



The European Synchrotron

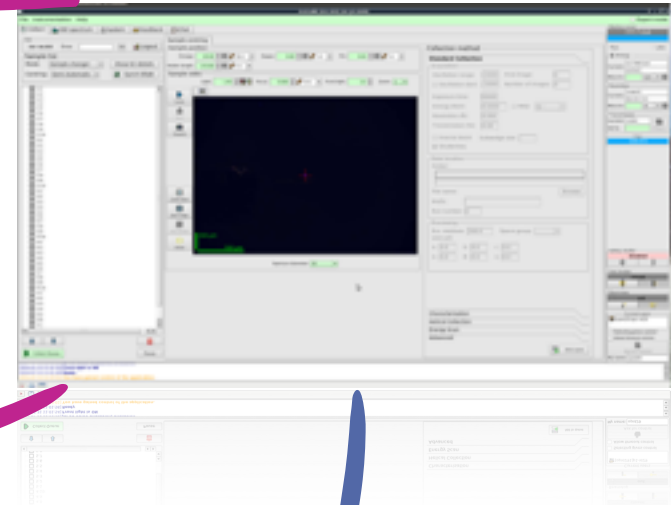
ID29

ISPyB



Sample information

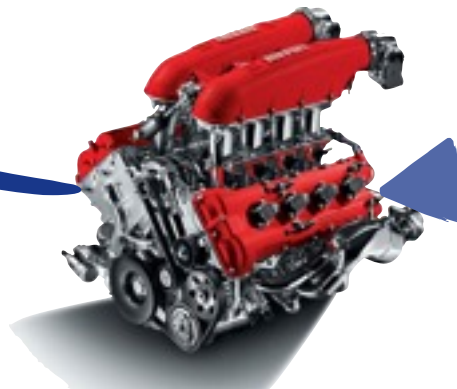
MXCuBE2

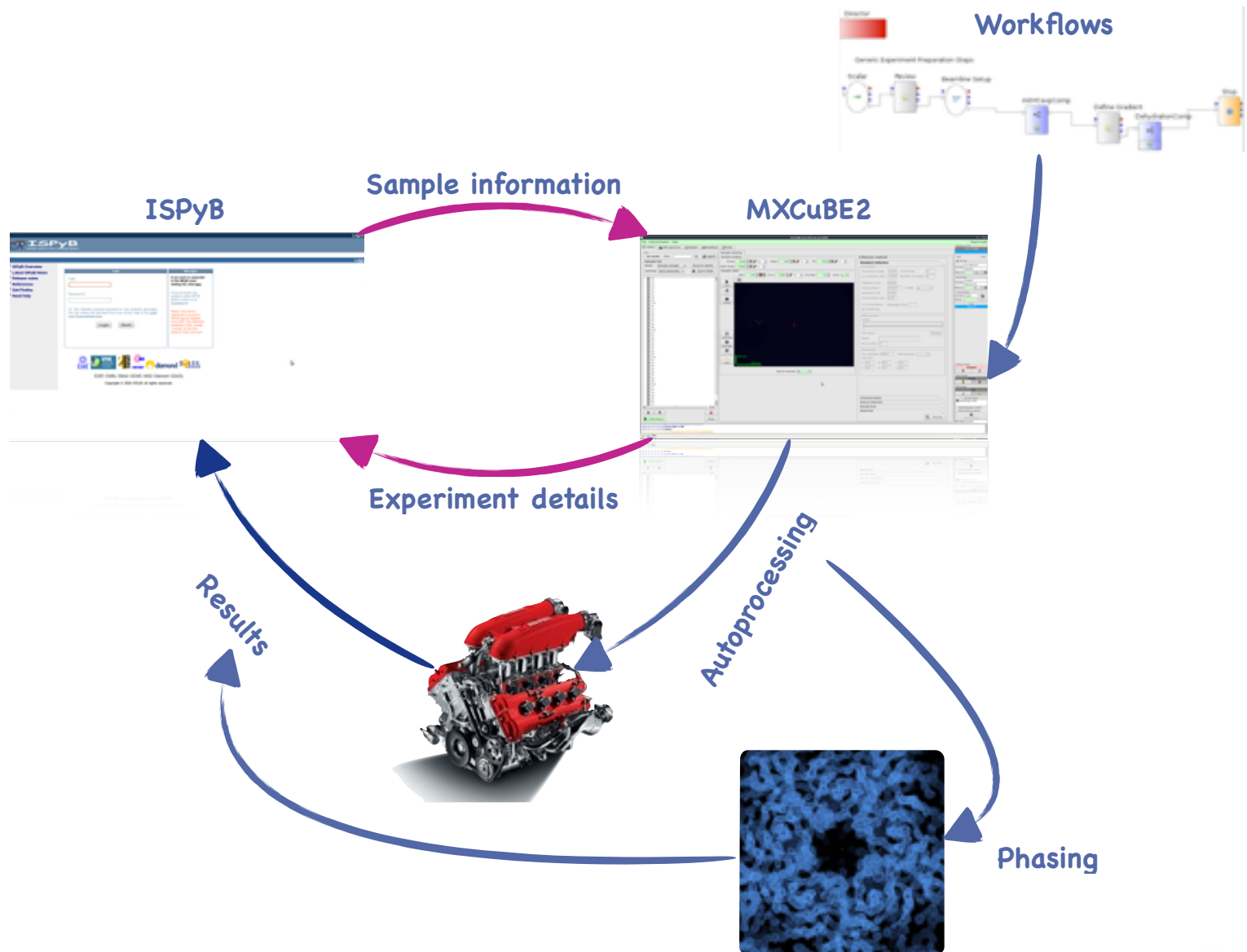


