Full wwPDB X-ray Structure Validation Report (i)

Jul 26, 2022 – 11:58 am BST

PDB ID	:	8AIC
Title	:	X-ray structure of the receptor binding domain of Env glycoprotein of Simian Foamy virus
Deposited on	:	2022-07-26
Resolution	:	2.80 Å(reported)

This wwPDB validation report is for manuscript review

This is a Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

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	:	2.29
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

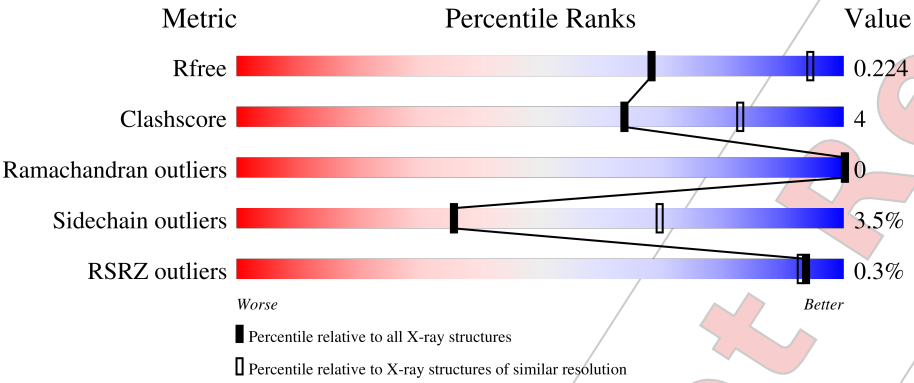
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1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	340	83% 13%
1	B	340	85% 11%
2	C	3	67% 33%
2	E	3	67% 33%

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Mol	Chain	Length	Quality of chain
2	G	3	100%
2	L	3	33% 33% 33%
3	D	2	50% 50%
3	H	2	50% 50%
3	I	2	50% 50%
3	J	2	100%
4	F	10	30% 50% 20%
5	K	9	11% 89%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BMA	L	3	-	-	-	X
3	NAG	D	2	-	-	-	X
3	NAG	H	2	-	-	-	X
3	NAG	J	2	-	-	-	X
4	MAN	F	9	-	-	-	X

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2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6086 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.

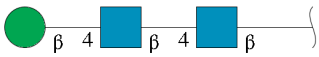
- Molecule 1 is a protein called Envelope glycoprotein gp130.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	15	0	0
			2716	1748	456	496	16			
1	B	330	Total	C	N	O	S	15	0	0
			2716	1746	457	497	16			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	553	ASP	-	expression tag	UNP K7YEW5
A	554	ASP	-	expression tag	UNP K7YEW5
A	555	ASP	-	expression tag	UNP K7YEW5
A	556	ASP	-	expression tag	UNP K7YEW5
A	557	LYS	-	expression tag	UNP K7YEW5
B	553	ASP	-	expression tag	UNP K7YEW5
B	554	ASP	-	expression tag	UNP K7YEW5
B	555	ASP	-	expression tag	UNP K7YEW5
B	556	ASP	-	expression tag	UNP K7YEW5
B	557	LYS	-	expression tag	UNP K7YEW5

- Molecule 2 is an oligosaccharide called 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
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	E	3	Total	C	N	O	0	0	0
			39	22	2	15			

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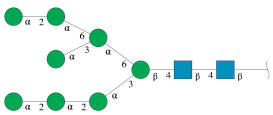
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	G	3	Total C N O 39 22 2 15	0	0	0
2	L	3	Total C N O 39 22 2 15	0	0	0

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	D	2	Total C N O 28 16 2 10	0	0	0
3	H	2	Total C N O 28 16 2 10	0	0	0
3	I	2	Total C N O 28 16 2 10	0	0	0
3	J	2	Total C N O 28 16 2 10	0	0	0

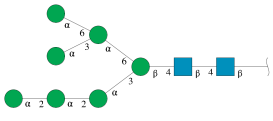
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
4	F	10	Total C N O 116 64 2 50	0	0	0

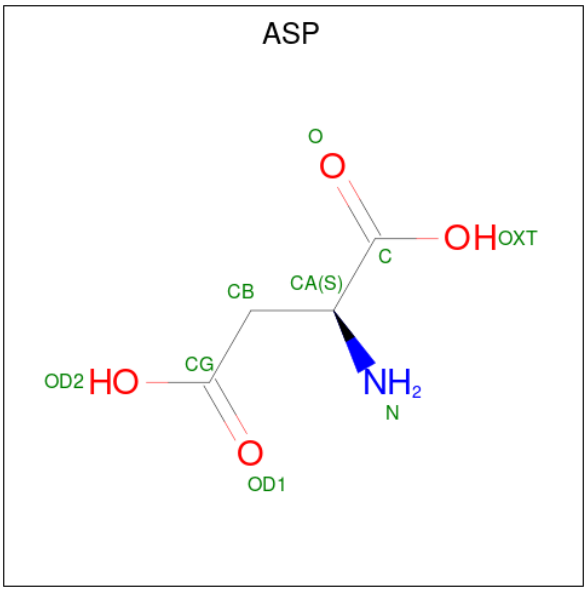
- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	K	9	Total	C	N	O	0	0	0
			105	58	2	45			

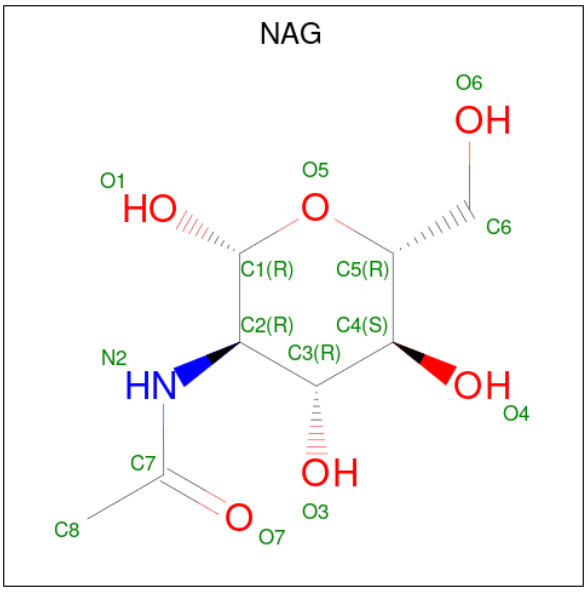
- Molecule 6 is ASPARTIC ACID (three-letter code: ASP) (formula: $C_4H_7NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			8	4	1	3		
6	A	1	Total	C	N	O	0	0
			8	4	1	3		

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

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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	63	Total O 63 63	0	0
8	B	44	Total O 44 44	0	0

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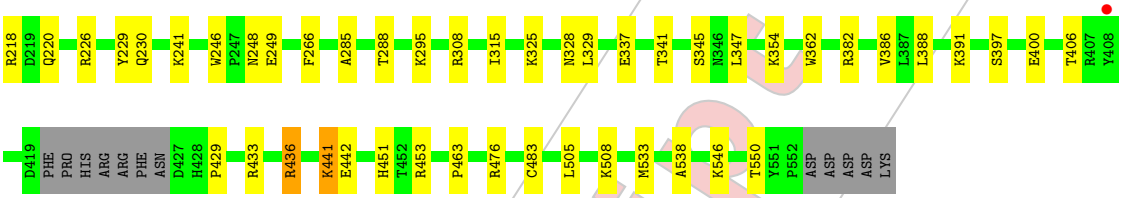
3 Residue-property plots (i)

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: Envelope glycoprotein gp130

Chain A:

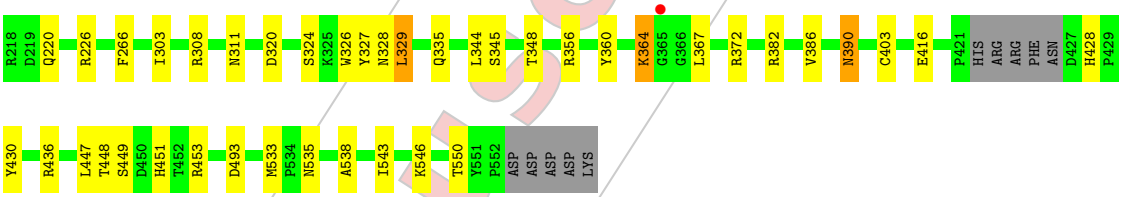




• Molecule 1: Envelope glycoprotein gp130

Chain B:





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

Chain C:





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

Chain E:

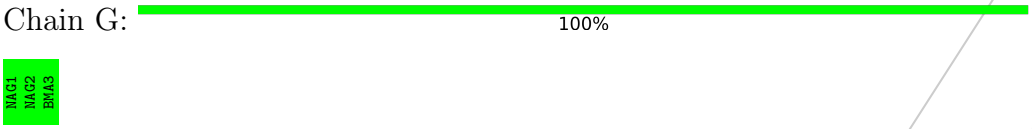




• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

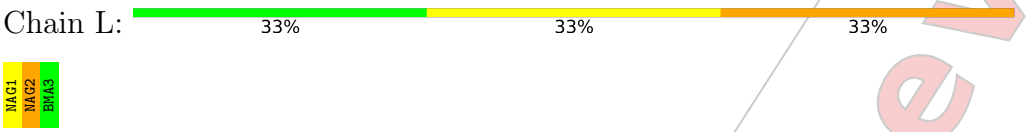
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Chain G:



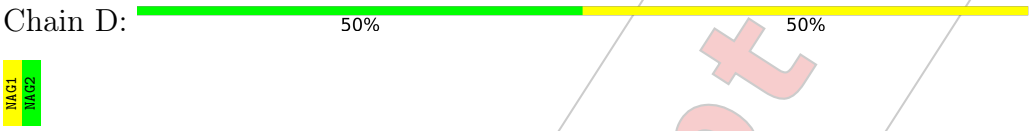
• Molecule 2: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:



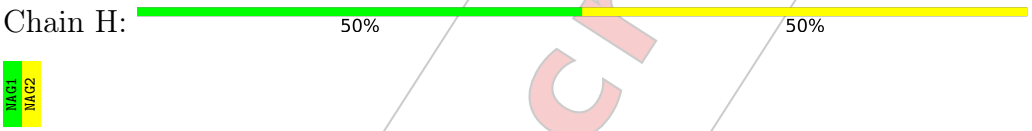
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:



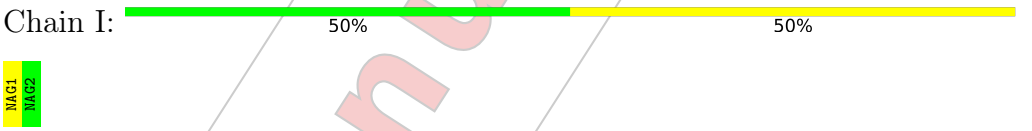
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:



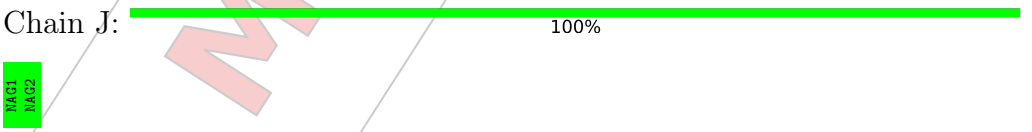
• Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:



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

Chain J:



• Molecule 4: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:



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• Molecule 5: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:





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4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	123.62Å 123.62Å 191.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.73 – 2.80 46.73 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (46.73-2.80) 94.2 (46.73-2.80)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 2.81Å)	Xtriage
Refinement program	BUSTER, PHENIX 1.19_4092	Depositor
R, R_{free}	0.194 , 0.229 0.190 , 0.224	Depositor DCC
R_{free} test set	2113 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å^2)	65.0	Xtriage
Anisotropy	0.210	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.038 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6086	wwPDB-VP
Average B, all atoms (Å^2)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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.

