

Genome-scale reconstruction of the metabolic network in *Pseudomonas stutzeri* A1501

Parizad Babaei, Sayed-Amir Marashi, Sedigheh Asad

Supplementary file S1:

Metabolic subsystems of unique reactions of *P. stutzeri*

There are 200 reactions which are unique to *iPB890*, the metabolic network of *P. stutzeri* A1501. Figure S2-1 summarizes the subsystems to which these reactions belong.

We also analyzed the reactions which are shared between the two template models, *iMO1086* and *iJP962*. We found 139 reactions which are shared by the template models and are not present in our model. These are either non-gene associated reactions which are not necessary for growth, or gene-associated reactions whose genes did not acceptably match any target gene in our BLASTp searches. The subsystems of these reactions are presented in Figure S2-2.

By comparing the two figures, it is obvious that in many subsystems the ratios are comparable. For example, the ratios of reactions which belong to metabolism of cofactors and vitamins, amino acid metabolism, nucleotide metabolism, and carbohydrate metabolism are more or less similar in the two reaction sets. However, transport reactions are much more common in the second reaction set (14% vs. 1%). This difference might be due to the frequent presence of non-gene associated transport reactions in the two models. On the other hand, among the unique reactions of *iPB890*, reactions of lipid metabolism, energy metabolism, and xenobiotics' metabolism show a higher ratio (when compared to the corresponding ratios in the set of shared reactions). This observation suggests that most of the unique reactions of *P. stutzeri* network model do not belong to the central metabolism, and represent the unique features of the metabolism of *P. stutzeri*.

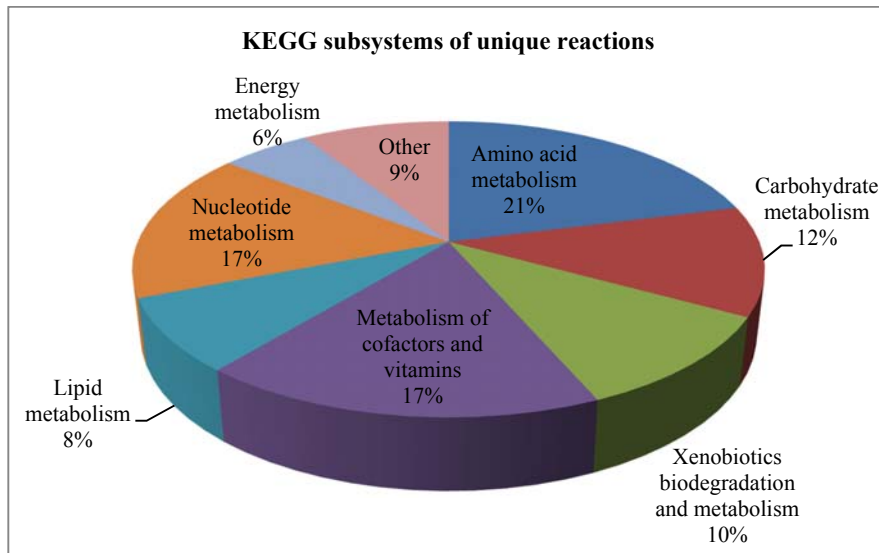


Figure S1-1. The subsystems of the unique reactions to *iPB890*.

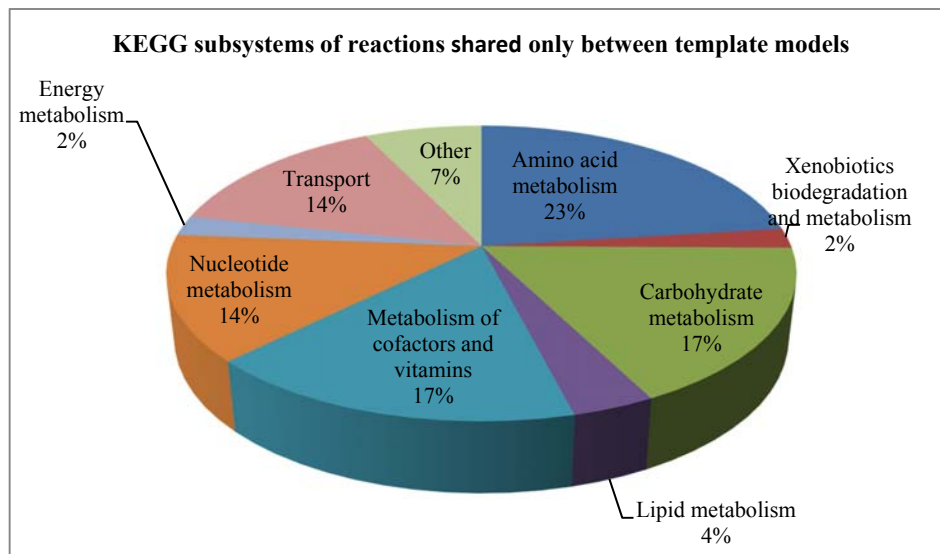


Figure S1-2. The metabolic subsystems of reactions shared between *iMO1086* and *iJP962* but absent in *iPB890*.