

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
- NEW** xmipp3 - deepEMhancer

Initial model

- chimerax - model from template

Rigid fitting

- phenix - dock in map
- chimerax - rigid fit

Flexible fitting

- phenix - real space refine
- phenix - search fit
- ccp4 - coot refinement
- ccp4 - refmac

Validation

- phenix - emringer
- phenix - molprobtity
- phenix - validation_cryoem
- NEW** xmipp3 - validate fsc-q

Tools-Calculators

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

Edit Copy Delete Browse Collapse Labels

View: Tree

Protocol Run: PhenixProtSearchFit

Phenix Protocol: phenix - search fit finished [Cite](#) [Help](#)

Run

Run name: phenix - search fit [Edit](#) Comment: [Edit](#)

Run mode: ☒ Continue ☐ Restart [?](#) Host: localhost

Parallel: ☒ Threads ☐ MPI 1 [?](#) Use queue? ☐ Yes ☒ No [?](#) [Edit](#)

Wait for: [?](#)

Expert Level: ☒ Normal ☐ Advanced

Input

Input Volume: xmipp3 - extract asymmetric unit.outputVolume [?](#) [Edit](#) [Delete](#)

Resolution (A): 3.2 [?](#) [Edit](#) [Delete](#)

Input atomic structure: chimerax - rigid fit.5ni1_chainA_94_118_MutALA_Atom_struct__3_001688 [?](#) [Edit](#) [Delete](#)

Test sequence: pwem - import sequence.outputSequence [?](#) [Edit](#) [Delete](#)

First residue: [{"residue": 90, "H"}] [?](#) [Edit](#) [Delete](#)

Last residue: [{"residue": 120, "P"}] [?](#) [Edit](#) [Delete](#)

Execute [Close](#) [Save](#)

