



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 05:13 PM UTC

PDB ID : 5D4E / pdb_00005d4e
Title : Crystal structure of Thermus thermophilus product complex for transcription initiation with 3'-dephosphate-CoA and CTP
Authors : Zhang, Y.; Ebright, R.H.
Deposited on : 2015-08-07
Resolution : 3.08 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

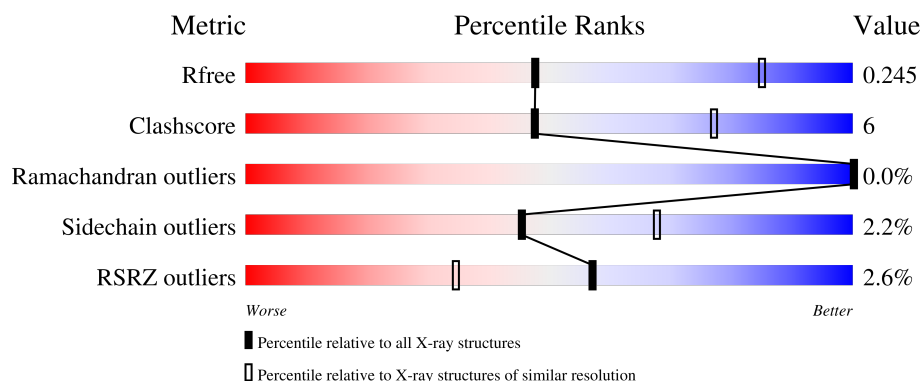
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.08 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}	180053	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. 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	<div> <div>2%</div> <div>61% 12% 27%</div> </div>
1	B	315	<div> <div>60% 11% 29%</div> </div>
1	K	315	<div> <div>% 60% 13% 27%</div> </div>
1	L	315	<div> <div>59% 11% 29%</div> </div>
2	C	1119	<div> <div>8% 80% 19% ..</div> </div>

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Mol	Chain	Length	Quality of chain
2	M	1119	
3	D	1524	
3	N	1524	
4	E	99	
4	O	99	
5	F	443	
5	P	443	
6	H	27	
6	S	27	
7	G	19	
7	R	19	

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 57723 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	231	Total	C	N	O	S	0	0	0
			1809	1155	315	337	2			
1	B	223	Total	C	N	O	S	0	0	0
			1758	1124	305	327	2			
1	K	231	Total	C	N	O	S	0	0	0
			1809	1155	315	337	2			
1	L	223	Total	C	N	O	S	0	0	0
			1758	1124	305	327	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1112	Total	C	N	O	S	0	0	0
			8774	5550	1565	1635	24			
2	M	1112	Total	C	N	O	S	0	1	0
			8783	5558	1565	1636	24			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1486	Total	C	N	O	S	0	0	0
			11738	7441	2067	2195	35			
3	N	1486	Total	C	N	O	S	0	0	0
			11738	7441	2067	2195	35			

- 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
			758	483	132	139	4			
4	O	94	Total	C	N	O	S	0	0	0
			758	483	132	139	4			

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

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	346	Total	C	N	O	S	0	0	0
			2807	1770	509	524	4			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-19	MET	-	initiating methionine	UNP Q72L95
F	-18	GLY	-	expression tag	UNP Q72L95
F	-17	SER	-	expression tag	UNP Q72L95
F	-16	SER	-	expression tag	UNP Q72L95
F	-15	HIS	-	expression tag	UNP Q72L95
F	-14	HIS	-	expression tag	UNP Q72L95
F	-13	HIS	-	expression tag	UNP Q72L95
F	-12	HIS	-	expression tag	UNP Q72L95
F	-11	HIS	-	expression tag	UNP Q72L95
F	-10	HIS	-	expression tag	UNP Q72L95
F	-9	SER	-	expression tag	UNP Q72L95
F	-8	SER	-	expression tag	UNP Q72L95
F	-7	GLY	-	expression tag	UNP Q72L95
F	-6	LEU	-	expression tag	UNP Q72L95
F	-5	VAL	-	expression tag	UNP Q72L95
F	-4	PRO	-	expression tag	UNP Q72L95
F	-3	ARG	-	expression tag	UNP Q72L95
F	-2	GLY	-	expression tag	UNP Q72L95
F	-1	SER	-	expression tag	UNP Q72L95
F	0	HIS	-	expression tag	UNP Q72L95
F	46	THR	ALA	conflict	UNP Q72L95
P	-19	MET	-	initiating methionine	UNP Q72L95
P	-18	GLY	-	expression tag	UNP Q72L95
P	-17	SER	-	expression tag	UNP Q72L95
P	-16	SER	-	expression tag	UNP Q72L95
P	-15	HIS	-	expression tag	UNP Q72L95
P	-14	HIS	-	expression tag	UNP Q72L95
P	-13	HIS	-	expression tag	UNP Q72L95
P	-12	HIS	-	expression tag	UNP Q72L95
P	-11	HIS	-	expression tag	UNP Q72L95
P	-10	HIS	-	expression tag	UNP Q72L95
P	-9	SER	-	expression tag	UNP Q72L95
P	-8	SER	-	expression tag	UNP Q72L95
P	-7	GLY	-	expression tag	UNP Q72L95

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-6	LEU	-	expression tag	UNP Q72L95
P	-5	VAL	-	expression tag	UNP Q72L95
P	-4	PRO	-	expression tag	UNP Q72L95
P	-3	ARG	-	expression tag	UNP Q72L95
P	-2	GLY	-	expression tag	UNP Q72L95
P	-1	SER	-	expression tag	UNP Q72L95
P	0	HIS	-	expression tag	UNP Q72L95
P	46	THR	ALA	conflict	UNP Q72L95

- Molecule 6 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	21	Total	C	N	O	P	0	0	0
			435	207	87	121	20			
6	S	21	Total	C	N	O	P	0	0	0
			435	207	87	121	20			

- Molecule 7 is a DNA chain called DNA (5'-D(*CP*C*TP*GP*CP*AP*TP*CP*CP*GP*T
P*GP*AP*GP*TP*AP*GP*AP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	16	Total	C	N	O	P	0	0	0
			327	156	62	94	15			
7	R	16	Total	C	N	O	P	0	0	0
			328	157	62	94	15			

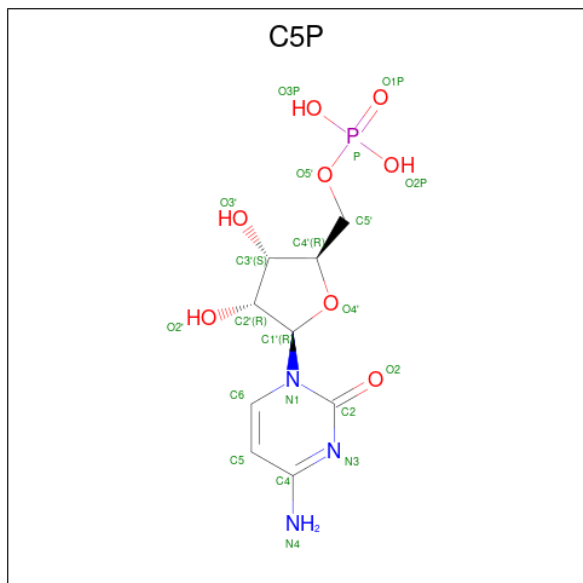
- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Mg	0	0
			1	1		
8	D	3	Total	Mg	0	0
			3	3		
8	F	1	Total	Mg	0	0
			1	1		
8	L	1	Total	Mg	0	0
			1	1		
8	N	2	Total	Mg	0	0
			2	2		
8	P	1	Total	Mg	0	0
			1	1		

