Backbone model of an aquareovirus virion by cryo-electron microscopy and bioinformatics

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Supplementary figure and movie legends:

Supplementary figure 1. Selected density regions from VP3A and VP3B revealing bulky side chain densities and a β-hairpin.

Supplementary figure 2. Illustration of our model refinement procedure using cryoEM density maps as constrains and homology models as templates. Note that the starting homology model of the amino-terminal segment of VP3B did not agree with the experimentally determined cryoEM map and our procedure was able to refine the model so that it fully agrees with the cryoEM density.

Supplementary figure 3. VP3A fitted with model. (a) VP3A model fitting into density map. (b) Rotated view of (a). An α-helix density attached to VP3A is attributable to VP2.
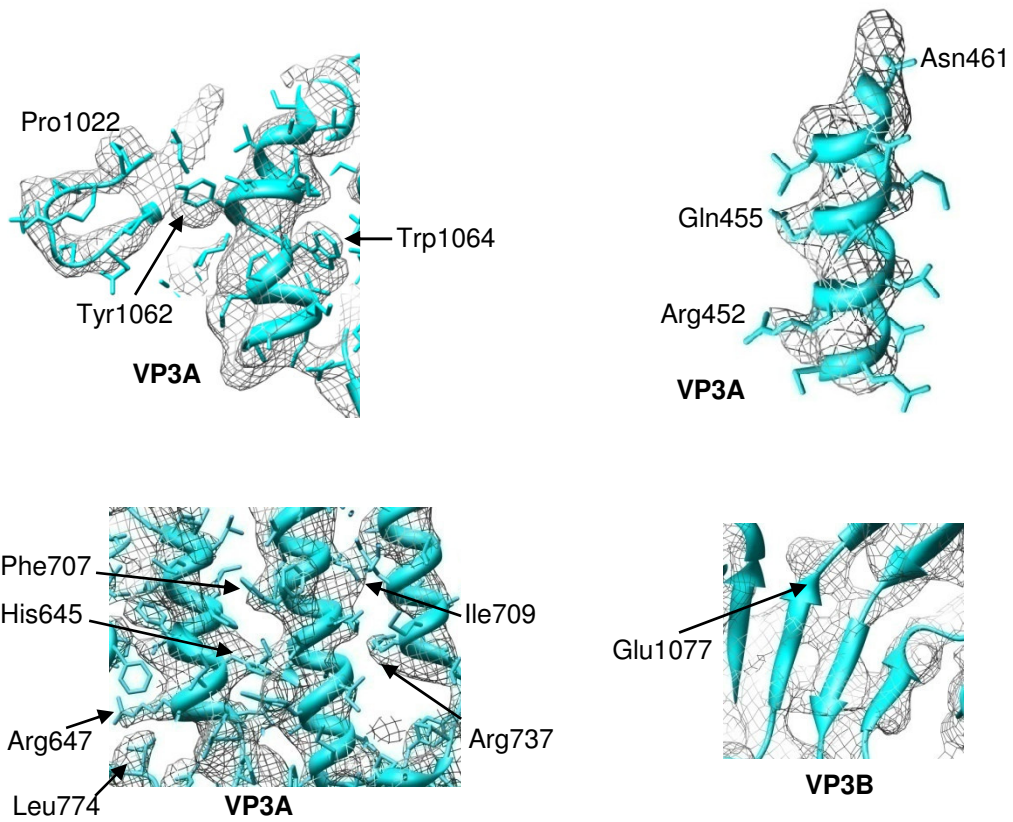
Supplementary movies:

Movie 1   Two α-helices from VP3A fitted with VP3A model showing resolved bulky side chains.

Movie 2   Core proteins segmented from GCRV virion are shown in different colors and superimposed with the cryoEM density maps of the core.

Movie 3   One asymmetric unit of the GCRV virion structure. The density map of the virion is shown first, followed by a superposition of one asymmetric unit containing five different capsid proteins shown as colored ribbons.

Movie 4   A copy of turret protein morphs between the open state (GCRV) and closed state (MRV). The color scheme for domains is the same as that of Fig. 4a.

