Supplemental Material

Bacteria associated with the fresh-water sponge *Spongilla lacustris* and their potential to produce secondary metabolites revealed via genomics, metagenomics and genome mining

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Table S1. Summary of MAGs retrieved from *Spongilla lacustris* metagenome and their GTDB-based taxonomy.

MAG	marker lineage	completeness	contamination	GC, %	genome size	scaffolds	contigs	longest scaffold	longest contig	phylum_gtdb	class_gtdb	order_gtdb	family_gtdb	genus_gtdb	gtdb_closest	environment
Spongilla lacustris MAG01	k__Bacteria	78.42	0.00	35.4	475425	5	8	206783	113061	Patescibacteria	Paceibacteria	UBA9983	UBA2163	J119	GCA_003694545.1	iron-rich hot spring
Spongilla lacustris MAG02	k__Bacteria	100.00	8.62	59.0	3101799	39	41	295652	295652	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Limnohabitans	GCA_005789825.1	freshwater lake
Spongilla lacustris MAG03	p__Bacteroidetes	98.57	0.95	40.7	4628720	74	86	411324	376971	Bacteroidota	Bacteroidia	AKYH767	B-17BO	-	GCA_002342065.1	freshwater lake
Spongilla lacustris MAG04	c__Gammaproteobacteria	87.26	0.00	36.5	1716532	16	30	476275	476275	Proteobacteria	Gammaproteobacteria	GCA-002705445	GCA-002716945	-	NA	NA
Spongilla lacustris MAG05	p__Bacteroidetes	98.52	1.97	38.9	2493715	127	129	88460	88460	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	UBA1312	GCA_002482815.1	water, biofilm
Spongilla lacustris MAG06	k__Bacteria	69.80	4.31	28.6	587916	85	118	40569	18454	Patescibacteria	Paceibacteria	UBA9984	UBA5272	-	GCA_003518045.1	groundwater
Spongilla lacustris MAG07	k__Bacteria	89.89	0.55	32.0	2551601	156	209	87631	83425	Bacteroidota	Bacteroidia	Cytophagales	-	-	NA	NA
Spongilla lacustris MAG08	p__Bacteroidetes	86.70	0.99	34.1	2276483	203	219	51600	51600	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Hydrotalea	NA	NA
Spongilla lacustris MAG09	c__Alphaproteobacteria	82.25	0.43	52.4	2299014	350	403	29586	27420	Proteobacteria	Alphaproteobacteria	Elsterales	-	-	NA	NA
Spongilla lacustris MAG10	c__Alphaproteobacteria	93.26	2.83	53.0	2719869	355	359	54419	54419	Proteobacteria	Alphaproteobacteria	-	-	-	NA	NA
Spongilla lacustris MAG11	p__Bacteroidetes	90.37	0.99	31.3	2716763	166	175	139035	139035	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	Sediminibacterium	NA	NA
Spongilla lacustris MAG12	k__Bacteria	78.98	0.07	67.7	2148011	426	429	26040	26040	Planctomycetota	Phycisphaerae	Phycisphaerales	SM1A02	SYIB01	GCA_005798965.1	freshwater lake
Spongilla lacustris MAG13	k__Bacteria	81.07	1.14	59.7	3350352	489	585	38525	38525	Planctomycetota	Phycisphaerae	Phycisphaerales	SM1A03	QWPT01	GCA_003671075.1	freshwater lake
Spongilla lacustris MAG14	o__Burkholderiales	54.73	0.06	44.0	1579445	270	278	26364	26364	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Symbiobacter	GCF_000477435.1	freshwater lake
Spongilla lacustris MAG15	k__Bacteria	87.23	1.35	53.1	1871277	100	163	165013	134855	Verrucomicrobiota	Verrucomicrobiae	Methylacidiphilales	UBA3015	UBA3015	GCA_001438005.1	Baltic Sea brackish surface water
Spongilla lacustris MAG16	k__Bacteria	96.77	1.08	48.9	1679970	91	119	152443	152443	Proteobacteria	Alphaproteobacteria	Elsterales	-	-	NA	NA
Spongilla lacustris MAG17	p__Bacteroidetes	96.85	1.23	36.1	3902886	134	235	123109	73227	Bacteroidota	Bacteroidia	Chitinophagales	Chitinophagaceae	-	NA	NA
Spongilla lacustris MAG18	p__Cyanobacteria	77.04	5.21	66.7	2492058	199	250	150199	94616	Cyanobacteria	Cyanobacteriia	PCC-6307	Cyanobiaceae	Cyanobium_A	GCA_007135755.1	hypersaline soda lake sediment
Spongilla lacustris MAG19	o__Burkholderiales	98.21	0.03	52.5	2643449	26	29	344907	344907	Proteobacteria	Gammaproteobacteria	Burkholderiales	Burkholderiaceae	Limnohabitans	GCA_005789825.1	freshwater lake
Spongilla lacustris MAG20	f__Flavobacteriaceae	98.23	3.49	31.2	4979690	313	339	202147	178244	Bacteroidota	Bacteroidia	Flavobacteriales	Flavobacteriaceae	Flavobacterium	NA	NA

Table S2. List of the oligonucleotide primers used in this work.

Name	Sequence (5´-3´)	Purpose
ermEp_Fw	GTCATCTAGAGGTGAACTTCGCACTTCG	Construction of pSET152_ermE*p plasmid
ermEp_Rv	TCCGGCTCGTATGTTGTG	Construction of pSET152_ermE*p plasmid
ctg3_1243_Fw	GTCAGCGGCCGCATGACCACGGCAATGCAG	Construction of pSET152_ermE*p_ctg3_1243 plasmid
ctg3_1243_Rv	GTCAGAATTCGCGACGACCTGGCCTGAC	Construction of pSET152_ermE*p_ctg3_1243 plasmid

Table S3. BGCs identified in the genome of *Streptomyces* sp. SL203 with antiSMASH version 6.1.1.

BGC	Type	From	To	Most similar known BGC	Similarity	Presence in another bacterium	Found and assigned NP
3.1	butyrolactone	237,860	246,265	-	-	*Streptomyces* sp. PAMC 26508	-
3.2	NRPS	319,354	372,367	rimosamide	21%	*Streptomyces* sp. PAMC 26508	detoxin S_1
3.3	PKSII, terpene	514,723	586,172	spore pigment	83%	*Streptomyces* sp. PAMC 26508	-
3.4	melanin	612,086	622,550	melanin	100%	*Streptomyces pratensis* ATCC 33331	-
3.5	PKSIII	719,172	760,230	-	-	*Streptomyces pratensis* ATCC 33331	-
3.6	RiPP-like	919,628	926,490	-	-	*Streptomyces pratensis* ATCC 33331	-
3.7	terpene, ectoine	957,073	977,440	ectoine	100%	*Streptomyces pratensis* ATCC 33331	ectoine
3.8	terpene	1,258,237	1,278,832	-	-	*Streptomyces pratensis* ATCC 33331	-
3.9	PKSII, PKS-like	1,323,735	1,396,271	cinerubin B	25%	*Streptomyces pratensis* ATCC 33331	coprisidin A/B
3.10	ectoine	1,758,007	1,768,405	ectoine	100%	*Streptomyces pratensis* ATCC 33331	ectoine
3.11	terpene	2,230,079	2,249,836	-	-	*Streptomyces* sp. PAMC 26508	-
3.12	lanthipeptide class III	2,690,330	2,712,981	-	-	*Streptomyces* sp. CB01580	-
3.13	siderophore	2,757,623	2,769,263	desferrioxamine B/E	83%	*Streptomyces* sp. PAMC 26508	(dehydroxy)nocardamine
3.14	NRPS, PKSI, NRPS-like	3,413,177	3,467,764	-	-	*Streptomyces pratensis* ATCC 33331	-
3.15	butyrolactone	3,667,911	3,678,837	-	-	*Streptomyces pratensis* ATCC 33331	-
3.16	RiPP-like	5,333,512	5,342,409	-	-	*Streptomyces* sp. PAMC 26508	-
3.17	terpene	5,500,170	5,520,316	-	-	*Streptomyces pratensis* ATCC 33331	-
3.18	siderophore	5,585,671	5,600,255	-	-	*Streptomyces pratensis* ATCC 33331	-
3.19	NRPS	5,872,256	5,927,100	-	-	*Streptomyces pratensis* ATCC 33331	-
3.20	lanthipeptide class I	5,947,894	5,974,342	-	-	*Streptomyces* sp. ADI97-07	-
3.21	RiPP-like	6,094,486	6,103,893	-	-	*Streptomyces* sp. ADI97-07	-
3.22	PKSI	6,320,692	6,408,208	sceliphrolactam	88%	*Streptomyces pratensis* ATCC 33331	sceliphrolactam
3.23	terpene	6,747,935	6,773,426	hopene	69%	*Streptomyces anulatus* ATCC 11523	-
3.24	β-lactam	6,831,354	6,850,351	clavulanic acid	20%	*Streptomyces* sp. PAMC 26508	-
3.25	RiPP-like	6,920,994	6,931,518	-	-	*Streptomyces pratensis* ATCC 33331	-
3.26	terpene	7,070,847	7,096,339	isorenieratene	100%	*Streptomyces pratensis* ATCC 33331	-
3.27	NRPS	7,110,740	7,160,490	coelichelin	90%	*Streptomyces pratensis* ATCC 33331	coelichelin
3.28	β-lactam, PKSI, NRPS	7,277,936	7,418,487	carbapenem MM4550	55%	*Streptomyces pratensis* ATCC 33331	-

Table S4. BGCs identified in the genome of *Streptomyces* sp. SL294 with antiSMASH version 6.1.1.

BGC	Type	From	To	Most similar known BGC	Similarity	Presence in another bacterium	Found and assigned NP
3.1	NRPS, PKSI, β-lactam	128,640	268,174	carbapenem MM4550	58%	*Streptomyces pratensis* ATCC 33331	-
3.2	NRPS	385,716	436,620	coelichelin	90%	*Streptomyces pratensis* ATCC 33331	coelichelin
3.3	terpene	451,251	475,851	isorenieratene	100%	*Streptomyces pratensis* ATCC 33331	-
3.4	RiPP-like	616,557	625,518	-	-	*Streptomyces pratensis* ATCC 33331	-
3.5	β-lactam	692,238	715,732	clavulanic acid	20%	*Streptomyces microflavus* CG 893	-
3.6	terpene	772,612	799,206	hopene	69%	*Streptomyces pratensis* ATCC 33331	-
3.7	PKSI	1,138,589	1,233,400	sceliphrolactam	88%	*Streptomyces pratensis* ATCC 33331	sceliphrolactam
3.8	RiPP-like	1,441,862	1,453,154	-	-	*Streptomyces* sp. ADI97-07	-
4.1	lanthipeptide class I	73,205	99,734	-	-	*Streptomyces* sp. ADI97-07	-
4.2	NRPS	120,528	175,401	-	-	*Streptomyces* sp. S501	-
4.3	siderophore	448,476	461,607	-	-	*Streptomyces pratensis* ATCC 33331	-
4.4	terpene	527,356	547,053	-	-	*Streptomyces pratensis* ATCC 33331	-
4.5	RiPP-like	705,268	714,816	-	-	*Streptomyces pratensis* ATCC 33331	-
4.6	butyrolactone	2,368,883	2,379,809	-	-	*Streptomyces pratensis* ATCC 33331	-
4.7	NRPS-like, PKSI, NRPS	2,579,964	2,634,827	-	-	*Streptomyces pratensis* ATCC 33331	-
4.8	siderophore	3,279,372	3,291,153	desferrioxamine B/E	83%	*Streptomyces microflavus* CG 893	(dehydroxy)nocardamine
4.9	lanthipeptide class III, lanthipeptide class II	3,335,681	3,366,663	-	-	*Streptomyces microflavus* CG 893	-
4.10	terpene	3,798,845	3,818,603	-	-	*Streptomyces microflavus* CG 893	-
4.11	ectoine	4,281,704	4,290,312	ectoine	100%	*Streptomyces pratensis* ATCC 33331	ectoine
4.12	PKSII, PKS-like	4,652,529	4,725,065	cinerubin B	25%	*Streptomyces pratensis* ATCC 33331	coprisidin A/B
4.13	terpene	4,769,968	4,790,570	-	-	*Streptomyces pratensis* ATCC 33331	-
4.14	terpene, ectoine	5,070,871	5,092,300	ectoine	100%	*Streptomyces pratensis* ATCC 33331	ectoine
4.15	RiPP-like	5,120,490	5,130,717	-	-	*Streptomyces pratensis* ATCC 33331	-

Table S5. ^{1}H (700 MHz, DMSO-d_6) and ^{13}C NMR data (176 MHz, DMSO-d_6) of **8** in comparison with literature data for coprisidin A (δ in ppm).

