



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 05:15 AM BST

PDB ID : 4BXK
Title : Crystal structure of the Angiotensin-1 converting enzyme N-domain in complex with a domain-specific inhibitor
Authors : Douglas, R.G.; Sharma, R.K.; Masuyer, G.; Lubbe, L.; Zamora, I.; Acharya, K.R.; Chibale, K.; Sturrock, E.D.
Deposited on : 2013-07-12
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

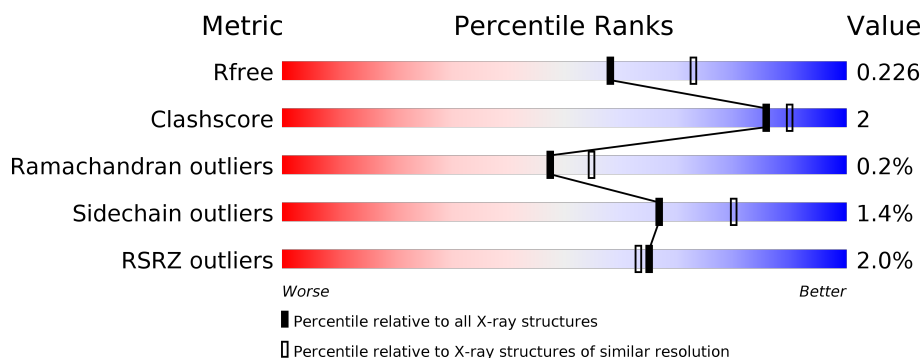
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	629	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div></div> </div> </div>
1	B	629	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div></div> </div> </div>
2	C	2	<div> <div></div> <div>100%</div> </div>
3	D	2	<div> <div></div> <div>100%</div> </div>
3	F	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
4	E	4	<div> <div></div> <div> <div>75%</div> <div>25%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
5	G	3	 A horizontal bar chart showing the quality of chain G. The bar is divided into two segments: a green segment on the left representing 33% and a yellow segment on the right representing 67%. The percentages are labeled below the bar.

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 10657 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 ANGIOTENSIN-CONVERTING ENZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	607	Total	C	N	O	S	0	3	0
			4965	3188	853	905	19			
1	B	607	Total	C	N	O	S	0	2	0
			4954	3184	848	903	19			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	629	LEU	-	expression tag	UNP P12821
A	9	GLN	ASN	engineered mutation	UNP P12821
A	25	GLN	ASN	engineered mutation	UNP P12821
A	82	GLN	ASN	engineered mutation	UNP P12821
A	117	GLN	ASN	engineered mutation	UNP P12821
A	131	GLN	ASN	engineered mutation	UNP P12821
A	289	GLN	ASN	engineered mutation	UNP P12821
A	545	ARG	GLN	engineered mutation	UNP P12821
A	576	LEU	PRO	engineered mutation	UNP P12821
B	629	LEU	-	expression tag	UNP P12821
B	9	GLN	ASN	engineered mutation	UNP P12821
B	25	GLN	ASN	engineered mutation	UNP P12821
B	82	GLN	ASN	engineered mutation	UNP P12821
B	117	GLN	ASN	engineered mutation	UNP P12821
B	131	GLN	ASN	engineered mutation	UNP P12821
B	289	GLN	ASN	engineered mutation	UNP P12821
B	545	ARG	GLN	engineered mutation	UNP P12821
B	576	LEU	PRO	engineered mutation	UNP P12821

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



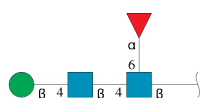
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 3 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
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 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.



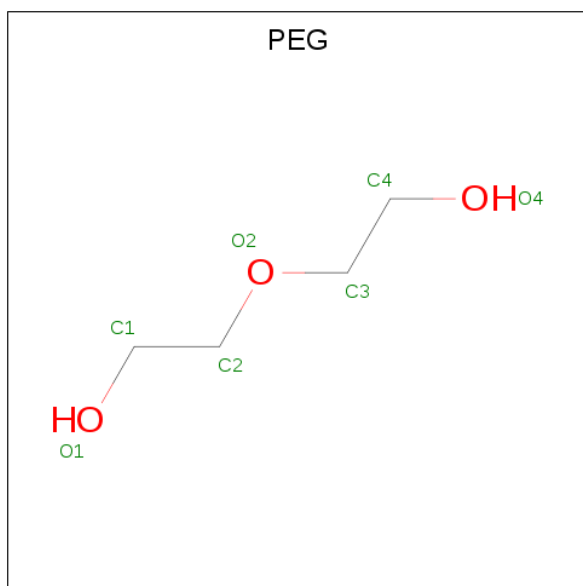
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 5 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.



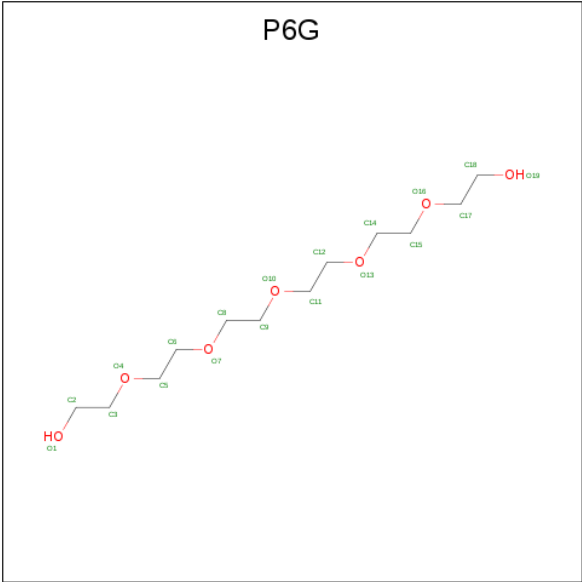
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



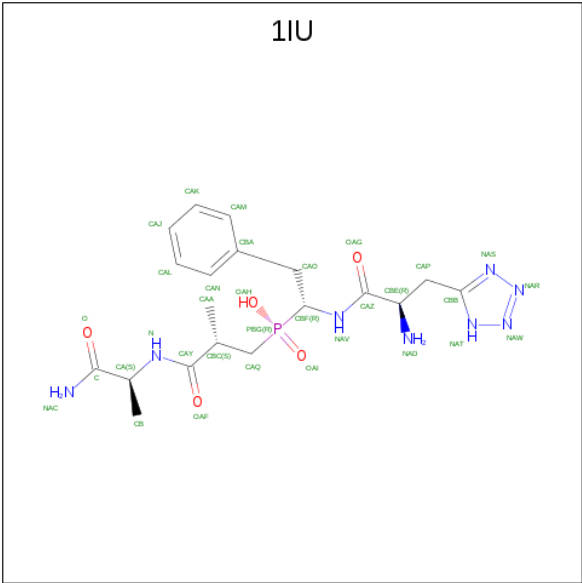
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			13	8	5		
7	B	1	Total	C	O	0	0
			19	12	7		

- Molecule 8 is [3-[[[(2S)-1-azanyl-1-oxidanylidene-propan-2-yl]amino]-2-methyl-3-oxidanylidene-propyl]-[(1R)-1-[[[(2R)-2-azanyl-3-(1H-1,2,3,4-tetrazol-5-yl)propanoyl]amino]-2-phenyl-ethyl]phosphinic acid (three-letter code: 1IU) (formula: C₁₉H₂₉N₈O₅P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	N	O	P	0	0
			33	19	8	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	N	O	P	0	0
			33	19	8	5	1		

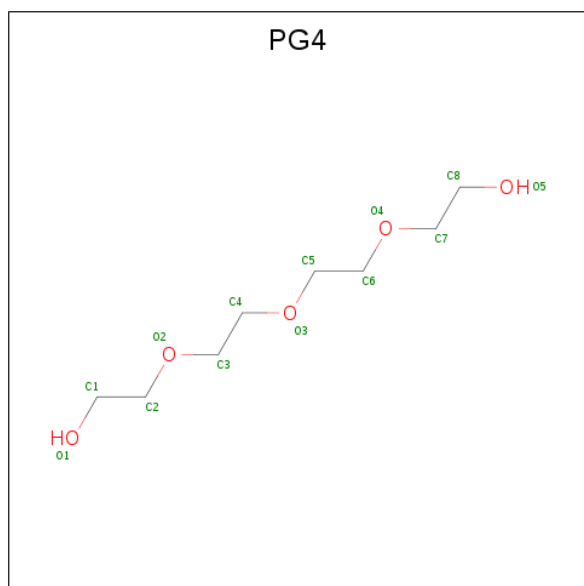
- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Zn	0	0
			1	1		
9	A	1	Total	Zn	0	0
			1	1		

- Molecule 10 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	1	Total	Cl	0	0
			1	1		
10	A	1	Total	Cl	0	0
			1	1		

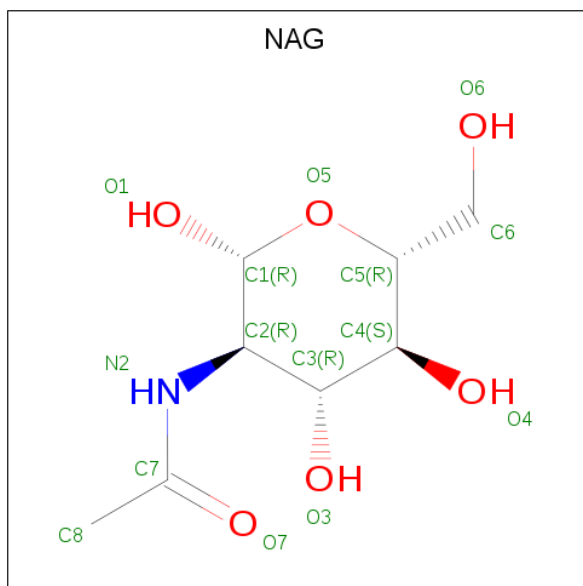
- Molecule 11 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG)

(formula: C₈H₁₅NO₆).



