# MASSIF-1 beamline upgrade

**Integration of the CrystalDirect harvester** 

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McCarthy Team - Marquez Team

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### MASSIF-1





- Fully autonomous beamline
  - no user control
  - data collection optimised for every sample
- Flexible booking, queuing system

Fixed energy: 12.84 keV

Highly intense beam: 5 x 10<sup>12</sup> ph/sec Flexible beamsize: 100 to 10 µm

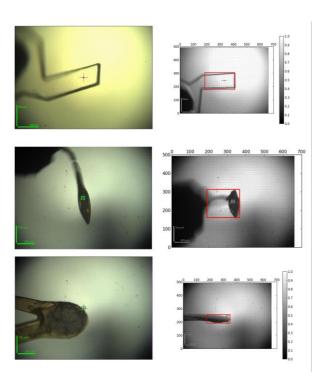
- Arinax MD2s diffractometer
- Flex HCD 368 samples capacity
- Pilatus3 2M
- CrystalDirect Harvester

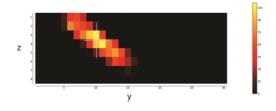


## Samples at MASSIF-1



### Diversity of sample holder (pins)

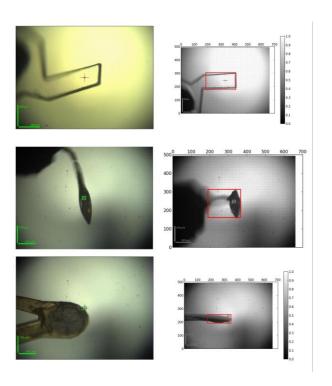




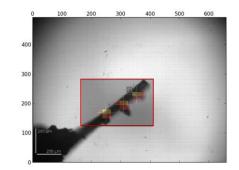
## Samples at MASSIF-1

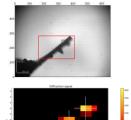


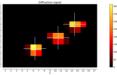
### Diversity of sample holder (pins)



### Multiple data collection



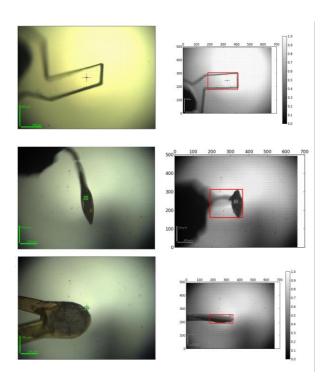




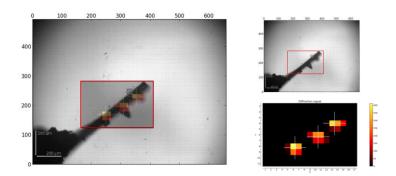
## Samples at MASSIF-1



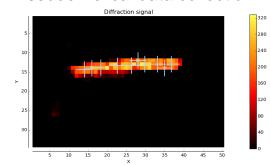
### Diversity of sample holder (pins)



