


- 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 - refrac
 - 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
 - chimerax - map subtraction
 - xmipp3 - map from atomic structure
 - Others
 - Exports
 - export to DB

B  **Protocol Run: PhenixProtRunRSRefine**

Protocol: phenix - real space refine Cite Help

Run

Run name phenix - real space refine (2) Comment

Run mode ☒ Continue ☐ Restart Host localhost

Parallel Threads 1 Use queue? ☐ Yes ☒ No Wait for

Expert Level ☐ Normal ☒ Advanced

Input

Input Volume Resolution (A): 3.0

Input atomic structure. 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