



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 04:36 am BST

PDB ID : 4E0J
Title : Protelomerase tela R255A mutant complexed with DNA hairpin product
Authors : Shi, K.; Aihara, H.
Deposited on : 2012-03-04
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

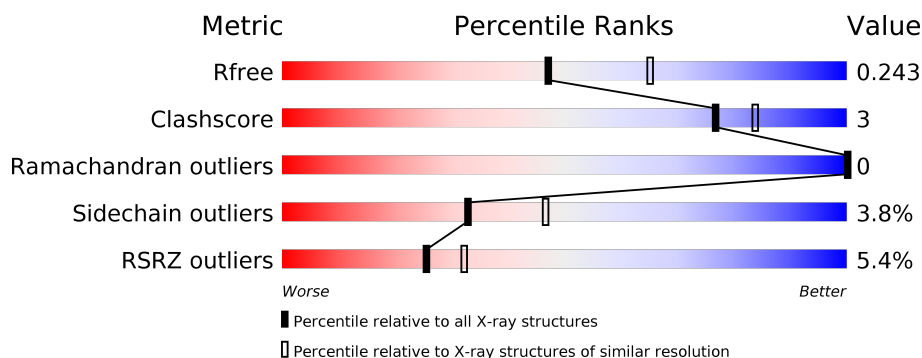
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	462	<div> <div>3%</div> <div> <div></div> <div>62%</div> <div>7%</div> <div>31%</div> </div> </div>
2	C	13	<div> <div>15%</div> <div> <div></div> <div>100%</div> </div> </div>
3	D	19	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>16%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3681 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 Protelomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	319	2600	1655	443	487	15	6	9	0

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q7CWW1
A	-18	GLY	-	EXPRESSION TAG	UNP Q7CWW1
A	-17	SER	-	EXPRESSION TAG	UNP Q7CWW1
A	-16	SER	-	EXPRESSION TAG	UNP Q7CWW1
A	-15	HIS	-	EXPRESSION TAG	UNP Q7CWW1
A	-14	HIS	-	EXPRESSION TAG	UNP Q7CWW1
A	-13	HIS	-	EXPRESSION TAG	UNP Q7CWW1
A	-12	HIS	-	EXPRESSION TAG	UNP Q7CWW1
A	-11	HIS	-	EXPRESSION TAG	UNP Q7CWW1
A	-10	HIS	-	EXPRESSION TAG	UNP Q7CWW1
A	-9	SER	-	EXPRESSION TAG	UNP Q7CWW1
A	-8	SER	-	EXPRESSION TAG	UNP Q7CWW1
A	-7	GLY	-	EXPRESSION TAG	UNP Q7CWW1
A	-6	LEU	-	EXPRESSION TAG	UNP Q7CWW1
A	-5	VAL	-	EXPRESSION TAG	UNP Q7CWW1
A	-4	PRO	-	EXPRESSION TAG	UNP Q7CWW1
A	-3	ARG	-	EXPRESSION TAG	UNP Q7CWW1
A	-2	GLY	-	EXPRESSION TAG	UNP Q7CWW1
A	-1	SER	-	EXPRESSION TAG	UNP Q7CWW1
A	0	HIS	-	EXPRESSION TAG	UNP Q7CWW1
A	1	MET	-	EXPRESSION TAG	UNP Q7CWW1
A	2	LEU	-	EXPRESSION TAG	UNP Q7CWW1
A	3	ALA	-	EXPRESSION TAG	UNP Q7CWW1
A	4	ALA	-	EXPRESSION TAG	UNP Q7CWW1
A	5	LYS	-	EXPRESSION TAG	UNP Q7CWW1
A	6	ARG	-	EXPRESSION TAG	UNP Q7CWW1
A	7	LYS	-	EXPRESSION TAG	UNP Q7CWW1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	8	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	9	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	10	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	11	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	12	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	13	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	14	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	15	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	16	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	17	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	18	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	19	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	20	PHE	-	EXPRESSION TAG	UNP Q7CWV1
A	21	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	22	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	23	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	24	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	25	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	26	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	27	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	28	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	29	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	30	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	31	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	32	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	33	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	34	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	35	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	36	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	37	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	38	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	39	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	40	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	41	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	42	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	43	TRP	-	EXPRESSION TAG	UNP Q7CWV1
A	44	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	45	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	46	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	47	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	48	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	49	TYR	-	EXPRESSION TAG	UNP Q7CWV1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	50	HIS	-	EXPRESSION TAG	UNP Q7CWV1
A	51	PHE	-	EXPRESSION TAG	UNP Q7CWV1
A	52	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	53	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	54	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	55	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	56	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	57	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	58	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	59	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	60	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	61	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	62	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	63	TYR	-	EXPRESSION TAG	UNP Q7CWV1
A	64	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	65	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	66	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	67	TYR	-	EXPRESSION TAG	UNP Q7CWV1
A	68	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	69	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	70	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	71	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	72	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	73	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	74	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	75	PHE	-	EXPRESSION TAG	UNP Q7CWV1
A	76	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	77	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	78	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	79	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	80	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	81	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	82	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	83	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	84	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	85	CYS	-	EXPRESSION TAG	UNP Q7CWV1
A	86	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	87	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	88	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	89	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	90	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	91	ARG	-	EXPRESSION TAG	UNP Q7CWV1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	92	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	93	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	94	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	95	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	96	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	97	TYR	-	EXPRESSION TAG	UNP Q7CWV1
A	98	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	99	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	100	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	101	GLY	-	EXPRESSION TAG	UNP Q7CWV1
A	102	ASP	-	EXPRESSION TAG	UNP Q7CWV1
A	255	ALA	ARG	engineered mutation	UNP Q7CWV1
A	422	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	423	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	424	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	425	ASN	-	EXPRESSION TAG	UNP Q7CWV1
A	426	GLU	-	EXPRESSION TAG	UNP Q7CWV1
A	427	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	428	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	429	LEU	-	EXPRESSION TAG	UNP Q7CWV1
A	430	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	431	GLN	-	EXPRESSION TAG	UNP Q7CWV1
A	432	MET	-	EXPRESSION TAG	UNP Q7CWV1
A	433	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	434	THR	-	EXPRESSION TAG	UNP Q7CWV1
A	435	ILE	-	EXPRESSION TAG	UNP Q7CWV1
A	436	ALA	-	EXPRESSION TAG	UNP Q7CWV1
A	437	PRO	-	EXPRESSION TAG	UNP Q7CWV1
A	438	VAL	-	EXPRESSION TAG	UNP Q7CWV1
A	439	SER	-	EXPRESSION TAG	UNP Q7CWV1
A	440	ARG	-	EXPRESSION TAG	UNP Q7CWV1
A	441	LYS	-	EXPRESSION TAG	UNP Q7CWV1
A	442	GLY	-	EXPRESSION TAG	UNP Q7CWV1

