WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Mar 5, 2024 – 06:21 PM EST

PDB ID	:	8SDF
Title	:	Crystal structure of SARS-CoV-2 receptor binding domain in complex with neutralizing antibody CC25.4
Authors	:	Yuan, M.; Wilson, I.A.
Deposited on	:	2023-04-06
Resolution	:	1.79 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

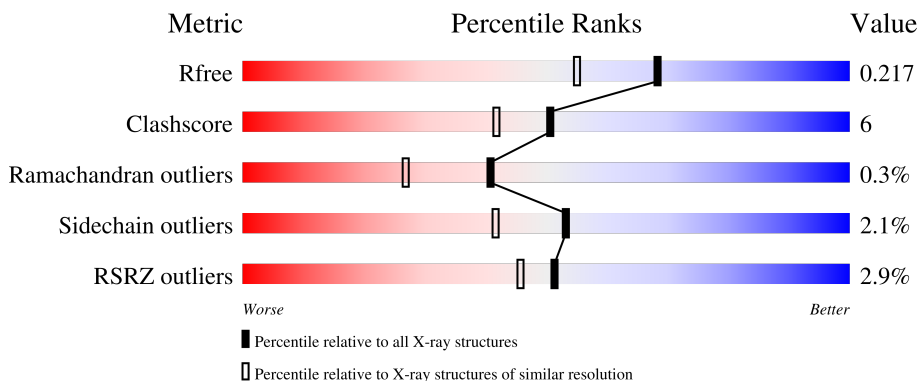|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.79 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.
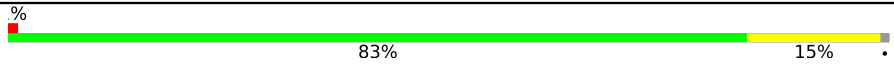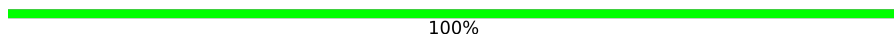

| | Percentile relative to all X-ray structures |
| | Percentile relative to X-ray structures of similar resolution |

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 >=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 <=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	4% — 81% — 13% · 5%
1	Z	205	.% — 86% — 9% — 5%
2	B	229	2% — 82% — 12% · 5%
2	H	229	2% — 87% — 12% ·
3	C	217	6% — 85% — 12% ··

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Mol	Chain	Length	Quality of chain
3	L	217	% 83% 15% .
4	D	3	100%

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 10506 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Z	195	Total	C	N	O	S	0	1	0
			1546	991	257	290	8			
1	A	194	Total	C	N	O	S	0	0	0
			1536	985	256	287	8			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	531	GLY	-	expression tag	UNP P0DTC2
Z	532	HIS	-	expression tag	UNP P0DTC2
Z	533	HIS	-	expression tag	UNP P0DTC2
Z	534	HIS	-	expression tag	UNP P0DTC2
Z	535	HIS	-	expression tag	UNP P0DTC2
Z	536	HIS	-	expression tag	UNP P0DTC2
Z	537	HIS	-	expression tag	UNP P0DTC2
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 Neutralizing antibody CC25.4 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	227	Total	C	N	O	S	0	0	0
			1748	1101	300	338	9			
2	B	217	Total	C	N	O	S	0	0	0
			1677	1062	289	317	9			

- Molecule 3 is a protein called Neutralizing Vantibody CC25.4 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total 1546	C 965	N 259	O 318	S 4	0	0	0
3	C	214	Total 1557	C 970	N 262	O 321	S 4	0	0	0

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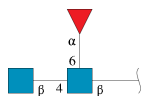
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	3	Total 38	C 22	N 2	O 14	0	0	0

