



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2023 – 06:09 PM JST

PDB ID : 8H9D  
Title : Crystal structure of Cas12a protein  
Authors : Jianwei, L.; Jobichen, C.; Sivaraman, J.  
Deposited on : 2022-10-25  
Resolution : 3.10 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.35  
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) : 2.35

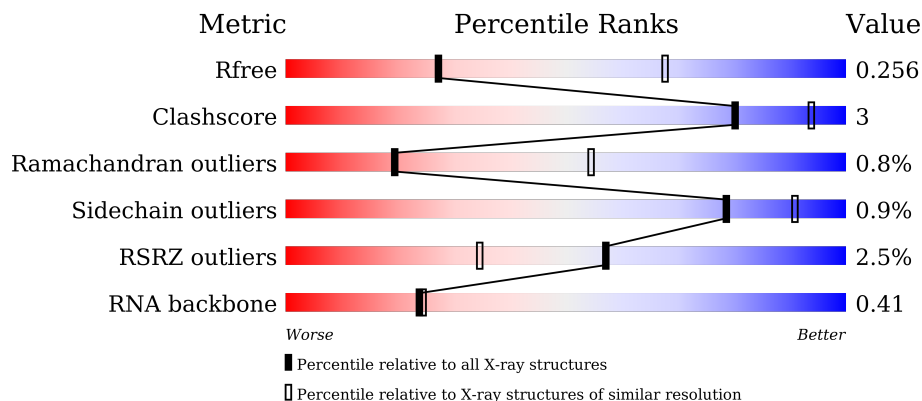
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

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	B	1206	 2% 75% 22%
2	A	1207	 2% 85% 7% 8%
3	G	21	 5% 67% 14% 14% 5%

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 16986 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 Cas12A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	946	7557	4835	1262	1439	21	0	0	0

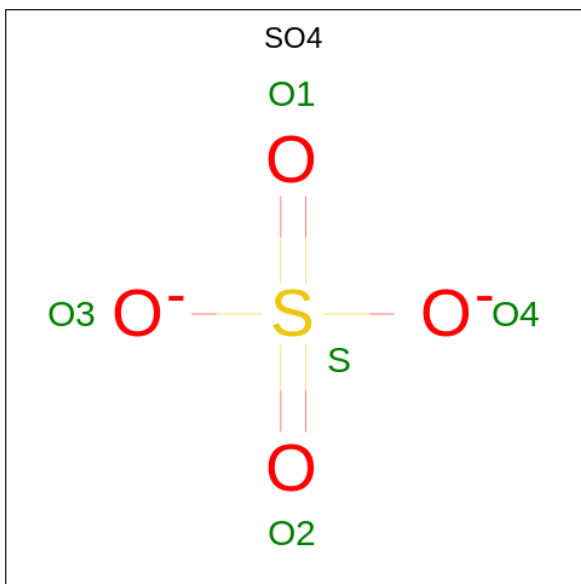
- Molecule 2 is a protein called Cas12A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	1114	8973	5713	1512	1726	22	0	0	0

- Molecule 3 is a RNA chain called RNA (5'-R(P\*AP\*AP\*UP\*UP\*UP\*CP\*UP\*AP\*CP\*UP\*AP\*AP\*GP\*UP\*GP\*UP\*AP\*GP\*AP\*UP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	G	21	443	199	75	148	21	0	0	0

- 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 5 4 1	0	0

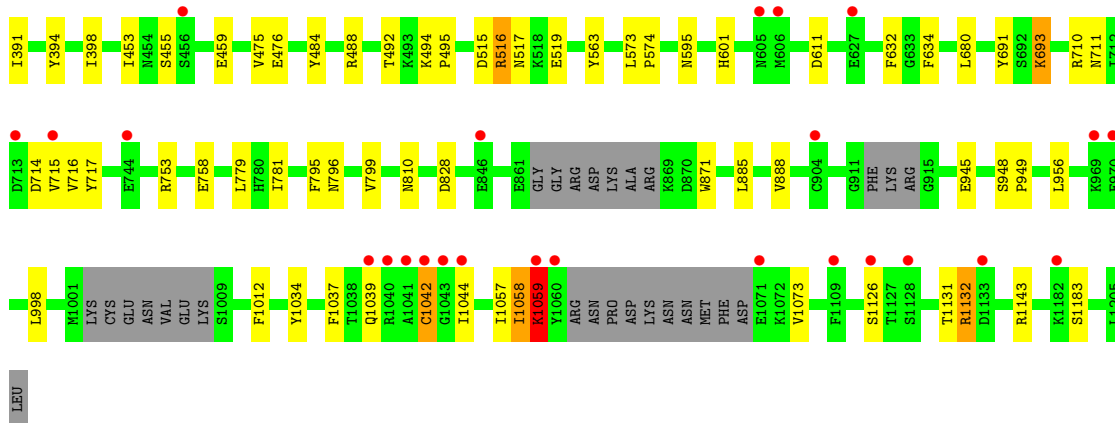
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0
5	G	1	Total Mg 1 1	0	0

