Full wwPDB X-ray Structure Validation Report

Aug 21, 2023 – 02:51 PM EDT

PDB ID	:	2PVW
Title	:	A high resolution structure of human glutamate carboxypeptidase II (GCPII) in complex with 2-(phosphonomethyl)pentanedioic acid (2-PMPA)
Authors	:	Barinka, C.; Lubkowski, J.
Deposited on	:	2007-05-10
Resolution	:	1.71 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:

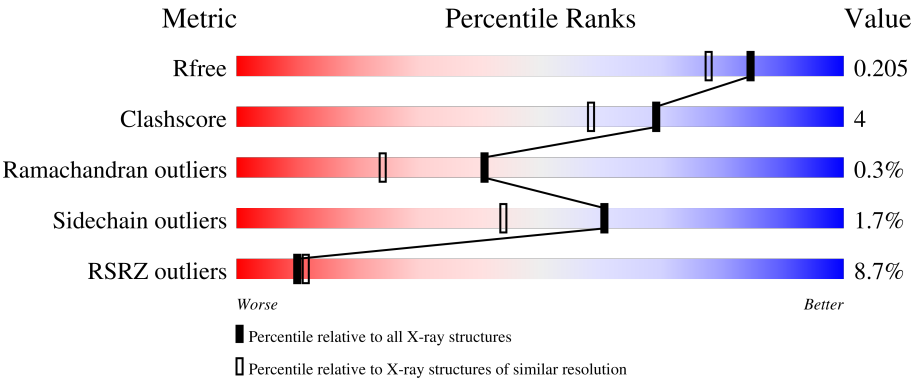
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 1.71 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	5722 (1.74-1.70)
Clashscore	141614	6152 (1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)
RSRZ outliers	127900	5629 (1.74-1.70)

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 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	709	8% 88% 9% .
2	B	2	100%
2	C	2	50% 50%
2	D	2	100%
3	E	4	25% 75%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6217 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.

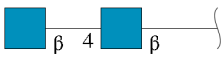
- Molecule 1 is a protein called Glutamate carboxypeptidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	690	Total	C	N	O	S	0	32	0
			5602	3607	936	1038	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	ARG	-	cloning artifact	UNP Q04609
A	43	SER	-	cloning artifact	UNP Q04609

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

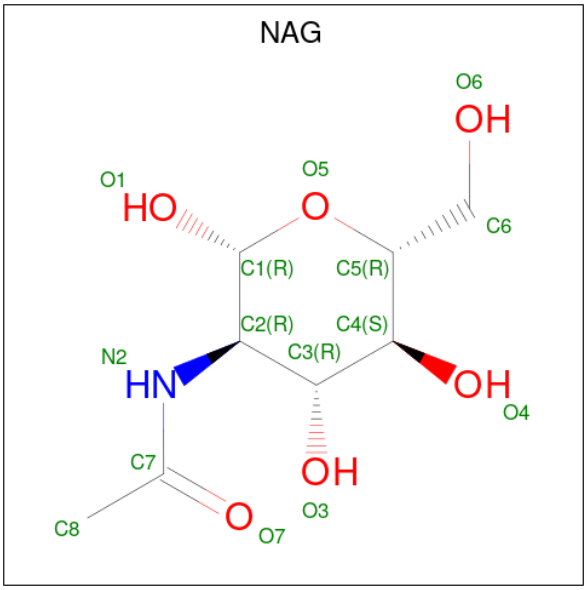


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- 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
3	E	4	Total C N O 50 28 2 20	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
4	A	1	Total C N O 14 8 1 5	0	0
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	2	Total Zn 2 2	0	0

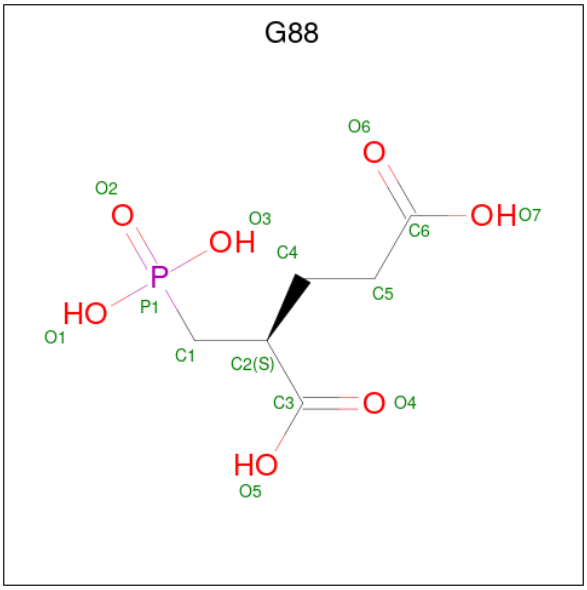
- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

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

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

- Molecule 8 is (2S)-2-(PHOSPHONOMETHYL)PENTANEDIOIC ACID (three-letter code: G88) (formula: $C_6H_{11}O_7P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O P 14 6 7 1	0	0

- Molecule 9 is water.

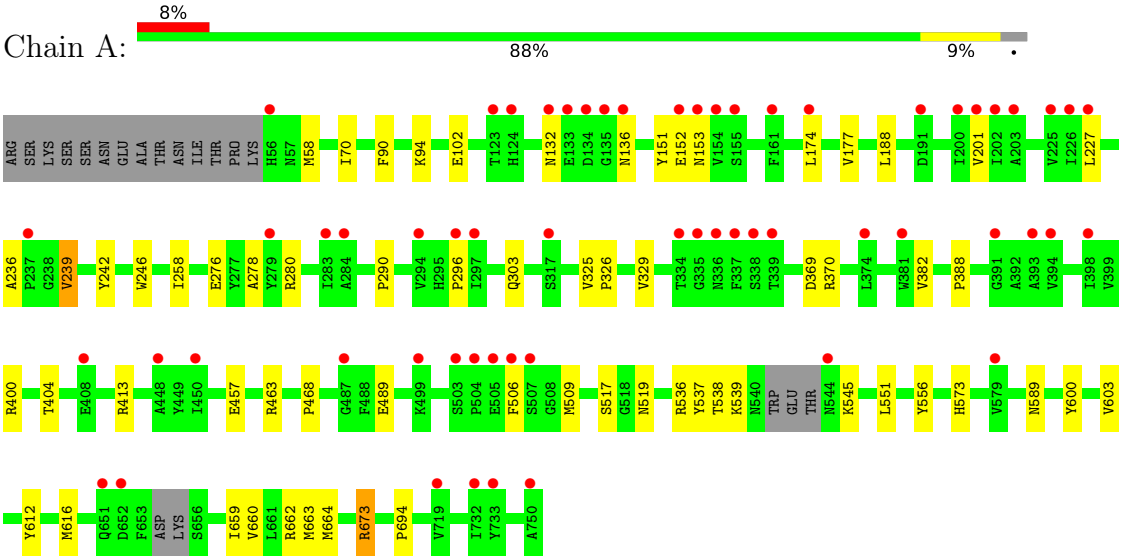
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	421	Total O 421 421	0	0

