

A

Project Help



(2018-10-)

View Protocols SPA

- ▶ ☒ Initial volume
- ▶ ☒ Preprocess
- ▶ ☒ Classify
- ▶ ☒ Refine
- ▶ ☒ Analysis
- ▶ ☒ Reconstruct

Tools

- ▶ ☒ Sets

Calculators

- ☐ xmipp3 - operate particles
- ☐ xmipp3 - operate volumes
- ☐ chimera - chimera operate
- ☐ chimera - chimera restore session
- ☐ phenix - superpose pdbs

Model Building

- ☐ xmipp3 - extract unit cell
- ☐ chimera - chimera rigid fit
- ☐ chimera - model from template
- ☐ powerfit_scipion - powerfit
- ☐ ccp4 - coot refinement
- ☒ **ccp4 - refmac**
- ☐ phenix - emringer
- ☐ phenix - real space refine
- ☐ phenix - molprobrity
- ☐ xmipp3 - 3d bionotes

B

Protocol Run: CCP4ProtRunRefmac

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 (Å): [?](#)

Min. Resolution (Å): [?](#)

Generate masked volume ☒ Yes ☐ No [?](#)

SFCALC mapradius: [?](#)

SFCALC mradius: [?](#)

Number of refinement iterations: [?](#)

Matrix refinement weight: [?](#)

B Factor: [?](#)

Extra parameters: [?](#)