

KINETICS OF LACTOSE FERMENTATION USING RECOMBINANT *Saccharomyces cerevisiae*

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This work presents a multi-route, nonstructural kinetic model for determination of ethanol fermentation on lactose using a recombinant *S. cerevisiae* flocculent strain expressing both the *LAC4* (coding for β -galactosidase) and *LAC12* (coding for lactose permease) genes of *Kluyveromyces lactis*. In this kind of modelling, the values of different metabolic pathways are calculated applying a modified Monod equation rate in which the growth rate is proportional to the concentration of a key enzyme controlling the single metabolic pathway. As a result, this type of model has a large number of parameters. In this study, three main metabolic routes for *S. cerevisiae* are considered: fermentation (producing ethanol), oxidation of lactose and oxidation of ethanol.

The main bioprocess variables determined experimentally were lactose, ethanol and biomass concentrations, dissolved oxygen and the composition of outgoing gas.

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