



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 9, 2023 – 11:20 AM EDT

PDB ID : 8DF8
Title : Structure of M. kandleri topoisomerase V in complex with DNA. 40 base pair symmetric DNA complex
Authors : Osterman, A.; Mondragon, A.
Deposited on : 2022-06-21
Resolution : 2.92 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

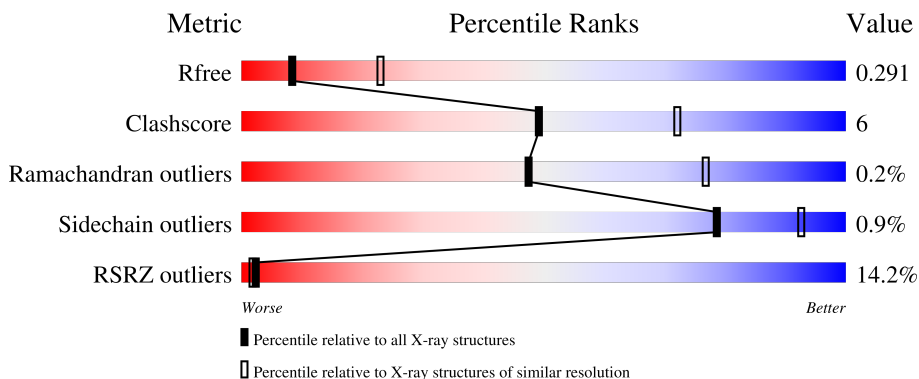
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.92 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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	854	
1	B	854	
2	U	42	
3	V	42	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 15241 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 Topoisomerase V.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	850	6807	4259	1222	1315	11	0	1	0
1	B	850	6807	4259	1222	1315	11	0	1	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	809	ALA	LYS	engineered mutation	UNP Q977W1
A	820	ALA	LYS	engineered mutation	UNP Q977W1
A	831	ALA	LYS	engineered mutation	UNP Q977W1
A	835	ALA	LYS	engineered mutation	UNP Q977W1
A	846	ALA	LYS	engineered mutation	UNP Q977W1
A	851	ALA	LYS	engineered mutation	UNP Q977W1
B	809	ALA	LYS	engineered mutation	UNP Q977W1
B	820	ALA	LYS	engineered mutation	UNP Q977W1
B	831	ALA	LYS	engineered mutation	UNP Q977W1
B	835	ALA	LYS	engineered mutation	UNP Q977W1
B	846	ALA	LYS	engineered mutation	UNP Q977W1
B	851	ALA	LYS	engineered mutation	UNP Q977W1

- Molecule 2 is a DNA chain called DNA (42-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	U	39	805	383	144	238	40	0	1	0

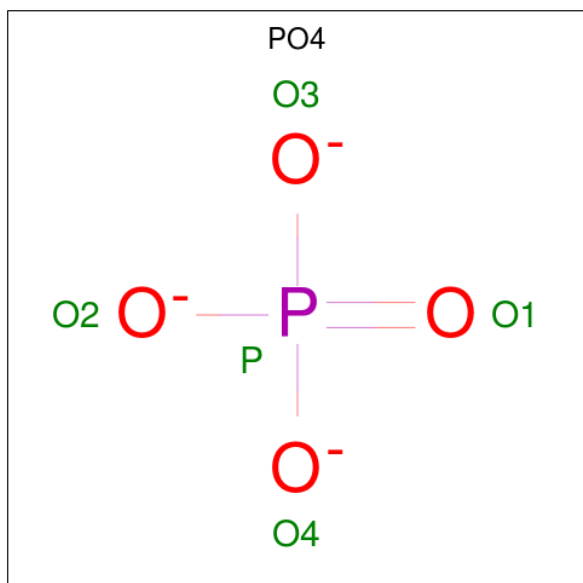
- Molecule 3 is a DNA chain called DNA (42-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	V	38	790	376	137	237	40	0	2	0

