Supplementary Information

Diversity of Bacterial Biosynthetic Genes in Maritime Antarctica

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Table S1 - Geographic location of the samples included in this study and environmental parameters measured: several trace elements (Cr, Ni, Cu, Zn, As, Pb, Cd and Hg) [1], organic matter (OM) and water content.

Sample	Latitude	Longitude	Cr	Ni	Cu	Zn	As	Pb	Cd	Hg	OM	Water
AC3	-62.1671	-58.8517	22.25	18.11	109.37	76.67	18.98	12.86	0.14	0.012	0.1	0.3
72	-62.1999	-58.9677	62.23	25.26	71.27	83.13	17.51	15.8	0.15	0.008	2.8	2.3
87	-62.1961	-58.9663	65.12	35.61	75.29	76.19	19.59	6.56	0.14	0.012	2.2	2.8
I1	-62.1960	-58.9611	68.64	34.35	105.7	216.19	19.36	418.49	1.19	0.074	2.8	0.5
TR1	-62.1991	-58.9589	52.23	21	83.19	104.09	18.73	6.66	0.21	0.007	1.8	1.3
TC3	-62.1993	-58.9620	63.35	33.49	95.45	79.16	20.5	14.41	0.15	0.025	1.8	1.5
54	-62.1994	-58.9656	29.33	16.59	100.31	98.58	17.42	5.19	0.14	0.026	4.1	3.6
66	-62.1973	-58.9654	31.41	15.83	65.65	86.97	17.48	7.28	0.61	0.005	2.2	1.8

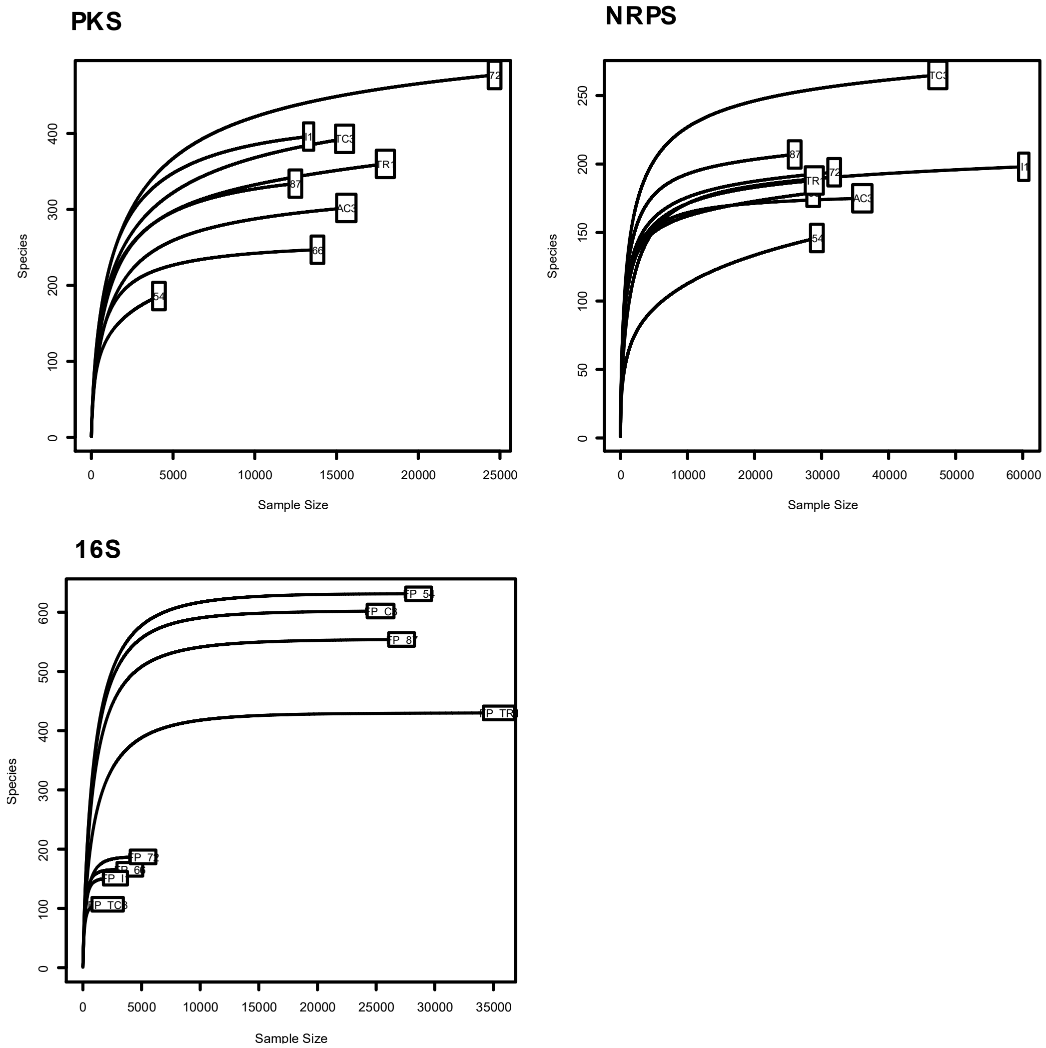


Figure S1 – Rarefaction plot of PKS and NRPS.

Table S2 – Sequence richness and diversity estimates for KS domain of PKS gene. Number of OTUs (grouped at 97% and in a second round at 95%), Chao1, Shannon and Simpson diversity index.

Sample	OTUs	Chao1	se.chao1	Shannon	Simpson
54	186	223.1429	15.530469	4.222633	0.9744810
66	247	251.4000	3.557533	4.260995	0.9700090
72	477	518.7576	15.070831	4.754638	0.9803395
87	334	346.6000	6.421924	4.477355	0.9696060
AC3	302	322.7143	9.968224	4.059967	0.9520663
I1	396	409.0526	6.277387	4.536398	0.9641627
TC3	393	436.3636	15.509294	4.654110	0.9789782
TR1	360	411.2727	19.724810	4.548058	0.9792373

Table S3– Sequence richness and diversity estimates for AD domain of NRPS gene. Number of OTUs (grouped at 97% and in a second round at 95%), Chao1, Shannon and Simpson diversity index.

