wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 04:53 PM GMT

PDB ID	:	4G7O
Title	:	Crystal structure of Thermus thermophilus transcription initiation complex containing 2 nt of RNA
Authors	:	Zhang, Y.; Ebright, R.H.
Deposited on	:	2012-07-20
Resolution	:	2.99 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

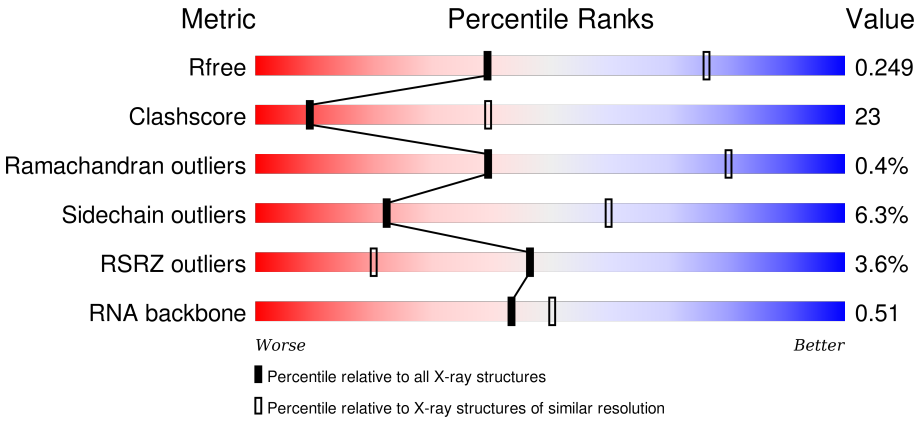
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)
RNA backbone	2183	1036 (3.40-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	315	44% 26% • 28%
1	B	315	% 41% 26% • 30%
1	K	315	48% 23% • 28%
1	L	315	% 43% 26% • 29%

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Mol	Chain	Length	Quality of chain
2	C	1119	3% 59% 38%
2	M	1119	8% 56% 40%
3	D	1524	3% 59% 34%
3	N	1524	4% 56% 38%
4	E	99	3% 68% 25% 5%
4	O	99	3% 71% 23% 5%
5	F	443	% 51% 25% 22%
5	P	443	4% 46% 28% 22%
6	G	21	48% 19% 10% 24%
6	Q	21	33% 43% 24%
7	H	27	52% 33% 11%
7	R	27	52% 37% 11%
8	I	2	100%
8	S	2	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	MG	D	2004	-	-	-	X
10	MG	K	1001	-	-	-	X
10	MG	N	2004	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 57231 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1782	1138	310	332	2			
1	B	222	Total	C	N	O	S	0	0	0
			1750	1118	304	326	2			
1	K	226	Total	C	N	O	S	0	0	0
			1782	1138	310	332	2			
1	L	225	Total	C	N	O	S	0	0	0
			1773	1133	308	330	2			

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1111	Total	C	N	O	S	0	0	0
			8770	5548	1564	1634	24			
2	M	1111	Total	C	N	O	S	0	0	0
			8770	5548	1564	1634	24			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1482	Total	C	N	O	S	0	0	0
			11704	7421	2059	2189	35			
3	N	1489	Total	C	N	O	S	0	0	0
			11746	7446	2066	2198	36			

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	94	Total	C	N	O	S	0	0	0
			761	486	132	139	4			
4	O	94	Total	C	N	O	S	0	0	0
			761	486	132	139	4			

- Molecule 5 is a protein called RNA polymerase sigma factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	346	Total	C	N	O	S	0	0	0
			2807	1770	509	524	4			
5	P	347	Total	C	N	O	S	0	0	0
			2814	1774	510	526	4			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-19	MET	-	EXPRESSION TAG	UNP Q5SKW1
F	-18	GLY	-	EXPRESSION TAG	UNP Q5SKW1
F	-17	SER	-	EXPRESSION TAG	UNP Q5SKW1
F	-16	SER	-	EXPRESSION TAG	UNP Q5SKW1
F	-15	HIS	-	EXPRESSION TAG	UNP Q5SKW1
F	-14	HIS	-	EXPRESSION TAG	UNP Q5SKW1
F	-13	HIS	-	EXPRESSION TAG	UNP Q5SKW1
F	-12	HIS	-	EXPRESSION TAG	UNP Q5SKW1
F	-11	HIS	-	EXPRESSION TAG	UNP Q5SKW1
F	-10	HIS	-	EXPRESSION TAG	UNP Q5SKW1
F	-9	SER	-	EXPRESSION TAG	UNP Q5SKW1
F	-8	SER	-	EXPRESSION TAG	UNP Q5SKW1
F	-7	GLY	-	EXPRESSION TAG	UNP Q5SKW1
F	-6	LEU	-	EXPRESSION TAG	UNP Q5SKW1
F	-5	VAL	-	EXPRESSION TAG	UNP Q5SKW1
F	-4	PRO	-	EXPRESSION TAG	UNP Q5SKW1
F	-3	ARG	-	EXPRESSION TAG	UNP Q5SKW1
F	-2	GLY	-	EXPRESSION TAG	UNP Q5SKW1
F	-1	SER	-	EXPRESSION TAG	UNP Q5SKW1
F	0	HIS	-	EXPRESSION TAG	UNP Q5SKW1
P	-19	MET	-	EXPRESSION TAG	UNP Q5SKW1
P	-18	GLY	-	EXPRESSION TAG	UNP Q5SKW1
P	-17	SER	-	EXPRESSION TAG	UNP Q5SKW1
P	-16	SER	-	EXPRESSION TAG	UNP Q5SKW1
P	-15	HIS	-	EXPRESSION TAG	UNP Q5SKW1
P	-14	HIS	-	EXPRESSION TAG	UNP Q5SKW1
P	-13	HIS	-	EXPRESSION TAG	UNP Q5SKW1
P	-12	HIS	-	EXPRESSION TAG	UNP Q5SKW1
P	-11	HIS	-	EXPRESSION TAG	UNP Q5SKW1
P	-10	HIS	-	EXPRESSION TAG	UNP Q5SKW1
P	-9	SER	-	EXPRESSION TAG	UNP Q5SKW1
P	-8	SER	-	EXPRESSION TAG	UNP Q5SKW1
P	-7	GLY	-	EXPRESSION TAG	UNP Q5SKW1
P	-6	LEU	-	EXPRESSION TAG	UNP Q5SKW1

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-5	VAL	-	EXPRESSION TAG	UNP Q5SKW1
P	-4	PRO	-	EXPRESSION TAG	UNP Q5SKW1
P	-3	ARG	-	EXPRESSION TAG	UNP Q5SKW1
P	-2	GLY	-	EXPRESSION TAG	UNP Q5SKW1
P	-1	SER	-	EXPRESSION TAG	UNP Q5SKW1
P	0	HIS	-	EXPRESSION TAG	UNP Q5SKW1

- Molecule 6 is a DNA chain called 5'-D(*CP*CP*T*GP*CP*AP*TP*CP*CP*GP*TP*GP*AP*GP*TP*CP*GP*AP*GP*GP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	16	Total	C	N	O	P	0	0	0
			328	156	63	94	15			
6	Q	16	Total	C	N	O	P	0	0	0
			328	156	63	94	15			

- Molecule 7 is a DNA chain called 5'-D(*TP*AP*TP*AP*AP*TP*GP*GP*GP*AP*GP*CP*TP*GP*TP*CP*AP*CP*GP*GP*AP*TP*GP*CP*AP*GP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	24	Total	C	N	O	P	0	0	0
			495	236	94	142	23			
7	R	24	Total	C	N	O	P	0	0	0
			495	236	94	142	23			

- Molecule 8 is a RNA chain called 5'-R(*GP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	2	Total	C	N	O	P	0	0	0
			42	20	10	11	1			
8	S	2	Total	C	N	O	P	0	0	0
			42	20	10	11	1			

- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	2	Total	Zn	0	0
			2	2		
9	N	2	Total	Zn	0	0
			2	2		

- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	D	2	Total Mg 2 2	0	0
10	K	1	Total Mg 1 1	0	0
10	N	2	Total Mg 2 2	0	0

- Molecule 11 is water.

