



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 7, 2022 – 05:58 PM EST

PDB ID : 7TOW  
Title : Antibody DH1058 Fab fragment bound to SARS-CoV-2 fusion peptide  
Authors : Gobeil, S.; Acharya, P.  
Deposited on : 2022-01-24  
Resolution : 2.15 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:

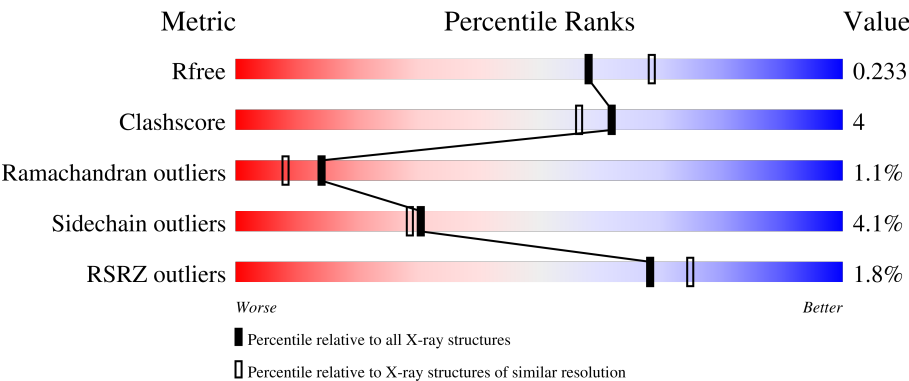
MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.26  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.26

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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.



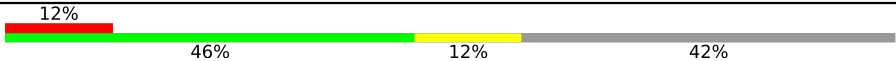
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	237	<div><div>2%</div><div>89%</div><div>10%</div><div>..</div></div>
1	H	237	<div><div>2%</div><div>87%</div><div>11%</div><div>.</div></div>
2	B	215	<div><div></div><div>88%</div><div>10%</div><div>.</div></div>
2	L	215	<div><div></div><div>87%</div><div>10%</div><div>.</div></div>
3	D	26	<div><div>15%</div><div>62%</div><div>23%</div><div>.</div><div>12%</div></div>

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Mol	Chain	Length	Quality of chain
3	E	26	

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
5	PO4	A	302	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8026 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 DH1058 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	236	Total	C	N	O	S	0	1	0
			1805	1124	321	351	9			
1	A	235	Total	C	N	O	S	0	0	0
			1780	1111	313	347	9			

- Molecule 2 is a protein called DH1058 Fab Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	1	0
			1657	1038	276	338	5			
2	B	214	Total	C	N	O	S	0	1	0
			1660	1040	279	336	5			

- Molecule 3 is a protein called Spike protein S2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	15	Total	C	N	O	0	1	0
			135	89	23	23			
3	D	23	Total	C	N	O	0	0	0
			183	120	30	33			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	2	Total	Ca	0	0
			2	2		
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



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

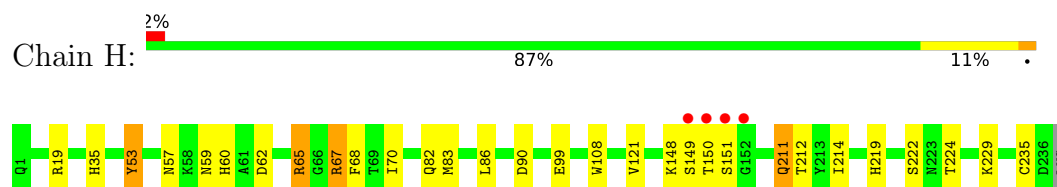
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	220	Total	O	0	0
			220	220		
6	L	160	Total	O	0	0
			160	160		
6	A	169	Total	O	0	0
			169	169		
6	B	196	Total	O	0	0
			196	196		
6	E	15	Total	O	0	0
			15	15		
6	D	33	Total	O	0	0
			33	33		

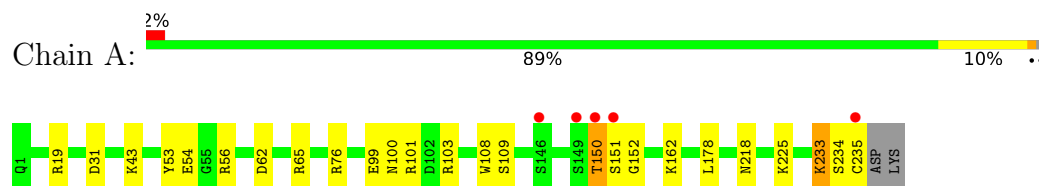
### 3 Residue-property plots [i](#)

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.

