



Supplementary Materials

Table S1. Origin data of Antarctic bacterial strains included in this study.

Strain ID*	Sampling Location	Sampling Date	Strain in Coculture
So1b	Fildes Bay (a)	2013/2014	So13.3
So13.3	Fildes Bay (a)	2013/2014	So1b
So64.6b	Ardley Island (ASPAs 150)	2013/2014	So32D
So5b	Collins Glacier beach area (ASPAs 125)	2013/2014	So27D
Se14.01b	Armonía point (b) (ASPAs 133)	2013/2014	Se41.02b
Se5.02b	Hannah point, Livingston Island (c) (ASPAs 126)	2013/2014	Se5.01b
Se18.01b	Fildes Bay (a)	2013/2014	Se63.02b
Se28.01b	Dee-Greenwich Island (a)	2013/2014	Se32.01b
Se32.01b	Dee-Greenwich Island (a)	2013/2014	Se28.01b
Se41.02b	Armonía point (ASPAs 133)	2013/2014	Se14.01b
Wa41.01b	Armonía point (ASPAs 133)	2013/2014	Dwa41.01b
So64.3b	Ardley Island (ASPAs 150)	2013/2014	So64.6b
So27D	Collins Glacier beach area (ASPAs 125)	2013/2014	So5b
So10b	Collins Glacier beach area (ASPAs 125)	2013/2014	So2b
So2b	Collins Glacier beach area (ASPAs 125)	2013/2014	So10b
So9b	Collins Glacier beach area (ASPAs 125)	2013/2014	So6b
Dwa41.01b	Fildes Bay (a)	2013/2014	Wa41.01
Se4.02b	Hannah point, Livingston Island (ASPAs 126)	2013/2014	Se5.02b
So11b	Collins Glacier beach area (ASPAs 125)	2013/2014	SoD9b
Se63.02b	Fildes Bay (a)	2013/2014	Se18.01
So1d	Collins Glacier beach area (ASPAs 125)	2013/2014	So5b
So13b	Fildes Bay (a)	2016	So02b
So3.2b	Robert Island (ASPAs 112)	2016	Se32.02b
Se32.02b	Robert Island (ASPAs 112)	2013/2014	So3.2b
Se5.01b	Hannah point, Livingston Island (ASPAs 126)	2013/2014	Se5.02b
So6b	Collins Glacier beach area (ASPAs 125)	2013/2014	So9b
SoD9b	Collins Glacier beach area (ASPAs 125)	2013/2014	So11b
So02b	Fildes Bay (a)	2016	So13b
Se16.2.2	Collins Glacier beach area (ASPAs 125)	2016	Se16.2.3
Se16.2.3	Collins Glacier beach area (ASPAs 125)	2016	Se16.2.2
Se16.2.5	Collins Glacier beach area (ASPAs 125)	2016	Se16.2.3
So16.8	Armonía point (ASPAs 133)	2016	So16.17
So16.17	Armonía point (ASPAs 133)	2016	So16.8
So16.14.3	Robert Island (ASPAs 112)	2016	So16.14.1

*Name codes *So*: soil, *Se*: sediment, *Wa*: water, *Dwa*: 10 m deep water, *ASPAs*: Antarctic Specially Protected Area number. (a) Area with human presence. (b) Lake sediment 0.3 m deep. (c) Marine sediment 0.3 m deep.

Table S2. Composition of culture media used in this study.

Media ID	Composition Per Liter
M1	Peptone (2.0 g)
	Yeast extract (4.0 g)
	Starch (1 0.0 g)
ISP2	Yeast extract (4.0 g)
	Malt extract (10.0 g)
	Glucose (4.0 g)
M2	Mannitol (40.0 g)
	Maltose (40.0 g)
	Yeast extract (10.0 g)
	K ₂ HPO ₄ (2.0 g)
	MgSO ₄ ·7H ₂ O (0.5 g)
	FeSO ₄ ·7H ₂ O (0.01 g)
SCA	Starch (10.0 g)
	Casein (0.3 g)
	KNO ₃ (2.0 g)
	NaCl (2.0 g)
	K ₂ HPO ₄ (2.0 g)
	MgSO ₄ ·7H ₂ O (0.05 g)
	CaCO ₃ (0.02 g)

