



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 12:38 pm BST

PDB ID : 3O41  
Title : Crystal Structure of 101F Fab Bound to 15-mer Peptide Epitope  
Authors : McLellan, J.S.; Chen, M.; Chang, J.S.; Yang, Y.; Kim, A.; Graham, B.S.;  
Kwong, P.D.  
Deposited on : 2010-07-26  
Resolution : 1.95 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.

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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)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

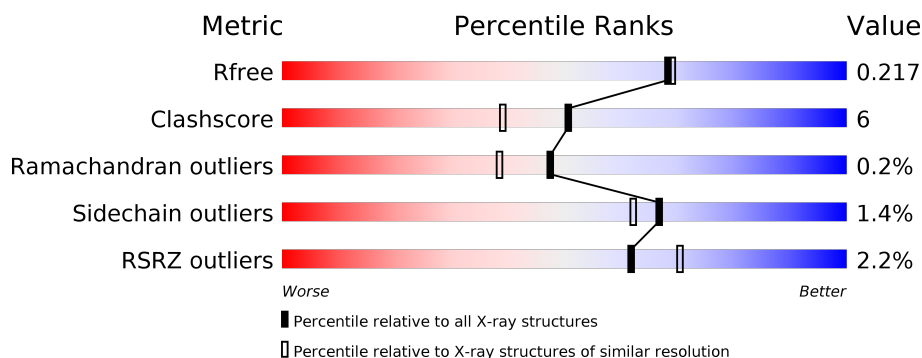
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (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 on 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	218	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>16%</div> <div>.</div> </div> </div>
1	L	218	<div> <div>%</div> <div> <div></div> <div>88%</div> <div>12%</div> </div> </div>
2	A	220	<div> <div>%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>..</div> </div> </div>
2	H	220	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>.</div> </div> </div>
3	C	17	<div> <div></div> <div> <div>59%</div> <div>41%</div> </div> </div>
3	P	17	<div> <div>6%</div> <div> <div></div> <div>59%</div> <div>6%</div> <div>35%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7652 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 Mouse monoclonal antibody 101F Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	218	Total	C	N	O	S	0	0	0
			1692	1059	284	342	7			
1	B	217	Total	C	N	O	S	0	0	0
			1686	1056	283	341	6			

- Molecule 2 is a protein called Mouse monoclonal antibody 101F Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	220	Total	C	N	O	S	0	0	0
			1669	1064	274	325	6			
2	A	217	Total	C	N	O	S	0	0	0
			1648	1052	270	320	6			

- Molecule 3 is a protein called Fusion glycoprotein F1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	11	Total	C	N	O	0	0	1
			82	52	17	13			
3	C	10	Total	C	N	O	0	0	1
			73	46	15	12			

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



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

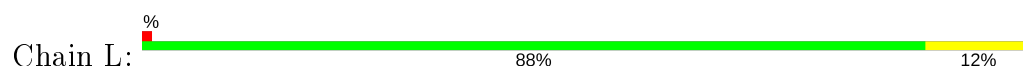
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	180	Total 180	O 180	0	0
5	H	184	Total 184	O 184	0	0
5	A	170	Total 170	O 170	0	0
5	B	180	Total 180	O 180	0	0
5	P	7	Total 7	O 7	0	0
5	C	11	Total 11	O 11	0	0

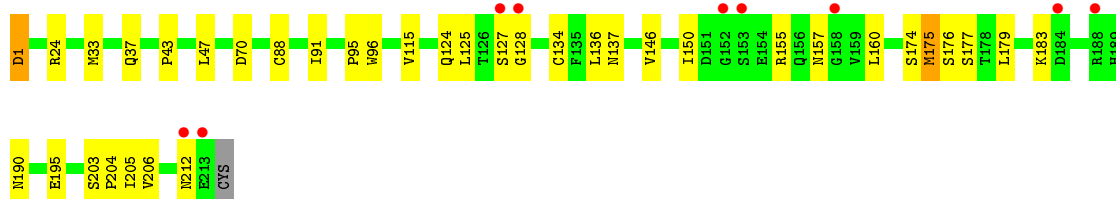
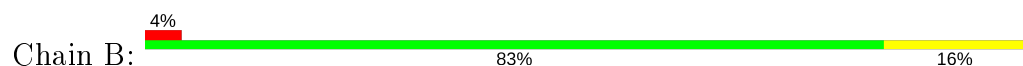
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

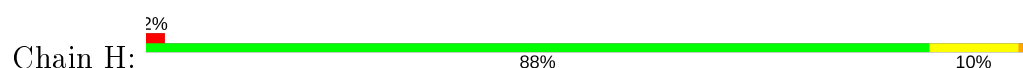
- Molecule 1: Mouse monoclonal antibody 101F Fab light chain



