



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 05:10 PM BST

PDB ID : 6C2W
Title : Crystal structure of human prothrombin mutant S101C/A470C
Authors : Chinnaraj, M.; Chen, Z.; Pelc, L.; Grese, Z.; Bystranowska, D.; Di Cera, E.; Pozzi, N.
Deposited on : 2018-01-09
Resolution : 4.12 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

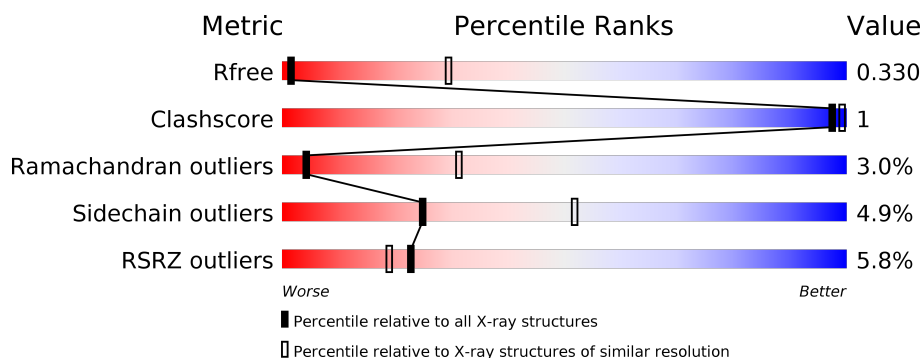
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.12 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	1024 (4.50-3.74)
Clashscore	141614	1011 (4.48-3.76)
Ramachandran outliers	138981	1043 (4.50-3.74)
Sidechain outliers	138945	1030 (4.50-3.74)
RSRZ outliers	127900	1041 (4.54-3.70)

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 ≥ 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	582	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>9%</div> </div> </div>
1	B	582	<div> <div>7%</div> <div> <div></div> <div>90%</div> <div>8%</div> </div> </div>
2	C	2	<div> <div></div> <div>100%</div> </div>
2	D	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </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
1	CGU	B	16	-	-	-	X
1	CGU	B	25	-	-	-	X

2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 9278 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 Prothrombin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	575	Total	C	N	O	S	0	0	0
			4594	2861	801	897	35			
1	B	575	Total	C	N	O	S	0	0	0
			4594	2861	801	897	35			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	101	CYS	SER	engineered mutation	UNP P00734
A	122	MET	THR	variant	UNP P00734
A	470	CYS	ALA	engineered mutation	UNP P00734
A	580	TYR	-	expression tag	UNP P00734
A	581	LEU	-	expression tag	UNP P00734
A	582	GLU	-	expression tag	UNP P00734
B	101	CYS	SER	engineered mutation	UNP P00734
B	122	MET	THR	variant	UNP P00734
B	470	CYS	ALA	engineered mutation	UNP P00734
B	580	TYR	-	expression tag	UNP P00734
B	581	LEU	-	expression tag	UNP P00734
B	582	GLU	-	expression tag	UNP P00734

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			25	14	1	10			

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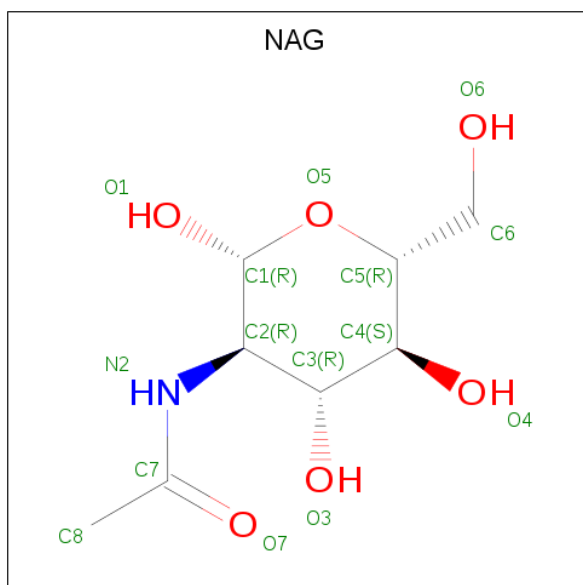
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	2	Total	C	N	O	0	0	0
			25	14	1	10			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	6	Total	Mg	0	0
			6	6		
3	A	6	Total	Mg	0	0
			6	6		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

