



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 04:34 PM UTC

PDB ID : 6TT4 / pdb_00006tt4
Title : Crystal structure of 'Res_S2 mutant human Angiotensin-1 converting enzyme
N-domain in complex with omapatrilat.
Authors : Cozier, G.E.; Acharya, K.R.
Deposited on : 2019-12-23
Resolution : 1.80 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

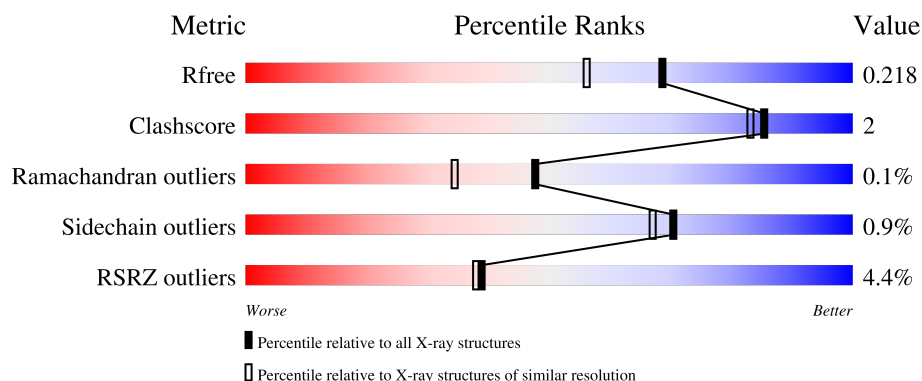
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	629	6% 91% 5%
1	B	629	3% 92% 5%
2	C	3	33% 33% 33%
3	D	3	67% 33%
4	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
5	F	5	 60%40%
6	G	2	 50%50%

2 Entry composition

There are 17 unique types of molecules in this entry. The entry contains 21503 atoms, of which 10031 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	604	Total	C	H	N	O	S	0	8	0
			9781	3208	4788	861	905	19			
1	B	611	Total	C	H	N	O	S	0	15	0
			9975	3269	4880	875	930	21			

There are 34 discrepancies between the modelled and reference sequences:

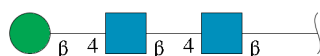
Chain	Residue	Modelled	Actual	Comment	Reference
A	9	GLN	ASN	conflict	UNP P12821
A	25	GLN	ASN	conflict	UNP P12821
A	82	GLN	ASN	conflict	UNP P12821
A	117	GLN	ASN	conflict	UNP P12821
A	131	GLN	ASN	conflict	UNP P12821
A	260	THR	SER	conflict	UNP P12821
A	262	SER	GLU	conflict	UNP P12821
A	289	GLN	ASN	conflict	UNP P12821
A	354	GLU	ASP	conflict	UNP P12821
A	357	VAL	SER	conflict	UNP P12821
A	358	VAL	THR	conflict	UNP P12821
A	369	PHE	TYR	conflict	UNP P12821
A	381	GLU	ARG	conflict	UNP P12821
A	431	ASP	GLU	conflict	UNP P12821
A	545	ARG	GLN	conflict	UNP P12821
A	576	LEU	PRO	conflict	UNP P12821
A	629	LEU	-	expression tag	UNP P12821
B	9	GLN	ASN	conflict	UNP P12821
B	25	GLN	ASN	conflict	UNP P12821
B	82	GLN	ASN	conflict	UNP P12821
B	117	GLN	ASN	conflict	UNP P12821
B	131	GLN	ASN	conflict	UNP P12821
B	260	THR	SER	conflict	UNP P12821
B	262	SER	GLU	conflict	UNP P12821
B	289	GLN	ASN	conflict	UNP P12821

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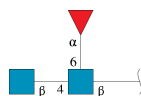
Chain	Residue	Modelled	Actual	Comment	Reference
B	354	GLU	ASP	conflict	UNP P12821
B	357	VAL	SER	conflict	UNP P12821
B	358	VAL	THR	conflict	UNP P12821
B	369	PHE	TYR	conflict	UNP P12821
B	381	GLU	ARG	conflict	UNP P12821
B	431	ASP	GLU	conflict	UNP P12821
B	545	ARG	GLN	conflict	UNP P12821
B	576	LEU	PRO	conflict	UNP P12821
B	629	LEU	-	expression tag	UNP P12821

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	3	Total	C	H	N	O	0	0	0
			76	22	37	2	15			

- Molecule 3 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.



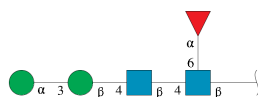
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	3	Total	C	H	N	O	0	0	0
			73	22	35	2	14			

- 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	E	2	Total	C	H	N	O	0	0	0
			55	16	27	2	10			

- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	5	Total	C	H	N	O	0	0	0
			116	34	56	2	24			

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



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	2	Total	C	H	N	O	0	0	0
			46	14	22	1	9			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).

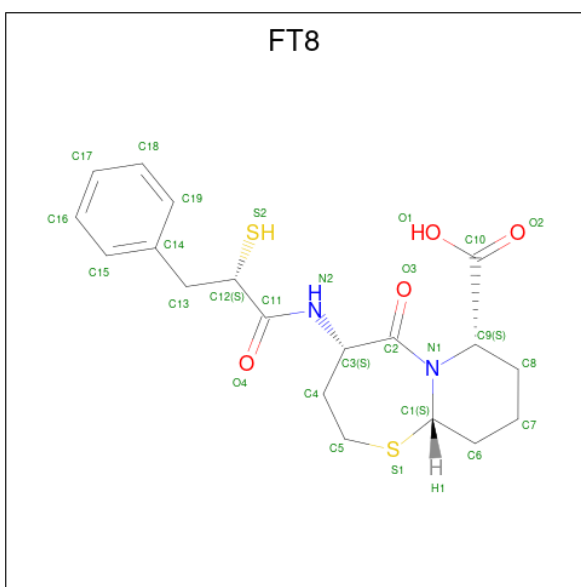


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 9 is Omapatrilat (CCD ID: FT8) (formula: C₁₉H₂₄N₂O₄S₂) (labeled as "Ligand of Interest" by depositor).

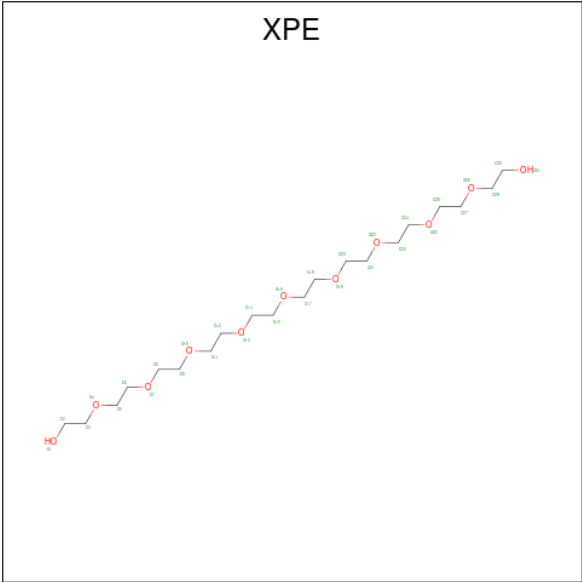


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	N	O	S	0	0
			27	19	2	4	2		
9	B	1	Total	C	N	O	S	0	0
			27	19	2	4	2		

- Molecule 10 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

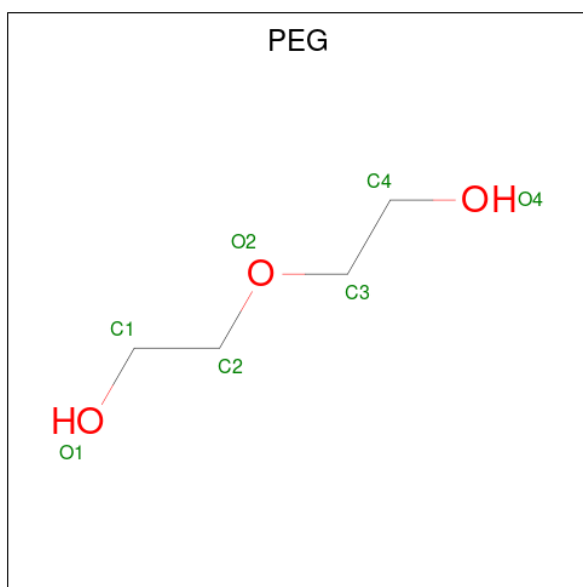
- Molecule 11 is 3,6,9,12,15,18,21,24,27-NONAOXANONACOSANE-1,29-DIOL (CCD ID: XPE) (formula: C₂₀H₄₂O₁₁).





