



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 23, 2024 – 07:20 AM EDT

PDB ID : 6DVC
Title : Crystal structure of Mycobacterium tuberculosis transcription initiation complex(ECF sigma factor L) containing 5nt RNA with 6nt spacer
Authors : Lin, W.; Das, K.; Feng, Y.; Ebright, R.H.
Deposited on : 2018-06-23
Resolution : 3.30 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

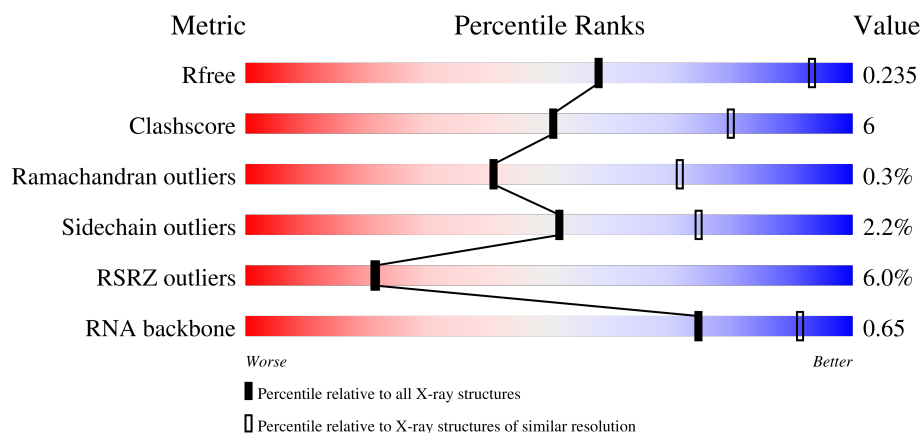
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



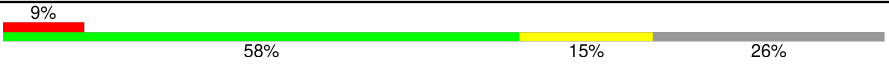

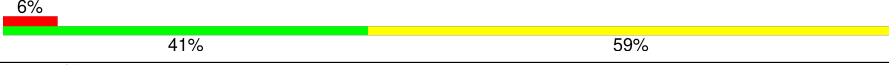
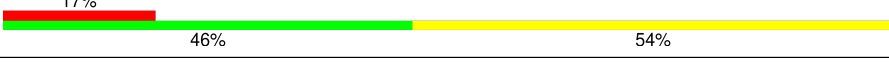

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)
RNA backbone	3102	1117 (3.70-2.90)

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	359	<div> <div>0%</div> <div> <div>50%</div> <div>13%</div> <div>37%</div> </div> </div>
1	B	359	<div> <div>4%</div> <div> <div>49%</div> <div>14%</div> <div>35%</div> </div> </div>
2	C	1178	<div> <div>4%</div> <div> <div>81%</div> <div>14%</div> </div> </div>
3	D	1316	<div> <div>7%</div> <div> <div>83%</div> <div>13%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
4	E	110	
5	F	177	
6	G	17	
7	H	24	
8	I	5	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 24983 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	225	Total	C	N	O	S	0	0	0
			1716	1080	296	338	2			
1	B	232	Total	C	N	O	S	0	0	0
			1732	1093	296	341	2			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP P9WGZ1
A	-10	GLY	-	expression tag	UNP P9WGZ1
A	-9	HIS	-	expression tag	UNP P9WGZ1
A	-8	HIS	-	expression tag	UNP P9WGZ1
A	-7	HIS	-	expression tag	UNP P9WGZ1
A	-6	HIS	-	expression tag	UNP P9WGZ1
A	-5	HIS	-	expression tag	UNP P9WGZ1
A	-4	HIS	-	expression tag	UNP P9WGZ1
A	-3	HIS	-	expression tag	UNP P9WGZ1
A	-2	HIS	-	expression tag	UNP P9WGZ1
A	-1	HIS	-	expression tag	UNP P9WGZ1
A	0	HIS	-	expression tag	UNP P9WGZ1
B	-11	MET	-	initiating methionine	UNP P9WGZ1
B	-10	GLY	-	expression tag	UNP P9WGZ1
B	-9	HIS	-	expression tag	UNP P9WGZ1
B	-8	HIS	-	expression tag	UNP P9WGZ1
B	-7	HIS	-	expression tag	UNP P9WGZ1
B	-6	HIS	-	expression tag	UNP P9WGZ1
B	-5	HIS	-	expression tag	UNP P9WGZ1
B	-4	HIS	-	expression tag	UNP P9WGZ1
B	-3	HIS	-	expression tag	UNP P9WGZ1
B	-2	HIS	-	expression tag	UNP P9WGZ1
B	-1	HIS	-	expression tag	UNP P9WGZ1
B	0	HIS	-	expression tag	UNP P9WGZ1