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

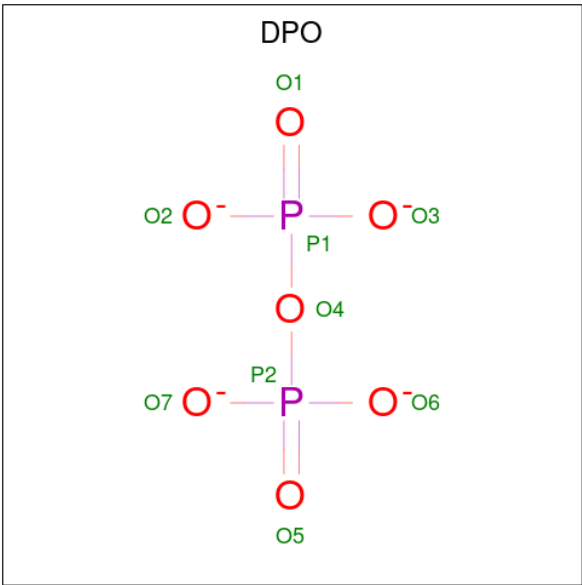
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	2	Total	Zn	0	0
			2	2		
9	N	2	Total	Zn	0	0
			2	2		

- Molecule 10 is CYTIDINE-5'-MONOPHOSPHATE (CCD ID: C5P) (formula: C₉H₁₄N₃O₈P).



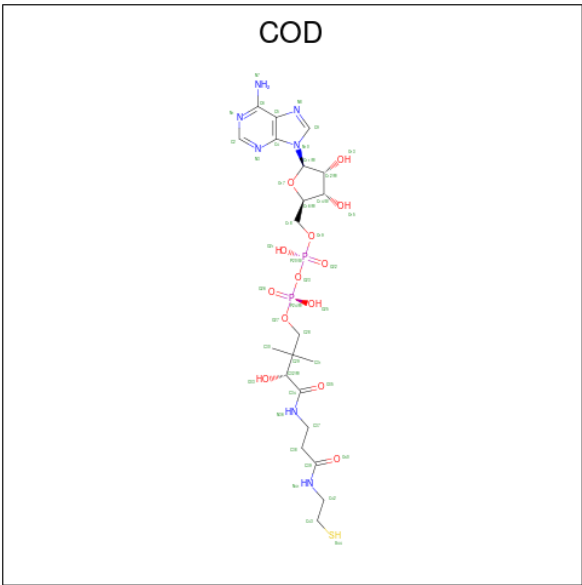
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	D	1	Total	C	N	O	P	0	0
			20	9	3	7	1		
10	N	1	Total	C	N	O	P	0	0
			20	9	3	7	1		

- Molecule 11 is DIPHOSPHATE (CCD ID: DPO) (formula: O₇P₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	D	1	Total	O	P	0	0
			9	7	2		
11	N	1	Total	O	P	0	0
			9	7	2		

- Molecule 12 is DEPHOSPHO COENZYME A (CCD ID: COD) (formula: $C_{21}H_{35}N_7O_{13}P_2S$).

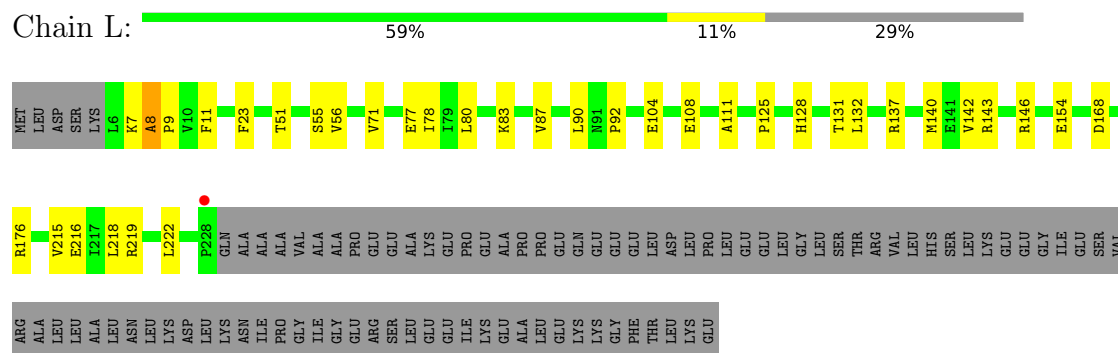


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	G	1	Total 28	C 11	N 5	O 10	P 2	0	0
12	R	1	Total 27	C 10	N 5	O 10	P 2	0	0

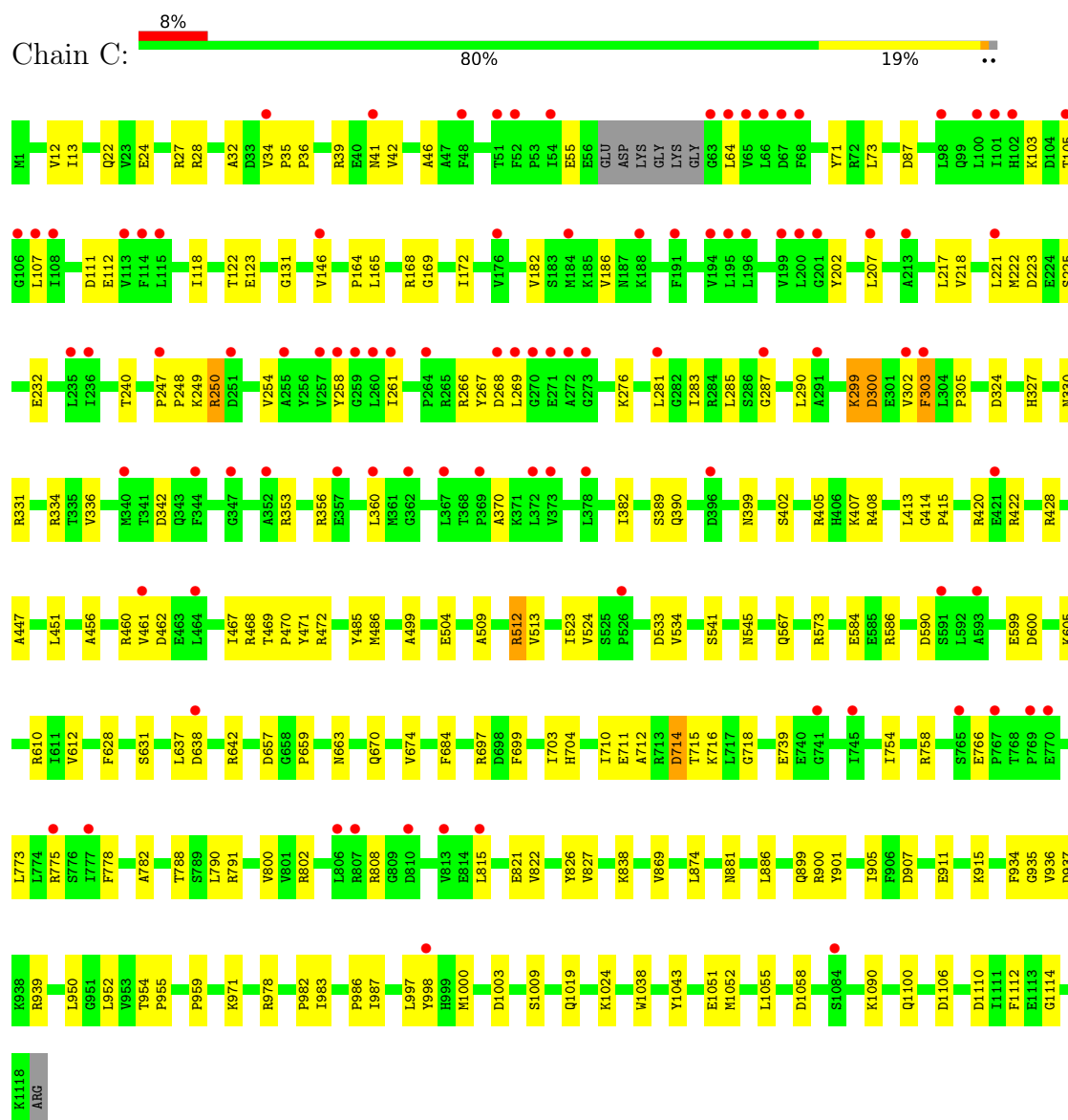
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	17	Total 17	O 17	0	0
13	B	10	Total 10	O 10	0	0
13	C	74	Total 74	O 74	0	0
13	D	144	Total 144	O 144	0	0
13	E	8	Total 8	O 8	0	0
13	F	17	Total 17	O 17	0	0
13	H	6	Total 6	O 6	0	0
13	G	3	Total 3	O 3	0	0
13	K	16	Total 16	O 16	0	0
13	L	14	Total 14	O 14	0	0
13	M	178	Total 178	O 178	0	0
13	N	217	Total 217	O 217	0	0
13	O	16	Total 16	O 16	0	0
13	P	41	Total 41	O 41	0	0
13	R	9	Total 9	O 9	0	0
13	S	5	Total 5	O 5	0	0

