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Beyond the Folding Structure of Biomolecules. Structural Chemistry and Molecular Recognition in Biomolecules Evolved at J-PARC. Nobuo Niimura, Inst. of Applied Beam Science, Ibaraki Univ., Hitachi 316 8511, Japan.

The J-PARC project in Japan for a 1 MW spallation neutron source is now under construction. There, the construction of dedicated neutron diffractometer for protein crystallography named BIX-P1 is also under construction. At the new instrument, the neutron intensity at the sample position will become about 100 times higher than at the current BIX-type diffractometer installed at JRR-4 in JAEA.

Neutron bio-macromolecular crystallography provides the accurate information of hydrogen & hydration in proteins and nucleic acids. This will open the new field beyond the folding structure of bio-macromolecules such as:

1) Recognition of proteins and nucleic acids through the network structure of water molecules surrounding bio-macromolecules, and

2) The nature of chemical bond in proteins and nucleic acids elucidated by the accumulation of accurate structural information of hydrogen atoms.