

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 - refmac**
 - Validation
 - phenix - emringer
 - phenix - molprobity
 - 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: CCP4ProtRunRefmac
Close
Save
Execute

CCP4
Protocol: ccp4 - refmac
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 (A):

Min. Resolution (A):

Generate masked volume
 Yes
 No

SFCALC mapradius:

SFCALC mradius:

Number of refinement iterations:

Matrix refinement weight:

B Factor:

Extra parameters: