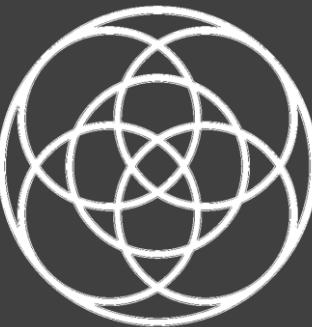


NMR

Ascend™  
Aeon

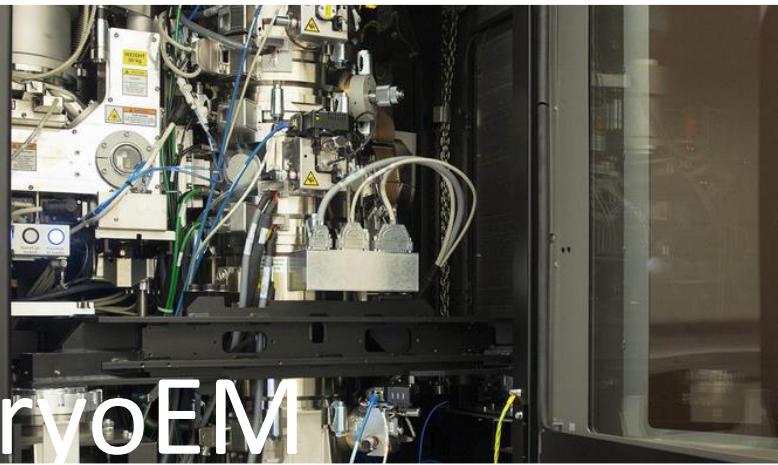
NMX



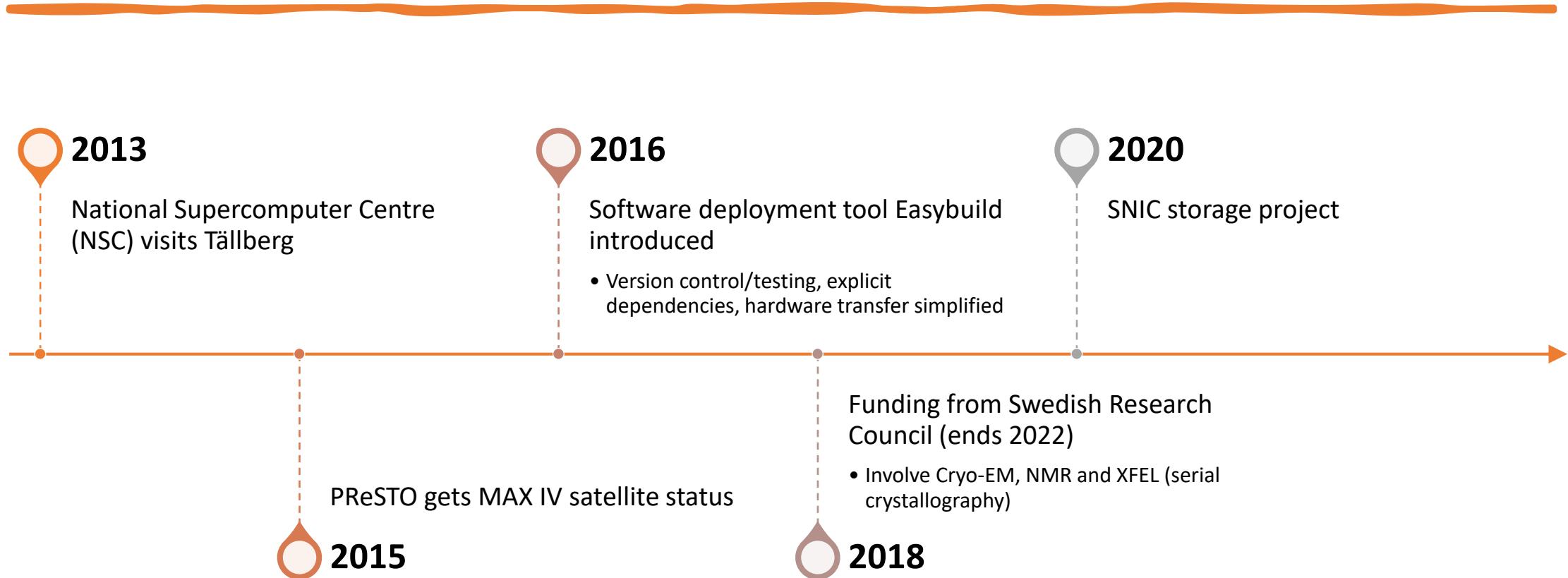
PReSTO – structural biology  
software in HPC environment