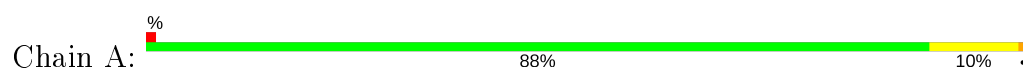
- Molecule 1: Mouse monoclonal antibody 101F Fab light chain



- Molecule 2: Mouse monoclonal antibody 101F Fab heavy chain

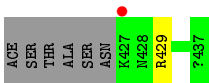


- Molecule 2: Mouse monoclonal antibody 101F Fab heavy chain

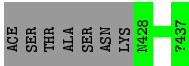


- Molecule 3: Fusion glycoprotein F1





● Molecule 3: Fusion glycoprotein F1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.90Å 92.98Å 141.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.08 – 1.95 33.08 – 1.95	Depositor EDS
% Data completeness (in resolution range)	90.4 (33.08-1.95) 90.4 (33.08-1.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.76 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.177 , 0.217 0.175 , 0.217	Depositor DCC
$R_{free}$ test set	3765 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	21.8	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 46.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7652	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.02% 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, NH2

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	0.27	0/1728	0.47	0/2352
1	L	0.27	0/1734	0.49	0/2360
2	A	0.29	0/1693	0.51	0/2316
2	H	0.29	0/1715	0.51	1/2348 (0.0%)
3	C	0.36	0/72	0.44	0/94
3	P	0.35	0/81	0.52	0/105
All	All	0.28	0/7023	0.50	1/9575 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	177	LEU	CA-CB-CG	5.42	127.76	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	B	1686	0	1605	26	0
1	L	1692	0	1610	20	0
2	A	1648	0	1626	18	0
2	H	1669	0	1647	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	73	0	77	0	0
3	P	82	0	90	4	0
4	A	15	0	0	0	0
4	B	15	0	0	0	0
4	H	15	0	0	0	0
4	L	25	0	0	0	0
5	A	170	0	0	3	0
5	B	180	0	0	1	0
5	C	11	0	0	0	0
5	H	184	0	0	0	0
5	L	180	0	0	2	0
5	P	7	0	0	0	0
All	All	7652	0	6655	77	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 (77) 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:L:155:ARG:HD3	1:L:179:LEU:HD11	1.65	0.76
1:B:190:ASN:HD21	1:B:212:ASN:ND2	1.85	0.74
1:B:127:SER:N	1:B:128:GLY:HA2	2.01	0.73
2:A:34:MET:HE1	2:A:94:ARG:HD2	1.73	0.70
1:L:14:SER:HA	1:L:107:LYS:HB2	1.81	0.62
1:B:190:ASN:HD21	1:B:212:ASN:HD22	1.47	0.60
1:L:78:VAL:HG11	1:L:106:ILE:HD12	1.84	0.60
1:B:127:SER:H	1:B:128:GLY:HA2	1.67	0.60
1:L:175:MET:HE2	1:L:177:SER:HB2	1.83	0.59
2:H:11:ILE:HB	2:H:147:PRO:HG3	1.84	0.59
1:B:175:MET:HE2	1:B:177:SER:HB2	1.84	0.59
1:B:125:LEU:O	1:B:183:LYS:HD3	2.04	0.58
1:L:80:GLU:HG2	5:L:730:HOH:O	2.04	0.57
1:L:150:ILE:HD11	1:L:179:LEU:HD21	1.86	0.57
1:B:136:LEU:HD11	1:B:146:VAL:HG22	1.86	0.57
2:A:186:SER:O	3:P:429:ARG:NH2	2.38	0.56
2:H:189:PRO:HB3	2:H:212:PRO:HG3	1.86	0.55
1:B:150:ILE:HD12	1:B:155:ARG:HD2	1.88	0.55
2:H:1:GLN:CD	2:H:1:GLN:N	2.59	0.55
1:B:1:ASP:HB3	1:B:95:PRO:HD2	1.89	0.55
