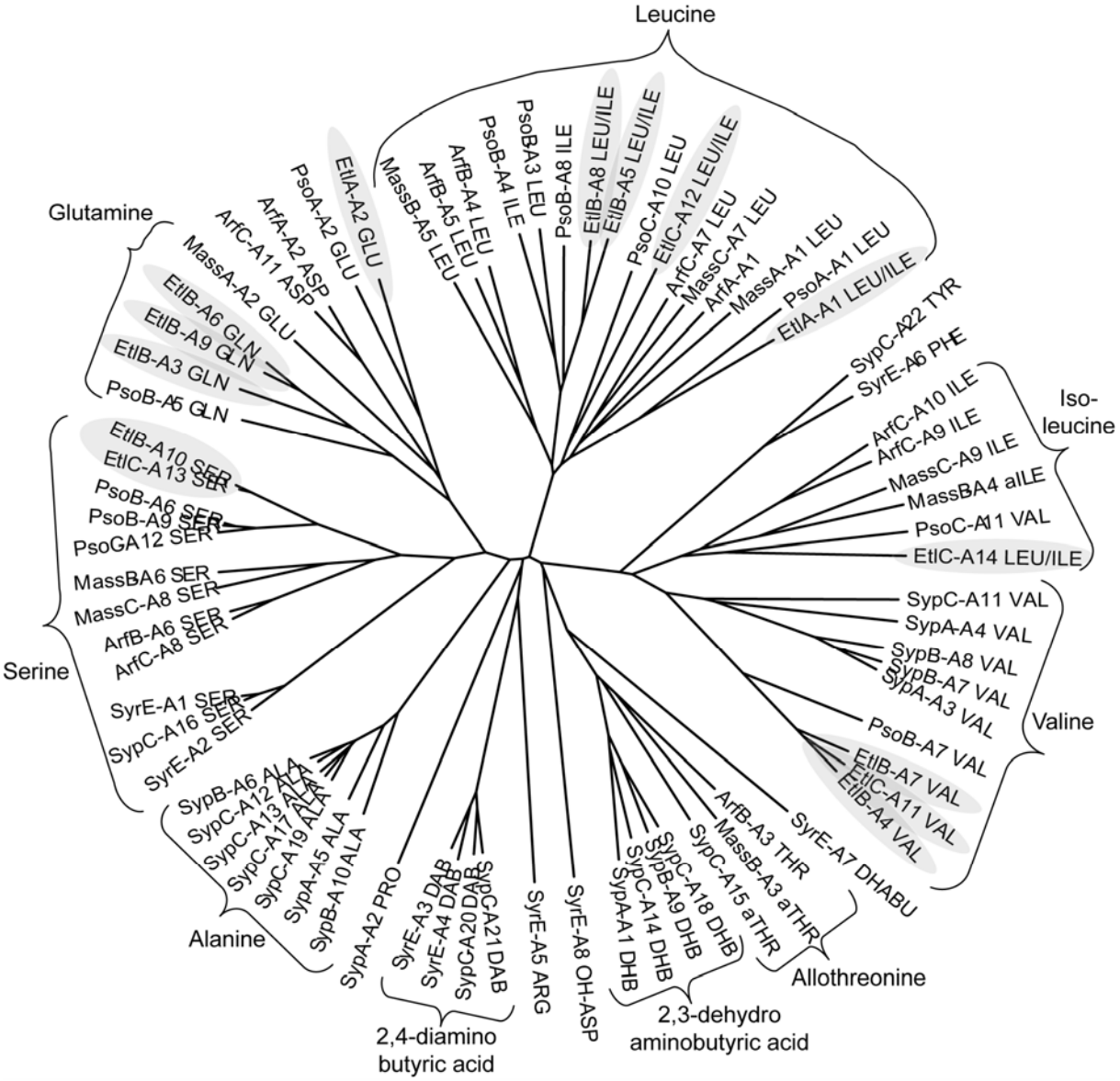

FIG S1 Phylogenetic analysis of the 14 substrate specificity regions (A domains) from the entolysin synthetases, EtlA, EtlB and EtlC and the regions of substrate specificity from the NRPS involved in massetolide A (MassA, MassB and MassC), putisolvins (PsoA, PsoB and PsoC), arthrofactin (ArfA, ArfB and ArfC), syringomycin (SyrE) and syringopeptin (SypA, SypB and SypC) biosynthesis. Numbering of the A domains is according to their order in the biosynthesis process. Amino acid abbreviations: Dab = 2,4-diaminobutyric acid, Dhb = 2,3-dehydroaminobutyric acid; and aThr = allothreonine. All other amino acids are identified by standard three-letter biochemical notation.

