



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:10 PM GMT

PDB ID : 4KN7
Title : X-ray crystal structure of the Escherichia coli RNA polymerase in complex with Benzoxazinorifamycin-2c
Authors : Murakami, K.S.
Deposited on : 2013-05-08
Resolution : 3.69 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

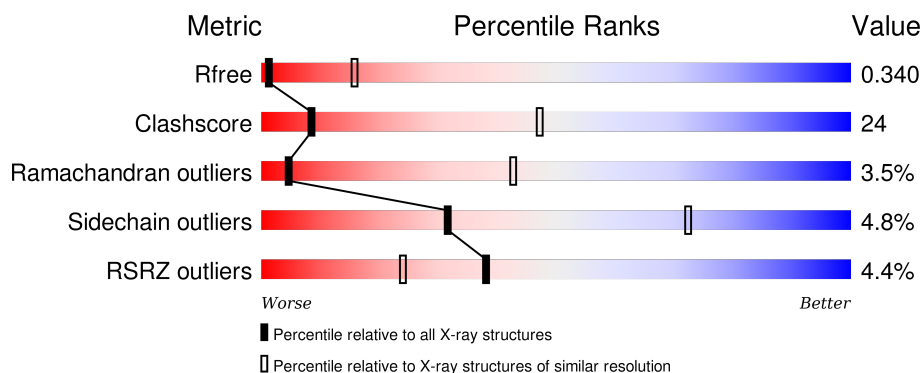
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.69 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	1033 (3.86-3.50)
Clashscore	102246	1148 (3.86-3.50)
Ramachandran outliers	100387	1100 (3.86-3.50)
Sidechain outliers	100360	1098 (3.86-3.50)
RSRZ outliers	91569	1040 (3.86-3.50)

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 $\leq 5\%$. 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	
1	B	329	
1	F	329	
1	G	329	
2	C	1342	

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Mol	Chain	Length	Quality of chain
2	H	1342	<div><div></div><div>6%</div><div>55%</div><div>39%</div><div>5%</div><div></div></div>
3	D	1407	<div><div></div><div>2%</div><div>40%</div><div>38%</div><div>5%</div><div>18%</div><div></div></div>
3	I	1407	<div><div></div><div>4%</div><div>41%</div><div>37%</div><div></div><div>18%</div><div></div></div>
4	E	91	<div><div></div><div>%</div><div>68%</div><div>27%</div><div></div><div></div><div></div></div>
4	J	91	<div><div></div><div>3%</div><div>52%</div><div>29%</div><div></div><div>16%</div><div></div></div>
5	X	613	<div><div></div><div>6%</div><div>49%</div><div>32%</div><div></div><div>16%</div><div></div></div>
5	Y	613	<div><div></div><div>5%</div><div>44%</div><div>29%</div><div></div><div>25%</div><div></div></div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 56331 atoms, of which 117 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	323	Total	C	N	O	S	0	0	0
			2514	1571	443	492	8			
1	B	221	Total	C	N	O	S	0	0	0
			1706	1065	300	335	6			
1	F	229	Total	C	N	O	S	0	0	0
			1775	1106	313	350	6			
1	G	217	Total	C	N	O	S	0	0	0
			1671	1045	293	327	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1335	Total	C	N	O	S	0	0	0
			10523	6601	1836	2043	43			
2	H	1335	Total	C	N	O	S	0	0	0
			10523	6601	1836	2043	43			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1160	Total	C	N	O	S	0	0	0
			9060	5695	1621	1697	47			
3	I	1160	Total	C	N	O	S	0	0	0
			9060	5695	1621	1697	47			

