



wwPDB X-ray Structure Validation Summary Report ⓘ

May 23, 2020 – 12:19 am BST

PDB ID : 6N61
Title : Escherichia coli RNA polymerase sigma70-holoenzyme bound to upstream fork promoter DNA and Capistruin
Authors : Braffman, N.; Hauver, J.; Campbell, E.A.; Darst, S.A.
Deposited on : 2018-11-24
Resolution : 3.25 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

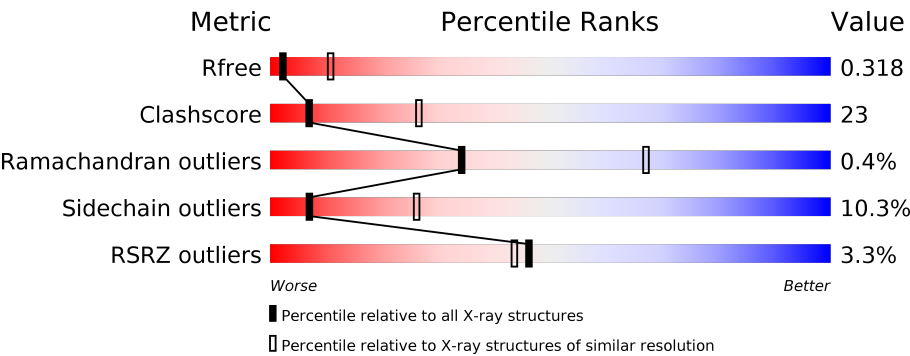
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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}	130704	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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 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	239	<div><div>4%</div><div><div></div><div>55%</div><div>36%</div><div>• 5%</div></div></div>
1	B	239	<div><div>7%</div><div><div></div><div>48%</div><div>37%</div><div>6%</div><div>9%</div></div></div>
2	C	1342	<div><div>%</div><div><div></div><div>56%</div><div>38%</div><div>5%</div><div>•</div></div></div>
3	D	1409	<div><div>3%</div><div><div></div><div>46%</div><div>36%</div><div>5%</div><div>12%</div></div></div>
4	E	90	<div><div>%</div><div><div></div><div>49%</div><div>37%</div><div>•</div><div>12%</div></div></div>
5	F	613	<div><div>4%</div><div><div></div><div>35%</div><div>26%</div><div>•</div><div>36%</div></div></div>

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Mol	Chain	Length	Quality of chain
6	N	29	
7	T	24	
8	I	19	

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
12	EPE	D	1504	-	-	X	-

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 28613 atoms, of which 23 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	228	Total	C	N	O	S	0	0	0
			1709	1067	300	336	6			
1	B	217	Total	C	N	O	S	0	0	0
			1658	1035	290	327	6			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	235	GLU	-	expression tag	UNP P0A7Z4
A	236	VAL	-	expression tag	UNP P0A7Z4
A	237	LEU	-	expression tag	UNP P0A7Z4
A	238	PHE	-	expression tag	UNP P0A7Z4
A	239	GLN	-	expression tag	UNP P0A7Z4
B	235	GLU	-	expression tag	UNP P0A7Z4
B	236	VAL	-	expression tag	UNP P0A7Z4
B	237	LEU	-	expression tag	UNP P0A7Z4
B	238	PHE	-	expression tag	UNP P0A7Z4
B	239	GLN	-	expression tag	UNP P0A7Z4

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1332	Total	C	N	O	S	0	0	0
			10489	6581	1829	2036	43			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1239	Total	C	N	O	S	0	0	0
			9649	6061	1733	1807	48			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1	VAL	-	expression tag	UNP P0A8T7
D	1408	LEU	-	expression tag	UNP P0A8T7
D	1409	GLU	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	79	Total	C	N	O	S	0	0	0
			627	382	118	126	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	395	Total	C	N	O	S	0	0	0
			3197	1993	578	603	23			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	149	ASN	ASP	conflict	UNP Q0P6L9

- Molecule 6 is a DNA chain called non-template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	N	29	Total	C	N	O	P	0	0	0
			595	284	106	176	29			

- Molecule 7 is a DNA chain called template strand DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	T	24	Total	C	N	O	P	0	0	0
			492	233	94	141	24			

- Molecule 8 is a protein called Capistrain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	I	17	Total	C	N	O	0	0	0
			126	80	24	22			

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	H	O	0	0
			10	2	6	2		

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

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

- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	D	2	Total	Zn	0	0
			2	2		

- Molecule 12 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	D	1	Total	C	H	N	O	S	
			32	8	17	2	4	1	0

