

1 Article

2 **The Structure of an AAV5-AAVR Complex at 2.5 Å**
3 **Resolution: Implications for Cellular and Immune**
4 **Neutralization of AAV Gene Therapy Vectors**
5 **Supplementary Materials**

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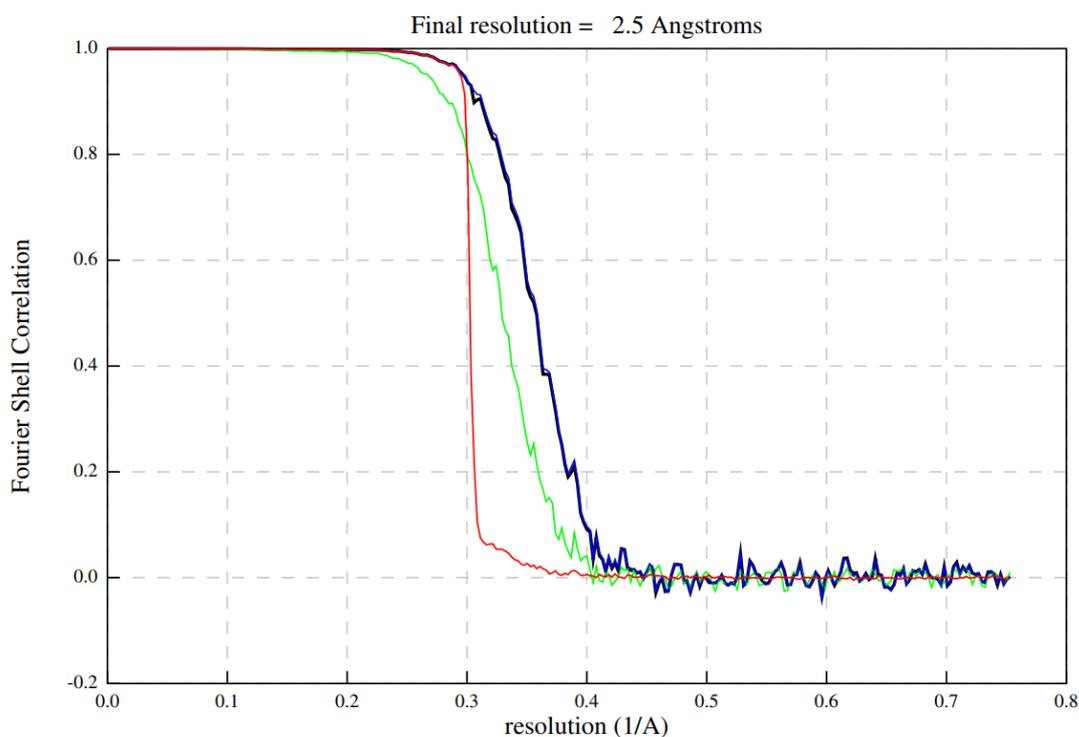
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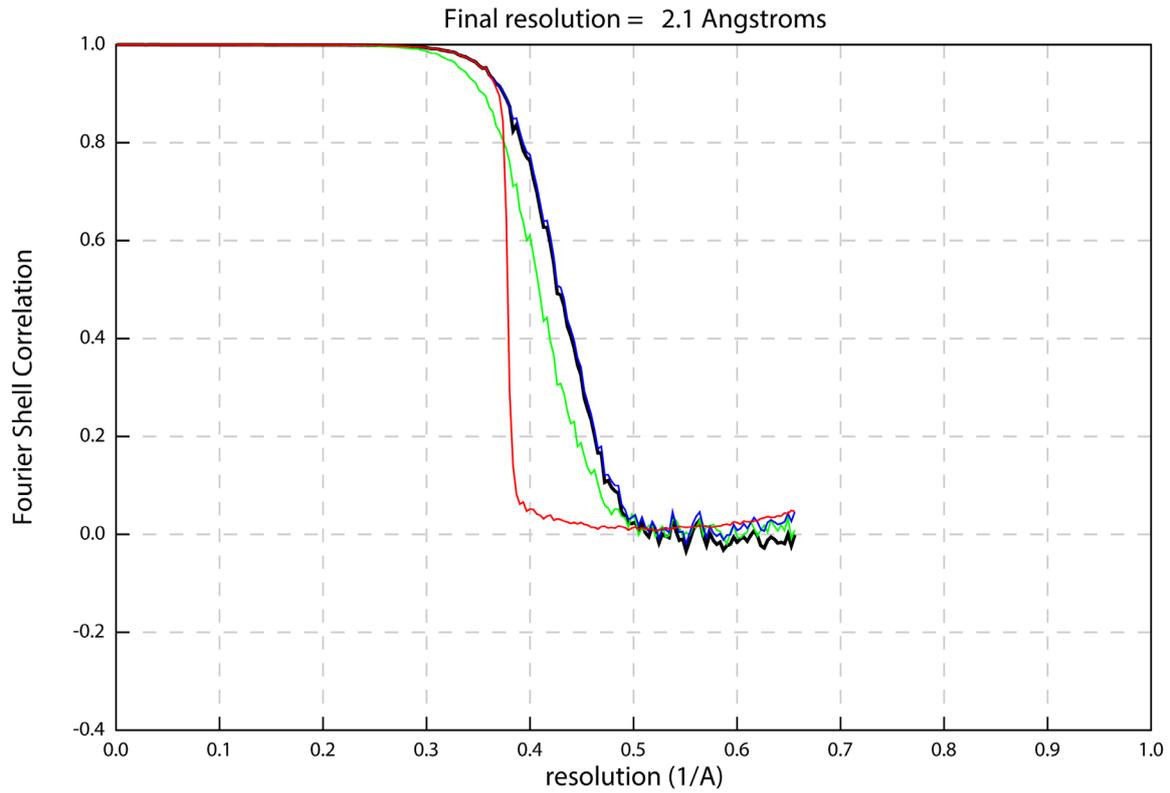
15 *Supplementary Figure S1*

