

**S3 Table. Cryo-EM data collection, processing, and validation**

Map	CZA97.012 SOSIP + 3BNC117 Fab
EMDB	EMD-40088
<b>Data collection</b>	
Microscope	Thermo Fisher Titan Krios
Voltage (kV)	300
Detector	Gatan K2 Summit
Recording mode	Counting
Nominal magnification	22,500
Movie micrograph pixel size (Å)	1.31
Dose rate (e <sup>-</sup> /[(camera pixel)*s])	10.0
Number of frames per movie micrograph	50
Frame exposure time (ms)	200
Movie micrograph exposure time (s)	10
Total dose (e <sup>-</sup> /Å <sup>2</sup> )	58
Defocus range (µm)	-1.0 to -2.7
<b>EM data processing</b>	
Number of movie micrographs	1,142
Number of molecular projection images in map	79,261
Symmetry	C3
Map resolution (FSC 0.143; Å)	3.4
Map sharpening B-factor (Å <sup>2</sup> )	-126
<b>Structure Building and Validation</b>	
<i>Number of atoms in deposited model</i>	
SOSIP gp120	10,707
SOSIP gp41	2,925
Fab Fv	5,349
glycans	1,677
MolProbity score	1.00
Clashscore	1.63
Map correlation coefficient	0.83
d FSC model (0.5)	3.6
EMRinger score	2.82
<i>RMSD from ideal</i>	
Bond length (Å)	0.006
Bond angles (°)	0.946
<i>Ramachandran plot</i>	
Favored (%)	97.57
Allowed (%)	2.43
Outliers (%)	0.00
Side chain rotamer outliers (%)	0.29
Cβ outliers (%)	0.00
PDB	8gje