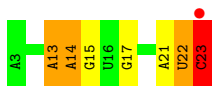
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	G	6	Total O 6 6	0	0





- Molecule 3: RNA (5'-R(P\*AP\*AP\*UP\*UP\*UP\*CP\*UP\*AP\*CP\*UP\*AP\*AP\*GP\*UP\*GP\*UP\*AP\*GP\*AP\*UP\*C)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	235.70Å 85.63Å 139.30Å 90.00° 110.15° 90.00°	Depositor
Resolution (Å)	29.98 – 3.10 29.98 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.98-3.10) 99.8 (29.98-3.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.16	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.37 (at 3.11Å)	Xtrriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, $R_{free}$	0.232 , 0.252 0.238 , 0.256	Depositor DCC
$R_{free}$ test set	1846 reflections (3.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	93.7	Xtrriage
Anisotropy	0.305	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 54.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	16986	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	98.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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: MG, 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	B	0.31	0/7671	0.55	0/10328
2	A	0.33	0/9126	0.56	0/12290
3	G	0.54	0/494	1.15	5/766 (0.7%)
All	All	0.33	0/17291	0.58	5/23384 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	22	U	P-O3'-C3'	11.39	133.37	119.70
3	G	23	C	O5'-P-OP2	8.14	120.47	110.70
3	G	23	C	OP1-P-OP2	-7.24	108.74	119.60
3	G	14	A	C2'-C3'-O3'	6.25	123.70	113.70
3	G	13	A	P-O3'-C3'	6.00	126.90	119.70

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	B	7557	0	7410	26	0
2	A	8973	0	8794	60	0
3	G	443	0	224	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	5	0	0	0	0
5	A	1	0	0	0	0
5	G	1	0	0	0	0
6	G	6	0	0	0	0
All	All	16986	0	16428	90	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 3.

