S8 Table: Cryo-EM data collection, refinement and validation statistics.

	BG505 SOSIP + Bess4 Fab + RM20A3 Fab (EMD-41498) (PDB: 8TQ1)
Data collection and processing	
Microscope	TFS Krios
Magnification	130,000x
Voltage (kV)	300
Electron exposure (e–/Å^2)	55.5
Defocus range (µm)	-0.7 to -1.7
Detector	Gatan K2 Summit
Recording mode	Counting
Pixel size (Å)	1.045
Symmetry imposed	C1
Micrographs (no.)	3,871
Initial particle images (no.)	494,075
Final particle images (no.)	82,374
Map resolution (Å)	3.3
FSC threshold	0.143
Map sharpening B factor (Å^2)	-83.5
Map pixel size (Å)	1.045
Map resolution range (Å)	2.4-5.0
Refinement	
Initial model used (PDB code)	6x9r
Model resolution (Å)	3.3
FSC threshold	0.5
Model resolution range (Å)	2.4-4.0
EMRinger score	3.95
Model composition	
Non-hydrogen atoms	19,788
Protein residues	2,400
Ligands	79
Mean B factors (Å^2)	
Protein	71
Ligand	96
R.m.s. deviations	
Bond lengths (Å)	0.006
Bond angles (°)	1.125
Validation	
MolProbity score	1.11
Clashscore	1.49
Poor rotamers (%)	0.19
Ramachandran plot	
Favored (%)	96.54
Allowed (%)	3.46
Disallowed (%)	0.00