



Routine room temperature structure determination from protein crystals *in situ* at the Diamond beamline VMXi using the Crystallisation Facility at Harwell



Dr Halina Mikolajek

CCP4 2023



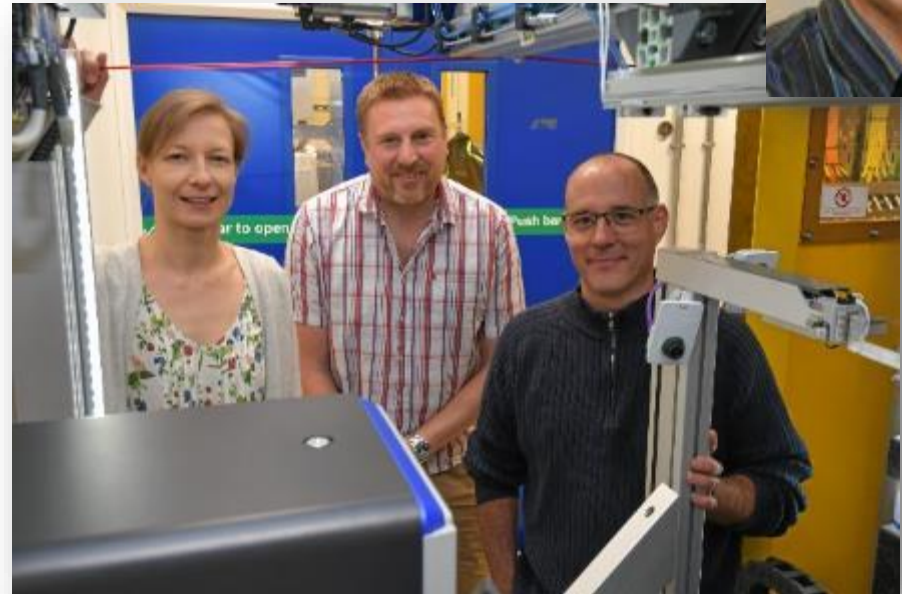
The VMXi team

Prof Mike Hough (PBS)

Dr Juan Sanchez-Weatherby (Senior Beamline Scientist)

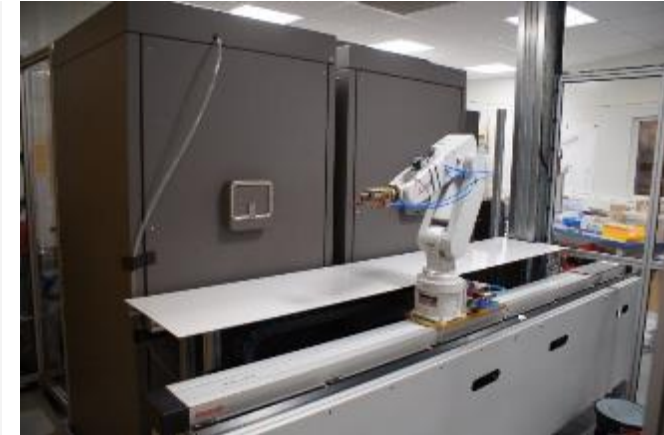
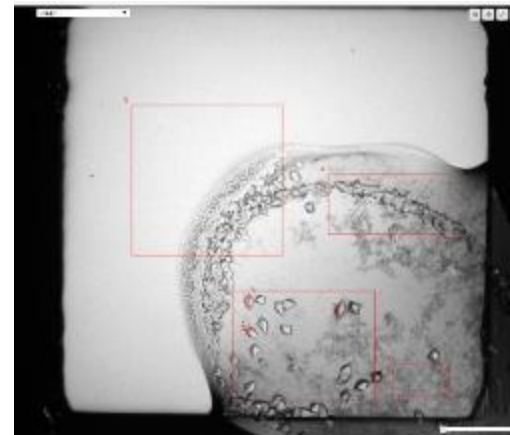
Dr James Sandy (Senior Beamline Scientist)

Dr Halina Mikolajek (Research Scientist and Crystallisation Facility Manager)



Beamline concept and vision

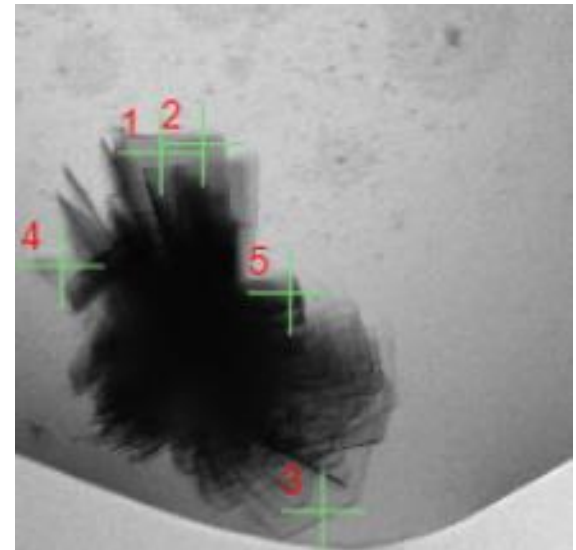
- VMXi is fully dedicated to room temperature experiments with samples in a number of different formats.
- $10 \times 10 \mu\text{m}^2$ beam size, pink beam 5×10^{13} ph/sec, 16 keV (tunable)
- Routine, high quality room temperature structures from multiple crystals of hundreds to $10 \mu\text{m}$ dimensions
- Highly automated operation including machine learning crystal finding and data processing
- Expanding remit to time resolved serial crystallography and fragment screening