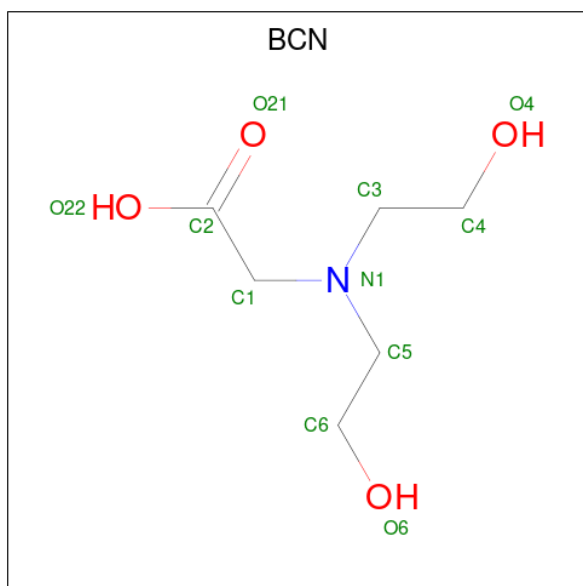
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	A	1	Total	C	H	O	0	0
			10	2	6	2		
13	A	1	Total	C	H	O	0	0
			10	2	6	2		
13	B	1	Total	C	H	O	0	0
			10	2	6	2		
13	B	1	Total	C	H	O	0	1
			20	4	12	4		
13	B	1	Total	C	H	O	0	0
			10	2	6	2		
13	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 14 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



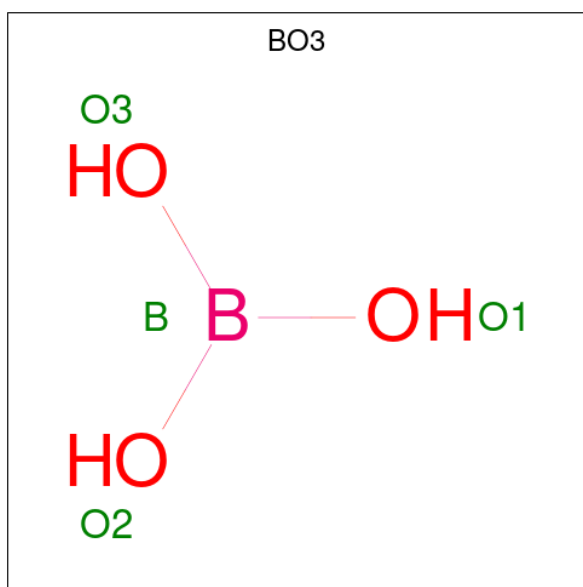
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
14	A	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 15 is BICINE (CCD ID: BCN) (formula: $C_6H_{13}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
15	A	1	Total	C	H	N	O	0	0
			23	6	12	1	4		
15	B	1	Total	C	H	N	O	0	0
			23	6	12	1	4		

- Molecule 16 is BORIC ACID (CCD ID: BO3) (formula: BH_3O_3).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
16	A	1	Total	B	H	O	0	0
			7	1	3	3		
16	A	1	Total	B	H	O	0	0
			7	1	3	3		
16	B	1	Total	B	H	O	0	0
			7	1	3	3		
16	B	1	Total	B	H	O	0	0
			7	1	3	3		

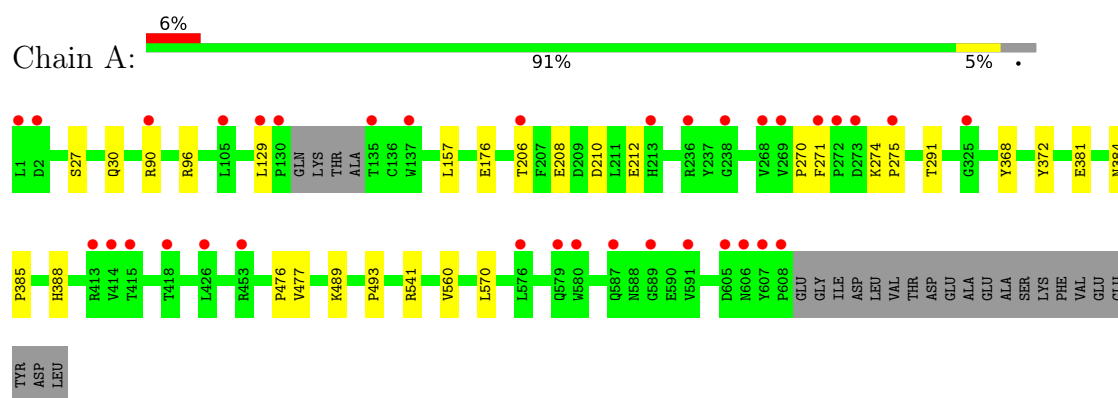
- Molecule 17 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
17	A	456	Total	O	0	4
			458	458		
17	B	527	Total	O	0	4
			531	531		

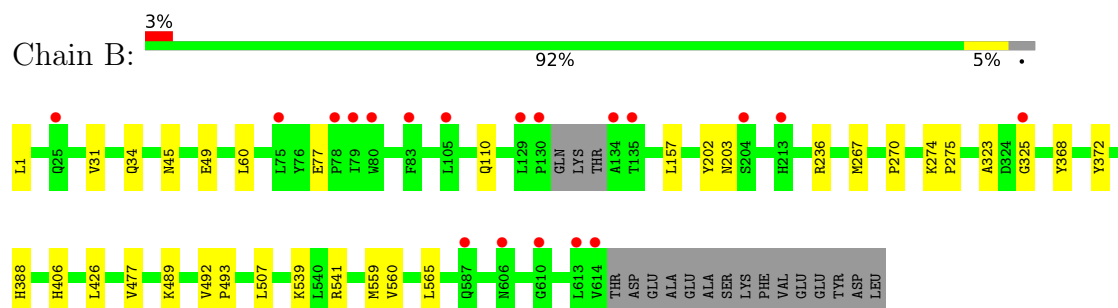
3 Residue-property plots [i](#)

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.

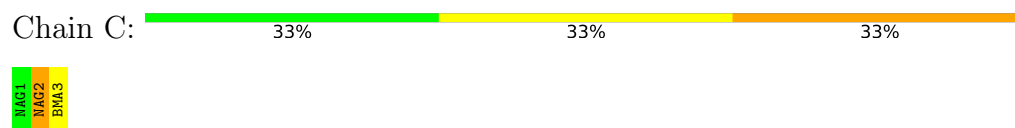
- Molecule 1: Angiotensin-converting enzyme



- Molecule 1: Angiotensin-converting enzyme



- Molecule 2: beta-D-mannopyranose-(1-4)-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)-[alpha-L-fucopyranose-(1-6)]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:  50% 50%



- Molecule 5: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  60% 40%



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

Chain G:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	74.37Å 78.83Å 89.69Å 92.43° 105.97° 114.60°	Depositor
Resolution (Å)	64.01 – 1.80 64.01 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.2 (64.01-1.80) 97.2 (64.01-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.13_2998, PHENIX 1.13_2998	Depositor
R, R_{free}	0.182 , 0.222 0.179 , 0.218	Depositor DCC
R_{free} test set	1396 reflections (0.60%)	wwPDB-VP
Wilson B-factor (Å ²)	27.1	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	21503	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% 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: XPE, ZN, EDO, BO3, BMA, FT8, PEG, NAG, BCN, FUC, CL, MAN, PGE

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	0.43	0/5166	0.54	0/7033
1	B	0.47	0/5270	0.56	0/7176
All	All	0.45	0/10436	0.55	0/14209

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	4993	4788	4757	18	0
1	B	5095	4880	4843	21	0
2	C	39	37	34	2	0
3	D	38	35	34	0	0
4	E	28	27	25	2	0
5	F	60	56	52	0	0
6	G	24	22	22	0	0
7	A	14	14	13	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
9	A	27	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	B	27	0	0	0	0
10	A	1	0	0	0	0
10	B	1	0	0	0	0
11	A	31	42	42	1	0
12	A	20	28	28	0	0
12	B	10	14	14	0	0
13	A	8	12	12	0	0
13	B	20	30	30	0	0
14	A	7	10	10	0	0
15	A	11	12	12	0	0
15	B	11	12	12	1	0
16	A	8	6	6	0	0
16	B	8	6	6	0	0
17	A	458	0	0	8	0
17	B	531	0	0	6	0
All	All	11472	10031	9952	45	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 45 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:A:176:GLU:OE1	17:A:801:HOH:O	2.01	0.79
4:E:2:NAG:H83	4:E:2:NAG:H3	1.67	0.74
1:A:90[A]:ARG:NH1	17:A:803:HOH:O	2.21	0.74
1:A:541[B]:ARG:NH1	17:A:806:HOH:O	2.26	0.67
1:A:541[A]:ARG:NH2	17:A:809:HOH:O	2.33	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	608/629 (97%)	595 (98%)	13 (2%)	0	100	100
1	B	622/629 (99%)	613 (99%)	8 (1%)	1 (0%)	43	31
All	All	1230/1258 (98%)	1208 (98%)	21 (2%)	1 (0%)	48	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	45	ASN

