

View Model building

- Model building
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 - import atomic structure
 - import sequence
 - Preprocess map
 - xmipp3 - create 3d mask
 - xmipp3 - local MonoRes
 - xmipp3 - localdeblur sharpening
 - xmipp3 - extract asymmetric unit
 - xmipp3 - deepEMhancer
 - Initial model
 - chimerax - model from template
 - Rigid fitting
 - phenix - dock in map
 - chimerax - rigid fit
 - Flexible fitting
 - ccp4 - coot refinement
 - ccp4 - refrac
 - phenix - real space refine
 - Validation
 - phenix - emringer
 - phenix - molprobtity
 - phenix - validation_cryoem
 - xmipp3 - validate fsc-q
 - Tools-Calculators
 - atomstructutils - operator
 - atomstructutils - convert_sym
 - phenix - superpose pdbs**
 - chimerax - operate
 - chimerax - restore session
 - chimerax - contacts
 - chimerax - map subtraction
 - xmipp3 - map from atomic structure
 - Others
 - Exports
 - export to DB

B

Protocol Run: PhenixProtRunSuperposePDBs

Phenix

Protocol: phenix - superpose pdbs

[Cite](#) [Help](#)

Run

Run name phenix - superpose pdbs (2) ✎ Comment ✎

Run mode ☒ Continue ☐ Restart ? Host localhost ▼

Use queue? ☐ Yes ☒ No ✎ ?

Wait for ?

Input

Fixed atomic structure 🔍 🗑️ 👁️ ?

Moving atomic structure 🔍 🗑️ 👁️ ?

✕ Close 💾 Save ⚙️ Execute