



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:51 AM UTC

PDB ID : 5ERD / pdb_00005erd
Title : Crystal structure of human Desmoglein-2 ectodomain
Authors : Brasch, J.; Harrison, O.J.; Shapiro, L.
Deposited on : 2015-11-13
Resolution : 2.90 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)
Xtrriage (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

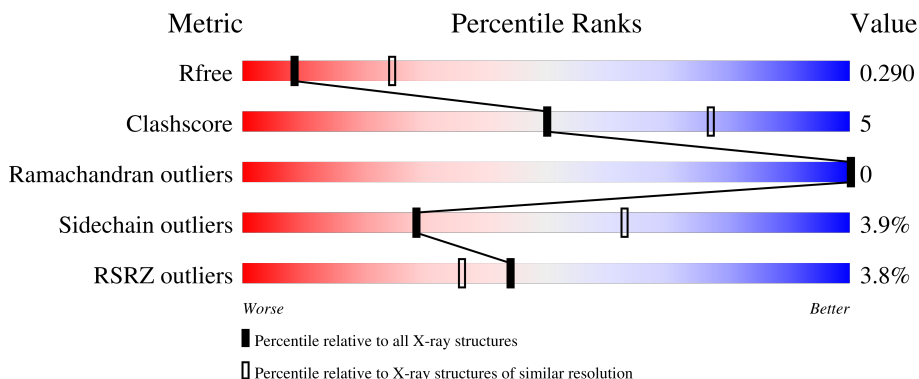
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

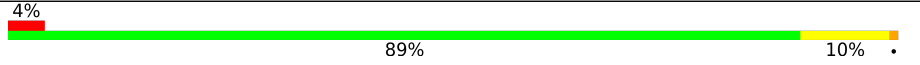
The reported resolution of this entry is 2.90 Å.

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.




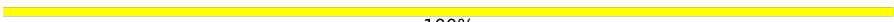

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	559	 3% 86% 12% ..
1	B	559	 4% 89% 10% .
2	C	3	 33% 33% 33%
2	D	3	 33% 67%
2	G	3	 100%

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Mol	Chain	Length	Quality of chain
3	E	4	 100%
4	F	2	 50% 50%
4	H	2	 100%
4	I	2	 50% 50%

2 Entry composition i

There are 9 unique types of molecules in this entry. The entry contains 18333 atoms, of which 8981 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.

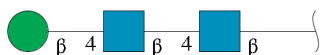
- Molecule 1 is a protein called Desmoglein-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	554	8661	2756	4295	726	873	11	0	2	0
1	B	559	8735	2782	4325	740	877	11	0	1	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	554	HIS	-	expression tag	UNP Q14126
A	555	HIS	-	expression tag	UNP Q14126
A	556	HIS	-	expression tag	UNP Q14126
A	557	HIS	-	expression tag	UNP Q14126
A	558	HIS	-	expression tag	UNP Q14126
A	559	HIS	-	expression tag	UNP Q14126
B	554	HIS	-	expression tag	UNP Q14126
B	555	HIS	-	expression tag	UNP Q14126
B	556	HIS	-	expression tag	UNP Q14126
B	557	HIS	-	expression tag	UNP Q14126
B	558	HIS	-	expression tag	UNP Q14126
B	559	HIS	-	expression tag	UNP Q14126

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



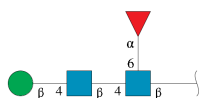
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	C	3	77	22	38	2	15	0	0	0

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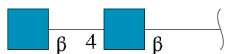
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	3	Total	C	H	N	O	0	0	0
			77	22	38	2	15			
2	G	3	Total	C	H	N	O	0	0	0
			77	22	38	2	15			

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	4	Total	C	H	N	O	0	0	0
			98	28	49	2	19			

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



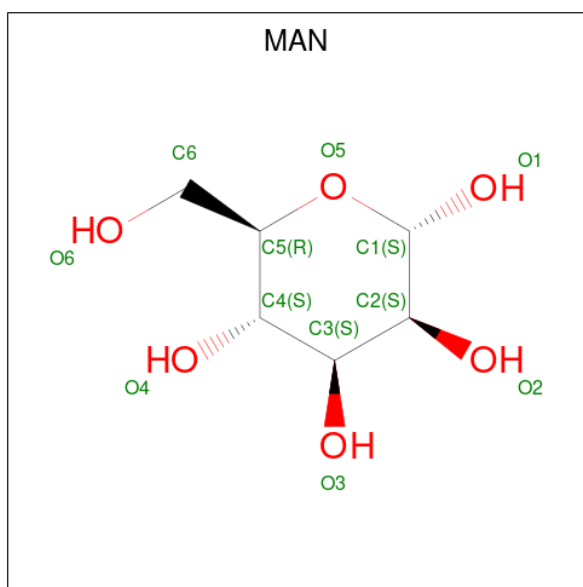
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	2	Total	C	H	N	O	0	0	0
			56	16	28	2	10			
4	H	2	Total	C	H	N	O	0	0	0
			56	16	28	2	10			
4	I	2	Total	C	H	N	O	0	0	0
			56	16	28	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
			Total	C	H	N			O	
5	A	1	Total	28	8	14	1	5	0	0
5	A	1	Total	28	8	14	1	5	0	0
5	B	1	Total	28	8	14	1	5	0	0

- Molecule 6 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	H	O			
6	A	1	Total	22	6	11	5	0	0

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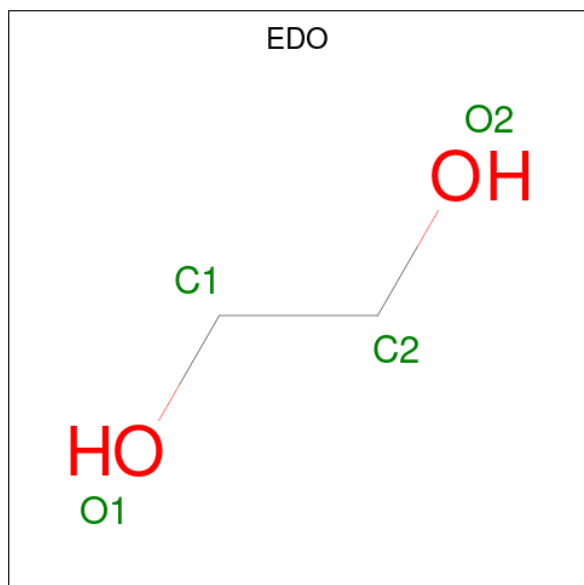
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			22	6	11	5		
6	A	1	Total	C	H	O	0	0
			22	6	11	5		
6	B	1	Total	C	H	O	0	0
			22	6	11	5		
6	B	1	Total	C	H	O	0	0
			22	6	11	5		
6	B	1	Total	C	H	O	0	0
			22	6	11	5		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	11	Total	Ca	0	0
			11	11		
7	B	11	Total	Ca	0	0
			11	11		

- Molecule 8 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	H	O	0	0
			10	2	6	2		

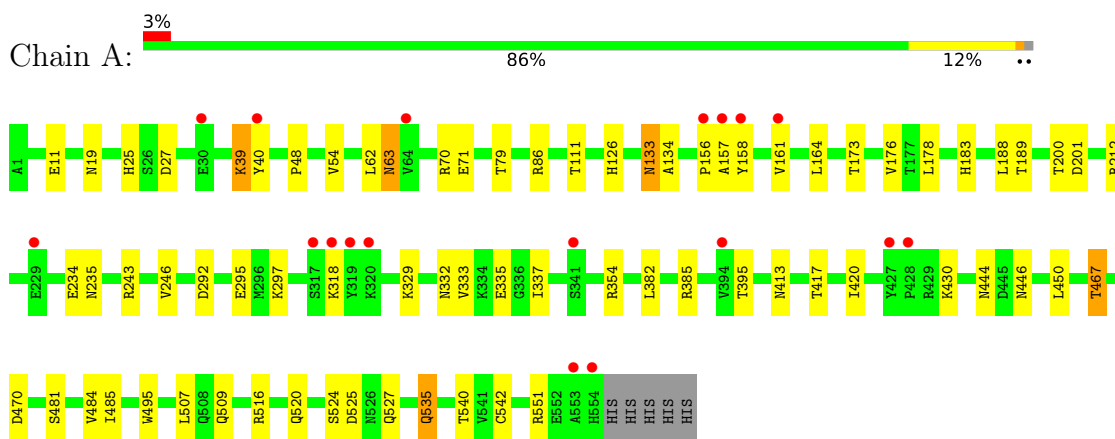
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	98	Total 98	O 98	0	0
9	B	94	Total 94	O 94	0	0

