

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 - 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 pdbs
- chimerax - operate
- chimerax - restore session
- chimerax - contacts
- chimerax - map subtraction
- xmipp3 - map from atomic structure

Edit Copy Delete Browse Collapse Labels

View: Tree

PROJECT

pwem - import volumes HEMOGLOBIN

pwem - import sequence HBA_HUMAN

Protocol Run: XmippProtDeepVolPostProc



Protocol: xmipp3 - deepEMhancer

finished Cite Help

Run

Run name xmipp3 - deepEMhancer

Comment

Run mode ☒ Continue ☐ Restart

Host localhost

GPU IDs 0

Use queue? ☐ Yes ☒ No

Wait for

Expert Level

☒ Normal ☐ Advanced

Input

Input

Would you like to use half maps? ☐ Yes ☒ No

Input Volume pwem - import volumes HEMOGLOBIN.outputVolume

Input normalization Automatic normalization

Model power highRes

Close

Save

Execute

SUMMARY

Input: raw data map

Normalization: auto

Analyze Results