



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 10:11 PM BST

PDB ID : 1RPQ
Title : High Affinity IgE Receptor (alpha chain) Complexed with Tight-Binding E131 'zeta' Peptide from Phage Display
Authors : Stamos, J.; Eigenbrot, C.; Nakamura, G.R.; Reynolds, M.E.; Yin, J.P.; Lowman, H.B.; Fairbrother, W.J.; Starovasnik, M.A.
Deposited on : 2003-12-03
Resolution : 3.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
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

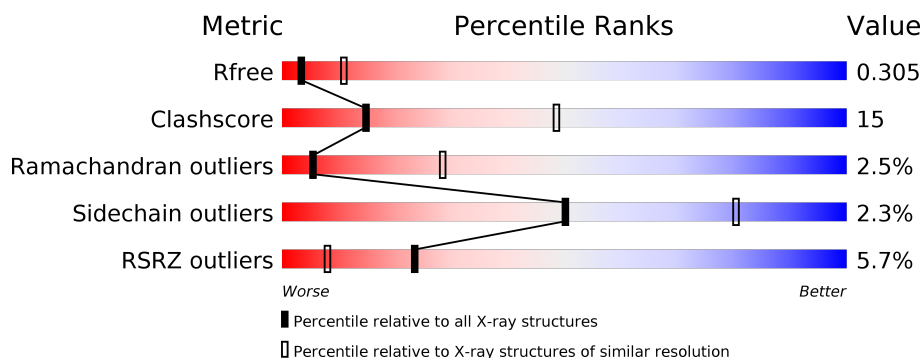
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	176	<div> <div>5%</div> <div> <div>68%</div> <div>25%</div> <div>6%</div> </div> </div>
1	B	176	<div> <div>6%</div> <div> <div>64%</div> <div>29%</div> <div>7%</div> </div> </div>
1	C	176	<div> <div>9%</div> <div> <div>61%</div> <div>31%</div> <div>6%</div> </div> </div>
1	D	176	<div> <div>3%</div> <div> <div>65%</div> <div>28%</div> <div>5%</div> </div> </div>
2	W	21	<div> <div>5%</div> <div> <div>86%</div> <div>14%</div> </div> </div>
2	X	21	<div> <div>62%</div> <div>38%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	Y	21	
2	Z	21	
3	E	3	
3	H	3	
4	F	5	
4	I	5	
4	L	5	
4	O	5	
5	G	3	
5	J	3	
5	M	3	
5	P	3	
6	K	2	
6	N	2	

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
4	BMA	I	3	-	-	-	X
4	BMA	I	4	-	-	-	X
4	BMA	I	5	-	-	-	X
4	BMA	L	3	-	-	X	-
4	BMA	L	5	-	-	-	X
4	BMA	O	4	-	-	-	X
4	BMA	O	5	-	-	-	X
5	NAG	G	2	-	-	-	X
5	BMA	G	3	-	-	-	X
5	NAG	J	2	-	-	-	X
5	BMA	J	3	-	-	-	X
5	NAG	M	2	-	-	-	X
5	BMA	M	3	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	P	2	-	-	-	X
5	BMA	P	3	-	-	-	X
6	NAG	N	2	-	-	-	X
7	NAG	A	340	X	-	-	-
7	NAG	B	340	X	-	-	-
7	NAG	C	340	X	-	-	X
7	NAG	D	340	X	-	-	X
8	SO4	A	401	-	-	-	X
9	CIT	C	403	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 6757 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.

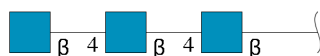
- Molecule 1 is a protein called High affinity immunoglobulin epsilon receptor alpha-subunit precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	165	Total	C	N	O	S	44	0	0
			1350	861	222	262	5			
1	B	164	Total	C	N	O	S	47	0	0
			1342	857	220	260	5			
1	C	166	Total	C	N	O	S	61	0	0
			1361	870	223	263	5			
1	D	167	Total	C	N	O	S	6	0	0
			1372	879	224	264	5			

- Molecule 2 is a protein called Peptide E131.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	W	21	Total	C	N	O	S	4	0	0
			175	114	24	33	4			
2	X	21	Total	C	N	O	S	0	0	0
			175	114	24	33	4			
2	Y	21	Total	C	N	O	S	0	0	0
			175	114	24	33	4			
2	Z	21	Total	C	N	O	S	0	0	0
			175	114	24	33	4			

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



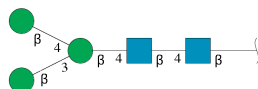
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	3	Total	C	N	O	0	0	0
			42	24	3	15			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	H	3	Total	C	N	O	0	0	0
			42	24	3	15			

- Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-4)]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	5	Total	C	N	O	0	0	0
			61	34	2	25			
4	I	5	Total	C	N	O	0	0	0
			61	34	2	25			
4	L	5	Total	C	N	O	0	0	0
			61	34	2	25			
4	O	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 5 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.



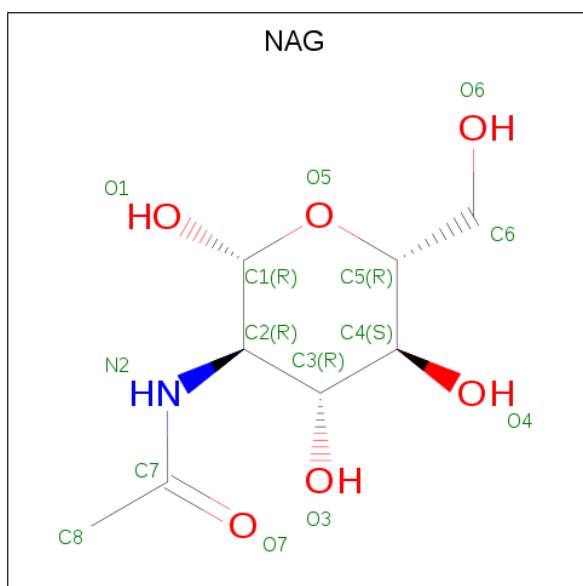
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	J	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	M	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	P	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 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
6	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
6	N	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



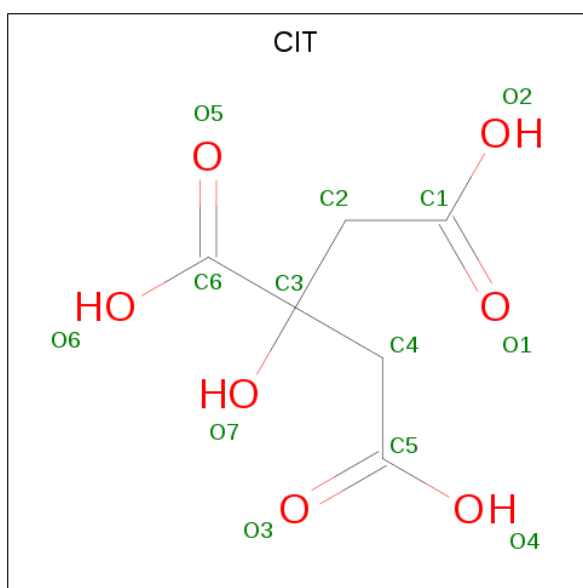
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	C	1	Total	C	N	O	0	0
			14	8	1	5		
7	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	3	0
			5	4	1		
8	Z	1	Total	O	S	4	0
			5	4	1		

- Molecule 9 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).

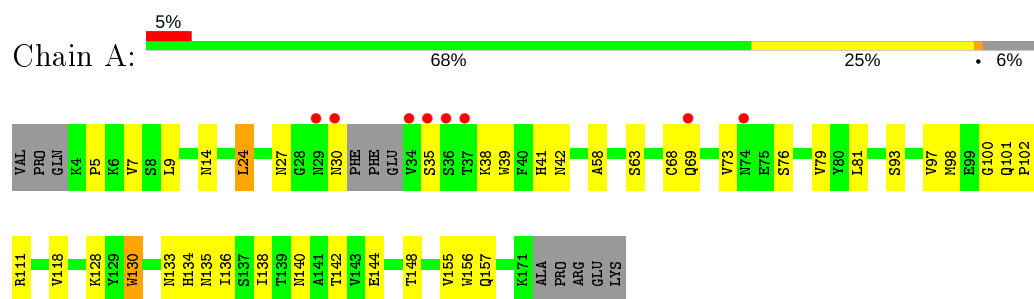


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	O	0	0
			13	6	7		
9	D	1	Total	C	O	0	0
			13	6	7		

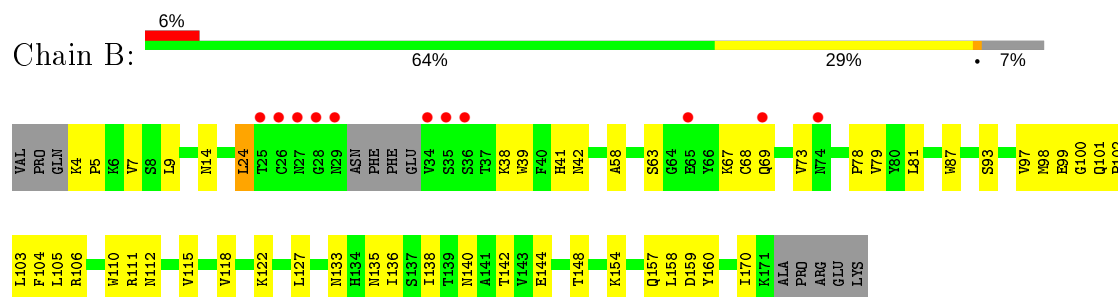
3 Residue-property plots [i](#)

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.

