



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2020 – 04:25 PM BST

PDB ID : 3N8W  
Title : Crystal Structure of R120Q/Native Cyclooxygenase-1 Heterodimer mutant in complex with Flurbiprofen  
Authors : Sidhu, R.S.  
Deposited on : 2010-05-28  
Resolution : 2.75 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

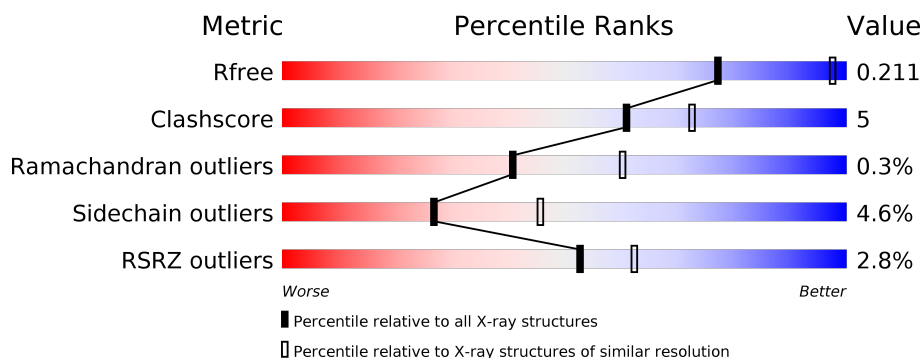
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.75 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.



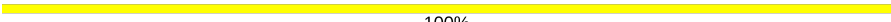
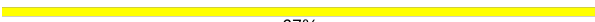

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	553	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>11%</div> </div> <div></div> </div>
2	B	553	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>10%</div> </div> <div></div> </div>
3	C	2	<div> <div></div> <div>100%</div> </div>
3	F	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
4	D	3	<div> <div></div> <div>100%</div> </div>
5	E	5	<div> <div></div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
6	G	3	 100%
7	H	3	 67%  33%

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
3	NAG	C	1	X	-	-	-
9	FLP	A	701	X	-	-	-

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 9505 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 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	0	0	0
			4437	2877	747	785	28			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	LEU	MET	conflict	UNP P05979

- Molecule 2 is a protein called Prostaglandin G/H synthase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	553	Total	C	N	O	S	0	8	0
			4472	2901	744	800	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	92	LEU	MET	conflict	UNP P05979
B	120	GLN	ARG	conflict	UNP P05979

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



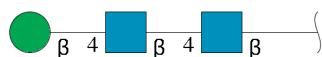
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

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

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



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

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 6 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.



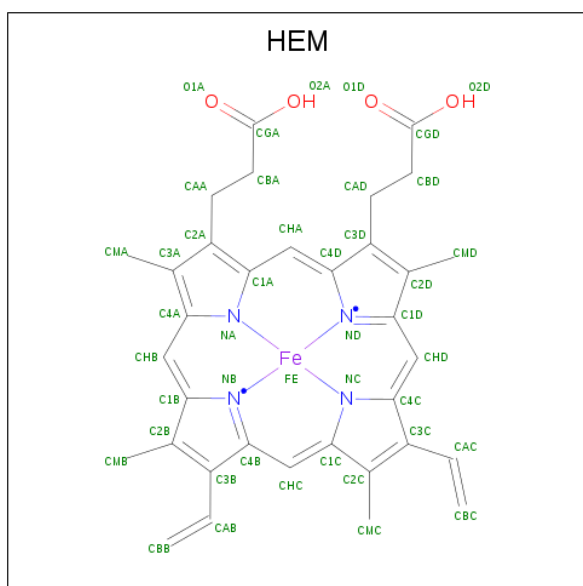
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	G	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 7 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



