



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 05:39 PM UTC

PDB ID : 3S17 / pdb_00003s17
Title : RNA Polymerase II Initiation Complex with a 9-nt RNA
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Deposited on : 2011-05-14
Resolution : 3.20 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

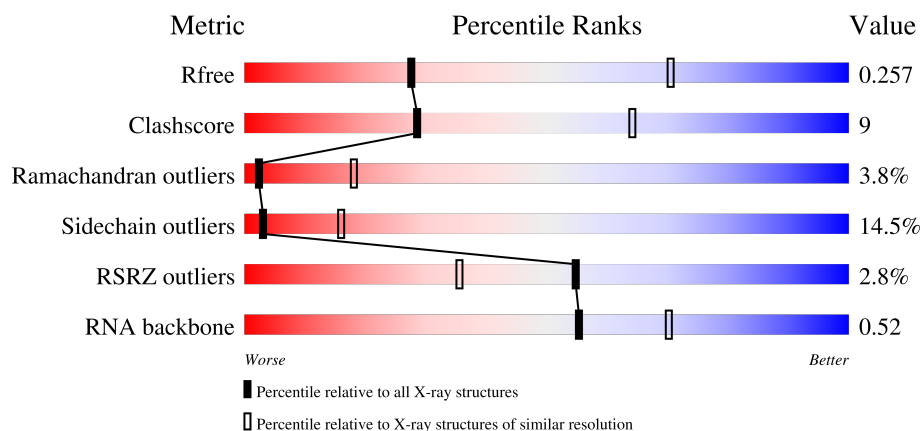
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)
RNA backbone	3983	1222 (3.50-2.90)

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	1733	2% 54% 21% 5% 19%
2	B	1224	3% 59% 25% 6% 9%
3	C	318	54% 25% 5% 16%
4	E	215	% 73% 24% .

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Mol	Chain	Length	Quality of chain
5	F	155	
6	H	146	
7	I	122	
8	J	70	
9	K	120	
10	L	70	
11	R	9	
12	T	29	

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 28757 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 II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1405	Total	C	N	O	S	0	0	0
			11043	6965	1936	2081	61			

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1114	Total	C	N	O	S	0	0	0
			8861	5610	1549	1647	55			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

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

- Molecule 4 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	214	Total	C	N	O	S	0	0	0
			1752	1111	309	321	11			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	85	Total	C	N	O	S	0	0	0
			688	439	116	130	3			

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	133	Total	C	N	O	S	0	0	0
			1068	673	180	211	4			

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB9.

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

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

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

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB11.

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

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

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

- Molecule 11 is a RNA chain called RNA (5'-R(*AP*UP*CP*GP*AP*GP*AP*GP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	R	9	Total	C	N	O	P	0	0	0
			195	88	40	59	8			

- Molecule 12 is a DNA chain called DNA (5'-D(*CP*TP*AP*CP*CP*GP*AP*TP*AP*AP*GP*CP*AP*GP*AP*CP*GP*AP*TP*CP*CP*TP*CP*TP*CP*GP*AP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	T	13	Total	C	N	O	P	0	0	0
			261	125	43	80	13			

- Molecule 13 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	2	Total	Zn	0	0
			2	2		

