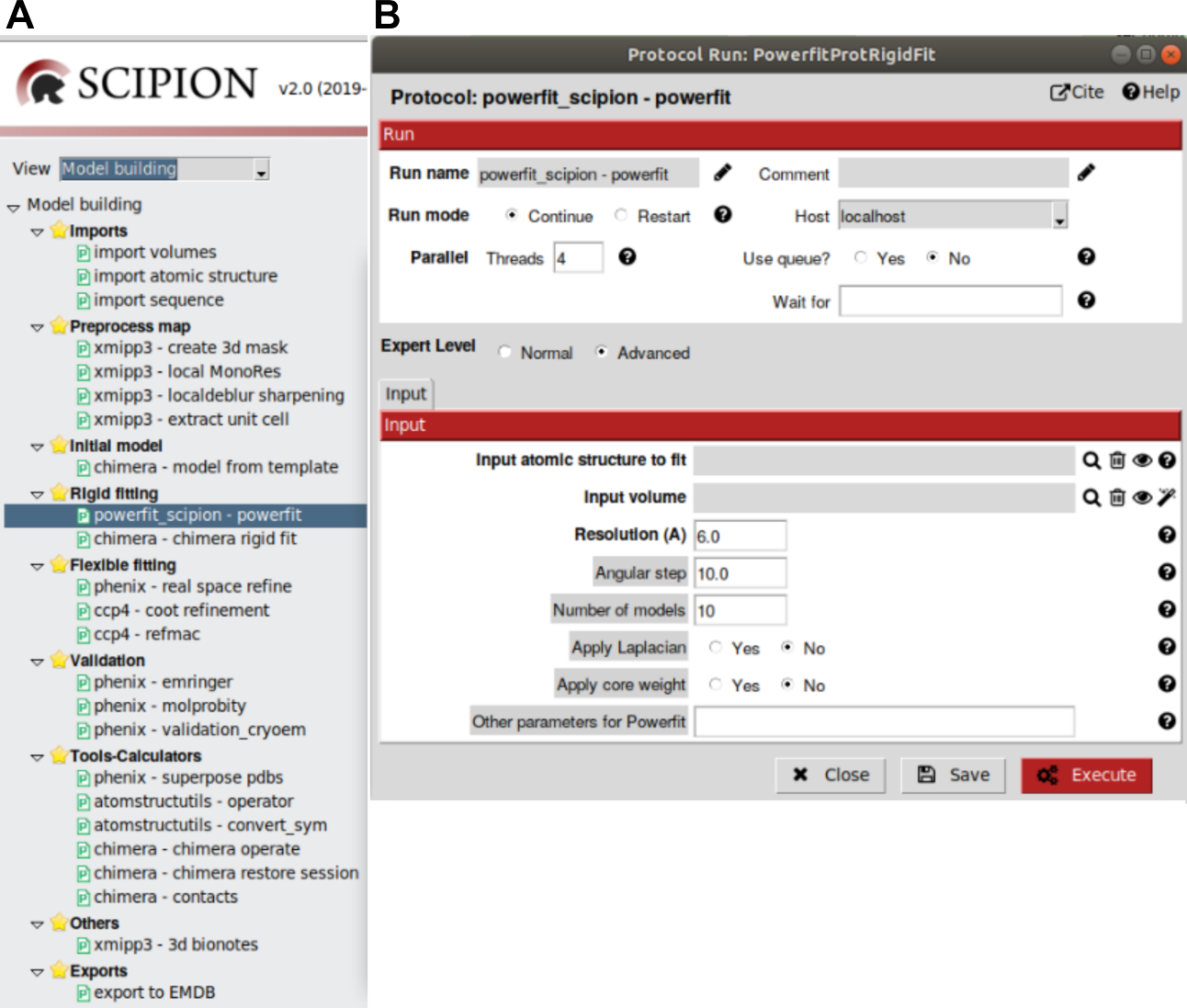
A
SCIPION
v2.0 (2019-
View
Model building
Model building
Imports
import volumes
import atomic structure
import sequence
Preprocess map
xmipp3 - create 3d mask
xmipp3 - local MonoRes
xmipp3 - localdeblur sharpening
xmipp3 - extract unit cell
Initial model
chimera - model from template
Rigid fitting
powerfit_scipion - 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
export to EMDB
B
Protocol Run: PowerfitProtRigidFit
Protocol: powerfit_scipion - powerfit
Cite
Help
Run
Run name
powerfit_scipion - powerfit
Comment
Run mode
Continue
Restart
Host
localhost
Parallel
Threads
4
Use queue?
Yes
No
Wait for
Expert Level
Normal
Advanced
Input
Input
Input atomic structure to fit
Input volume
Resolution (A)
6.0
Angular step
10.0
Number of models
10
Apply Laplacian
Yes
No
Apply core weight
Yes
No
Other parameters for Powerfit
Close
Save
Execute