Rational design for improving cell growth and protein production of a recombinant *Escherichia coli* strain using a proteomic approach

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To rational design for metabolic and cellular engineering, proteome profiling in response to the overexpression of human obese gene coding for leptin in *Escherichia coli*was investigated by 2-dimensional gel electrophoresis. We identified total of 88 proteins showing expression level variation. From the proteome analysis, we examined (i) the effects of the presence of plasmid, (ii) global physiological changes before and after induction, and (iii) inclusion body-associated proteins. We found two big burdens during overexpression of leptin. Especially, based on many physiological changes during overexpression of leptin, we firstly could design a strategy to enhance protein productivity by manipulating the target gene, *cysK*. We were able to recover cell growth rate reduced due to burden of plasmid presence, and to improve leptinproductivity by four times. Also, we demonstrated that this system could apply to production system of serine-rich proteins. This study was shown firstly that the use of such data by proteome analysis is critical to the design of the engineering of metabolic pathways needed for increase cell growth rate and the productivity of recombinant proteins in industrial bioprocesses.

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