

Cell, Volume 179

Supplemental Information

Structural Basis of *Poxvirus* Transcription:

Transcribing and Capping *Vaccinia* Complexes

Hauke S. Hillen, Julia Bartuli, Clemens Grimm, Christian Dienemann, Kristina Bedenk, Aladar A. Szalay, Utz Fischer, and Patrick Cramer

SUPPLEMENTARY TABLES

Table S1: Cryo-EM data collection, refinement and validation statistics. Related to Figure 1, Figure 2 and Figure S7.

	vRNAP EC (EMD-4889) (PDB 6RID)	vRNAP CCC (EMD-4890) (PDB 6RIE)	vRNAP Nucleic acid- free particle population (EMD-4891)
Data collection and processing			
Magnification	130,000	130,000	130,000
Voltage (kV)	300	300	300
Electron exposure (e-/Å ²)	40.63	40.63	40.63
Defocus range (μm)	-0.1 to -4.1	-0.2 to -4.1	-0.3 to -4.0
Pixel size (Å)	1.05	1.05	1.05
Symmetry imposed	C1	C1	C1
Initial particle images (no.)	632,458	632,458	632,458
Final particle images (no.)	110,733	77,706	12,433
Map resolution (Å)	2.87	3.05	4.15
FSC threshold	0.143	0.143	0.143
Map resolution range (Å)	2.7 – 3.6	2.8 – 4.1	3.9 – 9.9
Refinement			
Model resolution (Å)	2.9	3.1	
FSC threshold	0.5	0.5	
Map sharpening <i>B</i> factor (Å ²)	-46.4	-38.3	
Model composition			
Non-hydrogen atoms	26,705	36,583	
Protein/Nucleotide residues	3,223 / 34	4,418 / 40	
Ligands	4 x Zn, 1 x Mg	4 x Zn, 2 x Mg, 1 x GDP, 1 x SAM	
<i>B</i> factors (Å²)			
Protein/Nucleotide	37.2 / 108.6	29.9 / 86.8	
Ligand	66.5	54.6	
R.m.s. deviations			
Bond lengths (Å)	0.005	0.005	
Bond angles (°)	0.760	0.754	
Validation			
MolProbity score	1.38	1.51	
Clashscore	3.52	4.43	
Poor rotamers (%)	0.14	0.07	
Ramachandran plot			
Favored (%)	96.4	95.8	
Allowed (%)	3.6	4.2	
Disallowed (%)	0.00	0.00	