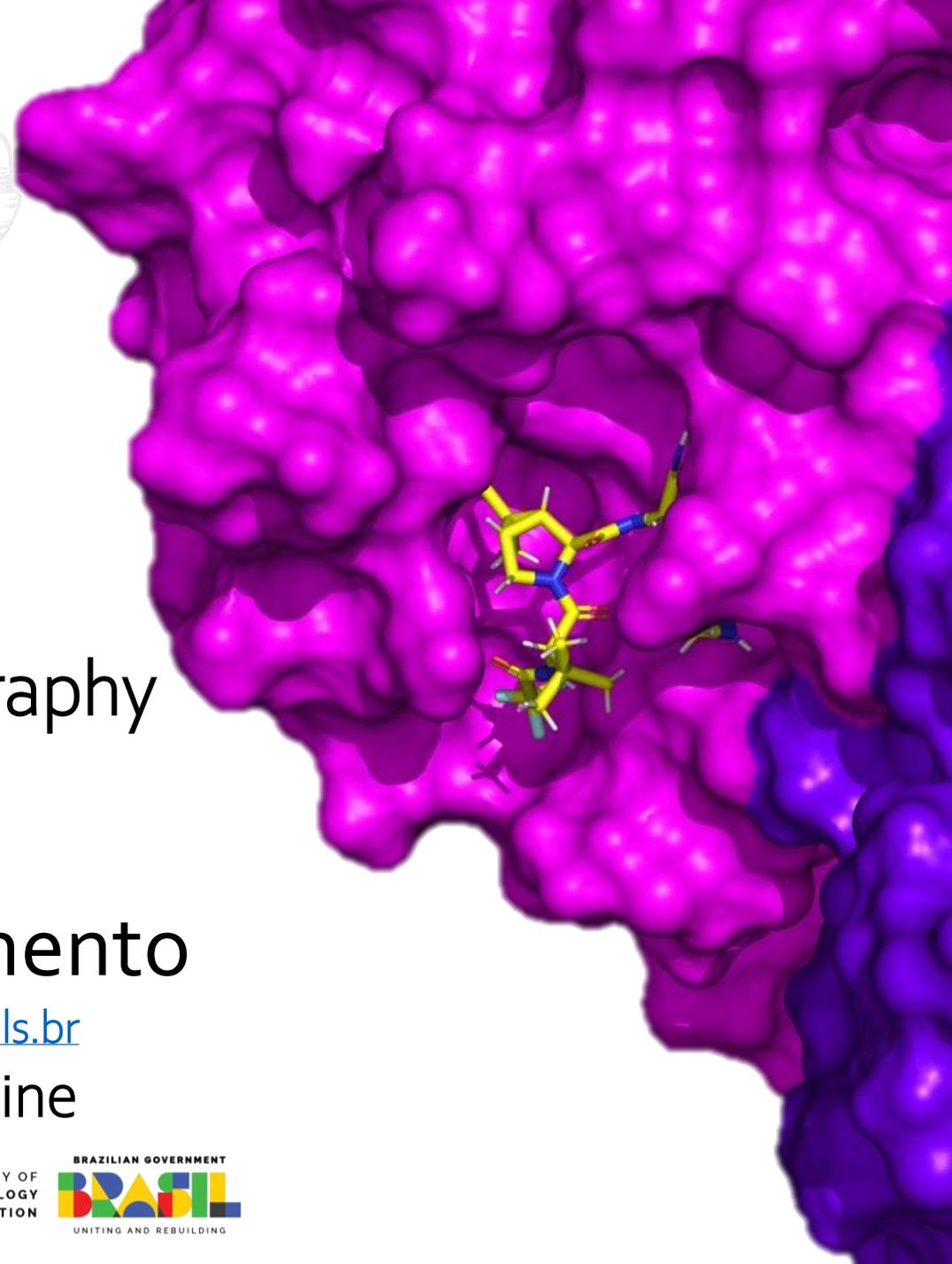




MXCuBE-ISPyB

Joint Meeting

Trieste, Italy / 20-22 November 2024



MANACÁ@Sirius

macromolecular and chemical crystallography

Andrey Nascimento

andrey.nascimento@lnls.br

MANACÁ beamline



MINISTRY OF
SCIENCE TECHNOLOGY
AND INNOVATION



Acknowledgment

MANACÁ group

Andrey Nascimento – coordinator

Evandro Araujo – researcher

Igor Maldonado – specialist

Felipe Ramos - dev. analyst

João Rodriguez - dev. analyst

Ana Julia Silva - intern

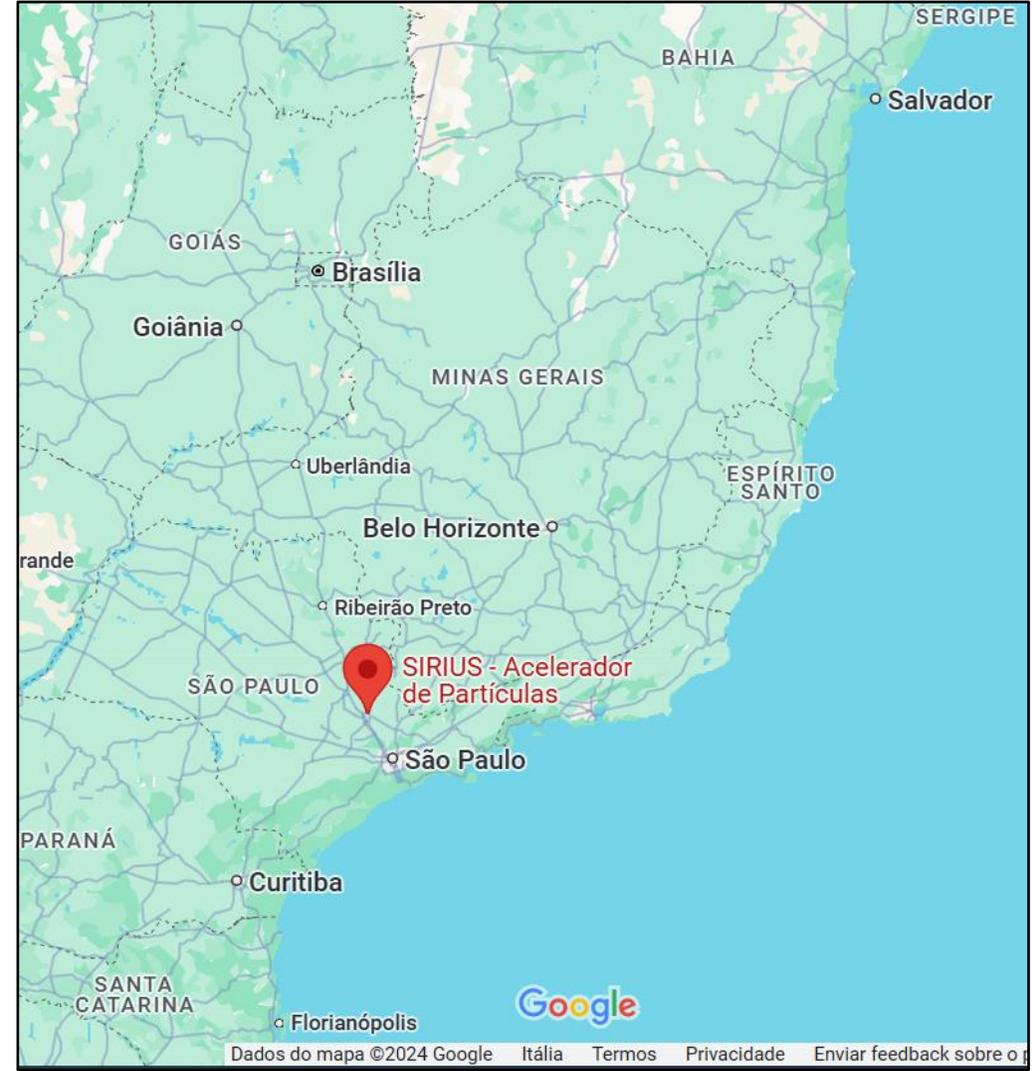
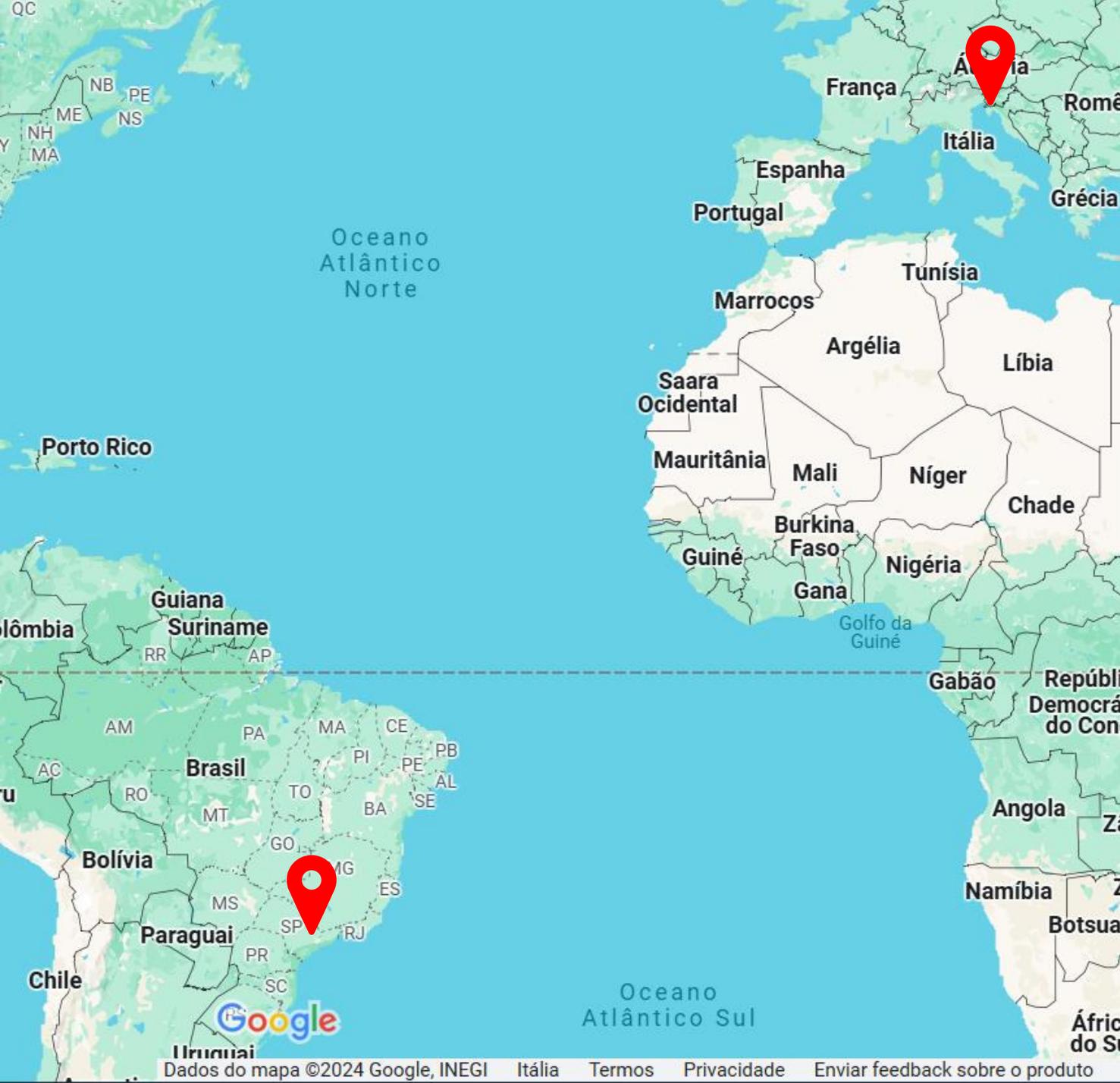
Pedro Benetton - intern

