

Table S1. Alterochromide A (alt) biosynthetic gene cluster annotation (scaffolds NZ_NSDG01000052, NZ_NSDG01000119 and NZ_NSDG01000203)

Protein Name	Protein ID (GenBank)	Length (aa)	Conserved domains (CD-Search)	Proposed function	MiBiG Protein Homolog	MiBiG Homolog Description	% ID	% Coverage	BLASTp Score	E-value	MiBiG Homolog Cluster	MiBiG Cluster Product	MiBiG Organism
AltA	WP_095728151	539	lyase class I like superfamily	lyase (C-N or C-O bond cleavage)	ERG36772	histidine ammonia-lyase	99.0	99.8	1037.0	5.90E-303	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltB	WP_095728150	97	PP-binding superfamily (phosphopantetheine attachment site)	T domain	ERG36773	hypothetical protein	92.0	100.0	121.0	1.00E-27	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltC	WP_095728149	498	PP-binding superfamily; 4 coum CoA lig superfamily (coumarate-CoA ligase)	loading T-A	ERG36774	AMP-dependent synthetase and ligase	94.0	100.0	933.0	1.10E-271	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltD	WP_095728148	727	KAS I and II; condensing enzymes superfamily	KS	ERG36775	3-oxoacyl-ACP synthase	97.0	100.0	1383.0	0	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltE	WP_010369407	255	CcmA superfamily (ABC-type multidrug transport system)	transporter	ERG36776	ABC transporter ATPase	100.0	100.0	513.0	1.80E-145	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltF	WP_010369409	371	YadH superfamily (ABC-type multidrug transport system, permease component)	transporter	ERG36777	ABC transporter permease	100.0	100.0	703.0	1.40E-202	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltG	WP_010369411	132	hot dog superfamily	DH	ERG36778	3-hydroxyacyl-ACP dehydratase	100.0	100.0	273.0	1.60E-73	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltH	WP_095728147	243	NADB Rossmann superfamily (NAD(P)H/NAD(P)(+) binding (NADB) domain)	KR	ERG36779	3-oxoacyl-[acyl-carrier-protein] reductase (FabG)	99.0	100.0	476.0	3.10E-134	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltI	WP_095728146	235	NA	unknown	ERG36780	hypothetical protein	95.0	100.0	435.0	4.40E-122	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltJ	WP_095728145	251	abhydrolase superfamily (alpha/beta hydrolase); GrsT (surfactin synthase thioesterase)	TEII	ERG36781	thioesterase	98.0	100.0	515.0	6.10E-146	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltK	WP_095728144	1517	PRK12467 (peptide synthase)	C-A-T-E	ERG36782	non-ribosomal peptide synthetase	98.0	100.0	2895.0	2895	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltL	WP_141240190	2615	AFD (adenylate forming domain), Class I superfamily; PP (phosphopantetheine)-binding superfamily	C-A-T-E-C-A-T	WP_010369428	non-ribosomal peptide synthetase	97.0	100.0	822.0	3.10E-238	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltM	WP_141240175	3280	PPK12316 (peptide synthase)	C-A-T-E-C-A-T-E-TE	WP_010369430	non-ribosomal peptide synthetase	96.0	100.0	4916.0	0	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>
AltN	WP_095730079	412	halo ClmS (chloramphenicol-biosynthetic FADH2-dependent halogenase)	halogenase	WP_010369433	tryptophan halogenase	96.0	100.0	805.0	4.90E-233	BGC0000299	alterochromide A (NRP)	<i>Pseudoalteromonas piscicida</i>

Gene clusters were mined with antiSMASH 5.1 then individual encoded enzymes were compared to those in the Conserved Domain database (NCBI) and MiBiG repository. *If a MiBiG homologue could not be detected, the closest BLASTp match from Genbank (NCBI) was recorded instead.

Table S2. Pseudoalterobactin biosynthetic (*pab*) gene cluster annotation (scaffold NZ_NSDG01000065)

