## NCCAT SPA workshop cryoSPARC practical

### NCCAT cryoSPARC server

In your web browser go to: http://3.228.94.38:39000/

The cryoSPARC login for the tutorial will be:

* Username: [\*\*\*\*\*]
* Password: {\*\*\*\*\*\*\*\*\*\*\*}

### cryoSPARC T20S tutorial link

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

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

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### Where to create projects?

You may use the existing project or create a new project here:

/beegfs/appion/projects/

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### Data available for processing during cryo-EM short course

The following directory names correspond to datasets available for processing. These are all located in the directory on our file system (/beegfs/appion/sworkshop/):

#### EMPIAR-10025-T20S-movies

* + [EMPIAR link](https://www.ebi.ac.uk/pdbe/emdb/empiar/entry/10025/)
	+ 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 need to be explicit with the path since you may be sharing the instance. You must type it out: /beegfs/appion/sworkshop/10025\_subset/norm-amibox05-0.mrc
	+ 8.1G /beegfs/appion/sworkshop/10025\_subset/\*tif

#### EMPIAR-10025-T20S-micrographs

* + [EMPIAR link](https://www.ebi.ac.uk/pdbe/emdb/empiar/entry/10025/)
	+ Micrographs (instead of movie files) that could be used in cryoSPARC tutorial dataset
	+ 42g /beegfs/appion/sworkshop/10025/data/14sep05c\_averaged\_196/
	+ Notes:
	2.0T /beegfs/appion/sworkshop/10025 (full dataset from EMPIAR)

#### EMPIAR-10215-Aldolase

* + [EMPIAR link](https://www.ebi.ac.uk/pdbe/emdb/empiar/entry/10215/)
	+ Micrographs (use motion corrected aligned images, raw moves are in bz2 format that need to be uncompressed before processing)
	+ 1.5T /beegfs/appion/sworkshop/10215

#### EMPIAR-10241-TMEM16

* + [EMPIAR link](https://www.ebi.ac.uk/pdbe/emdb/empiar/entry/10241/)
	+ Micrographs
	+ 163G /beegfs/appion/sworkshop/10241

#### EMPIAR-10256-TRPV5-CaM

* + [EMPIAR link](https://www.ebi.ac.uk/pdbe/emdb/empiar/entry/10256/)
	+ Extracted particle stack
	+ Particle meta path:
		- 10256/data/particles.star
	+ Particle data path:
		- 10256/data/Micrographs
	+ 119G /beegfs/appion/sworkshop/10256
* EMPIAR-10180-spliceosome
	+ [EMPIAR link](https://www.ebi.ac.uk/pdbe/emdb/empiar/entry/10180/)
	+ Extracted particle stack
	+ Particle meta path:
		- 10180/data/Example/consensus\_data.star
	+ Particle data path:
		- 10180/data/Micrographs\*
	+ 127G /beegfs/appion/sworkshop/10180

#### EMPIAR-10003-HIV-Trimer

* + (Infamous) [Einstein-from-noise dataset](https://www.ncbi.nlm.nih.gov/pubmed/24106306)
		- 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](https://www.ebi.ac.uk/pdbe/emdb/empiar/entry/10003/)
	+ 587G /beegfs/appion/sworkshop/10003
	+ See if you can solve an HIV trimer structure (!)