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Protocol Run: PowerfitProtRigidFit finished Cite ? Help

Protocol: powerfit_scipion - powerfit

Run

Run name **powerfit_scipion - powerfit** Comment

Run mode ☒ Continue ☐ Restart ? Host **localhost**

Parallel Threads **4** ? Use queue? ☐ Yes ☒ No ?

Wait for

Expert Level ☐ Normal ☒ Advanced

Input

Input atomic structure to fit chimera - model from template outputPdb_01

Input volume xmipp3 - extract unit cell sym C2.outputVolume

Resolution (A) **3.2**

Angular step **10.0**

Number of models **10**

Apply Laplacian ☐ Yes ☒ No

Apply core weight ☐ Yes ☒ No

Other parameters for Powerfit

Close **Save** **Execute**

Protocols | Da

extract unit cell sym finished

fit_scipion - powerfit finished

Analyze Results

volume=False)