

## SUPPLEMENTARY INFORMATION

### Insights into the ecological role of *Pseudomonas* spp. in an ant-plant symbiosis

Taise T. H. Fukuda<sup>1†</sup>; Camila F. Pereira<sup>1†</sup>; Weilan G. P. Melo<sup>1</sup>; Carla Menegatti<sup>1</sup>; Paulo H. M. Andrade<sup>2</sup>; Milton Groppo<sup>3</sup>; Paulo T. Lacava<sup>2</sup>; Cameron R. Currie<sup>4</sup>; Mônica T. Pupo<sup>1\*</sup>

<sup>†</sup>These authors contributed equally to this work.

<sup>1</sup>School of Pharmaceutical Sciences of Ribeirão Preto, University of São Paulo, Ribeirão Preto, SP, Brazil.

<sup>2</sup>Laboratory of Microbiology and Biomolecules, Department of Morphology and Pathology, Center of Biological Sciences and Health, Federal University of São Carlos, São Carlos, SP, Brazil

<sup>3</sup>Laboratory of Plant Systematics, Department of Biology, Faculty of Philosophy, Sciences and Letters at Ribeirão Preto, University of São Paulo, Ribeirão Preto, SP, Brazil

<sup>4</sup>Department of Bacteriology, University of Wisconsin-Madison, Madison, WI, USA.

