



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:52 AM UTC

PDB ID : 6BHQ / pdb_00006bhq
Title : Mouse Immunoglobulin G 2c Fc fragment with complex-type glycan
Authors : Falconer, D.; Barb, A.
Deposited on : 2017-10-31
Resolution : 2.05 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

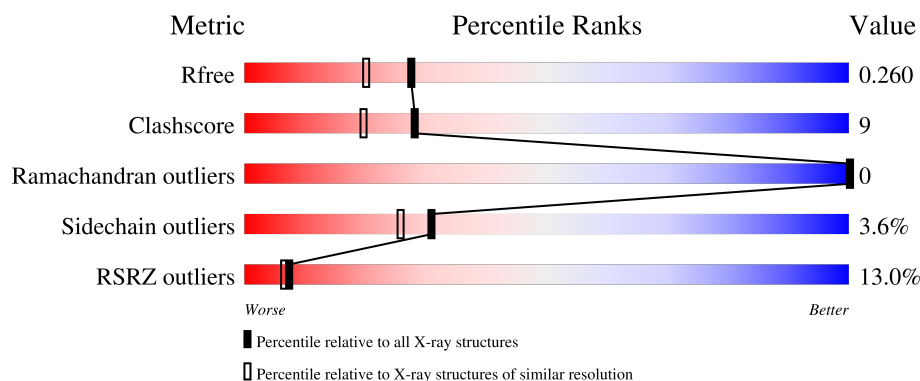
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	224	5% 79% 13% • 7%
1	B	224	19% 71% 15% • 11%
2	C	8	100%
2	D	8	100%

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
3	GOL	A	509	-	-	X	-

2 Entry composition [i](#)

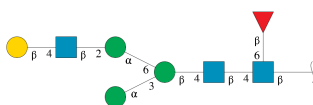
There are 4 unique types of molecules in this entry. The entry contains 3551 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Igh protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1618	1028	270	310	10			
1	B	199	Total	C	N	O	S	0	0	0
			1542	986	255	291	10			

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	0	0	0
			96	54	3	39			
2	D	8	Total	C	N	O	0	0	0
			96	54	3	39			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

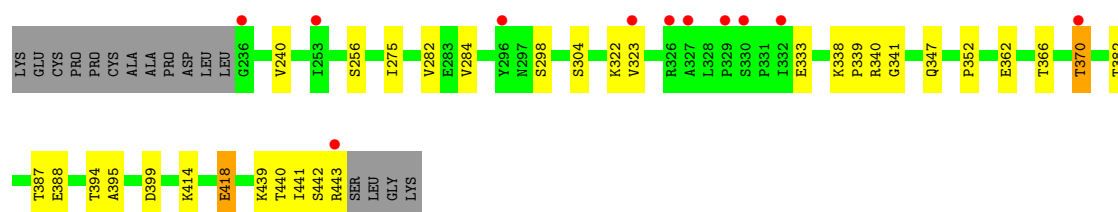
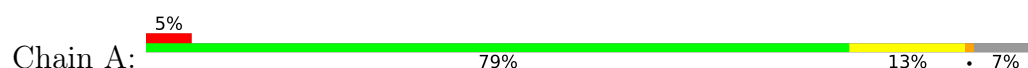
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	100	Total	O	0	0
			100	100		
4	B	93	Total	O	0	0
			93	93		

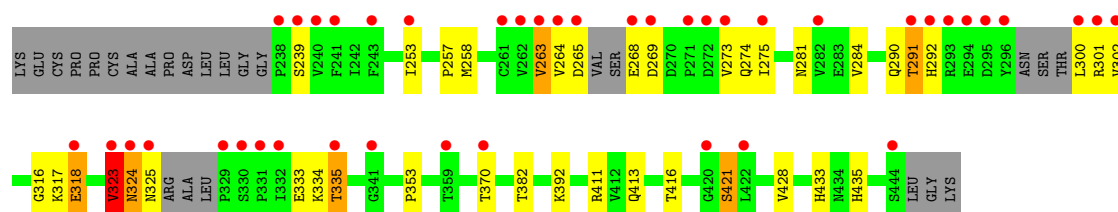
3 Residue-property plots

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: Igh protein



• Molecule 1: Igh protein



• Molecule 2: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 2: beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[beta-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



MAG1
MAG2
BMA3
MAN4
NAG5
GAL6
MAN7
FUL8

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.73Å 73.40Å 118.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.08 – 2.05 46.08 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.0 (46.08-2.05) 98.9 (46.08-2.05)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.05Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.237 , 0.258 0.239 , 0.260	Depositor DCC
R_{free} test set	4487 reflections (8.94%)	wwPDB-VP
Wilson B-factor (Å ²)	40.6	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.9	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	0.94	EDS
Total number of atoms	3551	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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, MAN, FUL, BMA, GAL, GOL