	FeSO ₄ ·7H ₂ O (0.01 g)
IMA	Yeast extract (4g)
	Malt extract (10g)
	Glucose (4g)
	Mannitol (40g)
SDB	Peptidic digest of animal tissue (5.0 g), Casein pancreatin digest (5.0 g), Dextrose (40.0 g)
	Glycerol (30g)
CCA	Peptone (2g)
	K ₂ HPO ₄ (1g)
	NaCl (1g)
	MgSO ₄ ·7H ₂ O (0.5g)
	Trace solution * (5mL)
	*Trace solution
	CaCl ₂ ·2H ₂ O (3g)
	MnSO ₄ (0.2g)
	ZnCl ₂ (0.1g)
	CuSO ₄ ·5H ₂ O (0.025g)
	Na ₂ B ₄ O ₇ ·10H ₂ O (0.02g)
	CoCl ₂ (0.004g)
	(NH ₄) ₆ Mo ₇ O ₂₄ ·4H ₂ O (0.01g)
YEME	Yeast extract (3g)
	Peptone (5g)
	Malt extract (3g)
	Glucose (10g)
	Sucrose (170g)
GYA	Yeast extract (4g)
	Malt extract (10g)
	Glucose (4g)
	CaCO ₃ (2g)
	Starch (20g)
YES	Sucrose (150 g)
	Yeast extract (20 g)
	MgSO ₄ ·7H ₂ O (0.5 g)
	ZnSO ₄ ·7H ₂ O (0.01 g)
	CuSO ₄ ·5H ₂ O (0.005 g)
ISP4	Starch (10.0 g)
	CaCO ₃ (2.0 g)
	(NH ₄) ₂ SO ₄ (2.0 g)
	K ₂ HPO ₄ (1.0 g)
	MgSO ₄ ·7H ₂ O (1.0 g)
	NaCl (1.0 g)
	FeSO ₄ ·7H ₂ O (1 mg)
	MnCl ₂ ·7H ₂ O (1.0 mg)
	ZnSO ₄ ·7H ₂ O (1.0 mg)
ES	100g of Antarctic soil (1 hour agitation prior filtering)
R2YE	[1]

- [1] Ghimire, G. P.; Koirala, N.; Sohng, J. K. Activation of cryptic hop genes from *Streptomyces peucetius* ATCC 27952 involved in hopanoid biosynthesis. *J. Microbiol. Biotechnol.* **2015**, doi:10.4014/jmb.1408.08058.

Table S3. Biosynthetic gene clusters (BGCs) identified on the genomes of selected Antarctic bacteria strains as potential source of novel antimicrobial compounds.