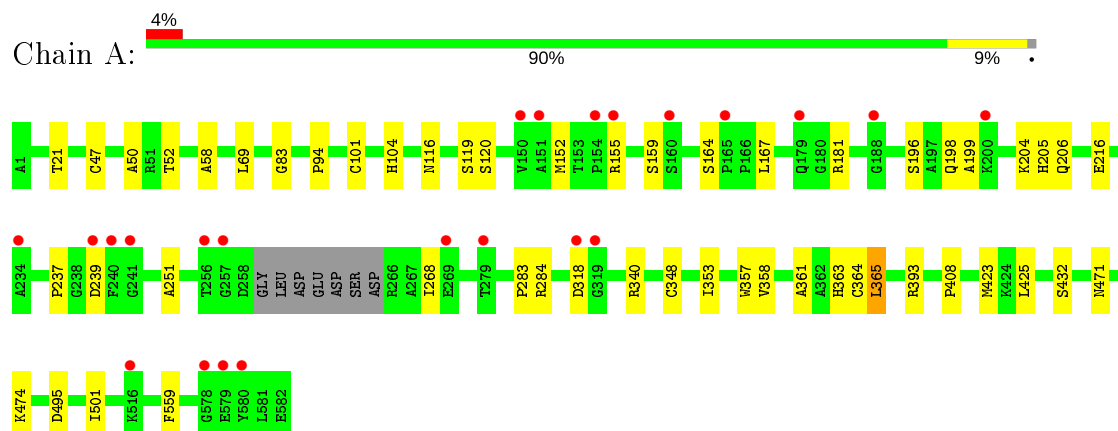


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

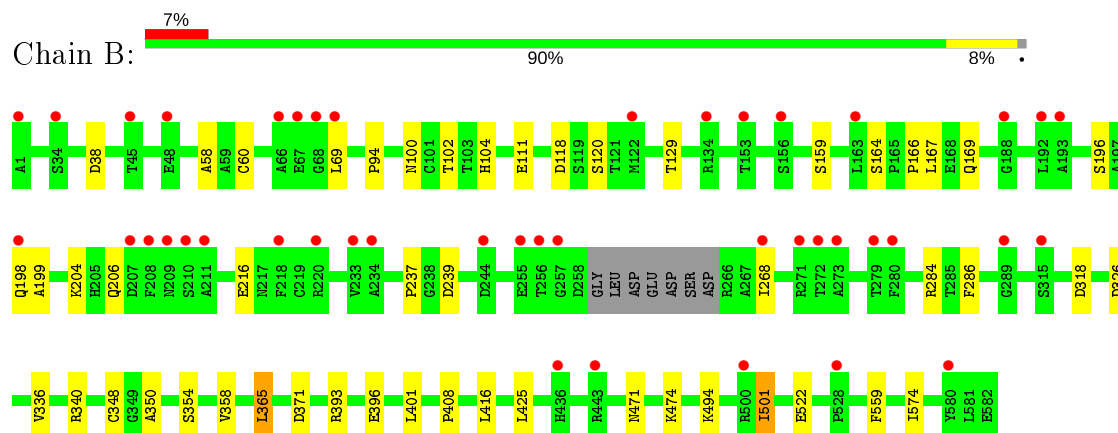
3 Residue-property plots

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.

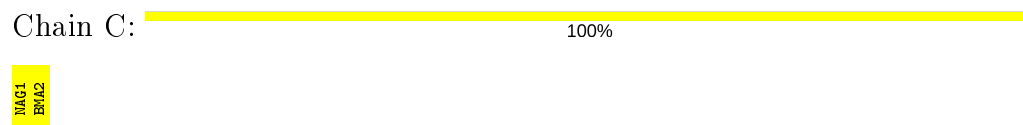
• Molecule 1: Prothrombin



• Molecule 1: Prothrombin



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



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





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	85.03Å 85.07Å 153.80Å 105.35° 90.00° 90.05°	Depositor
Resolution (Å)	30.32 – 4.12 30.32 – 4.12	Depositor EDS
% Data completeness (in resolution range)	88.0 (30.32-4.12) 96.5 (30.32-4.12)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 4.11Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.278 , 0.333 0.293 , 0.330	Depositor DCC
R_{free} test set	1508 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	171.3	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-l 0.046 for -h,k,-k-l 0.029 for -h,-k,k+l	Xtriage
Reported twinning fraction	0.290 for H, K, L 0.231 for h,-k,-l 0.214 for -H, -K, K+L 0.265 for -H, K, -K-L	Depositor
Outliers	0 of 30926 reflections	Xtriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	9278	wwPDB-VP
Average B, all atoms (Å ²)	194.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.45	0/4576	0.60	0/6190
1	B	0.44	0/4576	0.59	0/6190
All	All	0.44	0/9152	0.60	0/12380

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	4594	0	4330	7	0
1	B	4594	0	4330	7	0
2	C	25	0	22	0	0
2	D	25	0	22	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
All	All	9278	0	8730	14	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 1.