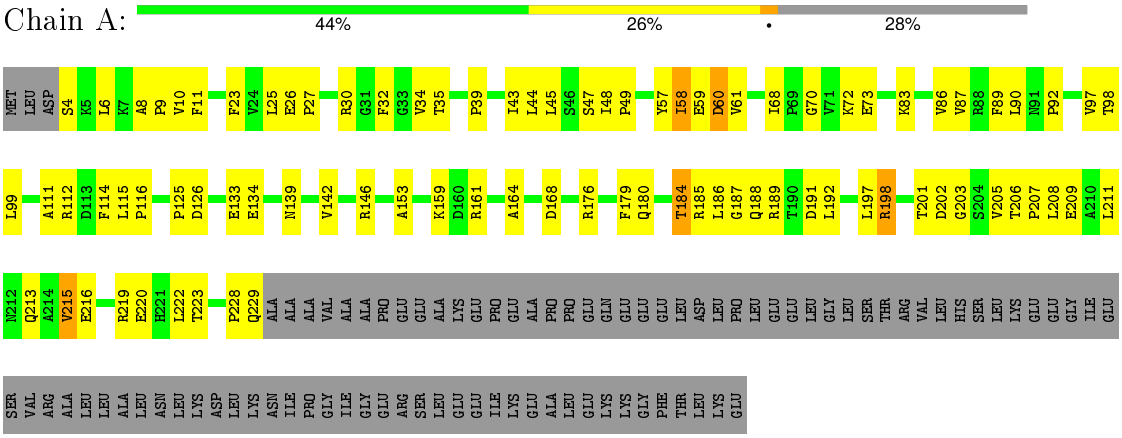
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	14	Total O 14 14	0	0
11	B	3	Total O 3 3	0	0
11	C	53	Total O 53 53	0	0
11	D	58	Total O 58 58	0	0
11	E	8	Total O 8 8	0	0
11	F	10	Total O 10 10	0	0
11	G	5	Total O 5 5	0	0
11	H	2	Total O 2 2	0	0
11	K	4	Total O 4 4	0	0
11	L	3	Total O 3 3	0	0
11	M	33	Total O 33 33	0	0
11	N	52	Total O 52 52	0	0
11	O	5	Total O 5 5	0	0
11	P	16	Total O 16 16	0	0
11	Q	2	Total O 2 2	0	0
11	R	3	Total O 3 3	0	0
11	S	1	Total O 1 1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

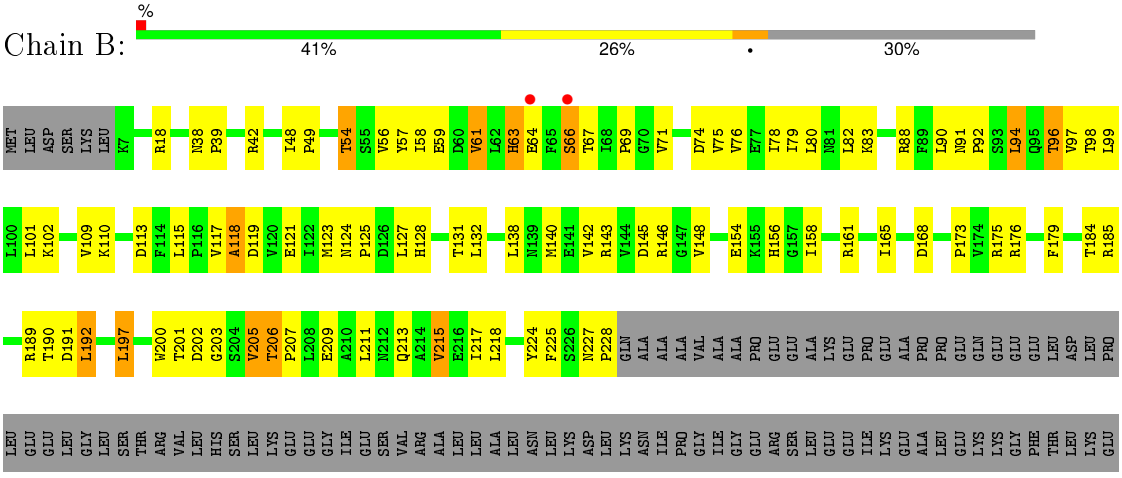
- Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain A:



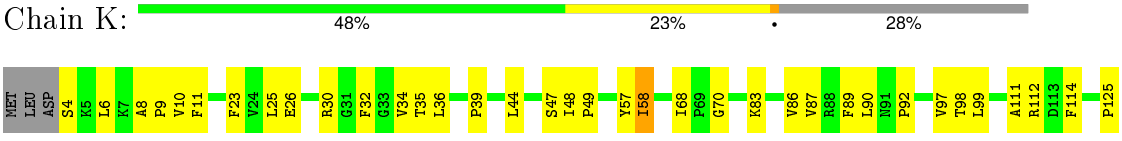
- Molecule 1: DNA-directed RNA polymerase subunit alpha

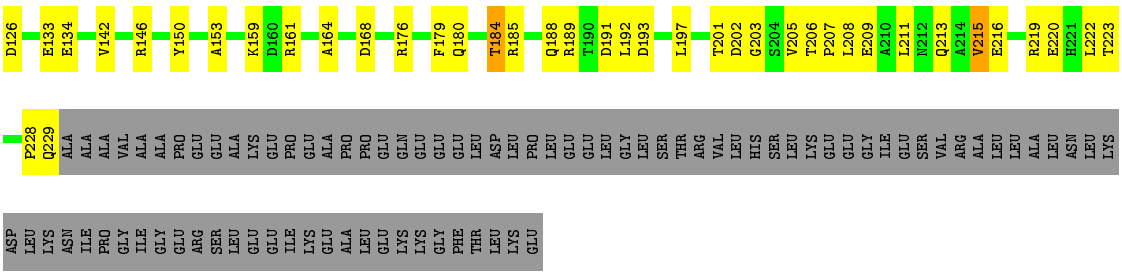
Chain B:



