Full wwPDB X-ray Structure Validation Report ⓘ

Jan 15, 2024 – 04:34 pm GMT

PDB ID	:	6HKZ
Title	:	X-ray structure of human glutamate carboxypeptidase II (GCPII) in complex with a inhibitor RNA 2-49-1
Authors	:	Motlova, L.; Novakova, Z.; Barinka, C.
Deposited on	:	2018-09-09
Resolution	:	2.09 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:

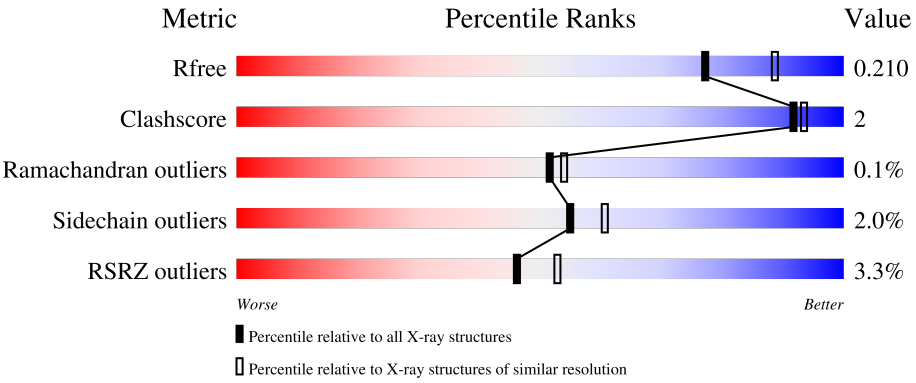
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 2.09 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	707	3%, 92%, 6%
2	B	2	50%, 50%
2	C	2	100%
3	D	4	100%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6205 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 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	694	5675	3643	951	1060	21	0	38	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 ZINC ION (three-letter code: ZN) (formula: Zn).

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

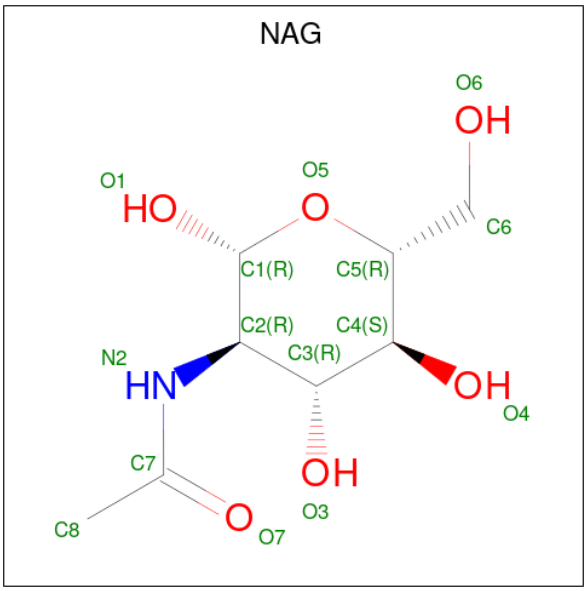
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

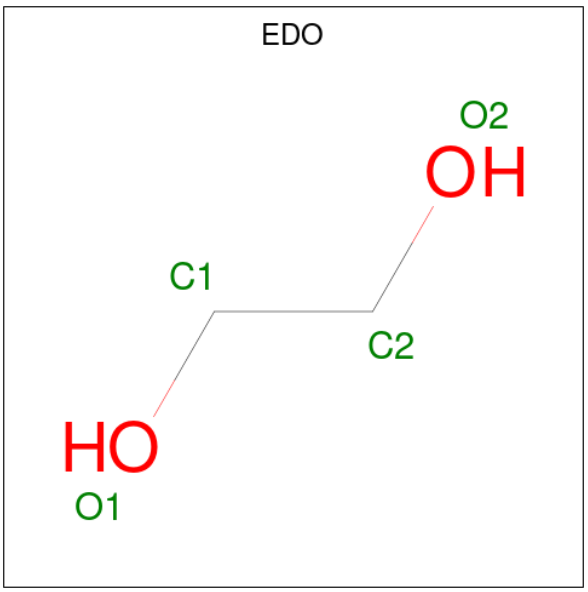
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Cl 1 1	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



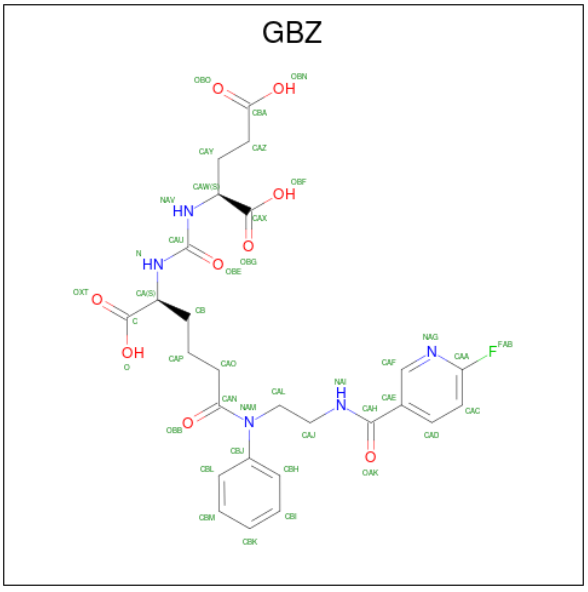
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N O 14 8 1 5	0	0
7	A	1	Total C N O 14 8 1 5	0	0
7	A	1	Total C N O 14 8 1 5	0	0
7	A	1	Total C N O 14 8 1 5	0	0

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 4 2 2	0	0

- Molecule 9 is (2 {S})-2-[[(2 {S})-6-[2-[(6-fluoranylpyridin-3-yl)carbonylamino]ethyl-phenyl-amino]-1-oxidanyl-1,6-bis(oxidanylidene)hexan-2-yl]carbamoylamino]pentanedioic acid (three-letter code: GBZ) (formula: $C_{26}H_{30}FN_5O_9$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C F N O 41 26 1 5 9	0	0

- Molecule 10 is water.

