



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:21 AM UTC

PDB ID : 4ZXB / pdb_00004zxb
Title : Structure of the human insulin receptor ectodomain, IRDeltabeta construct, in complex with four Fab molecules
Authors : Croll, T.; Smith, B.J.; Margetts, M.B.; Whittaker, J.; Weiss, M.A.; Ward, C.W.; Lawrence, M.C.
Deposited on : 2015-05-20
Resolution : 3.30 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

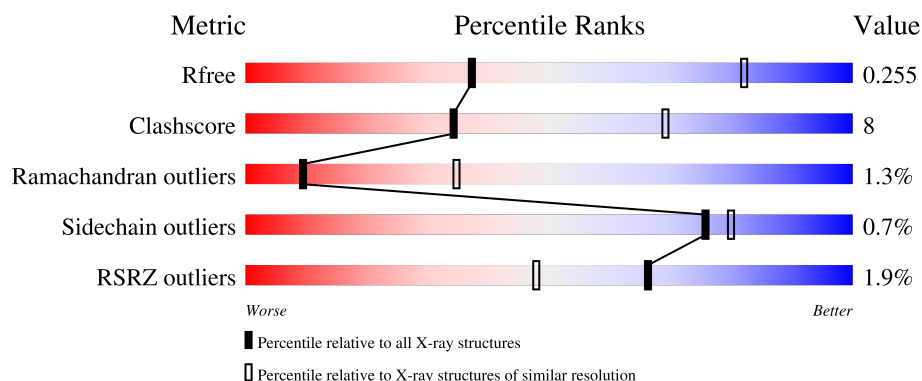
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.



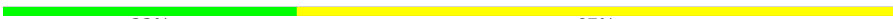
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	219	82% 15% .
2	B	219	84% 14% .
3	C	220	4% 65% 19% . 15%
4	D	214	2% 75% 9% . 15%
5	E	894	2% 66% 21% . 11%

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Mol	Chain	Length	Quality of chain
6	F	3	 100%
6	H	3	 67% 33%
6	K	3	 67% 33%
7	G	3	 100%
8	I	6	 33% 67%
9	J	2	 50% 50%
9	L	2	 50% 50%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 12918 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 Fab 83-7 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1611	1018	266	319	8			

- Molecule 2 is a protein called Fab 83-7 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	218	Total	C	N	O	S	0	0	0
			1706	1068	286	345	7			

- Molecule 3 is a protein called Fab 83-14 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	187	Total	C	N	O	S	0	0	0
			1427	917	234	271	5			

- Molecule 4 is a protein called Fab 83-14 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	182	Total	C	N	O	S	0	0	0
			1384	865	227	287	5			

- Molecule 5 is a protein called Insulin receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	800	Total	C	N	O	S	0	0	0
			6473	4106	1117	1202	48			

There are 28 discrepancies between the modelled and reference sequences:

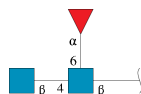
Chain	Residue	Modelled	Actual	Comment	Reference
E	144	HIS	TYR	engineered mutation	UNP P06213
E	?	-	ARG	deletion	UNP P06213

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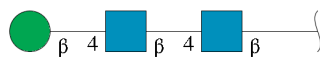
Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	LYS	deletion	UNP P06213
E	?	-	ARG	deletion	UNP P06213
E	?	-	ARG	deletion	UNP P06213
E	?	-	VAL	deletion	UNP P06213
E	?	-	THR	deletion	UNP P06213
E	?	-	VAL	deletion	UNP P06213
E	?	-	ALA	deletion	UNP P06213
E	?	-	VAL	deletion	UNP P06213
E	?	-	PRO	deletion	UNP P06213
E	?	-	THR	deletion	UNP P06213
E	?	-	VAL	deletion	UNP P06213
E	?	-	ALA	deletion	UNP P06213
E	?	-	ALA	deletion	UNP P06213
E	?	-	PHE	deletion	UNP P06213
E	?	-	PRO	deletion	UNP P06213
E	?	-	ASN	deletion	UNP P06213
E	?	-	THR	deletion	UNP P06213
E	?	-	SER	deletion	UNP P06213
E	?	-	SER	deletion	UNP P06213
E	?	-	THR	deletion	UNP P06213
E	?	-	SER	deletion	UNP P06213
E	?	-	VAL	deletion	UNP P06213
E	750	ALA	PRO	engineered mutation	UNP P06213
E	751	GLY	THR	engineered mutation	UNP P06213
E	752	ASN	SER	engineered mutation	UNP P06213
E	753	ASN	PRO	engineered mutation	UNP P06213

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



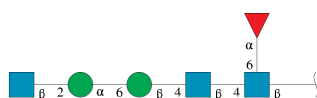
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	F	3	Total	C	N	O	0	0	0
			38	22	2	14			
6	H	3	Total	C	N	O	0	0	0
			38	22	2	14			
6	K	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 7 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
7	G	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 8 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-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.



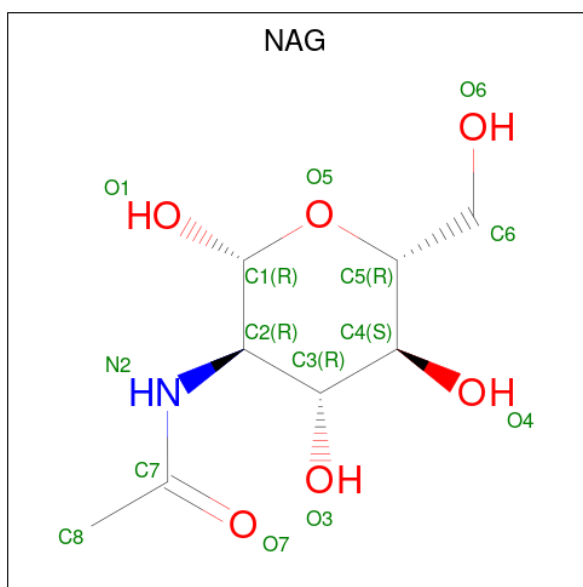
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	I	6	Total	C	N	O	0	0	0
			74	42	3	29			

- Molecule 9 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	J	2	Total	C	N	O	0	0	0
			24	14	1	9			
9	L	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

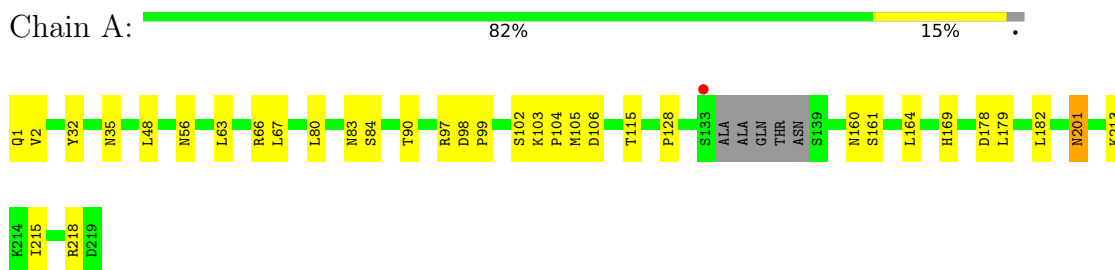


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	E	1	Total	C	N	O	0	0
			14	8	1	5		
10	E	1	Total	C	N	O	0	0
			14	8	1	5		
10	E	1	Total	C	N	O	0	0
			14	8	1	5		

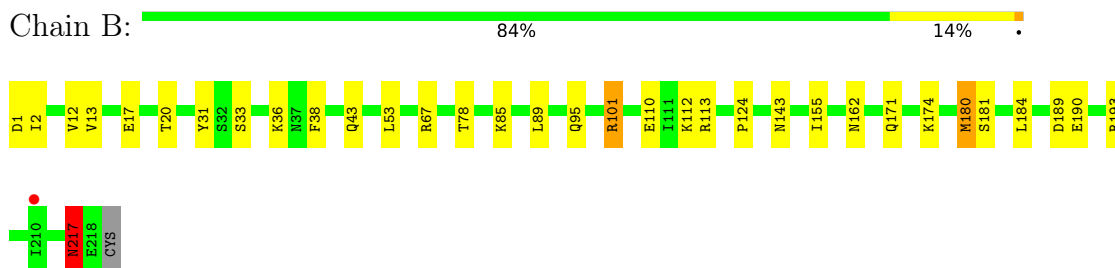
3 Residue-property plots [i](#)

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.

