Midterm Review
Protein Crystallography Research Group

Date: June 2011 (conducted by e-mail)
Reviewers:

- Dr. Yu-Shan Huang, Head of the Taiwan Beamline Office, National Synchrotron Radiation Research Center
- Dr. Masaki Takata, Deputy Director, RIKEN SPring-8 Center
- Dr. Yoshitsugu Shiro, Deputy Director, RIKEN SPring-8 Center
- Dr. Masaki Yamamoto, Director of Advanced Photon Technology Division, RIKEN SPring-8 Center

General Comments:

[Reviewer 1]

The information provided in the carefully preparatory documents is clear enough and allows the reviewer a detailed review of the PXRG performance. In brief, the overall appraisal of the level and quality of the PXRG's research activity is EXCELLENT* according to its quality and quantity of publications as well as its great contributions to the structural biology society. The overall appraisal of the level and quality of the PXRG's management is EXCELLENT* according to an efficient management proved by its solid research directions, very convincing results with limited manpower, international collaboration and industrial application, and growing funding from various sources. The reviewer is therefore sure that the PXRG's major group mission, being support for users both in-house and outside, has been very successfully executed.

*poor = 0-2, fair = 3-4, good = 5-6, excellent =7-9

[Reviewer 2]

The RSC Protein Crystallography Research Group (PCRG) is achieved an important mission by continuing and further developing the activities of the national structural genomics project of Japan's "Protein 3000" initiative (FY 2002-2006) and successfully took over the resources and functions of the High Through-Put Factory (HTPF) to launch the Protein Tectonics Platform (PTP) as an integrated research infrastructure for protein crystallography in

the SPring-8. As a result, the PTP promoted fruitful international collaboration with Taiwan NSRRC in addition to the basic infrastructural role for structural biology research at RIKEN SPring-8 Center (RSC).

In the RSC as a world-leading Photon Science Research Complex with the SPring-8 and SACLA, the area of the PCRG's activities, however, shall be transferred from the structural biology based on the crystallography to the photon control science, which allow an advanced visualization and/or creation of biological function such as "Bio-function photon science". Since this movement is the common with the trend of the materials science in RSC, the PCRG may be expected to cover the whole research area relating to the photon science. It is, therefore, the strategy concept and positioning of the PCRG in the Advanced Photon Technology Division should be reviewed and enhanced to facilitate activities of the newly-emerged RSC with SPring-8 and SACLA.

[Reviewer 3]

This Group started in 2008, which was based on the facilities and the research achievements of the national projects "Protein 3000" in the SPring-8 site. The "Protein 3000" was the big national project, the purpose of which was determination of 3000 protein structures by X-ray crystallographic and NMR techniques. To pursue the purpose, new facilities were launched and new technologies were developed. It is highly appreciated that the Group was established at the SPring-8 site after completion of the project, in order to broaden the achievement of the project to the general users of SPring-8 who are interested in structural biology. In the first 3 years, the group appeared to make efforts to establish the facilities and management systems, and is now settled down for its activities.

[Reviewer 4]

1. Present status of RSC Protein Crystallography Research Group

RSC Protein Crystallography Research Group (PCRG) was established as the successor to the High Through-Put Factory (HTPF) prepared by the national structural genomics project of Japan's "Protein 3000" initiative (FY 2002-2006). A vast of resources took over the HTPF were rearranged to the Protein Tectonics Platform (PTP) as a research infrastructure for protein crystallography in the SPring-8 campus. The PCRG steadily operate the PTP

in spite of the limited human resources. The PTP has been playing the important role as the basic infrastructures for structural biology research at RIKEN SPring-8 Center (RSC) and the international collaboration with Taiwan NSRRC.

PCRG has developed various technologies for the protein crystal engineering. A novel protein crystallization method using microporous zeolite as a heteroepitaxic nucleant is a unique and a promising technology to standardize the process of protein crystallization. More practical experiments to crystallize the structure unknown proteins will be strongly expected. A crystal contact design to improve diffraction quality of protein crystals by introducing mutations is an interesting study to improve the quality of the structure known crystals. In order to generalize this idea, more practical case studies will be recommended.

2. Future prospects for RSC biological research

PCRG are making important efforts for basic protein crystallography research at RSC. However, many types of equipment at the PTP are mainly focused on the High Through-Put protein crystallography for statistic structures of soluble proteins. Today's PTP based on the infrastructure prepared by "Protein 3000" before 2006 has been losing the competitive power in modern protein research according to the aging and changing the direction of protein science.

The leading edge targets of biological and protein science are moving from soluble proteins to membrane proteins and from statistic structures to dynamical structures according to the progress of the instrumentation and methods of SR and XFEL. At the SPring-8 campus, micro-focused X-rays at RIKEN Targeted protein beamline and X-ray Laser at SACLA have been utilized recently. Those will open the next door for biological and protein science. In order to accelerate and support the cutting-edge biological science at the SPring-8 campus, next generation infrastructures for biological research targeted not only proteins including membrane proteins but also higher order biological samples; for example, cell, cell organelle and supra molecule complexes, are strongly expected.