Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2023 – 11:53 AM JST

PDB ID	:	5Z65
Title	:	Crystal structure of porcine aminopeptidase N ectodomain in functional form
Authors	:	Sun, Y.G.; Li, R.; Jiang, L.G.; Qiao, S.L.; Zhang, G.P.
Deposited on	:	2018-01-22
Resolution	:	2.65 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

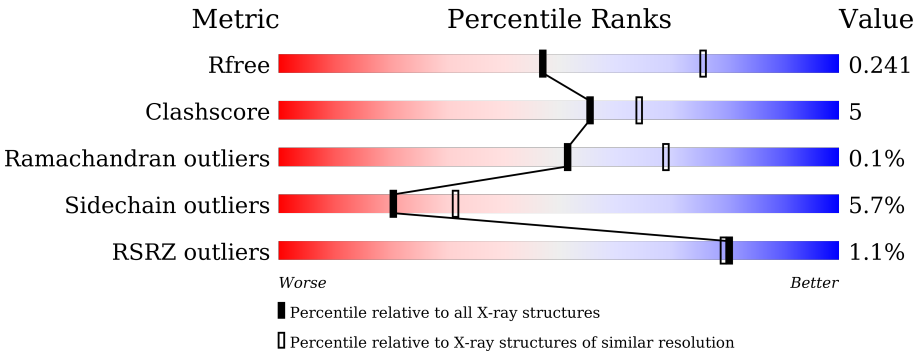
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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

Mol	Chain	Length	Quality of chain
1	A	913	% 87% 11% ••
2	B	3	67% 33%
2	C	3	100%
3	D	2	100%
3	E	2	100%
3	F	2	100%

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Mol	Chain	Length	Quality of chain
3	G	2	100%
3	H	2	100%
3	I	2	100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7530 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.

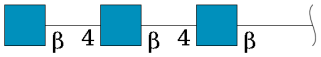
- Molecule 1 is a protein called Aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	900	Total	C	N	O	S	0	0	0
			7228	4617	1207	1374	30			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	ARG	-	see sequence details	UNP K7GMF9
A	62	SER	-	see sequence details	UNP K7GMF9
A	964	THR	-	see sequence details	UNP K7GMF9
A	965	ARG	-	see sequence details	UNP K7GMF9
A	966	THR	-	see sequence details	UNP K7GMF9
A	967	GLY	-	see sequence details	UNP K7GMF9
A	968	HIS	-	expression tag	UNP K7GMF9
A	969	HIS	-	expression tag	UNP K7GMF9
A	970	HIS	-	expression tag	UNP K7GMF9
A	971	HIS	-	expression tag	UNP K7GMF9
A	972	HIS	-	expression tag	UNP K7GMF9
A	973	HIS	-	expression tag	UNP K7GMF9

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

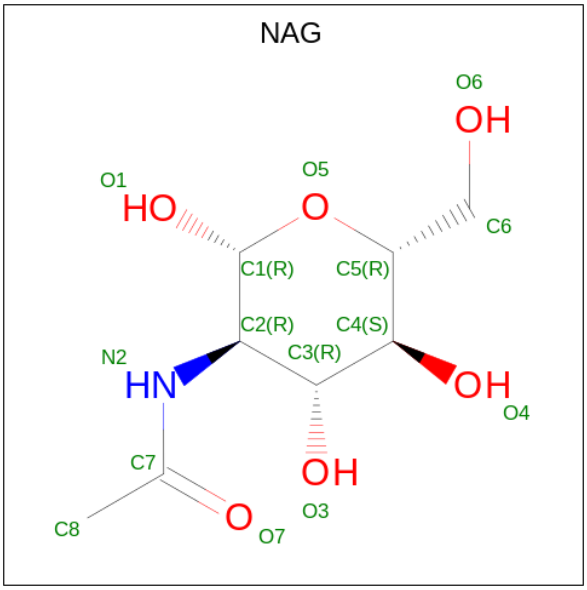


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			42	24	3	15			
2	C	3	Total	C	N	O	0	0	0
			42	24	3	15			

- Molecule 3 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
3	D	2	Total C N O 28 16 2 10	0	0	0
3	E	2	Total C N O 28 16 2 10	0	0	0
3	F	2	Total C N O 28 16 2 10	0	0	0
3	G	2	Total C N O 28 16 2 10	0	0	0
3	H	2	Total C N O 28 16 2 10	0	0	0
3	I	2	Total C N O 28 16 2 10	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Zn 1 1	0	0

- Molecule 6 is water.

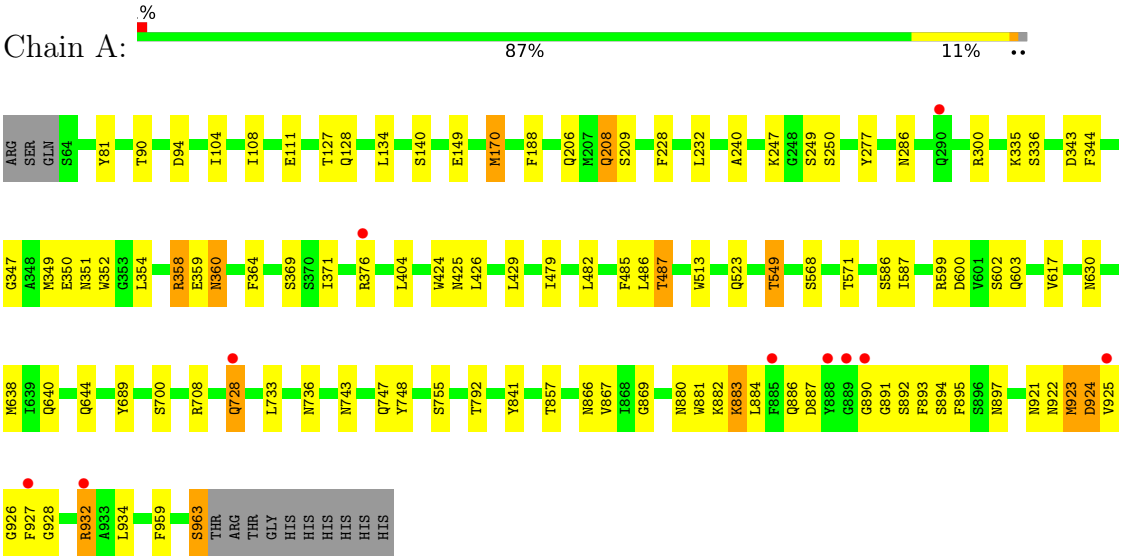
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	35	Total O 35 35	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Aminopeptidase

Chain A:

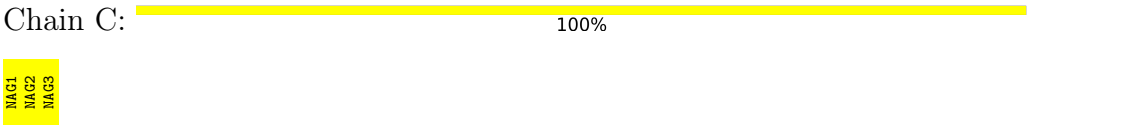


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

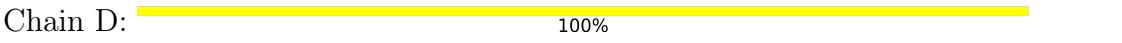
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

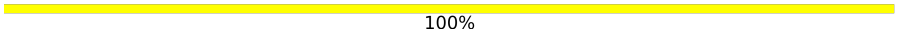


• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

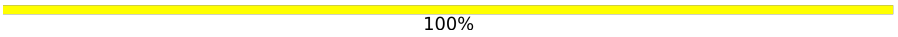
Chain D:



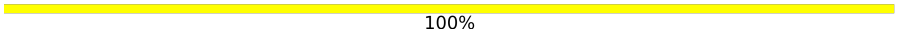
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 

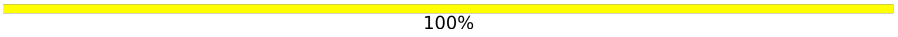
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F: 

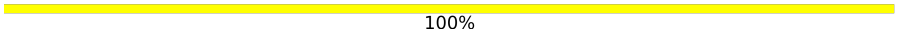
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 

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

Chain H: 

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

Chain I: 

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	260.33Å 62.31Å 80.57Å 90.00° 100.06° 90.00°	Depositor
Resolution (Å)	73.44 – 2.65 73.44 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.5 (73.44-2.65) 99.5 (73.44-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.41 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.196 , 0.251 0.201 , 0.241	Depositor DCC
R_{free} test set	1758 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å^2)	62.5	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 40.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	7530	wwPDB-VP
Average B, all atoms (Å^2)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.91% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 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	0.66	0/7417	0.77	0/10109

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	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	932	ARG	Peptide

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	7228	0	6985	75	0
2	B	42	0	37	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	42	0	37	0	0
3	D	28	0	25	0	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
3	G	28	0	25	0	0
3	H	28	0	25	0	0
3	I	28	0	25	0	0
4	A	14	0	13	0	0
5	A	1	0	0	0	0
6	A	35	0	0	0	0
All	All	7530	0	7222	75	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 5.

