



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:40 PM UTC

PDB ID : 8GB6 / pdb_00008gb6
Title : Crystal structure of SARS-CoV-2 receptor binding domain in complex with neutralizing antibody 21B6
Authors : Yuan, M.; Wilson, I.A.
Deposited on : 2023-02-24
Resolution : 1.75 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

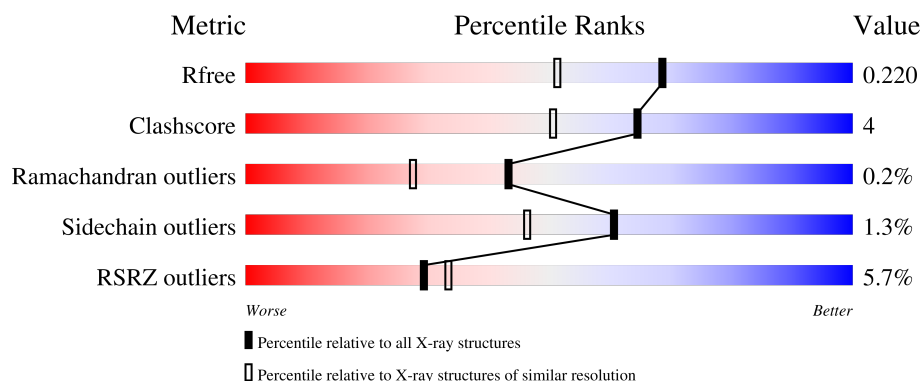
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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	205	10% 87% 7% 5%
2	H	226	4% 94% 5%
3	L	214	3% 93% 6%
4	B	3	67% 33%

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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	195	Total 1543	C 989	N 257	O 289	S 8	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	531	GLY	-	expression tag	UNP P0DTC2
A	532	HIS	-	expression tag	UNP P0DTC2
A	533	HIS	-	expression tag	UNP P0DTC2
A	534	HIS	-	expression tag	UNP P0DTC2
A	535	HIS	-	expression tag	UNP P0DTC2
A	536	HIS	-	expression tag	UNP P0DTC2
A	537	HIS	-	expression tag	UNP P0DTC2

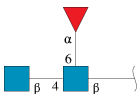
- Molecule 2 is a protein called 21B6 Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	226	Total 1681	C 1063	N 286	O 326	S 6	0	0	0

- Molecule 3 is a protein called 21B6 Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	0	0
			1634	1021	272	336	5			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	173	Total	O	0	0
			173	173		

Continued on next page...

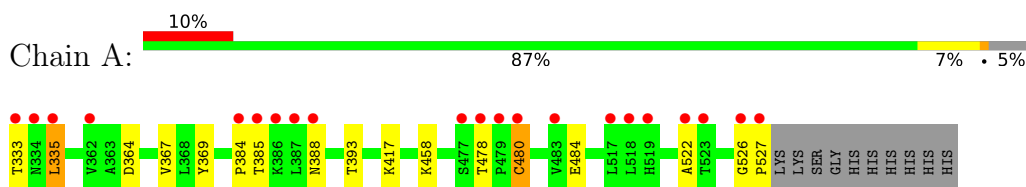
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	211	Total 211	O 211	0	0
6	L	203	Total 203	O 203	0	0

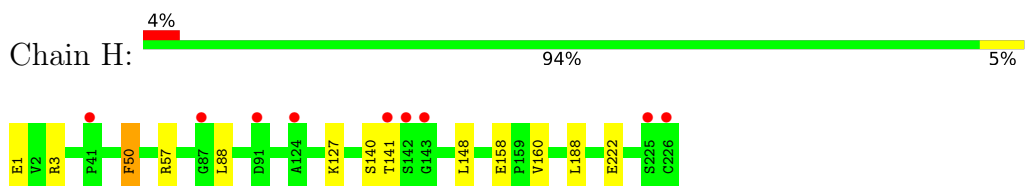
3 Residue-property plots [i](#)

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.