Experiment details

Results

Autoprocessing



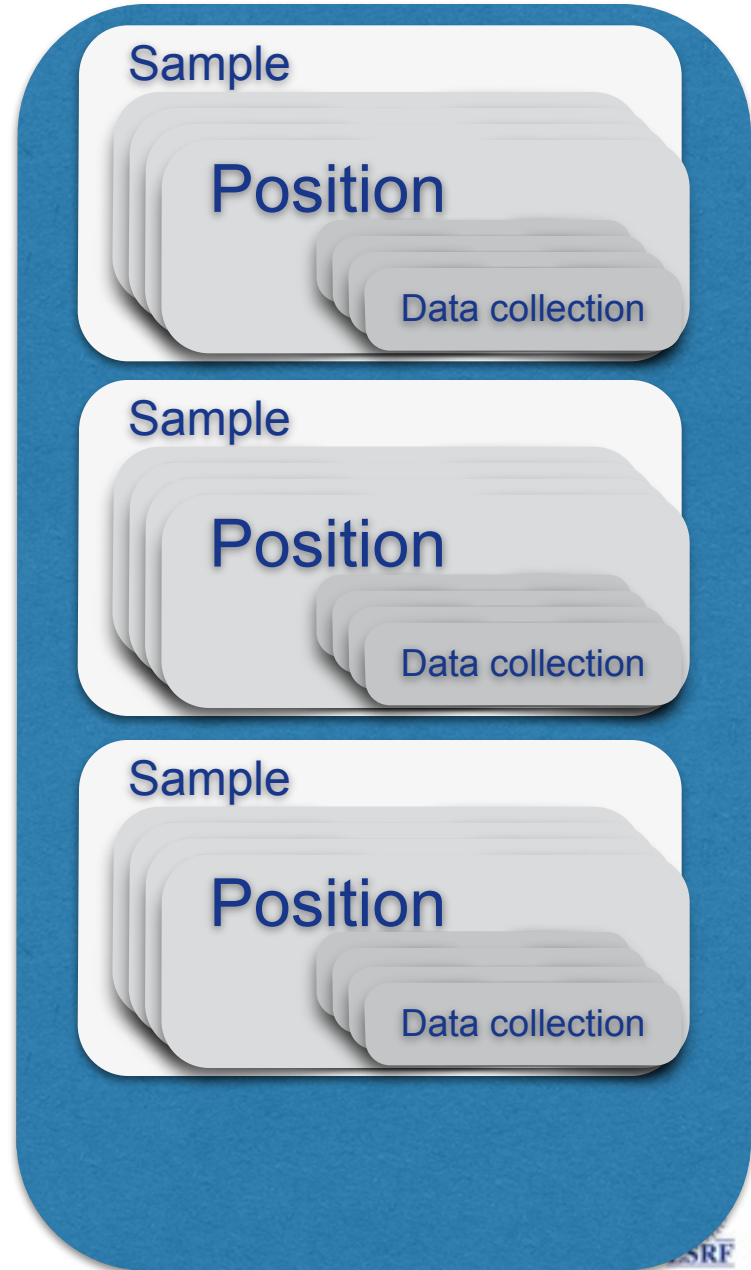
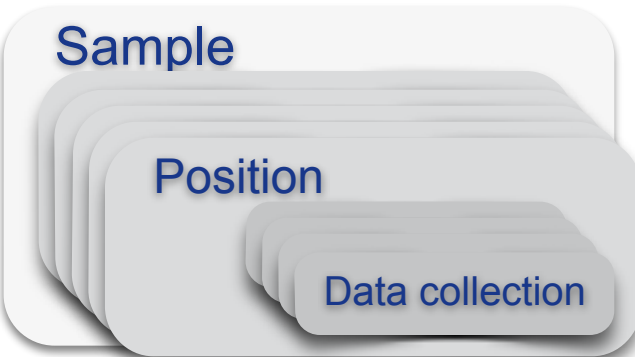
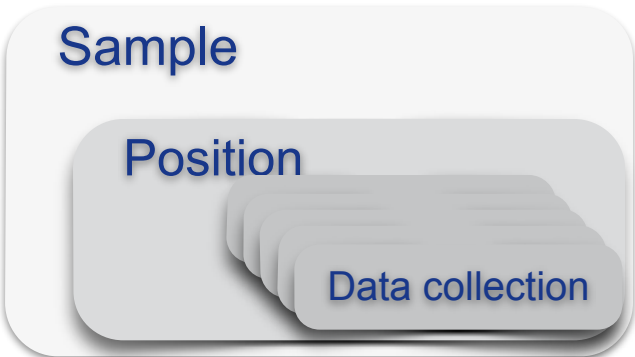
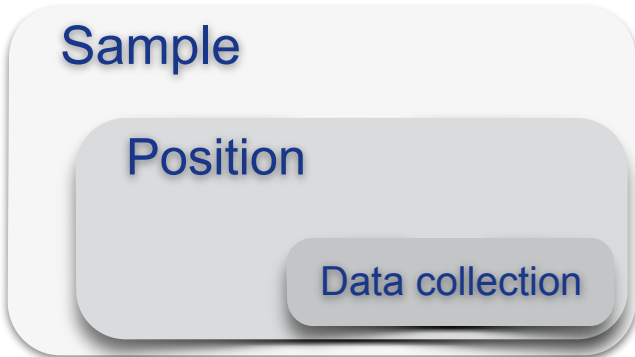


