

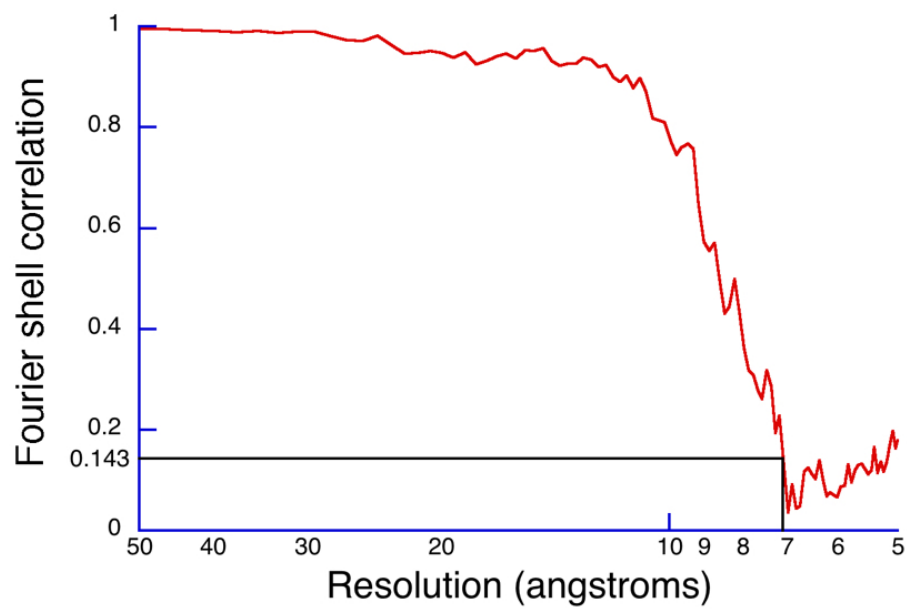
Cryo-Electron Microscopy Structure of the *Macrobrachium rosenbergii* Nodavirus

Capsid at 7 Angstroms Resolution

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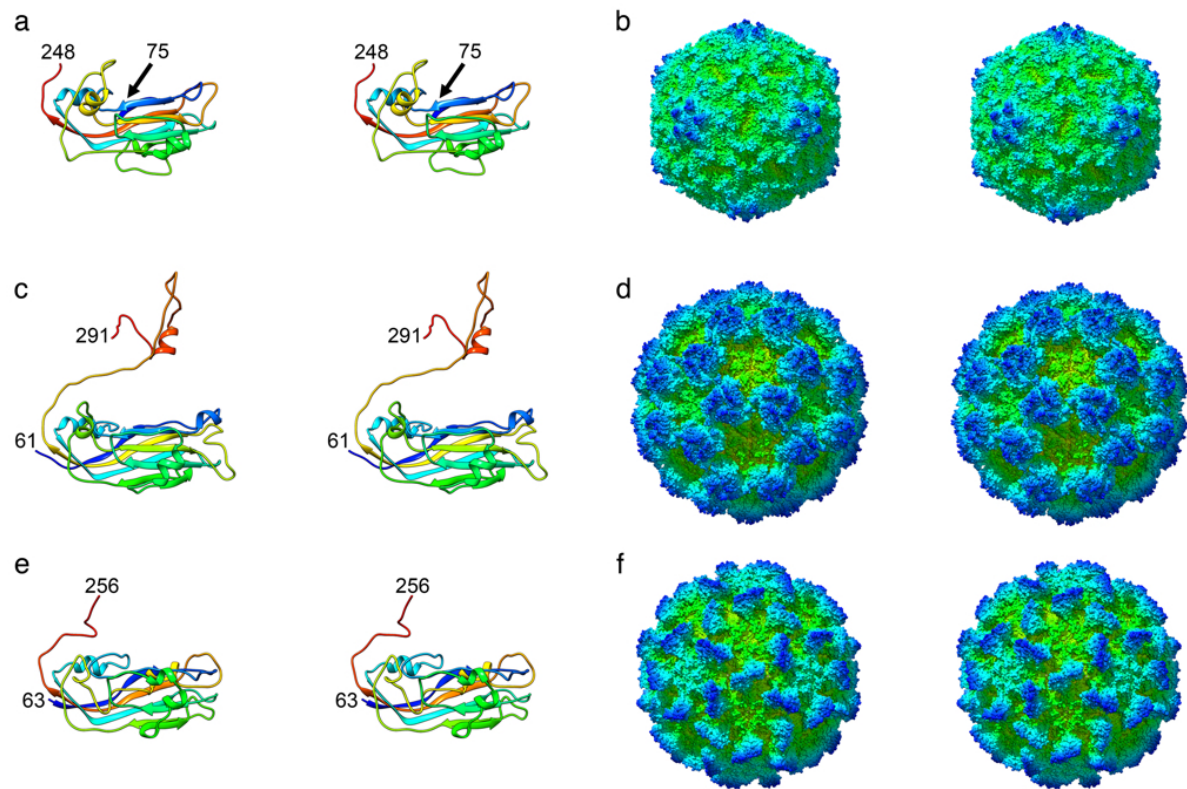
Supplemental figures

Figure S1.