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).
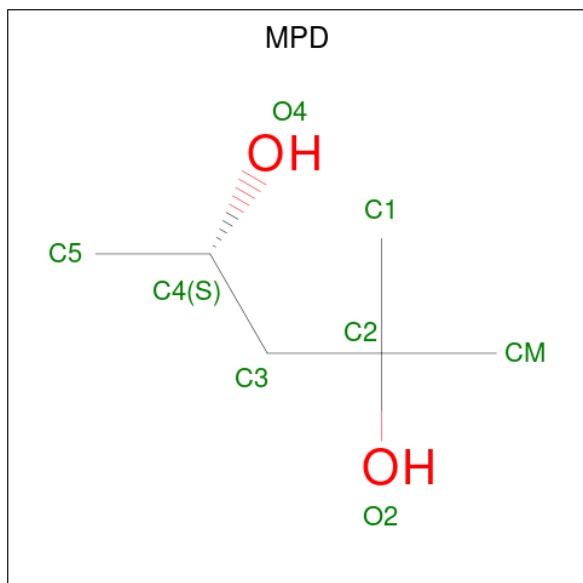
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	Z	1	Total 8	C 6	O 2	0	0
5	Z	1	Total 8	C 6	O 2	0	0
5	H	1	Total 8	C 6	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	1	Total 8	C 6	O 2	0	0
5	L	1	Total 8	C 6	O 2	0	0
5	A	1	Total 8	C 6	O 2	0	0
5	B	1	Total 8	C 6	O 2	0	0
5	C	1	Total 8	C 6	O 2	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).
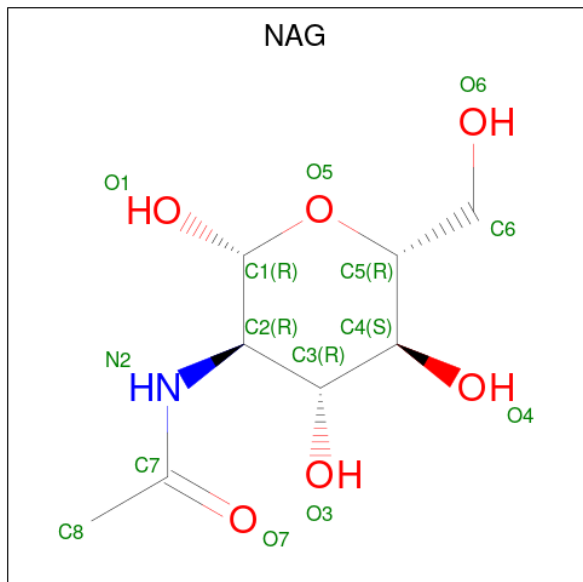
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total 14	C 8	N 1	O 5	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	Z	149	Total 149	O 149	0	0
7	H	186	Total 186	O 186	0	0
7	L	107	Total 107	O 107	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	104	Total 104	O 104	0	0
7	B	160	Total 160	O 160	0	0
7	C	74	Total 74	O 74	0	0

3 Residue-property plots ⓘ

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
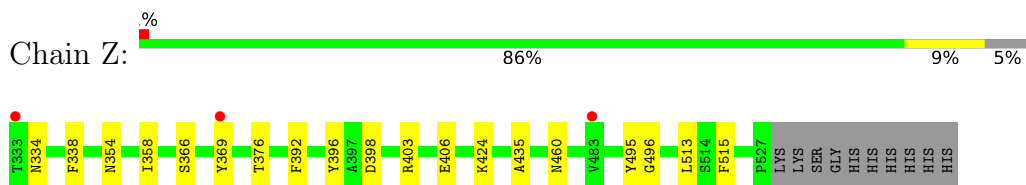
- Molecule 1: Spike protein S1
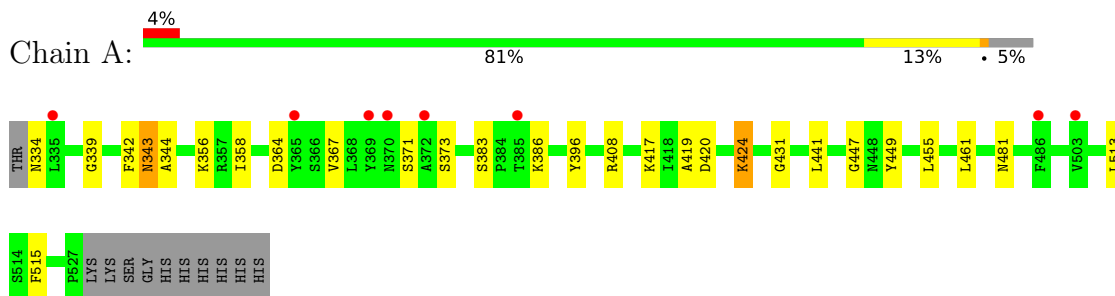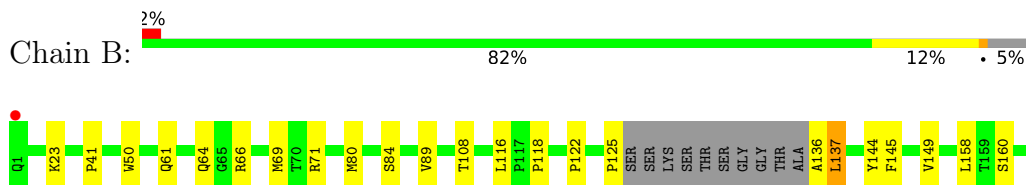

