



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:10 AM UTC

PDB ID : 6O9V / pdb_00006o9v
Title : KirBac3.1 mutant at a resolution of 3.1 Angstroms
Authors : Gulbis, J.M.; Black, K.A.; Miller, D.M.
Deposited on : 2019-03-15
Resolution : 3.09 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 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

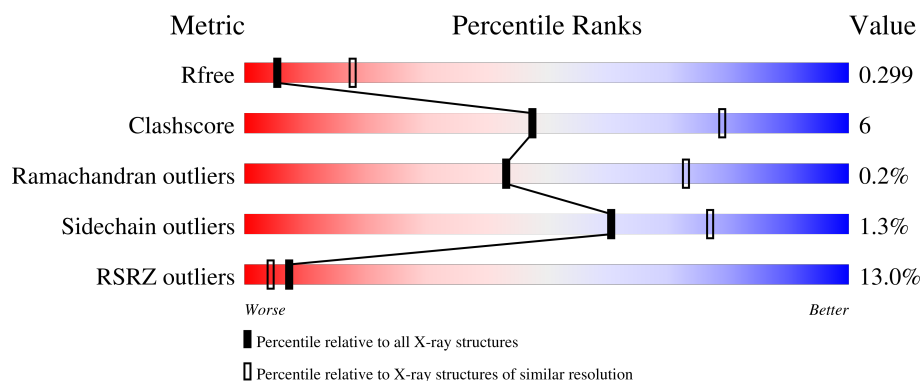
1 Overall quality at a glance

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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	301	11% 79% 12% 7%
1	B	301	14% 80% 14% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	TMO	B	403	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4420 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.

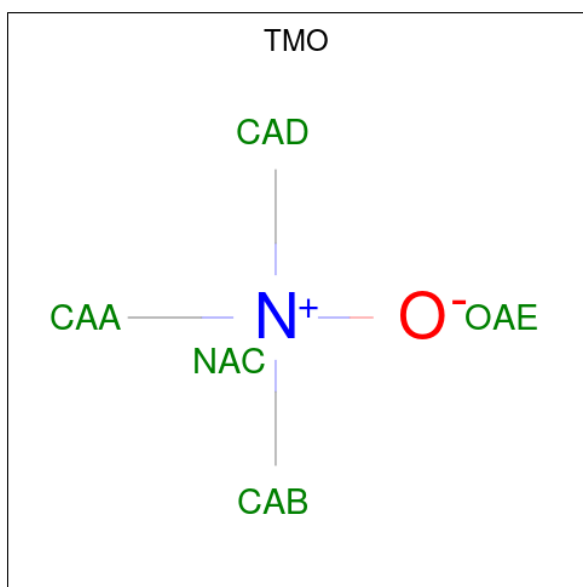
- Molecule 1 is a protein called Inward rectifier potassium channel Kirbac3.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	279	Total	C	N	O	S	0	0	0
			2170	1397	373	391	9			
1	B	282	Total	C	N	O	S	0	0	0
			2181	1401	376	395	9			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	VAL	CYS	engineered mutation	UNP D9N164
A	119	VAL	CYS	engineered mutation	UNP D9N164
A	129	CYS	SER	engineered mutation	UNP D9N164
A	135	CYS	PHE	engineered mutation	UNP D9N164
A	262	SER	CYS	engineered mutation	UNP D9N164
A	296	HIS	-	expression tag	UNP D9N164
A	297	HIS	-	expression tag	UNP D9N164
A	298	HIS	-	expression tag	UNP D9N164
A	299	HIS	-	expression tag	UNP D9N164
A	300	HIS	-	expression tag	UNP D9N164
A	301	HIS	-	expression tag	UNP D9N164
B	71	VAL	CYS	engineered mutation	UNP D9N164
B	119	VAL	CYS	engineered mutation	UNP D9N164
B	129	CYS	SER	engineered mutation	UNP D9N164
B	135	CYS	PHE	engineered mutation	UNP D9N164
B	262	SER	CYS	engineered mutation	UNP D9N164
B	296	HIS	-	expression tag	UNP D9N164
B	297	HIS	-	expression tag	UNP D9N164
B	298	HIS	-	expression tag	UNP D9N164
B	299	HIS	-	expression tag	UNP D9N164
B	300	HIS	-	expression tag	UNP D9N164
B	301	HIS	-	expression tag	UNP D9N164

- Molecule 2 is trimethylamine oxide (CCD ID: TMO) (formula: C₃H₉NO).