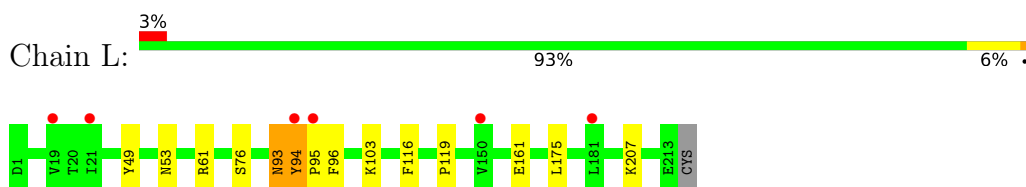
- Molecule 1: Spike protein S1



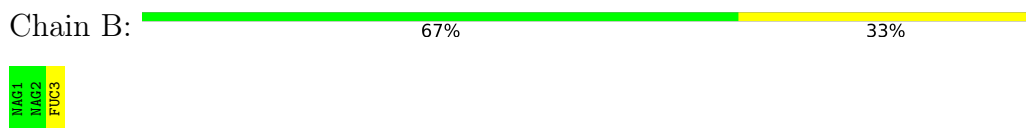
- Molecule 2: 21B6 Heavy chain



- Molecule 3: 21B6 Light chain



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.65Å 78.83Å 131.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.50 – 1.75 41.50 – 1.75	Depositor EDS
% Data completeness (in resolution range)	97.4 (41.50-1.75) 97.6 (41.50-1.75)	Depositor EDS
R_{merge}	0.99	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.75Å)	Xtriage
Refinement program	PHENIX 1.19.2	Depositor
R, R_{free}	0.182 , 0.221 0.181 , 0.220	Depositor DCC
R_{free} test set	2000 reflections (2.58%)	wwPDB-VP
Wilson B-factor (Å ²)	24.2	Xtriage
Anisotropy	0.661	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5523	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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, NAG, FUC

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	0.73	0/1587	0.83	1/2161 (0.0%)
2	H	0.75	0/1723	0.93	0/2349
3	L	0.70	0/1671	0.91	4/2272 (0.2%)
All	All	0.73	0/4981	0.89	5/6782 (0.1%)

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
2	H	0	1
3	L	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	480	CYS	CA-CB-SG	-7.37	97.45	114.40
3	L	94	TYR	CA-CB-CG	6.87	126.27	113.90
3	L	93	ASN	CA-C-N	6.33	137.24	121.80
3	L	93	ASN	C-N-CA	6.33	137.24	121.80
3	L	94	TYR	N-CA-CB	5.75	120.61	110.37

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	141	THR	Peptide
3	L	93	ASN	Peptide

