Table S1. Cryo-EM data collection and refinement statistics

	Multibody body 1	Multibody body 2	Consensus map
Data collection and processing			
Magnification	130,000	130,000	130,000
Voltage (kV)	300	300	300
Camera	Falcon 4	Falcon 4	Falcon 4
Electron exposure (e^-/Å^2)	50	50	50
Exposure rate (e-/pixel*s)	8.78	8.78	8.78
Number of frames	1323	1323	1323
Defocus range (μm)	-0.5 to -1.9	-0.5 to -1.9	-0.5 to -1.9
Pixel size (Å)	0.97	0.97	0.97
Symmetry imposed	C1	C1	C1
Movies collected (no.)	13,028 + 1202 (tilted stage)	13,028 + 1202 (tilted stage)	13,028 + 1202 (tilted stage)
Initial particle images (no.)	3,194,364 + 191,127 (tilted stage)	3,194,364 + 191,127 (tilted stage)	3,194,364 + 191,127 (tilted stage)
Final particle images (no.)	105,974 + 14,684 (tilted stage)	105,974 + 14,684 (tilted stage)	105,974 + 14,684 (tilted stage)
Map resolution (Å)			
FSC0.143 (unmasked/masked)	3.8/3.3	3.8/3.4	3.7/3.4
Map resolution range (Å)	3-10	3-11	3-11
Refinement			
Initial model used (PDB code)	8FYH	8FYH	8FYH
Resolution cutoff (Å)	4	4	4
Map sharpening *B* factor (Å^2)	0	0	0
Model composition			
Non-hydrogen atoms	12111	12103	24433
Protein residues	1793	1793	3586
Nucleotide residues	0	0	10
Ligands	ZN:7	ZN:7	ZN:14
B factors (Å^2)			
Protein	24.35	13.42	13.42
Ligand	44.27	22.70	22.70
RMSD			
Bond lengths (Å)	0.002 (0)	0.002 (0)	0.004 (0)
Bond angles (°)	0.521 (4)	0.536 (6)	0.971 (4)
Validation			
MolProbity score	2.25	2.27	2.26
Clashscore	9.77	8.81	9.57
Poor rotamers (%)	2.01	2.58	2.18
Ramachandran plot			
Favored (%)	91.43	92.12	91.66
Allowed (%)	8.45	7.77	8.17
Disallowed (%)	0.11	0.11	0.17