Dwa41.01b					
Region	Type	From	To	Most similar known cluster	Similarity
Region 1	ladderane,fatty_acid	75,852	118,134	pseudomonas quinolone signal	27%
Region 2	saccharide	271,126	294,546		
Region 3	saccharide	364,464	380,12		
Region 4	saccharide	1,126,731	1,151,389		
Region 5	saccharide	1,404,293	1,426,859		
Region 6	halogenated	1,466,276	1,491,000	WAP-8294A2	30%
Region 7	saccharide	1,500,477	1,535,607		
Region 8	saccharide	1,545,784	1,566,616		
Region 9	saccharide	1,706,299	1,752,277	exopolysaccharide	20%
Region 10	saccharide	2,181,871	2,200,672		
Region 11	saccharide	2,498,222	2,537,719		
Region 12	terpene	2,585,329	2,604,912		
Region 13	acyl_amino_acids	2,666,701	2,726,921		
Region 14	arylpolyyene	3,204,781	3,248,883	APE Vf	35%
Region 15	hserlactone	3,275,936	3,296,523		
Region 16	fatty_acid	3,375,525	3,398,099		
Region 17	saccharide	3,584,363	3,622,907	K53 capsular polysaccharide	15%
Region 18	saccharide	3,827,884	3,872,531		
Region 19	saccharide	4,186,168	4,207,395	lipopolysaccharide	5%
Region 20	terpene	4,301,655	4,325,256	carotenoid	100%
Region 21	saccharide	4,346,330	4,403,382		
Region 22	saccharide	4,479,885	4,530,756	lipopolysaccharide	14%
Region 23	saccharide	4,615,542	4,639,123	O-antigen	14%
Region 24	saccharide	4,812,304	4,836,129	lipopolysaccharide	5%
Region 25	saccharide	4,840,049	4,860,600		
Region 26	acyl_amino_acids,sacc	5,179,912	5,267,121	K53 capsular polysaccharide	10%
Region 27	fatty_acid	5,268,349	5,289,470	polyhydroxyalkanoate	50%
So1b					
Region	Type	From	To	Most similar known cluster	Similarity
Region 1	saccharide,T3PKS	333,107	430,53	dipeptide aldehydes	11%
Region 2	saccharide,terpene	435,276	473,443		
Region 3	NRPS,betalactone	536,424	618,887	fengycin	100%
Region 4	saccharide	665,202	685,619		
Region 5	transAT-PKS-	742,139	842,379	bacillaene	Similarity
Region 6	saccharide	1,006,994	1,027,472		
Region 7	saccharide	1,334,496	1,356,064		
Region 8	fatty_acid	1,385,610	1,406,452	chejuenolide A / chejuenolide B	11%
Region 9	terpene	1,433,936	1,454,715		
Region 10	saccharide	1,468,497	1,485,149	zwittermicin A	18%
Region 11	fatty_acid	1,501,606	1,522,487		
Region 12	halogenated	1,705,352	1,725,585		
Region 13	saccharide	1,785,201	1,807,273		
Region 14	NRPS	2,137,424	2,201,286	surfactin	78%
Region 15	saccharide	2,219,940	2,262,274		
Region 16	lanthipeptide	2,332,643	2,357,099	subtilomycin	100%
Region 17	saccharide	2,485,752	2,506,785		
Region 18	saccharide	2,758,084	2,778,117	bacillomycin D	20%
Region 19	saccharide	2,806,497	2,826,120		
Region 20	saccharide,other	2,852,963	2,910,931	bacilysin	100%
Region 21	sactipeptide,head_to_t	2,917,688	2,939,298	subtilosin A	100%
Region 22	saccharide	3,072,095	3,126,189	teichuronic acid	100%
Region 23	saccharide	3,194,906	3,256,035	K53 capsular polysaccharide	15%
Region 24	saccharide	3,277,735	3,303,013		
Region 25	NRPS	3,458,208	3,507,248	bacillibactin	100%
Region 26	saccharide	3,532,514	3,563,347		
Region 27	saccharide	3,587,706	3,621,555	scytophycin	11%
Region 28	saccharide	3,666,012	3,716,386		

