



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:44 AM GMT

PDB ID : 2E2I
Title : RNA polymerase II elongation complex in 5 mM Mg+2 with 2'-dGTP
Authors : Wang, D.; Bushnell, D.A.; Westover, K.D.; Kaplan, C.D.; Kornberg, R.D.
Deposited on : 2006-11-14
Resolution : 3.41 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

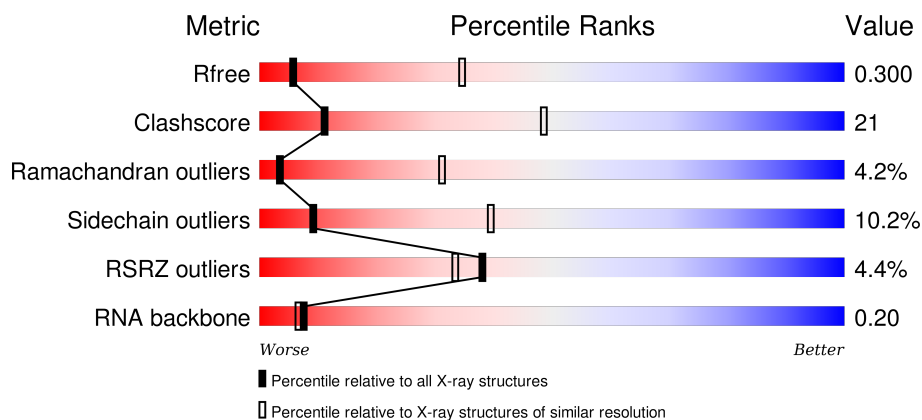
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.41 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	1049 (3.52-3.32)
Clashscore	102246	1032 (3.50-3.34)
Ramachandran outliers	100387	1002 (3.50-3.34)
Sidechain outliers	100360	1003 (3.50-3.34)
RSRZ outliers	91569	1054 (3.52-3.32)
RNA backbone	2183	1042 (4.02-2.80)

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	R	10	<div> <div>10%</div> <div>10% 20% 50% 20%</div> </div>
2	T	28	<div> <div>4%</div> <div>7% 75% 18%</div> </div>
3	N	14	<div> <div>7%</div> <div>7% 64% 29%</div> </div>
4	A	1733	<div> <div>5%</div> <div>51% 26% 19%</div> </div>

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Mol	Chain	Length	Quality of chain
5	B	1224	
6	C	318	
7	E	215	
8	F	155	
9	H	146	
10	I	122	
11	J	70	
12	K	120	
13	L	70	

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
16	DGT	B	1308[A]	-	-	-	X
16	DGT	B	1308[B]	-	-	-	X

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 29722 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 RNA chain called 5'-R(*AP*UP*CP*GP*AP*GP*AP*GP*GP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	10	Total	C	N	O	P	0	0	0
			216	98	45	64	9			

- Molecule 2 is a DNA chain called 28-MER DNA template strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	28	Total	C	N	O	P	0	0	0
			564	270	102	165	27			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	14	Total	C	N	O	P	0	0	0
			284	137	49	85	13			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	1411	Total	C	N	O	S	0	0	0
			11098	6989	1944	2104	61			

- Molecule 5 is a protein called DNA-directed RNA polymerase II 140 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	1143	Total	C	N	O	S	0	0	0
			9092	5753	1595	1688	56			

- Molecule 6 is a protein called DNA-directed RNA polymerase II 45 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	266	Total	C	N	O	S	0	0	0
			2095	1317	348	417	13			

- Molecule 7 is a protein called DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	E	213	Total	C	N	O	S	0	0	0
			1744	1107	308	318	11			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	F	86	Total	C	N	O	S	0	0	0
			697	445	118	131	3			

- Molecule 9 is a protein called DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	H	134	Total	C	N	O	S	0	0	0
			1076	678	181	212	5			

- Molecule 10 is a protein called DNA-directed RNA polymerase II subunit 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	I	119	Total	C	N	O	S	0	0	0
			971	596	179	186	10			

