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Platform for Protein Crystallization Studies: Screening and Optimization via Control of the Supersaturation Rate. Paul J.A. Kenis*, David Y. Kim, Sameer Talreja, Charles F. Zukoski, Dept. of Chemical and Biomolecular Engineering, Univ. of Illinois at Urbana-Champaign, Urbana, IL 61801.

Obtaining a high quality crystal of a protein for X-ray diffraction often requires screening of a wide range of solutions conditions in order to induce crystal nucleation and growth. Different phase transitions are often observed as a result of different solution conditions. In this presentation we present a novel platform that enables the rapid identification and optimization of crystallization conditions for proteins and other molecules by precise control of the evaporation rate. Our platform allows for precise control of the supersaturation rate and, in addition, guarantees a phase transition in every experiment. This leads to several key advantages over present crystallization screening platforms (hanging drop, free interface diffusion, microbatch): (i) Crystal producing conditions can be identified in the matter of days rather than weeks or months, (ii) every experiment provides information (through the occurrence of a phase transition) to guide the search to better crystallization conditions whereas in the presently used platforms 'hit' rates are typically less than 15% of the experiments, and, as a result, (iii) less of the often-precious biological material is needed.