



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 08:14 am BST

PDB ID : 5TJG
Title : Thermus aquaticus delta1.1-sigmaA holoenzyme/downstream-fork promoter complex with an open clamp
Authors : Darst, S.A.; Bae, B.
Deposited on : 2016-10-04
Resolution : 2.60 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

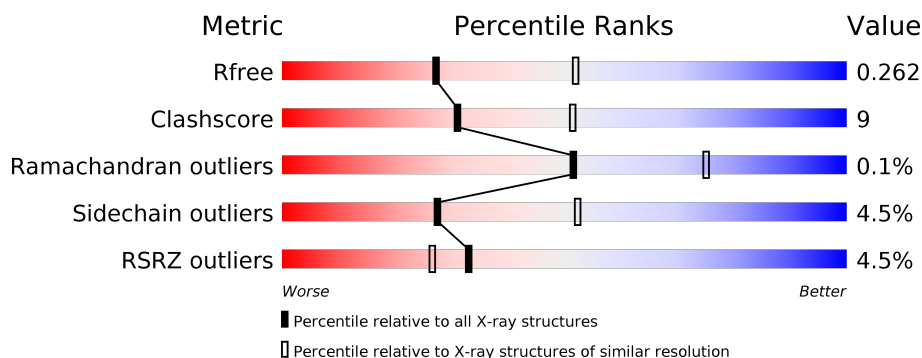
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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	314	<div> <div>5%</div> <div> <div>53%</div> <div>19%</div> <div>28%</div> </div> </div>
1	B	314	<div> <div>5%</div> <div> <div>54%</div> <div>17%</div> <div>28%</div> </div> </div>
2	C	1119	<div> <div>4%</div> <div> <div>75%</div> <div>23%</div> </div> </div>
3	D	1524	<div> <div>4%</div> <div> <div>73%</div> <div>23%</div> </div> </div>
4	E	99	<div> <div>7%</div> <div> <div>68%</div> <div>20%</div> <div>10%</div> </div> </div>
5	F	347	<div> <div>7%</div> <div> <div>77%</div> <div>18%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
6	G	31	 A horizontal bar chart showing the quality of chain G. The bar is divided into three segments: a green segment on the left labeled '19%', a yellow segment in the middle labeled '13%', and a grey segment on the right labeled '68%'. The segments are separated by thin white lines.

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 27767 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	227	Total	C	N	O	S	0	0	0
			1777	1134	309	331	3			
1	B	227	Total	C	N	O	S	0	0	0
			1777	1134	309	331	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	ARG	THR	conflict	UNP Q9KWU8
A	18	ARG	ASP	conflict	UNP Q9KWU8
B	14	ARG	THR	conflict	UNP Q9KWU8
B	18	ARG	ASP	conflict	UNP Q9KWU8

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	1112	Total	C	N	O	S	0	0	0
			8739	5531	1553	1632	23			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	1475	Total	C	N	O	S	0	0	0
			11657	7376	2066	2177	38			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	666	ILE	PHE	conflict	UNP Q9KWU6

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	89	Total	C	N	O	S	0	0	0
			730	464	129	133	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	334	Total	C	N	O	S	0	0	0
			2700	1702	485	509	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	10	Total	C	N	O	P	0	0	0
			207	100	41	57	9			

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

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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	18	Total	O	0	0
			18	18		
9	B	10	Total	O	0	0
			10	10		
9	C	48	Total	O	0	0
			48	48		
9	D	77	Total	O	0	0
			77	77		
9	E	7	Total	O	0	0
			7	7		
9	F	14	Total	O	0	0
			14	14		

