



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 07:09 PM BST

PDB ID : 3N8F  
Title : Crystal structure of the complex of goat lactoperoxidase with thiocyanate at 3.2 Å resolution  
Authors : Vikram, G.; Singh, A.K.; Singh, R.P.; Sinha, M.; Kaur, P.; Sharma, S.; Singh, T.P.  
Deposited on : 2010-05-28  
Resolution : 3.25 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](mailto: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.

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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



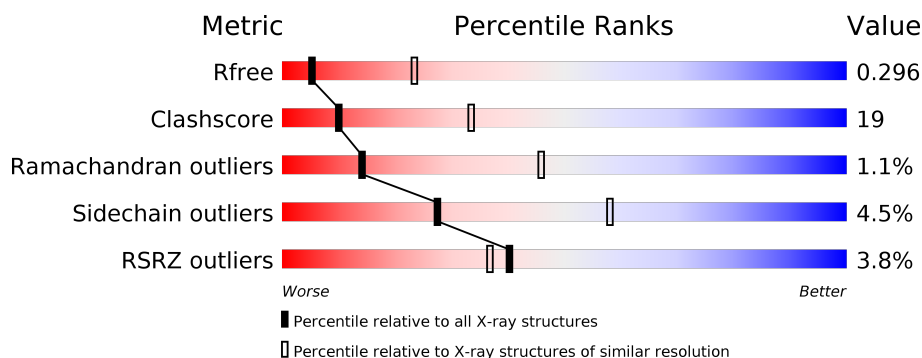
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.25 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	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)


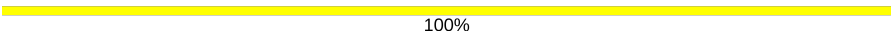
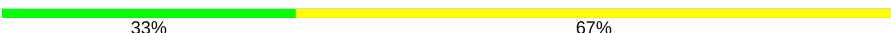
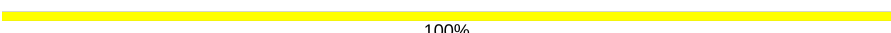
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria 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	595	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>26%</div> <div>.</div> </div> </div>
1	B	595	<div> <div>4%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>..</div> </div> </div>
2	C	2	<div> <div></div> <div>100%</div> </div>
2	E	2	<div> <div></div> <div>100%</div> </div>
2	F	2	<div> <div></div> <div>100%</div> </div>
2	G	2	<div> <div></div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
2	I	2	 50% 50%
2	J	2	 100%
3	D	3	 33% 67%
3	H	3	 100%

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	1	-	-	-	X
2	NAG	F	2	-	-	-	X
2	NAG	G	2	-	-	-	X
2	NAG	J	2	-	-	-	X
3	BMA	D	3	-	-	-	X
3	NAG	H	2	-	-	-	X
3	BMA	H	3	-	-	-	X
6	SCN	B	902	-	-	X	X
7	HEM	A	801	-	-	X	-



## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10057 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 Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	P	S	0	0	0
			4757	3021	844	865	1	26			
1	B	595	Total	C	N	O	P	S	0	0	0
			4757	3021	844	865	1	26			

- 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			
2	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

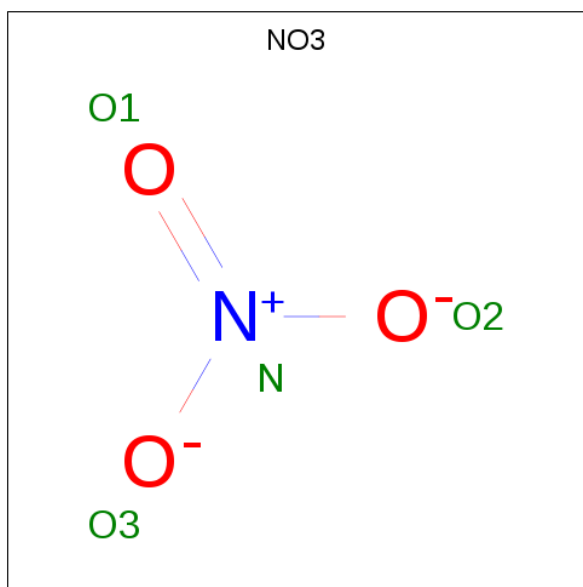
- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.





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

- Molecule 4 is NITRATE ION (three-letter code: NO3) (formula: NO<sub>3</sub>).



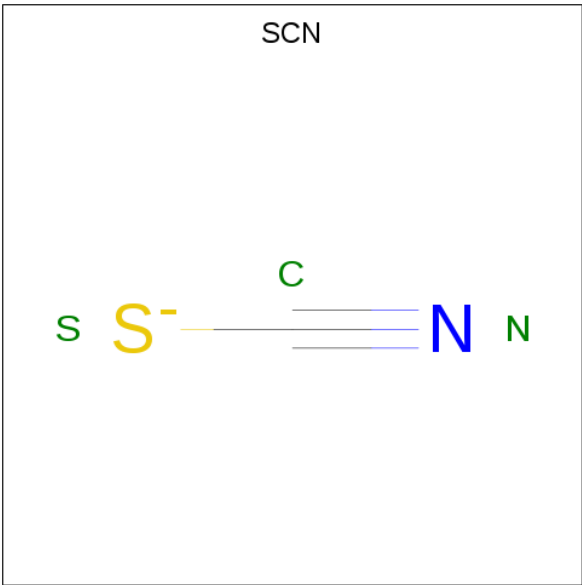
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	N	O	0	0
			4	1	3		
4	A	1	Total	N	O	0	0
			4	1	3		
4	B	1	Total	N	O	0	0
			4	1	3		
4	B	1	Total	N	O	0	0
			4	1	3		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		
5	A	1	Total	Ca	0	0
			1	1		

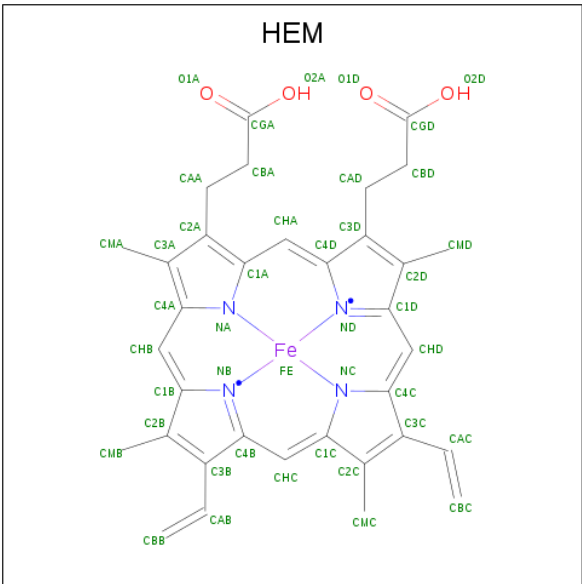
- Molecule 6 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	S	0	0
			3	1	1	1		
6	B	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 8 is water.

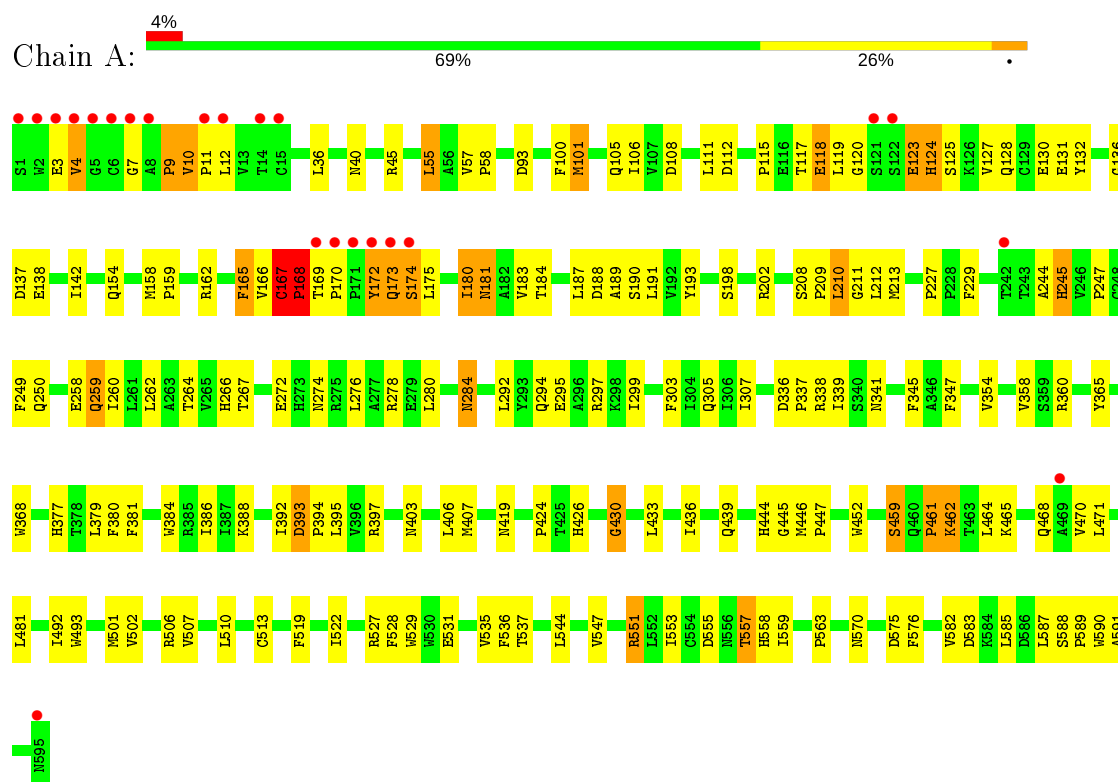
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	87	Total	O	0	0
			87	87		
8	B	100	Total	O	0	0
			100	100		



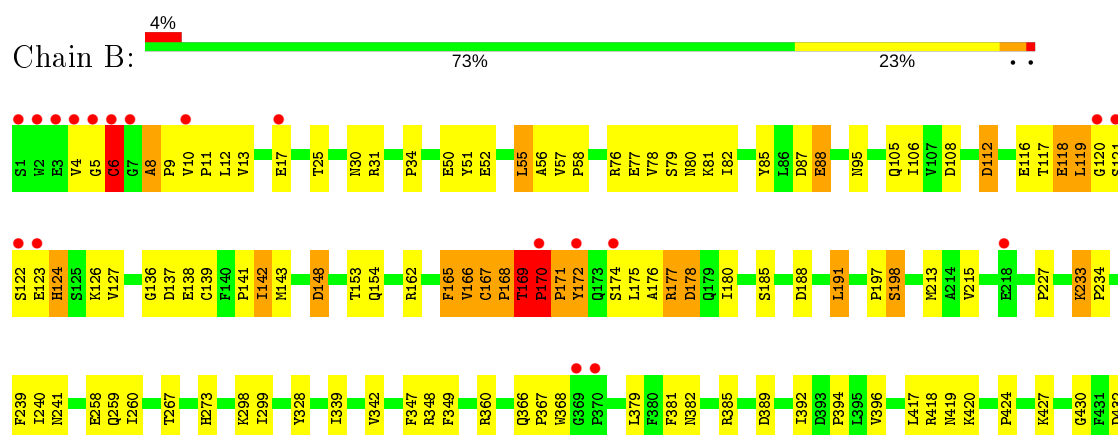
### 3 Residue-property plots [i](#)

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.