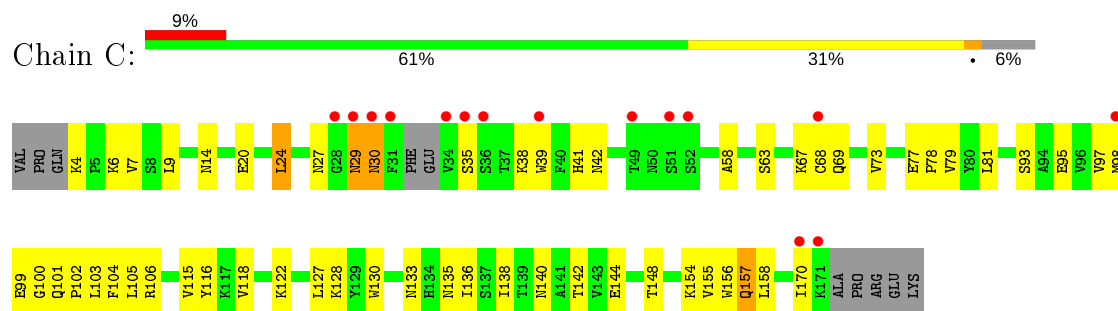
- Molecule 1: High affinity immunoglobulin epsilon receptor alpha-subunit precursor



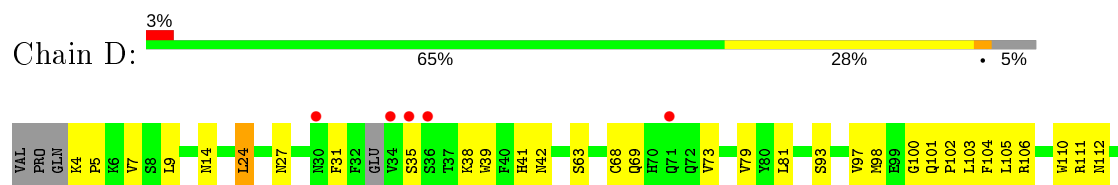
- Molecule 1: High affinity immunoglobulin epsilon receptor alpha-subunit precursor



- Molecule 1: High affinity immunoglobulin epsilon receptor alpha-subunit precursor

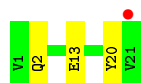
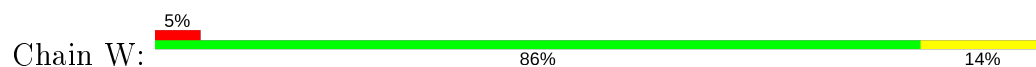


- Molecule 1: High affinity immunoglobulin epsilon receptor alpha-subunit precursor

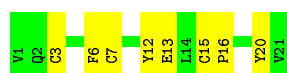




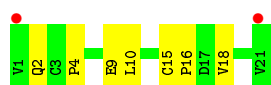
- Molecule 2: Peptide E131



- Molecule 2: Peptide E131



- Molecule 2: Peptide E131



- Molecule 2: Peptide E131



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

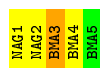


- Molecule 4: beta-D-mannopyranose-(1-3)-[beta-D-mannopyranose-(1-4)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

se

Chain F: 

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

Chain I: 

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

Chain L: 

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

Chain O: 

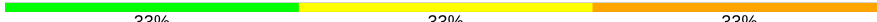
• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G: 

• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

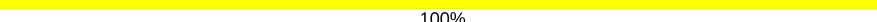
Chain J: 

• Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  33% 33% 33%


HA01
HA02
BO03

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain P:  100%

HA01
HA02
BO03

- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  50% 50%

HA01
HA02

- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%

HA01
HA02

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	199.70 Å 149.70 Å 104.10 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.00 30.02 – 3.01	Depositor EDS
% Data completeness (in resolution range)	96.5 (30.00-3.00) 97.2 (30.02-3.01)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 3.00 Å)	Xtriage
Refinement program	X-PLOR 98.1	Depositor
R, R_{free}	0.294 , 0.349 0.279 , 0.305	Depositor DCC
R_{free} test set	968 reflections (3.18%)	wwPDB-VP
Wilson B-factor (Å ²)	79.8	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 36.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	6757	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 9.70% 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: SO4, BMA, NAG, CIT

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	0.42	0/1387	0.60	0/1888
1	B	0.42	0/1379	0.64	0/1877
1	C	0.44	0/1399	0.63	0/1904
1	D	0.65	1/1411 (0.1%)	0.71	3/1920 (0.2%)
2	W	0.44	0/181	0.67	0/248
2	X	0.48	0/181	0.80	1/248 (0.4%)
2	Y	0.44	0/181	0.79	0/248
2	Z	0.49	0/181	0.74	0/248
All	All	0.49	1/6300 (0.0%)	0.66	4/8581 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	31	PHE	CB-CG	-18.18	1.20	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	31	PHE	CB-CG-CD1	-9.34	114.27	120.80
1	D	31	PHE	CA-CB-CG	9.09	135.71	113.90
1	D	31	PHE	CB-CG-CD2	8.20	126.54	120.80
2	X	15	CYS	CA-CB-SG	-5.27	104.52	114.00

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	1350	0	1265	33	0
1	B	1342	0	1259	34	0
1	C	1361	0	1273	48	0
1	D	1372	0	1283	37	0
2	W	175	0	152	1	0
2	X	175	0	152	4	0
2	Y	175	0	152	4	0
2	Z	175	0	152	7	0
3	E	42	0	37	3	0
3	H	42	0	37	3	0
4	F	61	0	52	6	0
4	I	61	0	52	2	0
4	L	61	0	52	8	0
4	O	61	0	52	4	0
5	G	39	0	34	0	0
5	J	39	0	34	1	0
5	M	39	0	34	1	0
5	P	39	0	34	5	0
6	K	28	0	25	2	0
6	N	28	0	25	0	0
7	A	14	0	13	0	0
7	B	14	0	13	0	0
7	C	14	0	13	0	0
7	D	14	0	13	0	0
8	A	5	0	0	0	0
8	Z	5	0	0	0	0
9	C	13	0	5	5	0
9	D	13	0	5	3	0
All	All	6757	0	6218	192	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 15.

The worst 5 of 192 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)
4:L:3:BMA:H61	4:L:5:BMA:O5	1.62	0.99
2:Z:6:PHE:HA	2:Z:9:GLU:HG2	1.42	0.99
3:E:2:NAG:H61	3:E:3:NAG:O5	1.67	0.95
4:O:3:BMA:H2	4:O:4:BMA:H2	1.50	0.91
4:O:3:BMA:C2	4:O:4:BMA:H2	2.10	0.82

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	161/176 (92%)	147 (91%)	9 (6%)	5 (3%)	4	23
1	B	160/176 (91%)	146 (91%)	12 (8%)	2 (1%)	12	45
1	C	162/176 (92%)	150 (93%)	7 (4%)	5 (3%)	4	23
1	D	163/176 (93%)	150 (92%)	10 (6%)	3 (2%)	8	37
2	W	19/21 (90%)	15 (79%)	4 (21%)	0	100	100
2	X	19/21 (90%)	16 (84%)	2 (10%)	1 (5%)	2	11
2	Y	19/21 (90%)	11 (58%)	7 (37%)	1 (5%)	2	11
2	Z	19/21 (90%)	18 (95%)	0	1 (5%)	2	11
All	All	722/788 (92%)	653 (90%)	51 (7%)	18 (2%)	5	28

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	27	ASN
1	A	27	ASN
2	Y	2	GLN
1	C	29	ASN
1	A	35	SER

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	151/161 (94%)	148 (98%)	3 (2%)	55	83
1	B	150/161 (93%)	146 (97%)	4 (3%)	44	77
1	C	152/161 (94%)	149 (98%)	3 (2%)	55	83
1	D	153/161 (95%)	148 (97%)	5 (3%)	38	73
2	W	21/21 (100%)	20 (95%)	1 (5%)	25	62
2	X	21/21 (100%)	21 (100%)	0	100	100
2	Y	21/21 (100%)	21 (100%)	0	100	100
2	Z	21/21 (100%)	21 (100%)	0	100	100
All	All	690/728 (95%)	674 (98%)	16 (2%)	50	80

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	24	LEU
1	C	148	THR
1	D	129	TYR
1	B	159	ASP
1	D	148	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	135	ASN
1	C	29	ASN
1	D	41	HIS
1	B	101	GLN
1	D	135	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 ⓘ

