

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 - reftmac
- phenix - real space refine

Validation

- phenix - emringer
- phenix - molprobtty
- phenix - validation_cryoem
- xmipp3 - validate fsc-q

Tools-Calculators

- atomstructutils - operator
- atomstructutils - convert_sym
- phenix - superpose pdbs
- chimerax - operate
- chimerax - restore session
- chimerax - contacts

Protocol Run: CCP4ProtRunReftmac

CCP4 Protocol: ccp4 - reftmac

finished Cite Help

Run

Run name Comment

Run mode ☒ Continue ☐ Restart Host

Use queue? ☐ Yes ☒ No

Wait for

Expert Level ☐ Normal ☒ Advanced

Input

Input Volume

Atomic structure to be refined

Max. Resolution (Å):

Min. Resolution (Å):

Generate masked volume ☒ Yes ☐ No

SFCALC mapradius:

SFCALC mradius:

Number of refinement iterations:

Matrix refinement weight:

B Factor:

Extra parameters:

Close Save Execute

Protocols | Data

Refres

Import atomic struct
finished

Max - model from te
finished

phenix - dock in ma
finished

chimerax - rigid fit
finished

ccp4 - coot refine
interactive

ccp4 - reftmac
finished

Analyze Results

volume=False)

volume=False)