



Full wwPDB X-ray Structure Validation Report ⓘ

May 19, 2026 – 10:10 pm BST

PDB ID : 9S1A / pdb_00009s1a
Title : WRN helicase in the absence of nucleotide or DNA
Authors : Fletcher, C.T.; Rucktooa, P.
Deposited on : 2025-07-18
Resolution : 1.96 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 : 1.8.4, CSD as541be (2020)
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

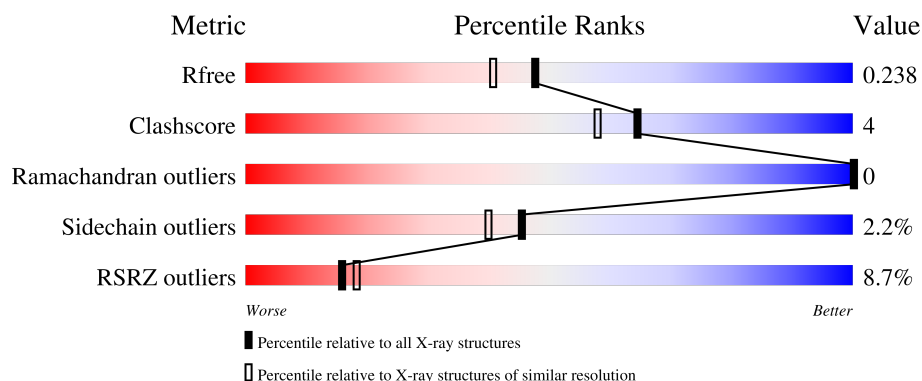
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	427	<div> <div>9%</div> <div>82%</div> <div>8%</div> <div>10%</div> </div>
1	B	427	<div> <div>7%</div> <div>85%</div> <div>8%</div> <div>5%</div> </div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6805 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 Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	386	Total	C	N	O	S	0	5	0
			3095	1966	544	556	29			
1	B	404	Total	C	N	O	S	0	11	0
			3290	2083	584	595	28			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	515	GLY	-	expression tag	UNP Q14191
A	516	MET	-	expression tag	UNP Q14191
B	515	GLY	-	expression tag	UNP Q14191
B	516	MET	-	expression tag	UNP Q14191

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

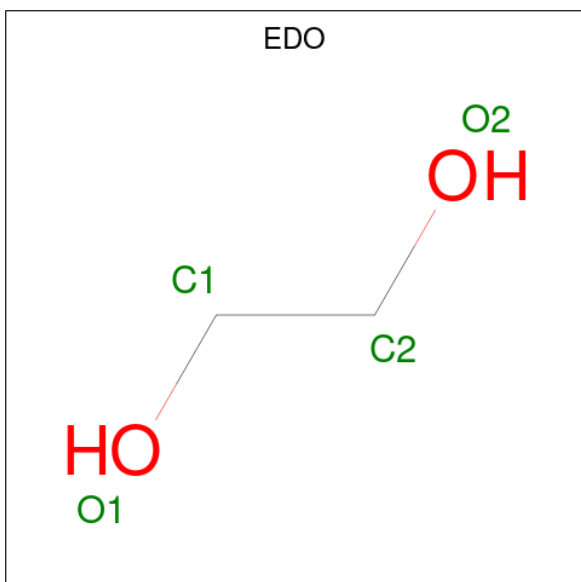
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



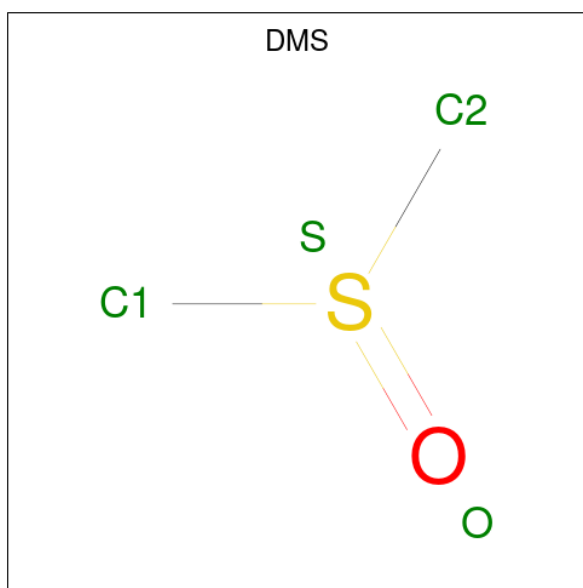
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	1
4	B	1	Total C O 4 2 2	0	0