All (14) 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:494:LYS:HA	1:B:501:ILE:HD11	1.86	0.57
1:B:69:LEU:HD13	1:B:120:SER:HB3	1.87	0.56
1:A:353:ILE:HD11	1:A:357:TRP:HB3	1.89	0.54
1:B:358:VAL:HG21	1:B:425:LEU:HD21	1.90	0.53
1:B:100:ASN:HD21	1:B:102:THR:HB	1.77	0.49
1:B:336:VAL:HB	1:B:350:ALA:HB3	1.97	0.47
1:A:361:ALA:HB3	1:A:364:CYS:SG	2.55	0.46
1:A:47:CYS:HB3	1:A:50:ALA:HB3	1.99	0.45
1:A:69:LEU:HD13	1:A:120:SER:HB3	1.99	0.44
1:A:358:VAL:HB	1:A:423:MET:HB2	2.00	0.43
1:B:401:LEU:HD23	1:B:425:LEU:HD23	2.02	0.42
1:A:361:ALA:HB1	1:A:363:HIS:CE1	2.55	0.42
1:A:358:VAL:HG21	1:A:425:LEU:HD21	2.02	0.41
1:B:286:PHE:HB2	1:B:574:ILE:HD13	2.02	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	561/582 (96%)	451 (80%)	92 (16%)	18 (3%)	4	30
1	B	561/582 (96%)	449 (80%)	96 (17%)	16 (3%)	4	32
All	All	1122/1164 (96%)	900 (80%)	188 (17%)	34 (3%)	4	31

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	164	SER
1	A	237	PRO

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Mol	Chain	Res	Type
1	B	237	PRO
1	A	58	ALA
1	A	83	GLY
1	A	199	ALA
1	A	318	ASP
1	B	164	SER
1	B	199	ALA
1	A	159	SER
1	A	251	ALA
1	A	283	PRO
1	B	58	ALA
1	B	159	SER
1	B	169	GLN
1	B	216	GLU
1	B	318	ASP
1	A	216	GLU
1	A	471	ASN
1	B	94	PRO
1	B	166	PRO
1	B	365	LEU
1	B	416	LEU
1	B	471	ASN
1	A	119	SER
1	A	155	ARG
1	A	181	ARG
1	A	196	SER
1	A	365	LEU
1	A	408	PRO
1	B	196	SER
1	B	371	ASP
1	B	408	PRO
1	A	94	PRO

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	484/490 (99%)	461 (95%)	23 (5%)	25	52
1	B	484/490 (99%)	460 (95%)	24 (5%)	24	51
All	All	968/980 (99%)	921 (95%)	47 (5%)	25	52

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	52	THR
1	A	101	CYS
1	A	104	HIS
1	A	116	ASN
1	A	152	MET
1	A	167	LEU
1	A	198	GLN
1	A	204	LYS
1	A	205	HIS
1	A	206	GLN
1	A	239	ASP
1	A	268	ILE
1	A	284	ARG
1	A	340	ARG
1	A	348	CYS
1	A	365	LEU
1	A	393	ARG
1	A	432	SER
1	A	474	LYS
1	A	495	ASP
1	A	501	ILE
1	A	559	PHE
1	B	38	ASP
1	B	60	CYS
1	B	104	HIS
1	B	111	GLU
1	B	118	ASP
1	B	129	THR
1	B	167	LEU
1	B	198	GLN
1	B	204	LYS
1	B	206	GLN
1	B	239	ASP
1	B	268	ILE

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Mol	Chain	Res	Type
1	B	284	ARG
1	B	326	ASP
1	B	340	ARG
1	B	348	CYS
1	B	354	SER
1	B	365	LEU
1	B	393	ARG
1	B	396	GLU
1	B	474	LYS
1	B	501	ILE
1	B	522	GLU
1	B	559	PHE

