

Analysis of the Genome-Scale Metabolic Model of *Pichia pastoris*

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Here we present the analysis of the genome-scale metabolic model of the yeast *Pichia pastoris*, an attractive host for heterologous protein production and capable of producing proteins of therapeutic value. Using the genome-scale metabolic model, characteristics and capacity towards the production of two proteins, human serum albumin (HSA) and human superoxide dismutase (hSOD), were analyzed and metabolic engineering targets were suggested to improve their production. Using genome-scale metabolic model, potential phenotypes can be screen in a high-throughput manner, accelerating the development of strategies for engineering improved strains. [This work was supported by the Korean Systems Biology Research Project (20100002164) of the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea, by the Austrian Science Fund (FWF), project I37-B03, and the Austrian Research Promotion Agency (program FHplus).]