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A Medium-scale, High-efficiency and Low-cost Platform for Structural Genomics Studies. Xiao-Dong Su^a, ^aCollege of Life Sciences, Peking Univ., Beijing 100871, China.

A platform for structural studies using Beckman Coulter Biomek FX and self-made automation systems has been set up at Peking University, the platform has a capacity to process about 2000 genes per year. So far, more than 470 *B. subtilis* and 1200 *S. mutans* genes, and hundreds of other genes, including human were selected as targets. More than 40 independent structures have been determined, among them, 11 are of novel structures by the criterion <30% sequence identity with known structures. More than 10 structures were determined *ab initio* by SAD/MAD phasing. We have adapted the genomic approaches in a moderately funded lab, and this adaptation has greatly improved the production of protein structures. Our goal is to solve a protein structure at an average cost of USD 10K.

As part of the platform, a low-cost, in-house developed, imaging robot for SBS crystallization plate has been constructed. It can scan a microplate in one to six minutes and a web-based crystallization database system has been developed, enabling users to follow their crystallization experiments from a web browser. The basic ideas for our system are simplicity, robustness and low-cost. The software consists of a controlling interface and an Image Management system, integrated with our in-house developed lab information management (LIMS).