

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 - refmac
- phenix - real space refine

Validation

- phenix - emringer
- phenix - molprobt
- 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

Protocol Run: ChimeraProtRigidFit

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 Volume xmipp3 - extract asymmetric unit HEMOGLOBIN.outputVolume

Object	Info
Input additional Volumes	

Atomic structure to be fitted phenix - dock in map.outputPdb

Object	Info
Other reference atomic structures	

SUMMARY

Produced files:
we have some result

Close Save Execute

BA_HORSE pwem -

chimerax - model from tem
finished

phenix - dock in map
finished

chimerax - rigid fit
finished

Analyze Results

= True)

= False)