



**A seamless CryoEM data processing  
pipeline utilizing an encompassing  
network, supercompute, clever scripting  
and virtual desktops**

**Dr. Farrah Blades**

**Cater group**

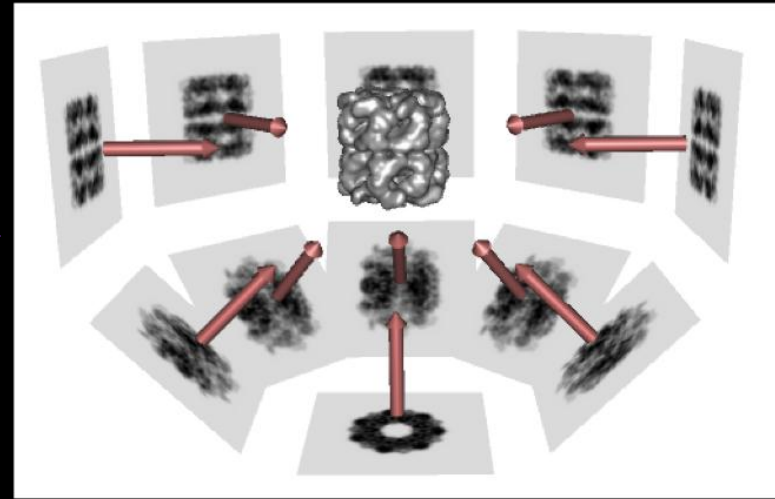
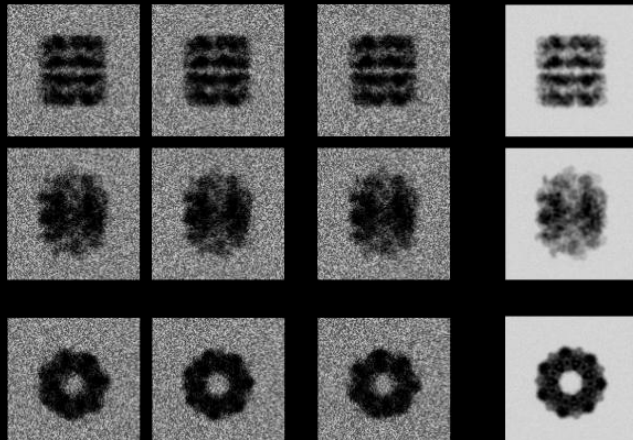
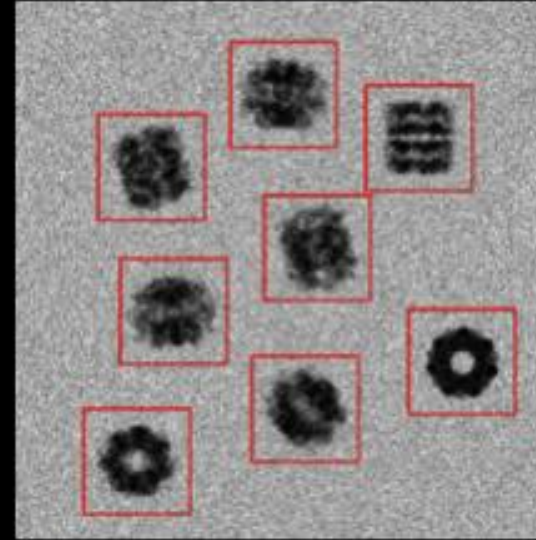
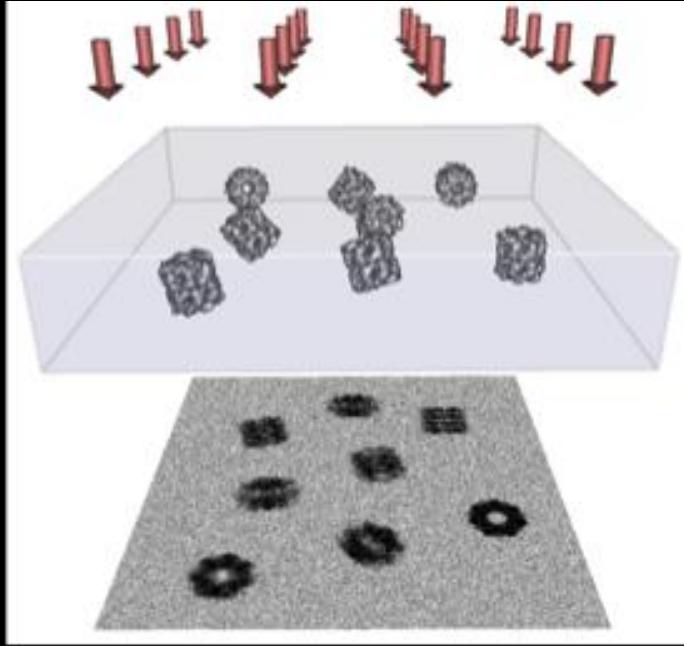
**Institute for Molecular Biosciences,**