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	1543	0	1459	14	0
2	H	1681	0	1652	10	0
3	L	1634	0	1570	15	0
4	B	38	0	34	0	0
5	A	10	0	0	1	0
5	H	20	0	0	0	0
5	L	10	0	0	0	0
6	A	173	0	0	6	0
6	H	211	0	0	5	0
6	L	203	0	0	4	0
All	All	5523	0	4715	38	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 (38) 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)
3:L:103:LYS:NZ	6:L:401:HOH:O	2.04	0.88
1:A:527:PRO:O	6:A:701:HOH:O	2.01	0.78
1:A:333:THR:HB	1:A:335:LEU:HD23	1.66	0.78
3:L:103:LYS:HD2	3:L:103:LYS:H	1.50	0.76
1:A:364:ASP:OD1	6:A:703:HOH:O	2.07	0.72
1:A:478:THR:OG1	6:A:702:HOH:O	2.06	0.71
2:H:158:GLU:HG3	6:H:401:HOH:O	1.95	0.66
2:H:127:LYS:NZ	6:H:404:HOH:O	2.27	0.66
3:L:103:LYS:HD2	3:L:103:LYS:N	2.13	0.63
1:A:417:LYS:NZ	6:A:707:HOH:O	2.29	0.62
2:H:158:GLU:OE2	6:H:401:HOH:O	2.16	0.61
2:H:140:SER:O	2:H:140:SER:OG	2.12	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:222:GLU:OE2	6:H:402:HOH:O	2.16	0.60
1:A:369:TYR:CD2	1:A:384:PRO:HB2	2.38	0.59
3:L:161:GLU:HG2	3:L:175:LEU:HD21	1.86	0.56
3:L:94:TYR:HB2	3:L:95:PRO:HD3	1.87	0.56
1:A:369:TYR:HD2	1:A:384:PRO:HB2	1.74	0.53
1:A:388:ASN:HB3	1:A:527:PRO:HD2	1.91	0.53
3:L:61:ARG:HG2	3:L:61:ARG:HH11	1.74	0.53
1:A:385:THR:OG1	6:A:705:HOH:O	2.18	0.52
2:H:140:SER:HA	3:L:116:PHE:HD2	1.76	0.51
2:H:57:ARG:HB2	6:H:434:HOH:O	2.11	0.51
3:L:119:PRO:O	6:L:402:HOH:O	2.18	0.51
3:L:103:LYS:HE3	6:L:408:HOH:O	2.12	0.48
3:L:103:LYS:NZ	6:L:408:HOH:O	2.44	0.48
3:L:61:ARG:HD2	3:L:76:SER:O	2.14	0.47
3:L:61:ARG:HG2	3:L:61:ARG:NH1	2.30	0.46
1:A:388:ASN:HA	1:A:526:GLY:HA3	1.99	0.45
1:A:458:LYS:HE3	6:A:753:HOH:O	2.17	0.44
2:H:88:LEU:HD23	2:H:88:LEU:HA	1.82	0.44
3:L:94:TYR:HB2	3:L:95:PRO:CD	2.47	0.44
1:A:478:THR:HG23	5:A:602:SO4:O4	2.18	0.43
2:H:50:PHE:C	2:H:50:PHE:CD1	2.97	0.43
1:A:393:THR:HA	1:A:522:ALA:HA	1.99	0.43
3:L:94:TYR:O	3:L:96:PHE:N	2.50	0.43
1:A:364:ASP:O	1:A:367:VAL:HG22	2.20	0.42
2:H:1:GLU:OE1	2:H:3:ARG:NH2	2.53	0.41
3:L:49:TYR:O	3:L:53:ASN:HB2	2.20	0.41

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	A	193/205 (94%)	186 (96%)	6 (3%)	1 (0%)	24	11
2	H	224/226 (99%)	212 (95%)	12 (5%)	0	100	100
3	L	211/214 (99%)	204 (97%)	7 (3%)	0	100	100
All	All	628/645 (97%)	602 (96%)	25 (4%)	1 (0%)	43	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	484	GLU

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	168/177 (95%)	166 (99%)	2 (1%)	63	49
2	H	186/186 (100%)	182 (98%)	4 (2%)	45	26
3	L	187/188 (100%)	186 (100%)	1 (0%)	81	75
All	All	541/551 (98%)	534 (99%)	7 (1%)	61	46

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	335	LEU
1	A	480	CYS
2	H	50	PHE
2	H	148	LEU
2	H	160	VAL
2	H	188	LEU
3	L	207	LYS

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

Mol	Chain	Res	Type
1	A	414	GLN

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 ⓘ

3 monosaccharides 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	NAG	B	1	4,1	14,14,15	0.51	0	17,19,21	0.72	0
4	NAG	B	2	4	14,14,15	0.48	0	17,19,21	0.43	0
4	FUC	B	3	4	10,10,11	1.64	3 (30%)	14,14,16	1.22	2 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	B	2	4	-	2/6/23/26	0/1/1/1
4	FUC	B	3	4	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	3	FUC	C1-C2	2.99	1.59	1.52
4	B	3	FUC	O5-C5	2.17	1.47	1.43
4	B	3	FUC	C4-C5	2.16	1.57	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	3	FUC	C1-O5-C5	2.60	119.09	112.97
4	B	3	FUC	C1-C2-C3	2.09	112.69	109.64

There are no chirality outliers.

