



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 04:54 AM UTC

PDB ID : 5XC2 / pdb_00005xc2
Title : Crystal structure of GH family 81 beta-1,3-glucanase from *Rhizomucor miehei* complexed with laminarihexaose
Authors : Qin, Z.; Yang, S.; Peng, Z.; Yan, Q.; Jiang, Z.
Deposited on : 2017-03-22
Resolution : 2.70 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

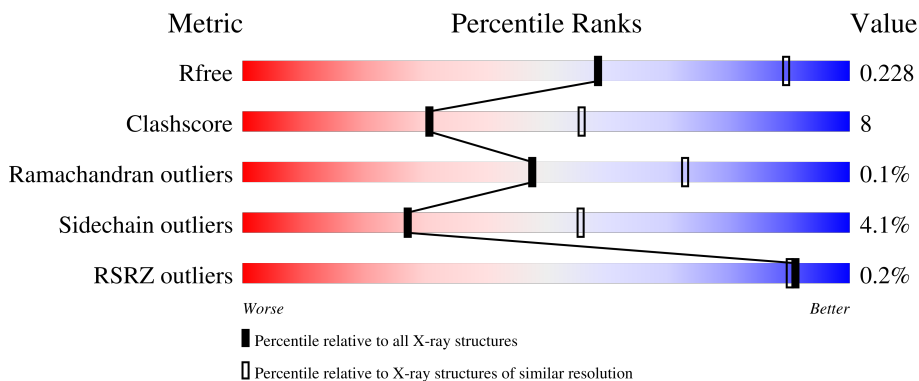
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	796	 76% 14% • 10%
1	B	796	 72% 17% • 10%
1	C	796	 66% 20% • 11%
1	D	796	 65% 16% • 19%
2	E	6	 50% 50%

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Mol	Chain	Length	Quality of chain
3	F	5	 80% 20%
3	M	5	 40% 60%
4	G	4	 75% 25%
4	L	4	 100%
4	O	4	 75% 25%
4	P	4	 50% 50%
4	Q	4	 25% 75%
5	H	3	 100%
5	I	3	 100%
5	N	3	 33% 67%
5	R	3	 67% 33%
6	J	2	 100%
6	K	2	 50% 50%

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
6	BGC	J	1	-	X	-	-
6	BGC	J	2	-	X	-	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 23075 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 Endo-beta-1,3-glucanase.

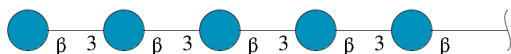
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	717	Total 5661	C 3624	N 947	O 1077	S 13	0	0	0
1	B	720	Total 5687	C 3638	N 951	O 1085	S 13	0	1	0
1	C	705	Total 5545	C 3553	N 923	O 1056	S 13	0	1	0
1	D	648	Total 5120	C 3298	N 851	O 959	S 12	0	1	0

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	E	6	Total 67	C 36	O 31	0	0	0

- Molecule 3 is an oligosaccharide called beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
3	F	5	Total 56	C 30	O 26	0	0	0

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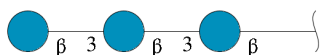
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	M	5	Total	C	O	0	0	0
			56	30	26			

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



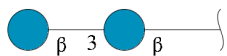
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	G	4	Total	C	O	0	0	0
			45	24	21			
4	L	4	Total	C	O	0	0	0
			45	24	21			
4	O	4	Total	C	O	0	0	0
			45	24	21			
4	P	4	Total	C	O	0	0	0
			45	24	21			
4	Q	4	Total	C	O	0	0	0
			45	24	21			

- Molecule 5 is an oligosaccharide called beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
5	H	3	Total	C	O	0	0	0
			33	18	15			
5	I	3	Total	C	O	0	0	0
			34	18	16			
5	N	3	Total	C	O	0	0	0
			34	18	16			
5	R	3	Total	C	O	0	0	0
			34	18	16			

- Molecule 6 is an oligosaccharide called beta-D-glucopyranose-(1-3)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
6	J	2	Total	C	O	0	0	0
			22	12	10			
6	K	2	Total	C	O	0	0	0
			22	12	10			

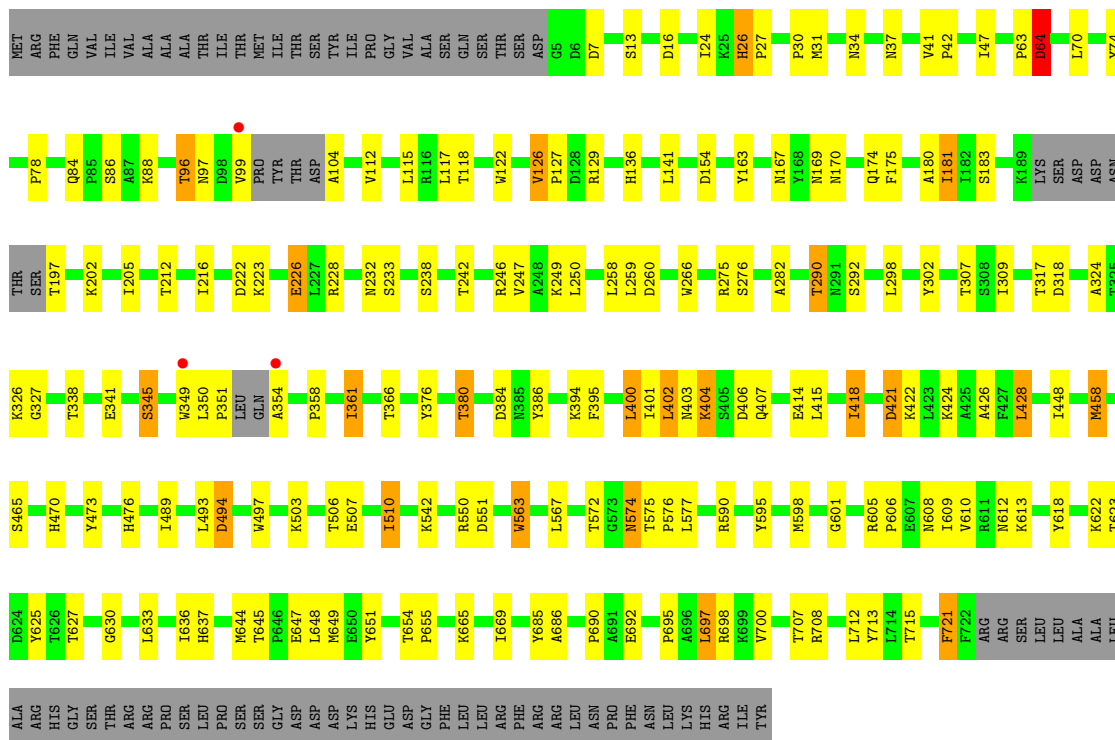
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	185	Total	O	0	0
			185	185		
7	B	143	Total	O	0	0
			143	143		
7	C	57	Total	O	0	0
			57	57		
7	D	94	Total	O	0	0
			94	94		

PRO	SER	GLY	ASP	ASP	ASP	LYS	HIS	GLU	ALA	GLY	ASP	GLY	PHE	LEU	LEU	LEU	ARG	PHE	ARG	ARG	ARG	ARG	LEU	ASN	GLY	VAL	PRO	PHE	PHE	ASN	ASN	LEU	LYS	HIS	ARG	ILE	TYR
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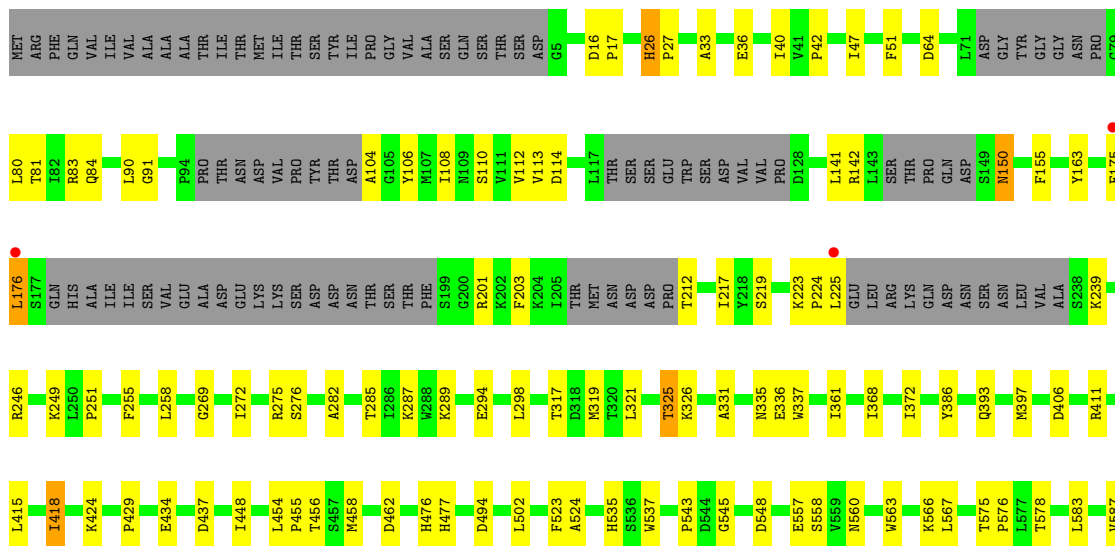
• Molecule 1: Endo-beta-1,3-glucanase

Chain C: 66% 20% 11%



• Molecule 1: Endo-beta-1,3-glucanase

Chain D: 65% 16% 19%





- Molecule 2: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain E: 50% 50%



- Molecule 3: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain F: 80% 20%



- Molecule 3: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain M: 40% 60%



- Molecule 4: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain G: 75% 25%



- Molecule 4: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain L: 100%




- Molecule 4: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain O: 75% 25%

BGC1
BGC2
BGC3
BGC4

- Molecule 4: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain P:  50% 50%

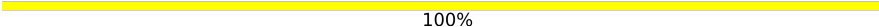
BGC1
BGC2
BGC3
BGC4

- Molecule 4: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain Q:  25% 75%

BGC1
BGC2
BGC3
BGC4

- Molecule 5: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain H:  100%

BGC1
BGC2
BGC3

- Molecule 5: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain I:  100%

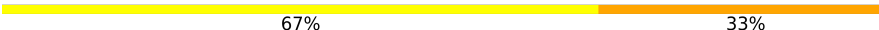
BGC1
BGC2
BGC3

- Molecule 5: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain N:  33% 67%

