

*Supplementary Files*

# Citrinin Monomer and Dimer Derivatives with Antibacterial and Cytotoxic Activities Isolated from the Deep Sea-Derived Fungus *Penicillium citrinum* NLG-S01-P1

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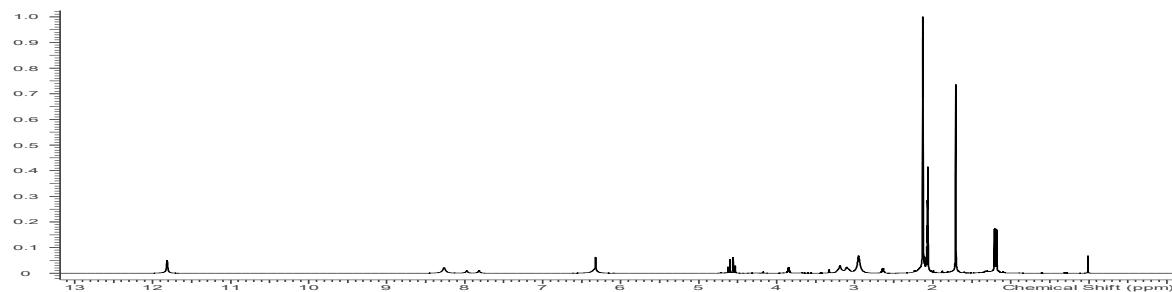


