Operation Schedule

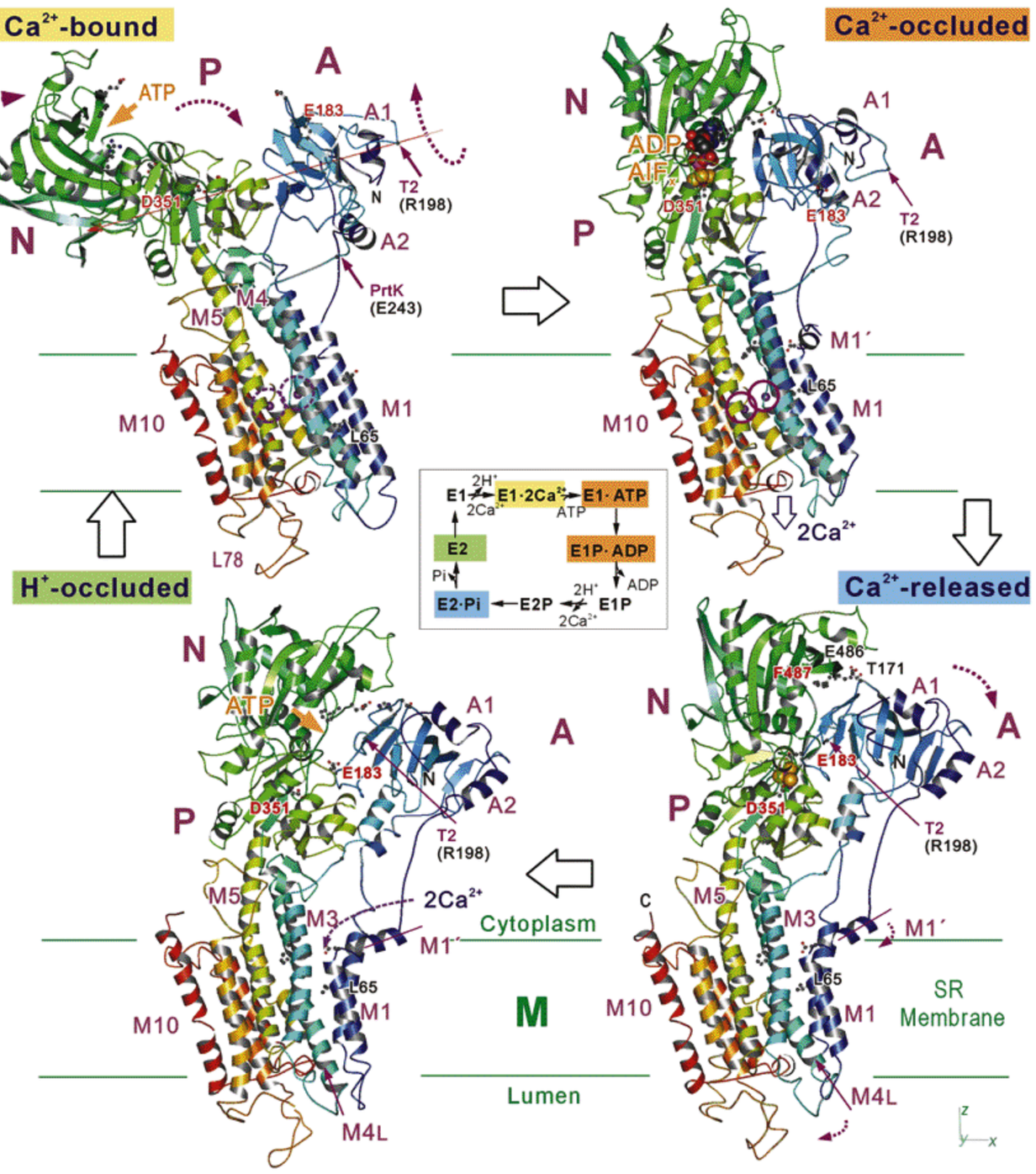
Due to the repair of the storage ring roof damaged by the series of typhoons last year, we are having a shutdown period till March 31, 2005. Operation schedule after April is available on the SPring-8 website.