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

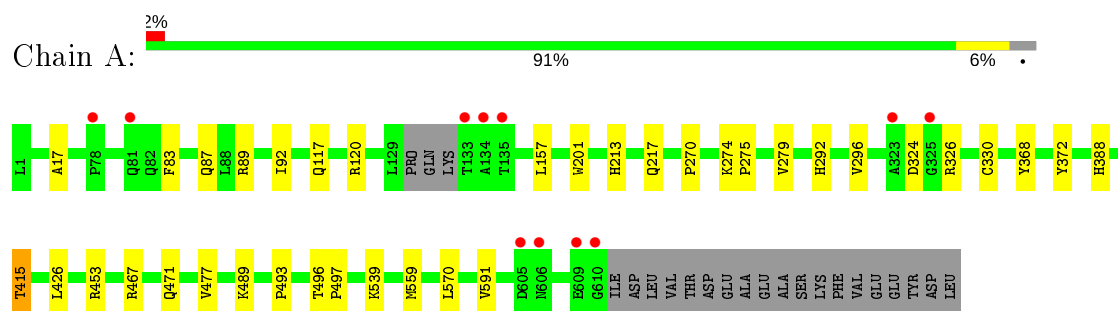
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	243	Total	O	0	0
			243	243		
13	B	166	Total	O	0	0
			166	166		

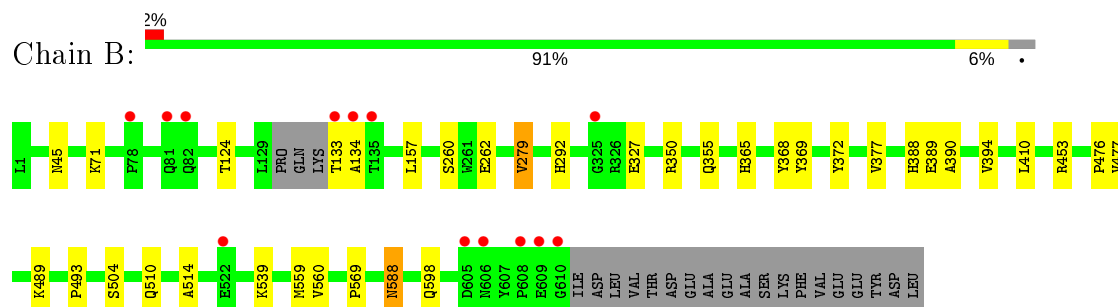
3 Residue-property plots

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.

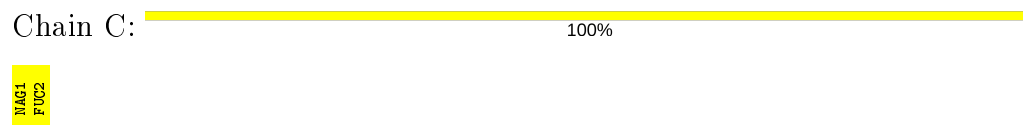
- Molecule 1: ANGIOTENSIN-CONVERTING ENZYME



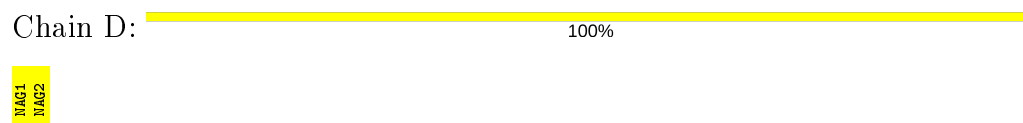
- Molecule 1: ANGIOTENSIN-CONVERTING ENZYME



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



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose




- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  50% 50%



- Molecule 4: 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:  75% 25%



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  33% 67%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.14Å 77.25Å 82.87Å 88.43° 64.28° 75.29°	Depositor
Resolution (Å)	29.69 – 2.20 29.67 – 2.20	Depositor EDS
% Data completeness (in resolution range)	91.4 (29.69-2.20) 91.4 (29.67-2.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.187 , 0.220 0.193 , 0.226	Depositor DCC
R_{free} test set	3660 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	27.0	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.6	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	0.95	EDS
Total number of atoms	10657	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.58% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, BMA, NAG, CL, PG4, FUC, P6G, 1IU, PEG

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	0.40	0/5127	0.56	0/6985
1	B	0.39	0/5116	0.55	0/6971
All	All	0.39	0/10243	0.56	0/13956

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	4965	0	4726	25	0
1	B	4954	0	4718	19	0
2	C	24	0	22	0	0
3	D	28	0	25	0	0
3	F	28	0	25	0	0
4	E	49	0	43	0	0
5	G	39	0	34	0	0
6	A	21	0	30	0	0
6	B	14	0	20	0	0
7	A	13	0	17	0	0
7	B	19	0	26	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	33	0	28	0	0
8	B	33	0	28	2	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
11	B	10	0	13	1	0
12	B	14	0	12	0	0
13	A	243	0	0	7	0
13	B	166	0	0	1	0
All	All	10657	0	9767	44	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 2.

The worst 5 of 44 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)
1:B:260:SER:OG	1:B:262:GLU:OE1	1.86	0.93
1:B:350:ARG:H	1:B:355:GLN:HE21	1.36	0.73
1:A:17:ALA:HB1	1:A:92:ILE:CD1	2.26	0.66
1:A:87[B]:GLN:NE2	13:A:2008:HOH:O	2.32	0.63
1:B:157:LEU:HD11	1:B:477:VAL:HG13	1.81	0.62

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	606/629 (96%)	592 (98%)	14 (2%)	0	100	100
1	B	605/629 (96%)	591 (98%)	11 (2%)	3 (0%)	29	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1211/1258 (96%)	1183 (98%)	25 (2%)	3 (0%)	47 55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	45	ASN
1	B	134	ALA
1	B	377	VAL

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	520/541 (96%)	513 (99%)	7 (1%)	69 81
1	B	519/541 (96%)	512 (99%)	7 (1%)	69 81
All	All	1039/1082 (96%)	1025 (99%)	14 (1%)	67 81

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	591	VAL
1	B	71	LYS
1	B	372	TYR
1	A	453	ARG
1	B	368	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	494	ASN
1	A	600	HIS
1	B	491	HIS
1	A	491	HIS
1	B	371	GLN

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 ⓘ

13 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	1,2	14,14,15	0.61	0	17,19,21	1.12	1 (5%)
2	FUC	C	2	2	10,10,11	0.86	0	14,14,16	2.17	3 (21%)
3	NAG	D	1	1,3	14,14,15	0.55	0	17,19,21	1.10	2 (11%)
3	NAG	D	2	3	14,14,15	0.44	0	17,19,21	1.07	1 (5%)
4	NAG	E	1	1,4	14,14,15	0.55	0	17,19,21	0.95	0
4	NAG	E	2	4	14,14,15	0.55	0	17,19,21	0.89	0
4	BMA	E	3	4	11,11,12	0.45	0	15,15,17	1.17	1 (6%)
4	FUC	E	4	4	10,10,11	0.68	0	14,14,16	0.59	0
3	NAG	F	1	1,3	14,14,15	0.62	0	17,19,21	1.10	2 (11%)
3	NAG	F	2	3	14,14,15	0.53	0	17,19,21	0.88	0
5	NAG	G	1	1,5	14,14,15	0.49	0	17,19,21	1.09	1 (5%)
5	NAG	G	2	5	14,14,15	0.52	0	17,19,21	0.81	0
5	BMA	G	3	5	11,11,12	0.44	0	15,15,17	1.92	3 (20%)

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	1,2	-	2/6/23/26	0/1/1/1
2	FUC	C	2	2	-	-	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
4	NAG	E	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	BMA	E	3	4	-	2/2/19/22	0/1/1/1
4	FUC	E	4	4	-	-	0/1/1/1
3	NAG	F	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
5	NAG	G	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	FUC	C1-C2-C3	6.12	117.19	109.67
5	G	3	BMA	C1-O5-C5	4.50	118.30	112.19
5	G	3	BMA	C1-C2-C3	4.49	115.18	109.67
2	C	2	FUC	C2-C3-C4	3.53	117.00	110.89
2	C	2	FUC	C3-C4-C5	3.17	114.71	109.77

There are no chirality outliers.

