

InfraLife

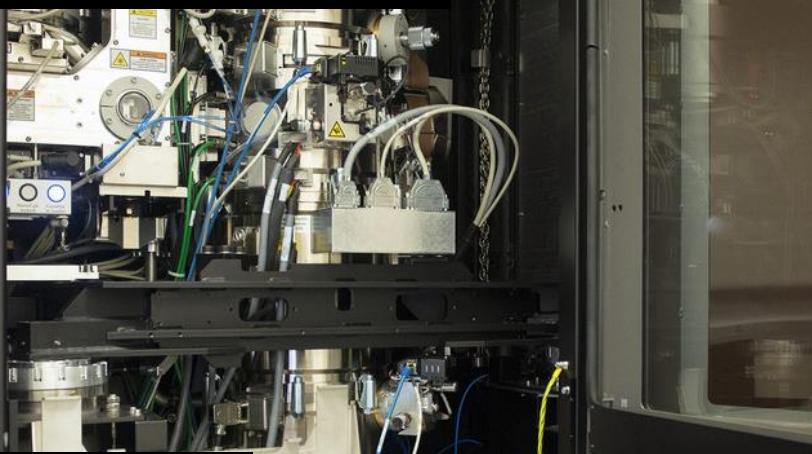
PReSTO – structural biology software in
high performance compute environment

Integrative Structural Biology Course, 22 Aug 2022
Martin Moche

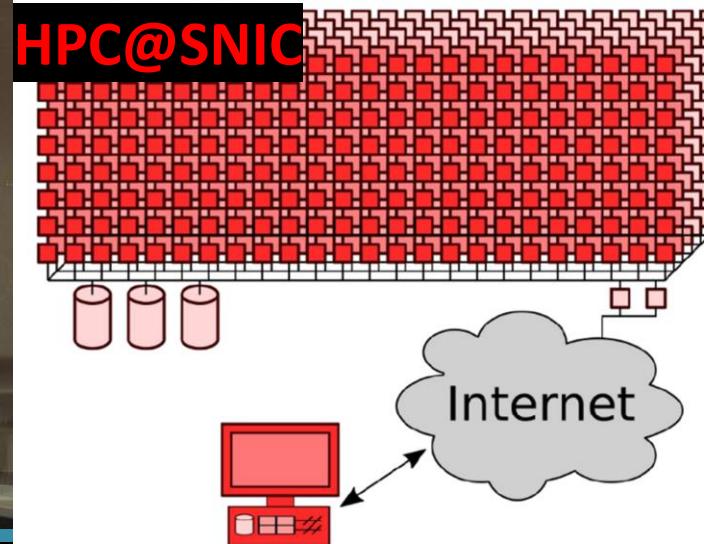
PReSTO "Integrated Structural Biology computing"

The PReSTO project installs, adapt and test structural biology software for use in Swedish high-performance compute (HPC) environments

CryoEM@SciLifeLab



HPC@SNIC



NMX&ESS



MX@MAXIV



NMR@SNC



XFEL@(MAXIV)EU



MAXIV
CPU
Local

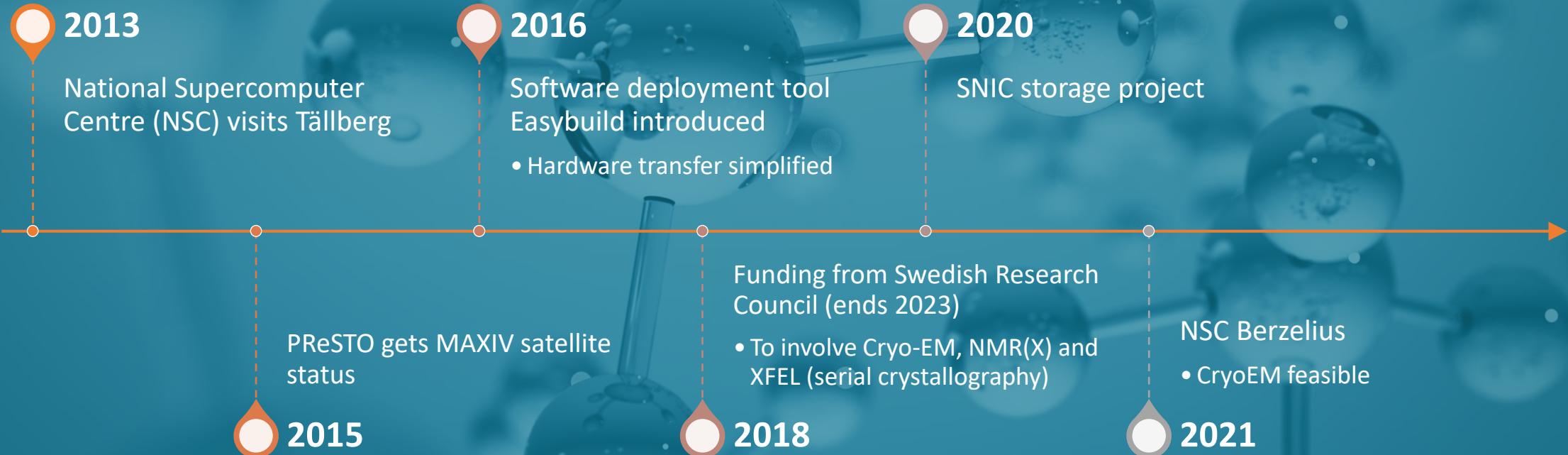
NSC Tetralith
CPU(GPU)
SNIC

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



PReSTO HPC hardware in 2022
- GitLab and Easybuild for software
installation transfer across hardware

PReSTO history



PReSTO@MAXIV



Online
Clu0-fe-1

Offline
Offline-fe1

maxiv.lu.se/fragmax/fragmaxapp/

PReSTO for
FragMAXapp

Data processing software selection

The screenshot shows the PrtK - JBS Data Analysis interface. On the left, a sidebar lists various options like Project, Soaking Planner, Home, Data Analysis, Pipedream, Pipedream Results, PanDDA analyse, PanDDA inspect, Giant PanDDA, Results, Download, Check HPC, and Logout. The main area is titled "Data processing software selection". It has three tabs: "Data processing", "Structure Refinement", and "Ligand fitting". Under "Data processing", there are checkboxes for Pipedream, XIA2/DIALS, XIA2/XDS/XSCALE, XDSAPP, and autoProc. Under "Structure Refinement", there are checkboxes for Pipedream, Dimple, BUSTER, and FS Pipeline. Under "Ligand fitting", there are checkboxes for Pipedream, RhoFit, Phenix LigFit, and PanDDA. A large green arrow points from the "Data processing" tab to the "Structure Refinement" tab. Another green arrow points from the "Structure Refinement" tab to the "Ligand fitting" tab. A third green arrow points from the "Ligand fitting" tab down to the "BUSTER Options" section. The "BUSTER Options" section includes fields for Water placement (use ARP/wARP, use Coot, use Phenix), Refinement mode (dropdown menu), Threshold for MR (0.4), Resolution cutoff (None), and Custom parameters (None). Below the tabs, there are buttons for RUN DATA PROCESSING, RUN REFINEMENT, and RUN LIGAND FITTING. At the bottom, tabs for DIALS, XDS/XSCALE, XDSAPP, autoPROC, DIMPLE, BUSTER, FS Pipeline, RhoFit, LigFit, PanDDA, Pipedream, and Hide are shown, with FS Pipeline highlighted in orange.

