

*In silico* analysis of the *Ralstonia eutropha* H<sub>16</sub> genome-scale metabolic model

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*Ralstonia eutropha* H16 is a Gram-negative lithoautotrophic bacterium that can use CO<sub>2</sub> and H<sub>2</sub> as sources of carbon and energy in the absence of organic substrates. It is the best known and most promising producer of polyhydroxyalkanoates (PHAs) from various carbon substrates. Systems metabolic engineering to improve its metabolic performance is essential to make *R. eutropha* H16 a more efficient and robust biofactory. Thus, we constructed the lithoautotrophic genome-scale metabolic model of *R. eutropha* H16 based on the annotated genome with biochemical and physiological information. The reconstructed genome-scale model, RehMBEL1391, is composed of 1391 reactions and 1171 metabolites. Furthermore, constraints-based flux analyses were applied 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) from the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea (NRF-2012-C1AAA001-2012M1A2A2026556)]