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	1.29	3/1659 (0.2%)	1.20	7/2264 (0.3%)
1	B	1.38	5/1580 (0.3%)	1.28	11/2152 (0.5%)
All	All	1.34	8/3239 (0.2%)	1.24	18/4416 (0.4%)

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	B	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	317	LYS	C-N	16.39	1.55	1.33
1	B	318	GLU	C-N	-9.43	1.21	1.33
1	A	395	ALA	C-O	6.14	1.32	1.23
1	B	370	THR	CA-C	5.92	1.59	1.52
1	B	284	VAL	CA-C	5.66	1.59	1.52
1	B	392	LYS	CA-C	5.40	1.59	1.52
1	A	284	VAL	CA-C	5.30	1.58	1.52
1	A	366	THR	N-CA	-5.21	1.39	1.46

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	317	LYS	CA-C-N	-9.88	105.53	122.92
1	B	317	LYS	C-N-CA	-9.88	105.53	122.92
1	A	418	GLU	N-CA-C	6.70	118.58	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	370	THR	N-CA-CB	-6.23	99.95	111.53
1	B	323	VAL	N-CA-C	6.08	117.34	108.53
1	A	256	SER	CA-C-N	-5.66	114.14	120.14
1	A	256	SER	C-N-CA	-5.66	114.14	120.14
1	B	318	GLU	CA-C-N	-5.51	115.40	123.00
1	B	318	GLU	C-N-CA	-5.51	115.40	123.00
1	B	324	ASN	N-CA-C	5.41	118.27	109.24
1	A	352	PRO	CA-C-N	-5.23	115.84	119.66
1	A	352	PRO	C-N-CA	-5.23	115.84	119.66
1	B	291	THR	N-CA-C	5.23	118.59	110.17
1	A	394	THR	N-CA-C	-5.22	103.50	110.55
1	B	316	GLY	N-CA-C	5.20	123.01	115.32
1	A	298	SER	N-CA-C	5.07	118.43	111.54
1	B	353	PRO	CA-C-N	-5.01	114.49	120.11
1	B	353	PRO	C-N-CA	-5.01	114.49	120.11

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	318	GLU	Mainchain

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	1618	0	1576	19	0
1	B	1542	0	1491	41	0
2	C	96	0	82	0	0
2	D	96	0	82	0	0
3	A	6	0	8	6	0
4	A	100	0	0	2	0
4	B	93	0	0	6	0
All	All	3551	0	3239	59	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 9.

