

A

Project Help



View Protocols SPA

2D

- Align
- Classify

3D

- Initial volume
- Preprocess
- Classify
- Refine
- Postprocess
- Analysis
- Reconstruct

Tools

- Sets
- Calculators
 - xmipp3 - operate particles
 - xmipp3 - operate volumes
 - chimera - chimera operate
 - chimera - chimera restore session
 - phenix - superpose pdbs

Model Building

- xmipp3 - extract unit cell
- chimera - chimera rigid fit
- chimera - model from template
- powerfit_scipion - powerfit
- ccp4 - coot refinement
- ccp4 - reflat
- phenix - emringer
- phenix - real space refine
- phenix - molprobit
- xmipp3 - 3d bionotes

B

Protocol Run: PhenixProtRunSuperposePDBs

Phenix Protocol: phenix - superpose pdbs Cite Help

Run

Run name phenix - superpose pdbs ✎ **Comment** ✎

Run mode ☒ Continue ☐ Restart ? **Host** localhost ▼

Use queue? ☐ Yes ☒ No ?

Wait for ?

Input

Fixed atomic structure 🔍 🗑️ 👁️ ?

Moving atomic structure 🔍 🗑️ 👁️ ?

✕ Close 💾 Save ⚙️ Execute