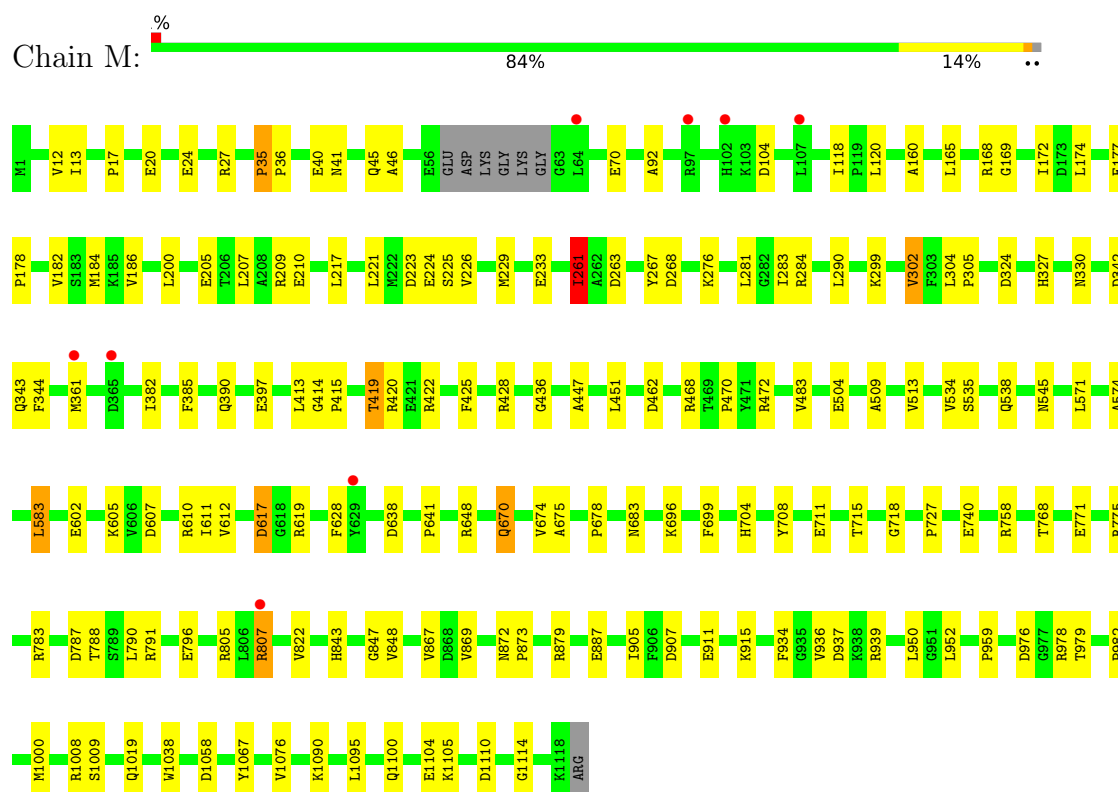
- Molecule 1: DNA-directed RNA polymerase subunit alpha



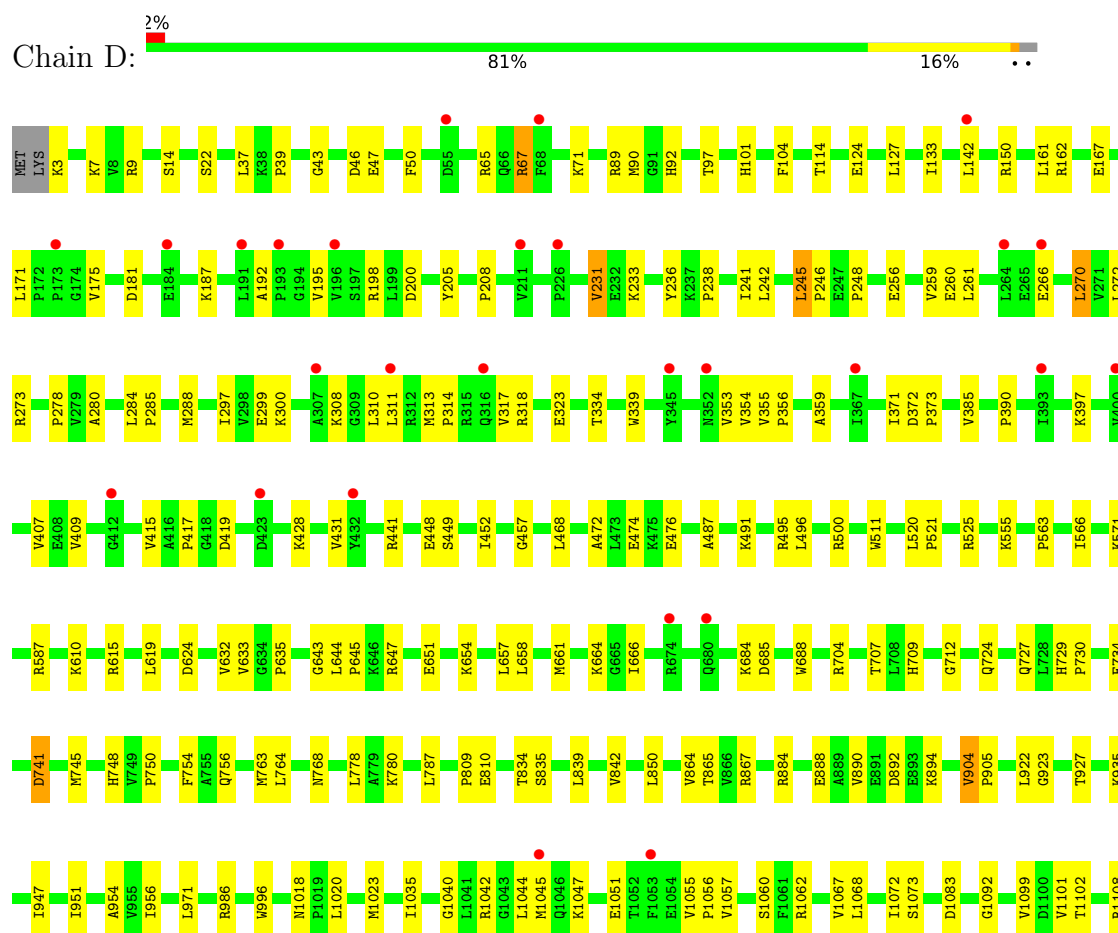
- Molecule 2: DNA-directed RNA polymerase subunit beta

