

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

PROJECT

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

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

Input

Sequence ID

Sequence name: HBA_HUMAN

Sequence description

Import sequence of: ☒ aminoacids ☐ nucleotides

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

UniProt name/ID: P69905

Analyze Results

Close Save Execute

Sequence of aminoacids:

Sequence HBA_HUMAN imported from UniProt ID P69905