



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 21, 2020 – 04:32 AM BST

PDB ID : 4E1G
Title : X-ray crystal structure of alpha-linolenic acid bound to the cyclooxygenase channel of cyclooxygenase-2
Authors : Vecchio, A.J.; Malkowski, M.G.
Deposited on : 2012-03-06
Resolution : 2.10 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

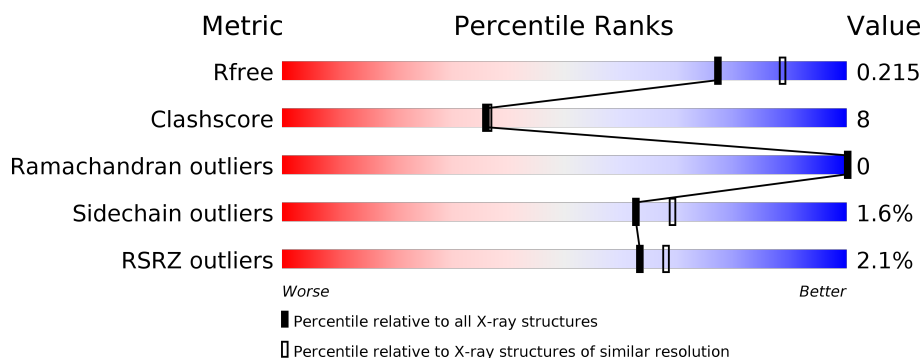
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	610	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>10%</div> </div> </div>
1	B	610	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>9%</div> <div>10%</div> </div> </div>
2	C	2	<div> <div></div> <div>50%</div> <div>50%</div> </div>
2	E	2	<div> <div></div> <div>100%</div> </div>
2	F	2	<div> <div></div> <div>50%</div> <div>50%</div> </div>
3	D	3	<div> <div></div> <div>33%</div> <div>67%</div> </div>

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
2	NAG	C	2	-	-	-	X
2	NAG	E	2	-	-	-	X
2	NAG	F	2	-	-	X	-
3	NAG	D	2	-	-	X	-
4	LNL	A	701	-	-	X	-
4	LNL	B	701	-	-	X	-
8	EDO	B	709	-	-	X	-
9	AKR	A	712	-	-	X	-
9	AKR	A	713	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 9967 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 Prostaglandin G/H synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	551	Total	C	N	O	S	0	5	0
			4436	2871	737	802	26			
1	B	551	Total	C	N	O	S	0	4	0
			4450	2880	741	803	26			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	HIS	-	expression tag	UNP Q05769
A	30	HIS	-	expression tag	UNP Q05769
A	31	HIS	-	expression tag	UNP Q05769
A	32	HIS	-	expression tag	UNP Q05769
A	33	HIS	-	expression tag	UNP Q05769
A	34	HIS	-	expression tag	UNP Q05769
A	594	ALA	ASN	engineered mutation	UNP Q05769
B	29	HIS	-	expression tag	UNP Q05769
B	30	HIS	-	expression tag	UNP Q05769
B	31	HIS	-	expression tag	UNP Q05769
B	32	HIS	-	expression tag	UNP Q05769
B	33	HIS	-	expression tag	UNP Q05769
B	34	HIS	-	expression tag	UNP Q05769
B	594	ALA	ASN	engineered mutation	UNP Q05769

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



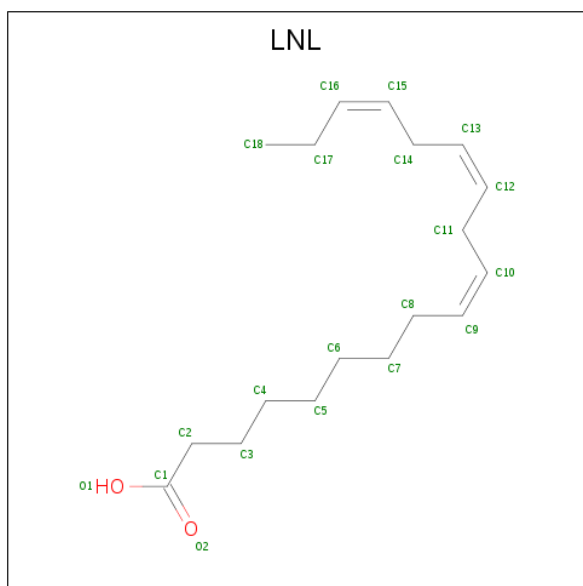
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



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

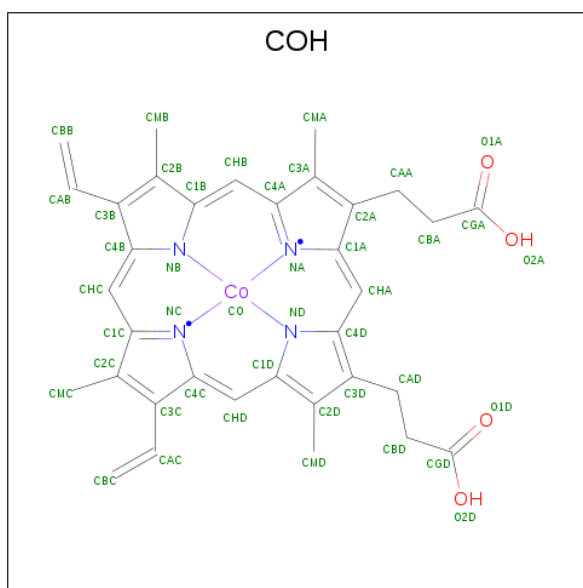
- Molecule 4 is ALPHA-LINOLENIC ACID (three-letter code: LNL) (formula: C₁₈H₃₀O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			20	18	2		
4	B	1	Total	C	O	0	0
			20	18	2		

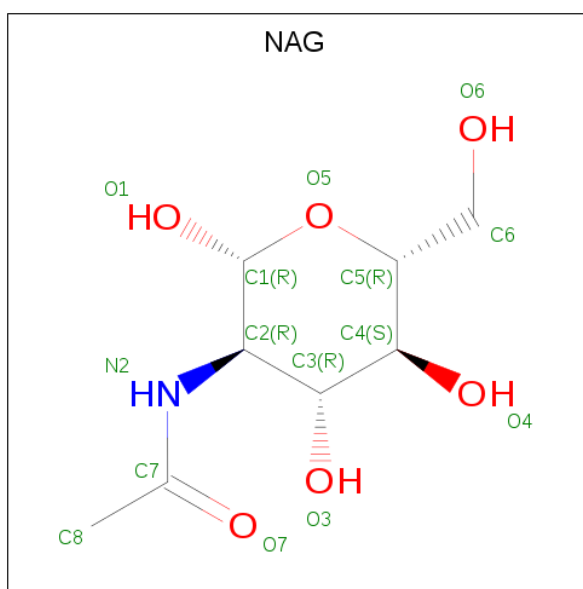
- Molecule 5 is PROTOPORPHYRIN IX CONTAINING CO (three-letter code: COH) (for-

mula: $C_{34}H_{32}CoN_4O_4$).



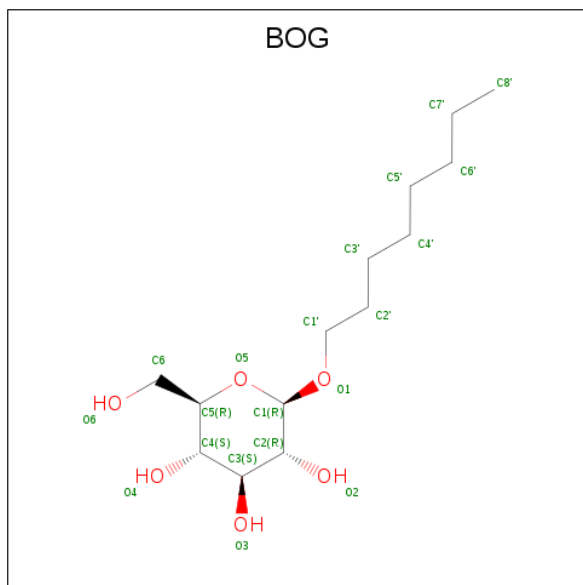
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Co	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Co	N	O	0	0
			43	34	1	4	4		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



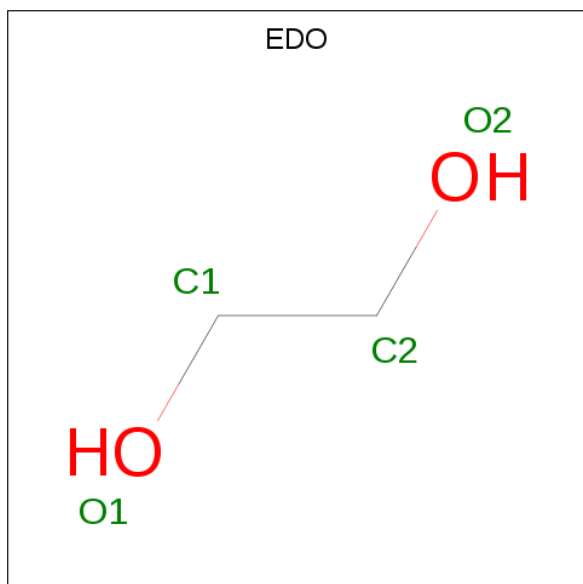
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula: $C_{14}H_{28}O_6$).