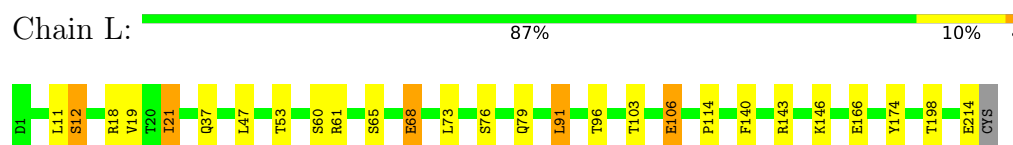
- Molecule 1: DH1058 Fab heavy chain



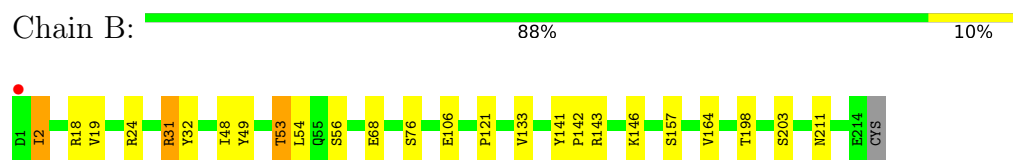
- Molecule 1: DH1058 Fab heavy chain



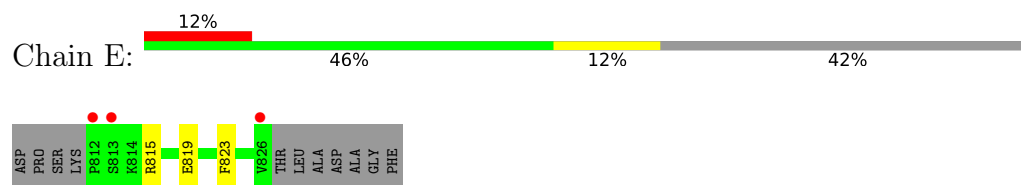
- Molecule 2: DH1058 Fab Light chain



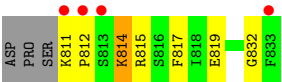
- Molecule 2: DH1058 Fab Light chain



- Molecule 3: Spike protein S2



- Molecule 3: Spike protein S2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.92Å 76.79Å 119.79Å 90.00° 100.85° 90.00°	Depositor
Resolution (Å)	39.21 – 2.15 39.21 – 2.15	Depositor EDS
% Data completeness (in resolution range)	92.7 (39.21-2.15) 92.7 (39.21-2.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.02 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, $R_{free}$	0.167 , 0.234 0.166 , 0.233	Depositor DCC
$R_{free}$ test set	1998 reflections (4.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.8	Xtriage
Anisotropy	0.211	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.031 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8026	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, PO4

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	0.36	0/1823	0.61	0/2477
1	H	0.42	0/1848	0.61	0/2509
2	B	0.42	0/1695	0.62	0/2303
2	L	0.42	0/1692	0.64	1/2300 (0.0%)
3	D	0.47	0/186	0.62	0/248
3	E	0.37	0/137	0.60	0/180
All	All	0.40	0/7381	0.62	1/10017 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	91	LEU	CA-CB-CG	5.30	127.50	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	67	ARG	Sidechain

