

**m01.o05****High-Quality Protein Crystallization in Space by JAXA-GCF Project**

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Japan Aerospace Exploration Agency (JAXA) has developed a package of technologies for obtaining high-quality protein crystals in space to contribute to the structural biology and the rational drug design, using modified crystallization method originally developed by European Space Agency (ESA) and Garcia-Ruiz's group [1]. In JAXA-GCF project, JAXA has constructed a user-friendly experimental frame work and provided regular flight opportunities, twice a year, using Russian flights. The success rate of crystallization, that is mostly the rate of improvement of the maximum resolution of diffraction, has been significantly increased to about 70% of the protein that had high purity and succeeded in the optimization of the crystallization condition. The most remarkable point of JAXA-GCF's result was that the maximum resolution was still improved even in the case that the ground-grown crystal showed excellent resolution, in the range of 1 to 1.5 Å [2]. In the near future, space experiment could be essential especially for obtaining atomic resolution crystals which will become significant for the drug design.

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[1] Garcia-Ruiz, J. M., Gonzalez-Ramirez, L. A., Gavira, J. A., Otalora, F. *Acta Cryst.*, D58, 1638 (2002).

[2] Tanaka, H., Inaka, K., Sato, M., Takahashi, S., Sugiyama, S., Yamanaka, M., Sano, S., Motohara, M., Kobayashi, T., Yoshitomi, S. *Acta Cryst.*, A61, C442 (2005).

**m02.o01****The new High-Throughput Crystallization at the EMBL-Hamburg**

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Progress in the life sciences depends on our understanding of complex biological processes at the molecular level, which in turn depends on our capability of rapidly determining the three-dimensional structures of all molecules involved in atomic detail. X-ray crystallography is the method of choice in structural analysis, contributing 85% of structures deposited in the PDB. A bottleneck specific to bio-crystallography is the need to produce large amounts (> 5mg) of chemically and structurally homogenous sample and to grow well diffracting crystals.

Despite numerous improvements in X-ray crystallographic methodology, it is still a comparatively slow technique. Since neither the ability to crystallise nor specific crystallization conditions for biological macromolecules can be predicted, a large number of different molecular constructs have to be scrutinized with respect to a large number of different crystallization solutions in order to identify appropriate crystallization conditions. As a consequence, the process of crystallization has been heavily automated.

The EMBL-Hamburg Outstation has established Europe's largest high-throughput crystallization facility that is open to the general user community. The facility has the capacity to generate 10,000 crystallization experiments in 8h and to store and image 1,000,000 experiments. During comprehensive validation in 2005, more than 83 users have submitted over 500 samples which were setup in 3,000 crystallization plates (~300,000 experiments). The platform consists of two highly integrated modules which are operated by one FTE.