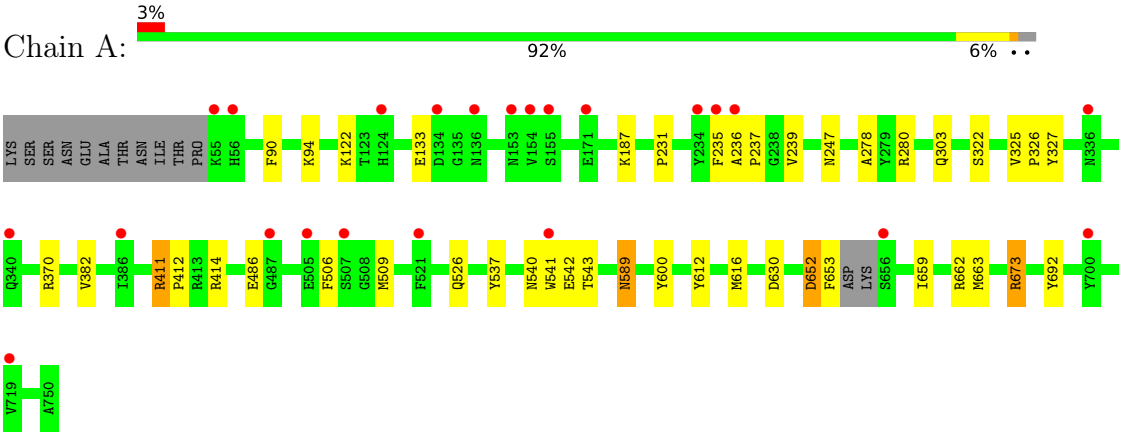
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	319	Total O 319 319	0	1

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: Glutamate carboxypeptidase 2

Chain A:

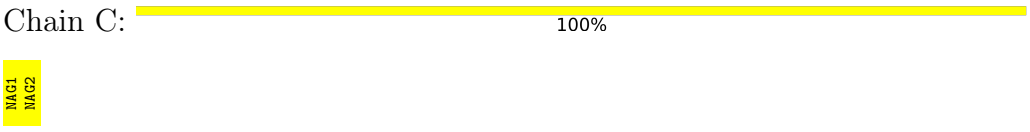


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

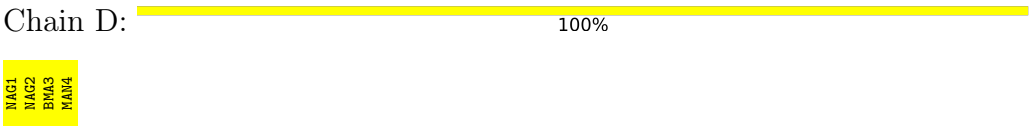
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:



• 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

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	102.96Å 132.26Å 161.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.59 – 2.09 47.73 – 2.09	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.59-2.09) 99.3 (47.73-2.09)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.30 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.170 , 0.203 0.181 , 0.210	Depositor DCC
R_{free} test set	2100 reflections (3.21%)	wwPDB-VP
Wilson B-factor (Å^2)	33.8	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 64.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6205	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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: GBZ, MAN, BMA, ZN, CA, CL, EDO, 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	0.78	0/5988	0.82	5/8109 (0.1%)

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	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	673	ARG	NE-CZ-NH2	-6.59	117.01	120.30
1	A	411	ARG	NE-CZ-NH2	-6.10	117.25	120.30
1	A	662	ARG	NE-CZ-NH2	-5.85	117.38	120.30
1	A	370	ARG	NE-CZ-NH2	-5.66	117.47	120.30
1	A	630	ASP	CB-CG-OD1	5.35	123.11	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	411	ARG	Sidechain
1	A	414	ARG	Sidechain

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	5675	0	5546	19	0
2	B	28	0	25	0	0
2	C	28	0	25	0	0
3	D	50	0	43	0	0
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	56	0	52	0	0
8	A	4	0	6	0	0
9	A	41	0	0	0	0
10	A	319	0	0	0	0
All	All	6205	0	5697	19	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 2.

All (19) 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:412:PRO:HA	1:A:589:ASN:HD21	1.37	0.90
1:A:235:PHE:HA	1:A:247:ASN:OD1	1.93	0.69
1:A:652:ASP:O	1:A:653:PHE:HB3	1.96	0.65
1:A:412:PRO:HA	1:A:589:ASN:ND2	2.11	0.62
1:A:236:ALA:HB1	1:A:237:PRO:CD	2.31	0.60
1:A:236:ALA:HB1	1:A:237:PRO:HD2	1.85	0.58
1:A:526[A]:GLN:OE1	1:A:692:TYR:O	2.27	0.52
1:A:659[B]:ILE:O	1:A:663[B]:MET:HG3	2.10	0.52
1:A:540:ASN:OD1	1:A:542:GLU:HG2	2.14	0.48
1:A:652:ASP:N	1:A:652:ASP:OD1	2.47	0.48
1:A:612:TYR:CZ	1:A:616:MET:HG3	2.48	0.47
1:A:231:PRO:HB3	1:A:235:PHE:HB3	2.00	0.44
1:A:542:GLU:O	1:A:543:THR:OG1	2.34	0.43
1:A:506:PHE:HB2	1:A:509:MET:HG3	2.00	0.42
1:A:325:VAL:HB	1:A:326:PRO:HD2	2.02	0.42
1:A:90:PHE:CE2	1:A:94:LYS:HE2	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:ALA:HB3	1:A:280[B]:ARG:NH1	2.35	0.41
1:A:326:PRO:O	1:A:327:TYR:HB2	2.21	0.41
1:A:486:GLU:CD	1:A:486:GLU:H	2.24	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	729/707 (103%)	708 (97%)	20 (3%)	1 (0%)	51 54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
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	631/603 (105%)	618 (98%)	13 (2%)	53 59