Gating Mechanism of Calcium Pump Revealed at Structural Biology Beamlines

In September 2004, Prof. Chikashi Toyoshima (the University of Tokyo) and his collaborative researchers determined the crystal structure of the calcium pump (calcium-ATPase) of skeletal muscle sarcoplasmic reticulum in the absence of Ca^{2+} but in the presence of a stable phosphate analogue, using the Structural Biology I Beamline, BL41XU, and the Macromolecular Assemblies Beamline, BL44XU (*Nature* AOP, published online 26 September 2004; *Nature* **432**, 361 - 368). The structure analysis revealed the gating mechanism of the pump for releasing the calcium ions into the lumen of the sarcoplasmic reticulum.

They have already reported the crystal structures of the calcium pump in three different states: 1) in the Ca^{2+}-bound state before transporting the calcium ions (*Nature* **405**, 647 - 655); 2) in the Ca^{2+}-free state after transporting the calcium ions (*Nature* **418**, 605 - 611); 3) with a bound ATP analogue, which revealed the mechanism for occluding the bound Ca^{2+} ions before releasing them into the lumen (*Nature* **430**, 529 - 535).

This structure analysis filled in the final missing link of the previous findings to provide the atomic models for all four principal states in the calcium pump reaction cycle.

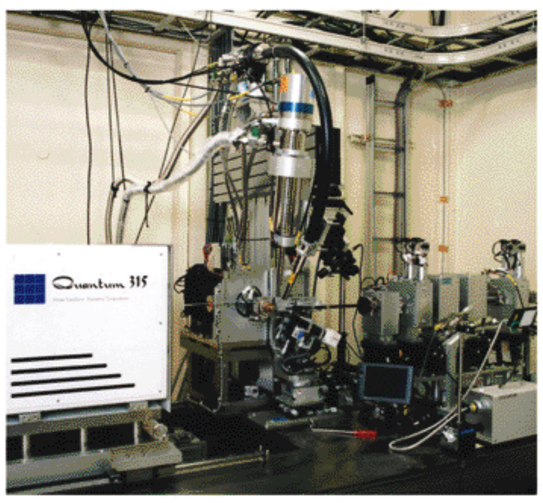


Structures of the calcium pump in four principal states

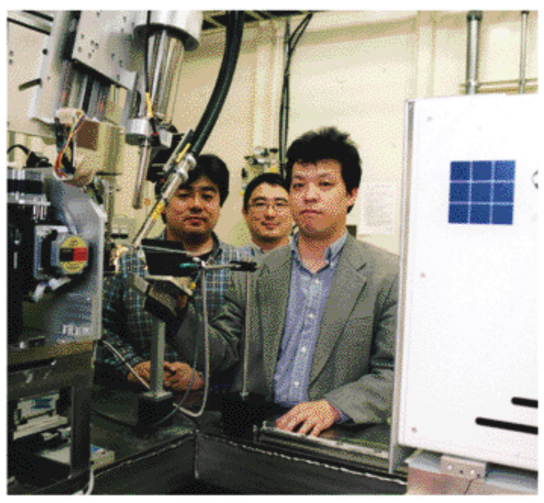
[Image: by courtesy of Prof. Chikashi Toyoshima]

Structural Biology I Beamline, BL41XU

The Structural Biology I Beamline, BL41XU, is operated to extend the applicable range of biological macromolecular crystallography in two regions : (i) larger unit cells and smaller crystal size taking advantage of high-brilliance X-rays, (ii) wider range of anomalous scattering element for multiple wavelength anomalous dispersion (MAD) method with higher energy X-rays. Its experimental station is equipped with a diffractometer with horizontal-axis goniometer and detectors. Two types of cryostream coolers, nitrogen gas and helium gas are installed on the diffractometer for experiments under cryogenic condition. The imaging plate detector and X-ray CCD detector are also available at this beamline.



Diffractometer for Protein X-ray Diffraction Experiment



Drs. N. Shimizu, H. Sakai and M. Kawamoto (Beamline Scientists)

XRM2005

The 8th International Conference on X-ray Microscopy, XRM2005, will be held at the Egret Himeji, Hyogo, Japan, from July 26 to 30, 2005.

http://xrm2005.spring8.or.jp/

SPring-8 **www.spring8.or.jp**