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

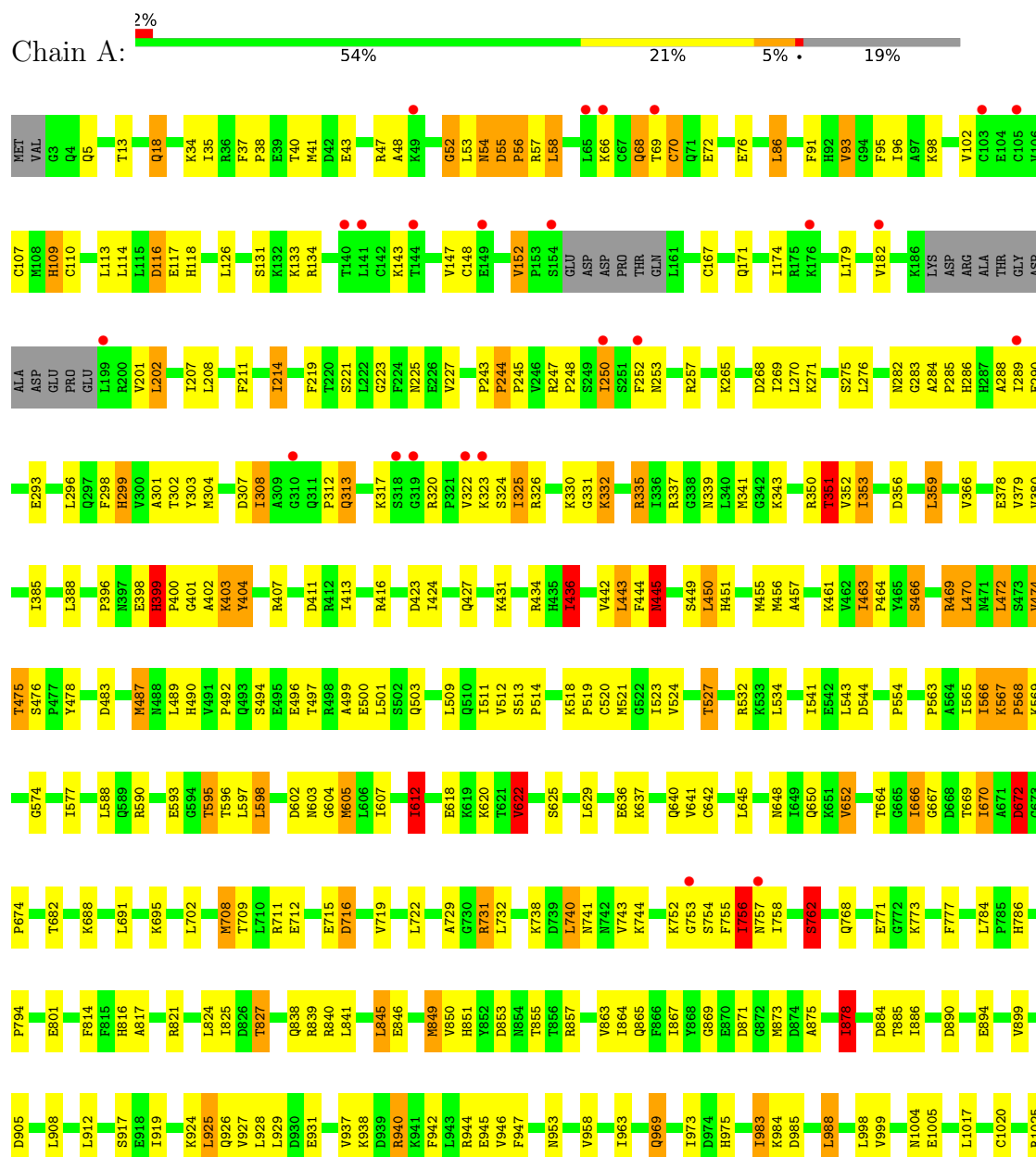
- Molecule 14 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

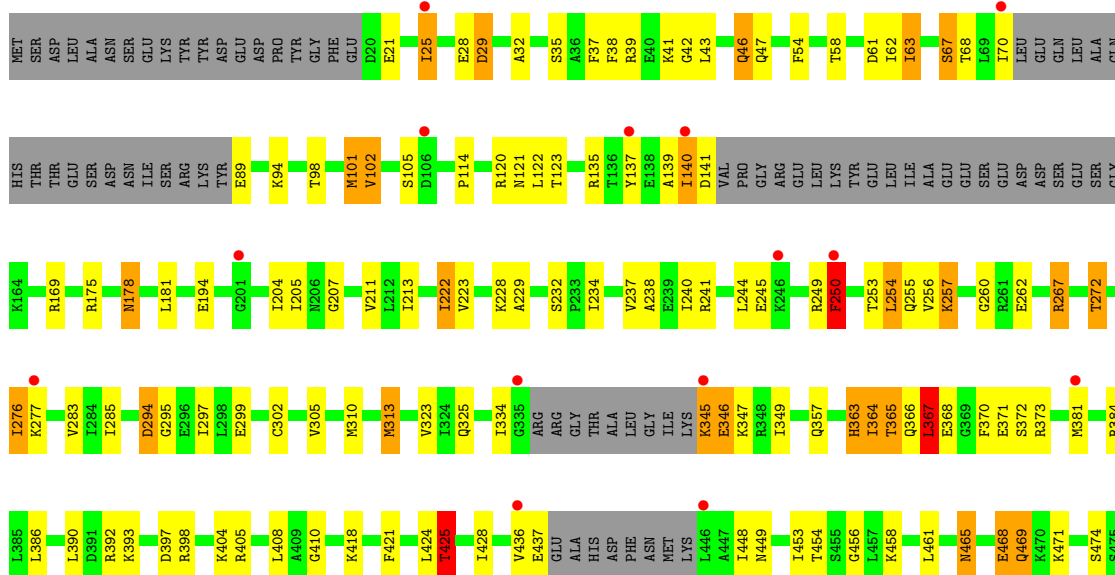
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	1	Total 1	Mg 1	0	0

