



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 04:10 PM UTC

PDB ID : 9CPX / pdb_00009cpx
Title : Crystal structure of SARS-CoV-2 receptor binding domain in complex with antibodies C03-0138 and CC12.3
Authors : Feng, Z.; Wilson, I.A.
Deposited on : 2024-07-18
Resolution : 2.70 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

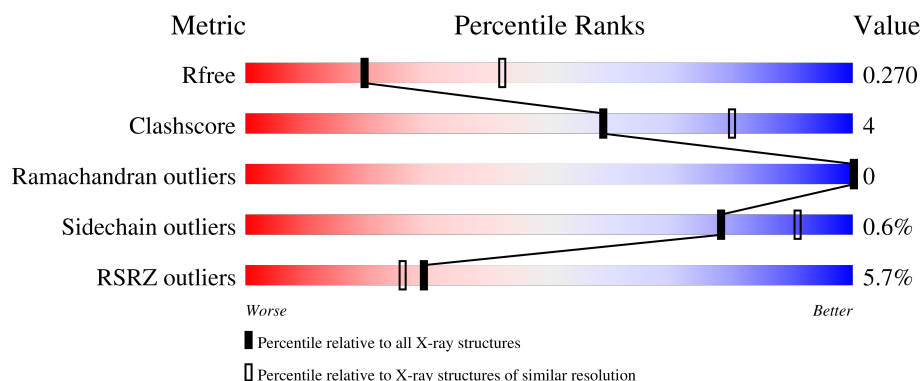
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

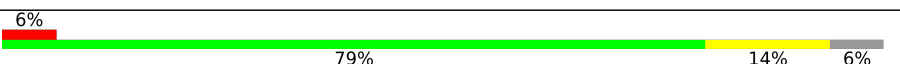
The reported resolution of this entry is 2.70 Å.

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.



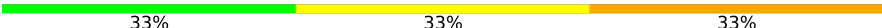
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	H	222	
2	L	220	
3	C	220	
4	D	214	
5	A	205	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
6	B	3	 33% 33% 33%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8124 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 C03-0138 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	220	Total	C	N	O	S	0	0	0
			1629	1036	264	320	9			

- Molecule 2 is a protein called C03-0138 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	217	Total	C	N	O	S	0	0	0
			1694	1068	279	342	5			

- Molecule 3 is a protein called CC12.3 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	212	Total	C	N	O	S	0	0	0
			1591	1010	262	313	6			

- Molecule 4 is a protein called CC12.3 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	211	Total	C	N	O	S	0	0	0
			1622	1014	277	327	4			

- Molecule 5 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	A	192	Total	C	N	O	S	0	0	0
			1529	983	254	284	8			

There are 7 discrepancies between the modelled and reference sequences:

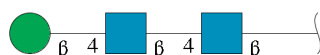
Chain	Residue	Modelled	Actual	Comment	Reference
A	531	GLY	-	expression tag	UNP P0DTC2
A	532	HIS	-	expression tag	UNP P0DTC2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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 6 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
6	B	3	Total	C	N	O	0	0	0
			39	22	2	15			

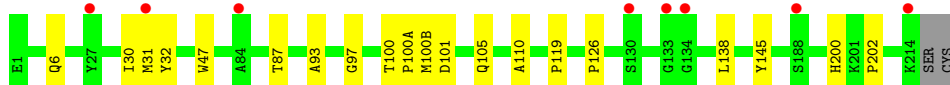
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	H	4	Total	O	0	0
			4	4		
7	L	1	Total	O	0	0
			1	1		
7	C	9	Total	O	0	0
			9	9		
7	D	1	Total	O	0	0
			1	1		
7	A	5	Total	O	0	0
			5	5		

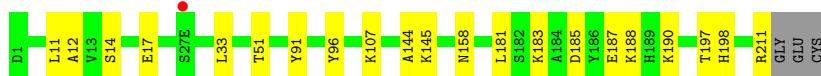
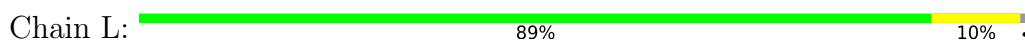
3 Residue-property plots [i](#)

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.