BGC1
BGC2
BGC3

- Molecule 5: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain R:  67% 33%

BGC1
BGC2
BGC3

- Molecule 6: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain J:  100%

BGC1
BGC2

- Molecule 6: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain K:  50%  50%

BGC1
BGC2

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	108.70Å 99.02Å 138.43Å 90.00° 111.35° 90.00°	Depositor
Resolution (Å)	29.73 – 2.70 29.73 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.73-2.70) 99.5 (29.73-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.68Å)	Xtrriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.176 , 0.232 0.183 , 0.228	Depositor DCC
R_{free} test set	2005 reflections (2.66%)	wwPDB-VP
Wilson B-factor (Å ²)	46.6	Xtrriage
Anisotropy	0.284	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	23075	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.53% 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: BGC

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	0.68	0/5821	0.96	10/7949 (0.1%)
1	B	0.62	0/5851	0.98	10/7991 (0.1%)
1	C	0.58	1/5704 (0.0%)	0.99	13/7791 (0.2%)
1	D	0.58	0/5265	0.97	13/7180 (0.2%)
All	All	0.62	1/22641 (0.0%)	0.97	46/30911 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	64	ASP	C-O	-5.06	1.17	1.24

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	16	ASP	CA-C-N	7.04	126.72	119.82
1	B	16	ASP	C-N-CA	7.04	126.72	119.82
1	A	232	ASN	N-CA-C	-6.76	104.78	113.16
1	C	418	ILE	N-CA-C	6.76	117.51	110.62
1	C	345	SER	CA-C-N	6.45	127.01	120.04

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	5661	0	5451	68	0
1	B	5687	0	5470	87	0
1	C	5545	0	5311	130	0
1	D	5120	0	4938	69	0
2	E	67	0	56	4	0
3	F	56	0	48	1	0
3	M	56	0	48	2	0
4	G	45	0	39	1	0
4	L	45	0	39	0	0
4	O	45	0	39	1	0
4	P	45	0	38	2	0
4	Q	45	0	38	4	0
5	H	33	0	27	0	0
5	I	34	0	28	0	0
5	N	34	0	30	4	0
5	R	34	0	30	3	0
6	J	22	0	13	5	0
6	K	22	0	17	1	0
7	A	185	0	0	6	1
7	B	143	0	0	7	0
7	C	57	0	0	10	0
7	D	94	0	0	4	1
All	All	23075	0	21660	365	1

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 8.

The worst 5 of 365 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)
6:J:1:BGC:C5	6:J:1:BGC:O5	1.64	1.42
1:C:64:ASP:OD2	1:C:302:TYR:OH	1.70	1.09
1:C:644:MET:HG3	1:C:649:MET:CE	1.93	0.98
1:C:644:MET:HG3	1:C:649:MET:HE3	1.52	0.89
1:B:363:GLU:OE1	1:B:698:ARG:NH2	2.07	0.88

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1068:HOH:O	7:D:952:HOH:O[2_848]	2.17	0.03

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	713/796 (90%)	678 (95%)	34 (5%)	1 (0%)	48	73
1	B	719/796 (90%)	678 (94%)	40 (6%)	1 (0%)	48	73
1	C	698/796 (88%)	656 (94%)	41 (6%)	1 (0%)	48	73
1	D	633/796 (80%)	604 (95%)	28 (4%)	1 (0%)	43	68
All	All	2763/3184 (87%)	2616 (95%)	143 (5%)	4 (0%)	48	73

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	64	ASP
1	B	64	ASP
1	D	64	ASP
1	C	64	ASP

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	603/685 (88%)	589 (98%)	14 (2%)	44	73
1	B	606/685 (88%)	581 (96%)	25 (4%)	27	56
1	C	587/685 (86%)	554 (94%)	33 (6%)	19	44
1	D	539/685 (79%)	515 (96%)	24 (4%)	24	52
All	All	2335/2740 (85%)	2239 (96%)	96 (4%)	27	56

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	404	LYS
1	C	707	THR
1	C	415	LEU
1	C	510	ILE
1	D	141	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	167	ASN
1	D	674	GLN
1	C	552	GLN
1	D	560	ASN
1	C	491	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

52 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BGC	E	1	2	12,12,12	0.85	0	17,17,17	2.45	4 (23%)
2	BGC	E	2	2	11,11,12	1.63	3 (27%)	15,15,17	1.23	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BGC	E	3	2	11,11,12	1.72	2 (18%)	15,15,17	2.02	6 (40%)
2	BGC	E	4	2	11,11,12	2.51	4 (36%)	15,15,17	2.37	6 (40%)
2	BGC	E	5	2	11,11,12	1.59	3 (27%)	15,15,17	1.28	2 (13%)
2	BGC	E	6	2	11,11,12	1.69	3 (27%)	15,15,17	1.62	3 (20%)
3	BGC	F	1	3	12,12,12	0.95	1 (8%)	17,17,17	2.36	7 (41%)
3	BGC	F	2	3	11,11,12	1.80	1 (9%)	15,15,17	2.60	4 (26%)
3	BGC	F	3	3	11,11,12	1.46	2 (18%)	15,15,17	1.22	2 (13%)
3	BGC	F	4	3	11,11,12	1.54	2 (18%)	15,15,17	1.01	0
3	BGC	F	5	3	11,11,12	1.81	3 (27%)	15,15,17	1.29	1 (6%)
4	BGC	G	1	4	12,12,12	1.16	1 (8%)	17,17,17	0.69	0
4	BGC	G	2	4	11,11,12	1.32	2 (18%)	15,15,17	1.45	3 (20%)
4	BGC	G	3	4	11,11,12	1.63	3 (27%)	15,15,17	1.09	1 (6%)
4	BGC	G	4	4	11,11,12	1.72	2 (18%)	15,15,17	1.15	1 (6%)
5	BGC	H	1	5	11,11,12	4.06	7 (63%)	15,15,17	4.26	9 (60%)
5	BGC	H	2	5	11,11,12	1.70	3 (27%)	15,15,17	2.45	5 (33%)
5	BGC	H	3	5	11,11,12	0.78	0	15,15,17	2.82	7 (46%)
5	BGC	I	1	5	12,12,12	1.23	1 (8%)	17,17,17	1.85	5 (29%)
5	BGC	I	2	5	11,11,12	3.43	3 (27%)	15,15,17	2.37	4 (26%)
5	BGC	I	3	5	11,11,12	1.93	1 (9%)	15,15,17	3.93	10 (66%)
6	BGC	J	1	6	11,11,12	5.87	8 (72%)	15,15,17	3.34	9 (60%)
6	BGC	J	2	6	11,11,12	7.49	8 (72%)	15,15,17	5.02	10 (66%)
6	BGC	K	1	6	11,11,12	1.69	3 (27%)	15,15,17	1.89	4 (26%)
6	BGC	K	2	6	11,11,12	1.92	3 (27%)	15,15,17	3.07	5 (33%)
4	BGC	L	1	4	12,12,12	1.08	1 (8%)	17,17,17	2.35	5 (29%)
4	BGC	L	2	4	11,11,12	1.77	2 (18%)	15,15,17	2.28	5 (33%)
4	BGC	L	3	4	11,11,12	1.56	1 (9%)	15,15,17	2.05	6 (40%)
4	BGC	L	4	4	11,11,12	1.80	3 (27%)	15,15,17	1.05	0
3	BGC	M	1	3	12,12,12	0.74	0	17,17,17	2.06	5 (29%)
3	BGC	M	2	3	11,11,12	1.68	3 (27%)	15,15,17	1.25	1 (6%)
3	BGC	M	3	3	11,11,12	1.68	3 (27%)	15,15,17	3.01	7 (46%)
3	BGC	M	4	3	11,11,12	1.85	3 (27%)	15,15,17	1.99	5 (33%)
3	BGC	M	5	3	11,11,12	1.48	2 (18%)	15,15,17	1.22	2 (13%)
5	BGC	N	1	5	12,12,12	1.33	1 (8%)	17,17,17	1.95	7 (41%)
5	BGC	N	2	5	11,11,12	2.69	2 (18%)	15,15,17	4.64	4 (26%)
5	BGC	N	3	5	11,11,12	1.92	5 (45%)	15,15,17	2.04	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BGC	O	1	4	12,12,12	1.18	1 (8%)	17,17,17	1.02	1 (5%)
4	BGC	O	2	4	11,11,12	1.69	3 (27%)	15,15,17	1.05	0
4	BGC	O	3	4	11,11,12	1.58	2 (18%)	15,15,17	1.26	2 (13%)
4	BGC	O	4	4	11,11,12	1.50	2 (18%)	15,15,17	1.70	2 (13%)
4	BGC	P	1	4	12,12,12	1.48	2 (16%)	17,17,17	2.13	5 (29%)
4	BGC	P	2	4	11,11,12	1.44	2 (18%)	15,15,17	2.90	6 (40%)
4	BGC	P	3	4	11,11,12	1.53	1 (9%)	15,15,17	2.42	7 (46%)
4	BGC	P	4	4	11,11,12	1.88	3 (27%)	15,15,17	1.46	4 (26%)
4	BGC	Q	1	4	12,12,12	1.08	1 (8%)	17,17,17	2.27	5 (29%)
4	BGC	Q	2	4	11,11,12	1.30	1 (9%)	15,15,17	2.18	4 (26%)
4	BGC	Q	3	4	11,11,12	1.81	6 (54%)	15,15,17	2.48	6 (40%)
4	BGC	Q	4	4	11,11,12	1.48	2 (18%)	15,15,17	3.02	5 (33%)
5	BGC	R	1	5	12,12,12	1.19	1 (8%)	17,17,17	0.76	1 (5%)
5	BGC	R	2	5	11,11,12	1.79	2 (18%)	15,15,17	2.90	8 (53%)
5	BGC	R	3	5	11,11,12	1.19	1 (9%)	15,15,17	1.82	5 (33%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BGC	E	1	2	-	2/2/22/22	0/1/1/1
2	BGC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	E	3	2	-	2/2/19/22	0/1/1/1
2	BGC	E	4	2	-	2/2/19/22	0/1/1/1
2	BGC	E	5	2	-	1/2/19/22	0/1/1/1
2	BGC	E	6	2	-	0/2/19/22	0/1/1/1
3	BGC	F	1	3	-	0/2/22/22	0/1/1/1
3	BGC	F	2	3	-	2/2/19/22	0/1/1/1
3	BGC	F	3	3	-	2/2/19/22	0/1/1/1
3	BGC	F	4	3	-	2/2/19/22	0/1/1/1
3	BGC	F	5	3	-	2/2/19/22	0/1/1/1
4	BGC	G	1	4	-	2/2/22/22	0/1/1/1
4	BGC	G	2	4	-	2/2/19/22	0/1/1/1
4	BGC	G	3	4	-	0/2/19/22	0/1/1/1
4	BGC	G	4	4	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BGC	H	1	5	-	1/2/19/22	0/1/1/1
5	BGC	H	2	5	-	2/2/19/22	0/1/1/1
5	BGC	H	3	5	-	1/2/19/22	0/1/1/1
5	BGC	I	1	5	-	0/2/22/22	0/1/1/1
5	BGC	I	2	5	-	0/2/19/22	0/1/1/1
5	BGC	I	3	5	-	2/2/19/22	0/1/1/1
6	BGC	J	1	6	-	2/2/19/22	0/1/1/1
6	BGC	J	2	6	-	2/2/19/22	0/1/1/1
6	BGC	K	1	6	-	0/2/19/22	0/1/1/1
6	BGC	K	2	6	-	2/2/19/22	0/1/1/1
4	BGC	L	1	4	-	0/2/22/22	0/1/1/1
4	BGC	L	2	4	-	0/2/19/22	0/1/1/1
4	BGC	L	3	4	-	0/2/19/22	0/1/1/1
4	BGC	L	4	4	-	1/2/19/22	0/1/1/1
3	BGC	M	1	3	-	2/2/22/22	0/1/1/1
3	BGC	M	2	3	-	0/2/19/22	0/1/1/1
3	BGC	M	3	3	-	1/2/19/22	0/1/1/1
3	BGC	M	4	3	-	2/2/19/22	0/1/1/1
3	BGC	M	5	3	-	2/2/19/22	0/1/1/1
5	BGC	N	1	5	-	0/2/22/22	0/1/1/1
5	BGC	N	2	5	-	0/2/19/22	0/1/1/1
5	BGC	N	3	5	-	2/2/19/22	0/1/1/1
4	BGC	O	1	4	-	0/2/22/22	0/1/1/1
4	BGC	O	2	4	-	2/2/19/22	0/1/1/1
4	BGC	O	3	4	-	0/2/19/22	0/1/1/1
4	BGC	O	4	4	-	0/2/19/22	0/1/1/1
4	BGC	P	1	4	-	2/2/22/22	0/1/1/1
4	BGC	P	2	4	-	1/2/19/22	0/1/1/1
4	BGC	P	3	4	-	1/2/19/22	0/1/1/1
4	BGC	P	4	4	-	2/2/19/22	0/1/1/1
4	BGC	Q	1	4	-	2/2/22/22	0/1/1/1
4	BGC	Q	2	4	-	2/2/19/22	0/1/1/1
4	BGC	Q	3	4	-	2/2/19/22	0/1/1/1
4	BGC	Q	4	4	-	2/2/19/22	0/1/1/1
5	BGC	R	1	5	-	2/2/22/22	0/1/1/1
5	BGC	R	2	5	-	2/2/19/22	0/1/1/1
5	BGC	R	3	5	-	0/2/19/22	0/1/1/1