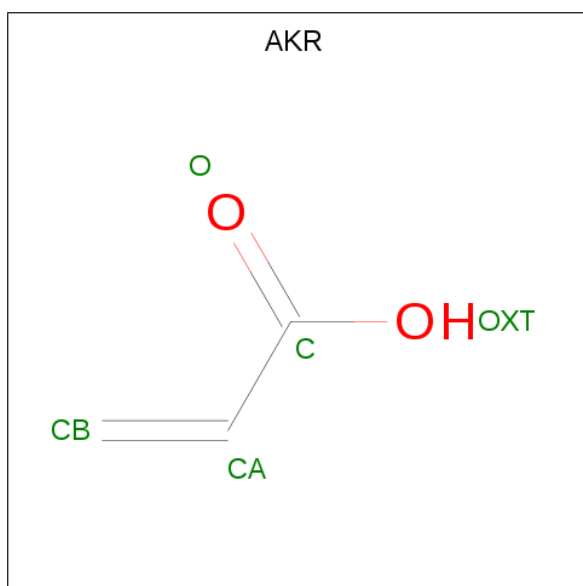
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			20	14	6		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C O 4 2 2	0	0
8	A	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0
8	B	1	Total C O 4 2 2	0	0

- Molecule 9 is ACRYLIC ACID (three-letter code: AKR) (formula: $C_3H_4O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C O 5 3 2	0	0
9	A	1	Total C O 5 3 2	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	395	Total O 395 395	0	0

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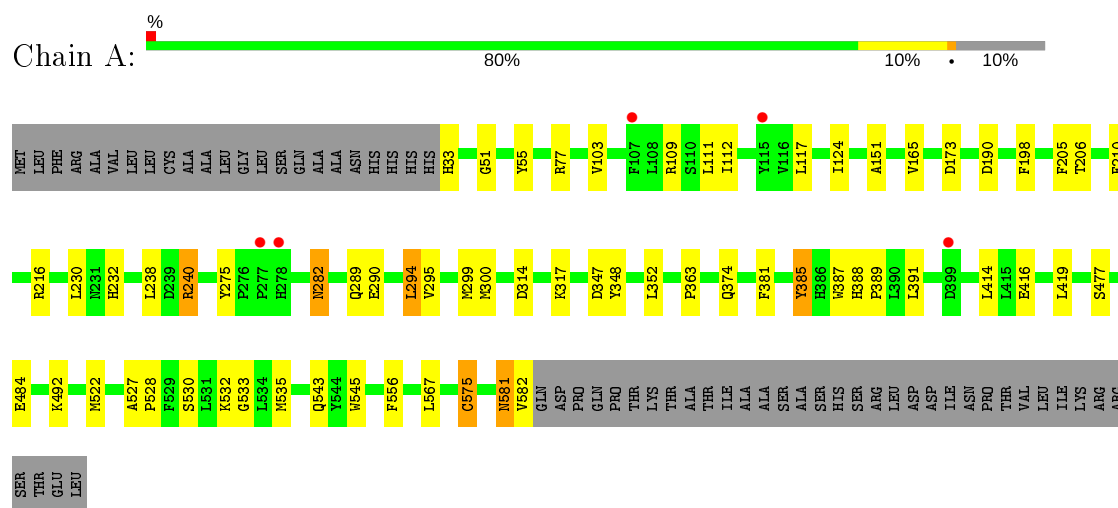
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	351	Total	O	0	0
			351	351		

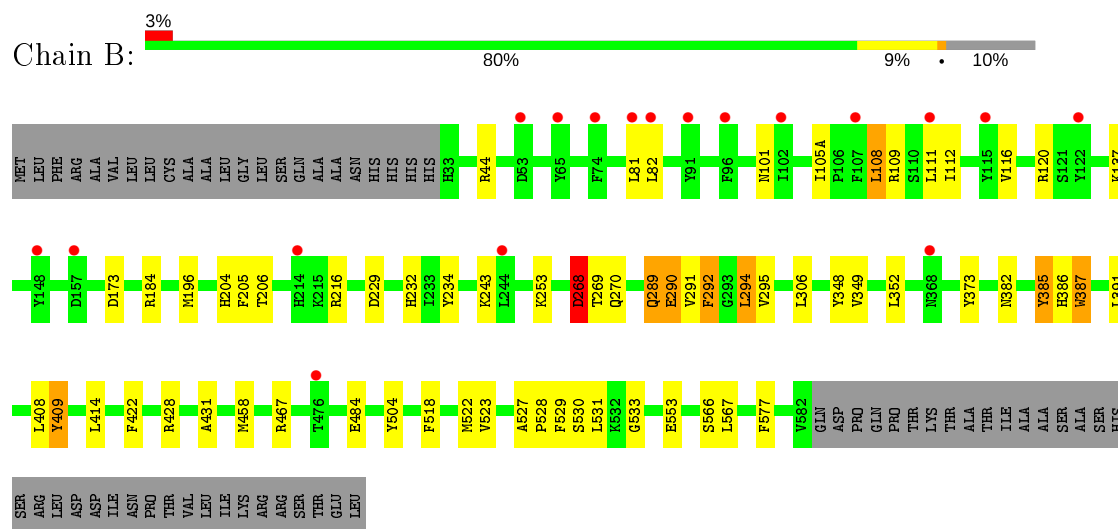
3 Residue-property plots [i](#)

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.

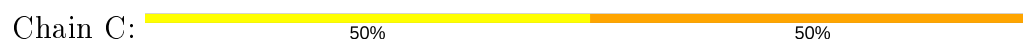
• Molecule 1: Prostaglandin G/H synthase 2



• Molecule 1: Prostaglandin G/H synthase 2



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



MAG1
MAG2

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

Chain E:  100%

MAG1
MAG2

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

Chain D:  33% 67%

MAG1
MAG2
MAG3

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	120.38Å 132.13Å 180.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.95 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.3 (20.00-2.10) 99.4 (19.95-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.159 , 0.203 0.175 , 0.215	Depositor DCC
R_{free} test set	4154 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.2	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9967	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, AKR, EDO, LNL, COH, BOG, MAN

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	1.13	6/4582 (0.1%)	0.92	12/6227 (0.2%)
1	B	1.11	11/4592 (0.2%)	0.94	10/6236 (0.2%)
All	All	1.12	17/9174 (0.2%)	0.93	22/12463 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	575	CYS	CB-SG	6.72	1.93	1.82
1	A	275	TYR	CD2-CE2	6.17	1.48	1.39
1	B	566	SER	CB-OG	5.97	1.50	1.42
1	B	290	GLU	CG-CD	-5.85	1.43	1.51
1	B	529	PHE	CE2-CZ	5.77	1.48	1.37

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	467	ARG	NE-CZ-NH2	-8.78	115.91	120.30
1	B	467	ARG	NE-CZ-NH1	8.15	124.38	120.30
1	A	299	MET	CG-SD-CE	-7.62	88.00	100.20
1	B	294	LEU	CA-CB-CG	6.80	130.94	115.30
1	B	173	ASP	CB-CG-OD2	6.68	124.32	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	581	ASN	Peptide

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	4436	0	4250	68	0
1	B	4450	0	4297	64	0
2	C	28	0	25	1	0
2	E	28	0	25	0	0
2	F	28	0	25	12	0
3	D	39	0	34	9	0
4	A	20	0	29	18	0
4	B	20	0	29	19	0
5	A	43	0	30	3	0
5	B	43	0	30	3	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0
7	A	20	0	28	1	0
8	A	8	0	12	2	0
8	B	20	0	30	6	0
9	A	10	0	6	6	0
10	A	395	0	0	12	0
10	B	351	0	0	3	0
All	All	9967	0	8876	145	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 145 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:581:ASN:HB2	10:A:1184:HOH:O	1.39	1.19
1:A:205:PHE:HE2	4:A:701:LNL:H13	1.04	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:ARG:NH1	3:D:2:NAG:H83	1.54	1.17
4:B:701:LNL:C5	4:B:701:LNL:H9	1.62	1.16
4:B:701:LNL:H51	4:B:701:LNL:H9	1.23	1.15

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	554/610 (91%)	535 (97%)	19 (3%)	0	100	100
1	B	553/610 (91%)	539 (98%)	14 (2%)	0	100	100
All	All	1107/1220 (91%)	1074 (97%)	33 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	475/542 (88%)	469 (99%)	6 (1%)	69	75
1	B	480/542 (89%)	471 (98%)	9 (2%)	57	63
All	All	955/1084 (88%)	940 (98%)	15 (2%)	62	69

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	81	LEU
1	B	82	LEU
1	B	289	GLN
1	A	556	PHE
1	B	268	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	A	400	GLN
1	B	289	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 ⓘ

9 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	0.86	0	17,19,21	2.04	5 (29%)
2	NAG	C	2	2	14,14,15	0.62	0	17,19,21	1.72	3 (17%)
3	NAG	D	1	1,3	14,14,15	1.03	1 (7%)	17,19,21	1.84	7 (41%)
3	NAG	D	2	3	14,14,15	0.80	0	17,19,21	2.28	5 (29%)
3	MAN	D	3	3	11,11,12	0.64	0	15,15,17	2.08	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	E	1	1,2	14,14,15	2.47	1 (7%)	17,19,21	3.33	7 (41%)
2	NAG	E	2	2	14,14,15	0.85	1 (7%)	17,19,21	1.42	2 (11%)
2	NAG	F	1	1,2	14,14,15	0.86	0	17,19,21	1.68	5 (29%)
2	NAG	F	2	2	14,14,15	0.97	0	17,19,21	2.79	6 (35%)

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	NAG	C	2	2	-	2/6/23/26	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	3/6/23/26	0/1/1/1
3	MAN	D	3	3	-	1/2/19/22	1/1/1/1
2	NAG	E	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	E	2	2	-	2/6/23/26	0/1/1/1
2	NAG	F	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	F	2	2	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	NAG	O5-C1	-8.74	1.29	1.43
2	E	2	NAG	O5-C1	-2.18	1.40	1.43
3	D	1	NAG	O5-C5	-2.04	1.39	1.43

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	NAG	C1-O5-C5	-10.13	98.46	112.19
2	F	2	NAG	C1-O5-C5	-6.42	103.50	112.19
3	D	3	MAN	C1-O5-C5	5.69	119.90	112.19
2	E	1	NAG	O5-C5-C6	5.65	116.06	107.20
2	F	2	NAG	O5-C5-C6	5.07	115.15	107.20

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	F	2	NAG	C8-C7-N2-C2
2	F	2	NAG	O7-C7-N2-C2
3	D	2	NAG	C8-C7-N2-C2

