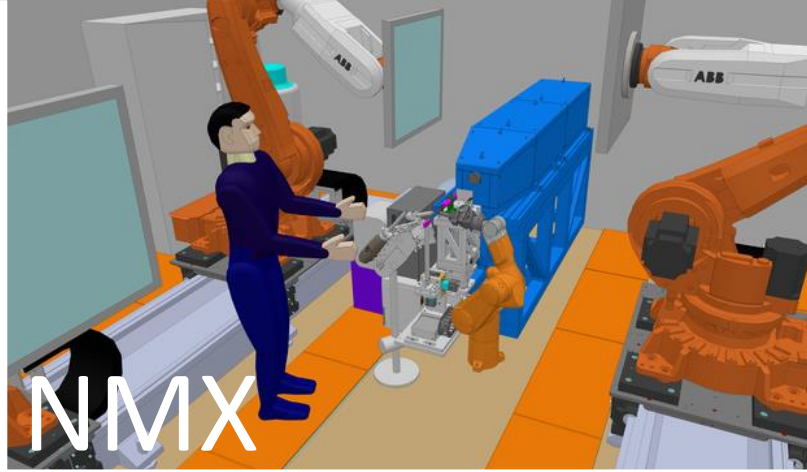
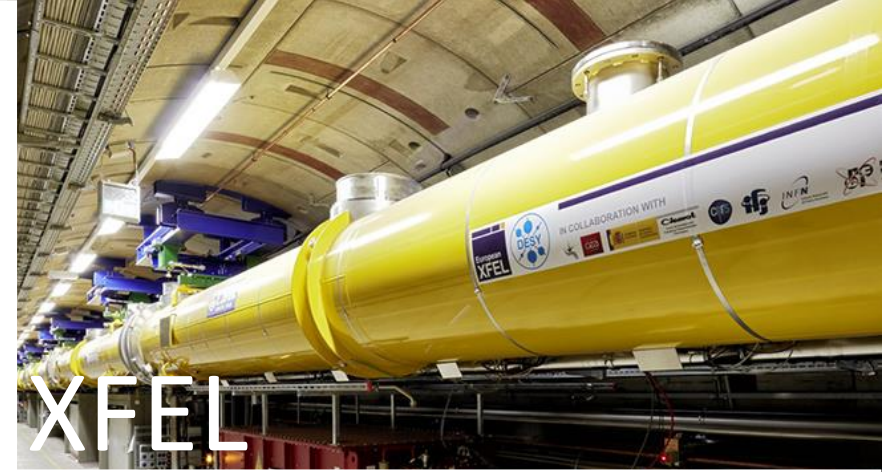




