



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 09:03 PM BST

PDB ID : 4WI3  
Title : Structural mapping of the human IgG1 binding site for FcRn: hu3S193 Fc mutation I253A  
Authors : Farrugia, W.; Burvenich, I.J.G.; Scott, A.M.; Ramsland, P.A.  
Deposited on : 2014-09-25  
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](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.

---

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 : 2.13.1  
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) : 2.13.1

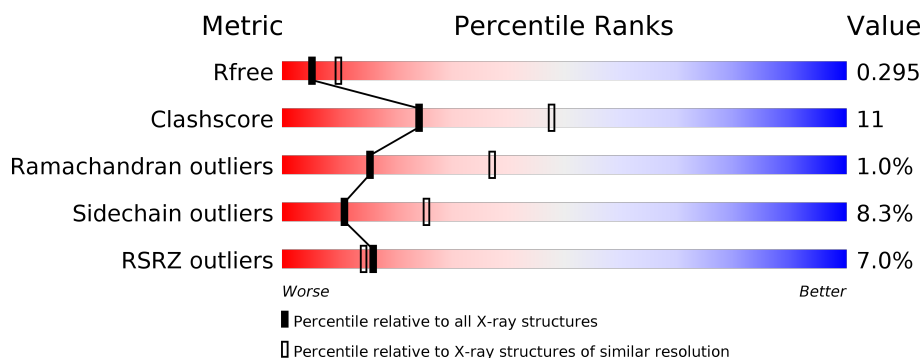
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (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 on 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	A	208	<div> <div>7%</div> <div>69%</div> <div>26%</div> <div>5%</div> </div>
1	B	208	<div> <div>7%</div> <div>72%</div> <div>23%</div> <div>5%</div> </div>
2	C	8	<div> <div>38%</div> <div>38%</div> <div>25%</div> </div>
2	D	8	<div> <div>50%</div> <div>38%</div> <div>13%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FUC	D	8	-	-	-	X

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3552 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.

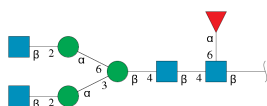
- Molecule 1 is a protein called Ig gamma-1 chain C region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1661	1056	280	319	6			
1	B	208	Total	C	N	O	S	0	0	0
			1661	1056	280	319	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	253	ALA	ILE	engineered mutation	UNP P01857
B	253	ALA	ILE	engineered mutation	UNP P01857

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	8	Total	C	N	O	0	0	0
			99	56	4	39			
2	D	8	Total	C	N	O	0	0	0
			99	56	4	39			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	14	Total	O	0	0
			14	14		

*Continued on next page...*

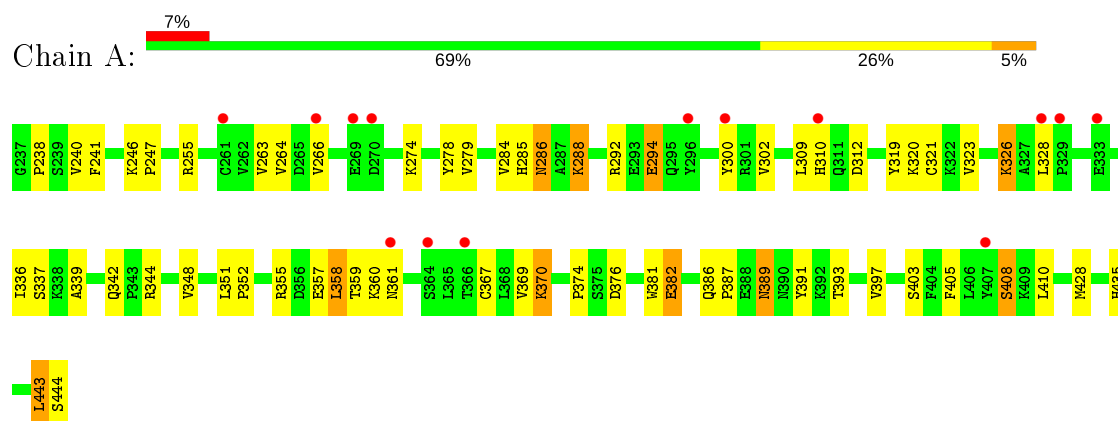
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	18	Total	O	0	0
			18	18		

