



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 10:15 AM UTC

PDB ID : 6SKA / pdb_00006ska
Title : Teneurin 2 in complex with Latrophilin 1 Lec-Olf domains
Authors : Chu, A.; Carrasquero, M.A.; Lowe, E.; Seiradake, E.
Deposited on : 2019-08-15
Resolution : 3.86 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

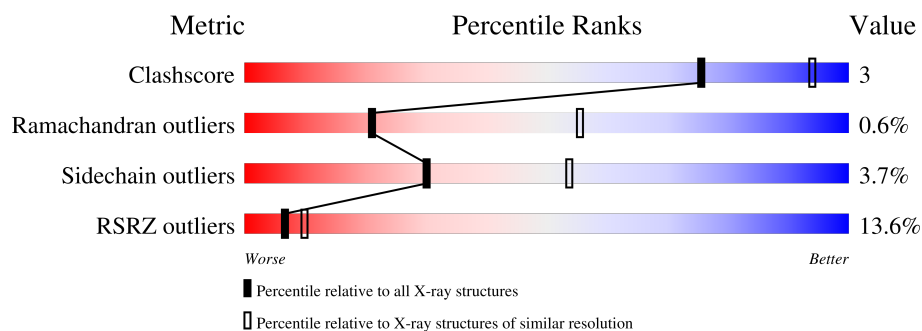
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.86 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))
Clashscore	190562	1207 (4.02-3.70)
Ramachandran outliers	187476	1149 (4.02-3.70)
Sidechain outliers	187428	1142 (4.02-3.70)
RSRZ outliers	180081	1164 (4.02-3.70)

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	1836	
2	D	347	
3	B	8	
4	C	2	
4	E	2	
4	F	2	
4	G	2	

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Mol	Chain	Length	Quality of chain
4	H	2	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17628 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 Teneurin-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1836	Total	C	N	O	S	0	1	0
			14513	9168	2508	2774	63			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LYS	deletion	UNP Q9DER5
A	?	-	THR	deletion	UNP Q9DER5
A	?	-	GLU	deletion	UNP Q9DER5
A	?	-	GLU	deletion	UNP Q9DER5
A	?	-	ASN	deletion	UNP Q9DER5
A	?	-	SER	deletion	UNP Q9DER5
A	?	-	ILE	deletion	UNP Q9DER5

- Molecule 2 is a protein called Adhesion G protein-coupled receptor L1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	347	Total	C	N	O	S	0	0	0
			2810	1775	479	539	17			

There are 11 discrepancies between the modelled and reference sequences:

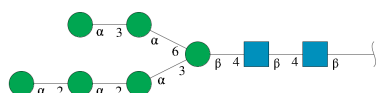
Chain	Residue	Modelled	Actual	Comment	Reference
D	132	VAL	ILE	conflict	UNP Q80TR1
D	?	-	VAL	deletion	UNP Q80TR1
D	?	-	TYR	deletion	UNP Q80TR1
D	?	-	VAL	deletion	UNP Q80TR1
D	?	-	ASP	deletion	UNP Q80TR1
D	?	-	ASP	deletion	UNP Q80TR1
D	?	-	ASP	deletion	UNP Q80TR1
D	?	-	SER	deletion	UNP Q80TR1
D	?	-	GLU	deletion	UNP Q80TR1

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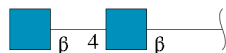
Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	ALA	deletion	UNP Q80TR1
D	?	-	ALA	deletion	UNP Q80TR1

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	8	Total	C	N	O	0	0	0
			94	52	2	40			

- 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	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



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

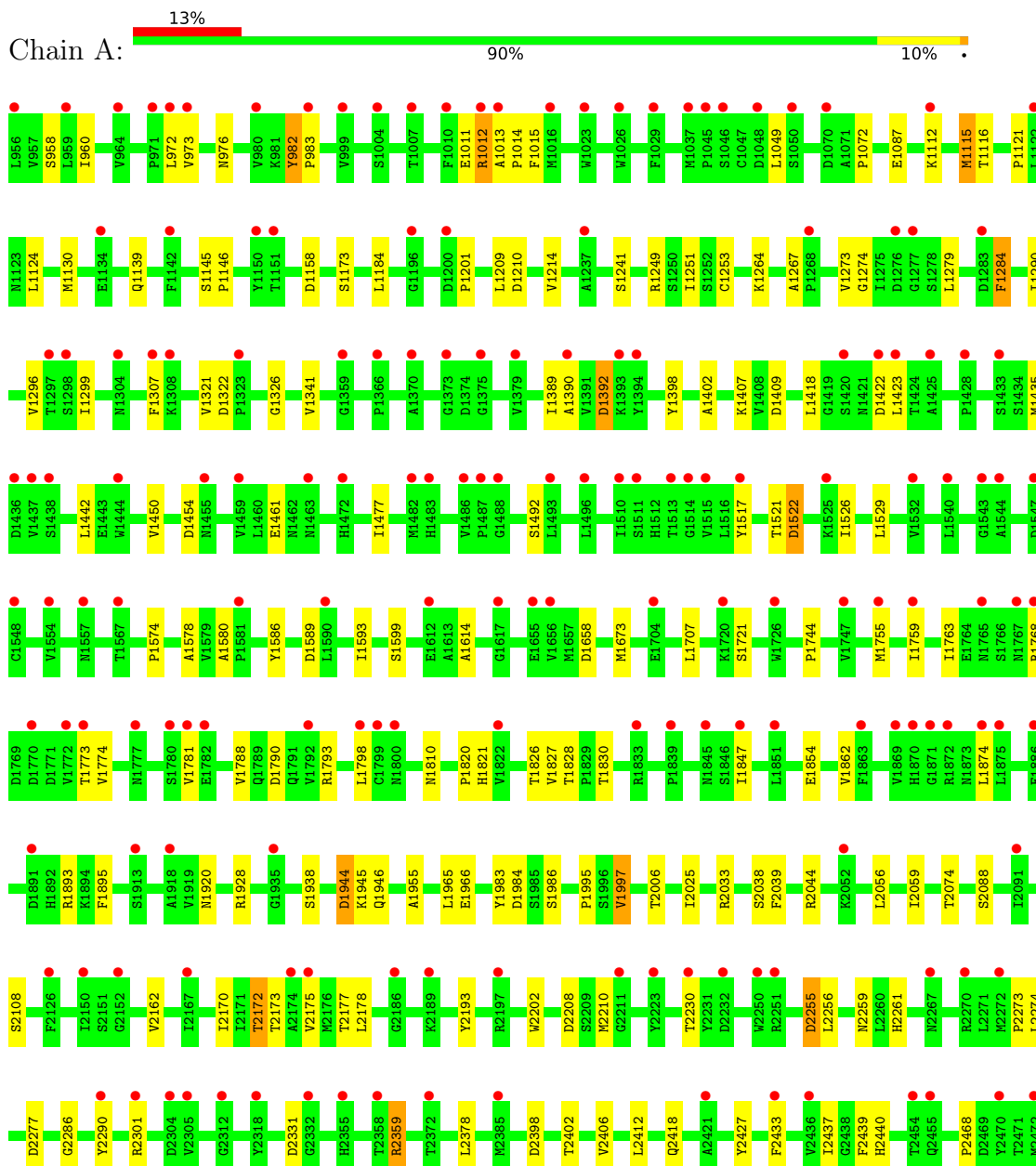
- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