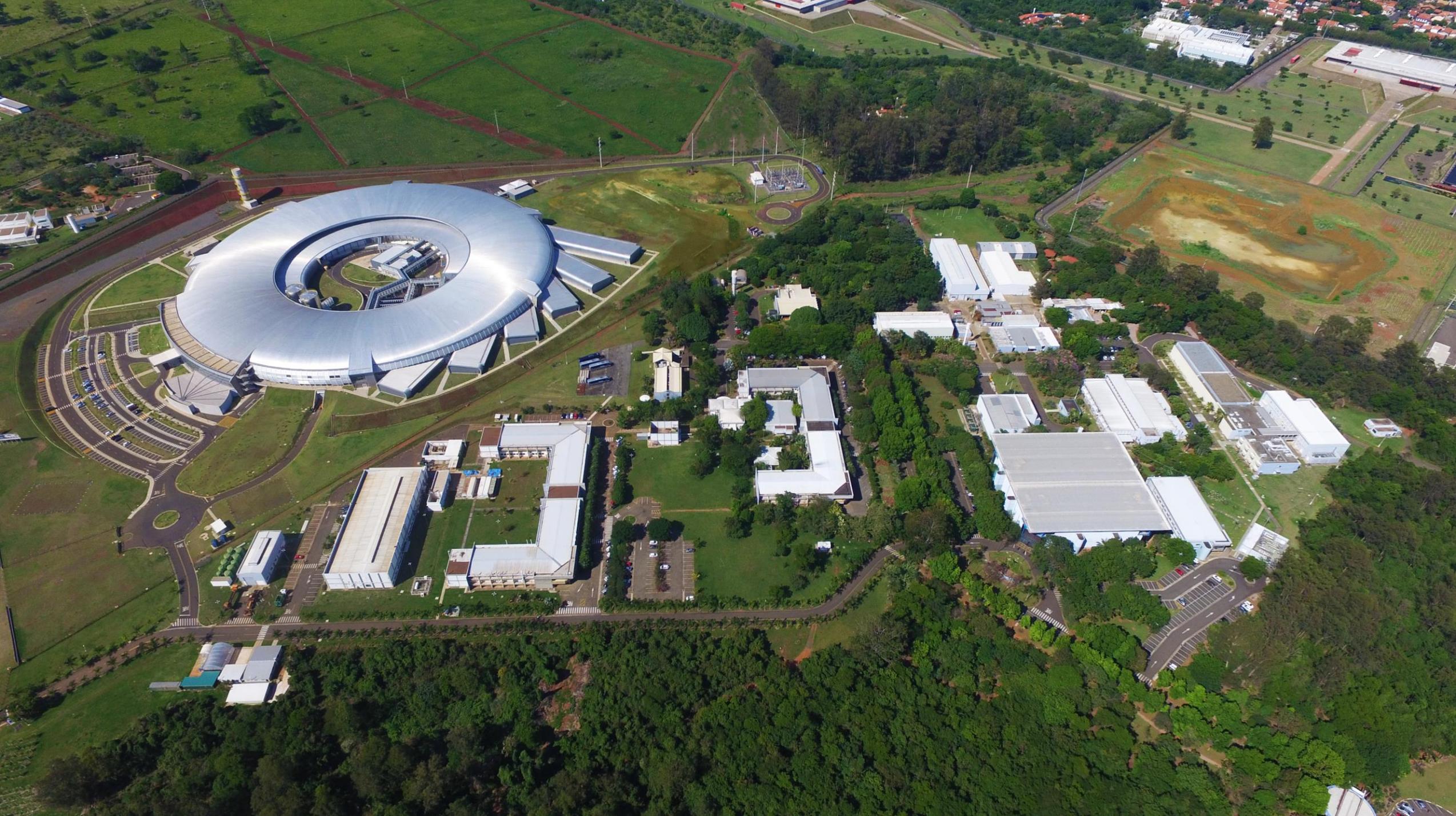
Ana Beatriz Carvalho - student

All the support teams.

Users!

