

A Light for Science

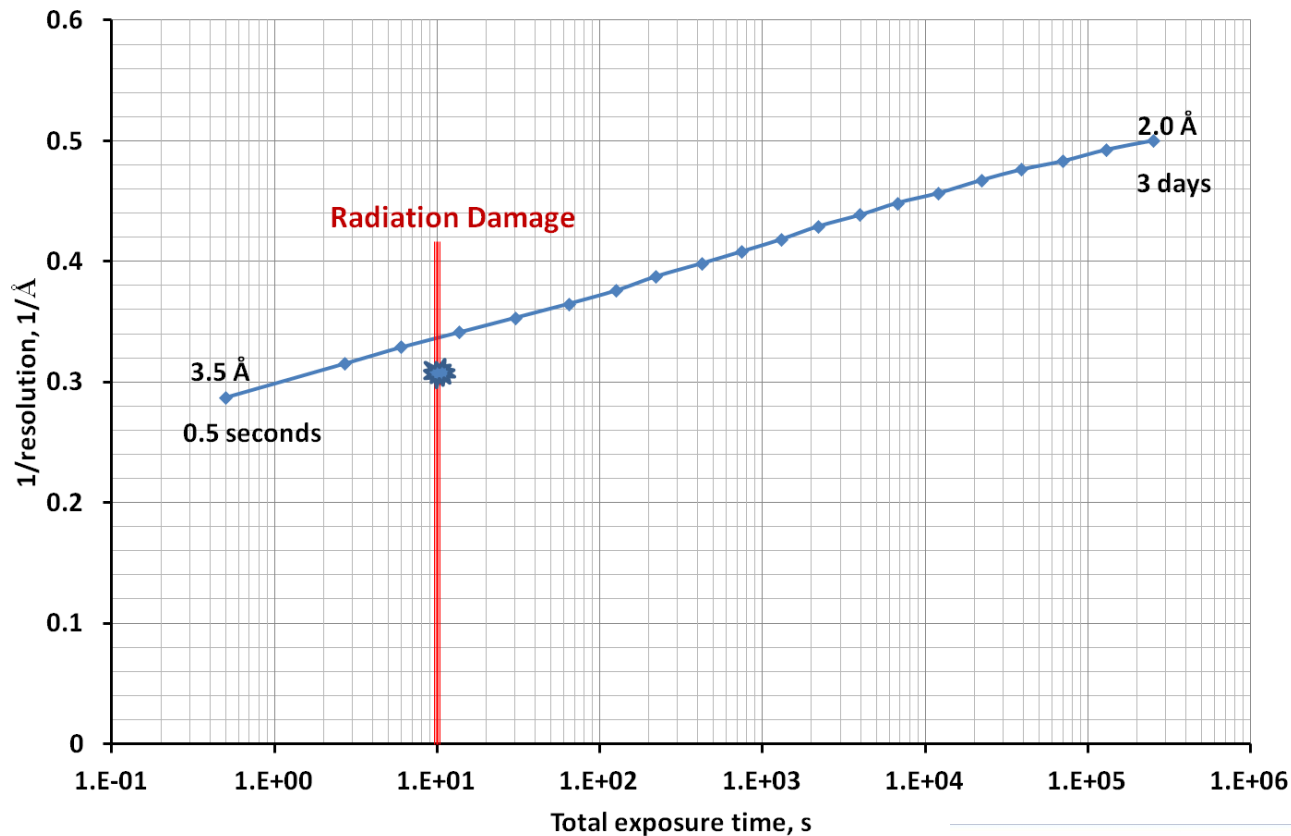


European Synchrotron Radiation Facility

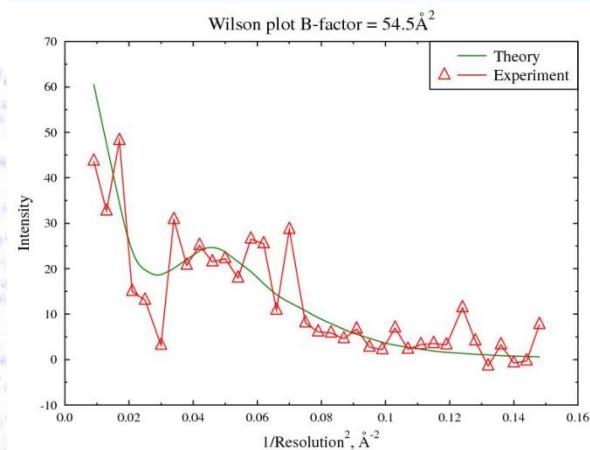
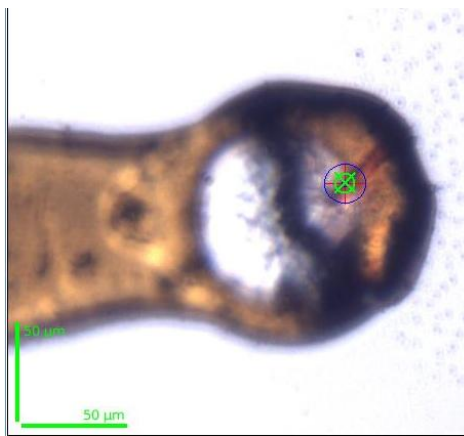
3-d Data Collection

Resolution vs. Total_exposure

BEST estimations, No radiation damage

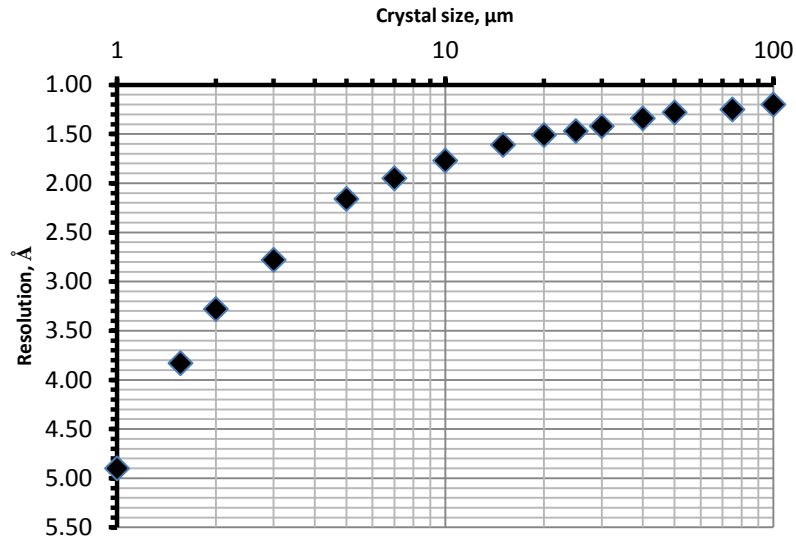


Macrhodopsin
ID23-1,
Aperture 20
Flux =4.7e+11 [photons/s]
Dose rate =0.5 Mgy/s

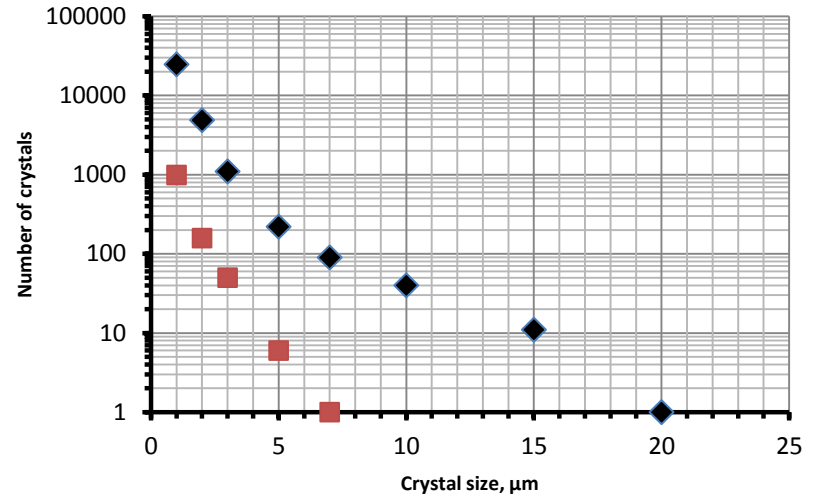


Micro-crystallography

- Thermolysin, Space Group $P6_122$; B-factor=11.5 Å²

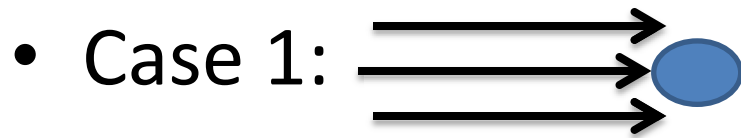


Complete data set resolution vs. crystal size



Number of cryocooled crystals of a given size required to achieve dataset resolutions of 1.5 Å (black) and 2.0 Å (blue).

- For a crystal $1 \times 1 \times 1 \mu\text{m}^3$ in dimensions partial data sets *from about 1000 crystals* would be needed to achieve a final data set resolution of $d_{\text{min}} = 2.0 \text{ \AA}$.



One-dimension DC



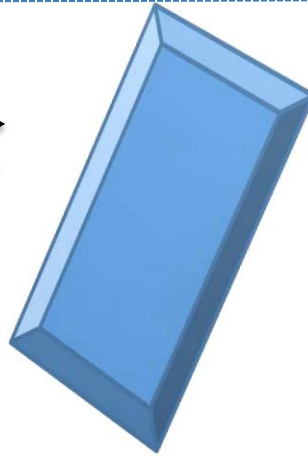
Two-dimension DC

- Case 3:



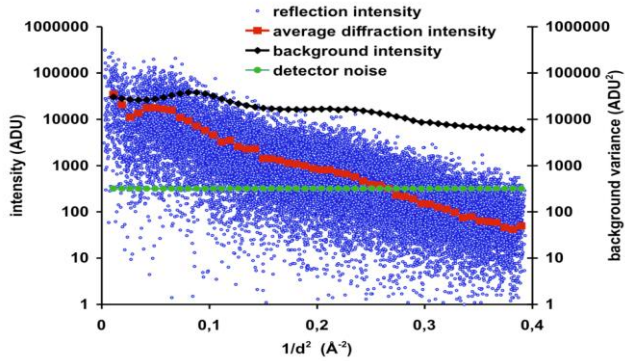
Three-dimension DC

- Case 3:



Case 1: One-dimension DC

Model for diffraction intensity vs. reciprocal space coordinate



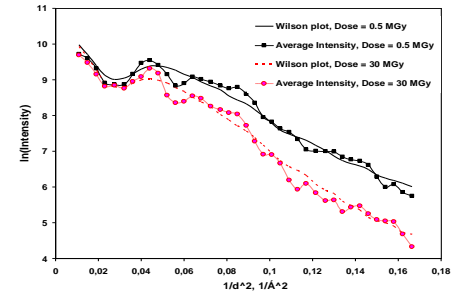
$$\hat{J}(\mathbf{h}) = \frac{1}{s} \cdot \hat{J}_u(h) \cdot \text{Exp}(-\mathbf{h} \cdot \mathbf{B} \cdot \mathbf{h}^T)$$

$$\hat{\sigma}_J(h, \varphi) = \frac{1}{2N} \sum_{i=1}^N \int_0^{\infty} \sqrt{k_{0i} + k_{1i} J + k_{2i} J^2} \left(p(J | \hat{J}(\mathbf{h}_{i1})) + p(J | \hat{J}(\mathbf{h}_{i2})) \right) dJ$$

Radiation-damage model

Resolution-dependent intensity decay:

$$\hat{J}(\mathbf{h}, D) = \hat{J}(\mathbf{h}, D=0) \text{scale}(D) \exp(-B(D)h^2 / 2)$$

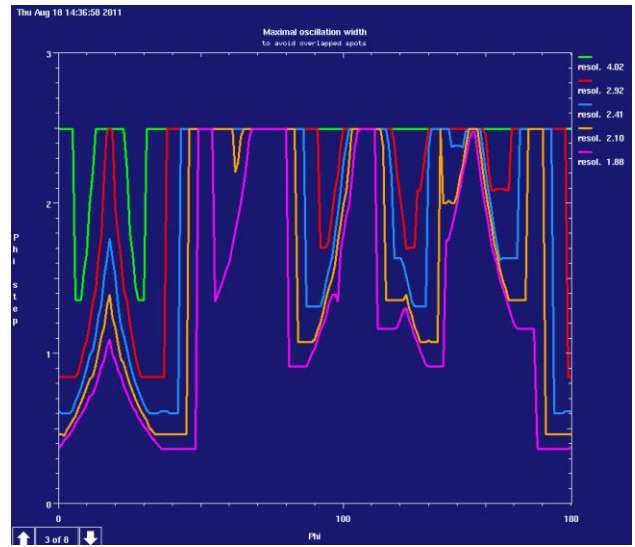
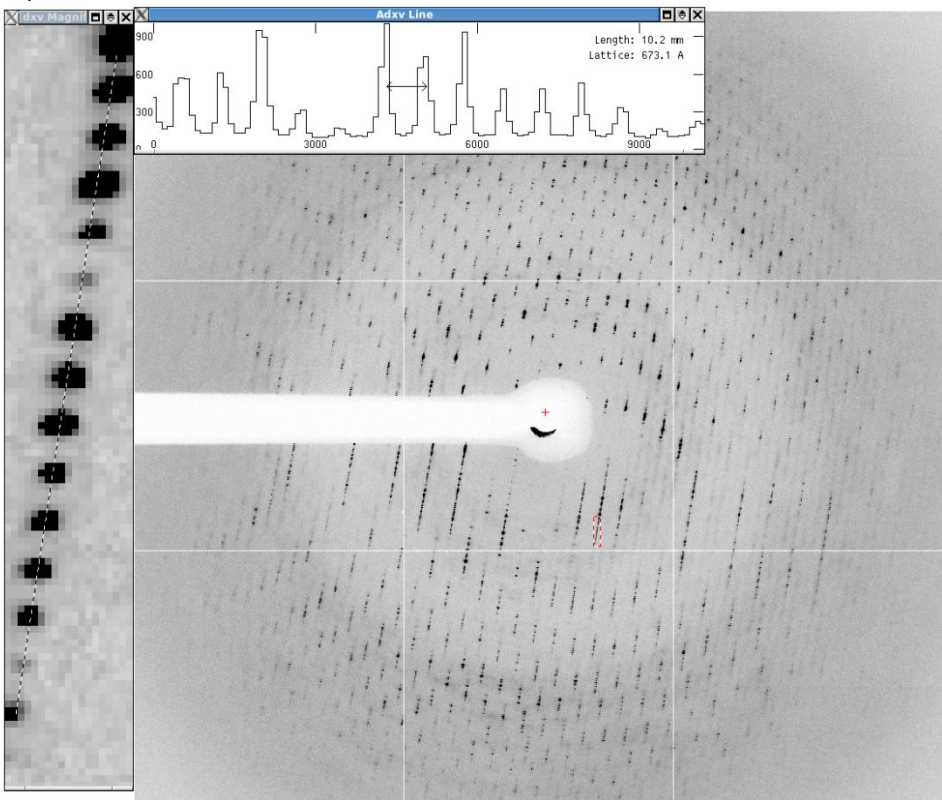


