

Supplementary Information

Bioprospecting Anticancer Compounds from the Marine-Derived Actinobacteria *Actinomadura* sp. Collected at the Saint Peter and Saint Paul Archipelago (Brazil)

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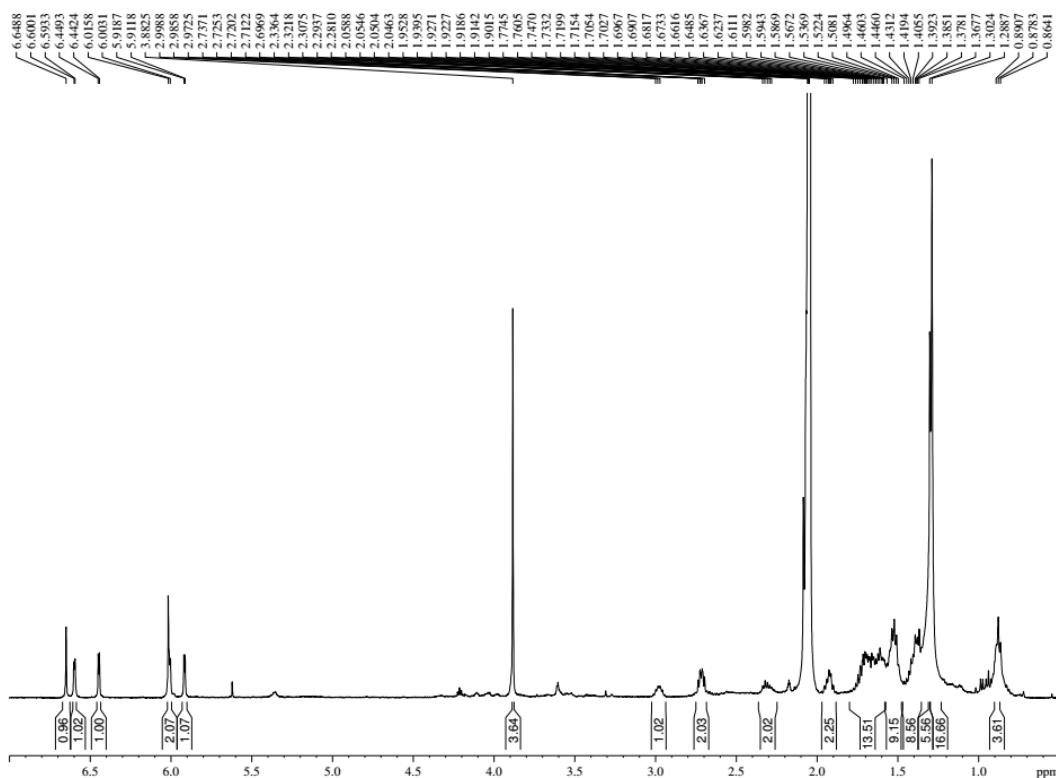


Figure S1. ¹H NMR spectrum (500 MHz, (CD₃)₂CO) of compound **1**.

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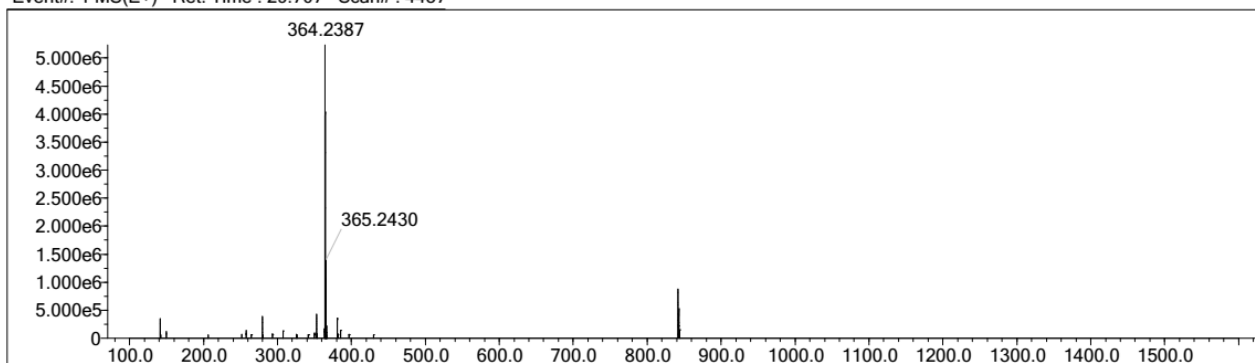


Figure S2. HRESIMS spectrum of compound 1.