**The University of Queensland, Australia.**

**[f.blades@imb.uq.edu.au](mailto:f.blades@imb.uq.edu.au)**

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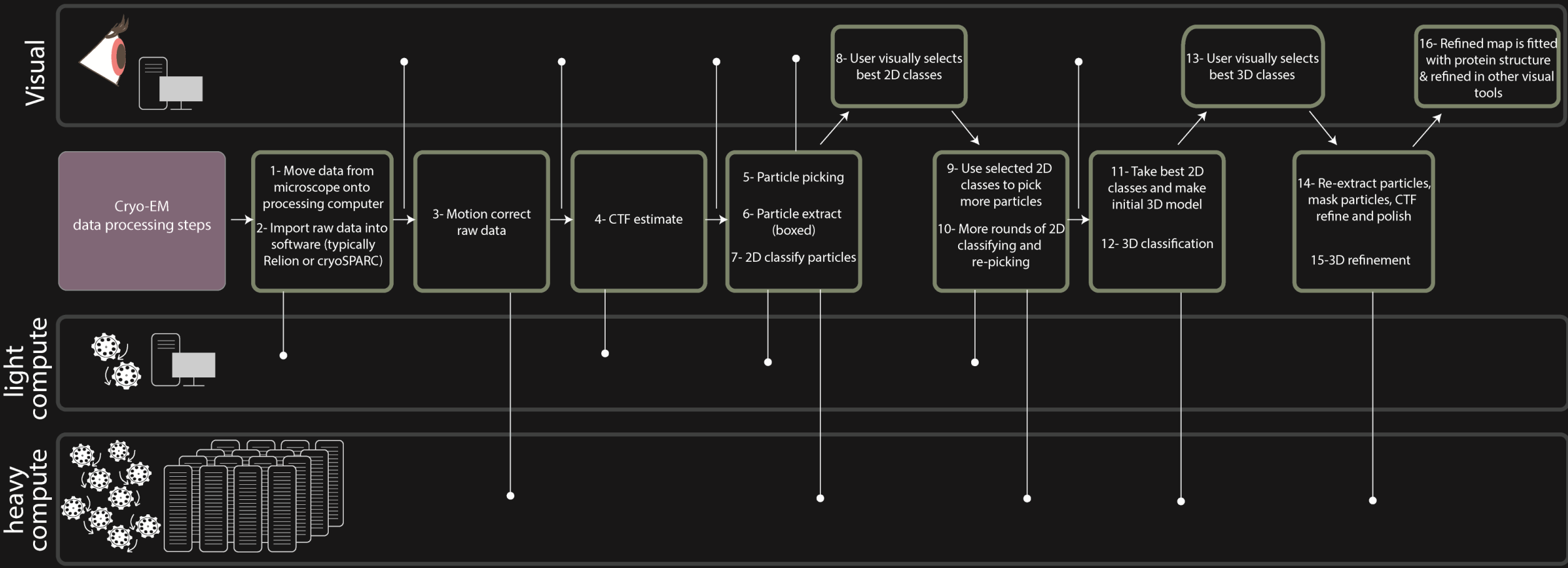
# Single particle cryogenic electron microscopy (Cryo-EM)



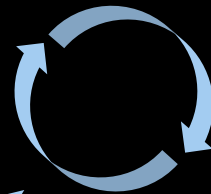
Thousands of  
micrographs

Millions of  
particles

# Typical Cryo-EM data processing workflow



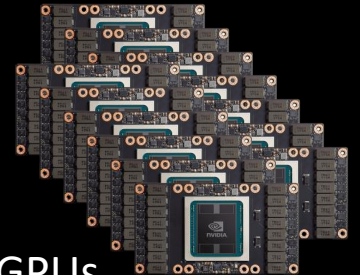
# How do we process these huge data sets?