Radiation-induced non-isomorphism:

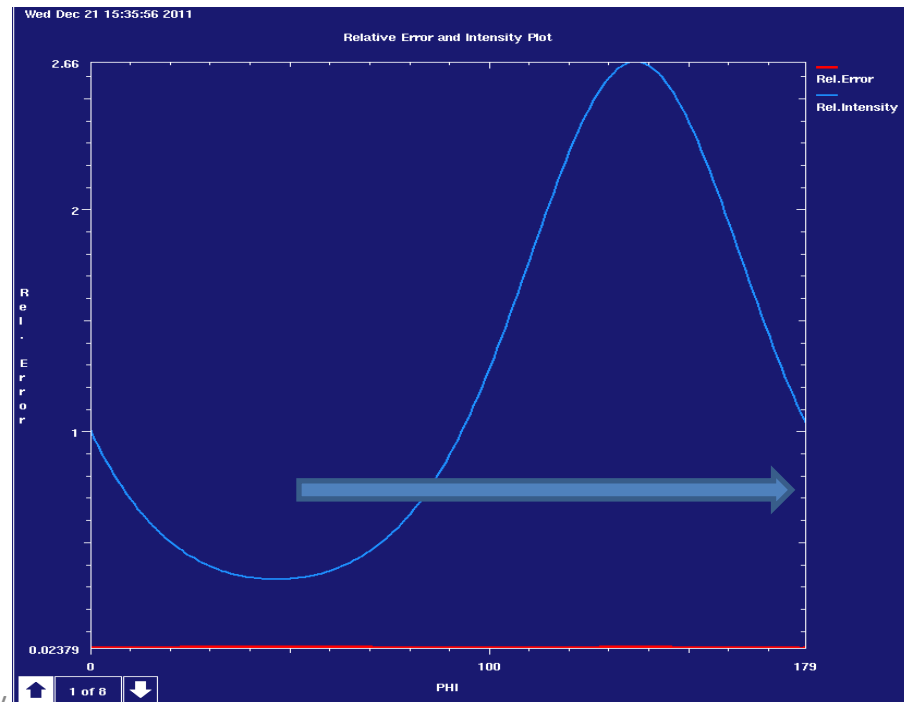
$$\sigma_a \approx e^{-\alpha D s^2}$$

$$R_{1I} = \left\langle \left| \frac{I_{D=0}}{\langle I_{D=0} \rangle} - \frac{I_D}{\langle I_D \rangle} \right| \right\rangle \approx (1 - \sigma_a^2)^{1/2}$$

Crystal : P 4
 Space Group : 141.55 141.55 671.01 90.00 90.00 90.00
 Cell :
 Mosaicity : 0.17 degree



Scaling
 Relative scale : 31.44
 Overall B-factor : 82.17 Angstrom^2
 B-factor eigenvalues : 51.11 118.04 118.04 Angstrom^2
 Scaling error : 3% at the resolution limit



Case 2: Two-dimension DC

(a) micrometre-sized crystals

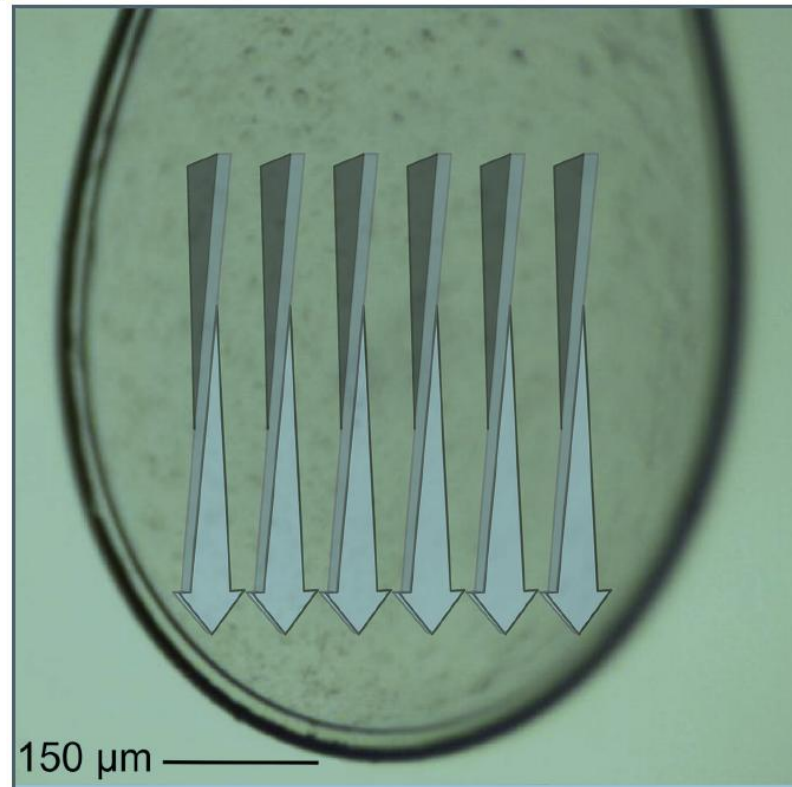
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BIOLOGY | MEDICINE

Serial crystallography on *in vivo* grown microcrystals using synchrotron radiation

Cornelius Gati,^{a,†} Gleb Bourenkov,^{b,†} Marco Klinge,^c Dirk Rehders,^c Francesco Stellato,^a Dominik Oberthür,^{a,d} Oleksandr Yefanov,^a Benjamin P. Sommer,^{d,e} Stefan Mogk,^e Michael Duszynski,^e Christian Betzel,^d Thomas R. Schneider,^{b,*} Henry N. Chapman^{a,f,*} and Lars Redecke^{c,*}

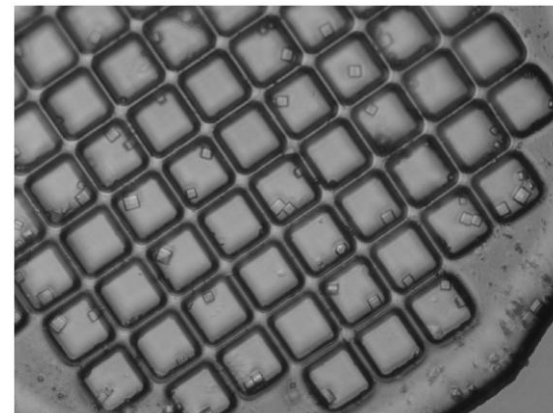
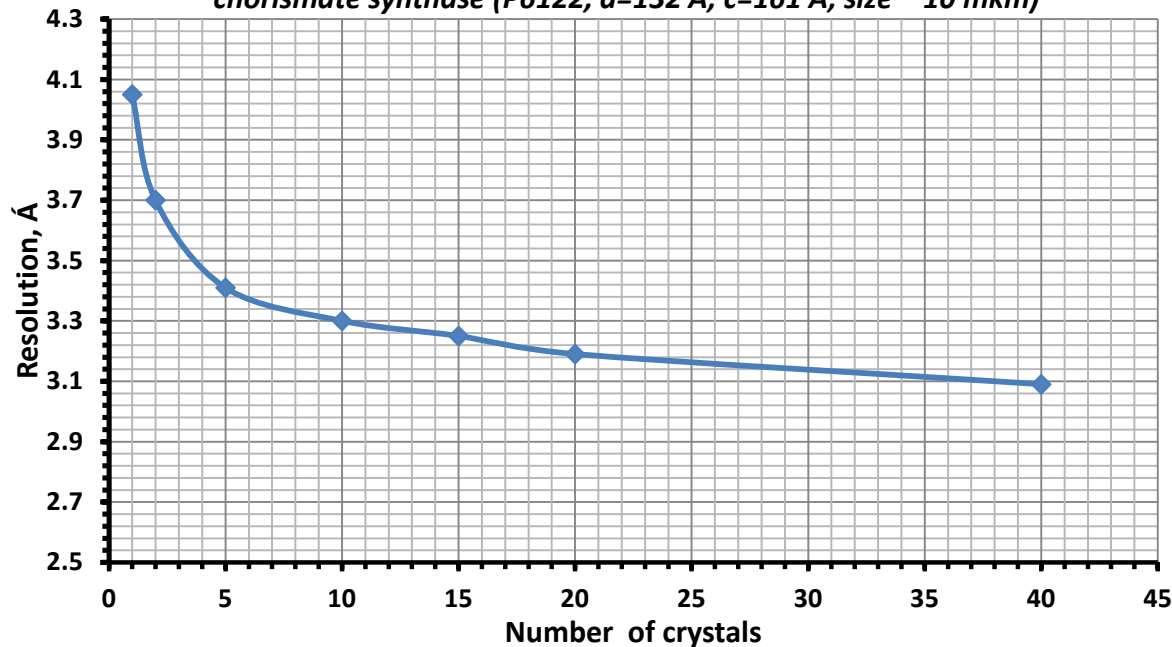
Received 7 November 2013
Accepted 16 December 2013

(b) sub-10 μm crystals
Can not be characterized



Case 2: Two-dimension DC (b) sub-10 μm crystals Crystals Can be characterized

Resolution vs. number of used crystals
chorismate synthase (P6122, $a=132 \text{ \AA}$, $c=161 \text{ \AA}$; size $\sim 10 \text{ mkm}$)



Cluster Analysis

xds_* Get Ref Data sets xds_x1_run1_1 Get Cell details

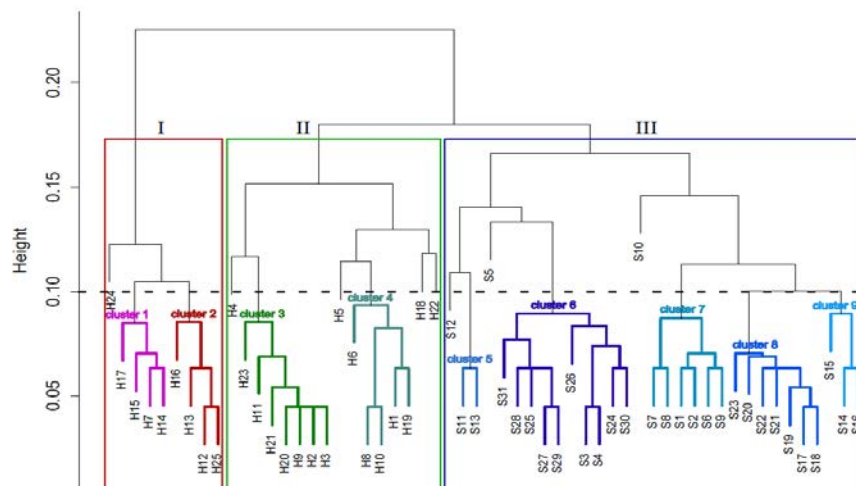
Space Group Unit Cell Parameters Friedel's law