Samples	Observed	Chao1	se.chao1	Shannon	Simpson
54	146	183.4000	17.144873	2.938287	0.9011069
66	179	200.8571	13.883750	3.869712	0.9534230
72	194	207.0000	9.258827	3.764392	0.9571343
87	207	222.1667	10.859490	3.741089	0.9389775
AC3	175	177.0000	2.585619	3.588332	0.9347654
I1	198	207.4286	7.257987	2.985950	0.8859579
TC3	265	288.3333	13.638560	3.691191	0.9323737
TR1	188	197.7500	7.201727	3.682722	0.9389044

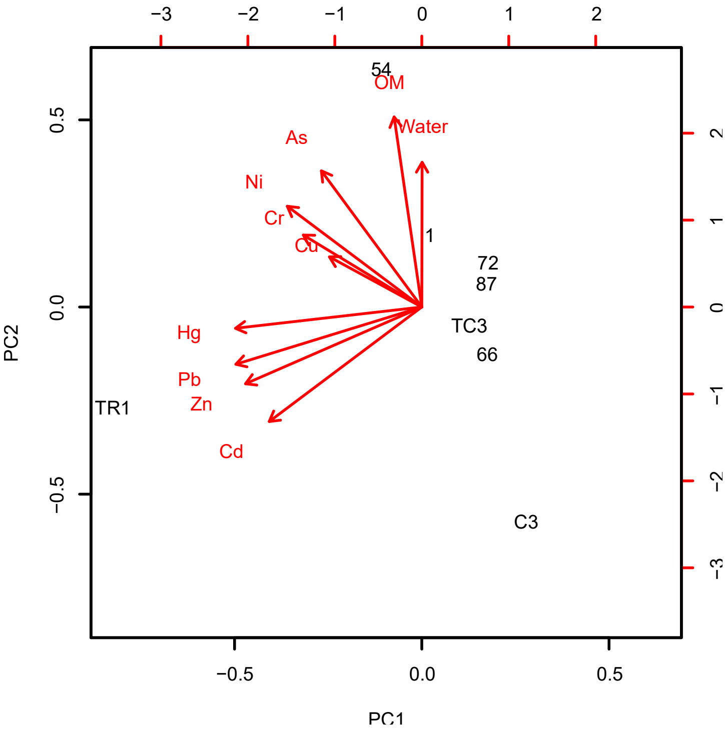


Figure S2 – Principal component analysis (PCA) of the environmental variables measured in this study.

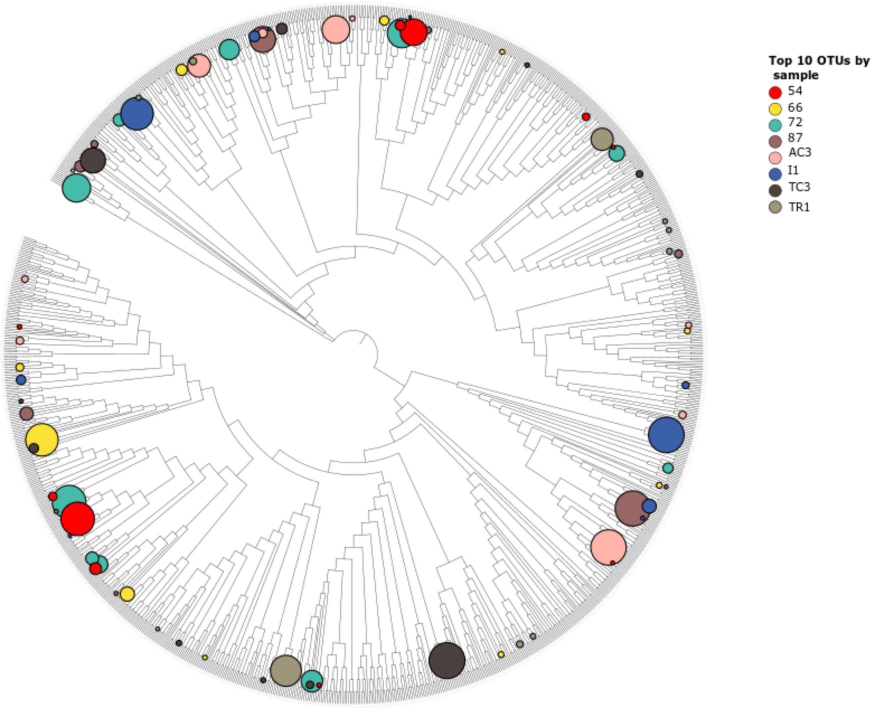


Figure S3 – Maximum likelihood phylogenetic tree of AD domain. The relative abundances of the 10 most abundant OTUs by sample is represented.

Table S4 – Relative abundance of KS domain provenience from actinobacterial genus.

	Samples							
	54	**66**	**72**	**87**	**AC3**	**I1**	**TC3**	**TR1**
Actinobacteria								
Other	3.030303	0.38624952	0.17812611	6.958608	13.2768362	0.0000000	6.97511392	2.60010400
Actinoalloteichus	0.000000	0.00000000	0.00000000	0.000000	0.0000000	64.4444444	0.03505082	0.00000000
Actinocrispum	0.000000	0.00000000	0.00000000	0.000000	0.2824859	0.0000000	0.00000000	0.26001040
Actinoplanes	0.000000	0.00000000	0.00000000	0.000000	0.0000000	0.0000000	3.01437084	0.29901196
Actinosynnema	0.000000	0.00000000	0.00000000	0.119976	0.0000000	0.0000000	0.00000000	0.00000000
Allokutzneria	0.000000	0.00000000	0.03562522	0.000000	2.2598870	0.0000000	0.00000000	0.00000000
Amycolatopsis	0.000000	0.34762457	0.00000000	0.000000	0.0000000	0.0000000	0.00000000	0.00000000
Auritidibacter	0.000000	0.00000000	0.07125045	0.000000	0.0000000	7.5213675	0.00000000	0.00000000
Couchioplanes	0.000000	0.27037466	0.00000000	0.000000	0.0000000	0.0000000	0.00000000	0.00000000
Frankia	0.000000	0.00000000	3.49127182	0.000000	0.0000000	1.5384615	0.00000000	0.00000000
Gordonia	0.000000	0.00000000	0.67687923	2.939412	0.0000000	0.0000000	0.03505082	0.00000000
Herbidospora	0.000000	0.00000000	0.00000000	1.499700	0.0000000	0.0000000	0.00000000	0.00000000
Kibdelosporangium	0.000000	0.00000000	0.00000000	0.000000	2.8248588	0.0000000	0.00000000	0.28601144