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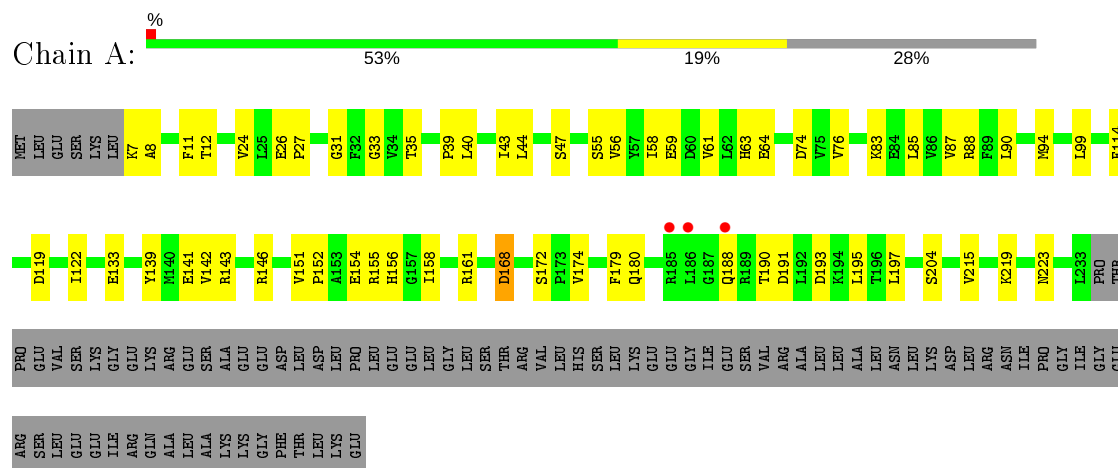
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	G	3	Total	O	0	0
			3	3		

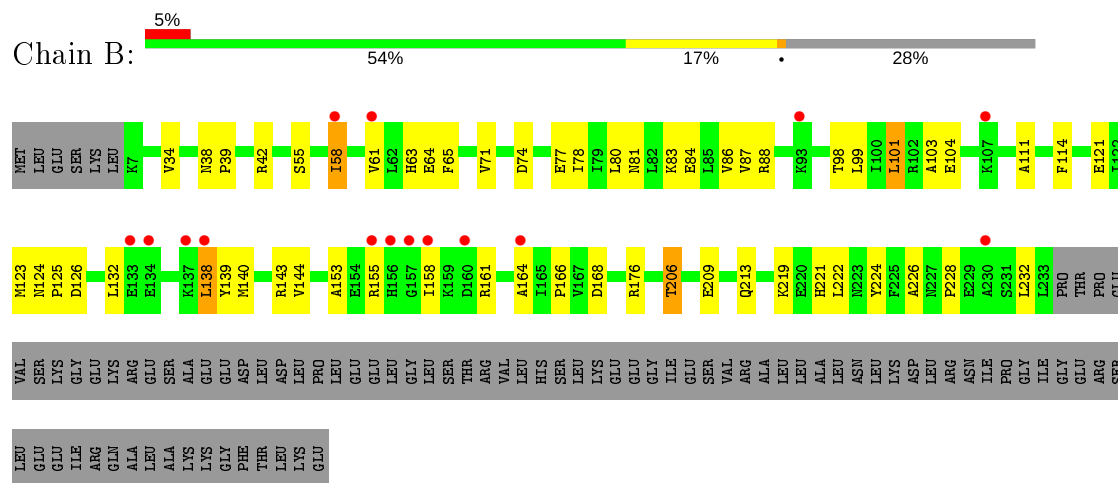
3 Residue-property plots [i](#)

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.

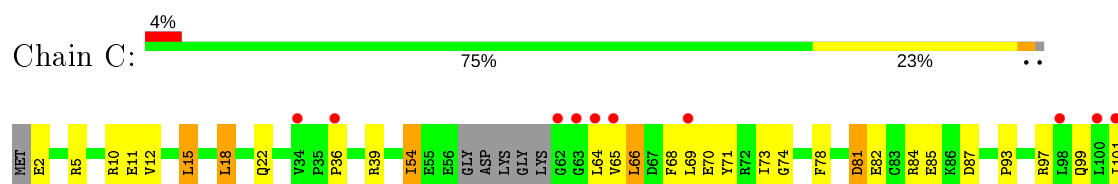
- Molecule 1: DNA-directed RNA polymerase subunit alpha