181 132.4 132.4 161.0 90.0 90.0 120.0 True False Process Ref Dataset

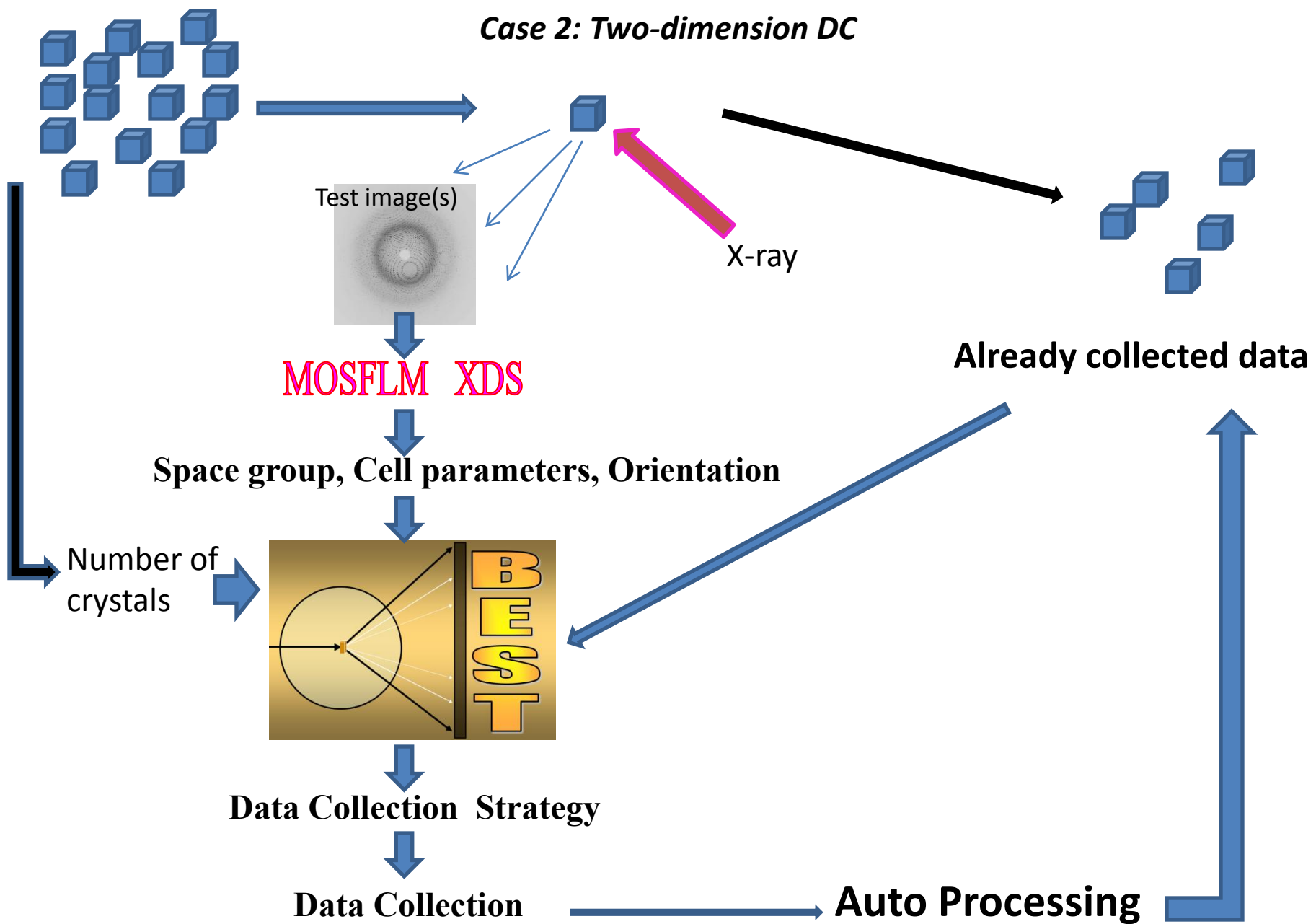
Folder name	Process in XDS	Include in XSCALE
1 xds_x1_run1_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
2 xds_x1_run2_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
3 xds_x2_run1_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
4 xds_x2_run2_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
5 xds_x3_run1_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
6 xds_x3_run2_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
7 xds_x4_run1_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
8 xds_x4_run2_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>
9 xds_x5_run1_1	<input type="checkbox"/>	<input checked="" type="checkbox"/>

Resolution up to: 2.0 Process all Datasets

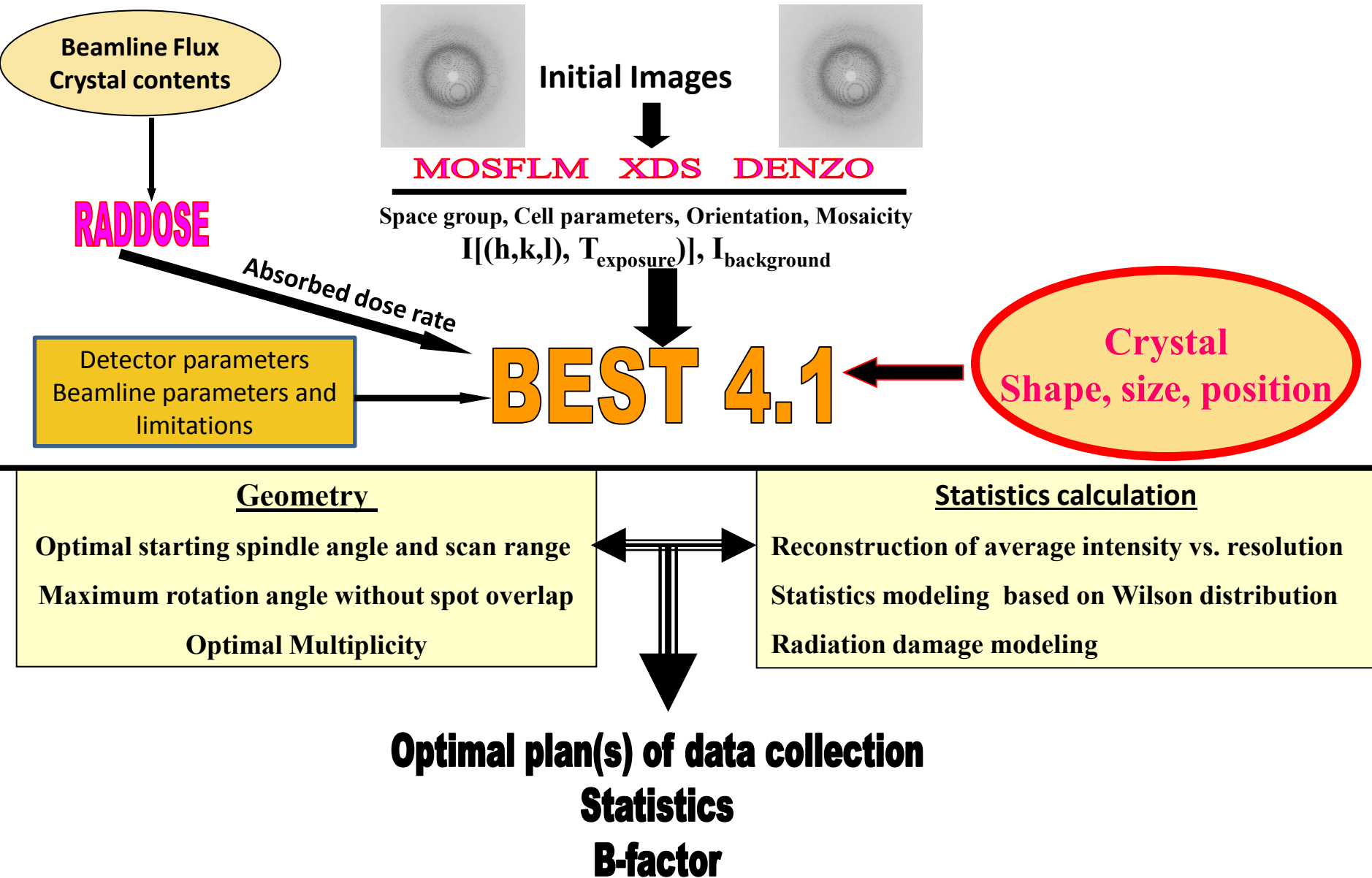
Searching Reference Datasets
 Getting symmetry from Reference Dataset: xds_x1_run1_1
 Searching Remaining Datasets
 Running XSCALE up to 2.0 Å resolution
 Running XSCALE



Case 2: Two-dimension DC



Data collection strategy accounting radiation damage

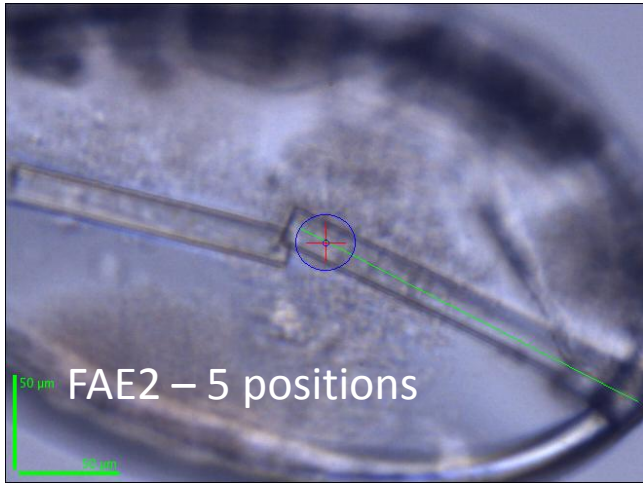


FAE crystals

ID23-1

E=12.75Kev, I=35 mA, Aperture=0.03 mm

Flux=1.5x10¹¹ Photon/sec



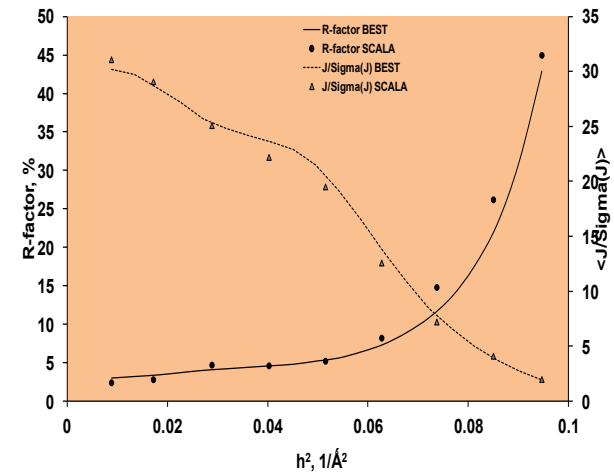
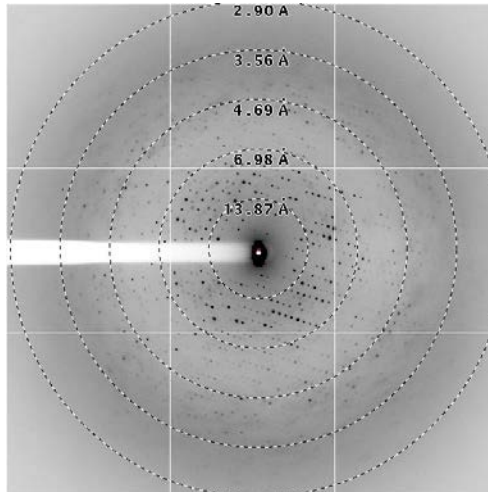
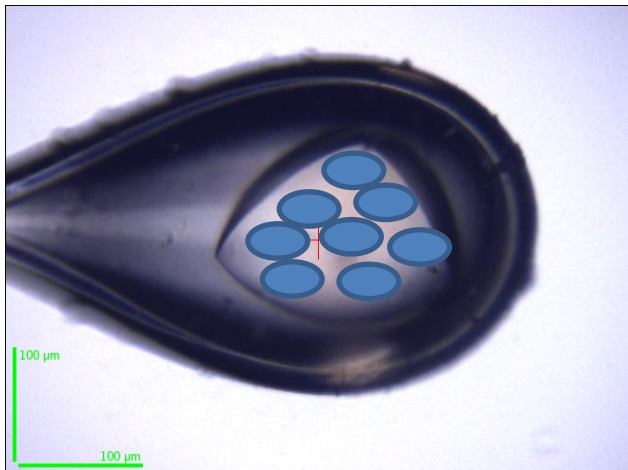
Multi-positions data collection

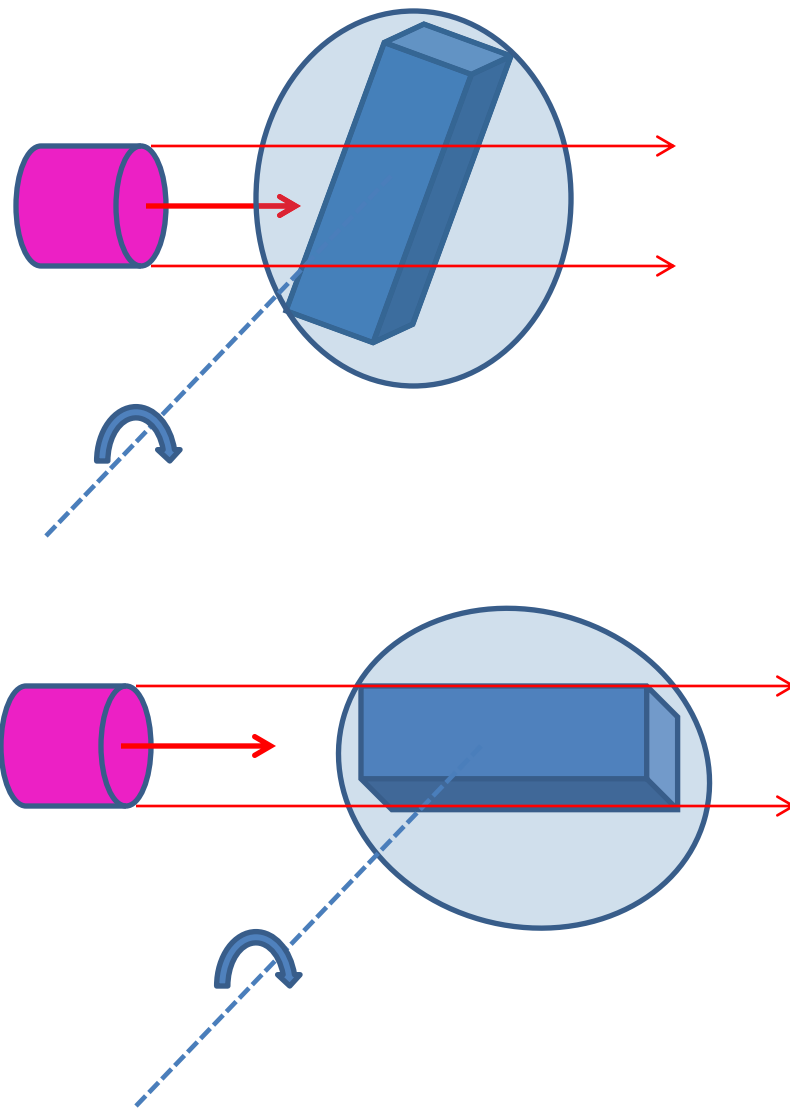
Resolution limit is set by the radiation damage
 Resolution limit = 1.73 Angstrom Transmission = 100.0% Distance = 244.6mm

WEDGE PARAMETERS					INFORMATION						
sub-We-dge	Phi-start degree	Rot-width degree	Exposure/image s	N.of images ges	Over-lap	Wedge width degree	Exposure/sWedge s	Exposure total s	Dose /sWedge MGy	Dose total MGy	Completeness %
Wedge number = 1 Crystal position = 1											
1	0.00	0.25	1.338	80	No	20.00	107.0	107.0	4.067	4.067	51.9
Wedge number = 2 Crystal position = 2											
1	20.00	0.25	1.338	80	No	20.00	107.0	107.0	4.067	4.067	85.6
Wedge number = 3 Crystal position = 3											
1	40.00	0.25	1.338	80	No	20.00	107.0	107.0	4.067	4.067	75.2
Wedge number = 4 Crystal position = 4											
1	60.00	0.25	1.338	80	No	20.00	107.0	107.0	4.067	4.067	88.1

