



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2020 – 03:29 AM BST

PDB ID : 6LBK
Title : Structure of rat GLD-2 (Terminal nucleotidyltransferase 2, TENT2)
Authors : Ma, X.Y.; Gao, S.
Deposited on : 2019-11-14
Resolution : 2.50 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 : 2.14.4.dev1
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) : 2.14.4.dev1

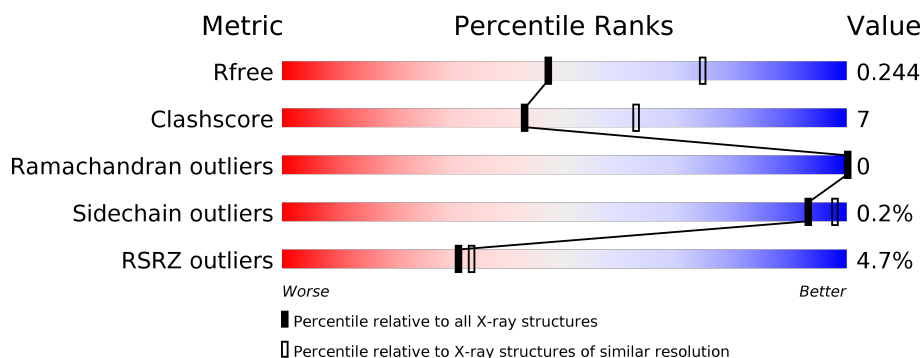
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	380	<div> <div>6%</div> <div>68%</div> <div>18%</div> <div>14%</div> </div>
1	B	380	<div> <div>2%</div> <div>73%</div> <div>11%</div> <div>16%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5274 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 Poly(A) RNA polymerase GLD2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	0	0
			2640	1688	468	473	11			
1	B	319	Total	C	N	O	S	0	0	0
			2595	1663	457	464	11			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	MET	-	expression tag	UNP Q5U315
A	106	GLY	-	expression tag	UNP Q5U315
A	107	SER	-	expression tag	UNP Q5U315
A	108	SER	-	expression tag	UNP Q5U315
A	109	HIS	-	expression tag	UNP Q5U315
A	110	HIS	-	expression tag	UNP Q5U315
A	111	HIS	-	expression tag	UNP Q5U315
A	112	HIS	-	expression tag	UNP Q5U315
A	113	HIS	-	expression tag	UNP Q5U315
A	114	HIS	-	expression tag	UNP Q5U315
A	115	SER	-	expression tag	UNP Q5U315
A	116	SER	-	expression tag	UNP Q5U315
A	117	GLY	-	expression tag	UNP Q5U315
A	118	LEU	-	expression tag	UNP Q5U315
A	119	GLU	-	expression tag	UNP Q5U315
A	120	VAL	-	expression tag	UNP Q5U315
A	121	LEU	-	expression tag	UNP Q5U315
A	122	PHE	-	expression tag	UNP Q5U315
A	123	GLN	-	expression tag	UNP Q5U315
A	124	GLY	-	expression tag	UNP Q5U315
A	125	PRO	-	expression tag	UNP Q5U315
A	126	HIS	-	expression tag	UNP Q5U315
A	127	MET	-	expression tag	UNP Q5U315
A	128	GLY	-	expression tag	UNP Q5U315
A	129	GLY	-	expression tag	UNP Q5U315

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Chain	Residue	Modelled	Actual	Comment	Reference
A	130	SER	-	expression tag	UNP Q5U315
A	279	ALA	ASP	engineered mutation	UNP Q5U315
B	105	MET	-	expression tag	UNP Q5U315
B	106	GLY	-	expression tag	UNP Q5U315
B	107	SER	-	expression tag	UNP Q5U315
B	108	SER	-	expression tag	UNP Q5U315
B	109	HIS	-	expression tag	UNP Q5U315
B	110	HIS	-	expression tag	UNP Q5U315
B	111	HIS	-	expression tag	UNP Q5U315
B	112	HIS	-	expression tag	UNP Q5U315
B	113	HIS	-	expression tag	UNP Q5U315
B	114	HIS	-	expression tag	UNP Q5U315
B	115	SER	-	expression tag	UNP Q5U315
B	116	SER	-	expression tag	UNP Q5U315
B	117	GLY	-	expression tag	UNP Q5U315
B	118	LEU	-	expression tag	UNP Q5U315
B	119	GLU	-	expression tag	UNP Q5U315
B	120	VAL	-	expression tag	UNP Q5U315
B	121	LEU	-	expression tag	UNP Q5U315
B	122	PHE	-	expression tag	UNP Q5U315
B	123	GLN	-	expression tag	UNP Q5U315
B	124	GLY	-	expression tag	UNP Q5U315
B	125	PRO	-	expression tag	UNP Q5U315
B	126	HIS	-	expression tag	UNP Q5U315
B	127	MET	-	expression tag	UNP Q5U315
B	128	GLY	-	expression tag	UNP Q5U315
B	129	GLY	-	expression tag	UNP Q5U315
B	130	SER	-	expression tag	UNP Q5U315
B	279	ALA	ASP	engineered mutation	UNP Q5U315

