BL12B2
NSRRC BM

The Taiwan beamline BL12B2 is one of the contract beamlines under collaboration between National Synchrotron Radiation Research Center in Taiwan (NSRRC), JASRI and RIKEN Harima Institute. BL12B2 has been maintained to serve for material science and protein crystallography users since 2000. The schematic layout of the beamline is shown in Figure1. The beamline is equipped with a collimating mirror (CM), a double crystal monochromater (DCM), a focusing mirror (FM). The measured spot size of the beam is about 250 μm×250 μm at protein end station and total flux is about 1.5×10^{11} at 12 keV. There are four end stations, EXAFS, x-ray diffraction, x-ray scattering, and protein crystallography (PX) end stations inside the experimental hutch of BL12B2.

The EXAFS experiment can be measured using two ion chambers at EXAFS table located at the most upper stream of the BL12B2 experiment hutch. The users can carry out their own experiment by placing their sample in between these two ion chambers. Powder x-ray diffraction can be 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 of these two experiments can be controlled the temperature from 400 K-20 K using heater and cryostat. High pressure x-ray diffraction can be carried out using CCD camera at protein crystallography table. The PX endstation is equipped with CCD and SPring-8 standard auto sample changer system have 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 successfully in 2011.

EXAFS, x-ray diffraction, x-ray scattering end stations are serving for material science users. The experiments are covering wide variety of material science topics, such as environmental science, nano science, geophysical science, etc. In 2012, BL12B2 users have published sixteen papers in SCI journals. The material science and protein crystallography users have published six and ten papers respectively. Selected results are shown in Fig. 2 (material science) and Fig. 3 (protein crystallography). Fig. 2 shows temperature dependent XRD patterns of the $(V_{1-x}Cr_x)_2O_3$ nanocrystals[1]. Fig. 3 shows crystal structure of rice cytosolic glyceraldehyde-3-phosphate dehydrogenase (GAPDH) complex with NAD and sulfate[14].

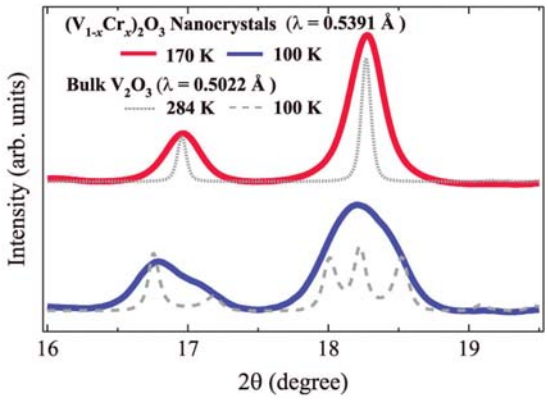

Fig.2 Temperature dependent XRD patterns of the $(V_{1-x}Cr_x)_2O_3$ nanocrystals. Red and blue line indicates high temperature 170 K and low temperature 100 K spectra, respectively. For comparison the data of the bulk $V_2O_{3.5}$ at high-temperature corundum phase (284 K) and the low-temperature monoclinic phase(100 K) are written in grey dotted and grey broken line, respectively[1].

The beamtime was shared for material science and protein crystallography users equally. The major users of the BL12B2 beamline in 2012 were from Taiwan. There are also international users from Japan and other place of the world. Users support has been provided by three beamline scientists and one engineer.

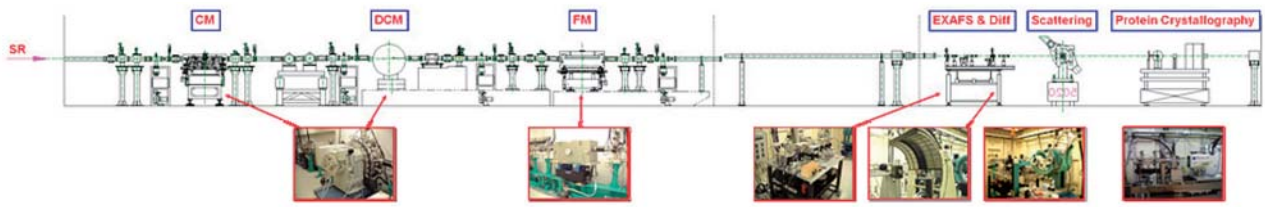

Fig.1 Schematic layout of BL12B2

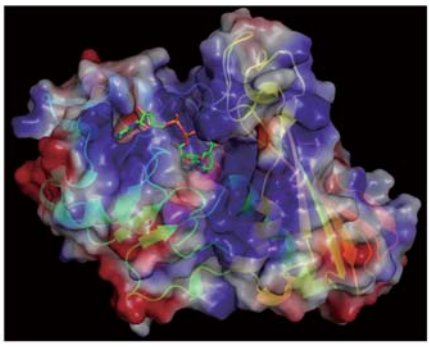

Fig.3 Crystal structure of rice cytosolic glyceraldehyde-3-phosphate dehydrogenase (GAPDH) complex with NAD and sulfate. The structure of GAPDH is presented as ribbons and the electrostatic surface (positive charges: blue; negatively charges: red). The NAD (in stick) is bound at the active-site pocket[14].

Publications

Material Science

[1] Y. Ishiwata, T. Shiraishi, N. Ito, S. Suehiro, T. Kida, H. Ishii, Y. Tezuka, Y. Inagaki, T. Kawae, H. Oosato, E. Watanabe, D. Tsuya, M. Nantoh and K. Ishibashi: "*Metal-insulator Transition Sustained by Cr-doping in V2O3 Nanocrystals*", Appl. Phys. Lett. **100** (2012) 043103.