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1126	Total	C	N	O	S	0	0	0
			8724	5459	1531	1695	39			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1264	Total	C	N	O	S	0	0	0
			9884	6189	1790	1865	40			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	81	Total	C	N	O		0	0	0
			630	403	106	121				

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	174	Total	C	N	O	S	0	0	0
			1352	840	256	254	2			

- Molecule 6 is a DNA chain called DNA (5'-D(*GP*CP*AP*TP*CP*CP*GP*TP*GP*AP*GP*TP*CP*GP*AP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	17	Total	C	N	O	P	0	0	0
			350	166	68	100	16			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	24	Total	C	N	O	P	0	0	0
			491	234	90	144	23			

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

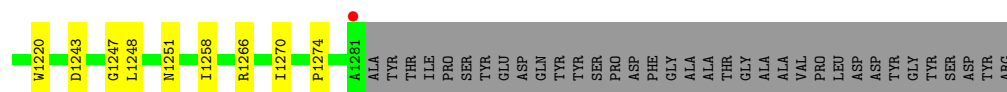
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	5	Total	C	N	O	P	0	0	0
			102	47	18	33	4			

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

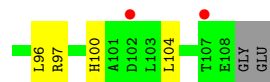
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	2	Total 2	Zn 2	0	0

- Molecule 1: DNA-directed RNA polymerase subunit alpha

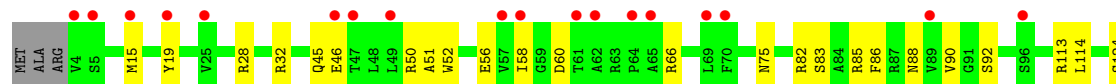
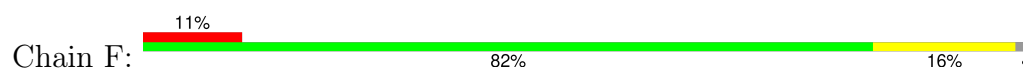




- Molecule 4: DNA-directed RNA polymerase subunit omega



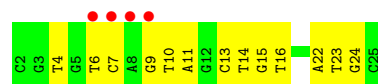
- Molecule 5: ECF RNA polymerase sigma factor SigL



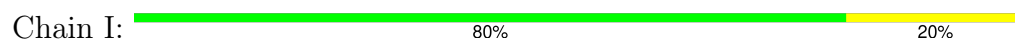
- Molecule 6: DNA (5'-D(*GP*CP*AP*TP*CP*CP*GP*TP*GP*AP*GP*TP*CP*GP*AP*GP*G)-3')



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



- Molecule 8: RNA (5'-R(*CP*UP*CP*GP*A)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	146.32Å 161.52Å 240.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	92.92 – 3.30 92.92 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.9 (92.92-3.30) 99.4 (92.92-3.30)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.198 , 0.235 0.196 , 0.235	Depositor DCC
R_{free} test set	4265 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	91.3	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 67.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	24983	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% 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

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	0.23	0/1742	0.44	0/2370
1	B	0.24	0/1758	0.44	0/2397
2	C	0.24	0/8883	0.42	0/12043
3	D	0.23	0/10049	0.40	0/13583
4	E	0.23	0/643	0.39	0/877
5	F	0.22	0/1374	0.38	0/1869
6	G	0.51	0/393	0.88	0/606
7	H	0.56	0/550	0.97	0/848
8	I	0.14	0/113	0.70	0/174
All	All	0.25	0/25505	0.45	0/34767

There are no bond length outliers.

