



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 02:39 AM BST

PDB ID : 4UNX
Title : Structure of the A_Equine_Newmarket_2_93 H3 haemagglutinin in complex with 3SLN
Authors : Vachieri, S.G.; Collins, P.J.; Haire, L.F.; Ogradowicz, R.W.; Martin, S.R.; Walker, P.A.; Xiong, X.; Gamblin, S.J.; Skehel, J.J.
Deposited on : 2014-05-31
Resolution : 3.20 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 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 : 2.13.1
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) : 2.13.1

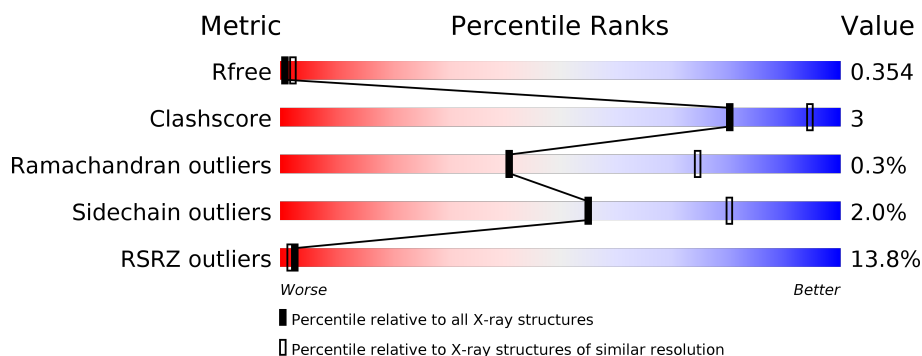
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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 $\leq 5\%$. 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	323	<div> <div>10%</div> <div>91%</div> <div>8%</div> <div>.</div> </div>
1	C	323	<div> <div>16%</div> <div>93%</div> <div>5%</div> <div>.</div> </div>
1	E	323	<div> <div>35%</div> <div>92%</div> <div>6%</div> <div>..</div> </div>
2	B	173	<div> <div>%</div> <div>92%</div> <div>6%</div> <div>..</div> </div>
2	D	173	<div> <div>%</div> <div>94%</div> <div>5%</div> <div>..</div> </div>
2	F	173	<div> <div>%</div> <div>94%</div> <div>5%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	2	
3	H	2	
3	L	2	
3	M	2	
3	P	2	
3	Q	2	
4	I	5	
4	R	5	
5	J	3	
6	K	2	
6	O	2	
6	S	2	
7	N	4	

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
3	NAG	G	2	-	-	-	X
3	NAG	H	2	-	-	-	X
3	NAG	L	1	-	-	-	X
3	NAG	L	2	-	-	-	X
3	NAG	P	1	-	-	-	X
3	NAG	P	2	X	-	-	X
4	MAN	I	4	-	-	-	X
4	MAN	R	4	-	-	-	X
6	FUC	K	2	X	-	-	-
6	FUC	O	2	X	-	-	-
6	NAG	S	1	-	-	-	X
6	FUC	S	2	X	-	-	X
7	BMA	N	3	-	-	-	X
9	SIA	E	701	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 12208 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 H3 HAEMAGGLUTININ HA1 CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	0	0
			2484	1553	438	479	14			
1	C	319	Total	C	N	O	S	0	0	0
			2484	1553	438	479	14			
1	E	319	Total	C	N	O	S	0	0	0
			2484	1553	438	479	14			

- Molecule 2 is a protein called H3 HAEMAGGLUTININ HA2 CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1396	870	245	275	6			
2	D	172	Total	C	N	O	S	0	0	0
			1396	870	245	275	6			
2	F	172	Total	C	N	O	S	0	0	0
			1396	870	245	275	6			

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



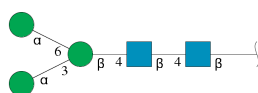
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

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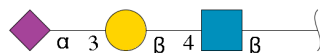
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	M	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	P	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	Q	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called 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	I	5	Total	C	N	O	0	0	0
			61	34	2	25			
4	R	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 5 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	J	3	Total	C	N	O	0	0	0
			46	25	2	19			

- Molecule 6 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



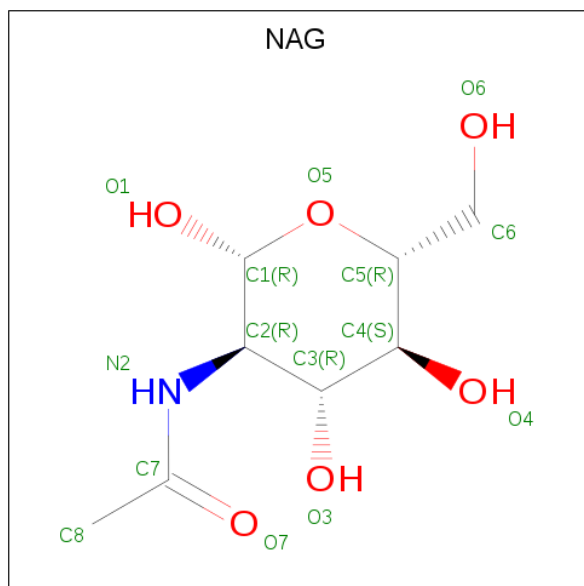
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	K	2	Total	C	N	O	0	0	0
			24	14	1	9			
6	O	2	Total	C	N	O	0	0	0
			24	14	1	9			
6	S	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 7 is an oligosaccharide called 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
7	N	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



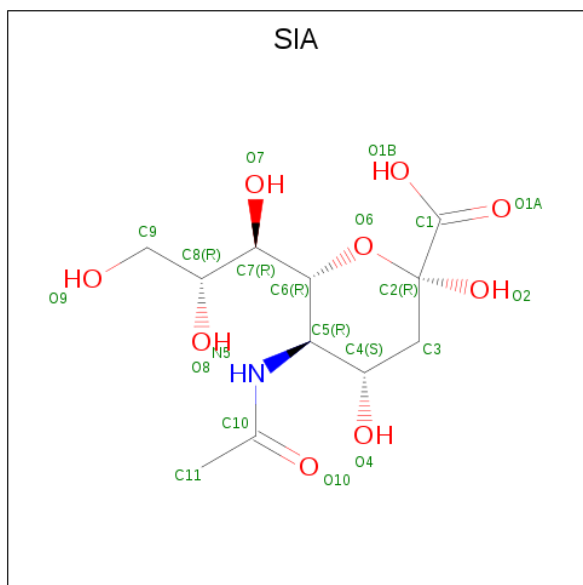
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 9 is N-acetyl-alpha-neuraminic acid (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).

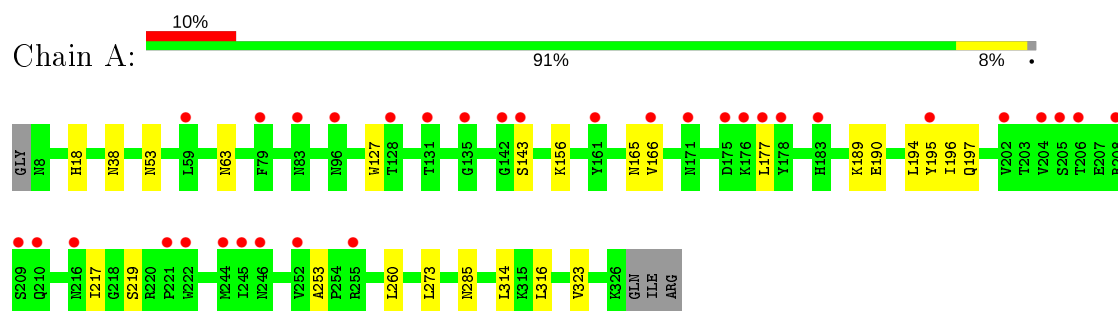


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	N	O	0	0
			20	11	1	8		
9	E	1	Total	C	N	O	0	0
			20	11	1	8		

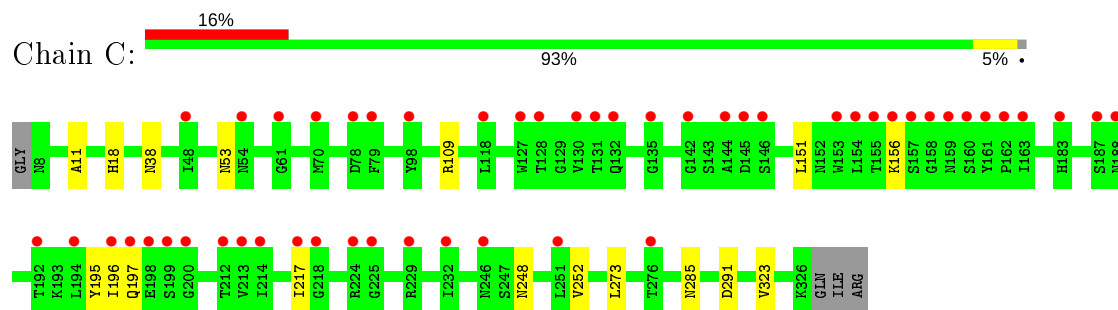
3 Residue-property plots [i](#)

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.

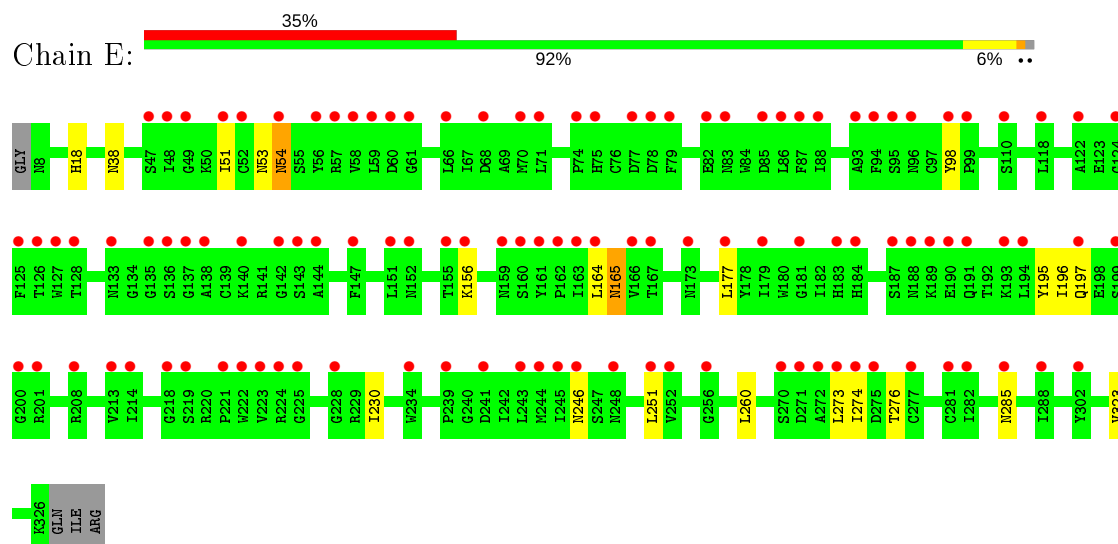
• Molecule 1: H3 HAEMAGGLUTININ HA1 CHAIN



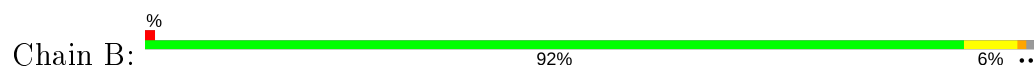
• Molecule 1: H3 HAEMAGGLUTININ HA1 CHAIN



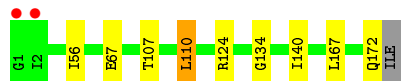
• Molecule 1: H3 HAEMAGGLUTININ HA1 CHAIN



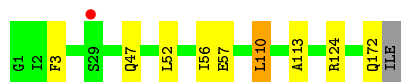
• Molecule 2: H3 HAEMAGGLUTININ HA2 CHAIN



• Molecule 2: H3 HAEMAGGLUTININ HA2 CHAIN



• Molecule 2: H3 HAEMAGGLUTININ HA2 CHAIN



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



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



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



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





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

Chain P:  100%



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

Chain Q:  50% 50%



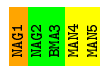
- Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  40% 40% 20%



- Molecule 4: 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 R:  40% 40% 20%



- Molecule 5: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  33% 33% 33%



- Molecule 6: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%



- Molecule 6: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  50% 50%


GAG1
FUC2

- Molecule 6: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain S:  100%

GAG1
FUC2

- Molecule 7: 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 N:  75% 25%

GAG1
GAG2
BNA3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	100.48Å 102.25Å 228.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	114.19 – 3.20 52.18 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (114.19-3.20) 99.2 (52.18-3.20)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.319 , 0.354 0.316 , 0.354	Depositor DCC
R_{free} test set	1971 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	73.3	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 55.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.055 for k,h,-l	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	12208	wwPDB-VP
Average B, all atoms (Å ²)	111.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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, NAG, SIA, GAL, FUC, 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	0.26	0/2537	0.44	0/3445
1	C	0.26	0/2537	0.44	0/3445
1	E	0.26	0/2537	0.43	0/3445
2	B	0.29	0/1421	0.47	0/1910
2	D	0.28	0/1421	0.46	0/1910
2	F	0.28	0/1421	0.45	0/1910
All	All	0.27	0/11874	0.45	0/16065

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 [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	2484	0	2432	18	0
1	C	2484	0	2432	11	0
1	E	2484	0	2432	15	0
2	B	1396	0	1318	7	0
2	D	1396	0	1318	8	0
2	F	1396	0	1318	6	0
3	G	28	0	25	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	28	0	25	1	0
3	L	28	0	25	1	0
3	M	28	0	25	1	0
3	P	28	0	25	3	0
3	Q	28	0	25	2	0
4	I	61	0	52	2	0
4	R	61	0	52	1	0
5	J	46	0	40	2	0
6	K	24	0	22	1	0
6	O	24	0	22	1	0
6	S	24	0	22	0	0
7	N	50	0	43	3	0
8	A	28	0	26	4	0
8	C	28	0	26	3	0
8	E	14	0	13	1	0
9	C	20	0	17	0	0
9	E	20	0	17	0	0
All	All	12208	0	11752	64	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 3.