The worst 5 of 125 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	J	2	BGC	O2-C2	-17.93	1.05	1.43
6	J	1	BGC	O3-C3	-12.15	1.12	1.43
6	J	1	BGC	O5-C5	10.96	1.64	1.43
5	I	2	BGC	O3-C3	-9.25	1.20	1.43
6	J	2	BGC	O5-C1	8.42	1.57	1.43

The worst 5 of 221 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	N	2	BGC	O5-C5-C6	-13.54	81.30	107.66
5	H	1	BGC	O5-C5-C6	-13.38	81.62	107.66
6	J	2	BGC	O5-C5-C6	-10.78	86.69	107.66
6	J	2	BGC	C1-C2-C3	9.26	123.12	109.64
4	Q	4	BGC	C1-C2-C3	-8.89	96.70	109.64

There are no chirality outliers.

5 of 63 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	P	4	BGC	O5-C5-C6-O6
4	O	2	BGC	C4-C5-C6-O6
4	Q	1	BGC	O5-C5-C6-O6
2	E	3	BGC	O5-C5-C6-O6
4	P	1	BGC	O5-C5-C6-O6

There are no ring outliers.

20 monomers are involved in 25 short contacts:

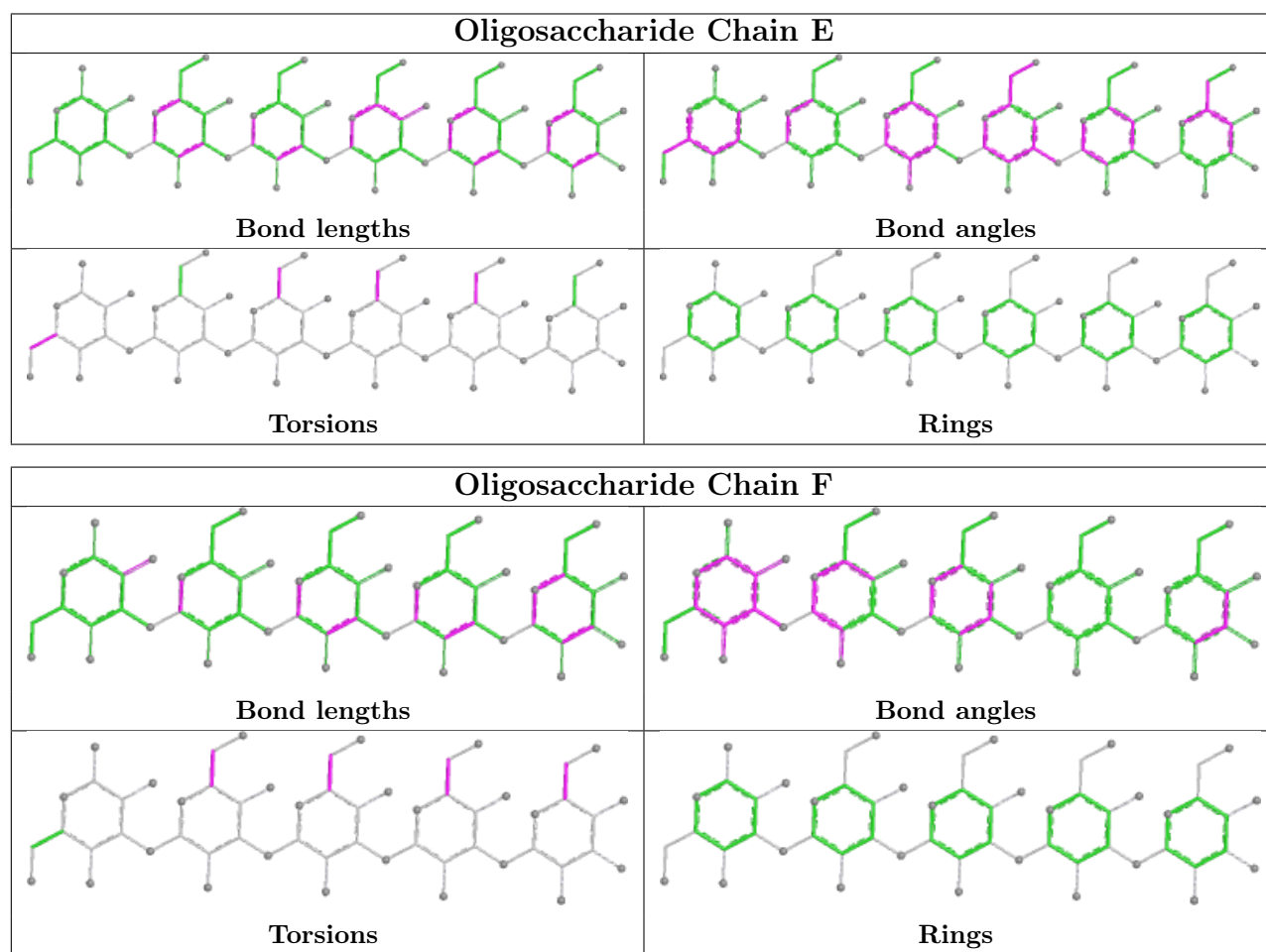
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	N	1	BGC	1	0
2	E	2	BGC	1	0
3	M	2	BGC	1	0
4	Q	2	BGC	2	0
2	E	3	BGC	2	0
3	M	3	BGC	1	0
6	J	1	BGC	5	0
4	Q	3	BGC	1	0
5	N	3	BGC	3	0
6	J	2	BGC	1	0
4	Q	1	BGC	1	0
4	P	3	BGC	1	0
3	M	4	BGC	1	0