- Molecule 1: DNA-directed RNA polymerase subunit alpha

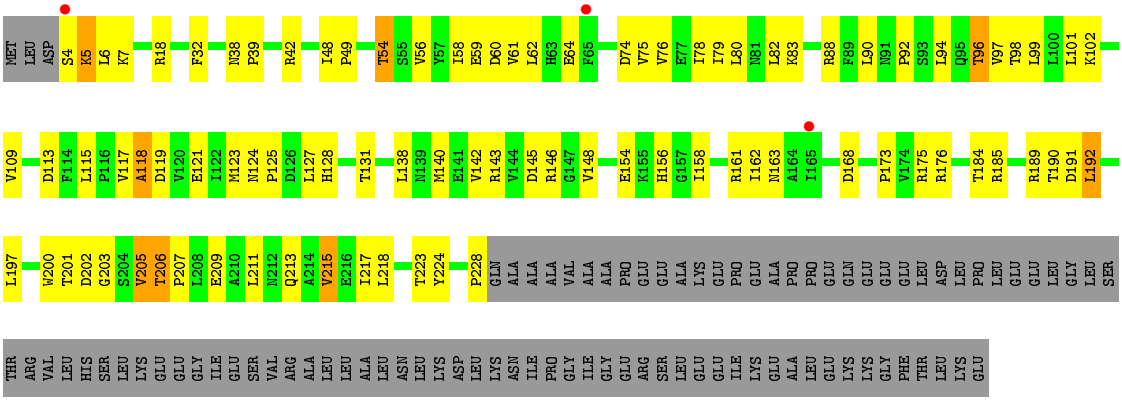
Chain K:





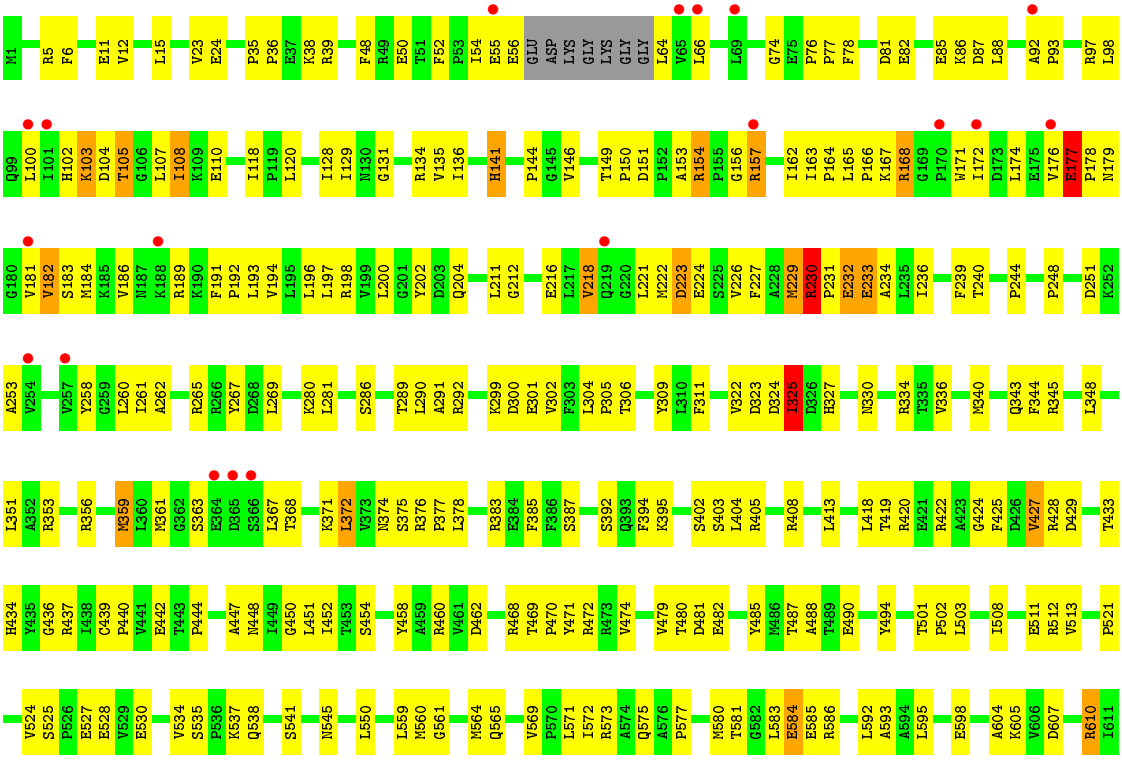
• Molecule 1: DNA-directed RNA polymerase subunit alpha

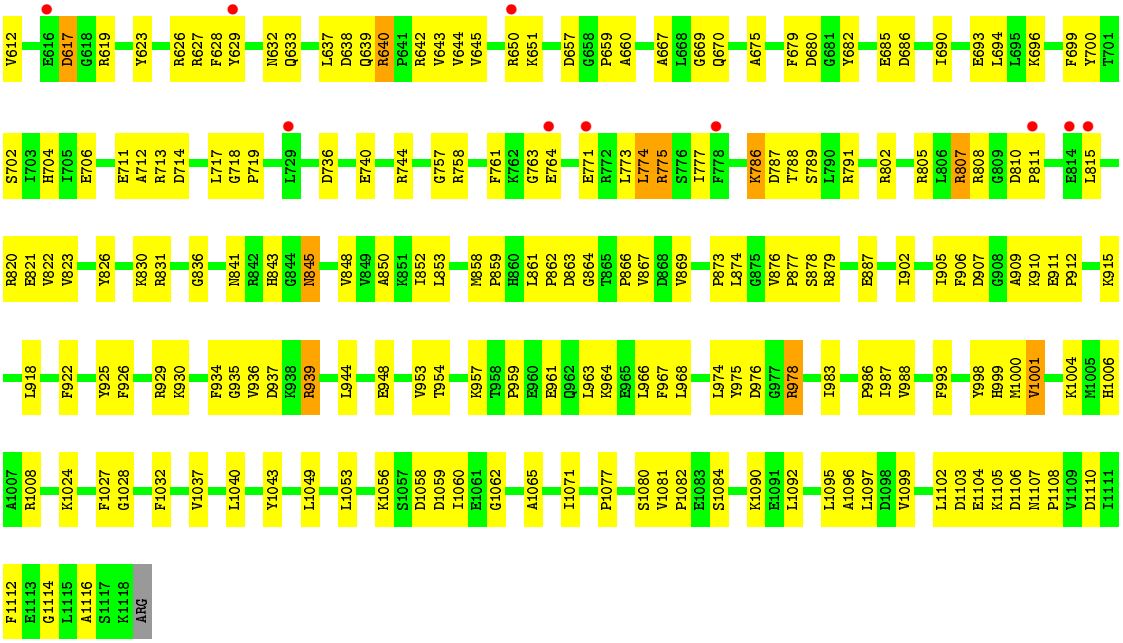
Chain L:



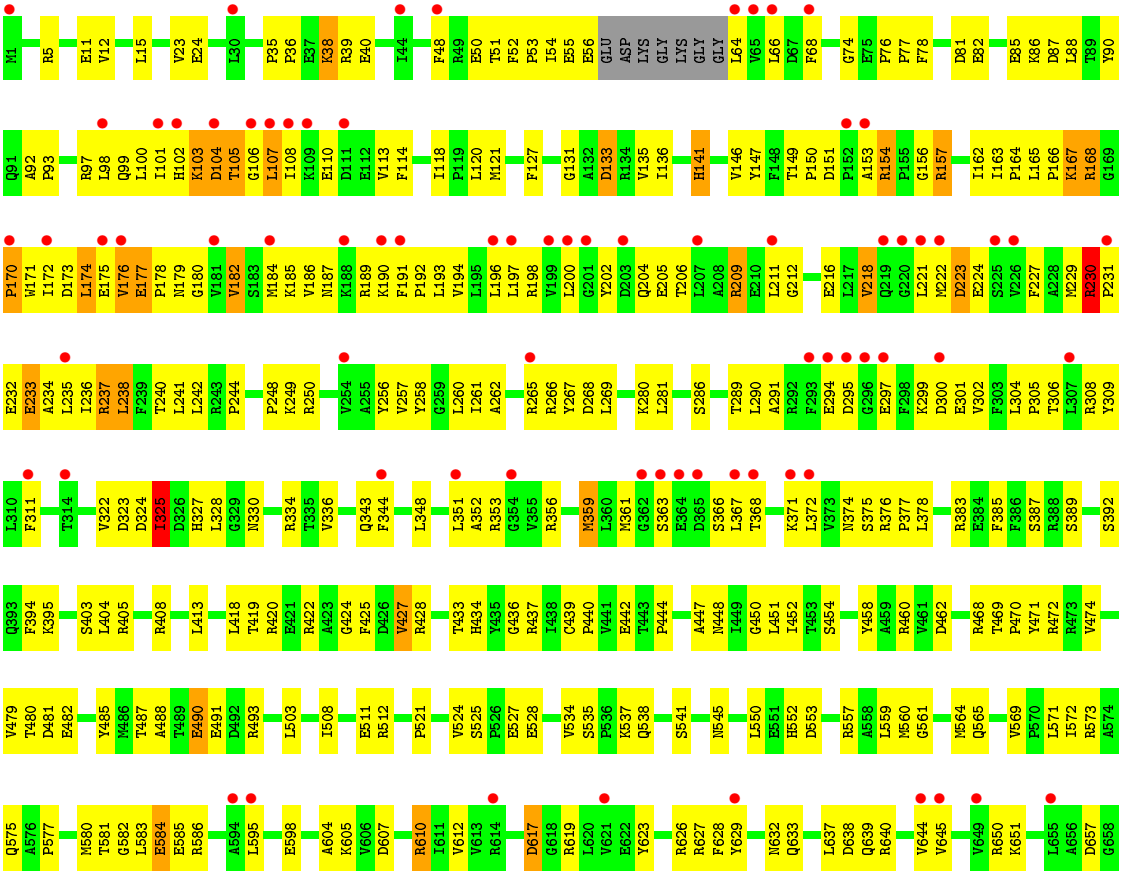
• Molecule 2: DNA-directed RNA polymerase subunit beta

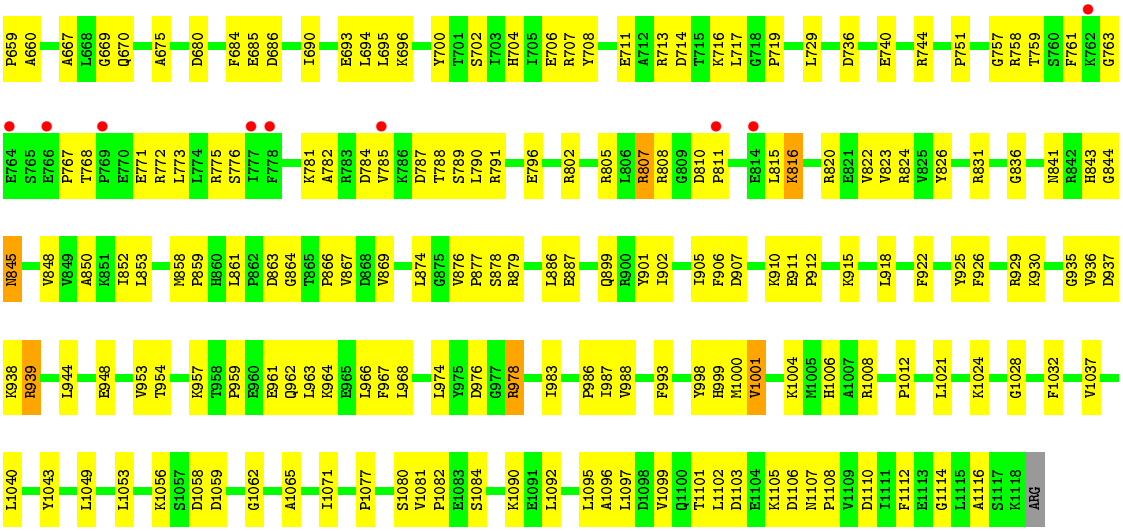
Chain C:





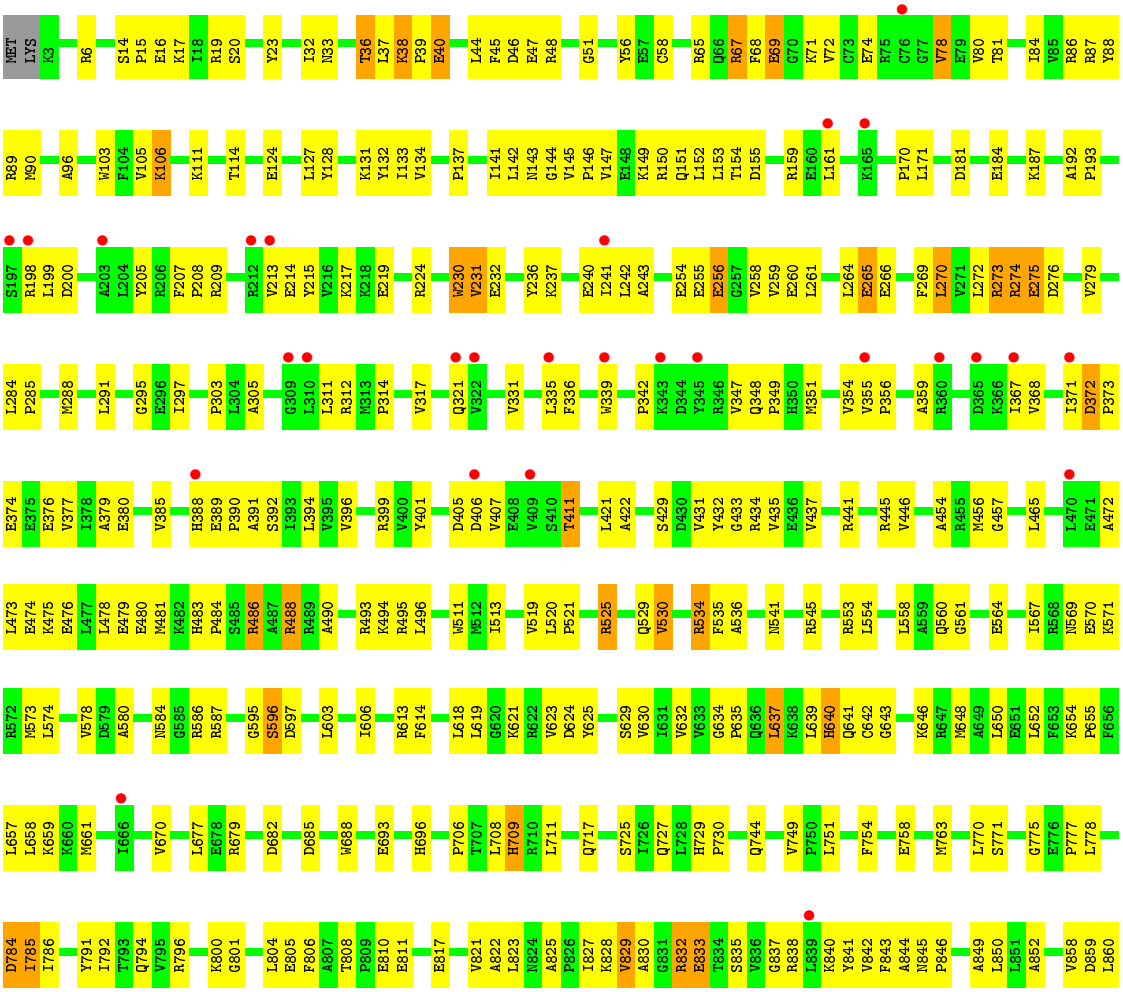
• Molecule 2: DNA-directed RNA polymerase subunit beta