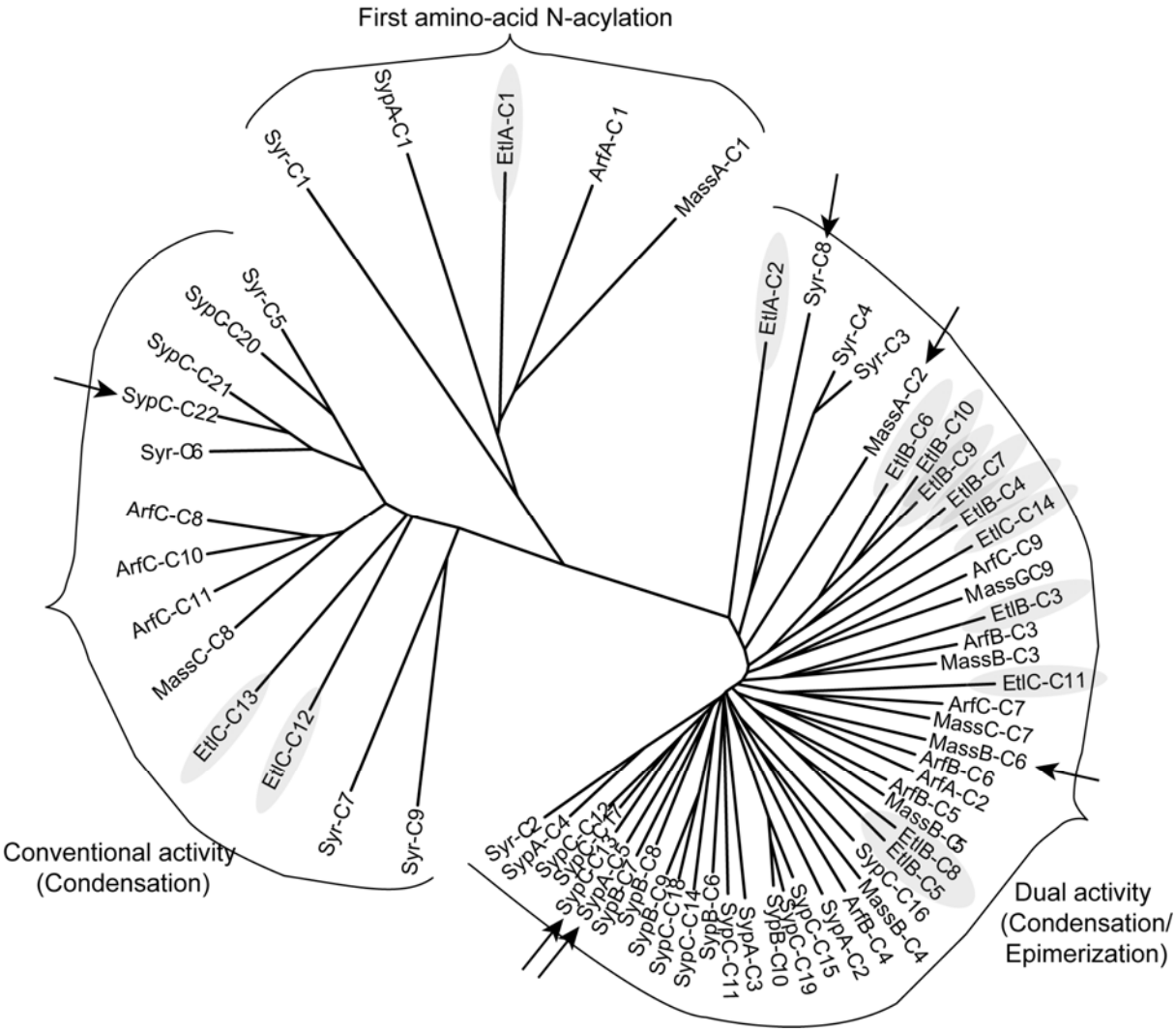

FIG S2 Phylogenetic analysis of the 14 C-domains from the entolysin synthetases, EtlA, EtlB and EtlC and the C-domains from the NRPS involved in massetolide A (MassA, MassB and MassC), arthrofactin (ArfA, ArfB and ArfC), syringomycin (SyrE) and syringopeptin (SypA, SypB and SypC) biosynthesis. Numbering of the C domains is according to their order in the biosynthesis process. Arrows indicate exception in the C-domain classification (domains involved in L amino acid addition clustering with dual C/E domain, or domains adding a D amino acid clustering with classical C domains).

