





# MXCuBE @ MAX IV: Status Report

Johan Unge

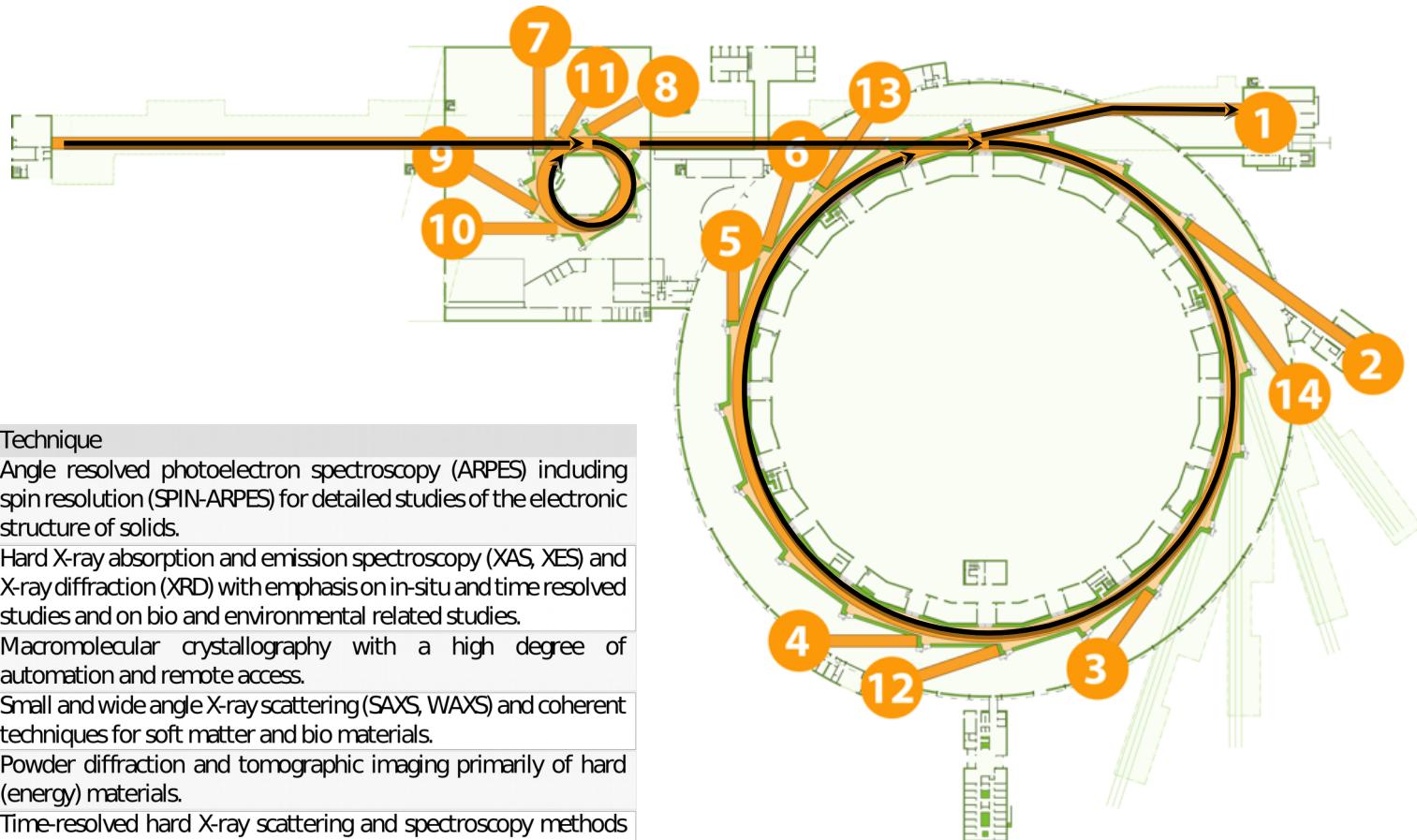
January 31, 2018



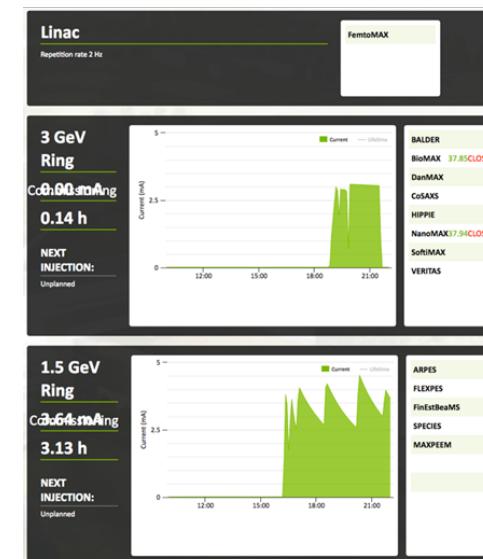
# 1 Linac

## 2 Rings

### 15 beamlines



Beamline	Accelerator	Technique
ARPES	7 1.5 GeV	Angle resolved photoelectron spectroscopy (ARPES) including spin resolution (SPIN-ARPES) for detailed studies of the electronic structure of solids.
Balder ★	3 3.0 GeV	Hard X-ray absorption and emission spectroscopy (XAS, XES) and X-ray diffraction (XRD) with emphasis on in-situ and time resolved studies and on bio and environmental related studies.
BioMAX ★	4 3.0 GeV	Macromolecular crystallography with a high degree of automation and remote access.
CoSAXS	12 3.0 GeV	Small and wide angle X-ray scattering (SAXS, WAXS) and coherent techniques for soft matter and bio materials.
DanMAX	14 3.0 GeV	Powder diffraction and tomographic imaging primarily of hard (energy) materials.
FemtoMAX ★	1 Linac	Time-resolved hard X-ray scattering and spectroscopy methods for studies of ultrafast processes
FinEstBeams	8 1.5 GeV	Electron spectroscopies and luminescence methods for studies of low density matter and solids.
FlexPES	11 1.5 GeV	Soft X-ray spectroscopies for studies of low density matter and solids.
HIPPIE ★	6 3.0 GeV	Near ambient pressure photoelectron spectroscopy on solids and liquids.
MAXPEEM	10 1.5 GeV	Aberration corrected photoelectron microscopy for investigation of surfaces and interfaces.
NanoMAX ★	2 3.0 GeV	Imaging with spectroscopic and structural contrast techniques and nanometre resolution.
SoftiMAX	13 3.0 GeV	Scanning transmission X-ray microscopy and coherent imaging methods.
SPECIES	9 1.5 GeV	Resonant inelastic X-ray scattering (RIXS) with high resolving power and near ambient pressure photoemission.
VERITAS ★	5 3.0 GeV	Resonant inelastic X-ray scattering (RIXS) with unique resolving power and high spatial resolution.