	8		Coprisidin A[a]	
Position	δ_H (J in Hz)	δ_C, type	δ_H (J in Hz)	δ_C, type
1	—	n.d.	—	183.7, C
1a	—	123.77, C	—	123.6, C
2	—	n.d.	—	147.2, C
3	—	n.d.	—	155.5, C
3-OH	10.61, br s	—	10.86, s	—
4	—	n.d.	—	131.0, C
5	7.44, s	120.54, CH	7.47, s	120.4, CH
5a	—	n.d.	—	122.3, C
6	—	n.d.	—	179.7, C
7	—	n.d.	—	154.1, C
7-OH	10.61, br s	—	10.60, br s	—
8	—	n.d.	—	124.6, C
9	2.37, t (7.5)	24.78, CH_2	2.38, t (7.0)	24.8, CH_2
10	1.40, qt (7.5, 7.4)	21.18, CH_2	1.41, qt (7.0, 7.0)	21.2, CH_2
11	0.87, t (7.4)	14.09, CH_3	0.88, t (7.0)	14.1, CH_3
12	3.76, s	n.d.	3.77, s	61.5, CH_3
NH	8.77, s	—	8.81, s	—
2′	—	170.35, C	—	170.3, C
3′	5.99, s	53.88, CH	6.00, s	53.8, CH
3′a	—	116.34, C	—	116.4, C
4′	—	155.24, C	—	155.3, C
4′-OH	9.64, s	—	9.80, s	—
5′	6.86, d (7.5)	113.93, CH	6.85, d (7.5)	113.9, CH
6′	7.31, dd (8.1, 7.5)	133.73, CH	7.32, dd (7.5, 7.5)	133.9, CH
7′	6.79, d (8.1)	115.02, CH	6.81, d (7.5)	115.2, CH
7′a	—	n.d.	—	149.3, C

[a] **Um, S., Bach, D. H., Shin, B., Ahn, C. H., Kim, S. H., Bang, H. S., Oh, K. B., Lee, S. K., Shin, J. and Oh, D. C., 2016. Naphthoquinone-Oxindole Alkaloids, Coprisidins A and B, from a Gut-Associated Bacterium in the Dung Beetle, Copris tripartitus. Organic letters, 18(22), 5792–5795.** ***https://doi.org/10.1021/acs.orglett.6b02555***

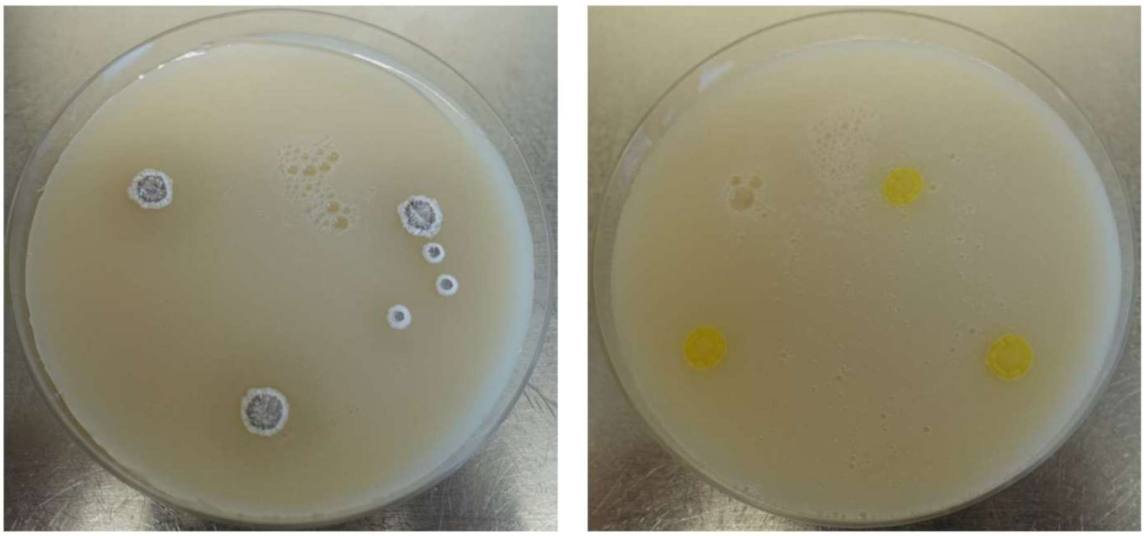
Table S6. ^{1}H (600 MHz, DMSO-d_6) and ^{13}C NMR data (151 MHz, DMSO-d_6) of **14** in comparison with literature data for saccharoquinoline (δ in ppm).

	14		Saccharoquinoline[a]	
Position	δ_H (J in Hz)	δ_C, type	δ_H (J in Hz)	δ_C, type
1	1.84, brd (12.5); 1.00, td (13.0, 2.9)	38.49, CH_2	1.83, d (14.3); 0.99, brd;	38.5, CH_2
2	1,65[b,c], m; 1,45[b,c], m	18.07, CH_2	1.66, m; 1.44, m	18.0, CH_2
3	1.39[b], brd; 1.17[b,c], m	41.36, CH_2	1.39; 1.18	41.3, CH_2
4	—	32.88, C	—	32.8, C
5	1.09, d (11.8)	55.33, CH	1.08	55.3, CH
6	1,74[b,c], m; 1,43[b,c], m	19.27, CH_2	1.74, m; 1.42, m	19.3, CH_2
7	2.14, m; 1,73[b,c], m	40.33, CH_2	2.15, dt (12.3, 3.6); 1.73	40.3, CH_2
8	—	78.17, C	—	78.1, C
9	1.67[b], dd (12.8, 5.1)	51.26, CH	1.67	51.2, CH
10	—	36.60, C	—	36.6, C
11	2.91, dd (16.4, 5.0); 2.70, dd (16.2, 13.1)	17.90, CH_2	2.91, dd (16.8, 13.1); 2.69, dd (16.8, 5.2)	17.9, CH_2
12	0.85, s	21.47, CH_3	0.85, s	21.5, CH_3
13	0.91, s	33.22, CH_3	0.90, s	33.2, CH_3
14	0.94, s	14.58, CH_3	0.94, s	14.6, CH_3
15	1.18[b], s	20.37, CH_3	1.18, s	20.3, CH_3
1′	—	104.86, C	—	104.9, C
2′	—	122.84, C	—	122.8, C
3′	—	133.60, C	—	133.6, C
4′	—	135.04, C	—	135.0, C
5′	—	136.96, C	—	136.9, C
6′	—	145.80, C	—	145.8, C
7′	8.40, d (8.6)	132.09, CH	8.40, d (8.6)	132.1, CH
8′	7.92, d (8.6)	116.93, CH	7.92, d (8.6)	116.9, CH
9′	—	140.90, C	—	140.8, C
10′	—	165.58, C	—	165.6, C

[a] Le, T. C., Lee, E. J., Lee, J., Hong, A., Yim, C. Y., Yang, I., Choi, H., Chin, J., Cho, S. J., Ko, J., Hwang, H., Nam, S. J. and Fenical, W., 2019. Saccharoquinoline, a Cytotoxic Alkaloidal Meroterpenoid from Marine-Derived Bacterium *Saccharomonospora* sp. *Marine Drugs*, *17*(2), 98. https://doi.org/10.3390/md17020098

[b] Overlapping signal. [c] Value determined from the HSQC spectrum.

Figure S1.



Streptomyces sp. SL203 *Streptomyces* sp. SL294

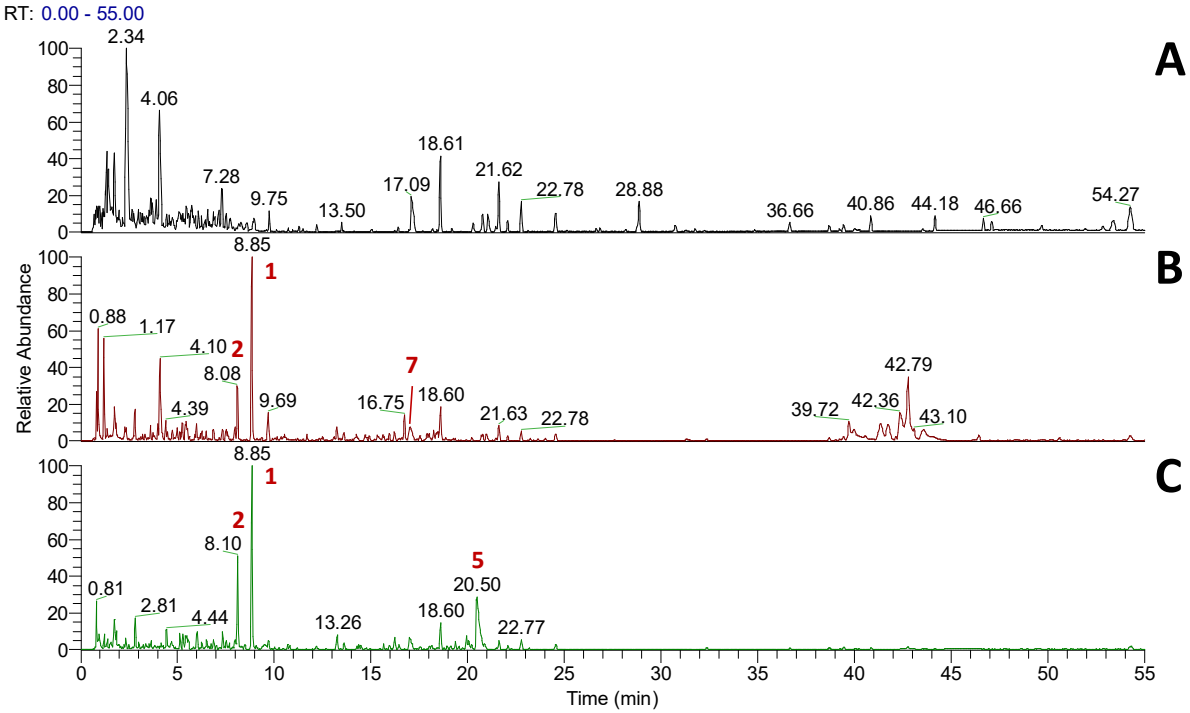


Figure S2. Base peak chromatograms (*m/z* 140-2000) obtained by LC-MS in positive ion mode of the extracts from SM17 medium control (A), strain SL203 pSET152_ermE*p grown in SM17 medium (B), and strain SL294 pSET152_ermE*p grown in SM17 medium (C). The peaks corresponding to nocardamine (**1**), dehydroxynocardamine (**2**), coproporphyrin (**5**), and detoxin S_1 (**7**) are labelled.

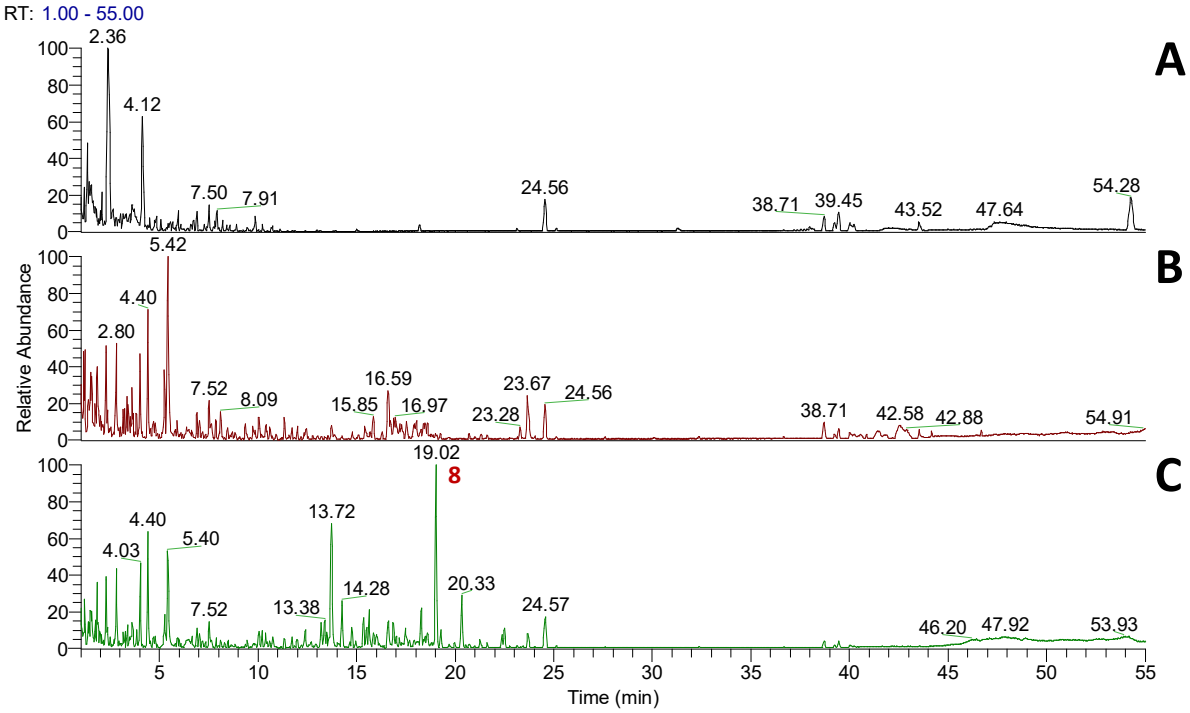


Figure S3. Base peak chromatograms (*m/z* 140-2000) obtained by LC-MS in positive ion mode of the extracts from MYM medium control (A), strain SL203 pSET152_ermE*p grown in MYM medium (B), and strain SL203 pSET152_ermE*p_ctg3_1243 grown in MYM medium (C). The peak corresponding to coprisidin A (**8**) is labelled.