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: Glutamate carboxypeptidase 2

Chain A:



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

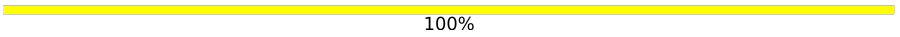
Chain B:

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

Chain C:

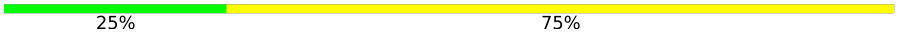
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:



• 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 E:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	101.85Å 130.82Å 159.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.71 29.61 – 1.71	Depositor EDS
% Data completeness (in resolution range)	97.7 (15.00-1.71) 97.7 (29.61-1.71)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.84 (at 1.72Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.182 , 0.207 0.180 , 0.205	Depositor DCC
R_{free} test set	5557 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	27.5	Xtriage
Anisotropy	0.578	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 54.0	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	0.97	EDS
Total number of atoms	6217	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% 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: MAN, CA, CL, G88, NAG, ZN, BMA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.94	1/5905 (0.0%)	0.88	6/7996 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	102	GLU	CG-CD	5.40	1.60	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	370	ARG	NE-CZ-NH1	7.14	123.87	120.30
1	A	673	ARG	NE-CZ-NH2	-6.02	117.29	120.30
1	A	174[A]	LEU	CA-CB-CG	5.72	128.46	115.30
1	A	174[B]	LEU	CA-CB-CG	5.72	128.46	115.30
1	A	369	ASP	CB-CG-OD1	5.29	123.06	118.30
1	A	370	ARG	NE-CZ-NH2	-5.23	117.68	120.30

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	5602	0	5467	40	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	28	0	25	2	0
2	C	28	0	25	1	0
2	D	28	0	25	0	0
3	E	50	0	43	0	0
4	A	42	0	39	1	0
5	A	2	0	0	0	0
6	A	1	0	0	0	0
7	A	1	0	0	0	0
8	A	14	0	8	0	0
9	A	421	0	0	6	0
All	All	6217	0	5632	43	0

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

All (43) 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:258[B]:ILE:HD13	1:A:290:PRO:HG3	1.37	1.01
1:A:151:TYR:O	1:A:153:ASN:N	1.99	0.94
1:A:258[B]:ILE:CD1	1:A:290:PRO:HG3	2.05	0.86
1:A:662[B]:ARG:HG2	1:A:662[B]:ARG:HH21	1.41	0.86
1:A:278:ALA:HB3	1:A:280[A]:ARG:NH1	1.95	0.81
1:A:659:ILE:O	1:A:663[B]:MET:HG3	1.84	0.78
1:A:662[B]:ARG:HH21	1:A:662[B]:ARG:CG	2.05	0.69
9:A:2103:HOH:O	2:C:2:NAG:H83	1.91	0.69
1:A:400:ARG:O	1:A:404[B]:THR:HG23	1.94	0.67
1:A:662[B]:ARG:HG2	1:A:662[B]:ARG:NH2	2.12	0.64
1:A:90[B]:PHE:CZ	1:A:94:LYS:HD3	2.35	0.62
1:A:132:ASN:HD21	1:A:136:ASN:HD22	1.47	0.62
1:A:188:LEU:HD21	1:A:329:VAL:HG11	1.81	0.61
1:A:660:VAL:O	1:A:664[A]:MET:HG2	2.00	0.60
1:A:612:TYR:CZ	1:A:616:MET:HG3	2.41	0.55
1:A:662[B]:ARG:NH2	9:A:1806:HOH:O	2.41	0.54
1:A:463:ARG:NH2	1:A:545:LYS:HG3	2.23	0.53
1:A:468:PRO:HG2	1:A:603:VAL:HG21	1.91	0.53
1:A:413:ARG:H	1:A:589[B]:ASN:HD22	1.59	0.51
1:A:325:VAL:HB	1:A:326:PRO:HD2	1.93	0.50
1:A:276[A]:GLU:HB2	9:A:1939:HOH:O	2.11	0.49
1:A:413:ARG:H	1:A:589[B]:ASN:ND2	2.12	0.47
1:A:278:ALA:HB3	1:A:280[A]:ARG:CZ	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:489:GLU:H	1:A:489:GLU:CD	2.18	0.47
1:A:242:TYR:OH	9:A:2167:HOH:O	2.01	0.46
1:A:188:LEU:CD2	1:A:329:VAL:HG11	2.45	0.46
1:A:188:LEU:HD21	1:A:329:VAL:CG1	2.44	0.45
1:A:90[B]:PHE:HE2	1:A:94:LYS:HZ3	1.64	0.45
1:A:236:ALA:O	1:A:239[A]:VAL:HG13	2.16	0.45
1:A:177:VAL:HG22	1:A:201[B]:VAL:HG13	1.99	0.44
1:A:246:TRP:CD1	4:A:1760:NAG:H83	2.53	0.43
1:A:551:LEU:HD22	1:A:556:TYR:HB2	1.99	0.43
9:A:2016:HOH:O	2:B:2:NAG:H81	2.19	0.42
1:A:517:SER:HB2	1:A:694:PRO:HG3	2.00	0.42
1:A:177:VAL:CG2	1:A:201[B]:VAL:HG13	2.50	0.42
1:A:90[B]:PHE:CE2	1:A:94:LYS:HE2	2.55	0.41
1:A:90[B]:PHE:CE2	1:A:94:LYS:CE	3.04	0.41
1:A:70:ILE:HG21	1:A:573:HIS:HB3	2.03	0.41
1:A:227:LEU:O	1:A:296:PRO:HA	2.20	0.40
1:A:457:GLU:HG3	1:A:538:THR:HA	2.03	0.40
9:A:2037:HOH:O	2:B:1:NAG:N2	2.29	0.40
1:A:506:PHE:HB2	1:A:509:MET:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	716/709 (101%)	696 (97%)	18 (2%)	2 (0%)	41 24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	GLU
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	619/605 (102%)	607 (98%)	12 (2%)	57 39