Custom definitions for
each software applied to all
datasets

Structure refinement using
three automated pipelines based
on different methods

Automatic ligand fitting
for each available refined
structure



Data processing takes place at
MAX IV Cluster

Extended options for
refinement, water placement
and blobs search

PReSTO@MAXIV



PReSTO for
FragMAXapp



Online
Clu0-fe-1

Offline
Offline-fe1

maxiv.lu.se/fragmax/fragmaxapp/

Electron density
and structure viewer on the browser

Navigation
tools for unexplained blobs and other structures

Information
about the model and ligand fitting scores

Display control
for ligand poses

Dual viewer
for improved binding mode comparison

Ligand representation
expected in the current dataset

Reciprocal lattice viewer

PReSTO in SB community 2022

	MX(NMX)	XFEL	CryoEM	NMR
infrastructure	MAXIV(ESS)	MAXIV	SciLifeLab	SNC
community	YES	YES	YES	yes
reason	available	available	data transfer	too few sw

User support

SNIC support - <https://supr.snic.se/support/>

login, using installed software/storage, SUPR, request software installation

PReSTO page: <https://www.nsc.liu.se/support/presto/>

Designed to support structural biology software use in HPC environment

No software manuals! Developers made these already

Phenix GUI slurm configuration

Known limitations (workarounds, issues, features)

Sub-page for MX, XFEL, NMR, Cryo-EM, NMX

List of software and releases in PReSTO

Acknowledgements and people involved

Access...

PReSTO training

- Upcoming InfraLife course practical's
- Additional NMR, NMX, XFEL and CryoEM training once used by community
- For additional MX? contact PSF martin.moche@ki.se
 - Require your own dataset and account on PReSTO resource
 - Several 2-hour zoom sessions (1-5 participants)
 - MX curriculum:
 - <https://www.nsc.liu.se/support/presto/MX-PReSTO%20training/>

How to support PReSTO?

1. Use PReSTO! Report issues and suggestions to SNIC support
2. Suggest software to be added into PReSTO - PyMOL plugins, CryoEM software
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)
5. Community representatives to be teached to perform 3 and 4

Trello for PReSTO management

PReSTO Gratis

Taylor
Medlemmar
Inställningar

Visningar av Arbetsytan
Tabell
Kalender

Dina taylor
PReSTO: Issues and work p...
PReSTO: Cryo-EM software que...
PReSTO: NMR
PReSTO: Work packages on hold
Project_meetings
Start up
WP3 - software platform at Ma...
Visa mindre

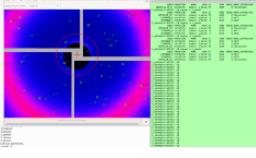
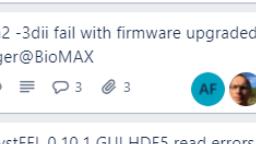
MX software dependencies

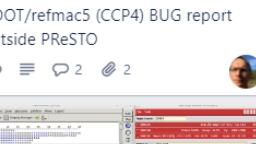
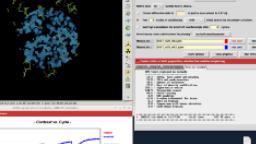
```
graph TD; XDS --> XDSViewer; XDS --> CCP4; XDSViewer --> autoPROC; XDSViewer --> XSDGUI; CCP4 --> XSDSTAT; CCP4 --> PHENIX; XSDSTAT --> XDSAPP; XSDAPP --> hkl2map; XSDAPP --> DIALS; XSDAPP --> SHARP; XSDAPP --> SHELXE; XSDAPP --> PReSTO
```

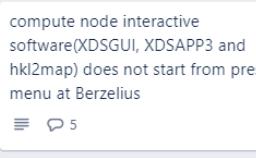
PReSTO: Issues and work packages

Information
Instruction on how to use this Trello board

Not started
MAX IV Make generate_XDS.INP point to correct path for neggia/durin plugins
Suggestion Install Arcimboldo
Bug dials.image_viewer does not work in vglrun
MAX IV Bug in upstream software Error loading pandda.inspect on gn/fe with missing numpy dep
MAX IV Add Cheetah GUI
MAX IV Make forkxds issue a warning instead of shutting down when oversubscribing a node
MAX IV Suggestion Install PAIREF
MAX IV Contact XDSAPP3 developers

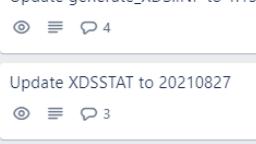
In progress
MAX IV try MAX IV jupyterhub

Bug Adapt CrystFEEL Slurm support to PReSTO?

Bug xia2 -3dii fail with firmware upgraded Eiger@BioMAX

Bug CrystFEEL 0.10.1 GUI HDF5 read errors

Bug COOT/refmac5 (CCP4) BUG report outside PReSTO

Bug Make xxdiff a dependency for XDSGUI

Done but not in repo (if applicable)
MAX IV Bug crystfel - libslurm

Bug compute node interactive software(XDSGUI, XDSAPP3 and hkl2map, DIALS, SHARP, SHELXE, PReSTO) does not start from presto menu at Berzelius

Bug Reinstall GlobalPhasing sw to update .licence

Bug Install DIALS 3.9.1 at NSC Tetralith

Bug XDS help programs XSCALE_ISOCLUSTER and spot2pdb are missing at MAX IV

Bug Install CCP4 8.0.001 at NSC Tetralith

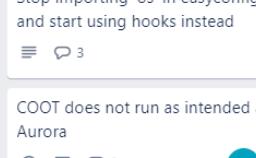
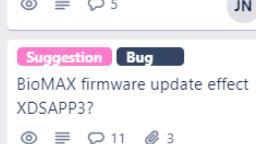
Bug Update autoPROC to 2022-06-08

Bug Update generate_XDS.INP to 1.13

Bug Update XDSSTAT to 20210827

Bug update XDSAPP3 v 1.6 at Tetralith


Queued for 7.2
+ Lägg till ett kort

Released
PReSTO menu does not work at NSC Tetralith for interactive jobs?

Stop importing 'os' in easyconfigs and start using hooks instead

COOT does not run as intended at Aurora

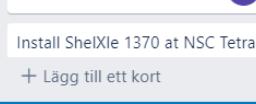
Add new nXDS to Tetralith & MAX IV

Suggestion Bug BioMAX firmware update effect XDSAPP3?

Bug in upstream software Send PR to EB upstream before a...