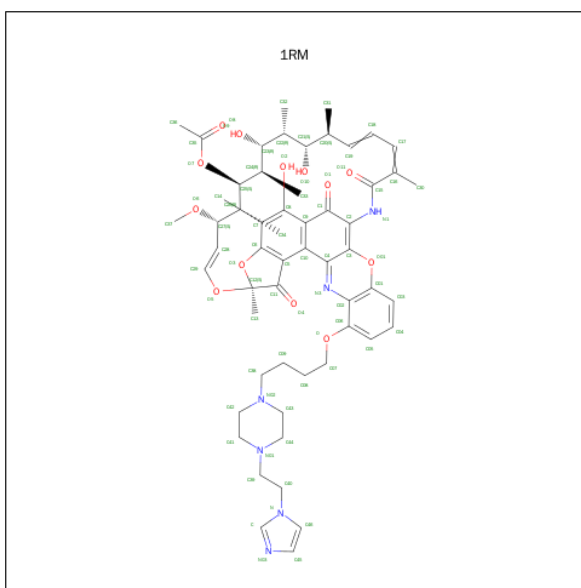
- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	90	Total	C	N	O	S	0	0	0
			708	430	136	141	1			
4	J	76	Total	C	N	O	S	0	0	0
			605	368	115	121	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	X	517	Total	C	N	O	S	0	0	0
			4198	2621	745	806	26			
5	Y	458	Total	C	N	O	S	0	0	0
			3732	2335	671	703	23			

- Molecule 6 is BENZOXAZINORIFAMYCIN-2C (three-letter code: 1RM) (formula: $C_{56}H_{70}N_6O_{13}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	C	1	Total	C	H	N	O	0	0
			145	56	70	6	13		
6	H	1	Total	C	H	N	O	0	0
			105	43	47	2	13		

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	I	2	Total	Zn	0	0
			2	2		
7	D	2	Total	Zn	0	0
			2	2		

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	I	1	Total 1	Mg 1	0	0
8	D	1	Total 1	Mg 1	0	0

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.

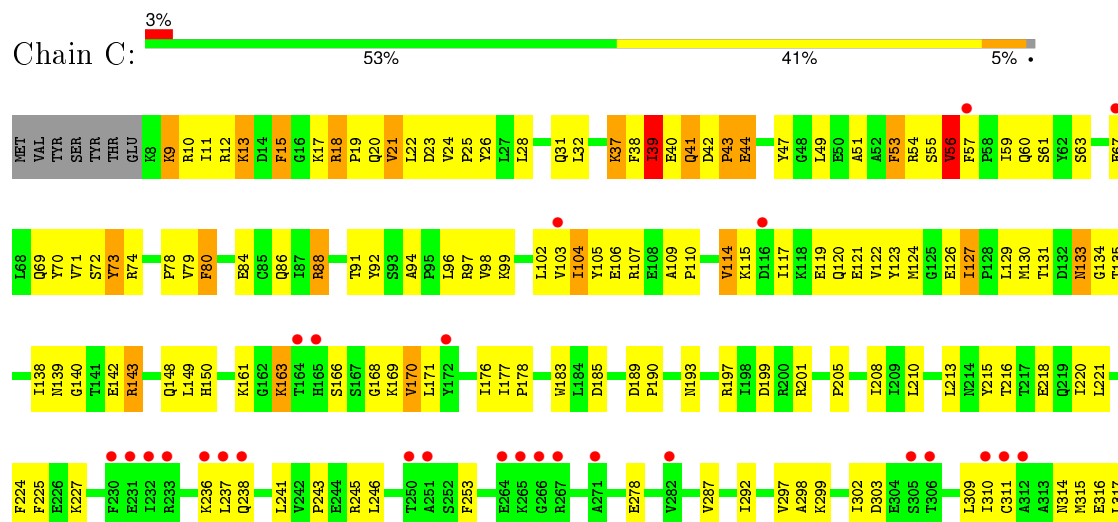
- Chain A:
-
- Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 0.20). The x-axis shows positions 1 to 300. A color scale at the top indicates conservation levels: 2% (red), 62% (green), and 33% (yellow). A legend at the bottom identifies amino acids by color: R310 (red), S313 (pink), L314 (light blue), G315 (green), K316 (dark green), L317 (light green), L318 (light blue), E319 (yellow), N320 (orange), K321 (dark green), F322 (red), P323 (pink), A324 (light blue), S325 (green), ILE (dark green), ALA (light green), ASP (light blue), and GLU (dark blue).

