Table S1. ^{1}H-NMR quantification of most primary and secondary metabolites detected in *Urginea* species; white squill (WS) and red squill (RS). Values are expressed as μg/mg dry powder ± S.D (n = 3). Chemical shifts used for metabolite quantification were determined in methanol-d_6 and expressed as relative values to HMDS (0.94 mM final concentration).

compound	**Protons used in quantification**	**WS**	**RS**
ω-9 fatty acid (M1)	H-3 CH_2	57.52 ±25.342	1.2437 ±0.525
ω-6 fatty acid (M2)	bis-allylic CH_2	32.1697±13.82	1.6003 ±0.0177
ω-3 fatty acid (M3)			
Rhamnose (M4)	H-6 CH_3	10.4557 ±1.119	11.39 ±0.285
β-glucose (M5)	H-1	15.0467 ±0.602	8.2347 ±0.721
α-glucose (M6)	H-1	15.5767 ±1.19	8.767 ±0.474
Sucrose (M7)	H-1	1.4733 ±0.463	8.2263 ±0.43
alanine (M8)	H-3	8.5873 ±1.631	0.3513 ±0.133
aspartic acid (M9)	H-1	43.07 ±7.217	38.3367 ±4.943
glycine (M10)	H-2	19.79 ±3.534	7.1673 ±1.032
Tyrosine (M11)	H-6	3.964 ±0.66	-
Tryptophan (M12)	H-10	2.2853 ±0.18	1.0087 ±0.115
bufalin (M13)	H-22	17.4867 ±7.502	-
Scilliradin (M14)			
dihydro kaempferol (M15)	H-6'		43.61 ±2.318
Coumarin (M16)	H-4	5.9703 ±0.282	4.6927 ±0.282

Table S2. RS and WS extract inhibition and viability values in different concentrations against different cancer cell lines measured by SRB assay.

Conc.														
	RS (MCF7)							**WS (MCF7)**						
µg/mL	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**MEAN±SD**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**MEAN±SD**
0	100	0	100	0	100	0		100	0	100	0	100	0	
0.01	99.291	0.709	97.48	2.52	101.1	-1.1		99.917	0.083	100	0	99.752	0.248	
0.1	74.567	25.433	74.409	25.591	74.488	25.512		99.089	0.911	100.5	-0.5	99.917	0.083	
1	24.882	75.118	25.433	74.567	26.063	73.937		25.828	74.172	26.325	73.675	25.414	74.586	
10	22.52	77.48	22.598	77.402	22.52	77.48		22.185	77.815	22.599	77.401	22.351	77.649	
100	17.48	82.52	17.323	82.677	17.008	82.992		14.983	85.017	16.06	83.94	16.887	83.113	
IC50		0.1636		0.1734		0.1593	**0.165±0.007**		0.326		0.3309		0.32	**0.326±0.005**
Conc.														
	RS (A-549)							**WS (A-549)**						
µg/mL	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**MEAN±SD**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**MEAN±SD**
0	100	0	100	0	100	0		100	0	100	0	100	0	
0.01	92.965	7.035	94.831	5.169	91.098	8.902		94.79	5.21	94.588	5.412	94.992	5.008	
0.1	84.35	15.65	84.853	15.147	83.202	16.798		55.446	44.554	56.726	43.274	55.985	44.015	
1	9.9067	90.0933	10.122	89.878	9.6195	90.3805		2.8296	97.1704	2.2906	97.7094	3.3685	96.6315	
10	3.1587	96.8413	3.8765	96.1235	2.4408	97.5592		2.9643	97.0357	2.0885	97.9115	2.2232	97.7768	
100	3.8047	96.1953	3.6612	96.3388	3.9483	96.0517		1.0779	98.9221	1.2127	98.7873	1.4148	98.5852	
IC50		0.2727		0.2661		0.2756	**0.271±0.005**		0.1053		0.1115		0.1079	**0.108±0.003**
Conc.														
	RS (SKOV-3)							**WS (SKOV-3)**						
µg/mL	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**MEAN±SD**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**Viability**	**Inhibition**	**MEAN±SD**
0	100	0	100	0	100	0		100	0	100	0	100	0	
0.01	92.074	7.926	90.415	9.585	89.585	10.415		81.267	18.733	79.89	20.11	84.022	15.978	
0.1	81.843	18.157	87.926	12.074	84.885	15.115		79.89	20.11	78.237	21.763	82.369	17.631	
1	45.069	54.931	43.963	56.037	44.516	55.484		33.196	66.804	31.956	68.044	34.435	65.565	
10	7.4654	92.5346	7.1889	92.8111	6.9124	93.0876		3.0303	96.9697	4.4077	95.5923	4.6832	95.3168	
100	2.4885	97.5115	2.765	97.235	2.4885	97.5115		1.1019	98.8981	1.6529	98.3471	1.6529	98.3471	
IC50		0.9077		0.8932		0.9357	**0.912±0.021**		0.7059		0.6708		0.6955	**0.690±0.018**

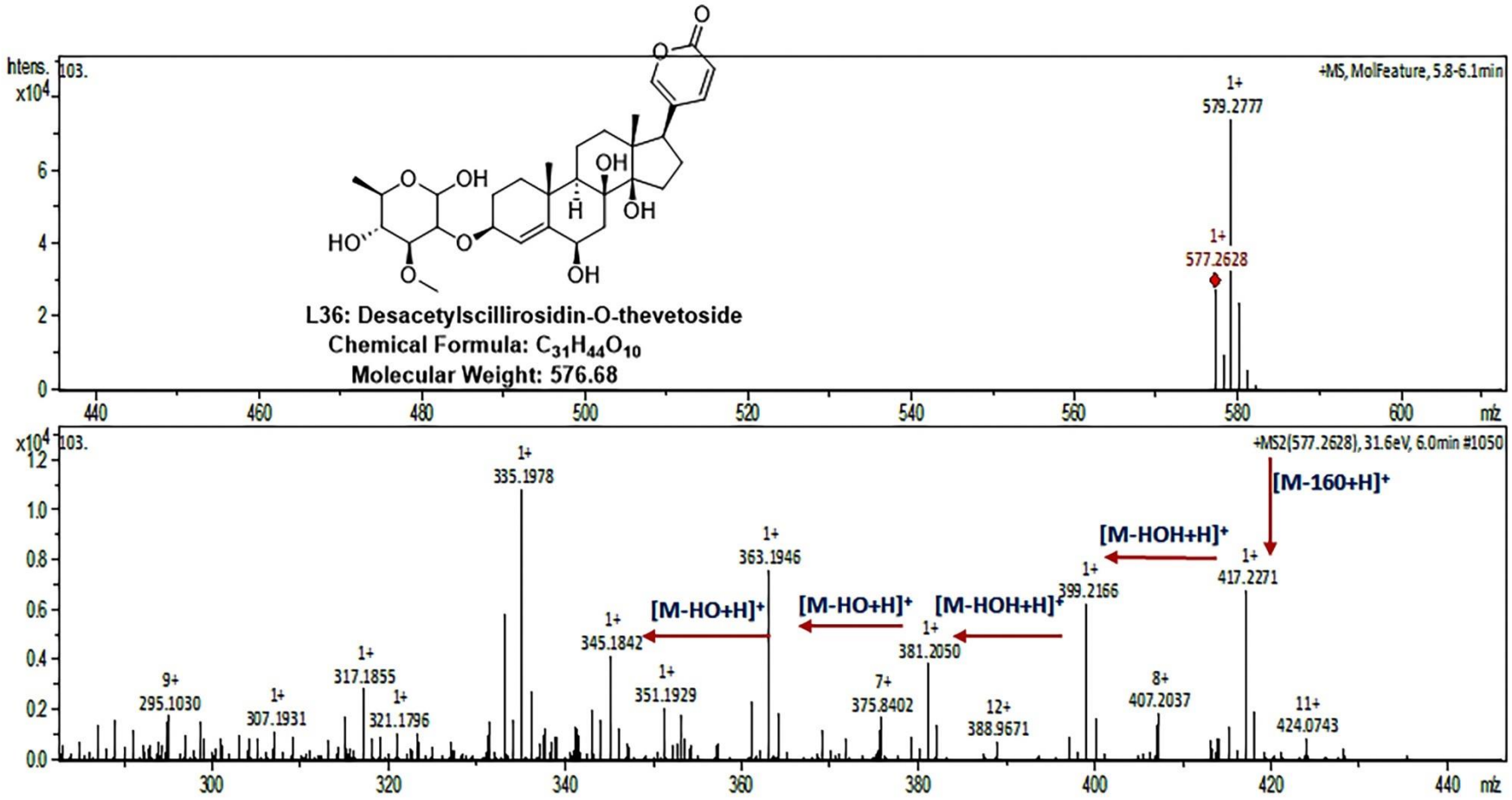

Figure S1.-A: ESI-MS/MS spectrum of L36 in the positive ion mode.