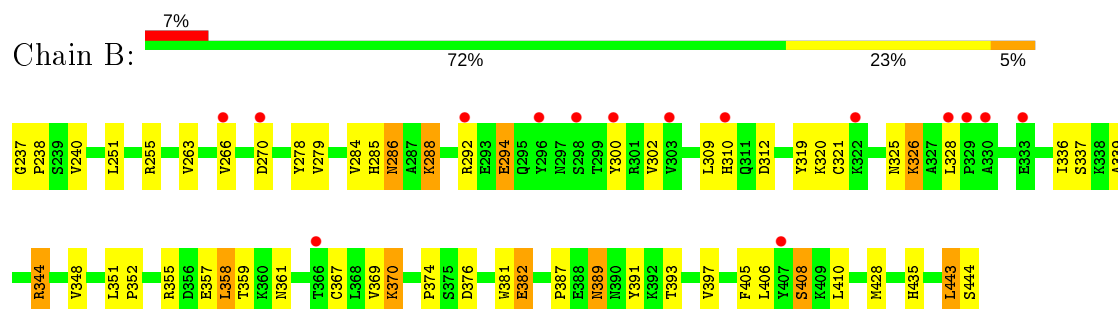
### 3 Residue-property plots [i](#)

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.

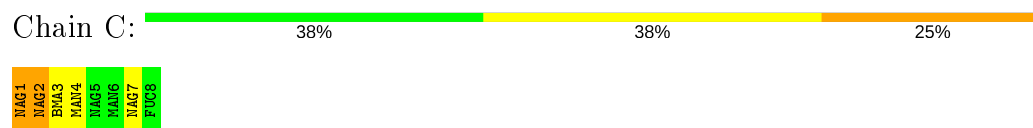
- Molecule 1: Ig gamma-1 chain C region



- Molecule 1: Ig gamma-1 chain C region



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



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

nose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  50% 38% 13%

MAG1	MAG2	BMJ3	MAG4	MAG5	MAG6	MAG7	FUC8
------	------	------	------	------	------	------	------

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.13 Å 75.91 Å 142.37 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.82 – 2.70 28.82 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.5 (28.82-2.70) 98.9 (28.82-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.22 (at 2.72 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.216 , 0.296 0.220 , 0.295	Depositor DCC
$R_{free}$ test set	1501 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.5	Xtriage
Anisotropy	1.025	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 73.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	3552	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 98.53 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1286e-11. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

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

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	0.39	0/1707	0.57	0/2326
1	B	0.39	0/1707	0.56	0/2326
All	All	0.39	0/3414	0.56	0/4652

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1661	0	1624	40	0
1	B	1661	0	1624	37	0
2	C	99	0	85	2	0
2	D	99	0	85	1	0
3	A	14	0	0	5	0
3	B	18	0	0	3	0
All	All	3552	0	3418	76	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 11.