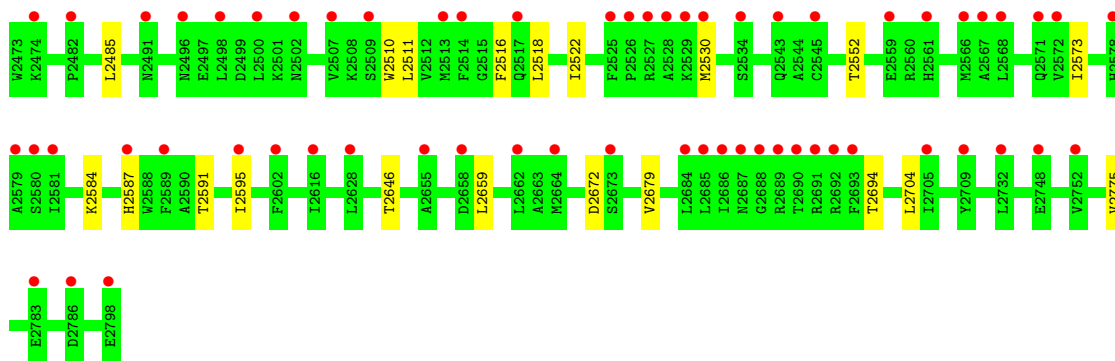
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	1	Total	Ca	0	0
			1	1		

3 Residue-property plots

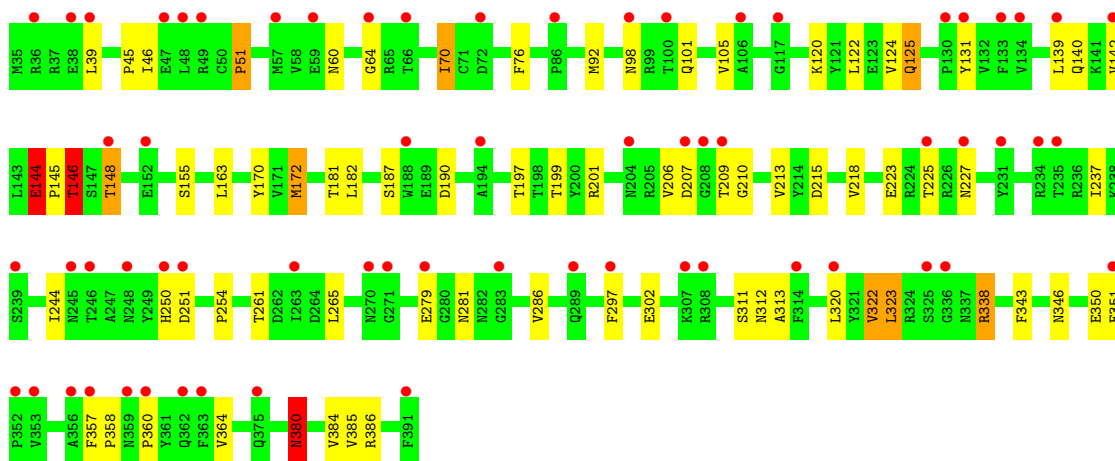
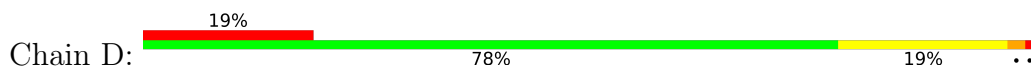
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Teneurin-2

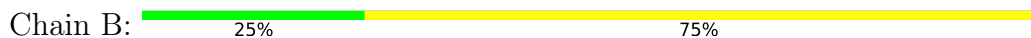




- Molecule 2: Adhesion G protein-coupled receptor L1



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



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



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

Chain E:  100%

MAG1
MAG2

- 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 G:  100%

MAG1
MAG2

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

Chain H:  50% 50%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	96.26Å 96.26Å 809.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.09 – 3.86 52.09 – 3.86	Depositor EDS
% Data completeness (in resolution range)	91.0 (52.09-3.86) 91.0 (52.09-3.86)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 3.89Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	(Not available) , (Not available) 0.285 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	104.8	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 112.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	17628	wwPDB-VP
Average B, all atoms (Å ²)	134.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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, MAN, CA

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	0.69	0/14825	1.14	30/20101 (0.1%)
2	D	0.72	1/2886 (0.0%)	1.11	1/3935 (0.0%)
All	All	0.70	1/17711 (0.0%)	1.13	31/24036 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	140	GLN	CA-C	5.45	1.55	1.52

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2331	ASP	CA-CB-CG	6.19	118.79	112.60
2	D	380	ASN	CA-CB-CG	6.18	118.78	112.60
1	A	1984	ASP	CA-CB-CG	6.16	118.76	112.60
1	A	1658	ASP	CA-CB-CG	6.10	118.70	112.60
1	A	2208	ASP	CA-CB-CG	6.07	118.67	112.60

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	14513	0	14252	75	0
2	D	2810	0	2639	30	0
3	B	94	0	79	0	0
4	C	28	0	25	0	0
4	E	28	0	25	0	0
4	F	28	0	25	0	0
4	G	28	0	25	0	0
4	H	28	0	25	0	0
5	A	70	0	65	0	0
6	D	1	0	0	0	0
All	All	17628	0	17160	103	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 103 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:364:VAL:HA	2:D:380:ASN:HB2	1.58	0.85
1:A:1821:HIS:HD2	1:A:1830:THR:HG21	1.44	0.81
1:A:982:TYR:HB3	1:A:983:PRO:HD3	1.63	0.78
1:A:982:TYR:HB3	1:A:983:PRO:CD	2.17	0.74
1:A:2468:PRO:HB3	1:A:2485:LEU:HB3	1.76	0.67

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	1829/1836 (100%)	1758 (96%)	63 (3%)	8 (0%)	30	64
2	D	343/347 (99%)	310 (90%)	27 (8%)	6 (2%)	7	35
All	All	2172/2183 (100%)	2068 (95%)	90 (4%)	14 (1%)	21	55

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	982	TYR
2	D	360	PRO
1	A	1284	PHE
2	D	210	GLY
1	A	1966	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	1601/1600 (100%)	1560 (97%)	41 (3%)	40	61
2	D	306/306 (100%)	277 (90%)	29 (10%)	8	29
All	All	1907/1906 (100%)	1837 (96%)	70 (4%)	30	54

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	227	ASN
2	D	265	LEU
2	D	338	ARG
1	A	1874	LEU
1	A	1847	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2549	GLN
2	D	60	ASN
2	D	346	ASN
1	A	2741	GLN
2	D	153	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

