



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 13, 2024 – 09:35 pm BST

PDB ID : 2YKG  
Title : Structural insights into RNA recognition by RIG-I  
Authors : Luo, D.; Pyle, A.M.  
Deposited on : 2011-05-27  
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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

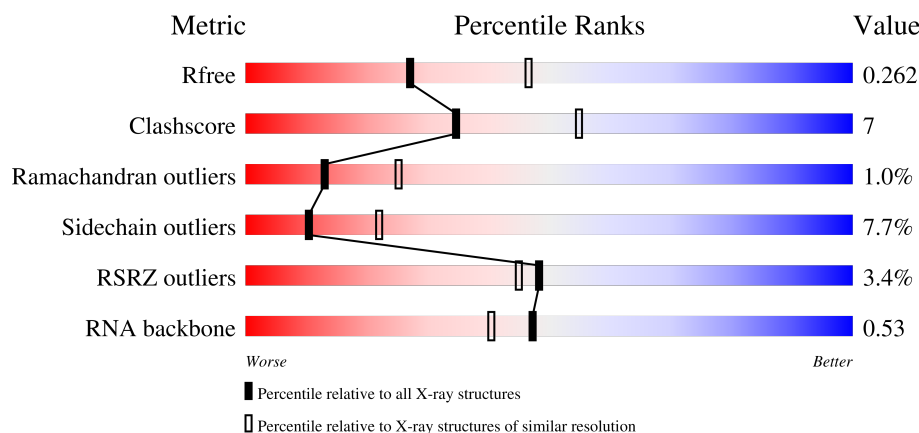
# 1 Overall quality at a glance

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))
$R_{free}$	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)
RNA backbone	3690	1181 (2.80-2.20)

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  $\geq 3$ , 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	696	 3% 73% 16% 9%
2	C	10	 70% 20% 10%
2	D	10	 70% 30%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5523 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 PROBABLE ATP-DEPENDENT RNA HELICASE DDX58.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	636	Total	C	N	O	S	5	1	0
			4994	3201	846	917	30			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	306	ASN	GLN	conflict	UNP O95786
A	419	THR	ASN	conflict	UNP O95786
A	828	ASP	GLU	conflict	UNP O95786

- Molecule 2 is a RNA chain called 5'-R(\*GP\*CP\*GP\*CP\*GP\*CP\*GP\*CP\*GP\*CP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	P	0	0	0
			212	95	40	68	9			
2	D	10	Total	C	N	O	P	0	0	0
			212	95	40	68	9			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

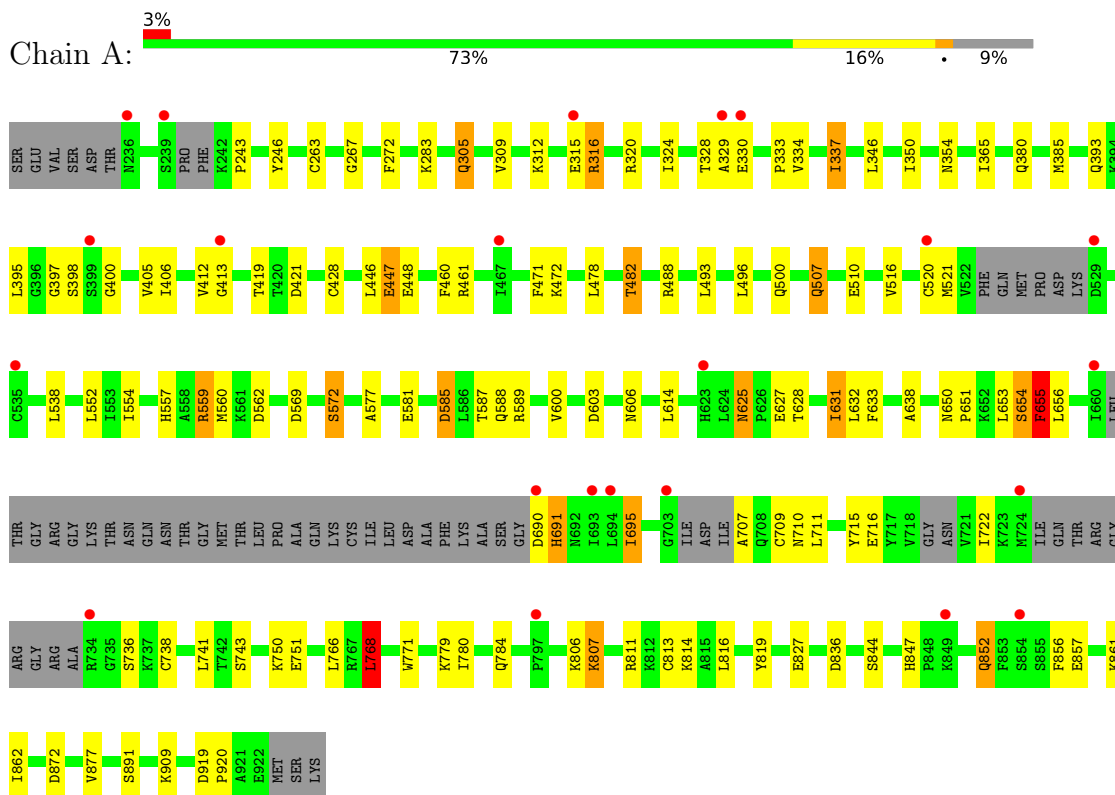
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	80	Total	O	0	0
			80	80		
5	C	11	Total	O	0	0
			11	11		
5	D	8	Total	O	0	0
			8	8		