All (76) 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:344:ARG:NH1	3:B:613:HOH:O	2.12	0.82
1:B:443:LEU:HD12	1:B:444:SER:H	1.52	0.74
1:A:443:LEU:HD12	1:A:444:SER:H	1.54	0.71
1:A:393:THR:OG1	1:A:408:SER:OG	2.09	0.70
1:B:393:THR:OG1	1:B:408:SER:OG	2.10	0.69
1:A:240:VAL:HG22	1:A:263:VAL:HG22	1.77	0.66
1:B:240:VAL:HG22	1:B:263:VAL:HG22	1.78	0.65
1:A:339:ALA:HB3	1:A:374:PRO:HB3	1.80	0.63
1:A:274:LYS:O	3:A:605:HOH:O	2.15	0.63
1:B:339:ALA:HB3	1:B:374:PRO:HB3	1.82	0.61
1:B:381:TRP:HE1	1:B:408:SER:HB3	1.67	0.60
1:A:294:GLU:HG2	1:A:300:TYR:HE1	1.67	0.59
1:B:294:GLU:HG2	1:B:300:TYR:HE1	1.68	0.59
1:B:355:ARG:HA	1:B:358:LEU:HD13	1.84	0.59
1:A:355:ARG:HA	1:A:358:LEU:HD13	1.85	0.59
1:A:444:SER:O	3:A:607:HOH:O	2.17	0.57
1:A:381:TRP:HE1	1:A:408:SER:HB3	1.68	0.57
1:A:323:VAL:HG13	3:A:605:HOH:O	2.06	0.56
1:B:255:ARG:O	1:B:310:HIS:NE2	2.37	0.56
1:A:370:LYS:HE2	1:B:357:GLU:OE2	2.06	0.56
1:A:255:ARG:O	1:A:310:HIS:NE2	2.40	0.52
1:A:397:VAL:HB	1:A:405:PHE:CE2	2.44	0.52
1:A:357:GLU:OE2	1:B:370:LYS:HE2	2.09	0.52
1:A:360:LYS:NZ	3:A:611:HOH:O	2.42	0.52
1:A:278:TYR:HD1	1:A:320:LYS:HD3	1.75	0.51
1:A:292:ARG:HB3	1:A:302:VAL:HG22	1.93	0.51
1:B:397:VAL:HB	1:B:405:PHE:CE2	2.46	0.51
1:B:278:TYR:HD1	1:B:320:LYS:HD3	1.76	0.50
1:B:393:THR:O	3:B:612:HOH:O	2.19	0.50
1:B:292:ARG:HB3	1:B:302:VAL:HG22	1.92	0.50
1:A:403:SER:OG	3:A:606:HOH:O	2.20	0.49
1:B:309:LEU:HB2	1:B:312:ASP:HB2	1.96	0.48
1:A:264:VAL:HG11	2:C:1:NAG:O4	2.14	0.48
1:A:286:ASN:OD1	1:A:286:ASN:N	2.45	0.48
1:A:326:LYS:H	1:A:326:LYS:HD2	1.79	0.48
1:B:286:ASN:OD1	1:B:286:ASN:N	2.46	0.48
1:A:309:LEU:HB2	1:A:312:ASP:HB2	1.95	0.47
1:B:367:CYS:HB2	1:B:381:TRP:CZ2	2.49	0.47
1:A:241:PHE:CE2	2:C:2:NAG:H4	2.49	0.47
1:B:326:LYS:H	1:B:326:LYS:HD2	1.80	0.47
1:B:389:ASN:OD1	1:B:389:ASN:N	2.43	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:TYR:HB2	1:A:320:LYS:HG2	1.97	0.47
1:A:367:CYS:HB2	1:A:381:TRP:CZ2	2.50	0.47
1:A:382:GLU:HB3	1:A:387:PRO:HA	1.97	0.47
1:B:382:GLU:HB3	1:B:387:PRO:HA	1.97	0.46
1:A:428:MET:HA	1:A:435:HIS:O	2.16	0.46
1:A:357:GLU:O	1:A:359:THR:N	2.46	0.46
1:B:348:VAL:HG22	1:B:369:VAL:HG13	1.97	0.46
1:A:391:TYR:HB3	1:A:410:LEU:CD1	2.46	0.46
1:B:278:TYR:HB2	1:B:320:LYS:HG2	1.98	0.46
1:B:288:LYS:HE2	1:B:288:LYS:HB2	1.55	0.45
1:A:279:VAL:HG22	1:A:319:TYR:CD1	2.53	0.44
1:A:389:ASN:N	1:A:389:ASN:OD1	2.46	0.44
1:A:238:PRO:HD2	1:A:328:LEU:HG	2.00	0.43
1:B:428:MET:HA	1:B:435:HIS:O	2.18	0.43
1:B:391:TYR:HB3	1:B:410:LEU:CD1	2.49	0.43
1:B:443:LEU:HA	1:B:443:LEU:HD13	1.91	0.43
1:A:336:ILE:HG12	1:A:337:SER:N	2.34	0.43
1:A:351:LEU:HA	1:A:352:PRO:HD2	1.74	0.43
1:B:443:LEU:HD12	1:B:444:SER:N	2.27	0.42
1:A:386:GLN:HA	1:A:387:PRO:HD3	1.88	0.42
1:B:238:PRO:HD2	1:B:328:LEU:HG	2.02	0.42
1:B:279:VAL:HG22	1:B:319:TYR:CD1	2.54	0.42
1:B:255:ARG:HD2	3:B:602:HOH:O	2.20	0.42
1:B:339:ALA:HB3	1:B:374:PRO:CB	2.49	0.42
1:A:342:GLN:HG2	1:A:342:GLN:H	1.70	0.42
1:B:270:ASP:O	1:B:325:ASN:ND2	2.35	0.42
1:B:237:GLY:HA3	1:B:238:PRO:HD3	1.89	0.41
1:B:357:GLU:O	1:B:359:THR:N	2.46	0.41
2:D:7:NAG:H2	2:D:7:NAG:H83	1.90	0.41
1:A:288:LYS:HB2	1:A:288:LYS:HE2	1.57	0.41
1:A:348:VAL:HG22	1:A:369:VAL:HG13	2.03	0.41
1:A:246:LYS:HA	1:A:247:PRO:HD3	1.94	0.41
1:A:339:ALA:HB3	1:A:374:PRO:CB	2.48	0.41
1:B:336:ILE:HG12	1:B:337:SER:N	2.34	0.41
1:B:351:LEU:HA	1:B:352:PRO:HD2	1.76	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	206/208 (99%)	193 (94%)	11 (5%)	2 (1%)	15	37
1	B	206/208 (99%)	194 (94%)	10 (5%)	2 (1%)	15	37
All	All	412/416 (99%)	387 (94%)	21 (5%)	4 (1%)	15	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	GLU
1	A	358	LEU
1	B	294	GLU
1	B	358	LEU

