.7718@hcd30.00 [85.0000-1;

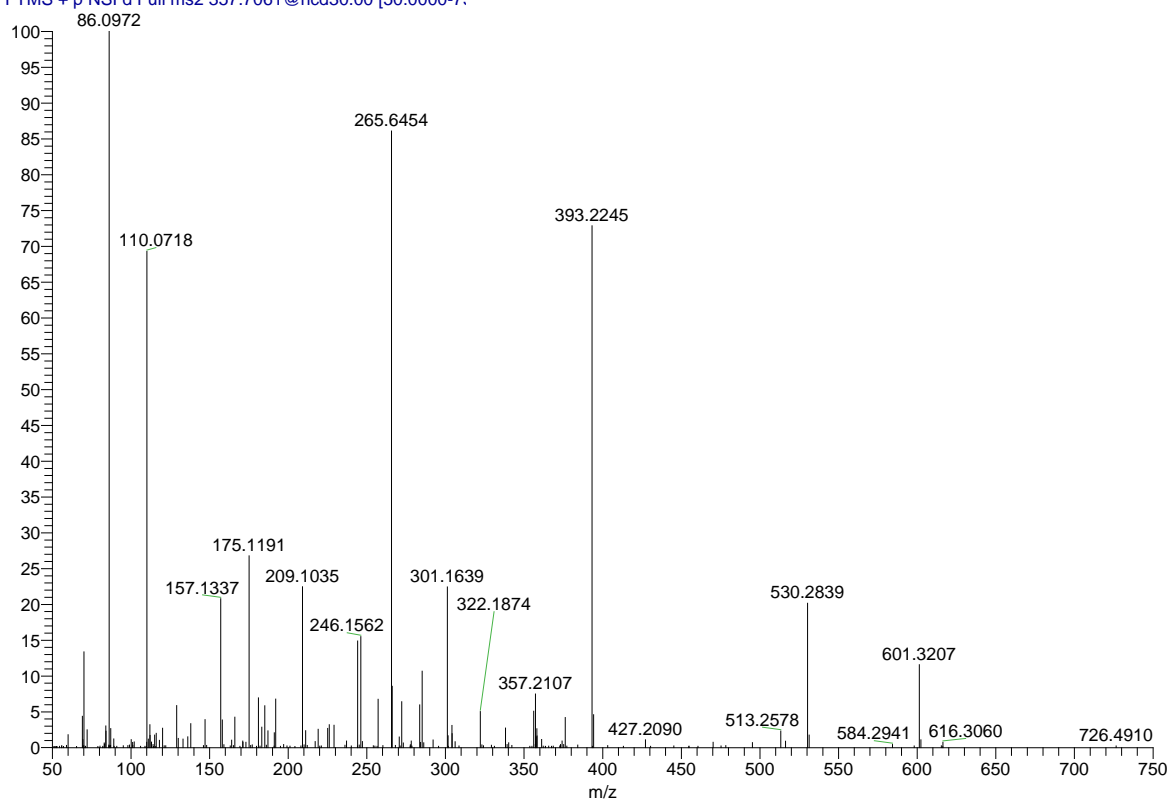


MS/MS mass 614.7718 m/z [M+H] ⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	L	---	---
	213.1599	213.1598	V	501.3145	501.3144
	326.2437	326.2438	L	402.2462	402.2459
	440.2867	440.2867	N	289.1620	289.1619
	---	---	R	175.1191	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **IAHFR**

170907_Skadi_peptide_35451 #45 RT: 0.65 AV: 1 NL: 1.21E6
 T: FTMS + p NSI d Full ms2 357.7061@hcd30.00 [50.0000-7!]

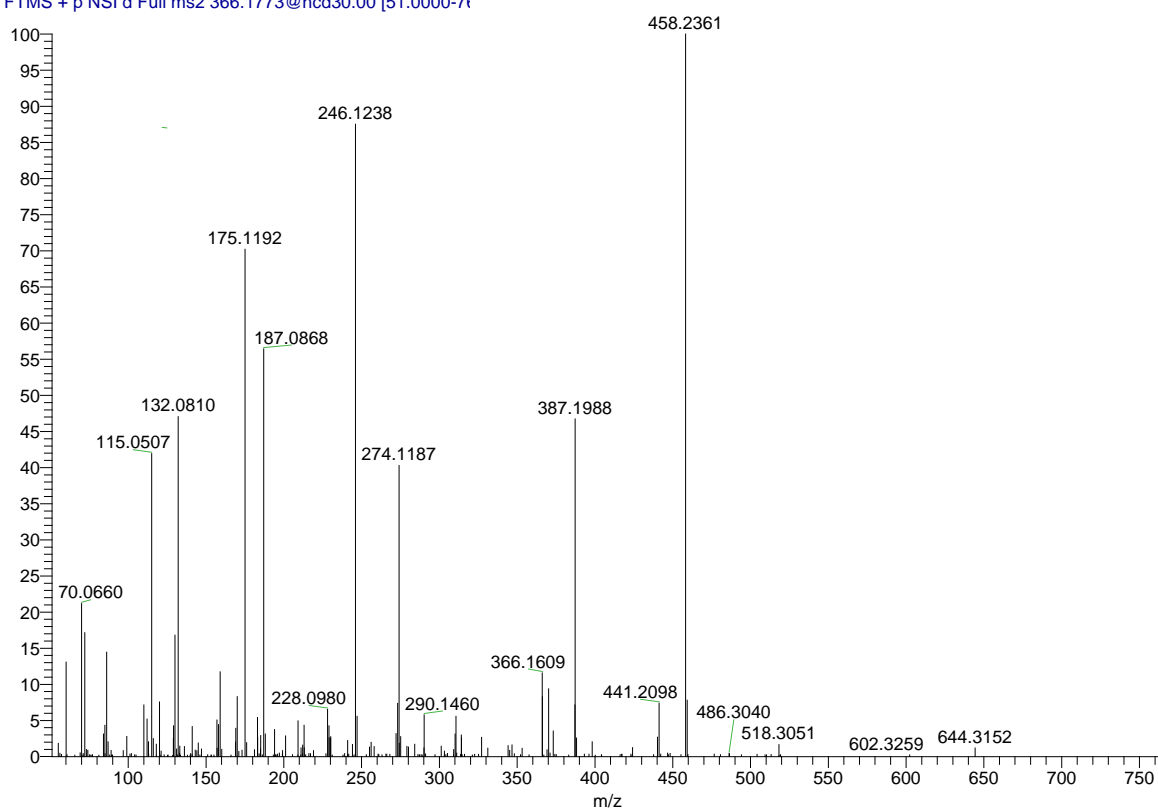


MS/MS mass 357.7061 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	I	---	---
	185.1286	185.1285	A	601.3207	601.3205
	322.1874	322.1874	H	530.2839	530.2834
	-	469.2558	F	393.2245	393.2245
	-	540.2929	A	246.1562	246.1561
	---	---	R	175.1191	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **SWAPDR**

170907_Skadi_peptide_35451 #74 RT: 0.81 AV: 1 NL: 3.76E5
T: FTMS + p NSI d Full ms2 366.1773@hcd30.00 [51.0000-7]

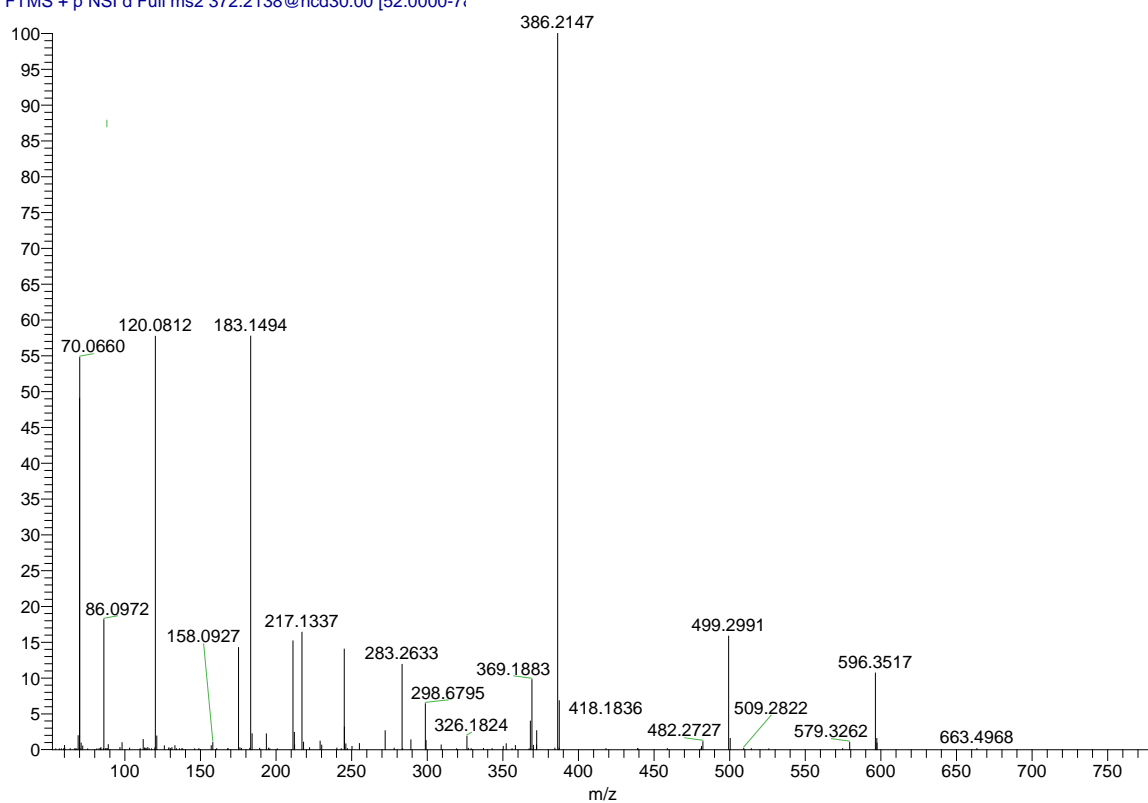


MS/MS mass 366.1773 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	S	---	---
	274.1187	274.1186	W	644.3152	644.3151
	345.1553	345.1557	A	458.2361	458.2358
	442.2141	442.2085	P	387.1988	387.1987
	-	557.2354	D	290.1460	290.1459
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **FPIPNR**

170907_Skadi_peptide_35451 #34-34 RT: 0.59-0.59 AV: 2 NL: 5.08E6
T: FTMS + p NSI d Full ms2 372.2138@hcd30.00 [52.0000-71

