



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 09:12 AM BST

PDB ID : 4IUG  
Title : Crystal structure of beta-galactosidase from *Aspergillus oryzae* in complex with galactose  
Authors : Maksimainen, M.; Rouvinen, J.  
Deposited on : 2013-01-21  
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 : 2.13.1  
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

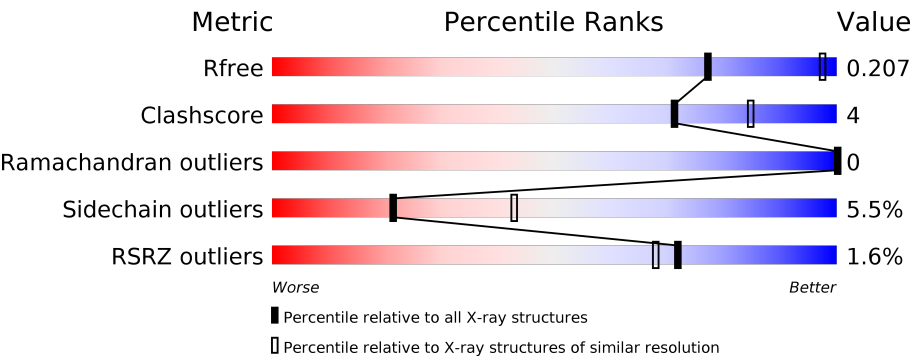
# 1 Overall quality at a glance i

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.



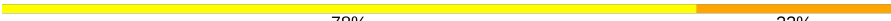
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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	1005	<div><div></div><div><div></div><div>84%</div><div>10%</div><div>5%</div></div></div>
2	B	5	<div><div></div><div><div></div><div>80%</div><div>20%</div></div></div>
3	C	7	<div><div></div><div><div></div><div>43%</div><div>29%</div><div>29%</div></div></div>
4	D	2	<div><div></div><div><div></div><div>100%</div></div></div>
4	E	2	<div><div></div><div><div></div><div>100%</div></div></div>
5	F	10	<div><div></div><div><div></div><div>20%</div><div>80%</div></div></div>

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Mol	Chain	Length	Quality of chain
6	G	9	 78% 22%

## 2 Entry composition [i](#)

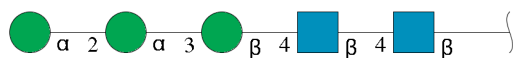
There are 10 unique types of molecules in this entry. The entry contains 8208 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Beta-galactosidase A.

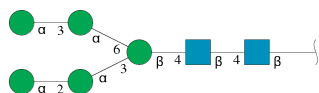
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	957	Total	C	N	O	P	S	0	0	0
			7441	4752	1227	1452	1	9			

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-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	B	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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.



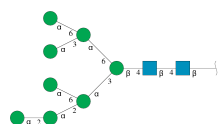
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



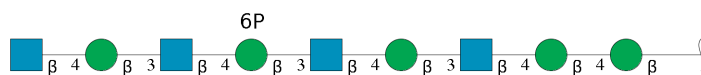
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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
5	F	10	Total	C	N	O	0	0	0
			116	64	2	50			

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

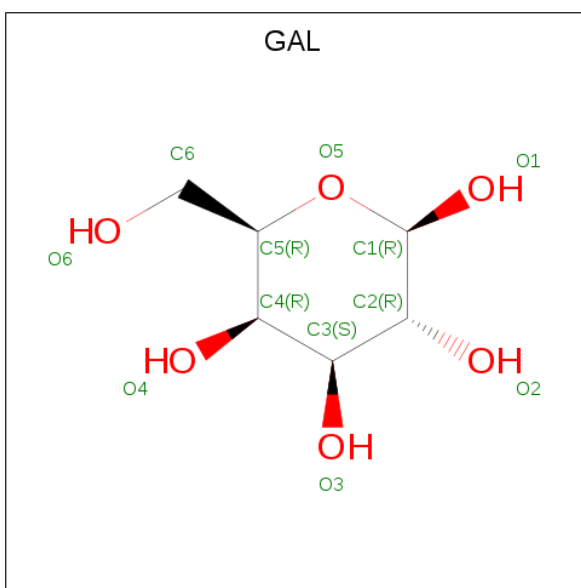


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	9	Total	C	N	O	P	0	0	0
			116	62	4	49	1			

- Molecule 7 is CADMIUM ION (three-letter code: CD) (formula: Cd).

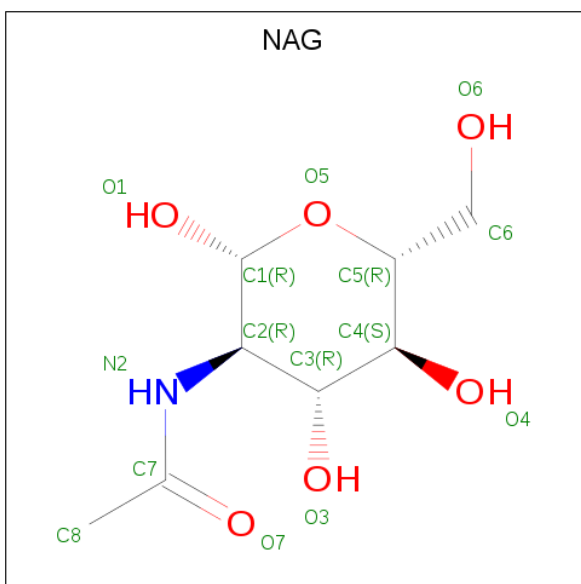
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	29	Total	Cd	0	0
			29	29		

- Molecule 8 is beta-D-galactopyranose (three-letter code: GAL) (formula:  $C_6H_{12}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			14	8	1	5		

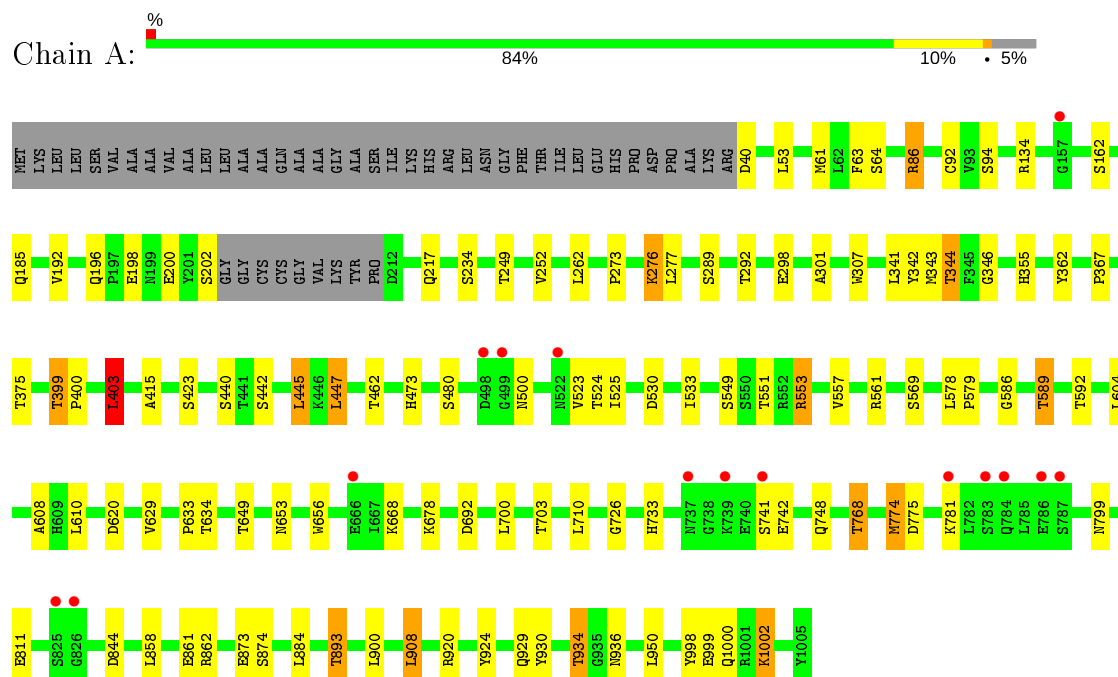
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	280	Total 280	O 280	0	0

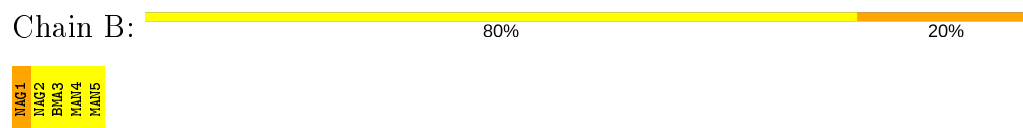
### 3 Residue-property plots

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.