Figure S1.  $^1\text{H}$  NMR spectrum of compound 1

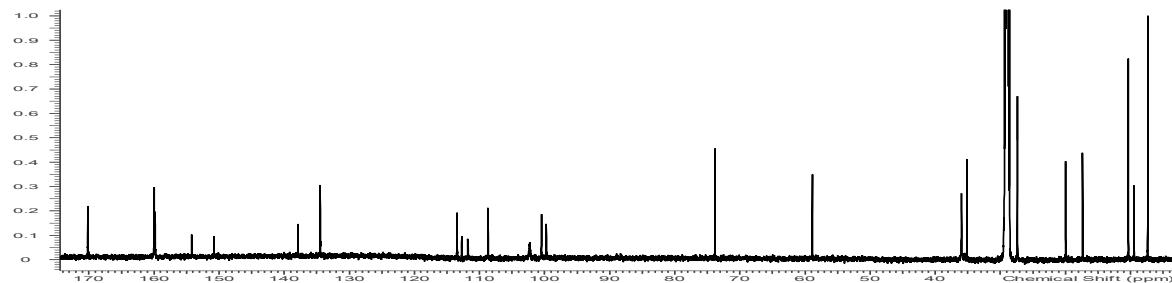


Figure S2.  $^{13}\text{C}$  NMR spectrum of compound 1

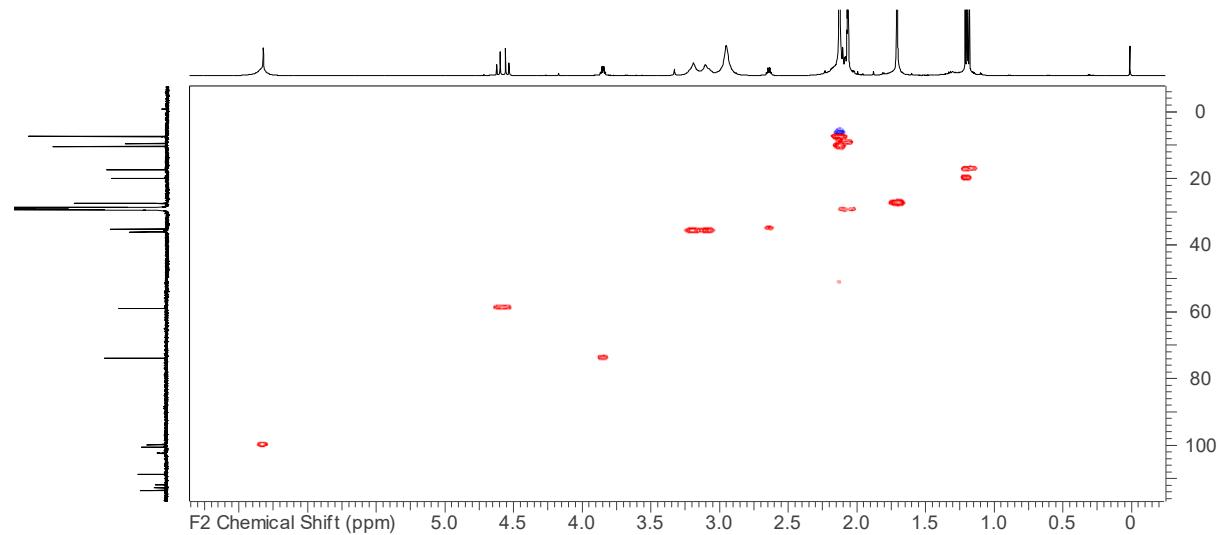


Figure S3. HSQC spectrum of compound 1

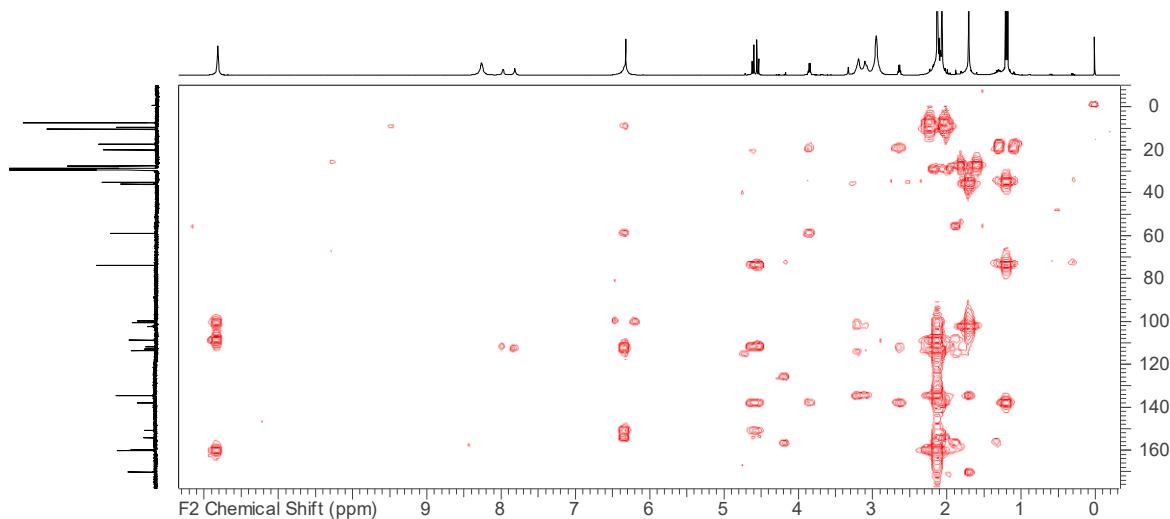


Figure S4. HMBC spectrum of compound 1

**Single Mass Analysis**

Tolerance = 15.0 mDa / DBE: min = -1.5, max = 50.0

Element prediction: Off

Number of isotope peaks used for i-FIT = 3

Mass	Calc. Mass	mDa	PPM	DBE	Formula	i-FIT	i-FIT Norm	Fit Conf %	C	H	N	O	N...
427.1747	427.1748	-0.1	-0.2	-0.5	C <sub>8</sub> H <sub>27</sub> N <sub>8</sub> O <sub>12</sub>	1119.4	5.363	0.47	8	27	8	12	
	427.1746	0.1	0.2	13.5	C <sub>23</sub> H <sub>24</sub> N <sub>4</sub> O <sub>3</sub> ...	1117.1	3.060	4.69	23	24	4	3	1
	427.1748	-0.1	-0.2	10.5	C <sub>6</sub> H <sub>15</sub> N <sub>22</sub> O <sub>2</sub>	1120.6	6.582	0.14	6	15	22	2	
	427.1751	-0.4	-0.9	6.5	C <sub>8</sub> H <sub>20</sub> N <sub>16</sub> O <sub>4</sub> ...	1119.8	5.810	0.30	8	20	16	4	1
	427.1743	0.4	0.9	17.5	C <sub>21</sub> H <sub>19</sub> N <sub>10</sub> O	1117.6	3.600	2.73	21	19	10	1	
	427.1738	0.9	2.1	1.5	C <sub>7</sub> H <sub>24</sub> N <sub>12</sub> O <sub>8</sub> ...	1119.7	5.630	0.36	7	24	12	8	1
	427.1757	-1.0	-2.3	11.5	C <sub>24</sub> H <sub>27</sub> O <sub>7</sub>	1116.7	2.696	6.75	24	27	7		
	427.1735	1.2	2.8	5.5	C <sub>5</sub> H <sub>19</sub> N <sub>18</sub> O <sub>6</sub>	1120.1	6.076	0.23	5	19	18	6	