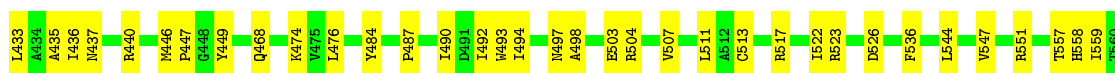
#### • Molecule 1: Lactoperoxidase



#### • Molecule 1: Lactoperoxidase







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

Chain C:  100%



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

Chain E:  100%



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

Chain F:  100%



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

Chain G:  100%



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

Chain I:  50% 50%



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

Chain J:  100%



MAG1  
MAG2

- Molecule 3: beta-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  
BVA3

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

Chain H:  100%

MAG1  
MAG2  
BVA3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	58.52Å 72.54Å 83.98Å 85.30° 84.06° 75.68°	Depositor
Resolution (Å)	24.98 – 3.25 24.98 – 3.25	Depositor EDS
% Data completeness (in resolution range)	94.6 (24.98-3.25) 94.8 (24.98-3.25)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.83 (at 3.23Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.205 , 0.248 0.210 , 0.296	Depositor DCC
$R_{free}$ test set	1011 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.2	Xtriage
Anisotropy	0.609	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 71.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	10057	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.72% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: SCN, NAG, SEP, CA, BMA, HEM, NO3

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	0.58	0/4875	0.67	7/6621 (0.1%)
1	B	0.55	1/4875 (0.0%)	0.67	5/6621 (0.1%)
All	All	0.57	1/9750 (0.0%)	0.67	12/13242 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	PHE	CD1-CE1	-5.40	1.28	1.39

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168	PRO	CA-N-CD	-13.40	92.74	111.50
1	B	169	THR	C-N-CD	-11.10	96.18	120.60
1	B	166	VAL	N-CA-C	6.07	127.39	111.00
1	A	10	VAL	N-CA-C	-5.80	95.35	111.00
1	A	7	GLY	N-CA-C	5.77	127.52	113.10

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	4757	0	4644	177	0
1	B	4757	0	4644	185	0
2	C	28	0	25	0	0
2	E	28	0	25	0	0
2	F	28	0	25	0	0
2	G	28	0	25	0	0
2	I	28	0	25	2	0
2	J	28	0	25	0	0
3	D	39	0	34	0	0
3	H	39	0	34	1	0
4	A	8	0	0	0	0
4	B	8	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	3	0	0	1	0
6	B	3	0	0	3	0
7	A	43	0	30	21	0
7	B	43	0	30	19	0
8	A	87	0	0	1	0
8	B	100	0	0	3	0
All	All	10057	0	9566	369	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 19.

The worst 5 of 369 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:258:GLU:OE2	7:B:821:HEM:CMB	1.63	1.46
1:B:108:ASP:OD2	7:B:821:HEM:CMD	1.65	1.45
1:A:258:GLU:OE2	7:A:801:HEM:CMB	1.67	1.39
1:B:170:PRO:CB	1:B:171:PRO:HD3	1.50	1.36
1:B:170:PRO:HB2	1:B:171:PRO:CD	1.46	1.36

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	592/595 (100%)	555 (94%)	30 (5%)	7 (1%)	13	43
1	B	592/595 (100%)	556 (94%)	30 (5%)	6 (1%)	15	47
All	All	1184/1190 (100%)	1111 (94%)	60 (5%)	13 (1%)	14	46

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	PRO
1	A	167	CYS
1	A	168	PRO
1	B	168	PRO
1	B	170	PRO

### 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	516/516 (100%)	493 (96%)	23 (4%)	27	58
1	B	516/516 (100%)	493 (96%)	23 (4%)	27	58
All	All	1032/1032 (100%)	986 (96%)	46 (4%)	27	58

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	537	THR

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Mol	Chain	Res	Type
1	B	55	LEU
1	B	177	ARG
1	A	551	ARG
1	B	6	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	377	HIS
1	A	468	GLN
1	B	250	GLN
1	A	341	ASN
1	B	437	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	SEP	B	198	1	8,9,10	1.66	1 (12%)	8,12,14	1.33	1 (12%)
1	SEP	A	198	1	8,9,10	1.68	1 (12%)	8,12,14	1.71	2 (25%)

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
1	SEP	B	198	1	-	1/5/8/10	-
1	SEP	A	198	1	-	2/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	P-O1P	3.73	1.62	1.50
1	B	198	SEP	P-O1P	3.73	1.62	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	OG-CB-CA	3.22	111.28	108.14
1	A	198	SEP	P-OG-CB	-2.60	111.14	118.30
1	B	198	SEP	OG-CB-CA	2.17	110.26	108.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	CB-OG-P-O2P
1	B	198	SEP	CA-CB-OG-P
1	A	198	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	198	SEP	2	0

## 5.5 Carbohydrates

18 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	1.11	2 (14%)	17,19,21	1.08	1 (5%)
2	NAG	C	2	2	14,14,15	1.41	3 (21%)	17,19,21	1.55	3 (17%)
3	NAG	D	1	1,3	14,14,15	0.72	0	17,19,21	0.75	0
3	NAG	D	2	3	14,14,15	0.79	0	17,19,21	1.53	2 (11%)
3	BMA	D	3	3	11,11,12	1.09	1 (9%)	15,15,17	1.67	4 (26%)
2	NAG	E	1	1,2	14,14,15	0.55	0	17,19,21	1.27	2 (11%)
2	NAG	E	2	2	14,14,15	0.57	0	17,19,21	1.81	3 (17%)
2	NAG	F	1	1,2	14,14,15	0.57	0	17,19,21	1.24	2 (11%)
2	NAG	F	2	2	14,14,15	0.65	0	17,19,21	1.55	3 (17%)
2	NAG	G	1	1,2	14,14,15	1.10	3 (21%)	17,19,21	1.08	1 (5%)
2	NAG	G	2	2	14,14,15	1.40	3 (21%)	17,19,21	1.54	2 (11%)
3	NAG	H	1	1,3	14,14,15	0.72	0	17,19,21	0.76	0
3	NAG	H	2	3	14,14,15	0.79	0	17,19,21	1.54	2 (11%)
3	BMA	H	3	3	11,11,12	1.08	1 (9%)	15,15,17	1.67	4 (26%)
2	NAG	I	1	1,2	14,14,15	0.45	0	17,19,21	1.45	2 (11%)
2	NAG	I	2	2	14,14,15	0.59	0	17,19,21	1.29	2 (11%)
2	NAG	J	1	1,2	14,14,15	0.60	0	17,19,21	1.52	2 (11%)
2	NAG	J	2	2	14,14,15	0.53	0	17,19,21	0.94	1 (5%)

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	BMA	H	3	3	-	2/2/19/22	0/1/1/1
2	NAG	I	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	I	2	2	-	2/6/23/26	0/1/1/1
2	NAG	J	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	J	2	2	-	3/6/23/26	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	2	NAG	C3-C2	2.90	1.58	1.52
2	C	2	NAG	C3-C2	2.87	1.58	1.52
3	H	3	BMA	C2-C3	2.80	1.56	1.52
3	D	3	BMA	C2-C3	2.79	1.56	1.52
2	G	2	NAG	C4-C3	2.40	1.58	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2	NAG	C1-O5-C5	5.27	119.33	112.19
3	H	2	NAG	C4-C3-C2	4.90	118.19	111.02
3	D	2	NAG	C4-C3-C2	4.86	118.14	111.02
2	C	2	NAG	C4-C3-C2	4.86	118.14	111.02
2	G	2	NAG	C4-C3-C2	4.83	118.09	111.02

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	1	NAG	C8-C7-N2-C2
2	E	1	NAG	O7-C7-N2-C2
2	J	1	NAG	O7-C7-N2-C2
2	J	2	NAG	O7-C7-N2-C2
2	F	2	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	I	1	NAG	2	0