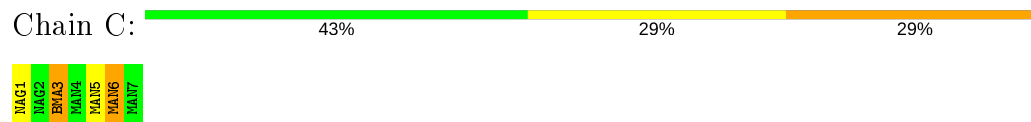
- Molecule 1: Beta-galactosidase A



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



- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[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





- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%

NAG1  
NAG2

- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%


NAG1  
NAG2

- Molecule 5: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]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 F:  20% 80%

NAG1  
NAG2  
MAN3  
MAN4  
MAN5  
MAN6  
MAN7  
MAN8  
MAN9  
MAN10

- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-6-O-phosphono-beta-D-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-beta-D-mannopyranose-(1-4)-beta-D-mannopyranose

Chain G:  78% 22%

MAN1  
MAN2  
MAN3  
MAN4  
MAN5  
MAN6  
MAN7  
MAN8  
MAN9

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	146.38Å 146.38Å 136.33Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.91 – 2.60 47.91 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.91-2.60) 99.9 (47.91-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.180 , 0.214 0.174 , 0.207	Depositor DCC
$R_{free}$ test set	2608 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.5	Xtriage
Anisotropy	0.091	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 34.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8208	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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, NAG, SEP, CD, GAL, M6D, 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	0.44	0/7640	0.59	1/10408 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	403	LEU	CA-CB-CG	6.28	129.75	115.30

There are no chirality outliers.

There are no planarity outliers.

### 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	A	7441	0	7109	52	0
2	B	61	0	52	1	0
3	C	83	0	70	1	0
4	D	28	0	25	0	0
4	E	28	0	25	0	0
5	F	116	0	97	0	0
6	G	116	0	93	1	0
7	A	29	0	0	0	0
8	A	12	0	12	2	0
9	A	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	A	280	0	0	1	0
All	All	8208	0	7496	54	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (54) 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:A:134:ARG:NH2	1:A:298:GLU:OE2	2.20	0.70
1:A:589:THR:HG22	1:A:592:THR:H	1.61	0.67
1:A:861:GLU:OE2	1:A:924:TYR:OH	2.14	0.65
1:A:298:GLU:OE1	8:A:1130:GAL:H1	1.95	0.65
1:A:134:ARG:HG2	1:A:196:GLN:HB3	1.85	0.58
1:A:200:GLU:OE2	8:A:1130:GAL:O1	2.24	0.54
1:A:579:PRO:HD2	1:A:608:ALA:O	2.08	0.53
1:A:742:GLU:HG2	1:A:781:LYS:HD2	1.90	0.53
1:A:86:ARG:NH2	1:A:586:GLY:O	2.42	0.52
1:A:774:MET:H	1:A:774:MET:CE	2.23	0.52
1:A:94:SER:OG	1:A:134:ARG:HD2	2.10	0.51
1:A:64:SER:HB2	1:A:92:CYS:HB3	1.93	0.51
1:A:604:LEU:HB3	1:A:620:ASP:HB2	1.94	0.49
1:A:341:LEU:HB2	1:A:344:THR:HG22	1.94	0.49
1:A:273:PRO:HB2	1:A:276:LYS:HD3	1.95	0.49
1:A:445:LEU:HD21	1:A:473:HIS:CD2	2.47	0.48
1:A:442:SER:HB3	1:A:462:THR:HG21	1.96	0.48
1:A:403:LEU:HD13	1:A:415:ALA:HB1	1.96	0.47
1:A:768:THR:HG23	1:A:936:ASN:ND2	2.29	0.47
1:A:445:LEU:HG	1:A:447:LEU:HD13	1.97	0.46
1:A:523:VAL:HG22	1:A:557:VAL:HG22	1.98	0.46
1:A:858:LEU:O	1:A:862:ARG:HG3	2.15	0.45
1:A:301:ALA:HB2	1:A:341:LEU:HB3	1.97	0.45
3:C:3:BMA:H61	3:C:6:MAN:H2	1.72	0.45
1:A:307:TRP:CZ3	1:A:934:THR:HG23	2.52	0.45
1:A:610:LEU:HD22	1:A:633:PRO:HG2	1.99	0.45
1:A:998:TYR:O	1:A:999:GLU:HG3	2.16	0.44
1:A:185:GLN:HA	1:A:192:VAL:HB	1.99	0.44
1:A:344:THR:HA	1:A:367:PRO:HD2	2.00	0.44
1:A:726:GLY:O	1:A:799:ASN:HB3	2.15	0.44
1:A:86:ARG:HD2	10:A:3223:HOH:O	2.17	0.44
1:A:678:LYS:HB2	1:A:893:THR:HG22	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:TYR:HA	1:A:343:MET:HA	1.90	0.43
1:A:692:ASP:OD2	1:A:733:HIS:NE2	2.47	0.43
1:A:561:ARG:NH1	1:A:653:ASN:HB3	2.34	0.43
1:A:629:VAL:HB	1:A:656:TRP:HB2	2.01	0.43
1:A:748:GLN:OE1	1:A:775:ASP:HB3	2.18	0.43
1:A:289:SER:HG	1:A:292:THR:HG1	1.67	0.43
1:A:920:ARG:HG2	1:A:934:THR:HB	2.00	0.43
1:A:549:SER:HB3	1:A:553:ARG:NH2	2.34	0.42
1:A:399:THR:HA	1:A:400:PRO:HD3	1.76	0.42
1:A:217:GLN:HB2	1:A:249:THR:HG23	2.01	0.42
6:G:6:M6D:H6A	6:G:7:NAG:C1	2.50	0.42
1:A:1002:LYS:HB3	1:A:1002:LYS:HE3	1.78	0.42
1:A:908:LEU:HD23	1:A:950:LEU:HD13	2.01	0.42
1:A:500:ASN:OD1	1:A:500:ASN:N	2.53	0.41
1:A:375:THR:HG21	2:B:1:NAG:H82	2.00	0.41
1:A:774:MET:H	1:A:774:MET:HE3	1.86	0.41
1:A:533:ILE:HD11	1:A:553:ARG:HG2	2.02	0.41
1:A:703:THR:HB	1:A:710:LEU:HD21	2.03	0.41
1:A:262:LEU:HD23	1:A:262:LEU:HA	1.83	0.40
1:A:346:GLY:HA3	1:A:362:TYR:O	2.22	0.40
1:A:525:ILE:HD12	1:A:530:ASP:HB3	2.02	0.40
1:A:234:SER:HB3	1:A:252:VAL:HG21	2.03	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	952/1005 (95%)	907 (95%)	45 (5%)	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	794/828 (96%)	750 (94%)	44 (6%)	21	43

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ASP
1	A	53	LEU
1	A	61	MET
1	A	63	PHE
1	A	86	ARG
1	A	162	SER
1	A	198	GLU
1	A	202	SER
1	A	276	LYS
1	A	277	LEU
1	A	344	THR
1	A	355	HIS
1	A	399	THR
1	A	403	LEU
1	A	423	SER
1	A	440	SER
1	A	445	LEU
1	A	447	LEU
1	A	480	SER
1	A	524	THR
1	A	551	THR
1	A	553	ARG
1	A	578	LEU
1	A	589	THR
1	A	634	THR
1	A	649	THR
1	A	668	LYS
1	A	700	LEU
1	A	741	SER
1	A	768	THR

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Mol	Chain	Res	Type
1	A	774	MET
1	A	811	GLU
1	A	844	ASP
1	A	873	GLU
1	A	874	SER
1	A	884	LEU
1	A	893	THR
1	A	900	LEU
1	A	908	LEU
1	A	929	GLN
1	A	930	TYR
1	A	934	THR
1	A	1000	GLN
1	A	1002	LYS

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 ⓘ

1 non-standard protein/DNA/RNA residue 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	$\# Z  > 2$
1	SEP	A	569	1	8,9,10	1.87	3 (37%)	8,12,14	2.21	2 (25%)

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
1	SEP	A	569	1	-	4/5/8/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	569	SEP	P-O1P	3.43	1.61	1.50
1	A	569	SEP	P-OG	2.35	1.67	1.60
1	A	569	SEP	P-O3P	2.10	1.62	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	569	SEP	OG-CB-CA	5.36	113.36	108.14
1	A	569	SEP	O3P-P-OG	2.08	112.27	106.73

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	569	SEP	CA-CB-OG-P
1	A	569	SEP	CB-OG-P-O1P
1	A	569	SEP	CB-OG-P-O2P
1	A	569	SEP	CB-OG-P-O3P

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

35 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	B	1	1,2	14,14,15	0.72	0	17,19,21	1.53	2 (11%)