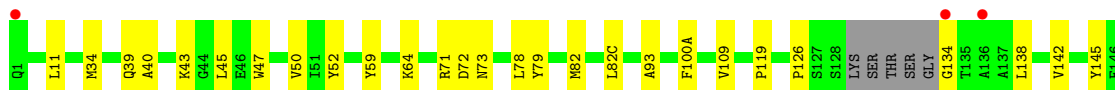
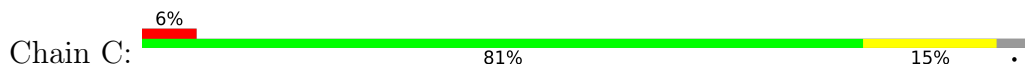
- Molecule 1: C03-0138 Fab heavy chain



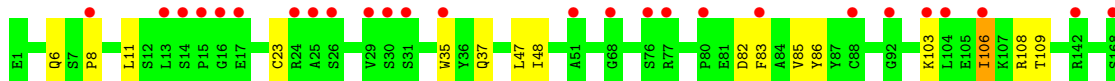
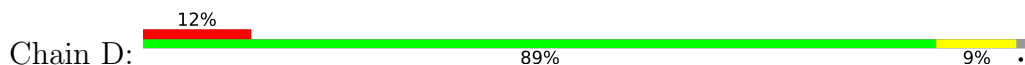
- Molecule 2: C03-0138 Fab light chain



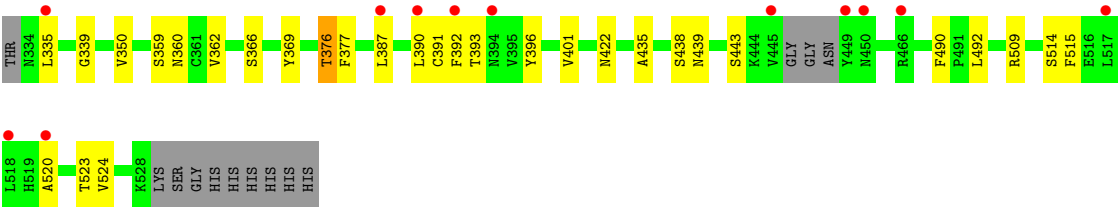
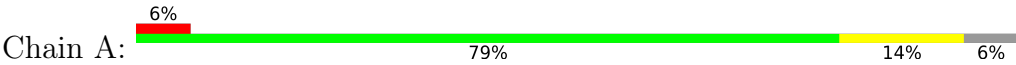
- Molecule 3: CC12.3 Fab heavy chain



- Molecule 4: CC12.3 Fab light chain



- Molecule 5: Spike protein S1



● Molecule 6: 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 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	110.17Å 110.17Å 226.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.54 – 2.70 49.54 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.1 (49.54-2.70) 99.4 (49.54-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 2.69Å)	Xtriage
Refinement program	PHENIX (1.21rc1_5127: ???)	Depositor
R, R_{free}	0.230 , 0.271 0.230 , 0.270	Depositor DCC
R_{free} test set	2000 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	39.0	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 30.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	8124	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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: NAG, BMA

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	H	0.12	0/1671	0.30	0/2275
2	L	0.10	0/1732	0.28	0/2354
3	C	0.11	0/1630	0.25	0/2220
4	D	0.10	0/1657	0.26	0/2249
5	A	0.11	0/1572	0.29	0/2138
All	All	0.11	0/8262	0.28	0/11236