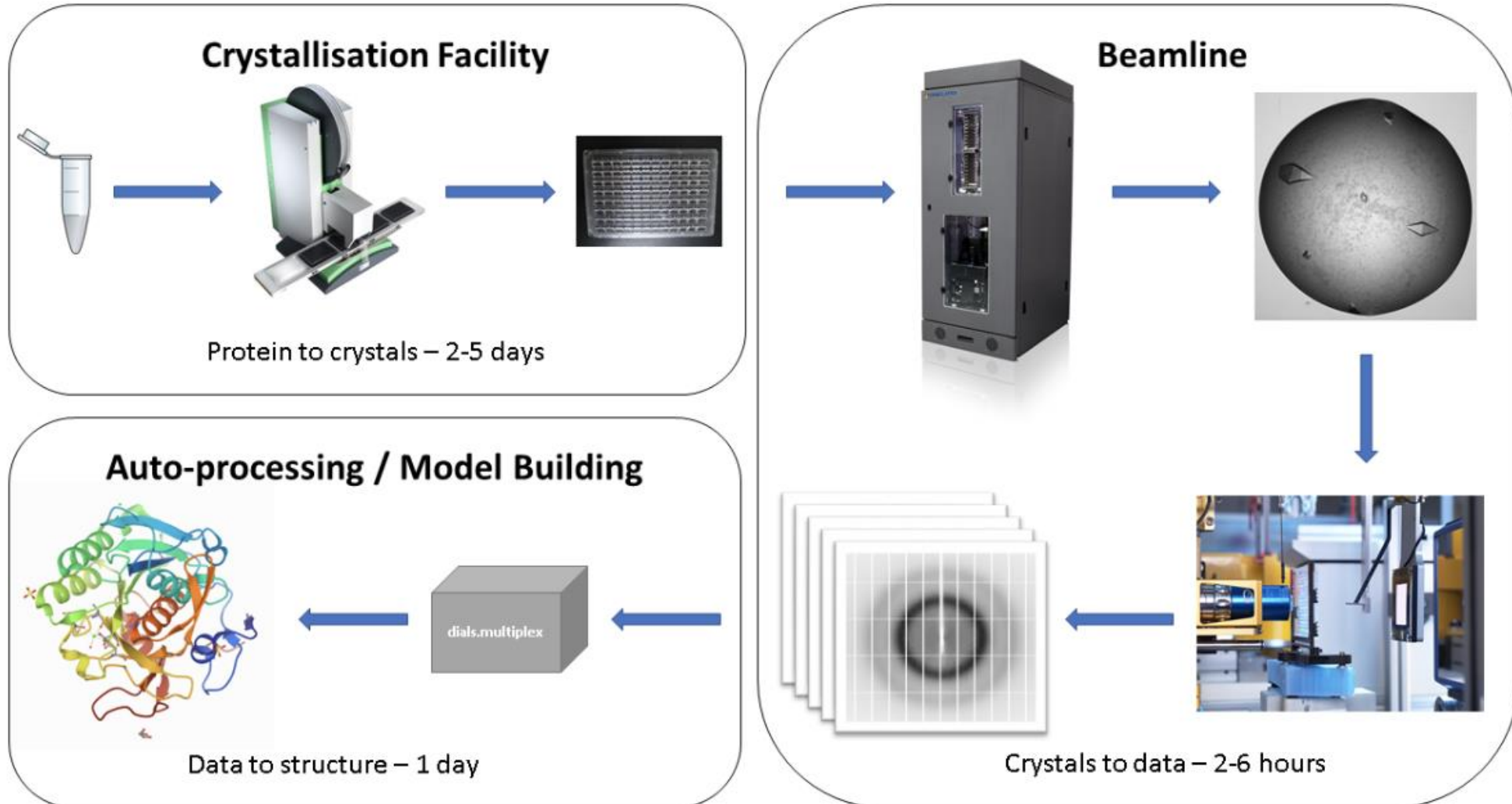
Why collect data at VMXi?

-> high quality RT datasets & structures

- Determining the intrinsic quality of crystal without introducing external variables
 - Dehydration
 - Manual handling
 - Cold shock
 - Cryoprotection
- Rapidly determining structures
 - Speeds up the early crystal optimisation cycles (hit finding and optimisation)
 - From click to structure in minutes
 - Not requiring fishing, cooling, cryo-optimising, transporting, loading, etc.
 - Rapidly solve and visualise multiple ligand structures
- Samples that do not cryo-protect well or are difficult to harvest
 - Complexes
 - Membrane proteins
 - Large crystals



Timelines at VMXi



Workflow at VMXi

Crystallisation plates arrive at the beamline

Beamline images crystallisation plates

User reviews results and selects point for DC

Beamline loads samples

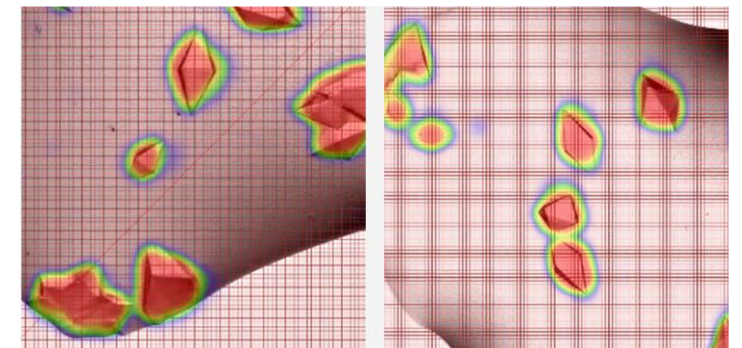
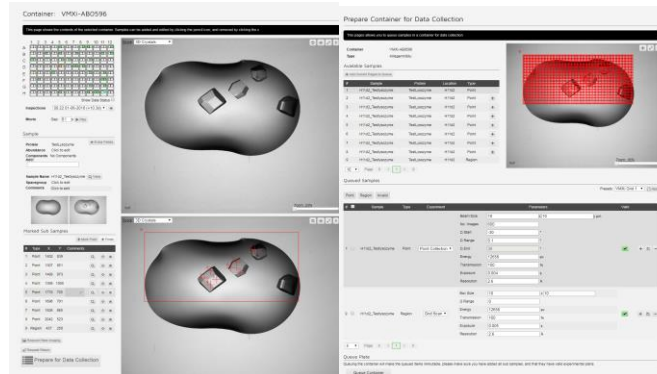
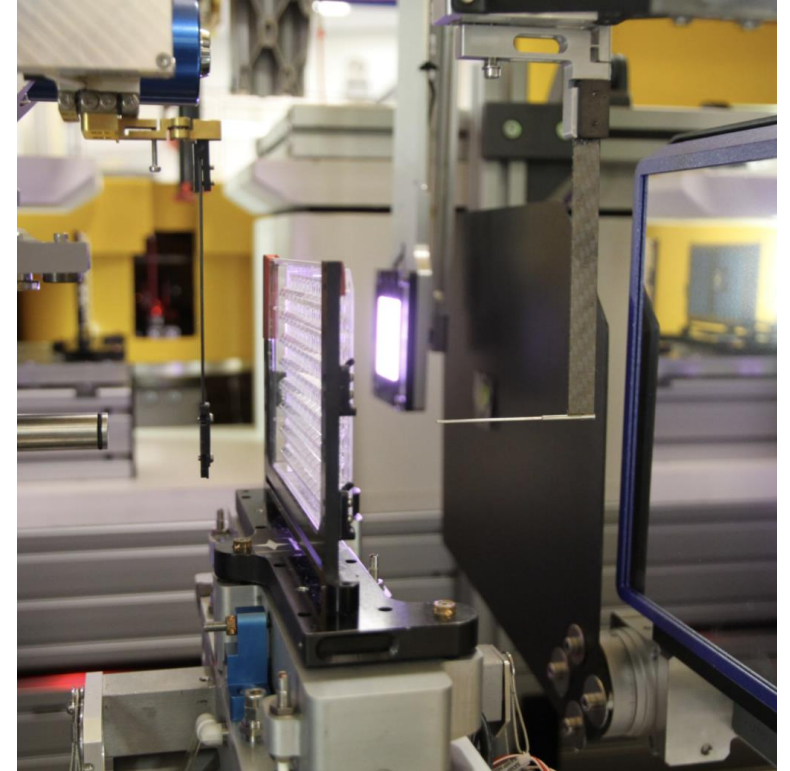
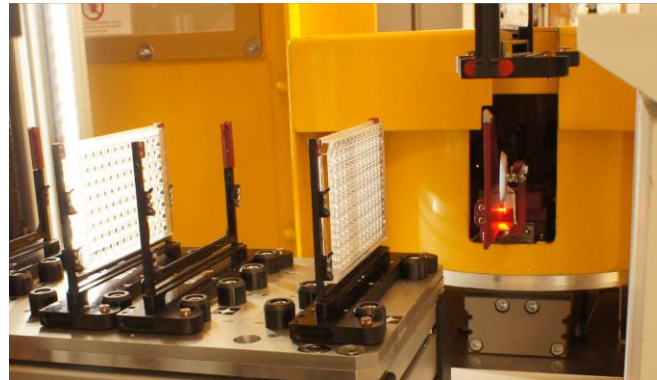
Beamline defines where users wants to collect data