All (59) 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:B:273:VAL:HG12	1:B:325:ASN:CB	1.41	1.47
1:B:273:VAL:CG1	1:B:325:ASN:HB2	1.50	1.41
1:B:273:VAL:CG1	1:B:325:ASN:CB	2.02	1.37
1:B:273:VAL:HG12	1:B:325:ASN:HB3	1.11	1.08
1:B:273:VAL:HA	1:B:324:ASN:O	1.56	1.04
1:B:273:VAL:HG13	1:B:325:ASN:HB2	1.36	1.03
1:B:416:THR:HG21	4:B:601:HOH:O	1.70	0.91
1:B:273:VAL:HG12	1:B:325:ASN:HB2	1.18	0.88
1:B:273:VAL:HG13	1:B:325:ASN:CB	1.93	0.86
1:B:273:VAL:CA	1:B:324:ASN:O	2.29	0.80
1:A:275:ILE:HG12	1:A:323:VAL:HG12	1.63	0.78
1:B:273:VAL:CG1	1:B:325:ASN:HB3	1.90	0.74
1:B:273:VAL:HG13	1:B:325:ASN:ND2	2.05	0.72
1:A:341:GLY:N	3:A:509:GOL:O3	2.24	0.70
1:A:442:SER:O	1:A:443:ARG:HB3	1.93	0.69
1:B:273:VAL:HG13	1:B:325:ASN:CG	2.20	0.67
1:A:399:ASP:CG	1:B:411:ARG:HH22	2.04	0.66
1:B:433:HIS:HD2	4:B:675:HOH:O	1.81	0.64
1:A:338:LYS:NZ	3:A:509:GOL:O1	2.25	0.62
1:A:339:PRO:O	3:A:509:GOL:H11	2.01	0.61
1:B:273:VAL:CG1	1:B:325:ASN:CG	2.73	0.60
1:A:347:GLN:HB3	1:A:370:THR:HG22	1.84	0.58
1:B:416:THR:CG2	4:B:601:HOH:O	2.40	0.58
1:B:290:GLN:NE2	1:B:292:HIS:CE1	2.73	0.57
1:B:273:VAL:HG13	1:B:325:ASN:HD22	1.67	0.57
1:B:413:GLN:O	1:B:416:THR:HG22	2.06	0.56
1:A:340:ARG:HA	3:A:509:GOL:H31	1.88	0.56
1:B:333:GLU:O	1:B:334:LYS:HD3	2.05	0.55
1:B:268:GLU:O	1:B:269:ASP:C	2.51	0.52
1:B:273:VAL:HG21	1:B:302:VAL:HG21	1.91	0.52
1:B:257:PRO:O	1:B:258:MET:HG2	2.11	0.50
1:B:416:THR:O	1:B:421:SER:OG	2.25	0.50
1:B:335:THR:HG23	4:B:677:HOH:O	2.12	0.50
1:A:399:ASP:OD1	1:B:411:ARG:NH2	2.42	0.49
1:B:263:VAL:O	1:B:301:ARG:HA	2.12	0.49
1:A:322:LYS:HG3	1:A:333:GLU:HG2	1.94	0.49
1:B:263:VAL:HG21	1:B:323:VAL:HG21	1.94	0.49
1:B:275:ILE:CD1	1:B:323:VAL:HG23	2.43	0.48
1:B:239:SER:O	1:B:264:VAL:HG22	2.13	0.48
1:A:340:ARG:HA	3:A:509:GOL:C3	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:LYS:NZ	4:A:604:HOH:O	2.46	0.47
1:B:433:HIS:CD2	4:B:675:HOH:O	2.63	0.47
1:B:292:HIS:HB2	1:B:301:ARG:O	2.15	0.47
1:A:382:THR:HG22	1:A:387:THR:HA	1.97	0.46
1:B:274:GLN:N	1:B:324:ASN:O	2.48	0.46
3:A:509:GOL:H12	4:A:674:HOH:O	2.16	0.45
1:A:240:VAL:HG21	1:A:323:VAL:HG21	1.99	0.45
1:A:275:ILE:HD12	1:A:304:SER:HB2	1.99	0.44
1:A:414:LYS:HE2	1:A:418:GLU:OE2	2.18	0.43
1:A:275:ILE:HG23	1:A:323:VAL:HG12	2.00	0.43
1:B:290:GLN:O	1:B:290:GLN:HG3	2.19	0.43
1:A:441:ILE:HG12	1:A:442:SER:N	2.34	0.43
1:B:273:VAL:CA	1:B:325:ASN:HB2	2.48	0.42
1:B:428:VAL:HA	1:B:435:HIS:O	2.20	0.42
1:B:273:VAL:HA	1:B:325:ASN:HB2	2.01	0.41
1:B:274:GLN:O	1:B:324:ASN:N	2.49	0.41
1:B:290:GLN:HE21	1:B:292:HIS:CE1	2.37	0.41
1:A:440:THR:HG22	1:A:441:ILE:N	2.35	0.41
1:B:382:THR:HG21	4:B:602:HOH:O	2.21	0.40

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	206/224 (92%)	204 (99%)	2 (1%)	0	100	100
1	B	191/224 (85%)	186 (97%)	5 (3%)	0	100	100
All	All	397/448 (89%)	390 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	185/203 (91%)	181 (98%)	4 (2%)	45	44
1	B	174/203 (86%)	165 (95%)	9 (5%)	21	14
All	All	359/406 (88%)	346 (96%)	13 (4%)	31	26

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	282	VAL
1	A	362	GLU
1	A	370	THR
1	A	388	GLU
1	B	253	ILE
1	B	263	VAL
1	B	265	ASP
1	B	281	ASN
1	B	291	THR
1	B	300	LEU
1	B	323	VAL
1	B	335	THR
1	B	421	SER

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

Mol	Chain	Res	Type
1	A	285	HIS
1	A	290	GLN
1	A	390	ASN
1	B	288	GLN
1	B	290	GLN
1	B	347	GLN
1	B	434	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 ⓘ

16 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$
2	NAG	C	1	1,2	14,14,15	0.87	0	17,19,21	2.08	3 (17%)
2	NAG	C	2	2	14,14,15	0.71	0	17,19,21	1.92	4 (23%)
2	BMA	C	3	2	11,11,12	0.40	0	15,15,17	1.33	1 (6%)
2	MAN	C	4	2	11,11,12	0.33	0	15,15,17	2.13	3 (20%)
2	NAG	C	5	2	14,14,15	0.86	1 (7%)	17,19,21	1.28	2 (11%)
2	GAL	C	6	2	11,11,12	1.35	2 (18%)	15,15,17	1.47	3 (20%)
2	MAN	C	7	2	11,11,12	0.79	0	15,15,17	1.15	2 (13%)
2	FUL	C	8	2	10,10,11	0.99	1 (10%)	14,14,16	1.91	5 (35%)
2	NAG	D	1	2	14,14,15	0.68	0	17,19,21	1.53	4 (23%)
2	NAG	D	2	2	14,14,15	0.41	0	17,19,21	1.67	3 (17%)
2	BMA	D	3	2	11,11,12	0.64	0	15,15,17	2.22	8 (53%)
2	MAN	D	4	2	11,11,12	0.58	0	15,15,17	1.50	2 (13%)
2	NAG	D	5	2	14,14,15	0.68	0	17,19,21	1.73	2 (11%)
2	GAL	D	6	2	11,11,12	1.18	1 (9%)	15,15,17	2.14	5 (33%)
2	MAN	D	7	2	11,11,12	1.09	1 (9%)	15,15,17	2.37	4 (26%)
2	FUL	D	8	2	10,10,11	0.58	0	14,14,16	1.65	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
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	1/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	NAG	C	5	2	-	0/6/23/26	0/1/1/1
2	GAL	C	6	2	-	1/2/19/22	0/1/1/1
2	MAN	C	7	2	-	2/2/19/22	0/1/1/1
2	FUL	C	8	2	-	-	0/1/1/1
2	NAG	D	1	2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	1/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1
2	NAG	D	5	2	-	2/6/23/26	0/1/1/1
2	GAL	D	6	2	-	0/2/19/22	0/1/1/1
2	MAN	D	7	2	-	0/2/19/22	0/1/1/1
2	FUL	D	8	2	-	-	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	6	GAL	O2-C2	2.80	1.49	1.43
2	C	8	FUL	C2-C3	-2.51	1.48	1.52
2	D	7	MAN	C2-C3	2.42	1.56	1.52
2	C	5	NAG	C2-N2	2.37	1.50	1.46
2	D	6	GAL	C1-C2	2.14	1.57	1.52
2	C	6	GAL	C2-C3	2.09	1.55	1.52

