



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2021 – 04:08 PM EDT

PDB ID : 7R8L  
Title : Structure of the SARS-CoV-2 RBD in complex with neutralizing antibody C099 and CR3022  
Authors : Barnes, C.O.; Bjorkman, P.J.  
Deposited on : 2021-06-26  
Resolution : 2.60 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](mailto: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.

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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 : 2.23.1  
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) : 2.23.1

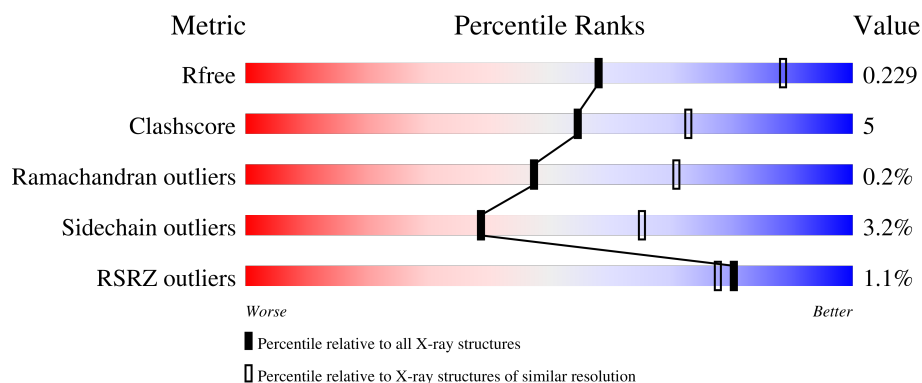
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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  $\geq 3$ , 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	218	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>10%</div> <div>..</div> </div> </div>
2	L	213	<div> <div>84%</div> <div>16%</div> </div>
3	E	195	<div> <div>86%</div> <div>13%</div> <div>..</div> </div>
4	C	222	<div> <div>%</div> <div>84%</div> <div>14%</div> <div>.</div> </div>
5	D	221	<div> <div>2%</div> <div>84%</div> <div>14%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
6	A	4	<div><div></div><div>50%</div><div></div><div>50%</div></div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8251 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 C099 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	214	Total	C	N	O	S	0	0	0
			1579	992	266	313	8			

- Molecule 2 is a protein called C099 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	0	0
			1623	1017	276	326	4			

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	194	Total	C	N	O	S	0	0	0
			1535	985	255	287	8			

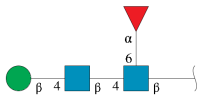
- Molecule 4 is a protein called CR3022 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	222	Total	C	N	O	S	0	0	0
			1647	1043	268	327	9			

- Molecule 5 is a protein called CR3022 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	D	221	Total	C	N	O	S	0	0	0
			1715	1076	284	350	5			

- Molecule 6 is an oligosaccharide called beta-D-mannopyranose-(1-4)-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
6	A	4	Total	C	N	O	0	0	0
			49	28	2	19			

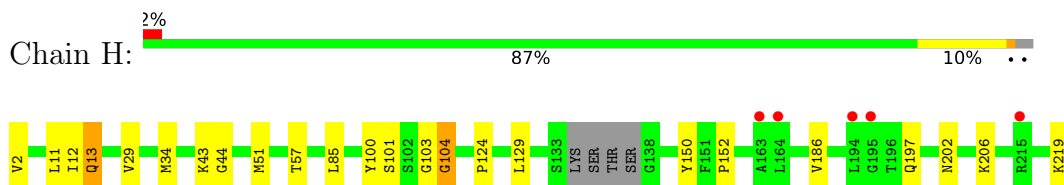
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	H	20	Total	O	0	0
			20	20		
7	L	19	Total	O	0	0
			19	19		
7	E	27	Total	O	0	0
			27	27		
7	C	18	Total	O	0	0
			18	18		
7	D	19	Total	O	0	0
			19	19		