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	MET
1	A	239[A]	VAL
1	A	239[B]	VAL
1	A	303	GLN
1	A	388	PRO
1	A	519	ASN
1	A	536[A]	ARG
1	A	536[B]	ARG
1	A	537	TYR
1	A	539	LYS
1	A	600	TYR
1	A	673	ARG

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

Mol	Chain	Res	Type
1	A	136	ASN
1	A	544	ASN
1	A	618	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

10 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	0.50	0	17,19,21	1.65	5 (29%)
2	NAG	B	2	2	14,14,15	0.70	0	17,19,21	1.05	1 (5%)
2	NAG	C	1	1,2	14,14,15	0.98	1 (7%)	17,19,21	1.33	2 (11%)
2	NAG	C	2	2	14,14,15	0.41	0	17,19,21	1.88	4 (23%)
2	NAG	D	1	1,2	14,14,15	0.92	1 (7%)	17,19,21	1.30	2 (11%)
2	NAG	D	2	2	14,14,15	0.51	0	17,19,21	1.14	1 (5%)
3	NAG	E	1	3,1	14,14,15	0.71	0	17,19,21	1.64	4 (23%)
3	NAG	E	2	3	14,14,15	0.70	0	17,19,21	1.23	1 (5%)
3	BMA	E	3	3	11,11,12	1.05	1 (9%)	15,15,17	0.91	0
3	MAN	E	4	3	11,11,12	0.44	0	15,15,17	0.89	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
2	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	4/6/23/26	0/1/1/1
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	3	BMA	O5-C1	-2.63	1.39	1.43
2	C	1	NAG	C1-C2	2.42	1.56	1.52
2	D	1	NAG	O7-C7	2.22	1.28	1.23

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	2	NAG	C2-N2-C7	4.24	128.94	122.90
2	C	2	NAG	C8-C7-N2	4.16	123.14	116.10
2	C	1	NAG	O5-C1-C2	-3.66	105.52	111.29
2	D	1	NAG	O5-C1-C2	-3.50	105.77	111.29
3	E	1	NAG	O5-C1-C2	-3.41	105.90	111.29
2	B	1	NAG	O3-C3-C4	-3.14	103.09	110.35
2	B	1	NAG	O4-C4-C3	-3.06	103.27	110.35
2	C	2	NAG	O7-C7-C8	-3.05	116.39	122.06
3	E	1	NAG	C6-C5-C4	-3.05	105.86	113.00
3	E	1	NAG	C1-O5-C5	2.79	115.97	112.19
2	B	1	NAG	O5-C5-C6	2.76	111.53	107.20
2	B	1	NAG	O5-C1-C2	-2.69	107.04	111.29
2	D	2	NAG	C8-C7-N2	2.61	120.52	116.10
2	B	2	NAG	C2-N2-C7	2.57	126.56	122.90
2	C	1	NAG	O5-C5-C6	2.28	110.78	107.20
2	D	1	NAG	O5-C5-C4	-2.27	105.30	110.83
3	E	2	NAG	C3-C4-C5	-2.23	106.27	110.24
2	B	1	NAG	C4-C3-C2	2.20	114.25	111.02
3	E	1	NAG	O4-C4-C5	-2.12	104.02	109.30
2	C	2	NAG	O5-C5-C6	2.09	110.47	107.20

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C8-C7-N2-C2
2	D	2	NAG	O7-C7-N2-C2
3	E	2	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	E	2	NAG	O7-C7-N2-C2
2	B	2	NAG	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6

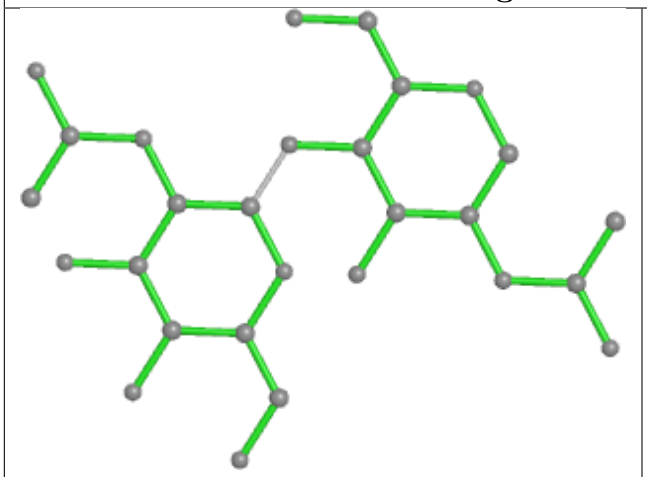
There are no ring outliers.

3 monomers are involved in 3 short contacts:

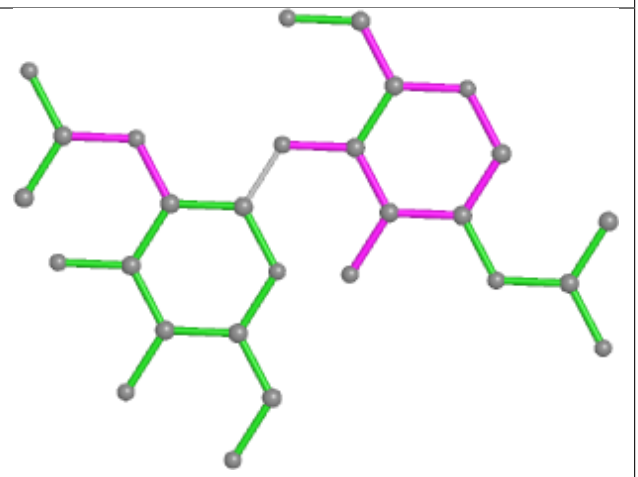
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
2	B	1	NAG	1	0
2	B	2	NAG	1	0