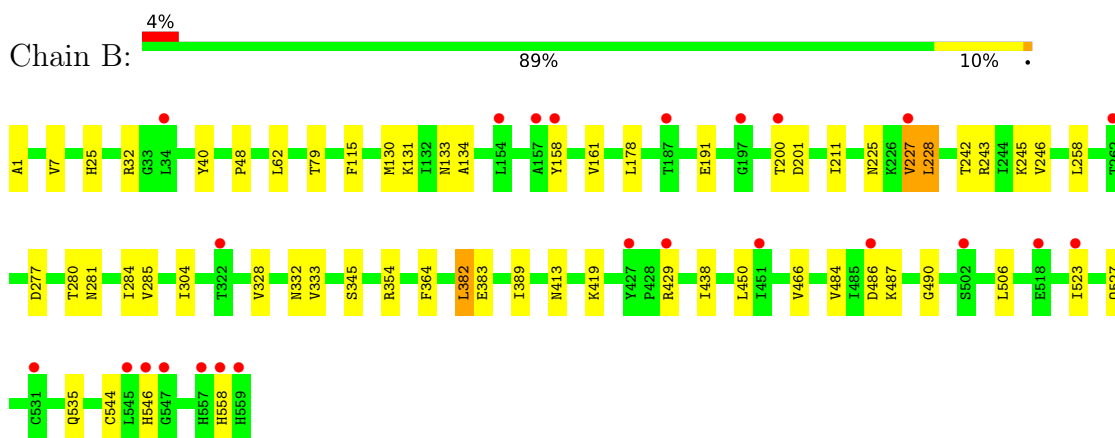
3 Residue-property plots [i](#)

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.

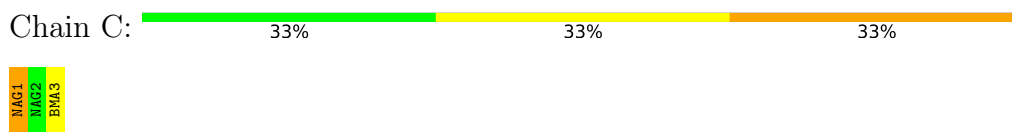
- Molecule 1: Desmoglein-2



- Molecule 1: Desmoglein-2



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



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

Chain D:  33% 67%

MAG1
MAG2
BMA3

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

Chain G:  100%

MAG1
MAG2
BMA3

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

Chain E:  100%

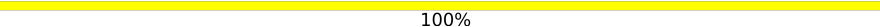
MAG1
MAG2
BMA3
FUC4

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

Chain F:  50% 50%

MAG1
MAG2

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

Chain H:  100%

MAG1
MAG2

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

Chain I:  50% 50%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.97Å 114.48Å 226.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.39 – 2.90 84.39 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (84.39-2.90) 86.4 (84.39-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.73 (at 2.91Å)	Xtrriage
Refinement program	PHENIX dev_1810	Depositor
R, R_{free}	0.241 , 0.287 0.246 , 0.290	Depositor DCC
R_{free} test set	2664 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	48.9	Xtrriage
Anisotropy	0.764	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18333	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.62% 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: NAG, BMA, CA, EDO, MAN, FUC

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	0.47	4/4455 (0.1%)	0.69	4/6049 (0.1%)
1	B	0.43	0/4501	0.66	1/6112 (0.0%)
All	All	0.45	4/8956 (0.0%)	0.67	5/12161 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	86	ARG	C-O	6.02	1.31	1.24
1	A	446	ASN	C-O	-5.34	1.17	1.23
1	A	86	ARG	CA-C	5.07	1.59	1.52
1	A	413	ASN	CG-ND2	5.04	1.43	1.33

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	48	PRO	O-C-N	7.19	124.53	121.15
1	A	446	ASN	CA-C-O	5.68	127.42	120.60
1	A	86	ARG	CA-C-O	5.67	126.62	120.55
1	A	318	LYS	N-CA-C	-5.61	106.44	113.28
1	A	48	PRO	O-C-N	5.05	123.53	121.15

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	4366	4295	4297	42	2
1	B	4410	4325	4325	30	1
2	C	39	38	34	3	0
2	D	39	38	34	6	0
2	G	39	38	34	7	0
3	E	49	49	43	6	0
4	F	28	28	25	4	0
4	H	28	28	25	0	0
4	I	28	28	25	3	0
5	A	28	28	26	3	0
5	B	14	14	13	1	0
6	A	33	33	30	0	0
6	B	33	33	29	2	1
7	A	11	0	0	0	0
7	B	11	0	0	0	0
8	A	4	6	5	0	0
9	A	98	0	0	5	0
9	B	94	0	0	2	0
All	All	9352	8981	8945	95	3

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 5.

The worst 5 of 95 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:D:1:NAG:C6	2:D:2:NAG:H2	2.04	0.88
1:A:133:ASN:OD1	1:A:134:ALA:N	2.13	0.82
2:G:2:NAG:O6	2:G:3:BMA:O5	1.98	0.81
2:D:1:NAG:O6	2:D:2:NAG:O7	2.00	0.80
4:I:2:NAG:H3	4:I:2:NAG:H82	1.65	0.79

All (3) 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)
1:A:235:ASN:O	6:B:901:MAN:O4[1_554]	1.67	0.53
1:A:158:TYR:OH	1:A:484:VAL:O[2_555]	1.97	0.23
1:B:158:TYR:OH	1:B:484:VAL:O[2_454]	2.01	0.19

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	554/559 (99%)	527 (95%)	27 (5%)	0	100	100
1	B	558/559 (100%)	527 (94%)	31 (6%)	0	100	100
All	All	1112/1118 (100%)	1054 (95%)	58 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	494/497 (99%)	476 (96%)	18 (4%)	31	65
1	B	498/497 (100%)	477 (96%)	21 (4%)	26	60
All	All	992/994 (100%)	953 (96%)	39 (4%)	28	63

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	328	VAL
1	B	506	LEU
1	B	345	SER
1	B	382	LEU
1	B	546	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	387	ASN
1	B	446	ASN
1	B	557	HIS
1	B	556	HIS
1	B	219	ASN

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](#)

19 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	NAG	C	1	2,1	14,14,15	0.75	1 (7%)	17,19,21	1.50	3 (17%)
2	NAG	C	2	2	14,14,15	0.49	0	17,19,21	0.81	0
2	BMA	C	3	2	11,11,12	2.89	8 (72%)	15,15,17	1.34	1 (6%)
2	NAG	D	1	2,1	14,14,15	2.06	1 (7%)	17,19,21	1.35	1 (5%)
2	NAG	D	2	2	14,14,15	2.03	2 (14%)	17,19,21	2.09	4 (23%)
2	BMA	D	3	2	11,11,12	2.98	8 (72%)	15,15,17	1.79	4 (26%)
3	NAG	E	1	3,1	14,14,15	1.14	1 (7%)	17,19,21	1.63	5 (29%)
3	NAG	E	2	3	14,14,15	0.89	2 (14%)	17,19,21	1.63	4 (23%)
3	BMA	E	3	3	11,11,12	2.39	6 (54%)	15,15,17	1.67	3 (20%)
3	FUC	E	4	3	10,10,11	1.37	2 (20%)	14,14,16	0.84	0
4	NAG	F	1	4,1	14,14,15	0.75	1 (7%)	17,19,21	2.16	3 (17%)
4	NAG	F	2	4	14,14,15	0.81	1 (7%)	17,19,21	0.84	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	G	1	2,1	14,14,15	0.80	0	17,19,21	2.02	3 (17%)
2	NAG	G	2	2	14,14,15	1.00	2 (14%)	17,19,21	1.59	3 (17%)
2	BMA	G	3	2	11,11,12	3.24	9 (81%)	15,15,17	1.35	2 (13%)
4	NAG	H	1	4,1	14,14,15	1.04	1 (7%)	17,19,21	1.04	0
4	NAG	H	2	4	14,14,15	1.41	2 (14%)	17,19,21	1.08	1 (5%)
4	NAG	I	1	4,1	14,14,15	0.99	2 (14%)	17,19,21	1.23	2 (11%)
4	NAG	I	2	4	14,14,15	0.78	1 (7%)	17,19,21	1.52	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	BMA	D	3	2	-	2/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1
3	BMA	E	3	3	-	1/2/19/22	0/1/1/1
3	FUC	E	4	3	-	-	0/1/1/1
4	NAG	F	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	F	2	4	-	1/6/23/26	0/1/1/1
2	NAG	G	1	2,1	-	3/6/23/26	0/1/1/1
2	NAG	G	2	2	-	1/6/23/26	0/1/1/1
2	BMA	G	3	2	-	2/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	4/6/23/26	0/1/1/1
4	NAG	I	2	4	-	5/6/23/26	0/1/1/1