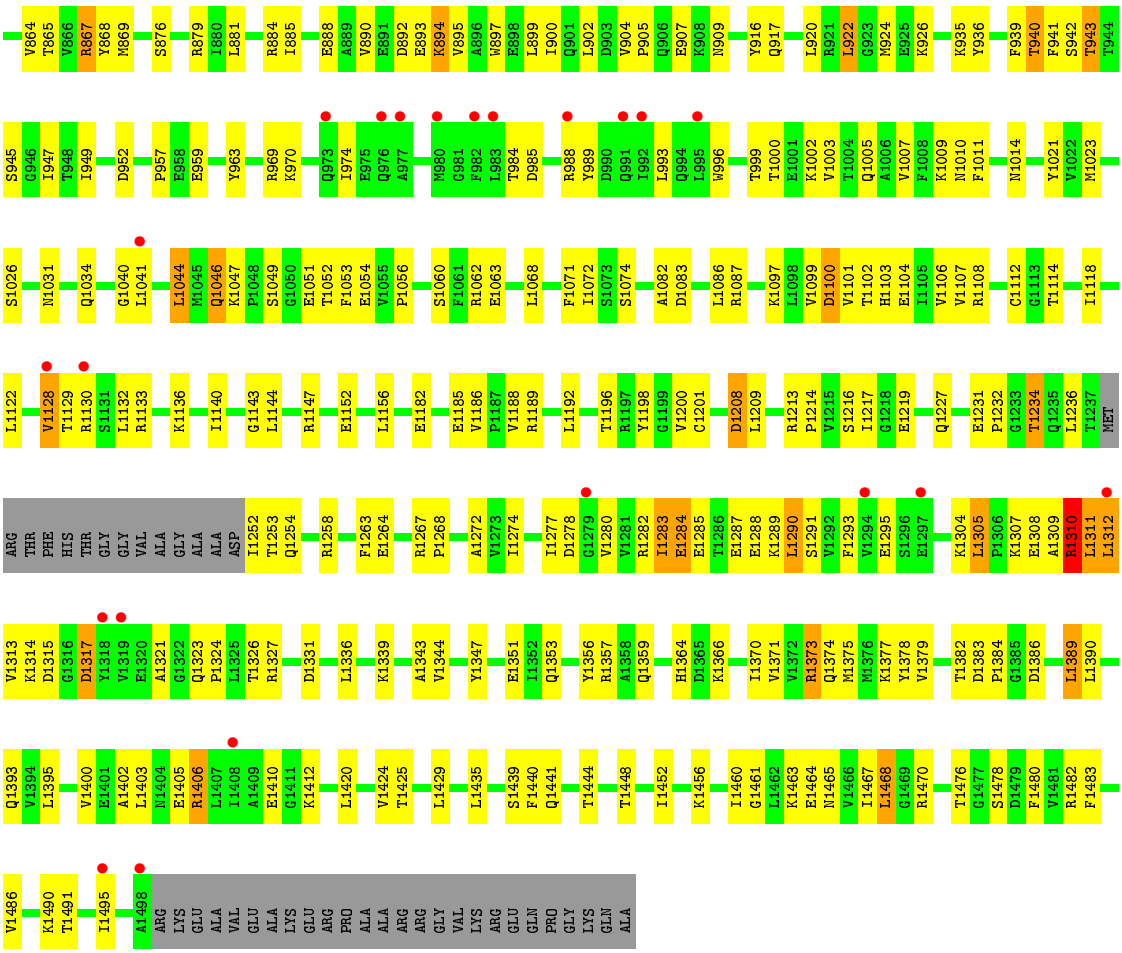




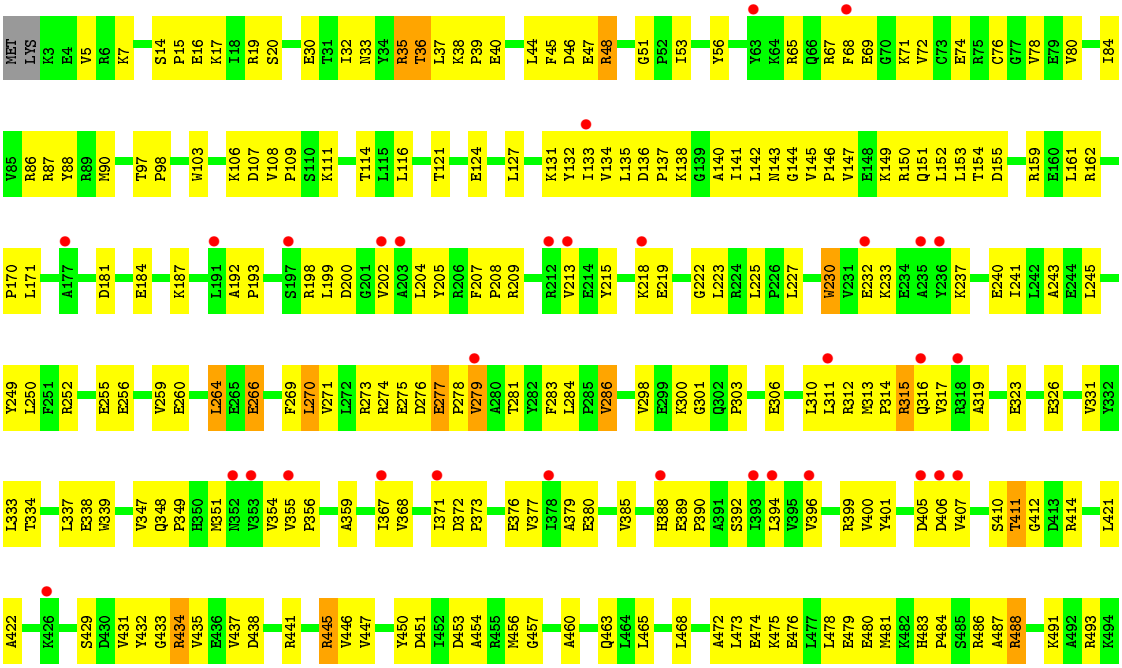
• Molecule 3: DNA-directed RNA polymerase subunit beta'