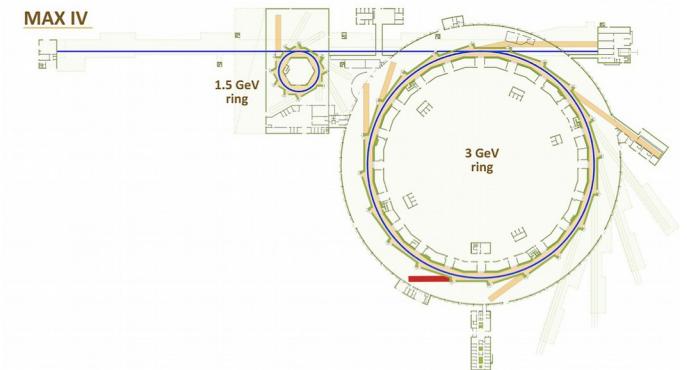


**Linac:**  
Injector 1.5 & 3 GeV & SPF  
*Injects both rings & delivers light to FemtoMAX*

**3 GeV:**  
200 mA, >5 Ah  
≈ (340±30) pm·rad  
≈ 8.5 mA single bunch  
*Delivers light to users*

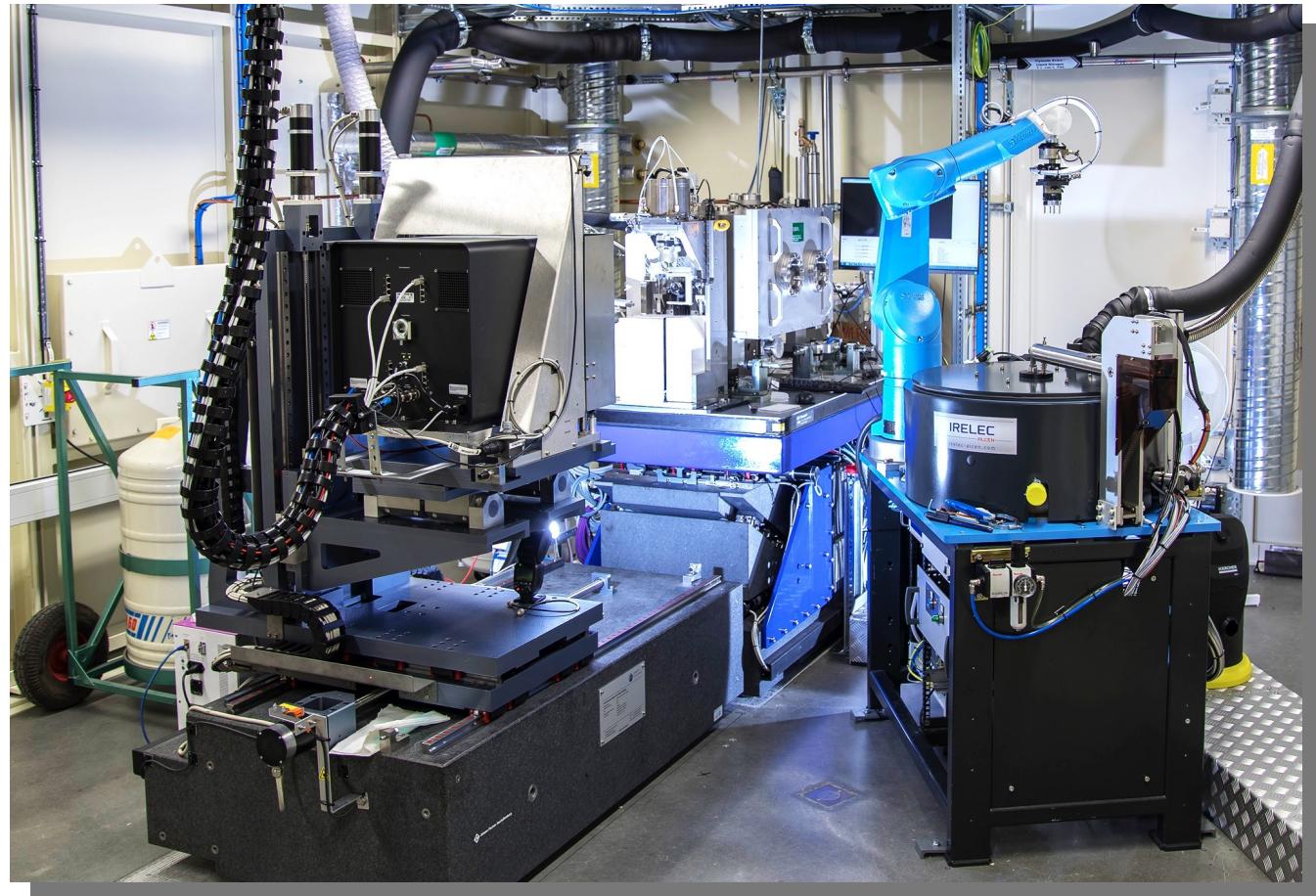
**1.5 GeV:**  
< 200 mA  
*Commissioning*