Protein Name	Protein ID (GenBank)	Length (aa)	Conserved domains (CD-Search)	Proposed function	MIBiG Protein Homolog	MIBiG Homolog Description	% ID	% Coverage	BLASTp Score	E-value	MIBiG Homolog Cluster	MIBiG Cluster Product	MIBiG Organism
PabS	WP_095728646	515	PRK00915 (isopropylmalate synthase) superfamily	substrate biosynthesis	AHZ61876	pyruvate carboxyltransferase/2-isopropylmalate synthase	38.0	66.2	213.0	1.00E-54	BGC0000240	lomaiviticin A (PK/Saccharide)	<i>Salinispora pacifica</i>
PabT	NA	358	Iso dh (isocitrate/isopropylmalate dehydrogenase) superfamily	substrate biosynthesis	WP_010374375*	3-isopropylmalate dehydrogenase	100.0	83.0	91.7	3e-20	NA	NA	<i>Pseudoalteromonas piscicida</i>
PabU	WP_095728645	467	aconitase superfamily (citrate/isocitrate isomerase)	substrate biosynthesis	ARO49575	3-isopropylmalate dehydratase large subunit	59.0	98.1	523.0	3.20E-148	BGC0001441	belactosin A	<i>Streptomyces</i> sp.
PabV	WP_095728644	199	aconitase swivel superfamily	substrate biosynthesis	AHZ61874	isopropylmalate dehydratase small subunit	37.0	97.5	133.0	4.00E-31	BGC0000240	lomaiviticin A (PK/Saccharide)	<i>Salinispora pacifica</i>
PabA	WP_095728639	67	MbtH superfamily	unknown	CAQ71824	MbtH-like protein	64.0	94.0	102.0	2.50E-22	BGC0001189	taiwachelin (NRP)	<i>Cupriavidus taiwanensis</i>
PabB	WP_095728638	1741	PRK05691	AL-T-C-A-T	WP_039806856	non-ribosomal peptide synthetase	38.0	102.0	1102.0	0	BGC0002001	crochelin A (NRP/PK)	<i>Azotobacter chroococcum</i>
PabC	WP_095728637	1463	cond enzymes superfamily; NADB Rossmann superfamily	KS-AT-KR-T	WP_039806854	type I polyketide synthase	41.0	103.0	977.0	2.00E-284	BGC0002001	crochelin A (NRP/PK)	<i>Azotobacter chroococcum</i>
PabD	WP_095728636	806	Ntn hydrolase superfamily (hydrolysis of amide bonds)	regulation	WP_081480190	acylase	36.0	100.4	517.0	4.00E-146	BGC0001716	odilorhabdins (NRP)	<i>Xenorhabdus nematophila</i>
PabE	WP_095728635	721	OM channels superfamily (porin)	transport	PHM29813	ferric alcaligin siderophore receptor	27.0	106.4	260.0	6.00E-69	BGC0001870	putrebactin (other)	<i>Xenorhabdus budapestensis</i>
PabF	WP_095728634	1538	PRK12467	C-A-T-C	AEH59100	nonribosomal peptide synthetase	33.0	99.0	690.0	6.50E-198	BGC0000385	lysobactin (NRP)	<i>Lysobacter</i> sp.
PabG	WP_095728633	3026	PRK12316	C-A-T-E-C-A-T-C	BAH43871	gramicidin non-ribosomal peptide synthetase LgrC	32.0	99.2	1446.0	0	BGC0000367	gramicidin (NRP)	<i>Brevibacillus brevis</i>
PabH	WP_095728632	353	CAS like superfamily	hydroxylation	CAQ71826	non-ribosomal peptide synthetase/dioxygenase/oxidoreductase	64.0	89.8	453.0	2.40E-127	BGC0001189	taiwachelin (NRP)	<i>Cupriavidus taiwanensis</i>
PabI	WP_095728631	1036	PPK12467; A NRPS; AFD class I superfamily	C-A-T	CAQ71827	non-ribosomal peptide synthetase	34.0	103.8	472.0	1.40E-132	BGC0001189	taiwachelin (NRP)	<i>Cupriavidus taiwanensis</i>
PabJ	WP_095728630	1334	PRK12467; abhydrolase superfamily	C-A-T-TE	WP_144411596	non-ribosomal peptide synthetase	33.0	88.4	537.0	8.00E-152	BGC0002001	crochelin A (NRP/PK)	<i>Azotobacter chroococcum</i>
PabK	WP_095728629	693	ligand gated channel; OM channels superfamily (porin)	receptor	ADJ63844	TonB-dependent siderophore receptor	26.0	103.9	199.0	1.60E-50	BGC0000424	serobactin C (NRP/siderophore)	<i>Herbaspirillum seropedicae</i>
PabL	WP_095728628	447	PepSY TM	receptor	AA93425	PepSY-associated TM helix domain protein	30.0	81.2	166.0	7.30E-41	BGC0000413	pyoverdin (NRP)	<i>Pseudomonas protegens</i>
PabM	WP_095728627	254	PRK08220 superfamily (2,3-dihydroxybenzoate-2,3-dehydrogenase)	DHB biosynthesis	YP_856989	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase	52.0	96.5	239.0	6.60E-63	BGC0001502	amonabactin P 750 (NRP)	<i>Aeromonas hydrophila</i>
PabN	WP_095728626	435	C NRPS-like superfamily	C-domain	YP_856990	nonribosomal peptide synthetase	29.0	96.1	173.0	5.80E-43	BGC0001502	amonabactin P 750 (NRP)	<i>Aeromonas hydrophila</i>
PabO	WP_095728625	288	cysteine hydrolase superfamily; PP-binding superfamily (e.g. isochorismatase)	DHB biosynthesis	ACR10711	isochorismatase	50.0	101.0	292.0	5.70E-79	BGC0000451	turnerbactin (NRP)	<i>Teredinibacter turnerae</i>
PabP	WP_095728624	538	EntE	A-domain	YP_856992	2,3-dihydroxybenzoate-AMP ligase	56.0	98.9	579.0	7.40E-165	BGC0001502	amonabactin P 750 (NRP)	<i>Aeromonas hydrophila</i>