- Molecule 11 is a protein called DNA-directed RNA polymerases I/II/III subunit 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 12 is a protein called DNA-directed RNA polymerase II 13.6 kDa polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	K	114	Total	C	N	O	S	0	0	0
			919	590	156	171	2			

- Molecule 13 is a protein called DNA-directed RNA polymerases I, II, and III 7.7 kDa polypep-

tide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	L	46	Total	C	N	O	S	0	0	0
			363	224	72	63	4			

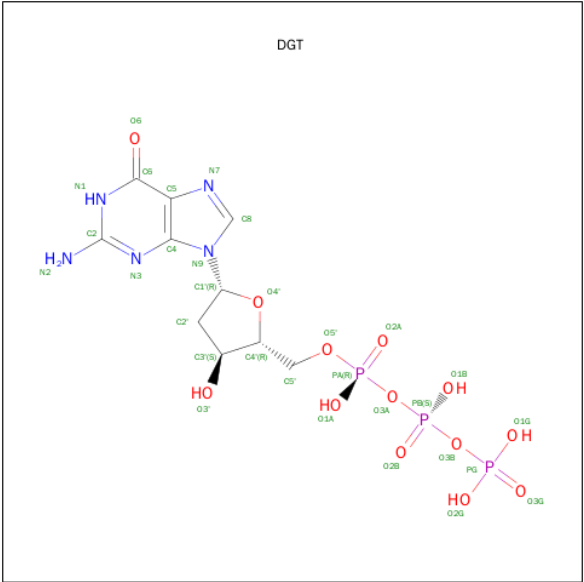
- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	J	1	Total	Zn	0	0
			1	1		
14	B	1	Total	Zn	0	0
			1	1		
14	I	2	Total	Zn	0	0
			2	2		
14	C	1	Total	Zn	0	0
			1	1		
14	A	2	Total	Zn	0	0
			2	2		
14	L	1	Total	Zn	0	0
			1	1		

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total	Mg	0	0
			1	1		

- Molecule 16 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
16	B	1	62	20	10	26	6	0	1

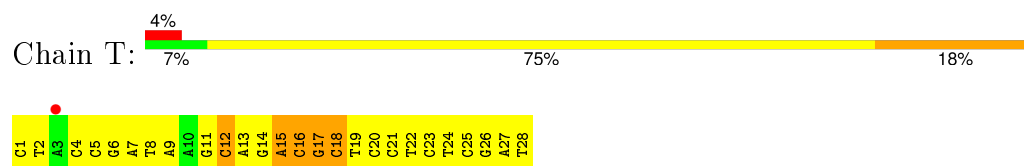
3 Residue-property plots

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

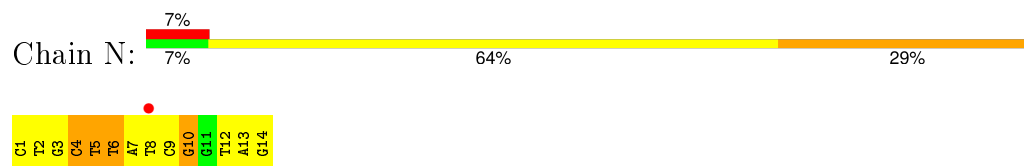
- Molecule 1: 5'-R(*AP*UP*CP*GP*AP*GP*AP*GP*GP*A)-3'