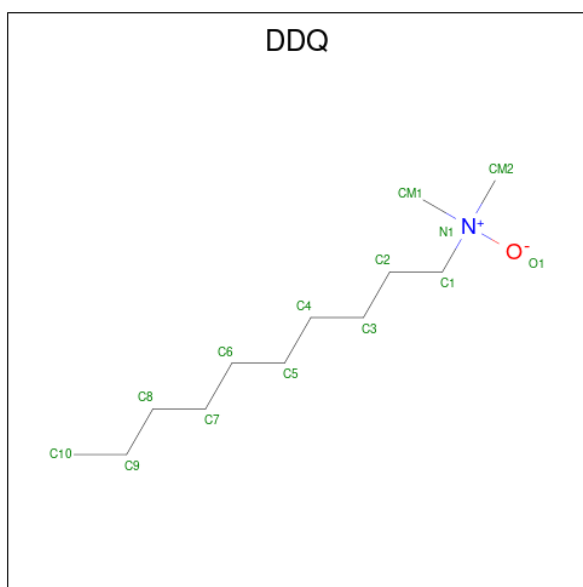


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			5	3	1	1		
2	B	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

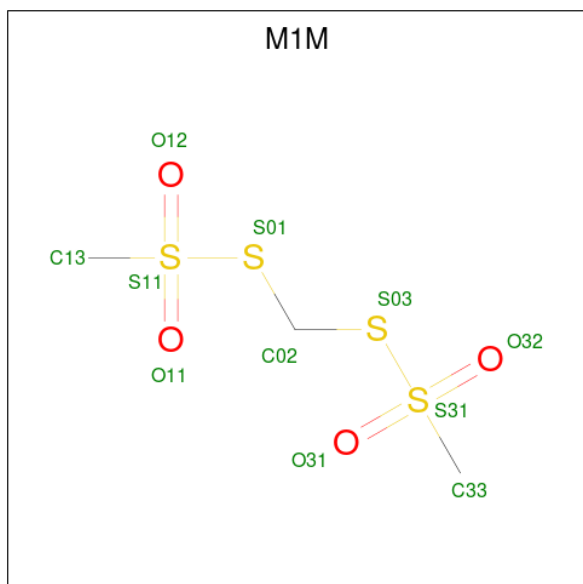
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	K	0	0
			3	3		

- Molecule 4 is DECYLAMINE-N,N-DIMETHYL-N-OXIDE (CCD ID: DDQ) (formula: C₁₂H₂₇NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	1
			20	16	2	2		
4	B	1	Total	C	N	O	0	0
			9	7	1	1		

- Molecule 5 is 1,1-Methanediyl Bismethanethiosulfonate (CCD ID: M1M) (formula: $C_3H_8O_4S_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	S	0	0
			3	1	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	S	0	0
			3	1	2		

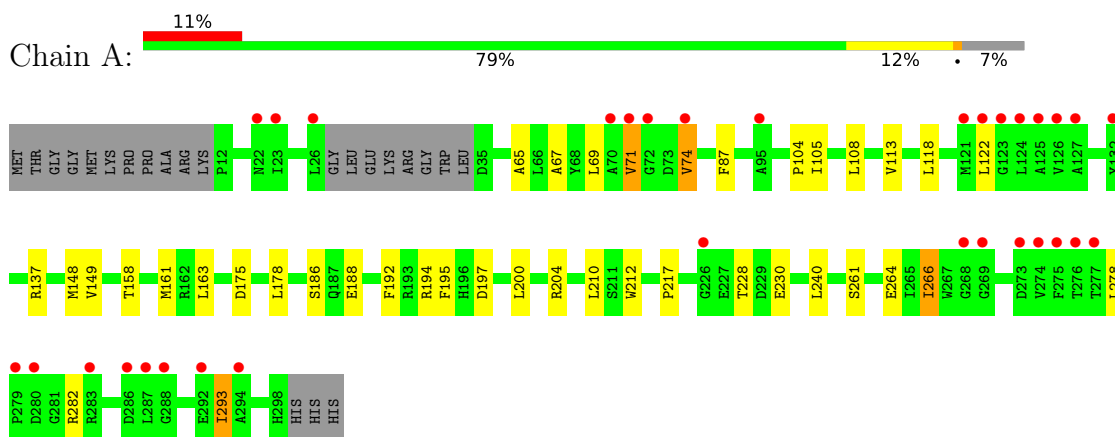
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	9	Total	O	0	0
			9	9		
6	B	12	Total	O	0	0
			12	12		