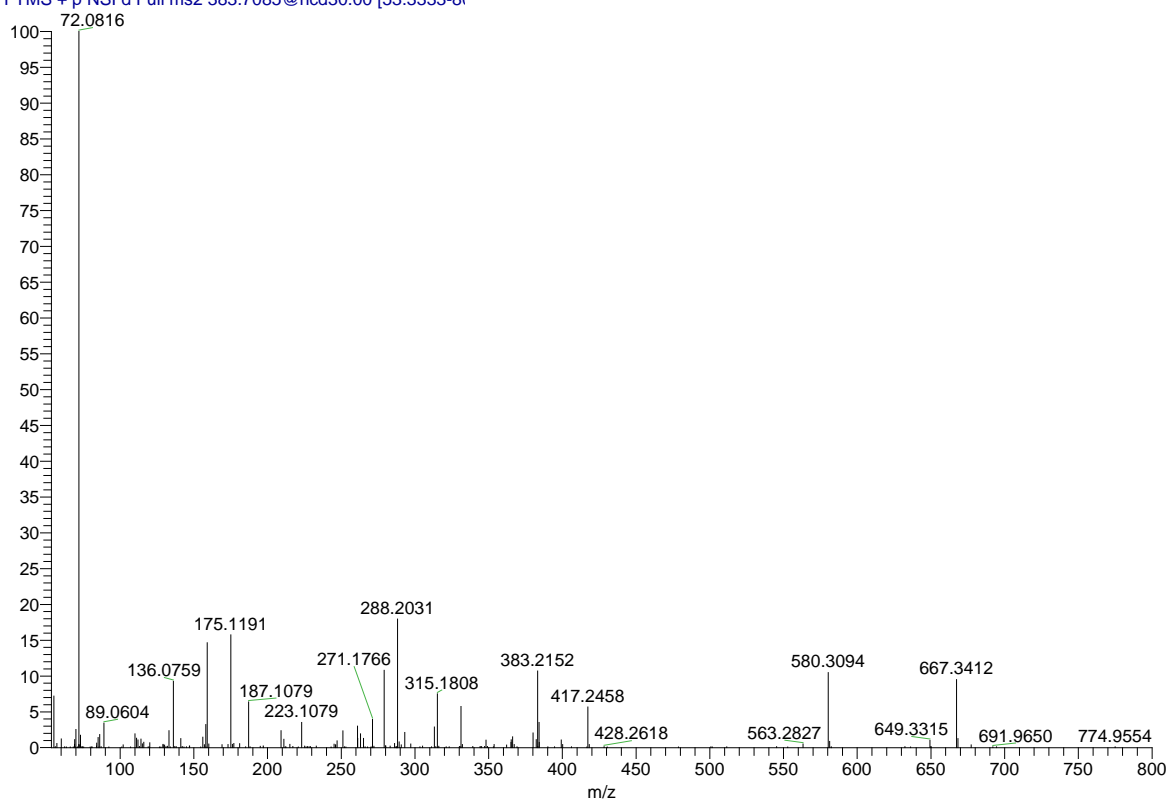


MS/MS mass 372.2138 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	F	---	---
	245.1286	245.1285	P	596.3517	596.3515
	358.2125	358.2125	I	499.2991	499.2987
	-	455.2653	P	386.2147	386.2146
	-	569.3082	N	289.1621	289.1619
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **VSYELR**

170907_Skadi_peptide_35451 #46-46 RT: 0.66-0.66 AV: 2 NL: 2.27E6
 T: FTMS + p NSI d Full ms2 383.7085@hcd30.00 [53.3333-8]

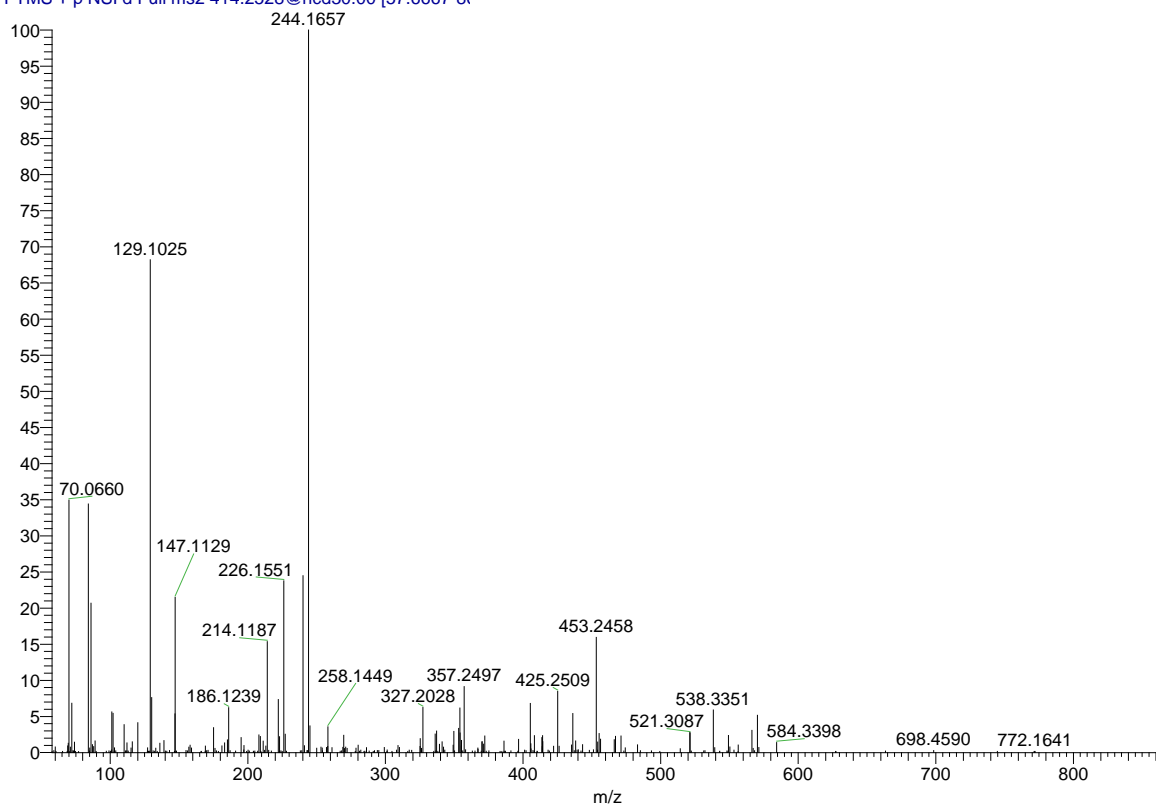


MS/MS mass 383.7085 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	V	---	---
	187.1079	187.1077	S	667.3412	667.3410
	-	350.1710	Y	580.3094	580.3089
	-	479.2136	E	417.2458	417.2456
	-	592.2977	L	288.2031	288.2030
	---	---	R	175.1191	175.1190

Mass spectrometry of **banana catalase** – MS/MS

MS/MS of fragment: **EKNVIPK**

170907_Skadi_peptide_35451 #65 RT: 0.76 AV: 1 NL: 5.60E5
 T: FTMS + p NSI d Full ms2 414.2528@hcd30.00 [57.6667-8]

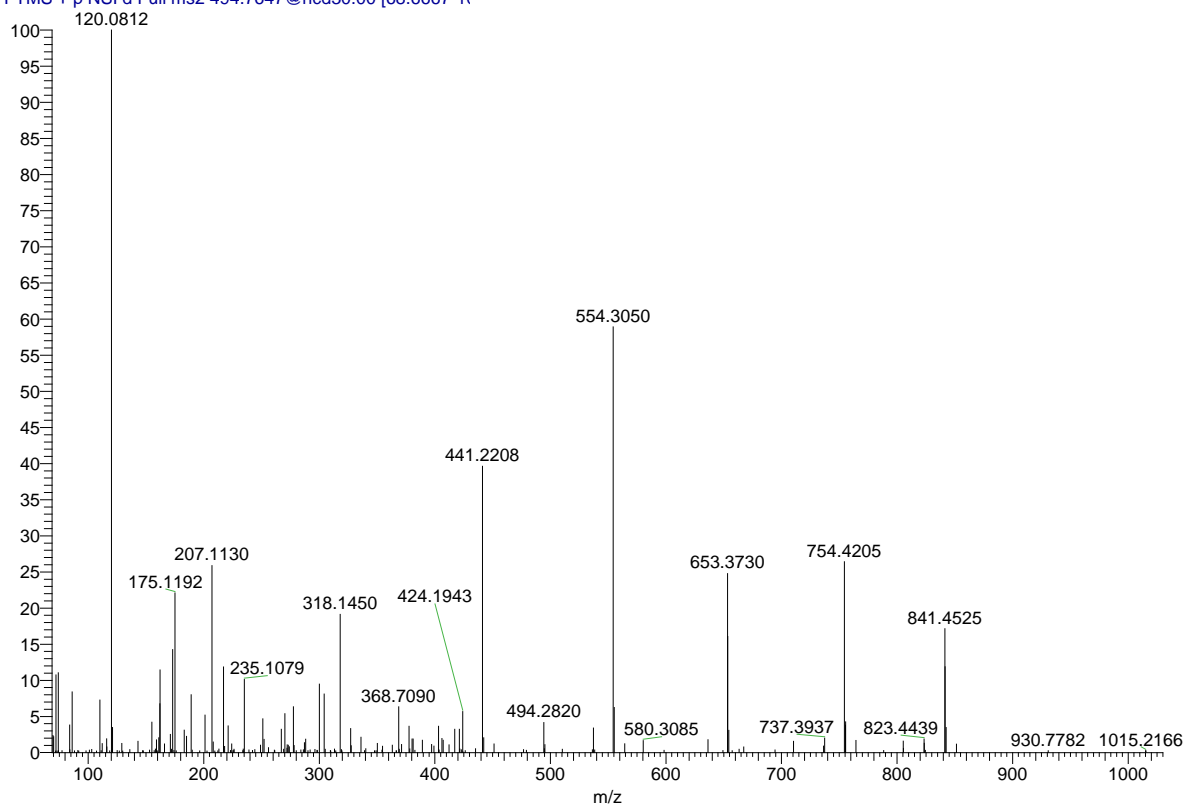


MS/MS mass 414.2528 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	E	---	---
	258.1449	258.1448	K	698.4590	698.4559
	372.1879	372.1878	N	570.3613	570.3610
	471.2567	471.2562	V	456.3179	456.3180
	584.3398	584.3402	I	357.2497	357.2496
	-	681.3930	P	244.1657	244.1656
	---	---	K	147.1129	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **FSTVIHER**

170907_Skadi_peptide_35451 #37 RT: 0.60 AV: 1 NL: 1.99E6
T: FTMS + p NSI d Full ms2 494.7647@hcd30.00 [68.6667-1]

