

High-throughput Protein Crystallization

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For high-throughput protein crystallography, we are developing a fully automated X-ray structural analysis system that consists of several subsystems for protein crystallization, harvesting and freezing crystals, mounting inside a hutch and data acquisition.

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 with the capability of setting up 240,000 crystallization trials per day. This system allows efficient crystallization trials of large protein complexes and structure-based drug design. It includes a crystallization tray supplier, a dispensing system using disposable tips which are specially designed for high dispensing accuracy, a sealing system, an observation system for taking images of drops in wells according to a pre-programmed schedule and storing them to the file server, incubators and a carrying robot which moves the trays between these components. Users can access the file server from anywhere in the world through a Web browser for checking the status of their crystal growth.

We will also describe a crystal harvesting system and automated sample exchange robots based on the SAM (SSR Automated Mounting) system as part of our efforts in automating X-ray structure determination.

Keywords: crystallization robots, automated crystallization, automated data collection