

View

Protocols SPA

Preprocess

Classify

Refine

Analysis

Reconstruct

Tools

Sets

Calculators

1xmipp3 - operate particles

xmipp3 - operate volumes

chimera - chimera operate

chimera - chimera restore session

phenix - superpose pdbs

Model Building

xmipp3 - extract unit cell

chimera - chimera rigid fit

chimera - model from template

powerfit\_scipion - powerfit

ccp4 - coot refinement

ccp4 - re mac

phenix - emringer

phenix - real space refine

phenix - molprobability

Protocol Run: PhenixProtRunSuperposePDBs

Phenix

Protocol: phenix - superpose pdbs

finished

Cite

Help

Run

Run namephenix - superpose pdbs refmz

Comment

Run modeContinueRestart

Hostlocalhost

Use queue?YesNo

Wait for

Input

Input

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

Moving atomic structureccp4 - re mac coot\_rsr.outputPdb (4)

2

3

Close

Save

4Execute

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

5

lume=True)

lume=False)