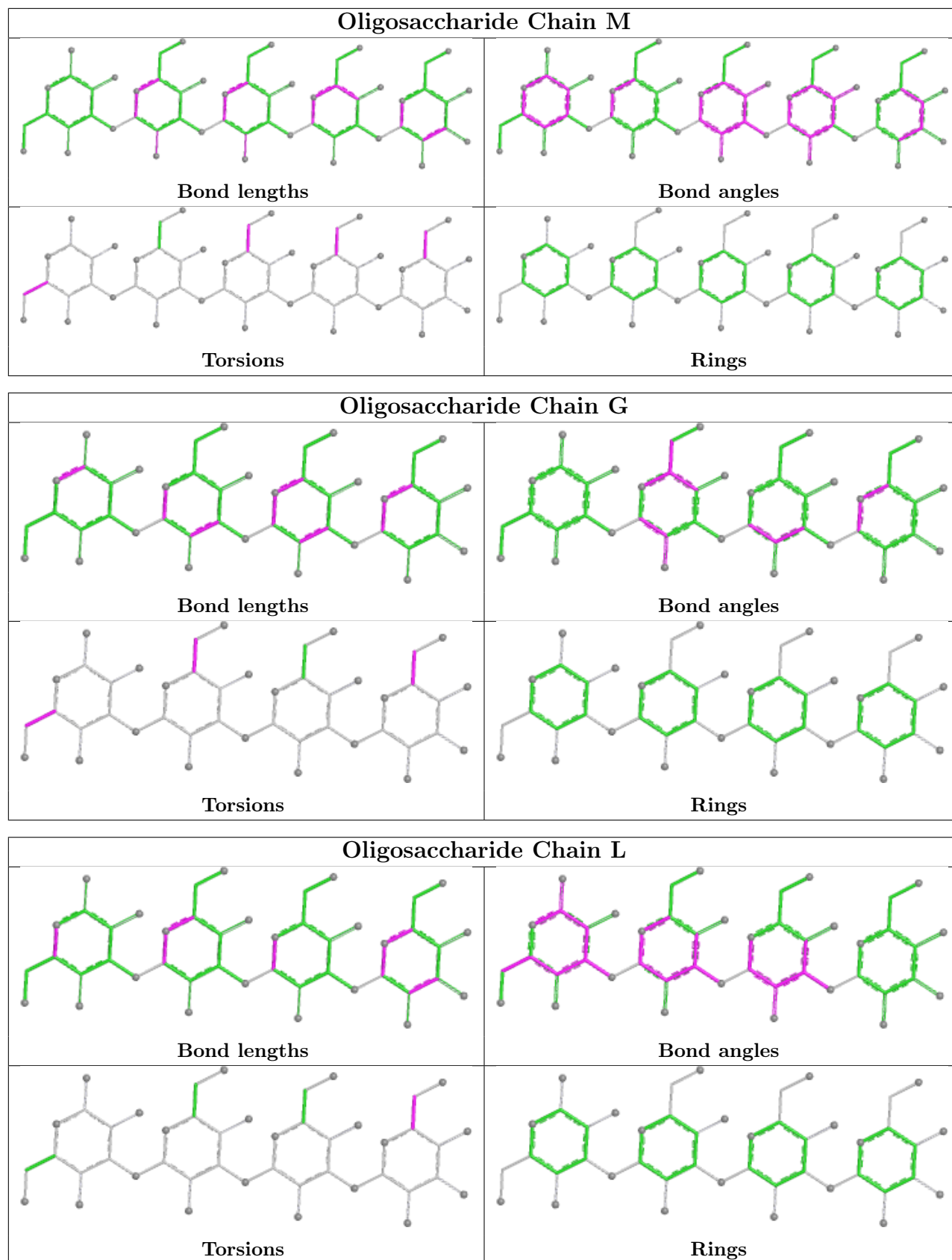
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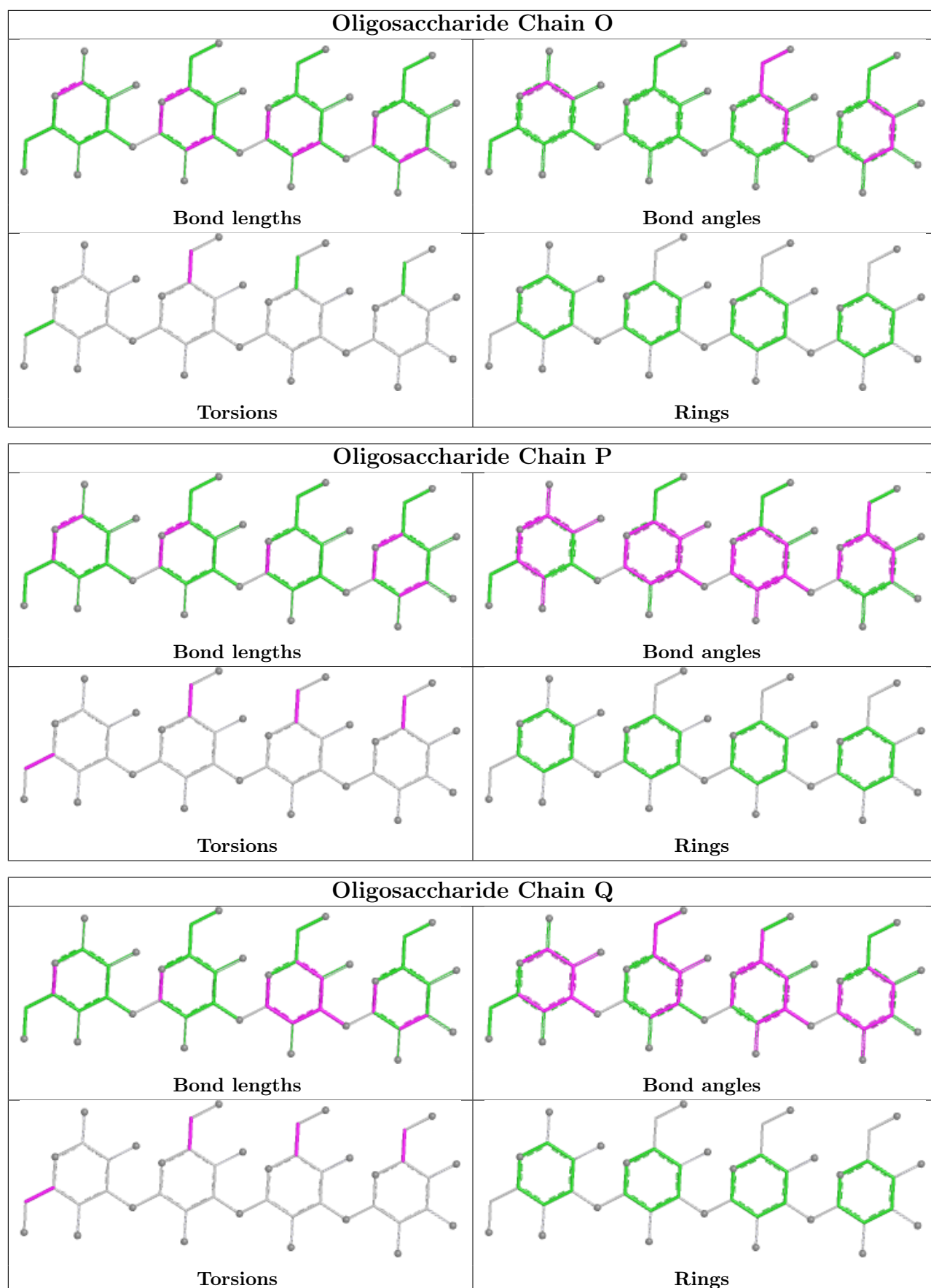
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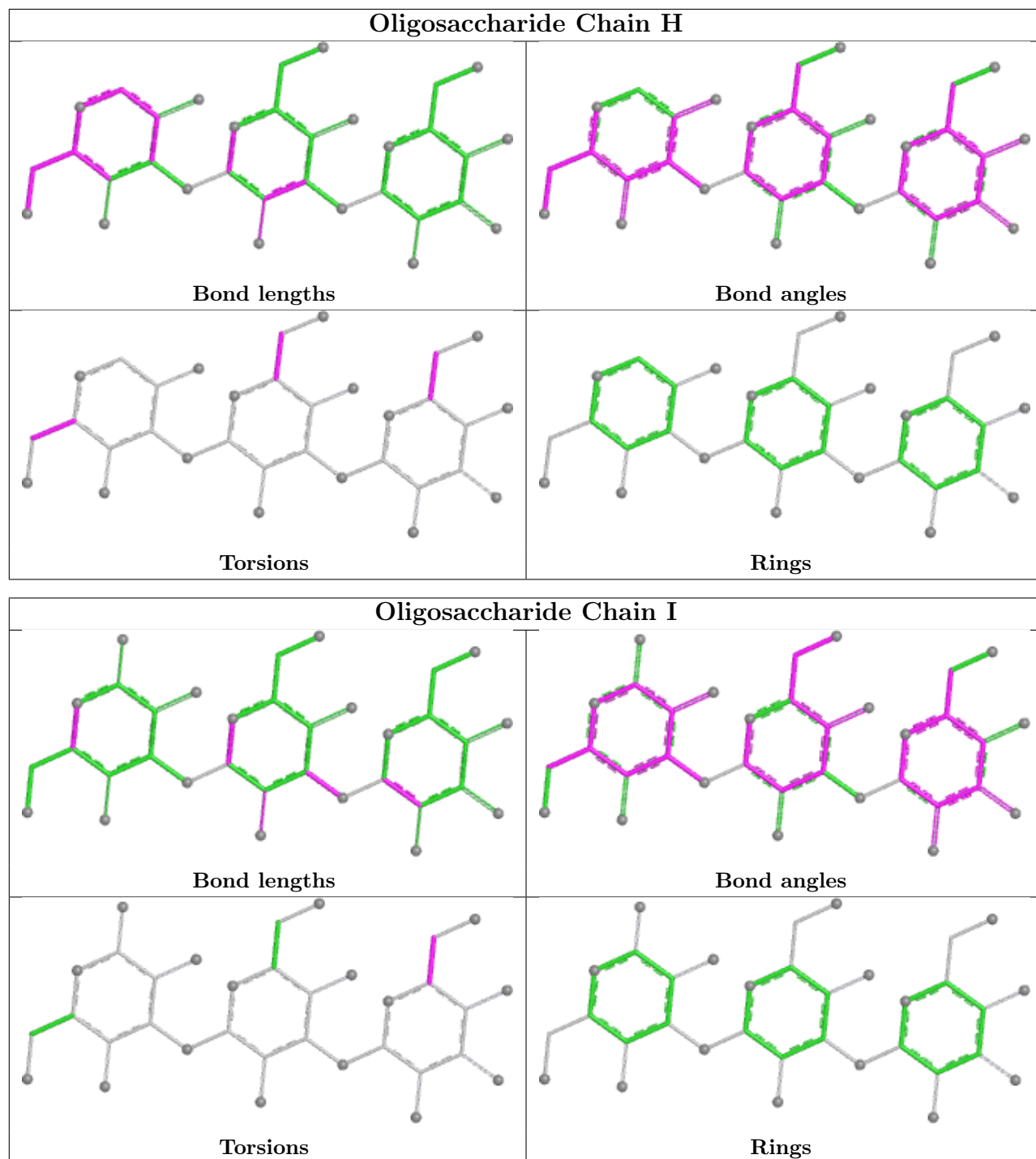
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	6	BGC	1	0
6	K	2	BGC	1	0
4	G	1	BGC	1	0
4	P	2	BGC	1	0
4	O	1	BGC	1	0
3	F	3	BGC	1	0
5	R	2	BGC	3	0