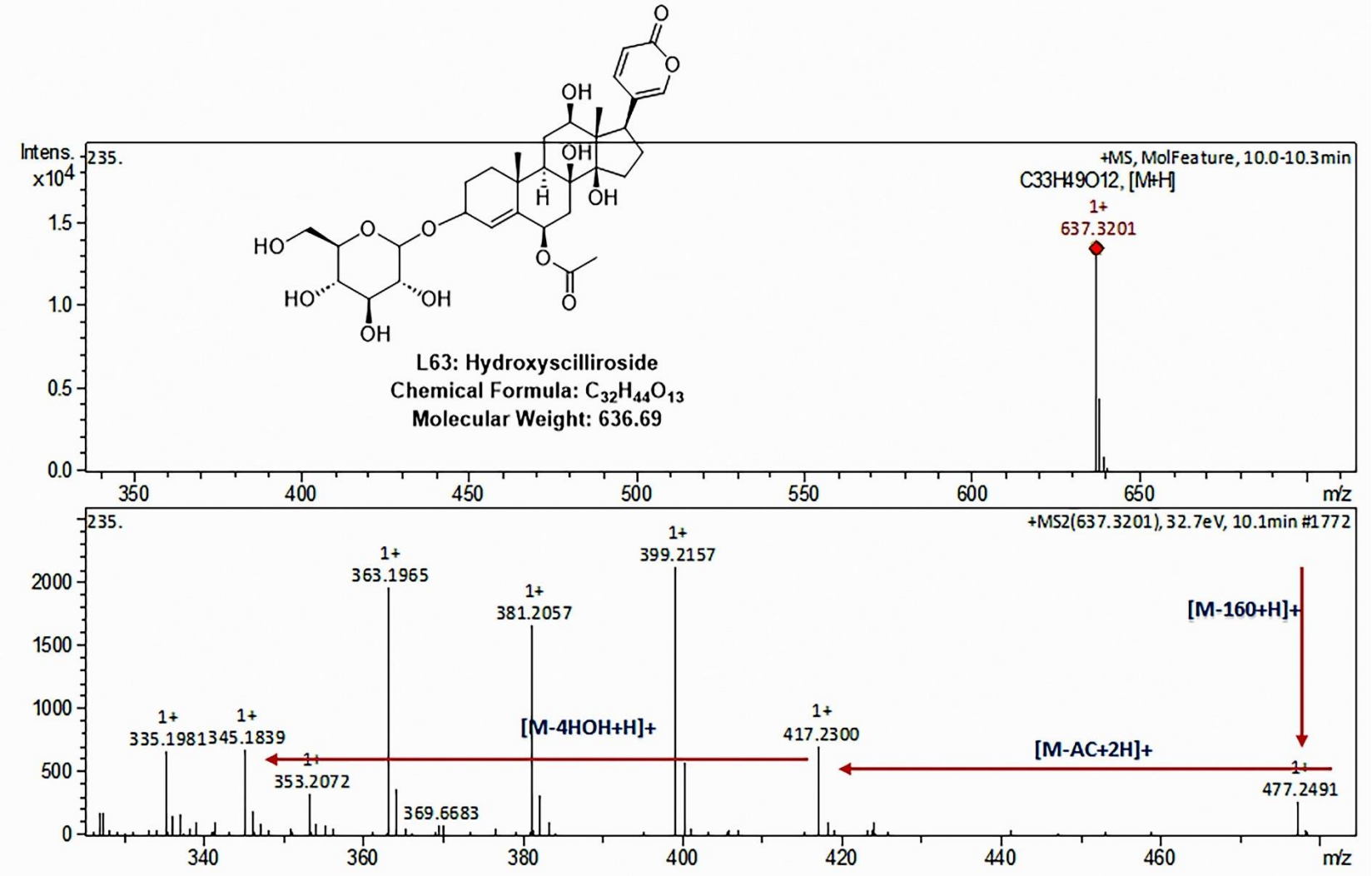

Figure S1.-B: ESI-MS/MS spectrum of L63 in the positive ion mode.

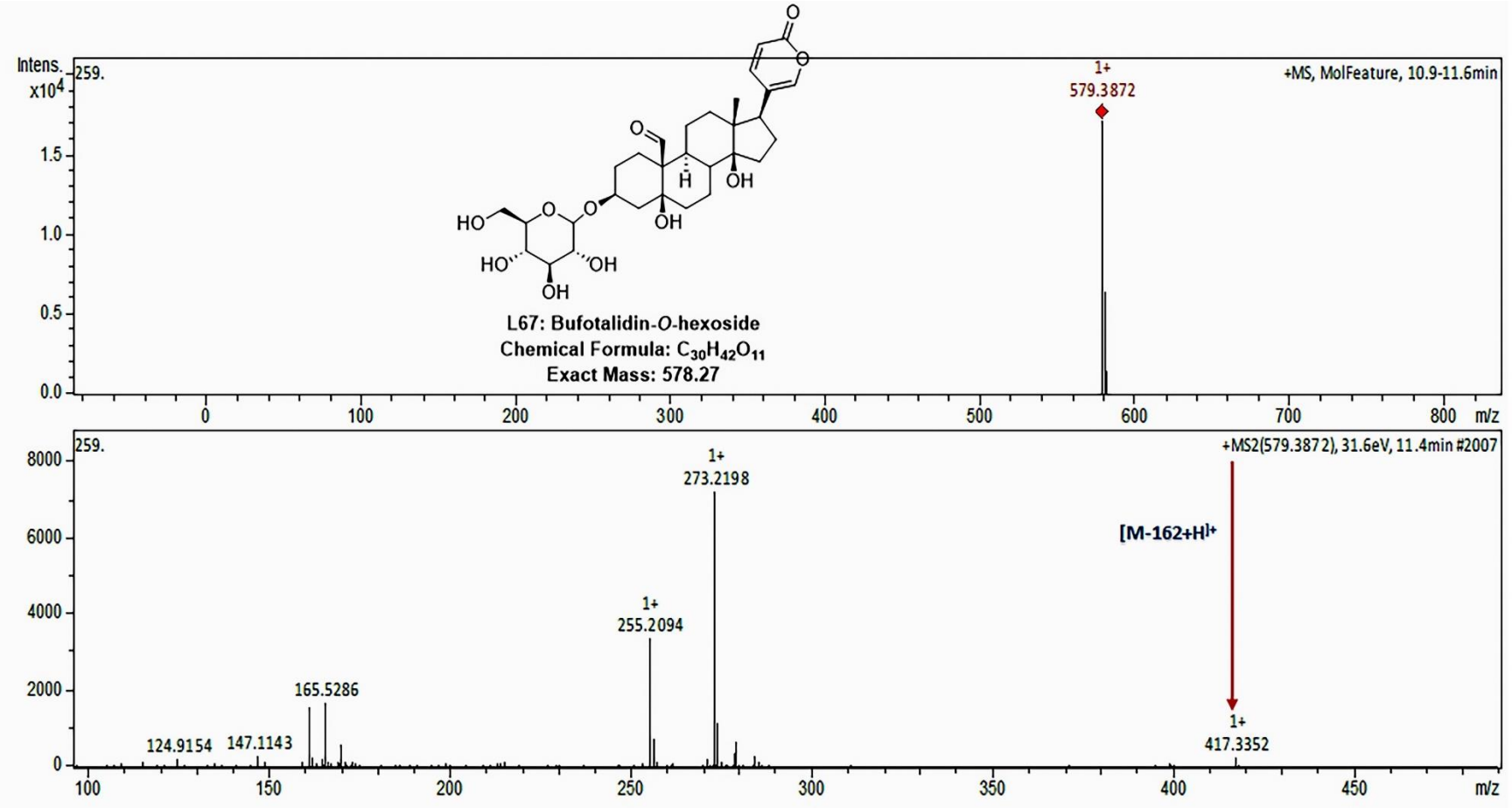

Figure S1.-C: ESI-MS/MS spectrum of L67 in the positive ion mode.

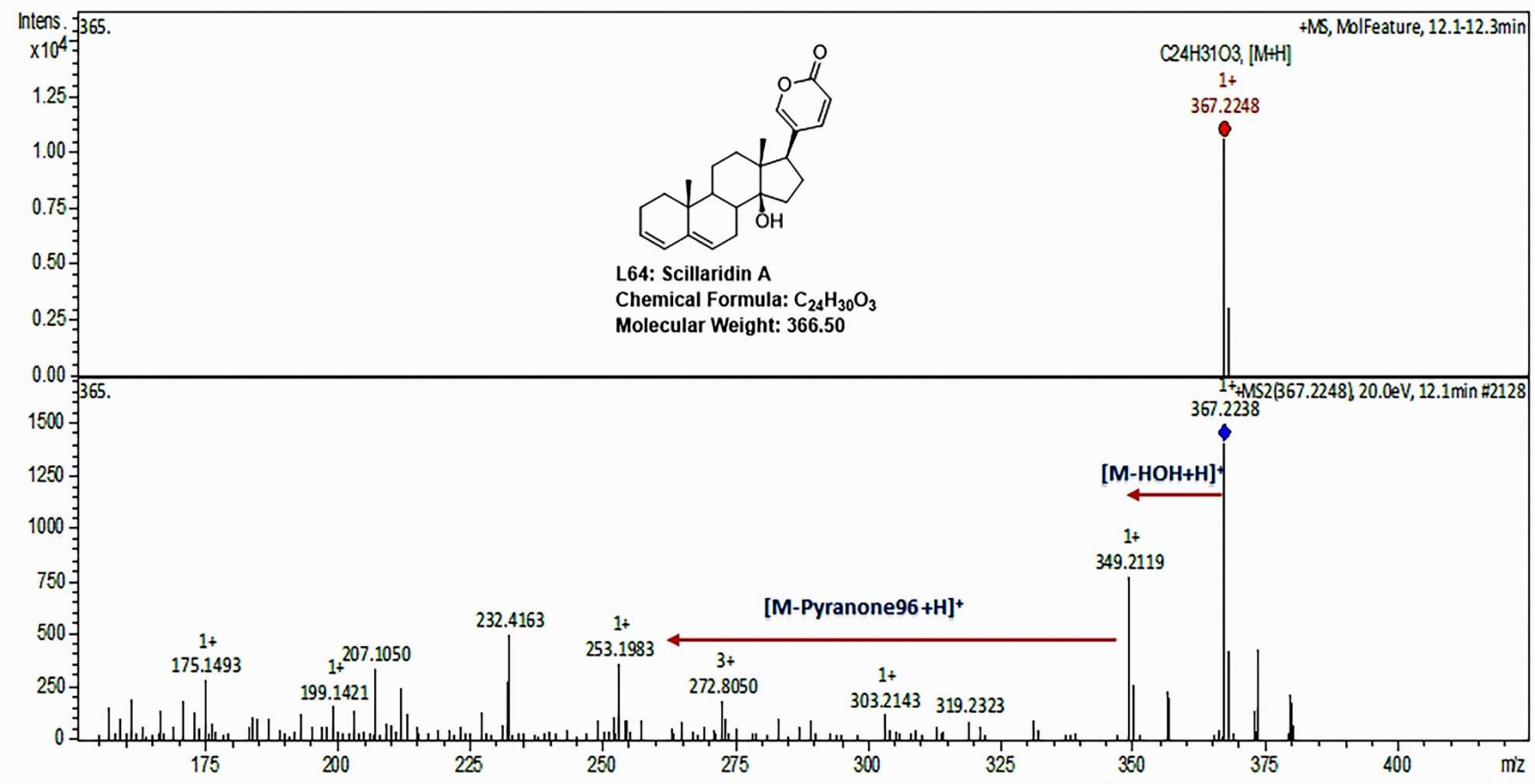

Figure S1.-D: ESI-MS/MS spectrum of L64 in the positive ion mode.