### 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	193/193 (100%)	178 (92%)	15 (8%)	12	29
1	B	193/193 (100%)	176 (91%)	17 (9%)	10	23
All	All	386/386 (100%)	354 (92%)	32 (8%)	11	25

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	266	VAL
1	A	284	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	285	HIS
1	A	286	ASN
1	A	288	LYS
1	A	321	CYS
1	A	326	LYS
1	A	344	ARG
1	A	361	ASN
1	A	370	LYS
1	A	376	ASP
1	A	382	GLU
1	A	389	ASN
1	A	408	SER
1	A	443	LEU
1	B	251	LEU
1	B	266	VAL
1	B	284	VAL
1	B	285	HIS
1	B	286	ASN
1	B	288	LYS
1	B	321	CYS
1	B	326	LYS
1	B	344	ARG
1	B	361	ASN
1	B	370	LYS
1	B	376	ASP
1	B	382	GLU
1	B	389	ASN
1	B	406	LEU
1	B	408	SER
1	B	443	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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	0.54	0	17,19,21	1.35	3 (17%)
2	NAG	C	2	2	14,14,15	0.56	0	17,19,21	1.20	2 (11%)
2	BMA	C	3	2	11,11,12	0.69	0	15,15,17	0.99	1 (6%)
2	MAN	C	4	2	11,11,12	0.63	0	15,15,17	0.89	1 (6%)
2	NAG	C	5	2	14,14,15	0.61	0	17,19,21	0.52	0
2	MAN	C	6	2	11,11,12	0.65	0	15,15,17	1.06	0
2	NAG	C	7	2	14,14,15	0.44	0	17,19,21	0.85	1 (5%)
2	FUC	C	8	2	10,10,11	0.64	0	14,14,16	0.78	0
2	NAG	D	1	1,2	14,14,15	0.51	0	17,19,21	0.94	1 (5%)
2	NAG	D	2	2	14,14,15	0.52	0	17,19,21	1.05	1 (5%)
2	BMA	D	3	2	11,11,12	0.68	0	15,15,17	1.22	1 (6%)
2	MAN	D	4	2	11,11,12	0.56	0	15,15,17	0.91	0
2	NAG	D	5	2	14,14,15	0.51	0	17,19,21	0.70	0
2	MAN	D	6	2	11,11,12	0.64	0	15,15,17	1.02	0
2	NAG	D	7	2	14,14,15	0.43	0	17,19,21	1.44	3 (17%)
2	FUC	D	8	2	10,10,11	0.59	0	14,14,16	0.95	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
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	-	2/2/19/22	0/1/1/1
2	MAN	C	4	2	-	2/2/19/22	0/1/1/1
2	NAG	C	5	2	-	2/6/23/26	0/1/1/1

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	C	6	2	-	0/2/19/22	0/1/1/1
2	NAG	C	7	2	-	1/6/23/26	0/1/1/1
2	FUC	C	8	2	-	-	0/1/1/1
2	NAG	D	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	BMA	D	3	2	-	1/2/19/22	0/1/1/1
2	MAN	D	4	2	-	2/2/19/22	0/1/1/1
2	NAG	D	5	2	-	2/6/23/26	0/1/1/1
2	MAN	D	6	2	-	0/2/19/22	0/1/1/1
2	NAG	D	7	2	-	3/6/23/26	0/1/1/1
2	FUC	D	8	2	-	-	0/1/1/1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	7	NAG	C1-O5-C5	3.92	117.51	112.19
2	C	1	NAG	C1-O5-C5	2.98	116.23	112.19
2	C	7	NAG	C1-O5-C5	2.87	116.08	112.19
2	D	3	BMA	C1-C2-C3	2.84	113.16	109.67
2	C	2	NAG	C3-C4-C5	2.67	115.00	110.24
2	D	7	NAG	C2-N2-C7	-2.65	119.13	122.90
2	C	2	NAG	C4-C3-C2	2.62	114.85	111.02
2	C	4	MAN	O5-C1-C2	-2.56	106.81	110.77
2	D	7	NAG	C4-C3-C2	-2.48	107.38	111.02
2	C	3	BMA	C1-C2-C3	2.38	112.59	109.67
2	C	1	NAG	C4-C3-C2	2.37	114.48	111.02
2	D	1	NAG	O5-C1-C2	-2.15	107.89	111.29
2	C	1	NAG	C3-C4-C5	2.12	114.03	110.24
2	D	2	NAG	C3-C4-C5	2.01	113.82	110.24

