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Effect of Reynolds number on 2-D protein crystallization at the air/water interface JAMES YOUNG, DAVID POSADA, AMIR HIRSA, Rensselaer Polytechnic Institute, JUAN LOPEZ, Arizona State University — X-ray diffraction is the primary technique used to obtain a detailed description of a protein on the molecular level and as such, has yielded essential information about protein structures and protein-ligand interactions. However a major drawback of this technique is that the protein must first be crystallized which is often a very difficult and inefficient process. It has been shown previously that the process of two-dimensional protein crystallization on lipid monolayers at the air/water interface can be enhanced by a shearing flow. Here we examine the relationship between Reynolds number and the crystal growth process using the deep-channel surface viscometer geometry, which consists of an annular region bounded by stationary inner and outer cylinders and driven by a constant rotation of the floor. The interfacial velocity measurements are compared to Navier-Stokes computations with the Boussinesq-Scriven surface model.

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