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	B	2	2	14,14,15	0.80	0	17,19,21	1.69	1 (5%)
2	BMA	B	3	2	11,11,12	2.20	4 (36%)	15,15,17	1.68	3 (20%)
2	MAN	B	4	2	11,11,12	0.73	0	15,15,17	1.25	2 (13%)
2	MAN	B	5	2	11,11,12	0.71	0	15,15,17	1.46	2 (13%)
3	NAG	C	1	1,3	14,14,15	0.59	0	17,19,21	1.28	3 (17%)
3	NAG	C	2	3	14,14,15	0.59	0	17,19,21	0.71	0
3	BMA	C	3	3	11,11,12	2.16	3 (27%)	15,15,17	2.63	9 (60%)
3	MAN	C	4	3	11,11,12	0.77	0	15,15,17	0.97	0
3	MAN	C	5	3	11,11,12	0.56	0	15,15,17	1.59	2 (13%)
3	MAN	C	6	3	11,11,12	0.66	0	15,15,17	1.16	2 (13%)
3	MAN	C	7	3	11,11,12	0.62	0	15,15,17	0.93	0
4	NAG	D	1	1,4	14,14,15	0.56	0	17,19,21	1.08	1 (5%)
4	NAG	D	2	4	14,14,15	0.52	0	17,19,21	1.43	2 (11%)
4	NAG	E	1	1,4	14,14,15	0.48	0	17,19,21	1.06	2 (11%)
4	NAG	E	2	4	14,14,15	0.55	0	17,19,21	0.86	1 (5%)
5	NAG	F	1	1,5	14,14,15	0.75	0	17,19,21	1.00	0
5	MAN	F	10	5	11,11,12	0.98	1 (9%)	15,15,17	1.87	4 (26%)
5	NAG	F	2	5	14,14,15	0.71	0	17,19,21	0.79	0
5	BMA	F	3	5	11,11,12	2.28	4 (36%)	15,15,17	1.11	1 (6%)
5	MAN	F	4	5	11,11,12	0.58	0	15,15,17	1.43	3 (20%)
5	MAN	F	5	5	11,11,12	0.54	0	15,15,17	1.01	1 (6%)
5	MAN	F	6	5	11,11,12	0.69	0	15,15,17	1.18	2 (13%)
5	MAN	F	7	5	11,11,12	0.85	1 (9%)	15,15,17	1.05	1 (6%)
5	MAN	F	8	5	11,11,12	0.64	0	15,15,17	2.48	4 (26%)
5	MAN	F	9	5	11,11,12	0.42	0	15,15,17	1.49	2 (13%)
6	BMA	G	1	6	12,12,12	1.50	2 (16%)	17,17,17	1.60	5 (29%)
6	BMA	G	2	7,6	11,11,12	1.14	1 (9%)	15,15,17	1.99	3 (20%)
6	NAG	G	3	6	14,14,15	0.70	0	17,19,21	1.27	2 (11%)
6	BMA	G	4	6	11,11,12	0.98	1 (9%)	15,15,17	2.19	3 (20%)
6	NAG	G	5	6	14,14,15	0.68	0	17,19,21	0.98	1 (5%)
6	M6D	G	6	6	15,15,16	1.12	3 (20%)	22,22,24	0.96	1 (4%)
6	NAG	G	7	6	14,14,15	0.60	0	17,19,21	1.56	2 (11%)
6	BMA	G	8	7,6	11,11,12	1.34	2 (18%)	15,15,17	2.05	4 (26%)
6	NAG	G	9	6	14,14,15	0.83	0	17,19,21	1.37	4 (23%)

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	B	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
2	MAN	B	4	2	-	1/2/19/22	0/1/1/1
2	MAN	B	5	2	-	2/2/19/22	0/1/1/1
3	NAG	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	1/2/19/22	0/1/1/1
3	MAN	C	5	3	-	2/2/19/22	0/1/1/1
3	MAN	C	6	3	-	0/2/19/22	0/1/1/1
3	MAN	C	7	3	-	0/2/19/22	0/1/1/1
4	NAG	D	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	NAG	E	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
5	NAG	F	1	1,5	-	2/6/23/26	0/1/1/1
5	MAN	F	10	5	-	0/2/19/22	0/1/1/1
5	NAG	F	2	5	-	0/6/23/26	0/1/1/1
5	BMA	F	3	5	-	0/2/19/22	0/1/1/1
5	MAN	F	4	5	-	1/2/19/22	0/1/1/1
5	MAN	F	5	5	-	0/2/19/22	0/1/1/1
5	MAN	F	6	5	-	0/2/19/22	0/1/1/1
5	MAN	F	7	5	-	0/2/19/22	0/1/1/1
5	MAN	F	8	5	-	2/2/19/22	0/1/1/1
5	MAN	F	9	5	-	2/2/19/22	0/1/1/1
6	BMA	G	1	6	-	2/2/22/22	0/1/1/1
6	BMA	G	2	7,6	-	2/2/19/22	0/1/1/1
6	NAG	G	3	6	-	2/6/23/26	0/1/1/1
6	BMA	G	4	6	-	2/2/19/22	0/1/1/1
6	NAG	G	5	6	-	0/6/23/26	0/1/1/1
6	M6D	G	6	6	-	2/6/23/26	0/1/1/1
6	NAG	G	7	6	-	2/6/23/26	0/1/1/1
6	BMA	G	8	7,6	-	2/2/19/22	0/1/1/1
6	NAG	G	9	6	-	0/6/23/26	0/1/1/1

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	3	BMA	C4-C3	-4.52	1.40	1.52
5	F	3	BMA	C4-C3	-4.25	1.41	1.52
5	F	3	BMA	C2-C3	-4.13	1.46	1.52
2	B	3	BMA	C2-C3	-3.94	1.46	1.52
2	B	3	BMA	C4-C3	-3.87	1.42	1.52
6	G	1	BMA	C4-C3	-3.81	1.42	1.52
3	C	3	BMA	C2-C3	-3.71	1.47	1.52
2	B	3	BMA	O5-C1	-3.43	1.38	1.43
5	F	3	BMA	O5-C1	-3.11	1.38	1.43
5	F	10	MAN	C2-C3	2.93	1.56	1.52
6	G	8	BMA	C2-C3	2.68	1.56	1.52
6	G	6	M6D	O4-C4	-2.59	1.36	1.43
6	G	8	BMA	O5-C1	-2.47	1.39	1.43
5	F	3	BMA	O2-C2	-2.47	1.38	1.43
2	B	3	BMA	O2-C2	-2.36	1.38	1.43
6	G	2	BMA	O5-C1	-2.28	1.40	1.43
5	F	7	MAN	O5-C1	-2.24	1.40	1.43
6	G	6	M6D	C4-C5	-2.22	1.48	1.53
6	G	4	BMA	C2-C3	2.13	1.55	1.52
3	C	3	BMA	O5-C1	-2.09	1.40	1.43
6	G	1	BMA	O2-C2	-2.06	1.38	1.43
6	G	6	M6D	C4-C3	-2.04	1.47	1.52