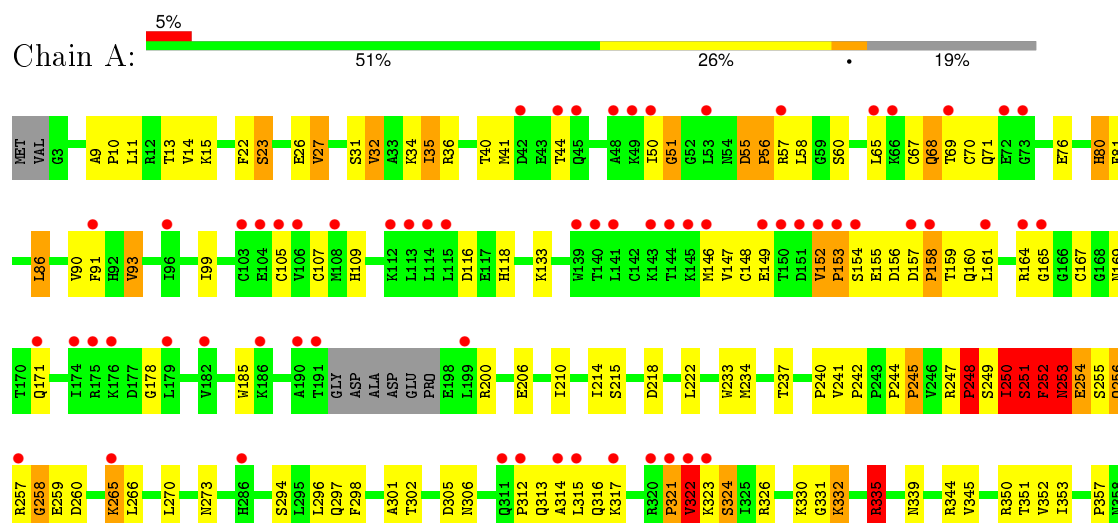
- Molecule 2: 28-MER DNA template strand



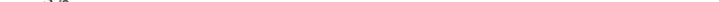
- Molecule 3: 5'-D(*CP*TP*GP*CP*TP*TP*AP*TP*CP*GP*GP*TP*AP*G)-3'



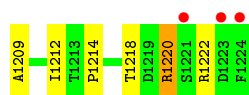
- Molecule 4: DNA-directed RNA polymerase II largest subunit