- Molecule 2: Neutralizing antibody CC25.4 heavy chain
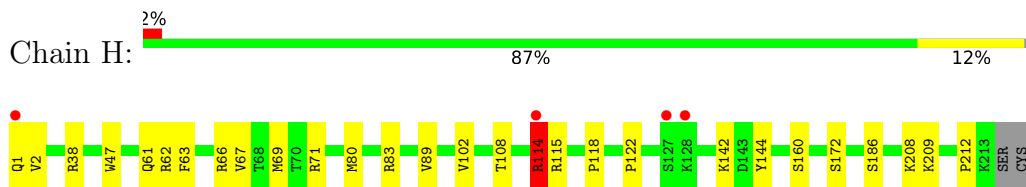
- Molecule 2: Neutralizing antibody CC25.4 heavy chain

- Molecule 3: Neutralizing antibody CC25.4 light chain
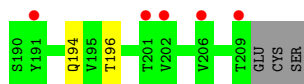
Chain L:

• Molecule 3: Neutralizing antibody CC25.4 light chain

Chain C:

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

Chain D:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	58.20Å 143.00Å 82.93Å 90.00° 94.13° 90.00°	Depositor
Resolution (Å)	58.05 – 1.79 58.05 – 1.79	Depositor EDS
% Data completeness (in resolution range)	99.2 (58.05-1.79) 99.2 (58.05-1.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.12 (at 1.78Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.185 , 0.218 0.185 , 0.217	Depositor DCC
R_{free} test set	6483 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	31.8	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 50.8	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	10506	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: FUC, MPD, NAG

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	0.50	0/1580	0.64	0/2151
1	Z	0.55	0/1593	0.67	1/2169 (0.0%)
2	B	0.51	0/1722	0.73	1/2349 (0.0%)
2	H	0.54	0/1794	0.72	0/2446
3	C	0.43	0/1595	0.66	2/2188 (0.1%)
3	L	0.46	0/1584	0.65	1/2175 (0.0%)
All	All	0.50	0/9868	0.68	5/13478 (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	Z	0	1
2	H	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(^{o})	Ideal(^{o})
3	C	47	LEU	CA-CB-CG	7.34	132.17	115.30
1	Z	495	TYR	C-N-CA	-6.04	109.61	122.30
3	L	47	LEU	CA-CB-CG	5.47	127.88	115.30
2	B	64	GLN	C-N-CA	-5.14	111.50	122.30
3	C	47	LEU	CB-CG-CD1	-5.07	102.39	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	114	ARG	Sidechain
1	Z	496	GLY	Peptide

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	A	1536	0	1452	17	0
1	Z	1546	0	1464	10	0
2	B	1677	0	1605	17	0
2	H	1748	0	1688	22	0
3	C	1557	0	1459	23	1
3	L	1546	0	1441	27	1
4	D	38	0	34	0	0
5	A	8	0	14	0	0
5	B	8	0	14	2	0
5	C	8	0	14	0	0
5	H	8	0	14	0	0
5	L	16	0	28	0	0
5	Z	16	0	28	0	0
6	A	14	0	13	1	0
7	A	104	0	0	2	0
7	B	160	0	0	4	1
7	C	74	0	0	4	0
7	H	186	0	0	7	1
7	L	107	0	0	7	0
7	Z	149	0	0	2	0
All	All	10506	0	9268	109	2

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.

The worst 5 of 109 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:B:61:GLN:NE2	3:C:1:GLN:OE1	1.95	0.97
1:A:343:ASN:O	7:A:701:HOH:O	1.87	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:180:LEU:O	7:C:401:HOH:O	1.90	0.88
3:L:79:GLN:NE2	7:L:401:HOH:O	2.11	0.82
2:H:209:LYS:NZ	7:H:401:HOH:O	2.00	0.78

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:H:565:HOH:O	7:B:538:HOH:O[2_556]	2.04	0.16
3:L:188:HIS:O	3:C:189:ARG:NH2[2_456]	2.18	0.02

