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 (SSRL Automated Mounting) system as part of our efforts in automating X-ray structure determination.

Keywords: crystallization robots, automated crystallizaton, automated data collection

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Miniaturization in Structural Biology Pipelines

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High-throughput (HT) structural biology is making significant contributions to our attempts at developing a complete understanding of biological systems. Process pipelines designed using HT approaches have now been implemented to explore protein fold/function space, to accelerate the Structure Based Drug Discovery, to study complete proteomes, and to develop and disseminate methods and technologies for working with integral membrane proteins.

The central theme of the technology development in our laboratory and that of our collaborators has been automation, integration, and miniaturization of processes in High-throughput structural analysis pipeline. These developments have dramatically increased success rates reducing the cost per structure by decreasing time from gene to structure, material usage, and number of personnel needed to accomplish large number of tasks. These factors also shorten feedback loops between processes leading to an almost two-fold decrease in time to arrive at a structure.

New tools for the HT pipeline include development of robust micro-expression protocols, use of NMR micro-probe for rapidly identifying protein targets amenable to further structural studies, use of nanocalorimetry or enthalpy array for biophysical characterization of interactions, and miniaturization, automation of the crystallization experiment, and use of workflow and GRID technologies for use in computational tasks in HT structure determination efforts.

Keywords: structural genomics, high-throughput structural biology, biophysical characterization

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High-resolution Data using short Wavelength Confocal Optics and a Cylindrical IP

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Combination of modern techniques for allows for new laboratory experiments that were previously inaccessible without specialized equipment. A new confocal optic for silver (Ag) radiation coupled with a rotating anode allows for greatly increased intensities at the sample position from this very short wavelength radiation.

By coupling this source with a cylindrical image-plate detector, very high resolution (high-Q) diffraction data can be obtained from a variety of samples, including single-crystal, powder, thin films, etc.

Several experiments are described and the results from high-resolution experiments are discussed.

Keywords: X-ray optics, high-Q, Ag radiation