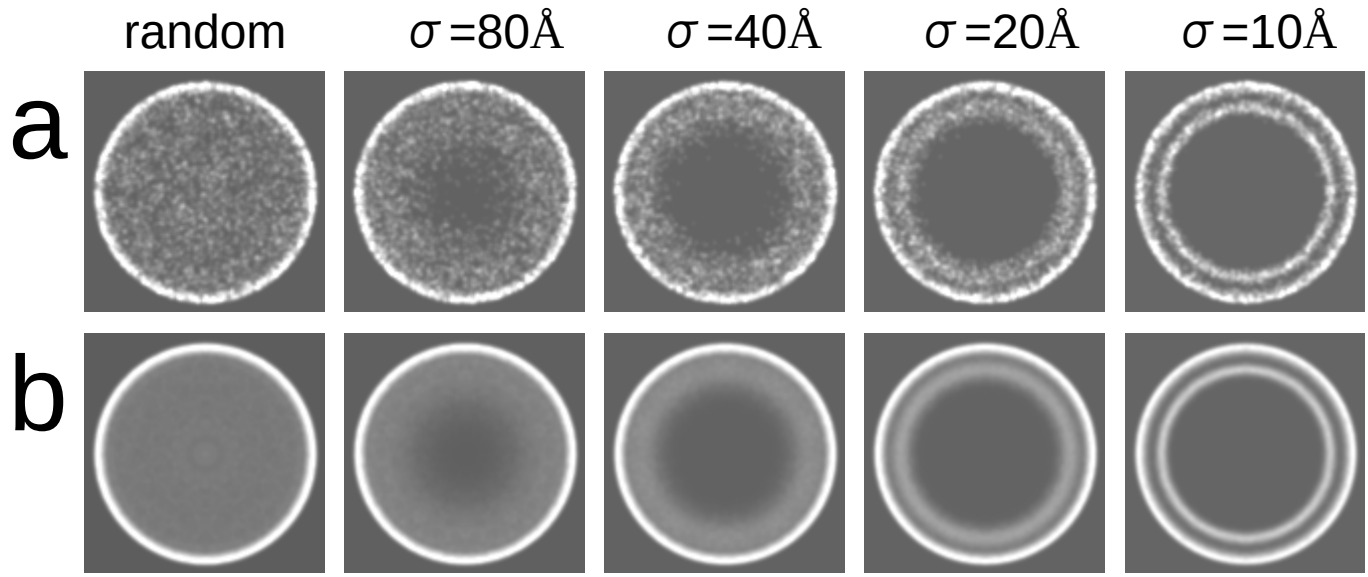


**Supplementary Figure 3.** Simulated ipDNA distributions. A protein shell was simulated using 145740 points (=420 * 347, one point for each residue in the T3 major shell protein, gp10A. These points were distributed randomly within a spherical protein shell of Gaussian shape with mean radius=275Å and standard deviation =15Å, to approximate the T3 phage protein shell. A 10.6 kb ipDNA was simulated with 64823 points inside this protein shell to approximate the total mass of the ipDNA (=(10600 * 650) / (420*36882) * 145740, assuming 650 Da per base pair on average). The ipDNA points are distributed either completely randomly (column 1) or in a Gaussian radial profile of mean radius=241Å and various ring standard deviations (widths). Ring width (column 2-4) was used to simulate the level of preferred clustering next to the inner surface of the protein shell. Each of the above 3-D distributions of points was then turned into a 3-D low resolution density map by representing each point as a 3-D gaussian blob of sigma=20Å. The central section of these 3-D density maps was shown before (a) and after (b) icosahedral averaging. From these simulations, the ipDNA density distribution in the 3-D reconstruction of cryo-EM images of 10.6 kb ipDNA-capsid is most consistent with random distribution inside the protein shell.