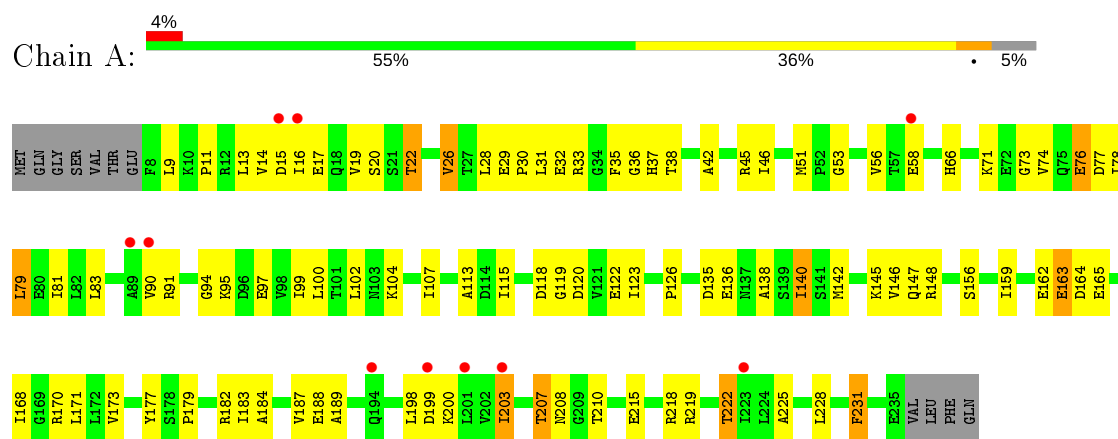
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	1	Total	O		
			1	1	0	0
13	B	2	Total	O		
			2	2	0	0
13	C	13	Total	O		
			13	13	0	0
13	D	3	Total	O		
			3	3	0	0
13	E	1	Total	O		
			1	1	0	0
13	F	5	Total	O		
			5	5	0	0
13	T	1	Total	O		
			1	1	0	0

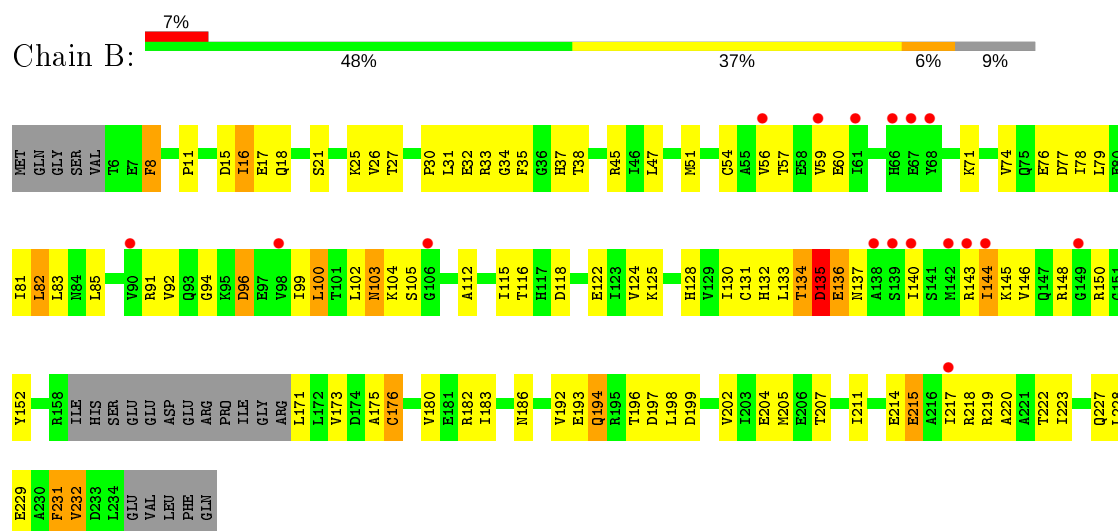
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

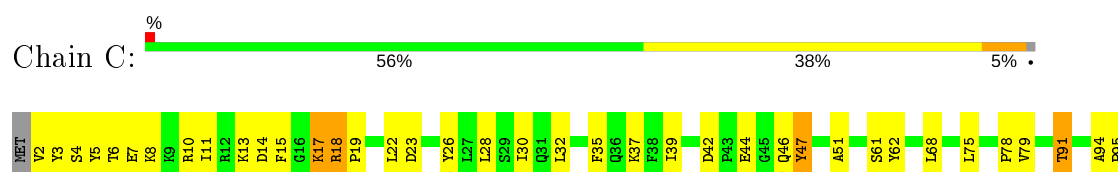
- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 1: DNA-directed RNA polymerase subunit alpha

