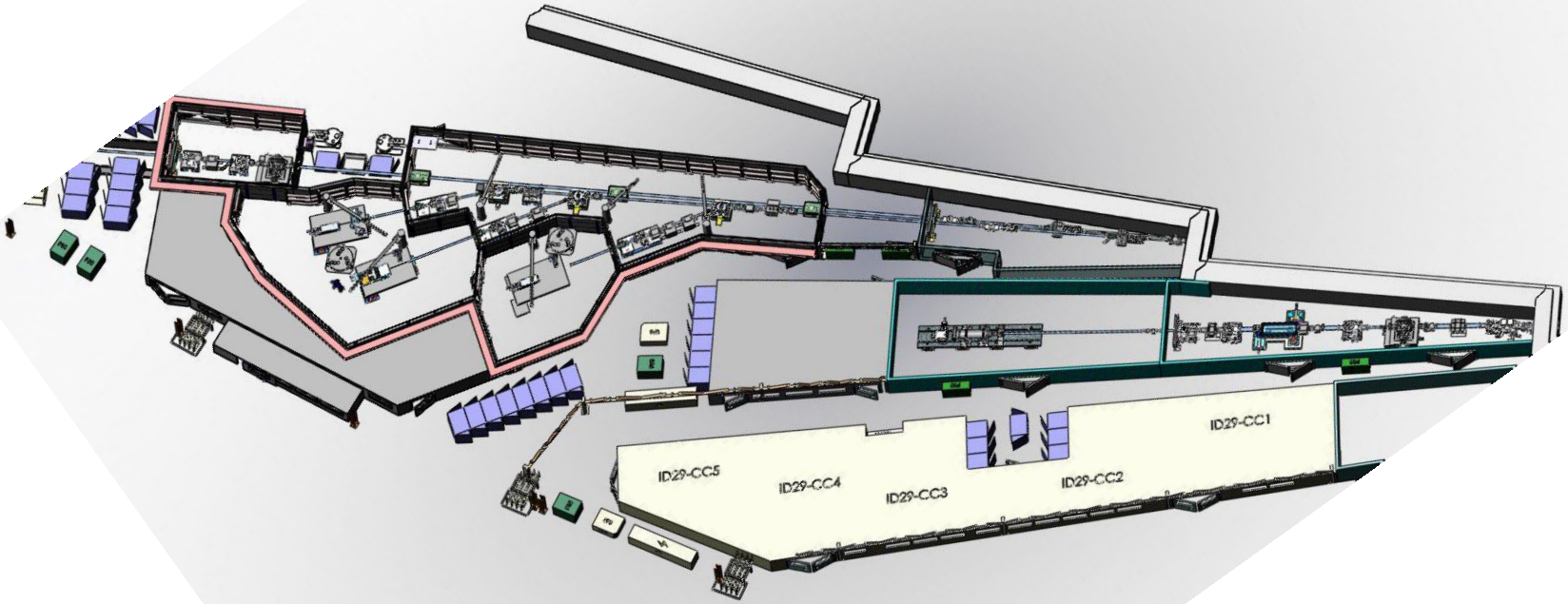
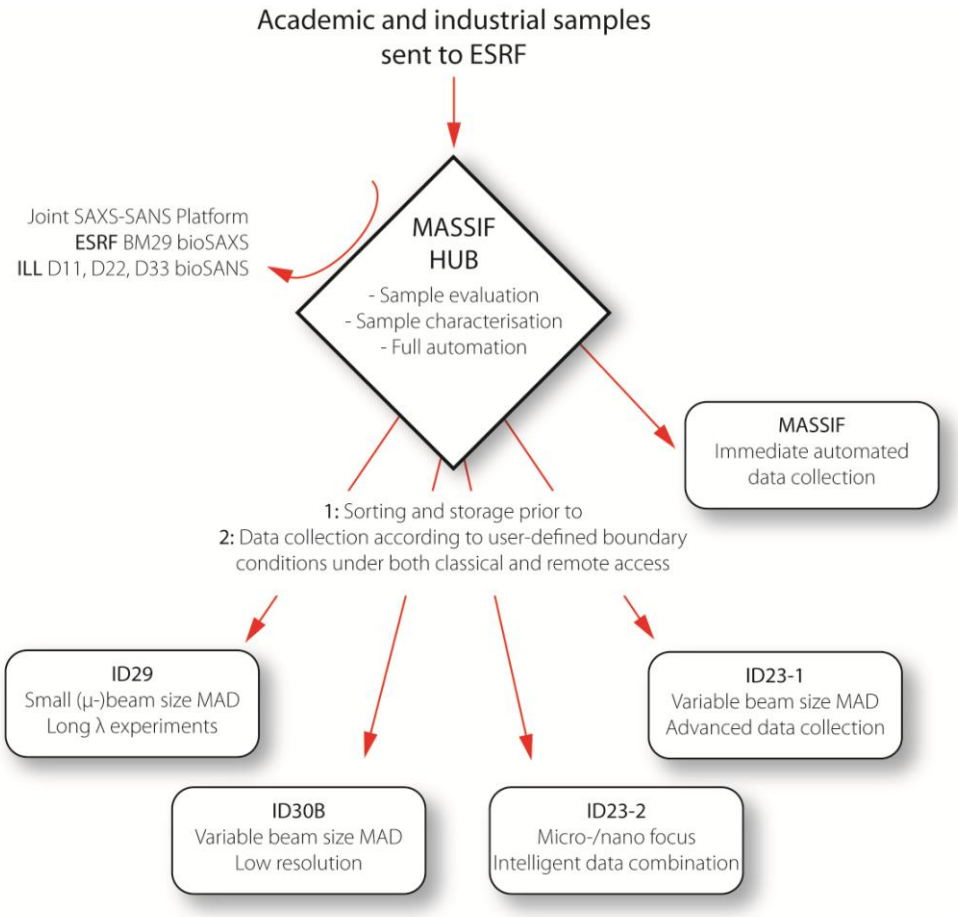
RoboDiff,
From Crystallography towards Serial Crystallography on MASSIF



ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY



Sample evaluation:

XRF spectrum

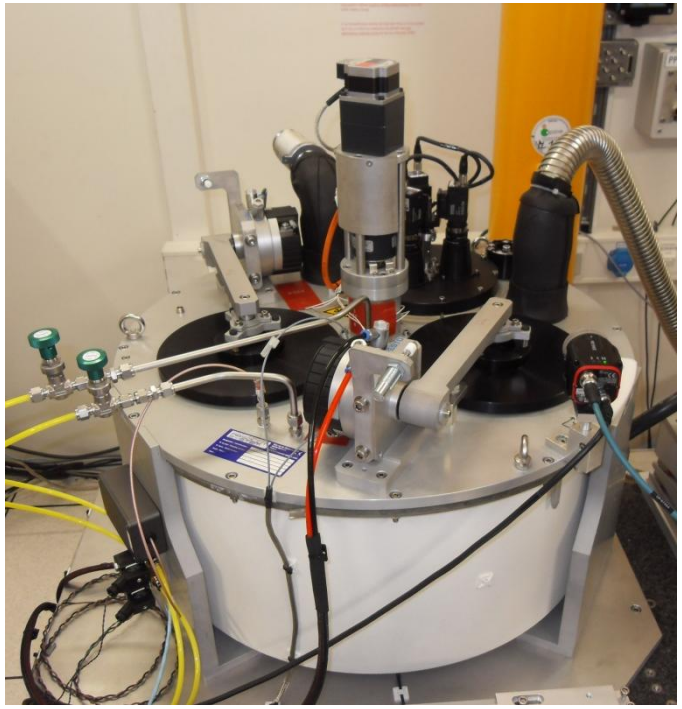
Microspectrophotometry

Xray Crystal centering

Crystal screening

HTP data collection

ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY



240 Samples in 8 cells of 3 pucks

3 independent ports

Pressure control system

Automatic refilling

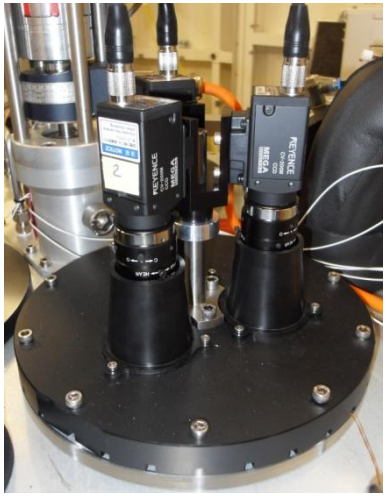
Low maintenance (Foam Dewar, no motor in LN2)

Unipuck potentiality

Barcode reader

Study owned by ESRF

ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY



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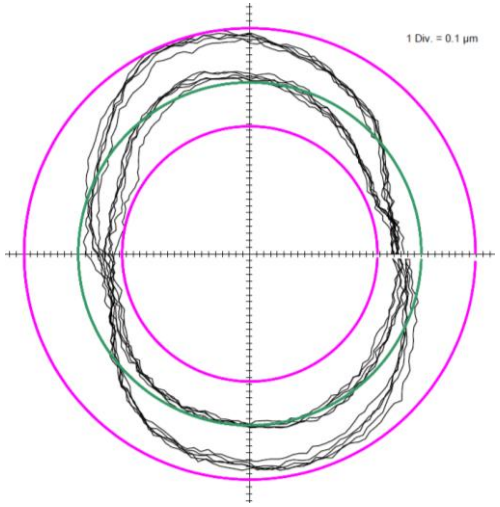
ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY

- Deported LN2 feeding point
- Independent automatic filling
- Flow control
- Compact system for easy integration on the Exp. Table
- Study owned by ESRF

ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY



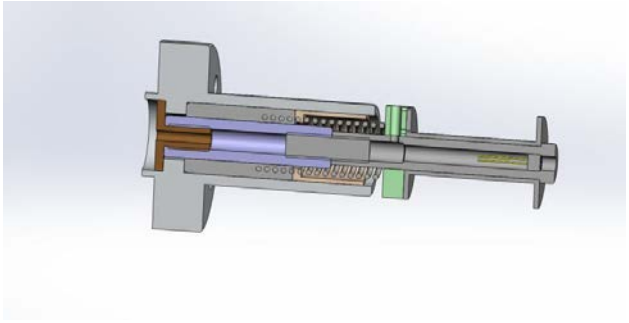
Air bearing with a SOC of 1.4µm

12 brushes slipring (18 in the new prototype)

