



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 19, 2023 – 07:29 PM JST

PDB ID : 6M4F
Title : Crystal structure of the E496A mutant of HsBglA
Authors : Uehara, R.; Iwamoto, R.; Aoki, S.; Yoshizawa, T.; Takano, K.; Matsumura, H.; Tanaka, S.-i.
Deposited on : 2020-03-06
Resolution : 2.20 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

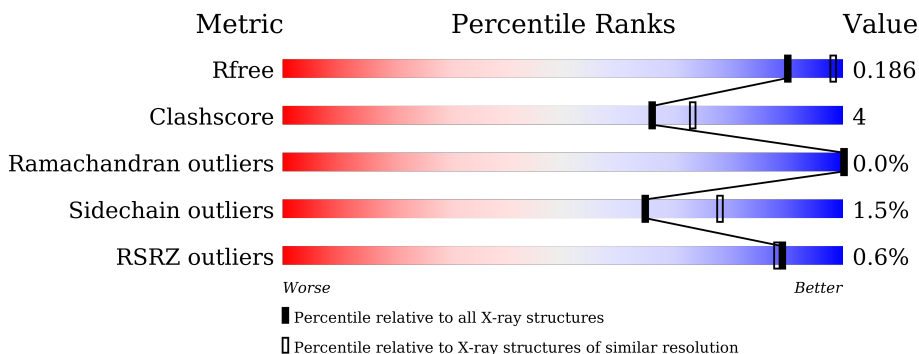
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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	578	 86% 8% 6%
1	C	578	 84% 10% 6%
1	E	578	 85% 9% 6%
1	G	578	 83% 11% 6%
2	B	2	 50% 50%
2	D	2	 100%

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Mol	Chain	Length	Quality of chain
2	F	2	 100%
2	H	2	 100%
2	I	2	 100%
2	J	2	 100%
2	K	2	 50%  50%
2	L	2	 50%  50%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 18617 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 Beta-galactosidase-like enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	542	4284	2753	712	810	9	0	0	0
1	C	543	4294	2759	715	811	9	0	0	0
1	E	542	4284	2753	712	810	9	0	0	0
1	G	544	4304	2765	718	812	9	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	496	ALA	GLU	engineered mutation	UNP Q564N5
A	595	HIS	-	expression tag	UNP Q564N5
A	596	HIS	-	expression tag	UNP Q564N5
A	597	HIS	-	expression tag	UNP Q564N5
A	598	HIS	-	expression tag	UNP Q564N5
A	599	HIS	-	expression tag	UNP Q564N5
A	600	HIS	-	expression tag	UNP Q564N5
C	496	ALA	GLU	engineered mutation	UNP Q564N5
C	595	HIS	-	expression tag	UNP Q564N5
C	596	HIS	-	expression tag	UNP Q564N5
C	597	HIS	-	expression tag	UNP Q564N5
C	598	HIS	-	expression tag	UNP Q564N5
C	599	HIS	-	expression tag	UNP Q564N5
C	600	HIS	-	expression tag	UNP Q564N5
E	496	ALA	GLU	engineered mutation	UNP Q564N5
E	595	HIS	-	expression tag	UNP Q564N5
E	596	HIS	-	expression tag	UNP Q564N5
E	597	HIS	-	expression tag	UNP Q564N5
E	598	HIS	-	expression tag	UNP Q564N5
E	599	HIS	-	expression tag	UNP Q564N5
E	600	HIS	-	expression tag	UNP Q564N5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	496	ALA	GLU	engineered mutation	UNP Q564N5
G	595	HIS	-	expression tag	UNP Q564N5
G	596	HIS	-	expression tag	UNP Q564N5
G	597	HIS	-	expression tag	UNP Q564N5
G	598	HIS	-	expression tag	UNP Q564N5
G	599	HIS	-	expression tag	UNP Q564N5
G	600	HIS	-	expression tag	UNP Q564N5

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



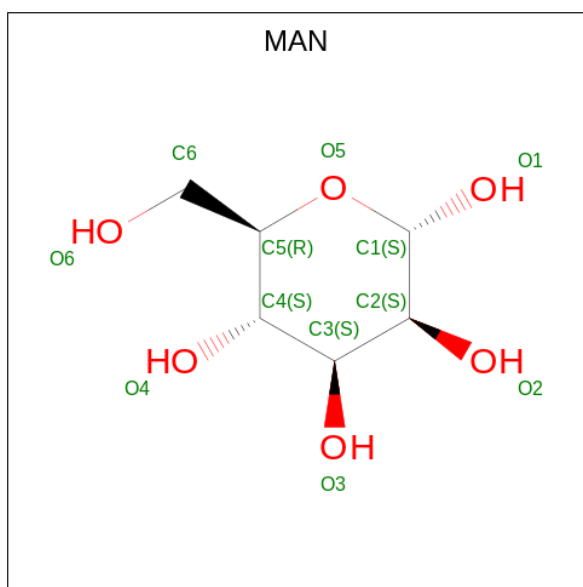
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0
2	D	2	28	16	2	10	0	0	0
2	F	2	28	16	2	10	0	0	0
2	H	2	28	16	2	10	0	0	0
2	I	2	28	16	2	10	0	0	0
2	J	2	28	16	2	10	0	0	0
2	K	2	28	16	2	10	0	0	0
2	L	2	28	16	2	10	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is alpha-D-mannopyranose (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 11 6 5	0	0
4	C	1	Total C O 11 6 5	0	0
4	C	1	Total C O 11 6 5	0	0
4	E	1	Total C O 11 6 5	0	0
4	G	1	Total C O 11 6 5	0	0

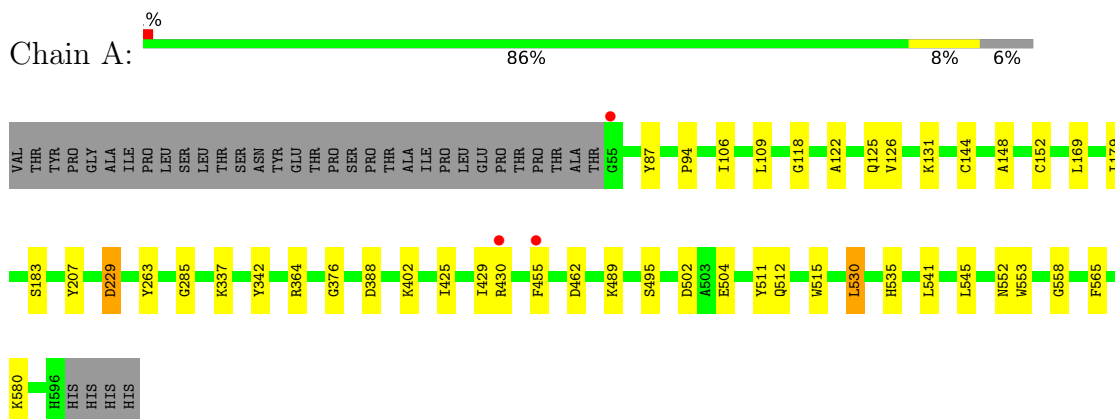
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	303	Total O 303 303	0	0
5	C	235	Total O 235 235	0	0
5	E	278	Total O 278 278	0	0
5	G	244	Total O 244 244	0	0

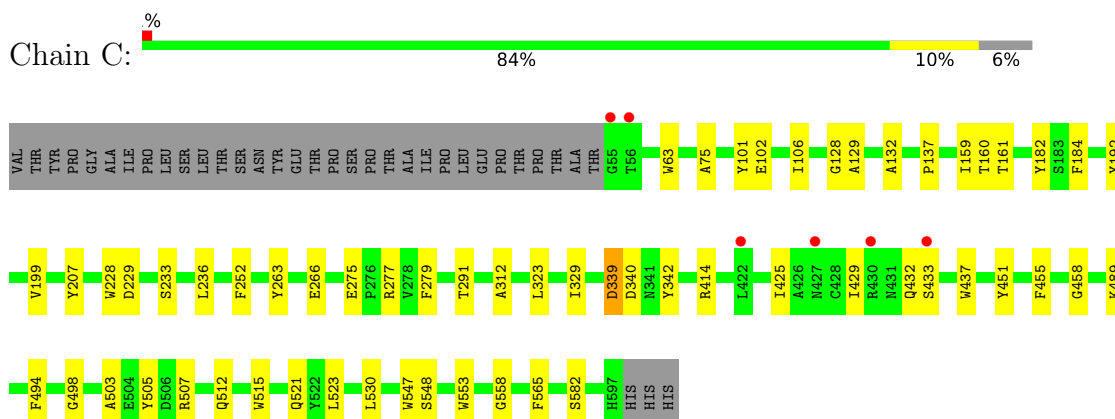
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