All (64) 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:E:165:ASN:HD21	3:Q:1:NAG:C1	1.74	1.00
1:C:285:ASN:HD21	7:N:1:NAG:C1	1.91	0.83
2:B:154:ASN:HD22	6:K:1:NAG:C1	1.93	0.80
1:E:165:ASN:ND2	3:Q:1:NAG:C1	2.45	0.79
1:A:53:ASN:HD21	3:G:1:NAG:C1	1.96	0.78
1:A:38:ASN:HD21	8:A:401:NAG:C1	1.98	0.76
1:A:63:ASN:HD21	3:H:1:NAG:C1	2.00	0.73
1:C:38:ASN:HD21	8:C:401:NAG:C1	2.04	0.70
1:A:285:ASN:HD21	4:I:1:NAG:C1	2.06	0.68
1:E:274:ILE:O	3:P:1:NAG:H83	1.97	0.65
1:A:38:ASN:ND2	8:A:401:NAG:C1	2.62	0.62
1:A:165:ASN:HD21	8:A:431:NAG:C1	2.14	0.61
1:A:194:LEU:HD21	5:J:3:SIA:O10	2.04	0.58
1:E:53:ASN:HD22	3:P:1:NAG:C1	2.16	0.58
8:C:421:NAG:C1	8:C:421:NAG:C8	2.82	0.58
1:C:53:ASN:HD21	3:L:1:NAG:C1	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:ASN:ND2	4:I:1:NAG:C1	2.67	0.57
1:E:38:ASN:HD21	8:E:401:NAG:C1	2.17	0.57
1:E:53:ASN:N	1:E:53:ASN:OD1	2.37	0.57
1:C:285:ASN:ND2	7:N:1:NAG:C1	2.67	0.56
2:F:56:ILE:HG22	2:F:57:GLU:HG2	1.90	0.53
1:A:127:TRP:CZ2	1:A:253:ALA:HB1	2.45	0.52
1:E:274:ILE:HD12	1:E:274:ILE:N	2.25	0.52
1:C:291:ASP:O	2:D:56:ILE:HG23	2.10	0.51
1:E:53:ASN:HD21	1:E:276:THR:HA	1.74	0.51
3:P:1:NAG:H3	3:P:2:NAG:O5	2.10	0.51
1:E:285:ASN:HD21	4:R:1:NAG:C1	2.24	0.51
1:A:165:ASN:ND2	8:A:431:NAG:C1	2.73	0.51
2:D:56:ILE:O	2:D:56:ILE:HG22	2.12	0.49
1:A:53:ASN:ND2	3:G:1:NAG:C1	2.72	0.49
1:A:219:SER:HB3	3:M:1:NAG:H82	1.94	0.49
2:B:6:ILE:HD12	2:B:112:ASP:HA	1.95	0.49
1:E:164:LEU:HD12	1:E:251:LEU:HD23	1.94	0.49
1:A:195:TYR:O	1:A:197:GLN:N	2.46	0.48
1:C:195:TYR:O	1:C:197:GLN:N	2.47	0.48
2:D:110:LEU:C	2:D:110:LEU:HD22	2.34	0.47
2:B:134:GLY:HA2	2:D:124:ARG:HD3	1.96	0.47
1:C:285:ASN:OD1	7:N:1:NAG:H83	2.14	0.47
1:C:11:ALA:HB3	2:D:140:ILE:HB	1.97	0.47
2:F:110:LEU:C	2:F:110:LEU:HD22	2.34	0.46
1:E:54:ASN:HD22	1:E:54:ASN:N	2.14	0.46
5:J:3:SIA:O6	5:J:3:SIA:O8	2.33	0.46
6:O:1:NAG:H82	6:O:1:NAG:O3	2.14	0.46
1:E:195:TYR:O	1:E:197:GLN:N	2.48	0.45
2:B:107:THR:HA	2:B:110:LEU:HD12	2.00	0.43
8:C:421:NAG:H83	8:C:421:NAG:C1	2.48	0.43
1:E:51:ILE:HB	1:E:274:ILE:HG13	2.00	0.43
1:A:189:LYS:HG3	1:A:190:GLU:N	2.33	0.42
2:B:158:ASP:HB3	2:B:161:ILE:HD12	2.01	0.42
1:A:177:LEU:HD22	1:A:260:LEU:HD21	2.00	0.42
2:F:3:PHE:CE1	2:F:113:ALA:HB2	2.55	0.42
3:G:1:NAG:O7	3:G:1:NAG:C1	2.67	0.41
2:D:134:GLY:HA2	2:F:124:ARG:HD3	2.03	0.41
1:A:217:ILE:HD12	1:A:217:ILE:N	2.36	0.41
1:E:177:LEU:HD22	1:E:260:LEU:HD21	2.03	0.41
1:C:151:LEU:HD23	1:C:252:VAL:HG11	2.03	0.40
1:C:217:ILE:HD12	1:C:217:ILE:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:98:TYR:CD2	1:E:230:ILE:HD12	2.57	0.40
1:A:316:LEU:HD23	2:B:52:LEU:HD13	2.04	0.40
1:C:109:ARG:NH1	2:D:67:GLU:OE2	2.53	0.40
2:F:47:GLN:OE1	2:F:110:LEU:HD23	2.21	0.40
1:A:314:LEU:HB3	2:B:100:VAL:HG21	2.04	0.40
2:D:107:THR:HA	2:D:110:LEU:HD12	2.04	0.40
2:F:52:LEU:HG	2:F:56:ILE:HD12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	317/323 (98%)	295 (93%)	20 (6%)	2 (1%)	25	64
1	C	317/323 (98%)	296 (93%)	20 (6%)	1 (0%)	41	74
1	E	317/323 (98%)	294 (93%)	22 (7%)	1 (0%)	41	74
2	B	170/173 (98%)	159 (94%)	11 (6%)	0	100	100
2	D	170/173 (98%)	158 (93%)	12 (7%)	0	100	100
2	F	170/173 (98%)	162 (95%)	8 (5%)	0	100	100
All	All	1461/1488 (98%)	1364 (93%)	93 (6%)	4 (0%)	41	74

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	143	SER
1	A	196	ILE
1	C	196	ILE
1	E	196	ILE

5.3.2 Protein sidechains ⓘ

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	280/283 (99%)	275 (98%)	5 (2%)	59	82
1	C	280/283 (99%)	275 (98%)	5 (2%)	59	82
1	E	280/283 (99%)	273 (98%)	7 (2%)	47	77
2	B	144/145 (99%)	141 (98%)	3 (2%)	53	79
2	D	144/145 (99%)	141 (98%)	3 (2%)	53	79
2	F	144/145 (99%)	142 (99%)	2 (1%)	67	86
All	All	1272/1284 (99%)	1247 (98%)	25 (2%)	55	80

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	156	LYS
1	A	166	VAL
1	A	273	LEU
1	A	323	VAL
2	B	110	LEU
2	B	127	ARG
2	B	172	GLN
1	C	18	HIS
1	C	156	LYS
1	C	248	ASN
1	C	273	LEU
1	C	323	VAL
2	D	110	LEU
2	D	167	LEU
2	D	172	GLN
1	E	18	HIS
1	E	54	ASN
1	E	156	LYS
1	E	165	ASN
1	E	246	ASN
1	E	273	LEU

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Mol	Chain	Res	Type
1	E	323	VAL
2	F	110	LEU
2	F	172	GLN

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

Mol	Chain	Res	Type
1	A	54	ASN
1	A	165	ASN
2	B	154	ASN
1	C	38	ASN
1	C	54	ASN
1	C	285	ASN
1	E	38	ASN
1	E	54	ASN
1	E	165	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

35 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	$\# Z > 2$
3	NAG	G	1	3	14,14,15	0.54	0	17,19,21	1.49	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	2	3	14,14,15	0.59	0	17,19,21	0.77	0
3	NAG	H	1	3	14,14,15	0.57	0	17,19,21	1.42	2 (11%)
3	NAG	H	2	3	14,14,15	0.68	0	17,19,21	2.37	4 (23%)
4	NAG	I	1	4	14,14,15	0.57	0	17,19,21	1.83	5 (29%)
4	NAG	I	2	4	14,14,15	0.55	0	17,19,21	0.76	0
4	BMA	I	3	4	11,11,12	0.32	0	15,15,17	0.56	0
4	MAN	I	4	4	11,11,12	0.62	0	15,15,17	1.10	1 (6%)
4	MAN	I	5	4	11,11,12	0.55	0	15,15,17	1.16	2 (13%)
5	NAG	J	1	5	15,15,15	0.47	0	21,21,21	1.73	4 (19%)
5	GAL	J	2	5	11,11,12	0.59	0	15,15,17	0.89	0
5	SIA	J	3	5	17,20,21	0.51	0	21,28,31	1.17	1 (4%)
6	NAG	K	1	6	14,14,15	0.53	0	17,19,21	0.86	0
6	FUC	K	2	6	10,10,11	0.85	0	14,14,16	1.72	4 (28%)
3	NAG	L	1	3	14,14,15	0.53	0	17,19,21	1.19	1 (5%)
3	NAG	L	2	3	14,14,15	0.62	0	17,19,21	1.18	3 (17%)
3	NAG	M	1	3	14,14,15	0.57	0	17,19,21	0.84	0
3	NAG	M	2	3	14,14,15	0.55	0	17,19,21	0.73	0
7	NAG	N	1	7	14,14,15	0.59	0	17,19,21	1.83	5 (29%)
7	NAG	N	2	7	14,14,15	0.38	0	17,19,21	1.78	3 (17%)
7	BMA	N	3	7	11,11,12	0.46	0	15,15,17	1.92	3 (20%)
7	MAN	N	4	7	11,11,12	0.57	0	15,15,17	1.27	3 (20%)
6	NAG	O	1	6	14,14,15	0.65	0	17,19,21	1.82	7 (41%)
6	FUC	O	2	6	10,10,11	0.62	0	14,14,16	0.67	0
3	NAG	P	1	3	14,14,15	0.71	0	17,19,21	1.66	3 (17%)
3	NAG	P	2	3	14,14,15	0.88	1 (7%)	17,19,21	1.67	5 (29%)
3	NAG	Q	1	3	14,14,15	0.60	0	17,19,21	1.21	2 (11%)
3	NAG	Q	2	3	14,14,15	0.51	0	17,19,21	0.74	0
4	NAG	R	1	4	14,14,15	0.54	0	17,19,21	1.37	3 (17%)
4	NAG	R	2	4	14,14,15	0.55	0	17,19,21	0.67	0
4	BMA	R	3	4	11,11,12	0.34	0	15,15,17	0.87	0
4	MAN	R	4	4	11,11,12	0.63	0	15,15,17	0.91	1 (6%)
4	MAN	R	5	4	11,11,12	0.55	0	15,15,17	1.23	2 (13%)
6	NAG	S	1	6	14,14,15	0.53	0	17,19,21	0.75	0
6	FUC	S	2	6	10,10,11	0.68	0	14,14,16	0.81	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
3	NAG	G	1	3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	1	3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1
4	NAG	I	1	4	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	0/6/23/26	0/1/1/1
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
4	MAN	I	4	4	-	1/2/19/22	0/1/1/1
4	MAN	I	5	4	-	2/2/19/22	1/1/1/1
5	NAG	J	1	5	-	2/6/26/26	0/1/1/1
5	GAL	J	2	5	-	1/2/19/22	0/1/1/1
5	SIA	J	3	5	-	6/14/34/38	0/1/1/1
6	NAG	K	1	6	-	3/6/23/26	0/1/1/1
6	FUC	K	2	6	1/1/4/5	-	0/1/1/1
3	NAG	L	1	3	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
3	NAG	M	1	3	-	1/6/23/26	0/1/1/1
3	NAG	M	2	3	-	2/6/23/26	0/1/1/1
7	NAG	N	1	7	-	2/6/23/26	0/1/1/1
7	NAG	N	2	7	-	1/6/23/26	0/1/1/1
7	BMA	N	3	7	-	2/2/19/22	0/1/1/1
7	MAN	N	4	7	-	2/2/19/22	0/1/1/1
6	NAG	O	1	6	-	4/6/23/26	0/1/1/1
6	FUC	O	2	6	1/1/4/5	-	0/1/1/1
3	NAG	P	1	3	-	3/6/23/26	0/1/1/1
3	NAG	P	2	3	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	Q	1	3	-	1/6/23/26	0/1/1/1
3	NAG	Q	2	3	-	2/6/23/26	0/1/1/1
4	NAG	R	1	4	-	4/6/23/26	0/1/1/1
4	NAG	R	2	4	-	0/6/23/26	0/1/1/1
4	BMA	R	3	4	-	2/2/19/22	0/1/1/1
4	MAN	R	4	4	-	2/2/19/22	0/1/1/1
4	MAN	R	5	4	-	0/2/19/22	1/1/1/1
6	NAG	S	1	6	-	2/6/23/26	0/1/1/1
6	FUC	S	2	6	1/1/4/5	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	2	NAG	C1-C2	2.74	1.56	1.52

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	2	NAG	C2-N2-C7	6.73	132.49	122.90
7	N	2	NAG	C1-O5-C5	5.30	119.37	112.19
7	N	3	BMA	C1-O5-C5	4.89	118.81	112.19
3	H	2	NAG	C8-C7-N2	4.79	124.21	116.10
3	P	1	NAG	C4-C3-C2	4.61	117.77	111.02
7	N	3	BMA	C1-C2-C3	4.53	115.23	109.67
5	J	3	SIA	C6-O6-C2	4.26	120.46	111.34
5	J	1	NAG	C1-C2-N2	4.19	115.58	110.73
6	K	2	FUC	O5-C1-C2	4.07	117.05	110.77
7	N	1	NAG	C8-C7-N2	3.95	122.78	116.10
4	I	1	NAG	C8-C7-N2	3.86	122.63	116.10
6	O	1	NAG	C2-N2-C7	3.60	128.03	122.90
4	I	5	MAN	C1-O5-C5	3.40	116.81	112.19
5	J	1	NAG	C4-C3-C2	3.38	115.29	110.34
3	H	1	NAG	O5-C1-C2	-3.36	105.98	111.29
7	N	2	NAG	C4-C3-C2	-3.31	106.16	111.02
4	I	1	NAG	O5-C1-C2	-3.29	106.09	111.29
4	R	5	MAN	C1-O5-C5	3.26	116.61	112.19
7	N	4	MAN	C1-O5-C5	3.26	116.61	112.19
7	N	1	NAG	C2-N2-C7	3.25	127.53	122.90
3	H	1	NAG	C3-C4-C5	3.15	115.86	110.24
6	O	1	NAG	C8-C7-N2	3.11	121.37	116.10
4	I	1	NAG	C3-C4-C5	3.08	115.74	110.24
7	N	1	NAG	C3-C4-C5	3.07	115.72	110.24
3	Q	1	NAG	C3-C4-C5	3.01	115.61	110.24
3	H	2	NAG	O7-C7-C8	-2.98	116.53	122.06
3	P	2	NAG	O5-C1-C2	2.97	115.98	111.29
5	J	1	NAG	C3-C4-C5	2.94	115.48	110.24
3	G	1	NAG	C1-C2-N2	2.88	115.41	110.49
3	P	2	NAG	C4-C3-C2	2.83	115.17	111.02
3	G	1	NAG	O5-C1-C2	-2.80	106.86	111.29
3	P	1	NAG	C3-C4-C5	2.74	115.12	110.24
7	N	2	NAG	O5-C5-C6	2.73	111.48	107.20
7	N	1	NAG	O7-C7-C8	-2.72	117.00	122.06
4	R	4	MAN	C1-C2-C3	2.71	113.00	109.67
4	I	4	MAN	C1-O5-C5	2.71	115.86	112.19
3	L	1	NAG	C4-C3-C2	2.68	114.95	111.02
4	I	1	NAG	C2-N2-C7	2.68	126.72	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	R	5	MAN	O5-C5-C6	2.64	111.34	107.20
3	P	2	NAG	C1-C2-N2	2.64	114.99	110.49
6	O	1	NAG	C1-C2-N2	-2.62	106.01	110.49
3	Q	1	NAG	O5-C1-C2	-2.58	107.22	111.29
6	K	2	FUC	C2-C3-C4	2.56	115.33	110.89
3	L	2	NAG	C3-C4-C5	2.52	114.73	110.24
5	J	1	NAG	C3-C2-N2	-2.51	105.88	110.62
3	P	2	NAG	O5-C5-C6	2.50	111.13	107.20
7	N	4	MAN	O5-C5-C6	2.50	111.12	107.20
6	K	2	FUC	C3-C4-C5	2.48	113.64	109.77
3	L	2	NAG	O5-C1-C2	-2.48	107.37	111.29
3	P	1	NAG	O5-C1-C2	-2.47	107.39	111.29
4	I	1	NAG	O7-C7-C8	-2.45	117.51	122.06
4	R	1	NAG	C4-C3-C2	2.45	114.60	111.02
7	N	3	BMA	O5-C1-C2	2.42	114.51	110.77
3	P	2	NAG	O5-C5-C4	-2.41	104.96	110.83
6	K	2	FUC	C1-O5-C5	-2.40	107.33	112.78
6	O	1	NAG	O7-C7-C8	-2.37	117.66	122.06
3	H	2	NAG	C1-C2-N2	-2.36	106.45	110.49
4	R	1	NAG	C3-C4-C5	2.30	114.35	110.24
6	O	1	NAG	O5-C1-C2	2.30	114.92	111.29
7	N	4	MAN	C1-C2-C3	2.30	112.49	109.67
3	L	2	NAG	C4-C3-C2	2.29	114.37	111.02
7	N	1	NAG	C4-C3-C2	2.28	114.35	111.02
4	I	5	MAN	O5-C5-C6	2.26	110.75	107.20
3	G	1	NAG	C2-N2-C7	2.23	126.08	122.90
3	G	1	NAG	C3-C4-C5	2.18	114.12	110.24
4	R	1	NAG	C8-C7-N2	2.17	119.78	116.10
3	G	1	NAG	O7-C7-C8	-2.07	118.22	122.06
6	O	1	NAG	O5-C5-C4	-2.06	105.81	110.83
6	O	1	NAG	O3-C3-C4	-2.03	105.66	110.35

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	K	2	FUC	C1
6	O	2	FUC	C1
3	P	2	NAG	C1
6	S	2	FUC	C1