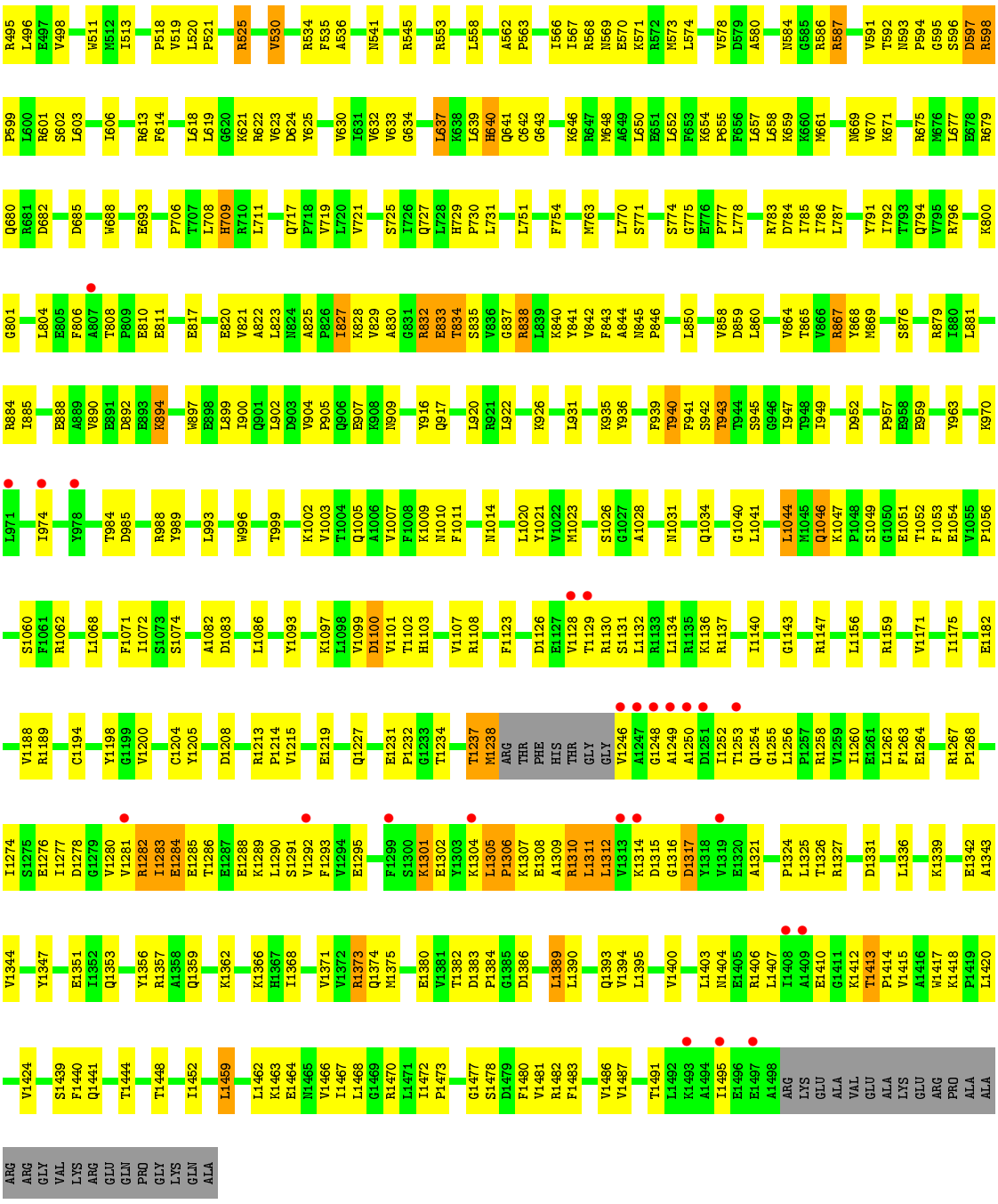
Chain D:



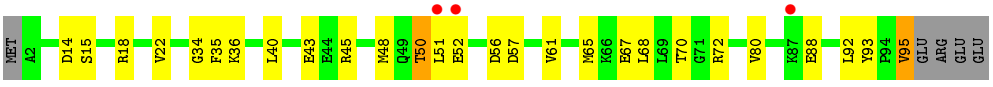


• Molecule 3: DNA-directed RNA polymerase subunit beta'

