Full wwPDB X-ray Structure Validation Report (i)

Dec 12, 2023 – 04:52 pm GMT

PDB ID	:	2XEG
Title	:	Human glutamate carboxypeptidase II in complex with Antibody- Recruiting Molecule ARM-P4
Authors	:	Zhang, A.X.; Murelli, R.P.; Barinka, C.; Michel, J.; Cocleaza, A.; Jorgensen, W.L.; Lubkowski, J.; Spiegel, D.A.
Deposited on	:	2010-05-14
Resolution	:	1.59 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 (i) 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 (i)) were used in the production of this report:

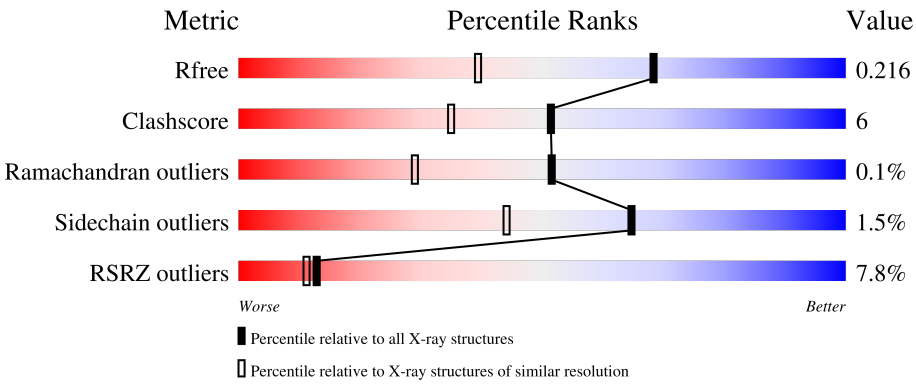
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 1.59 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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% 86% 11% • •
2	B	2	50% 50%
2	C	2	100%
2	D	2	100%

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Mol	Chain	Length	Quality of chain
3	E	4	75% 25%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 6618 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	5774	3716	964	1071	23	0	50	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	ARG	-	expression tag	UNP Q04609
A	43	SER	-	expression tag	UNP Q04609
A	593	GLN	LEU	conflict	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
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0
2	C	2	28	16	2	10	0	0	0
2	D	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	E	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
			Total	Zn		
4	A	2	2	2	0	0

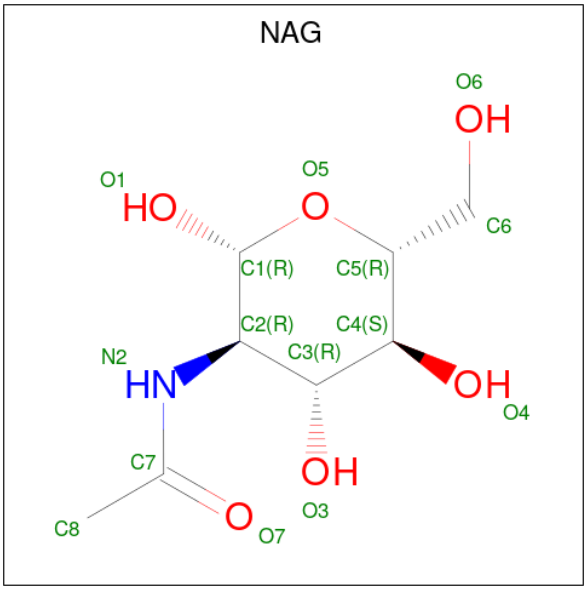
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

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

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

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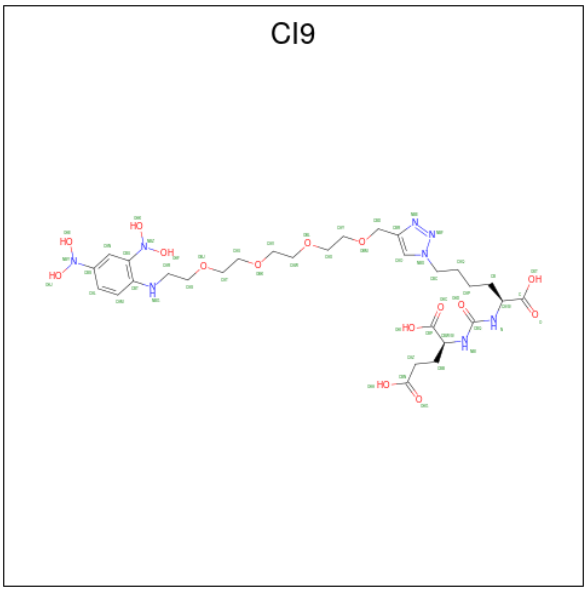
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
7	A	1	14	8	1	5	0	0
			Total	C	N	O		
7	A	1	14	8	1	5	0	0

- Molecule 8 is N-({(1S)-5-[4-(13-{[2,4-BIS(DIHYDROXYAMINO)PHENYL]AMINO}-2,5,8,11-TETRAOXATRIDEC-1-YL)-1H-1,2,3-TRIAZOL-1-YL]-1-CARBOXYPENTYL}CARBAMOYL)-L-GLUTAMIC ACID (three-letter code: CI9) (formula: $C_{29}H_{46}N_8O_{15}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
8	A	1	52	29	8	15	0	0

- Molecule 9 is water.

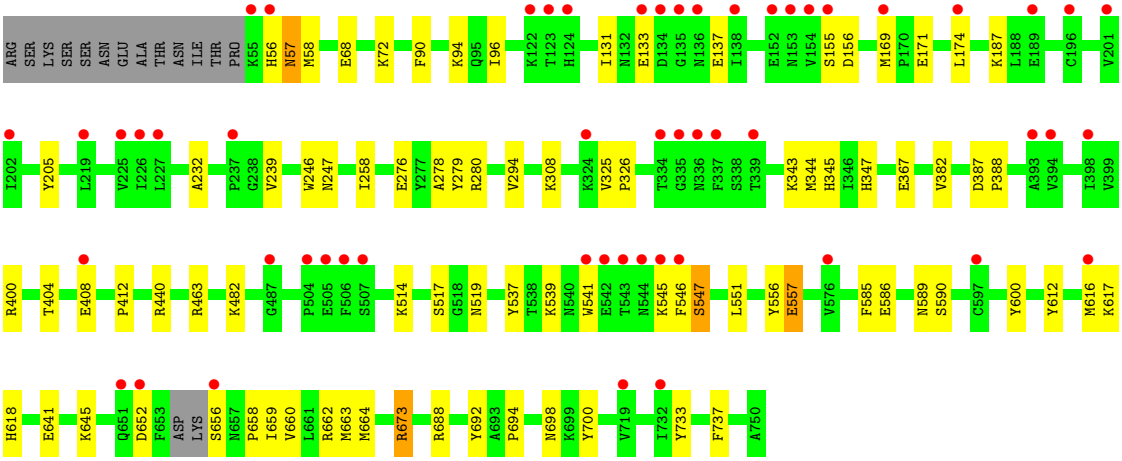
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
9	A	612	612	612	0	0