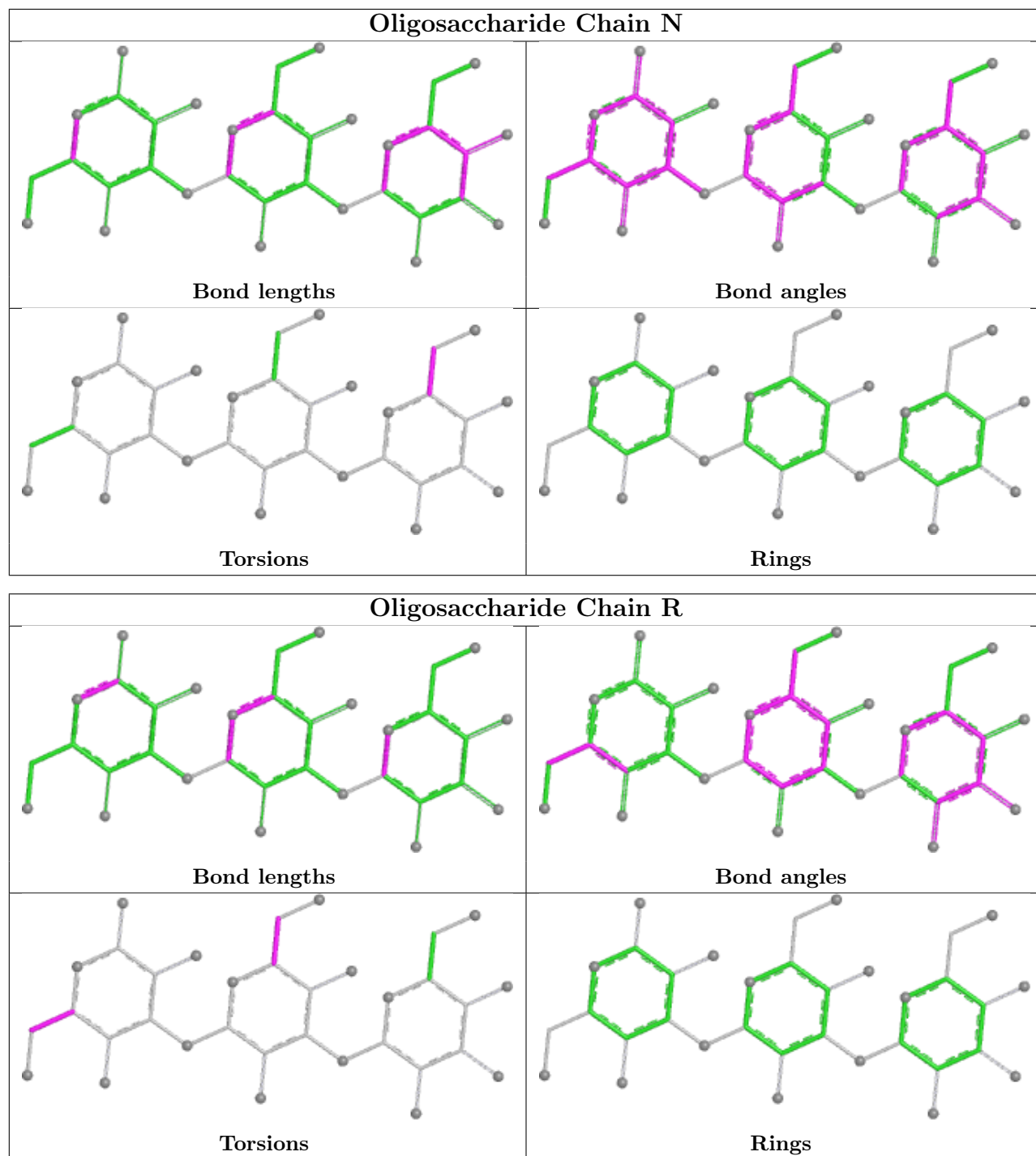
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

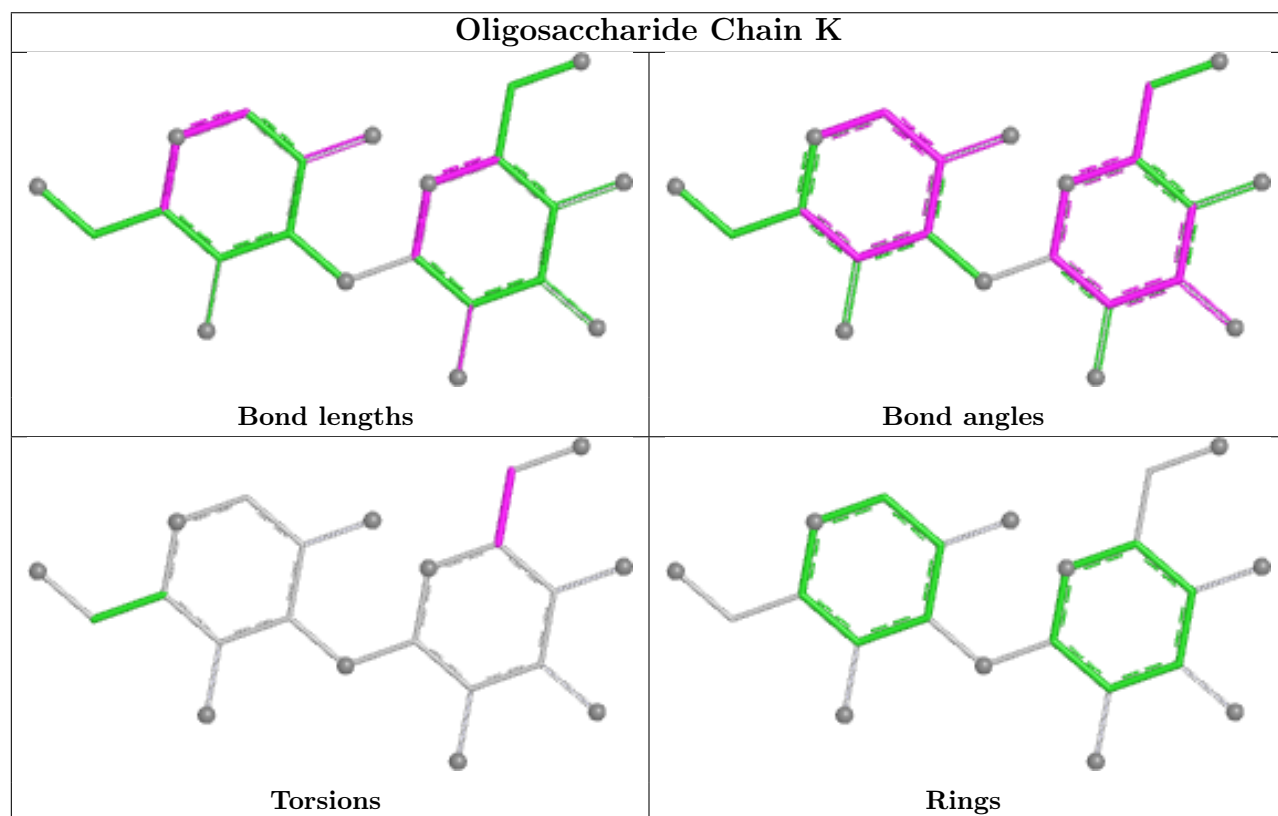
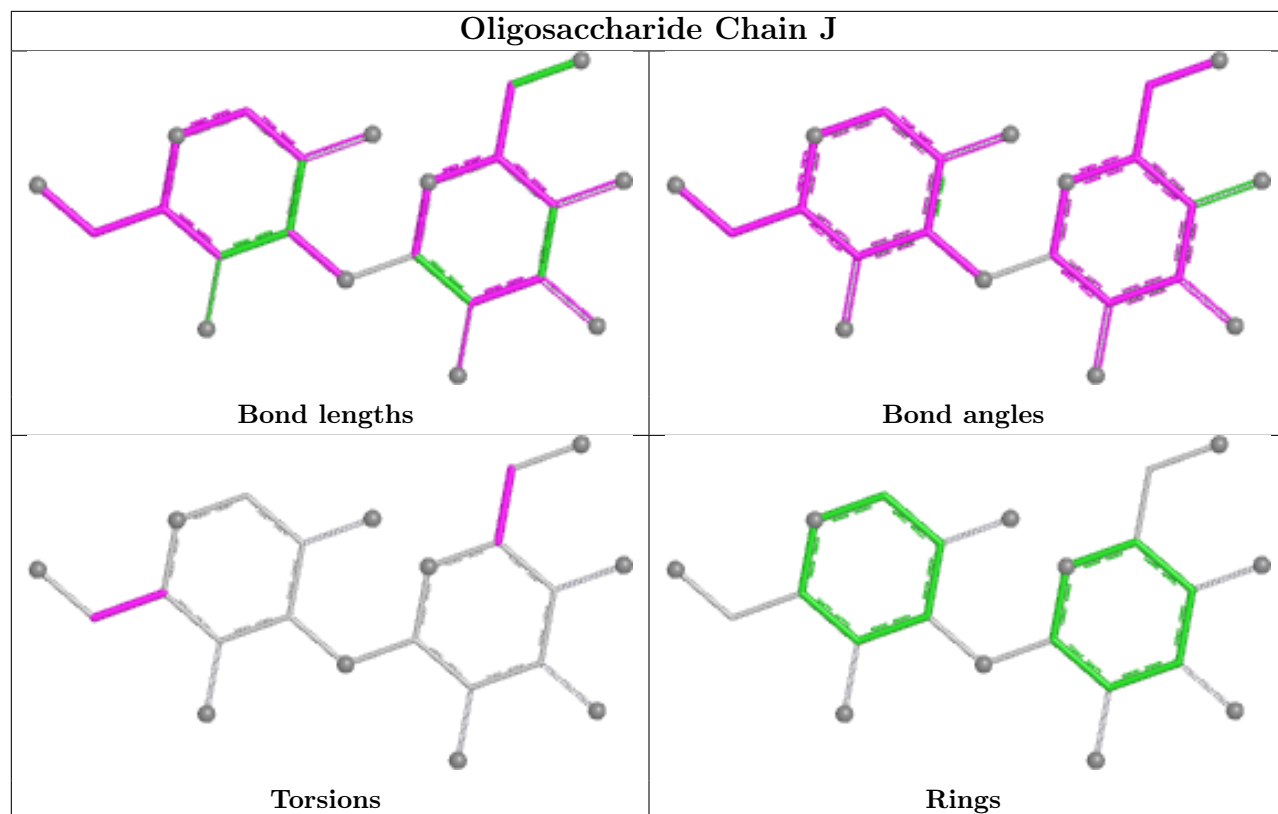