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	1	NAG	C1-C2-N2-C7
6	K	1	NAG	C3-C2-N2-C7
5	J	1	NAG	C1-C2-N2-C7
5	J	3	SIA	C6-C7-C8-O8
5	J	3	SIA	O7-C7-C8-O8
3	H	2	NAG	C3-C2-N2-C7
3	Q	2	NAG	O5-C5-C6-O6
6	S	1	NAG	O5-C5-C6-O6
7	N	3	BMA	O5-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
4	I	5	MAN	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
6	S	1	NAG	C4-C5-C6-O6
4	R	1	NAG	O5-C5-C6-O6
7	N	4	MAN	O5-C5-C6-O6
5	J	3	SIA	O7-C7-C8-C9
5	J	3	SIA	C6-C7-C8-C9
7	N	3	BMA	C4-C5-C6-O6
3	Q	2	NAG	C4-C5-C6-O6
6	K	1	NAG	C4-C5-C6-O6
4	R	1	NAG	C4-C5-C6-O6
4	I	1	NAG	C8-C7-N2-C2
4	I	1	NAG	O7-C7-N2-C2
4	R	1	NAG	C8-C7-N2-C2
4	R	1	NAG	O7-C7-N2-C2
6	O	1	NAG	C8-C7-N2-C2
6	O	1	NAG	O7-C7-N2-C2
7	N	1	NAG	C8-C7-N2-C2
7	N	1	NAG	O7-C7-N2-C2
3	H	2	NAG	C8-C7-N2-C2
3	H	2	NAG	O7-C7-N2-C2
4	R	4	MAN	C4-C5-C6-O6
7	N	4	MAN	C4-C5-C6-O6
6	K	1	NAG	O5-C5-C6-O6
4	R	3	BMA	C4-C5-C6-O6
6	O	1	NAG	C1-C2-N2-C7
4	R	4	MAN	O5-C5-C6-O6
3	P	2	NAG	O5-C5-C6-O6
4	I	5	MAN	C4-C5-C6-O6
4	I	4	MAN	O5-C5-C6-O6
3	Q	1	NAG	O5-C5-C6-O6
5	J	1	NAG	C3-C2-N2-C7
3	H	2	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
7	N	2	NAG	O5-C5-C6-O6
5	J	3	SIA	C7-C8-C9-O9
5	J	3	SIA	O8-C8-C9-O9
3	P	1	NAG	C4-C5-C6-O6
4	R	3	BMA	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
5	J	2	GAL	C4-C5-C6-O6
3	M	1	NAG	C3-C2-N2-C7
3	M	2	NAG	C4-C5-C6-O6
3	P	1	NAG	O5-C5-C6-O6
6	O	1	NAG	C3-C2-N2-C7
3	P	2	NAG	C3-C2-N2-C7
3	P	1	NAG	C3-C2-N2-C7
3	M	2	NAG	O5-C5-C6-O6

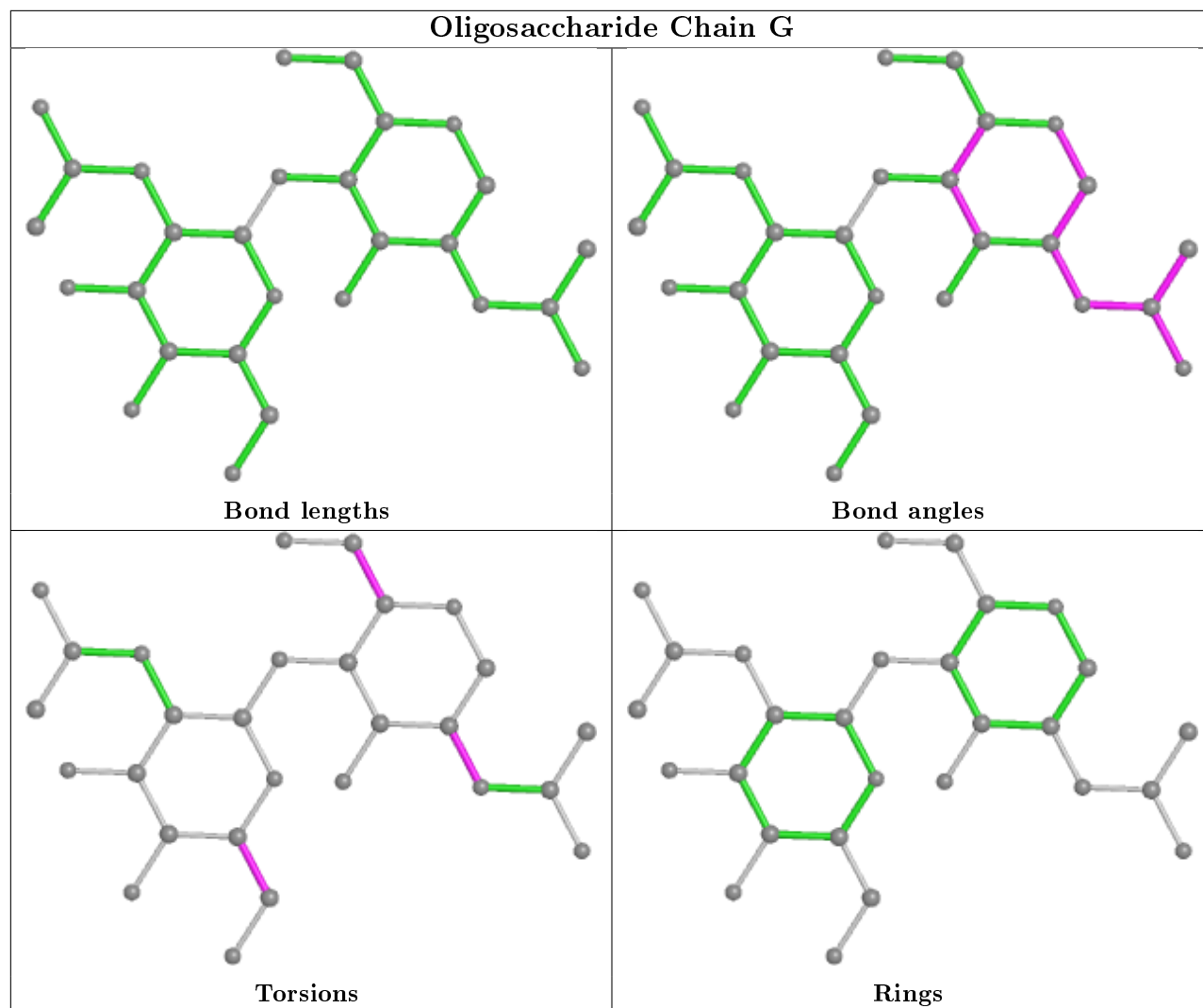
All (2) ring outliers are listed below:

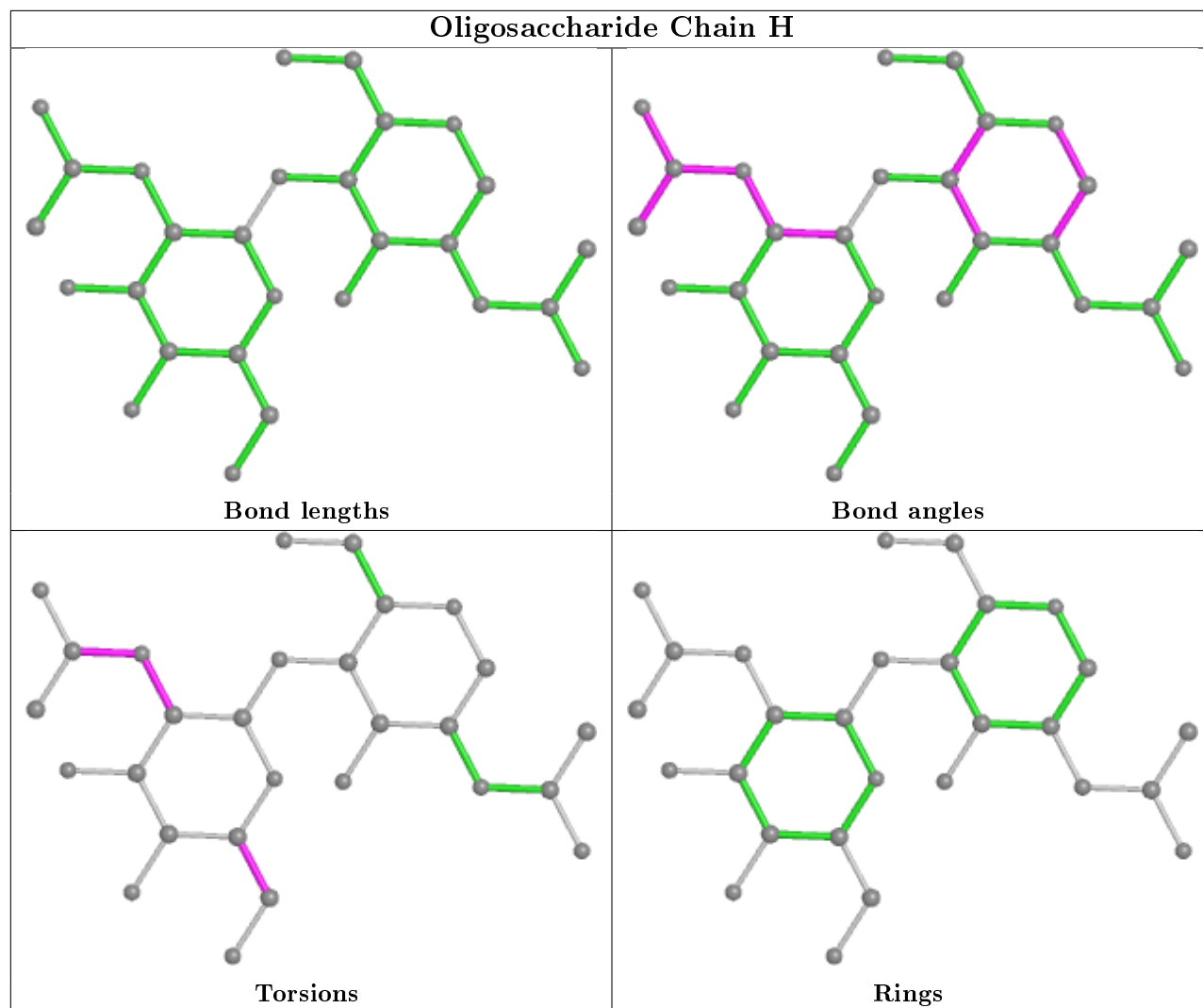
Mol	Chain	Res	Type	Atoms
4	R	5	MAN	C1-C2-C3-C4-C5-O5
4	I	5	MAN	C1-C2-C3-C4-C5-O5

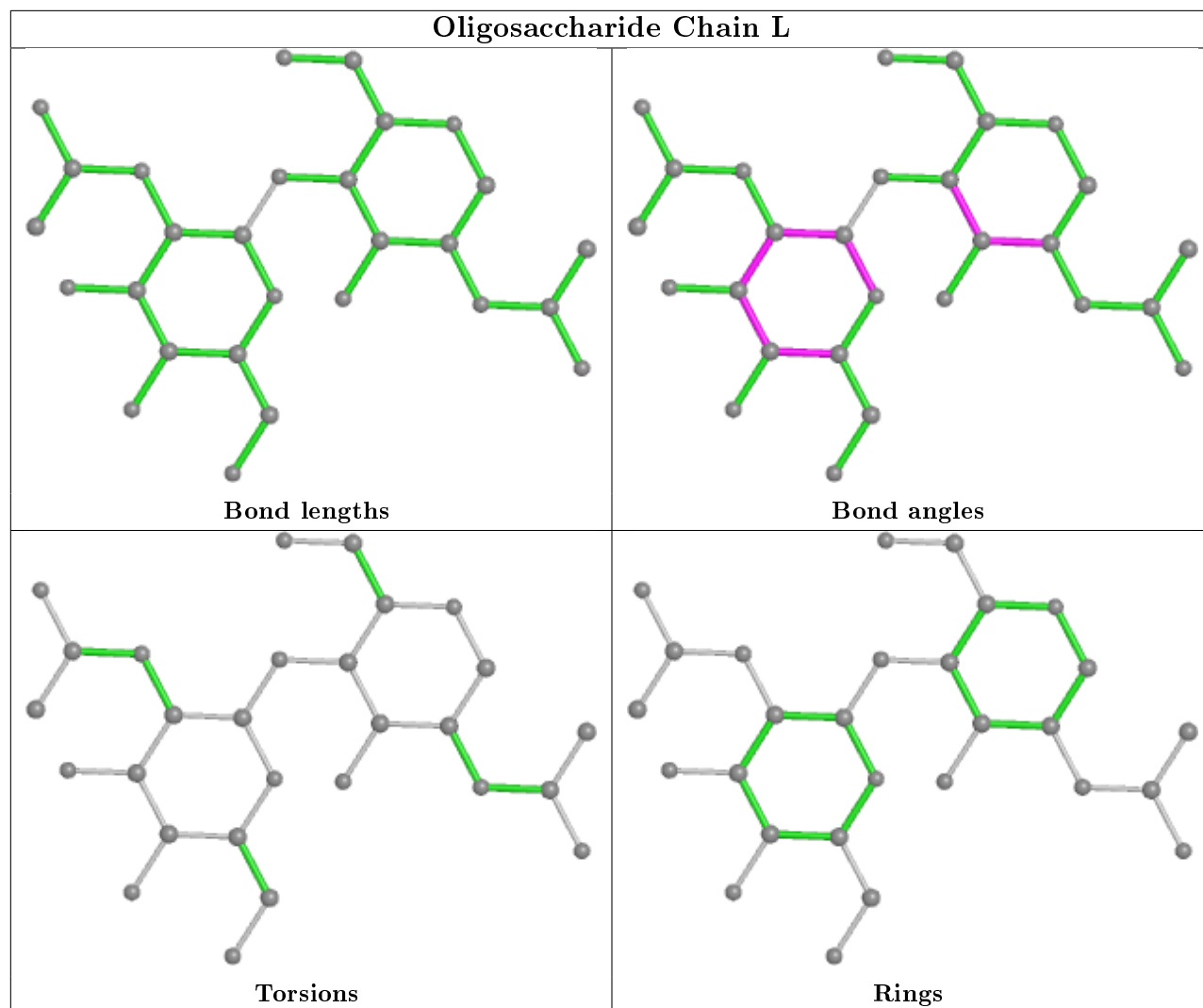
13 monomers are involved in 21 short contacts:

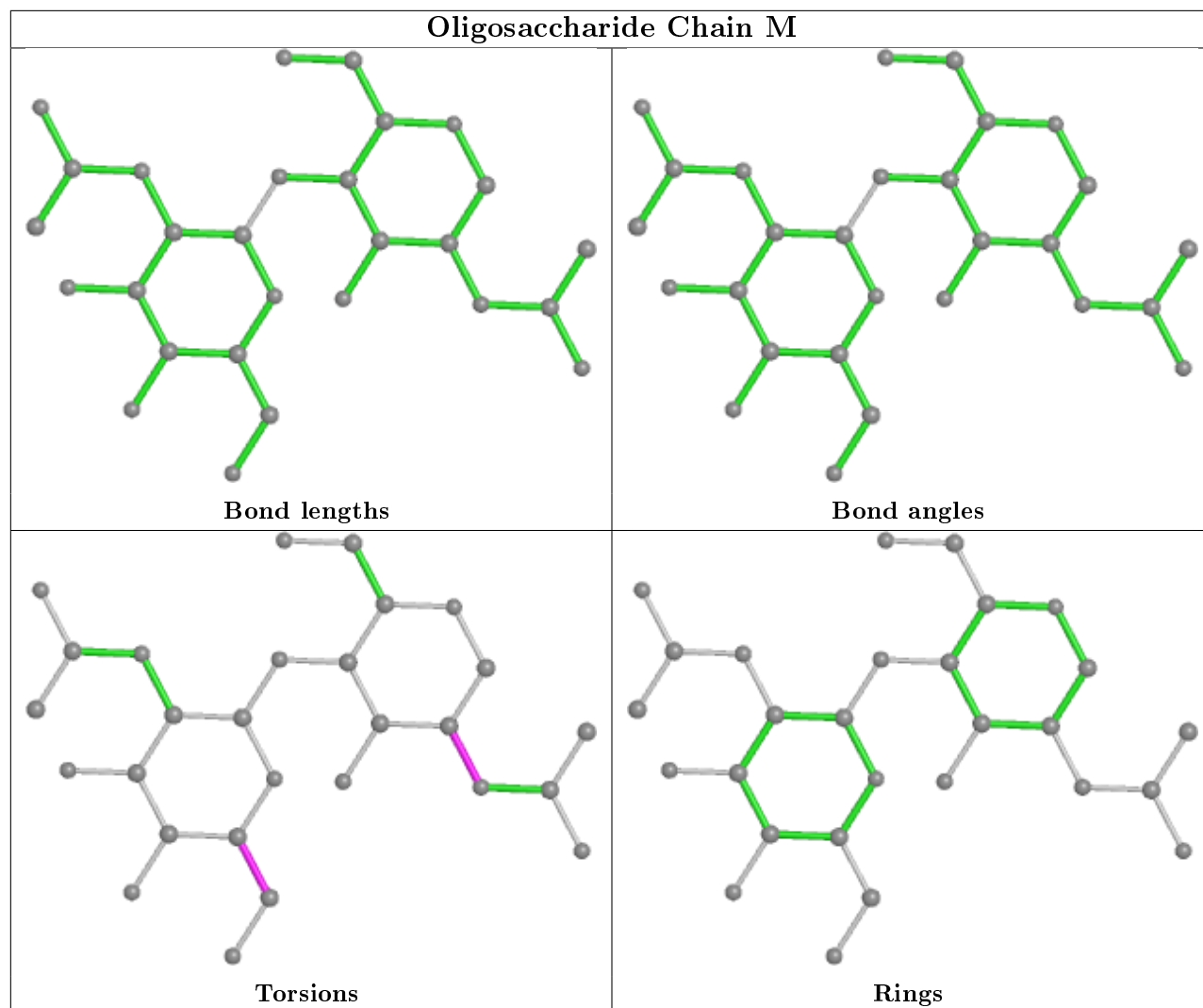
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	1	NAG	3	0
6	K	1	NAG	1	0
3	Q	1	NAG	2	0
3	L	1	NAG	1	0
4	I	1	NAG	2	0
4	R	1	NAG	1	0
5	J	3	SIA	2	0
6	O	1	NAG	1	0
3	M	1	NAG	1	0
3	P	2	NAG	1	0
3	P	1	NAG	3	0
7	N	1	NAG	3	0
3	H	1	NAG	1	0

