Full wwPDB X-ray Structure Validation Report (i)

Dec 16, 2023 – 09:06 am GMT

PDB ID	:	2WQR
Title	:	The high resolution crystal structure of IgE Fc
Authors	:	Dhaliwal, B.; Sutton, B.J.; Beavil, A.J.
Deposited on	:	2009-08-26
Resolution	:	1.90 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 (i) 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 (1)) were used in the production of this report:

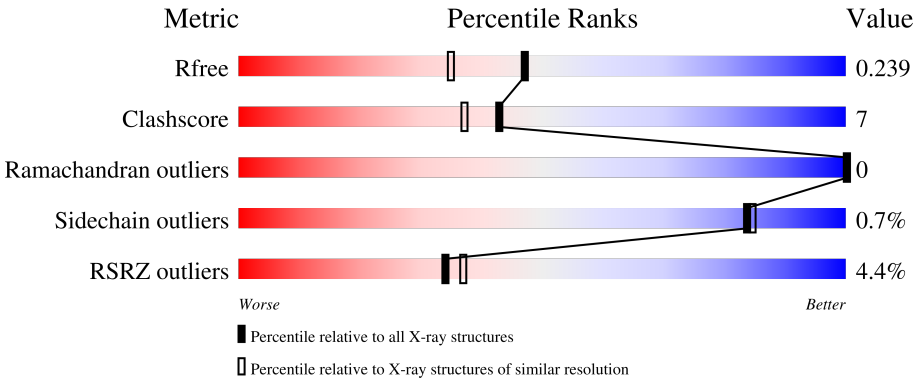
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	323	2% 89% 10%
1	B	323	7% 88% 11%
2	C	5	40% 60%
2	D	5	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
6	PG4	B	602	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 5725 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.

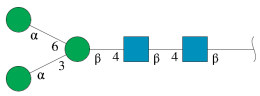
- Molecule 1 is a protein called IG EPSILON CHAIN C REGION.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	0	0
			2495	1557	443	484	11			
1	B	323	Total	C	N	O	S	23	0	0
			2522	1571	450	489	12			

There are 4 discrepancies between the modelled and reference sequences:

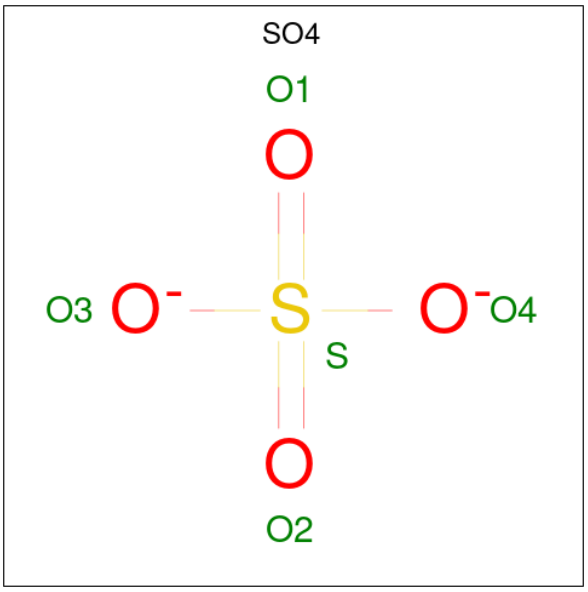
Chain	Residue	Modelled	Actual	Comment	Reference
A	265	GLN	ASN	engineered mutation	UNP P01854
A	371	GLN	ASN	engineered mutation	UNP P01854
B	265	GLN	ASN	engineered mutation	UNP P01854
B	371	GLN	ASN	engineered mutation	UNP P01854

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



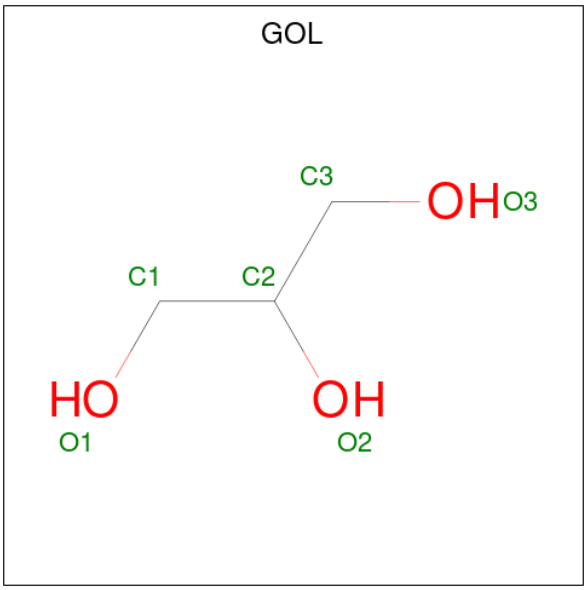
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	5	Total	C	N	O	0	0	0
			61	34	2	25			
2	D	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



