



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 16, 2023 – 03:17 am GMT

PDB ID : 8BE1
Title : SARS-CoV-2 RBD in complex with a Fab fragment of a neutralising antibody mRBD2
Authors : Lulla, A.; Brear, P.; Fischer, K.; Hollfelder, F.; Hyvonen, M.
Deposited on : 2022-10-21
Resolution : 1.98 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.3
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) : 2.31.3

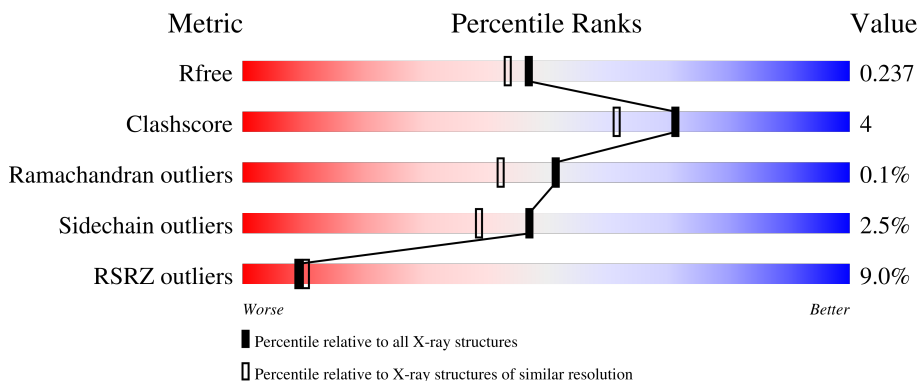
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.98 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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	230	
1	D	230	
2	B	215	
2	E	215	
3	C	198	

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Mol	Chain	Length	Quality of chain
3	F	198	 13% 86% 7% • 6%

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
4	SO4	A	301	-	X	X	-
4	SO4	D	302	-	X	-	-
4	SO4	E	301	-	X	X	-
4	SO4	F	601	-	-	X	-
4	SO4	F	603	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9866 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 Antibody heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	216	Total 1643	C 1040	N 271	O 326	S 6	0	0	0
1	D	213	Total 1622	C 1030	N 267	O 318	S 7	0	0	0

- Molecule 2 is a protein called Antibody light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	213	Total 1659	C 1032	N 279	O 342	S 6	0	0	0
2	E	213	Total 1659	C 1032	N 279	O 342	S 6	0	0	0

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	180	Total 1434	C 919	N 239	O 269	S 7	0	1	0
3	F	186	Total 1478	C 948	N 245	O 277	S 8	0	1	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	330	GLY	-	expression tag	UNP P0DTC2
C	331	SER	-	expression tag	UNP P0DTC2
C	332	GLY	-	expression tag	UNP P0DTC2
F	330	GLY	-	expression tag	UNP P0DTC2
F	331	SER	-	expression tag	UNP P0DTC2
F	332	GLY	-	expression tag	UNP P0DTC2

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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	C	1	Total	O	S	0	0
			5	4	1		
4	C	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		
4	E	1	Total	O	S	0	0
			5	4	1		

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

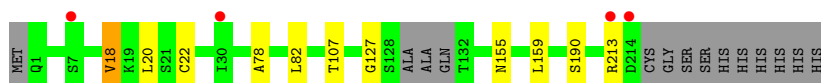
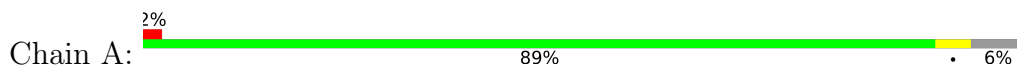
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	62	Total O 62 62	0	0
5	B	68	Total O 68 68	0	0
5	C	26	Total O 26 26	0	0
5	D	49	Total O 49 49	0	0
5	E	44	Total O 44 44	0	0
5	F	37	Total O 37 37	0	0