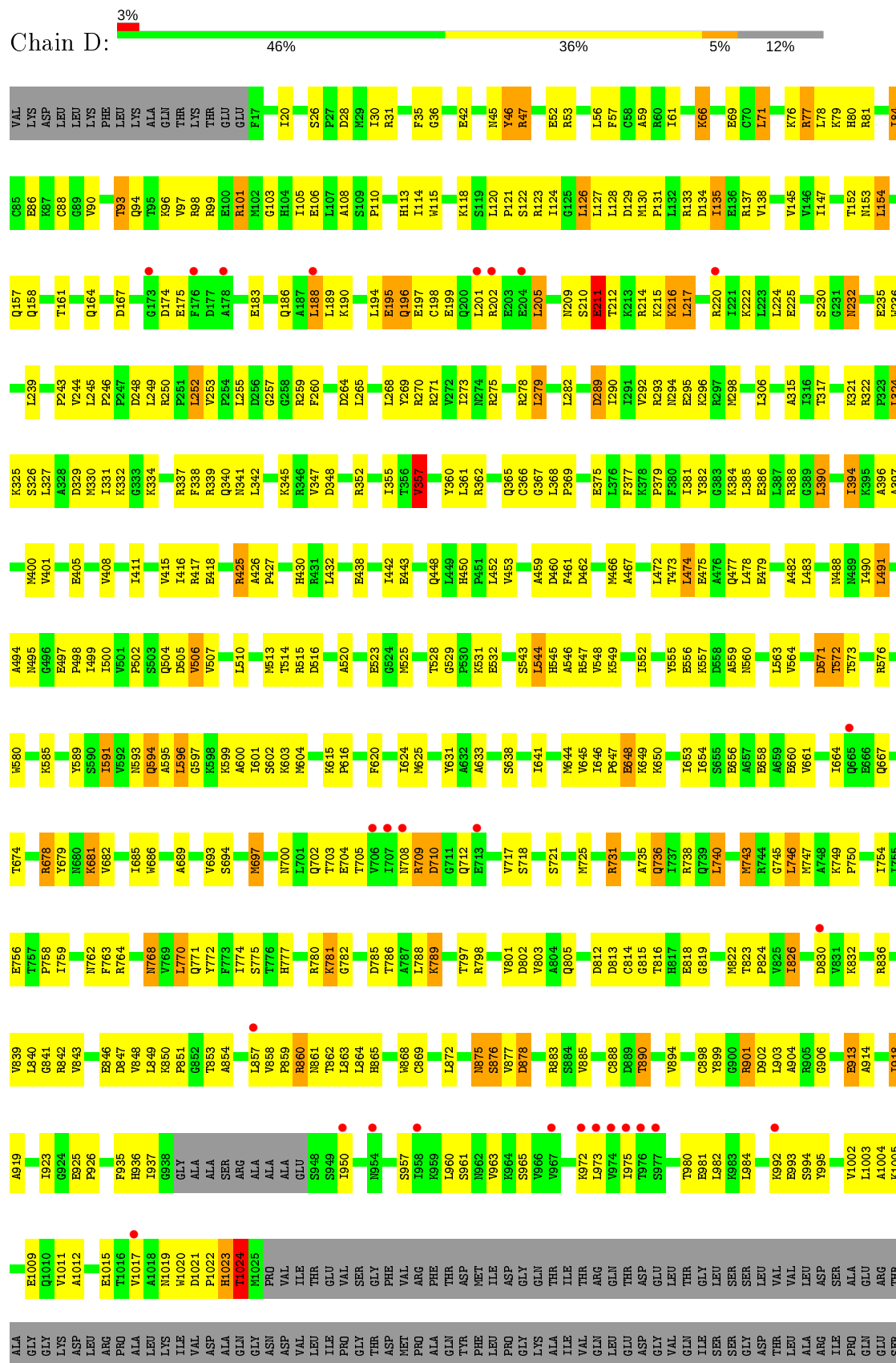


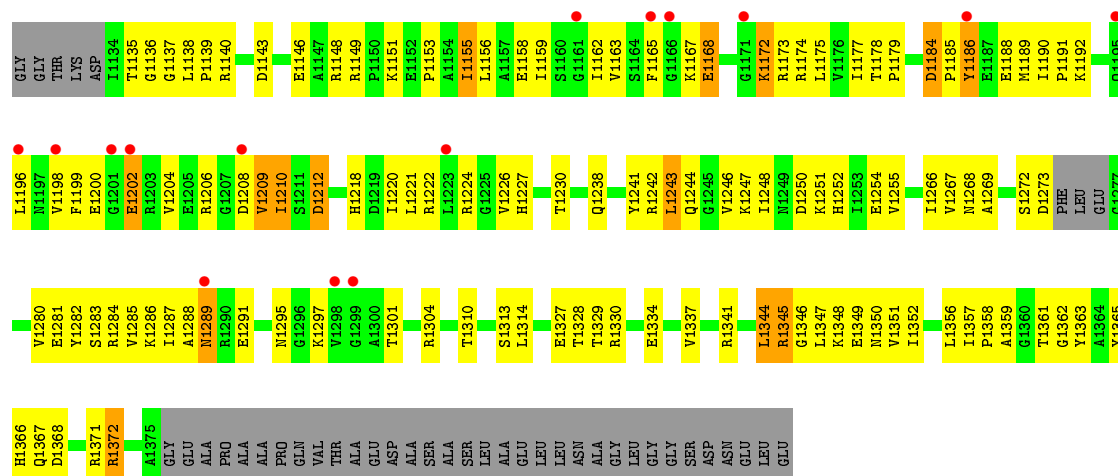
- Molecule 2: DNA-directed RNA polymerase subunit beta