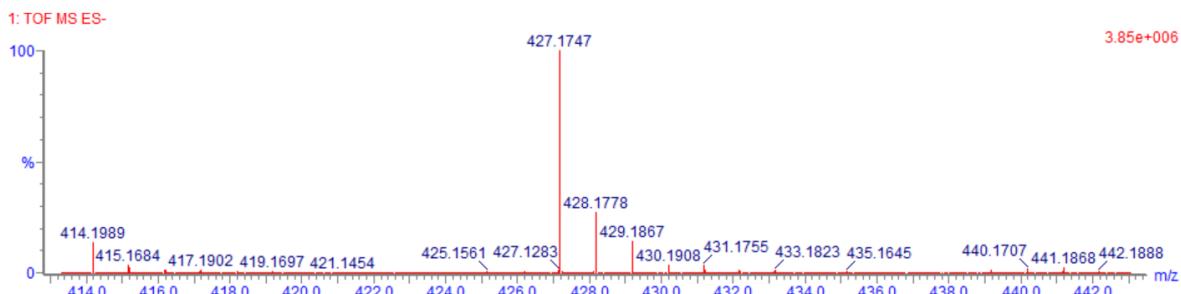


Figure S5. HRESIMS spectrum of compound 1

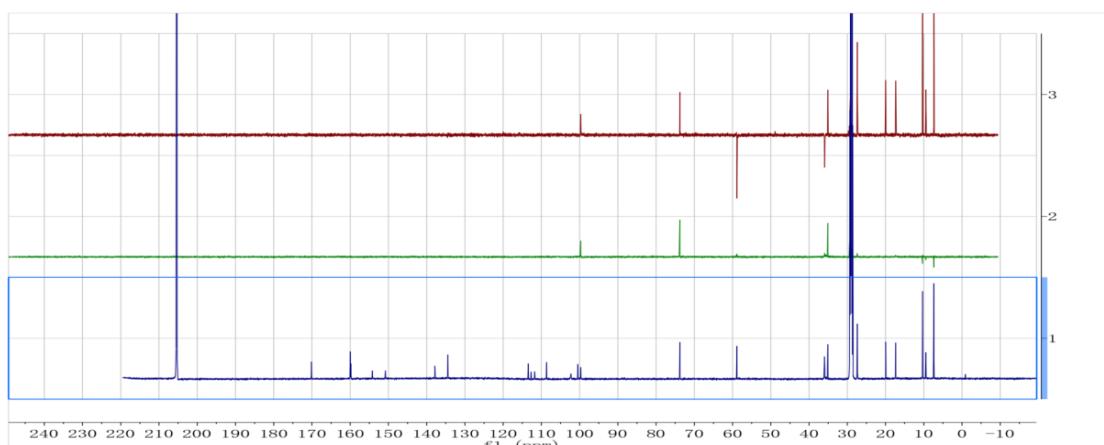


Figure S6. <sup>13</sup>C/DEPT spectrum of compound 1

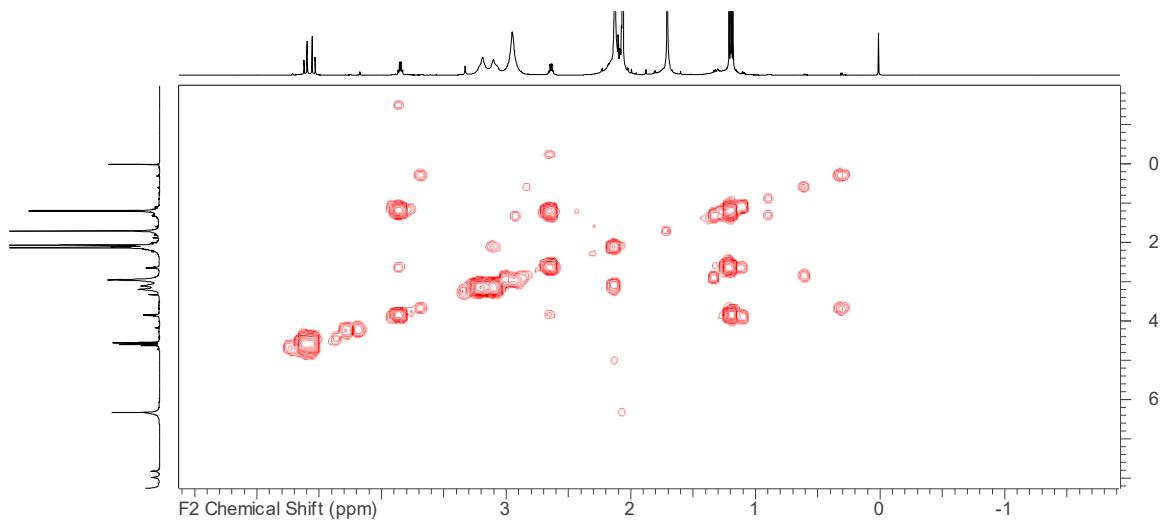


Figure S7. <sup>1</sup>H-<sup>1</sup>H COSY spectrum of compound 1