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	528/541 (98%)	523 (99%)	5 (1%)	70	67
1	B	540/541 (100%)	536 (99%)	4 (1%)	76	73
All	All	1068/1082 (99%)	1059 (99%)	9 (1%)	70	70

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	388	HIS
1	B	560	VAL
1	A	388	HIS
1	A	560	VAL
1	B	368	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	371	GLN
1	B	582	GLN
1	B	585	ASN
1	B	224	ASN
1	A	188	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 ⓘ

15 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	0.32	0	17,19,21	0.58	0
2	NAG	C	2	2	14,14,15	0.37	0	17,19,21	1.11	1 (5%)
2	BMA	C	3	2	11,11,12	0.95	0	15,15,17	1.16	1 (6%)
3	NAG	D	1	1,3	14,14,15	0.32	0	17,19,21	0.49	0
3	NAG	D	2	3	14,14,15	0.37	0	17,19,21	0.48	0
3	FUC	D	3	3	10,10,11	1.45	2 (20%)	14,14,16	0.97	0
4	NAG	E	1	1,4	14,14,15	0.36	0	17,19,21	0.54	0
4	NAG	E	2	4	14,14,15	0.32	0	17,19,21	1.14	1 (5%)
5	NAG	F	1	1,5	14,14,15	0.59	0	17,19,21	0.60	0
5	NAG	F	2	5	14,14,15	0.34	0	17,19,21	0.43	0
5	BMA	F	3	5	11,11,12	1.25	1 (9%)	15,15,17	1.16	1 (6%)
5	MAN	F	4	5	11,11,12	1.46	2 (18%)	15,15,17	1.16	1 (6%)
5	FUC	F	5	5	10,10,11	0.62	0	14,14,16	0.91	0
6	NAG	G	1	1,6	14,14,15	0.54	0	17,19,21	0.68	0
6	FUC	G	2	6	10,10,11	1.52	2 (20%)	14,14,16	1.11	1 (7%)

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

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	4	MAN	C1-C2	3.26	1.60	1.52
5	F	4	MAN	C2-C3	2.71	1.56	1.52
5	F	3	BMA	C1-C2	2.60	1.58	1.52
6	G	2	FUC	O5-C1	-2.54	1.39	1.43
6	G	2	FUC	C4-C3	2.44	1.58	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	2	NAG	C2-N2-C7	3.74	127.92	122.90
2	C	2	NAG	C2-N2-C7	3.60	127.72	122.90
5	F	4	MAN	C1-O5-C5	2.80	115.94	112.19
2	C	3	BMA	C1-O5-C5	2.78	115.91	112.19
5	F	3	BMA	C1-C2-C3	2.48	113.26	109.64

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	C1-C2-N2-C7
4	E	2	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6

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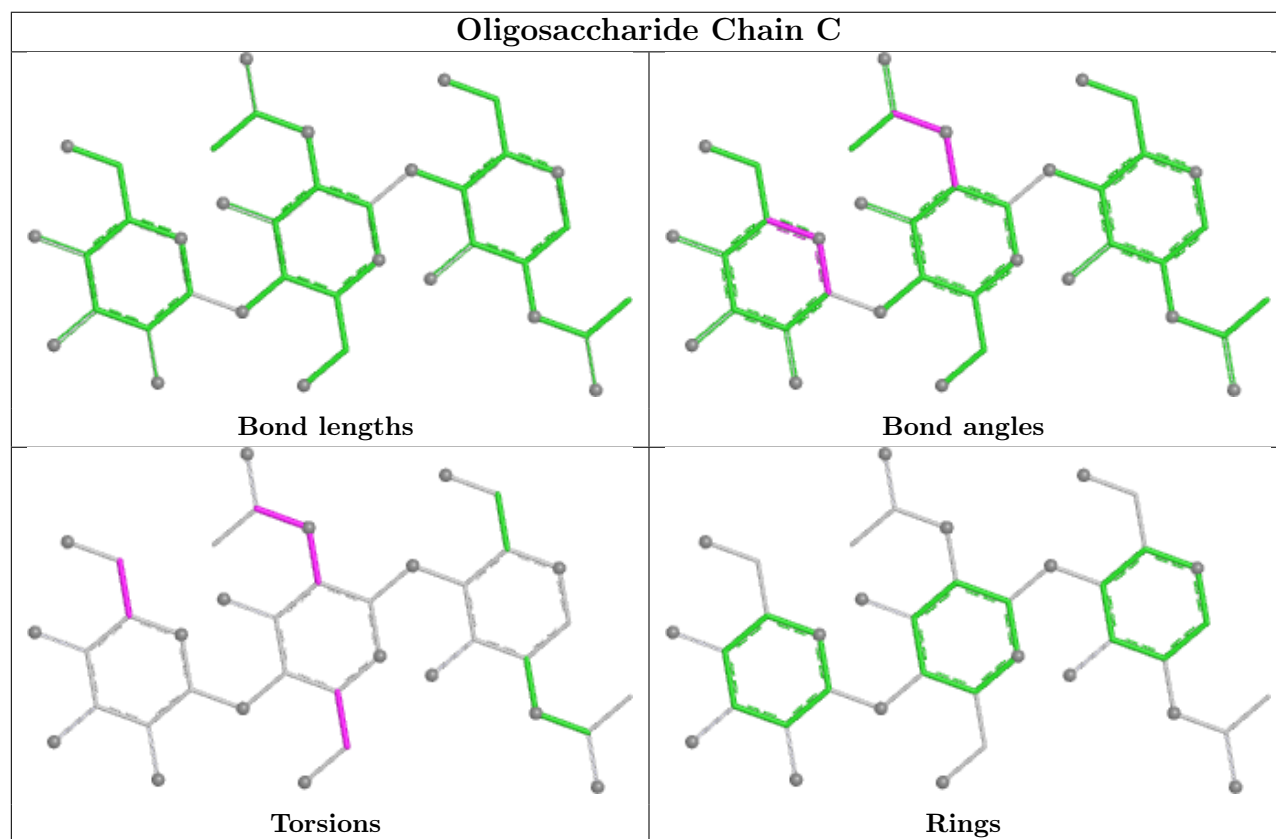
Mol	Chain	Res	Type	Atoms
4	E	2	NAG	C4-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6