18 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	B	1	1,3	14,14,15	0.43	0	17,19,21	0.69	1 (5%)
3	NAG	B	2	3	14,14,15	0.42	0	17,19,21	0.54	0
3	BMA	B	3	3	11,11,12	0.50	0	15,15,17	0.51	0
3	MAN	B	4	3	11,11,12	0.52	0	15,15,17	0.95	2 (13%)
3	MAN	B	5	3	11,11,12	0.58	0	15,15,17	0.87	1 (6%)
3	MAN	B	6	3	11,11,12	0.56	0	15,15,17	0.87	1 (6%)
3	MAN	B	7	3	11,11,12	0.56	0	15,15,17	0.88	1 (6%)
3	MAN	B	8	3	11,11,12	0.56	0	15,15,17	0.94	1 (6%)
4	NAG	C	1	1,4	14,14,15	0.44	0	17,19,21	0.70	0
4	NAG	C	2	4	14,14,15	0.45	0	17,19,21	0.60	0
4	NAG	E	1	1,4	14,14,15	0.43	0	17,19,21	0.66	0
4	NAG	E	2	4	14,14,15	0.44	0	17,19,21	0.59	0
4	NAG	F	1	1,4	14,14,15	0.43	0	17,19,21	0.68	1 (5%)
4	NAG	F	2	4	14,14,15	0.45	0	17,19,21	0.60	0
4	NAG	G	1	1,4	14,14,15	0.44	0	17,19,21	0.62	0
4	NAG	G	2	4	14,14,15	0.44	0	17,19,21	0.55	0
4	NAG	H	1	1,4	14,14,15	0.44	0	17,19,21	0.71	1 (5%)
4	NAG	H	2	4	14,14,15	0.43	0	17,19,21	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	B	2	3	-	2/6/23/26	0/1/1/1
3	BMA	B	3	3	-	0/2/19/22	0/1/1/1
3	MAN	B	4	3	-	2/2/19/22	0/1/1/1
3	MAN	B	5	3	-	1/2/19/22	0/1/1/1
3	MAN	B	6	3	-	0/2/19/22	0/1/1/1
3	MAN	B	7	3	-	0/2/19/22	0/1/1/1
3	MAN	B	8	3	-	0/2/19/22	0/1/1/1
4	NAG	C	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	C	2	4	-	3/6/23/26	0/1/1/1
4	NAG	E	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1
4	NAG	G	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	2/6/23/26	0/1/1/1
4	NAG	H	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	H	2	4	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	5	MAN	C1-O5-C5	2.73	115.85	112.19
3	B	8	MAN	C1-O5-C5	2.61	115.68	112.19
3	B	7	MAN	C1-O5-C5	2.39	115.39	112.19
3	B	4	MAN	C1-C2-C3	2.28	112.96	109.64
3	B	6	MAN	C1-O5-C5	2.24	115.19	112.19

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

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

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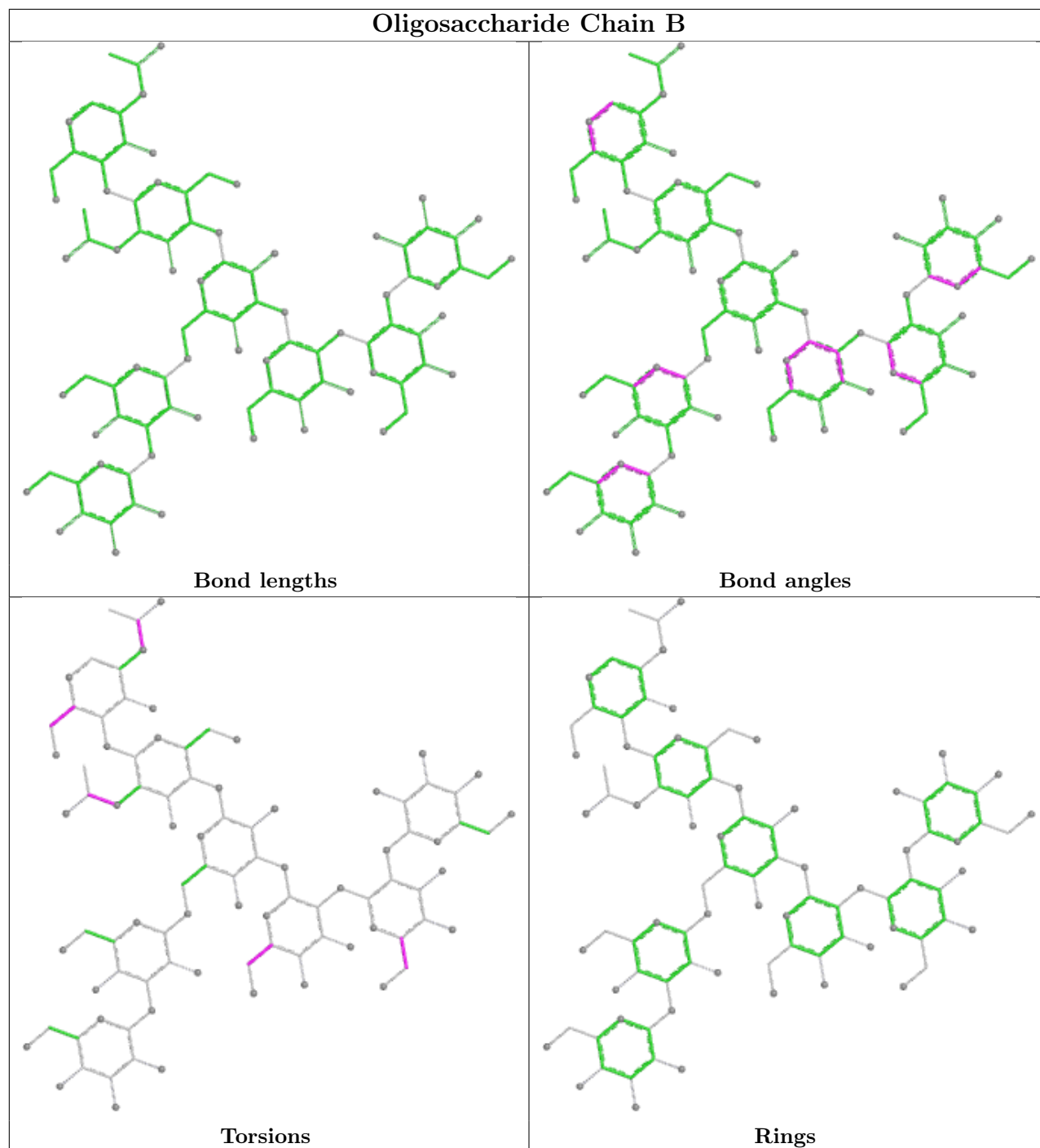
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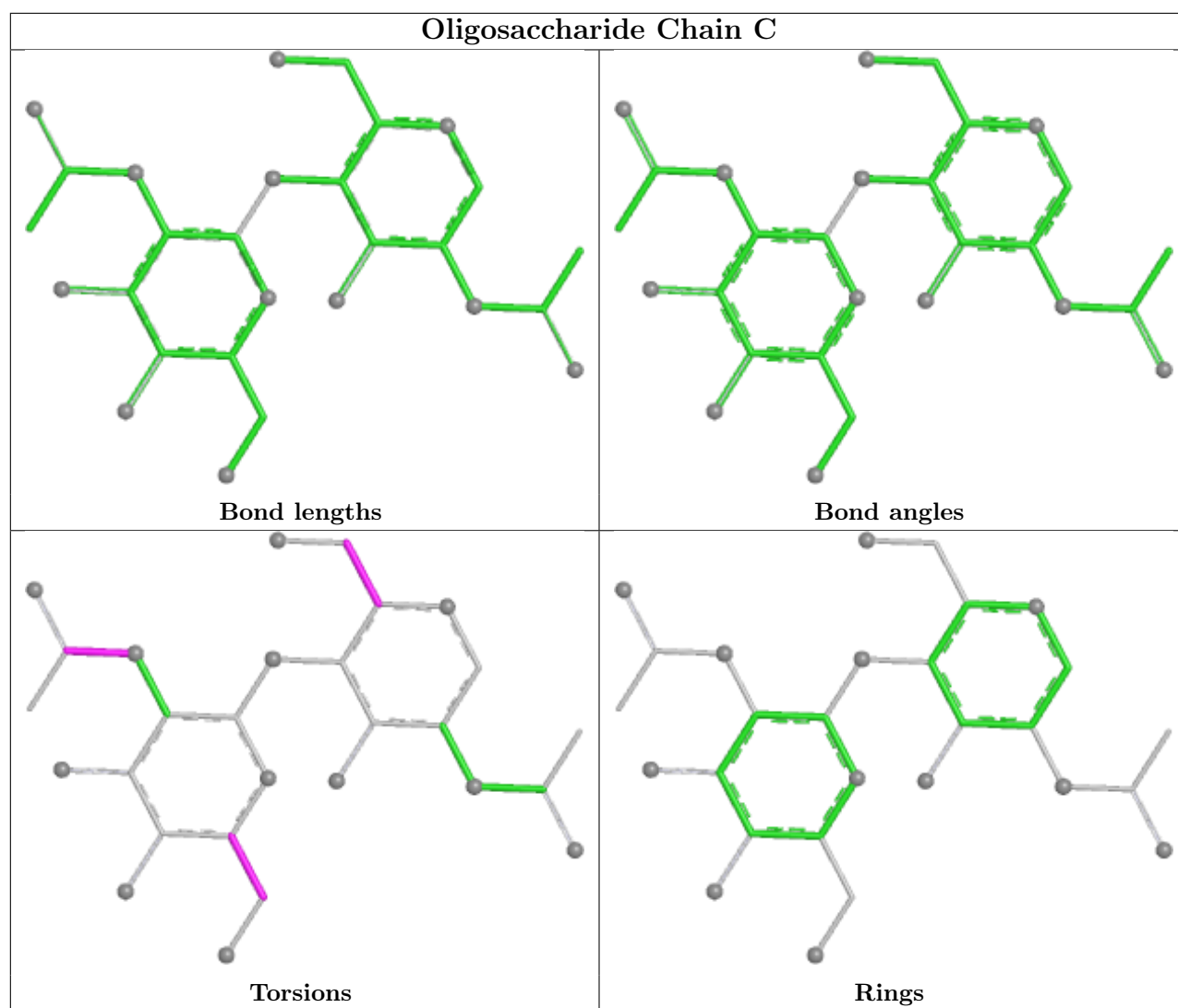
Mol	Chain	Res	Type	Atoms
3	B	2	NAG	O7-C7-N2-C2
4	C	2	NAG	C8-C7-N2-C2

