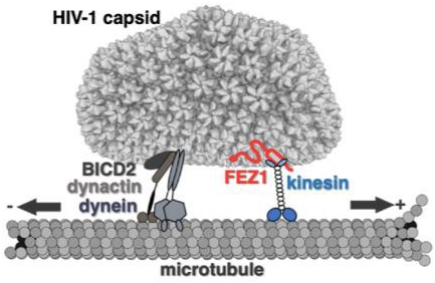

Fig1. Model of dynein-dynactin-BicD2 and FEZ1-Kinesin aid in shuttling the capsid on the microtubule.

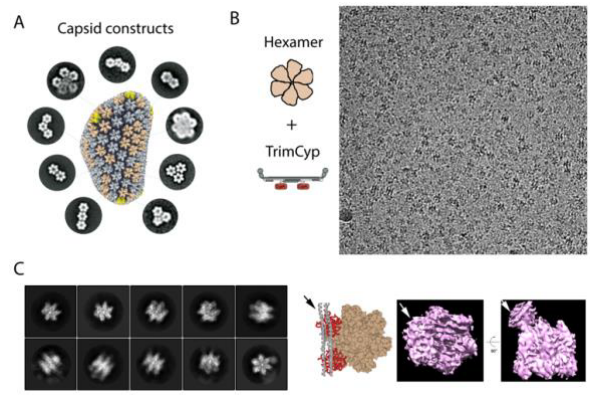

Fig2. TrimCyp complexed with HIV-1 hexamers A. Capsid constructs/assemblies created by our lab that replicate all possible cofactor binding interfaces. A cartoon of HIV-1 capsid is shown in the middle, surrounded by multi-hexamer/pentamer CA assemblies established in our study (negative-stain EM class averages). B. Left: Our sample is a complex of the CA hexamer and TrimCyp, Right: Cryo-EM micrograph of TrimCyp-hexamer complex taken at a Glacios microscope. C. 2D classification (left) and preliminary 3D reconstruction (right) of the TrimCyp-hexamer complex from a small screening data set (Glacios). A schematic of the expected complex is in the middle.

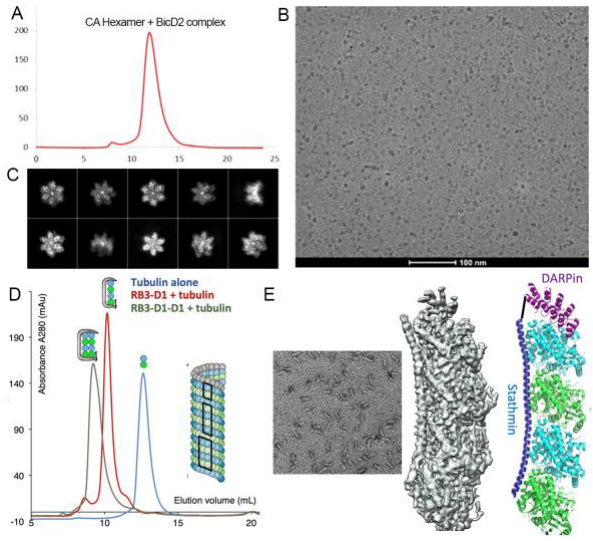

Fig. 3. Capsid-binding partners during microtubule tracking. A. Gel filtration profile of BICD2 with CA hexamers. B. cryo-EM micrograph (Talos L120C) of the complex. C. Top 2D class averages from a preliminary data set (Glacios). D. Purified tubulin assemblies for various microtubule structures (boxed). E. Negative stain micrograph (left), preliminary cryo-EM reconstruction (middle), and model of a tubulin hetero-tetramer (right).

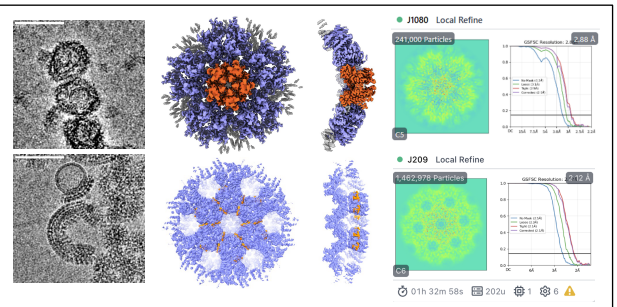

Fig4. Capsid-like particles with inhibitors. A. mature HIV casid-like particles with inhibitor-bound, resolved to 2.9Å resolution. B. immature Gag lattice of HIV-1 in vitro assembled on liposomes, resolved to 2.1Å resolution.