

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 - molprobtity
- 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

Exports

- export to DB

B

Protocol Run: PhenixProtRunValidationCryoEM

Phenix

Protocol: phenix - validation_cryoem [Cite](#) [Help](#)

Run

Run name phenix - validation_cryoem (3) [Edit](#) Comment [Edit](#)

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

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

Wait for [?](#)

Expert Level ☐ Normal ☒ Advanced

Input

Input

Input Volume [Search](#) [Delete](#) [Eye](#) [?](#)

Resolution (A): 3.0 [?](#)

Input atomic structure. [Search](#) [Delete](#) [Eye](#) [?](#)

Extra Params [?](#)

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