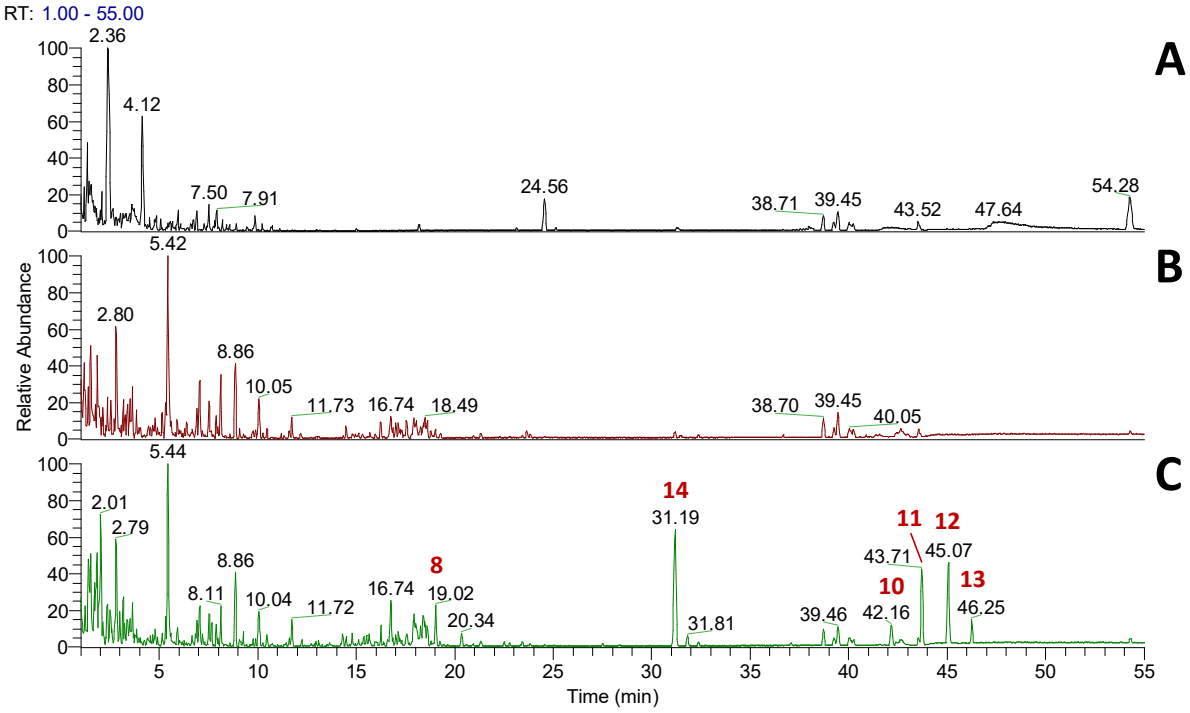


Figure S4. Base peak chromatograms (*m/z* 140-2000) obtained by LC-MS in positive ion mode of the extracts from MYM medium control (A), strain SL294 pSET152_ermE*p grown in MYM medium (B), and strain SL294 pSET152_ermE*p_ctg3_1243 grown in MYM medium (C). The peaks corresponding to coprisidin A (**8**), saccharoquinoline (**14**) and the congeners nonactin (**10**), monactin (**11**), isodinactin (**12**), and either trinactin or isotrinactin (**13**) are labelled.

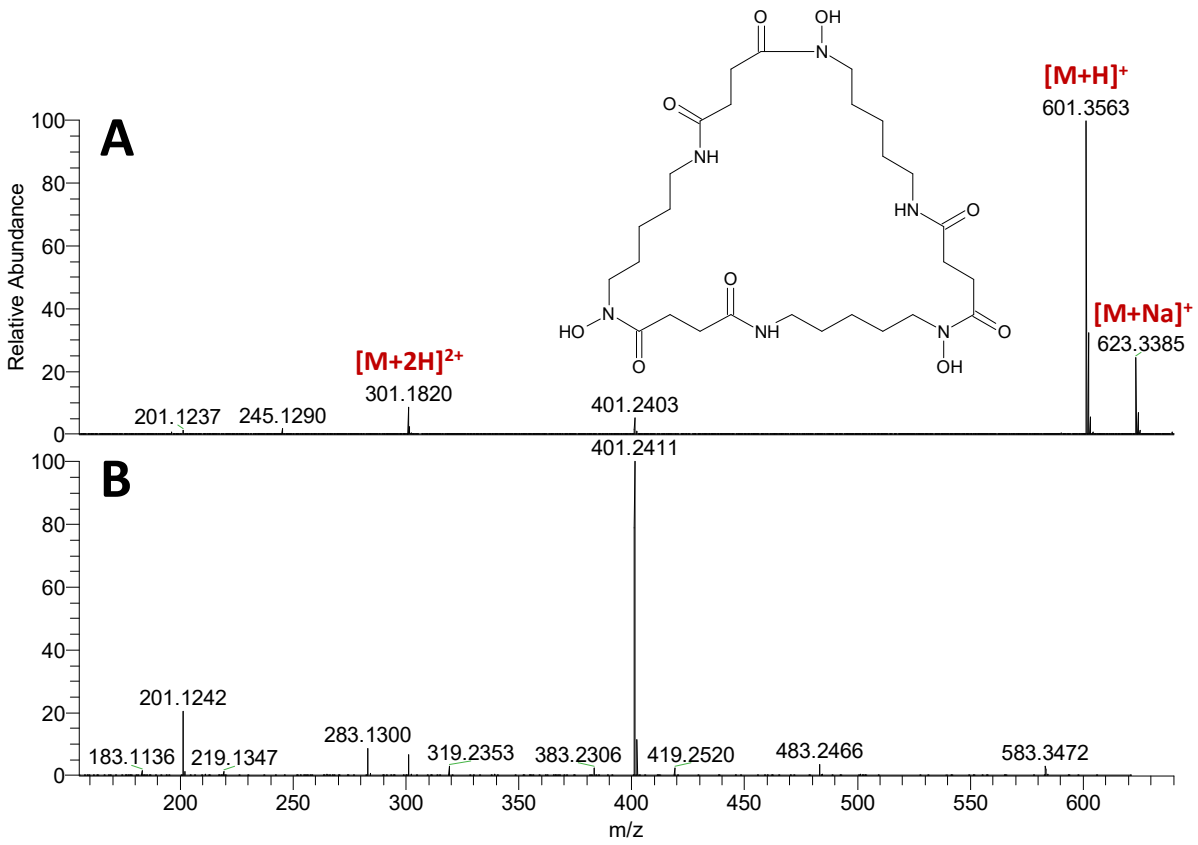


Figure S5. High resolution ESI mass spectrum of nocardamine (**1**) at R_t 8.76-8.94 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 601.3563 (B).

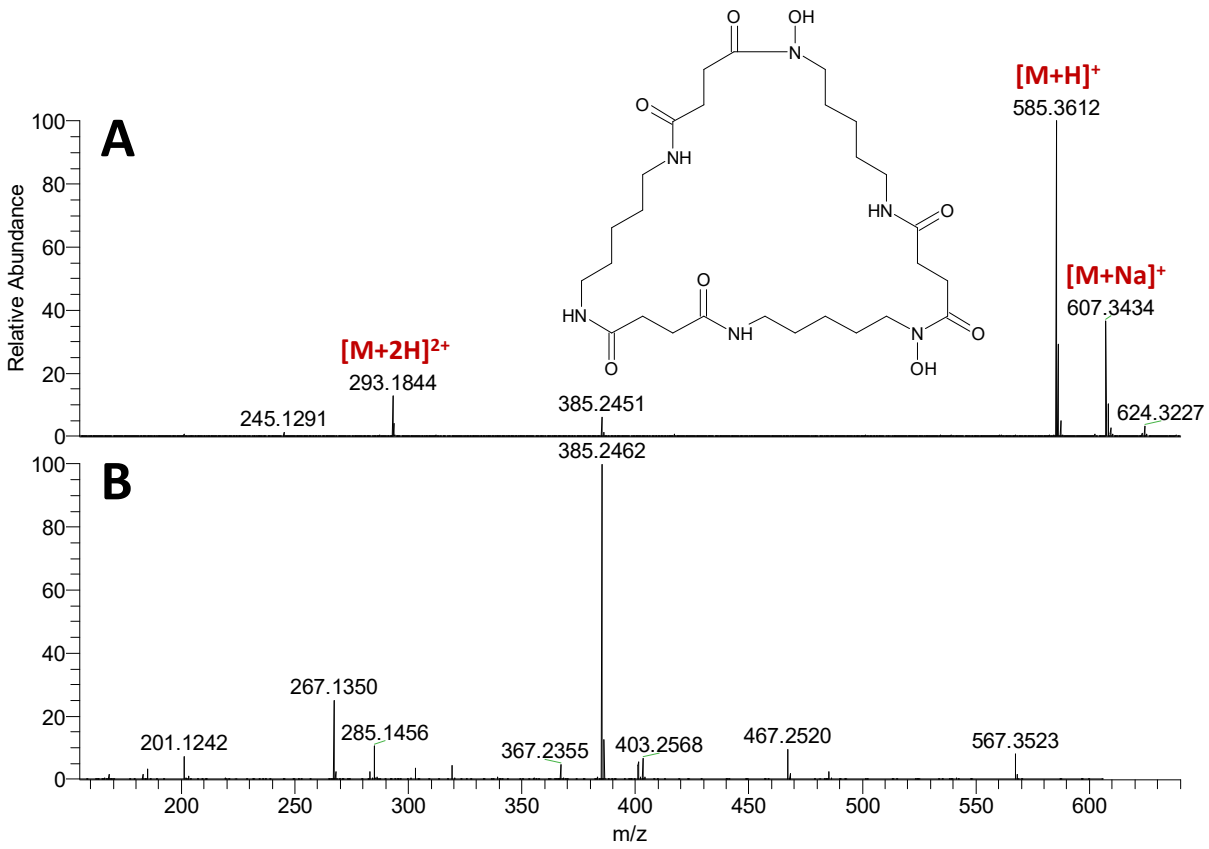


Figure S6. High resolution ESI mass spectrum of dehydroxynocardamine (**2**) at R_t 8.01-8.21 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 585.3612 (B).

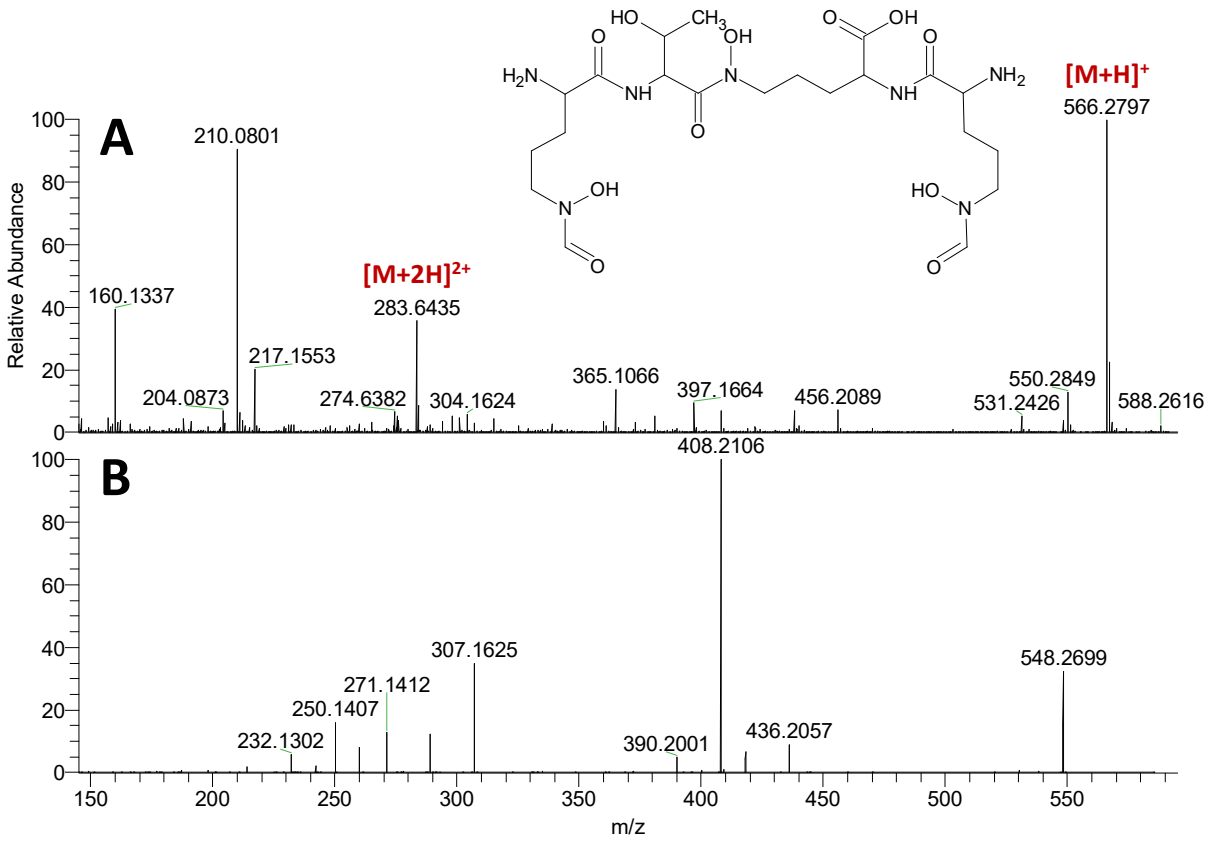


Figure S7. High resolution ESI mass spectrum of coelichelin (**3**) at R_t 1.10-1.13 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 566.2797 (B).