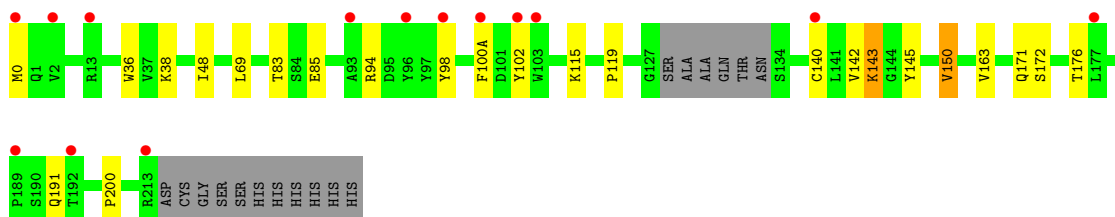
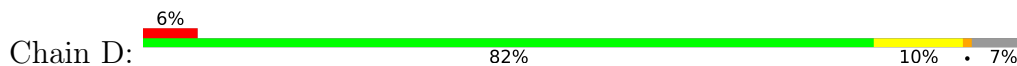
3 Residue-property plots [i](#)

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.

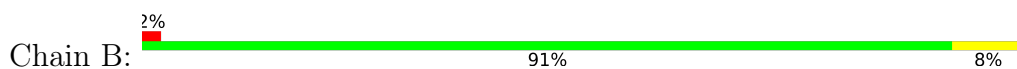
- Molecule 1: Antibody heavy chain



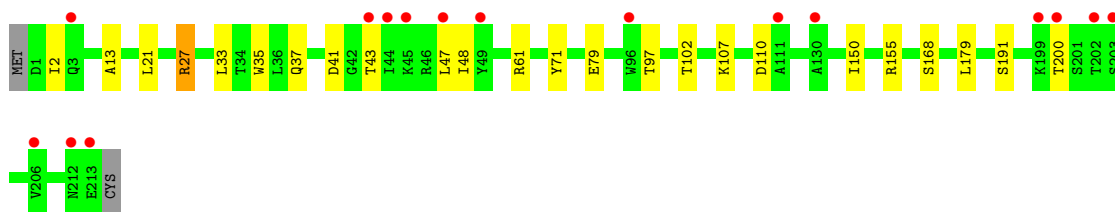
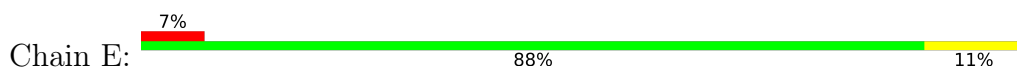
- Molecule 1: Antibody heavy chain



