BL12B2
NSRRC BM

BL12B2 has been maintained to serve for material science and protein crystallography users since 2000. The schematic layout of the beamline is presented in Figure 1. The beamline is equipped with collimating mirror (CM), double crystal monochromater (DCM), focusing mirror (FM). The measured spot size of the beam is about 250 μm square at protein end station and total flux 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 beamtime was shared between material science and protein crystallography users with equal amount. Most of the BL12B2 users were from Taiwan. There are also international users from Japan and other place of the world. User support of the beamline has been provided by three beamline scientist and one engineer.

The major upgrade of protein crystallography endstation has been carried out since 2009. In 2011 remote access capability has been tested successfully. 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 strongly correlated system, nano science, system under extreme conditions (high pressure), etc. In 2011, fifteen papers have been published from our users. Selected results of material science and protein crystallography are shown in Figure 2 and 3, respectively.

Publications

Material Science

[1] S. H. Chang, M. H. Yeh, C. J. Pan, K. J. Chen, H. Ishii, D. G. Liu, J. F. Lee, C. C. Liu, J. Rick, M. Y. Cheng and B. J. Hwang: "*CO-assisted Synthesis of Finely Sizecontrolled Platinum Nanoparticles*", Chem. Commun. **47** (2011) 3864.

[2] S. Hosokawa, N. Happo, K. Hayashi, K. Mimura, K. Wakita, W. Hu, H. Ishii, M. Yoshimura, J. Jeyakanthan and N. Mamedov: "*Three-dimensional Atomic Images of TlInSe2 Thermoelectric Material Obtained by X-ray Fluorescence*

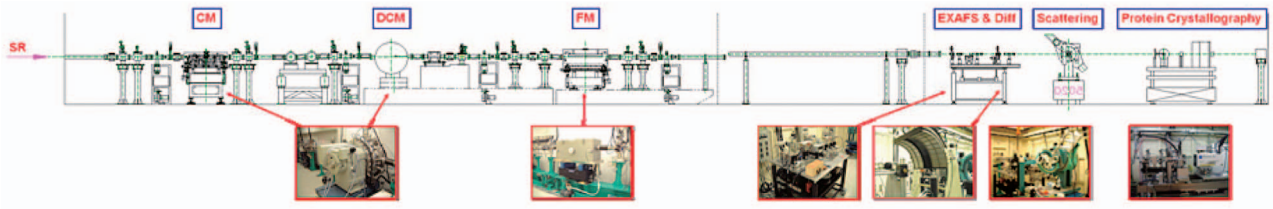

Fig.1 Schematic layout of BL12B2

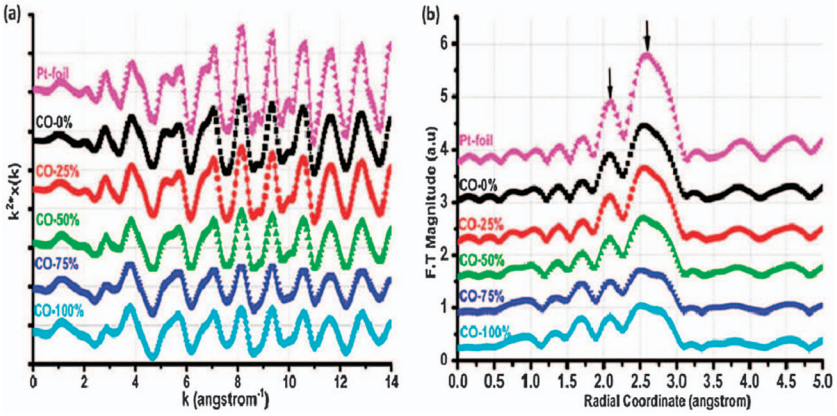

Fig.2 (a) k^2 -Weighted EXAFS of Pt nanoparticles at the Pt-L_{III} edge. (b) FT-EXAFS at the Pt-L_{III} edge. The arrow indicates the peaks corresponding to Pt-Pt coordination[1].

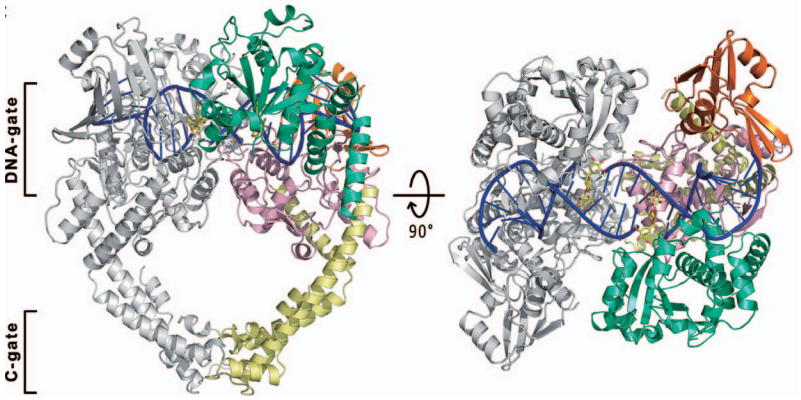

Fig.3 Structure of the hTOP2 β ^{core}-DNA cleavage complex stabilized by the anticancer drug etoposide. The dimeric enzyme displays a two-fold symmetric structure. One protein protomer is in gray, another is colored according to the domain organization of TOP2 enzymes[13].

Holography", Jpn. J. Appl. Phys. 1, **50** (2011) 05FC06.

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Protein Crystallography

[4] H.-C. Chan, Y.-T. Huang, S.-Y. Lyu, C.-J. Huang, Y.-S. Li, Y.-C. Liu, C.-C. Chou, M.-D.Tsai and T.-L. Li: "*Regioselective Deacetylation Based on Teicoplanincomplexed Orf2* Crystal Structures*", Mol. BioSyst. **7** (2011) 1224.

[5] C.-Y. Chou, T.-P. Ko, K.-J. Wu, K.-F. Huang, C.-H. Lin, C.-H. Wong and A. H.-J. Wang: "*Modulation of Substrate Specificities of D-sialic Acid Aldolase through Single Mutations of Val-251*", J. Biol. Chem. **286** (2011) 14057.

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