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	192/205 (94%)	182 (95%)	8 (4%)	2 (1%)	15	5
1	Z	194/205 (95%)	191 (98%)	3 (2%)	0	100	100
2	B	213/229 (93%)	206 (97%)	7 (3%)	0	100	100
2	H	225/229 (98%)	222 (99%)	3 (1%)	0	100	100
3	C	212/217 (98%)	199 (94%)	11 (5%)	2 (1%)	17	6
3	L	212/217 (98%)	202 (95%)	10 (5%)	0	100	100
All	All	1248/1302 (96%)	1202 (96%)	42 (3%)	4 (0%)	41	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	ASN
3	C	127	ALA
1	A	344	ALA
3	C	151	ASP

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	167/177 (94%)	163 (98%)	4 (2%)	49	36
1	Z	169/177 (96%)	169 (100%)	0	100	100
2	B	182/197 (92%)	174 (96%)	8 (4%)	28	14
2	H	194/197 (98%)	190 (98%)	4 (2%)	53	42
3	C	168/182 (92%)	164 (98%)	4 (2%)	49	36
3	L	165/182 (91%)	163 (99%)	2 (1%)	71	65
All	All	1045/1112 (94%)	1023 (98%)	22 (2%)	53	42

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	137	LEU
2	B	208	LYS
2	B	160	SER
3	C	12	SER
1	A	408	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	360	ASN
1	A	334	ASN
1	A	493	GLN
2	B	43	GLN
3	C	128	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 ⓘ

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	D	1	4,1	14,14,15	0.35	0	17,19,21	0.50	0
4	NAG	D	2	4	14,14,15	0.42	0	17,19,21	0.44	0
4	FUC	D	3	4	10,10,11	0.89	0	14,14,16	0.96	0

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	D	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	1/6/23/26	0/1/1/1
4	FUC	D	3	4	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

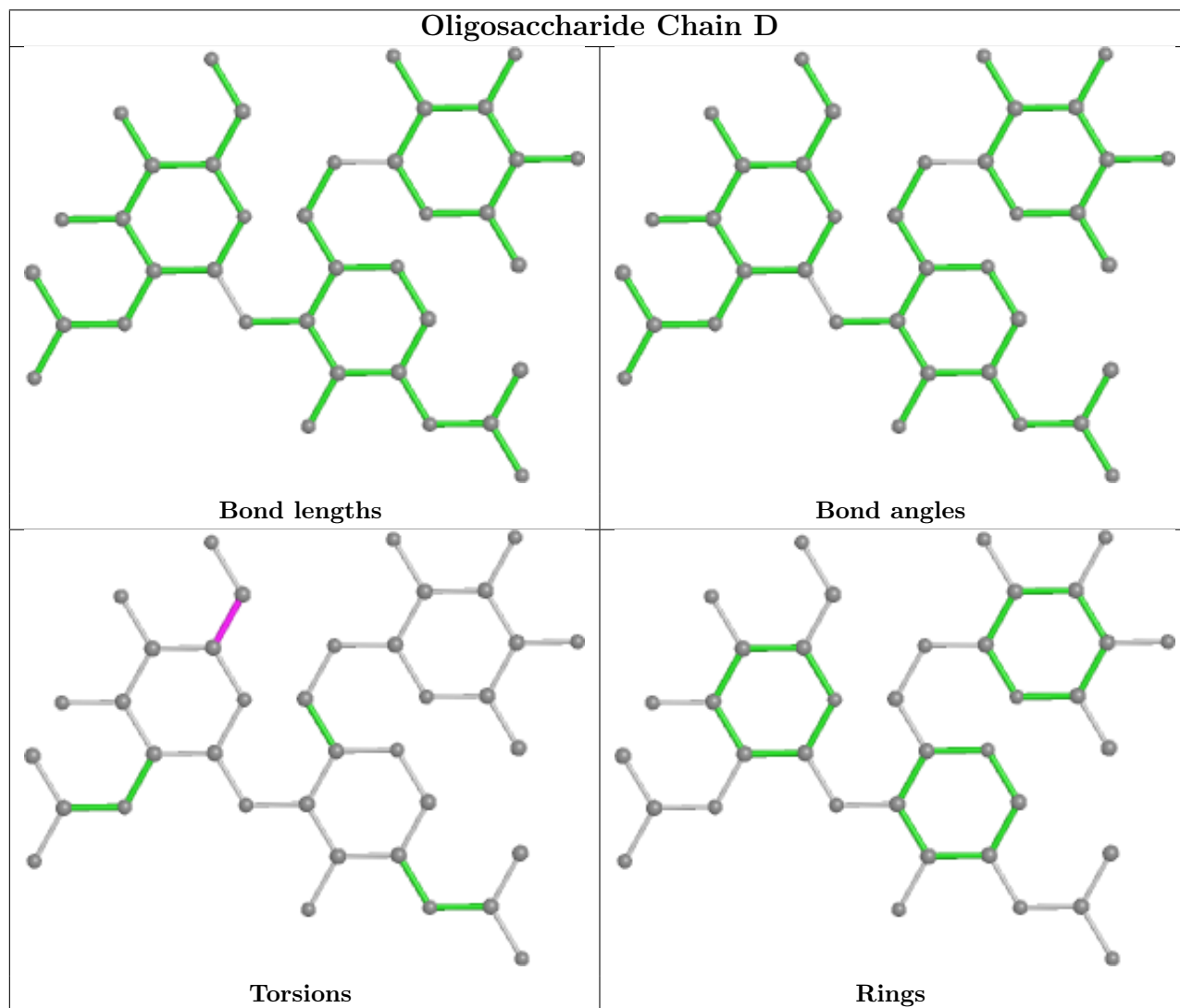All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	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 ⓘ