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

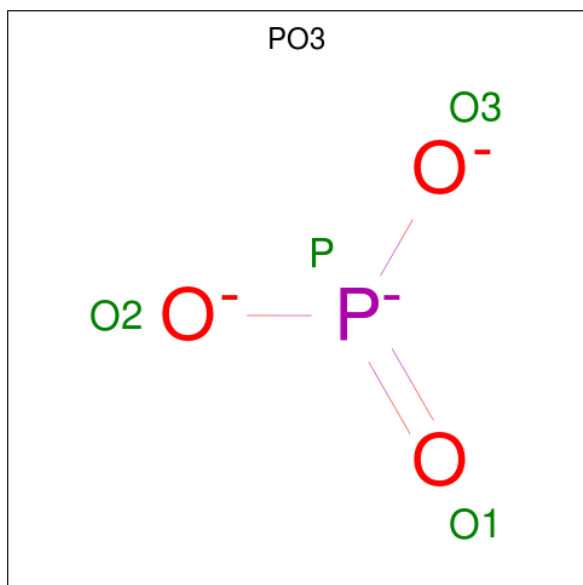
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total K 2 2	0	0
4	B	2	Total K 2 2	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total O P 5 4 1	0	0
5	B	1	Total O P 5 4 1	0	0
5	U	1	Total O P 5 4 1	0	0
5	U	1	Total O P 5 4 1	0	0

- Molecule 6 is PHOSPHITE ION (three-letter code: PO3) (formula: O₃P).

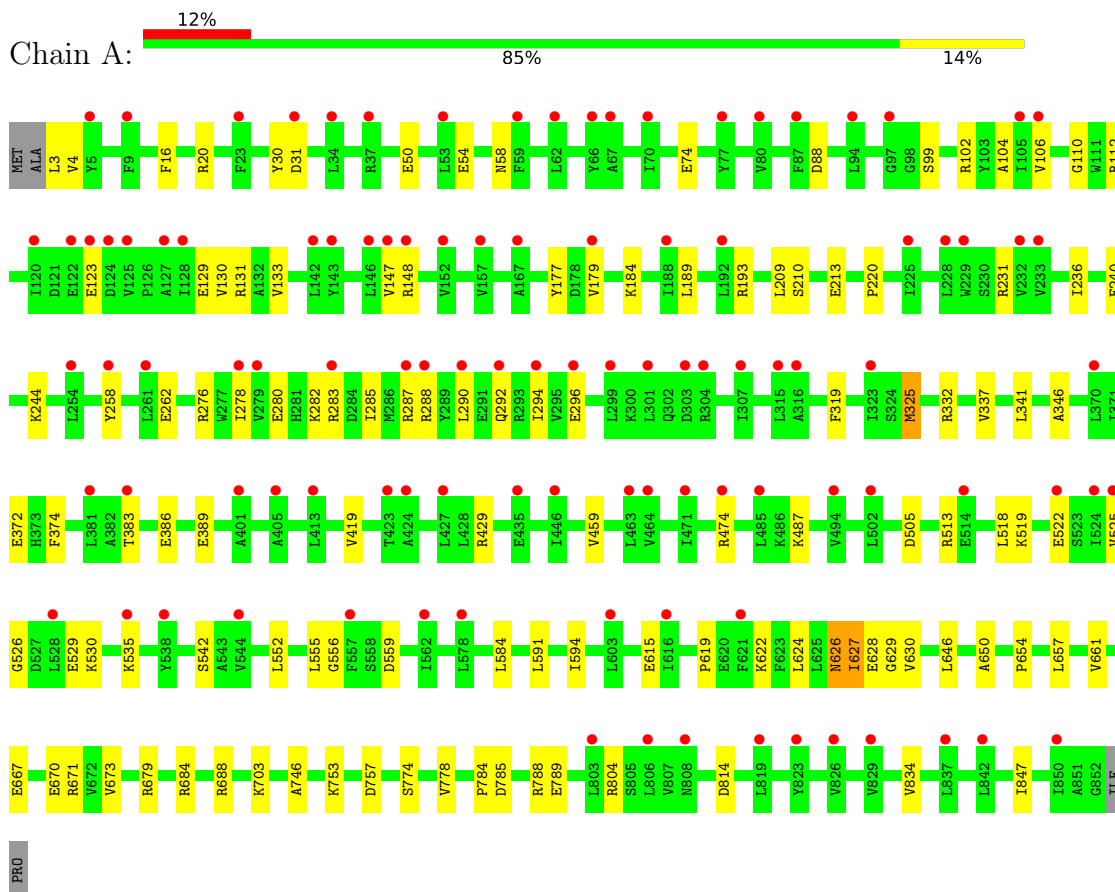


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	U	1	Total	O	P	0	0
			4	3	1		
6	V	1	Total	O	P	0	0
			4	3	1		