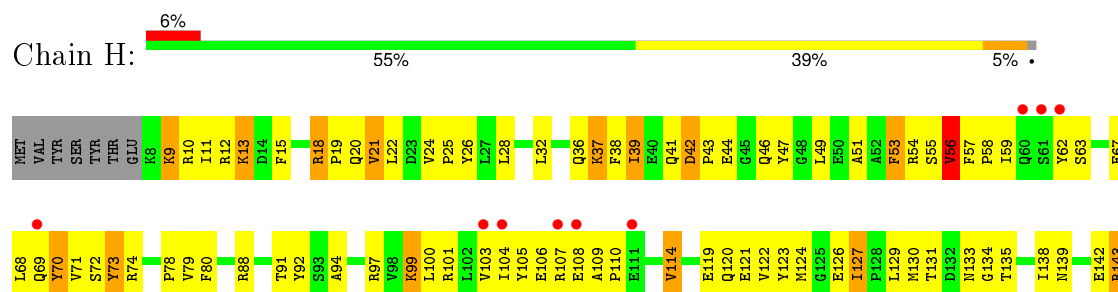
- Chain B:

3% 40% 24% 33%

MET GLN GLY SER VAL T6 E7 F8 L9 K10 P11 R12 L13 V14 D15 I16 E17 Q18 V19 S20 S21 T22 V26 T27 L28 E29 P30 L31 E32 R33 H37 T38 L39 G40 I41 A42 L43 R44 R45 I46 L47 L48 S49 S50 N51 P52 T57 I61 D62 G63 V64 L65 H66 E67 Y68 S69

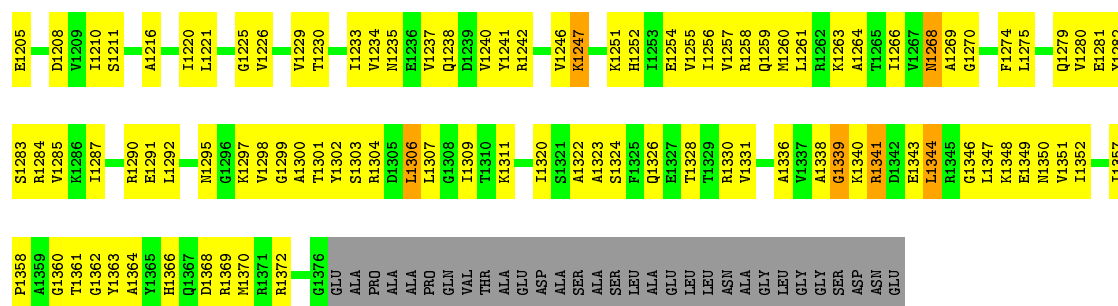
- Molecule 1: DNA-directed RNA polymerase subunit alpha