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	8	MAN	C1-O5-C5	6.80	121.41	112.19
6	G	4	BMA	C1-C2-C3	6.39	117.52	109.67
3	C	3	BMA	C6-C5-C4	-5.91	99.16	113.00
2	B	2	NAG	C2-N2-C7	-5.66	114.85	122.90
6	G	2	BMA	C1-C2-C3	5.60	116.55	109.67
6	G	8	BMA	C1-C2-C3	5.58	116.52	109.67
2	B	1	NAG	C1-O5-C5	4.75	118.63	112.19
6	G	7	NAG	C2-N2-C7	-4.71	116.20	122.90
3	C	5	MAN	C1-O5-C5	-4.33	106.33	112.19
4	D	2	NAG	C2-N2-C7	-4.13	117.02	122.90
2	B	5	MAN	O5-C1-C2	-4.08	104.47	110.77
5	F	8	MAN	C6-C5-C4	-3.98	103.69	113.00
6	G	2	BMA	C2-C3-C4	3.79	117.45	110.89
5	F	10	MAN	O3-C3-C2	3.79	117.25	109.99
6	G	4	BMA	C2-C3-C4	3.72	117.34	110.89
4	D	2	NAG	C1-O5-C5	3.68	117.18	112.19
3	C	3	BMA	C3-C4-C5	3.55	116.56	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	10	MAN	O2-C2-C3	3.51	117.17	110.14
6	G	8	BMA	C2-C3-C4	3.41	116.80	110.89
6	G	7	NAG	C1-O5-C5	3.38	116.78	112.19
5	F	8	MAN	C3-C4-C5	3.35	116.21	110.24
5	F	9	MAN	C2-C3-C4	-3.32	105.15	110.89
6	G	6	M6D	C1-O5-C5	-3.25	107.79	112.19
6	G	3	NAG	O3-C3-C2	3.15	115.98	109.47
3	C	3	BMA	O3-C3-C4	-3.15	103.08	110.35
5	F	9	MAN	C1-C2-C3	-3.11	105.84	109.67
2	B	3	BMA	C1-C2-C3	3.04	113.40	109.67
6	G	8	BMA	C1-O5-C5	-2.97	108.17	112.19
3	C	1	NAG	O5-C5-C6	2.96	111.84	107.20
3	C	3	BMA	O5-C1-C2	2.95	115.32	110.77
2	B	3	BMA	O3-C3-C2	-2.92	104.40	109.99
5	F	4	MAN	O5-C5-C6	2.85	111.67	107.20
3	C	3	BMA	O3-C3-C2	-2.79	104.65	109.99
3	C	5	MAN	O5-C5-C6	2.76	111.53	107.20
5	F	4	MAN	O5-C1-C2	-2.75	106.52	110.77
6	G	9	NAG	C3-C4-C5	-2.70	105.42	110.24
2	B	3	BMA	O4-C4-C5	-2.69	102.61	109.30
6	G	1	BMA	C1-C2-C3	2.69	115.89	110.31
4	D	1	NAG	C1-O5-C5	2.64	115.77	112.19
6	G	1	BMA	O5-C5-C6	2.64	112.99	106.44
5	F	8	MAN	O5-C5-C4	2.62	117.20	110.83
3	C	6	MAN	C1-C2-C3	2.60	112.87	109.67
3	C	3	BMA	O6-C6-C5	2.60	120.21	111.29
3	C	3	BMA	O5-C5-C6	2.58	111.25	107.20
6	G	1	BMA	O5-C1-C2	2.57	114.86	110.28
2	B	4	MAN	C1-O5-C5	2.55	115.65	112.19
2	B	1	NAG	O5-C1-C2	-2.55	107.27	111.29
5	F	10	MAN	O5-C1-C2	-2.54	106.86	110.77
6	G	5	NAG	C2-N2-C7	-2.47	119.39	122.90
3	C	1	NAG	C6-C5-C4	-2.47	107.22	113.00
6	G	9	NAG	O5-C5-C6	2.47	111.08	107.20
5	F	5	MAN	O5-C1-C2	-2.42	107.04	110.77
5	F	6	MAN	O5-C5-C6	2.41	110.99	107.20
2	B	4	MAN	O2-C2-C1	2.40	114.05	109.15
5	F	3	BMA	C1-C2-C3	2.32	112.52	109.67
3	C	1	NAG	O5-C1-C2	-2.30	107.65	111.29
6	G	3	NAG	C2-N2-C7	-2.30	119.63	122.90
6	G	8	BMA	O6-C6-C5	-2.28	103.46	111.29
6	G	1	BMA	C1-O5-C5	-2.27	109.38	113.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	3	BMA	C1-C2-C3	2.26	112.44	109.67
6	G	9	NAG	C1-O5-C5	-2.25	109.14	112.19
5	F	10	MAN	O4-C4-C5	2.22	114.80	109.30
4	E	1	NAG	O5-C1-C2	-2.17	107.86	111.29
4	E	1	NAG	C2-N2-C7	-2.17	119.82	122.90
6	G	4	BMA	O5-C5-C6	2.15	110.57	107.20
5	F	6	MAN	O5-C1-C2	-2.14	107.47	110.77
5	F	7	MAN	O5-C1-C2	-2.13	107.49	110.77
3	C	6	MAN	O5-C1-C2	-2.12	107.50	110.77
2	B	5	MAN	O3-C3-C2	2.10	114.01	109.99
5	F	4	MAN	O2-C2-C3	-2.05	106.04	110.14
6	G	9	NAG	O3-C3-C2	2.04	113.69	109.47
3	C	3	BMA	O4-C4-C5	-2.03	104.26	109.30
6	G	2	BMA	O6-C6-C5	-2.02	104.35	111.29
4	E	2	NAG	C2-N2-C7	-2.02	120.03	122.90
6	G	1	BMA	C4-C3-C2	2.02	114.34	110.82

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	G	6	M6D	C4-C5-C6-O6
6	G	6	M6D	O5-C5-C6-O6
6	G	4	BMA	O5-C5-C6-O6
2	B	5	MAN	O5-C5-C6-O6
6	G	7	NAG	O5-C5-C6-O6
6	G	4	BMA	C4-C5-C6-O6
6	G	8	BMA	O5-C5-C6-O6
2	B	5	MAN	C4-C5-C6-O6
6	G	7	NAG	C4-C5-C6-O6
4	E	2	NAG	O5-C5-C6-O6
3	C	5	MAN	C4-C5-C6-O6
6	G	1	BMA	O5-C5-C6-O6
5	F	8	MAN	O5-C5-C6-O6
6	G	1	BMA	C4-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
6	G	8	BMA	C4-C5-C6-O6
5	F	8	MAN	C4-C5-C6-O6
3	C	5	MAN	O5-C5-C6-O6
6	G	2	BMA	O5-C5-C6-O6
5	F	9	MAN	O5-C5-C6-O6
5	F	9	MAN	C4-C5-C6-O6

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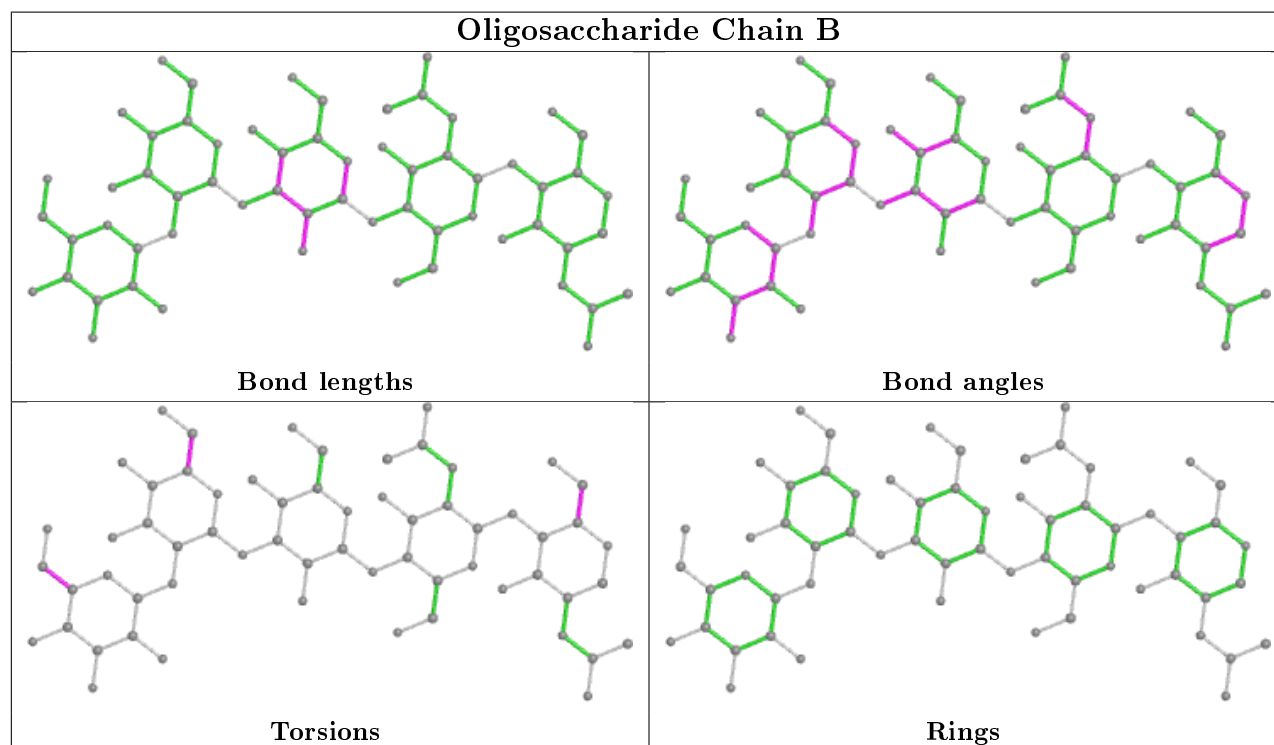
Mol	Chain	Res	Type	Atoms
6	G	3	NAG	C4-C5-C6-O6
5	F	4	MAN	O5-C5-C6-O6
6	G	2	BMA	C4-C5-C6-O6
3	C	4	MAN	O5-C5-C6-O6
6	G	3	NAG	O5-C5-C6-O6
5	F	1	NAG	O5-C5-C6-O6
2	B	4	MAN	O5-C5-C6-O6
5	F	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6