9 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	MPD	H	301	-	7,7,7	0.36	0	9,10,10	0.32	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
6	NAG	A	601	1	14,14,15	0.69	0	17,19,21	0.74	1 (5%)
5	MPD	Z	602	-	7,7,7	0.30	0	9,10,10	0.55	0
5	MPD	C	301	-	7,7,7	0.30	0	9,10,10	0.48	0
5	MPD	L	301	-	7,7,7	0.37	0	9,10,10	0.56	0
5	MPD	Z	601	-	7,7,7	0.32	0	9,10,10	0.64	0
5	MPD	B	301	-	7,7,7	0.32	0	9,10,10	0.54	0
5	MPD	A	602	-	7,7,7	0.31	0	9,10,10	0.83	0
5	MPD	L	302	1	7,7,7	0.50	0	9,10,10	0.64	0

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
5	MPD	H	301	-	-	3/5/5/5	-
6	NAG	A	601	1	-	0/6/23/26	0/1/1/1
5	MPD	Z	602	-	-	3/5/5/5	-
5	MPD	C	301	-	-	2/5/5/5	-
5	MPD	L	301	-	-	5/5/5/5	-
5	MPD	Z	601	-	-	2/5/5/5	-
5	MPD	B	301	-	-	1/5/5/5	-
5	MPD	A	602	-	-	2/5/5/5	-
5	MPD	L	302	1	-	1/5/5/5	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	601	NAG	C1-O5-C5	2.43	115.48	112.19

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	Z	601	MPD	C2-C3-C4-C5
5	Z	602	MPD	CM-C2-C3-C4
5	H	301	MPD	CM-C2-C3-C4
5	H	301	MPD	C2-C3-C4-O4
5	L	301	MPD	O2-C2-C3-C4

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	601	NAG	1	0
5	B	301	MPD	2	0

5.7 Other polymers ⓘ

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, 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	194/205 (94%)	0.17	8 (4%)	37	31	27, 42, 70, 77	0
1	Z	195/205 (95%)	-0.06	3 (1%)	73	70	25, 35, 59, 72	0
2	B	217/229 (94%)	0.11	4 (1%)	68	64	26, 40, 69, 87	0
2	H	227/229 (99%)	-0.04	4 (1%)	68	64	24, 34, 57, 74	0
3	C	214/217 (98%)	0.45	14 (6%)	18	15	27, 48, 80, 96	0
3	L	214/217 (98%)	0.24	3 (1%)	75	72	28, 44, 75, 84	0
All	All	1261/1302 (96%)	0.14	36 (2%)	51	46	24, 40, 70, 96	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	126	GLN	9.4
1	A	369	TYR	5.9
3	C	180	LEU	5.3
3	C	2	SER	4.7
1	Z	369	TYR	4.4