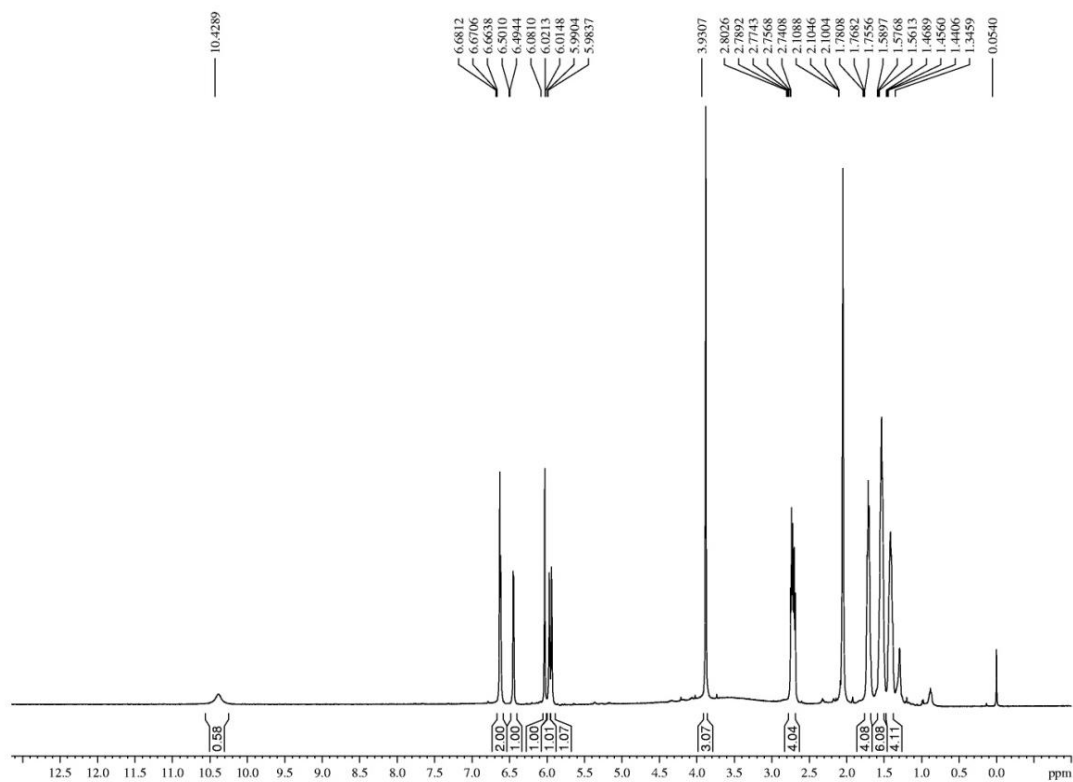


Figure S3. ^1H NMR spectrum (500 MHz, $(\text{CD}_3)_2\text{CO}$) of compound 2.