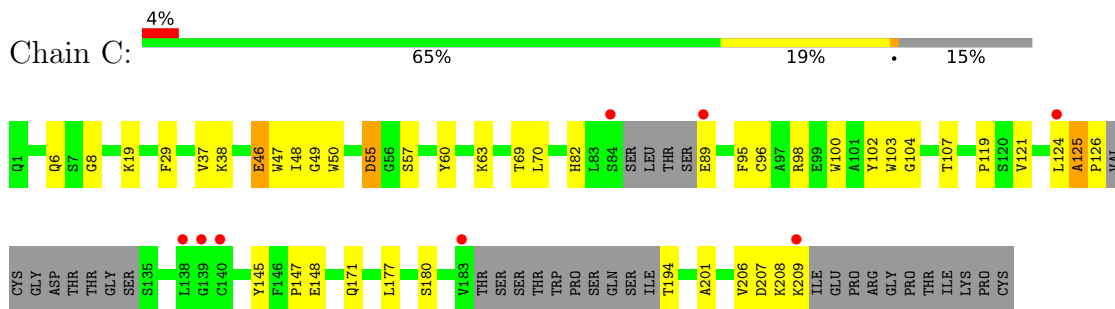
- Molecule 1: Fab 83-7 heavy chain



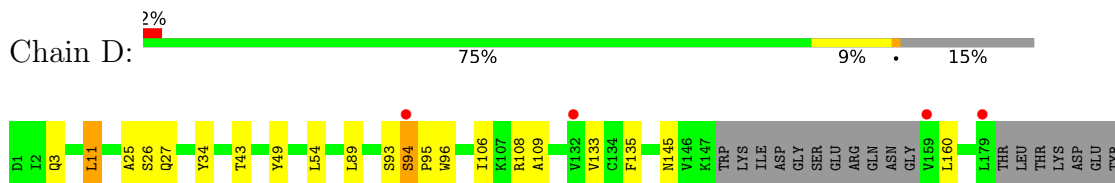
- Molecule 2: Fab 83-7 light chain



- Molecule 3: Fab 83-14 heavy chain

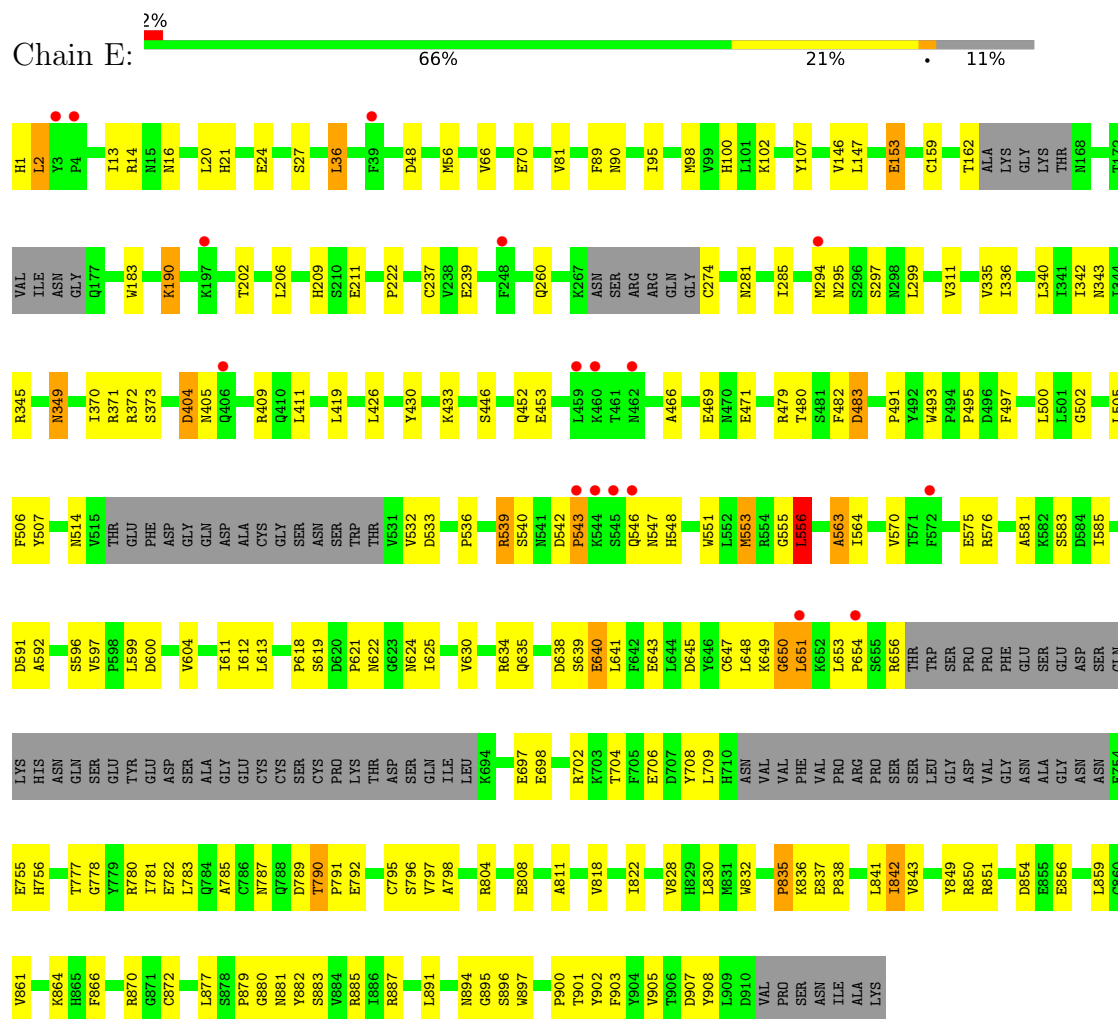


- Molecule 4: Fab 83-14 light chain

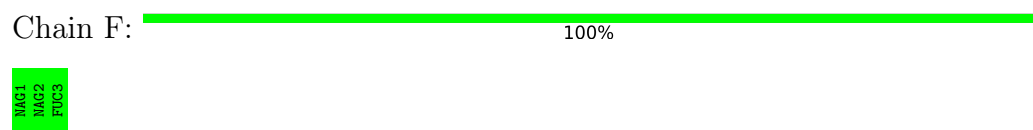


GLU	ARG	HIS	ASN	TYR	THR	CYS	GLU	ASN	ARG	GLY	CYS
A196	T197	F209	ASN	ARG	GLY	CYS					

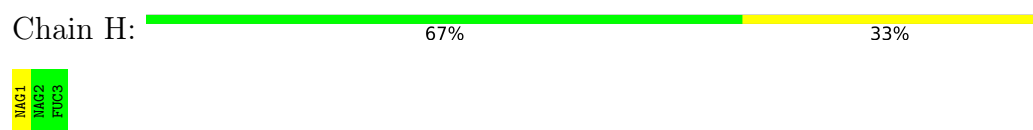
• Molecule 5: Insulin receptor



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



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

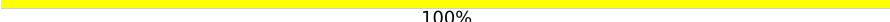


- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  67% 33%

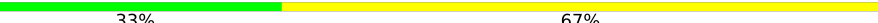

MAG1
MAG2
FUC3

- Molecule 7: 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
BM3

- Molecule 8: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)-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 I:  33% 67%


