

||||| 特集：国際宇宙ステーションの応用利用 |||||
(解説)

高品質結晶を利用したサブオングストロームレベルの
タンパク質構造・機能解析とその応用
—JAXA/ISS 応用利用研究拠点（大阪大学）での取り組み—

中川 敦史

**Structural and Functional Analyses of Proteins at Sub-angstrom
Resolution Using High-quality Crystals and Their Applications**

Atsushi NAKAGAWA

Abstract

Recent progress in protein x-ray crystallography has revealed many numbers of complex biological macromolecules. Structural biologists usually discuss the function of the molecules based on their atomic structures. However, most of these discussions are based on their structures without hydrogen, since atomic scattering factor (interaction with x-ray with atom) is proportional to the number of electrons and it is quite difficult to observe hydrogen by x-ray diffraction. Biological activities, or living process, is mostly based on chemical reaction of biological molecules. Not only biological macromolecules, but also water molecules and/or ions often play key roles in this process. Electron structure is also one of the most important information in chemical reaction. Atomic resolution ($\sim 1.2 \text{ \AA}$) data are required to observe hydrogen and much higher data are required to observe electrons. Also, higher-resolution data reveals more solvent structures and more disordered structures. We are working on the development of subangstrom structural biology as a collaborative program, and crystallization under microgravity is a key tool for the project.