Region 29	saccharide	3,915,985	3,956,517		
Se16.2.3					
Region	Type	From	To	Most similar known cluster	Similarity
Region 1	saccharide	61,393	85,833	O-antigen	9%
Region 2	saccharide	258,489	282,201	lipopolysaccharide	5%
Region 3	saccharide	284,796	306,672	pyoverdin	1%
Region 4	acyl_amino_acids,	626,909	711,754	K53 capsular polysaccharide	10%
Region 5	fatty_acid	716,652	734,902	polyhydroxyalkanoate	50%
Region 6	fatty_acid	882,123	909,289	pseudomonas quinolone signal	27%
Region 7	saccharide	1,066,648	1,089,120		
Region 8	saccharide	1,159,045	1,174,700		
Region 9	saccharide	1,922,274	1,946,138		
Region 10	halogenated	2,261,080	2,285,942	WAP-8294A2	30%
Region 11	saccharide	2,501,139	2,547,133	exopolysaccharide	20%
Region 12	saccharide	2,674,663	2,695,176		
Region 13	saccharide	2,973,950	2,996,371		
Region 14	saccharide	3,293,374	3,332,872		
Region 15	terpene	3,380,530	3,400,071		
Region 16	acyl_amino_acids	3,461,782	3,522,558		
Region 17	arylpolyyene	4,000,001	4,043,292	APE Vf	40%
Region 18	hserlactone	4,071,169	4,091,756		
Region 19	fatty_acid	4,170,318	4,194,832		
Region 20	saccharide	4,379,674	4,419,034	K53 capsular polysaccharide	15%
Region 21	saccharide	4,623,223	4,667,880		
Region 22	saccharide	4,981,635	5,002,858	lipopolysaccharide	5%
Region 23	terpene	5,097,337	5,120,843	carotenoid	83%
Region 24	saccharide	5,142,147	5,198,880		
Region 25	saccharide	5,274,999	5,326,287	lipopolysaccharide	17%
SoD9b					
Region	Type	From	To	Most similar known cluster	Similarity
Region 1	fatty_acid,saccharide	202,78	235,29	eicoseicosapentaenoic acid	15%
Region 2	fatty_acid	525,312	546,261		
Region 3	saccharide	569,733	626,198	lipopolysaccharide	54%
Region 4	saccharide	661,028	703,576		
Region 5	saccharide	727,413	749,236		
Region 6	fatty_acid	1,011,227	1,036,777		
Region 7	saccharide	1,138,471	1,168,349		
Region 8	bacteriocin	1,190,247	1,198,754		
Region 9	bacteriocin	1,497,254	1,508,128		
Region 10	saccharide	1,876,199	1,898,314	O-antigen	14%
Region 11	halogenated	2,292,133	2,311,229		
Region 12	saccharide	2,459,986	2,490,582	pseudopyronine A /	18%
Region 13	NRPS	2,503,908	2,550,336	streptobactin	23%
Region 14	saccharide	3,644,796	3,664,219		
Region 15	saccharide	3,853,356	3,881,455		
Region 16	saccharide	3,885,147	3,905,260		
Region 17	arylpolyyene,halogenat	4,222,695	4,266,297	APE Vf	35%
Region 18	saccharide	4,286,303	4,308,080		
So63.02b					
Region	Type	From	To	Most similar known cluster	Similarity
Region 1	saccharide	521,771	553,102		
Region 2	saccharide	644,353	690,098	kosinostatin	3%
Region 3	saccharide	1,026,342	1,063,007		
Region 4	saccharide	1,114,870	1,154,348		
Region 5	saccharide	1,488,720	1,563,242	phosphonoglycans	9%
Region 6	saccharide	1,926,695	1,951,760		
Region 7	fatty_acid	2,209,409	2,232,061		
Region 8	saccharide,betalactone	2,448,883	2,512,420	microansamycin	7%
Region 9	saccharide	2,527,091	2,550,083		
Region 10	saccharide	2,699,537	2,732,407		
Region 11	terpene	2,914,074	2,934,982	carotenoid	28%
Region 12	saccharide	3,222,694	3,245,310		