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

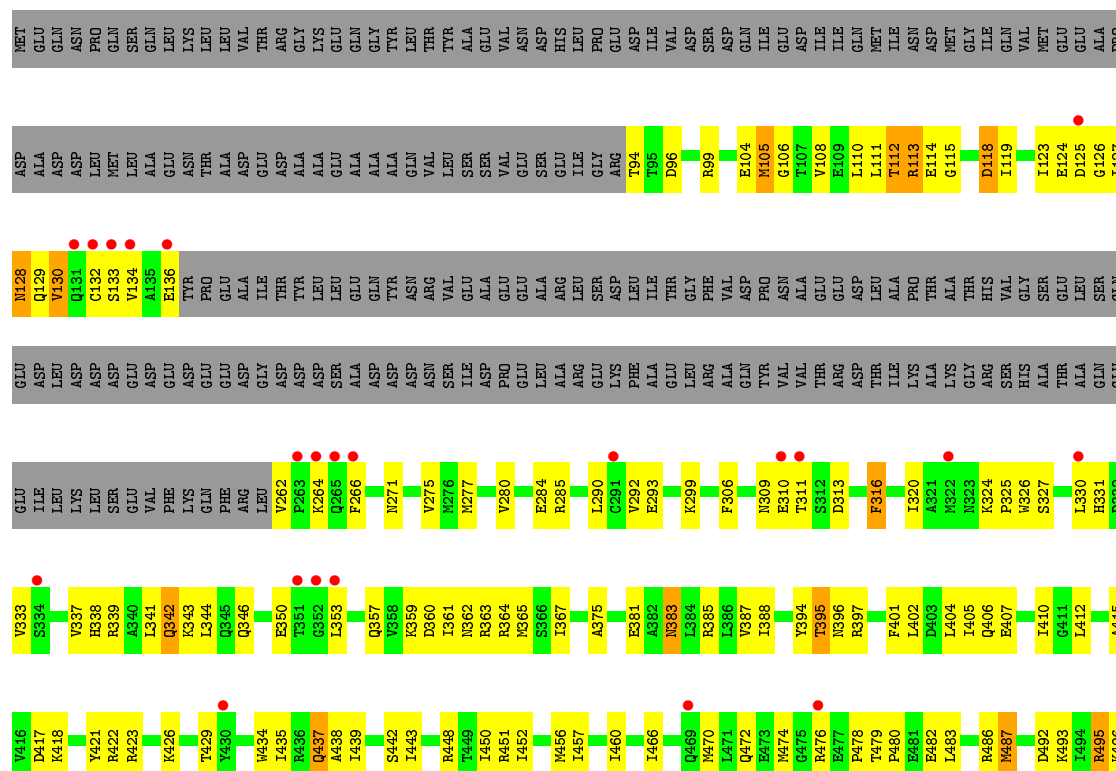


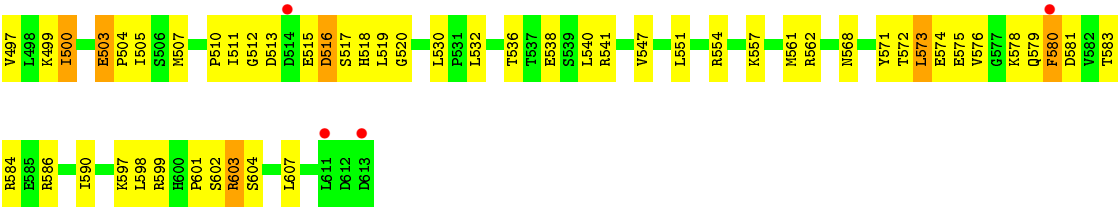


• Molecule 4: DNA-directed RNA polymerase subunit omega



• Molecule 5: RNA polymerase sigma factor RpoD

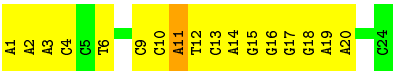
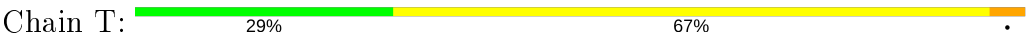




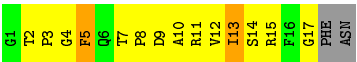
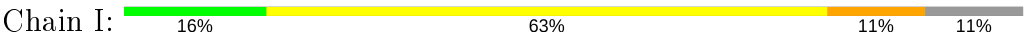
● Molecule 6: non-template strand DNA



● Molecule 7: template strand DNA



● Molecule 8: Capistruin



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	172.89Å 172.89Å 385.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.45 – 3.25 49.44 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.45-3.25) 99.0 (49.44-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 3.19Å)	Xtriage
Refinement program	PHENIX (1.13 _2998: ???)	Depositor
R, R_{free}	0.273 , 0.316 0.277 , 0.318	Depositor DCC
R_{free} test set	1980 reflections (2.07%)	wwPDB-VP
Wilson B-factor (Å ²)	99.1	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 53.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	28613	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.65% of the height of the origin peak. No significant pseudotranslation is detected.*

