A Probabilistic Superposing of Protein Structures

Tsuyoshi KATO
Computational Biology Research Center
e-mail: kato-tsuyoshi@aist.go.jp
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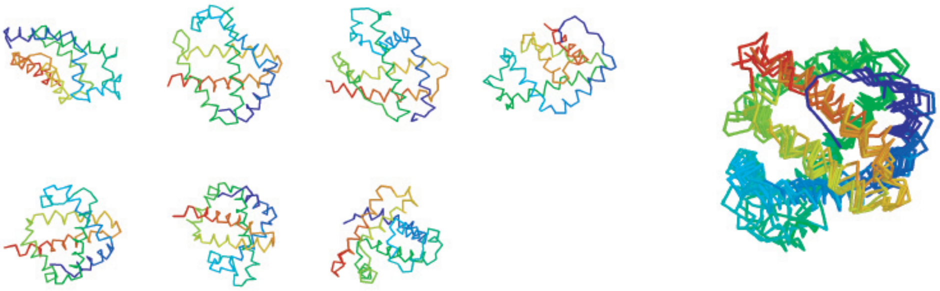
It is not easy to compare protein structures, as they tend to be translated and rotated in arbitrary ways. A set of proteins have to be superposed correctly to measure meaningful similarities among them. Therefore, it is a key to estimate the direction and location of each structure correctly. We focused on the probabilistic modeling for representing structures by employing the hidden Markov model which is one of the successful probabilistic models, and developed a novel algorithm for estimating the direction and location by maximum likelihood. We also adopted our algorithm for seven protein structures, and achieved almost perfect superposition, as illustrated in the figure.



Superposition of protein structures. Using seven protein structures shown in the left figure, our estimation algorithm found the almost optimal rotation and translation and the common shape, as shown in the right figure

Yeast Expression System at Low Temperature

Takehiko SAHARA
Institute for Biological Resources and Functions
e-mail: t-sahara@aist.go.jp
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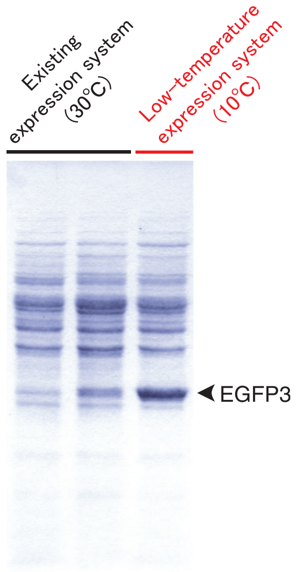
We have developed a novel expression system in yeast, *Saccharomyces cerevisiae*, at low temperature. In the expression system, target proteins can be produced only by lowering a culture temperature. A production yield of a protein in the expression system was higher than that in the existing expression systems in yeast at moderate temperature. Several proteins that were expressed as insoluble forms in *Escherichia coli* could be produced in functional and soluble forms in our expression system. Our expression system will greatly contribute to proteomics study and large-scale production of pharmaceutical and industrial proteins.



Effective production of EGFP3 in yeast at low temperature