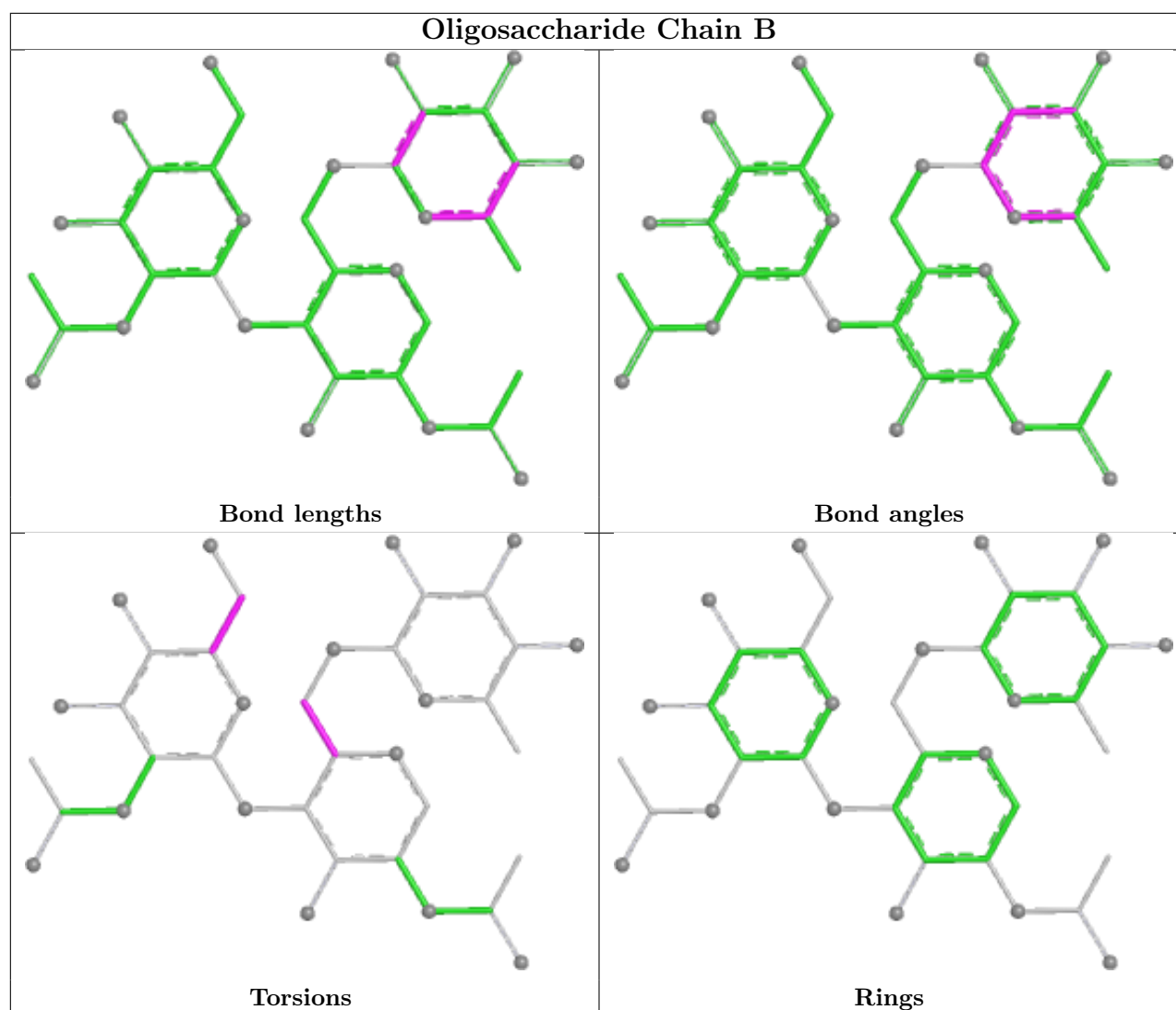
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1	NAG	C4-C5-C6-O6
4	B	1	NAG	O5-C5-C6-O6
4	B	2	NAG	C4-C5-C6-O6
4	B	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

