

Current and future trends in Macromolecular Crystallography experiments:

Focus on Automation, high data rate analysis and User Interfaces

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Outline

The P11 beamline at PETRA III

User Interface

Remote data collection

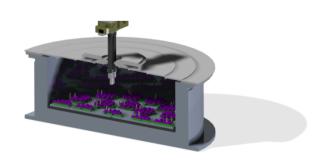
The 2020 year

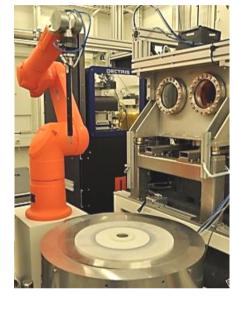
P11 – High Throughput MX beamline at PETRA III

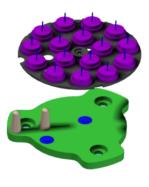
1) Crystallography experiment

- In user operation since 2013
- Broad energy range: 5.5 28 keV
- High-speed sample changer with capacity (23 unipcuks = 364 samples)
- Various focusing options (beamsize from 4 x 9 to 200 x 200 um)
- Pilatus 6M, Eiger2 16M (permanent)
- XRF for experimental phasing (SAD/ MAD) and element analysis
- Serial crystallography







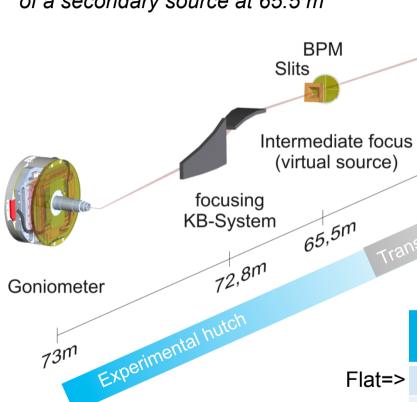


2 KB Systems:

73m

DESY.

> 1st KB system: 2 hor. and 1 vert. deflecting mirrors for generation of a secondary source at 65.5 m



Flexibility in beam size and flux by mirror bending and apertures:

37m 25m Frontend

Slits

Mono

BPM

Optics hutch

Mirrorsystem

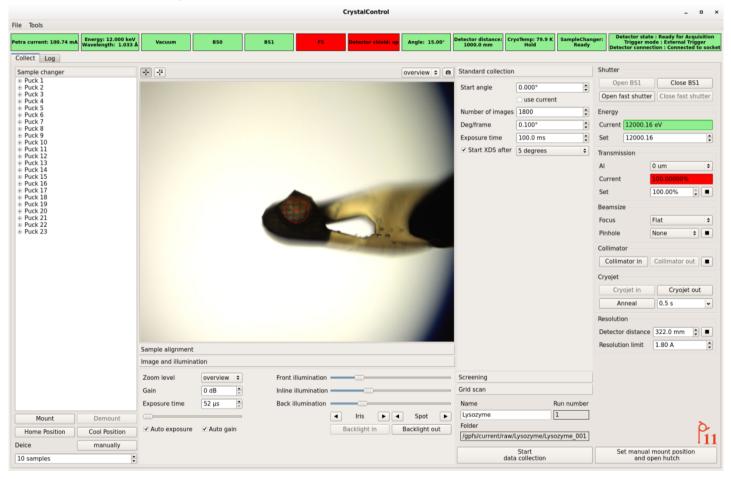
40m

Undulator

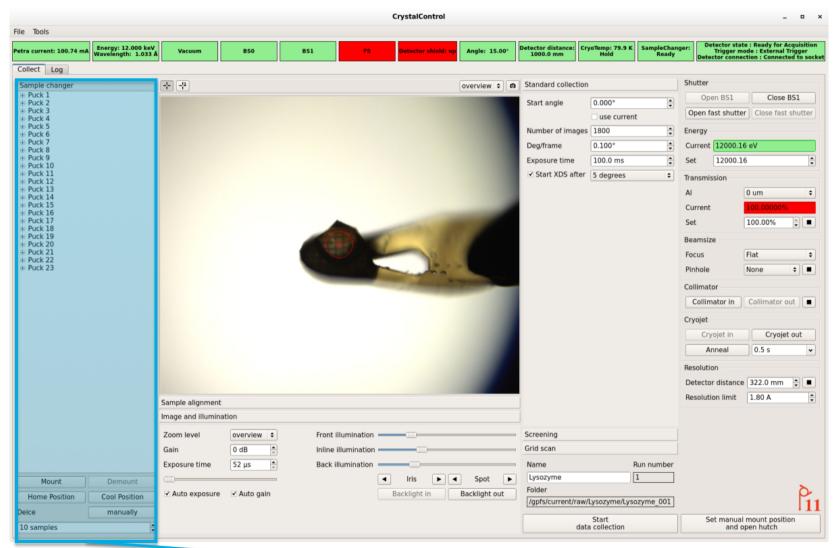
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	Beam size (μm)	Flux (ph/s)	T _{xtal} (s)
Flat=>	200 x 200	3.1e12	800
Focused=>	200 x 200	6,45e12	360
	100 x 100	1e13	40
	50 x 50	1e13	10
	20 x 20	1e13	1,6
	4 x 9	1e13	0,17

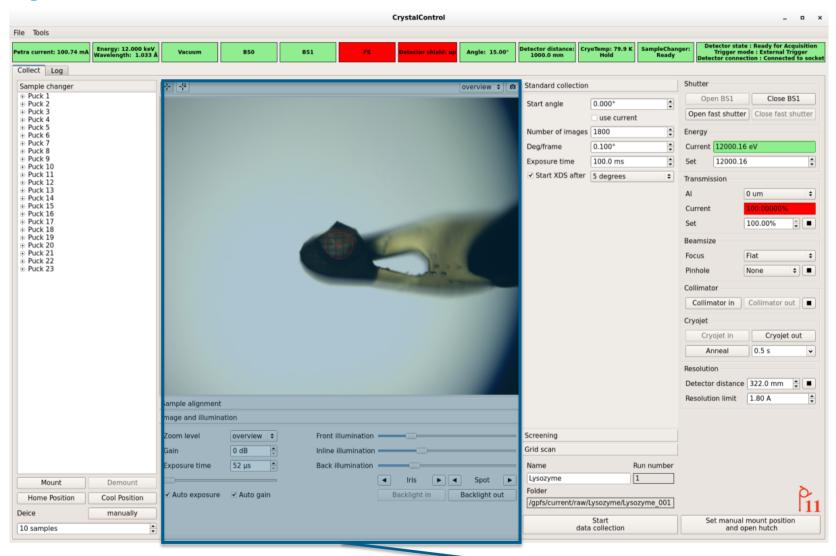
 Inhouse-developed Python-based GUI for standard MX applications including SAD/MAD phasing



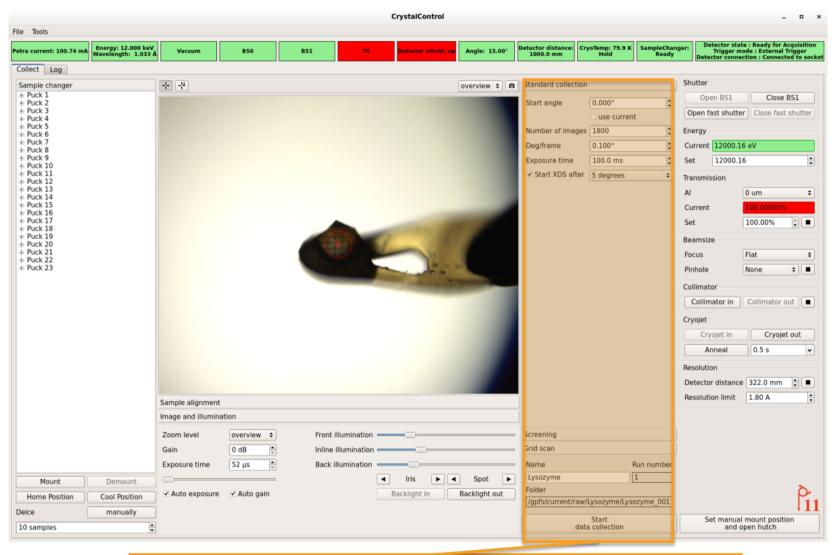
• Expert mode for beamline support (apertures, rotation axis, beam position...)