All (90) 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)
2:A:1059:LYS:CE	2:A:1126:SER:HB2	1.36	1.54
2:A:1059:LYS:CE	2:A:1126:SER:CB	2.30	1.10
2:A:1059:LYS:HE2	2:A:1126:SER:HB2	1.41	0.97
2:A:1059:LYS:HE3	2:A:1126:SER:HB2	0.97	0.96
2:A:1059:LYS:HE3	2:A:1126:SER:CB	1.90	0.96
2:A:716:VAL:HG12	2:A:717:TYR:H	1.40	0.86
2:A:998:LEU:HD13	2:A:1042:CYS:SG	2.19	0.82
2:A:998:LEU:CD1	2:A:1042:CYS:SG	2.72	0.77
2:A:1059:LYS:HE2	2:A:1126:SER:CB	2.09	0.74
3:G:23:C:OP2	3:G:23:C:H3'	1.89	0.71
2:A:711:ASN:HA	2:A:716:VAL:HG21	1.72	0.71
1:B:26:THR:HG21	1:B:680:LEU:H	1.58	0.69
2:A:1059:LYS:NZ	2:A:1126:SER:HB2	2.10	0.66
1:B:393:ASN:O	1:B:393:ASN:ND2	2.23	0.64
2:A:488:ARG:O	2:A:492:THR:HG22	1.99	0.62
2:A:516:ARG:N	2:A:563:TYR:O	2.31	0.62
2:A:26:THR:HG21	2:A:680:LEU:H	1.65	0.61
3:G:23:C:H2'	3:G:23:C:O2	2.02	0.59
1:B:450:LEU:HD12	1:B:477:LEU:CD1	2.31	0.59
1:B:1172:GLY:O	1:B:1175:VAL:HG22	2.02	0.59
1:B:393:ASN:HD22	1:B:393:ASN:C	2.03	0.58
2:A:179:PHE:HB3	2:A:180:PRO:HD3	1.86	0.57
2:A:716:VAL:HG12	2:A:717:TYR:N	2.17	0.56
2:A:885:LEU:HA	2:A:888:VAL:HG22	1.88	0.56
2:A:716:VAL:CG1	2:A:717:TYR:H	2.14	0.55
2:A:475:VAL:O	2:A:476:GLU:HB2	2.06	0.54
2:A:948:SER:N	2:A:949:PRO:HD3	2.22	0.54
1:B:496:PHE:CE2	1:B:537:ILE:HD11	2.43	0.54
1:B:1142:LYS:HG3	1:B:1206:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:21:A:H2'	3:G:22:U:O4'	2.08	0.53
2:A:716:VAL:HG22	2:A:956:LEU:HD22	1.90	0.52
2:A:394:TYR:CZ	2:A:398:ILE:HD11	2.45	0.52
2:A:183:LEU:O	2:A:186:VAL:HG22	2.10	0.52
1:B:838:SER:O	1:B:841:SER:HB2	2.10	0.51
2:A:515:ASP:OD1	2:A:563:TYR:CB	2.58	0.51
2:A:573:LEU:HB2	2:A:574:PRO:HD3	1.92	0.51
2:A:129:LEU:HB2	2:A:130:PRO:HD3	1.94	0.50
2:A:1057:ILE:HG12	2:A:1073:VAL:HG22	1.93	0.50
2:A:389:ASN:O	2:A:391:ILE:N	2.40	0.50
2:A:710:ARG:O	2:A:716:VAL:HG21	2.12	0.50
1:B:75:ILE:HA	1:B:78:GLU:OE2	2.12	0.49
2:A:795:PHE:C	2:A:795:PHE:CD1	2.86	0.49
1:B:1171:LYS:HE2	1:B:1197:TRP:CD2	2.47	0.49
2:A:82:LYS:HB2	2:A:84:GLN:OE1	2.13	0.48
2:A:455:SER:HB2	2:A:459:GLU:OE1	2.14	0.48
2:A:1132:ARG:NH1	2:A:1132:ARG:HB3	2.29	0.48
2:A:632:PHE:HB2	2:A:634:PHE:CE2	2.49	0.47
2:A:26:THR:CG2	2:A:680:LEU:H	2.28	0.46
1:B:450:LEU:CD1	1:B:477:LEU:CD1	2.92	0.46
2:A:23:ILE:O	2:A:26:THR:HG23	2.15	0.46
2:A:484:TYR:HH	2:A:871:TRP:HZ3	1.62	0.46
2:A:515:ASP:HA	2:A:563:TYR:CB	2.46	0.46
1:B:839:LEU:O	1:B:840:ASN:HB2	2.16	0.46
2:A:691:TYR:O	2:A:693:LYS:HE3	2.16	0.46
2:A:595:ASN:ND2	2:A:611:ASP:OD1	2.48	0.46
1:B:839:LEU:C	1:B:841:SER:H	2.19	0.45
1:B:450:LEU:CD1	1:B:477:LEU:HD12	2.46	0.45
2:A:810:ASN:OD1	2:A:828:ASP:HA	2.17	0.45
2:A:795:PHE:CD1	2:A:795:PHE:O	2.70	0.45
2:A:1058:ILE:HG22	2:A:1058:ILE:O	2.18	0.44
2:A:232:VAL:HG13	2:A:258:MET:HB2	1.98	0.44
2:A:1143:ARG:HD2	2:A:1143:ARG:H	1.82	0.44
2:A:779:LEU:HD21	2:A:781:ILE:HD11	2.00	0.44
2:A:186:VAL:HG12	2:A:211:PHE:HA	2.00	0.43
2:A:796:ASN:O	2:A:799:VAL:N	2.46	0.43
1:B:999:PHE:HB3	1:B:1001:MET:HG3	2.01	0.43
2:A:601:HIS:CD2	2:A:601:HIS:H	2.36	0.43
1:B:1166:TYR:CE2	1:B:1170:ARG:HD2	2.53	0.42
2:A:1012:PHE:CE1	2:A:1037:PHE:HE2	2.37	0.42
1:B:179:PHE:HB3	1:B:180:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:567:PRO:O	1:B:568:VAL:C	2.56	0.42
1:B:1034:TYR:HB2	1:B:1046:SER:HB2	2.01	0.42
2:A:475:VAL:HG12	2:A:476:GLU:N	2.35	0.42
2:A:494:LYS:HB3	2:A:495:PRO:HD2	2.02	0.42
2:A:1058:ILE:HD12	2:A:1058:ILE:H	1.85	0.42
2:A:389:ASN:O	2:A:390:LEU:HB2	2.20	0.42
2:A:717:TYR:N	2:A:717:TYR:CD1	2.88	0.42
1:B:496:PHE:CZ	1:B:537:ILE:HD11	2.54	0.41
2:A:453:ILE:HG22	2:A:453:ILE:O	2.20	0.41
2:A:714:ASP:C	2:A:716:VAL:N	2.73	0.41
1:B:121:ASP:OD1	1:B:121:ASP:N	2.52	0.41
1:B:1205:LEU:O	1:B:1206:LEU:HB2	2.20	0.41
1:B:652:VAL:HG12	1:B:652:VAL:O	2.19	0.41
2:A:39:ASP:OD1	2:A:42:ARG:NH1	2.53	0.41
2:A:517:ASN:C	2:A:519:GLU:H	2.24	0.41
2:A:46:TYR:CZ	2:A:50:LYS:HD2	2.56	0.41
1:B:1021:PHE:CE2	1:B:1023:ALA:HA	2.56	0.40
3:G:23:C:O2	3:G:23:C:C2'	2.67	0.40
1:B:480:VAL:HG22	1:B:480:VAL:O	2.21	0.40
1:B:129:LEU:H	1:B:130:PRO:CD	2.33	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	B	906/1206 (75%)	843 (93%)	56 (6%)	7 (1%)	19 54
2	A	1094/1207 (91%)	1034 (94%)	52 (5%)	8 (1%)	22 57
All	All	2000/2413 (83%)	1877 (94%)	108 (5%)	15 (1%)	19 54

