

A Metabolic Integrated Yeast Knowledgebase (MIYEASTK)

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Saccharomyces cerevisiae is one of the most widely used cell factories in industrial biotechnology. However, the development of optimized yeast strains for the production of novel compounds is a time-consuming process and represents a significant cost/time burden.

Genome-scale metabolic models are a valuable tool that helps to reduce cost and time in order to develop improved strains. Nevertheless, the existence of various genome-scale metabolic models for *S. cerevisiae*, with different metabolic information and predictability capabilities, increases the complexity of metabolic engineering studies.

Metabolic Integrated Yeast Knowledgebase (MIYEASTK) is scientific database that integrates several published genome-scale metabolic models of *S. cerevisiae*. The database enhances the annotation of individual metabolites, reactions, genes and gene rules with additional references from external databases such as KEGG, MetaCyc, etc. Moreover, integration with the myriad of information contained in SGD (*Saccharomyces* Genome Database) is provided via the metabolic genes within the models. This provides a valuable tool for users to compare yeast metabolic models.
