



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2022 – 12:09 PM EDT

PDB ID : 7N4J
Title : Crystal structure of SARS-CoV-2 receptor binding domain in complex with neutralizing human antibody WRAIR-2173.
Authors : Sankhala, R.S.; Joyce, M.G.
Deposited on : 2021-06-04
Resolution : 2.21 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 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	:	2.27
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)	:	2.27

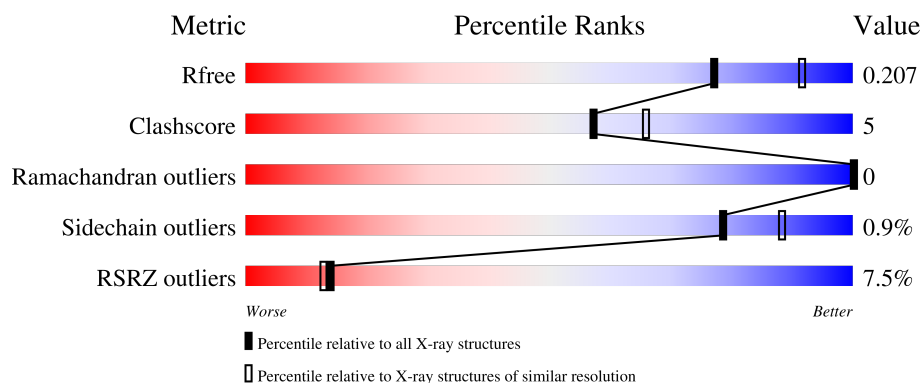
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	<div> <div>18%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
2	H	236	<div> <div>5%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>
3	L	218	<div> <div>%</div> <div>92%</div> <div>7%</div> <div>.</div> </div>
4	B	3	<div> <div>100%</div> </div>

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	BMA	B	3	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5277 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	A	202	Total	C	N	O	S	0	0	0
			1597	1020	271	298	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	528	GLY	-	expression tag	UNP P0DTC2
A	529	SER	-	expression tag	UNP P0DTC2
A	530	HIS	-	expression tag	UNP P0DTC2
A	531	HIS	-	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

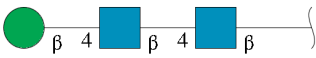
- Molecule 2 is a protein called WRAIR-2173 antibody Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	234	Total	C	N	O	S	0	0	0
			1766	1126	291	344	5			

- Molecule 3 is a protein called WRAIR-2173 antibody Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	216	Total	C	N	O	S	0	0	0
			1594	993	268	328	5			

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	3	Total	C	N	O	0	0	0
			39	22	2	15			

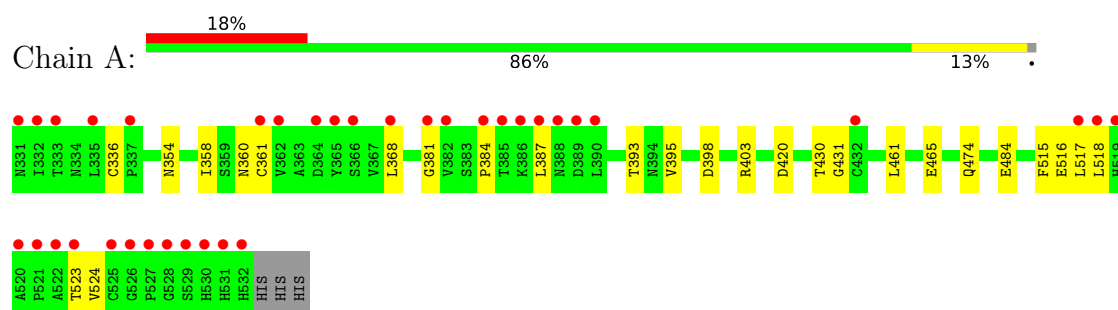
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	79	Total	O	0	0
			79	79		
5	H	101	Total	O	0	0
			101	101		
5	L	101	Total	O	0	0
			101	101		