# BioMAX experimental station



## Experimental environment

- MD3 micro-diffractometer
- Eiger 16M hybrid pixel detector
- ISARA sample changer
- HCLab humidifier
- Beam Condition Unit incl. XBPM
- Amptek fluorescence detector

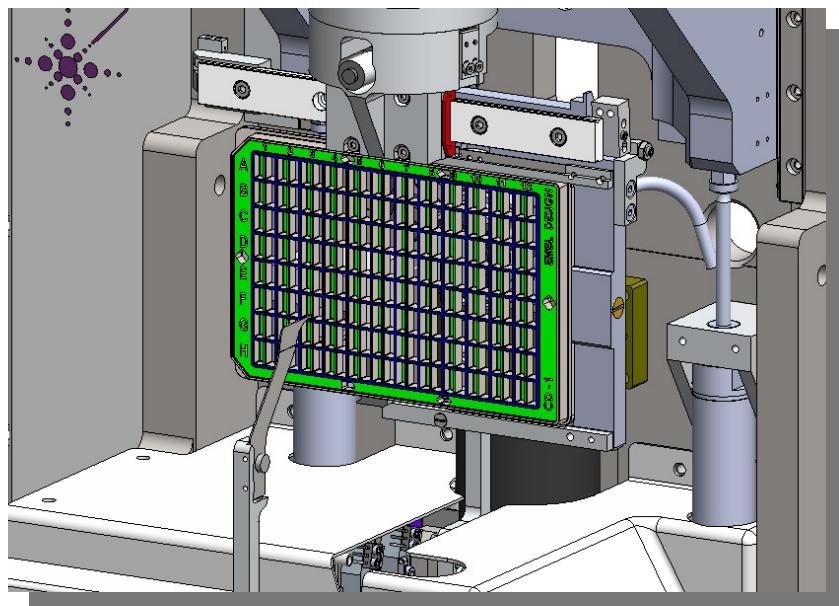


BioMAX experimental station

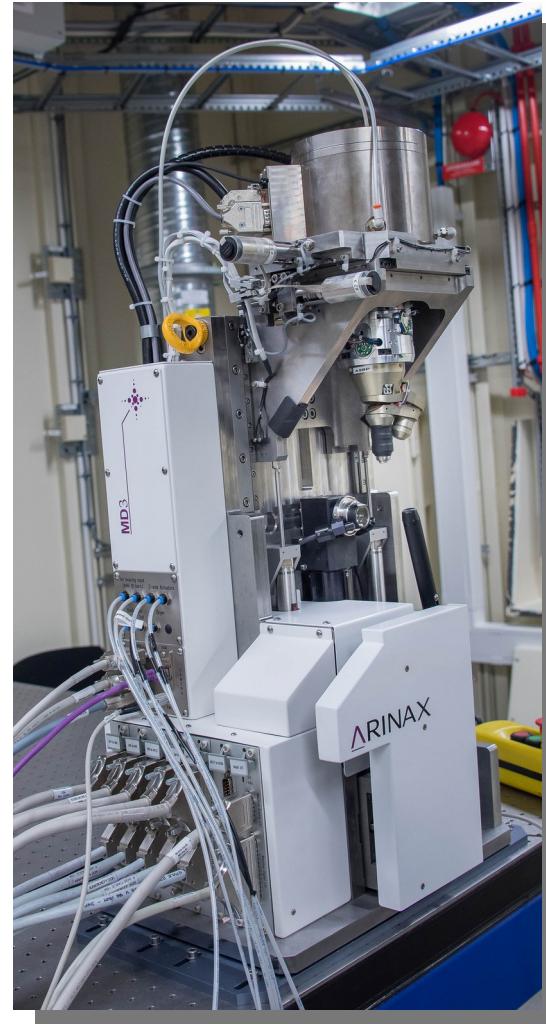
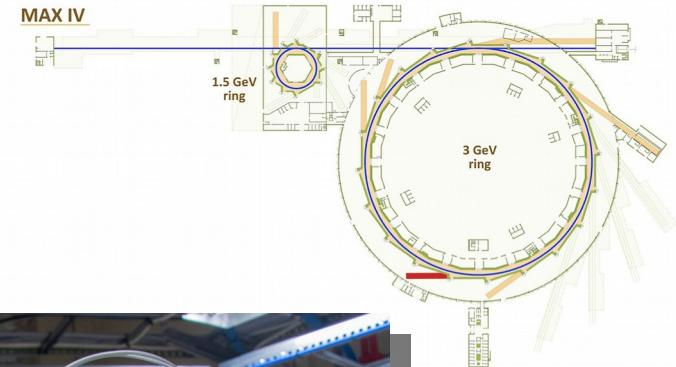
# Goniometry

## MD3 diffractometer:

- Ultra precise Omega-axis
  - Sphere-of-confusion  $r=100$  nm
  - Max. speed 800 deg/sec
- MK3 Mini-kappa goniometer
- Improved on-axis-microscope
- Crystallization plate holder



MD3 plate holder



MD3 at BioMAX experimental hutch

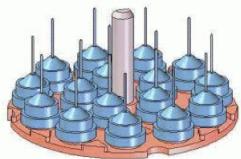
# Sample changer

## ISARA sample changer:

- Dewar capacity
  - 100 samples in SPINE pucks
  - 304 samples in UniPuck
- 4 crystallization plates
- 18 sec sample transfer time



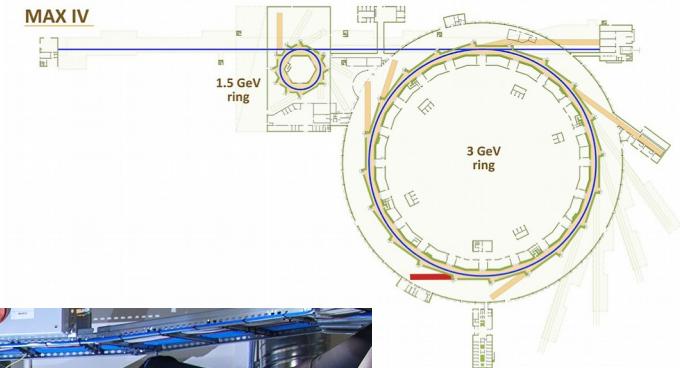
UniPuck



SPINEPuck

## Status

- Ice formation issues with new design
- Currently Unipuck is working
- Integrated into mxcube3, operation, maintenance page and hwobj

