

# A Genome-Scale *in silico* Model of Metabolic Network in *Saccharomyces cerevisiae*

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## ABSTRACT

A genome-scale metabolic representation of the model eukaryote *Saccharomyces cerevisiae* was constructed resulting in a biochemical reaction network consisting of 1212 reactions and 734 metabolites. Using flux balance analysis [1], the integrated functions of the reconstructed metabolic network, such as the P/O ratio and growth-associated ATP maintenance, were investigated and found to be quantitatively the same as those determined by independent experiments [2]. The consequences of gene knockouts on growth performance were predicted correctly for 499 cases out of 583 examined. Whole-cell functions of growth and metabolic by-product secretion in aerobic and anaerobic culture were quantitatively computed from the *in silico* model and the calculations of expression profiles for metabolic shifts were qualitatively consistent with experimental measurements [3, 4]. The combination of genome-scale metabolic reconstruction and quantitative constraints-based analysis allowed for a fundamental analysis of the integrated function of the metabolic network, and provided a bridge between the individual molecular components and whole-cell function.

## REFERENCES

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