Poster Presentation

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Increasing the probability of successful crystallization by using symmetric tag

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Recent progress in the techniques of bio-macromolecular crystallography makes crystal structure analysis more powerful and useful for life science. The structure analysis of huge super-molecular (eukaryotic Ribosome, Vault etc.) and membrane proteins related to diseases were successful. Moreover, the structure/fragment drug design using crystal structure analysis method is also becoming reliable. However, crystallization still remains as a major bottleneck for determining bio-macromolecular structures, although many methods have been developed such as crystallization kits, crystallization robot, crystallizing in gel, space, and magnetic field, laser excitation, using antibody, modification of protein surface, and so forth. The current situation of crystallization is still dependent on the accidental method searching for a crystallization reagent and the growth environment since the methodology for obtaining a quality crystal for structure analysis is not established yet. Therefore, further development of more advanced crystallization methods is required to increase the probability of successful crystallization. In principal, probability of successful crystallization could be increased by polymerized molecules with 2 or 3-fold rotation symmetry [1]. We have solved more than 100 structures, and found some fragments which is isolated from core structure, and seem to contribute to form high quality crystal by forming a polymer with 2 or 3-fold axial symmetry. Thus, we developed a novel method by fussing target protein with crystallization tags named 2/3RS-tag. These 2/3RS-tags polymerize target proteins with 2 or 3-fold axial symmetry, and consequently accelerate formation of crystal. We will report and discuss this new method in this presentation.

[1] *D. R. Banatao, D. Cascio, et. al., PNAS, 102, 16230-16235 (2006)*

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