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C1-O5-C5	5.88	120.06	112.19
2	D	5	NAG	C1-O5-C5	5.22	119.18	112.19
2	C	1	NAG	C1-O5-C5	4.91	118.76	112.19
2	C	4	MAN	C1-O5-C5	4.82	118.65	112.19
2	D	7	MAN	C1-O5-C5	4.68	118.46	112.19
2	C	1	NAG	C1-C2-N2	-4.65	103.11	110.43
2	D	7	MAN	C2-C3-C4	4.43	118.65	110.86
2	D	6	GAL	O3-C3-C2	-4.36	101.16	110.05
2	C	1	NAG	O5-C1-C2	-4.25	104.71	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3	BMA	C1-O5-C5	4.14	117.74	112.19
2	D	7	MAN	C1-C2-C3	4.02	115.49	109.64
2	D	4	MAN	C1-C2-C3	3.90	115.32	109.64
2	D	7	MAN	C3-C4-C5	3.86	117.24	110.23
2	D	6	GAL	C1-O5-C5	3.84	117.34	112.19
2	C	4	MAN	C1-C2-C3	3.83	115.22	109.64
2	C	4	MAN	O2-C2-C3	-3.82	102.23	110.15
2	D	2	NAG	C4-C3-C2	-3.71	105.58	111.02
2	D	3	BMA	O5-C5-C4	-3.69	101.86	110.83
2	D	3	BMA	C1-C2-C3	3.63	114.93	109.64
2	D	6	GAL	O2-C2-C1	3.45	117.12	109.22
2	D	1	NAG	O5-C1-C2	-3.33	106.14	111.29
2	D	8	FUL	C3-C4-C5	3.24	114.74	109.81
2	D	8	FUL	C1-C2-C3	3.15	114.23	109.64
2	D	3	BMA	O5-C5-C6	3.15	113.80	107.66
2	D	5	NAG	O4-C4-C3	-3.15	102.96	110.38
2	D	2	NAG	C1-O5-C5	3.08	116.31	112.19
2	D	2	NAG	C1-C2-N2	3.04	115.22	110.43
2	C	8	FUL	C1-O5-C5	3.00	120.05	112.97
2	D	3	BMA	O3-C3-C2	-2.97	104.00	110.05
2	C	6	GAL	O5-C5-C6	2.94	113.38	107.66
2	D	1	NAG	C1-O5-C5	2.91	116.08	112.19
2	C	6	GAL	O2-C2-C1	2.89	115.84	109.22
2	C	5	NAG	O3-C3-C2	-2.88	103.42	109.40
2	C	8	FUL	O5-C5-C4	2.78	114.56	109.55
2	C	8	FUL	C2-C3-C4	-2.75	106.03	110.86
2	C	8	FUL	C3-C4-C5	2.74	113.97	109.81
2	D	6	GAL	O2-C2-C3	-2.72	104.52	110.15
2	C	2	NAG	O5-C5-C4	2.61	117.18	110.83
2	D	3	BMA	C3-C4-C5	2.57	114.90	110.23
2	D	3	BMA	C2-C3-C4	2.46	115.19	110.86
2	C	7	MAN	C3-C4-C5	2.39	114.57	110.23
2	D	4	MAN	O5-C5-C6	2.38	112.30	107.66
2	D	1	NAG	C1-C2-N2	2.35	114.14	110.43
2	C	2	NAG	O4-C4-C5	-2.35	103.54	109.32
2	C	7	MAN	O4-C4-C3	-2.35	104.84	110.38
2	C	6	GAL	O5-C5-C4	-2.34	105.12	110.83
2	D	6	GAL	C1-C2-C3	2.27	112.95	109.64
2	D	3	BMA	O3-C3-C4	2.17	115.49	110.38
2	C	2	NAG	C1-C2-N2	-2.16	107.03	110.43
2	C	8	FUL	O2-C2-C3	-2.15	105.69	110.15
2	D	1	NAG	C4-C3-C2	-2.11	107.92	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	5	NAG	C2-N2-C7	-2.07	120.13	122.90
2	D	3	BMA	O5-C1-C2	2.05	115.69	110.79

There are no chirality outliers.

