



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 - re mac

Validation

phenix - emringer

phenix - molprobity

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 Run: ProtImportPdb



Protocol: scipion - import atomic structure

finished



Help

Run

Run name scipion - import atomic structu

Comment

Run mode

Continue

Restart



Host

localhost

Use queue?

Yes

No



Wait for

Input

Input

Import atomic structure from

id

file

Atomic structure ID

1pbx

Input Volume



Close



Save



Execute

Summary

Methods

Output Log

Input

Output

scipion - import atomic structure 1PBX -> outputPdb

AtomStruct (pseudoatoms=False, volume=False)

Analyze Results