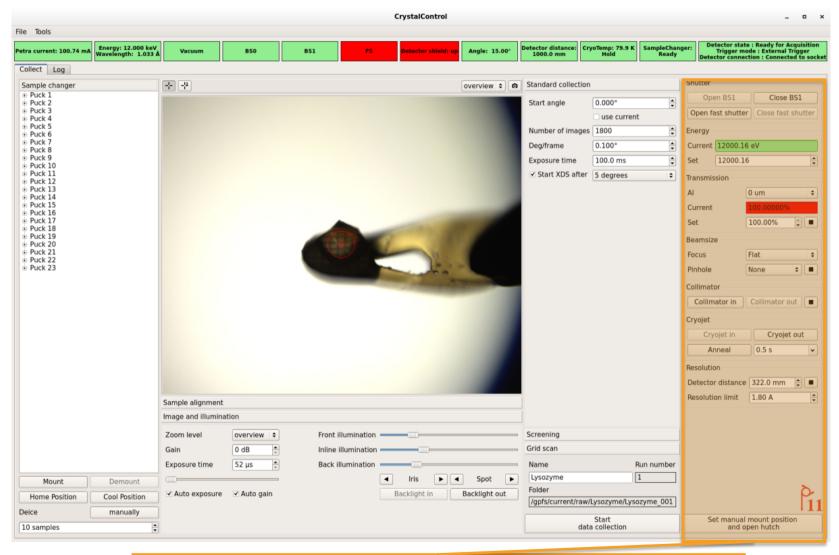
Sample changer: Puck and sample selection



Crystal View: zoom selection and 3 clicks centering

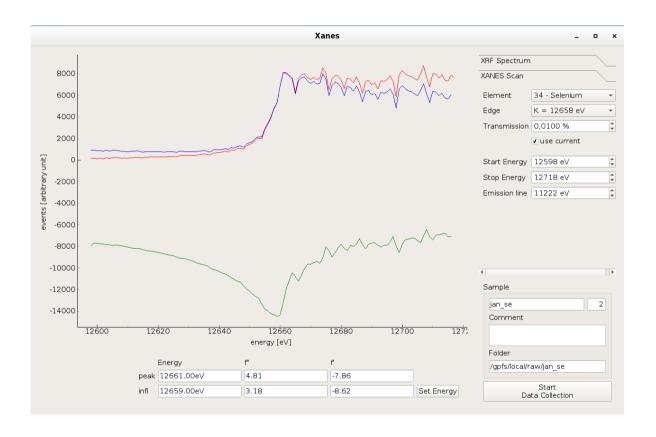


Data collection: Number of frames, exposure time, angular step

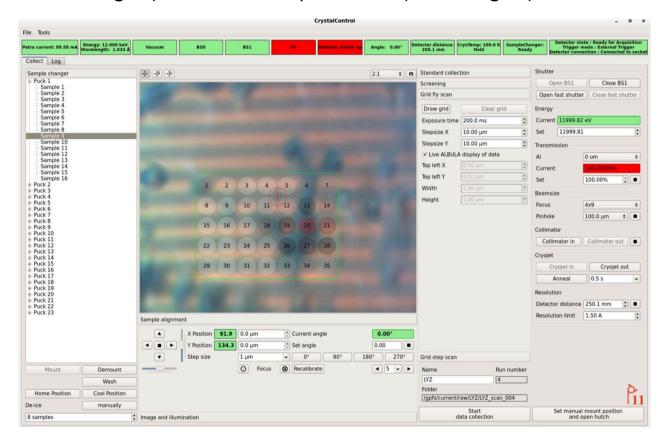


Data collection: Energy, Focus selection, Pinholes, transmission, resolution (det. distance)