SC - Queue

Sample - Position

Data Collection

[2014-01-31 22:42:34] Ready
 [2014-01-31 22:42:34] Centring in progress. Please save the suggested centring or re-center



1. Standard Collection
2. Characterisation
3. Helical Data Collection
4. Energy Scan
5. Advanced

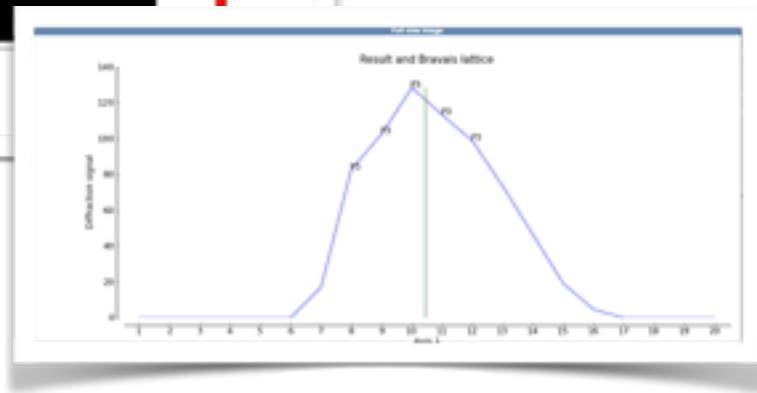
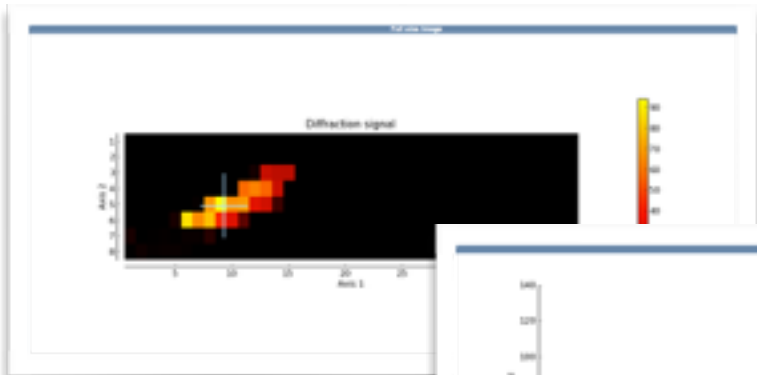
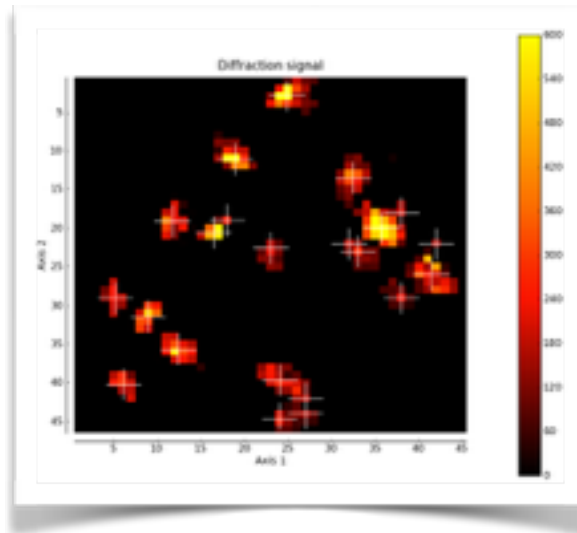
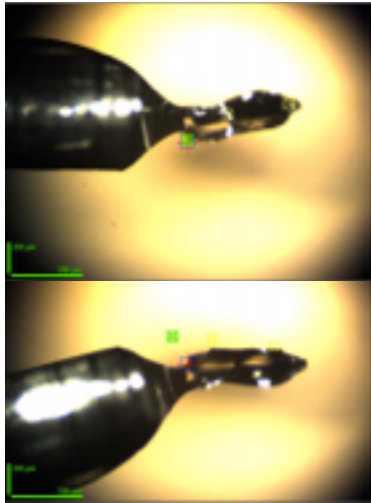
Powerful intuitive interface
 Close integration with ISPyB
 Enhancing automation
 Robust abstraction level
Open to external experiment descriptors

This design permits:
 Advance experiments: (ex.) MAD, multi
 positional MAD, multi kappa, raster &
 collect

The screenshot displays the 'Standard Collection' configuration window in the QUEUE software. The interface is organized into several sections:

- Collection method:** A dropdown menu showing 'Standard Collection' selected.
- Acquisition:** Contains input fields for 'Oscillation range' (0.1), 'First image' (1), 'Oscillation start' (45.0), 'Number of images' (1), 'Exposure time' (0.037), 'Energy (KeV)' (12.7), 'Resolution (Å)' (3.0), and 'Transmission (%)' (4.99). There are checkboxes for 'MAD' (unchecked), 'Inverse beam' (unchecked), and 'Shutterless' (checked). A 'Subwedge size' field is also present.
- Data location:** Includes a 'Folder' field with the path '/data/id29/inhouse/opid291/20140731/RAW_DATA', a 'File name' field with 'opid291_1_####.cbf', a 'Prefix' field with 'opid291', and a 'Run number' field with '1'. A 'Browse' button is located next to the file name field.
- Processing:** Features 'N.o. residues' (200), 'Space group' (dropdown), and 'Unit cell' parameters: 'a', 'b', 'c', 'α', 'β', and 'γ', all currently set to 0.
- Characterisation:** A section with a dropdown menu.
- Helical Collection:** A section with a dropdown menu.
- Energy Scan:** A section with a dropdown menu.
- Advanced:** A section with a dropdown menu.