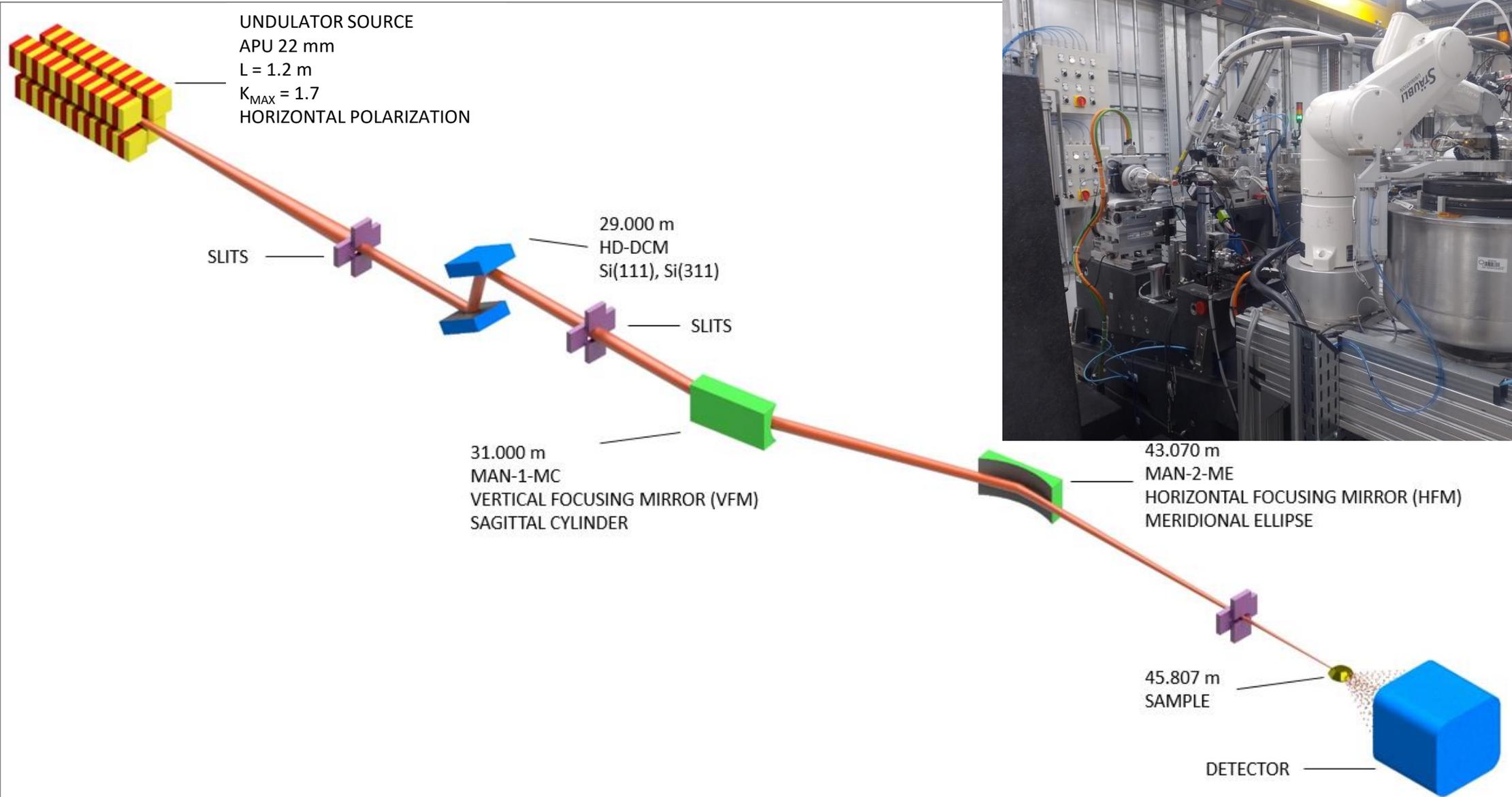






MANACÁ @ Sirius





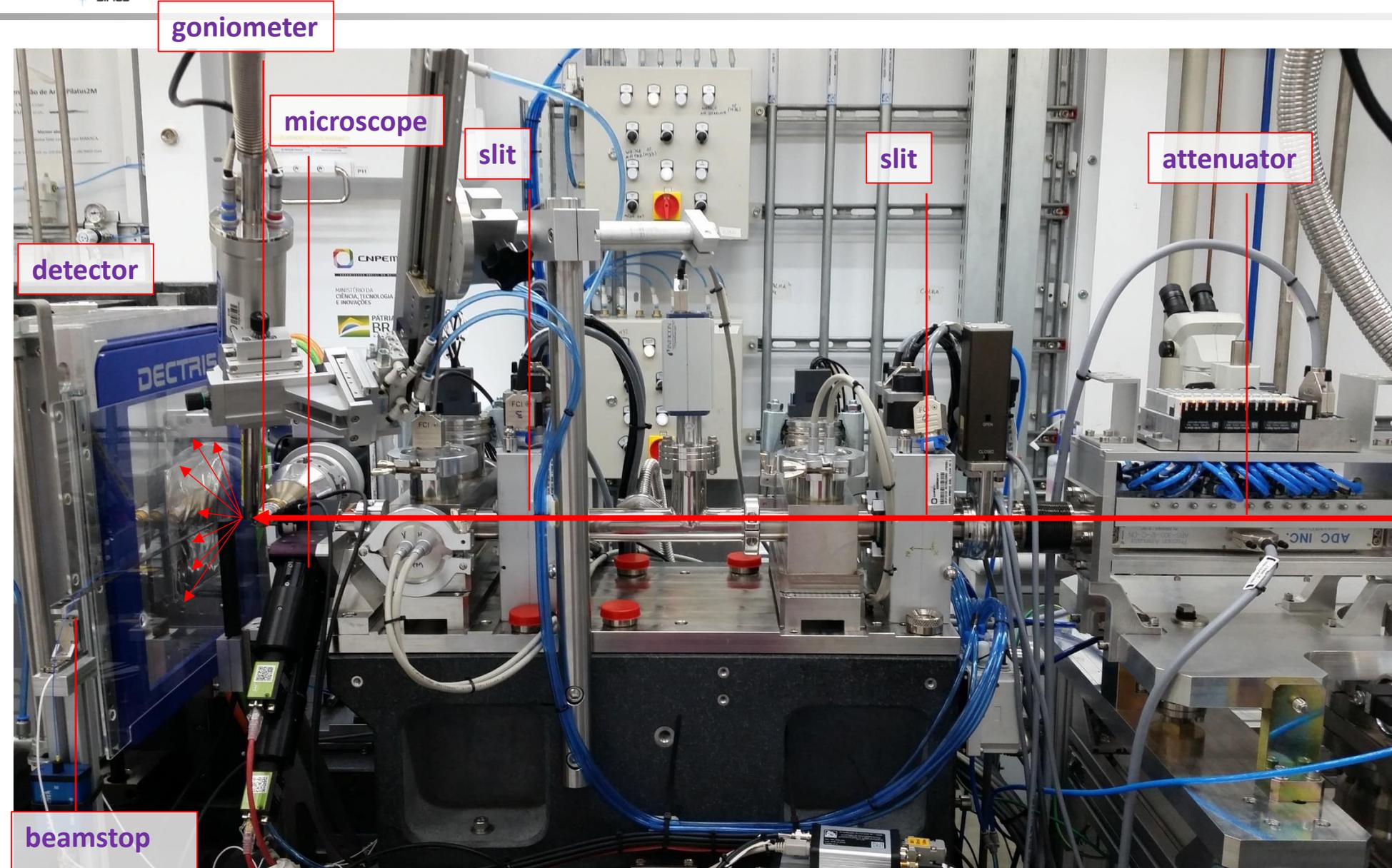
Experimental station

OAV microscope (Arinax)

Air bearing-based goniometer (in house)

PILATUS 2M detector (Dectris)

X ray



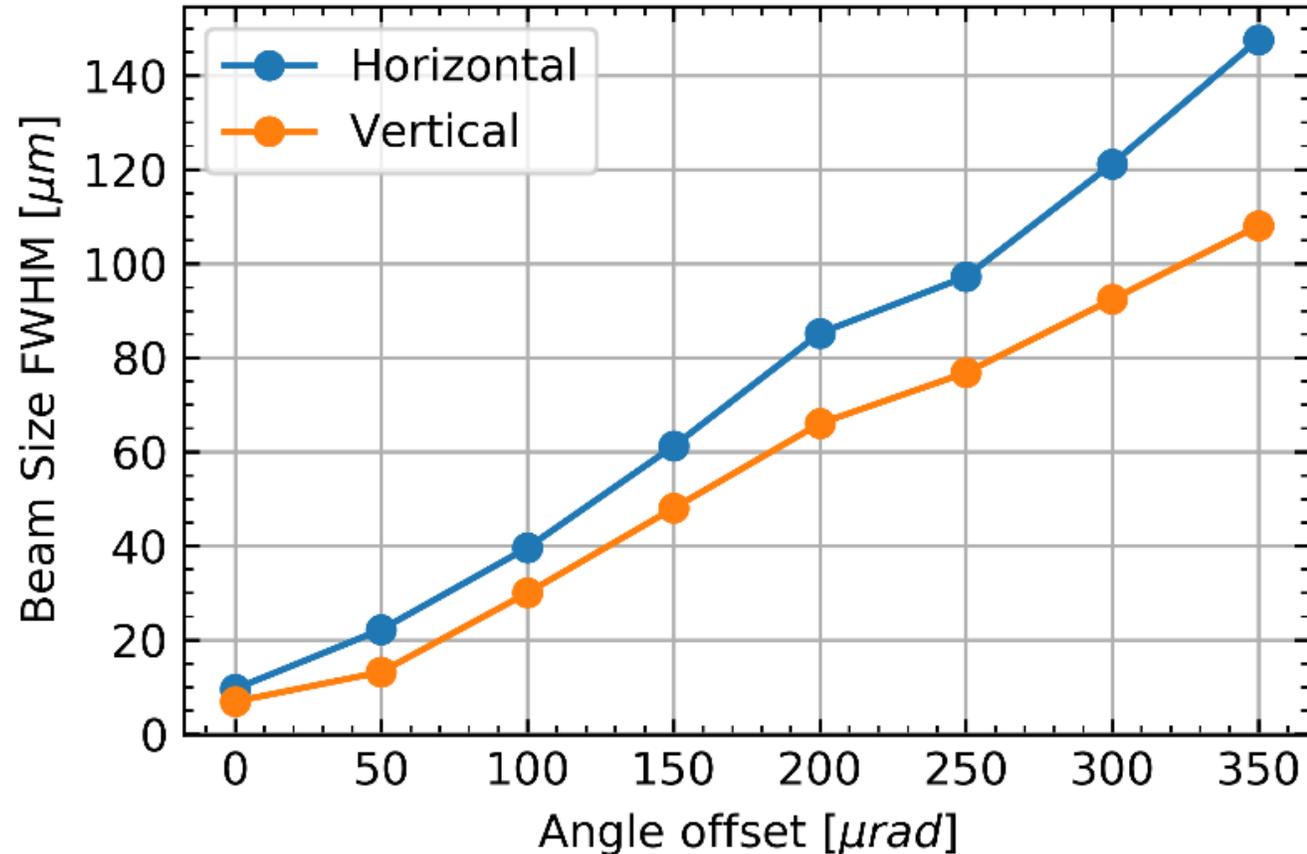
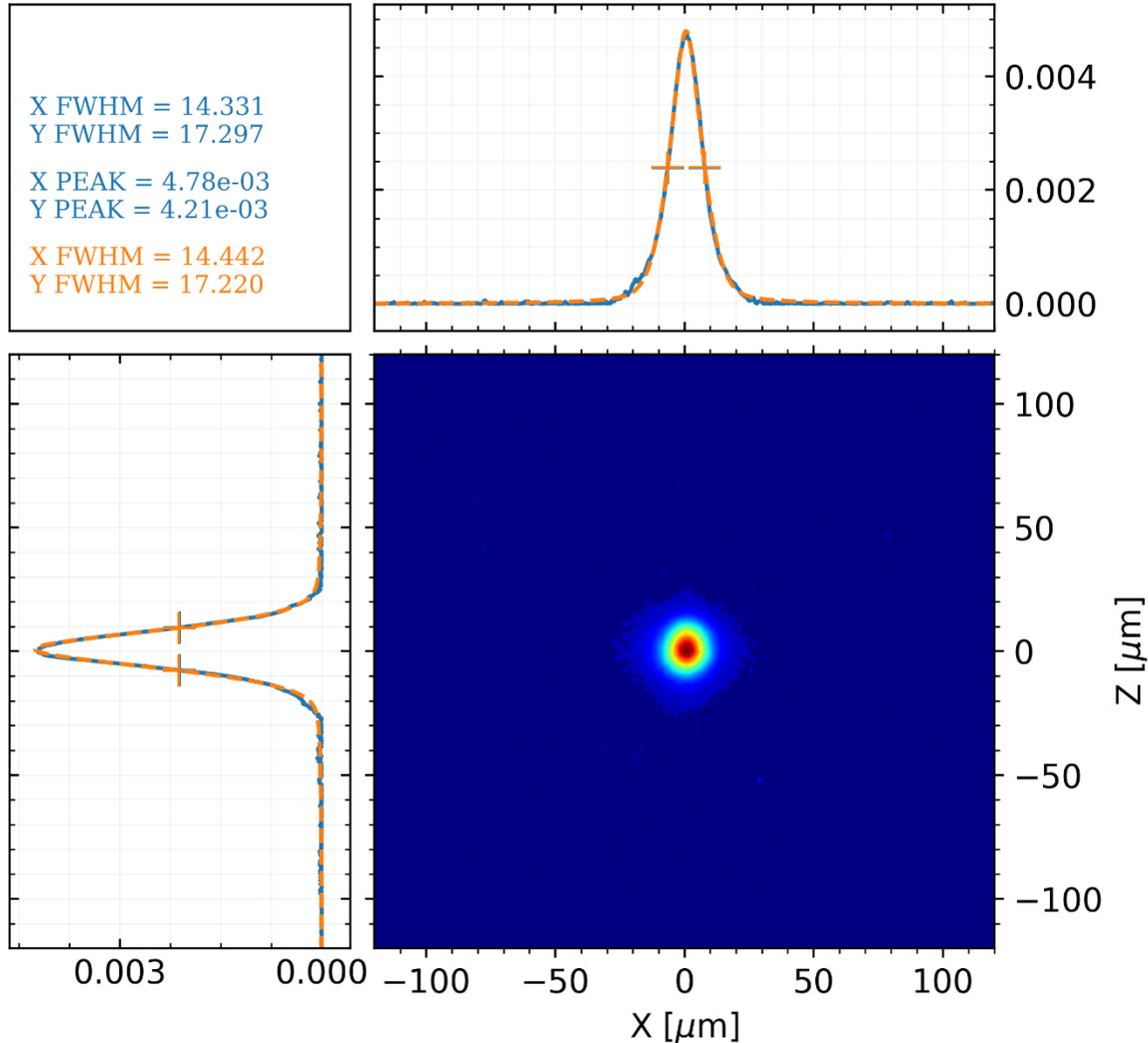
Beam size @ MANACA

Small and adjustable beam size.