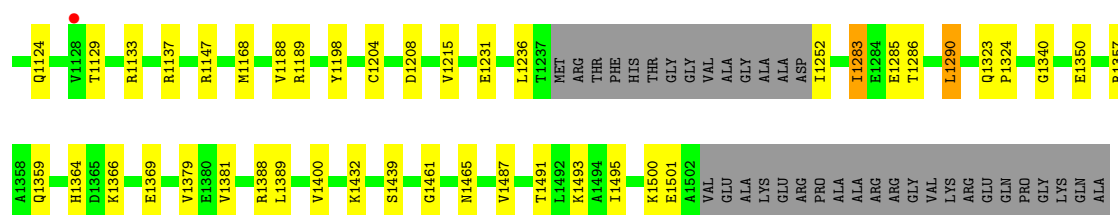


- Molecule 2: DNA-directed RNA polymerase subunit beta

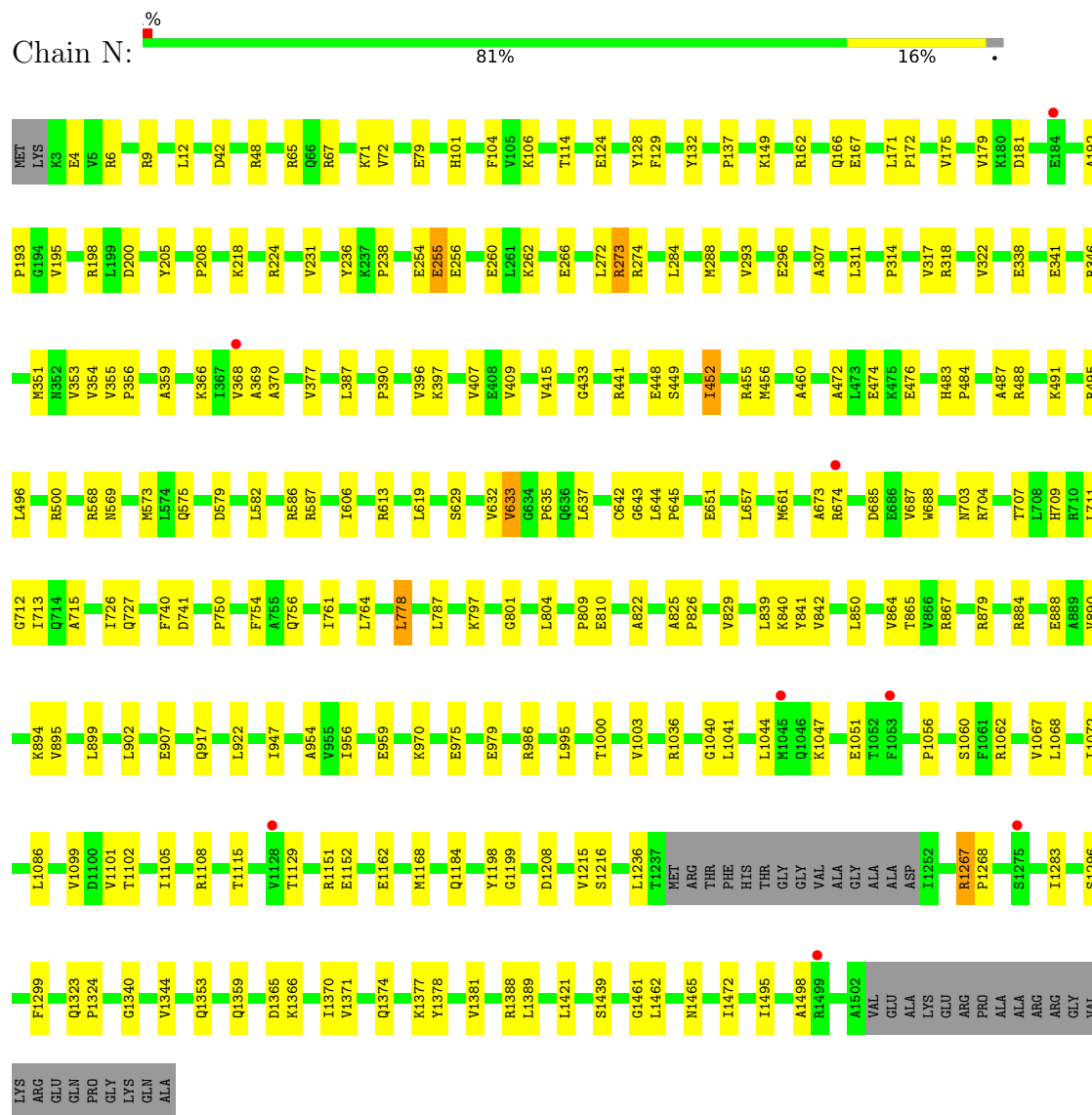


• Molecule 3: DNA-directed RNA polymerase subunit beta'





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




• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E:

83% 11% 5%



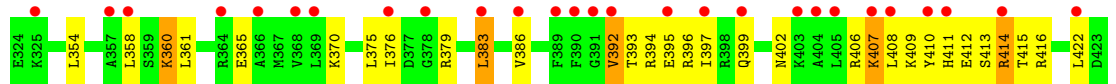
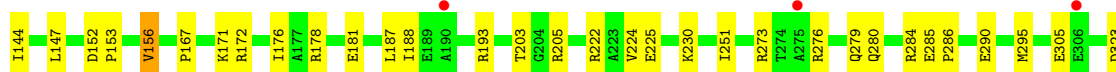
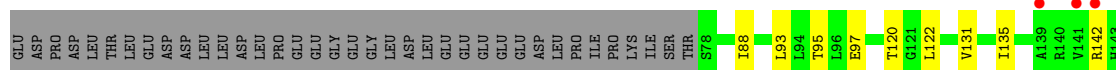
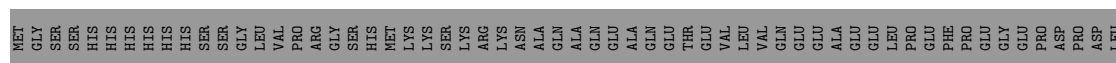
• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain O:  81% 14% 5%



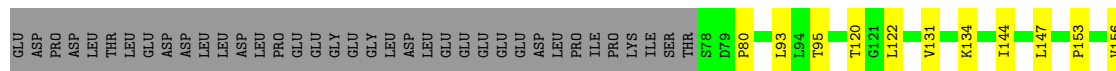
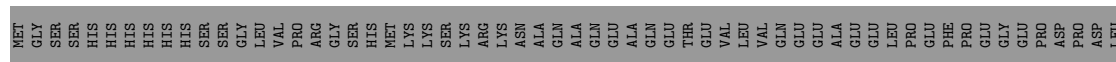
• Molecule 5: RNA polymerase sigma factor SigA

