Crystallography Times

Rigaku

Protein Crystallography Newsletter
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In this issue:

Continuing Education Webinar

Maintenance for a MicroMax-007 / 007 rotating anode X-ray generator.

Presenter: Adam Courville

July 16 at 12:00 PM EDT (16:00 GMT)

Crystallography in the news

June 24, 2009. Dutch software to weed out errors in Protein Data Bank. Protein structures are getting regular makeovers with the help of 're-refinement' software developed by Dutch structural biologists.

June 16, 2009. New research by scientists at The Scripps Research Institute and other institutions provides a close-up look at the cone-shaped shell that is the hallmark of human immunodeficiency virus (HIV), revealing how it is held together—and possible ways to break it apart.

June 16, 2009. The 2009 Carl Brändén Award was presented by Paul N. Swepston, Ph.D., President and General Manager of Rigaku Life Sciences, to **Dr. Bruce Alberts** (University of California, San Francisco and editor-in-chief of the journal *Science*) for his national and international commitment to the promotion of educational principles as well as the "creativity, openness and tolerance that are inherent to science."

June 11, 2009. Howard Hughes Medical Institute researchers are reporting the first detailed molecular snapshots of a deadly gastrointestinal virus as it is caught in the grasp of an immune system molecule with the capacity to destroy it. HHMI investigator Stephen C. Harrison and colleagues mapped the structure of an antiviral antibody clamped onto a protein called VP7 that stipples the surface of rotavirus.

Better performance AND less maintenance

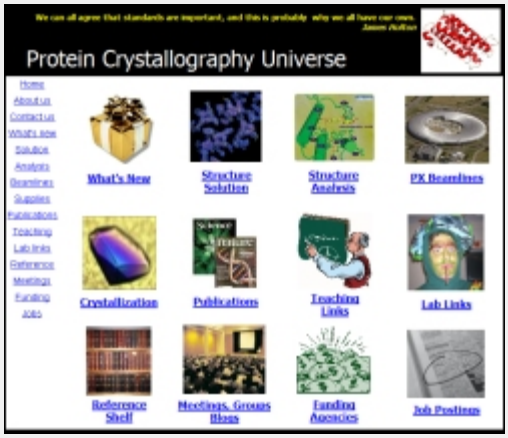
Since the introduction of the first sub-100 micron rotating anode in 2002, hundreds of Rigaku microfocus generators have been installed in protein crystallography labs around the world. The current model MicroMax-007 HF delivers performance comparable to a second generation beamline. The most challenging projects can now be performed in the home laboratory: screen crystals where no diffraction is seen on a standard system, collect full data sets on samples where only low resolution reflections would normally be observed, and solve previously intractable structures.

Contrary to intuition, higher performance does not mean higher maintenance. The MicroMax-007 HF actually requires less maintenance and service than its predecessors. Engineering design improvements have lengthened the time between routine service and made it easier and faster to perform maintenance. Featuring a unique and reliable direct-drive anode, the MicroMax-007 HF compact tower assembly contains both the vacuum chamber and turbo-molecular pump for fast pump downs. Pre-mounted, pre-crystallized filaments allow users to change filaments in a few minutes so they can quickly get back to collecting data.

Dramatically improved filament lifetimes, and anodes that only require maintenance about once a year, allow you to spend more time screening crystals and collecting data and less time on maintenance. When you do need to change the anode, customers can quickly swap out the old anode with a freshly rebuilt one. To maximize uptime, customers can purchase two anodes and sign up for our *Anode Storage Program* ? where we will ship you a freshly rebuilt anode when you need one so that you don't need to wait for your anode to be rebuilt.

Request a copy of the MicroMax-007 HF brochure or ask for more information about the Anode Storage Program.

MicroMax™-007 HF microfocus X-ray generator (top) and as part of the Rigaku Highflux HomeLab system (bottom).



Bookmark PXUniverse.com as your portal to the world of protein crystallography.

SURVEY QUESTION
Who is your favorite crystallization supply vendor?

◉	Emerald
○	Hampton Research
○	Jena Biosciences
○	Microlytic
○	Molecular Dimensions
○	Qiagen
○	Other

Submit Response

Use this link if the form doesn't work.