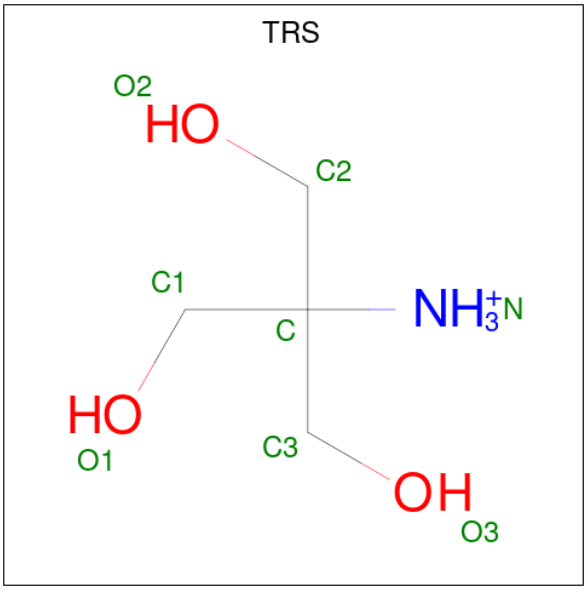
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	A	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



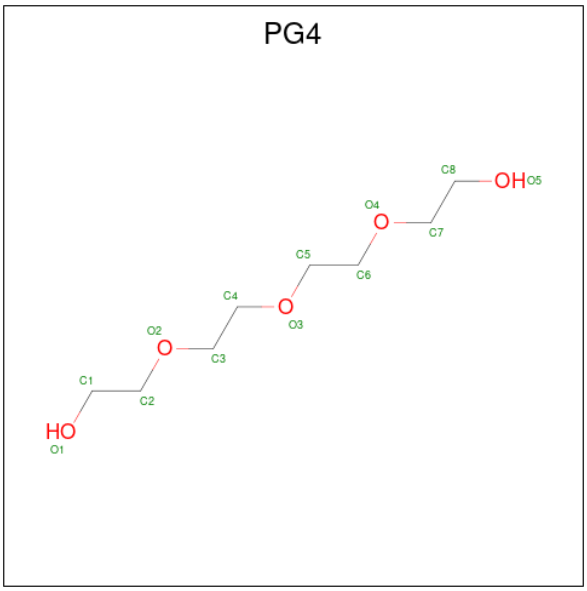
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 13 8 5	0	0

- Molecule 7 is water.

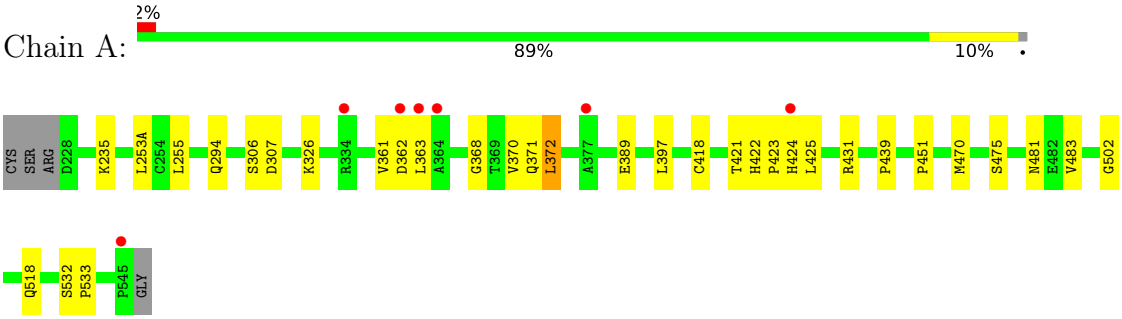
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	255	Total O 255 255	0	0
7	B	278	Total O 278 278	0	0

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.

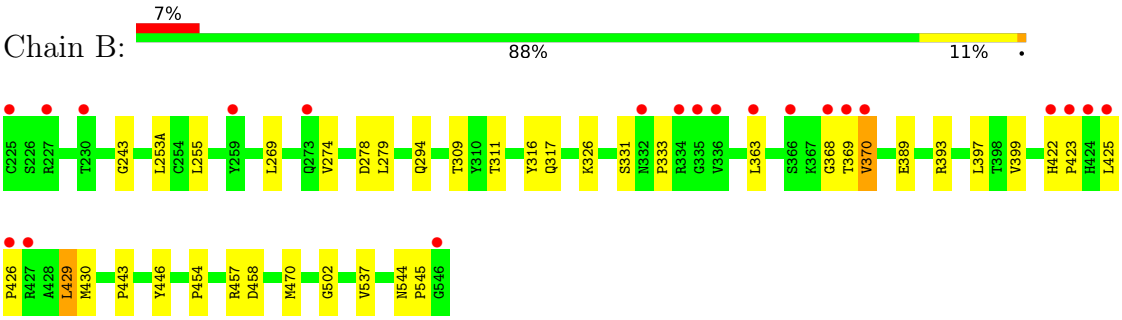
• Molecule 1: IG EPSILON CHAIN C REGION

Chain A:



• Molecule 1: IG EPSILON CHAIN C REGION

Chain B:

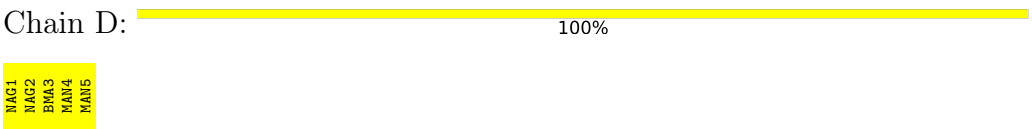


• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

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

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	130.50Å 75.28Å 79.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.00 – 1.90 49.31 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (36.00-1.90) 99.1 (49.31-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.53 (at 1.90Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.193 , 0.234 0.202 , 0.239	Depositor DCC
R_{free} test set	3110 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	28.0	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 48.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.018 for -h,l,k	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5725	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, MAN, NAG, GOL, PG4, TRS, SO4

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	0.30	0/2557	0.50	0/3486
1	B	0.30	0/2584	0.53	2/3521 (0.1%)
All	All	0.30	0/5141	0.51	2/7007 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	370	VAL	CB-CA-C	-6.33	99.38	111.40
1	B	370	VAL	N-CA-C	5.03	124.59	111.00

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	2495	0	2434	30	0
1	B	2522	0	2460	42	0
2	C	61	0	52	0	0
2	D	61	0	52	0	0
3	A	15	0	0	0	0
3	B	5	0	0	0	0
4	A	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	6	0	8	3	0
5	A	8	0	12	1	0
6	B	13	0	18	15	0
7	A	255	0	0	2	0
7	B	278	0	0	1	0
All	All	5725	0	5044	69	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 7.

All (69) 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:370:VAL:HG12	1:B:370:VAL:O	1.65	0.95
1:A:372:LEU:HD11	1:A:418:CYS:SG	2.19	0.82
1:B:393:ARG:HH11	4:B:601:GOL:H11	1.43	0.81
1:B:253(A):LEU:HD21	6:B:602:PG4:H61	1.64	0.78
1:B:393:ARG:NH1	4:B:601:GOL:H11	2.04	0.72
1:B:255:LEU:HD13	6:B:602:PG4:H12	1.73	0.70
1:A:370:VAL:HG22	1:A:422:HIS:HD2	1.58	0.68
1:B:389:GLU:HG2	1:B:399:VAL:HG22	1.75	0.68
1:A:294:GLN:OE1	6:B:602:PG4:H42	1.94	0.67
1:A:532:SER:HB2	1:A:533:PRO:HA	1.77	0.66
1:B:370:VAL:O	1:B:370:VAL:CG1	2.36	0.65
1:B:470:MET:HG3	1:B:502:GLY:HA2	1.81	0.63
1:B:255:LEU:CD1	6:B:602:PG4:H12	2.29	0.62
1:A:363:LEU:HD12	1:A:397:LEU:HB3	1.82	0.60
1:A:422:HIS:ND1	1:A:424:HIS:HB3	2.17	0.59
1:B:393:ARG:HD2	4:B:601:GOL:O3	2.03	0.58
1:B:294:GLN:OE1	6:B:602:PG4:H62	2.02	0.57
1:A:294:GLN:OE1	6:B:602:PG4:H32	2.05	0.57
1:B:422:HIS:CG	1:B:423:PRO:HD2	2.39	0.57
1:A:451:PRO:HD2	1:B:446:TYR:CD1	2.40	0.56
1:B:309:THR:HG21	1:B:393:ARG:HH22	1.70	0.55
1:B:317:GLN:O	1:B:317:GLN:HG3	2.07	0.55
1:A:326:LYS:HE2	1:B:243:GLY:O	2.06	0.54
1:B:269:LEU:HB2	1:B:311:THR:HB	1.88	0.54
1:A:253(A):LEU:HD22	6:B:602:PG4:H11	1.89	0.53
1:B:316:TYR:CE2	1:B:317:GLN:HG2	2.44	0.53
1:B:294:GLN:OE1	6:B:602:PG4:H51	2.09	0.53
1:A:371:GLN:HB2	1:A:421:THR:OG1	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:309:THR:HG21	1:B:393:ARG:NH2	2.24	0.52
1:A:294:GLN:OE1	6:B:602:PG4:C4	2.58	0.52
1:A:422:HIS:CE1	1:A:424:HIS:HB3	2.44	0.52
1:A:235:LYS:HE3	1:A:255:LEU:HD12	1.92	0.51
1:A:470:MET:HG3	1:A:502:GLY:HA2	1.94	0.50
1:B:368:GLY:H	1:B:422:HIS:HE2	1.60	0.49
1:A:475:SER:OG	5:A:610:TRS:H32	2.13	0.49
1:B:316:TYR:CD2	1:B:317:GLN:HG2	2.48	0.48
1:B:253(A):LEU:HD21	6:B:602:PG4:C6	2.41	0.48
1:B:363:LEU:CD1	1:B:370:VAL:HG21	2.44	0.47
1:A:389:GLU:HB2	1:A:397:LEU:HD11	1.95	0.47
1:A:370:VAL:HG22	1:A:422:HIS:CD2	2.44	0.47
1:B:363:LEU:HB2	1:B:397:LEU:HB3	1.98	0.46
1:B:369:THR:HG22	1:B:369:THR:O	2.15	0.46
1:A:235:LYS:HZ1	6:B:602:PG4:C8	2.29	0.46
1:A:439:PRO:HG3	1:B:278:ASP:HB3	1.97	0.45
1:B:370:VAL:H	1:B:422:HIS:HD2	1.65	0.45
1:B:269:LEU:HD23	1:B:274:VAL:HA	1.99	0.45
1:B:425:LEU:HA	1:B:426:PRO:HD3	1.85	0.45
1:A:431:ARG:NH2	7:A:705:HOH:O	2.49	0.44
1:A:235:LYS:NZ	6:B:602:PG4:C8	2.80	0.44
1:B:454:PRO:HA	1:B:457:ARG:HE	1.82	0.44
1:B:294:GLN:CD	6:B:602:PG4:H62	2.39	0.43
1:B:430:MET:HB3	1:B:430:MET:HE2	1.93	0.42
1:A:483:VAL:HG12	7:A:730:HOH:O	2.19	0.42
1:A:481:ASN:HB2	1:A:518:GLN:HE22	1.83	0.42
1:A:361:VAL:O	1:A:362:ASP:HB2	2.20	0.42
1:A:372:LEU:C	1:A:372:LEU:HD12	2.40	0.42
1:A:306:SER:O	1:A:307:ASP:HB2	2.19	0.42
1:B:363:LEU:HD13	1:B:370:VAL:HG21	2.02	0.42
1:B:326:LYS:HE2	7:B:785:HOH:O	2.19	0.41
1:B:370:VAL:N	1:B:422:HIS:HD2	2.18	0.41
1:A:425:LEU:HD23	1:A:425:LEU:HA	1.91	0.41
1:B:544:ASN:HA	1:B:545:PRO:HD3	1.92	0.41
1:A:294:GLN:OE1	6:B:602:PG4:C3	2.69	0.41
1:B:443:PRO:HG2	1:B:537:VAL:HG11	2.03	0.41
1:B:425:LEU:HD21	1:B:429:LEU:HD13	2.02	0.41
1:A:368:GLY:HA3	1:A:423:PRO:HG3	2.03	0.40
1:B:294:GLN:NE2	6:B:602:PG4:H62	2.36	0.40
1:B:368:GLY:H	1:B:422:HIS:CE1	2.39	0.40
1:B:331:SER:O	1:B:333:PRO:HD3	2.22	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	A	317/323 (98%)	310 (98%)	7 (2%)	0	100	100
1	B	321/323 (99%)	309 (96%)	12 (4%)	0	100	100
All	All	638/646 (99%)	619 (97%)	19 (3%)	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	283/286 (99%)	282 (100%)	1 (0%)	91	91
1	B	286/286 (100%)	283 (99%)	3 (1%)	76	76
All	All	569/572 (100%)	565 (99%)	4 (1%)	84	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	372	LEU
1	B	279	LEU
1	B	429	LEU
1	B	458	ASP

