High-throughput Protein Structural Analysis System at the Structural Biology Research Center in KEK-PF

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Obtaining X-ray quality crystals might require setting up thousands of crystallization trials on different conditions for protein solutions and precipitants. To this end, we have developed a large-scale protein crystallization system (PXS) that allowed efficient crystallization trials of large protein complexes and structure-based drug design. It includes a dispensing system, an observation system for acquiring images of drops according to a pre-programmed schedule and storing them to a file server, incubators and a plate-carrying robot. Users can access the file server from anywhere in the world through a Web browser for checking the status of their crystal growth.

Protein crystals which have grown large enough for X-ray diffraction experiment are harvested using cryo-loops and plunged into liquid nitrogen. We adopted a micro-manipulation system to overcome difficulties of harvesting crystals and we have succeeded in harvesting protein crystals from drops using a prototype harvesting system.

In order to pick up a frozen crystal from a Dewar and mount it onto a goniometer on an X-ray diffractometer automatically, we have installed two sample exchange robots based on the SAM (SSRL Automated Mounting) systems at our insertion device beam lines BL-5A and AR-NW12A at the Photon Factory. To reduce the time required for sample exchange further, a prototype of a double-tong system was developed. As a result of preliminary experiments, the sample exchange time was successfully reduced from 70 seconds to 10 seconds excluding the time required for pre-cooling and warming up the tongs. We plan to install the same type of robot at the new micro focus beam line BL-17A.
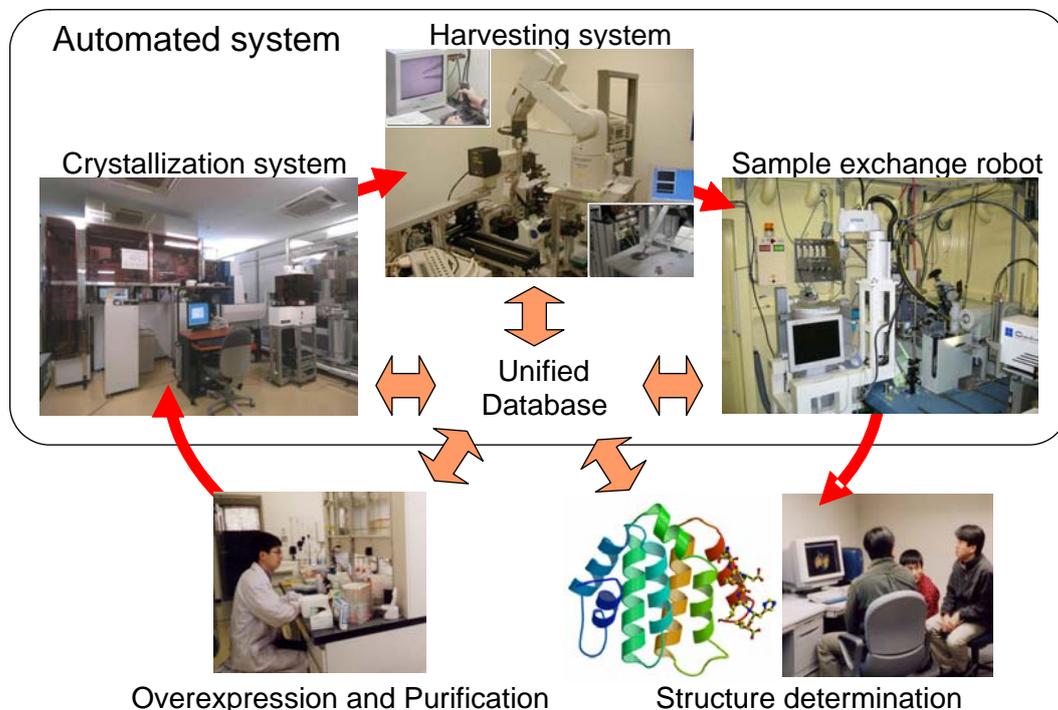
We are progressing developments of automated structural analysis system for high-throughput protein crystallography (Fig.1).