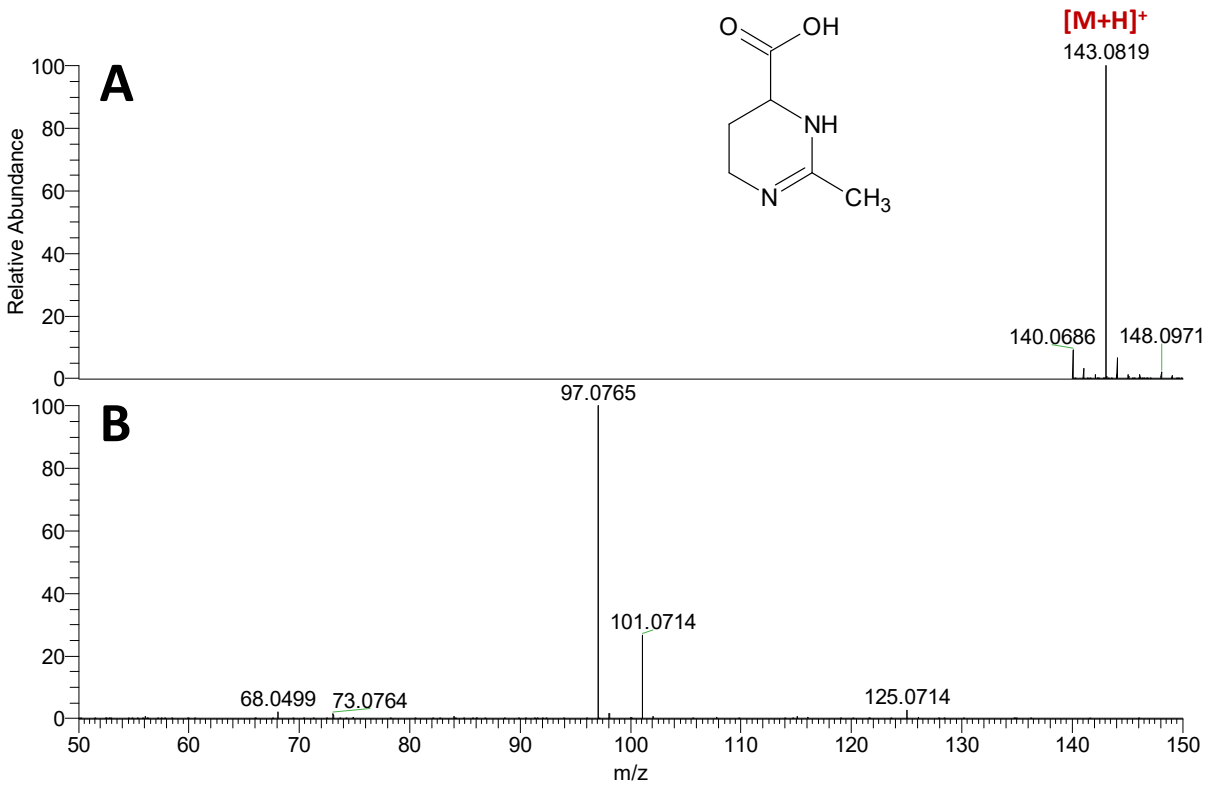


Figure S8. High resolution ESI mass spectrum of ectoine (**4**) at R_t 0.80-0.91 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 143.0819 (B).

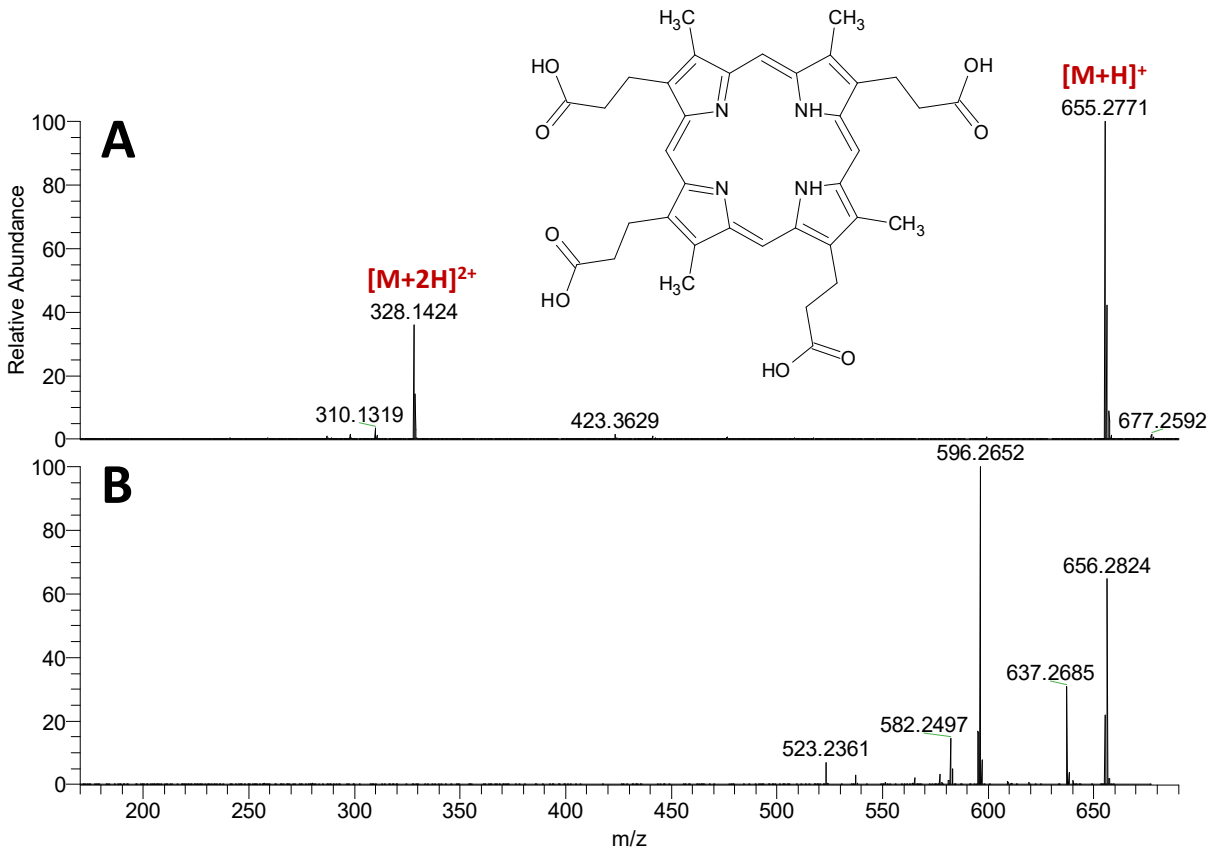


Figure S9. High resolution ESI mass spectrum of coproporphyrin (**5**) at R_t 20.41-20.82 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 655.2771 (B).

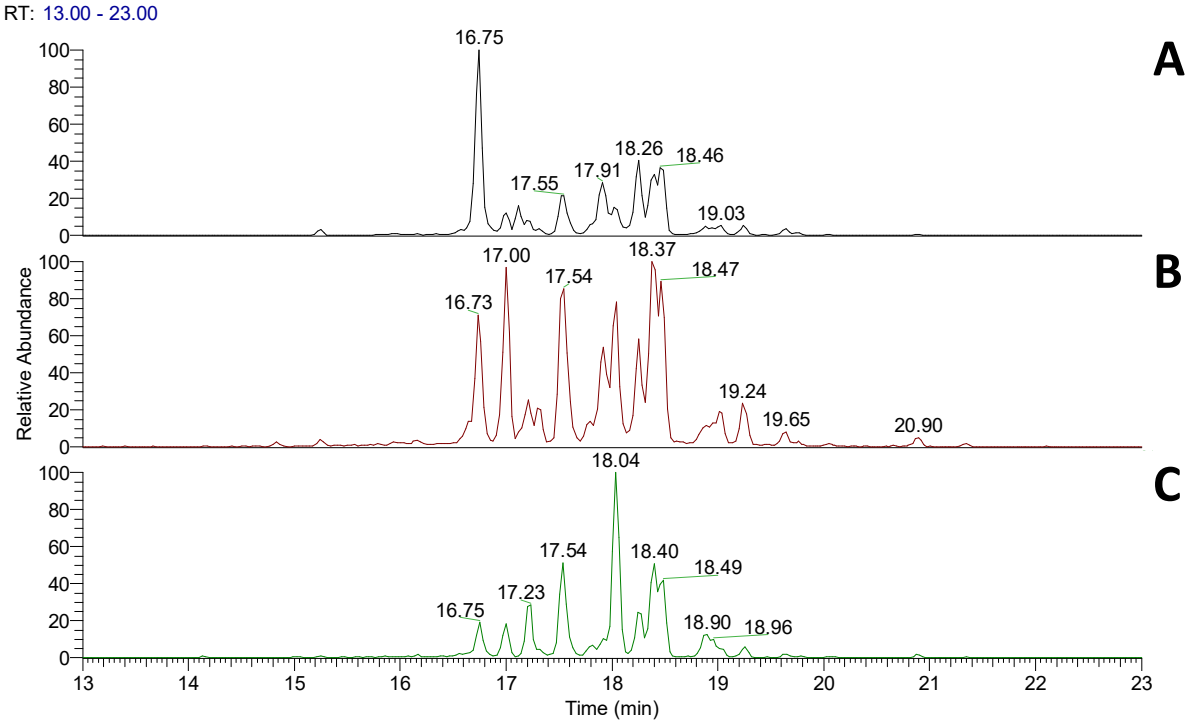


Figure S10. Extracted ion chromatograms (*m/z* 482.2537±0.0024) obtained by LC-MS in positive ion mode of the extracts from strain SL203 pSET152_ermE*p grown in SM17 medium (A), strain SL203 pSET152_ermE*p grown in MYM medium (B), and strain SL294 pSET152_ermE*p grown in SM17 medium (C). This *m/z* value corresponds to the $[M+H]^+$ ion of the various sceliphrolactam isomers.

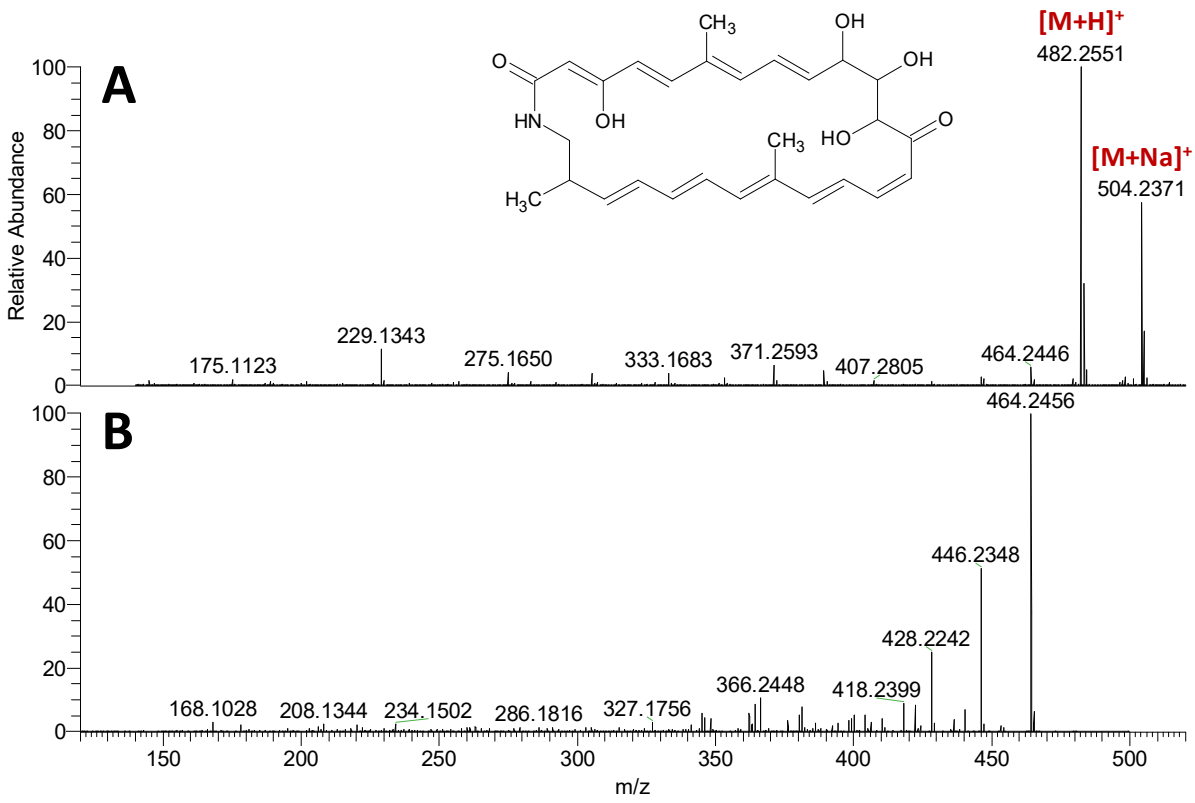


Figure S11. High resolution ESI mass spectrum of the sceliphrolactam isomer eluting at R_t 16.63-16.83 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 482.2551 (B). The structure shown is for sceliphrolactam as representative for the different isomers.