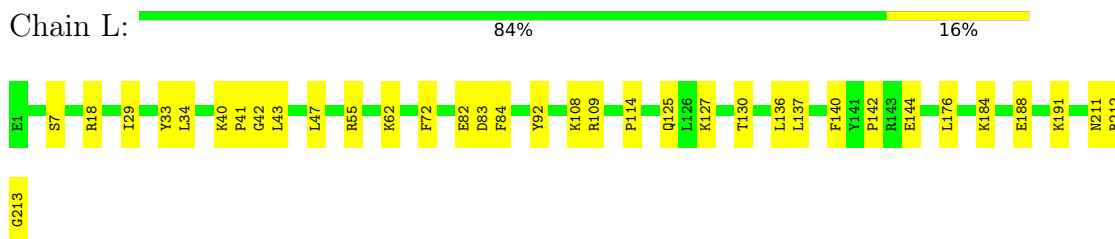
### 3 Residue-property plots

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.

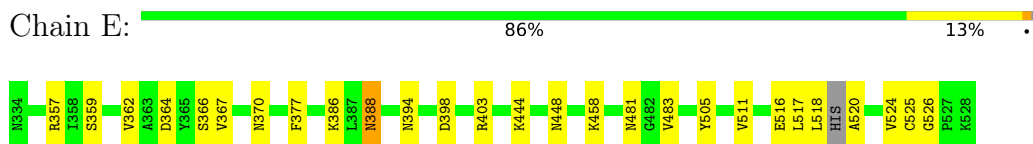
- Molecule 1: C099 Fab Heavy Chain



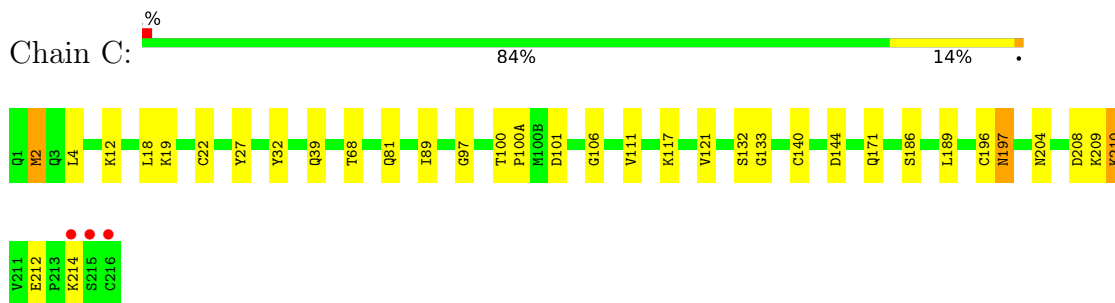
- Molecule 2: C099 Fab Light Chain



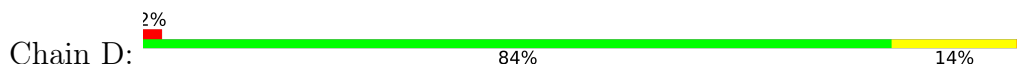
- Molecule 3: Spike protein S1

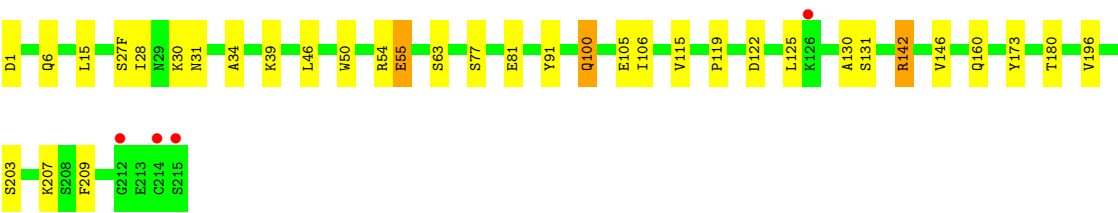


- Molecule 4: CR3022 Fab heavy chain



- Molecule 5: CR3022 Fab light chain





● Molecule 6: beta-D-mannopyranose-(1-4)-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 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.95Å 109.95Å 228.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.62 – 2.60 39.62 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.62-2.60) 100.0 (39.62-2.60)	Depositor EDS
$R_{merge}$	0.26	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.32 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, $R_{free}$	0.180 , 0.229 0.180 , 0.229	Depositor DCC
$R_{free}$ test set	2214 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.2	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 40.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8251	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, FUC, 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	H	0.45	0/1613	0.68	0/2194
2	L	0.46	0/1658	0.66	0/2249
3	E	0.47	0/1577	0.64	0/2144
4	C	0.45	0/1689	0.62	0/2299
5	D	0.48	0/1753	0.66	0/2383
All	All	0.46	0/8290	0.65	0/11269

