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Neutron Diffractometer for Protein Crystallography at Cold Neutron Beam Line of JRR-3

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The elucidation of the protein-protein interaction, especially among membrane proteins and protein complexes, is one of the most important research fields in life science. Such proteins have large molecular weights, and the lattice lengths of their crystals have large values. Cold neutrons contribute to improve the difficulty in separating Bragg peaks from those crystals. JRR-3 has three cold neutron beamlines in the beam hall facility, in which neutron guides have been recently upgraded to supermirror guides ($m=3$). The neutron intensity gain by the upgrading has also been estimated.

A diffractometer, to be installed at the cold neutron beamline, will be equipped a feature to choose a wavelength appropriate for data collection from crystals with a large unit cell. While BIX-3 and BIX-4 diffractometers with the Neutron Imaging Plate detector are now located in the reactor hall of JRR-3, this detector is more suitable to be used in the beam hall with a lower gamma-ray background. As the effectively usable angular divergence is limited for the single crystal diffraction method, neutron beam within the divergence of 1.0 degree at the cold beamline was simulated by the McStas program. From the calculation the peak wavelength of the spectrum at C1-3 beam port (a candidate port for the installation) was shifted from 0.4 nm to 0.29 nm, and the gain was one order of magnitude at the wavelength of 0.29 nm by the upgrading. The performance of the diffractometer will be discussed.

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