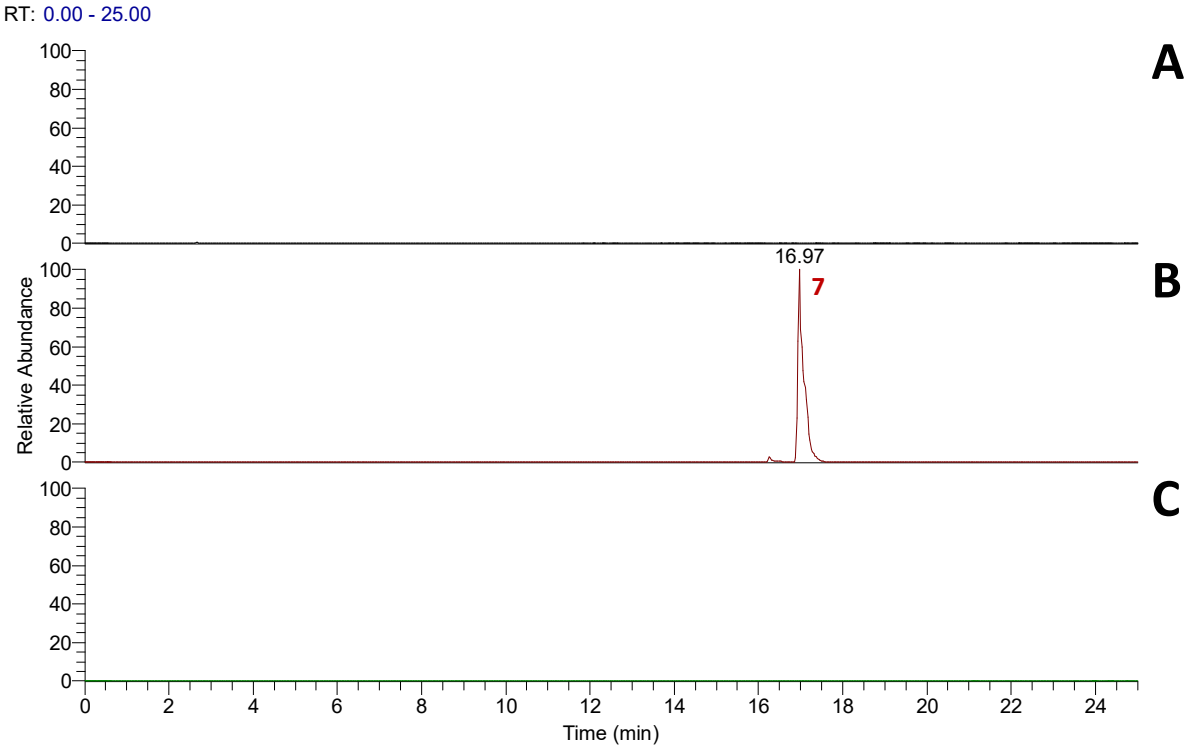


Figure S12. Extracted ion chromatograms (*m/z* 518.3225±0.0026) obtained by LC-MS in positive ion mode of the extracts from SM17 medium control (A), strain SL203 pSET152_ermE*p grown in SM17 medium (B), and strain SL294 pSET152_ermE*p grown in SM17 medium (C). This *m/z* value corresponds to the $[M+H]^+$ ion of detoxin S_1 (**7**).

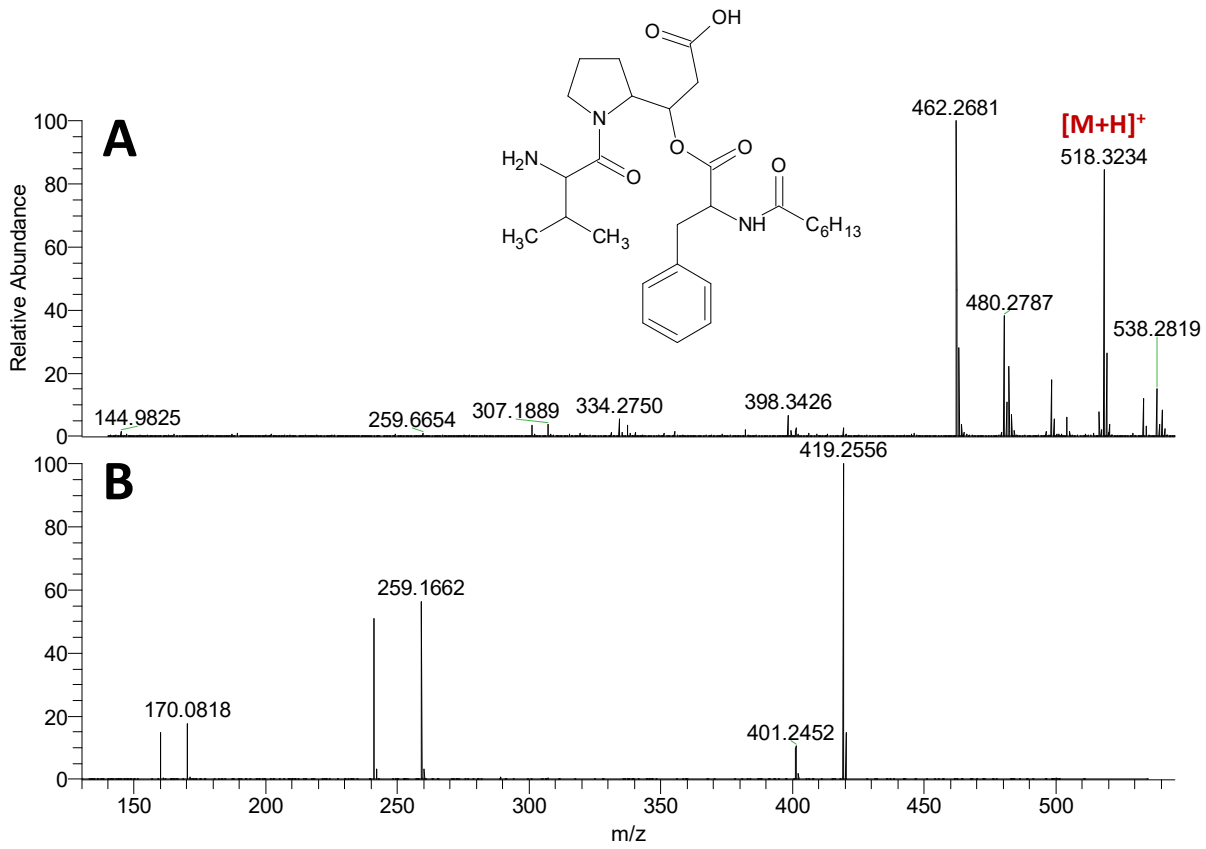


Figure S13. High resolution ESI mass spectrum of detoxin S_1 (**7**) at R_t 16.86-17.31 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 518.3234 (B). The structure of the *N*-acyl chain attached to the Phe is not known.

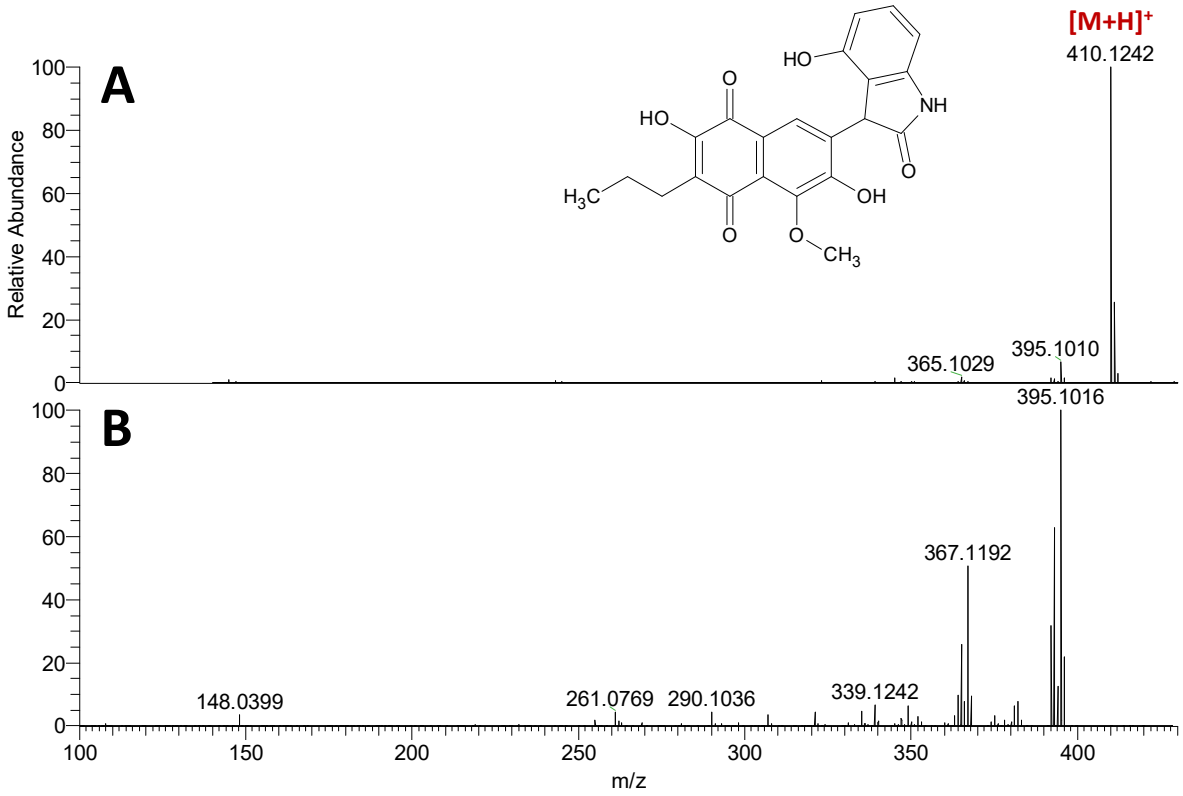


Figure S14. High resolution ESI mass spectrum of coprisidin A (**8**) at R_t 18.94-19.11 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 410.1242 (B).

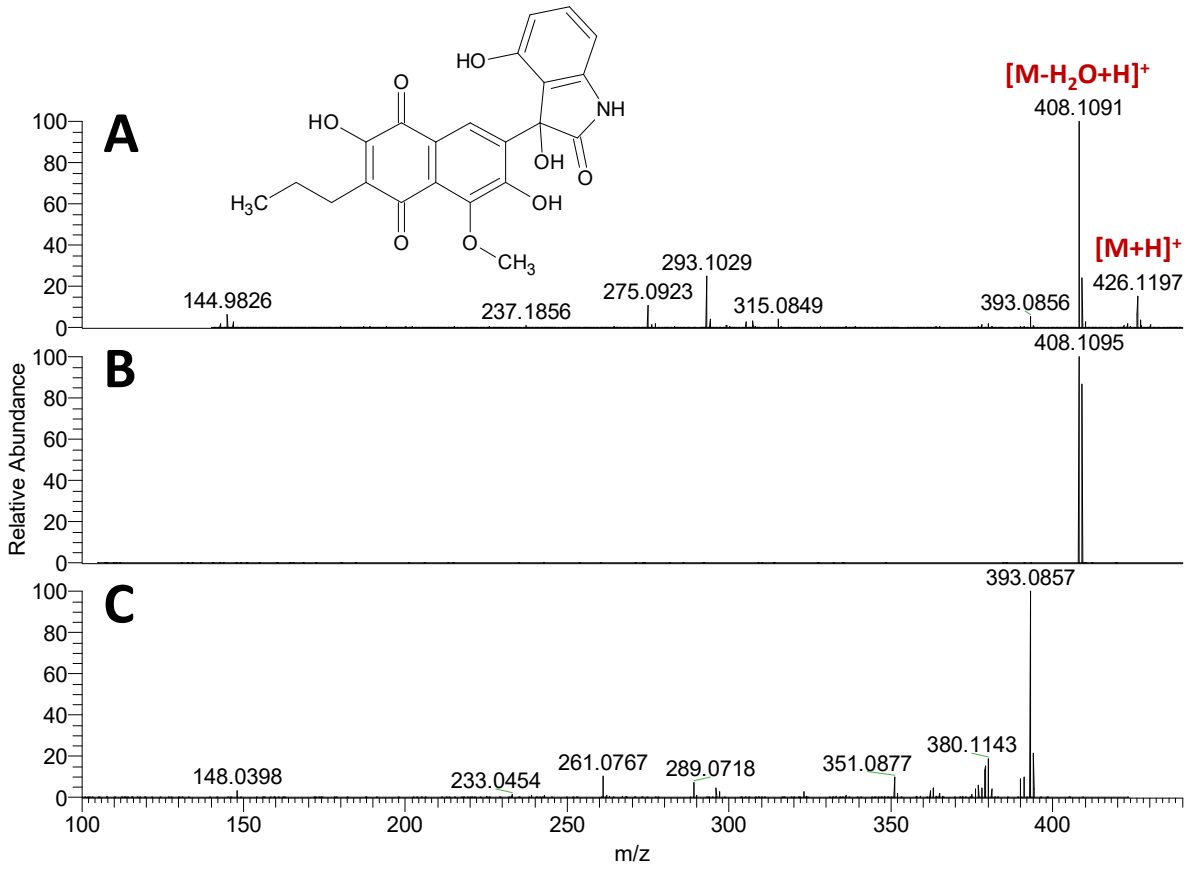


Figure S15. High resolution ESI mass spectrum of coprisidin B (**9**) at R_t 17.41-17.53 min (A), high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 426.1197 (B), and high resolution MS/MS spectrum of its $[M-H_2O+H]^+$ ion (formed via in source decay) at *m/z* 408.1091 (B).