MAG1
MAG2
BM3
BM4
MAG5
FUC6

- Molecule 9: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  50% 50%


MAG1
FUC2

- Molecule 9: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  50% 50%


MAG1
FUC2

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	121.87Å 321.25Å 199.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.46 – 3.30 34.46 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.0 (34.46-3.30) 97.9 (34.46-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 3.32Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.205 , 0.237 0.222 , 0.255	Depositor DCC
R_{free} test set	2911 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	106.7	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 122.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12918	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 2.57% 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, 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	0.86	3/1654 (0.2%)	1.18	3/2261 (0.1%)
2	B	0.75	1/1744 (0.1%)	1.14	6/2363 (0.3%)
3	C	0.76	0/1465	1.29	7/1995 (0.4%)
4	D	0.85	0/1412	1.26	8/1914 (0.4%)
5	E	0.86	5/6631 (0.1%)	1.36	66/8986 (0.7%)
All	All	0.83	9/12906 (0.1%)	1.29	90/17519 (0.5%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	95	ILE	CG1-CD1	-8.72	1.17	1.51
5	E	342	ILE	CG1-CD1	-8.21	1.19	1.51
2	B	180	MET	SD-CE	-7.63	1.60	1.79
1	A	215	ILE	CG1-CD1	-5.80	1.29	1.51
1	A	102	SER	CA-C	5.67	1.60	1.52

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	190	GLU	CB-CG-CD	8.70	127.38	112.60
3	C	55	ASP	CA-CB-CG	8.43	121.03	112.60
5	E	555	GLY	CA-C-N	8.40	137.59	121.54
5	E	555	GLY	C-N-CA	8.40	137.59	121.54
3	C	89	GLU	CB-CG-CD	7.75	125.78	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1611	0	1582	28	0
2	B	1706	0	1648	29	0
3	C	1427	0	1407	36	0
4	D	1384	0	1337	13	0
5	E	6473	0	6272	103	0
6	F	38	0	34	0	0
6	H	38	0	34	0	0
6	K	38	0	34	0	0
7	G	39	0	34	0	0
8	I	74	0	64	0	0
9	J	24	0	22	0	0
9	L	24	0	22	0	0
10	E	42	0	39	1	0
All	All	12918	0	12529	194	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 8.

The worst 5 of 194 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)
5:E:426:LEU:H	5:E:452:GLN:HE21	1.13	0.88
1:A:48:LEU:HD22	1:A:63:LEU:CD1	2.05	0.86
3:C:125:ALA:H	3:C:126:PRO:HD3	1.40	0.86
5:E:790:THR:HB	5:E:791:PRO:HD3	1.57	0.84
2:B:101:ARG:HH11	2:B:101:ARG:CG	1.93	0.81

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	210/219 (96%)	198 (94%)	11 (5%)	1 (0%)	24	55
2	B	216/219 (99%)	212 (98%)	4 (2%)	0	100	100
3	C	179/220 (81%)	169 (94%)	9 (5%)	1 (1%)	21	52
4	D	176/214 (82%)	171 (97%)	4 (2%)	1 (1%)	21	52
5	E	786/894 (88%)	715 (91%)	53 (7%)	18 (2%)	5	25
All	All	1567/1766 (89%)	1465 (94%)	81 (5%)	21 (1%)	9	35

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	125	ALA
4	D	94	SER
5	E	153	GLU
5	E	539	ARG
5	E	540	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	187/190 (98%)	186 (100%)	1 (0%)	81	83
2	B	196/197 (100%)	194 (99%)	2 (1%)	68	76
3	C	157/187 (84%)	156 (99%)	1 (1%)	78	81
4	D	161/190 (85%)	159 (99%)	2 (1%)	63	75
5	E	729/809 (90%)	725 (100%)	4 (0%)	81	83
All	All	1430/1573 (91%)	1420 (99%)	10 (1%)	76	80

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	E	349	ASN
5	E	640	GLU
5	E	651	LEU
3	C	69	THR
4	D	11	LEU

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

Mol	Chain	Res	Type
5	E	108	ASN
5	E	343	ASN
5	E	635	GLN
5	E	209	HIS
5	E	405	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

22 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	$\# Z > 2$
6	NAG	F	1	5,6	14,14,15	0.34	0	17,19,21	0.56	0
6	NAG	F	2	6	14,14,15	0.34	0	17,19,21	0.51	0
6	FUC	F	3	6	10,10,11	0.44	0	14,14,16	0.69	0
7	NAG	G	1	7,5	14,14,15	0.42	0	17,19,21	1.70	4 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	NAG	G	2	7	14,14,15	0.35	0	17,19,21	1.06	2 (11%)
7	BMA	G	3	7	11,11,12	0.43	0	15,15,17	0.74	1 (6%)
6	NAG	H	1	5,6	14,14,15	0.36	0	17,19,21	0.85	1 (5%)
6	NAG	H	2	6	14,14,15	0.46	0	17,19,21	0.59	0
6	FUC	H	3	6	10,10,11	0.52	0	14,14,16	0.72	0
8	NAG	I	1	5,8	14,14,15	0.32	0	17,19,21	0.87	1 (5%)
8	NAG	I	2	8	14,14,15	0.40	0	17,19,21	0.83	1 (5%)
8	BMA	I	3	8	11,11,12	0.32	0	15,15,17	0.42	0
8	MAN	I	4	8	11,11,12	0.50	0	15,15,17	0.94	1 (6%)
8	NAG	I	5	8	14,14,15	0.37	0	17,19,21	1.12	2 (11%)
8	FUC	I	6	8	10,10,11	0.54	0	14,14,16	0.70	0
9	NAG	J	1	5,9	14,14,15	0.45	0	17,19,21	0.73	1 (5%)
9	FUC	J	2	9	10,10,11	0.45	0	14,14,16	0.59	0
6	NAG	K	1	5,6	14,14,15	0.38	0	17,19,21	0.52	0
6	NAG	K	2	6	14,14,15	0.38	0	17,19,21	0.86	1 (5%)
6	FUC	K	3	6	10,10,11	0.45	0	14,14,16	0.49	0
9	NAG	L	1	5,9	14,14,15	0.45	0	17,19,21	1.35	1 (5%)
9	FUC	L	2	9	10,10,11	0.50	0	14,14,16	0.57	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
6	NAG	F	1	5,6	-	0/6/23/26	0/1/1/1
6	NAG	F	2	6	-	0/6/23/26	0/1/1/1
6	FUC	F	3	6	-	-	0/1/1/1
7	NAG	G	1	7,5	-	2/6/23/26	0/1/1/1
7	NAG	G	2	7	-	0/6/23/26	0/1/1/1
7	BMA	G	3	7	-	0/2/19/22	0/1/1/1
6	NAG	H	1	5,6	-	1/6/23/26	0/1/1/1
6	NAG	H	2	6	-	0/6/23/26	0/1/1/1
6	FUC	H	3	6	-	-	0/1/1/1
8	NAG	I	1	5,8	-	0/6/23/26	0/1/1/1
8	NAG	I	2	8	-	0/6/23/26	0/1/1/1
8	BMA	I	3	8	-	0/2/19/22	0/1/1/1
8	MAN	I	4	8	-	1/2/19/22	0/1/1/1
8	NAG	I	5	8	-	0/6/23/26	0/1/1/1
8	FUC	I	6	8	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	J	1	5,9	-	0/6/23/26	0/1/1/1
9	FUC	J	2	9	-	-	0/1/1/1
6	NAG	K	1	5,6	-	0/6/23/26	0/1/1/1
6	NAG	K	2	6	-	0/6/23/26	0/1/1/1
6	FUC	K	3	6	-	-	0/1/1/1
9	NAG	L	1	5,9	-	0/6/23/26	0/1/1/1
9	FUC	L	2	9	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	G	1	NAG	C1-O5-C5	4.67	118.44	112.19
9	L	1	NAG	C1-C2-N2	-4.05	104.05	110.43
7	G	1	NAG	C1-C2-N2	3.63	116.15	110.43
8	I	1	NAG	C1-O5-C5	3.03	116.24	112.19
8	I	4	MAN	C1-O5-C5	2.97	116.17	112.19

There are no chirality outliers.

