

## Biopharmaceutical Beamlines

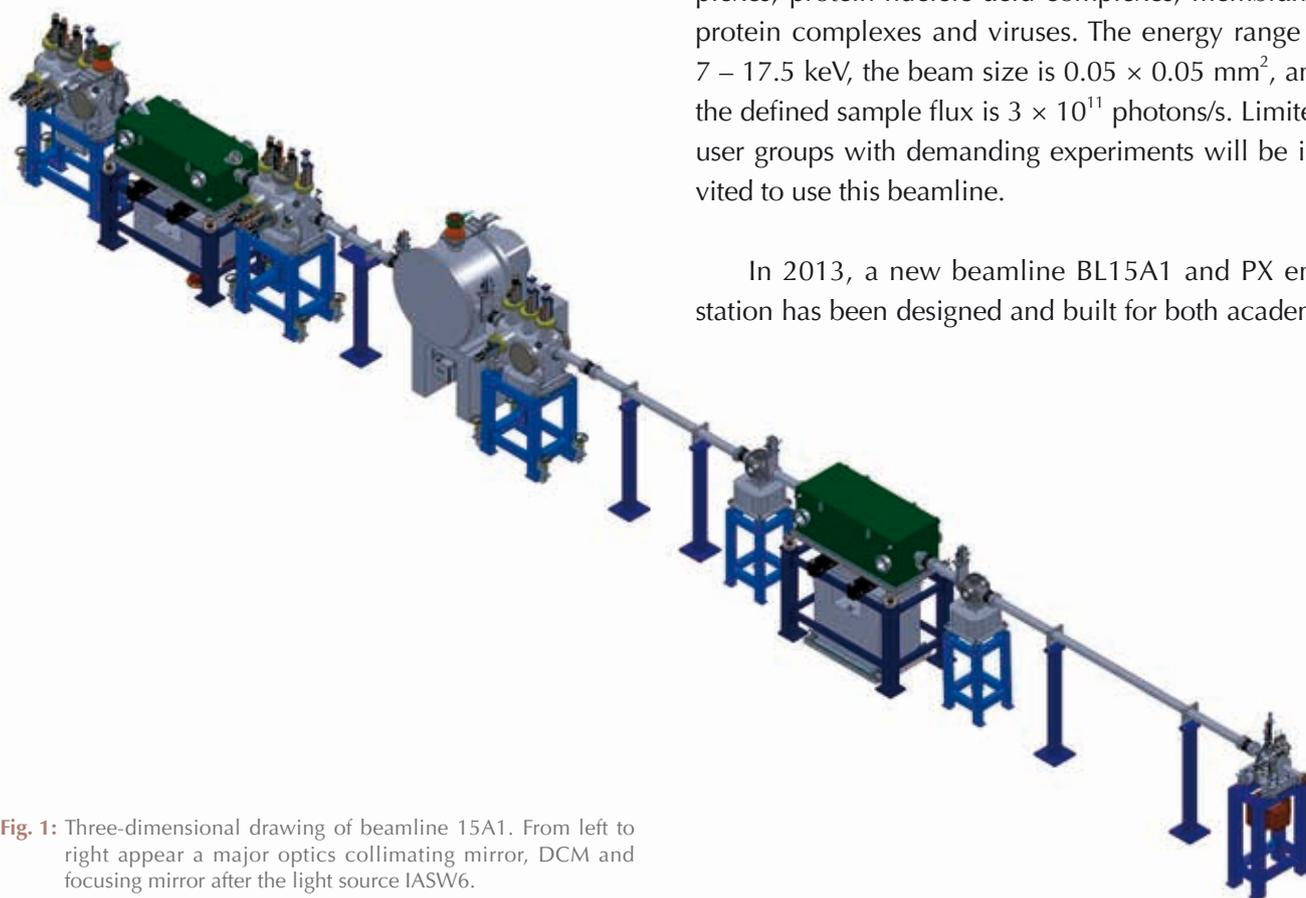
In NSRRC, we continuously provide our valuable users with scientific opportunities in using protein crystallography (PX) techniques. More than two beamlines of protein crystallography are smoothly operated, namely BL13B1 and BL13C1 at Taiwan Light Source, and BL44XU at SPring-8. Beamline 13B1 at TLS is a multiple anomalous-dispersion (MAD) beamline of PX operated since 2005. Beamline 13C1 at TLS is a monochromatic PX beamline operated since 2006.

Taiwan Beamline 12B2 at SPring-8 is a MAD beamline. The PX end station at BL12B2 has been in operation since 2002. The beamline is designed to provide an atomic-resolution structural probing environment for biostructure and material research. For

the PX end station, the measured flux at 1-Å wavelength at the sample position is about  $1.5 \times 10^{11}$  photons/s through a 0.25-mm aperture. The end station is equipped with a CCD detector (Rayonix MX225-HE), a highly precise goniometer (Kohzu, with a sphere of confusion less than 1  $\mu\text{m}$ ), and a SPring-8 SPACE sample changer. Half the total user time is allocated for research on protein crystallography.

Through international collaboration among Academia Sinica, NSRRC and Osaka University, about 10 % of the valuable beam time of BL44XU at SPring-8 is available for Taiwan users since 2010. This beamline is specially designed to collect high-quality X-ray diffraction data from biological macromolecular assemblies with a large unit cell, e.g. protein complexes, protein-nucleic acid complexes, membrane-protein complexes and viruses. The energy range is 7 – 17.5 keV, the beam size is  $0.05 \times 0.05 \text{ mm}^2$ , and the defined sample flux is  $3 \times 10^{11}$  photons/s. Limited user groups with demanding experiments will be invited to use this beamline.

In 2013, a new beamline BL15A1 and PX end station has been designed and built for both academ-



**Fig. 1:** Three-dimensional drawing of beamline 15A1. From left to right appear a major optics collimating mirror, DCM and focusing mirror after the light source IASW6.

ic and industrial users. This facility is fully automated with support for remote access, and is suitable for international collaboration between research groups, high-throughput crystal screening, high-resolution data collection, structure determination *de novo*, and other standard protein-crystallographic experiments.

To meet the requirements of biomedical research, a new facility for protein crystallography was designed and built by the Beamline and Protein Diffraction Groups at NSRRC.

The light source is an insertion device of a superconducting wiggler (In-Acromat, IASW6). The X-rays are collimated with a cylindrical collimating mirror, followed by a Si(111) double-crystal monochromator, and focused with a toroidal focusing mirror. To minimize the heat load on the silicon single crystal, the crystals are cooled with a liquid-nitrogen cryogenic system, which proved to be efficient on other similar beamlines. The energy range is 5.5 keV – 16 keV

(wavelengths 2.25 – 0.775 Å). At 1-Å wavelength, the measured flux at the sample position is about  $6 \times 10^{11}$  photons/s through an aperture  $200 \times 200 \mu\text{m}^2$ .

The end station has been in operation since January 2013. The major equipment in the end station includes a highly precise microdiffractometer, a cryo-cooler, and a CCD X-ray detector (Rayonix MX-300HE) hosted by a heavy-duty experimental table. The high-speed, highly precise air-bearing goniometer is important for highly efficient crystal screening and MAD/SAD phasing experiments, which are critical for a successful project in crystallography research. An SSR-style automatic sample changer is scheduled to be installed in February 2014. With this sample changer, the end station will become fully automatic and able to run without human intervention, but can be switched into manual control on demand. Remote access is also provided to facilitate international collaborations.



**Fig. 2:** Photograph of the end station. From right to left, the major components a highly precise microdiffractometer, a cryo-cooler, and a CCD X-ray detector.