Kitasatospora	42.424242	0.00000000	0.00000000	1.019796	0.0000000	0.0000000	0.07010165	0.19500780
Kocuria	0.000000	0.00000000	0.00000000	0.000000	0.0000000	0.8547009	0.00000000	0.00000000
Kribbella	0.000000	0.83043646	0.00000000	0.000000	0.0000000	0.0000000	0.14020329	0.00000000
Lechevalieria	0.000000	1.00424874	0.00000000	0.000000	0.0000000	0.0000000	0.31545741	0.00000000
Micromonospora	6.060606 2	0.64503669	1.78126113	0.299940	14.1242938	6.8376068	3.43498072	0.07800312
Millisia	0.000000	0.00000000	0.00000000	0.000000	0.0000000	0.0000000	3.04942166	0.00000000
Mycobacterium	3.030303 1	3.80842024	57.49910937	6.118776	9.6045198	12.3076923	22.74798458	22.47789912
Mycolicibacter	0.000000	0.00000000	0.99750623	0.000000	0.2824859	0.0000000	0.00000000	0.00000000
Mycolicibacterium	27.272727	0.03862495	0.10687567	0.299940	2.2598870	0.0000000	0.70101647	7.26729069
Nocardia	0.000000	1.58362302	0.00000000	0.239952	0.0000000	0.0000000	13.24921136	12.63650546
Nocardiopsis	0.000000	0.36693704	0.46312789	16.256749	0.0000000	0.0000000	0.00000000	0.18200728
Nonomuraea	0.000000	5.38818076	0.00000000	0.479904	0.0000000	0.0000000	2.06799860	0.00000000
Plantactinospora	0.000000	0.00000000	0.00000000	0.539892	0.0000000	0.0000000	1.78759201	0.00000000
Pseudonocardia	0.000000	7.30011587	0.00000000	2.039592	0.0000000	0.0000000	4.52155626	0.00000000
Rhodococcus	3.030303	0.05793743	0.28500178	22.615477	1.4124294	0.0000000	6.69470733	42.47269891
Saccharothrix	0.000000	0.38624952	0.00000000	0.000000	0.0000000	0.0000000	5.92358920	0.58502340
Salinispora	0.000000 1	8.79103901	7.58817243	0.000000	25.4237288	0.0000000	2.10304942	0.18200728
Streptomyces	15.151515 2	8.79490151	26.71891699	38.572286	28.2485876	5.9829060	23.13354364	9.20436817
Williamsia	0.000000	0.00000000	0.00000000	0.000000	0.0000000	0.0000000	0.00000000	1.23504940
Mycobacterium	0.000000	0.00000000	0.10687567	0.000000	0.0000000	0.5128205	0.00000000	0.03900156

Table S5 – Relative abundance of AD domain provenience from actinobacterial genus.

	Samples							
	54	**66**	**72**	**87**	**AC3**	**I1**	**TC3**	**TR1**
Actinobacteria								
Other	1.190476	2.6940942	2.49140893	2.34220907	36.1400894	5.5103884	12.86186517	1.74208915
Actinoplanes	0.000000	0.0000000	0.02863688	0.73964497	0.0000000	4.2457091	0.00000000	0.91867982
Actinospica	0.000000	3.0656934	0.00000000	0.00000000	0.0000000	0.0000000	0.00000000	0.00000000
Allosalinactinospora	0.000000	0.0000000	0.00000000	0.00000000	0.0000000	2.0776874	0.00000000	0.00000000
Amycolatopsis	0.000000	0.0000000	0.00000000	0.00000000	0.8196721	0.0000000	0.00000000	0.00000000
Arthrobacter	0.000000	0.0000000	0.00000000	0.00000000	2.5335320	0.0000000	0.00000000	0.00000000
Dactylosporangium	0.000000	0.0000000	0.00000000	2.44082840	0.0000000	0.0000000	0.00000000	0.00000000
Frankia	0.000000	4.0743198	0.00000000	1.28205128	0.0000000	0.0000000	0.05008514	0.00000000
Gordonia	0.000000	0.0000000	0.00000000	4.83234714	0.0000000	0.0000000	1.83311630	4.38924804
Herbidospora	0.000000	0.0000000	0.00000000	3.52564103	0.0000000	0.6323397	0.00000000	0.00000000
Kibdelosporangium	0.000000	2.5348374	0.00000000	0.00000000	0.0000000	0.0000000	0.00000000	1.96665532
Kitasatospora	0.000000	0.0000000	0.00000000	4.19132150	0.0000000	0.0000000	0.00000000	1.21810140
Kribbella	0.000000	0.0000000	0.00000000	0.88757396	0.0000000	0.0000000	0.00000000	0.00000000
Lentzea	34.523810	0.0000000	0.00000000	0.41913215	0.0000000	1.5356820	0.00000000	0.00000000
Micromonospora	0.000000	0.0000000	0.00000000	0.00000000	3.2414307	33.4236676	0.00000000	0.00000000
Murinocardiopsis	0.000000	0.0000000	0.77319588	0.00000000	0.0000000	0.0000000	0.00000000	0.00000000
Mycobacterium	26.190476	10.1393497	0.00000000	58.45660750	0.0000000	0.0000000	5.12871882	0.03402518
Nocardia	0.000000	0.5043132	60.05154639	0.39447732	0.0000000	0.0000000	30.97265351	37.39367132
Nonomuraea	0.000000	0.0000000	0.08591065	1.28205128	1.9001490	1.1743451	0.00000000	0.00000000
Rhodococcus	0.000000	8.1884539	3.89461627	1.62721893	29.6199702	6.7750678	22.54833216	28.09799251
Salinispora	0.000000	0.0000000	0.00000000	0.00000000	0.0000000	0.0000000	1.24211159	0.00000000
Sciscionella	0.000000	0.0000000	0.22909507	0.00000000	0.0000000	0.0000000	0.00000000	0.00000000
Smaragdicoccus	0.000000	0.0000000	2.09049255	0.00000000	0.0000000	0.0000000	0.05008514	23.43654304

Streptacidiphilus	0.000000	0.0000000	0.00000000	0.00000000	0.0000000	0.0000000	0.29049384	0.00000000
Streptomyces	38.095238	68.7989383	30.35509737	15.65581854	25.7451565	44.6251129	25.01252129	0.68730861
Streptosporangium	0.000000	0.0000000	0.00000000	0.32051282	0.0000000	0.0000000	0.00000000	0.00000000
Thermostaphylospora	0.000000	0.0000000	0.00000000	1.57790927	0.0000000	0.0000000	0.00000000	0.00000000
Williamsia	0.000000	0.0000000	0.00000000	0.02465483	0.0000000	0.0000000	0.01001703	0.11568561

Table S6 – Relative abundance of KS domain provenience from cyanobacterial genus.