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	246	HIS
1	A	313	GLN
1	A	383	ASN
1	A	518	GLN
1	B	286	GLN
1	B	317	GLN
1	B	392	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)

10 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	2,1	14,14,15	0.50	0	17,19,21	1.06	1 (5%)
2	NAG	C	2	2	14,14,15	0.57	0	17,19,21	1.11	2 (11%)
2	BMA	C	3	2	11,11,12	0.72	0	15,15,17	1.83	3 (20%)
2	MAN	C	4	2	11,11,12	0.68	0	15,15,17	0.71	0
2	MAN	C	5	2	11,11,12	0.67	0	15,15,17	0.88	0
2	NAG	D	1	2,1	14,14,15	0.46	0	17,19,21	1.37	2 (11%)
2	NAG	D	2	2	14,14,15	0.48	0	17,19,21	0.95	1 (5%)
2	BMA	D	3	2	11,11,12	0.68	0	15,15,17	1.48	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	MAN	D	4	2	11,11,12	0.68	0	15,15,17	0.97	1 (6%)
2	MAN	D	5	2	11,11,12	0.54	0	15,15,17	1.00	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
2	NAG	C	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	2/2/19/22	0/1/1/1
2	MAN	C	5	2	-	0/2/19/22	0/1/1/1
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	4/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	2/2/19/22	0/1/1/1
2	MAN	D	5	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	3	BMA	C1-C2-C3	4.32	114.97	109.67
2	D	3	BMA	C1-C2-C3	4.27	114.92	109.67
2	D	1	NAG	C1-O5-C5	4.11	117.76	112.19
2	C	3	BMA	O5-C5-C6	3.75	113.09	107.20
2	C	1	NAG	C1-O5-C5	2.98	116.22	112.19
2	C	3	BMA	O2-C2-C3	-2.77	104.60	110.14
2	C	2	NAG	C1-O5-C5	2.55	115.64	112.19
2	C	2	NAG	C4-C3-C2	2.52	114.71	111.02
2	D	2	NAG	C1-O5-C5	2.40	115.44	112.19
2	D	4	MAN	O5-C5-C6	2.30	110.81	107.20
2	D	1	NAG	C6-C5-C4	-2.25	107.74	113.00
2	D	5	MAN	C1-C2-C3	2.23	112.41	109.67

There are no chirality outliers.

