

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 - 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

Others

Edit Copy Delete Browse Collapse Labels

PROJECT

pwem - import volumes HEMOGLOBIN finished
pwem - import sequence HBA_HUMAN finished

View: Tree

Refr

Protocol Run: ProtImportSequence

Protocol: pwem - import sequence

finished Cite Help

Run

Run name pwem - import sequence HBA Comment

Run mode ☒ Continue ☐ Restart Host localhost

Use queue? ☐ Yes ☒ No

Wait for

Input

Sequence ID HBA_HUMAN_P69905

Sequence name HBA_HUMAN

Sequence description

Import sequence of ☒ aminoacids ☐ nucleotides

From ☐ plain text ☐ atomic structure ☐ file ☒ UniProt ID

UniProt name/ID P69905

Close Save Execute

Analyze Results

Sequence of aminoacids:

Sequence **HBA_HUMAN** imported from UniProt ID **P69905**