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**HPC and Grid Applications in High Throughput Protein Crystallography.** R. Keegan, D. Meredith, G. Winter, M. Winn, Daresbury Laboratory, Warrington, Cheshire, WA4 4AD, U.K.

We present details of work being carried out to aid the development of high throughput protein crystallography through the use of high performance computing and Grid technologies. We focus upon the speedup of data collection processes and structure solution, and upon the remote access to high-performance compute resources. Rapid feedback regarding the quality of data collected on a synchrotron beam-line is essential for the efficient operation of high-throughput systems. To achieve this goal, we have developed parallel versions of data processing codes and have also investigated the use of cheap “Beowulf” type clusters and clustering tools such as queuing systems. The developments in automated systems for post data collection structure solution are well suited to the utilization of HPC and Grid technologies. A parallel version of a molecular replacement code for running on a Beowulf type system has been developed. Access to these high-performance resources has been achieved through the use of web-services and Grid-enabled web-portal technologies. This facilitates the remote submission and monitoring of computationally intensive jobs in a secure, platform independent environment.