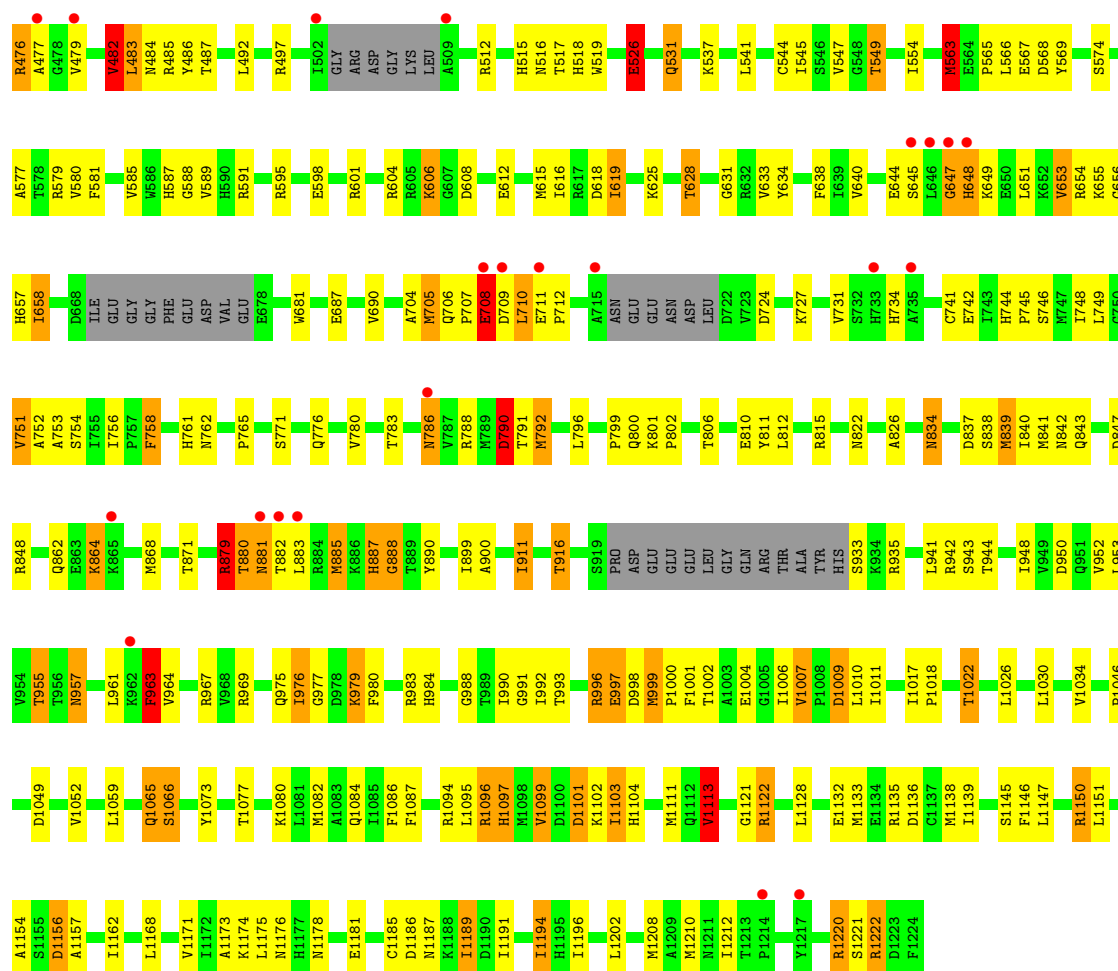
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 II subunit RPB1