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	LYS
1	A	133	GLU
1	A	187	LYS
1	A	239[A]	VAL
1	A	239[B]	VAL
1	A	303	GLN
1	A	322	SER
1	A	537	TYR
1	A	541	TRP
1	A	589	ASN
1	A	600	TYR
1	A	652	ASP
1	A	673	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	589	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)

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	0.41	0	17,19,21	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	NAG	B	2	2	14,14,15	0.42	0	17,19,21	1.49	3 (17%)
2	NAG	C	1	1,2	14,14,15	0.50	0	17,19,21	1.26	1 (5%)
2	NAG	C	2	2	14,14,15	0.48	0	17,19,21	1.26	2 (11%)
3	NAG	D	1	1,3	14,14,15	0.55	0	17,19,21	1.59	2 (11%)
3	NAG	D	2	3	14,14,15	0.47	0	17,19,21	1.40	2 (11%)
3	BMA	D	3	3	11,11,12	0.56	0	15,15,17	1.33	1 (6%)
3	MAN	D	4	3	11,11,12	0.43	0	15,15,17	1.26	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	B	1	1,2	-	0/6/23/26	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	-	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	-	4/6/23/26	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

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	1	NAG	C1-O5-C5	5.20	119.23	112.19
3	D	3	BMA	C1-C2-C3	3.85	114.39	109.67
2	B	2	NAG	C2-N2-C7	3.30	127.61	122.90
3	D	2	NAG	C1-O5-C5	3.23	116.58	112.19
2	B	2	NAG	C4-C3-C2	2.88	115.24	111.02
3	D	4	MAN	O5-C5-C6	2.85	111.67	107.20
2	C	2	NAG	C8-C7-N2	2.73	120.72	116.10
2	C	1	NAG	C1-O5-C5	2.66	115.80	112.19
3	D	1	NAG	O5-C1-C2	-2.50	107.33	111.29
2	B	2	NAG	C8-C7-N2	2.34	120.07	116.10
3	D	2	NAG	C8-C7-N2	2.27	119.94	116.10
2	C	2	NAG	O4-C4-C5	2.25	114.88	109.30

There are no chirality outliers.

All (12) torsion outliers are listed below:

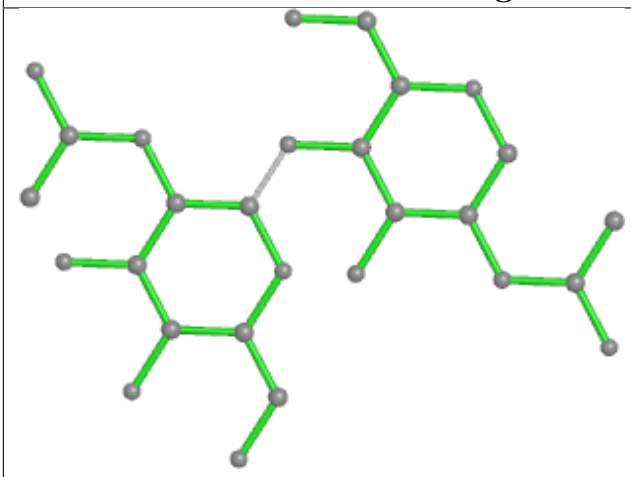
Mol	Chain	Res	Type	Atoms
3	D	2	NAG	C4-C5-C6-O6
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	C	1	NAG	C8-C7-N2-C2
2	C	1	NAG	O7-C7-N2-C2
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
3	D	1	NAG	C4-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6

There are no ring outliers.

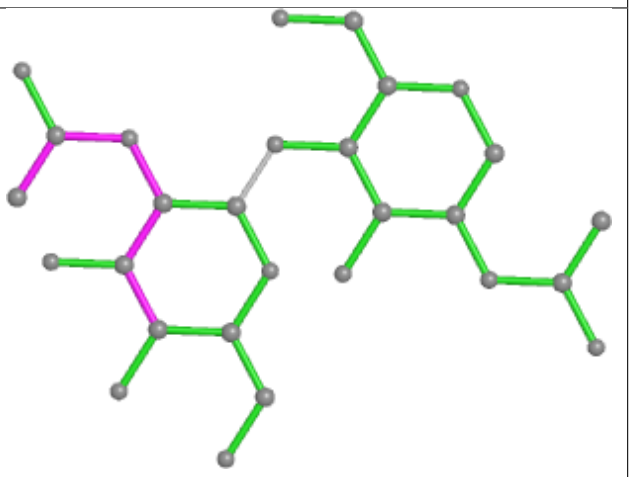
No monomer is involved in short contacts.