### 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: PROBABLE ATP-DEPENDENT RNA HELICASE DDX58



#### • Molecule 2: 5'-R(\*GP\*CP\*GP\*CP\*GP\*CP\*GP\*CP\*GP\*CP)-3'



#### • Molecule 2: 5'-R(\*GP\*CP\*GP\*CP\*GP\*CP\*GP\*CP\*GP\*CP)-3'



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	47.62Å 76.21Å 219.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 2.50 45.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.7 (45.00-2.50) 93.7 (45.00-2.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.220 , 0.273 0.214 , 0.262	Depositor DCC
$R_{free}$ test set	1341 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.1	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 57.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5523	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, ZN

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	0.77	1/5093 (0.0%)	0.69	4/6881 (0.1%)
2	C	0.86	0/236	1.30	3/367 (0.8%)
2	D	0.84	0/236	1.45	1/367 (0.3%)
All	All	0.77	1/5565 (0.0%)	0.78	8/7615 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	807	LYS	CE-NZ	-39.46	0.50	1.49

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	807	LYS	CD-CE-NZ	22.21	162.79	111.70
2	C	10	C	O4'-C1'-N1	7.00	113.80	108.20
1	A	768	LEU	CA-CB-CG	5.91	128.89	115.30
1	A	654	SER	N-CA-C	5.58	126.07	111.00
2	D	4	C	O4'-C1'-N1	5.42	112.53	108.20
2	C	2	C	O4'-C1'-N1	5.30	112.44	108.20
1	A	771	TRP	CA-CB-CG	5.13	123.44	113.70
2	C	3	G	O4'-C1'-N9	5.01	112.21	108.20

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	4994	0	4909	78	0
2	C	212	0	112	0	0
2	D	212	0	112	0	0
3	A	1	0	0	0	0
4	A	5	0	0	1	0
5	A	80	0	0	1	0
5	C	11	0	0	0	0
5	D	8	0	0	0	0
All	All	5523	0	5133	78	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 7.