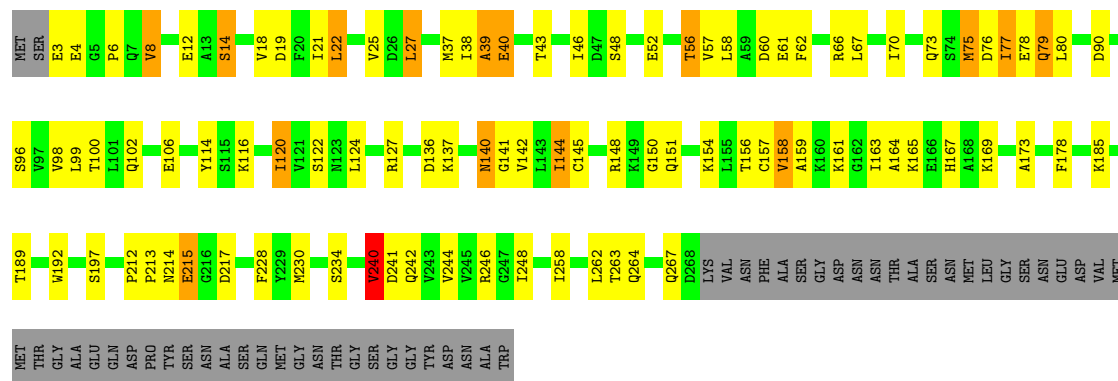






• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

Chain C: 54% 25% 5% 16%

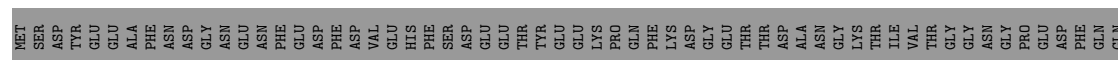
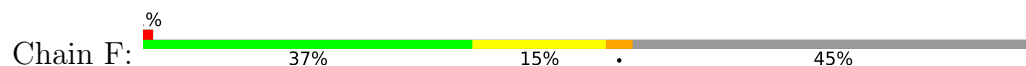


• Molecule 4: DNA-directed RNA polymerases I, II, and III subunit RPABC1

Chain E: 73% 24% 3%



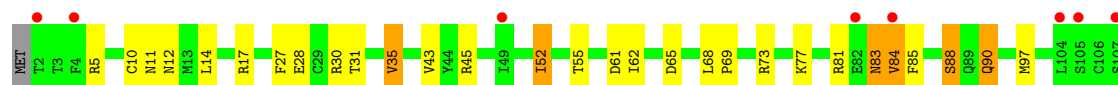
- Molecule 5: DNA-directed RNA polymerases I, II, and III subunit RPABC2



- Molecule 6: DNA-directed RNA polymerases I, II, and III subunit RPABC3



- Molecule 7: DNA-directed RNA polymerase II subunit RPB9

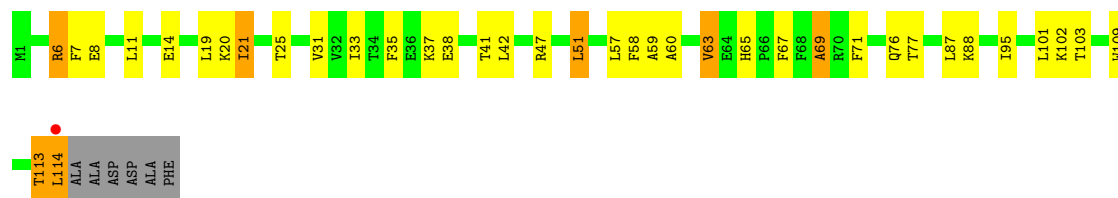


- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC5

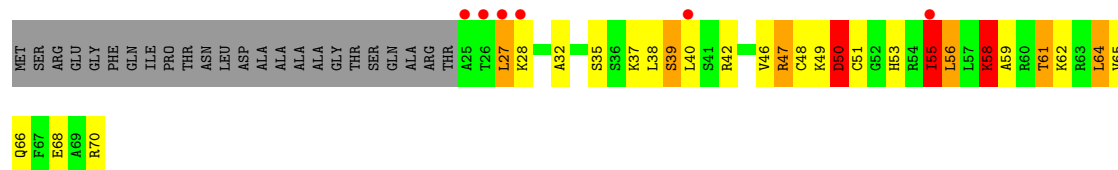
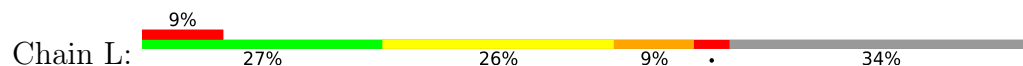


