

View Protocols SPA

- import micrographs
- import particles
- import volumes

more

Movies

Micrographs

- xmipp3 - preprocess micrographs
- CTF estimation

Particles

- Picking
- Extract
- Preprocess
- Filter
- Mask

2D

- Align
- Classify

3D

- Initial volume
 - relic - 3D initial model
 - xmipp3 - ransac
 - xmipp3 - reconstruct significant
 - xmipp3 - swarm consensus
 - xmipp3 - convert a PDB
 - eman2 - initial model
 - eman2 - initial model SGD
 - cryosparc2 - initial model

more

- Preprocess
- Classify
- Refine
- Postprocess
- Analysis
- Reconstruct

Protocol Run: ProtRelionInitialModel



Protocol: relic - 3D initial model

finished Cite Help

Run

Run name relic - 3D initial model

Comment

Run mode

Continue Restart

Host localhost

Parallel

Threads

1

MPI

3

Use queue?

Yes No

Wait for

Expert Level

Normal Advanced

Input

Optimisation

SGD

Compute

Input

Continue from a previous run? Yes No

Input particles apoParticles.outputParticles

Particle mask diameter (A) -1

CTF

Do CTF-correction? Yes No

Have data been phase-flipped? (Don't answer, see help)

Close

Save

Execute

Output

relic - 3D initial model -> outputVolume

relic - 3D initial model -> outputParticles

Volume (74 x 74 x 74, 1.98 Å/px)

SetOfParticles (5673 items, 74 x 74, 1.98 Å/px)

apoParticles
finished

relic - 3D initial model
finished

xmipp3 - convert to pseudoat
finished

atsas - convert PDB to SAXS c
finished

Analyze Results