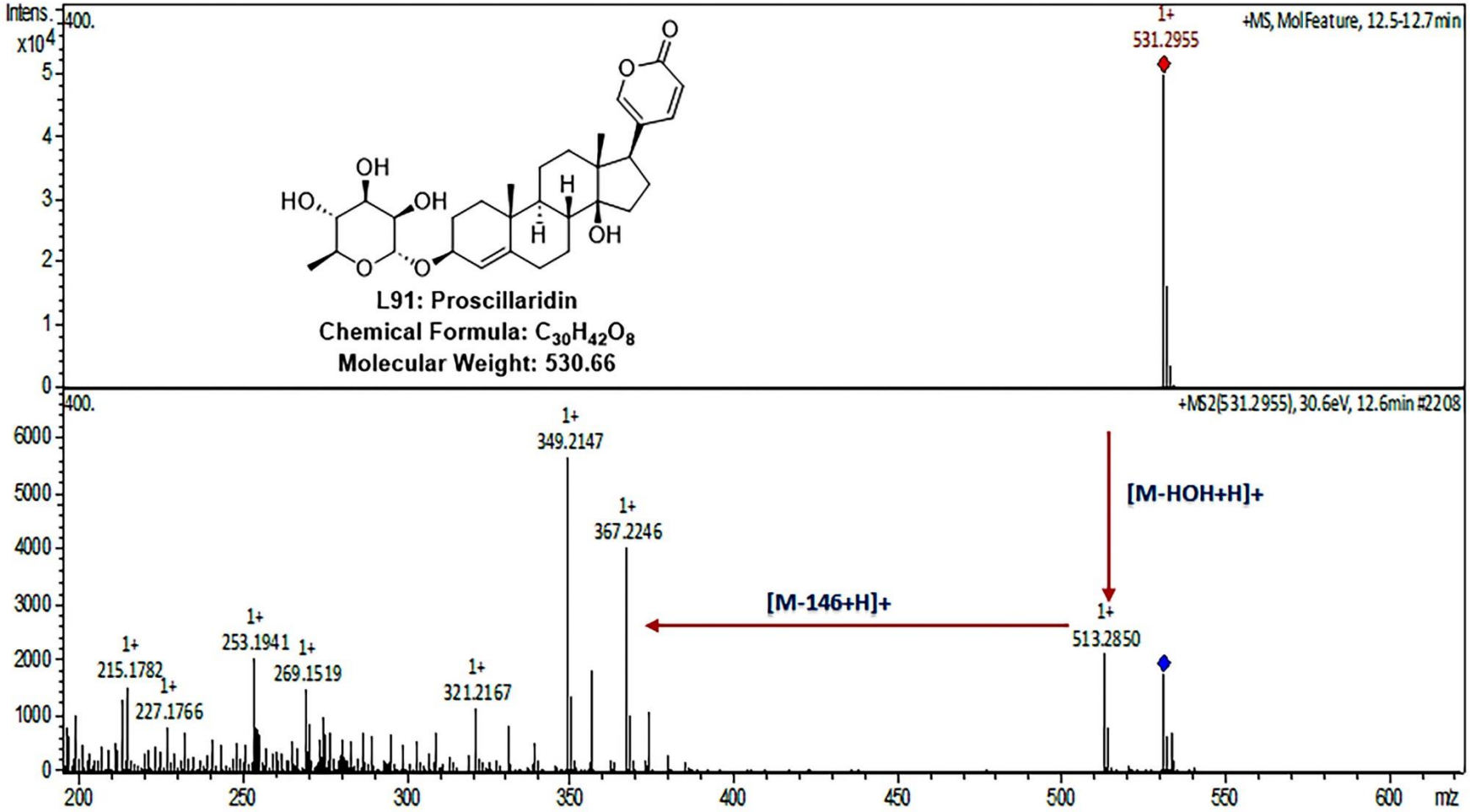

Figure S1.-E: ESI-MS/MS spectrum of L91 in the positive ion mode.

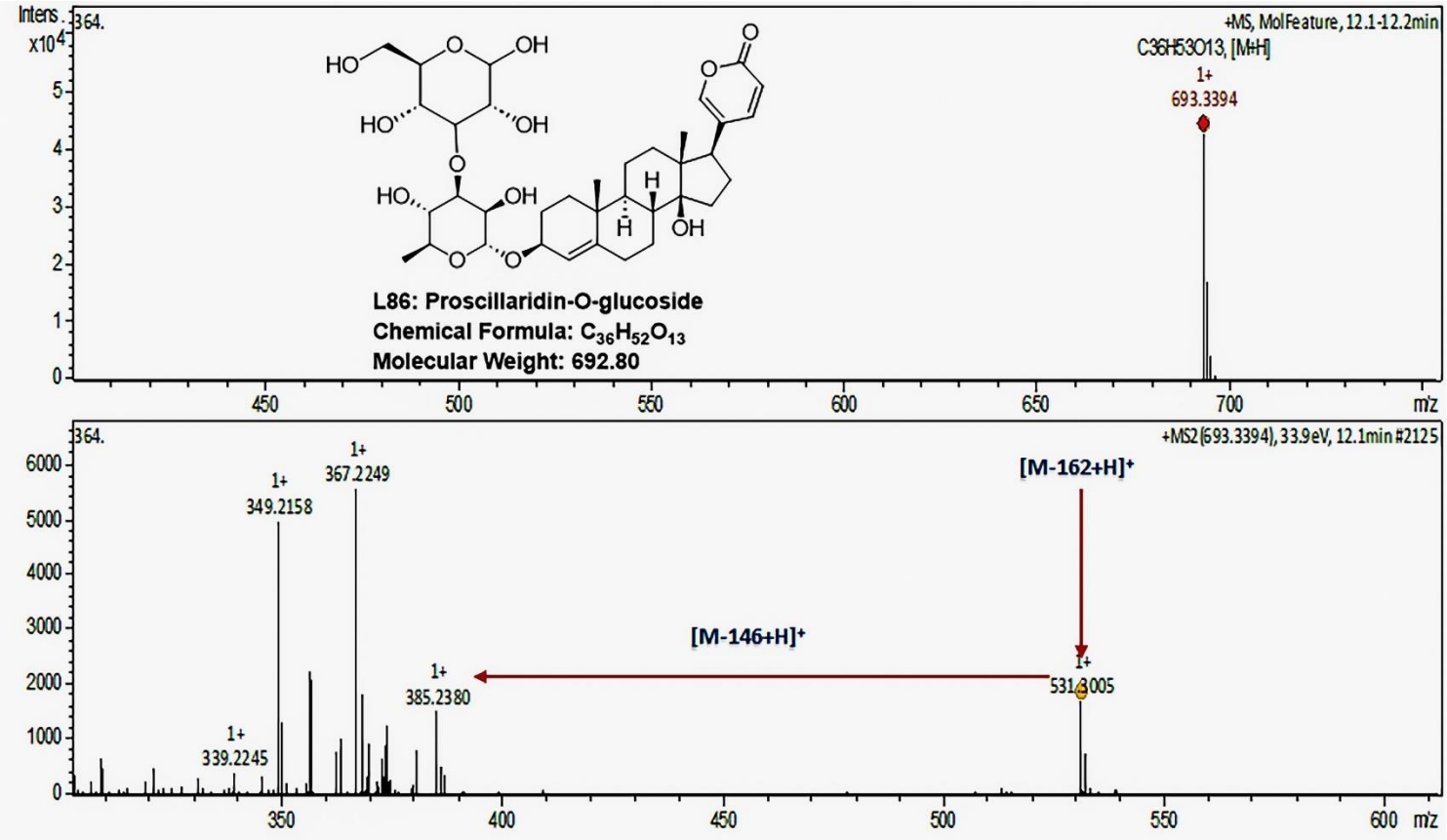

Figure S1.-F: ESI-MS/MS spectrum of L86 in the positive ion mode.

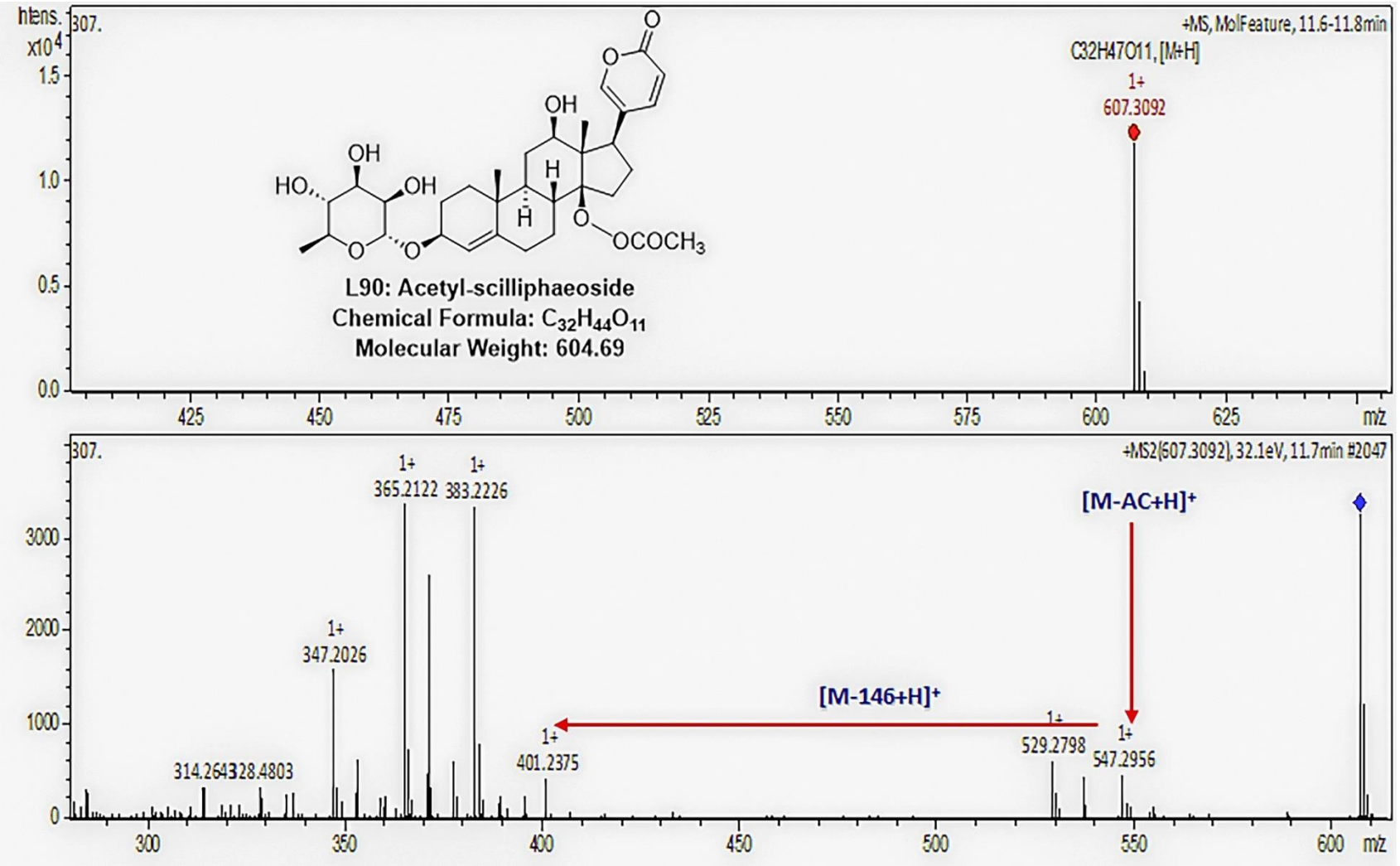

Figure S1.-G: ESI-MS/MS spectrum of L90 in the positive ion mode.