All (75) 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:884:LEU:HD12	1:A:895:PHE:CE2	1.68	1.28
1:A:884:LEU:HD12	1:A:895:PHE:CZ	1.75	1.20
1:A:884:LEU:CD1	1:A:895:PHE:CE2	2.28	1.16
1:A:358:ARG:HH11	1:A:376:ARG:NH2	1.47	1.13
1:A:358:ARG:NH1	1:A:376:ARG:HH21	1.56	1.02
1:A:887:ASP:HB3	1:A:893:PHE:CD2	1.97	0.97
1:A:887:ASP:O	1:A:891:GLY:O	1.85	0.94
1:A:358:ARG:NH1	1:A:376:ARG:NH2	2.17	0.92
1:A:884:LEU:CD1	1:A:895:PHE:CZ	2.49	0.88
1:A:886:GLN:O	1:A:890:GLY:HA3	1.73	0.87
1:A:959:PHE:O	1:A:963:SER:OG	1.93	0.85
1:A:486:LEU:O	1:A:487:THR:OG1	1.94	0.83
1:A:880:ASN:O	1:A:883:LYS:HD2	1.83	0.79
1:A:884:LEU:HD21	1:A:928:GLY:N	2.00	0.76
1:A:883:LYS:HD3	1:A:883:LYS:C	2.11	0.69
1:A:924:ASP:O	1:A:925:VAL:HG22	1.93	0.67
1:A:924:ASP:O	1:A:926:GLY:N	2.29	0.65
1:A:358:ARG:HH11	1:A:376:ARG:HH21	0.74	0.64
1:A:128:GLN:O	1:A:128:GLN:HG3	1.99	0.63
1:A:371:ILE:HD13	1:A:747:GLN:HE22	1.65	0.62
1:A:886:GLN:O	1:A:890:GLY:CA	2.47	0.60
1:A:426:LEU:HD23	1:A:429:LEU:HD12	1.84	0.59
1:A:206:GLN:OE1	1:A:349:MET:HG2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:ILE:HD11	1:A:424:TRP:CZ2	2.39	0.57
1:A:884:LEU:HD13	1:A:895:PHE:CE2	2.33	0.57
1:A:347:GLY:HA2	1:A:358:ARG:HG2	1.87	0.55
1:A:884:LEU:HD21	1:A:928:GLY:CA	2.36	0.55
1:A:708:ARG:HG2	1:A:867:VAL:CG2	2.37	0.55
1:A:925:VAL:HG23	1:A:926:GLY:N	2.20	0.55
1:A:600:ASP:OD1	1:A:600:ASP:N	2.38	0.53
1:A:108:ILE:HB	1:A:170:MET:HE3	1.92	0.52
1:A:925:VAL:CG2	1:A:926:GLY:N	2.73	0.51
1:A:404:LEU:HD12	1:A:479:ILE:HD11	1.93	0.51
1:A:887:ASP:CB	1:A:893:PHE:CD2	2.83	0.51
1:A:884:LEU:CD1	1:A:895:PHE:CD2	2.91	0.50
1:A:364:PHE:CE1	1:A:369:SER:HB2	2.46	0.49
1:A:887:ASP:O	1:A:893:PHE:HB2	2.12	0.49
1:A:689:TYR:CD1	1:A:748:TYR:HB3	2.48	0.48
1:A:108:ILE:HB	1:A:170:MET:CE	2.43	0.48
1:A:360:ASN:OD1	1:A:360:ASN:N	2.44	0.48
1:A:923:MET:O	1:A:924:ASP:HB2	2.13	0.47
1:A:921:ASN:HA	1:A:923:MET:CE	2.44	0.47
1:A:81:TYR:CD1	1:A:228:PHE:CE2	3.03	0.47
1:A:350:GLU:O	1:A:350:GLU:HG2	2.13	0.47
1:A:887:ASP:HB3	1:A:893:PHE:HD2	1.72	0.46
1:A:921:ASN:HA	1:A:923:MET:HE2	1.97	0.46
1:A:927:PHE:CZ	1:A:934:LEU:HD23	2.50	0.46
1:A:104:ILE:HG21	2:B:1:NAG:H82	1.97	0.45
1:A:371:ILE:HD13	1:A:747:GLN:NE2	2.31	0.45
1:A:549:THR:HA	1:A:630:ASN:O	2.17	0.44
1:A:728:GLN:HE21	1:A:728:GLN:HA	1.83	0.44
1:A:921:ASN:O	1:A:925:VAL:HG21	2.17	0.44
1:A:300:ARG:NH2	1:A:359:GLU:OE2	2.51	0.43
1:A:884:LEU:HD11	1:A:895:PHE:CZ	2.49	0.43
1:A:482:LEU:HA	1:A:485:PHE:CE2	2.53	0.43
1:A:857:THR:HG22	1:A:893:PHE:CE1	2.55	0.42
1:A:424:TRP:O	1:A:425:ASN:HB3	2.20	0.42
1:A:887:ASP:OD2	1:A:893:PHE:CE2	2.73	0.42
1:A:232:LEU:HD12	1:A:240:ALA:HB1	2.00	0.42
1:A:881:TRP:HZ2	1:A:927:PHE:HA	1.85	0.42
1:A:894:SER:OG	1:A:897:ASN:HB2	2.20	0.42
1:A:882:LYS:C	1:A:884:LEU:H	2.23	0.42
1:A:351:ASN:HB2	1:A:354:LEU:O	2.19	0.42
1:A:892:SER:O	1:A:895:PHE:CE1	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:924:ASP:HB3	1:A:925:VAL:HG13	2.02	0.41
1:A:640:GLN:O	1:A:644:GLN:OE1	2.38	0.41
1:A:866:ASN:O	1:A:869:GLY:N	2.52	0.41
1:A:884:LEU:HD12	1:A:884:LEU:HA	1.90	0.41
1:A:344:PHE:HB3	1:A:358:ARG:HA	2.03	0.41
1:A:927:PHE:CE1	1:A:934:LEU:CD2	3.04	0.41
1:A:208:GLN:HG3	1:A:209:SER:N	2.35	0.41
1:A:755:SER:HA	1:A:792:THR:HG21	2.03	0.41
1:A:923:MET:O	1:A:924:ASP:CB	2.69	0.40
1:A:883:LYS:HD3	1:A:883:LYS:N	2.36	0.40
1:A:364:PHE:CE1	1:A:369:SER:CB	3.05	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	898/913 (98%)	852 (95%)	45 (5%)	1 (0%)	51 69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	487	THR

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	795/807 (98%)	750 (94%)	45 (6%)	20 31

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90	THR
1	A	94	ASP
1	A	111	GLU
1	A	127	THR
1	A	134	LEU
1	A	140	SER
1	A	149	GLU
1	A	170	MET
1	A	188	PHE
1	A	208	GLN
1	A	247	LYS
1	A	249	SER
1	A	250	SER
1	A	277	TYR
1	A	286	ASN
1	A	335	LYS
1	A	336	SER
1	A	343	ASP
1	A	352	TRP
1	A	358	ARG
1	A	360	ASN
1	A	513	TRP
1	A	523	GLN
1	A	549	THR
1	A	568	SER
1	A	571	THR
1	A	586	SER
1	A	587	ILE
1	A	599	ARG
1	A	602	SER
1	A	603	GLN
1	A	617	VAL
1	A	638	MET
1	A	700	SER
1	A	728	GLN
1	A	733	LEU
1	A	736	ASN
1	A	743	ASN

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Mol	Chain	Res	Type
1	A	841	TYR
1	A	883	LYS
1	A	922	ASN
1	A	923	MET
1	A	924	ASP
1	A	932	ARG
1	A	963	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	448	HIS
1	A	728	GLN
1	A	760	ASN
1	A	775	GLN
1	A	812	GLN
1	A	814	GLN
1	A	878	GLN
1	A	917	GLN
1	A	922	ASN

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)

18 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	0.53	0	17,19,21	1.07	1 (5%)
2	NAG	B	2	2	14,14,15	0.83	0	17,19,21	2.12	7 (41%)
2	NAG	B	3	2	14,14,15	1.03	1 (7%)	17,19,21	1.62	2 (11%)
2	NAG	C	1	1,2	14,14,15	0.70	0	17,19,21	1.19	1 (5%)
2	NAG	C	2	2	14,14,15	0.89	0	17,19,21	1.41	3 (17%)
2	NAG	C	3	2	14,14,15	0.97	1 (7%)	17,19,21	1.46	3 (17%)
3	NAG	D	1	1,3	14,14,15	0.70	0	17,19,21	1.38	3 (17%)
3	NAG	D	2	3	14,14,15	0.79	0	17,19,21	1.21	1 (5%)
3	NAG	E	1	1,3	14,14,15	0.78	0	17,19,21	2.06	4 (23%)
3	NAG	E	2	3	14,14,15	0.55	0	17,19,21	1.12	2 (11%)
3	NAG	F	1	1,3	14,14,15	0.52	0	17,19,21	1.78	3 (17%)
3	NAG	F	2	3	14,14,15	1.08	2 (14%)	17,19,21	2.41	6 (35%)
3	NAG	G	1	1,3	14,14,15	0.96	0	17,19,21	2.32	7 (41%)
3	NAG	G	2	3	14,14,15	0.80	0	17,19,21	2.22	5 (29%)
3	NAG	H	1	1,3	14,14,15	0.93	0	17,19,21	2.76	6 (35%)
3	NAG	H	2	3	14,14,15	0.56	0	17,19,21	1.49	2 (11%)
3	NAG	I	1	1,3	14,14,15	0.76	1 (7%)	17,19,21	1.51	3 (17%)
3	NAG	I	2	3	14,14,15	0.56	0	17,19,21	1.48	2 (11%)

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	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	3/6/23/26	0/1/1/1
2	NAG	B	3	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	-	2/6/23/26	0/1/1/1
2	NAG	C	3	2	-	2/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	NAG	E	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	NAG	G	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	G	2	3	-	4/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1
3	NAG	I	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	NAG	C1-C2	2.76	1.56	1.52
2	C	3	NAG	C1-C2	2.66	1.56	1.52
3	F	2	NAG	C2-N2	2.27	1.50	1.46
3	I	1	NAG	O4-C4	2.16	1.48	1.43
3	F	2	NAG	C1-C2	2.06	1.55	1.52

