



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 04:57 AM BST

PDB ID : 2C6G  
Title : Membrane-bound glutamate carboxypeptidase II (GCPII) with bound glutamate  
Authors : Mesters, J.R.; Barinka, C.; Li, W.; Tsukamoto, T.; Majer, P.; Slusher, B.S.; Konvalinka, J.; Hilgenfeld, R.  
Deposited on : 2005-11-09  
Resolution : 2.20 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

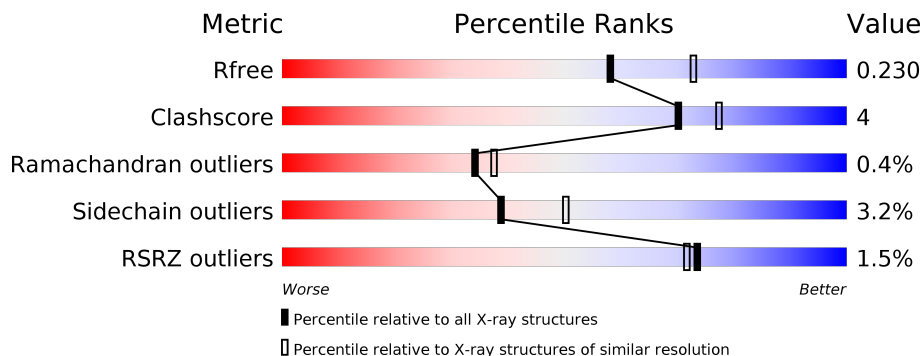
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	707	 83% 11% . .
2	B	2	 100%
2	C	2	 100%
3	D	4	 75% 25%

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
8	NAG	A	1759	X	-	-	-

## 2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 5571 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 GLUTAMATE CARBOXYPEPTIDASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	679	5266	3394	872	983	17	0	0	0

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



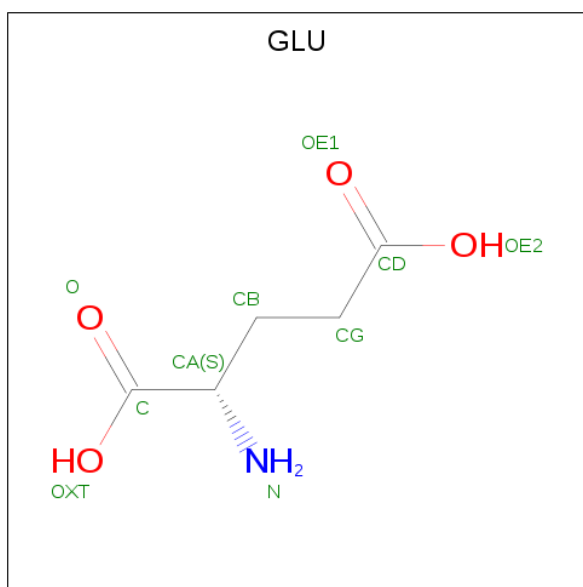
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0
2	C	2	28	16	2	10	0	0	0

- Molecule 3 is an oligosaccharide called 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
			Total	C	N	O			
3	D	4	50	28	2	20	0	0	0

- Molecule 4 is GLUTAMIC ACID (three-letter code: GLU) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	10	5	1	4	0	0

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
5	A	2	2	2	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
6	A	1	1	1	0	0

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
7	A	1	1	1	0	0

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

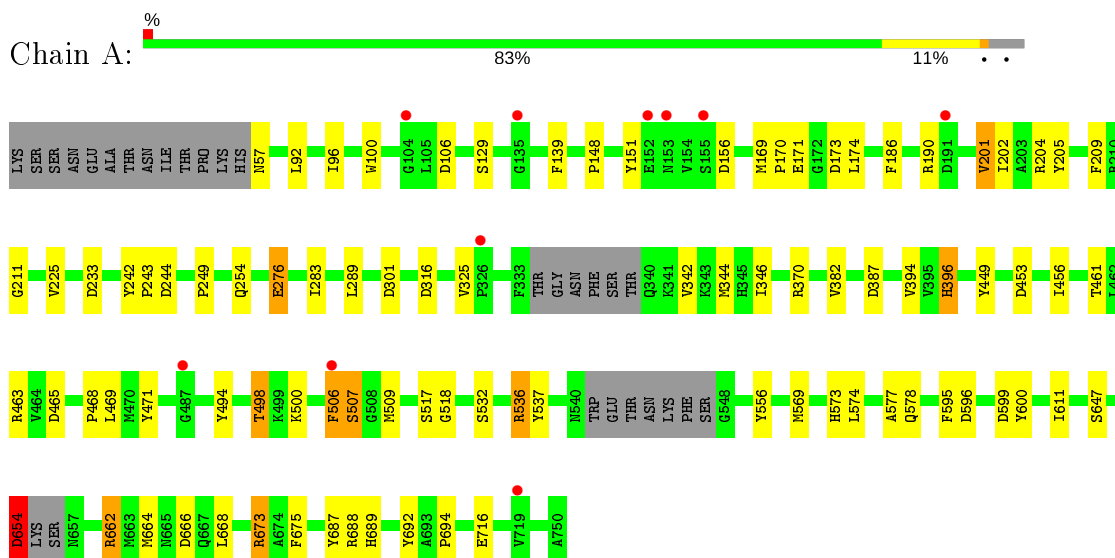
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	143	143	143	0	0

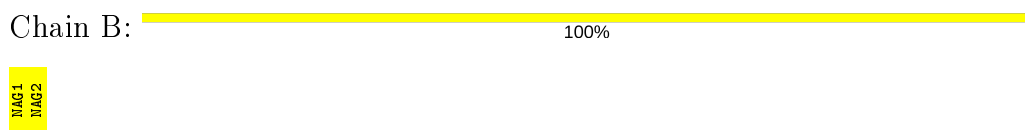
### 3 Residue-property plots

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.