All (11) torsion outliers are listed below:

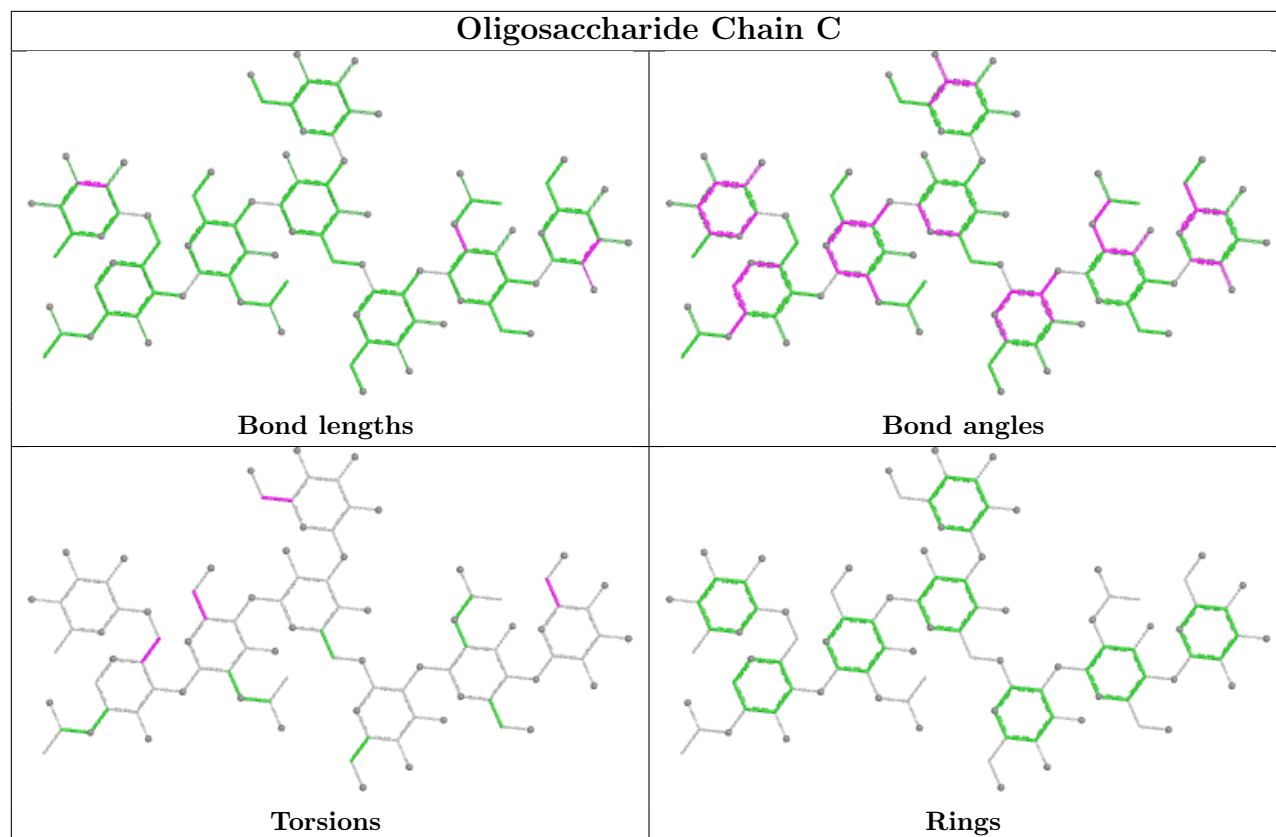
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	C	7	MAN	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
2	C	7	MAN	C4-C5-C6-O6
2	D	5	NAG	O5-C5-C6-O6
2	D	5	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	C	6	GAL	O5-C5-C6-O6

There are no ring outliers.