Chain F:  7% 62% 15% 22%



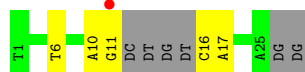
• Molecule 5: RNA polymerase sigma factor SigA

Chain P:  67% 10% 22%




• Molecule 6: DNA (27-MER)

Chain H:  4% 59% 19% 22%

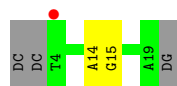
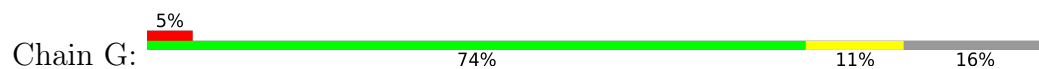


• Molecule 6: DNA (27-MER)

Chain S:  4% 44% 33% 22%



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	185.81Å 103.95Å 297.14Å 90.00° 98.47° 90.00°	Depositor
Resolution (Å)	39.68 – 3.08 39.68 – 3.08	Depositor EDS
% Data completeness (in resolution range)	89.9 (39.68-3.08) 90.1 (39.68-3.08)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.06Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.210 , 0.246 0.210 , 0.245	Depositor DCC
R_{free} test set	9379 reflections (4.50%)	wwPDB-VP
Wilson B-factor (Å ²)	62.5	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	57723	wwPDB-VP
Average B, all atoms (Å ²)	49.0	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 46.93 % 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 1.0674e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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, DPO, C5P, COD, 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	0.27	0/1841	0.76	2/2504 (0.1%)
1	B	0.35	0/1790	0.81	0/2435
1	K	0.27	0/1841	0.78	2/2504 (0.1%)
1	L	0.35	0/1790	0.82	0/2435
2	C	0.29	0/8941	0.75	3/12092 (0.0%)
2	M	0.30	0/8954	0.75	5/12110 (0.0%)
3	D	0.28	0/11944	0.75	8/16149 (0.0%)
3	N	0.28	0/11944	0.74	3/16149 (0.0%)
4	E	0.25	0/772	0.69	0/1040
4	O	0.26	0/772	0.73	0/1040
5	F	0.28	0/2852	0.76	2/3837 (0.1%)
5	P	0.27	0/2852	0.72	1/3837 (0.0%)
6	H	0.09	0/489	0.49	0/752
6	S	0.10	0/489	0.52	0/752
7	G	0.09	0/367	0.41	0/565
7	R	0.09	0/368	0.46	0/567
All	All	0.28	0/58006	0.74	26/78768 (0.0%)

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	245	LEU	CA-C-N	7.32	127.00	119.82
3	D	245	LEU	C-N-CA	7.32	127.00	119.82
3	D	1231	GLU	CA-C-N	-6.83	114.75	121.65
3	D	1231	GLU	C-N-CA	-6.83	114.75	121.65
3	N	1340	GLY	CA-C-N	6.72	126.23	119.24

There are no chirality outliers.

There are no planarity outliers.

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	1809	0	1863	24	0
1	B	1758	0	1808	24	0
1	K	1809	0	1863	25	0
1	L	1758	0	1808	22	0
2	C	8774	0	8877	129	0
2	M	8783	0	8886	101	0
3	D	11738	0	11971	140	0
3	N	11738	0	11971	137	0
4	E	758	0	770	6	0
4	O	758	0	770	10	0
5	F	2807	0	2882	41	0
5	P	2807	0	2882	30	0
6	H	435	0	238	4	0
6	S	435	0	238	6	0
7	G	327	0	179	3	0
7	R	328	0	182	3	0
8	B	1	0	0	0	0
8	D	3	0	0	0	0
8	F	1	0	0	0	0
8	L	1	0	0	0	0
8	N	2	0	0	0	0
8	P	1	0	0	0	0
9	D	2	0	0	0	0
9	N	2	0	0	0	0
10	D	20	0	11	1	0
10	N	20	0	11	3	0
11	D	9	0	0	0	0
11	N	9	0	0	0	0
12	G	28	0	11	0	0
12	R	27	0	11	0	0
13	A	17	0	0	0	0
13	B	10	0	0	0	0
13	C	74	0	0	2	0
13	D	144	0	0	0	0
13	E	8	0	0	0	0
13	F	17	0	0	0	0
13	G	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	H	6	0	0	0	0
13	K	16	0	0	0	0
13	L	14	0	0	0	0
13	M	178	0	0	3	0
13	N	217	0	0	2	0
13	O	16	0	0	0	0
13	P	41	0	0	0	0
13	R	9	0	0	0	0
13	S	5	0	0	0	0
All	All	57723	0	57232	641	0

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 6.

The worst 5 of 641 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:C:628:PHE:H	2:C:638:ASP:HB3	1.40	0.86
2:M:168:ARG:HD3	2:M:268:ASP:HB3	1.64	0.79
2:M:165:LEU:HB2	2:M:168:ARG:HG3	1.63	0.78
2:C:802:ARG:HB2	2:C:826:TYR:HB2	1.66	0.75
2:C:165:LEU:HB2	2:C:168:ARG:HG3	1.68	0.74

There are no symmetry-related clashes.

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	229/315 (73%)	224 (98%)	5 (2%)	0	100	100
1	B	221/315 (70%)	216 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	229/315 (73%)	225 (98%)	4 (2%)	0	100	100
1	L	221/315 (70%)	217 (98%)	3 (1%)	1 (0%)	24	54
2	C	1108/1119 (99%)	1075 (97%)	33 (3%)	0	100	100
2	M	1109/1119 (99%)	1080 (97%)	29 (3%)	0	100	100
3	D	1482/1524 (97%)	1445 (98%)	37 (2%)	0	100	100
3	N	1482/1524 (97%)	1447 (98%)	35 (2%)	0	100	100
4	E	92/99 (93%)	90 (98%)	2 (2%)	0	100	100
4	O	92/99 (93%)	90 (98%)	2 (2%)	0	100	100
5	F	344/443 (78%)	334 (97%)	9 (3%)	1 (0%)	36	64
5	P	344/443 (78%)	339 (98%)	5 (2%)	0	100	100
All	All	6953/7630 (91%)	6782 (98%)	169 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	F	376	ILE
1	L	8	ALA

5.3.2 Protein sidechains ⓘ

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	200/273 (73%)	197 (98%)	3 (2%)	57	73
1	B	196/273 (72%)	194 (99%)	2 (1%)	68	77
1	K	200/273 (73%)	198 (99%)	2 (1%)	68	77
1	L	196/273 (72%)	194 (99%)	2 (1%)	68	77
2	C	936/941 (100%)	920 (98%)	16 (2%)	53	71
2	M	937/941 (100%)	918 (98%)	19 (2%)	48	69
3	D	1253/1279 (98%)	1221 (97%)	32 (3%)	40	65
3	N	1253/1279 (98%)	1226 (98%)	27 (2%)	45	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	E	82/88 (93%)	79 (96%)	3 (4%)	30	58
4	O	82/88 (93%)	81 (99%)	1 (1%)	63	75
5	F	301/388 (78%)	285 (95%)	16 (5%)	20	48
5	P	301/388 (78%)	296 (98%)	5 (2%)	53	71
All	All	5937/6484 (92%)	5809 (98%)	128 (2%)	45	68