8 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	$\# Z > 2$
5	SO4	H	304	-	4,4,4	0.39	0	6,6,6	0.58	0
5	SO4	H	302	-	4,4,4	0.25	0	6,6,6	0.33	0
5	SO4	L	301	-	4,4,4	0.34	0	6,6,6	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SO4	H	301	-	4,4,4	0.38	0	6,6,6	0.37	0
5	SO4	H	303	-	4,4,4	0.24	0	6,6,6	0.34	0
5	SO4	A	601	-	4,4,4	0.49	0	6,6,6	0.59	0
5	SO4	A	602	-	4,4,4	0.31	0	6,6,6	1.13	0
5	SO4	L	302	-	4,4,4	0.32	0	6,6,6	0.21	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
5	A	602	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, 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	195/205 (95%)	0.49	21 (10%)	11 12	18, 28, 55, 89	0
2	H	226/226 (100%)	0.20	9 (3%)	42 48	18, 26, 46, 72	0
3	L	213/214 (99%)	0.30	6 (2%)	55 61	20, 29, 44, 66	0
All	All	634/645 (98%)	0.32	36 (5%)	29 33	18, 28, 50, 89	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	94	TYR	8.1
2	H	141	THR	6.8
1	A	483	VAL	5.8
1	A	333	THR	5.2
1	A	384	PRO	4.4
3	L	95	PRO	4.2
1	A	519	HIS	3.9
2	H	143	GLY	3.7
2	H	226	CYS	3.7
1	A	480	CYS	3.6
1	A	386	LYS	3.4
1	A	527	PRO	3.3
1	A	385	THR	3.2
2	H	142	SER	3.0
1	A	387	LEU	2.9
1	A	478	THR	2.8
3	L	21	ILE	2.7
1	A	362	VAL	2.7
1	A	388	ASN	2.7
1	A	477	SER	2.6
1	A	334	ASN	2.6
1	A	335	LEU	2.6
1	A	517	LEU	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	523	THR	2.5
2	H	225	SER	2.5
1	A	518	LEU	2.4
1	A	522	ALA	2.4
3	L	181	LEU	2.4
2	H	87	GLY	2.4
1	A	479	PRO	2.4
2	H	124	ALA	2.4
2	H	91	ASP	2.3
3	L	150	VAL	2.2
2	H	41	PRO	2.2
1	A	526	GLY	2.2
3	L	19	VAL	2.2

