Comprehensive Structure-based Functional Analysis on Transcription Factors

Hiroshi Itou[a], Ui Okada[b], Min Yao[b], Nobuhisa Watanabe[b], Isao Tanaka[b], [a]*Biomolecular Structure Laboratory, National Institute of Genetics, Mishima, Japan.* [b]*Graduate School of Science, Hokkaido University, Sapporo, Japan.* E-mail: hitou@lab.nig.ac.jp

Genomic-DNA analysis on number of organisms is now accomplished. Using these information, comprehensive structure analysis of transcription factors for their structure-based functional understanding is in progress. Our research target is transcription factors including putative ones from hyper-thermophilic archaeon *P.horikoshii*, mesophilic bacteria *C.glutamicum* and vertebrates *H.sapience.* Target proteins were cloned, over-expressed, purified and purified proteins were tried crystallization for X-ray crystal structure analysis. We had already succeeded in structure analysis of three of them, PH1161 [1] and PH1932 from *P.horikoshii* and CGL2612 from *C.glutamicum*. PH1161 protein is a homologue of bacterial transcriptional activator TenA, and PH1932 and CGL2612 are homologue of transcriptional repressor protein ArsR and QacR, respectively. As a further functional analysis, recognition DNA sequences of PH1932 and CGL2612 proteins were analyzed using the SELEX (Systematic Evolution of Ligand by EXponential enrichment) method. The SELEX suggested several consensus sequence of DNA recognized by these proteins, providing indispensable information to reveal their biological functions.

[1] Itou H., Yao M., Watanabe N., Tanaka I., *Acta. Cryst*, 2004, **D60**, 1094.

Keywords: structural genomics, transcription factor structure, x-ray crystal structure detemination