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	H	1	NAG	C1-O5-C5	8.49	123.69	112.19
3	G	2	NAG	O5-C5-C6	-6.48	97.05	107.20
3	F	2	NAG	C2-N2-C7	5.72	131.04	122.90
3	G	1	NAG	C3-C4-C5	-4.90	101.50	110.24
2	B	3	NAG	C4-C3-C2	4.78	118.02	111.02
2	B	2	NAG	C4-C3-C2	4.75	117.98	111.02
3	G	1	NAG	C1-O5-C5	4.55	118.36	112.19
3	F	2	NAG	C1-O5-C5	4.48	118.26	112.19
3	E	1	NAG	C1-O5-C5	4.35	118.08	112.19
3	E	1	NAG	C1-C2-N2	4.30	117.84	110.49
3	F	1	NAG	C1-C2-N2	4.09	117.47	110.49
3	I	2	NAG	O5-C5-C6	3.95	113.39	107.20
3	G	1	NAG	O5-C5-C6	-3.78	101.28	107.20
2	C	2	NAG	C4-C3-C2	3.70	116.44	111.02
3	F	2	NAG	C4-C3-C2	3.70	116.43	111.02
2	B	2	NAG	C1-O5-C5	3.62	117.10	112.19
3	E	1	NAG	C2-N2-C7	3.61	128.04	122.90
3	H	1	NAG	C8-C7-N2	3.61	122.21	116.10
3	F	1	NAG	O5-C1-C2	-3.56	105.66	111.29
3	H	2	NAG	C8-C7-N2	3.51	122.05	116.10
3	F	2	NAG	O5-C1-C2	3.39	116.64	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	G	2	NAG	C1-O5-C5	3.34	116.72	112.19
3	H	1	NAG	C3-C4-C5	3.29	116.10	110.24
2	C	3	NAG	O5-C5-C6	3.27	112.34	107.20
3	I	1	NAG	O5-C5-C6	-2.98	102.53	107.20
3	G	1	NAG	C4-C3-C2	2.91	115.28	111.02
3	F	1	NAG	C1-O5-C5	2.86	116.07	112.19
3	G	2	NAG	O6-C6-C5	-2.85	101.50	111.29
2	C	2	NAG	O5-C5-C6	2.82	111.62	107.20
3	E	1	NAG	C6-C5-C4	2.80	119.57	113.00
2	B	2	NAG	C8-C7-N2	2.79	120.82	116.10
3	G	2	NAG	O5-C1-C2	-2.73	106.98	111.29
2	B	1	NAG	C1-C2-N2	-2.71	105.87	110.49
3	G	1	NAG	O6-C6-C5	-2.70	102.03	111.29
2	B	2	NAG	O4-C4-C3	-2.70	104.11	110.35
3	D	1	NAG	O5-C5-C6	2.68	111.41	107.20
3	E	2	NAG	O5-C1-C2	-2.66	107.08	111.29
2	C	3	NAG	O5-C5-C4	-2.57	104.58	110.83
3	G	1	NAG	O5-C1-C2	-2.55	107.26	111.29
2	C	2	NAG	C1-C2-N2	-2.52	106.17	110.49
2	C	1	NAG	C4-C3-C2	2.49	114.66	111.02
2	B	2	NAG	O5-C5-C6	-2.42	103.41	107.20
3	D	2	NAG	C4-C3-C2	2.36	114.48	111.02
2	C	3	NAG	C2-N2-C7	2.36	126.27	122.90
3	H	1	NAG	C2-N2-C7	2.33	126.22	122.90
3	G	1	NAG	C1-C2-N2	-2.27	106.61	110.49
3	I	2	NAG	C1-O5-C5	2.27	115.27	112.19
3	E	2	NAG	C1-O5-C5	2.26	115.25	112.19
3	F	2	NAG	O7-C7-C8	-2.24	117.90	122.06
3	G	2	NAG	C6-C5-C4	-2.23	107.78	113.00
3	I	1	NAG	O4-C4-C5	2.21	114.79	109.30
3	D	1	NAG	O7-C7-C8	-2.20	117.97	122.06
3	I	1	NAG	O5-C1-C2	-2.17	107.86	111.29
3	H	2	NAG	O5-C1-C2	-2.17	107.86	111.29
3	H	1	NAG	O3-C3-C4	-2.17	105.34	110.35
2	B	3	NAG	O5-C5-C4	-2.16	105.57	110.83
2	B	2	NAG	C3-C4-C5	2.14	114.05	110.24
3	H	1	NAG	O4-C4-C3	-2.13	105.42	110.35
3	D	1	NAG	C2-N2-C7	2.11	125.91	122.90
2	B	2	NAG	O7-C7-C8	-2.08	118.19	122.06
3	F	2	NAG	O7-C7-N2	2.04	125.71	121.95

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	1	NAG	C3-C2-N2-C7
3	G	2	NAG	C8-C7-N2-C2
3	I	2	NAG	O5-C5-C6-O6
2	C	3	NAG	C4-C5-C6-O6
2	C	3	NAG	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
3	I	2	NAG	C4-C5-C6-O6
2	B	3	NAG	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	B	3	NAG	C4-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
3	G	2	NAG	O7-C7-N2-C2
3	H	2	NAG	O5-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
3	F	1	NAG	O5-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
3	H	1	NAG	C8-C7-N2-C2
3	H	1	NAG	O7-C7-N2-C2
3	H	2	NAG	C8-C7-N2-C2
3	H	2	NAG	O7-C7-N2-C2
3	G	2	NAG	O5-C5-C6-O6
3	F	2	NAG	C1-C2-N2-C7
3	H	2	NAG	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C1-C2-N2-C7

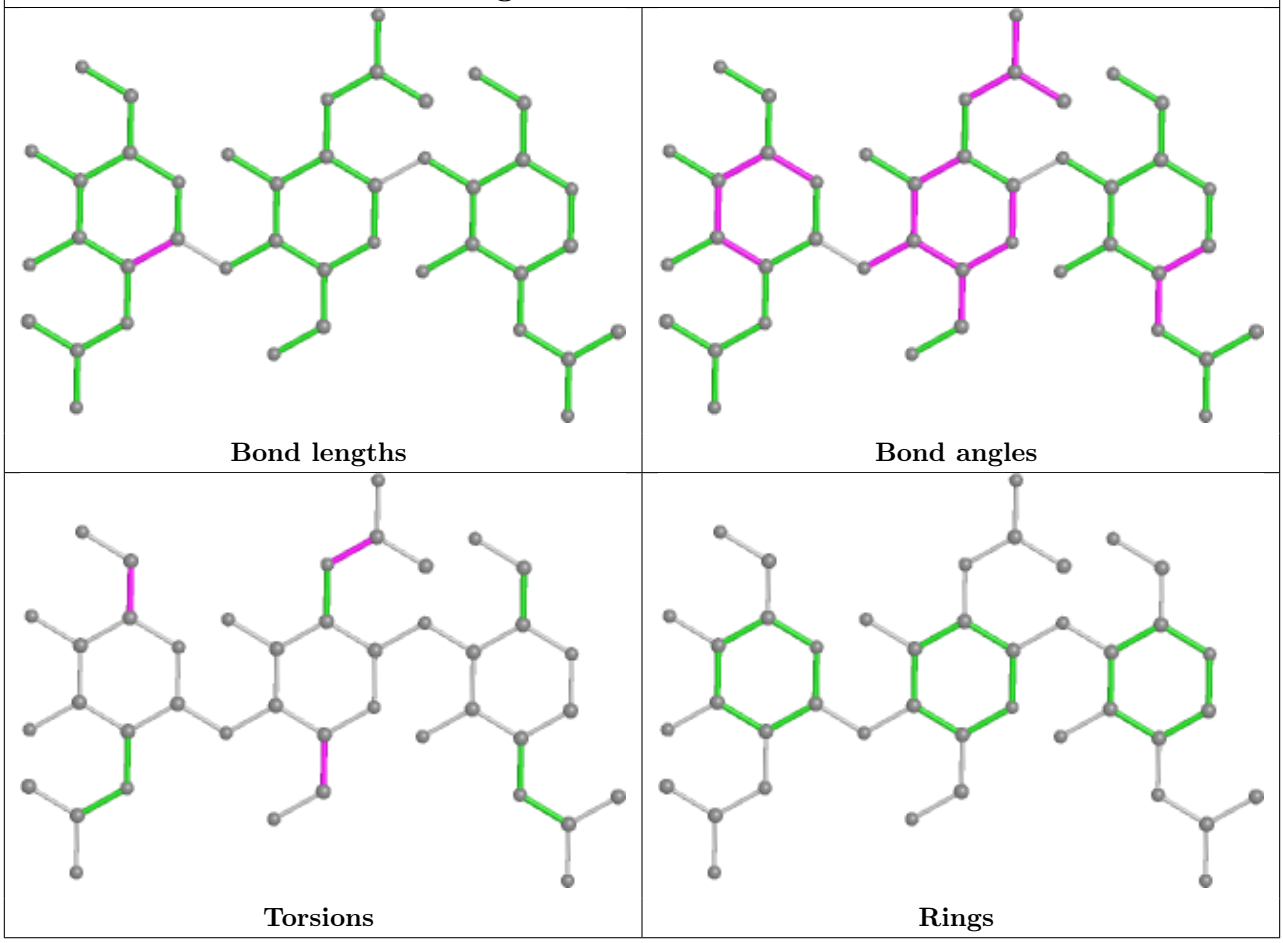
There are no ring outliers.

1 monomer is involved in 1 short contact:

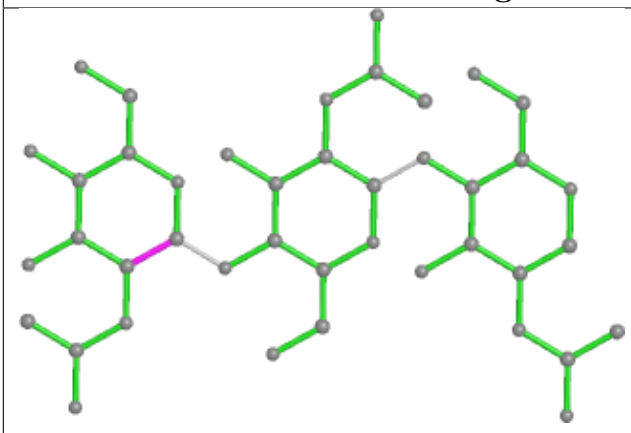
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1	NAG	1	0