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5 Model quality

5.1 Standard geometry

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

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	0.27	0/2797	0.53	0/3802
1	B	0.28	0/2796	0.53	0/3802
All	All	0.28	0/5593	0.53	0/7604

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2716	0	2602	26	0
1	B	2716	0	2588	24	0
2	C	39	0	34	0	0
2	E	39	0	34	0	0
2	G	39	0	34	0	0
2	L	39	0	34	1	0
3	D	28	0	25	0	0
3	H	28	0	25	1	0
3	I	28	0	25	1	0
3	J	28	0	25	0	0
4	F	116	0	97	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	K	105	0	88	1	0
6	A	16	0	7	0	0
7	A	14	0	13	0	0
7	B	28	0	26	0	0
8	A	63	0	0	0	0
8	B	44	0	0	0	0
All	All	6086	0	5657	48	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 (48) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:428:HIS:HD2	1:B:430:TYR:H	1.18	0.91
1:B:303:ILE:O	1:B:308:ARG:NH1	2.14	0.79
1:B:533:MET:HE2	1:B:538:ALA:HA	1.74	0.70
1:A:329:LEU:HD23	1:B:329:LEU:HB2	1.75	0.69
1:B:403:CYS:HA	3:I:1:NAG:H82	1.80	0.64
1:B:344:LEU:O	1:B:348:THR:HG23	2.02	0.59
1:A:546:LYS:NZ	1:A:550:THR:HG22	2.18	0.59
1:B:416:GLU:H	1:B:416:GLU:CD	2.06	0.58
1:B:220:GLN:O	1:B:220:GLN:HG3	2.04	0.58
1:B:320:ASP:OD1	1:B:535:ASN:ND2	2.33	0.58
1:B:428:HIS:CD2	1:B:430:TYR:H	2.10	0.58
1:A:226:ARG:O	1:A:230:GLN:HG2	2.04	0.57
1:A:533:MET:HE2	1:A:538:ALA:HA	1.87	0.56
1:A:441:LYS:HD2	1:A:441:LYS:H	1.71	0.55
1:A:229:TYR:CZ	1:A:337:GLU:HG3	2.42	0.55
1:B:546:LYS:NZ	1:B:550:THR:OG1	2.41	0.53
1:A:347:LEU:HA	1:A:354:LYS:HE2	1.91	0.52
1:A:505:LEU:O	1:A:508:LYS:HG2	2.11	0.50
1:A:266:PHE:O	1:B:226:ARG:HD3	2.12	0.49
1:B:533:MET:CE	1:B:538:ALA:HA	2.41	0.49
1:B:448:THR:OG1	1:B:449:SER:N	2.46	0.49
1:B:364:LYS:HD2	1:B:493:ASP:OD1	2.13	0.47
1:A:285:ALA:HB2	1:A:451:HIS:HB3	1.96	0.47
1:B:324:SER:HA	1:B:372:ARG:HB3	1.97	0.46
1:A:362:TRP:HA	1:A:391:LYS:HE3	1.97	0.46
1:B:367:LEU:HD23	1:B:367:LEU:HA	1.85	0.45
2:L:1:NAG:H62	2:L:2:NAG:N2	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:386:VAL:O	1:B:390:ASN:HB2	2.18	0.44
1:A:546:LYS:HZ2	1:A:550:THR:HG22	1.81	0.43
1:A:397:SER:HB3	1:A:483:CYS:HB3	2.01	0.43
1:A:337:GLU:O	1:A:341:THR:HG23	2.19	0.43
1:A:400:GLU:HG3	1:A:406:THR:HA	2.01	0.43
1:A:386:VAL:HG11	4:F:1:NAG:H82	2.00	0.42
1:A:436:ARG:NH1	1:A:463:PRO:HG3	2.33	0.42
1:A:476:ARG:HD2	4:F:9:MAN:H62	2.01	0.42
1:A:429:PRO:O	1:A:433:ARG:HD3	2.19	0.42
1:B:364:LYS:HD2	1:B:364:LYS:H	1.85	0.42
1:A:441:LYS:H	1:A:441:LYS:CD	2.32	0.42
1:B:386:VAL:HG11	5:K:1:NAG:H82	2.01	0.42
1:A:288:THR:HG23	1:A:442:GLU:OE1	2.20	0.42
1:A:246:TRP:HB3	1:A:308:ARG:HB3	2.02	0.42
1:A:218:ARG:O	1:A:220:GLN:N	2.54	0.41
1:B:326:TRP:CZ3	1:B:327:TYR:HB2	2.55	0.41
1:A:226:ARG:HD3	1:B:266:PHE:O	2.21	0.41
1:A:249:GLU:OE1	1:A:295:LYS:HE3	2.20	0.41
1:B:360:TYR:CD2	3:H:2:NAG:H81	2.55	0.41
1:B:311:ASN:HB3	1:B:543:ILE:HD13	2.03	0.41
1:A:315:ILE:HD12	1:A:388:LEU:HB3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	324/340 (95%)	312 (96%)	12 (4%)	0	100	100
1	B	326/340 (96%)	310 (95%)	16 (5%)	0	100	100
All	All	650/680 (96%)	622 (96%)	28 (4%)	0	100	100

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There are no Ramachandran outliers to report.

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	298/313 (95%)	289 (97%)	9 (3%)	41	75
1	B	296/313 (95%)	284 (96%)	12 (4%)	30	64
All	All	594/626 (95%)	573 (96%)	21 (4%)	36	70

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	241	LYS
1	A	248	ASN
1	A	325	LYS
1	A	328	ASN
1	A	345	SER
1	A	382	ARG
1	A	436	ARG
1	A	441	LYS
1	A	453	ARG
1	B	328	ASN
1	B	329	LEU
1	B	335	GLN
1	B	345	SER
1	B	356	ARG
1	B	364	LYS
1	B	382	ARG
1	B	390	ASN
1	B	436	ARG
1	B	447	LEU
1	B	451	HIS
1	B	453	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

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Mol	Chain	Res	Type
1	A	222	GLN
1	A	521	ASN
1	B	222	GLN
1	B	428	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)

39 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	C	1	2,1	14,14,15	0.18	0	17,19,21	0.92	1 (5%)
2	NAG	C	2	2	14,14,15	0.43	0	17,19,21	0.59	0
2	BMA	C	3	2	11,11,12	0.70	0	15,15,17	0.74	0
3	NAG	D	1	3,1	14,14,15	0.29	0	17,19,21	0.94	1 (5%)
3	NAG	D	2	3	14,14,15	0.53	0	17,19,21	0.60	0
2	NAG	E	1	2,1	14,14,15	0.30	0	17,19,21	0.53	0
2	NAG	E	2	2	14,14,15	0.22	0	17,19,21	0.47	0
2	BMA	E	3	2	11,11,12	0.80	0	15,15,17	1.08	1 (6%)
4	NAG	F	1	4,1	14,14,15	0.45	0	17,19,21	0.70	1 (5%)
4	MAN	F	10	4	11,11,12	0.74	0	15,15,17	1.01	2 (13%)
4	NAG	F	2	4	14,14,15	0.35	0	17,19,21	0.60	0
4	BMA	F	3	4	11,11,12	0.87	0	15,15,17	0.79	0
4	MAN	F	4	4	11,11,12	0.89	0	15,15,17	1.51	3 (20%)
4	MAN	F	5	4	11,11,12	0.64	0	15,15,17	0.99	2 (13%)

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Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	MAN	F	6	4	11,11,12	0.88	0	15,15,17	1.02	0
4	MAN	F	7	4	11,11,12	0.67	0	15,15,17	1.28	1 (6%)
4	MAN	F	8	4	11,11,12	0.86	0	15,15,17	0.93	1 (6%)
4	MAN	F	9	4	11,11,12	1.70	2 (18%)	15,15,17	2.18	4 (26%)
2	NAG	G	1	2,1	14,14,15	0.40	0	17,19,21	0.59	0
2	NAG	G	2	2	14,14,15	0.24	0	17,19,21	0.47	0
2	BMA	G	3	2	11,11,12	0.72	0	15,15,17	1.05	0
3	NAG	H	1	3,1	14,14,15	0.30	0	17,19,21	0.54	0
3	NAG	H	2	3	14,14,15	0.50	0	17,19,21	0.44	0
3	NAG	I	1	3,1	14,14,15	0.25	0	17,19,21	0.72	0
3	NAG	I	2	3	14,14,15	0.36	0	17,19,21	0.51	0
3	NAG	J	1	3,1	14,14,15	0.41	0	17,19,21	0.59	0
3	NAG	J	2	3	14,14,15	0.46	0	17,19,21	0.57	0
5	NAG	K	1	5,1	14,14,15	0.49	0	17,19,21	0.62	0
5	NAG	K	2	5	14,14,15	0.35	0	17,19,21	0.68	1 (5%)
5	BMA	K	3	5	11,11,12	0.69	0	15,15,17	0.80	0
5	MAN	K	4	5	11,11,12	0.86	1 (9%)	15,15,17	2.47	2 (13%)
5	MAN	K	5	5	11,11,12	0.73	0	15,15,17	1.52	3 (20%)
5	MAN	K	6	5	11,11,12	0.93	1 (9%)	15,15,17	1.10	1 (6%)
5	MAN	K	7	5	11,11,12	1.31	2 (18%)	15,15,17	2.07	2 (13%)
5	MAN	K	8	5	11,11,12	0.96	1 (9%)	15,15,17	0.87	1 (6%)
5	MAN	K	9	5	11,11,12	0.90	0	15,15,17	0.94	2 (13%)
2	NAG	L	1	2,1	14,14,15	0.32	0	17,19,21	0.67	0
2	NAG	L	2	2	14,14,15	0.41	0	17,19,21	0.77	1 (5%)
2	BMA	L	3	2	11,11,12	0.82	0	15,15,17	0.79	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	C	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	1/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
2	NAG	E	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BMA	E	3	2	-	2/2/19/22	0/1/1/1
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	MAN	F	10	4	-	0/2/19/22	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1
4	MAN	F	5	4	-	0/2/19/22	0/1/1/1
4	MAN	F	6	4	-	2/2/19/22	0/1/1/1
4	MAN	F	7	4	-	0/2/19/22	0/1/1/1
4	MAN	F	8	4	-	0/2/19/22	0/1/1/1
4	MAN	F	9	4	-	0/2/19/22	0/1/1/1
2	NAG	G	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	G	2	2	-	0/6/23/26	0/1/1/1
2	BMA	G	3	2	-	2/2/19/22	0/1/1/1
3	NAG	H	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	NAG	J	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	J	2	3	-	2/6/23/26	0/1/1/1
5	NAG	K	1	5,1	-	2/6/23/26	0/1/1/1
5	NAG	K	2	5	-	0/6/23/26	0/1/1/1
5	BMA	K	3	5	-	2/2/19/22	0/1/1/1
5	MAN	K	4	5	-	2/2/19/22	0/1/1/1
5	MAN	K	5	5	-	0/2/19/22	0/1/1/1
5	MAN	K	6	5	-	0/2/19/22	1/1/1/1
5	MAN	K	7	5	-	0/2/19/22	0/1/1/1
5	MAN	K	8	5	-	1/2/19/22	0/1/1/1
5	MAN	K	9	5	-	1/2/19/22	0/1/1/1
2	NAG	L	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	L	2	2	-	0/6/23/26	0/1/1/1
2	BMA	L	3	2	-	2/2/19/22	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	9	MAN	C1-C2	4.39	1.62	1.52
4	F	9	MAN	O5-C1	3.12	1.48	1.43
5	K	7	MAN	O5-C5	2.81	1.49	1.43
5	K	8	MAN	O5-C1	-2.57	1.39	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	K	7	MAN	O5-C1	2.33	1.47	1.43
5	K	4	MAN	O5-C5	2.26	1.48	1.43
5	K	6	MAN	C1-C2	2.23	1.57	1.52

