

## iOD962 - the first genome-scale metabolic model of *Kluyveromyces lactis*

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### Abstract

The genome-scale metabolic model of *Kluyveromyces lactis* was reconstructed from its genome annotation. The result was the partially compartmentalized (5 compartments) iOD962 metabolic model composed of 2038 reactions and 1561 metabolites. Previous chemostate experiments were used to adjust the maintenance ATP parameter, and the model proved valuable when predicting the biomass, oxygen and carbon dioxide yields. Also, the *in silico* knockouts predicted accurately the *in vivo* phenotypes, when compared to published experiments. This model allowed determining a minimal medium for cultivating *K. lactis* and will surely allow elucidating insights on the milk yeast metabolism as well as identifying engineering targets for the improvement of the production of by-products of interest by performing *in silico* simulations.