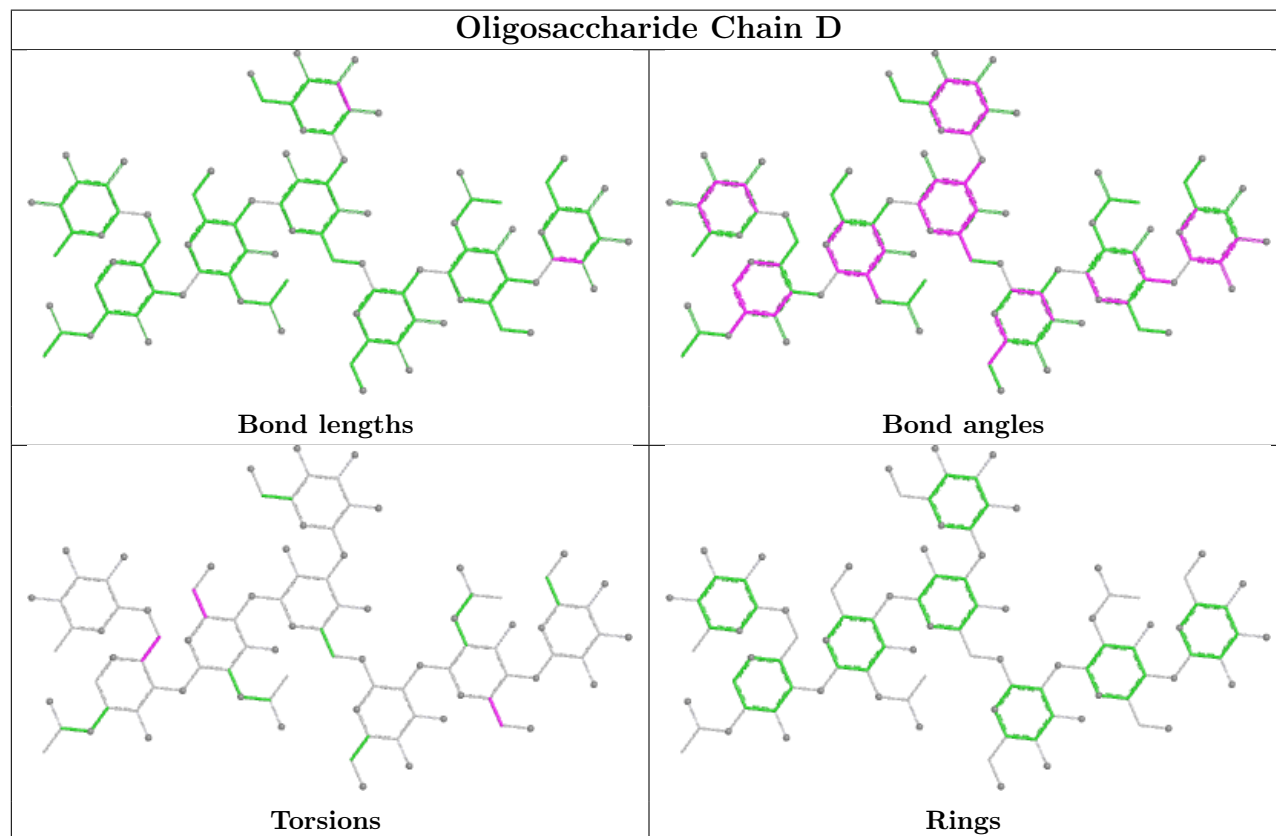
No monomer is involved in short contacts.

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

Oligosaccharide Chain C



Oligosaccharide Chain D



5.6 Ligand geometry

1 ligand is 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	$\# Z > 2$
3	GOL	A	509	-	5,5,5	0.38	0	5,5,5	0.71	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
3	GOL	A	509	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	509	GOL	C1-C2-C3-O3
3	A	509	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	509	GOL	6	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	208/224 (92%)	0.62	11 (5%) 32 32	28, 51, 72, 94	0
1	B	199/224 (88%)	1.11	42 (21%) 2 2	27, 49, 113, 143	0
All	All	407/448 (90%)	0.86	53 (13%) 7 6	27, 50, 94, 143	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	265	ASP	5.9
1	B	330	SER	5.6
1	B	300	LEU	5.2
1	B	240	VAL	5.2
1	B	329	PRO	5.1
1	B	272	ASP	5.1
1	B	273	VAL	5.1
1	B	332	ILE	5.0
1	B	444	SER	4.5
1	B	293	ARG	4.4
1	B	301	ARG	4.4
1	B	238	PRO	4.4
1	B	296	TYR	4.3
1	B	294	GLU	4.2
1	B	271	PRO	4.2
1	B	243	PHE	4.0
1	B	241	PHE	3.9
1	B	302	VAL	3.8
1	B	261	CYS	3.6
1	B	291	THR	3.6
1	B	323	VAL	3.5
1	B	331	PRO	3.4
1	A	236	GLY	3.3
1	B	262	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	264	VAL	3.1
1	B	292	HIS	3.0
1	B	275	ILE	2.9
1	B	324	ASN	2.9
1	B	282	VAL	2.9
1	B	239	SER	2.8
1	A	326	ARG	2.7
1	B	325	ASN	2.7
1	B	263	VAL	2.7
1	A	327	ALA	2.6
1	B	295	ASP	2.6
1	B	269	ASP	2.6
1	B	422	LEU	2.5
1	B	359	THR	2.5
1	B	420	GLY	2.5
1	A	253	ILE	2.5
1	A	323	VAL	2.4
1	B	370	THR	2.3
1	A	296	TYR	2.3
1	B	268	GLU	2.3
1	A	443	ARG	2.2
1	B	318	GLU	2.2
1	A	329	PRO	2.2
1	B	335	THR	2.2
1	B	253	ILE	2.1
1	A	330	SER	2.1
1	A	370	THR	2.1
1	A	332	ILE	2.1
1	B	341	GLY	2.1

