



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:00 AM UTC

PDB ID : 6TT3 / pdb_00006tt3
Title : Crystal structure of 'Res_S2 mutant human Angiotensin-1 converting enzyme N-domain in complex with SG6.
Authors : Cozier, G.E.; Acharya, K.R.
Deposited on : 2019-12-23
Resolution : 1.70 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

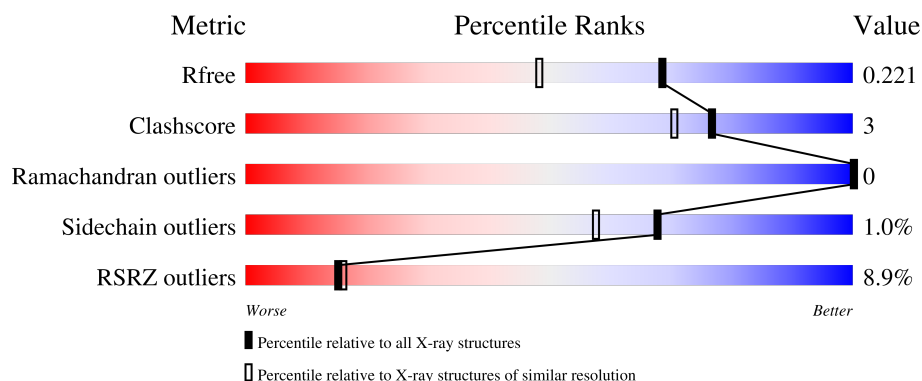
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	629	91%
1	B	629	16% 87% 9%
2	C	2	100%
2	F	2	50% 50%
3	D	4	100%

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Mol	Chain	Length	Quality of chain	
4	E	2		
4	G	2		

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
12	EDO	B	713	-	-	X	-

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 21134 atoms, of which 9908 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	603	Total	C	H	N	O	S	0	11	0
			9784	3212	4783	855	913	21			
1	B	603	Total	C	H	N	O	S	0	5	0
			9708	3189	4746	850	903	20			

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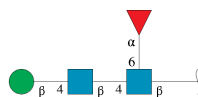
Chain	Residue	Modelled	Actual	Comment	Reference
B	354	GLU	ASP	conflict	UNP P12821
B	357	VAL	SER	conflict	UNP P12821
B	358	VAL	THR	conflict	UNP P12821
B	369	PHE	TYR	conflict	UNP P12821
B	381	GLU	ARG	conflict	UNP P12821
B	431	ASP	GLU	conflict	UNP P12821
B	545	ARG	GLN	conflict	UNP P12821
B	576	LEU	PRO	conflict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

- Molecule 2 is an oligosaccharide called 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	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			
2	F	2	Total	C	H	N	O	0	0	0
			53	16	25	2	10			

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



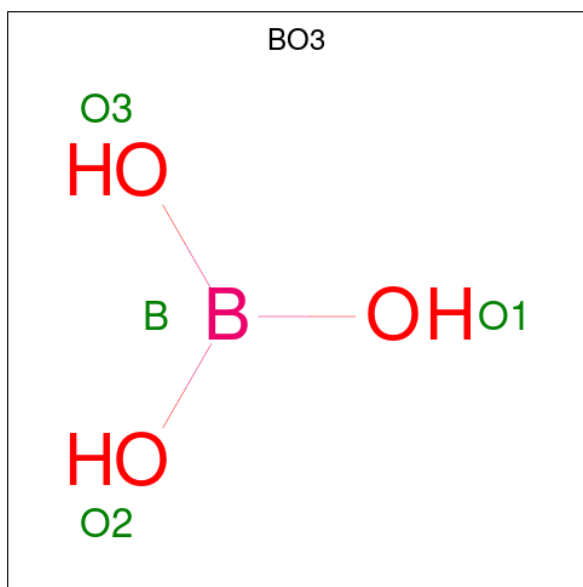
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	4	Total	C	H	N	O	0	0	0
			92	28	43	2	19			

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



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

- Molecule 5 is BORIC ACID (CCD ID: BO3) (formula: BH_3O_3).



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

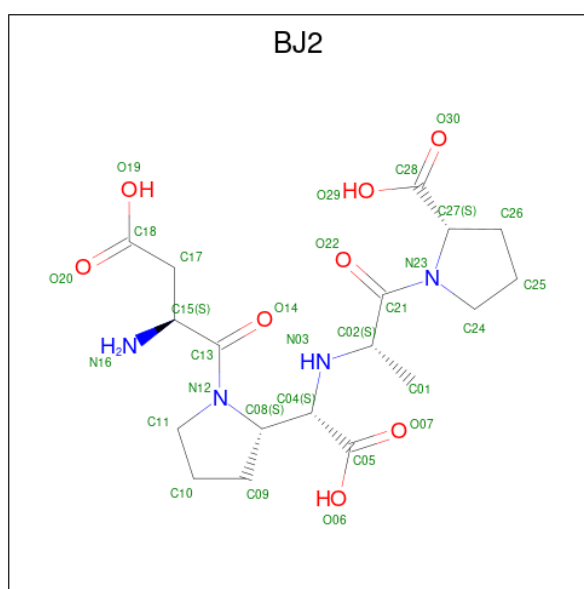
- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

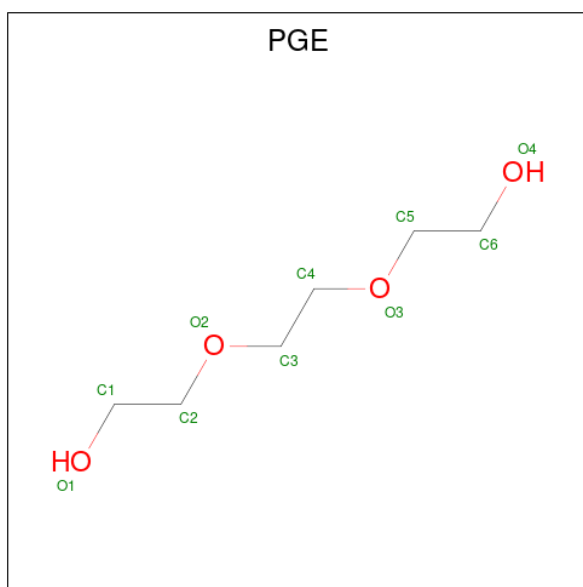
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		
7	B	1	Total	Cl	0	0
			1	1		

- Molecule 8 is (2 {S})-1-[(2 {S})-2-[(1 {S})-1-[(2 {S})-1-[(2 {S})-2-azanyl-4-oxidanyl-4-oxidanylidene-butanoyl]pyrrolidin-2-yl]-2-oxidanyl-2-oxidanylidene-ethyl]amino]propanoyl]pyrrolidine-2-carboxylic acid (CCD ID: BJ2) (formula: C₁₈H₂₈N₄O₈) (labeled as "Ligand of Interest" by depositor).



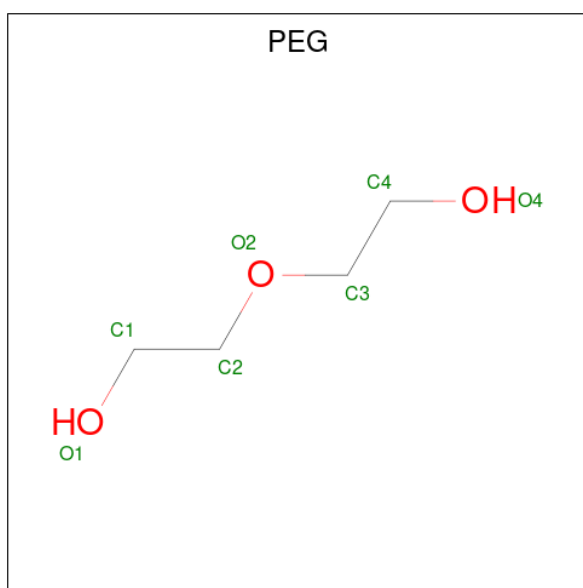
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	0	0
			55	18	25	4	8		
8	B	1	Total	C	H	N	O	0	0
			55	18	25	4	8		

- Molecule 9 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



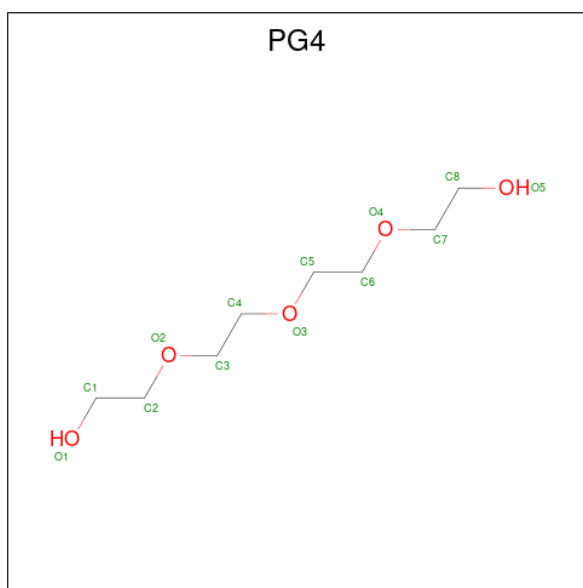
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	H	O	0	0
			24	6	14	4		
9	B	1	Total	C	H	O	0	1
			48	12	28	8		