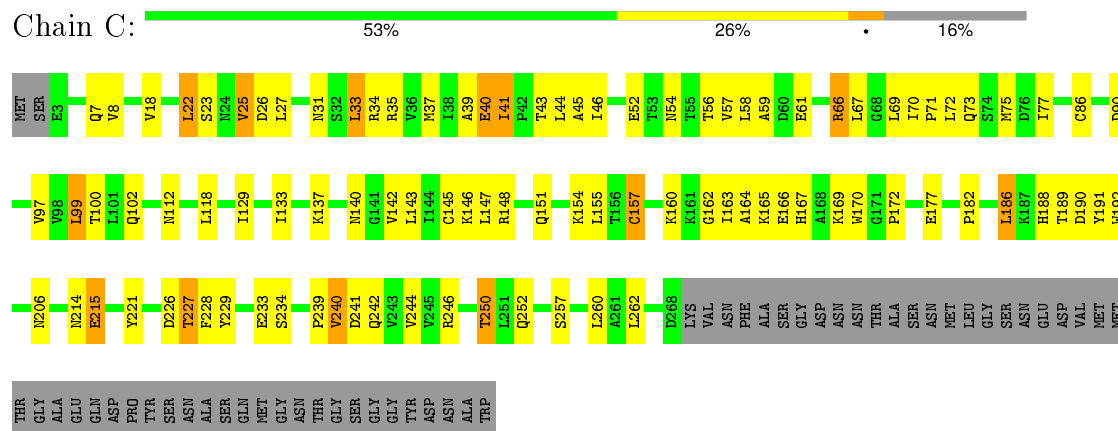


Chain B:  3% 52% 34% 6% • 7%

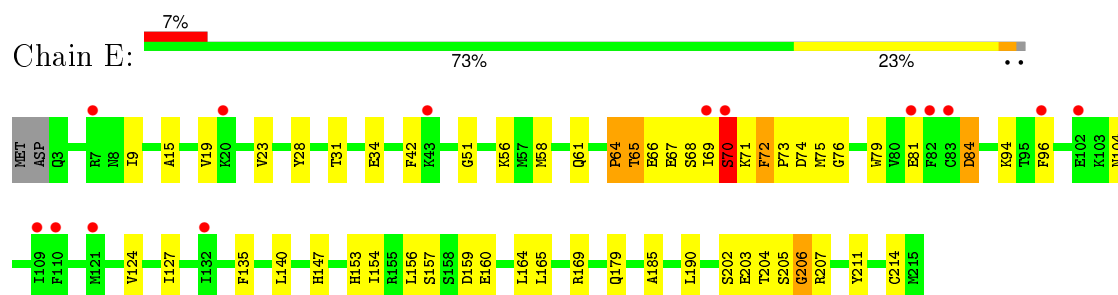




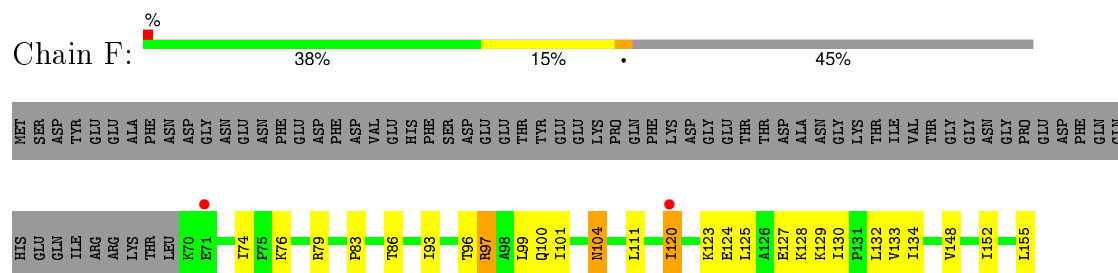
- Molecule 6: DNA-directed RNA polymerase II 45 kDa polypeptide



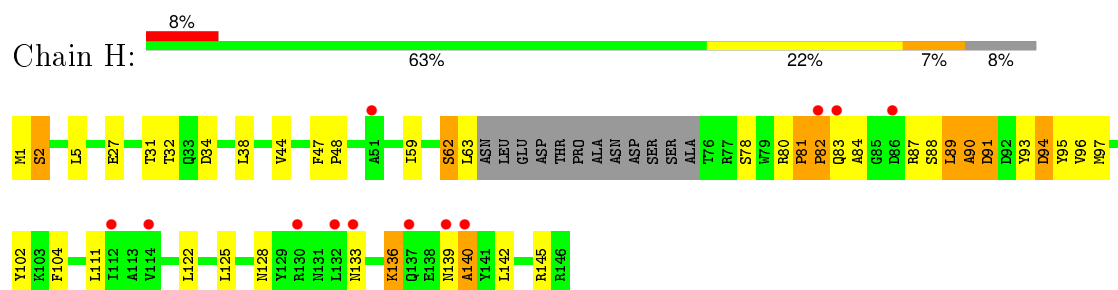
- Molecule 7: DNA-directed RNA polymerases I, II, and III 27 kDa polypeptide



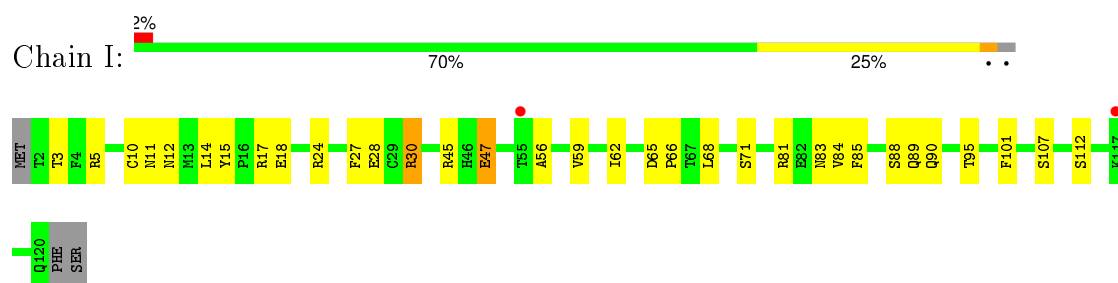
- Molecule 8: DNA-directed RNA polymerases I, II, and III 23 kDa polypeptide



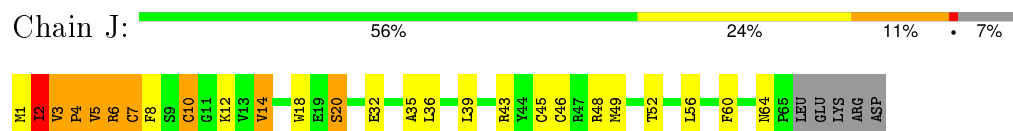
- Molecule 9: DNA-directed RNA polymerases I, II, and III 14.5 kDa polypeptide