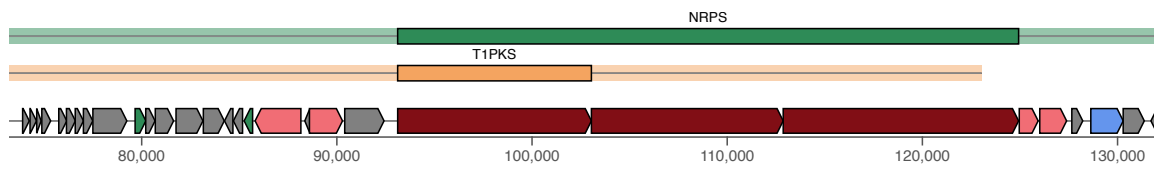
PabQ	WP_095728623	404	MenF (Isochorismate synthase)	DHB biosynthesis	ACR13729	isochorismate synthase DhbC	41.0	92.3	264.0	3.00E-70	BGC0000451	turnerbactin (NRP)	<i>Teredinibacter turnerae</i>
PabR	WP_095728622	246	Fe III red FhuF superfamily (siderophore-iron reductase)	regulation	WP_09903132 5*	(2Fe-2S)-binding protein	93.1	100.0	486.0	5e-173	NA	NA	<i>Pseudoalteromonas sp.</i>

Gene clusters were mined with antiSMASH 5.1 then individual encoded enzymes were compared to those in the Conserved Domain database (NCBI) and MIBiG repository. *If a MIBiG homologue could not be detected, the closest BLASTp match from Genbank (NCBI) was recorded instead.

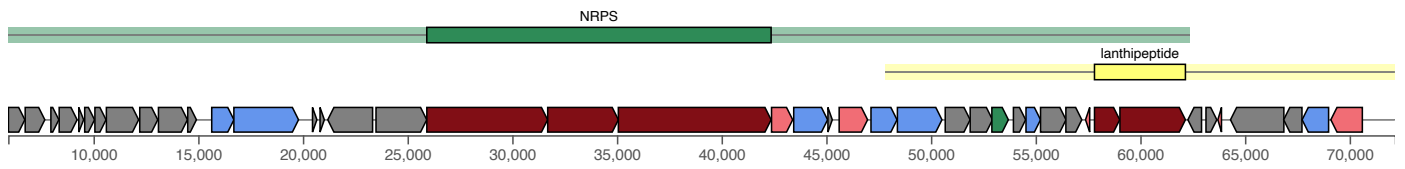
Table S3. Alteramide biosynthetic (*alm*) gene cluster annotation (scaffold NZ_NSDG01000081)

Protein Name	Protein ID (GenBank)	Length (aa)	Conserved domains (CD-Search)	Proposed function	MiBiG Protein Homolog	MiBiG Homolog Description	% ID	% Coverage	BLASTp Score	E-value	MiBiG Homolog Cluster	MiBiG Cluster Product	MiBiG Organism
AlmA	WP_095728960	434	zinc peptidase like superfamily	peptidase	WP_102056891*	succinyl-diaminopimelate desuccinylase	93.3	100.0	852.0	0	NA	NA	<i>Pseudoalteromonas</i> sp.
AlmB	WP_095728959	3113	cond enzymes superfamily; NADB Rossmann superfamily; PP-binding; PRK12467	KS-AT-DH-KR-T-C-A-T-TE	ABL86391	hybrid NRPS/PKS	44.0	101.2	2505.0	0	BGC0000999	heat-stable antifungal factor	<i>Lysobacter enzymogenes</i>
AlmC	WP_095728958	551	COG1233 superfamily (phytoene dehydrogenase-related protein)	dehydrogenase	BAG17641	FAD-dependent oxidoreductase	54.0	96.4	596.0	3.50E-170	BGC0001043	SGR PTMs (NRP/PK)	<i>Streptomyces griseus</i>
AlmD	WP_095728957	178	FMN red superfamily	reductase	WP_099029208*	flavodoxin FldB	98.3	100.0	356.0	6e-124	NA	NA	<i>Pseudoalteromonas</i> sp.
AlmE	WP_095728956	554	COG1233 superfamily (phytoene dehydrogenase-related protein)	dehydrogenase	AWO77089	FAD-dependent oxidoreductase	43.0	95.7	415.0	2.40E-126	BGC0001556	combamide (NRP/PK)	<i>Streptomyces</i> sp.
AlmF	WP_095728955	321	FA hydroxylase superfamily	hydroxylase	ABL86392	sterol desaturase-like protein	43.0	85.0	242.0	7.50E-64	BGC0000999	heat-stable antifungal factor	<i>Lysobacter enzymogenes</i>
AlmG	WP_095728954	459	MATE like superfamily	transport	CAN93353	MATE efflux family protein	43.0	96.9	356.0	6.70E-98	BGC0000179	etnangien (PK)	<i>Sorangium cellulosum</i>

