














View Protocols SPA

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

Protocol Run: ChimeraProtRigidFit

finished  

Protocol: chimera - chimera rigid fit

Run

Run name chimera - rigid fit HBA_HUMA

Comment

Run mode

☒ Continue ☐ Restart

Host

localhost

Use queue?

☐ Yes ☒ No

Wait for

Input

Help

Input

Input Volume xmipp3 - extract unit cell symC2 offs

Atomic structure to be fitted powerfit - powerfit HBA_HUMAN.ou

Other reference atomic structures

Object	Info
powerfit - powerfit HBA_HUMAN.outpu	PdbFile (pseudoatoms)

Close

Save

Execute