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	H	1629	0	1610	16	0
2	L	1694	0	1654	13	0
3	C	1591	0	1547	17	0
4	D	1622	0	1583	11	0
5	A	1529	0	1452	19	0
6	B	39	0	34	1	0
7	A	5	0	0	0	0
7	C	9	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	1	0	0	0	0
7	H	4	0	0	0	0
7	L	1	0	0	0	0
All	All	8124	0	7880	71	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 (71) 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:D:8:PRO:HG3	4:D:11:LEU:HD13	1.62	0.82
1:H:31:MET:SD	1:H:31:MET:N	2.56	0.79
2:L:33:LEU:HB3	2:L:51:THR:HG22	1.72	0.72
1:H:126:PRO:HG3	1:H:138:LEU:HB3	1.74	0.69
3:C:126:PRO:HG3	3:C:138:LEU:HB3	1.75	0.69
3:C:134:GLY:N	3:C:186:SER:HG	1.93	0.67
5:A:360:ASN:H	5:A:523:THR:HG23	1.64	0.62
3:C:138:LEU:HD13	3:C:211:VAL:HG21	1.83	0.60
5:A:439:ASN:O	5:A:443:SER:OG	2.17	0.60
3:C:11:LEU:HB2	3:C:147:PRO:HG3	1.85	0.58
1:H:31:MET:HE3	5:A:377:PHE:CD2	2.40	0.56
5:A:490:PHE:CE1	5:A:492:LEU:HB2	2.41	0.56
3:C:93:ALA:HB1	3:C:100(A):PHE:HB3	1.89	0.54
3:C:52:TYR:O	3:C:71:ARG:NH2	2.34	0.54
5:A:359:SER:HA	5:A:524:VAL:HG22	1.91	0.53
4:D:85:VAL:HG22	4:D:103:LYS:HD2	1.90	0.53
5:A:376:THR:HG23	5:A:435:ALA:HB3	1.91	0.52
3:C:59:TYR:HB2	3:C:64:LYS:HG3	1.92	0.51
5:A:392:PHE:CE1	5:A:515:PHE:HB3	2.46	0.51
3:C:119:PRO:HB3	3:C:145:TYR:HB3	1.93	0.50
2:L:14:SER:HB2	2:L:17:GLU:HG3	1.93	0.50
1:H:100(A):PRO:HD3	2:L:91:TYR:CZ	2.46	0.50
4:D:201:LEU:HD13	4:D:205:VAL:HG23	1.95	0.49
4:D:47:LEU:C	4:D:48:ILE:HD12	2.38	0.49
3:C:40:ALA:HB3	3:C:43:LYS:HB2	1.95	0.49
2:L:158:ASN:HD22	2:L:181:LEU:HD21	1.79	0.47
2:L:190:LYS:NZ	2:L:211:ARG:O	2.44	0.47
1:H:31:MET:HE2	5:A:369:TYR:HA	1.96	0.46
3:C:142:VAL:HG11	3:C:150:VAL:HG11	1.97	0.46
4:D:6:GLN:NE2	4:D:86:TYR:O	2.47	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:47:LEU:O	4:D:48:ILE:HD12	2.15	0.46
1:H:87:THR:HG23	1:H:110:ALA:HA	1.97	0.46
1:H:97:GLY:O	1:H:100:THR:HB	2.15	0.46
2:L:185:ASP:HA	2:L:188:LYS:HE3	1.98	0.46
5:A:335:LEU:HD23	5:A:335:LEU:H	1.80	0.45
1:H:100(A):PRO:HD3	2:L:91:TYR:CE2	2.51	0.45
1:H:32:TYR:HE2	1:H:101:ASP:OD1	1.99	0.45
