Summary of Protein 3000 Project in the Protein Crystallography Research Group and the next perspective

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We established a high-throughput crystallography system [1] utilizing the synchrotron radiation of SPring-8 as a contribution to the "National Project on Protein Structural and Functional Analyses". This project, also known as "Protein 3000", was a five-year structural genomics program that completed in March 2007 and was funded by the MEXT organization of Japan. The structure determination pipeline includes three newly developed technologies for automating X-ray protein crystallography: "TERA", an automated crystallization and observation robot system; the SPring-8 Precise Automatic Cryosample Exchanger (SPACE) for automated data collection; and the Package of Expert Researcher's Operation Network (PERON) for automated crystallographic computation from phasing to model checking. These facilities were developed in cooperation with other laboratories in the RIKEN SPring-8 Center. During the five years following April, 2002, this pipeline was used by seven researchers to determine 138 independent crystal structures (resulting from 437 purified proteins, 234 cryoloop-mountable crystals, and 175 diffraction data sets). The pipeline clearly made a significant contribution to the large-scale determination of protein crystal structures. During the Protein 3000 period, we also developed various elemental technologies for recalcitrant target proteins, such as the crystallization catalyst [2] and the crystal improvement by mutagenesis [3].

As of September 2008, as described below, we focuses on the application of the Protein 3000 resources to contribute to the X-ray free electron laser (XFEL) project and the integrated database project, both of which are funded by the MEXT grant. In near future, we will disseminate the project results for the benefit of national or international society, through releasing the protein analysis platform to inside and outside of RIKEN. Regarding the integrated database project, we will provide certain experimental data available in RIKEN to the database project by collaboration with the RIKEN Yokohama Institute, to benefit researchers in a broad range of life science fields. These data include the omics information of *Arabidopsis thaliana* and the analysis data from the Protein 3000 project. The experimental data to be provided will be compiled and annotated properly to enhance the scientific value of the data. We are responsible for the Protein 3000 data in the RIKEN Harima Institute.

Reference

- [1] Sugahara M. et al. (2008) J. Struct. Funct. Genomics, 9, in press (DOI 10.1007/s10969-008-9042-y)
- [2] Sugahara M. et al. (2008) Acta Cryst. D, 64, 686-695
- [3] Mizutani H. et al. (2008) Acta Cryst. D, 64, in press (DOI 10.1107/S0907444908023019)