

*In silico* genome-scale metabolic reconstruction of the fission yeast *Schizosaccharomyces pombe*

손승범, 김태용, 이상엽\*  
KAIST  
(leesy@kaist.ac.kr\*)

Here we present the genome-scale metabolic reconstruction of the fission yeast *Schizosaccharomyces pombe*, a model eukaryotic system. Although the budding yeast *Saccharomyces cerevisiae*, is more characterized and extensively studied, the cell cycle of *S. pombe* is highly similar to mitosis and is more ideal for studying cell cycle regulation. It has the smallest number of protein encoding genes in its genome, thereby making it a model for studying minimal cells. Here we present the genome-scale metabolic reconstruction of the fission yeast *S. pombe* and analysis of its metabolic network. With this metabolic model, the metabolism of this yeast is examined to attain a better understanding of its inner working and unique metabolic characteristics. [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. Further support by the World Class University Program (R32-2009-000-10142-0) through the National Research Foundation of Korea funded by the MEST is appreciated.]