

View **Model building**

- Model building
 - Imports
 - import volumes
 - import atomic structure
 - import sequence
 - Preprocess map
 - xmipp3 - create 3d mask
 - xmipp3 - local MonoRes
 - xmipp3 - localdeblur sharpening
 - xmipp3 - extract unit cell
 - Initial model
 - chimera - model from template
 - Rigid fitting
 - powerfit_scipion - powerfit
 - chimera - chimera rigid fit
 - Flexible fitting
 - phenix - real space refine
 - ccp4 - coot refinement
 - ccp4 - refmac
 - Validation
 - phenix - emringer
 - phenix - molprobtity
 - phenix - validation_cryoem
 - Tools-Calculators
 - phenix - superpose pdbs
 - atomstructutils - operator
 - atomstructutils - convert_sym
 - chimera - chimera operate
 - chimera - chimera restore session
 - chimera - contacts
 - Others
 - xmipp3 - 3d bionotes
 - Exports
 - export to EMDB

Protocol Run: PhenixProtRunValidationCryoEM

Phenix Protocol: phenix - validation_cryoem **finished** [Cite](#) [Help](#)

Run

Run name: phenix - validation_cryoem (2) [Edit](#) Comment: [Edit](#)

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

Parallel Threads: 1 [?](#) Use queue? ☐ Yes ☒ No [?](#) Wait for: [?](#)

Expert Level: ☒ Normal ☐ Advanced

Input

Input Volume: ccp4 - coot refinement (copy).output3DMap_0001 [Search](#) [Delete](#) [Eye](#) [?](#)

Resolution (Å): 3.2 [?](#)

Input atomic structure: phenix - real space refine.outputPdb [Search](#) [Delete](#) [Eye](#) [?](#)

Extra Params: [?](#)

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