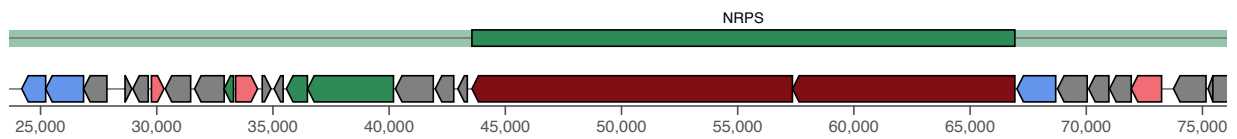
Gene clusters were mined with antiSMASH 5.1 then individual encoded enzymes were compared to those in the Conserved Domain database (NCBI) and MiBiG repository. *If a MiBiG homologue could not be detected, the closest BLASTp match from Genbank (NCBI) was recorded instead.



a) Hybrid NRPS-PKS 1



b) Hybrid Lanthipeptide-NRPS



c) NRPS

Figure S1. Orphan gene clusters identified in *Pseudoalteromonas* HM-SA03 genome by antiSMASH 5.1.2. Core biosynthetic genes (crimson), additional biosynthetic genes (salmon), transport-related genes (blue), regulatory genes (green), other genes (grey).

Table S4. Novel NRPS-TIPKS (siderophore) biosynthetic (sid) gene cluster annotation (scaffold NZ_NSDG01000022)

Protein Name	Protein ID (GenBank)	Length (aa)	Conserved domains (CD-Search)	Proposed function	MIBiG Protein Homolog	MIBiG Homolog Description	% ID	% Coverage	BLASTp Score	E-value	MIBiG Homolog Cluster	MIBiG Cluster Product	MIBiG Organism
SidA	WP_095727185	732	PRK10044 (ferrichrome outer membrane transporter)	regulation	CAQ71830	TonB-dependent siderophore receptor	36.0	101.1	421.0	2.10E-117	BGC0001189	taiwachelin (NRP)	<i>Cupriavidus taiwanensis</i>
SidB	None	85	K oxygenase	oxidoreductase	ADJ63845	L-ornithine N5-monoxygenase protein	51.0	97.7	97.0	1.40E-20	BGC0000424	serobactin C (NRP)	<i>Herbaspirillum seropedicae</i>
SidC	WP_095727186	138	ExbD superfamily (membrane bound transport proteins)	transport	WP_102056205*	biopolymer transporter ExbD	97.8	100.0	266.0	7.00E-90	NA	NA	<i>Pseudoalteromonas</i> sp.
SidD	WP_095727187	240	TolQ; MotA ExB superfamily (proton channel)	transport	WP_138580328*	MotA/TolQ/ExbB proton channel family protein	98.0	100.0	482.0	8.00E-172	NA	NA	<i>Pseudoalteromonas</i> sp.
SidE	WP_051009522	89	TonB C superfamily (receptor)	transport	WP_174170301*	energy transducer TonB	100.0	100.0	196.0	1.00E-61	NA	NA	<i>Pseudoalteromonas</i> sp.
SidF	WP_176474608	103	NA	unknown	PAA74211*	hypothetical protein	73.3	83.0	437.0	6.00E-18	NA	NA	<i>Macrostromum lignano</i>
SidG	WP_141240122	538	OM channels superfamily (porin)	regulation	WP_085297362*	TonB-dependent receptor	65.9	98.0	722.0	0	NA	NA	<i>Colwellia mytili</i>
SidH	WP_095727191	237	TrpE superfamily (anthranilate/para-aminobenzoate synthases)	isochorismate synthase	WP_063364360*	chorismate-binding protein	79.5	70.0	286.0	2.00E-92	NA	NA	<i>Pseudoalteromonas luteoviolacea</i>
SidI	WP_095727192	1739	PPK12467; A NRPS TImIV like; ADF class I superfamily	A-T-Cy-A-T	AEE88284	NRPS/PKS (CurF)	45.0	71.4	1050.0	2.80E-306	BGC0000976	curacin A (NRP/PK)	<i>Moorea producens</i>
SidJ	WP_095727193	1808	PksD; cond enzymes superfamily;NADB Rossmann superfamily; PP-binding	KS-AT-DH-KR-T	AAF19812	NRPS/PKS (MtaD)	42.0	99.2	1309.0	0	BGC0001024	myxothiazol (NRP/PK)	<i>Stigmatella aurantiaca</i>
SidK	WP_095727194	1201	TubC N; PPK12467	C-A-T	AXN93614	NRPS (PuwF)	43.0	96.3	894.0	1.40E-259	BGC0001953	puwainaphycin F (NRP)	<i>Anabaena</i> sp.
SidL	WP_095727195	1877	PksD; cond enzymes superfamily; PKS MT; KR 2 FAS SDR x; PP-binding	KS-AT-oMT-KR-T	DAB41916	PKS (ArzN)	44.0	100.5	1467.0	0	BGC0001884	aranazole A (NRP/PK)	<i>Fischerella</i> sp.
SidM	WP_176474609	1398	Cyc NRPS; AFD class-I superfamily; Nitro FMN reductase; PRK12467	Cy-A-Ox-T	DAB41917	NRPS (ArzO)	45.0	98.4	1193.0	0	BGC0001884	aranazole A (NRP/PK)	<i>Fischerella</i> sp.
SidN	WP_095727197	2028	cond enzymes superfamily; NADB Rossmann; PKS ER	KS-AT-DH-ER-KR	AEU11005	NRPS/PKS (NpnA)	46.0	103.0	1744.0	0	BGC0001029	nostophycin (NRP/PK)	<i>Nostoc</i> sp.
SidO	WP_095727198	93	PP-binding superfamily	T	ABM21570	PKS (CrpB)	41.0	73.1	62.0	4.00E-10	BGC0000975	cryptophycin-327 (NRP/PK)	<i>Nostoc</i> sp.
SidP	WP_095727199	1423	TubC; PPK12467; abhydrolase superfamily	C-A-T	AXN93602	NRPS (PuwF-G)	43.0	81.0	871.0	1.90E-252	BGC0001952	minutissamide A (NRP)	<i>Anabaena minutissima</i>
SidQ	WP_095727200	255	abhydrolase superfamily	TE	CAD29792	thioesterase (McyT)	45.0	92.9	216.0	4.60E-56	BGC0001015	microcystin (NRP/PK)	<i>Planktothrix agardhii</i>
SidR	WP_095727201	105	CM 2 superfamily (chorismate mutase type II)	salicylate synthase	AAO07762	Isochorismate pyruvate-lyase	56.0	101.0	134.0	7.20E-32	BGC0000460	vulnibactin (NRP)	<i>Vibrio vulnificus</i>