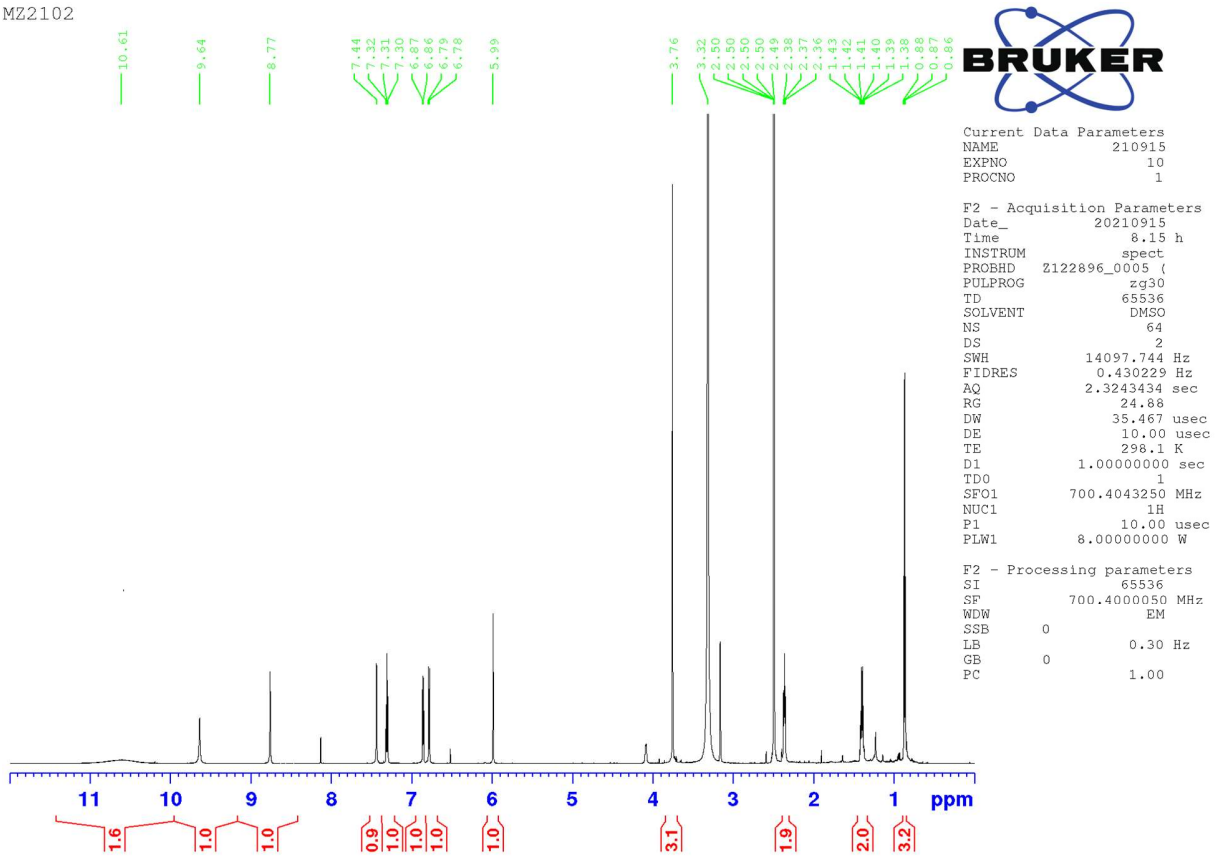


Figure S16. ^{1}H NMR spectrum of coprisidin A (**1**) in DMSO-d_6 at 700 MHz.

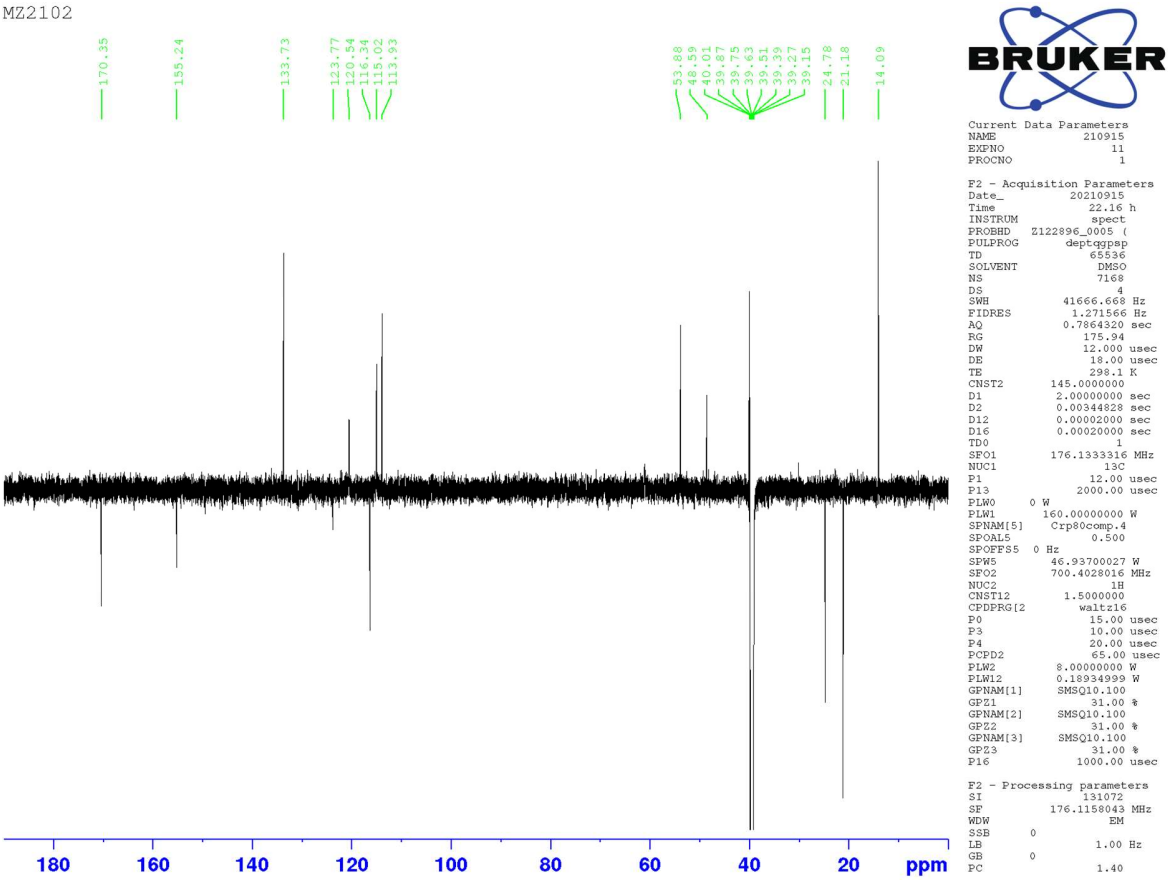


Figure S17. ^{13}C NMR spectrum of coprisidin A (**1**) in DMSO-d_6 at 176 MHz.

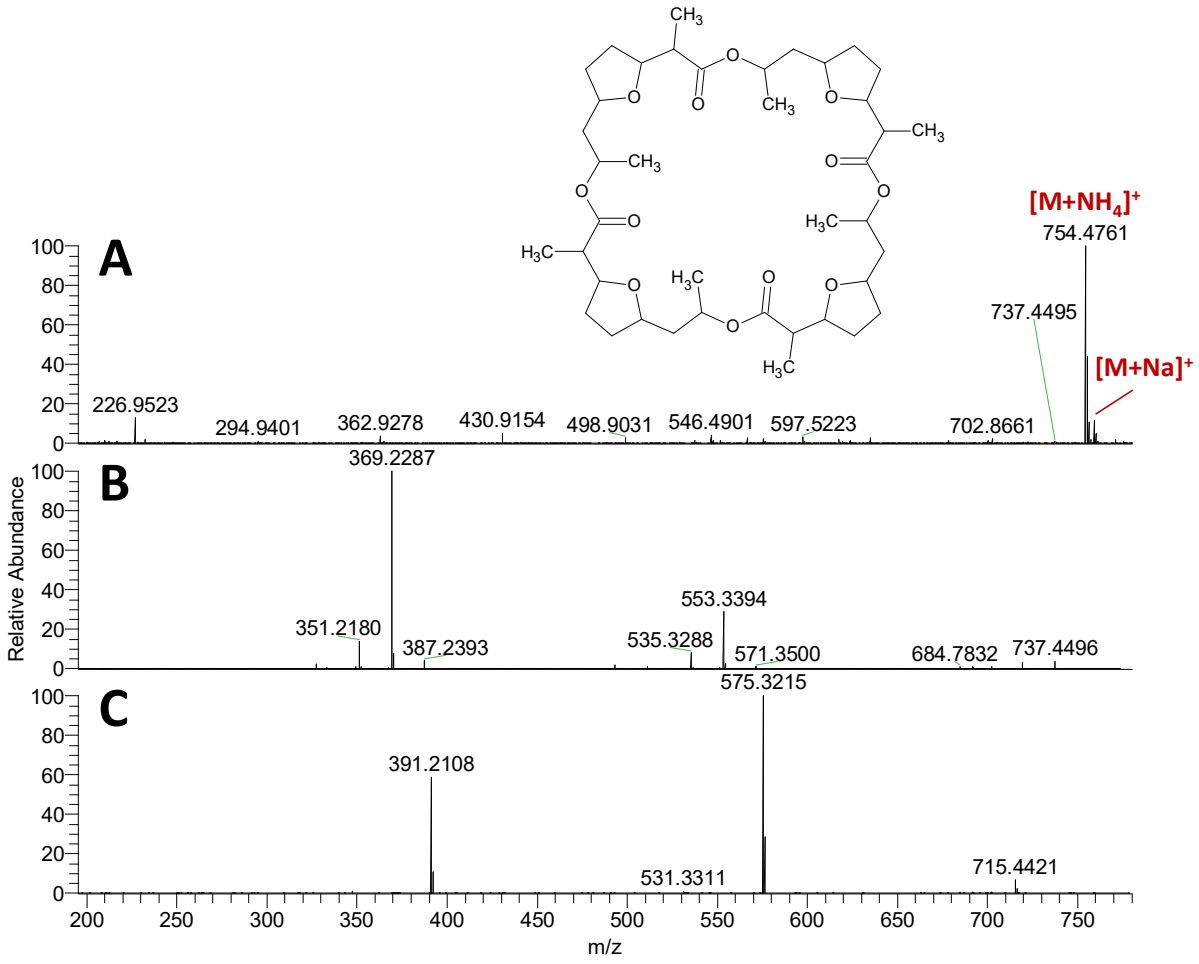


Figure S18. High resolution ESI mass spectrum of nonactin (**10**) at R_t 42.05-42.26 min (A), high resolution MS/MS spectrum of its $[M+NH_4]^+$ ion at *m/z* 754.4761 (B), and high resolution MS/MS spectrum of its $[M+Na]^+$ ion at *m/z* 759.4316 (B).