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	5	NAG	C8-C7-N2-C2
2	D	5	NAG	O7-C7-N2-C2
2	C	5	NAG	C8-C7-N2-C2

*Continued on next page...*

*Continued from previous page...*

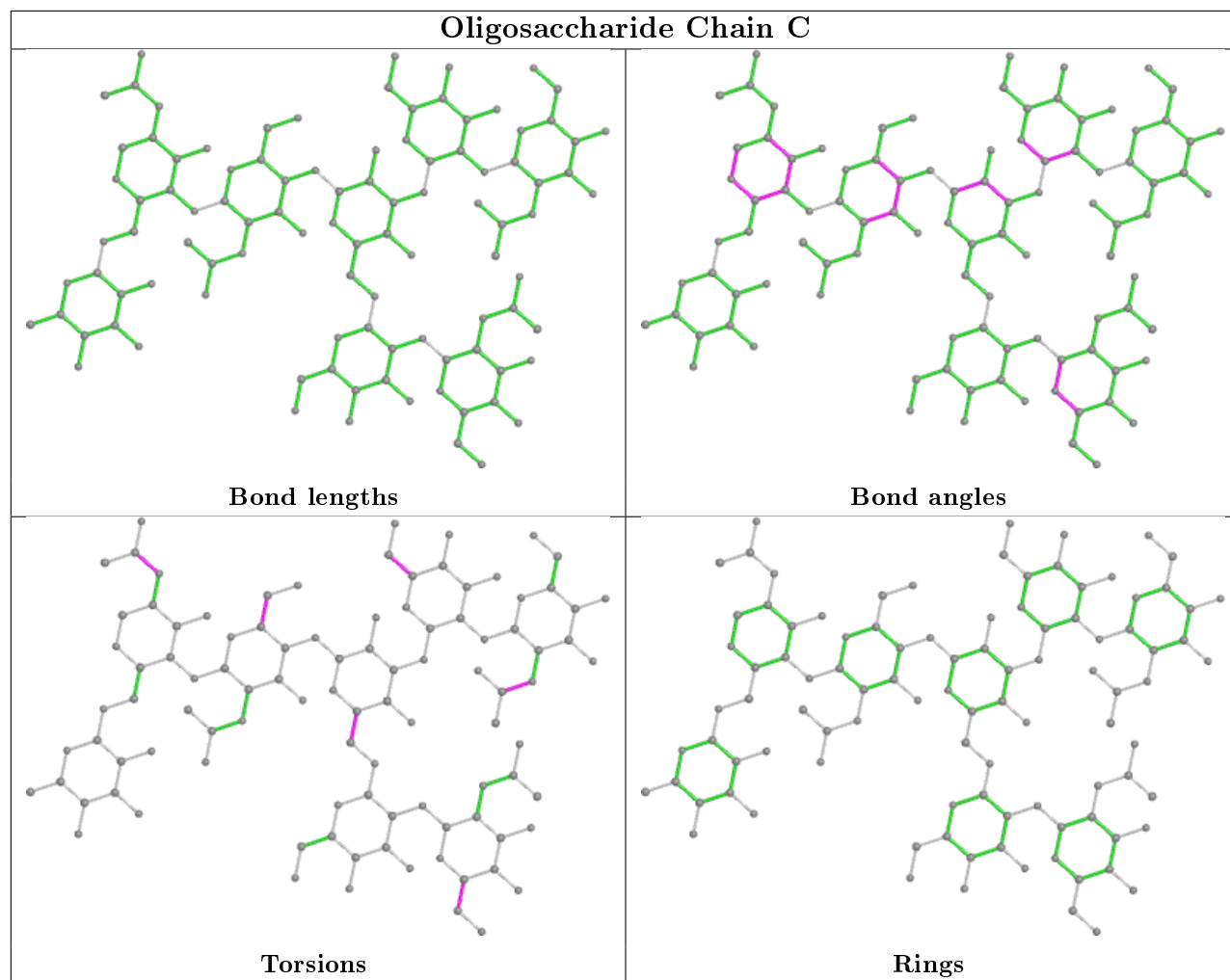
Mol	Chain	Res	Type	Atoms
2	C	5	NAG	O7-C7-N2-C2
2	D	7	NAG	C8-C7-N2-C2
2	D	7	NAG	O7-C7-N2-C2
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
2	C	4	MAN	O5-C5-C6-O6
2	C	4	MAN	C4-C5-C6-O6
2	D	4	MAN	C4-C5-C6-O6
2	D	7	NAG	O5-C5-C6-O6
2	C	3	BMA	O5-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	D	4	MAN	O5-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
2	C	7	NAG	O5-C5-C6-O6
2	D	2	NAG	O5-C5-C6-O6
2	C	3	BMA	C4-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	D	3	BMA	O5-C5-C6-O6