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C O S 4 2 1 1	0	0
5	B	1	Total C O S 4 2 1 1	0	0

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

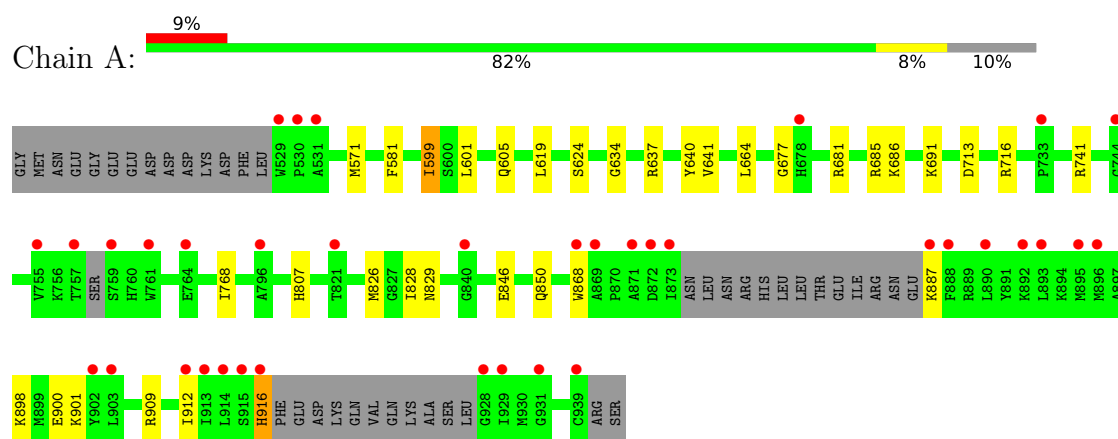
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	156	Total	O	0	0
			156	156		
7	B	185	Total	O	0	1
			185	185		

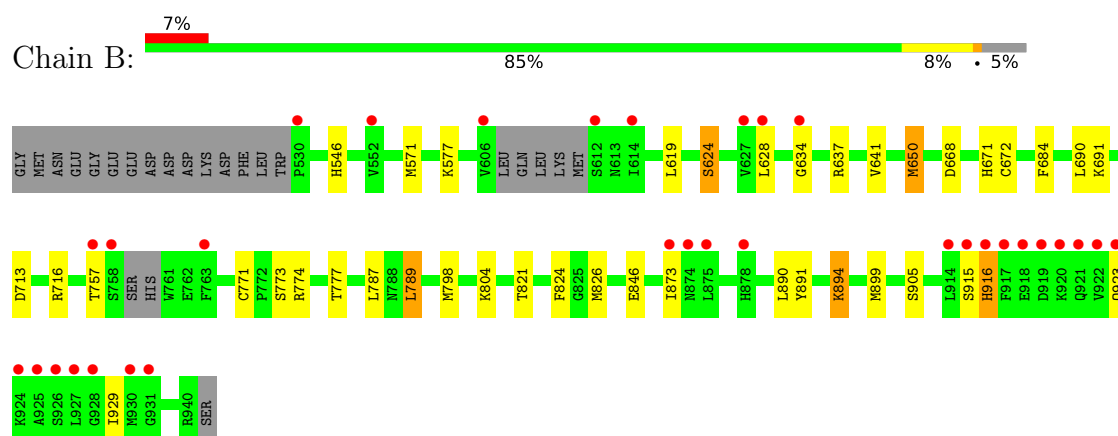
3 Residue-property plots

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: Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN



- Molecule 1: Bifunctional 3'-5' exonuclease/ATP-dependent helicase WRN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.76Å 80.24Å 83.09Å 90.00° 90.27° 90.00°	Depositor
Resolution (Å)	57.72 – 1.96 57.72 – 1.96	Depositor EDS
% Data completeness (in resolution range)	90.3 (57.72-1.96) 90.3 (57.72-1.96)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 1.95Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.207 , 0.247 0.201 , 0.238	Depositor DCC
R_{free} test set	3087 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.008 for -h,l,k 0.024 for -h,-l,-k 0.045 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6805	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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: GOL, EDO, ZN, DMS, SO4

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	0.72	0/3164	1.00	0/4269
1	B	0.74	3/3373 (0.1%)	1.01	1/4547 (0.0%)
All	All	0.73	3/6537 (0.0%)	1.01	1/8816 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	826	MET	SD-CE	-8.29	1.58	1.79
1	B	899	MET	SD-CE	-7.07	1.61	1.79
1	B	650	MET	SD-CE	-6.93	1.62	1.79

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	824	PHE	CA-CB-CG	11.08	124.88	113.80

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	3095	0	3125	27	0
1	B	3290	0	3322	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	0	0	0
3	B	15	0	0	0	0
4	A	8	0	12	0	0
4	B	24	0	36	6	0
5	B	8	0	12	1	0
6	B	12	0	16	2	0
7	A	156	0	0	0	0
7	B	185	0	0	2	0
All	All	6805	0	6523	51	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 4.