	Samples							
	54	66	72	87	AC3	I1	TC3	TR1
Cyanobacteria								
Other	0.0000000	1.3024602	1.07863605	0.0000000	1.0455564	2.56678889	0.00000000	0.2751032
Anabaena	0.0000000	2.6049204	0.06958942	0.0000000	0.0000000	0.00000000	0.47892720	0.0000000
Aphanothece	0.0000000	0.0000000	0.00000000	0.0000000	0.0000000	1.10005238	0.00000000	0.0000000
Calothrix	0.0000000	0.0000000	0.55671538	0.0000000	5.0784167	2.09533787	7.18390805	0.1375516
Chroococcopsis	0.0000000	0.0000000	0.00000000	0.0000000	0.0000000	0.00000000	5.65134100	0.0000000
Coleofasciculus	0.0000000	0.0000000	0.34794711	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Crocosphaera	0.5703422	0.1447178	2.08768267	0.0000000	0.0000000	0.00000000	1.43678161	0.0000000
Cyanobium	0.0000000	0.0000000	1.73973556	0.0000000	1.0455564	0.89051860	0.00000000	0.0000000
Cyanosarcina	0.0000000	0.0000000	0.00000000	0.1795332	0.0000000	0.00000000	3.63984674	0.0000000
Desertifilum	0.1901141	0.0000000	0.00000000	0.0000000	0.0000000	0.00000000	2.68199234	0.0000000
Fischerella	0.0000000	0.0000000	0.06958942	0.0000000	0.8215086	2.25248821	0.28735632	0.1375516
Fortiea	0.0000000	0.0000000	0.00000000	0.0000000	0.0000000	0.47145102	7.37547893	0.0000000
Geitlerinema	0.0000000	0.0000000	0.00000000	0.0000000	0.0000000	0.20953379	0.00000000	0.0000000
Gloeothece	0.0000000	0.2894356	0.00000000	0.0000000	0.1493652	0.00000000	0.00000000	0.0000000
Halothece cluster	0.0000000	0.0000000	0.00000000	0.0000000	0.0000000	0.62860136	0.00000000	0.0000000
Hassallia	0.0000000	0.0000000	0.00000000	0.0000000	0.0000000	0.41906757	0.00000000	0.0000000
Hydrococcus	0.0000000	0.0000000	0.00000000	0.3590664	0.0000000	0.10476689	0.00000000	0.0000000
Kamptonema	0.0000000	0.0000000	0.20876827	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Leptolyngbya	0.0000000	0.1447178	7.20250522	10.2333932	0.0000000	2.72393924	0.19157088	0.0000000
Limnoraphis	0.0000000	0.0000000	5.21920668	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Lyngbya	0.0000000	0.0000000	1.14822547	0.0000000	1.2696042	0.00000000	0.00000000	0.0000000
Mastigocoleus	0.0000000	1.4471780	0.00000000	0.0000000	0.0000000	0.00000000	0.19157088	0.0000000
Microcystis	0.0000000	0.8683068	0.00000000	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Moorea	0.0000000	2.7496382	7.82881002	2.8725314	70.0522778	53.79779990	6.70498084	2.7510316
Myxosarcina	0.0000000	0.0000000	0.00000000	0.0000000	0.0000000	0.89051860	0.00000000	0.0000000
Nodularia	0.1901141	1.4471780	8.24634656	0.0000000	0.5974608	0.05238345	0.57471264	4.9518569
Nostoc	30.7984791	47.9015919	59.95128740	13.8240575	13.3681852	16.13410162	26.72413793	39.2022008
Nunduva	0.0000000	1.7366136	0.00000000	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Phormidesmis	0.0000000	0.0000000	0.00000000	0.7181329	0.0000000	0.00000000	0.09578544	0.0000000
Planktothrix	0.0000000	4.9204052	0.00000000	0.7181329	0.2240478	2.30487166	0.00000000	0.0000000
Plectonema	0.0000000	1.4471780	0.06958942	0.0000000	0.0000000	0.00000000	0.00000000	8.9408528
Pleurocapsa	0.0000000	0.5788712	0.00000000	0.0000000	0.0000000	0.26191723	0.19157088	5.0894085
Pseudanabaena	0.0000000	0.0000000	0.10438413	0.0000000	3.4353996	0.00000000	0.00000000	0.0000000
Rivularia	0.0000000	0.0000000	1.28740431	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Scytonema	68.2509506	20.6946454	0.55671538	63.9138241	2.9126214	10.68622315	33.90804598	0.1375516
Stanieria	0.0000000	4.3415340	0.00000000	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Symploca	0.0000000	0.0000000	0.41753653	0.0000000	0.0000000	0.10476689	1.53256705	0.0000000
Tolypothrix	0.0000000	0.0000000	0.00000000	0.7181329	0.0000000	0.00000000	0.38314176	0.0000000

Trichodesmium	0.0000000	0.1447178	0.00000000	0.0000000	0.0000000	0.00000000	0.76628352	0.0000000
Trichormus	0.0000000	6.2228654	1.70494085	6.4631957	0.0000000	2.30487166	0.00000000	38.3768913
Westiellopsis	0.0000000	1.0130246	0.00000000	0.0000000	0.0000000	0.00000000	0.00000000	0.0000000
Moorea	0.0000000	0.0000000	0.10438413	0.0000000	0.0000000	0.00000000	0.00000000	0.00000000

Table S7 – Relative abundance of AD domain provenience from cyanobacterial genus.