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 ⓘ

20 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CGU	A	20	1	3,11,12	0.65	0	1,14,16	0.96	0
1	CGU	B	20	1	3,11,12	0.71	0	1,14,16	0.76	0
1	CGU	A	14	1,3	3,11,12	0.54	0	1,14,16	1.21	0
1	CGU	B	16	1,3	3,11,12	0.57	0	1,14,16	0.68	0
1	CGU	A	6	1	3,11,12	0.69	0	1,14,16	0.45	0
1	CGU	B	29	1,3	3,11,12	0.56	0	1,14,16	0.71	0
1	CGU	A	25	1	3,11,12	0.59	0	1,14,16	1.08	0
1	CGU	A	19	1,3	3,11,12	0.65	0	1,14,16	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CGU	A	26	1,3	3,11,12	0.59	0	1,14,16	0.61	0
1	CGU	A	29	1,3	3,11,12	0.69	0	1,14,16	1.00	0
1	CGU	B	14	1	3,11,12	0.58	0	1,14,16	0.44	0
1	CGU	A	32	1,3	3,11,12	0.64	0	1,14,16	1.44	0
1	CGU	B	32	1	3,11,12	0.64	0	1,14,16	1.03	0
1	CGU	B	25	1	3,11,12	0.71	0	1,14,16	1.59	0
1	CGU	B	6	1	3,11,12	0.78	0	1,14,16	0.00	0
1	CGU	A	16	1,3	3,11,12	0.74	0	1,14,16	0.57	0
1	CGU	A	7	1	3,11,12	0.68	0	1,14,16	0.27	0
1	CGU	B	19	1,3	3,11,12	0.67	0	1,14,16	0.76	0
1	CGU	B	26	1,3	3,11,12	0.60	0	1,14,16	0.68	0
1	CGU	B	7	1	3,11,12	0.74	0	1,14,16	0.54	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
1	CGU	A	20	1	-	3/5/14/16	-
1	CGU	B	20	1	-	1/5/14/16	-
1	CGU	A	14	1,3	-	0/5/14/16	-
1	CGU	B	16	1,3	-	0/5/14/16	-
1	CGU	A	6	1	-	3/5/14/16	-
1	CGU	B	29	1,3	-	0/5/14/16	-
1	CGU	A	25	1	-	0/5/14/16	-
1	CGU	A	19	1,3	-	2/5/14/16	-
1	CGU	A	26	1,3	-	0/5/14/16	-
1	CGU	A	29	1,3	-	0/5/14/16	-
1	CGU	B	14	1	-	0/5/14/16	-
1	CGU	A	32	1,3	-	1/5/14/16	-
1	CGU	B	32	1	-	1/5/14/16	-
1	CGU	B	25	1	-	0/5/14/16	-
1	CGU	B	6	1	-	2/5/14/16	-
1	CGU	A	16	1,3	-	0/5/14/16	-
1	CGU	A	7	1	-	4/5/14/16	-
1	CGU	B	19	1,3	-	2/5/14/16	-
1	CGU	B	26	1,3	-	0/5/14/16	-
1	CGU	B	7	1	-	4/5/14/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	20	CGU	O-C-CA-CB
1	A	20	CGU	CA-CB-CG-CD1
1	A	20	CGU	CA-CB-CG-CD2
1	B	20	CGU	O-C-CA-CB
1	A	32	CGU	N-CA-CB-CG
1	B	32	CGU	N-CA-CB-CG
1	B	6	CGU	CA-CB-CG-CD1
1	B	6	CGU	CA-CB-CG-CD2
1	A	7	CGU	N-CA-CB-CG
1	A	7	CGU	C-CA-CB-CG
1	A	7	CGU	CA-CB-CG-CD1
1	A	6	CGU	CA-CB-CG-CD1
1	A	6	CGU	CA-CB-CG-CD2
1	A	19	CGU	CA-CB-CG-CD1
1	A	19	CGU	CA-CB-CG-CD2
1	A	7	CGU	CA-CB-CG-CD2
1	B	7	CGU	CA-CB-CG-CD1
1	B	7	CGU	CA-CB-CG-CD2
1	A	6	CGU	C-CA-CB-CG
1	B	7	CGU	C-CA-CB-CG
1	B	19	CGU	CA-CB-CG-CD1
1	B	19	CGU	CA-CB-CG-CD2
1	B	7	CGU	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

4 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	0.65	0	17,19,21	0.94	1 (5%)
2	BMA	C	2	2	11,11,12	0.61	0	15,15,17	1.12	1 (6%)
2	NAG	D	1	1,2	14,14,15	0.64	0	17,19,21	0.85	0
2	BMA	D	2	2	11,11,12	0.61	0	15,15,17	1.02	1 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	1,2	-	1/6/23/26	0/1/1/1
2	BMA	C	2	2	-	2/2/19/22	0/1/1/1
2	NAG	D	1	1,2	-	1/6/23/26	0/1/1/1
2	BMA	D	2	2	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	BMA	C1-C2-C3	2.37	112.58	109.67
2	C	2	BMA	C2-C3-C4	2.27	114.83	110.89
2	C	1	NAG	C1-O5-C5	2.07	114.99	112.19

There are no chirality outliers.