Infinite rotation for shutterless data collection

13152 step/° encoder for high accuracy positioning

ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY



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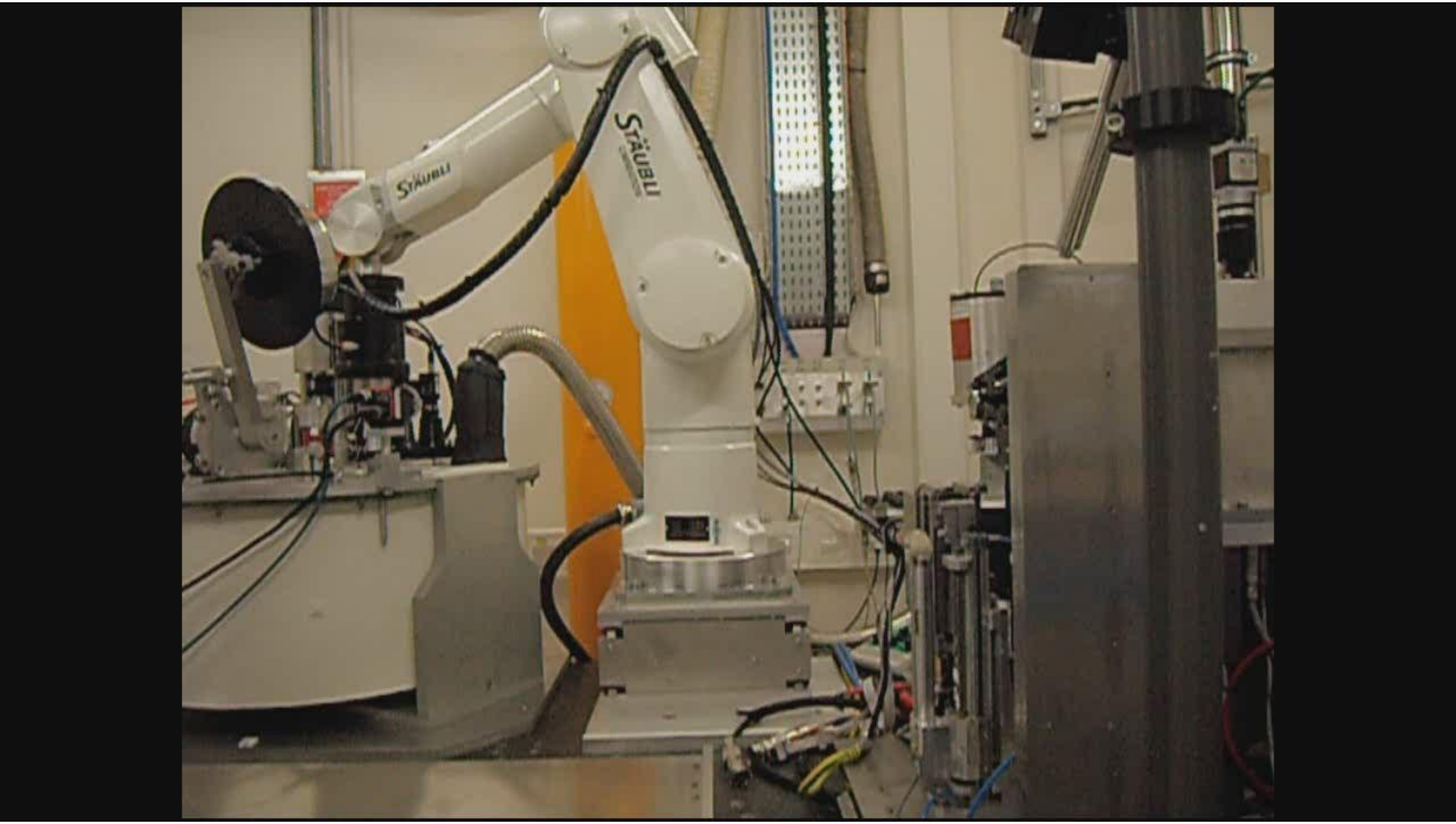
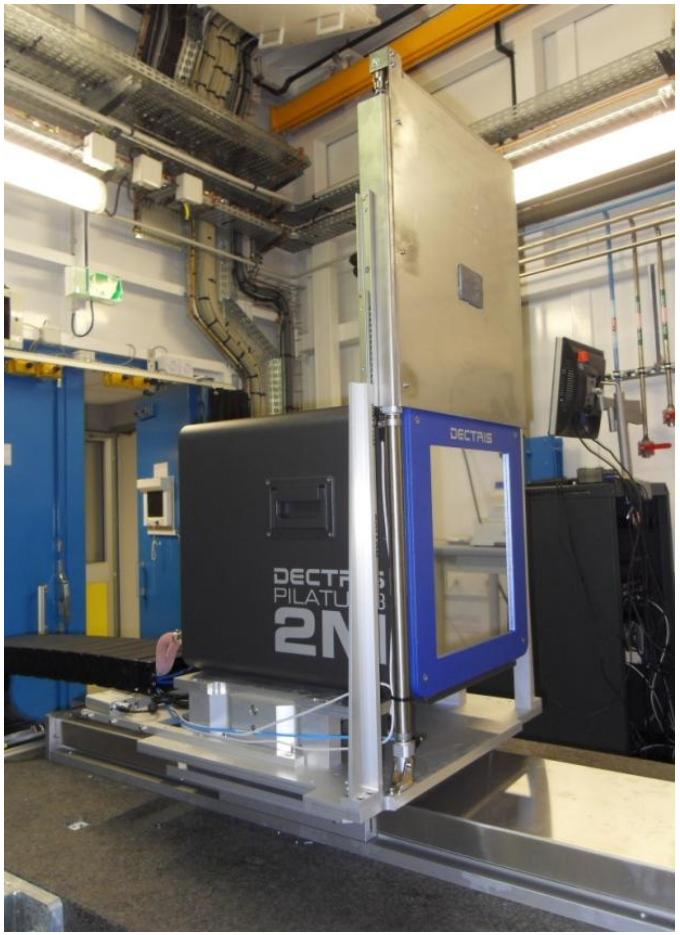




