

Biology



Introduction

The wiggler 17B2 and SPring-8 12B2 stations have been routinely operated in the year 2004 and 2005 to provide the users with reliable protein crystallography facilities for structural biology research in Taiwan. The number of protein structures with high impacts determined by various phasing approaches, such as MIR/SIR, MAD/SAD and MR, has greatly increased in the last two years. Following research highlights are selected from the protein structures recently published by the user groups. These include the crystal structure of *Escherichia coli* primosomal protein PriB by C.-D. Hsiao of Academia Sinica, the structural implication of Fungal Volvatoxin A2 by Y.-C. Liaw of Academia Sinica, structure of the topoisomerase IV C-terminal domain from *Bacillus stearothermophilus* by N.-L. Chan of National Chung Hsing University, and venom citrate-dependent heparan sulfate-mediated cell surface retention of cardiotoxin A3 by C.-J. Chen of National Synchrotron Radiation Research Center.

As the 17B2 station is phased out, two new protein crystallography beamlines BL13B and BL13C at NSRRC funded by the National Science and Technology Program for Genomic Medicine (NRPGM) will be opened in September 2005 and continue to serve users. With the new state-of-art facilities, user friendly programs and increased dedicated beamtime, it is expected that many more important biological structures will be solved in the coming years.