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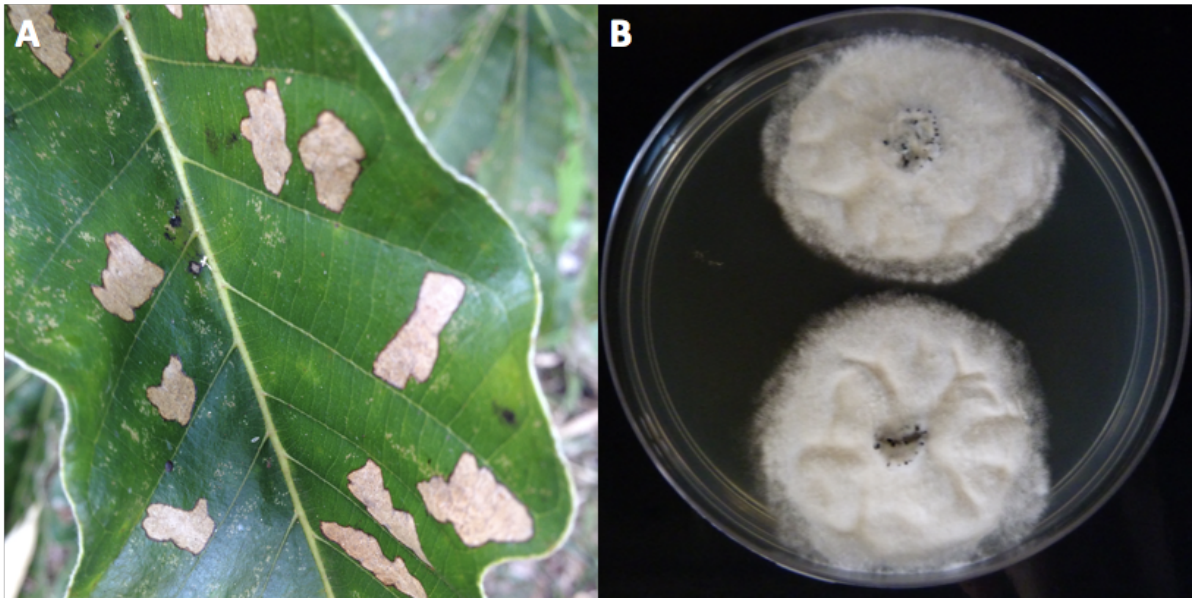
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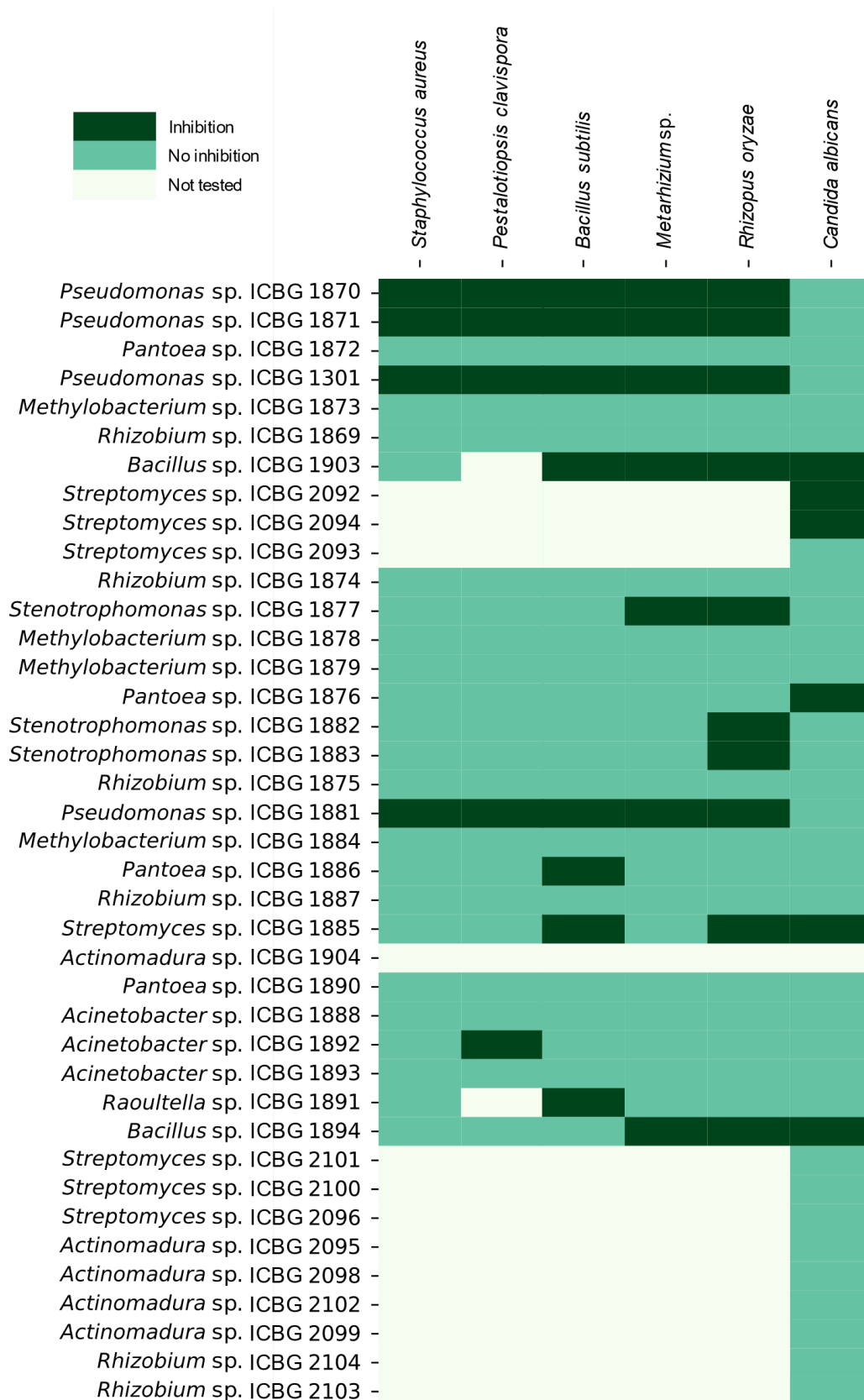
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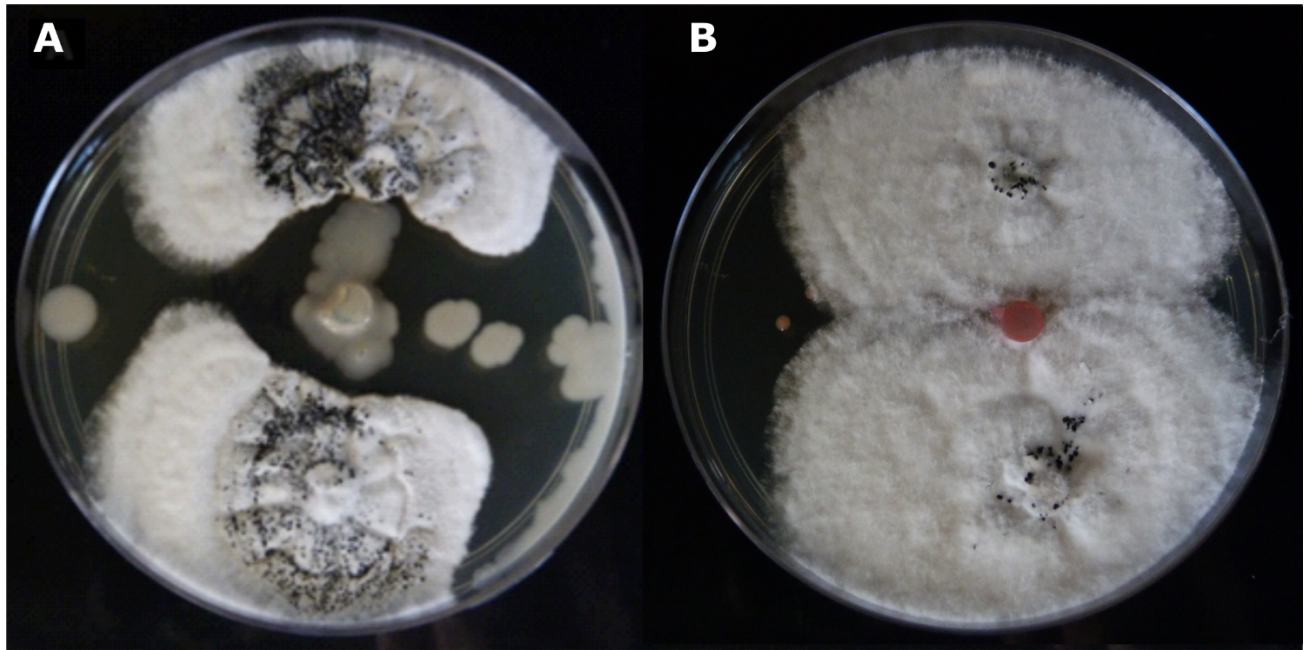
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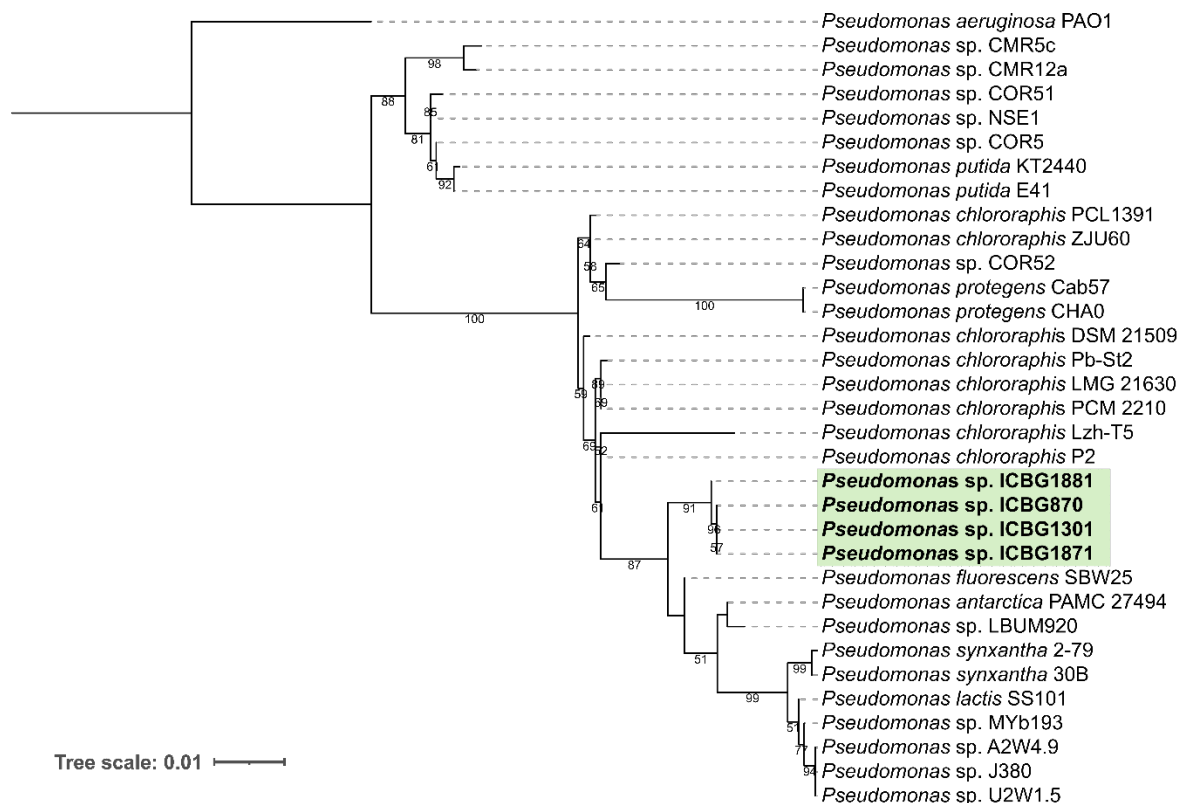
**Figure S1.** Isolation of the phytopathogen *Pestalotiopsis clavispora* from *Cecropia* leaves. **(A)** *Cecropia* sp. leaf contaminated with a fungal pathogen. **(B)** *P. clavispora* FB1 isolated from *Cecropia* sp.



**Figure S2.** Heatmap of the biological activity of *Cecropia-Azteca* microbial strains against human pathogens, phytopathogens and an entomopathogen.