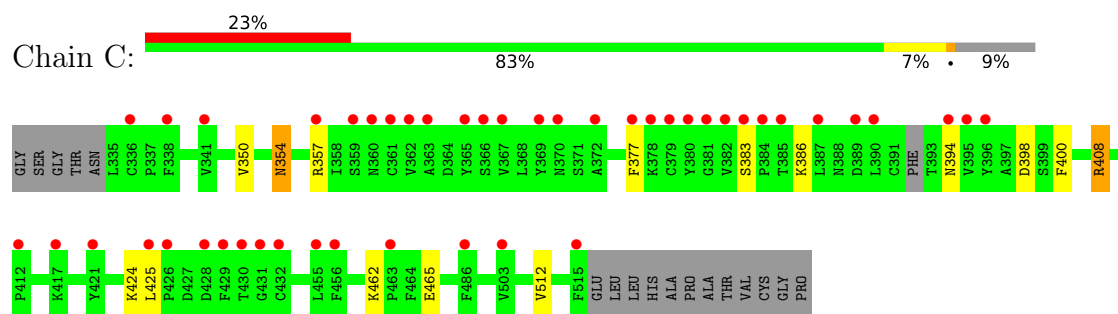
- Molecule 2: Antibody light chain



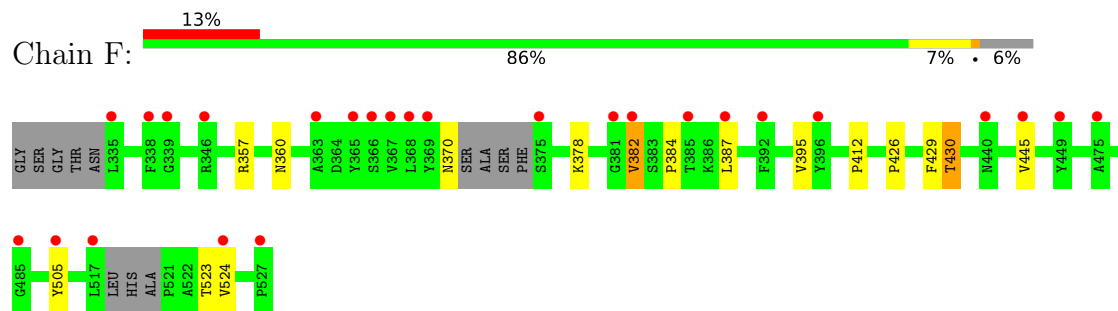
- Molecule 2: Antibody light chain



- Molecule 3: Spike protein S1



- Molecule 3: Spike protein S1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.47Å 194.62Å 62.09Å 90.00° 97.16° 90.00°	Depositor
Resolution (Å)	39.02 – 1.98 39.02 – 1.98	Depositor EDS
% Data completeness (in resolution range)	98.2 (39.02-1.98) 98.2 (39.02-1.98)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 1.98Å)	Xtrriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.247 , 0.284 0.238 , 0.237	Depositor DCC
R_{free} test set	4659 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	55.7	Xtrriage
Anisotropy	0.267	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9866	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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: 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	0.45	0/1685	0.64	0/2298
1	D	0.43	0/1664	0.61	0/2268
2	B	0.44	0/1695	0.62	0/2298
2	E	0.43	0/1695	0.62	0/2298
3	C	0.37	0/1466	0.55	0/1990
3	F	0.45	0/1510	0.59	0/2048
All	All	0.43	0/9715	0.61	0/13200

There are no bond length outliers.

There are no bond angle outliers.

