

view **Protocols SPA**

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▶ **Initial volume**

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▶ **Refine**

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▶ **Tools**

▼ **Model Building**

▶ **xmipp3 - extract unit cell**

▶ **chimera - chimera rigid fit**

▶ **chimera - model from template**

▶ **powerfit\_scipion - powerfit**

▶ **ccp4 - coot refinement**

▶ **ccp4 - refrac**

▶ **phenix - emringer**

▶ **phenix - real space refine**

▶ **phenix - molprobability**

▶ **xmipp3 - 3d bionotes**
**Phenix**

Protocol: phenix - molprobability

finished

Cite

? Help

Run

Run name **phenix - molprobability**

Comment

Run mode

☒ Continue ☐ Restart

Host

localhost

Use queue?

☐ Yes ☒ No

Wait for

Input

Input

Input Volume **xmipp3 - extract unit cell symC2 off**

Resolution (A):

3.2

Input atomic structure.

**ccp4 - refrac HBA\_HUMAN.output**

Close

Save

Execute

### SUMMARY

MolProbability statistics:

Ramachandran outliers: 0.00 % (Goal: &lt; 0.2%) Ramachandran favored: 94.96 % (Goal: &gt; 98%)

Rotamer outliers: 3.54 % (Goal: &lt; 1%) C-beta outliers: 0 (Goal: 0)

Clashscore: 1.81 Overall score: 1.71

Refres

HUMAN (coot)

d

SK

me=False)

Analyze Results

ox)

ume=False)