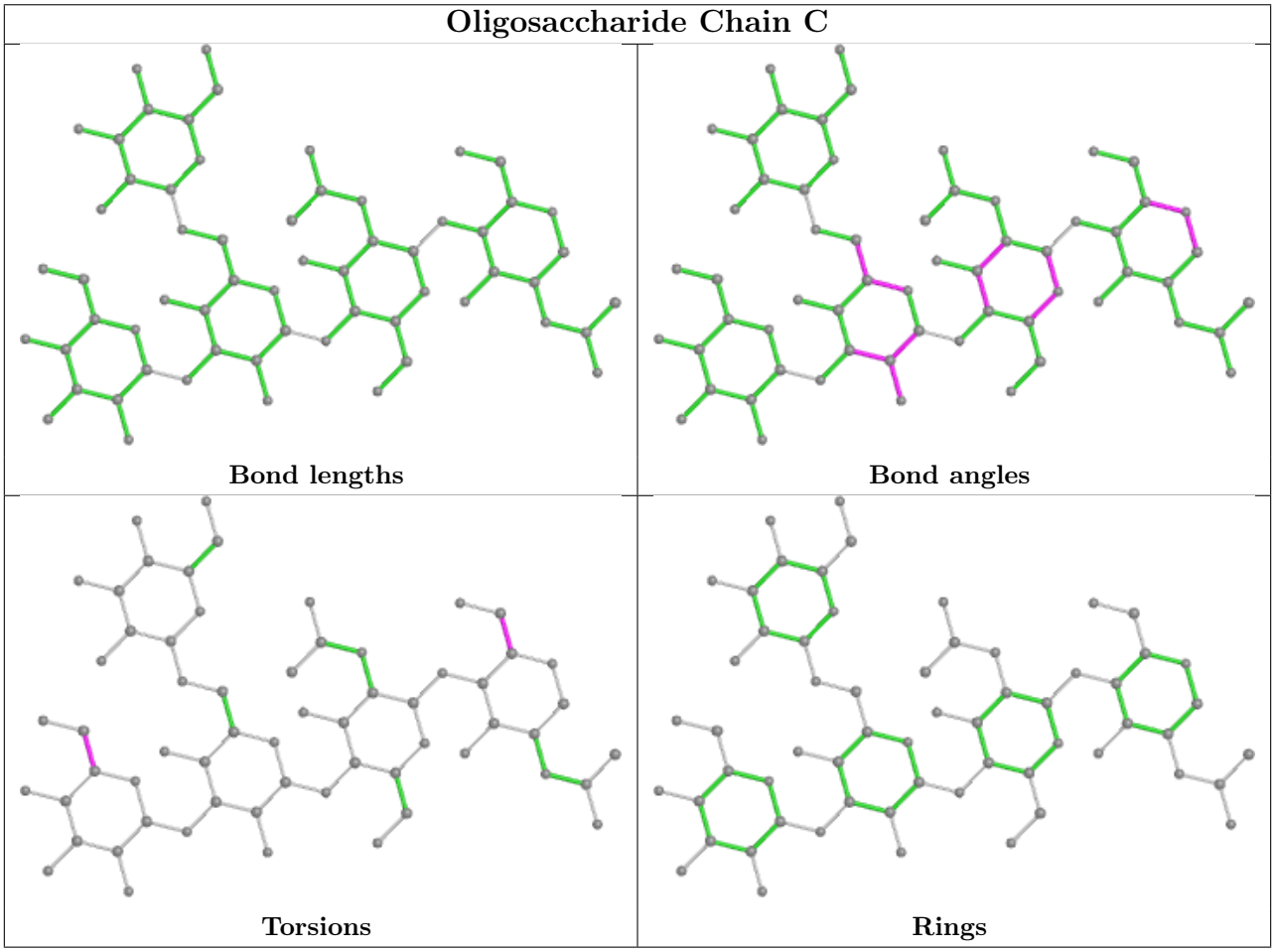
All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	4	MAN	O5-C5-C6-O6
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
2	C	1	NAG	O5-C5-C6-O6
2	C	4	MAN	O5-C5-C6-O6
2	D	4	MAN	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	C	4	MAN	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6