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:

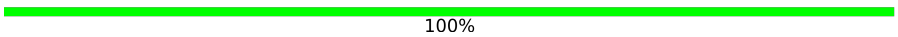


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:

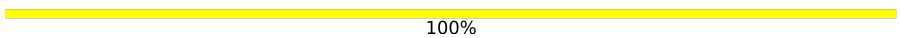
• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

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	101.71Å 130.04Å 159.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.59 28.56 – 1.59	Depositor EDS
% Data completeness (in resolution range)	97.6 (30.00-1.59) 97.6 (28.56-1.59)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.84 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.4.0057	Depositor
R, R_{free}	0.169 , 0.191 0.195 , 0.216	Depositor DCC
R_{free} test set	1373 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å^2)	20.5	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 57.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6618	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, CI9, CA, NAG, CL, MAN, ZN

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	0.90	3/6069 (0.0%)	0.86	7/8215 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	557	GLU	CB-CG	-6.32	1.40	1.52
1	A	205	TYR	CE1-CZ	5.63	1.45	1.38
1	A	737	PHE	CD2-CE2	5.14	1.49	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	673	ARG	NE-CZ-NH2	-8.29	116.15	120.30
1	A	440	ARG	NE-CZ-NH2	-8.02	116.29	120.30
1	A	688[A]	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	A	688[B]	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	A	652	ASP	CB-CA-C	-5.26	99.87	110.40
1	A	174[A]	LEU	CA-CB-CG	5.02	126.86	115.30
1	A	174[B]	LEU	CA-CB-CG	5.02	126.86	115.30

There are no chirality outliers.

There are no planarity outliers.

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	5774	0	5671	64	1
2	B	28	0	25	2	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
3	E	50	0	43	0	1
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	42	0	39	1	0
8	A	52	0	43	10	0
9	A	612	0	0	16	2
All	All	6618	0	5871	67	3

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 6.

All (67) 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:660[A]:VAL:O	1:A:664[A]:MET:HG2	1.17	1.28
1:A:660[A]:VAL:O	1:A:664[A]:MET:CG	2.14	0.94
1:A:541:TRP:CH2	8:A:1768:CI9:HAR1	2.12	0.85
1:A:90[B]:PHE:HE2	1:A:94:LYS:HZ3	1.27	0.83
1:A:482:LYS:HE2	9:A:2359:HOH:O	1.78	0.82
1:A:733:TYR:HE2	9:A:2579:HOH:O	1.66	0.78
1:A:541:TRP:CZ2	8:A:1768:CI9:HAR1	2.23	0.74
1:A:400:ARG:O	1:A:404[B]:THR:HG23	1.90	0.71
1:A:698:ASN:HD21	8:A:1768:CI9:HAY2	1.55	0.71
1:A:645[B]:LYS:HE3	9:A:2489:HOH:O	1.90	0.71
1:A:239[A]:VAL:HG22	1:A:247:ASN:ND2	2.09	0.68
1:A:698:ASN:HD21	8:A:1768:CI9:CAY	2.06	0.68
1:A:463[A]:ARG:HH21	8:A:1768:CI9:HAS1	1.57	0.68
1:A:612:TYR:CZ	1:A:616:MET:HG3	2.32	0.65
1:A:131:ILE:HG22	1:A:137:GLU:HG2	1.79	0.64
1:A:90[B]:PHE:CE2	1:A:94:LYS:NZ	2.66	0.62
1:A:641:GLU:HG3	9:A:2482:HOH:O	2.00	0.62
1:A:463[A]:ARG:HE	8:A:1768:CI9:HAR2	1.63	0.62
1:A:656[B]:SER:O	1:A:658[B]:PRO:HD3	2.05	0.56
1:A:733:TYR:CE2	9:A:2579:HOH:O	2.50	0.55
1:A:90[B]:PHE:CE2	1:A:94:LYS:CE	2.90	0.55
1:A:547:SER:HB3	9:A:2146:HOH:O	2.07	0.55
1:A:308:LYS:HB2	9:A:2250:HOH:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:VAL:HB	1:A:326:PRO:HD2	1.90	0.53
1:A:278:ALA:HB3	1:A:280[B]:ARG:NH1	2.23	0.53
1:A:514[A]:LYS:HG3	9:A:2382:HOH:O	2.08	0.53
1:A:586[B]:GLU:OE2	1:A:590[B]:SER:OG	2.27	0.53
1:A:347:HIS:HE1	9:A:2071:HOH:O	1.91	0.51
1:A:700:TYR:HB2	8:A:1768:CI9:HAY1	1.92	0.51
1:A:58[B]:MET:HG3	1:A:585:PHE:CG	2.46	0.51
1:A:232:ALA:O	1:A:545:LYS:HE2	2.10	0.50
1:A:276[A]:GLU:HB2	9:A:2211:HOH:O	2.11	0.50
9:A:2032:HOH:O	2:B:2:NAG:H81	2.10	0.50
1:A:171[A]:GLU:HG2	1:A:343:LYS:HG3	1.94	0.50
1:A:90[B]:PHE:CE2	1:A:94:LYS:HE2	2.47	0.50
1:A:56:HIS:HE1	1:A:408:GLU:OE2	1.95	0.49
1:A:367:GLU:OE1	1:A:662[B]:ARG:NH1	2.47	0.48
1:A:239[A]:VAL:HG22	1:A:247:ASN:CG	2.34	0.47
1:A:539:LYS:NZ	1:A:546:PHE:O	2.48	0.47
1:A:90[B]:PHE:HE2	1:A:94:LYS:NZ	2.02	0.47
1:A:137:GLU:OE2	1:A:345:HIS:HE1	1.98	0.47
1:A:617:LYS:NZ	9:A:2457:HOH:O	2.47	0.47
1:A:412:PRO:HA	1:A:589[B]:ASN:OD1	2.15	0.46
1:A:347:HIS:CE1	9:A:2071:HOH:O	2.67	0.46
1:A:463[A]:ARG:NE	8:A:1768:CI9:HAR2	2.29	0.46
1:A:246:TRP:CD1	7:A:1760:NAG:H83	2.51	0.46
1:A:90[B]:PHE:CZ	1:A:94:LYS:HD3	2.51	0.45
9:A:2595:HOH:O	2:B:2:NAG:H83	2.16	0.45
1:A:96[B]:ILE:HD13	9:A:2314:HOH:O	2.15	0.45
1:A:514[A]:LYS:HD2	1:A:692:TYR:HE1	1.83	0.44
1:A:137:GLU:OE2	1:A:345:HIS:CE1	2.71	0.44
1:A:169:MET:HA	1:A:344:MET:O	2.18	0.44
1:A:258:ILE:HD13	1:A:294:VAL:HB	2.00	0.44
1:A:131:ILE:CG2	1:A:137:GLU:HG2	2.48	0.43
1:A:278:ALA:HB3	1:A:280[B]:ARG:CZ	2.49	0.43
1:A:517:SER:HB2	1:A:694:PRO:HG3	1.99	0.43
1:A:551:LEU:HD22	1:A:556:TYR:HB2	2.01	0.43
1:A:645[B]:LYS:HD3	1:A:645[B]:LYS:HA	1.85	0.42
1:A:698:ASN:HD21	8:A:1768:CI9:CAX	2.31	0.42
1:A:68:GLU:OE1	1:A:72:LYS:HE3	2.18	0.42
1:A:659[B]:ILE:O	1:A:663[B]:MET:HG3	2.20	0.42
1:A:618:HIS:HE1	9:A:2553:HOH:O	2.02	0.42
1:A:57:ASN:C	1:A:57:ASN:HD22	2.23	0.42
1:A:155:SER:O	1:A:156:ASP:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:ASP:HA	1:A:388:PRO:HA	1.89	0.41
8:A:1768:CI9:HAV2	8:A:1768:CI9:HAT1	1.74	0.41