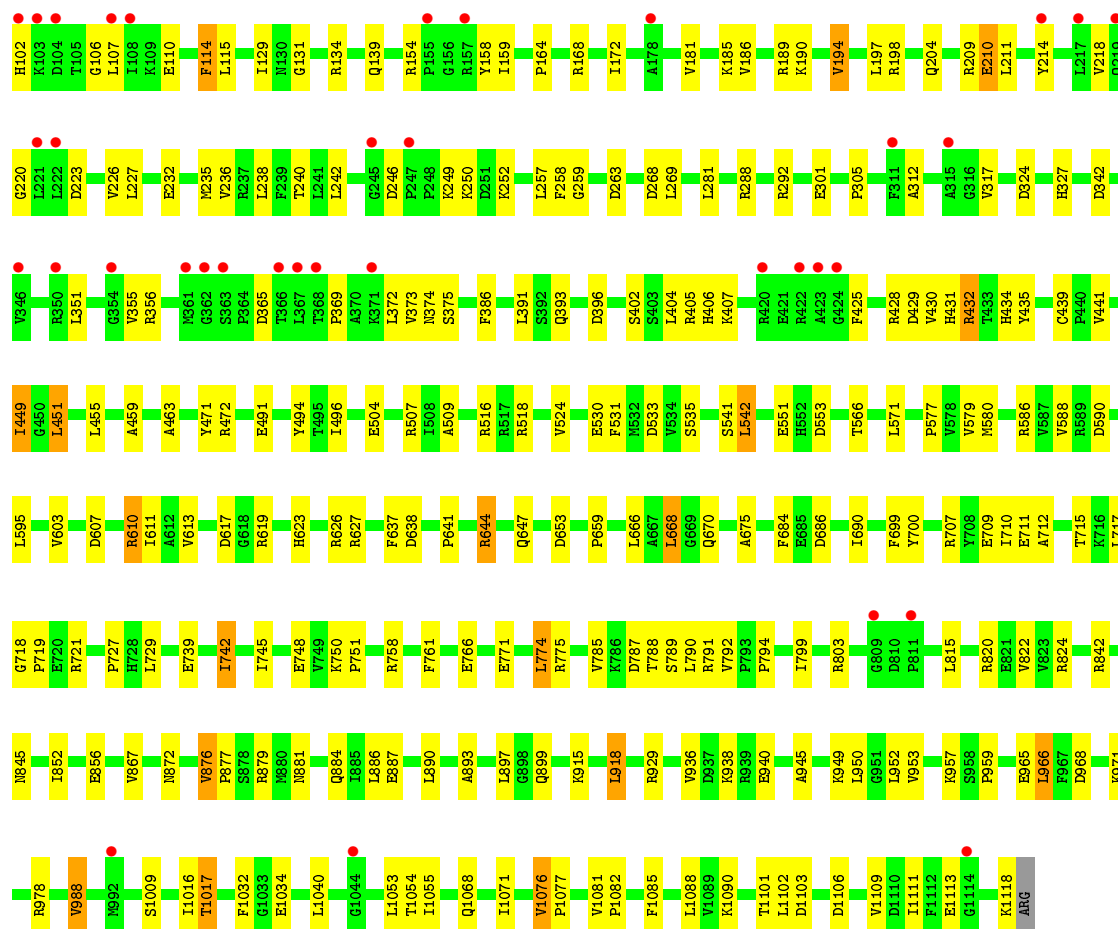


- Molecule 1: DNA-directed RNA polymerase subunit alpha

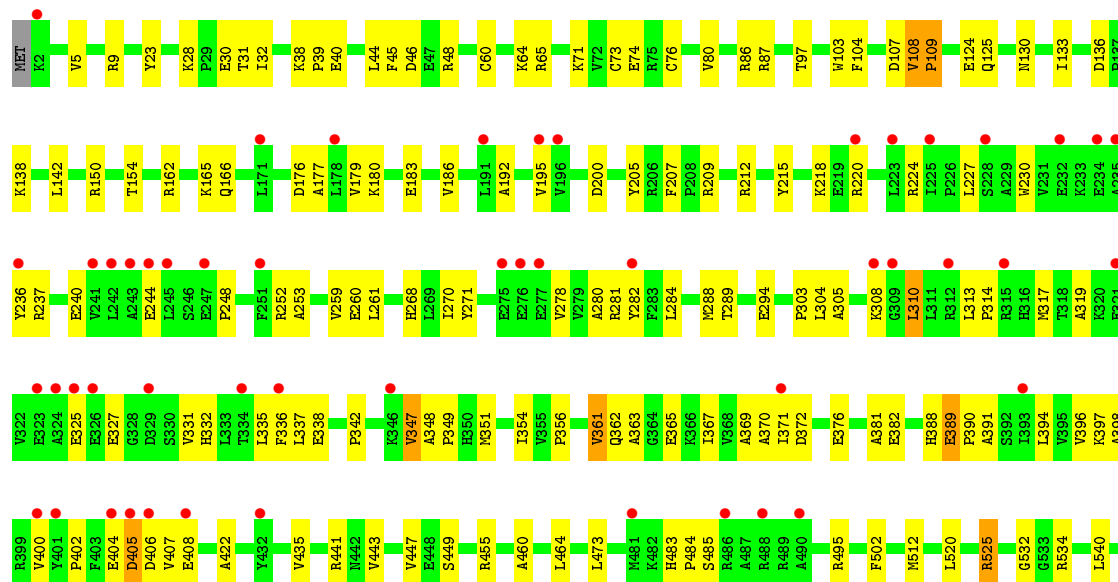