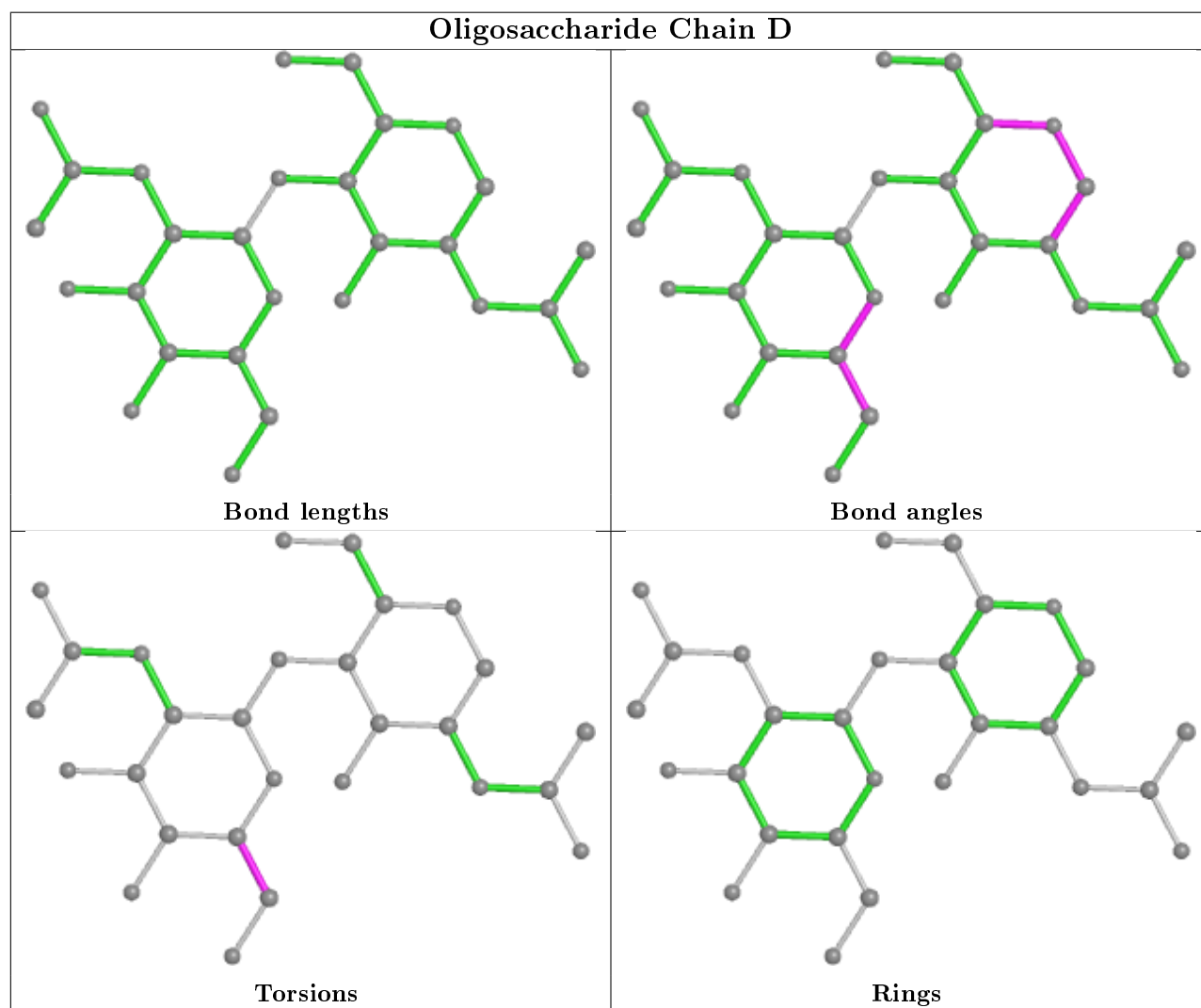
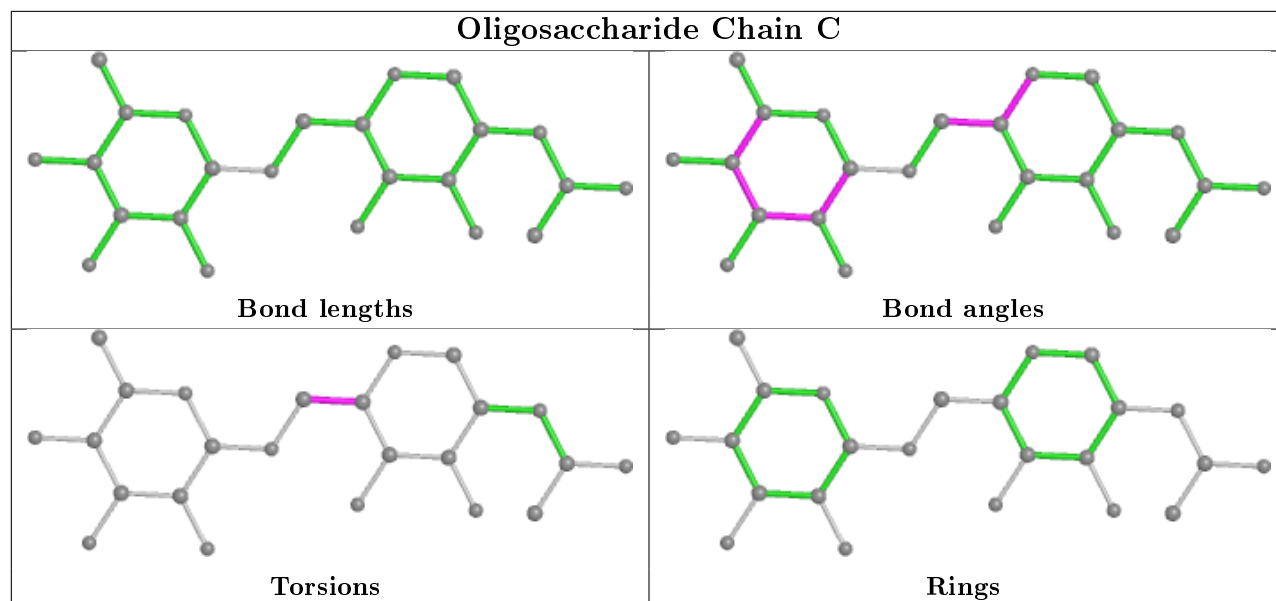
5 of 10 torsion outliers are listed below:

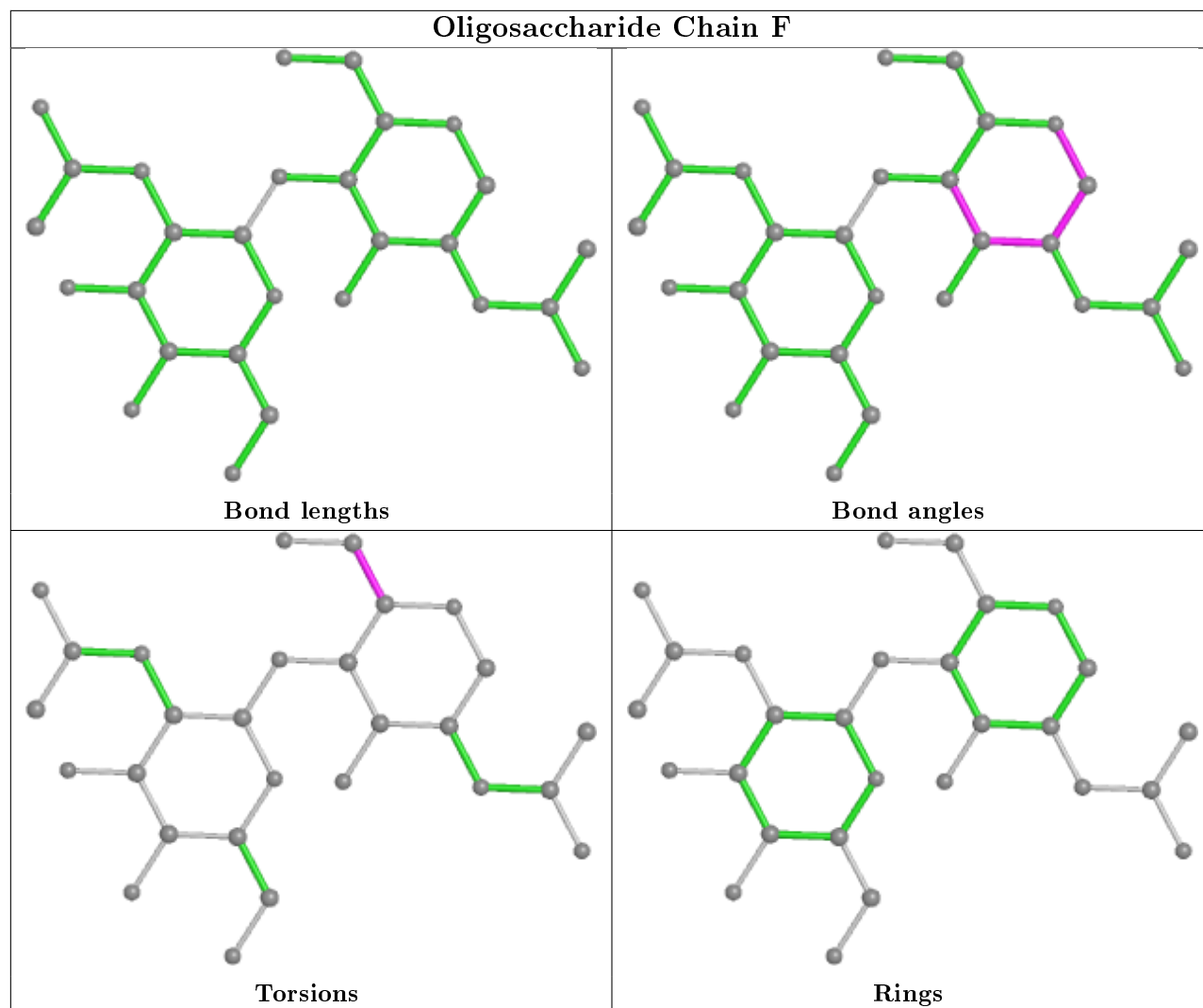
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6

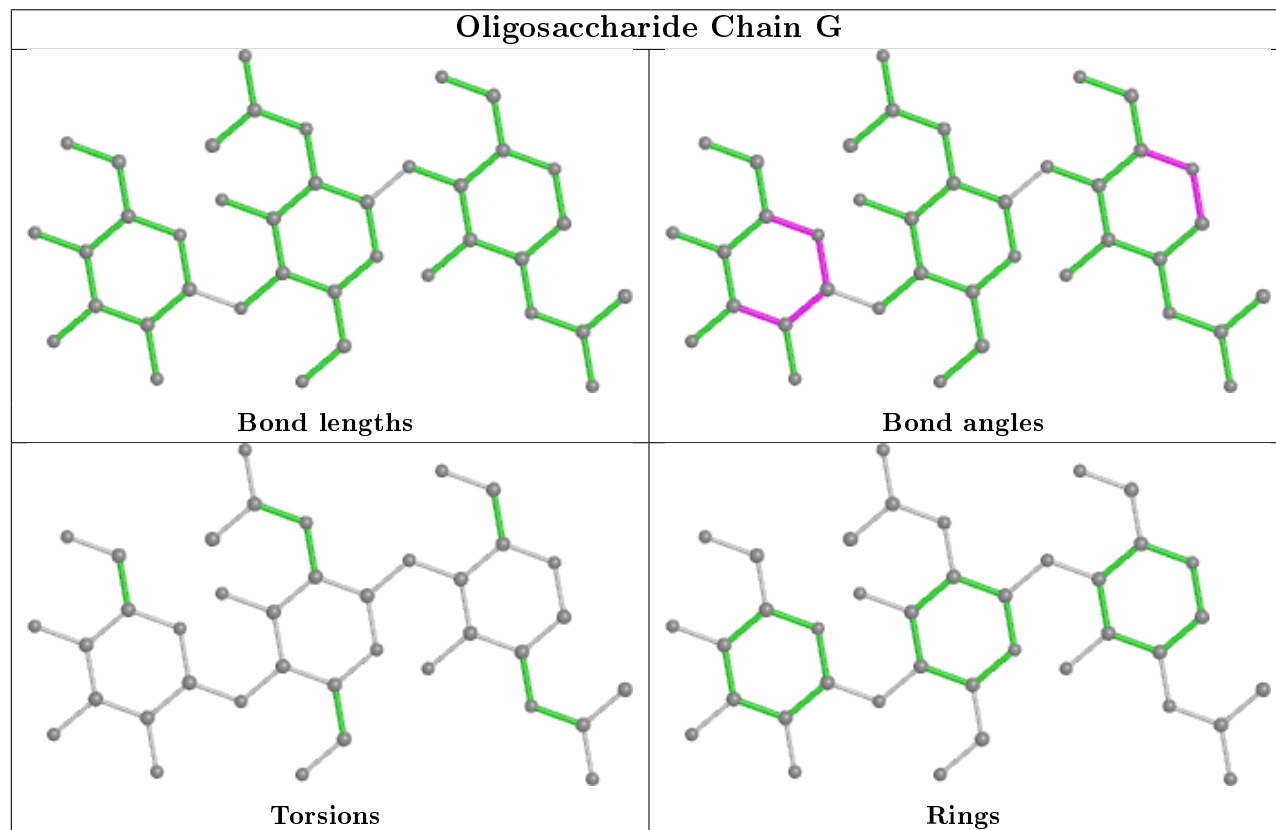
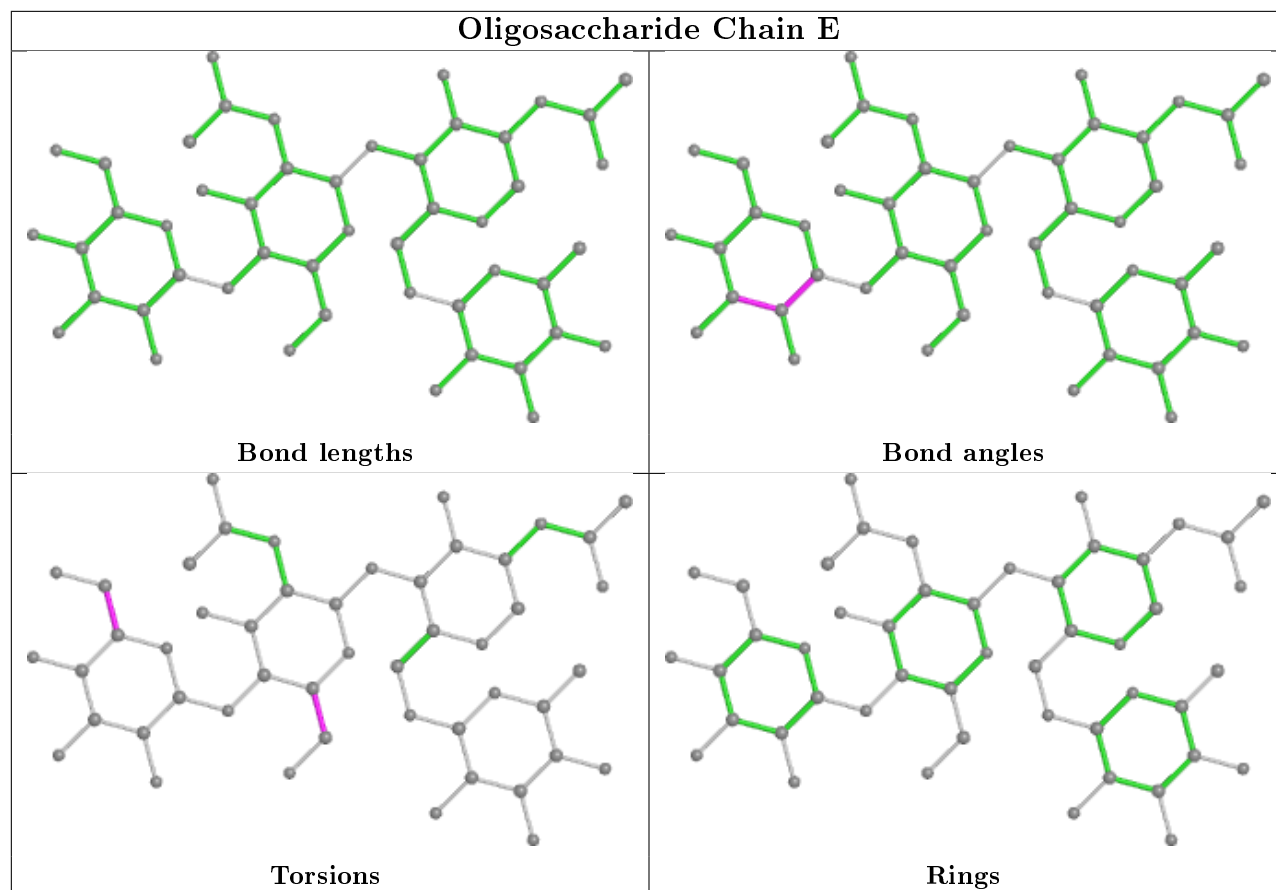
There are no ring outliers.