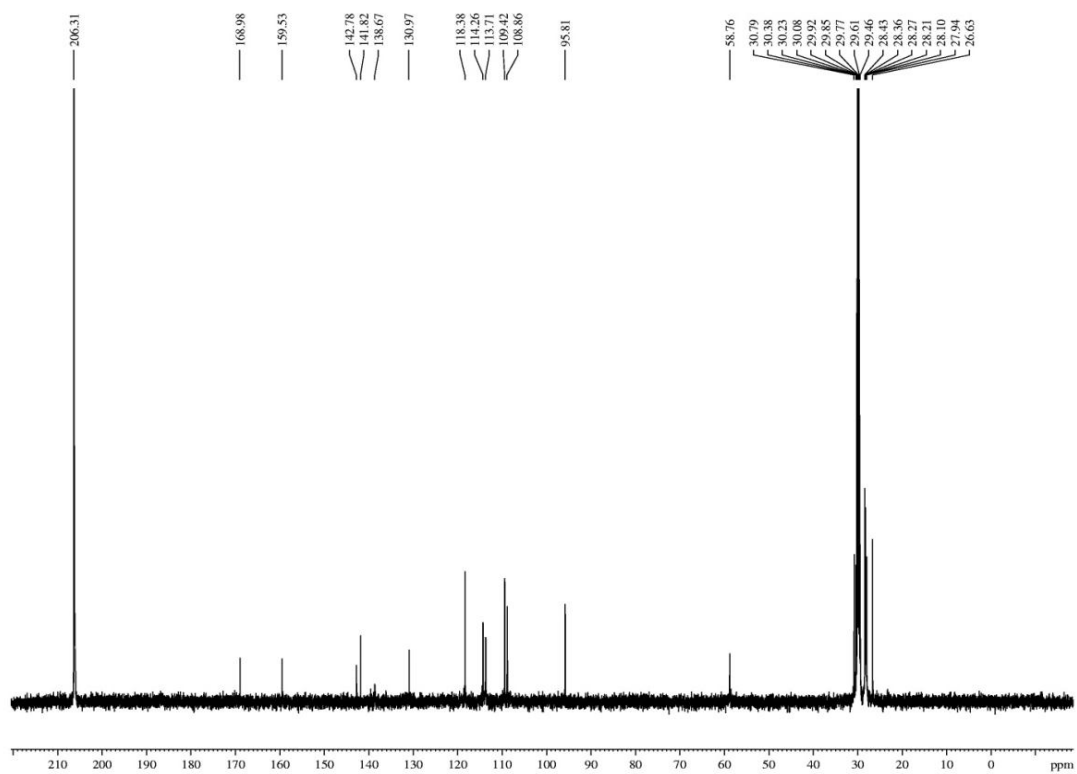


Figure S4. ^{13}C NMR spectra (125 MHz, $(\text{CD}_3)_2\text{CO}$) of compound **2**.

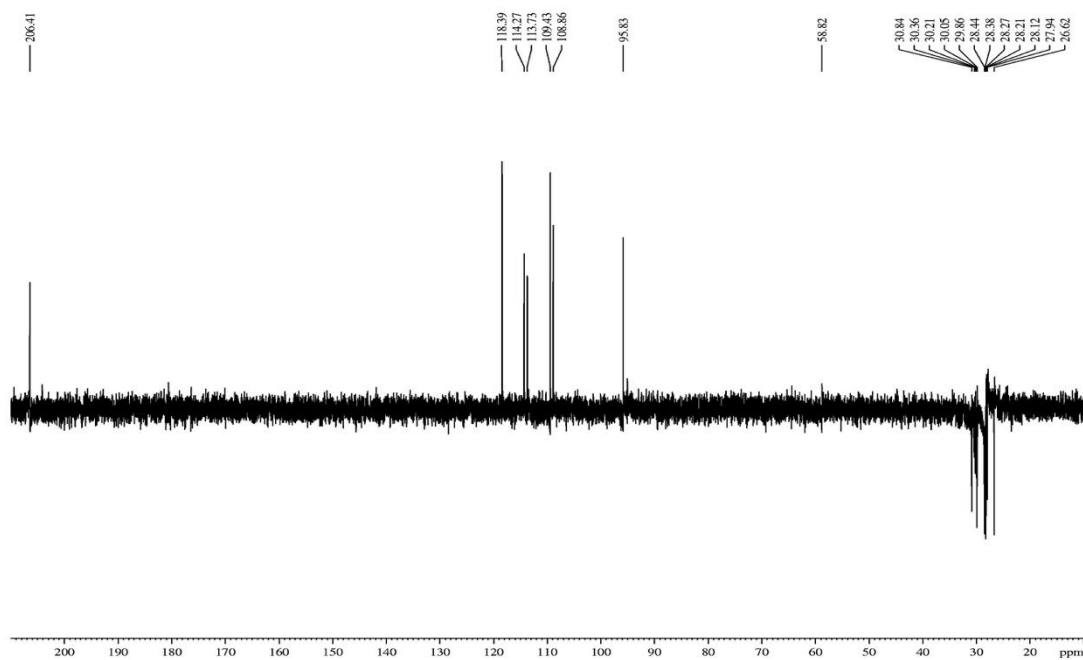


Figure S5. ^{13}C NMR DEPT 135° spectra (125 MHz, $(\text{CD}_3)_2\text{CO}$) of compound **2**.