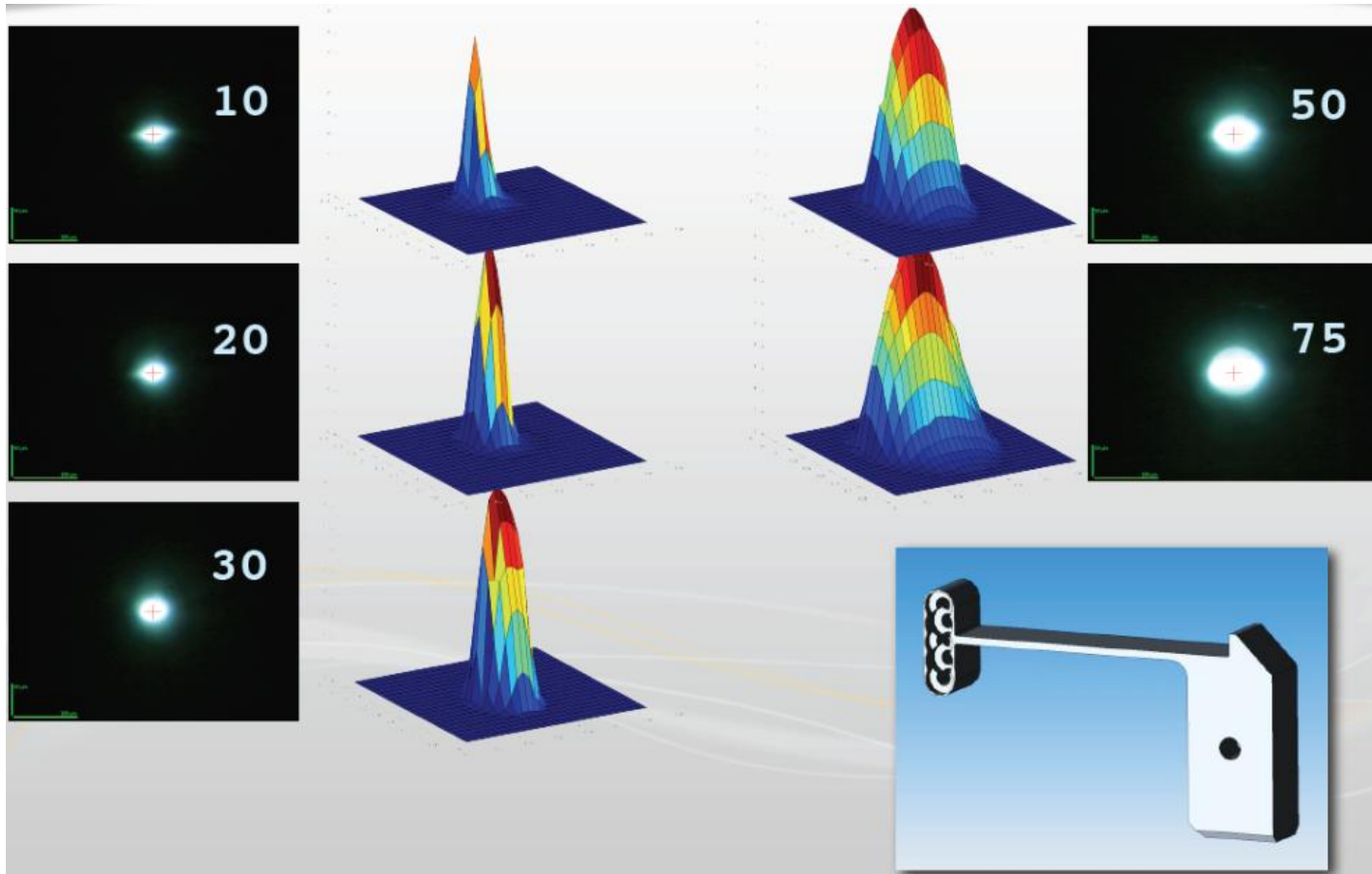
Phi_start - Phi_finish : 0.00 - 80.00
 Total rotation range : 80.00 degree
 Total N.of images : 320
 Overall Completeness : 98.6%
 Redundancy : 3.18
 R-factor (outer shell) : 5.6% (36.8%)
 I/Sigma (outer shell) : 22.9 (3.3)
 Total Exposure time : 428.1 sec (0.119 hour)
 Total Data Collection time : 1228.1 sec (0.341 hour)

The 70 kDa membrane protein FtsH from Aquifex aeolicus I222, a = 137.9, b = 162.1, c = 170





$$\hat{J}(\mathbf{h}, D, \Omega) = \hat{J}(\mathbf{h}, D = 0) \text{scale}(D, \Omega) \exp(-\mathbf{h} \cdot \mathbf{B}(D, \Omega) \cdot \mathbf{h}^T / 2)$$



Flux
 σ_x σ_y
 Aperture
 Slit sizes

Diffraction sample Modeling

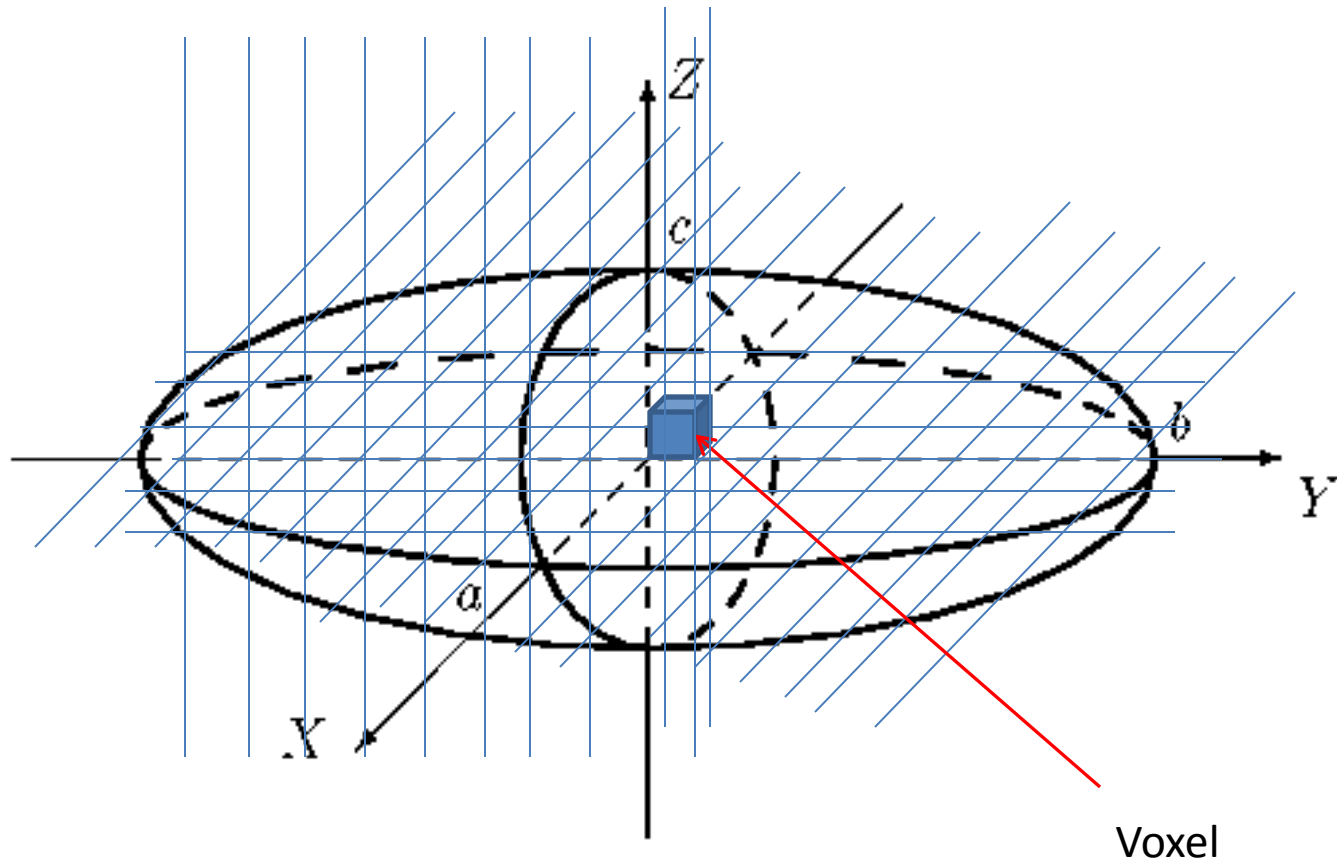
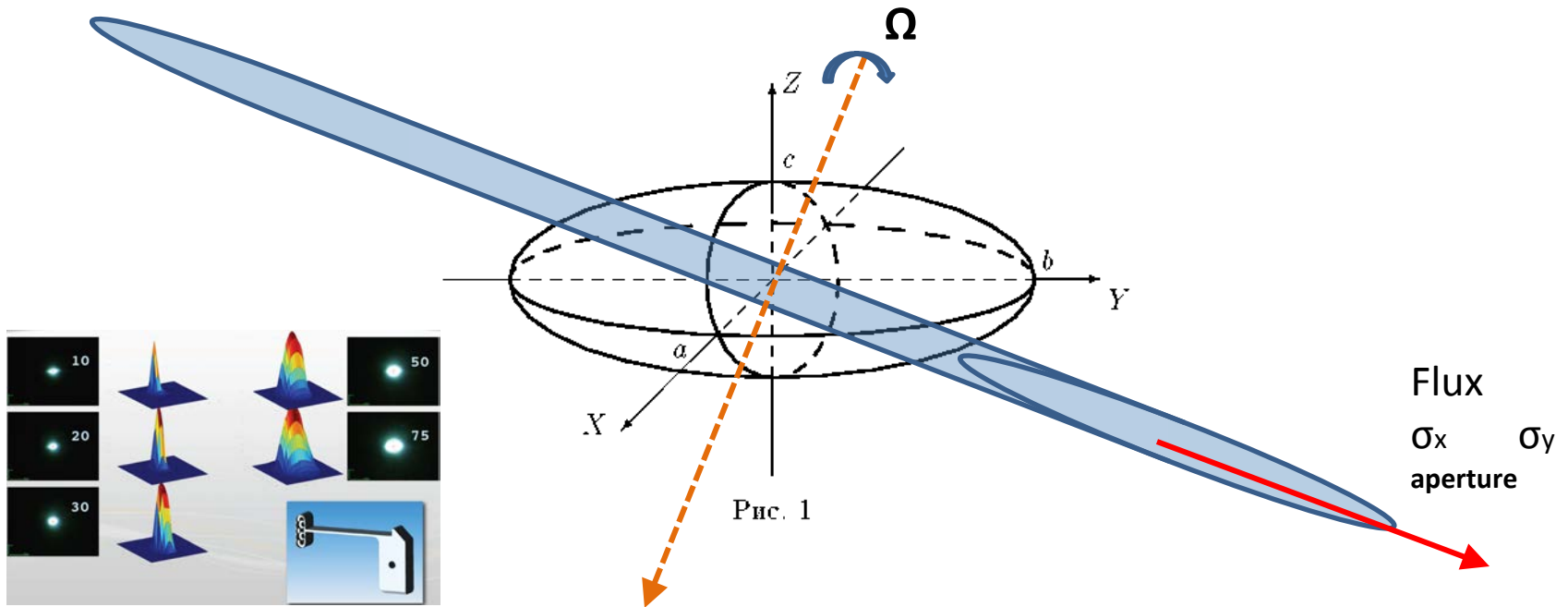


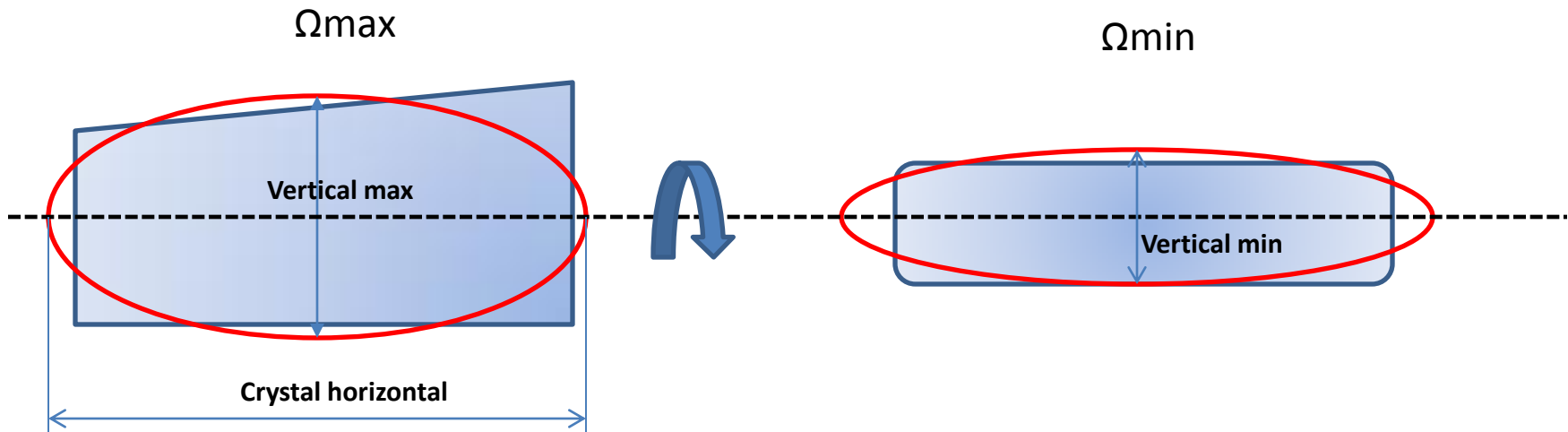
Рис. 1

Volumetric Picture Element

$$Scale(\Omega) = Scale(voxel) \times NumberVoxel(\Omega)$$



$$\hat{J}(\mathbf{h}, D) = \hat{J}_o(h) \sum_{voxel} \sum_{x,y} I_{x,y}(beam) \times scale(voxel, D_{voxel}) \exp(-\mathbf{h} \cdot \mathbf{B}(D_{voxel}) \cdot \mathbf{h}^T / 2)$$