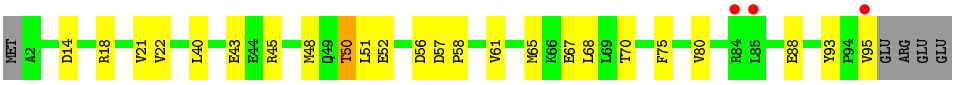




• Molecule 4: DNA-directed RNA polymerase subunit omega

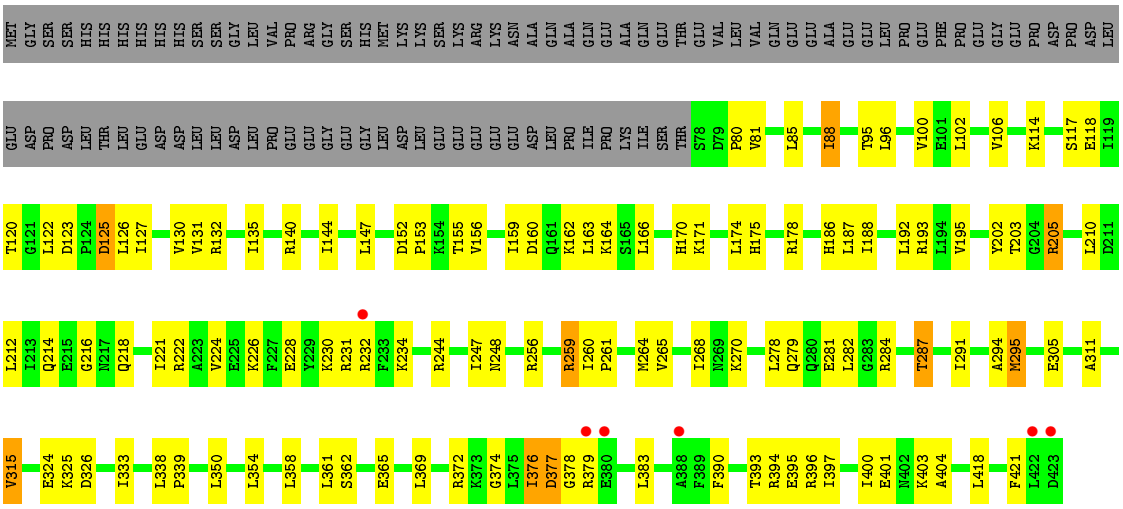


• Molecule 4: DNA-directed RNA polymerase subunit omega



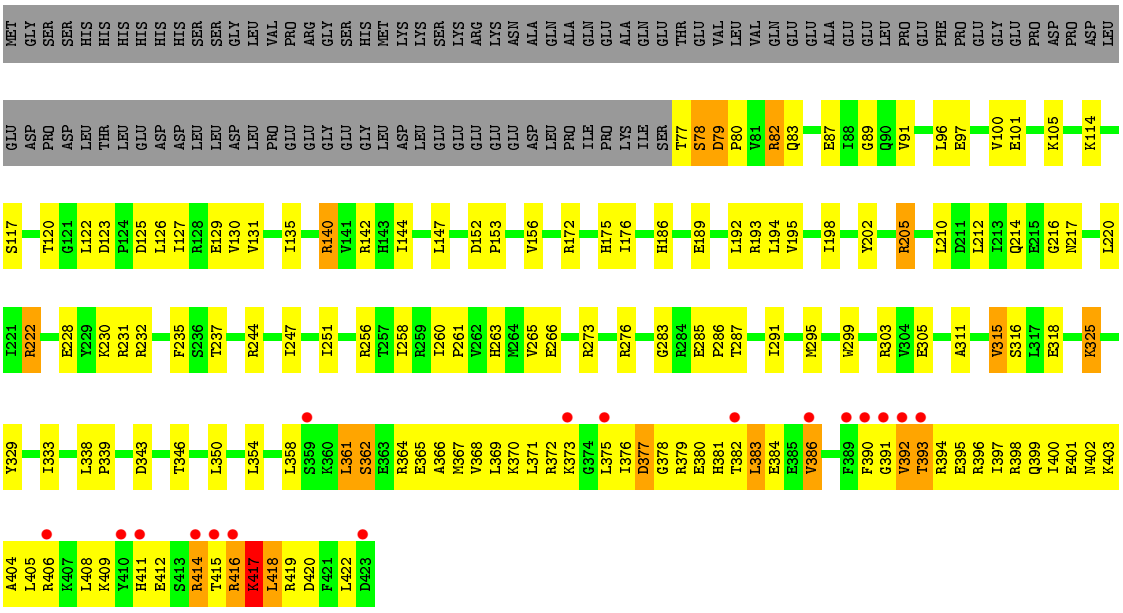
• Molecule 5: RNA polymerase sigma factor

Chain F:



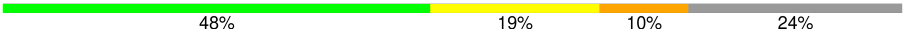
• Molecule 5: RNA polymerase sigma factor

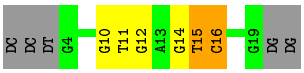
Chain P:



• Molecule 6: 5'-D(*CP*CP*T*GP*CP*AP*TP*CP*CP*GP*TP*GP*AP*GP*TP*CP*GP*AP*GP*GP*G)-3'

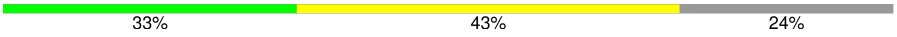
Chain G:





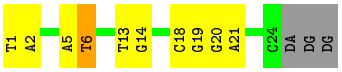
• Molecule 6: 5'-D(*CP*CP*T*GP*CP*AP*TP*CP*CP*GP*TP*GP*AP*GP*TP*CP*GP*AP*GP*GP*G)-3'

Chain Q:



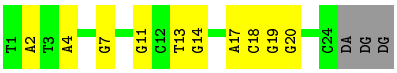
• Molecule 7: 5'-D(*TP*AP*TP*AP*AP*TP*GP*GP*GP*AP*GP*CP*TP*GP*TP*CP*AP*CP*GP*GP*AP*TP*GP*CP*AP*GP*G)-3'

Chain H:



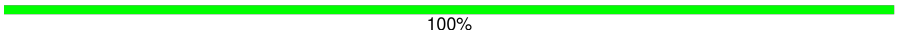
• Molecule 7: 5'-D(*TP*AP*TP*AP*AP*TP*GP*GP*GP*AP*GP*CP*TP*GP*TP*CP*AP*CP*GP*GP*AP*TP*GP*CP*AP*GP*G)-3'

Chain R:



• Molecule 8: 5'-R(*GP*A)-3'

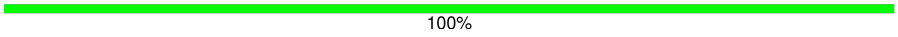
Chain I:



There are no outlier residues recorded for this chain.

• Molecule 8: 5'-R(*GP*A)-3'

Chain S:



There are no outlier residues recorded for this chain.

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	185.48Å 103.88Å 297.34Å 90.00° 98.23° 90.00°	Depositor
Resolution (Å)	46.61 – 2.99 49.59 – 2.99	Depositor EDS
% Data completeness (in resolution range)	95.6 (46.61-2.99) 95.5 (49.59-2.99)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	0.17	Depositor
$< I/\sigma(I) >$ [1]	1.99 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.205 , 0.247 0.205 , 0.249	Depositor DCC
R_{free} test set	1903 reflections (0.88%)	DCC
Wilson B-factor (Å^2)	65.4	Xtriage
Anisotropy	0.459	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 42.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	6 of 221179 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	57231	wwPDB-VP
Average B, all atoms (Å^2)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.33 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 5.0787e-04.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.29	0/1814	0.50	0/2466
1	B	0.27	0/1782	0.49	0/2424
1	K	0.27	0/1814	0.49	0/2466
1	L	0.28	0/1805	0.51	0/2454
2	C	0.30	0/8937	0.49	0/12087
2	M	0.31	0/8937	0.50	0/12087
3	D	0.31	1/11910 (0.0%)	0.49	0/16105
3	N	0.31	1/11952 (0.0%)	0.50	0/16162
4	E	0.28	0/775	0.44	0/1045
4	O	0.26	0/775	0.44	0/1045
5	F	0.28	0/2852	0.46	0/3837
5	P	0.28	0/2859	0.45	0/3847
6	G	0.55	0/368	1.09	2/567 (0.4%)
6	Q	0.47	0/368	1.05	0/567
7	H	0.51	0/556	1.26	3/858 (0.3%)
7	R	0.52	0/556	1.23	2/858 (0.2%)
8	I	0.35	0/47	0.68	0/72
8	S	0.25	0/47	0.55	0/72
All	All	0.31	2/58154 (0.0%)	0.53	7/79019 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	M	0	1
5	P	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	599	PRO	C-N	5.34	1.46	1.34
3	D	105	VAL	C-N	5.13	1.45	1.34

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	R	17	DA	O4'-C1'-N9	6.77	112.74	108.00
7	H	6	DT	O4'-C1'-N1	-6.45	103.49	108.00
7	H	20	DG	C1'-O4'-C4'	-6.17	103.93	110.10
6	G	16	DC	O4'-C4'-C3'	-5.77	102.19	104.50
7	R	20	DG	C1'-O4'-C4'	-5.40	104.70	110.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	M	104	ASP	Peptide
5	P	82	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1782	0	1834	81	0
1	B	1750	0	1797	92	0
1	K	1782	0	1834	60	0
1	L	1773	0	1826	76	0
2	C	8770	0	8872	436	0
2	M	8770	0	8871	518	2
3	D	11704	0	11934	544	1
3	N	11746	0	11974	664	0
4	E	761	0	778	26	0
4	O	761	0	778	25	0
5	F	2807	0	2882	111	0
5	P	2814	0	2888	168	1
6	G	328	0	181	4	0
6	Q	328	0	181	6	0
7	H	495	0	272	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	R	495	0	272	14	0
8	I	42	0	23	0	0
8	S	42	0	23	0	0
9	D	2	0	0	0	0
9	N	2	0	0	0	0
10	D	2	0	0	0	0
10	K	1	0	0	0	0
10	N	2	0	0	0	0
11	A	14	0	0	0	0
11	B	3	0	0	0	0
11	C	53	0	0	0	0
11	D	58	0	0	0	0
11	E	8	0	0	0	0
11	F	10	0	0	0	0
11	G	5	0	0	0	0
11	H	2	0	0	0	0
11	K	4	0	0	0	0
11	L	3	0	0	0	0
11	M	33	0	0	1	0
11	N	52	0	0	1	0
11	O	5	0	0	0	0
11	P	16	0	0	0	0
11	Q	2	0	0	0	0
11	R	3	0	0	0	0
11	S	1	0	0	0	0
All	All	57231	0	57220	2617	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 23.