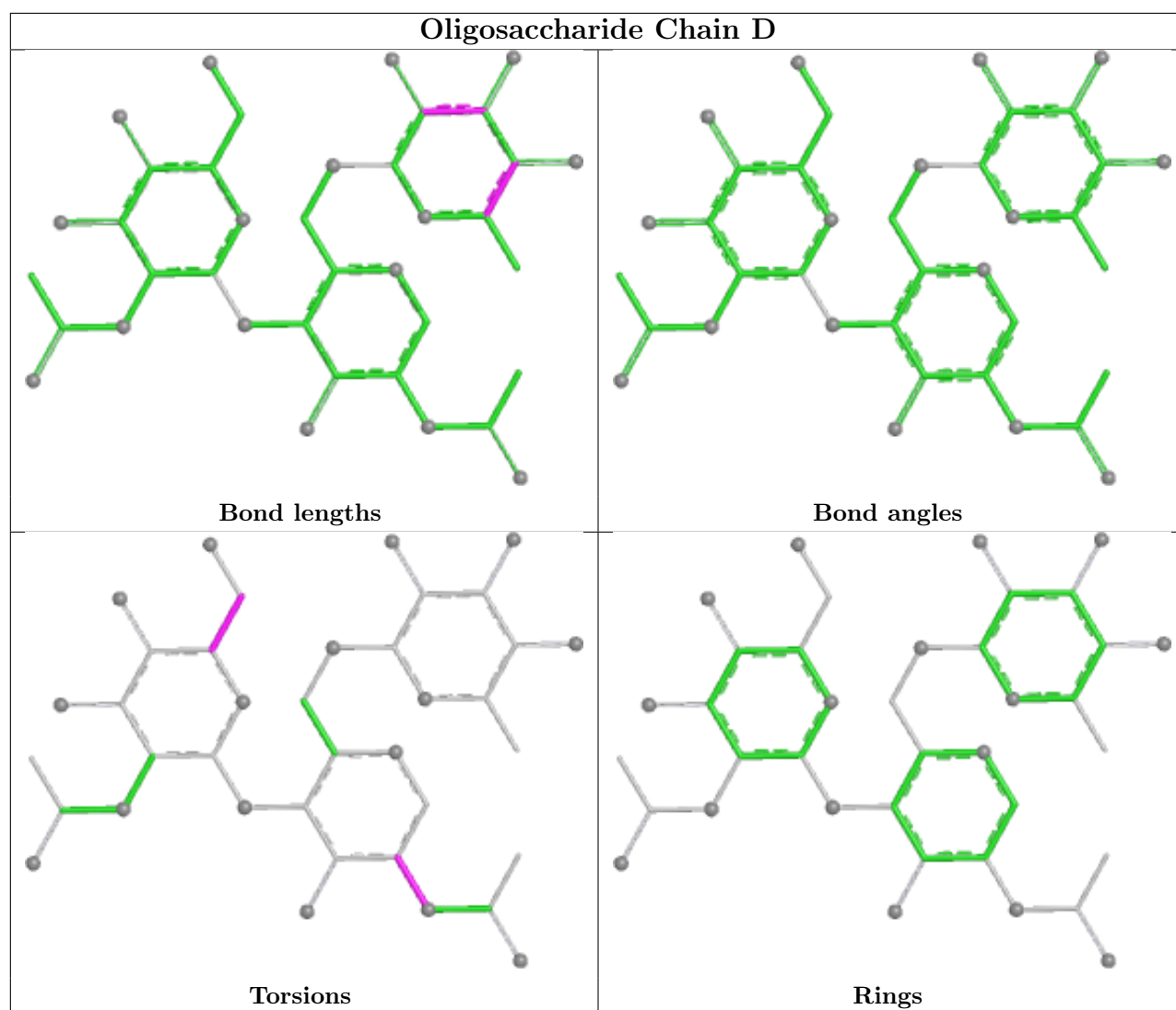
There are no ring outliers.

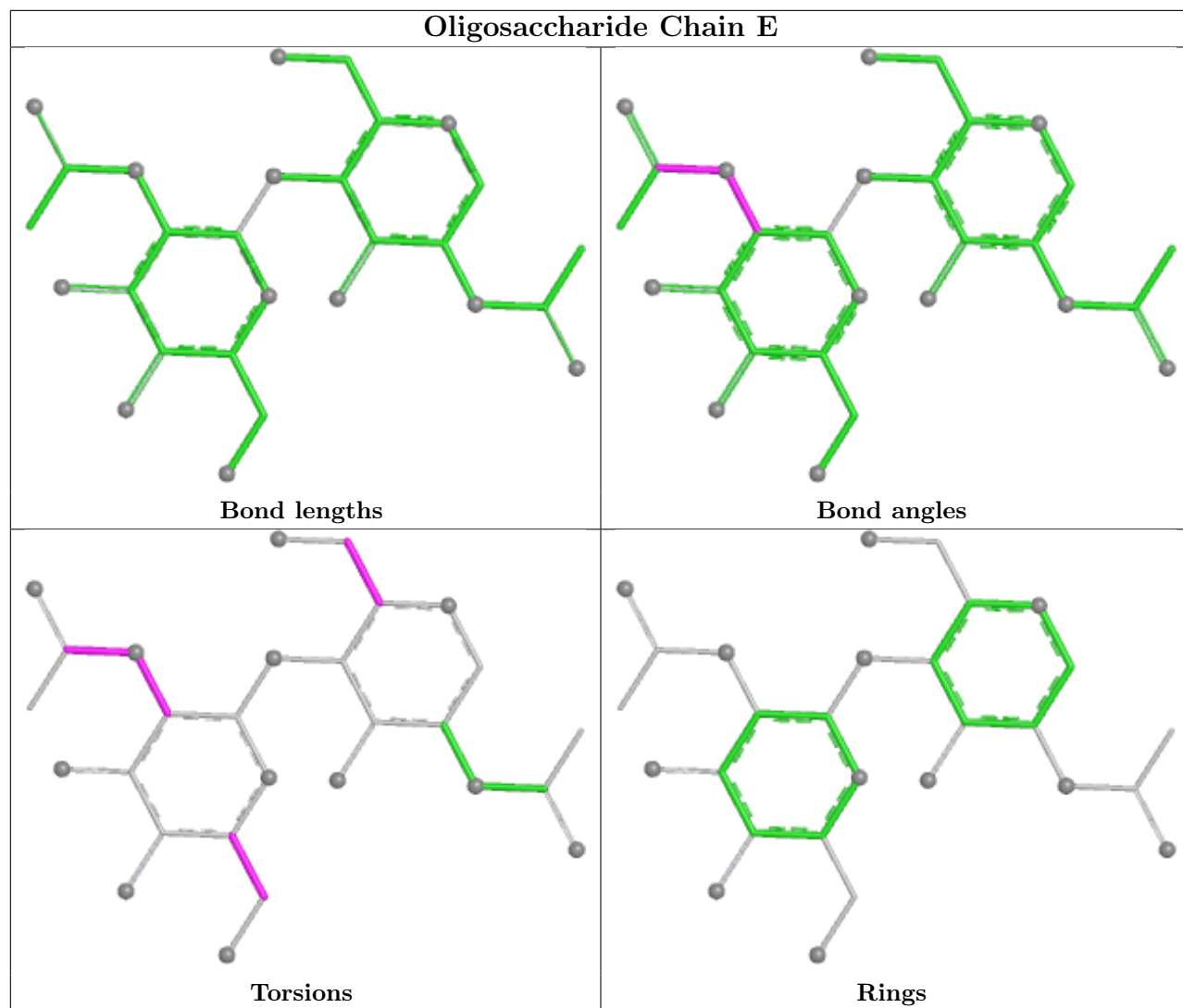
2 monomers are involved in 4 short contacts:

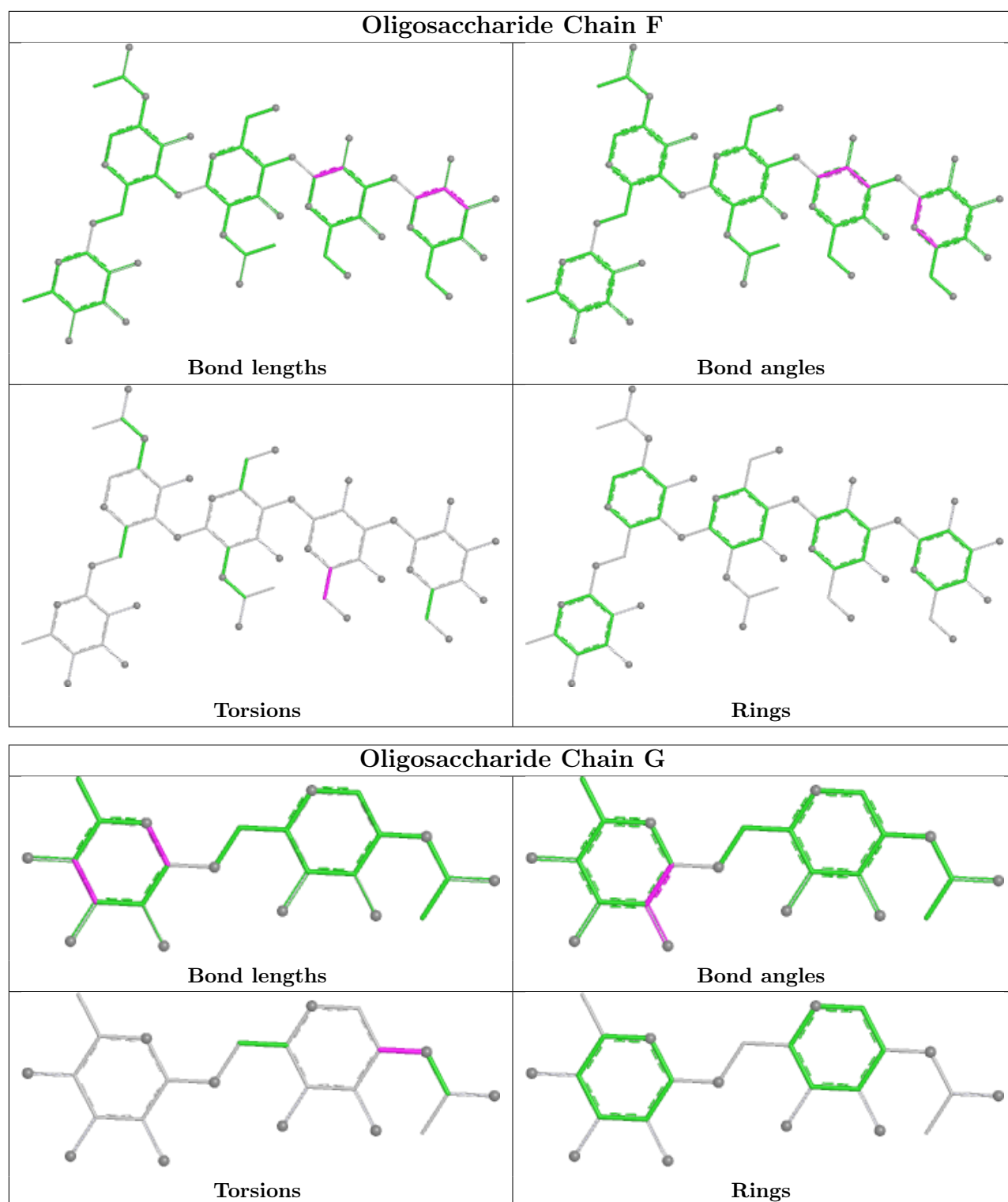
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	2	0
4	E	2	NAG	2	0