Region 13	saccharide	3,426,715	3,445,479		
Region 14	saccharide	3,473,784	3,494,764		
So64.6b					
Region	Type	From	To	Most similar known cluster	Similarity
Region 1	saccharide	402,957	428,867		
Region 2	saccharide	666,331	689,678		
Region 3	saccharide	717,381	736,371		
Region 4	saccharide	833,072	877,204	glycopeptidolipid	5%
Region 5	saccharide	883,546	910,762		
Region 6	saccharide	983,304	1,024,979	nogabecin	8%
Region 7	lassopeptide,hserlacto	1,448,221	1,470,598		
Region 8	fatty_acid	1,532,944	1,561,119		
Region 9	saccharide	1,842,988	1,871,436		
Region 10	saccharide	2,255,557	2,285,856	O&K-antigen	4%
Region 11	halogenated	2,349,570	2,368,140		
Region 12	saccharide	2,549,397	2,570,096	lipopolysaccharide	5%
Region 13	saccharide	2,722,855	2,745,868	gellan polysaccharide	7%
Region 14	saccharide,lassopeptid	3,440,244	3,499,720		
Region 15	T3PKS	3,889,391	3,930,452		
Region 16	terpene	4,072,179	4,096,869	carotenoid	30%
Region 17	fatty_acid	4,115,483	4,136,445		
Region 18	saccharide	4,154,895	4,177,593		
Region 19	halogenated	4,231,676	4,252,788		
Region 20	saccharide	4,417,107	4,453,510		
So13.3					
Region	Type	From	To	Most similar known cluster	Similarity
Region 1	lanthipeptide	68,939	91,332	SapB	100%
Region 2	fatty_acid	181,707	201,626	actinomycin D	10%
Region 3	T3PKS	366,627	406,159	A-47934	23%
Region 4	NRPS,other	460,304	527,487	actinomycin D	89%
Region 5	CDPS,T3PKS	913,307	960,433	alkylresorcinol	100%
Region 6	lassopeptide	1,067,644	1,090,272	clavulanic acid	8%
Region 7	NRPS	1,403,665	1,453,533	deimino-antipain	66%
Region 8	terpene	1,517,889	1,534,894	ebelactone	5%
Region 9	fatty_acid,T2PKS,NRP	1,561,713	1,657,640	spore pigment	83%
Region 10	saccharide,terpene	1,799,022	1,834,067	pristinol	100%
Region 11	NRPS-	1,855,463	1,902,275	marineosin A / marineosin B	86%
Region 12	saccharide	2,110,127	2,134,781		
Region 13	saccharide	2,279,201	2,299,855	daptomycin	10%
Region 14	saccharide	2,382,299	2,405,253	steffimycin D	5%
Region 15	ectoine,saccharide	2,924,964	2,969,079	ectoine	100%
Region 16	saccharide	3,110,074	3,133,370		
Region 17	saccharide	3,256,328	3,306,690	acarviostatin I03 / acarviostatin	29%
Region 18	saccharide	3,318,888	3,351,341	glycopeptidolipid	5%
Region 19	fatty_acid	3,574,310	3,595,405		
Region 20	siderophore	3,643,627	3,657,431		
Region 21	saccharide	3,753,455	3,778,710		
Region 22	saccharide	4,115,700	4,140,963		
Region 23	saccharide	4,296,616	4,316,343		
Region 24	saccharide	4,469,278	4,496,601	cathomycin	20%
Region 25	saccharide	4,690,571	4,715,758	neocarzinostatin	6%
Region 26	saccharide	4,917,327	4,950,799		
Region 27	melanin,saccharide	5,141,629	5,170,222	melanin	100%
Region 28	halogenated	5,542,357	5,562,337		
Region 29	saccharide	5,618,194	5,657,873	TP-1161	41%
Region 30	saccharide	5,886,722	5,928,571	napyradiomycin A80915C	9%
Region 31	saccharide	6,092,627	6,116,746		
Region 32	T1PKS,fatty_acid,NRP	6,242,873	6,377,035	macrotermycins	46%
Region 33	saccharide	6,508,813	6,527,699		
Region 34	saccharide,other,halog	6,531,244	6,581,567	A-503083 A / A-503083 B / A-	3%
Region 35	siderophore	6,943,207	6,957,918	ficellomycin	3%
Region 36	NRPS	7,092,437	7,137,408	enduracidin	10%

Region 37	bacteriocin	7,142,716	7,153,177		
Region 38	saccharide	7,155,120	7,188,902	ashimides	12%
Region 39	saccharide	7,368,836	7,390,778	belactosin A / belactosin C	20%
Region 40	terpene	7,486,846	7,510,747	hopene	76%
Region 41	NRPS,fatty_acid	7,755,098	7,815,348	myxothiazol	28%
Region 42	terpene	7,922,434	7,942,364	nenestatin	3%
Region 43	lanthipeptide,terpene	7,942,457	7,984,662	geosmin	100%
Region 44	saccharide	8,017,247	8,057,061		
Region 45	T1PKS,LAP	8,059,656	8,109,323	maduropeptin	3%
Region 46	NRPS,fatty_acid	8,118,137	8,162,078	diisonitrile antibiotic SF2768	61%
Region 47	T1PKS,T2PKS,fatty_ac	8,241,505	8,323,840	lysolipin I	65%
Region 48	NRPS-like	8,454,616	8,497,189	borrelidin	5%
Region 49	bacteriocin	8,508,335	8,520,242		
Region 50	melanin	8,793,470	8,803,892	melanin	28%
Region 51	NRPS	9,104,379	9,167,226	qinichelins	44%
Region 52	saccharide	9,250,594	9,271,013	cosmomycin C	3%
Region 53	lanthipeptide	9,293,335	9,315,935	polyoxin A / polyoxin H	5%
Region 54	saccharide	9,436,178	9,469,306	acarviostatin I03 / acarviostatin	18%