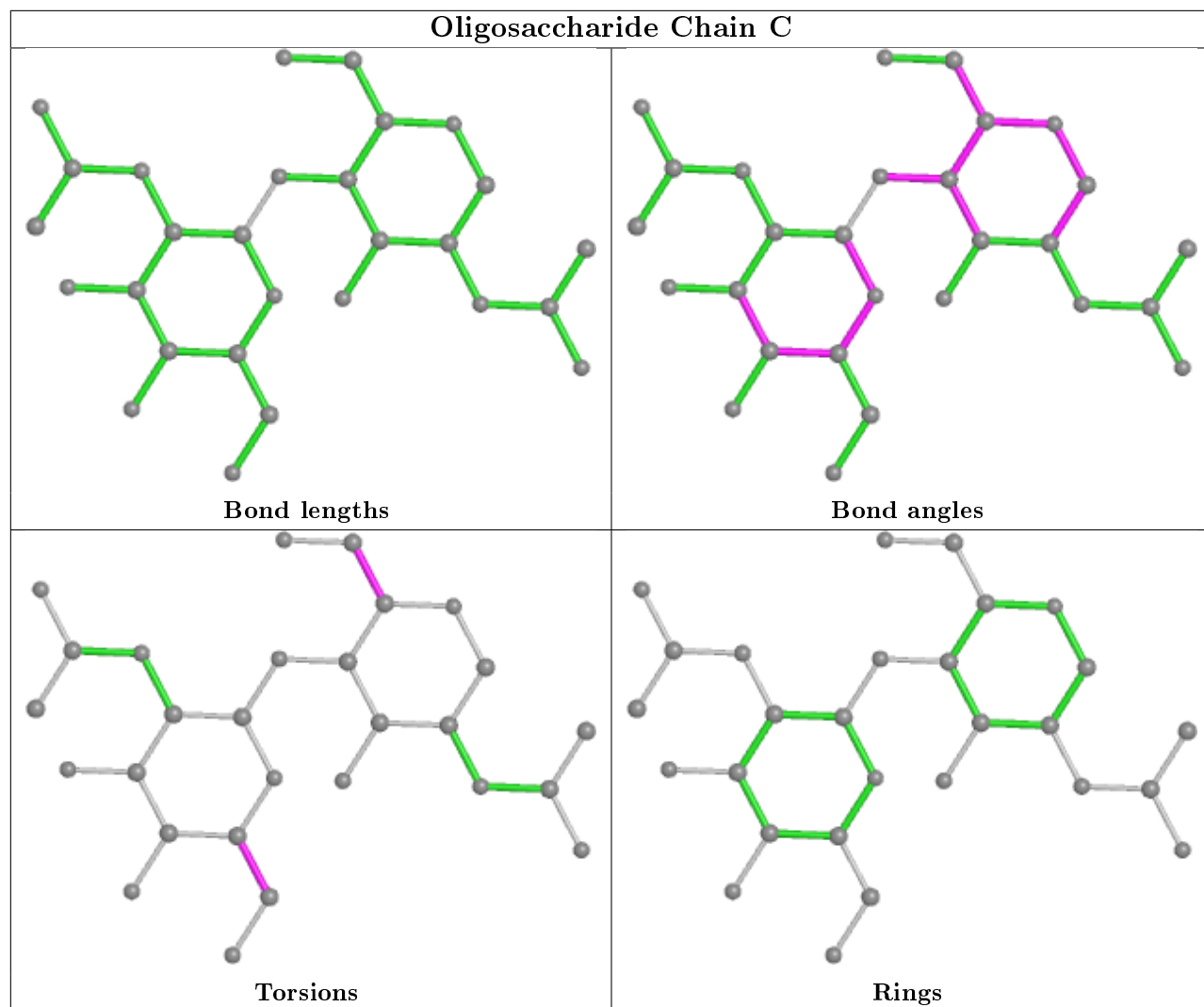
All (1) ring outliers are listed below:

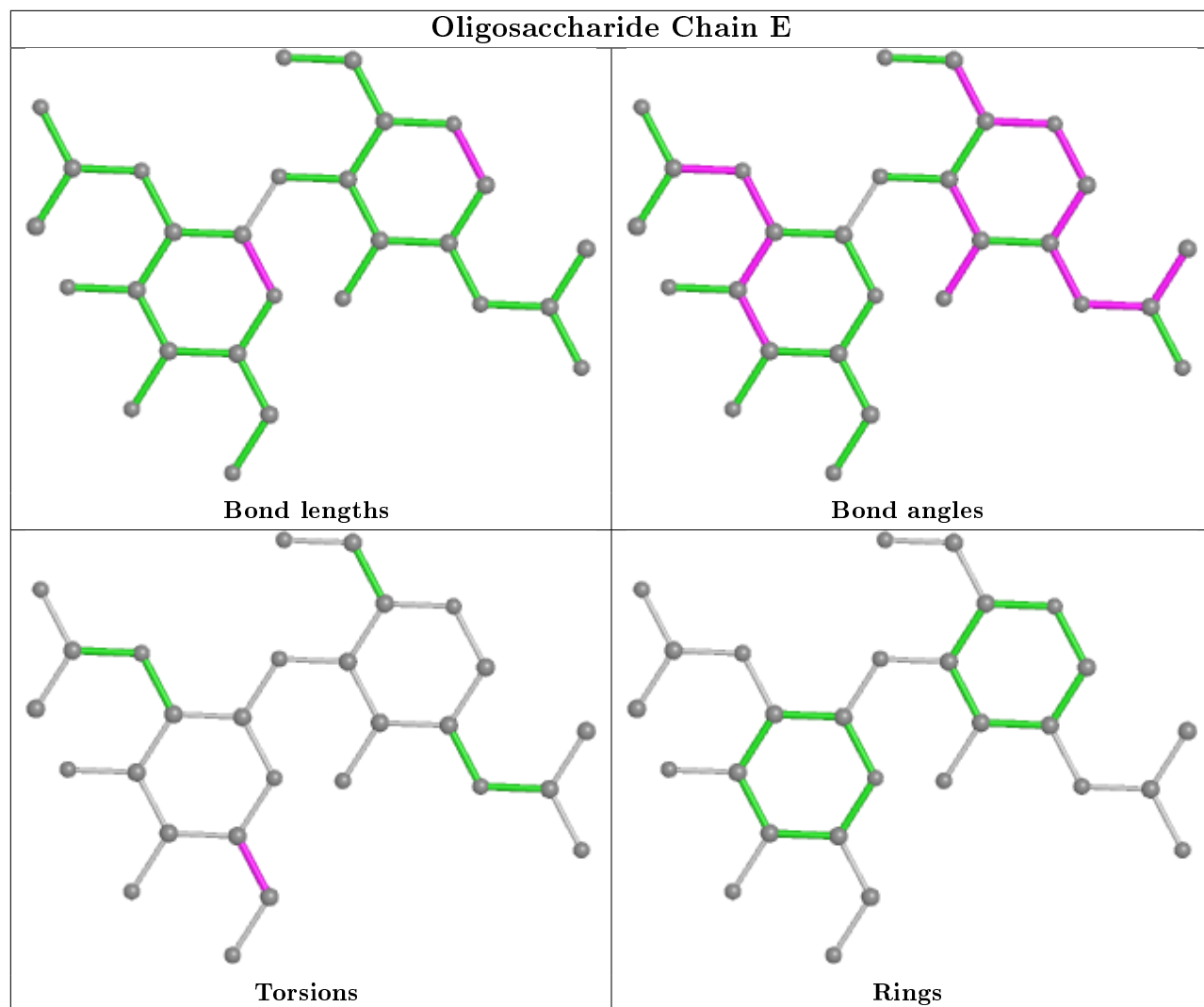
Mol	Chain	Res	Type	Atoms
3	D	3	MAN	C1-C2-C3-C4-C5-O5

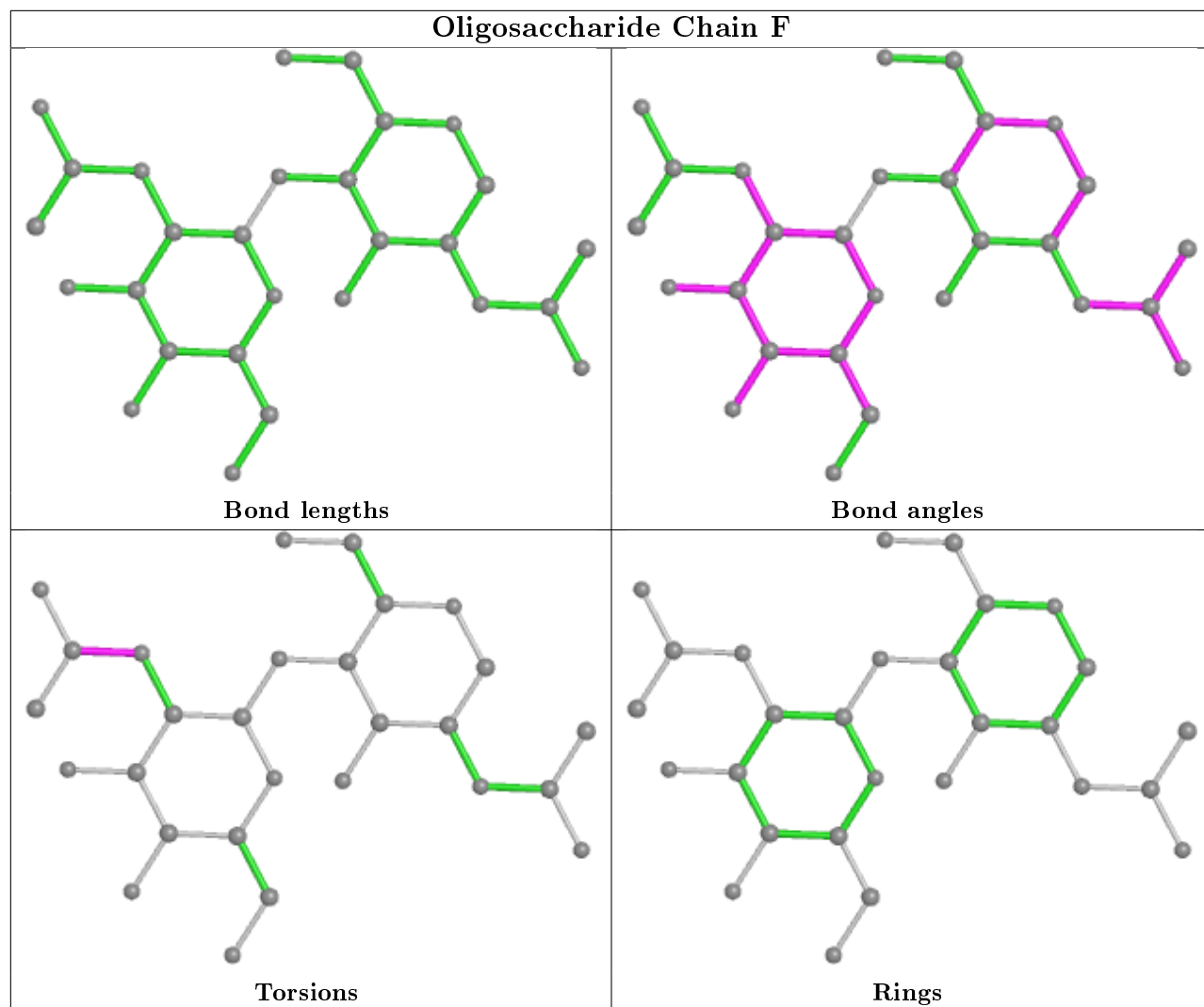
4 monomers are involved in 22 short contacts:

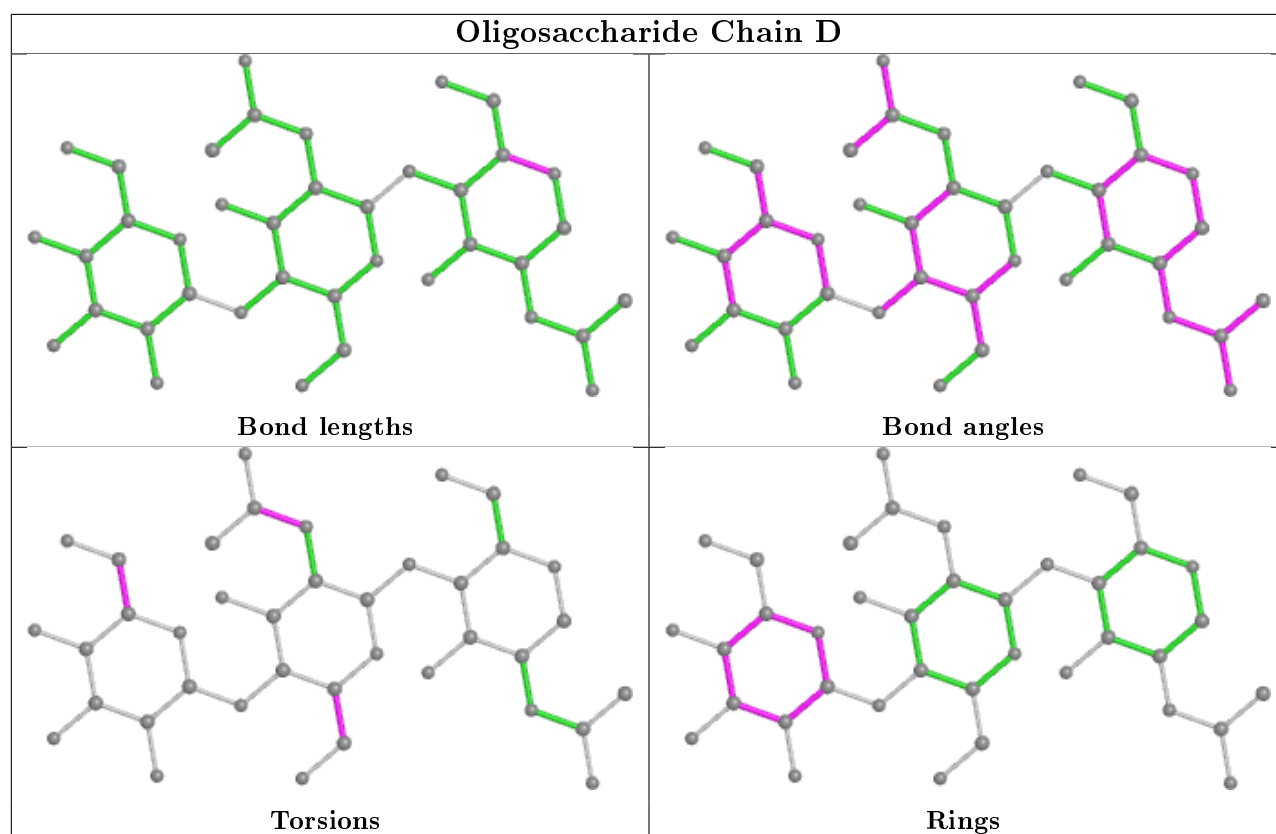
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	NAG	1	0
3	D	3	MAN	2	0
2	F	2	NAG	12	0
3	D	2	NAG	7	0

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](#)

16 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
8	EDO	B	709	-	3,3,3	0.11	0	2,2,2	1.72	1 (50%)
9	AKR	A	713	-	1,4,4	1.97	0	0,4,4	0.00	-
5	COH	A	702	1	31,50,50	5.50	23 (74%)	23,82,82	4.84	12 (52%)
4	LNL	A	701	-	16,19,19	1.73	3 (18%)	14,19,19	1.35	3 (21%)
8	EDO	B	710	-	3,3,3	0.66	0	2,2,2	0.36	0
6	NAG	B	707	1	14,14,15	0.68	0	17,19,21	1.45	4 (23%)
9	AKR	A	712	-	1,4,4	1.63	0	0,4,4	0.00	-
8	EDO	A	711	-	3,3,3	0.60	0	2,2,2	0.42	0
8	EDO	B	711	-	3,3,3	0.49	0	2,2,2	0.89	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	EDO	A	710	-	3,3,3	1.06	0	2,2,2	1.03	0
8	EDO	B	708	-	3,3,3	0.96	0	2,2,2	1.16	0
4	LNL	B	701	-	16,19,19	1.85	3 (18%)	14,19,19	0.81	0
8	EDO	B	712	-	3,3,3	0.57	0	2,2,2	0.36	0
7	BOG	A	709	-	20,20,20	0.87	1 (5%)	25,25,25	0.89	1 (4%)
6	NAG	A	708	1	14,14,15	0.78	0	17,19,21	2.02	4 (23%)
5	COH	B	702	1	31,50,50	5.61	24 (77%)	23,82,82	4.89	11 (47%)

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	EDO	B	709	-	-	1/1/1/1	-
9	AKR	A	713	-	-	0/0/2/2	-
5	COH	A	702	1	-	3/8/94/94	-
4	LNL	A	701	-	-	5/15/17/17	-
8	EDO	B	710	-	-	0/1/1/1	-
6	NAG	B	707	1	-	2/6/23/26	0/1/1/1
9	AKR	A	712	-	-	0/0/2/2	-
8	EDO	A	711	-	-	0/1/1/1	-
8	EDO	B	711	-	-	1/1/1/1	-
8	EDO	A	710	-	-	1/1/1/1	-
8	EDO	B	708	-	-	1/1/1/1	-
4	LNL	B	701	-	-	9/15/17/17	-
8	EDO	B	712	-	-	0/1/1/1	-
7	BOG	A	709	-	-	2/11/31/31	0/1/1/1
6	NAG	A	708	1	-	0/6/23/26	0/1/1/1
5	COH	B	702	1	-	5/8/94/94	-

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	702	COH	C1D-ND	12.56	1.41	1.34
5	B	702	COH	C1D-ND	12.53	1.41	1.34
5	B	702	COH	C4B-NB	11.39	1.40	1.34
5	A	702	COH	C4D-ND	11.00	1.40	1.34
5	B	702	COH	C4D-ND	10.88	1.40	1.34

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	702	COH	CHC-C1C-NC	11.31	126.77	110.12
5	B	702	COH	CHB-C4A-NA	11.04	126.37	110.12
5	B	702	COH	CHD-C4C-NC	10.94	126.22	110.12
5	A	702	COH	CHB-C4A-NA	10.87	126.12	110.12
5	A	702	COH	CHA-C1A-NA	10.25	125.21	110.12

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	702	COH	C1A-C2A-CAA-CBA
5	A	702	COH	C3A-C2A-CAA-CBA
4	B	701	LNL	C1-C2-C3-C4
5	A	702	COH	C2A-CAA-CBA-CGA
5	B	702	COH	C2A-CAA-CBA-CGA