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, EPE, MG, EDO

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	0.24	0/1729	0.46	0/2349
1	B	0.24	0/1677	0.47	0/2274
2	C	0.25	0/10654	0.43	0/14375
3	D	0.25	0/9794	0.44	0/13212
4	E	0.22	0/629	0.39	0/847
5	F	0.24	0/3239	0.40	0/4352
6	N	0.55	1/666 (0.2%)	0.90	0/1026
7	T	0.57	1/552 (0.2%)	0.84	0/849
8	I	0.30	0/129	0.55	0/173
All	All	0.26	2/29069 (0.0%)	0.46	0/39457

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
1	B	0	2
2	C	0	4
3	D	0	2
All	All	0	8

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	T	11	DA	C1'-N9	-5.97	1.38	1.47
6	N	12	DG	C1'-N9	-5.60	1.39	1.47

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	135	ASP	Peptide
1	B	231	PHE	Peptide
2	C	198	ILE	Peptide
2	C	234	ASP	Peptide
2	C	985	GLU	Peptide

5.2 Too-close contacts [i](#)

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	1709	0	1700	69	0
1	B	1658	0	1669	86	0
2	C	10489	0	10490	455	0
3	D	9649	0	9859	531	0
4	E	627	0	634	31	0
5	F	3197	0	3251	148	0
6	N	595	0	329	36	0
7	T	492	0	269	36	0
8	I	126	0	123	22	0
9	C	4	6	6	1	0
10	D	1	0	0	0	0
11	D	2	0	0	0	0
12	D	15	17	17	7	0
13	A	1	0	0	1	0
13	B	2	0	0	0	0
13	C	13	0	0	2	0
13	D	3	0	0	3	0
13	E	1	0	0	0	0
13	F	5	0	0	0	0
13	T	1	0	0	1	0
All	All	28590	23	28347	1306	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 23.