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

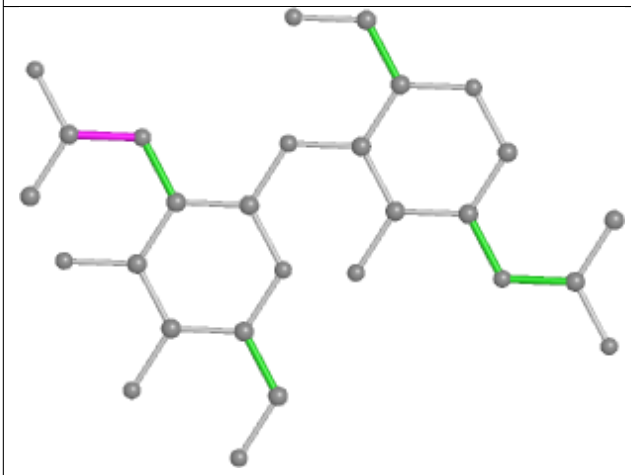
Oligosaccharide Chain B



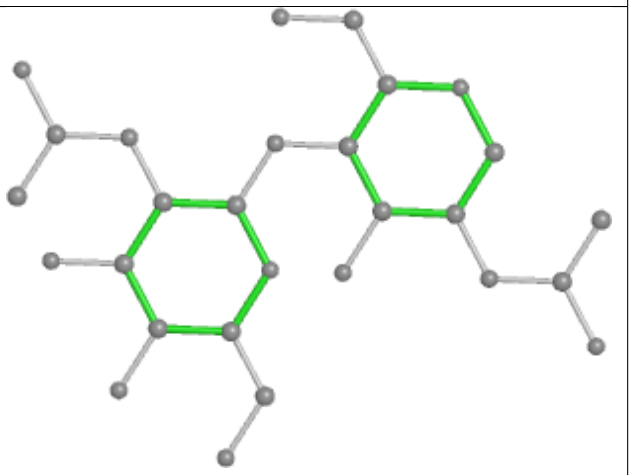
Bond lengths



Bond angles

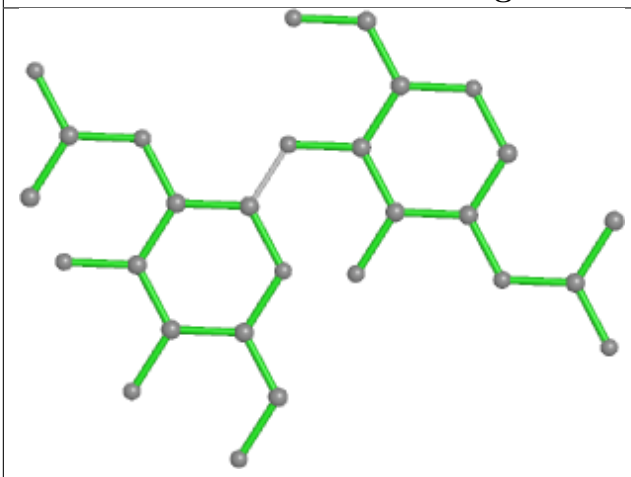


Torsions

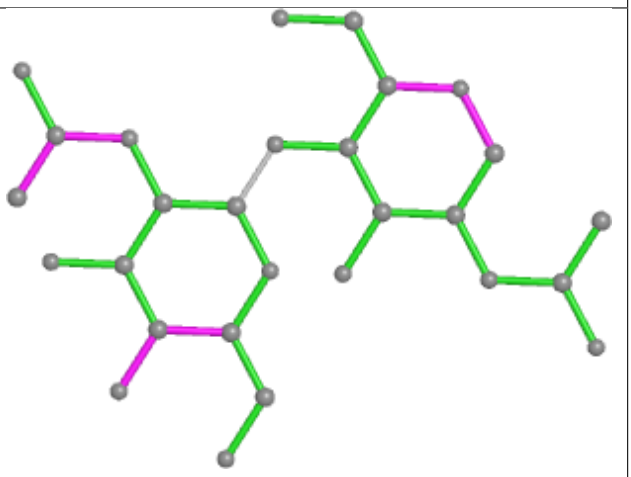


Rings

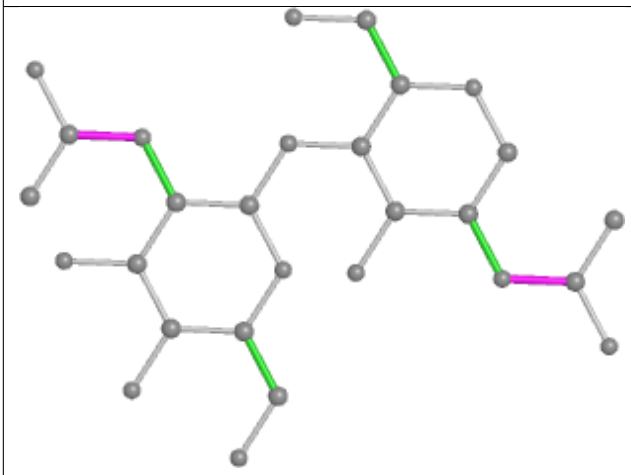
Oligosaccharide Chain C



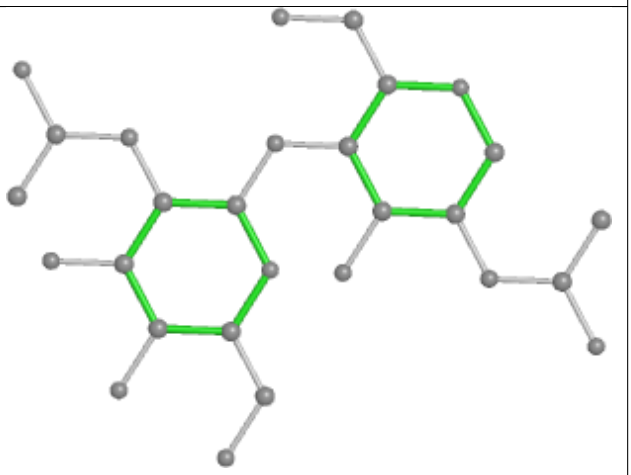
Bond lengths



Bond angles

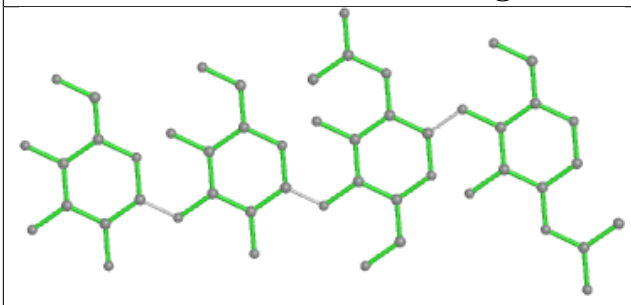


Torsions

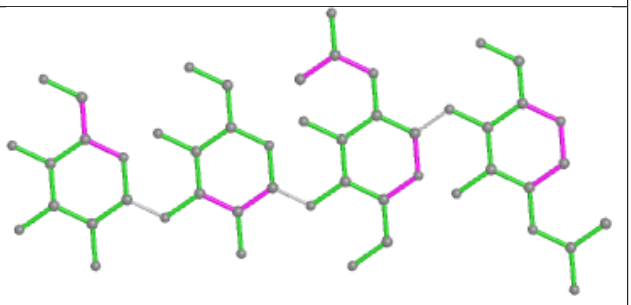


Rings

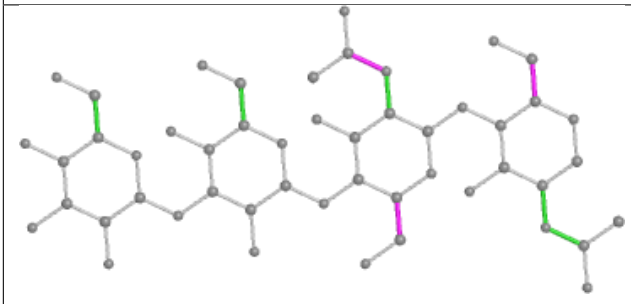
Oligosaccharide Chain D



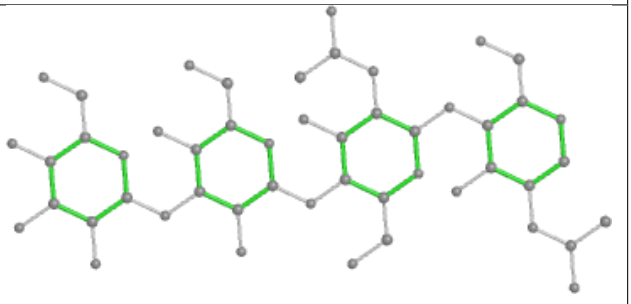
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	$\#\|Z\| > 2$
7	NAG	A	809	1	14,14,15	0.74	0	17,19,21	2.30	6 (35%)
8	EDO	A	817	-	3,3,3	0.46	0	2,2,2	0.37	0
9	GBZ	A	818	4	42,42,42	1.79	7 (16%)	54,55,55	3.22	14 (25%)
7	NAG	A	807	1	14,14,15	0.61	0	17,19,21	1.88	5 (29%)
7	NAG	A	810	1	14,14,15	0.46	0	17,19,21	1.42	2 (11%)
7	NAG	A	808	1	14,14,15	0.99	1 (7%)	17,19,21	1.31	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
7	NAG	A	809	1	-	2/6/23/26	0/1/1/1
8	EDO	A	817	-	-	1/1/1/1	-
9	GBZ	A	818	4	-	0/45/45/45	0/2/2/2
7	NAG	A	807	1	-	2/6/23/26	0/1/1/1
7	NAG	A	810	1	-	2/6/23/26	0/1/1/1
7	NAG	A	808	1	-	0/6/23/26	0/1/1/1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	818	GBZ	CAA-NAG	5.38	1.36	1.30
9	A	818	GBZ	CAE-CAH	-5.29	1.39	1.50
9	A	818	GBZ	CAF-NAG	3.94	1.42	1.34
9	A	818	GBZ	CBJ-NAM	-3.33	1.36	1.43
9	A	818	GBZ	CAO-CAN	2.99	1.57	1.51