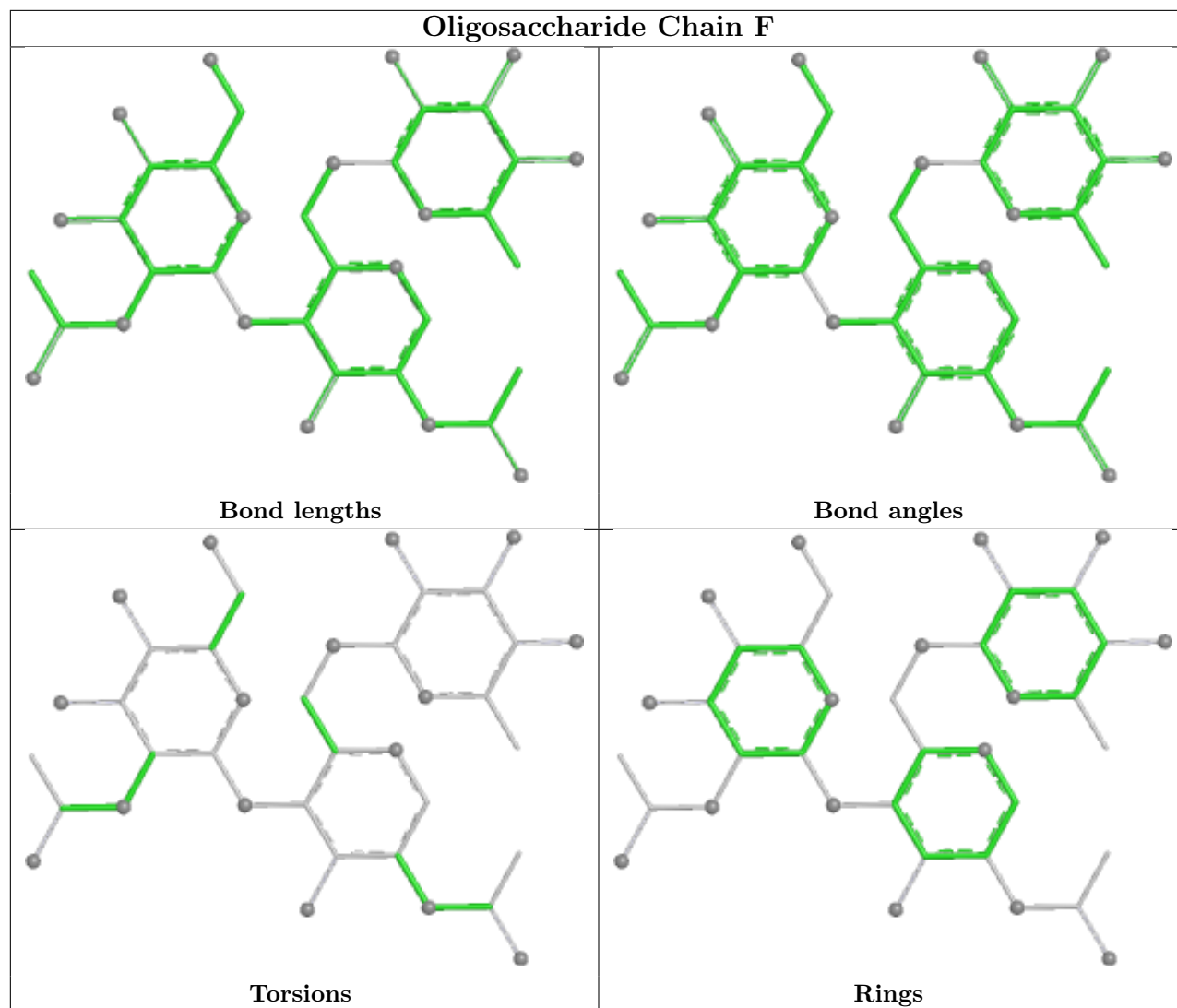
All (4) torsion outliers are listed below:

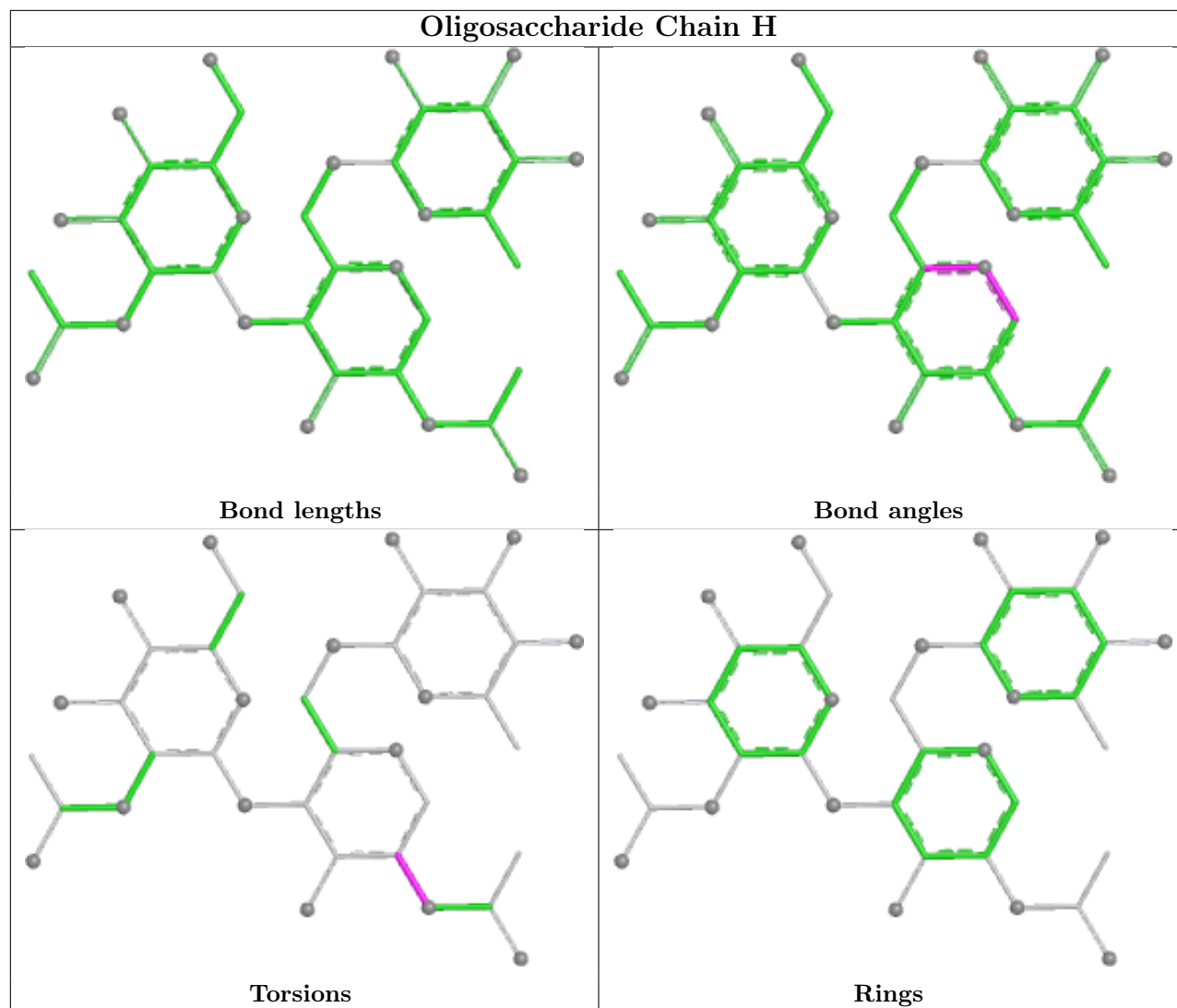
Mol	Chain	Res	Type	Atoms
8	I	4	MAN	O5-C5-C6-O6
7	G	1	NAG	O5-C5-C6-O6
6	H	1	NAG	C1-C2-N2-C7
7	G	1	NAG	C1-C2-N2-C7