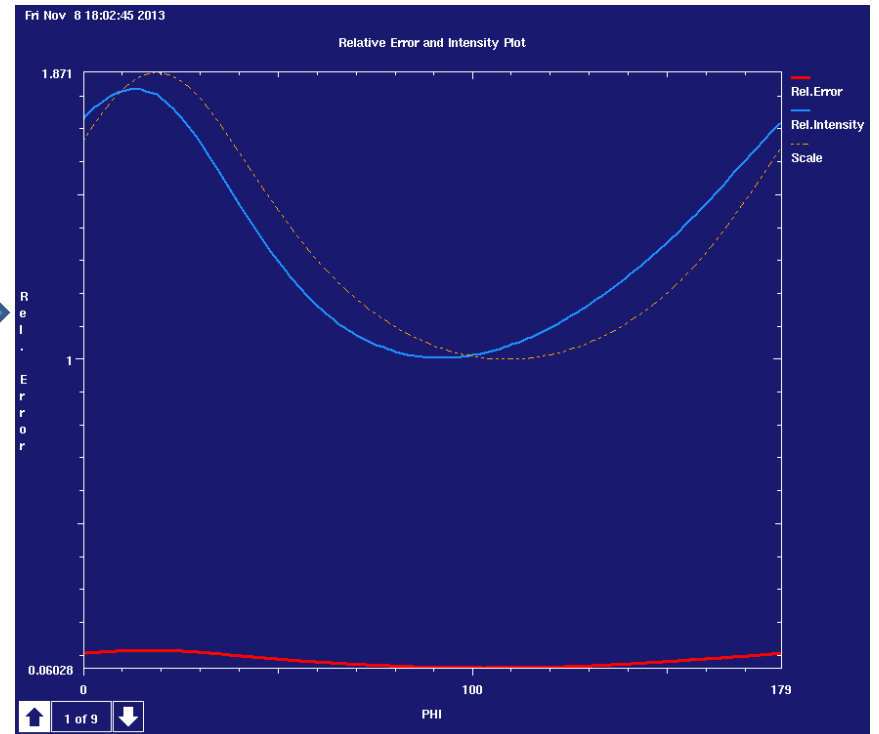
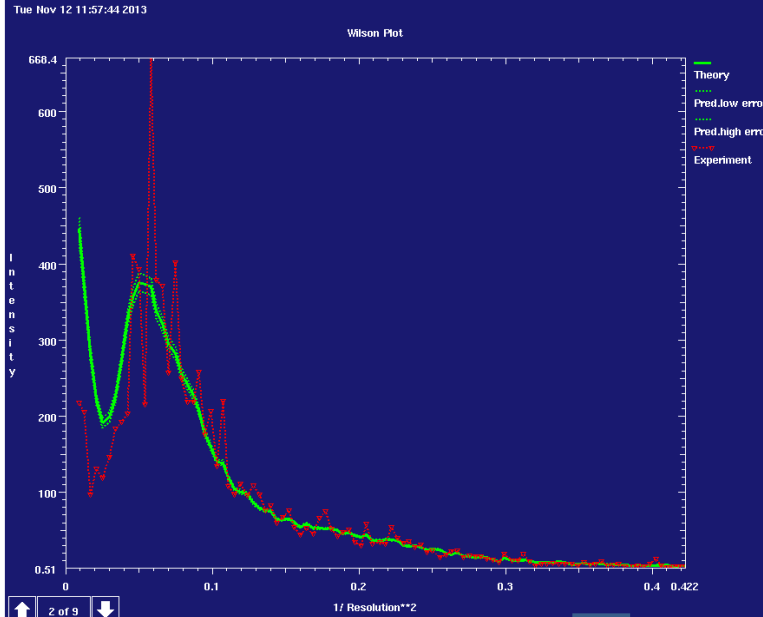