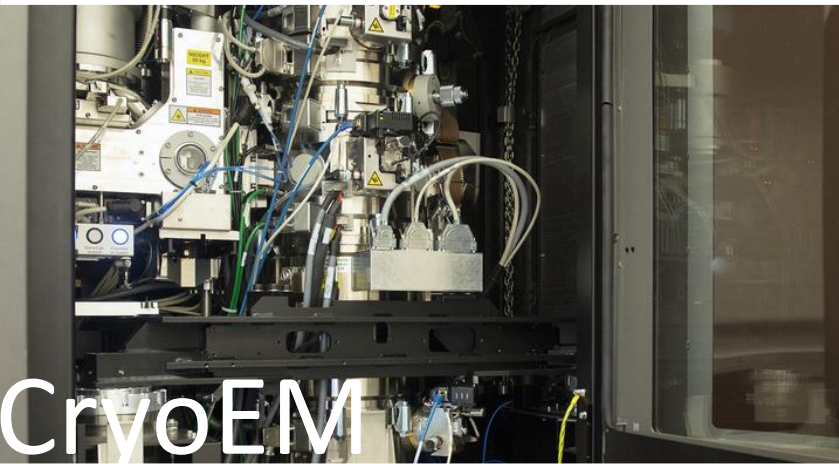
NMR



NMX



XFEL



CryoEM



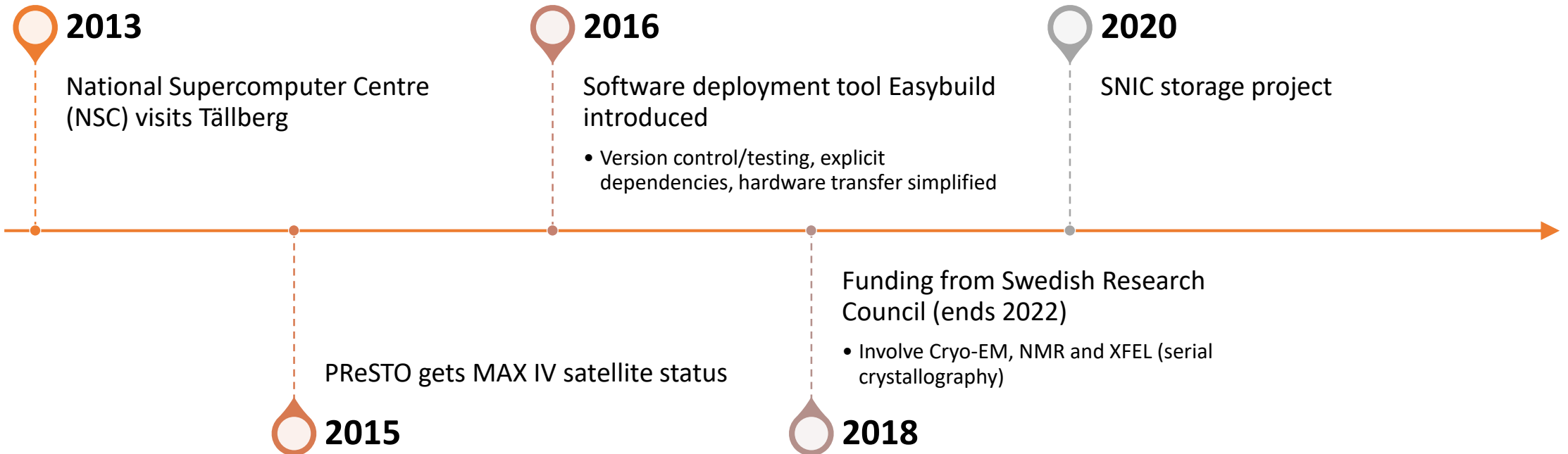
MX



PRestO – structural biology software in HPC environment

Status report June 2021

PReSTO history



Software in PReSTO – June 2021



MX (XDS, CCP4, PHENIX, GlobalPhasing, PyMOL, ChimeraX, USF)

tbd: Python2->Python3 transfer, DIALS3, CCP4 v.7.1, CSD, automated testing



XFEL (CrystFEL, Cheetah, nXDS)

tbd: cctbx-xfel, DatView



Cryo-EM (Scipion, Relion, CisTEM, EMAN2, Gctf, Gautomatch, Motion2Cor, CTFFIND)

tbd: CryoSPARC, CryoDRG, eTomo, Dynamo, EMClarity, PEET,..



NMR (NMRPipe, MddNMR)

tbd: CS_Rosetta, Catia, PINT, CYANA, FLYA, ARIA,..

PreSTO usage June 2021

	MX	XFEL	CryoEM	NMR
infrastructure	MAX IV	MAX IV	SciLifeLab	SNC
community	YES	YES	NO	NO
reason	available	available	data transfer	too few sw

