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From thermodynamics to fluid mechanics: Enhancing the 2-D protein crystallization process JAMES YOUNG, DAVID POSADA, AMIR HIRSA, Rensselaer Polytechnic Institute, JUAN LOPEZ, Arizona State University — The leading method to determine protein structure is to perform X-ray diffraction on protein crystals. However, crystallizing protein is a challenging task which is usually met with limited success. 2-D protein crystals at the air/water interface are commonly obtained under quiescent conditions. Recently, the formation of such crystals was shown to be enhanced by the presence of flow. Here, we examine both the kinetics of the process, including the detrimental effects of protein aggregation, as well as the fluid dynamics associated with successful crystallization events. The deep-channel surface viscometer geometry is utilized which consists of the annular flow between two stationary cylinders and a rotating floor. For a particular protein surface concentration, a Reynolds number threshold has been identified above which crystals grow and below which they do not. This flow system also allows for the determination of the surface shear viscosity, which provides an indication of the mesoscale interactions associated with protein crystals.

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