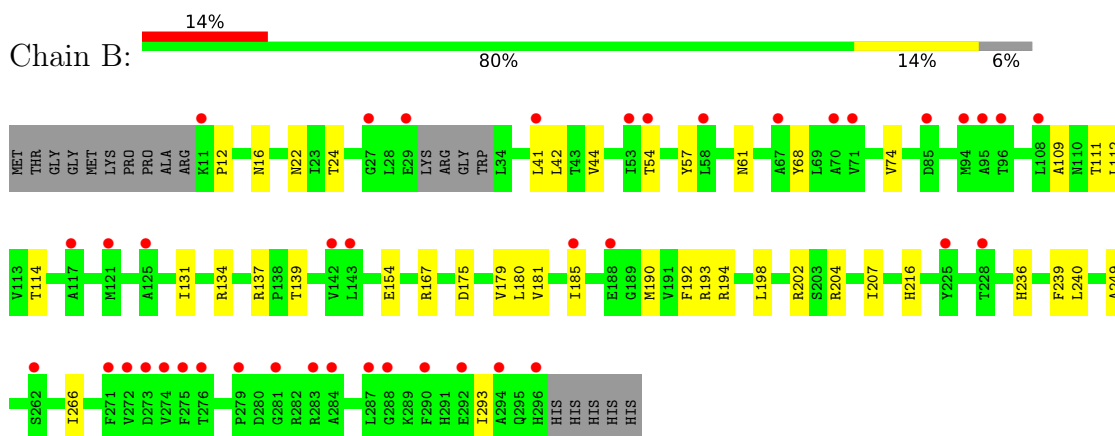
3 Residue-property plots

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: Inward rectifier potassium channel Kirbac3.1



- Molecule 1: Inward rectifier potassium channel Kirbac3.1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	83.30Å 114.68Å 89.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.73 – 3.09 44.73 – 3.09	Depositor EDS
% Data completeness (in resolution range)	98.9 (44.73-3.09) 98.9 (44.73-3.09)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 3.07Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.248 , 0.294 0.258 , 0.299	Depositor DCC
R_{free} test set	835 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å ²)	86.2	Xtriage
Anisotropy	0.560	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 44.9	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	0.88	EDS
Total number of atoms	4420	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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

Bond lengths and bond angles in the following residue types are not validated in this section: TMO, DDQ, K, M1M

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	0.14	0/2225	0.32	0/3030
1	B	0.12	0/2235	0.29	0/3046
All	All	0.13	0/4460	0.31	0/6076

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

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	2170	0	2123	27	0
1	B	2181	0	2117	27	0
2	A	5	0	9	0	0
2	B	5	0	9	0	0
3	A	3	0	0	0	0
4	A	20	0	32	4	0
4	B	9	0	14	1	0
5	B	6	0	0	0	0
6	A	9	0	0	0	0
6	B	12	0	0	0	0
All	All	4420	0	4304	49	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.