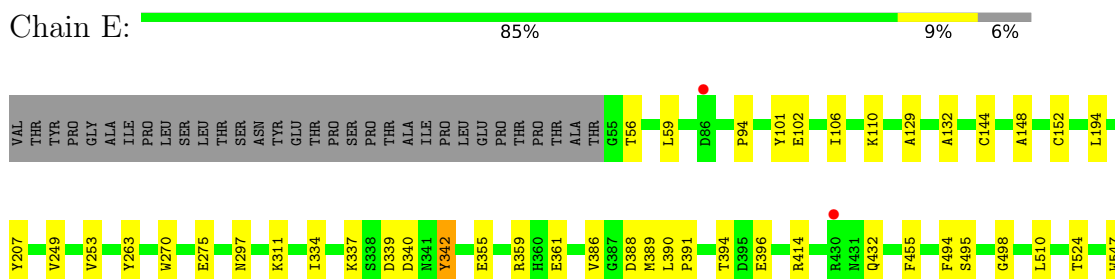
- Molecule 1: Beta-galactosidase-like enzyme



- Molecule 1: Beta-galactosidase-like enzyme

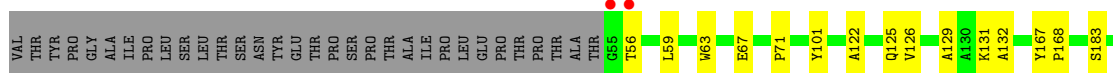
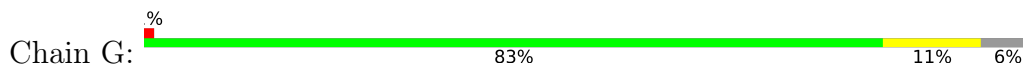


- Molecule 1: Beta-galactosidase-like enzyme





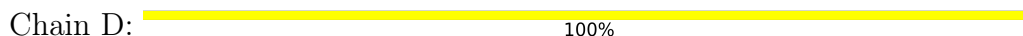
- Molecule 1: Beta-galactosidase-like enzyme



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



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




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



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




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

Chain I:  100%


MAG1
MAG2

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

Chain J:  100%


MAG1
MAG2

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

Chain K:  50% 50%

MAG1
MAG2

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

Chain L:  50% 50%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	192.75Å 67.62Å 200.87Å 90.00° 104.07° 90.00°	Depositor
Resolution (Å)	48.71 – 2.20 48.71 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.71-2.20) 99.4 (48.71-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.20Å)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.186 , 0.186 0.186 , 0.186	Depositor DCC
R_{free} test set	6359 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	41.3	Xtrriage
Anisotropy	0.290	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 36.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18617	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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: MAN, NAG

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	0.46	0/4418	0.58	0/6029
1	C	0.45	0/4429	0.55	0/6044
1	E	0.44	0/4418	0.57	0/6029
1	G	0.47	0/4440	0.58	0/6059
All	All	0.45	0/17705	0.57	0/24161

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	4284	0	4025	29	0
1	C	4294	0	4031	33	0
1	E	4284	0	4026	29	0
1	G	4304	0	4038	41	0
2	B	28	0	25	1	0
2	D	28	0	25	3	0
2	F	28	0	25	0	0
2	H	28	0	25	3	0
2	I	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	28	0	25	3	0
2	K	28	0	25	2	0
2	L	28	0	25	1	0
3	A	28	0	26	2	0
3	C	14	0	13	0	0
3	E	28	0	26	1	0
3	G	42	0	39	4	0
4	C	33	0	30	0	0
4	E	11	0	10	0	0
4	G	11	0	10	0	0
5	A	303	0	0	0	0
5	C	235	0	0	1	0
5	E	278	0	0	0	0
5	G	244	0	0	1	0
All	All	18617	0	16474	136	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 136 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)
2:J:1:NAG:H62	2:J:2:NAG:HN2	1.36	0.90
1:C:160:THR:HG23	1:C:161:THR:H	1.39	0.85
1:A:455:PHE:HE2	1:C:515:TRP:CE3	1.99	0.81
1:G:354:GLU:O	1:G:358:LYS:HD3	1.86	0.76
1:A:455:PHE:CE2	1:C:515:TRP:CE3	2.76	0.73

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	540/578 (93%)	524 (97%)	16 (3%)	0	100	100
1	C	541/578 (94%)	520 (96%)	20 (4%)	1 (0%)	47	55
1	E	540/578 (93%)	524 (97%)	16 (3%)	0	100	100
1	G	542/578 (94%)	523 (96%)	19 (4%)	0	100	100
All	All	2163/2312 (94%)	2091 (97%)	71 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	340	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	442/474 (93%)	437 (99%)	5 (1%)	73	85
1	C	443/474 (94%)	433 (98%)	10 (2%)	50	63
1	E	442/474 (93%)	434 (98%)	8 (2%)	59	72
1	G	444/474 (94%)	440 (99%)	4 (1%)	78	88
All	All	1771/1896 (93%)	1744 (98%)	27 (2%)	65	78

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	565	PHE
1	E	388	ASP
1	G	414	ARG
1	E	342	TYR
1	E	414	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	151	GLN

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](#)

16 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	B	1	1,2	14,14,15	0.29	0	17,19,21	0.61	0
2	NAG	B	2	2	14,14,15	0.30	0	17,19,21	0.62	0
2	NAG	D	1	1,2	14,14,15	0.30	0	17,19,21	0.61	0
2	NAG	D	2	2	14,14,15	0.29	0	17,19,21	0.61	0
2	NAG	F	1	1,2	14,14,15	0.29	0	17,19,21	0.61	0
2	NAG	F	2	2	14,14,15	0.30	0	17,19,21	0.61	0
2	NAG	H	1	1,2	14,14,15	1.47	2 (14%)	17,19,21	2.89	6 (35%)
2	NAG	H	2	2	14,14,15	0.90	1 (7%)	17,19,21	2.37	9 (52%)
2	NAG	I	1	1,2	14,14,15	1.18	1 (7%)	17,19,21	1.01	2 (11%)
2	NAG	I	2	2	14,14,15	1.05	1 (7%)	17,19,21	1.27	2 (11%)
2	NAG	J	1	1,2	14,14,15	0.30	0	17,19,21	0.61	0
2	NAG	J	2	2	14,14,15	0.29	0	17,19,21	0.61	0
2	NAG	K	1	1,2	14,14,15	0.23	0	17,19,21	0.56	0
2	NAG	K	2	2	14,14,15	0.41	0	17,19,21	1.22	1 (5%)
2	NAG	L	1	1,2	14,14,15	1.17	0	17,19,21	1.99	5 (29%)
2	NAG	L	2	2	14,14,15	0.89	1 (7%)	17,19,21	2.12	5 (29%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	2/6/23/26	0/1/1/1
2	NAG	D	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	F	2	2	-	1/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	H	2	2	-	6/6/23/26	0/1/1/1
2	NAG	I	1	1,2	-	1/6/23/26	0/1/1/1
2	NAG	I	2	2	-	4/6/23/26	0/1/1/1
2	NAG	J	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	J	2	2	-	6/6/23/26	0/1/1/1
2	NAG	K	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	K	2	2	-	4/6/23/26	0/1/1/1
2	NAG	L	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	L	2	2	-	2/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	1	NAG	O5-C1	-4.23	1.37	1.43
2	I	2	NAG	C1-C2	3.69	1.57	1.52
2	H	1	NAG	O5-C1	-3.48	1.38	1.43
2	L	2	NAG	C2-N2	-2.64	1.41	1.46
2	H	1	NAG	C1-C2	-2.32	1.48	1.52

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	NAG	C4-C3-C2	-7.94	99.38	111.02
2	H	1	NAG	O5-C1-C2	-6.05	101.74	111.29
2	H	2	NAG	C1-C2-N2	-4.64	102.56	110.49
2	L	2	NAG	C4-C3-C2	-4.53	104.37	111.02
2	L	2	NAG	C1-O5-C5	4.46	118.24	112.19

There are no chirality outliers.

5 of 49 torsion outliers are listed below:

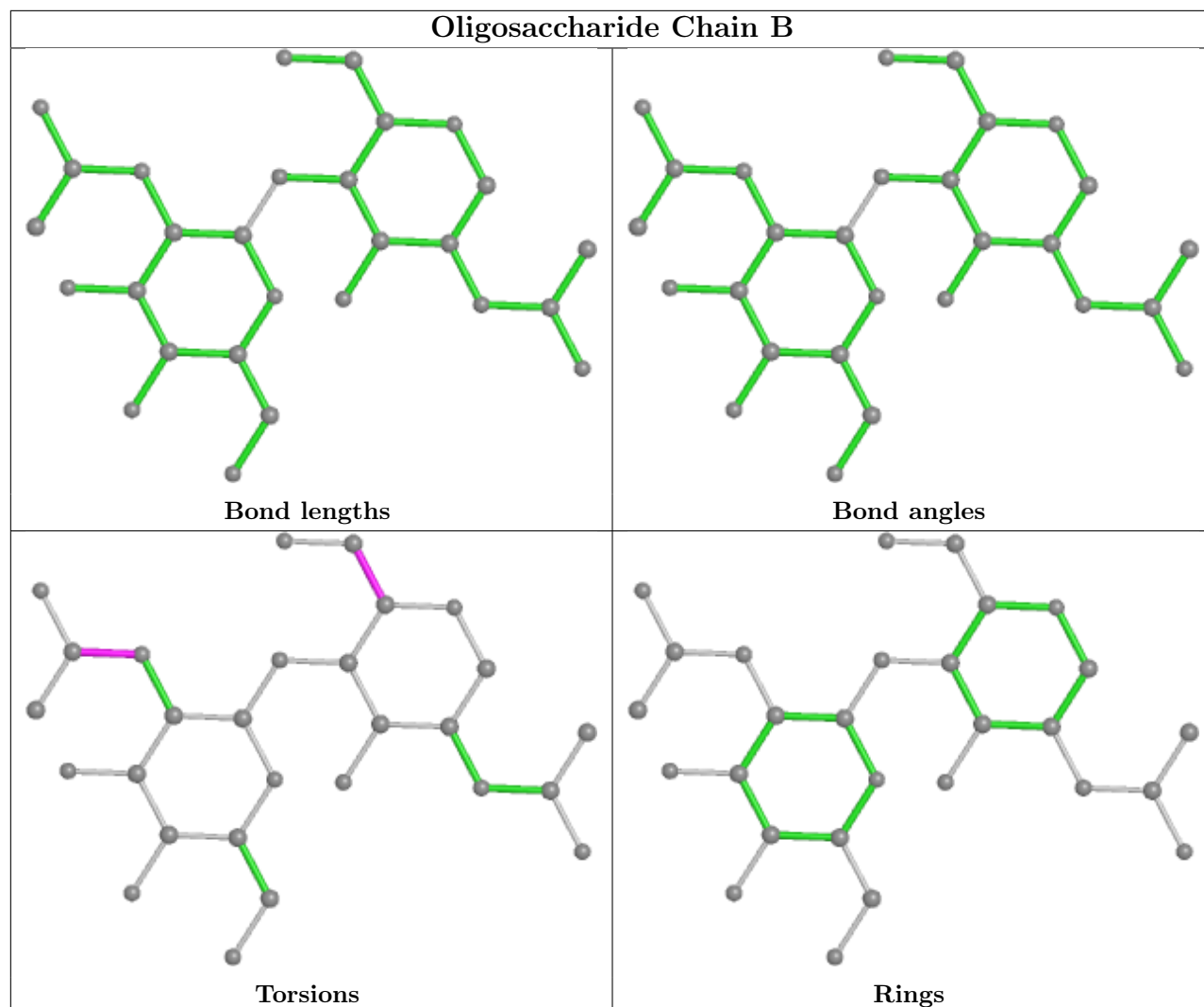
Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	H	2	NAG	C8-C7-N2-C2
2	H	2	NAG	O7-C7-N2-C2
2	J	1	NAG	C8-C7-N2-C2

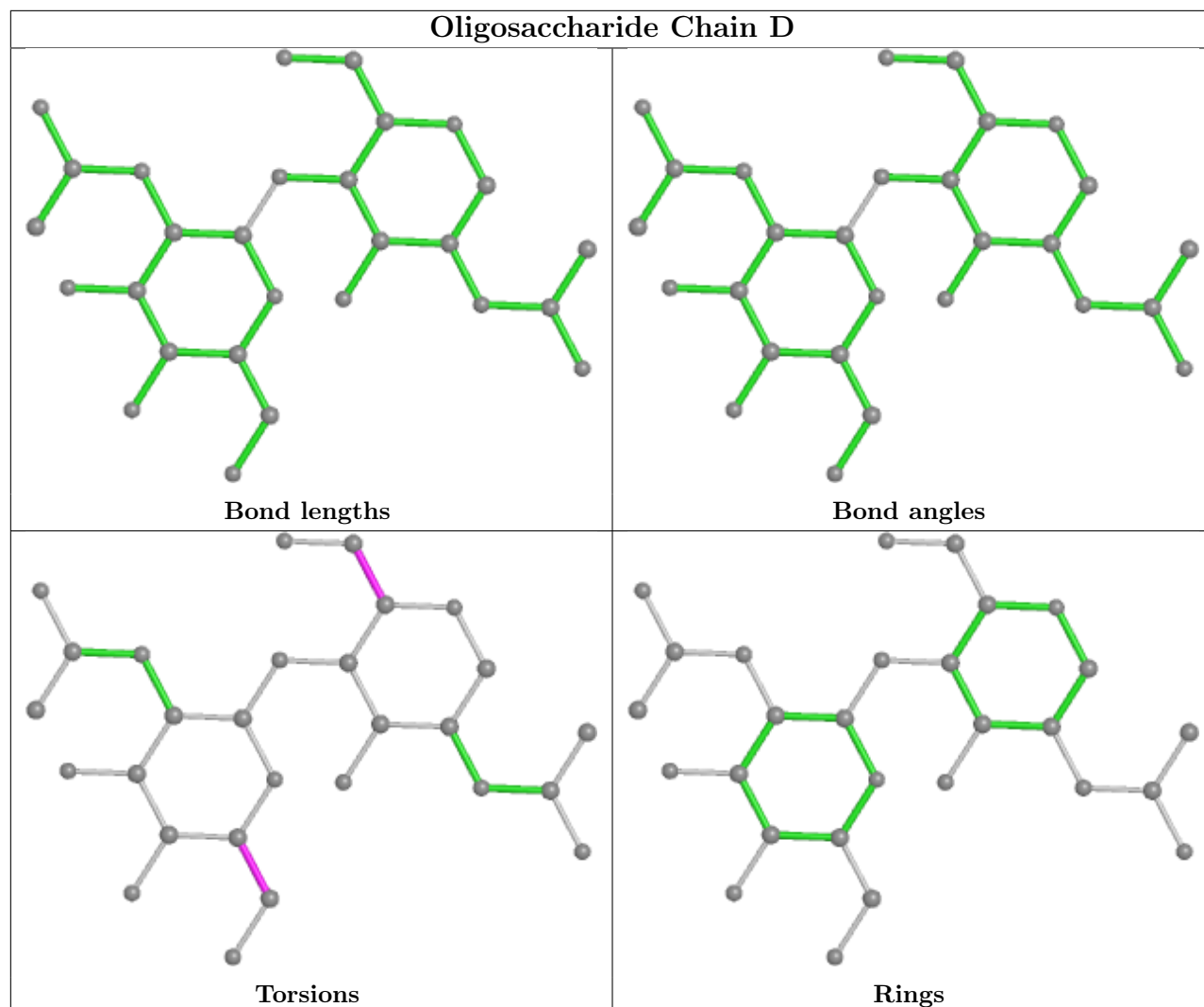
There are no ring outliers.

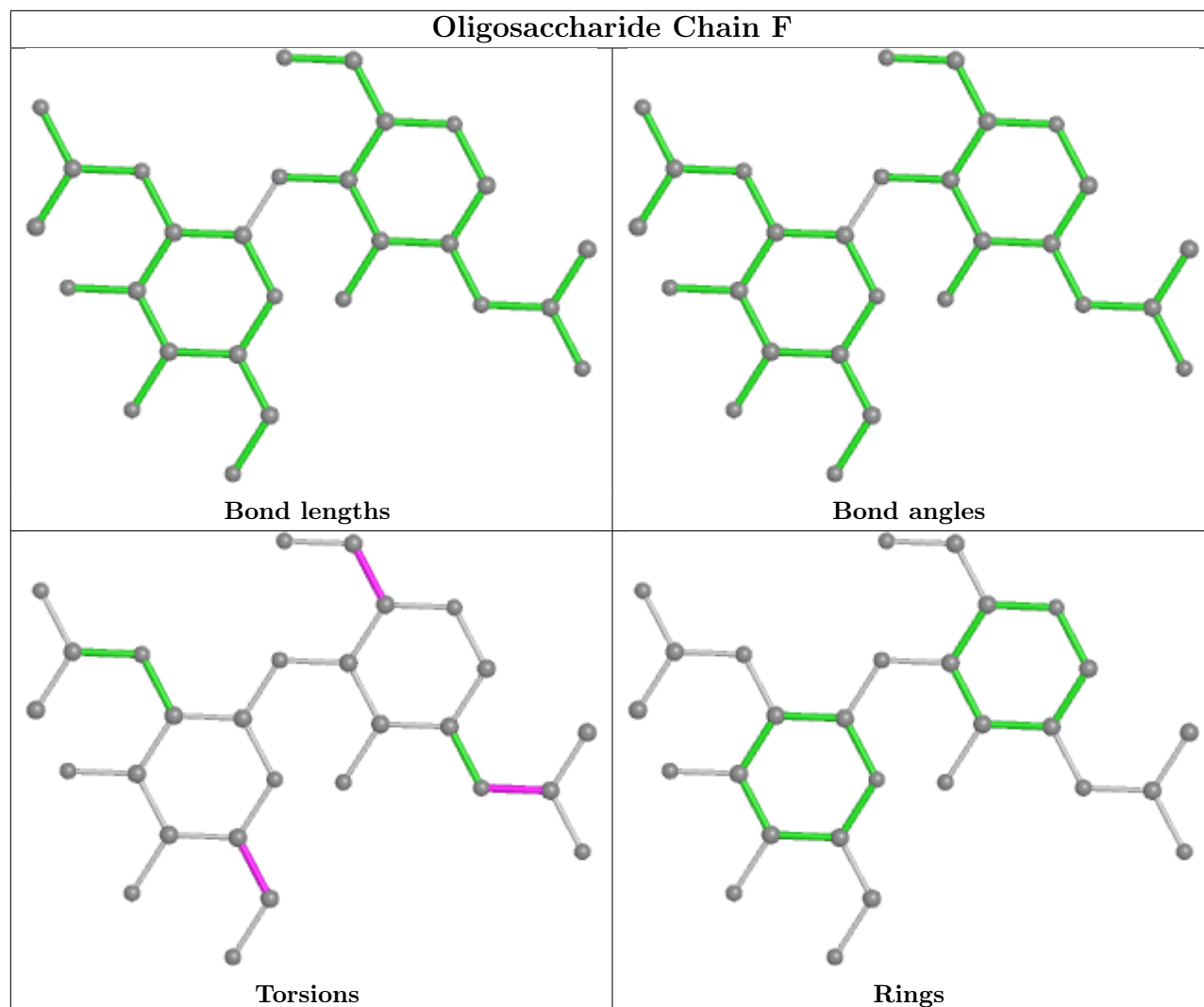
10 monomers are involved in 13 short contacts:

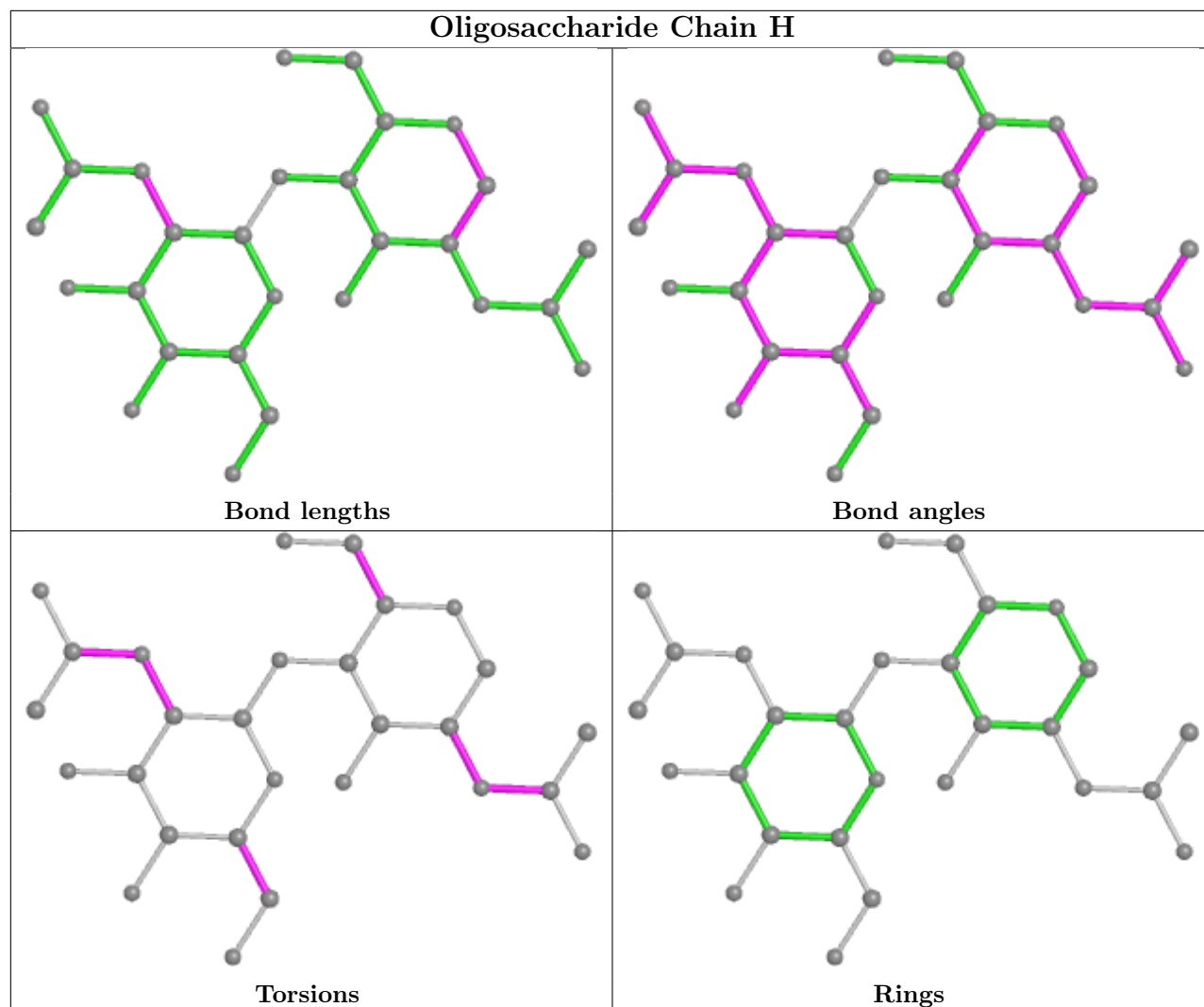
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	K	2	NAG	1	0
2	D	2	NAG	3	0
2	J	1	NAG	3	0
2	B	1	NAG	1	0
2	J	2	NAG	2	0
2	L	1	NAG	1	0
2	H	1	NAG	3	0
2	H	2	NAG	1	0
2	D	1	NAG	1	0
2	K	1	NAG	1	0

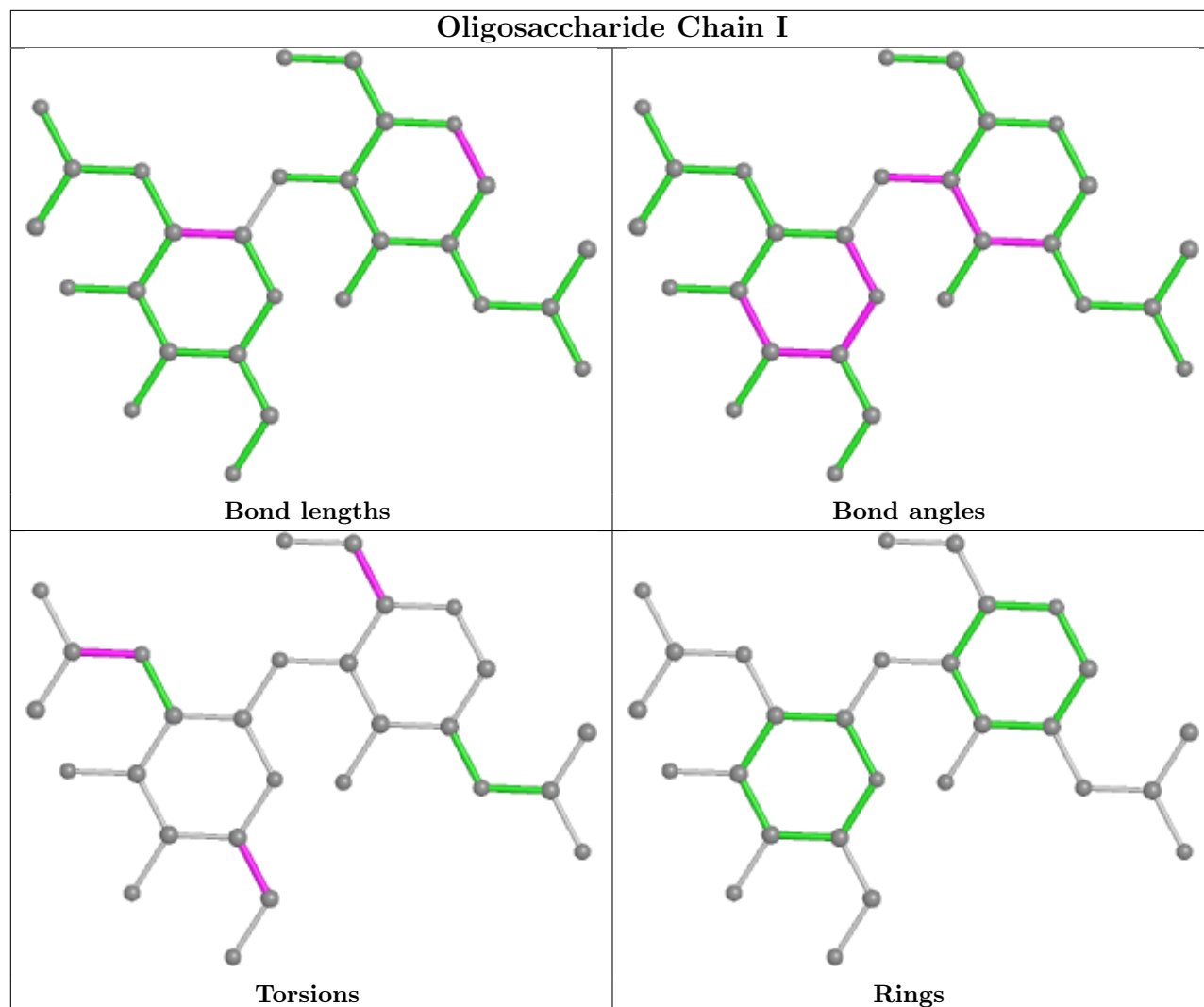
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

