S3 Table. Cryo-EM data collection, refinement and validation statistics for HMPV F in complex with scFv MPE8.

	HMPV F in complex with scFv MPE8 (EMD-28891) (PDB ID: 8F6X)
Data collection and processing	
Magnification	105,000
Voltage (kV)	300
Electron exposure (e–/Å^2)	58.06
Defocus range (μm)	-1.0 to -2.5 μm
Pixel size (Å)	0.83
Symmetry imposed	C3
Final particle images (no.)	192259
Map resolution (Å)	3.25
FSC threshold	0.5
Refinement	
Initial model used (PDB code)	7LZE
Model resolution (Å)	3.23
FSC threshold	0.5
Map sharpening B factor (Å^2)	-152.1
Model composition	
Non-hydrogen atoms	14952
Protein residues	1980
Ligands	3 NAG
B factors (Å^2)(mean)	
Protein	49.5
Ligand	79.1
R.m.s. deviations	
Bond lengths (Å)	0.002
Bond angles (°)	0.507
Validation	
MolProbity score	1.86
Clash score	8.9
Poor rotamers (%)	0.06
Ramachandran plot	
Favored (%)	94.29
Allowed	5.66
Disallowed	0.05