**\*\*Command line skills\*\***  
Writing scripts  
Logging into HPC by command line  
Submitting jobs by command line

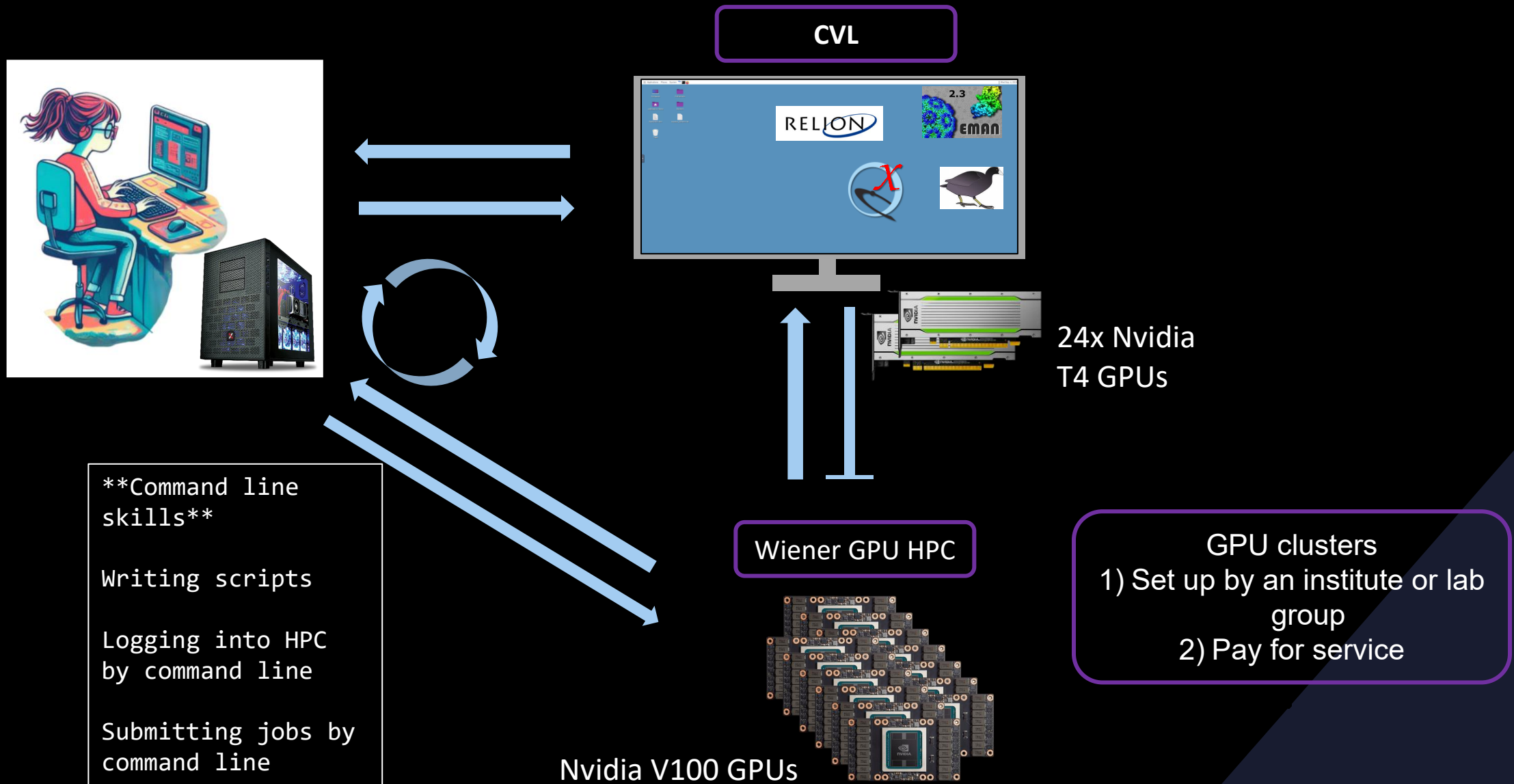
Wiener GPU HPC

GPU clusters  
1) Set up by an institute or lab group  
2) Pay for service



Nvidia V100 GPUs

# First attempts to solve the issue at UQ- Characterisation Virtual Laboratory (CVL)



# Easiest solution



- Expiration countdown begins as soon as its built
- Maintenance
- Cannot store or process our data set sizes
- New techniques pushing capacity even further
- Moving data on and off
- Arduous script writing skills to run big jobs still required

Data movement and processing

=

**Can be one of the largest bottlenecks for  
CryoEM groups**

# How did we get here?

## BIOLOGISTS

It needs to be as easy as possible, once I find a way that works, I will do it forever

I don't want to and I don't have the time to learn command line

Extreme time and funding pressure

Somewhat risk averse

I just want my result

Finding an easier way to get the data processed

## COMPUTE

**\*\*Command line skills\*\***

Writing scripts

Logging into HPC by command line

Submitting jobs by command line

Software requests

We can build what we think you need

Things being built that don't meet needs and aren't convenient

# Fixing a university (and nation?) wide issue

## BIOLOGISTS

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## COMPUTE

```
**Command line skills**
```