42 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	E	1	1,3	14,14,15	0.73	0	17,19,21	1.08	1 (5%)
3	NAG	E	2	3	14,14,15	0.78	1 (7%)	17,19,21	1.02	1 (5%)
3	NAG	E	3	3	14,14,15	0.58	0	17,19,21	0.79	0
4	NAG	F	1	1,4	14,14,15	0.46	0	17,19,21	0.74	0
4	NAG	F	2	4	14,14,15	0.67	0	17,19,21	1.63	2 (11%)
4	BMA	F	3	4	11,11,12	0.90	1 (9%)	15,15,17	1.67	3 (20%)
4	BMA	F	4	4	11,11,12	0.51	0	15,15,17	0.36	0
4	BMA	F	5	4	11,11,12	0.44	0	15,15,17	0.33	0
5	NAG	G	1	1,5	14,14,15	0.58	0	17,19,21	0.77	0
5	NAG	G	2	5	14,14,15	0.38	0	17,19,21	0.72	0
5	BMA	G	3	5	11,11,12	0.36	0	15,15,17	0.26	0
3	NAG	H	1	1,3	14,14,15	0.57	0	17,19,21	1.00	2 (11%)
3	NAG	H	2	3	14,14,15	0.61	0	17,19,21	0.73	0
3	NAG	H	3	3	14,14,15	0.54	0	17,19,21	0.68	0
4	NAG	I	1	1,4	14,14,15	0.63	0	17,19,21	0.91	1 (5%)
4	NAG	I	2	4	14,14,15	0.70	0	17,19,21	1.97	4 (23%)
4	BMA	I	3	4	11,11,12	0.53	0	15,15,17	1.15	1 (6%)
4	BMA	I	4	4	11,11,12	0.41	0	15,15,17	0.59	0
4	BMA	I	5	4	11,11,12	0.35	0	15,15,17	0.48	0
5	NAG	J	1	1,5	14,14,15	0.63	0	17,19,21	0.67	0
5	NAG	J	2	5	14,14,15	0.47	0	17,19,21	0.60	0
5	BMA	J	3	5	11,11,12	0.35	0	15,15,17	0.44	0
6	NAG	K	1	1,6	14,14,15	0.62	0	17,19,21	0.79	1 (5%)
6	NAG	K	2	6	14,14,15	0.39	0	17,19,21	0.63	0
4	NAG	L	1	1,4	14,14,15	0.56	0	17,19,21	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	L	2	4	14,14,15	0.70	0	17,19,21	2.00	3 (17%)
4	BMA	L	3	4	11,11,12	0.70	0	15,15,17	1.01	1 (6%)
4	BMA	L	4	4	11,11,12	0.56	0	15,15,17	0.64	1 (6%)
4	BMA	L	5	4	11,11,12	0.51	0	15,15,17	0.39	0
5	NAG	M	1	1,5	14,14,15	0.67	0	17,19,21	1.07	2 (11%)
5	NAG	M	2	5	14,14,15	0.64	0	17,19,21	0.64	0
5	BMA	M	3	5	11,11,12	0.38	0	15,15,17	0.25	0
6	NAG	N	1	1,6	14,14,15	0.63	0	17,19,21	0.72	0
6	NAG	N	2	6	14,14,15	0.55	0	17,19,21	0.67	0
4	NAG	O	1	1,4	14,14,15	0.54	0	17,19,21	0.86	0
4	NAG	O	2	4	14,14,15	0.81	0	17,19,21	1.99	3 (17%)
4	BMA	O	3	4	11,11,12	0.59	0	15,15,17	1.11	2 (13%)
4	BMA	O	4	4	11,11,12	0.40	0	15,15,17	0.45	0
4	BMA	O	5	4	11,11,12	0.35	0	15,15,17	0.36	0
5	NAG	P	1	1,5	14,14,15	0.72	0	17,19,21	0.70	0
5	NAG	P	2	5	14,14,15	0.49	0	17,19,21	0.63	0
5	BMA	P	3	5	11,11,12	0.37	0	15,15,17	0.30	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	E	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	3/6/23/26	0/1/1/1
3	NAG	E	3	3	-	2/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	2/2/19/22	0/1/1/1
4	BMA	F	4	4	-	0/2/19/22	0/1/1/1
4	BMA	F	5	4	-	2/2/19/22	0/1/1/1
5	NAG	G	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	NAG	H	3	3	-	1/6/23/26	0/1/1/1
4	NAG	I	1	1,4	-	2/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	I	2	4	-	1/6/23/26	0/1/1/1
4	BMA	I	3	4	-	2/2/19/22	0/1/1/1
4	BMA	I	4	4	-	0/2/19/22	0/1/1/1
4	BMA	I	5	4	-	0/2/19/22	0/1/1/1
5	NAG	J	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	J	2	5	-	1/6/23/26	0/1/1/1
5	BMA	J	3	5	-	2/2/19/22	0/1/1/1
6	NAG	K	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	K	2	6	-	0/6/23/26	0/1/1/1
4	NAG	L	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	L	2	4	-	2/6/23/26	0/1/1/1
4	BMA	L	3	4	-	0/2/19/22	0/1/1/1
4	BMA	L	4	4	-	2/2/19/22	0/1/1/1
4	BMA	L	5	4	-	0/2/19/22	0/1/1/1
5	NAG	M	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	M	2	5	-	2/6/23/26	0/1/1/1
5	BMA	M	3	5	-	2/2/19/22	0/1/1/1
6	NAG	N	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	N	2	6	-	2/6/23/26	0/1/1/1
4	NAG	O	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	O	2	4	-	0/6/23/26	0/1/1/1
4	BMA	O	3	4	-	2/2/19/22	0/1/1/1
4	BMA	O	4	4	-	2/2/19/22	0/1/1/1
4	BMA	O	5	4	-	2/2/19/22	0/1/1/1
5	NAG	P	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	P	2	5	-	2/6/23/26	0/1/1/1
5	BMA	P	3	5	-	0/2/19/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	3	BMA	C1-C2	2.36	1.57	1.52
3	E	2	NAG	C4-C5	2.02	1.57	1.53

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	2	NAG	C4-C3-C2	-6.56	101.41	111.02

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	O	2	NAG	C4-C3-C2	-6.46	101.56	111.02
4	I	2	NAG	C4-C3-C2	-6.44	101.58	111.02
4	F	2	NAG	C4-C3-C2	-5.10	103.54	111.02
4	F	3	BMA	C1-C2-C3	5.00	115.82	109.67

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

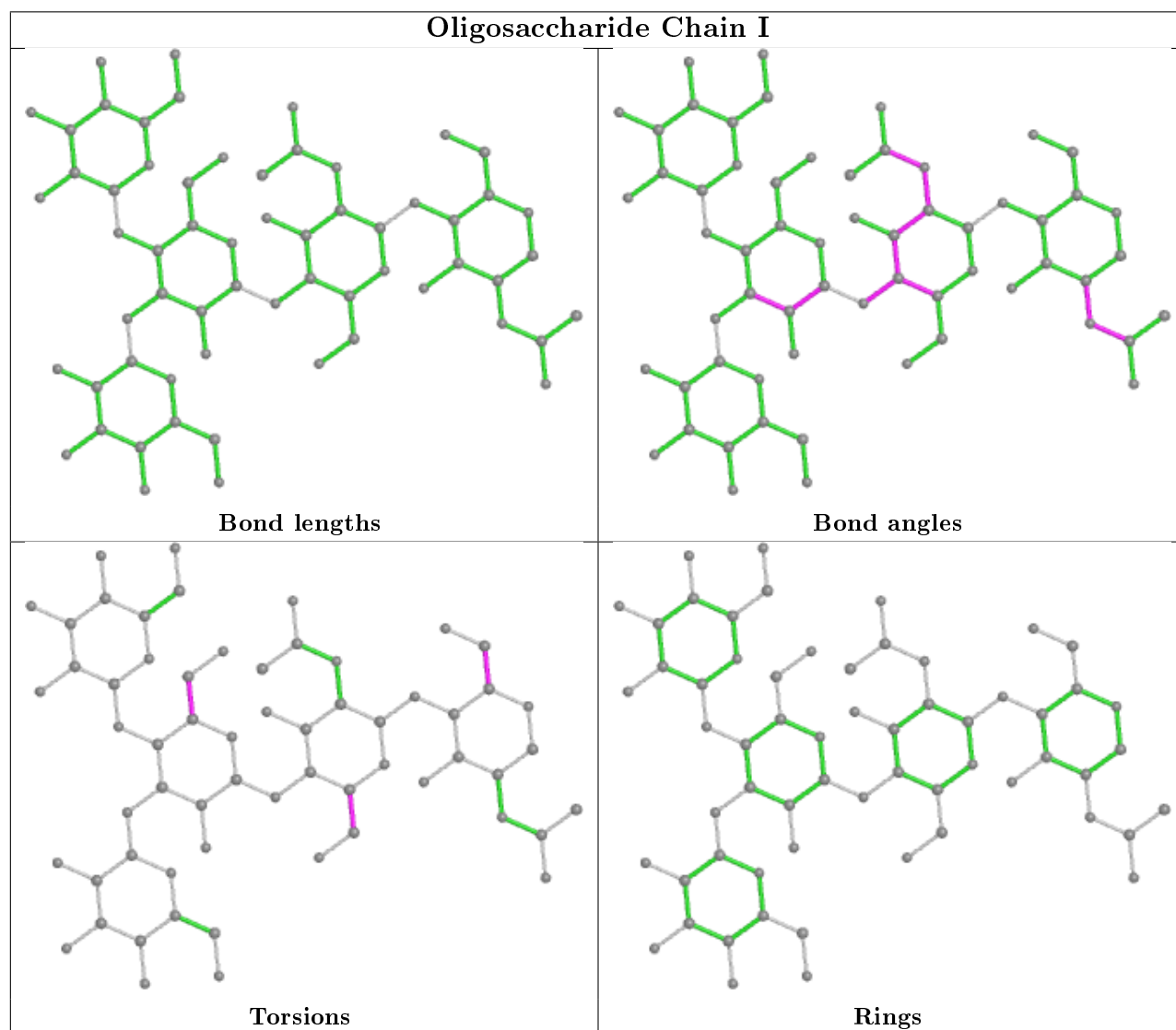
Mol	Chain	Res	Type	Atoms
3	H	3	NAG	C3-C2-N2-C7
4	O	3	BMA	C4-C5-C6-O6
5	M	2	NAG	O5-C5-C6-O6
4	L	4	BMA	C4-C5-C6-O6
4	O	3	BMA	O5-C5-C6-O6