All (78) 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:560:MET:HE3	1:A:600:VAL:HG12	1.41	1.00
1:A:654:SER:H	1:A:655:PHE:HB3	1.28	0.98
1:A:560:MET:CE	1:A:600:VAL:HG12	1.94	0.96
1:A:471:PHE:HB2	1:A:560:MET:HE3	1.46	0.95
1:A:654:SER:N	1:A:655:PHE:HB3	1.87	0.88
1:A:690:ASP:HA	1:A:691:HIS:CB	2.07	0.84
1:A:471:PHE:HB2	1:A:560:MET:CE	2.10	0.81
1:A:653:LEU:HB3	1:A:656:LEU:HD12	1.61	0.81
1:A:780:ILE:O	1:A:784:GLN:HG3	1.81	0.80
1:A:428:CYS:SG	1:A:779:LYS:NZ	2.54	0.79
1:A:557:HIS:CE1	1:A:716:GLU:HG2	2.18	0.78
1:A:654:SER:CA	1:A:655:PHE:HB3	2.17	0.73
1:A:461:ARG:HB2	1:A:741:LEU:HD23	1.71	0.73
1:A:585:ASP:O	1:A:589:ARG:HG3	1.89	0.72
1:A:460:PHE:HE1	1:A:751:GLU:HG2	1.55	0.71
1:A:560:MET:HE3	1:A:600:VAL:CG1	2.21	0.70
1:A:263:CYS:SG	5:A:2007:HOH:O	2.00	0.67
1:A:412:VAL:HG23	1:A:413:GLY:N	2.09	0.66
1:A:631:ILE:HD12	1:A:633:PHE:CE1	2.34	0.62
1:A:560:MET:HE1	1:A:600:VAL:HG12	1.80	0.61
1:A:656:LEU:HB3	1:A:695:ILE:HD11	1.82	0.61
1:A:460:PHE:CE1	1:A:751:GLU:HG2	2.36	0.59
1:A:246:TYR:HD2	1:A:448:GLU:OE1	1.86	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:654:SER:H	1:A:655:PHE:CB	2.09	0.58
1:A:559:ARG:HD3	1:A:562:ASP:OD2	2.04	0.57
1:A:447:GLU:H	1:A:447:GLU:CD	2.08	0.57
1:A:603:ASP:O	1:A:606:ASN:HB2	2.06	0.56
1:A:419:THR:HG22	1:A:421:ASP:H	1.69	0.56
1:A:496:LEU:HD23	1:A:516:VAL:HG13	1.88	0.54
1:A:844:SER:HB3	1:A:862:ILE:HG22	1.90	0.54
1:A:625:ASN:ND2	1:A:627:GLU:H	2.06	0.54
1:A:632:LEU:HD11	1:A:715:TYR:HB2	1.90	0.53
1:A:315:GLU:O	1:A:316:ARG:CB	2.57	0.53
1:A:329:ALA:HB1	1:A:330:GLU:HA	1.90	0.53
1:A:312:LYS:O	1:A:315:GLU:HG2	2.09	0.52
1:A:478:LEU:O	1:A:482:THR:CG2	2.57	0.52
1:A:690:ASP:CA	1:A:691:HIS:CB	2.84	0.52
1:A:334:VAL:HG11	1:A:354:ASN:OD1	2.10	0.52
1:A:807:LYS:HD2	1:A:816:LEU:HD13	1.92	0.52
1:A:813:CYS:O	1:A:814:LYS:HB2	2.10	0.50
1:A:412:VAL:CG2	1:A:413:GLY:N	2.74	0.49
1:A:569:ASP:O	1:A:572:SER:HB3	2.13	0.49
1:A:507:GLN:H	1:A:507:GLN:CD	2.15	0.49
1:A:554:ILE:HD11	1:A:638:ALA:HB1	1.95	0.48
1:A:267:GLY:N	4:A:1923:SO4:O1	2.33	0.47
1:A:333:PRO:O	1:A:337:ILE:HD12	2.15	0.47
1:A:768:LEU:HD12	1:A:768:LEU:C	2.35	0.47
1:A:460:PHE:CE1	1:A:751:GLU:CG	2.98	0.47
1:A:710:ASN:HA	1:A:736:SER:HB3	1.97	0.46
1:A:807:LYS:HG2	1:A:819:TYR:CE1	2.50	0.46
1:A:872:ASP:O	1:A:891:SER:OG	2.30	0.45
1:A:393:GLN:HG3	1:A:398:SER:HB2	1.99	0.45
1:A:628:THR:HA	1:A:710:ASN:HD21	1.81	0.45
1:A:380:GLN:HA	1:A:385:MET:HE3	1.99	0.45
1:A:521:MET:H	1:A:521:MET:HG3	1.59	0.44
1:A:631:ILE:HD13	1:A:632:LEU:N	2.33	0.44
1:A:632:LEU:HD11	1:A:715:TYR:CB	2.48	0.44
1:A:405:VAL:O	1:A:406:ILE:HD13	2.18	0.43
1:A:559:ARG:HH11	1:A:562:ASP:CG	2.22	0.43
1:A:478:LEU:O	1:A:482:THR:HG23	2.16	0.43
1:A:625:ASN:C	1:A:625:ASN:HD22	2.21	0.43
1:A:324:ILE:HB	1:A:346:LEU:CD2	2.48	0.43
1:A:243:PRO:HB3	1:A:272:PHE:HE2	1.83	0.43
1:A:560:MET:HE1	1:A:600:VAL:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:919:ASP:HA	1:A:920:PRO:HD2	1.86	0.43
1:A:650:ASN:HA	1:A:651:PRO:HD2	1.89	0.43
1:A:305:GLN:O	1:A:309:VAL:HG23	2.19	0.42
1:A:246:TYR:CD2	1:A:448:GLU:OE1	2.69	0.42
1:A:478:LEU:O	1:A:482:THR:HG22	2.18	0.42
1:A:655:PHE:C	1:A:655:PHE:CD1	2.92	0.42
1:A:472:LYS:HG3	1:A:552:LEU:HD22	2.01	0.42
1:A:560:MET:HE1	1:A:600:VAL:C	2.40	0.42
1:A:710:ASN:O	1:A:736:SER:HA	2.20	0.42
1:A:707:ALA:C	1:A:709:CYS:H	2.22	0.41
1:A:398:SER:O	1:A:400:GLY:HA3	2.22	0.40
1:A:852:GLN:HG2	1:A:857:GLU:HB2	2.02	0.40
1:A:847:HIS:HD2	1:A:861:LYS:HG2	1.87	0.40
1:A:856:PHE:HB2	1:A:877:VAL:HB	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	623/696 (90%)	583 (94%)	34 (6%)	6 (1%)	13 25