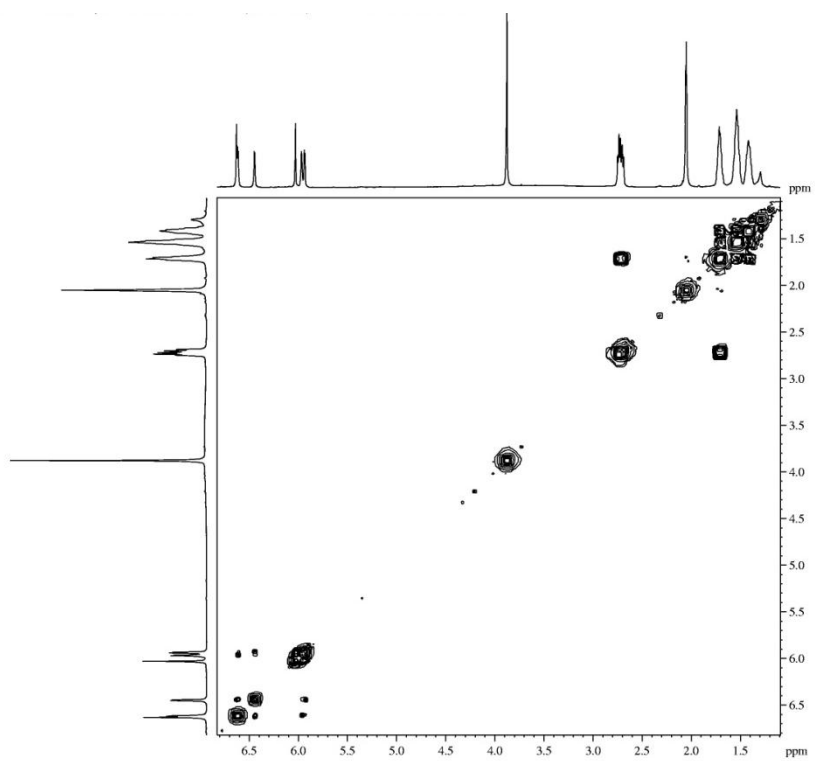


Figure S6. COSY spectrum of compound **2**.

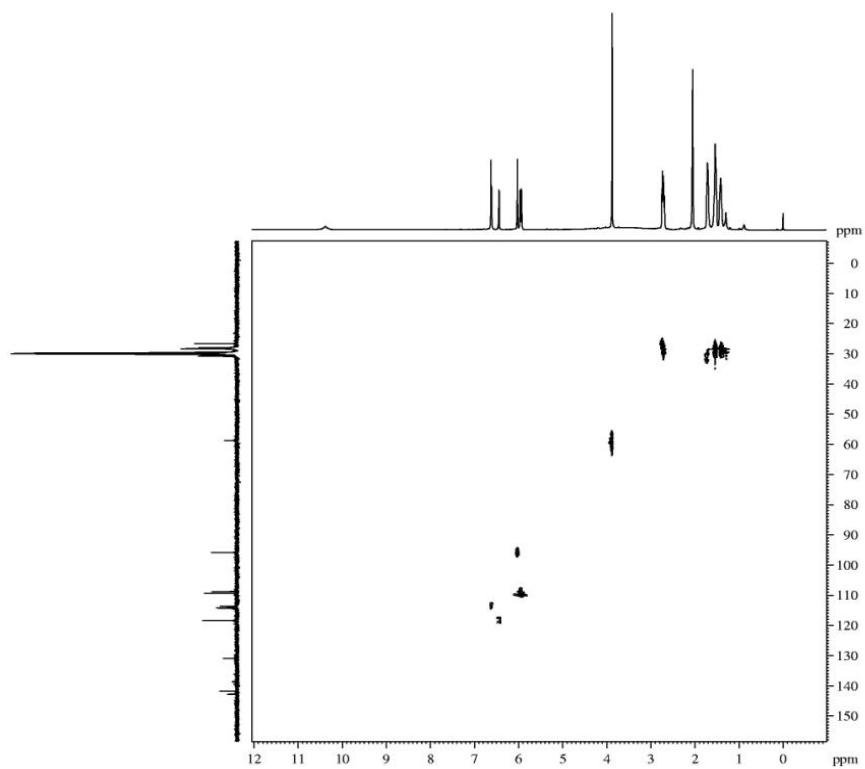


Figure S7. HSQC spectrum of compound **2**.