	Samples							
	54	66	72	87	AC3	I1	TC3	TR1
Cyanobacteria								
Other	57.094477249	12.30684327	0.4418262	5.48621190	0.5956433	31.60124259 1	1.42032571	0.2022927
Acaryochloris	0.000000000	0.00000000	0.0000000	0.05805515	0.0000000	0.00000000	0.55658627	0.0000000
Anabaena	0.000000000	0.00000000	0.0000000	3.30914369	1.0551396	0.00000000	0.00000000	0.0000000
Aphanothece	0.703369225	0.00000000	0.0000000	0.00000000	0.0000000	0.00000000	0.00000000	0.0000000
Calothrix	0.078152136	5.84988962	0.9327442	1.04499274	3.4547311	6.60830274	0.32982890	0.0000000
Chamaesiphon	0.000000000	0.00000000	3.1909671	0.00000000	0.2212389	29.14430952	0.43290043	1.2137559
Chlorogloeopsis	0.000000000	0.00000000	2.0127639	0.00000000	0.0000000	0.00000000	0.00000000	0.0000000
Coleofasciculus	0.000000000	0.55187638	0.0000000	0.14513788	0.0000000	0.00000000	0.00000000	0.0000000
Crinalium	0.000000000	0.00000000	0.0000000	7.16981132	0.0000000	0.00000000	0.00000000	0.0000000
Crocosphaera	0.000000000	5.24282561	0.0000000	0.00000000	0.0000000	0.00000000	0.00000000	0.0000000
Cyanobacterium	0.000000000	0.00000000	0.0000000	0.00000000	1.1402314	0.02824061	0.00000000	0.2697235
Cyanothece	4.307051059	15.50772627	0.0000000	3.16400581	0.0000000	0.00000000	8.49309421	0.0000000
Cylindrospermum	5.748523793	0.00000000	0.0000000	8.85341074	0.3914227	0.00000000 4	3.94970109	0.0000000
Fischerella	0.000000000	0.00000000	0.0000000	0.08708273	0.0000000	0.00000000	0.00000000	0.2697235
Gloeocapsa	0.017367141	0.00000000	0.0000000	0.02902758	0.0000000	1.49675233	1.03071532	6.2710722
Hassallia	0.000000000	0.00000000	0.0000000	0.00000000	0.3914227	0.00000000	0.00000000	0.0000000
Leptolyngbya	0.000000000	0.00000000	0.4909180	0.00000000	0.0000000	0.00000000	0.37105751	3.7761295
Mastigocoleus	0.008683571	48.67549669	0.0000000	0.00000000	0.0000000	0.00000000	4.76190476	0.0000000
Merismopedia	0.000000000	1.10375276	0.0000000	25.51523948	0.2382573	0.00000000 1	1.42032571	0.0000000
Microcoleus	0.000000000	0.00000000	0.0000000	1.07402032	0.0000000	0.00000000	0.26798598	0.0000000
Microcystis	0.000000000	0.00000000	10.9474718	0.00000000	0.8168822	3.78424174	0.00000000	0.0000000
Moorea	0.069468565	0.05518764	0.1472754	2.00290276	8.1688223	0.76249647	2.28818800	0.0000000
Myxosarcina	0.000000000	0.00000000	0.5891016	0.00000000	0.0000000	0.00000000	0.00000000	0.0000000
Nostoc	14.102118791	3.91832230	23.4658812	37.41654572	14.3635126	21.74526970	7.02947846	4.6527310
Oscillatoria	0.000000000	0.00000000	0.0000000	0.00000000	0.6126617	3.75600113	0.00000000	0.0000000
Phormidium	0.000000000	0.00000000	4.0255277	0.00000000	65.7420014	0.11296244	0.22675737 8	3.3445718
Planktothrix	17.749218479	0.00000000	0.4418262	0.00000000	0.0000000	0.28240610	0.02061431	0.0000000
Pseudanabaena	0.008683571	0.00000000	1.0800196	0.31930334	2.3144997	0.36712793	0.00000000	0.0000000
Scytonema	0.104202848	5.68432671	31.7623957	4.15094340	0.3744044	0.00000000	1.93774479	0.0000000
Stanieria	0.008683571	0.00000000	0.0000000	0.17416546	0.0000000	0.00000000	5.46279118	0.0000000
Synechococcus	0.000000000	1.10375276	0.0000000	0.00000000	0.0000000	0.00000000	0.00000000	0.0000000
Tolypothrix	0.000000000	0.00000000	20.4712813	0.00000000	0.0000000	0.31064671	0.00000000	0.0000000
Trichormus	0.000000000	0.00000000	0.0000000	0.00000000	0.1191287	0.00000000	0.00000000	0.0000000

Table S8 – Relative abundance of KS domain provenience from Firmicutes genera.

	Samples							
	54	**66**	**72**	**87**	**AC3**	**I1**	**TC3**	**TR1**
Firmicutes								
Other	0.000000	1.840491	0.0000000	0.000000	0.000000	0.000000	0.000000	0.000000
Bacillus	0.000000	6.441718	5.3927813	10.294118	4.545455	46.391753	7.118644	2.857143
Brevibacillus	35.057471	8.588957	17.7070064	0.000000	0.000000	0.000000	0.000000	0.000000

Clostridium	0.000000	0.000000	0.0000000	11.029412	0.000000	0.000000	0.000000	0.000000
Enterococcus	1.149425	0.000000	0.3397028	5.514706	15.909091	5.154639	0.000000	2.857143
Lihuaxuella	0.000000	0.000000	0.0000000	0.000000	47.727273	0.000000	0.000000	0.000000
Lysinibacillus	0.000000	0.000000	1.3588110	0.000000	0.000000	0.000000	0.000000	0.000000
Marininema	0.000000	0.000000	0.2972399	0.000000	0.000000	0.000000	0.000000	0.000000
Paenibacillus	63.793103	18.711656	74.9044586	54.044118	31.818182	48.453608	85.649718	94.285714
Ruminiclostridium	0.000000	64.417178	0.0000000	7.352941	0.000000	0.000000	7.231638	0.000000
Sporomusa	0.000000	0.000000	0.0000000	6.250000	0.000000	0.000000	0.000000	0.000000
Thermoflavimicrobium	0.000000	0.000000	0.0000000	5.514706	0.000000	0.000000	0.000000	0.000000

Table S9 – Relative abundance of AD domain provenience from Firmicutes genera.

	Samples							
	54	**66**	**72**	**87**	**AC3**	**I1**	**TC3**	**TR1**
Firmicutes								
	0.000000	3.459821	0.0000000	0.0000000	0.000000	0.61309679	0.0000000	0.0000000
Acetonema	0.000000	0.000000	0.0000000	1.2562814	0.000000	0.00000000	0.0000000	0.0000000
Anaerobacterium	0.000000	0.000000	0.0000000	0.0000000	0.000000	0.00000000	2.0238095	0.4950495
Aneurinibacillus group	5.797511	0.000000	0.9018759	0.0000000	15.961801	47.15627446	0.0000000	2.4752475
Bacillus	4.609729	19.084821	55.5194805	15.0753769	21.521146	45.38220715	2.9761905	7.5907591
Brevibacillus	3.563348	39.174107	26.4550265	26.3819095	2.216917	0.07826768	36.5476190	0.0000000
Desmospora	0.000000	0.000000	0.0962001	0.0000000	0.000000	0.02608923	0.0000000	0.1650165
Desulfocucumis	0.000000	27.790179	0.0000000	0.0000000	0.000000	0.00000000	0.0000000	0.0000000
Dorea	0.000000	0.000000	0.0000000	0.0000000	0.000000	0.00000000	0.0000000	11.0561056
Fontibacillus	0.000000	0.000000	0.0000000	0.0000000	0.000000	0.00000000	1.7857143	0.0000000
Hungateiclostridium	0.000000	2.120536	0.0000000	0.0000000	0.000000	0.00000000	0.0000000	0.0000000
Lihuaxuella	0.000000	0.000000	0.0000000	0.5025126	0.000000	0.00000000	0.0000000	0.0000000
Oceanobacillus	0.000000	0.000000	0.0000000	0.0000000	0.000000	0.00000000	2.0238095	0.0000000
Paenibacillus	2.743213	4.910714	2.5012025	12.8140704	16.200546	2.16540569	24.4047619	70.2970297
Paludifilum	0.000000	0.000000	0.1202501	0.0000000	0.000000	0.00000000	0.0000000	0.0000000
Ruminiclostridium	0.000000	0.000000	0.0000000	2.0100503	0.000000	0.00000000	0.2380952	0.0000000
Seinonella	0.000000	0.000000	0.0000000	6.1557789	0.000000	0.00000000	0.0000000	0.0000000
Syntrophomonas	0.000000	0.000000	0.0000000	0.0000000	0.000000	0.80876598	0.0000000	0.0000000
Thermoactinomyces	0.000000	0.000000	0.0000000	0.0000000	0.000000	1.39577355	0.0000000	0.8250825
Thermoflavimicrobium	0.000000	0.000000	0.0000000	0.0000000	1.057299	0.00000000	0.0000000	0.0000000
Tumebacillus	83.286199	3.459821	14.4059644	35.8040201	43.042292	2.37411949	30.0000000	7.0957096

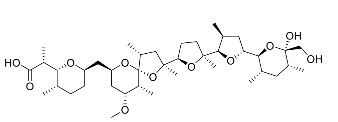
Table S10 – Relative abundance of KS domain provenience from Verrucomicrobia genera.