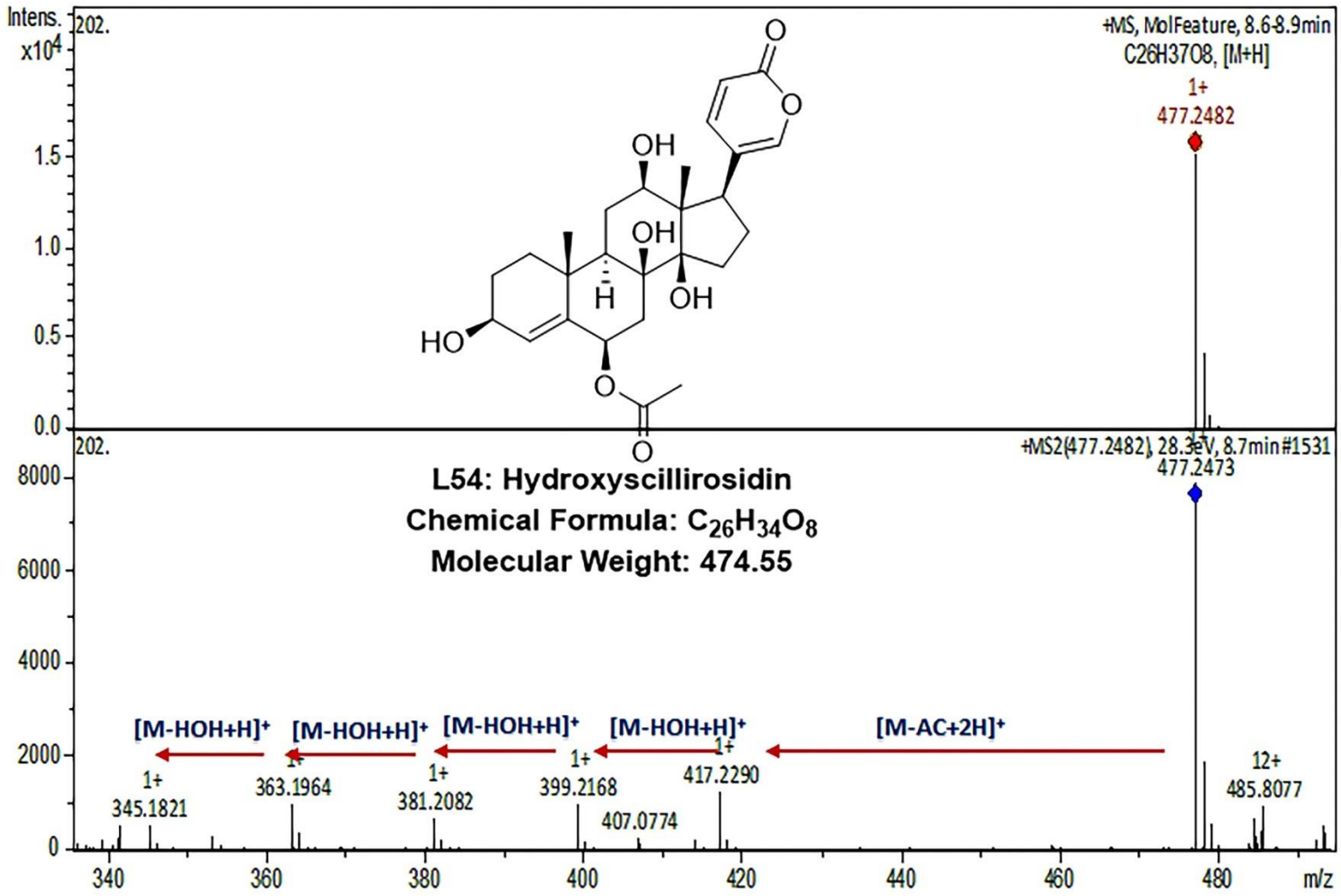

Figure S1.-H: ESI-MS/MS spectrum of L54 in the positive ion mode.

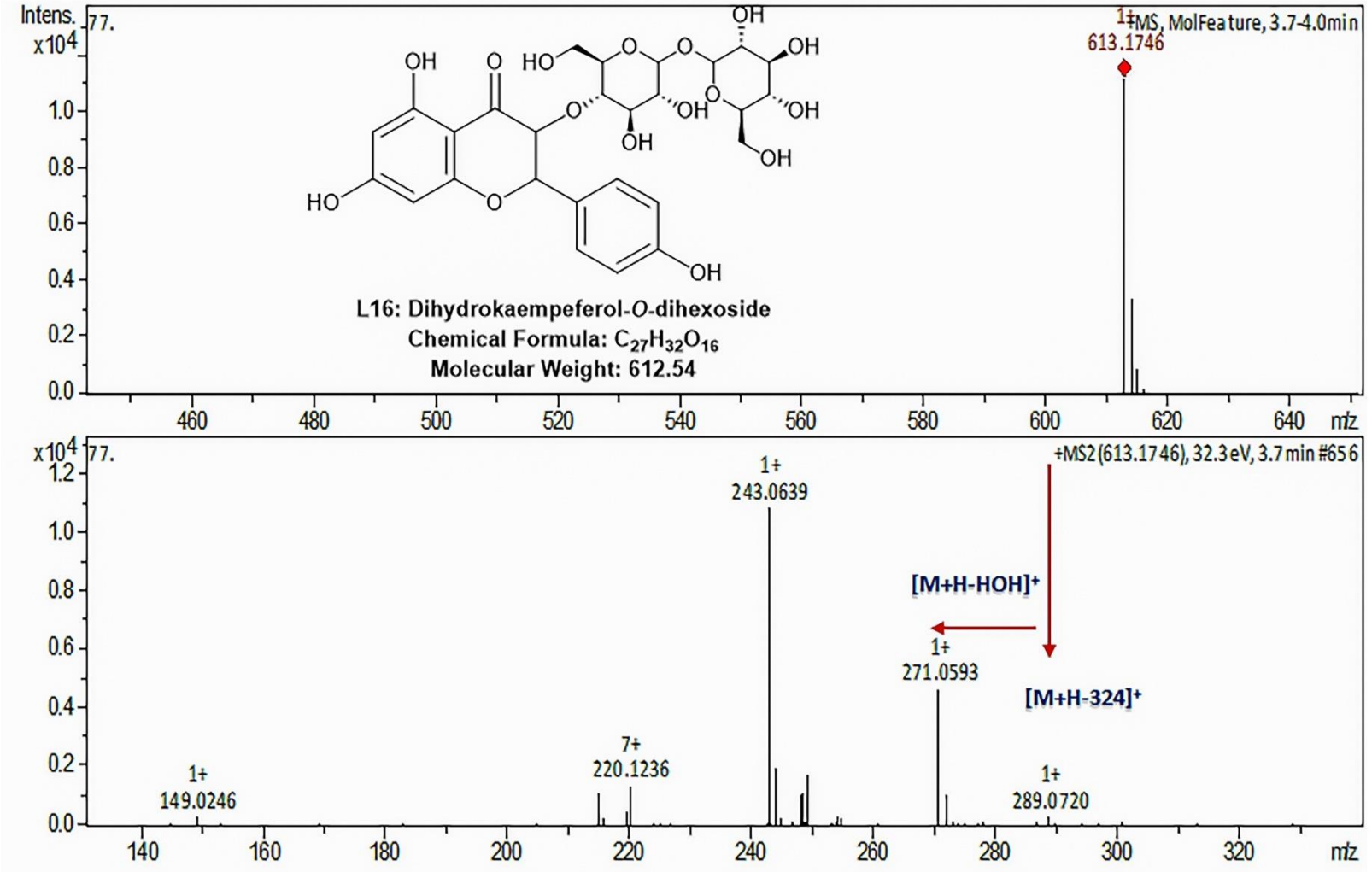

Figure S1.-I: ESI-MS/MS spectrum of L16 in the positive ion mode.