5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	717/796 (90%)	-0.81	0	100 100	2, 10, 33, 60	0
1	B	720/796 (90%)	-0.77	0	100 100	4, 16, 37, 69	1 (0%)
1	C	705/796 (88%)	-0.11	3 (0%)	88 87	11, 37, 68, 83	1 (0%)
1	D	648/796 (81%)	-0.29	3 (0%)	87 86	6, 29, 63, 82	1 (0%)
All	All	2790/3184 (87%)	-0.50	6 (0%)	91 90	2, 21, 59, 83	3 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	175	PHE	4.1
1	C	99	VAL	2.5
1	C	354	ALA	2.4
1	D	225	LEU	2.2
1	D	176	LEU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
6	BGC	J	2	11/12	0.64	0.11	30,45,52,59	0
5	BGC	H	3	11/12	0.68	0.09	46,50,63,64	0

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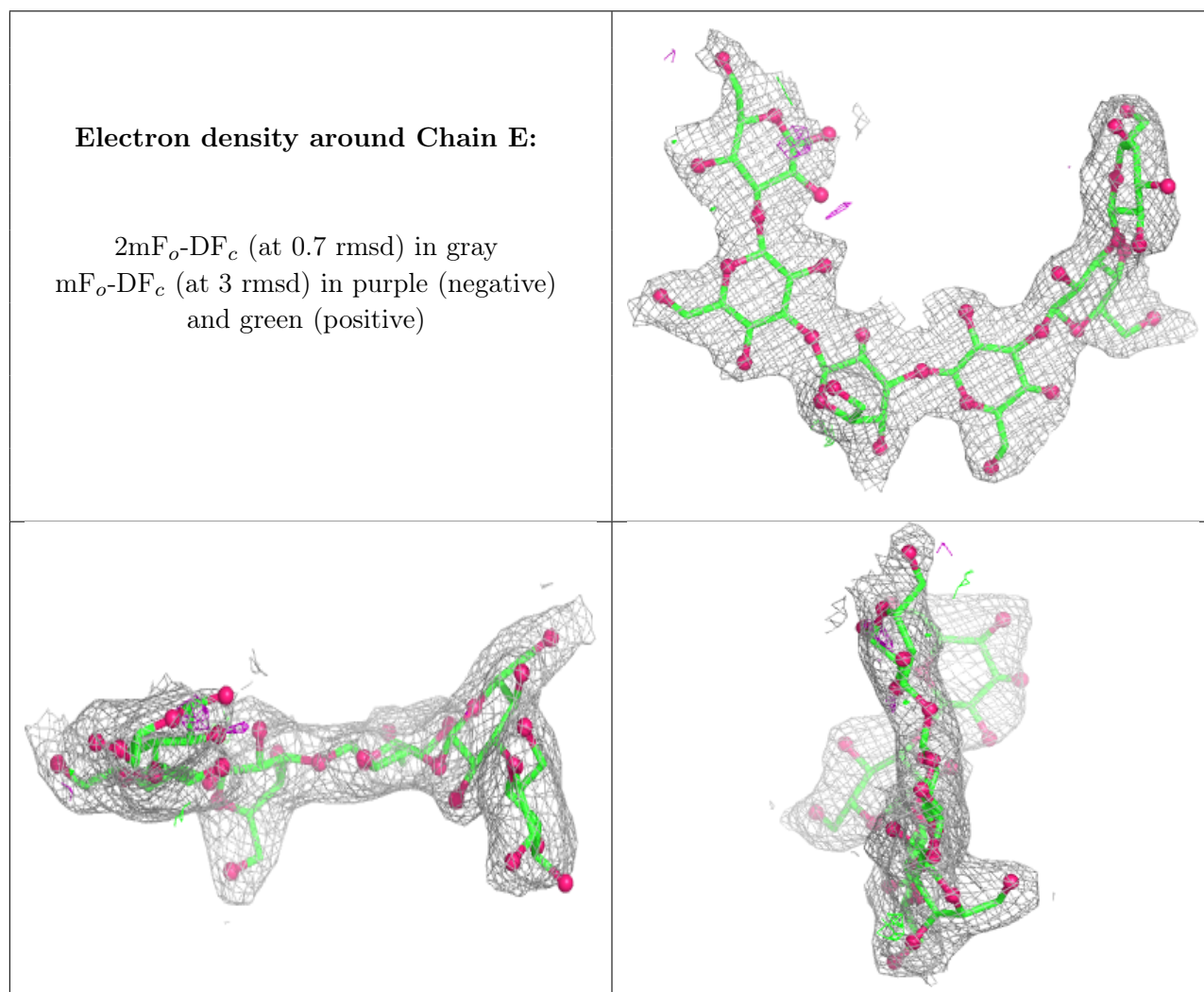
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	BGC	Q	4	11/12	0.68	0.12	34,41,53,63	0
3	BGC	F	1	12/12	0.79	0.11	28,40,46,52	0
2	BGC	E	1	12/12	0.82	0.12	13,30,41,42	0
4	BGC	G	4	11/12	0.86	0.09	9,25,34,39	0
3	BGC	M	5	11/12	0.87	0.09	27,35,42,44	0
2	BGC	E	6	11/12	0.87	0.08	27,33,36,46	0
4	BGC	O	1	12/12	0.87	0.08	27,32,47,52	0
6	BGC	K	1	11/12	0.87	0.07	9,15,24,33	0
5	BGC	H	2	11/12	0.88	0.07	17,27,46,46	0
4	BGC	O	4	11/12	0.88	0.07	28,37,45,47	0
4	BGC	Q	1	12/12	0.88	0.08	26,30,43,45	0
4	BGC	G	1	12/12	0.88	0.08	18,28,42,48	0
5	BGC	R	3	11/12	0.89	0.08	18,32,38,53	0
3	BGC	F	5	11/12	0.90	0.07	21,28,31,33	0
6	BGC	J	1	11/12	0.90	0.08	12,14,24,25	0
4	BGC	L	1	12/12	0.90	0.07	18,26,38,46	0
4	BGC	L	4	11/12	0.90	0.06	21,29,37,47	0
3	BGC	M	1	12/12	0.91	0.07	24,29,35,41	0
5	BGC	I	1	12/12	0.92	0.07	12,16,26,28	0
5	BGC	R	2	11/12	0.92	0.06	24,29,36,46	0
5	BGC	H	1	11/12	0.92	0.07	7,12,15,18	0
3	BGC	F	2	11/12	0.93	0.06	14,19,22,23	0
4	BGC	P	1	12/12	0.93	0.06	21,28,33,36	0
4	BGC	P	4	11/12	0.93	0.06	15,20,30,33	0
4	BGC	O	2	11/12	0.93	0.07	14,20,24,25	0
4	BGC	Q	3	11/12	0.93	0.06	20,24,31,32	0
5	BGC	N	1	12/12	0.94	0.05	18,25,28,35	0
5	BGC	N	3	11/12	0.94	0.06	21,22,28,34	0
3	BGC	M	2	11/12	0.94	0.07	12,17,22,22	0
4	BGC	P	2	11/12	0.94	0.06	15,18,22,24	0
3	BGC	M	3	11/12	0.94	0.06	19,22,27,30	0
2	BGC	E	4	11/12	0.94	0.08	6,8,10,12	0
4	BGC	L	3	11/12	0.94	0.06	11,15,20,23	0
5	BGC	R	1	12/12	0.95	0.06	19,23,26,28	0
2	BGC	E	2	11/12	0.95	0.07	4,10,16,18	0
3	BGC	M	4	11/12	0.95	0.05	21,25,28,29	0
2	BGC	E	5	11/12	0.95	0.05	10,15,18,19	0
5	BGC	N	2	11/12	0.95	0.06	12,16,21,23	0
4	BGC	Q	2	11/12	0.95	0.05	21,23,28,29	0
4	BGC	O	3	11/12	0.96	0.04	20,23,34,34	0
5	BGC	I	2	11/12	0.96	0.06	7,9,14,15	0
5	BGC	I	3	11/12	0.96	0.06	8,11,14,15	0

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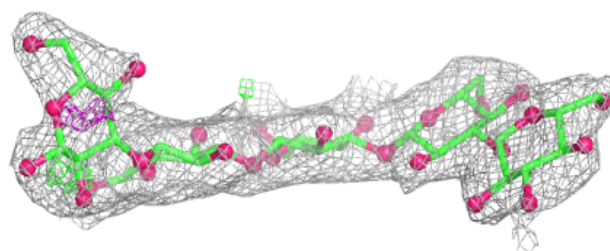
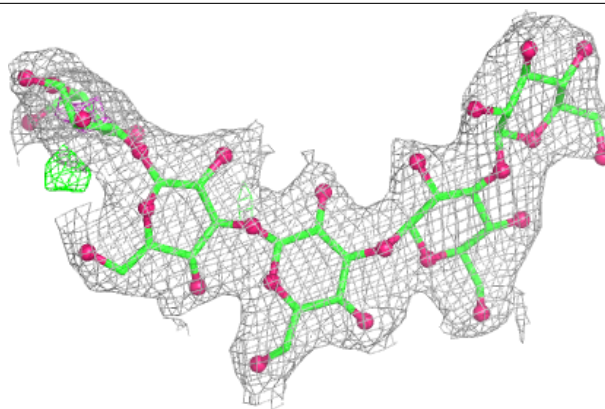
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	BGC	F	3	11/12	0.96	0.05	6,11,16,17	0
4	BGC	G	2	11/12	0.96	0.06	8,10,12,16	0
4	BGC	G	3	11/12	0.96	0.05	7,9,13,14	0
4	BGC	L	2	11/12	0.97	0.05	8,11,13,14	0
3	BGC	F	4	11/12	0.97	0.06	9,11,19,19	0
2	BGC	E	3	11/12	0.97	0.04	7,9,11,12	0
4	BGC	P	3	11/12	0.97	0.04	11,15,17,20	0
6	BGC	K	2	11/12	0.97	0.05	7,9,13,13	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.