All (49) 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:67:ALA:O	1:A:71:VAL:HG12	1.79	0.81
1:A:210:LEU:H	4:A:405[A]:DDQ:HM12	1.50	0.77
1:B:266:ILE:HD11	1:B:293:ILE:HG21	1.74	0.70
1:A:71:VAL:HG22	1:A:108:LEU:HD13	1.77	0.64
1:A:197:ASP:OD1	1:B:202:ARG:NH2	2.32	0.63
1:A:195:PHE:O	1:B:202:ARG:NH1	2.35	0.59
1:A:148:MET:HG2	1:A:161:MET:HB3	1.85	0.59
1:A:137:ARG:NH1	1:B:249:ALA:O	2.37	0.58
1:A:266:ILE:HG21	1:A:293:ILE:HD12	1.86	0.57
1:A:122:LEU:HD22	1:B:131:ILE:HD11	1.87	0.57
1:A:228:THR:HG23	1:A:230:GLU:H	1.70	0.55
1:B:41:LEU:O	1:B:134:ARG:NH1	2.42	0.53
1:A:261:SER:H	1:A:264:GLU:HG3	1.72	0.53
1:B:175:ASP:OD1	1:B:204:ARG:NE	2.30	0.53
1:B:42:LEU:HB3	1:B:137:ARG:NH2	2.24	0.52
1:B:139:THR:O	1:B:167:ARG:NH1	2.37	0.51
1:A:186:SER:HB3	1:A:192:PHE:CE2	2.45	0.51
1:A:178:LEU:HB3	1:A:200:LEU:HD21	1.93	0.50
1:B:111:THR:HA	1:B:114:THR:HG22	1.95	0.49
1:A:118:LEU:HD11	1:B:54:THR:HA	1.94	0.49
1:A:175:ASP:OD2	1:A:204:ARG:NH2	2.46	0.49
1:A:210:LEU:N	4:A:405[B]:DDQ:O1	2.46	0.47
1:A:158:THR:HG22	1:A:217:PRO:HA	1.96	0.47
1:B:42:LEU:HB3	1:B:137:ARG:HH22	1.79	0.47
1:A:74:VAL:HB	1:A:105:ILE:HB	1.97	0.46
1:B:44:VAL:O	1:B:134:ARG:NH2	2.45	0.46
1:B:181:VAL:HG22	1:B:193:ARG:HH21	1.80	0.45
1:A:278:LEU:HD12	1:A:282:ARG:HB2	1.99	0.45
1:A:240:LEU:HD21	1:B:207:ILE:HD12	1.98	0.45
4:B:404:DDQ:HM21	4:B:404:DDQ:H22	1.78	0.45
1:A:192:PHE:CE1	1:A:194:ARG:HG3	2.51	0.44
1:B:12:PRO:HD2	1:B:236:HIS:CE1	2.52	0.44
1:B:57:TYR:O	1:B:61:ASN:ND2	2.39	0.44
1:B:179:VAL:O	1:B:240:LEU:N	2.45	0.44
1:B:68:TYR:CD1	1:B:112:LEU:HD23	2.53	0.44
1:A:186:SER:HB3	1:A:192:PHE:HE2	1.82	0.44
1:B:180:LEU:HD13	1:B:239:PHE:CZ	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:TRP:CD1	4:A:405[A]:DDQ:H42	2.53	0.43
1:B:74:VAL:HB	1:B:109:ALA:HB2	2.00	0.43
1:B:185:ILE:HA	1:B:190:MET:O	2.18	0.43
1:A:149:VAL:HG12	1:A:266:ILE:HG23	2.00	0.43
1:A:188:GLU:OE1	1:B:154:GLU:N	2.50	0.42
1:B:192:PHE:HZ	1:B:194:ARG:HH21	1.68	0.42
1:A:104:PRO:HG3	1:A:113:VAL:HG21	2.01	0.42
1:B:190:MET:HE2	1:B:192:PHE:HB3	2.02	0.41
1:B:198:LEU:HB3	1:B:216:HIS:ND1	2.36	0.41
1:A:65:ALA:HB2	1:A:87:PHE:HA	2.02	0.41
1:B:16:ASN:OD1	1:B:22:ASN:HB2	2.21	0.41
4:A:405[B]:DDQ:HM11	4:A:405[B]:DDQ:H22	1.88	0.40

There are no symmetry-related clashes.

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	275/301 (91%)	264 (96%)	10 (4%)	1 (0%)	30	61
1	B	278/301 (92%)	266 (96%)	12 (4%)	0	100	100
All	All	553/602 (92%)	530 (96%)	22 (4%)	1 (0%)	43	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	71	VAL

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	232/256 (91%)	227 (98%)	5 (2%)	45	71
1	B	231/256 (90%)	230 (100%)	1 (0%)	84	86
All	All	463/512 (90%)	457 (99%)	6 (1%)	61	77

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	LEU
1	A	74	VAL
1	A	163	LEU
1	A	266	ILE
1	A	293	ILE
1	B	24	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	221	HIS
1	B	77	ASN
1	B	236	HIS
1	B	252	GLN
1	B	270	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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	M1M	B	402	1	2,2,10	1.23	0	0,1,15	-	-
4	DDQ	A	405[B]	-	7,9,13	2.17	1 (14%)	8,11,15	0.29	0
4	DDQ	B	404	-	6,8,13	2.33	1 (16%)	7,10,15	0.26	0
4	DDQ	A	405[A]	-	7,9,13	2.20	1 (14%)	8,11,15	0.33	0
5	M1M	B	401	1	2,2,10	1.31	0	0,1,15	-	-
2	TMO	B	403	-	4,4,4	1.90	3 (75%)	6,6,6	0.23	0
2	TMO	A	401	-	4,4,4	1.90	3 (75%)	6,6,6	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DDQ	A	405[B]	-	-	2/7/7/11	-
4	DDQ	B	404	-	-	2/6/6/11	-
4	DDQ	A	405[A]	-	-	2/7/7/11	-

