



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

Run

Run name xmipp3 - local MonoRes

Run mode Continue Restart

Host localhost

Parallel Threads 4

Use queue? Yes No

Wait for

Expert Level Normal Advanced

Input

Input

Would you like to use half volumes? Yes No

3 Input volume scipion - import volumes HEMOGLOBIN.outputVolume
Binary Mask xmipp3 - create 3d mask.outputMask

Extra parameters

Resolution Range (Å) High 0.0 Low 6.0 Step

Significance 0.95

Mask threshold 0.5

4 Is the original premasked? Yes No
5 Spherical mask radius (px) 43.0

Filter input volume with local resolution? Yes No

Close

Save

Execute