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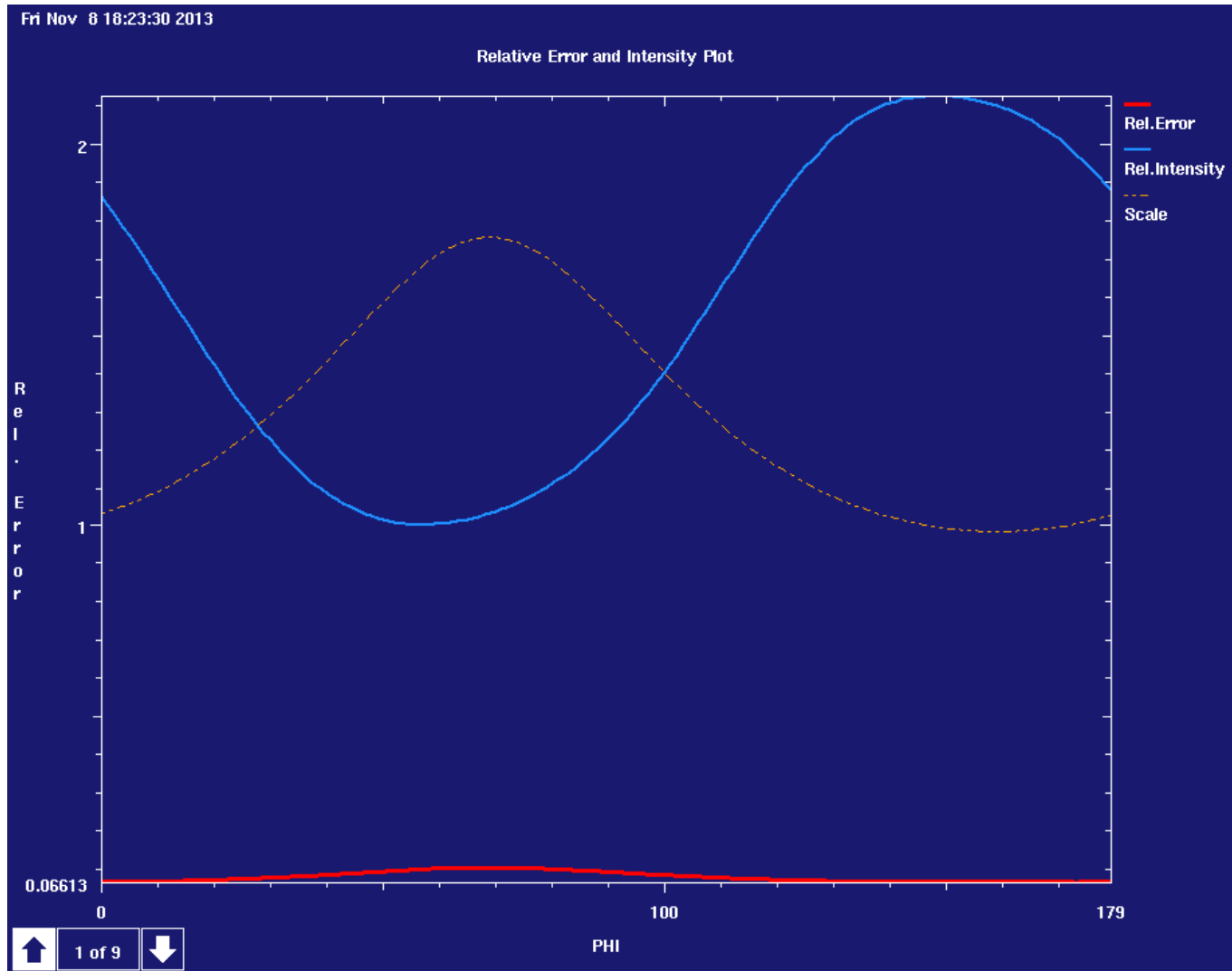
beam_crystal.dat - /mntdirect/_users/apopov/BEST4.1/
File Edit Search Preferences Shell Macro Windows Help
! - this is a comments
! all sizes in mm
horizontal_size 0.045
vertical_size 0.035
aperture_size 0.030
!default: no aperture
!horizontal slit 0.1000
!vertical slit 0.1000
beam_shift 0.01
!vertical shift relative to the rotation axis
!beam flux 2.0e12
flux_2_dose 2.0e-5
!
crystal_vert_max 0.170
crystal_vert_min 0.090
crystal_hor 0.100
omega_min 20
!description of crystal shape and position- a, c, b
end

```

First step - scaling



First step - scaling



Main Wedge

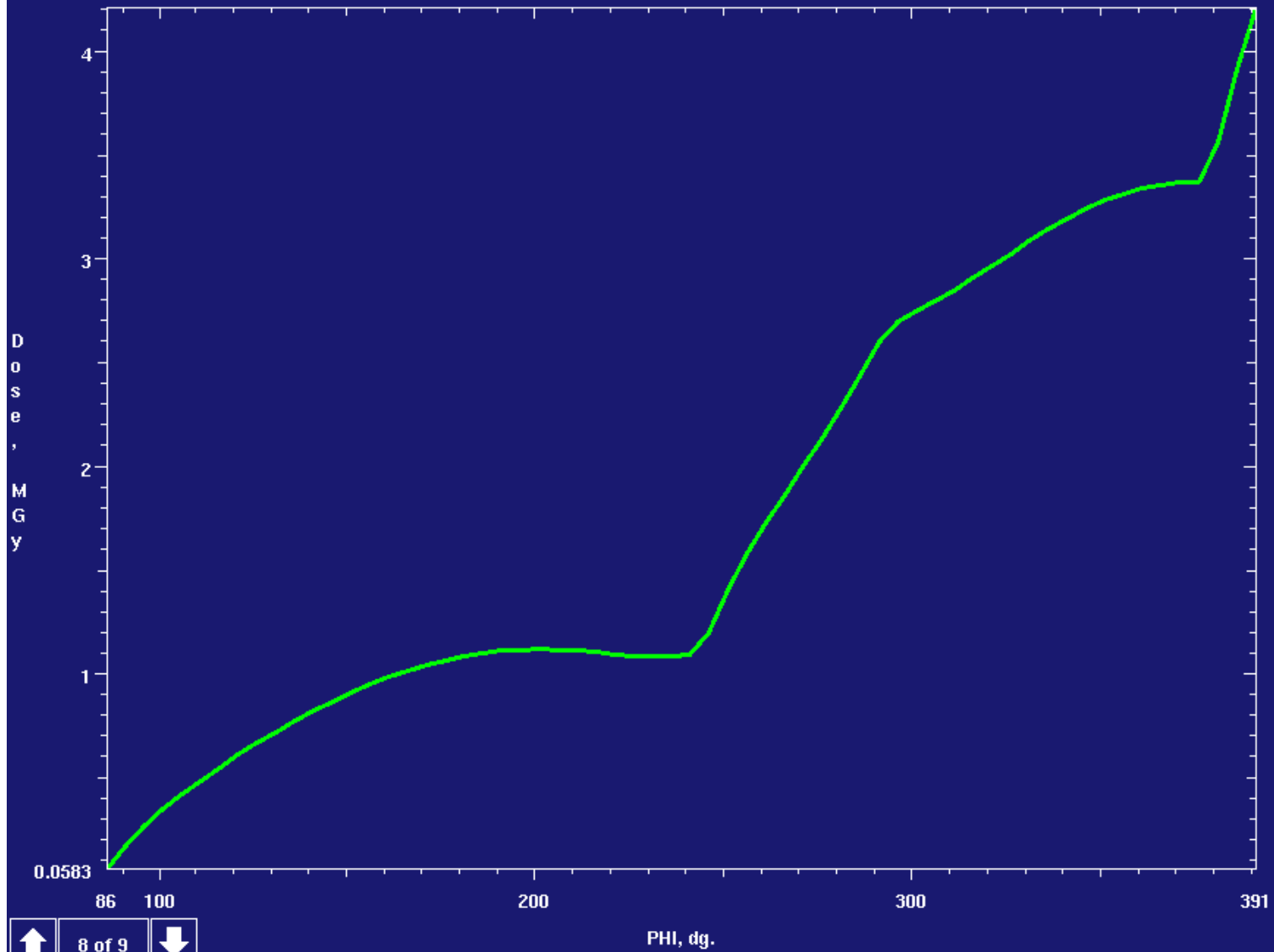
Resolution limit is set by the radiation damage
 Resolution limit = 1.61 Angstrom Transmission = 100.0% Distance = 306.2mm

WEDGE PARAMETERS					INFORMATION						
sub-We-dge	Phi-start degree	Rot. width degree	Exposure /image s	N.of ima-ges	Over-lap	sWedge width degree	Exposure /sWedge s	Exposure total s	Dose /sWedge MGy	Dose total MGy	Comple-teness %
1	81.00	0.15	0.122	1067	No	160.05	130.5	130.5	3.581	3.581	99.9
2	241.05	0.15	0.358	333	No	49.95	119.3	249.9	3.274	6.855	100.0
3	291.00	0.15	0.223	567	No	85.05	126.2	376.1	3.463	10.319	100.0
4	376.05	0.15	0.647	100	No	15.00	64.7	440.8	1.774	12.093	100.0

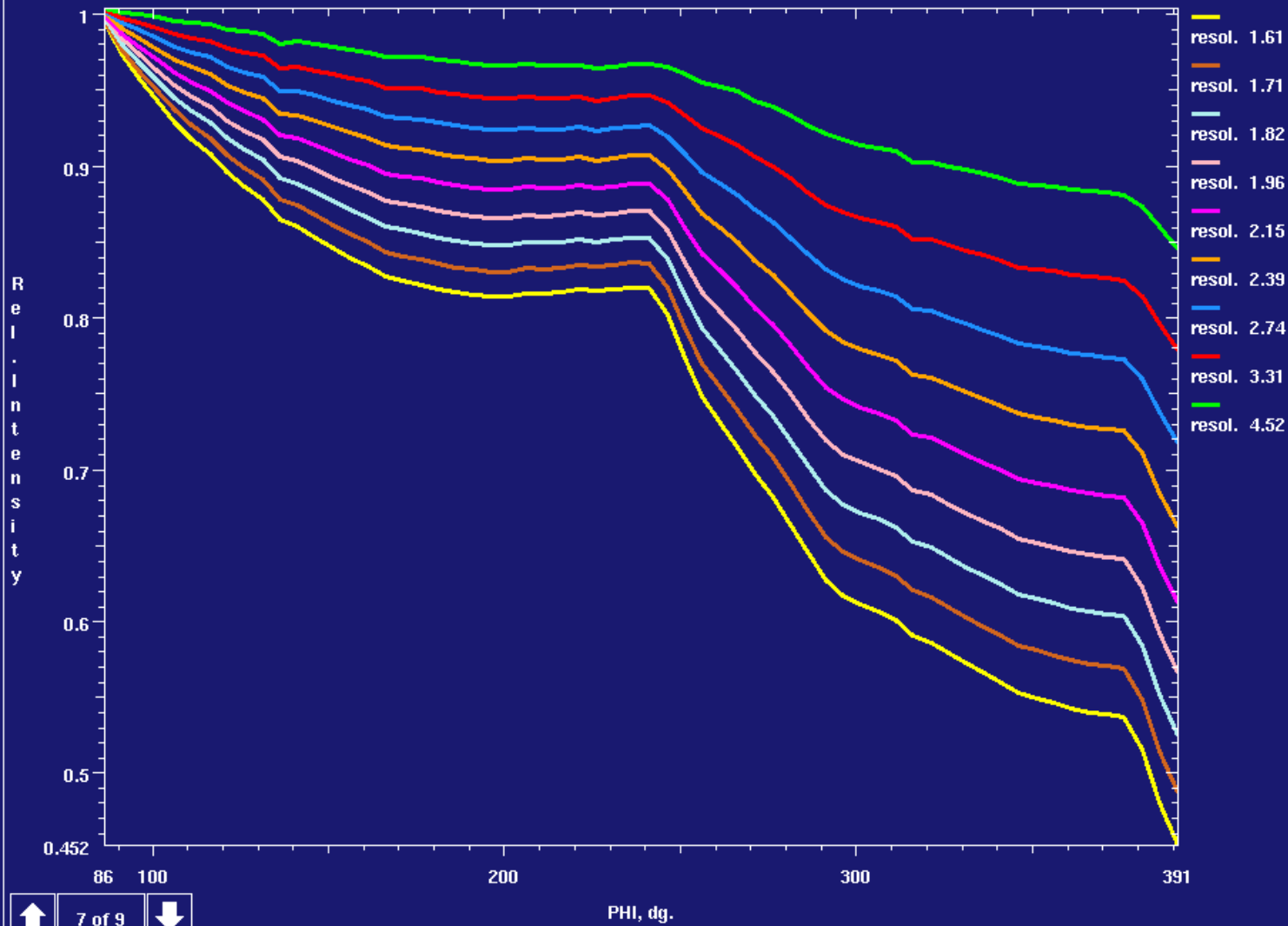
Phi_start - Phi_finish : 81.00 - 391.05
 Total rotation range : 310.05 degree
 Total N.of images : 2067
 Overall Completeness : 100.0%
 Redundancy : 12.69
 R-factor (outer shell) : 10.5% (89.7%)