Nominal: 10 (H) x 7 (V) μm^2

Current operation: 20 (H) x 20 (V) μm^2

Flux: $6 \cdot 10^{11}$ ph/s/100 mA @ 12.7 keV



Energy range @ MANACA

The energy can be adjusted from 5.6 – 20 keV.

Benzamidine inhibitor bound to bovine trypsin (solved by native SAD).

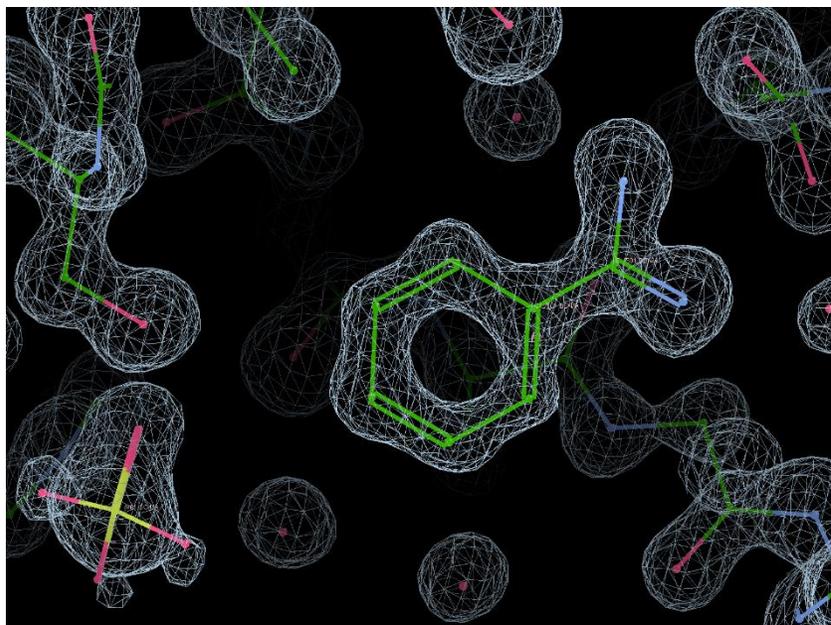
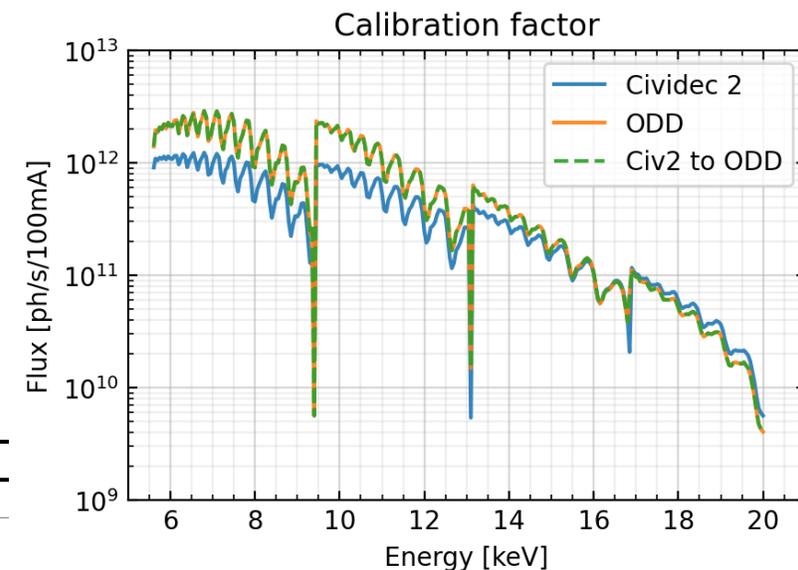


Table 2. Data collection statistics of trypsin.

	Single crystal	Merged (4 crystals)
Energy (keV)	5.627	5.627
Resolution range	43.23 - 2.09 (2.165 - 2.09)	47.26 - 2.09 (2.165 - 2.09)
Space group	P 3 ₁ 2 1	P 3 ₁ 2 1
Unit cell (Å, °) (a=b c, α=β=90° γ=120°)	54.57 106.98	54.57 106.98
Total reflections	178059 (4294)	706448 (17246)
Unique reflections	11180 (867)	11405 (1078)
Multiplicity	15.9 (5.0)	61.9 (16.0)
Completeness (%)	97.81 (78.68)	99.78 (97.82)
Mean I/sigma(I)	33.76 (11.71)	54.10 (17.30)
Wilson B-factor	15.40	15.50
R-meas	0.0706 (0.0918)	0.0870 (0.1181)
CC1/2	0.999 (0.992)	1 (0.993)
Anomalous signal	1.307	1.859

Statistics for the highest-resolution shell are shown in parentheses.

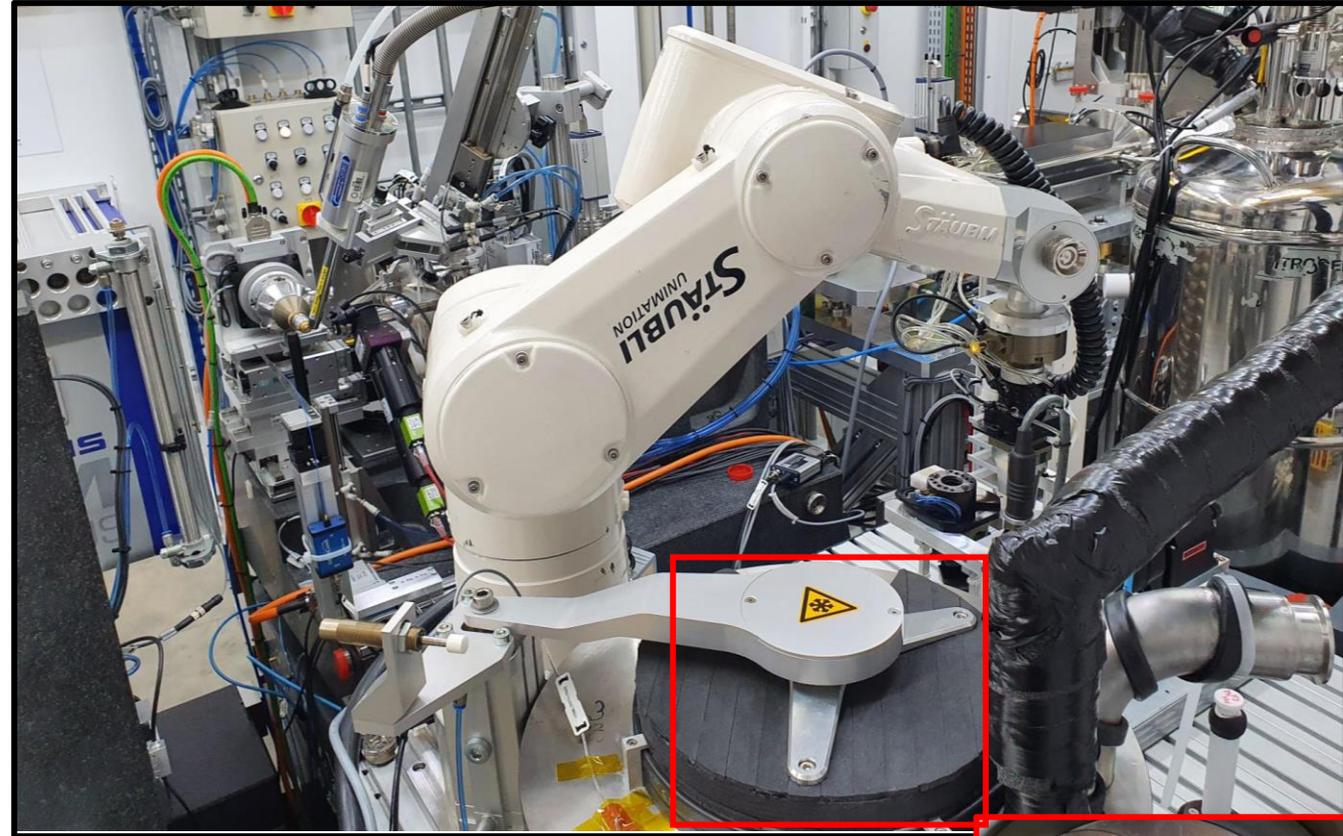


High flux at low energy.

~2x10¹² ph/s/100 mA @ 6-8 keV

Sample Changer @ MANACA

Automatic and fast sample mounting.