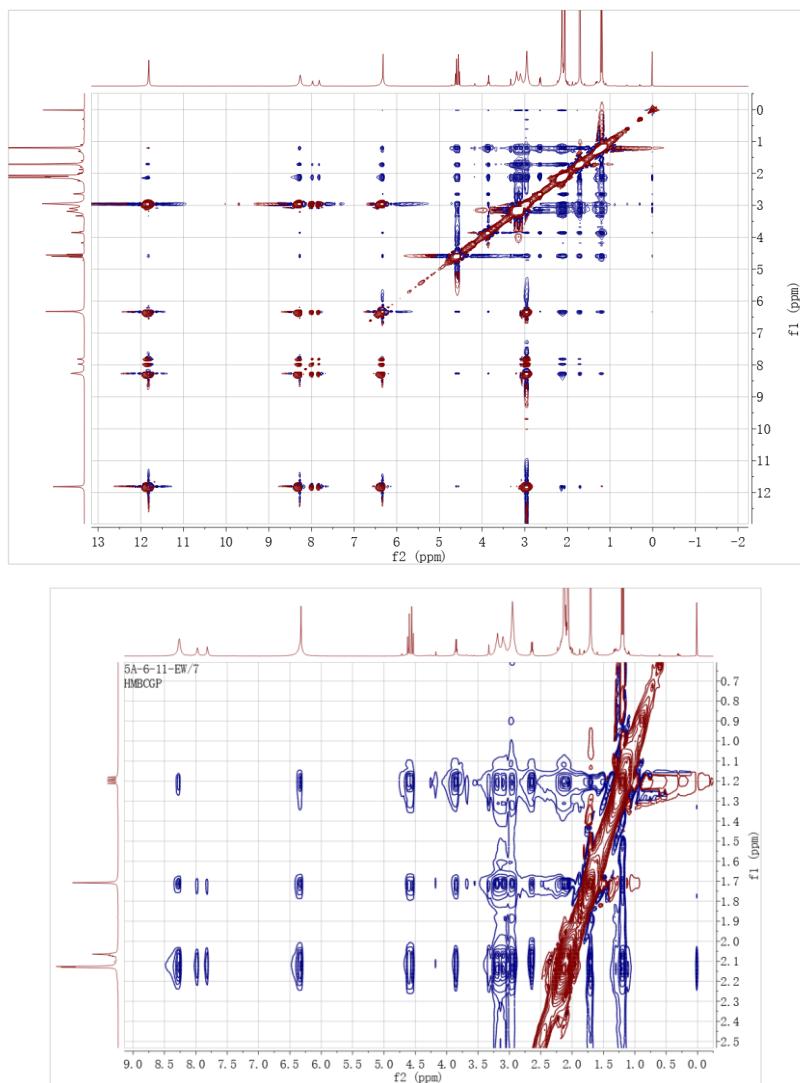


Figure S8. NOESY spectrum of compound 1

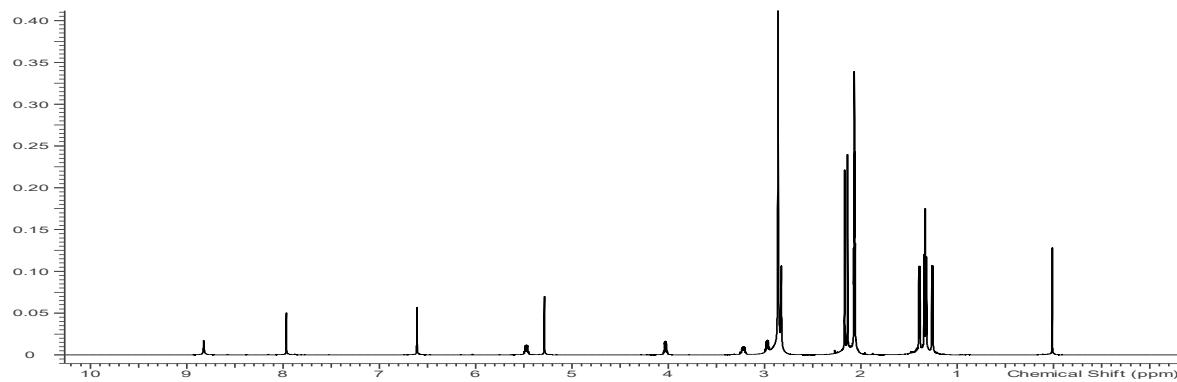


Figure S9. <sup>1</sup>H NMR spectrum of compound 2

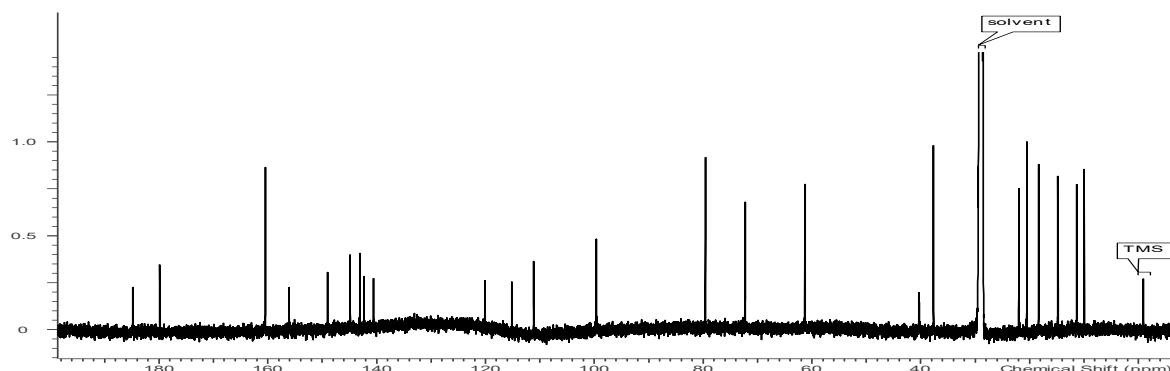


Figure S10. <sup>13</sup>C NMR spectrum of compound 2

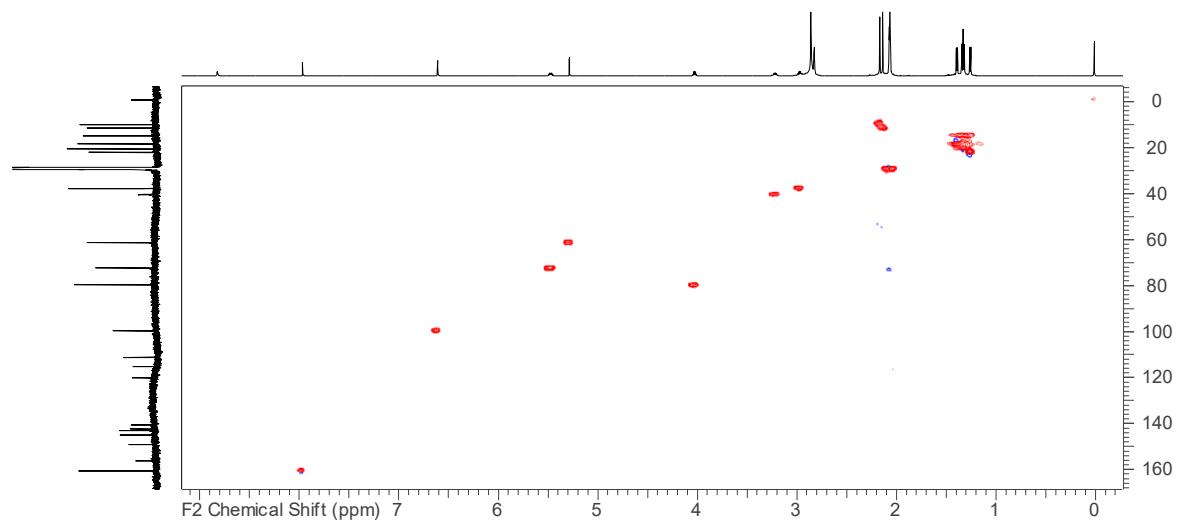


