

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 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 - reftac
- 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



### Protocol: chimera - rigid fit

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

#### Run

Run name **chimerax - rigid fit**

Comment

Run mode

☒ Continue ☐ Restart

Host **localhost**

Use queue? ☐ Yes ☒ No

Wait for

Input

Help

#### Input

##### Input Volume

xmipp3 - extract asymmetric unit HEMOGLOBIN.outputVolume

Input additional Volumes

Object

Info

Atomic structure to be fitted

phenix - dock in map.outputPdb

Other reference atomic structures

Object

Info

Close

Save

Execute