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	K	4	MAN	C1-O5-C5	8.66	123.93	112.19
4	F	9	MAN	C1-O5-C5	7.06	121.76	112.19
5	K	7	MAN	C1-O5-C5	6.18	120.57	112.19
5	K	5	MAN	C1-O5-C5	3.86	117.42	112.19
4	F	7	MAN	C1-O5-C5	3.83	117.38	112.19
4	F	4	MAN	O2-C2-C3	-3.48	103.17	110.14
5	K	7	MAN	O3-C3-C2	3.28	116.27	109.99
4	F	4	MAN	C1-O5-C5	3.22	116.56	112.19
2	C	1	NAG	C1-O5-C5	3.14	116.44	112.19
5	K	6	MAN	C1-O5-C5	2.87	116.08	112.19
5	K	5	MAN	O2-C2-C3	-2.79	104.55	110.14
2	L	2	NAG	C1-O5-C5	2.55	115.65	112.19
4	F	10	MAN	C1-O5-C5	2.51	115.59	112.19
2	E	3	BMA	C1-C2-C3	2.36	112.56	109.67
4	F	9	MAN	C1-C2-C3	2.34	112.54	109.67
5	K	9	MAN	C1-O5-C5	2.29	115.29	112.19
4	F	9	MAN	O2-C2-C3	-2.27	105.58	110.14
4	F	10	MAN	O2-C2-C3	-2.26	105.61	110.14
4	F	1	NAG	C1-O5-C5	2.25	115.25	112.19
4	F	9	MAN	O5-C1-C2	2.22	114.19	110.77
5	K	4	MAN	O5-C5-C4	2.18	116.13	110.83
4	F	8	MAN	C1-O5-C5	2.17	115.13	112.19
4	F	5	MAN	C1-O5-C5	2.16	115.12	112.19
5	K	5	MAN	C1-C2-C3	-2.15	107.03	109.67
4	F	5	MAN	O2-C2-C3	-2.14	105.85	110.14
4	F	4	MAN	C2-C3-C4	-2.12	107.23	110.89
5	K	8	MAN	O2-C2-C3	-2.10	105.93	110.14
5	K	9	MAN	O2-C2-C3	-2.06	106.02	110.14
3	D	1	NAG	O4-C4-C5	2.04	114.36	109.30
5	K	2	NAG	C1-O5-C5	2.00	114.91	112.19

There are no chirality outliers.

All (35) torsion outliers are listed below:

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Mol	Chain	Res	Type	Atoms
3	D	1	NAG	O5-C5-C6-O6
2	L	3	BMA	O5-C5-C6-O6
5	K	4	MAN	O5-C5-C6-O6
2	E	2	NAG	C4-C5-C6-O6
3	I	2	NAG	C4-C5-C6-O6
2	L	3	BMA	C4-C5-C6-O6
5	K	1	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
5	K	4	MAN	C4-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6
4	F	6	MAN	C4-C5-C6-O6
5	K	1	NAG	C4-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
2	E	2	NAG	O5-C5-C6-O6
3	J	2	NAG	O5-C5-C6-O6
2	G	3	BMA	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
4	F	6	MAN	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	G	3	BMA	O5-C5-C6-O6
3	D	1	NAG	C1-C2-N2-C7
2	C	3	BMA	O5-C5-C6-O6
5	K	3	BMA	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
3	J	2	NAG	C4-C5-C6-O6
5	K	3	BMA	C4-C5-C6-O6
5	K	9	MAN	O5-C5-C6-O6
5	K	8	MAN	O5-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
2	E	1	NAG	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
2	E	3	BMA	C4-C5-C6-O6
2	E	3	BMA	O5-C5-C6-O6

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	K	6	MAN	C1-C2-C3-C4-C5-O5

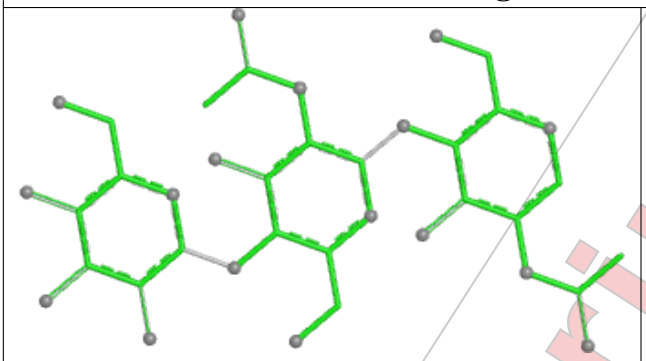
7 monomers are involved in 6 short contacts:

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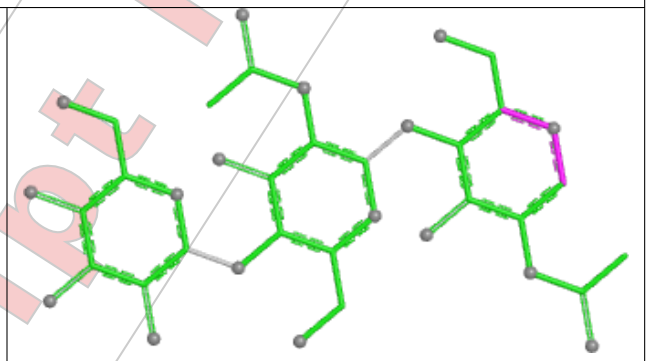
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	2	NAG	1	0
4	F	9	MAN	1	0
4	F	1	NAG	1	0
3	H	2	NAG	1	0
3	I	1	NAG	1	0
2	L	1	NAG	1	0
5	K	1	NAG	1	0

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

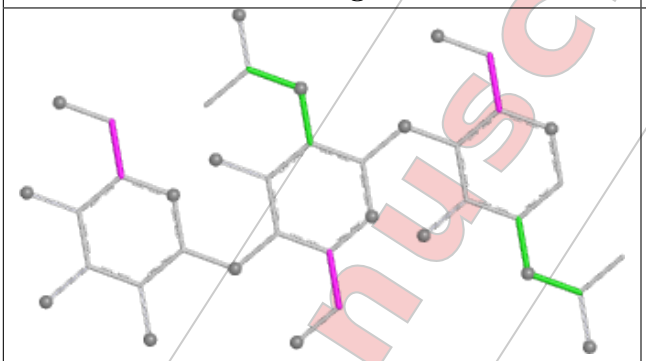
Oligosaccharide Chain C



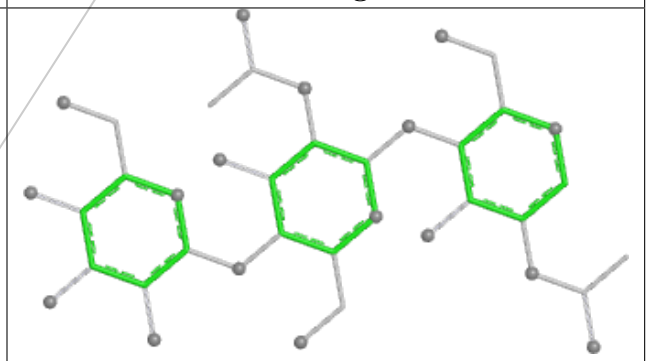
Bond lengths



Bond angles



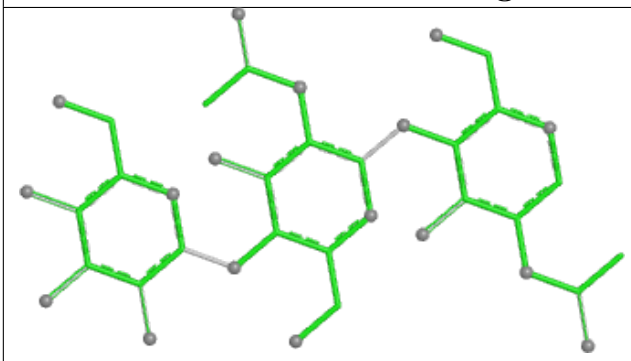
Torsions



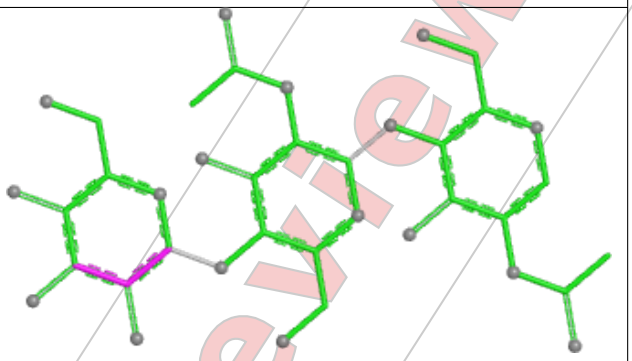
Rings

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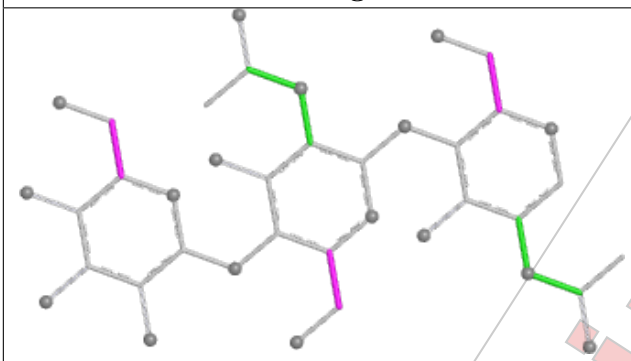
Oligosaccharide Chain E



