

	Nucleosome EMD-53596 PDB-9R5W	Complex I EMD-53590 PDB-9R5K	Complex II EMD-53597	Complex III EMD-53595 PDB-9R5S
<u>Data collection and processing</u>				
Magnification	81,000	81,000	81,000	81,000
Voltage(kV)	300	300	300	300
Detector	K3	K3	K3	K3
Electron exposure	46.8	46.8	46.8	46.8
Defocus Range	(1.5-3.2)	(1.5-3.2)	(1.5-3.2)	(1.5-3.2)
Pixel size	0.55	0.55	0.55	0.55
Initial particle images (no.)	500,179	500,179	500,179	500,179
Final particle images (no.)	105,495	135,523	147,140	110,285
Map resolution (Å)	3.74	4.08	4.22	3.83
FSC threshold	0.143	0.143	0.143	0.143
<u>Models</u>				
	DNA, Histones	DNA,Histone	DNA,Histone	DNA,Histone, Chd1
<u>Refinement</u>				
Initial Model	3LZ0	3LZ0,6ftx,7tn3	3LZ0,6ftx,7tn4	3LZ0,6ftx,7tn5
Map sharpening B factor (Å ²)	180	180	180	180
Model Composition				
Non-hydrogen atoms	12494	12495	11905	17426
Hydrogens	9773	9774	6695	9675
Protein residues	742	742	735	1390
DNA bases	324	324	298	320
r.m.s deviations				
Bond lengths (Å)	0.004	0.004	0.015	0.006
Bond Angles (°)	0.702	0.735	1.4	0.837
Validation				
MolProbity score	1.51	1.56	1.8	1.75
Clashscore	7.55	8.58	6.67	6.7
CaBLAM outliers (%)	0.7	0.7	0.57	1.64
Rotamer outliers (%)	0	0	0.17	0.09
Cβ outliers (%)	0	0	0.15	0
Ramachandran plot				
Favoured (%)	97.52	97.52	97.64	94.5
Allowed (%)	2.48	2.48	2.36	5.5
Disallowed (%)	0	0	0	0