XDS default version expires 23 mars

New ADXV version 1.15 to NSC Tetralith

Install ShelXle 1370 at NSC Tetralith


PReSTO team acknowledgement

Sebastian Thorarensen

Karl Hörnell

Torben Rasmussen

Torbjörn Lönnemark

Filip Polbratt

Anton Haglund

Johan Raber



Anders Sjöström

Anders Follin



Maria Sunnerhagen
Alexandra Ahlner

Tavelmedlemmar ×

Sök medlemmar

Medlemmar i Arbetsytan





Gäster





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



Zdenek Matej

Jie Nan

Oskar Aurelius

Aaron Finke

Elmir Jagudin

Thomas Eriksson

Ana Gonzales

Aleksander Cehovin

Johan Unge

Gustavo Lima

Anastasia Shilova



THANK YOU SPONSORS



CryoNET

exillum



Live DEMO start



Trash



File System



Home



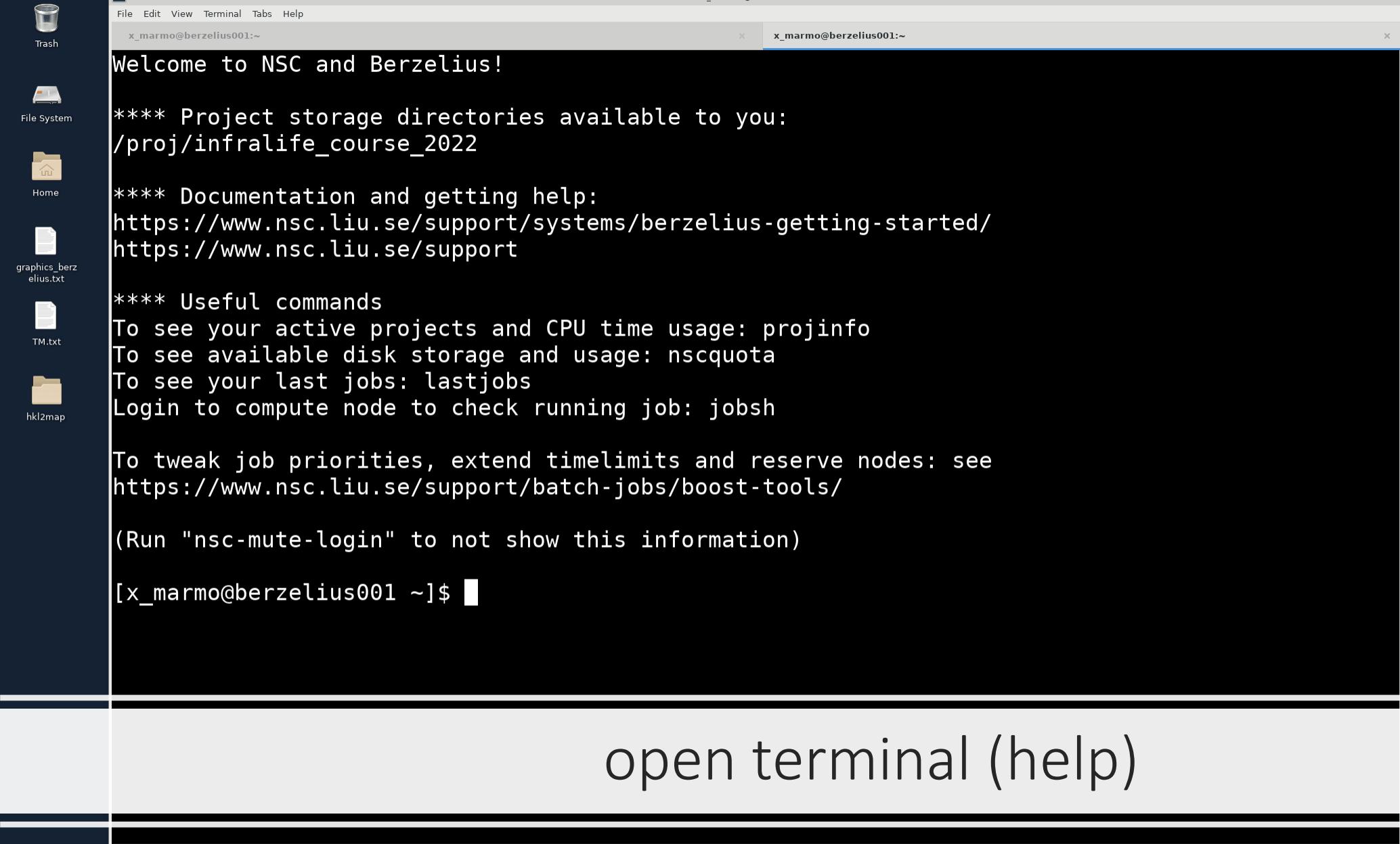
graphics_berz
elius.txt



mia.txt

Remote desktop at Berzelius login node





x_marmo@berzelius001 - ThinLinc Client

Applications Terminal - x_marmo@berzelius001:~ Fri 12 Aug, 09:56 Martin Moche

[x_marmo@berzelius001 ~]\$ projinfo

You are a member of 1 active project.

Berzelius-2022-123

Principal Investigator (PI): Maria Josefin Lundgren Gawell
Project storage directory: /proj/infralife_course_2022
Slurm account: berzelius-2022-123
Current core time allocation: 720 h/month
Consumed compute resource time during the last 30 days:

User	Name	Hours
x_marmo	Martin Moche	1.20
torbenr	torbenr	0.00
x_cecpe	x_cecpe	0.00
x_eskok	Esko Oksanen	0.00
x_mahed	Mattias Hedenström	0.00
x_micha	Michael Hall	0.00
x_ulrbr	x_ulrbr	0.00
Total:		1.20