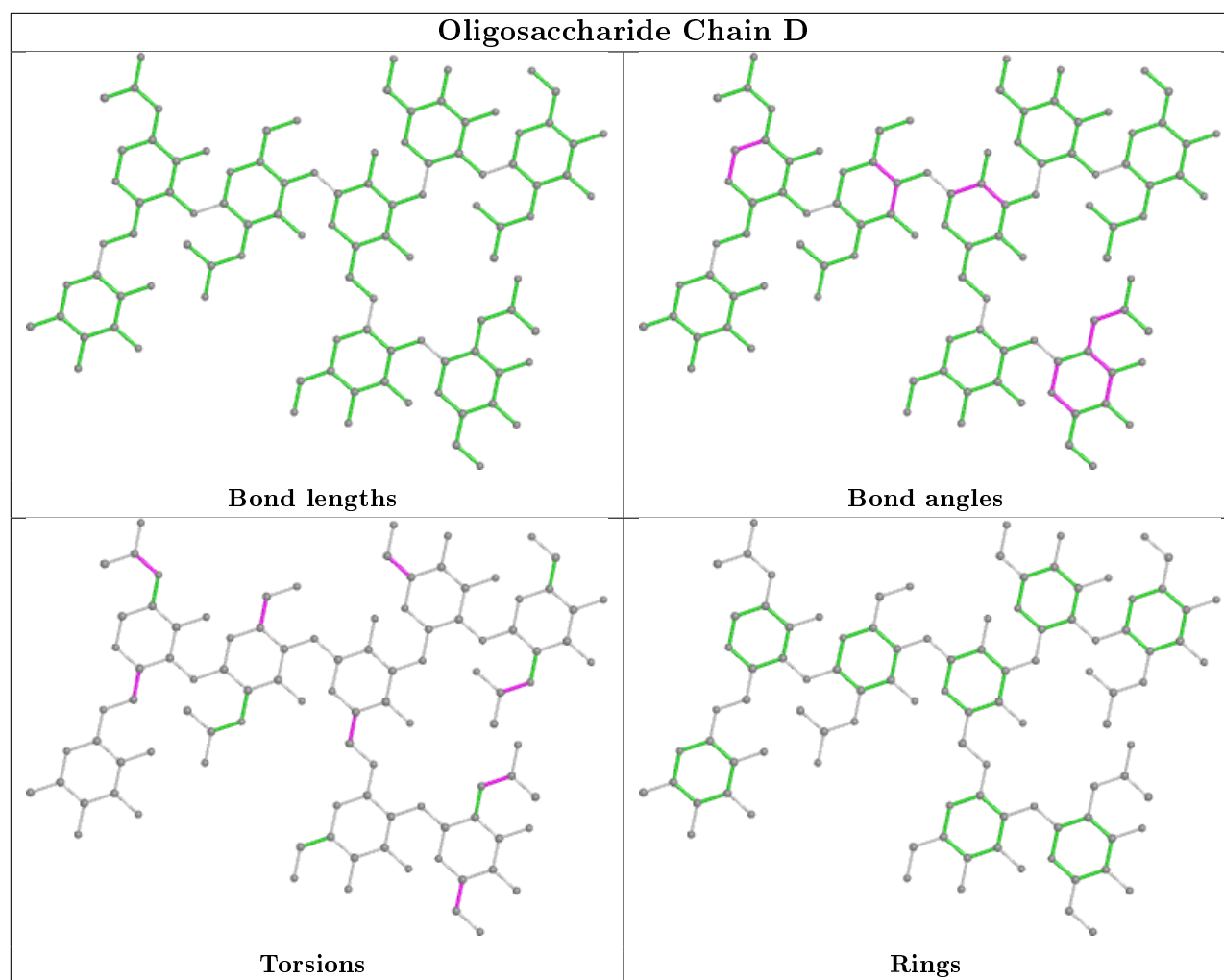
There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
2	D	7	NAG	1	0
2	C	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, 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	A	208/208 (100%)	0.32	14 (6%)	17 16	51, 104, 183, 213	0
1	B	208/208 (100%)	0.32	15 (7%)	15 13	53, 106, 183, 213	0
All	All	416/416 (100%)	0.32	29 (6%)	16 14	51, 105, 183, 213	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	300	TYR	5.6
1	B	300	TYR	5.3
1	A	310	HIS	3.2
1	B	266	VAL	3.1
1	B	333	GLU	2.9
1	B	296	TYR	2.9
1	B	329	PRO	2.8
1	A	407	TYR	2.8
1	A	329	PRO	2.7
1	B	366	THR	2.7
1	B	310	HIS	2.7
1	A	270	ASP	2.6
1	A	266	VAL	2.6
1	B	322	LYS	2.6
1	A	366	THR	2.5
1	A	261	CYS	2.4
1	B	407	TYR	2.3
1	B	328	LEU	2.3
1	A	364	SER	2.2
1	A	333	GLU	2.2
1	A	296	TYR	2.2
1	B	270	ASP	2.2
1	B	330	ALA	2.2
1	B	303	VAL	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	328	LEU	2.1
1	A	361	ASN	2.0
1	B	292	ARG	2.0
1	A	269	GLU	2.0
1	B	298	SER	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](#)