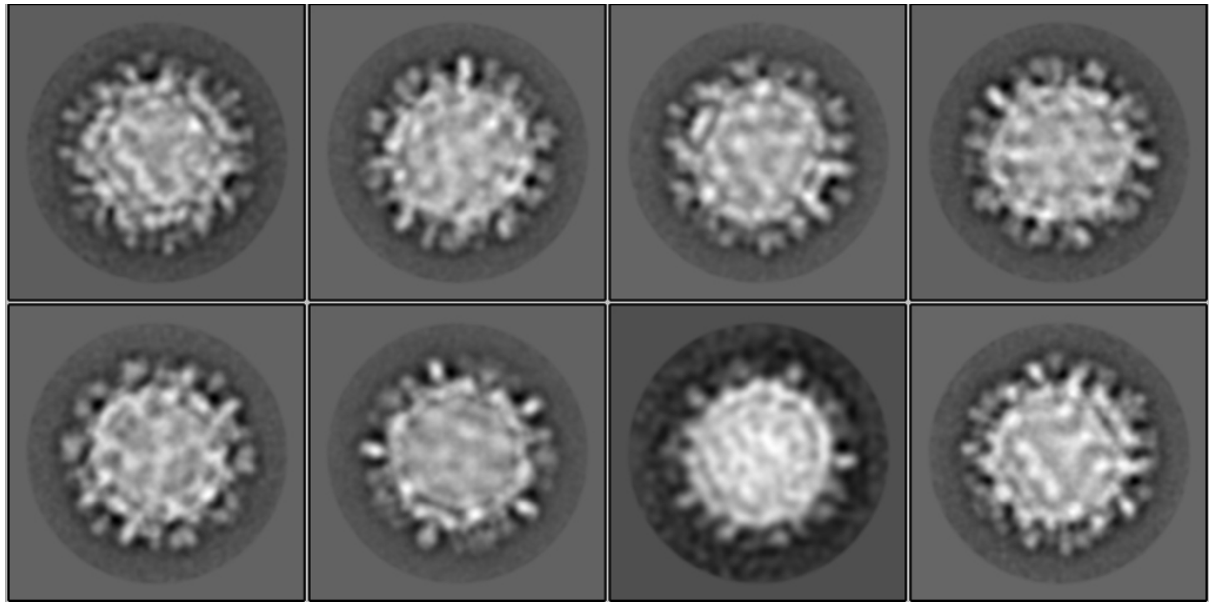
Gold-standard Fourier shell correlation plot for the *MrNV* 3D reconstruction, indicating a resolution of 7 angstroms was achieved assuming an FSC cut-off of 0.143.

Figure S2



Structure prediction was performed using the known structures of several plant and animal viruses from both *nodaviridae* and *tombusviridae* determined by X-ray crystallography. The previously published homology modelling against cucumber necrosis virus – PDB ID 4LLF is presented in the article as figure 4. Here three other viruses were used for modelling. Left-hand panels show ribbon diagrams of the homology models, while the right-hand panels show solvent excluding surface representations of the viral capsid structures that informed the homology model. (a,b) cocksfoot mottle virus 2 – PDB ID 1NG0, (c,d) Orsay virus – PDB ID 4NWV and (e,f) carnation mottle virus PDB ID 1OPO. These models show a common eight-stranded anti-parallel beta-barrel topology in the S-domain. The N and C terminal residues for each ribbon diagram are labelled, indicating the extent of the capsid sequence that was modelled.

Figure S3



A subset of class-averages of MrNV VLPs showing the presence of pronounced spikes on the capsid surface.