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

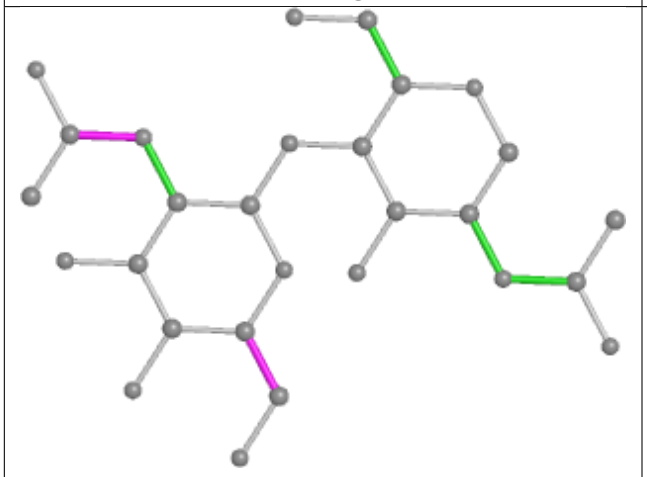
Oligosaccharide Chain B



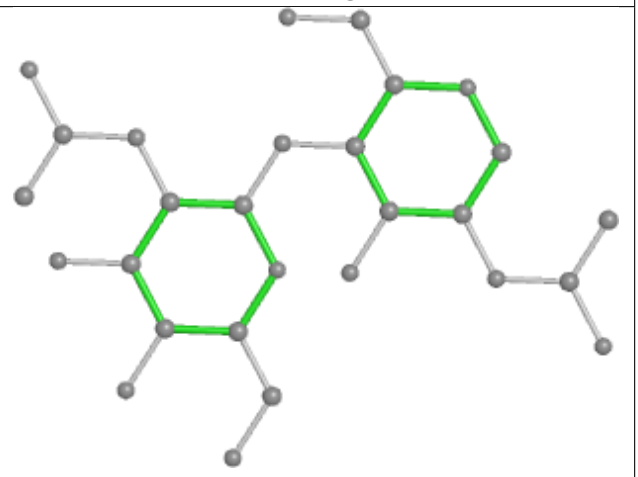
Bond lengths



Bond angles

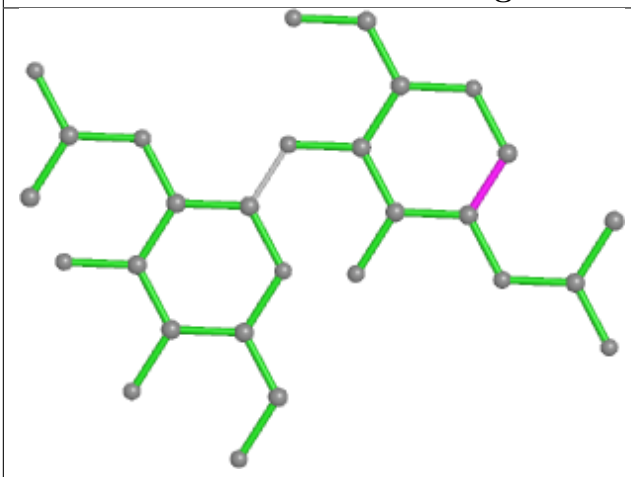


Torsions

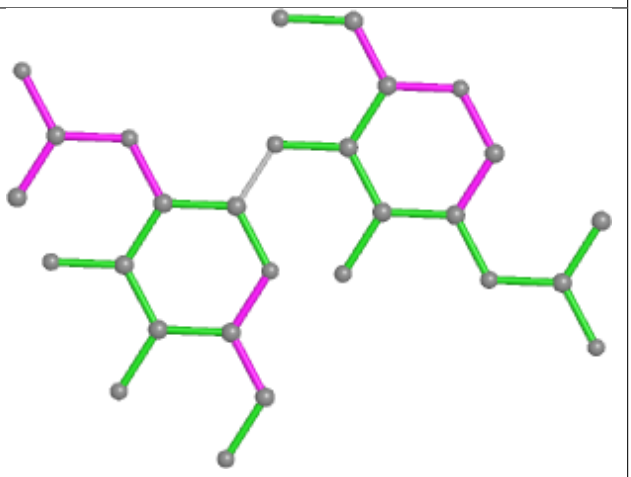


Rings

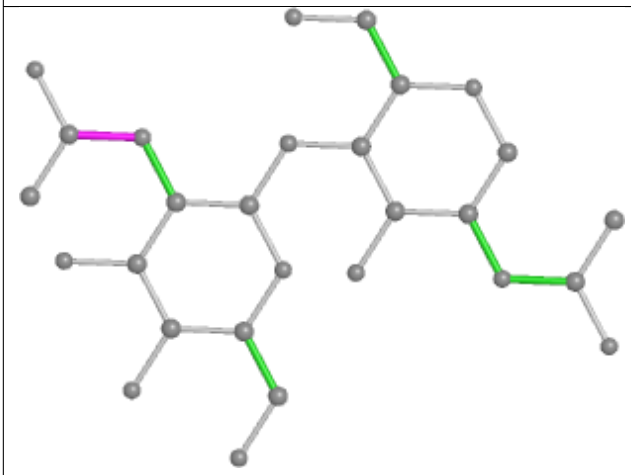
Oligosaccharide Chain C



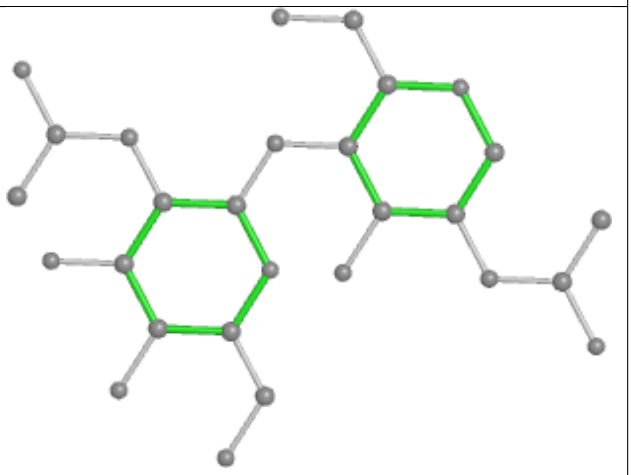
Bond lengths



Bond angles

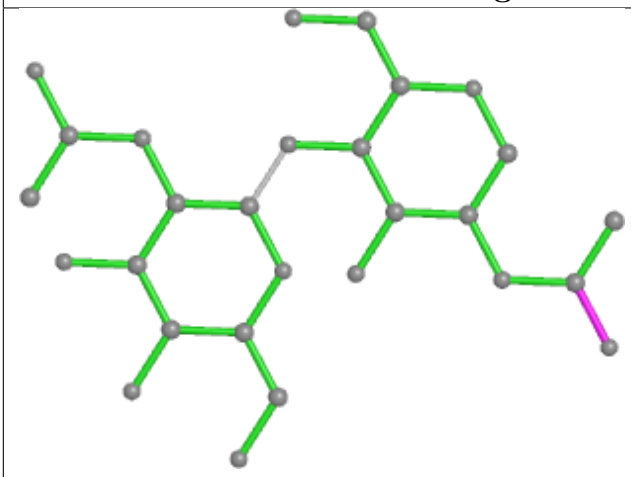


Torsions

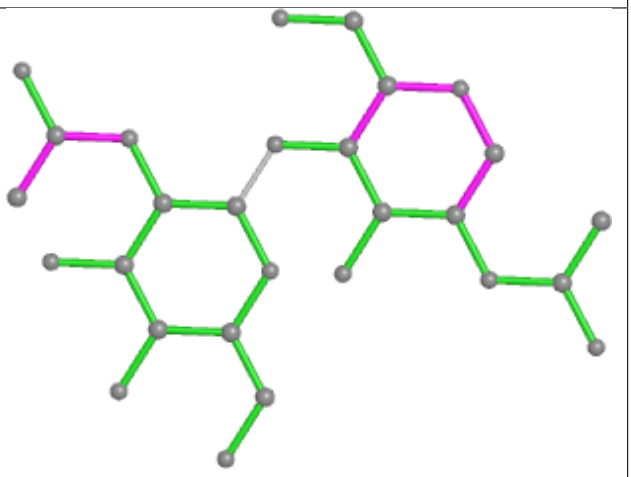


Rings

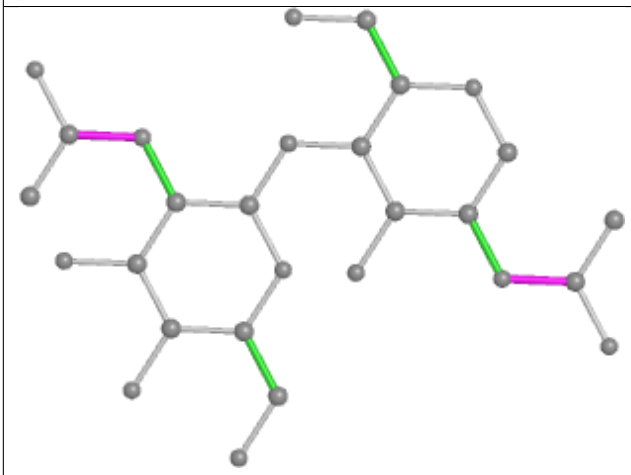
Oligosaccharide Chain D



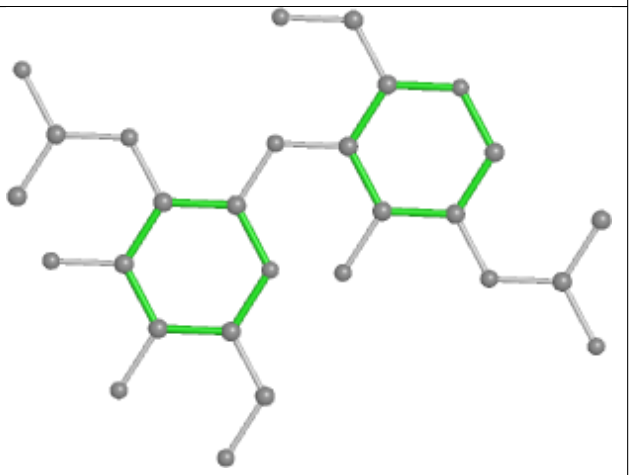
Bond lengths



Bond angles

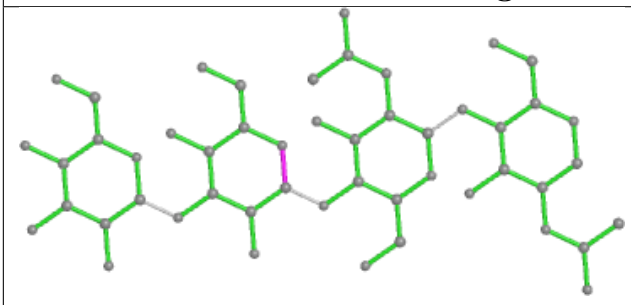


Torsions

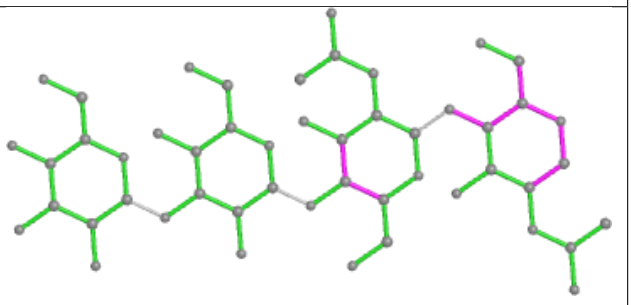


Rings

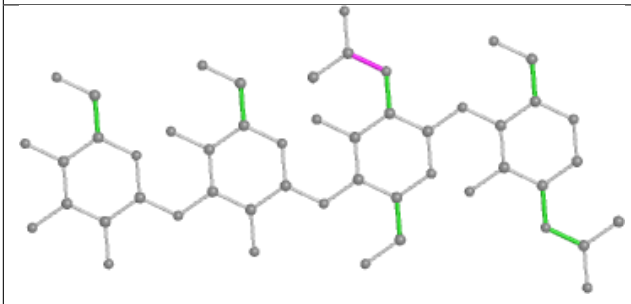
Oligosaccharide Chain E



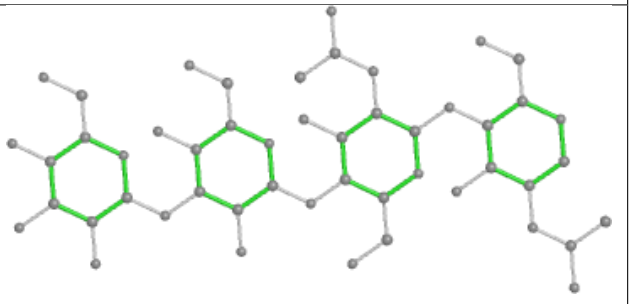
Bond lengths



Bond angles



Torsions



Rings

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
8	G88	A	1768	5	12,13,13	2.26	4 (33%)	17,18,18	1.39	4 (23%)
4	NAG	A	1757	1	14,14,15	0.58	0	17,19,21	1.97	3 (17%)
4	NAG	A	1759	1	14,14,15	0.49	0	17,19,21	1.12	1 (5%)
4	NAG	A	1760	1	14,14,15	0.63	0	17,19,21	1.62	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