[x_marmo@berzelius001 ~]\$

File Edit View Terminal Tabs Help

Trash

File System

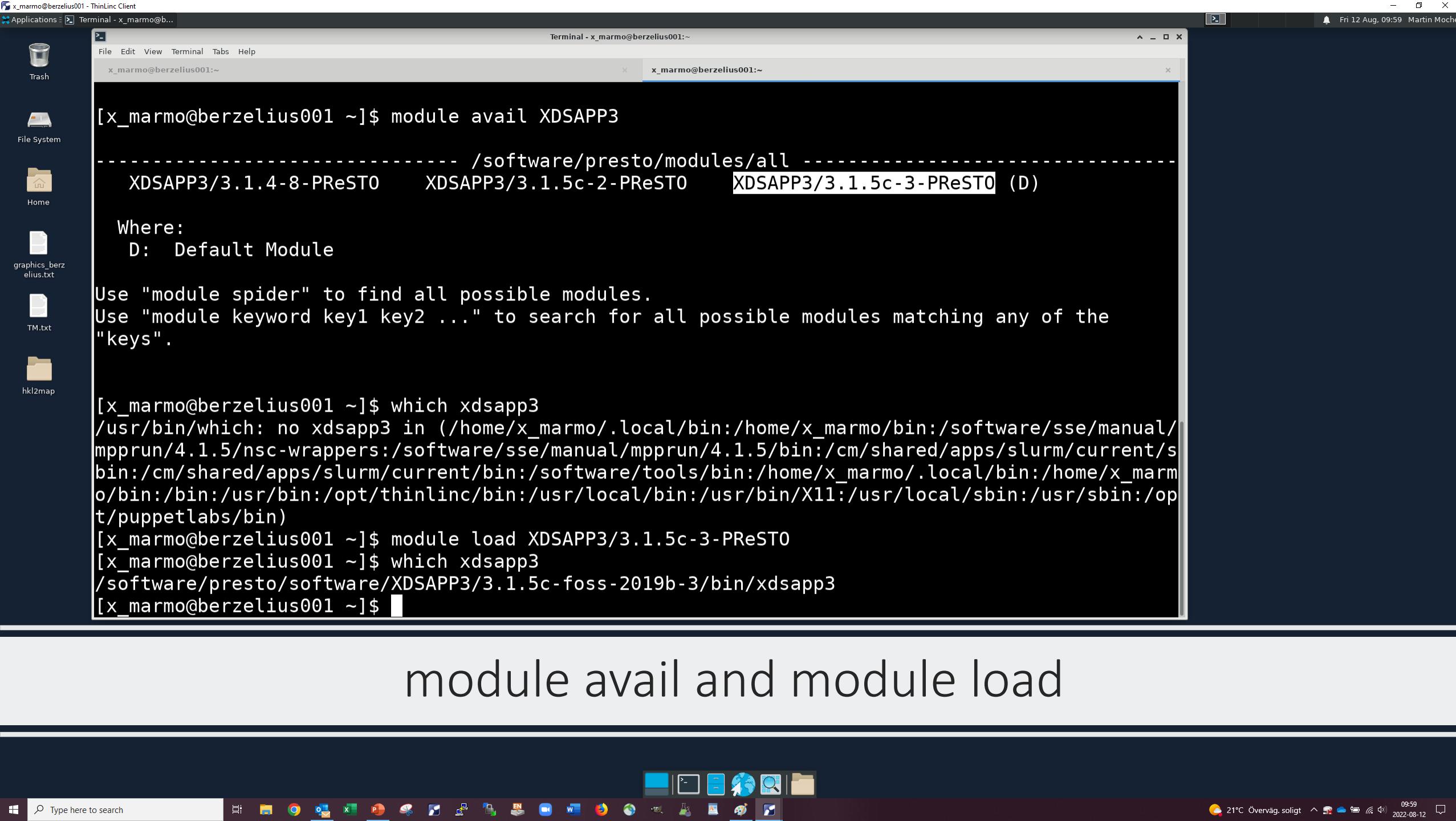
Home

graphics_berzelius.txt

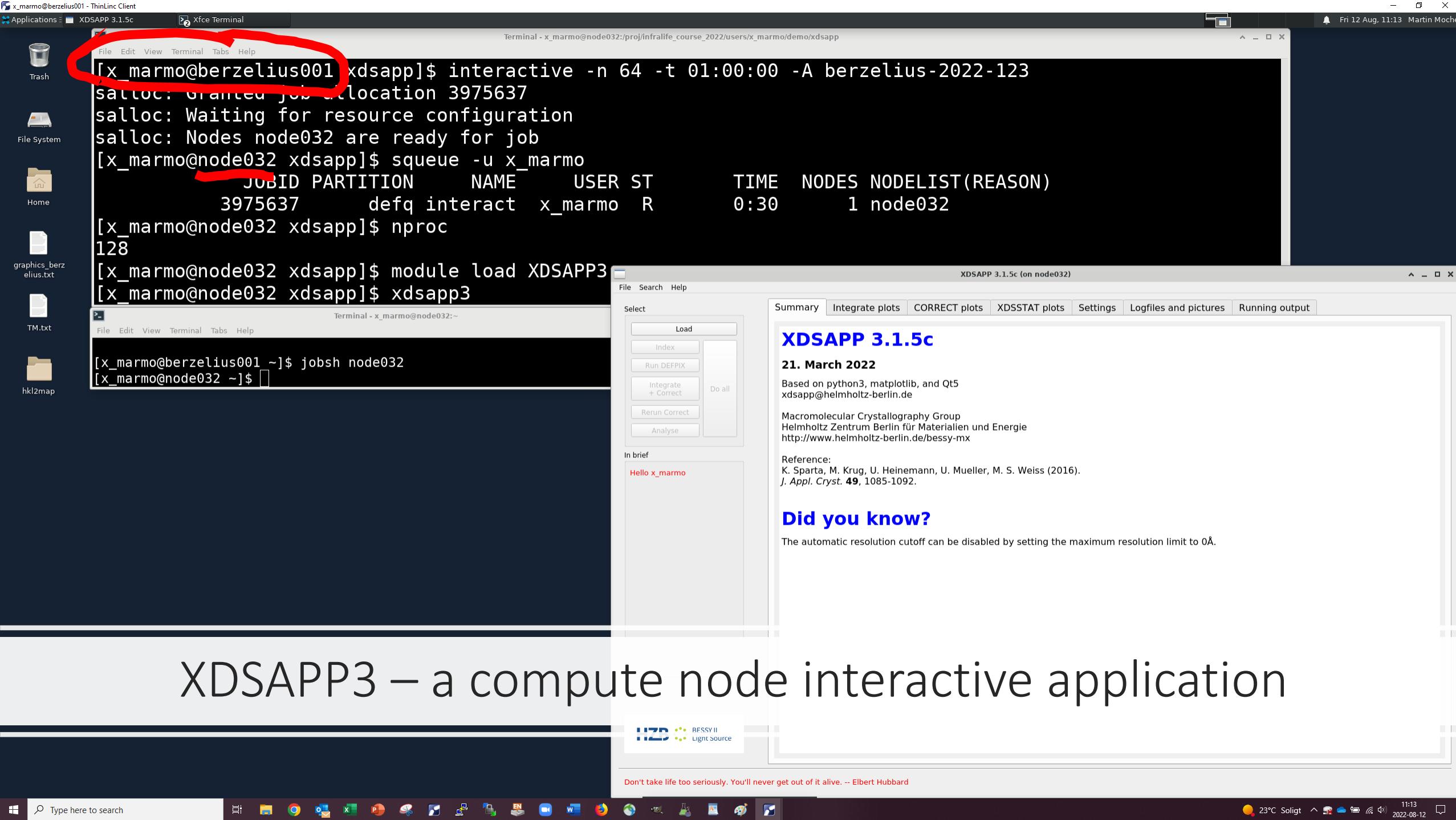
TM.txt

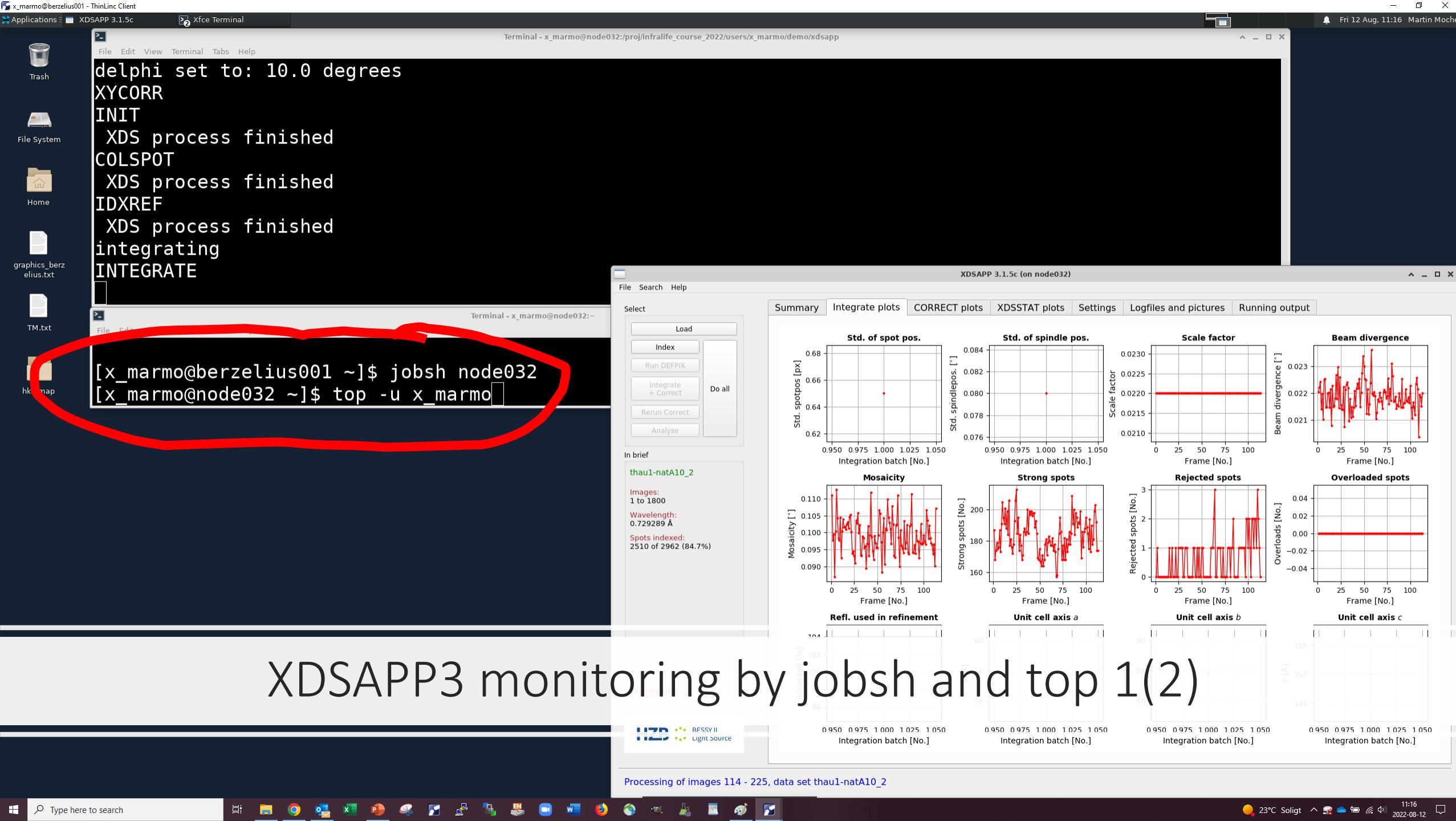
hkl2map

projinfo



module avail and module load

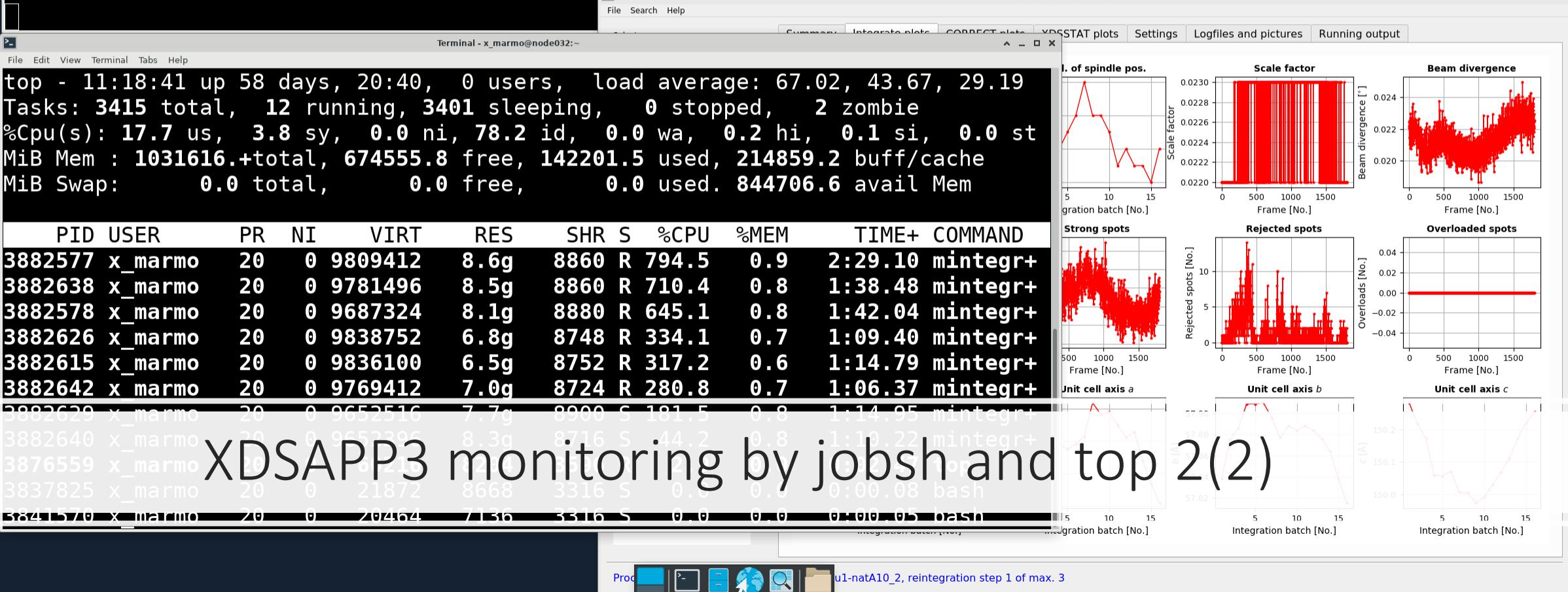


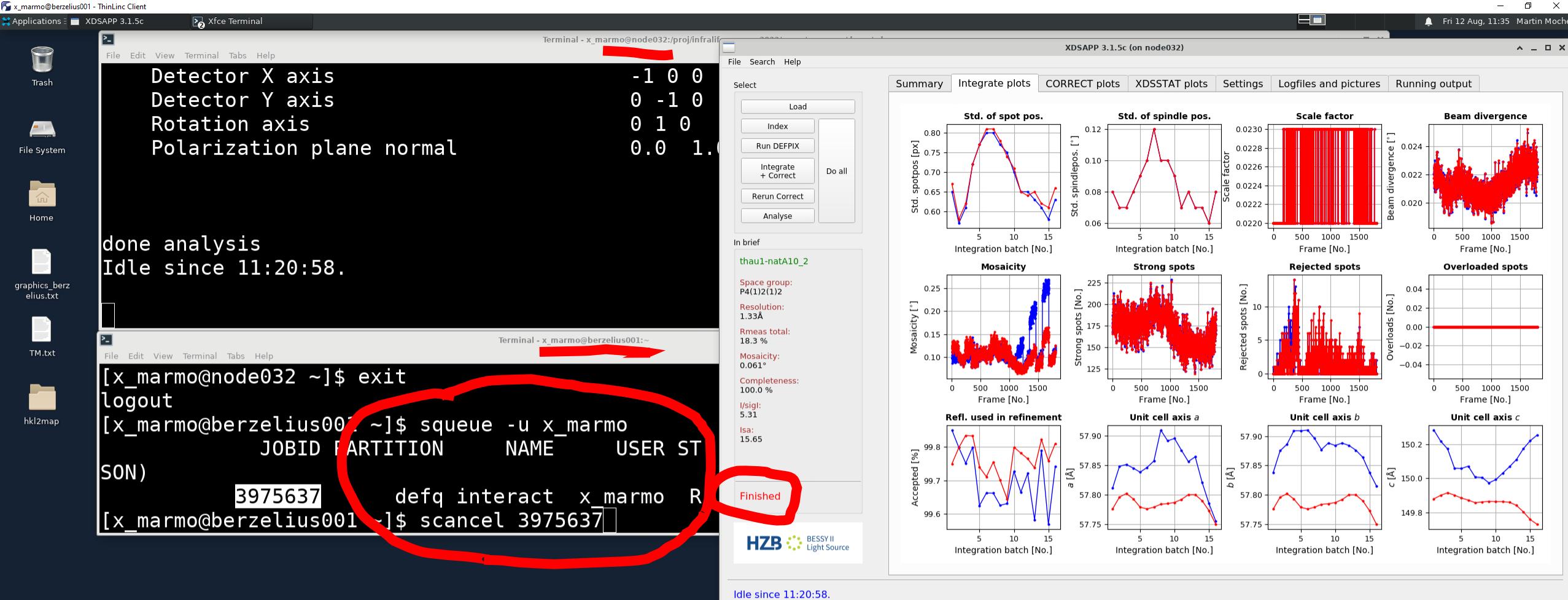


XDSAPP3 monitoring by jobsh and top 1(2)



```
File Edit View Terminal Tabs Help
Terminal - x_marmo@node032:/proj/infralife_course_2022/users/x_marmo/demo/xdsapp
1.03 -0.21 80.6 509.0 2.5