 I/Sigma (outer shell) : 30.7 (3.2)
 Total Exposure time : 440.8 sec (0.122 hour)
 Total Data Collection time : 449.0 sec (0.125 hour)

1. SUMMARY END - (CONT.)

Average dose vs.PHI



Intensity decrease due to radiation damage

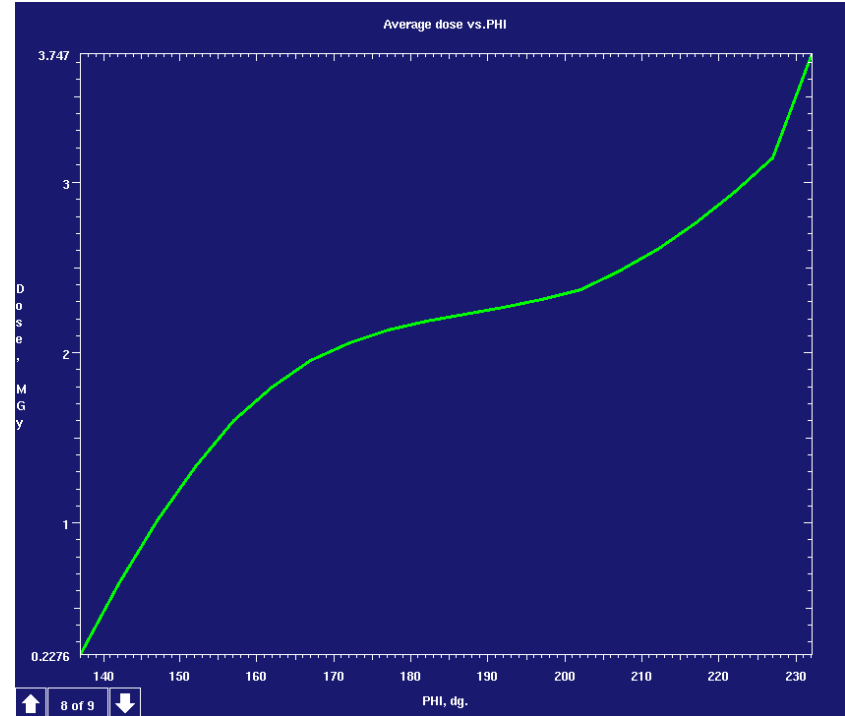
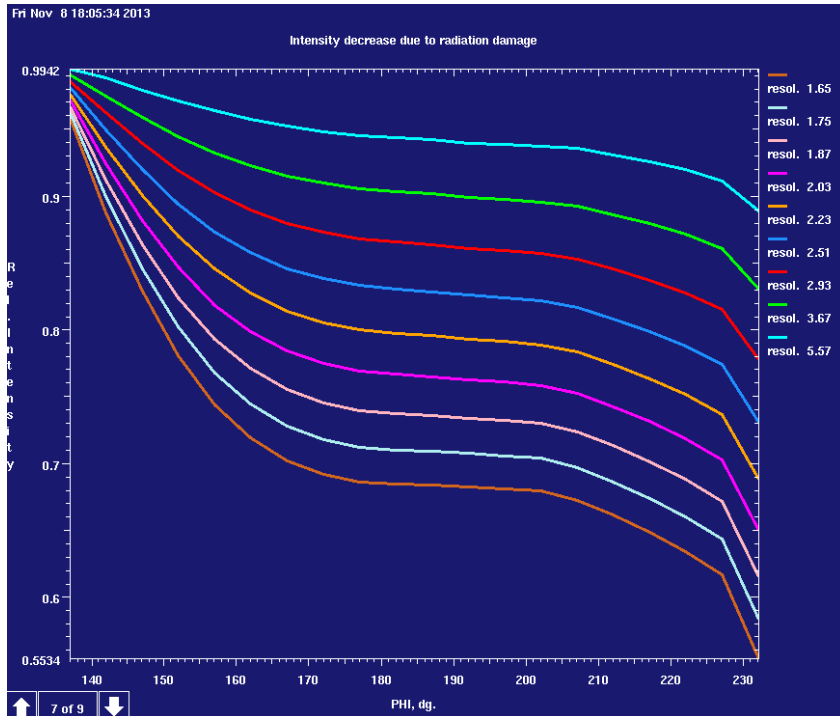


Main Wedge

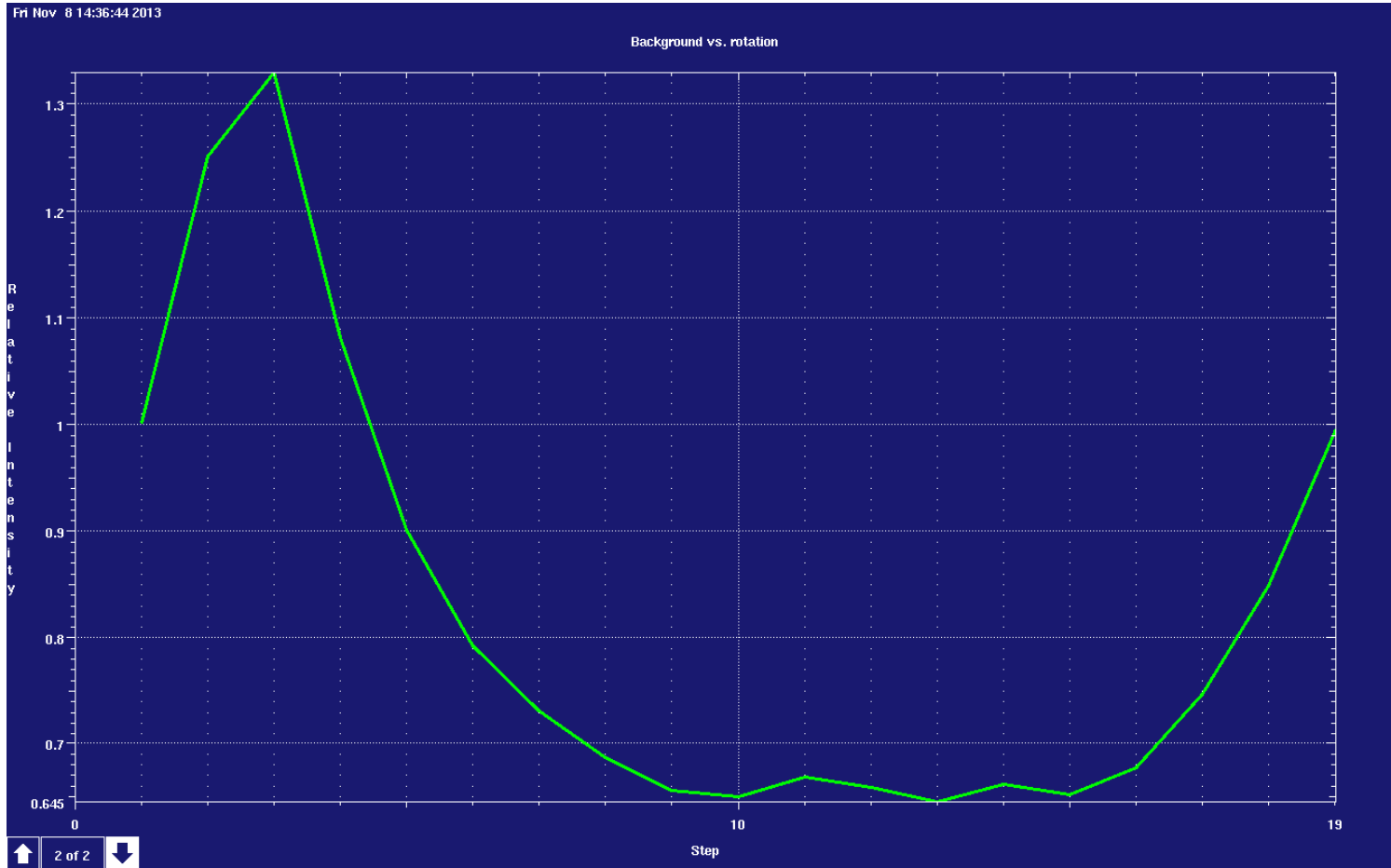
Resolution limit is set by the radiation damage
 Resolution limit = 1.65 Angstrom Transmission = 100.0% Distance = 315.4mm

WEDGE PARAMETERS					INFORMATION						
sub-We-dge	Phi-start degree	Rot. width degree	Exposure /image s	N.of ima-ges	Over-lap	sWedge width degree	Exposure /sWedge s	Exposure total s	Dose /sWedge MGy	Dose total MGy	Completeness %
1	132.00	0.15	0.478	634	No	95.10	303.1	303.1	8.315	8.315	97.0
2	227.10	0.15	1.328	33	No	4.95	43.8	346.9	1.202	9.518	99.0

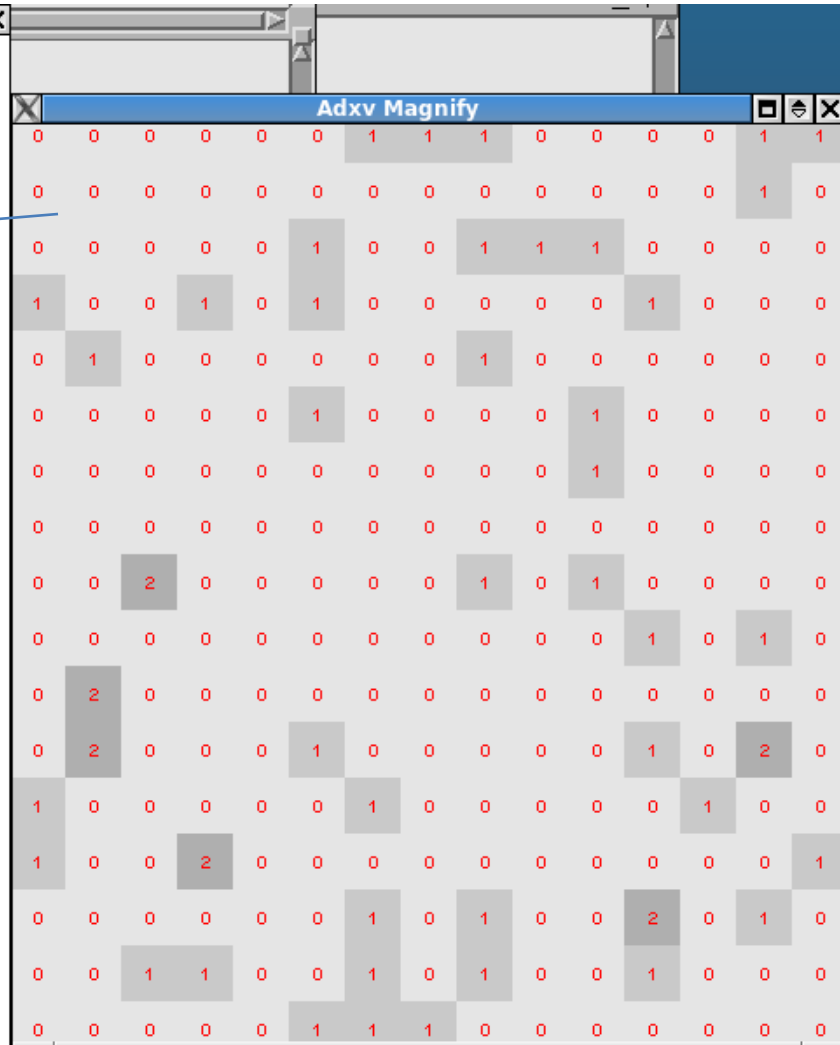
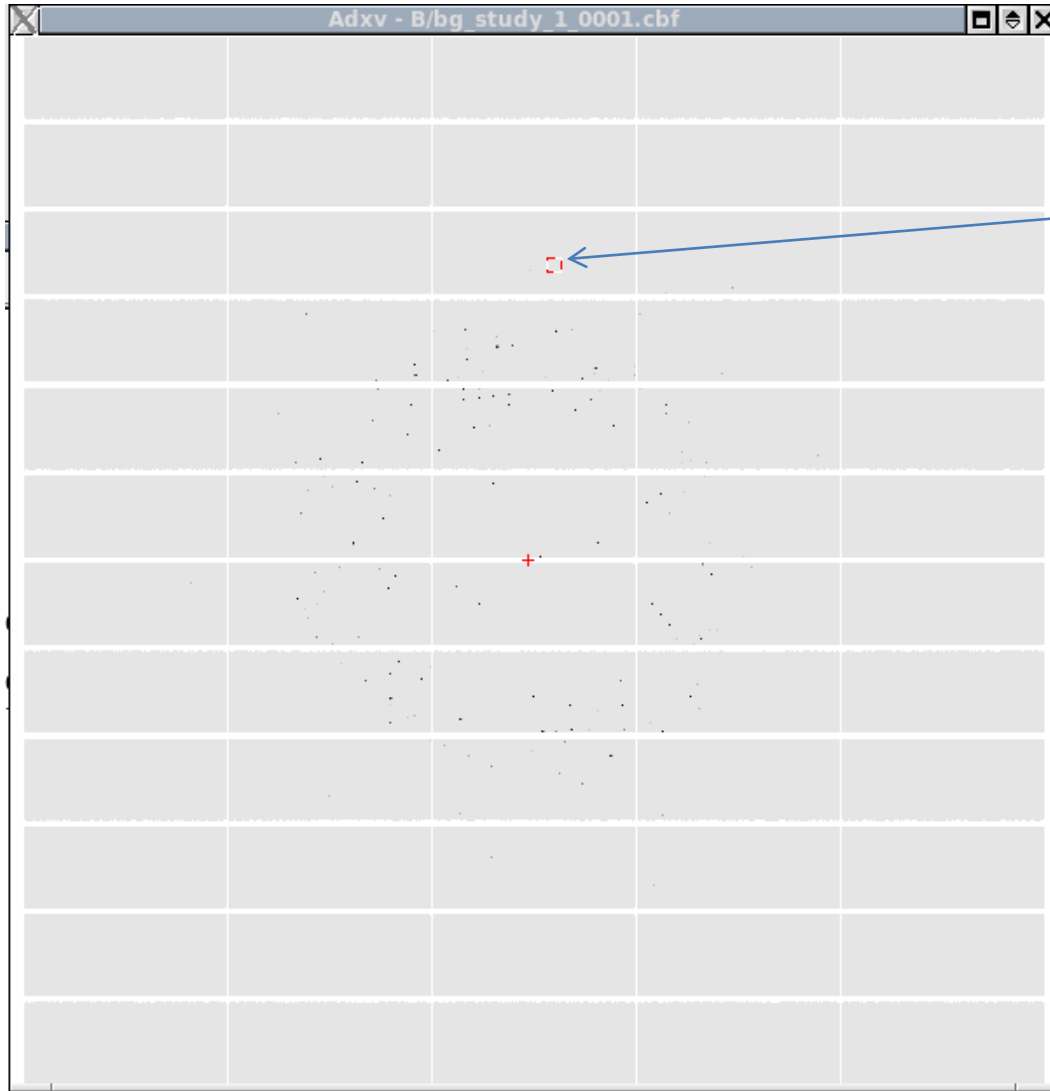
Phi_start - Phi_finish : 132.00 - 232.05
 Total rotation range : 100.05 degree
 Total N.of images : 667
 Overall Completeness : 99.0%
 Redundancy : 4.13
 R-factor (outer shell) : 6.3% (48.1%)
 I/Sigma (outer shell) : 27.2 (2.9)
 Total Exposure time : 346.9 sec (0.096 hour)
 Total Data Collection time : 349.6 sec (0.097 hour)



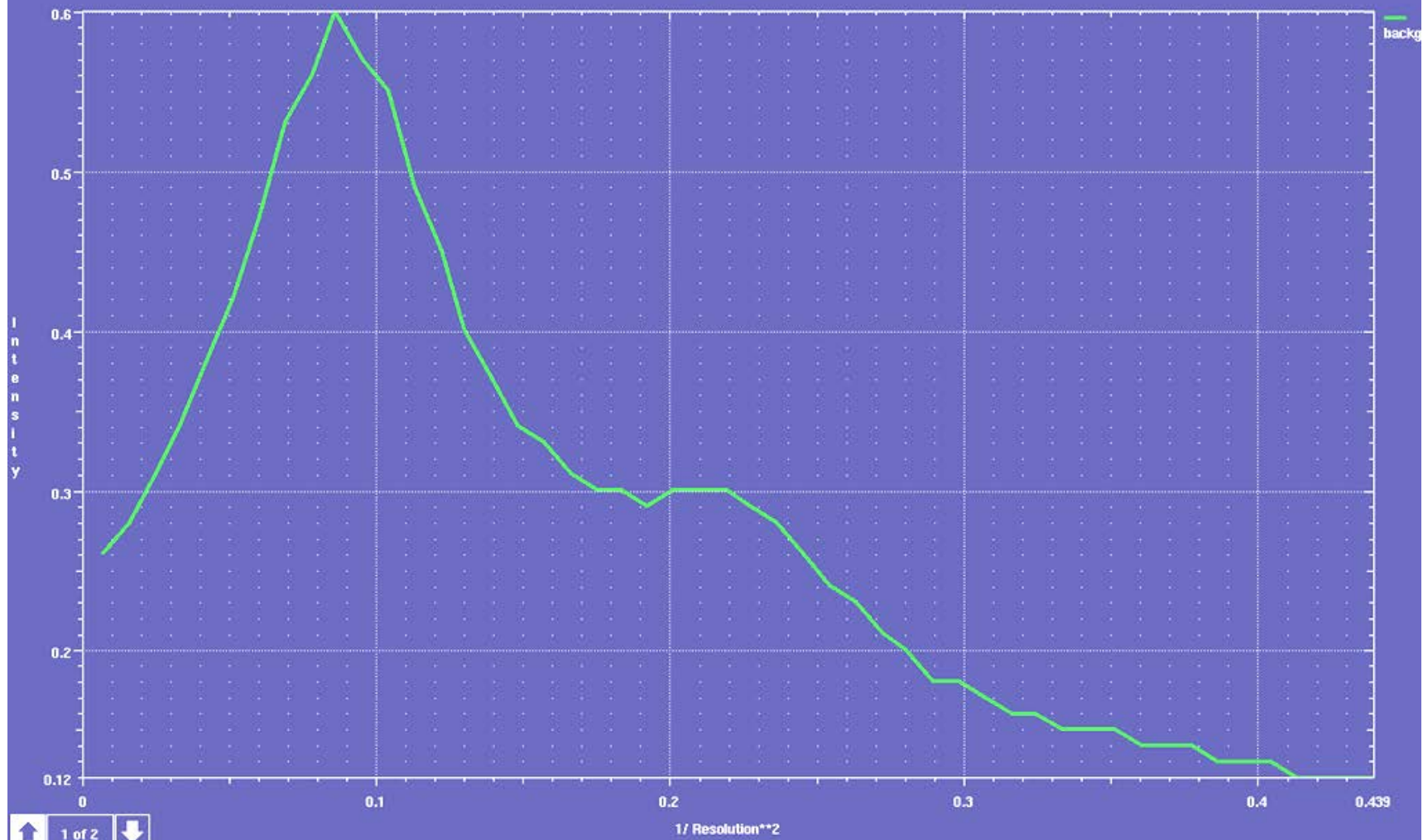
Background vs. Crystal position

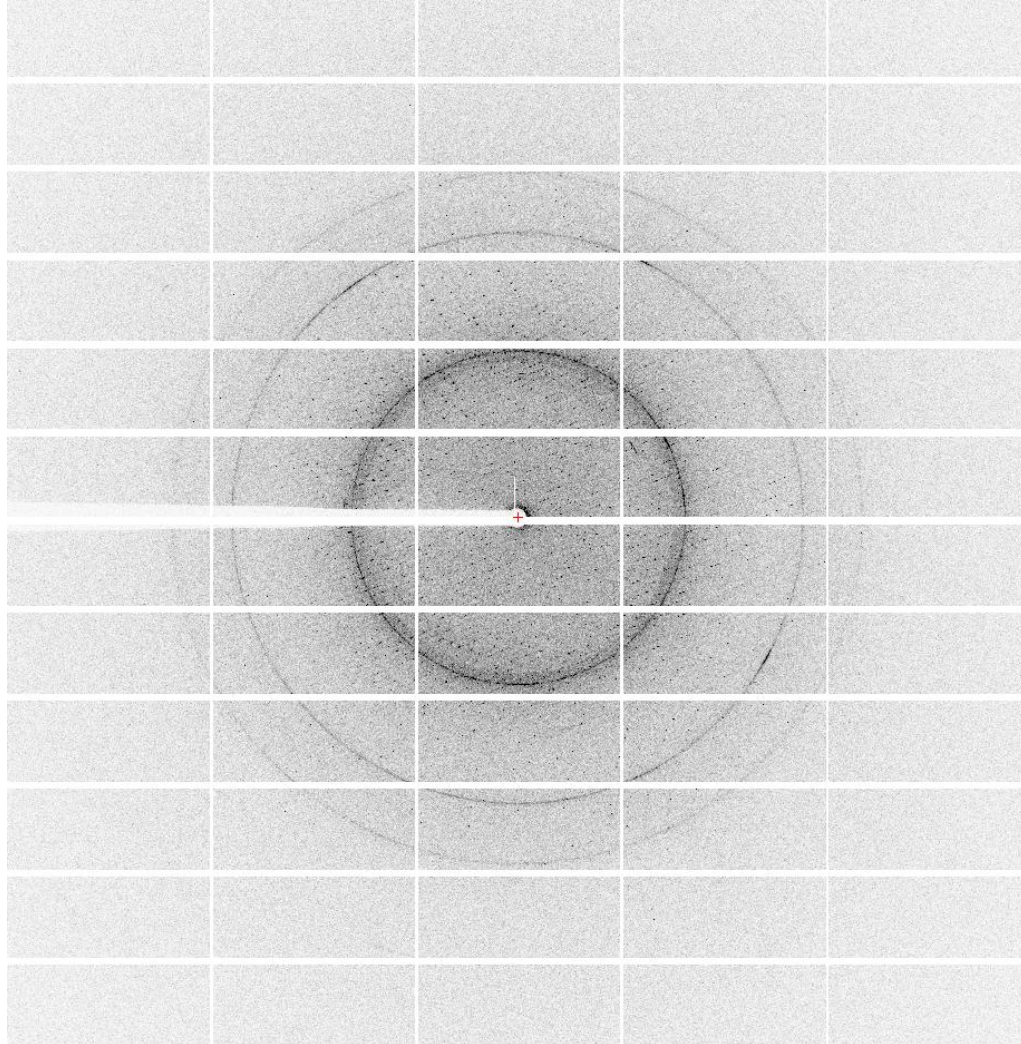


Background vs. Crystal position



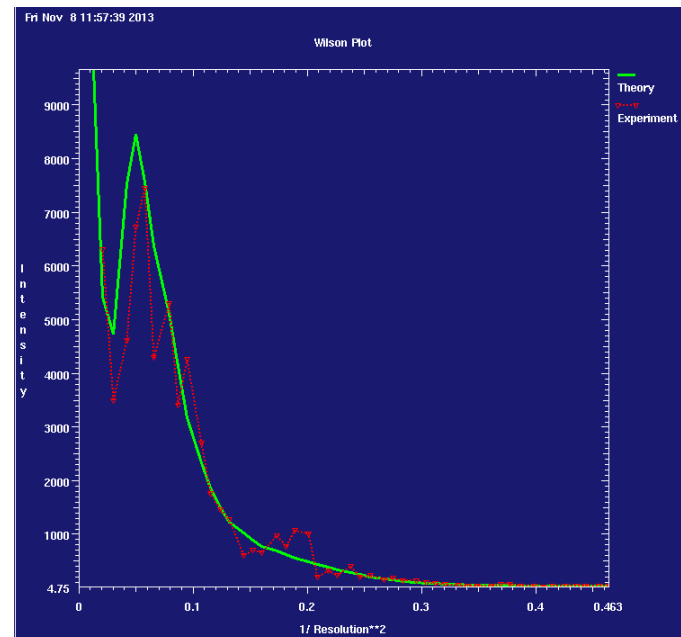
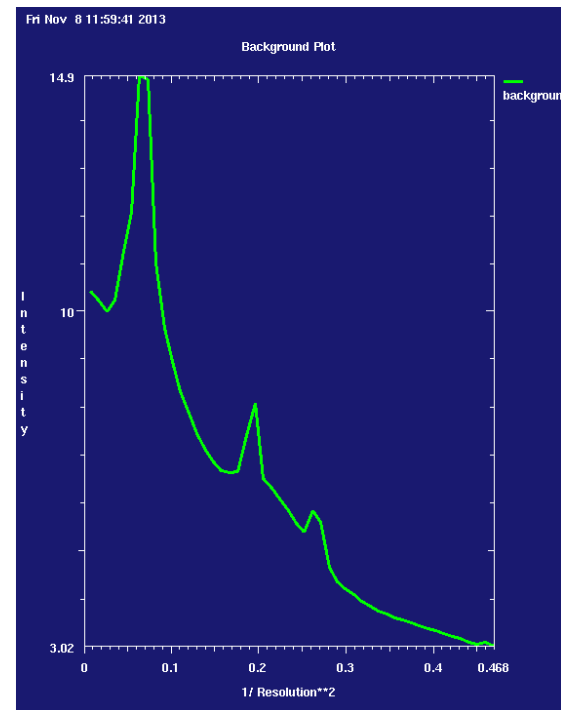
Background Plot



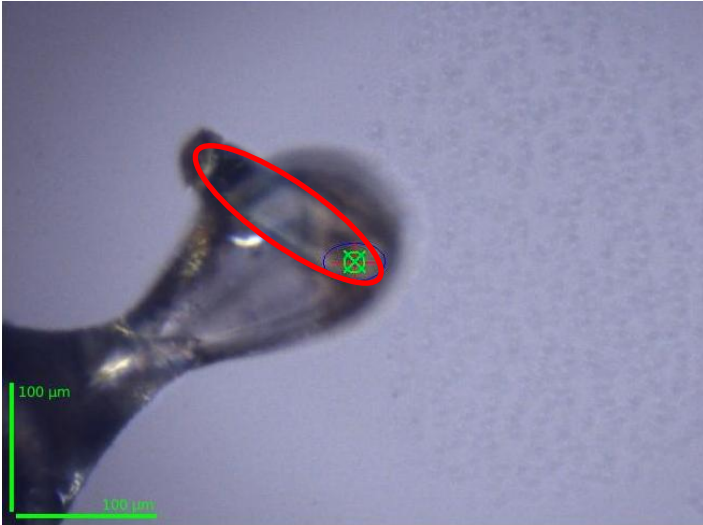
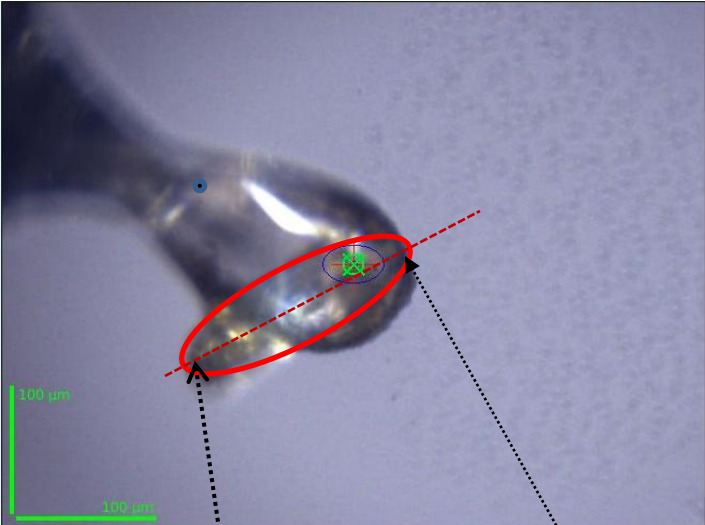