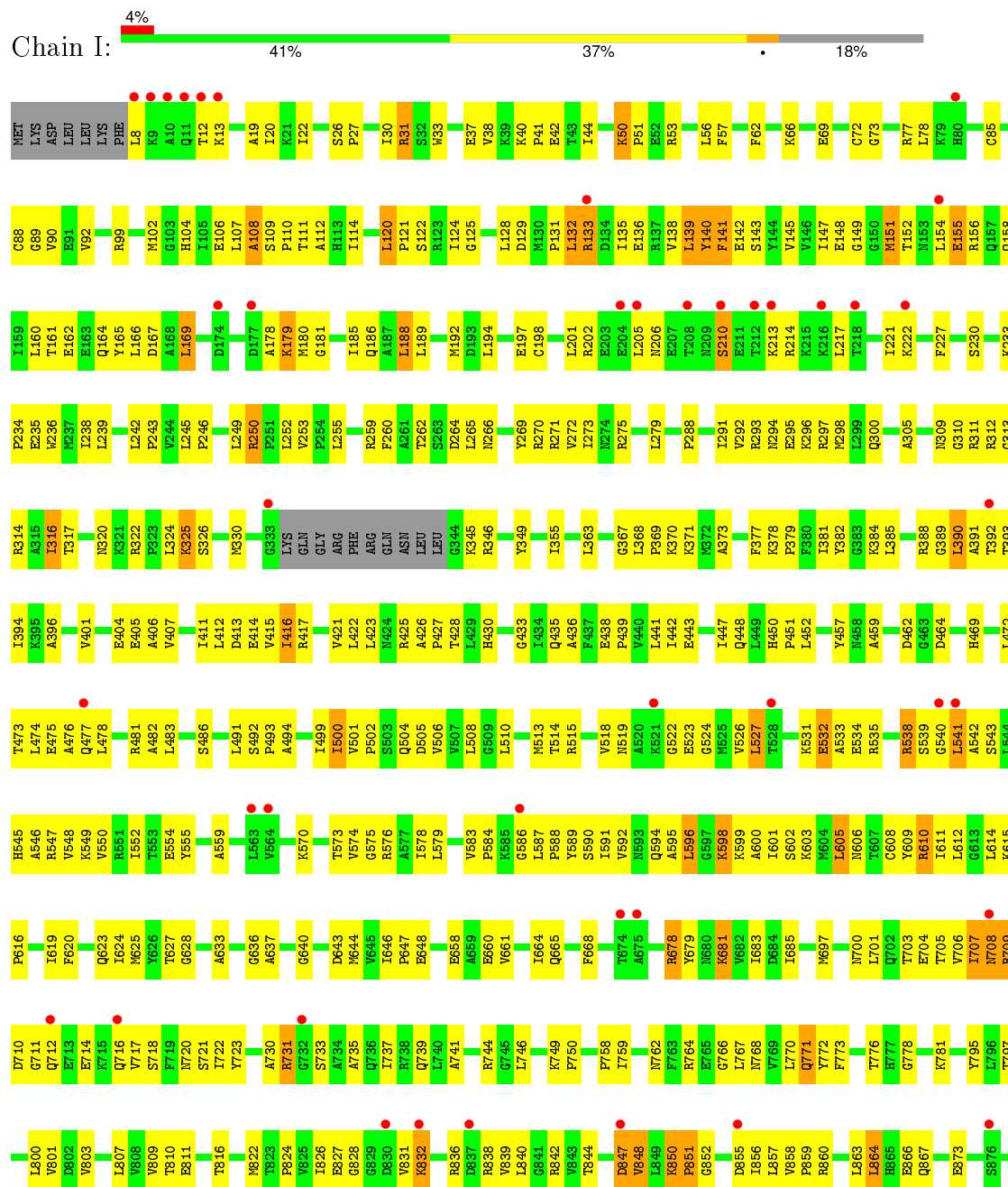


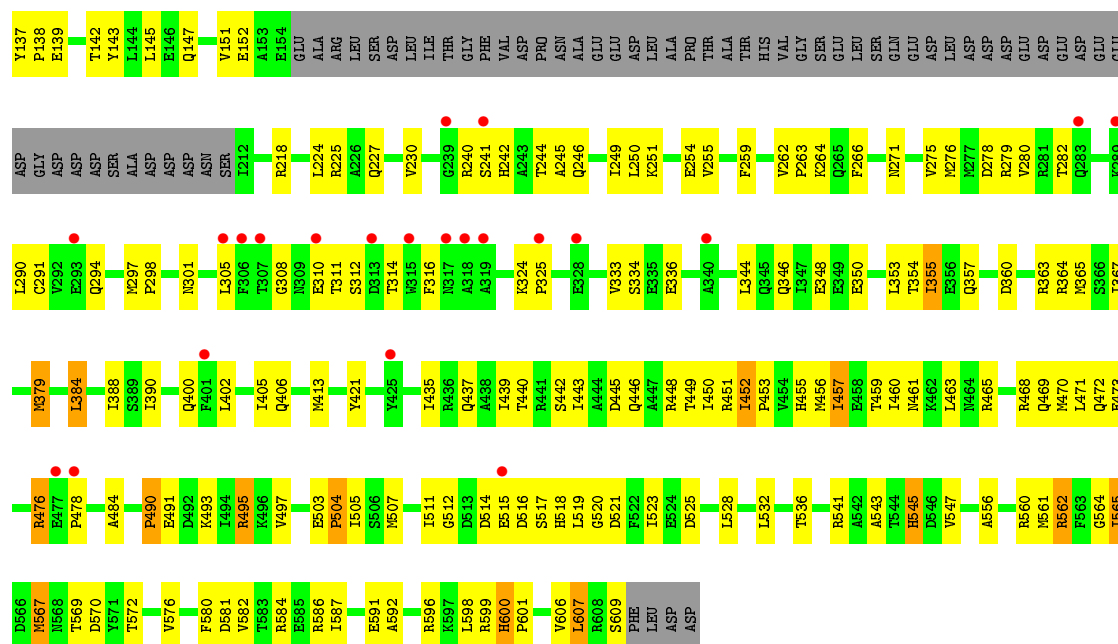




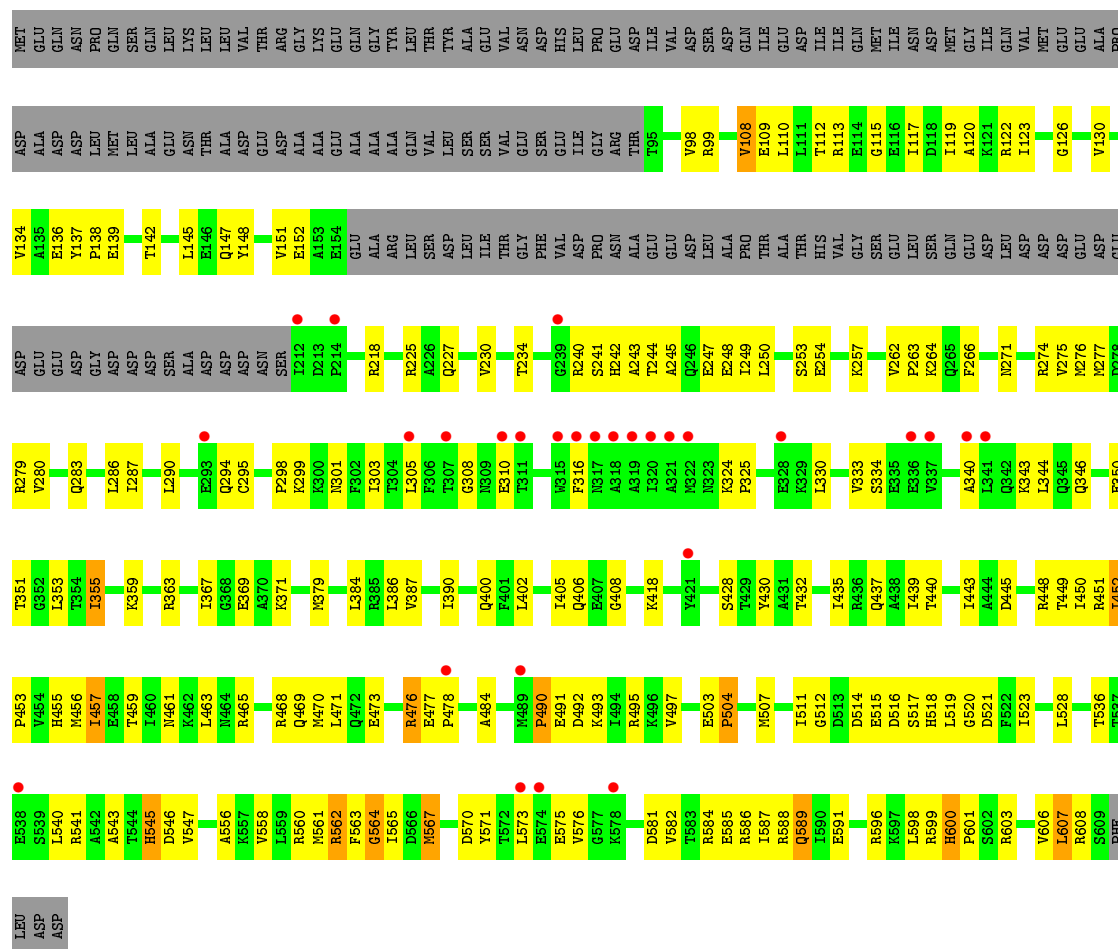


• Molecule 3: DNA-directed RNA polymerase subunit beta'





• Molecule 5: RNA polymerase sigma factor RpoD



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	185.83Å 204.58Å 308.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.88 – 3.69 29.88 – 3.69	Depositor EDS
% Data completeness (in resolution range)	93.1 (29.88-3.69) 87.0 (29.88-3.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 3.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.252 , 0.309 0.293 , 0.340	Depositor DCC
R_{free} test set	5907 reflections (5.63%)	DCC
Wilson B-factor (Å ²)	117.0	Xtriage
Anisotropy	0.274	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 28.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	1 of 118179 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	56331	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.73% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN, 1RM