- Molecule 10 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



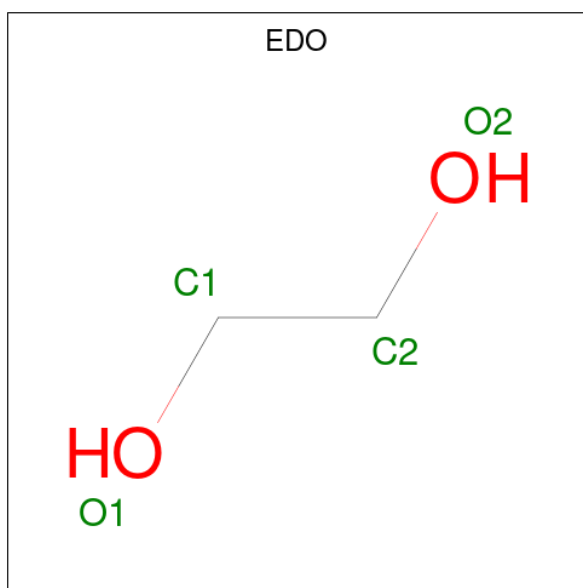
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	H	O	0	0
			17	4	10	3		
10	B	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 11 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	A	1	Total	C	H	O	0	0
			31	8	18	5		

- Molecule 12 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



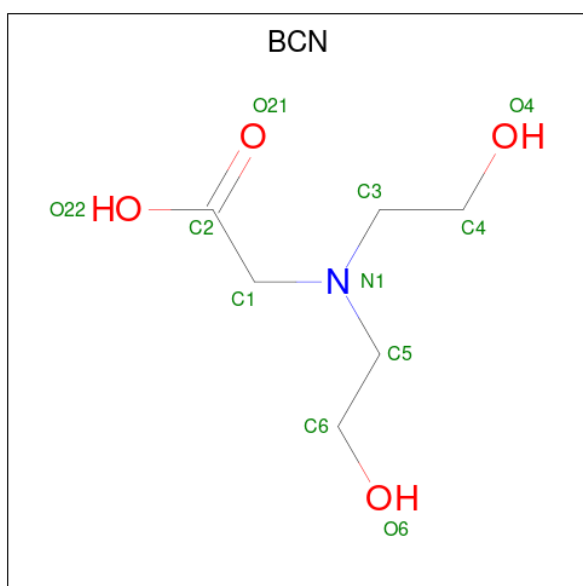
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	A	1	Total	C	H	O	0	0
			10	2	6	2		
12	A	1	Total	C	H	O	0	0
			10	2	6	2		

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

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



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

- Molecule 14 is CALCIUM ION (CCD ID: CA) (formula: Ca).

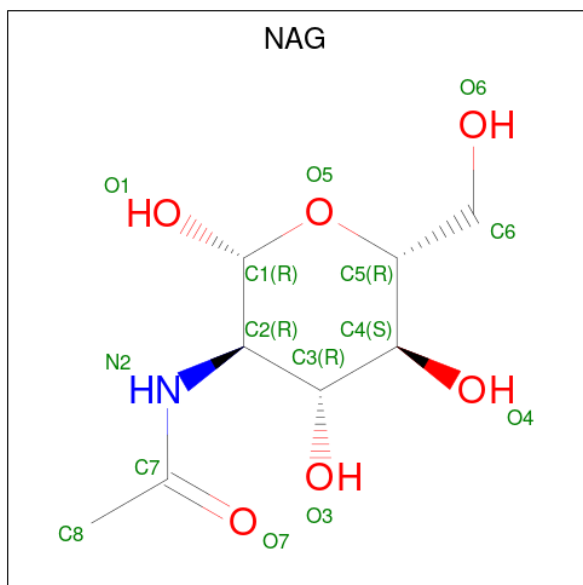
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	B	1	Total	Ca	0	0
			1	1		

- Molecule 15 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
15	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

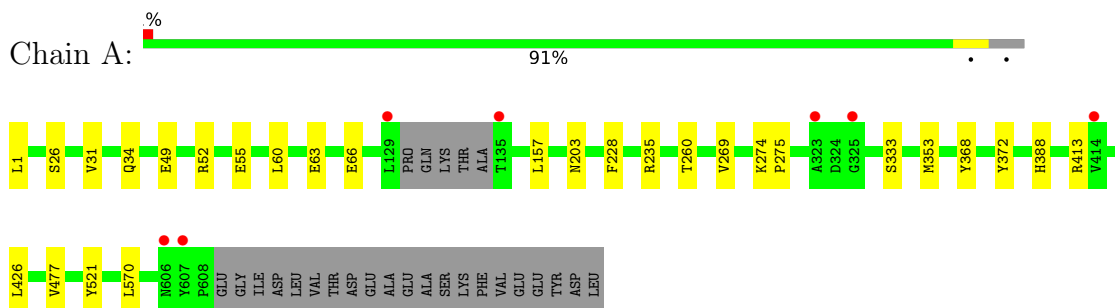
- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	539	Total	O	0	7
			545	545		
16	B	338	Total	O	0	5
			343	343		

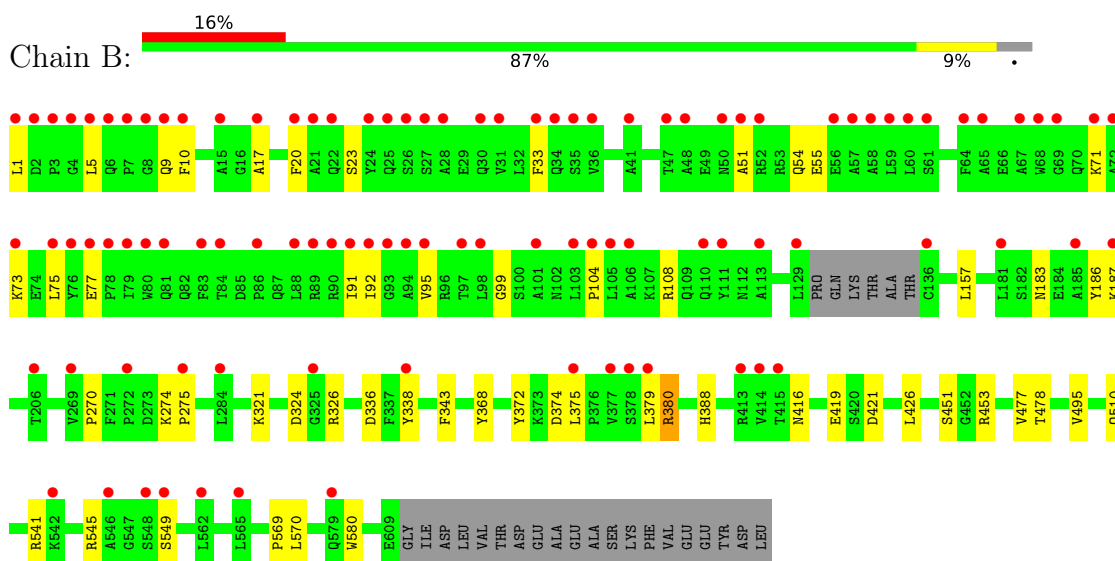
3 Residue-property plots [i](#)

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.