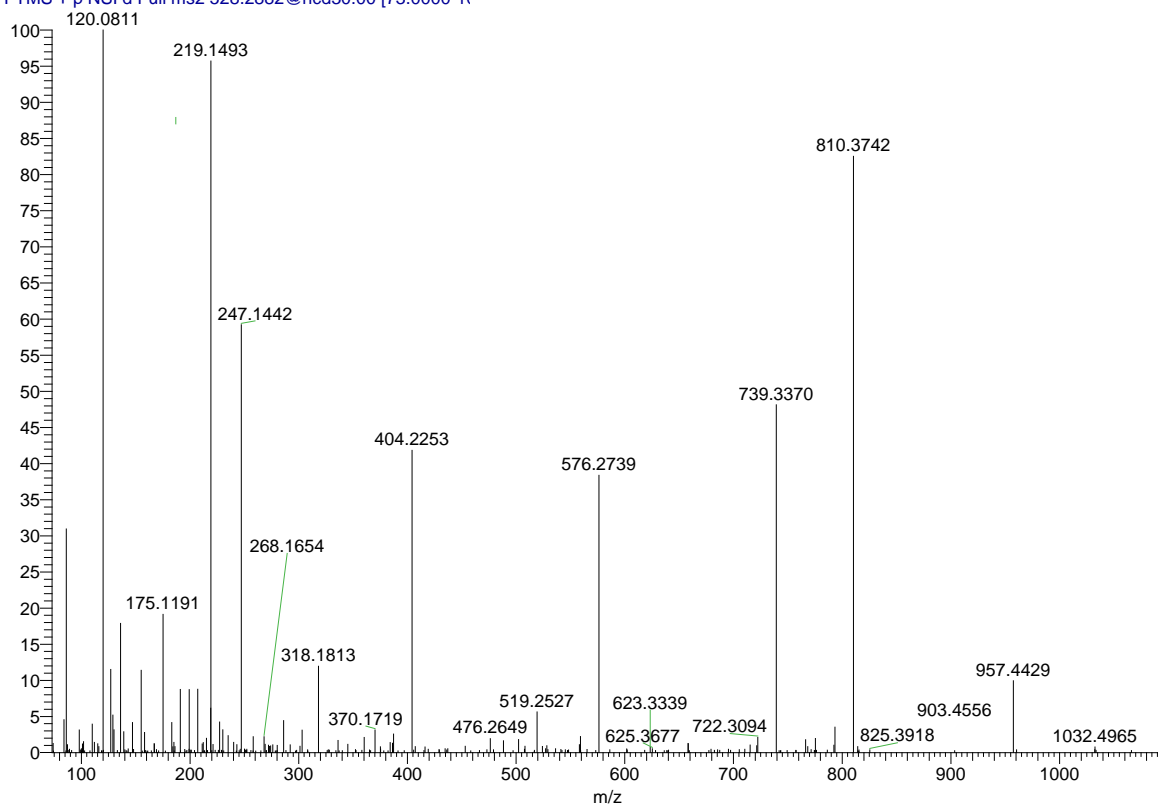


MS/MS mass 494.7647 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	F	---	---
	235.1079	235.1077	S	841.4525	841.4526
	336.1555	336.1554	T	754.4205	754.4206
	435.2240	435.2238	V	653.3730	653.3729
	-	548.3079	I	554.3050	554.3045
	-	685.3668	H	441.2208	441.2205
	-	814.4094	E	304.1617	304.1615
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **VFAYGDTQR**

170907_Skadi_peptide_35451 #92 RT: 0.92 AV: 1 NL: 7.78E5
 T: FTMS + p NSI d Full ms2 528.2882@hcd30.00 [73.0000-1(

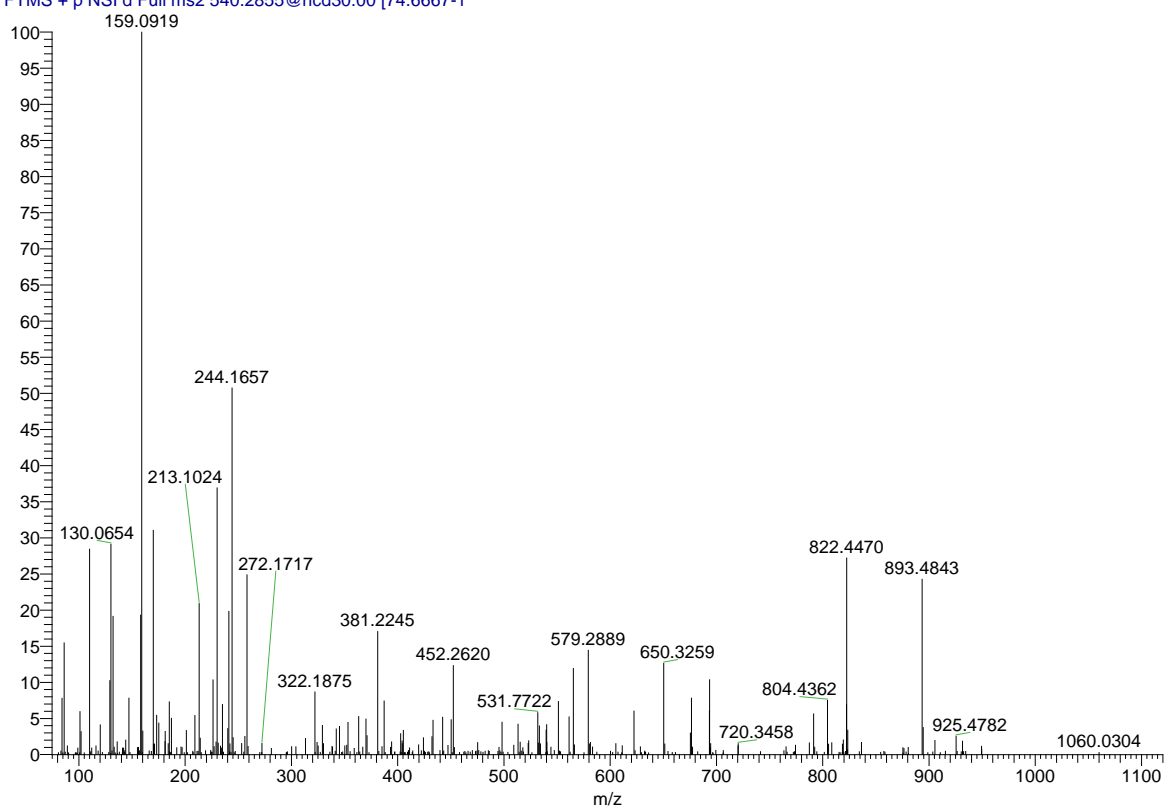


MS/MS mass 528.2882 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	V	---	---
	247.1442	247.1441	F	957.4429	957.4425
	318.1813	318.1812	A	810.3742	810.3741
	-	481.2445	Y	739.3370	739.3369
	-	538.2660	G	576.2739	576.2736
	-	653.2930	D	519.2527	519.2522
	-	754.3406	T	404.2253	404.2252
	-	882.3992	Q	303.1776	303.1775
	---	---	R	175.1191	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **WAEQLAHPK**

170907_Skadi_peptide_35451 #58 RT: 0.72 AV: 1 NL: 7.11E5
 T: FTMS + p NSI d Full ms2 540.2855@hcd30.00 [74.6667-1]

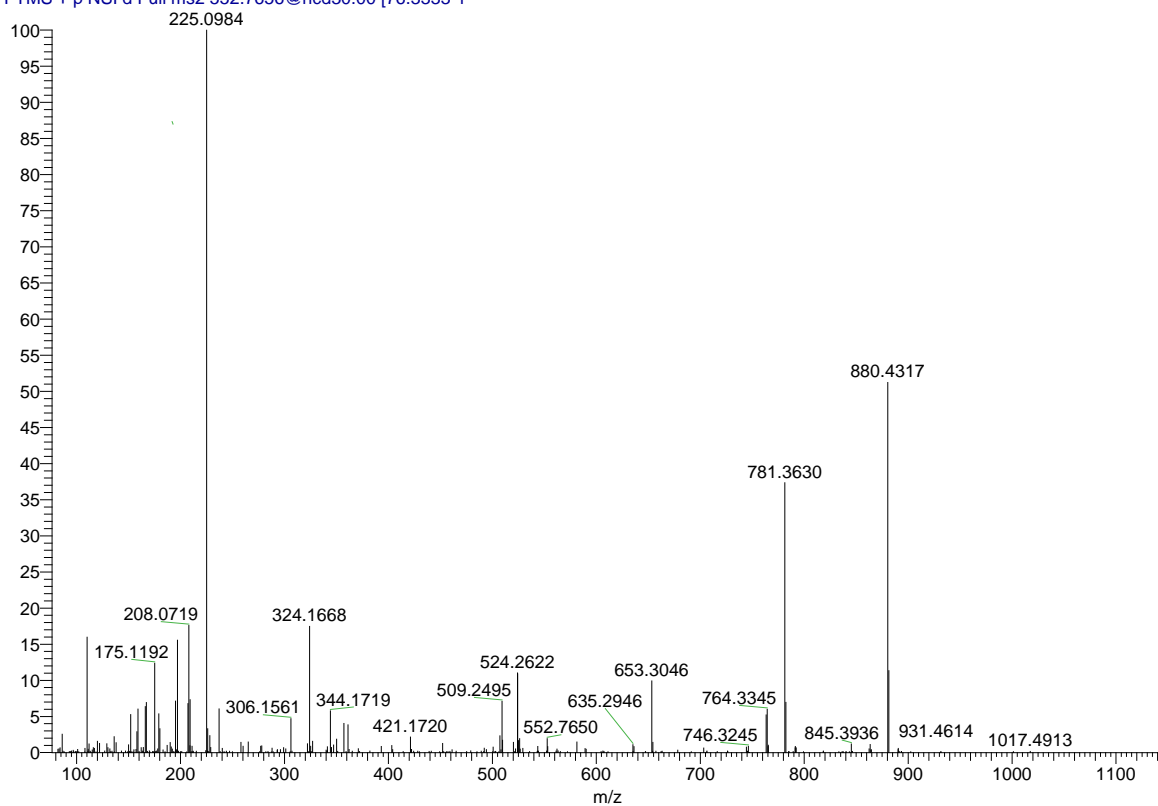


MS/MS mass 540.2855 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
		---	---	W	---
	258.1238	258.1237	A	893.4843	893.4839
	387.1664	387.1663	E	822.4470	822.4468
	515.2262	515.2249	Q	693.4043	693.4042
	628.3081	628.3089	L	565.3461	565.3457
	699.3445	699.3461	A	452.2620	452.2616
	836.4040	836.4050	H	381.2245	381.2245
	-	933.4577	P	244.1657	244.1656
	---	---	K	147.1130	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **SHVQEYWR**