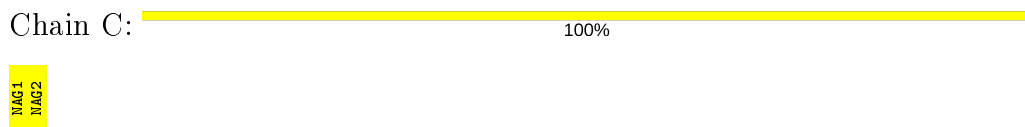
- Molecule 1: GLUTAMATE CARBOXYPEPTIDASE II



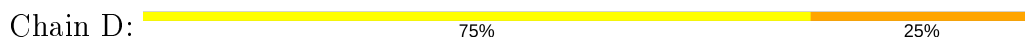
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



- Molecule 3: 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



MAC1  
MAC2  
BMA3  
MAT4



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.44Å 130.43Å 159.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.20 47.25 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.6 (100.00-2.20) 95.6 (47.25-2.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.186 , 0.228 0.193 , 0.230	Depositor DCC
$R_{free}$ test set	1324 reflections (2.55%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.9	Xtrriage
Anisotropy	0.032	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 34.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5571	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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: ZN, BMA, NAG, CL, CA, 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	0.94	0/5412	0.95	21/7354 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	662	ARG	NE-CZ-NH1	9.72	125.16	120.30
1	A	387	ASP	CB-CG-OD2	8.65	126.08	118.30
1	A	599	ASP	CB-CG-OD2	8.29	125.76	118.30
1	A	662	ARG	NE-CZ-NH2	-8.27	116.16	120.30
1	A	106	ASP	CB-CG-OD2	7.90	125.41	118.30
1	A	654	ASP	CB-CG-OD2	7.27	124.84	118.30
1	A	244	ASP	CB-CG-OD2	6.83	124.44	118.30
1	A	370	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	A	173	ASP	CB-CG-OD2	6.09	123.78	118.30
1	A	370	ARG	NE-CZ-NH2	-5.99	117.31	120.30
1	A	301	ASP	CB-CG-OD2	5.98	123.68	118.30
1	A	688	ARG	NE-CZ-NH1	5.97	123.28	120.30
1	A	453	ASP	CB-CG-OD2	5.96	123.67	118.30
1	A	316	ASP	CB-CG-OD2	5.95	123.65	118.30
1	A	233	ASP	CB-CG-OD2	5.65	123.39	118.30
1	A	507	SER	N-CA-C	-5.64	95.77	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	673	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	A	596	ASP	CB-CG-OD2	5.54	123.28	118.30
1	A	202	ILE	N-CA-C	5.42	125.63	111.00
1	A	156	ASP	CB-CG-OD2	5.24	123.02	118.30
1	A	204	ARG	NE-CZ-NH1	5.06	122.83	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	VAL	Peptide
1	A	289	LEU	Peptide
1	A	346	ILE	Peptide
1	A	506	PHE	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5266	0	4957	38	1
2	B	28	0	25	0	0
2	C	28	0	25	0	0
3	D	50	0	43	0	1
4	A	10	0	5	0	0
5	A	2	0	0	0	0
6	A	1	0	0	0	0
7	A	1	0	0	0	0
8	A	42	0	39	0	0
9	A	143	0	0	2	0
All	All	5571	0	5094	38	1