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









5.6 Ligand geometry [i](#)

Of 25 ligands modelled in this entry, 4 are monoatomic - leaving 21 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
16	BO3	B	719	-	3,3,3	0.20	0	3,3,3	0.19	0
13	EDO	B	717	-	3,3,3	0.55	0	2,2,2	0.03	0
14	PEG	A	715	-	6,6,6	0.52	0	5,5,5	0.47	0
16	BO3	B	720	-	3,3,3	0.24	0	3,3,3	0.12	0
13	EDO	B	714	-	3,3,3	0.45	0	2,2,2	0.36	0
13	EDO	A	713	-	3,3,3	0.61	0	2,2,2	0.39	0
9	FT8	B	711	8	25,29,29	2.24	5 (20%)	26,40,40	1.41	5 (19%)
16	BO3	A	717	-	3,3,3	0.20	0	3,3,3	0.32	0
12	PGE	A	712[B]	-	9,9,9	0.32	0	8,8,8	0.43	0
11	XPE	A	711	-	30,30,30	0.55	0	29,29,29	0.41	0
13	EDO	B	716	-	3,3,3	0.51	0	2,2,2	0.25	0
12	PGE	A	712[A]	-	9,9,9	0.36	0	8,8,8	0.40	0
16	BO3	A	718	-	3,3,3	0.38	0	3,3,3	0.22	0
12	PGE	B	713	-	9,9,9	0.37	0	8,8,8	0.35	0
7	NAG	A	701	1	14,14,15	0.54	0	17,19,21	0.57	0
13	EDO	A	714	-	3,3,3	0.55	0	2,2,2	0.24	0
9	FT8	A	709	8	25,29,29	2.37	3 (12%)	26,40,40	1.32	4 (15%)
13	EDO	B	715[B]	-	3,3,3	0.55	0	2,2,2	0.17	0
15	BCN	A	716	-	10,10,10	0.95	0	11,11,11	1.16	1 (9%)
13	EDO	B	715[A]	-	3,3,3	0.44	0	2,2,2	0.34	0
15	BCN	B	718	-	10,10,10	0.78	0	11,11,11	1.50	1 (9%)

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
7	NAG	A	701	1	-	1/6/23/26	0/1/1/1
13	EDO	A	714	-	-	1/1/1/1	-
9	FT8	A	709	8	-	0/14/44/44	0/2/3/3
12	PGE	A	712[A]	-	-	3/7/7/7	-
13	EDO	B	715[B]	-	-	0/1/1/1	-
12	PGE	B	713	-	-	3/7/7/7	-
15	BCN	B	718	-	-	2/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	BCN	A	716	-	-	2/10/10/10	-
13	EDO	B	716	-	-	0/1/1/1	-
12	PGE	A	712[B]	-	-	3/7/7/7	-
13	EDO	B	717	-	-	1/1/1/1	-
14	PEG	A	715	-	-	3/4/4/4	-
13	EDO	B	714	-	-	0/1/1/1	-
11	XPE	A	711	-	-	14/28/28/28	-
13	EDO	A	713	-	-	1/1/1/1	-
13	EDO	B	715[A]	-	-	1/1/1/1	-
9	FT8	B	711	8	-	1/14/44/44	0/2/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	709	FT8	C2-N1	9.39	1.45	1.35
9	B	711	FT8	C2-N1	8.04	1.44	1.35
9	B	711	FT8	C11-N2	4.92	1.44	1.34
9	A	709	FT8	C11-N2	4.76	1.44	1.34
9	A	709	FT8	C9-N1	3.66	1.53	1.47

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	709	FT8	C8-C9-N1	4.33	116.80	110.26
9	B	711	FT8	C8-C9-N1	3.40	115.41	110.26
15	B	718	BCN	C2-C1-N1	-3.40	103.00	113.77
15	A	716	BCN	C2-C1-N1	-3.03	104.15	113.77
9	B	711	FT8	C13-C12-C11	-2.64	106.74	112.46

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

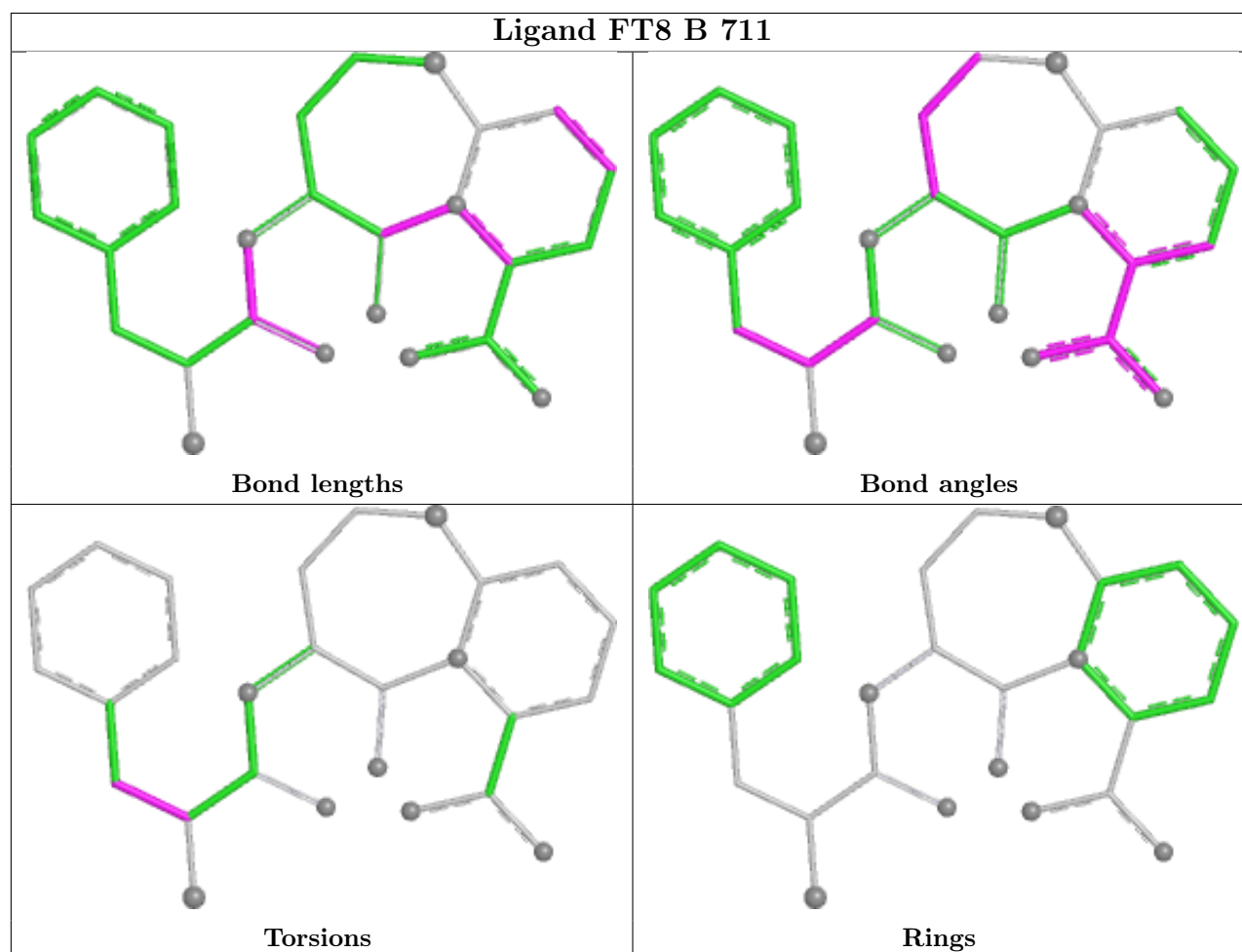
Mol	Chain	Res	Type	Atoms
11	A	711	XPE	C6-C5-O4-C3
15	B	718	BCN	N1-C1-C2-O21
12	A	712[A]	PGE	O2-C3-C4-O3
11	A	711	XPE	O19-C20-C21-O22
15	B	718	BCN	N1-C1-C2-O22