### Multiple data collection



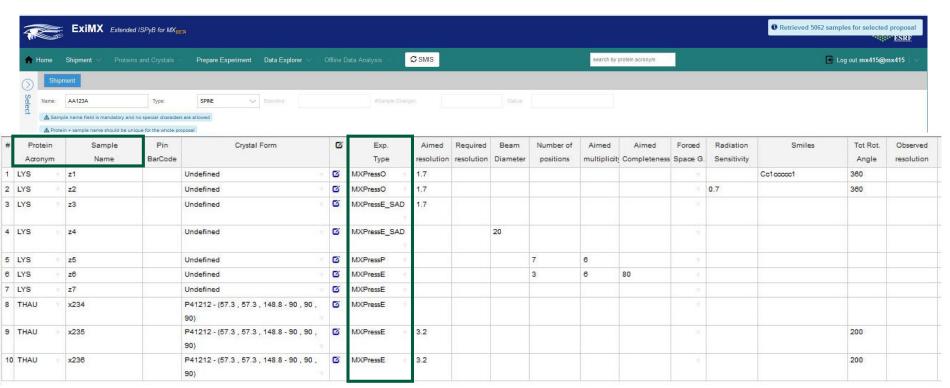
### Pseudo-helical data collection



### Diffraction Plan

### Tutorial on Feb 7th, afternoon

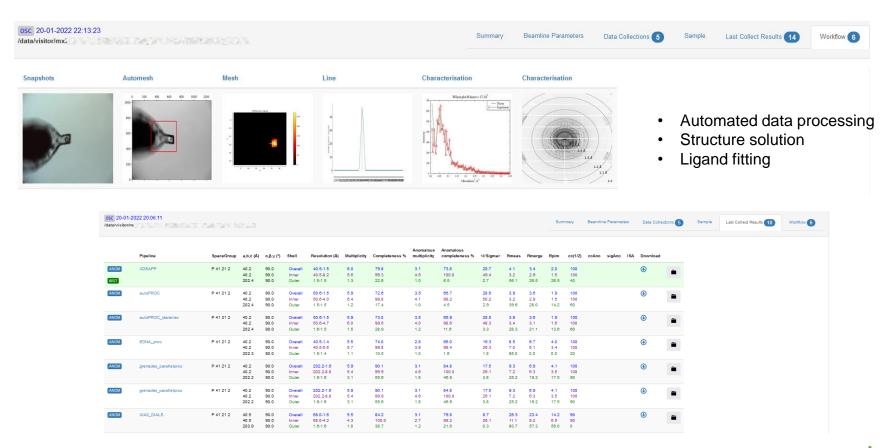
#### Workflows



Workflow details: <a href="https://www.esrf.fr/MXPressWF">https://www.esrf.fr/MXPressWF</a>



### Data collection results

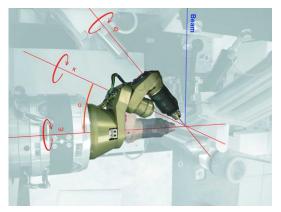




## Data collection of low symmetry space groups

Automated crystal reorientation and additional data collection





Mini-k goniometer head

### Space group P1: small amount of data lost in the blind region

- Mini kappa opening
- Second data collection at different crystal orientation

vefix	Run	#images	Exposure Time	Res. (corner)	Wavelength	Transmission	Directory and image template	Time	Run status	Indicators	View Results	Phasing	Comments					
- 73 5 5 5 6 5 6 5	0	306	0.05 s	1.3 Å (1.0 Å)	0.9655 Å	100%	•	07:43:30	Data collection successful				G					
	1	100	0.05 s	1.0 Å (1.0 Å)	0.9655 Å	100%	•	07:45:00	Data collection successful				Ø					
H.	1	0	0.1 s	1.3 Å (1.0 Å)	0.9655 Å	100%	•	07:46:13	Data collection successful				Ø					
200.00.000	1	1800	0.02 s	1.5 Å (1.1 Å)	0.9655 Å	80.10%	•	07:47:55	Data collection successful	***	٠		P1 Overall Inner Outer	Res. 47.78-1.42 47.78-7.77 1.44-1.42	Completeness 95, 1% 95, 8% 97, 2%	Rmerge 8.0 1.0 250.1	l/sigma 9:3 40.1 0:3	CC1/2 99.5 99.7 15.2
eshi	1	60	0.05 s	1.3 Å (1.0 Å)	0.9655 Å	100%	•	07:50:18	Data collection successful	•			Ø					
	2	15	0.1 s	1.3 Å (1.0 Å)	0.9655 Å	50.24%	•	07:51:35	Data collection successful				Ø					
275.11.6361	2	1800	0.02 s	1.5 Å (1.1 Å)	0.9555 Å	86.10%	•	07:52:30	Data collection successful	•	۰		P 1 Overall Inner Outer	Res. 47.90-1.51 47.90-8.25 1.53-1.51	Completeness 95.3% 93.3% 84.0%	4.5 1.0 245.2	Vsigma 11.4 50.0 0.4	CC1/2 99.6 99.8 15.2

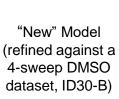


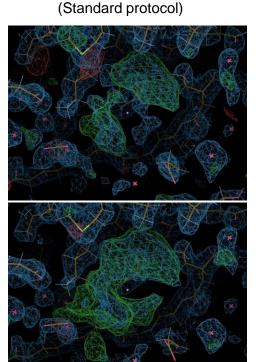
## Data collection of 1057 (pilot project: P1)