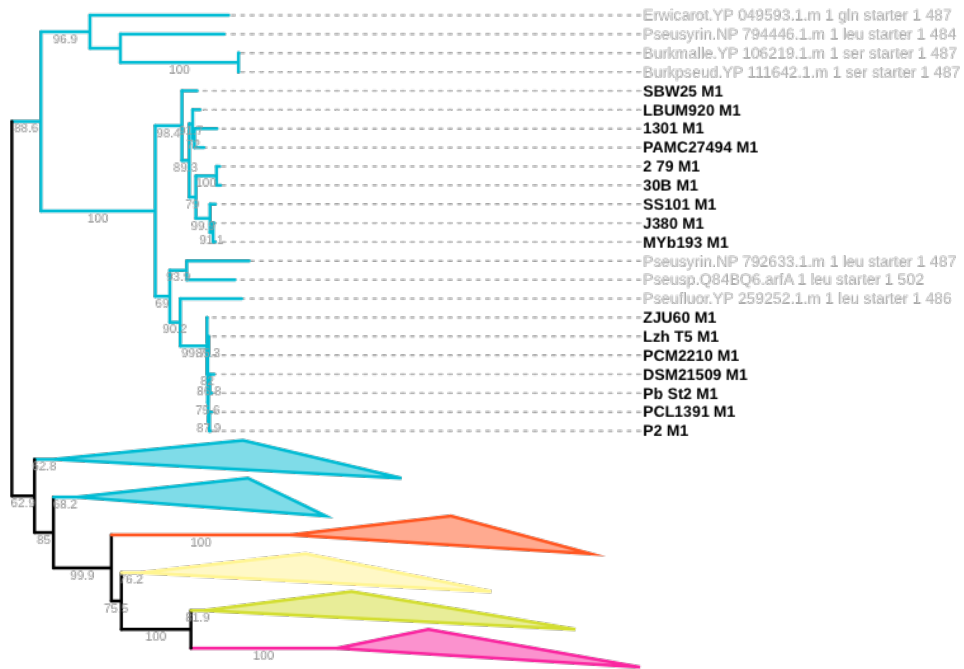


**Figure S3.** Antifungal activity of *Pseudomonas* sp. ICBG1870 against *Pestalotiopsis clavispora* FB1. **(A)** Inhibition zone of *Pseudomonas* sp. ICBG1870 against *P. clavispora*. **(B)** *Methylobacterium* sp. ICBG1884 against *P. clavispora*, negative control.

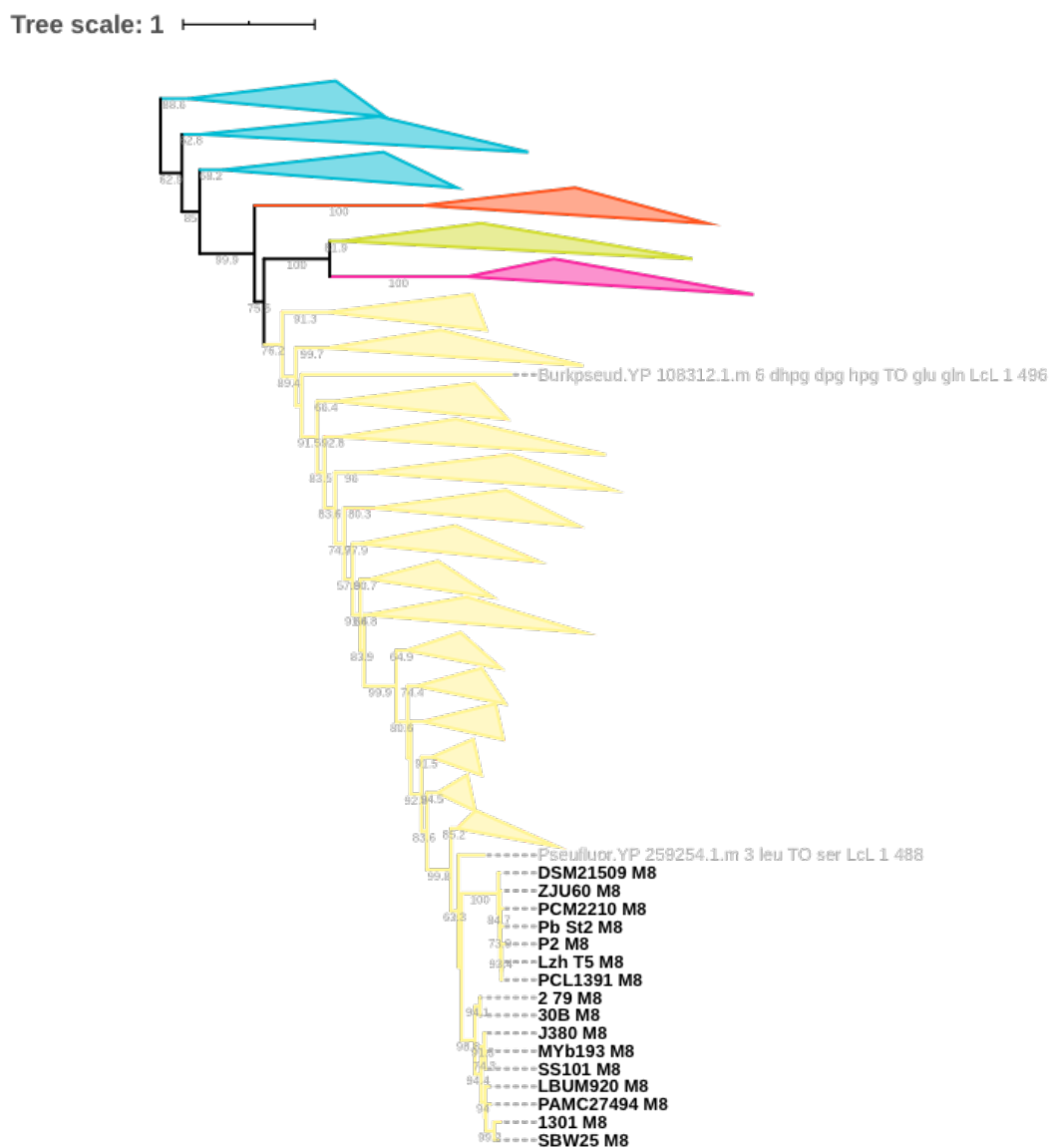


**Figure S4.** Phylogenetic analysis based on the 16S rRNA gene of viscosin-producers. The bootstrap support values are based on 1000 bootstrap replicates. The phylogeny was reconstructed using IQ-TREE, using the TPM3+F+R2 model of nucleotide substitution and including *P. aeruginosa* PAO1 as outgroup.