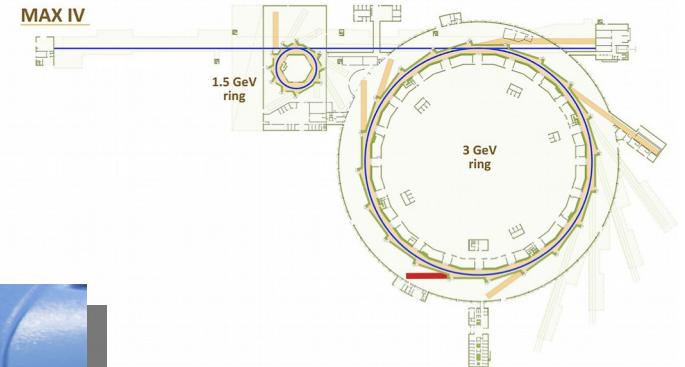


ISARA sample changer (IRELEC)

# HCLab - Room temperature



HCLab facility operational



First Si chip operation at BioMAX,  
(B. Vestergaard, UC)

# MXCuBE3

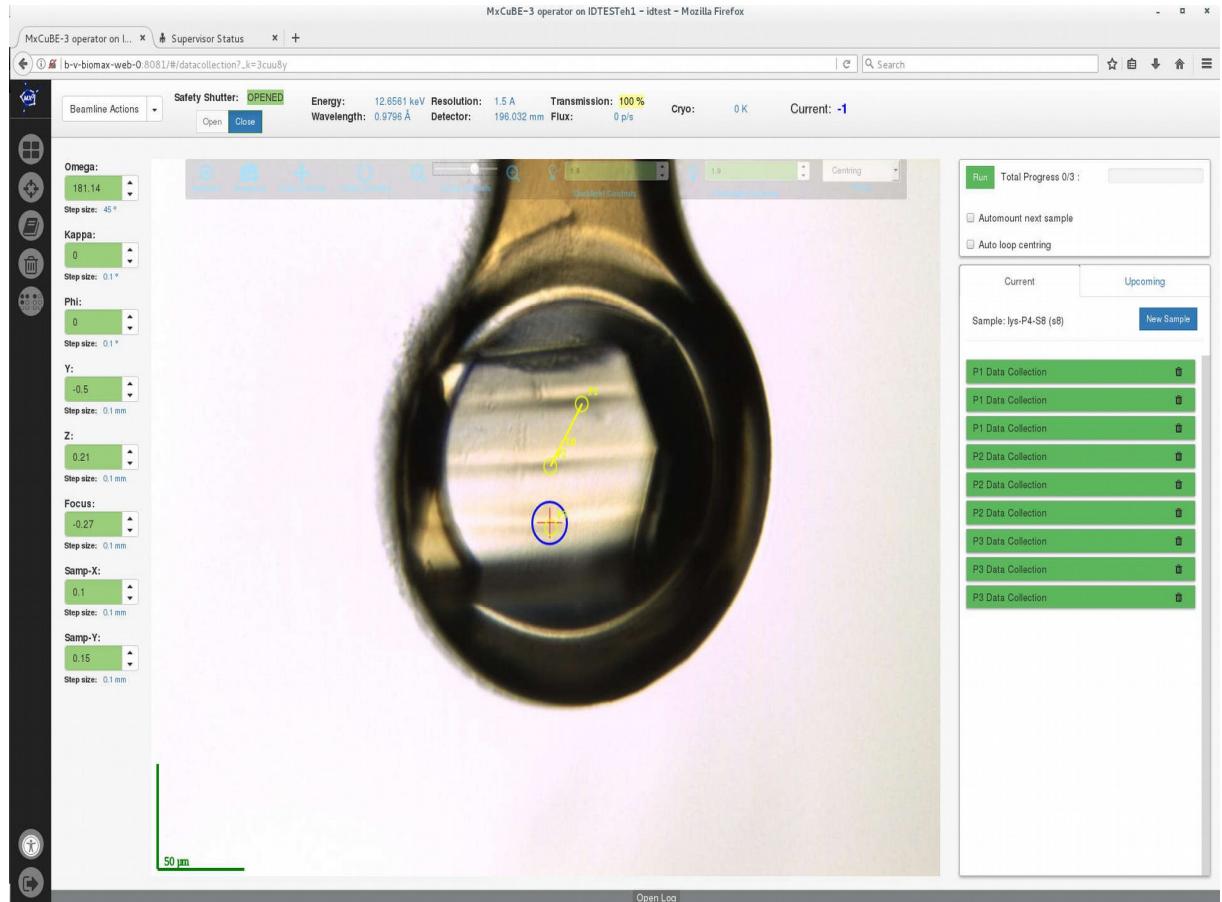
## MXCuBE3 data collection view

- *Current Status, major features*

- Sample Centering
- Standard Oscillation
- Characterization
- Helical Scan
- Sample Changer
- ISARA adaptation for Tango device and HWO
- Mesh Scan
- In Situ

- *In progress and todo*

- Stability maturation
- XRF, XANES
- Parallel processing for spot finding for MESH scan
- ISPyB and SDM integration