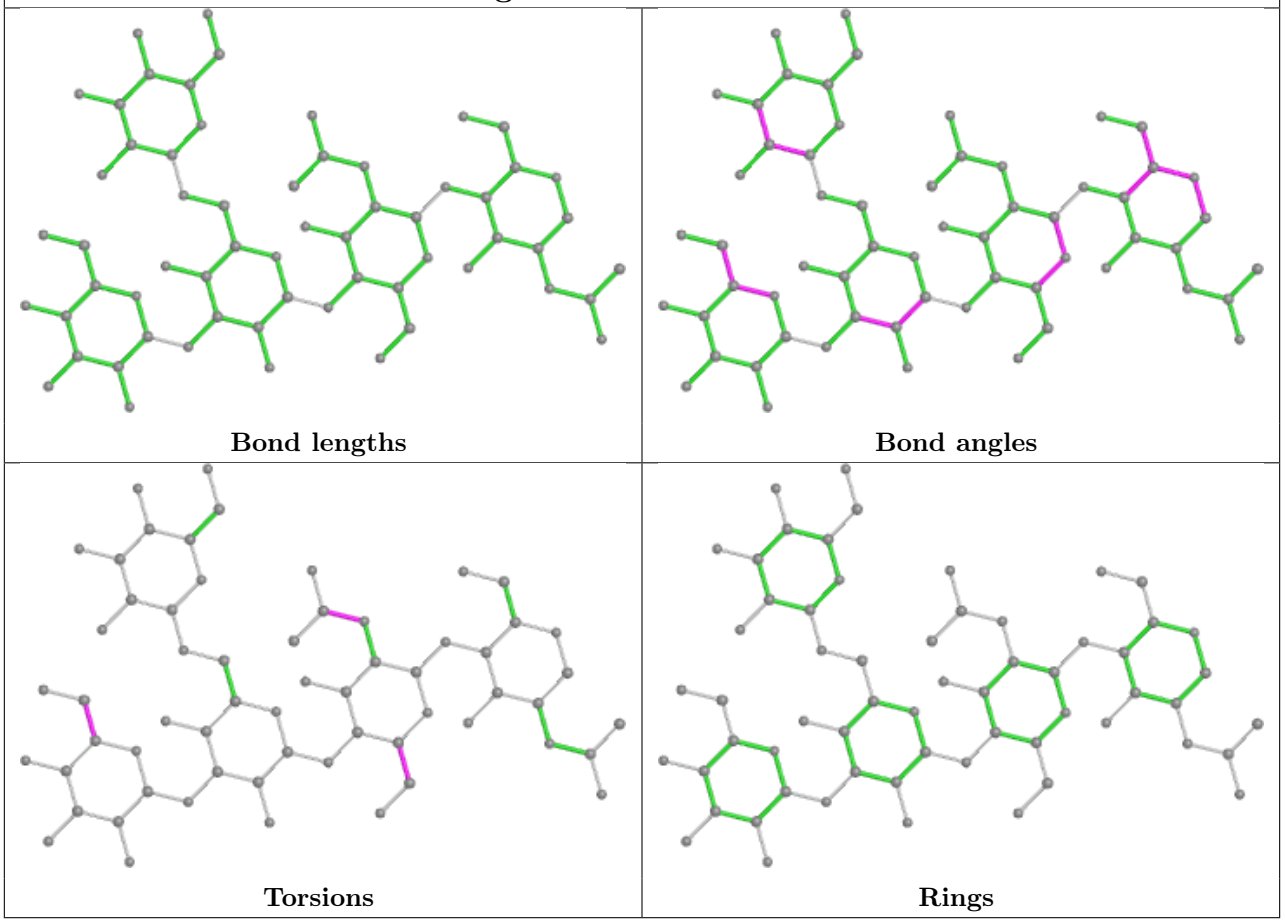
There are no ring outliers.

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.



Oligosaccharide Chain D



5.6 Ligand geometry (i)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	A	608	-	4,4,4	0.24	0	6,6,6	0.11	0
4	GOL	B	601	-	5,5,5	0.33	0	5,5,5	0.28	0
3	SO4	A	606	-	4,4,4	0.12	0	6,6,6	0.11	0
4	GOL	A	609	-	5,5,5	0.38	0	5,5,5	0.30	0
3	SO4	B	603	-	4,4,4	0.14	0	6,6,6	0.10	0
3	SO4	A	607	-	4,4,4	0.14	0	6,6,6	0.10	0
5	TRS	A	610	-	7,7,7	0.33	0	9,9,9	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	PG4	B	602	-	12,12,12	0.56	0	11,11,11	1.41	1 (9%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	TRS	A	610	-	-	9/9/9/9	-
4	GOL	A	609	-	-	2/4/4/4	-
6	PG4	B	602	-	-	7/10/10/10	-
4	GOL	B	601	-	-	4/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	B	602	PG4	O4-C6-C5	2.00	119.43	110.39

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	609	GOL	C1-C2-C3-O3
5	A	610	TRS	C2-C-C1-O1
5	A	610	TRS	C1-C-C3-O3
5	A	610	TRS	C2-C-C3-O3
5	A	610	TRS	N-C-C3-O3
4	A	609	GOL	O2-C2-C3-O3
4	B	601	GOL	O1-C1-C2-C3
4	B	601	GOL	C1-C2-C3-O3
4	B	601	GOL	O2-C2-C3-O3
6	B	602	PG4	O2-C3-C4-O3
5	A	610	TRS	C3-C-C1-O1
5	A	610	TRS	C1-C-C2-O2
6	B	602	PG4	O4-C7-C8-O5
4	B	601	GOL	O1-C1-C2-O2
5	A	610	TRS	N-C-C2-O2
6	B	602	PG4	C8-C7-O4-C6
6	B	602	PG4	C3-C4-O3-C5

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Mol	Chain	Res	Type	Atoms
6	B	602	PG4	C1-C2-O2-C3
5	A	610	TRS	C3-C-C2-O2
6	B	602	PG4	C4-C3-O2-C2
5	A	610	TRS	N-C-C1-O1
6	B	602	PG4	O3-C5-C6-O4

There are no ring outliers.