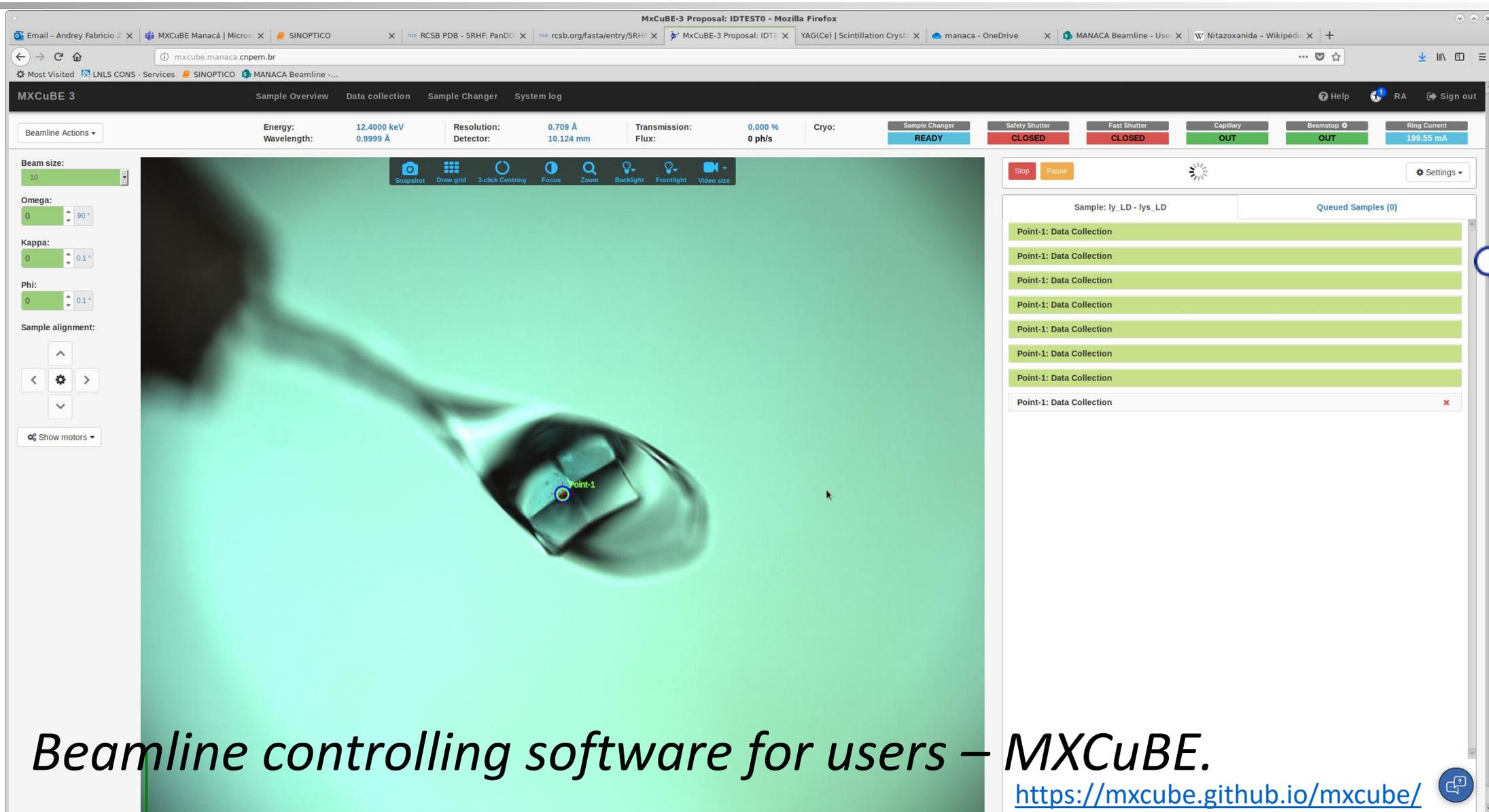


In operation with users since April/2021.

- Capacity for 48 samples (3 Unipucks; SPINE caps).
- Changes a sample in ~50 seconds (unmount/mount).
- Full user control through graphical interface (MXCuBE).



Friendly usage - MXCuBE @ MANACA



MXCuBE-3 Proposal: IDTEST0 - Mozilla Firefox

mxcube.manaca.cnpem.br

Sample Overview Data collection Sample Changer System log Help RA Sign out

Beamline Actions

Energy: 12.4000 keV Resolution: 0.709 Å Transmission: 0.000 % Cryo: READY
Wavelength: 0.9999 Å Detector: 10.124 mm Flux: 0 ph/s

Sample Changer: READY Safety Shutter: CLOSED Fast Shutter: CLOSED Capillary: OUT Beamstop: OUT Ring Current: 199.55 mA

Beam size: 10

Omega: 0 90°

Kappa: 0 0.1°

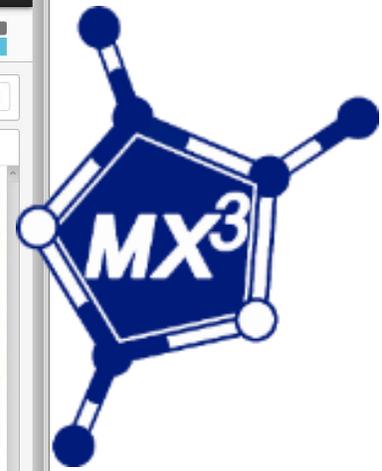
Phi: 0 0.1°

Sample alignment: Show motors

Stop Pause Settings

Sample: ly_LD - lys_LD Queued Samples (0)

- Point-1: Data Collection



Beamline controlling software for users – MXCuBE.

<https://mxcube.github.io/mxcube/>



Data processing - MANACAutoProc

MANACAutoProc Web: interface for data processing.

No ssh connection or HPC setup required. Accessible from any OS through CNPEM's VPN.

MANACAutoProc Web

Display Documentation

Login

Username

Password

Macromolecules Small Molecules

Login

MANACAutoProc Web

Proposal Selection

Go to Home

20240031

Proposal Data for: 20240031

Visualize data/Process new data

Day of Data Acquisition: 06/04/2024

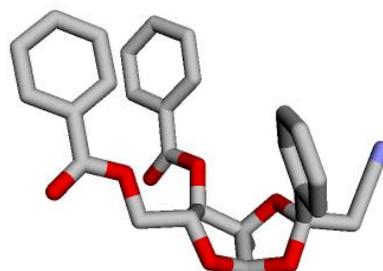
Search by experiment reference

Experiment Reference (Puck ID)	Run Number	Number of Images	Process Status	R-Free	Date/Time of Processing	Actions
CPS-4613-1-01	0	3600	XDS	----	06/04/2024 16:18:39	Copy Log Path Plot Data View Table HTML File Phasing Options Download Main Files Download All Files
CPS-4613-1-01	1	3600	XDS, SAD	----	08/04/2024 18:31:42	Copy Log Path Plot Data View Table HTML File Phasing Options Download Main Files Download All Files
CPS-4613-1-02	0	3600	XDS	----	06/04/2024 16:36:09	Copy Log Path Plot Data View Table HTML File Phasing Options Download Main Files Download All Files

Molecular Structure for CRD005-1-01_0001_run0:

Shelxl Shelxt

Close



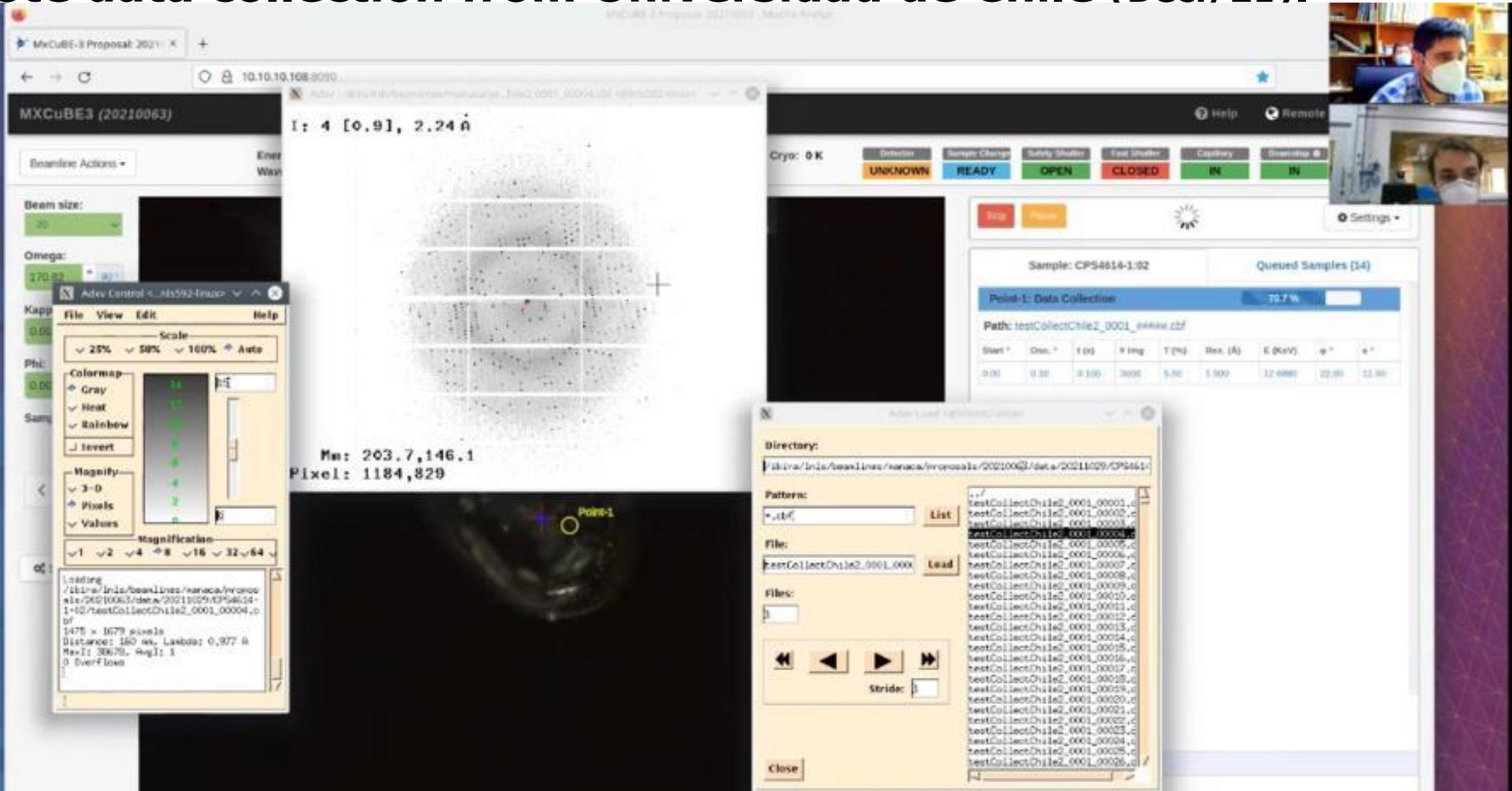
CIF file was found

For protein and small molecules.

