

Table of contents:

Table of contents:	1
Accessing cryoSPARC	1
Known issues	1
General notes about using cryoSPARC during workshop	1
cryoSPARC T20S tutorial link	2
Data available for processing during cryo-EM workshop at ACA	2
EMPIAR-10025-T20S-movies	2
EMPIAR-10025-T20S-micrographs	2
EMPIAR-10215-Aldolase	2
EMPIAR-10241-TMEM16	2
EMPIAR-10256-TRPV5-CaM	2
EMPIAR-10180-spliceosome	2
EMPIAR-10003-HIV-Trimer	3
Configuration details for cryoSPARC on AWS	3
Slack channel invite link	3

Accessing cryoSPARC

1. Type web address in Google Chrome [officially supported web browser for cryoSPARC] that was emailed to you by mcianfro@umich.edu
2. Login using the following username / password:
 - Username: participant@noreply.com
 - Password: ACA2019
3. PLEASE only connect one device to private wifi for cryo-EM workshop

Known issues

- Motion correction does not work
- CTFFIND4 and Gctf do not work

General notes about using cryoSPARC during workshop

- For organizational purposes, please select `/home/ubuntu/cryosparc-project-directories/` as the output directory for any new projects in cryosparc

- Your machine only has 800 GB, you may fill up the hard drive which will require you to clean up the hard drive if it fills up
- You only have ONE GPU on your machine, so you can only run one job at a time

cryoSPARC T20S tutorial link

Please follow this link for detailed step-by-step instructions for the T20S tutorial:

<https://cryosparc.com/docs/tutorials/t20s/>

Data available for processing during cryo-EM workshop at ACA

The following directory names correspond to datasets available for processing. These are all located in the home directory (`/home/ubuntu/`):

- EMPIAR-10025-T20S-movies
 - [EMPIAR link](#)
 - Movie files [corresponds to cryoSPARC tutorial dataset]
 - Angstroms per pixel=0.6575
 - keV=300
 - Cs=2.7 [spherical aberration]
 - Total dose=53 e⁻/Å²
 - When importing the gain reference, you cannot have the wilde \$HOME in the path.
You must type it out: `/home/ubuntu/`
- EMPIAR-10025-T20S-micrographs
 - [EMPIAR link](#)
 - Micrographs (instead of movie files) that could be used in cryoSPARC tutorial dataset
- EMPIAR-10215-Aldolase
 - [EMPIAR link](#)
 - Micrographs
- EMPIAR-10241-TMEM16
 - [EMPIAR link](#)
 - Micrographs
- EMPIAR-10256-TRPV5-CaM
 - [EMPIAR link](#)
 - Extracted particle stack
 - Particle meta path:
 - `EMPIAR-10256-TRPV5-CaM/particles.star`
 - Particle data path:
 - `EMPIAR-10256-TRPV5-CaM/`
- EMPIAR-10180-spliceosome
 - [EMPIAR link](#)
 - Extracted particle stack

- Particle meta path:
 - EMPIAR-10180-spliceosome/Example/consensus_data.star
- Particle data path:
 - EMPIAR-10180-spliceosome/
- EMPIAR-10003-HIV-Trimer
 - (Infamous) [Einstein-from-noise dataset](#)
 - Dataset was collected at very low defocus, particles could not be seen
 - Authors used HIV trimer as a *template* to pick the data
 - Refined to 6Å structure that did not have reliable structural features
 - Example of model bias in cryo-EM data processing
 - [EMPIAR link](#)
 - See if you can solve an HIV trimer structure (!)

Configuration details for cryoSPARC on AWS

You are running cryoSPARC v2.9.0 on [p2.xlarge AWS instance](#) with the following specs:

- 4 vCPUs
- 1 GPU (NVIDIA K80)
- 31 GM RAM
- 800 GB storage
- Hourly rate: \$0.90/hr

Slack channel invite link

https://join.slack.com/t/cryoem-aca2019/shared_invite/enQtNzAzMjg1MDgxNzAyLTQzYzhlMzFIYTNkYjQwY2YxNTZkZDkzNzQ0Y2ZlOTU0YmQ1M2M5OTAzYTBiZTk0NGU5MzUwYjAwNzRiYTViNTY