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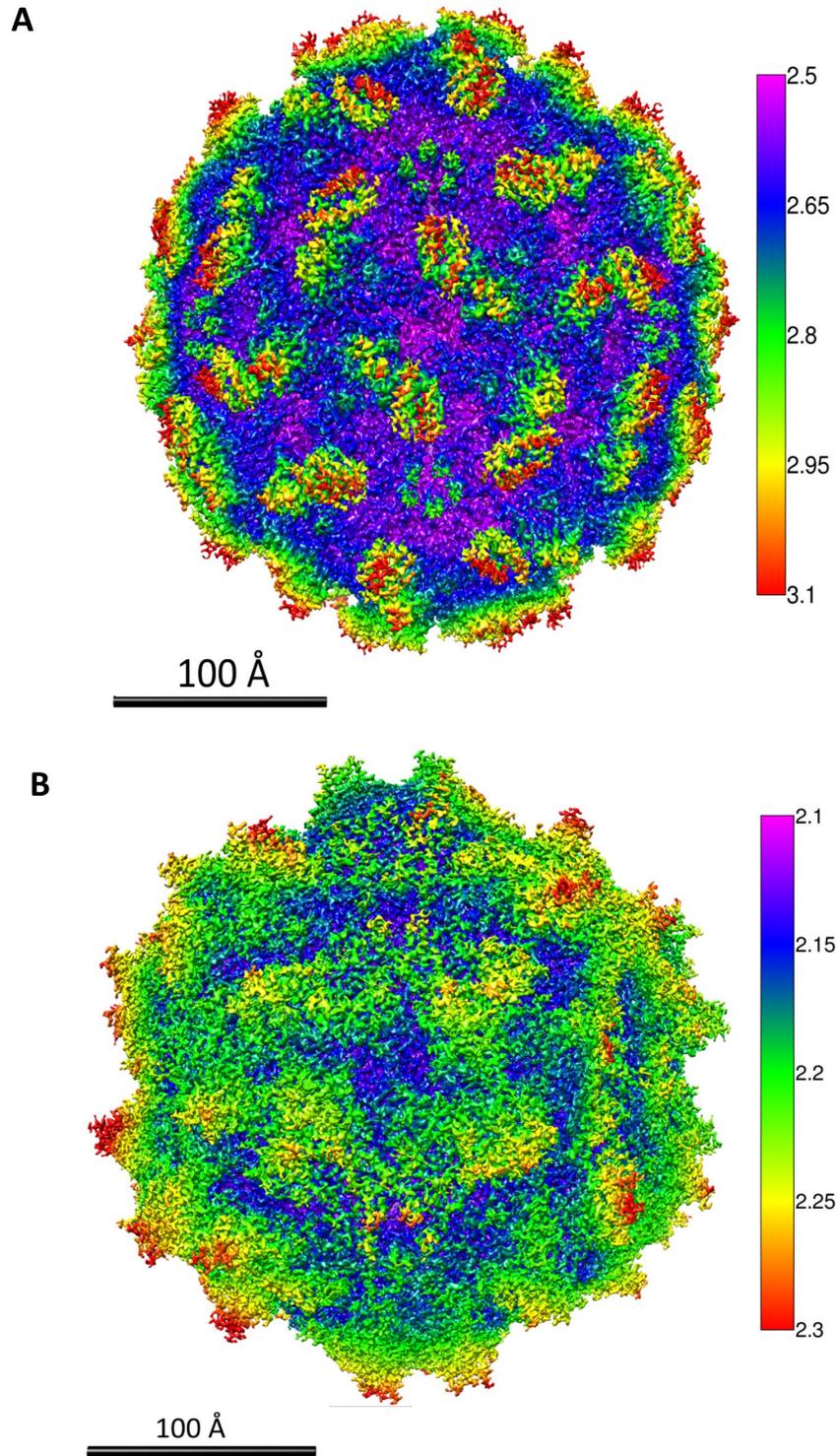
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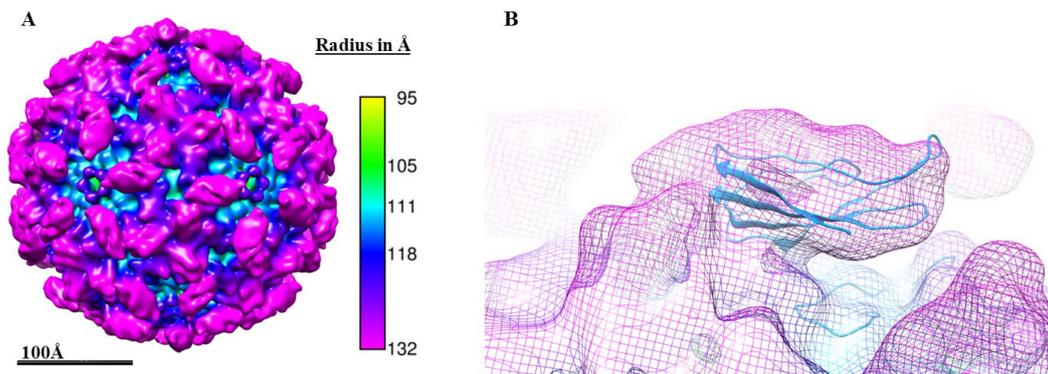
Figure S1. Fourier Shell correlation (FSC) curves from the Relion program Postprocess [1] for AAV5 reconstructions: **(A)** The AAVR-bound dataset; and **(B)** uncomplexed AAV5, showing the final resolution of the EM maps. FSC curves are shown for the unmasked map (green), the masked map (blue), the maps with Fourier components ≤ 3.32 and 3.08 Å replaced by random noise and then masked for A and B respectively (red), the masked corrected map (black) which shows the true resolution by factoring potential resolution artifacts due to masking. This is done by subtracting the random noise FSC from the masked FSC and dividing by 1 minus the random noise FSC [2].