3 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	601	GOL	3	0
5	A	610	TRS	1	0
6	B	602	PG4	15	0

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, 95^{th} 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	319/323 (98%)	-0.06	7 (2%)	62	64	23, 39, 96, 183	0
1	B	320/323 (99%)	0.22	21 (6%)	18	20	21, 39, 90, 148	0
All	All	639/646 (98%)	0.08	28 (4%)	34	37	21, 39, 96, 183	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	427	ARG	7.5
1	B	334	ARG	5.7
1	B	425	LEU	5.4
1	B	225	CYS	5.0
1	B	426	PRO	4.8
1	A	545	PRO	4.7
1	B	363	LEU	4.5
1	B	424	HIS	4.5
1	B	423	PRO	3.8
1	B	422	HIS	3.5
1	B	366	SER	3.1
1	B	369	THR	2.9
1	B	370	VAL	2.9
1	A	363	LEU	2.8
1	B	368	GLY	2.7
1	A	334	ARG	2.7
1	B	335	GLY	2.7
1	B	230	THR	2.6
1	B	336	VAL	2.6
1	B	546	GLY	2.5
1	A	364	ALA	2.4
1	B	227	ARG	2.4
1	B	273	GLN	2.4
1	A	424	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	377	ALA	2.2
1	B	332	ASN	2.2
1	A	362	ASP	2.2
1	B	259	TYR	2.2

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)

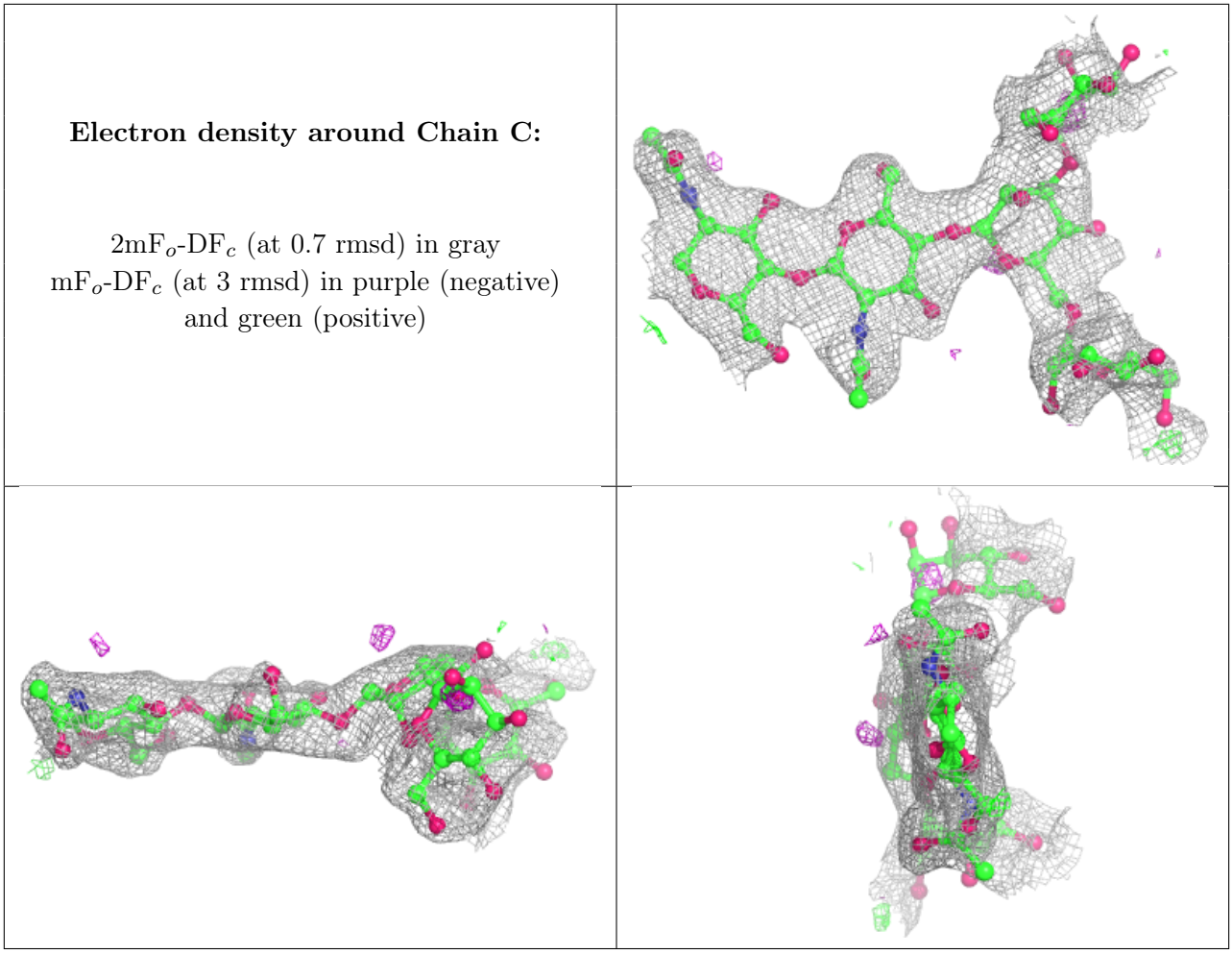
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
2	MAN	C	4	11/12	0.28	0.32	116,121,128,129	0
2	MAN	C	5	11/12	0.72	0.27	113,116,120,122	0
2	MAN	D	4	11/12	0.82	0.23	88,94,99,101	0
2	BMA	C	3	11/12	0.85	0.16	99,107,114,125	0
2	MAN	D	5	11/12	0.88	0.14	78,85,97,99	0
2	NAG	C	2	14/15	0.89	0.16	79,84,91,92	0
2	BMA	D	3	11/12	0.89	0.14	52,67,74,80	0
2	NAG	C	1	14/15	0.91	0.17	82,88,100,102	0
2	NAG	D	2	14/15	0.95	0.09	41,54,58,64	0
2	NAG	D	1	14/15	0.95	0.09	49,55,64,72	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