	Samples							
	54	**66**	**72**	**87**	**AC3**	**I1**	**TC3**	**TR1**
Verrucomicrobia								
	83.3333333	90.5252317	30.59777	51.7094017	75.59809	41.76072	93.01629531	99.137931
Chthoniobacter	15.8730159	8.1359423	28.47011	47.6495726	24.40191	45.82393	5.75324243	0.862069
Opitutus	0.7936508	0.2059732	0.00000	0.0000000	0.00000	0.00000	0.43232458	0.000000
Pedosphaera	0.0000000	1.1328527	0.00000	0.0000000	0.00000	0.00000	0.00000000	0.000000
Roseimicrobium	0.0000000	0.0000000	0.00000	0.2136752	0.00000	0.00000	0.76488194	0.000000
Verrucomicrobium	0.0000000	0.0000000	40.93212	0.4273504	0.00000	12.41535	0.03325574	0.000000

Table S11 – Distribution of KS OTUs with higher identity (above 80%) to the MiBIG database.

OTU_ID	BGC_acession	main_product	Identity	Query cover	evalue	Bioactivity
Uniq540	BGC0000148	spinosad	90.000	99	1.70e-33	Insecticide[2]
Uniq1276	BGC0001597	fluvirucin b2	89.474	99	1.03e-26	Antifungal and antiviral [3]
Uniq1728	BGC0001700	niphimycins C-E	88.750	99	4.96e-41	Antibiotic [4]
Uniq155	BGC0000021	apoptolidin	88.710	86	3.06e-29	Cytotoxic [5]
Uniq623	BGC0000021	apoptolidin	88.710	80	2.20e-29	Cytotoxic [5]
Uniq4837	BGC0000994	FK520	87.931	87	5.50e-27	Immunosupressant [6]
Uniq477	BGC0001199	akaeolide	87.719	98	4.73e-25	Antibiotic [7]
Uniq4169	BGC0001619	ibomycin	87.719	93	1.61e-25	Antifungal [8]
Uniq3055	BGC0000105	nanchangmycin	87.500	99	4.16e-39	Antibiotic [9]
Uniq44	BGC0000105	nanchangmycin	87.500	99	4.10e-40	Antibiotic [9]
Uniq1866	BGC0000954	ajudazol	86.842	84	1.28e-37	Antifungal [10]
Uniq3083	BGC0001013	meridamycin	86.420	89	1.77e-39	Nonimmunosuppressive [11]
Uniq3683	BGC0000954	ajudazol	86.207	99	1.16e-46	Antifungal [10]
Uniq29	BGC0001597	fluvirucin b2	85.965	99	8.80e-26	Antifungal and antiviral [3]
Uniq66	BGC0000086	lasalocid	85.965	83	4.27e-26	Antibiotic [12]
Uniq2030	BGC0001204	versipelostatin	85.915	93	8.55e-28	Antitumor [13]
Uniq2920	BGC0000002	aculeximycin	85.714	76	3.03e-23	Antibiotic [14]
Uniq4051	BGC0000105	nanchangmycin	85.714	100	6.83e-41	Antibiotic [9]
Uniq62	BGC0001470	macrobrevin	85.366	99	1.10e-42	Antibiotic [15]
Uniq940	BGC0000075	hygrocin	85.246	99	1.30e-25	Antitumor [16]
Uniq368	BGC0001200	lorneic acid A	85.000	99	1.04e-39	PDE5 inhibition activity[17] [17]
Uniq5011	BGC0000050	E-837	84.932	92	4.88e-34	electron transport inhibitor [18]
Uniq4143	BGC0001559	crocagin A / crocagin B	84.810	95	1.08e-37	[19]
Uniq2579	BGC0001165	curacin	84.615	79	6.44e-37	Antimitotic, Antiproliferative, and Brine Shrimp Toxic [20]
Uniq2154	BGC0000086	lasalocid[21]	84.615	93	5.10e-37	Antibiotic [21]
Uniq3137	BGC0000179	etnangien	84.483	99	4.46e-27	Antibiotic [22]
Uniq852	BGC0001200	lorneic acid A	84.127	81	2.29e-27	PDE5 inhibition activity (Zhou et al. 2015)
Uniq3161	BGC0001700	niphimycins C-E	83.871	99	5.74e-43	Antibiotic [4]
Uniq4274	BGC0000114	nigericin	83.750	58	2.52e-37	Antibiotic [23]
Uniq810	BGC0001559	crocagin A / crocagin B	83.750	98	2.18e-39	[19]
Uniq2814	BGC0001338	citrinin	83.750	99	3.00e-40	Micotoxin [24]
Uniq324	BGC0001338	citrinin	83.750	99	3.00e-40	Micotoxin [24]
Uniq2046	BGC0000122	[25] A	83.750	99	2.49e-38	multidrug resistance reversal agent [25]
Uniq5107	BGC0000122	phenylnannolone A	83.750	99	1.19e-39	multidrug resistance reversal agent [25]
Uniq503	BGC0001287	chaxamycin A-D	83.750	78	3.27e-37	Antibiotic [26]
Uniq753	BGC0000042	cremimycin	83.750	84	5.21e-38	Antibiotic [27]
Uniq2553	BGC0001066	kendomycin	83.750	99	6.41e-36	Antibiotic [28]
Uniq4297	BGC0001165	curacin	83.636	84	9.57e-26	Antimitotic, Antiproliferative, and Brine Shrimp Toxic [20]
Uniq3486	BGC0001619	ibomycin	83.544	94	1.30e-36	Antifungal [8]
Uniq1208	BGC0000172	basiliskamides	82.927	99	9.31e-42	Antifungal and antibiotic [29]
Uniq1207	BGC0001099	kalimantacin / batumin	82.716	99	5.35e-43	Antibiotic [30]
Uniq1559	BGC0001357	carbamidocyclophane A-U	82.667	96	4.33e-36	Cytotoxic and antibiotic [31]
Uniq265	BGC0001200	lorneic acid A	82.540	81	6.21e-27	PDE5 inhibition activity [4]
Uniq4801	BGC0001520	aurantinins B-D	82.500	99	5.17e-40	Antibiotic [32]
Uniq4002	BGC0001125	puwainaphycins	82.500	97	1.01e-38	Cytotoxic [33]
Uniq1922	BGC0000122	phenylnannolone A	82.500	99	3.94e-37	multidrug resistance reversal agent [25]
Uniq1733	BGC0001357	carbamidocyclophane A-U	82.500	99	2.82e-39	Cytotoxic and antibiotic [31]
Uniq2850	BGC0001357	Carbamidocyclophane A-U	82.500	99	1.82e-39	Cytotoxic and antibiotic [31]
Uniq4564	BGC0001287	chaxamycin A-D	82.500	78	4.05e-37	Antibiotic [26]
Uniq655	BGC0001199	akaeolide	82.500	85	2.52e-37	Antibiotic [7]

