

Stress-induced Proteome Network of *Escherichia coli*

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Through 2-DE-based quantitative proteomics, we systematically analyzed and integrated the dynamic characteristics of overall proteome profiles of *Escherichia coli* BL21 strain under four different stresses influencing redox potential and protein folding. By comparative analysis, we focused on the proteins that showed significantly notable increase in expression levels. Then, we classified these proteins were classified into 3 groups on the basis of their functions ; heat shock proteins/foldases, metabolic enzymes, and other stress responsive proteins. Consequently, these studies allowed us to design and construct the new fusion tags as effective folding enhancers for desired recombinant proteins. Surprisingly, some of stress induced fusion candidates enhanced protein folding of heterologous proteins remarkably.