

Materials List for

Enhancing Density Maps by Removing the Majority of Particles in Single Particle Cryogenic Electron Microscopy Final Stacks

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Materials

Name	Company	Catalog Number	Comments
CryoSPARC	Structura Biotechnology Inc. Toronto, Canada		CryoSPARC (Cryo-EM Single Particle Ab-Initio Reconstruction and Classification) is a state of the art HPC software solution for complete processing of single-particle cryo-electron microscopy (cryo-EM) data. CryoSPARC is useful for solving cryo-EM structures of membrane proteins, viruses, complexes, flexible molecules, small particles, phase plate data and negative stain data.
EMPIAR-10097 Dataset		https://ftp.ebi.ac.uk/empair/world_availability/10097/data/Particle-Stack/T40_HA_130K-Equalized-Particle-Stack.mrcs	This dataset comprises single-particle cryo-EM data of the Influenza Hemagglutinin trimer, characterized by its highly preferred orientation, collected using a 40-degree tilted collection strategy.
initial.mrc		https://github.com/mxhulab/cryosieve-demos/tree/master/EMPIAR-10097	
mask.mrc		https://github.com/mxhulab/cryosieve-demos/tree/master/EMPIAR-10097	
RELION		4.0-beta-2	RELION (REGularised LIkelihood Optimisation) is an open-source software for cryo-electron microscopy (cryo-EM) data processing, particularly for refining macromolecular structures. Utilizing a Bayesian approach, it excels in separating signal from noise, enabling high-resolution structure

			determination. RELION supports single-particle analysis, tomography, and sub-tomogram averaging, and has become widely used in structural biology due to its effectiveness and user-friendly interface.
T40_HA_130K-Equalized_run-data_CryoSPARC_refined.star		https://github.com/mxhulab/cryosieve-demos/tree/master/EMPIAR-10097	Metadata file for the final stack of particles from EMPIAR-10097