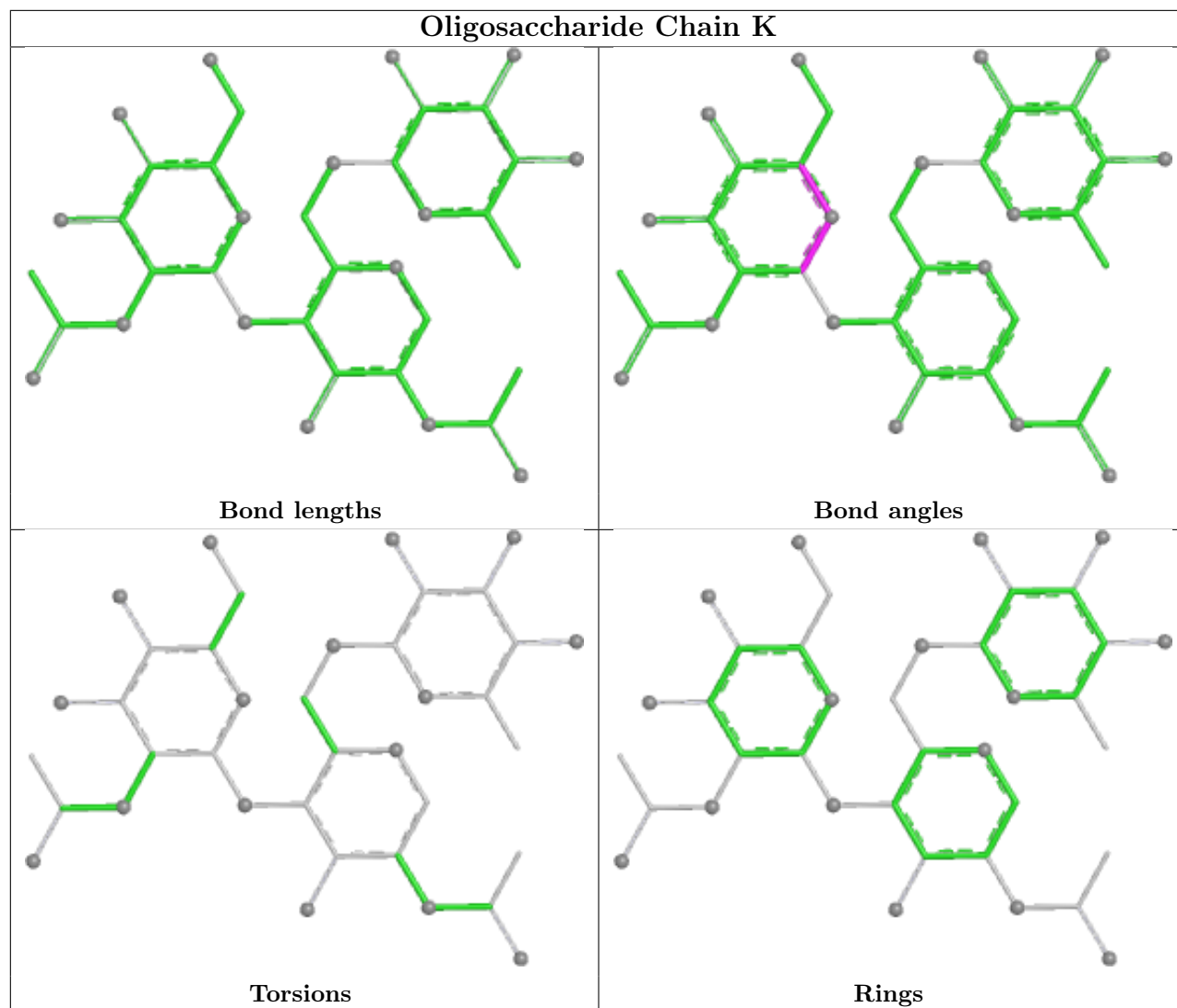
There are no ring outliers.

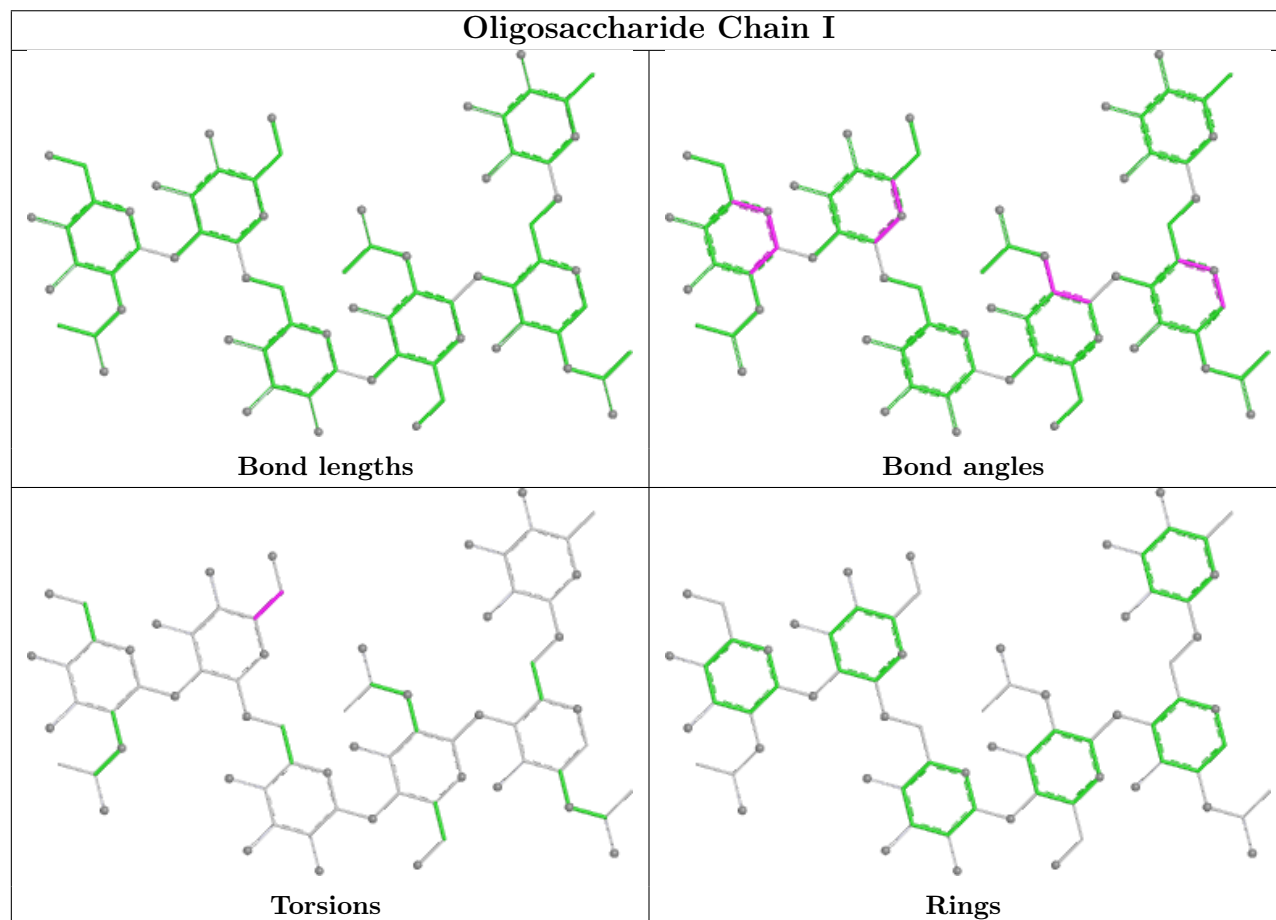
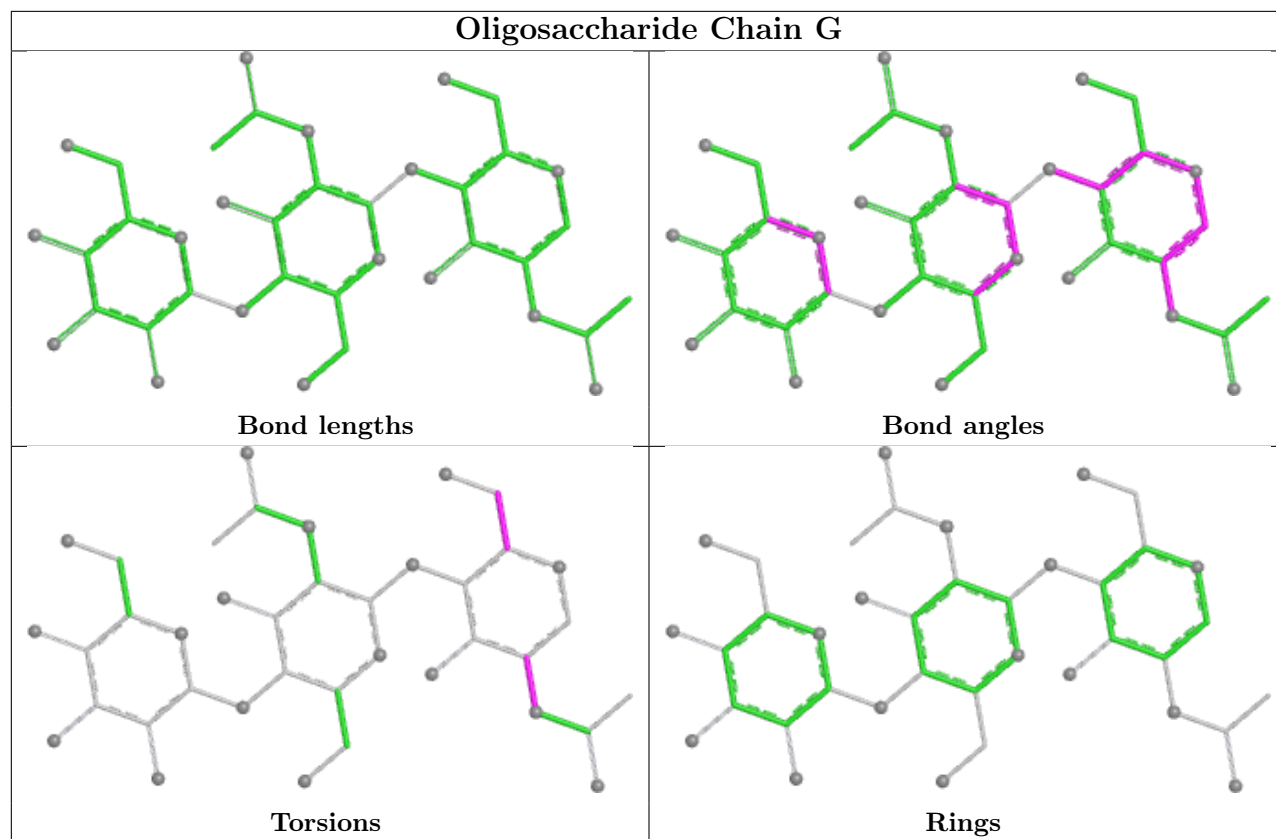
No monomer is involved in short contacts.

