



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 16, 2017 – 12:24 AM EST

PDB ID : 5KBJ
Title : Structure of Rep-DNA complex
Authors : Schumacher, M.
Deposited on : unknown
Resolution : 3.09 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030345

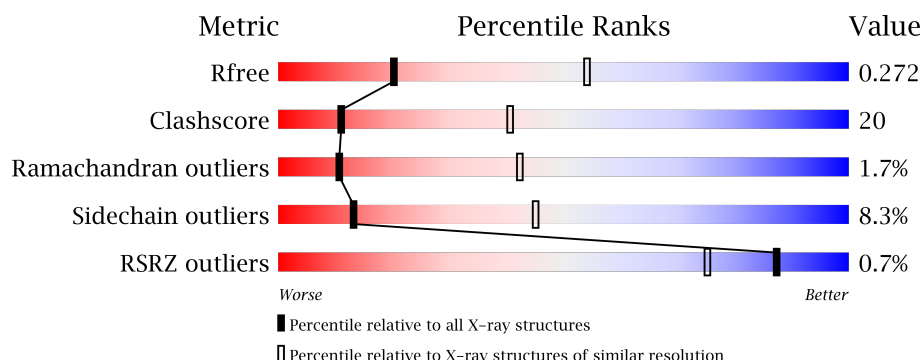
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.09 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}	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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	A	132	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 49%, yellow 43%, orange 6%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 49% 43% 6% • </div> </div>
1	B	132	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 55%, yellow 39%, orange 5%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 55% 39% 5% • </div> </div>
1	C	132	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 63%, yellow 28%, orange 5%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 63% 28% • 5% </div> </div>
1	D	132	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 54%, yellow 36%, orange 8%, red 2%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 54% 36% 8% •• </div> </div>
1	E	132	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 54%, yellow 38%, orange 7%, grey 0%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 100% 54% 38% 7% • </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	132	<div> <div></div> <div>56%</div> <div>39%</div> <div>• •</div> </div>
1	G	132	<div> <div></div> <div>44%</div> <div>47%</div> <div>7% •</div> </div>
1	H	132	<div> <div></div> <div>66%</div> <div>27%</div> <div>• •</div> </div>
2	R	32	<div> <div></div> <div>34%</div> <div>63%</div> <div>•</div> </div>
3	W	32	<div> <div></div> <div>44%</div> <div>53%</div> <div>•</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10059 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 Replication initiator A, N-terminal.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	130	Total	C	N	O	S	0	0	0
			1105	712	183	206	4			
1	B	130	Total	C	N	O	S	0	0	0
			1106	713	183	206	4			
1	C	125	Total	C	N	O	S	0	0	0
			1059	683	173	199	4			
1	H	127	Total	C	N	O	S	0	0	0
			1078	694	180	200	4			
1	D	130	Total	C	N	O	S	0	0	0
			1106	713	183	206	4			
1	E	130	Total	C	N	O	S	0	0	0
			1099	707	183	205	4			
1	F	130	Total	C	N	O	S	0	0	0
			1099	707	183	205	4			
1	G	129	Total	C	N	O	S	0	0	0
			1095	703	184	204	4			

- Molecule 2 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	32	Total	C	N	O	P	0	0	0
			657	312	126	187	32			

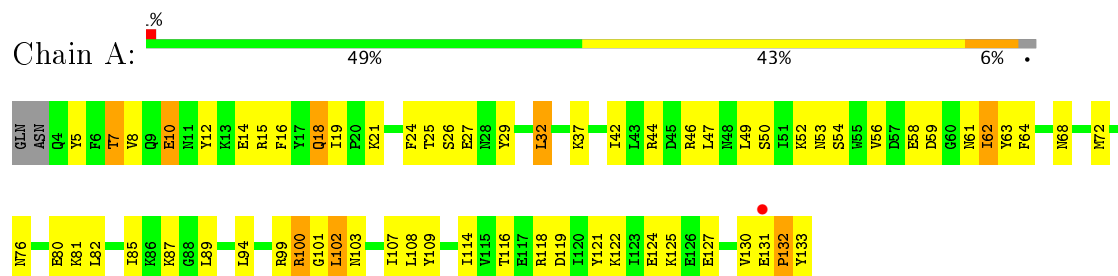
- Molecule 3 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	W	32	Total	C	N	O	P	0	0	0
			655	313	113	197	32			