1.06 -0.20 93.2 447.2 3.0
1.10 -0.17 99.7 395.9 3.3
1.14 -0.18 100.0 349.9 6.4
1.19 -0.19 100.0 321.1 6.2
1.24 -0.08 100.0 271.5 12.4*
1.30 0.08 100.0 223.0 17.8*
1.37 0.37 100.0 169.7 46.9*
Data will be used up to 1.30
INTEGRATE
```





scancel or exit to save compute time



PReSTO menu

3.

1.

Did you know?

Hovering with the mouse over an input field in the settings tab will pop-up a contextual help.

True science teaches, above all, to doubt and to be ignorant. -- Miguel de Unamuno

2.

Run XDSAPP3 on a compute node

XDSAPP3 needs to be submitted as an interactive job to the queue system and run on a compute node. Please set the parameters for the job:

- Account: snic2021-5-376
- Number of cores: 32
- Time limit [HH:MM]: 01:00

Cancel Continue

21. March 2022

Based on python3, matplotlib, and Qt5
xdsapp@helmholtz-berlin.de

Protein Crystallography Group
Helmholtz Zentrum Berlin für Materialien und Energie
www.helmholtz-berlin.de/bessy-mx

ence:
arta, M. Krug, U. Heinemann, U. Mueller, M. S. Weiss (2016).
J. Cryst. **49**, 1085–1092.

XDSAPP 3.1.5c

Summary Integrate plots CORRECT plots XDSSTAT plots Settings Logfiles and pictures Running output

