

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 - chimera from template

## Rigid fitting

- powerfit\_sciption - powerfit
- chimera - chimera rigid fit

## Flexible fitting

- phenix - real space refine
- ccp4 - coot refinement
- ccp4 - reformat

## Validation

- phenix - emringer
- phenix - molprobity
- 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: XmippProtLocSharp



Protocol: xmipp3 - localdeblur sharpening

finished

Cite Help

## Run

Run name **xmipp3 - localdeblur sharpenin**

Comment

Run mode

☒ Continue ☐ Restart

Host localhost

Parallel

Threads 4

Use queue?

☐ Yes ☒ No

Wait for

## Expert Level

☐ Normal☒ Advanced

## Input

## Input

Input Map **scipion - import volumes HEMOGLOBIN.outputVolume**Resolution Map **xmipp3 - local MonoRes.resolution\_Volume**

lambda 1.0

K 0.025

Close

Save

Execute

## SUMMARY

LocalDeblur Map