Supplementary Figure 1 Supplementary Fig. 1. Selected density regions from VP3A and VP3B revealing bulky side-chain densities and a β-hairpin.
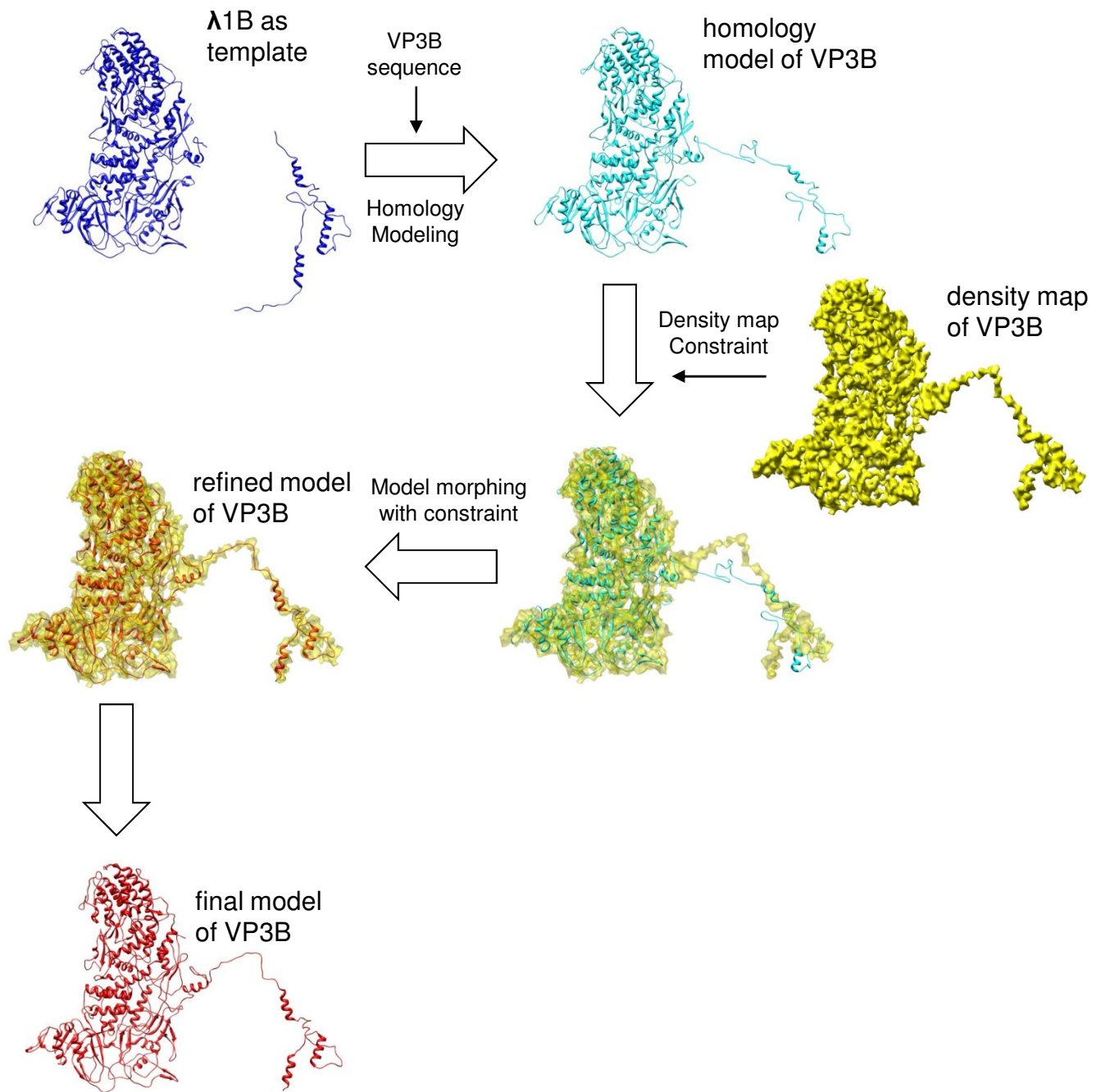
Supplementary Figure 2 Supplementary Fig. 2. Illustration of our model refinement procedure using cryo-EM density maps as constraints and homology models as templates. Note that the starting homology model of the amino-terminal segment of VP3B did not agree with the experimentally determined cryo-EM map and our procedure was able to refine the model so that it fully agrees with the cryo-EM density.
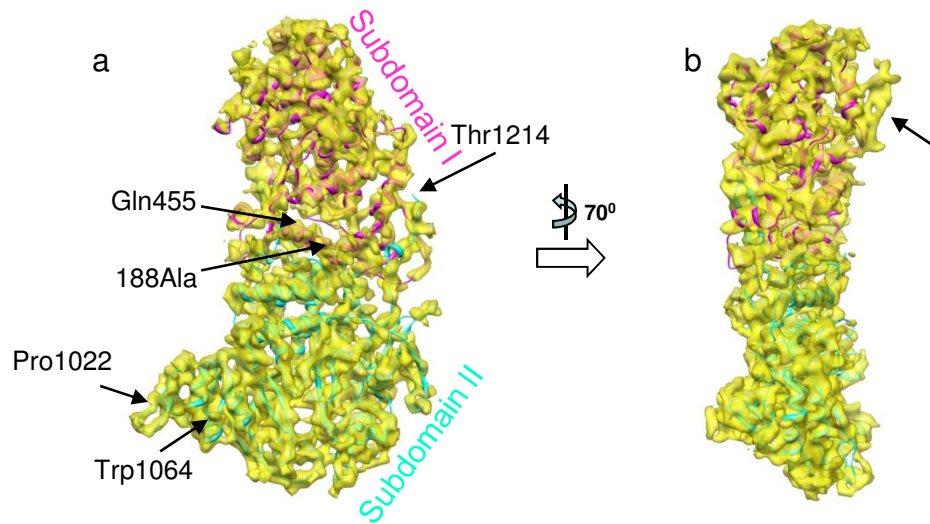
Supplementary Figure 3 Supplementary Fig. 3. VP3A fitted with model. (a) VP3A model fitting into density map. (b) Rotated view of (a). An α-helix density attached to VP3A is attributable to VP2.