170907_Skadi_peptide_35451 #47 RT: 0.66 AV: 1 NL: 2.03E6
T: FTMS + p NSI d Full ms2 552.7656@hcd30.00 [76.3333-1]

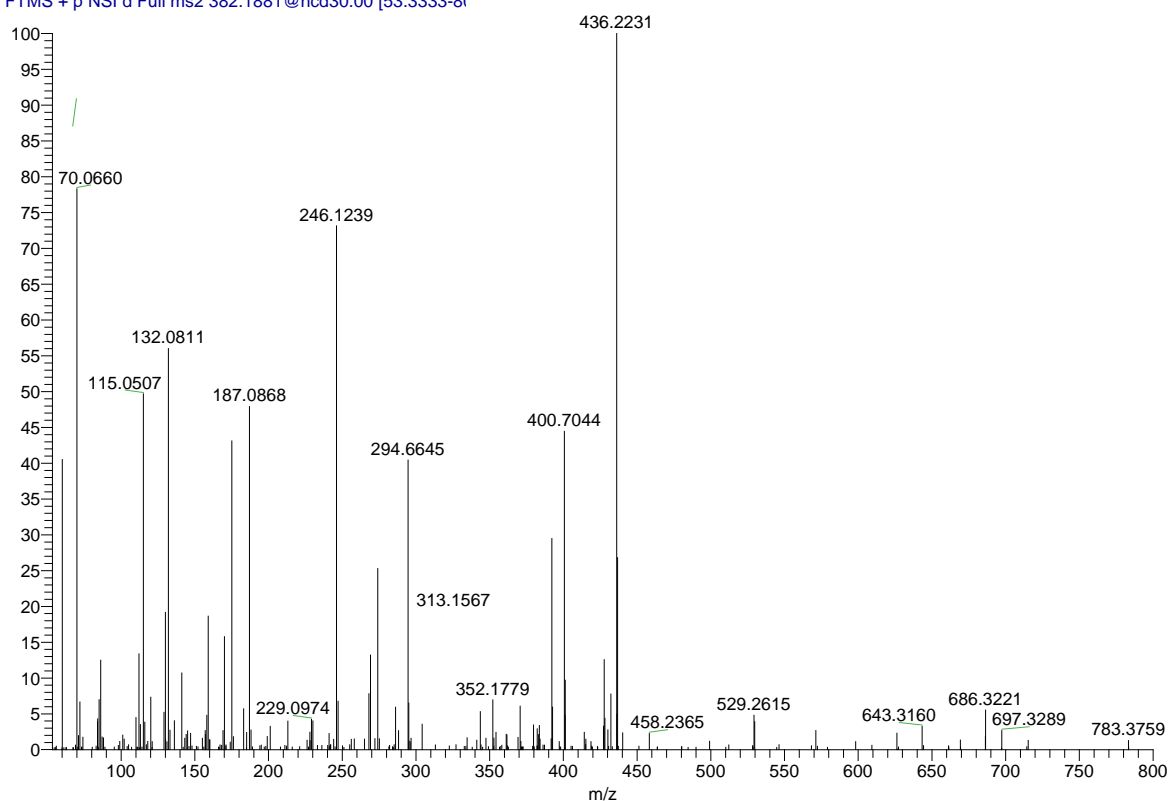


MS/MS mass 552.7656 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	S	---	---
	225.0984	225.0982	H	1017.4913	1017.4901
	324.1668	324.1666	V	880.4317	880.4312
	452.2253	452.2252	Q	781.3630	781.3628
	581.2675	581.2678	E	653.3046	653.3042
	744.3320	744.3311	Y	524.2622	524.2616
	-	930.4104	W	361.1985	361.1983
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **SWAPDRQER**

170907_Skadi_peptide_35451 #170 RT: 1.38 AV: 1 NL: 1.96E5
 T: FTMS + p NSI d Full ms2 382.1881 @hcd30.00 [53.3333-8]

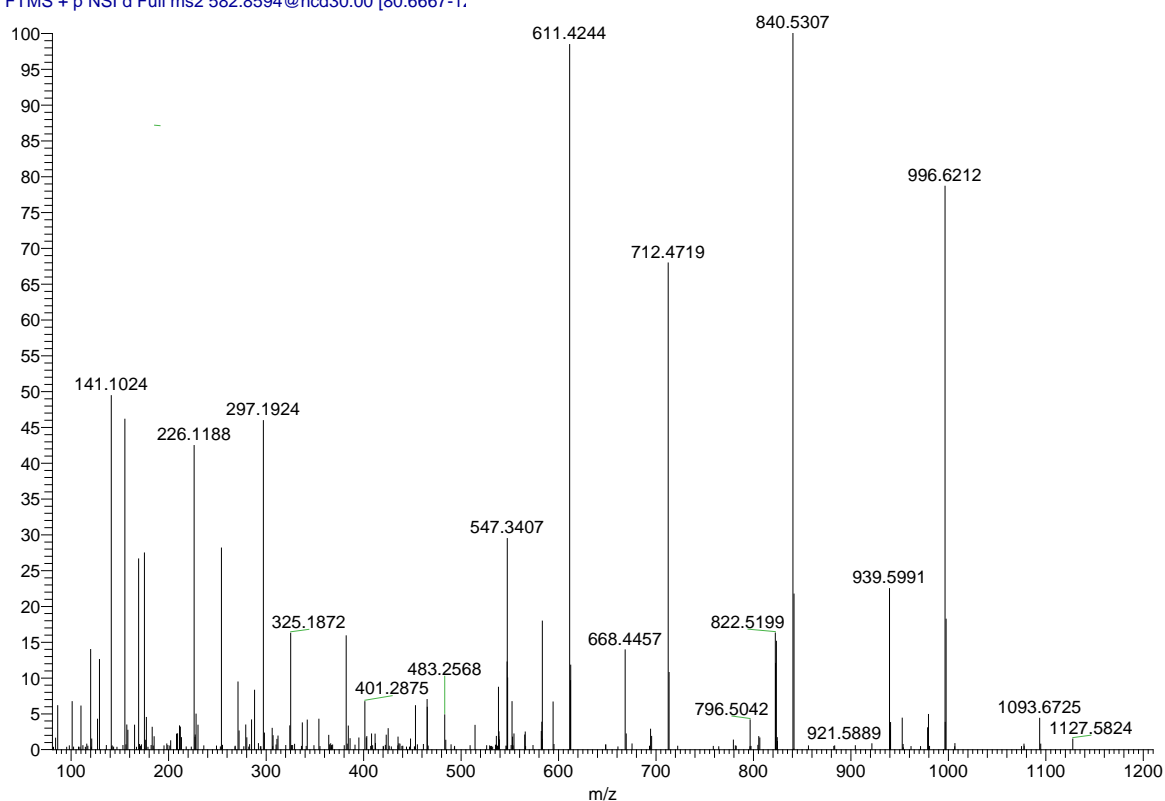


MS/MS mass 382.1881 m/z [M+H] ³⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y ²⁺ -ion determined	Mass y ²⁺ -ion thero.
	---	---	S	---	---
	274.1187	274.1186	W	529.2615	529.2623
	345.1555	345.1557	A	436.2231	436.2227
	-	442.2085	P	400.7044	400.7041
	-	557.2354	D	352.1779	352.1777
	-	713.3365	R	294.6645	294.6643
	-	841.3951	Q	-	216.6137
	-	970.4377	E	-	152.5844
	---	---	R	88.0400	88.0631

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **APGVQTPPIILR**

170907_Skadi_peptide_35451 #35 RT: 0.59 AV: 1 NL: 2.06E6
T: FTMS + p NSI d Full ms2 582.8594@hcd30.00 [80.6667-1]

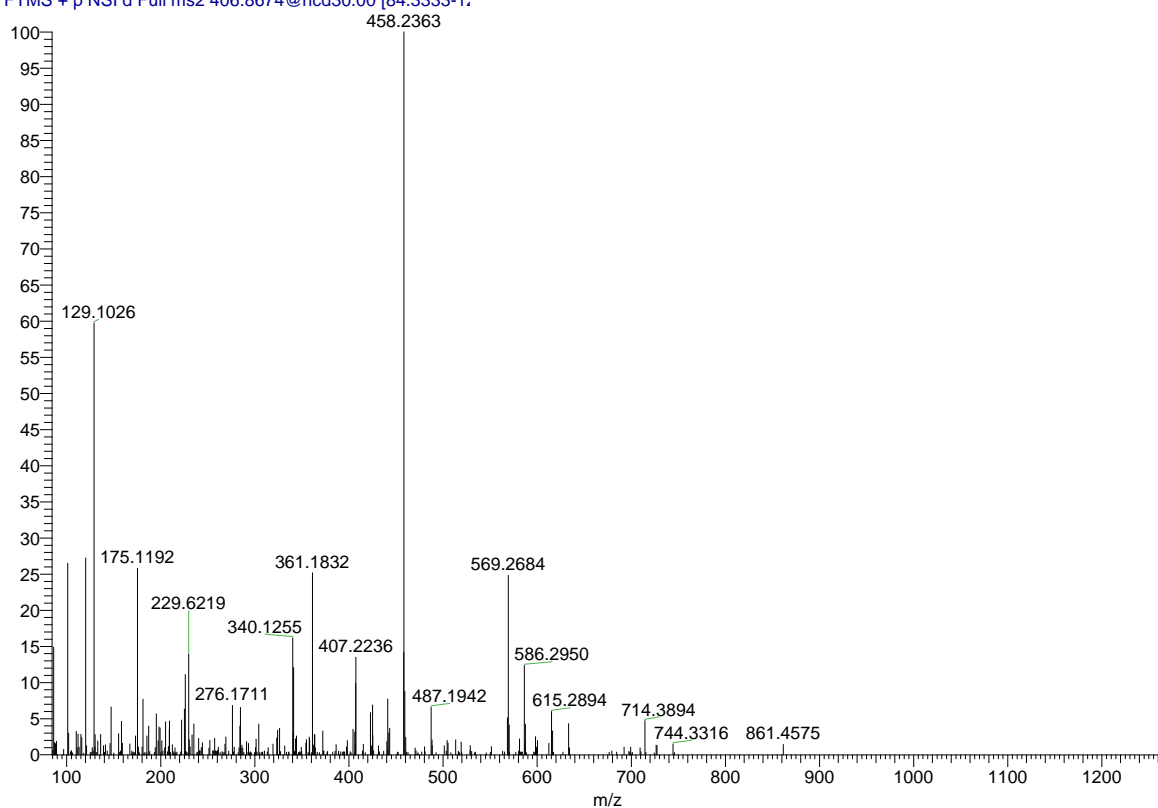


MS/MS mass 582.8594 m/z [M+H] ²⁺ :	Mass b-ion	Mass b-ion	Amino Acid sequence	Mass y-ion	Mass y-ion
	determined	thero.		determined	thero.
	---	---	A	---	---
	169.0974	169.0972	P	1093.6725	1093.6728
	226.1188	226.1186	G	996.6212	996.6200
	325.1872	325.1870	V	939.5991	939.5986
	453.2461	453.2456	Q	840.5307	840.5302
	554.2941	554.2933	T	712.4719	712.4716
	-	651.3461	P	611.4244	611.4239
	764.4304	764.4301	I	514.3727	514.3711
	-	877.5142	I	401.2875	401.2871
	-	990.5982	L	288.2032	288.2030
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **QNDFKQPGER**:

170907_Skadi_peptide_35451 #149 RT: 1.26 AV: 1 NL: 2.26E5
T: FTMS + p NSI d Full ms2 406.8674@hcd30.00 [84.3333-1;

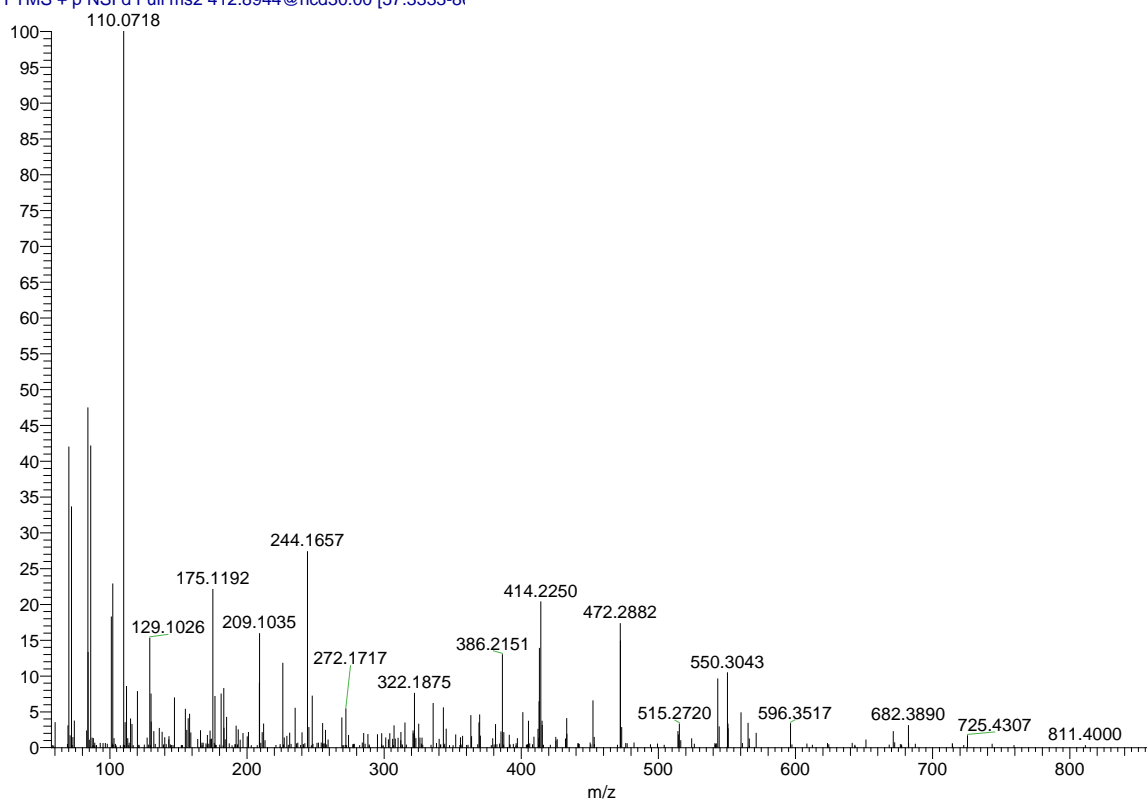


MS/MS mass 406.8674 m/z [M+H] ³⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	Q	---	---
	-	243.1088	N	-	1090.5276
	358.1354	358.1357	D	-	976.4847
	505.2047	505.2041	F	861.4575	861.4577
	633.2996	633.2991	K	714.3894	714.3893
	-	761.3577	Q	586.2950	586.2944
	-	858.4104	P	458.2363	458.2358
	-	915.4319	G	361.1832	361.1830
	-	1044.4745	E	304.1618	304.1615
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **RWAEQLAHPK**

170907_Skadi_peptide_35451 #128 RT: 1.13 AV: 1 NL: 3.17E5
 T: FTMS + p NSI d Full ms2 412.8944@hcd30.00 [57.3333-8f]

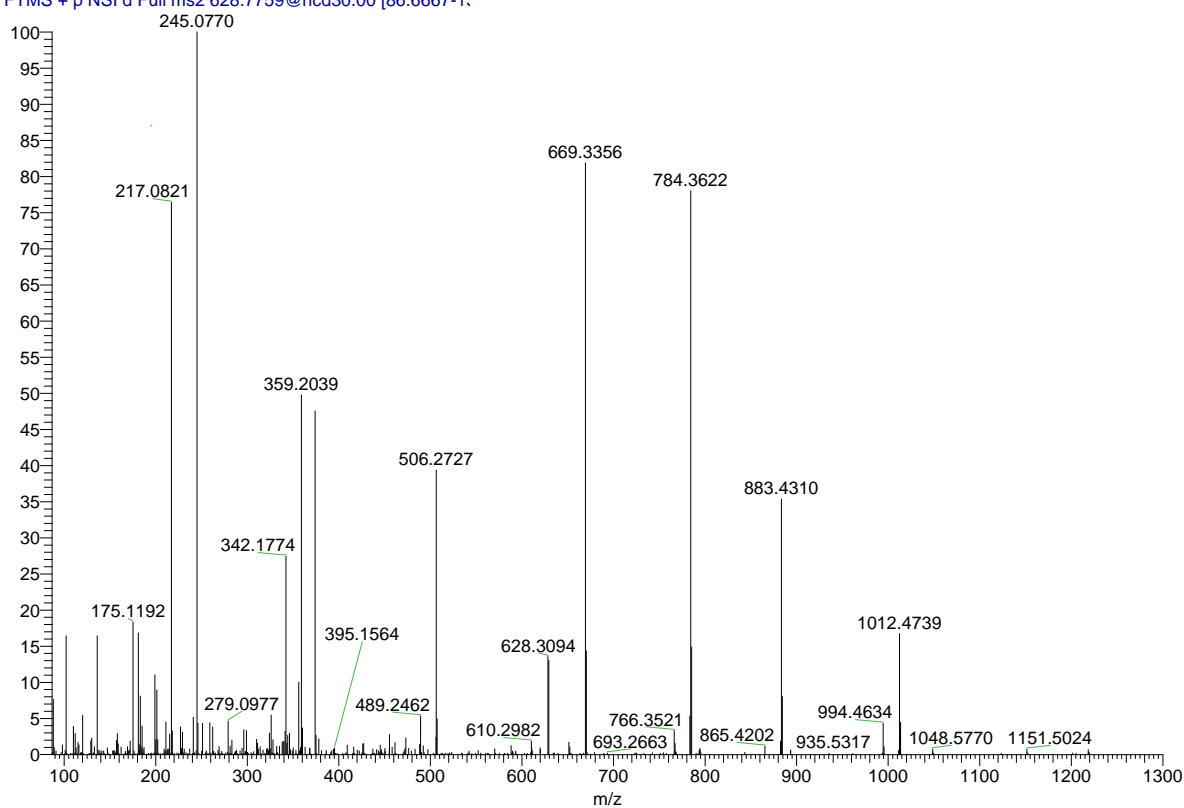


MS/MS mass 412.8944 m/z [M+H] ³⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	R	---	---
	343.1878	343.1877	W	-	1079.5633
	414.2250	414.2248	A	-	893.4839
	543.2676	543.2674	E	-	822.4468
	671.3250	671.3260	Q	-	693.4042
	-	784.4100	L	565.3453	565.3457
	-	855.4472	A	452.2619	452.2616
	-	992.5061	H	381.2245	381.2245
	-	1089.5588	P	244.1657	244.1656
	---	---	K	147.1129	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **DEEVDYFPSR**

170907_Skadi_peptide_35451 #54 RT: 0.69 AV: 1 NL: 5.66E5
T: FTMS + p NSI d Full ms2 628.7759@hcd30.00 [86.6667-1;

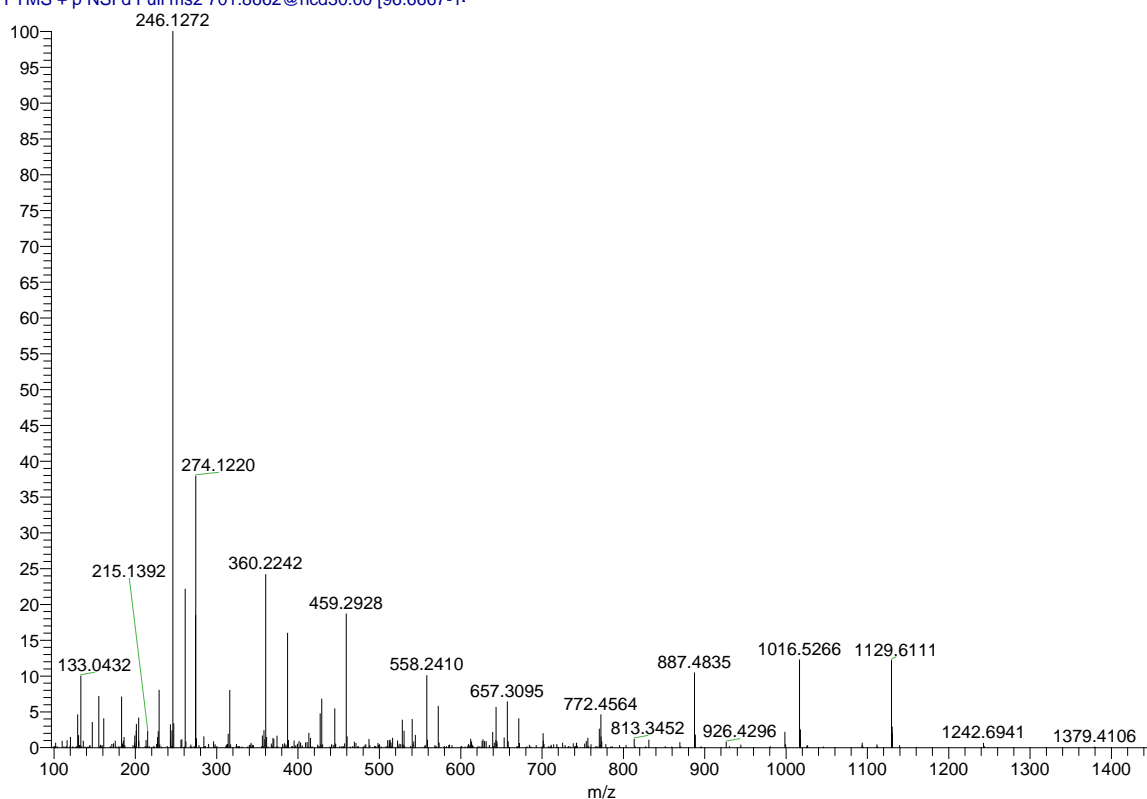


MS/MS mass 628.7759 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	D	---	---
	245.0770	245.0768	E	-	1141.5160
	374.1195	374.1194	E	1012.4739	1012.4734
	473.1885	473.1878	V	883.4310	883.4308
	588.2153	588.2148	D	784.3622	784.3624
	751.2764	751.2781	Y	669.3356	669.3355
	-	898.3465	F	506.2727	506.2722
	-	995.3993	P	359.2039	359.2037
	-	1082.4313	S	262.1511	262.1510
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **CLLEDEAIVVGGK**

