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Protein Crystallization By Counter-Diffusion Coupled To Pipeline Crystallography Using a 96 Capillary Automated Loading Device. J. D. Ng¹, Z.-J. Liu², T. Lewis³, O. Carlton³, S. Hardin³, K. Hougland³, J. M. Garcia-Ruiz⁴, L. DeLucas³ and B-C Wang²,¹Univ of AL, Huntsville, AL 35899 USA, ²Univ of Georgia, Athens, GA 30602 USA, ³Univ. of AL, Birmingham, AL 35294,USA, ⁴IACT-CSIC-UGRA, Facultad de Ciencias, Granada 18002 Spain.

A crystallization device has been constructed to quickly screen or optimize protein crystallization conditions in a 96 array configuration by counter-diffusion in a restricted geometry. Model and recombinant proteins targeted by the Southeast Collaboratory for Structural Genomics were able to be loaded in capillary trays for finding optimal crystal growth conditions. Proteins were grown in cryoprotectant solution and used for immediate X-ray data collection for structural determination by Single Anomalous Scattering or Molecular Replacement techniques without any crystal manipulation. Ninety-six counter-diffusion processes can be performed at one time in an automated manner. The development of this high-throughput tool coupled to the advances in X-ray crystallography, the streamlining of tedious and time consuming events in determining three-dimensional structures can be realized.

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