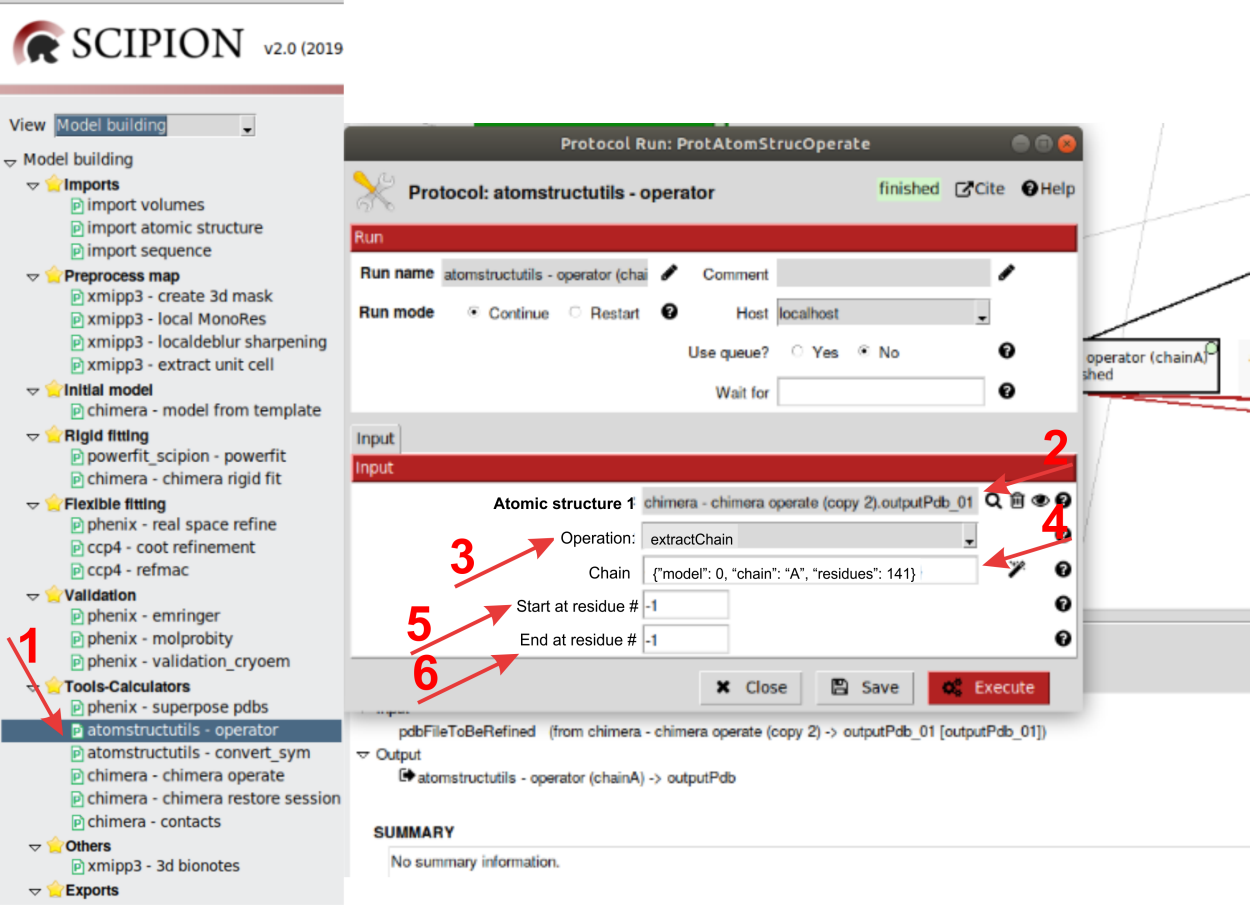
SCIPION v2.0 (2019
View Model building
Model building
Imports
import volumes
import atomic structure
import sequence
Preprocess map
xmipp3 - create 3d mask
xmipp3 - local MonoRes
xmipp3 - localdeblur sharpening
xmipp3 - extract unit cell
Initial model
chimera - model from template
Rigid fitting
powerfit_scipion - 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
chimera - chimera operate
chimera - chimera restore session
chimera - contacts
Others
xmipp3 - 3d bionotes
Exports
1
Protocol Run: ProtAtomStrucOperate
Protocol: atomstructutils - operator
finished
Cite
Help
Run
Run name atomstructutils - operator (chai
Comment
Run mode Continue Restart
Host localhost
Use queue? Yes No
Wait for
Input
Input
Atomic structure 1 chimera - chimera operate (copy 2).outputPdb_01
Operation: extractChain
Chain {"model": 0, "chain": "A", "residues": 141}
Start at residue # -1
End at residue # -1
2
3
4
5
6
Close
Save
Execute
pdbFileToBeRefined (from chimera - chimera operate (copy 2) -> outputPdb_01 [outputPdb_01])
Output
atomstructutils - operator (chainA) -> outputPdb
operator (chainA)
shed
SUMMARY
No summary information.