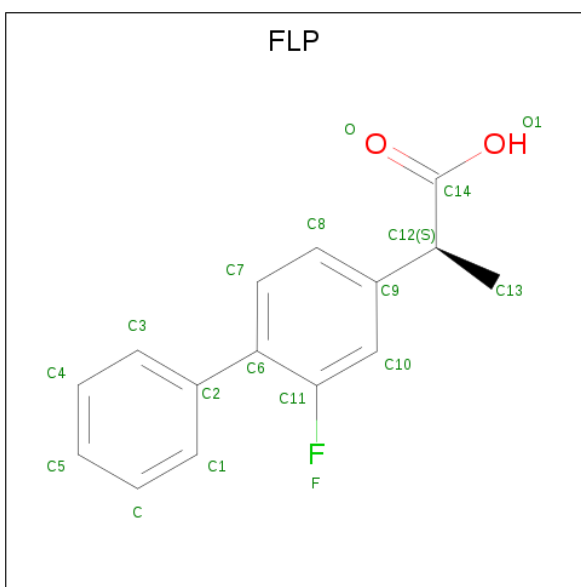
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	H	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 8 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



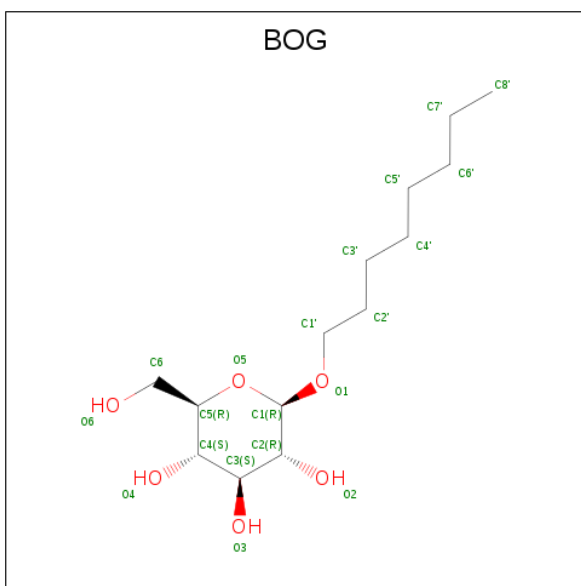
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	Fe	N	O	0
			43	34	1	4	4	
8	B	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

- Molecule 9 is FLURBIPROFEN (three-letter code: FLP) (formula:  $C_{15}H_{13}FO_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	F	O	0	0
			18	15	1	2		

- Molecule 10 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula:  $C_{14}H_{28}O_6$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			20	14	6		
10	B	1	Total	C	O	0	0
			13	7	6		
10	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 11 is water.

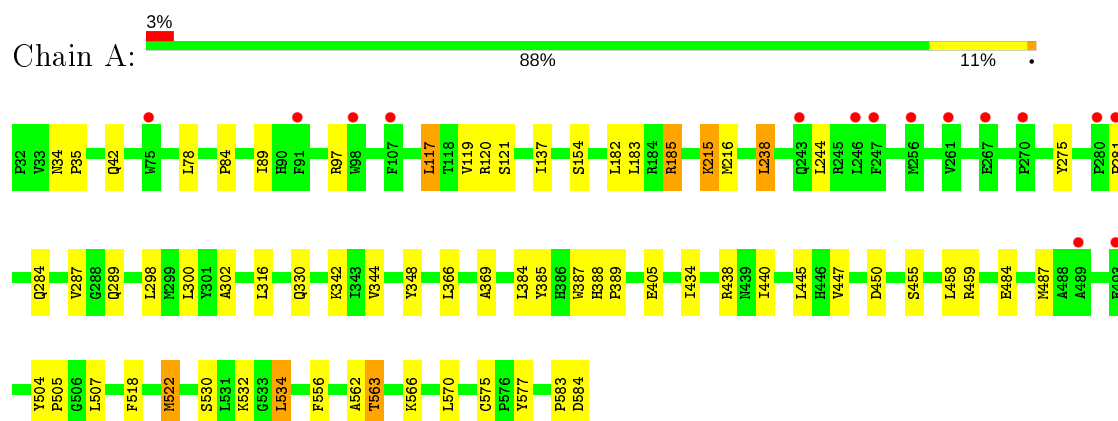
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	105	Total 105	O 105	0	0
11	B	108	Total 108	O 108	0	0