The worst 5 of 1306 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)
7:T:10:DC:H2"	7:T:11:DA:H5'	1.27	1.11
1:A:26:VAL:HG23	1:A:203:ILE:HG13	1.37	1.07
2:C:746:ALA:HB1	2:C:747:GLY:HA3	1.33	1.06
3:D:426:ALA:HB3	3:D:427:PRO:HD3	1.40	1.02
1:B:192:VAL:HG21	1:B:198:LEU:HD22	1.46	0.96

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	226/239 (95%)	206 (91%)	19 (8%)	1 (0%)	34	67
1	B	213/239 (89%)	196 (92%)	14 (7%)	3 (1%)	11	40
2	C	1326/1342 (99%)	1245 (94%)	75 (6%)	6 (0%)	29	62
3	D	1231/1409 (87%)	1145 (93%)	83 (7%)	3 (0%)	47	77
4	E	77/90 (86%)	73 (95%)	3 (4%)	1 (1%)	12	41
5	F	391/613 (64%)	378 (97%)	13 (3%)	0	100	100
8	I	15/19 (79%)	12 (80%)	3 (20%)	0	100	100
All	All	3479/3951 (88%)	3255 (94%)	210 (6%)	14 (0%)	34	67

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	163	GLU
2	C	199	ASP
2	C	200	ARG
3	D	1345	ARG
2	C	235	ASN

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	181/206 (88%)	166 (92%)	15 (8%)	11	36
1	B	181/206 (88%)	163 (90%)	18 (10%)	8	28
2	C	1144/1157 (99%)	1033 (90%)	111 (10%)	8	29
3	D	1035/1170 (88%)	921 (89%)	114 (11%)	6	24
4	E	67/74 (90%)	64 (96%)	3 (4%)	27	58
5	F	350/540 (65%)	308 (88%)	42 (12%)	5	20
8	I	13/15 (87%)	11 (85%)	2 (15%)	2	12
All	All	2971/3368 (88%)	2666 (90%)	305 (10%)	7	26

5 of 305 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	1236	ASN
3	D	232	ASN
5	F	437	GLN
2	C	1339	LEU
3	D	93	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	1268	GLN
3	D	341	ASN
5	F	362	ASN
2	C	1314	GLN
3	D	164	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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
9	EDO	C	1401	-	3,3,3	0.44	0	2,2,2	0.58	0
12	EPE	D	1504	-	15,15,15	0.90	1 (6%)	18,20,20	2.09	6 (33%)

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
9	EDO	C	1401	-	-	0/1/1/1	-
12	EPE	D	1504	-	-	3/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	D	1504	EPE	C10-S	3.09	1.81	1.77

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	D	1504	EPE	C7-N4-C5	4.36	122.38	111.23

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
12	D	1504	EPE	O2S-S-C10	3.98	111.71	106.92
12	D	1504	EPE	C5-N4-C3	3.13	115.88	108.83
12	D	1504	EPE	C7-N4-C3	2.85	118.52	111.23
12	D	1504	EPE	O3S-S-C10	2.64	110.04	105.77

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	D	1504	EPE	C8-C7-N4-C3
12	D	1504	EPE	C9-C10-S-O3S
12	D	1504	EPE	C9-C10-S-O2S

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	C	1401	EDO	1	0
12	D	1504	EPE	7	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	228/239 (95%)	0.22	10 (4%) 34 32	73, 115, 173, 204	0
1	B	217/239 (90%)	0.39	17 (7%) 13 12	74, 133, 174, 188	0
2	C	1332/1342 (99%)	-0.04	20 (1%) 73 71	36, 92, 163, 211	0
3	D	1239/1409 (87%)	0.12	42 (3%) 45 42	45, 104, 181, 218	0
4	E	79/90 (87%)	-0.04	1 (1%) 77 75	71, 95, 155, 183	0
5	F	395/613 (64%)	0.28	26 (6%) 18 17	68, 140, 182, 213	0
6	N	29/29 (100%)	-0.13	2 (6%) 16 16	124, 171, 253, 256	0
7	T	24/24 (100%)	-0.22	0 100 100	114, 179, 256, 268	0
8	I	17/19 (89%)	0.12	0 100 100	97, 108, 127, 131	0
All	All	3560/4004 (88%)	0.09	118 (3%) 46 43	36, 107, 178, 268	0

The worst 5 of 118 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	90	VAL	6.9
3	D	972	LYS	6.1
3	D	973	LEU	6.0
2	C	230	PHE	5.9
5	F	352	GLY	5.8

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. 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	EPE	D	1504	15/15	0.70	0.33	114,143,172,178	0
9	EDO	C	1401	4/4	0.83	0.20	98,117,137,139	0
11	ZN	D	1503	1/1	0.90	0.24	108,108,108,108	0
11	ZN	D	1502	1/1	0.95	0.14	126,126,126,126	0
10	MG	D	1501	1/1	0.99	0.31	54,54,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.