SAD/MAD phasing



• ISMO scantool: GUI for fixed-target SSX, data collection with (rotation wedges) and without φ rotation (still images)



Heat map overlayed on the sample view

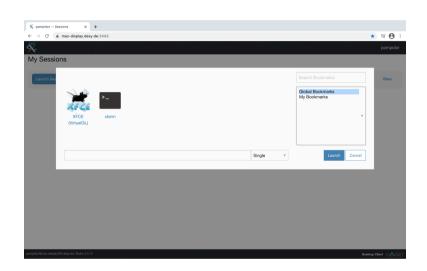
Implementation of remote data collection

- Beamline control by one user only
- Access to needed functionalities only
- Monitoring of user actions
- Possibility to take back the control at any time for the local contacts
- No need of special hardware, software or OS dependencies for the user community
- Authentication against personalized account
- Remote access dependent on valid safety training

Technical Implementation (Spring 2020)

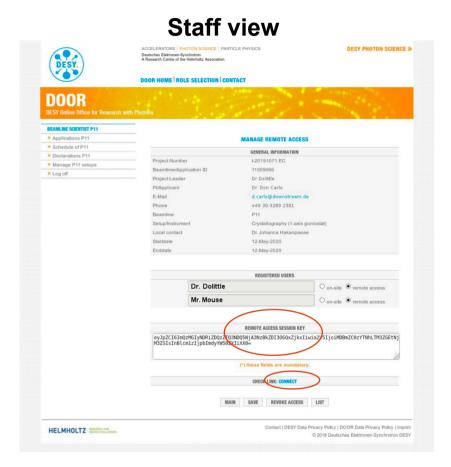
FastX

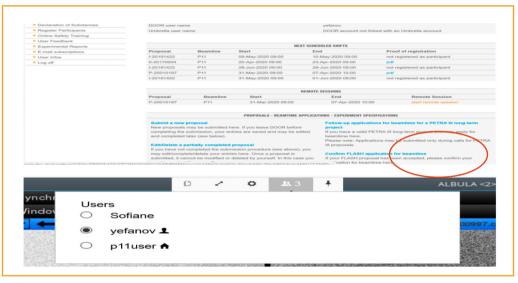
- Commercial software for Linux remote desktop
- X server from a web browser
- Similar to Maxwell Cluster (computing at DESY)
- Sessions between several users with only one controlling
- Running on a dedicated host