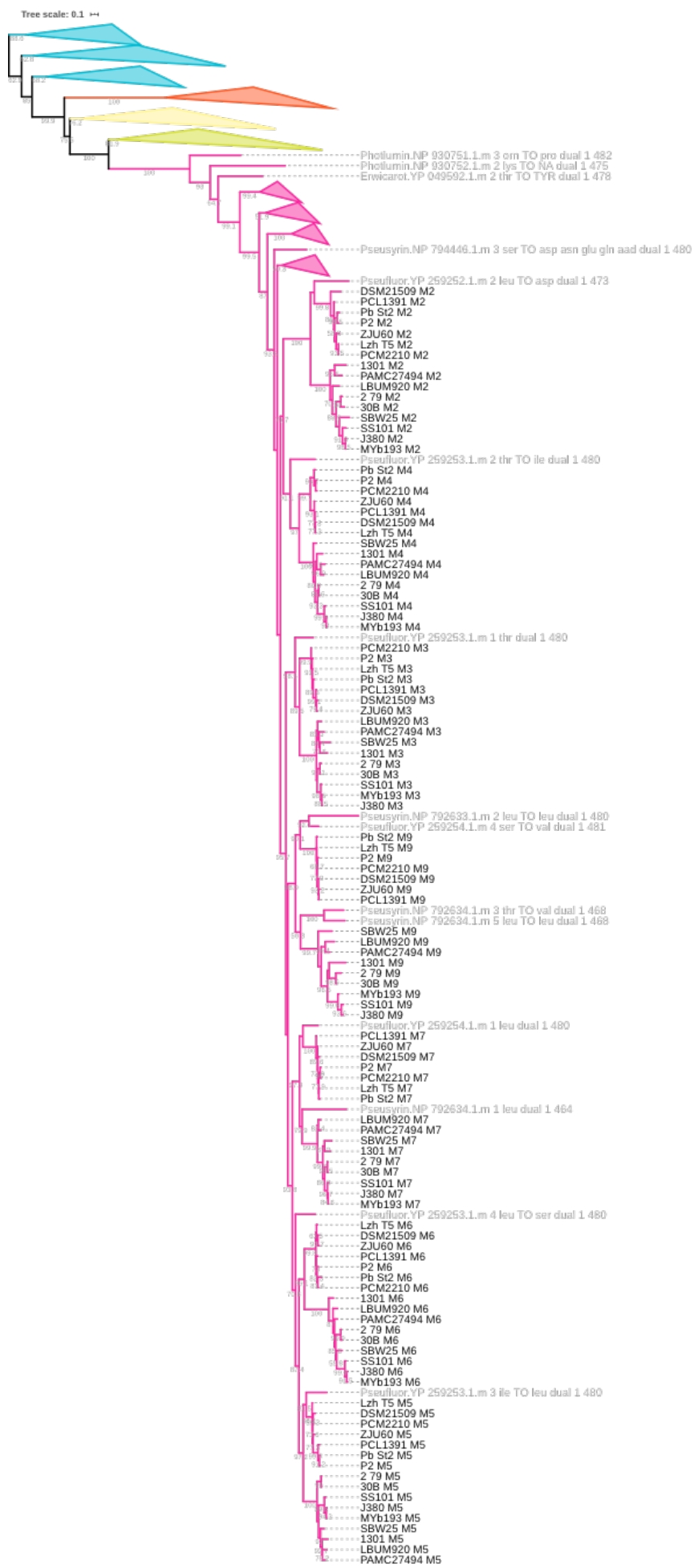
Tree scale: 1



**Figure S5.** Phylogeny of condensation domains. The phylogeny was reconstructed using IQ-TREE, using the LG+F+R10 amino acid substitution model. Support values are based on 1000 bootstrap replicas. Blue: clade that comprises  $C_{\text{starter}}$  modules; orange: Cyc; yellow: LCL; green: DCL; pink:  $C_{\text{dual}}$ . The clade that comprises the condensation domains of module 1 viscosins-producers is highlighted in bold. Other clades were collapsed.



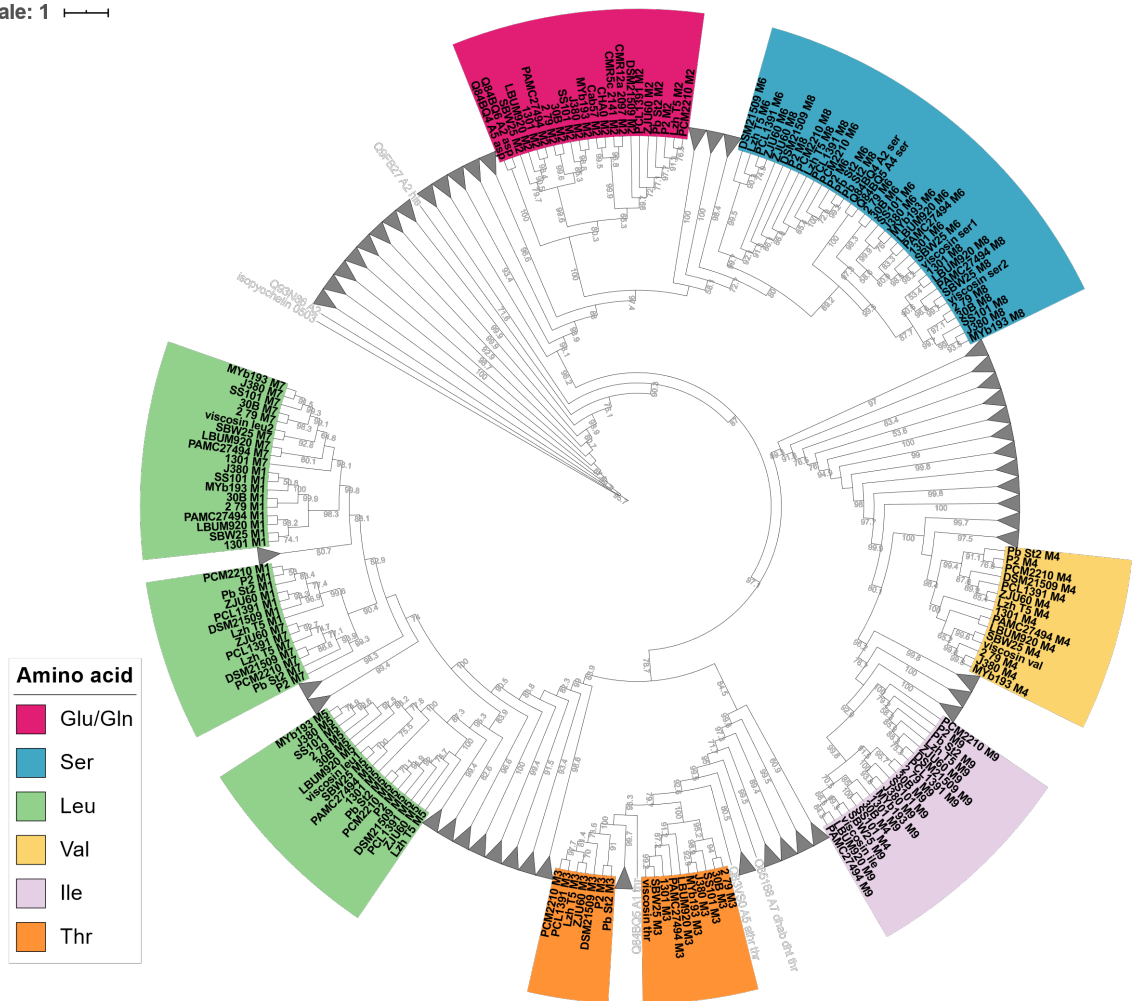
**Figure S6.** Phylogeny of condensation domains. The phylogeny was reconstructed using IQ-TREE, using the LG+F+R10 amino acid substitution model. Support values are based on 1000 bootstrap replicas. Blue: clade that comprises  $C_{\text{starter}}$  modules; orange:  $C_{\text{yc}}$ ; yellow: LCL; green: DCL; pink:  $C_{\text{dual}}$ . The clade that comprises the condensation domains of module 8 viscosins-producers is highlighted in bold. Other clades were collapsed.