- *Advantage*  
Joint collaboration with ESRF
- *Challenges*

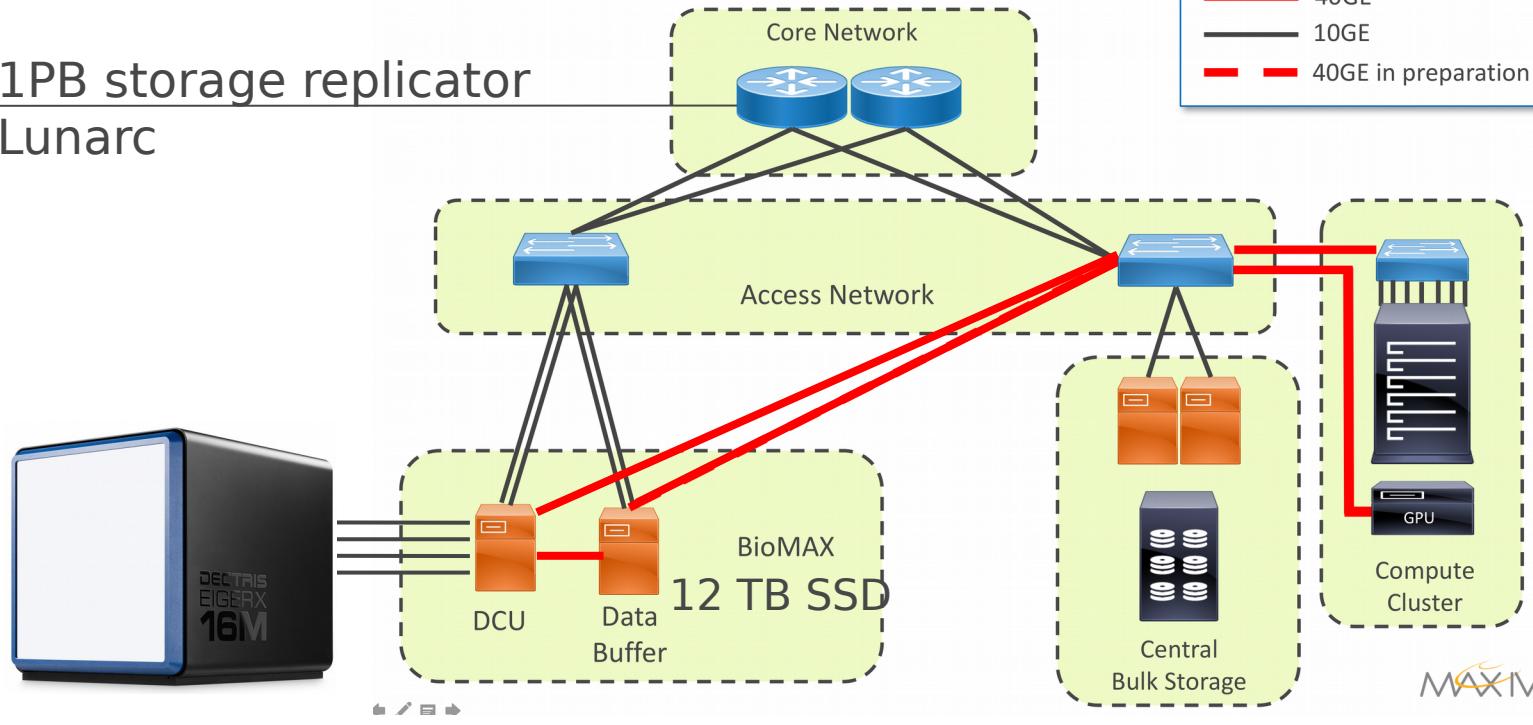
Software stability, user-friendliness and integration with various hardware + software

# IT environment

## Eiger 16M IT-environment

1PB storage replicator

Lunarc



Courtesy of Artur Barczyk

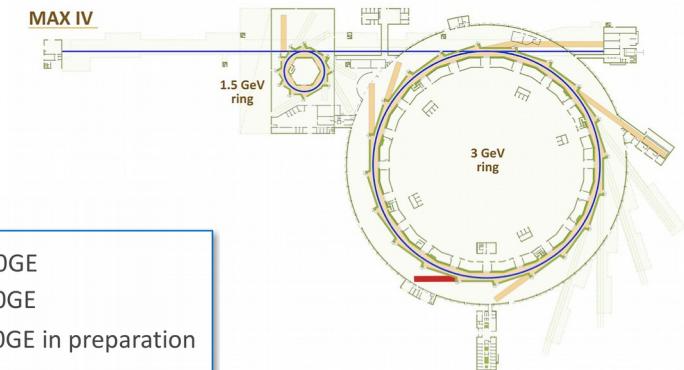
250 TB installed  
GPFS file system

~ 1100 CPU cores

60 nodes 2017

25 dedicated to BioMAX

- Alternative data retrieval via Globus ([www.globus.org](http://www.globus.org))
- DUO (proposal management) in place and will be used soon
- Account and data management system (SDM) → talk by Fredrik



# Data reduction and performance

- Three pipelines currently used
  - fast\_dp, autoPROC, BioMAX\_Pipeline
- System to install all MX software on cluster, PreSTO, collaboration with National Supercomputer Centre and Lunarc.
  - Thinlinc to create simple interface to cluster
  - XDS and central GPFS file system? XDS makes many small I/O operations...testing alternatives

MAX IV, GPFS system (1)	Lunarc, Same blades type (1)	4 Nodes, NFS mount 8 XDS-jobs 24 processes (2)	8 Nodes NFS mount 16 XDS-jobs 24 processes (2)
134.0 sec	52 sec	56.2 sec	45.6 sec