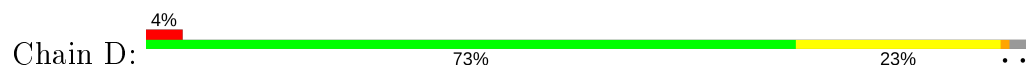


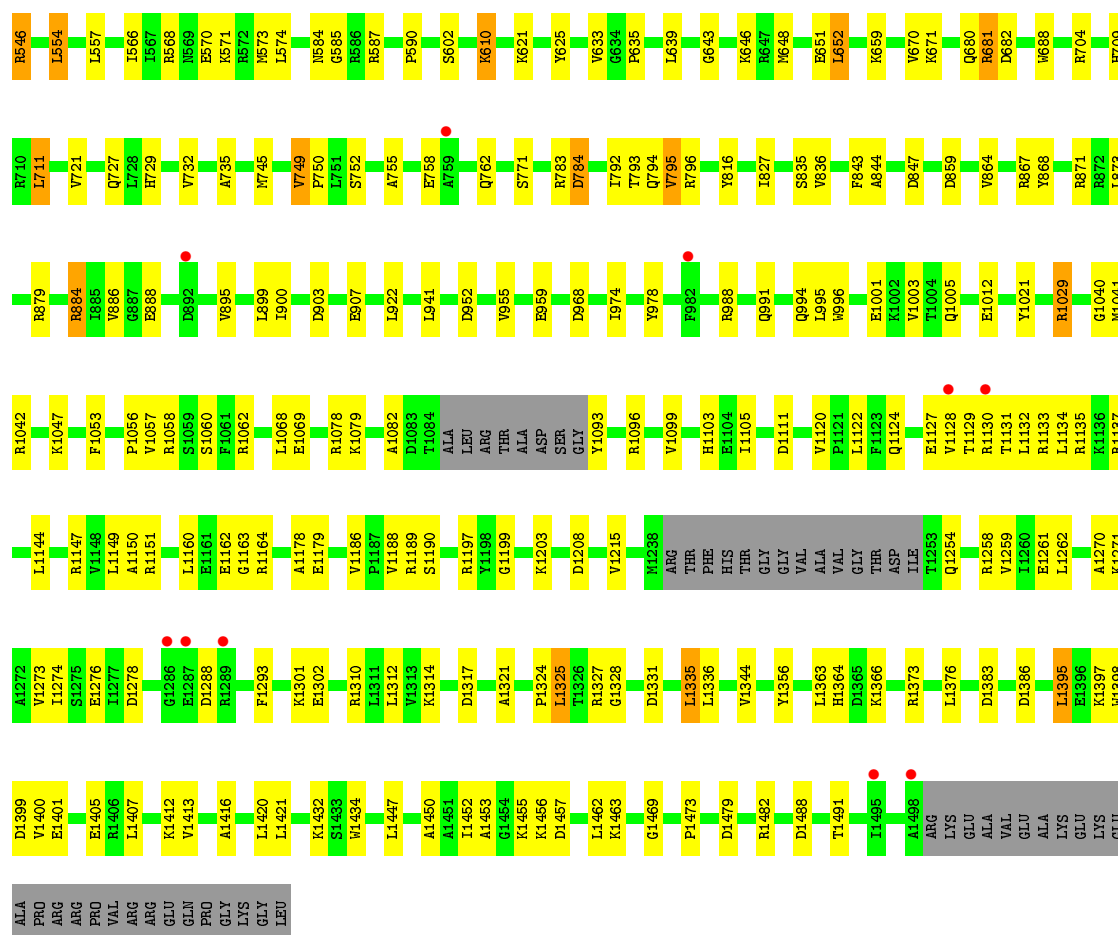
- Molecule 2: DNA-directed RNA polymerase subunit beta





