# Enhanced Production of Recombinant Protein in *Escherichia coli* by the Coexpression of the Down-Regulated Genes Identified by Transcriptome Profiling

Jong Hyun Choi, Sang Yup Lee
Department of Chemical and Biomolecular Engineering
and BioProcess Engineering Research Center, KAIST
Tel: +82-42-869-3930, FAX: 82-42-869-8800

## Abstract

*Escherichia coli* has been the workhorse for the production of various useful recombinant proteins. Changes in gene expression in response to environmental change during production of recombinant protein are important in finding cures that could increase the productivity of recombinant proteins in *E. coli*. Analysis of gene expression pattern may provide information for the construction of metabolic pathway as well as engineering of overexpression system in *E. coli*. This global analysis can provide important information on metabolic changes under protein production, and consequently can be used to identify connections between regulatory and metabolic pathways that were previously unknown.

In this study, we report analysis of transcriptomes of *E. coli* during overexpression of recombinant IGF-I proteins using glycerol as a carbon source by using Panorama DNA array and we were able to rationally select two down-regulated genes after induction, and subsequently used them to develop engineered strains that were capable of enhanced production of IGF-I.

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