

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

Edit Copy Delete Steps Browse Db Collapse Labels

Protocol Run: PhenixProtRunValidationCryoEM

Phenix

Protocol: phenix - validation_cryoem

finished

Cite Help

Run

Run name phenix - validation_cryoem (2)

Comment

Run mode

Continue

Restart

Host

localhost

Parallel

Threads

1

Use queue?

Yes

No

Wait for

Expert Level

Normal

Advanced

Input

Input

Input Volume ccp4 - coot refinement (copy).output3DMap_0001

Resolution (A):

3.2

Input atomic structure

phenix - real space refine.outputPdb

Close

Save

Execute

Summary

Methods

Output Log

Input

inputVolume (from ccp4 - coot refinement (copy) -> output3DMap_0001 [output3DMap_0001])

inputStructure (from phenix - real space refine -> outputPdb [outputPdb])