

View Protocols SPA

Micrographs

- xmipp3 - preprocess micrographs
- xmipp3 - ctf estimation
- CTF estimation

more

Particles

- Picking
- Extract
- Preprocess
- Filter
- Mask

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
 - atomstructutils - operator
 - phenix - superpose pdbs

Model Building

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

Protocol Run: ProtAtomStrucOperate

Protocol: atomstructutils - operator finished [Cite](#) [Help](#)

Run

Run name atomstructutils - operator (chainA) [Edit](#) Comment [Add](#)

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

Use queue? ☐ Yes ☒ No [?](#)

Wait for [?](#)

Input

Atomic structure 1 chimera - chimera operate (copy 2) outputPdb_01 [Search](#) [Refresh](#) [Help](#)

Operation: extractChain [Help](#)

Chain { "model": 0, "chain": "A", "residues": 141 } [Edit](#) [Help](#)

Start at residue # -1 [Help](#)

End at residue # -1 [Help](#)

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

Output

pdbeFileToBeRefined (from chimera - chimera operate (copy 2) -> outputPdb_01 [outputPdb_01])

atomstructutils - operator (chainA) -> outputPdb

SUMMARY

No summary information.

operator (chainA)
shed