170907_Skadi_peptide_35451_#61 RT: 0.74 AV: 1 NL: 1.38E6
T: FTMS + p NSI d Full ms2 701.8662@hcd30.00 [96.6667-1

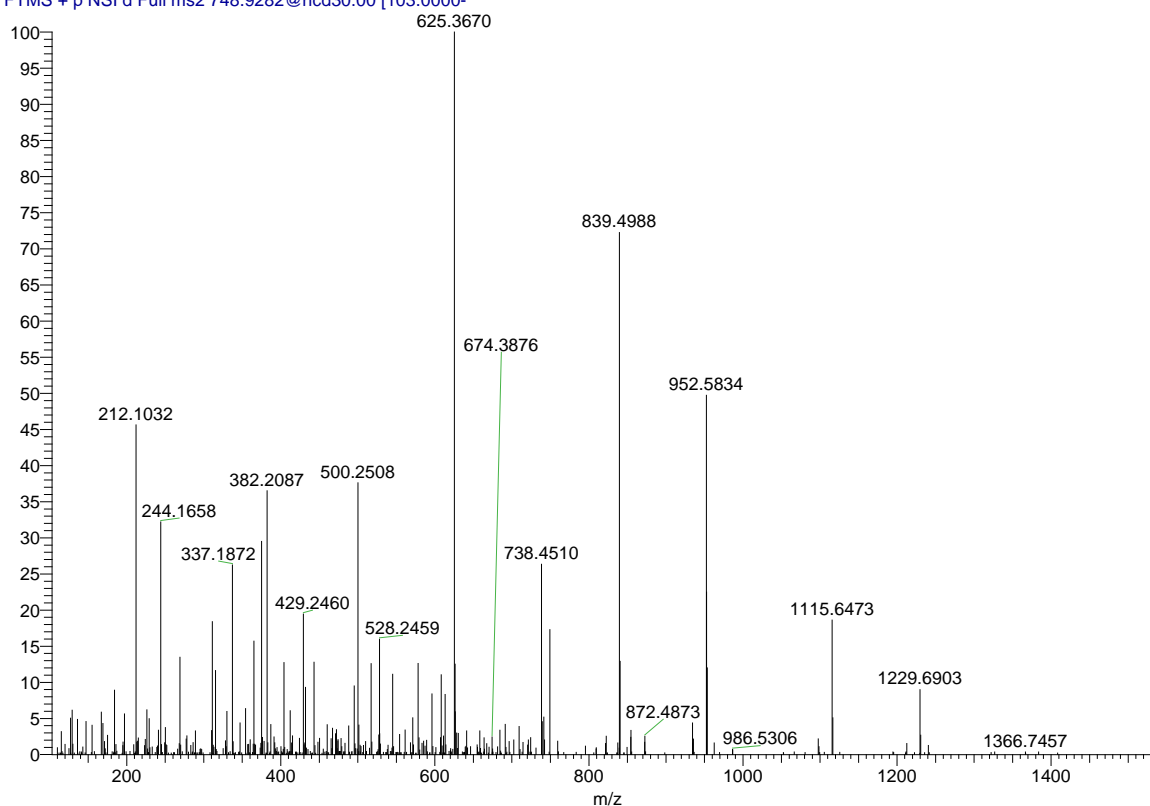


MS/MS mass 701.8662 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	C (CAM)	---	---
	274.1220	274.1220	L	1242.6941	1242.6940
	387.2062	387.2061	L	1129.6111	1129.6099
	516.2488	516.2486	E	1016.5266	1016.5259
	631.2759	631.2756	D	887.4835	887.4833
	760.3184	760.3182	E	772.4564	772.4563
	831.3561	831.3553	A	643.4141	643.4137
	944.4405	944.4394	I	572.3770	572.3766
	-	1043.5078	V	459.2928	459.2926
	-	1142.5762	V	360.2242	360.2241
	-	1199.5977	G	261.1559	261.1557
	-	1256.6191	G	204.1345	204.1343
	---	---	K	147.1130	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **LGPNYLTLPVNAPK**

170907_Skadi_peptide_35451 #48 RT: 0.67 AV: 1 NL: 9.99E5
T: FTMS + p NSI d Full ms2 748.9282@hcd30.00 [103.0000-]



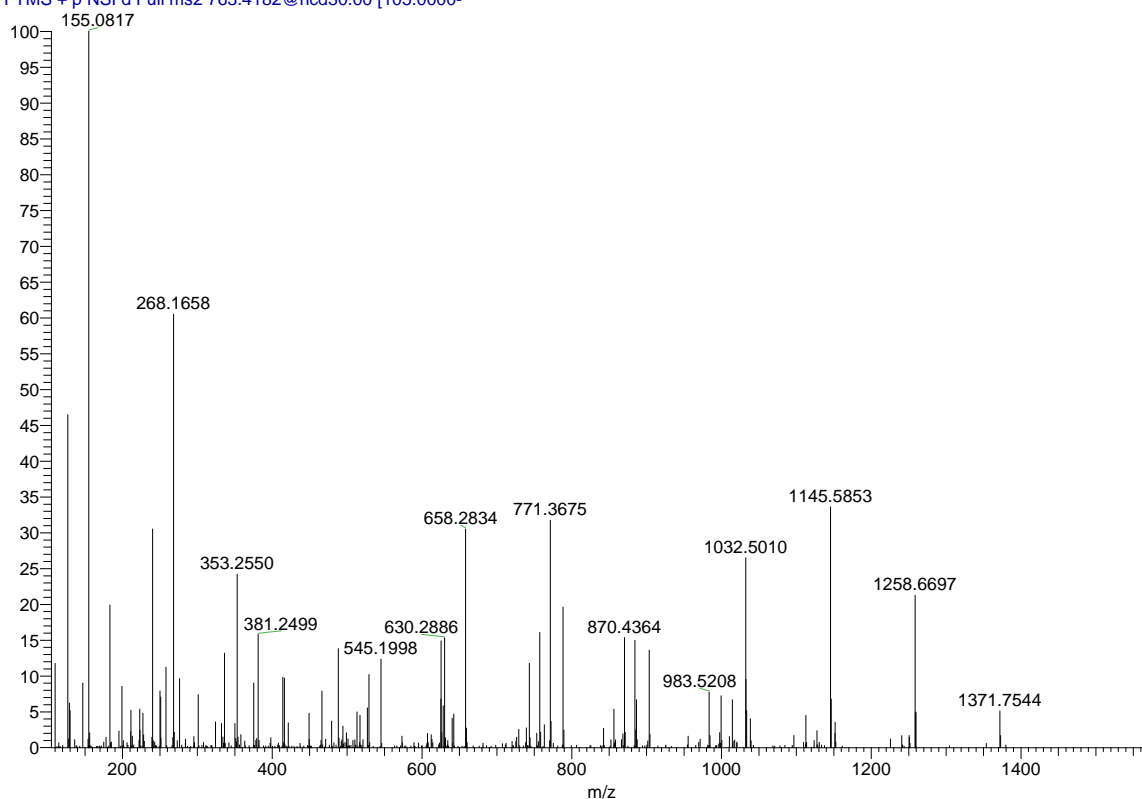
MS/MS mass
748.9282 m/z
[M+H]²⁺:

Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
---	---	L	---	---
171.1129	171.1128	G	1383.7668	1383.7631
268.1658	268.1656	P	1326.7396	1326.7416
382.2087	382.2085	N	1229.6903	1229.6888
545.2723	545.2718	Y	1115.6473	1115.6459
658.3563	658.3559	L	952.5834	952.5826
759.4048	759.4036	T	839.4988	839.4985
872.4873	872.4876	L	738.4510	738.4509
969.5087	969.5404	P	625.3670	625.3668
-	1068.6088	V	528.3144	528.3140
-	1182.6517	N	429.2460	429.2456
-	1253.6888	A	315.2029	315.2027
-	1350.7416	P	244.1658	244.1656
---	---	K	147.1129	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **GPILLEDYHLVEK**

170907_Skadi_peptide_35451 #50 RT: 0.67 AV: 1 NL: 1.22E6
 T: FTMS + p NSI d Full ms2 763.4182@hcd30.00 [105.0000-