8	G88	A	1768	5	-	2/14/14/14	-
4	NAG	A	1757	1	-	4/6/23/26	0/1/1/1
4	NAG	A	1759	1	-	2/6/23/26	0/1/1/1
4	NAG	A	1760	1	-	2/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1768	G88	P1-C1	5.16	1.84	1.78
8	A	1768	G88	P1-O2	3.37	1.57	1.50
8	A	1768	G88	P1-O1	-2.74	1.48	1.54
8	A	1768	G88	P1-O3	-2.31	1.49	1.54

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1757	NAG	C1-O5-C5	4.91	118.84	112.19
4	A	1760	NAG	C1-O5-C5	4.71	118.58	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1757	NAG	O5-C5-C6	4.05	113.56	107.20
4	A	1759	NAG	C1-O5-C5	3.85	117.40	112.19
4	A	1757	NAG	C8-C7-N2	2.63	120.55	116.10
8	A	1768	G88	C5-C4-C2	-2.53	108.56	113.34
8	A	1768	G88	O1-P1-O3	2.49	115.35	108.08
8	A	1768	G88	O3-P1-O2	-2.43	105.95	112.39
8	A	1768	G88	O2-P1-C1	-2.35	107.19	111.54
4	A	1760	NAG	O7-C7-N2	2.21	126.02	121.95

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1757	NAG	C8-C7-N2-C2
4	A	1757	NAG	O7-C7-N2-C2
4	A	1759	NAG	O5-C5-C6-O6
4	A	1759	NAG	C4-C5-C6-O6
4	A	1757	NAG	O5-C5-C6-O6
4	A	1760	NAG	C4-C5-C6-O6
4	A	1760	NAG	O5-C5-C6-O6
4	A	1757	NAG	C4-C5-C6-O6
8	A	1768	G88	C2-C1-P1-O1