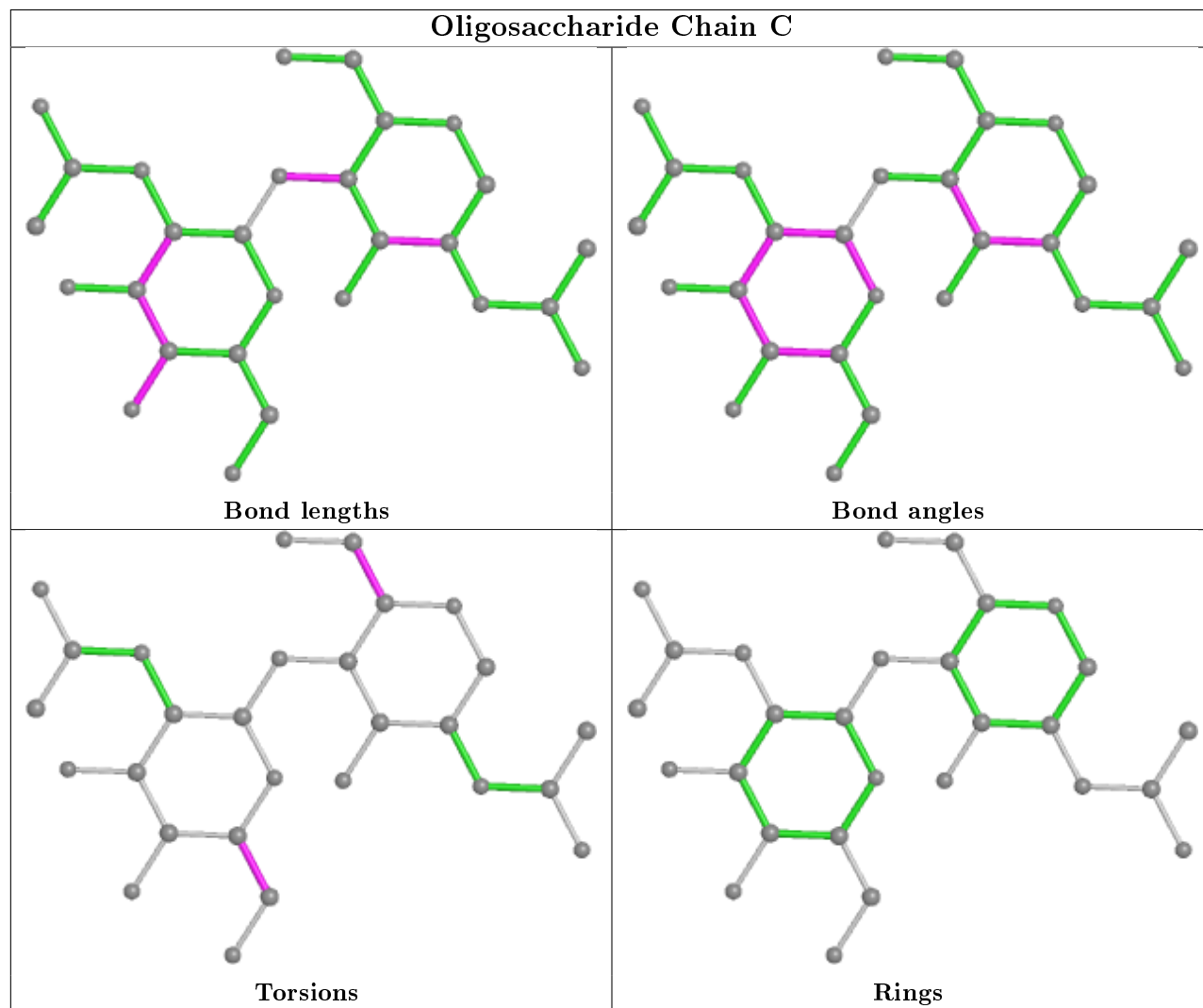
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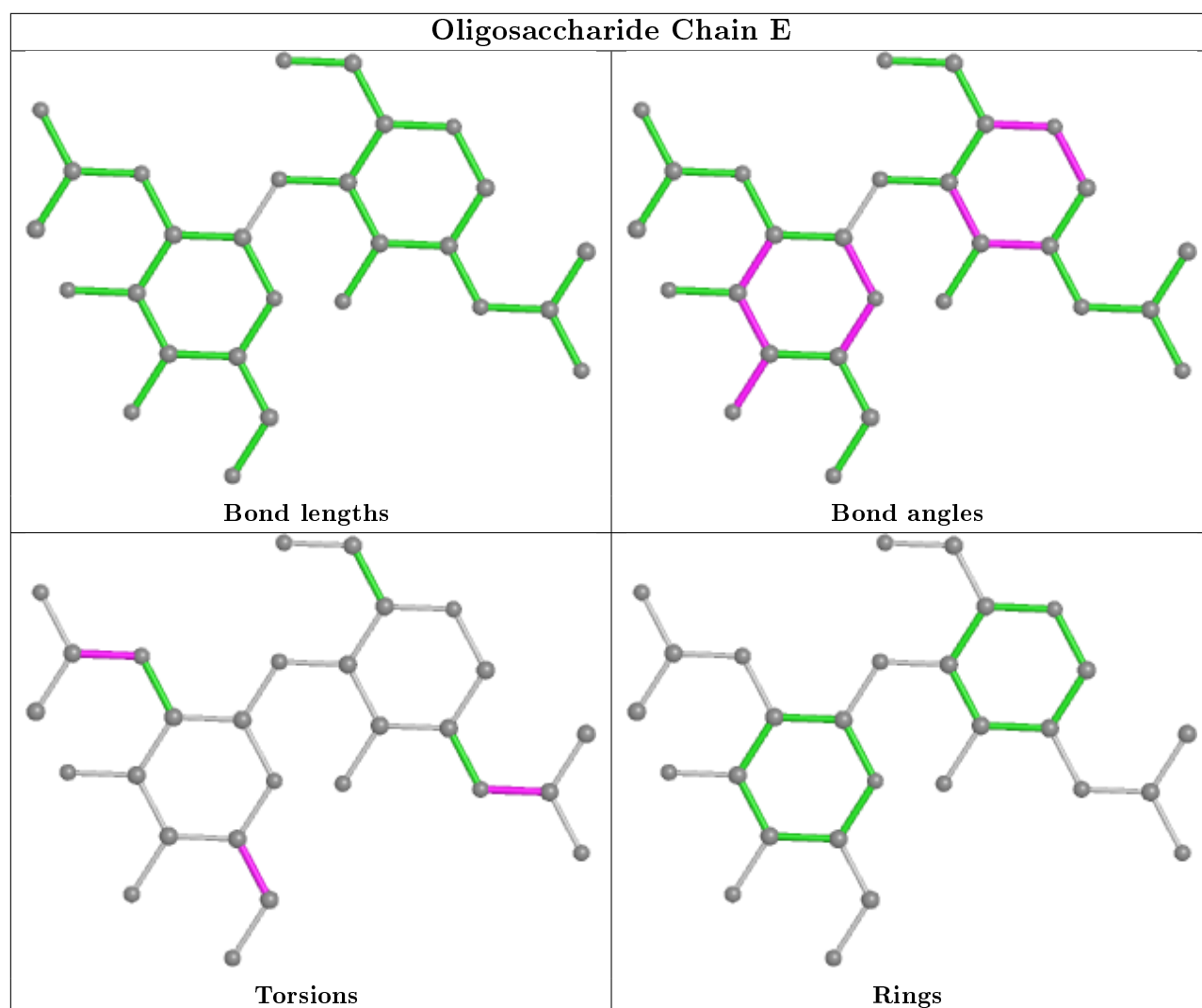
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	NAG	1	0

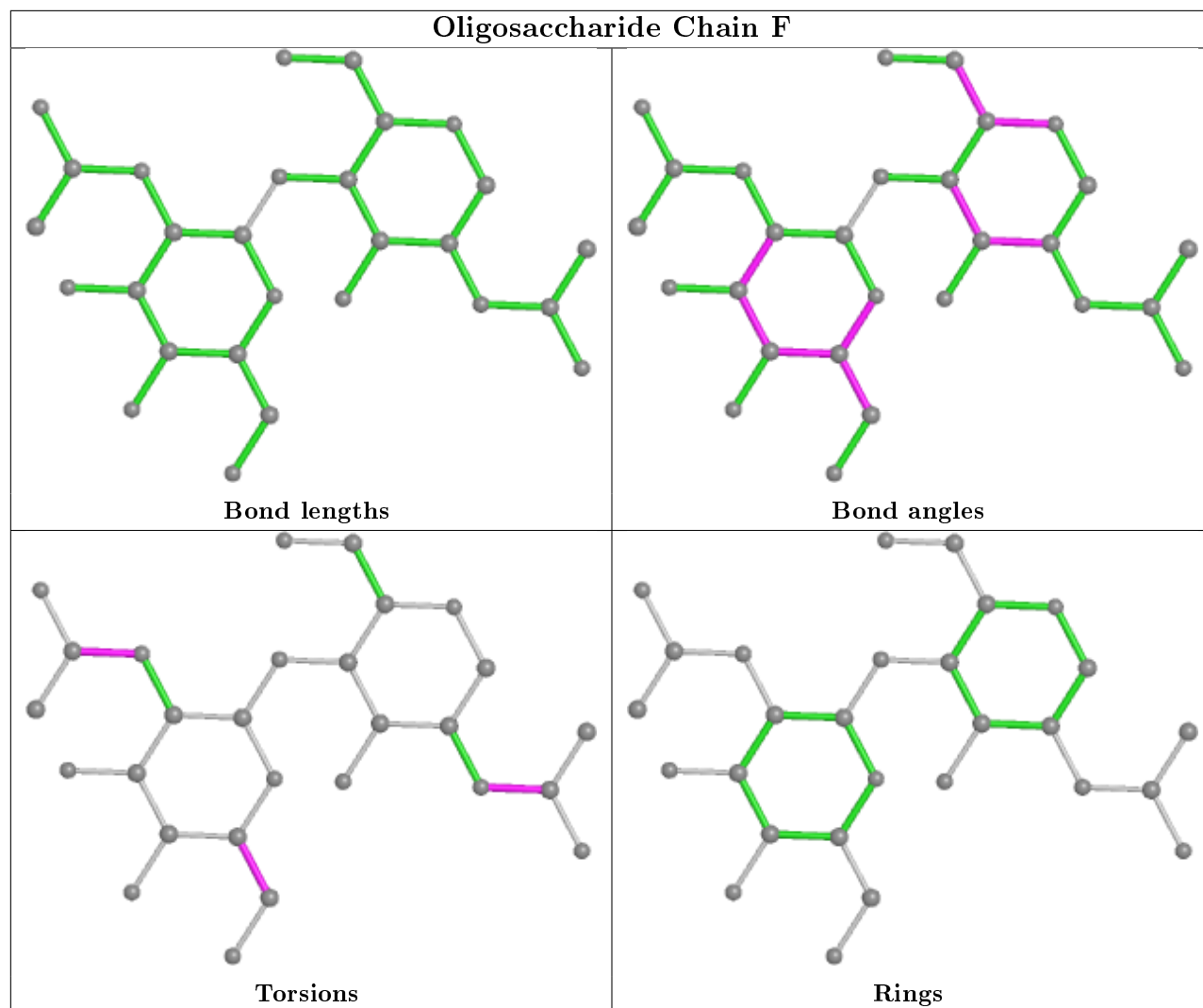
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