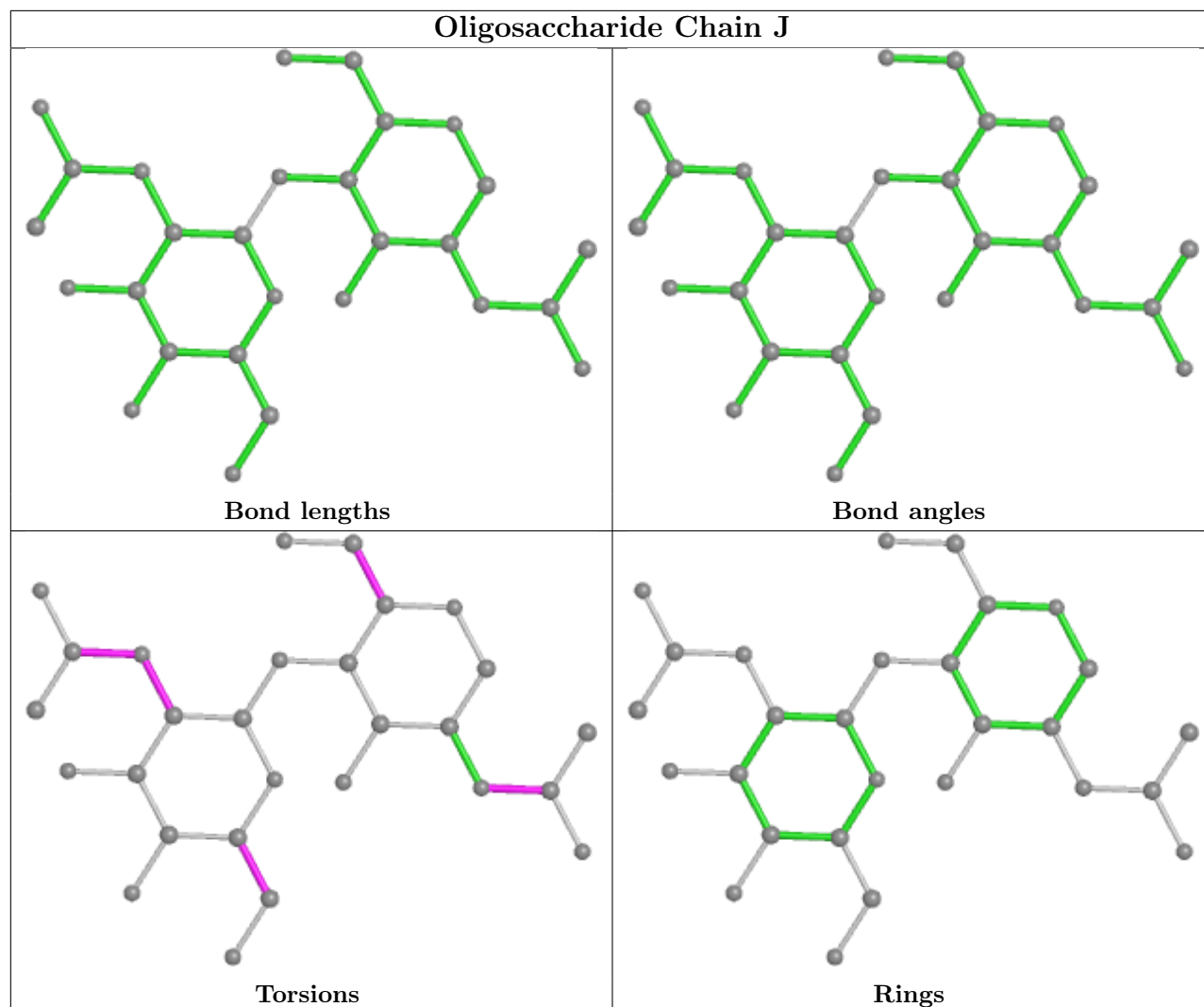


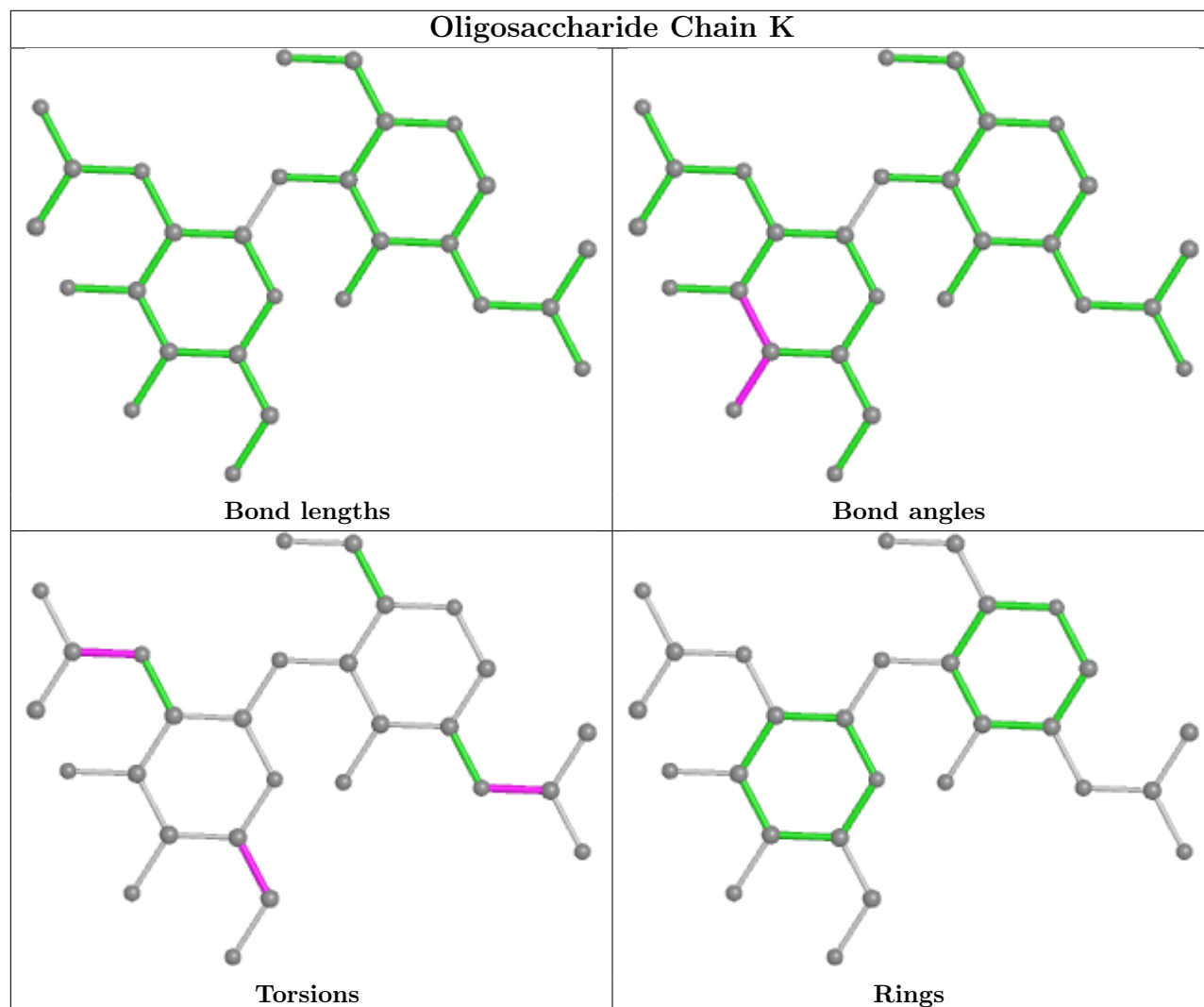


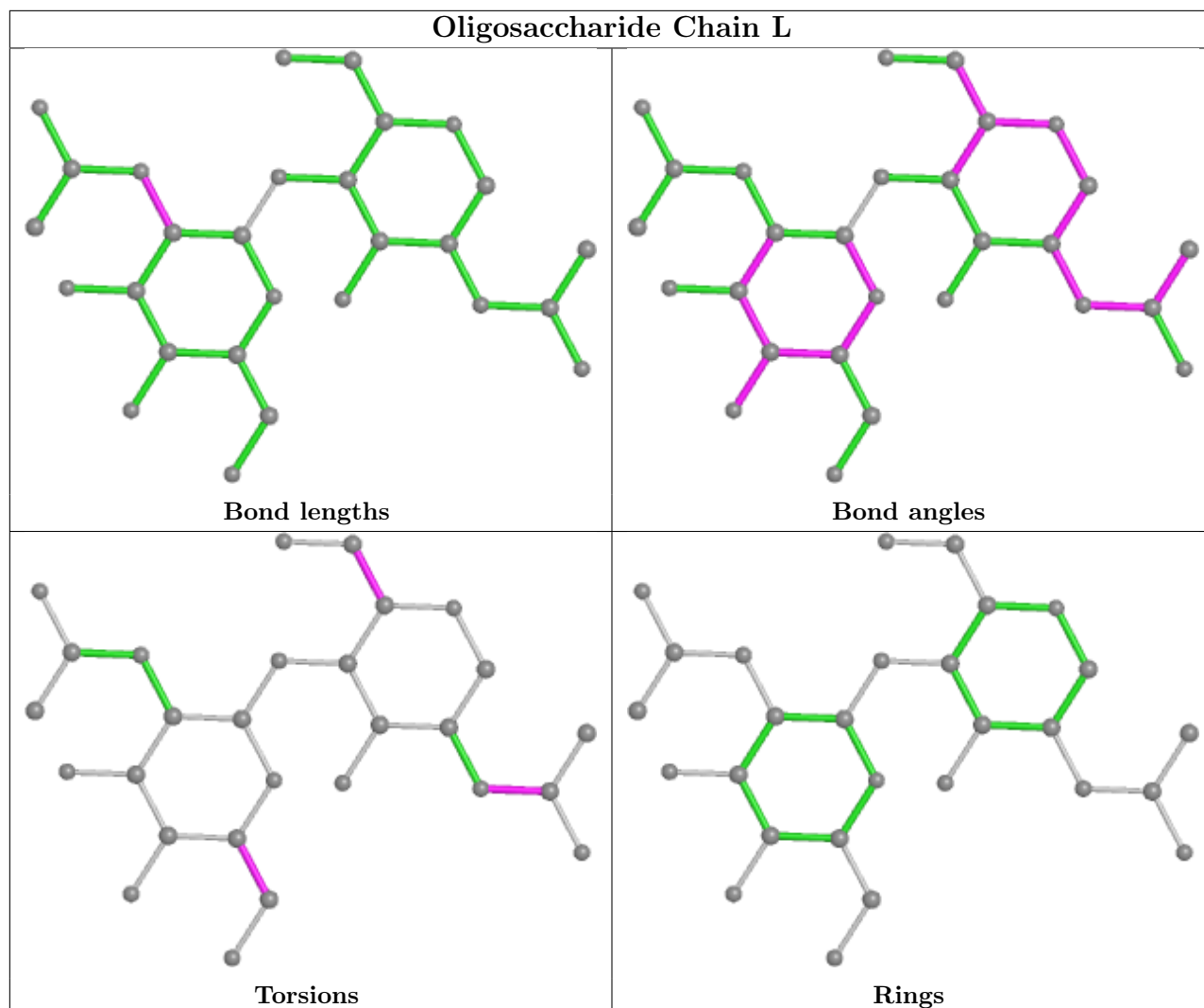












5.6 Ligand geometry [i](#)

13 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$
4	MAN	C	701	1	11,11,12	0.26	0	15,15,17	0.64	0
4	MAN	G	701	1	11,11,12	1.01	1 (9%)	15,15,17	1.04	2 (13%)
3	NAG	G	702	1	14,14,15	1.44	3 (21%)	17,19,21	2.50	6 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	701	1	14,14,15	0.34	0	17,19,21	1.44	3 (17%)
3	NAG	A	702	1	14,14,15	1.24	1 (7%)	17,19,21	1.24	3 (17%)
3	NAG	E	702	1	14,14,15	0.42	0	17,19,21	0.75	0
4	MAN	E	701	1	11,11,12	1.28	1 (9%)	15,15,17	0.93	0
3	NAG	E	703	1	14,14,15	1.16	1 (7%)	17,19,21	0.75	0
4	MAN	C	702	1	11,11,12	0.71	0	15,15,17	1.54	3 (20%)
3	NAG	G	704	1	14,14,15	1.21	1 (7%)	17,19,21	1.28	1 (5%)
4	MAN	C	703	1	11,11,12	0.87	1 (9%)	15,15,17	1.07	1 (6%)
3	NAG	G	703	1	14,14,15	0.86	1 (7%)	17,19,21	1.17	2 (11%)
3	NAG	C	704	1	14,14,15	0.80	1 (7%)	17,19,21	0.95	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
4	MAN	C	701	1	-	1/2/19/22	0/1/1/1
4	MAN	G	701	1	-	1/2/19/22	0/1/1/1
3	NAG	G	702	1	-	4/6/23/26	0/1/1/1
3	NAG	A	701	1	-	5/6/23/26	0/1/1/1
3	NAG	A	702	1	-	2/6/23/26	0/1/1/1
3	NAG	E	702	1	-	1/6/23/26	0/1/1/1
4	MAN	E	701	1	-	2/2/19/22	0/1/1/1
3	NAG	E	703	1	-	2/6/23/26	0/1/1/1
4	MAN	C	702	1	-	1/2/19/22	0/1/1/1
3	NAG	G	704	1	-	2/6/23/26	0/1/1/1
4	MAN	C	703	1	-	2/2/19/22	0/1/1/1
3	NAG	G	703	1	-	0/6/23/26	0/1/1/1
3	NAG	C	704	1	-	0/6/23/26	0/1/1/1

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	703	NAG	O5-C1	-4.01	1.37	1.43
3	G	702	NAG	O5-C1	-2.90	1.39	1.43