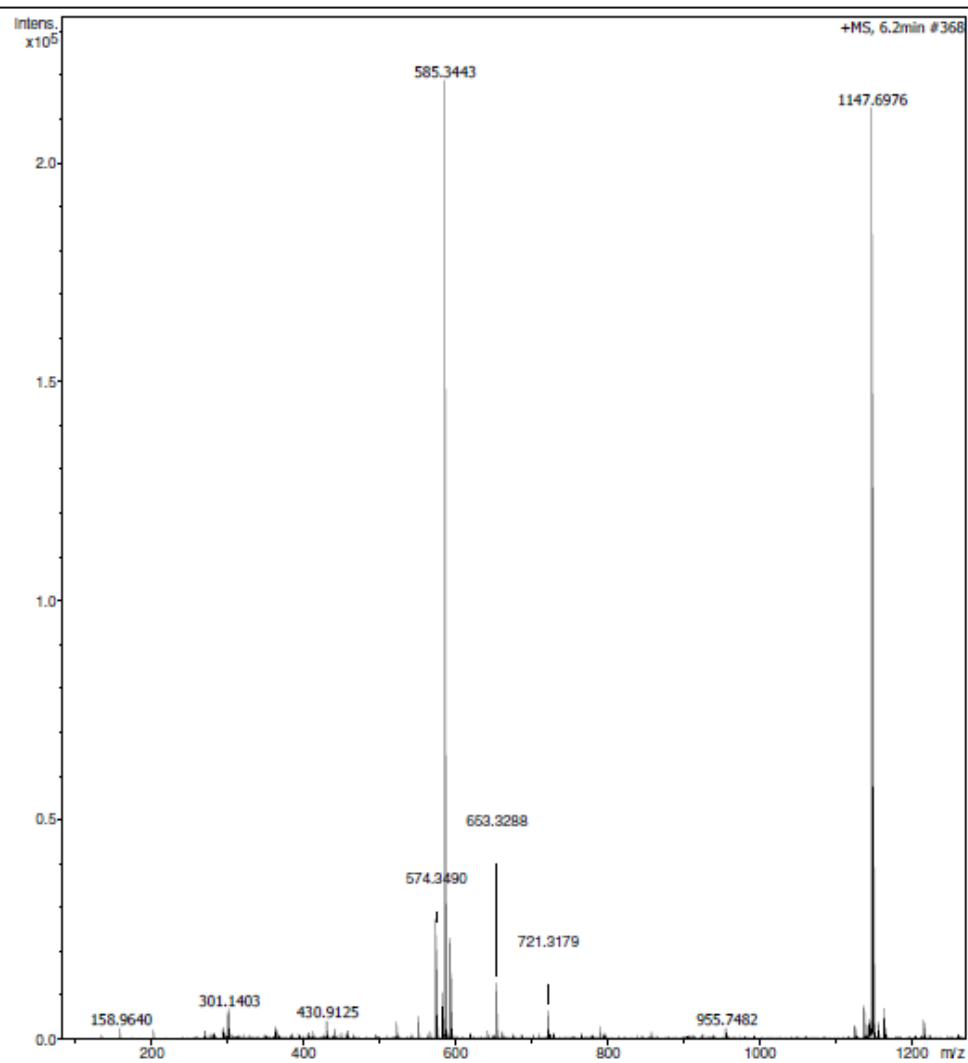


**Figure S7.** Phylogeny of condensation domains. The phylogeny was reconstructed using IQ-TREE, using the LG+F+R10 amino acid substitution model. Support values are based on 1000 bootstrap replicas. Blue: clade that comprises  $C_{\text{starter}}$  modules; orange: C<sub>yc</sub>; yellow: LCL; green: DCL; pink:  $C_{\text{dual}}$ . The clade that comprises the  $C_{\text{dual}}$  domains of viscosins-producers is highlighted in bold. Other clades were collapsed.

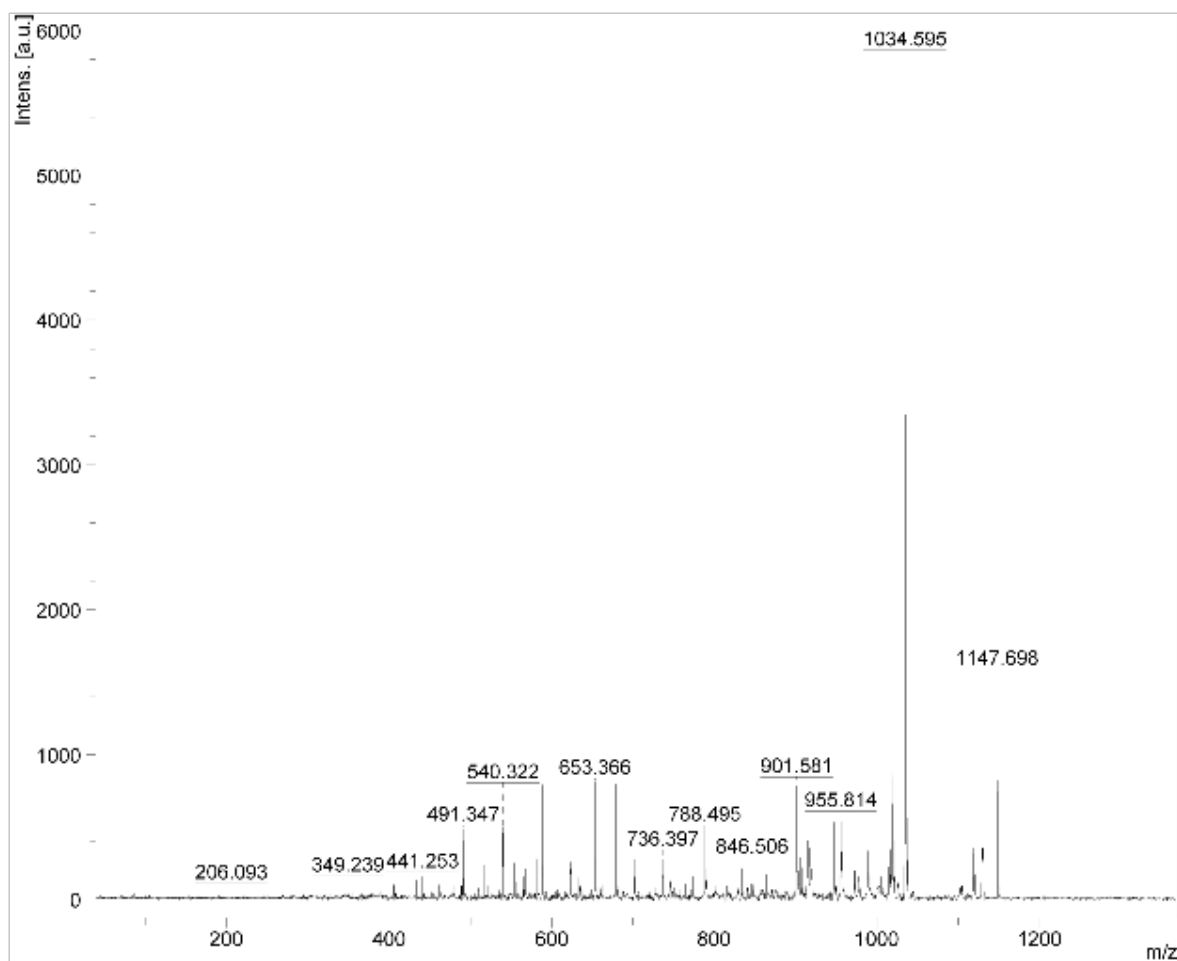
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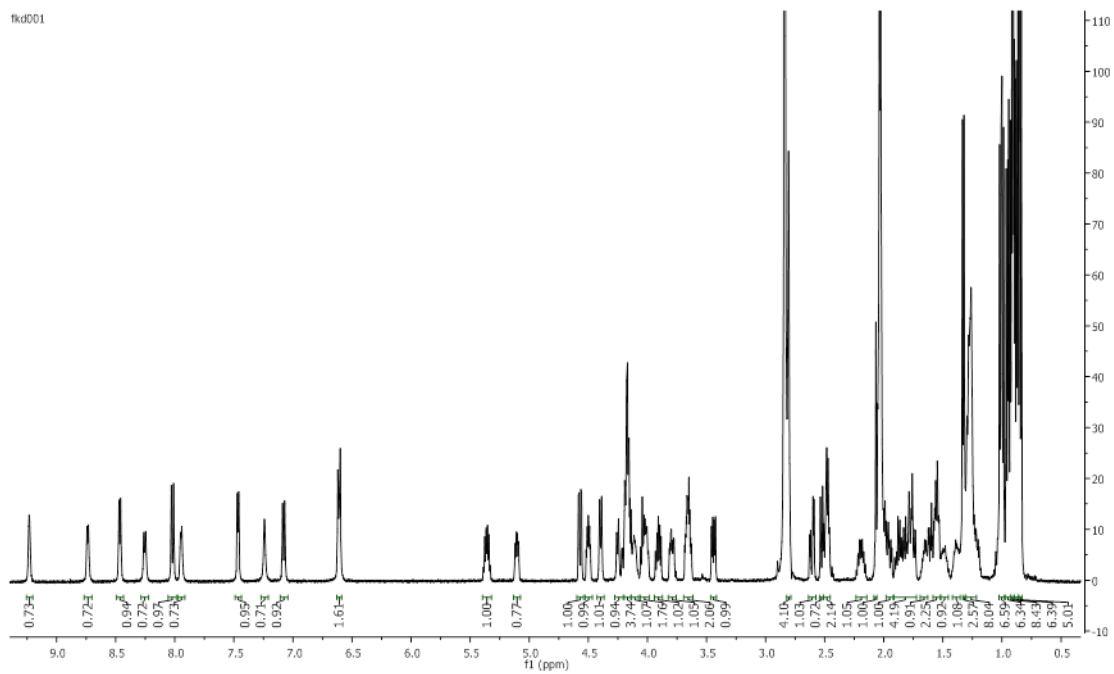
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**Figure S9.** HRESI-MS spectrum of viscosinamide.