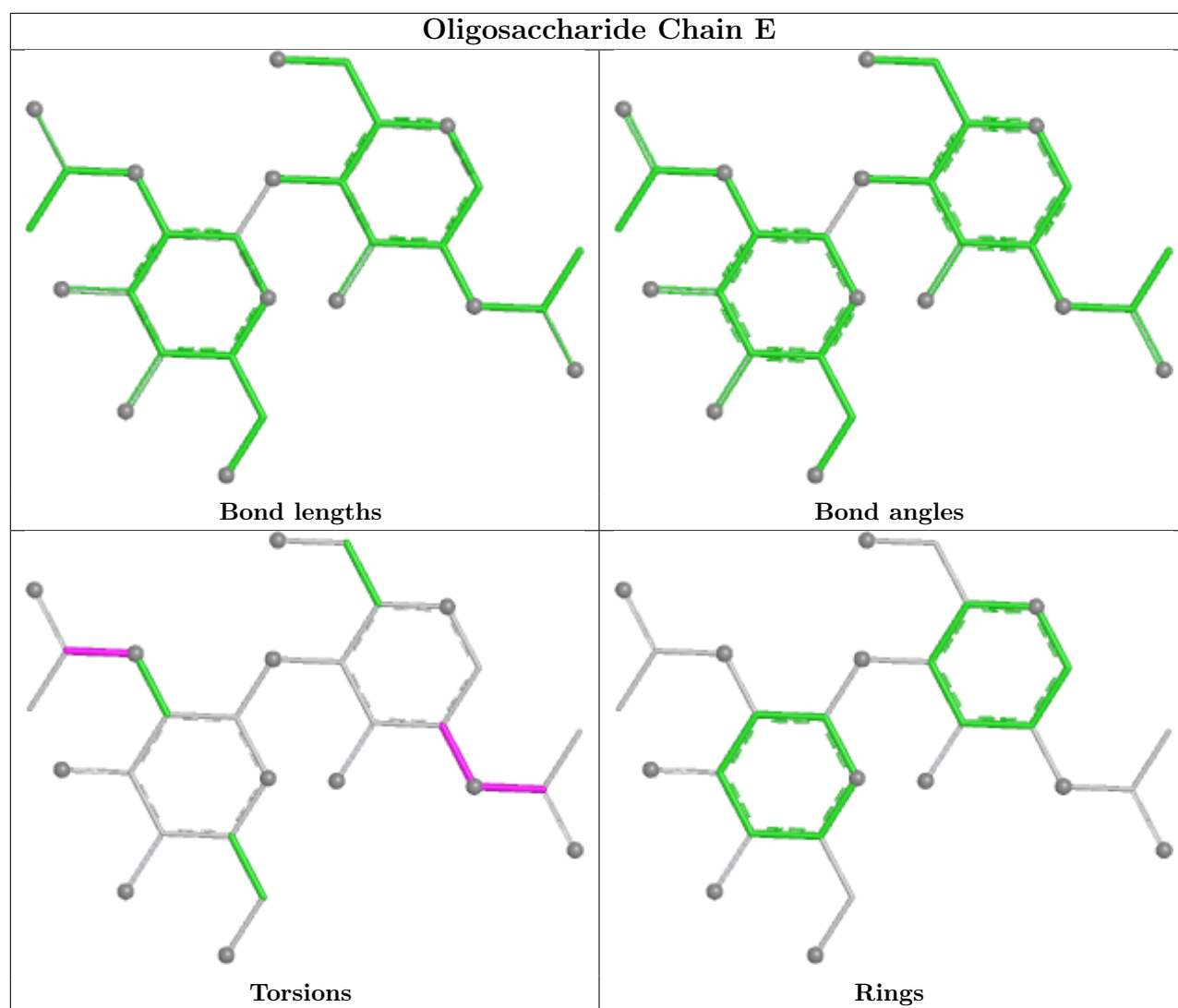
There are no ring outliers.