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

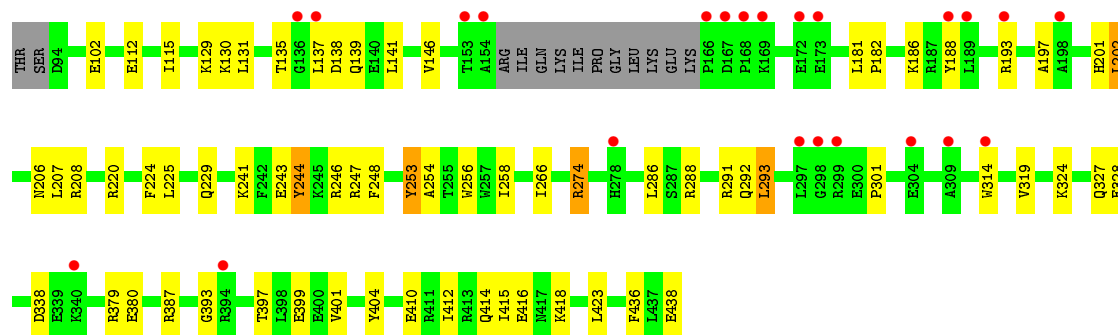
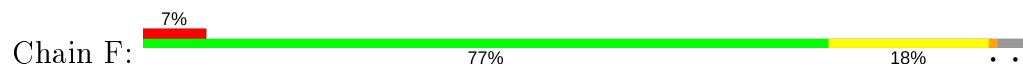




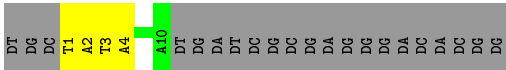
- Molecule 4: DNA-directed RNA polymerase subunit omega



- Molecule 5: RNA polymerase sigma factor SigA



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	104.10Å 111.42Å 143.18Å 104.12° 99.66° 109.43°	Depositor
Resolution (Å)	38.63 – 2.60 38.63 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.4 (38.63-2.60) 84.7 (38.63-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.90 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.10.1-2155-000	Depositor
R, R_{free}	0.224 , 0.262 0.224 , 0.262	Depositor DCC
R_{free} test set	8519 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	52.7	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 54.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	27767	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.26	0/1811	0.47	0/2462
1	B	0.26	0/1811	0.47	0/2462
2	C	0.25	0/8905	0.45	0/12040
3	D	0.25	0/11857	0.45	0/16021
4	E	0.23	0/743	0.44	1/999 (0.1%)
5	F	0.23	0/2740	0.41	0/3683
6	G	0.58	0/233	0.94	0/359
All	All	0.25	0/28100	0.45	1/38026 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	51	LEU	CA-CB-CG	5.18	127.22	115.30

