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New Possibilities Offered by Current Progress in Neutron Macromolecule Crystallography. Flora Meilleur, Institut Laue Langevin, BP156, 38042 Grenoble, France, meilleur@ill.fr

Neutron macromolecule crystallographic studies are providing unique and complementary insights on hydrogen and hydration in protein crystal structures that are not available from X-ray structures alone. Recent progress in neutron protein crystallography instrumentation have dramatically improved the speed and precision with which neutron protein structures can now be determined. Ongoing developments will further extend the size and complexity of systems that can be studied. Parallel improvements in modern molecular biology now allow fully (per)deuterated protein samples to be produced for neutron scattering that essentially eradicate the large hydrogen incoherent scattering background that has hampered such studies in the past. High quality neutron data can now be collected to near atomic resolution ($\sim 2.0\text{\AA}$) for proteins of up to ~ 50 kDa molecular weight using crystals of volume $\sim 0.1\text{ mm}^3$. The ability to flash-cool and collect high resolution neutron data from protein crystals at cryogenic temperature (15 K) now opens the way for kinetic crystallography on freeze trapped systems.