4	G	701	MAN	O5-C1	-2.85	1.39	1.43
3	G	702	NAG	O5-C5	-2.82	1.37	1.43
4	E	701	MAN	O5-C1	-2.76	1.39	1.43

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	702	NAG	C1-O5-C5	-5.58	104.63	112.19
4	C	702	MAN	C1-O5-C5	4.77	118.65	112.19
3	G	702	NAG	C2-N2-C7	4.53	129.36	122.90
3	A	701	NAG	C2-N2-C7	4.37	129.12	122.90
3	G	702	NAG	O5-C1-C2	-4.07	104.86	111.29

There are no chirality outliers.

5 of 23 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	G	702	NAG	C1-C2-N2-C7
3	A	701	NAG	C4-C5-C6-O6
3	A	701	NAG	C8-C7-N2-C2
3	A	701	NAG	O7-C7-N2-C2
3	A	702	NAG	C8-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	702	NAG	2	0
3	A	701	NAG	2	0
3	E	703	NAG	1	0
3	G	704	NAG	1	0
3	G	703	NAG	1	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 [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	542/578 (93%)	-0.33	3 (0%) 89 88	28, 39, 52, 71	0
1	C	543/578 (93%)	-0.21	6 (1%) 80 79	29, 42, 57, 81	0
1	E	542/578 (93%)	-0.29	2 (0%) 92 91	29, 40, 54, 77	0
1	G	544/578 (94%)	-0.23	3 (0%) 89 88	26, 41, 55, 85	0
All	All	2171/2312 (93%)	-0.27	14 (0%) 89 88	26, 40, 55, 85	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	56	THR	3.5
1	G	55	GLY	3.2
1	C	55	GLY	3.1
1	G	430	ARG	2.7
1	E	86	ASP	2.6

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

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

6.3 Carbohydrates [i](#)

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

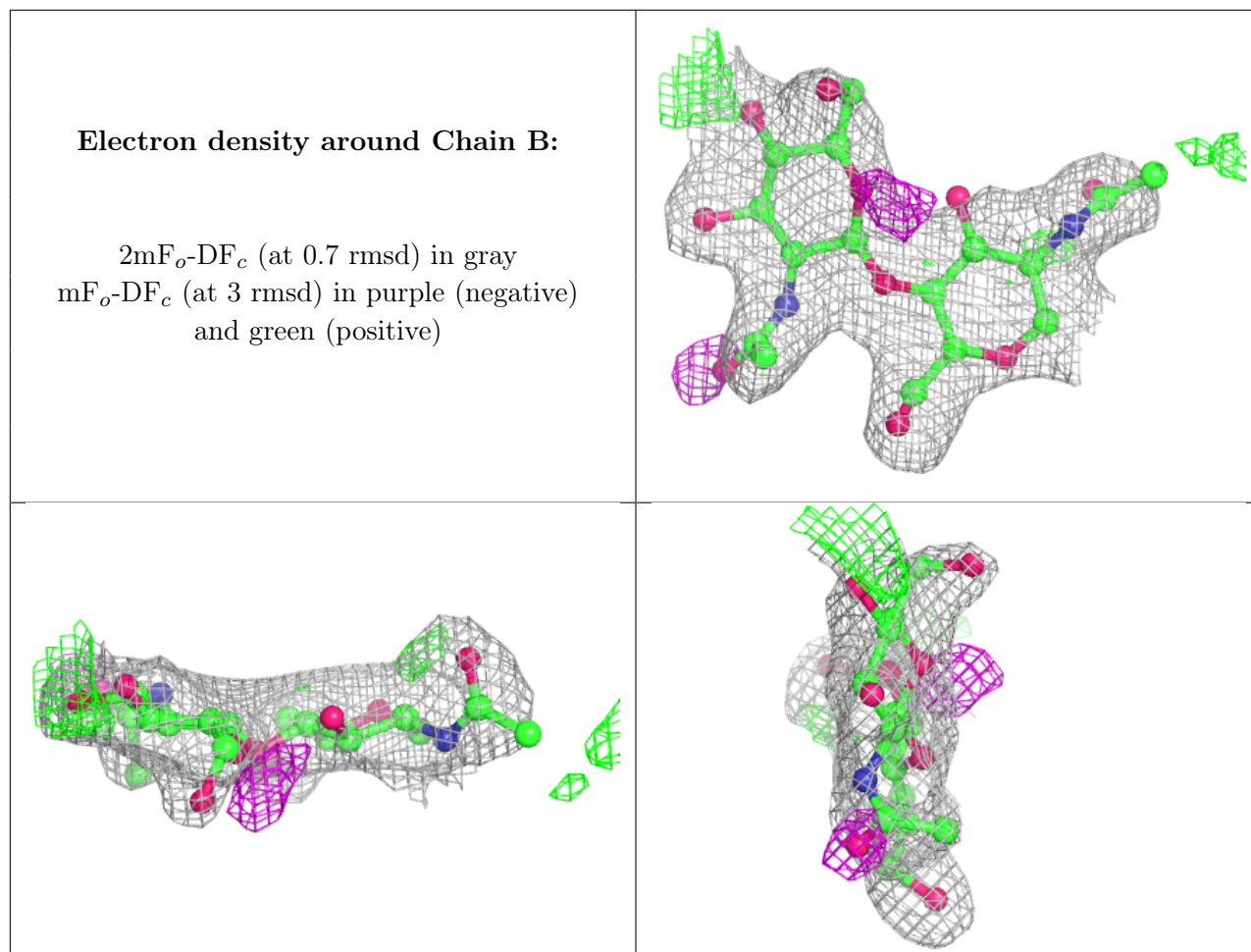
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	I	2	14/15	0.74	0.34	73,80,89,93	0
2	NAG	L	2	14/15	0.80	0.21	63,75,81,85	0