27 Supplementary Figure S2



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Figure S2. Coulombic potential maps colored by local resolution. Maps for both (A) AAV5 in complex with PKD1-2 and (B) uncomplexed AAV5 contoured at 1.6 sigma. The color keys are by resolution in Å

32 *Supplementary Figure S3*

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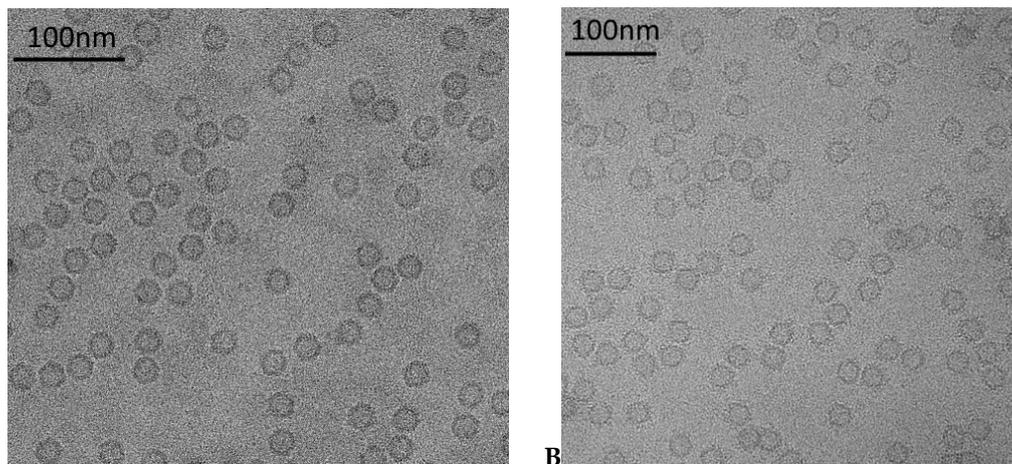
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Figure S3. The 10 Å lowpass filtered cryo-EM coulombic potential map for AAV5 in complex with PKD1-2. **(A)** The view is along a 2-fold, with 2-fold axes also on horizontal and vertical axes. Three-fold axes can be seen above and below center, while 5-fold axes are left and right of center. The map is colored by distance from the center of the map. **(B)** A zoomed in image of A with a PKD1 domain inserted into the density. The lowpass filtered map shows the region of PKD1 close to the 5-fold axis of symmetry that cannot be seen at high resolution.