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

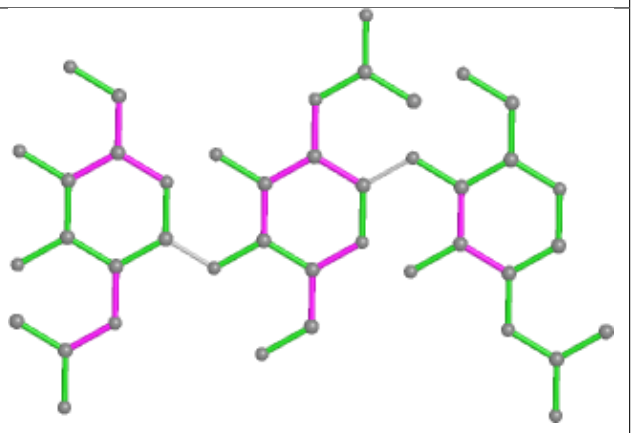
Oligosaccharide Chain B



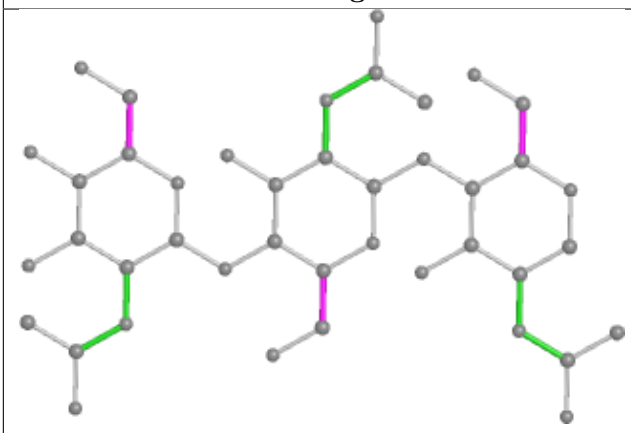
Oligosaccharide Chain C



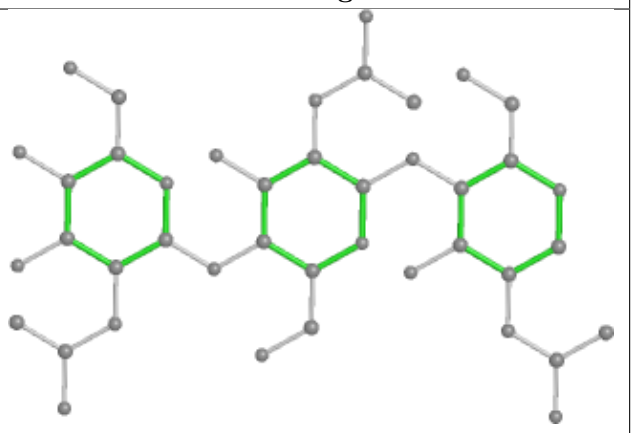
Bond lengths



Bond angles

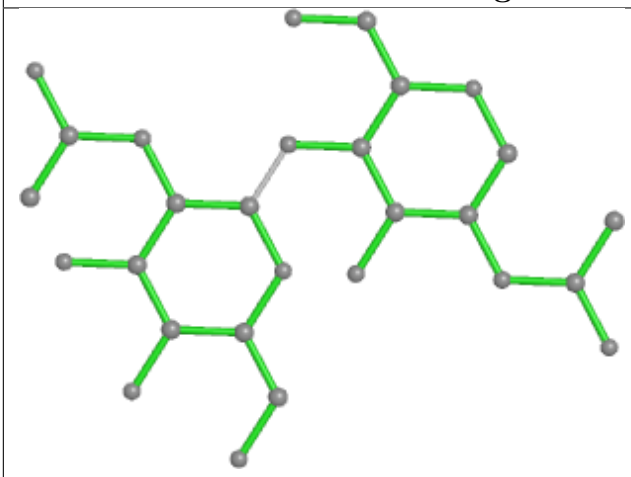


Torsions

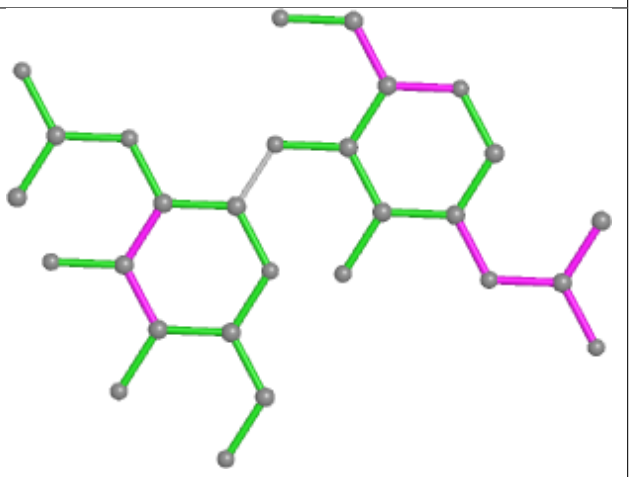


Rings

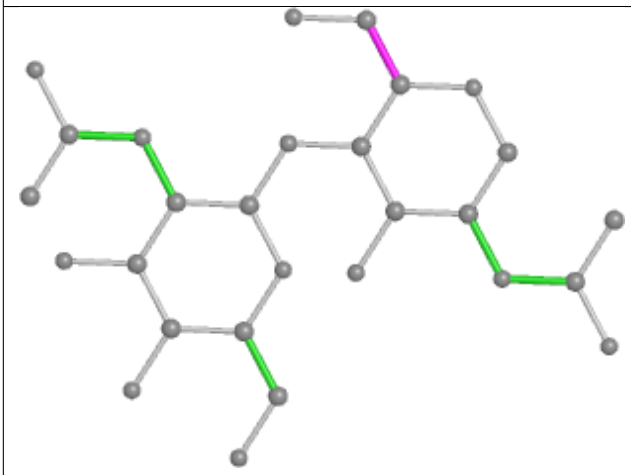
Oligosaccharide Chain D



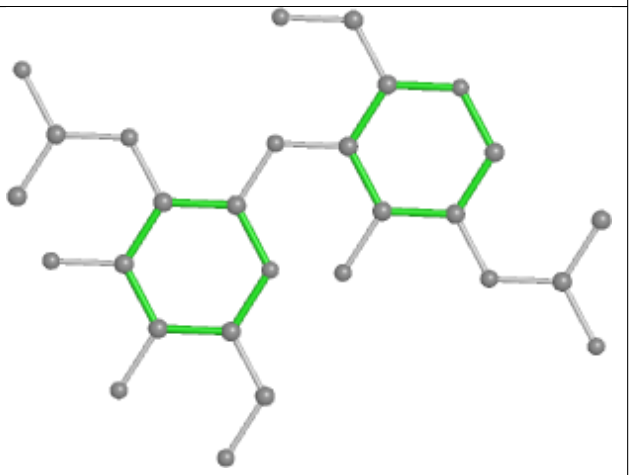
Bond lengths



Bond angles

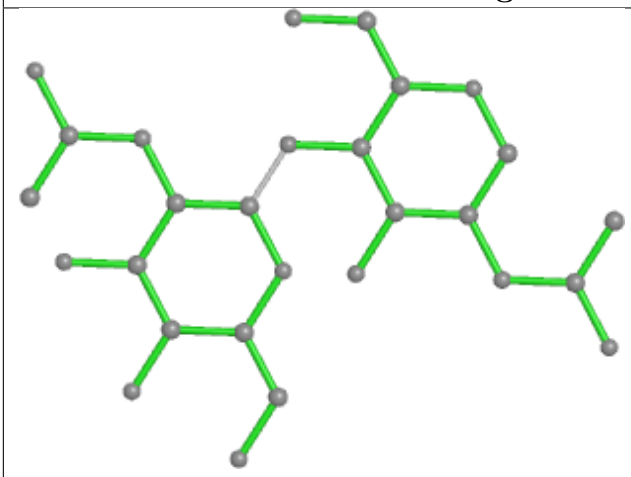


Torsions

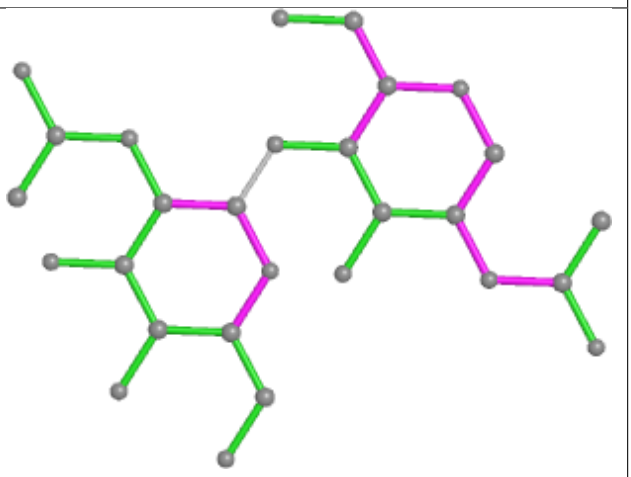


Rings

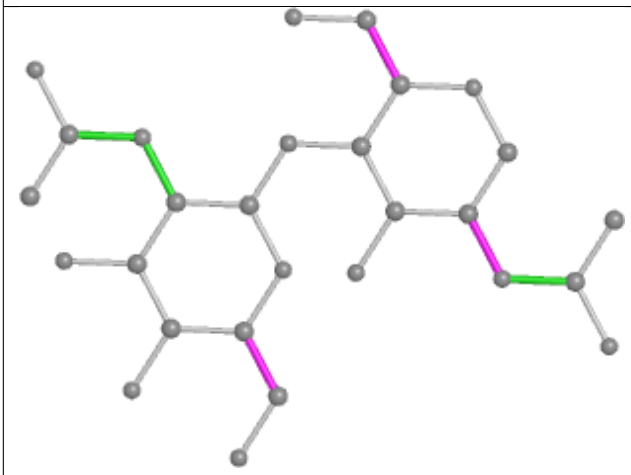
Oligosaccharide Chain E



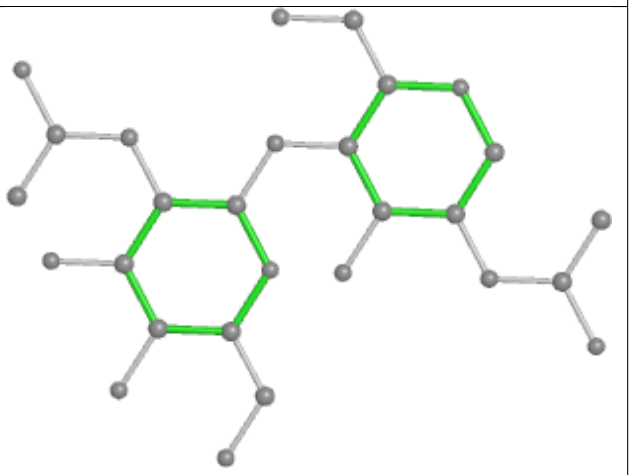
Bond lengths



Bond angles

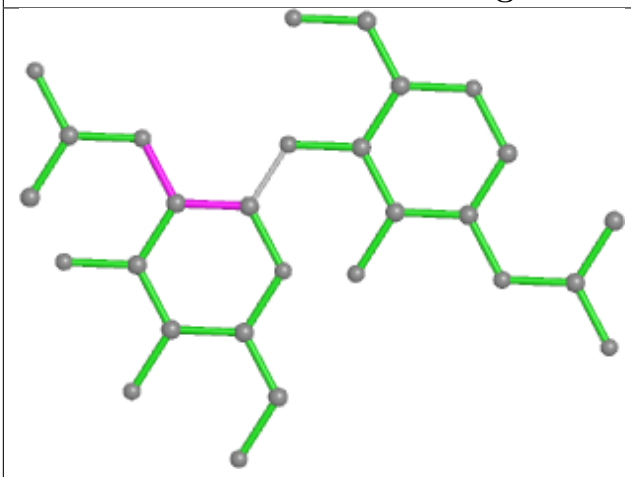


Torsions

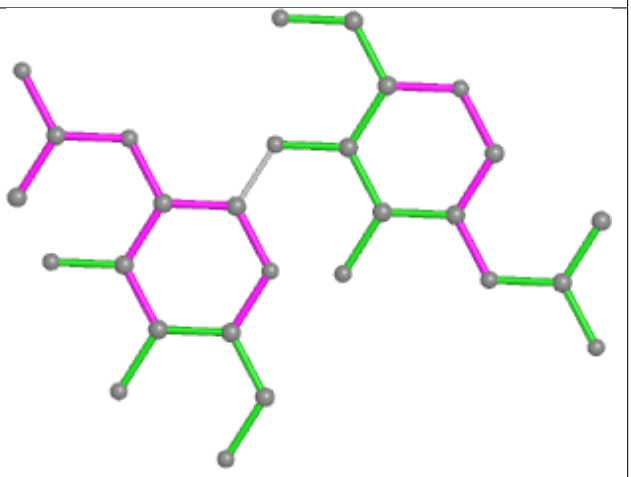


Rings

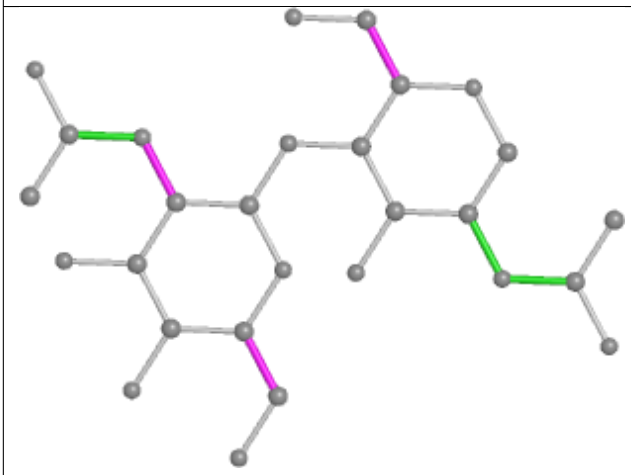
Oligosaccharide Chain F



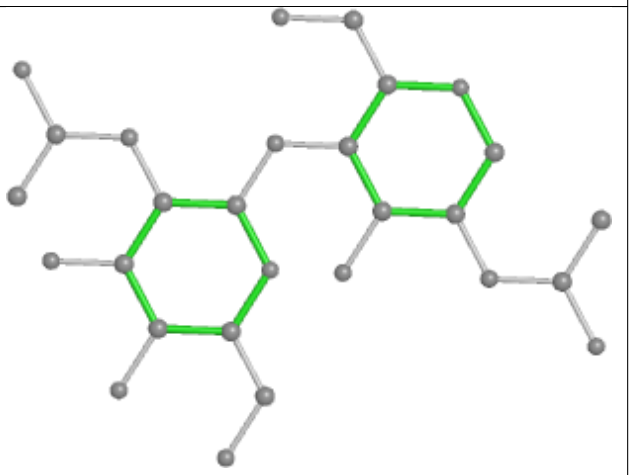
Bond lengths



Bond angles

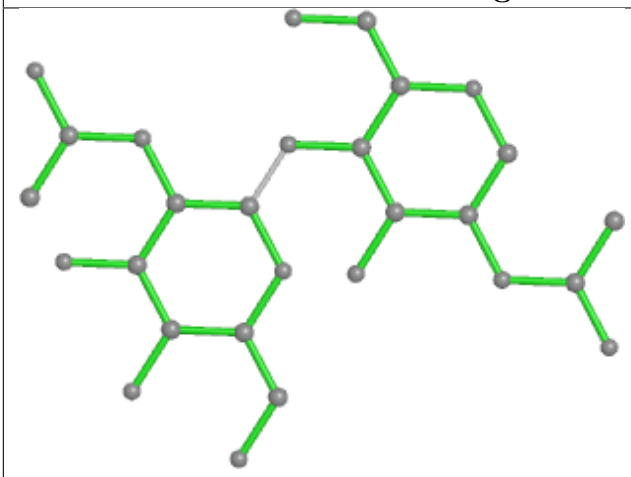


Torsions

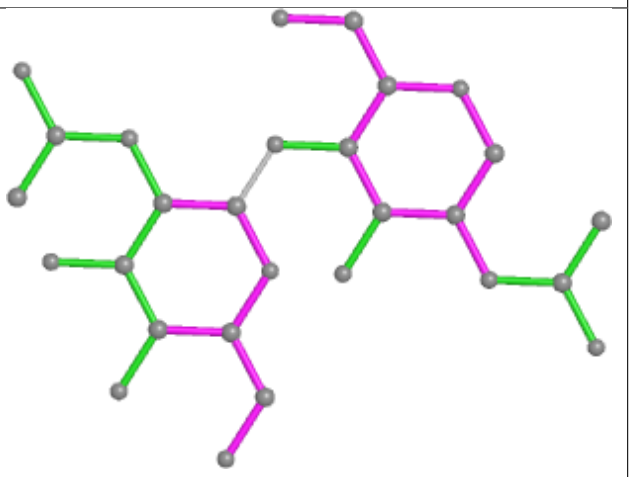


Rings

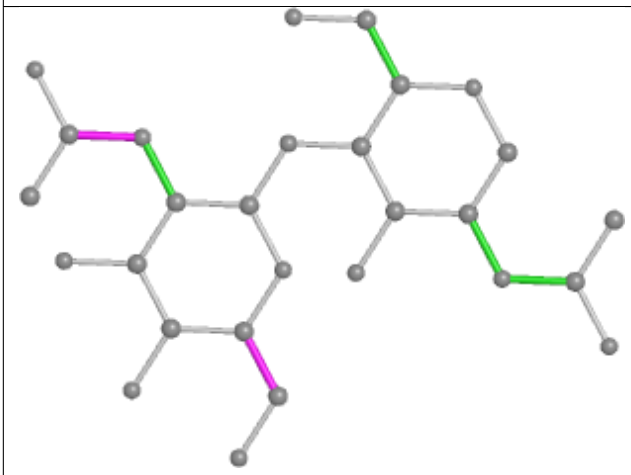