5 of 128 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	N	907	GLU
3	N	1184	GLN
3	D	1283	ILE
3	D	1252	ILE
3	N	1283	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
5	F	411	HIS
3	N	386	HIS
5	P	185	GLN
2	M	219	GLN
2	M	683	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 19 ligands modelled in this entry, 13 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
11	DPO	N	1605	8	6,8,8	1.02	0	12,13,13	0.78	0
10	C5P	N	1604	8,12	18,21,22	0.28	0	25,30,33	0.36	0
10	C5P	D	2005	8,12	18,21,22	0.30	0	25,30,33	0.36	0
12	COD	R	101	10	28,29,46	1.65	6 (21%)	43,45,68	1.32	4 (9%)
12	COD	G	101	10	30,30,46	1.59	6 (20%)	43,46,68	1.33	4 (9%)
11	DPO	D	2006	8	6,8,8	0.99	0	12,13,13	0.89	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	DPO	N	1605	8	-	0/6/6/6	-
10	C5P	N	1604	8,12	-	0/7/25/26	0/2/2/2
10	C5P	D	2005	8,12	-	2/7/25/26	0/2/2/2
12	COD	R	101	10	-	6/16/32/59	0/3/3/3
12	COD	G	101	10	-	3/19/35/59	0/3/3/3
11	DPO	D	2006	8	-	0/6/6/6	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	R	101	COD	C6-N7	3.76	1.43	1.34
12	G	101	COD	C6-N7	3.75	1.43	1.34
12	R	101	COD	C18-C16	3.21	1.61	1.51
12	G	101	COD	C2-N3	3.21	1.39	1.33
12	G	101	COD	C18-C16	3.16	1.61	1.51

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	R	101	COD	N3-C2-N1	-5.29	120.57	128.58
12	G	101	COD	N3-C2-N1	-5.26	120.61	128.58
12	G	101	COD	C14-C12-C11	3.39	107.87	101.46
12	R	101	COD	C14-C12-C11	2.72	106.61	101.46
12	G	101	COD	O17-C16-C18	2.24	116.52	109.33

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

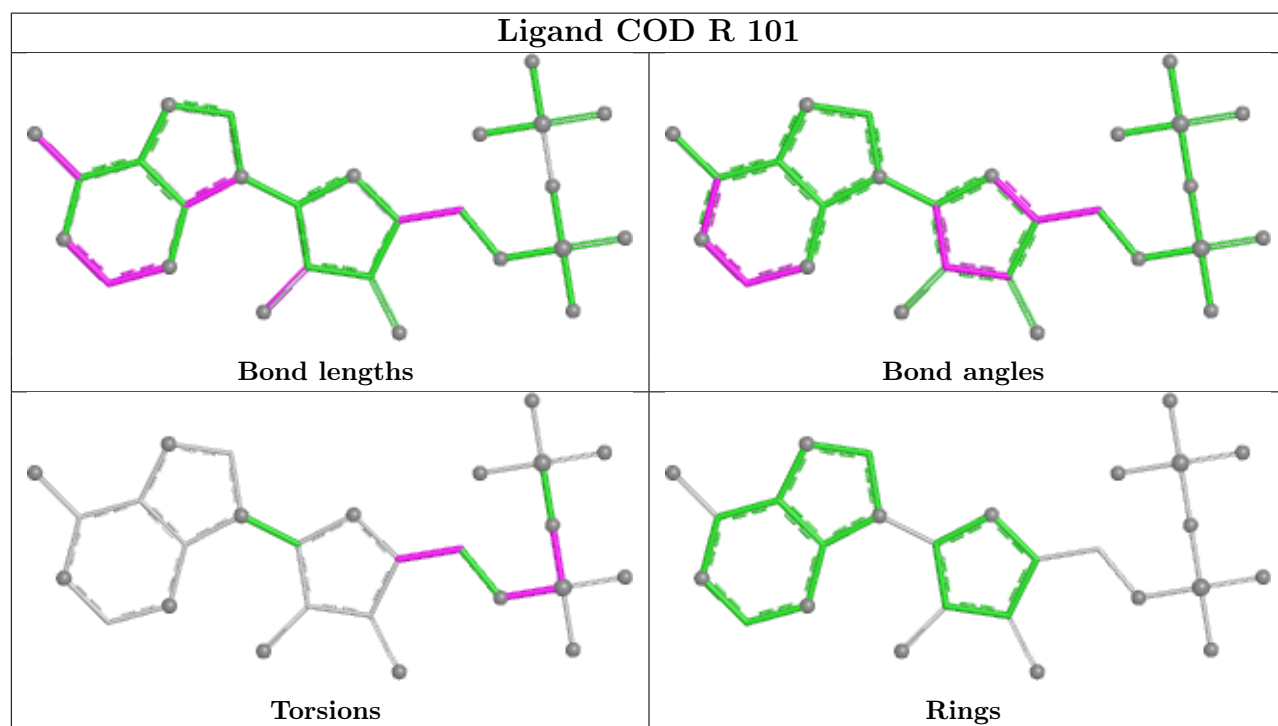
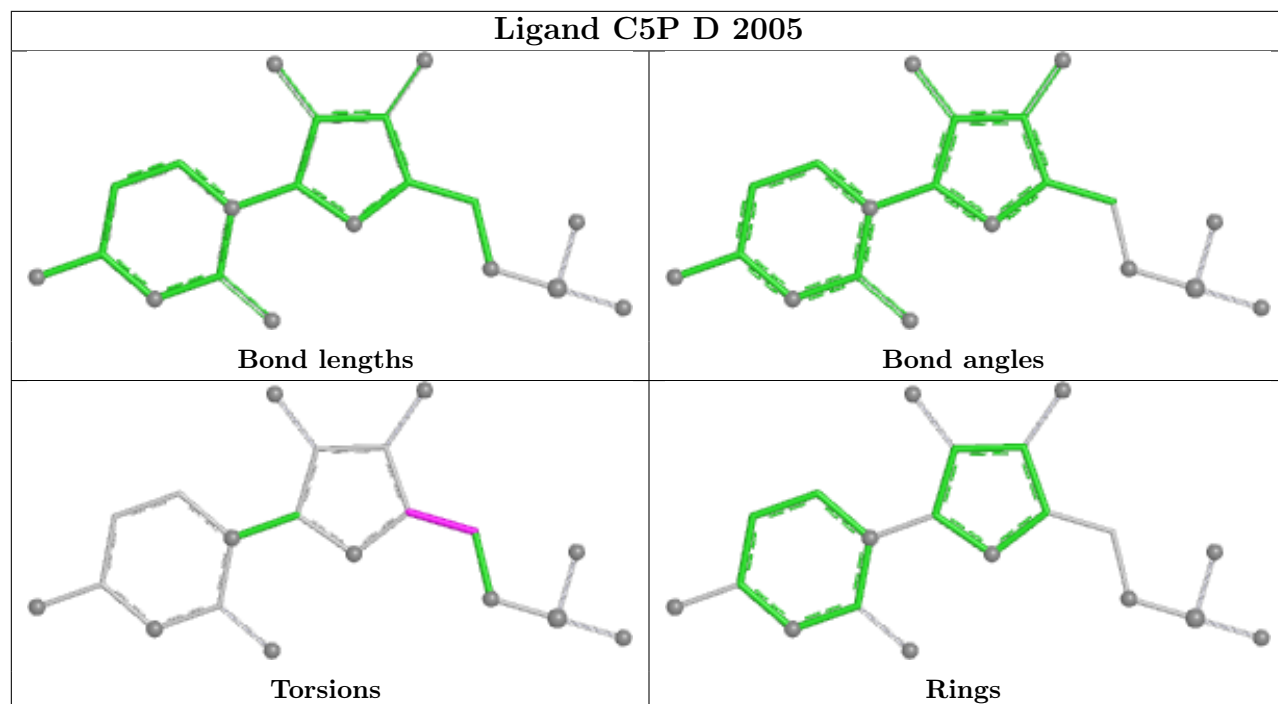
Mol	Chain	Res	Type	Atoms
10	D	2005	C5P	O4'-C4'-C5'-O5'
12	R	101	COD	C18-O19-P20-O21
12	R	101	COD	C18-O19-P20-O22
12	R	101	COD	C18-O19-P20-O23
10	D	2005	C5P	C3'-C4'-C5'-O5'