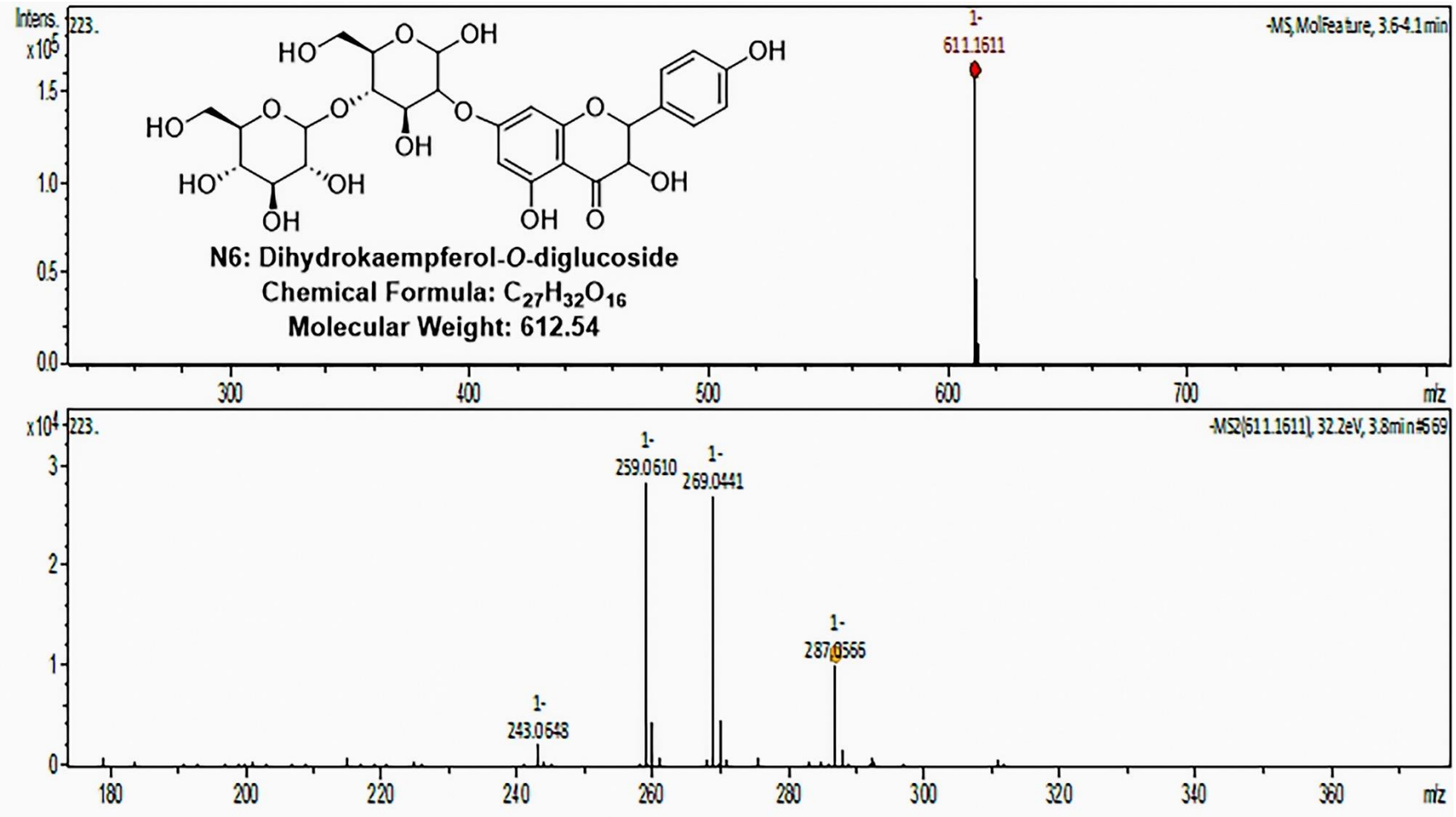

Figure S1.-J: ESI-MS/MS spectrum of N6 in the negative ion mode.

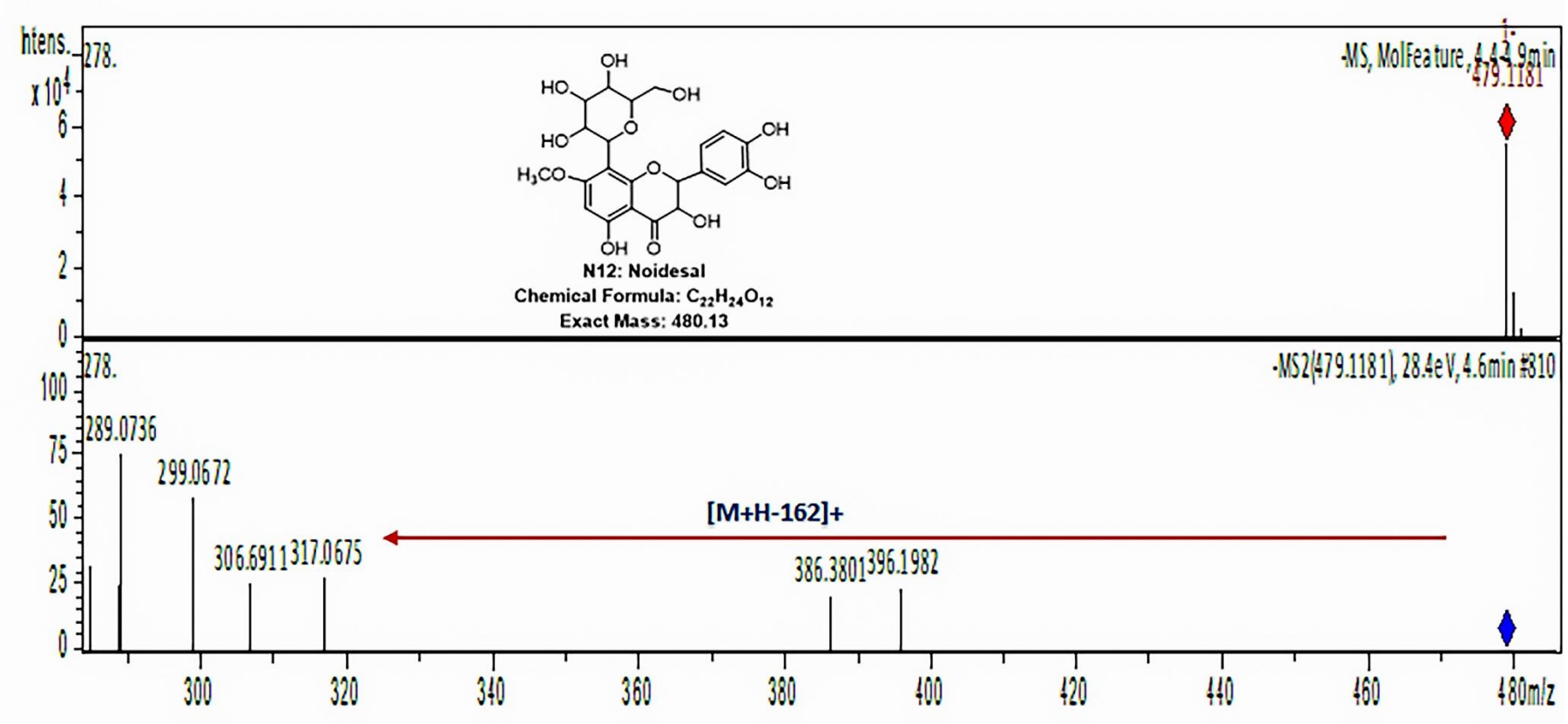

Figure S1.-K: ESI-MS/MS spectrum of N12 in the negative ion mode.

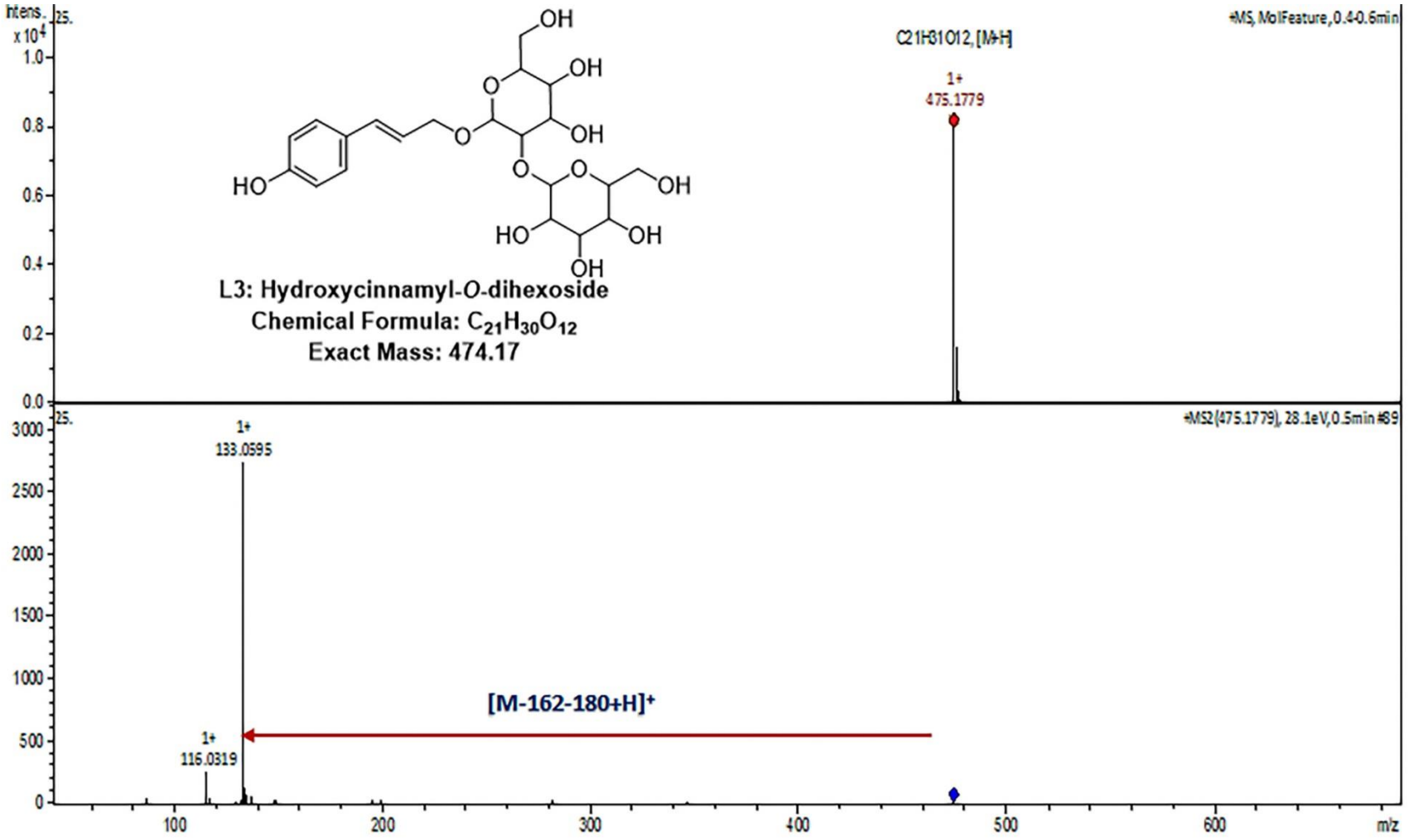

Figure S1.-L: ESI-MS/MS spectrum of L3 in the positive ion mode.