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 (38) 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:569:MET:CE	1:A:569:MET:SD	2.05	1.42
1:A:494:TYR:O	1:A:498:THR:CG2	2.36	0.73
1:A:494:TYR:O	1:A:498:THR:HG22	1.92	0.69
1:A:100:TRP:HE1	1:A:396:HIS:HD2	1.43	0.65
1:A:654:ASP:N	1:A:654:ASP:OD1	2.35	0.59
1:A:666:ASP:OD2	9:A:2106:HOH:O	2.15	0.59
1:A:169:MET:HA	1:A:344:MET:O	2.04	0.58
1:A:494:TYR:O	1:A:498:THR:HG23	2.03	0.57
1:A:249:PRO:HG2	1:A:556:TYR:CE2	2.44	0.53
1:A:242:TYR:CG	1:A:243:PRO:HA	2.44	0.52
1:A:100:TRP:HE1	1:A:396:HIS:CD2	2.25	0.52
1:A:205:TYR:CE1	1:A:254:GLN:HB3	2.43	0.52
1:A:129:SER:HA	1:A:139:PHE:O	2.10	0.52
1:A:716:GLU:CD	1:A:716:GLU:H	2.13	0.52
1:A:687:TYR:CZ	1:A:694:PRO:HG2	2.47	0.49
1:A:662:ARG:HD2	9:A:2106:HOH:O	2.13	0.48
1:A:689:HIS:HB3	1:A:692:TYR:O	2.14	0.48
1:A:456:ILE:HD13	1:A:573:HIS:HE1	1.81	0.46
1:A:148:PRO:HG2	1:A:151:TYR:CD2	2.51	0.45
1:A:209:PHE:CE2	1:A:211:GLY:HA3	2.51	0.45
1:A:201:VAL:HG23	1:A:225:VAL:HG13	2.00	0.44
1:A:169:MET:N	1:A:170:PRO:CD	2.81	0.43
1:A:675:PHE:CB	1:A:689:HIS:CE1	3.02	0.43
1:A:517:SER:HB2	1:A:694:PRO:HG3	2.01	0.43
1:A:186:PHE:O	1:A:190:ARG:HB2	2.19	0.42
1:A:611:ILE:HA	1:A:611:ILE:HD12	1.87	0.42
1:A:456:ILE:HG13	1:A:456:ILE:O	2.19	0.42
1:A:463:ARG:NE	1:A:536:ARG:NH2	2.68	0.41
1:A:171:GLU:HA	1:A:342:VAL:O	2.20	0.41
1:A:517:SER:OG	1:A:518:GLY:N	2.52	0.41
1:A:468:PRO:HA	1:A:471:TYR:CE1	2.56	0.41
1:A:461:THR:HB	1:A:500:LYS:HD3	2.01	0.41
1:A:675:PHE:HB3	1:A:689:HIS:CE1	2.55	0.41
1:A:469:LEU:O	1:A:595:PHE:HA	2.21	0.41
1:A:394:VAL:HG13	1:A:577:ALA:HB2	2.04	0.40
1:A:449:TYR:O	1:A:532:SER:HA	2.21	0.40
1:A:574:LEU:O	1:A:578:GLN:HG3	2.21	0.40
1:A:92:LEU:O	1:A:96:ILE:HG12	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:GLU:OE2	3:D:3:BMA:O2[2_565]	2.12	0.08

### 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	671/707 (95%)	636 (95%)	32 (5%)	3 (0%)	34 37

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	506	PHE
1	A	507	SER
1	A	382	VAL

#### 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	531/603 (88%)	514 (97%)	17 (3%)	39 50

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	174	LEU
1	A	276	GLU

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Mol	Chain	Res	Type
1	A	283	ILE
1	A	325	VAL
1	A	396	HIS
1	A	465	ASP
1	A	498	THR
1	A	509	MET
1	A	536	ARG
1	A	537	TYR
1	A	600	TYR
1	A	647	SER
1	A	654	ASP
1	A	664	MET
1	A	668	LEU
1	A	673	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	136	ASN
1	A	396	HIS
1	A	573	HIS

### 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](#)

8 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	0.64	0	17,19,21	1.80	4 (23%)
2	NAG	B	2	2	14,14,15	0.77	0	17,19,21	2.33	5 (29%)
2	NAG	C	1	1,2	14,14,15	1.14	1 (7%)	17,19,21	1.84	4 (23%)
2	NAG	C	2	2	14,14,15	0.66	0	17,19,21	1.03	1 (5%)
3	NAG	D	1	1,3	14,14,15	0.57	0	17,19,21	1.61	2 (11%)
3	NAG	D	2	3	14,14,15	0.77	0	17,19,21	1.71	4 (23%)
3	BMA	D	3	3	11,11,12	0.84	0	15,15,17	2.08	3 (20%)
3	MAN	D	4	3	11,11,12	0.69	0	15,15,17	1.47	3 (20%)

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	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	MAN	D	4	3	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	NAG	O5-C1	-2.93	1.39	1.43

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3	BMA	C1-C2-C3	6.12	117.19	109.67
3	D	1	NAG	C1-O5-C5	4.90	118.83	112.19
2	C	1	NAG	O5-C1-C2	-4.66	103.93	111.29
2	B	2	NAG	C8-C7-N2	4.65	123.97	116.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	C2-N2-C7	4.37	129.13	122.90
2	B	2	NAG	C4-C3-C2	4.22	117.21	111.02
2	B	1	NAG	O5-C5-C6	4.21	113.80	107.20
2	B	1	NAG	O4-C4-C3	-3.76	101.66	110.35
2	C	1	NAG	C1-O5-C5	3.61	117.09	112.19
3	D	2	NAG	C1-C2-N2	3.55	116.55	110.49
3	D	4	MAN	O5-C5-C6	3.50	112.69	107.20
2	B	2	NAG	O3-C3-C2	-3.16	102.94	109.47
2	B	1	NAG	C1-O5-C5	3.01	116.26	112.19
3	D	3	BMA	O3-C3-C2	-2.92	104.41	109.99
3	D	2	NAG	C1-O5-C5	2.90	116.12	112.19
3	D	2	NAG	C4-C3-C2	-2.75	106.99	111.02
3	D	4	MAN	C3-C4-C5	-2.75	105.34	110.24
3	D	2	NAG	C8-C7-N2	2.69	120.65	116.10
2	B	1	NAG	O5-C1-C2	-2.65	107.10	111.29
2	C	1	NAG	O4-C4-C5	2.50	115.52	109.30
2	B	2	NAG	O7-C7-C8	-2.40	117.60	122.06
3	D	4	MAN	C1-O5-C5	2.31	115.32	112.19
2	C	1	NAG	O4-C4-C3	-2.17	105.33	110.35
3	D	3	BMA	O2-C2-C3	-2.15	105.84	110.14
2	C	2	NAG	O4-C4-C5	2.12	114.55	109.30
3	D	1	NAG	O5-C1-C2	-2.05	108.05	111.29