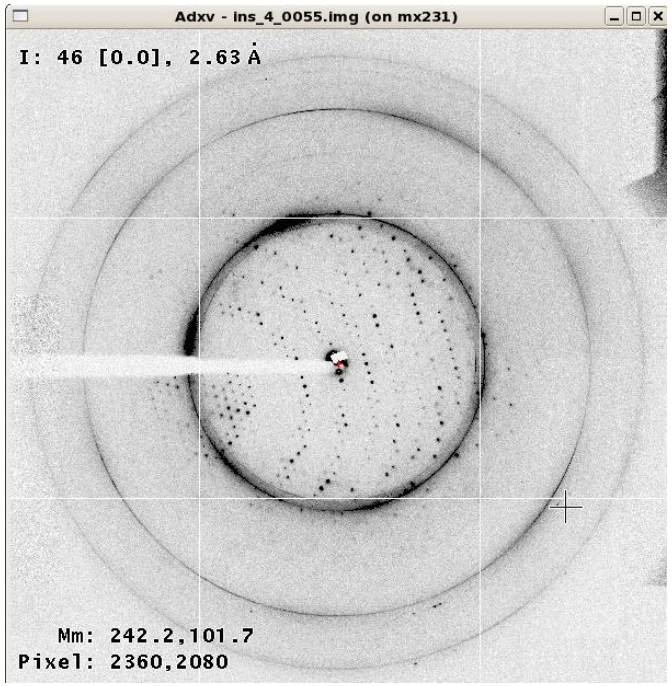
Pilatus3 2M

253.7 x 288.8 mm^2 active area

3x8 detector modules

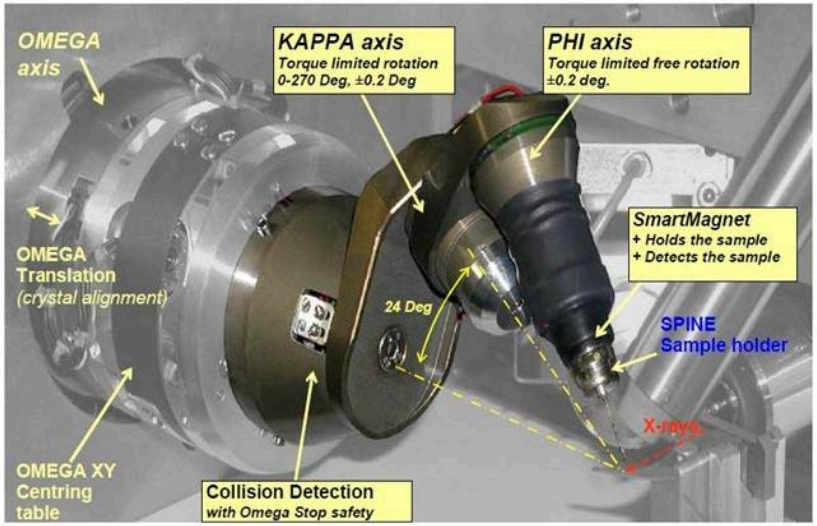
172x172 mm^2 pixel size (2’476’525 pixels)

Frame rate max 250Hz (4.95 ms/frame)