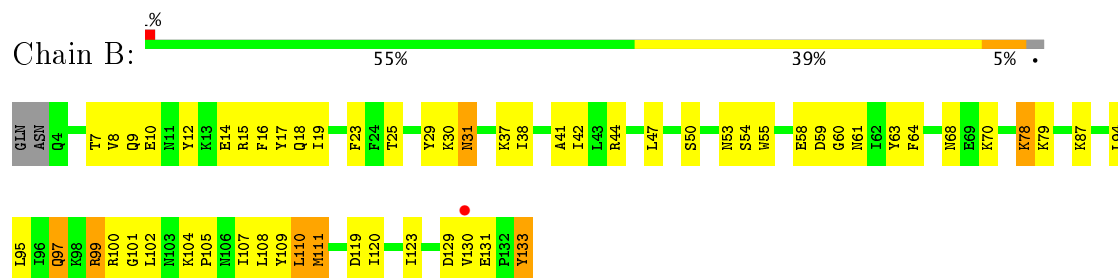
3 Residue-property plots [i](#)

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.

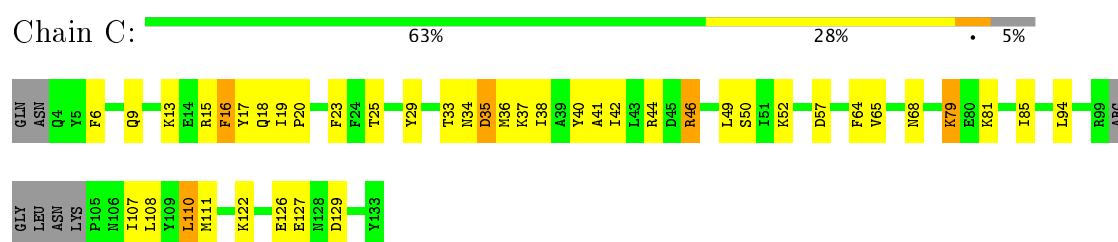
- Molecule 1: Replication initiator A, N-terminal



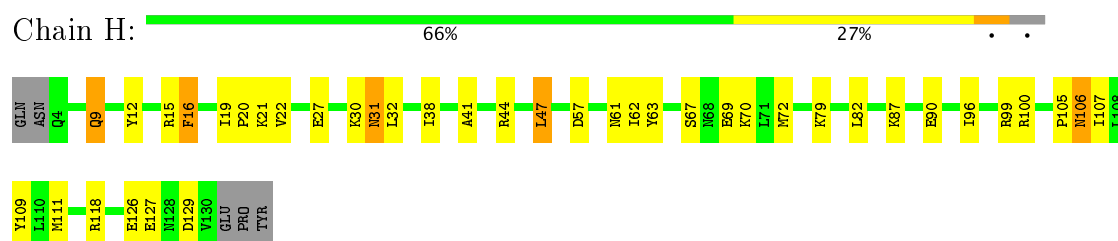
- Molecule 1: Replication initiator A, N-terminal



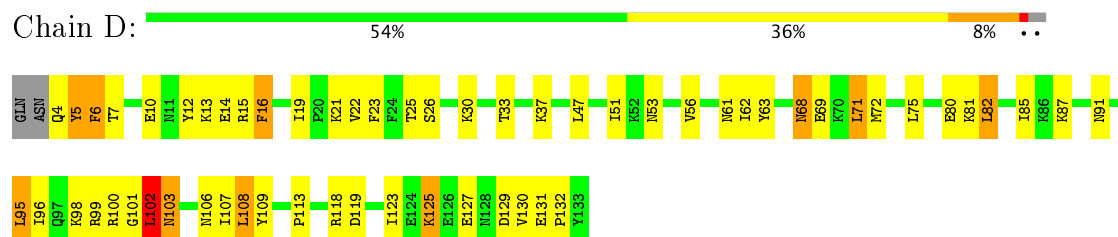
- Molecule 1: Replication initiator A, N-terminal



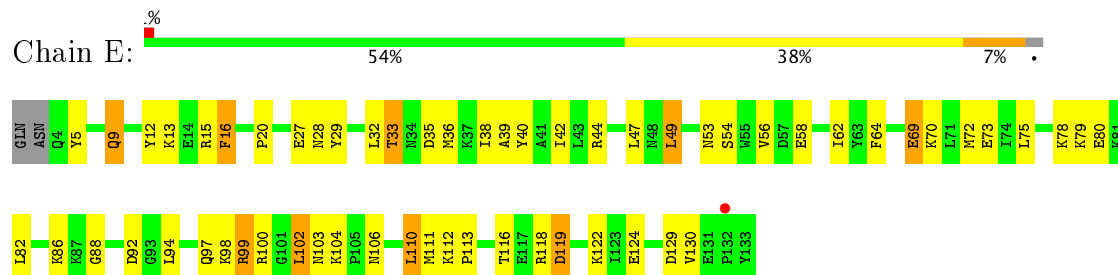
- Molecule 1: Replication initiator A, N-terminal