[2] Y. Ishiwata, S. Suehiro, T. Kida, H. Ishii, Y. Tezuka, H.Oosato, E. Watanabe, D. Tsuya, Y. Inagaki, T. Kawae, M. Nantoh and K. Ishibashi: "*Spontaneous Uniaxial Strain and Disappearance of the Metal-insulator Transition in Monodisperse V2O3 Nanocrystals*", Phys. Rev. B **86** (2012) 035449.

[3] Y.-C. Kao, T. Huang, D.-Y. Lin, Y.-S. Huang, K.-K. Tiong, H.-Y. Lee, J.-M. Lin, H.-S. Sheu and C.-M. Lin: "*Anomalous Structural Phase Transition Properties in ReSe2 and Au-doped ReSe2*", J. Chem. Phys. **137** (2012) 024509.

[4] C. Wang, F. Casper, Y. Guo, T. Gasi, V. Ksenofontov, B. Balke, G. H. Fecher, C. Felser, Y.-K. Hwu and J.-J. Lee: "*Resolving the Phase Structure of Nonstoichiometric Co2FeGa Heusler Nanoparticles*", J. Appl. Phys. **112** (2012) 124314.

[5] C. Wang, F. Casper, T. Gasi, V. Ksenofontov, B. Balke, G. H. Fecher, C. Felser, Y.-K. Hwu and J.-J. Lee: "*Structural and Magnetic Properties of Fe2CoGa Heusler Nanoparticles*", J. Phys. D- Appl. Phys. **45** (2012) 295001.

[6] S.-C. Weng, Y.-R. Lee, C.-G. Chen, C.-H. Chu, Y.-L. Soo and S.-L. Chang: "*Direct Observation of Charge Ordering in Magnetite Using Resonant Multiwave X-ray Diffraction*", Phys. Rev. Lett. **108** (2012) 146404.

Protein X-ray Crystallography

[7] C.-D. Chen, C.-H. Lin, P. Chuankhayan, Y.-C. Huang, Y.-C. Hsieh, T.-F. Huang, H.-H. Guan, M.-Y. Liu, W.-C. Chang and C.-J. Chen: "*Crystal Structures of Complexes of the Branched-chain Aminotransferase from Deinococcus Radiodurans with α-Ketoisocaproate and L-Glutamate Suggest the Radiation Resistance of This Enzyme for Catalysis*", J. Bacteriol. **194** (2012) 6206.

[8] W.-C. Cheng, Y.-F. Chen, H.-J. Wang, K.-C. Hsu, S.-C. Lin, T.-J. Chen, J.-M. Yang and W.-C. Wang: "*Structures of Helicobacter Pylori Shikimate Kinase Reveal a Selective Inhibitor-induced-fit Mechanism*", PLoS One **7** (2012) e33481.

[9] K.-H. Chin, W.-T. Kuo, Y.-J. Yu, Y.-T. Liao, M.-T. Yang and S.-H. Chou: "*Structural Polymorphism of c-di-GMP Bound to an EAL Domain and in Complex with a Type II PilZ-domain Protein*", Acta Crystallogr. D **68** (2012) 1380.

[10] J.-W. Huang, Y.-S. Cheng, T.-P. Ko, C.-Y. Lin, H.-L. Lai, C.-C. Chen, Y. Ma, Y. Zheng, C.-H. Huang, P. Zou, J.-R. Liu and R.-T. Guo: "*Rational Design to Improve Thermostability and Specific Activity of the Truncated Fibrobacter Succinogenes 1,3-1,4-β-D-glucanase*", Appl. Microbiol. Biotechnol. **94** (2012) 111.

[11] Y.-T. Liao, K.-H. Chin, W.-T. Kuo, M. L.-C. Chuah, Z.-X. Liang and S.-H. Chou: "*Crystallization and Preliminary X-ray diffraction Characterization of the XccFimXEAL-c-di-GMP and XccFimXEAL-c-di-GMP-XccPilZ Complexes from Xanthomonas Campestris*", Acta Crystallogr. F **68** (2012) 301.

[12] W.-R. Liu, B. H. Lin, C. C. Kuo, W. C. Lee, M. Hong, J. Kwo, C.-H. Hsu and W. F. Hsieh: "*Thickness-dependent Lattice Relaxation and the Associated Optical Properties of ZnO Epitaxial Films Grown on Si (111)*", CrystEngComm **14** (2012) 8103.

[13] V. S. Tadwal, L. Sundararaman, M. S. S. Manimekalai, C. Hunke and G. Grüber: "*Relevance of the Conserved Histidine and Asparagine Residues in the Phosphate-binding Loop of the Nucleotide Binding Subunit B of A1AO ATP Synthases*", J. Struct. Biol. **180** (2012) 509.

[14] Y. -C. Tien , P. Chuankhayan , Y. -C. Huang , C. -D. Chen, J. Alikhajeh, S.-L. Chang and C.-J. Chen: "*Crystal Structures of Rice (Oryza Sativa) Glyceraldehyde-3-phosphate Dehydrogenase Complexes with NAD and Sulfate Suggest Involvement of Phe37 in NADBinding for Catalysis*", Plant Mol. Biol. **80** (2012) 389.

[15] H.-H. Wu, P.-Y. Wu, K.-F. Huang, Y.-Y. Kao and M.-D. Tsai: "*Structural Delineation of MDC1-FHA Domain Binding with CHK2-pThr68*", Biochemistry **51** (2012) 575.

[16] H.-M. Wu, Y.-C. Kuan, C.-H. Chu, W.-H. Hsu and W.-C. Wang: "*Crystal Structures of Lysine-preferred Racemases, the Non-antibiotic Selectable Markers for Transgenic Plants*", PLoS One **7** (2012) e48301.

M. Yoshimura, J.-M. Lin, T. Tatsumi and H. Ishii
NSRRC, Taiwan