<https://mncautoproc-manaca.lnls.br>

Remote Access @ MANACA

Remote data collection from Universidad de Chile (Dec./21).



The screenshot displays the MXCuBE3 (20210063) remote access interface. The central window shows a diffraction pattern with a crosshair and the following data: $\lambda: 4 [0.9], 2.24 \text{ \AA}$. Below the pattern, the coordinates are given as $Mn: 203.7, 146.1$ and $Pixel: 1184, 829$. A 'Point-1' is marked on a lower-resolution image below.

The left sidebar contains 'Beamline Actions', 'Beam size: 20', 'Omega: 170.82', and 'Kappa: 0.00'. A 'Adev Control' window is open, showing 'Scale' (25%, 50%, 100%, Auto) and 'Colormap' (Gray, Heat, Rainbow, Invert) options.

The right sidebar shows the status: 'Cryo: 0 K', 'Detector: UNKNOWN', 'Sample Change: READY', 'Safety Shutter: OPEN', 'Test Shutter: CLOSED', 'Cooling: IN', and 'Overstop: IN'. The 'Sample: CPS4614-1.02' is listed with 'Quoted Samples (14)'. A progress bar for 'Point-1: Data Collection' is at 73.7%. Below is a table of data collection parameters:

Start	End	Time	#img	T (s)	Res. (Å)	E (keV)	ϕ	ω
0:00	0:30	0:100	3000	5.50	1.500	12.0000	22.00	11.00

The bottom window shows a file browser with the directory `/sirius/lnls/beamlines/manaca/proposals/20210063/data/20211029/CPS4614-1.02/testCollectChile2_0001_00004.cbf`. The file list contains numerous files named `testCollectChile2_0001_00001.cbf` through `testCollectChile2_0001_00026.cbf`.

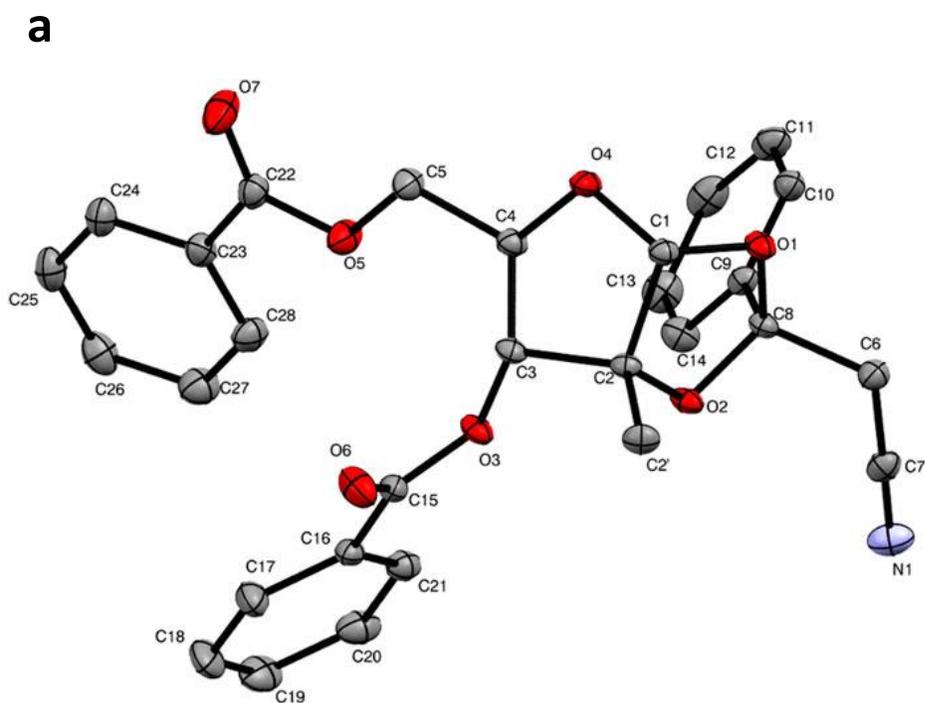
In the top right corner, a video call window shows two participants wearing face masks.



Recent developments

for protein and chemical crystallography

Chemical Crystallography – Small Molecules

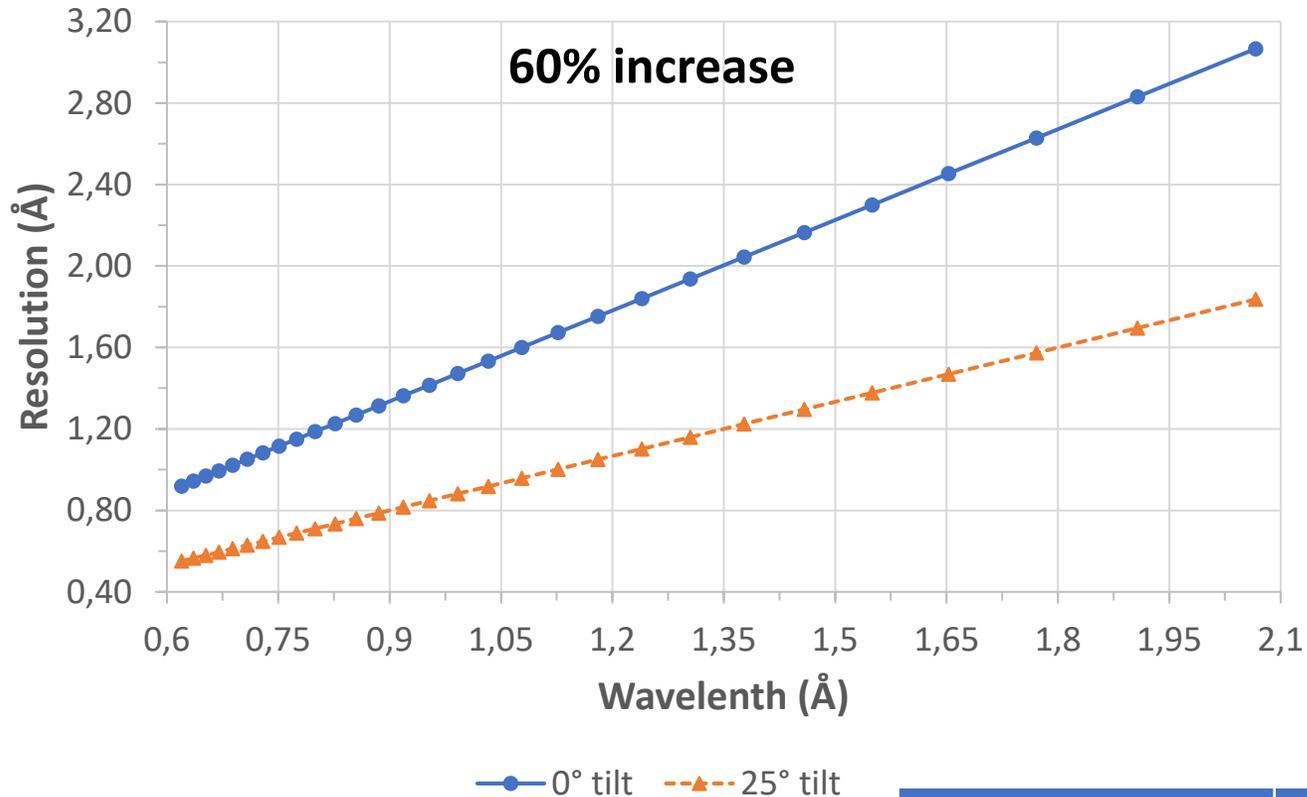


b



a, first structure of a small molecule solved at MANACÁ beamline (Naciuk et al., *Front. Chem.* 11, 2023). **b**, small molecule data collection by advanced users. After an one-week intensive work several high-quality data sets were collected, confirming the potential of MANACÁ beamline for Chemical crystallography Community. From left to right: Prof. Javier Ellena (USP, São Carlos), Prof. Leopoldo Suescun (Udelar, Montevideo), Dr. Andrey Nascimento (MANACÁ, LNLS), Prof. Alejandro Ayala (UFC, Fortaleza) and Prof. Florencia Di Salvo (UBA, Buenos Aires).

Detector tilt: increase 2theta (*commiss.*).



Energy (keV) / Wavel. (Å)	Resolution (Å)	
	@112 mm	<i>tilted</i>
18.5 / 0.65	0.75	<i>0.60</i>
17.462 / 0.71 (Mo-K)	0.80	<i>0.63</i>
8.051 / 1.54 (Cu-K)	1.73	<i>1.37</i>



Room Temperature Macromolecular Crystallography

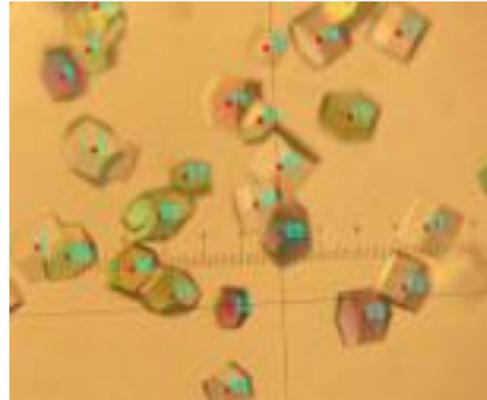
From plate to structure pipeline.