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

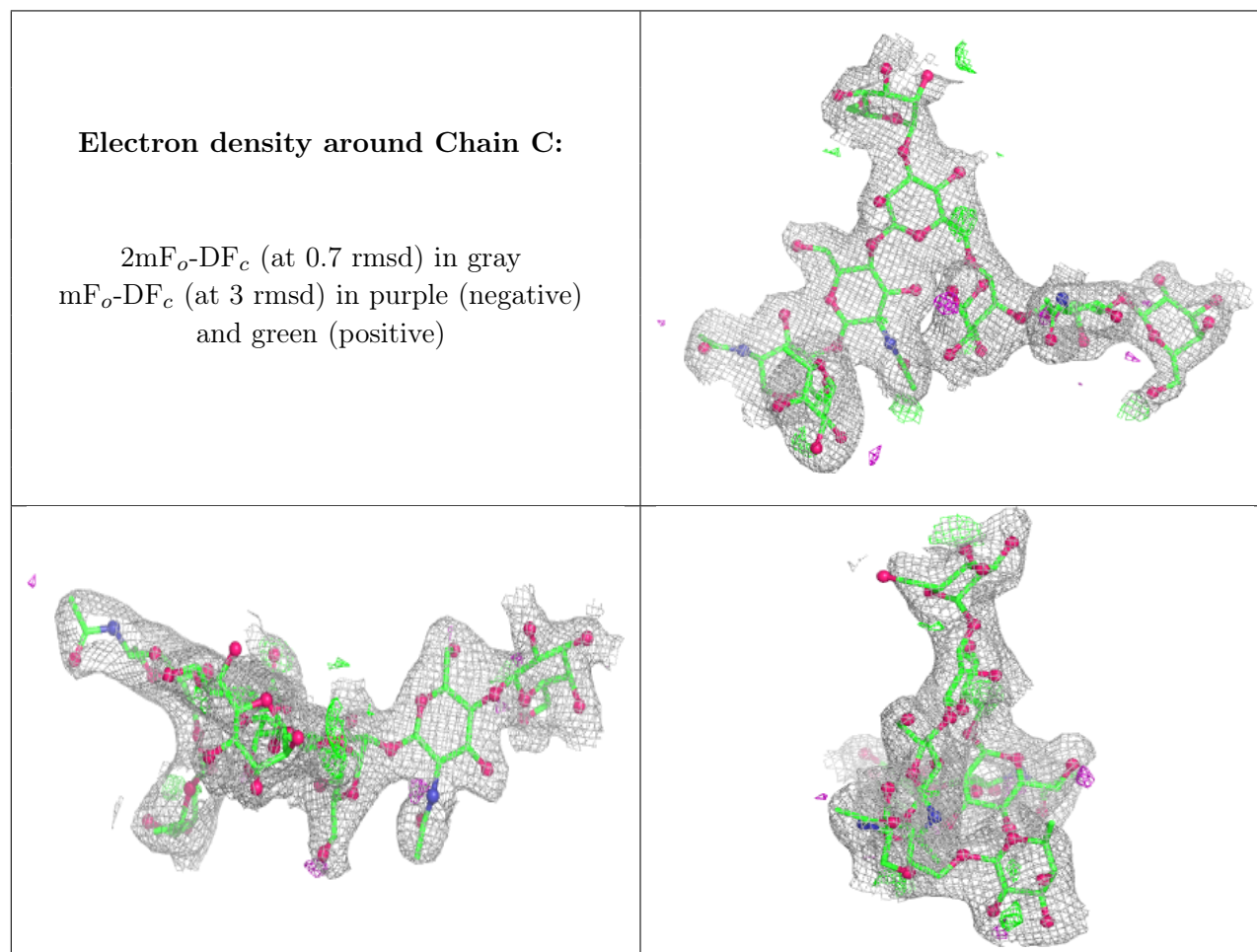
There are no non-standard protein/DNA/RNA residues in this entry.