9	A	818	GBZ	CAC-CAA	2.22	1.39	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	818	GBZ	CAY-CAW	2.13	1.58	1.53
7	A	808	NAG	C1-C2	2.04	1.55	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	A	818	GBZ	CAF-NAG-CAA	14.57	120.50	115.75
9	A	818	GBZ	FAB-CAA-NAG	10.69	121.89	114.95
9	A	818	GBZ	CAC-CAA-NAG	-10.34	121.16	126.83
7	A	809	NAG	C1-O5-C5	5.92	120.21	112.19
7	A	807	NAG	C1-O5-C5	5.18	119.22	112.19
9	A	818	GBZ	CAD-CAC-CAA	4.26	119.53	116.35
7	A	810	NAG	C1-O5-C5	3.85	117.41	112.19
9	A	818	GBZ	CAE-CAF-NAG	-3.73	118.46	123.67
7	A	809	NAG	O5-C1-C2	-3.33	106.04	111.29
7	A	809	NAG	C6-C5-C4	-3.31	105.26	113.00
7	A	809	NAG	O5-C5-C6	3.03	111.96	107.20
7	A	808	NAG	C1-O5-C5	2.78	115.95	112.19
9	A	818	GBZ	CAL-NAM-CBJ	2.71	121.94	117.06
9	A	818	GBZ	CA-N-CAU	2.67	126.75	120.64
7	A	807	NAG	C8-C7-N2	2.66	120.60	116.10
9	A	818	GBZ	OAK-CAH-CAE	-2.61	116.29	120.94
9	A	818	GBZ	CAX-CAW-NAV	-2.59	104.42	110.55
7	A	810	NAG	C4-C3-C2	-2.55	107.28	111.02
9	A	818	GBZ	FAB-CAA-CAC	-2.45	116.95	118.71
7	A	807	NAG	O5-C5-C6	2.41	110.98	107.20
9	A	818	GBZ	CB-CAP-CAO	-2.35	106.97	113.36
7	A	809	NAG	C8-C7-N2	2.32	120.03	116.10
9	A	818	GBZ	CAD-CAE-CAF	2.17	120.09	117.63
9	A	818	GBZ	OBE-CAU-NAV	-2.15	118.70	122.62
7	A	807	NAG	O5-C1-C2	-2.12	107.94	111.29
9	A	818	GBZ	CBL-CBJ-NAM	2.11	123.27	120.18
7	A	809	NAG	C3-C4-C5	2.09	113.96	110.24
7	A	807	NAG	O4-C4-C5	2.06	114.42	109.30
7	A	808	NAG	C2-N2-C7	2.06	125.83	122.90

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	810	NAG	C4-C5-C6-O6
7	A	810	NAG	O5-C5-C6-O6

Continued on next page...

Continued from previous page...