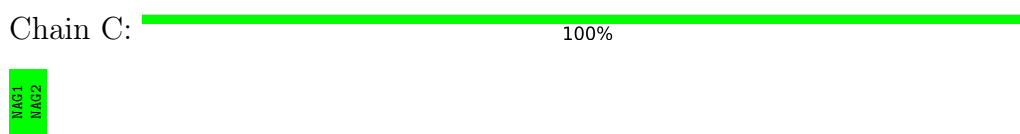
- Molecule 1: Angiotensin-converting enzyme



- Molecule 1: Angiotensin-converting enzyme



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



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

Chain F:  50% 50%

MAG1
MAG2

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

Chain D:  100%

MAG1
MAG2
BMJ3
FUC4

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

Chain E:  50% 50%

MAG1
FUC2

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

Chain G:  50% 50%

MAG3
FUC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.62Å 78.20Å 83.79Å 88.64° 64.35° 74.64°	Depositor
Resolution (Å)	75.11 – 1.70 75.11 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.2 (75.11-1.70) 97.2 (75.11-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.13_2998, PHENIX 1.13_2998	Depositor
R, R_{free}	0.188 , 0.221 0.190 , 0.221	Depositor DCC
R_{free} test set	2061 reflections (1.16%)	wwPDB-VP
Wilson B-factor (Å ²)	24.3	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.5	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	21134	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.26% 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: BO3, CL, NAG, BMA, PG4, CA, BCN, FUC, BJ2, ZN, PEG, PGE, EDO

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	0.45	0/5169	0.56	0/7038
1	B	0.38	0/5125	0.52	0/6979
All	All	0.42	0/10294	0.54	0/14017

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5001	4783	4764	22	0
1	B	4962	4746	4737	36	0
2	C	28	25	25	0	0
2	F	28	25	25	1	0
3	D	49	43	43	0	0
4	E	24	22	22	0	0
4	G	24	22	22	1	0
5	A	12	9	9	0	0
5	B	8	6	6	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	30	25	0	0	0
8	B	30	25	0	0	0
9	A	10	14	14	0	0
9	B	20	28	28	0	0
10	A	7	10	10	0	0
10	B	7	10	9	0	0
11	A	13	18	18	0	0
12	A	20	30	30	4	0
12	B	12	18	18	4	0
13	A	22	24	22	2	0
13	B	11	12	12	0	0
14	A	1	0	0	0	0
14	B	1	0	0	0	0
15	B	14	13	13	0	0
16	A	545	0	0	6	0
16	B	343	0	0	3	0
All	All	11226	9908	9827	59	0

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

The worst 5 of 59 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:375:LEU:O	1:B:380:ARG:NH2	2.16	0.79
1:B:55:GLU:OE2	16:B:801:HOH:O	2.03	0.77
1:B:91:ILE:O	1:B:95:VAL:HG23	1.87	0.76
1:B:416:ASN:ND2	2:F:1:NAG:O7	2.23	0.71
1:A:49:GLU:OE1	1:A:52:ARG:NH2	2.24	0.71

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	610/629 (97%)	602 (99%)	8 (1%)	0	100	100
1	B	604/629 (96%)	587 (97%)	17 (3%)	0	100	100
All	All	1214/1258 (96%)	1189 (98%)	25 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	529/541 (98%)	525 (99%)	4 (1%)	73	65
1	B	524/541 (97%)	518 (99%)	6 (1%)	65	54
All	All	1053/1082 (97%)	1043 (99%)	10 (1%)	68	62

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

Mol	Chain	Res	Type
1	B	388	HIS
1	B	419	GLU
1	B	421	ASP
1	A	388	HIS
1	B	368	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	371	GLN
1	B	527	GLN
1	A	582	GLN
1	A	588	ASN
1	B	50	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 ⓘ

12 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	0.41	0	17,19,21	0.61	0
2	NAG	C	2	2	14,14,15	0.36	0	17,19,21	0.45	0
3	NAG	D	1	1,3	14,14,15	0.48	0	17,19,21	0.47	0
3	NAG	D	2	3	14,14,15	0.32	0	17,19,21	0.63	0
3	BMA	D	3	3	11,11,12	0.83	0	15,15,17	0.70	0
3	FUC	D	4	3	10,10,11	0.67	0	14,14,16	0.72	0
4	NAG	E	1	1,4	14,14,15	0.32	0	17,19,21	0.72	0
4	FUC	E	2	4	10,10,11	0.92	1 (10%)	14,14,16	1.24	2 (14%)
2	NAG	F	1	1,2	14,14,15	0.81	2 (14%)	17,19,21	0.58	0
2	NAG	F	2	2	14,14,15	0.26	0	17,19,21	0.52	0
4	NAG	G	1	1,4	14,14,15	0.28	0	17,19,21	0.50	0
4	FUC	G	2	4	10,10,11	0.92	0	14,14,16	0.97	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
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	2	FUC	C1-C2	2.32	1.57	1.52
2	F	1	NAG	C1-C2	2.15	1.55	1.52
2	F	1	NAG	O5-C1	2.05	1.47	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	2	FUC	C1-C2-C3	2.94	113.93	109.64
4	E	2	FUC	O5-C1-C2	2.04	115.67	110.79

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

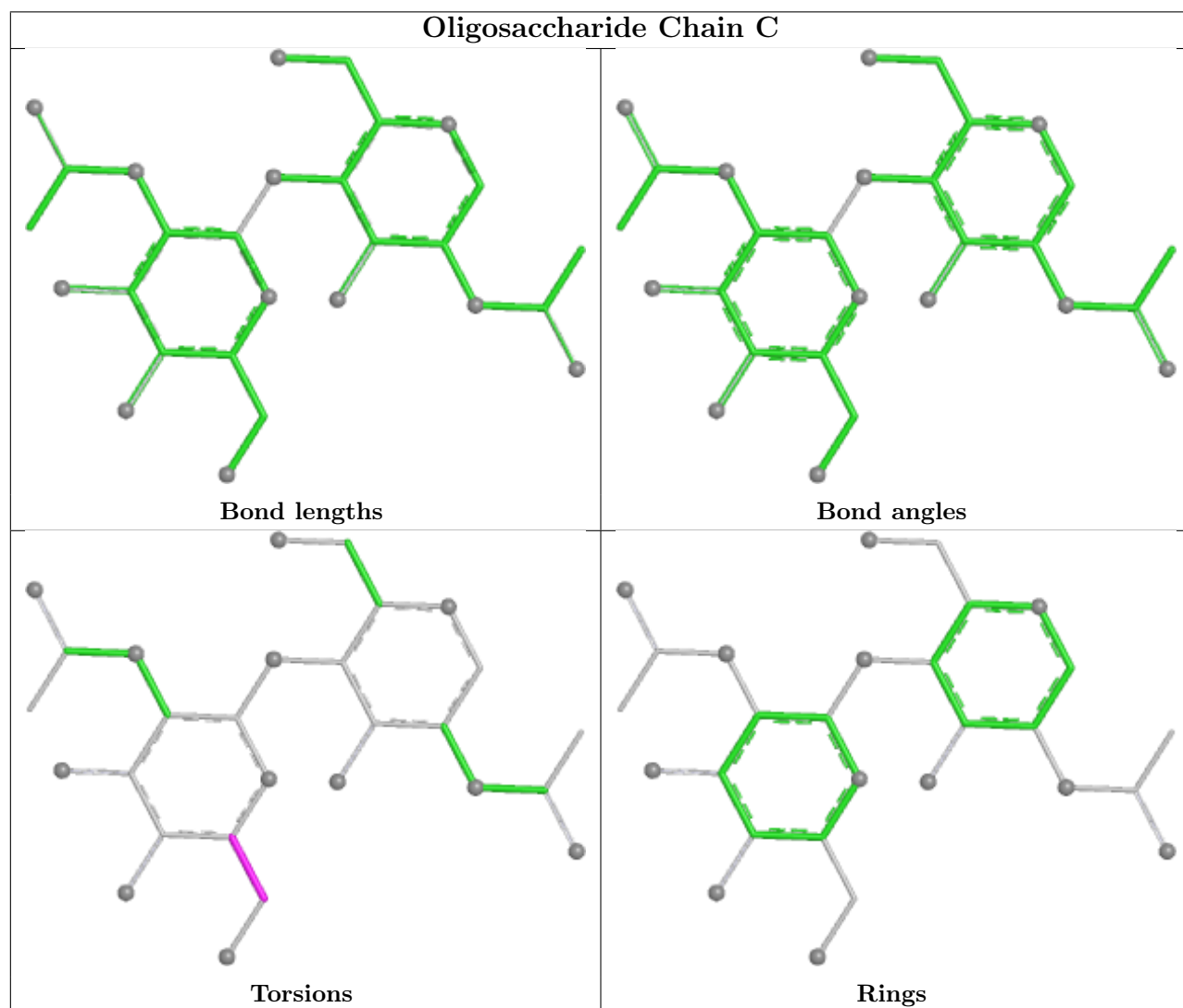
Mol	Chain	Res	Type	Atoms
2	F	1	NAG	C1-C2-N2-C7
4	E	1	NAG	O5-C5-C6-O6
2	F	1	NAG	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	F	1	NAG	C4-C5-C6-O6