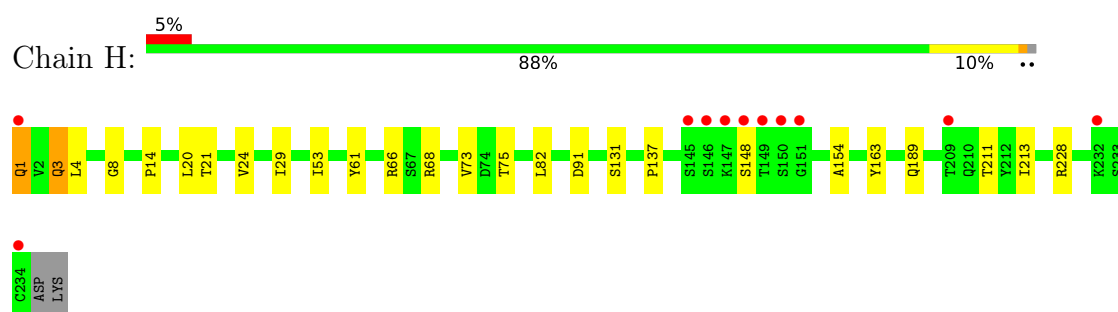
3 Residue-property plots

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.

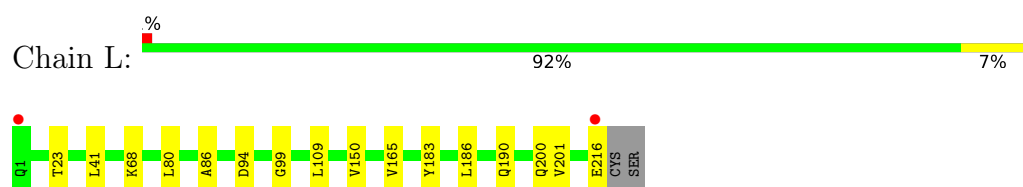
- Molecule 1: Spike protein S1



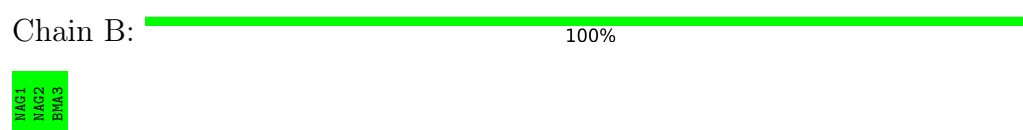
- Molecule 2: WRAIR-2173 antibody Fab heavy chain



- Molecule 3: WRAIR-2173 antibody Fab light chain



- Molecule 4: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.26Å 70.46Å 107.25Å 90.00° 98.19° 90.00°	Depositor
Resolution (Å)	44.40 – 2.21 44.40 – 2.21	Depositor EDS
% Data completeness (in resolution range)	97.7 (44.40-2.21) 97.7 (44.40-2.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.172 , 0.207 0.172 , 0.207	Depositor DCC
R_{free} test set	1686 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5277	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 4.94% 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: BMA, 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	0.27	0/1644	0.48	0/2237
2	H	0.27	0/1815	0.51	0/2487
3	L	0.28	0/1632	0.50	0/2227
All	All	0.27	0/5091	0.49	0/6951

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	1597	0	1497	21	0
2	H	1766	0	1750	17	0
3	L	1594	0	1544	10	0
4	B	39	0	34	0	0
5	A	79	0	0	8	1
5	H	101	0	0	3	0
5	L	101	0	0	3	1
All	All	5277	0	4825	48	1

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 5.