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	516	ARG
2	A	945	GLU
1	B	124	ASP
2	A	715	VAL
2	A	1042	CYS
2	A	1059	LYS
1	B	129	LEU
1	B	205	GLU
2	A	1058	ILE
2	A	1131	THR
1	B	508	SER
1	B	633	GLY
1	B	1130	GLY
1	B	568	VAL
2	A	130	PRO

### 5.3.2 Protein sidechains [i](#)

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	B	812/1110 (73%)	806 (99%)	6 (1%)	84 93
2	A	975/1111 (88%)	965 (99%)	10 (1%)	76 90
All	All	1787/2221 (80%)	1771 (99%)	16 (1%)	78 91

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	121	ASP
1	B	135	ASP
1	B	393	ASN
1	B	449	GLU
1	B	523	LEU
1	B	1205	LEU
2	A	223	ASP
2	A	693	LYS
2	A	753	ARG

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Mol	Chain	Res	Type
2	A	758	GLU
2	A	1034	TYR
2	A	1039	GLN
2	A	1044	ILE
2	A	1059	LYS
2	A	1132	ARG
2	A	1183	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	48	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	G	20/21 (95%)	5 (25%)	1 (5%)

All (5) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	G	13	A
3	G	14	A
3	G	15	G
3	G	17	G
3	G	23	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	G	14	A

## 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](#)

Of 3 ligands modelled in this entry, 2 are 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	1301	-	4,4,4	0.16	0	6,6,6	0.10	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.

No monomer is involved in short contacts.

## 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	B	946/1206 (78%)	0.00	22 (2%) 60 39	30, 100, 139, 168	0
2	A	1114/1207 (92%)	0.00	29 (2%) 56 33	30, 95, 137, 169	0
3	G	21/21 (100%)	0.39	1 (4%) 30 14	60, 66, 95, 125	0
All	All	2081/2434 (85%)	0.01	52 (2%) 57 34	30, 97, 139, 169	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	1042	CYS	7.1
1	B	204	GLU	5.2
1	B	203	GLY	4.9
2	A	1109	PHE	4.4
2	A	605	ASN	4.3
1	B	772	TYR	4.1
1	B	512	ASN	3.9
2	A	268	ASP	3.7
1	B	200	ASP	3.5
2	A	606	MET	3.5
1	B	970	GLU	3.4
2	A	1133	ASP	3.4
3	G	23	C	3.3
2	A	1040	ARG	3.3
1	B	633	GLY	3.2
2	A	970	GLU	3.2
1	B	141	GLU	3.2
2	A	904	CYS	3.2
2	A	1059	LYS	3.2
2	A	1060	TYR	3.1
2	A	1043	GLY	3.1
1	B	1066	ASN	3.1
2	A	1044	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
2	A	456	SER	3.1
2	A	1041	ALA	3.0
1	B	635	LYS	3.0
1	B	1186	GLU	2.7
1	B	127	GLU	2.6
1	B	636	PHE	2.6
1	B	570	ASN	2.5
2	A	382	ASN	2.5
2	A	627	GLU	2.4
2	A	969	LYS	2.4
1	B	1087	TYR	2.4
1	B	1059	LYS	2.3
2	A	1039	GLN	2.3
2	A	715	VAL	2.3
2	A	846	GLU	2.3
2	A	713	ASP	2.3
1	B	373	LYS	2.3
2	A	744	GLU	2.2
1	B	1187	LYS	2.2
2	A	1126	SER	2.2
1	B	1070	ASP	2.2
1	B	205	GLU	2.2
2	A	1071	GLU	2.1
1	B	135	ASP	2.1
2	A	201	GLY	2.1
2	A	1182	LYS	2.1
2	A	1128	SER	2.1
1	B	321	LYS	2.0
2	A	388	CYS	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 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	1301	5/5	0.65	0.28	111,113,140,145	0
5	MG	A	1302	1/1	0.97	0.57	66,66,66,66	0
5	MG	G	101	1/1	0.97	0.06	63,63,63,63	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.