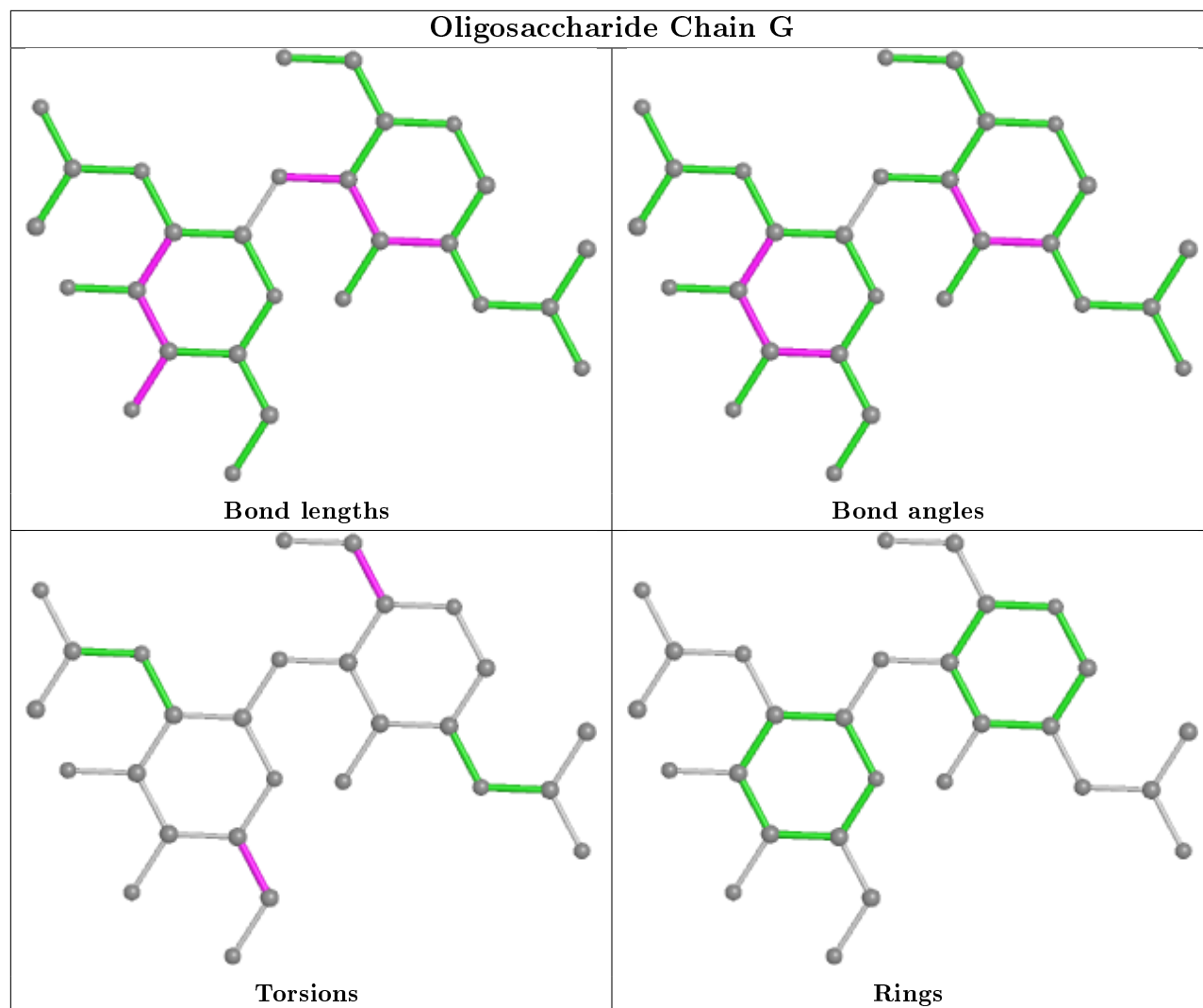




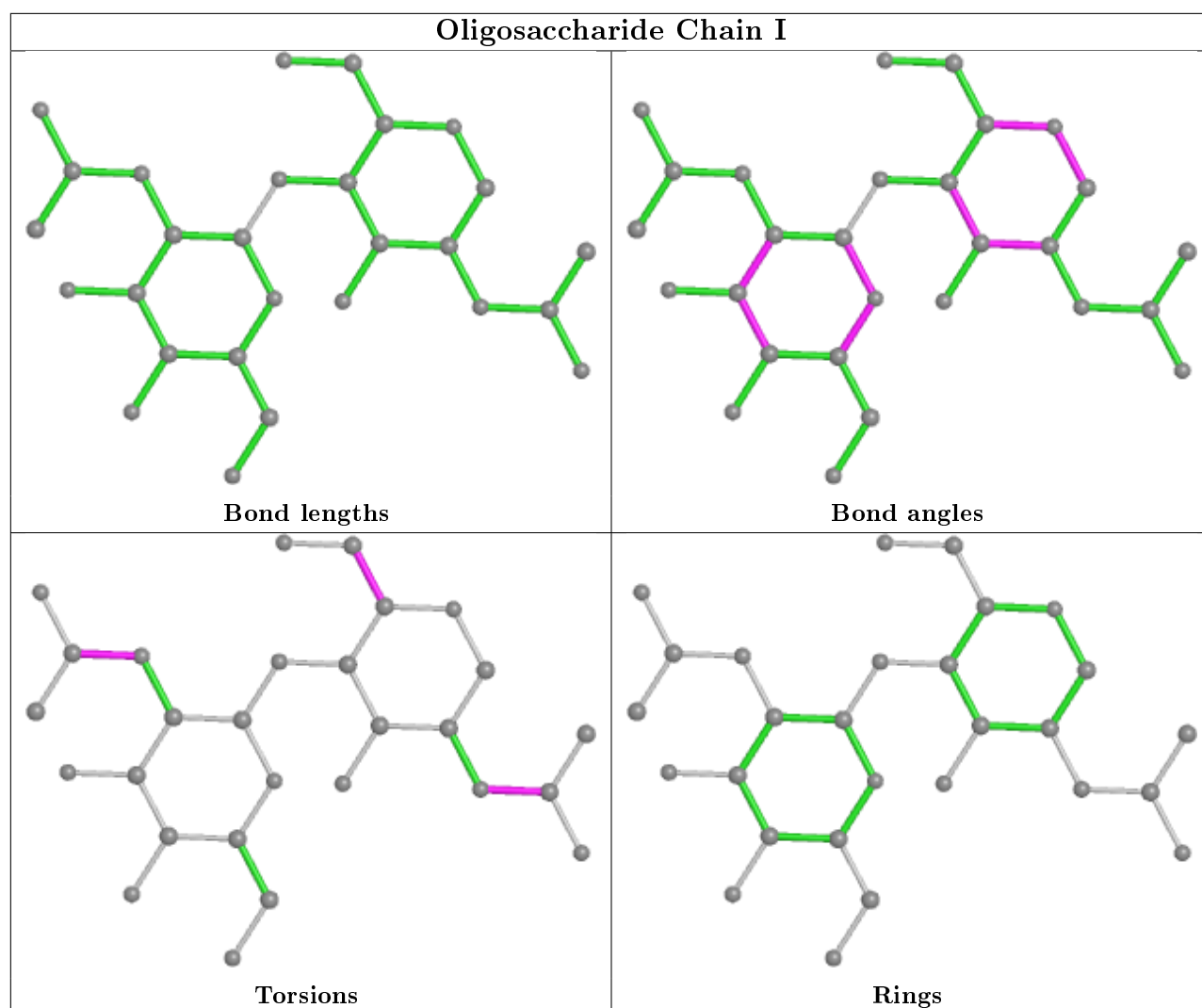




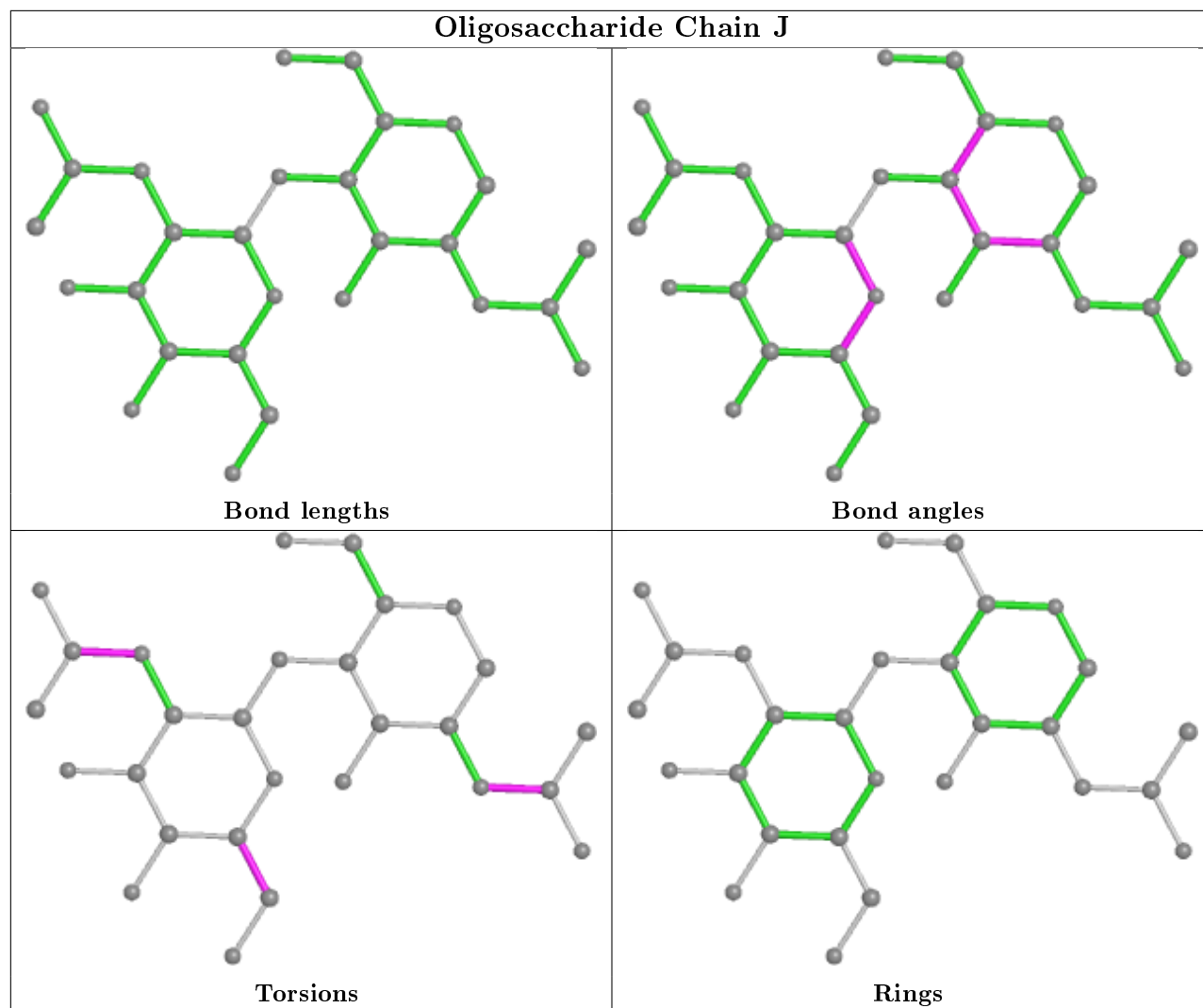




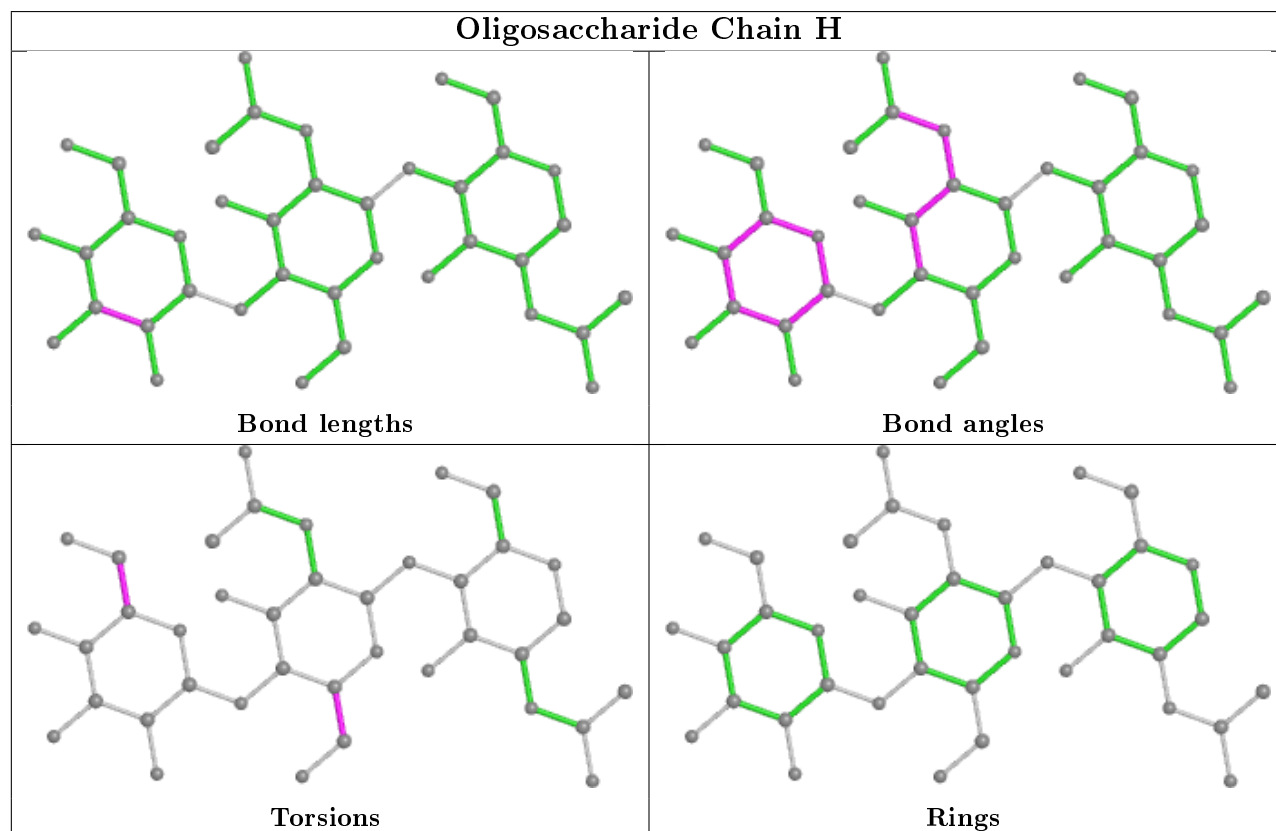
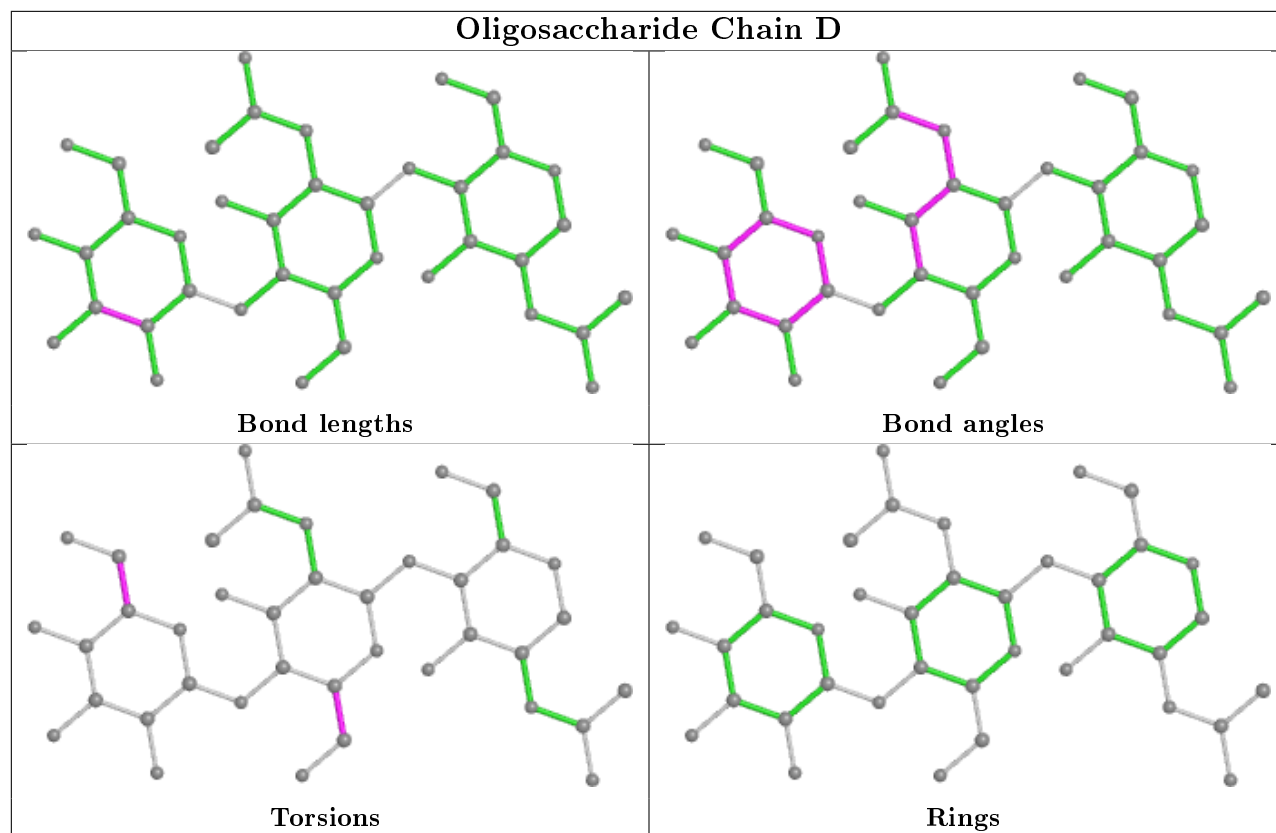














## 5.6 Ligand geometry

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
4	NO3	A	607	-	1,3,3	3.68	1 (100%)	0,3,3	0.00	-
6	SCN	A	901	-	1,2,2	3.68	1 (100%)	0,1,1	0.00	-
7	HEM	A	801	1,8	27,50,50	2.18	6 (22%)	17,82,82	1.51	2 (11%)
6	SCN	B	902	-	1,2,2	3.22	1 (100%)	0,1,1	0.00	-
4	NO3	B	608	-	1,3,3	3.38	1 (100%)	0,3,3	0.00	-
7	HEM	B	821	1,8	27,50,50	2.14	6 (22%)	17,82,82	1.63	5 (29%)
4	NO3	B	607	-	1,3,3	3.69	1 (100%)	0,3,3	0.00	-
4	NO3	A	608	-	1,3,3	3.57	1 (100%)	0,3,3	0.00	-

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	HEM	A	801	1,8	-	2/6/54/54	-
7	HEM	B	821	1,8	-	0/6/54/54	-

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	821	HEM	C3D-C2D	5.27	1.53	1.37
7	A	801	HEM	C3D-C2D	5.27	1.53	1.37
7	B	821	HEM	C3B-C2B	-4.30	1.34	1.40
7	A	801	HEM	C3B-C2B	-4.06	1.34	1.40
7	A	801	HEM	C3C-CAC	4.00	1.56	1.47

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



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	801	HEM	CBD-CAD-C3D	-3.54	105.96	112.48
7	B	821	HEM	CAD-CBD-CGD	-3.44	106.89	112.67
7	B	821	HEM	CBD-CAD-C3D	-2.71	107.48	112.48
7	B	821	HEM	C1D-C2D-C3D	-2.11	105.53	107.00
7	A	801	HEM	CAA-CBA-CGA	-2.11	109.14	112.67

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	801	HEM	C1A-C2A-CAA-CBA
7	A	801	HEM	C3A-C2A-CAA-CBA