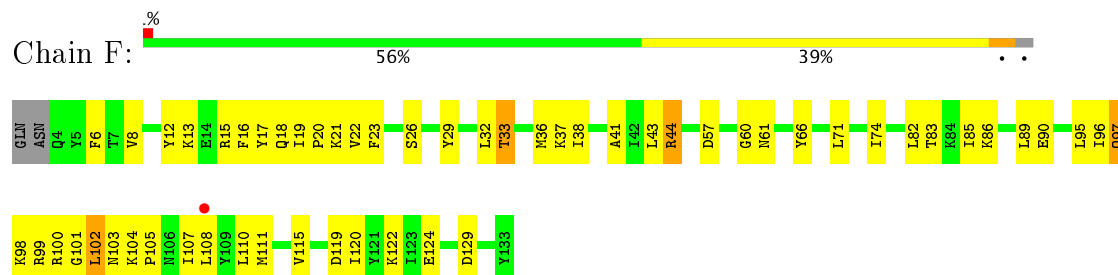
- Molecule 1: Replication initiator A, N-terminal



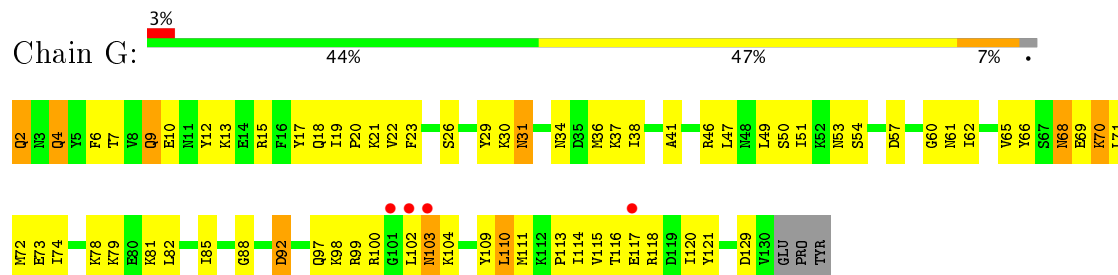
- Molecule 1: Replication initiator A, N-terminal



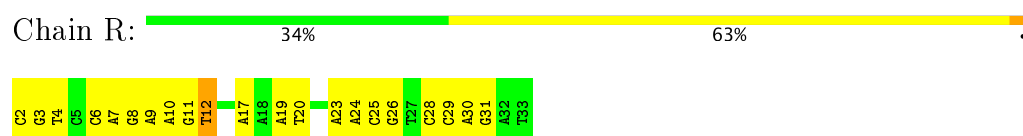
- Molecule 1: Replication initiator A, N-terminal



- Molecule 1: Replication initiator A, N-terminal



- Molecule 2: DNA (32-MER)



- Molecule 3: DNA (32-MER)



A3	T4	C5	T6	G7	G8	A9	C10	G11	T12	T13	G14	G15	A16	T17	T18	T19	T20	G30	C33	G34
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.20 Å 77.50 Å 100.70 Å 80.80° 75.50° 71.90°	Depositor
Resolution (Å)	97.10 – 3.09 97.10 – 3.09	Depositor EDS
% Data completeness (in resolution range)	94.5 (97.10-3.09) 92.1 (97.10-3.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 3.07 Å)	Xtriage
Refinement program	PHENIX 1.6.4 _486	Depositor
R, R_{free}	0.225 , 0.277 0.217 , 0.272	Depositor DCC
R_{free} test set	3675 reflections (12.92%)	DCC
Wilson B-factor (Å ²)	62.6	Xtriage
Anisotropy	0.777	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10059	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.55% 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