Oligosaccharide Chain G



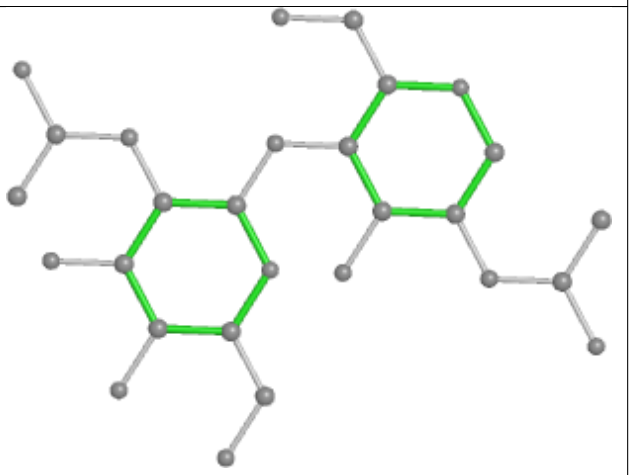
Bond lengths



Bond angles

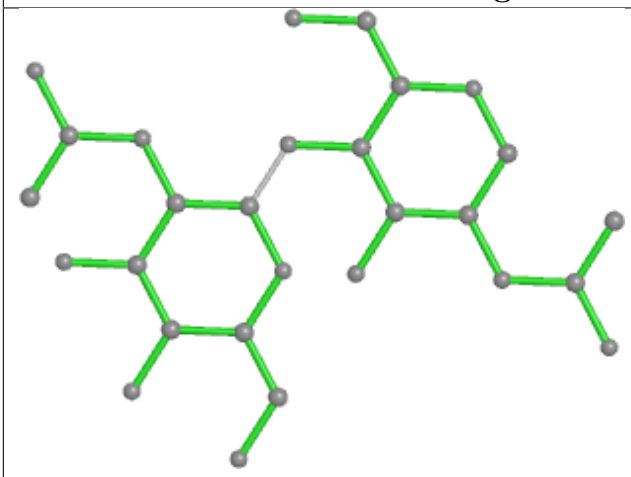


Torsions

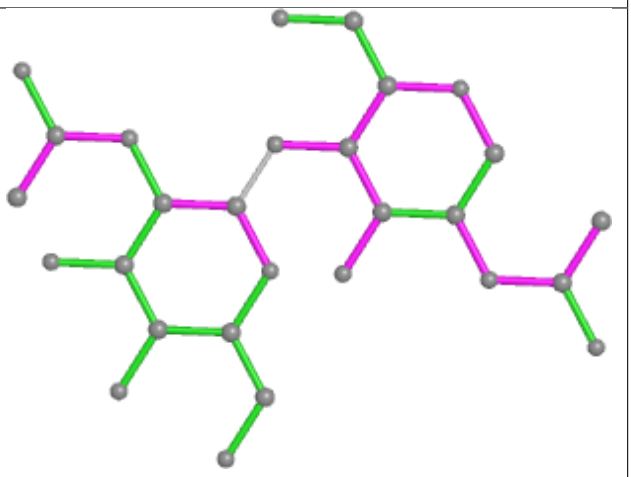


Rings

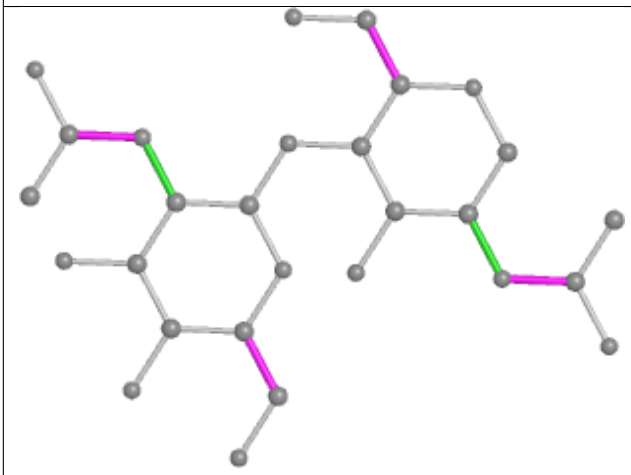
Oligosaccharide Chain H



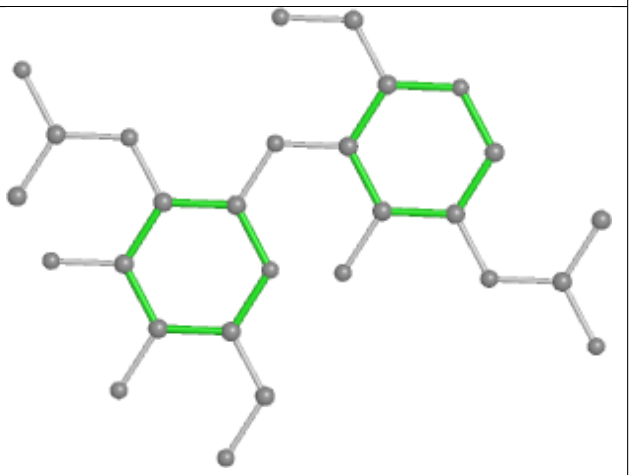
Bond lengths



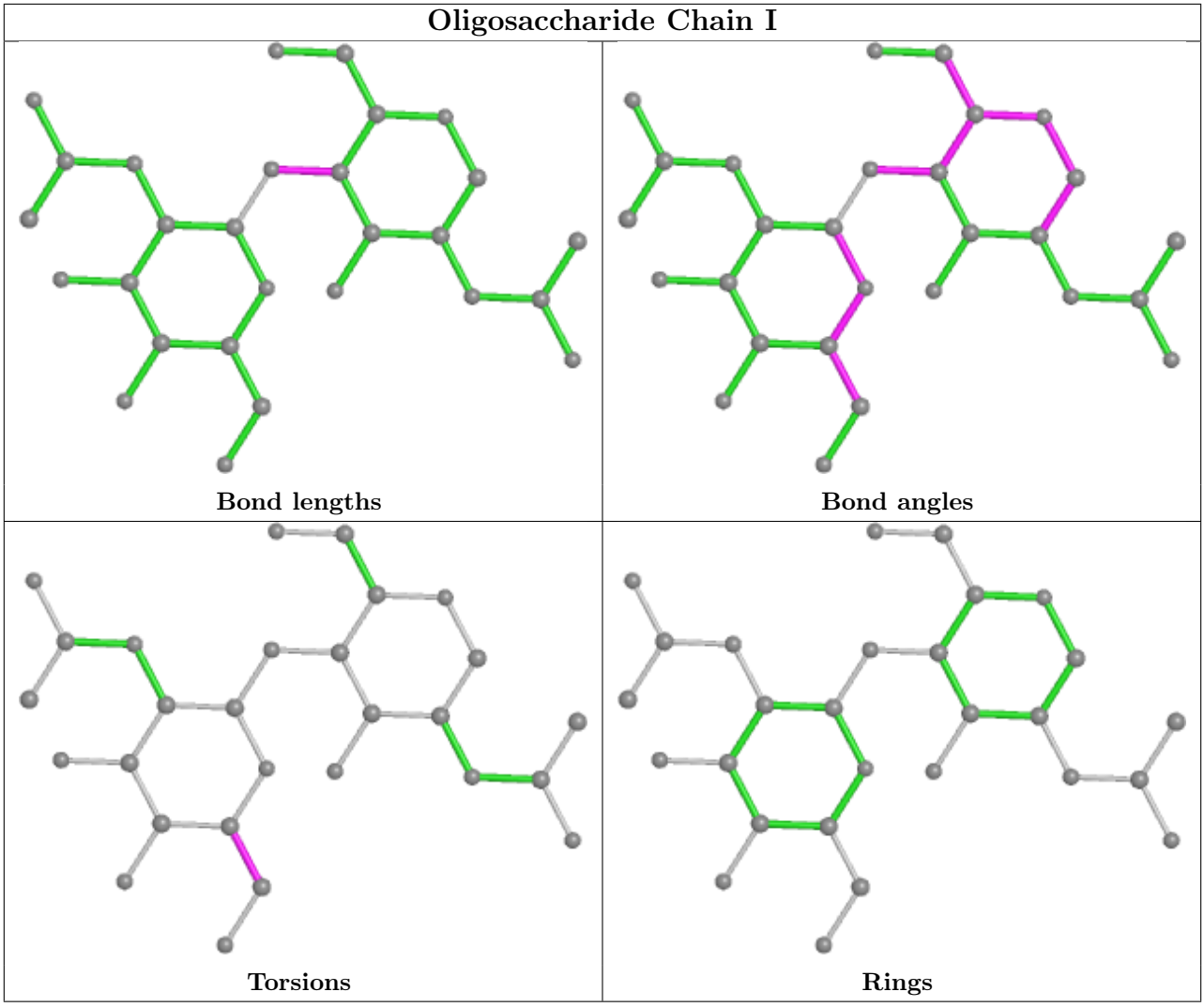
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	A	1019	1	14,14,15	0.80	0	17,19,21	1.60	2 (11%)

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	A	1019	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1019	NAG	O5-C5-C6	4.66	114.50	107.20
4	A	1019	NAG	O5-C1-C2	-2.70	107.02	111.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1019	NAG	C4-C5-C6-O6
4	A	1019	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	900/913 (98%)	0.12	10 (1%)	80	79	41, 67, 107, 185	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	889	GLY	8.7
1	A	890	GLY	5.4
1	A	888	TYR	4.2
1	A	932	ARG	3.8
1	A	885	PHE	3.4
1	A	290	GLN	3.2
1	A	927	PHE	2.8
1	A	728	GLN	2.7
1	A	925	VAL	2.2
1	A	376	ARG	2.1

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