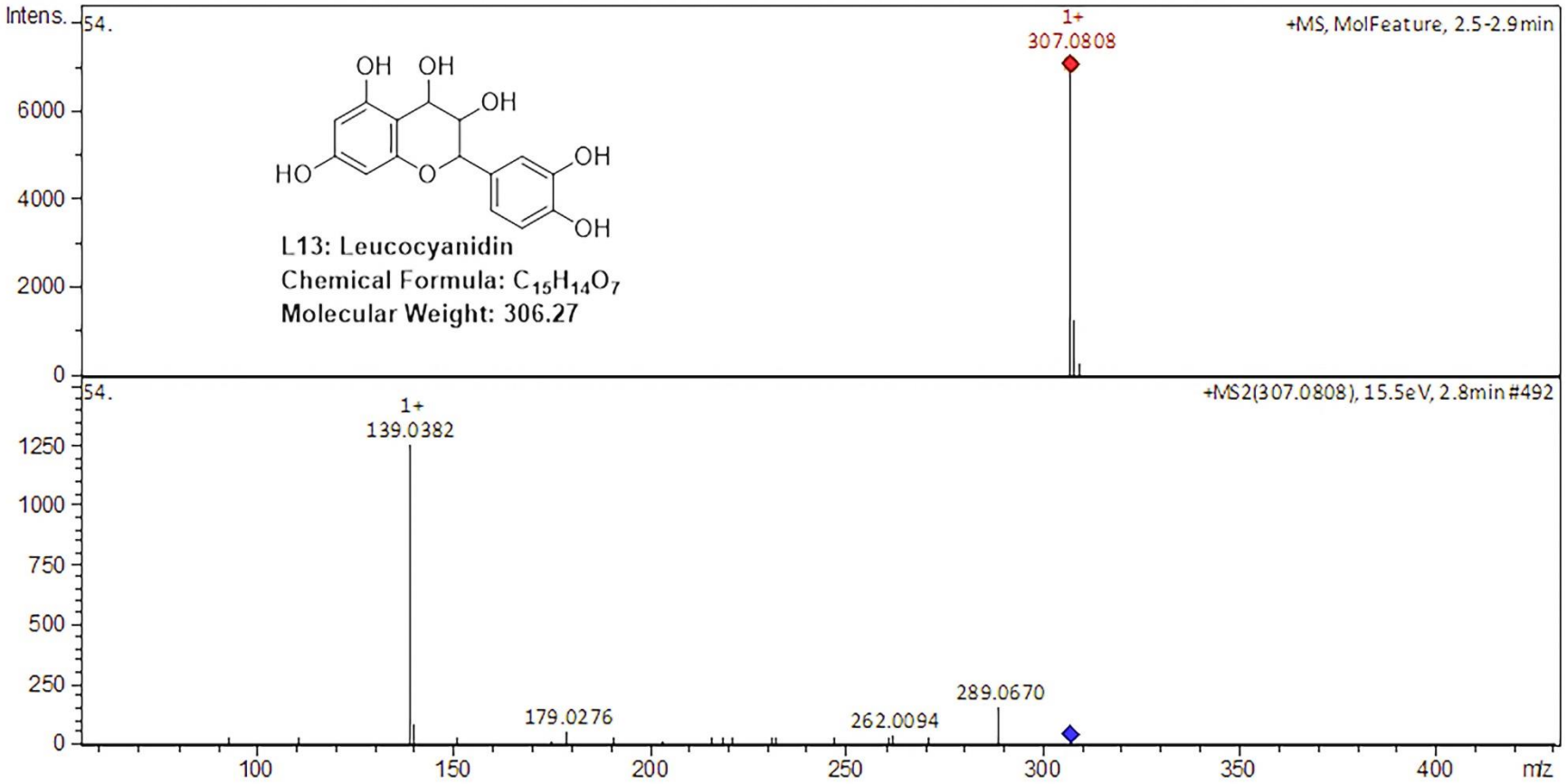

Figure S1.-M: ESI-MS/MS spectrum of L13 in the positive ion mode.

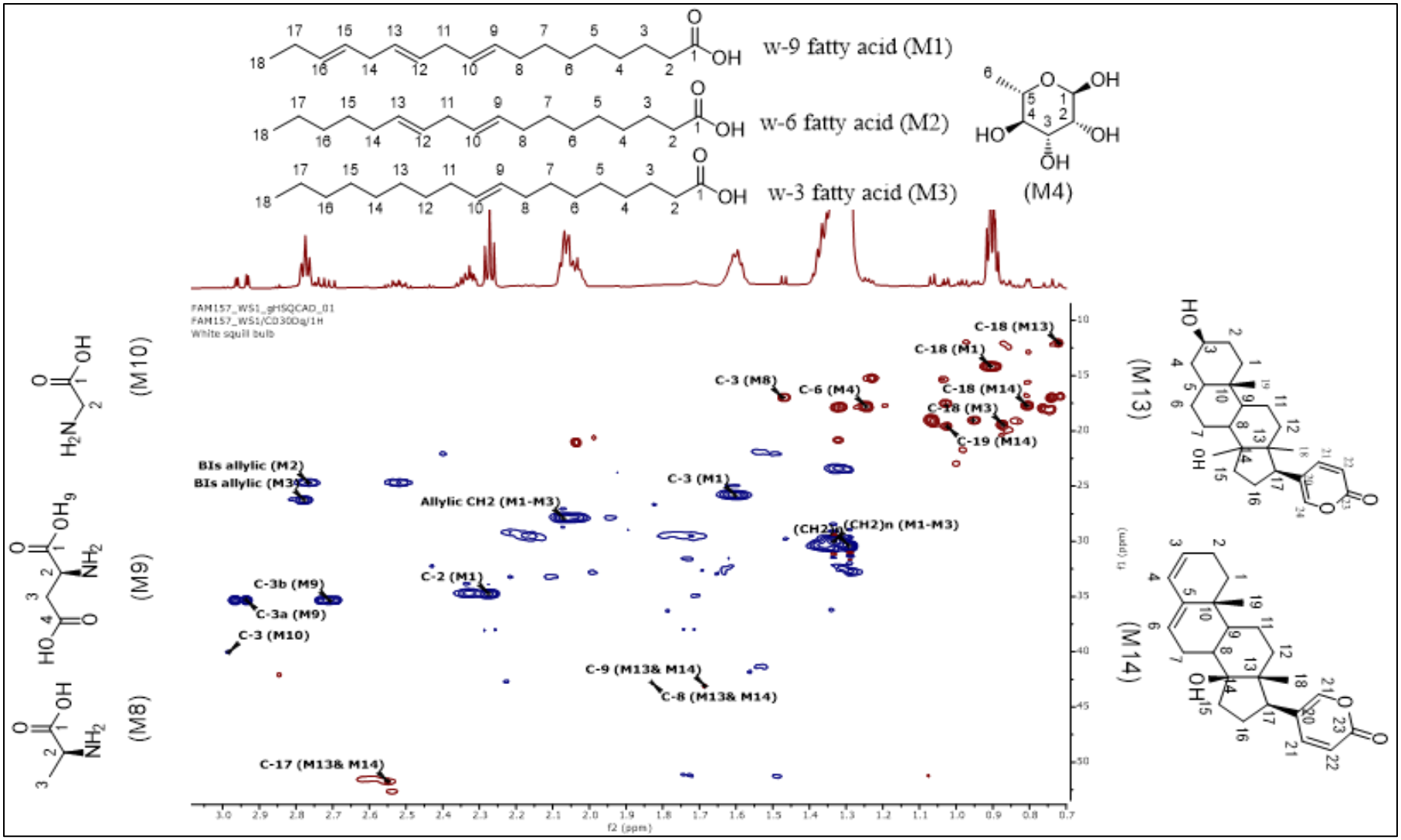

Figure S2. Signal assignment of the ^{1}H-NMR markers for fatty acids (**M1**-**M3**), rhamnose (**M4**), alanine (**M8**), aspartic acid (**M9**), glycine (**M10**) and bufadienolides (**M13&M14**) using ^{1}H-^{13}C correlations observed in the HSQC spectrum of squill methanol extract.

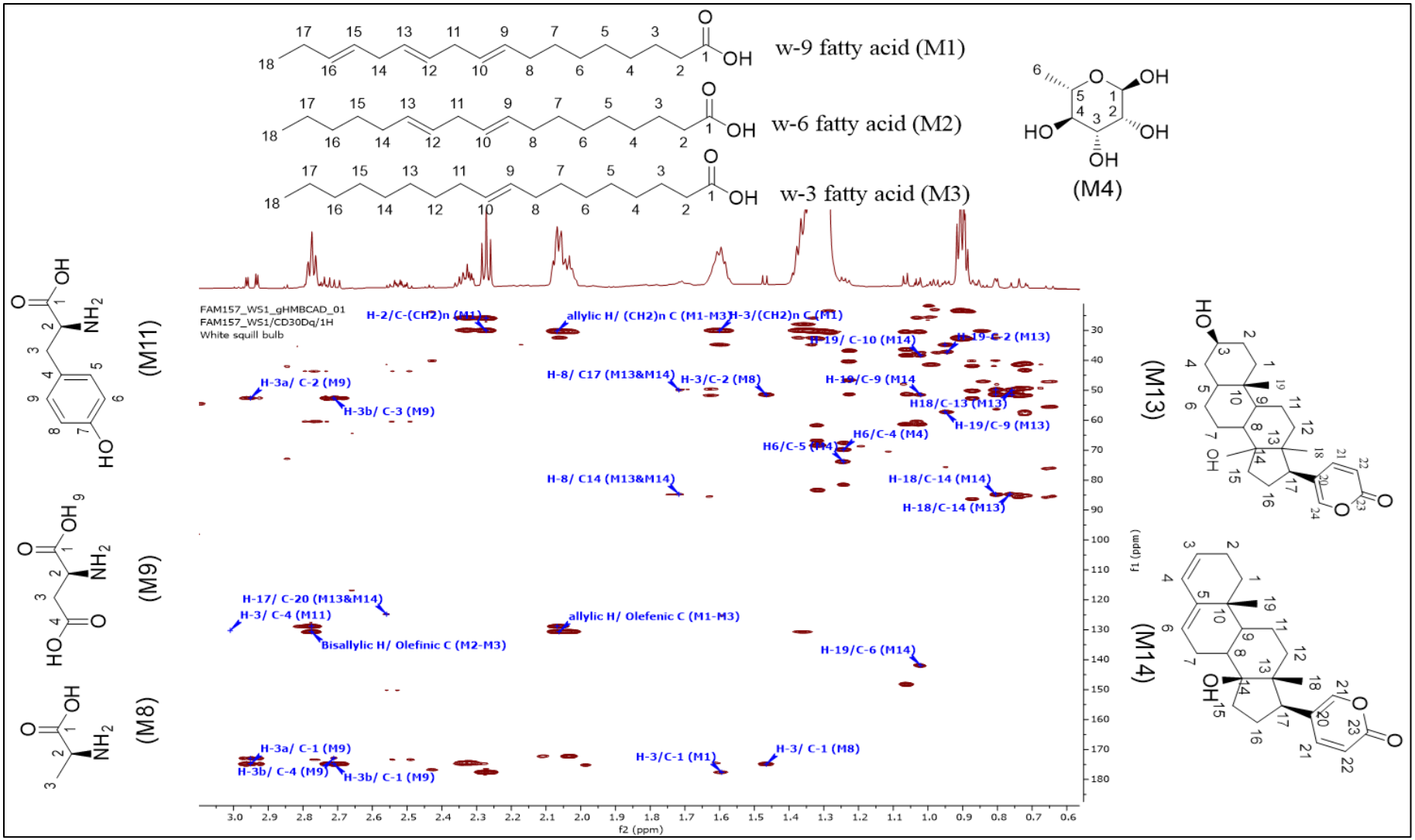

Figure S3. Signal assignment of the ^{1}H-NMR markers for fatty acids (**M1**-**M3**), rhamnose (**M4**), alanine (**M8**), aspartic acid (**M9**), glycine (**M10**) and bufadienolides (**M13&M14**) using ^{1}H-^{13}C correlations observed in the HMBC spectrum of squill methanol extract.