1:L:205:ILE:HD11	5:L:406:HOH:O	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:30:SER:OG	2:H:73:THR:HG21	2.07	0.55
1:L:78:VAL:CG1	1:L:106:ILE:HD12	2.37	0.54
1:L:210:ASN:HB2	1:L:213:GLU:HG2	1.89	0.54
2:H:13:GLN:HG3	2:H:14:PRO:HD2	1.90	0.54
1:L:37:GLN:HB2	1:L:47:LEU:HD11	1.91	0.53
2:A:34:MET:HE1	2:A:94:ARG:CD	2.39	0.52
2:A:173:ASP:HB3	5:A:518:HOH:O	2.09	0.52
1:B:127:SER:N	1:B:128:GLY:CA	2.74	0.51
2:A:105:GLN:HA	1:B:43:PRO:HG3	1.92	0.51
2:H:133:ASN:O	2:H:185:SER:HB3	2.11	0.51
1:B:205:ILE:HD11	5:B:504:HOH:O	2.12	0.50
1:L:43:PRO:HG3	2:H:105:GLN:HA	1.93	0.50
2:A:169:VAL:HG11	1:B:160:LEU:HG	1.93	0.50
1:L:16:GLY:HA2	1:L:77:PRO:HB2	1.93	0.49
1:B:175:MET:CE	1:B:177:SER:HB2	2.42	0.49
1:B:37:GLN:HB2	1:B:47:LEU:HD11	1.95	0.49
2:A:34:MET:HE1	2:A:94:ARG:CG	2.43	0.49
1:L:33:MET:SD	1:L:88:CYS:HB2	2.51	0.49
1:L:136:LEU:HD21	1:L:146:VAL:HG22	1.94	0.49
2:A:189:PRO:HB3	2:A:212:PRO:HG3	1.94	0.49
2:A:9:PRO:HG3	5:A:286:HOH:O	2.12	0.48
2:H:96:TYR:CE1	3:P:429:ARG:HD2	2.49	0.48
1:B:195:GLU:HG2	1:B:206:VAL:HG22	1.96	0.47
1:B:33:MET:SD	1:B:88:CYS:HB2	2.55	0.47
1:B:24:ARG:HD3	1:B:70:ASP:OD1	2.16	0.46
2:H:61:PRO:HA	2:H:64:LYS:HB2	1.97	0.45
1:L:175:MET:HG2	1:L:176:SER:N	2.31	0.45
1:B:203:SER:HA	1:B:204:PRO:HD3	1.84	0.45
2:H:96:TYR:CZ	3:P:429:ARG:HD2	2.52	0.45
1:L:80:GLU:H	1:L:80:GLU:CD	2.19	0.44
2:A:184:PRO:HB2	2:A:187:THR:HG23	1.98	0.44
1:L:213:GLU:O	1:L:214:CYS:HB2	2.18	0.44
2:A:187:THR:HG22	5:A:512:HOH:O	2.18	0.44
2:A:34:MET:HB3	2:A:34:MET:HE2	1.64	0.44
1:B:124:GLN:O	1:B:127:SER:HB2	2.18	0.44
1:B:115:VAL:HG22	1:B:136:LEU:HD22	2.00	0.43
1:B:150:ILE:HD11	1:B:179:LEU:HD21	1.99	0.43
2:A:66:ARG:HD2	2:A:82(A):THR:O	2.19	0.43
2:H:96:TYR:CD1	3:P:429:ARG:HD2	2.54	0.43
2:H:14:PRO:O	2:H:15:SER:CB	2.65	0.42
2:A:14:PRO:O	2:A:15:SER:CB	2.66	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:ILE:HG22	1:B:96:TRP:HB3	2.00	0.42
2:A:39:GLN:HB2	2:A:45:LEU:HD23	2.00	0.42
2:H:17:THR:CG2	2:H:81:LYS:HG3	2.49	0.42
1:B:137:ASN:HD22	1:B:174:SER:HB3	1.85	0.41
2:H:161:SER:OG	2:A:1:GLN:HG3	2.20	0.41
2:H:122:TYR:HA	2:H:123:PRO:HD3	1.84	0.41
1:L:150:ILE:HD12	1:L:155:ARG:HD2	2.01	0.41
1:L:203:SER:HA	1:L:204:PRO:HD3	1.86	0.41
1:L:213:GLU:O	1:L:214:CYS:CB	2.69	0.41
2:A:172:SER:O	2:A:173:ASP:HB2	2.21	0.41
2:H:12:LEU:HD12	2:H:12:LEU:N	2.36	0.41
1:B:155:ARG:NH1	1:B:157:ASN:O	2.53	0.41
2:A:12:LEU:CD1	2:A:111:VAL:HG22	2.51	0.41
2:H:119:PRO:HB3	2:H:145:TYR:HB3	2.03	0.41
1:B:175:MET:HG2	1:B:176:SER:N	2.37	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	B	215/218 (99%)	208 (97%)	7 (3%)	0	100	100
1	L	216/218 (99%)	208 (96%)	8 (4%)	0	100	100
2	A	213/220 (97%)	209 (98%)	3 (1%)	1 (0%)	29	17
2	H	218/220 (99%)	210 (96%)	7 (3%)	1 (0%)	29	17
3	C	8/17 (47%)	7 (88%)	1 (12%)	0	100	100
3	P	9/17 (53%)	8 (89%)	1 (11%)	0	100	100
All	All	879/910 (97%)	850 (97%)	27 (3%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	15	SER
2	A	15	SER