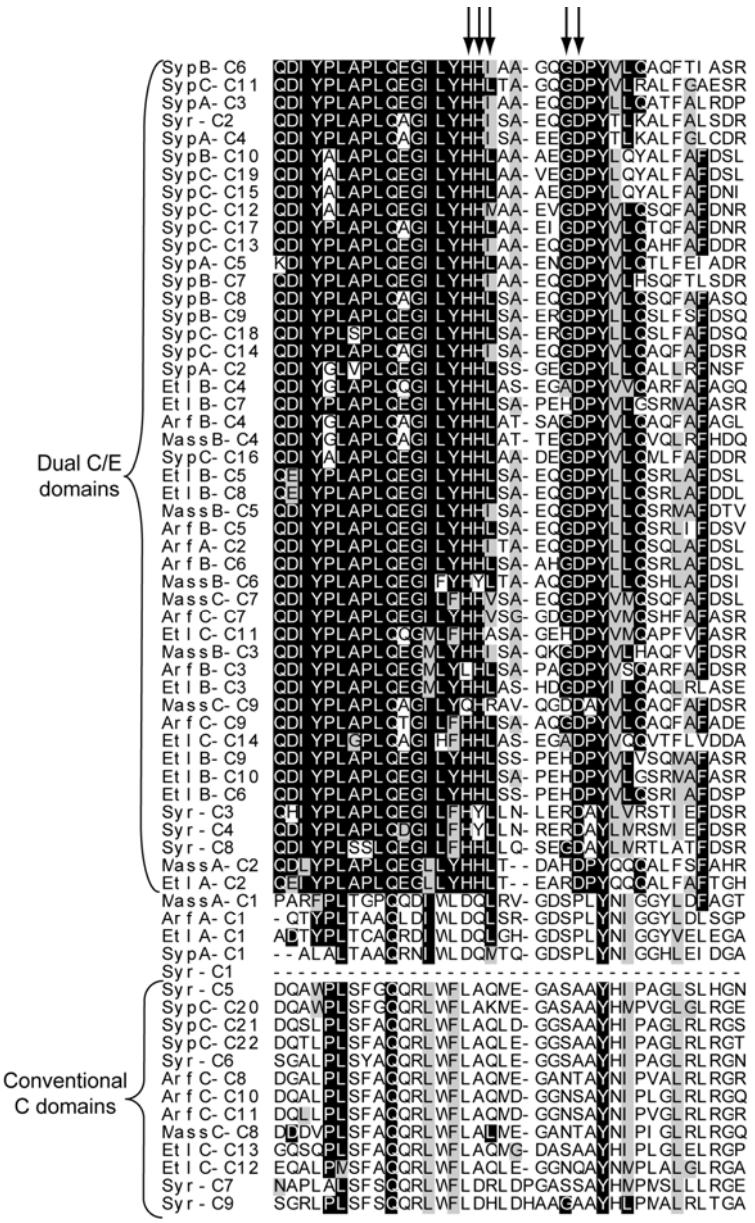

FIG S3 Primary sequence alignment of the 14 C-domains from the entolysin synthetases, EtlA, EtlB and EtlC and the C-domains from the NRPS involved in massetolide A (MassA, MassB and MassC), arthrofactin (ArfA, ArfB and ArfC), syringomycin (SyrE) and syringopeptin (SypA, SypB and SypC) biosynthesis. Conserved residues are indicated by arrows. Residues