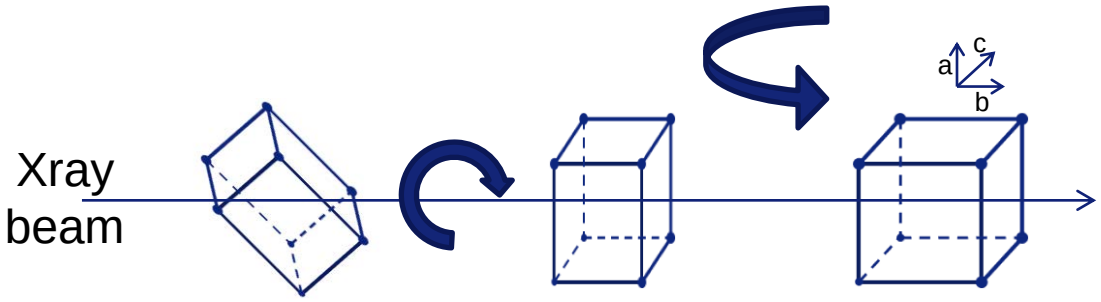


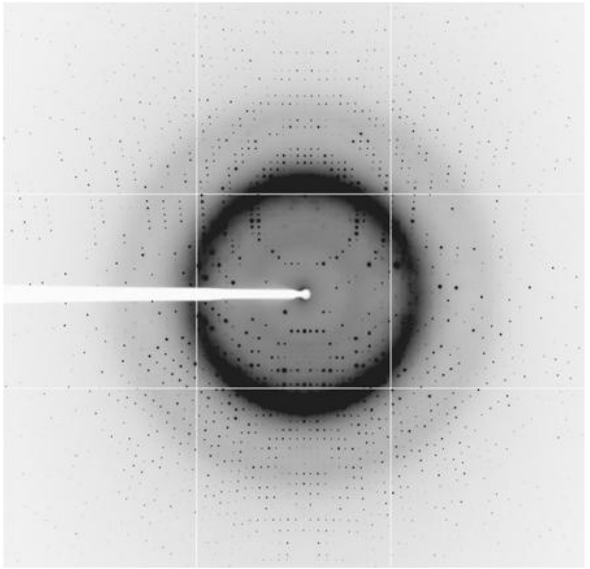
First Insulin crystal (22/11/2013)

Wavelength in Å (Energy in keV)	0.9650 (12.848)
Nb of images	90
Space group	I23
Cell dimension (Å)	80.0
Exposure time(s)	0.1
Oscillation range (°)	0.5
Detector	ADSC q315r
Resolution in Å (low, high bin)	20-2.8 (8.85, 2.95)
R_{sym}(%)	10.3(3.0, 10.3)
I/σI	9.3(18.4, 3.4)
Completeness	94.5 (86.6, 97.5)
Multiplicity	4.6 (5.0, 4.5)