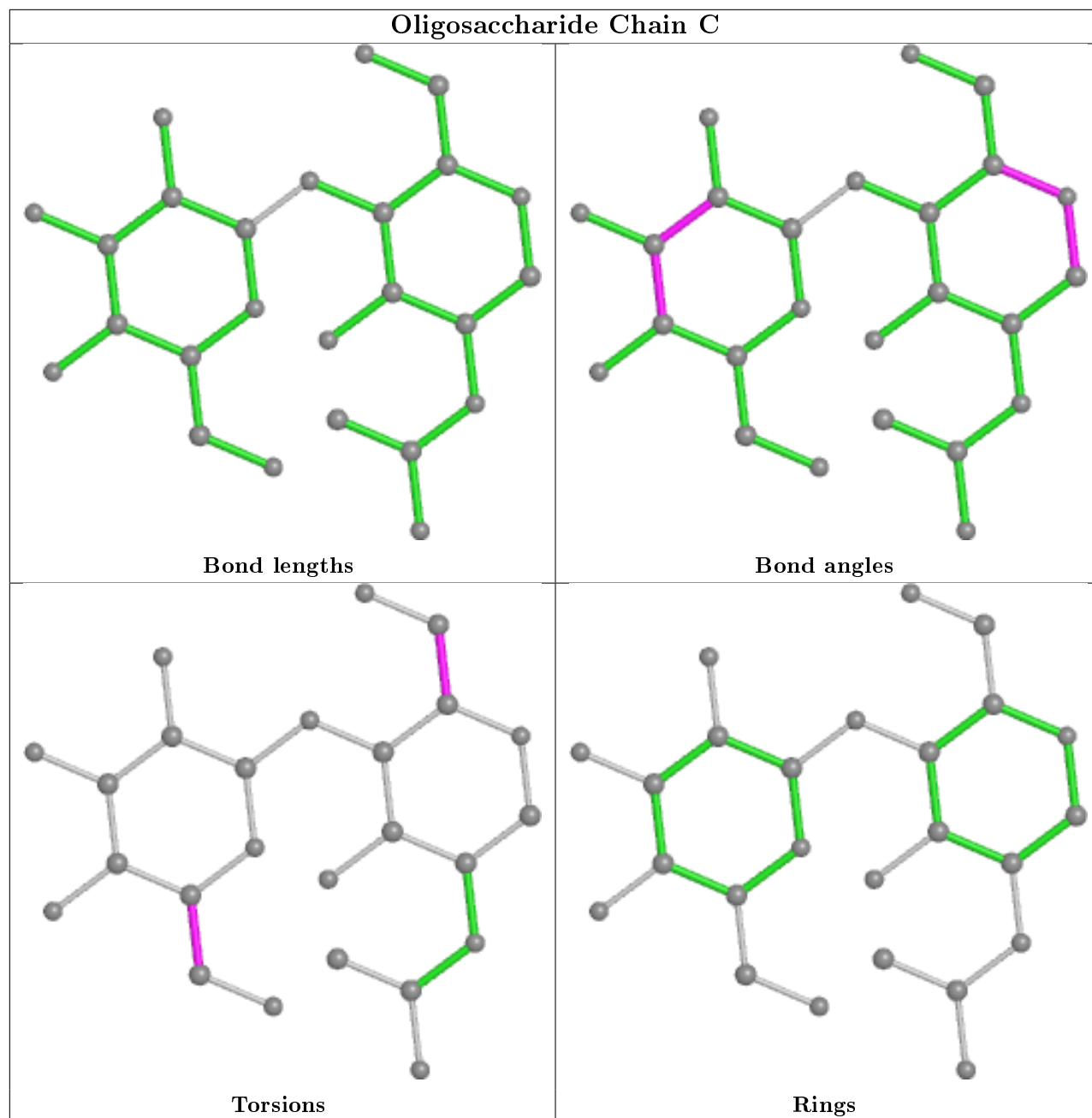
All (6) torsion outliers are listed below:

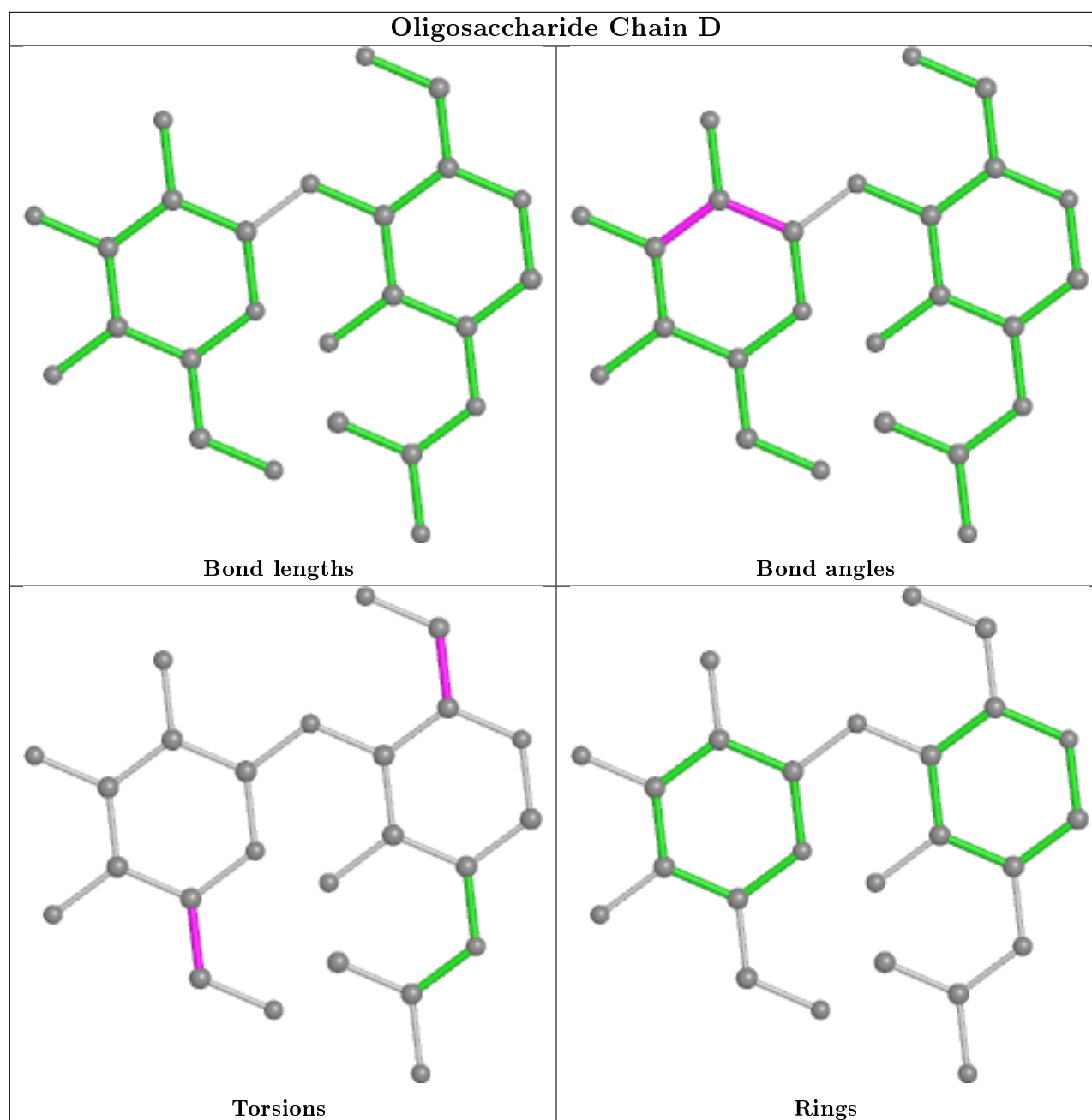
Mol	Chain	Res	Type	Atoms
2	D	2	BMA	O5-C5-C6-O6
2	C	2	BMA	O5-C5-C6-O6
2	C	2	BMA	C4-C5-C6-O6
2	D	2	BMA	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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





5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 12 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
4	NAG	B	609	1	14,14,15	0.50	0	17,19,21	0.86	1 (5%)
4	NAG	A	609	1	14,14,15	0.66	0	17,19,21	1.22	3 (17%)

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
4	NAG	B	609	1	-	0/6/23/26	0/1/1/1
4	NAG	A	609	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	609	NAG	C4-C3-C2	2.40	114.54	111.02
4	A	609	NAG	O5-C5-C6	2.36	110.91	107.20
4	A	609	NAG	C1-O5-C5	2.11	115.06	112.19
4	B	609	NAG	C4-C3-C2	2.03	114.00	111.02

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	609	NAG	C4-C5-C6-O6
4	A	609	NAG	O5-C5-C6-O6

