

Applications of the genome-scale metabolic model of fission yeast *Schizosaccharomyces pombe*

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Yeast has been studied extensively as a model system for higher eukaryotic organisms, including *Homo sapiens* and has contributed greatly towards a better understanding of higher eukaryotic cellular functions. The fission yeast *Schizosaccharomyces pombe*, is an attractive system as a model due to the similarity in cell division with mammals, fission as opposed to budding, which is used in the more characterized yeast *Saccharomyces cerevisiae*. Additionally, *S. pombe* possesses genes that are similar to genes that are found in humans and are responsible for a number of genetic diseases. Here we have reconstructed the genome-scale metabolic model of the fission yeast *S. pombe* to serve as a platform for better understanding the metabolic phenotype of *S. pombe*. [This work was supported by the Korean Systems Biology Research Project (20090065571) of the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea (NRF). Further supports by the World Class University Program (R32-2008-000-10142-0) of the MEST, LG Chem Chair Professorship, IBM SUR program, and Microsoft are appreciated.]