

Supplementary information for

**Comparative genomic and functional analyses: unearthing the
diversity and specificity of nematicidal factors in *Pseudomonas putida*
strain 1A00316**

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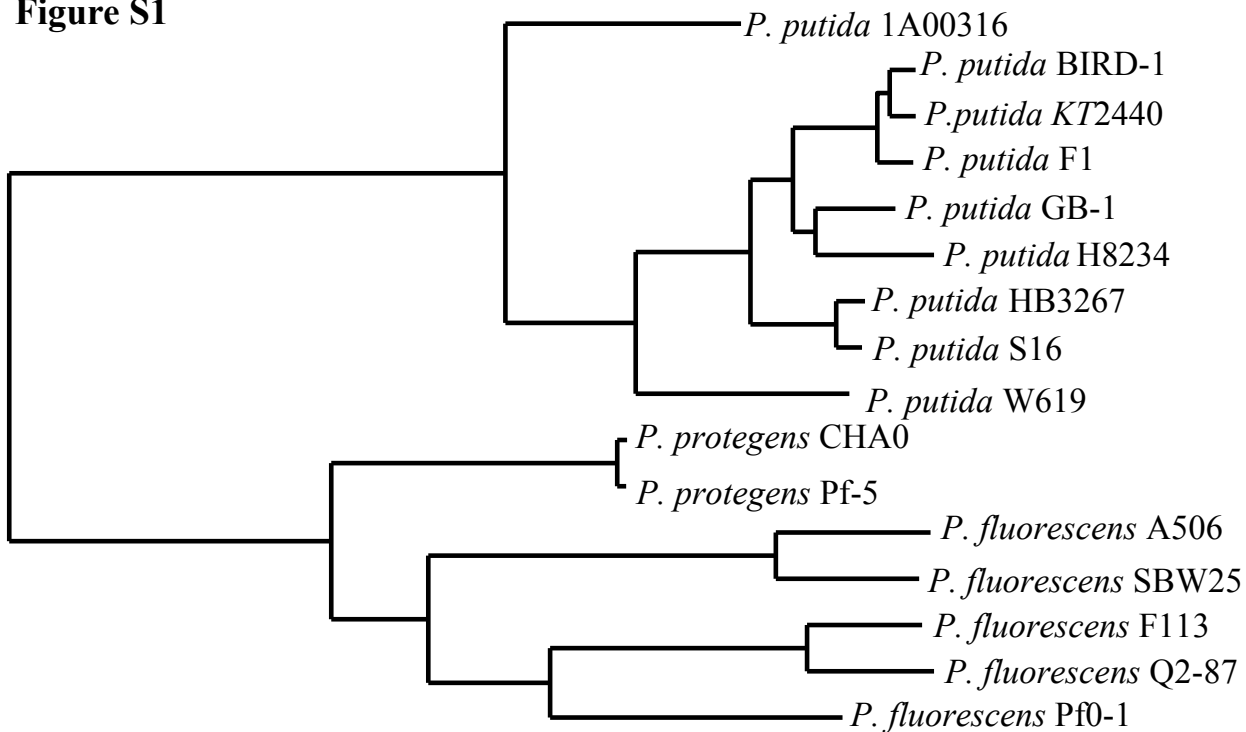
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Figure S1. Maximum likelihood phylogeny inferred from 2,408 single-copy conserved protein-coding genes in the *P. putida* 1A00316 genome.

Figure S2. Sequence alignment of the AprA protein in various *Pseudomonas* strains. Green sequence fragments are the ZnMc_serralysin_like domain, and red amino acids are active sites.

Figure S1



0.05

Figure S2