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

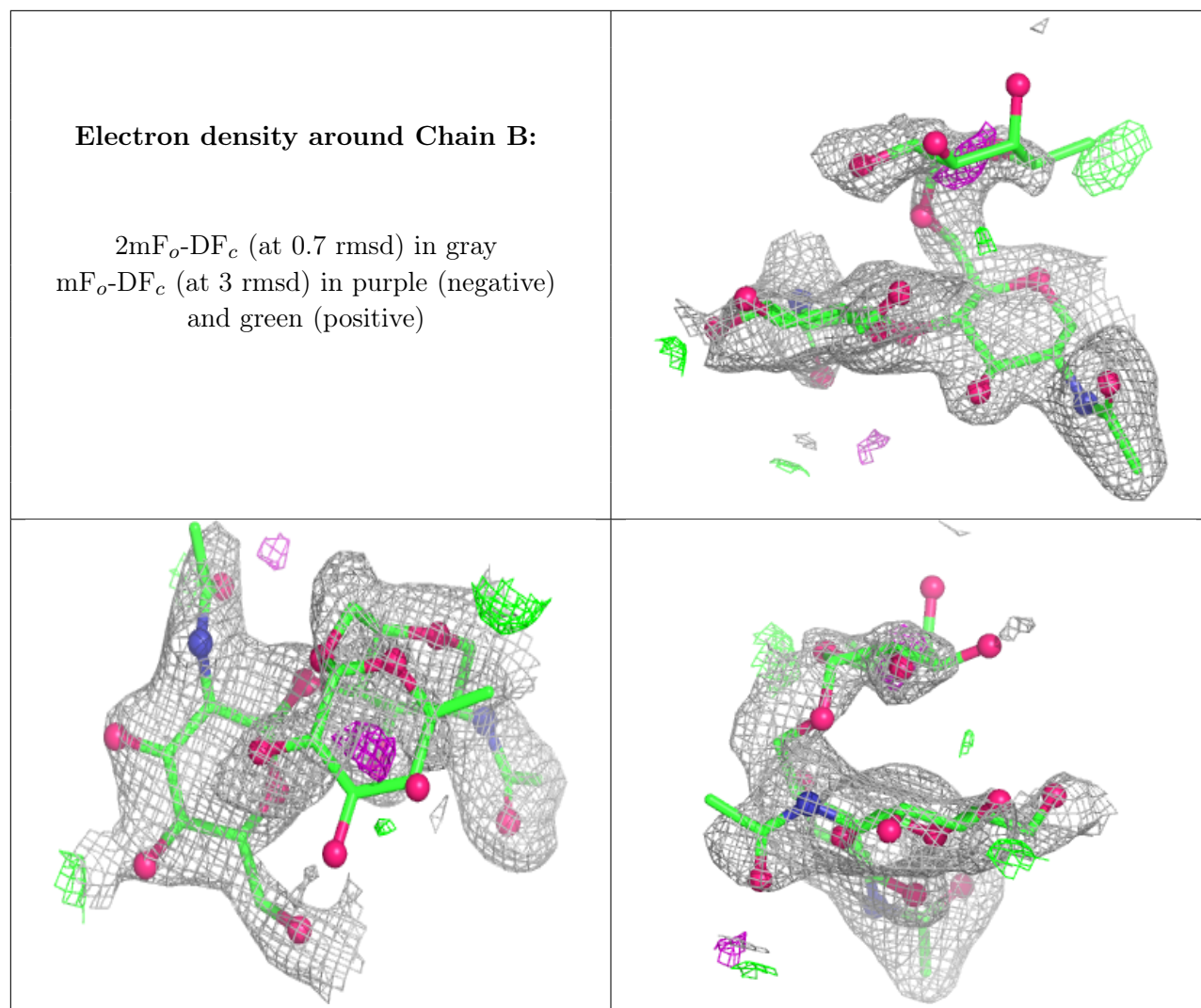
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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	NAG	B	1	14/15	-	-	30,41,60,74	0
4	NAG	B	2	14/15	-	-	65,74,85,91	0
4	FUC	B	3	10/11	-	-	75,79,91,94	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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($\text{\AA}^2$)	Q<0.9
5	SO4	L	301	5/5	0.76	0.11	59,62,76,88	0
5	SO4	H	301	5/5	0.81	0.10	46,64,71,79	0
5	SO4	L	302	5/5	0.85	0.10	57,57,71,77	0
5	SO4	H	302	5/5	0.86	0.09	61,66,68,69	0
5	SO4	H	303	5/5	0.88	0.09	45,58,64,76	0
5	SO4	H	304	5/5	0.91	0.10	50,52,61,62	0
5	SO4	A	602	5/5	0.92	0.09	41,41,46,47	0
5	SO4	A	601	5/5	0.97	0.06	35,37,39,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.