highlighted in black are highly conserved, and residues highlighted in grey are moderately conserved.

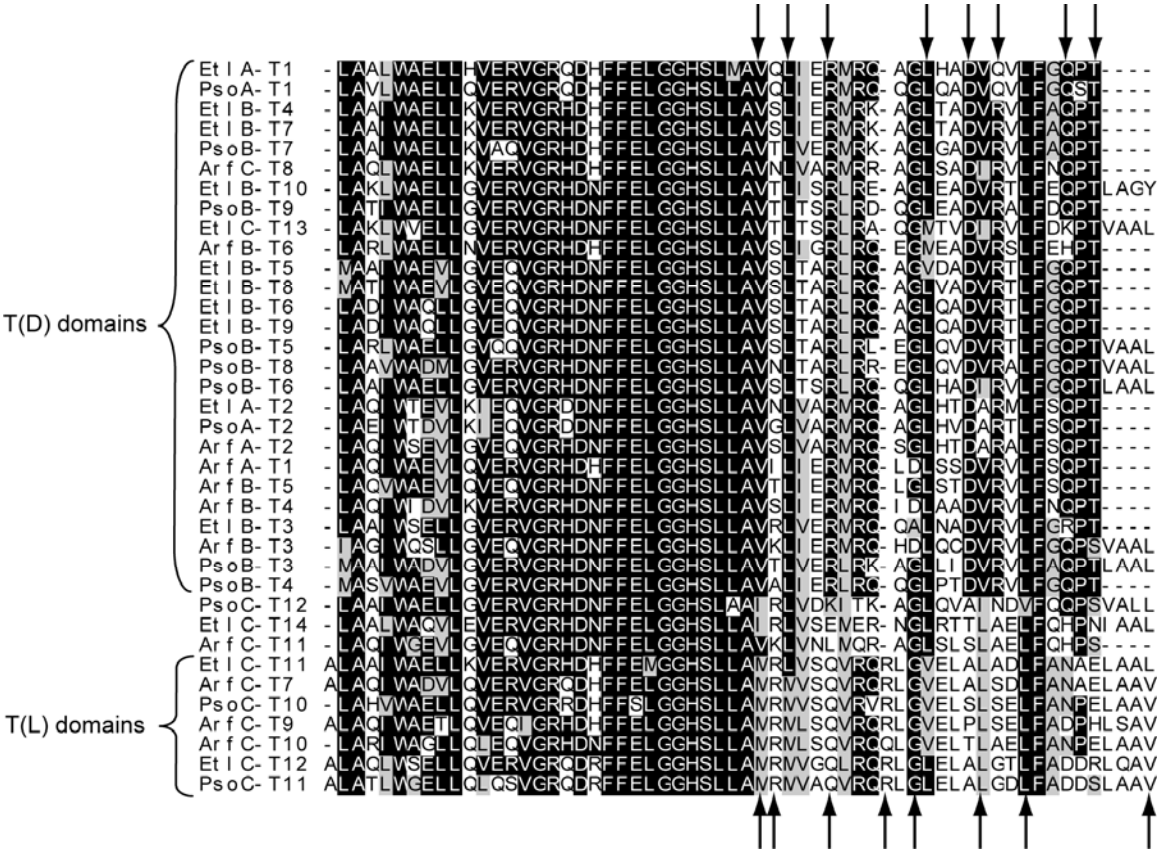

FIG S4 Primary sequence alignment of the 14 T-domains from the entolysin synthetases, EtlA, EtlB and EtlC and the T-domains from the NRPS involved in arthrofactin (ArfA, ArfB and ArfC) and putisolvins (PsoA, PsoB and PsoC) biosynthesis.

