

Genome-scale Reconstruction of the metabolic network of *Schizosaccharomyces pombe*

유재용, 손승범, 이상엽*
한국과학기술원
(leesy@kaist.ac.kr*)

The fission yeast *Schizosaccharomyces pombe*, is one of two yeast systems that have been central in the study of higher eukaryotes, the other being *Saccharomyces cerevisiae*, as a model system. Physiological similarities in cell division between *S. pombe* and mammalian cells and genetic similarity of several genes found in human have made *S. pombe* an important model system in elucidating higher eukaryotic function. The genome-scale metabolic model maps the metabolic network of *S. pombe* which allows for a more better understanding and study of the metabolism behind the observed physiology. This tool further allows for prediction of novel physiological characteristics, given a set genetic perturbation linked to the metabolic network. As a result, insights into the metabolic physiology of *S. pombe*, can be examined and applied towards the improvement of human life.