PanDDA analysis 135 datasets did not detect any binding for this ligand



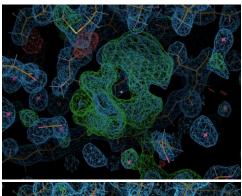
"Old" Model (refined against best standard dataset)

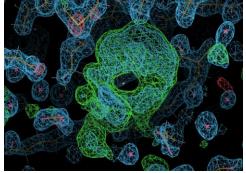




"Old" data for complex

"New" data for complex (4-sweep protocol on ID30-B)





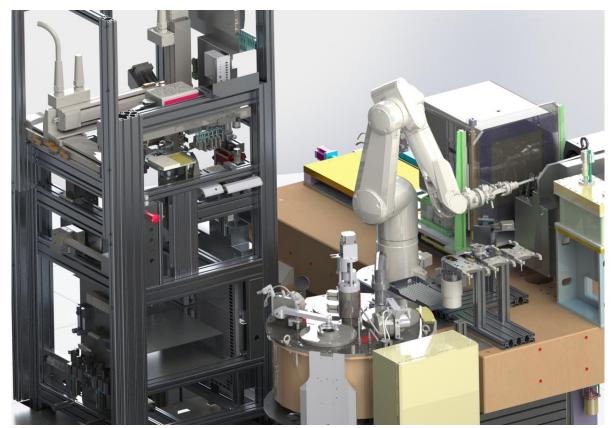


(Collaboration: Merck KGaA and Marquez Team)

## Integration of the CrystalDirect harvester

ESRF

Commissioning ongoing





## CrystalDirect harvester



Fully automated crystallography pipeline controlled through CRIMS interface



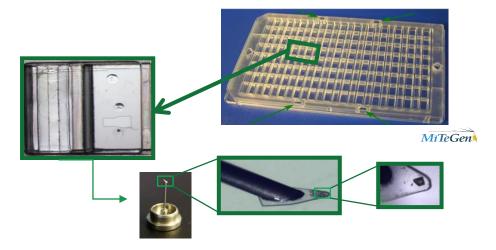
#### Crystallization facility at EMBL:

- Online Crystallography (Protein to Structure)
- Fragment Screening
- Serial crystallography for membrane proteins