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	NAG	O5-C1	-7.43	1.31	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NAG	C1-C2	6.50	1.61	1.52
2	D	3	BMA	O5-C1	5.15	1.52	1.43
2	G	3	BMA	O2-C2	5.15	1.54	1.43
2	C	3	BMA	O2-C2	4.54	1.52	1.43

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1	NAG	C2-N2-C7	6.50	131.61	122.90
2	D	2	NAG	C1-O5-C5	-5.85	104.35	112.19
2	G	1	NAG	C2-N2-C7	5.72	130.57	122.90
4	I	2	NAG	C2-N2-C7	5.17	129.83	122.90
3	E	2	NAG	C1-O5-C5	4.85	118.69	112.19

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

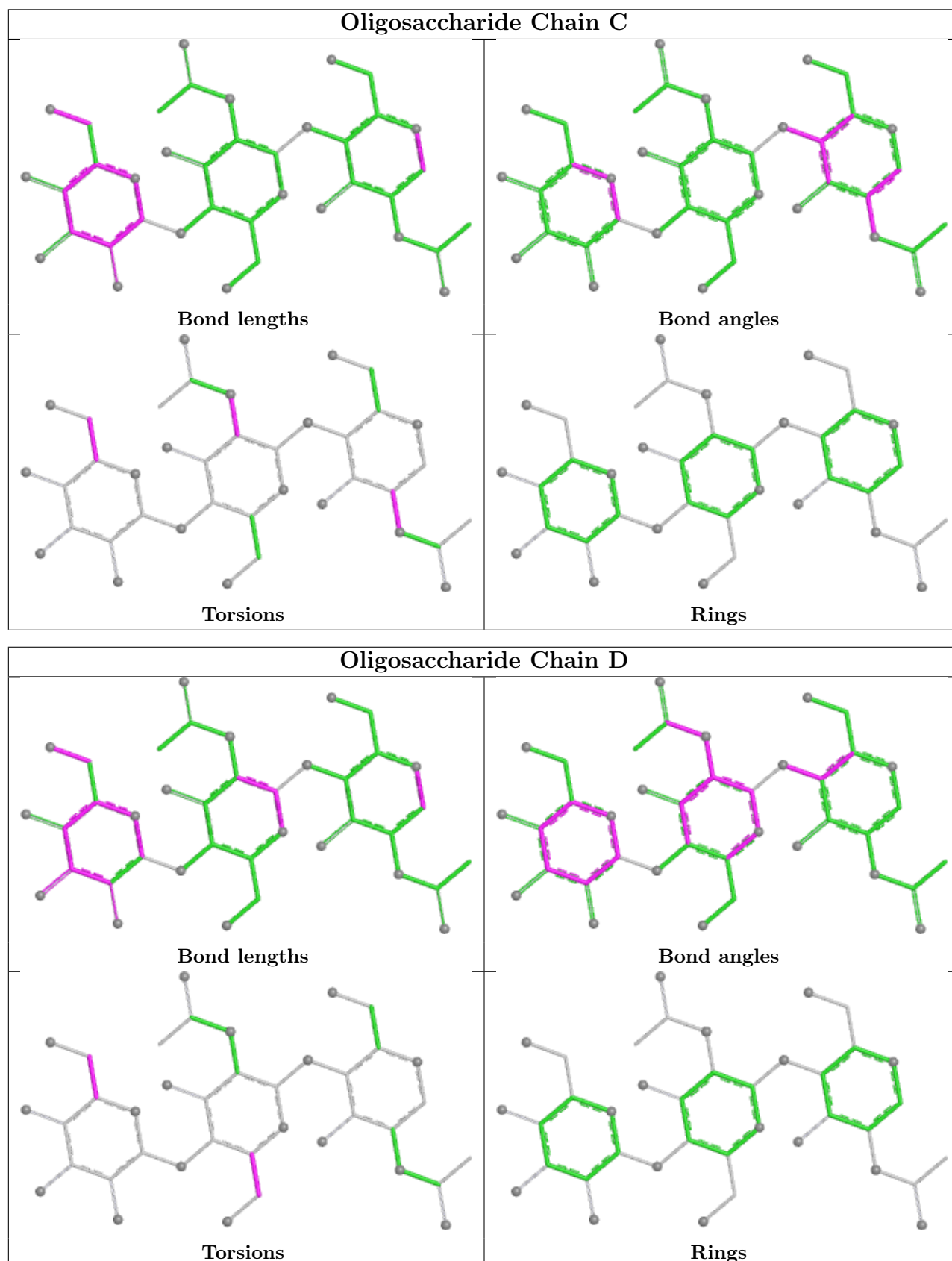
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C1-C2-N2-C7
2	G	1	NAG	C3-C2-N2-C7
2	G	2	NAG	C1-C2-N2-C7
3	E	1	NAG	C1-C2-N2-C7
4	F	1	NAG	C3-C2-N2-C7