Beamline sets correct DC parameters

Beamline collects data

Beamline unloads samples

Beamline automatically processes data



Access

If you would like access to VMXi, please email:

VMXi@diamond.ac.uk or [Dr Halina Mikolajek](#) for soluble proteins and [Dr Andrew Quigley](#) for membrane proteins.

Complete a project form describing the proposed experiments, enter sample into ERA of active MX proposal.

Courier sample or visit site with sample or plates

Options include

- *Bringing plates to RCaH or VMXi directly*
- *Sending a researcher to setup plates in Research Complex*
- *Sending protein (by prior arrangement/discussion)*

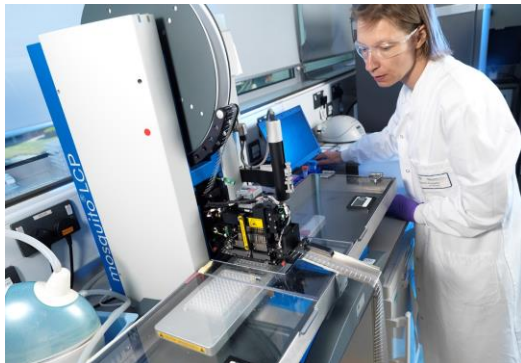
Access to VMXi and Crystallisation laboratory within RCaH

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-
- Crystallisation robotics: Mosquito and Gryphon (4°C & 20°C, humidity & light control, LCP)
 - Scorpion and Formulatrix for making screens
 - Automated imaging systems with MFI technology (4°C & 20°C, LCP) with remote viewing



Crystallisation laboratory

Screens

- Molecular Dimensions
- Hampton Research



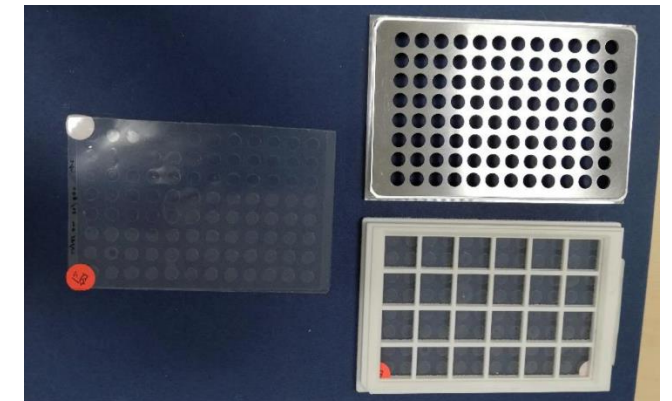
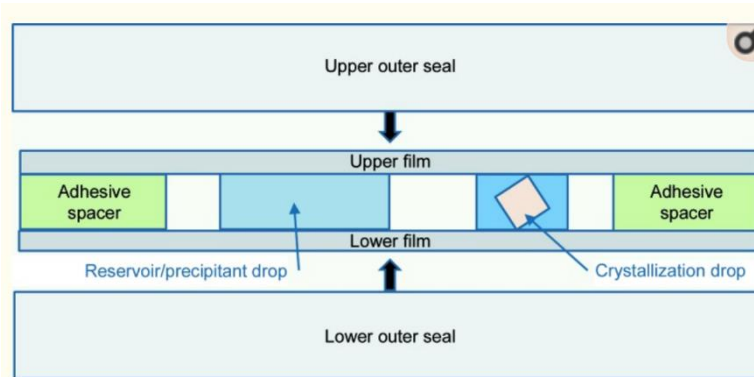
Plate types for VMXi