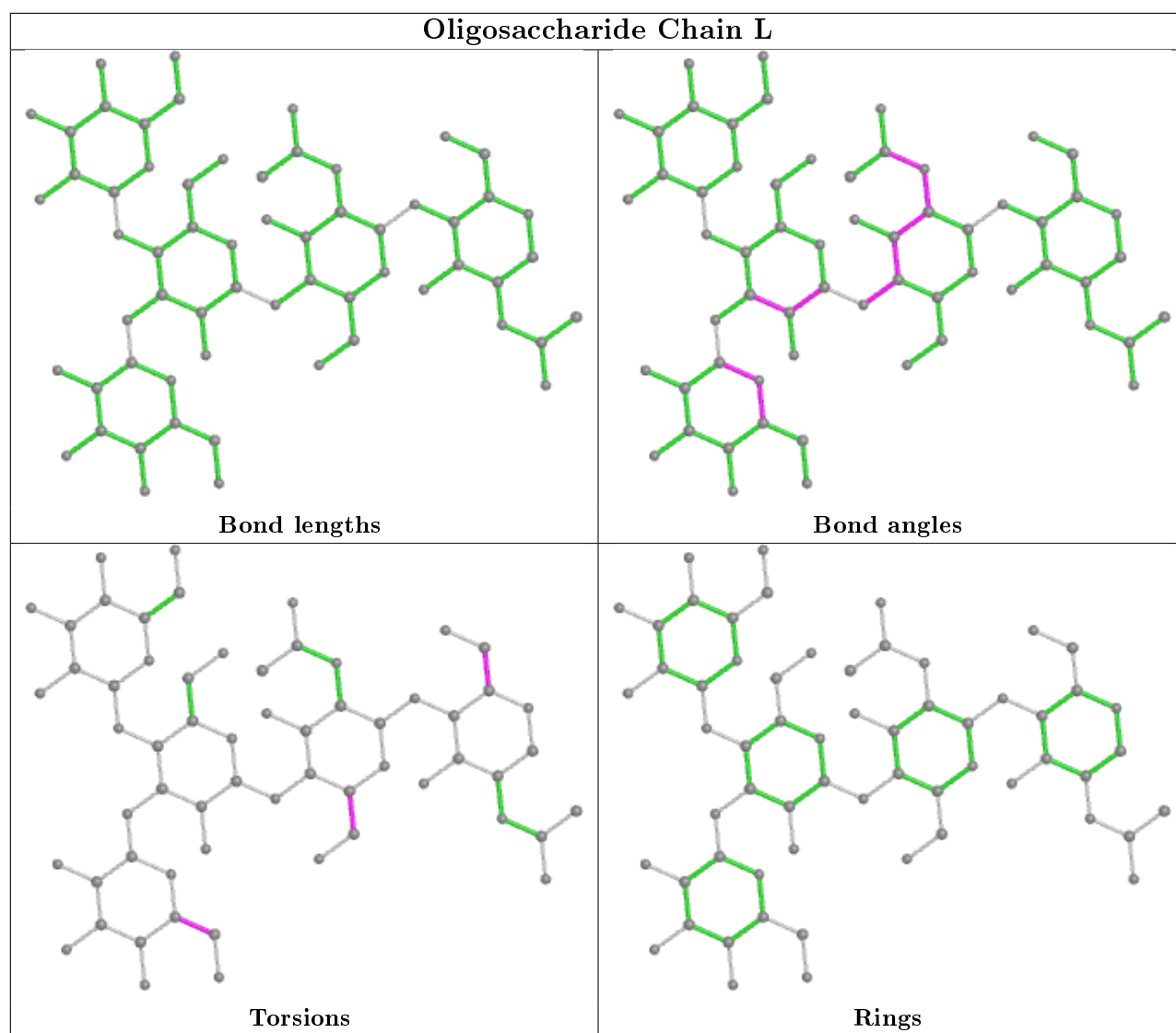
There are no ring outliers.

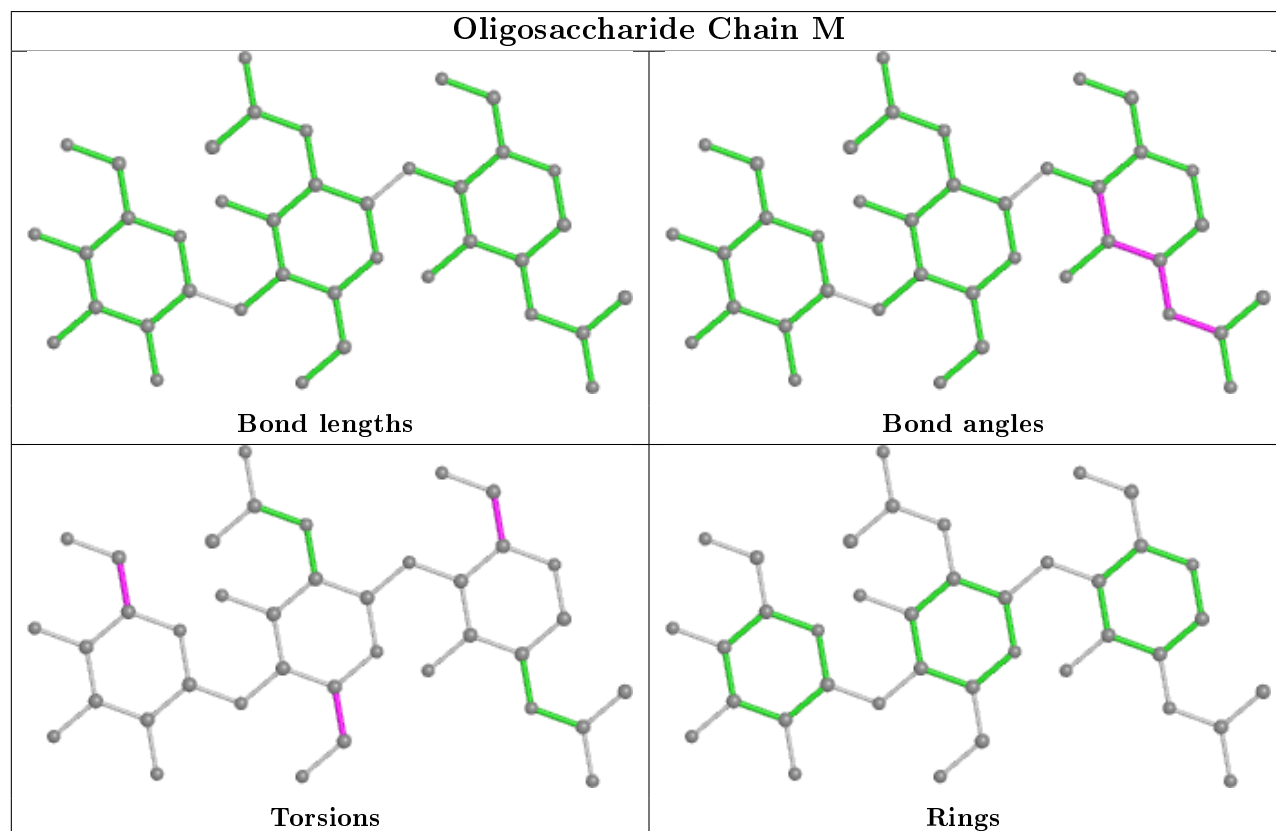
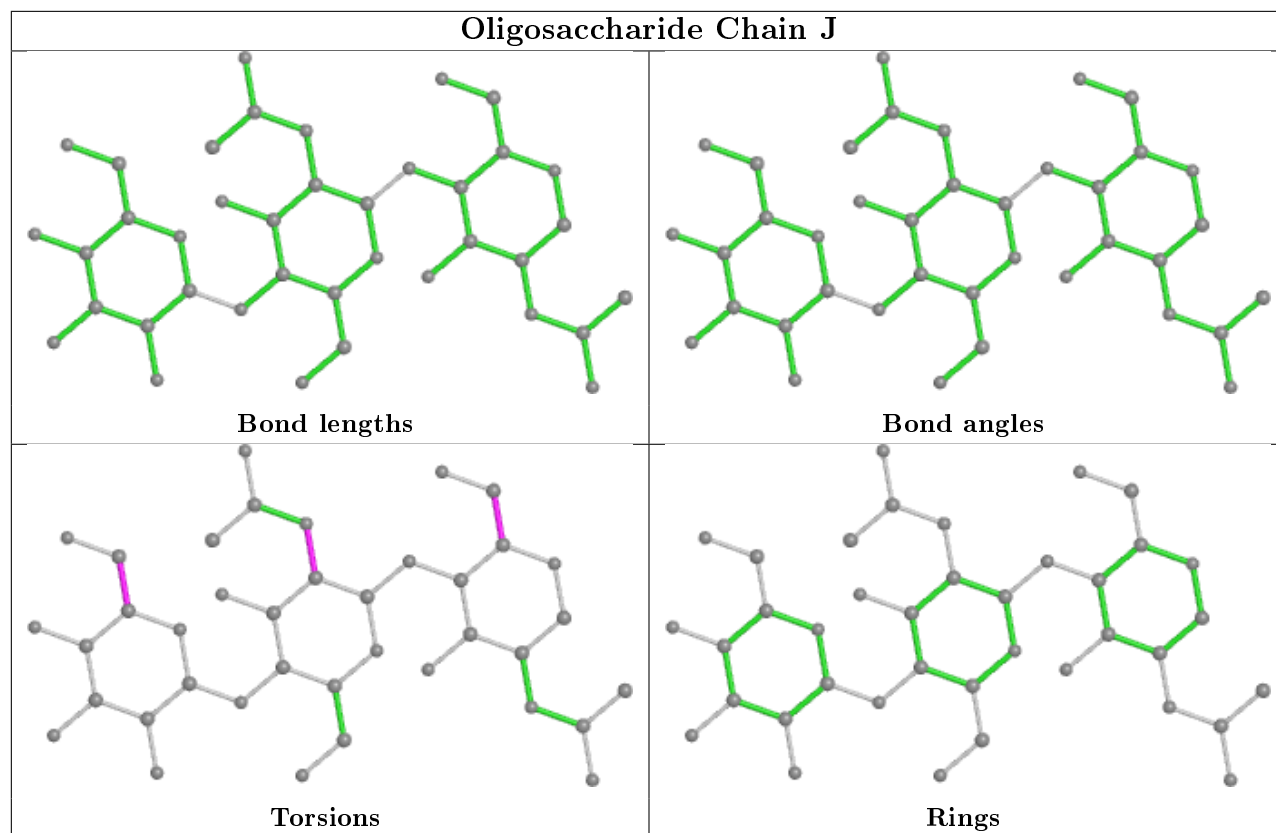
23 monomers are involved in 35 short contacts:

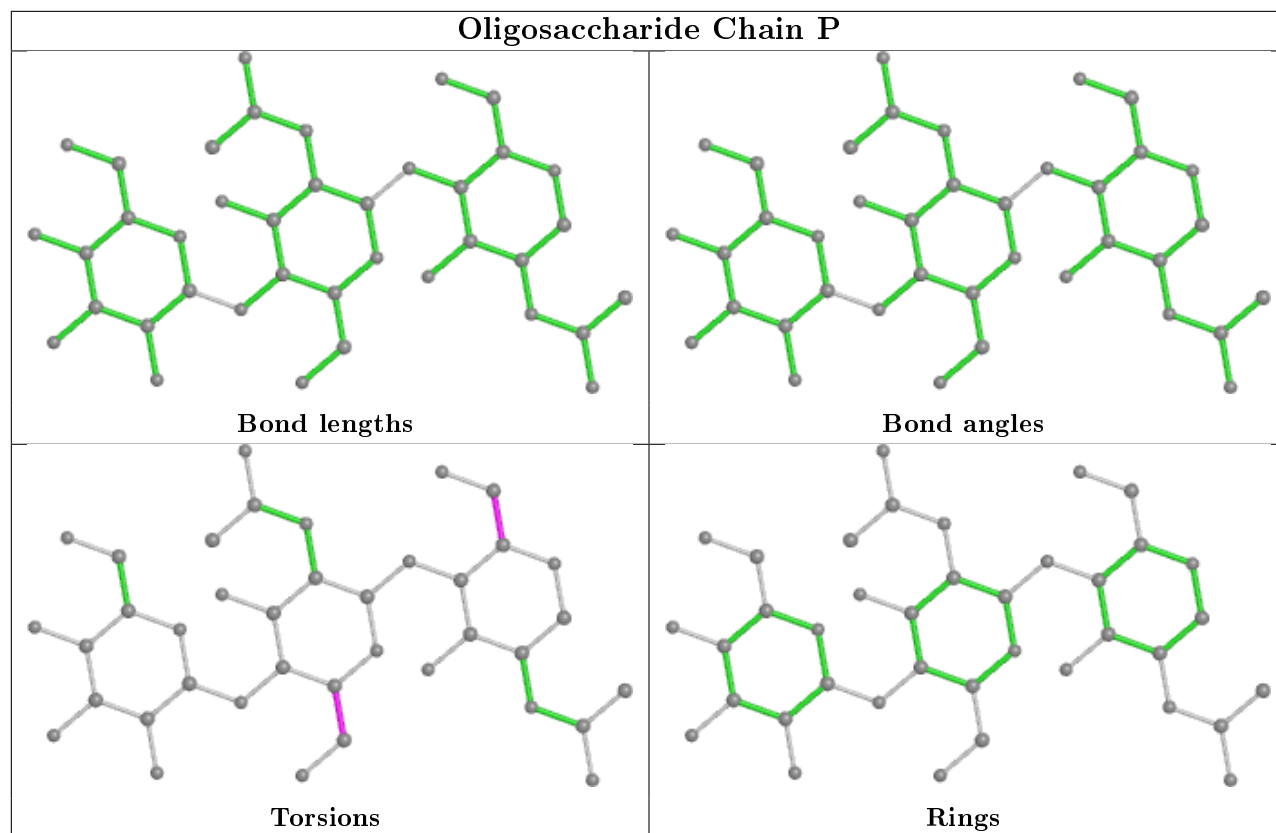
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	1	NAG	1	0
4	F	5	BMA	5	0
6	K	1	NAG	2	0
4	O	3	BMA	3	0
5	P	1	NAG	4	0
4	I	4	BMA	2	0
5	M	2	NAG	1	0
3	H	3	NAG	3	0
5	P	3	BMA	1	0
4	O	1	NAG	1	0
3	E	2	NAG	3	0
6	K	2	NAG	1	0
3	E	3	NAG	3	0
4	I	3	BMA	2	0
4	O	4	BMA	3	0
4	L	2	NAG	2	0
4	F	3	BMA	5	0
5	J	2	NAG	1	0
4	L	3	BMA	6	0
4	L	1	NAG	2	0
5	P	2	NAG	4	0
4	L	5	BMA	5	0
4	F	1	NAG	1	0

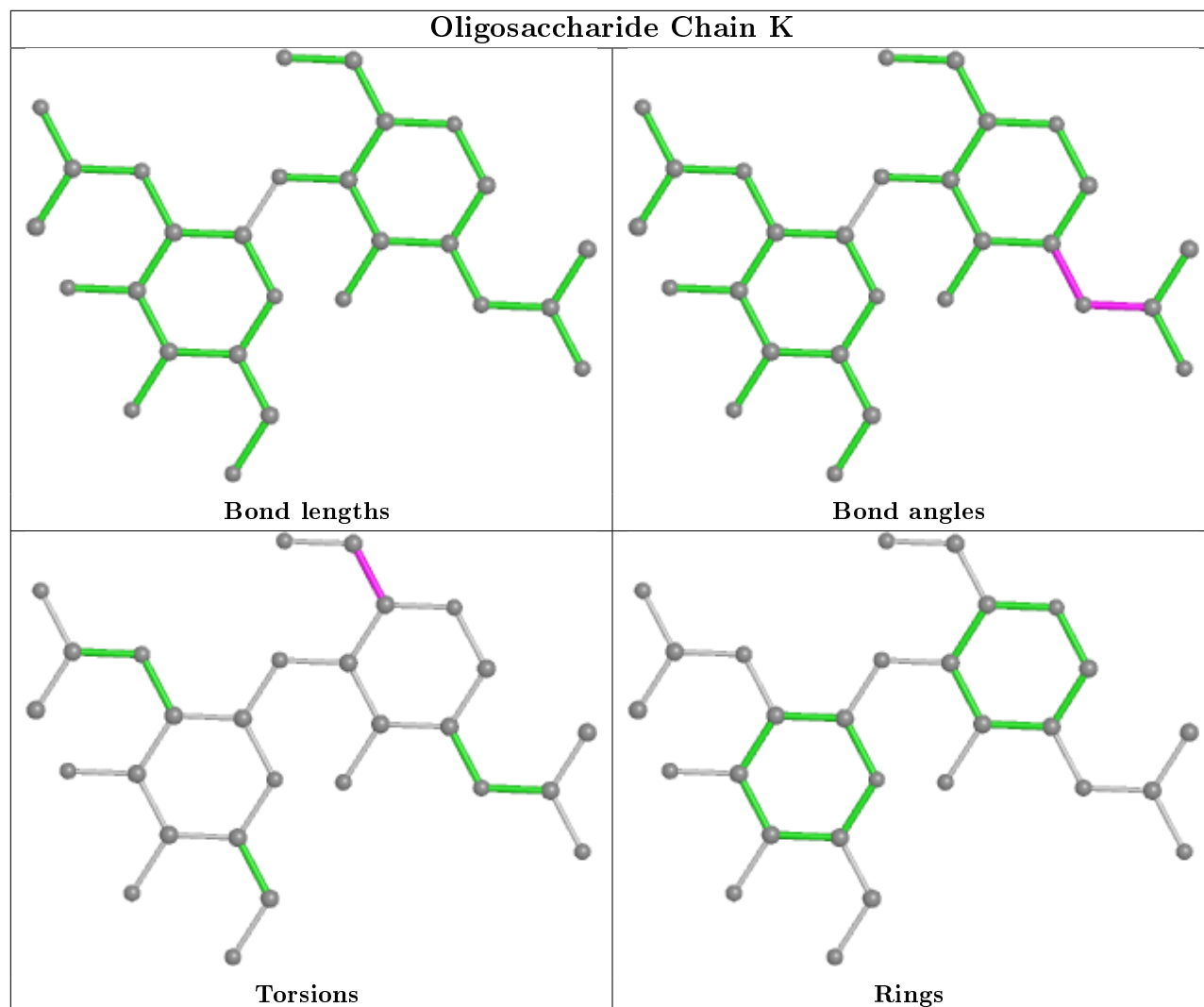
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