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:A:2507:HOH:O	9:A:2507:HOH:O[2_565]	1.07	1.13
1:A:276[A]:GLU:OE1	3:E:3:BMA:O2[2_565]	1.97	0.23
9:A:2319:HOH:O	9:A:2580:HOH:O[2_565]	2.02	0.18

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	737/709 (104%)	720 (98%)	16 (2%)	1 (0%)	51 29

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	639/605 (106%)	630 (99%)	9 (1%)	67 47

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	133	GLU
1	A	187	LYS
1	A	519	ASN
1	A	537	TYR
1	A	547	SER
1	A	557	GLU
1	A	600	TYR
1	A	673	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS
1	A	57	ASN
1	A	91	GLN
1	A	303	GLN
1	A	345	HIS
1	A	618	HIS
1	A	698	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)

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	2,1	14,14,15	0.50	0	17,19,21	1.26	2 (11%)
2	NAG	B	2	2	14,14,15	0.65	0	17,19,21	1.30	1 (5%)
2	NAG	C	1	2,1	14,14,15	0.59	0	17,19,21	1.04	0
2	NAG	C	2	2	14,14,15	0.42	0	17,19,21	0.95	0
2	NAG	D	1	2,1	14,14,15	0.90	1 (7%)	17,19,21	1.27	2 (11%)
2	NAG	D	2	2	14,14,15	0.51	0	17,19,21	1.41	2 (11%)
3	NAG	E	1	3,1	14,14,15	0.62	0	17,19,21	1.02	1 (5%)
3	NAG	E	2	3	14,14,15	0.84	1 (7%)	17,19,21	1.09	1 (5%)
3	BMA	E	3	3	11,11,12	0.62	0	15,15,17	1.13	1 (6%)
3	MAN	E	4	3	11,11,12	0.57	0	15,15,17	1.31	3 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	2,1	-	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	2,1	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	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	-	2/6/23/26	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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	2	NAG	O5-C1	-2.54	1.39	1.43
2	D	1	NAG	O7-C7	2.50	1.28	1.23

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	NAG	C2-N2-C7	3.90	128.45	122.90
2	D	2	NAG	C8-C7-N2	3.19	121.51	116.10
2	D	1	NAG	O5-C5-C4	-2.97	103.59	110.83
3	E	3	BMA	O3-C3-C2	-2.84	104.56	109.99
2	D	1	NAG	O5-C1-C2	-2.65	107.11	111.29
2	B	1	NAG	O5-C1-C2	-2.61	107.16	111.29
3	E	4	MAN	C1-C2-C3	2.61	112.87	109.67
3	E	1	NAG	O5-C1-C2	-2.60	107.19	111.29
3	E	4	MAN	C1-O5-C5	2.41	115.46	112.19
3	E	2	NAG	C1-O5-C5	2.41	115.45	112.19
2	B	1	NAG	C2-N2-C7	-2.37	119.52	122.90
3	E	4	MAN	O5-C5-C6	2.07	110.44	107.20
2	D	2	NAG	O5-C5-C6	2.04	110.40	107.20

There are no chirality outliers.

All (10) 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	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
3	E	2	NAG	O7-C7-N2-C2
3	E	1	NAG	C4-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6

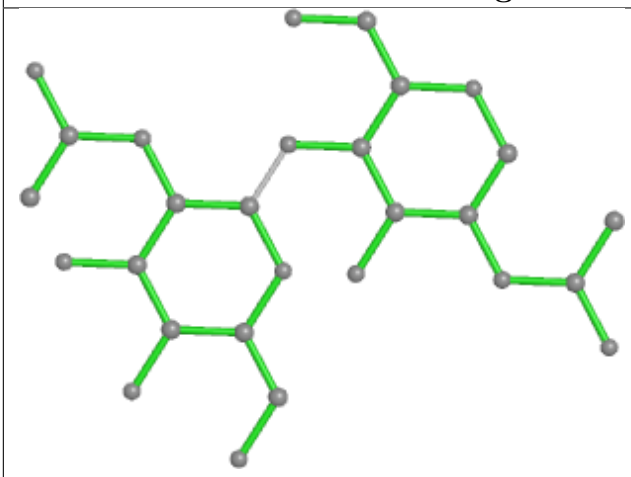
There are no ring outliers.

