

Project Help

SCIPION

(2018)

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 - molprobrity

Protocol Run: ChimeraModelFromTemplate

Protocol: scipion - model from template

Cite Help

Run

Run name: scipion - model from template Comment: [text box]

Run mode: ☒ Continue ☐ Restart ? Host: localhost

Use queue? ☐ Yes ☒ No ?

Wait for: [text box] ?

Input Help

Input

PDBx/mmCIF file template: scipion - import structure 1pbx.outpu

Chain: [model: 0, chain: A, 142 residues]

Target sequence: scipion - import sequence HBA_HUI

Additional sequences to align? ☒ Yes ☐ No

Other sequences to align

Object	Info
scipion - import sequence HORSE.outp	HBA_HORSE_P01958
scipion - import sequence RABIT.outp	HBA_RABIT_P01948
scipion - import sequence MELGA.outp	HBA_MELGA_P81023
scipion - import sequence ALDGI.outp	HBAD_ALDGI_P83134

Multiple alignment tool: Clustal Omega

Close Save Execute

Protocols | Data

scipion - import se
finishe

Analyze Results