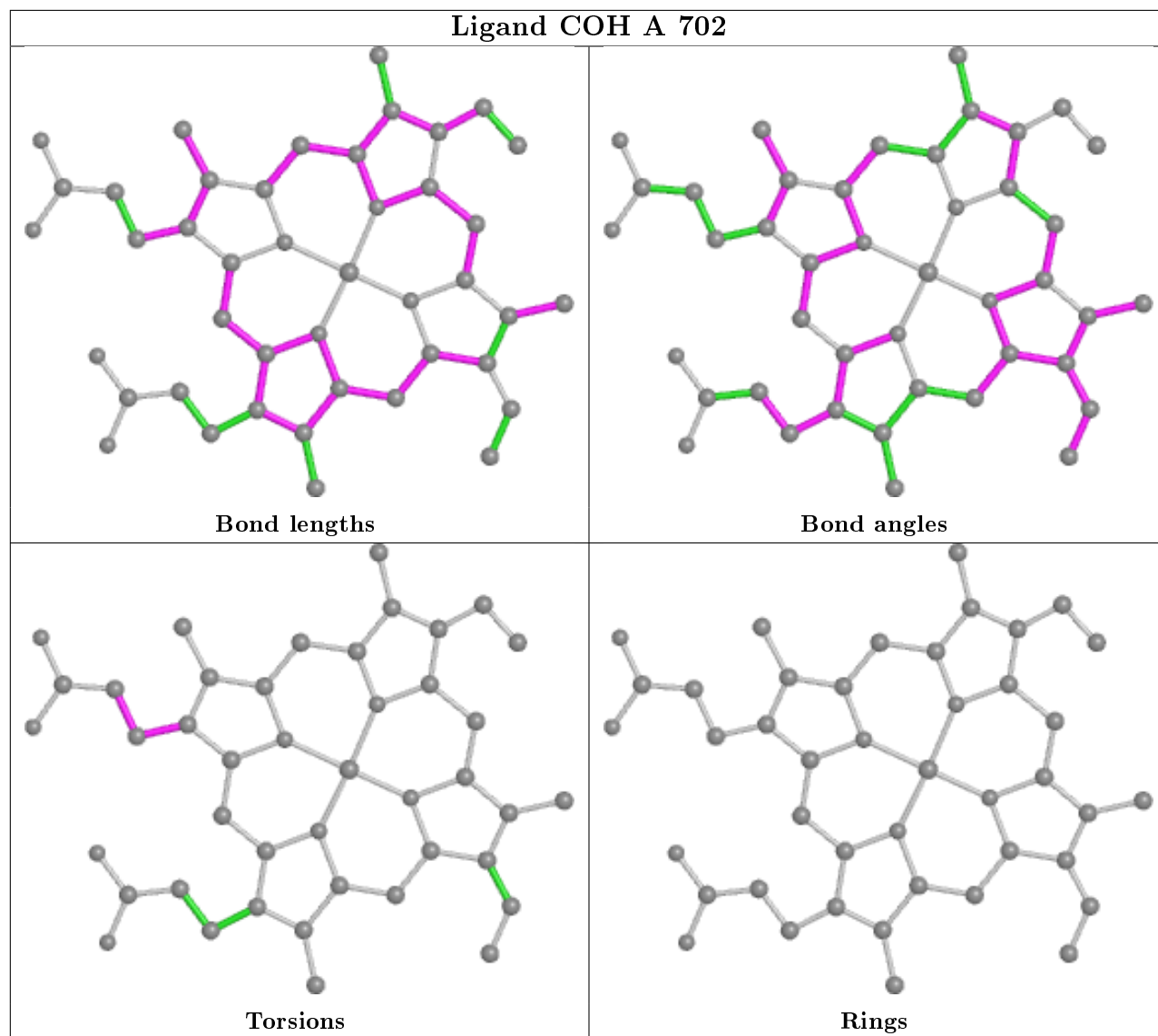
There are no ring outliers.

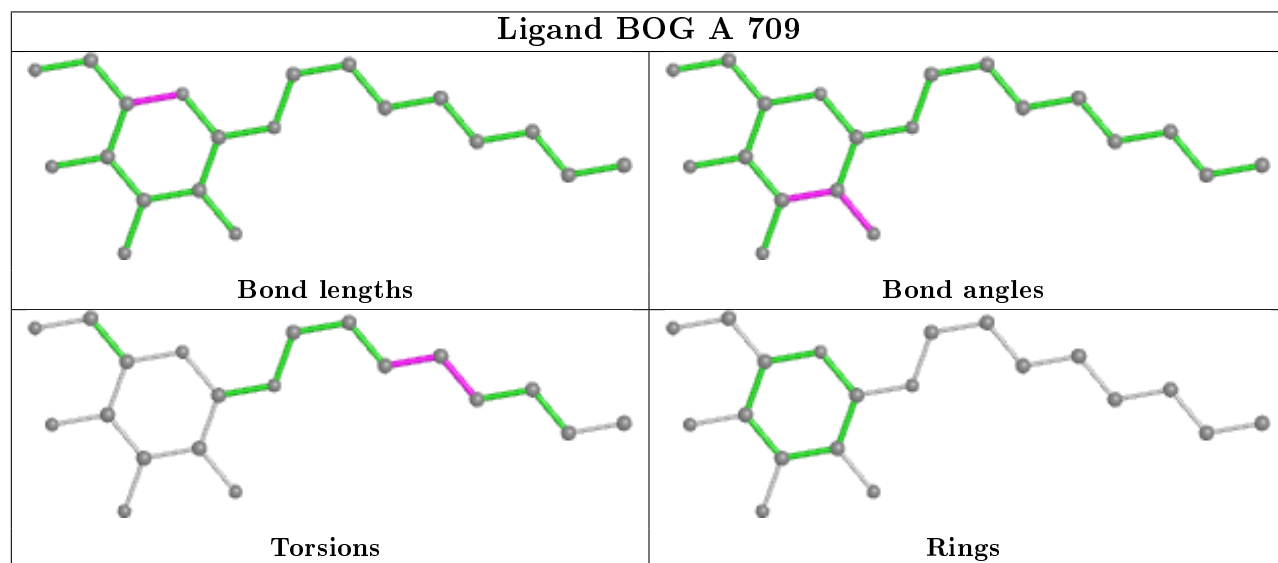
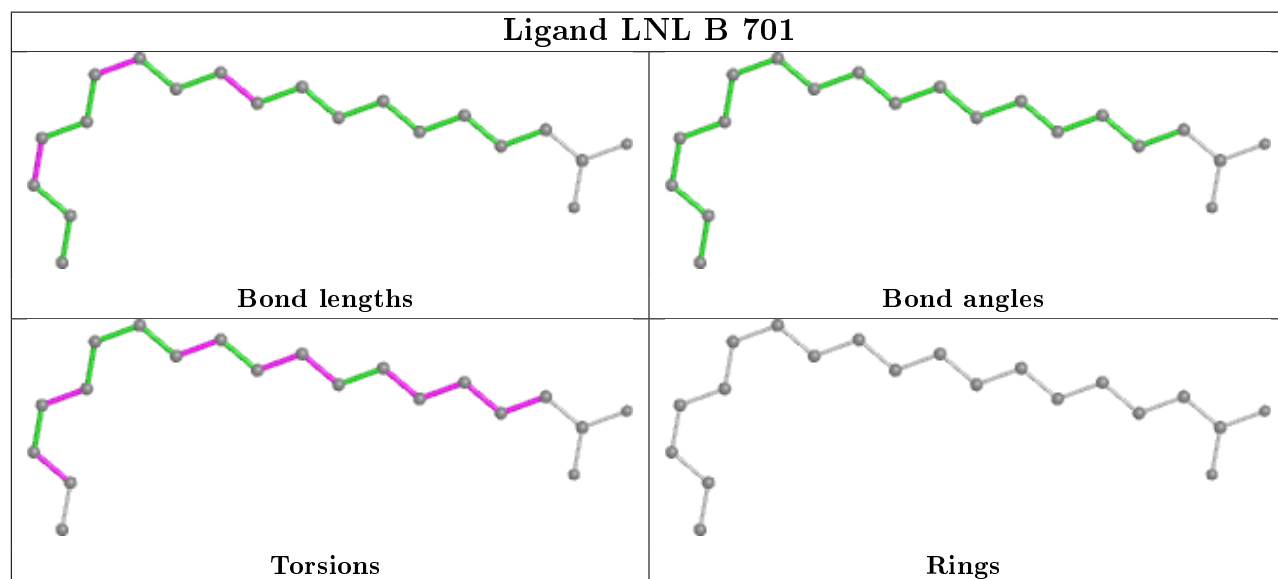
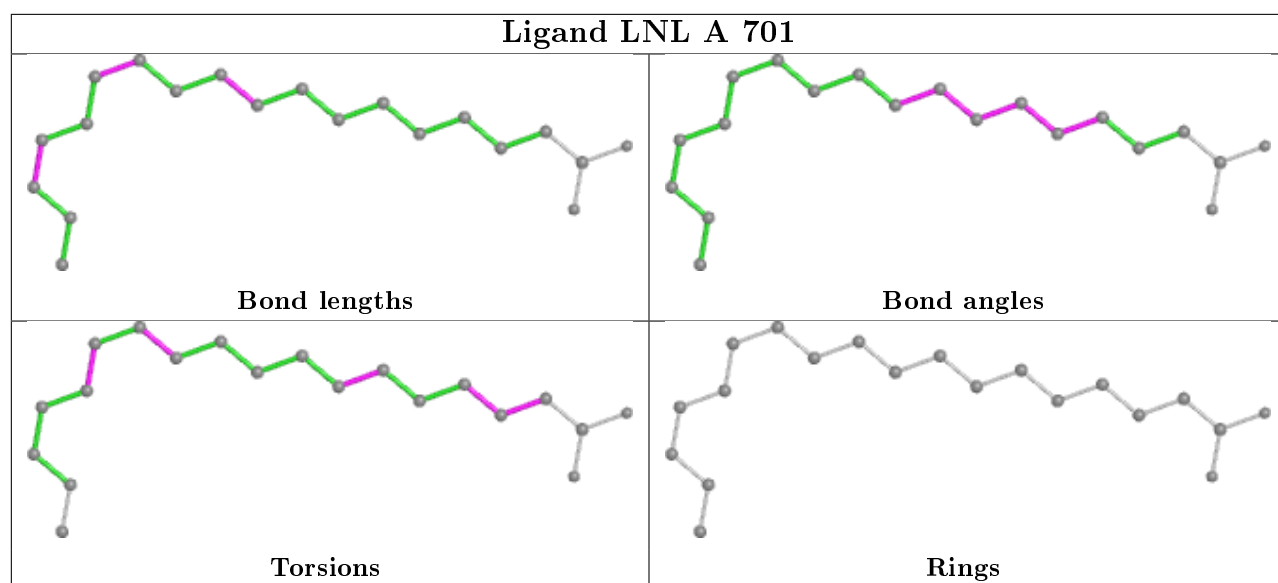
11 monomers are involved in 58 short contacts:

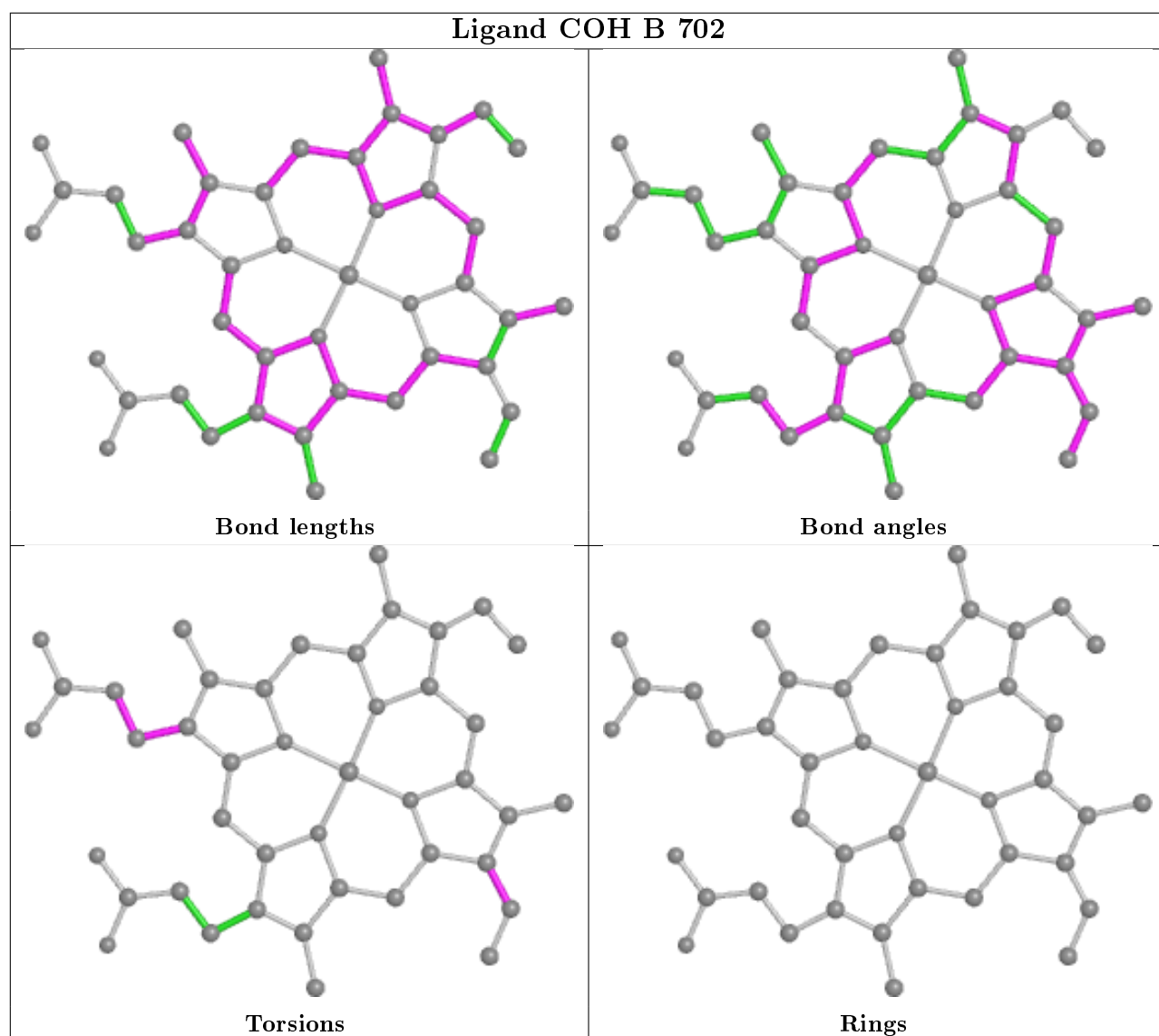
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	709	EDO	4	0
9	A	713	AKR	3	0
5	A	702	COH	3	0
4	A	701	LNL	18	0
9	A	712	AKR	3	0
8	A	711	EDO	2	0
8	B	711	EDO	1	0
4	B	701	LNL	19	0
8	B	712	EDO	1	0
7	A	709	BOG	1	0
5	B	702	COH	3	0

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	551/610 (90%)	-0.39	5 (0%) 84 86	15, 25, 39, 52	0
1	B	551/610 (90%)	-0.11	18 (3%) 46 53	17, 29, 46, 54	0
All	All	1102/1220 (90%)	-0.25	23 (2%) 63 68	15, 27, 44, 54	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	82	LEU	5.2
1	B	91	TYR	4.6
1	B	122	TYR	4.2
1	B	102	ILE	4.1
1	B	81	LEU	4.1

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

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

6.3 Carbohydrates ⓘ

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.

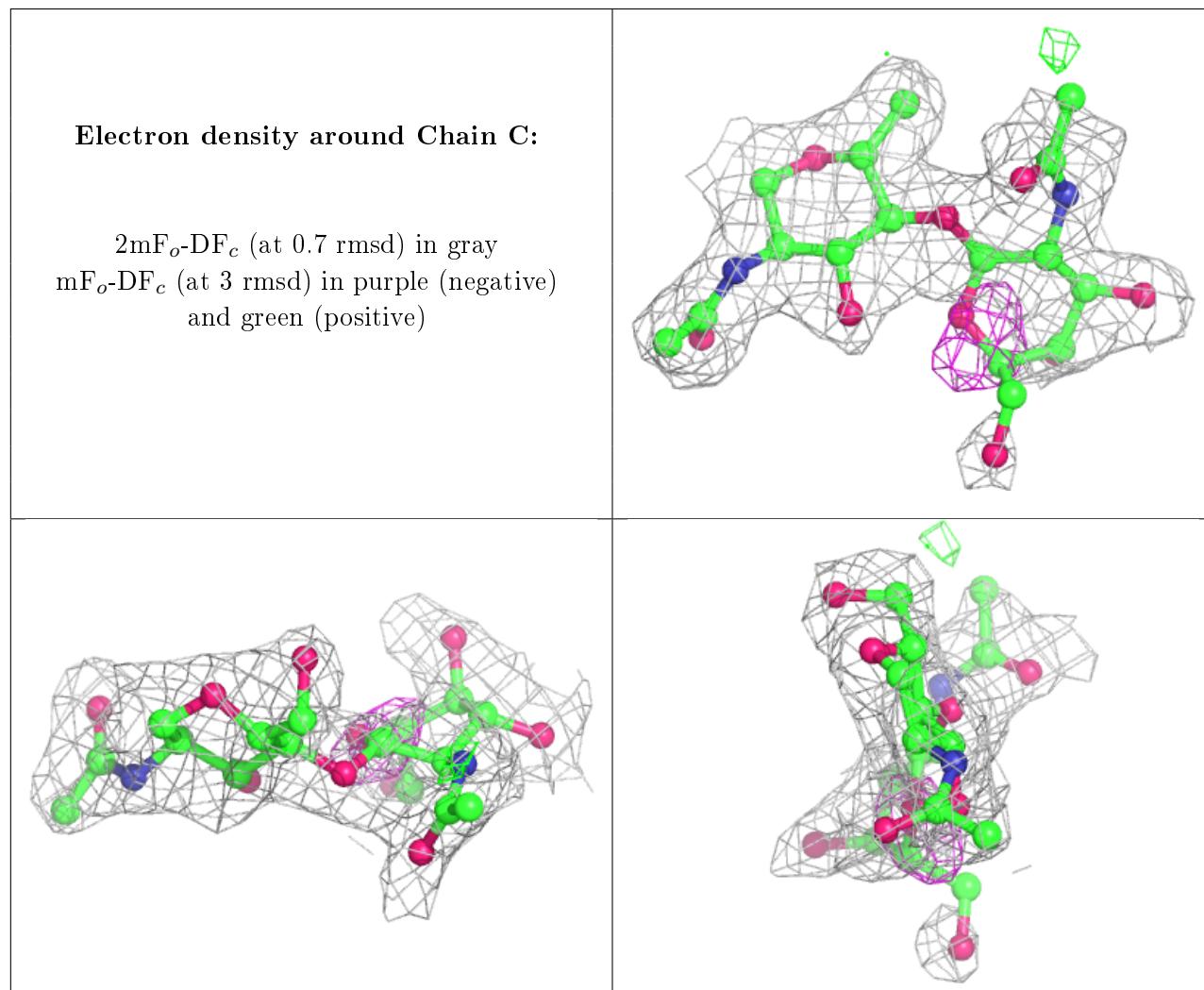
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	C	2	14/15	0.59	0.43	69,73,74,76	0
3	MAN	D	3	11/12	0.73	0.38	65,70,73,74	0
2	NAG	E	2	14/15	0.77	0.42	72,76,78,80	0
2	NAG	E	1	14/15	0.79	0.29	46,52,58,66	0
2	NAG	F	2	14/15	0.81	0.30	37,49,56,58	0

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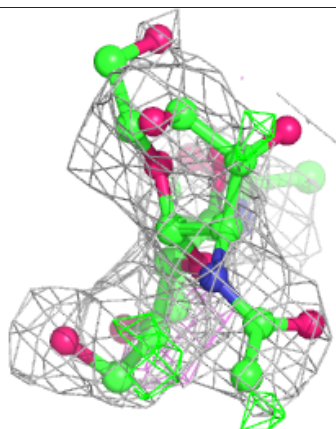
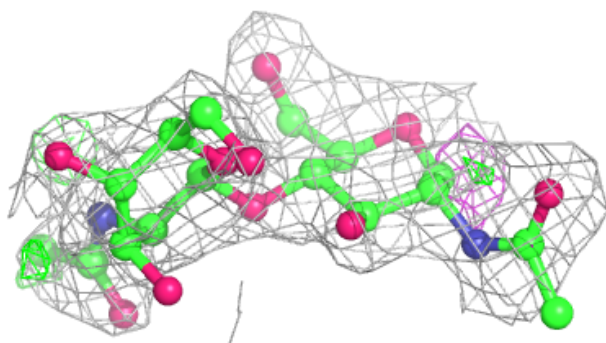
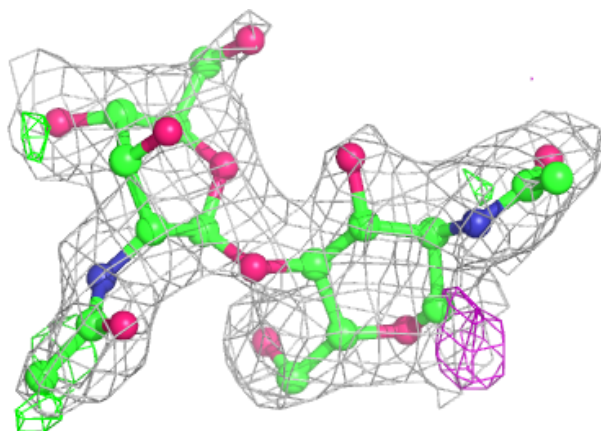
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	C	1	14/15	0.90	0.21	42,49,56,61	0
3	NAG	D	2	14/15	0.91	0.16	33,43,49,59	0
3	NAG	D	1	14/15	0.96	0.08	24,29,34,35	0
2	NAG	F	1	14/15	0.97	0.08	21,27,29,37	0

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.