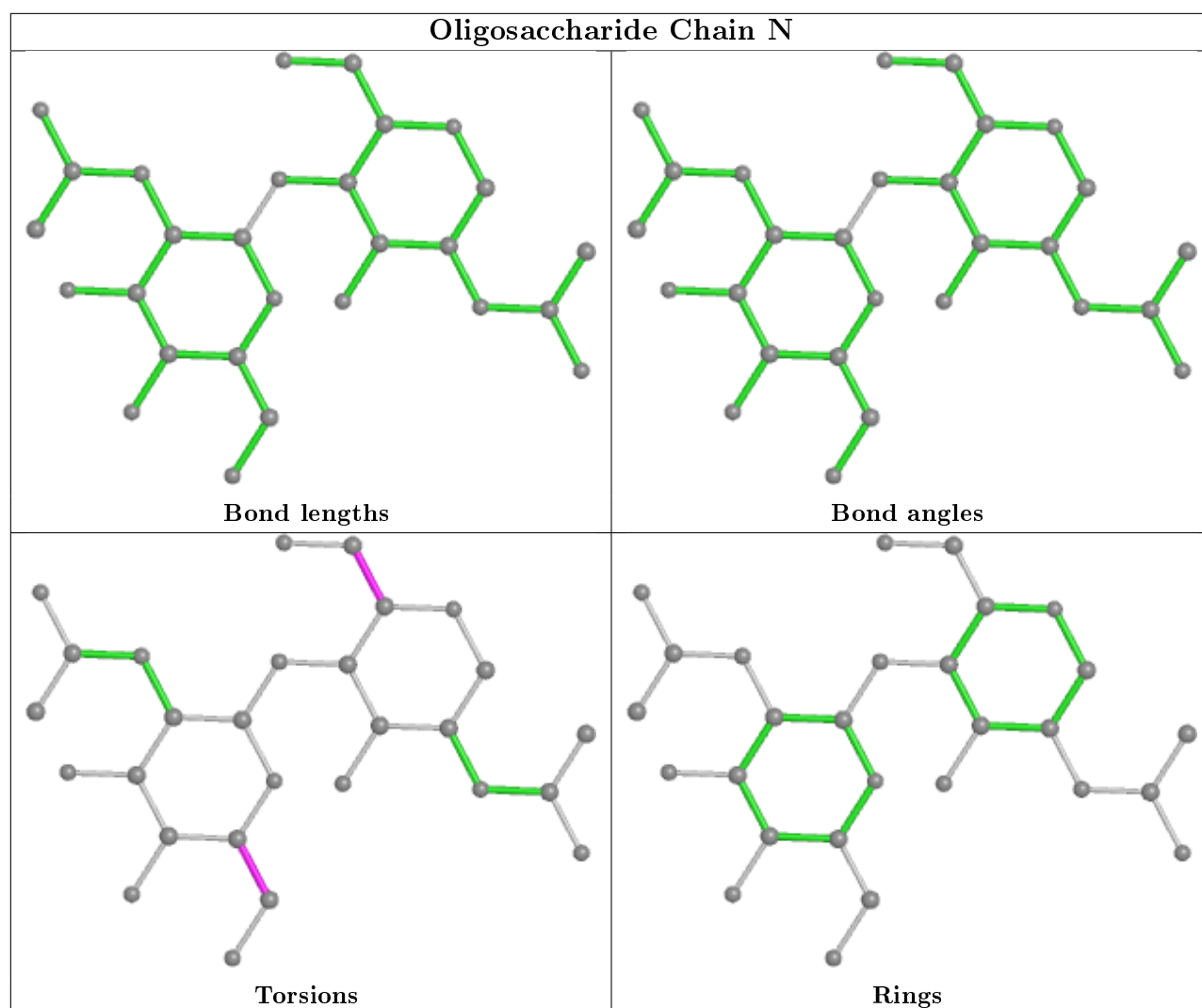


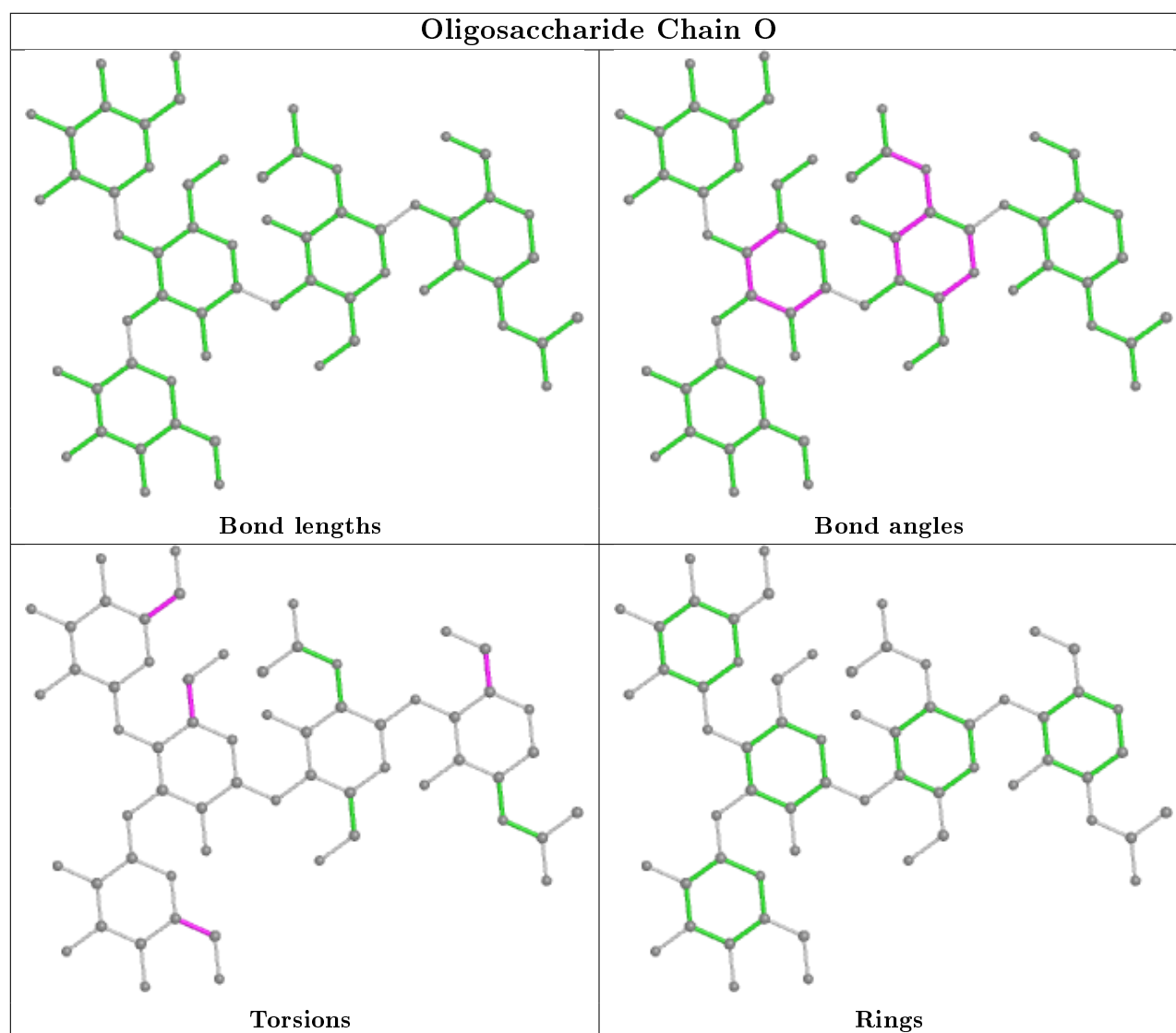












5.6 Ligand geometry [i](#)

8 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	$\# Z > 2$
8	SO4	Z	402	-	4,4,4	0.18	0	6,6,6	0.16	0
8	SO4	A	401	-	4,4,4	0.23	0	6,6,6	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	CIT	D	404	-	3,12,12	1.39	1 (33%)	3,17,17	1.94	1 (33%)
7	NAG	D	340	1	14,14,15	0.39	0	17,19,21	0.77	1 (5%)
7	NAG	C	340	1	14,14,15	0.41	0	17,19,21	0.67	0
9	CIT	C	403	-	3,12,12	1.18	0	3,17,17	1.74	1 (33%)
7	NAG	B	340	1	14,14,15	0.53	0	17,19,21	0.72	1 (5%)
7	NAG	A	340	1	14,14,15	0.67	0	17,19,21	0.85	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
9	CIT	D	404	-	-	1/6/16/16	-
7	NAG	D	340	1	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	C	340	1	1/1/5/7	0/6/23/26	0/1/1/1
9	CIT	C	403	-	-	3/6/16/16	-
7	NAG	B	340	1	1/1/5/7	2/6/23/26	0/1/1/1
7	NAG	A	340	1	1/1/5/7	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	D	404	CIT	O7-C3	2.23	1.46	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	D	404	CIT	C3-C2-C1	3.30	120.27	114.98
9	C	403	CIT	C3-C2-C1	2.96	119.72	114.98
7	B	340	NAG	C2-N2-C7	-2.28	119.66	122.90
7	D	340	NAG	C2-N2-C7	-2.09	119.92	122.90

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	C	340	NAG	C1
7	D	340	NAG	C1
7	B	340	NAG	C1
7	A	340	NAG	C1

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	C	403	CIT	C1-C2-C3-O7
9	C	403	CIT	C1-C2-C3-C4
9	C	403	CIT	C1-C2-C3-C6
7	B	340	NAG	C4-C5-C6-O6
7	A	340	NAG	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	D	404	CIT	3	0
9	C	403	CIT	5	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	161/176 (91%)	-0.02	8 (4%) 28 10	29, 62, 111, 118	8 (4%)
1	B	160/176 (90%)	0.02	11 (6%) 16 5	34, 64, 110, 117	7 (4%)
1	C	162/176 (92%)	0.12	15 (9%) 8 3	32, 66, 110, 114	11 (6%)
1	D	167/176 (94%)	0.00	5 (2%) 50 22	31, 65, 111, 116	8 (4%)
2	W	21/21 (100%)	-0.14	1 (4%) 30 11	50, 66, 92, 96	1 (4%)
2	X	21/21 (100%)	-0.17	0 100 100	50, 67, 93, 94	0
2	Y	21/21 (100%)	0.10	2 (9%) 8 3	48, 65, 93, 98	0
2	Z	21/21 (100%)	-0.25	0 100 100	49, 68, 92, 99	0
All	All	734/788 (93%)	0.01	42 (5%) 23 8	29, 65, 110, 118	35 (4%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	34	VAL	17.1
1	D	35	SER	13.2
1	C	34	VAL	12.8
1	D	34	VAL	9.5
1	C	35	SER	8.2

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.

