Genome-scale metabolic model of the fission yeast Schizosaccharomyce pombe

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The fission yeast *Schizosaccharomyces pombe* is a model yeast for cell cycle regulation. Unlike the more popular budding yeast Saccharomyces cerevisae, its cell cycle is highly similar to mitosis. Furthermore, it is able to exist in both haploid and diploids states. Additionally, it has the smallest number of protein encoding genes in its genome, making it a model for studying minimal cells. Here we present the genome-scale metabolic reconstruction of the fission yeast *S. pombe*. Using this metabolic model, we examine the metabolism of this yeast to attain a better understanding of its inner working and unique metabolic characteristics. [This work was supported by the Korean Systems Biology (MEST) through the National Research Foundation of Korea. Further support by the World Class University Program (R32-2008-000-10142-0) through the National Research Foundation of Korea funded by the MEST is appreciated.]