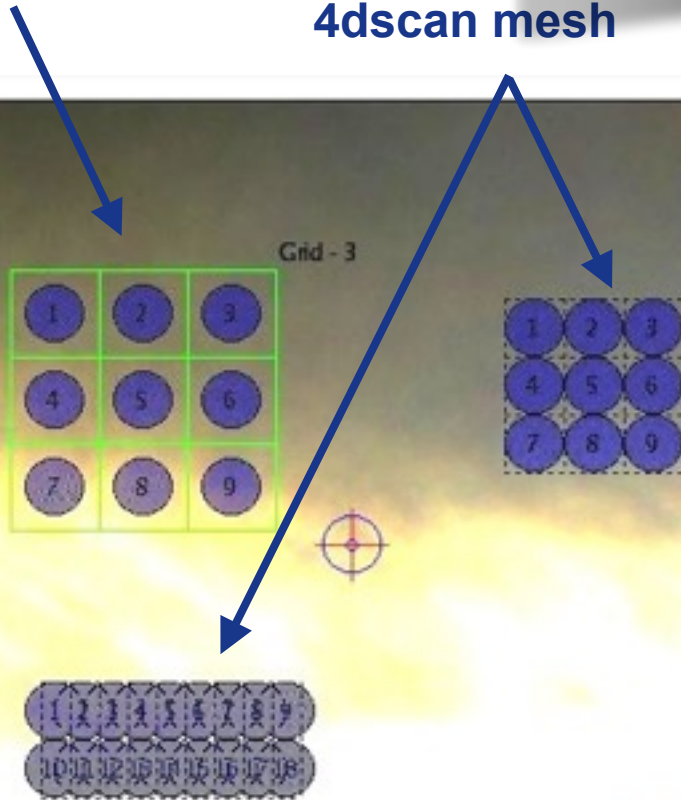
At the bottom right, there is a green 'Add to queue' button.



- Fast meshes available via ICEPAP on all beamlines

Discrete mesh

4dscan mesh



Data location

Folder:

Prefix

Run number

Grid Tool

Name	Beam Height	Beam Width	Horizontal Step	Vertical Step
Grid - 3	10.0	10.0	5.0	5.0
Grid - 4	10.0	10.0	0.0	0.0
Grid - 5	10.0	10.0	-5.0	0.0

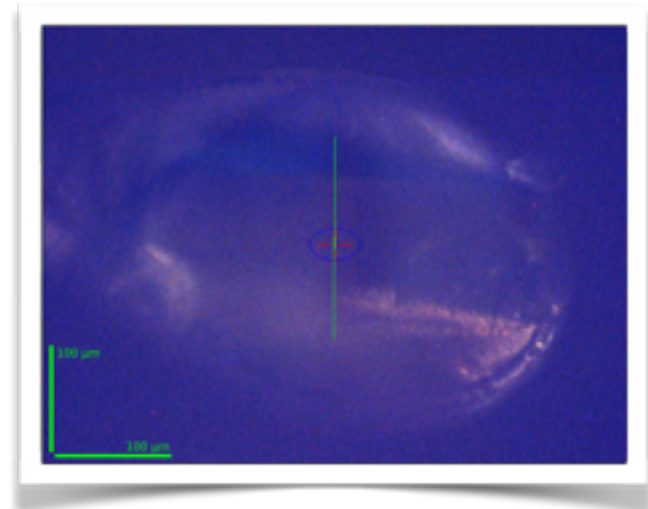
Horizontal step:

Vertical step:

+ -

Hide

- Use full dynamic range of OAV
- Getting more and more independent from SPEC
 - New beamlines are SPEC-free for what concerns data collection
 - ID29 on the way
 - More new application as Advanced Collection Methods
- MXCuBE collaboration growing: two new partners
 - ESRF, EMBL, SOLEIL, MAXLAB, BESSY, Global Phasing, ALBA and DESY
 - Plans for future development



ISPyB
Information System for Protein Crystallography Beamlines

-- Select Technique -- Logoff mx1hr1

Shipment Create Shipment

Lab-contacts Shipment Samples Prepare experiment Data collection Feedback References Help Logoff

Create

- Shipment
- Puck
- CSV upload

View

- Shipments
- Dewars

Search

- Shipment
- Dewar

Shipment	
Name	test
Creation date	01-08-2014
Status	opened
Back to this Shipment	

Upload Shipment from Excel file

Help

Dewar1 +

(*) mandatory field for each sample

- A new web tool is available to fill the sample name and details for each sample in the sample changer - no need for xls file upload - can be done in a couple of minutes at the beamline