Writing scripts

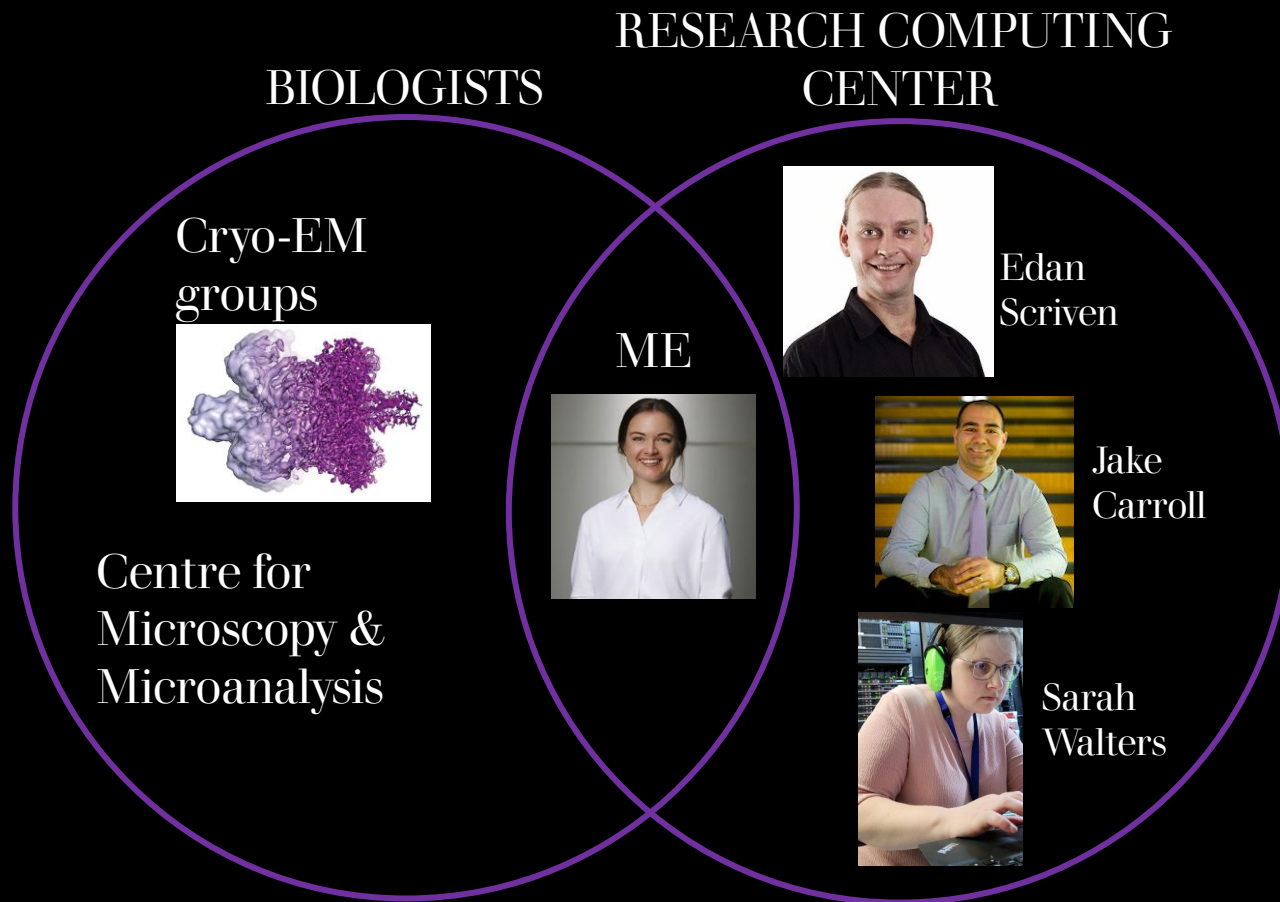
Logging into HPC by command line

Submitting jobs by command line

Software requests

We can build what we think you need

# Right people, right place, right time, right funding



# HPC Bunya: UQ's new supercomputer, grass roots build

## Phase 1 & 2

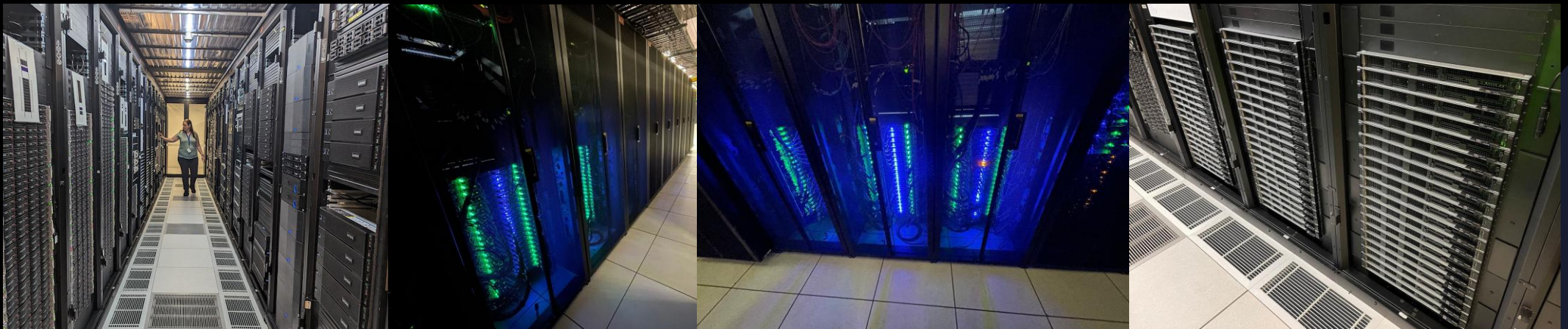
- RCC took many lessons from Wiener HPC, CVL and the feedback from the CryoEM community.
- ~10,000 cores of AMD Milan and Genoa CPUs.
- 2TB of DDR5 memory per node.
- 200Gbit/sec RDMA networking.
- SLURM entry but also cloud desktop.
- GPUs: Nvidia H100s, A100s, L40s and AMD's MI210s.
  - **21x H100s 80GB GPU RAM**
  - **8x A100s 80GB " "**
  - **3x A100 MIG 10GB (21 slices)**
  - **18x L40s 48GB " "**
  - **6x MI210 64GB " "**

## Phase 3

- RCC took more lessons from trench 1 & 2 and the viz community
- ~2,000 additional cores of AMD Milan and Genoa CPUs
  - **16x H100 SXMs 320GB GPU RAM**
  - **9x A16s 16GB " "**

**Each can run 4x desktops = 32 desktops**

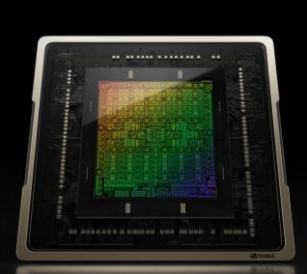
  - **6x L40s 24GB " "**
  - **AMD MI300 server access**
- **2x MI300x boxes with 8xGPUs each**



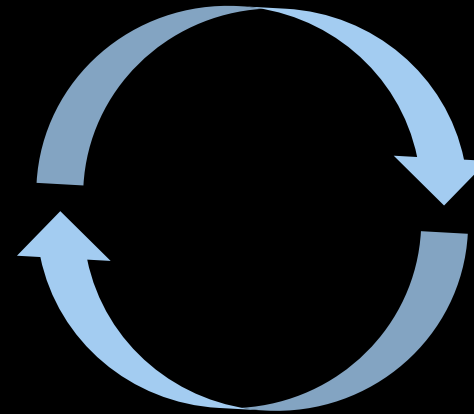
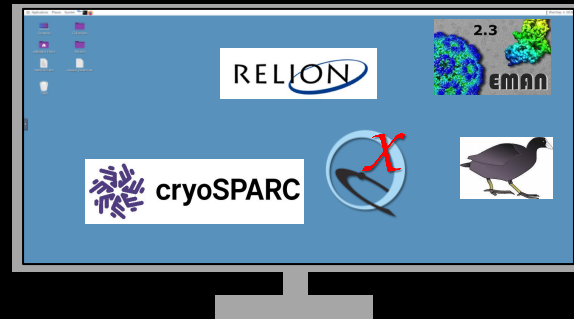
# HPC Bunya: UQ's new GPU and CPU supercomputer

