



# wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 5NWT  
Title : Crystal Structure of Escherichia coli RNA polymerase - Sigma54 Holoenzyme complex  
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Deposited on : unknown  
Resolution : 3.76 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20029824
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20029824

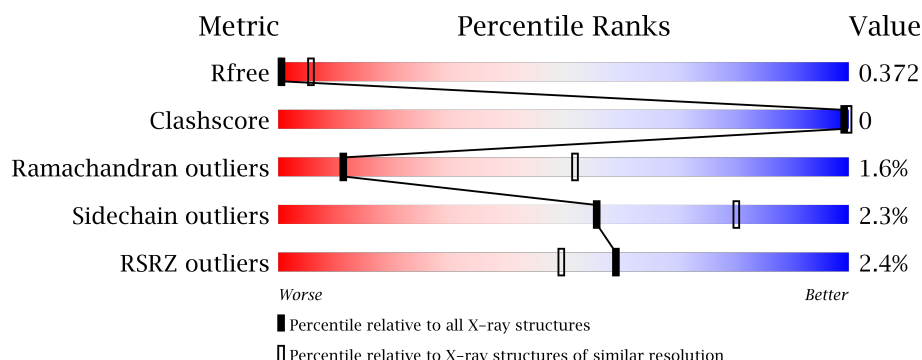
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.76 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))
$R_{free}$	100719	1423 (4.02-3.50)
Clashscore	112137	1087 (4.00-3.52)
Ramachandran outliers	110173	1047 (4.00-3.52)
Sidechain outliers	110143	1041 (4.00-3.52)
RSRZ outliers	101464	1011 (4.00-3.52)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	329	<div> <div>91%</div> <div>7%</div> </div>
1	B	329	<div> <div>65%</div> <div>35%</div> </div>
2	C	1342	<div> <div>4%</div> <div>96%</div> <div>2%</div> </div>
3	D	1407	<div> <div>2%</div> <div>94%</div> <div>2%</div> </div>
4	E	91	<div> <div>85%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
5	M	477	<div><div><div>%</div><div><div></div></div><div>86%</div><div><div></div><div></div></div><div>10%</div></div></div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 22461 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	307	Total	C	N	O	S	0	0	0
			1888	1159	348	375	6			
1	B	215	Total	C	N	O	S	0	0	0
			1272	781	233	254	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1318	Total	C	N	O	S	0	0	0
			8247	5047	1515	1661	24			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1358	Total	C	N	O	S	0	0	0
			8092	4936	1535	1598	23			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	78	Total	C	N	O	S	0	0	0
			589	358	108	122	1			

- Molecule 5 is a protein called RNA polymerase sigma-54 factor, RNA polymerase sigma-54 factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	M	431	Total	C	N	O	Se	51	0	0
			2370	1442	444	476	8			

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

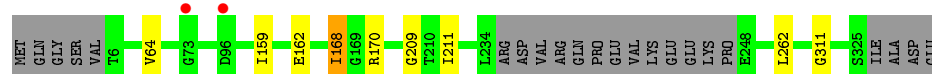
- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

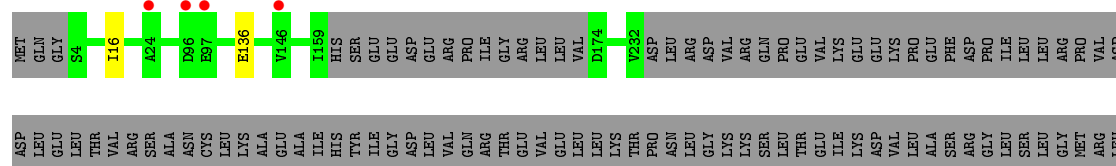
### 3 Residue-property plots

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.

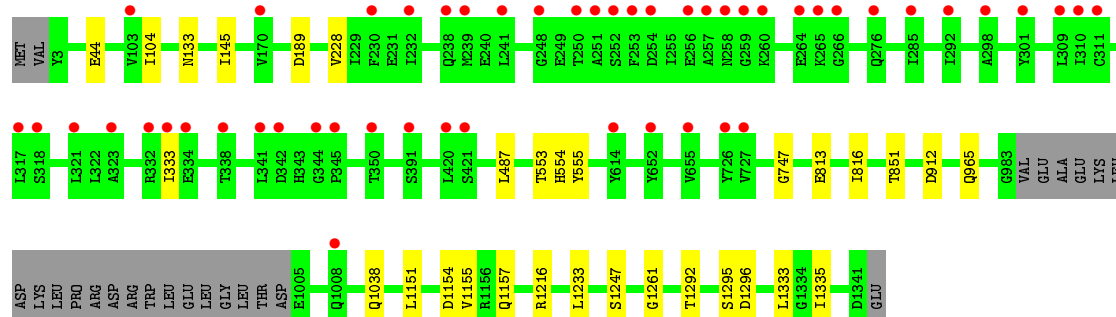
- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 1: DNA-directed RNA polymerase subunit alpha