2 monomers are involved in 3 short contacts:

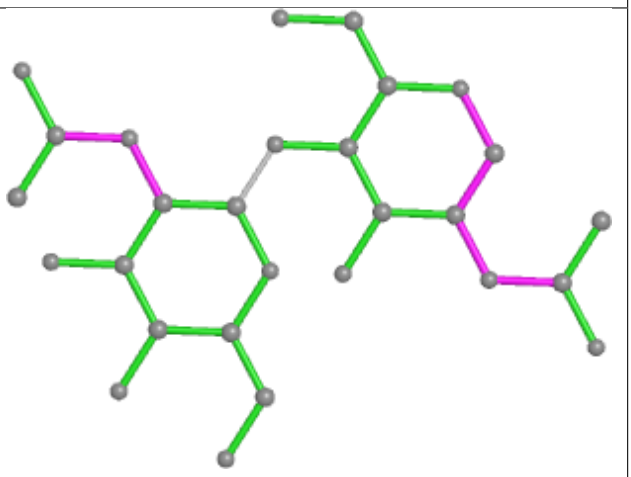
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	3	BMA	0	1
2	B	2	NAG	2	0

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

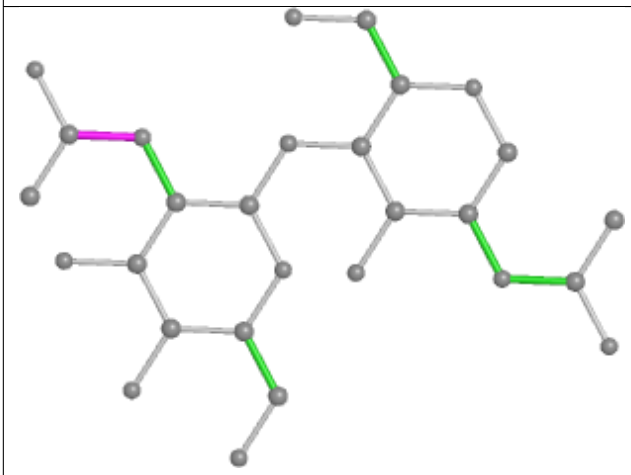
Oligosaccharide Chain B



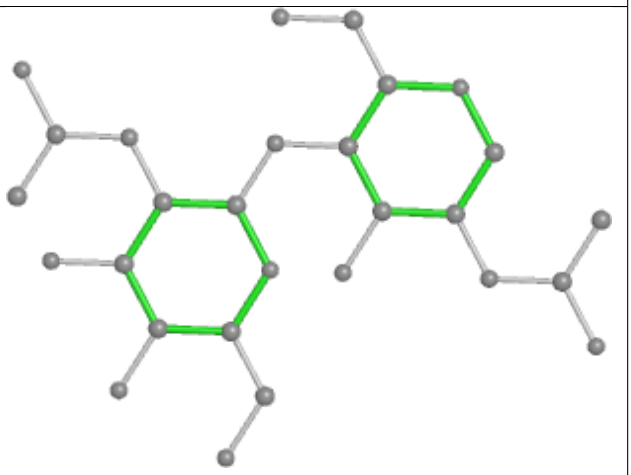
Bond lengths



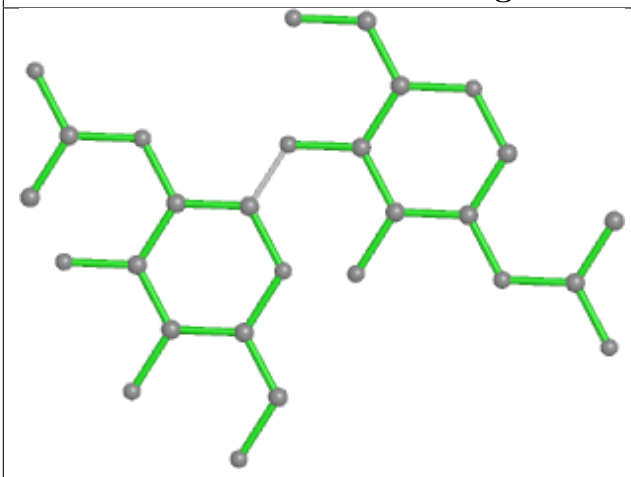
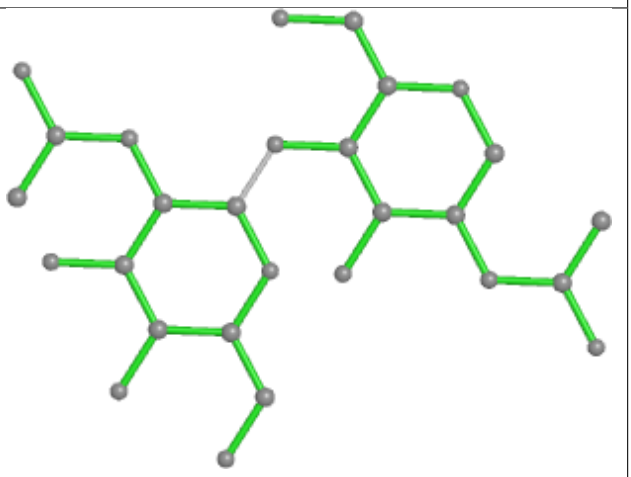
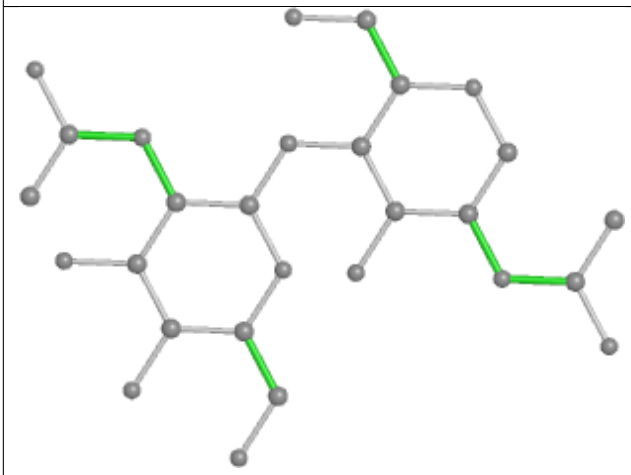
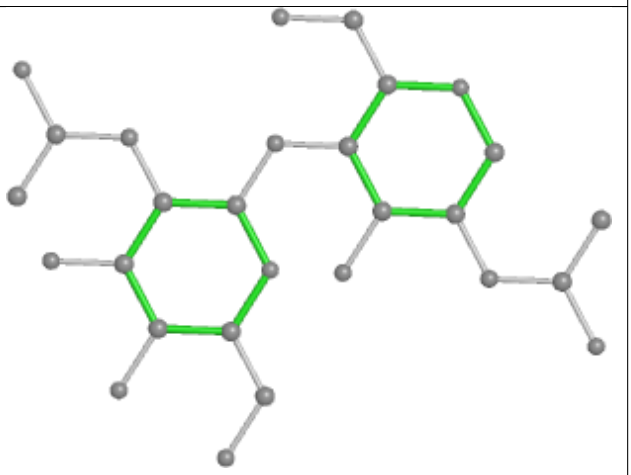
Bond angles