There are no non-standard protein/DNA/RNA residues in this entry.

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^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	B	3	14/15	0.50	0.33	132,157,166,167	0
3	NAG	F	2	14/15	0.57	0.26	95,128,137,141	0

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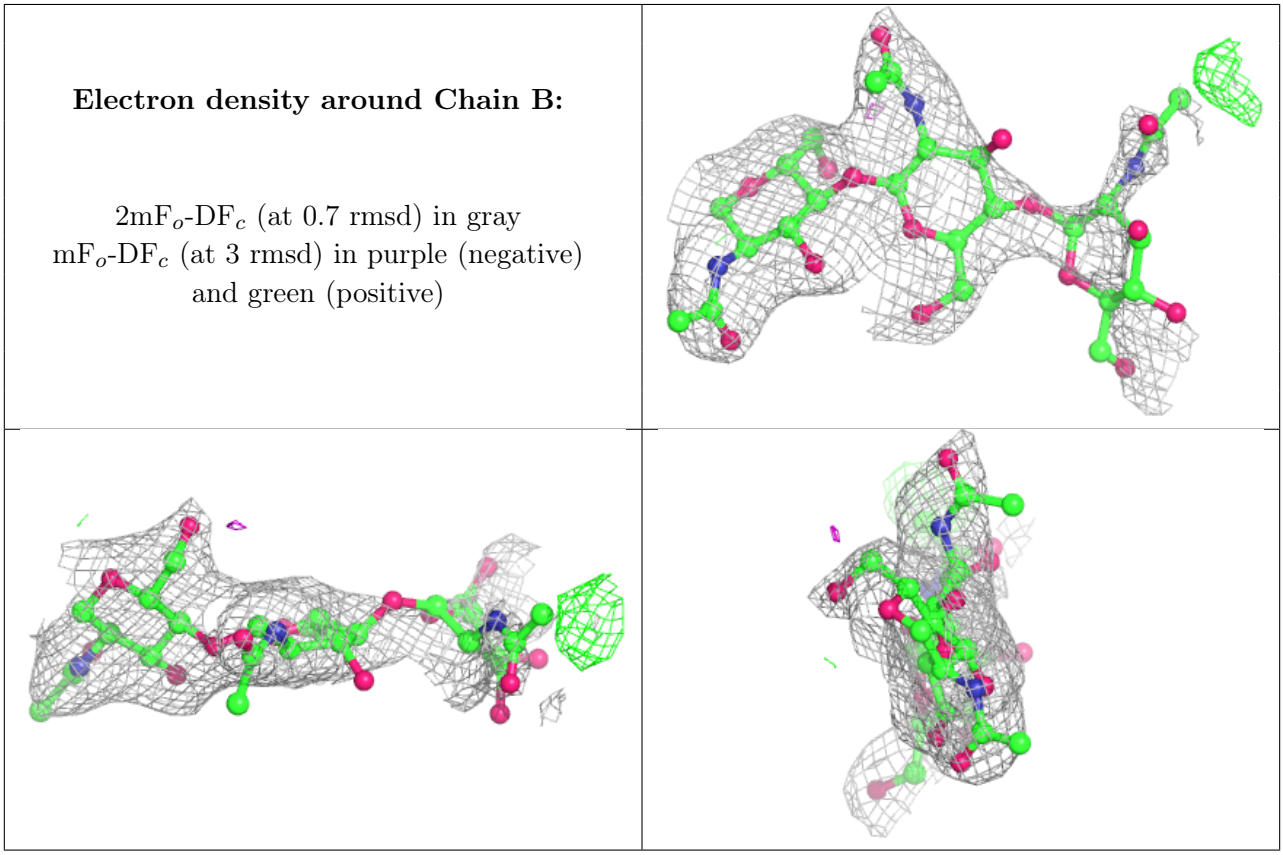
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	C	3	14/15	0.58	0.22	127,153,172,174	0
2	NAG	C	2	14/15	0.72	0.24	112,144,160,180	0
3	NAG	I	2	14/15	0.82	0.20	98,115,126,133	0
3	NAG	H	2	14/15	0.85	0.18	112,129,136,137	0
3	NAG	E	2	14/15	0.85	0.30	97,122,146,147	0
2	NAG	B	2	14/15	0.87	0.22	88,105,124,145	0
3	NAG	G	2	14/15	0.89	0.14	69,91,101,103	0
2	NAG	C	1	14/15	0.89	0.28	64,93,107,133	0
3	NAG	E	1	14/15	0.89	0.15	85,97,105,116	0
3	NAG	F	1	14/15	0.90	0.16	82,105,115,126	0
3	NAG	H	1	14/15	0.90	0.15	68,105,116,116	0
3	NAG	D	2	14/15	0.91	0.14	76,92,101,101	0
3	NAG	I	1	14/15	0.95	0.13	62,76,85,88	0
2	NAG	B	1	14/15	0.96	0.15	59,66,74,82	0
3	NAG	G	1	14/15	0.97	0.12	58,63,69,82	0
3	NAG	D	1	14/15	0.97	0.18	46,58,72,77	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.

