

Reconstruction of *Ralstonia eutropha* H16 genome-scale metabolic model and *in silico* analyses for polyhydroxyalkanoate production

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Ralstonia eutropha H16 that found in both soil and water is a Gram-negative lithoautotrophic bacterium that can make use of CO₂ and H₂ as its sources of carbon and energy in the absence of organic substrates. We constructed the lithoautotrophic genome-scale model of *R. eutropha* H16 based on the annotated genome sequence with biochemical and physiological information. The stoichiometric model, RehMBEL1391, is comprised of 1391 reactions including 229 transport reactions and 1171 metabolites. 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 Advanced Biomass R&D Center(ABC) of Global Frontier Project funded by the Ministry of Education, Science and Technology. Further supports by the World Class University Program(R32-2008-000-10142-0) of the MEST were appreciated.]