Data collection		
Electron microscope	Titan Krios G4	
Camera	K3	
Magnification	81,000	
Voltage (kV)	300	
Defocus range (μm)	0.6-2.0	
Pixel size (Å)	1.058 (physical pixels)	
Number of movies	4,864	
Frame exposure time (s)	3.21	
Number of frames	50	
Total electron dose (e-/Å2)	57.36	
Reconstruction		
	Whole virus	**Local reconstruction of one asymmetric unit**
Symmetry imposed	icosahedral	C1
Number of particle images	92,484	5,550,000
Resolution (Å)	3.10	2.51
Map sharpening B factor (Å2)	-101.7	-91.6
FSC threshold	0.143	0.143
Refinement		
EMD accession code	EMD-78948	EMD-78949
PDB accession code	38NK	38NL
Model composition		
Non-hydrogen atoms	30,868	
Protein residues	3,996	
Ligand	12	
Ramachandran plot		
Favored (%)	95.29	
Allowed (%)	4.71	
Disallowed (%)	0.00	
Validation		
MolProbity score	1.64	
Clashscore	5.74	
Rotamer outliers (%)	0.00	
R.m.s. deviations		
Bond lengths (Å)	0.005 (0)	
Bond angles (°)	0.643 (0)	
Cβ outliers (%)	0.00	