

View Protocols SPA

- Micrographs
 - xmipp3 - preprocess micrographs
 - CTF estimation
 - gctf - ctf estimation
 - relicon - export ctf
 - xmipp3 - ctf estimation
 - xmipp3 - ctf consensus
 - eman2 - ctf auto
 - grigoriefflab - ctfind4
- more
- Particles
 - Picking
 - relicon - auto-picking
 - xmipp3 - particle boxsize
 - xmipp3 - manual-picking (step 1)
 - xmipp3 - auto-picking (step 2)
 - xmipp3 - deep consensus picking
 - xmipp3 - assign tiltpairs
 - xmipp3 - picking consensus
 - sphere - cryolo picking
 - sphere - cryolo training
 - eman2 - boxer
 - eman2 - boxer auto
 - eman2 - sparx gaussian picker
 - bsoft - particle picking
 - Extract
 - Preprocess
 - Filter
 - xmipp3 - filter particles
 - xmipp3 - denoise particles

Protocol Run: SphireProtCRYOLOPicking

Protocol: sphere - cryolo picking finished [Cite](#) [Help](#)

Run

Run name: sphere - cryolo picking [Edit](#) Comment: [Edit](#)

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

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

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

Expert Level: ☒ Normal ☐ Advanced

Input Streaming

Input

Input Micrographs: xmipp3 - ctf consensus.outputMicrographs [Search](#) [Delete](#) [Eye](#) [?](#)

Use previous model: ☒ general ☐ other [?](#)

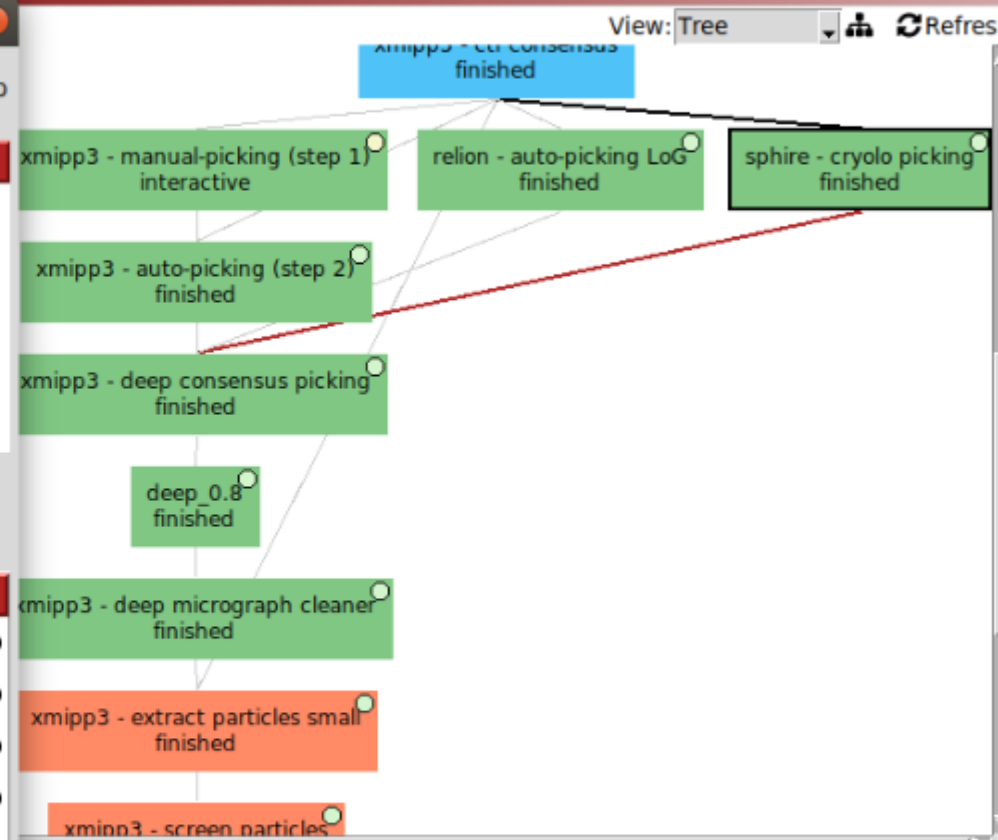
Confidence threshold: [?](#)

Low-pass filter: ☐ Yes ☒ No [?](#)

Box Size: [Search](#) [?](#)

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

- Input
 - inputMicrographs (from xmipp3 - ctf consensus -> outputMicrographs [outputMicrographs])
- Output
 - sphere - cryolo picking -> outputCoordinates



SetOfMicrographs (47 items, 3710 x 3838, 0.49 Å/px)

SetOfCoordinates (6491 items, 300 x 300)

[Analyze Results](#)