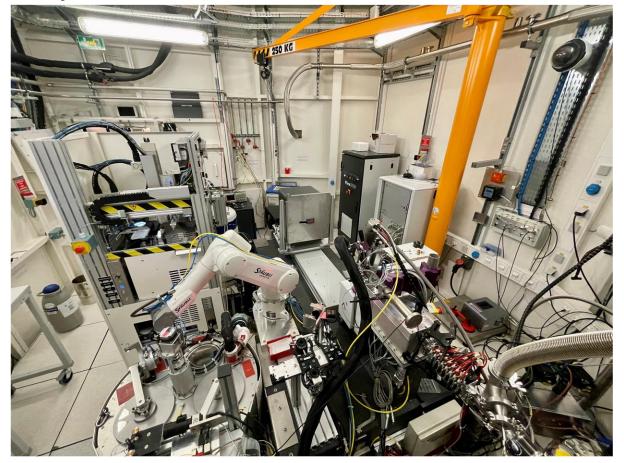






## CrystalDirect harvester at MASSIF-1







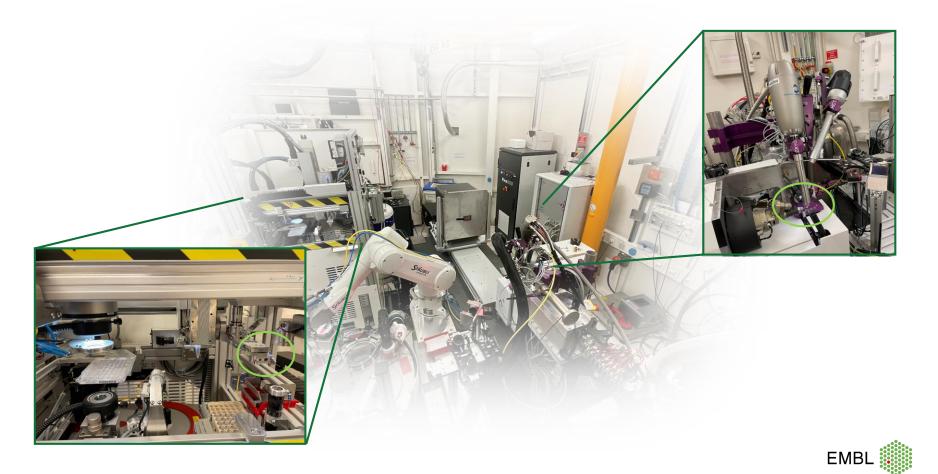
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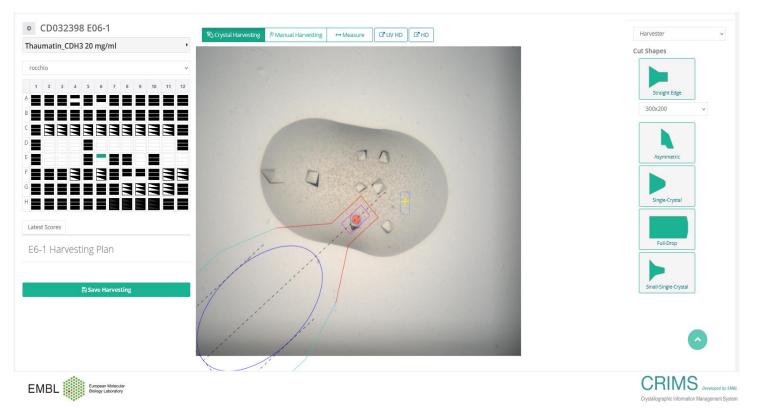


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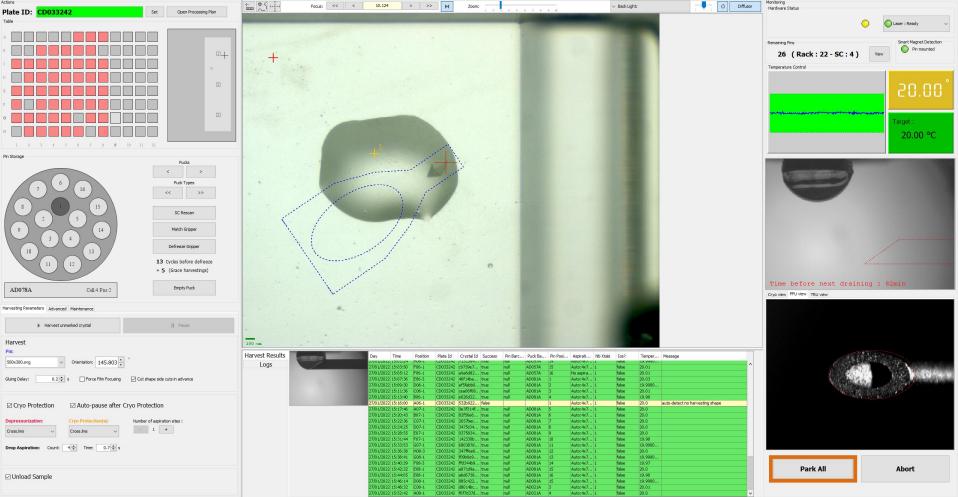