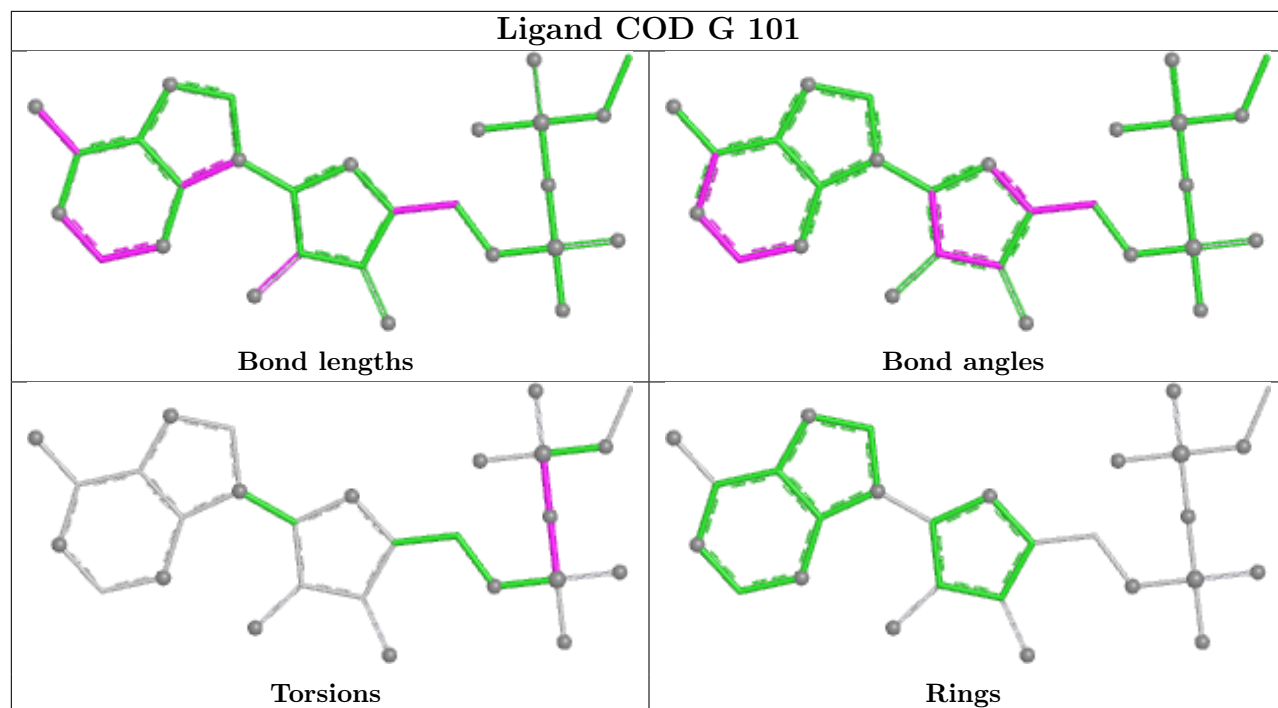
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	N	1604	C5P	3	0
10	D	2005	C5P	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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, 95th 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	231/315 (73%)	0.24	7 (3%) 52 30	29, 51, 78, 126	1 (0%)
1	B	223/315 (70%)	0.08	0 100 100	26, 53, 93, 122	0
1	K	231/315 (73%)	-0.10	3 (1%) 75 53	22, 38, 65, 128	1 (0%)
1	L	223/315 (70%)	-0.00	1 (0%) 88 75	21, 49, 82, 102	0
2	C	1112/1119 (99%)	0.59	94 (8%) 16 9	12, 58, 115, 132	3 (0%)
2	M	1112/1119 (99%)	-0.20	8 (0%) 84 66	5, 32, 82, 118	4 (0%)
3	D	1486/1524 (97%)	0.05	28 (1%) 66 44	7, 43, 96, 131	4 (0%)
3	N	1486/1524 (97%)	-0.19	8 (0%) 87 72	4, 34, 85, 125	4 (0%)
4	E	94/99 (94%)	0.03	0 100 100	22, 44, 88, 102	0
4	O	94/99 (94%)	-0.17	0 100 100	14, 31, 67, 85	0
5	F	346/443 (78%)	0.75	33 (9%) 14 7	33, 70, 134, 152	0
5	P	346/443 (78%)	-0.04	0 100 100	14, 43, 93, 112	0
6	H	21/27 (77%)	0.85	1 (4%) 35 18	47, 92, 134, 155	0
6	S	21/27 (77%)	0.42	1 (4%) 35 18	35, 73, 118, 146	0
7	G	16/19 (84%)	0.72	1 (6%) 26 13	49, 77, 129, 134	0
7	R	16/19 (84%)	0.31	0 100 100	31, 60, 131, 137	0
All	All	7058/7722 (91%)	0.08	185 (2%) 57 34	4, 44, 99, 155	17 (0%)

The worst 5 of 185 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	63	GLY	8.3
2	C	200	LEU	5.6
2	C	196	LEU	5.6
2	C	807	ARG	5.5
2	C	48	PHE	5.4

