



APS Data Collection

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Template originally designed by Michael S. Chapman; modified by Thayumanasamy Somasundaram



SER-CAT APS Trip, Date: 00/00/00;

Data collection at SER-CAT beam line 22-ID-X

Data collection members: Thayumanasamy Somasundaram

Project Name: PI_0000

Beam line contact:

Date, SER-CAT, Beamline 22-ID-X, Advanced Photon Source

Argonne National Laboratory, Argonne, IL 60439



Crystallization, Buffers and Solution Preparation

Crystal Mounting & Storage

Needed Accessories

			
CryoCap	CryoLoop	Mounted CryoLoop	Cryo Tong
			
CryoWand	Vial Clamp	Cryo Dewar	Cryo Coder
			
Cryo Cap Magnetic	Vial Clamp	Cryo Sleeve	Cryo Cane
<p><i>All images courtesy of Hampton Research, Aliso Viejo, CA 92656</i></p>			

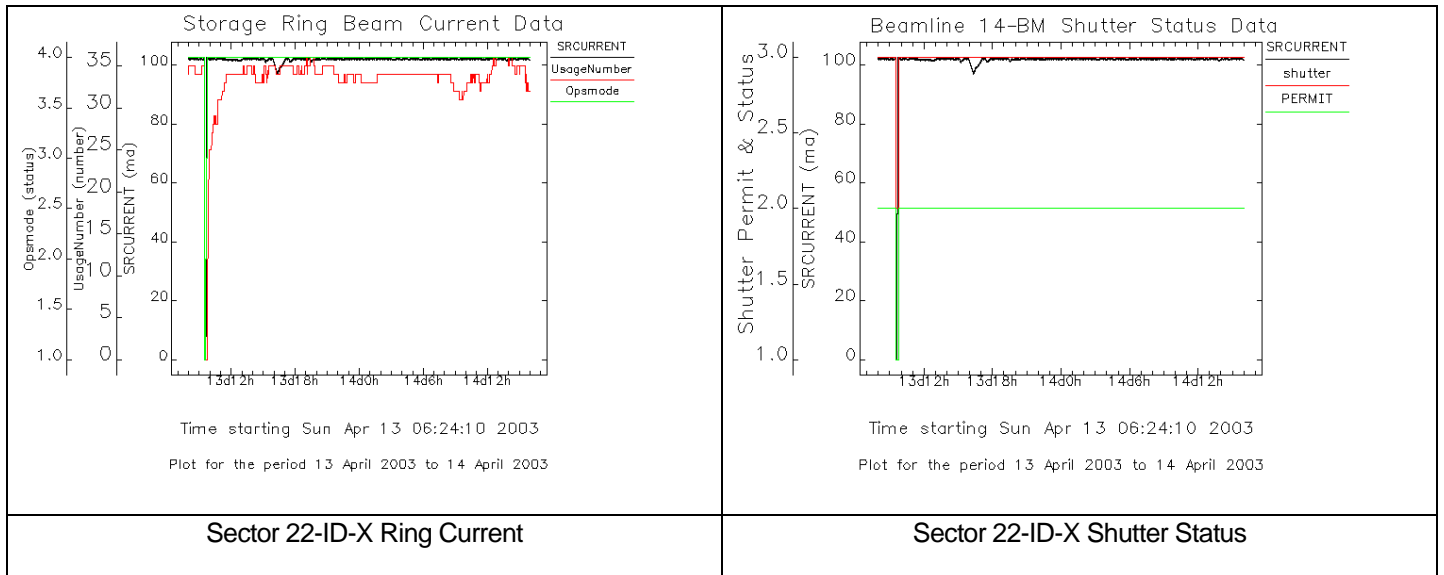
Cryo Pak Charging

Cryo Pak series from Taylor-Wharton (1-800-898-2657) biological shippers are designed for transporting small quantities of biological materials at cryogenic temperatures. The shipper (sometimes referred to as 'Dry Shipper') contains unique absorbent material that holds several liters of liquid nitrogen with out spilling any liquid even if they are tipped over. Cryo Pak needs to be 'charged' before usage. Charging and loading the samples should be done outside the shipping enclosure (black box). First weigh the shipper with its lid on and without the canister (4.40 kg). Then fill it with liquid nitrogen to the top of the shipper and allow to stand for ½ h. Add liquid nitrogen as needed and repeat the procedure until no further liquid nitrogen is needed. At this stage the shipper is considered fully 'charged' and all remaining liquid nitrogen **should be poured out**. The charged shipper is again weighed with its lid on and without the canister (7.90 kg). The difference in weight between the 'charged' and the empty should be close to 3.5 kg. Now shipper is ready to accept samples for extended storage (24-30 days) at cryogenic temperatures. Pictures of [CX100 Cryo Express](#) dry shippers.



CryoPak Dry Shipper & Protective Shipping Enclosure

Beam line Details



Crystal Trials

Xtal1:

First trials were John Doe's hand-carried Xtal1 crystals.

Xtal2:

Jane Doe's samples were tried after John's data collection was half-way over.

Data collection													
	Project:				Sample type				Crystal		Frozen		
Sample	Prep. #		Date		OD _{280/260}		Conc. (mg/ml; after dialysis)		Glycerol (%)		Mg ⁺⁺ (mM)		
Crystallization setup	Date	Tray #	Well #	Temp (C)	Drop: PEG (%)	Glycerol (%)	Size (μL)	Well: PEG (%)	glycerol (%)	Size (μL)	Growth time (d)		
Crystal	Size (mm)		Appearance				Sketch:						
Mounting	Loop or capillary? – size (mm):		Date	Experimenter									
Storage	Cane #		Vial #		Change for		Cane #		Vial #				
Diffraction	Date	Temp (K)	Collimator (mm)	Beam trim vertical (%)	Horizontal (%)	2-theta	Wave length (A)	Appearance on centering					
Files	Directory			Oscillation file prefix		Snapshot file prefix		Experimenters					
Backup	Tape #1	Date	Place	Tape#2	Date	Place	CD1 #	date	CD2 #	date			
Backup format	DDS?	Verified?	Machine	DDS?	Verified?	Machine	8500/8200?	Verified?	8500/8200?	Verified?			
Run # or "Snap"	Start frame	End frame	Start φ	Time(A M/PM)	Exposure(sec)	Oscillation	Sample-detector (mm)	Beam position X	Beam position Y	Start current (mA)	Start counts (kps)	End current (mA)	End counts (kps)

Inspection	Crystal:		Run/Snap:	Run	Frame(s):	180	Inspectors:		Date:
Resolution limits (Å)	Detector edge	Detector corner	Farthest spot	Pattern	Ice rings?	Twinning?	Mosaicity (guessed)	Spot profile	Diffuse scatter?
Lattice	Spot separation	Lune separation	Streaking?	Crystal form guess	Background	Other comments			

Indexing	Crystal: 1		Run/Snap: 1	Frame(s): 338	Processor: TS		Date: 10/2/01		
	Program		Directory						
Peak selection	Resolution cut	Floor etc.			Number	Comments			
Indexing parameters	Vector length	Non-integer tolerance							
Unit cell	System	Distortion	a	b	c	α	β	γ	Orientation angles
Results	% peaks found		Rms error (mm)		Comments				