

Table S2: Cryo-EM data collection and processing information. Related to Figures S1 to S4 and STAR Methods.

Data collection and pre-processing										
Magnification	130,000x									
Voltage (kV)	300									
Electron exposure (e ⁻ /Å ²)	43.6									
Defocus range (μm)	0.5-4.0									
Pixel size (Å)	1.05									
Initial particle images (#)	4 323 739									
Model/Map Name	Consensus PIC^a	Closed complex^a	CC^{dist} complex^a	Intermediate complex^a	Open complex^a	Contracted TFIIH^a	Expanded TFIIH^a	Pol II-TFIIIB^a	TFIIF^a	Upstream complex
EMDB identifier (EMD-)	12720	12743	12744	12719	12745	12721	12722	12725	12724	12723
PDB identifier	7O4J	7O72	7O73	7O4I	7O75	7O4K	7O4L	-	-	-
Symmetry imposed	C1	C1	C1	C1	C1	C1	C1	C1	C1	C1
Final particle images (#)	107 644	11 014	10 163	16 495	23 887	24 671	34 198	934 763	173 154	156 629
Map resolution (Å)	2.9	3.4	3.4	3.2	3.2	3.6	3.4	2.6	2.8	3.2
FSC threshold = 0.143										
Map resolution range (Å)	2.6-7.0	3.0-10.1	3.1-10.0	3.0-9.0	3.0-8.3	3.2-8.0	3.1-7.9	2.4-3.0	2.6-3.7	3.2-5.0
Refinement										
Initial model used (PDB code)	5OQJ, 1RM1, 3DOM	5OQJ, 1RM1, 3DOM	5OQJ, 1RM1, 3DOM	5OQJ, 1RM1, 3DOM	5OQJ, 1RM1, 3DOM	5OQJ 3DOM	5OQJ 3DOM	-	-	-
Model resolution (Å) ^b	2.8	3.4	3.3	3.2	3.1	3.3	3.2	-	-	-
FSC threshold = 0.5										
Map sharpening B factor (Å ²)	-77	-81	-71	-86	-103	-87	-93	-	-	-
Model composition										
Non-hydrogen atoms	73 026	73 681	73 769	73 946	73 886	34 264	35 160	-	-	-
Protein residues	8889	8868	8880	8892	8901	4216	4330	-	-	-
Nucleotides	90	130	130	134	127	20	20	-	-	-
Ligands	ZN: 17 ADP: 1 MG: 2 SF4: 1 BEF: 1	ZN: 17 ADP: 1 MG: 2 SF4: 1 BEF: 1	ZN: 17 ADP: 1 MG: 2 SF4: 1 BEF: 1	ZN: 17 ADP: 1 MG: 2 SF4: 1 BEF: 1	ZN: 17 ADP: 1 MG: 2 SF4: 1 BEF: 1	ZN: 10 ADP: 1 MG: 2 SF4: 1 BEF: 1	ZN: 11 ADP: 1 MG: 1 SF4: 1 BEF: 1		-	-
Mean B factors (Å²)										
Protein	49.11	121.30	119.47	108.27	92.77	91.45	88.13	-	-	-
Nucleotides	103.37	273.76	254.84	220.22	205.63	98.72	126.37	-	-	-
Ligand	65.71	195.45	188.64	167.99	138.65	75.41	98.41	-	-	-
R.m.s. deviations										
Bond lengths (Å)	0.002	0.002	0.002	0.002	0.002	0.002	0.002	-	-	-
Bond angles (°)	0.489	0.467	0.435	0.478	0.449	0.439	0.427	-	-	-
Validation										
MolProbity score	1.32	1.20	1.23	1.33	1.27	1.12	1.25	-	-	-
Clashscore	4.29	3.94	4.07	4.59	4.13	3.31	3.96	-	-	-
Poor rotamers (%)	0.01	0.00	0.00	0.00	0.00	0.00	0.00	-	-	-
Ramachandran plot										
Favored (%)	97.44	97.92	97.85	97.53	97.65	98.03	97.70	-	-	-
Allowed (%)	2.56	2.07	2.14	2.47	2.35	1.97	2.30	-	-	-
Disallowed (%)	0.00	0.01	0.01	0.00	0.00	0.00	0.00	-	-	-

^a composite map

^b The model-map correlation was determined using locally filtered and sharpened final maps. As an artefact of the local filtering, the determined resolution for the model-map fit in some cases extended beyond the resolution determined for the half-map correlation (i.e. the map resolution). This was dependent on the distribution of well- and poorly resolved regions within the map. As expected, the corresponding conventionally post-processed maps (i.e. the same original half-maps were utilized for reconstruction but sharpened and filtered with globally applied parameters) did not cause this effect when used for determination of the model-map correlation.