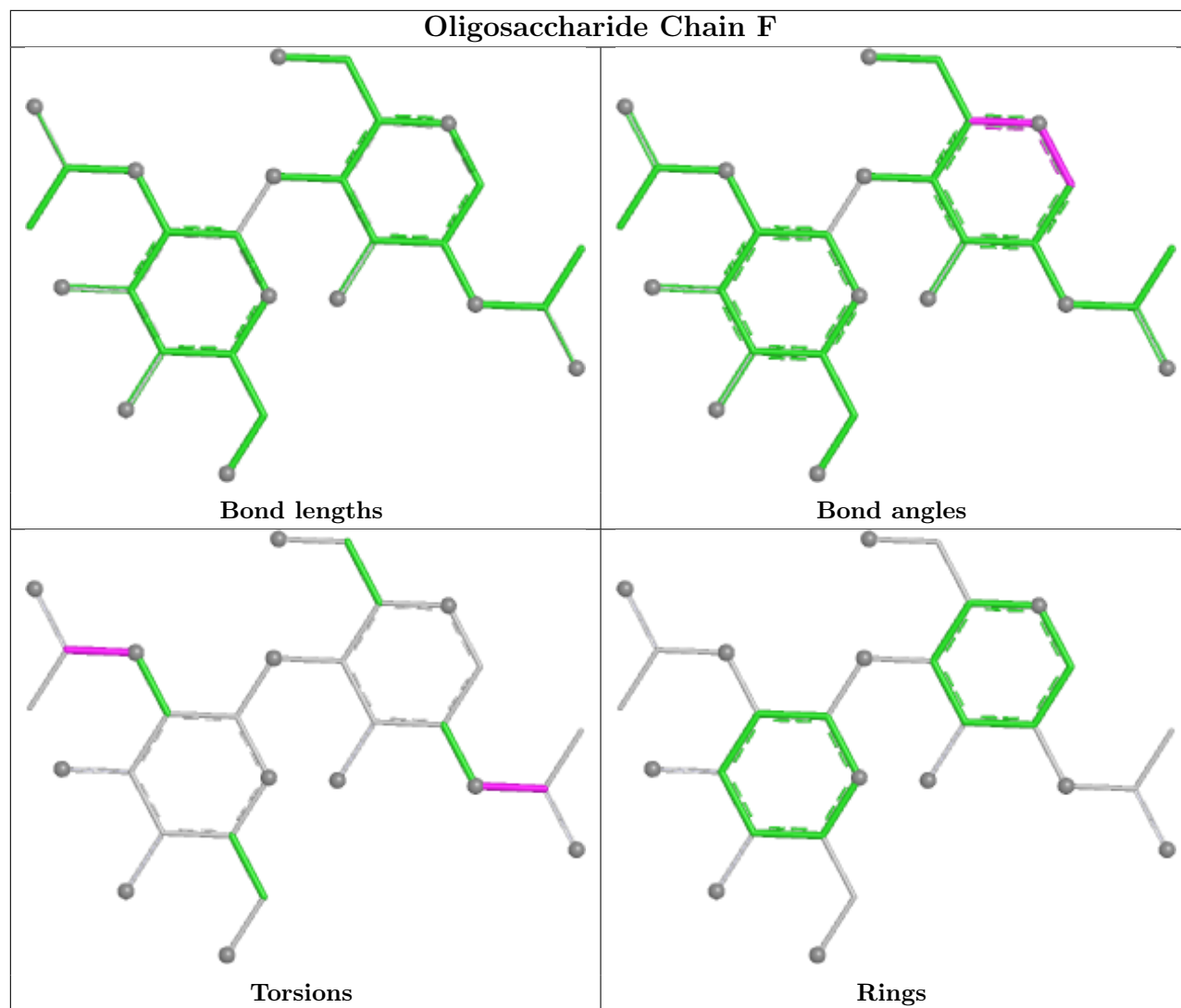
No monomer is involved in short contacts.

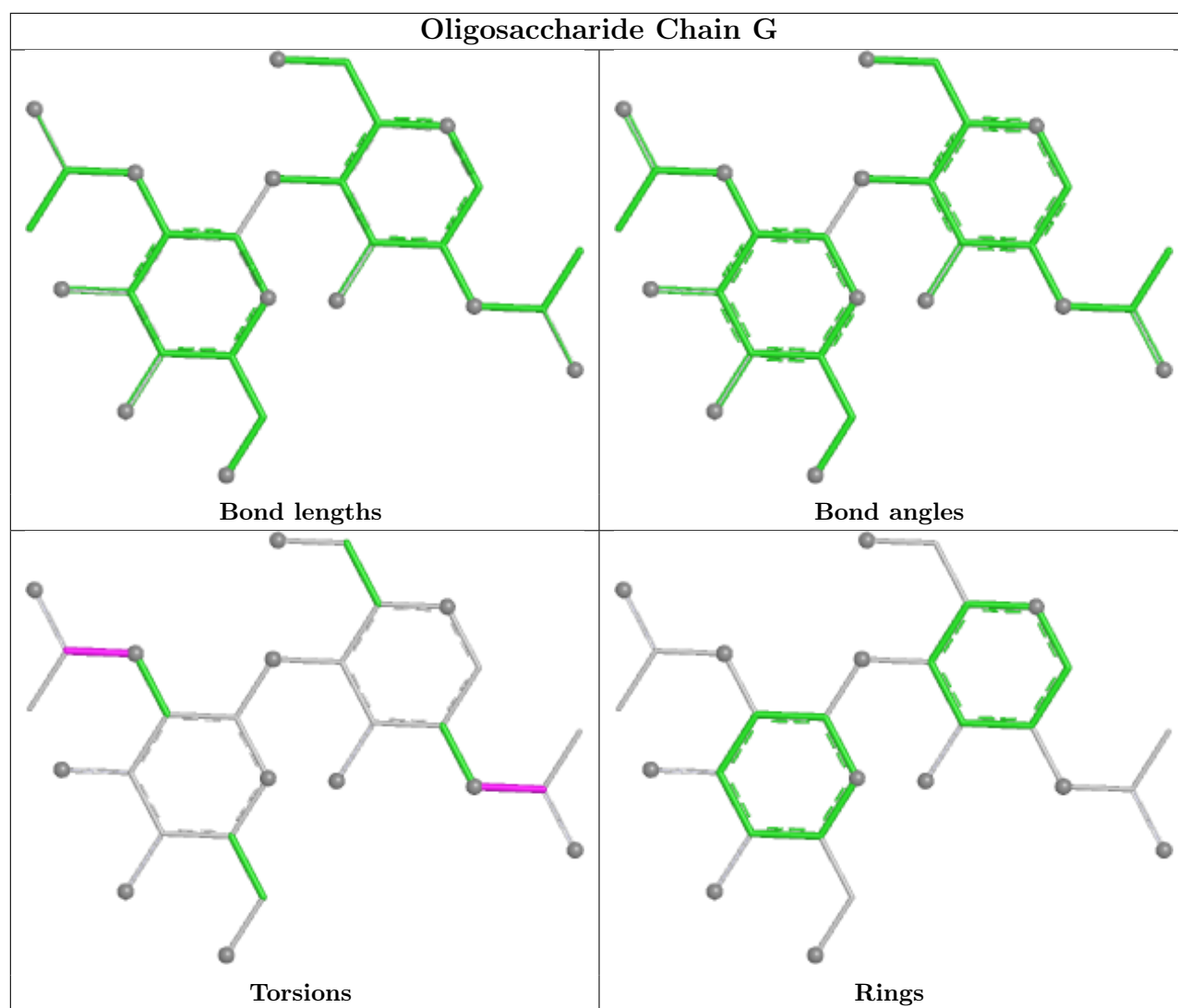
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