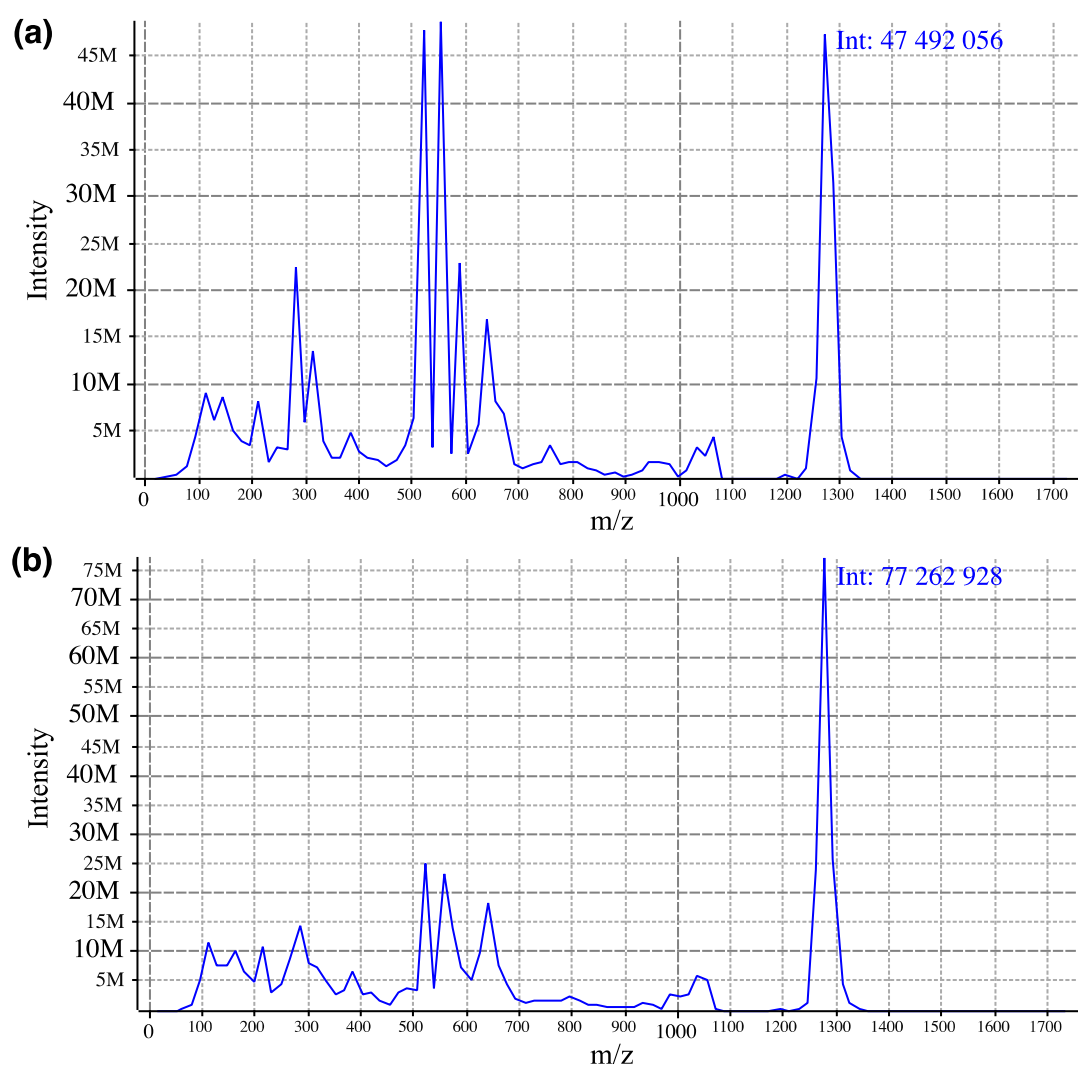
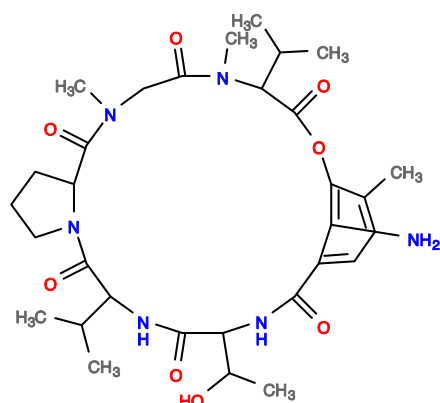
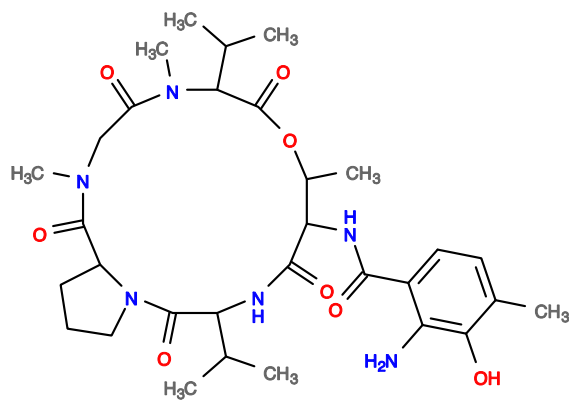