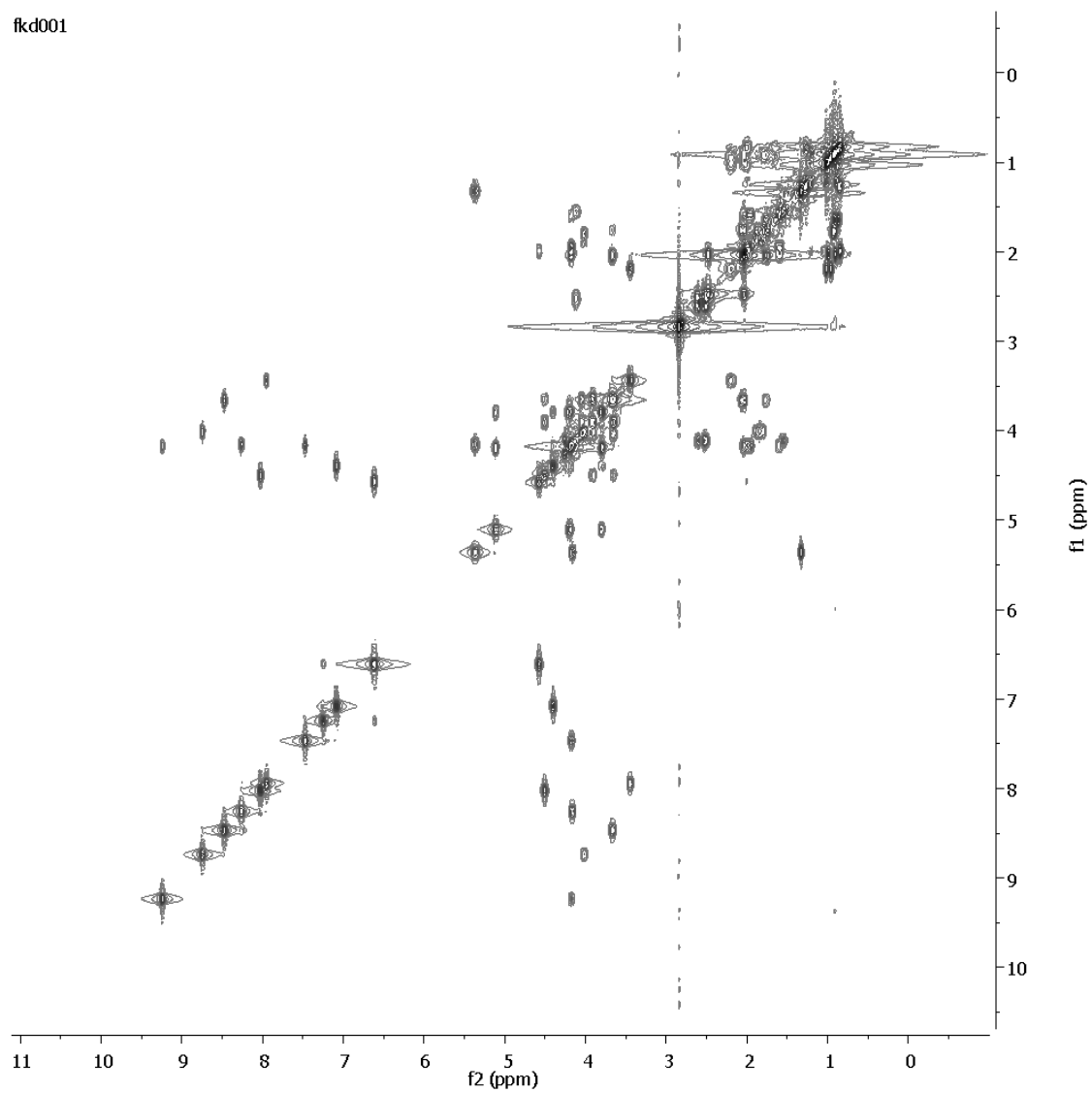


**Figure S10.** MALDI-MS/MS spectrum of viscosinamide.

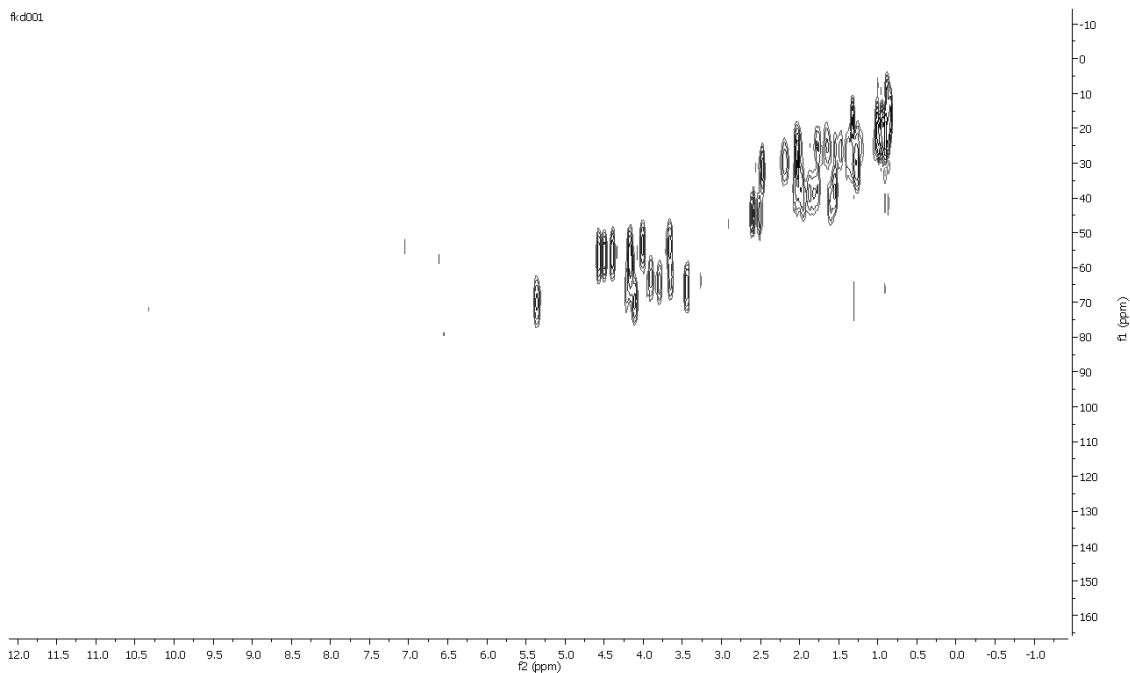


**Figure S11.**  $^1\text{H}$  NMR spectrum of viscosinamide ( $\text{CD}_3\text{COCD}_3$ , 500 MHz).

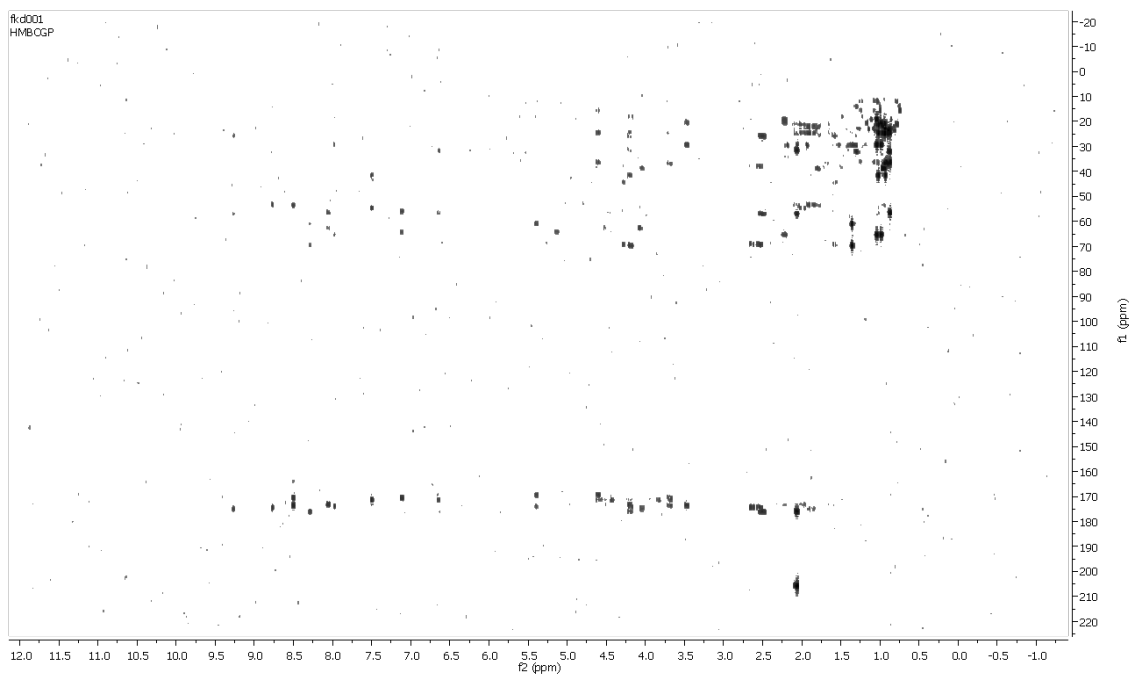
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**Figure S12.**  $^1\text{H}$ ,  $^1\text{H}$ -COSY spectrum of viscosinamide ( $\text{CD}_3\text{COCD}_3$ , 500 MHz).



**Figure S13.** gHSQC spectrum of viscosinamide ( $\text{CD}_3\text{COCD}_3$ , 500 MHz).



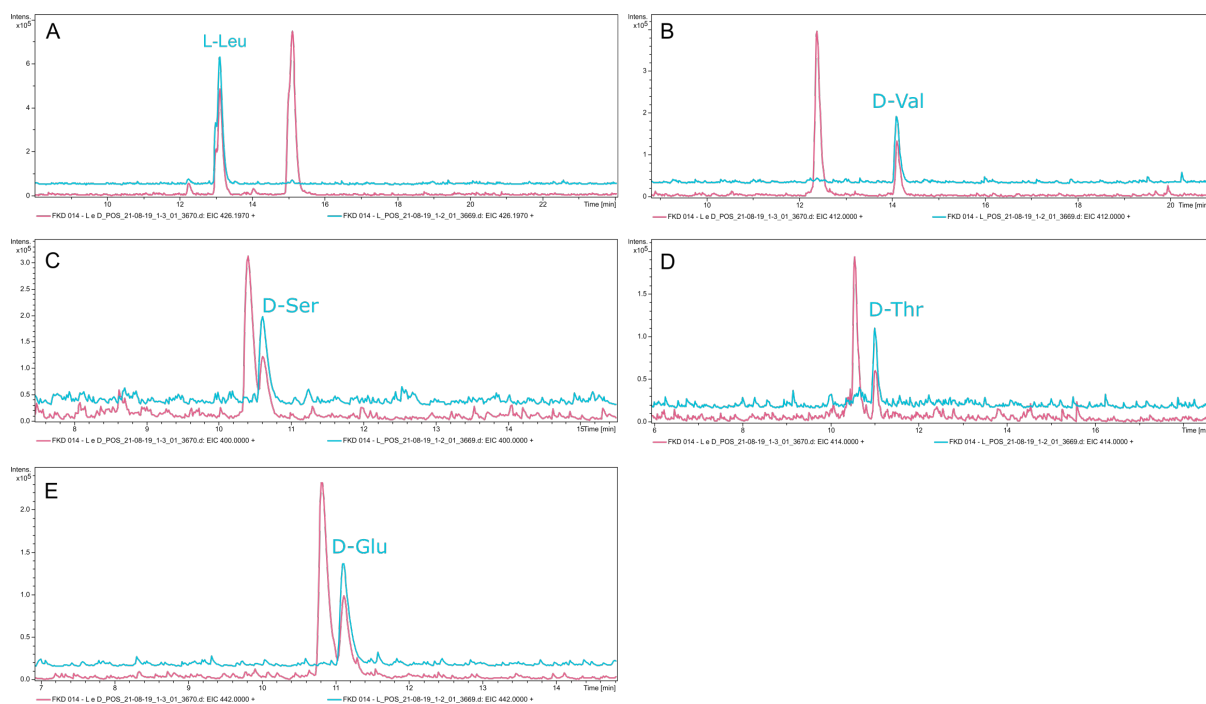
**Figure S14.** gHMBC spectrum of viscosinamide ( $\text{CD}_3\text{COCD}_3$ , 500 MHz).