ISPYB: PREPARE EXPERIMENT

Help

Dewar1

aaa001a

Save Reset Change sample name automatically

Sample Positio	Protein Acronym (*)	Sample Name (*)	PinBarcode	Space Group	Pre-Ob resolut	Needle resolut	Oscilla Range	Experimen Type	Unit Ce a	Unit Ce b	Unit Ce c	Unit Ce alpha	Unit Ce beta	Unit Ce gamma	SMILES	Comments	Action
1	raj1 - Undefined	sample01		Undefi...				Default	0	0	0	0	0	0			
2	raj1 - Undefined	sample02		Undefi...				Default	0	0	0	0	0	0			
3	raj1 - Undefined	sample03		Undefi...				Default	0	0	0	0	0	0			
4	raj1 - Undefined	sample04		Undefi...				Default	0	0	0	0	0	0			
5	raj1 - Undefined	sample05		Undefi...				Default	0	0	0	0	0	0			
6	raj1 - Undefined	sample06		Undefi...				Default	0	0	0	0	0	0			
7	raj1 - Undefined	sample07		Undefi...				Default	0	0	0	0	0	0			
8	raj1 - Undefined	sample08		Undefi...				Default	0	0	0	0	0	0			
9	raj1 - Undefined	sample09		Undefi...				Default	0	0	0	0	0	0			
10	raj1 - Undefined	sample10		Undefi...				Default	0	0	0	0	0	0			

(*) mandatory field for each sample


- minimal information required but
 - space group unit cell can be specified
 - SMILES for ligand study (more later)

Sample list

Mode: **Sample changer**

Show SC-details

Centring: **Semi Automatic**

 **Synch ISPyB**

- 1:1 - CER-sampA01
- 1:2 - CER-sampA02
- 1:3 - CER-sampA03
- 1:4 - CER-sampA04
- 1:5 - CER-sampA05
- 1:6 - CER-sampA06
- 1:7 - CER-sampA07
- 1:8 - CER-sampA08
- 1:9 - CER-sampA09
- 1:10 - CER-sampA10
- 2:1 - CER-sampB01
- 2:2 - CER-sampB02
- 2:3 - CER-sampB03
- 2:4 - CER-sampB04
- 2:5 - CER-sampB05
- 2:6 - CER-sampB06
- 2:7 - CER-sampB07
- 2:8 - CER-sampB08
- 2:9 - CER-sampB09
- 2:10 - CER-sampB10
- 3:1 - CER-sampC01
- 3:2 - CER-sampC02
- 3:3 - CER-sampC03
- 3:4 - CER-sampC04
- 3:5 - CER-sampC05
- 3:6 - CER-sampC06
- 3:7 - CER-sampC07
- 3:8 - CER-sampC08
- 3:9 - CER-sampC09
- 3:10 - CER-sampC10
- 4:1 - Mnth-sample-E01
- 4:2 - Mnth-sample-E02
- 4:3 - Mnth-sample-E03
- 4:4 - Mnth-sample-E04
- 4:5 - Mnth-sample-E05
- 4:6 - Mnth-sample-E06
- 4:7 - Mnth-sample-E07
- 4:8 - Mnth-sample-E08
- 4:9 - Mnth-sample-E09
- 4:10 - Mnth-sample-E10
- 5:1 - PFLU-SampD01
- 5:2 - PFLU-SampD02

Expert mode

Machine current: **777.7 mA**

Flux: ? ph/s

Energy

Current: 12.7000 keV

Move to: keV

Resolution: 3.000 Å

Current: 612.01 mm

Move to: A

Transmission: Current: 4.99%

Set to: Filters

Cryo: 100.0 K

Safety shutter: **disabled**

Fast shutter: **closed**

Beamstop: **out**

Current users: [opid291]p1-429

Selecting gives control

Allow timeout control

Ask for control

My name: [opid29]

Collection method

Standard Collection

Acquisition

Oscillation start: 0.0000

Oscillation range: 0.0000

First image: 0

Number of images: 0

Exposure time: 00000

Energy (KeV): 0.0000

MAD ip: -

Resolution (Å): 0.000

Transmission (%): 0.00

Inverse beam

Subwedge size:

Shutterless

Data location

Folder:

File name:

Prefix:

Run number:

Processing

N.o. residues: 200.0

Space group:

Unit cell:

a: 0.0 b: 0.0 c: 0.0

α: 0.0 β: 0.0 γ: 0.0

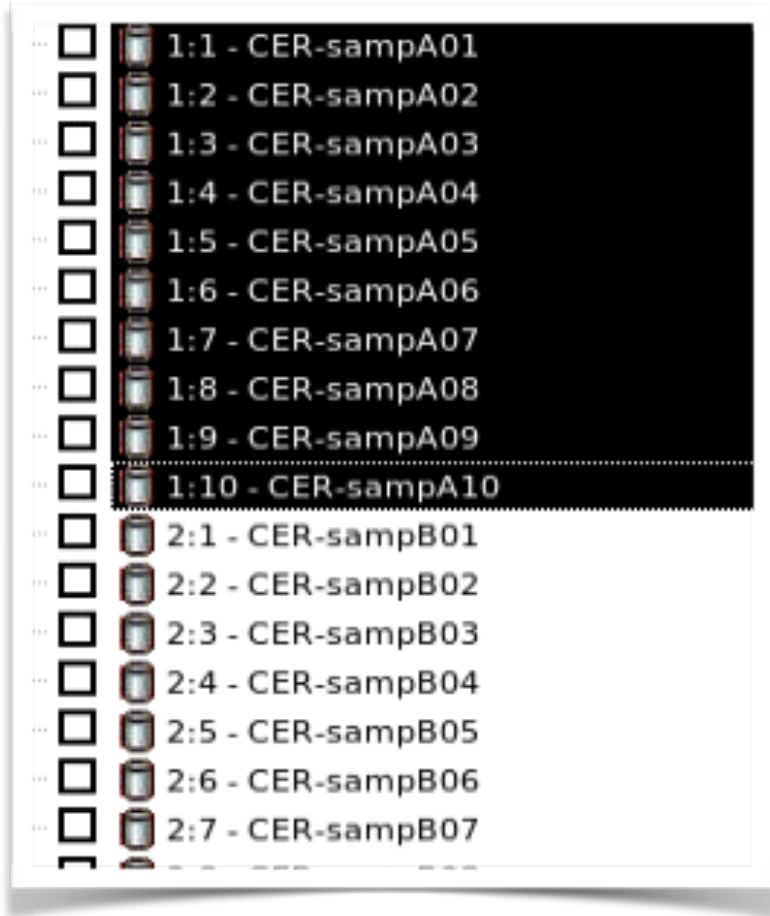
Characterisation

Helical Collection

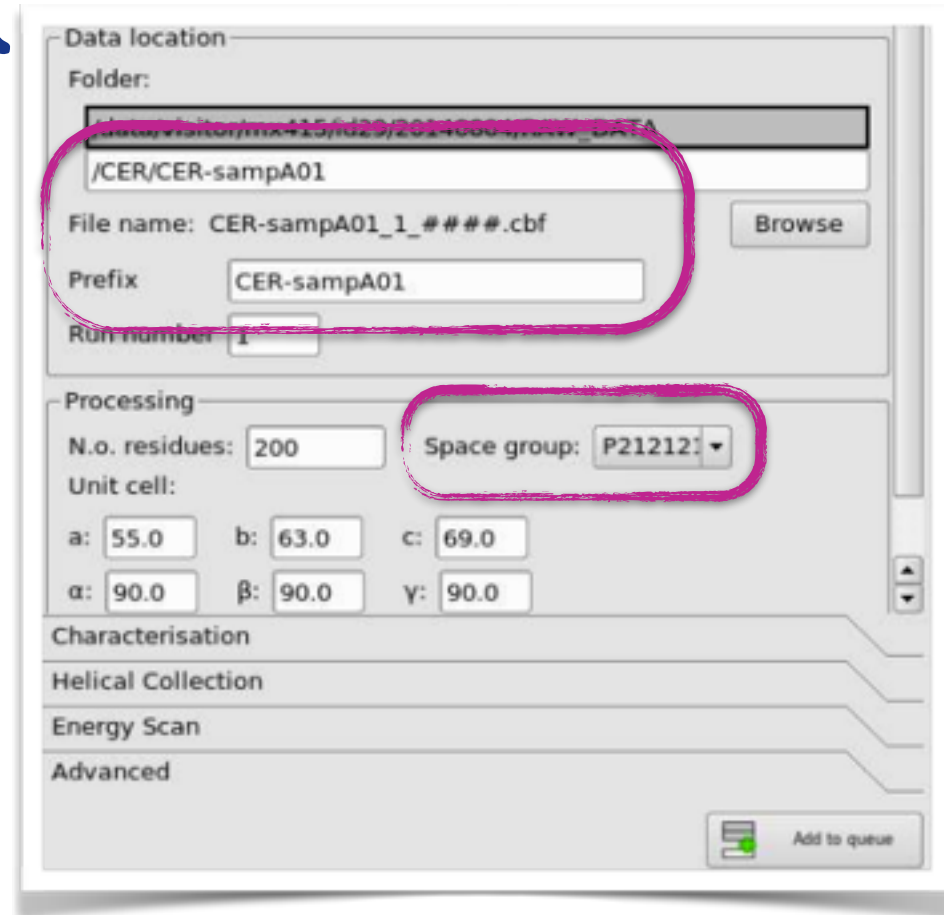
Energy Scan

Advanced

ISPyB Sample names



Data Collection



A screenshot of the Data Collection panel in the ISPyB interface. The panel is divided into several sections:

- Data location:** Folder: (highlighted with a pink circle). File name: CER-sampA01_1_####.cbf. Prefix: CER-sampA01. Run number: 1.
- Processing:** N.o. residues: 200. Space group: P21212 (highlighted with a pink circle). Unit cell: a: 55.0, b: 63.0, c: 69.0, α : 90.0, β : 90.0, γ : 90.0.
- Characterisation:** Helical Collection, Energy Scan, Advanced.


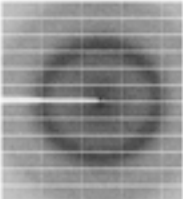
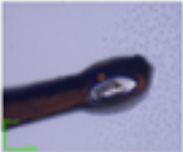
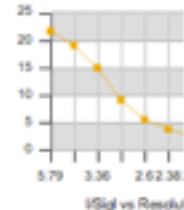
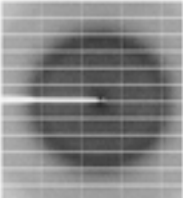
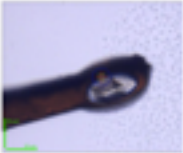
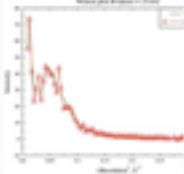
An "Add to queue" button is located at the bottom right.

