

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 - refrac
- phenix - real space refine


## Validation

- phenix - emringer
- phenix - molprobt
- phenix - validation\_cryoem
- xmipp3 - validate fsc-q

## Tools-Calculators

- atomstructutills - operator

Protocol Run: XmippProtExtractUnit


**Protocol: xmipp3 - extract asymmetric unit**
finished
Cite
Help

**Run**

Run name **xmipp3 - extract asymmetric u**
Comment

Run mode ☒ Continue ☐ Restart
Host localhost

Use queue? ☐ Yes ☒ No

Wait for

Input

**Input**

**Input Volume** pwem - import volumes HEMOGLOBIN.outputVolume

Symmetry Cn (Cn)

Symmetry Order 2

offset -45.0

Inner Radius (px) 0.0

Outer Radius (px) 40.0

Expand Factor 0.2

☒ Analyze Results

Close Save Execute

m - import sequence HBA  
finished

xmipp3 - de  
fini

xmipp3 - extract asym  
fini