

Table 1. Cryo-EM data collection, refinement and validation statistics

	MmCAT1:Arg: FrMLV-RBD (EMDB-50669) (PDB 9FQU)	MmCAT1:Lys: FrMLV-RBD (EMDB-50670) (PDB 9FQV)	MmCAT1:Orn: FrMLV-RBD (EMDB-50671) (PDB 9FQW)	MmCAT1(apo) :FrMLV-RBD (EMDB-50668) (PDB 9FQT)
Data collection and processing				
Magnification	105k	105k	105k	105k
Voltage (kV)	300	300	300	300
Electron exposure (e-/Å ²)	50	50	50	50
Defocus range (µm)	1.2-2.4	1.2-2.4	1.2-2.4	1.2-2.6
Pixel size (Å)	0.825	0.825	0.825	0.825
Symmetry imposed	C1	C1	C1	C1
Initial particle picks (no.)	2,375,463	3,150,614	1,567,413	2,482,628
Particles after 2D (no.)	772,292	684,030	579,080	517,673
Final particles (no.)	386,193	417,283	247,271	263,131
Map resolution (Å) (GSFSC=0.143)	8.88 - 2.79	26.39 - 2.95	45.23 - 3.01	37.34 - 3.50
Refinement				
Initial model used	AlphaFold & 1AOL	AlphaFold & 1AOL	AlphaFold & 1AOL	AlphaFold & 1AOL
Model resolution (Å) (FSC=0.5)	3.0	3.1	3.2	3.8
Map sharpening <i>B</i> factor (Å ²)	-120.3	-138.7	-129.2	-155.1
Model composition				
Non-hydrogen atoms	6059	6031	6031	5922
Protein residues	770	770	768	760
Ligands	13	11	12	11
<i>B</i> factors (Å ²)				
Protein	61.64	62.96	66.79	66.80
Ligand	67.29	68.89	68.17	66.92
R.M.S. deviations				
Bond lengths (Å)	0.002	0.002	0.002	0.003
Bond angles (°)	0.478	0.465	0.502	0.609
Validation				
MolProbity score	1.24	1.27	1.23	1.49
Clashscore	4.63	5.15	4.57	9.17
Poor rotamers (%)	0.16	0.00	0.00	0.16
Ramachandran plot				
Favored (%)	98.03	98.03	98.68	98.81
Allowed (%)	1.97	1.97	1.32	1.19
Disallowed (%)	0.00	0.00	0.00	0.00