There are no chirality outliers.

All (10) torsion outliers are listed below:

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

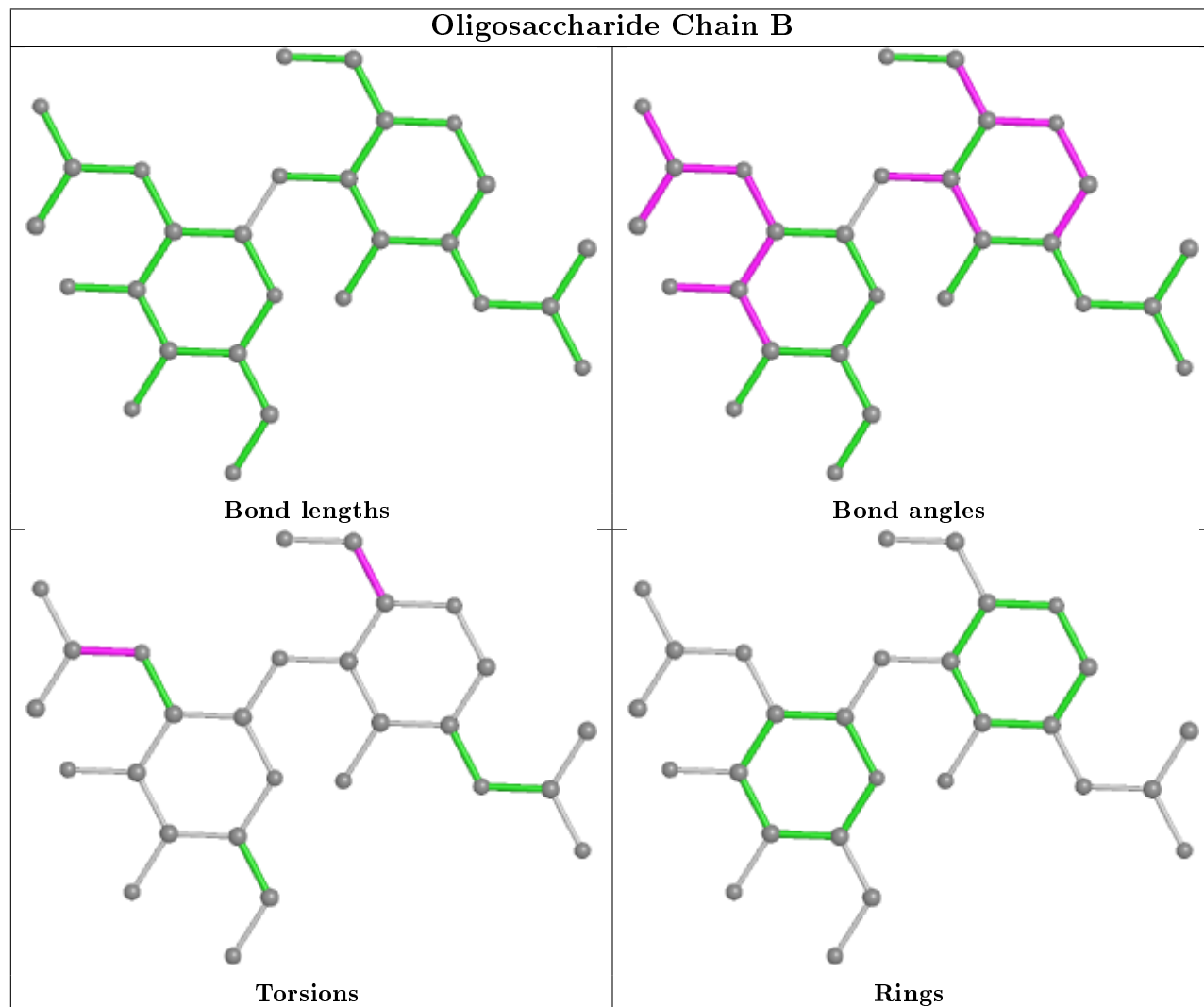
There are no ring outliers.