**Table S1.** NMR spectroscopic data of viscosinamide (CD<sub>3</sub>COCD<sub>3</sub>).

Amino acid	Position	$\delta$ C	$\delta$ H	Multiplicity (Hz)	COSY	HMBC
Fatty acid	1	174.7	--			
	2	44.7	2.61	dd (14.23; 4.04)	3	1, 3
	3	69.7	4.11	d (9.47)	3	1, 3, 4, 5
	4	38.3	1.55	m	4	
	5	26.3	1.48	m	5	
	6	n.a.	n.a.			
	7	n.a.	n.a.			
	8	n.a.	n.a.			
	9	n.a.	n.a.			
	10	n.a.	n.a.			
	11	n.a.	n.a.			
Leu1*	12		8.74	d (5.88)	13	13, 14
	13	53.4	3.99	m	12, 15	15,14
	14	174.9	--			
	15	38.9	1.87	m	13, 16	16, 17, 13,
	16	25.3	1.77	m	15, 17	13, 17
	17	22.3	0.91	m	16	16, 13
	18	21.3	0.91	m	16	16, 13
Gln2	19	--	8.25	d (7.10)	20	20
	20	58.3	4.15	m	22	23, 21,
	21	176.6	--			
	22	28.7	2.02	m	20, 23	23,20,24
	23	31.7	2.48	dt (11.10; 5.92)	22	24, 20,
	24	176.5	--			
	25	--	7.24/6.61	s		
Thr3	26		9.23	br s	27	27, 28
	27	57.0	4.17	m	29	28, 21,30, 29
	28	174.5	--			
	29	71	5.36	dq (12.00; 5.89)	27, 30	28, 63
	30	17.9	1.32	d (6.00)	29	
Val4	31	--	7.95	d (5.21)	32	32, 34, 33
	32	65.8	3.44	dd (11.08; 5.63)	34	35, 34,
	33	174.1	--			
	34	29.7	2.19	m	35,36	33,35, 32
	35	20.3	1.01	m	34	36
	36	19.5	0.96	m	34	35,34,32
	Leu5*	37	--	8.47	d (6.75)	38
38		54	3.67	m	40	41, 39, 33
39		171.1	--			
40		38.8	1.77	m	38,41	38, 40, 43
41		25.6	1.62	m	42,43	43
42		21.3	0.92	m	41	43, 41
43		21.8	0.94	m	41	41, 40
Ser6		44	--	07.08	d (5.69)	45
	45	56.4	4.4	m	44,47	46,47
	46	171.9	--			
	47	64.5	3.79	m	45,48	46
	48	--	5.11	dd (8.98; 5.59)	47	47
Leu7*	49	--	7.47	d (8.45)	50	46, 52
	50	56.2	4.16	dt (8.42; 2.43)	49	52, 51, 46

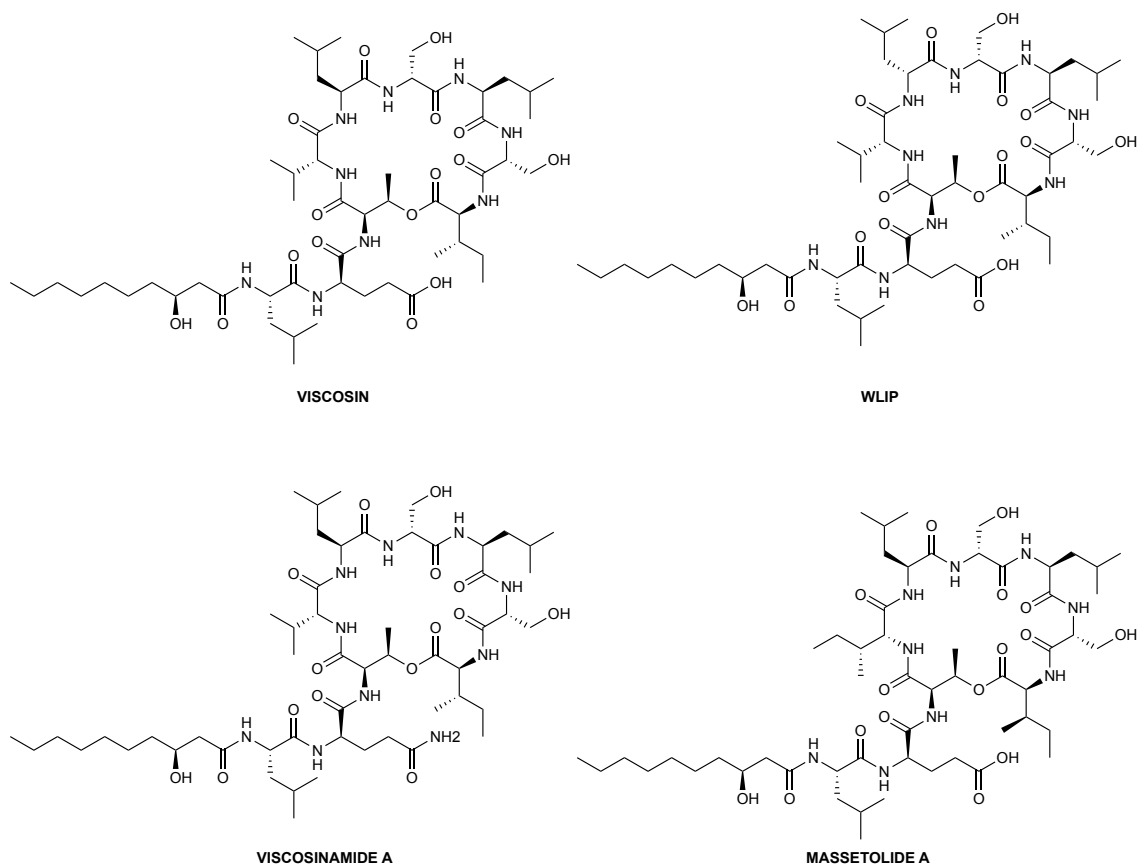
	51	173.6	--			
	52	41.6	1.60	m	53	50
	53	36.1	1.98	m		50, 51
	54	16	0.84	m		50
	55	16	0.85	m		50
Ser8	56	--	8.02	d (9.14)	57	57, 51, 59
	57	56.7	4.50	dt (8.88; 4.45)	56, 59	59, 58, 51
	58	171.7	--			
	59	62.4	3.65	m	60, 57	58
	60	--	4.04	m	59	59
Ile9	61	--	6.61	d (9.99)	62	62, 58, 63
	62	56.7	4.57	dd (10.15; 3.03)	61, 64	64, 65, 66, 63, 58
	63	170.1	--			
	64	36.1	1.98	m	62, 65, 66	66, 67
	65	16	0.85	m	64	64, 66, 67, 62
	66	25.1	1.6	m	67, 64	62
	67	21.3	0.94	m	66	66

\* Interchangeable.



**Figure S15.** Chromatograms of viscosinamide products after hydrolysis and advanced Marfey derivatization. In blue, the chromatograms of the product of the reaction with L-FDLA are represented, and in pink, with L, D-FDLA. (A) EIC *m/z* 426.45, corresponding to L-Leu. (B) EIC *m/z* 412.43, corresponding to D-Val. (C) EIC *m/z* 400.37, corresponding to D-Ser. (D) EIC *m/z* 414.4, corresponding to D-Thr. (E) EIC *m/z* 442.41, corresponding to D-Glu.





**Figure S16.** Chemical structures of viscosin, WLIP, viscosinamide A and massetolide A.