## Automated crystal harvesting and data collection pipeline

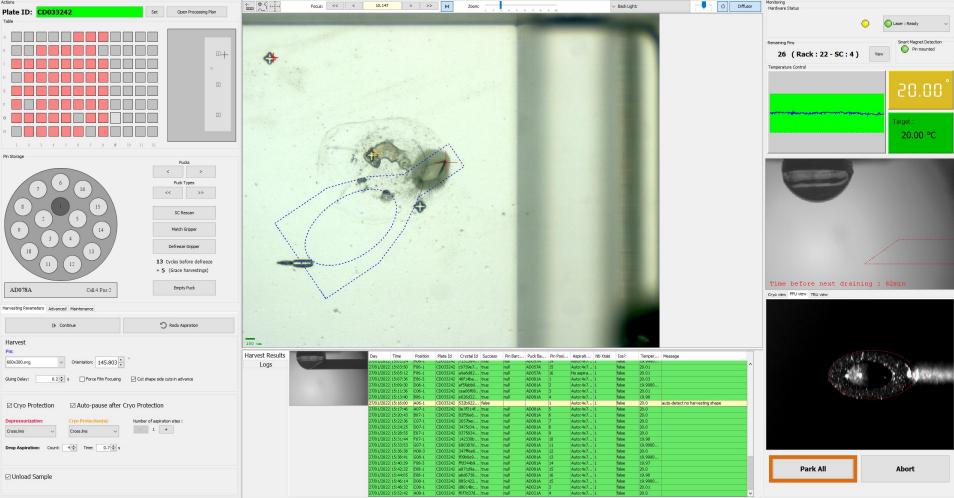
Harvesting plan preparation in CRIMS interface







Ready



Admin 16:00:39 ()