Figure S11. HSQC spectrum of compound 2

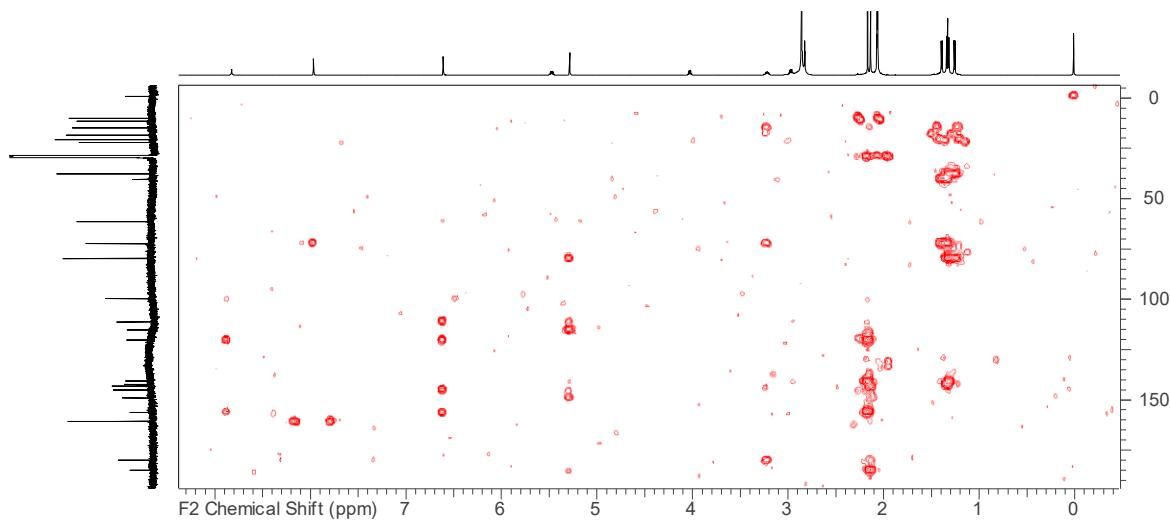


Figure S12. HMBC spectrum of compound 2

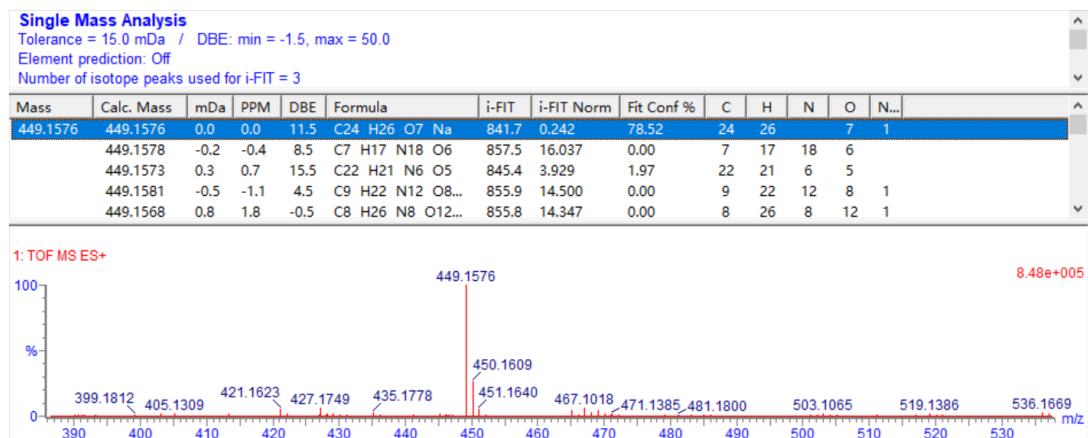


Figure S13. HRESIMS spectrum of compound 2

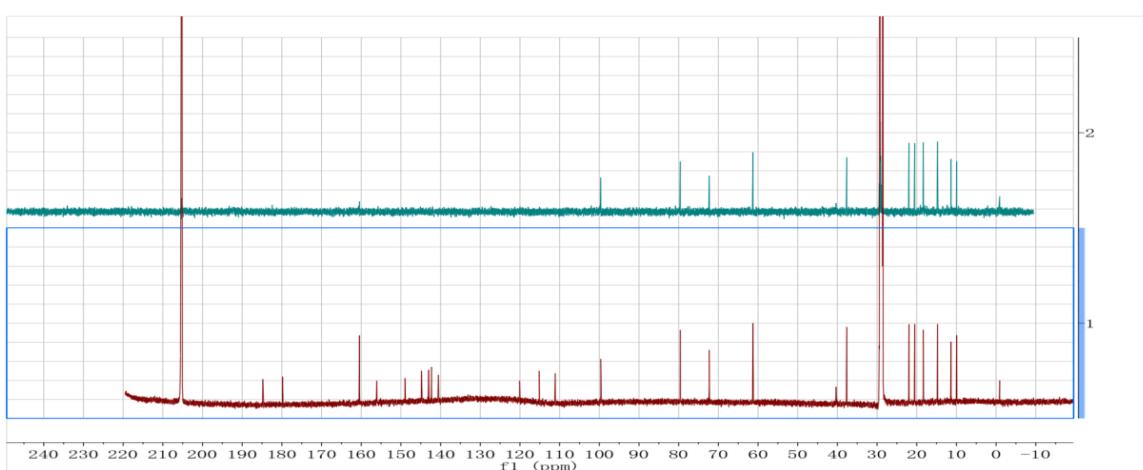


Figure S14. <sup>13</sup>C/DEPT spectrum of compound 2