All (51) 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:624:SER:HB3	7:B:1101:HOH:O	1.71	0.91
1:B:546:HIS:ND1	5:B:1011:DMS:H21	1.92	0.85
1:B:915:SER:HA	1:B:923:GLN:HG3	1.65	0.79
1:B:619:LEU:HB3	1:B:641[B]:VAL:HG12	1.69	0.75
1:B:916:HIS:HE1	4:B:1007:EDO:O1	1.70	0.75
1:B:650:MET:HE1	1:B:690:LEU:HD23	1.70	0.71
1:B:787:LEU:HB2	1:B:789:LEU:HD22	1.74	0.69
1:A:619:LEU:HB3	1:A:641[B]:VAL:CG1	2.23	0.68
1:A:601:LEU:HD21	1:B:624:SER:HB3	1.77	0.67
1:B:774[B]:ARG:HE	4:B:1009[B]:EDO:H22	1.60	0.66
1:A:807:HIS:HE1	1:A:829:ASN:O	1.78	0.66
1:A:599:ILE:HD11	1:A:640:TYR:HB3	1.78	0.65
1:A:681:ARG:HE	1:A:685:ARG:NH1	1.93	0.65
1:B:915:SER:HA	1:B:923:GLN:CG	2.27	0.65
1:A:619:LEU:HB3	1:A:641[B]:VAL:HG12	1.81	0.61
1:A:619:LEU:HB3	1:A:641[A]:VAL:HG22	1.82	0.60
1:B:916:HIS:CE1	4:B:1007:EDO:O1	2.54	0.59
1:B:846:GLU:HG3	4:B:1007:EDO:H12	1.87	0.56
1:A:677:GLY:O	1:A:681:ARG:HB2	2.07	0.55
1:A:686:LYS:NZ	4:B:1010:EDO:H21	2.22	0.55
1:B:773:SER:O	1:B:777:THR:HG23	2.09	0.52
1:B:634:GLY:O	1:B:637:ARG:NH1	2.43	0.51
1:B:798:MET:O	7:B:1101:HOH:O	2.18	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:741:ARG:NH1	1:A:868:TRP:CH2	2.79	0.50
1:A:898:LYS:HA	1:A:901:LYS:CE	2.43	0.49
1:B:774[A]:ARG:HD3	1:B:821:THR:HG21	1.95	0.48
1:A:768:ILE:HD11	1:A:828:ILE:HG21	1.94	0.48
1:A:634:GLY:O	1:A:637:ARG:NH1	2.46	0.48
1:A:898:LYS:HA	1:A:901:LYS:HE3	1.97	0.47
1:B:771:CYS:HB2	1:B:777:THR:HG22	1.96	0.46
1:A:619:LEU:HD23	1:A:641[B]:VAL:HG11	1.98	0.46
1:B:713:ASP:OD1	1:B:716:ARG:NH1	2.49	0.46
1:B:672:CYS:HB3	1:B:684:PHE:HB2	1.98	0.45
1:B:650:MET:HE1	1:B:690:LEU:HA	1.96	0.45
1:B:891:TYR:CE1	6:B:1012:GOL:H31	2.51	0.45
1:A:686:LYS:HZ2	4:B:1010:EDO:H21	1.80	0.45
1:A:713:ASP:OD1	1:A:716:ARG:NH1	2.50	0.45
1:B:668:ASP:OD2	1:B:671:HIS:ND1	2.44	0.45
1:B:905:SER:HA	6:B:1006:GOL:H2	1.97	0.45
1:B:890:LEU:O	1:B:894:LYS:HG2	2.17	0.45
1:A:681:ARG:HE	1:A:685:ARG:HH12	1.64	0.44
1:A:898:LYS:NZ	1:A:916:HIS:HA	2.33	0.44
1:A:846:GLU:O	1:A:850:GLN:HG3	2.18	0.44
1:A:691:LYS:HD2	1:A:691:LYS:HA	1.85	0.43
1:A:909:ARG:HA	1:A:912:ILE:HD12	2.03	0.41
1:B:691:LYS:HD2	1:B:691:LYS:HA	1.91	0.41
1:A:581:PHE:HA	1:A:664[A]:LEU:HD11	2.01	0.41
1:A:571:MET:HE2	1:A:571:MET:HB3	1.94	0.41
1:A:768:ILE:CD1	1:A:828:ILE:HG21	2.51	0.40
1:A:581:PHE:HZ	1:A:605:GLN:HE22	1.69	0.40
1:B:571:MET:HE2	1:B:571:MET:HB3	1.97	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	383/427 (90%)	375 (98%)	8 (2%)	0	100	100
1	B	409/427 (96%)	398 (97%)	11 (3%)	0	100	100
All	All	792/854 (93%)	773 (98%)	19 (2%)	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	344/377 (91%)	339 (98%)	5 (2%)	57	54
1	B	367/377 (97%)	357 (97%)	10 (3%)	39	32
All	All	711/754 (94%)	696 (98%)	15 (2%)	45	41