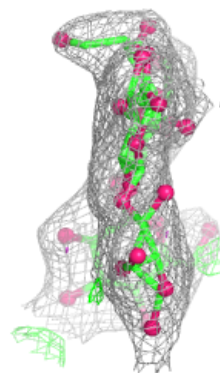
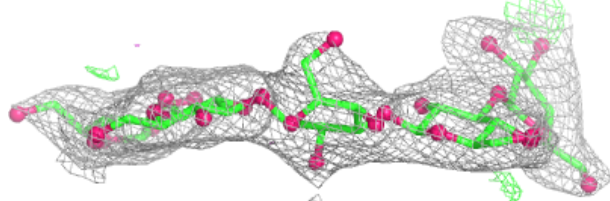
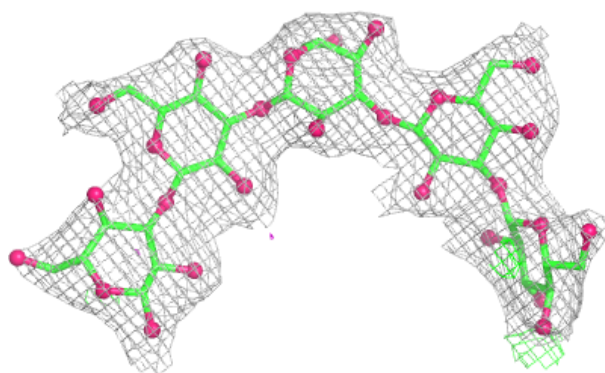


Electron density around Chain F:

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

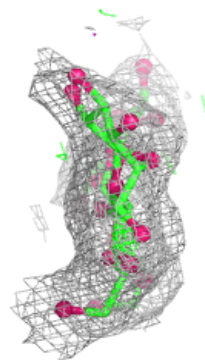
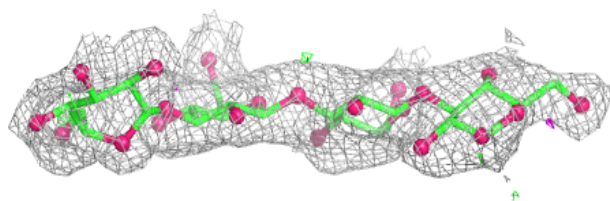
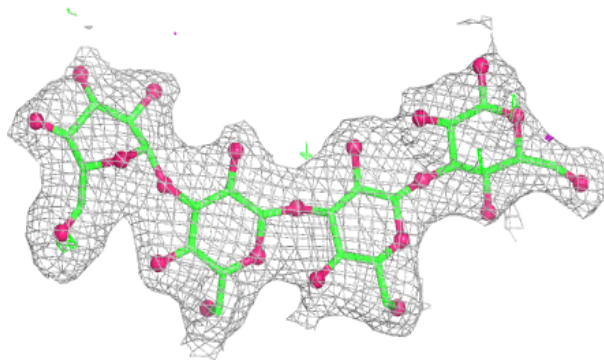
**Electron density around Chain M:**

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

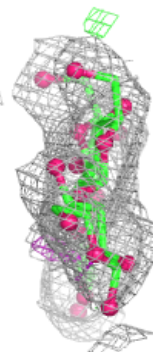
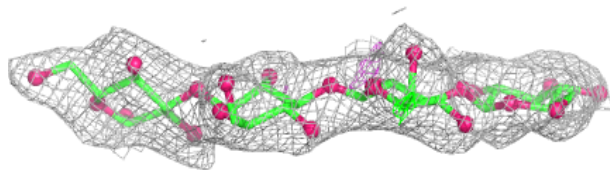
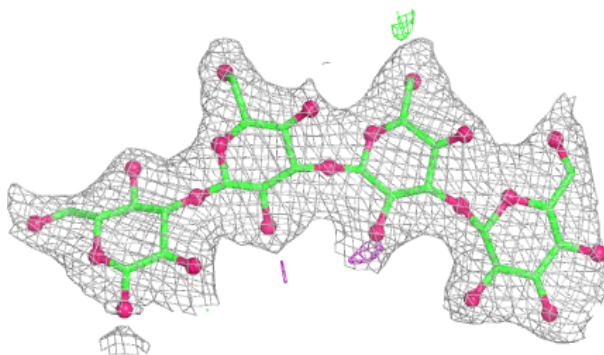


Electron density around Chain G:

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

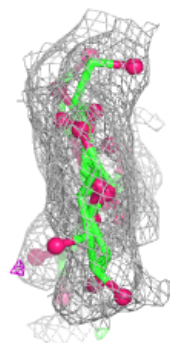
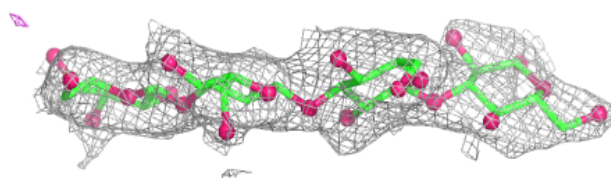
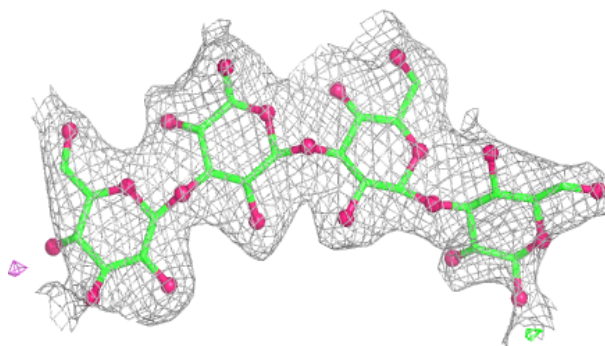
**Electron density around Chain L:**

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

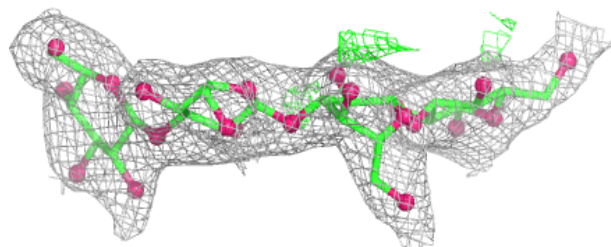
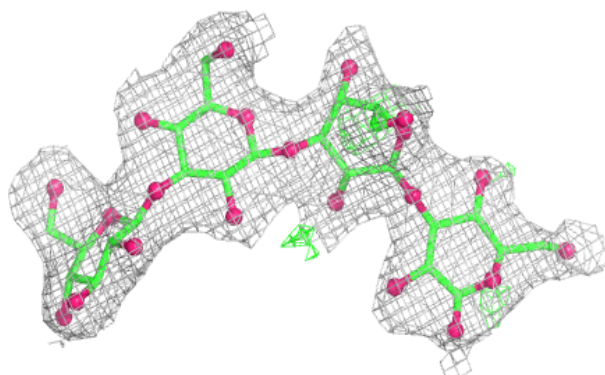


Electron density around Chain O:

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

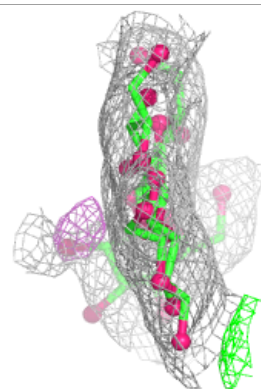
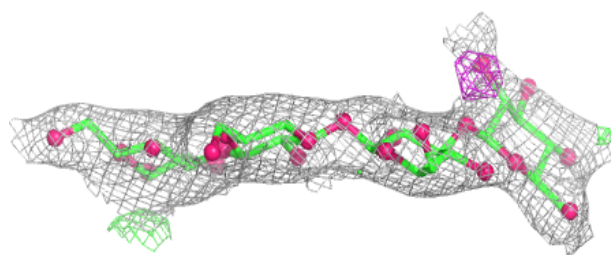
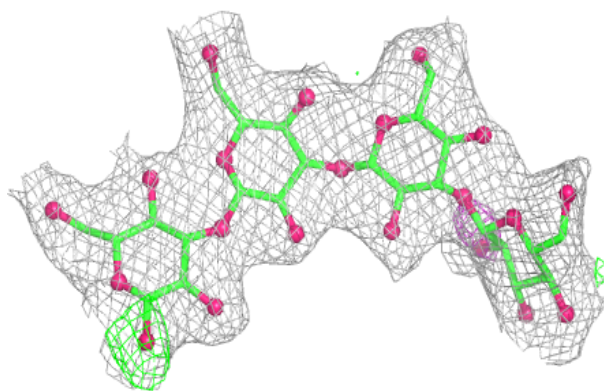
**Electron density around Chain P:**

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

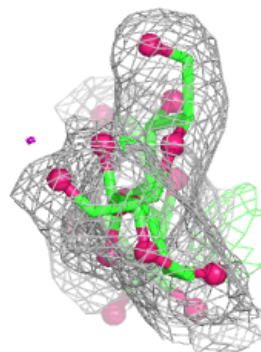
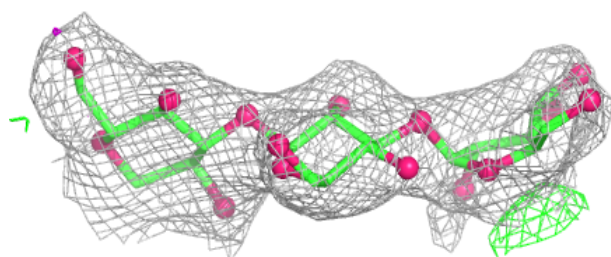
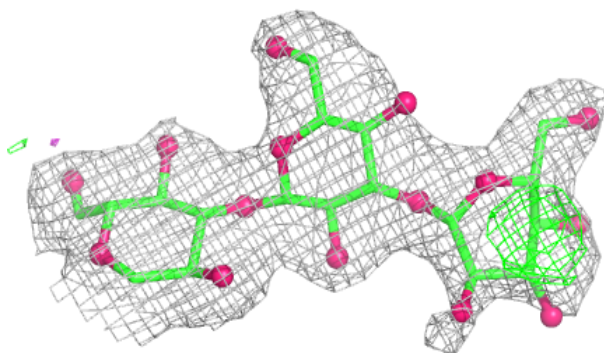


