



## 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

Atomic structure used as 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

1

Tools

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 - molprobability
- xmipp3 - 3d bionotes

Protocols | Dat

Refre

scipion - import se  
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Analyze Results