3:C:82:MET:HE1	3:C:109:VAL:HG21	1.97	0.45
2:L:144:ALA:HB2	2:L:198:HIS:HD2	1.81	0.45
3:C:72:ASP:HB2	3:C:79:TYR:HE2	1.82	0.45
5:A:401:VAL:HG22	5:A:509:ARG:HG3	1.99	0.44
2:L:183:LYS:O	2:L:187:GLU:HG2	2.18	0.44
3:C:200:HIS:CD2	3:C:202:PRO:HD2	2.52	0.44
3:C:47:TRP:HZ2	3:C:50:VAL:HG12	1.83	0.44
1:H:100(B):MET:HE3	1:H:100(B):MET:HB2	1.81	0.44
1:H:119:PRO:HB3	1:H:145:TYR:HB3	2.00	0.44
5:A:387:LEU:HD21	5:A:515:PHE:CZ	2.52	0.44
1:H:6:GLN:H	1:H:105:GLN:HE22	1.66	0.44
3:C:82:MET:HB3	3:C:82(C):LEU:HD21	1.99	0.43
5:A:339:GLY:HA2	6:B:1:NAG:H83	2.01	0.43
4:D:82:ASP:O	4:D:86:TYR:OH	2.34	0.43
2:L:14:SER:OG	2:L:107:LYS:HE3	2.18	0.43
1:H:200:HIS:CD2	1:H:202:PRO:HD2	2.54	0.43
5:A:335:LEU:HA	5:A:362:VAL:O	2.18	0.43
1:H:30:ILE:HG23	1:H:31:MET:SD	2.59	0.43
2:L:145:LYS:HB3	2:L:197:THR:HB	2.01	0.43
5:A:393:THR:HG21	5:A:520:ALA:HB3	2.01	0.43
4:D:23:CYS:HB2	4:D:35:TRP:CH2	2.54	0.42
3:C:39:GLN:HB2	3:C:45:LEU:HD23	2.00	0.42
4:D:108:ARG:HH21	4:D:109:THR:HG23	1.85	0.42
5:A:396:TYR:HB2	5:A:514:SER:HB3	2.00	0.42
3:C:34:MET:HB3	3:C:78:LEU:HD22	2.01	0.42
4:D:37:GLN:HB2	4:D:47:LEU:HD11	2.00	0.42
1:H:47:TRP:CG	2:L:96:TYR:HB2	2.54	0.42
1:H:93:ALA:HB1	1:H:100(B):MET:HB3	2.02	0.42
5:A:366:SER:HA	5:A:369:TYR:CE2	2.55	0.41
5:A:438:SER:CB	5:A:509:ARG:HD2	2.50	0.41
2:L:11:LEU:HD12	2:L:12:ALA:H	1.85	0.41
5:A:350:VAL:HG22	5:A:422:ASN:HB3	2.03	0.41
5:A:390:LEU:HD13	5:A:391:CYS:N	2.37	0.40
4:D:83:PHE:CE1	4:D:106:ILE:HB	2.56	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	H	218/222 (98%)	217 (100%)	1 (0%)	0	100	100
2	L	215/220 (98%)	212 (99%)	3 (1%)	0	100	100
3	C	208/220 (94%)	207 (100%)	1 (0%)	0	100	100
4	D	209/214 (98%)	203 (97%)	6 (3%)	0	100	100
5	A	188/205 (92%)	183 (97%)	5 (3%)	0	100	100
All	All	1038/1081 (96%)	1022 (98%)	16 (2%)	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	H	183/185 (99%)	183 (100%)	0	100	100
2	L	194/196 (99%)	194 (100%)	0	100	100
3	C	179/186 (96%)	178 (99%)	1 (1%)	78	91
4	D	183/185 (99%)	180 (98%)	3 (2%)	55	80
5	A	167/177 (94%)	166 (99%)	1 (1%)	78	91
All	All	906/929 (98%)	901 (99%)	5 (1%)	78	91

