






















View Protocols SPA

▷  Classify▼ **3D**▷  Initial volume▷  Preprocess▷  Classify▷  Refine▷  Analysis▷  Reconstruct▼ **Tools**▷  Sets▼  Calculators xmipp3 - operate particles xmipp3 - operate volumes chimera - chimera operate chimera - chimera restore sessi phenix - superpose pdbs▼ **Model Building** xmipp3 - extract unit cell chimera - rigid fit scipion - model from template powerfit - powerfit ccp4 - coot refinement ccp4 - reftmac phenix - emringer phenix - real space refine phenix - molprobit

Protocol Run: PowerfitProtRigidFit

Protocol: powerfit - powerfit

 Cite  Help

Run

Run name powerfit - powerfit HBA_HUM

Comment

Run mode ☒ Continue ☐ Restart

Host localhost

Parallel Threads 4

Use queue? ☐ Yes ☒ No

Wait for

Expert Level

☐ Normal ☒ Advanced

Input

Input

Input PDBx/mmCIF scipion - model from template HBA_

Input volume xmipp3 - extract unit cell symC2 off

Resolution (Å) 3.2

Angular step 10.0

Number of models 10

Apply Laplacian ☐ Yes ☒ NoApply core weight ☐ Yes ☒ No

Other parameters for Powerfit

Close

Save

Execute