Uniq4940	BGC0001349	heronamide	82.500	99	6.20e-41	n.d. [34]
Uniq149	BGC0001034	pellasoren	82.456	83	1.54e-25	Cytotoxic [35]
Uniq879	BGC0000111	neocarzilin	82.456	83	1.40e-25	Cytotoxic [36]
Uniq3503	BGC0000184	sorangicin	82.051	98	5.01e-39	Antibiotic [37]
Uniq924	BGC0001099	kalimantacin / batumin	81.944	98	6.32e-49	Antibiotic [30]
Uniq3379	BGC0000163	tetronasin	81.944	94	2.93e-33	Antibiotic [38]
Uniq4882	BGC0000183	paenimacrolidin	81.707	99	7.12e-44	Antibiotic [39]
Uniq1630	BGC0001559	crocagin A / crocagin B	81.667	99	2.74e-26	[19]
Uniq4087	BGC0001034	pellasoren	81.667	83	1.01e-26	Cytotoxic [35]
Uniq1978	BGC0000954	ajudazol	81.481	99	1.46e-28	Antifungal [10]
Uniq4903	BGC0001770	sceliphrolactam	81.481	84	2.38e-38	Antifungal [40]
Uniq3461	BGC0001066	kendomycin	81.481	92	3.48e-27	Antibiotic [28]
Uniq1662	BGC0001737	phenalamide	81.333	96	1.43e-33	HIV-1 inhibitor [41]
Uniq1810	BGC0001470	macrobrevin	81.250	99	5.80e-41	Antibiotic [15]
Uniq2659	BGC0000954	ajudazol	81.250	100	1.41e-35	Antifungal [10]
Uniq46	BGC0000954	ajudazol	81.250	87	1.38e-35	Antifungal [10]
Uniq922	BGC0001559	crocagin A / crocagin B	81.250	99	2.53e-36	[19]
Uniq1066	BGC0001125	puwainaphycins	81.250	97	3.81e-38	Cytotoxic [33]
Uniq3016	BGC0001125	puwainaphycins	81.250	99	8.98e-37	Cytotoxic [33]
Uniq1724	BGC0001024	myxothiazol	81.250	98	7.30e-38	Antibiotic [42]
Uniq3169	BGC0000954	ajudazol	81.034	100	1.89e-21	Antifungal [10]
Uniq120	BGC0001298	4-Z-annimycin	81.013	74	7.79e-36	Inhibition of sporulation in certain Actinobacteria [43]
Uniq1325	BGC0001165	curacin	80.723	99	9.43e-40	Antimitotic, Antiproliferative, and Brine Shrimp Toxic [20]
Uniq1850	BGC0000027	azaphilone	80.556	94	1.94e-37	antimicrobial, antiviral, cytotoxic, anticancer, and anti-inflammatory [44]
Uniq135	BGC0001470	macrobrevin	80.488	99	9.97e-39	Antibiotic [15]
Uniq757	BGC0000954	ajudazol	80.488	75	1.58e-35	Antifungal [10]
Uniq834	BGC0001491	67-121C	80.488	99	3.01e-35	Antifungal [45]
Uniq524	BGC0001099	kalimantacin / batumin	80.488	99	1.98e-37	Antibiotic [30]
Uniq771	BGC0000153	stigmatellin	80.488	99	6.57e-36	Antibiotic [46]
Uniq2192	BGC0001663	merocyclophane C / merocyclophane D	80.357	99	5.52e-26	Cytotoxic [47]
Uniq3359	BGC0000183	paenimacrolidin	80.247	99	1.11e-42	Antibiotic [39]
Uniq367	BGC0000183	paenimacrolidin	80.247	99	3.77e-41	Antibiotic [39]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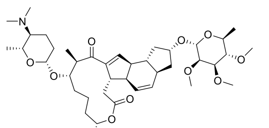
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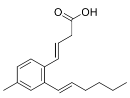
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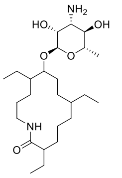
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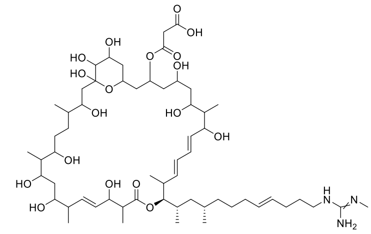
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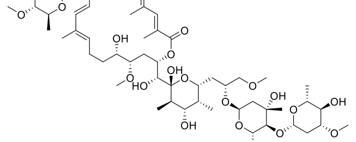
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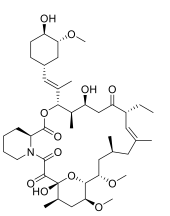
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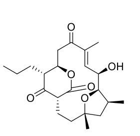
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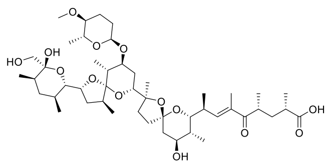
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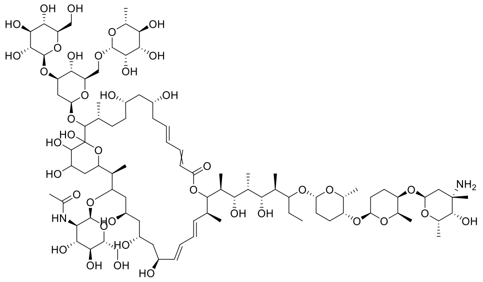
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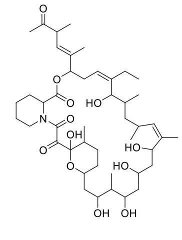
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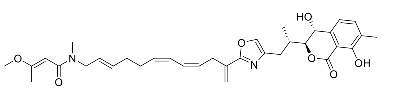
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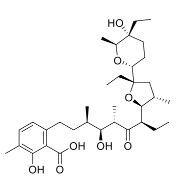
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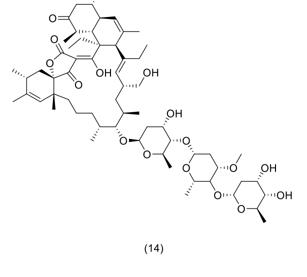
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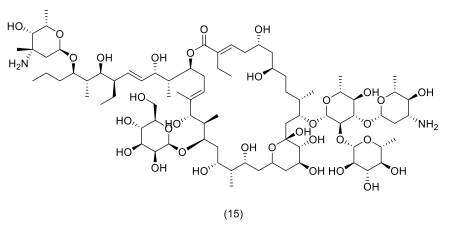
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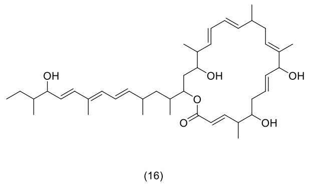
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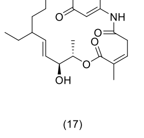
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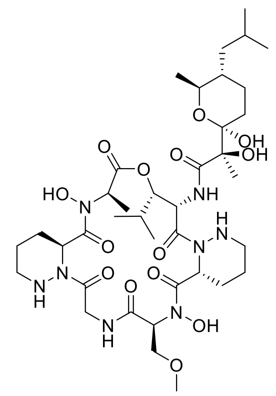
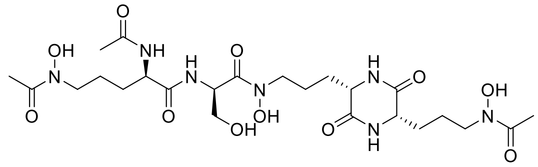
Figure S4 –For KS domain, 24 OTU sequences were associated with over 85% of identity to BGCs involved in the production of 17 different compounds in MiBiG database. Their chemical structures, presented here, were retrieved using ChemDraw v19.0.1.28. (1) – nigericin, (2) – spinosad, (3) – lorneic acid A, (4) – fluviricin b2, (5) – niphymicin, (6) – apoptolidin, (7) – FK520, (8) – akaeolide, (9) – ibomycin, (10) – nanchangmycin, (11) – ajudazol A, (12) – meridamycin, (13) – lasalocid, (14) – versipelostatin, (15) – aculeximycin, (16) – macrobrevin, (17) - hygrocin A.