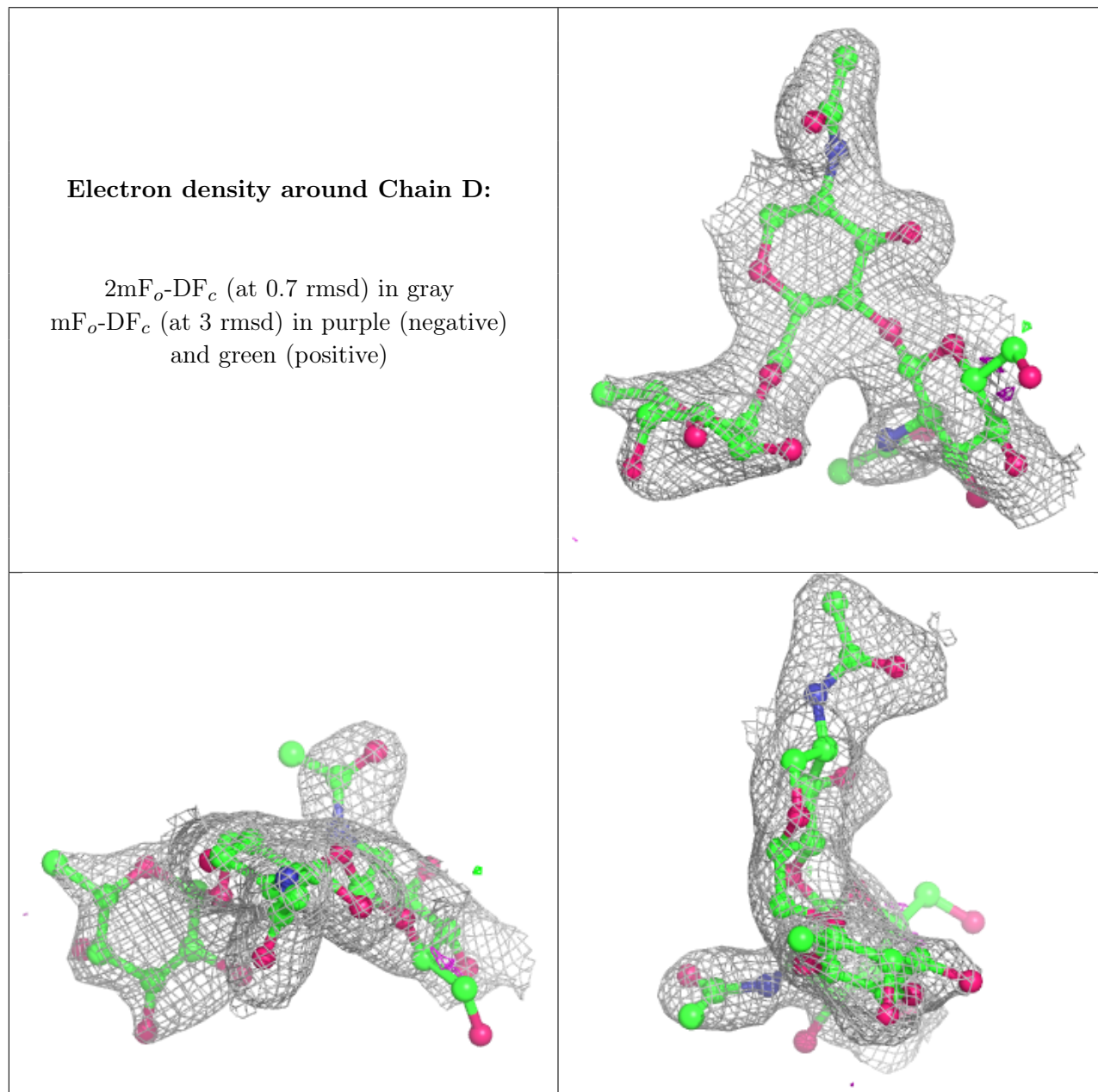## 6.2   Non-standard residues in protein, DNA, RNA chains ⓘ

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($\mathring{A}^2$)	Q<0.9
4	NAG	D	2	14/15	0.83	0.28	63,77,92,100	0
4	FUC	D	3	10/11	0.87	0.24	57,69,75,81	0
4	NAG	D	1	14/15	0.95	0.07	30,39,54,67	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.

Electron density around Chain D:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

6.4 Ligands ⓘ

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
5	MPD	L	302	8/8	0.70	0.23	55,63,66,69	0
6	NAG	A	601	14/15	0.71	0.22	65,75,86,92	0
5	MPD	Z	602	8/8	0.80	0.22	58,67,71,73	0
5	MPD	A	602	8/8	0.83	0.28	52,66,78,84	0
5	MPD	Z	601	8/8	0.88	0.19	52,61,65,74	0
5	MPD	C	301	8/8	0.89	0.19	43,50,67,75	0
5	MPD	H	301	8/8	0.90	0.22	50,59,69,74	0
5	MPD	L	301	8/8	0.90	0.20	44,54,68,77	0
5	MPD	B	301	8/8	0.94	0.10	37,46,52,53	0

6.5 Other polymers ⓘ

There are no such residues in this entry.