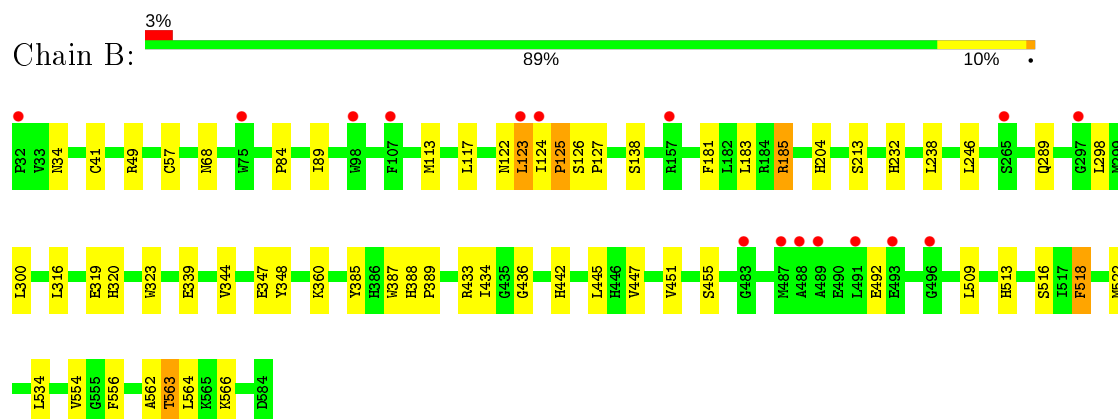
### 3 Residue-property plots [i](#)

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.

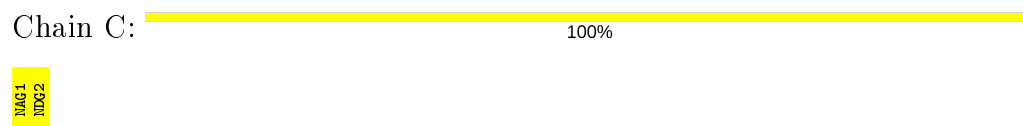
- Molecule 1: Prostaglandin G/H synthase 1



- Molecule 2: Prostaglandin G/H synthase 1



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

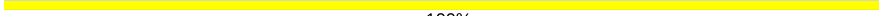


- Molecule 3: 2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  50% 50%

UAG1  
UDG2

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

Chain D:  100%

UAG1  
UDG2  
BMA3

- Molecule 5: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

UAG1  
UDG2  
BMA3  
MAN4  
MAN5

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

Chain G:  100%

UAG1  
UDG2  
MAN3

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  67% 33%

UAG1  
UDG2  
BMA3

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	182.48Å 182.48Å 103.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.91 – 2.75 46.91 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.0 (46.91-2.75) 99.5 (46.91-2.75)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.178 , 0.201 0.191 , 0.211	Depositor DCC
$R_{free}$ test set	1712 reflections (3.38%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.6	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 32.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	0.064 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.532 for H, K, L 0.468 for -H-K, K, -L	Depositor
Outliers	0 of 50719 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9505	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, FLP, NDG, HEM, 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	0.35	0/4576	0.51	0/6224
2	B	0.35	0/4612	0.51	0/6281
All	All	0.35	0/9188	0.51	0/12505

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	4437	0	4280	36	0
2	B	4472	0	4299	47	0
3	C	28	0	24	0	0
3	F	28	0	24	0	0
4	D	39	0	34	0	0
5	E	61	0	51	0	0
6	G	39	0	33	0	0
7	H	39	0	33	1	0
8	A	43	0	30	1	0
8	B	43	0	30	1	0
9	A	18	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	A	20	0	28	1	0
10	B	25	0	22	0	0
11	A	105	0	0	5	0
11	B	108	0	0	5	0
All	All	9505	0	8900	82	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 5.

