

A

Project Help



View Protocols SPA

▷ Classify

▼ 3D

▷ Initial volume

▷ Preprocess

▷ Classify

▷ Refine

▷ Analysis

▷ Reconstruct

▼ Tools

▷ Sets

▼ Calculators

xmipp3 - operate particles

xmipp3 - operate volumes

chimera - chimera operate

chimera - chimera restore s

phenix - superpose pdbs

▼ Model Building

xmipp3 - extract unit cell

chimera - chimera rigid fit

chimera - model from template

powerfit_scipion - powerfit

ccp4 - coot refinement

ccp4 - refmac

phenix - emringer

phenix - real space refine

phenix - molprobit

xmipp3 - 3d bionotes

B

Protocol Run: ChimeraModelFromTemplate



Protocol: scipion - model from template

Cite Help

Run

Run name scipion - model from template

Comment

Run mode

☒ Continue
 ☐ Restart

Host localhost

Use queue?

☐ Yes
 ☒ No

Wait for

Input

Help

Input

Atomic structure used as template

Chain

Target sequence

Additional sequences to align?

☒ Yes
 ☐ No

Other sequences to align

Object

Info

Multiple alignment tool:

Clustal Omega

Close

Save

Execute