Figure S1. HPLC-MS/MS spectra of organic crude extracts from the Antarctic strain *Streptomyces fildesensis* So13.3 under different culture conditions: (a) IMA medium with no elicitation treatment (basal condition) and (b) IMA medium with coculture elicitation strains So13.3 + So1b. Peak correspondent to putative Actinomycin D is showed and labeled with the intensity of this compound detected for each culture condition.

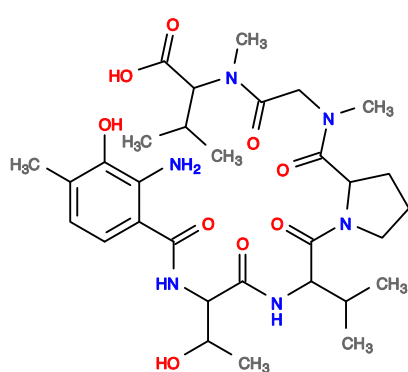
Figure S2. Maximum-likelihood phylogenetic tree based on complete 16S rRNA gene sequences showing the genetic distances between Antarctic bacterial strains (highlighted in color and bold) and closely related species based on 16S rRNA reference sequences from DDBJ/ENA/GenBank database. Numbers at nodes represent the bootstrap support (%). Accession number of 16S rRNA gene sequences are shown after the species name.



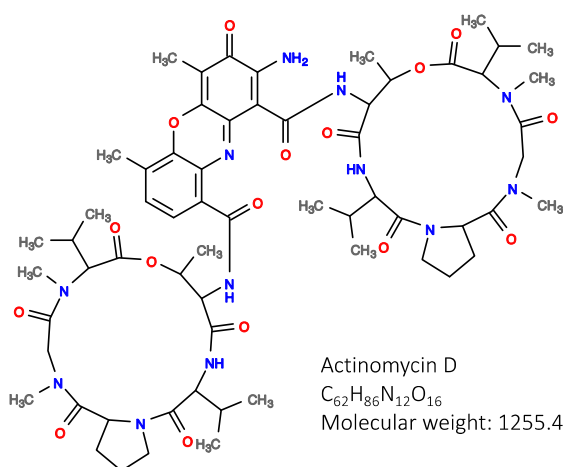
Scaffold 1 predicted from So13.3 gene cluster
 $C_{31}H_{46}N_6O_8$
 Molecular weight: 630.730



Scaffold 2 predicted from So13.3 gene cluster
 $C_{31}H_{46}N_6O_8$
 Molecular weight: 630.730



Scaffold 3 predicted from So13.3 gene cluster
 $C_{31}H_{46}N_6O_9$
 Molecular weight: 648.750



Actinomycin D
 $C_{62}H_{86}N_{12}O_{16}$
 Molecular weight: 1255.420

Figure S3. Chemical structures predicted for biosynthetic gene cluster similar to Actinomycin D from the Antarctic strain So13.3 genome (Scaffolds 1-3) compared to the structure of the known drug. The predicted structures were based on the core biosynthetic genes using PRISM 4 (<http://grid.adapsyn.com/prism/#!/prism>).