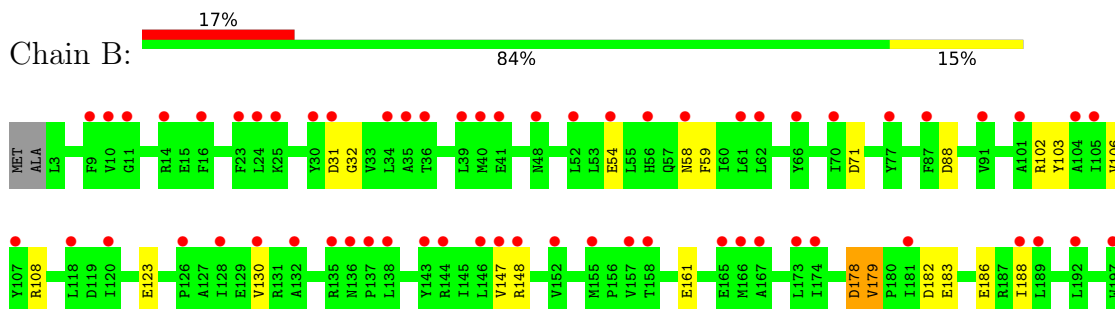
3 Residue-property plots [i](#)

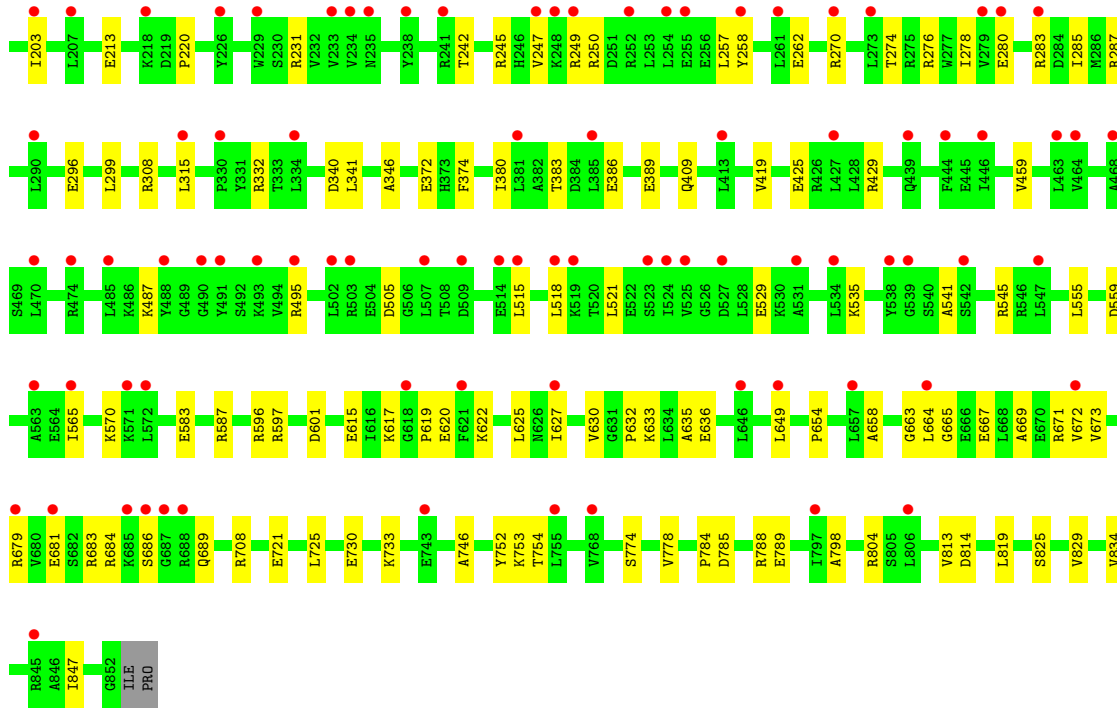
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Topoisomerase V

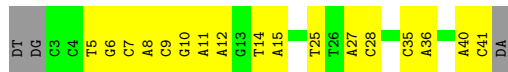


- Molecule 1: Topoisomerase V





• Molecule 2: DNA (42-MER)



• Molecule 3: DNA (42-MER)