All (48) 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:474:GLN:OE1	5:A:601:HOH:O	1.99	0.81
1:A:361:CYS:SG	5:A:646:HOH:O	2.39	0.80
1:A:420:ASP:OD1	5:A:602:HOH:O	1.99	0.80
1:A:336:CYS:SG	5:A:646:HOH:O	2.41	0.78
3:L:200:GLN:NE2	5:L:303:HOH:O	2.22	0.73
2:H:29:ILE:HD11	2:H:75:THR:HA	1.71	0.73
1:A:361:CYS:O	5:A:603:HOH:O	2.08	0.72
1:A:465:GLU:OE2	5:A:604:HOH:O	2.11	0.67
1:A:360:ASN:H	1:A:523:THR:HG22	1.58	0.66
1:A:395:VAL:HG13	1:A:524:VAL:HG21	1.76	0.66
1:A:381:GLY:HA3	1:A:430:THR:HG22	1.78	0.66
2:H:4:LEU:HD22	2:H:24:VAL:HG22	1.78	0.65
3:L:216:GLU:O	5:L:301:HOH:O	2.15	0.64
1:A:461:LEU:HD22	1:A:465:GLU:HG3	1.80	0.64
1:A:484:GLU:OE1	5:A:605:HOH:O	2.16	0.58
2:H:189:GLN:OE1	5:H:301:HOH:O	2.17	0.58
2:H:211:THR:HG23	2:H:228:ARG:HD2	1.85	0.57
2:H:211:THR:HG23	2:H:228:ARG:HH11	1.69	0.57
2:H:14:PRO:HD2	2:H:131:SER:HB3	1.88	0.56
1:A:393:THR:O	1:A:523:THR:HB	2.05	0.56
2:H:148:SER:HB3	2:H:154:ALA:HA	1.88	0.54
1:A:354:ASN:O	1:A:398:ASP:HA	2.07	0.54
1:A:403:ARG:NH1	5:A:608:HOH:O	2.41	0.53
3:L:186:LEU:HB3	3:L:190:GLN:HG3	1.91	0.52
1:A:516:GLU:HG2	1:A:518:LEU:HG	1.92	0.52
1:A:358:ILE:HB	1:A:395:VAL:HG23	1.92	0.52
1:A:431:GLY:HA2	1:A:515:PHE:CE2	2.46	0.50
2:H:68:ARG:NH2	2:H:91:ASP:OD2	2.39	0.50
3:L:80:LEU:HD11	3:L:109:LEU:HD21	1.94	0.49
3:L:23:THR:HG23	5:L:325:HOH:O	2.12	0.48
3:L:41:LEU:HD23	3:L:86:ALA:HB2	1.95	0.48
2:H:68:ARG:HH22	2:H:91:ASP:CG	2.17	0.48
2:H:137:PRO:HB3	2:H:163:TYR:HB3	1.95	0.47
2:H:61:TYR:O	5:H:302:HOH:O	2.20	0.47
1:A:517:LEU:HD23	1:A:517:LEU:H	1.81	0.46
3:L:165:VAL:HA	3:L:183:TYR:O	2.16	0.46
1:A:384:PRO:HA	1:A:387:LEU:HG	1.98	0.45
2:H:8:GLY:HA3	2:H:20:LEU:HD23	1.98	0.45
3:L:94:ASP:O	3:L:99:GLY:HA2	2.18	0.44
1:A:395:VAL:HG12	1:A:515:PHE:HD1	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:150:VAL:CG2	3:L:201:VAL:HG13	2.48	0.43
2:H:1:GLN:NE2	2:H:3:GLN:OE1	2.52	0.43
1:A:368:LEU:HD23	1:A:368:LEU:HA	1.83	0.43
2:H:53:ILE:HD13	2:H:73:VAL:HG23	2.00	0.43
2:H:1:GLN:HG3	5:H:325:HOH:O	2.20	0.42
3:L:150:VAL:HG21	3:L:201:VAL:HG13	2.02	0.42
2:H:213:ILE:HD13	2:H:228:ARG:HB2	2.02	0.41
2:H:20:LEU:HD12	2:H:82:LEU:HD23	2.04	0.40

All (1) 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)
5:A:666:HOH:O	5:L:394:HOH:O[2_345]	2.13	0.07

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	200/205 (98%)	189 (94%)	11 (6%)	0	100	100
2	H	232/236 (98%)	223 (96%)	9 (4%)	0	100	100
3	L	214/218 (98%)	207 (97%)	7 (3%)	0	100	100
All	All	646/659 (98%)	619 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	174/177 (98%)	174 (100%)	0	100	100
2	H	205/207 (99%)	201 (98%)	4 (2%)	55	69
3	L	179/181 (99%)	178 (99%)	1 (1%)	86	93
All	All	558/565 (99%)	553 (99%)	5 (1%)	78	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	1	GLN
2	H	3	GLN
2	H	21	THR
2	H	66	ARG
3	L	68	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	1	GLN
2	H	3	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	1,4	14,14,15	0.36	0	17,19,21	0.46	0
4	NAG	B	2	4	14,14,15	0.27	0	17,19,21	0.59	0
4	BMA	B	3	4	11,11,12	0.80	0	15,15,17	0.90	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	B	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	B	2	4	-	2/6/23/26	0/1/1/1
4	BMA	B	3	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

