

View Protocols SPA

Preprocess

Classify

Refine

Analysis

Reconstruct

Tools

Sets

Calculators

1 xmipp3 - operate particles

xmipp3 - operate volumes

chimera - chimera operate

chimera - chimera restore session

phenix - superpose pdbs

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 - molprobability

Protocol Run: PhenixProtRunSuperposePDBs

Phenix

Protocol: phenix - superpose pdbs

finished

Cite

Help

Run

Run name phenix - superpose pdbs refm

Comment

Run mode

Continue

Restart

Host localhost

Use queue?

Yes

No

Wait for

Input

Fixed atomic structure chimera - rigid fit.outputPdb\_01 (280)

Moving atomic structure ccp4 - refmac coot\_rsr.outputPdb (4)

Close

Save

Execute

SUMMARY

RMSD between fixed and moving atoms (start): 0.39

RMSD between fixed and moving atoms (final): 0.384

phenix - superpose pdbs finished

Analyze Results

lume=True)

lume=False)