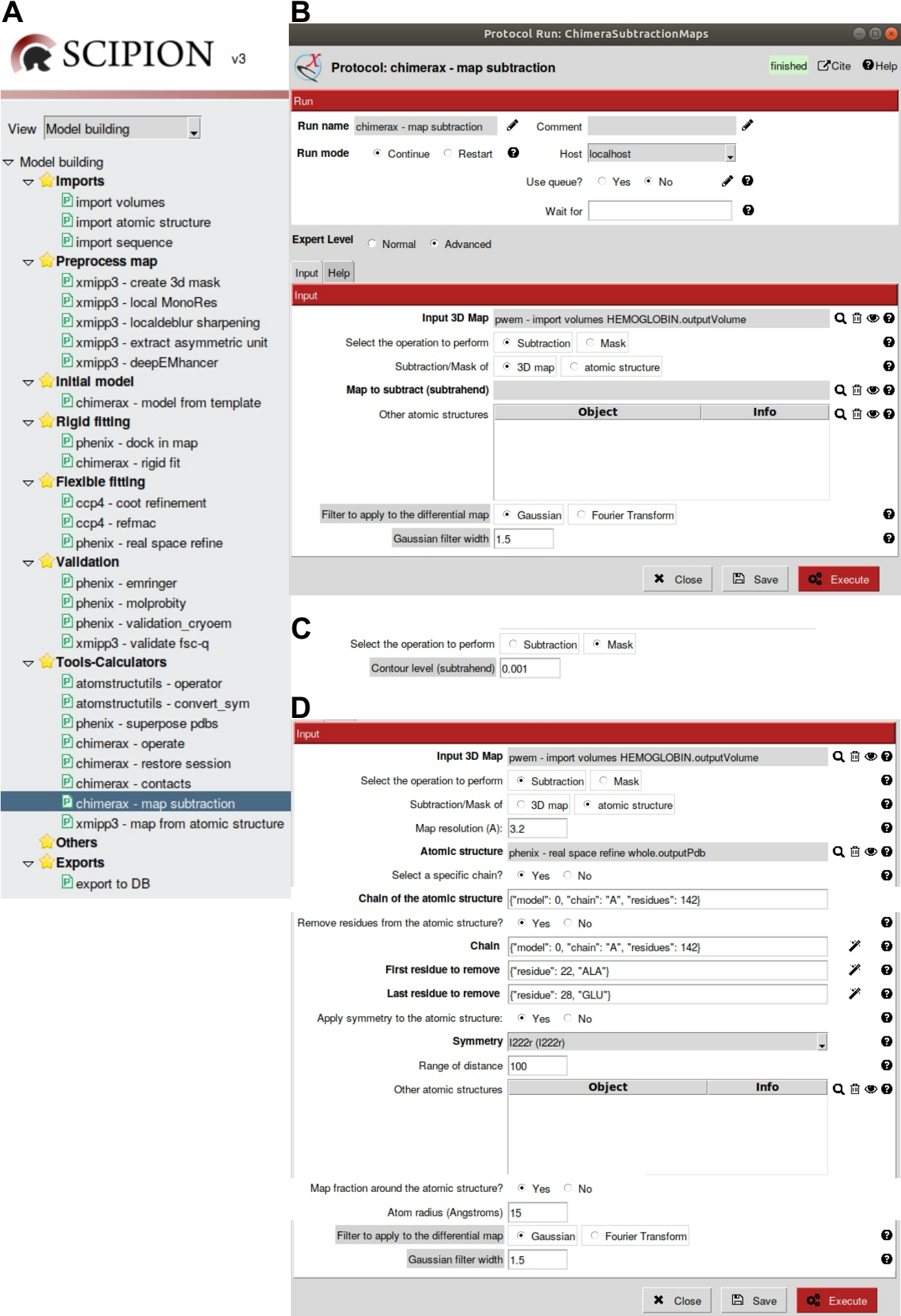
A
SCIPION v3
View Model building
Model building
Imports
import volumes
import atomic structure
import sequence
Preprocess map
xmipp3 - create 3d mask
xmipp3 - local MonoRes
xmipp3 - localdeblur sharpening
xmipp3 - extract asymmetric unit
xmipp3 - deepEMhancer
Initial model
chimerax - model from template
Rigid fitting
phenix - dock in map
chimerax - rigid fit
Flexible fitting
ccp4 - coot refinement
ccp4 - refmac
phenix - real space refine
Validation
phenix - emringer
phenix - molprobity
phenix - validation_cryoem
xmipp3 - validate fsc-q
Tools-Calculators
atomstructutils - operator
atomstructutils - convert_sym
phenix - superpose pdbs
chimerax - operate
chimerax - restore session
chimerax - contacts
chimerax - map subtraction
xmipp3 - map from atomic structure
Others
Exports
export to DB
B
Protocol Run: ChimeraSubtractionMaps
Protocol: chimerax - map subtraction
finished
Cite
Help
Run
Run name chimerax - map subtraction
Comment
Run mode Continue Restart
Host localhost
Use queue? Yes No
Wait for
Expert Level Normal Advanced
Input Help
Input
Input 3D Map pwem - import volumes HEMOGLOBIN.outputVolume
Select the operation to perform Subtraction Mask
Subtraction/Mask of 3D map atomic structure
Map to subtract (subtrahend)
Other atomic structures
Object Info
Filter to apply to the differential map Gaussian Fourier Transform
Gaussian filter width 1.5
Close
Save
Execute
C
Select the operation to perform Subtraction Mask
Contour level (subtrahend) 0.001
D
Input
Input 3D Map pwem - import volumes HEMOGLOBIN.outputVolume
Select the operation to perform Subtraction Mask
Subtraction/Mask of 3D map atomic structure
Map resolution (A): 3.2
Atomic structure phenix - real space refine whole.outputPdb
Select a specific chain? Yes No
Chain of the atomic structure {"model": 0, "chain": "A", "residues": 142}
Remove residues from the atomic structure? Yes No
Chain {"model": 0, "chain": "A", "residues": 142}
First residue to remove {"residue": 22, "ALA"}
Last residue to remove {"residue": 28, "GLU"}
Apply symmetry to the atomic structure: Yes No
Symmetry I222r (I222r)
Range of distance 100
Other atomic structures
Object Info
Map fraction around the atomic structure? Yes No
Atom radius (Angstroms) 15
Filter to apply to the differential map Gaussian Fourier Transform
Gaussian filter width 1.5
Close
Save
Execute