The worst 5 of 82 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)
2:B:124[B]:ILE:O	2:B:126[B]:SER:N	1.71	1.21
2:B:122[B]:ASN:O	2:B:124[B]:ILE:N	1.87	1.07
2:B:185:ARG:HG3	2:B:185:ARG:HH11	1.24	1.02
2:B:122[B]:ASN:C	2:B:124[B]:ILE:H	1.63	1.01
2:B:124[B]:ILE:C	2:B:126[B]:SER:H	1.65	0.99

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	551/553 (100%)	525 (95%)	26 (5%)	0	100	100
2	B	559/553 (101%)	528 (94%)	26 (5%)	5 (1%)	17	31
All	All	1110/1106 (100%)	1053 (95%)	52 (5%)	5 (0%)	41	47

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	123[A]	LEU
2	B	123[B]	LEU
2	B	125[A]	PRO
2	B	125[B]	PRO
2	B	204	HIS

### 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	475/488 (97%)	449 (94%)	26 (6%)	21	37
2	B	480/488 (98%)	462 (96%)	18 (4%)	33	53
All	All	955/976 (98%)	911 (95%)	44 (5%)	27	46

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	522	MET
1	A	575	CYS
2	B	534	LEU
1	A	534	LEU
1	A	563	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	400	GLN
2	B	581	HIS

### 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 ⓘ

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$
3	NAG	C	1	1,3	14,14,15	0.43	0	17,19,21	1.25	1 (5%)
3	NDG	C	2	3	14,14,15	0.56	0	17,19,21	1.62	4 (23%)
4	NAG	D	1	1,4	14,14,15	1.90	1 (7%)	17,19,21	2.20	4 (23%)
4	NAG	D	2	4	14,14,15	0.39	0	17,19,21	1.33	2 (11%)
4	BMA	D	3	4	11,11,12	0.57	0	15,15,17	1.55	3 (20%)
5	NAG	E	1	1,5	14,14,15	0.61	0	17,19,21	1.32	2 (11%)
5	NDG	E	2	5	14,14,15	0.61	0	17,19,21	1.95	2 (11%)
5	BMA	E	3	5	11,11,12	0.61	0	15,15,17	0.92	1 (6%)
5	MAN	E	4	5	11,11,12	0.54	0	15,15,17	1.65	3 (20%)
5	MAN	E	5	5	11,11,12	0.62	0	15,15,17	1.53	3 (20%)
3	NAG	F	1	3,2	14,14,15	0.46	0	17,19,21	0.85	0
3	NDG	F	2	3	14,14,15	0.48	0	17,19,21	1.07	1 (5%)
6	NAG	G	1	2,6	14,14,15	0.72	0	17,19,21	1.70	4 (23%)
6	NAG	G	2	6	14,14,15	0.48	0	17,19,21	1.03	1 (5%)
6	MAN	G	3	6	11,11,12	0.55	0	15,15,17	1.12	1 (6%)
7	NAG	H	1	2,7	14,14,15	0.50	0	17,19,21	1.20	1 (5%)
7	NDG	H	2	7	14,14,15	0.64	0	17,19,21	1.98	5 (29%)
7	BMA	H	3	7	11,11,12	0.60	0	15,15,17	1.04	1 (6%)

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
3	NAG	C	1	1,3	1/1/5/7	0/6/23/26	0/1/1/1
3	NDG	C	2	3	-	1/6/23/26	0/1/1/1
4	NAG	D	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
5	NAG	E	1	1,5	-	0/6/23/26	0/1/1/1
5	NDG	E	2	5	-	2/6/23/26	0/1/1/1
5	BMA	E	3	5	-	2/2/19/22	0/1/1/1
5	MAN	E	4	5	-	0/2/19/22	0/1/1/1
5	MAN	E	5	5	-	0/2/19/22	0/1/1/1
3	NAG	F	1	3,2	-	1/6/23/26	0/1/1/1
3	NDG	F	2	3	-	0/6/23/26	0/1/1/1
6	NAG	G	1	2,6	-	2/6/23/26	0/1/1/1
6	NAG	G	2	6	-	0/6/23/26	0/1/1/1
6	MAN	G	3	6	-	0/2/19/22	0/1/1/1
7	NAG	H	1	2,7	-	0/6/23/26	0/1/1/1
7	NDG	H	2	7	-	1/6/23/26	0/1/1/1
7	BMA	H	3	7	-	1/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1	NAG	O5-C1	-6.85	1.32	1.43

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	2	NDG	C1-O5-C5	6.44	120.92	112.19
4	D	1	NAG	C1-O5-C5	-5.84	104.28	112.19
4	D	1	NAG	O5-C1-C2	-4.92	103.53	111.29
5	E	4	MAN	C1-O5-C5	4.69	118.55	112.19
6	G	1	NAG	C4-C3-C2	4.69	117.89	111.02