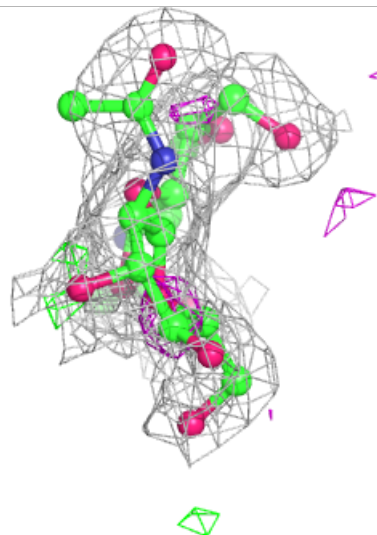
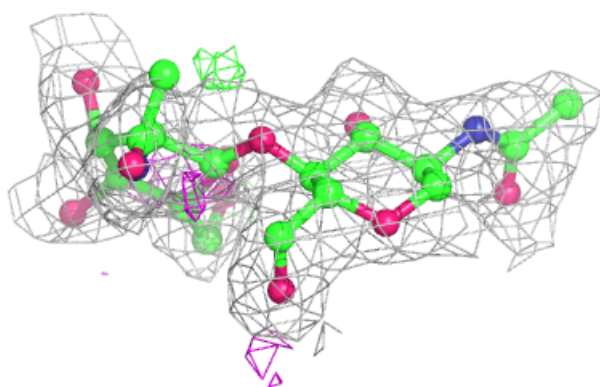
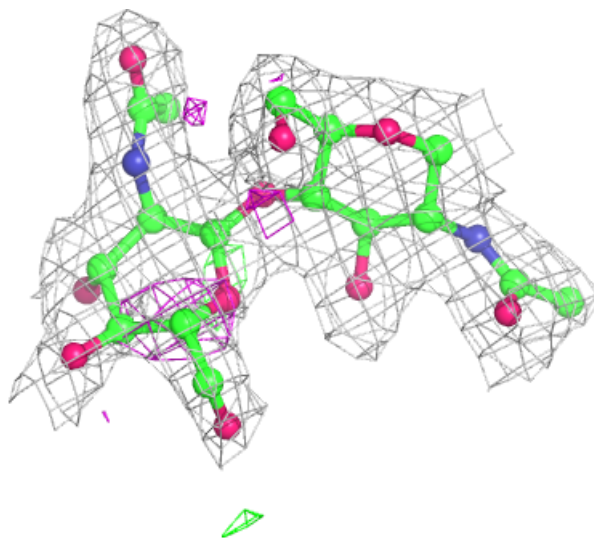
Electron density around Chain E:

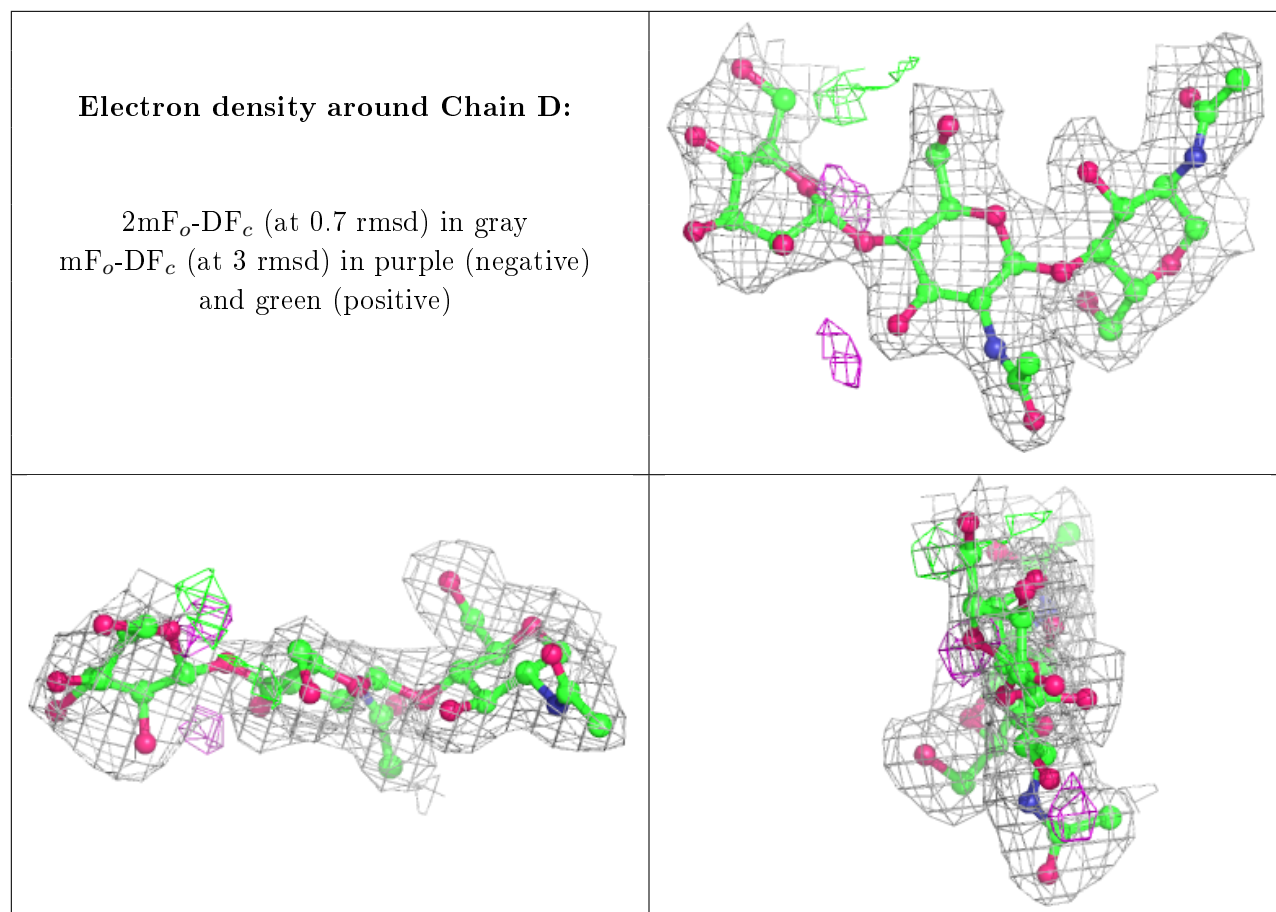
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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
5	COH	B	702	43/43	0.70	0.29	61,75,82,85	0
5	COH	A	702	43/43	0.74	0.25	61,76,86,88	0
4	LNL	B	701	20/20	0.77	0.23	32,52,63,65	0
6	NAG	B	707	14/15	0.80	0.32	56,62,65,66	0
4	LNL	A	701	20/20	0.81	0.23	36,47,55,56	0
6	NAG	A	708	14/15	0.90	0.27	43,47,52,54	0
9	AKR	A	713	5/5	0.92	0.24	42,43,44,45	0
9	AKR	A	712	5/5	0.93	0.17	42,43,44,45	0
8	EDO	B	709	4/4	0.93	0.16	43,44,46,47	0
8	EDO	B	711	4/4	0.95	0.09	43,44,45,46	0
7	BOG	A	709	20/20	0.95	0.10	28,34,39,40	0
8	EDO	B	710	4/4	0.96	0.12	23,26,28,32	0

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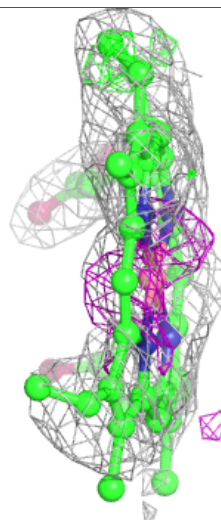
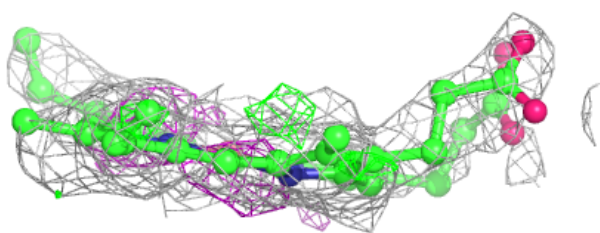
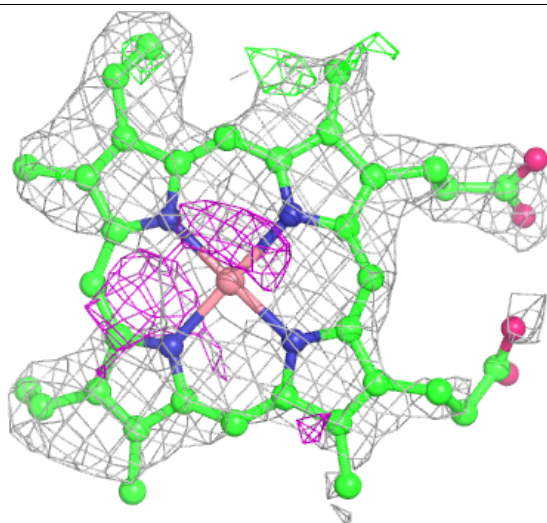
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	EDO	A	710	4/4	0.96	0.13	29,30,33,39	0
8	EDO	B	708	4/4	0.96	0.10	29,31,34,42	0
8	EDO	A	711	4/4	0.97	0.10	26,27,30,30	0
8	EDO	B	712	4/4	0.97	0.09	25,26,30,33	0

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.

