BL12B2
NSRRC BM

BL12B2 is one of the two contact beamlines based on the collaborative Memorandum of Understanding between National Synchrotron Radiation Research Center (NSRRC, Taiwan), Japan Synchrotron Radiation Research Institute (JASRI), and RIKEN SPring-8 Center (RSC) since 1998. The user support and end station maintenance of the beamlines have been provided by NSRRC. BL12B2 has been maintained to serve for material science and protein crystallography users since 2000. The current schematic layout of the beamline is presented in Figure 1. The beamline is equipped with collimating mirror (CM), double crystal monochromator (DCM), and focusing mirror (FM). The measured spot size and total flux of the beam is about 250 μm square and about 1.5×10^{11} photons respectively at the protein end station at incident photon energy of 12 keV. Four end stations, EXAFS, X-ray diffraction, X-ray scattering, and protein crystallography (PX) end stations, are equipped tandemly inside the experimental hutch of BL12B2.

The EXAFS experiment is measured using two ion chambers at EXAFS table located at most upper stream of the BL12B2 experiment hutch. The users can carry out experiment by placing their sample in between these two ion chambers. Powder X-ray diffraction is measured using image plate at XRD table located next to the EXAFS table. X-ray scattering experiment can be carried out using six circle diffractometer. The sample environment of these two experiments can be changed from 20-400 K. High pressure X-ray diffraction can be carried out using CCD camera at protein crystallography table. Protein crystallography (PX) end station which is equipped with CCD and SPring-8 standard auto sample changer system has been installed since 2009. The user interface software of PX is SPring-8 standard BSS. Remote access capability of this PX system has been tested and operated from 2011. The CCD detector has been upgraded from Quantum 210r to Raynox MX225-HE in 2014. The fast read out and wide detection area of the new detector will help user to collect high quality data. We have planned to carry out mail-in powder diffraction experiment using this PX setup. In 2015, control program BSS has been updated for mail-in powder diffraction experiment.

EXAFS, X-ray diffraction, X-ray scattering end stations are serving for material science users. The material science experiments are covering wide area of topics, such as environmental science, nano science, geophysical science, etc.

In 2015, BL12B2 users have published eighteen papers in SCI (Science Citation Index) journals. The material science and protein crystallography users have published eleven and seven papers, respectively. Figure 2 shows the selected result from material science user Dr. J.-M. Chen's group (NSRRC). They studied pressure dependence of Yb compounds. They found crossover from a heavy fermion to intermediate valence state in noncetrosymmetric $Yb_2Ni_{12}(P,As)_7$. Figure 3 shows the selected result from protein crystallography user Dr. C-J. Chen's group (NSRRC). Betanodaviruses cause massive mortality in marine fish species with viral nervous necrosis. It is expected that the structural mapping of the GNNV P-domain also provide a clue for the development of vaccine strategies in the fish aquaculture industry. The atomic-resolution crystal

