N	Gene	Size (aa)	Homolog	ID/SM (%)	Origin	Accession Number
1	orf-4	644	putative serine/threonine protein kinase	45/55	Myxococcus stipitatus DSM 14675	YP_007358846.1
2	orf-3	311	hypothetical protein	51/64	Myxococcus xanthus DK 1622	YP_630142.1
3	orf-2	337	hypothetical protein	73/81	Myxococcus sp. (contaminant ex DSM 436)	WP_002637734.1
4	orf-1	248	hypothetical protein	63/74	Corallococcus coralloides DSM 2259	YP_005366892.1
5	M	351	hydroxyneurosporene-O-methyltransferase	52/67	Synechococcus sp. PCC 6312	YP_007063273.1
6	B	1142	chromopyrrolic acid synthase StaD	44/57	Streptomyces sp. TP-A0274	BAC15759.1
7	C	445	Rieske (2Fe-2S) domain-containing protein	49/64	Pusillimonas noertemannii	WP_017524407.1
8	E	198	prodeoxyviolacein synthase VioE	46/60	Pseudoalteromonas sp. 520P1	BAJ62033.1
9	orf+1	535	serine/threonine protein kinase	48/63	Myxococcus xanthus DK 1622	YP_629143.1
10	orf+2	204	hypothetical protein	47/62	Stigmatella aurantiaca DW4/3-1	YP_003956677.1
11	orf+3	246	putative keratin associated protein	30/37	Cystobacter fuscus	WP_002623966.1
12	orf+4	274	hypothetical protein	78/86	Myxococcus sp. (contaminant ex DSM 436)	WP_002640891.1
13	orf+5	124	response regulator	83/90	Myxococcus xanthus DK 1622	YP_628978.1
14	orf+6	491	hypothetical protein	83/91	Myxococcus fulvus HW-1	YP_004664046.1
15	orf+7	447	short-chain fatty acid transporter	88/93	Myxococcus stipitatus DSM 14675	YP_007357717.1
16	orf+8	168	hypothetical protein	78/89	Myxococcus fulvus HW-1	YP_004664050.1
17	orf+9	2082	polyketide synthase	81/88	Myxococcus sp. (contaminant ex DSM 436)	WP_002634960.1
18	orf+10	254	hypothetical protein	58/67	Myxococcus xanthus DK 1622	YP_631014.1
19	orf+11	1560	non-ribosomal peptide synthetase	79/88	Myxococcus xanthus DK 1622	YP_631013.1
20	orf+12	119	hypothetical protein	34/47	Maricaulis maris MCS10	YP_755404.1
21	orf+13	368	hypothetical protein	47/60	Stigmatella aurantiaca DW4/3-1	YP_003954527.1
22	orf+14	566	hypothetical protein	68/78	Myxococcus sp. (contaminant ex DSM 436)	WP_002633419.1

NM343 Amplicon:

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TTGATGCTCCAGTACACGTACGCGGCCTGGTCGCTGCCCAACTACGTGACGGGGTGCGAGTATGTGGAGCGCGGGCTGTGGACGCCCGAGC
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GGCGGCGAGCACCACCTGTTCCTGCACGAGGCCATCAACCGCAAGCACCCGGACTACCAGCTCCAG
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Figure S1. Annotation of the *mar* gene cluster found in clone NM343 (GenBank accession: KF551863). Annotations are based on a BLASTP homology search of translated genes predicted by FGENESB.

Methylarcyriarubin (1): UV (methanol) λ_{max} 227, 276, 377, 475; ^{1}H NMR (600 MHz, DMSO-d_6) δ3.05 (3H, s, H$_3$-13), 6.63 (2H, t, J = 7.5 Hz, H-10), 6.80 (2H, d, J = 8.0 Hz, H-11), 6.97 (2H, t, J = 7.5 Hz, H-9), 7.37 (2H, d, J = 8.1 Hz, H-8), 7.75 (2H, s, H-5), 11.66 (2H, bs, N-4);^{13}C NMR (150 MHz, DMSO-d_6) δ24.0 (C-13), 105.6 (C-6), 111.7 (C-8), 119.3 (C-10), 120.9 (C-11), 121.6 (C-9), 125.3 (C-12), 127.1 (C-3), 129.1 (C-5), 136.0 (C-7), 171.8 (C-2); HR-ESI-MS m/z 342.1237 [M-H]$^+$ (calcd for $C_{21}H_{16}N_3O_2$, 342.1243).

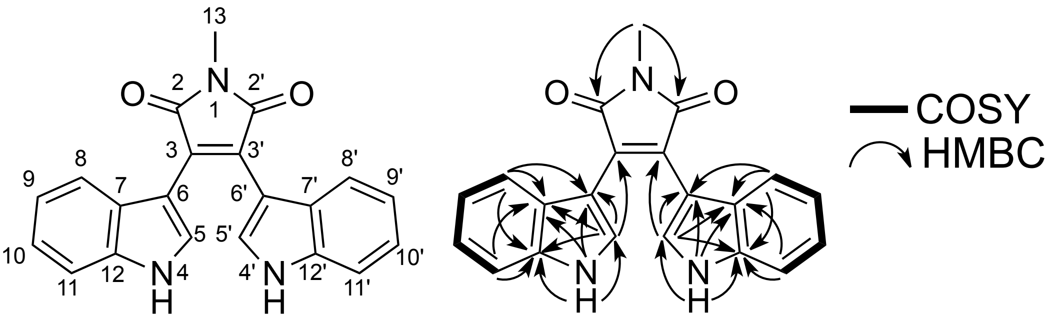

Figure S2. Spectroscopic data for methylarcyriarubin (**1**). This data is consistent with that reported from the synthesis of compound **1**.[30] **Top:** UV, ^{1}H NMR, ^{13}C NMR, and HR-ESI-MS data summary of **1**. **Bottom:** Correlations observed in HMBC and ^{1}H-^{1}H COSY NMR spectra of **1**.