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	1643	0	1598	5	0
1	D	1622	0	1585	13	0
2	B	1659	0	1591	9	0
2	E	1659	0	1591	13	0
3	C	1434	0	1355	6	0
3	F	1478	0	1398	13	0
4	A	10	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	10	0	0	0	0
4	C	10	0	0	1	0
4	D	25	0	0	3	0
4	E	15	0	0	6	0
4	F	15	0	0	5	0
5	A	62	0	0	0	0
5	B	68	0	0	0	0
5	C	26	0	0	0	0
5	D	49	0	0	0	0
5	E	44	0	0	0	0
5	F	37	0	0	1	0
All	All	9866	0	9118	66	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 (66) 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)
4:E:301:SO4:S	4:E:301:SO4:O3	1.03	1.41
4:A:301:SO4:O4	4:A:301:SO4:S	1.01	1.41
4:E:301:SO4:O3	4:E:301:SO4:O2	1.65	1.12
4:A:301:SO4:O4	4:A:301:SO4:O3	1.69	1.08
4:A:301:SO4:O4	4:A:301:SO4:O2	1.74	1.02
4:A:301:SO4:O4	4:A:301:SO4:O1	1.78	1.00
4:E:301:SO4:O3	4:E:301:SO4:O1	1.84	0.96
4:E:301:SO4:O3	4:E:301:SO4:O4	1.83	0.95
1:D:119:PRO:HB3	1:D:145:TYR:HB3	1.67	0.76
2:E:150:ILE:HD12	2:E:155:ARG:HD2	1.79	0.65
2:E:155:ARG:HG3	4:E:302:SO4:O1	1.98	0.64
2:B:39:LYS:NZ	2:B:81:GLU:HG2	2.12	0.63
3:C:408:ARG:NH2	4:C:601:SO4:O4	2.32	0.62
2:B:39:LYS:HZ1	2:B:81:GLU:HG2	1.63	0.62
3:F:505:TYR:HD2	4:F:602:SO4:O4	1.85	0.59
3:F:430:THR:O	4:F:603:SO4:O3	2.22	0.57
2:E:61:ARG:CZ	2:E:79:GLU:HG3	2.35	0.57
3:F:429:PHE:HD1	4:F:603:SO4:O4	1.87	0.57
2:B:21:LEU:HD22	2:B:102:THR:HG21	1.86	0.57
3:F:395:VAL:HG23	3:F:524:VAL:HG11	1.86	0.56
3:C:462:LYS:HG2	3:C:465:GLU:HB2	1.87	0.56
1:A:18:VAL:HG12	1:A:82:LEU:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:383:SER:HB3	3:C:386:LYS:HG2	1.90	0.54
2:E:13:ALA:HA	2:E:107:LYS:HE3	1.90	0.54
1:D:143:LYS:HE3	1:D:176:THR:HG21	1.91	0.51
1:D:143:LYS:HE2	1:D:171:GLN:OE1	2.11	0.51
2:E:150:ILE:HD11	2:E:179:LEU:HD21	1.92	0.51
2:E:97:THR:HA	4:E:301:SO4:O1	2.12	0.49
2:E:33:LEU:HD22	2:E:71:TYR:HB3	1.95	0.49
3:F:505:TYR:CD1	4:F:601:SO4:O4	2.67	0.48
1:D:142:VAL:HG11	1:D:150:VAL:HG11	1.96	0.47
3:F:412:PRO:HG3	3:F:429:PHE:HB3	1.96	0.47
1:D:83:THR:HG23	1:D:85:GLU:H	1.80	0.46
1:D:36:TRP:CD1	1:D:69:LEU:HD22	2.50	0.46
2:E:37:GLN:HB2	2:E:47:LEU:HD11	1.99	0.45
3:F:360:ASN:H	3:F:523:THR:HB	1.82	0.45
3:F:412:PRO:HB3	3:F:426:PRO:O	2.17	0.45
1:D:38:LYS:HB2	1:D:48:ILE:HD11	1.99	0.45
1:A:155:ASN:HB2	1:A:159:LEU:HG	1.99	0.45
1:D:163:VAL:HG21	4:D:304:SO4:O3	2.17	0.44
1:D:98:TYR:CD2	4:D:303:SO4:O4	2.70	0.44
2:E:110:ASP:HB3	2:E:200:THR:HG22	2.00	0.44
3:F:384:PRO:HA	3:F:387:LEU:HD12	1.99	0.43
1:A:20:LEU:HD22	1:A:107:THR:HG21	2.00	0.43
1:D:119:PRO:CB	1:D:145:TYR:HB3	2.44	0.43
3:F:505:TYR:CE1	4:F:601:SO4:O4	2.72	0.42
3:C:354:ASN:O	3:C:398:ASP:HA	2.19	0.42
1:A:22:CYS:HB3	1:A:78:ALA:HB3	2.01	0.42
2:B:166:GLN:HG3	2:B:173:TYR:CZ	2.53	0.42
2:E:35:TRP:HB2	2:E:48:ILE:HB	2.02	0.42
3:F:360:ASN:H	3:F:523:THR:CB	2.33	0.42
3:F:378:LYS:NZ	5:F:705:HOH:O	2.52	0.42
1:A:127:GLY:HA2	1:A:213:ARG:HD2	2.01	0.42
2:B:125:LEU:O	2:B:183:LYS:HD2	2.20	0.41
2:E:2:ILE:HG12	2:E:27:ARG:HG3	2.02	0.41
3:F:382:VAL:HG23	3:F:387:LEU:HG	2.02	0.41
2:B:39:LYS:NZ	2:B:81:GLU:CG	2.83	0.41
2:B:169:LYS:HB2	1:D:102:TYR:CE2	2.55	0.41
2:E:21:LEU:HD22	2:E:102:THR:HG21	2.03	0.41
2:B:113:PRO:HG3	2:B:144:ILE:HD11	2.03	0.41
3:C:425:LEU:HD21	3:C:512:VAL:HG11	2.01	0.41
1:D:200:PRO:HA	4:D:305:SO4:O3	2.21	0.41
1:D:94:ARG:O	1:D:100(A):PHE:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:41:ASP:OD1	2:E:43:THR:HG22	2.21	0.41
2:B:124:GLN:HG2	2:B:129:GLY:O	2.21	0.41
3:C:350:VAL:HA	3:C:400:PHE:HB2	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	212/230 (92%)	209 (99%)	3 (1%)	0	100	100
1	D	209/230 (91%)	205 (98%)	3 (1%)	1 (0%)	29	16
2	B	211/215 (98%)	206 (98%)	5 (2%)	0	100	100
2	E	211/215 (98%)	206 (98%)	5 (2%)	0	100	100
3	C	176/198 (89%)	164 (93%)	12 (7%)	0	100	100
3	F	180/198 (91%)	172 (96%)	8 (4%)	0	100	100
All	All	1199/1286 (93%)	1162 (97%)	36 (3%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	172	SER

