

A

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 - refrac

## 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

B

Protocol Run: ChimeraModelFromTemplate

Protocol: scipion - model from template

Cite ? Help

**Run**

Run name:  Comment:

Run mode: ☒ Continue ☐ Restart ? Host:

Use queue? ☐ Yes ☒ No ?

Wait for:  ?

Input Help

**Input**

Atomic structure used as template:  ?

Chain:  ?

Target sequence:  ?

Additional sequences to align? ☒ Yes ☐ No ?

Other sequences to align:

Object	Info	?

Multiple alignment tool:  ?

Close Save Execute