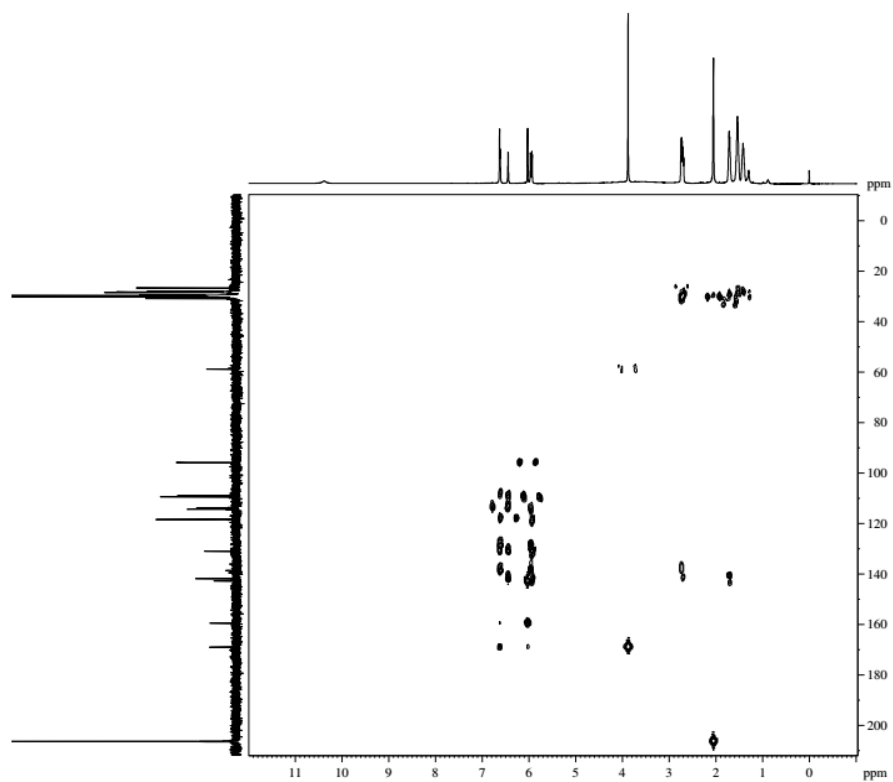


Figure S8. HMBC spectrum of compound **2**.

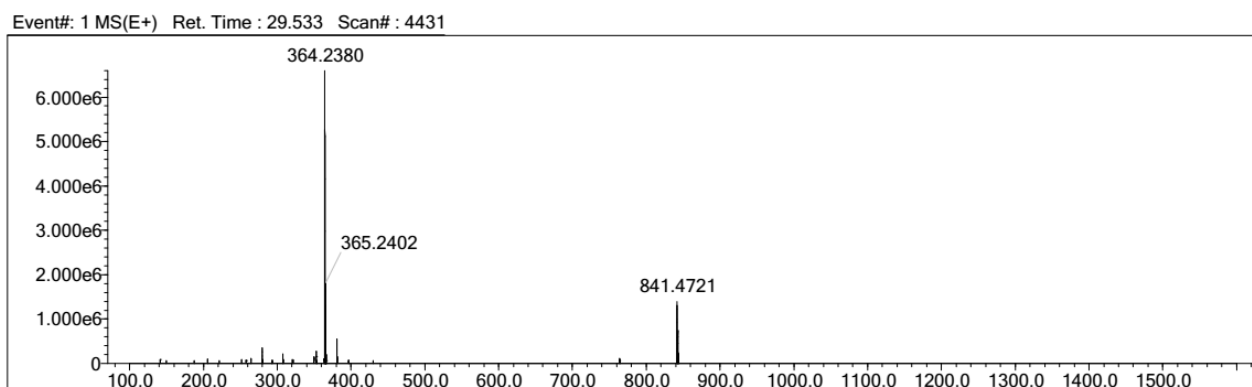


Figure S9. HRESIMS spectrum of compound **2**.