- Molecule 2: DNA-directed RNA polymerase subunit beta



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





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	208.48 Å   151.53 Å   195.28 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	195.28 – 3.76 29.64 – 3.76	Depositor EDS
% Data completeness (in resolution range)	98.2 (195.28-3.76) 98.5 (29.64-3.76)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.26 (at 3.75 Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, $R_{free}$	0.313   ,   0.370 0.316   ,   0.372	Depositor DCC
$R_{free}$ test set	3077 reflections (5.19%)	DCC
Wilson B-factor (Å <sup>2</sup> )	142.0	Xtriage
Anisotropy	0.740	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.22 , 166.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	22461	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	194.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, 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	0.33	0/1913	0.48	0/2643
1	B	0.32	0/1284	0.45	0/1779
2	C	0.34	0/8363	0.47	0/11499
3	D	0.33	0/8201	0.48	0/11314
4	E	0.37	0/591	0.51	0/801
5	M	0.34	0/1986	0.47	0/2746
All	All	0.34	0/22338	0.48	0/30782

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	1888	0	1450	1	0
1	B	1272	0	946	0	0
2	C	8247	0	6196	2	0
3	D	8092	0	5804	4	0
4	E	589	0	559	0	0
5	M	2370	0	1363	6	0
6	D	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	1	0	0	0	0
All	All	22461	0	16318	13	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 0.

The worst 5 of 13 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)
5:M:152:GLY:O	5:M:260:PRO:HG3	1.65	0.96
3:D:72:CYS:SG	6:D:1501:ZN:ZN	1.81	0.70
5:M:152:GLY:HA3	5:M:260:PRO:HG2	1.81	0.61
5:M:152:GLY:HA3	5:M:260:PRO:CG	2.34	0.57
3:D:322:ARG:CB	3:D:323:PRO:CD	2.84	0.56

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	303/329 (92%)	260 (86%)	36 (12%)	7 (2%)	7	46
1	B	211/329 (64%)	186 (88%)	23 (11%)	2 (1%)	20	63
2	C	1310/1342 (98%)	1156 (88%)	140 (11%)	14 (1%)	17	60
3	D	1354/1407 (96%)	1182 (87%)	152 (11%)	20 (2%)	12	53
4	E	76/91 (84%)	69 (91%)	6 (8%)	1 (1%)	14	56
5	M	349/477 (73%)	276 (79%)	59 (17%)	14 (4%)	3	34
All	All	3603/3975 (91%)	3129 (87%)	416 (12%)	58 (2%)	11	52

5 of 58 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	119	SER
1	B	16	ILE
2	C	333	ILE
3	D	120	LEU
3	D	322	ARG

### 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	127/286 (44%)	125 (98%)	2 (2%)	68	86
1	B	77/286 (27%)	77 (100%)	0	100	100
2	C	546/1157 (47%)	532 (97%)	14 (3%)	51	78
3	D	439/1168 (38%)	426 (97%)	13 (3%)	46	75
4	E	59/75 (79%)	59 (100%)	0	100	100
5	M	82/314 (26%)	80 (98%)	2 (2%)	54	79
All	All	1330/3286 (40%)	1299 (98%)	31 (2%)	56	80

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	1233	LEU
3	D	190	LYS
3	D	857	LEU
2	C	1296	ASP
3	D	245	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	450	ASN
3	D	11	GLN
3	D	861	ASN
3	D	1367	GLN

### 5.3.3 RNA [i](#)

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 3 ligands modelled in this entry, 3 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	C	2
5	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	66:UNK	C	85:UNK	N	16.93

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	336:LEU	C	337:PHE	N	3.66
1	C	225:PHE	C	226:GLU	N	3.29

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	307/329 (93%)	-0.45	2 (0%) 87 82	91, 180, 277, 375	0
1	B	215/329 (65%)	-0.26	4 (1%) 67 59	141, 222, 314, 352	0
2	C	1318/1342 (98%)	-0.16	51 (3%) 40 32	78, 189, 358, 534	0
3	D	1358/1407 (96%)	-0.31	24 (1%) 69 60	79, 189, 316, 397	0
4	E	78/91 (85%)	-0.23	0 100 100	127, 187, 317, 381	0
5	M	341/477 (71%)	-0.64	6 (1%) 69 60	30, 141, 223, 314	6 (1%)
All	All	3617/3975 (90%)	-0.29	87 (2%) 59 49	30, 185, 323, 534	6 (0%)

The worst 5 of 87 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	252	SER	17.5
2	C	253	PHE	13.2
2	C	265	LYS	9.1
2	C	254	ASP	7.8
2	C	251	ALA	7.4

### 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 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<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
6	ZN	D	1503	1/1	0.88	0.16	-0.41	156,156,156,156	0
6	ZN	D	1501	1/1	0.91	0.12	-0.77	120,120,120,120	0
7	MG	D	1502	1/1	0.87	0.38	-	163,163,163,163	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.