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Table S5. Novel NRPS biosynthetic gene cluster (scaffold NZ_NSDG01000113)

Protein Name	Protein ID (GenBank)	Length (aa)	Conserved domains (CD-Search)	Proposed function	MiBiG Protein Homolog	MiBiG Homolog Description	% ID	% Coverage	BLASTp Score	E-value	MiBiG Homolog Cluster	MiBiG Cluster Product	MiBiG Organism
WP_095729892		434	AAT I superfamily	transamination, racemization, decarboxylation, or various side-chain reactions	WP_013184465	diaminobutyrate-2-oxoglutarate transaminase	56.0	95.9	496.0	5.10E-140	BGC0001716	odilorhabdins (NRP)	<i>Xenorhabdus nematophila</i>
WP_095729891		310	cupin like superfamily	unknown	WP_021711495*	cupin-like domain-containing protein	71.0	84.0	486.0	6.00E-164	NA	NA	<i>Vibrio azureus</i>
WP_095729890		290	cupin like superfamily	unknown	WP_010846017	hypothetical protein	45.0	99.0	262.0	8.30E-70	BGC0001716	odilorhabdins (NRP)	<i>Xenorhabdus nematophila</i>
WP_176474729		424	metL (aspartate kinase II/homoserine dehydrogenase II)	kinase/dehydrogenase	EWM63050	aspartate kinase 2	30.0	45.0	79.0	1.10E-14	BGC0000679	diazepinomicin (Terpene)	<i>Micromonospora</i> sp.
WP_095729888		556	PudE (ABC-type siderophore export system)	transport	WP_010846011	cyclic peptide export ABC transporter	41.0	98.0	396.0	9.20E-110	BGC0001716	odilorhabdins (NRP)	<i>Xenorhabdus nematophila</i>
WP_095729887		3188	PPK12467; PRK05691 (NRPS)	C-A-T-C-A-T-C-A-T	AXN93590	non-ribosomal peptide synthetase PuwF-G	37.0	101.3	1953.0	0	BGC0001951	puwainaphycin F (NRP)	<i>Cylindrospermum alatosporum</i>
WP_095729886		4597	PRK12316; PRK12467 (NRPS)	C-A-T-C-A-T-C-A-T-C-A-T-TE	ABI26078	nonribosomal peptide synthetase OciB	39.0	91.6	2889.0	0	BGC0000331	cyanopeptin (NRP)	<i>Planktothrix agardhii</i>
WP_095729885		135	DAGK IM like superfamily (Integral membrane diacylglycerol kinase)	ATP-dependent phosphorylation	BAG50454	diacylglycerol kinase	50.0	84.4	103.0	2.30E-22	BGC0000780	O&K-antigen (Saccharide)	<i>Vibrio parahaemolyticus</i>
WP_095729884		264	PAP2 like	phosphatase/oxidase	WP_071564087*	phosphatase PAP2 family protein	48.0	66.0	243.0	2e-76	NA	NA	<i>Bathymodiolus thermophilus thioautotrophic gill symbiont</i>
WP_095729883		542	PRK11598	hydrolase	NQY65624*	phosphoethanolamine-lipid A transferase	51.0	68.0	591.0	0	NA	NA	<i>Alteromonadaceae bacterium</i>
WP_095729882		1231	PAS 4; PRK11107 (sensory histidine kinase)	signal transduction	WP_091320338	HAMP domain-containing protein	29.0	39.1	187.0	1.40E-46	BGC0002007	atolypene A (Terpene)	<i>Amycolatopsis tolypomycina</i>
WP_095729881		300	PleD	response regulator	ACV42481	putative adenylate/guanylate cyclase	27.0	62.0	76.0	8.70E-14	BGC0000043	curacin A (PK)	<i>Moorea producens</i>
WP_095729880		129	NA	unknown	KID36715*	hypothetical protein	93.0	94.0	240.0	9.00E-80	NA	NA	<i>Pseudoalteromonas elyakovii</i>
WP_095729879		126	DUF3192	unknown	WP_138582242*	DUF3192 domain-containing protein	98.0	99.0	259.0	2e-87	NA	NA	<i>Pseudoalteromonas</i> sp.
WP_095729878		315	NADB Rossmann; 2-Hacid dh 4	dehydrogenase	BAK64657	putative dehydrogenase	31.0	95.9	104.0	2.40E-22	BGC0000135	reveromycin A (PK)	<i>Streptomyces</i> sp.