```

image number =      1
Relative scale   :   9.08
Overall B-factor : 23.74 Angstrom^2
Resolution used  :   1.7 Angstrom
Correlation =    84.6 %
Rfactor =       17.7 %
  
```



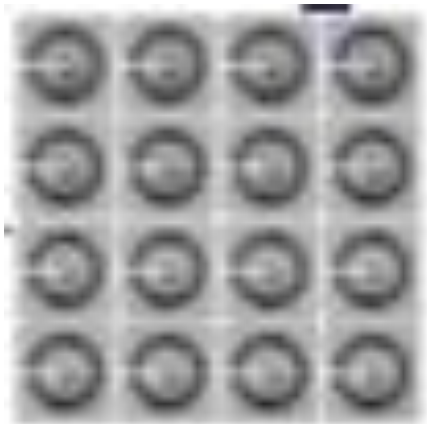
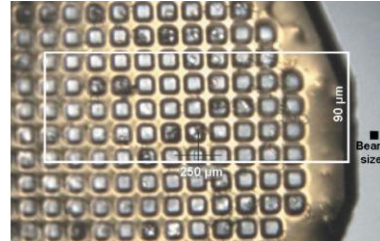
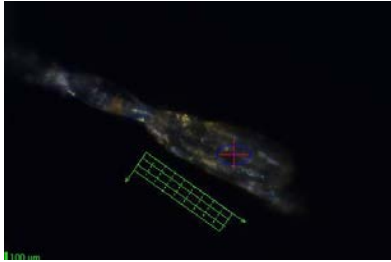
How to define a form and the position of a crystal?



Point 1

Point 2

crystal detection and characterization



computer programs



Journal of
**Applied
Crystallography**
ISSN 0021-8898

Automated diffraction image analysis and spot searching for high-throughput crystal screening

Zepu Zhang,^a Nicholas K. Sauter,^b Henry van den Bedem,^c Gyorgy Snell^d and Ashley M. Deacon^{c*}

Received 1 September 2005
Accepted 5 December 2005

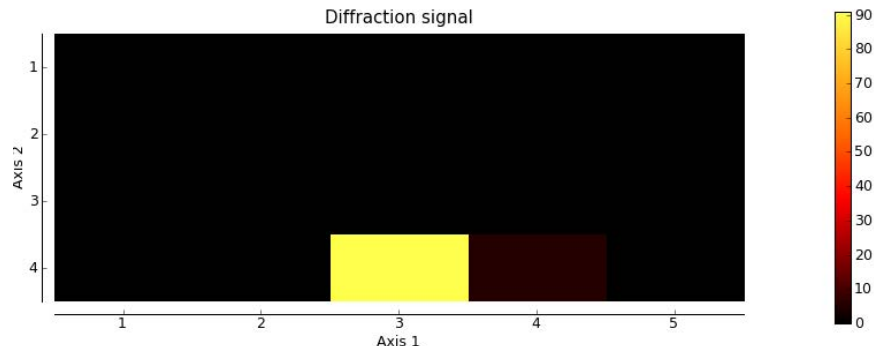
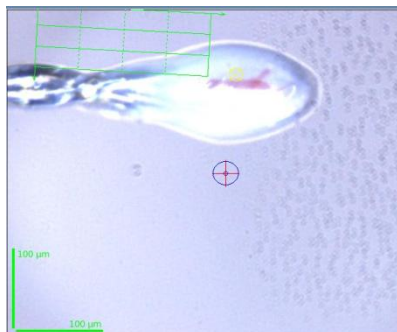
LABELIT
MOSFLM

Best position

Grid index Y	Grid index Z	Image file	sampx	sampy	phiy	Total integrated intensity	Bravais lattice
10	2	mesh2d-opid291_1_0020.cbf	-0.089	0.005	-0.545	1.3e+07	P3

All positions

Grid index Y	Grid index Z	Image file	sampx	sampy	phiy	Total integrated intensity	Bravais lattice
1	1	mesh2d-opid291_1_0001.cbf	-0.043	-0.041	-0.345	1.61e+06	—
2	1	mesh2d-opid291_1_0002.cbf	-0.046	-0.038	-0.367	6.17e+06	—
3	1	mesh2d-opid291_1_0003.cbf	-0.049	-0.035	-0.390	9.35e+06	—
4	1	mesh2d-opid291_1_0004.cbf	-0.053	-0.031	-0.413	1.08e+07	P3
5	1	mesh2d-opid291_1_0005.cbf	-0.056	-0.028	-0.436	1.14e+07	—
6	1	mesh2d-opid291_1_0006.cbf	-0.059	-0.025	-0.458	9e+06	—
7	1	mesh2d-opid291_1_0007.cbf	-0.062	-0.022	-0.481	6.49e+06	—
8	1	mesh2d-opid291_1_0008.cbf	-0.065	-0.019	-0.504	3.04e+06	—



Best position

The sample has automatically been moved to the best position.

In order to move the sample to an other position please copy/paste the commands from the right column into SPEC EXP.

Axis 1	Axis 2	Image file	Signal 1	Signal 2	Bravais lattice	SPEC command for moving sample to position
3	4	mesh-x_1_0018.cbf	90.9	75846	P1	mv sampx 0.280; mv sampy -0.382; mv phiy 22.465

Signal 1: Criteria that uses intensities over background vs resolution. Popov 2014, to be published.

Signal 2: Labelit distl spotfinder total integrated intensity.

All positions

Axis 1	Axis 2	Image file	Signal 1	Signal 2	Bravais lattice	SPEC command for moving sample to position
3	4	mesh-x_1_0018.cbf	90.9	75846	P1	mv sampx 0.280; mv sampy -0.382; mv phiy 22.465
4	4	mesh-x_1_0019.cbf	5.2	8975	_	mv sampx 0.278; mv sampy -0.381; mv phiy 22.515
1	1	mesh-x_1_0001.cbf	0	165	_	mv sampx 0.351; mv sampy -0.415; mv phiy 22.370
2	1	mesh-x_1_0002.cbf	0	368	_	mv sampx 0.348; mv sampy -0.414; mv phiy 22.419
3	1	mesh-x_1_0003.cbf	0	87	_	mv sampx 0.346; mv sampy -0.413; mv phiy 22.469
4	1	mesh-x_1_0004.cbf	0	199	_	mv sampx 0.344; mv sampy -0.411; mv phiy 22.519
5	1	mesh-x_1_0005.cbf	0	811	_	mv sampx 0.341; mv sampy -0.410; mv phiy 22.569
1	2	mesh-x_1_0006.cbf	0	274	_	mv sampx 0.329; mv sampy -0.405; mv phiy 22.368
3	2	mesh-x_1_0008.cbf	0	365	_	mv sampx 0.324; mv sampy -0.402; mv phiy 22.468
4	2	mesh-x_1_0009.cbf	0	514	_	mv sampx 0.322; mv sampy -0.401; mv phiy 22.518
5	2	mesh-x_1_0010.cbf	0	281	_	mv sampx 0.319; mv sampy -0.400; mv phiy 22.567
1	3	mesh-x_1_0011.cbf	0	825	_	mv sampx 0.307; mv sampy -0.394; mv phiy 22.367
2	3	mesh-x_1_0012.cbf	0	690	_	mv sampx 0.305; mv sampy -0.393; mv phiy 22.417
3	3	mesh-x_1_0013.cbf	0	1251	_	mv sampx 0.302; mv sampy -0.392; mv phiy 22.467
4	3	mesh-x_1_0014.cbf	0	4402	_	mv sampx 0.300; mv sampy -0.391; mv phiy 22.516
5	3	mesh-x_1_0015.cbf	0	76	_	mv sampx 0.297; mv sampy -0.390; mv phiy 22.566
1	4	mesh-x_1_0016.cbf	0	553	_	mv sampx 0.285; mv sampy -0.384; mv phiy 22.366
2	4	mesh-x_1_0017.cbf	0	539	_	mv sampx 0.283; mv sampy -0.383; mv phiy 22.416
5	4	mesh-x_1_0020.cbf	0	83	_	mv sampx 0.276; mv sampy -0.380; mv phiy 22.565
2	2	mesh-x_1_0007.cbf	-0.005	6889	_	mv sampx 0.327; mv sampy -0.403; mv phiy 22.418

Number	Scaler	B-factor	Resolution	Correlation	R-factor
1	7.896	310.8	5.3	12.4	74.9
2	43.779	124.7	4.1	39	43.6
3	74.18	53.1	3	71.2	20.4
4	89.461	43.6	2.9	76.2	20
5	108.249	37.1	2.9	78.1	21.9
6	255	38.5	3.1	77.9	22.6
7	916.497	46.1	5.3	60.5	49.7
8	2075.394	67.8	5.3	10.7	87.6
9	0	0	0	0	0
10	0	0	0	0	0
11	424.232	43.5	4.8	62.5	36.2
12	31.177	34.8	2.4	80.5	17.4
13	14.481	28.3	2	84	15.4
14	8.728	31.3	1.9	81.7	17.9
15	5.714	37.1	2	78.7	18.5
16	5.048	38.9	2.1	77.2	20.3
17	6.151	34	1.9	79.7	17.4
18	11.242	29.3	1.9	83.7	15.1
19	15.979	38.7	2.1	76.6	21.5
20	51.573	39.3	2.9	76	22.7
21	0	0	0	0	0
22	203.738	49.6	3.1	71.4	27.2
23	37.04	47.9	2.9	73.1	21.5
24	13.783	49.1	2.4	71	24.4
25	14.12	30.1	2.4	82.5	16.6
26	7.71	34.2	2	79.3	19.3
27	5.854	35.4	1.9	80	17.1
28	5.696	37.9	2	79.1	16.9
29	6.887	35.6	1.9	79.5	16.3
30	9.08	23.7	1.7	84.6	17.7
31	0	0	0	0	0
32	0	0	0	0	0
33	0	0	0	0	0
34	0	0	0	0	0
35	219.289	42.8	3.1	74.7	26.8
36	166.848	-9.9	2.4	37.6	62.2
37	49.944	12.6	2.4	85.5	24.5
38	17.325	40.3	2.4	74.9	24.2
39	11.697	49.7	2.4	70.9	24.9
40	15.37	36.1	2.1	77.9	20.8