Status report June 2021

MX



# 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



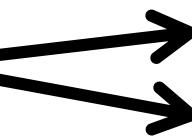
NSC Berzelius

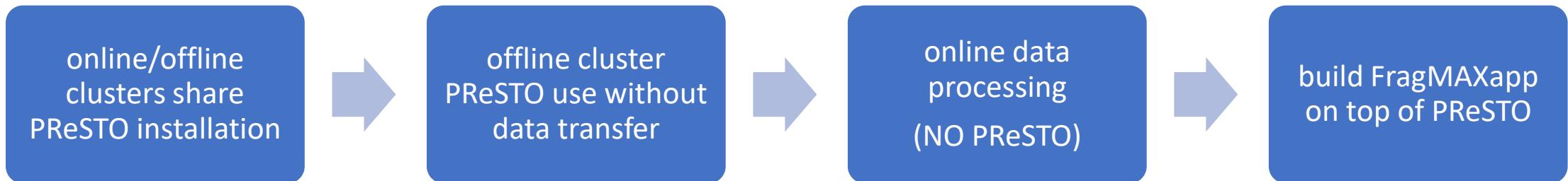


NSC Tetralith

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

Screenshot of a Trello board titled "PReSTO: Issues and work packages". The board is organized into several columns:

- Information:** issue with upgrading Albulia 4.0.1 at MAXIV (local installation)
- Instruction on how to use this Trello board:**
- MAX IV messages:** 46 @ 6
- MX software dependencies:** A diagram showing dependencies between XDS, CCP4, XDS-Viewer, autoPROC, BUSTER, XSDGUIL, XDSAPP, XDSSTAT, PHENIX, hkl2map, XDSME, DIALS, SHARP, SHELXLE, and PReSTO.
- Not started:**
  - Ha en flagga per modul i menu-config.yaml som bestämmer om gamla versioner ska visas
  - Install CCP4M
  - Implement a way to use DIALS in multinode mode for BioMAX
  - Make cctbx.xfel in Phenix work (requires MySQL/MariaDB)
  - Install Arcimboldo
  - dials.image\_viewer does not work in vglrun
  - Error loading pandda.inspect on gn/fe with missing numpy dep
  - Add Cheetah GUI
  - Make forkxds issue a warning instead of shutting down when oversubscribing a node
  - Add CCP4 7.1
- In progress:**
  - 24 cores in PReSTO-menu at LUNARC for XDSAPP and XDSGUI, ShelXle does not work, ...
  - Port PReSTO-MX from Python 2 to Python3
  - install and test autoPROC/BUSTER version 20210420 at NSC Teralith
- Done but not in repo (if applicable):**
  - XDS 20210323 installed and tested at Teralith
  - XDS-Viewer version 0.7
  - Phenix BUG? GUI sbatch scheduling not ok for all wizards!
  - [Bug] xdsapp crashing on MAX IV
  - Install cxiview (Cheetah image viewer)
  - Testing nXDS and nXSCALE
  - PReSTO XDSAPP not working with
- Queued for 5.2:** + Lägg till ett kort
- Queued for 6.0:**
  - NMRPipe 10.9
  - MddNMR 2.7
  - Scipion 3.0.7
  - EMAN 2.91
- Released:**
  - XDSGUI 20201022 not OK at MAX IV compute nodes

**MX software dependencies:**

```
graph TD; XDS --> XDSViewer; XDS --> CCP4; XDSViewer --> autoPROC; XDSViewer --> BUSTER; XDSViewer --> XSDGUIL; XDSViewer --> XDSAPP; CCP4 --> XDSSTAT; CCP4 --> PHENIX; autoPROC --> BUSTER; XSDGUIL --> XDSAPP; XDSAPP --> XDSSTAT; XDSAPP --> PHENIX; hkl2map[Xhl2map, XDSME, DIALS, SHARP, SHELXLE, PReSTO] --- XDS; hkl2map --- CCP4; hkl2map --- XDSViewer; hkl2map --- autoPROC; hkl2map --- BUSTER; hkl2map --- XSDGUIL; hkl2map --- XDSAPP; hkl2map --- XDSSTAT; hkl2map --- PHENIX;
```

# 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 x

Sök medlemmar

MEDLEMMAR I ARBETSUTRYMMET

A circular grid of 12 circular icons representing team members. Some icons contain letters (T, A, AS, FP, J, MS, EJ, AC, O, TE) and others contain small profile pictures. The icons are arranged in three rows: top row (T, A, AS, FP, J), middle row (MS, EJ, AC), and bottom row (O, TE).

GÄSTER

A circular grid of 7 circular icons representing guests. The icons contain letters (AC, A, EJ, JN, O, TE) and small profile pictures. The icons are arranged in two rows: top row (AC, A, EJ, JN, O), bottom row (TE).

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

SciLifeLab

The central part of the slide displays a screenshot of a web-based member directory titled 'Tavelmedlemmar'. It includes a search bar, sections for 'MEDLEMMAR I ARBETSUTRYMMET' (with a grid of icons for each member), and a section for 'GÄSTER' (with a grid of icons for each guest). Below this, the names of four additional team members are listed: Michael Hall, Stefan Fleichmann, Jose Miguel de la Rosa Trevin, and Björn Forsberg. At the bottom, the logos for NSC and LUNARC are shown, along with the SciLifeLab logo.

Zdenek Matej

Jie Nan

Oskar Aurelius

Alexander Cehovni

Elmir Jagudin

Thomas Eriksson

Ana Gonzales

Johan Unge

Gustavo Lima

Anastasia Shilova

