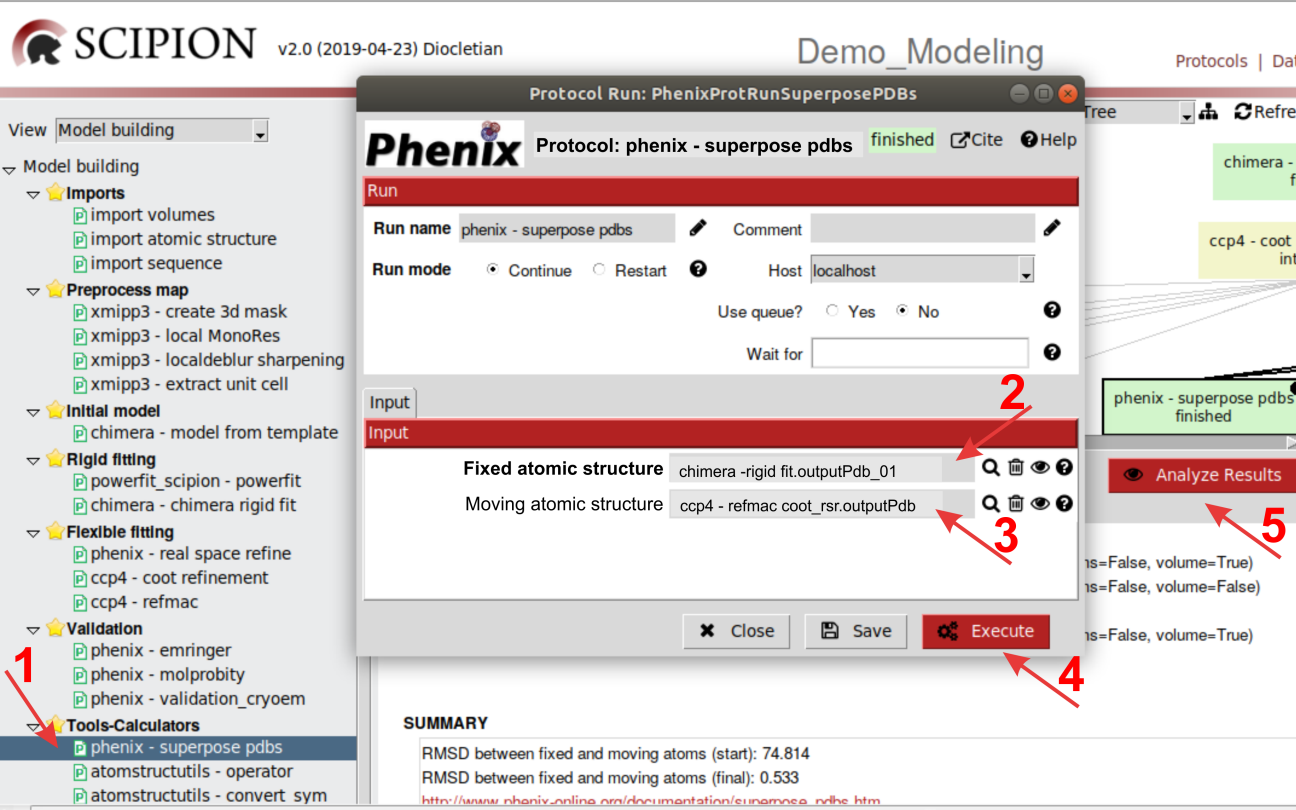
SCIPION
v2.0 (2019-04-23) Diocletian
Demo_Modeling
Protocols | Dat
Protocol Run: PhenixProtRunSuperposePDBs
Phenix
Protocol: phenix - superpose pdbs
finished
Cite
Help
Run
Run name
phenix - superpose pdbs
Comment
Run mode
Continue
Restart
Host
localhost
Use queue?
Yes
No
Wait for
Input
Input
Fixed atomic structure
chimera -rigid fit.outputPdb_01
Moving atomic structure
ccp4 - refmac coot_rsr.outputPdb
Close
Save
Execute
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 - refmac
Validation
phenix - emringer
phenix - molprobity
phenix - validation_cryoem
Tools-Calculators
phenix - superpose pdbs
atomstructutils - operator
atomstructutils - convert_sym
Tree
Refre
chimera -
ccp4 - coot
int
phenix - superpose pdbs
finished
Analyze Results
ns=False, volume=True)
ns=False, volume=False)
ns=False, volume=True)
SUMMARY
RMSD between fixed and moving atoms (start): 74.814
RMSD between fixed and moving atoms (final): 0.533
1
2
3
4
5