A

SCIPION v3.0.3 ()

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 - deepEMhancer
    📄 xmipp3 - extract asymmetric unit
  ▽ ⭐ 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
    📄 xmipp3 - validate fsc-q
    📄 phenix - emringer
    📄 phenix - molprobity
    📄 phenix - validation_cryoem
  ▽ ⭐ Tools-Calculators

B

Protocol Run: ProtImportSequence

Protocol: pwem - import sequence   ☐Cite ❓Help

Run

Run name pwem - import sequence ✏   Comment ✏

Run mode   ⦿ Continue ○ Restart ❓   Host localhost ▾

                                Use queue? ○ Yes ⦿ No ✏ ❓

                                Wait for ❓

Input

Input

Sequence ID ❓

Sequence name ❓

Sequence description ❓

Import sequence of   ⦿ aminoacids ○ nucleotides ❓

From   ⦿ plain text ○ atomic structure ○ file ○ UniProt ID ❓

IUPAC Protein alphabet: ⦿ Extended Protein ○ Protein ❓

Write your sequence here: ❓

✖ Close   💾 Save   ⚙ Execute