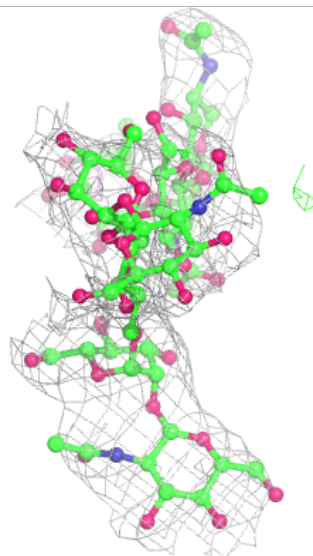
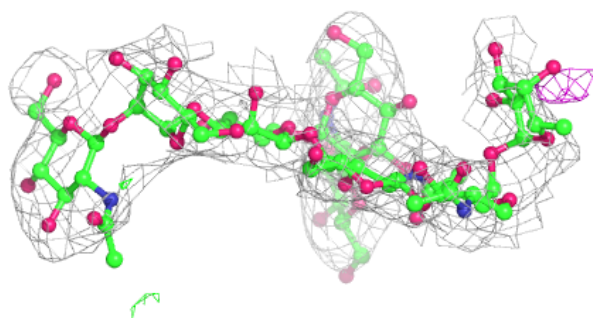
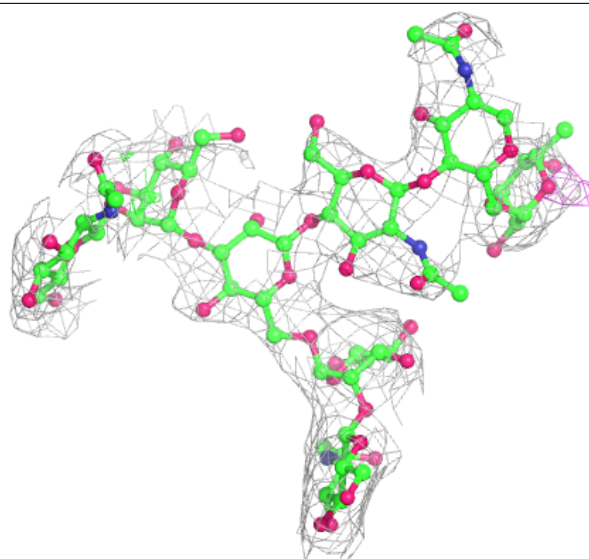
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

