

View Protocols SPA

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View: Tree Refres

- Micrographs
 - xmipp3 - preprocess micrographs
 - CTF estimation
 - gctf - ctf estimation
 - relion - export ctf
 - xmipp3 - ctf estimation
 - xmipp3 - ctf consensus
 - eman2 - ctf auto
 - grigoriefflab - ctffind4
- Particles
 - Picking
 - relion - 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
 - Mask
- 2D
 - Align
 - Classify
- 3D
 - Initial volume
 - Preprocess
 - Classify

Protocol Run: XmippParticlePickingAutomatic

Protocol: xmipp3 - auto-picking (step 2) finished Cite Help

Run

Run name: xmipp3 - auto-picking (step 2) Comment

Run mode: ☒ Continue ☐ Restart Host: localhost

Parallel: ☒ Threads ☐ MPI 1 Use queue? ☐ Yes ☒ No

Wait for

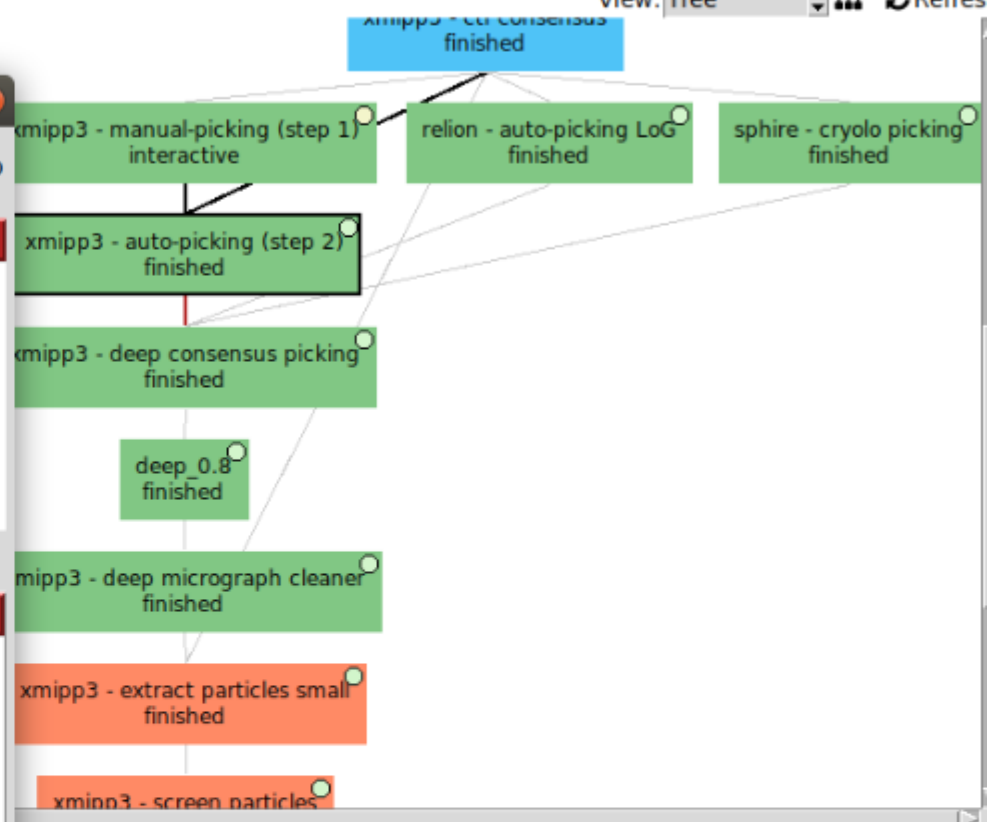
Input Streaming

Xmipp particle picking run: xmipp3 - manual-picking (step 1)

Micrographs to pick: ☐ Same as supervised ☒ Other

Micrographs: xmipp3 - ctf consensus.outputMicrographs

Close Save Execute



Analyze Results

Summary Methods Output Log

Input

xmippParticlePicking (from xmipp3 - manual-picking (step 1))

inputMicrographs (from xmipp3 - ctf consensus -> outputMicrographs [outputMicrographs])

Output

xmipp3 - auto-picking (step 2) -> outputCoordinates

729 particles picked (from 47 micrographs)

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

SetOfCoordinates (6388 items, 300 x 300)

SUMMARY

Number of input micrographs: 47

outputCoordinates:

Previous run: xmipp3 - manual-picking (step 1)

Manual particles picked: 28