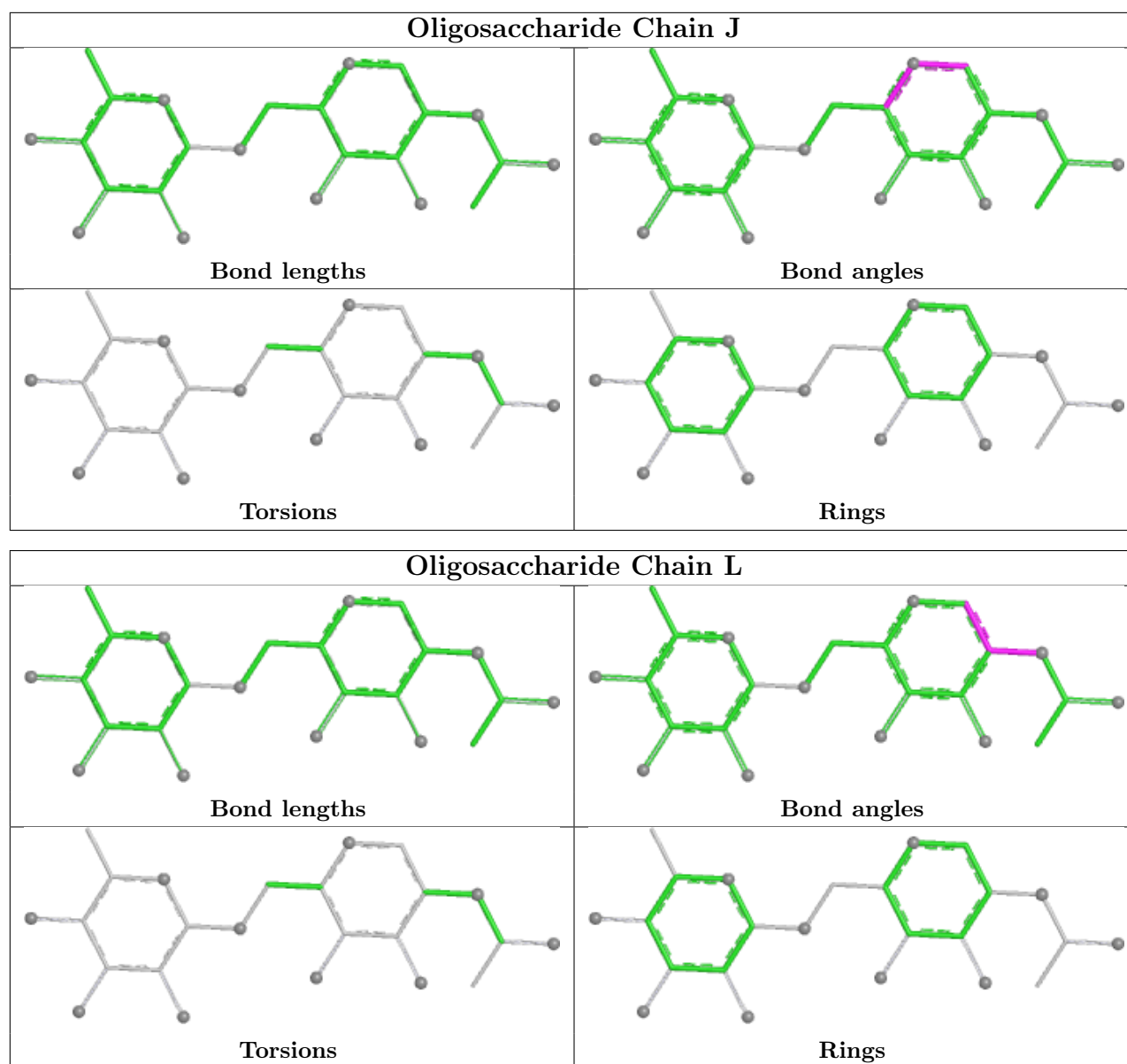
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

3 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
10	NAG	E	1020	5	14,14,15	0.39	0	17,19,21	1.06	2 (11%)
10	NAG	E	1001	5	14,14,15	0.40	0	17,19,21	0.61	0
10	NAG	E	1008	5	14,14,15	0.31	0	17,19,21	2.32	2 (11%)

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
10	NAG	E	1020	5	-	0/6/23/26	0/1/1/1
10	NAG	E	1001	5	-	0/6/23/26	0/1/1/1
10	NAG	E	1008	5	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	E	1008	NAG	C1-C2-N2	-8.90	96.40	110.43
10	E	1020	NAG	C1-O5-C5	2.91	116.08	112.19
10	E	1020	NAG	C1-C2-N2	2.50	114.37	110.43
10	E	1008	NAG	O5-C1-C2	2.49	115.15	111.29

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	E	1008	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	E	1008	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	214/219 (97%)	-0.28	1 (0%) 87 76	78, 111, 146, 168	0
2	B	218/219 (99%)	-0.23	1 (0%) 87 76	84, 121, 155, 175	0
3	C	187/220 (85%)	0.11	8 (4%) 40 25	87, 155, 199, 214	0
4	D	182/214 (85%)	-0.02	4 (2%) 62 43	78, 123, 204, 217	0
5	E	800/894 (89%)	-0.06	17 (2%) 63 44	72, 135, 186, 228	0
All	All	1601/1766 (90%)	-0.09	31 (1%) 66 48	72, 129, 190, 228	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	139	GLY	4.5
3	C	84	SER	4.4
5	E	4	PRO	3.5
5	E	459	LEU	3.4
5	E	543	PRO	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
7	BMA	G	3	11/12	0.35	0.14	160,165,169,169	0