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	0.19	0/2548	0.37	0/3454
1	B	0.19	0/1725	0.41	0/2337
1	F	0.19	0/1797	0.40	0/2436
1	G	0.20	0/1690	0.40	0/2290
2	C	0.20	0/10690	0.39	0/14423
2	H	0.20	0/10690	0.39	0/14423
3	D	0.20	0/9198	0.40	0/12413
3	I	0.20	0/9198	0.40	0/12413
4	E	0.19	0/710	0.36	0/956
4	J	0.19	0/607	0.37	0/817
5	X	0.20	0/4253	0.37	0/5719
5	Y	0.20	0/3783	0.37	0/5083
All	All	0.20	0/56889	0.39	0/76764

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 [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	2514	0	2566	102	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1706	0	1738	86	0
1	F	1775	0	1800	65	0
1	G	1671	0	1706	80	0
2	C	10523	0	10546	566	0
2	H	10523	0	10546	538	0
3	D	9060	0	9257	589	0
3	I	9060	0	9256	532	0
4	E	708	0	719	31	0
4	J	605	0	612	28	0
5	X	4198	0	4250	180	0
5	Y	3732	0	3809	139	0
6	C	75	70	70	9	0
6	H	58	47	46	8	0
7	D	2	0	0	0	0
7	I	2	0	0	0	0
8	D	1	0	0	0	0
8	I	1	0	0	0	0
All	All	56214	117	56921	2717	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 24.

The worst 5 of 2717 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:H:1119:MET:HG2	2:H:1228:GLY:HA2	1.26	1.17
3:D:1173:ARG:HA	3:D:1174:ARG:HB2	1.28	1.14
3:D:310:GLY:HA3	3:D:311:ARG:HB2	1.22	1.13
2:C:1119:MET:HG2	2:C:1228:GLY:HA2	1.31	1.10
3:I:1173:ARG:HA	3:I:1174:ARG:HB2	1.29	1.09

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	321/329 (98%)	266 (83%)	40 (12%)	15 (5%)	3	33
1	B	217/329 (66%)	187 (86%)	22 (10%)	8 (4%)	4	40
1	F	227/329 (69%)	196 (86%)	25 (11%)	6 (3%)	7	48
1	G	213/329 (65%)	187 (88%)	22 (10%)	4 (2%)	10	55
2	C	1333/1342 (99%)	1069 (80%)	216 (16%)	48 (4%)	4	41
2	H	1333/1342 (99%)	1069 (80%)	215 (16%)	49 (4%)	4	40
3	D	1154/1407 (82%)	918 (80%)	194 (17%)	42 (4%)	4	41
3	I	1154/1407 (82%)	920 (80%)	192 (17%)	42 (4%)	4	41
4	E	88/91 (97%)	78 (89%)	5 (6%)	5 (6%)	2	27
4	J	74/91 (81%)	65 (88%)	4 (5%)	5 (7%)	1	23
5	X	511/613 (83%)	449 (88%)	49 (10%)	13 (2%)	7	49
5	Y	454/613 (74%)	410 (90%)	34 (8%)	10 (2%)	8	52
All	All	7079/8222 (86%)	5814 (82%)	1018 (14%)	247 (4%)	4	43

5 of 247 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	52	PRO
1	A	319	GLU
1	B	20	SER
1	B	52	PRO
2	C	21	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	281/286 (98%)	273 (97%)	8 (3%)	51	82
1	B	189/286 (66%)	186 (98%)	3 (2%)	70	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	197/286 (69%)	193 (98%)	4 (2%)	63	87
1	G	185/286 (65%)	179 (97%)	6 (3%)	46	80
2	C	1150/1157 (99%)	1083 (94%)	67 (6%)	25	67
2	H	1150/1157 (99%)	1085 (94%)	65 (6%)	25	68
3	D	971/1168 (83%)	920 (95%)	51 (5%)	28	70
3	I	971/1168 (83%)	920 (95%)	51 (5%)	28	70
4	E	74/75 (99%)	72 (97%)	2 (3%)	52	83
4	J	65/75 (87%)	63 (97%)	2 (3%)	47	81
5	X	460/540 (85%)	443 (96%)	17 (4%)	41	77
5	Y	407/540 (75%)	391 (96%)	16 (4%)	39	77
All	All	6100/7024 (87%)	5808 (95%)	292 (5%)	31	72