- Mitegen *in situ*
- Greiner Crystal Quick X

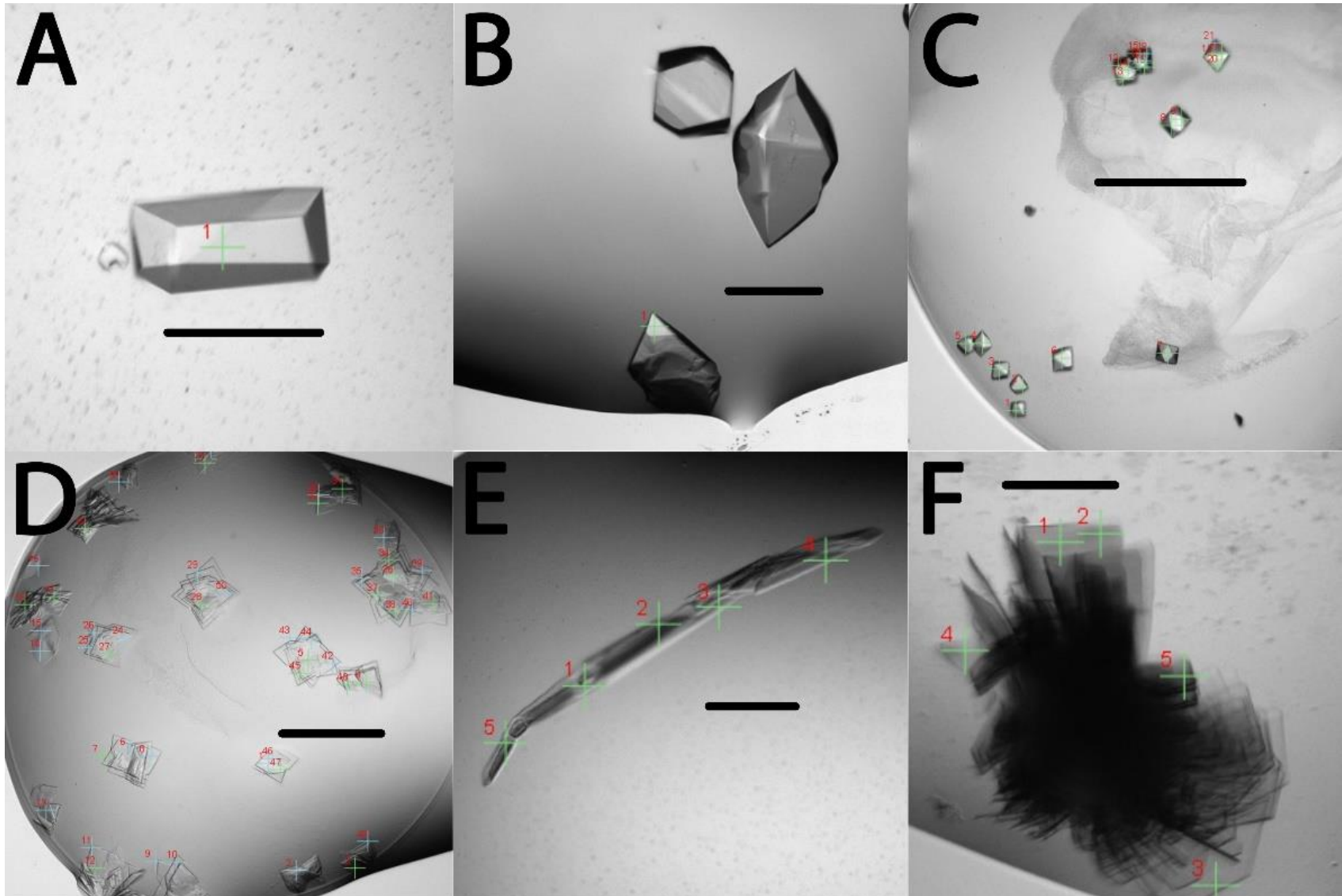


Films

- Very low background
- Ideal for small wedge data collection
- Ideal for microcrystals

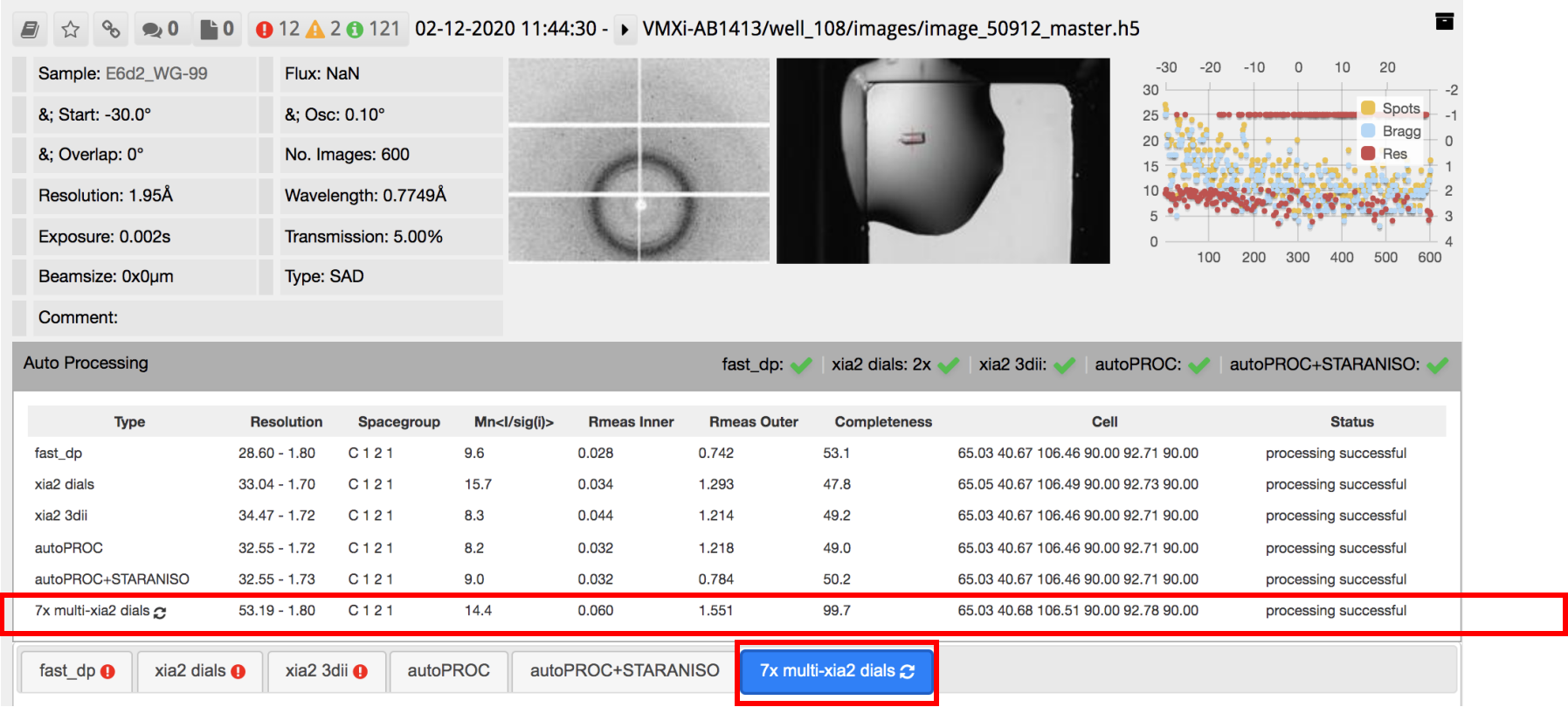
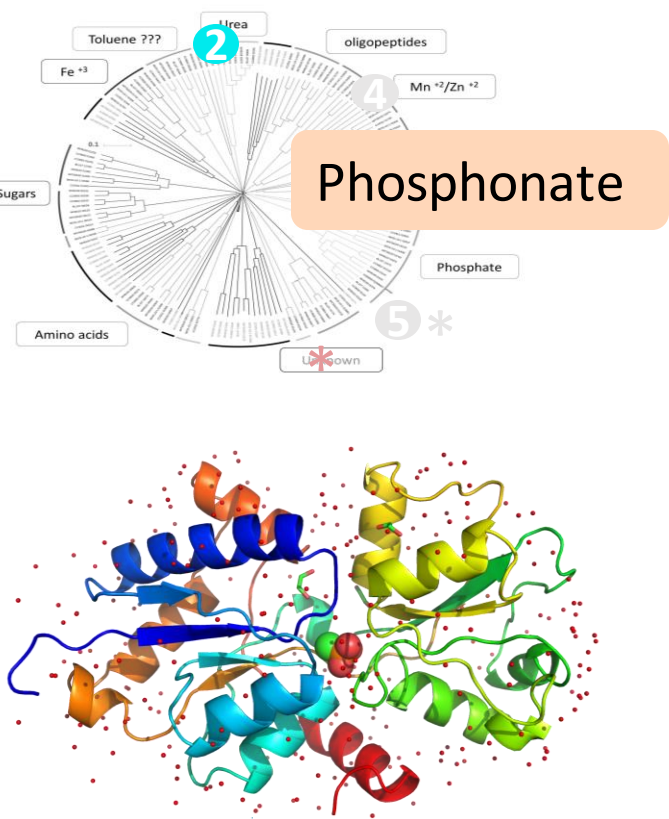