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

Of 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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
8	1IU	A	1001	9	30,34,34	2.53	5 (16%)	34,47,47	1.35	6 (17%)
6	PEG	A	703	-	6,6,6	0.39	0	5,5,5	0.36	0
7	P6G	A	704	-	12,12,18	0.50	0	11,11,17	0.34	0
7	P6G	B	709	-	18,18,18	0.62	0	17,17,17	0.60	0
6	PEG	A	701	-	6,6,6	0.51	0	5,5,5	0.39	0
11	PG4	B	704	-	9,9,12	0.41	0	8,8,11	0.29	0
6	PEG	A	702	-	6,6,6	0.50	0	5,5,5	0.25	0
6	PEG	B	711	-	6,6,6	0.40	0	5,5,5	0.31	0
8	1IU	B	1001	9	30,34,34	1.71	4 (13%)	34,47,47	1.08	3 (8%)
12	NAG	B	1612	1	14,14,15	0.69	0	17,19,21	1.78	2 (11%)
6	PEG	B	701	-	6,6,6	0.50	0	5,5,5	0.31	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
8	1IU	A	1001	9	-	7/32/39/39	0/2/2/2
6	PEG	A	703	-	-	1/4/4/4	-
7	P6G	A	704	-	-	4/10/10/16	-
7	P6G	B	709	-	-	10/16/16/16	-
6	PEG	A	701	-	-	3/4/4/4	-
11	PG4	B	704	-	-	4/7/7/10	-
6	PEG	A	702	-	-	3/4/4/4	-
6	PEG	B	711	-	-	2/4/4/4	-
8	1IU	B	1001	9	-	8/32/39/39	0/2/2/2
12	NAG	B	1612	1	-	3/6/23/26	0/1/1/1
6	PEG	B	701	-	-	1/4/4/4	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1001	1IU	NAT-NAW	-8.44	1.22	1.34
8	A	1001	1IU	NAS-NAR	-7.94	1.23	1.34
8	B	1001	1IU	NAT-NAW	-5.48	1.26	1.34
8	A	1001	1IU	PBG-OAI	4.42	1.58	1.49
8	B	1001	1IU	NAS-NAR	-3.87	1.29	1.34

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	1612	NAG	C4-C3-C2	5.48	119.05	111.02
8	A	1001	1IU	CBE-CAZ-NAV	3.49	121.00	116.15
8	A	1001	1IU	CBC-CAY-N	-3.22	112.97	116.42
12	B	1612	NAG	O5-C5-C6	3.15	112.14	107.20
8	B	1001	1IU	OAH-PBG-CBF	2.94	113.46	106.87

There are no chirality outliers.

5 of 46 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	1001	1IU	OAG-CAZ-CBE-CAP
8	A	1001	1IU	NAV-CAZ-CBE-CAP
8	A	1001	1IU	CBC-CAQ-PBG-OAI
8	A	1001	1IU	CBC-CAQ-PBG-OAH
8	B	1001	1IU	OAG-CAZ-CBE-CAP

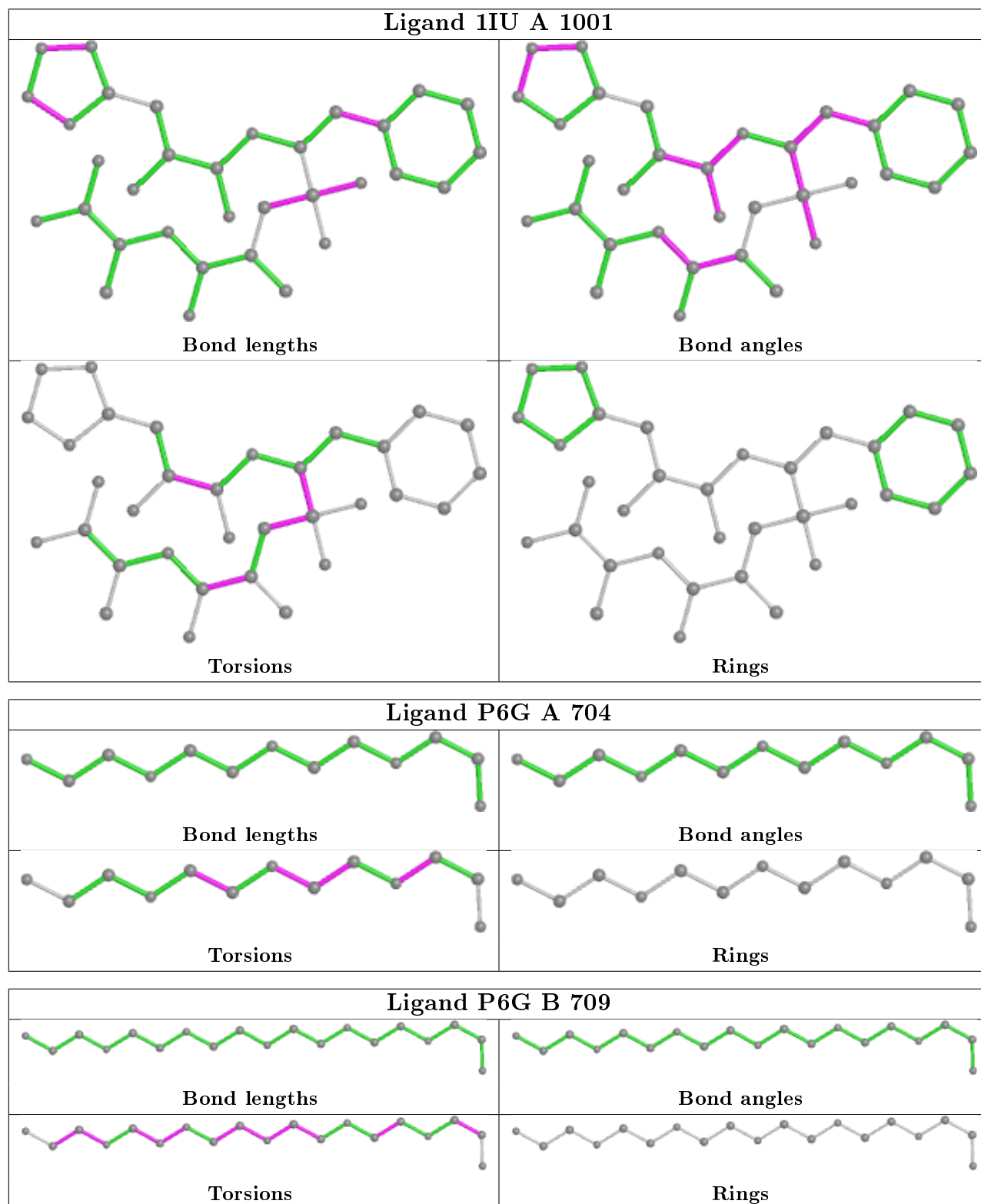
There are no ring outliers.