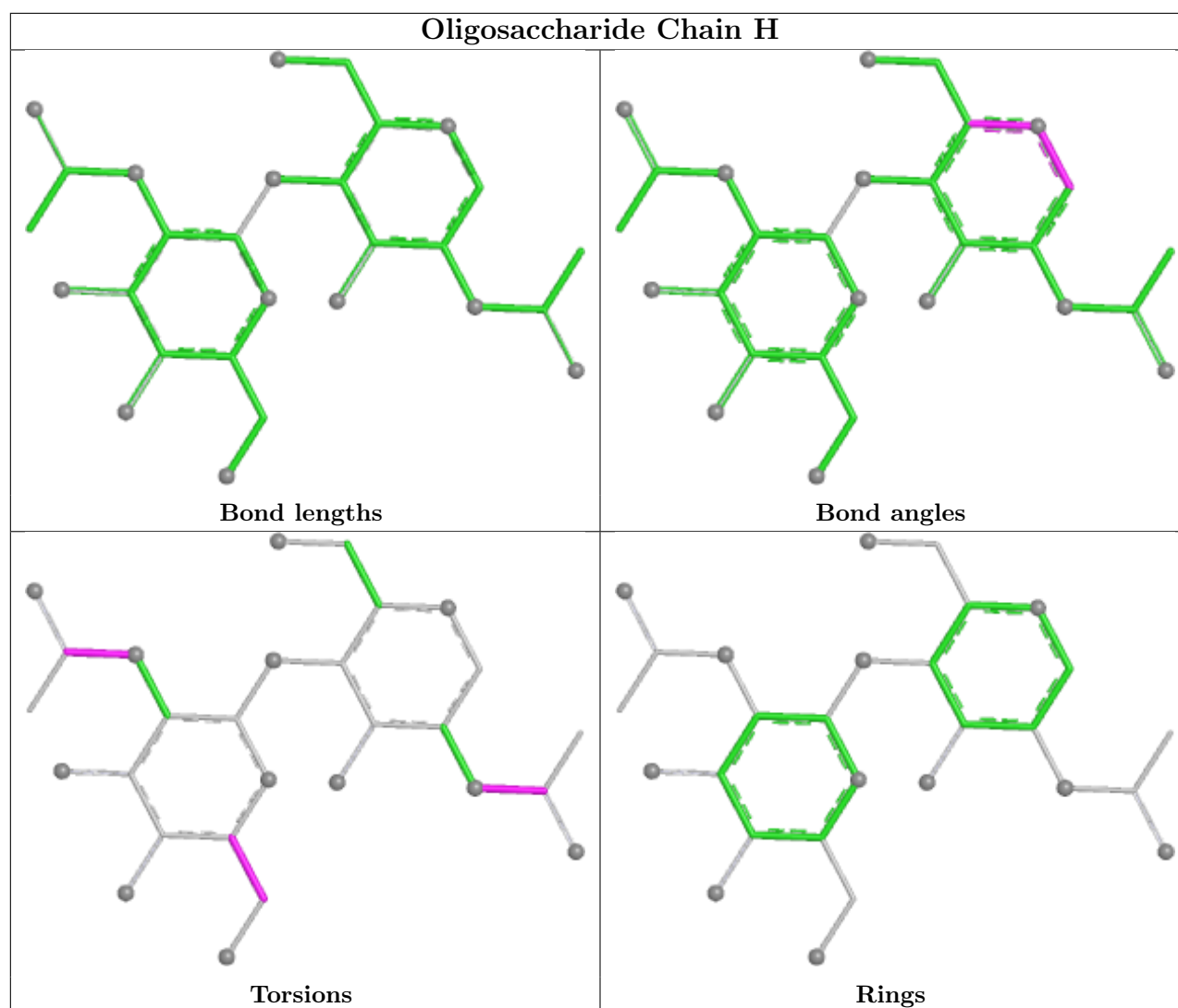












5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	3022	1	14,14,15	0.44	0	17,19,21	0.69	0
5	NAG	A	3019	1	14,14,15	0.46	0	17,19,21	0.64	0
5	NAG	A	3000	1	14,14,15	0.44	0	17,19,21	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	3014	1	14,14,15	0.44	0	17,19,21	1.18	2 (11%)
5	NAG	A	3011	1	14,14,15	0.44	0	17,19,21	0.65	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	3022	1	-	4/6/23/26	0/1/1/1
5	NAG	A	3019	1	-	2/6/23/26	0/1/1/1
5	NAG	A	3000	1	-	2/6/23/26	0/1/1/1
5	NAG	A	3014	1	-	4/6/23/26	0/1/1/1
5	NAG	A	3011	1	-	5/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	3014	NAG	C1-C2-N2	3.27	115.59	110.43
5	A	3014	NAG	C2-N2-C7	3.26	127.27	122.90

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	3000	NAG	C8-C7-N2-C2
5	A	3000	NAG	O7-C7-N2-C2
5	A	3011	NAG	C8-C7-N2-C2
5	A	3011	NAG	O7-C7-N2-C2
5	A	3014	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3
2	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1037:MET	C	1045:PRO	N	15.82
1	D	325:SER	C	336:GLY	N	7.27
1	A	1891:ASP	C	1892:HIS	N	3.08
1	A	1145:SER	C	1146:PRO	N	2.74

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	1836/1836 (100%)	1.07	232 (12%) 8 11	45, 123, 188, 241	1 (0%)
2	D	347/347 (100%)	1.22	65 (18%) 3 6	70, 144, 230, 300	0
All	All	2183/2183 (100%)	1.09	297 (13%) 7 10	45, 126, 194, 300	1 (0%)

The worst 5 of 297 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	263	ILE	5.7
1	A	2568	LEU	5.7
1	A	2684	LEU	5.3
1	A	2530	MET	5.1
1	A	2571	GLN	5.0

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.