## 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	1780	0	1715	17	0
1	H	1805	0	1742	19	0
2	B	1660	0	1618	13	0
2	L	1657	0	1611	9	0
3	D	183	0	188	9	0
3	E	135	0	144	6	0
4	A	1	0	0	0	0
4	H	2	0	0	0	0
5	A	5	0	0	2	0
5	H	5	0	0	0	0
6	A	169	0	0	4	0
6	B	196	0	0	3	0
6	D	33	0	0	2	0
6	E	15	0	0	0	0
6	H	220	0	0	0	0
6	L	160	0	0	1	0
All	All	8026	0	7018	63	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 (63) 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:233:LYS:HE3	1:A:234:SER:H	1.49	0.77
1:H:108:TRP:CE2	3:E:815:ARG:HG3	2.21	0.74
1:A:54:GLU:OE2	6:A:401:HOH:O	2.06	0.73
1:A:53:TYR:CE1	3:D:815:ARG:HD2	2.25	0.70
1:A:218:ASN:HD22	1:A:225:LYS:HG2	1.58	0.68
1:H:62:ASP:OD1	1:H:65[B]:ARG:NH1	2.26	0.67
1:A:150:THR:O	1:A:152:GLY:N	2.30	0.65
2:B:146:LYS:HB3	2:B:198:THR:HB	1.77	0.65
1:A:54:GLU:HG3	1:A:56:ARG:H	1.63	0.64
2:B:24:ARG:NH2	6:B:304:HOH:O	2.32	0.63
3:D:811:LYS:N	6:D:902:HOH:O	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:143[A]:ARG:HH21	2:B:164:VAL:HG11	1.64	0.62
2:L:12:SER:OG	2:L:106:GLU:OE2	2.17	0.62
1:H:53:TYR:CZ	3:E:815:ARG:HD2	2.35	0.62
2:L:146:LYS:HB3	2:L:198:THR:HB	1.82	0.61
1:H:59:ASN:OD1	1:H:65[A]:ARG:NH1	2.34	0.61
3:E:815:ARG:HD3	3:E:819:GLU:OE2	2.02	0.60
1:H:67:ARG:NH2	1:H:90:ASP:OD2	2.25	0.59
1:A:108:TRP:CE2	3:D:815:ARG:HG3	2.37	0.59
2:L:11:LEU:HD11	2:L:19:VAL:HG13	1.84	0.59
1:H:60:HIS:HD1	1:H:65[A]:ARG:NH2	2.01	0.58
3:D:814:LYS:NZ	6:D:901:HOH:O	2.28	0.58
1:H:53:TYR:CE1	3:E:815:ARG:HD2	2.39	0.58
2:L:106:GLU:OE1	2:L:174:TYR:OH	2.12	0.58
1:A:62:ASP:OD1	1:A:65:ARG:NH1	2.37	0.57
1:A:108:TRP:CZ2	3:D:815:ARG:HG3	2.41	0.55
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.88	0.55
3:D:815:ARG:HD3	3:D:819:GLU:OE2	2.06	0.54
1:H:211:GLN:HG3	1:H:212:THR:N	2.23	0.53
2:L:21:ILE:HG21	2:L:103:THR:HG21	1.90	0.53
1:H:219:HIS:ND1	1:H:222:SER:HB2	2.24	0.53
3:D:814:LYS:HG3	3:D:817:PHE:H	1.73	0.52
1:H:148:LYS:C	1:H:150:THR:H	2.12	0.52
1:H:108:TRP:CZ2	3:E:815:ARG:HG3	2.47	0.49
2:B:49:TYR:O	2:B:53:THR:HG23	2.11	0.49
6:A:418:HOH:O	2:B:53:THR:HG21	2.12	0.48
1:A:76:ARG:NH1	6:A:403:HOH:O	2.31	0.48
2:B:143[A]:ARG:NH2	6:B:314:HOH:O	2.46	0.47
2:L:61:ARG:CZ	2:L:79:GLN:HG3	2.44	0.46
1:A:101:ARG:O	5:A:302:PO4:P	2.72	0.46
2:B:31:ARG:HD2	2:B:32:TYR:CE1	2.51	0.45
1:H:68:PHE:HA	1:H:82:GLN:O	2.17	0.45
1:A:103:ARG:HB2	2:B:49:TYR:OH	2.17	0.44
2:B:141:TYR:CG	2:B:142:PRO:HA	2.53	0.44
1:H:235:CYS:SG	6:L:404:HOH:O	2.62	0.44
1:A:99:GLU:HG2	6:A:434:HOH:O	2.18	0.43
2:L:18:ARG:HG2	2:L:76:SER:HA	2.00	0.43
1:A:233:LYS:CE	1:A:234:SER:H	2.26	0.43
3:D:814:LYS:HA	3:D:814:LYS:HD3	1.88	0.43
1:H:57:ASN:HB3	3:E:823:PHE:CG	2.54	0.42
1:A:162:LYS:HE2	6:B:316:HOH:O	2.17	0.42
2:L:114:PRO:HB3	2:L:140:PHE:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:214:ILE:HD13	1:H:229:LYS:HA	2.02	0.42
1:H:83:MET:HE2	1:H:86:LEU:HD21	2.02	0.42
1:H:60:HIS:NE2	1:H:70:ILE:HG22	2.34	0.42
1:H:222:SER:HB3	1:H:224:THR:OG1	2.19	0.42
1:A:100:ASN:OD1	5:A:302:PO4:P	2.78	0.42
1:H:35:HIS:HE2	1:H:99:GLU:HG3	1.85	0.41
2:B:211:ASN:HD22	2:B:211:ASN:N	2.17	0.41
1:A:53:TYR:CZ	3:D:815:ARG:HD2	2.56	0.41
2:B:48:ILE:HD13	2:B:54:LEU:HA	2.03	0.40
2:B:121:PRO:HD3	2:B:133:VAL:HG22	2.04	0.40
2:B:18:ARG:HG3	2:B:76:SER:HA	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	233/237 (98%)	223 (96%)	8 (3%)	2 (1%)	17	11
1	H	235/237 (99%)	225 (96%)	8 (3%)	2 (1%)	17	11
2	B	213/215 (99%)	204 (96%)	7 (3%)	2 (1%)	17	11
2	L	212/215 (99%)	205 (97%)	6 (3%)	1 (0%)	29	22
3	D	21/26 (81%)	18 (86%)	0	3 (14%)	0	0
3	E	14/26 (54%)	13 (93%)	1 (7%)	0	100	100
All	All	928/956 (97%)	888 (96%)	30 (3%)	10 (1%)	14	8