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	A	185/196 (94%)	183 (99%)	2 (1%)	73	70
1	D	182/196 (93%)	176 (97%)	6 (3%)	38	26
2	B	189/191 (99%)	184 (97%)	5 (3%)	46	37
2	E	189/191 (99%)	186 (98%)	3 (2%)	62	56
3	C	155/169 (92%)	149 (96%)	6 (4%)	32	19
3	F	160/169 (95%)	155 (97%)	5 (3%)	40	28
All	All	1060/1112 (95%)	1033 (98%)	27 (2%)	47	39

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	VAL
1	A	190	SER
2	B	9	SER
2	B	10	SER
2	B	60	LYS
2	B	105	GLU
2	B	153	SER
3	C	354	ASN
3	C	357	ARG
3	C	377	PHE
3	C	394	ASN
3	C	408	ARG
3	C	424	LYS
1	D	0	MET
1	D	115	LYS
1	D	140	CYS
1	D	143	LYS
1	D	150	VAL
1	D	191	GLN
2	E	27	ARG
2	E	168	SER
2	E	191	SER
3	F	357	ARG
3	F	370	ASN
3	F	382	VAL
3	F	430	THR
3	F	445	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

17 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	A	302	-	4,4,4	0.65	0	6,6,6	0.55	0
4	SO4	E	303	-	4,4,4	0.29	0	6,6,6	0.21	0
4	SO4	F	603	-	4,4,4	0.38	0	6,6,6	0.50	0
4	SO4	D	303	-	4,4,4	1.52	1 (25%)	6,6,6	0.77	0
4	SO4	D	305	-	4,4,4	0.28	0	6,6,6	0.29	0
4	SO4	A	301	-	4,4,4	4.78	4 (100%)	6,6,6	1.03	0
4	SO4	D	304	-	4,4,4	0.78	0	6,6,6	0.78	0
4	SO4	E	302	-	4,4,4	2.04	2 (50%)	6,6,6	1.25	1 (16%)
4	SO4	D	301	-	4,4,4	0.41	0	6,6,6	0.46	0
4	SO4	C	601	-	4,4,4	0.13	0	6,6,6	0.15	0
4	SO4	B	302	-	4,4,4	0.21	0	6,6,6	0.30	0
4	SO4	C	602	-	4,4,4	0.24	0	6,6,6	0.18	0
4	SO4	F	602	-	4,4,4	0.31	0	6,6,6	0.36	0
4	SO4	D	302	-	4,4,4	3.10	3 (75%)	6,6,6	1.68	2 (33%)
4	SO4	F	601	-	4,4,4	2.38	2 (50%)	6,6,6	0.91	0
4	SO4	E	301	-	4,4,4	4.74	4 (100%)	6,6,6	1.22	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	B	301	-	4,4,4	1.22	0	6,6,6	0.99	0