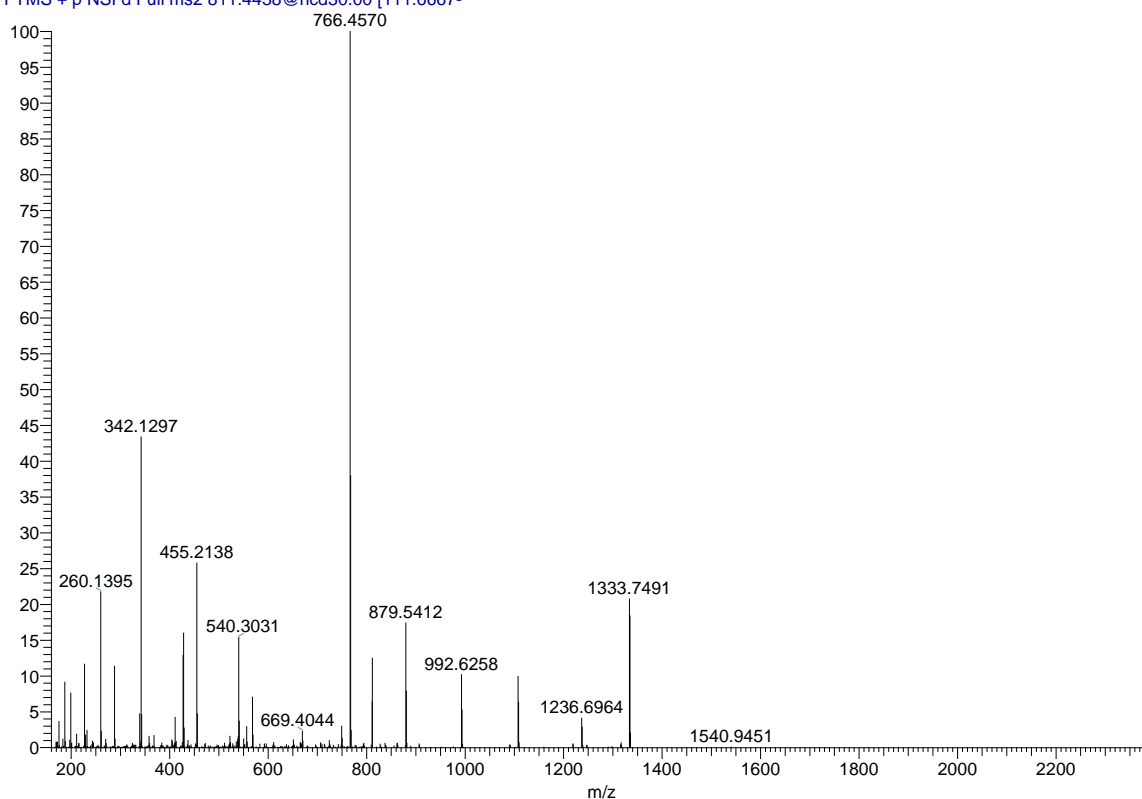


MS/MS mass 763.4182 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	G	---	---
	155.0817	155.0815	P	-	1468.8046
	268.1658	268.1656	I	1371.7544	1371.7518
	381.2499	381.2496	L	1258.6697	1258.6678
	494.3343	494.3337	L	1145.5853	1145.5837
	623.3776	623.3763	E	1032.5010	1032.4997
	738.4037	738.4032	D	903.4576	903.4571
	901.4672	901.4666	Y	788.4307	788.4301
	1038.5264	1038.5255	H	625.3672	625.3668
	1151.6112	1151.6095	L	488.3084	488.3079
	1250.6803	1250.6780	V	375.2241	375.2238
	1379.7177	1379.7205	E	276.1556	276.1554
	---	---	K	147.1130	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **TWPEDLLPLQPVGR**

170907_Skadi_peptide_35451 #53 RT: 0.69 AV: 1 NL: 1.70E6
 T: FTMS + p NSI d Full ms2 811.4438@hcd30.00 [111.6667-111.6667]

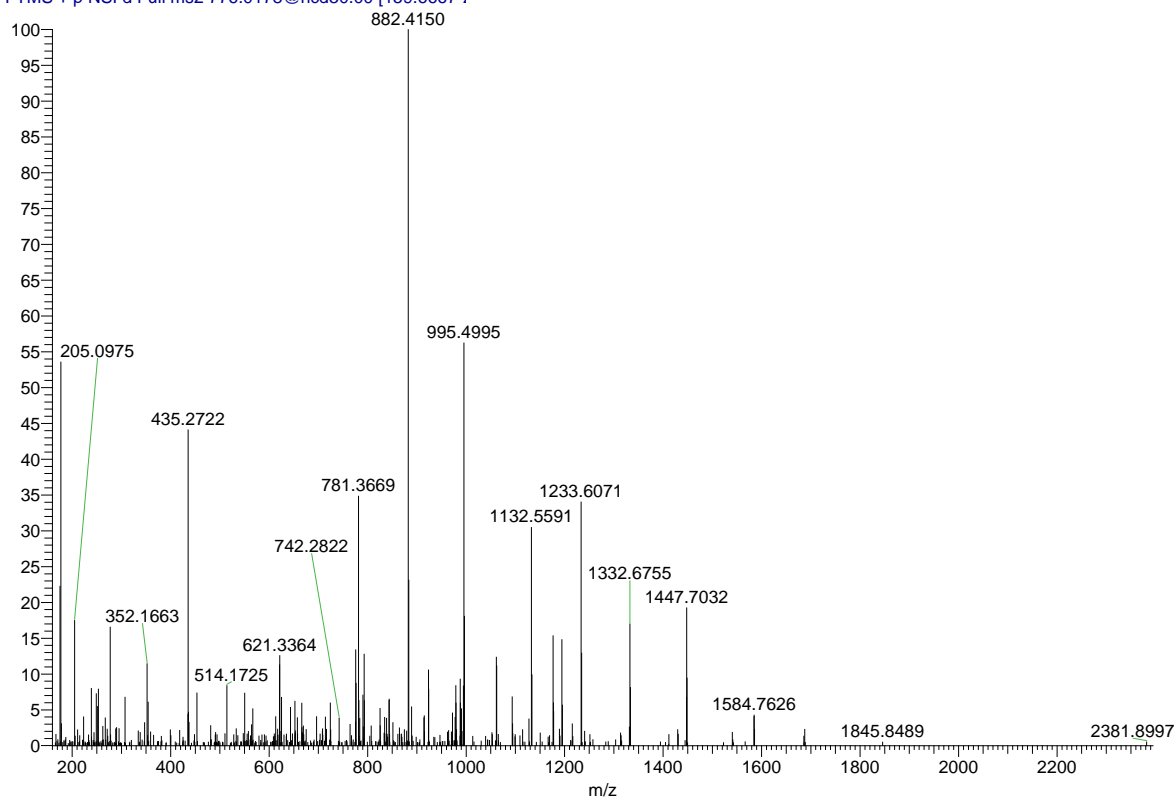


MS/MS mass 811.4438 m/z [M+H] ²⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	T	---	---
	288.1343	288.1343	W	-	1519.8267
	-	385.1870	P	1333.7491	1333.7474
	514.2299	514.2296	E	1236.6964	1236.6947
	629.2562	629.2566	D	1107.6530	1107.6521
	742.3405	742.3406	L	992.6258	992.6251
	855.4257	855.4247	L	879.5412	879.5411
	-	952.4775	P	766.4570	766.4570
	-	1065.5615	L	669.4044	669.4042
	-	1193.6201	Q	556.3206	556.3202
	-	1290.6729	P	428.3002	428.2616
	-	1389.7413	V	331.2090	331.2088
	-	1446.7627	G	232.1405	232.1404
	---	---	R	175.1192	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **GFFECTHDVTHLTCADFLR**

170907_Skadi_peptide_35451 #278 RT: 2.03 AV: 1 NL: 1.67E5
 T: FTMS + p NSI d Full ms2 776.0178@hcd30.00 [159.6667-4



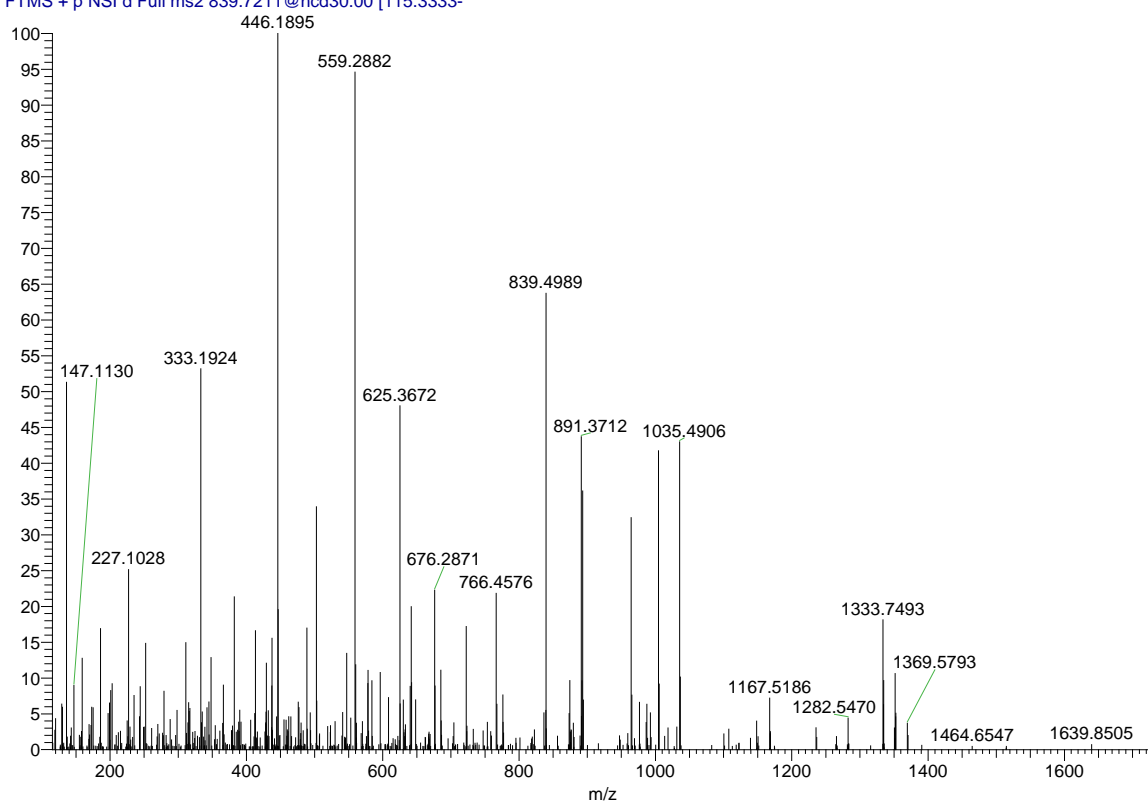
MS/MS mass
 776.0178 m/z
 [M+H]³⁺:

Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
---	---	G	---	---
205.0975	205.0972	F	-	2269.0165
352.1663	352.1656	F	-	2121.9481
481.2082	481.2082	E	-	1974.8797
641.2401	641.2388	C (CAM)	1845.8489	1845.8371
742.2822	742.2865	T	1685.8091	1685.8064
879.3464	879.3454	H	1584.7626	1584.7587
994.3741	994.3723	D	1447.7032	1447.6998
1093.4393	1093.4408	V	1332.6755	1332.6729
1194.4906	1194.4884	T	1233.6071	1233.6045
1331.5518	1331.5473	H	1132.5591	1132.5568
1444.6368	1444.6314	L	995.4995	995.4979
-	1545.6791	T	882.4150	882.4138
-	1705.7097	C (CAM)	781.3669	781.3661
-	1776.7469	A	621.3364	621.3355
-	1891.7738	D	550.2993	550.2984
-	2038.8422	F	435.2722	435.2714
-	2151.9263	L	288.2032	288.2030
---	---	R	175.1193	175.1190