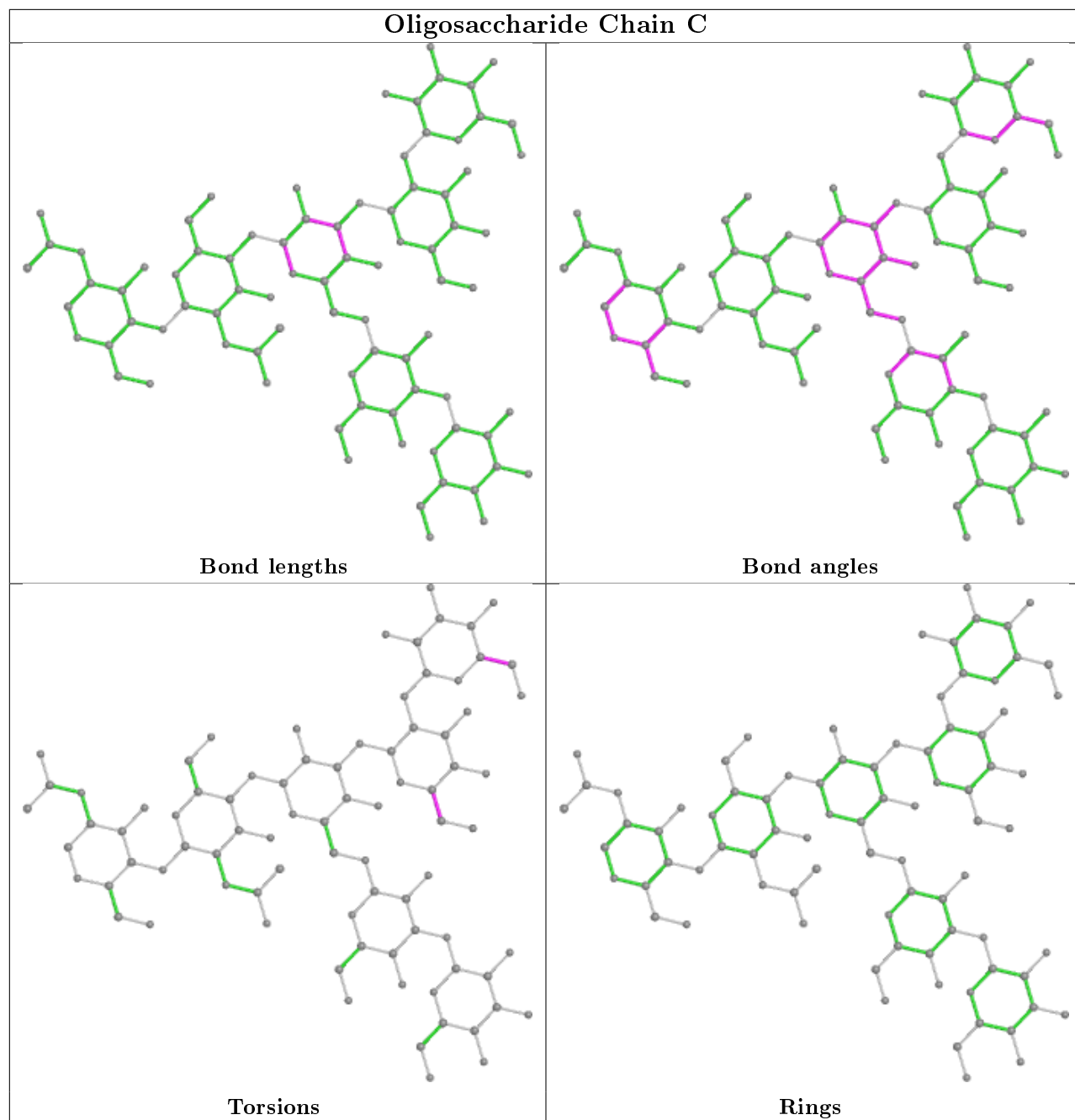
There are no ring outliers.

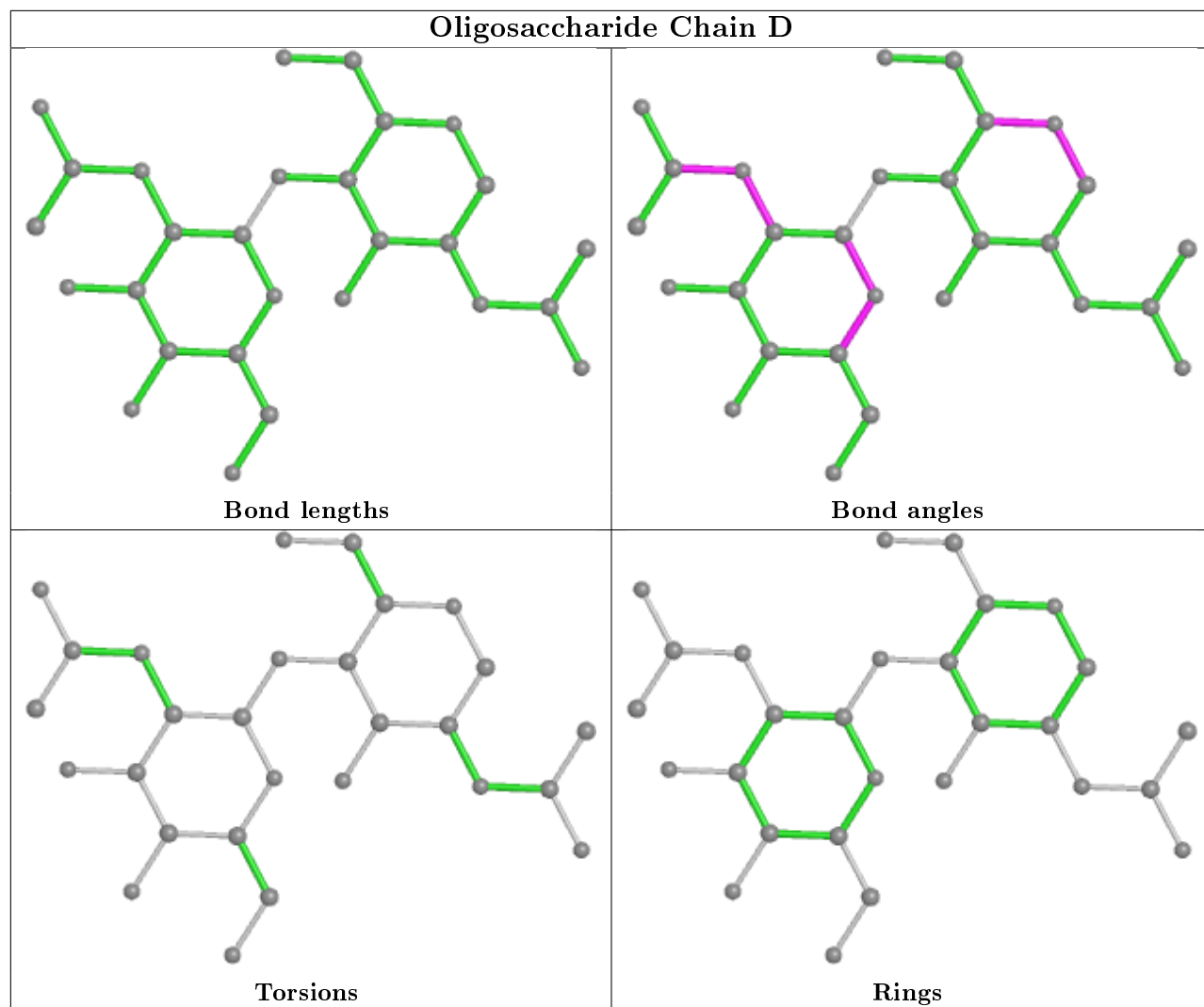
5 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	3	BMA	1	0
3	C	6	MAN	1	0
6	G	7	NAG	1	0
6	G	6	M6D	1	0
2	B	1	NAG	1	0

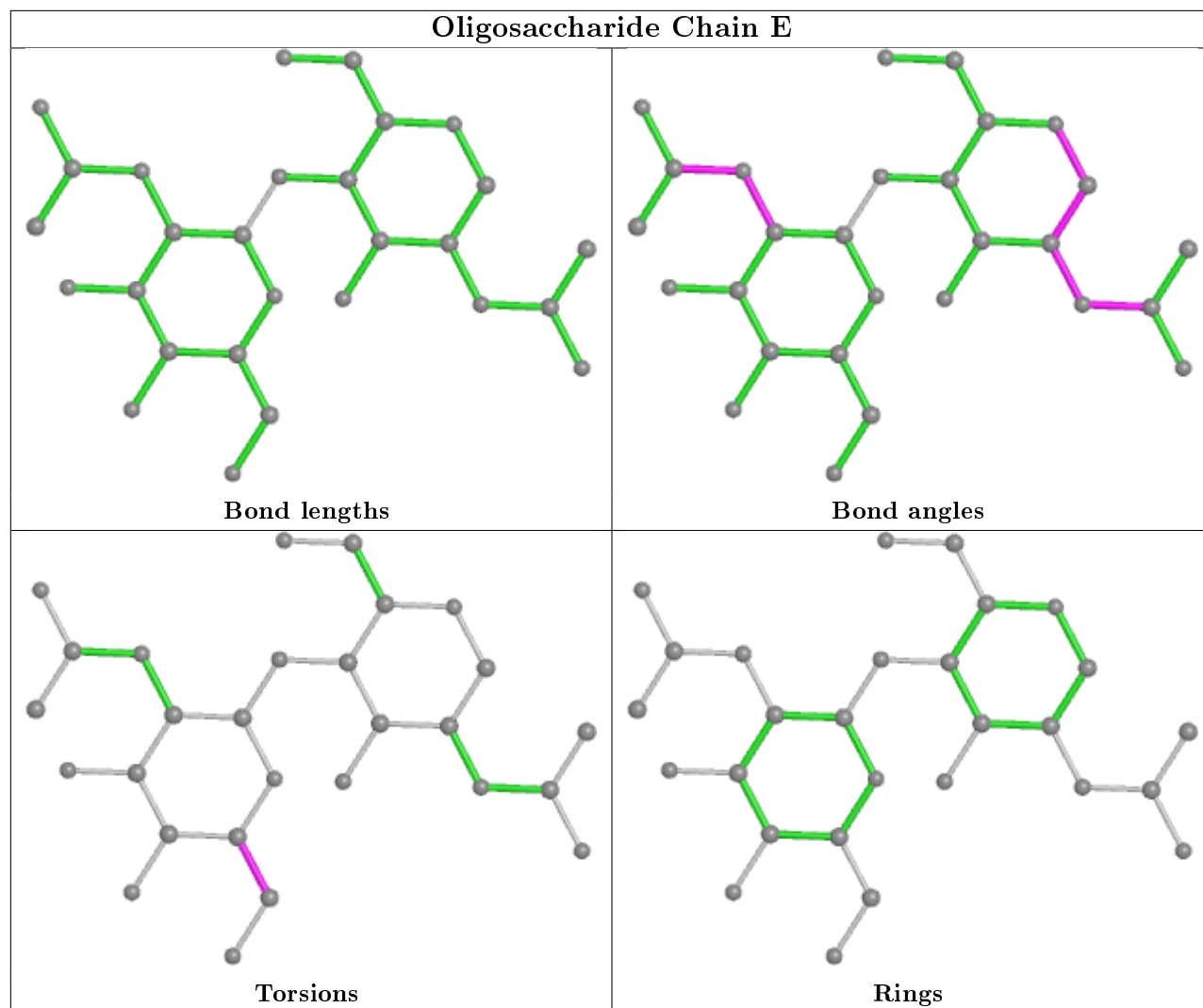
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