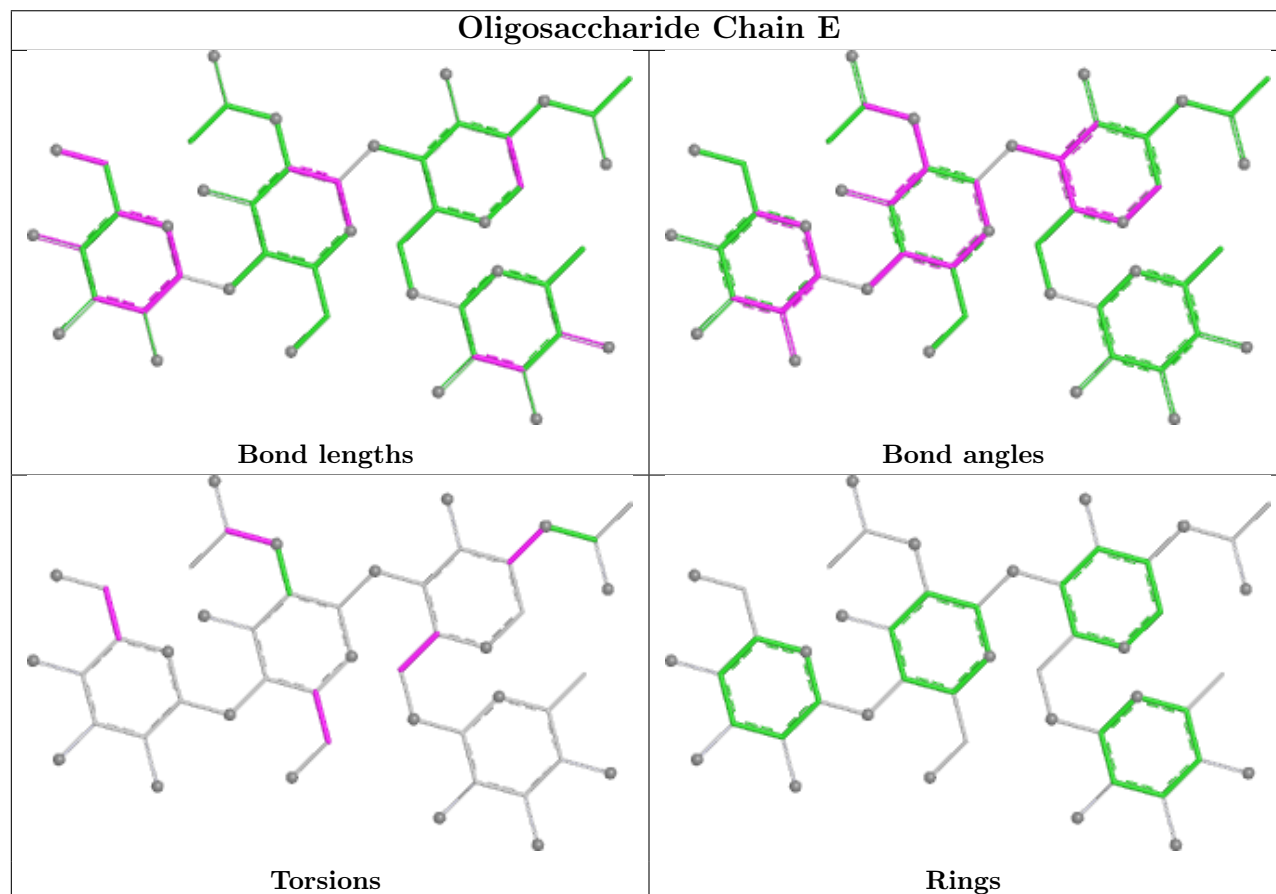
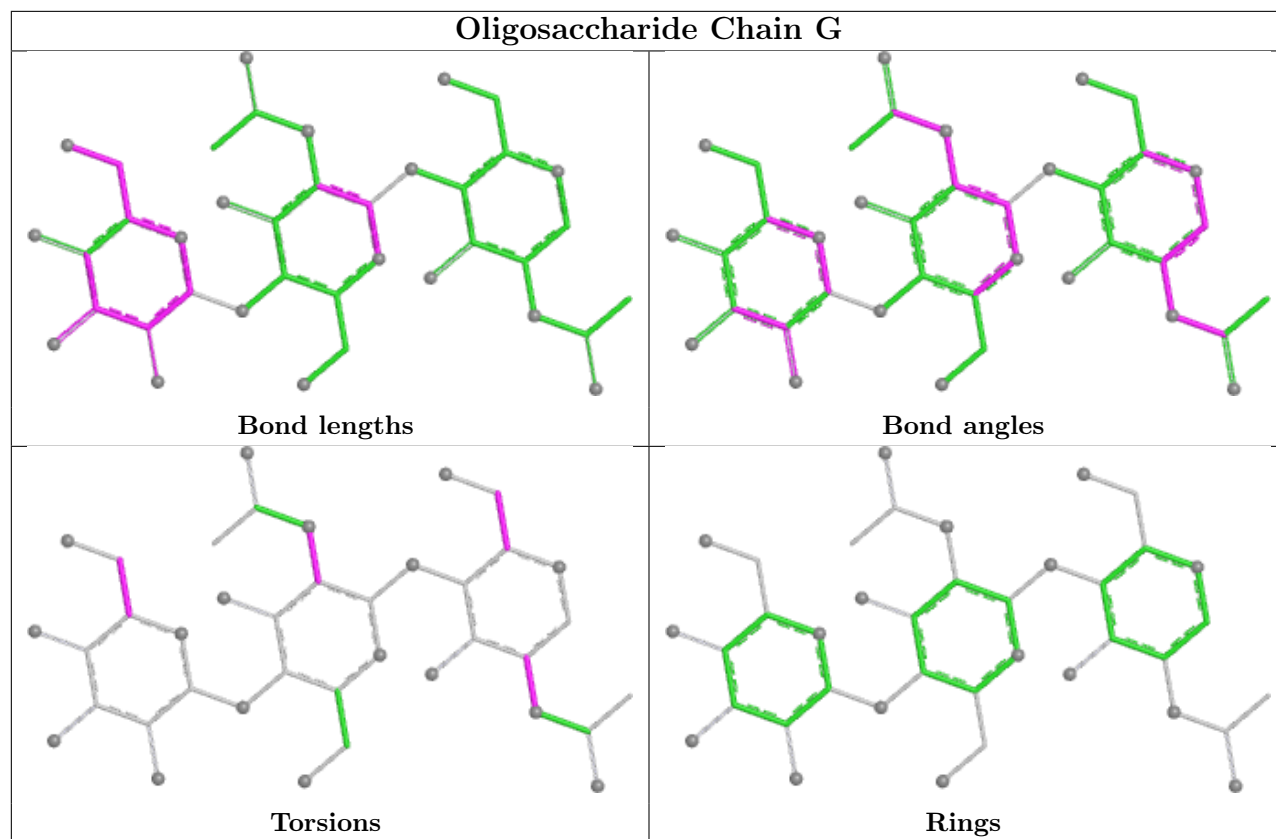
There are no ring outliers.

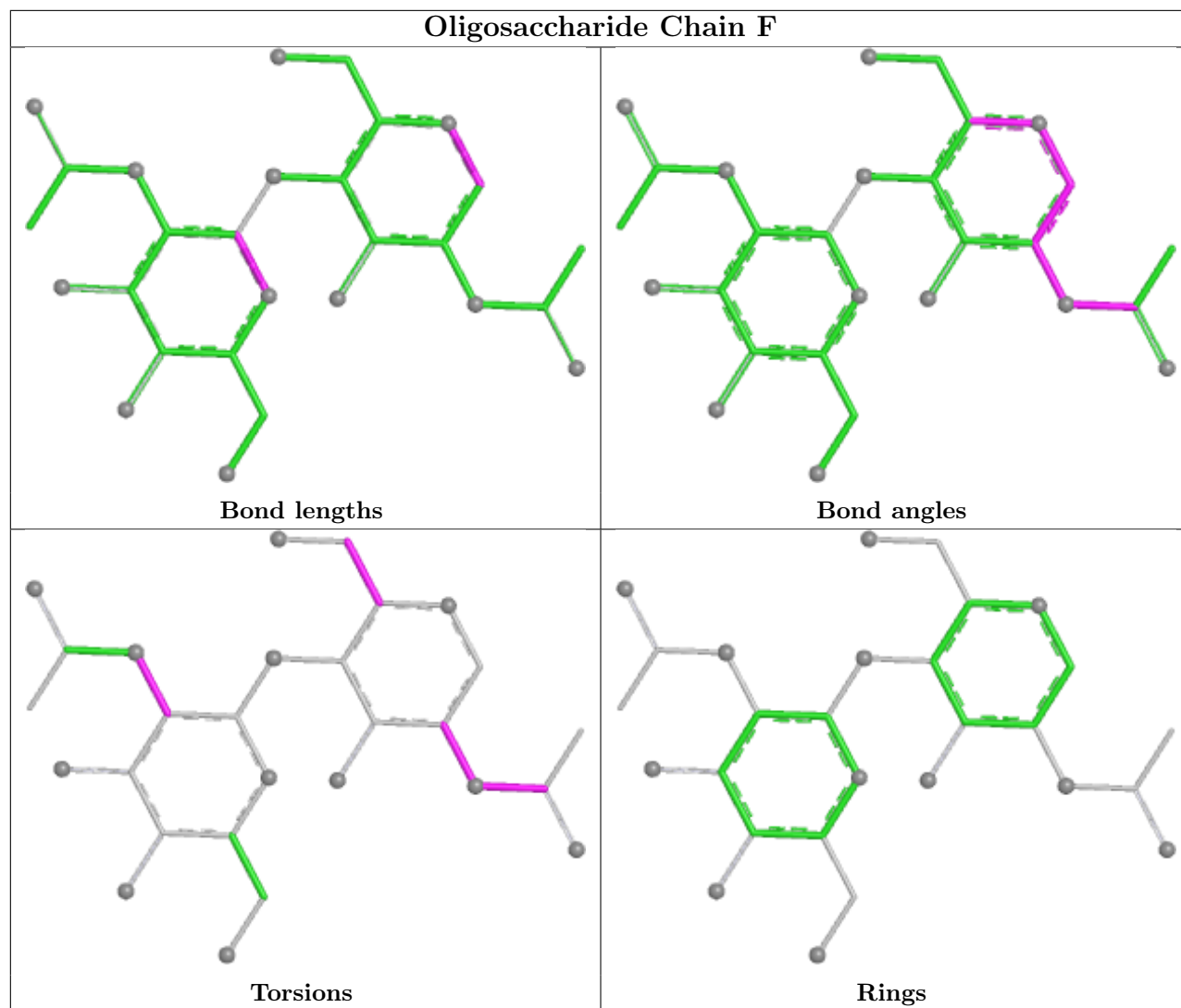
12 monomers are involved in 29 short contacts:

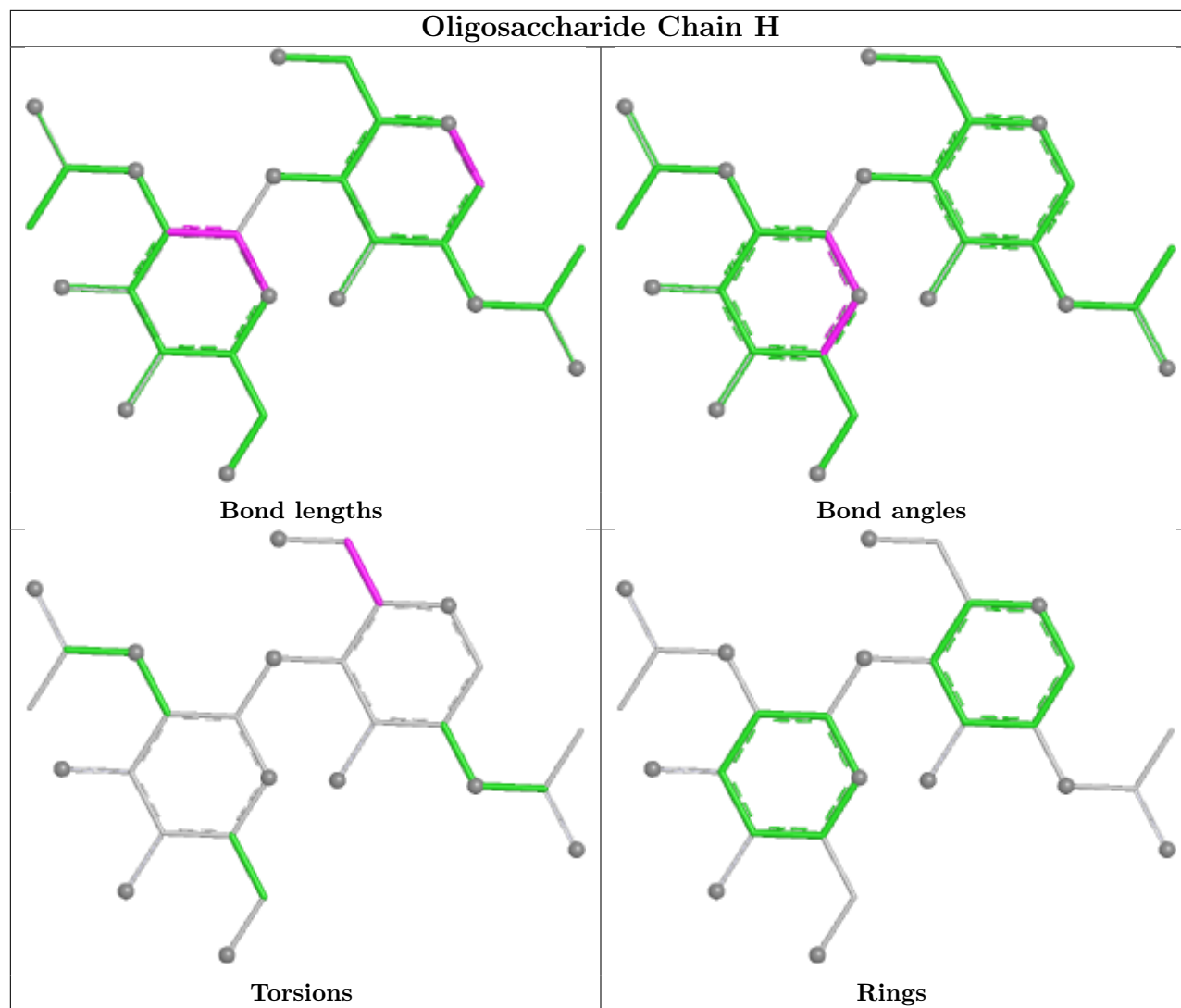
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1	NAG	4	0
4	I	2	NAG	3	0
2	G	1	NAG	4	0
2	D	2	NAG	6	0
3	E	4	FUC	2	0
3	E	2	NAG	4	0
2	C	1	NAG	3	0
3	E	3	BMA	1	0
2	G	2	NAG	3	0
2	D	1	NAG	6	0
4	F	1	NAG	4	0
2	G	3	BMA	1	0

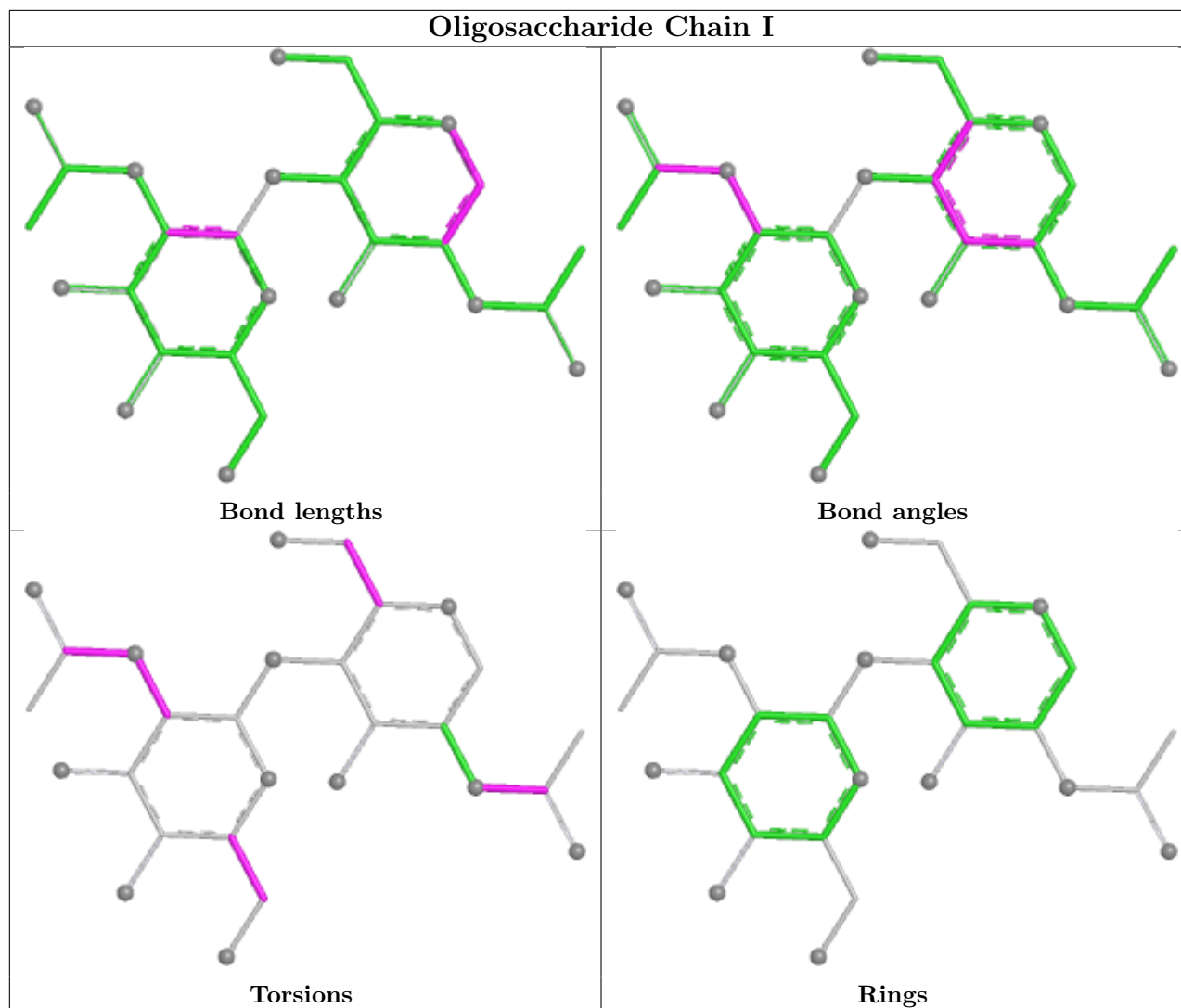
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 22 are monoatomic - leaving 10 for Mogul analysis.