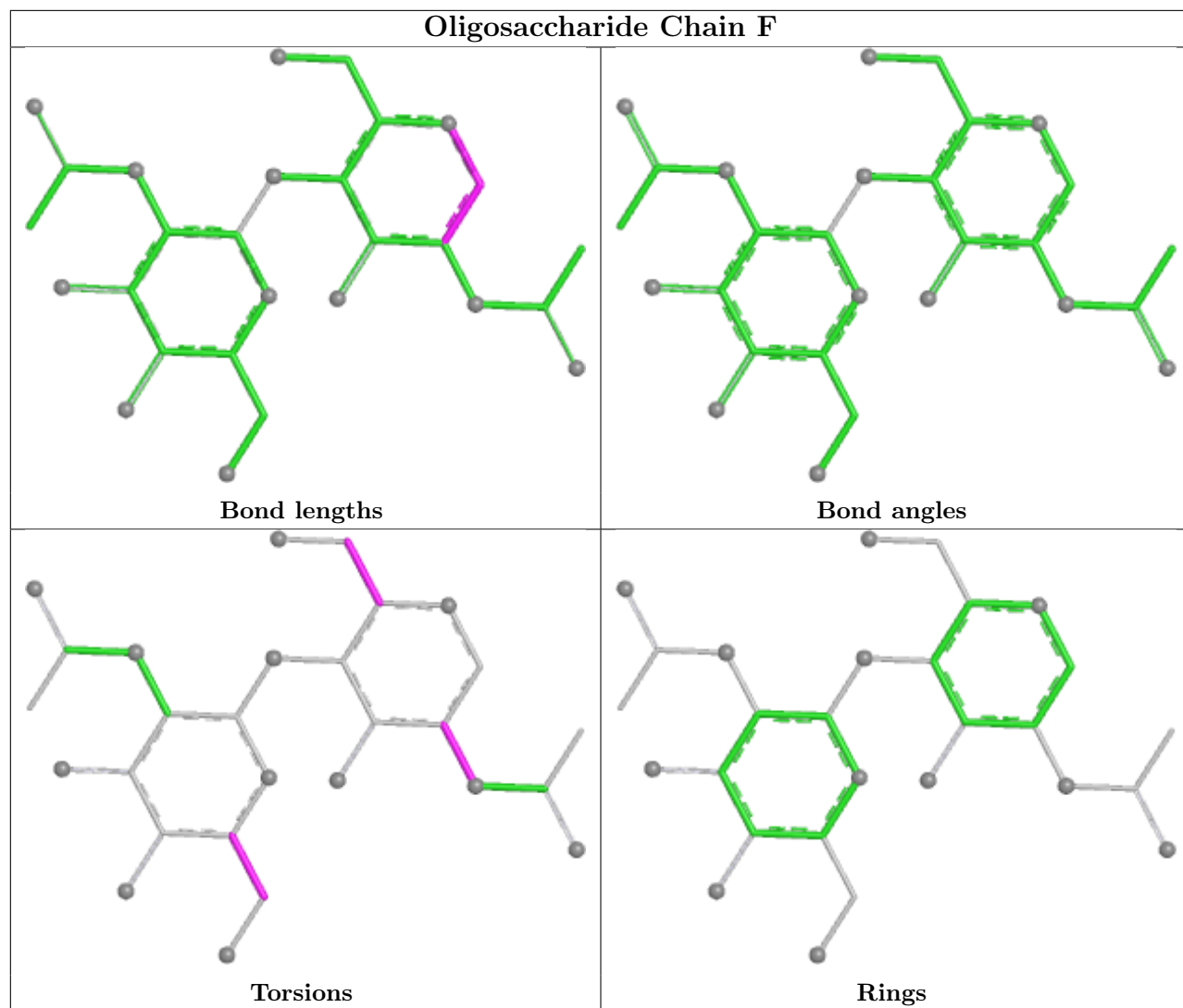
There are no ring outliers.

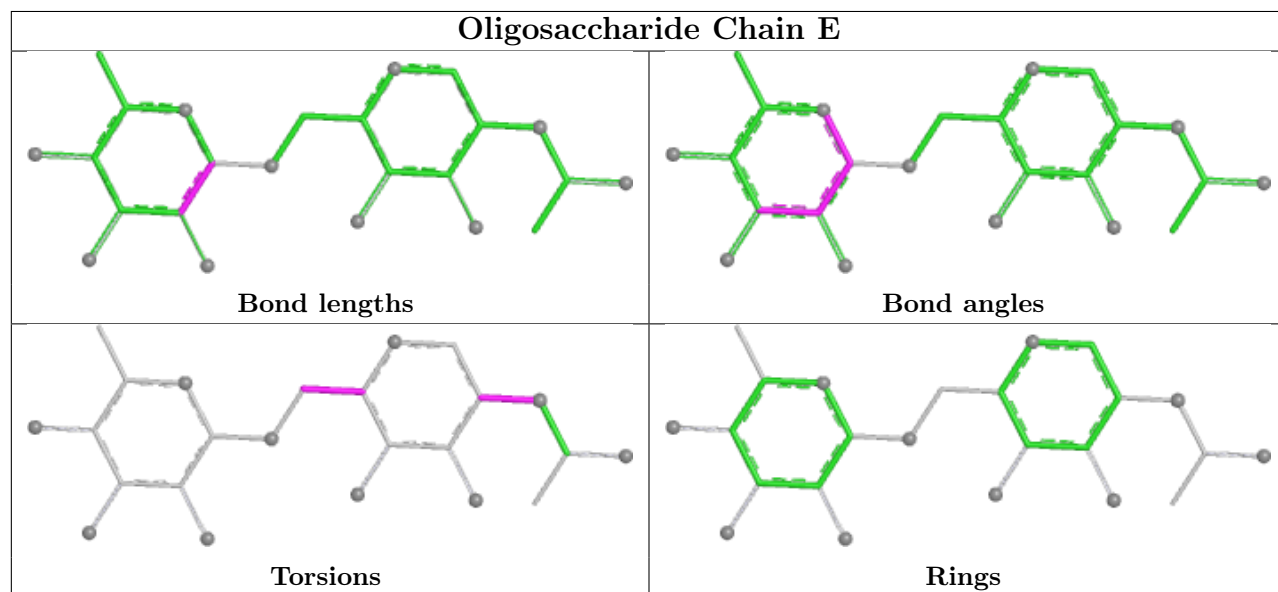
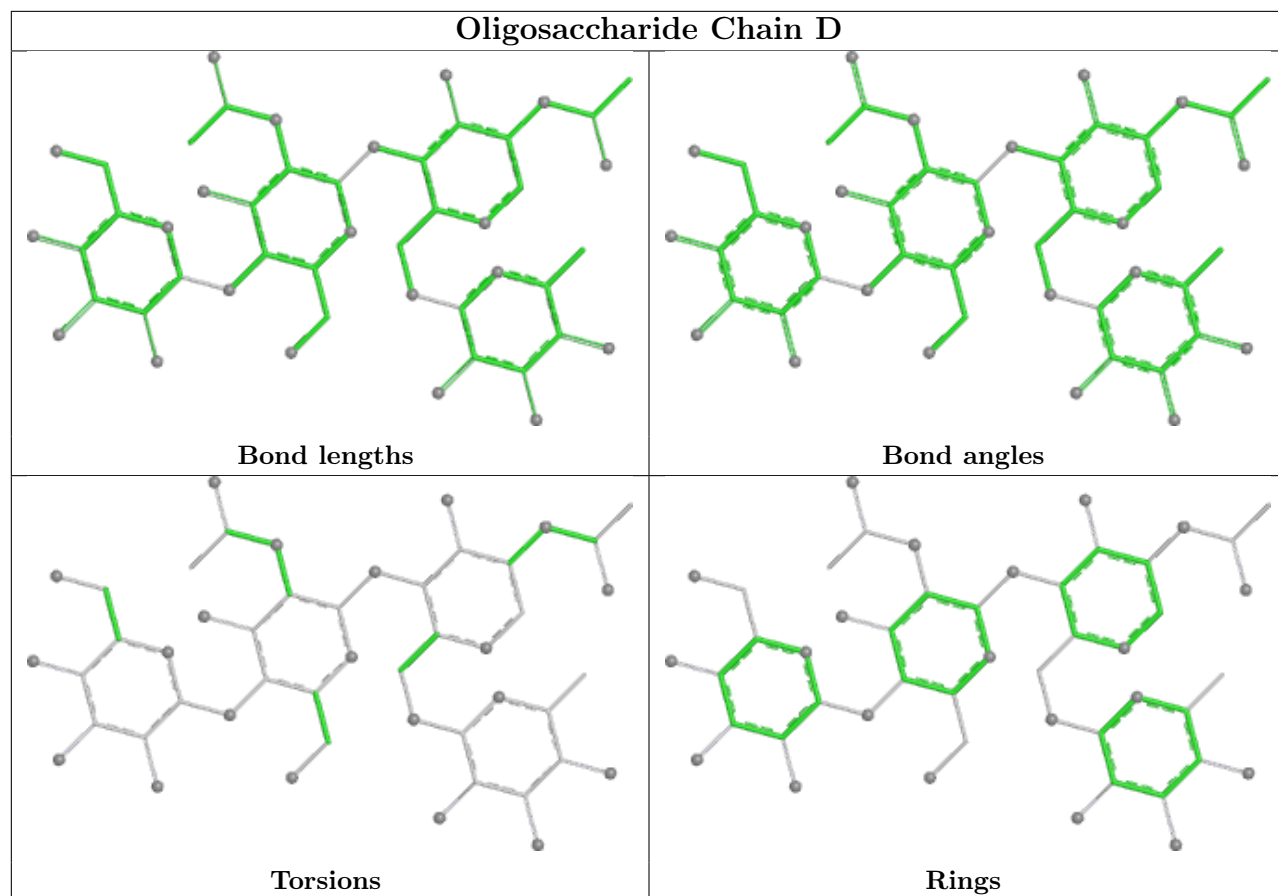
2 monomers are involved in 2 short contacts:

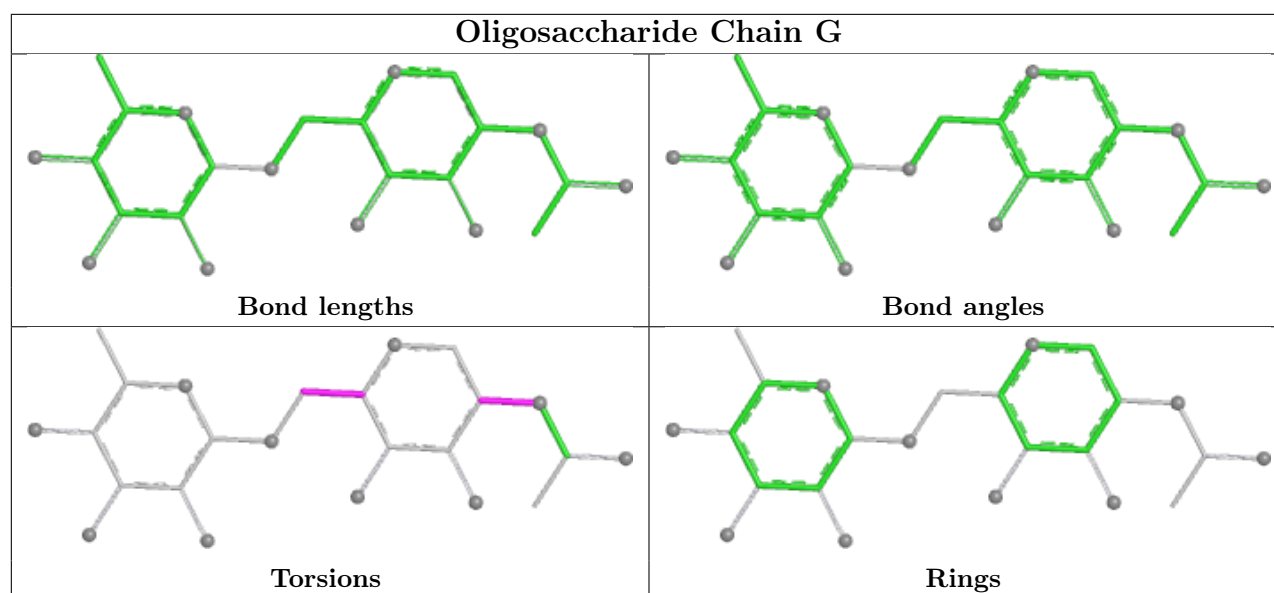
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1	NAG	1	0
4	G	2	FUC	1	0

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









5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 6 are monoatomic - leaving 25 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	$\# Z > 2$
9	PGE	B	711[A]	-	9,9,9	0.34	0	8,8,8	0.26	0
12	EDO	A	720[B]	-	3,3,3	0.61	0	2,2,2	0.28	0
10	PEG	B	712	14	6,6,6	0.52	0	5,5,5	0.28	0
12	EDO	B	714	-	3,3,3	0.49	0	2,2,2	0.31	0
13	BCN	B	716	14	10,10,10	1.27	1 (10%)	11,11,11	1.39	2 (18%)
5	BO3	A	709	-	3,3,3	0.45	0	3,3,3	0.43	0
15	NAG	B	701	1	14,14,15	1.01	1 (7%)	17,19,21	0.87	0
12	EDO	A	719	-	3,3,3	0.47	0	2,2,2	0.32	0
5	BO3	B	706	-	3,3,3	0.25	0	3,3,3	0.20	0
5	BO3	B	707	-	3,3,3	0.27	0	3,3,3	0.19	0
12	EDO	B	715	-	3,3,3	0.48	0	2,2,2	0.11	0
9	PGE	A	715	-	9,9,9	0.38	0	8,8,8	0.56	0
5	BO3	A	710	-	3,3,3	0.54	0	3,3,3	0.07	0
8	BJ2	B	710	14,6	31,31,31	3.55	14 (45%)	37,44,44	1.53	7 (18%)
10	PEG	A	716	-	6,6,6	0.45	0	5,5,5	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	PGE	B	711[B]	-	9,9,9	0.31	0	8,8,8	0.32	0
12	EDO	A	720[A]	-	3,3,3	0.49	0	2,2,2	0.28	0
5	BO3	A	711	-	3,3,3	0.26	0	3,3,3	0.14	0
12	EDO	A	721	-	3,3,3	0.46	0	2,2,2	0.29	0
13	BCN	A	723	14	10,10,10	1.21	1 (10%)	11,11,11	1.09	0
12	EDO	A	718	-	3,3,3	0.47	0	2,2,2	0.32	0
12	EDO	B	713	-	3,3,3	0.51	0	2,2,2	0.09	0
8	BJ2	A	714	14,6	31,31,31	3.36	12 (38%)	37,44,44	1.48	10 (27%)
13	BCN	A	722	14	10,10,10	1.18	0	11,11,11	1.16	1 (9%)
11	PG4	A	717	-	12,12,12	0.57	0	11,11,11	0.43	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
9	PGE	B	711[A]	-	-	4/7/7/7	-
12	EDO	A	720[B]	-	-	0/1/1/1	-
10	PEG	B	712	14	-	0/4/4/4	-
12	EDO	B	714	-	-	0/1/1/1	-
13	BCN	B	716	14	-	1/10/10/10	-
15	NAG	B	701	1	-	2/6/23/26	0/1/1/1
12	EDO	A	719	-	-	0/1/1/1	-
12	EDO	B	715	-	-	1/1/1/1	-
9	PGE	A	715	-	-	3/7/7/7	-
10	PEG	A	716	-	-	3/4/4/4	-
8	BJ2	B	710	14,6	-	5/36/56/56	0/2/2/2
12	EDO	A	720[A]	-	-	0/1/1/1	-
9	PGE	B	711[B]	-	-	2/7/7/7	-
12	EDO	A	721	-	-	0/1/1/1	-
13	BCN	A	723	14	-	1/10/10/10	-
12	EDO	A	718	-	-	0/1/1/1	-
12	EDO	B	713	-	-	0/1/1/1	-
8	BJ2	A	714	14,6	-	5/36/56/56	0/2/2/2
13	BCN	A	722	14	-	4/10/10/10	-
11	PG4	A	717	-	-	4/10/10/10	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	714	BJ2	C08-N12	8.36	1.57	1.46
8	B	710	BJ2	C08-N12	8.24	1.56	1.46
8	A	714	BJ2	C09-C08	-8.11	1.40	1.53
8	B	710	BJ2	C09-C08	-7.77	1.40	1.53
8	B	710	BJ2	C27-N23	6.22	1.59	1.47

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	710	BJ2	C28-C27-N23	-4.31	103.90	112.54
8	A	714	BJ2	C28-C27-N23	-3.90	104.72	112.54
8	B	710	BJ2	O06-C05-O07	-3.09	117.06	124.08
13	B	716	BCN	C5-N1-C3	-3.00	104.29	111.44
8	B	710	BJ2	C08-C04-N03	-2.97	103.98	110.02

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	714	BJ2	N03-C04-C08-C09
15	B	701	NAG	O5-C5-C6-O6
15	B	701	NAG	C4-C5-C6-O6
9	A	715	PGE	O1-C1-C2-O2
10	A	716	PEG	O1-C1-C2-O2

