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A Simplified and High-Density Counter-Diffusion Method for a Protein Crystallization. Masaru Sato,¹ Hiroaki Tanaka,² Koji Inaka,³ Shigeru Sugiyama,³ Sachiko Takahashi,² Satoshi Sano,¹ and Susumu Yoshitomi¹; ¹Japan Aerospace Exploration Agency, Ibaraki, 305-8505, Japan; ²Japan Space Utilization Promotion Center, Tokyo, 169-8624, Japan; ³Maruwa Food Industries, Inc., Nara, 639-1123, Japan.

We previously reported 'Gel-Tube' method for a protein crystallization using a simplified counter-diffusion method for optimising crystallization conditions using only readily available in the laboratory^[1]. The one capillary could continuously scan a wide range of crystallization conditions unless crystallization occurred, which meant that single capillary may be equivalent to many drops of the vapour-diffusion method. In addition, if 1-dimensional (1-D) simulations of the crystal growth based on the 1-D diffusion model would be combined with the crystallization in the capillary, we could estimate the solution concentrations in the capillary at which the crystallization occurred.

Based on this method, we introduce our new modified crystallization device. It requires less amount of the crystallization solutions. Crystallization cells are individual and packed in high-density. This device will be applicable for the space experiment in the future.

[1] Tanaka, H. *et al.*, *J. Synchrotron Rad.* (2004). 11, 45-48