Gene clusters were mined with antiSMASH 5.1 then individual encoded enzymes were compared to those in the Conserved Domain database (NCBI) and MiBiG repository. *If a MiBiG homologue could not be detected, the closest BLASTp match from Genbank (NCBI) was recorded instead.

Table S6. Novel NRPS-PKS 1 biosynthetic gene cluster (scaffold NZ_NSDG01000004)

Protein Name	Protein ID (GenBank)	Length (aa)	Conserved domains (CD-Search)	Proposed function	MiBiG Protein Homolog	MiBiG Homolog Description	% ID	% Coverage	BLASTp Score	E-value	MiBiG Homolog Cluster	MiBiG Cluster Product	MiBiG Organism
WP_095726664		564	G glu transpept (gamma-glutamyltranspeptidase)	gamma-glutamyltransferase	AOC89013	putative gamma-glutamyltransferase-like hydrolase	31.0	104.3	267.0	3.83-71	BGC0001652	limazepine C (NRP)	<i>Streptomyces</i> sp.
WP_095726665		671	metallo-dependent hydrolase (amidohydrolase) superfamily	amidohydrolase	TXD00011	amidohydrolase family protein	25.0	67.7	98.0	3.70E-20	BGC0001877	cyphomycin (PK)	<i>Streptomyces</i> sp.
WP_095726666		3308	FAAL; PP-; cond enzymes; HemL; PPK12467; AFD classI	AL-T-KS-AT-T-AmT-C-A-T	CAD17792	NRPS-PKS	33.0	114.6	1668.0	0	BGC0001754	ralsolamycin (NRP/PK)	<i>Ralstonia solanacearum</i>
WP_095726667		3275	TubC; PRK12316; PRK12467	C-A-T-C-A-T-C-A-T	AAF17280	NRPS (NosC)	32.0	103.5	1488.0	0	BGC0001028	nostopeptolide A2 (NRP/PK)	<i>Nostoc</i> sp.
WP_095726668		4020	PPK12467	C-A-T-C-A-T-E-C-A-TE	AEU11003	NRPS (NpnC)	32.0	100.9	1798.0	0	BGC0001029	nostophycin (NRP/PK)	<i>Nostoc</i> sp.
WP_095726669		322	TauD; CAS like superfamily	hydroxylase	AVI26391	putative dioxygenase (TnaD)	47.0	89.1	285.0	7.80E-77	BGC0001800	theonellamide (NRP/PK)	<i>Candidatus Entotheonella sarta</i>
WP_095726670		458	beta-lactamase; transpeptidase superfamily	serine hydrolase	WP_17417055 g*	Serine hydrolase	951.0	99.0	99.0	0	NA	NA	<i>Pseudoalteromonas</i> sp.
WP_010607109		186	DUF697	unknown	AFL68049	uncharacterized protein associated with GTPases	42.0	66.1	106.0	6.40E-23	BGC0001524	barnesin A (NRP/PK)	<i>Sulfurospirillum barnesii</i>
WP_017217212		58	NA	unknown	WP_17243988 g*	hypothetical protein	98.0	100.0	116.0	7.00E-33	NA	NA	<i>Pseudoalteromonas</i> sp.
WP_095726671		553	PudE (ABC-type siderophore export system)	transport	AFL68050	ABC transporter	37.0	93.5	358.0	2.80E-98	BGC0001524	barnesin A (NRP/PK)	<i>Sulfurospirillum barnesii</i>
WP_095726672		360	SPFH prohibitin	chaperone	AFL68051	membrane protease subunit, stomatin/prohibitin	41.0	76.7	189.0	1.10E-47	BGC0001524	barnesin A (NRP/PK)	<i>Sulfurospirillum barnesii</i>

