

View **Model building**

Model building

Imports

- import volumes
- import atomic structure
- import sequence

Preprocess map

- xmipp3 - create 3d mask
- xmipp3 - local MonoRes
- xmipp3 - localdeblur sharpening
- xmipp3 - extract unit cell

Initial model

- chimera - model from template

Rigid fitting

- powerfit_scipion - powerfit
- chimera - chimera rigid fit

Flexible fitting

- phenix - real space refine
- ccp4 - coot refinement
- ccp4 - refrac

Validation

- phenix - emringer
- phenix - molprobrity
- phenix - validation_cryoem

Tools-Calculators

- phenix - superpose pdbs
- atomstructutils - operator
- atomstructutils - convert_sym
- chimera - chimera operate
- chimera - chimera restore session
- chimera - contacts**

Others

- xmipp3 - 3d bionotes

Exports

- export to EMDB

Protocol: chimera - contacts

finished Cite Help

Run

Run name: chimera - contacts (unit cell) Comment:

Run mode: ☒ Continue ☐ Restart ? Host: localhost

Use queue? ☐ Yes ☒ No ?

Wait for:

Expert Level: ☒ Normal ☐ Advanced

Input

Input

Atomic Structure: atomstructutils - operator (unit cell).outputPdb ? ? ? ?

Chain Labeling: {"A": "chainA", "A002": "HEM_A", "B": "chainB", "B002": "H ? ? ? ?

Apply symmetry: ☒ Yes ☐ No

Symmetry: Cn

Symmetry Order: 2

Close Save Execute

Entry Grid

	<i>label</i>
A	chainA
A002	HEM_A
B	chainB
B002	HEM_B
OK	