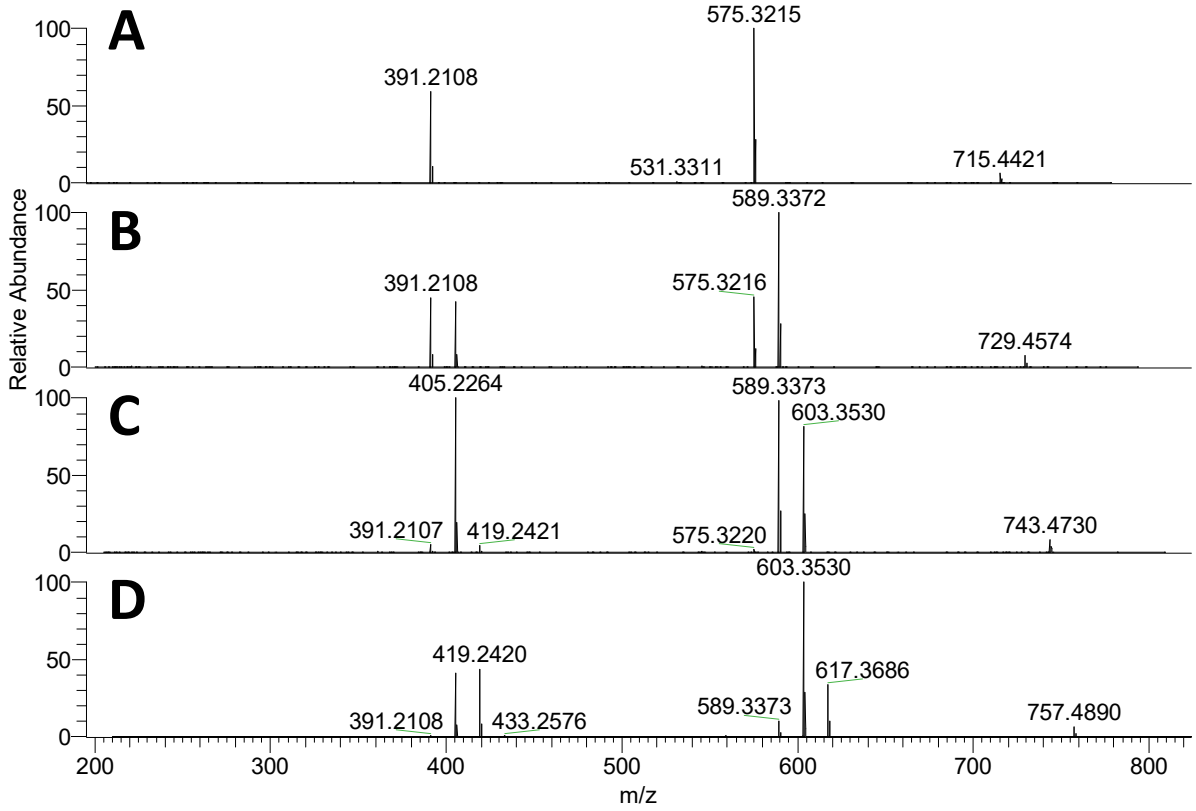


Figure S19. High resolution MS/MS spectra of the $[M+Na]^+$ ions of nonactin (**10**) at *m/z* 759.4316 (A), monactin (**11**) at *m/z* 773.4463 (B), isodinactin (**12**) at *m/z* 787.4616 (C), and either trinactin or isotrinactin (**13**) at *m/z* 801.4781 (D).

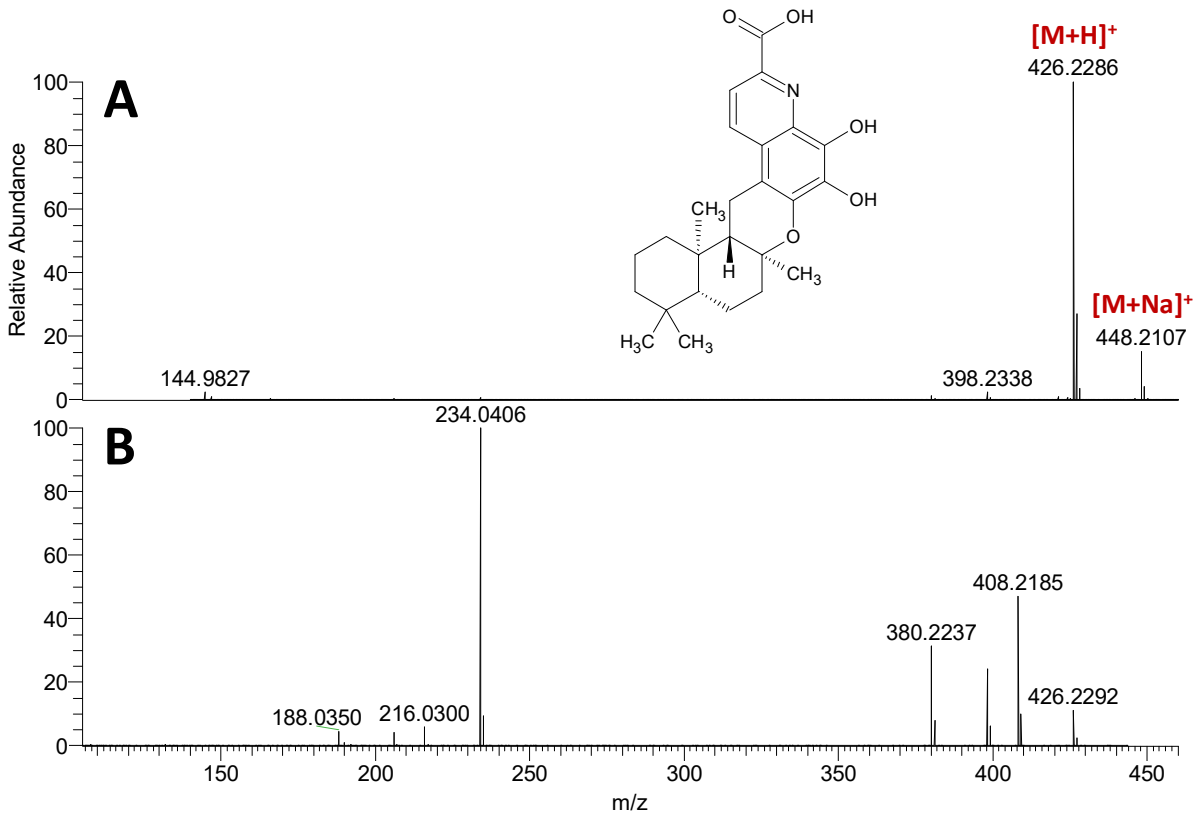


Figure S20. High resolution ESI mass spectrum of saccharoquinoline (**14**) at R_t 31.04-31.31 min (A) and high resolution MS/MS spectrum of its $[M+H]^+$ ion at *m/z* 426.2286 (B).

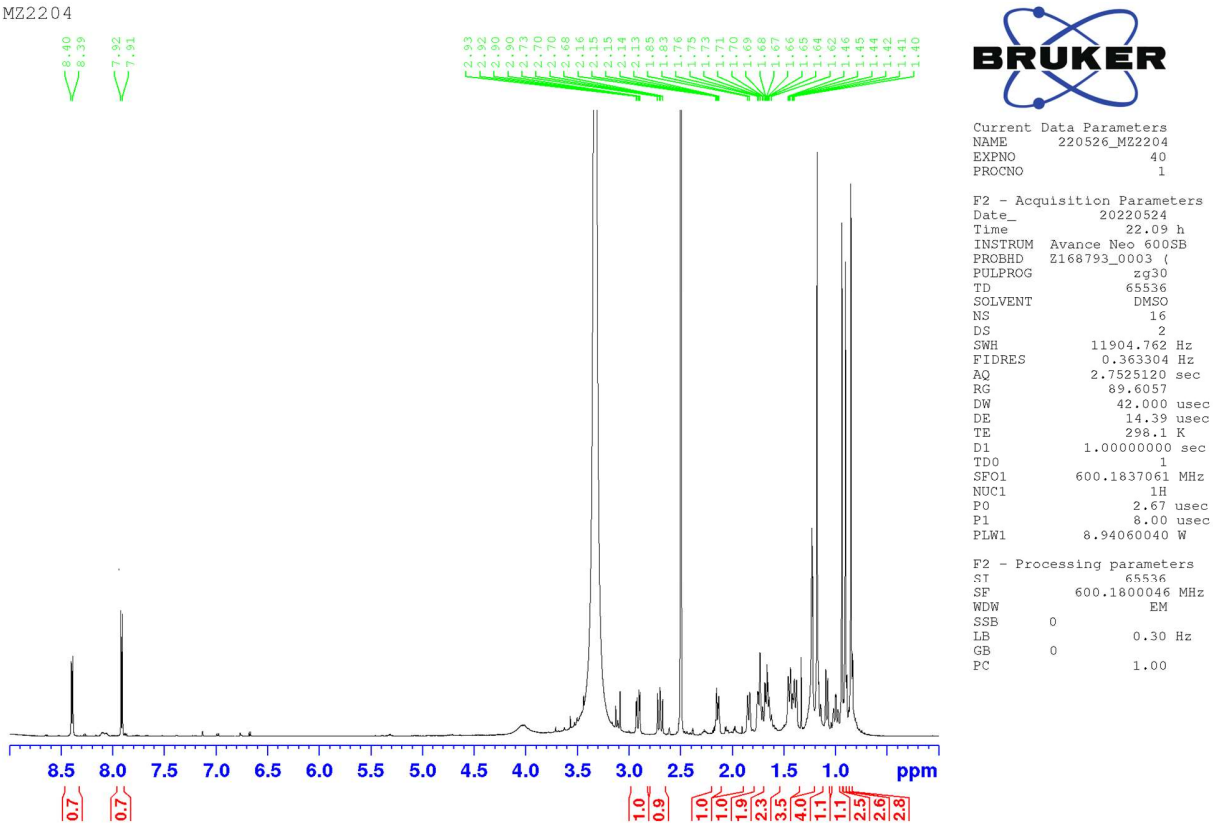


Figure S21. ^{1}H NMR spectrum of saccharoquinoline (**14**) in DMSO-d_6 at 600 MHz.

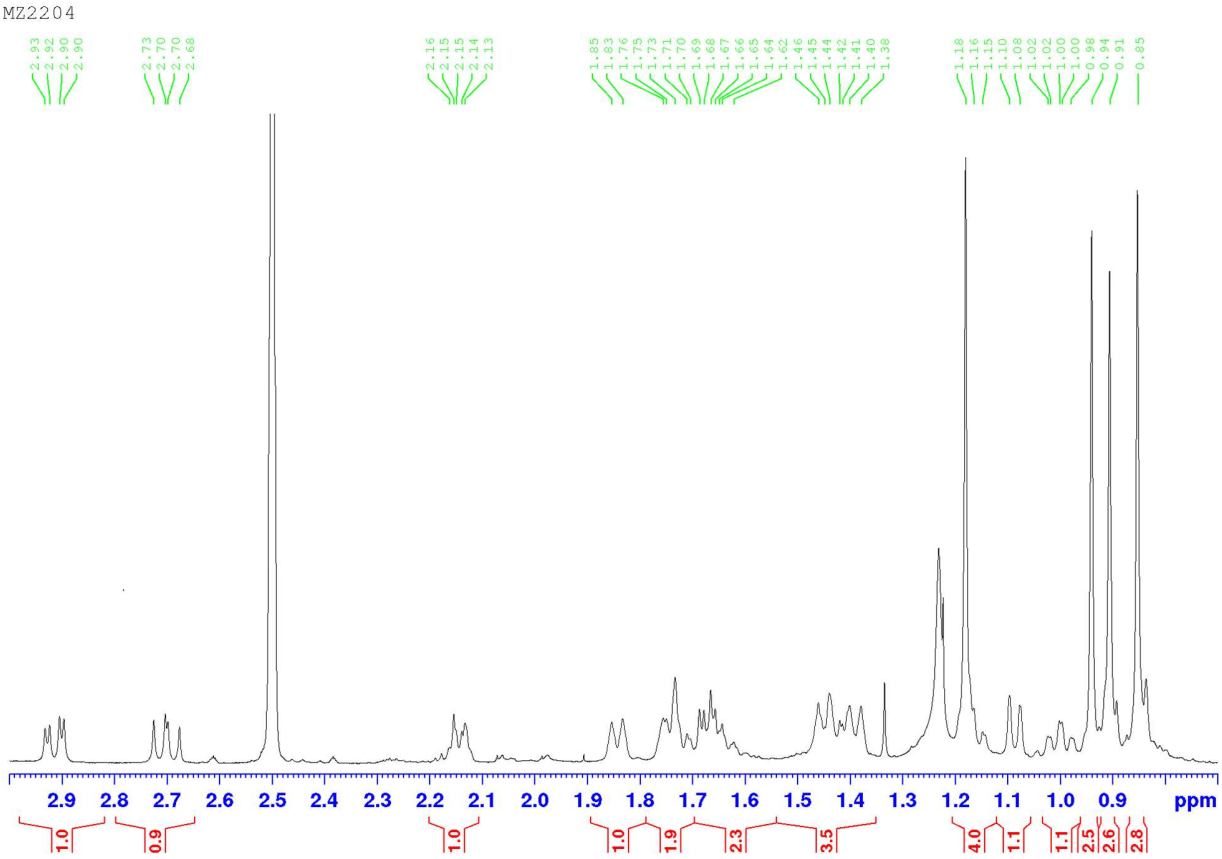


Figure S22. ^{1}H NMR spectrum of saccharoquinoline (**14**) in DMSO-d_6 at 600 MHz (zoom).