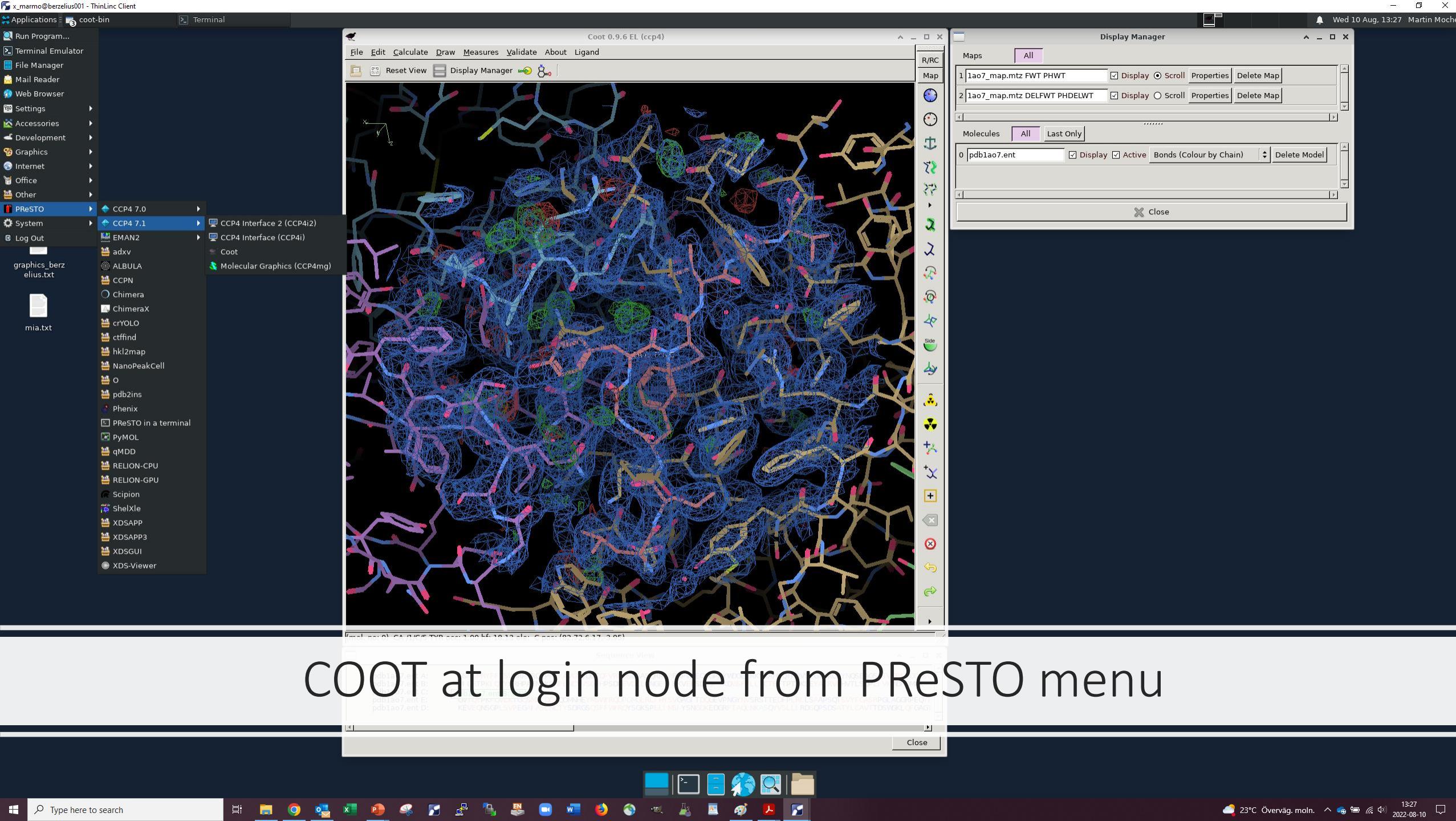
File Search Help

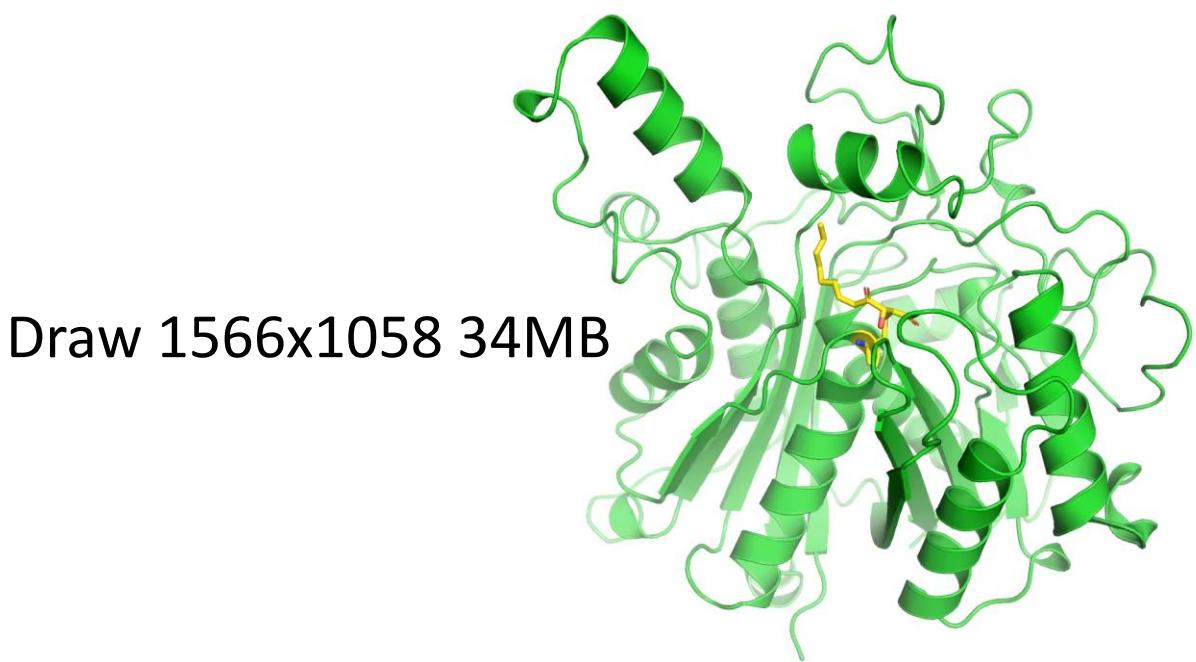
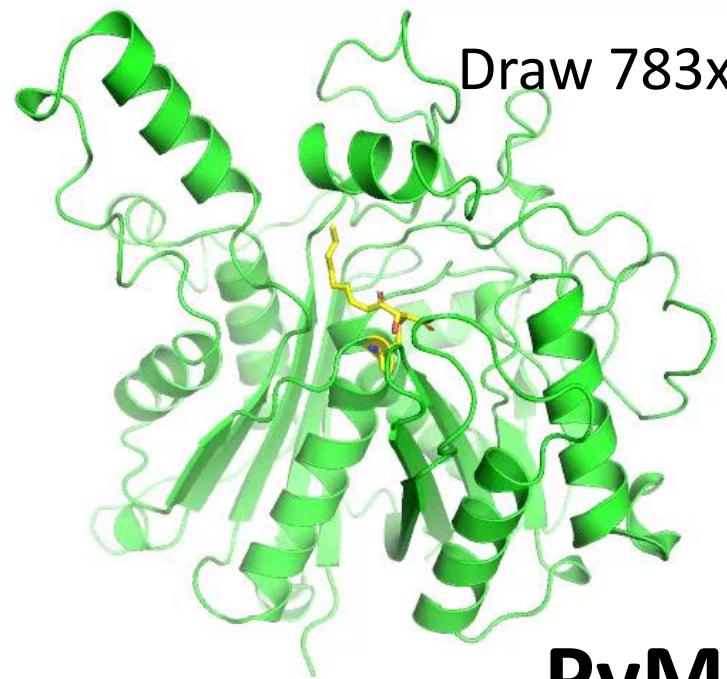
Select Load Index Run DEPIX Integrate + Correct Do all