Crystallization



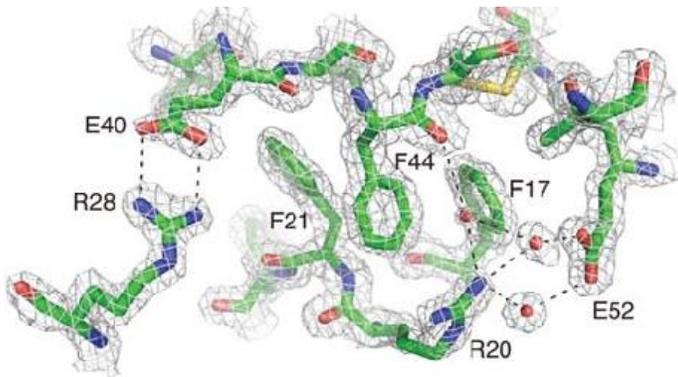
Mount



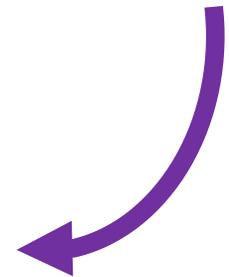
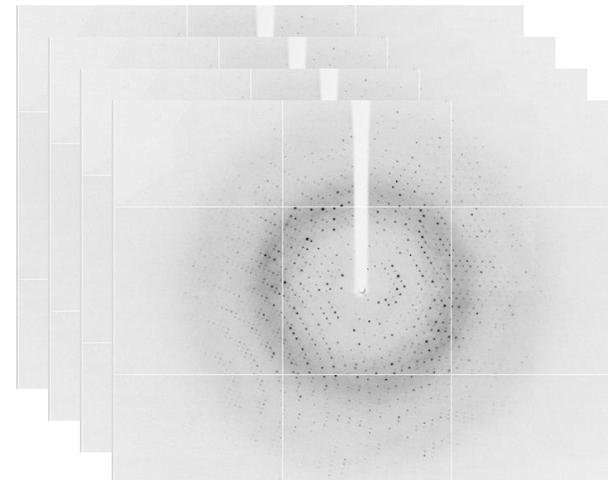
Crystal selection



Data collection
(small wedge, e.g. 10°)



Automatic multi-crystal
data processing



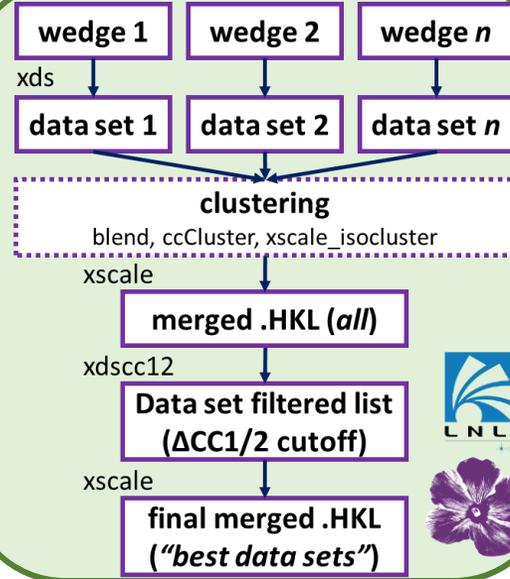
Room Temperature Macromolecular Crystallography

Automatic crystal selection
(deep learning)

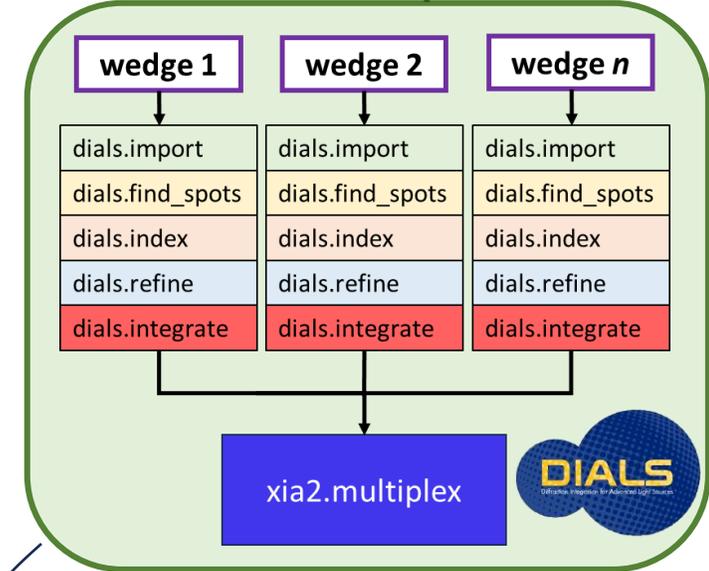
Data collection

Data reduction options

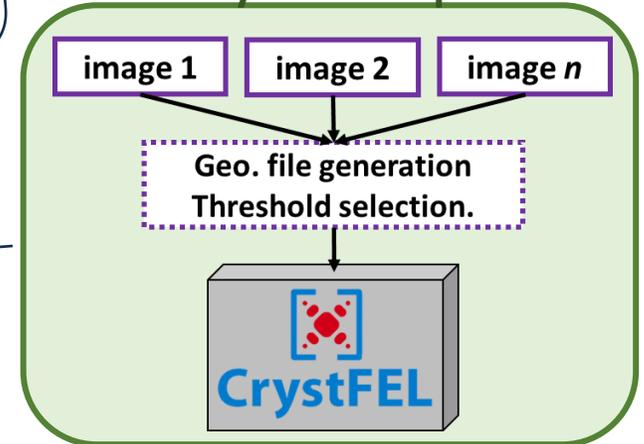
mncautoproc multixtal



xia2.multiplex



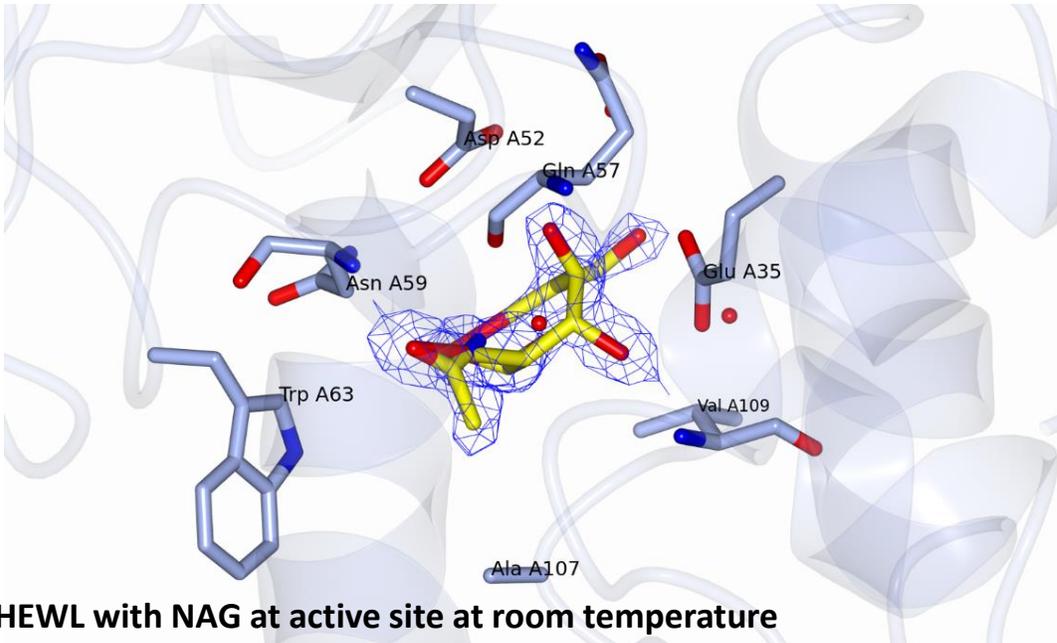
CrystFEL script



.mtz file

Phasing & Refinement

phaser, phenix.refine



HEWL with NAG at active site at room temperature

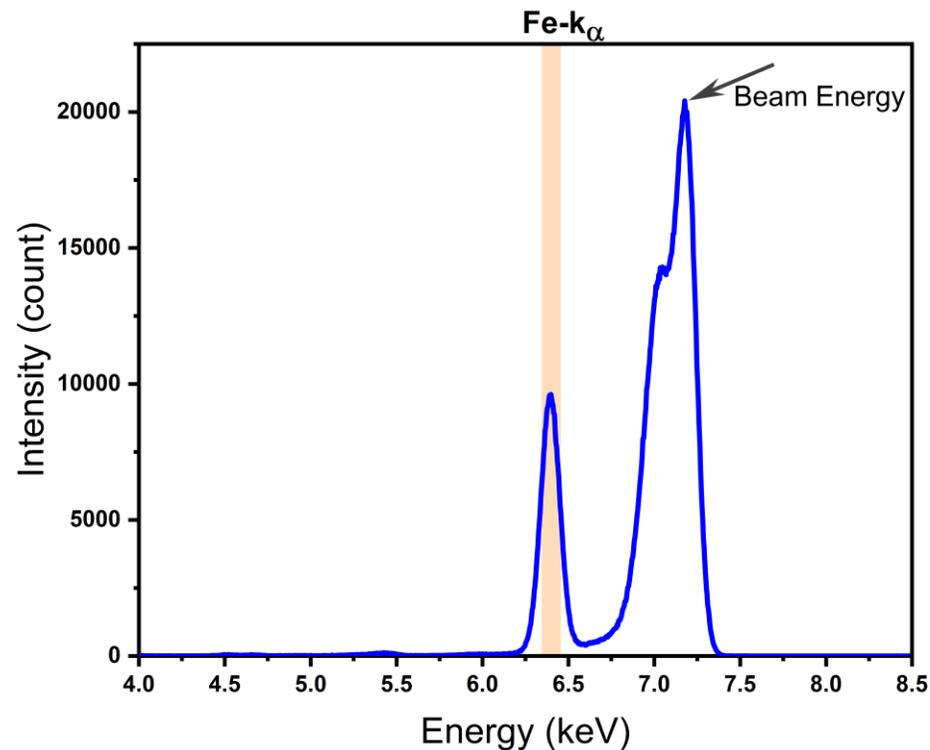
Automatic pipeline!

White et al., J. Appl. Cryst. **45** (2012).
 Gildea et al. Acta Cryst. D **78** (2022).
 Kabsch et al. Acta Cryst. D **66** (2010).

MAD scan and XRF (*under commissioning*). Phasing and element search in the crystal.