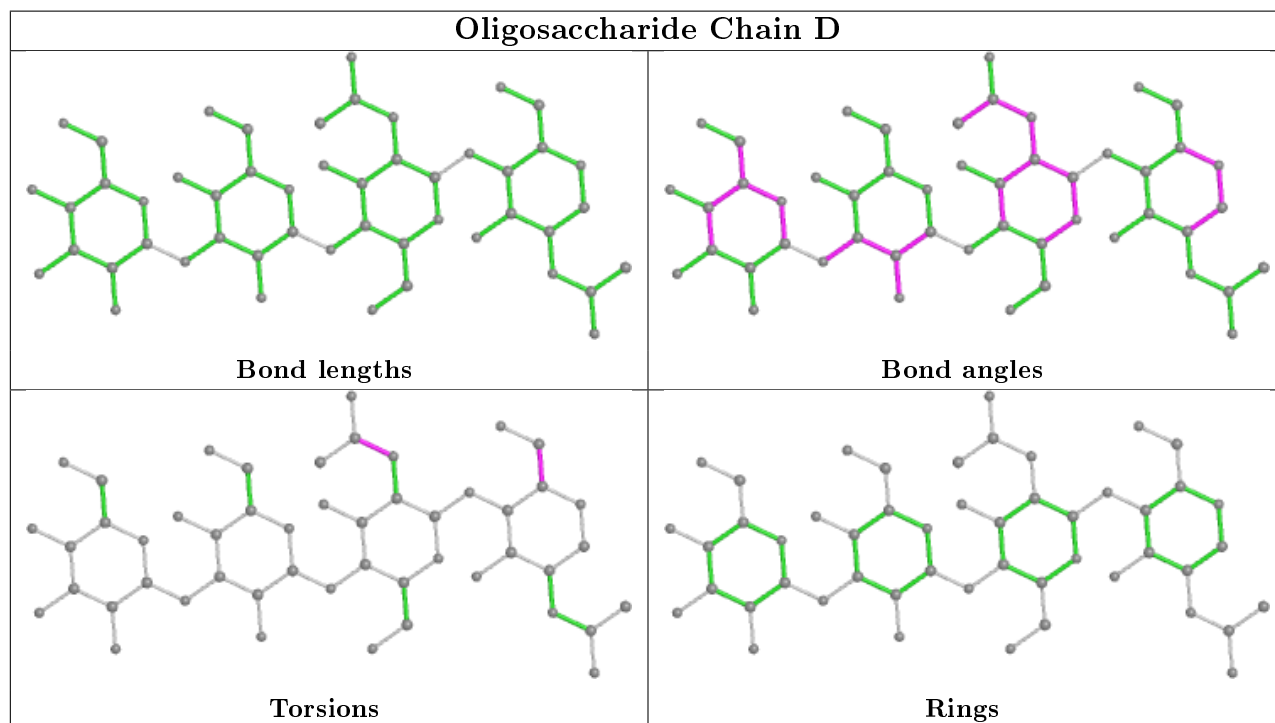
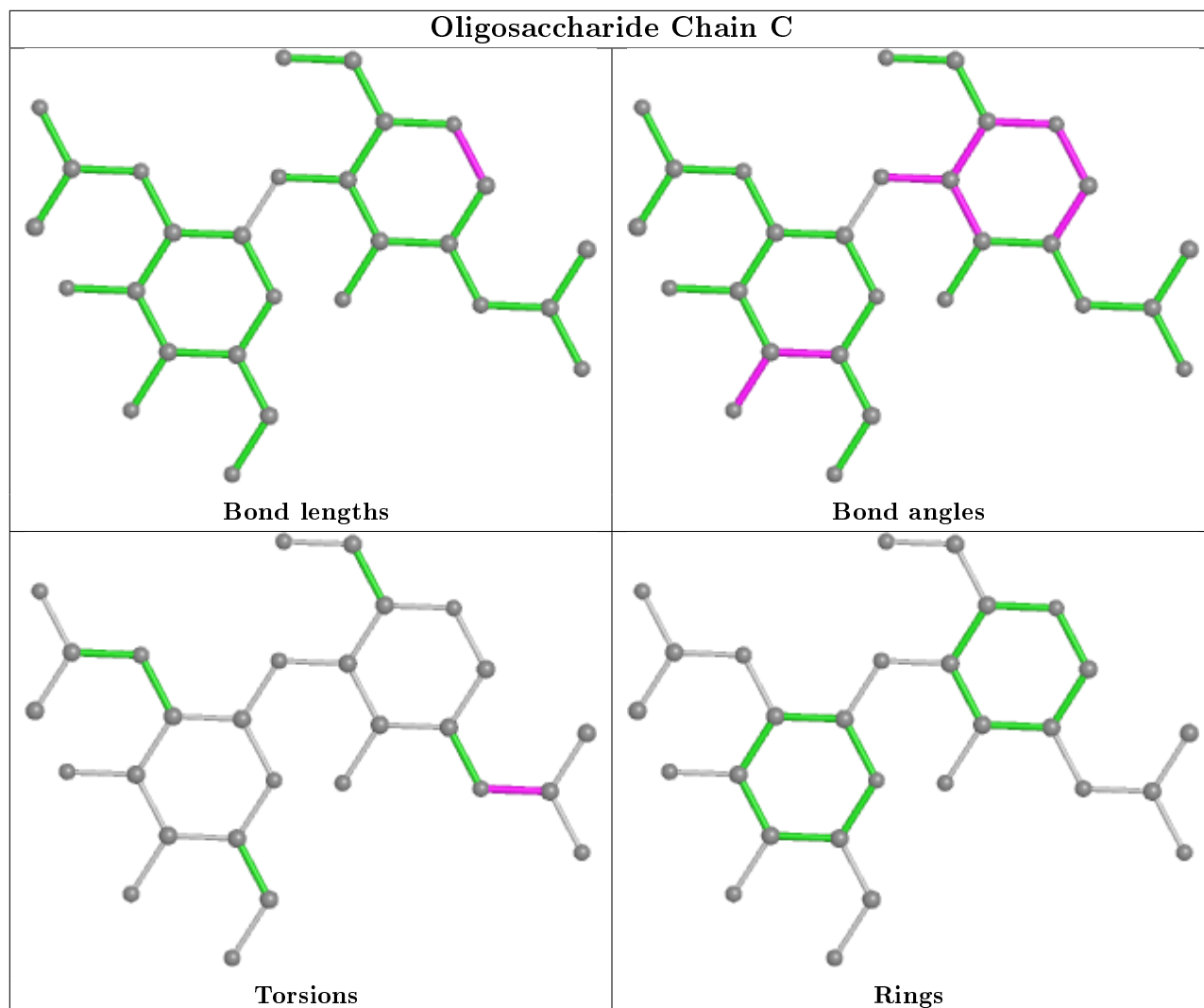
1 monomer is involved in 1 short contact:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	3	BMA	0	1