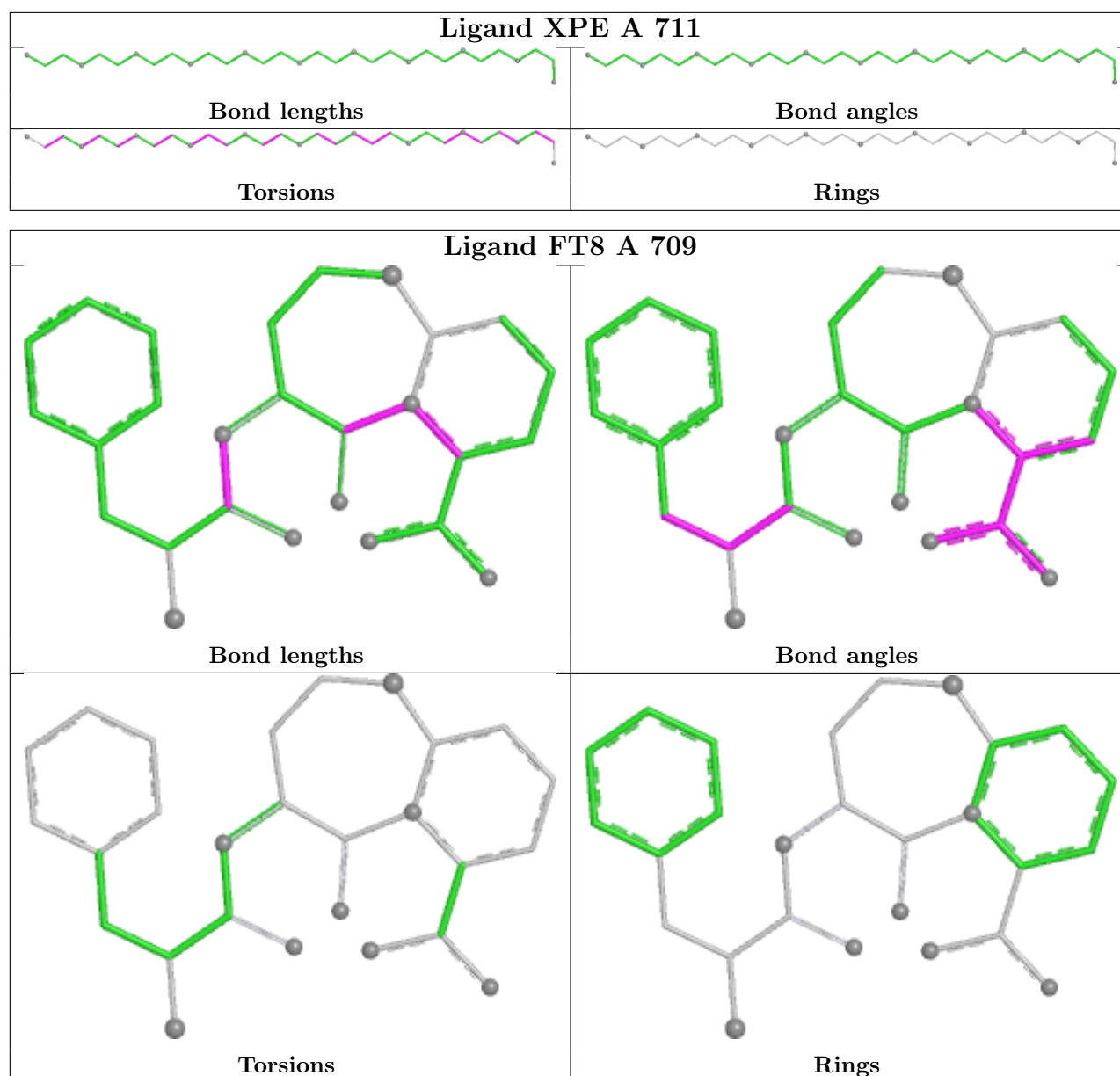
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	711	XPE	1	0
15	B	718	BCN	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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	604/629 (96%)	0.46	35 (5%)	29 27	19, 39, 63, 103	6 (0%)
1	B	611/629 (97%)	0.18	19 (3%)	51 51	13, 34, 58, 92	13 (2%)
All	All	1215/1258 (96%)	0.32	54 (4%)	39 38	13, 37, 62, 103	19 (1%)

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	129	LEU	5.8
1	A	130	PRO	5.5
1	B	130	PRO	5.1
1	B	135	THR	5.1
1	B	325	GLY	4.6

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

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

6.3 Carbohydrates [i](#)

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

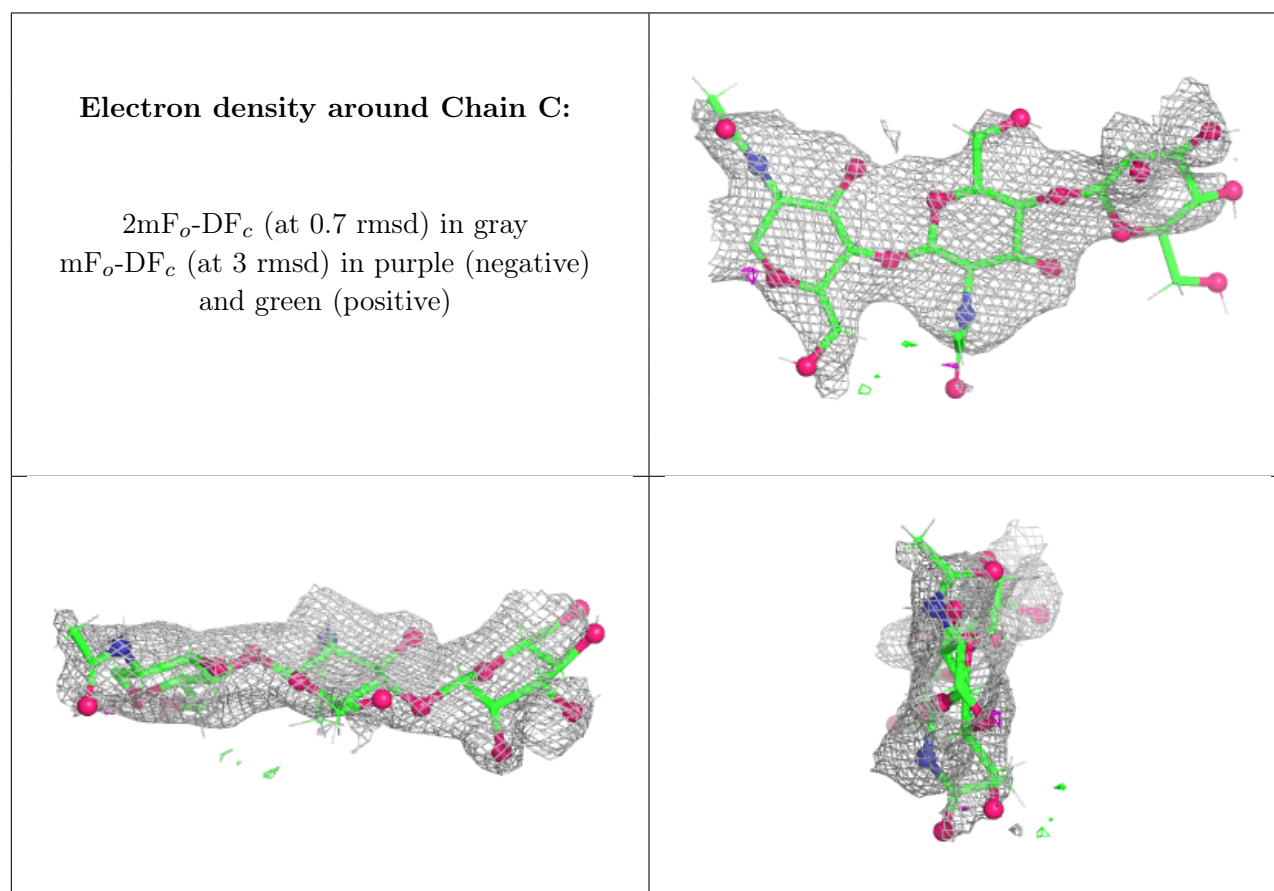
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q < 0.9
5	MAN	F	4	11/12	0.48	0.20	82,92,108,110	0
2	BMA	C	3	11/12	0.57	0.16	84,95,112,113	0
5	BMA	F	3	11/12	0.60	0.17	74,84,97,101	0
4	NAG	E	2	14/15	0.66	0.18	83,102,123,125	0
3	NAG	D	2	14/15	0.70	0.17	59,79,101,108	0