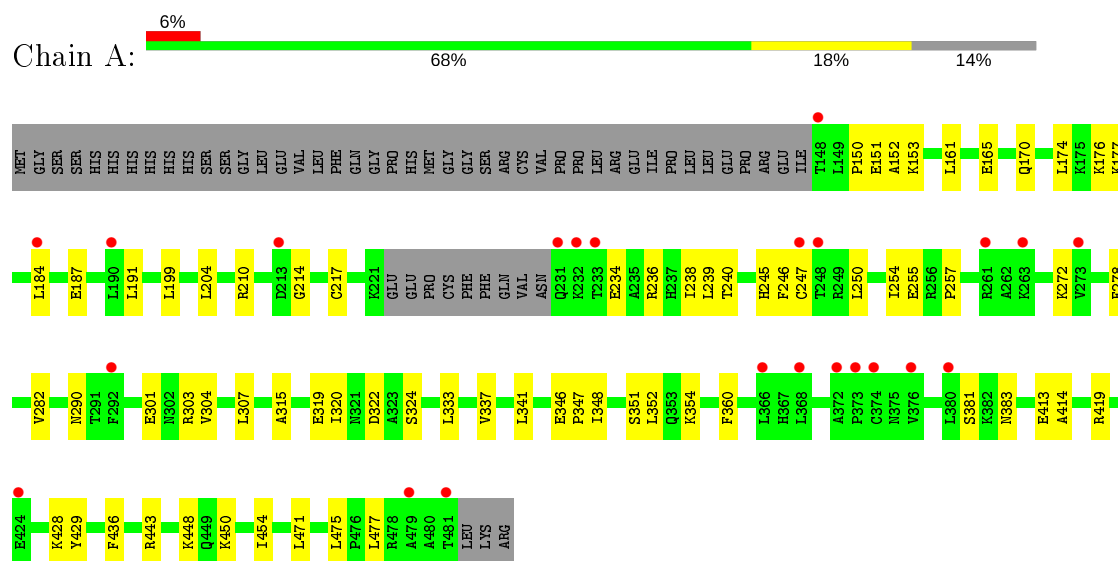
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	20	Total O 20 20	0	0
2	B	19	Total O 19 19	0	0

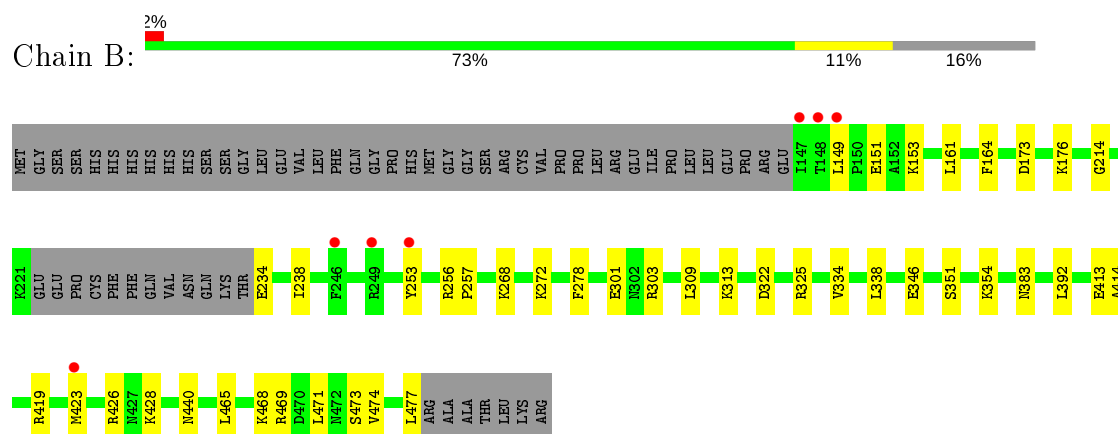
3 Residue-property plots [i](#)

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: Poly(A) RNA polymerase GLD2