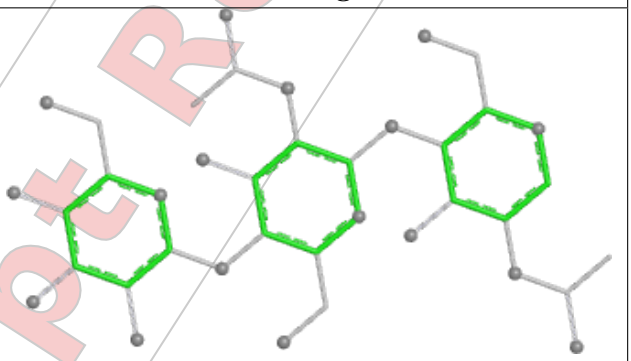
Bond lengths



Bond angles

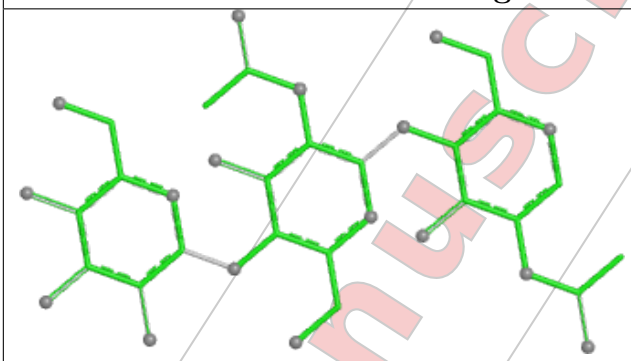


Torsions

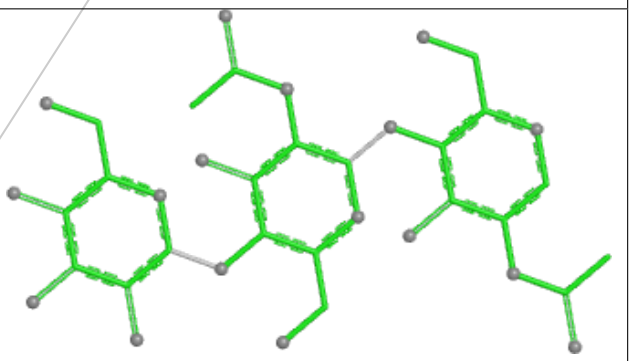


Rings

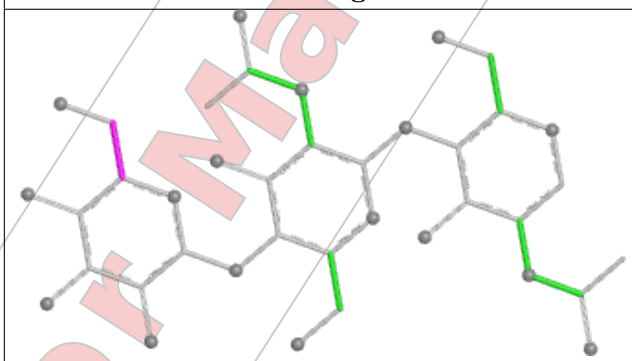
Oligosaccharide Chain G



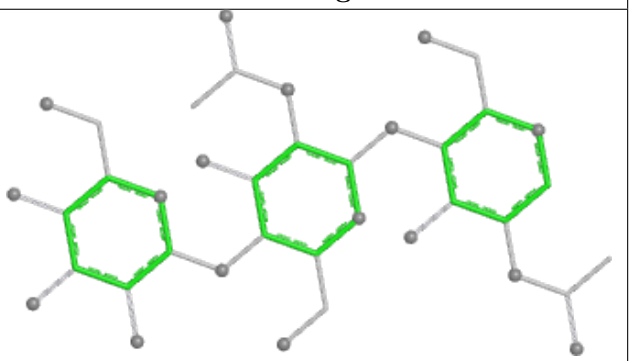
Bond lengths



Bond angles

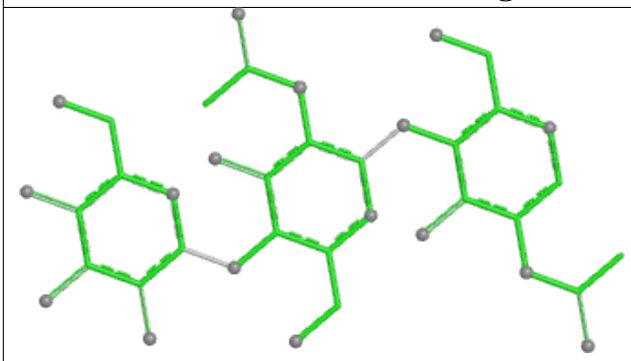
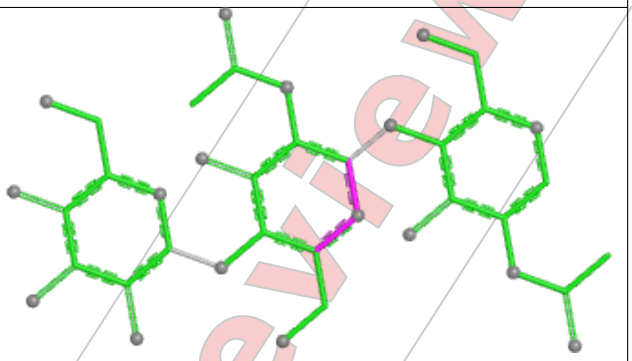
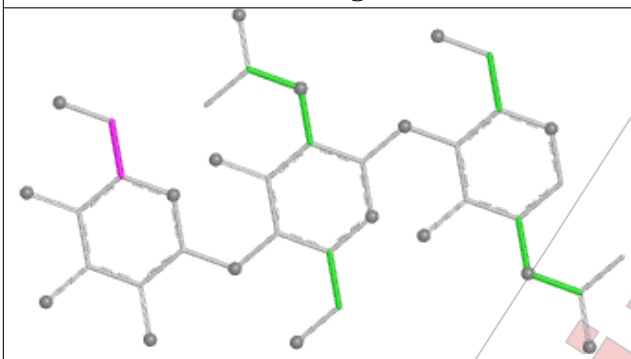
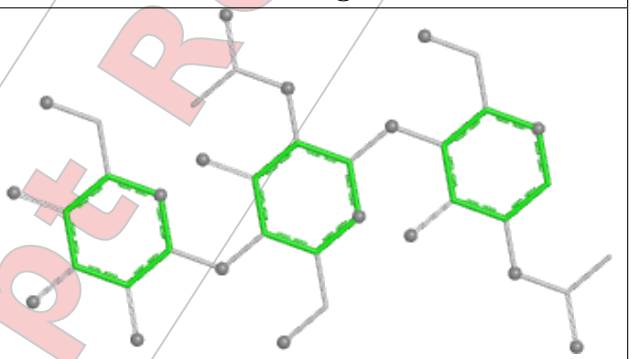


Torsions



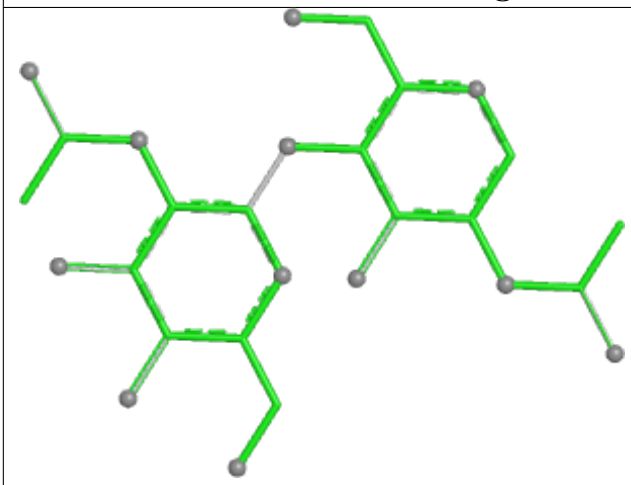
Rings

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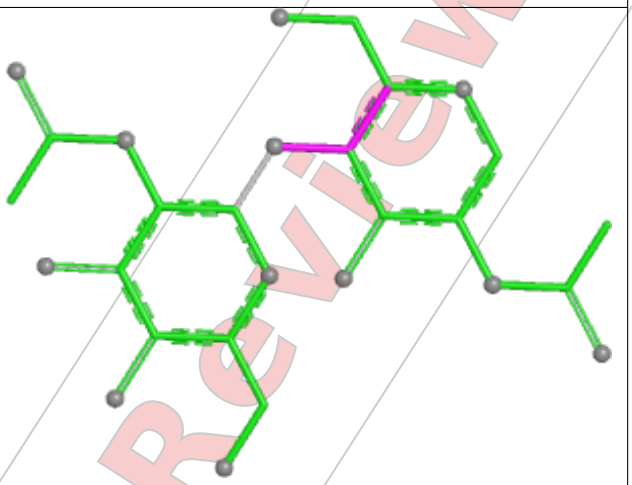
Oligosaccharide Chain L	
 Bond lengths	 Bond angles
 Torsions	 Rings

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Oligosaccharide Chain D



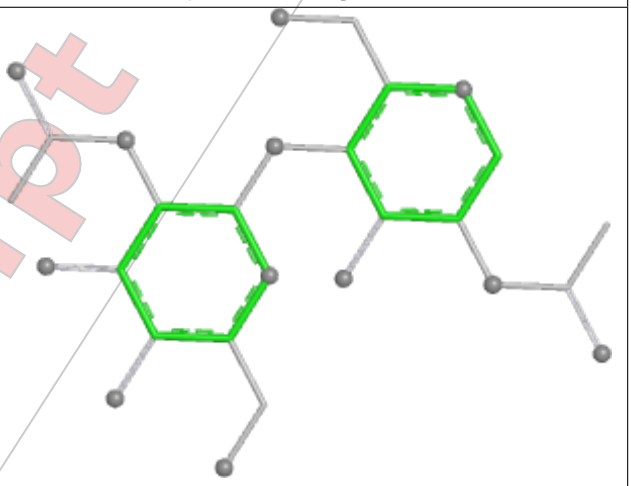
Bond lengths



Bond angles

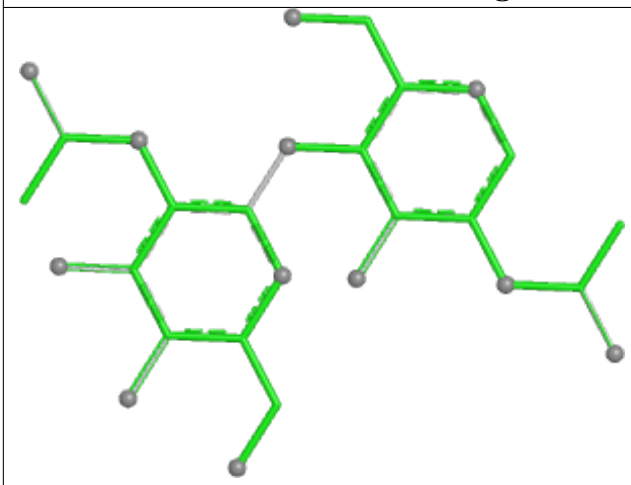
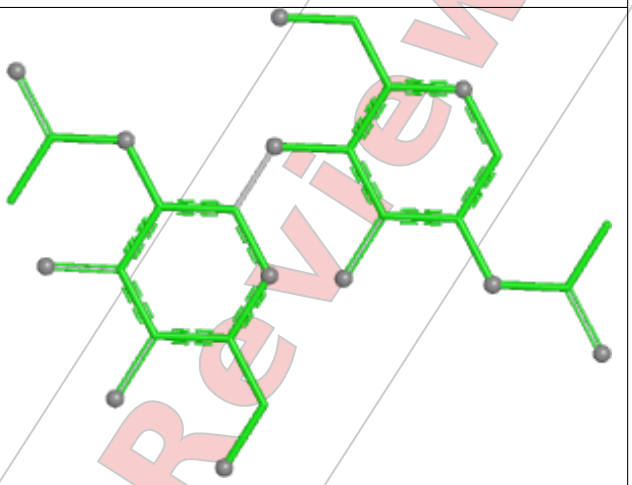
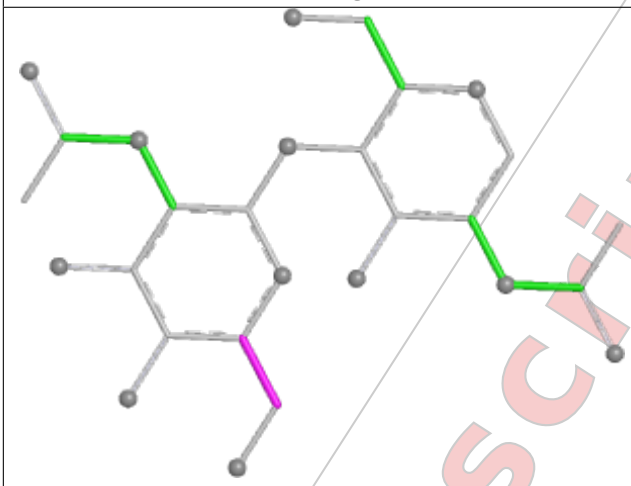
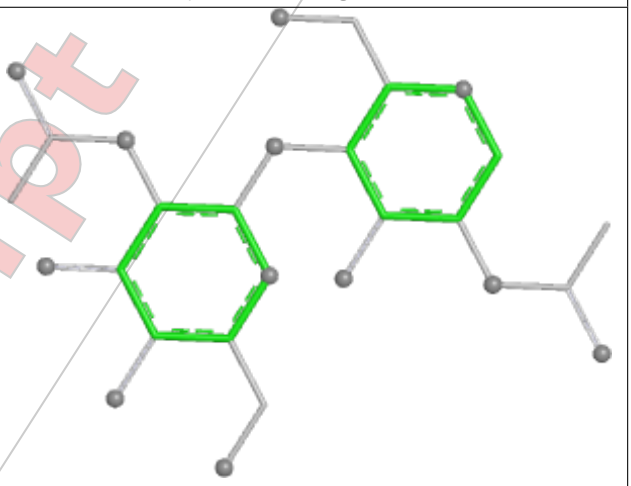


