



Figure S1. Cladogram representation of a maximum-likelihood tree inferred from amino acid sequence alignment of condensation domains extracted from characterized *Pseudomonas* NRPSs. The lipopeptide-specific codes are specified in Fig. 3, with the xantholysin-related ones in bold. Clusters are differentiated according to the type of C-domain by color: conventional domains (green), dual epimerization/condensation domains (blue), and N-acylating starter domains (red). The tree was rooted with the divergent C1 domain of SyrE (black).