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	H	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	104	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	H	1579	0	1549	14	0
2	L	1623	0	1588	20	0
3	E	1535	0	1457	18	0
4	C	1647	0	1623	20	0
5	D	1715	0	1659	21	0
6	A	49	0	43	0	0
7	C	18	0	0	1	0
7	D	19	0	0	2	0
7	E	27	0	0	1	0
7	H	20	0	0	3	0
7	L	19	0	0	1	0
All	All	8251	0	7919	84	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 5.

All (84) 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:C:121:VAL:O	4:C:209:LYS:NZ	2.12	0.81
2:L:144:GLU:N	2:L:144:GLU:OE2	2.18	0.75
3:E:518:LEU:O	3:E:520:ALA:N	2.22	0.72
5:D:6:GLN:H	5:D:100:GLN:HE21	1.42	0.67
5:D:54:ARG:NE	7:D:301:HOH:O	2.16	0.66
3:E:444:LYS:HG3	3:E:448:ASN:HB2	1.77	0.65
4:C:19:LYS:NZ	7:C:301:HOH:O	2.24	0.65
1:H:29:VAL:HG13	1:H:34:MET:HG3	1.78	0.65
2:L:184:LYS:O	2:L:188:GLU:HG2	1.98	0.64
3:E:357:ARG:NH1	7:E:601:HOH:O	2.29	0.62
1:H:2:VAL:N	7:H:302:HOH:O	2.34	0.61
5:D:142:ARG:NH2	7:D:302:HOH:O	2.35	0.60
1:H:186:VAL:HG11	2:L:136:LEU:HD22	1.84	0.60
2:L:108:LYS:HG2	2:L:109:ARG:H	1.67	0.59
3:E:364:ASP:OD2	3:E:366:SER:HB3	2.02	0.58
2:L:55:ARG:HD2	7:L:302:HOH:O	2.02	0.58
2:L:142:PRO:HB2	2:L:144:GLU:OE2	2.04	0.57
4:C:89:ILE:HD11	4:C:106:GLY:HA3	1.86	0.56
3:E:362:VAL:HA	3:E:525:CYS:O	2.05	0.56
3:E:394:ASN:HB2	3:E:516:GLU:OE1	2.06	0.56
1:H:43:LYS:N	7:H:301:HOH:O	2.29	0.55
3:E:370:ASN:HB3	4:C:27:TYR:HB3	1.88	0.55
5:D:115:VAL:HG12	5:D:207:LYS:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:388:ASN:HA	3:E:526:GLY:HA3	1.90	0.54
2:L:62:LYS:NZ	2:L:83:ASP:OD2	2.33	0.53
1:H:100:TYR:CD1	2:L:92:TYR:HB2	2.44	0.53
1:H:11:LEU:HB2	1:H:152:PRO:HG3	1.92	0.52
5:D:6:GLN:O	5:D:100:GLN:NE2	2.43	0.51
4:C:12:LYS:HE3	4:C:18:LEU:HD13	1.93	0.51
5:D:39:LYS:HE2	5:D:81:GLU:O	2.11	0.51
5:D:46:LEU:HD23	5:D:55:GLU:HG3	1.92	0.50
4:C:186:SER:O	4:C:189:LEU:HB2	2.13	0.49
3:E:359:SER:HB3	3:E:394:ASN:ND2	2.28	0.49
4:C:68:THR:HB	4:C:81:GLN:HG2	1.94	0.48
4:C:2:MET:HG2	4:C:32:TYR:CE2	2.47	0.48
4:C:210:LYS:HD2	4:C:212:GLU:OE2	2.14	0.48
3:E:481:ASN:O	3:E:483:VAL:HG23	2.13	0.47
3:E:370:ASN:CB	4:C:27:TYR:HB3	2.44	0.47
1:H:124:PRO:HB3	1:H:150:TYR:HB3	1.96	0.47
