

Specific Rate of Protein Crystallization Determined by the Guggenheim Method

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Knowledge of the three-dimensional arrangement of the atoms in a protein molecule often serves as the key to understanding the biological function of the protein. Although X-ray diffraction from single crystals can be employed to solve for the molecular structure, use of this method is often impeded by the slow rate of precipitation of the crystals from the growth solution. In order to discover ways of adjusting the conditions in the growth solution to speed up the kinetics, the measurement of the specific rate of crystallization is of interest [1]. Because the crystals are denser than the growth solution, the process of crystallization can be followed by growing the crystals in a dilatometer [1]. To determine the specific rate of crystallization, the height of the fluid in the capillary side arm of the dilatometer is measured as a function of the elapsed time. In the case of the protein, canavalin, for example, the time required to reach solubility equilibrium is four to five days. If, however, the height vs. time measurements of the fluid in the side arm are collected in groups at equally spaced times, the data can be analyzed by the Guggenheim method [2]. There is no need to wait until the experiment has reached equilibrium. We show that use of the Guggenheim method reduces the time required to determine the specific rate of crystallization to about two days.

[1] K. G. Caraballo, J. K. Baird, and J. D. Ng., *Cryst. Growth Des.* **6**, 874 (2006).

[2] J. W. Moore and R. G. Pearson, *Kinetics and Mechanism*, John Wiley and Sons, New York, 1981. p.71.