### **Electronic Supplementary Information**

# Guanidyl modification of the 1-azabicyclo[3.1.0]hexane ring in ficellomycin essential for its biological activity

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Oligonualaatida	Sequence	Description
Oligonucleotide	(Restriction enzyme sites are underlined)	(Restriction enzyme)
∆ <i>fic15</i> UpFw		gene deletion
	5-IGC <u>ICIAGAAAGCII</u> CACCICGICGGCCGICAC-3	(XbaI and HindIII)
∆ <i>fic15</i> UpRv	5'-CCG <u>GAATTC</u> GCTGGCCGAGGCGATCCA-3'	gene deletion (EcoRI)
∆ <i>fic15</i> DnFw	5'-CCG <u>GAATTC</u> GACTCGTGACCGGTGGGT-3'	gene deletion (EcoRI)
∆ <i>fic15</i> DnRv	5'-CCC <u>AAGCTT</u> GGCTCGCCGACGACATCG-3'	gene deletion (HindIII)
		gene complementation
∆ <i>fic15</i> compFw	5'- CUC <u>AAGUII</u> CGUGGUUGGUUGIGAGA-3'	(HindIII)
		gene complementation
Δ <i>fic15</i> compRv	5'-IGC <u>ICTAGA</u> CGCICAACGGACGGGCIC- <i>3</i> '	(XbaI)
∆ <i>fic15</i> checkFw	5'-GGCCGGACACGCCGAGTA-3'	colony PCR
∆ <i>fic15</i> checkRv	5'-TACCGGGCTGCCGGAATG-3'	colony PCR
		gene deletion
∆ <i>fic16</i> UpFw	5'-IGC <u>ICTAGAAAGCTI</u> CGCGAGCCGIICCIGGII-3'	(XbaI and HindIII)
∆ <i>fic16</i> UpRv	5'-CCG <u>GAATTC</u> GGCTGACCGGAAACCGAC-3'	gene deletion (EcoRI)
∆ <i>fic16</i> DnFw	5'-CCG <u>GAATTC</u> CATGGCGTGGTTCACCCT-3'	gene deletion (EcoRI)
Δ <i>fic16</i> DnRv	5'-CCC <u>AAGCTT</u> CTGCAGACCCTGCCCCTG-3'	gene deletion (HindIII)
		gene complementation
∆ <i>fic16</i> compFw	5'-CCC <u>AAGCTT</u> CCCCGTGAACCACATGCG-3'	(HindIII)
		gene complementation
Δ <i>fic16</i> compRv	5'-IGC <u>ICTAGA</u> CGGICAGCCCAGCACGIC-3'	(XbaI)
∆ <i>fic16</i> checkFw	5'-CGGGGACTCGTGACCGGT-3'	colony PCR
∆ <i>fic16</i> checkRv	5'-ATCCTCACCGCCGAGCCG-3'	colony PCR
∆ <i>fic22</i> UpFw	5'-CCC <u>AAGCTT</u> GTACGGGCCGGTGGTCGC-3'	gene deletion (HindIII)
∆ <i>fic22</i> UpRv	5'-CGG <u>ACTAGT</u> ATCGTGGCGCTGAGCCCG-3'	gene deletion (SpeI)
∆ <i>fic22</i> DnFw	5'-CGG <u>ACTAGT</u> CATGTGAGGTGTCCTTTC-3'	gene deletion (SpeI)
∆ <i>fic22</i> DnRv	5'-CCC <u>AAGCTT</u> GGCTACCCCTGGACCGTG-3'	gene deletion (HindIII)
Δ <i>fic22</i> compFw		gene complementation
	5'-CCC <u>AAGCTT</u> AGGAACACCTCGTCGACC-3'	(HindIII)
		gene complementation
∆ <i>fic22</i> compRv	5'-CCC <u>AAGCTT</u> CTACTCCCCCAGTCCTC-3'	(XbaI)
∆ <i>fic22</i> checkFw	5'-GACCGCGTCGCAGTCCTC-3'	colony PCR
∆ <i>fic22</i> checkRv	5'-GTGACCGTCGAGGAGCAC-3'	colony PCR
	1	1