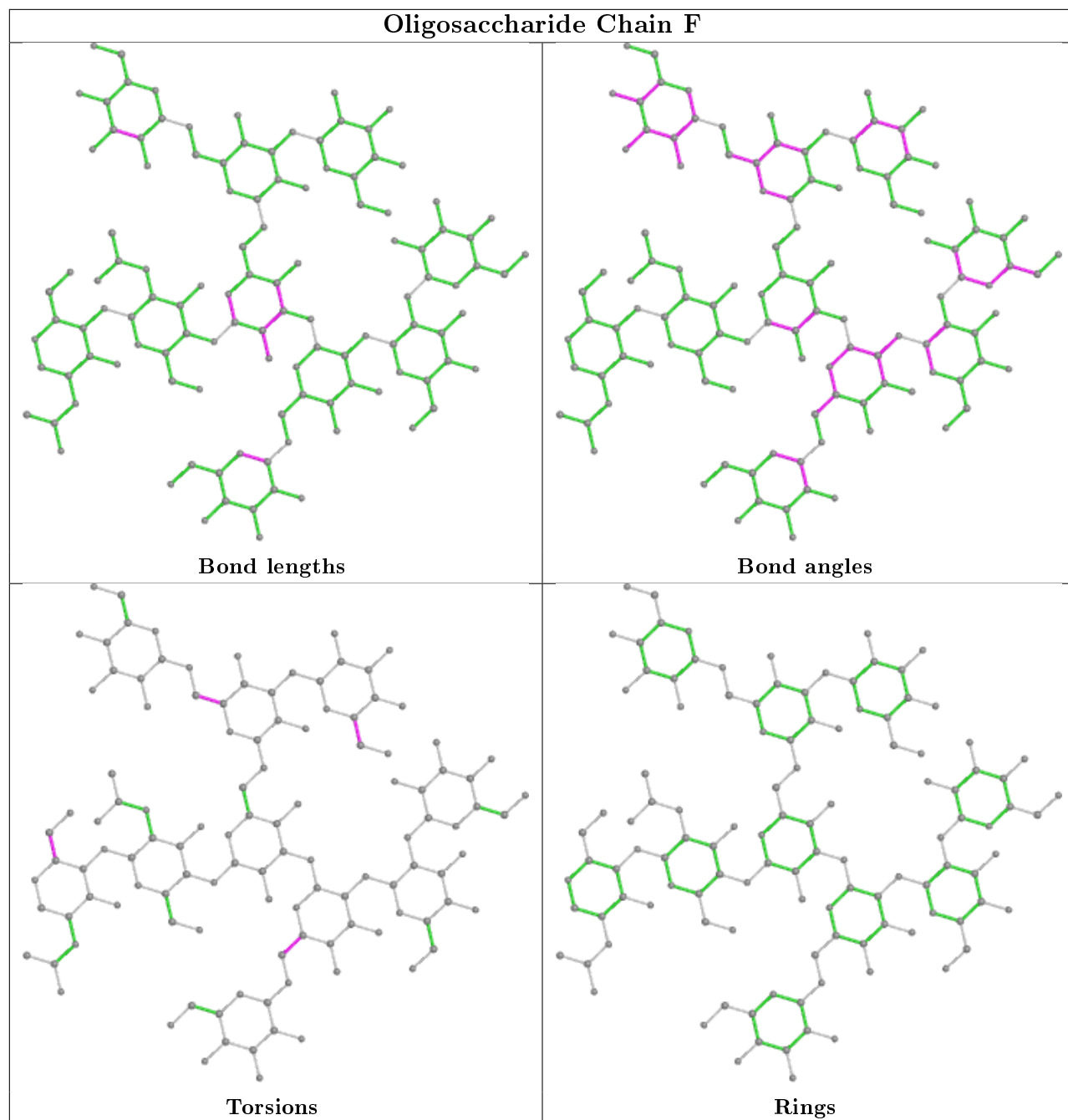


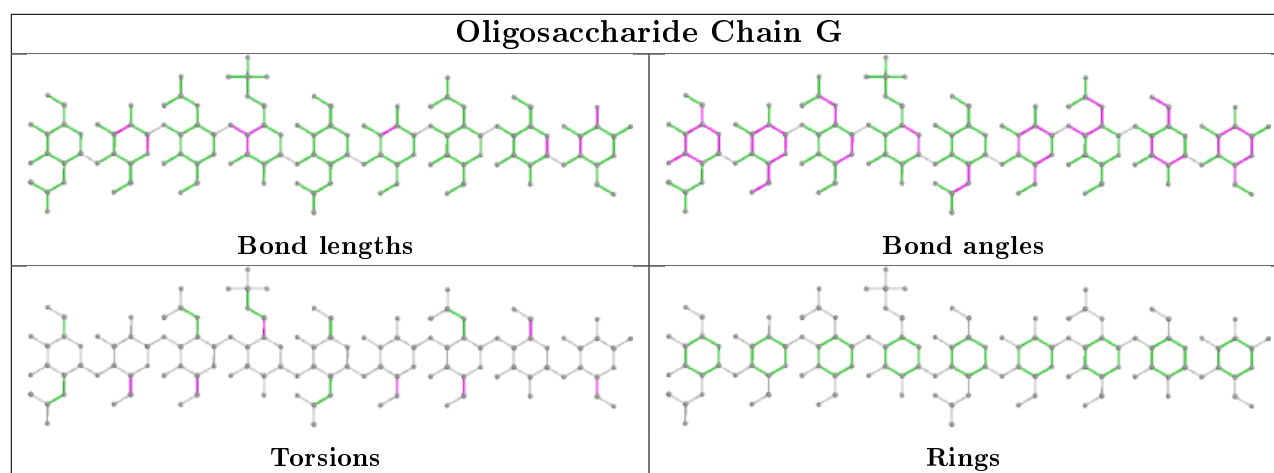












## 5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 29 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z  > 2$
9	NAG	A	1136	1	14,14,15	0.50	0	17,19,21	1.36	4 (23%)
8	GAL	A	1130	-	12,12,12	0.83	1 (8%)	17,17,17	1.05	1 (5%)

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
9	NAG	A	1136	1	-	2/6/23/26	0/1/1/1
8	GAL	A	1130	-	-	1/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1130	GAL	O2-C2	-2.16	1.37	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1136	NAG	C2-N2-C7	-3.09	118.50	122.90
8	A	1130	GAL	O5-C5-C4	-2.19	105.72	109.69
9	A	1136	NAG	O5-C1-C2	-2.15	107.90	111.29
9	A	1136	NAG	C1-O5-C5	2.15	115.10	112.19
9	A	1136	NAG	C3-C4-C5	-2.03	106.61	110.24

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	1136	NAG	C8-C7-N2-C2
9	A	1136	NAG	O7-C7-N2-C2
8	A	1130	GAL	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1130	GAL	2	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 [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	A	956/1005 (95%)	-0.40	15 (1%) 72 68	24, 32, 47, 64	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	498	ASP	4.7
1	A	499	GLY	3.3
1	A	739	LYS	3.3
1	A	781	LYS	2.9
1	A	787	SER	2.8
1	A	741	SER	2.6
1	A	737	ASN	2.5
1	A	826	GLY	2.4
1	A	786	GLU	2.4
1	A	666	GLU	2.3
1	A	784	GLN	2.2
1	A	783	SER	2.1
1	A	522	ASN	2.1
1	A	157	GLY	2.1
1	A	825	SER	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	A	569	10/11	0.93	0.13	32,34,39,41	0