2:L:40:LYS:NZ	2:L:82:GLU:HG3	2.29	0.46
4:C:4:LEU:HD22	4:C:22:CYS:SG	2.55	0.46
5:D:146:VAL:HG22	5:D:196:VAL:HG22	1.97	0.46
3:E:359:SER:HA	3:E:524:VAL:HG22	1.97	0.46
2:L:33:TYR:HA	2:L:92:TYR:CE1	2.50	0.46
1:H:12:ILE:HG21	1:H:85:LEU:HD13	1.98	0.46
5:D:131:SER:OG	5:D:180:THR:HG22	2.16	0.46
2:L:42:GLY:O	2:L:43:LEU:HD23	2.16	0.46
2:L:125:GLN:HG2	2:L:130:THR:O	2.16	0.45
2:L:191:LYS:HD2	2:L:191:LYS:HA	1.69	0.45
5:D:30:LYS:HA	5:D:30:LYS:HD3	1.45	0.45
1:H:104:GLY:HA3	2:L:47:LEU:HD13	1.98	0.45
4:C:12:LYS:O	4:C:111:VAL:HA	2.17	0.44
4:C:197:ASN:ND2	4:C:208:ASP:OD1	2.44	0.44
1:H:44:GLY:N	7:H:301:HOH:O	2.29	0.44
5:D:6:GLN:N	5:D:100:GLN:HE21	2.12	0.44
1:H:100:TYR:O	1:H:103:GLY:O	2.36	0.44
4:C:117:LYS:HE2	4:C:144:ASP:O	2.18	0.43
3:E:388:ASN:N	3:E:388:ASN:OD1	2.51	0.43
2:L:34:LEU:HD13	2:L:72:PHE:CD2	2.54	0.43
2:L:29:ILE:HG22	3:E:505:TYR:CE1	2.53	0.43
2:L:211:ASN:O	2:L:213:GLY:N	2.52	0.43
5:D:125:LEU:HA	5:D:125:LEU:HD23	1.85	0.43
3:E:364:ASP:O	3:E:367:VAL:HG12	2.18	0.43
3:E:517:LEU:HD21	5:D:28:ILE:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:214:LYS:HA	4:C:214:LYS:HD2	1.74	0.43
4:C:97:GLY:O	4:C:100:THR:HB	2.19	0.42
3:E:386:LYS:NZ	4:C:101:ASP:OD1	2.48	0.42
5:D:15:LEU:HD23	5:D:15:LEU:HA	1.84	0.42
5:D:119:PRO:HB3	5:D:209:PHE:CZ	2.54	0.42
1:H:12:ILE:HD12	1:H:13:GLN:H	1.83	0.42
1:H:129:LEU:HD23	1:H:129:LEU:HA	1.89	0.42
5:D:31:ASN:O	5:D:50:TRP:HA	2.20	0.42
5:D:106:ILE:HD13	5:D:106:ILE:HA	1.85	0.42
4:C:39:GLN:HB3	4:C:89:ILE:HG23	2.02	0.42
2:L:114:PRO:HB3	2:L:140:PHE:CD2	2.55	0.41
1:H:51:MET:HG3	1:H:57:THR:HG22	2.01	0.41
2:L:137:LEU:HD22	2:L:176:LEU:HD22	2.03	0.41
3:E:398:ASP:O	3:E:511:VAL:HA	2.20	0.41
4:C:100:THR:HG23	4:C:100(A):PRO:HD2	2.03	0.41
5:D:125:LEU:HD21	5:D:130:ALA:HB2	2.03	0.41
5:D:105:GLU:OE1	5:D:173:TYR:OH	2.22	0.40
2:L:41:PRO:HG3	2:L:84:PHE:HE2	1.87	0.40
4:C:171:GLN:HA	5:D:160:GLN:HE22	1.86	0.40
5:D:34:ALA:HB2	5:D:91:TYR:HE1	1.86	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	210/218 (96%)	203 (97%)	7 (3%)	0	100	100
2	L	211/213 (99%)	206 (98%)	4 (2%)	1 (0%)	29	52
3	E	190/195 (97%)	182 (96%)	8 (4%)	0	100	100
4	C	220/222 (99%)	213 (97%)	6 (3%)	1 (0%)	29	52