User cases



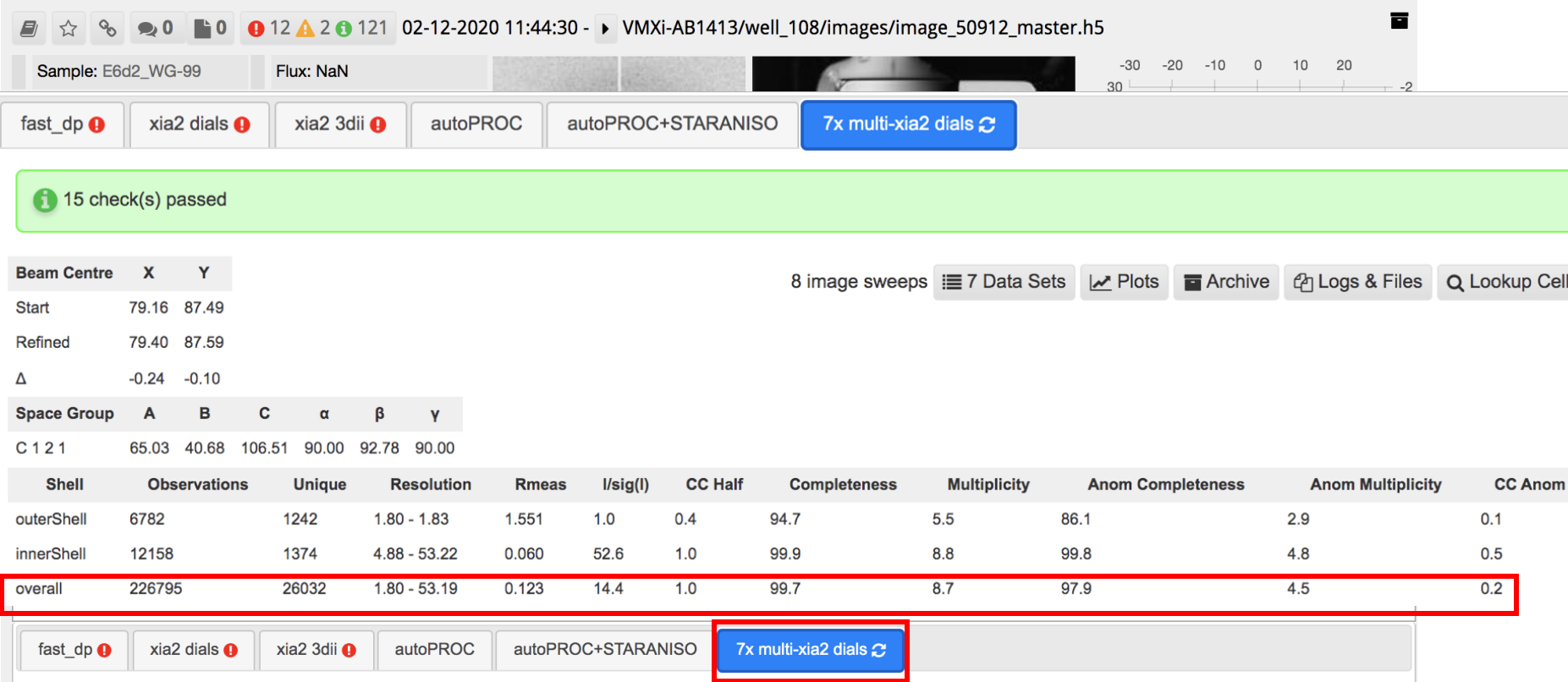
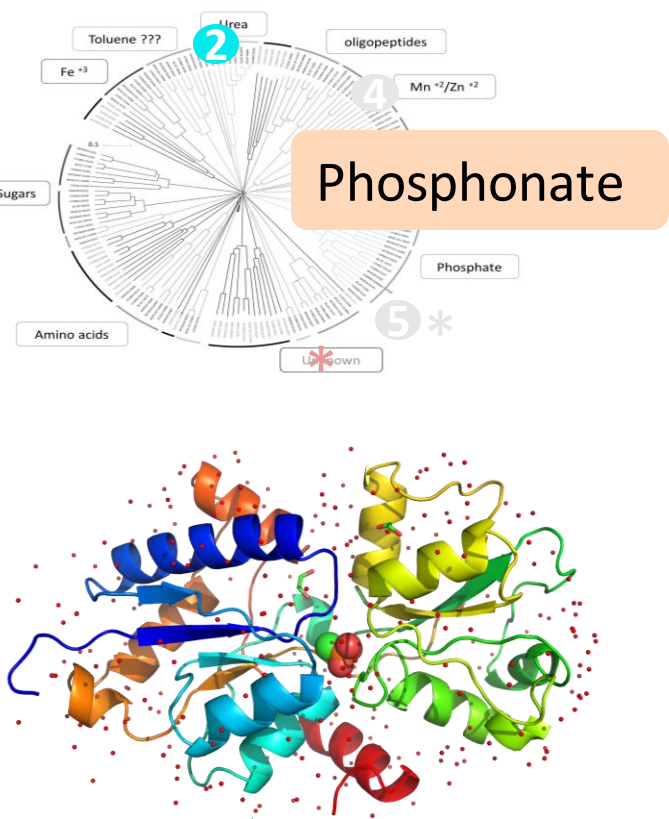
User 1: RT Crystal structures of Substrate Binding Proteins

This project required merging from 7 crystals using multi-xia2 dials to obtain a complete dataset.