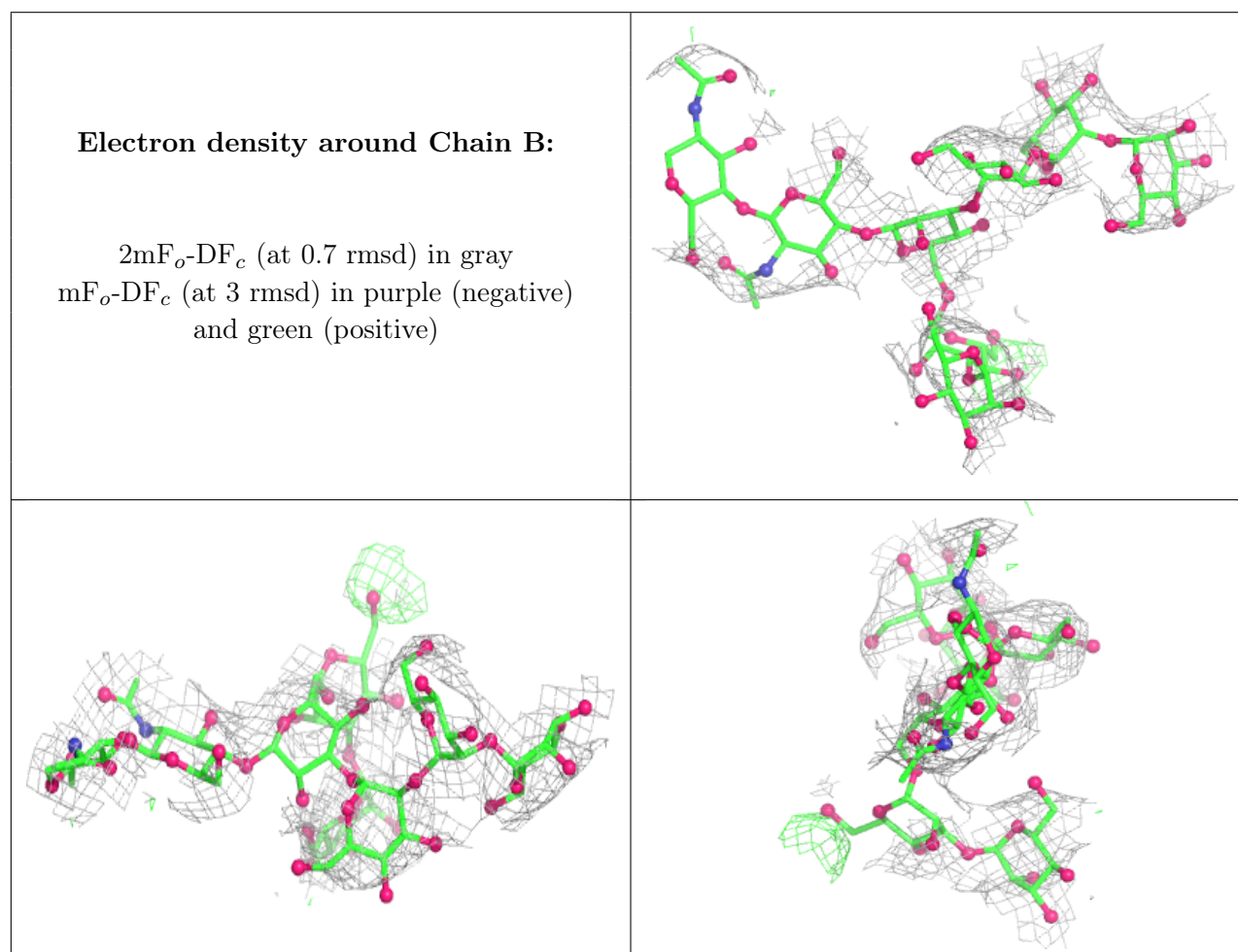
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	B	1	14/15	-	-	151,158,168,169	0
3	NAG	B	2	14/15	-	-	168,177,183,189	0
3	BMA	B	3	11/12	-	-	194,198,204,207	0
3	MAN	B	4	11/12	-	-	201,202,203,205	0
3	MAN	B	5	11/12	-	-	208,209,210,213	0

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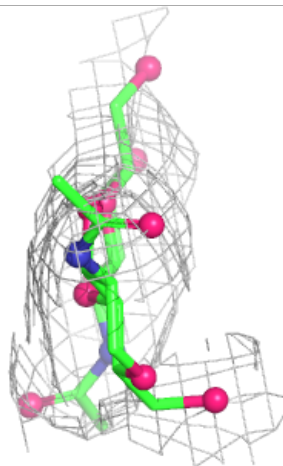
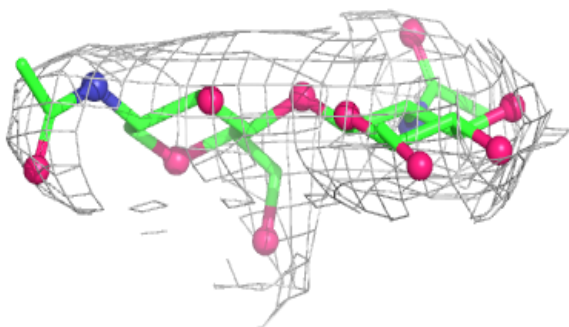
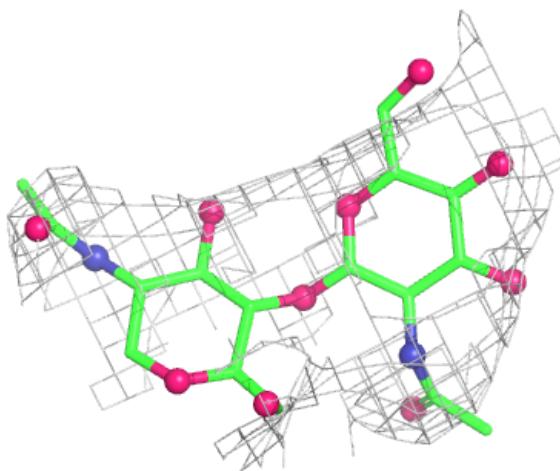
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MAN	B	6	11/12	-	-	215,217,218,219	0
3	MAN	B	7	11/12	-	-	210,212,213,213	0
3	MAN	B	8	11/12	-	-	212,213,214,215	0
4	NAG	G	2	14/15	0.26	0.20	152,155,160,161	0
4	NAG	F	2	14/15	0.49	0.16	156,160,165,166	0
4	NAG	G	1	14/15	0.59	0.17	128,137,143,147	0
4	NAG	H	2	14/15	0.69	0.16	139,140,142,144	0
4	NAG	C	2	14/15	0.73	0.15	145,151,157,160	0
4	NAG	H	1	14/15	0.75	0.15	122,132,138,138	0
4	NAG	C	1	14/15	0.78	0.15	129,133,137,141	0
4	NAG	E	2	14/15	0.81	0.16	155,158,162,164	0
4	NAG	E	1	14/15	0.82	0.17	137,140,145,149	0
4	NAG	F	1	14/15	0.89	0.10	125,138,146,150	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.