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*AP*TP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	P	0	0	0
			263	128	52	71	12			

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

GP*TP*TP*AP*TP*TP*AP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	19	Total	C	N	O	P	0	3	0
			450	219	75	135	21			

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

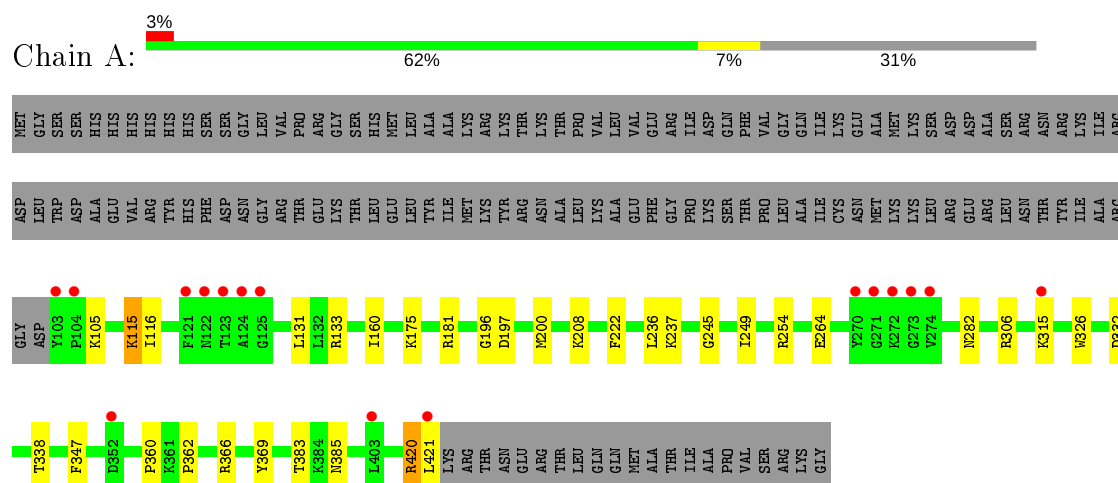
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	274	Total	O	1	3
			277	277		
6	C	35	Total	O	0	0
			35	35		
6	D	54	Total	O	0	0
			54	54		

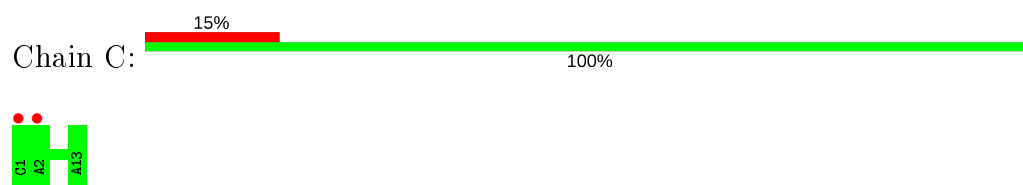
3 Residue-property plots [i](#)

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.