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	655	PHE
1	A	316	ARG
1	A	397	GLY
1	A	691	HIS
1	A	577	ALA
1	A	722	ILE

### 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	536/624 (86%)	495 (92%)	41 (8%)	11	22

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	283	LYS
1	A	305	GLN
1	A	320	ARG
1	A	328	THR
1	A	337	ILE
1	A	350	ILE
1	A	365	ILE
1	A	395	LEU
1	A	446	LEU
1	A	447	GLU
1	A	482	THR
1	A	488	ARG
1	A	493	LEU
1	A	500	GLN
1	A	507	GLN
1	A	510	GLU
1	A	520	CYS
1	A	538	LEU
1	A	559	ARG
1	A	572	SER
1	A	581	GLU
1	A	585	ASP
1	A	587	THR
1	A	588	GLN
1	A	614	LEU
1	A	625	ASN
1	A	631	ILE
1	A	655	PHE
1	A	695	ILE
1	A	711	LEU

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Mol	Chain	Res	Type
1	A	738	CYS
1	A	743	SER
1	A	750	LYS
1	A	766	LEU
1	A	768	LEU
1	A	806	LYS
1	A	811	ARG
1	A	827	GLU
1	A	836	ASP
1	A	852	GLN
1	A	909	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	619	GLN
1	A	625	ASN
1	A	645	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	9/10 (90%)	1 (11%)	0
2	D	9/10 (90%)	2 (22%)	0
All	All	18/20 (90%)	3 (16%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	10	C
2	D	9	G
2	D	10	C

There are no RNA pucker outliers to report.

## 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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z  > 2$
4	SO4	A	1923	-	4,4,4	0.16	0	6,6,6	0.30	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1923	SO4	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	636/696 (91%)	0.14	22 (3%)	47	44	22, 57, 91, 116	4 (0%)
2	C	10/10 (100%)	-0.63	0	100	100	35, 56, 110, 133	0
2	D	10/10 (100%)	-0.63	0	100	100	44, 56, 93, 107	0
All	All	656/716 (91%)	0.12	22 (3%)	48	45	22, 57, 93, 133	4 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	724	MET	3.9
1	A	529	ASP	3.5
1	A	693	ILE	3.5
1	A	413	GLY	3.4
1	A	660	ILE	3.1
1	A	399	SER	2.9
1	A	797	PRO	2.9
1	A	734	ARG	2.8
1	A	239	SER	2.8
1	A	849	LYS	2.8
1	A	329	ALA	2.8
1	A	690	ASP	2.7
1	A	330	GLU	2.7
1	A	467	ILE	2.6
1	A	315	GLU	2.5
1	A	623	HIS	2.5
1	A	236	ASN	2.5
1	A	520	CYS	2.5
1	A	535	CYS	2.4
1	A	703	GLY	2.3
1	A	694	LEU	2.2
1	A	854	SER	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](#)

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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	SO4	A	1923	5/5	0.94	0.07	63,63,64,64	0
3	ZN	A	927	1/1	0.98	0.04	72,72,72,72	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.