

Supplementary information, Table. S1 | Cryo-EM data collection, refinement and validation statistics

		H3K9 deacetylation state	H3/H4 deacetylation states			Alternative deacetylation state	Linker tightening state	Rpd3S-Hho1 co-existing state
	Apo Rpd3S (EMD- 37096,PD B 8KC7)	Rpd3S- NCP ^{187bp} /MLA/K 9Q (EMD- 37123,PDB 8KD3)	Rpd3S- NCP ^{187bp} /MLA Class1 (EMD- 37124,PDB 8KD4)	Rpd3S- NCP ^{187bp} /MLA Class2 (EMD- 37125,PDB 8KD5)	Rpd3S- NCP ^{187bp} /MLA Class3 (EMD- 37126,PDB 8KD6)	Rpd3S- NCP ^{167bp} /MLA (EMD- 37127,PDB 8KD7)	Rpd3S- NCP ^{187bp} (EMD- 37122,PD B 8KD2)	NCP ^{187bp} _ Hho1
Data collection and processing								
Magnification	45,000	165,000	165,000	165,000	165,000	165,000	165,000	165,000
Voltage(kV)	200	300	300	300	300	300	300	300
Electron exposure(e ⁻ /Å ²)	60	50	50	50	50	50	50	50
Energy filter slit width(eV)	—	10	10	10	10	10	10	10
Defocus range(μm)	-0.8 to -2.2	-0.8 to -2.2	-0.8 to -2.2	-0.8 to -2.2	-0.8 to -2.2	-0.8 to -2.2	-0.8 to -2.2	-0.8 to -2.2
Pixel size(Å)	0.88	0.71	0.71	0.71	0.71	0.71	0.71	0.71
Symmetry imposed	C1	C1	C1	C1	C1	C1	C1	C1
Movies(no.)	15,087	12,467	12,412	12,412	12,412	11,990	10,632	22,499
Initial particle images(no.)	2,767,513	1,149,836	983,865	983,865	983,865	1,061,981	965,584	2,114,187
Final particle images(no.)	287,163	117,400	100,597	109,319	68,388	56,949	72,121	54,692
Map resolution(Å) FSC threshold 0.143	3.46	2.90	2.93	2.90	3.07	3.09	3.02	6
Refinement								
Initial model used (PDB code)	2LKM, 1C3P, 2N2H and 6XAW	2LKM, 1C3P, 2N2H, 6XAW and 4LD9	2LKM, 1C3P, 2N2H, 6XAW and 4LD9	2LKM, 1C3P, 2N2H, 6XAW and 4LD9	2LKM, 1C3P, 2N2H, 6XAW and 4LD9	2LKM, 1C3P, 2N2H, 6XAW and 4LD9	2LKM, 1C3P, 2N2H, 6XAW and 4LD9	4LD9 and 7PFX
Map sharpening B factor(Å ²)	-137.78	-31.94	-45.19	-41.23	-45.26	-43.48	-38.68	
Model composition Non-hydrogen atoms Protein/Nucleotide	14,330 1,748	27,587 2,562/328	27,055 2,497/328	26,888 2,500/319	26,971 2,488/328	24,922 2,299/305	24715 2164/348	
R.m.s deviations Bond lengths(Å) Bond angles(°)	0.003 0.706	0.004 0.761	0.004 0.833	0.003 0.747	0.004 0.870	0.004 0.884	0.004 0.717	
Validation								
MolProbity score	1.89	1.74	1.78	1.73	1.72	1.77	1.73	
Clashscore	8.63	7.10	7.96	7.82	7.46	7.80	7.93	
Poor rotamers(%)	0.93	0.09	0.59	0.54	0.77	0.25	0.57	
Ramachandran plot Favored(%) Allowed(%) Disallowed(%)	93.43 6.57 0.00	95.01 4.99 0.00	95.05 4.95 0.00	95.70 4.30 0.00	95.47 4.53 0.00	95.10 4.90 0.00	95.69 4.31 0.00	
Model to map CC (mask, box, peaks, volume)	0.78/0.8/ 0.71/0.78	0.66/0.74/ 0.61/0.66	0.74/0.77/ 0.65/0.74	0.74/0.76/ 0.64/0.74	0.71/0.76/ 0.61/0.71	0.67/0.75/ 0.61/0.67	0.74/0.78/ 0.66/0.73	