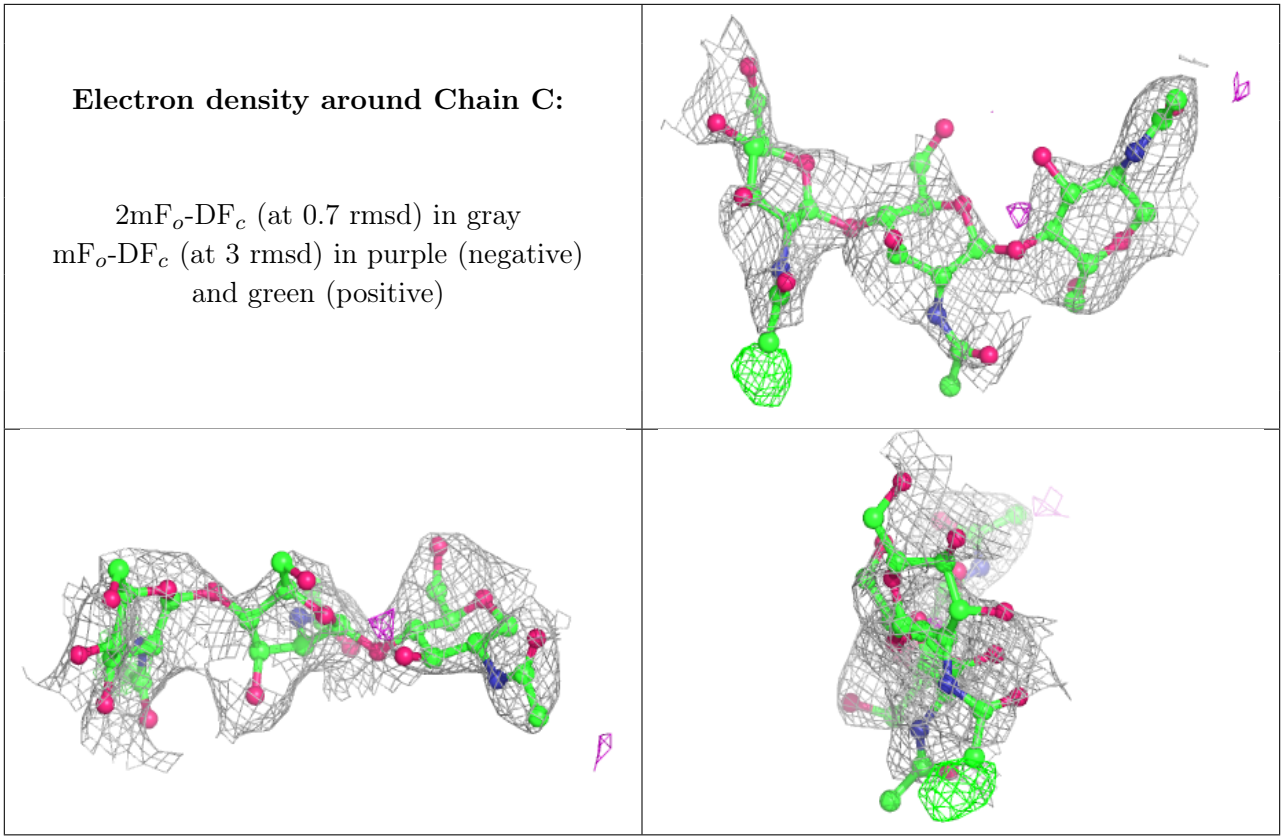
Electron density around Chain B:

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



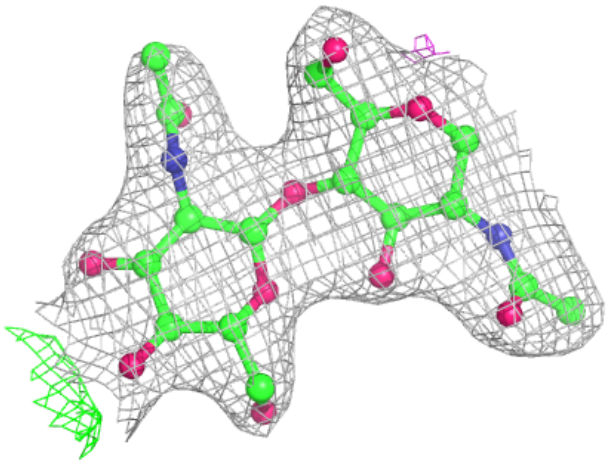
Electron density around Chain C:

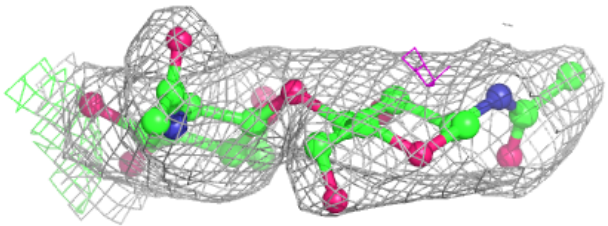
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

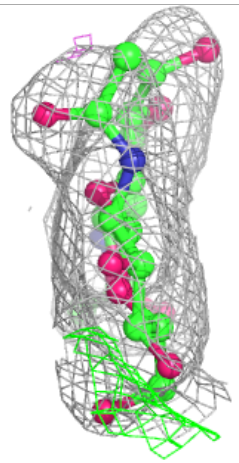


Electron density around Chain D:

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

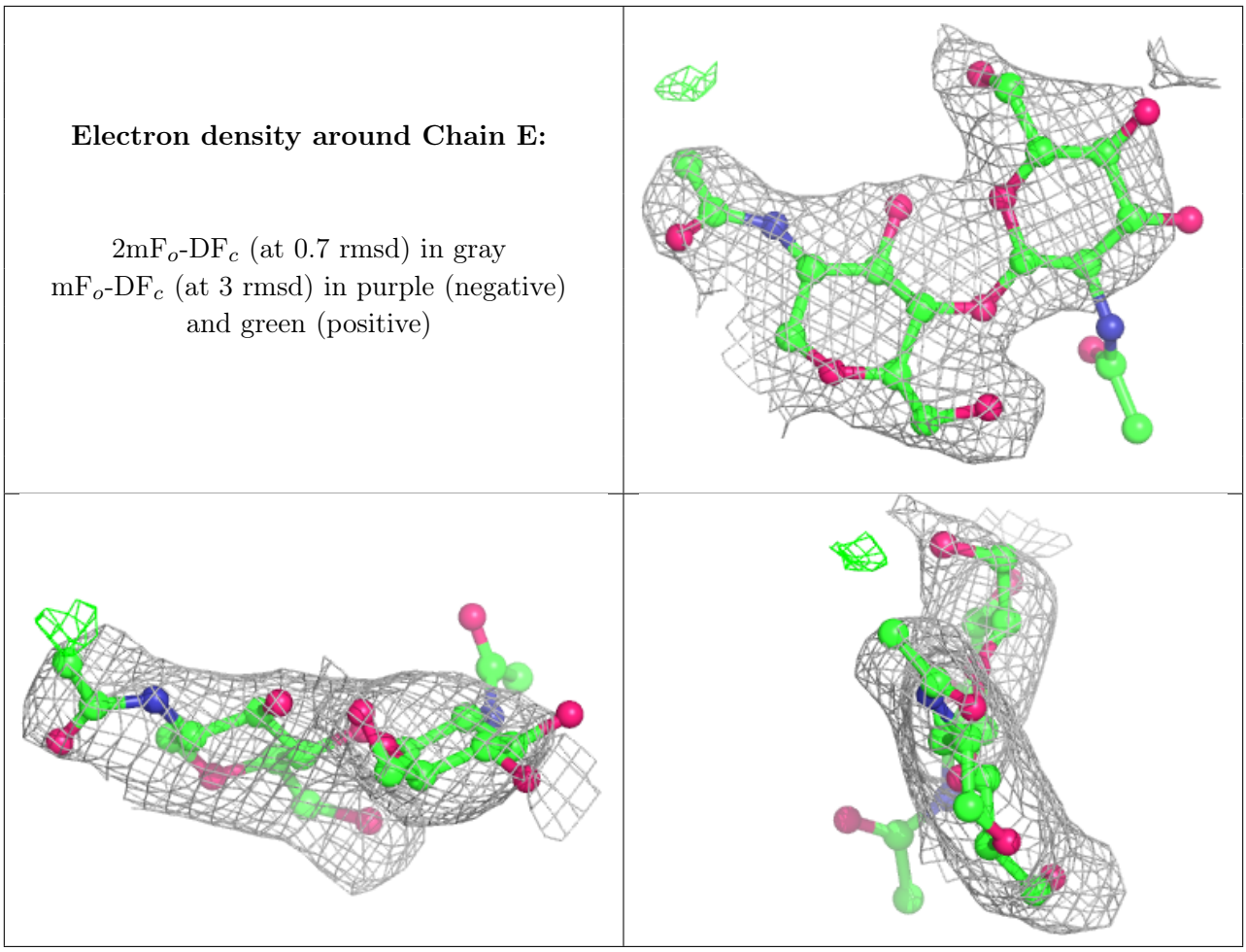






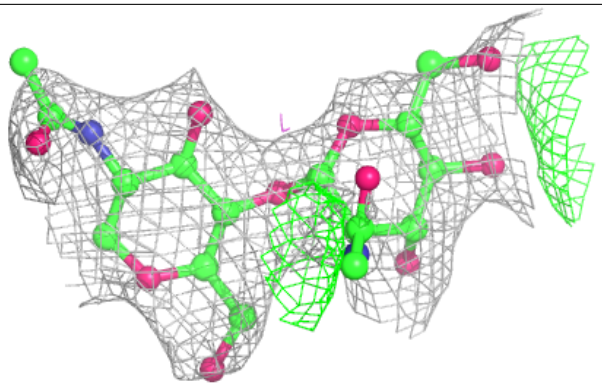
Electron density around Chain E:

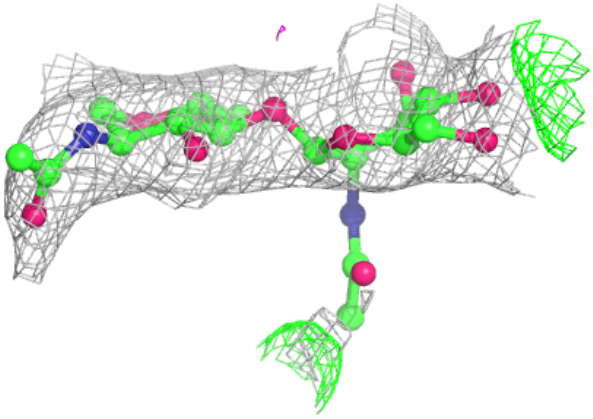
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

