

 **SCIPION** v3.0.6

View: Protocols SPA

- Protocols SPA
 - Imports
 - Movies
 - Micrographs
 - CTF estimation
 - Preprocess
 - Particles
 - Picking
 - xmipp3 - particle boxsize
 - xmipp3 - manual-picking (stac)
 - xmipp3 - auto-picking (stac)
 - xmipp3 - deep consensus picker
 - xmipp3 - deep micrograph classifier
 - xmipp3 - assign tiltpairs
 - xmipp3 - picking consensus
 - xmipp3 - pick noise
 - xmipp3 - remove duplicates
 - sphere - cryolo picking
 - sphere - cryolo training
 - relion - auto-picking
 - relion - auto-picking LoG
 - gautomatch - auto-picking
 - eman2 - boxer
 - eman2 - boxer auto
 - eman2 - sparx gaussian picker
 - cistem - find particles
 - Extract
 - Preprocess
 - Filter
 - Mask
 - 2D
 - Align
 - Classifu
 - 3D
 - Initial volume
 - Preprocess
 - Classifu
 - Refine
 - Postprocess
 - Analysis
 - Reconstruct
 - Tools
 - Exports

Protocol Run: SparxGaussianProtPicking

Protocol: eman2 - sparx gaussian picker finished [Cite](#) [Help](#)

Run

Run name: eman2 - sparx gaussian picker [Edit](#) Comment: [Edit](#)

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

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

Wait for: [Help](#)

Expert Level: ☒ Normal ☐ Advanced

Input

Input Micrographs: xmipp3 - ctf consensus GCTF+CTFFind4+Xmipp.outputMicrographs [Search](#) [Delete](#) [Eye](#) [Help](#)

Box Size: 300 [Search](#) [Edit](#) [Help](#)

Picker range: Lower 0.2 Higher 30.0 [Edit](#) [Help](#)

Gauss Width: 30.0 [Edit](#) [Help](#)

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

Summary **Methods** **Output Log**

Input

- inputMicrographs (from xmipp3 - ctf consensus GCTF+CTFFind4+Xmipp -> output.M SetOfMicrographs (28 items, 3710 x 3838, 0.49 Å/px))

Output

- eman2 - sparx gaussian picker -> outputCoordinates SetOfCoordinates (6656 items, 300 x 300)

[Ana](#)

View: Tree

- nsensus GCTF+CTFFind4+... finished
- er
- sphere - cryolo pick finished