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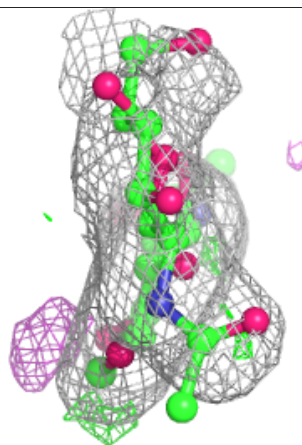
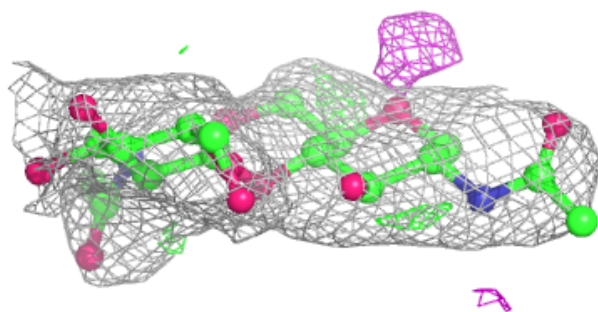
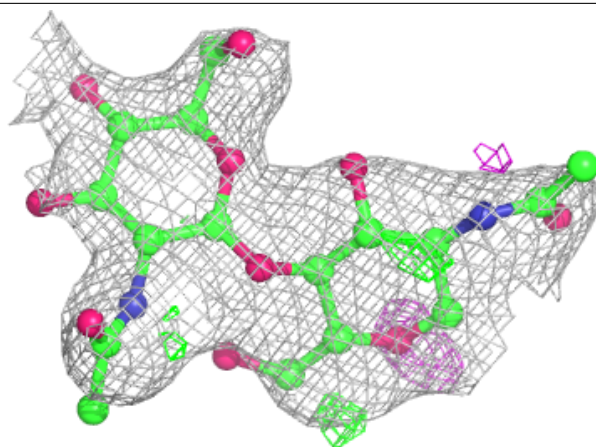
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	D	2	14/15	0.82	0.26	66,76,81,82	0
2	NAG	J	1	14/15	0.83	0.14	54,60,66,66	0
2	NAG	H	2	14/15	0.85	0.23	70,75,88,91	0
2	NAG	K	2	14/15	0.85	0.17	63,71,76,83	0
2	NAG	F	2	14/15	0.85	0.32	65,70,78,87	0
2	NAG	B	2	14/15	0.87	0.20	58,60,70,78	0
2	NAG	J	2	14/15	0.87	0.23	72,78,88,92	0
2	NAG	F	1	14/15	0.88	0.15	49,56,63,64	0
2	NAG	I	1	14/15	0.90	0.14	33,46,56,65	0
2	NAG	B	1	14/15	0.90	0.15	48,53,59,69	0
2	NAG	D	1	14/15	0.90	0.16	50,59,68,74	0
2	NAG	H	1	14/15	0.91	0.14	58,60,68,70	0
2	NAG	L	1	14/15	0.92	0.14	52,61,69,72	0
2	NAG	K	1	14/15	0.94	0.11	51,59,65,67	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.



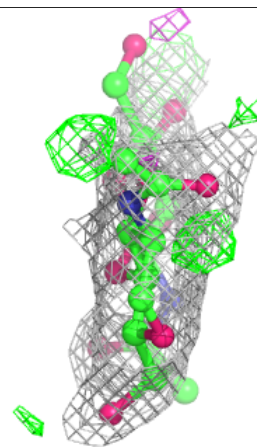
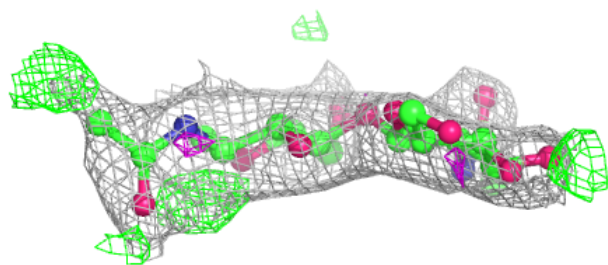
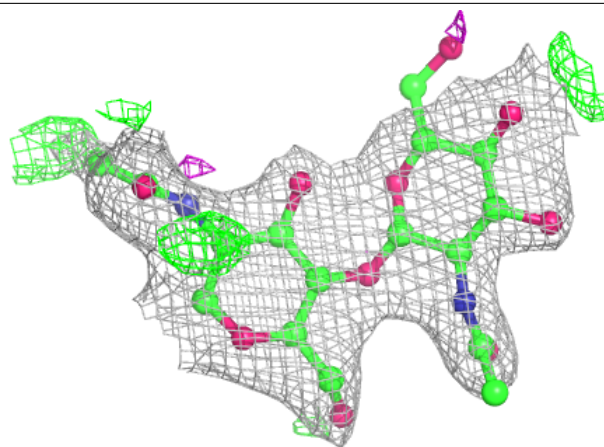
Electron density around Chain D:

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



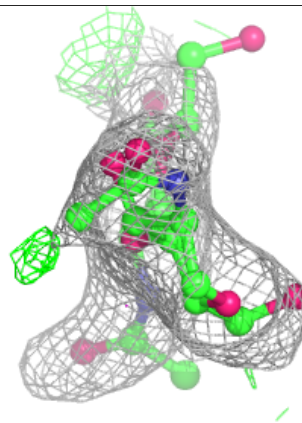
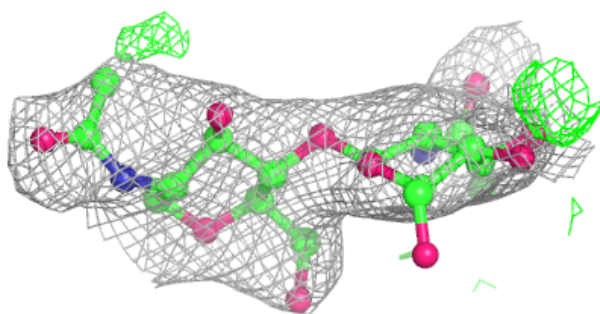
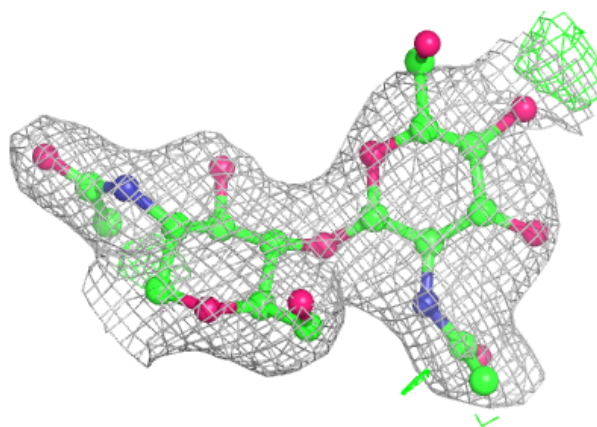
Electron density around Chain F:

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

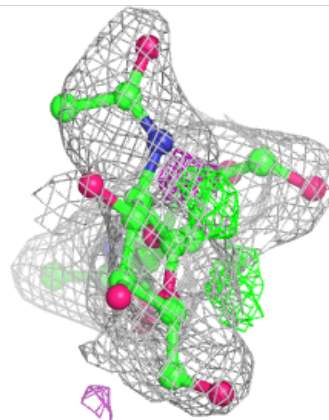
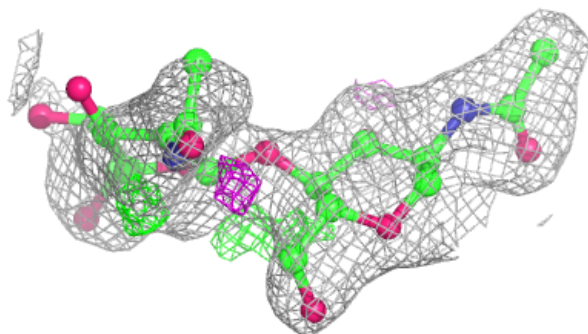
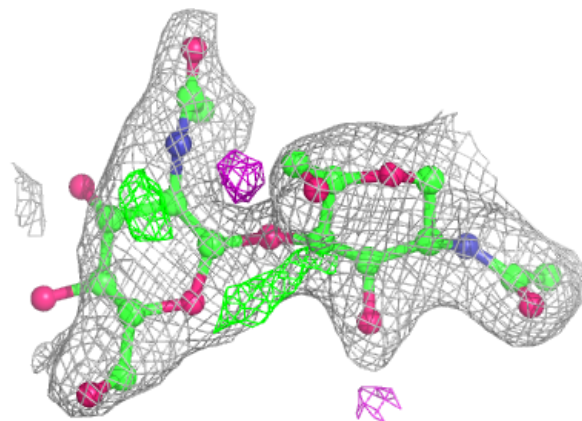