Conserved residues are indicated by arrows. Residues highlighted in black are highly conserved, and residues highlighted in grey are moderately conserved. Conserved residues are indicated by arrows. Residues highlighted in black are highly conserved, and residues highlighted in grey are moderately conserved.

TABLE S1 Amino analysis data

Amino acid	Experimental molar ratio	Molar ratio predicted from proposed structure
Ser	2	2
Glu + Gln	4	4
Val	2.2	3
Ile	1	5*
Leu	3.5	

Ser: serine; Glu: glutamic acid; Gln: glutamine; Val: valine; Ile: isoleucine; Leu: leucine

* The molar ratios of Ile and Leu are presented together as they cannot be discriminated by the mass spectrometric techniques used to date.

TABLE S2 Prediction and selectivity-conferring code of the amino-acid-specific adenylation domains (A-domains) of the entolysin synthesis genes.

A-domain	**Selectivity-conferring amino acid at position:**										**Amino acid**
	235	**236**	**239**	**278**	**299**	**301**	**322**	**330**	**331**	**527**	
EtlA-A1	D	A	W	F	L	G	N	V	V	K	**Leu**
EtlA-A2	D	G	W	K	F	G	V	V	D	K	**Glu**
EtlB-A3	D	A	W	Q	V	G	V	V	D	K	**Gln**
EtlB-A4	D	A	L	W	M	G	G	T	F	K	**Val**
EtlB-A5	D	A	F	F	L	G	N	V	V	K	**Leu**
EtlB-A6	D	A	W	Q	V	G	V	V	D	K	**Gln**
EtlB-A7	D	A	L	W	M	G	G	T	F	K	**Val**
EtlB-A8	D	A	W	P	L	G	N	V	V	K	**Leu**
EtlB-A9	D	A	W	Q	V	G	V	V	D	K	**Gln**
EtlB-A10	D	V	W	H	L	S	L	V	D	K	**Ser**
EtlC-A11	D	A	L	W	M	G	G	T	F	K	**Val**
EtlC-A12	D	A	W	A	L	G	N	V	V	K	**Leu**
EtlC-A13	D	V	W	H	L	S	L	V	D	K	**Ser**
EtlC-A14	D	A	M	F	L	G	C	T	F	K	**Leu**

Ser: serine; Glu: glutamic acid; Gln: glutamine; Val: valine; Leu: leucine ;

TABLE S3 Ability of *P. entomophila*, a *gacA* mutant and an entolysin deficient mutant to protect cucumber seedling from Pythium damping-off and root rot*

Bacterial strain added**	*Pythium* added	Surviving plants per flask (%)	Plant fresh weight per flask (g)	Shoot fresh weight per flask (g)	Root fresh weight per flask (g)
None	-	100	2.10	1.75	0.35
P. fluorescens CHA0	-	100	2.45	1.95	0.50
P. entomophila (Pe)	-	100	2.36	1.86	0.50
ΔgacA	-	100	2.28	1.85	0.43
IM3044	-	92	2.35	1.89	0.46
None	+	25	0.21	0.15	0.06
CHA0	+	96	2.36	1.94	0.42
Pe	+	100	2.62	2.12	0.50
ΔgacA	+	88	1.55	1.26	0.29
IM3044	+	100	2.51	1.99	0.52

* Data represent the averages from eight replicates (flasks containing three cucumber plants) per treatment.

** Bacterial strains were added at 10^7 CFU/g of natural soil contained within 200 ml flasks (60g of soil per flask), after planting three 72h-old. sterile-grown cucumber seedlings per flask. *Pythium ultimum* was added as a millet-seed inoculum at 2.5 g/kg of soil before planting. Plants were harvested after 7 days.