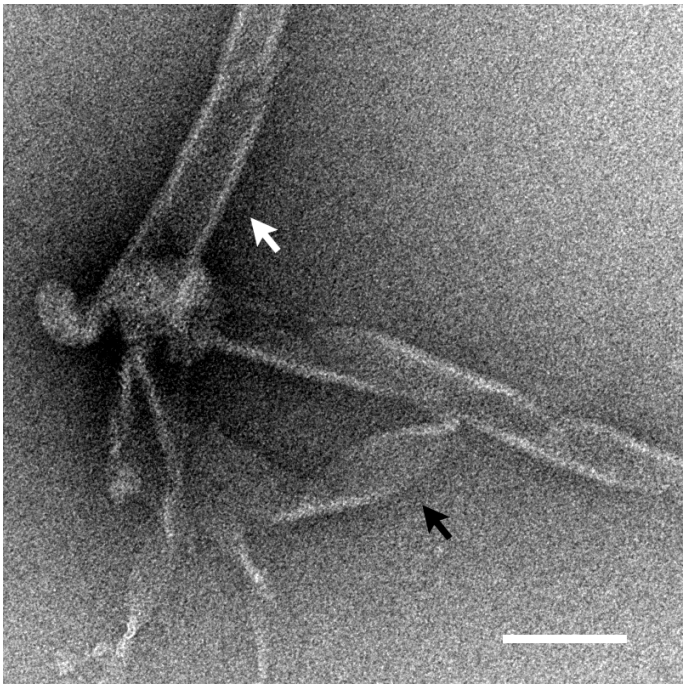
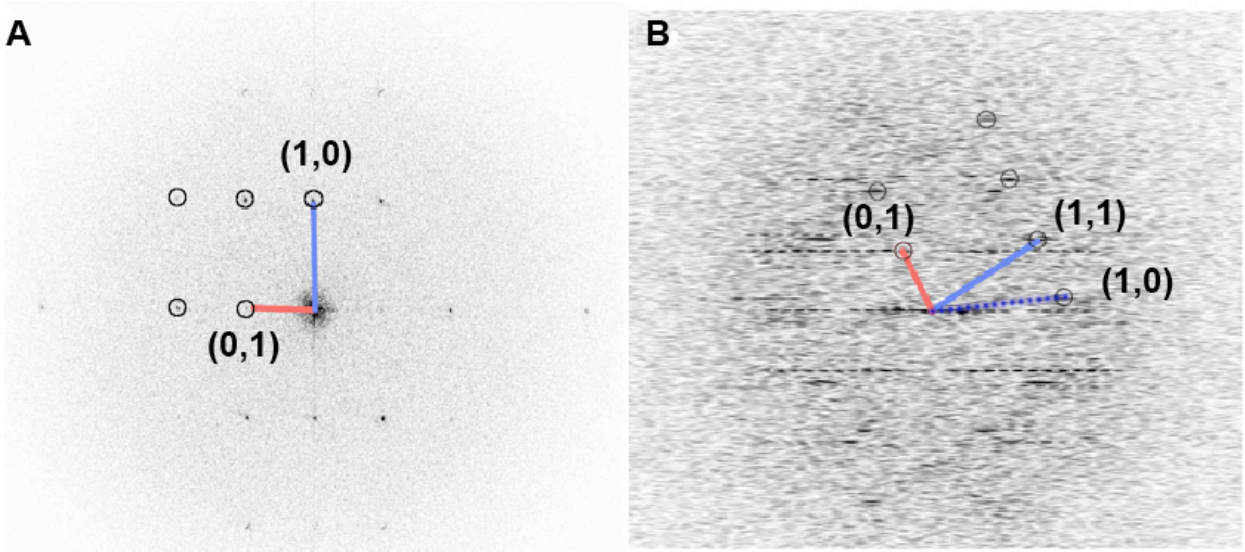
Supplementary Materials

Surface for Catalysis by Poliovirus RNA-Dependent RNA Polymerase, by Wang, Lyle, Bullitt



Supplementary Fig. 1. *Oligomeric form of purified 3Dpol (Electron micrograph of negatively stained sample)*. 3Dpol formed short tubes (white arrow) and ribbons (black arrow) after incubation for 5 min at 30 ^{o}C. Scale bar 100 nm.



Supplementary Fig 2. *Dimensions of unit cells are similar for planar and helical arrays of 3Dpol*. **(a)** The computed Fourier transform (FT) of a 3Dpol planar array, with unit cell parameters a= 53 Å (blue), b= 87 Å (red), $\gamma = 89^{o}$. **(b)** The computed FT of a 3Dpol tube belonging to the (-32, 6) family, with the length of the unit cell vector (0, 1) that points to the beating layer line 90 $Å^{-1}$(red). The resulting unit cell size defined by the (0, 1) and (1, 0) vectors (blue dotted line) is different than that of the planar arrays. However, the (1, 1) vector (blue continuous line) of the helical diffraction pattern is 47 $Å^{-1}$ long. The unit cell size is therefore similar to that of the planar arrays when the unit cell is defined by the (0,1) and (1,1) vectors, which includes an interaxial angle 82^{o}.