Torsions



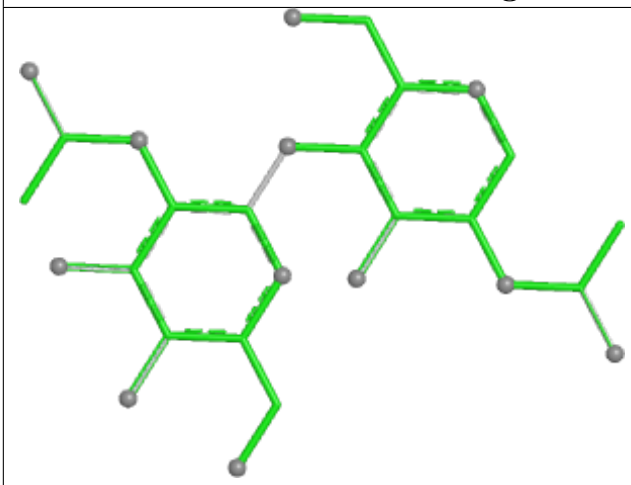
Rings

For Manuscript Review

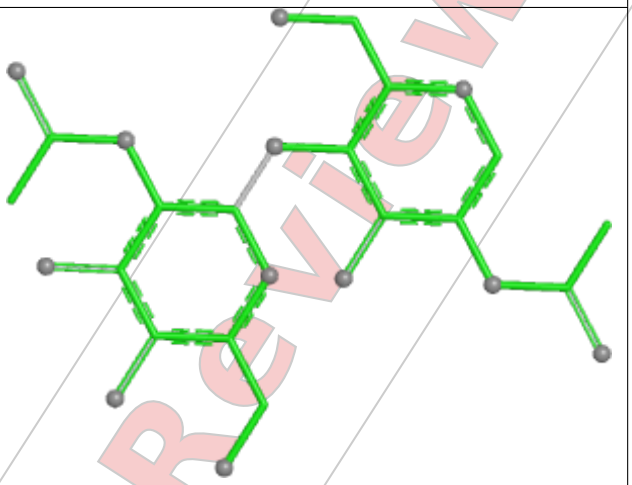
Oligosaccharide Chain H	
 Bond lengths	 Bond angles
 Torsions	 Rings

