Cryo-EM data collection, refinement and validation statistics

	Maf1-Pol III (EMD-10595, PDB 6TUT)
Data collection and processing	
Magnification	130 000
Voltage (kV)	300
Electron exposure (e^{-}/Å^2)	60.5
Defocus range (μm)	-0.75 to -3.5
Pixel size (Å)	1.041
Symmetry imposed	none
Initial particle images (no.)	1 688 795
Final particle images (no.)	117 442
Map resolution (Å)	3.25
FSC threshold	0.143
Map resolution range (Å)	2.9 to 5.0
Refinement	
Initial model used (PDB code)	6eu3
Model resolution (Å)	3.1
FSC threshold	0.5
Map sharpening *B* factor (Å^2)	-109
Model composition	
Nonhydrogen atoms	40 653
Protein residues	5 131
Ligands	7
B factors (Å^2)	
Protein	64
Ligand	68
R.m.s. deviations	
Bond lengths (Å)	0.01
Bond angles (°)	1.21
Validation	
MolProbity score	1.89
Clashscore	6.36
Poor rotamers (%)	0.87
Ramachandran plot	
Favored (%)	90.33
Allowed (%)	9.55
Disallowed (%)	0.12