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	SER

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Mol	Chain	Res	Type
3	D	814	LYS
1	H	149	SER
2	L	68	GLU
1	A	150	THR
3	D	832	GLY
2	B	2	ILE
1	H	151	SER
2	B	68	GLU
3	D	812	PRO

### 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	197/200 (98%)	190 (96%)	7 (4%)	35	33
1	H	200/200 (100%)	194 (97%)	6 (3%)	41	40
2	B	189/189 (100%)	181 (96%)	8 (4%)	30	28
2	L	189/189 (100%)	176 (93%)	13 (7%)	15	10
3	D	20/23 (87%)	20 (100%)	0	100	100
3	E	16/23 (70%)	16 (100%)	0	100	100
All	All	811/824 (98%)	777 (96%)	34 (4%)	30	28

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	19	ARG
1	H	53	TYR
1	H	65[A]	ARG
1	H	65[B]	ARG
1	H	121	VAL
1	H	211	GLN
2	L	12	SER
2	L	21	ILE
2	L	53	THR

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Mol	Chain	Res	Type
2	L	60	SER
2	L	65	SER
2	L	68	GLU
2	L	73	LEU
2	L	91	LEU
2	L	96	THR
2	L	106	GLU
2	L	143	ARG
2	L	166	GLU
2	L	214	GLU
1	A	19	ARG
1	A	31	ASP
1	A	43	LYS
1	A	109	SER
1	A	178	LEU
1	A	233	LYS
1	A	235	CYS
2	B	2	ILE
2	B	19	VAL
2	B	31	ARG
2	B	53	THR
2	B	56	SER
2	B	106	GLU
2	B	157	SER
2	B	203	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	B	211	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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	PO4	A	302	-	4,4,4	1.09	0	6,6,6	1.90	2 (33%)
5	PO4	H	303	-	4,4,4	0.98	0	6,6,6	1.07	0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	302	PO4	O3-P-O2	3.57	119.44	107.97
5	A	302	PO4	O3-P-O1	-2.22	102.76	110.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	302	PO4	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	235/237 (99%)	-0.20	5 (2%) 63 71	13, 25, 47, 81	0
1	H	236/237 (99%)	-0.35	4 (1%) 70 76	11, 20, 39, 78	0
2	B	214/215 (99%)	-0.40	1 (0%) 91 93	12, 21, 34, 65	0
2	L	214/215 (99%)	-0.38	0 100 100	13, 25, 37, 49	0
3	D	23/26 (88%)	0.78	4 (17%) 1 1	19, 27, 47, 58	0
3	E	15/26 (57%)	0.71	3 (20%) 1 1	23, 26, 57, 65	0
All	All	937/956 (98%)	-0.29	17 (1%) 68 75	11, 23, 40, 81	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	833	PHE	7.5
1	A	150	THR	5.8
3	E	813	SER	5.8
3	D	812	PRO	5.6
1	H	151	SER	4.8
1	H	150	THR	4.7
1	A	151	SER	4.6
1	H	149	SER	4.5
1	A	149	SER	3.8
3	E	826	VAL	3.7
2	B	1	ASP	3.6
1	H	152	GLY	3.4
3	D	811	LYS	3.4
3	D	813	SER	3.1
3	E	812	PRO	3.1
1	A	146	SER	2.5
1	A	235	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
5	PO4	H	303	5/5	0.89	0.16	35,36,40,41	0
5	PO4	A	302	5/5	0.94	0.15	17,31,42,42	0
4	CA	A	301	1/1	0.99	0.04	21,21,21,21	0
4	CA	H	301	1/1	0.99	0.05	29,29,29,29	0
4	CA	H	302	1/1	0.99	0.04	21,21,21,21	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.