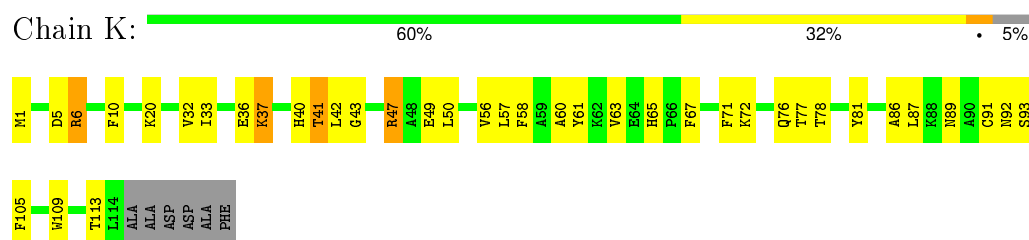
- Molecule 10: DNA-directed RNA polymerase II subunit 9



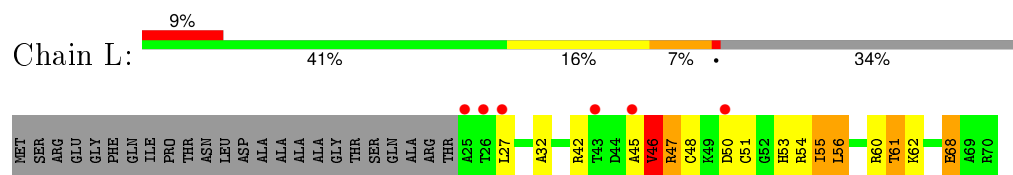
- Molecule 11: DNA-directed RNA polymerases I/II/III subunit 10



- Molecule 12: DNA-directed RNA polymerase II 13.6 kDa polypeptide



- Molecule 13: DNA-directed RNA polymerases I, II, and III 7.7 kDa polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	168.68Å 223.52Å 193.94Å 90.00° 100.54° 90.00°	Depositor
Resolution (Å)	50.00 – 3.41 49.77 – 3.41	Depositor EDS
% Data completeness (in resolution range)	98.0 (50.00-3.41) 98.0 (49.77-3.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.266 , 0.316 0.257 , 0.300	Depositor DCC
R_{free} test set	4732 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	92.7	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 72.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 94165 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	29722	wwPDB-VP
Average B, all atoms (Å ²)	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	R	1.15	0/243	1.89	10/378 (2.6%)
2	T	0.87	0/631	1.67	12/970 (1.2%)
3	N	0.81	0/317	1.53	9/488 (1.8%)
4	A	0.65	3/11294 (0.0%)	0.74	3/15270 (0.0%)
5	B	0.80	4/9268 (0.0%)	0.87	9/12496 (0.1%)
6	C	0.74	1/2133 (0.0%)	0.79	1/2891 (0.0%)
7	E	0.51	0/1780	0.64	0/2395
8	F	0.55	0/709	0.69	0/956
9	H	0.51	0/1094	0.66	0/1480
10	I	0.60	0/989	0.66	0/1331
11	J	0.85	1/541 (0.2%)	0.91	0/727
12	K	0.72	1/937 (0.1%)	0.72	0/1265
13	L	0.81	2/365 (0.5%)	0.91	0/485
All	All	0.71	12/30301 (0.0%)	0.84	44/41132 (0.1%)

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
4	A	0	7
5	B	0	11
7	E	0	1
11	J	0	2
All	All	0	21

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	J	10	CYS	CB-SG	7.21	1.94	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	86	CYS	CB-SG	-6.58	1.71	1.82
5	B	302	CYS	CB-SG	-6.13	1.71	1.82
12	K	91	CYS	CB-SG	-6.02	1.72	1.82
5	B	147	LEU	C-O	5.98	1.34	1.23