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	301	SO4	O4-S	-5.60	1.01	1.47
4	E	301	SO4	O2-S	-5.48	1.16	1.46
4	E	301	SO4	O3-S	-5.36	1.03	1.47
4	A	301	SO4	O2-S	-5.15	1.18	1.46
4	E	301	SO4	O1-S	-4.51	1.21	1.46
4	D	302	SO4	O4-S	-4.15	1.13	1.47
4	A	301	SO4	O3-S	-4.13	1.13	1.47
4	A	301	SO4	O1-S	-4.05	1.24	1.46
4	D	302	SO4	O1-S	-3.65	1.26	1.46
4	F	601	SO4	O2-S	-3.51	1.27	1.46
4	E	301	SO4	O4-S	-3.28	1.21	1.47
4	E	302	SO4	O1-S	-2.53	1.32	1.46
4	D	303	SO4	O2-S	-2.41	1.33	1.46
4	F	601	SO4	O1-S	-2.35	1.33	1.46
4	E	302	SO4	O2-S	-2.23	1.33	1.46
4	D	302	SO4	O3-S	-2.23	1.29	1.47

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	302	SO4	O4-S-O1	-2.59	95.81	109.31
4	E	302	SO4	O4-S-O1	-2.30	97.29	109.31
4	E	301	SO4	O3-S-O2	-2.29	97.38	109.31
4	D	302	SO4	O3-S-O2	2.13	120.45	109.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	603	SO4	2	0
4	D	303	SO4	1	0
4	D	305	SO4	1	0
4	A	301	SO4	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	304	SO4	1	0
4	E	302	SO4	1	0
4	C	601	SO4	1	0
4	F	602	SO4	1	0
4	F	601	SO4	2	0
4	E	301	SO4	5	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	216/230 (93%)	0.47	4 (1%) 66 68	46, 60, 78, 87	0
1	D	213/230 (92%)	0.63	14 (6%) 18 20	44, 66, 83, 93	0
2	B	213/215 (99%)	0.35	4 (1%) 66 68	47, 58, 72, 86	0
2	E	213/215 (99%)	0.68	16 (7%) 14 16	40, 63, 79, 105	0
3	C	180/198 (90%)	1.34	46 (25%) 0 0	57, 74, 110, 120	0
3	F	186/198 (93%)	0.88	26 (13%) 2 3	44, 63, 95, 111	0
All	All	1221/1286 (94%)	0.70	110 (9%) 9 10	40, 63, 91, 120	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	390	LEU	7.4
3	C	361	CYS	6.3
3	C	360	ASN	6.3
3	C	365	TYR	5.9
3	F	368	LEU	5.7
3	C	380	TYR	5.4
3	C	396	TYR	5.1
2	E	212	ASN	4.8
3	C	336	CYS	4.8
3	C	338	PHE	4.7
3	C	382	VAL	4.6
3	F	527	PRO	4.6
3	C	394	ASN	4.6
3	C	429	PHE	4.6
3	C	363	ALA	4.5
3	F	335	LEU	4.5
3	C	395	VAL	4.4
3	F	445	VAL	4.4
3	C	369	TYR	4.4