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

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	565/582 (97%)	0.08	23 (4%) 37 30	102, 186, 247, 305	0
1	B	565/582 (97%)	0.30	43 (7%) 13 12	111, 200, 265, 336	0
All	All	1130/1164 (97%)	0.19	66 (5%) 23 19	102, 193, 256, 336	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	579	GLU	7.6
1	A	318	ASP	7.5
1	B	68	GLY	6.5
1	B	234	ALA	6.4
1	A	155	ARG	6.0
1	B	233	VAL	5.6
1	A	256	THR	5.5
1	B	279	THR	4.7
1	A	150	VAL	4.7
1	A	151	ALA	4.6
1	B	67	GLU	4.5
1	B	153	THR	4.4
1	B	315	SER	4.3
1	A	241	GLY	3.7
1	B	209	ASN	3.6
1	B	256	THR	3.6
1	A	239	ASP	3.6
1	B	244	ASP	3.5
1	B	193	ALA	3.4
1	A	257	GLY	3.4
1	B	207	ASP	3.4
1	B	289	GLY	3.3
1	A	154	PRO	3.3
1	B	210	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	578	GLY	3.1
1	B	156	SER	3.1
1	B	580	TYR	3.0
1	A	160	SER	2.9
1	B	272	THR	2.9
1	B	257	GLY	2.9
1	A	179	GLN	2.9
1	B	163	LEU	2.8
1	B	48	GLU	2.7
1	A	200	LYS	2.7
1	A	188	GLY	2.7
1	A	319	GLY	2.7
1	A	165	PRO	2.7
1	B	45	THR	2.6
1	A	279	THR	2.6
1	B	122	MET	2.6
1	B	34	SER	2.6
1	B	280	PHE	2.5
1	B	198	GLN	2.5
1	A	269	GLU	2.4
1	B	218	PHE	2.4
1	B	211	ALA	2.4
1	B	134	ARG	2.4
1	B	188	GLY	2.4
1	B	273	ALA	2.4
1	B	500	ARG	2.4
1	A	580	TYR	2.4
1	A	240	PHE	2.2
1	B	66	ALA	2.2
1	B	1	ALA	2.2
1	B	255	GLU	2.2
1	A	516	LYS	2.2
1	B	208	PHE	2.2
1	B	436	HIS	2.2
1	B	271	ARG	2.1
1	B	268	ILE	2.1
1	B	528	PRO	2.1
1	B	192	LEU	2.1
1	B	220	ARG	2.1
1	A	234	ALA	2.0
1	B	443	ARG	2.0
1	B	69	LEU	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CGU	B	20	12/13	0.60	0.32	158,178,182,188	0
1	CGU	B	16	12/13	0.65	0.44	216,227,233,235	0
1	CGU	A	7	12/13	0.77	0.33	168,177,190,191	0
1	CGU	B	14	12/13	0.78	0.29	128,171,178,188	0
1	CGU	B	25	12/13	0.79	0.45	135,158,163,166	0
1	CGU	B	19	12/13	0.79	0.39	97,157,178,182	0
1	CGU	A	25	12/13	0.80	0.36	139,169,178,180	0
1	CGU	B	6	12/13	0.81	0.19	119,156,167,169	0
1	CGU	A	6	12/13	0.82	0.34	129,145,175,181	0
1	CGU	B	26	12/13	0.82	0.19	111,151,158,160	0
1	CGU	A	16	12/13	0.85	0.29	113,133,157,161	0
1	CGU	B	32	12/13	0.85	0.16	133,151,195,199	0
1	CGU	A	20	12/13	0.85	0.23	186,201,204,205	0
1	CGU	B	29	12/13	0.85	0.15	206,227,242,251	0
1	CGU	B	7	12/13	0.86	0.38	147,173,179,180	0
1	CGU	A	19	12/13	0.87	0.22	96,131,184,190	0
1	CGU	A	14	12/13	0.87	0.21	115,146,168,174	0
1	CGU	A	29	12/13	0.88	0.16	174,198,208,216	0
1	CGU	A	26	12/13	0.89	0.21	110,133,152,157	0
1	CGU	A	32	12/13	0.89	0.15	110,144,171,180	0

6.3 Carbohydrates ⓘ

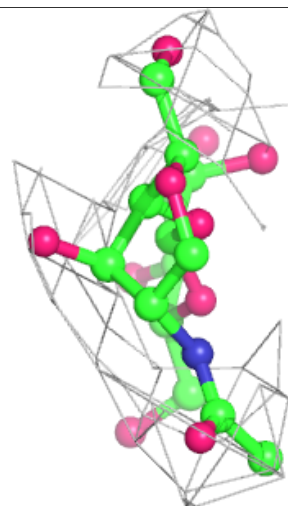
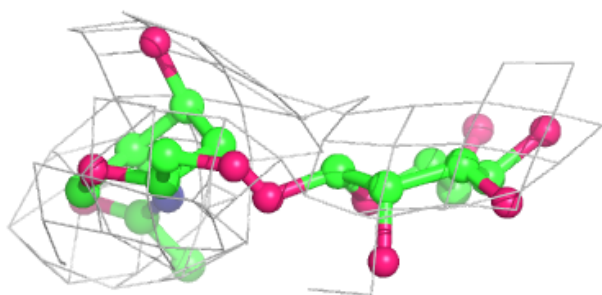
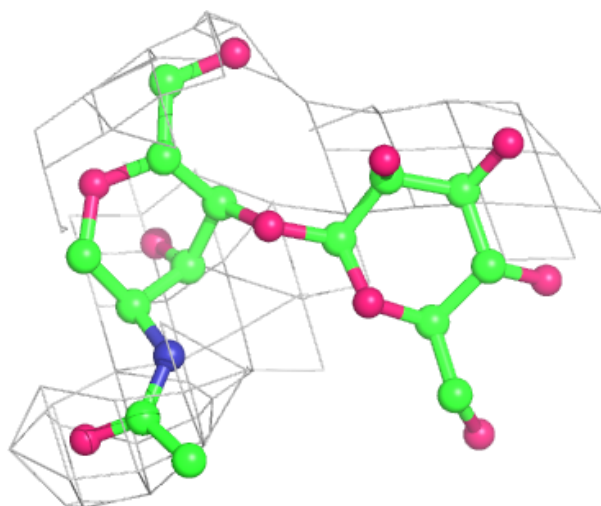
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