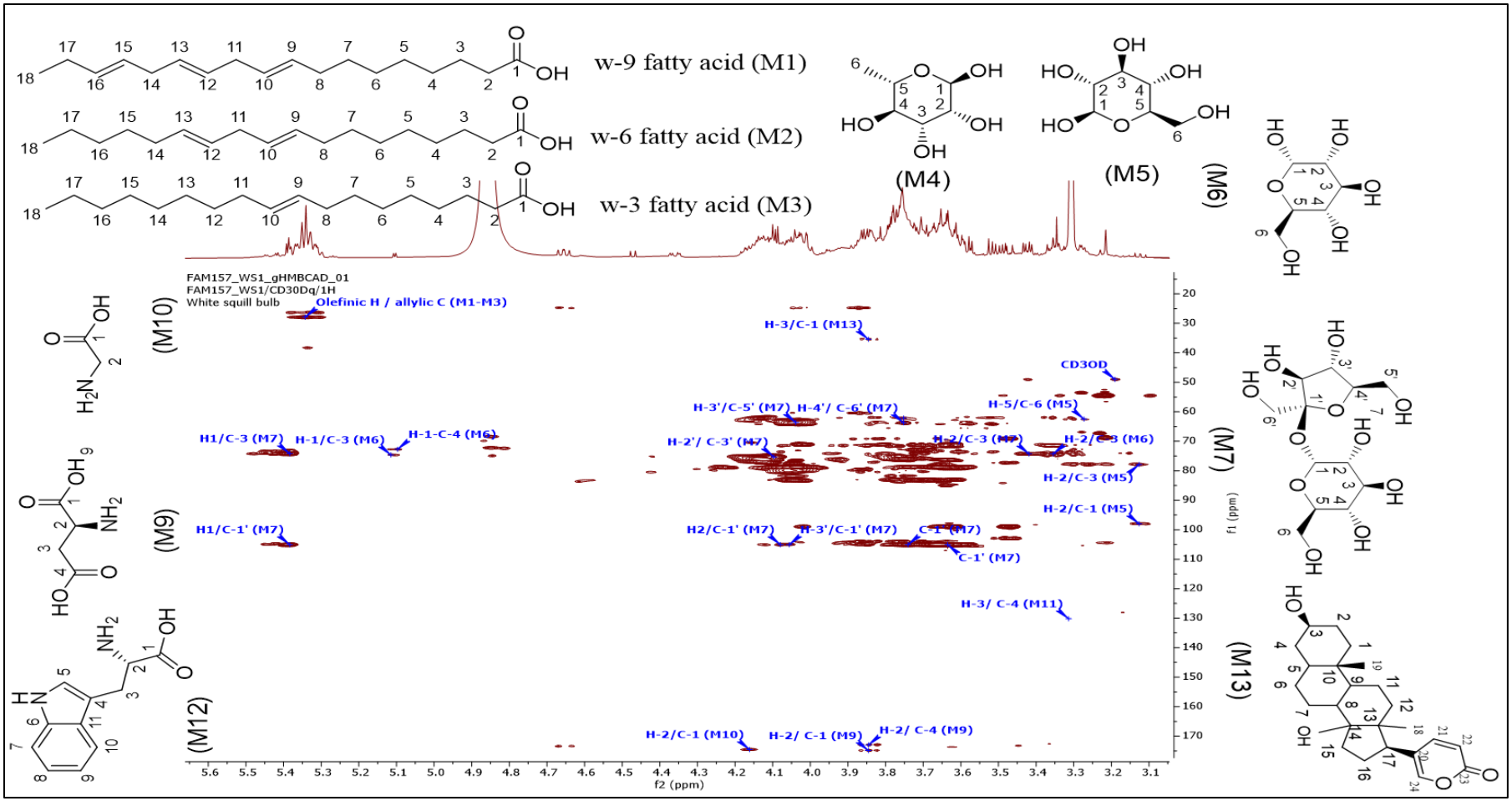

Figure S4. Signal assignment of the ^{1}H-NMR markers for fatty acids (**M1-M3**), rhamnose (**M4**), β, α glucose **(M5& M6)**, sucrose **(M7),** aspartic acid (**M9**), glycine (**M10**), tryptophan **(M12)** and bufalin (**M13**) using ^{1}H-^{13}C correlations observed in the HMBC spectrum of squill methanol extract.

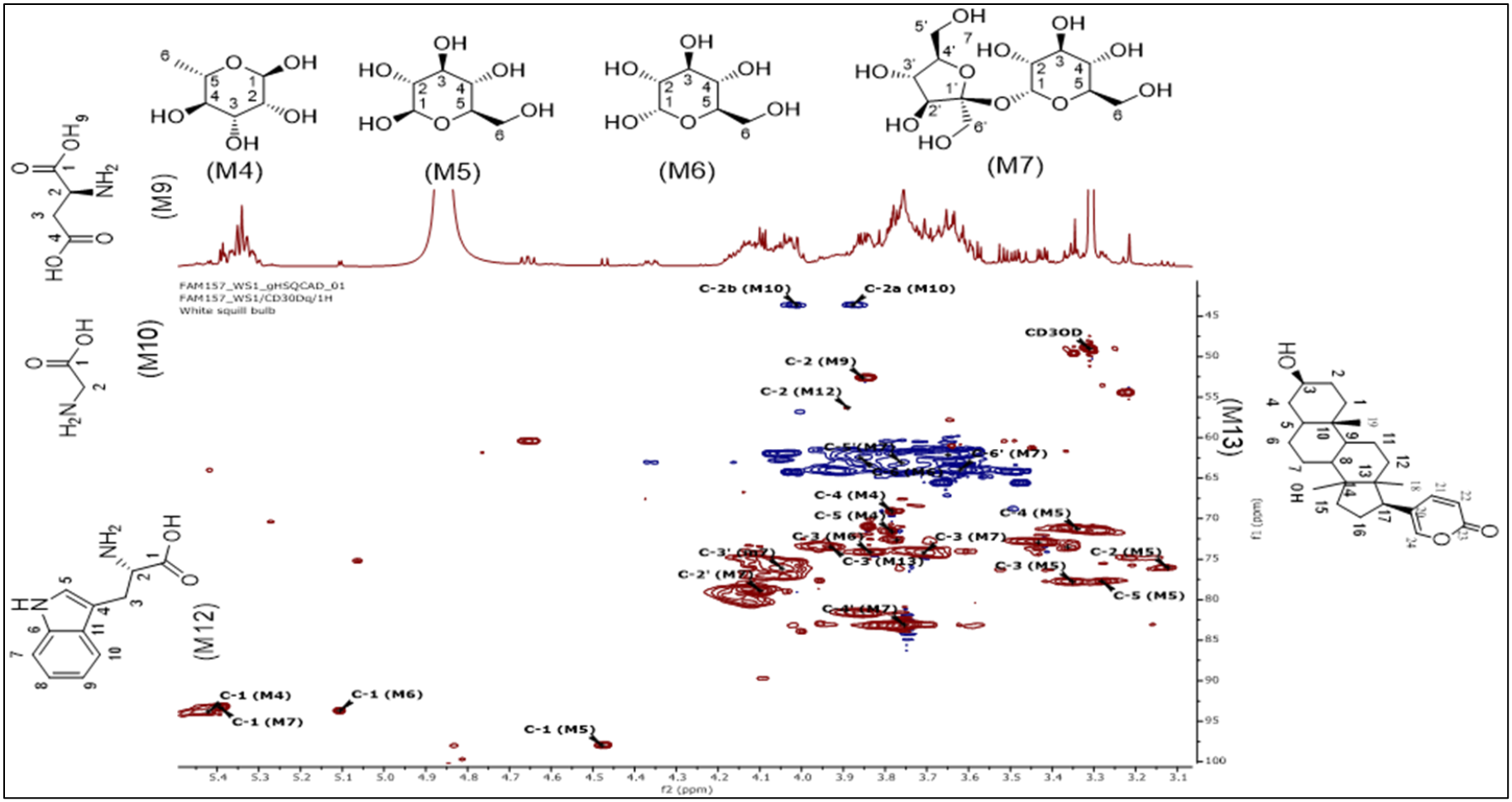

Figure S5. Signal assignment of the ^{1}H-NMR markers for rhamnose (**M4**), β, α glucose **(M5& M6)**, sucrose **(M7),** aspartic acid (**M9**), glycine (**M10**), tryptophan **(M12)** and bufalin (**M13**) using ^{1}H-^{13}C correlations observed in the HSQC spectrum of squill methanol extract.