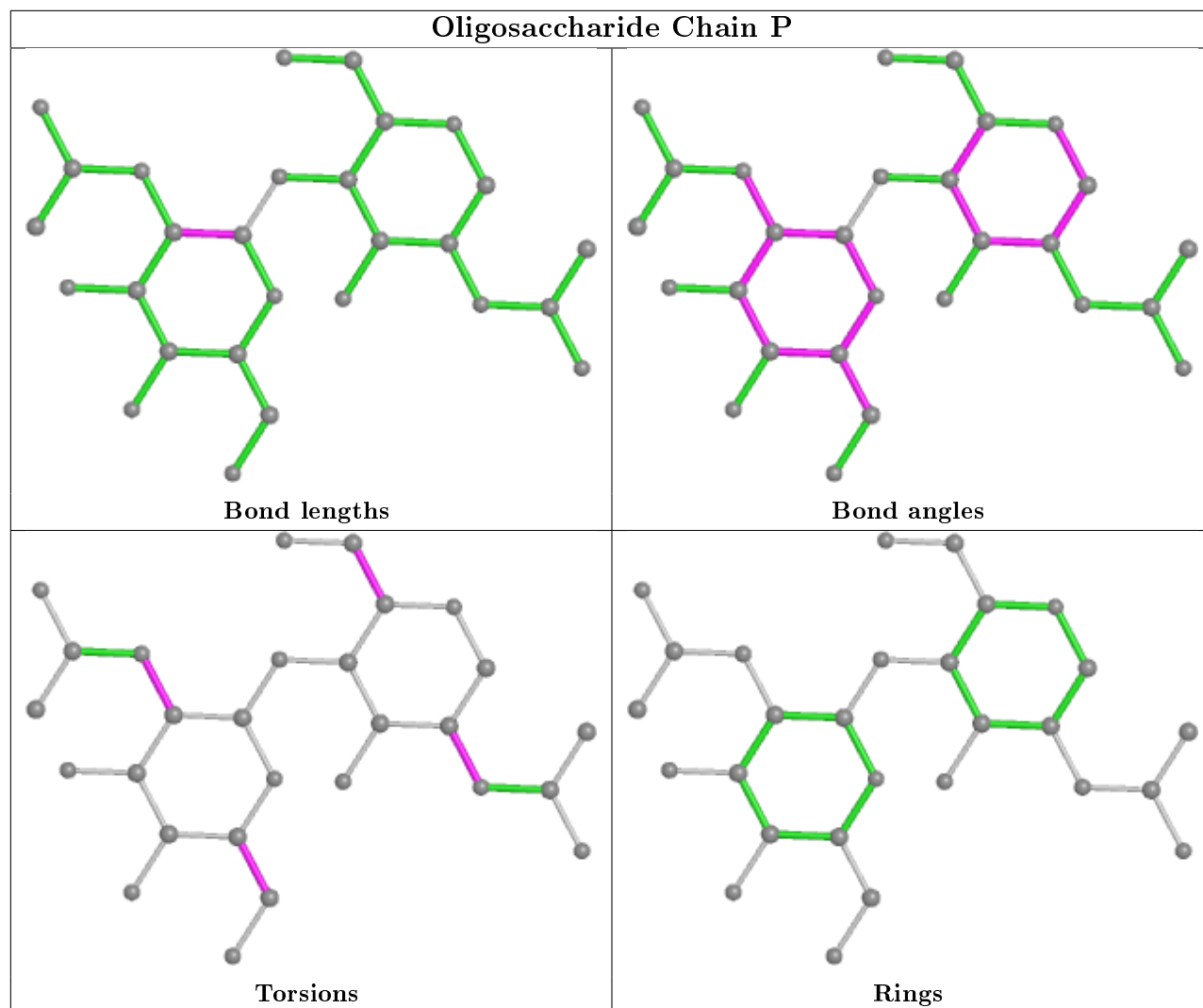
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

