

Project Help

SCIPIO

View Protocols SPA

Protocols SPA

- Imports
 - import movies
 - import micrographs
 - import particles
 - import volumes
- more
- Movies
- Micrographs
 - CTF estimation
 - Preprocess
- Particles
 - Picking
 - Extract
 - Preprocess
 - Filter
 - Mask
- 2D
 - Align
 - Classify
- 3D
 - Initial volume
 - Preprocess
 - Classify
 - Refine
 - xmipp3 - high
 - xmipp3 - pro.i
 - xmipp3 - estimate local defocus
 - relion - 3D auto-refine
 - relion - ctf refinement
 - relion - bayesian polishing
 - relion - 3D multi-body
 - eman2 - refine easy
 - cryosparc2 - 3D homogeneous refinement**
 - cryosparc2 - 3D non-uniform refinement
 - cryosparc2 - local ctf refinement (BETA)
 - cryosparc2 - global ctf refinement (BETA)
 - more
 - Postprocess
 - Analysis

Protocol Run: ProtCryoSparcRefine3D

cryoSPARC Protocol: cryosparc2 - 3D homogeneous refinement **finished** [Cite](#) [Help](#)

Run

Run name: cryosparc2 - 3D homogeneous refinement [Edit](#) Comment: [Edit](#)

Run mode: ☒ Continue ☐ Restart [?](#) Host: localhost

Parallel Threads: 1 MPI: 1 [?](#) Use queue? ☐ Yes ☒ No [?](#)

GPU IDs: 0 [?](#) Wait for: [?](#)

Expert Level: ☒ Normal ☐ Advanced

Input Refinement Compute settings

Input

Input particles: xmipp3 - extract particles 2/3 size,outputParticles [Q](#) [X](#) [E](#) [?](#)

Input volume: xmipp3 - crop/resize volumes 2/3,outputVol [Q](#) [X](#) [E](#) [?](#)

Mask to be applied to this map(Optional): [Q](#) [X](#) [E](#) [?](#)

[Close](#) [Save](#) [Execute](#)