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	1	NAG	C1

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	G	1	NAG	C1-C2-N2-C7

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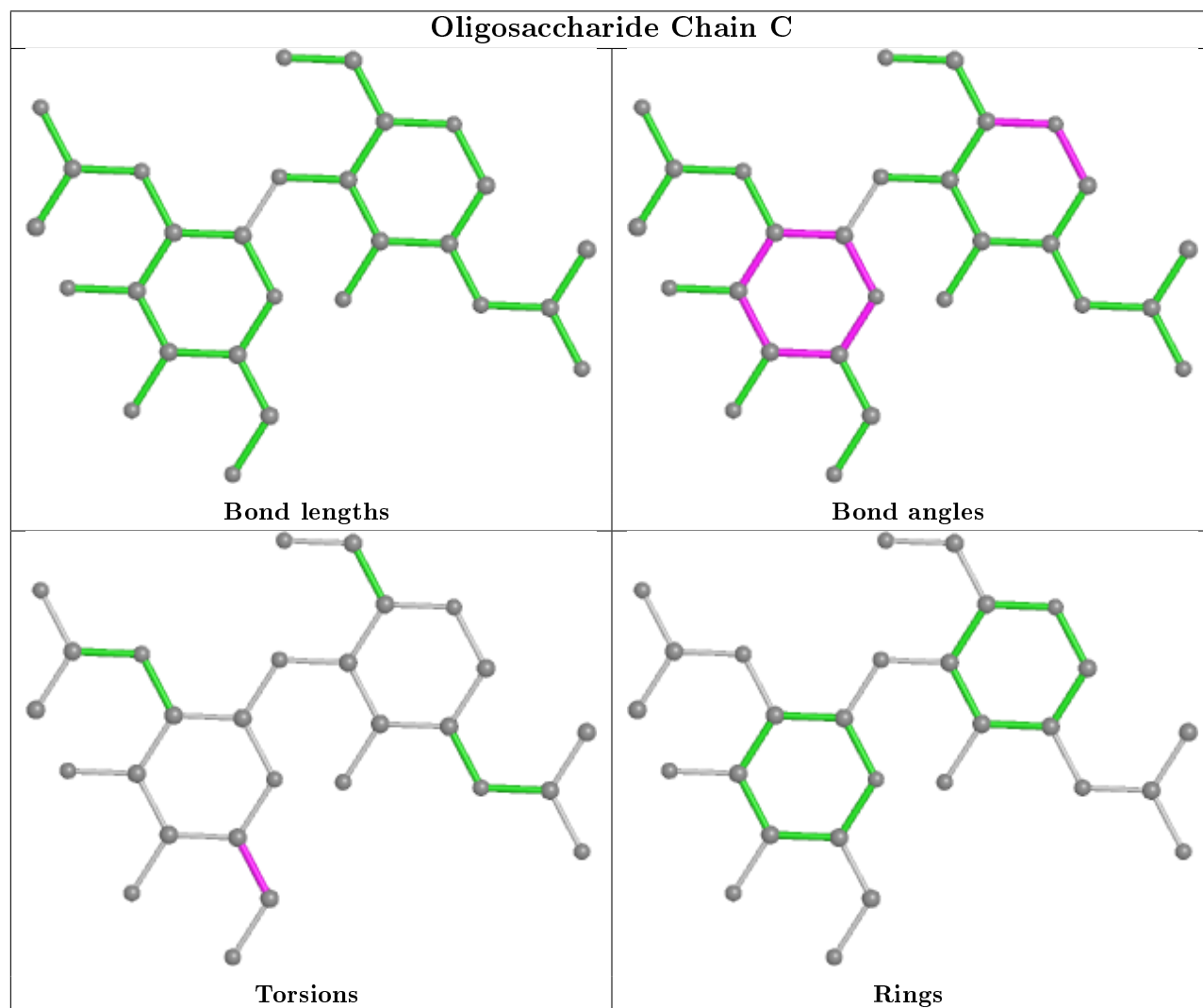
Mol	Chain	Res	Type	Atoms
5	E	2	NDG	C3-C2-N2-C7
4	D	1	NAG	O5-C5-C6-O6
5	E	3	BMA	O5-C5-C6-O6
7	H	3	BMA	O5-C5-C6-O6