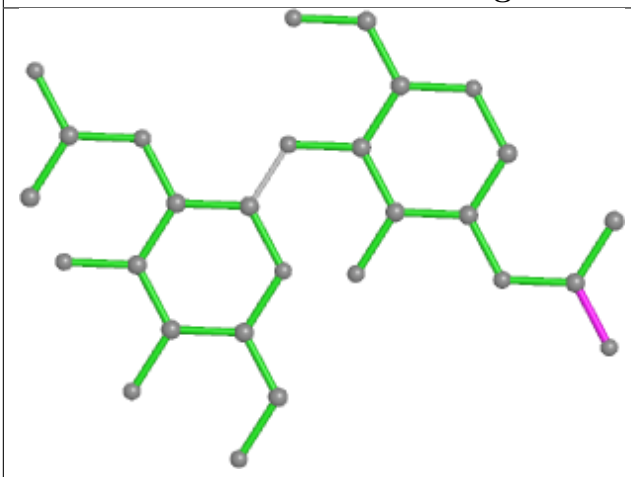
Torsions



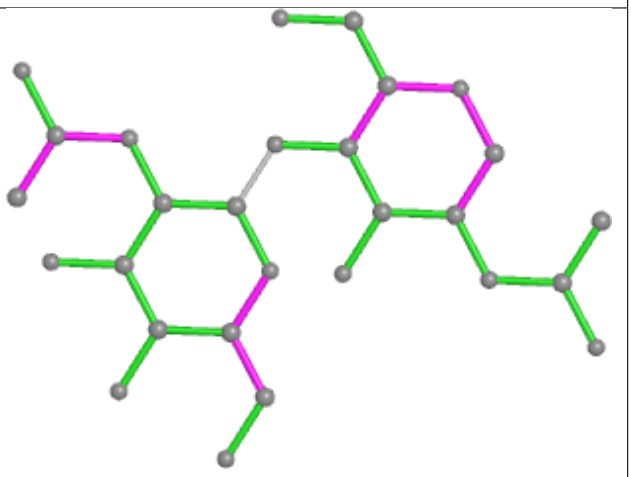
Rings

Oligosaccharide Chain C	
 Bond lengths	 Bond angles
 Torsions	 Rings

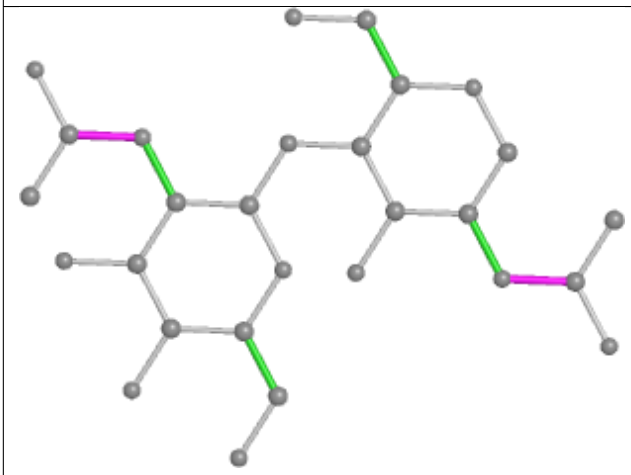
Oligosaccharide Chain D



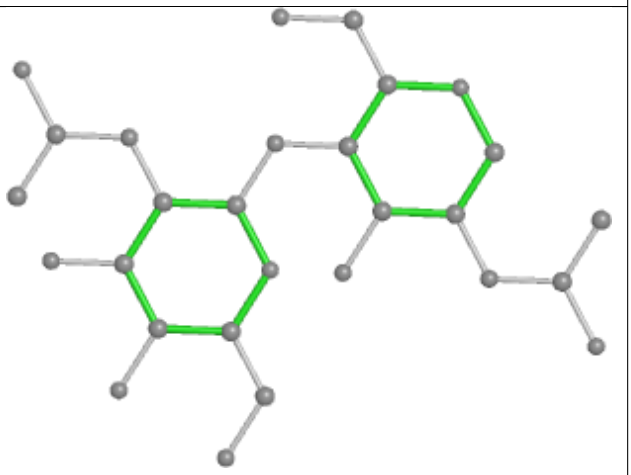
Bond lengths



Bond angles

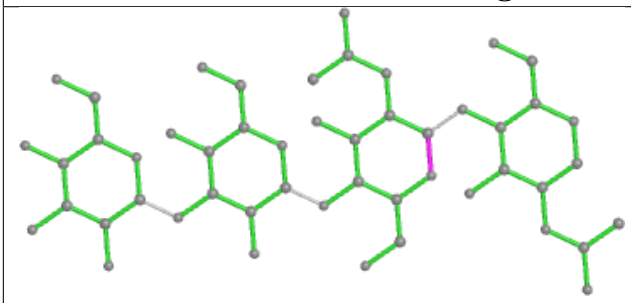


Torsions

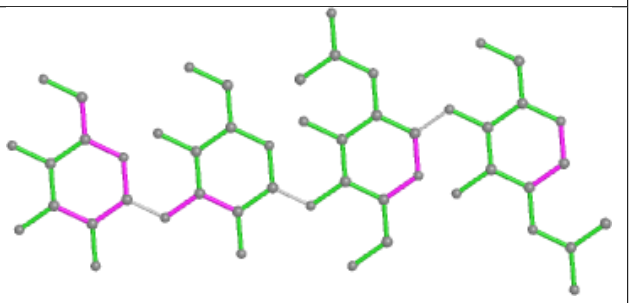


Rings

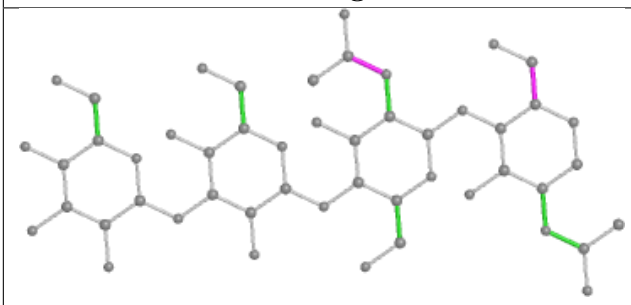
Oligosaccharide Chain E



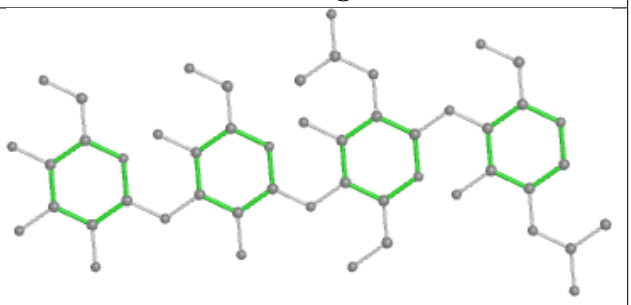
Bond lengths



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	CI9	A	1768	4	52,53,53	1.53	5 (9%)	58,67,67	2.71	13 (22%)
7	NAG	A	1757	1	14,14,15	0.70	0	17,19,21	1.39	3 (17%)
7	NAG	A	1760	1	14,14,15	0.64	0	17,19,21	1.58	5 (29%)
7	NAG	A	1759	1	14,14,15	0.43	0	17,19,21	2.35	4 (23%)