(1) 900 images, thaumatin, 0.1 deg/image, (2) 900 images, Dectris data

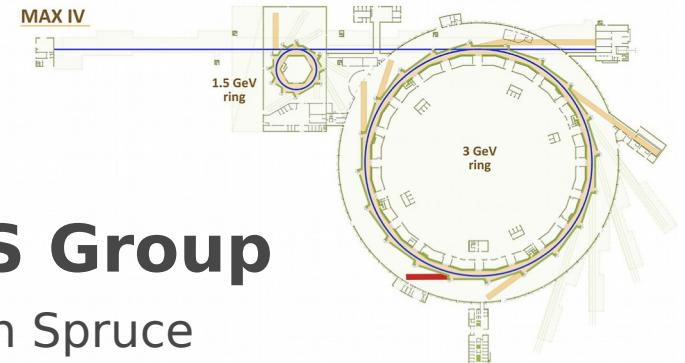
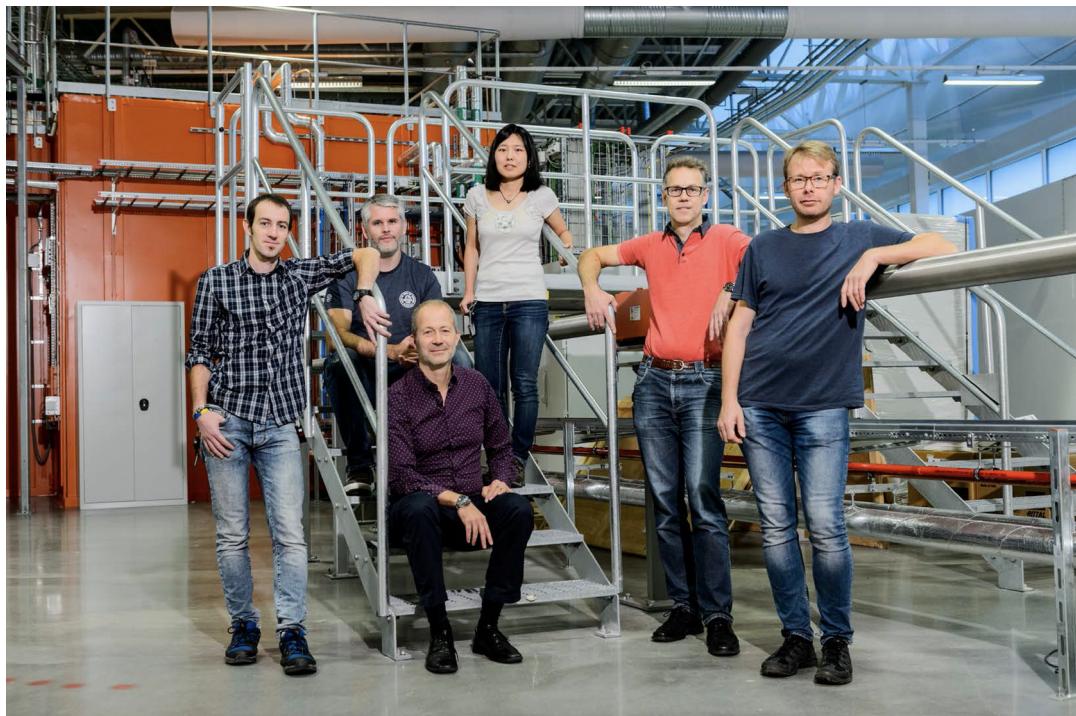
# Outlook

- Remote operation using web based MXCuBE. This will be critical during 2018. Involves MAXIV IT systems.
- ISARA sample changer: all functionalities and a lot of testing -> ready to users!
- Remaining equipment to integrate...
- Extend beamline capabilities (energy tuneability, beam stability feedback systems, MESH scan, XRF, minikappa...)

# Acknowledgement

## MX Group

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Jie Nan  
Thomas Ursby  
Johan Unge  
Roberto Appio  
Ross Friel



## KITS Group

Darren Spruce  
Mikel Eguiraun  
Fredrik Bolmsten  
Antonio Milán-Otero  
Artur Barczyk  
Zdenek Matej

## User Office

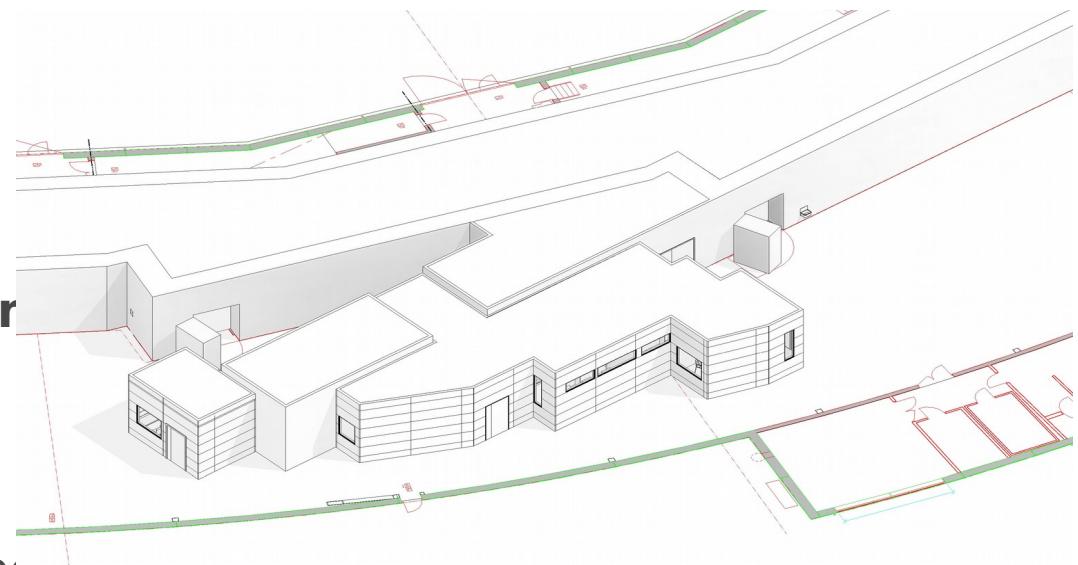
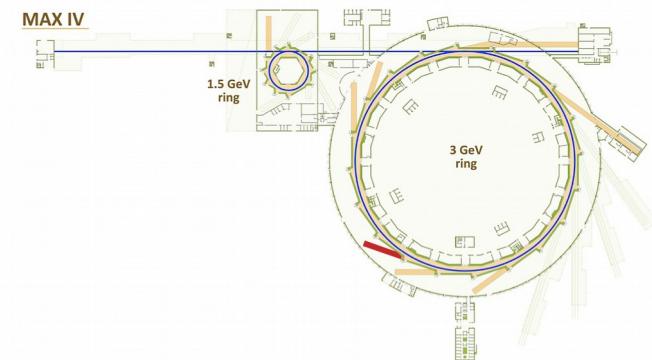
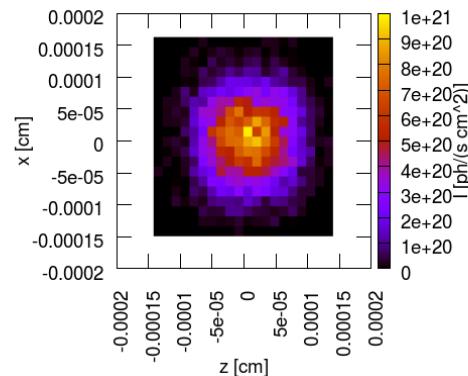
Marjolein Thunnissen

