



View: **Model building** 1

- 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 - refrac
 - phenix - real space refine
 - Validation
 - phenix - emringer
 - phenix - molprobtity
 - phenix - validation_cryoem
 - xmipp3 - validate fsc-q
 - Tools-Calculators
 - atomstructutils - operator
 - atomstructutils - convert_sym
 - phenix - superpose pdb
 - chimerax - operate
 - chimerax - restore session
 - chimerax - contacts
 - chimerax - map subtraction
 - xmipp3 - map from atomic structure
 - Others
 - Exports

PROJECT

pwem - import volumes HEMOGLOBIN

Protocol Run: ProtImportVolumes

Protocol: pwem - import volumes finished [Cite](#) [Help](#)

Run

Run name: pwem - import volumes HEMC [Edit](#) Comment: [Edit](#)

Run mode: ☒ Continue ☐ Restart [?](#) Host: localhost [?](#)

Use queue? ☐ Yes ☒ No [?](#)

Wait for: [?](#)

Expert Level ☒ Normal ☐ Advanced

Import **Streaming**

Import

Import from: local file [?](#)

Files directory: /model_building_tutorial/volumes/emd_3488.map [?](#)

Pattern: [?](#)

Set half maps: ☐ Yes ☒ No [?](#)

Pixel size ("sampling rate") (Å/px): 1.05 [?](#)

Set origin of coordinates: ☐ Yes ☒ No [?](#)

Analyze Results 3

Execute 2

Volume 2_outputVolume.46 imported from:
/home/marta/software/scipion_plugin/data/tests/model_building_tutorial/volumes/emd_3488.map
Sampling rate: 1.05 (Å/px)