Remote identification via user database: Door

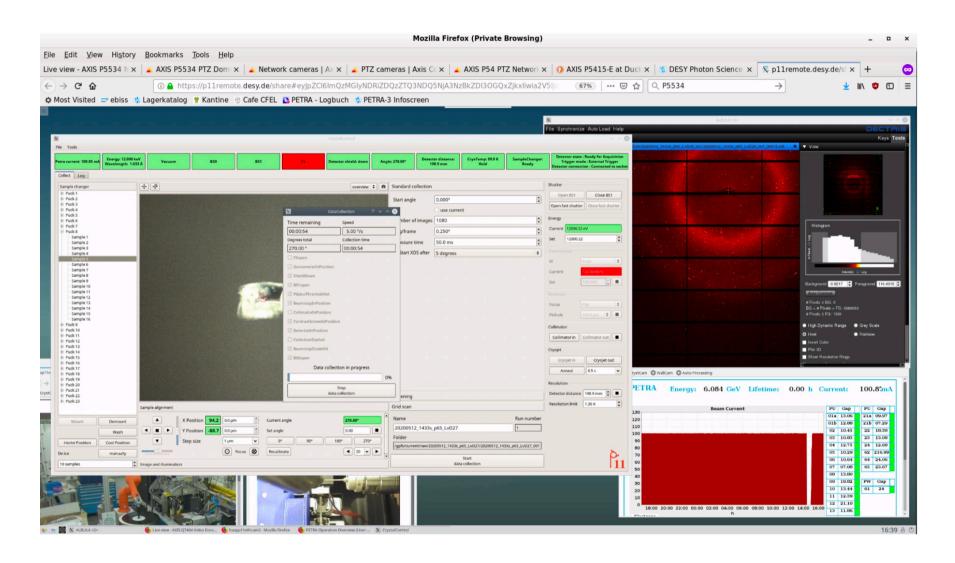
User view





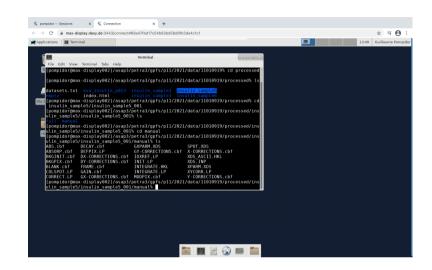
- Selection of 'remote', 'onsite' or 'data-access' during user registration
- Automated e-mail notification once the remote is open
- All participants can log-in at the same time from different locations, one has control over the experiment, can be swapped independently among the users
- Detailed instructions on our public webpage for shipment, remote session and data processing
- Support via zoom
- Successful operation also with users who were never onsite;
 connection stabile and shipments running e.g. to China and India

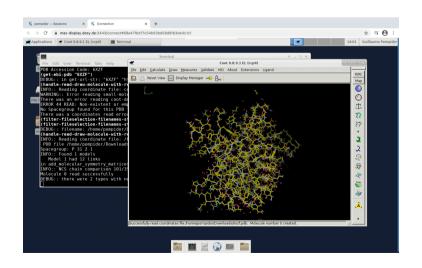
Remote data collection



Remote data processing on Maxwell Cluster

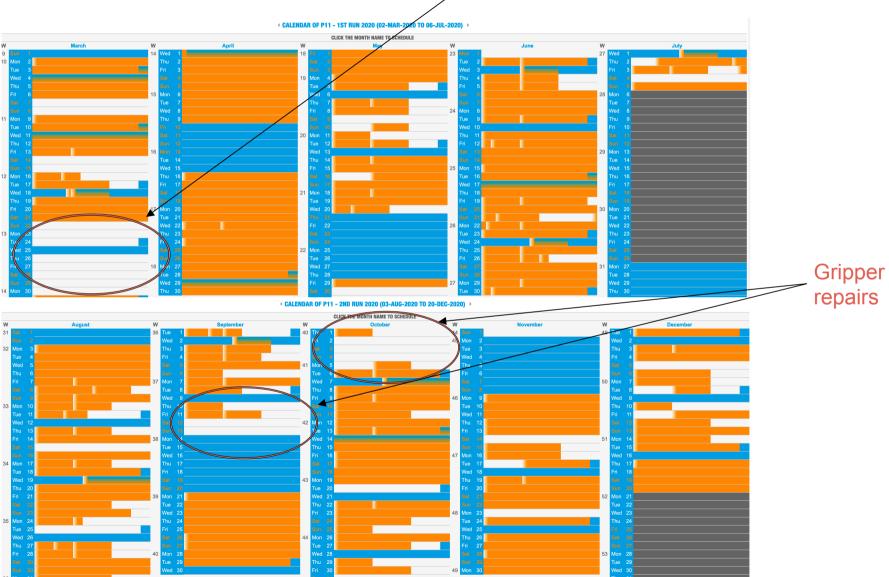
- Computing cluster for DESY
- Access via scientific account
- Backup (or via Gamma portal)
- Data processing
 - Albula, adxv
 - XDS, imosflm
 - ccp4, Phenix
 - Coot, Chimera







Machine down due to the lock-down!