Electron density around Chain Q:

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

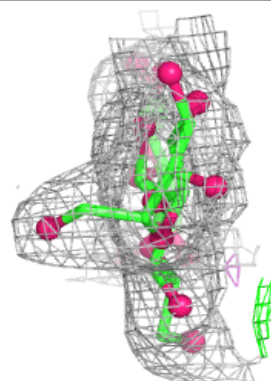
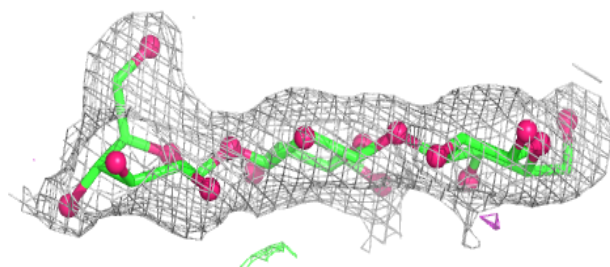
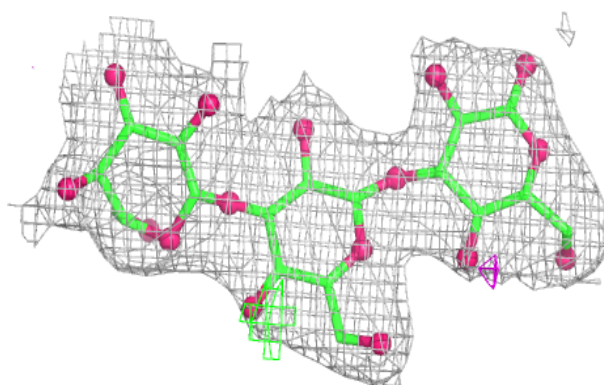
**Electron density around Chain H:**

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

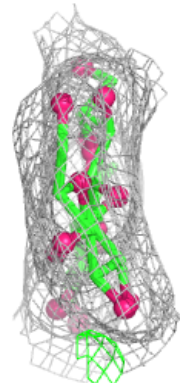
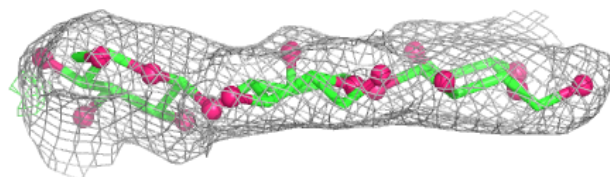
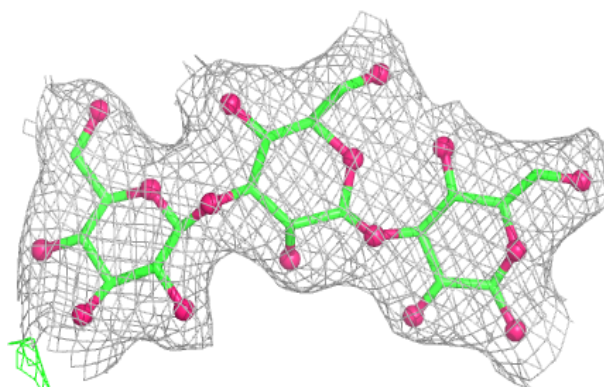


Electron density around Chain I:

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

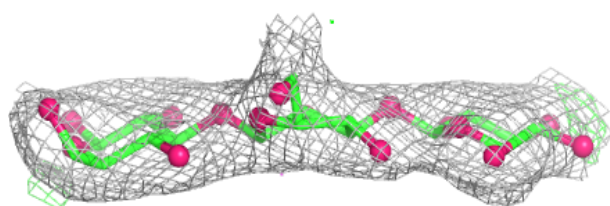
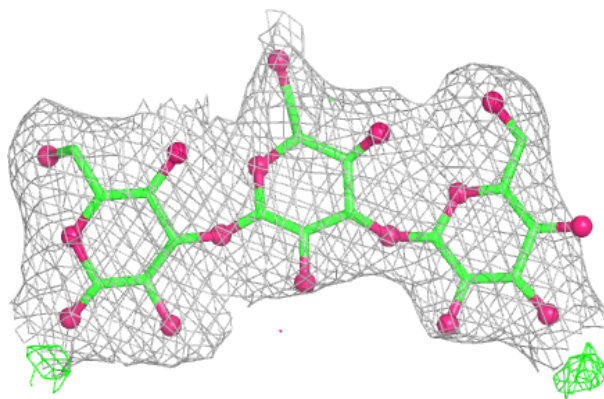
**Electron density around Chain N:**

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

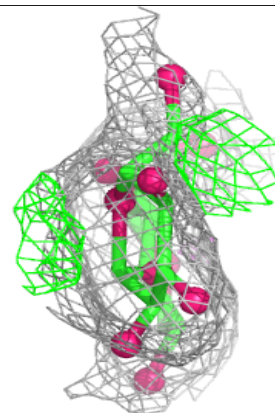
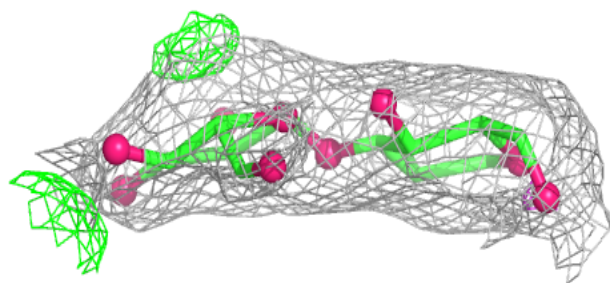
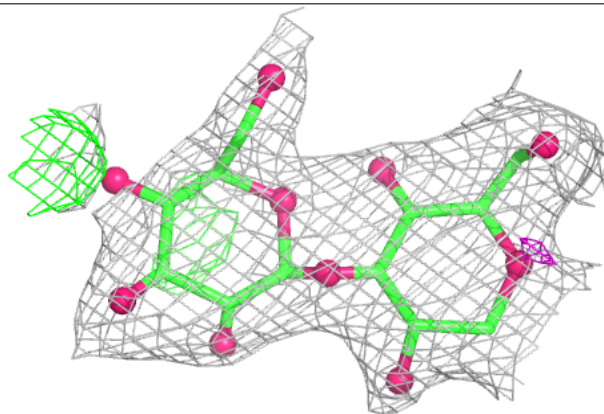


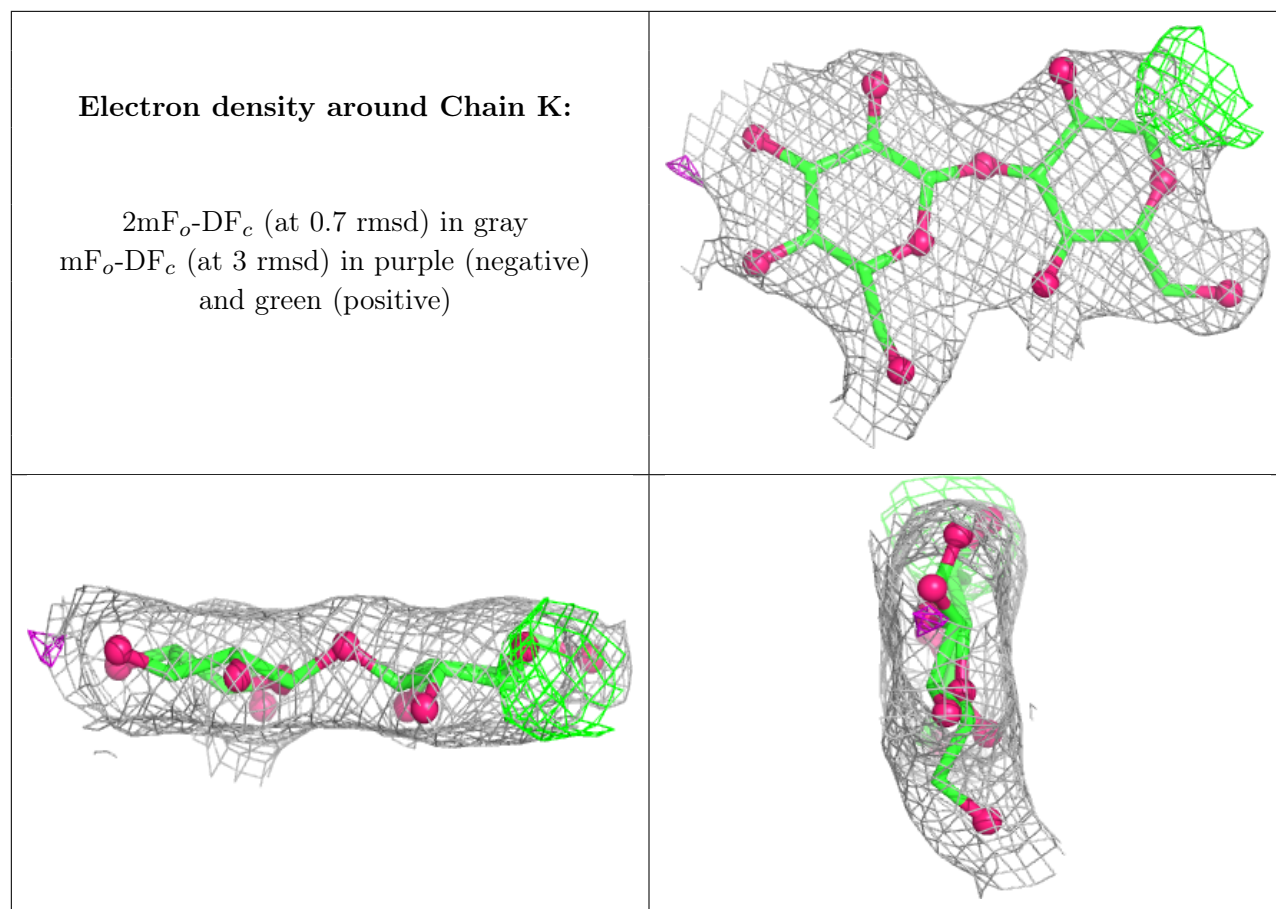
Electron density around Chain R:

$2mF_o-DF_c$ (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)





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.