MAX IV



LUNARC



NSC Berzelius



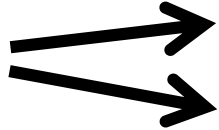
NSC Tetralith

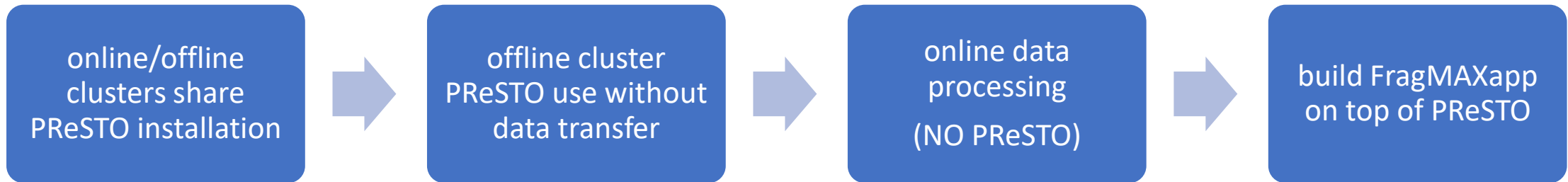


Hardware with PReSTO today and tomorrow



PReSTO at MAX IV

MAX IV cluster divided into  online@beamtime
offline@home



NSC Tetralith (2018) vs Berzelius (2021) GPU nodes



NSC	Nodes	CPU type	CPUs	RAM	GPU	/scratch/local
Tetralith	170	2x Intel Xeon Gold 6130	32	96 GiB	1 NVIDIA® T4	2 TB NVMe SSD
Berzelius	60	2 AMD Epyc™ 7742	128	1 TB	8 NVIDIA® A100 Tensor Core	15 TB NVMe SSD

Gitlab and easybuild simplifies moving PReSTO to new hardware

Cryo-EM PReSTO at Berzelius

Researchers not using AI/ML methods may apply provided

- ✓ Their project show efficient NVIDIA GPU use by their software
- ✓ NSC support for non-AI/ML workflows will only be provided if time allows
- ✓ Outside of the focus area of Berzelius, no special compute environment or software are supported by NSC
- ✓ The researcher must be able to manage their own software stack

<https://www.nsc.liu.se/support/systems/resource-allocations-on-berzelius/>



PReSTO support and training...

PReSTO homepage(MX only)

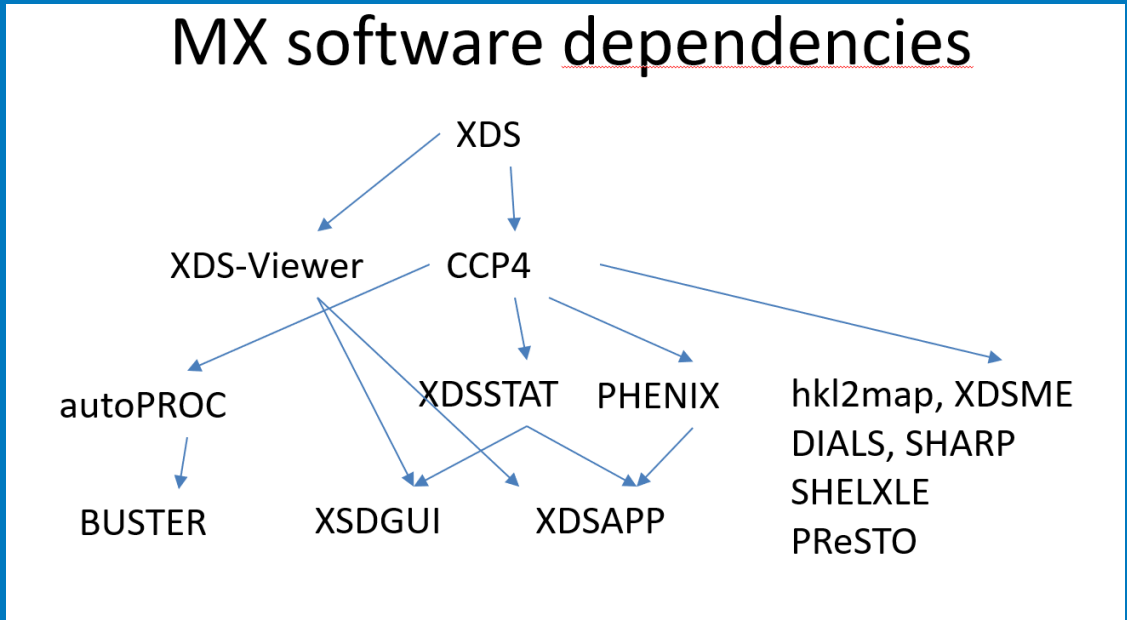
- <https://www.nsc.liu.se/support/presto/>
- MX software and CrystFEL startup scripts
- Phenix GUI slurm configuration
- Login vs compute nodes

