High-throughput Protein Crystallization at the Center for Eukaryotic Structural Genomics

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The Center for Eukaryotic Strucural Genomics (CESG) solves structures of selected, unique eukaryotic proteins. Here we report the status and performance of our integrated robotic WHITE ICE system (Wisconsin HI-Throughput Extensible and Integrated Crystallization Environment) consisting of a Tecan Genesis™ crystallization platform, CrystalScore™ and CrystalFarm™ imaging systems, and Sesame, our laboratory information management system. We also present a preliminary analysis of the Fluidigm Topaz™ microfluidic chip-based crystallization and imaging platform, and evaluate its performance relative to microliter-scale crystallization experiments. The relative performance of protein samples prepared by micro- and large-scale protein production pipeline methods is also evaluated. The screening success rate for CESG fold-space targets is over 30%, and ~80% for test targets. We report analysis of our initial screening strategy and results from a salvage pathway encompassing alternative screens, perturbation screening, reductive methylation, and mutagenesis. Supported by Protein Structure Initative NIH grant P50 GM64598.

Keywords: crystallization, structural genomics, protein crystallography