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	0/1124	0.38	0/1508
1	B	0.23	0/1126	0.39	0/1512
1	C	0.23	0/1077	0.38	0/1445
1	D	0.24	0/1126	0.39	0/1512
1	E	0.24	0/1118	0.38	0/1501
1	F	0.27	0/1118	0.43	0/1501
1	G	0.23	0/1113	0.37	0/1493
1	H	0.24	0/1096	0.38	0/1470
2	R	0.51	0/738	1.21	3/1136 (0.3%)
3	W	0.47	0/732	1.21	1/1128 (0.1%)
All	All	0.29	0/10368	0.60	4/14206 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	12	DT	O4'-C1'-N1	7.45	113.22	108.00
2	R	12	DT	C1'-O4'-C4'	-7.38	102.72	110.10
3	W	13	DT	O4'-C1'-N1	5.19	111.63	108.00
2	R	17	DA	O4'-C1'-N9	5.13	111.59	108.00

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	1105	0	1120	58	0
1	B	1106	0	1125	63	0
1	C	1059	0	1072	38	0
1	D	1106	0	1125	49	0
1	E	1099	0	1118	56	0
1	F	1099	0	1118	58	0
1	G	1095	0	1117	68	0
1	H	1078	0	1103	40	0
2	R	657	0	359	28	0
3	W	655	0	364	25	0
All	All	10059	0	9621	395	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 20.

The worst 5 of 395 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:F:18:GLN:HB2	1:F:44:ARG:HD3	1.41	1.02
1:B:101:GLY:HA3	3:W:30:DG:H1'	1.43	0.98
1:E:102:LEU:HD23	1:E:103:ASN:H	1.32	0.94
2:R:11:DG:H1'	2:R:12:DT:OP1	1.66	0.92
2:R:19:DA:H61	3:W:17:DT:H3	1.13	0.89

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	128/132 (97%)	107 (84%)	18 (14%)	3 (2%)	7	33
1	B	128/132 (97%)	111 (87%)	15 (12%)	2 (2%)	11	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	121/132 (92%)	114 (94%)	7 (6%)	0	100	100
1	D	128/132 (97%)	112 (88%)	10 (8%)	6 (5%)	3	17
1	E	128/132 (97%)	112 (88%)	16 (12%)	0	100	100
1	F	128/132 (97%)	108 (84%)	17 (13%)	3 (2%)	7	33
1	G	127/132 (96%)	102 (80%)	22 (17%)	3 (2%)	7	32
1	H	125/132 (95%)	116 (93%)	9 (7%)	0	100	100
All	All	1013/1056 (96%)	882 (87%)	114 (11%)	17 (2%)	11	42

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	130	VAL
1	B	105	PRO
1	D	101	GLY
1	D	103	ASN
1	F	101	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	123/126 (98%)	110 (89%)	13 (11%)	8	30
1	B	124/126 (98%)	115 (93%)	9 (7%)	16	50
1	C	119/126 (94%)	110 (92%)	9 (8%)	15	49
1	D	124/126 (98%)	113 (91%)	11 (9%)	11	41
1	E	123/126 (98%)	107 (87%)	16 (13%)	5	21
1	F	123/126 (98%)	120 (98%)	3 (2%)	54	83
1	G	123/126 (98%)	111 (90%)	12 (10%)	9	35
1	H	121/126 (96%)	113 (93%)	8 (7%)	19	54
All	All	980/1008 (97%)	899 (92%)	81 (8%)	13	45

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	106	ASN
1	D	100	ARG
1	G	70	LYS
1	H	126	GLU
1	D	68	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	97	GLN
1	D	53	ASN
1	G	31	ASN
1	H	106	ASN
1	D	4	GLN

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

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	130/132 (98%)	0.02	1 (0%) 86 71	59, 85, 118, 163	0
1	B	130/132 (98%)	-0.01	1 (0%) 86 71	47, 80, 110, 142	0
1	C	125/132 (94%)	-0.02	0 100 100	58, 86, 116, 133	0
1	D	130/132 (98%)	-0.06	0 100 100	47, 83, 108, 140	0
1	E	130/132 (98%)	-0.03	1 (0%) 86 71	50, 78, 112, 133	0
1	F	130/132 (98%)	0.17	1 (0%) 86 71	70, 103, 125, 143	0
1	G	129/132 (97%)	0.14	4 (3%) 49 26	71, 98, 128, 149	0
1	H	127/132 (96%)	-0.07	0 100 100	62, 83, 114, 127	0
2	R	32/32 (100%)	-0.26	0 100 100	71, 85, 101, 110	0
3	W	32/32 (100%)	-0.32	0 100 100	65, 86, 96, 108	0
All	All	1095/1120 (97%)	-0.00	8 (0%) 87 75	47, 87, 119, 163	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	101	GLY	4.8
1	G	102	LEU	2.8
1	G	117	GLU	2.8
1	G	103	ASN	2.7
1	B	130	VAL	2.6

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.