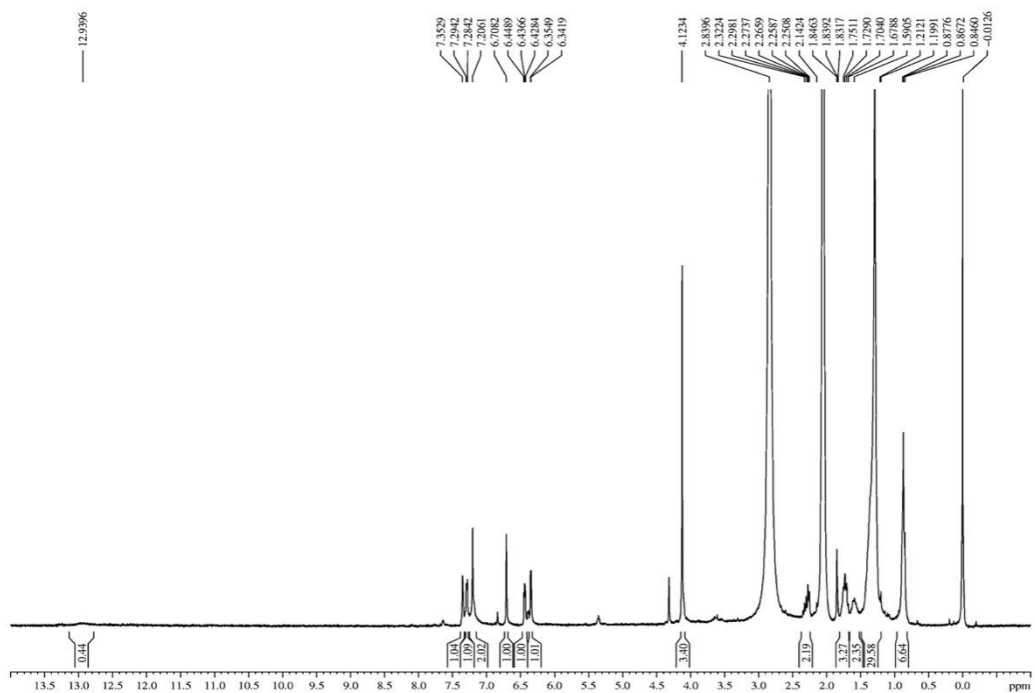


Figure S10. ^1H NMR spectrum (300 MHz, $(\text{CD}_3)_2\text{CO}$) of compound **3**.

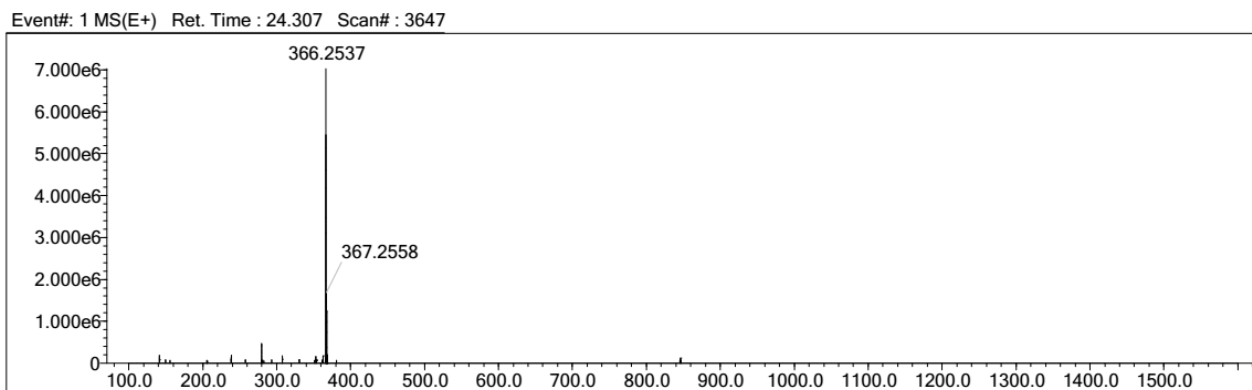


Figure S11. HRMSIMS spectrum of compound **3**.