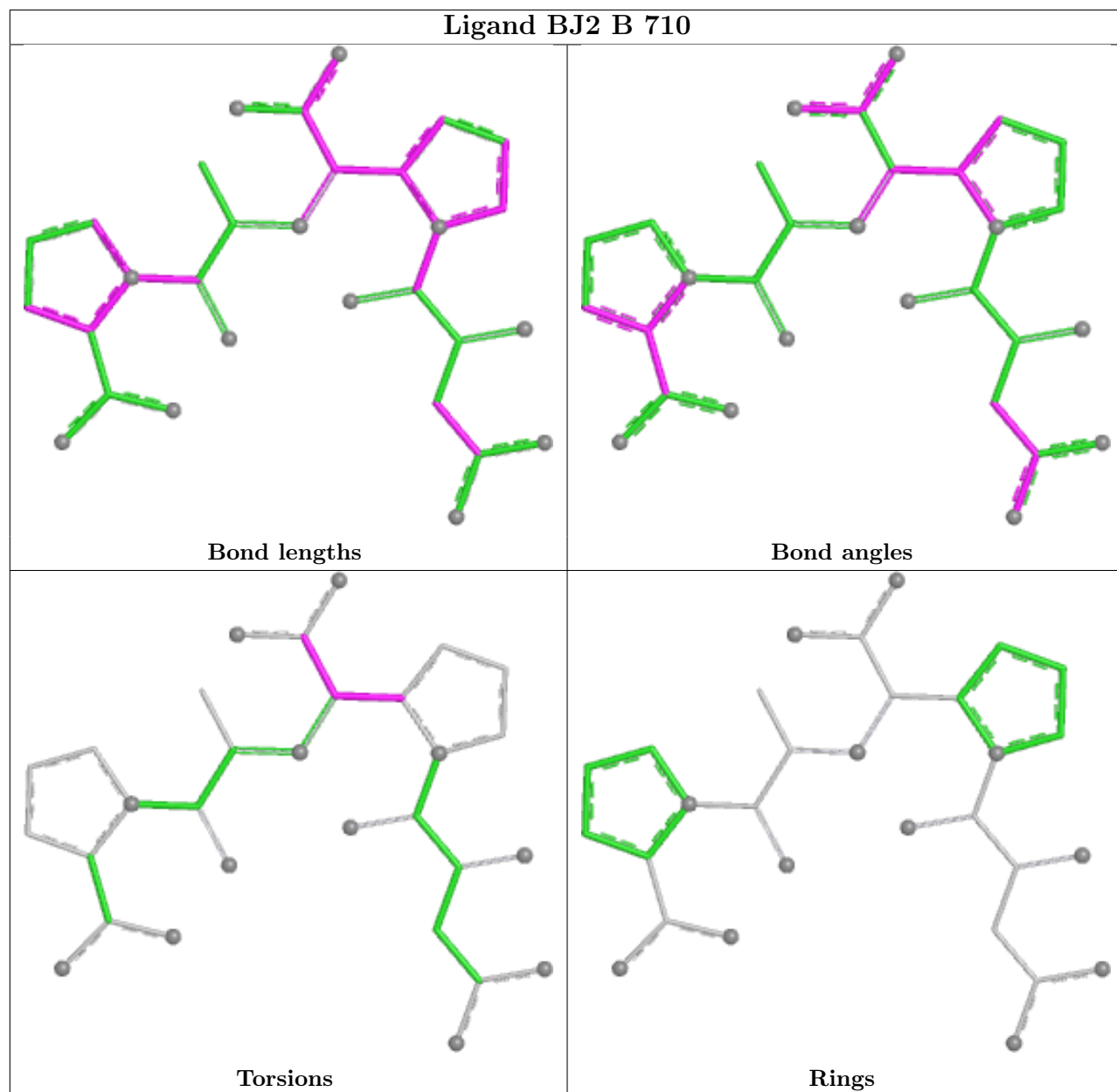
There are no ring outliers.

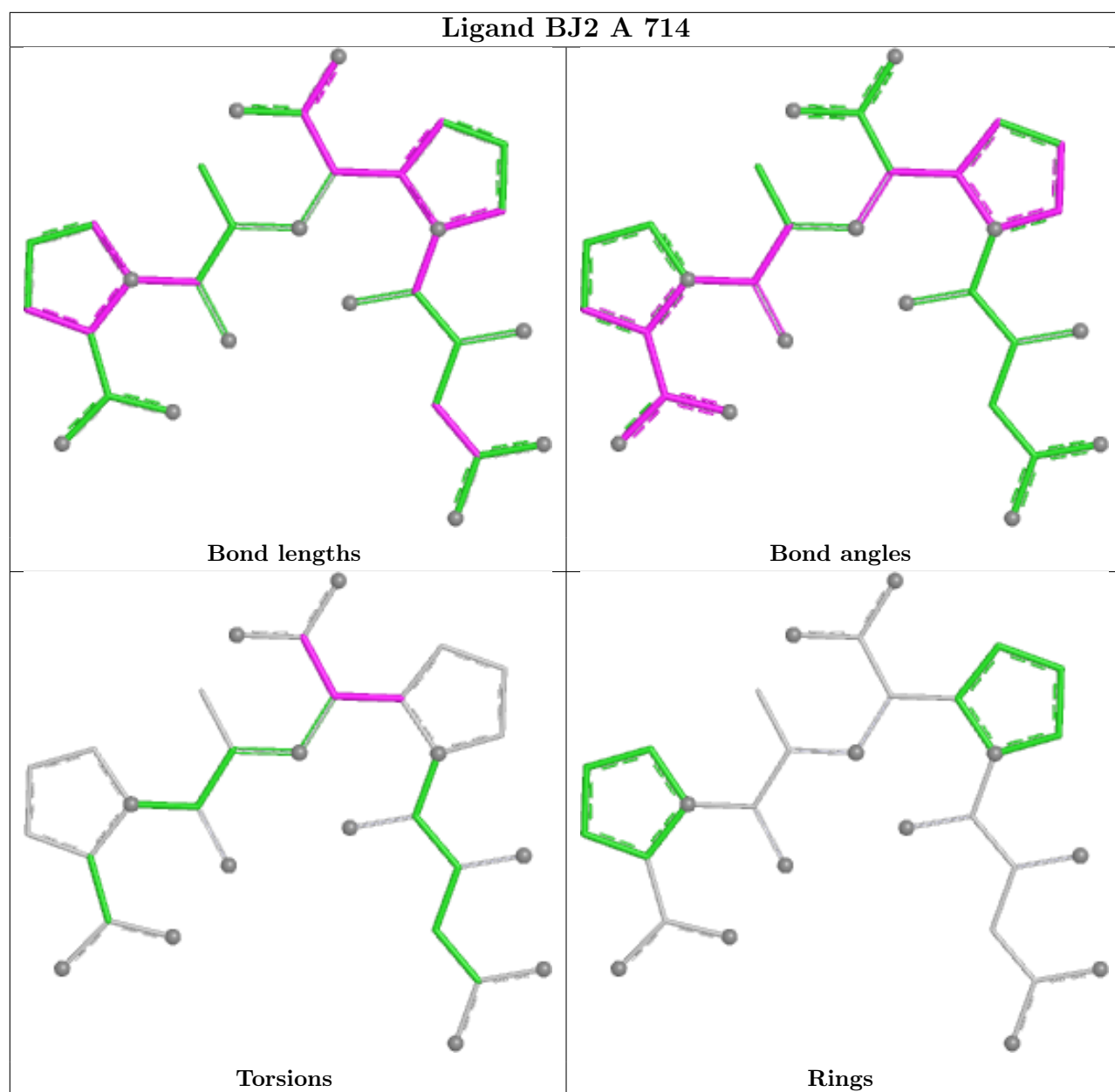
4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	A	720[B]	EDO	3	0
12	A	721	EDO	1	0
12	B	713	EDO	4	0
13	A	722	BCN	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	603/629 (95%)	-0.30	7 (1%) 76 80	11, 29, 53, 106	9 (1%)
1	B	603/629 (95%)	0.66	100 (16%) 4 4	14, 40, 80, 109	4 (0%)
All	All	1206/1258 (95%)	0.18	107 (8%) 15 16	11, 33, 73, 109	13 (1%)

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	92	ILE	6.1
1	B	1	LEU	5.7
1	B	129	LEU	5.5
1	B	24	TYR	5.2
1	B	68	TRP	4.9