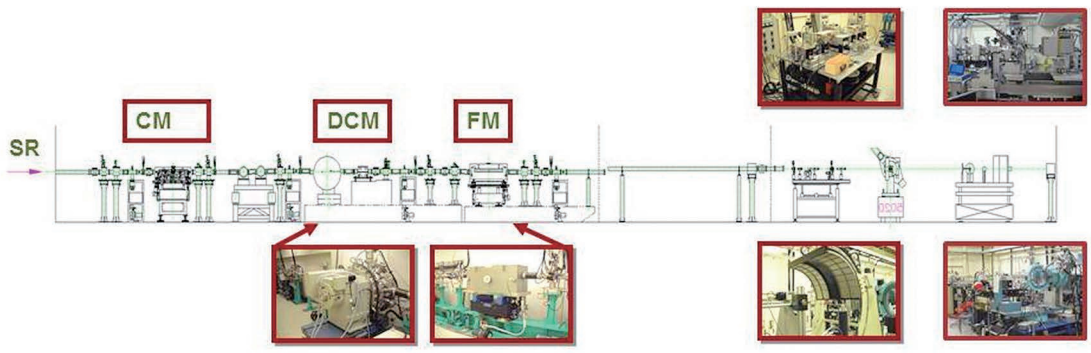

Fig.1 Schematic layout of BL12B2

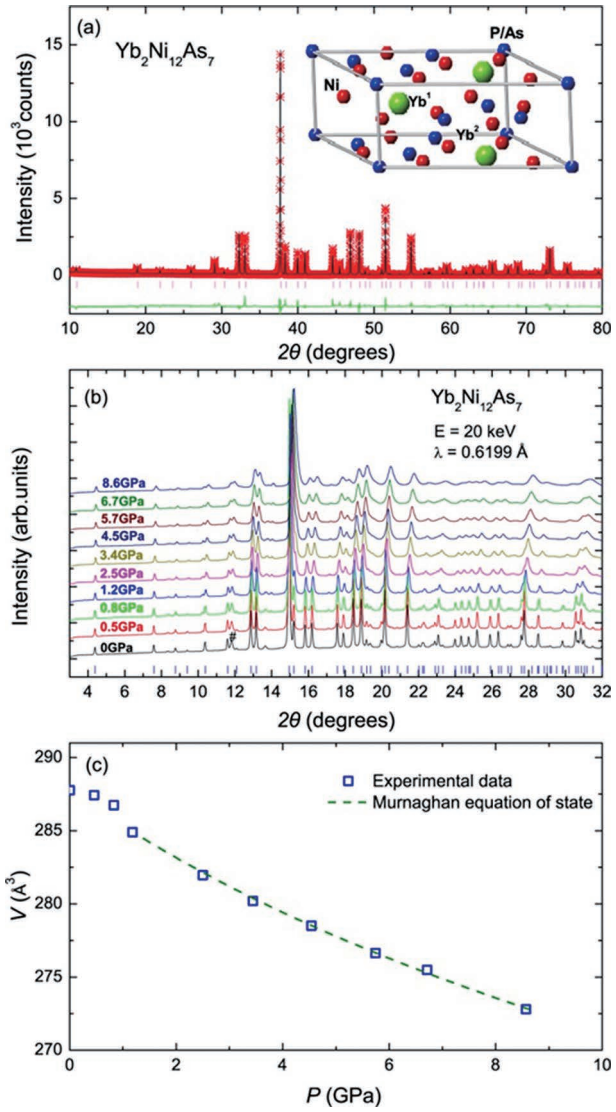

Fig.2 (a) Powder X-ray diffraction pattern of polycrystalline $Yb_2Ni_{12}As_7$. The red crosses and black solid line denote the experimental data and calculated profiles, respectively, while the vertical bars indicate the theoretical Bragg peak positions. The crystal structure of the compounds is shown in the inset. (b) Powder X-ray diffraction patterns of $Yb_2Ni_{12}As_7$ measured under applied hydrostatic pressure. (c) Pressure dependence of the unit cell volume, obtained from refinements of the unit cell volume, obtained from refinements of the XRD data. The dashed line shows a fit to the Murnaghan equation of state.[P8]

structure of GNNV, a piscine betanodavirus, was first revealed by X-ray crystallography. The structural studies of GNNV together with the biological assays shed insights into the role of the P-domain of GNNV in the capsid assembly and viral infection by this betanodavirus.

The beam time was shared between material science and protein crystallography users with equal amount. We will reconsider this ratio in 2016. The major users of the BL12B2 beamline in 2015 were from Taiwan. There are also

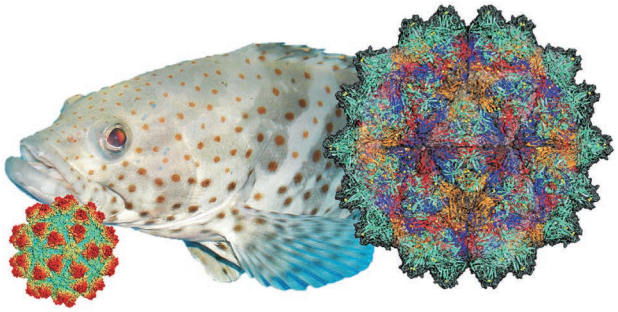

Fig.3 Orange-spotted Grouper fish and Grouper Nervous Necrosis Virus (GNNV). [P15]

international users from Japan and other place of the world. Users support has been provided by three local beamline scientists and one engineer.

Publications

Material Science

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