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	CI9	A	1768	4	-	14/47/53/53	0/2/2/2
7	NAG	A	1757	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1760	1	-	0/6/23/26	0/1/1/1
7	NAG	A	1759	1	-	3/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1768	CI9	NBE-NBF	-5.55	1.24	1.34
8	A	1768	CI9	NBF-NBX	-4.71	1.25	1.34
8	A	1768	CI9	CBD-CBR	-4.61	1.39	1.50
8	A	1768	CI9	CAZ-CBN	2.62	1.56	1.50
8	A	1768	CI9	CBS-NBY	-2.53	1.35	1.44

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	1768	CI9	OAJ-NBY-CBS	8.81	121.56	108.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	A	1768	CI9	OAK-NBZ-CBU	8.56	122.63	106.67
8	A	1768	CI9	OAE-NBY-CBS	7.90	120.22	108.62
7	A	1759	NAG	C1-O5-C5	7.57	122.45	112.19
8	A	1768	CI9	OAF-NBZ-CBU	7.53	120.71	106.67
8	A	1768	CI9	CB-CA-N	-6.16	98.42	110.88
8	A	1768	CI9	NBE-NBF-NBX	5.03	111.11	107.31
7	A	1757	NAG	O5-C5-C6	3.21	112.24	107.20
8	A	1768	CI9	CAL-CBS-NBY	3.10	121.57	119.25
7	A	1760	NAG	C1-O5-C5	3.06	116.34	112.19
7	A	1759	NAG	C6-C5-C4	-2.93	106.13	113.00
8	A	1768	CI9	OAD-CBQ-NBI	-2.85	117.43	122.62
8	A	1768	CI9	CAQ-CAP-CB	-2.84	103.57	113.62
7	A	1759	NAG	C8-C7-N2	2.80	120.84	116.10
7	A	1757	NAG	C1-C2-N2	-2.61	106.03	110.49
8	A	1768	CI9	OBM-CBD-CBR	2.58	118.29	110.94
7	A	1760	NAG	O5-C5-C6	2.45	111.04	107.20
7	A	1760	NAG	O5-C1-C2	-2.34	107.59	111.29
7	A	1760	NAG	C2-N2-C7	-2.32	119.59	122.90
8	A	1768	CI9	CAM-CBT-NBG	-2.22	118.01	121.80
7	A	1760	NAG	O7-C7-C8	-2.22	117.93	122.06
8	A	1768	CI9	O-C-CA	-2.13	115.27	122.26
7	A	1759	NAG	C2-N2-C7	2.04	125.80	122.90
7	A	1757	NAG	O3-C3-C2	-2.03	105.27	109.47
8	A	1768	CI9	CBB-CBW-CBP	-2.00	105.53	110.35

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1768	CI9	CBU-CBT-NBG-CAR
8	A	1768	CI9	CAL-CBS-NBY-OAJ
8	A	1768	CI9	CAL-CBS-NBY-OAE
8	A	1768	CI9	CAN-CBS-NBY-OAJ
8	A	1768	CI9	CAN-CBS-NBY-OAE
8	A	1768	CI9	CAM-CBT-NBG-CAR
8	A	1768	CI9	OBJ-CAT-CAU-OBK
7	A	1759	NAG	C8-C7-N2-C2
7	A	1759	NAG	O7-C7-N2-C2
8	A	1768	CI9	CAS-CAR-NBG-CBT
8	A	1768	CI9	CAT-CAU-OBK-CAV
8	A	1768	CI9	OBK-CAV-CAW-OBL
7	A	1759	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
8	A	1768	CI9	CBR-CBD-OBM-CAY
8	A	1768	CI9	CAV-CAW-OBL-CAX
8	A	1768	CI9	CAU-CAT-OBJ-CAS
8	A	1768	CI9	CAY-CAX-OBL-CAW

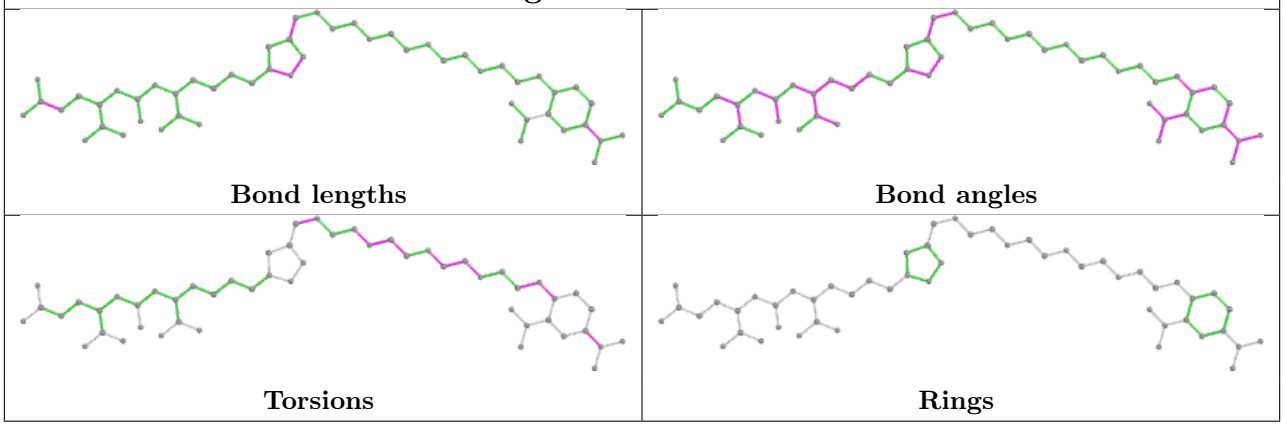
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	1768	CI9	10	0
7	A	1760	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 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 CI9 A 1768