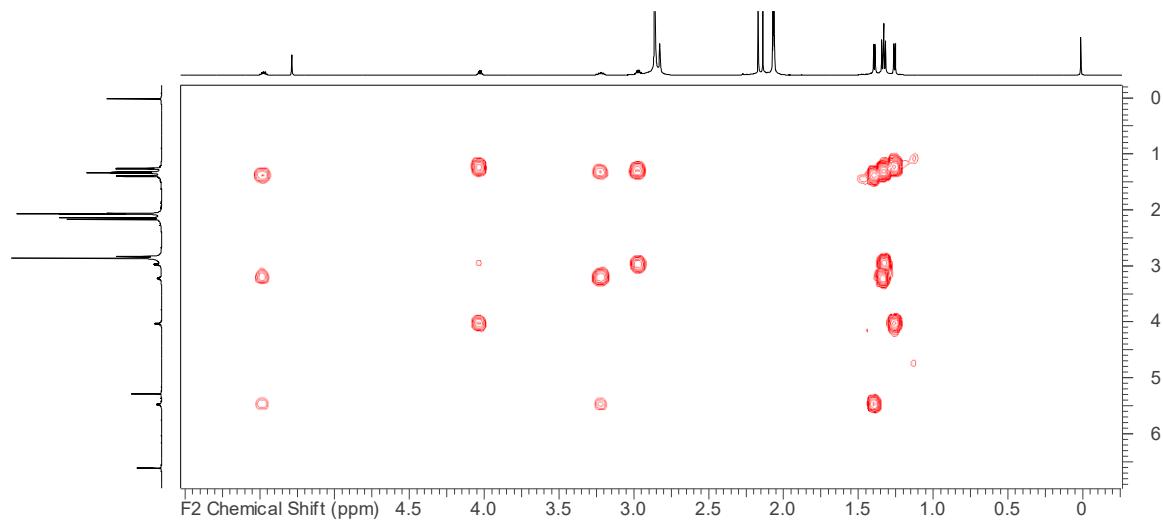


Figure S15. <sup>1</sup>H-<sup>1</sup>H COSY spectrum of compound 2

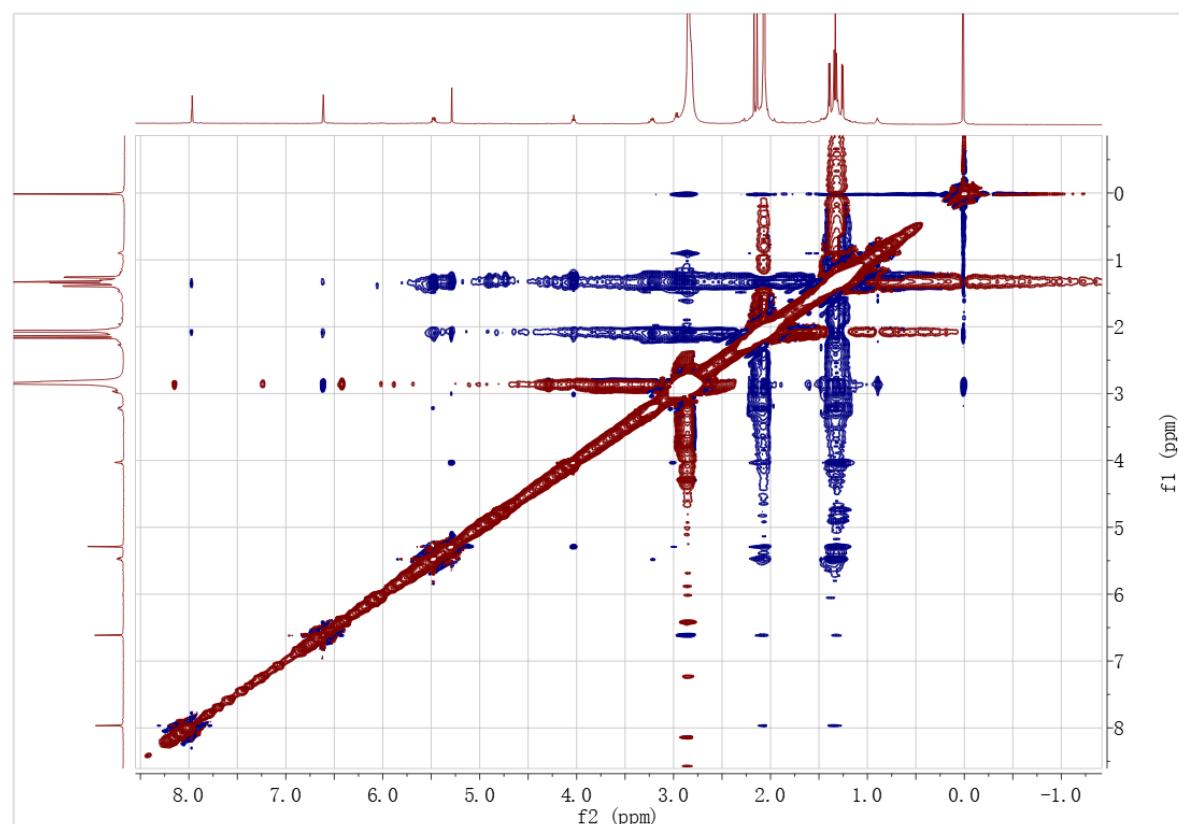


Figure S16. NOESY spectrum of compound 2

Table S1. Gibbs free energies <sup>a</sup> and equilibrium populations <sup>b</sup> of low-energy conformers of (*3S, 4R, 3'R*)-1

configuration	conformer	structure	$\Delta G$ (kcal/mol)	Percent
(3 <i>S, 4R, 3'R</i> )-1	a		0.00000	29.29%
	b		0.00188	29.20%
	c		0.24221	19.46%
	d		0.24472	19.38%
	e		1.41815	2.67%

<sup>a</sup> B3LYP/6-31G(d), in kcal/mol. <sup>b</sup> From  $\Delta G$  values at 298.15 K.