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

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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
8	NAG	A	1758	1	14,14,15	1.03	1 (7%)	17,19,21	1.67	3 (17%)
8	NAG	A	1759	1	14,14,15	0.70	0	17,19,21	2.52	8 (47%)
8	NAG	A	1757	1	14,14,15	0.76	0	17,19,21	2.42	8 (47%)

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
8	NAG	A	1758	1	-	0/6/23/26	0/1/1/1
8	NAG	A	1759	1	1/1/5/7	2/6/23/26	0/1/1/1
8	NAG	A	1757	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1758	NAG	C4-C5	2.14	1.57	1.53

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1757	NAG	C1-O5-C5	6.83	121.44	112.19
8	A	1759	NAG	C1-O5-C5	6.24	120.65	112.19
8	A	1758	NAG	O5-C1-C2	-4.15	104.74	111.29
8	A	1759	NAG	O5-C1-C2	4.11	117.77	111.29
8	A	1759	NAG	C4-C3-C2	-3.87	105.34	111.02
8	A	1757	NAG	C3-C4-C5	3.71	116.85	110.24
8	A	1758	NAG	C1-O5-C5	2.95	116.19	112.19
8	A	1759	NAG	O5-C5-C6	2.86	111.69	107.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1757	NAG	C4-C3-C2	2.76	115.07	111.02
8	A	1757	NAG	O5-C5-C4	2.51	116.92	110.83
8	A	1757	NAG	C8-C7-N2	2.41	120.18	116.10
8	A	1757	NAG	O5-C5-C6	2.38	110.94	107.20
8	A	1759	NAG	C1-C2-N2	-2.33	106.51	110.49
8	A	1757	NAG	O5-C1-C2	-2.33	107.61	111.29
8	A	1759	NAG	O7-C7-C8	-2.32	117.75	122.06
8	A	1759	NAG	O5-C5-C4	2.26	116.33	110.83
8	A	1758	NAG	O7-C7-C8	-2.14	118.09	122.06
8	A	1759	NAG	O7-C7-N2	2.13	125.86	121.95
8	A	1757	NAG	O7-C7-C8	-2.03	118.29	122.06

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
8	A	1759	NAG	C1

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1759	NAG	C4-C5-C6-O6
8	A	1759	NAG	O5-C5-C6-O6
8	A	1757	NAG	C8-C7-N2-C2
8	A	1757	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

## 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	679/707 (96%)	-0.36	10 (1%) 73 72	20, 36, 63, 75	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	153	ASN	4.3
1	A	506	PHE	3.4
1	A	155	SER	3.4
1	A	719	VAL	3.0
1	A	135	GLY	2.9
1	A	487	GLY	2.4
1	A	104	GLY	2.3
1	A	152	GLU	2.2
1	A	326	PRO	2.1
1	A	191	ASP	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.