© CrystalDirect
File Devices Help

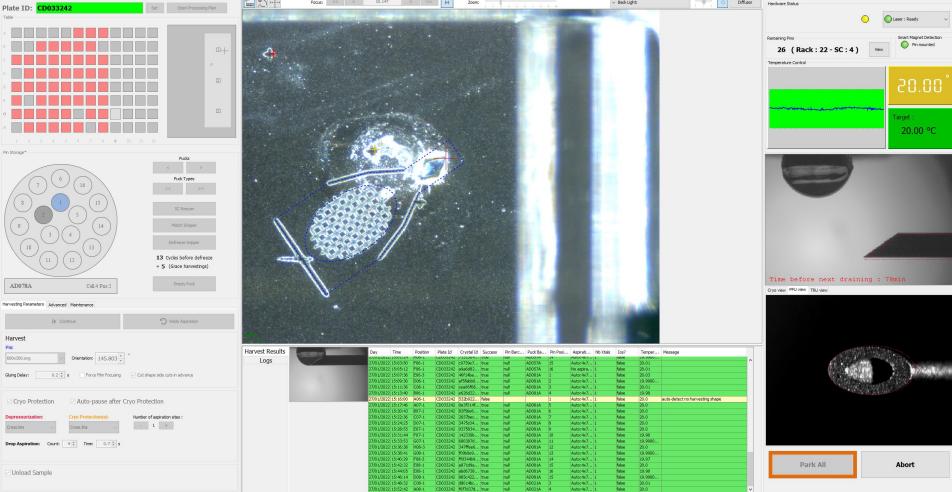
Actors

Plate ID: CD033242

Set Cpon Processing Plan

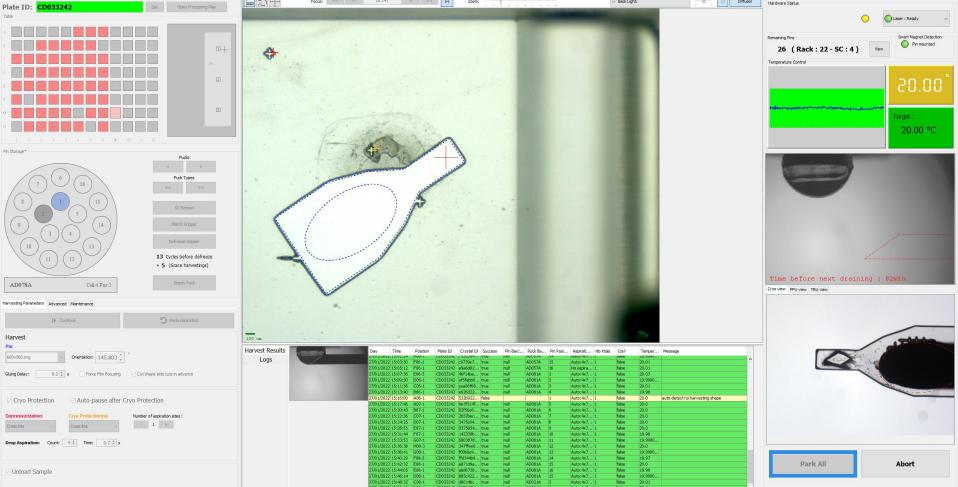
Focus: < < 10.147 > >> № Zoom: CD033242

Bed Light: O Diffusor Herburge Status



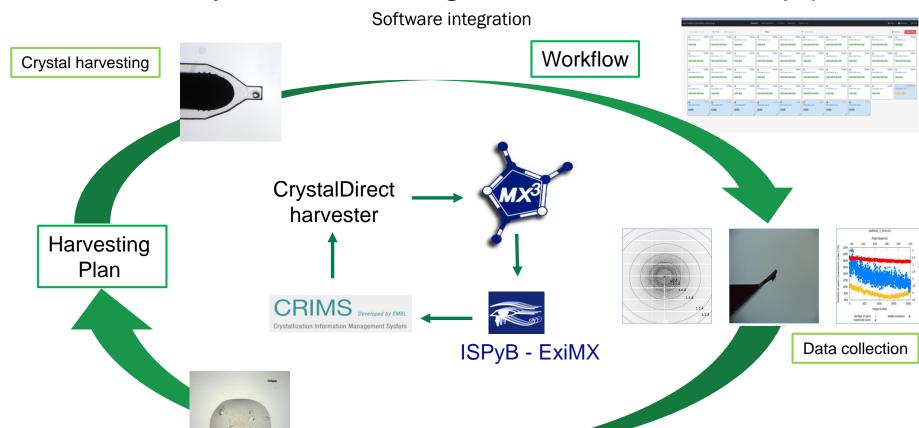
Finishing Harvesting Admin 16:01:05 C

CrystalDirect - o × File Devices Help Actions Monitoring ₩ 5 Focus: << < 10.147 Diffusor ∨ Back Light: Hardware Status Plate ID: CD033242



Finishing Harvesting

## Automated crystal harvesting and data collection pipeline



Protein crystallisation



### **Current status**

#### Validation of different data collection modalities

### Data collection at cryogenic temperature

- Samples harvested and collected in automated mode without user intervention
- Systematic analysis of crystallization conditions
- MXPressR: small fast mesh + EDNA

#### Dehydration screening

- Improve crystal diffraction quality
- Queue system to shorten the experimental set up
- MXPressR\_dehydration: batch configurable parameter

#### Data collection at room temperature

- Protein dynamic, ligand binding site interactions, protein allosteric sites
- MXPressR\_180: small fast mesh with batch configurable dose adapted to beam size



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### Conclusion

The integration of CrystalDirect harvester at MASSIF-1 will expand the beamline automated services.

The beamline upgrade will open to new experimental possibilities allowing the development of new automated and target-based data collection modalities.

### **Plate-to-beam Applications**

- ✓ Increased efficiency for fragment screening and high throughput applications
  - Automated dehydration experiments
    - ✓ Systematic studies at RT
    - √ Time course experiments
  - ✓ Systematic analysis of crystallization conditions







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### **Future Plans**

User acces: mid 2022

- High throughput large scale RT data collection series
  - Workflow optimization (muliple target systems)
- RT serial crystallography
- In situ screening and data collection