For Manuscript Review

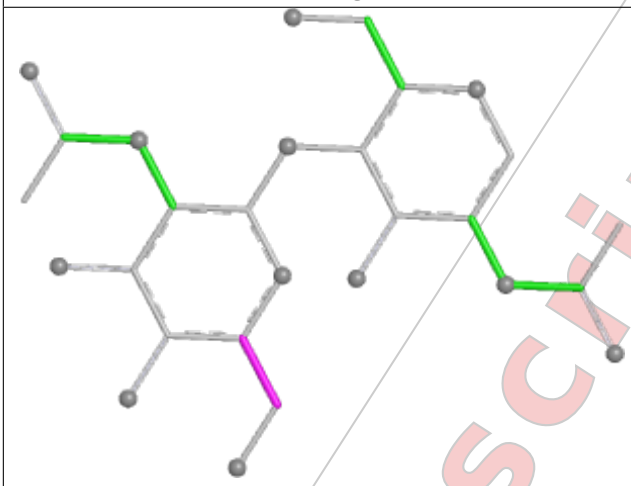
Oligosaccharide Chain I



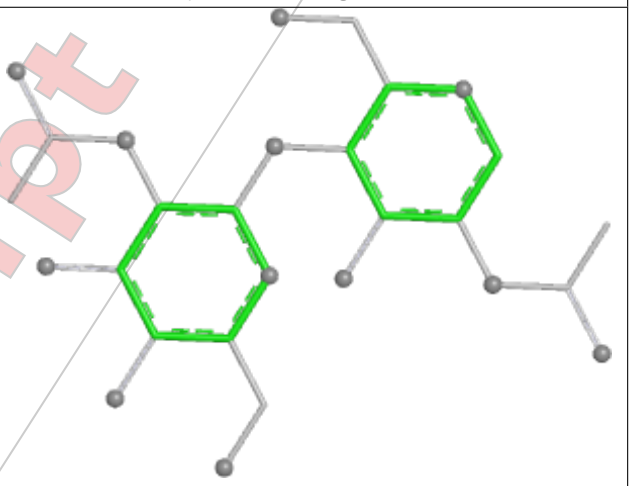
Bond lengths



Bond angles



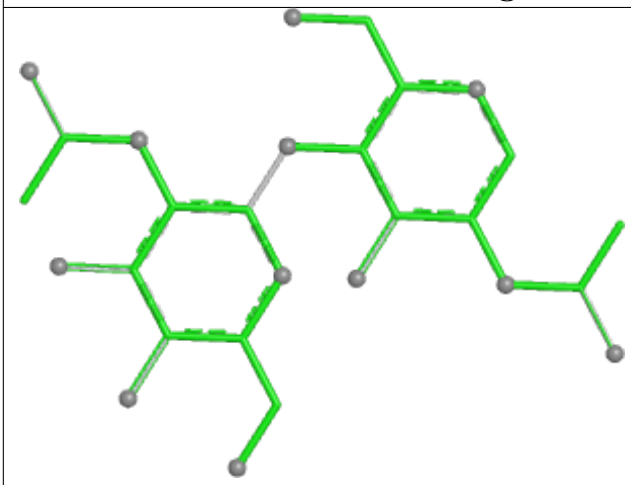
Torsions



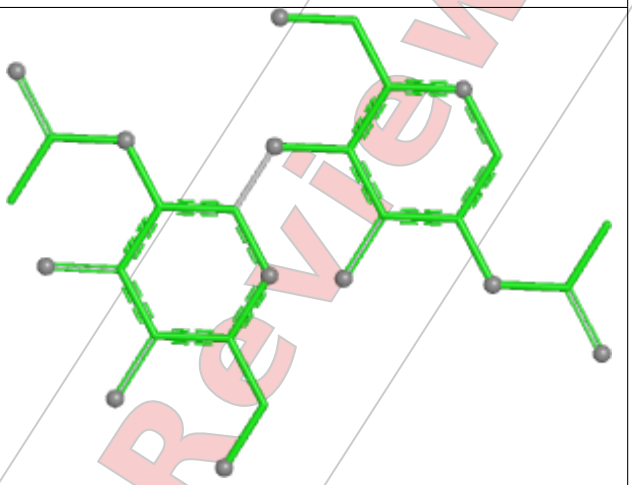
Rings

For Manuscript Review

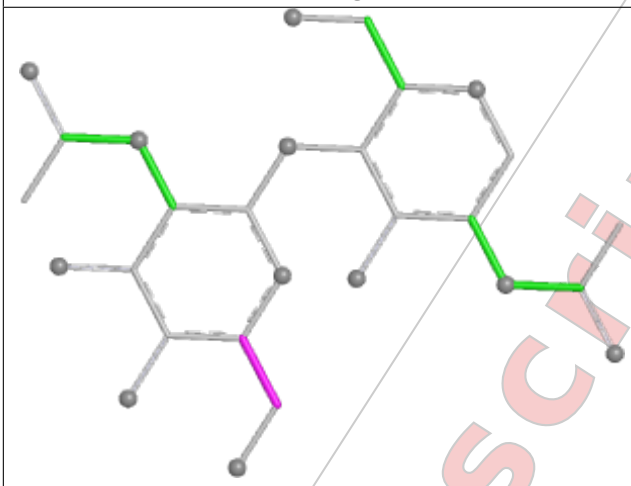
Oligosaccharide Chain J



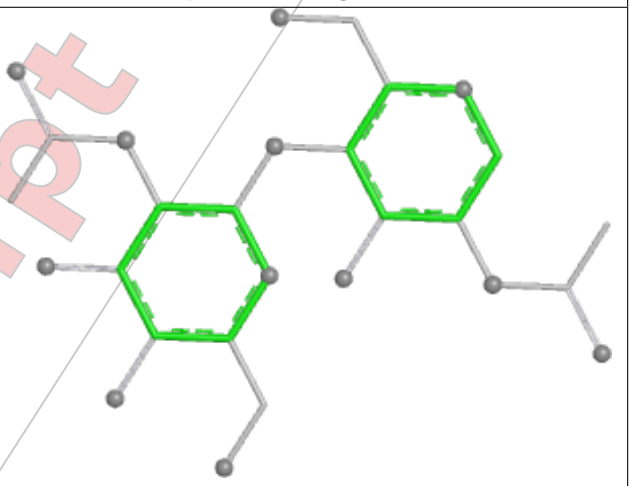
Bond lengths



Bond angles



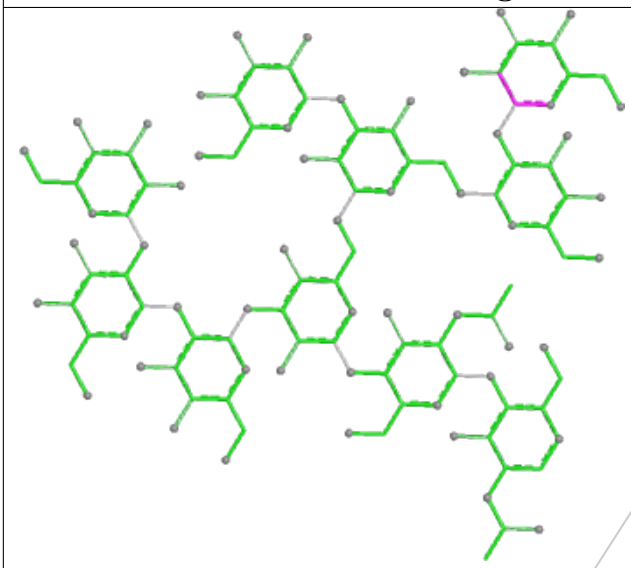
Torsions



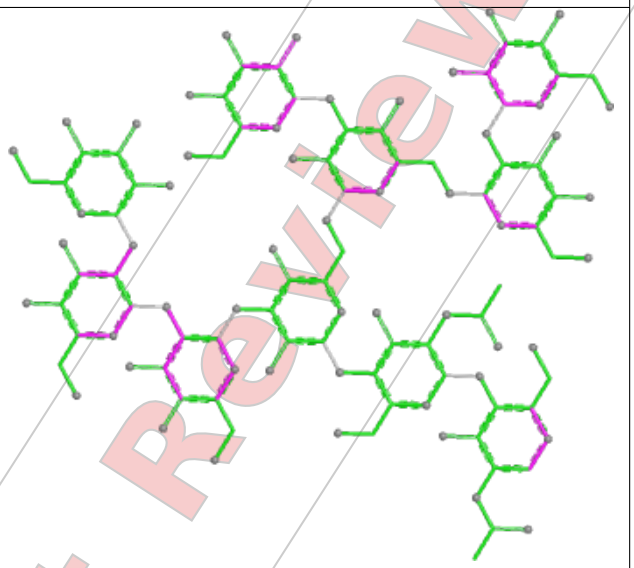
Rings

For Manuscript Review

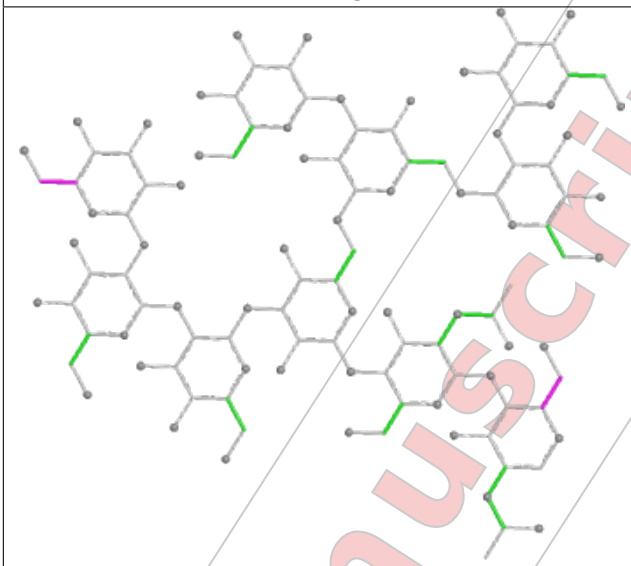
Oligosaccharide Chain F



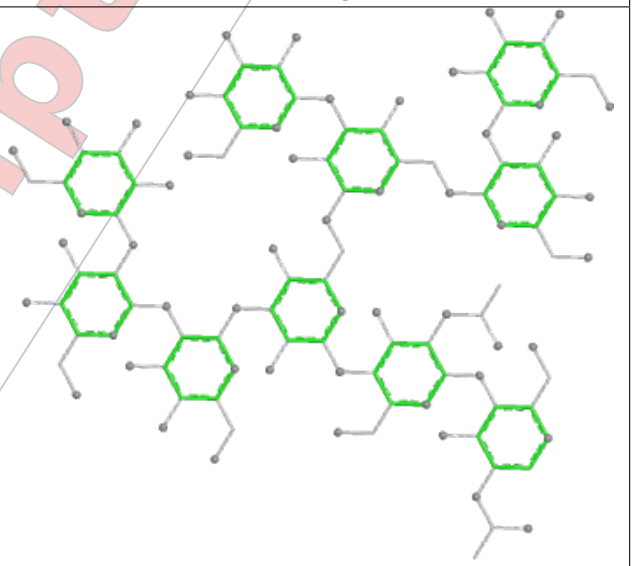
Bond lengths



Bond angles



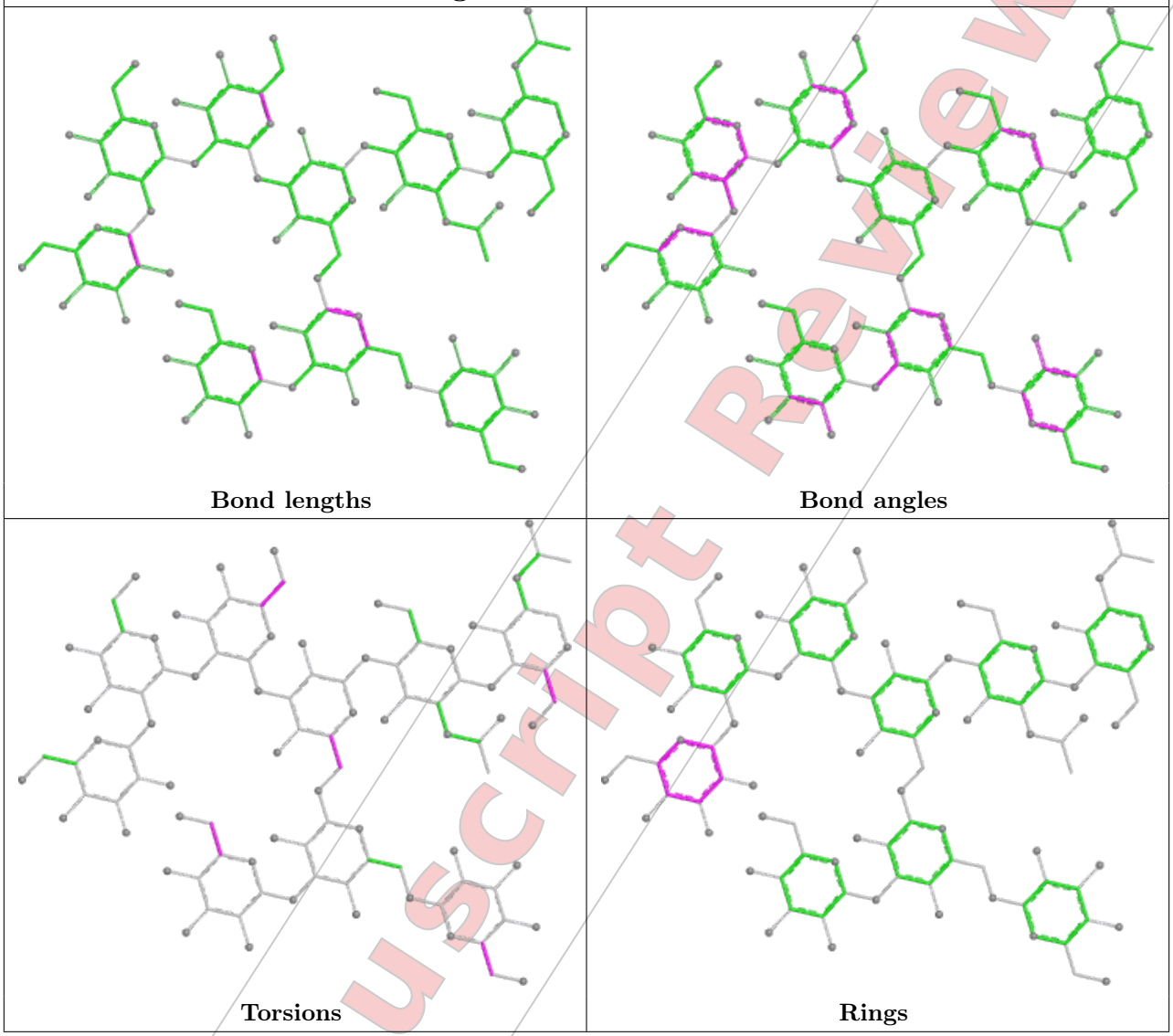
Torsions



Rings

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Oligosaccharide Chain K



5.6 Ligand geometry

5 ligands 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	$\#\|Z\| > 2$
7	NAG	B	602	1	14,14,15	0.24	0	17,19,21	0.57	0

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Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
7	NAG	B	601	1	14,14,15	0.26	0	17,19,21	0.57	0
7	NAG	A	603	1	14,14,15	0.20	0	17,19,21	0.43	0
6	ASP	A	601	-	6,7,8	0.88	0	5,8,10	0.85	0
6	ASP	A	602	-	6,7,8	0.89	0	5,8,10	0.97	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
7	NAG	B	602	1	-	2/6/23/26	0/1/1/1
7	NAG	B	601	1	-	2/6/23/26	0/1/1/1
7	NAG	A	603	1	-	0/6/23/26	0/1/1/1
6	ASP	A	601	-	-	1/5/6/8	-
6	ASP	A	602	-	-	0/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	601	ASP	O-C-CA-CB
7	B	601	NAG	C1-C2-N2-C7
7	B	602	NAG	C3-C2-N2-C7
7	B	602	NAG	C1-C2-N2-C7
7	B	601	NAG	C3-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

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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	326/340 (95%)	-0.28	1 (0%)	94	93	39, 58, 91, 141	0
1	B	328/340 (96%)	-0.24	1 (0%)	94	93	45, 67, 96, 129	0
All	All	654/680 (96%)	-0.26	2 (0%)	94	93	39, 62, 95, 141	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	365	GLY	2.5
1	A	408	TYR	2.4

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

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

6.3 Carbohydrates

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	J	2	14/15	0.62	0.50	121,162,171,174	0
5	MAN	K	9	11/12	0.65	0.35	131,148,155,157	0
4	MAN	F	9	11/12	0.66	0.43	139,162,174,174	0
2	BMA	C	3	11/12	0.67	0.34	129,152,167,171	0
5	MAN	K	8	11/12	0.74	0.27	110,137,153,153	0
3	NAG	D	2	14/15	0.74	0.42	107,156,166,168	0
2	BMA	L	3	11/12	0.77	0.45	123,159,170,175	0

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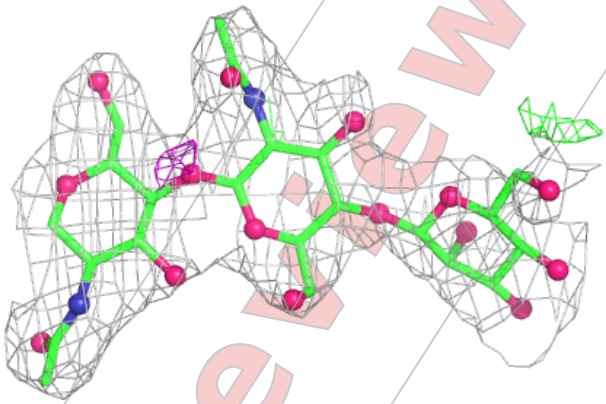
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	D	1	14/15	0.78	0.23	79,118,129,132	0
3	NAG	H	2	14/15	0.78	0.41	101,139,161,162	0
2	BMA	E	3	11/12	0.79	0.35	116,145,153,157	0
5	MAN	K	6	11/12	0.79	0.39	101,121,139,147	0
5	MAN	K	7	11/12	0.80	0.18	116,123,137,149	0
3	NAG	I	2	14/15	0.81	0.38	85,136,146,150	0
4	MAN	F	6	11/12	0.82	0.31	96,116,124,124	0
2	NAG	L	2	14/15	0.83	0.41	131,172,180,180	0
4	MAN	F	8	11/12	0.84	0.23	128,144,154,157	0
3	NAG	I	1	14/15	0.84	0.18	58,87,116,123	0
2	BMA	G	3	11/12	0.84	0.24	129,146,156,158	0
4	MAN	F	10	11/12	0.86	0.18	117,130,140,141	0
2	NAG	E	2	14/15	0.87	0.40	109,138,169,177	0
2	NAG	G	1	14/15	0.88	0.22	53,75,88,93	0
4	MAN	F	7	11/12	0.89	0.13	96,114,127,136	0
2	NAG	L	1	14/15	0.90	0.28	100,128,148,159	0
2	NAG	C	2	14/15	0.90	0.24	78,114,143,148	0
3	NAG	J	1	14/15	0.91	0.27	80,115,137,148	0
2	NAG	E	1	14/15	0.92	0.17	56,83,96,96	0
4	MAN	F	5	11/12	0.93	0.17	72,83,98,110	0
5	MAN	K	5	11/12	0.93	0.15	75,85,106,113	0
2	NAG	G	2	14/15	0.94	0.33	78,104,129,143	0
2	NAG	C	1	14/15	0.95	0.13	66,78,90,98	0
4	NAG	F	2	14/15	0.95	0.13	51,58,76,76	0
5	MAN	K	4	11/12	0.95	0.17	83,91,101,114	0
3	NAG	H	1	14/15	0.95	0.10	73,88,107,114	0
5	NAG	K	2	14/15	0.97	0.17	47,61,79,88	0
5	BMA	K	3	11/12	0.97	0.12	64,75,96,112	0
4	BMA	F	3	11/12	0.97	0.10	61,81,92,99	0
4	MAN	F	4	11/12	0.97	0.14	65,80,94,103	0
4	NAG	F	1	14/15	0.98	0.18	40,49,56,63	0
5	NAG	K	1	14/15	0.98	0.21	40,52,62,64	0

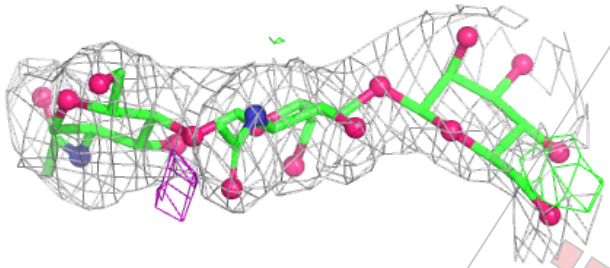
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