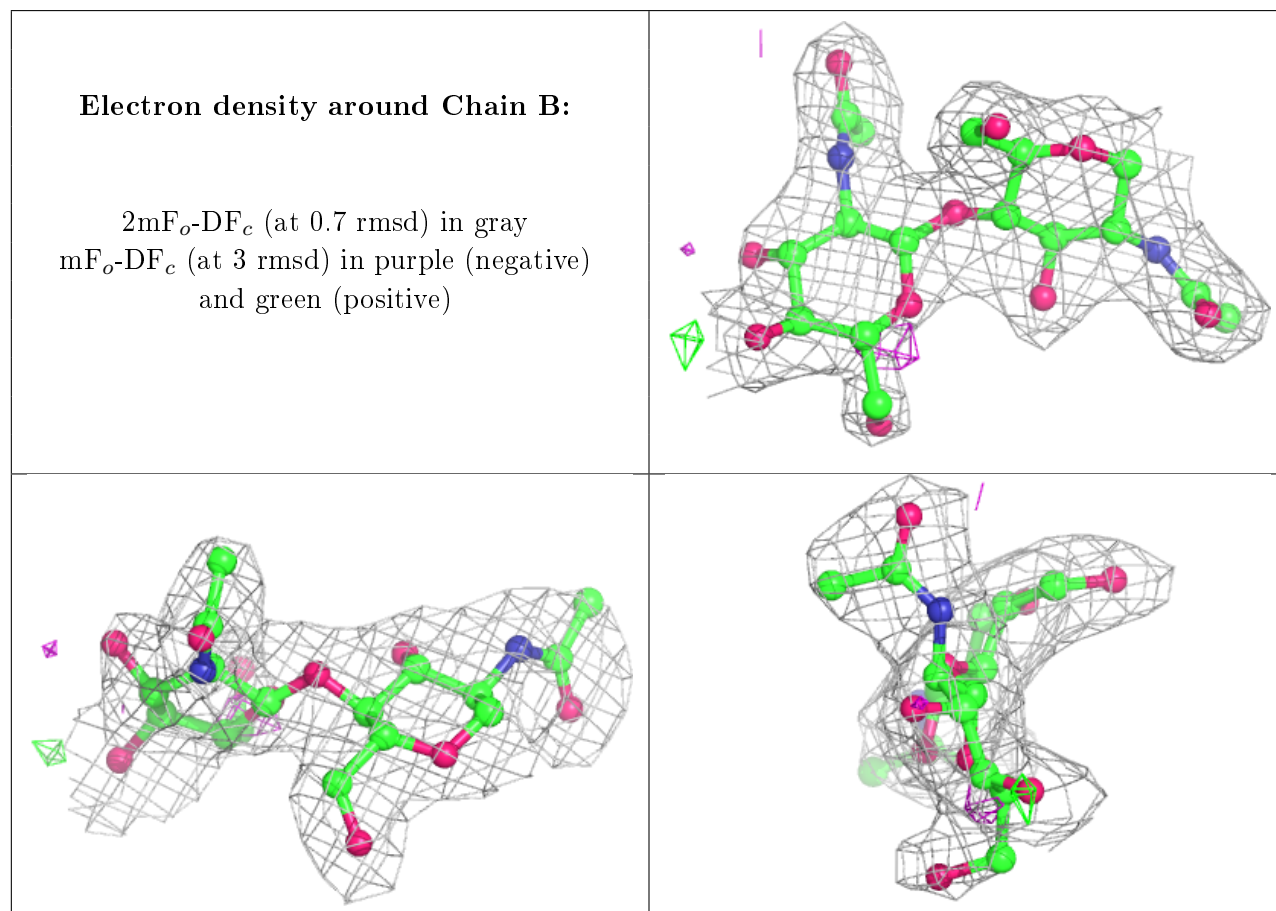
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	B	2	14/15	0.79	0.31	62,70,73,73	0
3	BMA	D	3	11/12	0.85	0.12	68,71,72,72	0

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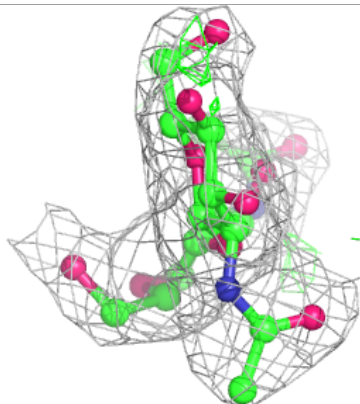
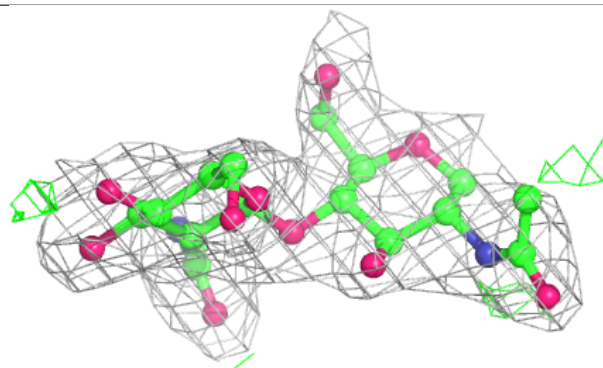
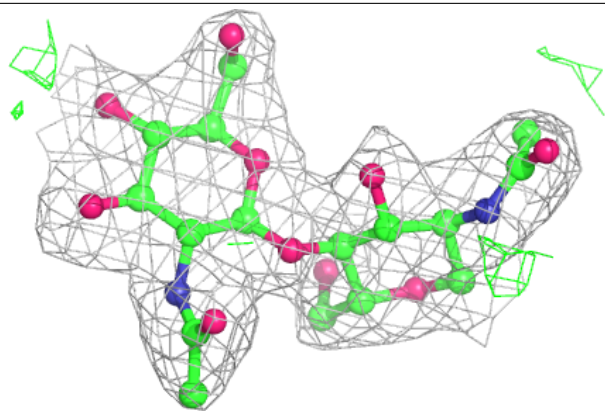
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	D	2	14/15	0.90	0.13	54,60,64,65	0
3	MAN	D	4	11/12	0.91	0.11	74,75,78,80	0
2	NAG	C	2	14/15	0.93	0.11	57,61,63,64	0
2	NAG	C	1	14/15	0.94	0.10	44,50,55,55	0
2	NAG	B	1	14/15	0.94	0.14	47,54,57,60	0
3	NAG	D	1	14/15	0.96	0.08	32,37,49,49	0

