

## 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 - 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



## Protocol: xmipp3 - viewer extract unit cell

Visualization of input volume and extracted unit cell

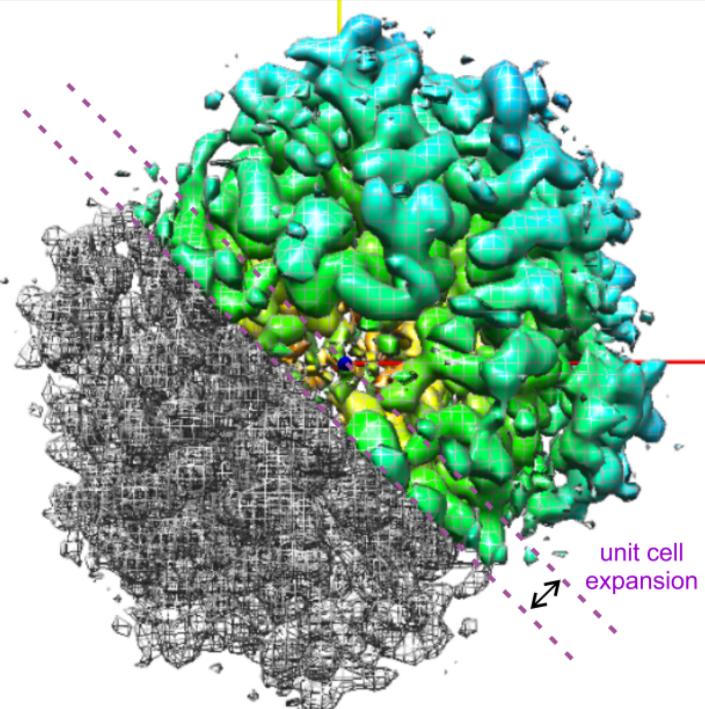
Visualization of input volume and extracted unit cell

Display volume with  chimera  slices

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UCSF Chimera

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phenix - superpose p  
finished

Summary Methods Output

## Input

inputVolumes (from scipion)

## Output

xmipp3 - extract unit cell