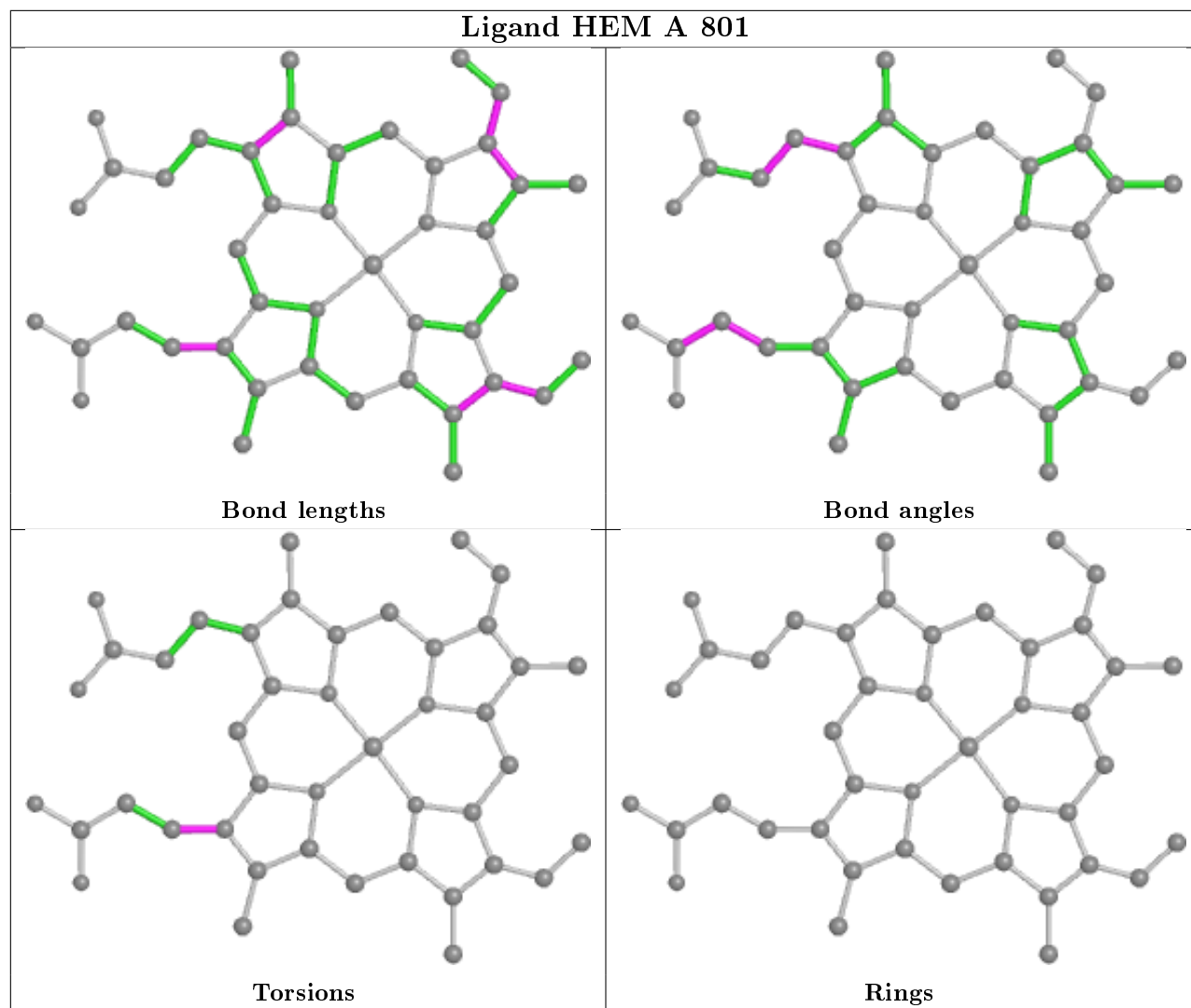
There are no ring outliers.

4 monomers are involved in 42 short contacts:

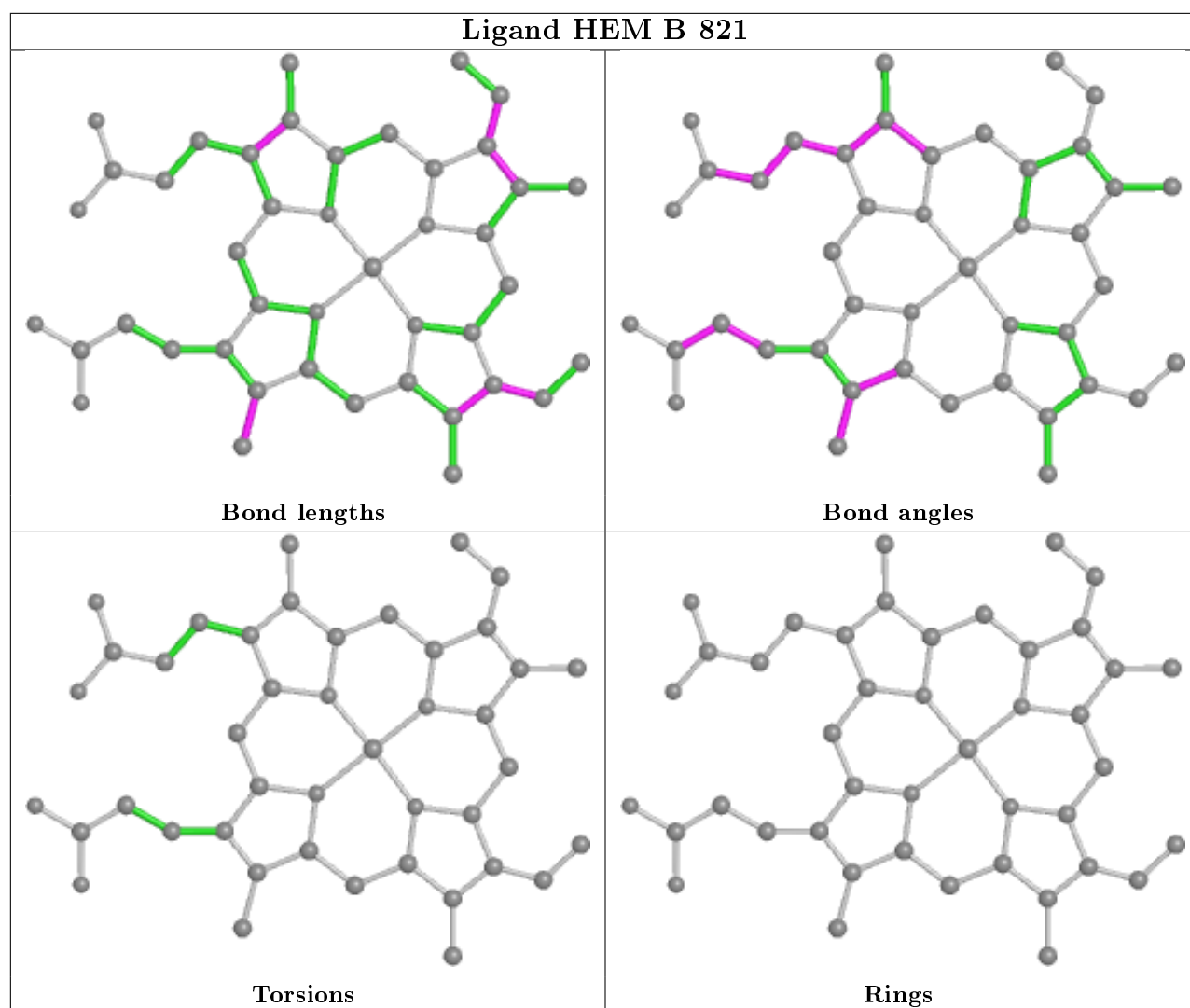
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	901	SCN	1	0
7	A	801	HEM	21	0
6	B	902	SCN	3	0
7	B	821	HEM	19	0

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	594/595 (99%)	-0.24	23 (3%) 39 36	6, 21, 48, 75	0
1	B	594/595 (99%)	-0.20	22 (3%) 41 38	4, 22, 46, 71	0
All	All	1188/1190 (99%)	-0.22	45 (3%) 40 37	4, 22, 47, 75	0

The worst 5 of 45 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	595	ASN	5.7
1	B	6	CYS	5.6
1	B	5	GLY	5.0
1	A	172	TYR	4.9
1	B	121	SER	4.9

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	SEP	A	198	10/11	0.84	0.51	31,32,38,39	0
1	SEP	B	198	10/11	0.89	0.34	29,30,35,35	0

### 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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.



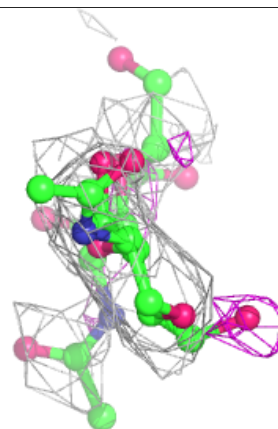
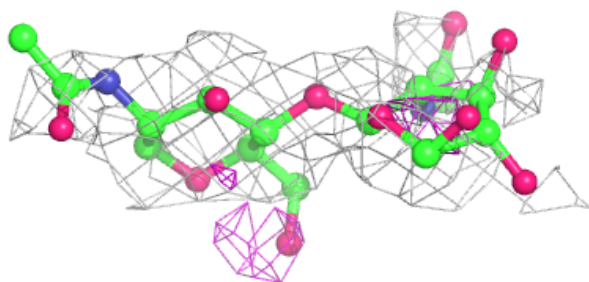
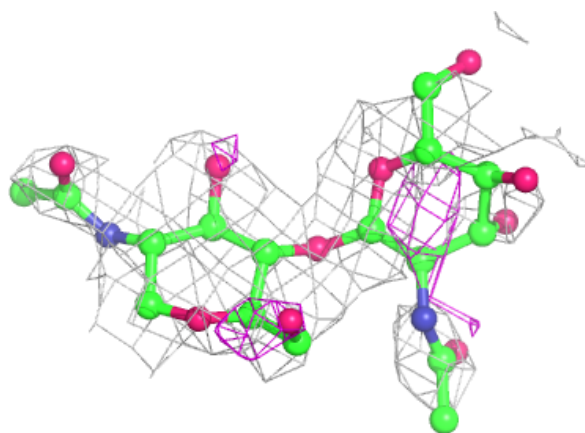
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	G	2	14/15	0.61	0.59	35,39,39,39	0
3	BMA	D	3	11/12	0.64	0.69	36,38,39,39	0
2	NAG	F	2	14/15	0.65	0.59	52,52,53,53	0
2	NAG	E	2	14/15	0.66	0.46	49,52,53,54	0
3	NAG	H	2	14/15	0.68	0.59	30,37,39,39	0
2	NAG	F	1	14/15	0.69	0.43	44,47,48,50	0
2	NAG	C	2	14/15	0.69	0.54	35,39,39,39	0
3	BMA	H	3	11/12	0.69	0.79	36,38,39,39	0
2	NAG	I	2	14/15	0.77	0.39	50,53,54,56	0
2	NAG	J	2	14/15	0.77	0.72	49,51,51,51	0
2	NAG	G	1	14/15	0.81	0.44	30,31,38,39	0
2	NAG	C	1	14/15	0.83	0.41	30,31,38,39	0
3	NAG	D	2	14/15	0.84	0.33	30,37,39,39	0
2	NAG	J	1	14/15	0.86	0.35	37,40,43,46	0
3	NAG	D	1	14/15	0.91	0.20	30,35,39,39	0
3	NAG	H	1	14/15	0.92	0.20	30,35,39,39	0
2	NAG	I	1	14/15	0.94	0.15	38,40,42,46	0
2	NAG	E	1	14/15	0.94	0.15	38,40,42,46	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.