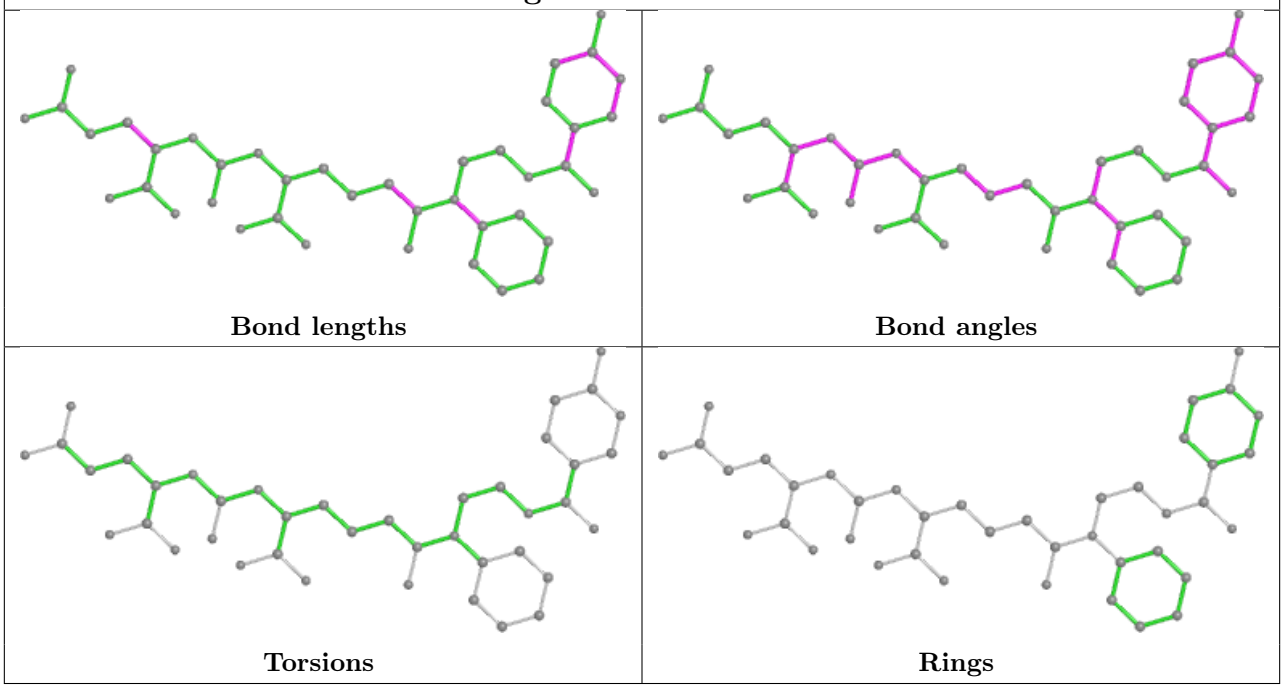
Mol	Chain	Res	Type	Atoms
7	A	807	NAG	C8-C7-N2-C2
7	A	807	NAG	O7-C7-N2-C2
7	A	809	NAG	C8-C7-N2-C2
7	A	809	NAG	O7-C7-N2-C2
8	A	817	EDO	O1-C1-C2-O2

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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand GBZ A 818



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{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	694/707 (98%)	0.13	23 (3%) 46 53	41, 56, 82, 110	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	TYR	4.8
1	A	155	SER	4.5
1	A	235	PHE	4.5
1	A	656[A]	SER	4.0
1	A	236	ALA	3.5
1	A	55	LYS	3.5
1	A	154	VAL	3.3
1	A	507	SER	3.1
1	A	153	ASN	2.9
1	A	541	TRP	2.8
1	A	505	GLU	2.8
1	A	386	ILE	2.7
1	A	56	HIS	2.3
1	A	336	ASN	2.3
1	A	124	HIS	2.2
1	A	340	GLN	2.2
1	A	171[A]	GLU	2.2
1	A	487	GLY	2.2
1	A	719	VAL	2.2
1	A	134	ASP	2.1
1	A	700	TYR	2.1
1	A	521	PHE	2.1
1	A	136	ASN	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)

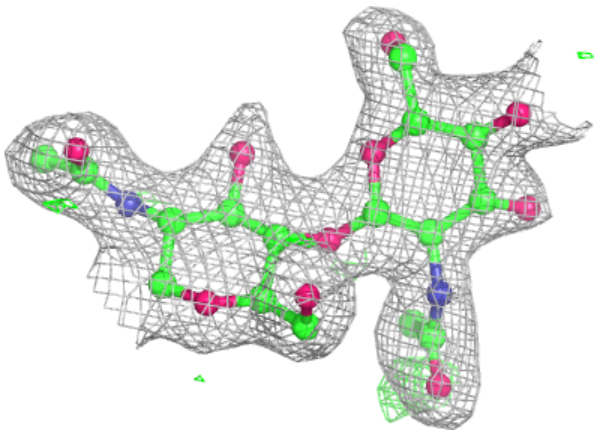
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

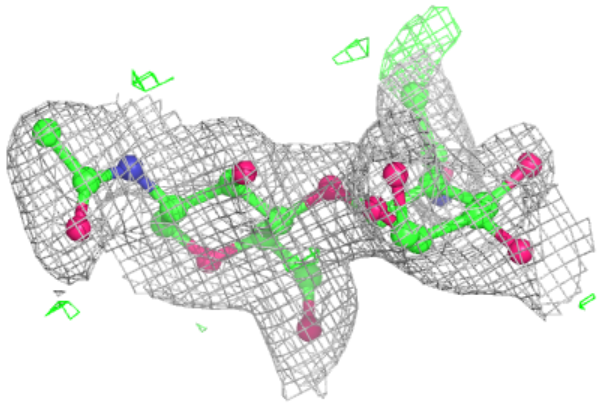
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	B	2	14/15	0.73	0.32	71,87,97,101	0
3	BMA	D	3	11/12	0.83	0.13	76,79,86,87	0
3	NAG	D	1	14/15	0.85	0.12	50,57,72,74	0
2	NAG	C	2	14/15	0.89	0.13	63,71,81,82	0
3	MAN	D	4	11/12	0.89	0.12	88,93,98,98	0
2	NAG	C	1	14/15	0.90	0.11	57,60,63,67	0
3	NAG	D	2	14/15	0.90	0.18	72,78,91,95	0
2	NAG	B	1	14/15	0.91	0.18	60,67,74,84	0