The worst 5 of 2617 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:M:157:ARG:NH1	2:M:176:VAL:HG11	1.23	1.47
2:C:64:LEU:N	2:C:103:LYS:NZ	1.61	1.47
2:M:64:LEU:N	2:M:103:LYS:NZ	1.64	1.45
2:M:107:LEU:HD12	2:M:108:ILE:N	1.11	1.40
2:M:740:GLU:OE1	2:M:805:ARG:NH1	1.57	1.36

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:1314:LYS:NZ	2:M:784:ASP:OD2[1_445]	1.83	0.37
2:M:40:GLU:OE1	5:P:364:ARG:NH1[1_545]	2.03	0.17

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	224/315 (71%)	218 (97%)	5 (2%)	1 (0%)	39 80
1	B	220/315 (70%)	212 (96%)	6 (3%)	2 (1%)	21 64
1	K	224/315 (71%)	218 (97%)	6 (3%)	0	100 100
1	L	223/315 (71%)	213 (96%)	8 (4%)	2 (1%)	21 64
2	C	1107/1119 (99%)	1066 (96%)	37 (3%)	4 (0%)	39 80
2	M	1107/1119 (99%)	1063 (96%)	39 (4%)	5 (0%)	34 76
3	D	1478/1524 (97%)	1423 (96%)	53 (4%)	2 (0%)	56 90
3	N	1485/1524 (97%)	1423 (96%)	57 (4%)	5 (0%)	46 84
4	E	92/99 (93%)	89 (97%)	3 (3%)	0	100 100
4	O	92/99 (93%)	88 (96%)	4 (4%)	0	100 100
5	F	344/443 (78%)	335 (97%)	9 (3%)	0	100 100
5	P	345/443 (78%)	329 (95%)	12 (4%)	4 (1%)	16 56
All	All	6941/7630 (91%)	6677 (96%)	239 (3%)	25 (0%)	39 80

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	325	ILE
2	M	325	ILE
5	P	78	SER
5	P	417	LYS
3	D	1310	ARG

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	199/273 (73%)	189 (95%)	10 (5%)	30	70
1	B	195/273 (71%)	182 (93%)	13 (7%)	20	57
1	K	199/273 (73%)	189 (95%)	10 (5%)	30	70
1	L	198/273 (72%)	188 (95%)	10 (5%)	29	69
2	C	936/941 (100%)	880 (94%)	56 (6%)	24	62
2	M	936/941 (100%)	873 (93%)	63 (7%)	20	57
3	D	1250/1279 (98%)	1165 (93%)	85 (7%)	20	56
3	N	1253/1279 (98%)	1169 (93%)	84 (7%)	20	57
4	E	83/88 (94%)	80 (96%)	3 (4%)	42	79
4	O	83/88 (94%)	81 (98%)	2 (2%)	57	87
5	F	301/388 (78%)	287 (95%)	14 (5%)	32	72
5	P	302/388 (78%)	280 (93%)	22 (7%)	17	52
All	All	5935/6484 (92%)	5563 (94%)	372 (6%)	22	60

5 of 372 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	F	117	SER
2	M	107	LEU
3	N	1389	LEU
5	F	218	GLN
1	K	185	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	M	187	ASN
2	M	330	ASN
3	N	1195	GLN
3	D	1172	HIS

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Mol	Chain	Res	Type
1	L	221	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	I	1/2 (50%)	0	0
8	S	1/2 (50%)	0	0
All	All	2/4 (50%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	226/315 (71%)	-0.27	0 100 100	47, 67, 98, 118	0
1	B	222/315 (70%)	-0.17	2 (0%) 85 64	50, 79, 119, 142	0
1	K	226/315 (71%)	-0.21	0 100 100	49, 73, 103, 122	0
1	L	225/315 (71%)	-0.14	3 (1%) 79 53	51, 81, 126, 148	0
2	C	1111/1119 (99%)	-0.02	29 (2%) 59 29	34, 62, 122, 168	0
2	M	1111/1119 (99%)	0.26	84 (7%) 17 6	38, 76, 142, 179	0
3	D	1482/1524 (97%)	0.03	50 (3%) 49 21	32, 66, 130, 178	1 (0%)
3	N	1489/1524 (97%)	0.07	57 (3%) 44 18	34, 69, 129, 201	1 (0%)
4	E	94/99 (94%)	-0.07	3 (3%) 51 23	44, 66, 113, 121	0
4	O	94/99 (94%)	-0.09	3 (3%) 51 23	49, 72, 116, 130	0
5	F	346/443 (78%)	-0.14	6 (1%) 73 45	42, 70, 124, 147	0
5	P	347/443 (78%)	0.05	17 (4%) 33 13	46, 83, 156, 214	0
6	G	16/21 (76%)	-0.45	0 100 100	42, 78, 172, 179	0
6	Q	16/21 (76%)	-0.60	0 100 100	53, 80, 182, 183	0
7	H	24/27 (88%)	-0.35	0 100 100	67, 95, 146, 201	0
7	R	24/27 (88%)	-0.35	0 100 100	65, 106, 160, 210	0
8	I	2/2 (100%)	-0.37	0 100 100	50, 50, 50, 55	0
8	S	2/2 (100%)	-0.35	0 100 100	62, 62, 62, 63	0
All	All	7057/7730 (91%)	0.02	254 (3%) 46 20	32, 71, 132, 214	2 (0%)

The worst 5 of 254 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	M	363	SER	6.6
5	P	392	VAL	6.1
5	P	411	HIS	6.0

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Mol	Chain	Res	Type	RSRZ
2	M	191	PHE	6.0
5	P	375	LEU	5.7

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
10	MG	K	1001	1/1	0.89	0.66	11.75	69,69,69,69	0
10	MG	N	2004	1/1	0.83	0.37	2.41	65,65,65,65	0
10	MG	D	2004	1/1	0.97	0.44	1.92	63,63,63,63	0
9	ZN	N	2001	1/1	0.98	0.20	1.27	62,62,62,62	0
9	ZN	D	2001	1/1	0.99	0.13	-0.59	62,62,62,62	0
9	ZN	N	2002	1/1	0.99	0.05	-1.45	107,107,107,107	0
9	ZN	D	2002	1/1	0.98	0.08	-1.85	83,83,83,83	0
10	MG	D	2003	1/1	0.94	0.24	-	40,40,40,40	0
10	MG	N	2003	1/1	0.79	0.20	-	46,46,46,46	0

6.5 Other polymers (i)

There are no such residues in this entry.