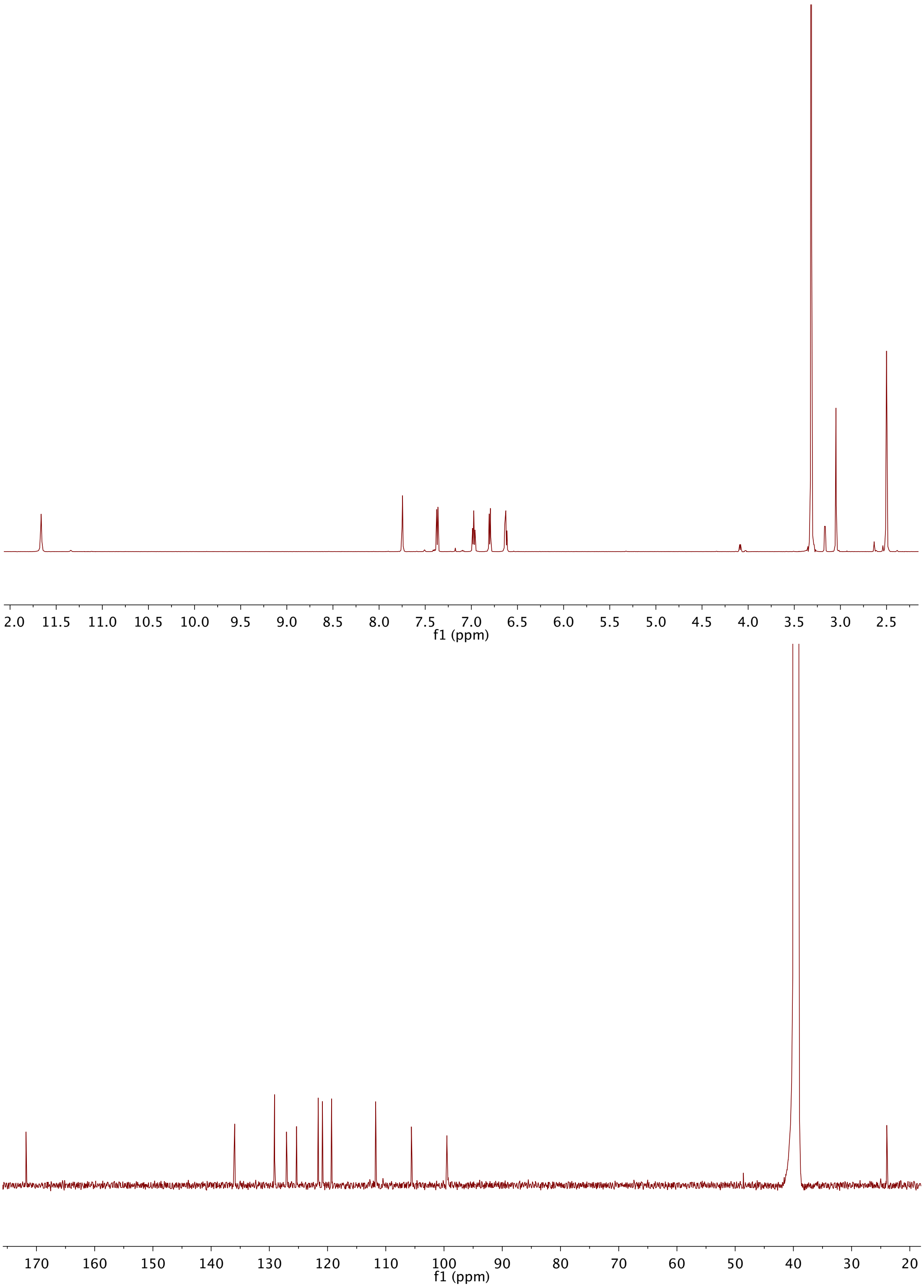

Figure S3. ^{1}H NMR (**top,** 600 MHz) and ^{13}C NMR (**bottom,** 150 MHz) of methylarcyriarubin (**1**) in DMSO-*d*$_6$.

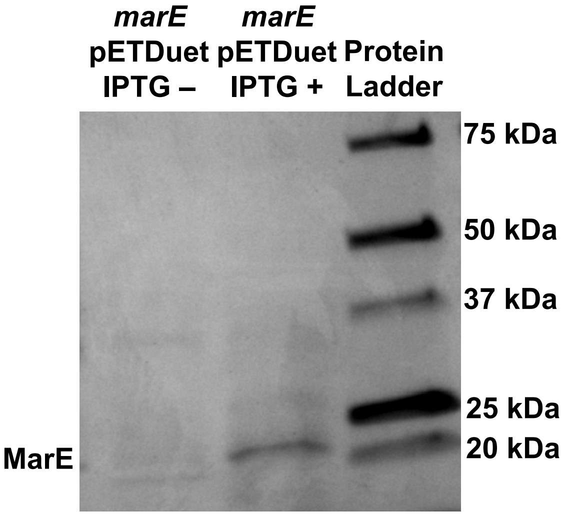

Figure S4. Soluble protein extract of *marE*/pETDuet harboring *E. coli* with or without IPTG induction (200 rpm, 37 °C, 2 hours after OD_{600} ~0.5). IPTG-dependent expression of a protein with the size corresponding to MarE (~22 kDa) is observed.