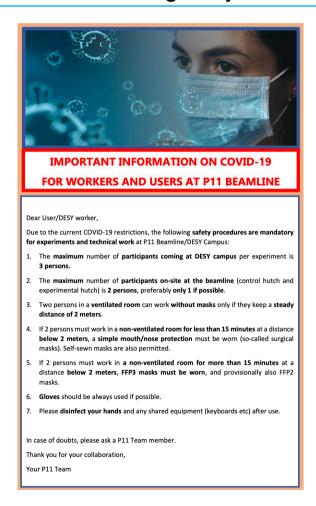
DESY.

Pandemic vs user operations 2020

Suspended user operations mid-March - April 2020: only Fast-track open

Masks & distancing: May-October 2020

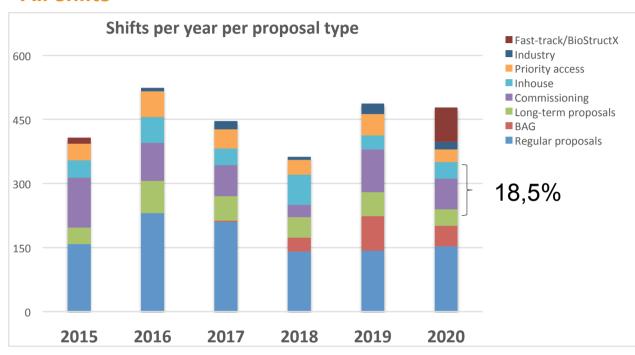
Enhanced remote at P11 since October 2020 Covid-tests since November 2020





User statistics

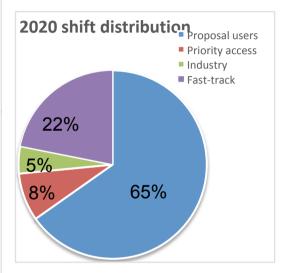
All shifts

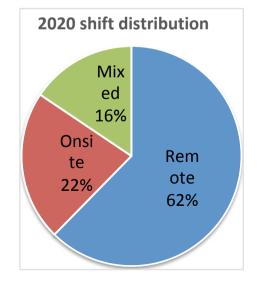


Numbers extracted from shifts actually carried out Inhouse and commissioning are by P11 staff only Serial Synchrotron Crystallography with tape-drive 24 shifts, with chips 18 shifts

Some empty days due to repairs and short-notice cancellation 11 shifts given out from INH for 'friendly users' i.e. users with no valid proposal => need for rolling access scheme

Excluding inhouse/ commissioning





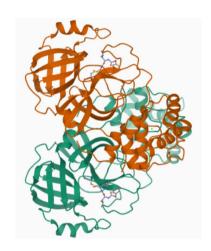
DESY.

SARS-CoV2 -related research arising from P11

Also outside of the fast-track procedure

37 structures deposited from P11 (Main Protease)

- 30 from the fast-track screening campaign by Alke Meents
- 3 through other fast-track projects
- 2 through priority access
- 2 through regular proposals



Publications:

- "Crystal structure of SARS-CoV-2 main protease provides a basis for design of improved α-ketoamide inhibitor" (Zhang et al., 2020, Science, 368, 409-412)
- "Catalytic cleavage of HEAT and subsequent covalent binding of the tetralone moiety by the SARS-CoV-2 main protease" (Günther et al., 2020)
- "SARS-CoV-2 MPro inhibitors and activity base probes for patient-sample imaging" (Rut et al., Nat. Chem. Biol., 2020)

"Repurposing the HCV NS3–4A protease drug boceprevir as COVID-19 therapeutics" (Oerlemans et al., RSC Medicinal Chemistry 2021)

Thank you

Johanna Hakanpää

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Jan-Peter Kurz