Table S12 – Distribution of AD OTUs with higher identity (above 80%) to the MiBIG database.

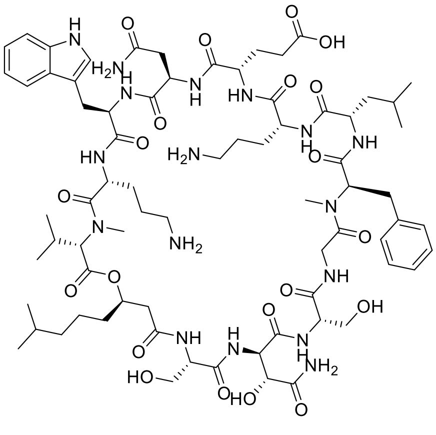
OTU_ID	**BGC_acc.**	**main_product**	**Identity %**	**query cover (%)**	**E-value**	**Bioactivity**
Uniq443	BGC0001519	aurantimycin	95.833	97	1.08e-24	Antibiotic and cytotoxic [48]
Uniq1538	BGC0000349	erythrochelin	87.931	91	1.31e-29	Siderophore [49]
Uniq3185	BGC0000349	erythrochelin	87.500	91	5.96e-44	Siderophore [49]
Uniq6572	BGC0000461	WAP-8294A$_2$ (lotilibcin)	87.273	97	9.70e-26	Antibiotic [50]
Uniq7256	BGC0000413	pyoverdine	86.207	99	7.69e-26	Siderophore [51]
Uniq482	BGC0001036	polyoxypeptin	84.810	99	8.39e-37	Apoptotic[52]
Uniq7256	BGC0000413	pyoverdine	84.810	99	5.18e-42	Siderophore [51]
Uniq315	BGC0001312	viscosin	82.759	95	1.92e-20	Biosurfactant, antibiotic and antiviral [53]
Uniq1441	BGC0000331	cyanopeptin	82.759	99	5.75e-32	Protease inhibitor[54]
Uniq3128	BGC0000331	cyanopeptin	82.759	99	1.84e-31	Protease inhibitor[54]
Uniq3997	BGC0000413	pyoverdine	82.759	99	2.48e-28	Siderophore [51]
Uniq577	BGC0001328	rakicidin A / rakicidin B	82.456	99	1.13e-22	Cytotoxic [55]
Uniq772	BGC0001657	lysocin	81.481	97	1.89e-25	Antibiotic [56]
Uniq6572	BGC0000461	WAP-8294A2 (lotilibcin)	81.132	97	9.40e-21	Antibiotic [50]
Uniq1939	BGC0001125	puwainaphycins	81.034	99	2.36e-29	Cytotoxic [33]
Uniq3781	BGC0001028	nostopeptolide	81.034	99	1.26e-28	Unknown
Uniq6075	BGC0000397	nostocyclopeptide	81.034	99	1.57e-28	Antitoxin [57]
Uniq7312	BGC0001608	glidopeptin	80.769	97	1.39e-38	Weak antibiotic and cytotoxic [58]
Uniq31	BGC0001657	lysocin	80.702	99	1.44e-25	Antibiotic [56]



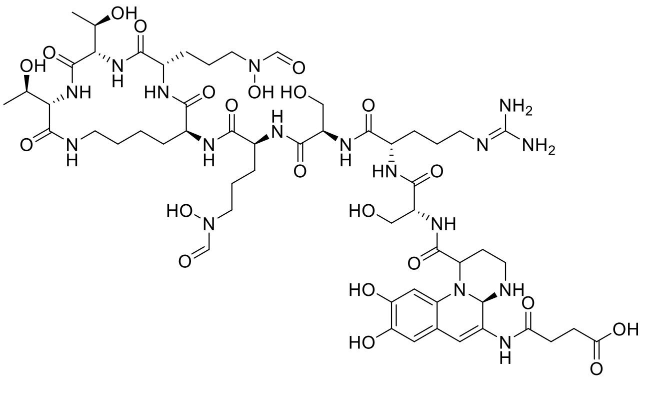
(1)



(2)



(3)



(4)

Figure S5 - For AD domain, 5 OTU sequences were associated with over 85% of identity to BGCs involved in the production of 4 different compounds. Their chemical structures, presented here, were retrieved using ChemDraw v19.0.1.28. (1) – aurantamycin A, (2) – erythrochelin, (3) - P-8294A2 (lotilibcin), (4) – pyoverdine.

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