

BL12B2

NSRRC BM

The NSRRC-contracted protein crystallography station at SPring-8 Beamline 12B2 has served for Taiwan users of structural biology since the beginning of operation in 2002B. The station with the advanced facilities provides MAD/SAD, MIR/SIR and MR capabilities, and numerous protein structures have already been determined since last year. This year, the Taiwan PX users share about 50% of the user beamtime available in every period and are sufficiently supported by the capable and knowledgeable beamline scientists and staffs. In total 27 PX user groups travelling from Taiwan to SPring-8 have used the BL12B2 beamtime in year 2007. A number of research papers with the high impact factor have been published by user groups within recent two years which shows a great successful operation and research output.

Following highlight research work are selected from the protein structures determined using the BL12B2 beamline, including "Dual binding sites for translocation catalysis by Escherichia Coli glutathionylspermidine synthetase" by A. H.-J. Wang of Academia Sinica (EMBO J. 2006, 25, 5970); "Structure and mechanism of Helicobacter Pylori fucosyltransferase: a basis for lipopolysaccharide variation and inhibitor design" by A. H.-J. Wang of Academia Sinica (J. Biol. Chem. 2007, 282, 9973); "Structure of the SARS coronavirus nucleocapsid protein RNA-binding dimerization domain suggests a mechanism for helical packaging of viral RNA" by C.-D. Hsiao of Academia Sinica (J. Mol. Biol. 2007, 368, 1075); "Crystal structure of a bifunctional deaminase and reductase from Bacillus Subtilis involved in riboflavin biosynthesis" by S.-H. Liaw of National Yang-Ming University (J. Biol. Chem. 2006, 281, 7605); "Structure-based drug design of a novel family of PPAR γ partial agonists: virtual screening, X-ray crystallography, and in vitro/in vivo biological Activities" by S.-Y. Wu of National Health Research Institutes (J. Med. Chem. 2006, 49, 2703) and "Crystal structure of Helicobacter Pylori formamidase AmiF reveals a cysteine-glutamate-lysine catalytic triad" by W.-C. Wang of the National Tsing Hua University (J. Biol. Chem. 2007, 282, 12220). Other protein structures and functions have also been revealed using BL12B2 beamline.

In March 2007, the MOU has been signed as the joint force of NSRRC and IPR-Osaka to develop and construct laboratories for sample preparation and characterization at SPring-8. In the

coming year, BL12B2 beamline PX station will be fully upgraded to the automatic operation mode in collaboration with the REKEN beamline facility. It is expected that many more important biological structures will be explored in the coming years.