

Our study showed that HIV-2 particles had a uniform particle diameter, with a homogeneous and often complete capsid lattice (**Figure 1A**). We determined a 5.5 Å single particle reconstruction map of the HIV-2 Gag lattice from immature viral-like particles (**Figure 1B**). The resolution of the reconstruction is limited, likely due to limitation of orientations and noises from membrane and nucleic acids. Tomographic analysis of the immature particles confirmed there is high occupancy of capsid hexamers along the radii of the viral like particles, resulting in few gaps (**Figure 1C**)

Please see Talledge et al., DOI: <https://doi.org/10.1101/2022.02.01.478508>.

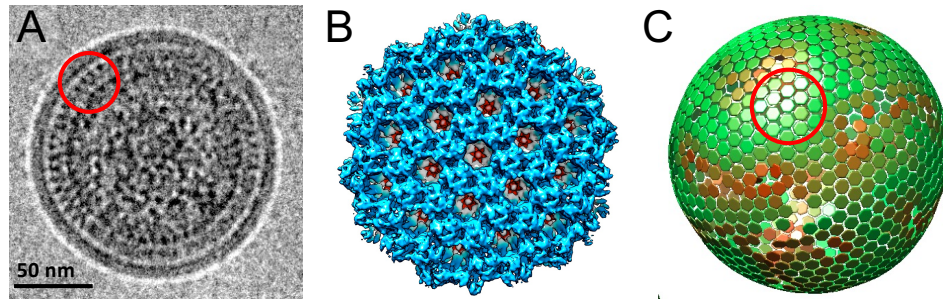


Figure. 1 Cryo-EM Image, 3D map and Gag lattice distribution of HIV-2 immature virus-like particles. (A) Cryo-EM image of one HIV-2 immature particle. The red circle marks a boxed region subjected to the single particle reconstruction calculation. (B) The 3D map (5.5 Å resolution) determined by the single-particle reconstruction method. (C) The locations of Gag hexamers in one HIV-2 immature particle determined by cryo-ET and subtomogram averaging methods. The red circle marks the equivalent size of the reconstruction map in B.

We have purified portions of the HIV-2 Gag polyprotein which assembles efficiently into spherical structures. The cryo-EM images of these assemblies reveal features of immature Gag lattice structure (**Figure 2**). We propose to collect high-resolution images of this sample and solve the structure at near atomic resolution.

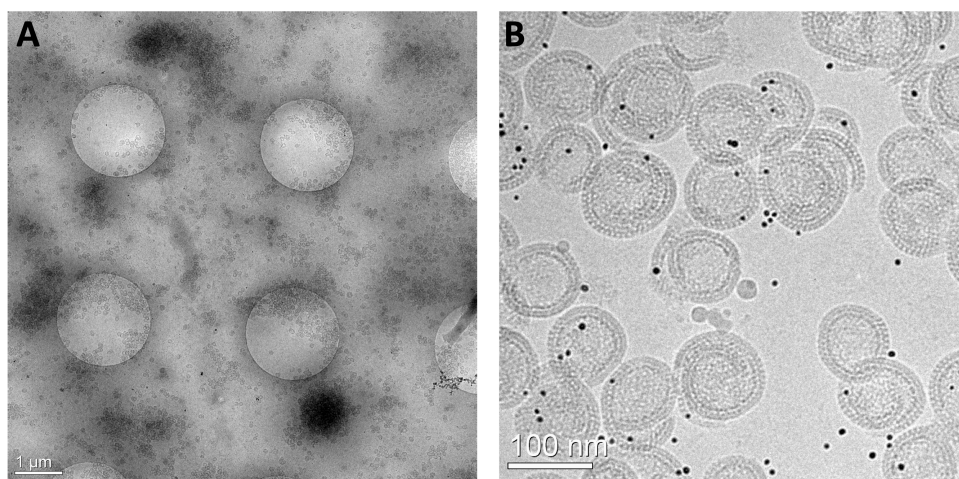


Figure 2. Cryo-EM images of assembled HIV-2 Gag lattice. (A) Low magnification view showing the distribution of vitreous ice. (B) Images of the assembled particles.