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	D	219/221 (99%)	208 (95%)	11 (5%)	0	100	100
All	All	1050/1069 (98%)	1012 (96%)	36 (3%)	2 (0%)	47	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	133	GLY
2	L	212	ARG

### 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	H	177/181 (98%)	171 (97%)	6 (3%)	37	63
2	L	181/181 (100%)	178 (98%)	3 (2%)	60	81
3	E	167/168 (99%)	163 (98%)	4 (2%)	49	74
4	C	187/187 (100%)	180 (96%)	7 (4%)	34	60
5	D	196/196 (100%)	187 (95%)	9 (5%)	27	51
All	All	908/913 (100%)	879 (97%)	29 (3%)	39	65

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	13	GLN
1	H	101	SER
1	H	197	GLN
1	H	202	ASN
1	H	206	LYS
1	H	219	LYS
2	L	7	SER
2	L	18	ARG
2	L	127	LYS
3	E	377	PHE

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Mol	Chain	Res	Type
3	E	388	ASN
3	E	403	ARG
3	E	458	LYS
4	C	2	MET
4	C	132	SER
4	C	140	CYS
4	C	196	CYS
4	C	197	ASN
4	C	204	ASN
4	C	210	LYS
5	D	1	ASP
5	D	27(F)	SER
5	D	55	GLU
5	D	63	SER
5	D	77	SER
5	D	100	GLN
5	D	122	ASP
5	D	142	ARG
5	D	203	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
3	E	394	ASN
4	C	199	ASN
4	C	204	ASN
5	D	100	GLN

### 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](#)

4 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	A	1	6,3	14,14,15	0.52	0	17,19,21	0.62	0
6	NAG	A	2	6	14,14,15	0.28	0	17,19,21	0.75	1 (5%)
6	BMA	A	3	6	11,11,12	1.15	2 (18%)	15,15,17	0.85	0
6	FUC	A	4	6	10,10,11	1.04	0	14,14,16	0.75	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
6	NAG	A	1	6,3	-	0/6/23/26	0/1/1/1
6	NAG	A	2	6	-	1/6/23/26	0/1/1/1
6	BMA	A	3	6	-	0/2/19/22	0/1/1/1
6	FUC	A	4	6	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	3	BMA	C4-C5	2.29	1.57	1.53
6	A	3	BMA	C1-C2	2.21	1.57	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	2	NAG	C1-O5-C5	2.67	115.81	112.19

There are no chirality outliers.