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	599	ILE
1	A	826	MET
1	A	887	LYS
1	A	900	GLU
1	A	916	HIS
1	B	577	LYS
1	B	624	SER
1	B	628	LEU
1	B	757	THR
1	B	789	LEU
1	B	804	LYS
1	B	873	ILE
1	B	894	LYS
1	B	916	HIS
1	B	929	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	546	HIS
1	A	605	GLN
1	A	722	ASN
1	A	779	GLN
1	A	807	HIS
1	A	861	GLN
1	A	916	HIS
1	A	938	ASN
1	B	605	GLN
1	B	722	ASN
1	B	748	GLN
1	B	778	GLN
1	B	779	GLN
1	B	829	ASN
1	B	835	GLN
1	B	861	GLN
1	B	916	HIS
1	B	938	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 2 are monoatomic - leaving 17 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
3	SO4	B	1013	-	4,4,4	0.10	0	6,6,6	1.02	0
4	EDO	B	1008	-	3,3,3	0.22	0	2,2,2	0.34	0
4	EDO	B	1010	-	3,3,3	0.38	0	2,2,2	0.16	0
6	GOL	B	1006	-	5,5,5	0.04	0	5,5,5	0.31	0
3	SO4	A	1002	-	4,4,4	0.10	0	6,6,6	0.27	0
3	SO4	A	1005	-	4,4,4	0.12	0	6,6,6	0.90	0
4	EDO	A	1003	-	3,3,3	0.15	0	2,2,2	0.33	0
4	EDO	B	1003	-	3,3,3	0.43	0	2,2,2	0.36	0
4	EDO	B	1007	-	3,3,3	0.13	0	2,2,2	0.54	0
6	GOL	B	1012	-	5,5,5	0.07	0	5,5,5	0.30	0
5	DMS	B	1004	-	3,3,3	0.57	0	3,3,3	0.54	0
3	SO4	B	1014	-	4,4,4	0.16	0	6,6,6	0.80	0
4	EDO	A	1004	-	3,3,3	0.18	0	2,2,2	0.42	0
3	SO4	B	1002	-	4,4,4	0.07	0	6,6,6	0.85	0
5	DMS	B	1011	-	3,3,3	0.67	0	3,3,3	0.38	0
4	EDO	B	1005	-	3,3,3	0.12	0	2,2,2	0.42	0
4	EDO	B	1009[B]	-	3,3,3	0.25	0	2,2,2	0.24	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
6	GOL	B	1006	-	-	0/4/4/4	-
4	EDO	B	1008	-	-	1/1/1/1	-
4	EDO	B	1010	-	-	1/1/1/1	-
4	EDO	B	1003	-	-	0/1/1/1	-
4	EDO	B	1007	-	-	0/1/1/1	-
4	EDO	A	1003	-	-	1/1/1/1	-
6	GOL	B	1012	-	-	1/4/4/4	-
4	EDO	A	1004	-	-	0/1/1/1	-
4	EDO	B	1005	-	-	0/1/1/1	-
4	EDO	B	1009[B]	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1010	EDO	O1-C1-C2-O2
6	B	1012	GOL	C1-C2-C3-O3
4	B	1009[B]	EDO	O1-C1-C2-O2
4	A	1003	EDO	O1-C1-C2-O2
4	B	1008	EDO	O1-C1-C2-O2

There are no ring outliers.