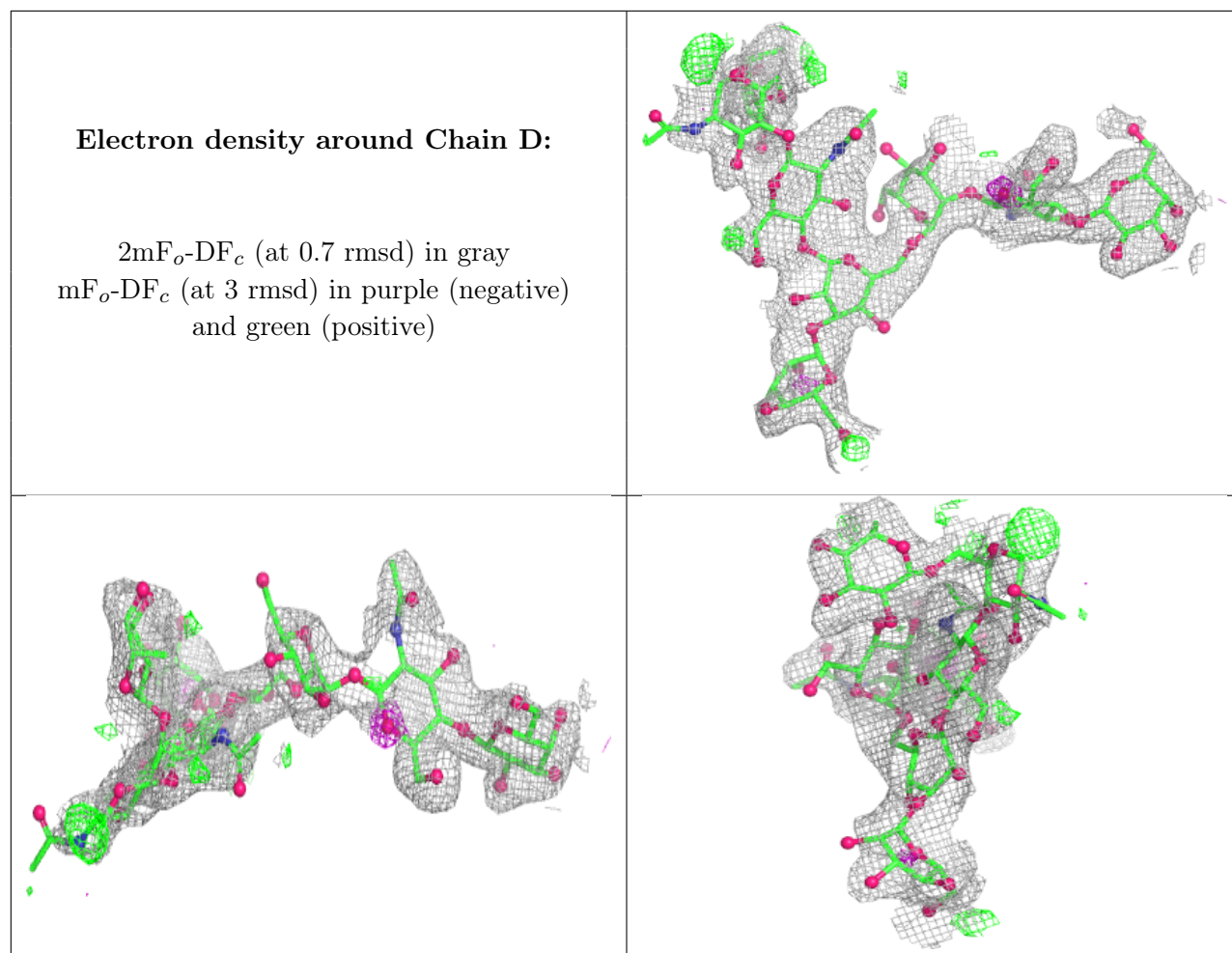
6.3 Carbohydrates ⓘ

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($\text{\AA}^2$)	Q<0.9
2	MAN	D	7	11/12	0.33	0.18	96,101,106,107	0
2	NAG	D	1	14/15	0.39	0.20	116,125,141,142	0
2	FUL	D	8	10/11	0.44	0.18	98,105,109,110	0
2	MAN	D	4	11/12	0.67	0.14	105,112,114,118	0
2	MAN	C	7	11/12	0.68	0.15	92,94,96,98	0
2	NAG	D	2	14/15	0.70	0.16	101,107,114,115	0
2	NAG	D	5	14/15	0.74	0.15	76,82,84,85	0
2	FUL	C	8	10/11	0.85	0.14	67,68,69,70	0
2	BMA	D	3	11/12	0.85	0.11	80,84,91,94	0
2	GAL	C	6	11/12	0.87	0.15	52,52,55,56	0
2	MAN	C	4	11/12	0.88	0.10	51,53,54,54	0
2	BMA	C	3	11/12	0.89	0.09	50,53,54,56	0
2	GAL	D	6	11/12	0.89	0.12	63,66,69,71	0
2	NAG	C	5	14/15	0.91	0.11	51,52,53,54	0
2	NAG	C	1	14/15	0.91	0.10	53,56,58,58	0
2	NAG	C	2	14/15	0.91	0.10	51,52,56,57	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
3	GOL	A	509	6/6	0.74	0.36	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.