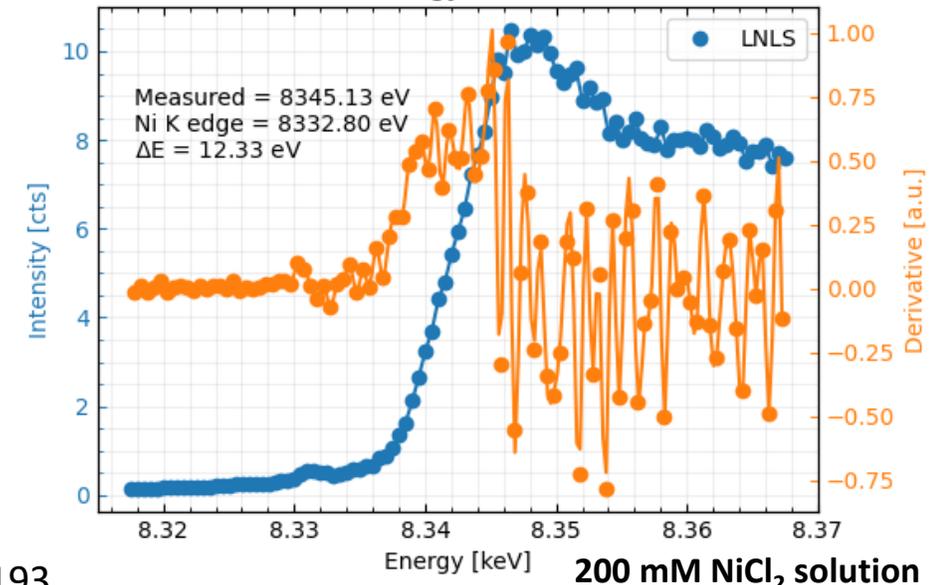


Descarboxylase with Fe - XRF



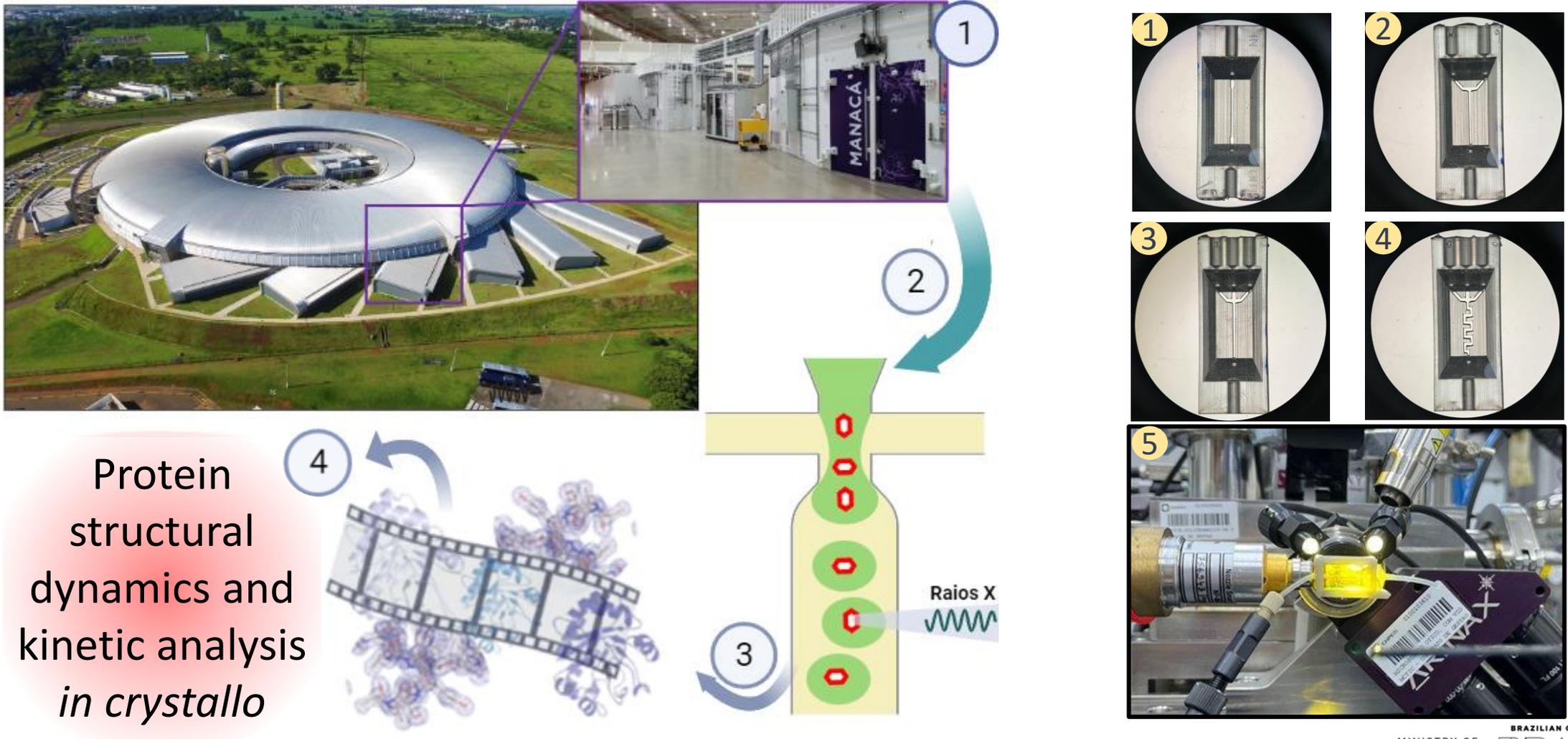
MANACÁ's first fluorescence scan

MAN - Ni-K Energy Scan 2024-03-07



Time-resolved and serial crystallography

Time resolved crystallography for study reaction mechanism of enzymes at atomic level.



1

2

3

4

5

Raios X

4

Protein structural dynamics and kinetic analysis *in crystallo*

Microfluidic sample holders for serial crystallography. *Under development.*



MXCuBE at LNLS/Sirius

Status Report

on behalf of Nicolas Moliterno (COMP)

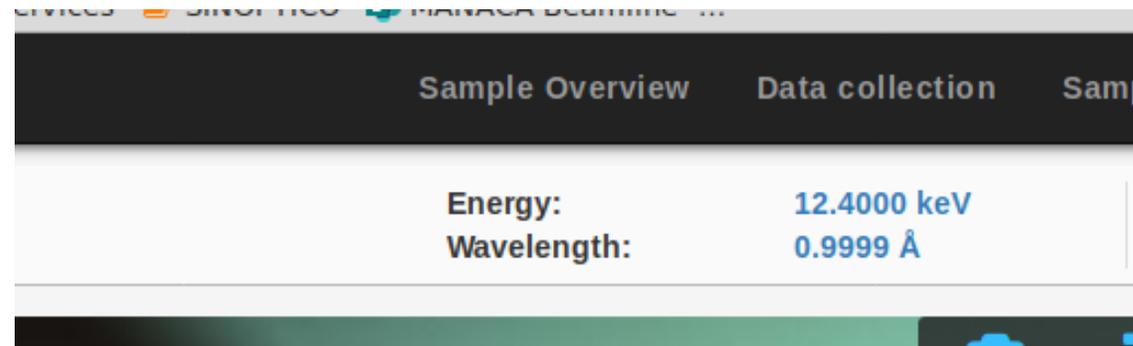
- **Production Version:**
Web MXCuBE3 - Backend and Frontend

- **Development Version:**
Web MXCuBE3, Web MXCuBE4, mxcubecore

- Other Deployments
 - Exploring Bluesky to replace legacy scans relying on older Python versions
- Cybersecurity
 - MXCuBE is accessed via VPN
 - Cybersecurity is managed by the CNPEM-IT Team.

Developments since last meeting

- Refactor: EPICSActuator Class
 - Integrated new devices.
- Update: LNLSEnergy Class
 - Previously, only allowed reading DCM Energy. Now it can set Energy as well.
 - IOC DCM refactor enabled new functionalities related to energy, overcoming previous equipment configuration limitations.



The screenshot shows a control interface with a dark header containing three tabs: "Sample Overview", "Data collection", and "Sample". Below the header, there is a table with two rows of data. The first row shows "Energy:" followed by "12.4000 keV". The second row shows "Wavelength:" followed by "0.9999 Å".

Energy:	12.4000 keV
Wavelength:	0.9999 Å

Developments since last meeting

- BlueSky with MXCuBE in LNLS
 - New class LNLSWorkflow
 - Include WF mesh scan
 - Live view of grid design
 - Integrate a bluesky API for saving metadata
 - Scan control and live monitoring of generated data
 - Helical scan in development

Developments since last meeting

- Refactor: LNLSTransmission Class & Associated Equipment
 - Previously: A Python script controlled transmission actuators, performing calculations using variables like energy.
 - Now: The script is replaced by an EPICS IOC featuring:
 - State Machine with an ALU (Arithmetic Logic Unit).
 - This update replaces Python-script-controlled equipment within MXCuBE, leaving only scans, post-processing scripts, or motor subroutines.
- Update: LNLSDetDistMotor Class
 - With the granite base update for the detector, movements are now handled by kinematics, replacing the real motor.

Plans for the next six months

- Update scan routines
- Integrate new equipment (e.g. mini-kappa, det. tilt), update of LNLS class files
- Update LNLSCollect
- Test MXCuBE 4/5 with new scan routines (bluesky).

Beamline plans for near future

- Integrate RT data collection.
- Implement a web diffraction image viewer (Braggy, h5web, ?).
- Improve automatic data processing at MXCuBE (currently only data reduction is performed).
- Implement characterization software (EDNA/DOZR).
- Start the implementation of a LIMS (ISPyB, ICAT, ?).

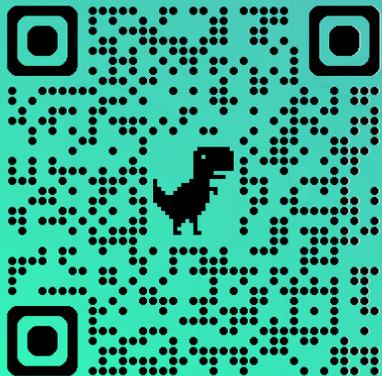
THANK YOU!

Andrey Nascimento
andrey.nascimento@lnls.br

<https://lnls.cnpem.br/facilities/manaca-en/>

GRAZIE!

OBRIGADO!



CNPem
Brazilian Center for Research
in Energy and Materials

MINISTRY OF
SCIENCE TECHNOLOGY
AND INNOVATION

