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Supplemental Information

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Mature P22 Bacteriophage**

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Resolution and Probabilistic Structural Models of Subcomponents Derived from CryoEM Maps of Mature P22 Bacteriophage

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Supporting Material

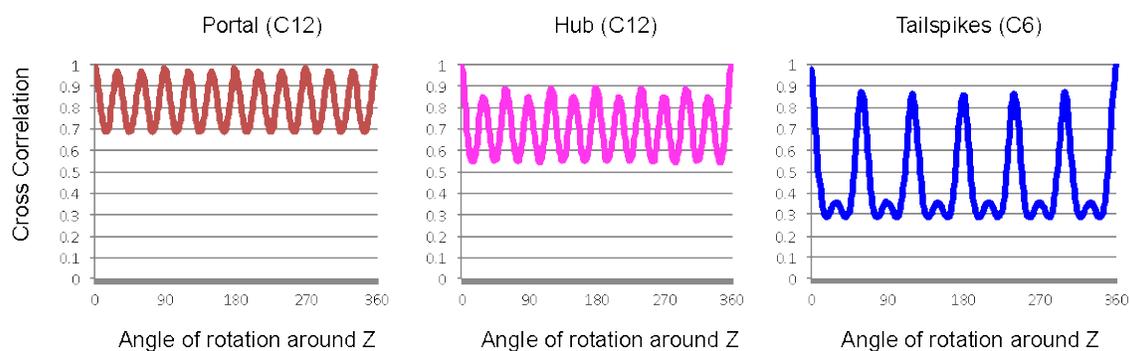


Figure S1. Rotational cross-correlation through individual components extracted from the entire map – portal, hub and tailspikes. The portal and hub have C12 symmetry, thus 12 peaks are seen the CC plot as the densities are rotated through 360° around the z-axis. For the portal, every 3rd peak is practically at $CC \sim 1.0$, and all others are just slightly less; overall the 12 portal proteins are very similar. For the hub, another interesting pattern can be seen: every second peak (except the one at Angle=0) has $CC \sim 0.89$, and all others have $CC \sim 0.85$. Because the peak at Angle=0 is the highest, this means that each protein in the hub can be somewhat different from all others. This may be explained by the fact that the C12 hub has to connect the C12 portal to the C6 tailspike trimers. The C6 tailspike trimers' density has 6 major peaks in the CC rotational plot – each peak except at Angle=0 has $CC \sim 0.88$. Thus, the 6 trimers are similar but not exactly the same in conformation.

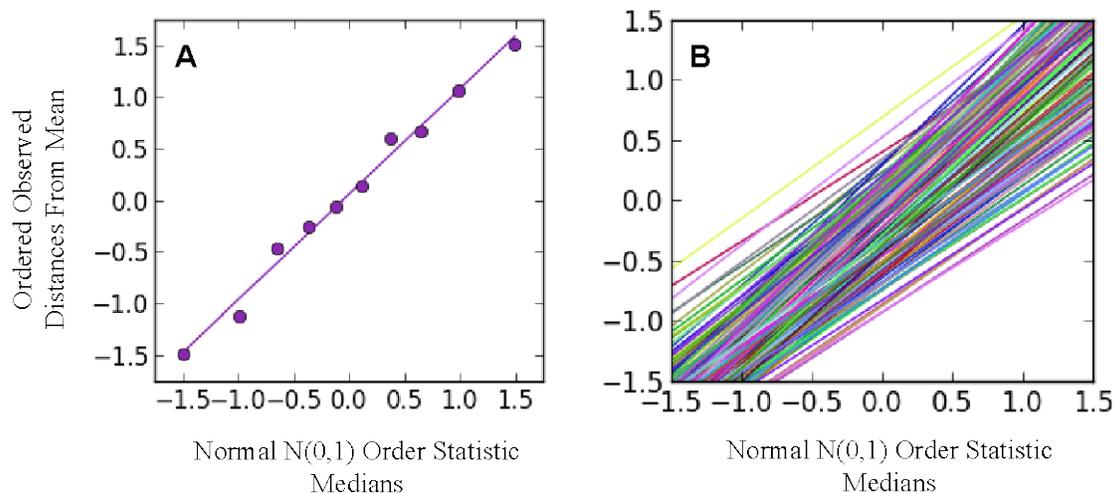


Figure S2. Normal probability plot to test whether backbone atoms positions can be represented with a normal distribution. (A) A shows a normal probability plot for the backbone atom position of a single residue, showing data points (circles), and line fitted to the points. (B) Lines fitted to sample points for all residues. Lines that have $\sim 45^\circ$ slope indicate that the samples fall very close to a normal distribution.