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	1777	0	1814	42	0
1	B	1777	0	1814	45	0
2	C	8739	0	8841	165	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	11657	0	11875	244	0
4	E	730	0	744	13	0
5	F	2700	0	2768	47	0
6	G	207	0	115	3	0
7	D	2	0	0	0	0
8	D	1	0	0	0	0
9	A	18	0	0	1	0
9	B	10	0	0	8	0
9	C	48	0	0	7	0
9	D	77	0	0	20	0
9	E	7	0	0	2	0
9	F	14	0	0	5	0
9	G	3	0	0	0	0
All	All	27767	0	27971	507	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 507 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)
3:D:124:GLU:OE2	3:D:587:ARG:NH2	2.06	0.88
3:D:260:GLU:HB3	3:D:271:TYR:HB2	1.57	0.84
3:D:1163:GLY:O	9:D:2102:HOH:O	1.96	0.82
3:D:1124:GLN:HG3	3:D:1135:ARG:HG2	1.61	0.81
3:D:1310:ARG:HG3	3:D:1327:ARG:HG3	1.62	0.81

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	225/314 (72%)	218 (97%)	7 (3%)	0	100	100
1	B	225/314 (72%)	210 (93%)	15 (7%)	0	100	100
2	C	1108/1119 (99%)	1065 (96%)	40 (4%)	3 (0%)	41	64
3	D	1469/1524 (96%)	1416 (96%)	51 (4%)	2 (0%)	51	75
4	E	87/99 (88%)	84 (97%)	3 (3%)	0	100	100
5	F	330/347 (95%)	324 (98%)	6 (2%)	0	100	100
All	All	3444/3717 (93%)	3317 (96%)	122 (4%)	5 (0%)	51	75

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	1128	VAL
3	D	109	PRO
2	C	876	VAL
2	C	164	PRO
2	C	727	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	
1	A	194/270 (72%)	189 (97%)	5 (3%)	46	72
1	B	194/270 (72%)	188 (97%)	6 (3%)	40	66
2	C	931/936 (100%)	873 (94%)	58 (6%)	18	37
3	D	1244/1281 (97%)	1194 (96%)	50 (4%)	31	57
4	E	79/88 (90%)	76 (96%)	3 (4%)	33	59
5	F	287/299 (96%)	276 (96%)	11 (4%)	33	59
All	All	2929/3144 (93%)	2796 (96%)	133 (4%)	27	52

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	966	LEU
3	D	227	LEU
5	F	137	LEU
2	C	988	VAL
2	C	1102	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	388	HIS
3	D	483	HIS
3	D	1364	HIS
3	D	130	ASN
3	D	1445	HIS

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](#)

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	227/314 (72%)	-0.24	3 (1%) 77 73	49, 70, 108, 133	0
1	B	227/314 (72%)	0.24	15 (6%) 18 13	60, 94, 142, 176	0
2	C	1112/1119 (99%)	0.10	46 (4%) 37 30	35, 77, 136, 170	0
3	D	1475/1524 (96%)	0.09	61 (4%) 37 30	36, 75, 136, 163	0
4	E	89/99 (89%)	0.19	7 (7%) 12 9	56, 85, 141, 147	0
5	F	334/347 (96%)	0.22	23 (6%) 16 12	49, 97, 145, 166	0
6	G	10/31 (32%)	-0.53	0 100 100	100, 109, 139, 151	0
All	All	3474/3748 (92%)	0.10	155 (4%) 33 26	35, 80, 137, 176	0

The worst 5 of 155 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	F	168	PRO	8.5
3	D	1495	ILE	7.7
2	C	64	LEU	7.4
2	C	100	LEU	7.2
1	B	155	ARG	7.1

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. 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
7	ZN	D	2002	1/1	0.67	0.36	216,216,216,216	0
7	ZN	D	2001	1/1	0.92	0.26	110,110,110,110	0
8	MG	D	2003	1/1	0.97	0.08	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.