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$
5	NAG	A	608	1	14,14,15	0.92	1 (7%)	17,19,21	1.54	3 (17%)
6	MAN	B	902	1	11,11,12	1.26	2 (18%)	15,15,17	1.92	3 (20%)
6	MAN	A	613	1	11,11,12	0.82	0	15,15,17	1.92	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	MAN	A	614	1	11,11,12	1.06	1 (9%)	15,15,17	2.25	3 (20%)
6	MAN	B	903	1	11,11,12	1.30	2 (18%)	15,15,17	1.93	4 (26%)
5	NAG	B	911	1	14,14,15	0.37	0	17,19,21	0.48	0
6	MAN	B	901	1	11,11,12	1.79	3 (27%)	15,15,17	2.24	6 (40%)
5	NAG	A	601	1	14,14,15	1.07	1 (7%)	17,19,21	2.45	5 (29%)
6	MAN	A	615	1	11,11,12	0.89	1 (9%)	15,15,17	1.39	3 (20%)
8	EDO	A	627	-	3,3,3	0.63	0	2,2,2	0.60	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
5	NAG	A	608	1	-	1/6/23/26	0/1/1/1
6	MAN	B	902	1	-	2/2/19/22	0/1/1/1
6	MAN	A	613	1	-	2/2/19/22	0/1/1/1
6	MAN	A	614	1	-	0/2/19/22	0/1/1/1
6	MAN	B	903	1	-	2/2/19/22	0/1/1/1
5	NAG	B	911	1	-	2/6/23/26	0/1/1/1
6	MAN	B	901	1	-	1/2/19/22	0/1/1/1
5	NAG	A	601	1	-	2/6/23/26	0/1/1/1
6	MAN	A	615	1	-	0/2/19/22	0/1/1/1
8	EDO	A	627	-	-	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)
6	B	901	MAN	O4-C4	-4.28	1.32	1.43
6	B	903	MAN	C1-C2	3.50	1.60	1.52
6	B	902	MAN	C1-C2	3.29	1.60	1.52
6	A	614	MAN	C1-C2	3.15	1.59	1.52
5	A	601	NAG	C1-C2	3.06	1.56	1.52

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	601	NAG	C1-O5-C5	7.57	122.33	112.19
6	A	614	MAN	C1-O5-C5	6.65	121.11	112.19
6	A	613	MAN	C1-O5-C5	5.81	119.97	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	903	MAN	C1-O5-C5	5.11	119.04	112.19
6	B	902	MAN	C1-O5-C5	5.11	119.03	112.19

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	608	NAG	C3-C2-N2-C7
6	A	613	MAN	O5-C5-C6-O6
6	B	902	MAN	O5-C5-C6-O6
6	A	613	MAN	C4-C5-C6-O6
6	B	902	MAN	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	608	NAG	3	0
6	B	903	MAN	1	0
5	B	911	NAG	1	0
6	B	901	MAN	1	1

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	554/559 (99%)	0.39	18 (3%)	50 41	45, 77, 107, 203	2 (0%)
1	B	559/559 (100%)	0.46	24 (4%)	40 31	46, 79, 117, 145	1 (0%)
All	All	1113/1118 (99%)	0.43	42 (3%)	44 36	45, 78, 114, 203	3 (0%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	554	HIS	4.5
1	B	559	HIS	4.2
1	A	427	TYR	4.0
1	B	322	THR	3.8
1	B	502	SER	3.4

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.

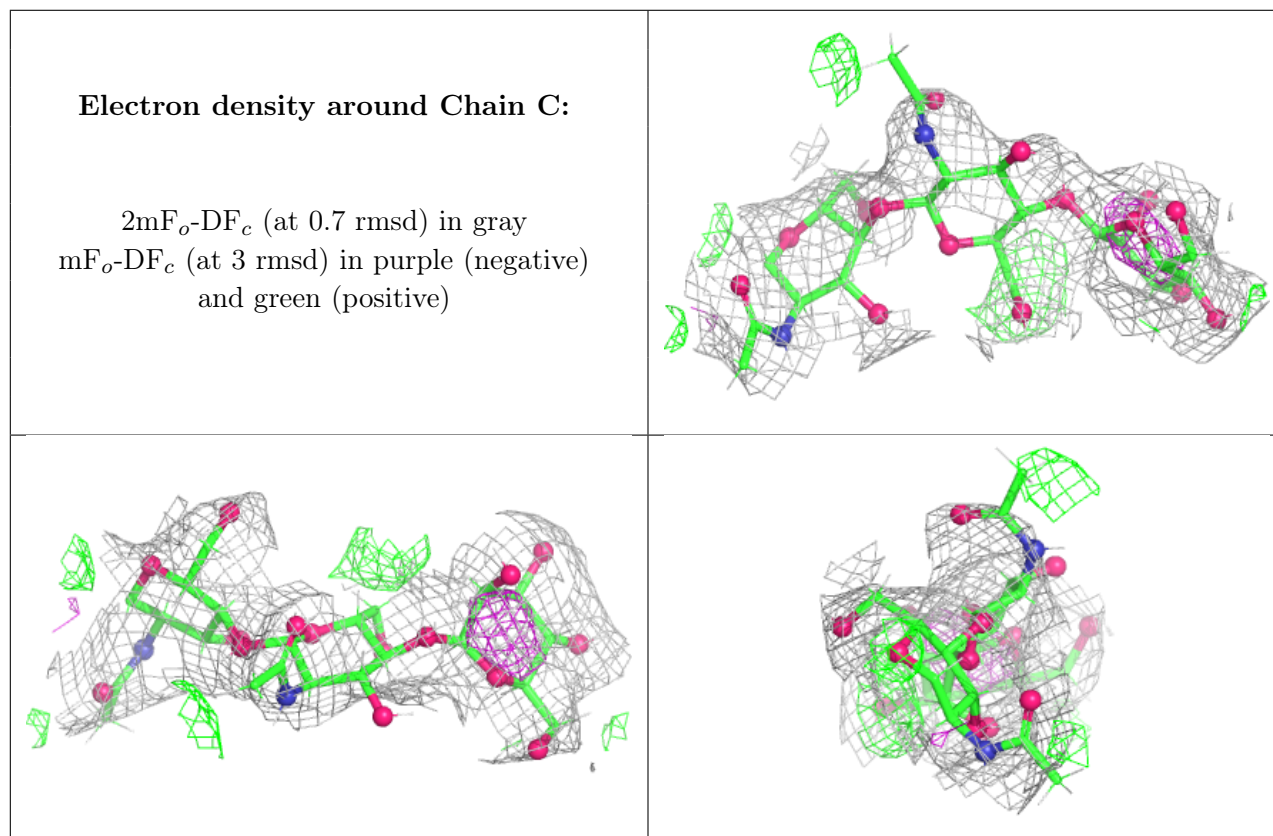
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	H	2	14/15	0.36	0.21	65,82,98,102	0
4	NAG	I	2	14/15	0.39	0.19	93,128,157,162	0
2	NAG	D	2	14/15	0.42	0.16	68,126,154,161	0
2	NAG	G	2	14/15	0.47	0.15	90,130,157,162	0
2	BMA	G	3	11/12	0.49	0.16	70,87,104,109	0