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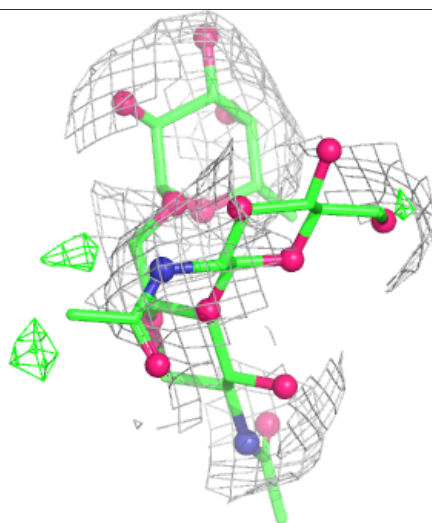
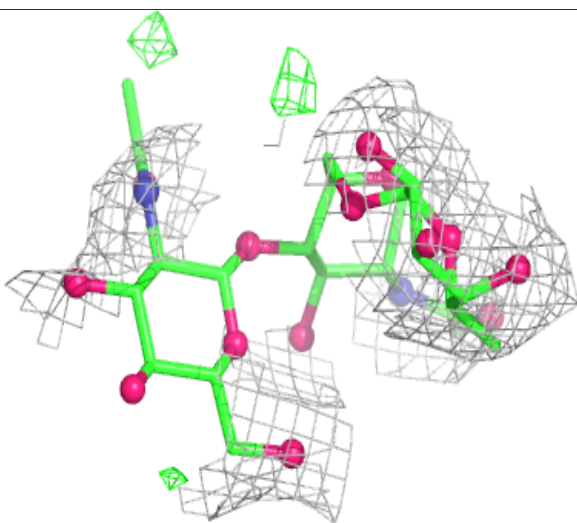
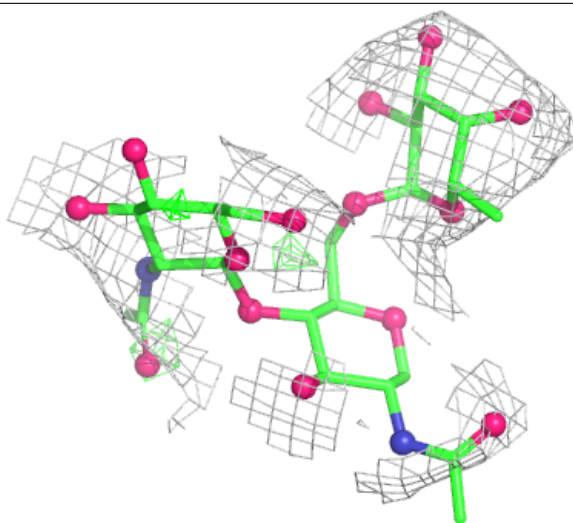
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	BMA	I	3	11/12	0.50	0.10	186,198,199,200	0
9	NAG	J	1	14/15	0.60	0.12	181,187,195,196	0
8	MAN	I	4	11/12	0.61	0.13	185,197,203,208	0
9	FUC	L	2	10/11	0.63	0.15	187,197,205,206	0
6	NAG	F	2	14/15	0.67	0.11	179,204,207,207	0
6	FUC	F	3	10/11	0.71	0.10	177,185,193,194	0
6	NAG	H	2	14/15	0.72	0.12	146,173,183,183	0
8	NAG	I	5	14/15	0.76	0.13	160,168,180,181	0
6	FUC	K	3	10/11	0.77	0.13	180,188,194,201	0
8	NAG	I	2	14/15	0.79	0.09	153,185,196,200	0
8	NAG	I	1	14/15	0.79	0.12	147,159,171,177	0
8	FUC	I	6	10/11	0.83	0.10	161,170,173,174	0
6	NAG	F	1	14/15	0.84	0.09	177,187,197,204	0
9	FUC	J	2	10/11	0.84	0.14	178,184,186,189	0
6	NAG	K	2	14/15	0.84	0.10	173,193,201,203	0
9	NAG	L	1	14/15	0.87	0.10	152,159,173,184	0
6	NAG	K	1	14/15	0.91	0.09	155,179,193,198	0
7	NAG	G	2	14/15	0.92	0.10	133,151,167,174	0
6	FUC	H	3	10/11	0.92	0.12	146,154,162,162	0
6	NAG	H	1	14/15	0.95	0.08	135,148,159,159	0
7	NAG	G	1	14/15	0.96	0.08	138,152,170,180	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

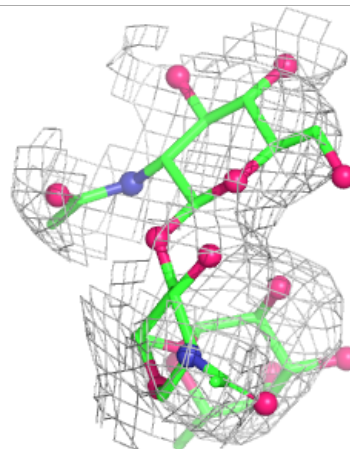
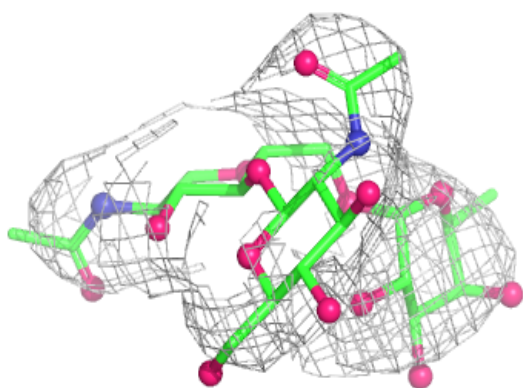
Electron density around Chain F:

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



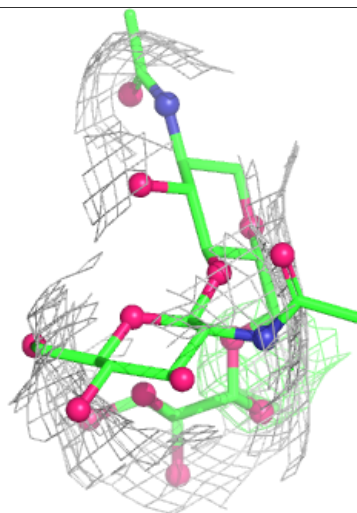
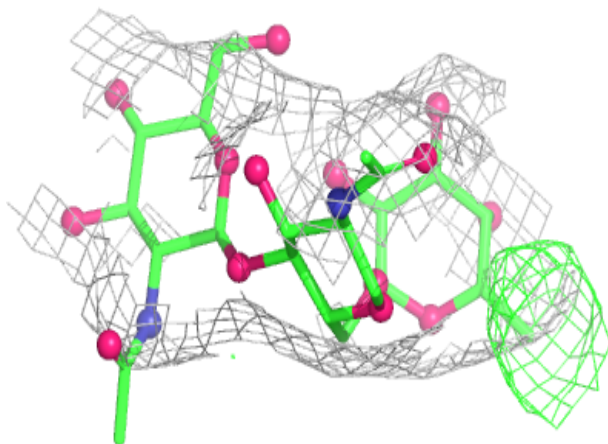
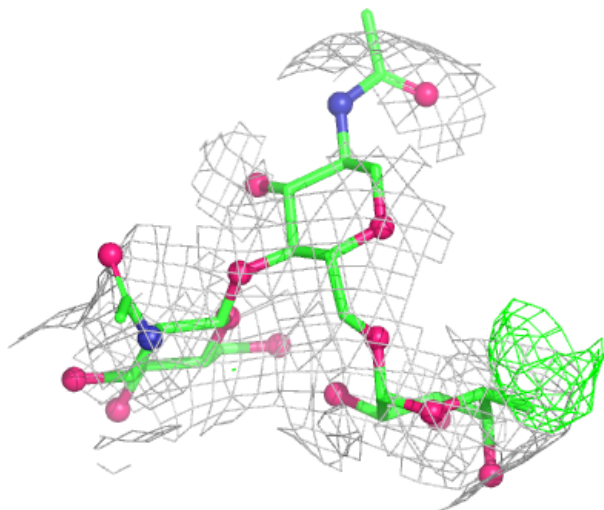
Electron density around Chain H:

