

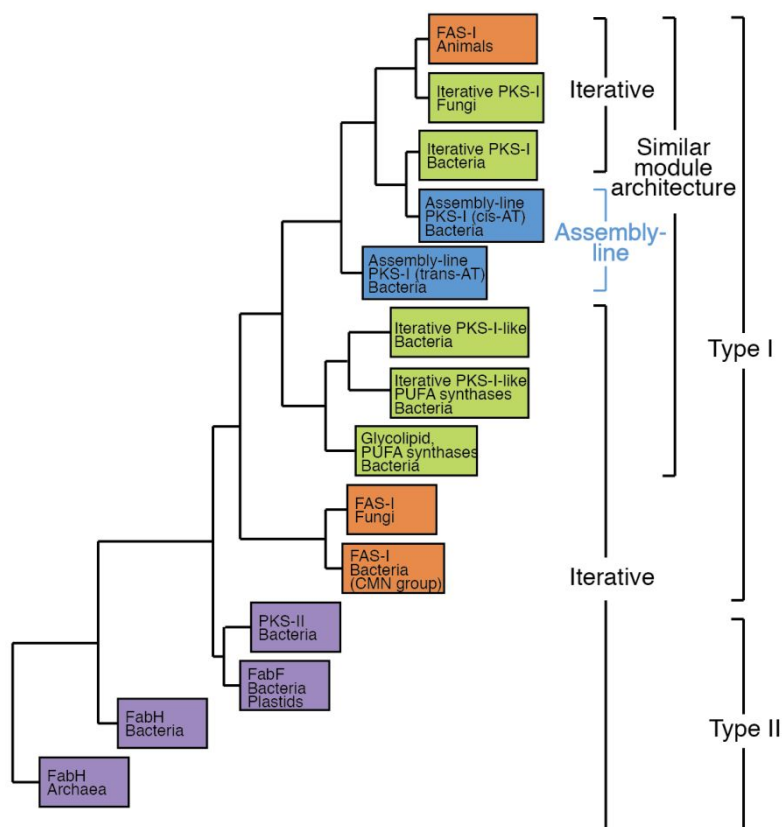
# Evolution and Diversity of Assembly-Line Polyketide Synthases

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## Supplementary information



**Supplementary Figure S1.** Schematic representation of phylogenetic relationships between KS domains from different types of FASs and PKSs, as inferred by Bayesian statistics. Adapted from Jenke-Kodama *et al.* 2005<sup>1</sup> and Jenke-Kodama *et al.* 2009.<sup>2</sup>



**Supplementary Figure S2.** Network of 3,551 distinct assembly-line PKS clusters, visualized by Cytoscape 3.7.2<sup>3</sup>. Nodes correspond to known clusters (larger circles) and "orphans" (smaller circles), color coded according to the phylum of their host (graphical legend). Edges represent >50% sequence similarity between two clusters, calculated as described in <sup>4</sup>.

The catalog, the dendrogram and the network file are available online:  
[http://web.stanford.edu/group/orphan\\_pks/](http://web.stanford.edu/group/orphan_pks/)

The code used in this work is available on GitHub:  
[https://github.com/aleksnivina/Orphan\\_PKS\\_catalog](https://github.com/aleksnivina/Orphan_PKS_catalog)

- (1) Jenke-Kodama, H.; Sandmann, A.; Müller, R.; Dittmann, E. Evolutionary Implications of Bacterial Polyketide Synthases. *Mol. Biol. Evol.* **2005**, *22*, 2027–2039.
- (2) Jenke-Kodama, H.; Dittmann, E. Evolution of Metabolic Diversity: Insights From Microbial Polyketide Synthases. *Phytochemistry* **2009**, *70*, 1858–1866.
- (3) Shannon, P.; Markiel, A.; Ozier, O.; Baliga, N. S.; Wang, J. T.; Ramage, D.; Amin, N.; Schwikowski, B.; Ideker, T. Cytoscape: a Software Environment for Integrated Models of Biomolecular Interaction Networks. *Genome Res.* **2003**, *13*, 2498–2504.
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