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Mol	Chain	Res	Type	RSRZ
3	F	381	GLY	4.4
3	C	381	GLY	4.3
1	D	0	MET	4.0
3	F	387	LEU	3.9
1	D	213	ARG	3.8
3	F	517	LEU	3.8
3	C	515	PHE	3.8
3	C	366	SER	3.7
3	C	362	VAL	3.7
3	C	359	SER	3.7
3	F	339	GLY	3.6
2	E	202	THR	3.6
3	C	384	PRO	3.6
3	C	383	SER	3.4
3	C	425	LEU	3.4
3	C	372	ALA	3.4
3	C	370	ASN	3.3
3	F	367	VAL	3.2
3	F	524	VAL	3.2
2	E	200	THR	3.2
3	C	421	TYR	3.1
3	C	456	PHE	3.1
2	E	203	SER	3.1
3	C	389	ASP	3.0
3	C	379	CYS	3.0
3	C	385	THR	3.0
3	F	385	THR	3.0
1	D	96	TYR	2.9
2	B	57	GLY	2.9
1	D	189	PRO	2.9
3	C	357	ARG	2.9
3	C	341	VAL	2.8
3	C	426	PRO	2.8
3	C	378	LYS	2.7
3	F	396	TYR	2.7
3	C	387	LEU	2.7
1	D	192	THR	2.7
1	D	93	ALA	2.7
3	F	365	TYR	2.7
3	F	449	TYR	2.7
3	C	417	LYS	2.6
1	D	100(A)	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
3	F	366	SER	2.6
3	F	375	SER	2.6
2	B	67	SER	2.6
1	D	103	TRP	2.6
1	A	214	ASP	2.6
3	F	382	VAL	2.6
3	F	369	TYR	2.6
3	F	505	TYR	2.5
1	D	2	VAL	2.5
2	E	44	ILE	2.5
3	C	430	THR	2.5
1	D	102	TYR	2.5
3	C	432	CYS	2.5
3	F	346	ARG	2.5
2	E	199	LYS	2.4
1	A	30	ILE	2.4
1	D	177	LEU	2.4
2	E	49	TYR	2.4
2	E	43	THR	2.4
3	C	367	VAL	2.4
3	F	338	PHE	2.4
3	C	455	LEU	2.3
3	C	377	PHE	2.3
2	E	47	LEU	2.3
3	F	440	ASN	2.3
3	C	431	GLY	2.3
3	C	463	PRO	2.3
3	F	392	PHE	2.2
2	E	111	ALA	2.2
3	C	503	VAL	2.2
3	C	486	PHE	2.2
3	F	363	ALA	2.2
1	A	7	SER	2.2
2	E	130	ALA	2.2
3	C	428	ASP	2.2
1	D	140	CYS	2.1
3	F	485	GLY	2.1
2	E	3	GLN	2.1
2	E	96	TRP	2.1
3	C	412	PRO	2.1
2	E	206	VAL	2.1
2	B	213	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	213	GLU	2.1
2	E	45	LYS	2.1
2	B	212	ASN	2.1
1	D	98	TYR	2.0
1	A	213	ARG	2.0
1	D	13	ARG	2.0
3	F	475	ALA	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, 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
4	SO4	C	601	5/5	0.85	0.13	120,120,120,120	0
4	SO4	F	602	5/5	0.85	0.34	96,96,97,97	0
4	SO4	C	602	5/5	0.86	0.20	102,102,102,103	0
4	SO4	D	305	5/5	0.88	0.15	96,96,97,97	0
4	SO4	B	302	5/5	0.92	0.23	83,83,83,83	0
4	SO4	F	603	5/5	0.92	0.17	81,81,82,82	0
4	SO4	E	303	5/5	0.95	0.19	84,84,84,84	0
4	SO4	A	302	5/5	0.96	0.15	62,62,64,64	0
4	SO4	D	301	5/5	0.96	0.14	64,64,65,66	0
4	SO4	D	302	5/5	0.97	0.19	37,40,41,42	0
4	SO4	D	303	5/5	0.97	0.18	49,50,53,53	0
4	SO4	B	301	5/5	0.97	0.14	51,51,55,55	0
4	SO4	E	302	5/5	0.98	0.20	47,47,50,51	0
4	SO4	F	601	5/5	0.98	0.14	44,46,46,49	0
4	SO4	A	301	5/5	0.99	0.19	31,31,37,37	0
4	SO4	D	304	5/5	0.99	0.15	63,63,64,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	E	301	5/5	1.00	0.18	31,32,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.