

 **SCIPION** v3.0.6 -

View: Protocols SPA

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

RELION Protocol: relion - auto-picking LoG finished [Cite](#) [Help](#)

Run

Run name: relion - auto-picking LoG [Edit](#) Comment: [Edit](#)

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

Parallel: MPI 4 [?](#) Use queue? ☐ Yes ☒ No [Edit](#) [?](#)

Wait for: [?](#)

Input **Streaming**

Input

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

Box size (px): 300 [?](#)

Laplacian of Gaussian

Diameter for LoG filter (A): Min 100 Max 200 [Edit](#) [?](#)

Are the particles white? ☐ Yes ☒ No [?](#)

Maximum resolution to consider (A): 20.0 [?](#)

Adjust default threshold (stddev): 0.0 [Edit](#) [?](#)

Upper threshold (stddev): 999.0 [Edit](#) [?](#)

Additional arguments: [?](#)

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

relion - auto-picking LoG -> outputCoordinates SetOfCoordinates (4291 items, 300 x 300)

View: Tree

consensus GCTF+CTFFind4+... finished

sphere - cryolo pick finished

Ana

710 x 3838, 0.49 Å/px)