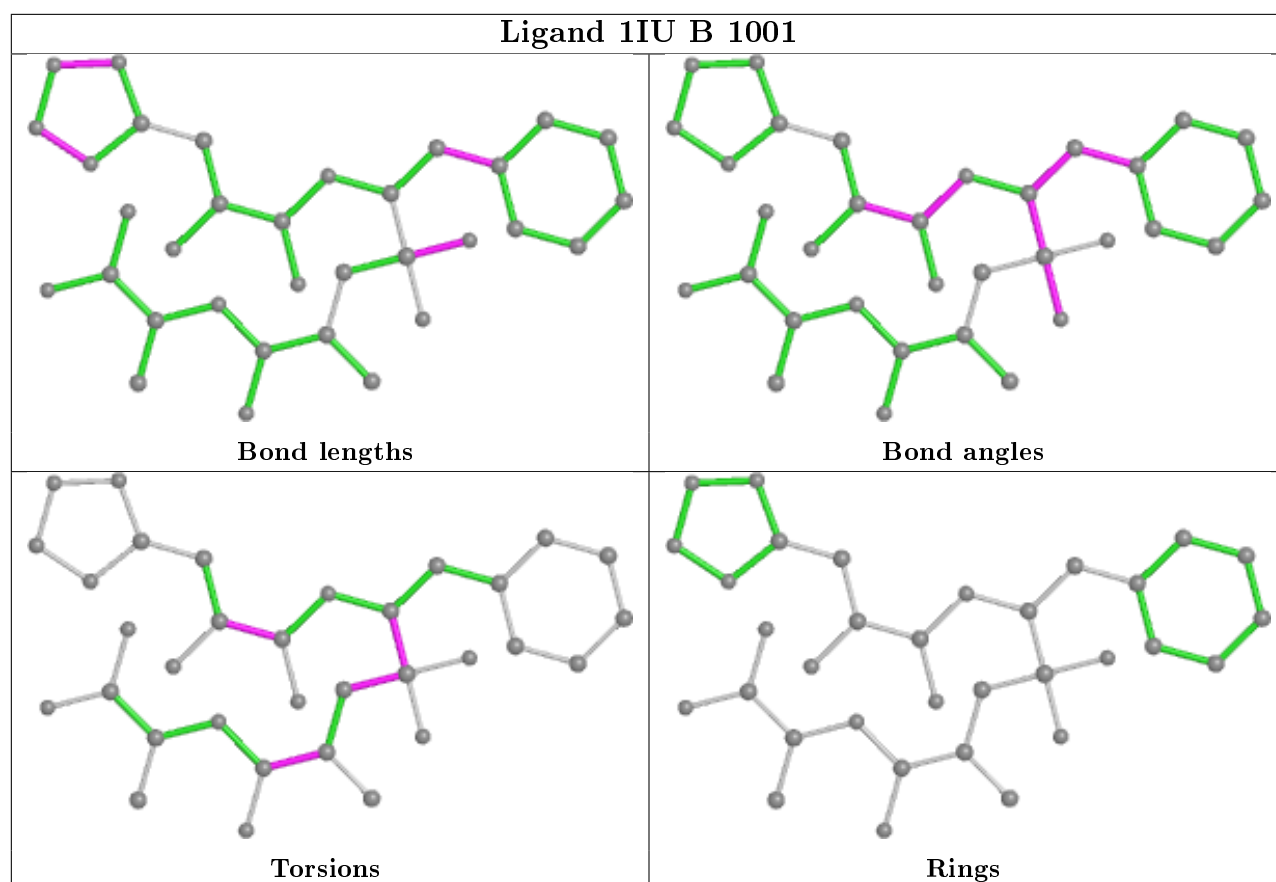
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	709	P6G	2	0
11	B	704	PG4	1	0
8	B	1001	1IU	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	607/629 (96%)	-0.40	11 (1%) 68 66	13, 24, 44, 79	0
1	B	607/629 (96%)	-0.30	13 (2%) 63 61	13, 28, 50, 70	0
All	All	1214/1258 (96%)	-0.35	24 (1%) 65 63	13, 26, 49, 79	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	325	GLY	5.9
1	B	135	THR	4.1
1	B	133	THR	4.0
1	A	78	PRO	3.8
1	B	134	ALA	3.7

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

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

6.3 Carbohydrates [i](#)

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

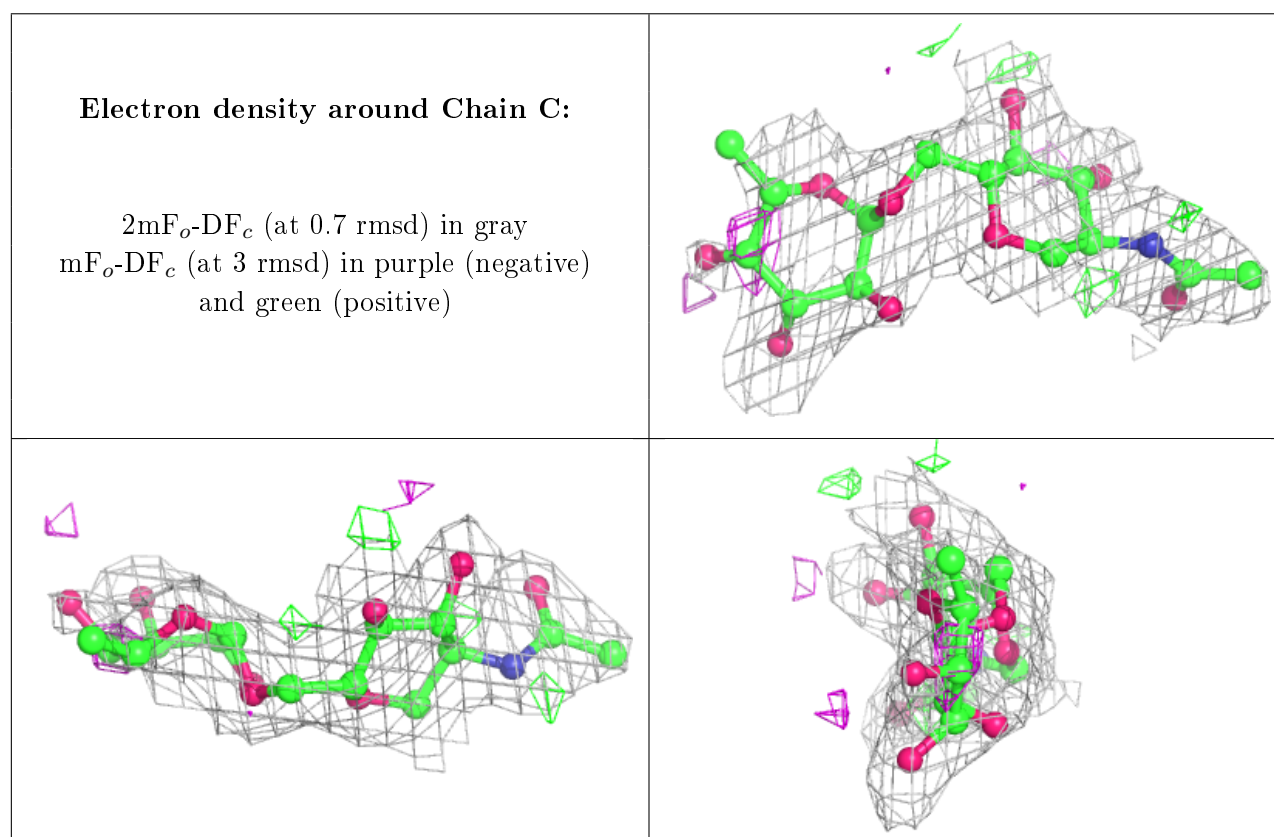
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FUC	C	2	10/11	0.77	0.34	53,56,58,59	0
3	NAG	D	2	14/15	0.79	0.34	47,53,56,57	0
4	BMA	E	3	11/12	0.80	0.24	55,59,60,60	0
5	BMA	G	3	11/12	0.81	0.36	76,78,79,82	0
4	FUC	E	4	10/11	0.83	0.22	42,43,45,45	0

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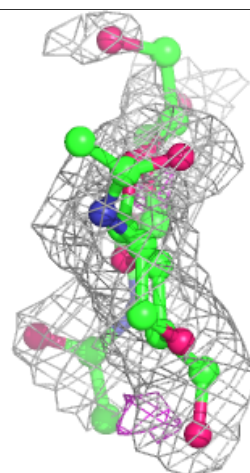
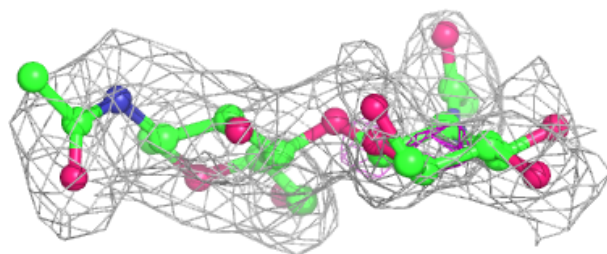
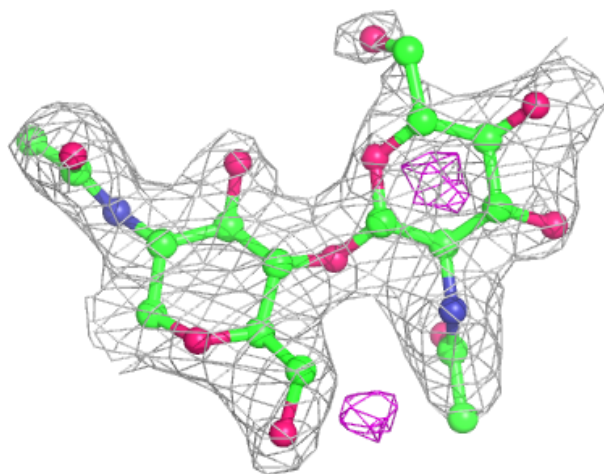
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	F	2	14/15	0.85	0.42	61,64,65,66	0
3	NAG	D	1	14/15	0.86	0.22	42,45,47,49	0
4	NAG	E	2	14/15	0.90	0.19	44,48,52,53	0
3	NAG	F	1	14/15	0.90	0.27	45,47,51,57	0
5	NAG	G	1	14/15	0.90	0.20	53,55,57,61	0
5	NAG	G	2	14/15	0.90	0.40	66,70,71,74	0
2	NAG	C	1	14/15	0.92	0.16	32,36,41,47	0
4	NAG	E	1	14/15	0.95	0.13	37,39,42,42	0