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

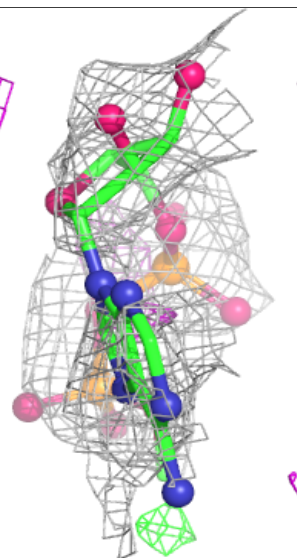
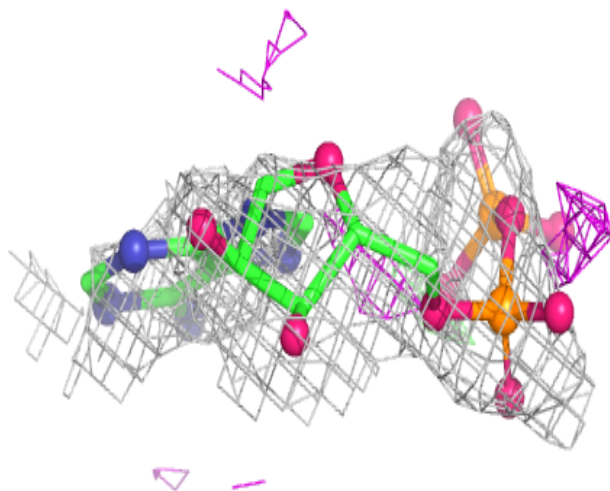
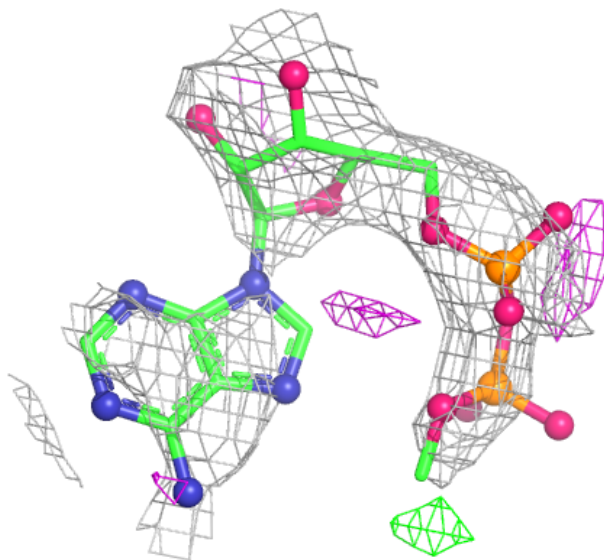
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
12	COD	G	101	28/44	0.64	0.17	50,73,102,116	28
8	MG	F	2001	1/1	0.71	0.09	92,92,92,92	0
10	C5P	D	2005	20/21	0.80	0.16	43,61,71,80	20
8	MG	B	2001	1/1	0.85	0.10	71,71,71,71	0
10	C5P	N	1604	20/21	0.86	0.15	24,34,49,57	20
11	DPO	D	2006	9/9	0.86	0.07	45,68,84,98	0
8	MG	D	2004	1/1	0.86	0.32	27,27,27,27	0
12	COD	R	101	27/44	0.86	0.13	35,43,62,65	27
11	DPO	N	1605	9/9	0.87	0.08	26,51,74,84	0
8	MG	L	1601	1/1	0.88	0.28	25,25,25,25	0
8	MG	N	1606	1/1	0.88	0.07	36,36,36,36	0
8	MG	P	2001	1/1	0.90	0.06	38,38,38,38	0
8	MG	D	2007	1/1	0.91	0.06	49,49,49,49	0
9	ZN	D	2002	1/1	0.97	0.06	92,92,92,92	0
8	MG	N	1603	1/1	0.98	0.06	13,13,13,13	0
8	MG	D	2003	1/1	0.98	0.04	22,22,22,22	0
9	ZN	D	2001	1/1	1.00	0.02	20,20,20,20	0
9	ZN	N	1601	1/1	1.00	0.02	16,16,16,16	0
9	ZN	N	1602	1/1	1.00	0.02	50,50,50,50	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

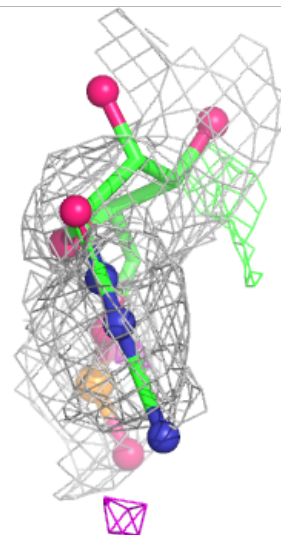
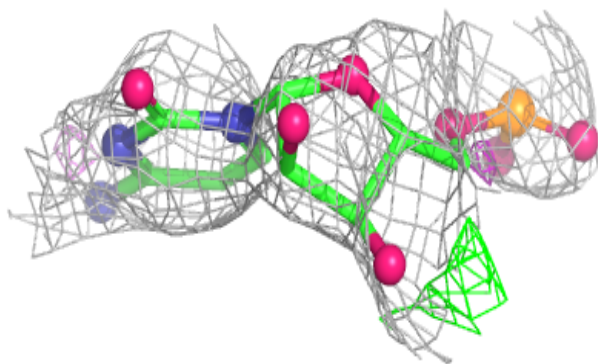
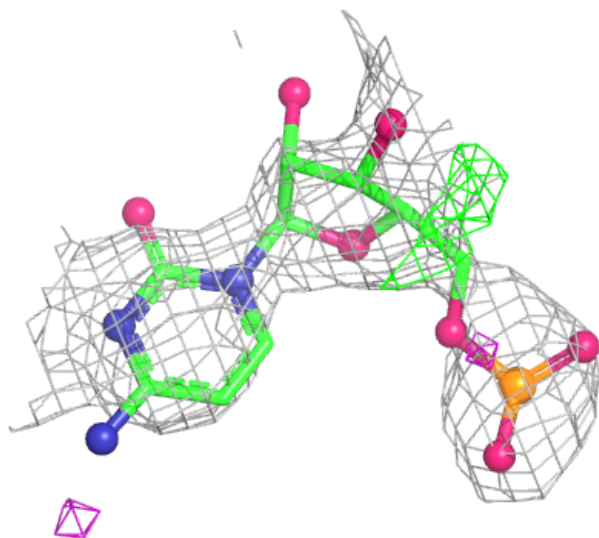
Electron density around COD G 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



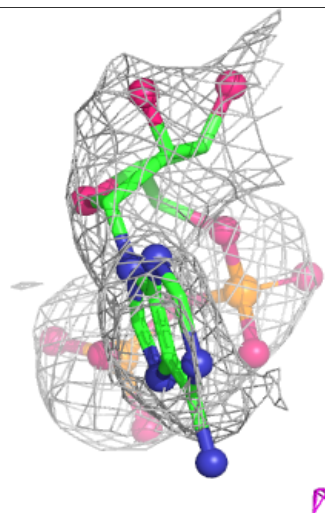
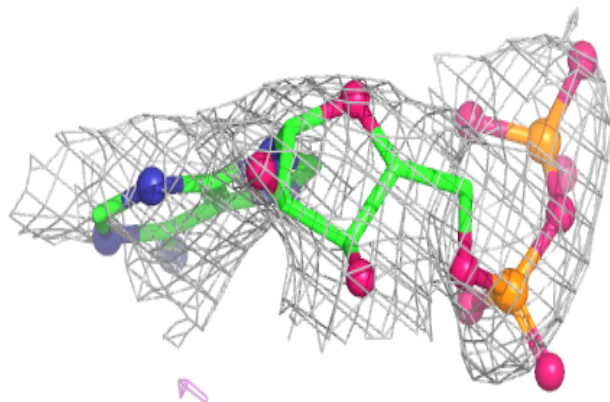
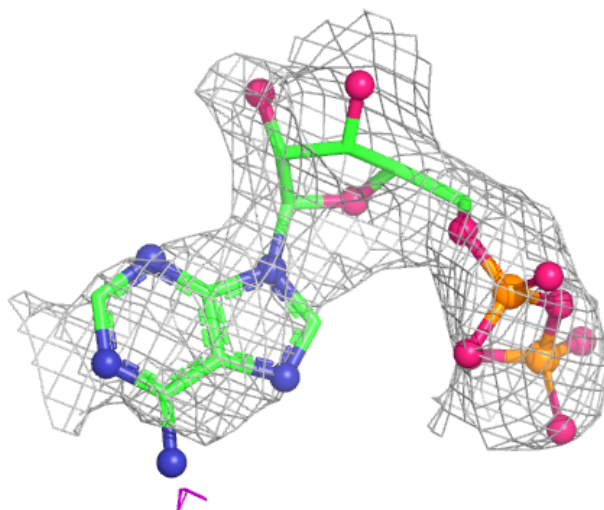
Electron density around C5P D 2005:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around COD R 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.