Gene clusters were mined with antiSMASH 5.1 then individual encoded enzymes were compared to those in the Conserved Domain database (NCBI) and MiBiG repository. *If a MiBiG homologue could not be detected, the closest BLASTp match from Genbank (NCBI) was recorded instead.

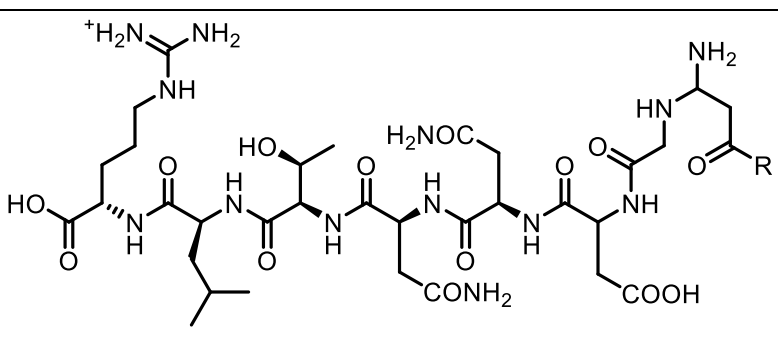
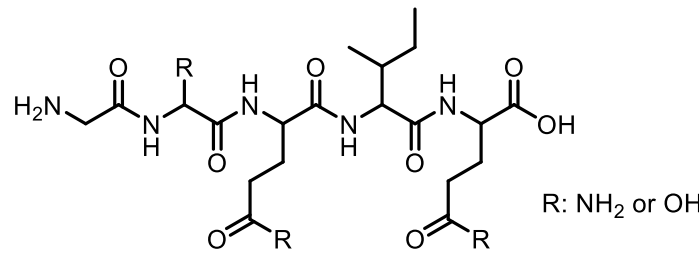
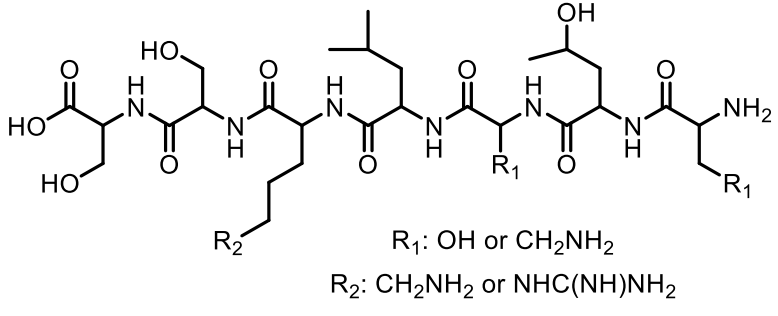
Table S7. Novel Lanthipeptide-NRPS biosynthetic gene cluster (scaffold NZ_NSDG01000099)