- Molecule 9: DNA-directed RNA polymerase II subunit RPB11





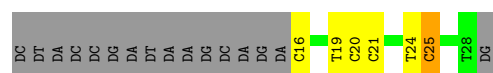
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 11: RNA (5'-R(*AP*UP*CP*GP*AP*GP*AP*GP*G)-3')



- Molecule 12: DNA (5'-D(*CP*TP*AP*CP*CP*GP*AP*TP*AP*AP*GP*CP*AP*GP*AP*C
P*GP*AP*TP*CP*CP*TP*CP*TP*CP*GP*AP*TP*G)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	159.97Å 220.90Å 192.03Å 90.00° 98.16° 90.00°	Depositor
Resolution (Å)	43.65 – 3.20 43.65 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (43.65-3.20) 99.9 (43.65-3.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 3.19Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.8.0, BUSTER 2.8.0	Depositor
R, R_{free}	0.188 , 0.236 0.208 , 0.257	Depositor DCC
R_{free} test set	5511 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	73.9	Xtriage
Anisotropy	0.836	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 88.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	28757	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% 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: MG, 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	0.82	3/11241 (0.0%)	1.47	79/15199 (0.5%)
2	B	0.85	3/9033 (0.0%)	1.45	69/12181 (0.6%)
3	C	0.80	1/2133 (0.0%)	1.43	18/2891 (0.6%)
4	E	0.78	0/1788	1.42	12/2406 (0.5%)
5	F	0.80	0/700	1.37	8/945 (0.8%)
6	H	0.80	0/1086	1.36	15/1470 (1.0%)
7	I	0.82	0/989	1.38	5/1331 (0.4%)
8	J	0.83	0/541	1.57	10/727 (1.4%)
9	K	0.75	0/937	1.40	6/1265 (0.5%)
10	L	0.87	0/365	1.59	7/485 (1.4%)
11	R	0.61	0/219	1.17	2/341 (0.6%)
12	T	0.42	0/290	1.32	3/444 (0.7%)
All	All	0.82	7/29322 (0.0%)	1.45	234/39685 (0.6%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	758	PHE	CA-C	6.28	1.57	1.53
2	B	705	MET	SD-CE	-6.10	1.64	1.79
2	B	563	MET	SD-CE	-5.60	1.65	1.79
3	C	212	PRO	CA-C	5.58	1.54	1.51
1	A	605	MET	SD-CE	-5.50	1.65	1.79

The worst 5 of 234 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	647	GLY	CA-C-N	11.15	141.78	121.70
2	B	647	GLY	C-N-CA	11.15	141.78	121.70
3	C	39	ALA	N-CA-C	9.80	123.74	111.69
10	L	55	ILE	N-CA-C	9.78	120.55	111.45
1	A	116	ASP	CA-C-N	9.66	139.09	121.70

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	11043	0	11133	202	0
2	B	8861	0	8884	201	0
3	C	2095	0	2051	47	0
4	E	1752	0	1776	21	0
5	F	688	0	707	11	0
6	H	1068	0	1040	18	0
7	I	971	0	927	13	0
8	J	532	0	542	18	0
9	K	919	0	929	23	0
10	L	363	0	386	10	0
11	R	195	0	99	1	0
12	T	261	0	148	3	0
13	A	2	0	0	0	0
13	B	1	0	0	0	0
13	C	1	0	0	0	0
13	I	2	0	0	0	0
13	J	1	0	0	0	0
13	L	1	0	0	0	0
14	A	1	0	0	0	0
All	All	28757	0	28622	506	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 9.

The worst 5 of 506 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:567:LYS:HB2	1:A:568:PRO:HD2	1.44	1.00
4:E:77:SER:HB3	4:E:105:PHE:HA	1.53	0.89
1:A:1123:GLY:HA3	1:A:1124:HIS:HB2	1.52	0.89
2:B:519:TRP:HZ2	2:B:705:MET:HE1	1.39	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:783:THR:HG22	8:J:63:TYR:HE1	1.39	0.87