## Virtual Desktop = OnBunya

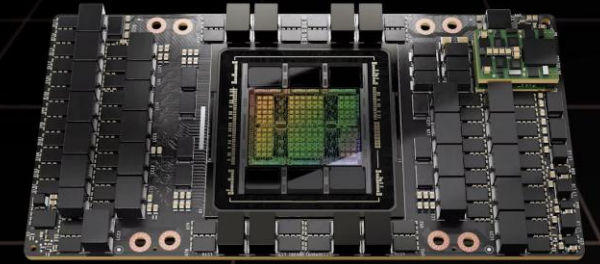
**OPEN**  
**OnDemand**  
OnDemand provides an integrated, single access point for all of your HPC resources.



Use powerful visual L40 GPUs for the desktop workloads



## Working nodes



Use powerful AI/ML GPUs (A100, H100, MI210) or L40 for compute jobs

User input



Cryo-EM  
with local  
data collect



1.

5.

8. (repeat 5-7)

3.



Launch v-desktop through  
OPEN OnDemand web

4.

v-desktop launches per  
requested resource  
(i.e 1x L40 GPU)

Heavy jobs passed  
to Bunya SLURM  
(i.e 3x A100 GPUs)

6.

7.

completed job output  
available real time  
on v-desktop

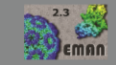
GPUs re-enter SLURM  
pool

v-desktop

User's RDM

Research group  
scratch drive

cryoSPARC



Liber-TEM

crY@LO

RELION

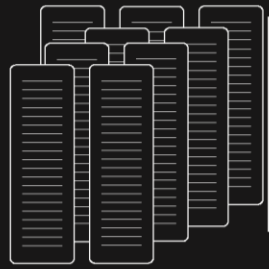


blender

Automatic

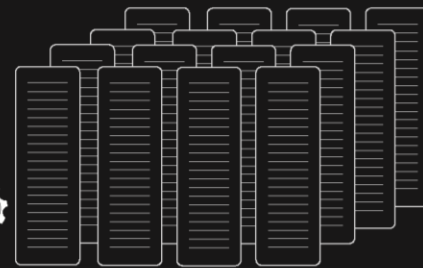
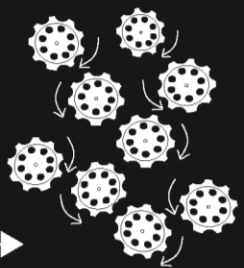


2.