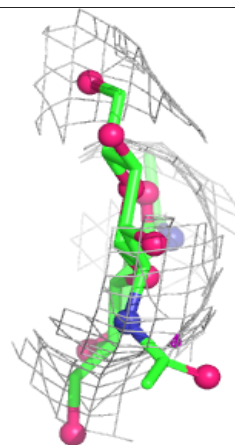
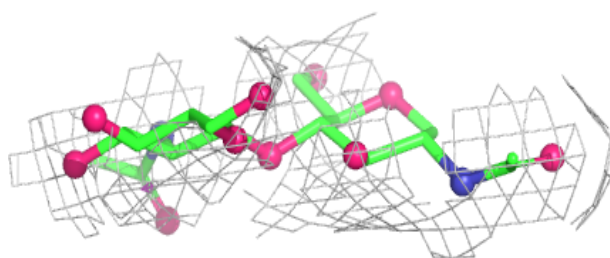
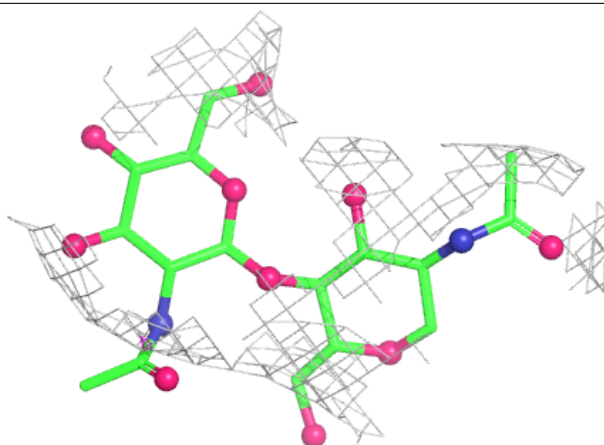
Electron density around Chain C:

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

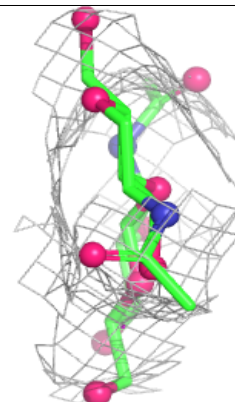
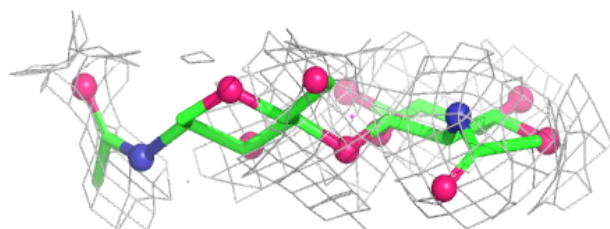
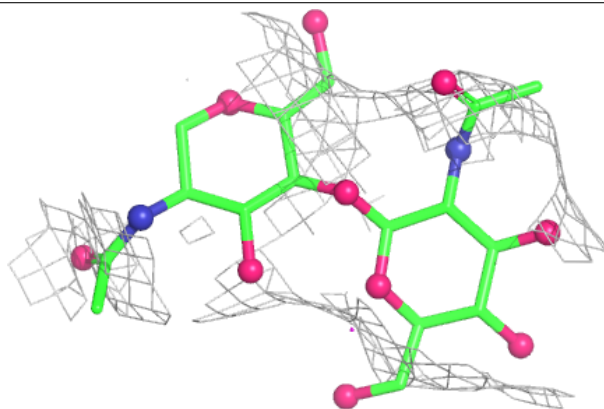


Electron density around Chain E:

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

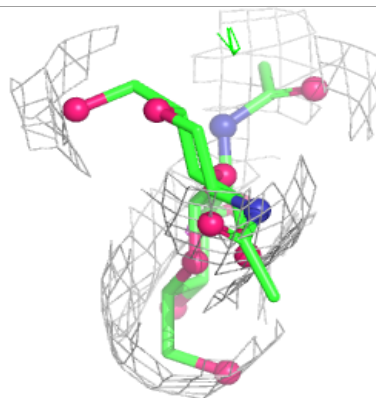
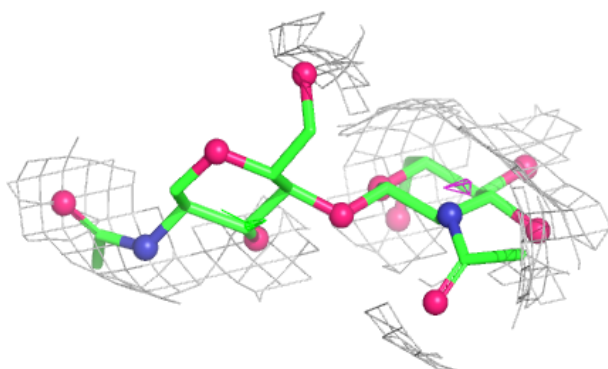
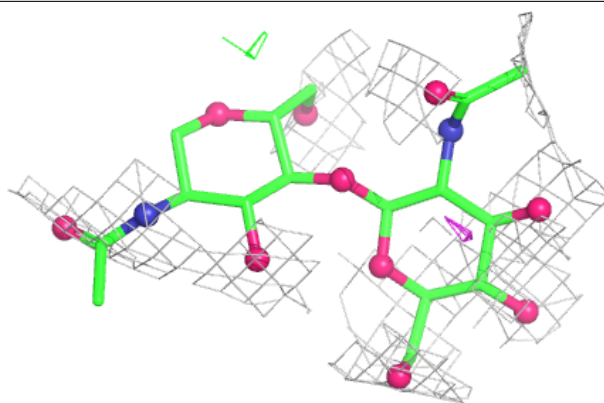
**Electron density around Chain F:**

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

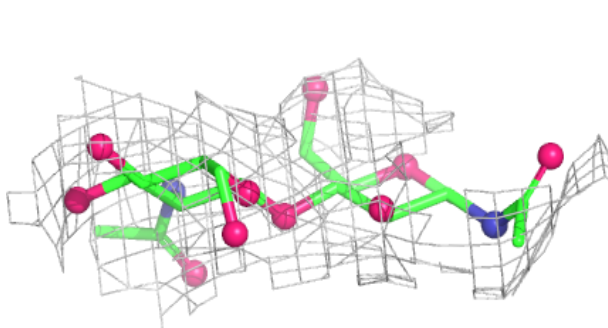
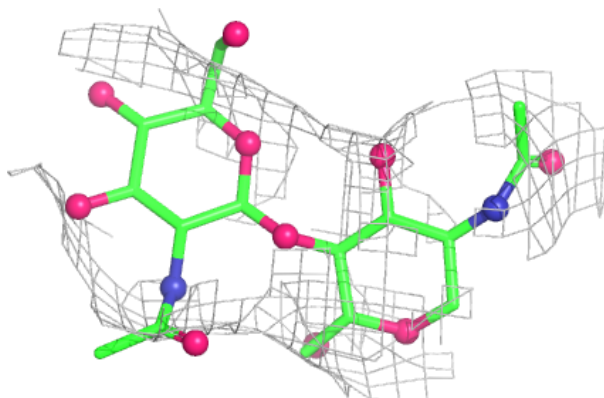


Electron density around Chain G:

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

**Electron density around Chain H:**

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



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($\text{\AA}^2$)	Q<0.9
5	NAG	A	3014	14/15	0.42	0.21	152,156,159,159	0
5	NAG	A	3019	14/15	0.43	0.18	215,217,218,219	0
5	NAG	A	3000	14/15	0.62	0.18	224,225,228,228	0
5	NAG	A	3022	14/15	0.63	0.14	187,190,194,194	0
5	NAG	A	3011	14/15	0.75	0.18	139,144,149,149	0
6	CA	D	1100	1/1	0.99	0.14	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.