There are no bond angle outliers.

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	1716	0	1756	28	0
1	B	1732	0	1754	36	0
2	C	8724	0	8651	101	0
3	D	9884	0	9939	107	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	630	0	622	13	0
5	F	1352	0	1346	21	0
6	G	350	0	192	9	0
7	H	491	0	272	22	0
8	I	102	0	56	1	0
9	D	2	0	0	0	0
All	All	24983	0	24588	282	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 282 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)
1:A:40:ARG:HE	1:B:33:THR:HG22	1.32	0.93
2:C:467:ARG:HG3	7:H:16:DT:H5'	1.63	0.79
2:C:593:MET:HA	2:C:628:THR:HG21	1.68	0.74
1:A:4:SER:HB3	1:B:144:ARG:HH12	1.52	0.74
3:D:363:PRO:HG2	5:F:15:MET:HG3	1.70	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	223/359 (62%)	217 (97%)	5 (2%)	1 (0%)	34	66
1	B	230/359 (64%)	213 (93%)	16 (7%)	1 (0%)	34	66
2	C	1124/1178 (95%)	1071 (95%)	48 (4%)	5 (0%)	34	66
3	D	1258/1316 (96%)	1205 (96%)	51 (4%)	2 (0%)	47	77
4	E	79/110 (72%)	76 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	F	172/177 (97%)	168 (98%)	4 (2%)	0	100	100
All	All	3086/3499 (88%)	2950 (96%)	127 (4%)	9 (0%)	41	71

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	159	ILE
2	C	370	ILE
2	C	732	GLU
3	D	1089	PHE
2	C	32	VAL

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	194/308 (63%)	190 (98%)	4 (2%)	53	75
1	B	191/308 (62%)	185 (97%)	6 (3%)	40	67
2	C	950/998 (95%)	932 (98%)	18 (2%)	57	77
3	D	1049/1095 (96%)	1026 (98%)	23 (2%)	52	74
4	E	66/90 (73%)	66 (100%)	0	100	100
5	F	134/136 (98%)	128 (96%)	6 (4%)	27	58
All	All	2584/2935 (88%)	2527 (98%)	57 (2%)	52	74

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	82	VAL
5	F	85	ARG
3	D	443	LEU
5	F	66	ARG
3	D	910	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	I	4/5 (80%)	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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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 [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	225/359 (62%)	0.19	5 (2%) 62 60	48, 74, 136, 172	0
1	B	232/359 (64%)	0.62	13 (5%) 24 23	62, 95, 148, 179	0
2	C	1126/1178 (95%)	0.29	42 (3%) 41 38	44, 85, 156, 184	0
3	D	1264/1316 (96%)	0.42	93 (7%) 14 14	42, 90, 176, 221	0
4	E	81/110 (73%)	0.69	10 (12%) 4 3	68, 97, 172, 188	0
5	F	174/177 (98%)	0.85	20 (11%) 4 4	60, 101, 168, 190	0
6	G	17/17 (100%)	0.42	1 (5%) 22 22	77, 88, 163, 163	0
7	H	24/24 (100%)	0.97	4 (16%) 1 1	100, 150, 211, 215	0
8	I	5/5 (100%)	1.33	0 100 100	74, 75, 90, 117	0
All	All	3148/3545 (88%)	0.41	188 (5%) 21 21	42, 89, 164, 221	0

The worst 5 of 188 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	3	ILE	7.1
3	D	1053	VAL	6.0
3	D	1099	LEU	6.0
3	D	1064	ILE	5.5
1	B	4	SER	5.5

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides 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
9	ZN	D	2002	1/1	0.98	0.08	105,105,105,105	0
9	ZN	D	2001	1/1	0.99	0.10	100,100,100,100	0

6.5 Other polymers [i](#)

There are no such residues in this entry.