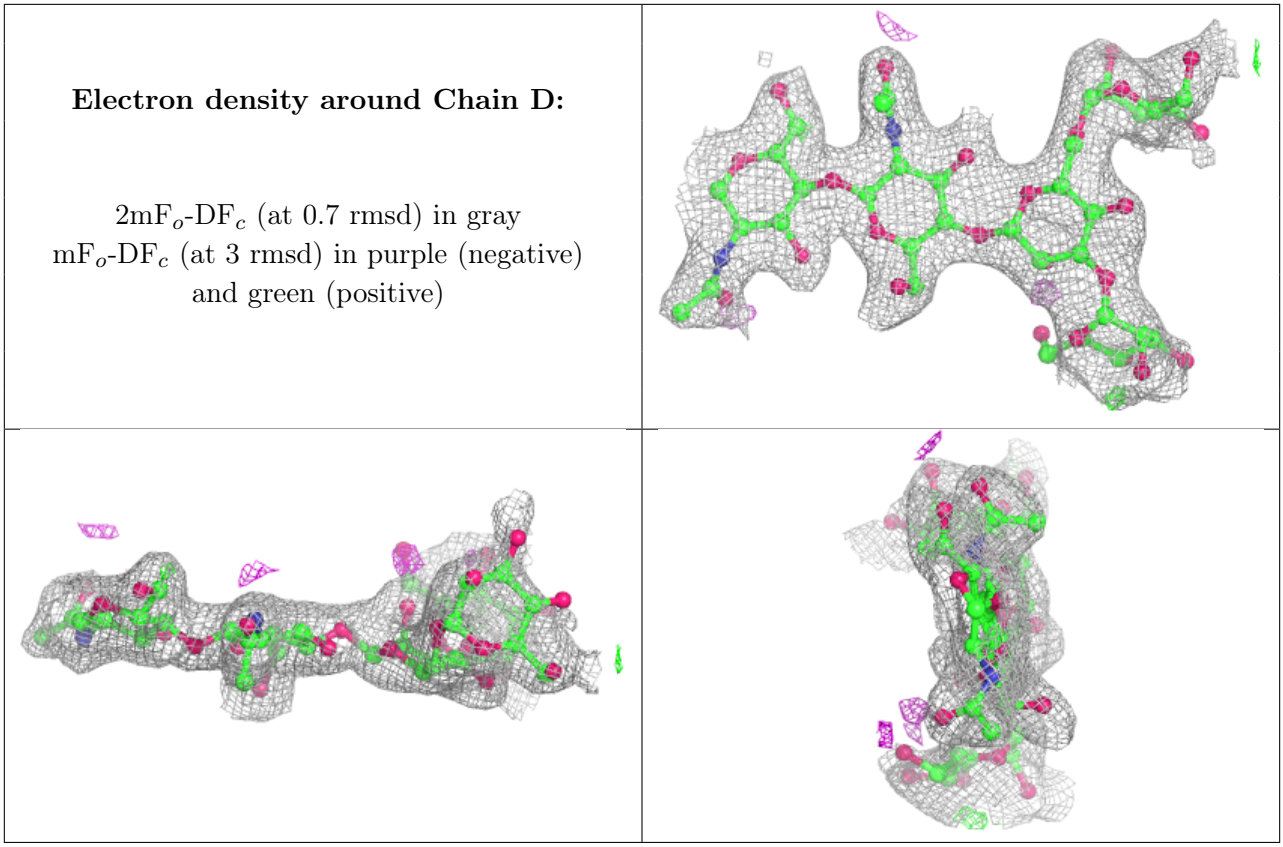
Electron density around Chain C:

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



Electron density around Chain D:

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



6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	TRS	A	610	8/8	0.75	0.26	64,73,96,104	0
4	GOL	B	601	6/6	0.79	0.17	83,88,90,93	0
6	PG4	B	602	13/13	0.84	0.66	66,74,83,86	0
4	GOL	A	609	6/6	0.86	0.23	76,79,93,99	0
3	SO4	A	607	5/5	0.89	0.15	107,109,114,114	0
3	SO4	A	608	5/5	0.91	0.11	103,109,111,111	0
3	SO4	B	603	5/5	0.93	0.12	66,67,77,79	0
3	SO4	A	606	5/5	0.98	0.15	53,61,71,78	0

6.5 Other polymers

There are no such residues in this entry.