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	120.94Å 120.94Å 497.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	58.76 – 2.92 108.77 – 2.92	Depositor EDS
% Data completeness (in resolution range)	68.9 (58.76-2.92) 69.0 (108.77-2.92)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.33 (at 2.91Å)	Xtriage
Refinement program	BUSTER, PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.257 , 0.288 0.265 , 0.291	Depositor DCC
R_{free} test set	2846 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	98.8	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 66.5	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	0.89	EDS
Total number of atoms	15241	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.10% 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: K, PO3, PO4

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	0.24	0/6906	0.51	0/9302
1	B	0.24	0/6906	0.51	0/9302
2	U	0.48	0/901	0.90	0/1386
3	V	0.47	0/894	0.93	1/1376 (0.1%)
All	All	0.28	0/15607	0.58	1/21366 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	V	39	DC	O4'-C1'-N1	5.13	111.59	108.00

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	6807	0	6873	81	0
1	B	6807	0	6873	77	0
2	U	805	0	444	18	0
3	V	790	0	431	17	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	10	0	0	0	0
5	U	10	0	0	0	0
6	U	4	0	0	0	0
6	V	4	0	0	1	0
All	All	15241	0	14621	174	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 6.

The worst 5 of 174 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:V:24:DC:H2''	3:V:25:DT:H5''	1.64	0.78
1:A:220:PRO:HB3	1:A:231:ARG:HG3	1.66	0.78
1:A:285:ILE:HD11	2:U:5:DT:P	2.26	0.75
1:A:542:SER:HB2	2:U:28[A]:DC:H5''	1.70	0.73
3:V:39:DC:H2''	3:V:40:DA:H5'	1.72	0.70

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	849/854 (99%)	828 (98%)	19 (2%)	2 (0%)	47 77
1	B	849/854 (99%)	828 (98%)	19 (2%)	2 (0%)	47 77
All	All	1698/1708 (99%)	1656 (98%)	38 (2%)	4 (0%)	47 77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	628	GLU
1	B	663	GLY
1	B	178	ASP
1	A	627	ILE

5.3.2 Protein sidechains [i](#)

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	713/715 (100%)	706 (99%)	7 (1%)	76	91
1	B	713/715 (100%)	706 (99%)	7 (1%)	76	91
All	All	1426/1430 (100%)	1412 (99%)	14 (1%)	78	91

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	88	ASP
1	B	108	ARG
1	B	649	LEU
1	B	555	LEU
1	B	559	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	$\# Z > 2$
5	PO4	U	103	-	4,4,4	0.66	0	6,6,6	0.43	0
5	PO4	B	901	-	4,4,4	0.65	0	6,6,6	0.43	0
5	PO4	U	101	-	4,4,4	0.66	0	6,6,6	0.43	0
5	PO4	B	904	-	4,4,4	0.67	0	6,6,6	0.43	0
6	PO3	V	101	3	0,3,3	-	-	0,3,3	-	-
6	PO3	U	102	2	0,3,3	-	-	0,3,3	-	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	V	101	PO3	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	U	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	U	27:DA	O3'	28[B]:DC	P	2.55

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	850/854 (99%)	0.94	104 (12%) 4 3	26, 93, 145, 176	0
1	B	850/854 (99%)	1.14	148 (17%) 1 1	29, 96, 168, 351	0
2	U	39/42 (92%)	0.28	0 100 100	84, 110, 166, 167	0
3	V	38/42 (90%)	0.28	1 (2%) 56 53	55, 111, 136, 145	0
All	All	1777/1792 (99%)	1.00	253 (14%) 2 2	26, 96, 158, 351	0

The worst 5 of 253 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	166	MET	9.9
1	B	192	LEU	7.8
1	B	138	LEU	5.9
1	A	557	PHE	5.6
1	A	287	ARG	5.5

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 monosaccharides 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
5	PO4	U	103	5/5	0.78	0.20	146,154,157,159	0
4	K	A	902	1/1	0.80	0.19	109,109,109,109	0
4	K	B	903	1/1	0.84	0.61	114,114,114,114	0
4	K	A	901	1/1	0.85	0.20	95,95,95,95	0
5	PO4	B	904	5/5	0.87	0.47	129,130,146,147	5
5	PO4	B	901	5/5	0.88	0.35	87,99,116,123	5
6	PO3	U	102	4/4	0.88	0.16	153,166,168,173	0
4	K	B	902	1/1	0.90	0.24	89,89,89,89	0
5	PO4	U	101	5/5	0.90	0.13	90,101,123,125	0
6	PO3	V	101	4/4	0.91	0.18	120,133,148,161	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.