MX trainee requires

- Own data to analyze
- User account on SNIC/MAX IV cluster with PReSTO
- Multiple 2-hour zoom sessions until saturation/satisfaction
- <https://www.nsc.liu.se/support/presto/MX-PReSTO%20training/>

Trello for project management

The screenshot shows a Trello board for 'PReSTO: Issues and work packages'. The board is organized into columns representing different stages of work: Information, Not started, In progress, Done but not in repo (if applicable), Queued for 5.2, Queued for 6.0, and Released. Each column contains several cards with titles and descriptions of tasks or issues. For example, in the 'Not started' column, there is a card 'Ha en flagga per modul i menu-config.yaml...' and another 'Implement a way to use DIALS in multinode mode for BioMAX'. In the 'In progress' column, cards include '24 cores in PReSTO-menu at LUNARC for XDSAPP and XDSGUI, ShelXie does not work...' and 'Port PReSTO-MX from Python 2 to Python3'. The 'Released' column shows cards like 'XDSGUI 20201022 not OK at MAX IV compute nodes'.



How can you support PReSTO?

1. Use PReSTO!
report BUGs to SNIC support (or PReSTO team members)
2. Suggest software to be added into PReSTO
What is most important NMR/Cryo-EM/XFEL package to add?
3. Perform software updates (require PReSTO admin rights)
Free up time for PReSTO staff to deal with new installs and issues
4. Add new software to PReSTO (require PReSTO admin rights)
PReSTO to educate interested community representatives

PReSTO acknowledgements

Lima, G.M.A. et al. FragMAXapp: crystallographic fragment-screening data-analysis and project-management system. *Acta Crystallogr D Struct Biol* **77**, 799-808 (2021).

Anandapadamanaban, M. et al. E3 ubiquitin-protein ligase TRIM21-mediated lysine capture by UBE2E1 reveals substrate-targeting mode of a ubiquitin-conjugating E2. *J Biol Chem* **294**, 11404-11419 (2019).

Anandapadamanaban, M. et al. Mutation-Induced Population Shift in the MexR Conformational Ensemble Disengages DNA Binding: A Novel Mechanism for MarR Family Derepression. *Structure* **24**, 1311-1321 (2016).

Brock, J.S. et al. A dynamic Asp-Arg interaction is essential for catalysis in microsomal prostaglandin E2 synthase. *Proc Natl Acad Sci U S A* **113**, 972-7 (2016).

Janfalk Carlsson, A. et al. Laboratory-Evolved Enzymes Provide Snapshots of the Development of Enantioconvergence in Enzyme-Catalyzed Epoxide Hydrolysis. *Chembiochem* (2016).

PRESTO team acknowledgement

Sebastian Thorarensen
Torbjörn Lönnemark
Filip Polbratt
Karl Hörnell
Anton Haglund
Torben Rasmussen
Johan Raber



Anders Sjöström



Tavelmedlemmar ×

🔍 sök medlemmar

MEDLEMMAR I ARBETSUTRYMMET

GÄSTER

Michael Hall
Stefan Fleischmann
Jose Miguel de la Rosa Trevin
Björn Forsberg

The SciLifeLab logo features a stylized green and yellow molecular structure icon to the left of the text 'SciLifeLab' in a bold, black font.

Zdenek Matej
Jie Nan
Oskar Aurelius
Alexander Cehovni
Elmir Jagudin
Thomas Eriksson
Ana Gonzales
Johan Unge
Gustavo Lima
Anastasia Shilova