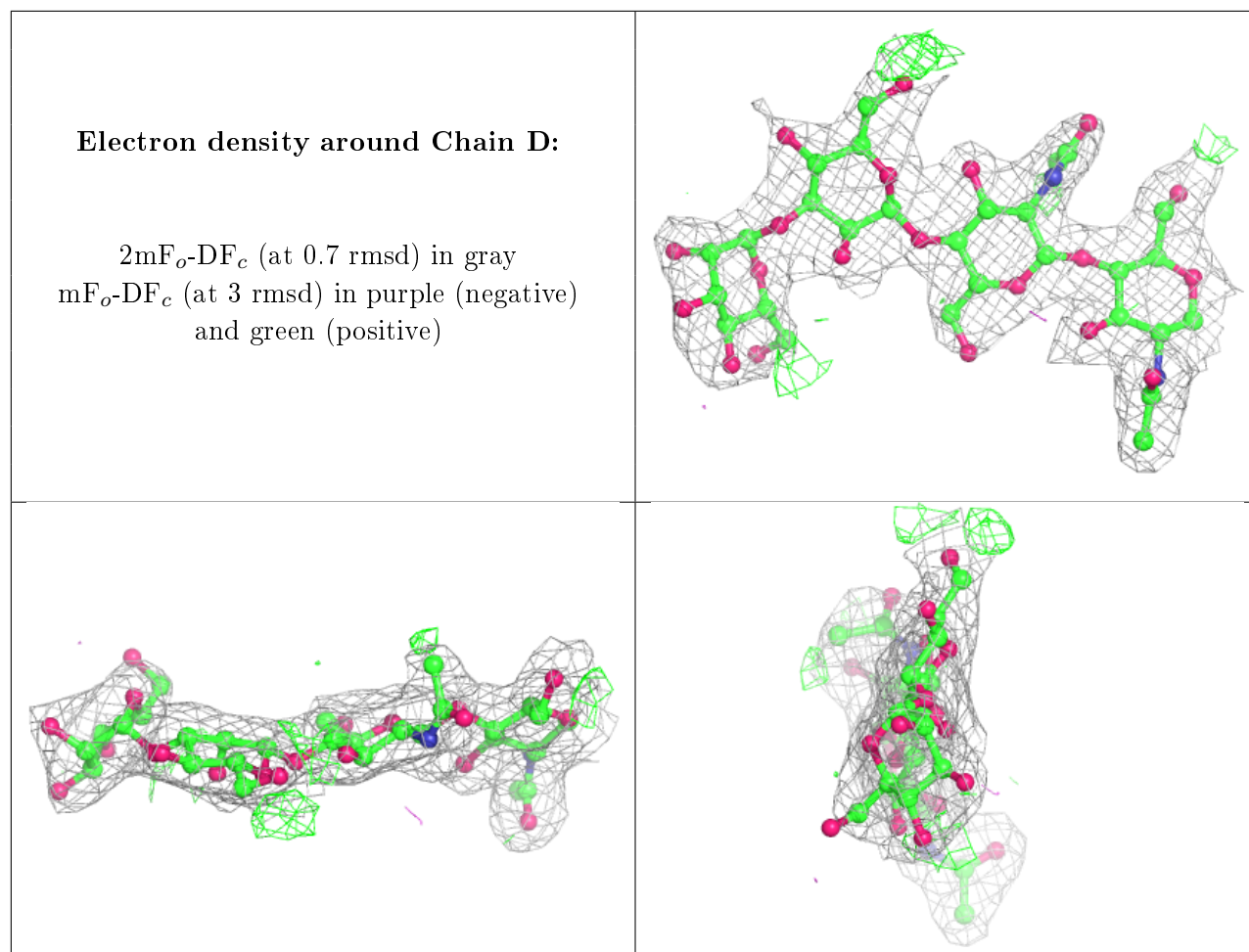
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



**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](#)

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
8	NAG	A	1758	14/15	0.75	0.19	61,64,66,68	0
8	NAG	A	1757	14/15	0.80	0.33	73,77,82,83	0
8	NAG	A	1759	14/15	0.86	0.14	44,58,68,70	0
4	GLU	A	1766	10/10	0.97	0.11	25,27,28,28	0
5	ZN	A	1751	1/1	0.99	0.12	27,27,27,27	0
6	CA	A	1753	1/1	1.00	0.09	21,21,21,21	0
5	ZN	A	1752	1/1	1.00	0.10	25,25,25,25	0
7	CL	A	1754	1/1	1.00	0.15	31,31,31,31	0



## 6.5 Other polymers

There are no such residues in this entry.