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



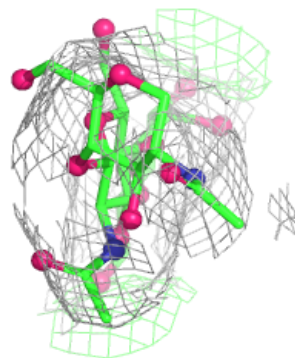
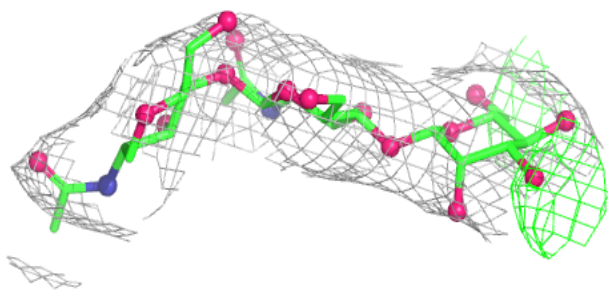
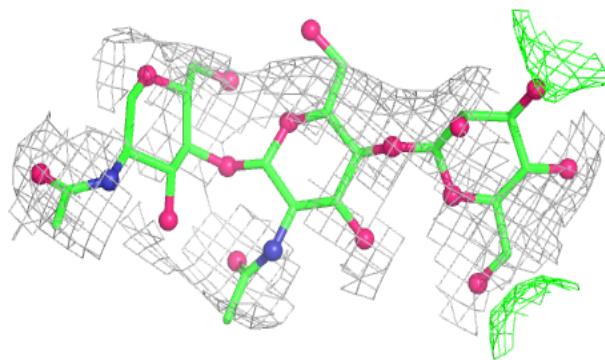
Electron density around Chain K:

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



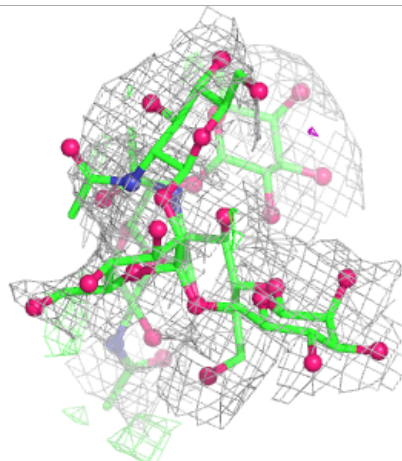
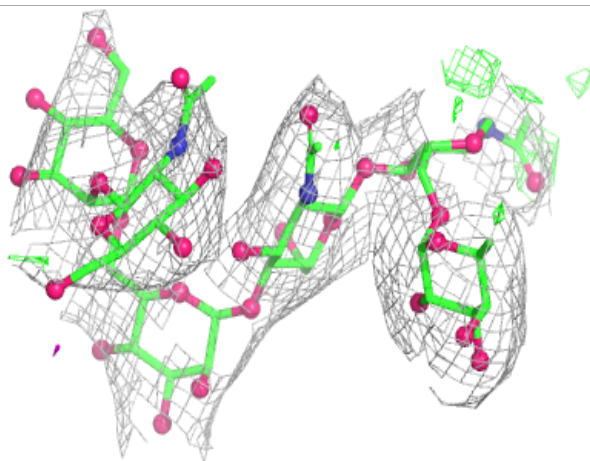
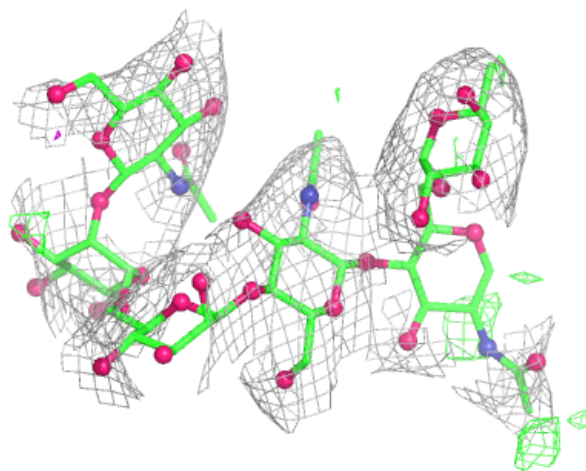
Electron density around Chain G:

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



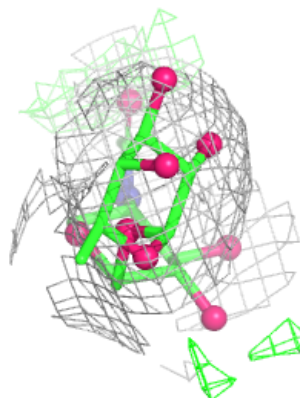
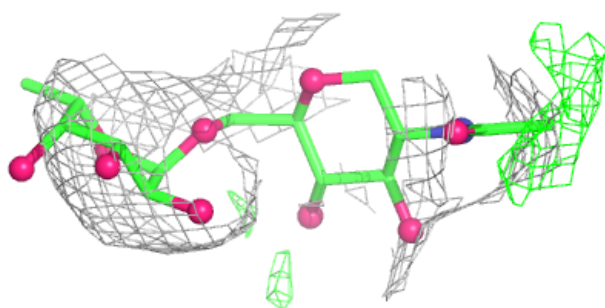
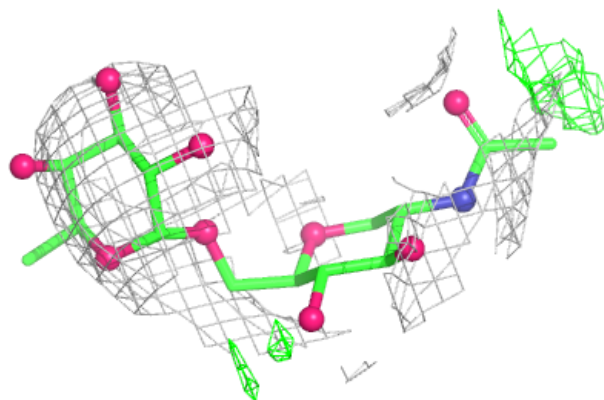
Electron density around Chain I:

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

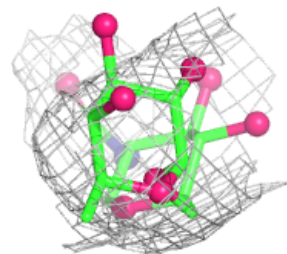
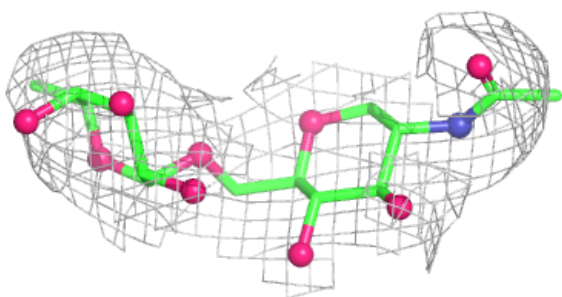
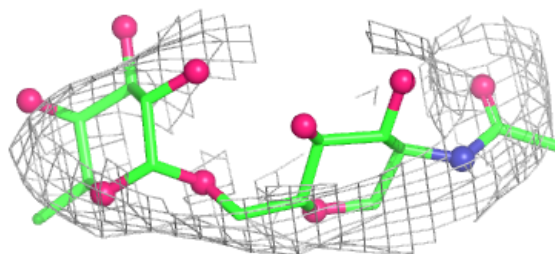


Electron density around Chain J:

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

**Electron density around Chain 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($\text{\AA}^2$)	Q<0.9
10	NAG	E	1001	14/15	0.73	0.10	152,163,168,169	0
10	NAG	E	1008	14/15	0.76	0.12	134,150,160,163	0
10	NAG	E	1020	14/15	0.80	0.08	155,162,168,169	0

6.5 Other polymers [i](#)

There are no such residues in this entry.