Figure S4a

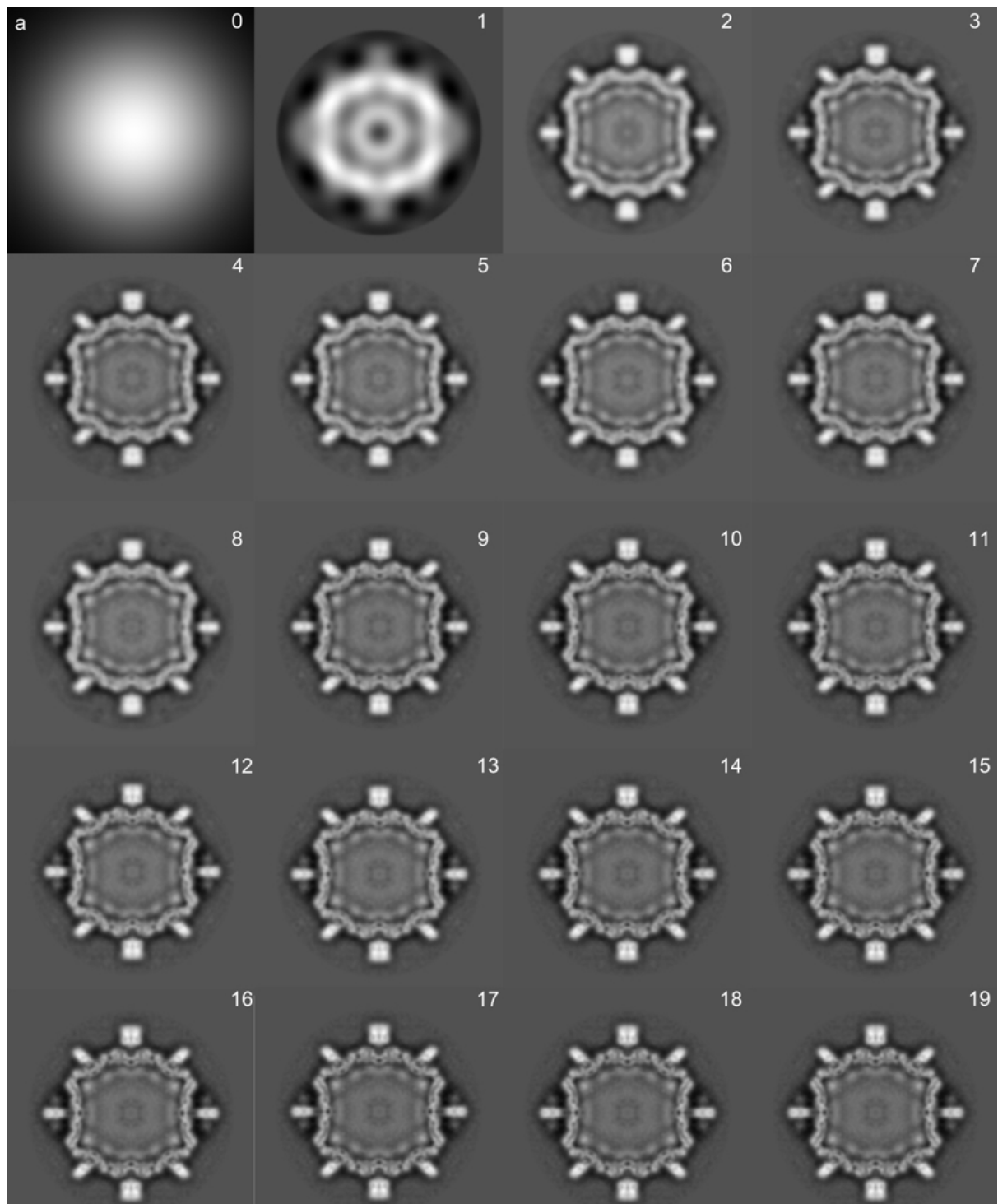
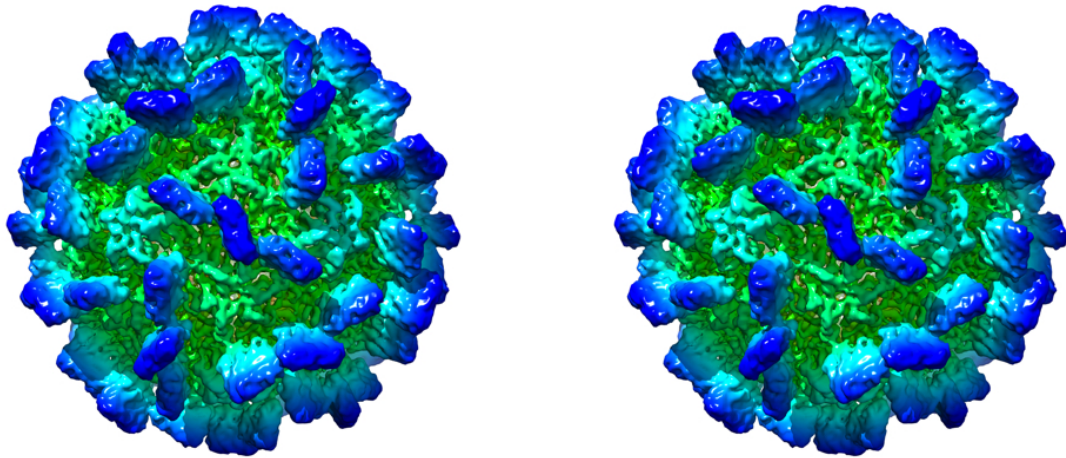


Figure S4b

b



To ensure that our three-dimensional reconstruction was not the product of a model-biased refinement, we prepared a reference-free reconstruction. A subset of binned particles was selected following 2D and 3D classification in Relion. These were then subjected to a 3D auto-refine procedure for which a Gaussian sphere was used as a starting model. (a) Central sections through reconstructions calculated from half-datasets at each iteration of the refinement are given, iteration 0 represents the input starting model. (b) A surface view of the 7-angstrom resolution reconstruction that was determined by iteration 19.