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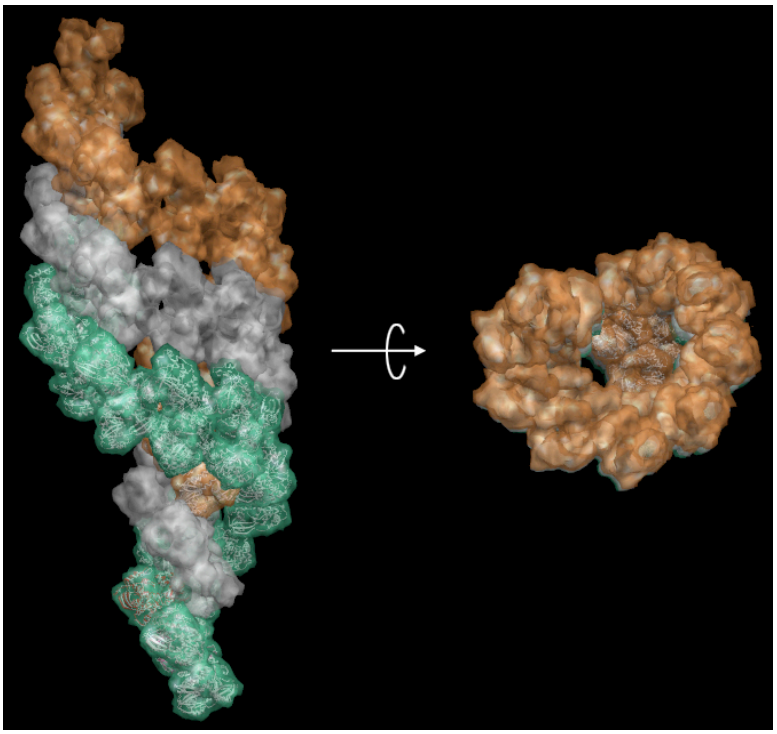
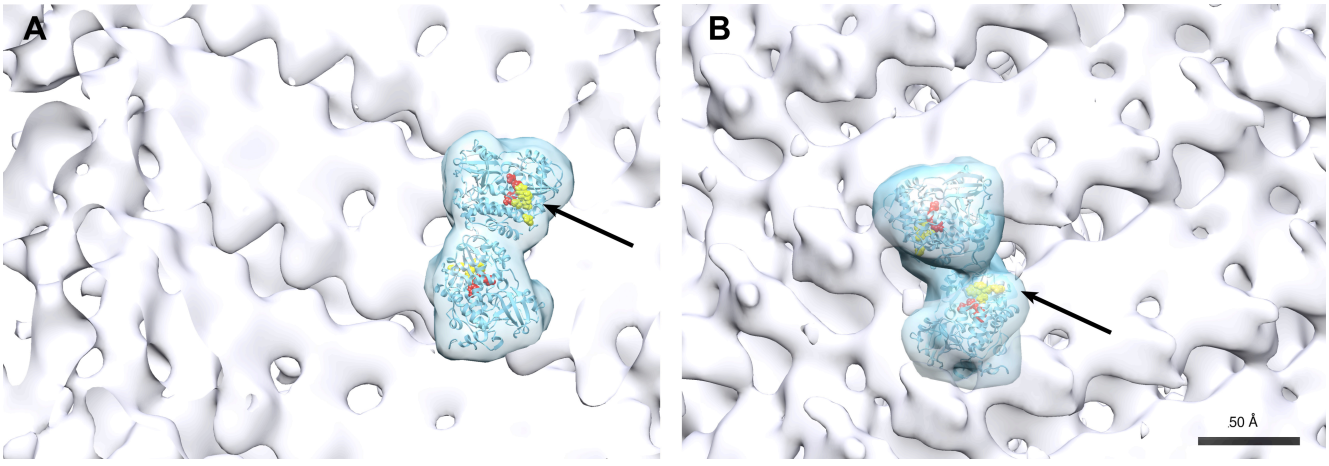


Supplementary Fig. 3. *Extendability test of 3Dpol tetramer*. Two parallel interface-I dimers predicted by computational modeling were first extended by superimposition along interface-II producing the green strand. Two more strands (gray and orange) were superimposed along interface-I. The complex spirals up with increasing diameter, resembling a waffle cone. This illustrates visually that strict propagation of parallel interface-I dimers does not form planar arrays . However, our new experimental data strongly support a parallel arrangement of interface-I filaments in planar arrays of 3Dpol through quasi-equivalent interactions between subunits.



Supplementary Fig. 4. *Potential binding sites for 3Dpol to membrane via membrane-associated 3AB.* There are accessible binding sites for 3AB on both the inside and outside surfaces of polymerase tubes, as seen when a 3Dpol dimer is fitted into the EM map. Known VPg binding

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sites on 3Dpol are shown as yellow spheres, and the active sites are shown in red. Magnification bar 50 Å.

Helical Family	# of Tubes	% of Tubes
(-29, 5)	1	2.9
(-30, 5)	2	5.9
(-31, 5)	2	5.9
(-33, 5)	1	2.9
(-31, 6)	2	5.9
(-32, 6)	9	26.5
(-33, 6)	3	8.8
(-34, 6)	6	17.6
(-36, 6)	1	2.9
(-30, 7)	2	5.9
(-32, 7)	1	2.9
(-35, 7)	1	2.9
(-33, 8)	1	2.9
(-36, 8)	2	5.9

Supplementary Table. *Helical familes of poliovirus polymerase tubes.* Symmetry was determined for 34 tubes imaged by cryoEM. The majority of tubes were of the (-32,6) or (34,6) family.