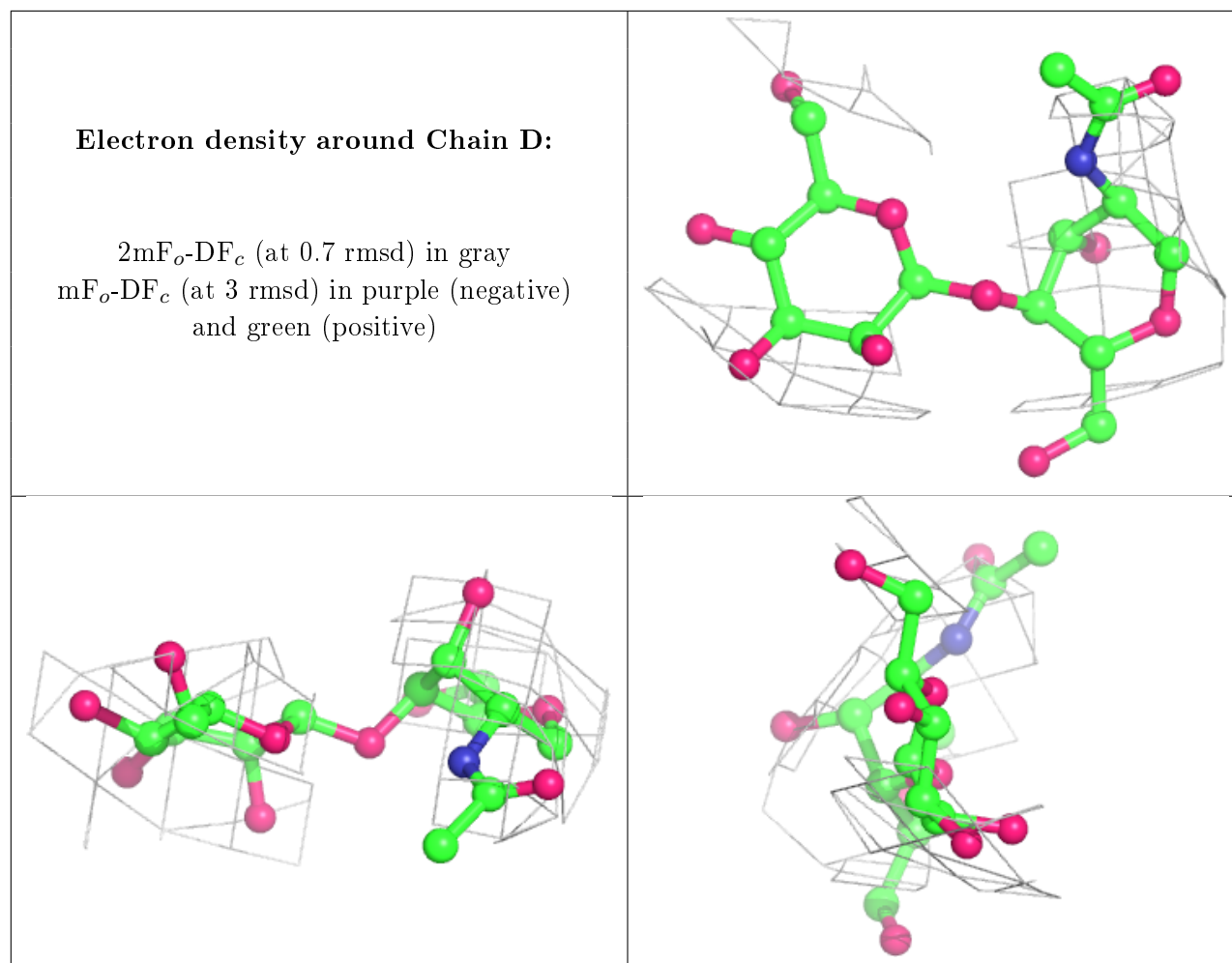
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BMA	D	2	11/12	0.72	0.27	162,190,200,204	0
2	BMA	C	2	11/12	0.82	0.27	119,144,147,148	0
2	NAG	D	1	14/15	0.86	0.45	157,204,221,228	0
2	NAG	C	1	14/15	0.91	0.27	116,152,167,179	0

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 ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	B	602	1/1	0.74	0.32	92,92,92,92	0
3	MG	B	606	1/1	0.79	0.16	43,43,43,43	0
3	MG	B	605	1/1	0.81	0.21	79,79,79,79	0
3	MG	A	603	1/1	0.84	0.20	92,92,92,92	0
4	NAG	B	609	14/15	0.84	0.24	196,208,224,224	0
3	MG	B	604	1/1	0.88	0.35	83,83,83,83	0
3	MG	A	605	1/1	0.88	0.12	90,90,90,90	0
3	MG	A	602	1/1	0.88	0.16	84,84,84,84	0
4	NAG	A	609	14/15	0.90	0.15	126,185,213,218	0
3	MG	A	601	1/1	0.90	0.56	133,133,133,133	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	B	601	1/1	0.91	0.35	116,116,116,116	0
3	MG	B	603	1/1	0.94	0.10	84,84,84,84	0
3	MG	A	606	1/1	0.96	0.22	57,57,57,57	0
3	MG	A	604	1/1	0.97	0.26	102,102,102,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.