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	18	DC	O4'-C4'-C3'	-16.51	96.09	106.00
2	T	28	DT	C1'-O4'-C4'	-12.85	97.25	110.10
2	T	18	DC	C4'-C3'-C2'	-12.19	92.13	103.10
1	R	9	G	C5'-C4'-C3'	-9.98	100.04	116.00
2	T	18	DC	C1'-O4'-C4'	-8.74	101.36	110.10

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	248	PRO	Peptide
4	A	250	ILE	Peptide
4	A	251	SER	Peptide
4	A	252	PHE	Peptide
4	A	254	GLU	Peptide

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	R	216	0	109	13	0
2	T	564	0	316	88	0
3	N	284	0	161	19	0
4	A	11098	0	11174	428	0
5	B	9092	0	9135	504	0
6	C	2095	0	2051	95	0
7	E	1744	0	1772	46	0
8	F	697	0	720	19	0
9	H	1076	0	1052	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	I	971	0	928	16	0
11	J	532	0	542	48	0
12	K	919	0	929	37	0
13	L	363	0	388	6	0
14	A	2	0	0	0	0
14	B	1	0	0	0	0
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	0	0
14	L	1	0	0	0	0
15	A	1	0	0	0	0
16	B	62	0	24	2	0
All	All	29722	0	29301	1225	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 21.

The worst 5 of 1225 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:B:69:LEU:HG	5:B:70:ILE:CG2	1.32	1.55
2:T:19:DT:H2'	2:T:20:DC:C6	1.41	1.51
5:B:142:VAL:CG1	5:B:144:GLY:HA3	1.43	1.45
5:B:142:VAL:HG13	5:B:144:GLY:CA	1.57	1.34
5:B:69:LEU:CA	5:B:70:ILE:HB	1.58	1.28

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	
4	A	1401/1733 (81%)	1186 (85%)	160 (11%)	55 (4%)	4	33
5	B	1129/1224 (92%)	938 (83%)	133 (12%)	58 (5%)	2	25
6	C	264/318 (83%)	226 (86%)	33 (12%)	5 (2%)	10	50
7	E	211/215 (98%)	176 (83%)	29 (14%)	6 (3%)	6	42
8	F	84/155 (54%)	74 (88%)	7 (8%)	3 (4%)	4	36
9	H	130/146 (89%)	104 (80%)	21 (16%)	5 (4%)	4	34
10	I	117/122 (96%)	95 (81%)	19 (16%)	3 (3%)	7	43
11	J	63/70 (90%)	55 (87%)	4 (6%)	4 (6%)	2	19
12	K	112/120 (93%)	102 (91%)	8 (7%)	2 (2%)	11	51
13	L	44/70 (63%)	30 (68%)	7 (16%)	7 (16%)	0	2
All	All	3555/4173 (85%)	2986 (84%)	421 (12%)	148 (4%)	3	31

5 of 148 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	50	ILE
4	A	55	ASP
4	A	56	PRO
4	A	250	ILE
4	A	312	PRO

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	
4	A	1233/1520 (81%)	1121 (91%)	112 (9%)	12	45
5	B	991/1061 (93%)	871 (88%)	120 (12%)	6	29
6	C	234/274 (85%)	214 (92%)	20 (8%)	13	49
7	E	195/197 (99%)	185 (95%)	10 (5%)	29	69
8	F	76/137 (56%)	70 (92%)	6 (8%)	15	52
9	H	118/128 (92%)	105 (89%)	13 (11%)	8	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	I	113/116 (97%)	101 (89%)	12 (11%)	8	37
11	J	60/65 (92%)	53 (88%)	7 (12%)	7	31
12	K	99/102 (97%)	86 (87%)	13 (13%)	5	26
13	L	40/57 (70%)	32 (80%)	8 (20%)	1	7
All	All	3159/3657 (86%)	2838 (90%)	321 (10%)	9	39

5 of 321 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	384	ARG
5	B	658	ILE
11	J	20	SER
5	B	412	LEU
5	B	484	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
5	B	366	GLN
5	B	657	HIS
9	H	139	ASN
5	B	415	GLN
5	B	515	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	R	9/10 (90%)	5 (55%)	1 (11%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	R	2	U
1	R	3	C
1	R	7	A
1	R	8	G
1	R	9	G