Electron density around Chain H:

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

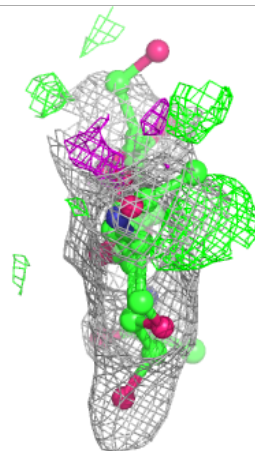
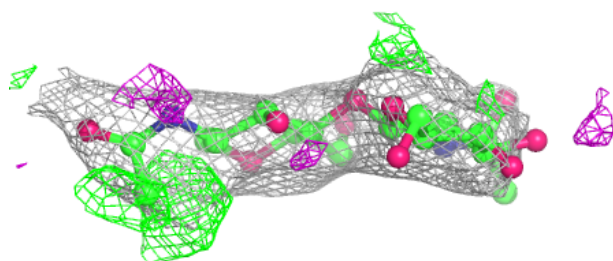
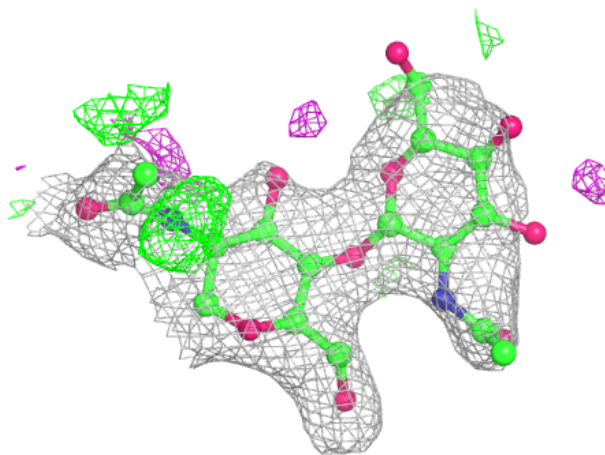
**Electron density around Chain I:**

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



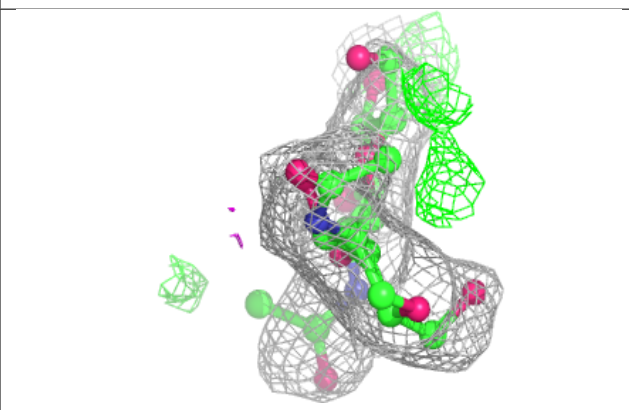
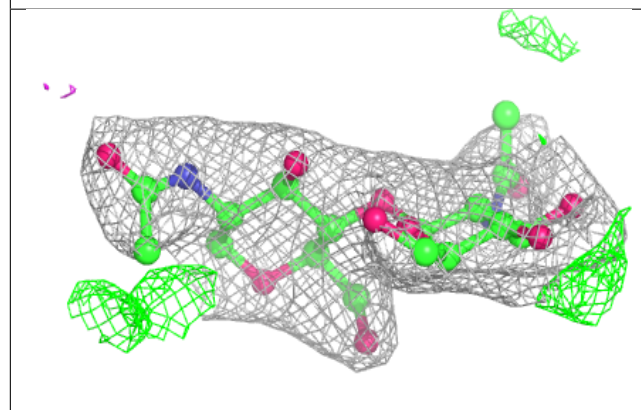
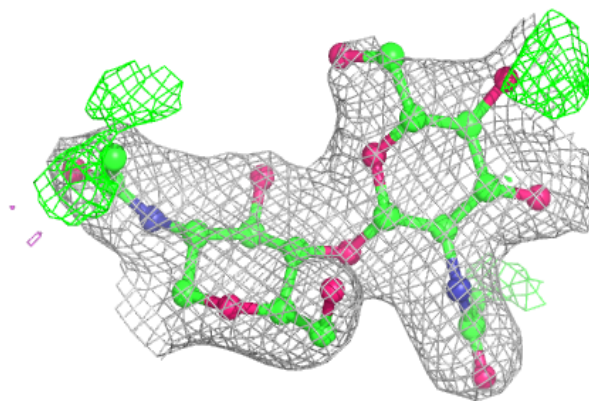
Electron density around Chain J:

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

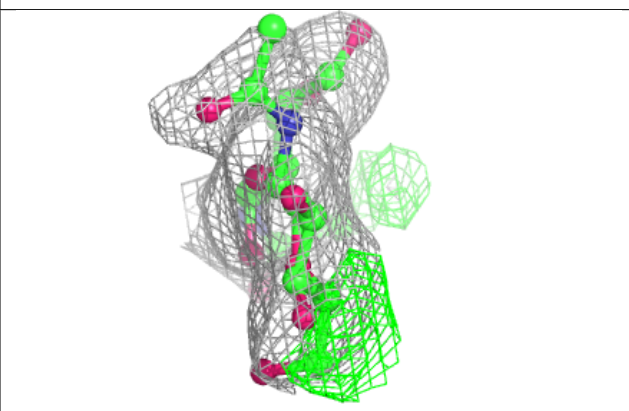
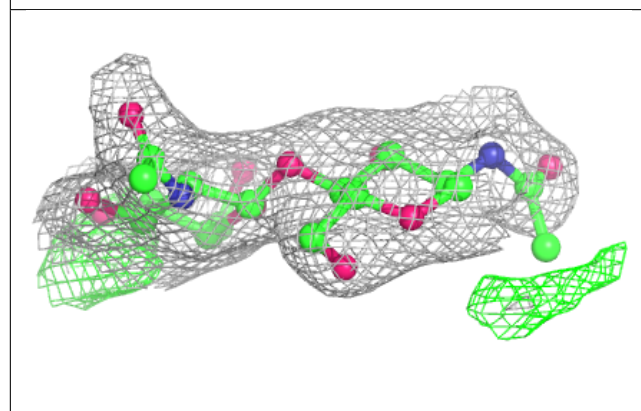
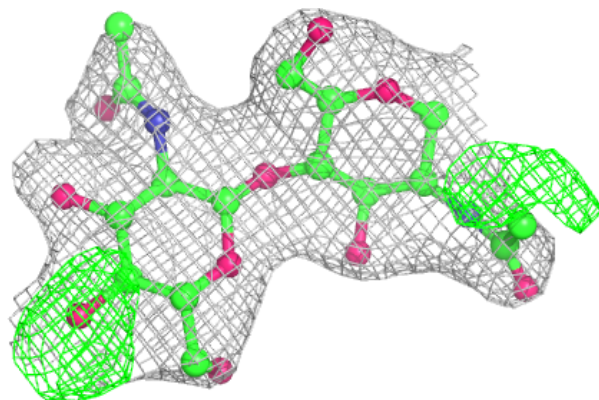


Electron density around Chain K:

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

**Electron density around Chain L:**

$2mF_o-DF_c$ (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
4	MAN	C	701	11/12	0.78	0.29	57,62,68,70	0
3	NAG	G	702	14/15	0.81	0.16	58,66,70,74	0
3	NAG	G	703	14/15	0.82	0.27	64,69,78,86	0
3	NAG	C	704	14/15	0.83	0.26	65,68,81,88	0
3	NAG	A	701	14/15	0.86	0.29	57,62,74,76	0
4	MAN	C	702	11/12	0.88	0.26	63,68,74,75	0
3	NAG	A	702	14/15	0.89	0.15	32,52,64,78	0
4	MAN	G	701	11/12	0.89	0.28	55,58,63,64	0
3	NAG	E	703	14/15	0.91	0.13	28,45,55,66	0
4	MAN	C	703	11/12	0.91	0.26	54,58,64,65	0
3	NAG	E	702	14/15	0.91	0.19	55,61,68,72	0
4	MAN	E	701	11/12	0.93	0.18	49,51,55,63	0
3	NAG	G	704	14/15	0.93	0.10	34,47,60,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.