### 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	B	189/190 (100%)	186 (98%)	3 (2%)	62	58
1	L	190/190 (100%)	189 (100%)	1 (0%)	88	88
2	A	189/191 (99%)	186 (98%)	3 (2%)	62	58
2	H	191/191 (100%)	187 (98%)	4 (2%)	53	46
3	C	8/13 (62%)	8 (100%)	0	100	100
3	P	9/13 (69%)	9 (100%)	0	100	100
All	All	776/788 (98%)	765 (99%)	11 (1%)	67	62

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	202	THR
2	H	1	GLN
2	H	12	LEU
2	H	29	LEU
2	H	177	LEU
2	A	12	LEU
2	A	43	LYS
2	A	177	LEU
1	B	1	ASP
1	B	134	CYS
1	B	175	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	137	ASN

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Mol	Chain	Res	Type
1	L	210	ASN
2	H	131	GLN
2	A	13	GLN
1	B	37	GLN
1	B	137	ASN
1	B	212	ASN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

14 ligands are modelled in this entry.

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	L	217	-	4,4,4	0.14	0	6,6,6	0.07	0
4	SO4	A	214	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	L	218	-	4,4,4	0.13	0	6,6,6	0.07	0
4	SO4	H	216	-	4,4,4	0.14	0	6,6,6	0.17	0
4	SO4	B	217	-	4,4,4	0.14	0	6,6,6	0.08	0
4	SO4	A	215	-	4,4,4	0.13	0	6,6,6	0.08	0
4	SO4	L	215	-	4,4,4	0.13	0	6,6,6	0.11	0
4	SO4	H	215	-	4,4,4	0.14	0	6,6,6	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	SO4	L	216	-	4,4,4	0.14	0	6,6,6	0.07	0
4	SO4	A	216	-	4,4,4	0.14	0	6,6,6	0.14	0
4	SO4	B	216	-	4,4,4	0.14	0	6,6,6	0.12	0
4	SO4	L	219	-	4,4,4	0.14	0	6,6,6	0.08	0
4	SO4	B	215	-	4,4,4	0.14	0	6,6,6	0.06	0
4	SO4	H	214	-	4,4,4	0.14	0	6,6,6	0.06	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	217/218 (99%)	0.05	9 (4%) 37 46	15, 26, 62, 85	4 (1%)
1	L	218/218 (100%)	-0.07	3 (1%) 75 82	16, 27, 40, 52	4 (1%)
2	A	217/220 (98%)	-0.07	3 (1%) 75 82	14, 22, 39, 76	0
2	H	220/220 (100%)	-0.03	4 (1%) 68 76	13, 23, 45, 80	0
3	C	9/17 (52%)	-0.16	0 100 100	14, 18, 33, 60	0
3	P	10/17 (58%)	0.17	1 (10%) 7 11	16, 19, 59, 76	0
All	All	891/910 (97%)	-0.03	20 (2%) 62 70	13, 25, 50, 85	8 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	212	ASN	4.5
2	H	133	ASN	4.3
2	H	64	LYS	4.1
2	A	133	ASN	3.7
1	L	214	CYS	3.4
2	A	1	GLN	3.1
1	B	153	SER	3.0
1	B	184	ASP	2.9
1	B	127	SER	2.9
2	A	128	SER	2.8
1	L	202	THR	2.7
1	L	126	THR	2.7
1	B	128	GLY	2.6
3	P	427	LYS	2.4
2	H	1	GLN	2.3
1	B	188	ARG	2.2
2	H	171	GLN	2.2
1	B	152	GLY	2.1
1	B	158	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	213	GLU	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 carbohydrates 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(Å <sup>2</sup> )	Q<0.9
4	SO4	A	215	5/5	0.69	0.28	106,107,107,108	0
4	SO4	H	215	5/5	0.73	0.28	107,107,108,108	0
4	SO4	L	217	5/5	0.81	0.22	84,84,86,87	0
4	SO4	L	218	5/5	0.81	0.27	116,116,116,116	0
4	SO4	H	214	5/5	0.86	0.24	101,101,102,103	0
4	SO4	B	217	5/5	0.88	0.33	101,102,102,102	0
4	SO4	L	216	5/5	0.90	0.20	90,90,91,91	0
4	SO4	A	214	5/5	0.90	0.20	95,95,95,96	0
4	SO4	H	216	5/5	0.91	0.30	82,82,84,84	0
4	SO4	L	219	5/5	0.92	0.15	79,80,81,81	0
4	SO4	A	216	5/5	0.93	0.26	69,70,71,72	0
4	SO4	B	216	5/5	0.94	0.11	58,59,62,62	0
4	SO4	B	215	5/5	0.97	0.14	51,51,52,55	0
4	SO4	L	215	5/5	0.98	0.14	46,46,48,48	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.