










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 - rigid fit
-  scipion - model from template
-  powerfit - powerfit
-  ccp4 - coot refinement
-  ccp4 - refmac
-  **phenix - emringer**
-  phenix - real space refine
-  phenix - molprobtity

**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 Volume xmipp3 - extract unit cell symC2 offs

Input atomic structure ccp4 - refmac 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 - emring finished

mac HBA\_HUMAN No\_MA finished

nix - emringer (copy 9) finished

Analyze Results

Å/px)  
volume=False)