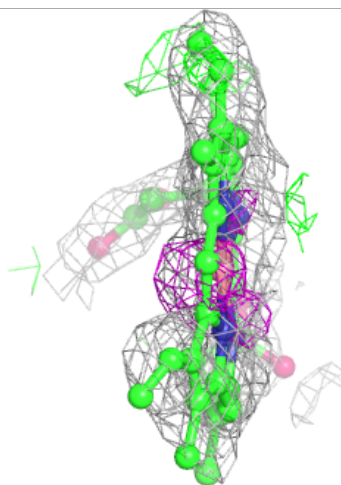
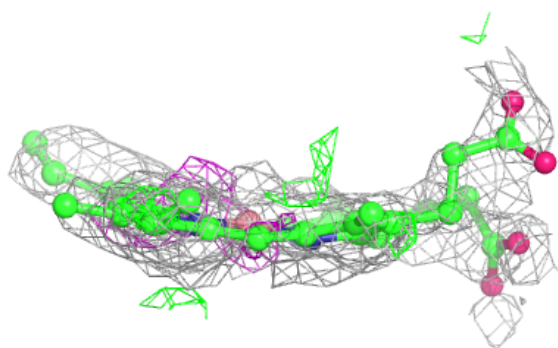
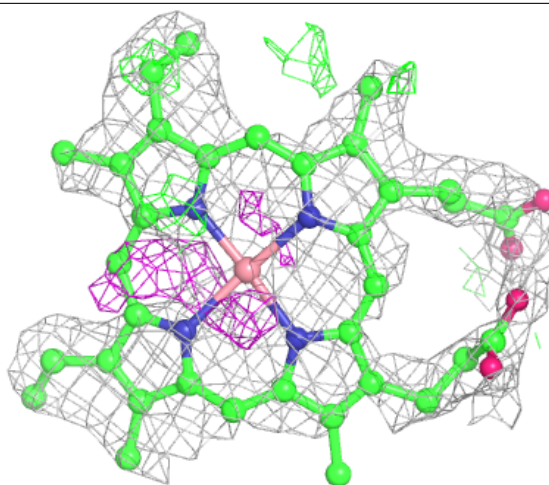
Electron density around COH B 702:

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



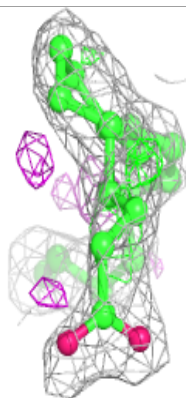
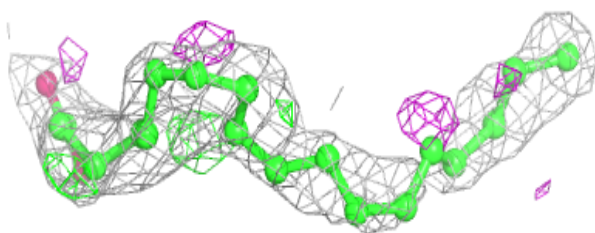
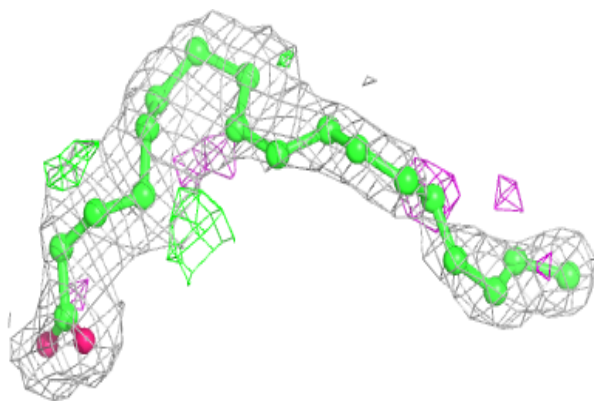
Electron density around COH A 702:

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

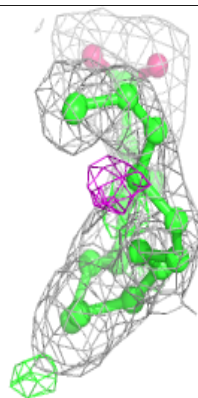
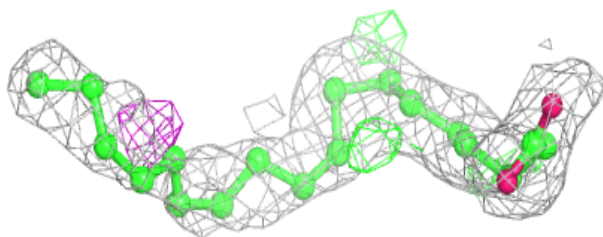
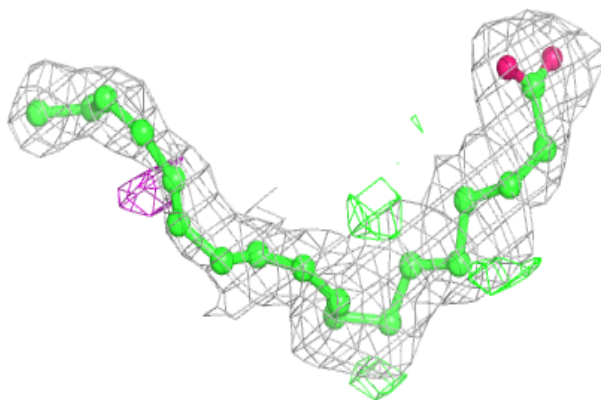


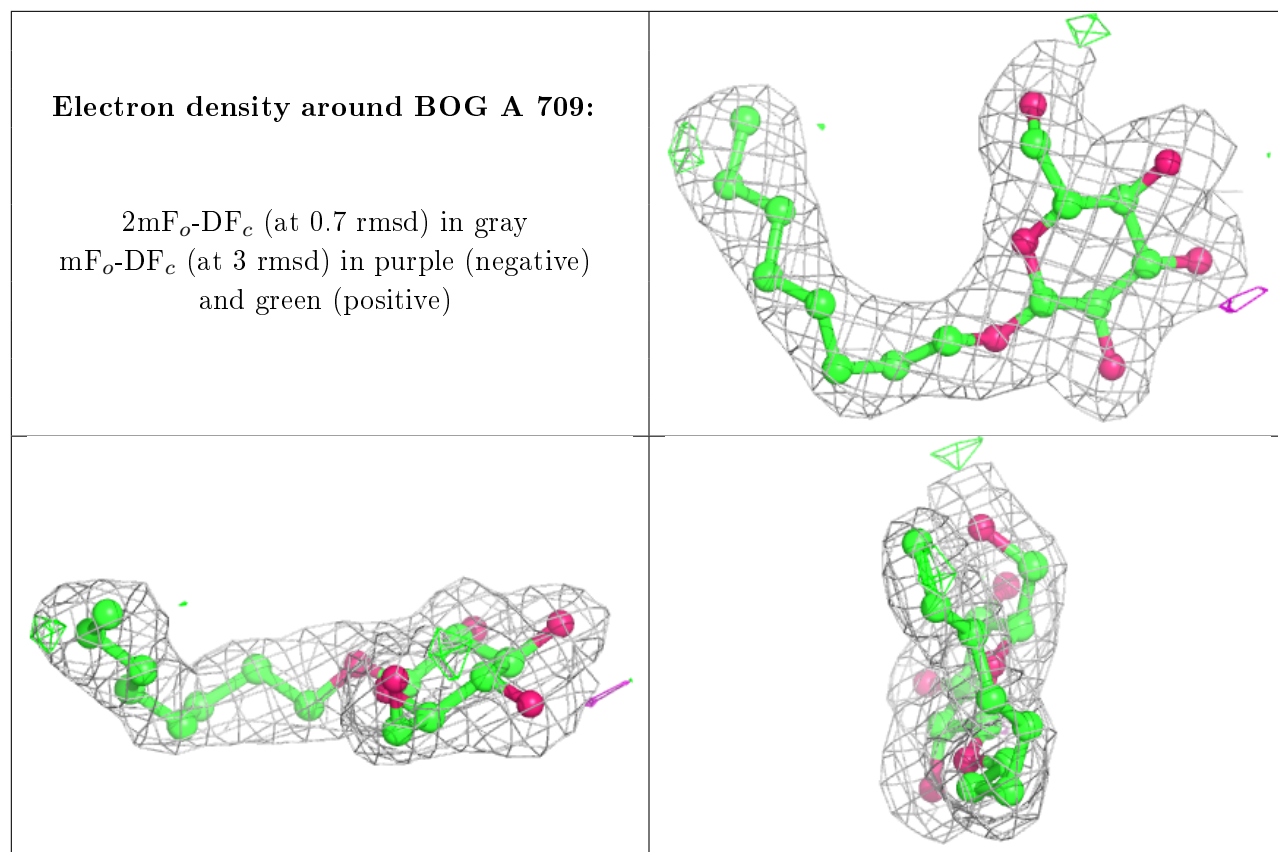
Electron density around LNL B 701:

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

**Electron density around LNL A 701:**

$2mF_o-DF_c$ (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.