

A

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 - reftmac

Validation

- phenix - emringer
- phenix - molprobtity
- 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

B

Protocol Run: PhenixProtRunRSRefine

Phenix Protocol: phenix - real space refine [Cite](#) [Help](#)

Run

Run name **phenix - real space refine** [Edit](#) Comment [Edit](#)

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

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

Wait for [?](#)

Expert Level ☐ Normal ☒ Advanced

Input

Input Volume [?](#) [Trash](#) [Eye](#)

Resolution (Å): **3.0** [?](#)

Input atomic structure. [?](#) [Trash](#) [Eye](#)

Extra Params [?](#)

Secondary structure ☒ Yes ☐ No [?](#)

Macro cycles **5** [?](#)

Optimization strategy options

Global minimization: ☒ Yes ☐ No [?](#)

Rigid body: ☐ Yes ☒ No [?](#)

Local grid search: ☐ Yes ☒ No [?](#)

Morphing ☐ Yes ☒ No [?](#)

Simulated annealing ☐ Yes ☒ No [?](#)

Atomic Displacement Parameters (ADPs) ☒ Yes ☐ No [?](#)

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