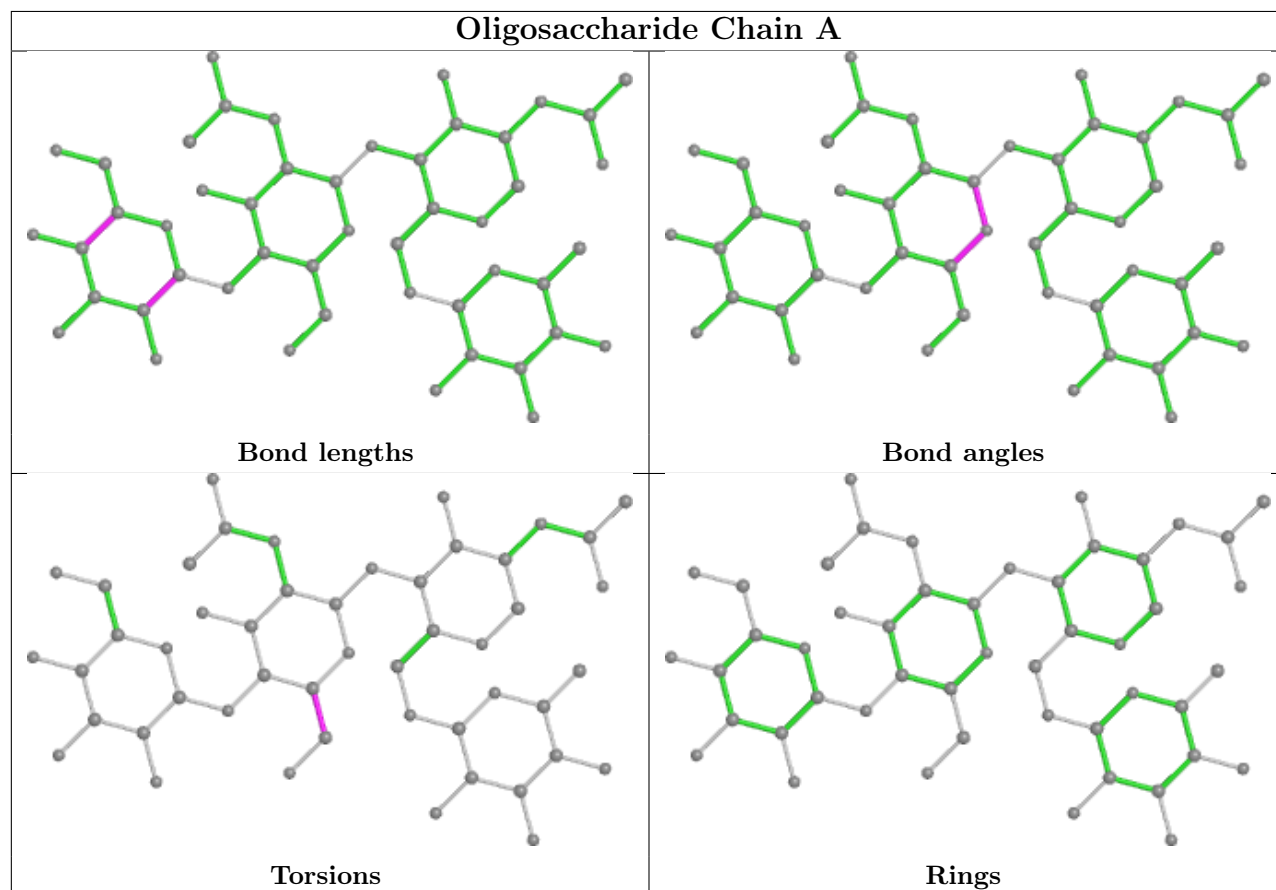
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	H	214/218 (98%)	-0.16	5 (2%) 60 54	42, 59, 104, 113	0
2	L	213/213 (100%)	-0.37	0 100 100	43, 56, 74, 98	0
3	E	194/195 (99%)	-0.26	0 100 100	41, 53, 91, 127	0
4	C	222/222 (100%)	-0.21	3 (1%) 75 71	45, 59, 85, 180	0
5	D	221/221 (100%)	-0.31	4 (1%) 68 64	43, 56, 79, 131	0
All	All	1064/1069 (99%)	-0.26	12 (1%) 80 78	41, 57, 86, 180	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	C	216	CYS	9.2
5	D	215	SER	7.8
4	C	215	SER	6.7
5	D	214	CYS	5.0
5	D	212	GLY	3.4
4	C	214	LYS	2.8
1	H	215	ARG	2.8
1	H	164	LEU	2.6
1	H	194	LEU	2.3
1	H	195	GLY	2.2
5	D	126	LYS	2.2
1	H	163	ALA	2.1