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	694/709 (97%)	0.34	54 (7%) 13 11	12, 22, 40, 59	1 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	506	PHE	5.5
1	A	55	LYS	5.4
1	A	545	LYS	5.3
1	A	507	SER	4.9
1	A	546	PHE	4.8
1	A	153	ASN	4.8
1	A	656[A]	SER	4.4
1	A	155	SER	4.4
1	A	541	TRP	4.4
1	A	336	ASN	4.3
1	A	335	GLY	4.1
1	A	544	ASN	4.0
1	A	542	GLU	4.0
1	A	134	ASP	3.9
1	A	337	PHE	3.9
1	A	136	ASN	3.7
1	A	719	VAL	3.5
1	A	135	GLY	3.4
1	A	123	THR	3.3
1	A	652	ASP	3.1
1	A	237	PRO	3.0
1	A	543	THR	2.9
1	A	154	VAL	2.9
1	A	334	THR	2.9
1	A	487	GLY	2.9
1	A	138	ILE	2.8
1	A	651	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	122	LYS	2.7
1	A	169	MET	2.7
1	A	174[A]	LEU	2.7
1	A	226	ILE	2.7
1	A	227	LEU	2.7
1	A	394	VAL	2.6
1	A	133	GLU	2.6
1	A	219	LEU	2.6
1	A	196	CYS	2.6
1	A	56	HIS	2.5
1	A	124	HIS	2.5
1	A	189	GLU	2.5
1	A	408	GLU	2.4
1	A	202	ILE	2.4
1	A	616	MET	2.3
1	A	324	LYS	2.3
1	A	152	GLU	2.3
1	A	201	VAL	2.3
1	A	505	GLU	2.2
1	A	732	ILE	2.2
1	A	339	THR	2.1
1	A	225	VAL	2.1
1	A	597	CYS	2.1
1	A	504	PRO	2.1
1	A	393	ALA	2.1
1	A	398	ILE	2.0
1	A	576	VAL	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	B	2	14/15	0.63	0.29	38,44,49,52	0

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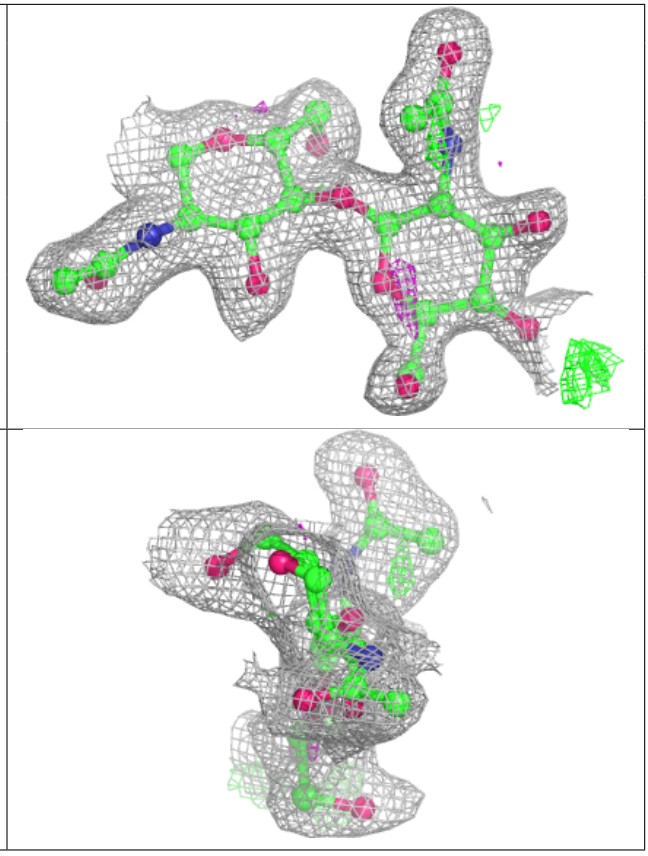
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	C	1	14/15	0.80	0.18	36,39,43,49	0
2	NAG	C	2	14/15	0.80	0.30	53,57,61,62	0
3	NAG	E	2	14/15	0.83	0.24	34,37,46,49	0
3	BMA	E	3	11/12	0.84	0.18	32,35,37,38	0
3	NAG	E	1	14/15	0.87	0.11	19,24,32,42	0
3	MAN	E	4	11/12	0.87	0.19	38,42,44,45	0
2	NAG	D	2	14/15	0.88	0.17	30,35,40,43	0
2	NAG	D	1	14/15	0.90	0.13	23,26,31,37	0
2	NAG	B	1	14/15	0.91	0.11	28,34,40,43	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.

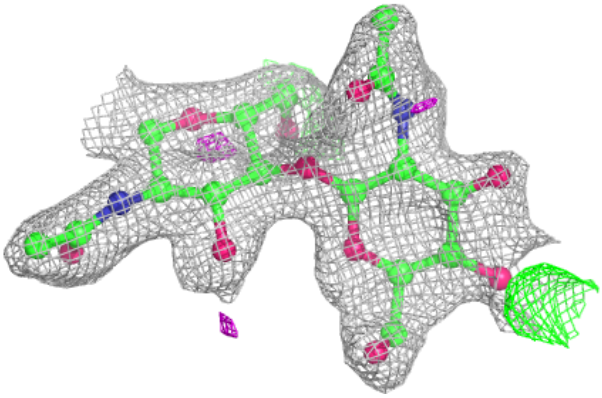
Electron density around Chain B:

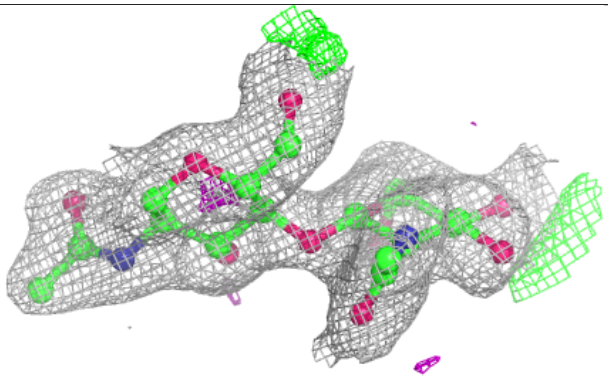
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

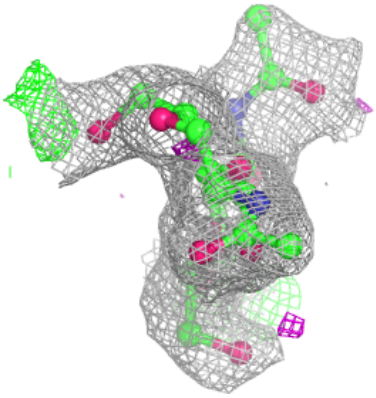


Electron density around Chain C:

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

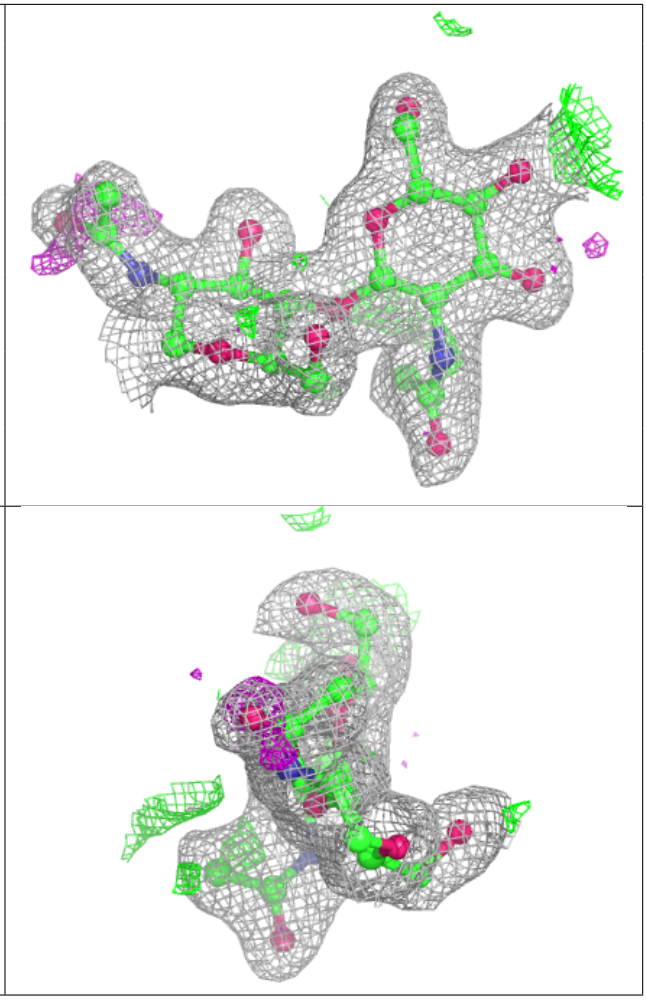






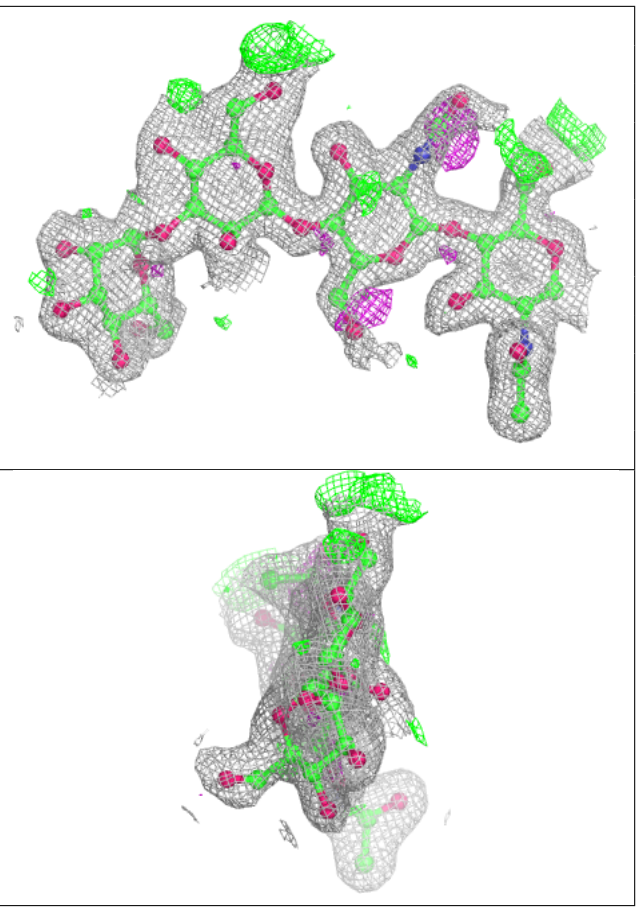
Electron density around Chain D:

$2mF_o$-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)

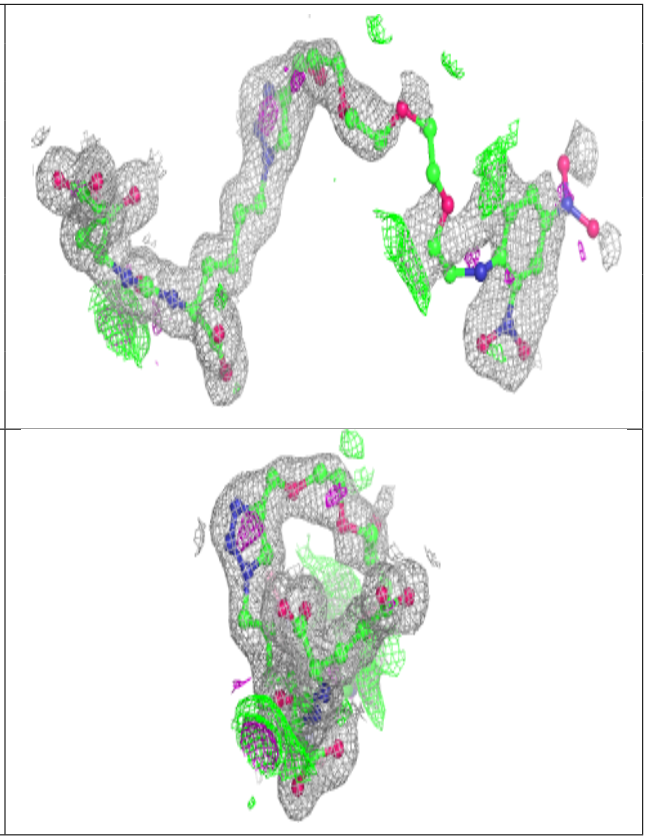
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	NAG	A	1757	14/15	0.71	0.27	40,47,51,52	0
7	NAG	A	1759	14/15	0.72	0.21	56,62,66,68	0
7	NAG	A	1760	14/15	0.83	0.18	26,43,46,48	0
8	CI9	A	1768	52/52	0.91	0.16	13,49,78,81	0
4	ZN	A	1751	1/1	1.00	0.12	5,5,5,5	0
4	ZN	A	1752	1/1	1.00	0.12	5,5,5,5	0
5	CA	A	1753	1/1	1.00	0.09	4,4,4,4	0
6	CL	A	1754	1/1	1.00	0.13	5,5,5,5	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 CI9 A 1768:

$2mF_o$-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.