ISPYB: RESULTS

Session

Save Comments View All DataCollection

Expand All Collapse All Clear Grouping

Experiment Type	Acronym Sample name	Image Prefix	Run#	Parameters	Results	Image Thumbnail	Crystal snapshot	Graph	Comments
11-07-2014 (1 Item)									
OSC	AtFuT1-gdpfuc02	AtFuT1-gdpfuc02_w	1	<p>Nb images: 2230 Exp. time: 0.04 s Phi range: 0.10 ° Flux: 2.03E11 ph/sec Detector resolution: 2.1... Transmission: 21.47 Wavelength: 0.976 Å Total expo time: 82.51 s</p>	<p>EDNA dp ● GrenADES fp ● GrenADES pp ● Space Group: P 1 21 1 Completeness:</p> 				
Start time: 17:11:01 11-07-2014 (1 Item)									
Characte...	AtFuT1-gdpfuc02	ref: AtFuT1-gdpfuc02	1	<p>Nb images: 2 Exp. time: 0.04 s Phi range: 1.00 ° Flux: 8.89E11 ph/sec Detector resolution: 2.3... Transmission: 100.00 Wavelength: 0.976 Å Total expo time:</p>	<p>Indexing ● Strategy ● Space Group: P2 Unit Cell: a, b, c: 87.99, 85.53, 150.55 O±, OI, OI: 90.00, 96.31, 90.00 Mosaicity: 0.02 Å Ranking Resolution: 2.16 Å</p>				

Characterisation Results (EDNA log file)

Data collection info

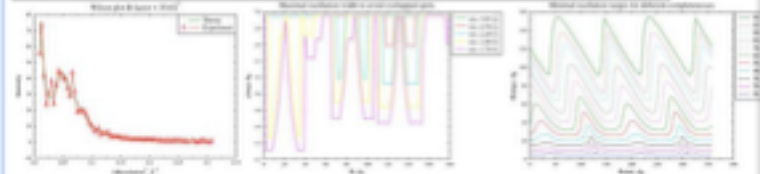
Data collection date:	2014Jul11 17:11:28.631
Image prefix:	ref-AiFuT1-gdpluc02_1
Directory:	/data/d22sb1/beamline/br1/20140711/RAW_DATA/AiFuT1-AiFuT1-gdpluc02

Diffraction Plan

Forced space group	Anomalous data	Aimed multiplicity	Aimed completeness	Aimed Strategy at highest res.	Aimed resolution (Å)
P2	Yes	4.00	0.99	2.00	0.99

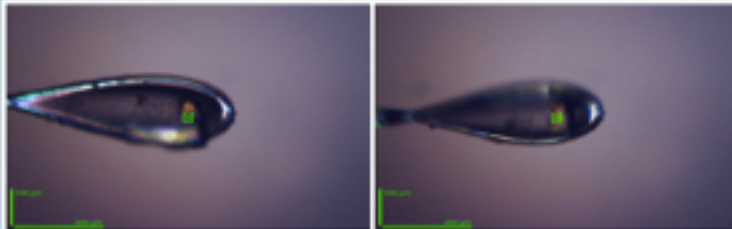
Collection plan strategy (RADDOSE log file, BEST log file)

Resolution limit is set by the radiation damage							
Wedge/subwedge	Start (°)	Width (°)	No. images	Exp. time (s)	Coll. res. (Å)	Rot. trans. (%)	Distance (mm)
1	1	129.00	0.10	2250	0.04	2.34	21.54



Indexing summary: Selected spacegroup: P2

Crystal Snapshots



Main Output Parameters

Overall:

- Overall Resolution: 49.91-1.94 Å
- Overall Completeness: 96.8%
- Overall I over Sigma: 8.7
- Overall Rsymm: 8.9%
- Overall Multiplicity: 4.1

Outer Shell:

- Outer Shell Resolution: 2.01-1.94 Å
- Outer Shell Completeness: 75.9%
- Outer Shell I over Sigma: 0.9
- Outer Shell Rsymm: 108.9%
- Outer Shell Multiplicity: 3.1

Unit Cell:

- Unit Cell A: 87.9 Å
- Unit Cell B: 85.8 Å
- Unit Cell C: 150.6 Å
- Unit Cell Alpha: 90.0 °
- Unit Cell Beta: 96.22 °
- Unit Cell Gamma: 90.0 °

Files

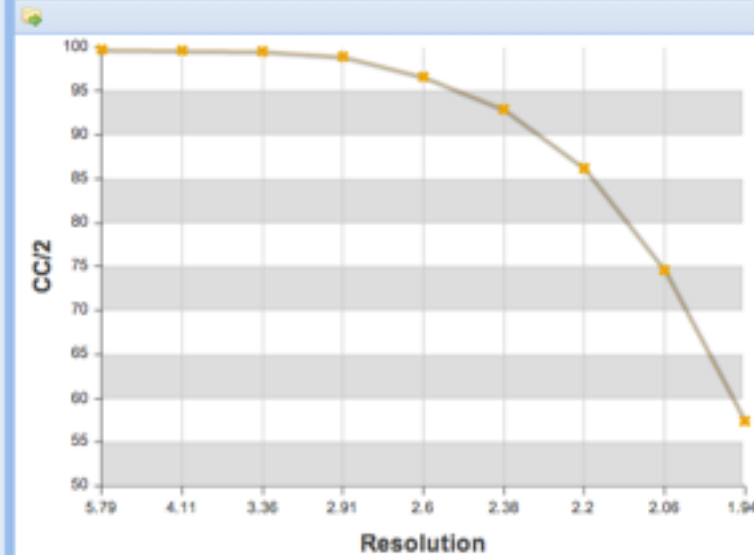
Download

XDS | XSCALE | SCALA/AIMLESS | SCALEPACK | TRUNCATE

Log Files:

- AiFuT1-gdpluc02_w1_run1_merger_anom_XSCALE.LP
- AiFuT1-gdpluc02_w1_run1_unmerged_anom_XSCALE.LP
- AiFuT1-gdpluc02_w1_run1_merger_noanom_XSCALE.LP
- AiFuT1-gdpluc02_w1_run1_unmerged_noanom_XSCALE.LP

Plot: Completeness vs Resolution | R-factor vs Resolution | CC/2 vs Resolution



Session

Save Comments View All DataCollection

Expand All Collapse All Clear Grouping

Experiment Type	Acronym Sample name	Image Pref	Run#	Parameters	Results	Image Thumbnail	Crystal snapshot	Graph	Second Graph	Comments
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Start time: 02:07:47
27-07-2014 (1 Item)

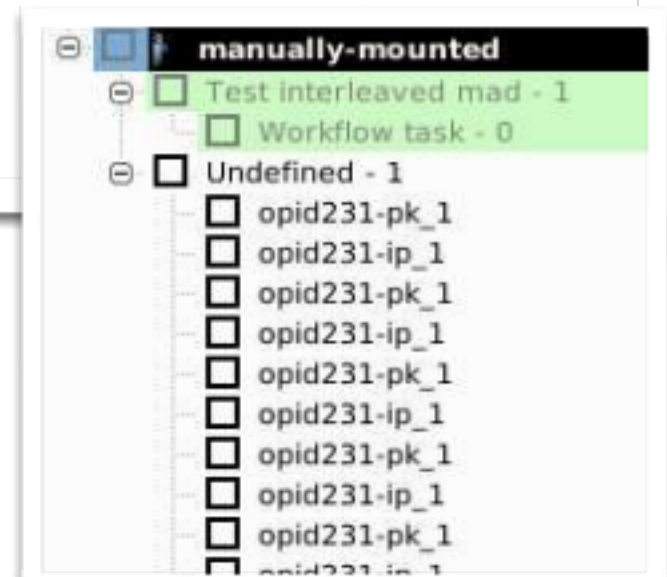
MXPressE	Ogg1-TFA-22_CD003054_F9-3_S	Ogg1-TFA-22_CD003054_F9-3_S	1	<p>Nb tot images: 1544 Nb images: 1544 Exp. time: 0.04 s Phi range: 0.10 ° Flux: 6.39E11 ph/sec Detector resolution: 1... Transmission: 22.26 Wavelength: 0.969 Å Total expo time: 42.9...</p>	<p>MXPressE ● EDNA dp ● GrenADES fp ● GrenADES pp ● Space Group: P 61 Completeness:</p> 					
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Start time: 01:59:08
27-07-2014 (1 Item)

MXPressE	Ogg1-TFA-22_CD003054_F9-2_S	Ogg1-TFA-22_CD003054_F9-2_S	1	<p>Nb tot images: 1264 Nb images: 1264 Exp. time: 0.04 s Phi range: 0.20 ° Flux: 1.65E12 ph/sec Detector resolution: 2... Transmission: 55.07 Wavelength: 0.969 Å Total expo time: 33.3...</p>	<p>MXPressE ● EDNA dp ● GrenADES fp ● GrenADES pp ● Space Group: P 1 Completeness:</p> 					
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- Autoprocessing
- New cluster being installed during User meeting
 - EDNAdp
 - Fast autoprocessing in best SG
 - If SG and Unit cell are given runs in these
 - Check data quality with phenix.xtrriage
 - If pdb is given runs DIMPLE
 - Grenades
 - Fast autoprocessing
 - Parallel autoprocessing
 - In best multiple space groups
 - If SG is given runs `_also_` in this
 - Triggers AutoSAD if anomalous signal is detected
 - Triggers AutoMR if same SG and unit cell are found in PDB
 - Triggers MR if pdb is given

- Advanced (Workflows)
 - Make complicated tasks simple to perform with minimal user input
 - MASSIF-1
 - Kappa
 - X-ray centring/mesh
 -
 - Just moved to a new platform: improved reliability and monitoring
 - Among latest development:
 - MAD
 - Interleaved MAD
 - HCA - multicrystal data collections



- MXCuBE2
 - Start work on web platform
 - Integrate latest developments
 - Multi-axis goniometer
 - beam definition
 - Minimize SPEC dependency

- ISPyB
 - A lot of ideas are on the pipeline. ISPyB is and will be the central platform. Short term plans include:
 - Evolve ISPyB to latest layout
 - Add sequence and make use of it
 - Report results for phasing
 - Define data collection (wished) plans beforehand
 - Add reprocessing functionalities
 - Introduction of new sample tracking tools (TAG)

- Autoprocessing (EDNAdp + Grenades) and Workflows
 - Complete integration of the pipeline
 - Phasing results into ISPyB
 - Add reprocessing functionalities
 - Multicrystal analysis (TAG)
 - Hierarchical cluster analysis
 - Eiger detector data reduction

- Software development is crucial for better science at MX beamlines
 - mesh, MXCuBE2 MAD/Multipos, kappa, ...
 - We do not have more resources than the minimum