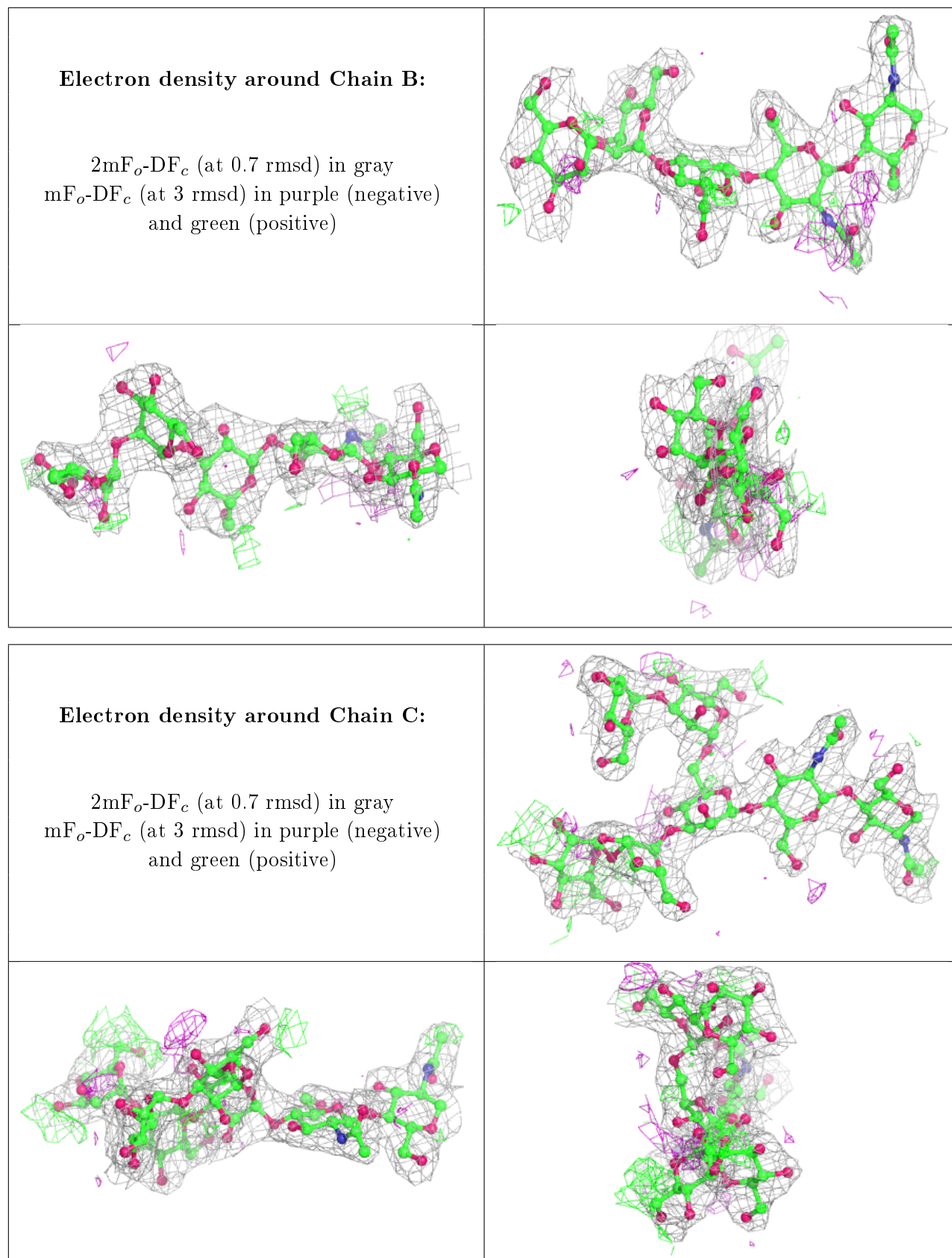
## 6.3 Carbohydrates ⓘ

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, 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
5	MAN	F	10	11/12	0.74	0.21	48,50,51,52	0
4	NAG	D	2	14/15	0.81	0.23	50,58,62,62	0
6	M6D	G	6	15/16	0.83	0.20	47,52,59,60	0
3	MAN	C	5	11/12	0.85	0.22	49,54,57,57	0
5	MAN	F	9	11/12	0.87	0.23	38,41,46,49	0
6	BMA	G	1	12/12	0.87	0.24	50,55,60,65	0
2	MAN	B	5	11/12	0.87	0.30	50,53,56,56	0
6	NAG	G	7	14/15	0.90	0.14	51,52,54,55	0
4	NAG	E	2	14/15	0.92	0.26	55,58,61,63	0
6	NAG	G	9	14/15	0.92	0.14	45,50,51,52	0
6	BMA	G	4	11/12	0.93	0.11	35,37,39,42	0
6	BMA	G	2	11/12	0.94	0.16	42,44,47,48	0
3	BMA	C	3	11/12	0.95	0.11	29,32,35,35	0
4	NAG	D	1	14/15	0.95	0.12	42,46,51,52	0
5	MAN	F	6	11/12	0.95	0.13	31,32,34,35	0
4	NAG	E	1	14/15	0.95	0.14	36,43,50,52	0
5	MAN	F	8	11/12	0.95	0.12	37,41,43,44	0
6	BMA	G	8	11/12	0.95	0.11	51,53,53,54	0
3	MAN	C	6	11/12	0.95	0.14	30,32,34,34	0
3	NAG	C	1	14/15	0.96	0.10	26,29,30,30	0
5	MAN	F	7	11/12	0.96	0.11	32,33,34,38	0
2	BMA	B	3	11/12	0.96	0.09	35,38,39,39	0
2	MAN	B	4	11/12	0.96	0.12	38,41,44,47	0
6	NAG	G	3	14/15	0.96	0.11	36,39,41,42	0
2	NAG	B	2	14/15	0.96	0.12	30,32,34,37	0
5	NAG	F	2	14/15	0.96	0.13	28,31,35,35	0
3	MAN	C	7	11/12	0.97	0.09	31,32,35,38	0
5	MAN	F	5	11/12	0.97	0.12	31,33,34,35	0
3	NAG	C	2	14/15	0.97	0.09	27,29,30,30	0
5	NAG	F	1	14/15	0.97	0.10	27,30,35,37	0
3	MAN	C	4	11/12	0.98	0.10	35,36,41,45	0
6	NAG	G	5	14/15	0.98	0.10	36,40,42,43	0
5	MAN	F	4	11/12	0.98	0.08	31,32,33,34	0
5	BMA	F	3	11/12	0.98	0.11	30,31,33,37	0
2	NAG	B	1	14/15	0.98	0.12	25,28,31,33	0

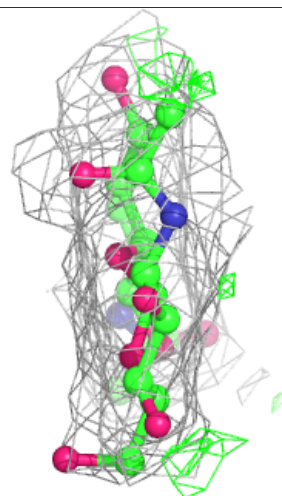
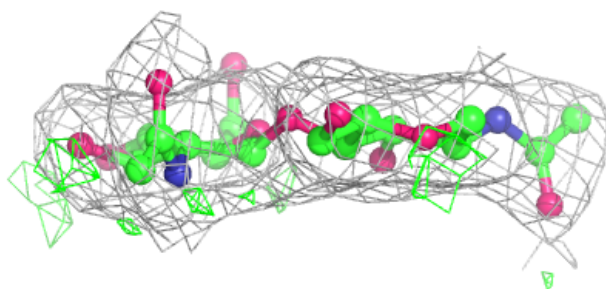
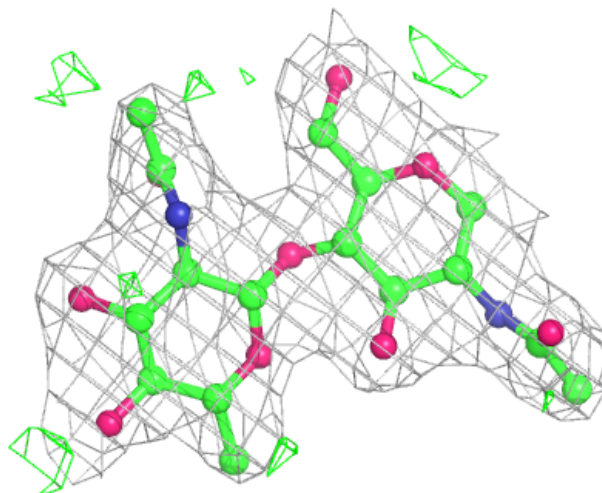
The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.