## Table S1. Oligonucleotides used in this study.

Fic13-pHis8Fw	5'-CGC <u>GGATCC</u> ATGAGTGATTTCGCAGGA-3'	overexpression (BamHI)
Fic13-pHis8Rv	5'-CCC <u>AAGCTT</u> CTACGGCTGGGCTGGCGG-3'	overexpression (HindIII)
Fic15-pHis8Fw	5'-CGC <u>GGATCC</u> ATGTCCATCGACGCCGTA-3'	overexpression (BamHI)
Fic15-pHis8Rv	5'-CCC <u>AAGCTT</u> TCAACGGACGGGCTCGGT-3'	overexpression (HindIII)
Fic16-pHis8Fw	5'-CGC <u>GGATCC</u> ATGAACCCGACCCCGGAC-3'	overexpression (BamHI)
Fic16-pHis8Rv	5'-CCC <u>AAGCTT</u> TCAGCCCAGCACGTCGGC-3'	overexpression (HindIII)
Fic36-pHis8Fw	5'-CGC <u>GGATCC</u> ATGAGCCTGGTCAATGTC-3'	overexpression (BamHI)
Fic36-pHis8Rv	5'-CCC <u>AAGCTT</u> CTACCGGTAGGTGGCGAG-3'	overexpression (HindIII)

(Solvent: d6-DMSO, <sup>1</sup> H NMR: 600 MHz, <sup>13</sup> C NMR: 150 MHz)					
	$\delta_{\mathrm{C}}$	$\delta_{\mathrm{H}}$	$(m, J_H \text{ in Hz})$		
1	168.9				
2	59.0	4.23	(dd, 3.2, 6.6)		
3	60.4	4.15	(ddd, 3.3, 8.1, 11.5)		
4a	31.1	2.75	(dd, 11.9, 18.0)		
4b		1.82	(dd, 7.8, 18.1)		
5	211.0				
6	41.7	2.33	(dd, 2.3, 6.3)		
7a	28.1	2.20	(d, 2.2)		
7b		1.71	(d, 6.4)		
N8		9.77	(d, 6.7)		
9	148.0				
10	117.3	7.29	(d, 9.8)		
11	130.4	8.18	(dd, 2.7, 9.7)		
12	134.8				
13	124.3	8.86	(d, 2.8)		
14	130.1				

#### Table S2. Characterization of 2-DNP

NMR chemical shift

 $\frac{\text{Optical rotation}}{[\alpha]_D^{28} = -6.9 \text{ (c } 0.0034 \text{, water)}}$ 



Fig. S1 Structure determination of 2-DNP. (a) The key correlations of HMBC and double quantum filtered-COSY (DQF-COSY) are shown. (b)(c) The relative stereochemistry of 2-DNP. The key correlations of NOESY are shown in the part of structure containing (b) the azabicyclo hexane ring or (c) DNP unit, respectively.

Ο

Н

 $\Gamma_{13}$ H

3

 $\dot{R}_2$ 

















Fig. S8 MS/MS analysis of 1. The m/z values with 98 and 80 of the azabicyclo hexane ring-containing fragments indicated the presence and absence of the hydroxy group at the C4 position of the ring.



**Fig. S9** SDS-PAGE of Fic13, Fic16, Fic36, and Fic15. All enzymes were purified with proposed mass of 28, 45, 41, and 49 kDa, respectively.



**Fig. S10** LC-MS analysis of the *in vitro* reaction mixture for Fic13. EIC chromatograms for 1 and 2 (m/z 173.09 [M + H]<sup>+</sup> and m/z 171.08 [M + H]<sup>+</sup>) are shown.



**Fig. S11** LC-MS analysis of the *in vitro* reaction mixture for Fic16 using various amino acids as substrates. EIC chromatograms for **2**  $(m/z \ 171.08 \ [M + H]^+)$  are shown.



**Fig. S12** LC-MS analysis of the *in vitro* coupling reaction mixture of Fic16 and Fic36. EIC chromatograms for 4-DNP (m/z 380.13 [M+H]<sup>+</sup>) are shown.



Fig. S13 MS/MS analysis of 4-DNP. The m/z value of 60 was annotated as the guanidyl unit and those of 139 and 80 of the azabicyclo hexane ring-containing fragments indicated the presence and absence of the guanidyl unit at the C4 position of the ring. The m/z volume of 222 was comparable to the fragment with the DNP unit at the  $\alpha$ -amino group.



**Fig. S14** Metabolite analysis of *S. ficellus*  $\Delta fic15$ . Extracted ion count (EIC) chromatograms for ficellomycin (m/z 313.20 [M + H]<sup>+</sup>) is shown.