**Research  
Data  
Manager**  
Designed at The University of Queensland

Data storage centre



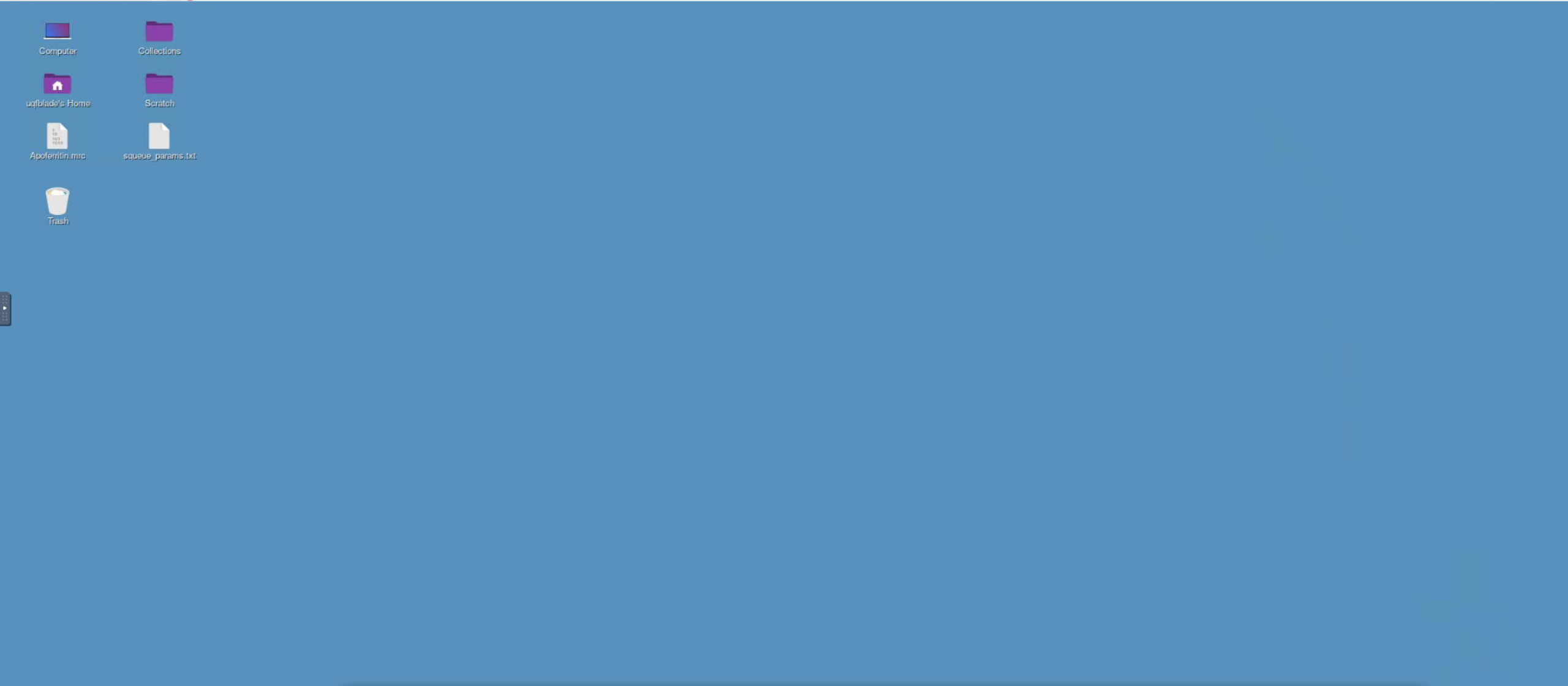
Bunya HPC

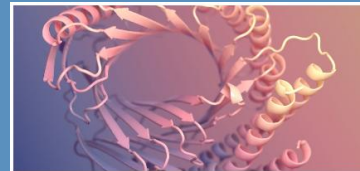
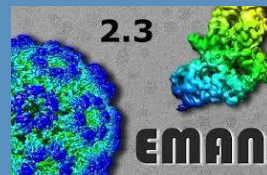
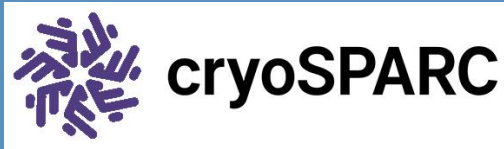
The desktop environment shows a file manager window with the following items:

- Computer
- uqfblade's Home
- Link to Farrah
- Trash
- Link

```
Mate Terminal
File Edit View Search Terminal Help
Every 0.1s: squeue --me bun078: Wed Nov 22 13:26:15 2023
JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)
6570917 gpu_viz Viz_Desk uqfblade R 15:35:55 1 bun078
```

```
Relion
File Edit View Search Terminal Help
[uqfblade@bun078 NewRelion4]$
```





RFdiffusion: A generative model for protein design



AlphaFold



```
Male Terminal
File Edit View Search Terminal Help
Every 0.1s: queue --me bun078: Wed Nov 22 13:26:15 2023
JOBID PARTITION NAME USER ST TIME NODES NODELIST(REASON)
6570917 gpu_viz Viz_Desk uqfblade R 15:35:55 1 bun078
```

```
Relion
File Edit View Search Terminal Help
[uqfblade@bun078 NewRelion4]$
```

# Users (so far)

Beta-testing Dec 2023

Official launch May 2024

Users of OnBunya = 595

~43% of Bunya HPC users are  
using OnBunya

“OnBunya has proven to be extremely useful, helpful, and convenient for our need”

## Testimonies

“Without OnBunya more than half of our people wouldn’t have [means] to do their processing at all and would have to wait”

“for the future, OnBunya should be the main place people do their processing, it is a no-brainer”

“It will help with publications and future grant applications”

“I extensively use the OnBunya desktop”

# Why is this platform so successful?

**User designed**

**User tested**

**Trust across disciplines**

**Grass roots HPC build**

**Workshops to increase user confidence**

**Data access**

**Storage and scratch space**

**Everything user needs in one place**

**It is at least 5x better than the next best alternative**

# Where to from here?

- We have found a scalable solution to moving large data sets and processing them in house and we hope to help other universities do the same
- A national service as smooth as OnBunya...

# Acknowledgements

My email: [f.blades@imb.uq.edu.au](mailto:f.blades@imb.uq.edu.au)  
[www.linkedin.com/in/farrah-blades](http://www.linkedin.com/in/farrah-blades)



