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Mixing it up for Protein Crystallization CARL HANSEN, Physics and Astronomy, University of British Columbia, MORTEN SOMMER, CCS, University of Copenhagen, JAMES BERGER, Molecular Biology, UC Berkeley, STEPHEN QUAKE, Bioengineering, Stanford — In the post-genomic era, X-ray crystallography has emerged as the workhorse of large-scale structural biology initiatives that seek to understand protein function and interaction at the atomic scale. Despite impressive technological advances in X-ray sources, phasing techniques, and computing power, the determination of protein structure continues to be severely hampered by the difficulties in obtaining high-quality protein crystals. Emergent technologies utilizing microfluidics now have the potential to solve these problems on several levels. We will present two microfluidic devices that have been shown to dramatically improve protein crystallization. The first is a formulation device which allows for the rapid combinatorial mixing of reagents to systematically explore protein solubility behavior. *A priori* solubility mapping allows for the rational design of optimal crystallization screens that are tailored to a specific target. A second screening device allows for massively parallel sample processing while exploiting the properties of mass transport manifest at the micron scale to ensure slow and efficient mixing kinetics that are difficult to achieve in macroscopic reactors.

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