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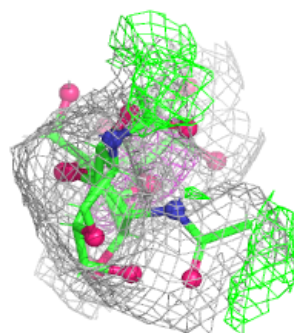
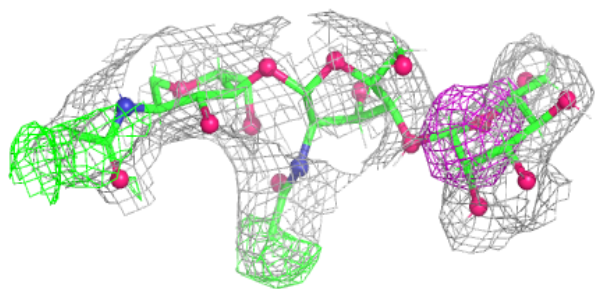
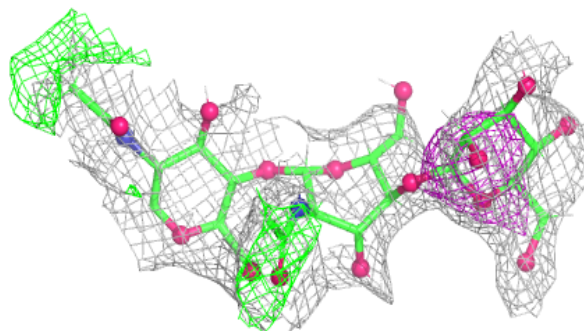
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	D	1	14/15	0.52	0.20	84,115,138,143	0
3	FUC	E	4	10/11	0.52	0.20	116,140,167,174	0
2	BMA	C	3	11/12	0.53	0.16	71,84,95,111	0
2	NAG	C	2	14/15	0.55	0.20	89,117,145,153	0
2	BMA	D	3	11/12	0.57	0.16	65,84,101,111	0
3	NAG	E	2	14/15	0.58	0.15	112,129,149,154	0
2	NAG	G	1	14/15	0.61	0.16	118,141,167,175	0
4	NAG	F	2	14/15	0.63	0.17	91,116,139,144	0
3	BMA	E	3	11/12	0.67	0.12	60,77,94,99	0
4	NAG	H	1	14/15	0.67	0.15	68,83,97,102	0
4	NAG	I	1	14/15	0.73	0.18	87,120,146,162	0
4	NAG	F	1	14/15	0.75	0.20	86,110,129,138	0
2	NAG	C	1	14/15	0.82	0.13	78,99,119,148	0
3	NAG	E	1	14/15	0.84	0.15	84,115,141,162	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.

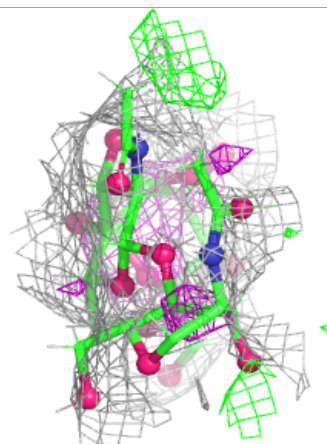
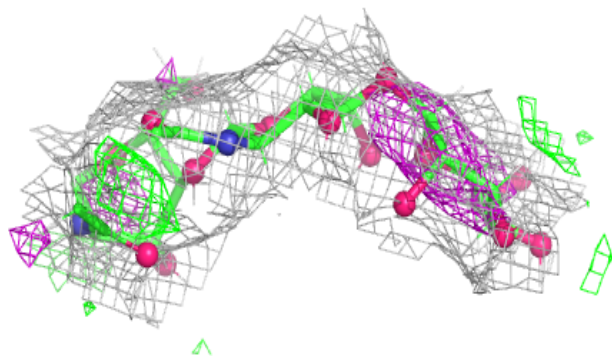
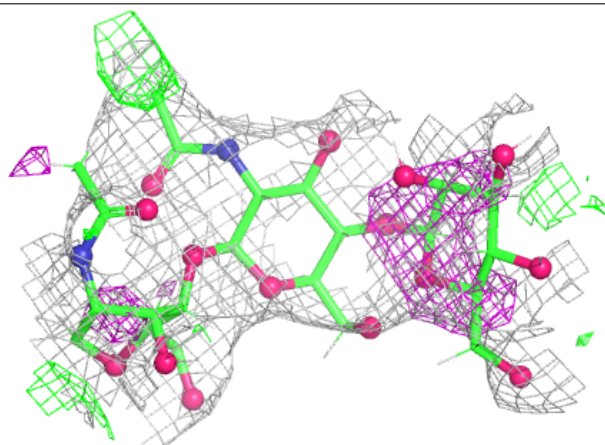


Electron density around Chain D:

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

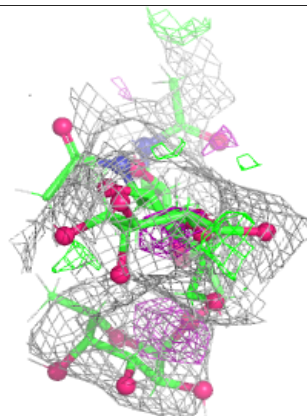
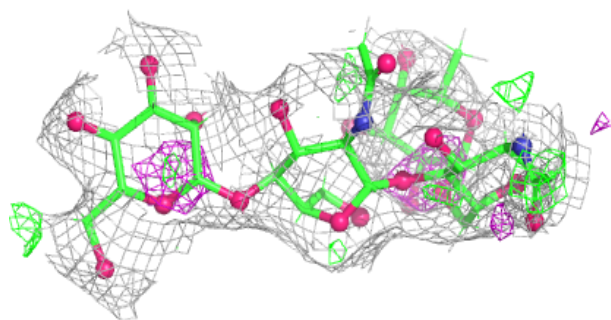
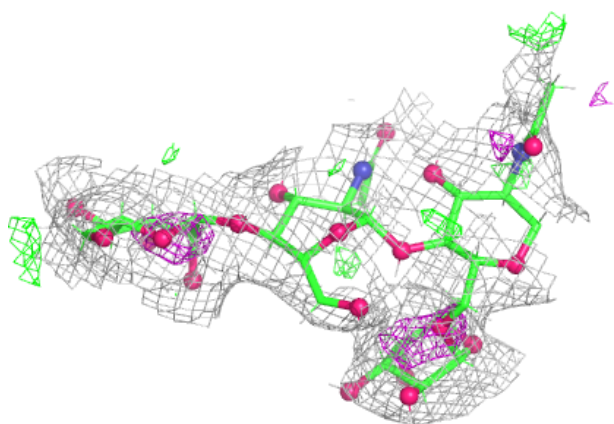
**Electron density around Chain G:**

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



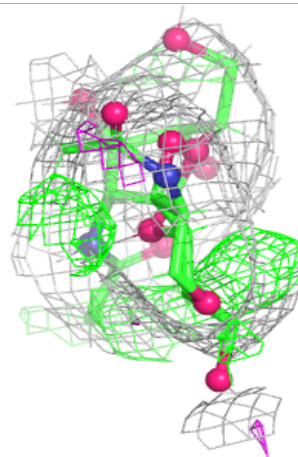
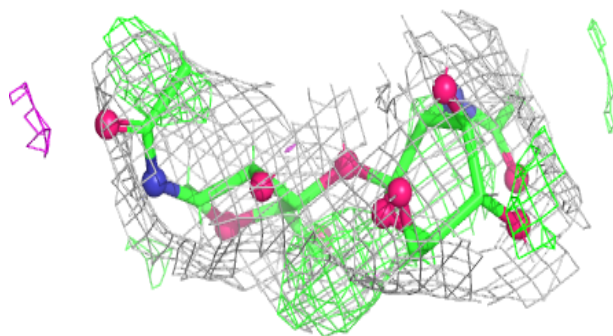
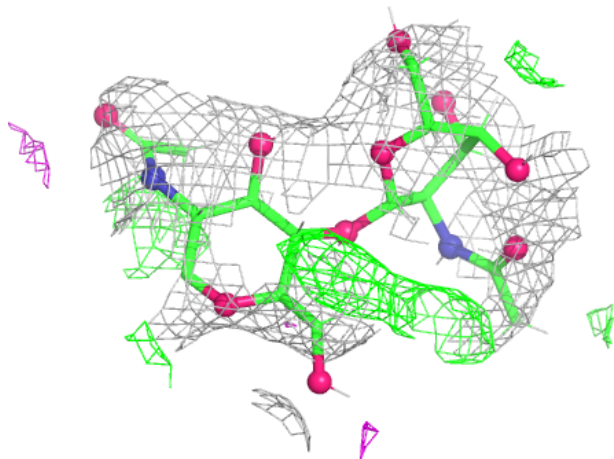
Electron density around Chain E:

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



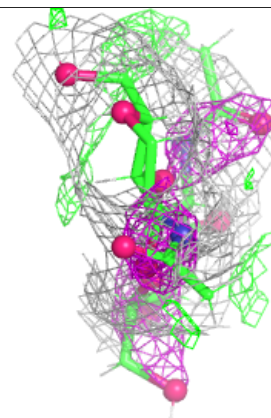
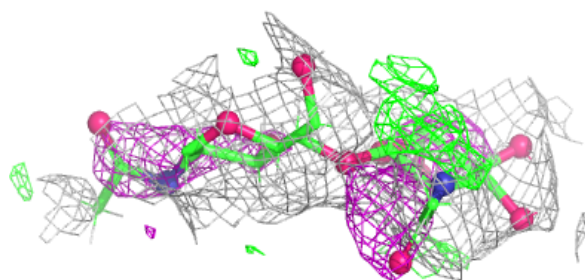
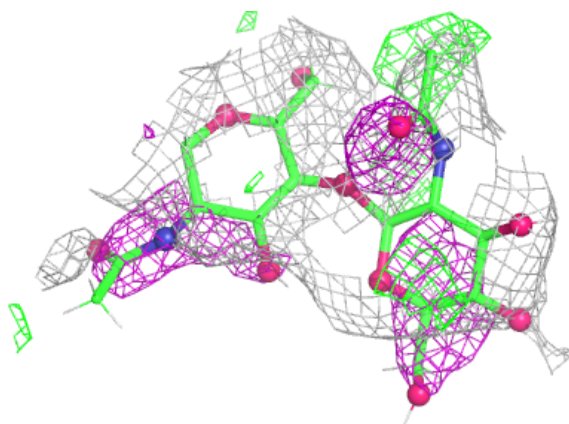
Electron density around Chain F:

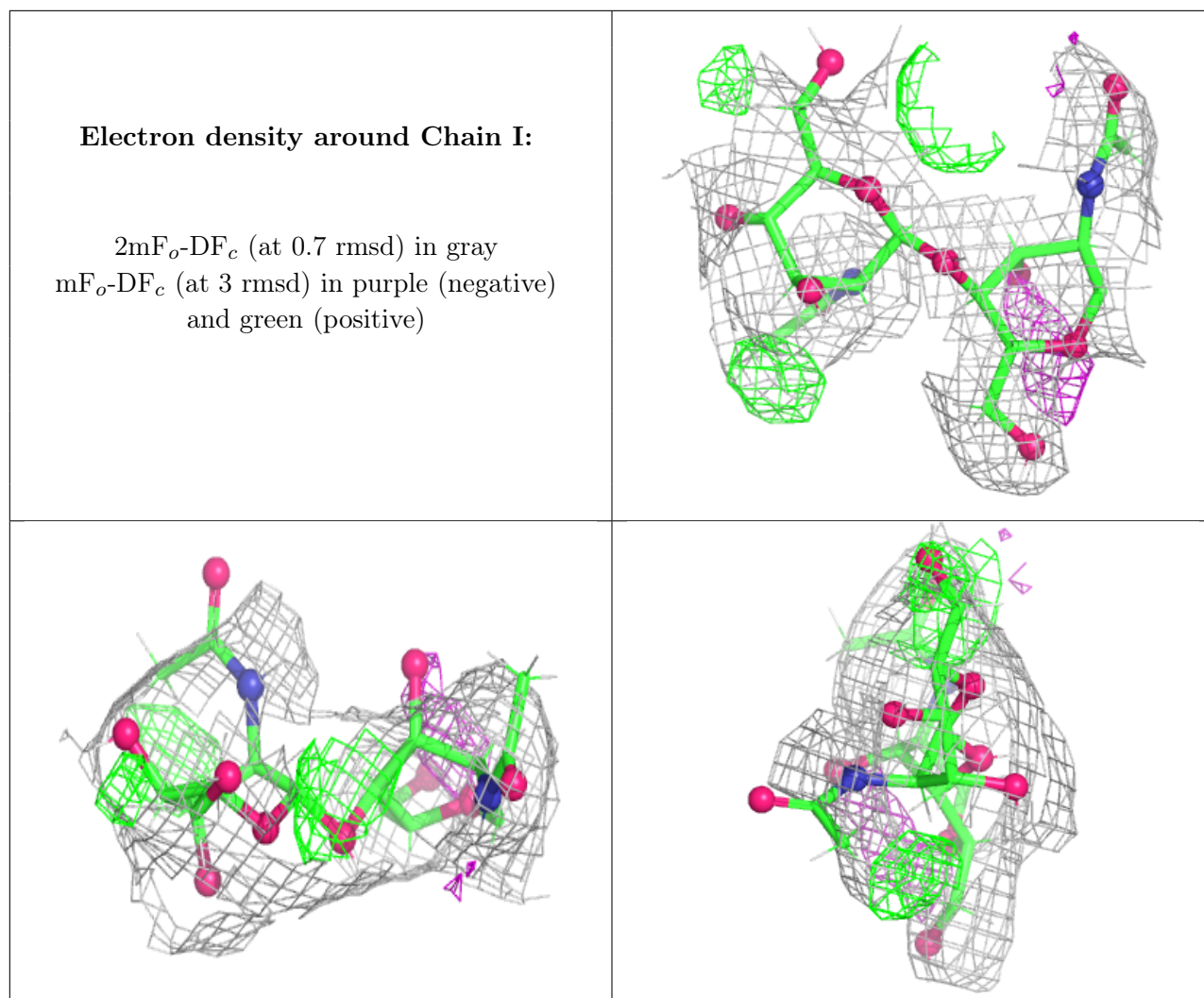
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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
5	NAG	A	601	14/15	0.30	0.17	113,165,199,201	0
6	MAN	A	615	11/12	0.54	0.19	98,118,134,158	0
5	NAG	A	608	14/15	0.62	0.17	80,114,137,146	0
5	NAG	B	911	14/15	0.65	0.14	97,138,173,175	0
6	MAN	B	903	11/12	0.65	0.18	93,111,129,133	0
6	MAN	B	902	11/12	0.75	0.16	77,99,115,134	0
6	MAN	A	613	11/12	0.75	0.17	98,123,141,148	0
6	MAN	B	901	11/12	0.76	0.21	92,116,139,157	0
6	MAN	A	614	11/12	0.79	0.19	109,129,150,155	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	EDO	A	627	4/4	0.85	0.19	63,77,99,119	0
7	CA	A	623	1/1	0.90	0.10	79,79,79,79	0
7	CA	B	924	1/1	0.91	0.09	71,71,71,71	0
7	CA	B	917	1/1	0.91	0.09	71,71,71,71	0
7	CA	A	620	1/1	0.92	0.07	78,78,78,78	0
7	CA	B	915	1/1	0.93	0.09	79,79,79,79	0
7	CA	A	621	1/1	0.94	0.06	58,58,58,58	0
7	CA	B	918	1/1	0.94	0.07	70,70,70,70	0
7	CA	A	626	1/1	0.95	0.06	78,78,78,78	0
7	CA	A	624	1/1	0.95	0.08	65,65,65,65	0
7	CA	B	920	1/1	0.96	0.07	69,69,69,69	0
7	CA	B	919	1/1	0.97	0.06	63,63,63,63	0
7	CA	B	923	1/1	0.97	0.06	77,77,77,77	0
7	CA	A	617	1/1	0.98	0.06	71,71,71,71	0
7	CA	A	625	1/1	0.98	0.04	58,58,58,58	0
7	CA	A	618	1/1	0.98	0.04	71,71,71,71	0
7	CA	B	921	1/1	0.98	0.05	51,51,51,51	0
7	CA	B	922	1/1	0.98	0.05	59,59,59,59	0
7	CA	A	622	1/1	0.98	0.05	64,64,64,64	0
7	CA	B	916	1/1	0.98	0.05	46,46,46,46	0
7	CA	A	619	1/1	0.98	0.04	48,48,48,48	0
7	CA	B	914	1/1	0.99	0.04	64,64,64,64	0
7	CA	A	616	1/1	0.99	0.03	66,66,66,66	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.