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

Mol	Chain	Res	Type
3	C	73	ASN
4	D	106	ILE
4	D	185	ASP
4	D	211	ARG
5	A	376	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	164	HIS
3	C	39	GLN
4	D	38	GLN
4	D	189	HIS
4	D	199	GLN
5	A	439	ASN
5	A	501	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	$\# Z > 2$
6	NAG	B	1	5,6	14,14,15	0.68	0	17,19,21	1.26	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	NAG	B	2	6	14,14,15	0.69	0	17,19,21	0.94	0
6	BMA	B	3	6	11,11,12	0.82	0	15,15,17	1.80	1 (6%)

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
6	NAG	B	1	5,6	-	2/6/23/26	0/1/1/1
6	NAG	B	2	6	-	0/6/23/26	0/1/1/1
6	BMA	B	3	6	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	3	BMA	C1-O5-C5	5.71	119.84	112.19
6	B	1	NAG	C2-N2-C7	2.77	126.61	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

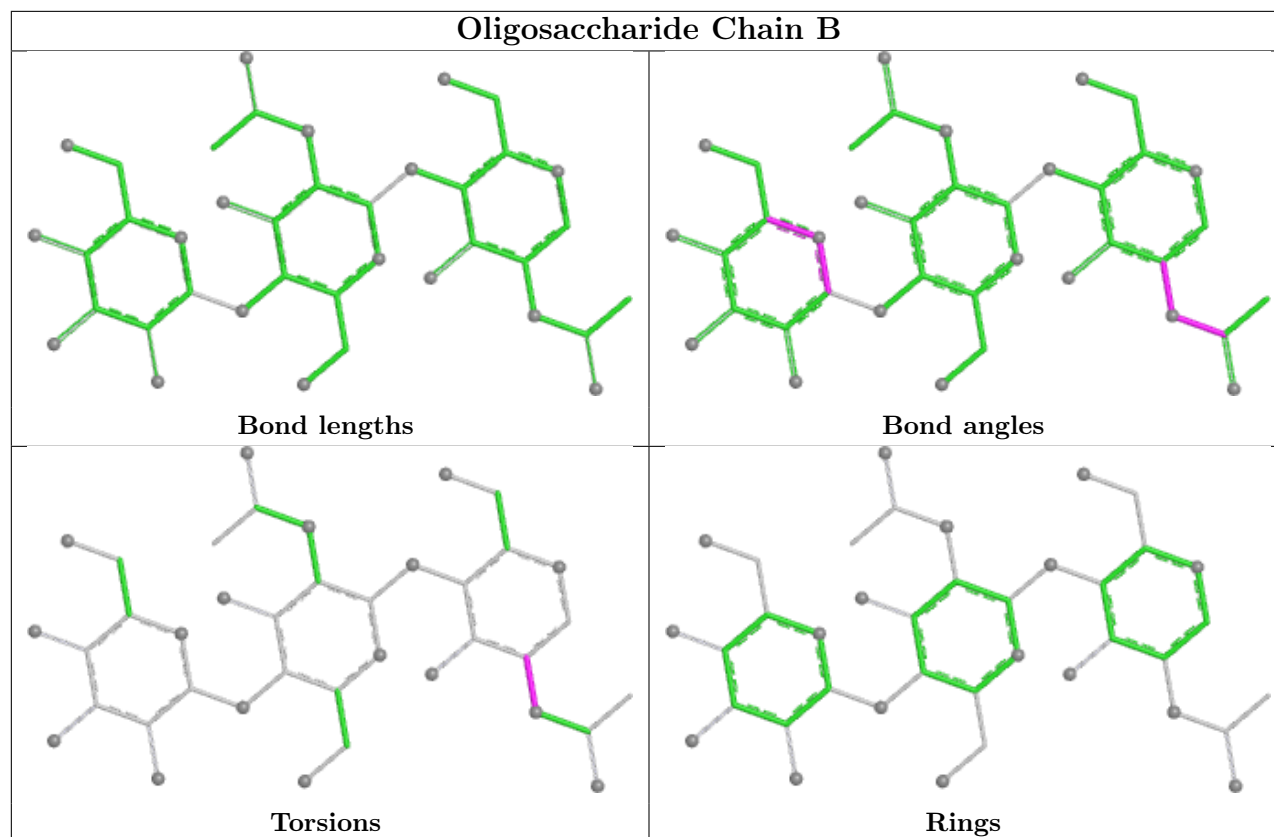
Mol	Chain	Res	Type	Atoms
6	B	1	NAG	C1-C2-N2-C7
6	B	1	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1	NAG	1	0

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	H	220/222 (99%)	0.28	8 (3%) 46 42	15, 34, 58, 76	0
2	L	217/220 (98%)	0.24	1 (0%) 87 86	17, 36, 52, 66	0
3	C	212/220 (96%)	0.35	13 (6%) 27 24	18, 34, 65, 83	0
4	D	211/214 (98%)	0.85	26 (12%) 8 7	24, 45, 68, 81	0
5	A	192/205 (93%)	0.45	12 (6%) 26 23	18, 34, 67, 79	0
All	All	1052/1081 (97%)	0.43	60 (5%) 29 26	15, 37, 64, 83	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	A	390	LEU	5.2
1	H	133	GLY	5.0
3	C	158	ALA	4.7
1	H	27	TYR	4.6
5	A	445	VAL	3.8
4	D	29	VAL	3.8
5	A	449	TYR	3.5
5	A	518	LEU	3.4
3	C	182	VAL	3.4
4	D	13	LEU	3.3
3	C	159	LEU	3.3
4	D	51	ALA	3.2
3	C	1	GLN	3.2
1	H	31	MET	3.1
1	H	214	LYS	2.8
4	D	83	PHE	2.8
5	A	450	ASN	2.8
3	C	163	VAL	2.7
4	D	92	GLY	2.7
4	D	80	PRO	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	130	SER	2.6
3	C	189	LEU	2.5
4	D	26	SER	2.5
3	C	213	PRO	2.5
5	A	394	ASN	2.5
2	L	27(E)	SER	2.5
4	D	104	LEU	2.5
4	D	106	ILE	2.4
4	D	35	TRP	2.4
5	A	335	LEU	2.4
4	D	30	SER	2.3
4	D	31	SER	2.3
1	H	188	SER	2.2
4	D	168	SER	2.2
4	D	25	ALA	2.2
4	D	88	CYS	2.2
4	D	142	ARG	2.2
3	C	157	GLY	2.2
3	C	154	TRP	2.2
3	C	136	ALA	2.2
5	A	387	LEU	2.2
5	A	392	PHE	2.2
4	D	8	PRO	2.1
4	D	15	PRO	2.1
4	D	16	GLY	2.1
4	D	14	SER	2.1
4	D	103	LYS	2.1
4	D	68	GLY	2.1
5	A	466	ARG	2.1
5	A	517	LEU	2.1
1	H	134	GLY	2.1
1	H	84	ALA	2.1
4	D	17	GLU	2.1
4	D	77	ARG	2.1
5	A	520	ALA	2.1
3	C	193	THR	2.1
3	C	134	GLY	2.1
3	C	161	SER	2.0
4	D	76	SER	2.0
4	D	24	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