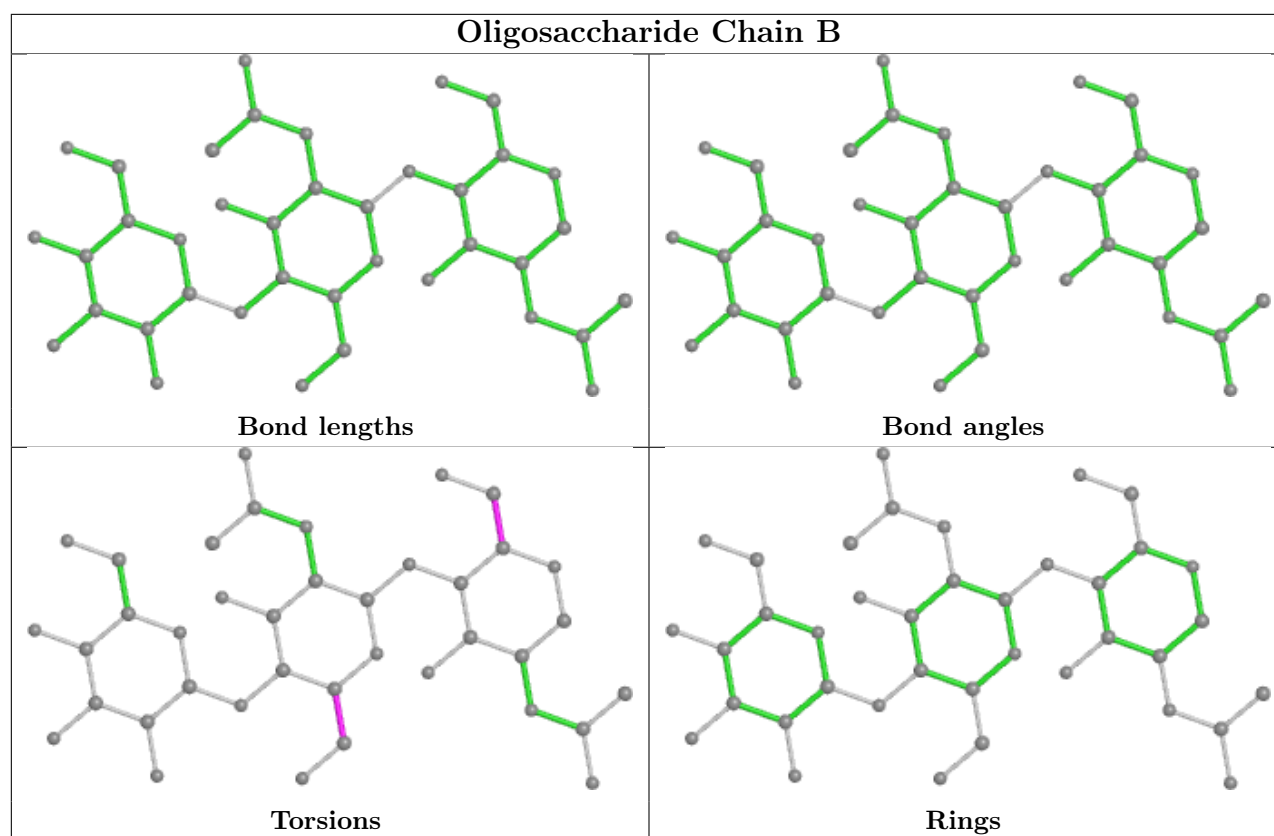
All (4) torsion outliers are listed below:

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

There are no ligands in this entry.

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	202/205 (98%)	0.76	36 (17%) 1 1	19, 44, 124, 144	0
2	H	234/236 (99%)	0.06	11 (4%) 31 30	16, 35, 78, 169	0
3	L	216/218 (99%)	-0.26	2 (0%) 84 83	17, 32, 57, 92	0
All	All	652/659 (98%)	0.17	49 (7%) 14 13	16, 35, 105, 169	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	331	ASN	16.6
2	H	149	THR	12.4
2	H	150	SER	9.2
1	A	532	HIS	8.3
1	A	332	ILE	8.3
1	A	530	HIS	8.2
1	A	531	HIS	7.2
1	A	519	HIS	6.6
2	H	151	GLY	6.6
1	A	335	LEU	6.0
3	L	1	GLN	4.8
2	H	148	SER	4.7
1	A	521	PRO	4.7
1	A	522	ALA	4.7
1	A	384	PRO	4.6
2	H	234	CYS	4.5
1	A	527	PRO	4.4
1	A	517	LEU	4.3
3	L	216	GLU	4.3
1	A	385	THR	4.1
1	A	361	CYS	4.1
1	A	529	SER	4.0
1	A	389	ASP	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	365	TYR	3.9
2	H	146	SER	3.7
2	H	147	LYS	3.6
1	A	364	ASP	3.6
1	A	390	LEU	3.5
1	A	528	GLY	3.4
1	A	523	THR	3.4
1	A	518	LEU	3.4
1	A	520	ALA	3.4
1	A	366	SER	3.3
1	A	382	VAL	3.2
1	A	333	THR	3.0
1	A	386	LYS	3.0
2	H	209	THR	3.0
1	A	526	GLY	3.0
1	A	381	GLY	2.9
2	H	232	LYS	2.8
1	A	337	PRO	2.6
1	A	388	ASN	2.4
2	H	145	SER	2.3
1	A	432	CYS	2.3
1	A	387	LEU	2.3
1	A	368	LEU	2.2
2	H	1	GLN	2.1
1	A	525	CYS	2.1
1	A	362	VAL	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](#)

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.