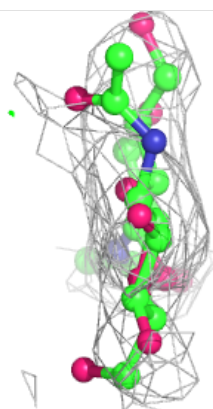
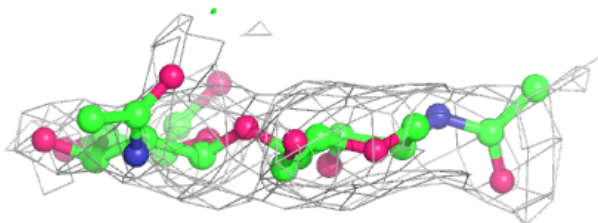
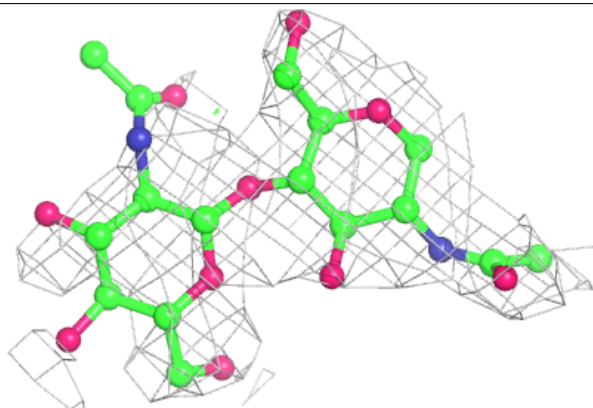


**Electron density around Chain C:**

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

**Electron density around Chain E:**

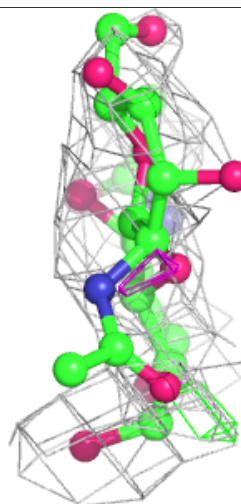
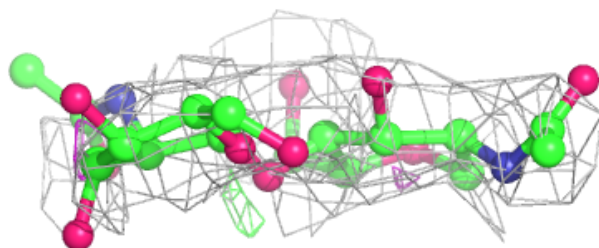
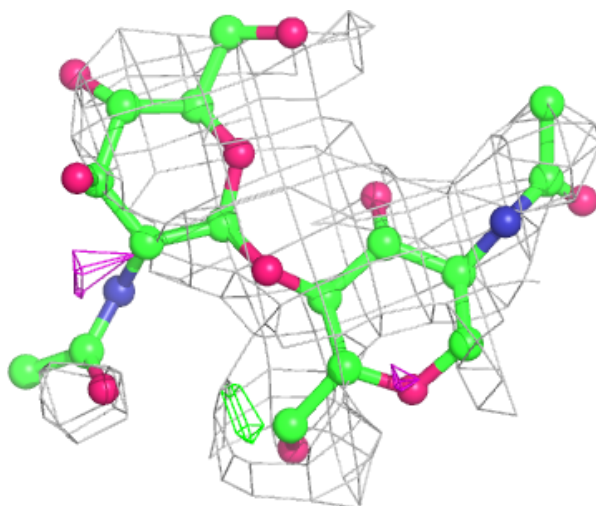
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
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and green (positive)





**Electron density around Chain F:**

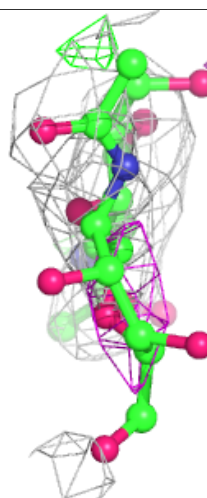
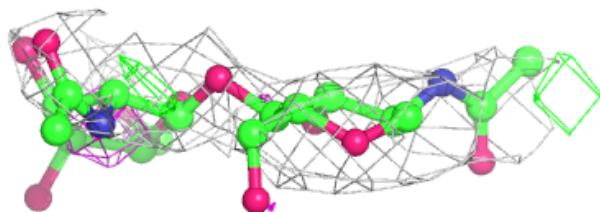
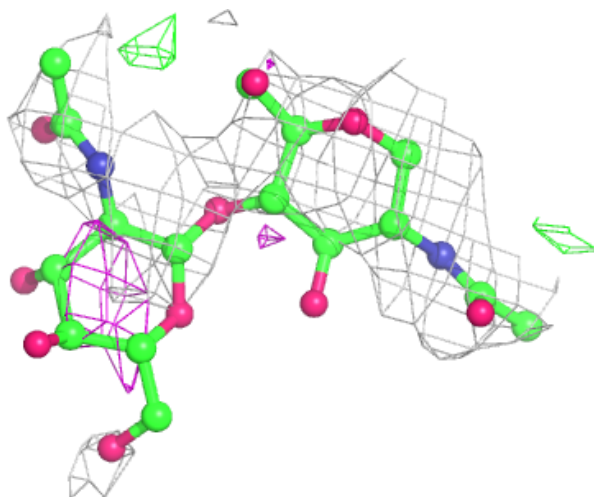
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 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around Chain G:**

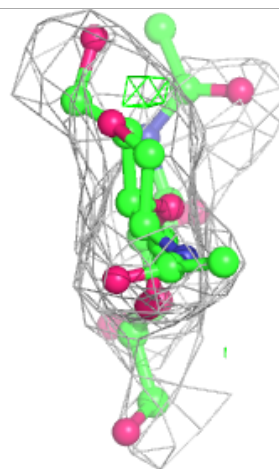
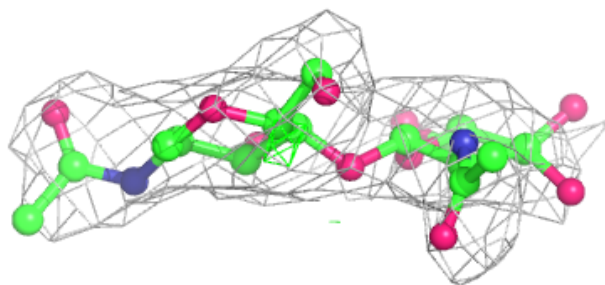
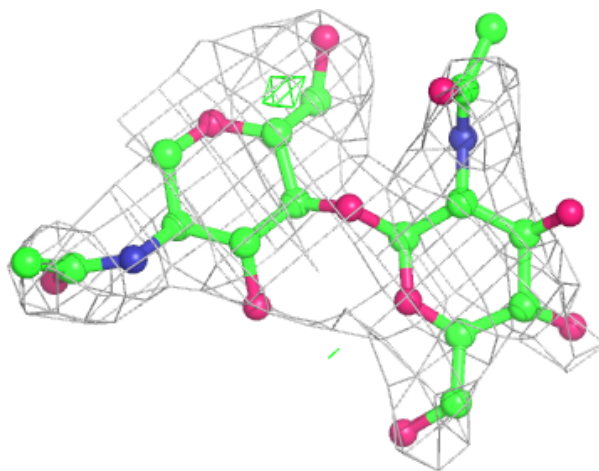
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around Chain I:**

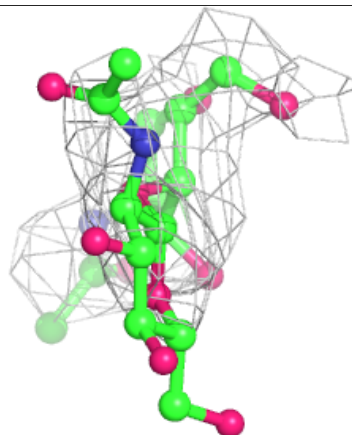
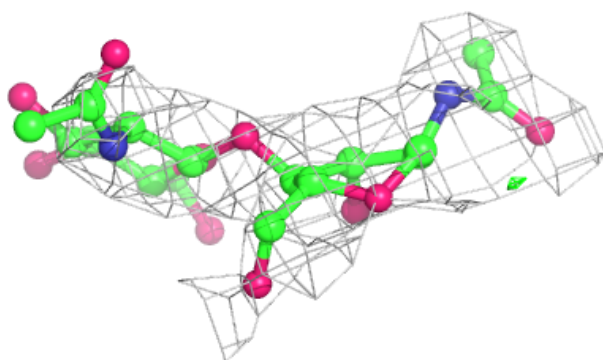
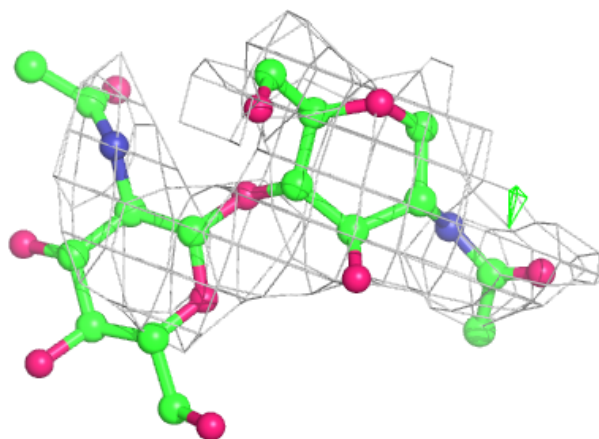
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