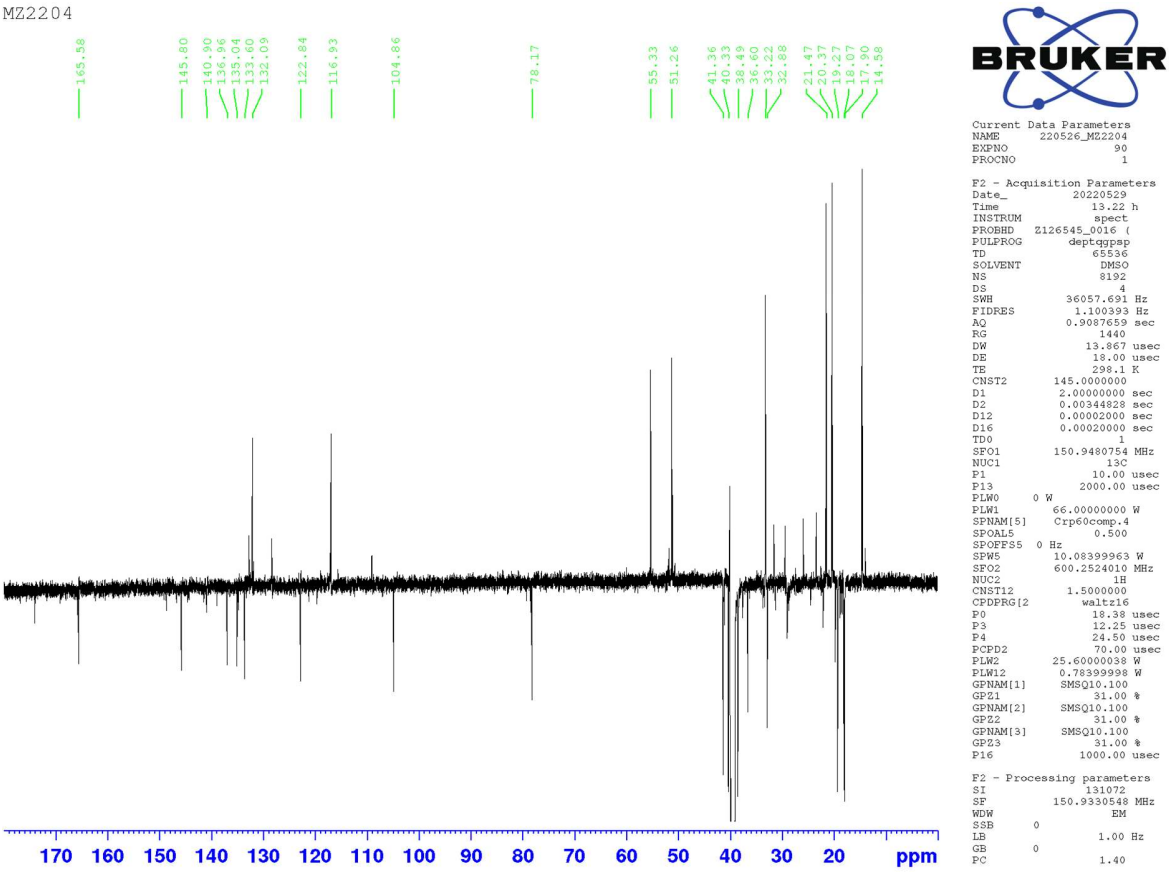


Figure S23. ^{13}C NMR spectrum of saccharoquinoline (**14**) in DMSO-d_6 at 151 MHz.

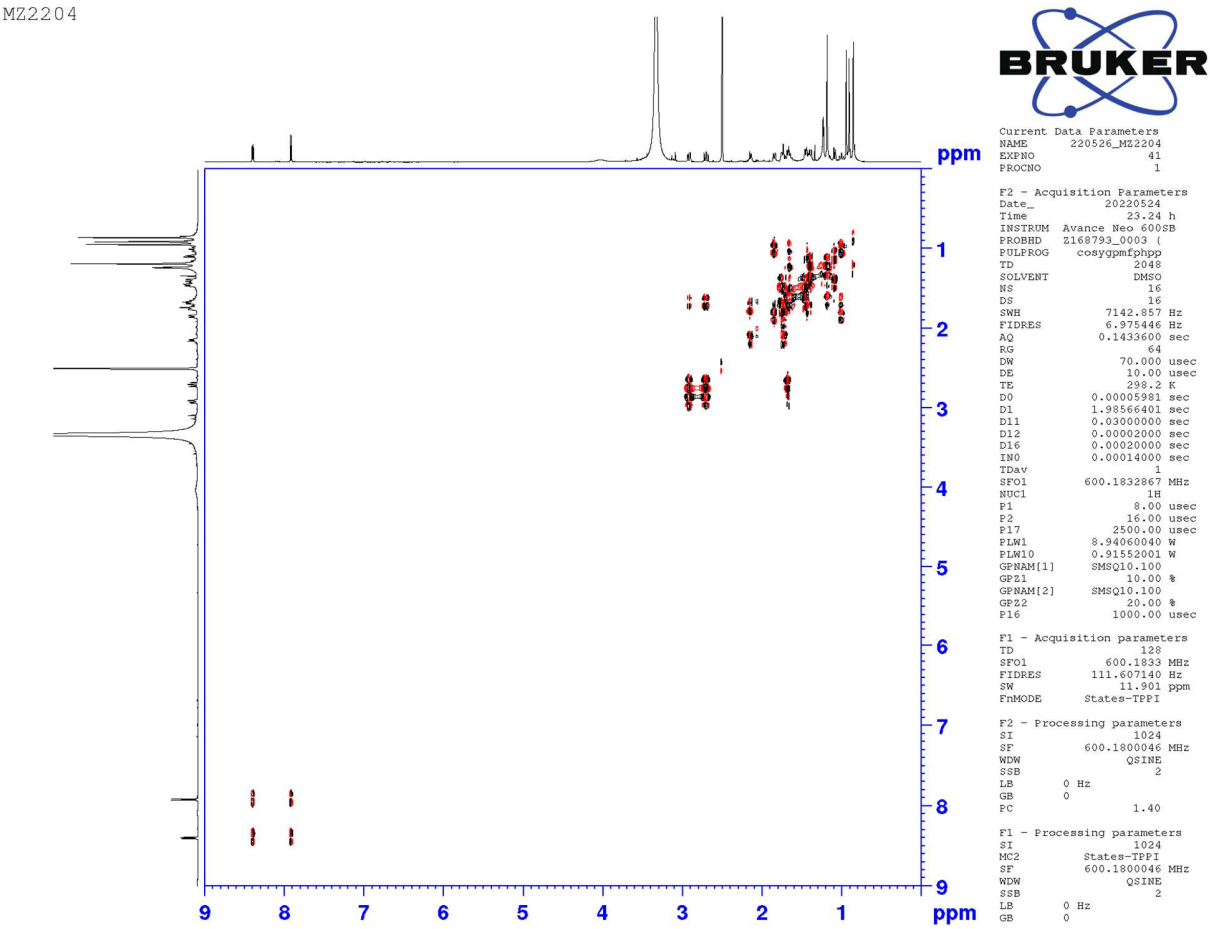


Figure S24. COSY spectrum of saccharoquinoline (**14**) in DMSO-d_6 at 600 MHz.

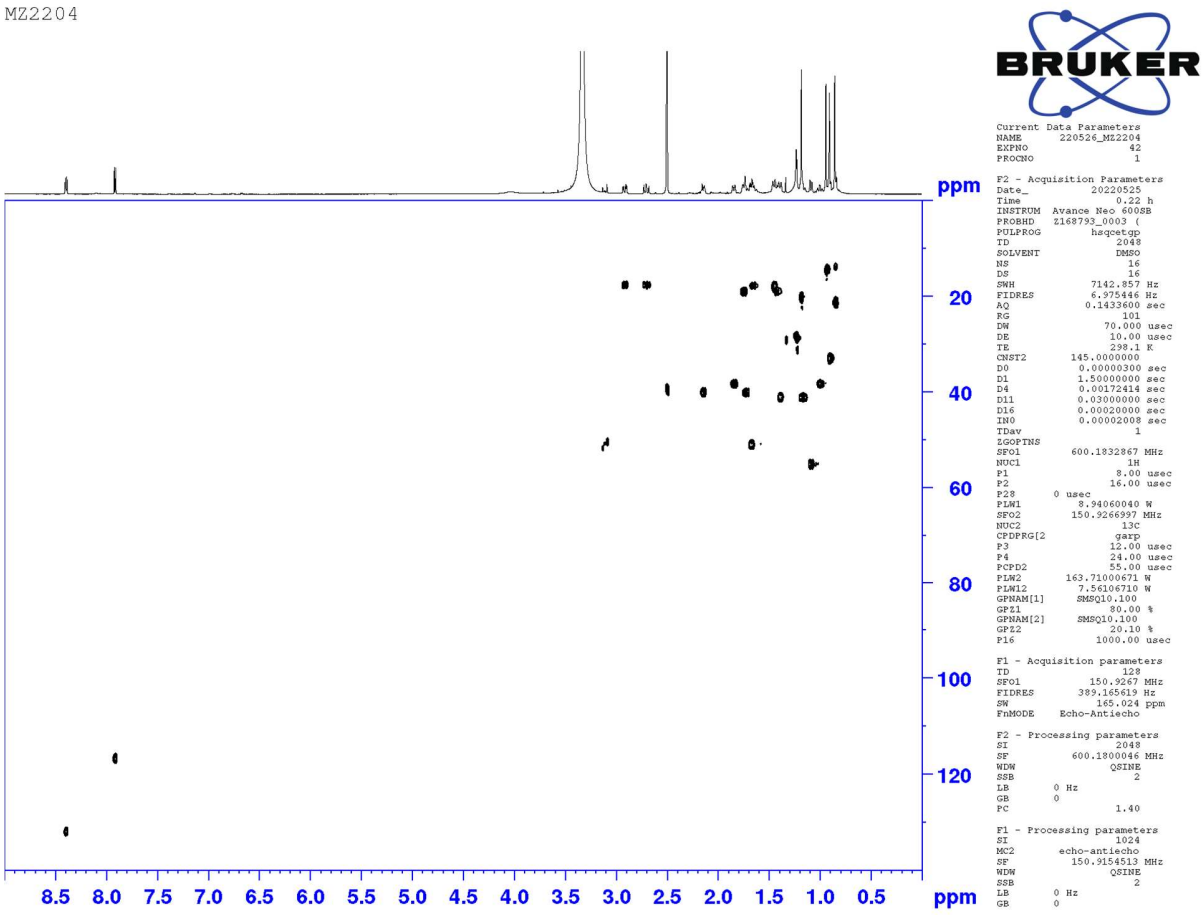


Figure S25. HSQC spectrum of saccharoquinoline (**14**) in DMSO-d_6 at 600 MHz.

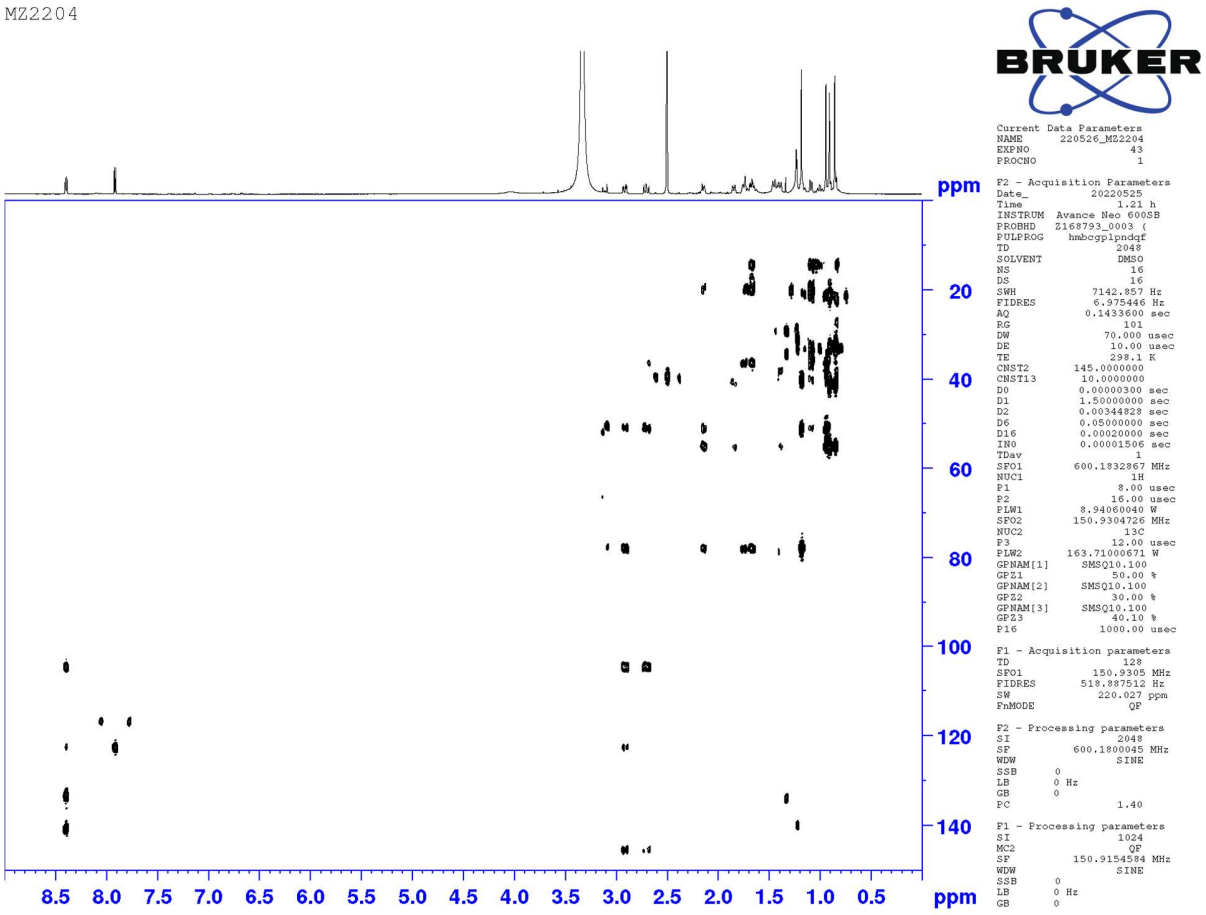


Figure S26. HMBC spectrum of saccharoquinoline (**14**) in DMSO-d_6 at 600 MHz.