- Molecule 1: Poly(A) RNA polymerase GLD2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.96 Å 40.72 Å 105.00 Å 90.00° 100.20° 90.00°	Depositor
Resolution (Å)	47.20 – 2.50 47.20 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.20-2.50) 99.1 (47.20-2.50)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.48 Å)	Xtriage
Refinement program	PHENIX 1.12 _2829	Depositor
R, R_{free}	0.205 , 0.243 0.205 , 0.244	Depositor DCC
R_{free} test set	1213 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	60.4	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 57.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5274	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.99 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.2541e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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](#)

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	0.50	1/2696 (0.0%)	0.65	1/3646 (0.0%)
1	B	0.53	0/2651	0.69	0/3586
All	All	0.51	1/5347 (0.0%)	0.67	1/7232 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	217	CYS	CB-SG	-5.81	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	475	LEU	CA-CB-CG	5.46	127.87	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	2640	0	2700	44	1
1	B	2595	0	2653	28	1
2	A	20	0	0	3	0
2	B	19	0	0	1	0
All	All	5274	0	5353	72	1

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 7.

All (72) 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:B:256:ARG:NH2	2:B:501:HOH:O	2.14	0.80
1:A:174:LEU:HD12	2:A:501:HOH:O	1.87	0.74
1:B:428:LYS:HD3	1:B:440:ASN:HD22	1.56	0.71
1:A:184:LEU:HD21	1:A:254:ILE:HD11	1.76	0.68
1:A:150:PRO:HD2	1:A:161:LEU:HD21	1.80	0.64
1:B:428:LYS:HD3	1:B:440:ASN:ND2	2.13	0.63
1:B:419:ARG:NH2	1:B:428:LYS:O	2.33	0.62
1:B:351:SER:HB2	1:B:414:ALA:HB2	1.82	0.61
1:A:354:LYS:HE3	1:A:413:GLU:HA	1.81	0.61
1:B:301:GLU:OE2	1:B:303:ARG:NH2	2.32	0.60
1:A:471:LEU:HB3	1:A:477:LEU:HD21	1.83	0.59
1:B:471:LEU:HD23	1:B:477:LEU:HD21	1.85	0.59
1:A:429:TYR:OH	1:A:448:LYS:CG	2.52	0.58
1:A:419:ARG:NH2	1:A:428:LYS:O	2.36	0.58
1:B:173:ASP:O	1:B:176:LYS:HG2	2.05	0.57
1:B:234:GLU:O	1:B:238:ILE:HG12	2.04	0.57
1:A:301:GLU:OE2	1:A:303:ARG:NH2	2.36	0.57
1:A:170:GLN:OE1	1:A:210:ARG:HD3	2.05	0.56
1:B:423:MET:SD	1:B:426:ARG:NE	2.80	0.55
1:A:429:TYR:OH	1:A:448:LYS:HG2	2.07	0.53
1:B:423:MET:HA	1:B:426:ARG:HE	1.74	0.53
1:A:307:LEU:HD23	1:A:337:VAL:HG13	1.90	0.52
1:A:236:ARG:O	1:A:240:THR:HG22	2.10	0.52
1:A:246:PHE:CD1	1:A:250:LEU:HD12	2.46	0.51
1:A:255:GLU:HG3	1:A:272:LYS:HD2	1.91	0.51
1:A:234:GLU:HG3	1:A:238:ILE:HD11	1.93	0.51
1:B:214:GLY:O	1:B:278:PHE:HA	2.12	0.50
1:A:304:VAL:HG22	1:A:341:LEU:HD13	1.93	0.50
1:A:320:ILE:HB	1:A:454:ILE:HD13	1.93	0.49
1:A:429:TYR:OH	1:A:448:LYS:HG3	2.11	0.49
1:A:290:ASN:HA	1:A:436:PHE:HE2	1.78	0.49
1:A:187:GLU:HG2	1:A:250:LEU:HD11	1.94	0.48
1:B:151:GLU:HG2	1:B:153:LYS:HG2	1.95	0.48
1:A:347:PRO:O	1:A:381:SER:HB2	2.15	0.47
1:A:161:LEU:O	1:A:165:GLU:HG3	2.14	0.47
1:A:176:LYS:HA	1:A:176:LYS:HD2	1.57	0.47
1:B:164:PHE:HD1	1:B:309:LEU:HD23	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:LEU:HD22	1:B:161:LEU:CD2	2.44	0.47
1:A:346:GLU:O	1:A:383:ASN:HB2	2.15	0.47
1:B:334:VAL:O	1:B:338:LEU:HG	2.14	0.46
1:A:322:ASP:OD1	1:A:324:SER:OG	2.27	0.46
1:B:392:LEU:HD12	1:B:469:ARG:NH1	2.30	0.46
1:B:164:PHE:HA	1:B:309:LEU:HD23	1.98	0.46
1:A:352:LEU:HB3	1:A:360:PHE:CE2	2.51	0.45
1:A:471:LEU:HD23	1:A:477:LEU:HD11	1.98	0.45
1:A:191:LEU:HD11	1:A:245:HIS:HB2	1.99	0.45
1:A:450:LYS:O	1:A:454:ILE:HG12	2.17	0.44
1:B:354:LYS:HE3	1:B:413:GLU:HA	2.00	0.44
1:A:177:LYS:HB2	2:A:501:HOH:O	2.16	0.44
1:A:151:GLU:HG2	1:A:153:LYS:HG3	1.99	0.44
1:A:301:GLU:OE1	1:A:348:ILE:HG23	2.18	0.44
1:B:346:GLU:O	1:B:383:ASN:HB2	2.18	0.43
1:A:187:GLU:HG2	1:A:250:LEU:CD1	2.48	0.43
1:A:351:SER:HB2	1:A:414:ALA:HB2	2.00	0.43
1:A:301:GLU:CD	1:A:348:ILE:HG23	2.39	0.43
1:A:304:VAL:HG22	1:A:341:LEU:CD1	2.49	0.43
1:B:465:LEU:HB2	1:B:474:VAL:HG21	2.00	0.43
1:A:152:ALA:HB2	1:A:161:LEU:HD12	2.01	0.43
1:A:214:GLY:HA3	1:A:278:PHE:CD1	2.54	0.42
1:A:199:LEU:CD1	2:A:501:HOH:O	2.67	0.42
1:B:257:PRO:HA	1:B:268:LYS:O	2.18	0.42
1:A:247:CYS:SG	1:A:257:PRO:HG2	2.59	0.42
1:B:322:ASP:HB3	1:B:325:ARG:HB2	2.02	0.42
1:B:423:MET:HA	1:B:426:ARG:NE	2.35	0.42
1:A:315:ALA:CB	1:A:333:LEU:HD11	2.50	0.42
1:A:204:LEU:HD12	1:A:204:LEU:HA	1.88	0.41
1:B:253:TYR:HA	1:B:272:LYS:HD3	2.02	0.41
1:B:309:LEU:HD11	1:B:313:LYS:HE2	2.03	0.41
1:B:468:LYS:HD2	1:B:473:SER:HB3	2.02	0.41
1:A:255:GLU:HG3	1:A:272:LYS:CG	2.51	0.41
1:B:468:LYS:HD2	1:B:473:SER:CB	2.51	0.41
1:A:239:LEU:HD13	1:A:282:VAL:HG23	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:ARG:CD	1:B:151:GLU:OE1[2_657]	2.17	0.03