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	1395/1733 (80%)	1221 (88%)	131 (9%)	43 (3%)	3	22
2	B	1096/1224 (90%)	952 (87%)	91 (8%)	53 (5%)	2	14
3	C	264/318 (83%)	238 (90%)	22 (8%)	4 (2%)	8	37
4	E	212/215 (99%)	199 (94%)	8 (4%)	5 (2%)	4	28
5	F	83/155 (54%)	73 (88%)	7 (8%)	3 (4%)	2	19
6	H	129/146 (88%)	100 (78%)	16 (12%)	13 (10%)	0	2
7	I	117/122 (96%)	101 (86%)	14 (12%)	2 (2%)	7	35
8	J	63/70 (90%)	58 (92%)	3 (5%)	2 (3%)	3	21
9	K	112/120 (93%)	106 (95%)	6 (5%)	0	100	100
10	L	44/70 (63%)	27 (61%)	9 (20%)	8 (18%)	0	0
All	All	3515/4173 (84%)	3075 (88%)	307 (9%)	133 (4%)	2	18

5 of 133 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	40	THR
1	A	55	ASP
1	A	66	LYS
1	A	250	ILE
1	A	283	GLY

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	1225/1520 (81%)	1036 (85%)	189 (15%)	2	14
2	B	967/1061 (91%)	835 (86%)	132 (14%)	3	18
3	C	234/274 (85%)	203 (87%)	31 (13%)	4	19
4	E	196/197 (100%)	175 (89%)	21 (11%)	6	27
5	F	75/137 (55%)	66 (88%)	9 (12%)	5	23
6	H	117/128 (91%)	95 (81%)	22 (19%)	1	9
7	I	113/116 (97%)	97 (86%)	16 (14%)	3	17
8	J	60/65 (92%)	52 (87%)	8 (13%)	4	19
9	K	99/102 (97%)	84 (85%)	15 (15%)	3	14
10	L	40/57 (70%)	29 (72%)	11 (28%)	0	2
All	All	3126/3657 (86%)	2672 (86%)	454 (14%)	3	16

5 of 454 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	404	LYS
10	L	27	LEU
2	B	955	THR
9	K	77	THR
6	H	109	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	822	ASN
3	C	112	ASN
2	B	984	HIS
2	B	1161	HIS
3	C	167	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	R	8/9 (88%)	1 (12%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	R	10	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 9 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	1405/1733 (81%)	0.20	39 (2%)	55	35	52, 98, 181, 233	0
2	B	1114/1224 (91%)	0.21	36 (3%)	50	31	53, 88, 148, 200	0
3	C	266/318 (83%)	0.03	0	100	100	62, 86, 123, 171	0
4	E	214/215 (99%)	0.21	2 (0%)	81	64	72, 128, 183, 201	0
5	F	85/155 (54%)	-0.04	1 (1%)	76	58	73, 100, 144, 162	0
6	H	133/146 (91%)	0.43	8 (6%)	27	17	94, 138, 168, 181	0
7	I	119/122 (97%)	0.27	8 (6%)	24	15	68, 101, 140, 152	0
8	J	65/70 (92%)	-0.04	0	100	100	57, 77, 111, 127	0
9	K	114/120 (95%)	-0.07	1 (0%)	81	64	61, 89, 116, 131	0
10	L	46/70 (65%)	0.82	6 (13%)	7	6	80, 124, 153, 164	0
11	R	9/9 (100%)	-0.12	0	100	100	79, 103, 145, 148	0
12	T	13/29 (44%)	0.49	0	100	100	85, 110, 168, 175	0
All	All	3583/4211 (85%)	0.19	101 (2%)	55	35	52, 96, 167, 233	0

The worst 5 of 101 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	708	GLU	5.7
2	B	715	ALA	5.4
2	B	335	GLY	4.9
10	L	27	LEU	4.8
2	B	883	LEU	4.8

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
13	ZN	A	1734	1/1	0.92	0.07	230,230,230,230	0
14	MG	A	2001	1/1	0.98	0.03	45,45,45,45	0
13	ZN	B	1307	1/1	0.99	0.04	144,144,144,144	0
13	ZN	C	319	1/1	0.99	0.03	88,88,88,88	0
13	ZN	I	203	1/1	0.99	0.03	104,104,104,104	0
13	ZN	A	1735	1/1	0.99	0.06	128,128,128,128	0
13	ZN	J	101	1/1	1.00	0.03	71,71,71,71	0
13	ZN	L	105	1/1	1.00	0.02	117,117,117,117	0
13	ZN	I	204	1/1	1.00	0.02	78,78,78,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.