Maintenance for a rotating anode X-ray generator

Rigaku Life Sciences Webinar Series continues on July 16th with a discussion on maintenance and routine service for microfocus rotating anode X-ray generators. Hosted by analytical X-ray systems specialist Adam Courville, this complementary continuing education seminar is recommended viewing for any MicroMax-007 or 007HF users and for people interested in learning about what maintenance is required for a state-of-the-art rotating anode generator.

Useful links for crystallography

The 2009 Dorothy Crowfoot Hodgkin Award, sponsored by Genentech and granted in recognition of exceptional contributions in protein science, was presented to Dr. Janet Thornton (European Bioinformatics Institute) on June 15, 2009 for her pioneering work in the field of bioinformatics. Thorton's lab offer several web based tools to aid in the analysis of protein structures:

ProFunc - for analysis of a protein's 3D structure to help identify its likely biochemical function.

Catalytic Site Atlas - obtain catalytic residue details.

PDBsum - provides an at-a-glance overview of every macromolecular structure deposited in the Protein Data Bank (PDB), giving schematic diagrams of the molecules in each structure and of the interactions between them.

Selected recent crystallographic papers

The p22 tail machine at subnanometer resolution reveals the architecture of an infection conduit. G.C. Lander, R. Khayat, R. Li, P.E. Prevelige, C.S. Potter, B. Carragher and J.E. Johnson.
Structure **17**, No. 6, 789-799 (2009).

Structure and mechanism of an amino acid antiporter. Xiang Gao, Feiran Lu, Lijun Zhou, Shangyu Dang, Linfeng Sun, Xiaochun Li, Jiawei Wang and Yigong Shi.
Science **324**, No. 5934, 1565-1568 (2009).

Cellular mechanisms of membrane protein folding. William R. Skach.
Nature Structural & Molecular Biology **16**, No. 6, 606-612 (2009).

Crystal Structure of the sodium-potassium pump at 2.4 Å resolution. T. Shinoda, H. Ogawa, F. Cornelius and C. Toyoshima.
Nature **459**, 446-450 (2009).

FAQ: How to get better spot separation and data

When diffraction spots are too close together, it implies that your detector is too close to the sample and/or your crystal has a long unit cell axis. There are several experiments you can do to test for optimal data collection parameters which will result in better separation between spots. One common sense way is to increase the crystal-to-detector distance. This usually helps unless you have a highly divergent optic in which case you want to try and keep the detector as close to the crystal as possible.

A second approach is to either collimate the beam or, in the case of VariMax optics, close the slits a bit. Both of these options have the disadvantage that you will also decrease the flux on your crystal which will result in the need for longer exposure times.

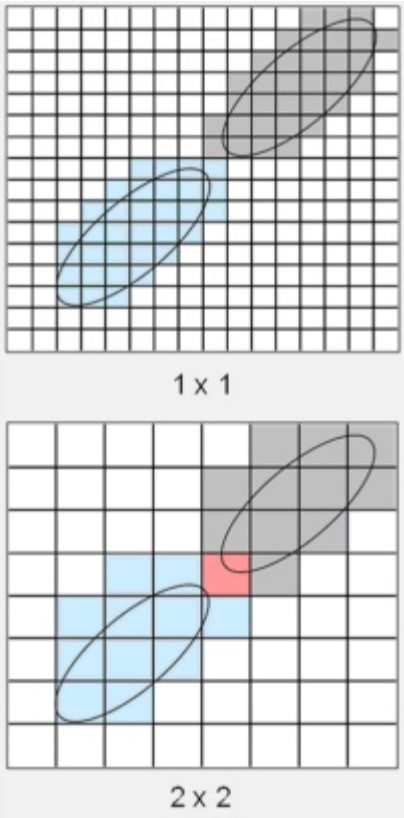


Illustration of how collecting data in 1x1 binning mode can help resolve diffraction spots.

Another method you can easily try is to collect images in unbinned (1x1) mode. The usual default bin mode for most CCDs is 2x2. As the image (at left) illustrates, finer sampling of the detector space with unbinned images can sometimes resolve spots. More likely than not, if you have a challenging system you will need a combination of these techniques. And if all else fails at home, there's always the synchrotron.

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