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Supplementary Figure S4

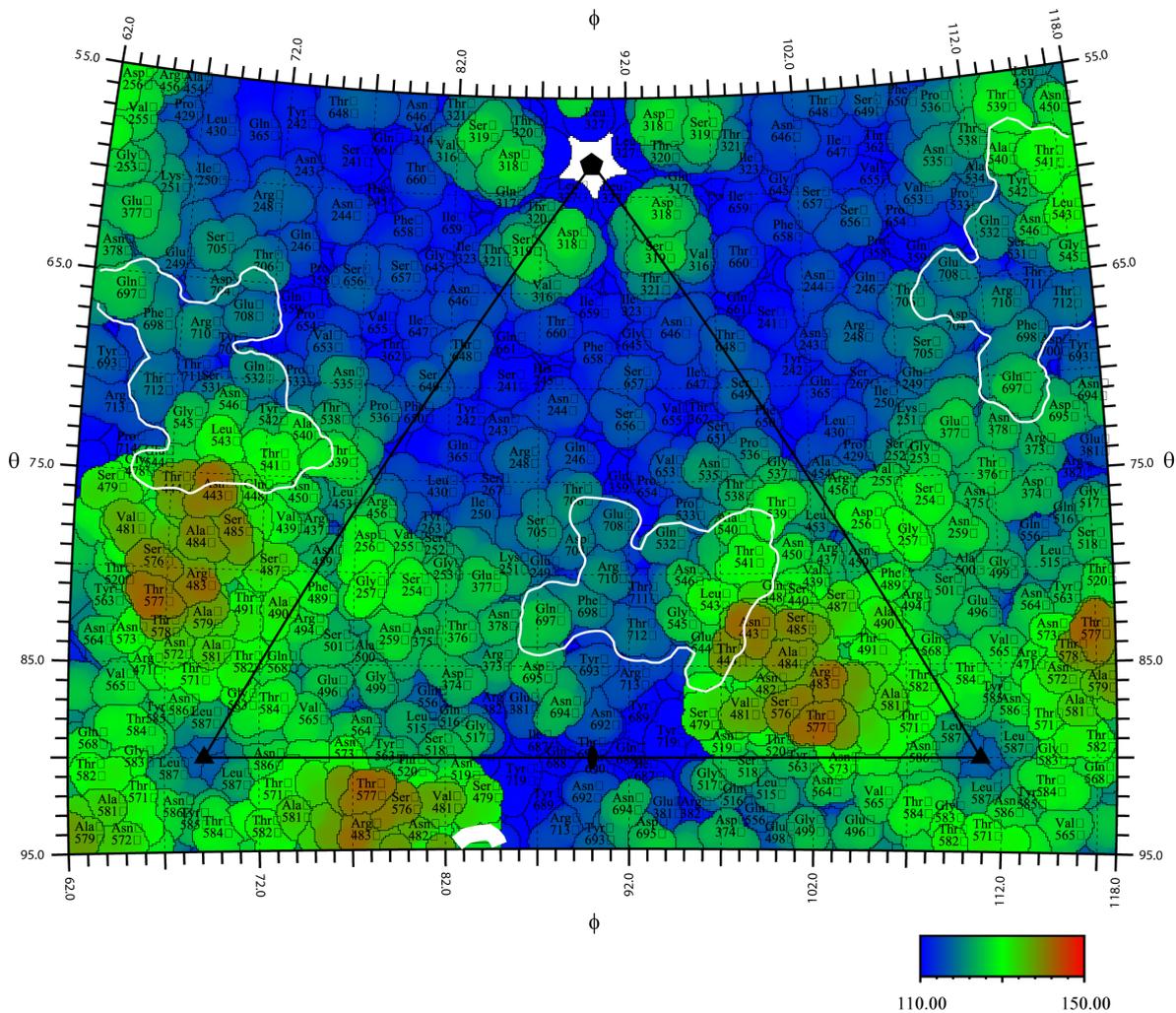
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Figure S4. Typical Micrographs from the datasets. **(A)** Native AAV5 lowpass filtered at 20 Å shows VLPs in vitreous ice. **(B)** same as A but with AAV5-PKD1-2 bound

44 Supplementary Figure S5



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46 **Figure S5** A full sized roadmap of PKD1 footprints on AAV5. Footprints of PKD1 are outlined in
 47 white and amino acids are labeled. Amino acids are colored by their distance from the center of the
 48 particle. Color scale is by distance in Å.

49 References

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