












View Protocols SPA

- ▷  Preprocess
- ▷  Filter
- ▷  Mask

2D











- ▷  Align
- ▷  Classify

3D

- ▷  Initial volume
- ▷  Preprocess
- ▷  Classify
- ▷  Refine
- ▷  Analysis
- ▷  Reconstruct

Tools

Model Building

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

Phenix

Protocol: phenix - emringer

finished

Cite

? Help

Run

Run name

phenix - emringer

Comment

Run mode

☒ Continue

☐ Restart

Host

localhost

Use queue?

☐ Yes

☒ No

Wait for

Input

Input

Input Volume

xmipp3 - extract unit cell symC2 offs

Input atomic structure

ccp4 - reframe HBA_HUMAN.output

Close

Save

Execute

SUMMARY

Optimal Threshold: 0.14 Rotamer-Ratio: 0.87

Max Zscore: 4.77 Model Length: 84

EMRinger Score: 5.20

phenix - emringer
finished

mac HBA_HUMAN No_MA
finished

phenix - emringer (copy 9)
finished

Analyze Results

Å/px)
volume=False)