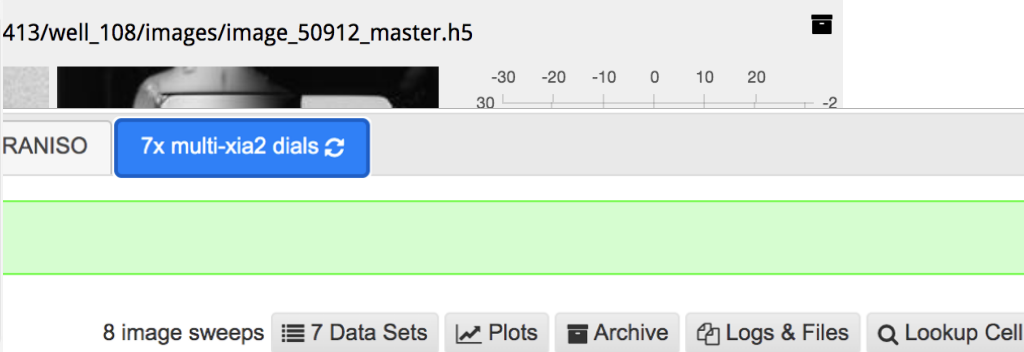
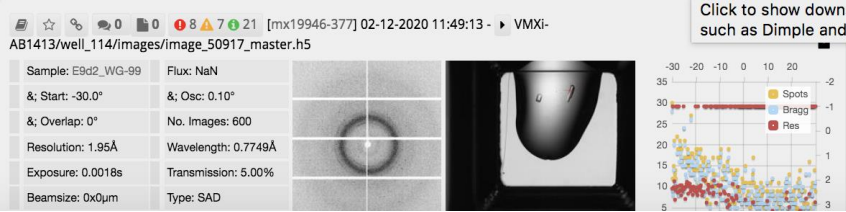
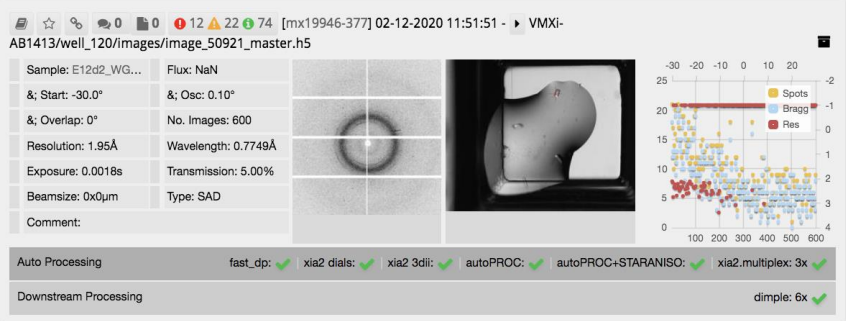
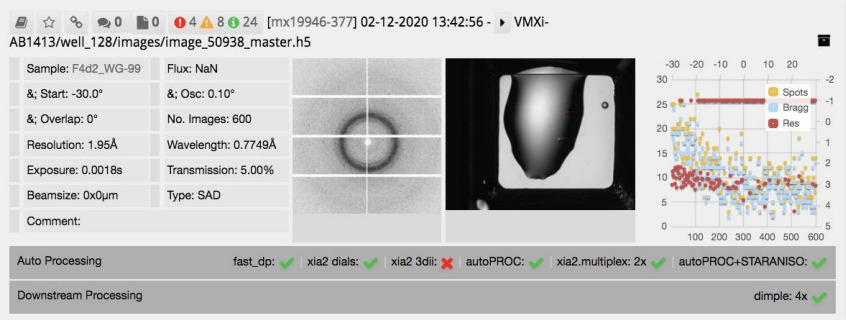
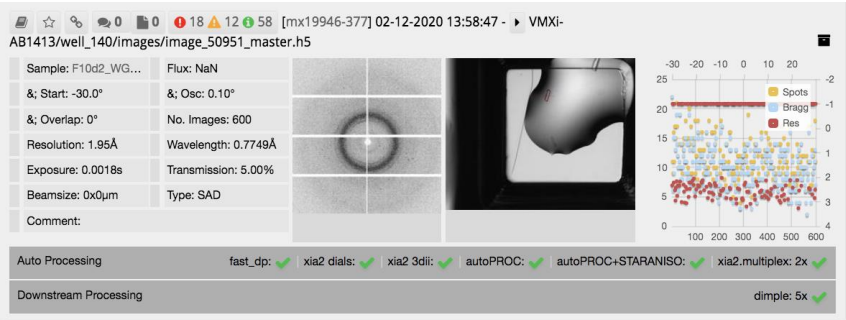