8	A	1768	G88	C2-C1-P1-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1760	NAG	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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	690/709 (97%)	0.33	60 (8%)	10	11	20, 31, 50, 66	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	506	PHE	5.8
1	A	719	VAL	5.2
1	A	201[A]	VAL	5.0
1	A	226	ILE	4.8
1	A	202	ILE	4.3
1	A	135	GLY	4.1
1	A	336	ASN	4.1
1	A	505	GLU	4.1
1	A	133	GLU	4.0
1	A	153	ASN	4.0
1	A	134	ASP	4.0
1	A	123	THR	3.8
1	A	335	GLY	3.8
1	A	225	VAL	3.7
1	A	544	ASN	3.6
1	A	652	ASP	3.5
1	A	155	SER	3.5
1	A	154	VAL	3.4
1	A	487	GLY	3.3
1	A	504	PRO	3.3
1	A	203	ALA	3.3
1	A	227	LEU	3.3
1	A	507	SER	3.2
1	A	152	GLU	3.2
1	A	394	VAL	3.1
1	A	174[A]	LEU	3.1
1	A	191	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	334	THR	2.8
1	A	200	ILE	2.8
1	A	56	HIS	2.8
1	A	733	TYR	2.7
1	A	338	SER	2.7
1	A	124	HIS	2.7
1	A	339	THR	2.6
1	A	398	ILE	2.6
1	A	408	GLU	2.6
1	A	161	PHE	2.6
1	A	294	VAL	2.6
1	A	237	PRO	2.6
1	A	337	PHE	2.5
1	A	297	ILE	2.5
1	A	283[A]	ILE	2.5
1	A	393	ALA	2.5
1	A	374	LEU	2.5
1	A	296	PRO	2.4
1	A	579	VAL	2.3
1	A	732	ILE	2.3
1	A	651	GLN	2.2
1	A	391	GLY	2.2
1	A	450	ILE	2.2
1	A	381	TRP	2.2
1	A	284	ALA	2.2
1	A	279[A]	TYR	2.1
1	A	132	ASN	2.1
1	A	136	ASN	2.1
1	A	499	LYS	2.1
1	A	503	SER	2.1
1	A	448	ALA	2.0
1	A	750	ALA	2.0
1	A	317	SER	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)