## ESRF

Matias Guijarro  
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Daniele De Sanctis  
Antonia Beteva

# MicroMAX

Thomas Ursby: email: thomas.ursby@maxiv.lu.se



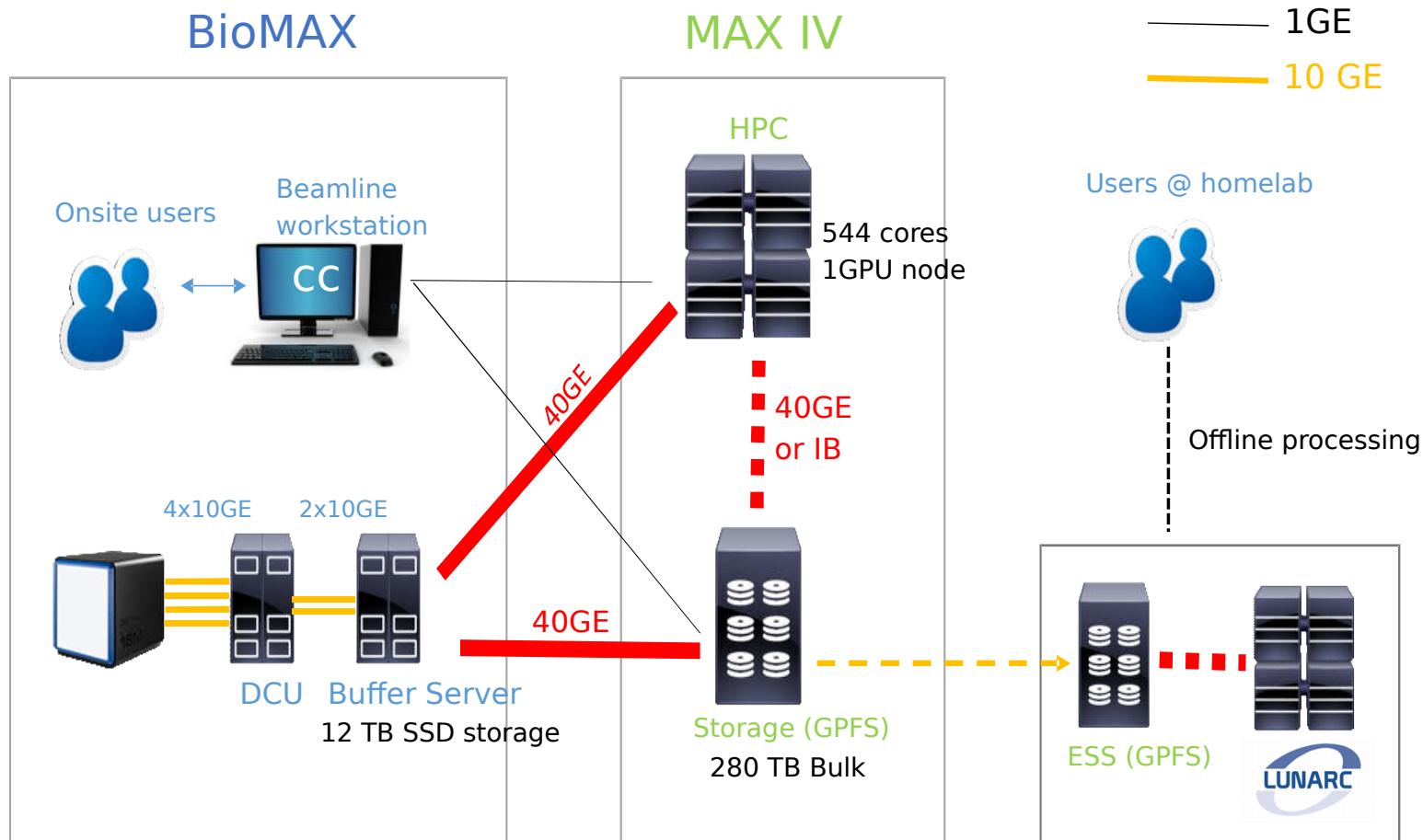
## Plans for the second MX beam

- Microfocus beamline
- **$1 \times 0.7 \mu\text{m}^2$**  beam at sample
- Photon flux  **$10^{13} - 10^{15}$  phot/sec**
- Traditional setup (goniometry, sample environment)
- Exploratory setup (serial crystallography, fixed target single shot)
- Optimal source for most demanding projects (large complexes, membrane proteins)

Status: funded by Novo Nordisk Foundation



# BioMAX - IT Infrastructure



# Data reduction and performance

- Automatic processing
  - Fast\_dp
  - autoPROC
  - Biomax\_pipeline

	HPC - 4 nodes (24 cores, CPU E5-cores, CPU E5- 2650 v4 @ 2.20GHz)	HPC - 8 nodes (24 cores, CPU E5-cores, CPU E5- 2650 v4 @ 2.20GHz)	BufferServer 2643 v4 @ 3.4GHz)	Kay32 cpus, HPSLS - 4 nodes cores, E5-269 @2.70 GHz)	
Time*	53s	36s	136s	120 s	76.6 s