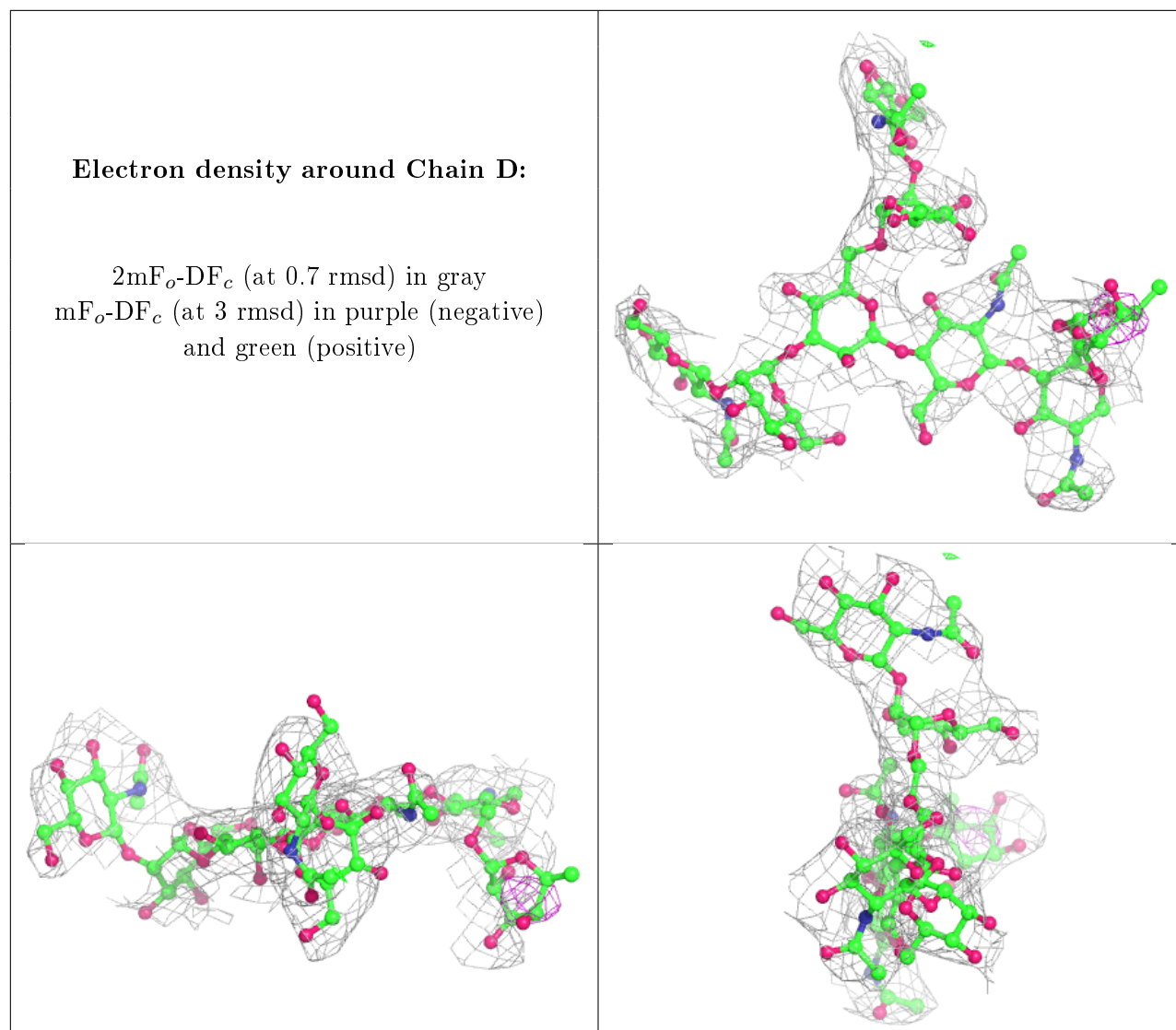
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	FUC	D	8	10/11	0.58	0.44	146,175,208,221	0
2	FUC	C	8	10/11	0.71	0.38	171,192,202,203	0
2	NAG	D	1	14/15	0.79	0.25	104,158,186,212	0
2	NAG	C	2	14/15	0.83	0.26	124,171,201,208	0
2	NAG	D	5	14/15	0.85	0.16	121,159,173,178	0
2	NAG	D	7	14/15	0.85	0.18	109,132,139,152	0
2	NAG	C	5	14/15	0.87	0.17	131,160,185,185	0
2	NAG	C	1	14/15	0.87	0.23	131,161,190,211	0
2	NAG	D	2	14/15	0.87	0.23	129,178,203,208	0
2	NAG	C	7	14/15	0.88	0.17	107,126,138,139	0
2	BMA	D	3	11/12	0.92	0.15	111,143,164,176	0
2	BMA	C	3	11/12	0.92	0.15	107,141,164,167	0
2	MAN	D	4	11/12	0.93	0.20	158,170,190,204	0
2	MAN	C	6	11/12	0.93	0.17	113,128,152,154	0
2	MAN	D	6	11/12	0.95	0.15	119,131,146,156	0
2	MAN	C	4	11/12	0.96	0.20	139,161,181,194	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)





## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.