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



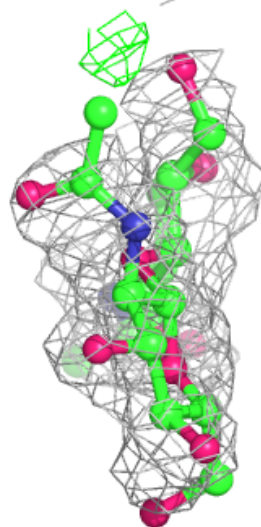
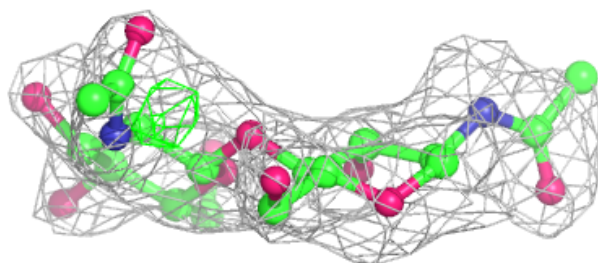
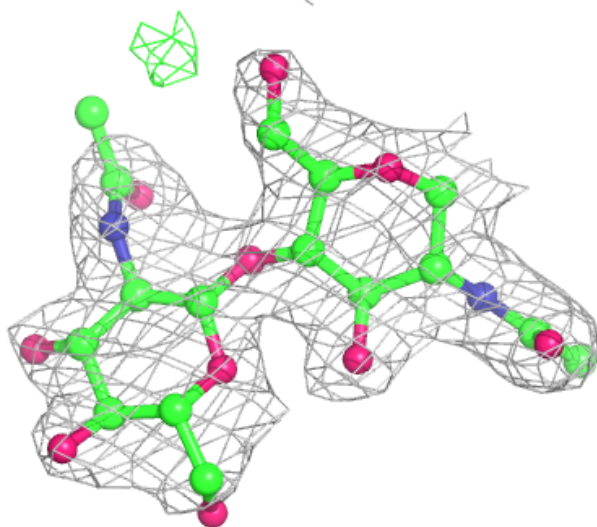
Electron density around Chain D:

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



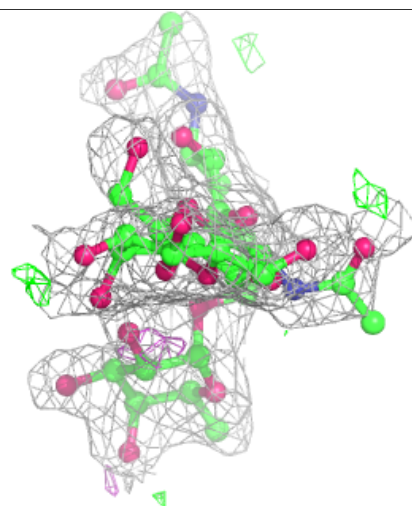
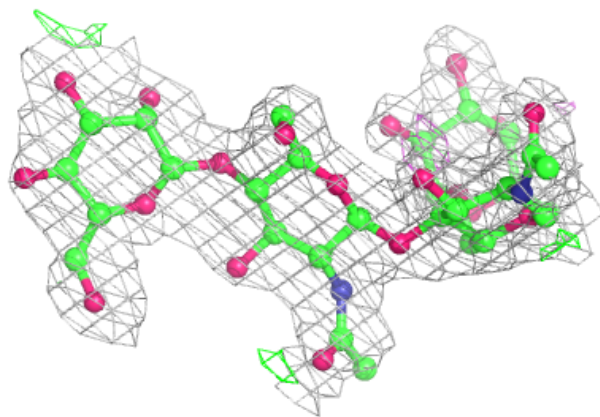
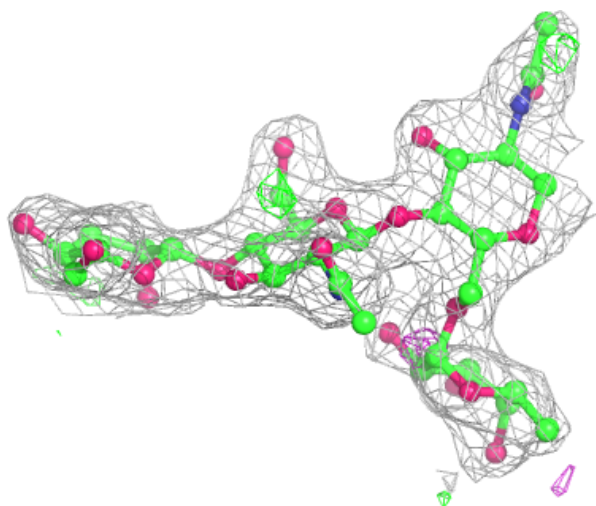
Electron density around Chain F:

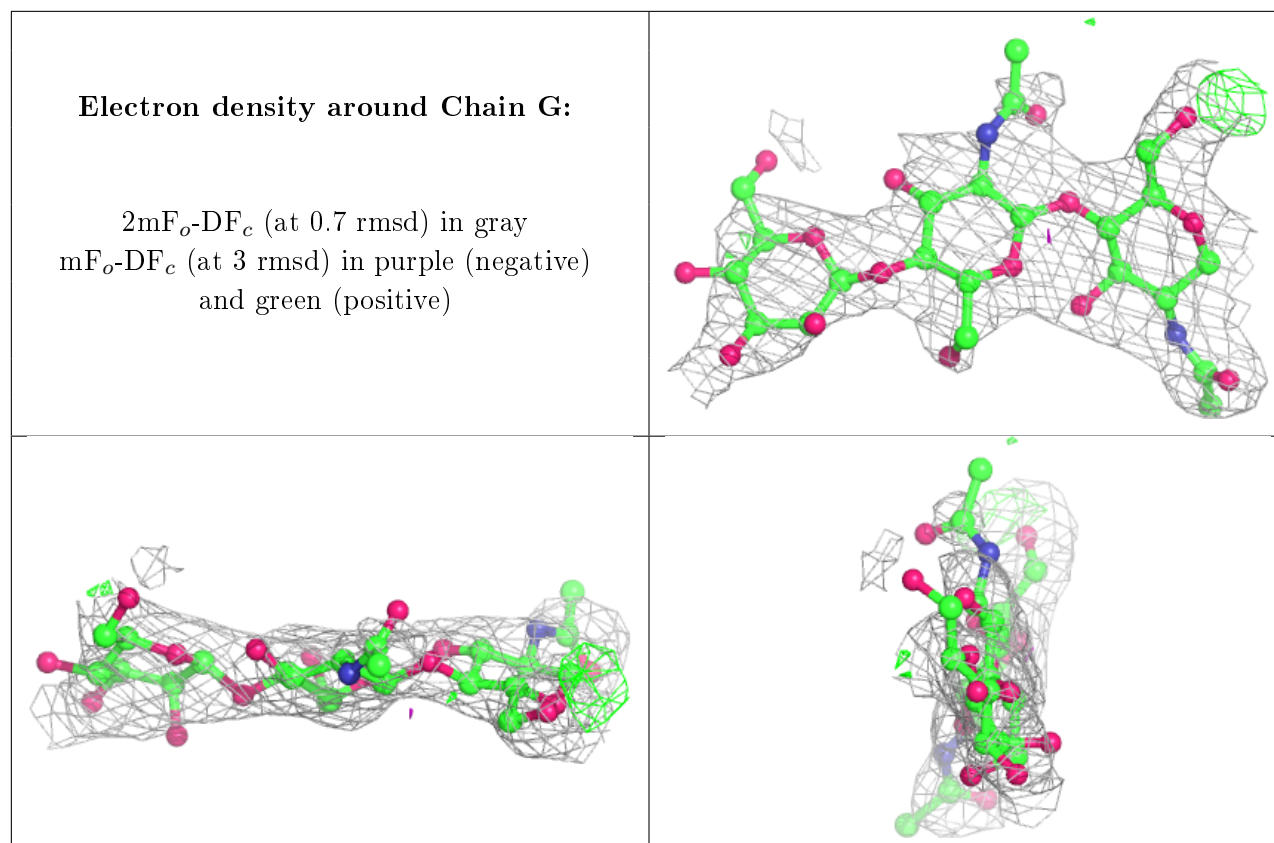
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain E:

$2mF_o-DF_c$ (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(\AA^2)	Q<0.9
7	P6G	B	709	19/19	0.76	0.15	33,39,42,42	0
6	PEG	A	702	7/7	0.77	0.21	56,58,59,59	0
6	PEG	A	701	7/7	0.80	0.23	47,48,49,49	0
6	PEG	B	701	7/7	0.80	0.23	42,46,46,48	0
7	P6G	A	704	13/19	0.83	0.17	42,43,48,48	0
12	NAG	B	1612	14/15	0.85	0.14	37,40,43,43	0
6	PEG	B	711	7/7	0.86	0.15	34,35,42,43	0
6	PEG	A	703	7/7	0.91	0.16	42,44,44,44	0
11	PG4	B	704	10/13	0.93	0.13	37,37,39,39	0
8	1IU	A	1001	33/33	0.96	0.11	18,20,26,26	0
8	1IU	B	1001	33/33	0.97	0.11	14,17,23,23	0
10	CL	A	1621	1/1	0.99	0.07	17,17,17,17	0
9	ZN	B	1619	1/1	1.00	0.09	14,14,14,14	0
10	CL	B	1620	1/1	1.00	0.07	22,22,22,22	0

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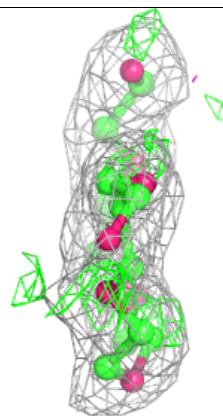
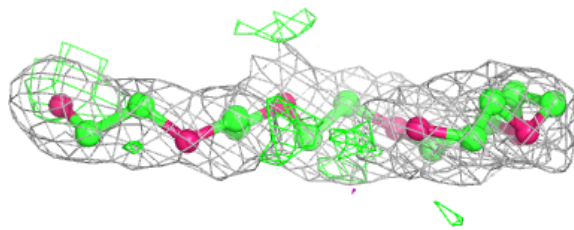
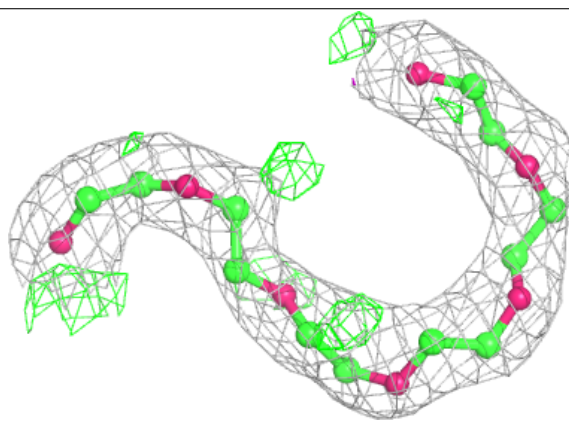
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
9	ZN	A	1620	1/1	1.00	0.09	17,17,17,17	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

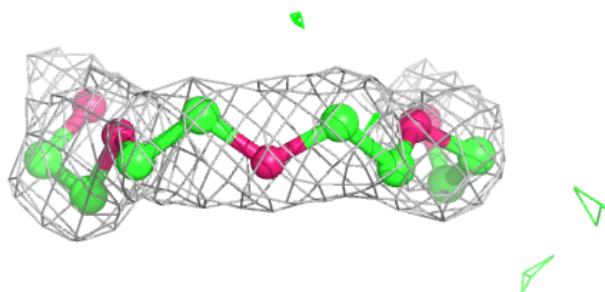
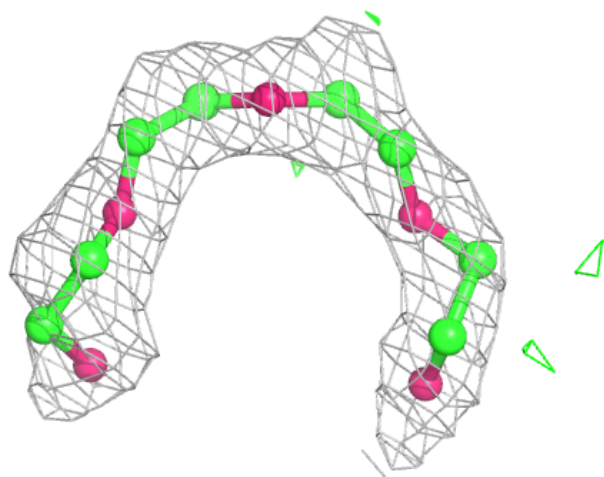
Electron density around P6G B 709:

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



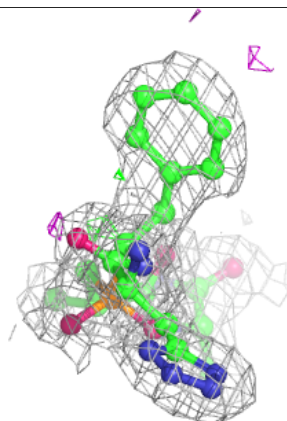
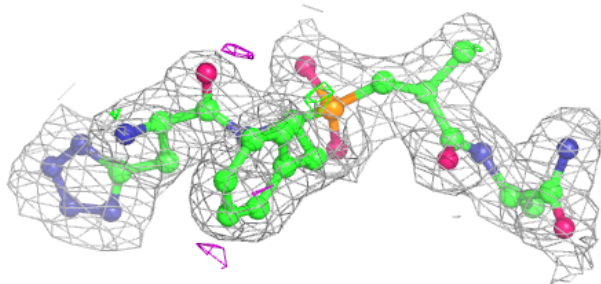
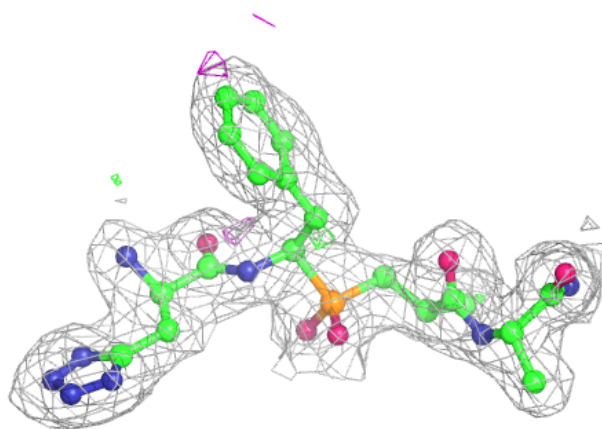
Electron density around P6G A 704:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

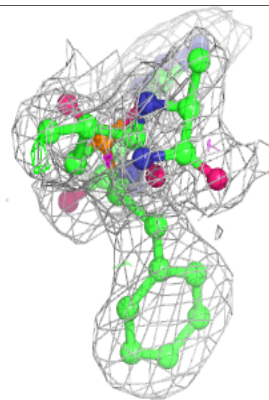
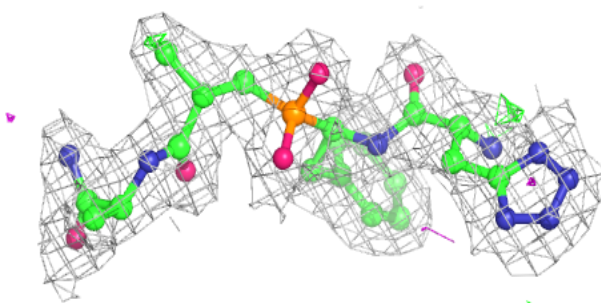
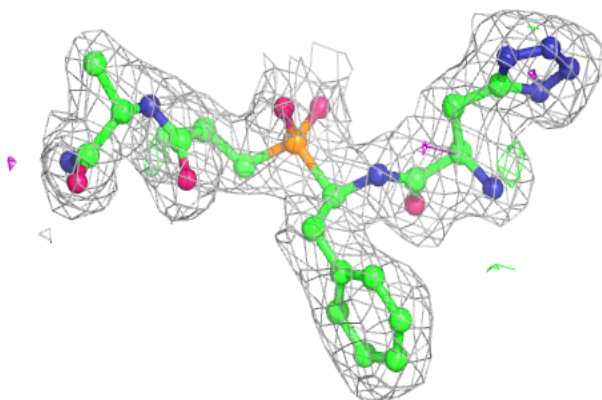


Electron density around 1IU A 1001:

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

**Electron density around 1IU B 1001:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.