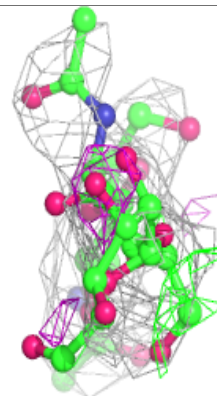
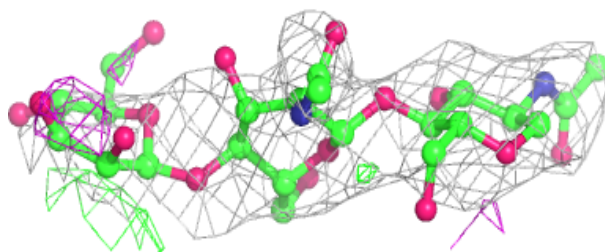
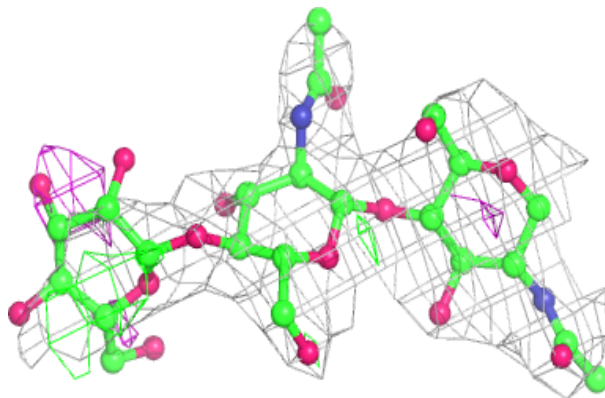


**Electron density around Chain J:**

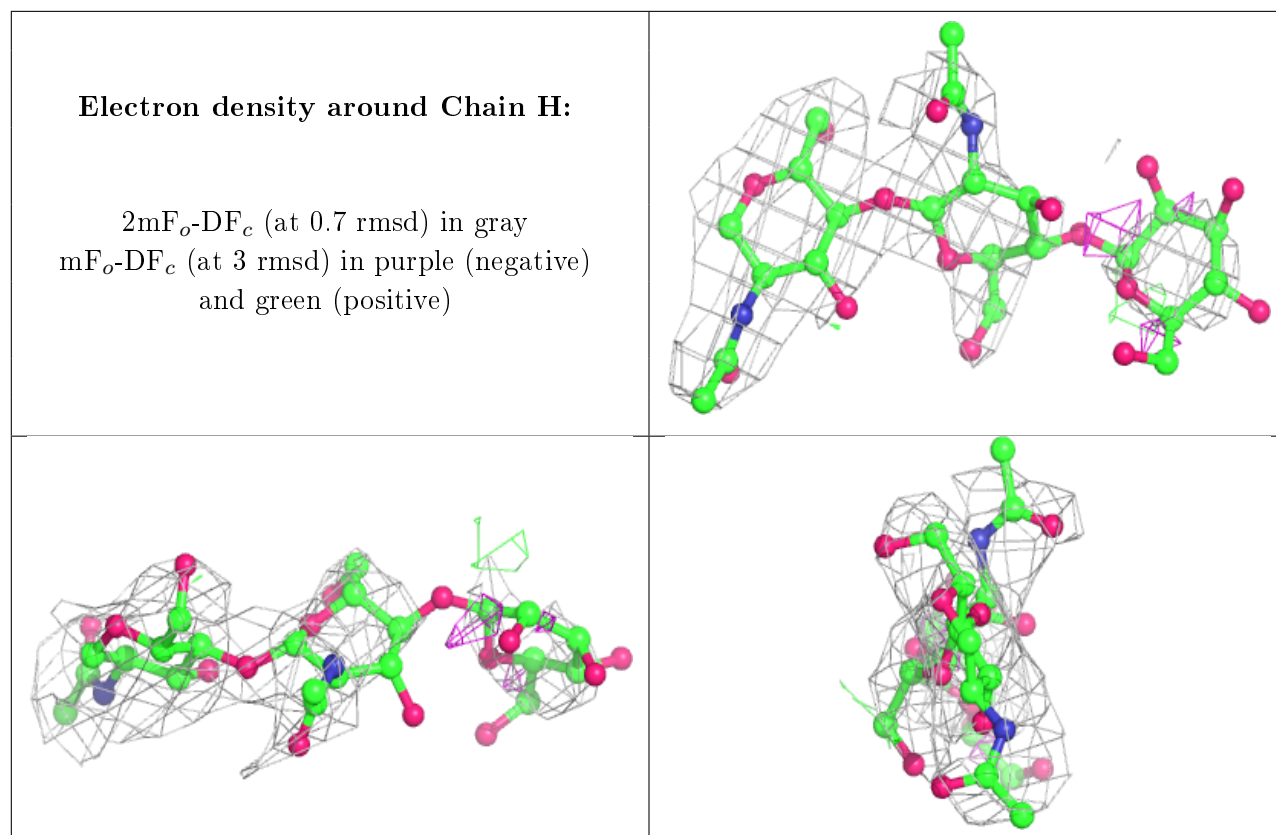
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around Chain D:**

$2mF_o - DF_c$  (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, 95<sup>th</sup> 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.

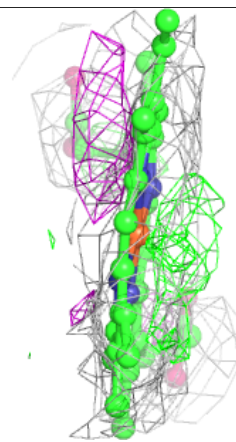
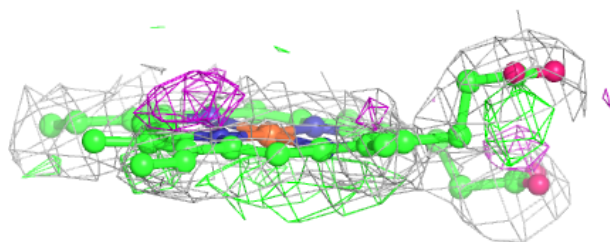
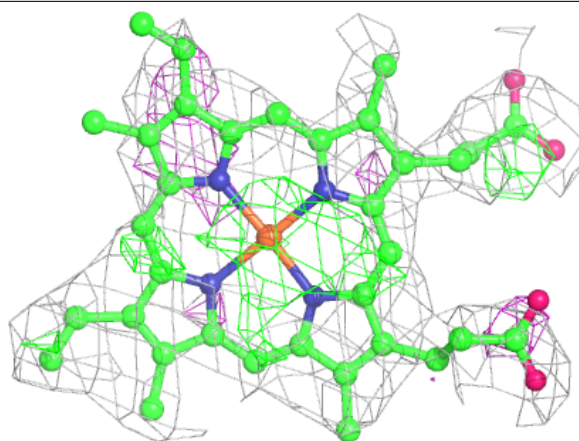
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	SCN	B	902	3/3	0.76	0.41	23,23,23,24	0
6	SCN	A	901	3/3	0.82	0.27	26,26,26,26	0
7	HEM	A	801	43/43	0.84	0.28	22,24,26,27	0
7	HEM	B	821	43/43	0.84	0.28	15,18,18,19	0
4	NO3	A	607	4/4	0.91	0.27	69,69,69,69	0
4	NO3	B	607	4/4	0.92	0.32	44,44,44,44	0
5	CA	A	704	1/1	0.95	0.10	28,28,28,28	0
4	NO3	B	608	4/4	0.97	0.18	11,11,11,11	0
4	NO3	A	608	4/4	0.98	0.16	25,25,26,26	0
5	CA	B	724	1/1	0.99	0.09	21,21,21,21	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 HEM A 801:**

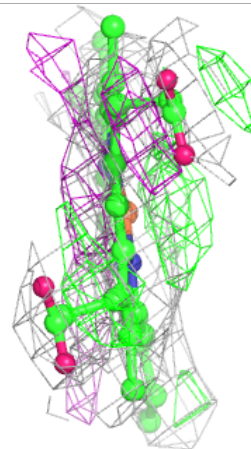
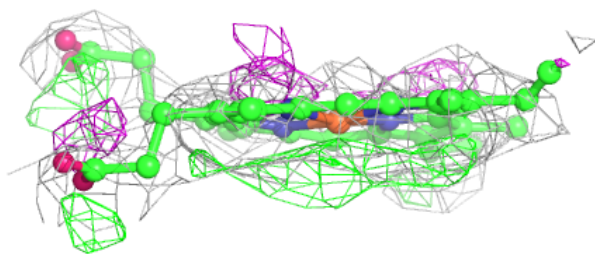
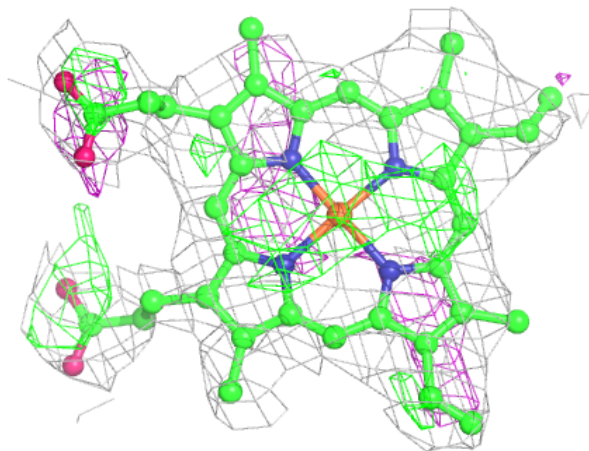
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around HEM B 821:**

$2mF_o-DF_c$  (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.