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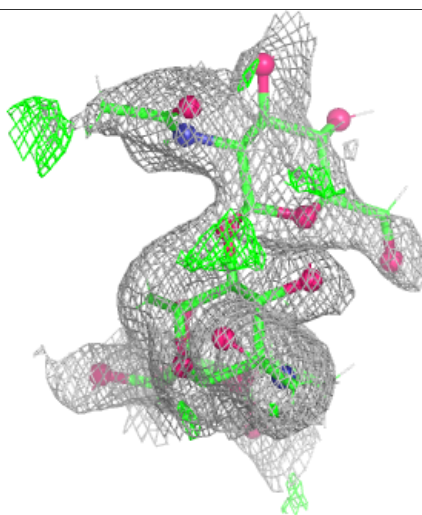
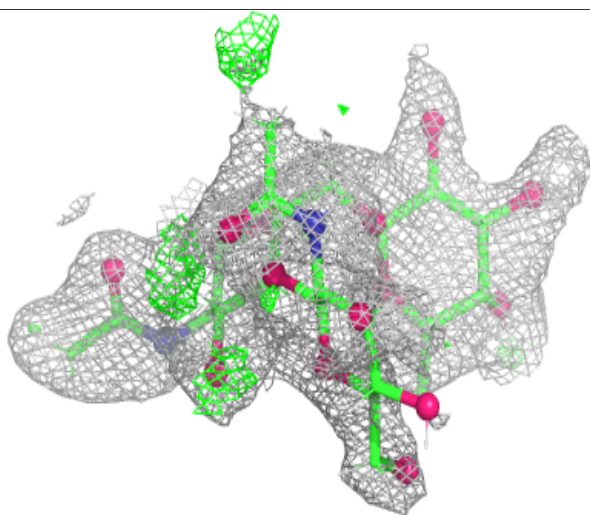
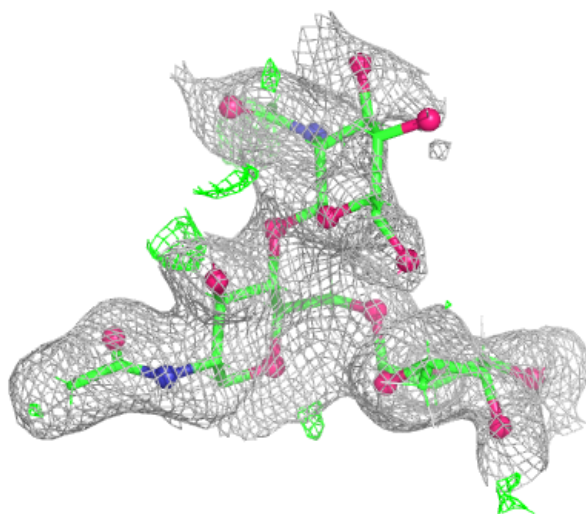
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	C	2	14/15	0.71	0.18	77,91,105,105	0
3	FUC	D	3	10/11	0.73	0.19	57,66,78,79	0
6	FUC	G	2	10/11	0.75	0.20	52,60,70,72	20
2	NAG	C	1	14/15	0.78	0.15	69,80,96,101	0
4	NAG	E	1	14/15	0.82	0.15	51,65,84,93	0
6	NAG	G	1	14/15	0.83	0.16	51,63,76,79	0
5	FUC	F	5	10/11	0.86	0.13	53,62,70,74	0
3	NAG	D	1	14/15	0.87	0.13	44,58,72,76	0
5	NAG	F	2	14/15	0.89	0.13	51,62,75,77	0
5	NAG	F	1	14/15	0.93	0.09	41,48,57,58	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.



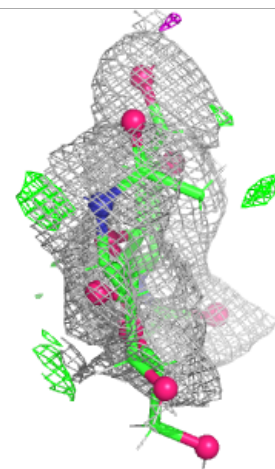
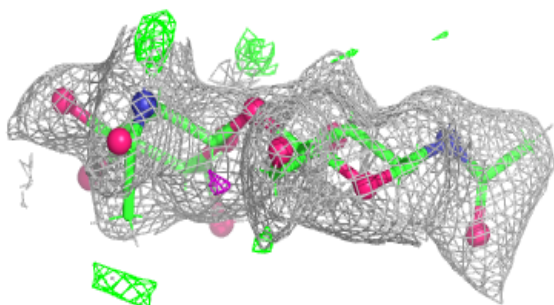
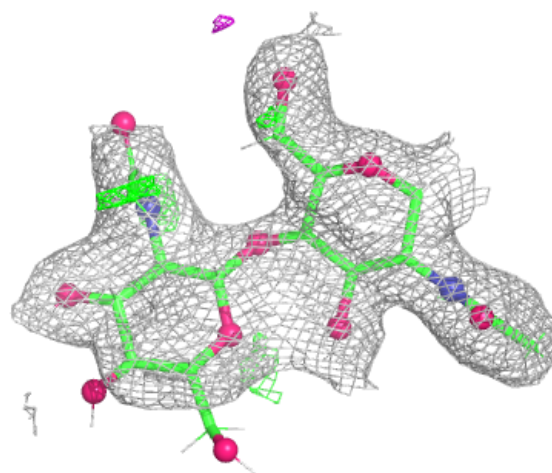
Electron density around Chain D:

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



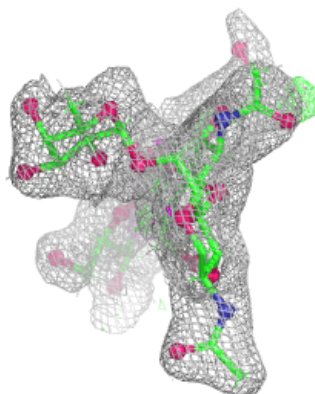
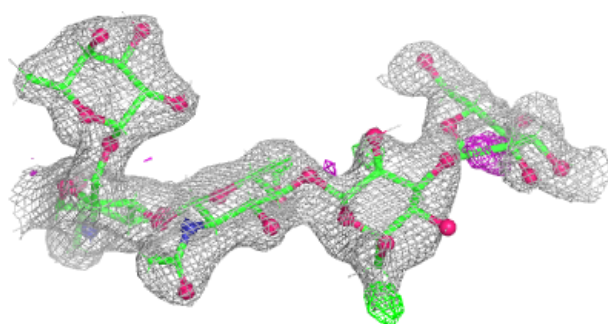
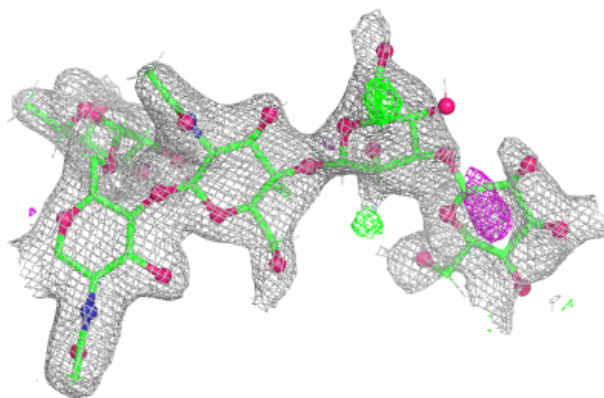
Electron density around Chain E:

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

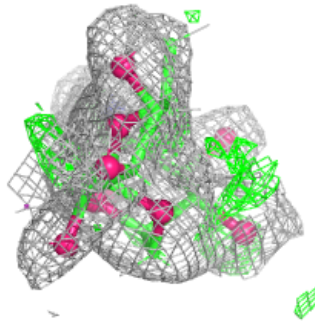
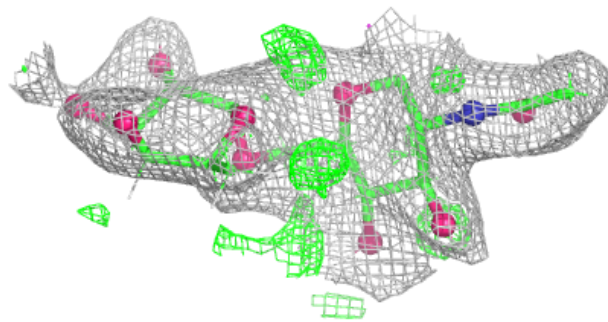
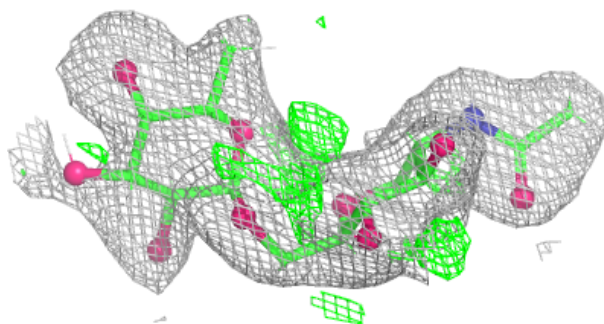


Electron density around Chain F:

$2mF_o - DF_c$ (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)



6.4 Ligands ⓘ

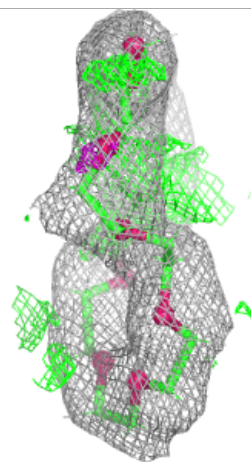
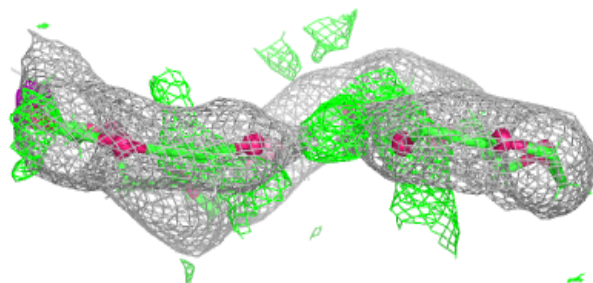
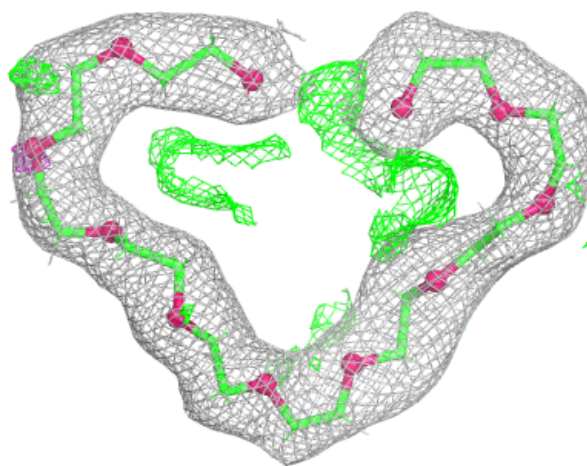
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
13	EDO	A	713	4/4	0.73	0.20	48,57,62,63	0
13	EDO	B	716	4/4	0.73	0.19	47,57,60,64	0
12	PGE	B	713	10/10	0.78	0.17	45,62,72,74	0
13	EDO	B	715[A]	4/4	0.79	0.20	42,50,54,54	10
13	EDO	B	715[B]	4/4	0.79	0.20	38,46,55,55	10
7	NAG	A	701	14/15	0.79	0.16	44,58,72,83	0
15	BCN	A	716	11/11	0.80	0.17	40,49,57,59	23
15	BCN	B	718	11/11	0.81	0.19	37,45,53,55	23
14	PEG	A	715	7/7	0.83	0.16	45,56,65,65	0
16	BO3	A	718	4/4	0.85	0.13	52,55,67,68	0
13	EDO	B	717	4/4	0.87	0.15	40,51,56,61	0
16	BO3	B	720	4/4	0.87	0.13	48,58,70,77	0
11	XPE	A	711	31/31	0.88	0.12	37,48,57,61	0
16	BO3	B	719	4/4	0.88	0.13	41,46,55,56	0
16	BO3	A	717	4/4	0.88	0.17	40,44,52,57	0
13	EDO	B	714	4/4	0.89	0.12	44,53,60,63	0
12	PGE	A	712[A]	10/10	0.90	0.15	31,39,42,43	24
12	PGE	A	712[B]	10/10	0.90	0.15	34,41,44,44	24
13	EDO	A	714	4/4	0.90	0.13	43,52,60,61	0
9	FT8	A	709	27/27	0.96	0.10	26,29,45,48	0
9	FT8	B	711	27/27	0.97	0.09	23,26,45,46	0
10	CL	A	710	1/1	0.99	0.04	27,27,27,27	0
10	CL	B	712	1/1	0.99	0.03	26,26,26,26	0
8	ZN	A	708	1/1	1.00	0.03	27,27,27,27	0
8	ZN	B	710	1/1	1.00	0.03	26,26,26,26	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.

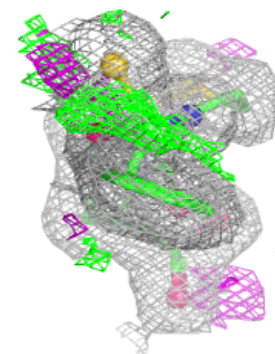
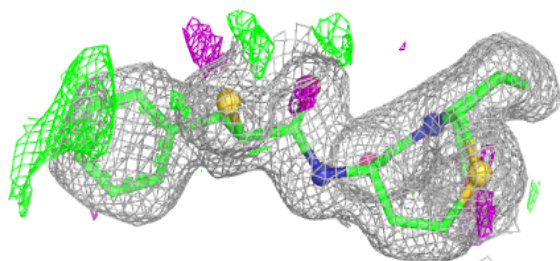
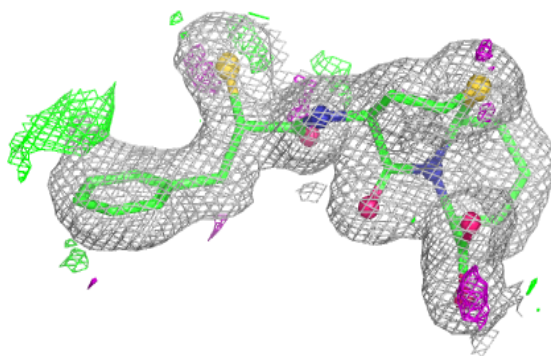
Electron density around XPE A 711:

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

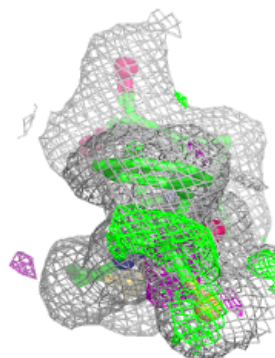
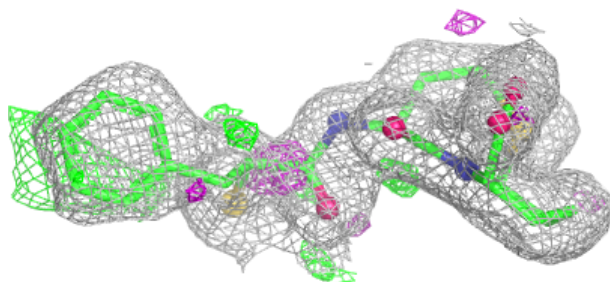
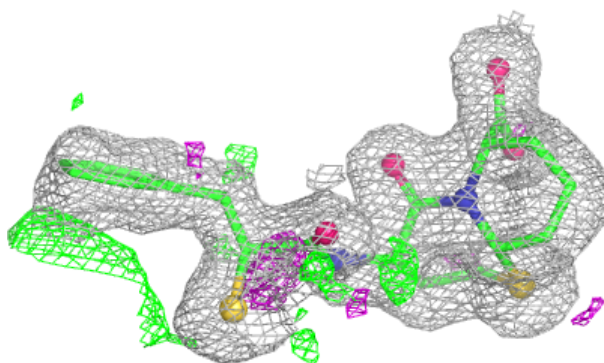


Electron density around FT8 A 709:

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

**Electron density around FT8 B 711:**

$2mF_o-DF_c$ (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.