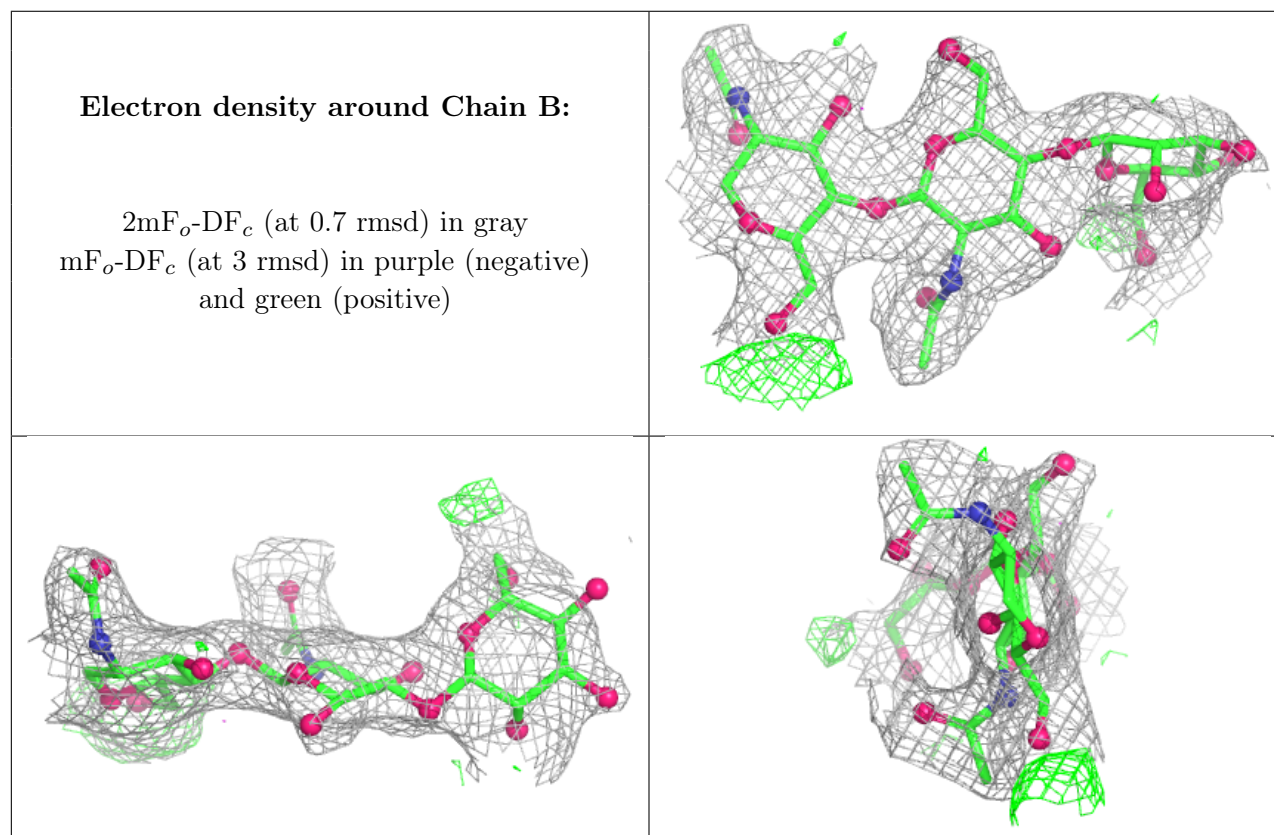
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
6	NAG	B	1	14/15	-	-	30,45,51,53	0
6	NAG	B	2	14/15	-	-	46,61,66,80	0
6	BMA	B	3	11/12	-	-	70,75,80,92	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.