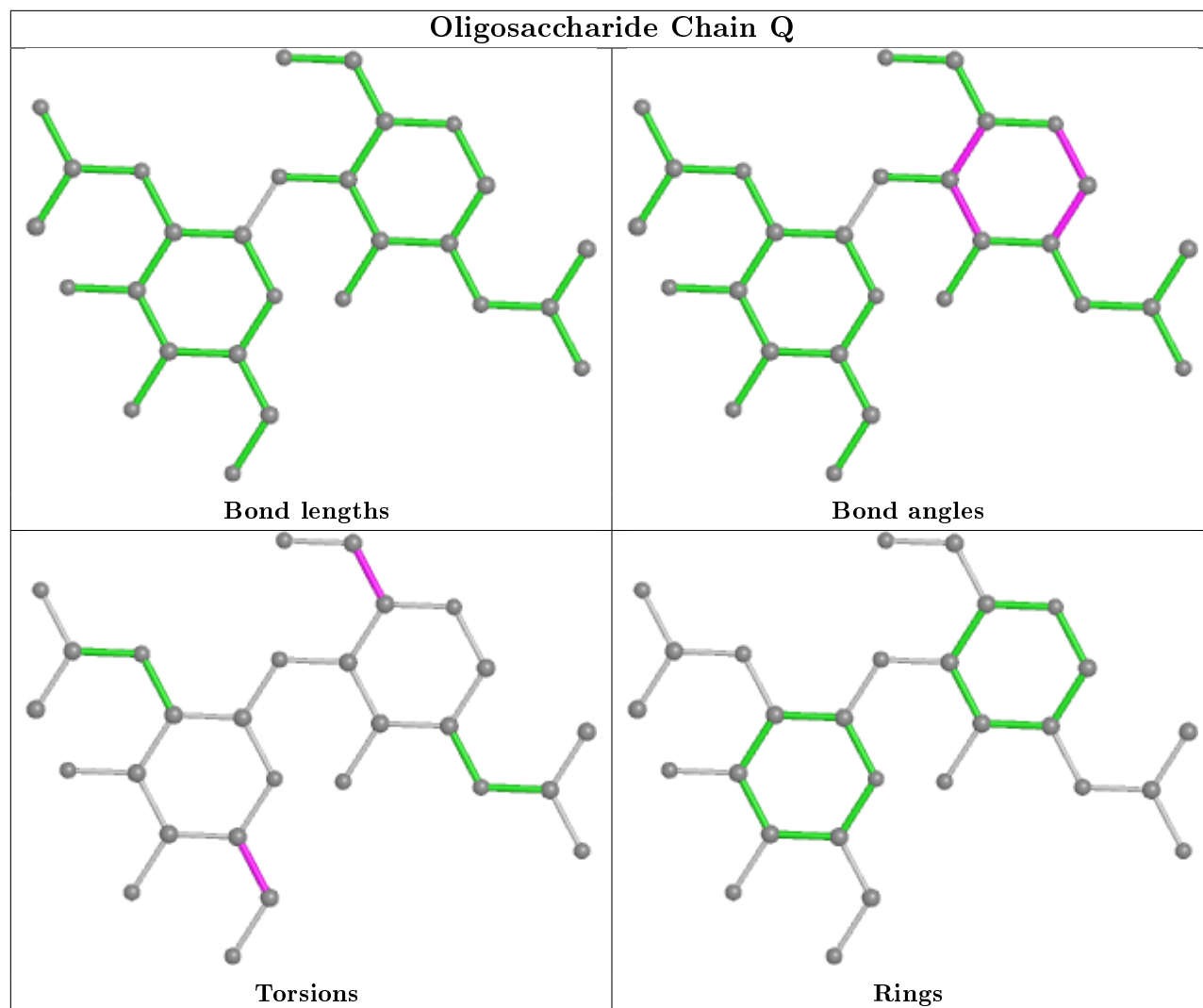


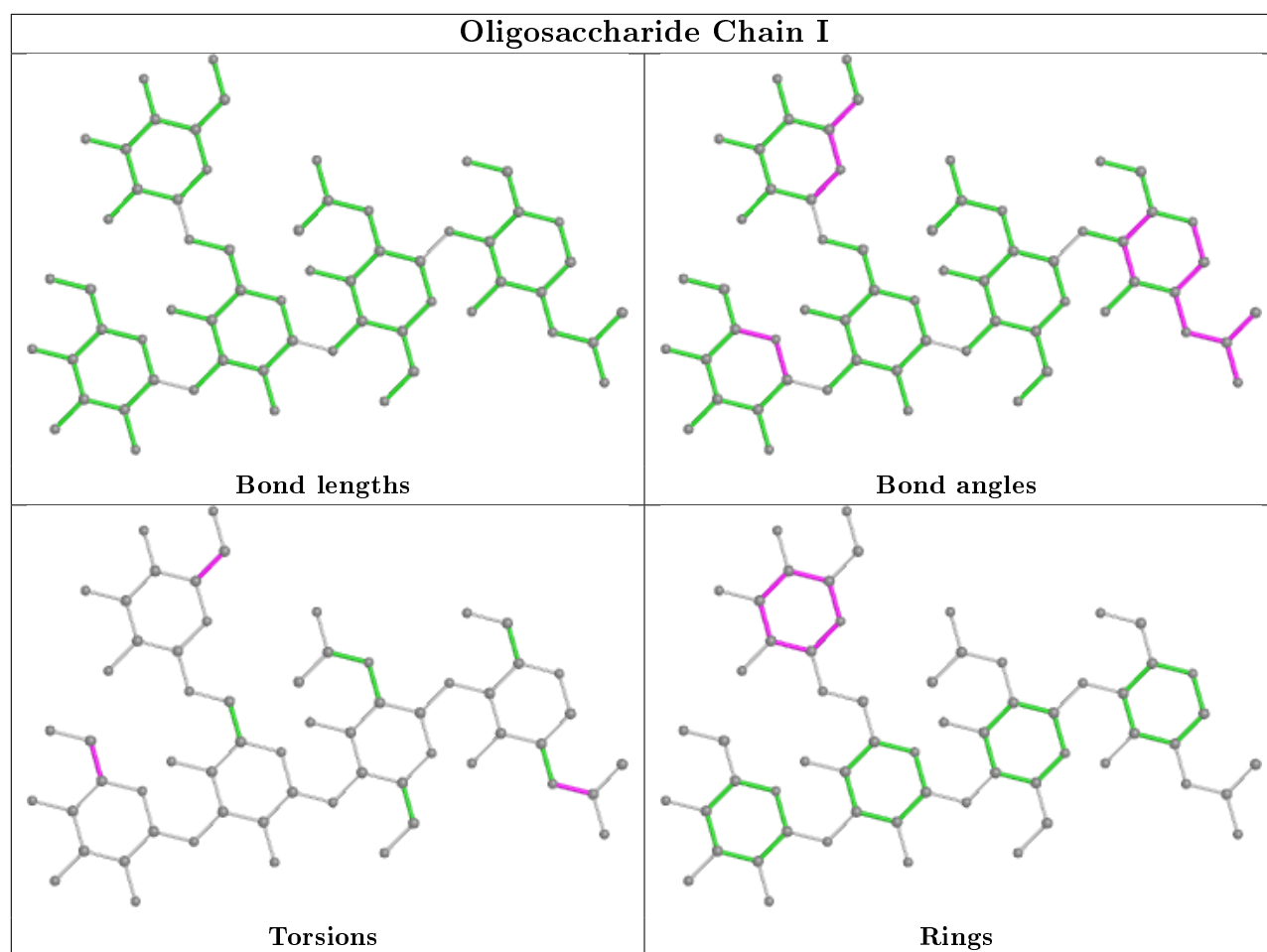


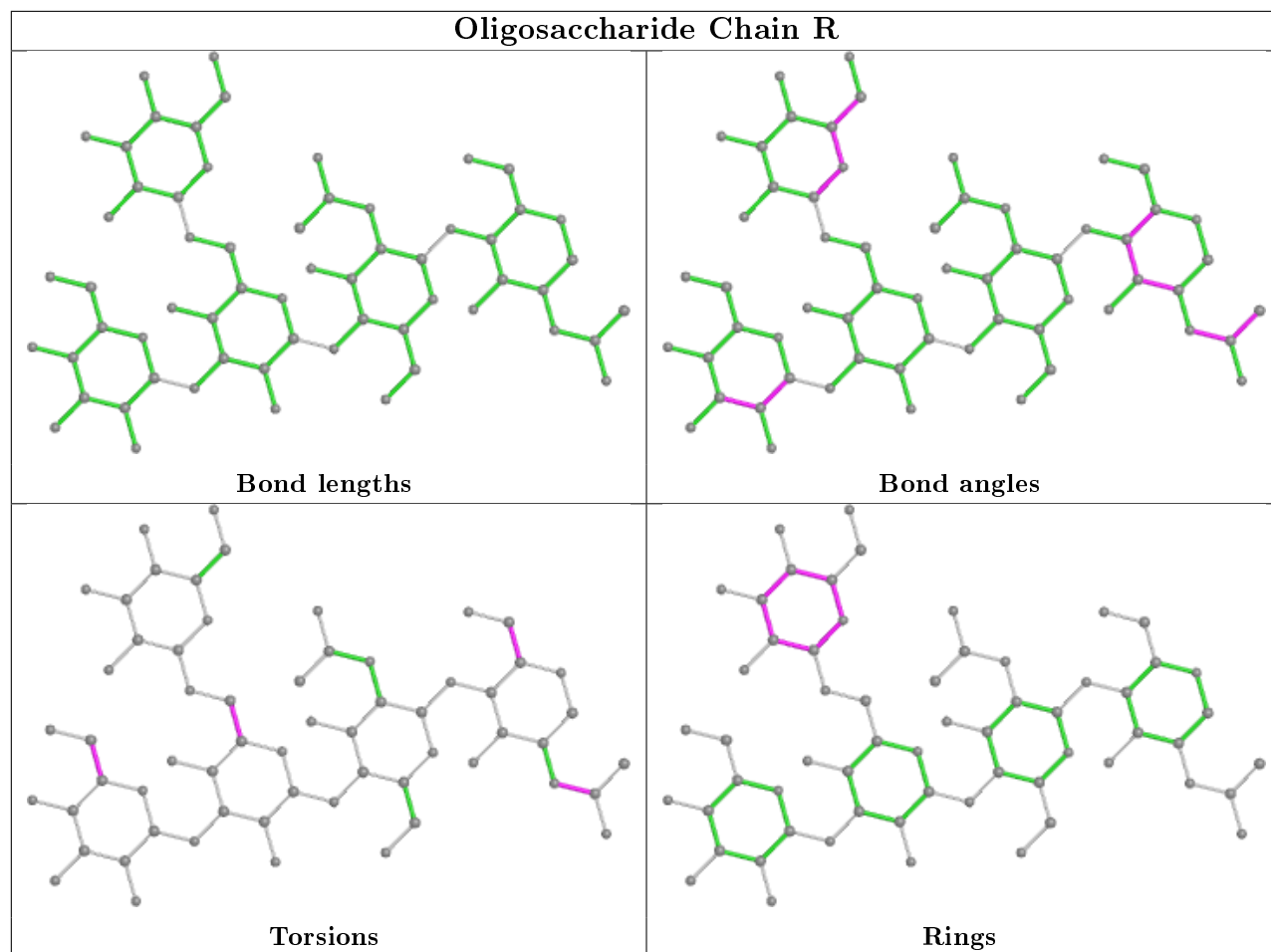




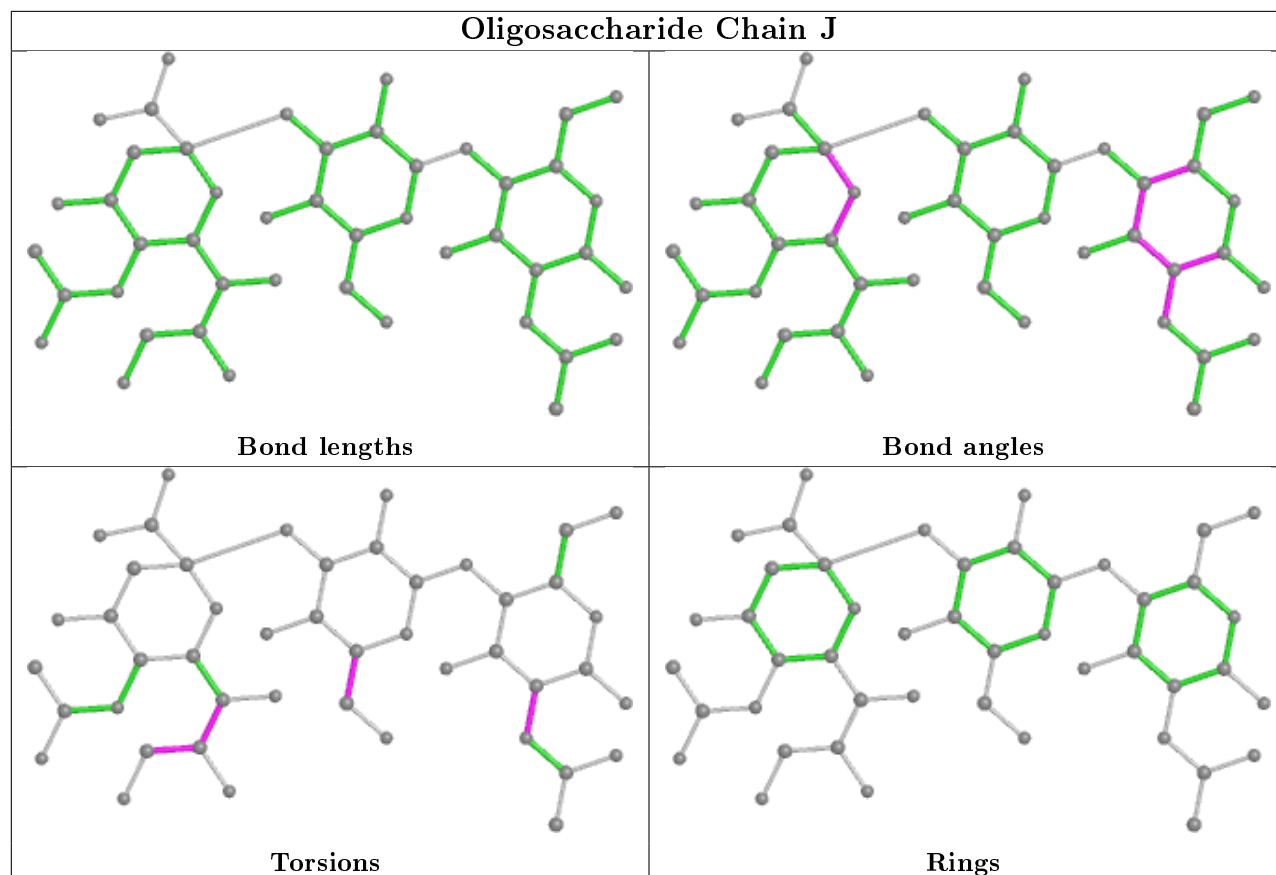




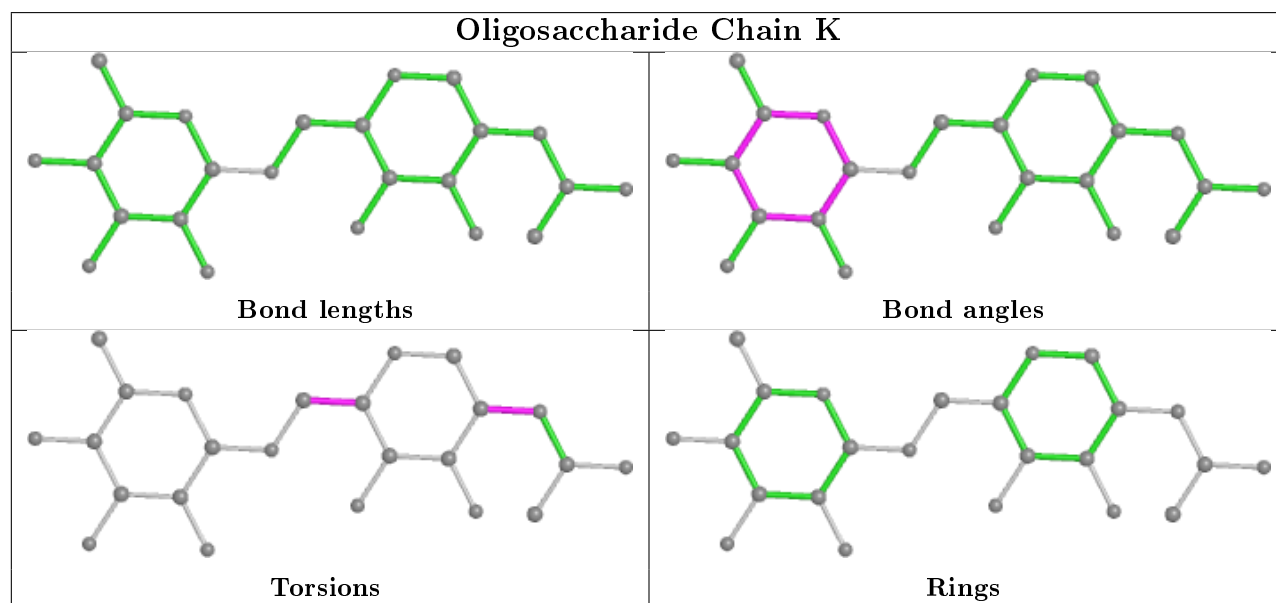


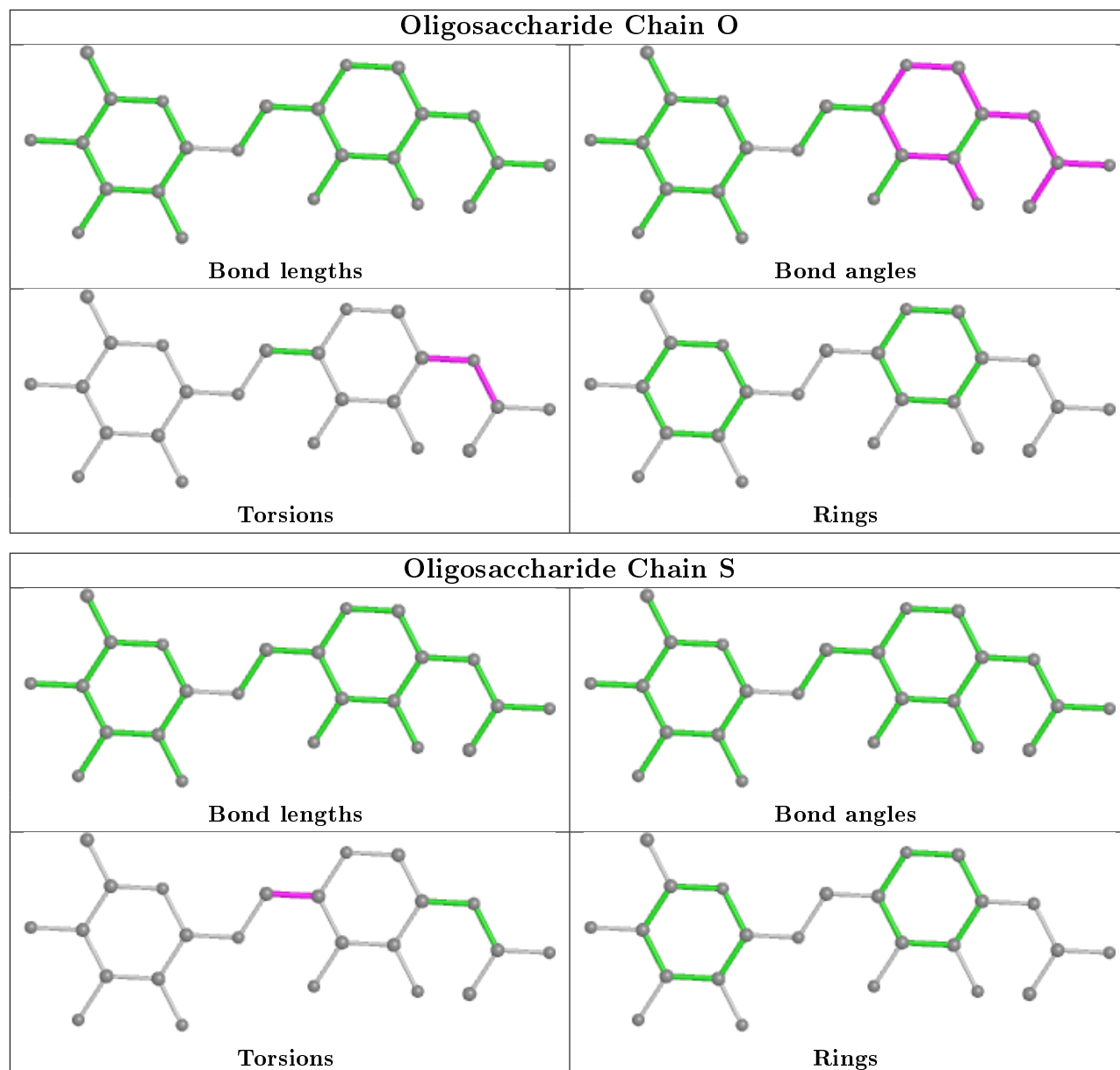


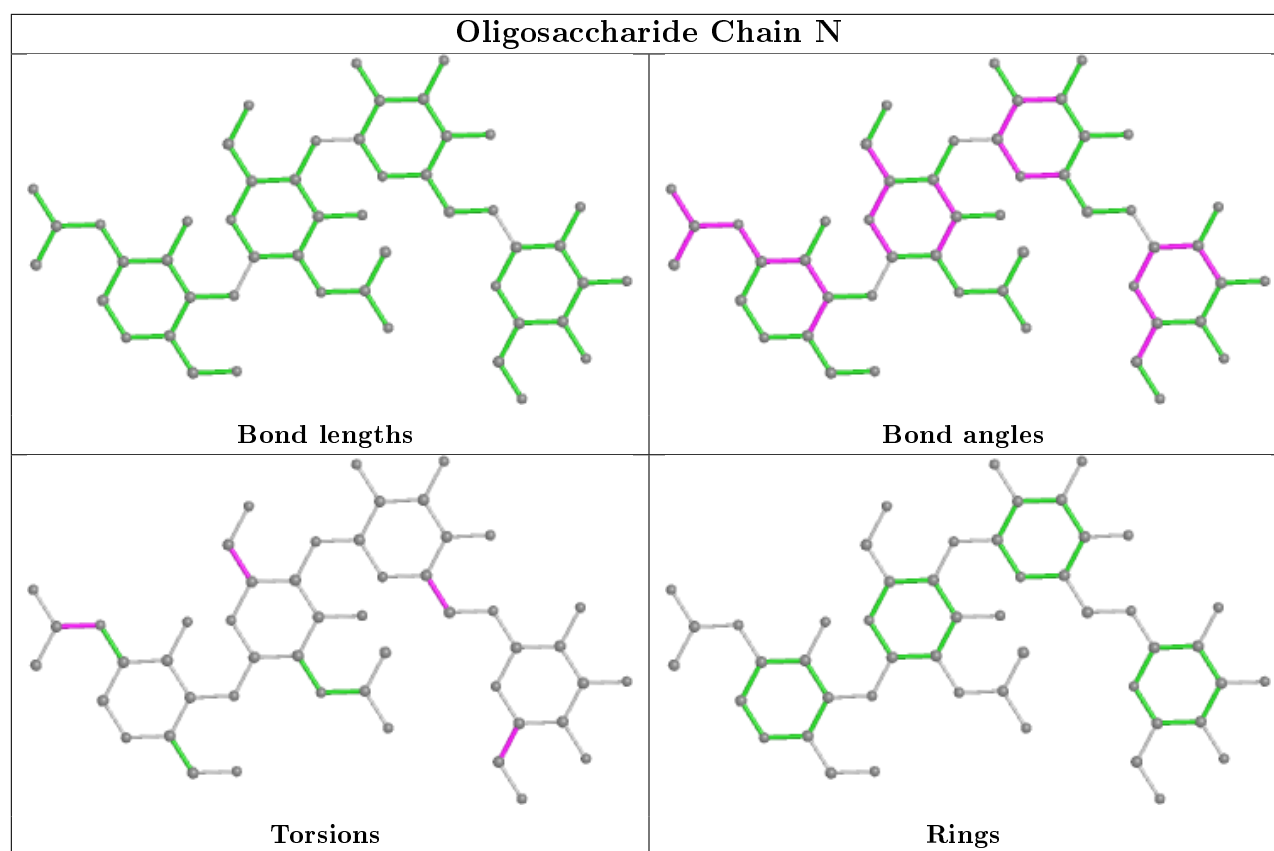
Oligosaccharide Chain J



Oligosaccharide Chain K







5.6 Ligand geometry [i](#)

7 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	$\# Z > 2$
9	SIA	C	701	-	17,20,21	0.24	0	21,28,31	0.77	1 (4%)
8	NAG	E	401	-	14,14,15	0.57	0	17,19,21	0.83	0
9	SIA	E	701	-	17,20,21	0.25	0	21,28,31	0.88	1 (4%)
8	NAG	A	401	-	14,14,15	0.66	0	17,19,21	1.35	2 (11%)
8	NAG	C	401	-	14,14,15	0.48	0	17,19,21	1.31	2 (11%)
8	NAG	A	431	-	14,14,15	0.50	0	17,19,21	1.09	1 (5%)
8	NAG	C	421	-	14,14,15	0.55	0	17,19,21	2.03	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
9	SIA	C	701	-	-	1/14/34/38	0/1/1/1
8	NAG	E	401	-	-	0/6/23/26	0/1/1/1
9	SIA	E	701	-	-	0/14/34/38	0/1/1/1
8	NAG	A	401	-	-	2/6/23/26	0/1/1/1
8	NAG	C	401	-	-	1/6/23/26	0/1/1/1
8	NAG	A	431	-	-	2/6/23/26	0/1/1/1
8	NAG	C	421	-	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	421	NAG	C2-N2-C7	4.77	129.69	122.90
8	C	421	NAG	C8-C7-N2	4.11	123.06	116.10
8	C	401	NAG	C1-O5-C5	3.70	117.20	112.19
8	C	421	NAG	C1-C2-N2	3.62	116.67	110.49
8	A	401	NAG	C4-C3-C2	3.30	115.85	111.02
9	E	701	SIA	C6-O6-C2	2.81	117.34	111.34
8	C	421	NAG	O7-C7-C8	-2.79	116.88	122.06
8	A	401	NAG	C3-C4-C5	2.66	114.99	110.24
9	C	701	SIA	C6-O6-C2	2.47	116.64	111.34
8	C	401	NAG	C3-C4-C5	2.45	114.61	110.24
8	A	431	NAG	O5-C1-C2	-2.37	107.55	111.29

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	C	421	NAG	C1-C2-N2-C7
8	A	431	NAG	O5-C5-C6-O6
8	A	431	NAG	C4-C5-C6-O6
8	A	401	NAG	O5-C5-C6-O6
8	A	401	NAG	C4-C5-C6-O6
8	C	421	NAG	C8-C7-N2-C2
8	C	421	NAG	O7-C7-N2-C2
8	C	401	NAG	O5-C5-C6-O6
9	C	701	SIA	C4-C5-N5-C10