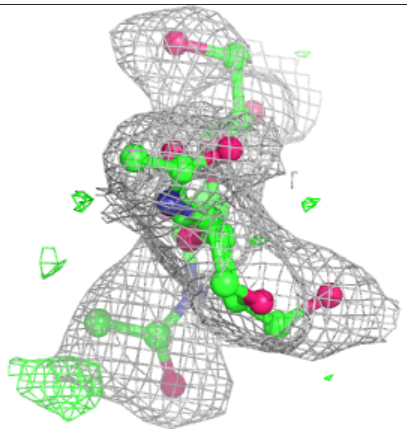
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

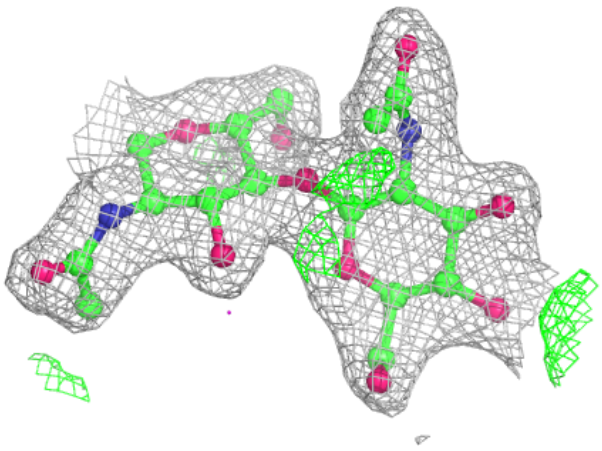


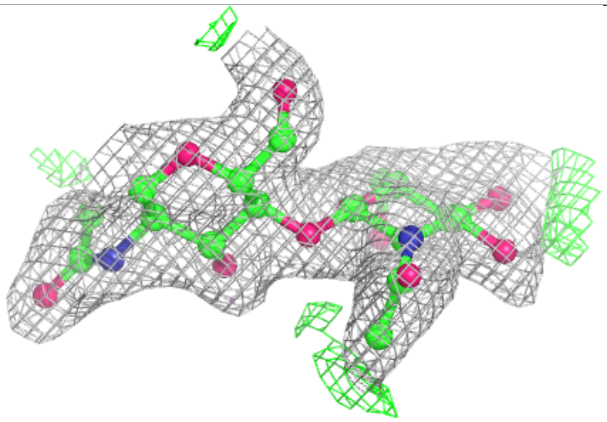


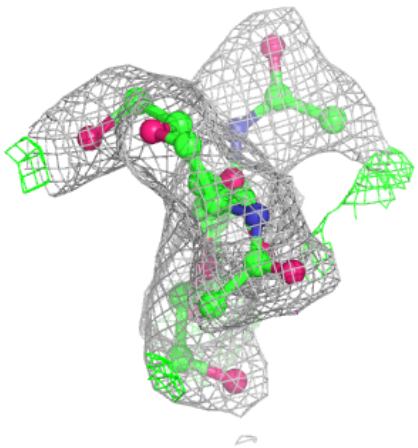


Electron density around Chain C:

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

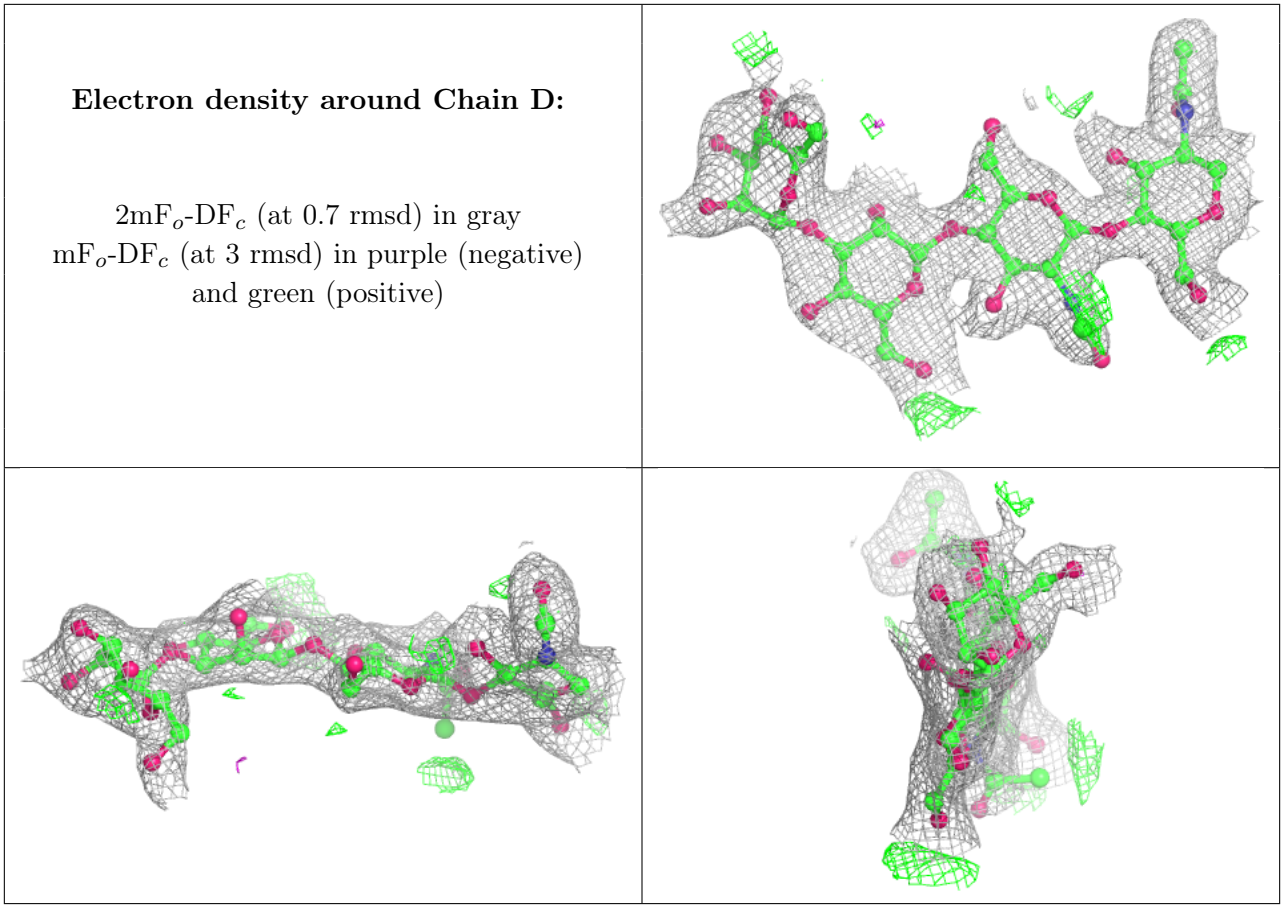






Electron density around Chain D:

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



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.

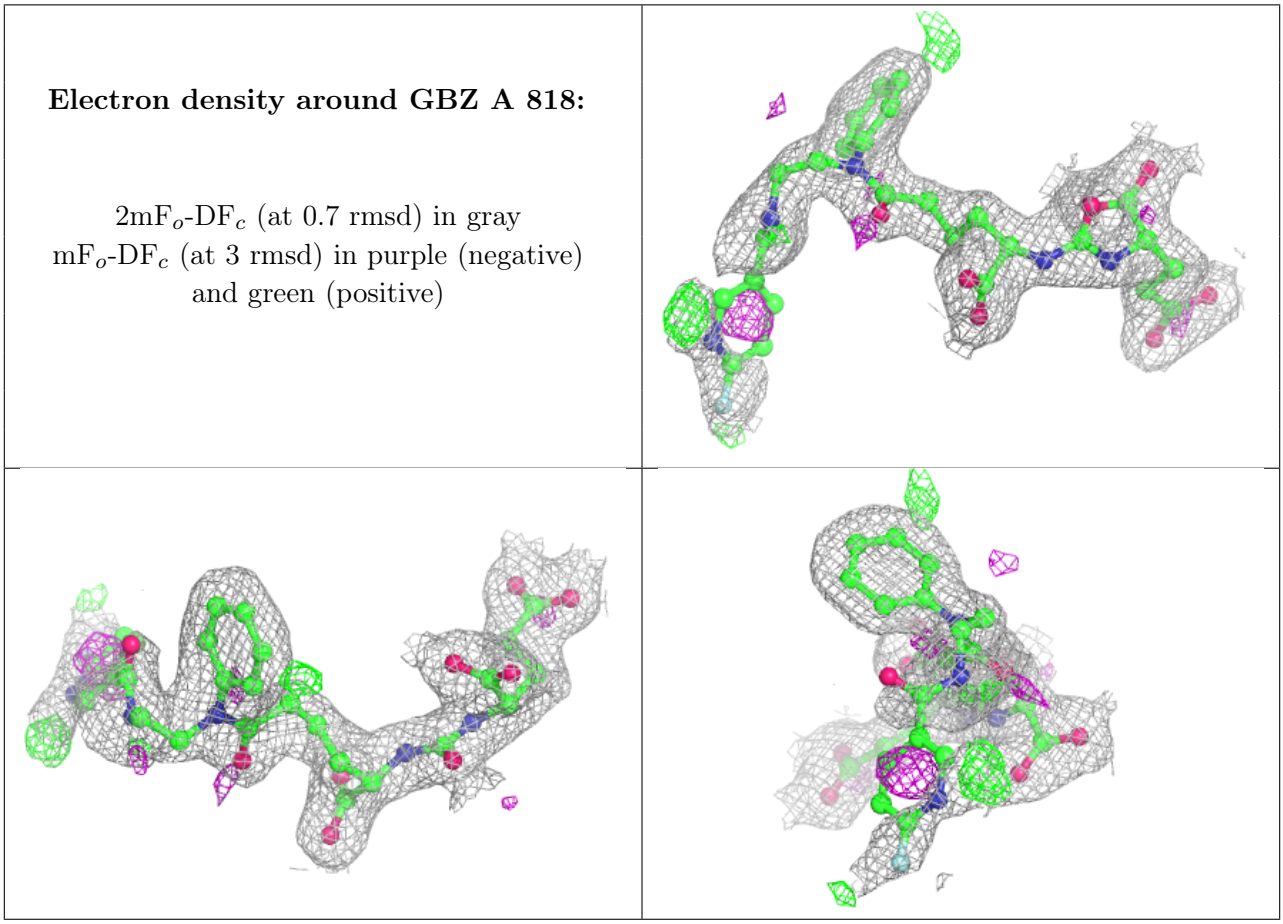
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	NAG	A	809	14/15	0.60	0.23	89,93,100,101	0
7	NAG	A	808	14/15	0.72	0.22	67,73,77,79	0
7	NAG	A	807	14/15	0.74	0.26	73,84,111,116	0
7	NAG	A	810	14/15	0.78	0.17	64,83,98,100	0
8	EDO	A	817	4/4	0.80	0.28	72,74,77,82	0
9	GBZ	A	818	41/41	0.92	0.21	43,54,125,132	0
5	CA	A	803	1/1	1.00	0.10	44,44,44,44	0
6	CL	A	804	1/1	1.00	0.24	49,49,49,49	0
4	ZN	A	801	1/1	1.00	0.10	48,48,48,48	0
4	ZN	A	802	1/1	1.00	0.10	47,47,47,47	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around GBZ A 818:

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



6.5 Other polymers (i)

There are no such residues in this entry.