

W0442

A Preliminary Screen To Optimize Protein Solubility And Improve Crystal Screen Results. Aude Izaac, Stephen J. Tomanicek, Timothy C. Mueser, Dept. of Chemistry, The University of Toledo, Toledo, OH 43606.

Crystallization of protein and protein complexes is a multi-parametric problem that involves investigation of a vast number of physical and chemical conditions. The buffers, salts and additives used to prepare the protein solution will be present in every crystallization condition. In many cases, we have observed a correlation between maximizing the solubility of a protein and the success of crystal screening. Using a preliminary solubility screen, we determine the solubility profile of a protein in various salt and buffer conditions. The proteins are dialyzed into the optimal buffer and salt solution and then concentrated. This approach has enabled us to improve the solubility of the proteins prior to crystallization experiments. Comparison of test proteins in optimized solution conditions versus standard solution conditions (Tris-HCl, NaCl) show improvement in the quality of crystals in the initial screens. The crystal screens were carried out at room temperature in 96 well, three drop Greiner crystal trays. All trays were poured with the 96 well Cartesian robot and set up using the honeybee sitting drop robot from Genomic Solutions. Crystal hits were recorded using the Rhombix imaging system from DCA. For the proteins that effectively crystallized, the optimized protein solution yielded large diffraction quality crystals directly in the screens, whereas in the same condition, the standard solution produced only clear drops, precipitates or microcrystals at best.