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **NHSHATQDLYDSIAAGNYPEWK**

170907_Skadi_peptide_35451 #345 RT: 2.43 AV: 1 NL: 1.57E5
 T: FTMS + p NSI d Full ms2 839.7211@hcd30.00 [115.3333-1639.8505]

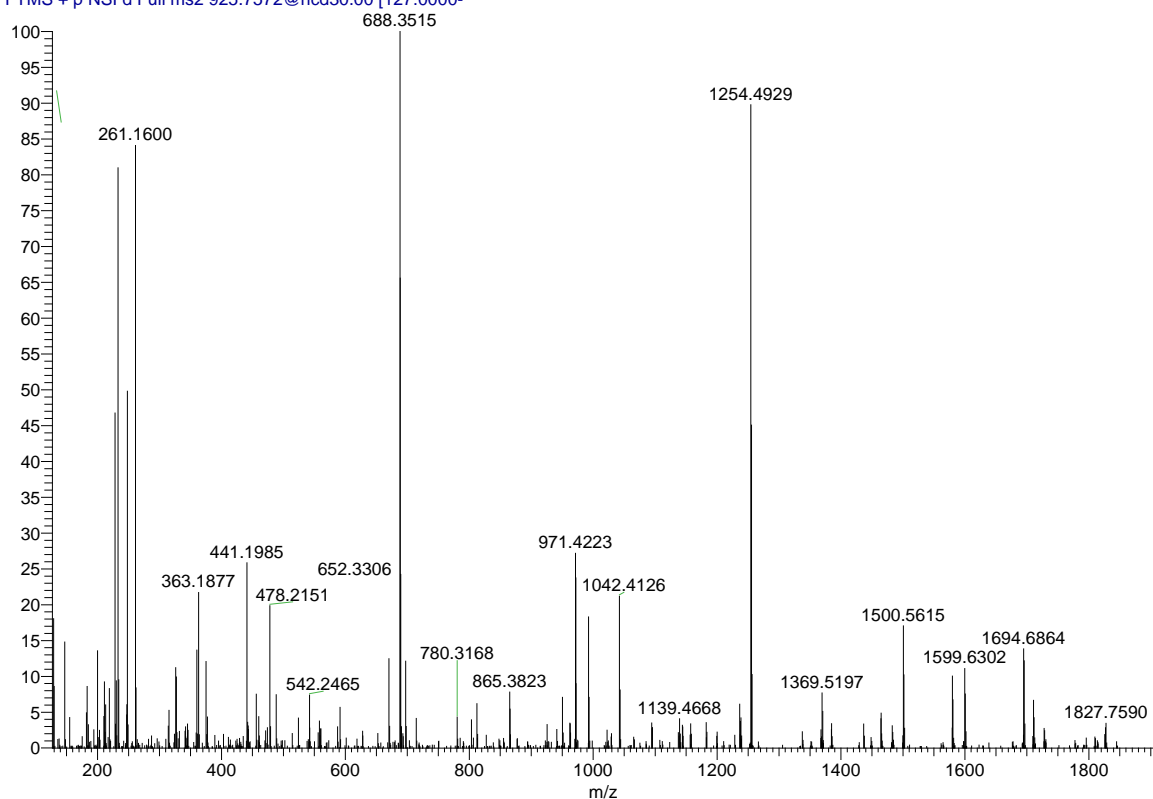


MS/MS mass 839.7211 m/z [M+H] ³⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
	---	---	N	---	---
	252.1094	252.1091	H	-	2403.1000
	339.1414	339.1411	S	-	2266.0411
	476.2011	476.2001	H	-	2179.0091
	547.2382	547.2372	A	-	2041.9502
	648.2863	648.2848	T	-	1970.9130
	776.3434	776.3434	Q	-	1869.8654
	891.3712	891.3704	D	-	1741.8068
	1004.4556	1004.4544	L	-	1626.7798
	1167.5186	1167.5178	Y	-	1513.6958
	1282.5470	1282.5447	D	1350.6389	1350.6325
	1369.5739	1369.5767	S	1235.6080	1235.6055
	-	1482.6608	I	1148.5747	1148.5735
	-	1553.6979	A	1035.4906	1035.4894
	-	1624.7350	A	964.4534	964.4523
	-	1681.7565	G	893.4161	893.4152
	-	1795.7994	N	836.3937	836.3937
	-	1958.8627	Y	722.3513	722.3508
	-	2055.9155	P	559.2882	559.2875
	-	2184.9581	E	462.2354	462.2347
	-	2371.0374	W	333.1924	333.1921
	---	---	K	147.1130	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **LFVQVMDPDTEDRYDFDPLDDTK** (without oxidation)

170907_Skadi_peptide_35451 #100 RT: 0.97 AV: 1 NL: 3.85E5
T: FTMS + p NSI d Full ms2 925.7572@hcd30.00 [127.0000-1827.7590]



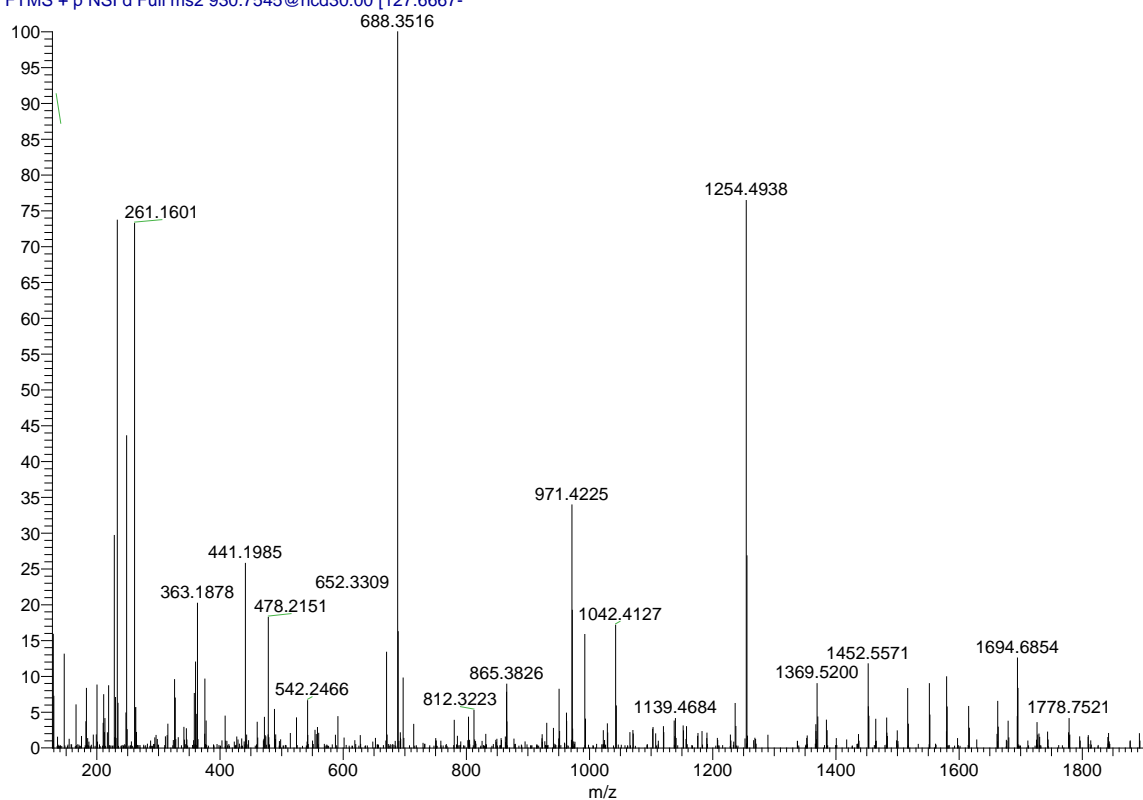
MS/MS mass
925.7572 m/z
[M+H]³⁺:

Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
---	---	L	---	---
261.1600	261.1598	F	-	2661.1661
360.2285	360.2282	V	-	2514.0977
488.2873	488.2867	Q	-	2415.0293
587.3556	587.3552	V	-	2286.9707
718.8193	718.3956	M	-	2187.9023
833.4254	833.4226	D	-	2056.8618
-	930.4754	P	-	1941.8349
-	1045.5023	D	1844.7825	1844.7821
-	1146.5500	T	1729.7632	1729.7552
-	1275.5926	E	1628.7104	1628.7075
-	1390.6195	D	1499.6694	1499.6649
-	1546.7206	R	1384.6411	1384.6379
-	1709.7839	Y	1228.5388	1228.5368
-	1824.8109	D	1065.4730	1065.4735
-	1971.8793	F	950.4476	950.4466
-	2086.9062	D	803.3790	803.3781
-	2183.9590	P	688.3515	688.3512
-	2297.0431	L	591.2990	591.2984
-	2412.0700	D	478.2151	478.2144
-	2527.0970	D	363.1877	363.1874
-	2628.1446	T	248.1608	248.1605
---	---	K	147.1130	147.1128

Mass spectrometry of banana catalase – MS/MS

MS/MS of fragment: **LFVQVMDPDTEDRYDFDPLDDTK (with methionine oxidation)**

170907_Skadi_peptide_35451 #146 RT: 1.24 AV: 1 NL: 3.00E5
T: FTMS + p NSI d Full ms2 930.7545@hcd30.00 [127.6667-]



MS/MS mass 930.7545 m/z [M+H] ³⁺ :	Mass b-ion determined	Mass b-ion thero.	Amino Acid sequence	Mass y-ion determined	Mass y-ion thero.
		---	---	L	---
	261.1601	261.1598	F	-	2677.1610
	360.2285	360.2282	V	-	2530.0926
	488.2873	488.2867	Q	-	2431.0242
	587.3555	587.3552	V	-	2302.9656
	-	734.3906	M (MSO)	-	2203.8972
	849.4175	849.4175	D	-	2056.8618
	-	946.4703	P	-	1941.8349
	-	1061.4972	D	1844.7927	1844.7821
	-	1162.5449	T	1729.7524	1729.7552
	-	1291.5875	E	1628.7085	1628.7075
	-	1406.6144	D	1499.6682	1499.6649
	-	1562.7155	R	1384.6417	1384.6379
	-	1725.7789	Y	1228.5408	1228.5368
	-	1840.8058	D	1065.4771	1065.4735
	-	1987.8742	F	950.4482	950.4466
	-	2102.9012	D	803.3796	803.3781
	-	2199.9539	P	688.3516	688.3512
	-	2313.0380	L	591.2985	591.2984
	-	2428.0649	D	478.2151	478.2144
	-	2543.0919	D	363.1878	363.1874
	-	2644.1396	T	248.1608	248.1605
	---	---	K	147.1131	147.1128