6 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1010	EDO	2	0
6	B	1006	GOL	1	0
4	B	1007	EDO	3	0
6	B	1012	GOL	1	0
5	B	1011	DMS	1	0
4	B	1009[B]	EDO	1	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	386/427 (90%)	0.54	37 (9%) 13 15	10, 42, 76, 88	5 (1%)
1	B	404/427 (94%)	0.35	32 (7%) 18 21	12, 33, 55, 81	11 (2%)
All	All	790/854 (92%)	0.44	69 (8%) 16 18	10, 37, 72, 88	16 (2%)

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	873	ILE	5.2
1	B	758	SER	4.5
1	A	928	GLY	4.4
1	A	529	TRP	4.4
1	B	875	LEU	4.3
1	B	925	ALA	4.0
1	B	927	LEU	3.9
1	B	922	VAL	3.9
1	B	757	THR	3.9
1	A	871	ALA	3.8
1	A	757	THR	3.4
1	B	530	PRO	3.4
1	B	873	ILE	3.3
1	B	917	PHE	3.3
1	A	896	MET	3.2
1	B	931	GLY	3.1
1	B	914	LEU	3.0
1	A	929	ILE	3.0
1	A	890	LEU	2.9
1	A	913	ILE	2.9
1	B	924	LYS	2.9
1	A	939	CYS	2.8
1	B	627	VAL	2.8
1	B	916	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	930	MET	2.8
1	A	931	GLY	2.7
1	A	903	LEU	2.7
1	B	614	ILE	2.7
1	B	552	VAL	2.7
1	A	914	LEU	2.6
1	A	887	LYS	2.6
1	A	902	TYR	2.6
1	A	733	PRO	2.6
1	A	893	LEU	2.5
1	B	919	ASP	2.5
1	B	634	GLY	2.5
1	B	874	ASN	2.5
1	B	878	HIS	2.5
1	B	921	GLN	2.5
1	A	764	GLU	2.5
1	B	612	SER	2.5
1	A	888	PHE	2.4
1	B	920	LYS	2.4
1	A	678	HIS	2.4
1	A	916	HIS	2.4
1	B	915	SER	2.4
1	B	923	GLN	2.4
1	A	755	VAL	2.4
1	B	918	GLU	2.3
1	A	869	ALA	2.3
1	A	759	SER	2.3
1	B	763[A]	PHE	2.2
1	B	926	SER	2.2
1	A	761	TRP	2.2
1	A	895	MET	2.2
1	A	531	ALA	2.2
1	A	744	GLY	2.2
1	A	868	TRP	2.1
1	A	840	GLY	2.1
1	B	928	GLY	2.1
1	A	530	PRO	2.1
1	B	628	LEU	2.1
1	A	821	THR	2.1
1	A	796	ALA	2.1
1	A	872	ASP	2.1
1	A	892	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	915	SER	2.0
1	A	912	ILE	2.0
1	B	606	VAL	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
5	DMS	B	1011	4/4	0.63	0.23	106,106,106,106	0
4	EDO	A	1004	4/4	0.76	0.21	67,67,67,67	0
4	EDO	B	1005	4/4	0.80	0.20	68,68,68,68	0
6	GOL	B	1012	6/6	0.80	0.20	62,62,63,63	0
4	EDO	B	1003	4/4	0.82	0.14	37,37,37,37	0
6	GOL	B	1006	6/6	0.82	0.14	62,62,62,63	0
4	EDO	A	1003	4/4	0.82	0.21	54,54,54,54	0
4	EDO	B	1009[B]	4/4	0.83	0.13	44,45,45,46	4
4	EDO	B	1007	4/4	0.86	0.18	59,59,59,60	0
4	EDO	B	1008	4/4	0.86	0.14	55,55,55,55	0
4	EDO	B	1010	4/4	0.89	0.13	56,56,57,57	0
5	DMS	B	1004	4/4	0.91	0.14	48,48,48,48	0
3	SO4	A	1005	5/5	0.94	0.11	47,47,47,47	0
3	SO4	B	1002	5/5	0.94	0.09	54,54,55,55	0
3	SO4	A	1002	5/5	0.97	0.06	47,47,47,47	0
3	SO4	B	1014	5/5	0.97	0.08	36,37,37,38	0
3	SO4	B	1013	5/5	0.98	0.05	28,29,29,30	0
2	ZN	A	1001	1/1	0.99	0.04	61,61,61,61	0
2	ZN	B	1001	1/1	1.00	0.02	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.