

Reconstruction and *in silico* analysis of genome-scale metabolic model of *Ralstonia eutropha* H16

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*Ralstonia eutropha* H16 is a lithoautotrophic Gram-negative bacterium using CO<sub>2</sub> and H<sub>2</sub> as main sources of carbon and energy without any organic substrates. It is known for polyhydroxyalkanoates (PHAs) producer and is an environmentally promising bacterium because of its capability of degradation of aromatic compounds. Systems metabolic engineering to improve its metabolic performance is applied here to make *R. eutropha* H16 a more efficient and robust biofactory. Here, a genome-scale model called RehMBEL1391 composed of 1391 reactions 1171 metabolites was constructed. Constraints-based flux analyses were performed to refine and validate the genome-scale metabolic model under environmental and genetic perturbations. [This work was supported by the Technology Development Program to Solve Climate Changes (systems metabolic engineering for biorefineries) (NRF-2012-C1AAA001-2012M1A2A2026556) and by the Intelligent Synthetic Biology Center of Global Frontier Project (2011-0031963) from the Ministry of Education, Science and Technology (MEST)]