Protein Name	Protein ID (GenBank)	Length (aa)	Conserved domains (CD-Search)	Proposed function	MIBiG Protein Homolog	MIBiG Homolog Description	% ID	% Coverage	BLASTp Score	E-value	MIBiG Homolog Cluster	MIBiG Cluster Product	MIBiG Organism
WP_095729408		807	penicillin amidase superfamily	amidase/acylase	ADQ55483	penicillin acylase	24.0	95.0	205.0	2.60E-52	BGC0000350	ET-743 (NRP/Beta-lactam)	uncultured organism
WP_095729409		1923	PPK12467	C-A-T-C-A-T	AAO23333	nonribosomal peptide synthetase NcpA	29.0	94.6	752.0	2.30E-216	BGC0000397	nostocyclopeptide A2 (NRP)	<i>Nostoc</i> sp.
WP_095729410		1125	TubC N; PRK12467	C-A-T	AAO23333	nonribosomal peptide synthetase NcpA	38.0	98.1	718.0	1.30E-206	BGC0000397	nostocyclopeptide A2 (NRP)	<i>Nostoc</i> sp.
WP_095729411		2432	TubC N; PRK12467	C-A-T-C-A-T-TE	WP_06411855_9	nonribosomal peptide synthetase	33.0	100.0	1141.0	0	BGC0001509	anikasin (NRP)	<i>Pseudomonas fluorescens</i>
WP_095729412		336	CAS like superfamily	hydroxylase	ABL74947	SyrP-like regulatory protein/ Dioxygenase	41.0	92.0	274.0	3.20E-73	BGC0001048	tallysomylin A (NRP/Glycopeptide/PK)	<i>Streptoalloteichus hindustanus</i>
WP_095729413		539	PRK10522 (multidrug transporter membrane component/ATP-binding component)	transport	WP_01084601_1	cyclic peptide export ABC transporter	35.0	97.6	314.0	3.40E-85	BGC0001716	odilorhabdins (NRP)	<i>Xenorhabdus nematophila</i>
WP_095729414		69	NA	unknown	WP_13012721_6*	hypothetical protein	88.0	92.0	105.0	3.00E-28	NA	NA	<i>Pseudoalteromonas</i> sp.
WP_095729415		452	glmU (UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase)	unknown	AAD13560	dTDP-1-glucose synthase	36.0	25.0	72.0	1.90E-12	BGC0000239	landomycin A (Polyketide:Type II + Saccharide:Hybrid/tailoring)	<i>Pseudoalteromonas piscicida</i>
WP_095729416		414	type I hlyD (secretion membrane fusion protein)	transport	WP_04118287_3	HlyD family efflux transporter periplasmic adaptor subunit	25.0	92.8	117.0	6.20E-26	BGC0002005	RaxX (RiPP)	<i>Xanthomonas oryzae</i>
	None	708	SunT superfamily (bacteriocin/lantibiotic exporters)	transport	AAI08400	ABC transporter protein MceG	40.0	93.0	425.0	2.10E-118	BGC0000586	microcin E492 (RiPP)	<i>Klebsiella pneumoniae</i>
WP_095729417		396	NA	unknown	WP_13852455_1*	hypothetical protein	91.0	94.0	761.0	0	NA	NA	<i>Pseudoalteromonas</i> sp.
WP_095729418		355	LytS (sensor histidine kinase)	signalling	WP_08853218_8*	histidine kinase	88.0	93.0	632.0	0	NA	NA	<i>Pseudoalteromonas piscicida</i>
WP_095729419		262	LytT (DNA-binding response regulator)	regulation	CBD77761	regulatory protein	26.0	92.7	81.0	2.40E-15	BGC0000974	crocacin (NRP/PK)	<i>Chondromyces crocatus</i>
WP_095729420		194	NA	unknown	WP_13852454_7*	hypothetical protein	95.0	98.0	368.0	3.00E-128	NA	NA	<i>Pseudoalteromonas</i> sp.
WP_095729421		231	P-loop NTPase superfamily (nucleoside triphosphate hydrolases)	transport	AKP45406	ABC transporter ATP-binding protein	44.0	97.4	204.0	1.60E-52	BGC0001413	cystobactamide (NRP)	<i>Cystobacter</i> sp.
WP_095729422		405	LoIE superfamily (ABC-type permease)	transport	AKP45404	efflux ABC transporter	24.0	74.8	72.0	2.20E-12	BGC0001413	cystobactamide (NRP)	<i>Cystobacter</i> sp.
WP_095729423		253	LoIA superfamily (outer membrane lipoprotein-sorting protein)	transport	WP_12872720_7*	outer membrane lipoprotein-sorting protein	94.0	97.0	479.0	3.00E-170	NA	NA	<i>Pseudoalteromonas</i> sp.
WP_039493184		66	NA	Lanthipeptide leader/core peptide	WP_08853218_0*	hypothetical protein	98.0	100.0	140.0	4.00E-42	NA	NA	<i>Pseudoalteromonas piscicida</i>

WP_095729424	401	LanC superfamily (cyclase)	lanthionine synthase	AEK64493	EtnC	25.0	91.5	86.0	8.60E-17	BGC0000506	entianin (RiPP/Lanthipeptide)	<i>Bacillus subtilis</i> subsp. <i>spizizenii</i>
WP_095729425	1042	Lant dehydr N; Lant dehydr C	lantibiotic dehydratase	AHF21234	lanthionine biosynthesis protein PabB	23.0	104.3	230.0	1.60E-59	BGC0000542	paenicidin B (RiPP/Lanthipeptide)	<i>Paenibacillus terrae</i>

Gene clusters were mined with antiSMASH 5.1 then individual encoded enzymes were compared to those in the Conserved Domain database (NCBI) and MIBiG repository. *If a MIBiG homologue could not be detected, the closest BLASTp match from Genbank (NCBI) was recorded instead.

Table S8. Predicted products of orphan NRPS/PKS biosynthesis gene clusters in HM-SA03

Cluster	Size (kbp)	Type	Predicted structure*
HYBR1	31.8	Hybrid NRPS-PKS (lipopeptide)	
HYBR2	16.4	Hybrid Lanthipeptide- NRPS (pentapeptide)	 <p>R: NH₂ or OH</p>
NRPS2	23.4	NRPS (heptapeptide)	 <p>R₁: OH or CH₂NH₂ R₂: CH₂NH₂ or NHC(NH)NH₂</p>

*Putative linear peptide is depicted