Table S2. Gibbs free energies <sup>a</sup> and equilibrium populations <sup>b</sup> of low-energy conformers of (*3S, 4R, 3'S*)-1

configuration	conformer	structure	$\Delta G$ (kcal/mol)	Percent
(3 <i>S, 4R, 3'S</i> )-1	a		0.00000	68.58%
	b		0.72037	20.31%
	c		1.28449	7.83%
	d		1.80155	3.27%

<sup>a</sup> B3LYP/6-31G(d), in kcal/mol. <sup>b</sup> From  $\Delta G$  values at 298.15 K.

Table S3. Gibbs free energies <sup>a</sup> and equilibrium populations <sup>b</sup> of low-energy conformers of (1*S*, 3*R*, 4*S*, 7'*S*, 8'*R*)-2

configuration	conformer	structure	$\Delta G$ (kcal/mol)	Percent
(1 <i>S</i> , 3 <i>R</i> , 4 <i>S</i> , 7' <i>S</i> , 8' <i>R</i> )-2	a		0.00000	58.25%
	b		0.72727	17.06%
	c		0.86783	13.45%
	d		1.50851	4.56%
	e		1.69174	3.35%
	f		1.69362	3.33%

<sup>a</sup> B3LYP/6-31G(d), in kcal/mol. <sup>b</sup> From  $\Delta G$  values at 298.15 K.

Table S4. Gibbs free energies <sup>a</sup> and equilibrium populations <sup>b</sup> of low-energy conformers of (1*R*, 3*R*, 4*S*, 7'*S*, 8'*R*)-3

configuration	conformer	structure	$\Delta G$ (kcal/mol)	Percent
(1 <i>R</i> , 3 <i>R</i> , 4 <i>S</i> , 7' <i>S</i> , 8' <i>R</i> )-3	a		0.00000	48.79%
	b		0.78312	13.00%
	c		0.80696	12.49%
	d		0.80885	12.45%
	e		1.54930	3.56%
	f		1.55494	3.53%
	g		1.85740	2.12%
	h		1.85928	2.11%
	i		1.90572	1.95%

<sup>a</sup> B3LYP/6-31G(d), in kcal/mol. <sup>b</sup> From  $\Delta G$  values at 298.15 K.

Text S1. ITS1-5.8S-ITS2 rDNA sequence of strain NLG-S01-P1

LOCUS Seq1 487 bp DNA linear PLN 05-DEC-2018  
DEFINITION *Penicillium citrinum* NLG-S01-P1 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.  
ACCESSION Seq1  
VERSION  
KEYWORDS .  
SOURCE *Penicillium citrinum*  
ORGANISM *Penicillium citrinum*  
Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;  
Eurotiomycetes; Eurotiomycetidae; Eurotiales; Aspergillaceae;  
*Penicillium*.  
REFERENCE 1 (bases 1 to 487)  
AUTHORS Wang,W.  
TITLE Citrinin Monomer and Dimer Derivatives with Antibacterial and Cytotoxic Activities Isolated from the Deep Sea Derived Fungus *Penicillium citrinum* NLG-S01-P1  
JOURNAL unpublished  
REFERENCE 2 (bases 1 to 487)  
AUTHORS Wang,W.  
TITLE Direct Submission  
JOURNAL Submitted (05-DEC-2018) Key Laboratory of Marine Biogenetic Resources, Third Institute of Oceanography, State Oceanic Administration, 178 Daxue Road, Xiamen, Fujian 361005, China  
COMMENT Bankit Comment: ALT EMAIL:wywang\_cas@163.com  
Bankit Comment: TOTAL # OF SEQS:1  
##Assembly-Data-START##  
Sequencing Technology :: Sanger dideoxy sequencing  
##Assembly-Data-END##  
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/isolation\_source="seawater"  
/bio\_material="Penicillium citrinum"  
/db\_xref="taxon:5077"  
/collected\_by="Yanping Hou"  
/identified\_by="Weiyi Wang"  
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61 catacgctcg aggaccggac gcgggtgccgc cgctgcctt cgggcccgtc ccccccggcgg  
121 gggggacggg gcccaacaca caagccggc ttgagggcag caatgacgct cggacaggca  
181 tgccctccgg aataccagag ggcgcaatgt gcgttcaaag actcgatgtatcactgaatt  
241 ctgcaattca cattagttat cgcatatcg tgcgttcttc atcgatccg gaaccaagag  
301 atccgttgtt gaaagttta actaatttc ttataggctc cagactgcaa ctccagacag  
361 cggtcagggg ggccgtccgc gggcgccccccc cccggcagg caacatagggt tcgggcaaca  
421 cgggggggag gttggccccc gagggcccg cactcgtaa tgatcctcc gcagggtcac  
481 ctacgga

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