5 of 292 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	X	28	ASN
2	H	41	GLN
3	I	1247	LYS
5	X	266	PHE
1	F	37	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 90 such sidechains are listed below:

Mol	Chain	Res	Type
5	X	8	GLN
5	X	461	ASN
5	Y	242	HIS
5	X	28	ASN
5	X	54	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 8 ligands modelled in this entry, 6 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	$\# Z > 2$
6	1RM	C	1401	-	76,82,82	1.86	15 (19%)	102,120,120	1.93	27 (26%)
6	1RM	H	1401	-	59,63,82	2.08	14 (23%)	80,96,120	1.87	20 (25%)

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
6	1RM	C	1401	-	-	0/68/97/97	0/3/8/8
6	1RM	H	1401	-	-	0/55/74/97	0/1/6/8

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1401	1RM	O7-C25	-4.42	1.37	1.44
6	H	1401	1RM	O7-C25	-4.33	1.38	1.44
6	H	1401	1RM	C12-C11	-3.19	1.38	1.54
6	C	1401	1RM	C12-C11	-3.13	1.39	1.54
6	C	1401	1RM	C32-C22	-2.37	1.48	1.53

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	1401	1RM	C12-O3-C6	-6.62	99.42	107.82
6	H	1401	1RM	C12-O3-C6	-6.17	99.99	107.82
6	H	1401	1RM	C3-O01-C01	-3.85	116.89	122.30
6	C	1401	1RM	C6-C5-C11	-3.81	100.59	107.64
6	C	1401	1RM	C3-O01-C01	-3.67	117.15	122.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	1401	1RM	9	0
6	H	1401	1RM	8	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 ⓘ

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	323/329 (98%)	-0.09	8 (2%) 61 43	0, 59, 154, 247	0
1	B	221/329 (67%)	0.17	11 (4%) 32 20	5, 86, 172, 210	0
1	F	229/329 (69%)	0.22	13 (5%) 27 16	20, 107, 186, 257	0
1	G	217/329 (65%)	0.29	16 (7%) 17 10	23, 106, 166, 211	0
2	C	1335/1342 (99%)	-0.19	38 (2%) 56 39	0, 35, 155, 279	0
2	H	1335/1342 (99%)	0.06	78 (5%) 26 15	1, 78, 192, 314	0
3	D	1160/1407 (82%)	-0.13	26 (2%) 65 48	0, 30, 149, 264	0
3	I	1160/1407 (82%)	0.01	54 (4%) 35 22	1, 49, 170, 288	0
4	E	90/91 (98%)	-0.37	1 (1%) 82 69	0, 32, 101, 141	0
4	J	76/91 (83%)	-0.03	3 (3%) 43 28	7, 72, 156, 198	0
5	X	517/613 (84%)	0.14	36 (6%) 19 11	1, 95, 219, 329	0
5	Y	458/613 (74%)	0.13	28 (6%) 25 14	2, 98, 217, 320	0
All	All	7121/8222 (86%)	-0.01	312 (4%) 38 24	0, 62, 183, 329	0

The worst 5 of 312 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	10	ALA	11.8
2	H	1002	LEU	9.4
2	H	1003	THR	7.7
5	Y	239	GLY	7.7
2	C	311	CYS	7.3

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 [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, 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	LLDF	B-factors(\AA^2)	Q<0.9
6	1RM	C	1401	75/75	0.76	0.37	0.99	20,20,20,20	0
6	1RM	H	1401	58/75	0.83	0.32	0.83	20,20,20,20	0
7	ZN	I	1502	1/1	0.97	0.15	-0.39	49,49,49,49	0
7	ZN	D	1502	1/1	0.97	0.20	-0.49	8,8,8,8	0
7	ZN	D	1501	1/1	0.97	0.10	-0.92	54,54,54,54	0
7	ZN	I	1501	1/1	0.95	0.10	-1.50	60,60,60,60	0
8	MG	D	1503	1/1	0.84	0.49	-	24,24,24,24	0
8	MG	I	1503	1/1	0.93	0.73	-	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.