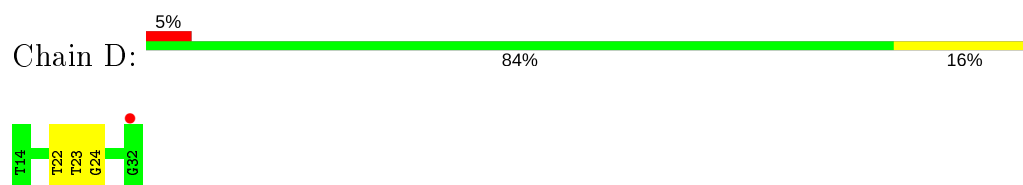
- Molecule 1: Protelomerase



- Molecule 2: DNA (5'-D(*CP*AP*TP*AP*AP*TP*AP*AP*CP*AP*AP*TP*A)-3')



- Molecule 3: DNA (5'-D(*TP*CP*AP*TP*GP*AP*TP*AP*TP*TP*GP*TP*TP*AP*TP*TP*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	117.56Å 120.08Å 56.76Å 90.00° 111.68° 90.00°	Depositor
Resolution (Å)	39.50 – 2.30 47.77 – 2.30	Depositor EDS
% Data completeness (in resolution range)	85.2 (39.50-2.30) 85.2 (47.77-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.205 , 0.252 0.203 , 0.243	Depositor DCC
R_{free} test set	1409 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	30.2	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 70.7	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	0.94	EDS
Total number of atoms	3681	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% 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: NA, CL

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	0/2658	0.42	0/3593
2	C	0.48	0/296	1.09	0/454
3	D	0.45	0/503	1.10	0/776
All	All	0.30	0/3457	0.66	0/4823

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	2600	0	2564	17	0
2	C	263	0	148	0	0
3	D	450	0	255	2	0
4	A	1	0	0	0	0
5	A	1	0	0	0	0
6	A	277	0	0	3	0
6	C	35	0	0	0	0
6	D	54	0	0	0	0
All	All	3681	0	2967	18	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 3.

All (18) 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:115:LYS:HD2	1:A:131:LEU:HD21	1.79	0.64
1:A:181:ARG:NH1	6:A:617:HOH:O	2.30	0.63
1:A:196:GLY:HA3	1:A:200:MET:HE2	1.79	0.63
1:A:420:ARG:O	1:A:420:ARG:HG2	2.02	0.58
1:A:306:ARG:NH2	6:A:653:HOH:O	2.38	0.56
1:A:175:LYS:NZ	6:A:823:HOH:O	2.41	0.54
1:A:264:GLU:HB2	1:A:282:ASN:HB3	1.90	0.54
1:A:366:ARG:O	1:A:369:TYR:HB3	2.09	0.53
3:D:22:DT:H2'	3:D:23:DT:C6	2.45	0.52
1:A:362:PRO:HG2	3:D:24:DG:OP2	2.10	0.51
1:A:383[A]:THR:HG22	1:A:385:ASN:H	1.80	0.46
1:A:105:LYS:HE2	1:A:105:LYS:HB2	1.92	0.42
1:A:315:LYS:HA	1:A:315:LYS:HD3	1.69	0.41
1:A:245:GLY:O	1:A:249:ILE:HG13	2.20	0.41
1:A:326:TRP:HE1	1:A:338:THR:HG1	1.67	0.41
1:A:133:ARG:CZ	1:A:160:ILE:HG13	2.51	0.41
1:A:116:ILE:HD11	1:A:131:LEU:HB3	2.03	0.40
1:A:347[B]:PHE:HA	1:A:360:PRO:HG2	2.03	0.40

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	326/462 (71%)	311 (95%)	15 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	273 / 389 (70%)	263 (96%)	10 (4%)	34	48

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	LYS
1	A	197	ASP
1	A	208	LYS
1	A	222	PHE
1	A	236	LEU
1	A	237	LYS
1	A	254	ARG
1	A	332	ASP
1	A	420	ARG
1	A	421	LEU

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 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

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	319/462 (69%)	0.24	16 (5%) 28 35	16, 44, 83, 105	0
2	C	13/13 (100%)	0.47	2 (15%) 2 3	23, 41, 103, 106	0
3	D	19/19 (100%)	0.29	1 (5%) 26 33	20, 42, 84, 103	0
All	All	351/494 (71%)	0.25	19 (5%) 25 32	16, 44, 84, 106	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	271	GLY	5.1
1	A	103	TYR	4.4
3	D	32	DG	3.8
1	A	104	PRO	3.6
1	A	272	LYS	3.5
1	A	270	TYR	3.2
1	A	124	ALA	3.0
1	A	274	VAL	3.0
2	C	2	DA	2.9
2	C	1	DC	2.8
1	A	273	GLY	2.8
1	A	121	PHE	2.4
1	A	421	LEU	2.3
1	A	123	THR	2.2
1	A	403	LEU	2.1
1	A	352	ASP	2.0
1	A	315	LYS	2.0
1	A	122	ASN	2.0
1	A	125	GLY	2.0

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
4	NA	A	501	1/1	0.72	0.29	67,67,67,67	0
5	CL	A	502	1/1	0.90	0.11	76,76,76,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.