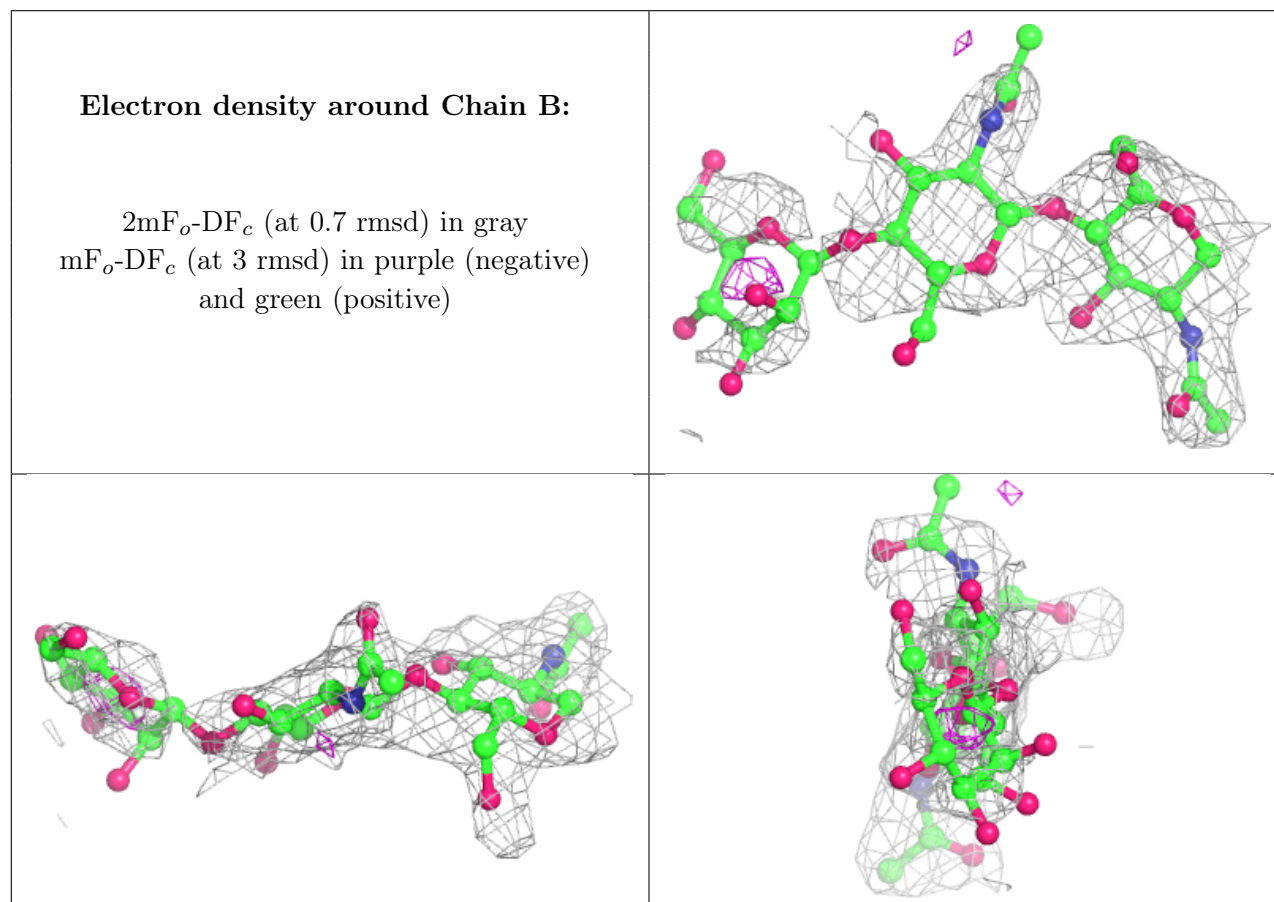
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	B	3	11/12	0.55	0.40	100,108,110,110	0
4	NAG	B	2	14/15	0.83	0.28	90,95,106,106	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	B	1	14/15	0.87	0.18	49,71,78,90	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.