

Genome-scale reconstruction of *Pseudomonas putida* KT2440 and applications

손승범, 김태용, 김현욱, 이상엽*

Dept. of Chemical and Biomolecular Eng., KAIST

(ehukim@kaist.ac.kr*)

Pseudomonas putida is a Gram-negative bacterium known for its versatility and adaptability under a number of stressful conditions. Its ability to survive and thrive in toxic environments and use toxins as a source of nutrients has garnered much interest in utilizing these microbes in biotechnological applications. With the reconstruction of a genome-scale model, simulations can be used to predict physiologies of any metabolic engineering modifications, resulting in the selection of optimal connections in the network to suit various goals. With *P. putida*'s ability to utilize a number of exotic compounds, new and potentially low cost substrates can be utilized and directed to producing high value products. In the process of designing network connectivity for such applications, knowledge of bacterial biosystems can be better understood, resulting in an enhanced knowledge of other biological systems. [This work was supported by the Korean Systems Biology Research Program (M10309020000-03B5002-00000) of the Ministry of Education, Science and Technology through the Korea Science and Engineering Foundation. Further supports by the BK21 program, LG Chem Chair Professorship, and IBM SUR program are appreciated]