

Comparative Metabolic flux analysis in *E.coli* using MetaFluxNet

방현옥, 김태용, 홍순호, 이상엽*
한국과학기술원 생명화학공학과
(leesy@kaist.ac.kr*)

Metabolic engineering can be defined as directed modification of cellular metabolism and properties using recombinant DNA. In these days, metabolic flux analysis, which allows calculation of the intracellular metabolic fluxes by the measurement of extracellular metabolite concentrations in combination with the stoichiometry of intracellular reactions, has become an essential tools for metabolic engineering. In this study, we applied new MFA software (MetaFluxNet) to identify metabolic characteristics of *Escherichia coli*. The variation of intracellular metabolic flux distributions of *E. coli* was estimated by MFA under various conditions, and the response of metabolic fluxes were evaluated. From the results of this study, we identified functions of certain metabolic pathways. As verified in this study, MFA could be used for the identification of new metabolic pathways, and considering the simplicity of MFA wide application of MFA for the pathway function identification of various microorganisms is predicted.