Table S1. Nonilprodiginine and cycled derivatives BGC and proposed functions

RAST ORF	ANTISMASH BGC	Ptn size / aa	BLASTp best hit	E-value (% of aa identity)	Prodigiosins BGCs orthologous (E-value)
fig 1989.4.peg.5306	ctg330_13	83	acyl carrier protein [<i>Actinomadura latina</i>]	1e-44 (83%)	MarQ [<i>Streptomyces</i> sp. CNQ-617] (1e-16)
fig 1989.4.peg.5305	ctg330_12	86	acyl carrier protein [<i>Actinomadura latina</i>]	4e-37(93%)	MarO [<i>Streptomyces</i> sp. CNQ-617] (3e-22)
fig 1989.4.peg.5304	ctg330_11	622	8-amino-7-oxononanoate synthase [<i>Actinomadura latina</i>]	0.0 (95%)	MarN [<i>Streptomyces</i> sp. CNQ-617] (0.0)
fig 1989.4.peg.5303	ctg330_10	528	D-alanine--poly(phosphoribitol) ligase [<i>Actinomadura latina</i>]	0.0 6(87%)	MarM [<i>Streptomyces</i> sp. CNQ-617] (0.0)
fig 1989.4.peg.5302	ctg330_9	2600	type I polyketide synthase [<i>Actinomadura madurae</i>]	0.0 (82%)	MarL [<i>Streptomyces</i> sp. CNQ-617] (0.0)
fig 1989.4.peg.5301	ctg330_8	265	thioesterase [<i>Actinomadura madurae</i>]	1e-138 (86%)	MarJ [<i>Streptomyces</i> sp. CNQ-617] (7e-83)
fig 1989.4.peg.5300	ctg330_7	349	SAM-dependent methyltransferase [<i>Actinomadura latina</i>]	0.0 (95%)	MarI [<i>Streptomyces</i> sp. CNQ-617] (2e-137)
fig 1989.4.peg.5299	ctg330_6	892	phosphoenolpyruvate-utilizing enzyme [<i>Actinomadura latina</i>]	0.0 (95%)	MarH [<i>Streptomyces</i> sp. CNQ-617] (0.0)
fig 1989.4.peg.5298	ctg330_5	381	hypothetical protein [<i>Actinomadura latina</i>]	0.0 (93%)	MarG [<i>Streptomyces</i> sp. CNQ-617] (1e-122)
fig 1989.4.peg.5297	ctg330_4	896	polyketide synthase [<i>Actinomadura latina</i>]	0.0(89%)	MarX [<i>Streptomyces</i> sp. CNQ-617] (0.0)
fig 1989.4.peg.5296	ctg330_3	387	acyl-CoA dehydrogenase [<i>Actinomadura latina</i>]	0.0 (94%)	RedW [<i>Streptomyces</i> sp. CNQ-617] (0.0)
fig 1989.4.peg.5295	ctg330_2	103	RedY protein [<i>Actinomadura latina</i>]	5e-62 (89%)	MarY [<i>Streptomyces</i> sp. CNQ-617] (8e-32)
fig 1989.4.peg.5294	ctg330_1	289	SARP family transcriptional regulator [<i>Actinomadura latina</i>]	4e-167 (91%)	MarD [<i>Streptomyces</i> sp. CNQ-617](7e-85)
fig 1989.4.peg.6340	ND	203	TetR family transcriptional regulator [<i>Actinomadura madurae</i>]	1e-89 (82%)	trkA1
fig 1989.4.peg.6341	ND	743	hypothetical protein [<i>Actinomadura latina</i>]	0.0 (95%)	ND
fig 1989.4.peg.6342	ND	181	TetR family transcriptional regulator [<i>Dactylosporangium aurantiacum</i>]	5e-34 (43%)	trkA2
fig 1989.4.peg.6343	ND	371	hypothetical protein [<i>Actinomadura latina</i>]	0.0 (90%)	RedV protein [<i>Streptomyces coelicolor</i>] (3e-94)
fig 1989.4.peg.6344	ND	243	hypothetical protein [<i>Actinomadura latina</i>]	8e-58 (51%)	MarU [<i>Streptomyces</i> sp. CNQ-617] (2e-57)
fig 1989.4.peg.6345	ND	296	hypothetical protein [<i>Actinomadura latina</i>]	0.0 (94%)	MarT [<i>Streptomyces</i> sp. CNQ-617] (4e-139)
fig 1989.4.peg.6346	ND	409	3-oxoacyl-ACP synthase [<i>Actinomadura latina</i>]	0.0 (95%)	MarR [<i>Streptomyces</i> sp. CNQ-617] (7e-180)
fig 1989.4.peg.6347	ND	221	3-oxoacyl-ACP synthase [<i>Actinomadura latina</i>]	1e-129 (89%)	MarP [<i>Streptomyces</i> sp. CNQ-617] (1e-76)