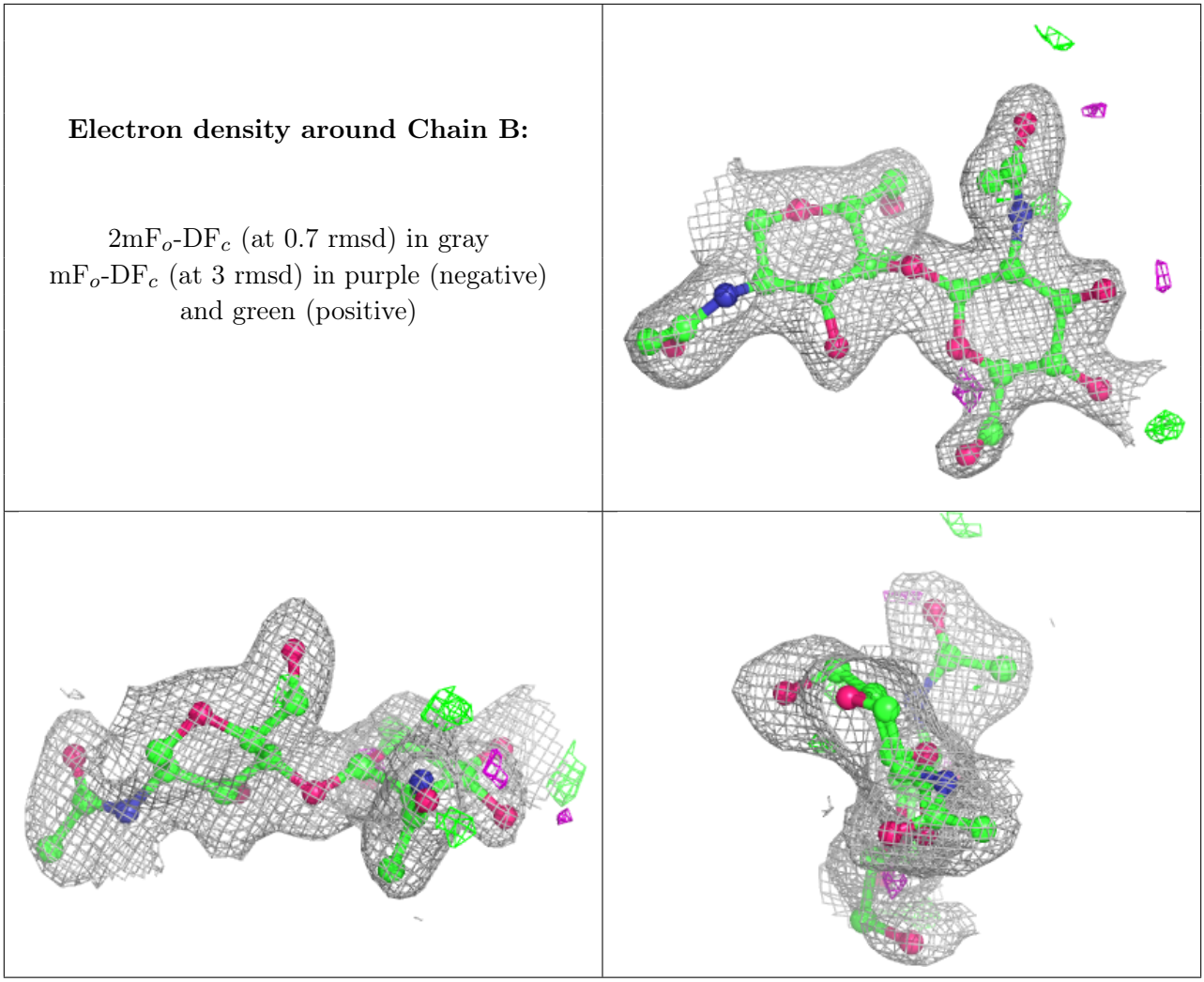
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	0.70	0.33	51,58,62,64	0
2	NAG	C	2	14/15	0.78	0.33	57,61,65,65	0
2	NAG	C	1	14/15	0.88	0.15	41,45,49,51	0
2	NAG	D	2	14/15	0.89	0.24	47,52,57,58	0
2	NAG	D	1	14/15	0.92	0.14	35,40,44,48	0
2	NAG	B	1	14/15	0.93	0.09	39,47,51,54	0
3	NAG	E	2	14/15	0.93	0.22	39,42,50,55	0
3	NAG	E	1	14/15	0.94	0.08	25,32,39,46	0
3	MAN	E	4	11/12	0.94	0.18	47,50,55,57	0
3	BMA	E	3	11/12	0.95	0.14	40,43,45,46	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.

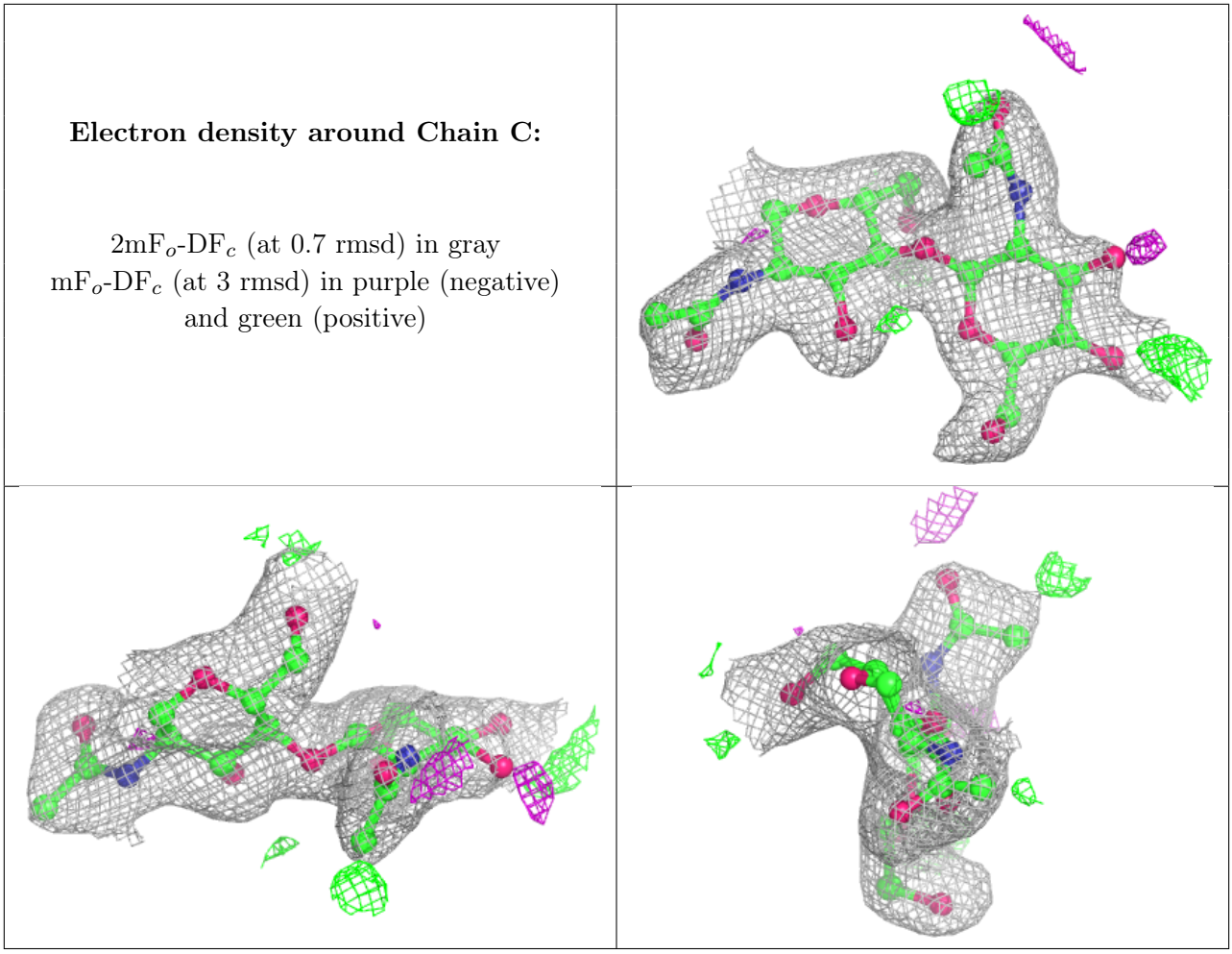
Electron density around Chain B:

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



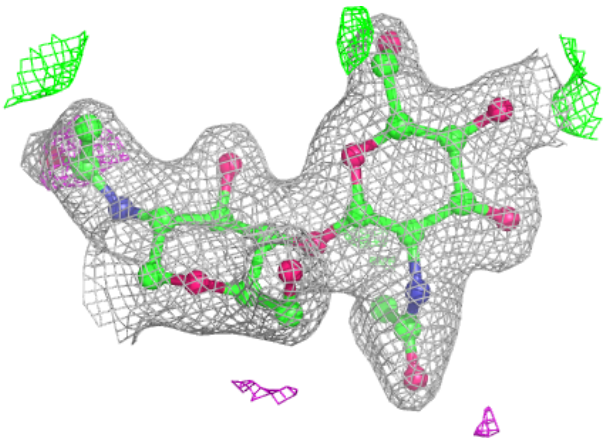
Electron density around Chain C:

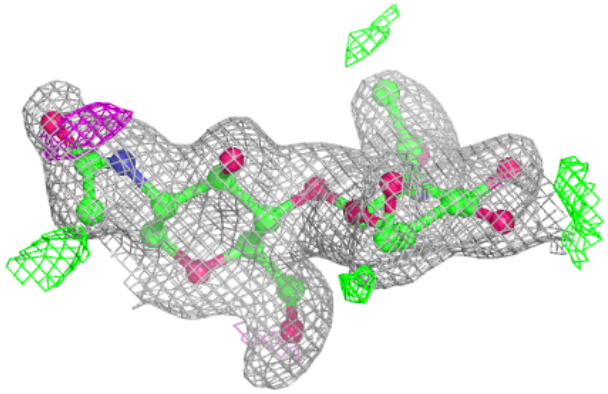
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

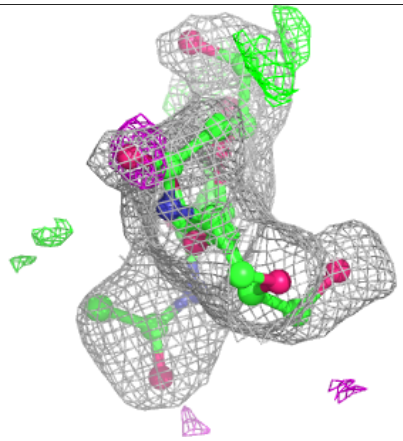


Electron density around Chain D:

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

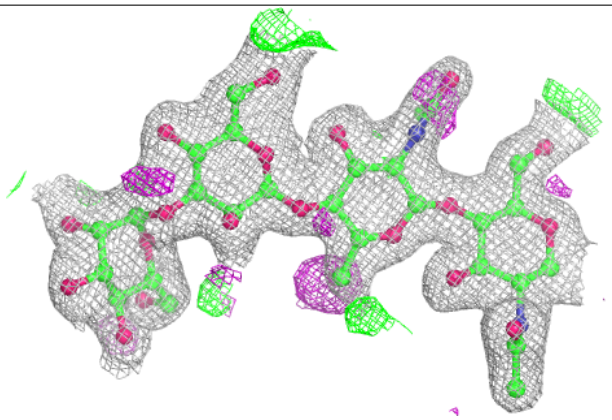


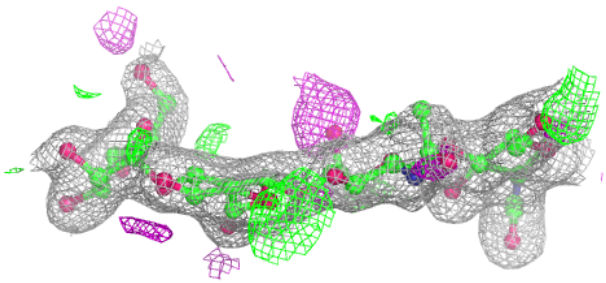


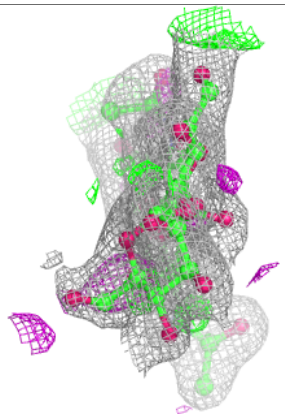


Electron density around Chain E:

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







6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{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	1757	14/15	0.72	0.31	54,59,66,66	0
4	NAG	A	1760	14/15	0.81	0.18	38,53,61,62	0
4	NAG	A	1759	14/15	0.88	0.27	70,75,77,79	0
8	G88	A	1768	14/14	0.97	0.11	25,29,37,37	0
5	ZN	A	1752	1/1	1.00	0.08	26,26,26,26	0
6	CA	A	1753	1/1	1.00	0.08	22,22,22,22	0
7	CL	A	1754	1/1	1.00	0.02	35,35,35,35	0
5	ZN	A	1751	1/1	1.00	0.09	25,25,25,25	0

6.5 Other polymers (i)

There are no such residues in this entry.