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	R	1	A

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 11 ligands modelled in this entry, 9 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	$\# Z > 2$
16	DGT	B	1308[A]	-	25,33,33	1.14	2 (8%)	35,52,52	1.76	8 (22%)
16	DGT	B	1308[B]	-	25,33,33	1.08	2 (8%)	35,52,52	1.73	6 (17%)

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
16	DGT	B	1308[A]	-	-	0/18/34/34	0/3/3/3
16	DGT	B	1308[B]	-	-	0/18/34/34	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	B	1308[B]	DGT	C5-C4	3.12	1.47	1.40
16	B	1308[A]	DGT	C5-C4	3.20	1.47	1.40
16	B	1308[B]	DGT	C6-C5	3.58	1.48	1.41
16	B	1308[A]	DGT	C6-C5	3.78	1.48	1.41

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	B	1308[B]	DGT	C6-C5-C4	-4.07	116.03	120.90
16	B	1308[B]	DGT	C5-C6-N1	-3.94	118.21	123.59
16	B	1308[A]	DGT	C6-C5-C4	-3.93	116.20	120.90
16	B	1308[A]	DGT	C5-C6-N1	-3.89	118.28	123.59
16	B	1308[A]	DGT	N3-C2-N1	-3.28	122.45	127.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	B	1308[A]	DGT	2	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	R	10/10 (100%)	0.04	1 (10%) 9 10	72, 93, 202, 234	0
2	T	28/28 (100%)	0.49	1 (3%) 46 41	118, 195, 427, 447	0
3	N	14/14 (100%)	0.48	1 (7%) 19 18	270, 338, 424, 426	0
4	A	1411/1733 (81%)	0.29	80 (5%) 27 24	56, 105, 206, 247	0
5	B	1143/1224 (93%)	0.16	41 (3%) 46 41	27, 88, 156, 185	0
6	C	266/318 (83%)	-0.11	0 100 100	59, 91, 135, 151	0
7	E	213/215 (99%)	0.38	14 (6%) 22 19	96, 142, 228, 233	0
8	F	86/155 (55%)	0.02	2 (2%) 64 58	83, 117, 137, 141	0
9	H	134/146 (91%)	0.70	12 (8%) 12 12	35, 140, 171, 175	0
10	I	119/122 (97%)	0.06	2 (1%) 73 67	85, 121, 156, 165	0
11	J	65/70 (92%)	-0.17	0 100 100	60, 82, 110, 117	0
12	K	114/120 (95%)	0.04	0 100 100	77, 102, 119, 122	0
13	L	46/70 (65%)	1.04	6 (13%) 5 5	87, 165, 176, 179	0
All	All	3649/4225 (86%)	0.22	160 (4%) 38 33	27, 103, 198, 447	0

The worst 5 of 160 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	L	26	THR	9.4
4	A	69	THR	8.2
4	A	152	VAL	7.9
4	A	144	THR	6.9
4	A	150	THR	6.5

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 [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(Å ²)	Q<0.9
16	DGT	B	1308[A]	31/31	0.87	0.41	7.73	126,132,152,153	31
16	DGT	B	1308[B]	31/31	0.87	0.41	6.43	80,86,113,113	31
14	ZN	I	203	1/1	0.97	0.15	-0.31	131,131,131,131	0
14	ZN	B	1307	1/1	0.97	0.13	-0.51	143,143,143,143	0
14	ZN	C	319	1/1	0.99	0.10	-0.86	95,95,95,95	0
14	ZN	I	204	1/1	0.99	0.12	-0.93	106,106,106,106	0
14	ZN	A	1735	1/1	0.94	0.10	-1.70	139,139,139,139	0
14	ZN	A	1734	1/1	0.94	0.04	-2.48	226,226,226,226	0
14	ZN	L	105	1/1	0.98	0.07	-2.91	190,190,190,190	0
14	ZN	J	101	1/1	0.99	0.13	-3.65	105,105,105,105	0
15	MG	A	2001	1/1	0.98	0.40	-	116,116,116,116	0

6.5 Other polymers [i](#)

There are no such residues in this entry.