5.3 Torsion angles

5.3.1 Protein backbone

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	321/380 (84%)	308 (96%)	13 (4%)	0	100	100
1	B	315/380 (83%)	305 (97%)	10 (3%)	0	100	100
All	All	636/760 (84%)	613 (96%)	23 (4%)	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	297/347 (86%)	296 (100%)	1 (0%)	92	97
1	B	293/347 (84%)	293 (100%)	0	100	100
All	All	590/694 (85%)	589 (100%)	1 (0%)	93	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	319	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	449	GLN
1	B	183	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 monosaccharides 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 [i](#)

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	325/380 (85%)	0.29	23 (7%) 16 16	42, 83, 138, 178	0
1	B	319/380 (83%)	-0.03	7 (2%) 62 65	38, 72, 127, 168	0
All	All	644/760 (84%)	0.14	30 (4%) 31 33	38, 76, 133, 178	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	148	THR	5.2
1	A	479	ALA	5.0
1	A	373	PRO	4.0
1	B	423	MET	3.9
1	A	368	LEU	3.7
1	A	261	ARG	3.7
1	A	232	LYS	3.5
1	A	248	THR	3.2
1	A	481	THR	3.2
1	A	366	LEU	3.1
1	A	263	LYS	3.0
1	A	233	THR	3.0
1	A	374	CYS	3.0
1	A	148	THR	3.0
1	A	380	LEU	2.7
1	A	247	CYS	2.7
1	A	184	LEU	2.7
1	A	376	VAL	2.5
1	A	424	GLU	2.5
1	A	190	LEU	2.4
1	A	213	ASP	2.3
1	A	273	VAL	2.3
1	B	147	ILE	2.3
1	A	231	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	292	PHE	2.3
1	B	149	LEU	2.2
1	A	372	ALA	2.1
1	B	249	ARG	2.1
1	B	246	PHE	2.1
1	B	253	TYR	2.1

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 monosaccharides 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.