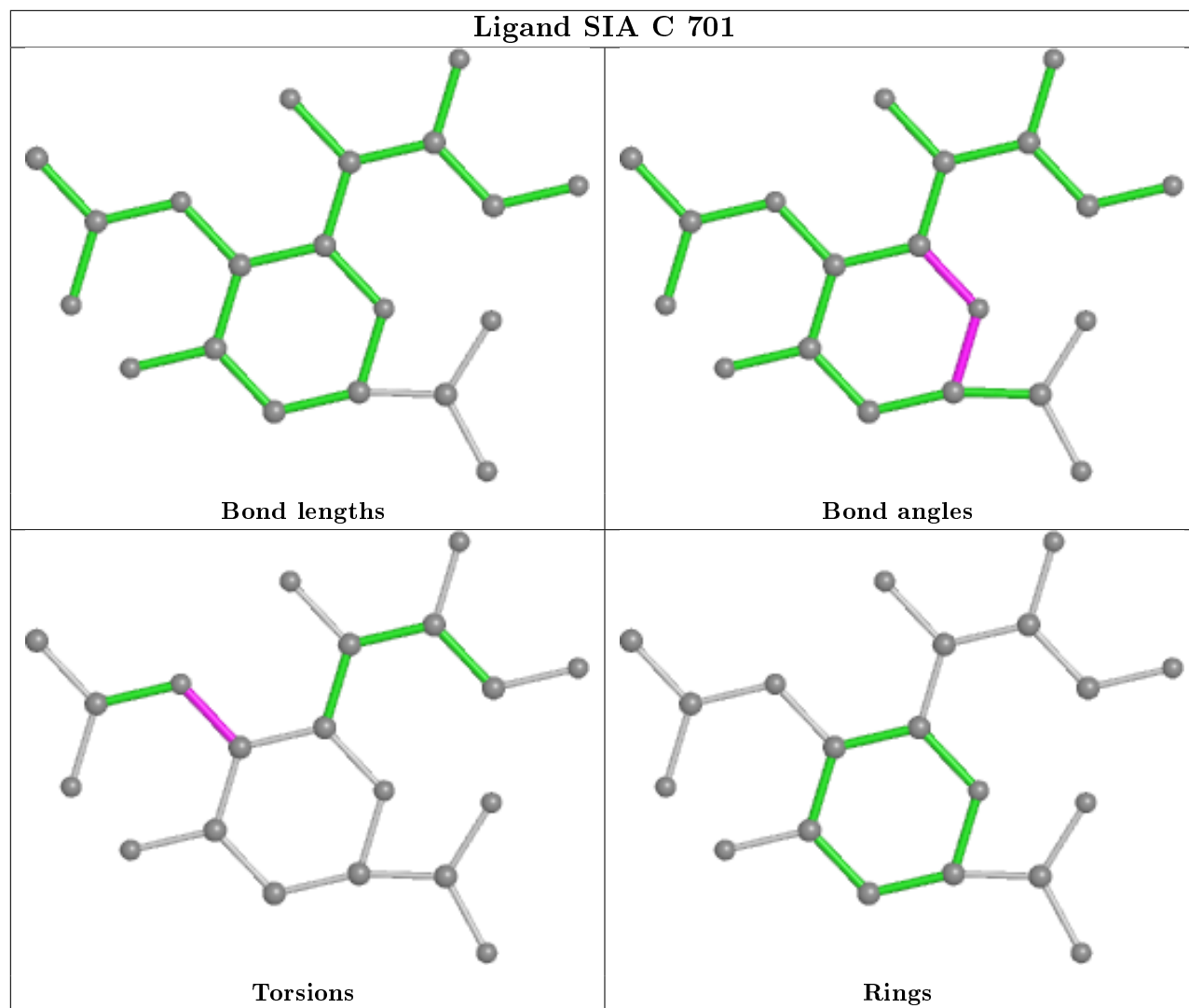
There are no ring outliers.

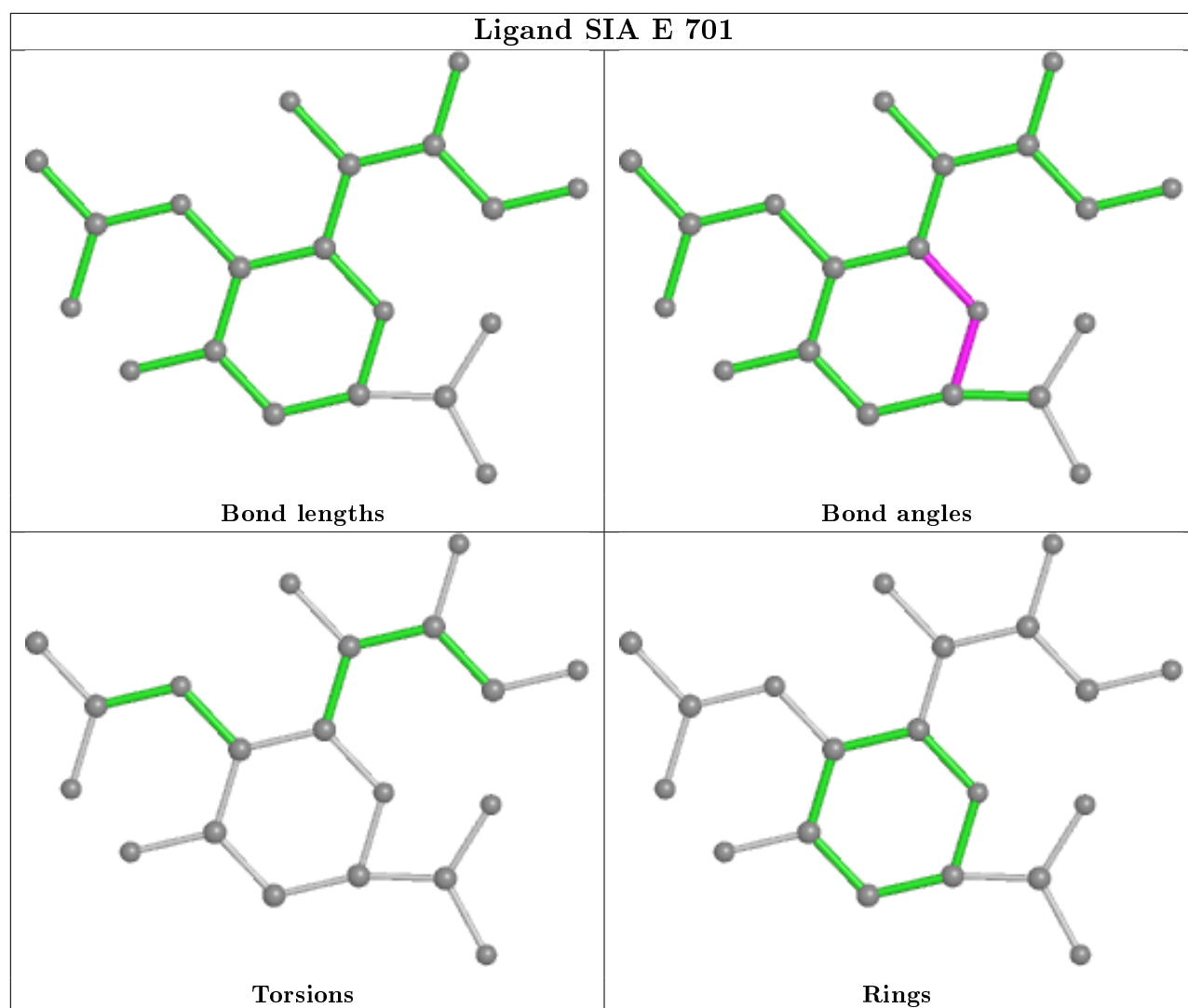
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	E	401	NAG	1	0
8	A	401	NAG	2	0
8	C	401	NAG	1	0
8	A	431	NAG	2	0
8	C	421	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 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 than 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 SIA C 701





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, 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	319/323 (98%)	0.76	33 (10%) 6 4	73, 109, 145, 155	0
1	C	319/323 (98%)	1.01	51 (15%) 1 1	91, 120, 162, 175	0
1	E	319/323 (98%)	1.81	114 (35%) 0 0	108, 150, 173, 186	0
2	B	172/173 (99%)	0.29	2 (1%) 79 67	64, 79, 108, 121	0
2	D	172/173 (99%)	0.22	2 (1%) 79 67	64, 76, 108, 122	0
2	F	172/173 (99%)	0.19	1 (0%) 89 83	68, 86, 110, 124	0
All	All	1473/1488 (98%)	0.86	203 (13%) 2 2	64, 108, 163, 186	0

All (203) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	58	VAL	9.1
1	E	243	LEU	8.1
1	E	59	LEU	7.3
1	E	179	ILE	7.1
1	C	200	GLY	6.6
1	E	222	TRP	6.4
1	C	199	SER	5.8
1	C	161	TYR	5.6
1	C	157	SER	5.6
1	E	218	GLY	5.5
1	E	127	TRP	5.4
1	E	151	LEU	5.2
1	E	143	SER	5.2
1	C	187	SER	5.1
1	A	245	ILE	5.0
1	E	159	ASN	5.0
1	E	199	SER	5.0
1	A	206	THR	5.0
1	C	158	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
1	C	198	GLU	4.7
1	E	147	PHE	4.7
1	E	223	VAL	4.7
1	A	210	GLN	4.7
1	E	126	THR	4.6
1	E	272	ALA	4.6
1	E	155	THR	4.6
1	C	154	LEU	4.6
1	E	47	SER	4.5
1	C	159	ASN	4.4
1	E	60	ASP	4.4
1	E	136	SER	4.3
1	E	273	LEU	4.3
1	E	79	PHE	4.2
1	E	191	GLN	4.2
1	C	135	GLY	4.1
1	E	194	LEU	4.1
1	E	245	ILE	4.1
1	E	160	SER	4.1
1	E	66	LEU	4.1
1	E	82	GLU	4.0
1	E	162	PRO	4.0
1	E	71	LEU	3.9
1	E	144	ALA	3.9
1	E	140	LYS	3.9
1	C	70	MET	3.9
1	E	244	MET	3.9
1	E	224	ARG	3.9
1	E	135	GLY	3.8
1	E	288	ILE	3.8
1	A	246	ASN	3.8
1	E	94	PHE	3.7
1	E	96	ASN	3.7
1	E	86	LEU	3.6
1	C	155	THR	3.6
1	A	205	SER	3.6
1	E	275	ASP	3.6
1	A	161	TYR	3.5
1	A	222	TRP	3.5
1	E	189	LYS	3.5
1	A	142	GLY	3.5
1	E	142	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	E	56	TYR	3.5
1	E	118	LEU	3.5
1	E	83	ASN	3.5
1	E	219	SER	3.5
1	E	197	GLN	3.5
1	E	138	ALA	3.5
1	E	166	VAL	3.4
1	E	256	GLY	3.4
1	E	161	TYR	3.4
1	E	282	ILE	3.4
1	E	200	GLY	3.4
1	A	244	MET	3.3
1	E	241	ASP	3.2
1	A	195	TYR	3.2
1	C	224	ARG	3.2
1	E	221	PRO	3.2
1	E	234	TRP	3.2
1	C	128	THR	3.2
1	E	48	ILE	3.2
1	A	79	PHE	3.2
1	A	83	ASN	3.2
1	C	218	GLY	3.1
1	E	61	GLY	3.1
1	E	128	THR	3.1
1	C	251	LEU	3.1
1	C	145	ASP	3.1
1	E	246	ASN	3.0
1	C	229	ARG	3.0
1	C	130	VAL	3.0
1	C	162	PRO	3.0
1	E	52	CYS	3.0
1	C	156	LYS	3.0
1	E	74	PRO	3.0
1	C	118	LEU	3.0
1	E	78	ASP	2.9
1	E	75	HIS	2.9
1	E	190	GLU	2.9
1	A	175	ASP	2.9
1	C	194	LEU	2.9
1	A	204	VAL	2.8
1	C	132	GLN	2.8
1	E	177	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	176	LYS	2.8
1	E	167	THR	2.8
1	E	125	PHE	2.8
1	E	88	ILE	2.8
1	E	70	MET	2.8
1	C	225	GLY	2.8
1	E	239	PRO	2.8
1	E	57	ARG	2.8
1	E	85	ASP	2.8
1	E	164	LEU	2.8
1	A	183	HIS	2.8
1	E	201	ARG	2.8
1	E	156	LYS	2.7
1	E	214	ILE	2.7
1	E	152	ASN	2.7
2	D	1	GLY	2.7
1	E	281	CYS	2.7
1	A	221	PRO	2.7
1	A	216	ASN	2.7
1	C	153	TRP	2.7
1	A	209	SER	2.7
1	E	188	ASN	2.7
1	A	208	ARG	2.7
1	E	95	SER	2.6
1	C	212	THR	2.6
1	A	255	ARG	2.6
1	A	178	TYR	2.6
1	E	208	ARG	2.6
1	E	87	PHE	2.6
1	E	163	ILE	2.6
1	A	59	LEU	2.5
1	E	122	ALA	2.5
1	A	96	ASN	2.5
1	C	232	ILE	2.5
1	E	225	GLY	2.5
1	C	144	ALA	2.5
1	E	228	GLY	2.5
1	E	184	HIS	2.5
1	C	213	VAL	2.5
1	C	48	ILE	2.5
1	A	252	VAL	2.4
1	C	160	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	79	PHE	2.4
1	C	131	THR	2.4
1	E	54	ASN	2.4
1	E	248	ASN	2.4
1	C	196	ILE	2.4
2	B	61	GLU	2.4
1	C	192	THR	2.4
1	E	98	TYR	2.4
1	E	302	TYR	2.4
1	A	143	SER	2.4
1	E	252	VAL	2.4
1	C	183	HIS	2.4
1	A	128	THR	2.4
1	E	99	PRO	2.4
1	E	271	ASP	2.4
1	E	49	GLY	2.4
1	C	54	ASN	2.4
1	C	61	GLY	2.3
1	A	171	ASN	2.3
1	C	142	GLY	2.3
1	E	187	SER	2.3
1	E	124	GLY	2.3
1	A	177	LEU	2.3
1	C	217	ILE	2.2
1	E	183	HIS	2.2
1	E	77	ASP	2.2
1	C	197	GLN	2.2
1	C	163	ILE	2.2
1	E	68	ASP	2.2
1	E	93	ALA	2.2
1	E	251	LEU	2.2
1	C	127	TRP	2.2
1	A	131	THR	2.2
1	E	213	VAL	2.1
2	F	29	SER	2.1
1	E	133	ASN	2.1
1	E	173	ASN	2.1
1	A	166	VAL	2.1
2	B	81	GLU	2.1
1	C	214	ILE	2.1
1	A	202	VAL	2.1
1	E	110	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	135	GLY	2.1
1	E	285	ASN	2.1
1	E	270	SER	2.1
1	C	78	ASP	2.1
1	C	188	ASN	2.1
1	C	276	THR	2.1
1	E	51	ILE	2.1
1	E	277	CYS	2.1
1	C	146	SER	2.1
1	E	137	GLY	2.1
1	E	274	ILE	2.0
1	E	193	LYS	2.0
2	D	2	ILE	2.0
1	E	181	GLY	2.0
1	C	246	ASN	2.0
1	C	98	TYR	2.0

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, 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
3	NAG	H	2	14/15	0.43	0.59	125,130,136,137	0
4	MAN	R	4	11/12	0.44	0.69	143,147,149,151	0
3	NAG	L	2	14/15	0.49	0.45	134,140,143,145	0
4	MAN	I	4	11/12	0.51	0.49	102,104,106,107	0
3	NAG	L	1	14/15	0.52	0.44	120,125,130,133	0
7	BMA	N	3	11/12	0.54	0.45	128,131,137,139	0
6	FUC	S	2	10/11	0.56	0.56	96,101,103,104	0
3	NAG	P	1	14/15	0.56	0.56	159,163,167,167	0
3	NAG	P	2	14/15	0.58	0.71	170,174,179,179	0
4	MAN	R	5	11/12	0.61	0.34	130,133,136,138	0
3	NAG	G	1	14/15	0.62	0.33	109,112,118,118	0
7	MAN	N	4	11/12	0.62	0.34	122,127,134,135	0

