

View Protocols SPA

- ▶ C Preprocess
- ▶ C Filter
- ▶ C Mask

2D

- ▶ C Align
- ▶ C Classify

3D

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

Tools

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 - molprobit
- ▶ xmipp3 - 3d bionotes

Edit Copy

ccp4 - coot

phenix - real

Summary Me

Input

inputVolume (from xmipp3 - extract unit cell symC2 offset -45 -> outputVolume Volume (101 x 101 x 101, 1.05 Å/px)

SUMMARY

Phenix

Protocol: phenix - real space refine

Cite Help

Run

Run name phenix - real space refine HBA

Comment

Run mode ☒ Continue ☐ Restart

Host

localhost

Use queue?

☐ Yes

☒ No

Wait for

Expert Level

☒ Normal

☐ Advanced

Input

Input

Input Volume ccp4 - coot refinement.output

Resolution (Å): 3.2

Input atomic structure.

chimera - rigid fit HBA_HUMAN.out

Close

Save

Execute

Analyze Results