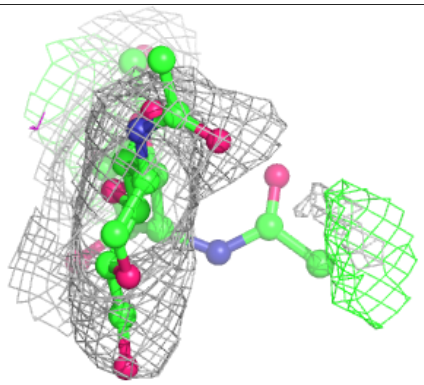


Electron density around Chain F:

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

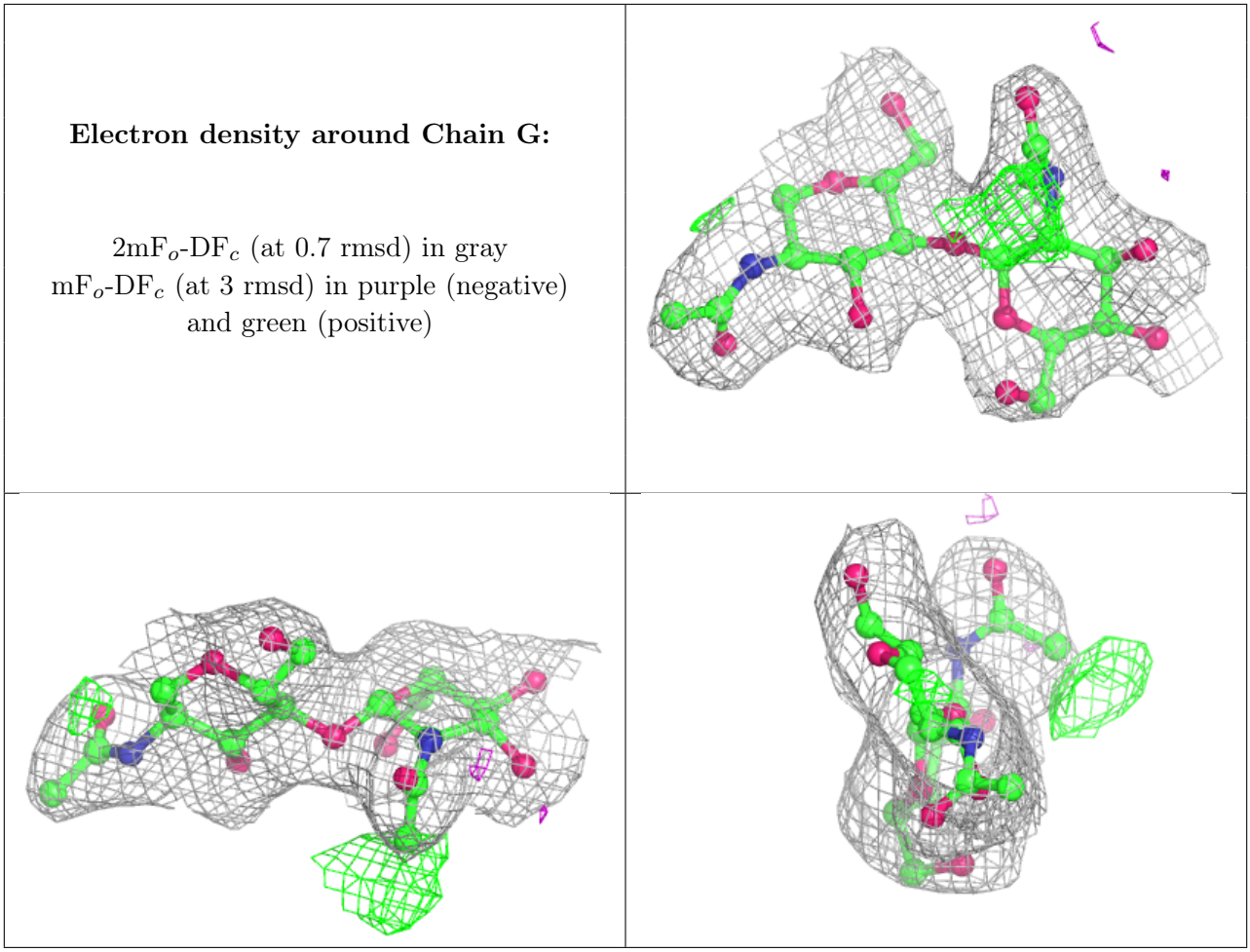






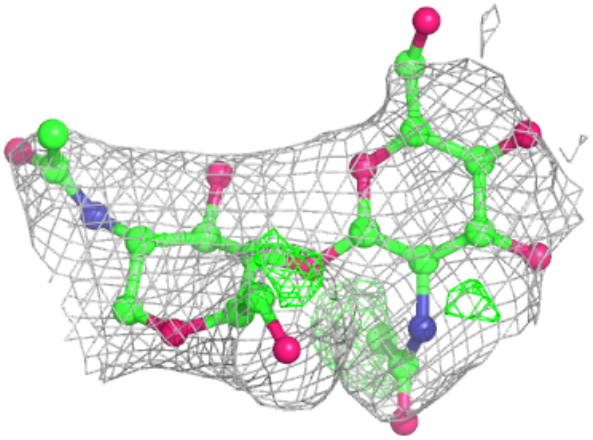
Electron density around Chain G:

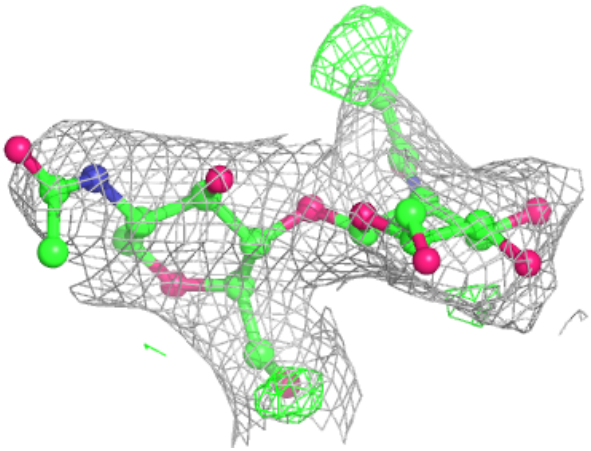
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

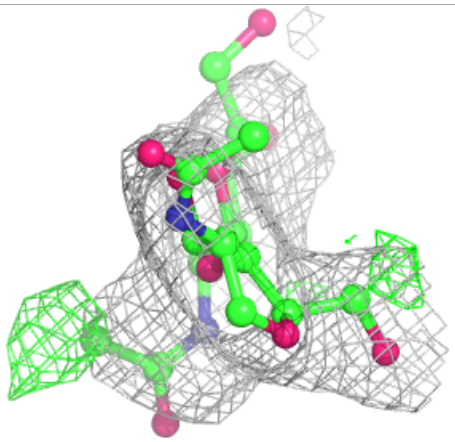


Electron density around Chain H:

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

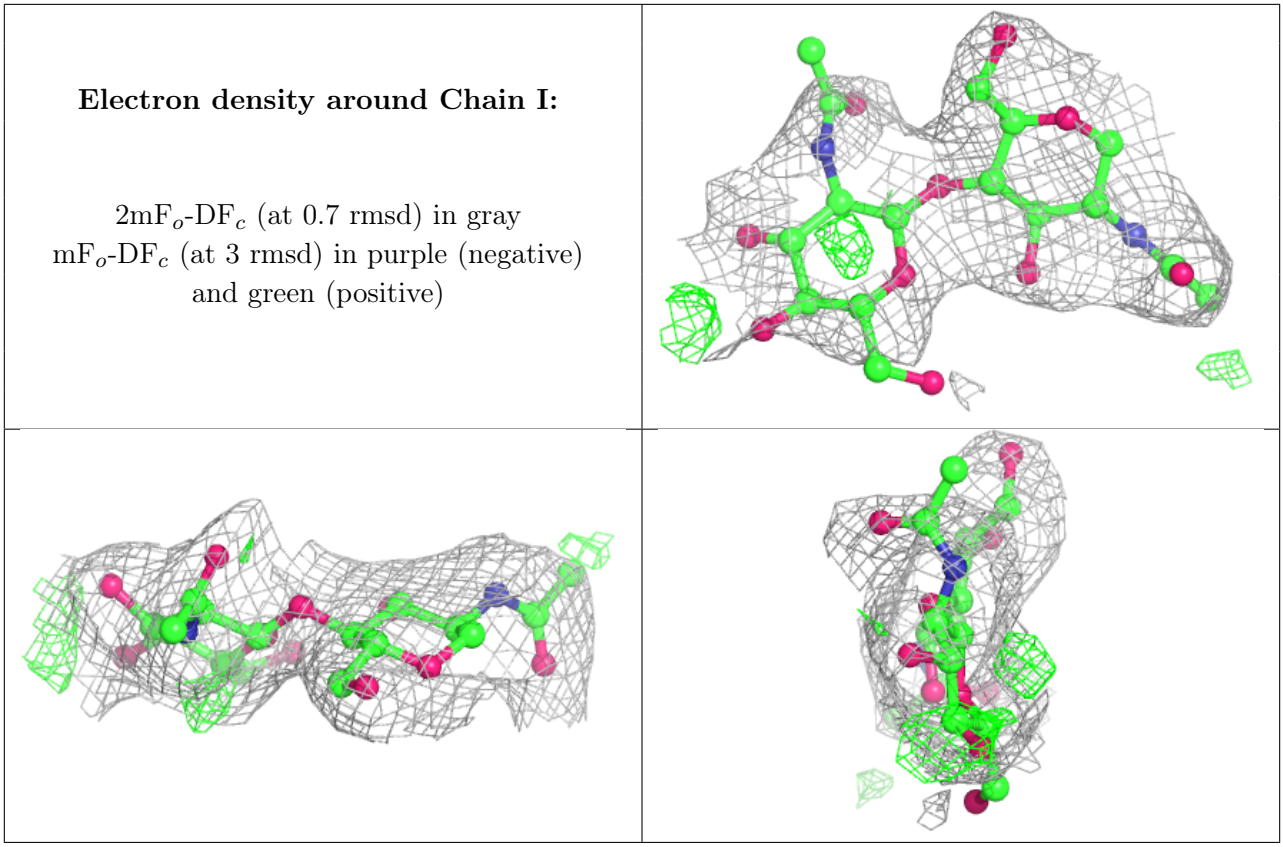






Electron density around Chain I:

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



6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	NAG	A	1019	14/15	0.76	0.24	104,119,126,126	0
5	ZN	A	1020	1/1	0.99	0.20	51,51,51,51	0

6.5 Other polymers

There are no such residues in this entry.