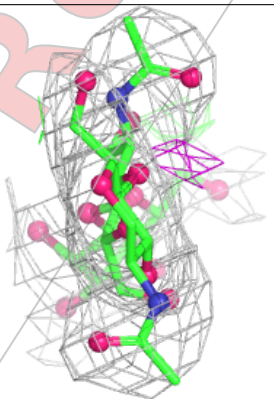
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Electron density around Chain C:

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

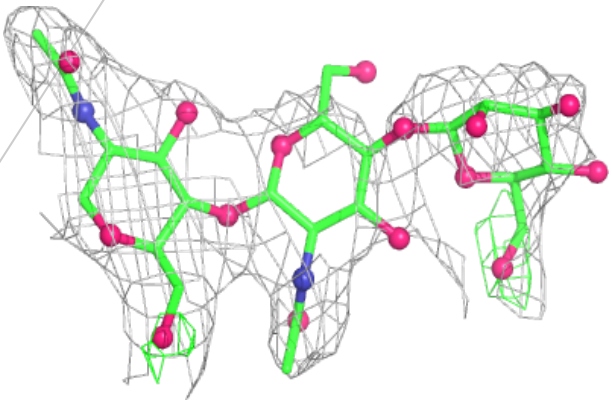


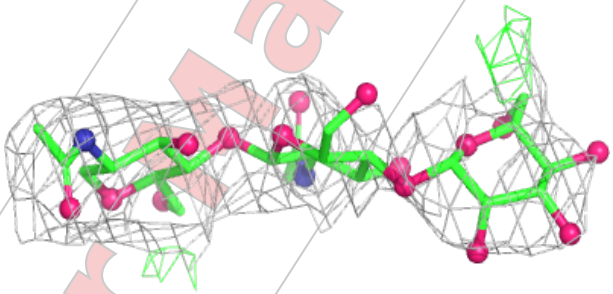


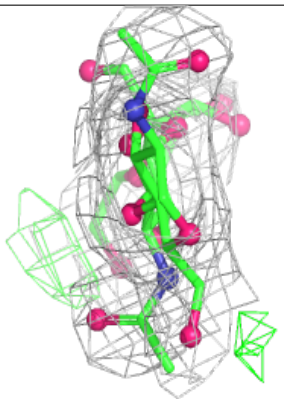


Electron density around Chain E:

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



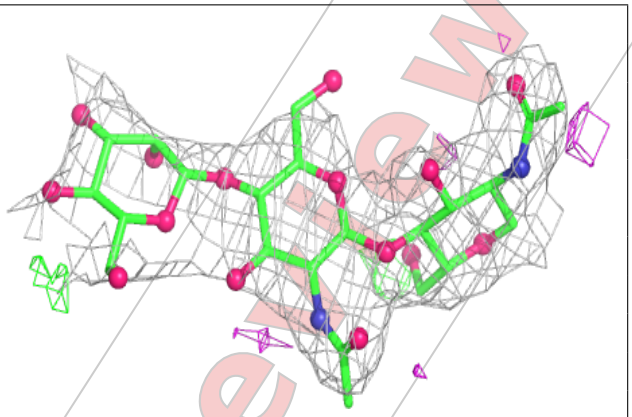


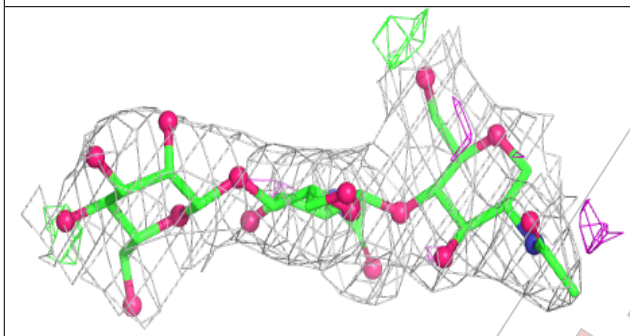


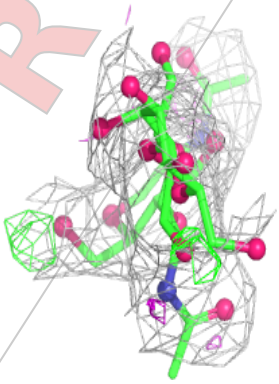
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Electron density around Chain G:

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

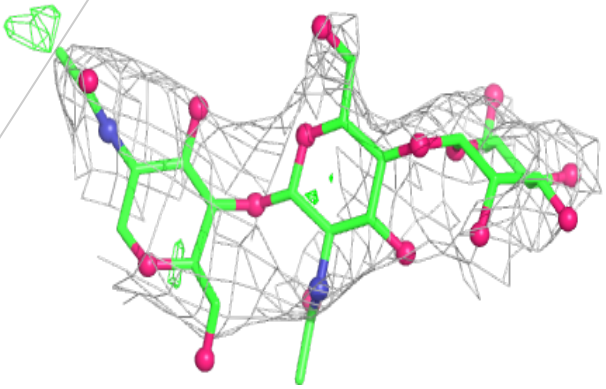


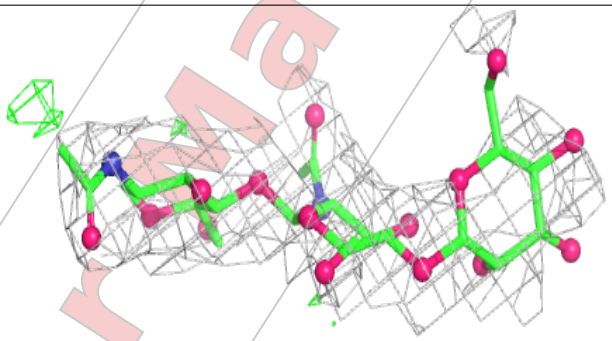


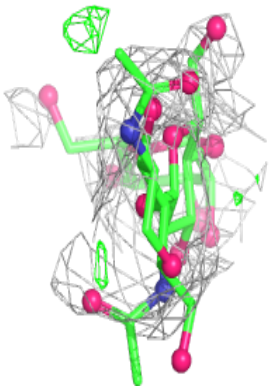


Electron density around Chain L:

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



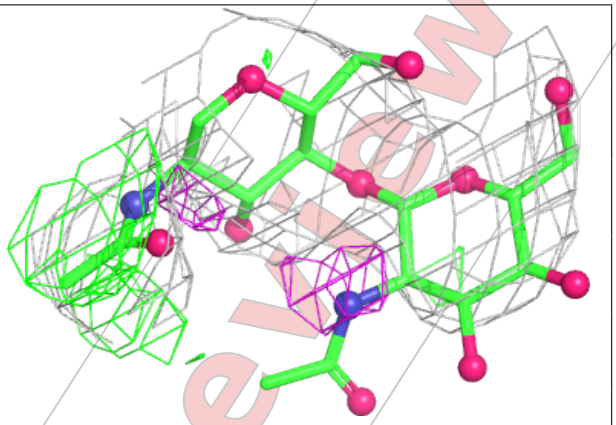


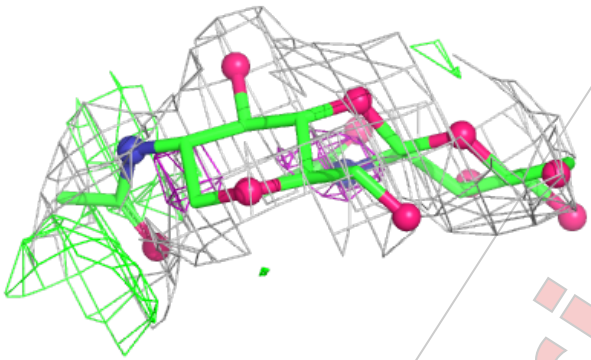


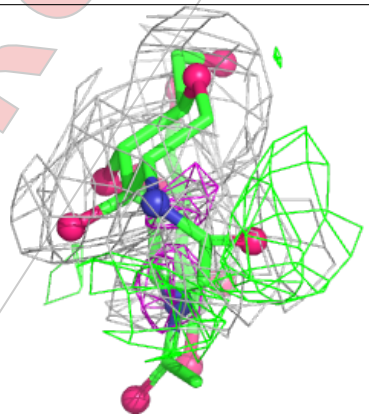
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Electron density around Chain D:

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



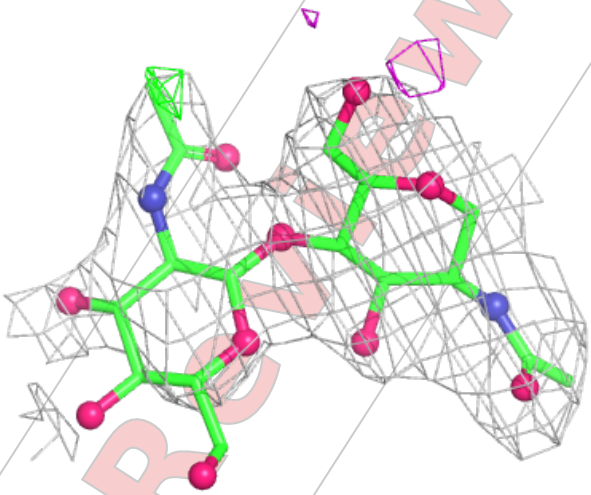


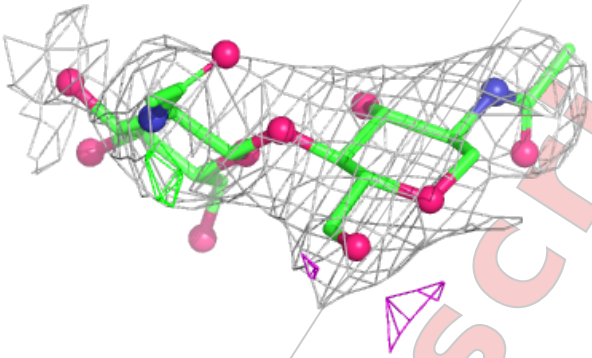


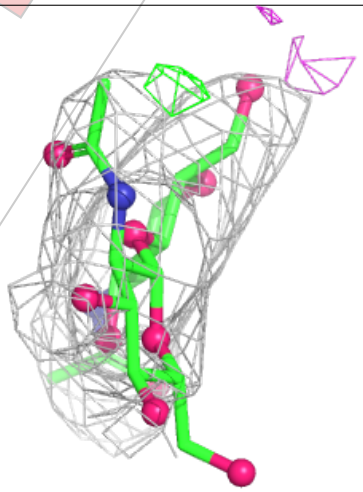
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Electron density around Chain H:

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



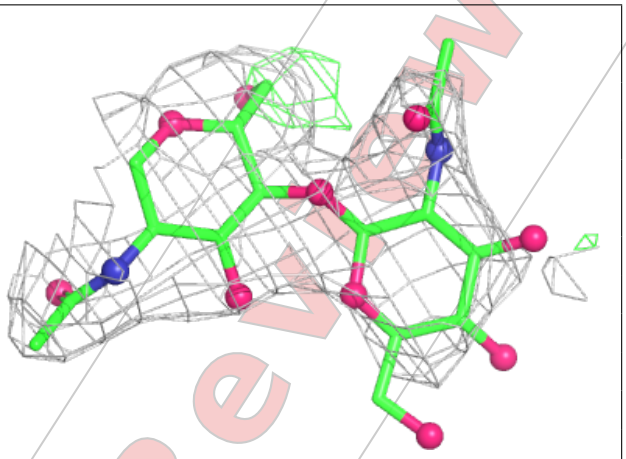


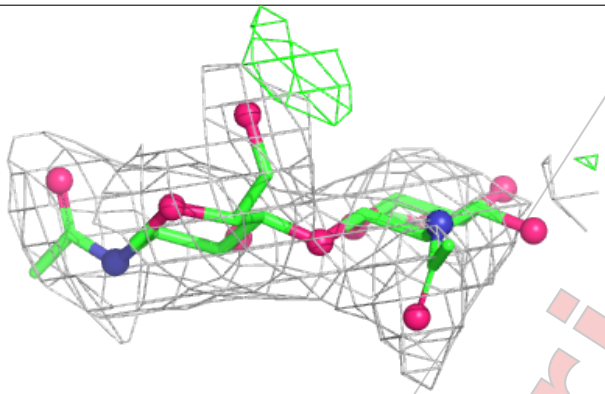


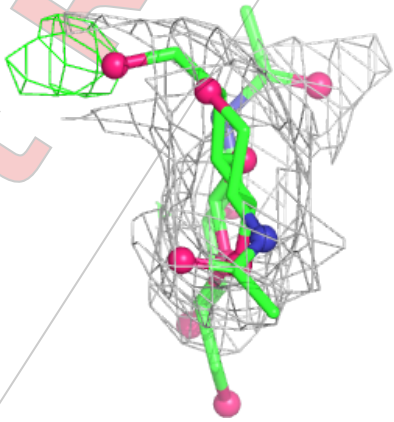
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Electron density around Chain I:

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



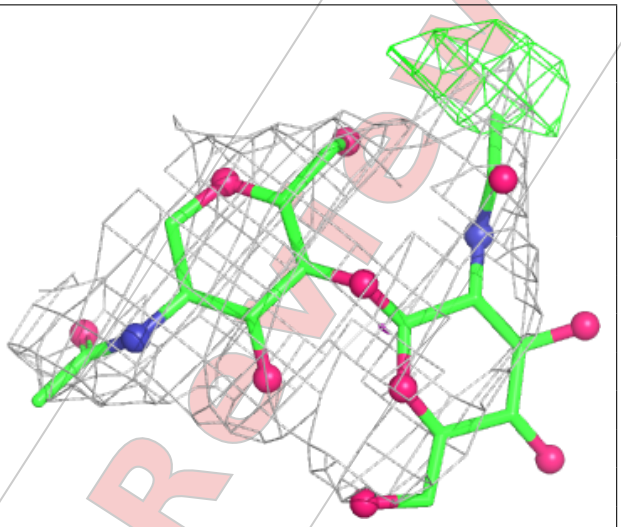


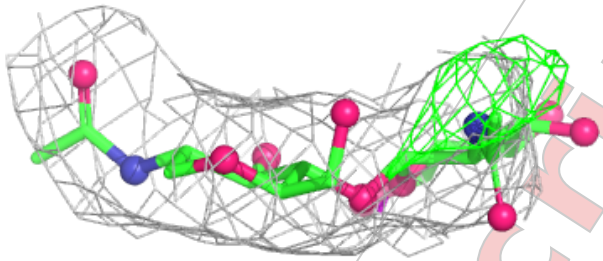


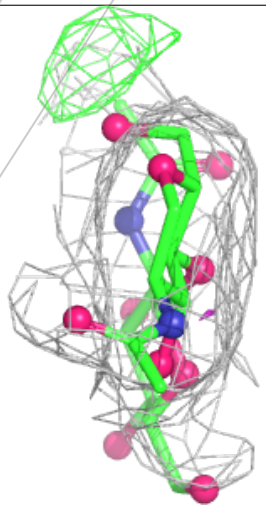
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Electron density around Chain J:

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



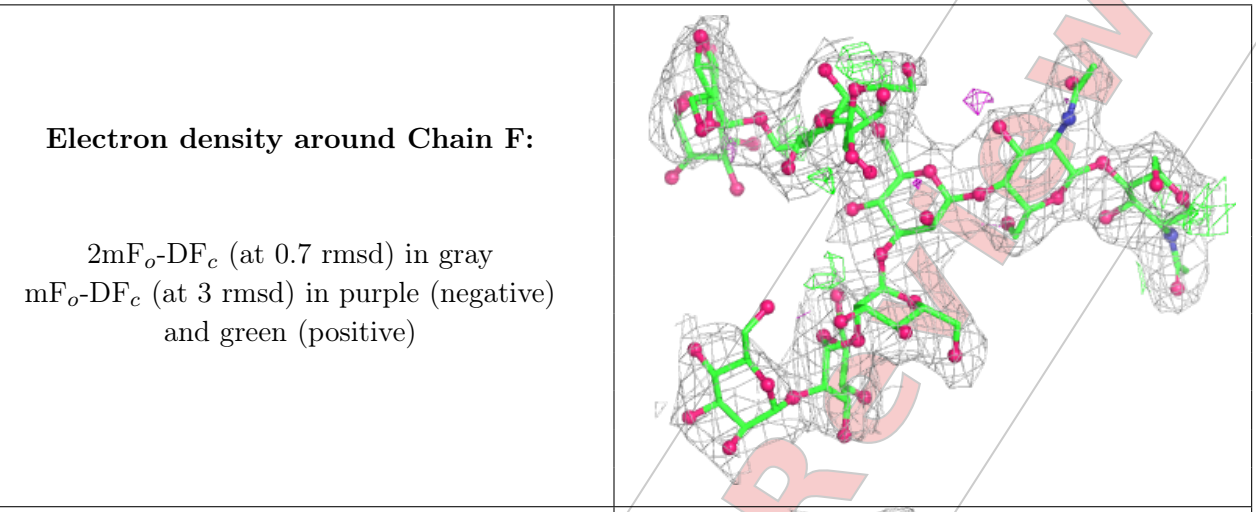


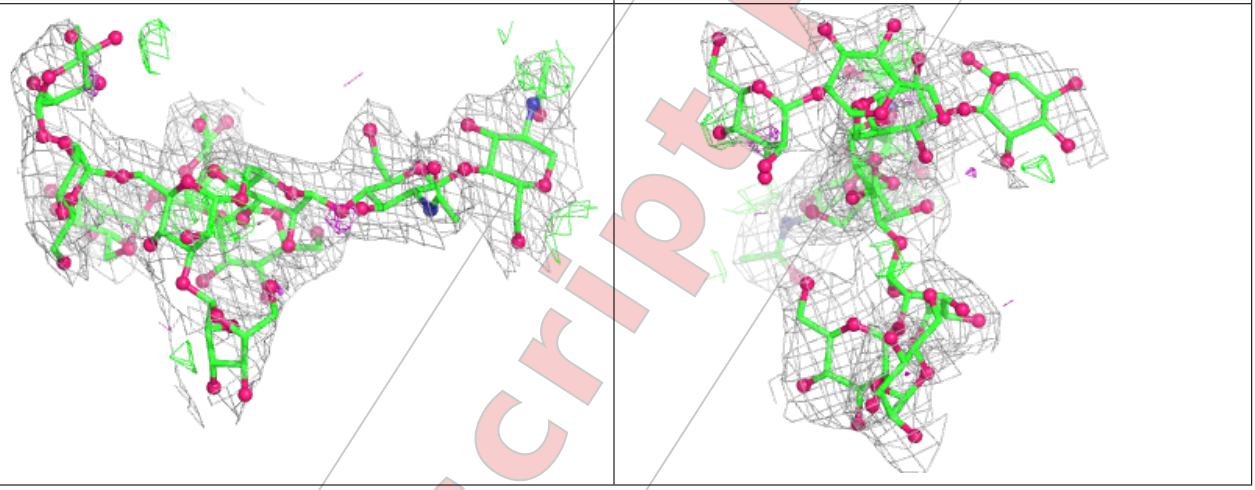


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Electron density around Chain F:

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

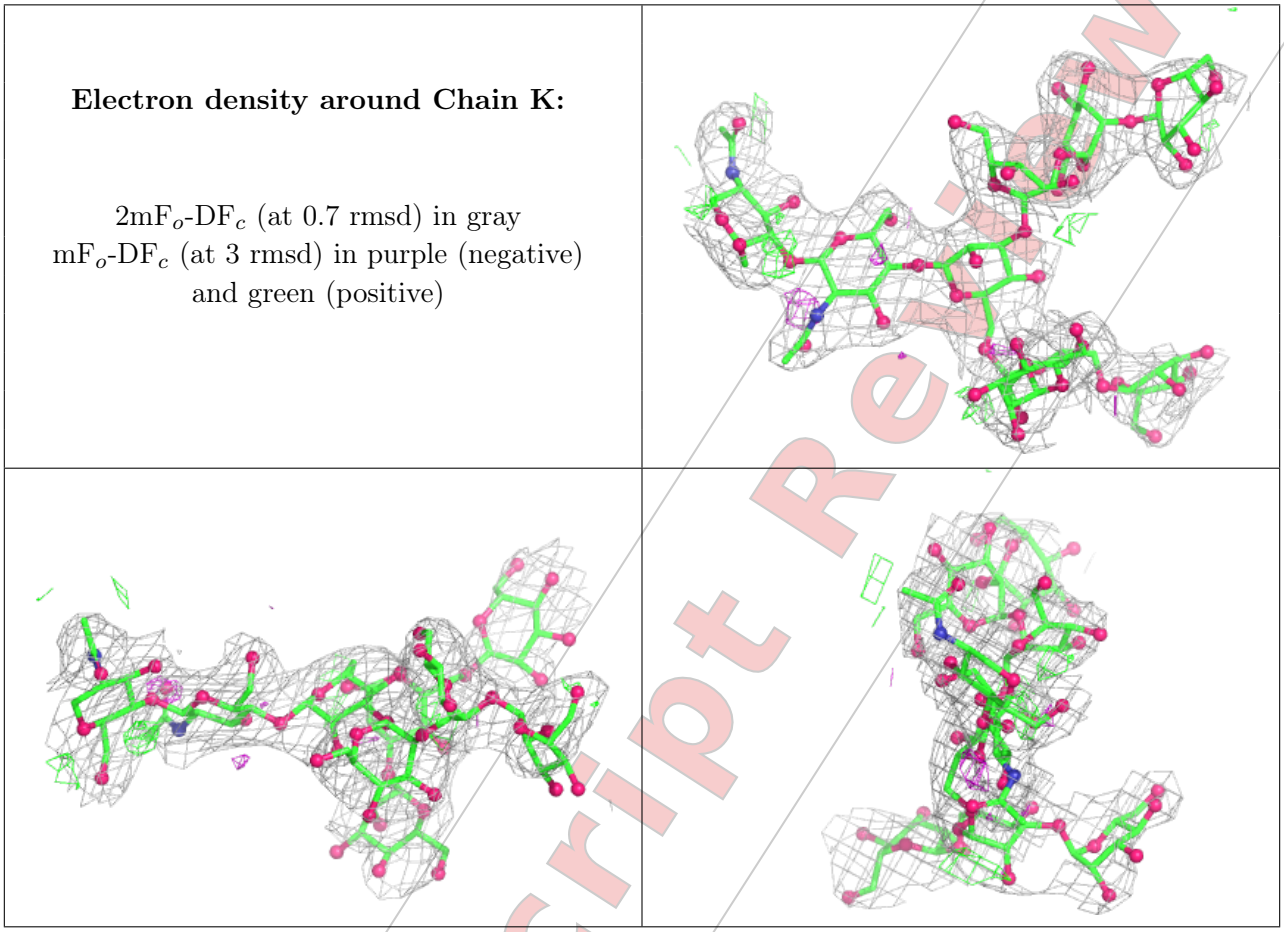




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Electron density around Chain K:

$2mF_o$-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
6	ASP	A	602	8/9	0.74	0.36	108,130,137,143	0
6	ASP	A	601	8/9	0.75	0.21	131,140,146,147	0
7	NAG	A	603	14/15	0.88	0.30	89,126,134,140	0
7	NAG	B	601	14/15	0.89	0.30	119,133,144,148	0
7	NAG	B	602	14/15	0.90	0.22	89,115,122,126	0

6.5 Other polymers

There are no such residues in this entry.

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