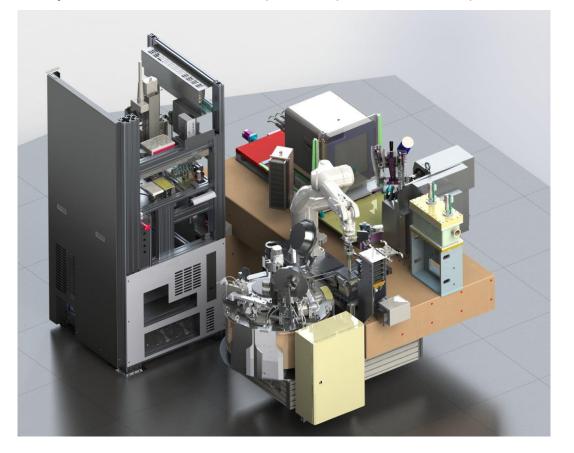




## Future development

Fully automation of the entire process: plate holder and pin station

Instrumentation Team





## Acknowledgements



Andrew McCarthy
Matthew Bowler
Jean Baptiste Florial
Nicolas Foos

José Antonio Márquez
Florine Dupeux
Anne-Sophie Humm
Peter Murphy



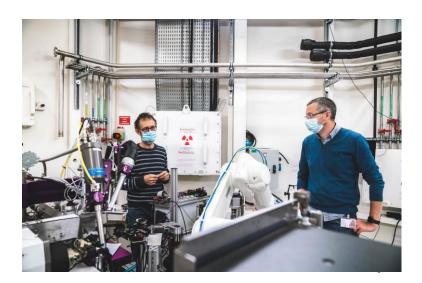
**Instrumentation Team** 

Gergely Papp Jeremy Sinoir Marcos Lopez Marrero Frank Felisaz



Gordon Leonard SB Group

Didier Nurizzo Olof Svensson



### Poster Session

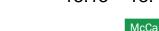
13:15 - 13:45

8 Feb, 2022











# Fully autonomous end-to-end protein to structure pipelines: the CrystalDirect harvester at MASSIF-1

S Rocchio<sub>1</sub>, J Sinoir<sub>1</sub>, JB Florial<sub>1</sub>, M Lopez-Merraro<sub>1</sub>, F Felisaz<sub>1</sub>, P Murphy<sub>1</sub>, F Dupex<sub>1</sub>, AS Humm<sub>1</sub>, D Nurizzo<sub>2</sub>, O Svesson<sub>2</sub>, N Foos<sub>1</sub>, GA Leonard<sub>2</sub>, G Papp<sub>1</sub>, AA McCarthy<sub>1</sub>, JA Marquez<sub>1</sub>, MW Bowler<sub>1</sub>.

1 European Molecular Biology Laboratory (EMBL) - Grenoble; 2 European Synchrotron Radiation Facility (ESRF)

Automation is changing the way in which opstallographic data are collected, allowing large amounts of high-quality data to be collected efficiently and paving the way to the development of more specific methods [1,2]. Here, the possibility to explore different data collection modalities is important to keep up with modern structural biology projects. The <u>CrystalDireg</u>t harvester allows access to a fully automated protein crystallography worldflow, integrating protein crystallography worldflow, integrating protein crystallography worldflow, as many protein crystallography worldflow, integrating protein crystallography worldflow, integrating protein crystallography worldflow, and the protein crystallography worldflow, integrating protein crystallography worldflow, and the protein crystallography worldflow in the crystallography worldflow in the protein crystallography worldflow in the protein crystallography worldflow in the protein crystallography worldflow, integrating protein crystallography wor



13:45 - 14:15











Nicolas Foos

McCarthy Synchrotron

# Performing *in-situ* data collection : service provision for the most complex experiments

N.Foos<sub>1</sub>, M.Bowler<sub>1</sub>, D.Nurizzo<sub>2</sub>, S.Rocchio<sub>1</sub>, J.Sinoir<sub>1</sub>, J.B.Florial<sub>1</sub>, C.Mueller-Dieckmann<sub>2</sub>, G.A.Leonard<sub>2</sub>, J.Márquez<sub>1</sub>, G.Papp<sub>1</sub>, A.A.McCarthy<sub>1</sub> 1: Distr. Genome Out-Station, 2: ESHF

Being fast, reliable and automated is what makes X-ray crystallography efficient, popular, successful and in constant improvement. The right beam offered by the ESPI-ESB makes possible to collect excellent data from micro to nano-crystals using the latest developments in serial approaches. Our project aims to address the issue of high throughput in structural biology or projects, while at the same time pushing forward more classical experiments hanks to the implementation of the EMDL Genoble HTX platform which offers a robust solution for automated crystal harvesting. To achieve this we are creating the convergence between the final diffraction experiment and the original crystal harvesting.

Our project takes advantage of the FLEX robot and its versatility to make the missing link between the HTX high throughput crystallization platform, the Opstal Christ harvester and the MDSS diffractoriset on the beamline, in order to create a comprise pipeline we are implementing an automated in-situ screening and data-collection service. To drive the experiment and make it user triendly, we are developing an efficient workflow integrating automated decision making to achieve a fully automated data collection beginning from crystal growing devices (plates as well as microflution chips).