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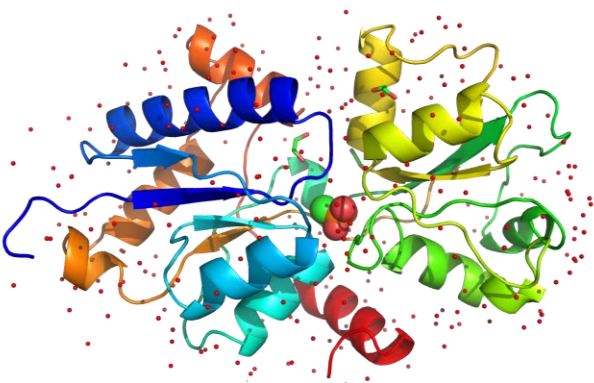
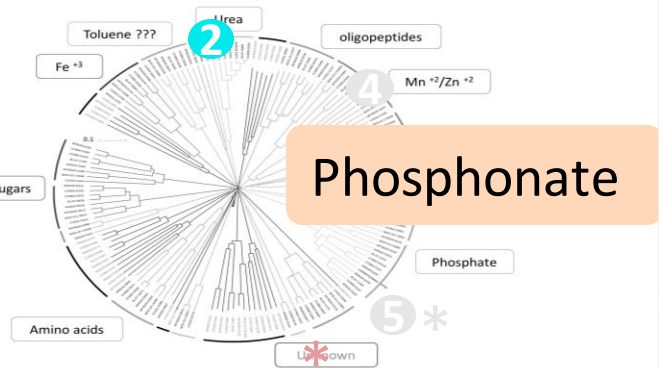
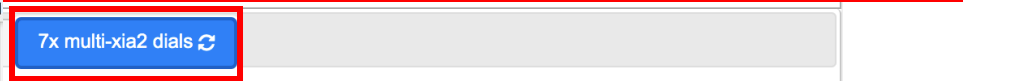
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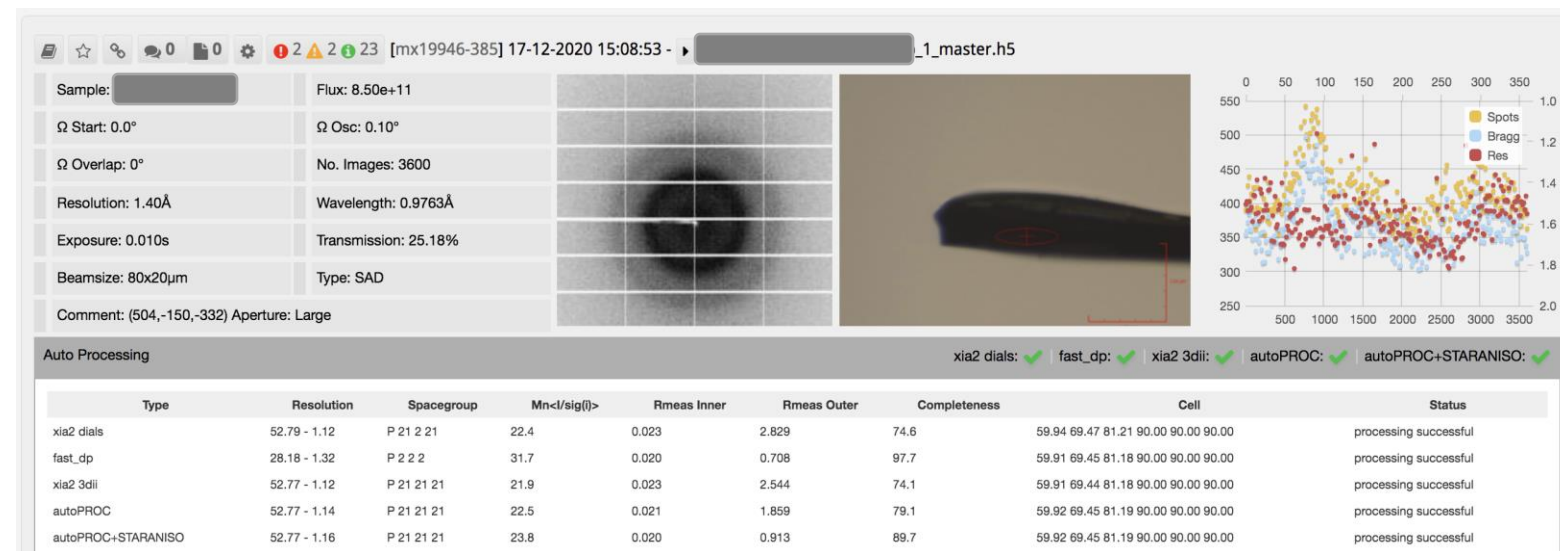
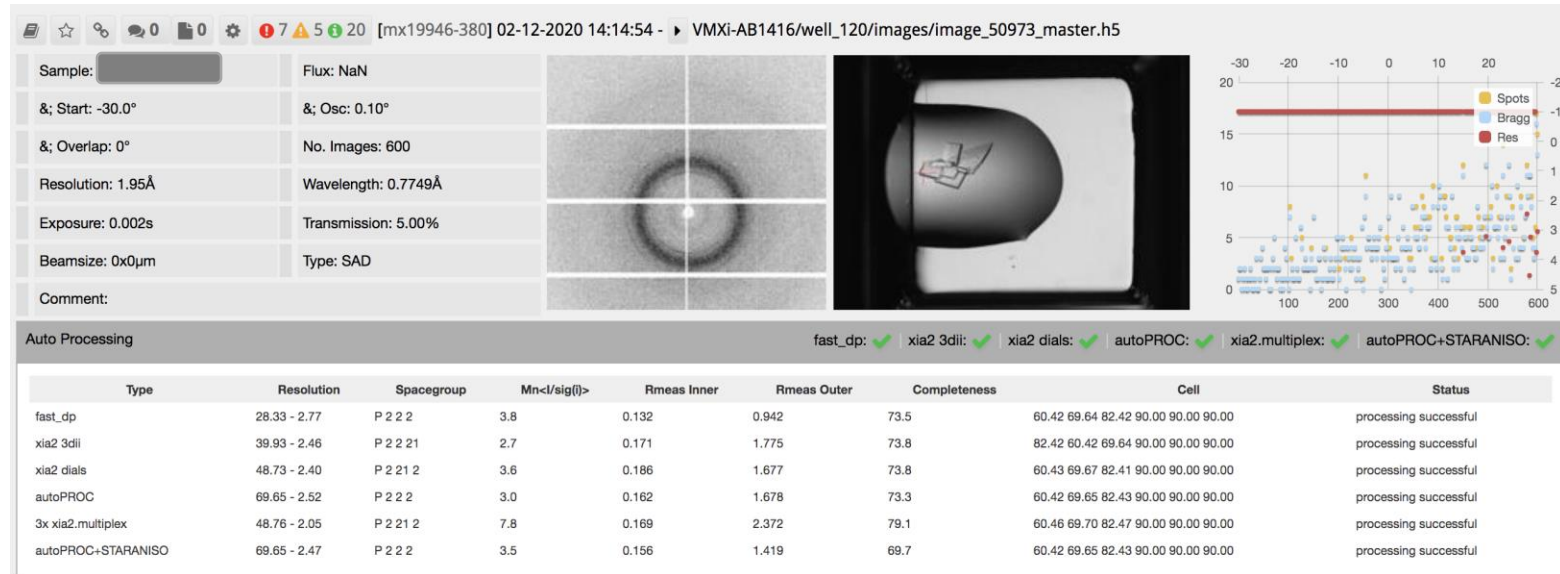
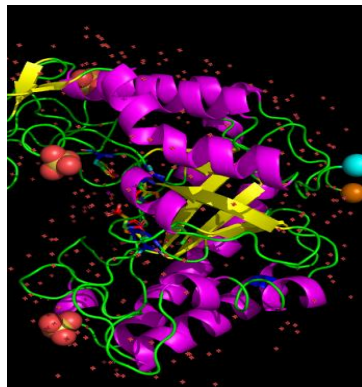


Half	Completeness	Multiplicity	Anom Completeness	Anom Multiplicity	CC Anom
	94.7	5.5	86.1	2.9	0.1
	99.9	8.8	99.8	4.8	0.5
	99.7	8.7	97.9	4.5	0.2



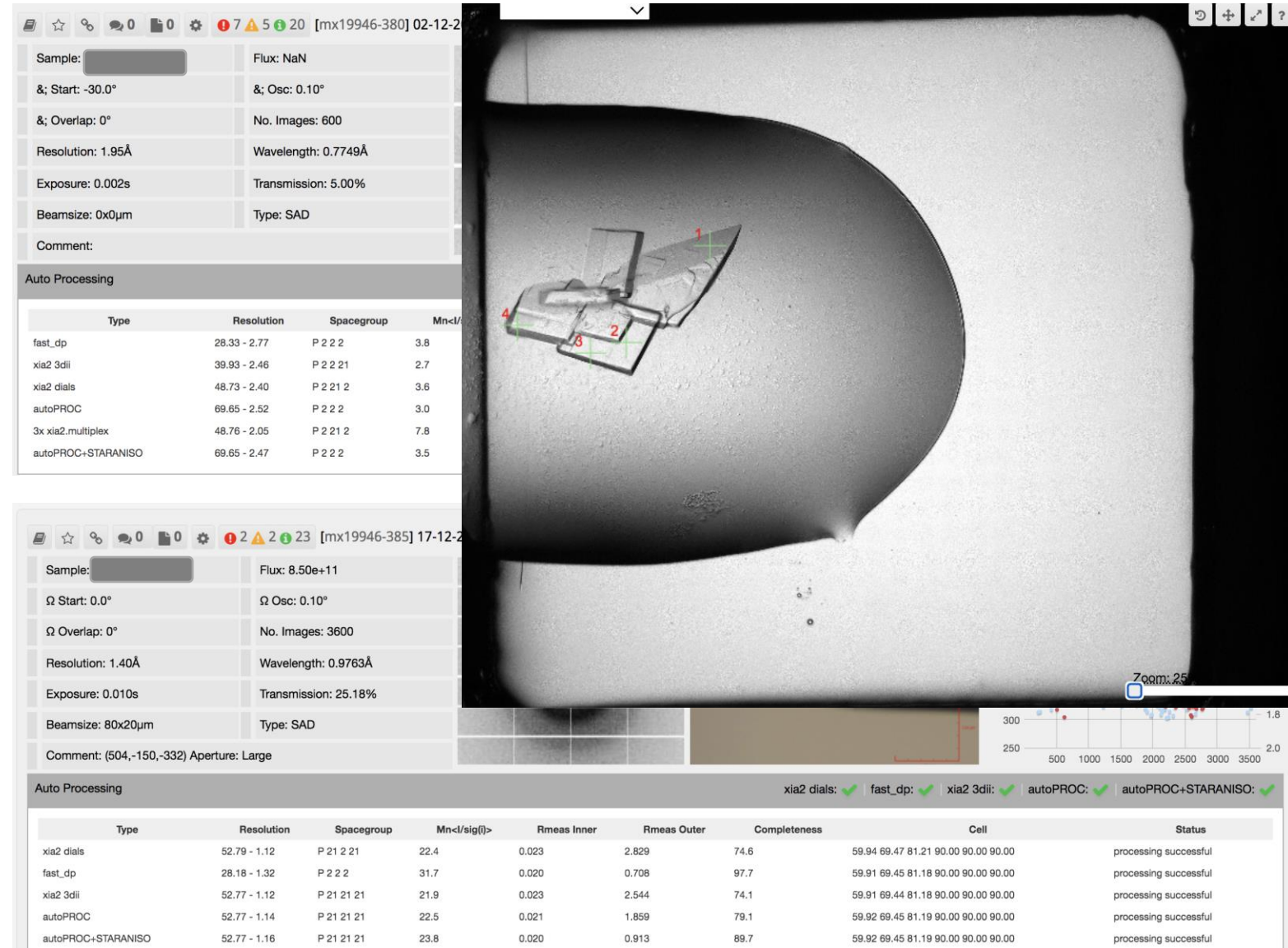
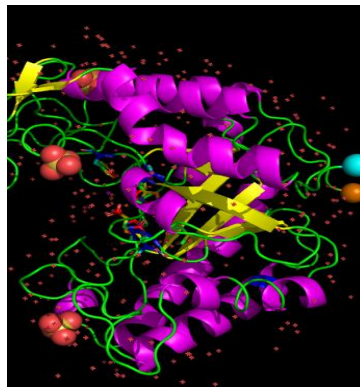
User 2: Quick feedback on difficult to harvest crystals -> Biofuel Project