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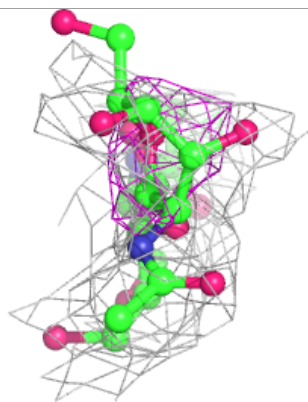
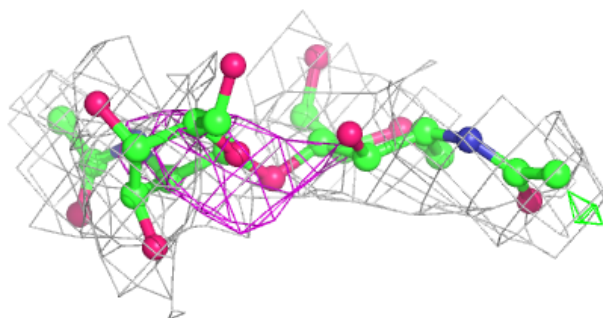
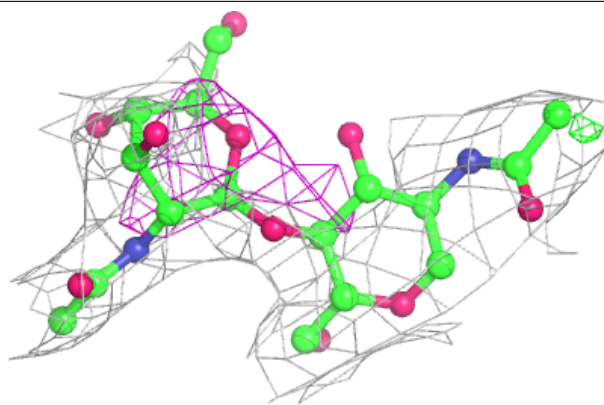
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	J	1	15/15	0.64	0.37	137,142,148,148	0
3	NAG	G	2	14/15	0.64	0.56	121,126,129,129	0
3	NAG	Q	2	14/15	0.65	0.35	164,170,175,176	0
4	BMA	I	3	11/12	0.69	0.33	96,99,102,103	0
7	NAG	N	2	14/15	0.71	0.36	118,121,125,128	0
4	MAN	I	5	11/12	0.72	0.23	92,95,99,99	0
4	BMA	R	3	11/12	0.73	0.30	135,138,142,143	0
3	NAG	M	2	14/15	0.73	0.35	133,141,146,147	0
6	NAG	S	1	14/15	0.74	0.40	99,102,107,108	0
4	NAG	R	2	14/15	0.74	0.29	130,134,138,138	0
3	NAG	Q	1	14/15	0.76	0.25	165,167,169,169	0
6	NAG	O	1	14/15	0.78	0.27	85,91,99,102	0
6	FUC	K	2	10/11	0.78	0.35	90,98,102,103	0
6	FUC	O	2	10/11	0.79	0.28	83,88,92,94	0
4	NAG	I	2	14/15	0.80	0.29	89,91,94,95	0
5	SIA	J	3	20/21	0.81	0.22	125,129,132,133	0
3	NAG	H	1	14/15	0.82	0.47	114,116,121,122	0
3	NAG	M	1	14/15	0.85	0.21	135,138,142,143	0
4	NAG	R	1	14/15	0.85	0.26	132,133,136,137	0
7	NAG	N	1	14/15	0.87	0.24	112,116,119,120	0
5	GAL	J	2	11/12	0.87	0.17	130,133,135,135	0
6	NAG	K	1	14/15	0.89	0.20	93,98,105,106	0
4	NAG	I	1	14/15	0.91	0.18	84,87,89,90	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.

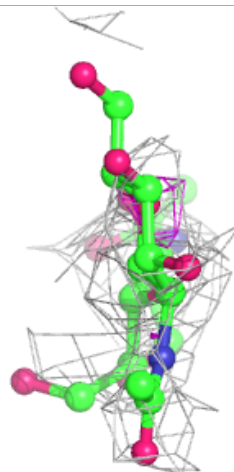
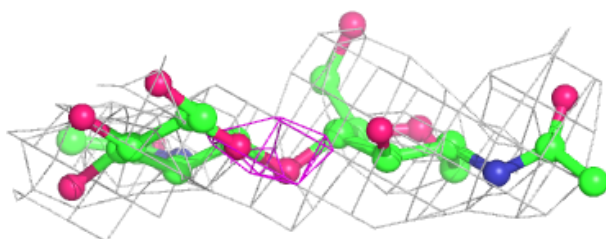
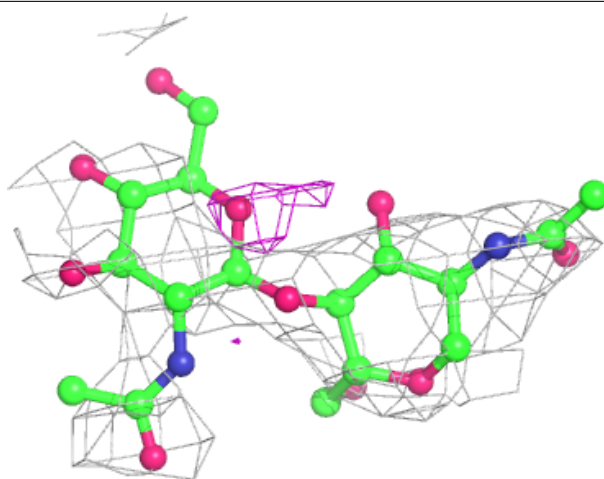
Electron density around Chain G:

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



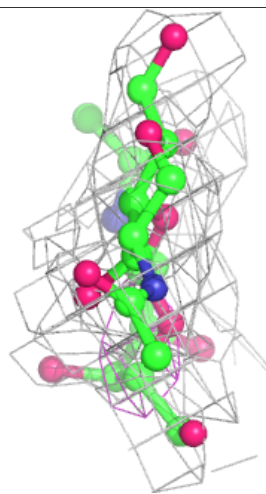
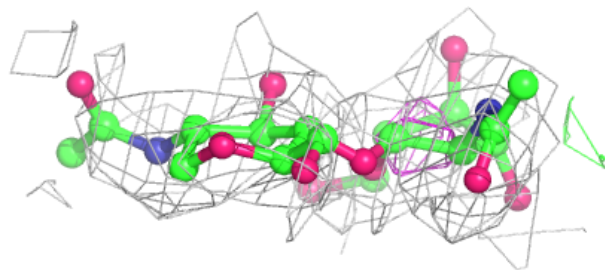
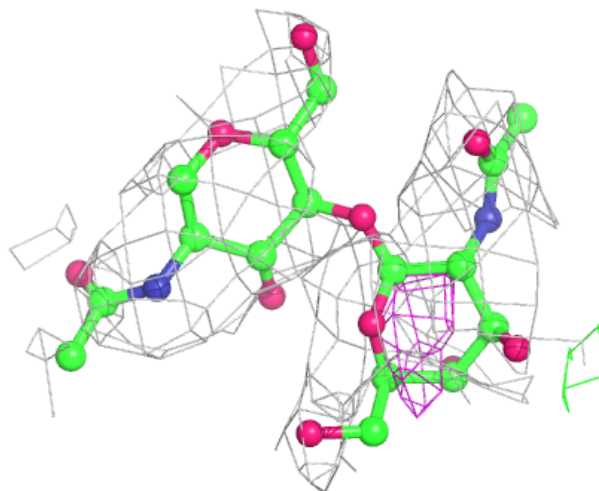
Electron density around Chain H:

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



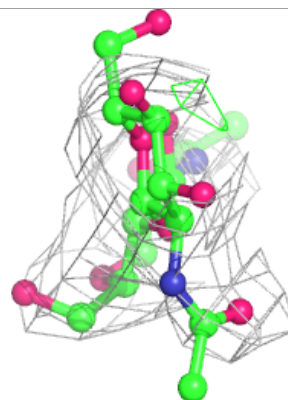
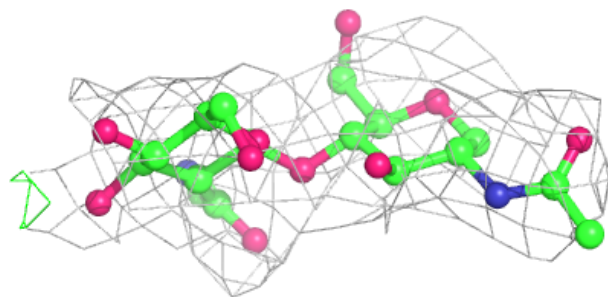
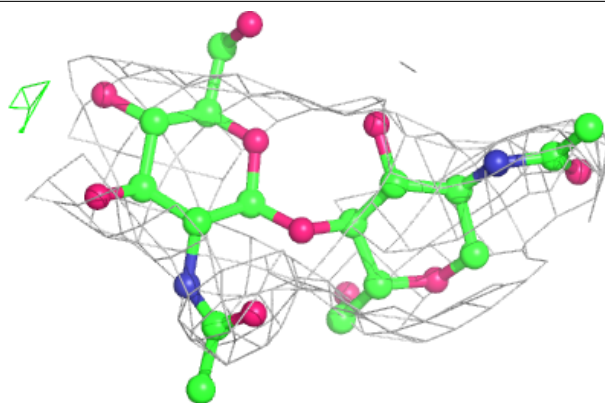
Electron density around Chain L:

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



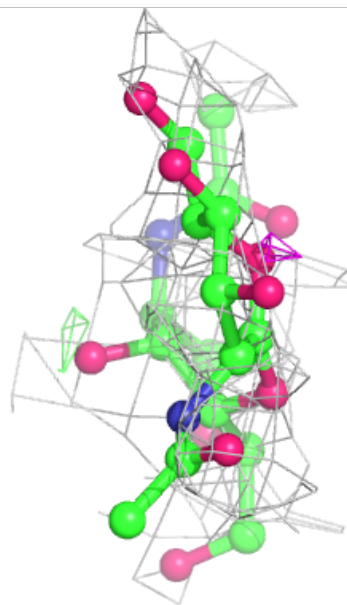
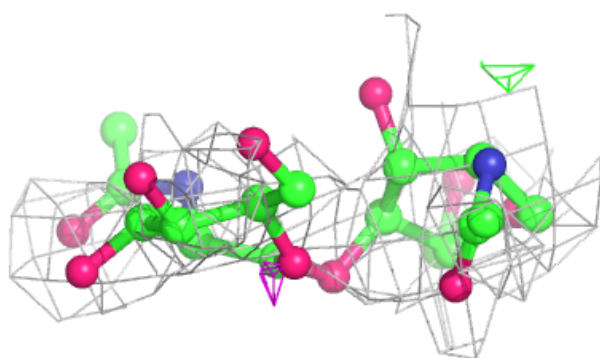
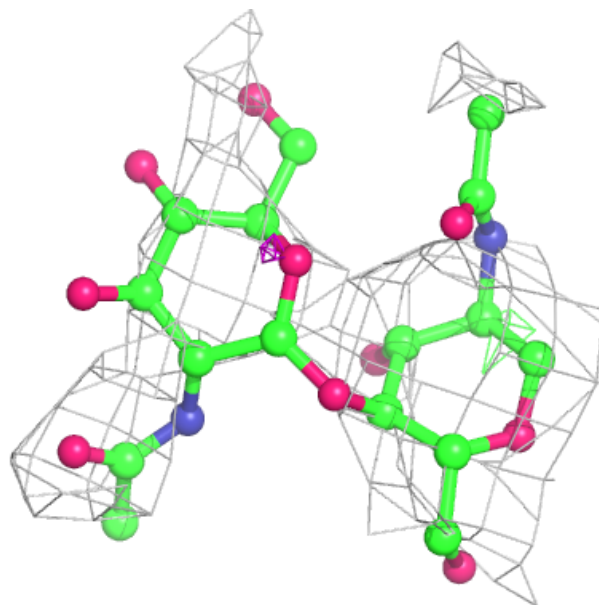
Electron density around Chain M:

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



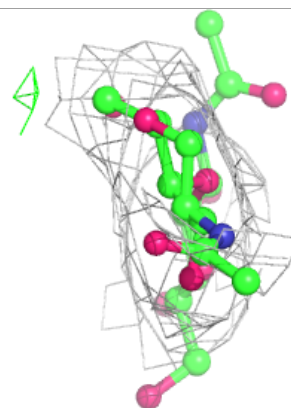
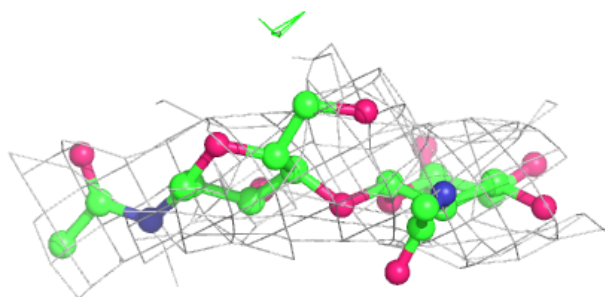
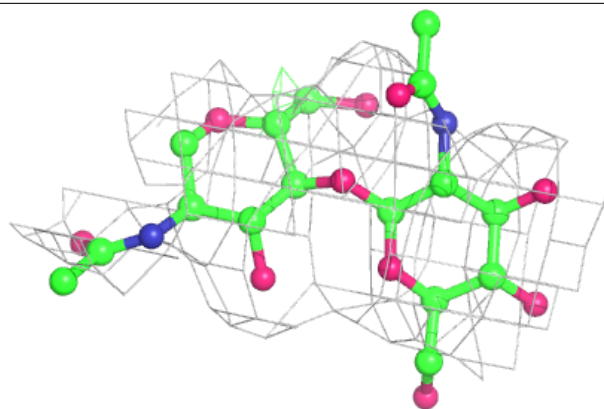
Electron density around Chain P:

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



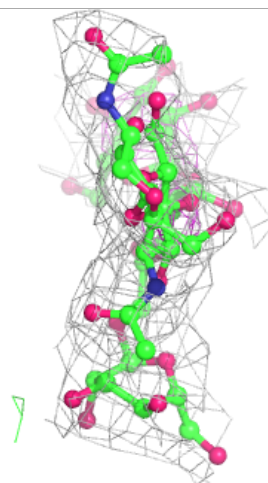
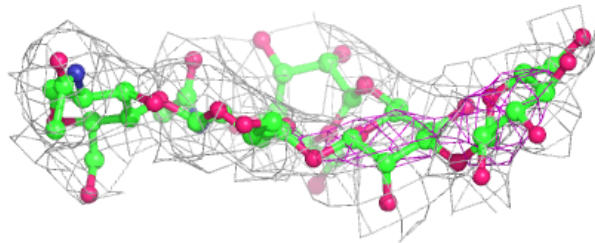
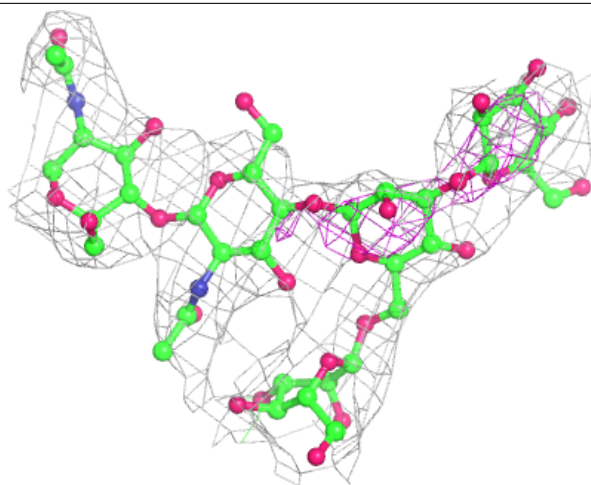
Electron density around Chain Q:

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



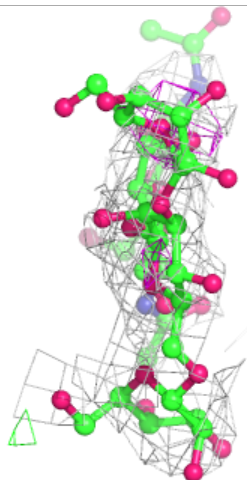
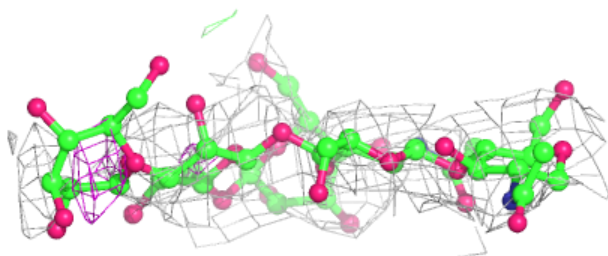
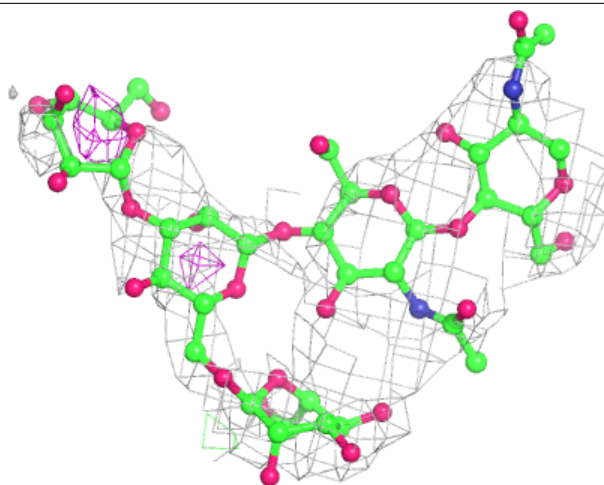
Electron density around Chain I:

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



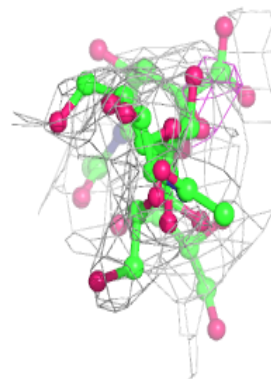
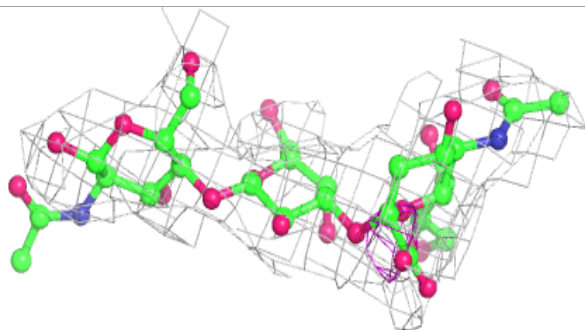
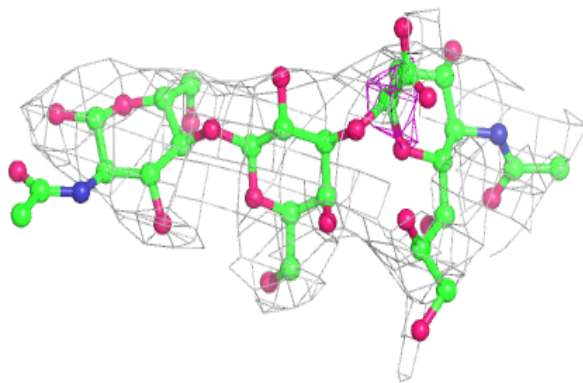
Electron density around Chain R:

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

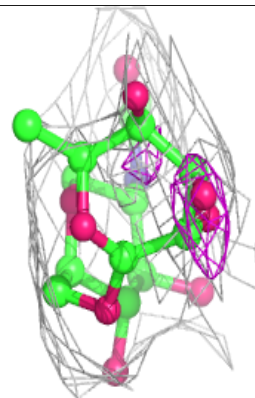
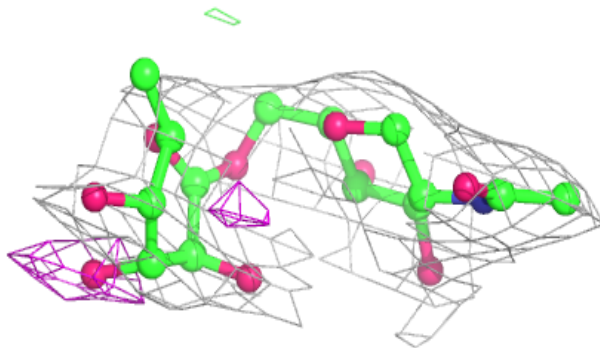
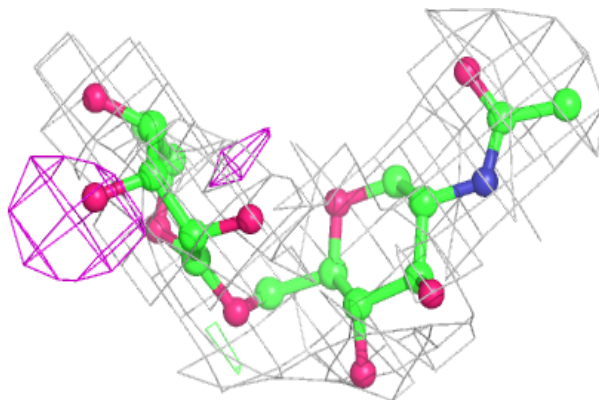


Electron density around Chain J:

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

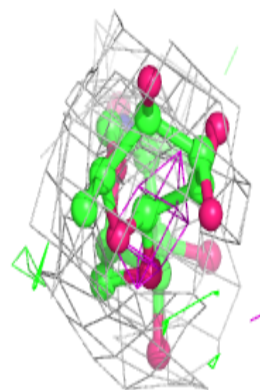
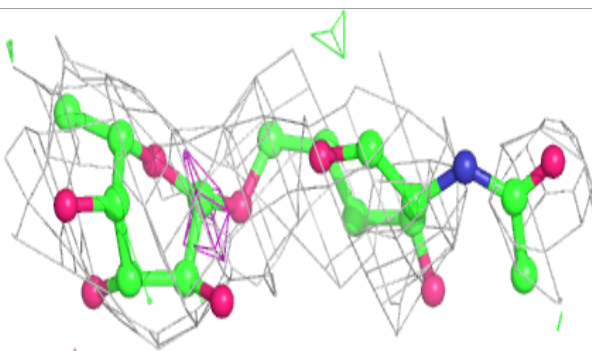
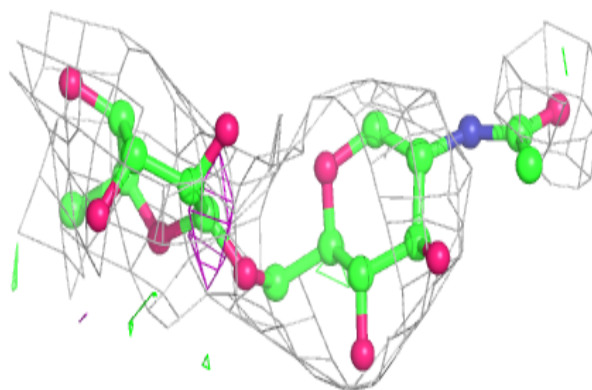
**Electron density around Chain K:**

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

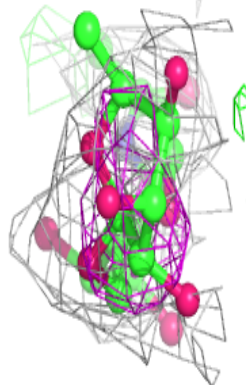
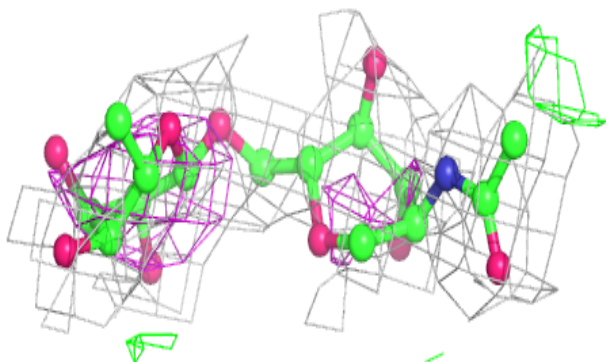
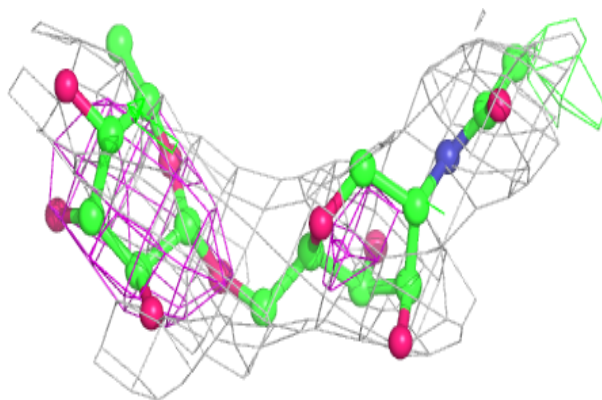


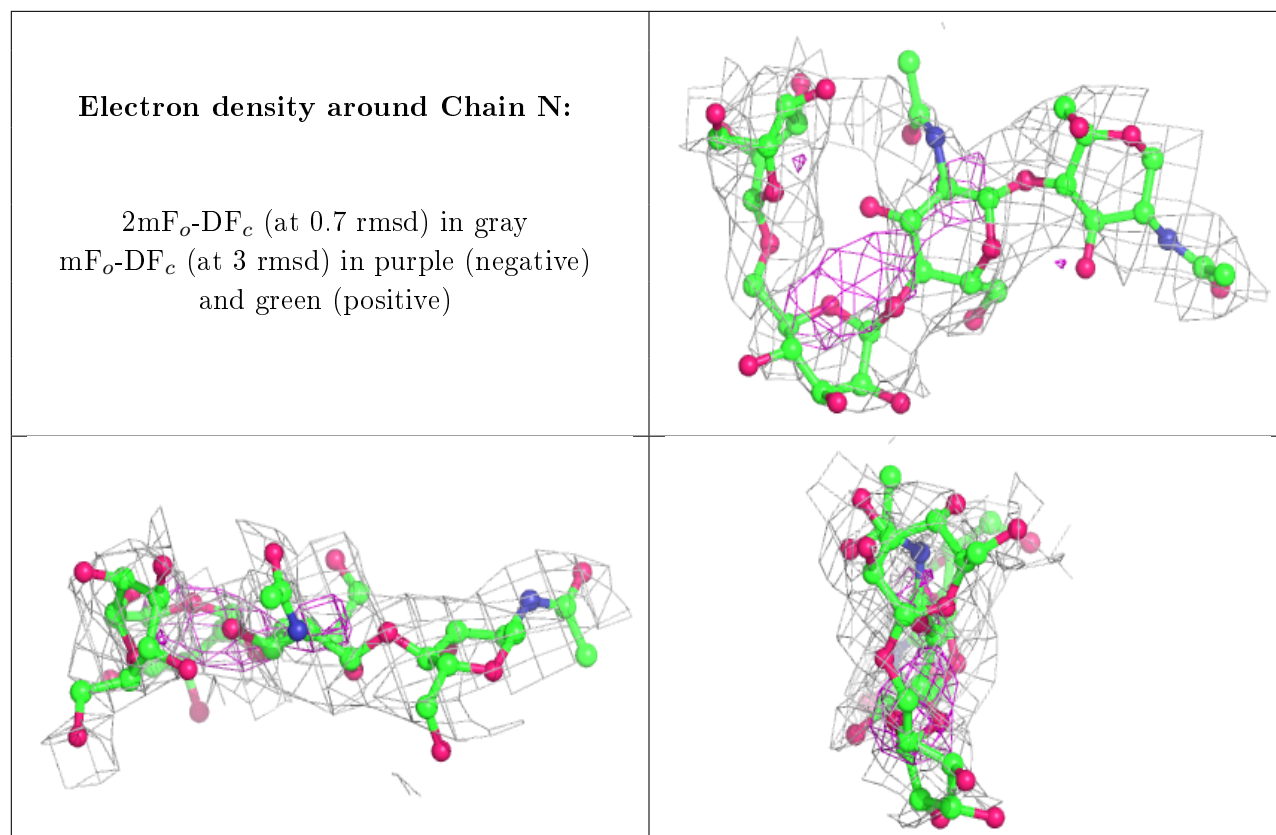
Electron density around Chain O:

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

**Electron density around Chain S:**

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





6.4 Ligands [i](#)

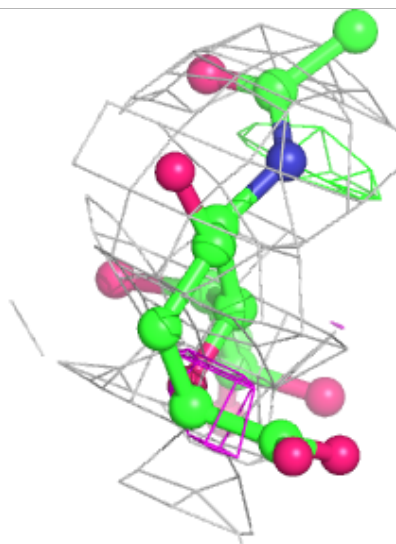
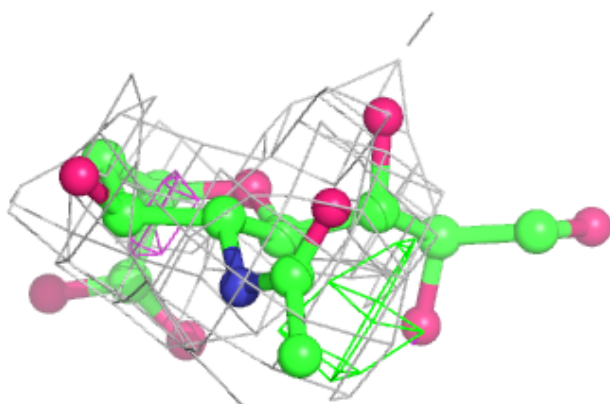
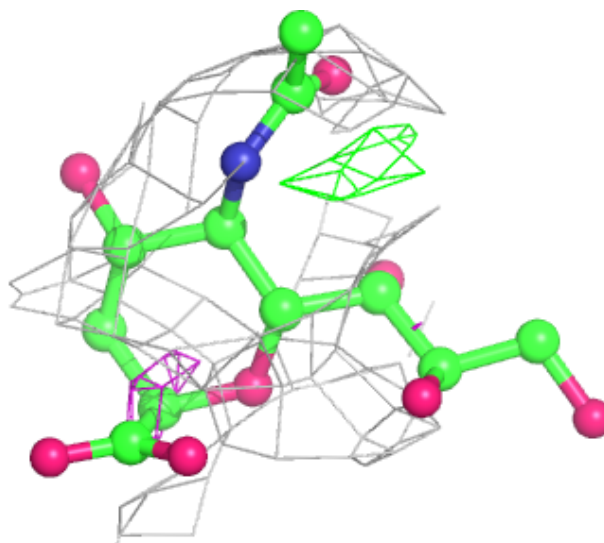
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	SIA	E	701	20/21	0.49	0.60	164,170,175,175	0
8	NAG	C	421	14/15	0.49	0.35	137,145,152,155	0
9	SIA	C	701	20/21	0.60	0.37	151,156,161,162	0
8	NAG	A	431	14/15	0.68	0.33	157,161,164,167	0
8	NAG	E	401	14/15	0.78	0.27	127,130,134,137	0
8	NAG	A	401	14/15	0.79	0.27	77,79,81,82	0
8	NAG	C	401	14/15	0.85	0.24	93,96,97,98	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.

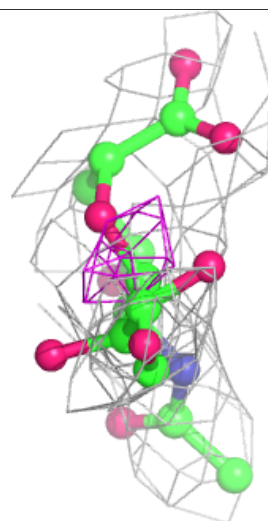
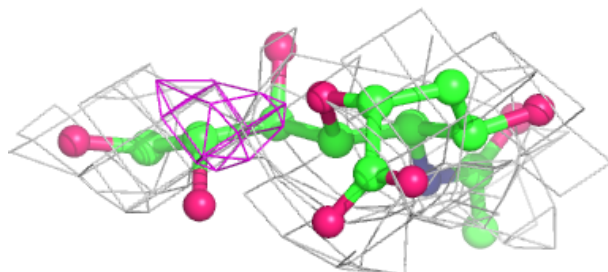
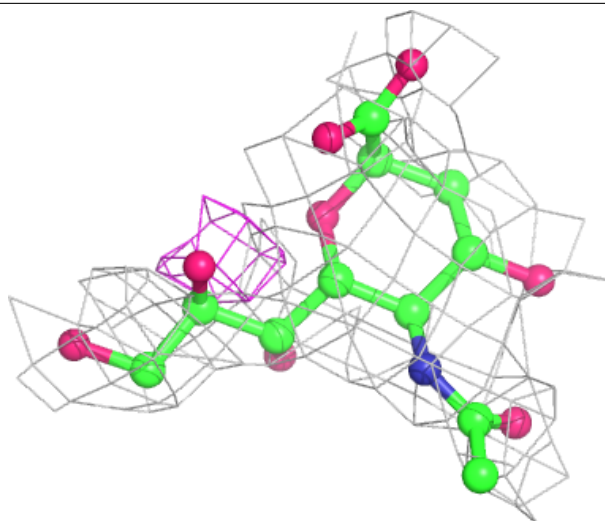
Electron density around SIA E 701:

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



Electron density around SIA C 701:

$2mF_o-DF_c$ (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.