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	405[A]	DDQ	C1-N1	-5.77	1.45	1.51
4	A	405[B]	DDQ	C1-N1	-5.68	1.45	1.51
4	B	404	DDQ	C1-N1	-5.64	1.45	1.51
2	A	401	TMO	CAB-NAC	-2.08	1.45	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	TMO	CAA-NAC	-2.06	1.45	1.48
2	B	403	TMO	CAA-NAC	-2.04	1.45	1.48
2	B	403	TMO	CAB-NAC	-2.04	1.45	1.48
2	B	403	TMO	CAD-NAC	-2.04	1.45	1.48
2	A	401	TMO	CAD-NAC	-2.02	1.45	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	405[A]	DDQ	C1-C2-C3-C4
4	A	405[B]	DDQ	C2-C3-C4-C5
4	A	405[A]	DDQ	C2-C3-C4-C5
4	B	404	DDQ	N1-C1-C2-C3
4	A	405[B]	DDQ	C3-C4-C5-C6
4	B	404	DDQ	C2-C3-C4-C5

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	405[B]	DDQ	2	0
4	B	404	DDQ	1	0
4	A	405[A]	DDQ	2	0

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	279/301 (92%)	0.73	32 (11%) 9 5	59, 88, 126, 154	0
1	B	282/301 (93%)	0.85	41 (14%) 6 3	56, 91, 129, 165	0
All	All	561/602 (93%)	0.79	73 (13%) 7 4	56, 90, 128, 165	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	276	THR	10.6
1	A	71	VAL	10.5
1	B	71	VAL	8.1
1	B	275	PHE	7.2
1	B	276	THR	6.9
1	B	95	ALA	6.9
1	A	279	PRO	6.7
1	B	70	ALA	6.2
1	A	70	ALA	6.2
1	A	286	ASP	5.6
1	A	275	PHE	5.3
1	B	283	ARG	5.3
1	B	284	ALA	5.2
1	A	125	ALA	5.0
1	B	29	GLU	4.9
1	A	121	MET	4.8
1	A	294	ALA	4.7
1	A	95	ALA	4.7
1	B	117	ALA	4.6
1	A	72	GLY	4.4
1	B	143	LEU	4.4
1	A	277	THR	4.4
1	B	27	GLY	4.3
1	A	280	ASP	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	287	LEU	3.9
1	A	288	GLY	3.9
1	B	121	MET	3.9
1	B	67	ALA	3.9
1	B	274	VAL	3.8
1	A	287	LEU	3.8
1	A	126	VAL	3.6
1	B	281	GLY	3.5
1	B	296	HIS	3.4
1	B	292	GLU	3.4
1	A	283	ARG	3.3
1	B	85	ASP	3.3
1	B	272	VAL	3.2
1	A	23	ILE	3.2
1	B	294	ALA	3.0
1	A	122	LEU	3.0
1	A	124	LEU	3.0
1	B	94	MET	2.9
1	B	185	ILE	2.8
1	A	123	GLY	2.8
1	B	142	VAL	2.8
1	B	41	LEU	2.8
1	B	273	ASP	2.7
1	A	26	LEU	2.6
1	A	274	VAL	2.6
1	B	58	LEU	2.6
1	A	292	GLU	2.5
1	B	96	THR	2.4
1	B	288	GLY	2.4
1	B	125	ALA	2.4
1	B	54	THR	2.3
1	A	268	GLY	2.3
1	B	108	LEU	2.3
1	A	127	ALA	2.2
1	B	271	PHE	2.2
1	A	273	ASP	2.2
1	B	290	PHE	2.2
1	A	132	TYR	2.1
1	B	262	SER	2.1
1	B	279	PRO	2.1
1	A	22	ASN	2.1
1	B	53	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	11	LYS	2.1
1	A	269	GLY	2.1
1	B	188	GLU	2.1
1	A	74	VAL	2.0
1	B	225	TYR	2.0
1	B	228	THR	2.0
1	A	226	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 oligosaccharides 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(Å ²)	Q<0.9
2	TMO	B	403	5/5	0.75	0.57	60,62,75,91	5
4	DDQ	B	404	9/14	0.79	0.20	61,73,83,92	0
4	DDQ	A	405[B]	10/14	0.83	0.21	71,82,86,128	10
4	DDQ	A	405[A]	10/14	0.83	0.21	73,83,86,127	10
2	TMO	A	401	5/5	0.85	0.29	78,86,94,96	5
3	K	A	403	1/1	0.88	0.10	109,109,109,109	1
5	M1M	B	401	3/11	0.89	0.20	91,91,96,153	0
5	M1M	B	402	3/11	0.91	0.14	92,92,112,113	0
3	K	A	402	1/1	0.93	0.07	104,104,104,104	1
3	K	A	404	1/1	0.95	0.10	79,79,79,79	1

6.5 Other polymers [i](#)

There are no such residues in this entry.