- User obtained crystals after 75 days. Screened at VMXi and determined crystal to be protein. Tricky MR and low completeness meant harvesting of remaining crystal and collecting at I03. Structure solved.
- Crystal turned out to contain truncated protein. Knowledge from structure led to construct redesign. New crystal form highly diffracting and suitable for ligand screening.



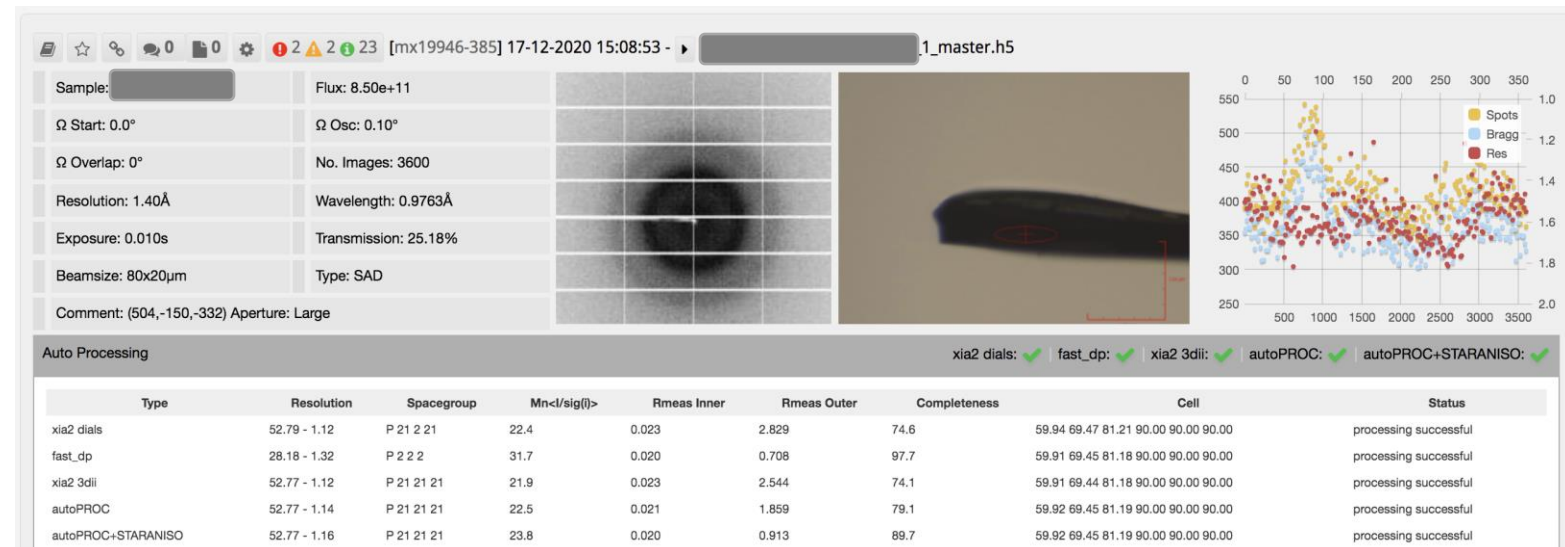
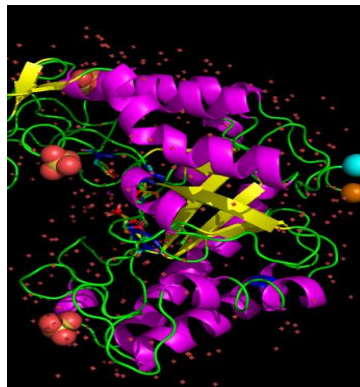
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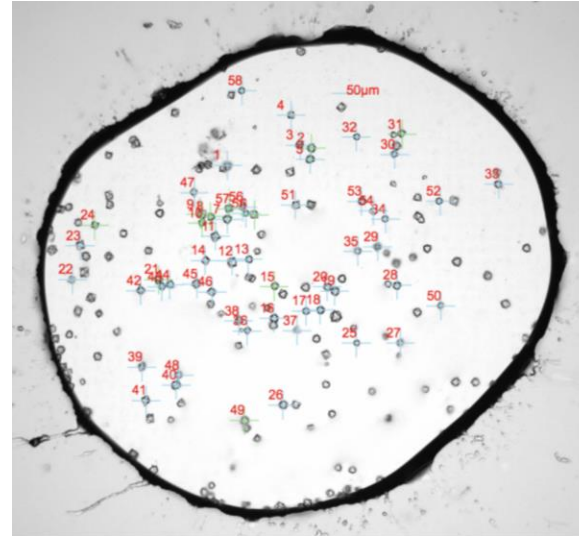
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Future directions for VMXi

- Thin film for serial static and serial-oscillation options (small wedge data collection) for batch grown microcrystals



- Time resolved serial crystallography
- Integration with XCHEM for fragments and ligands at room temperature