## HANKAMER GROUP

Prof Ben Hankamer

## Centre for Microscopy & Microanalysis UQ

Dr Matthias Floetenmeyer

Dr Lou Brillault

Dr Na'ama Koifman

Professor Roger Wepf



Edan Scriven



## Research Computing Centre



Jake Carroll



Sarah Walters

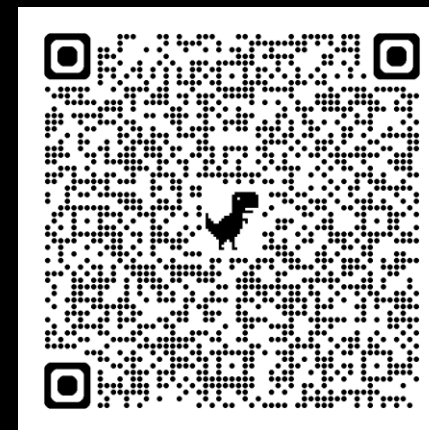
Marlies Hankel  
Irek Porebski



## Code sharing

All open access: <https://github.com/UQ-RCC/hpc-docs>

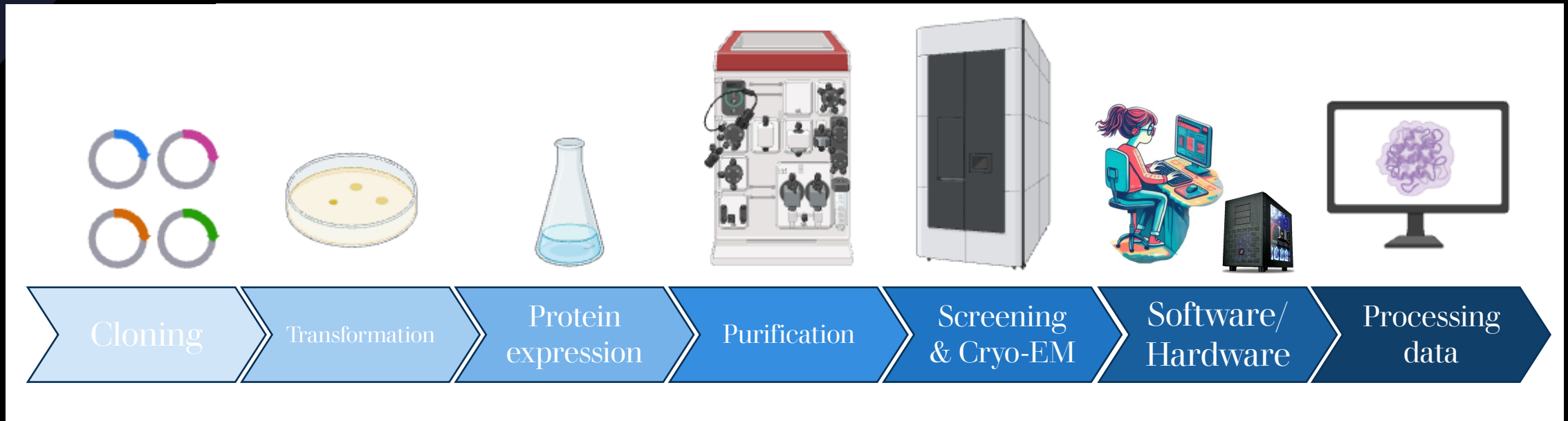
we hope to show others how to tackle this huge data/  
big viz and big compute problem