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

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

6.3 Carbohydrates [i](#)

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

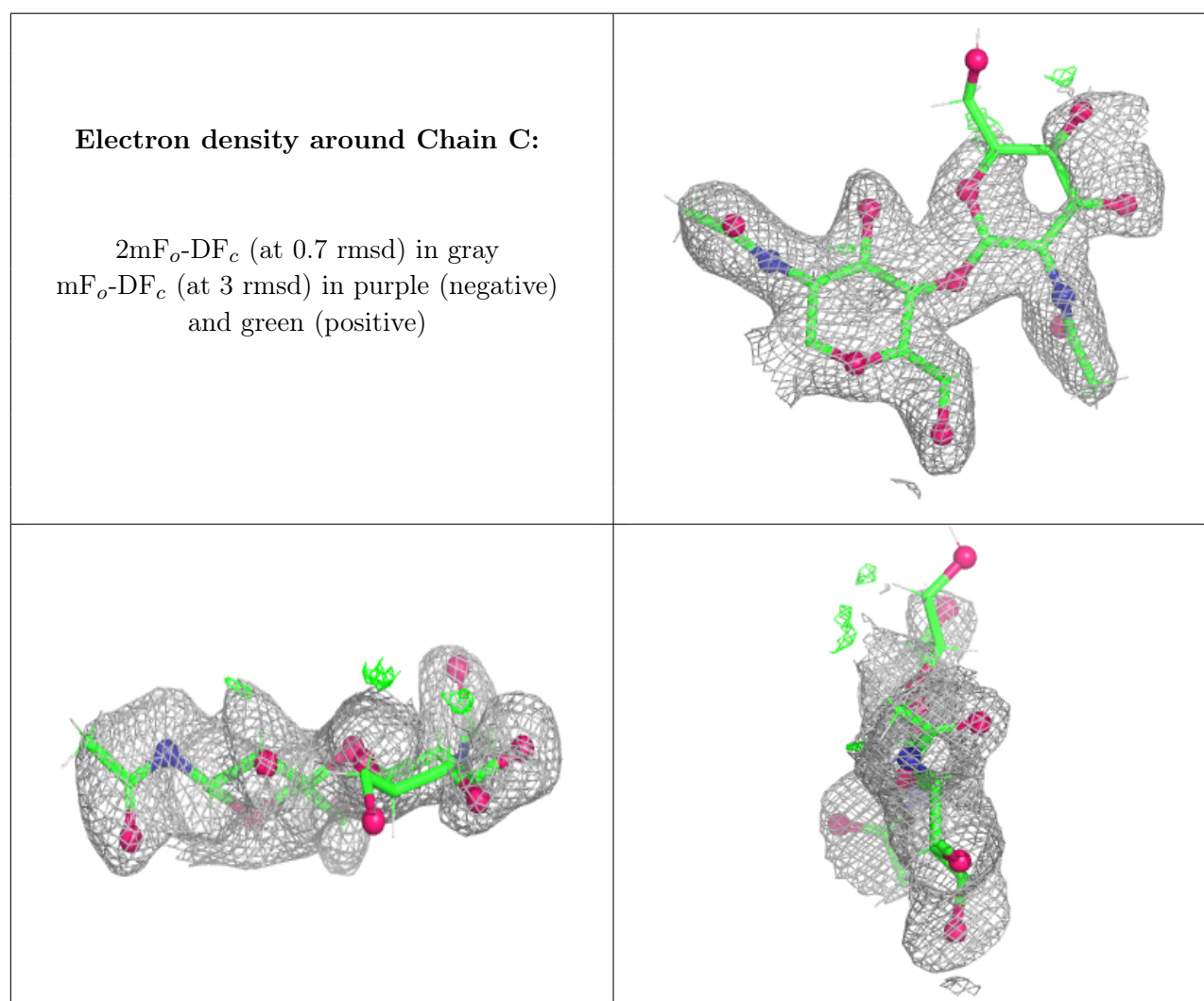
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	FUC	E	2	10/11	0.69	0.20	56,78,104,109	0
3	BMA	D	3	11/12	0.77	0.12	55,78,94,97	0
2	NAG	F	1	14/15	0.77	0.13	51,65,75,78	26
2	NAG	F	2	14/15	0.78	0.13	67,82,112,112	0
4	FUC	G	2	10/11	0.79	0.15	55,78,111,119	0

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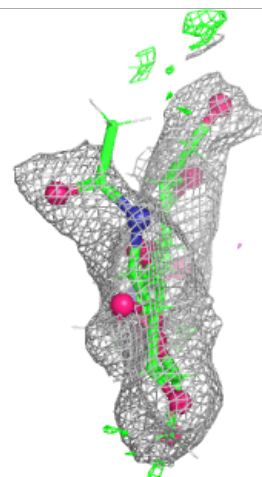
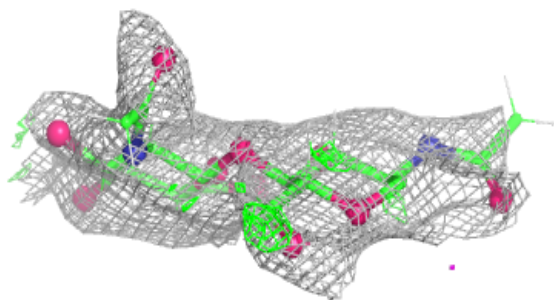
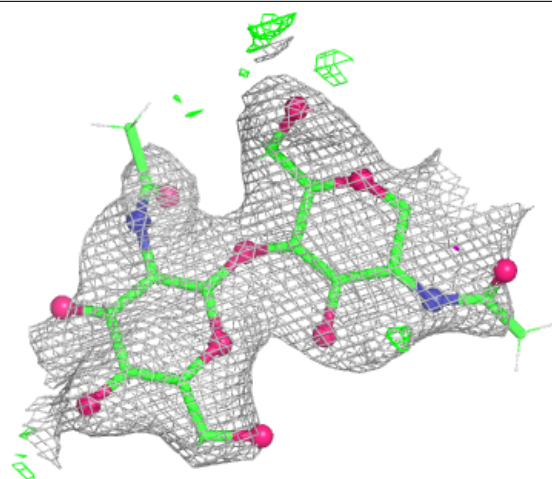
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	C	2	14/15	0.81	0.14	51,71,108,109	0
3	FUC	D	4	10/11	0.86	0.12	42,55,63,76	0
4	NAG	G	1	14/15	0.87	0.10	39,53,71,85	0
2	NAG	C	1	14/15	0.88	0.11	44,54,65,75	0
3	NAG	D	2	14/15	0.90	0.10	43,57,82,82	0
4	NAG	E	1	14/15	0.92	0.10	35,46,65,70	0
3	NAG	D	1	14/15	0.92	0.09	31,44,60,60	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.



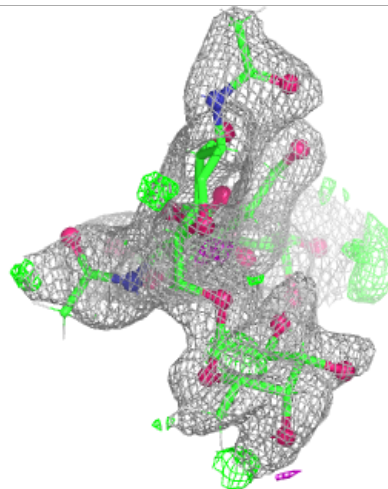
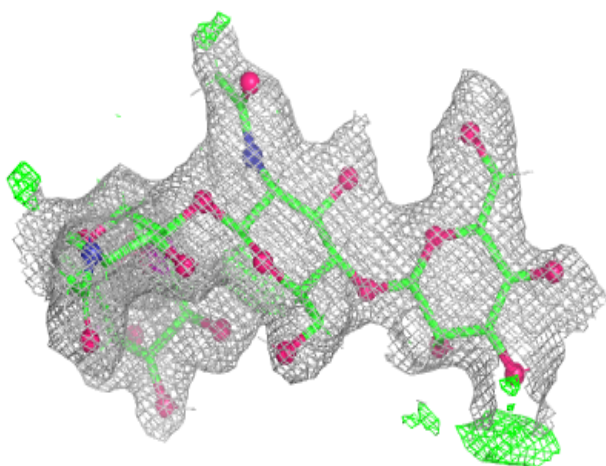
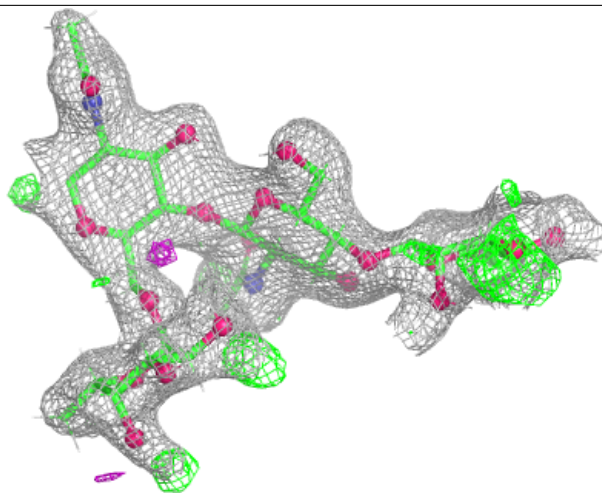
Electron density around Chain F:

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



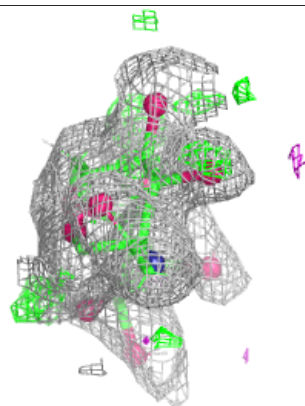
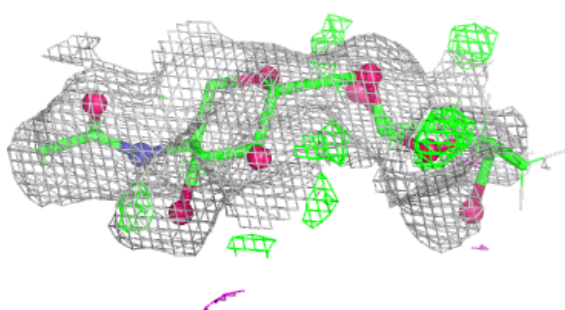
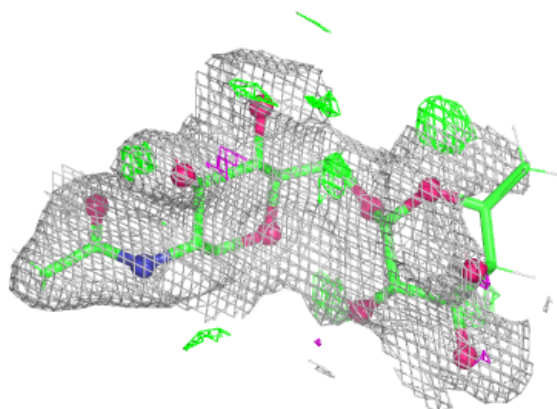
Electron density around Chain D:

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

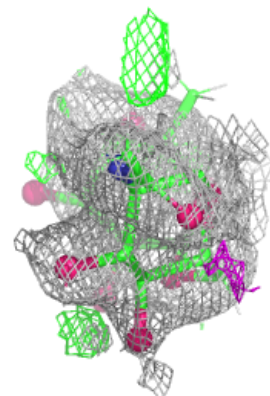
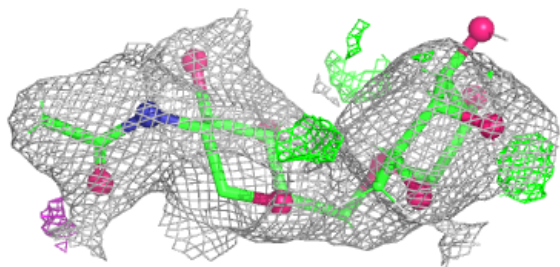
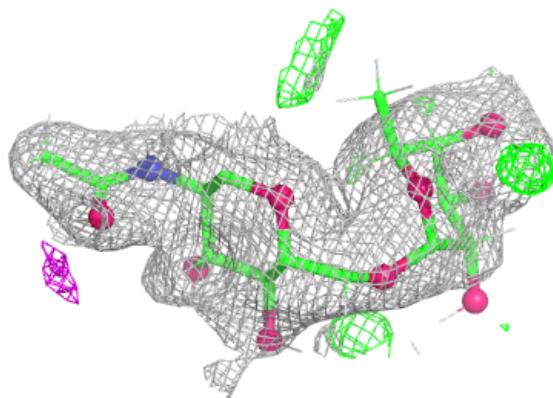


Electron density around Chain E:

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

**Electron density around Chain 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 ⓘ

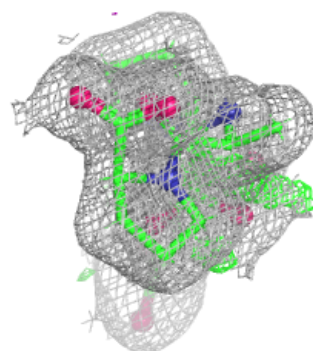
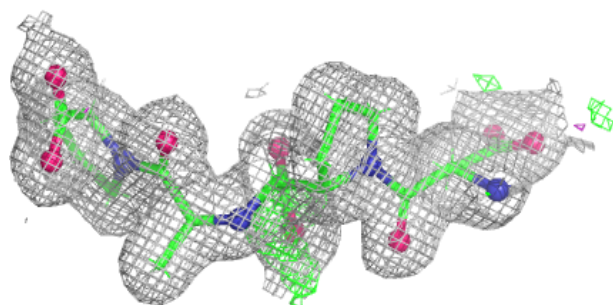
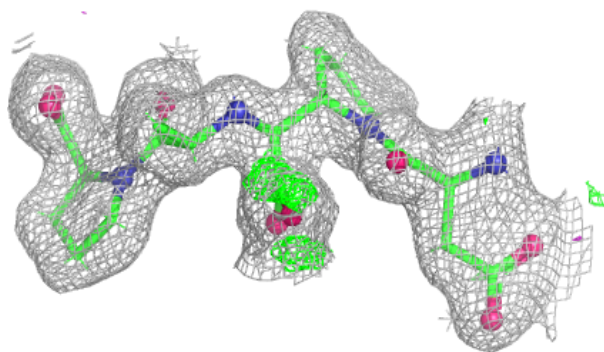
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
15	NAG	B	701	14/15	0.71	0.17	67,82,101,110	0
12	EDO	B	713	4/4	0.79	0.24	36,55,66,69	0
12	EDO	B	715	4/4	0.81	0.15	56,67,78,78	0
10	PEG	B	712	7/7	0.83	0.13	41,59,70,70	0
9	PGE	B	711[B]	10/10	0.85	0.15	30,38,45,50	24
12	EDO	B	714	4/4	0.85	0.10	42,52,62,69	0
9	PGE	B	711[A]	10/10	0.85	0.15	25,37,43,44	24
13	BCN	B	716	11/11	0.85	0.13	40,59,70,80	0
11	PG4	A	717	13/13	0.85	0.14	41,55,67,67	0
12	EDO	A	719	4/4	0.87	0.12	50,60,64,67	0
13	BCN	A	722	11/11	0.89	0.11	27,45,65,79	0
12	EDO	A	720[B]	4/4	0.89	0.12	23,42,51,57	10
12	EDO	A	720[A]	4/4	0.89	0.12	30,42,55,55	10
9	PGE	A	715	10/10	0.90	0.12	34,50,63,75	0
5	BO3	B	706	4/4	0.90	0.18	40,46,55,56	0
12	EDO	A	718	4/4	0.91	0.10	43,52,60,63	0
10	PEG	A	716	7/7	0.92	0.09	35,44,58,65	0
12	EDO	A	721	4/4	0.92	0.13	36,50,61,61	0
5	BO3	A	710	4/4	0.93	0.10	36,43,59,62	0
5	BO3	A	711	4/4	0.93	0.12	29,35,43,49	0
14	CA	B	717	1/1	0.94	0.09	43,43,43,43	0
13	BCN	A	723	11/11	0.94	0.09	27,39,54,56	0
5	BO3	A	709	4/4	0.95	0.13	37,39,46,47	0
8	BJ2	B	710	30/30	0.96	0.06	17,26,39,43	0
5	BO3	B	707	4/4	0.96	0.11	30,35,38,45	0
8	BJ2	A	714	30/30	0.97	0.05	16,22,28,31	0
7	CL	B	709	1/1	0.98	0.05	26,26,26,26	0
14	CA	A	724	1/1	0.99	0.02	24,24,24,24	1
7	CL	A	713	1/1	1.00	0.03	17,17,17,17	0
6	ZN	A	712	1/1	1.00	0.02	18,18,18,18	0
6	ZN	B	708	1/1	1.00	0.02	23,23,23,23	0

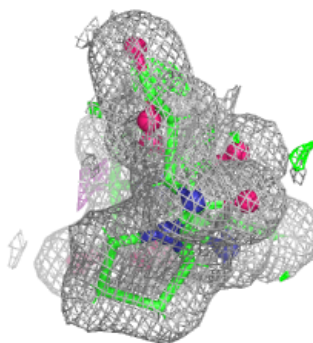
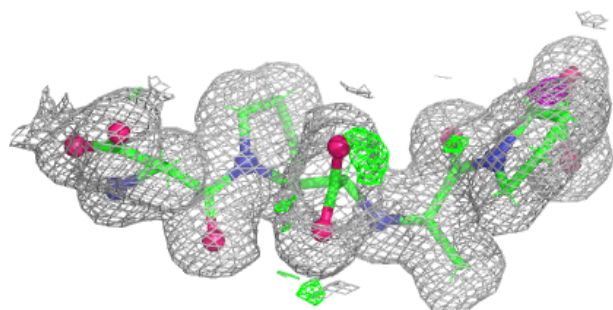
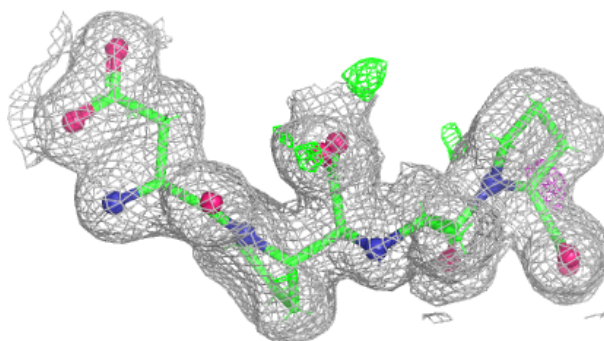
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around BJ2 B 710:

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

**Electron density around BJ2 A 714:**

$2mF_o-DF_c$ (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.