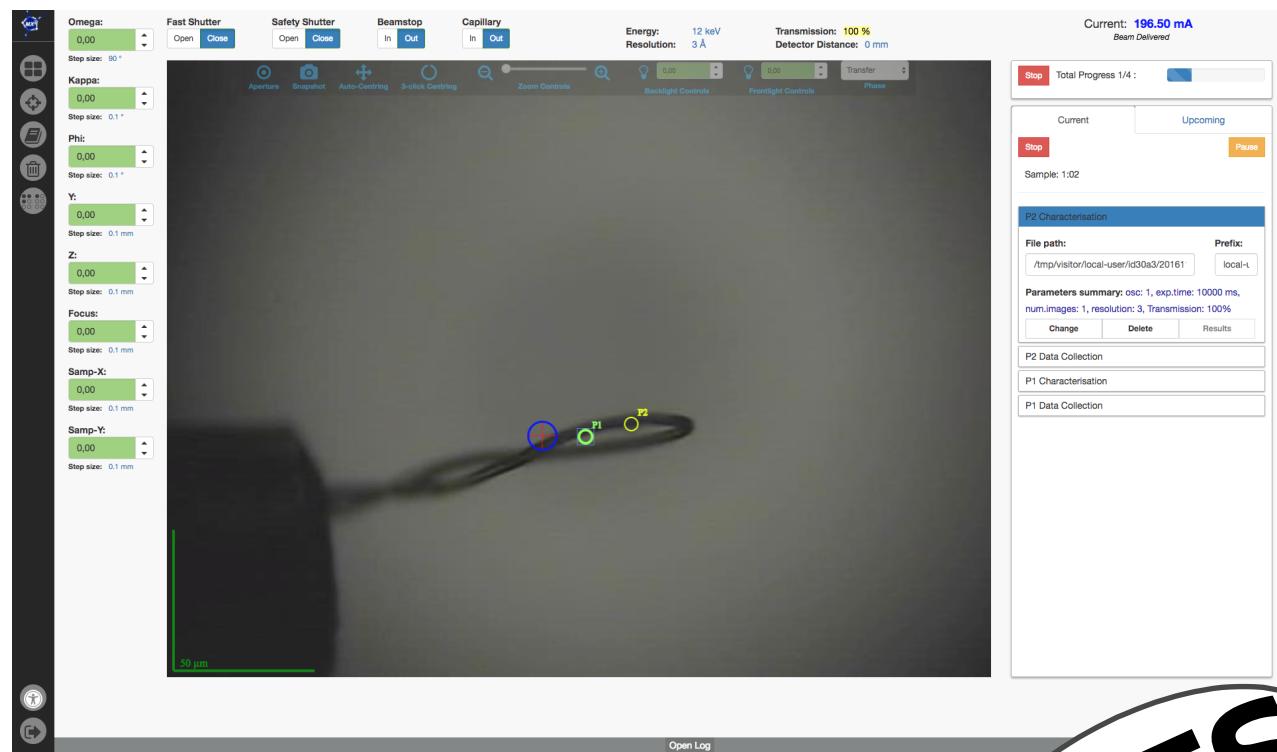
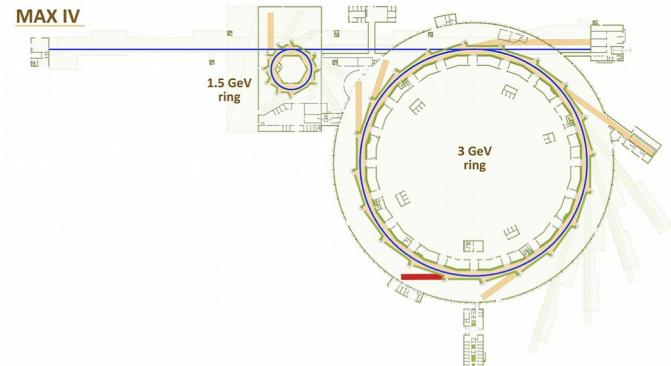
EIGER\_16M\_Nov2015.tar.bz2, 900 images in 9 containers, 0.1 osc, from Dectris website

- Run XDS with SLURM on HPC

[https://github.com/JieNanMAXIV/xds\\_slurm](https://github.com/JieNanMAXIV/xds_slurm)

# MXCuBE3

- Current Status, major features
  - Sample Centering
  - Standard Oscillation
  - Characterization
  - Helical Scan
  - Sample Changer
  - Mesh Scan
- Todo
  - Stability maturation
  - XRF, XANES
- Advantage
  - Joint collaboration with ESRF
- Challenges
  - Integration with of various hardware, software,
  - Software stability and user-friendliness



MXCuBE3 data collection view

KITS

# MXCuBE3 at BioMAX

The screenshot shows the MXCuBE3 software interface running in Mozilla Firefox. The main window displays a micrograph of a sample with several yellow and blue markers indicating beam position and orientation. On the left, there are controls for Omega, Kappa, Phi, Y, Z, Focus, Samp-X, and Samp-Y, each with a slider and step size indicator. The top bar shows beamline actions (Safety Shutter: OPENED), energy (12.6561 keV, 0.9796 Å), resolution (1.5 Å, 196.032 mm), transmission (100%), cryo status (0 K), current (-1), and detector flux (0 p/s). The right side features a 'Run' button, a progress bar for 'Total Progress 0/3', and a list of tasks: 'Automount next sample' and 'Auto loop centring'. Below this is a 'Queue' section with 'Current' and 'Upcoming' tabs, showing a list of data collections for sample 'lys-P4-S8 (s8)'. The bottom of the interface includes a '50 μm' scale bar and an 'Open Log' button.

Manual mounting  
Over 40 samples, 500GB / 8h shift

## Main features

- Sample Video
  - 3 click Centering
  - 2D Centring
  - Auto-Loop Centring
- MD3 controls
  - Motors
  - Zoom
  - Light
  - phase
- Data Collection
  - Standard collection
  - Characterization
  - Helical Scan
- Processing
  - Launched on HPC
- Queue