

3

1

2

Figure S1. Resolution of the wt and D263A and F55A MVM capsids. Fourier shell
correlation (FSC) resolution curve for wt (red) and D263A (green) and F55A (blue) capsids.
Resolutions based on the 0.143 criteria are indicated. For the 0.143 threshold, values for the wt
capsid were at 3.42 Å. and those for D263A and F55A capsids were at 3.36 Å and 3.26 Å,

8 respectively.



9

10 Figure S2. Comparison between the cryo-EM and X-ray structures of wt MVM VP2. (A)

- 11 Plot showing the C α -C α distances after the superimpositions of all equivalent C α atoms in the
- 12 VP2 structures obtained by either cryo-EM or X-ray crystallography. Dashed lines are traced
- 13 at a C α -C α distance of 0.8 and 1.4 Å. (B) Ribbon representation of the superimposition of the
- 14 VP2 backbone atoms. Regions with C α -C α distances > 0.8 Å are colored red.
- 15



16

17 Figure S3. Comparison between X-ray crystallography B-factors and cryo-EM LR values

and B-factors for the wt MVM capsid protein and different protein complexes. (A) 18 19 Residue-by-residue comparison of crystallographic relative B-factors and cryo-EM relative LR 20 values and B-factors for the wt MVM capsid. Color distribution along the VP2 sequence is 21 based on relative X-ray B-bactors, relative cryo-EM LR values or relative cryo-EM B-factors 22 (X-ray), as indicated in the color scales at right. (B) Residue-by-residue comparison of the 23 crystallographic relative B-factors and cryo-EM relative LR values and B-factors for β-24 galactosidase, DMFase, apoferritin and PCV-2. Color distribution along the protein sequences is as in A. 25

- 26
- 27

28 Data S1. dat PDB coordinates for wt MVM capsid protein that include relative LR

- 29 values (separate file).
- 30