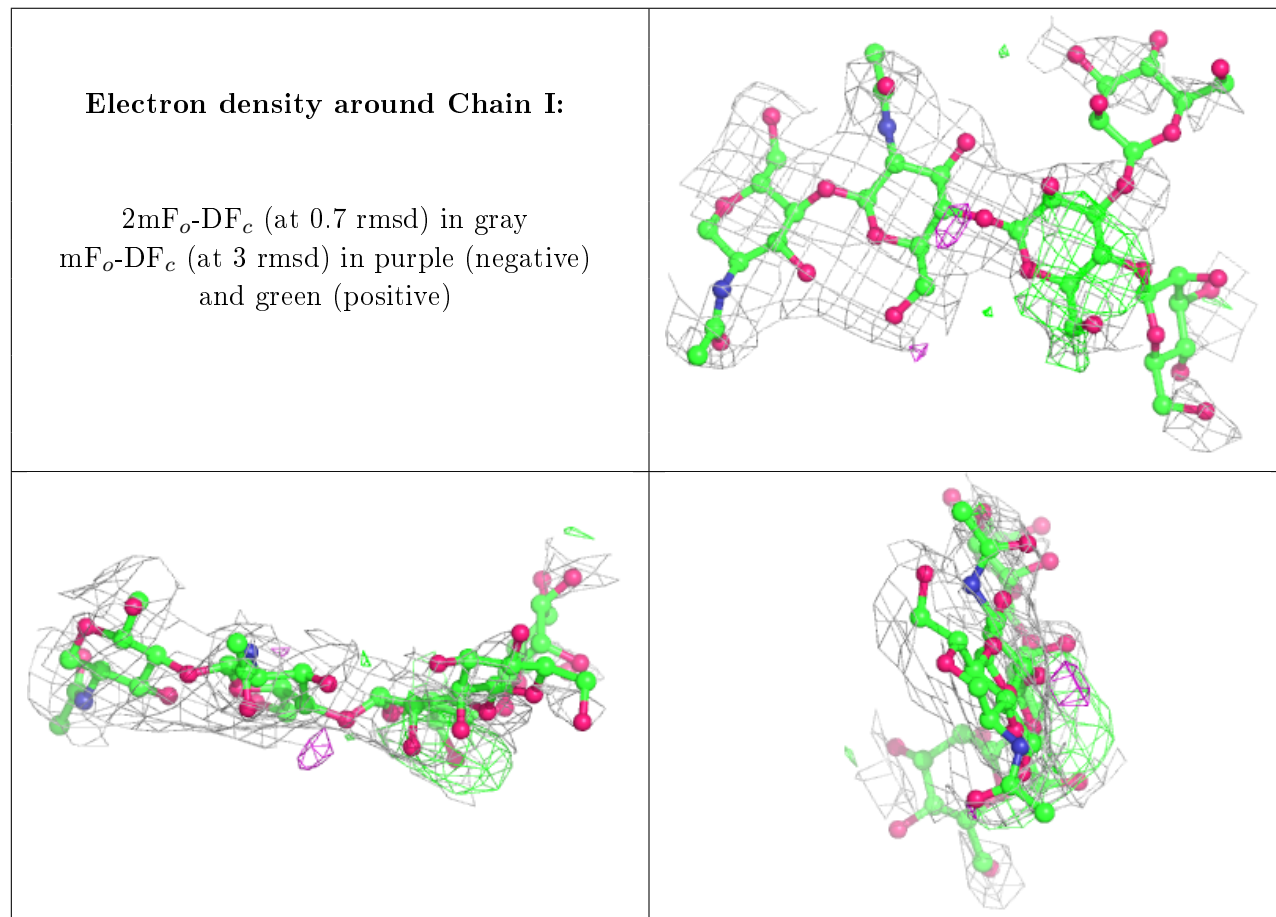
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	BMA	I	5	11/12	-0.12	1.13	50,51,52,53	11
5	BMA	J	3	11/12	0.07	1.16	64,66,67,67	11
5	BMA	M	3	11/12	0.21	1.26	67,67,68,68	11
5	BMA	P	3	11/12	0.25	0.87	70,71,71,72	11
4	BMA	F	5	11/12	0.25	0.34	78,85,86,86	11
5	BMA	G	3	11/12	0.25	0.72	52,54,55,56	11
5	NAG	M	2	14/15	0.33	0.59	70,74,76,76	14
4	BMA	L	5	11/12	0.36	0.47	88,93,95,95	11
5	NAG	P	2	14/15	0.48	0.71	70,73,75,76	14
4	BMA	I	3	11/12	0.50	0.62	46,51,54,56	11
4	BMA	I	4	11/12	0.52	0.55	36,39,41,42	11
5	NAG	G	2	14/15	0.56	0.45	53,57,61,62	14
4	BMA	O	4	11/12	0.58	0.49	59,62,64,65	11
5	NAG	J	2	14/15	0.60	0.55	59,65,65,66	14
4	BMA	O	5	11/12	0.61	0.52	64,67,69,69	11
4	BMA	F	4	11/12	0.63	0.35	56,61,63,65	11
6	NAG	N	2	14/15	0.69	0.47	89,89,91,91	14
4	BMA	F	3	11/12	0.71	0.31	71,79,87,89	0
3	NAG	H	3	14/15	0.74	0.29	41,46,48,49	14
4	BMA	L	3	11/12	0.75	0.32	88,92,97,97	0
3	NAG	E	3	14/15	0.76	0.26	72,79,85,91	0
4	BMA	L	4	11/12	0.77	0.23	96,101,102,102	0
5	NAG	M	1	14/15	0.78	0.30	75,81,84,84	14
5	NAG	G	1	14/15	0.79	0.23	69,75,77,78	0
6	NAG	K	2	14/15	0.80	0.38	95,96,97,97	14
4	BMA	O	3	11/12	0.80	0.20	71,73,75,76	0
5	NAG	J	1	14/15	0.81	0.23	68,75,85,86	14
5	NAG	P	1	14/15	0.81	0.37	80,84,85,85	14
6	NAG	N	1	14/15	0.86	0.17	82,88,94,97	0
3	NAG	H	1	14/15	0.87	0.24	61,76,82,82	0
3	NAG	E	2	14/15	0.88	0.23	60,75,81,82	0
4	NAG	O	2	14/15	0.89	0.21	64,70,79,80	0
4	NAG	L	2	14/15	0.90	0.21	67,71,76,80	0
3	NAG	E	1	14/15	0.90	0.23	72,76,83,83	0
4	NAG	L	1	14/15	0.91	0.14	51,55,59,62	0
3	NAG	H	2	14/15	0.91	0.26	44,49,52,53	14
4	NAG	I	2	14/15	0.92	0.19	63,69,79,80	0
6	NAG	K	1	14/15	0.92	0.16	92,96,100,101	0
4	NAG	F	2	14/15	0.92	0.25	55,61,63,71	0
4	NAG	I	1	14/15	0.94	0.15	59,61,69,69	0

Continued on next page...

Continued from previous page...

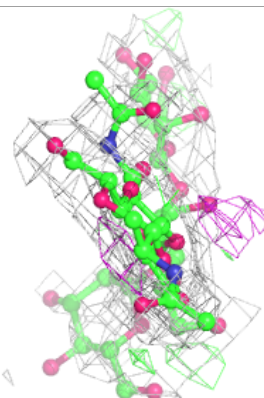
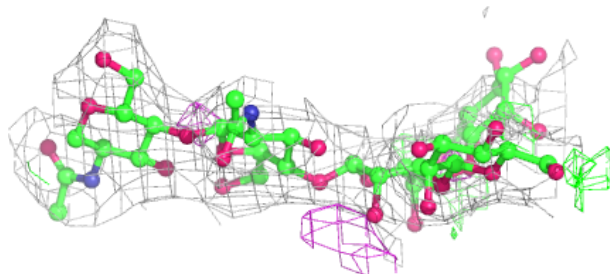
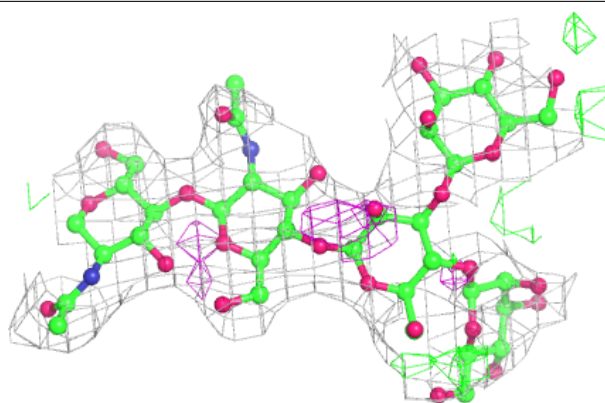
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	NAG	O	1	14/15	0.96	0.19	60,62,67,69	0
4	NAG	F	1	14/15	0.97	0.18	53,55,63,66	0

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.

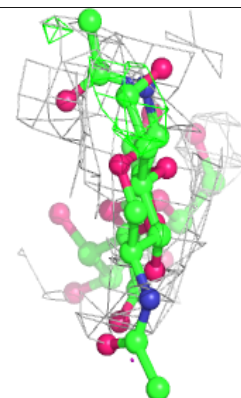
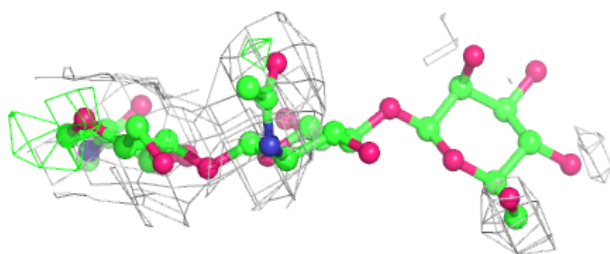
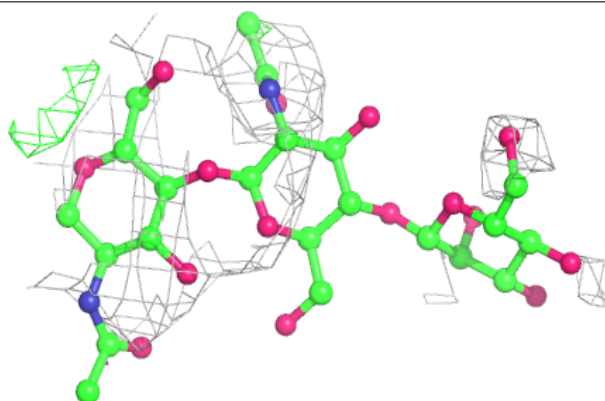


Electron density around Chain L:

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

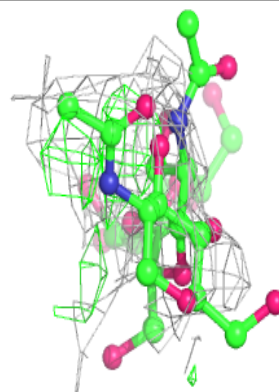
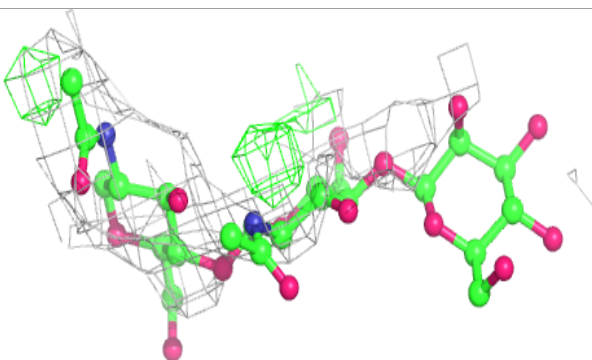
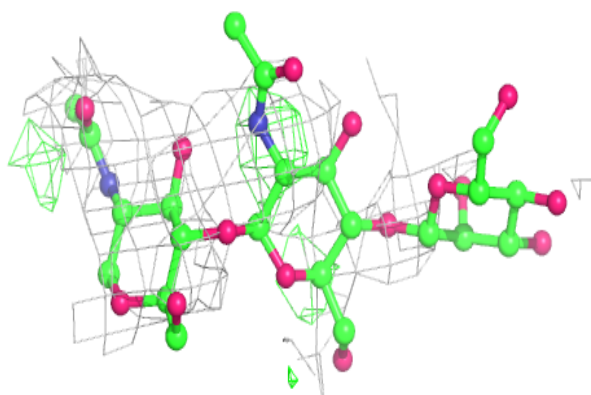
**Electron density around Chain J:**

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

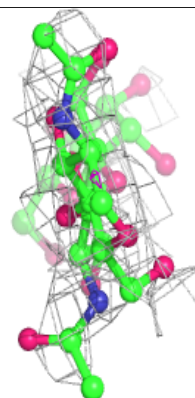
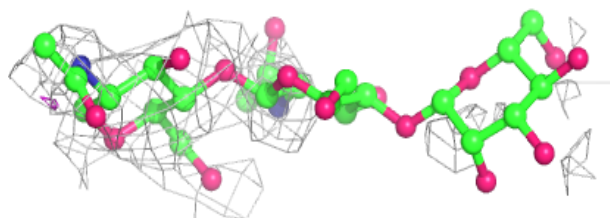
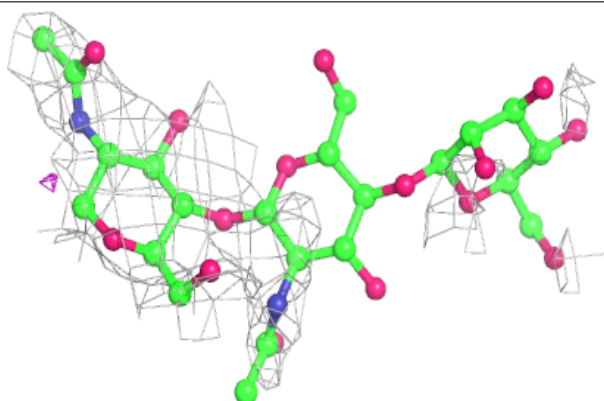


Electron density around Chain M:

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

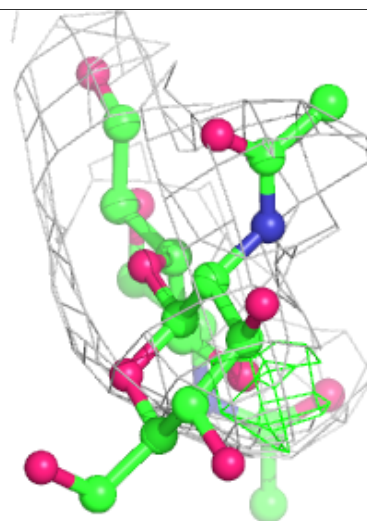
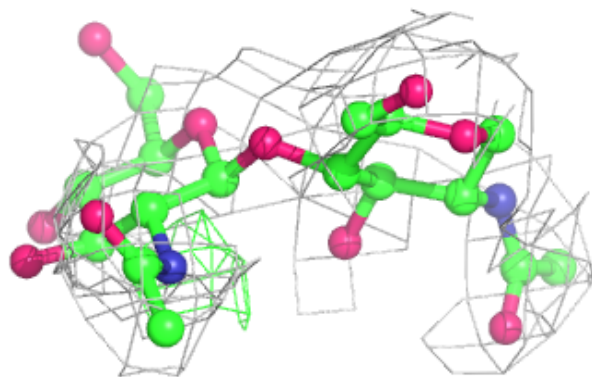
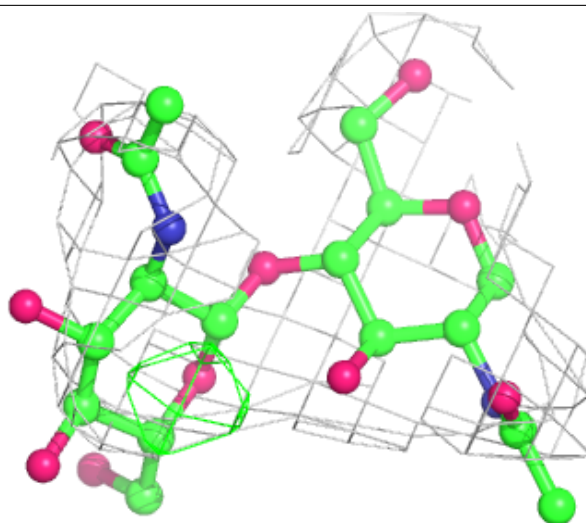
**Electron density around Chain P:**

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



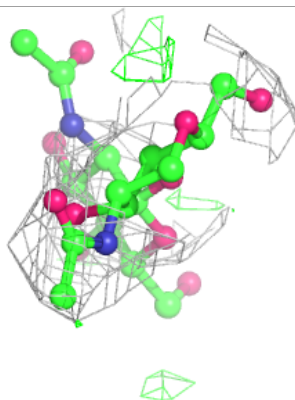
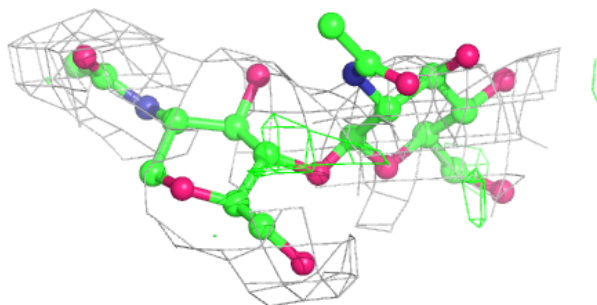
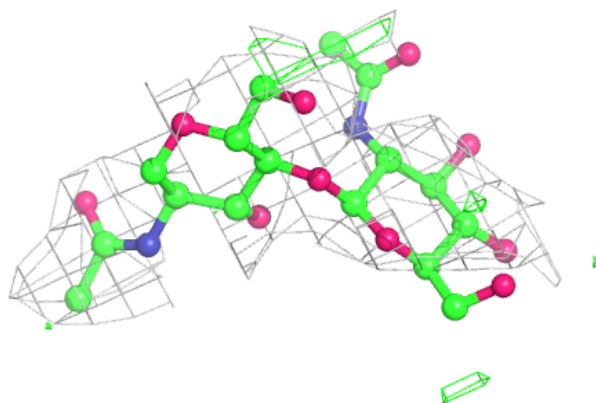
Electron density around Chain K:

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

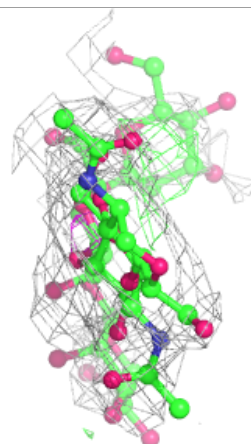
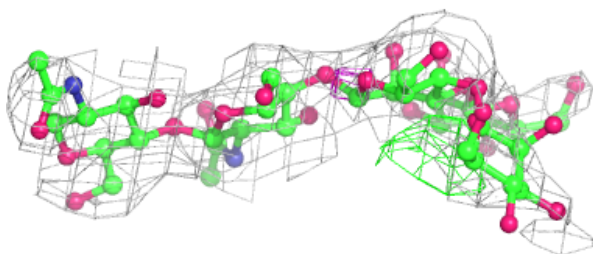
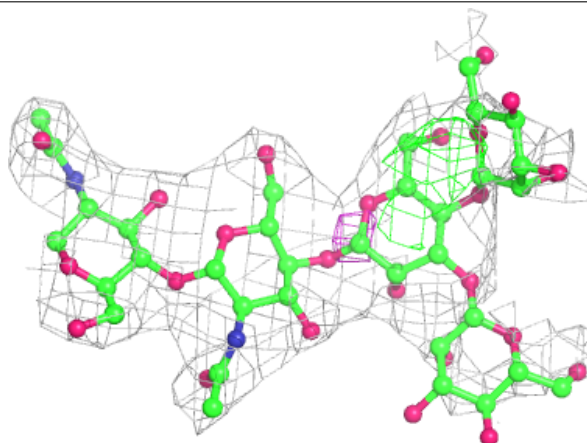


Electron density around Chain N:

$2mF_o-DF_c$ (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)



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
8	SO4	A	401	5/5	0.34	1.27	119,120,120,120	5
7	NAG	C	340	14/15	0.43	0.41	71,73,75,76	14
7	NAG	D	340	14/15	0.44	0.54	70,73,76,77	14
7	NAG	A	340	14/15	0.71	0.33	45,47,51,53	14
7	NAG	B	340	14/15	0.77	0.27	60,67,69,69	14
9	CIT	D	404	13/13	0.79	0.38	118,119,120,120	0
9	CIT	C	403	13/13	0.79	0.44	107,109,110,110	0
8	SO4	Z	402	5/5	0.94	0.69	25,25,26,26	5

6.5 Other polymers [i](#)

There are no such residues in this entry.