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

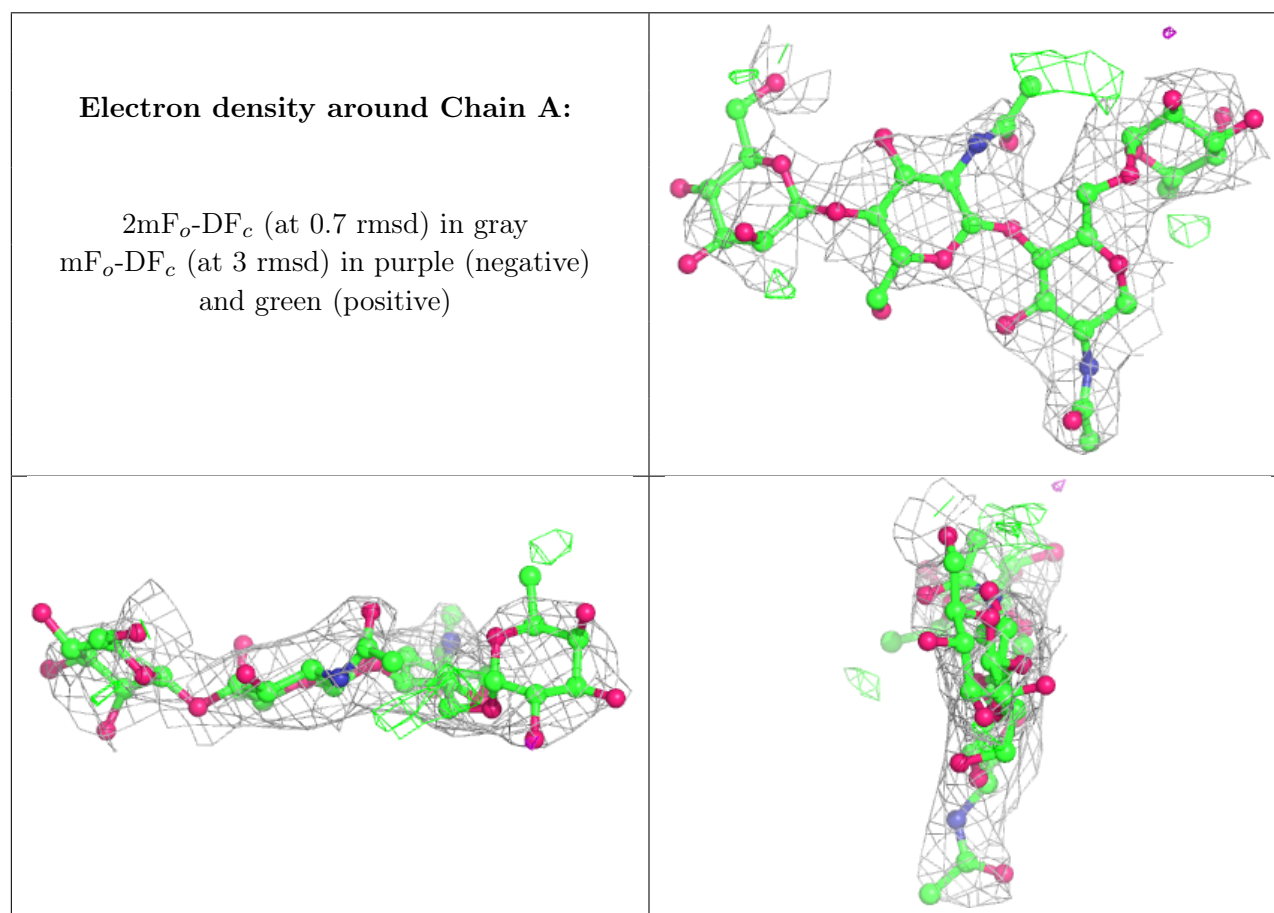
There are no non-standard protein/DNA/RNA residues in this entry.

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	BMA	A	3	11/12	0.52	0.34	130,142,149,150	0
6	NAG	A	2	14/15	0.90	0.23	99,107,120,130	0
6	FUC	A	4	10/11	0.91	0.16	100,108,109,111	0
6	NAG	A	1	14/15	0.95	0.12	71,85,95,96	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.