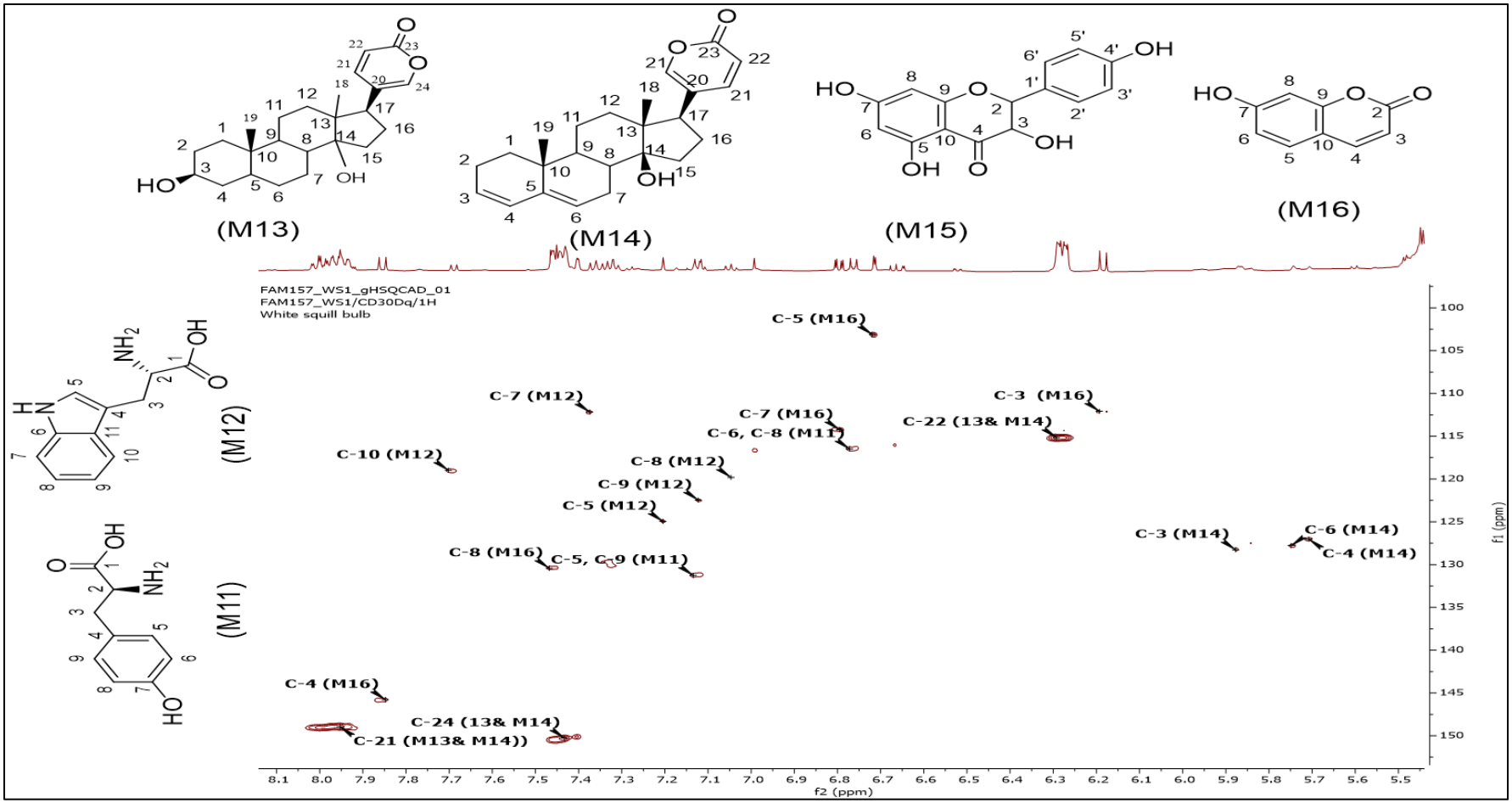

Figure S6: Signal assignment of the ^{1}H-NMR markers for tyrosine (**M11**), tryptophan **(M12)**, bufalin **(M13),** scilliridin (**M14**), dihydro kaempferol (**M15**), and coumarin **(M16)**, ^{1}H-^{13}C correlations observed in the HSQC spectrum of squill methanol extract.

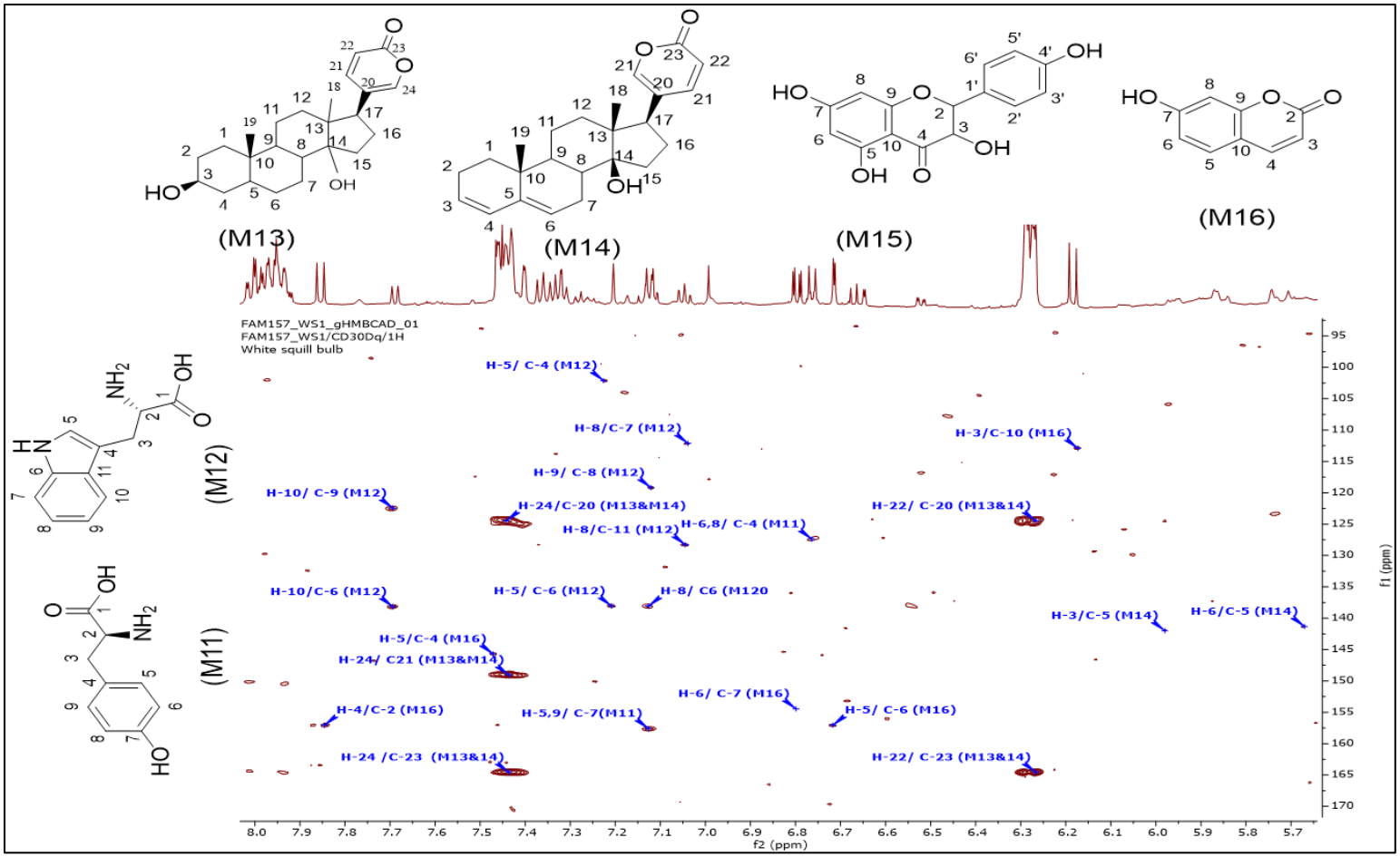

Figure S7. Signal assignment of the ^{1}H-NMR markers for tyrosine (**M11**), tryptophan **(M12)**, bufalin **(M13),** scilliridin (**M14**), dihydro kaempferol (**M15**), and coumarin **(M16)**, ^{1}H-^{13}C correlations observed in the HMBC spectrum of squill methanol extract.

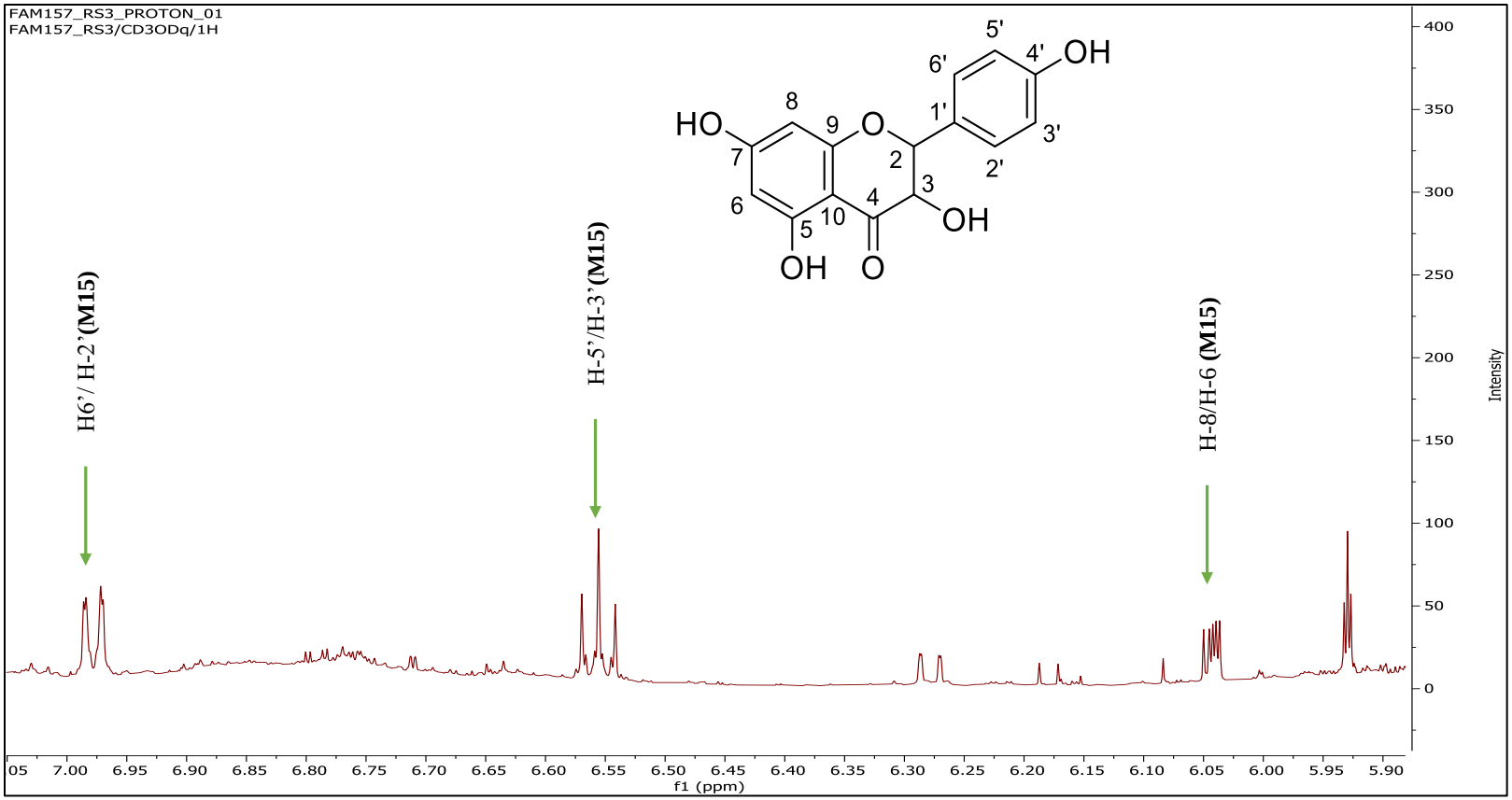

Figure S8. Signal assignment of the proton markers for dihydro kaempferol (**M15**) observed in the ^{1}H-NMR spectrum of RS methanol extract.