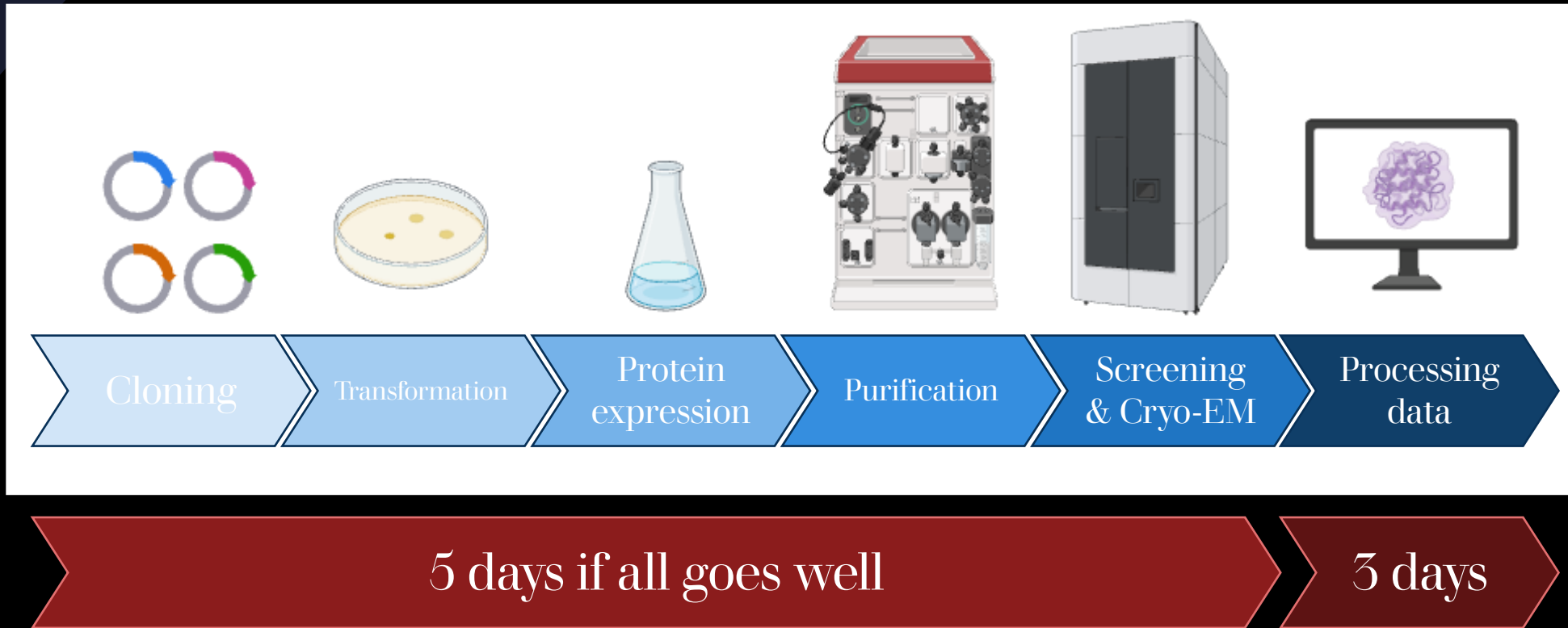
24 hour Run-a-thon for Lifeline



# Community examples- Meihan Liu (Collins Group)



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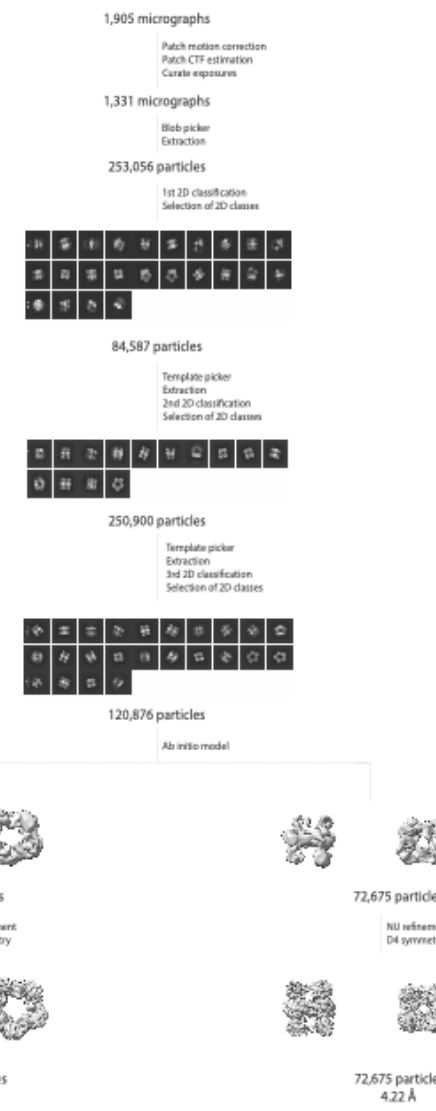
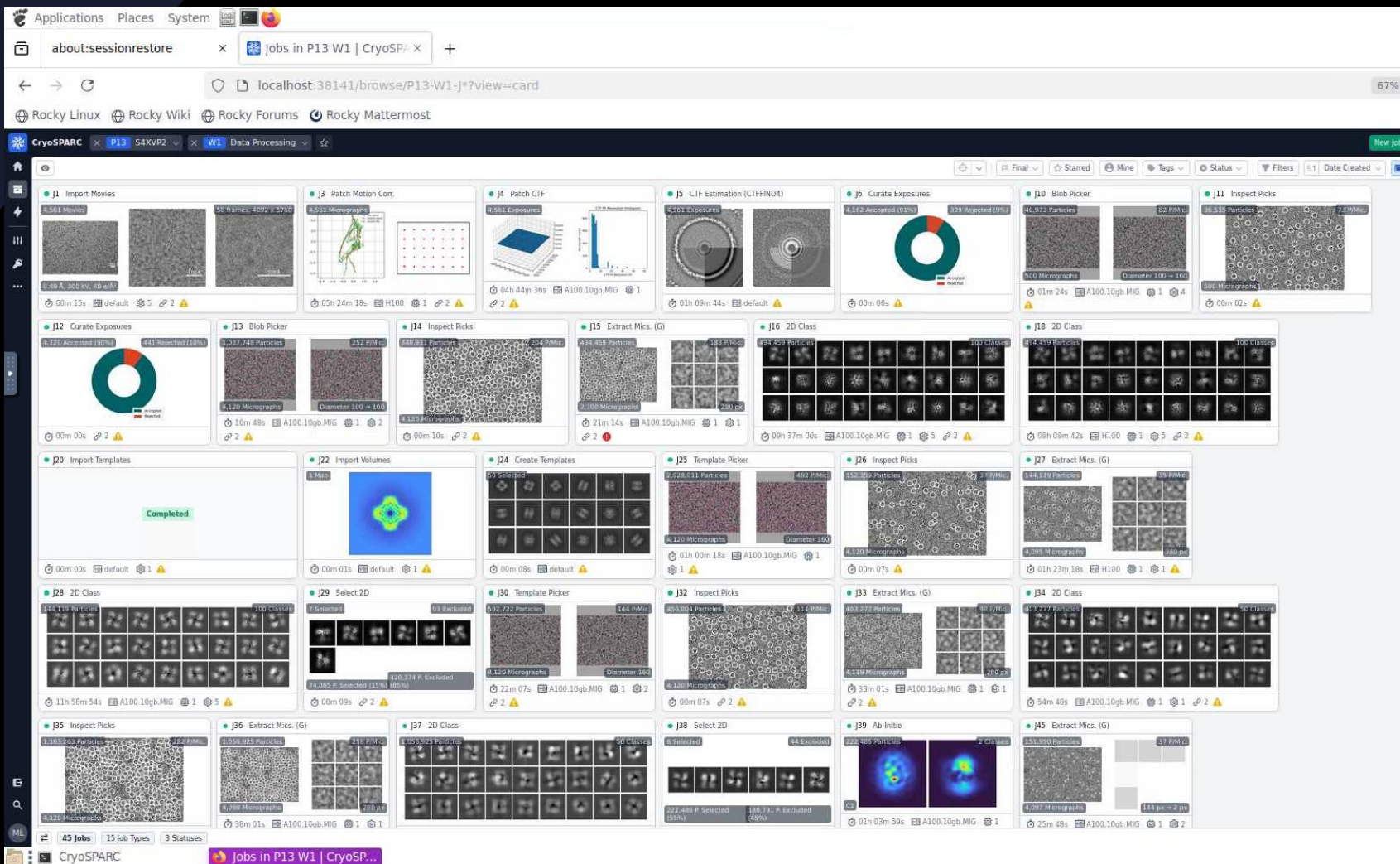


Figure A: CryoSPARC workflow for cryoEM structure determination of MBK5214510.