PReSTO menu for interactive applications at

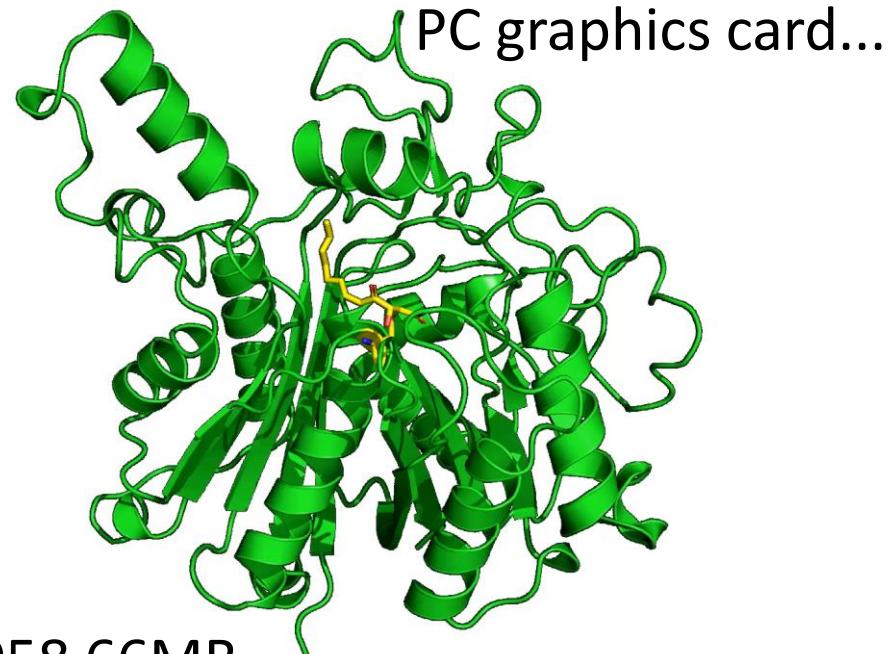
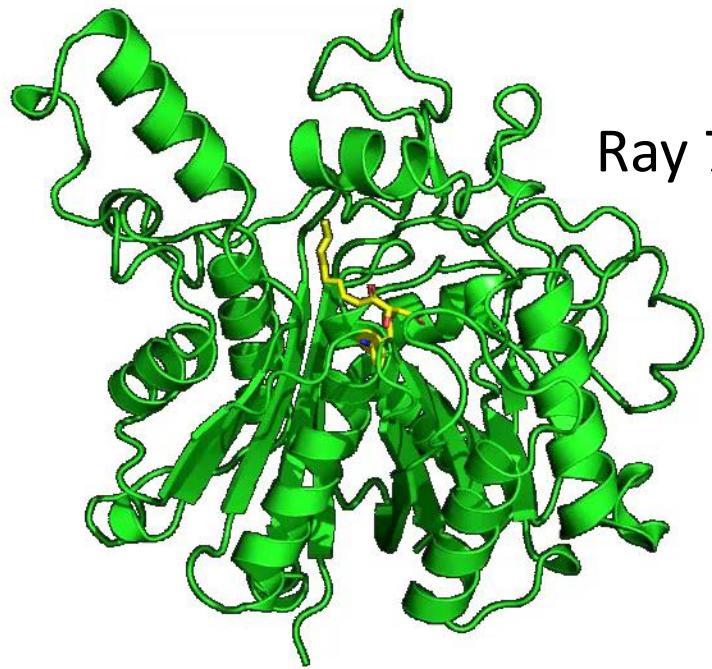
a) login node: COOT, PyMOL, Chimera, ADXV (graphics applications)

b) interactive compute node: XDSAPP3, XDSGUI, hkl2map (parallel computing)





PyMOL movies for PowerPoint



Live DEMO end

Berzelius test-login

- Download and install thinlinc from
<https://www.cendio.com/thinlinc/download>
- Install "Google authenticator" on your phones
- Can you login to Berzelius?
- Can you see the PReSTO menu?

THE END

Enjoy the course!

Login and compute nodes for MX software

Use login node for:

1. Interactive graphics software: PyMOL, COOT, Chimera, ADXV, ALBULA
2. GUIs doing non-parallel computing: ccp4i, ccp4i2
PHASER is parallel => ccp4i, ccp4i2 at interactive compute node
3. GUIs with SLURM: Phenix, CrystFEL

Use interactive compute node for

1. XDSAPP3, hkl2map, XDSGUI
i.e. software running in parallel mode once started from GUI

Use sbatch script at compute node for

1. BUSTER, XDS, DIALS, autoPROC, SHARP, archimboldo

File transfer by WinSCP, filezilla, rsync

The screenshot shows the WinSCP interface comparing two directory structures. On the left, the local directory structure is displayed under 'C:\Users\marmoc\OneDrive - Karolinska Institutet\Dokument\' with many subfolders and their details. On the right, the remote directory structure is shown under '/home/x_marmo/' with files and their details. The interface includes tabs for Transfer Settings and Default, and various file operations like Synchronize, Queue, Find Files, Upload, Download, and Properties.

Name	Type	Size	Changed	Rights	Owner
..	Parent directory		2022-08-15 09:22:43		
2020	File folder		2021-10-04 15:52:29		
2021	File folder		2021-10-04 15:52:32		
Anpassade Office-mallar	File folder		2021-10-04 15:45:40		
anställning_PSF	File folder		2021-10-04 15:45:40		
applications	File folder		2021-10-04 15:45:40		
articles	File folder		2022-03-31 15:35:29		
beamline	File folder		2022-06-27 10:06:51		
Biomedicum	File folder		2021-11-09 17:43:24		
BoxSyncOLD	File folder		2021-10-04 15:49:48		
cache	File folder		2021-10-04 15:49:29		
carpentry	File folder		2021-10-04 15:47:36		
certificate	File folder		2021-10-04 15:46:11		
Choir	File folder		2022-05-31 16:00:04		
Custom Office Templates	File folder		2021-10-06 10:06:04		
Drupal_8	File folder		2021-10-04 15:45:42		
ELN	File folder		2021-10-04 15:45:42		
emails	File folder		2022-04-29 12:55:10		
EndNote	File folder		2021-10-04 15:45:44		
EndNote2	File folder		2022-08-12 17:53:32		
excel	File folder		2021-10-04 15:45:57		

Name	Type	Size	Changed	Rights	Owner
..	Parent directory		2022-08-15 10:30:17	rwxr-xr-x	root
Desktop	File folder		2022-08-15 16:13:37	rwxrwxr-x	x_marm...
xdsapp	File folder		2022-08-12 10:37:43	rwxrwxr-x	x_marm...
coot-download	File folder		2022-08-10 13:22:10	rwxrwxr-x	x_marm...
Phenix	File folder		2022-06-16 16:39:38	rwxrwxr-x	x_marm...
demo	File folder		2022-06-16 10:04:23	rwxrwxr-x	x_marm...
Downloads	File folder		2022-06-16 09:26:31	rwxr-xr-x	x_marm...
CCP4MG_DOWNLOAD	File folder		2022-06-16 08:45:29	rwxrwxr-x	x_marm...
0-coot-history.scm	File	1 KB	2022-08-10 14:48:31	rw-rw-r--	x_marm...
0-coot-history.py	File	2 KB	2022-08-10 14:48:31	rw-rw-r--	x_marm...
0-coot.state.scm	File	2 KB	2022-08-10 14:48:31	rw-rw-r--	x_marm...
0-coot.state.py	File	2 KB	2022-08-10 14:48:31	rw-rw-r--	x_marm...
1b3n.cif	File	318 KB	2022-06-02 16:42:28	rw-rw-r--	x_marm...

```
rsync -rvplt x_marmo@berzelius.nsc.liu.se:/proj/infralife_course_2022/users/x_marmo/ .
```

Ways to transfer large amount of data and many files?

Things not discussed in this presentation

- Easybuild structure
 - easyconfigs, easyblocks
- sbatch script examples
- How to write compute and storage applications to SNIC

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).