**Electron density around Chain D:**

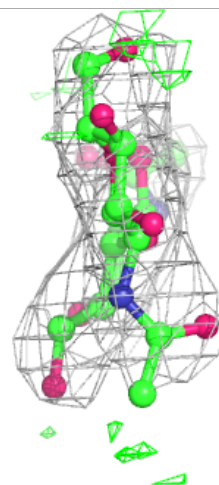
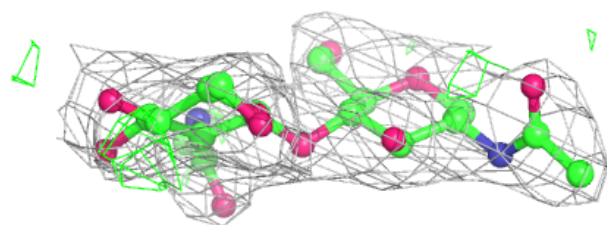
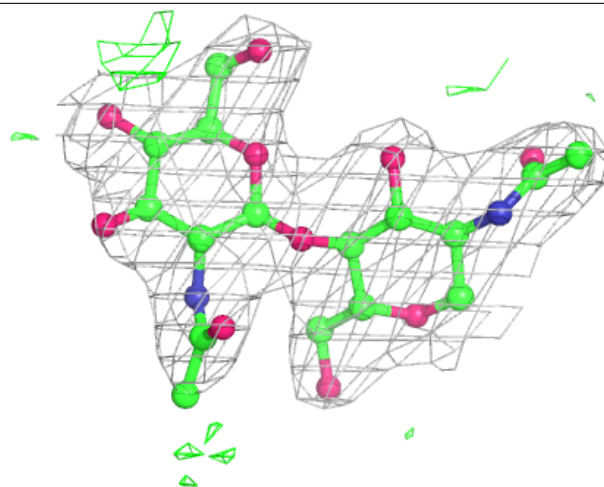
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





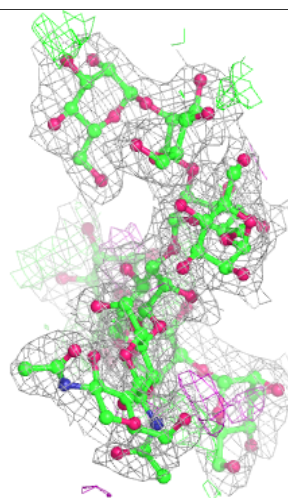
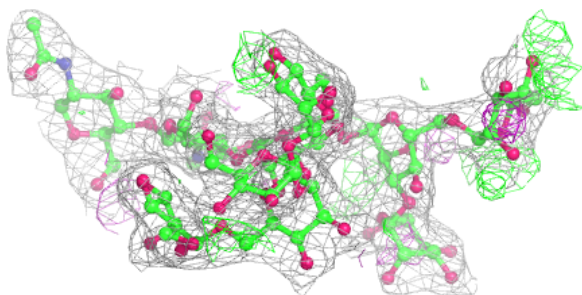
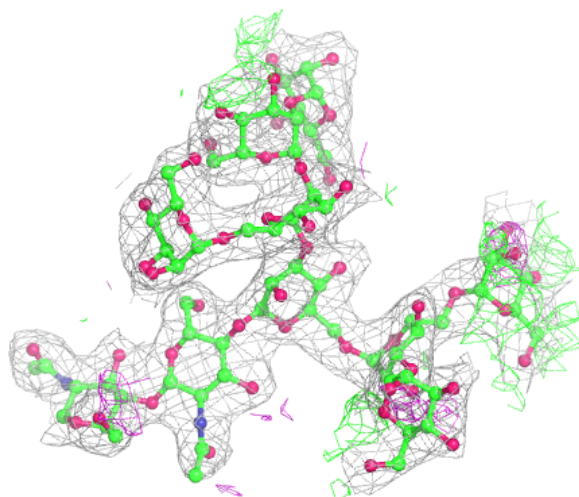
**Electron density around Chain E:**

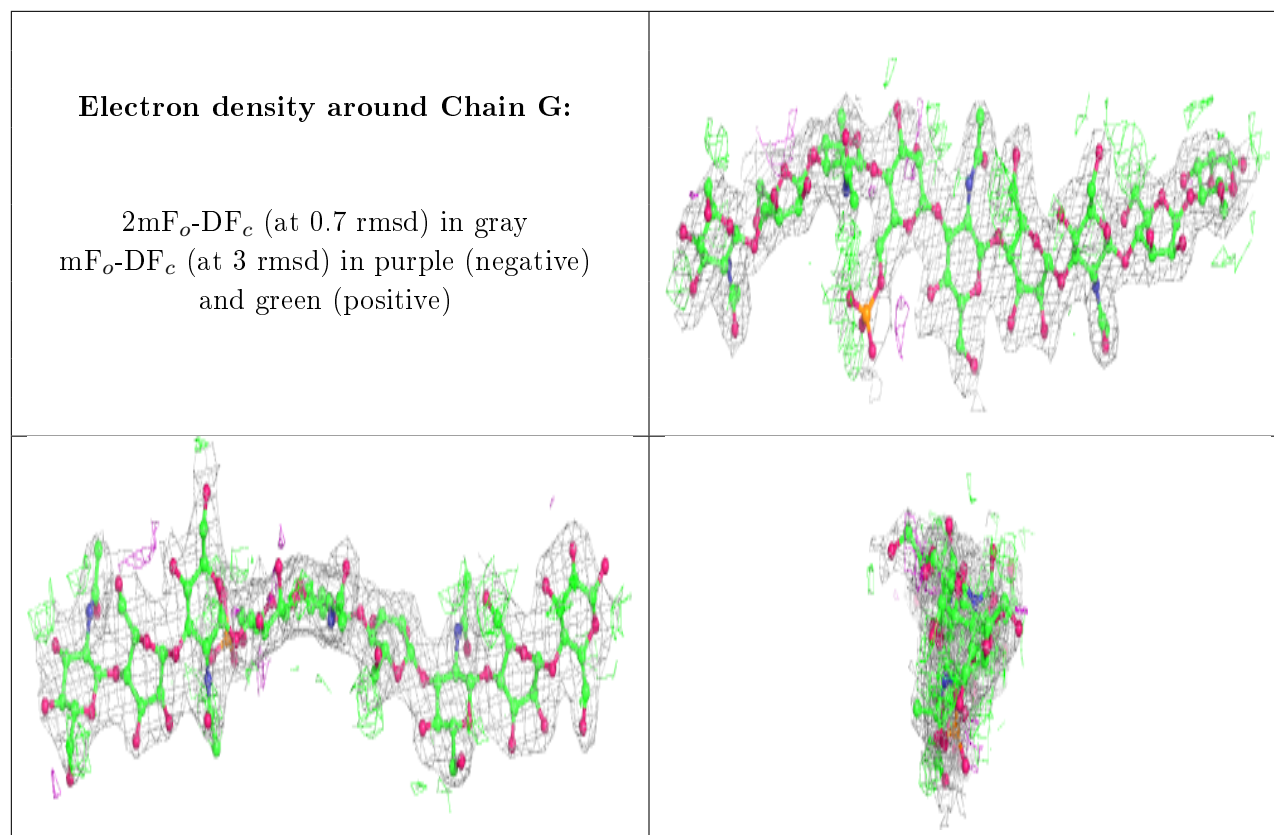
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around Chain F:**

$2mF_o-DF_c$  (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<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( $\text{\AA}^2$ )	Q<0.9
7	CD	A	1111	1/1	0.79	0.26	108,108,108,108	0
9	NAG	A	1136	14/15	0.85	0.34	42,47,50,50	0
8	GAL	A	1130	12/12	0.87	0.20	27,30,34,35	0
7	CD	A	1117	1/1	0.87	0.17	119,119,119,119	0
7	CD	A	1118	1/1	0.88	0.08	110,110,110,110	0
7	CD	A	1127	1/1	0.88	0.19	113,113,113,113	0
7	CD	A	1116	1/1	0.90	0.17	113,113,113,113	0
7	CD	A	1121	1/1	0.91	0.13	104,104,104,104	0
7	CD	A	1129	1/1	0.91	0.06	108,108,108,108	0
7	CD	A	1101	1/1	0.92	0.17	104,104,104,104	0
7	CD	A	1119	1/1	0.93	0.06	88,88,88,88	0
7	CD	A	1113	1/1	0.95	0.09	94,94,94,94	0
7	CD	A	1112	1/1	0.95	0.09	96,96,96,96	0
7	CD	A	1114	1/1	0.95	0.09	84,84,84,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
7	CD	A	1123	1/1	0.96	0.16	105,105,105,105	0
7	CD	A	1126	1/1	0.96	0.15	110,110,110,110	0
7	CD	A	1109	1/1	0.96	0.14	95,95,95,95	0
7	CD	A	1122	1/1	0.97	0.08	95,95,95,95	0
7	CD	A	1107	1/1	0.97	0.05	97,97,97,97	0
7	CD	A	1120	1/1	0.98	0.07	98,98,98,98	0
7	CD	A	1125	1/1	0.98	0.03	89,89,89,89	0
7	CD	A	1115	1/1	0.98	0.03	78,78,78,78	0
7	CD	A	1110	1/1	0.98	0.05	91,91,91,91	0
7	CD	A	1106	1/1	0.98	0.03	85,85,85,85	0
7	CD	A	1124	1/1	0.98	0.12	91,91,91,91	0
7	CD	A	1103	1/1	0.99	0.06	47,47,47,47	0
7	CD	A	1102	1/1	0.99	0.08	49,49,49,49	0
7	CD	A	1108	1/1	0.99	0.06	70,70,70,70	0
7	CD	A	1128	1/1	0.99	0.06	73,73,73,73	0
7	CD	A	1104	1/1	1.00	0.10	42,42,42,42	0
7	CD	A	1105	1/1	1.00	0.11	42,42,42,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.