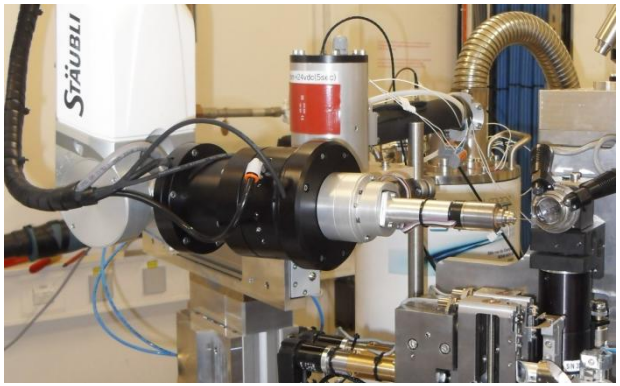


A κ goniometer has a fix spindle rotation orientation



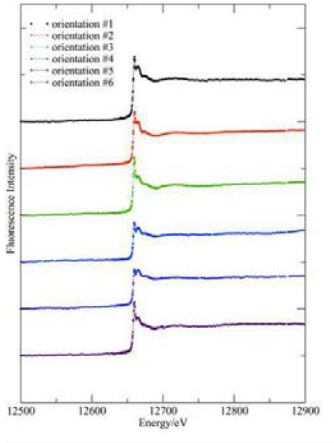


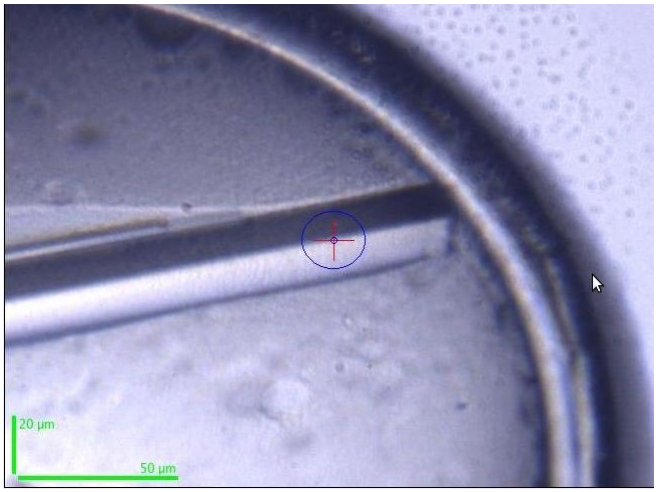
ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY

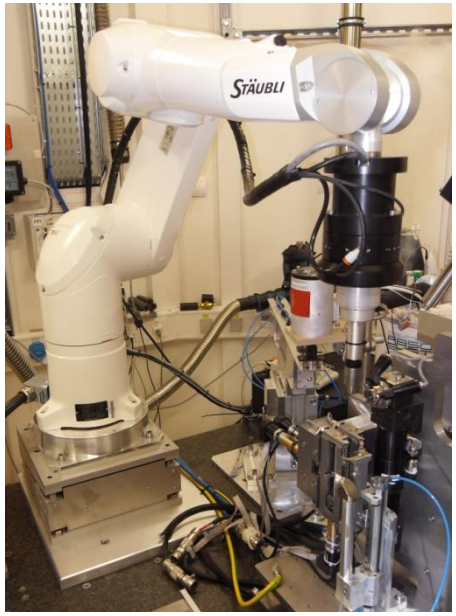


RoboDiff will be able to collect from any accessible orientation without deteriorating the SOC

Improve anisothropic anomalous signal using the polarised X-ray beam





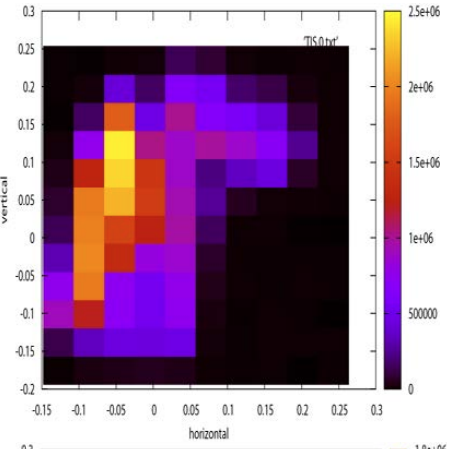


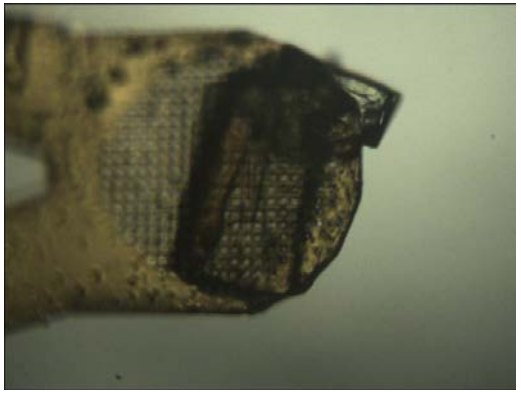
Dynamic Mode:

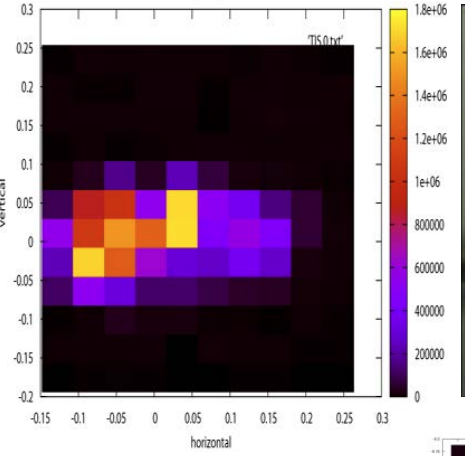
helical data collection

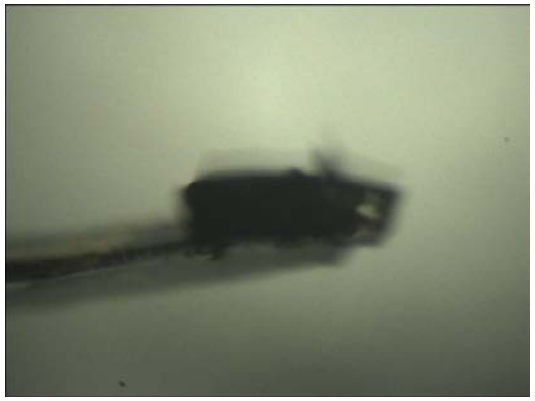
Synchronisation of the centering table with Y table / Ω axis / detector / centering table

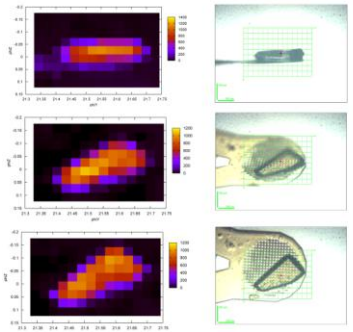
ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY











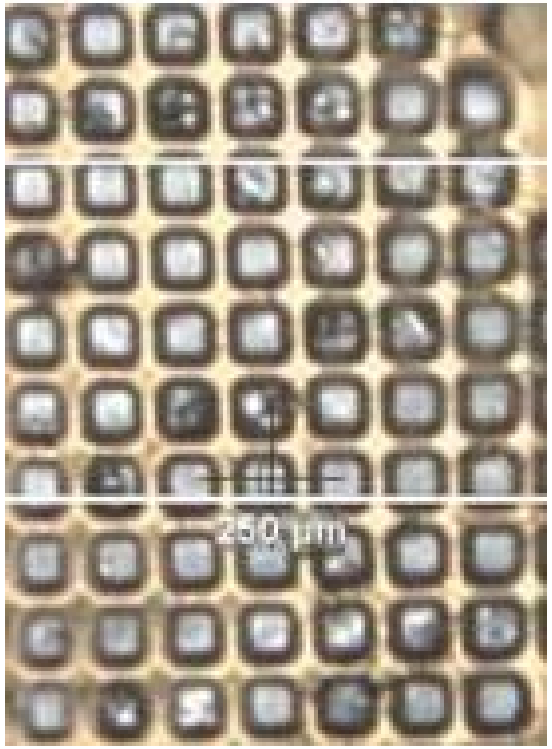
Dynamic Mode:

3D rastering reconstruction

Automatic crystal centering

Quality crystal analysis

ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY



Mesh scan in shutterless mode

4D scan using microbeam

Reduction of anisothropy due to cryo condition changes

ROBODIFF, FROM CRYSTALLOGRAPHY TOWARDS SERIAL CRYSTALLOGRAPHY

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Jose-Maria Clement
Hervé Gonzalez

Structural Biology Group

Gordon Leonard
Christoph Mueller-Dieckmann
Daniele de Sanctis

Nicolas Guichard
Mario Lentini
John Surr
Thierry Giraud
Hugo Caserotto
Fabien Dobias

Beamline Control Unit

Matias Guijarro
Marcus Oskarsson
Antonia Beteva

EMBL

Florent Cipriani
Gergely Papp
Alexandre Gobbo

Hope to see you in JULY