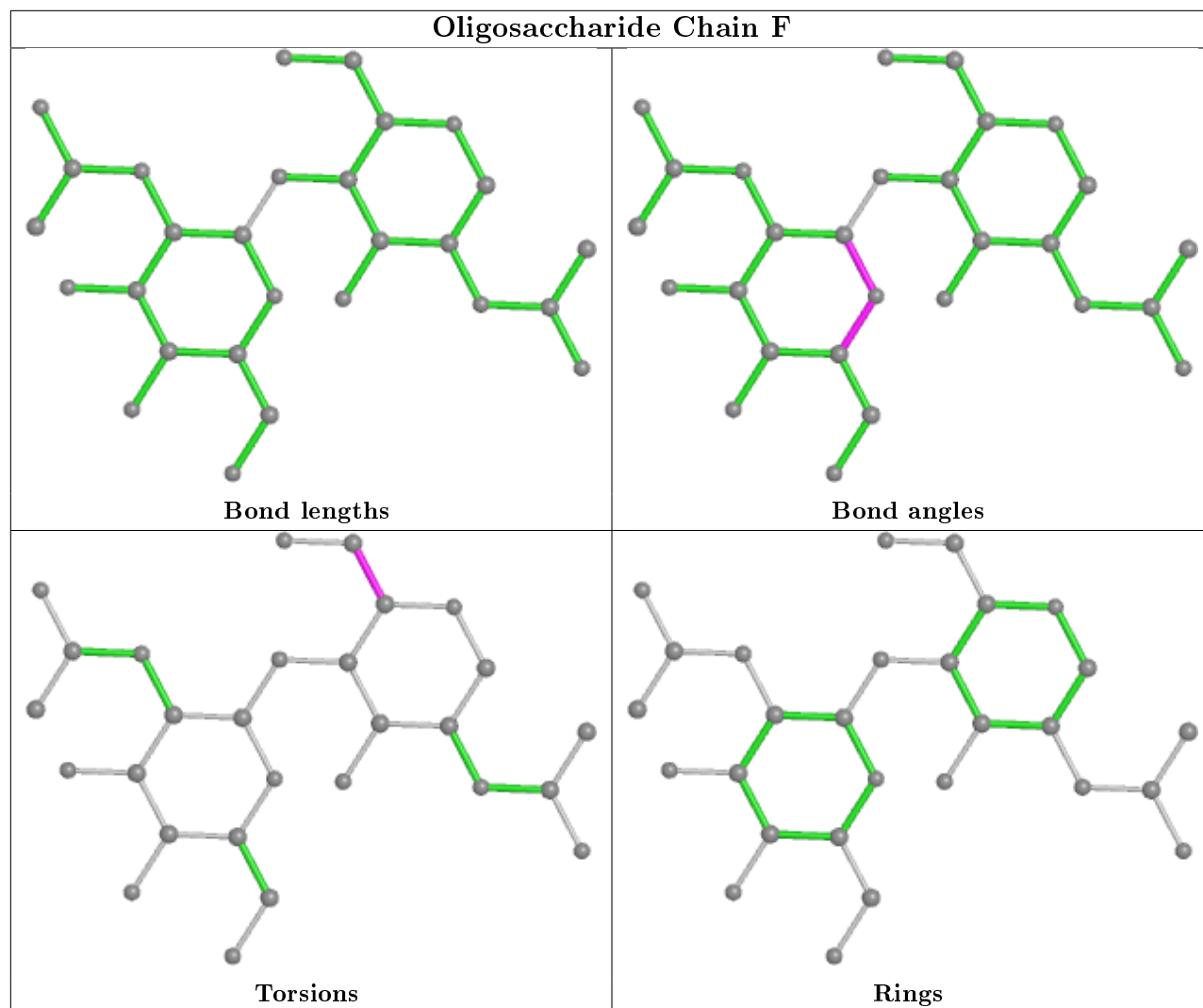
There are no ring outliers.

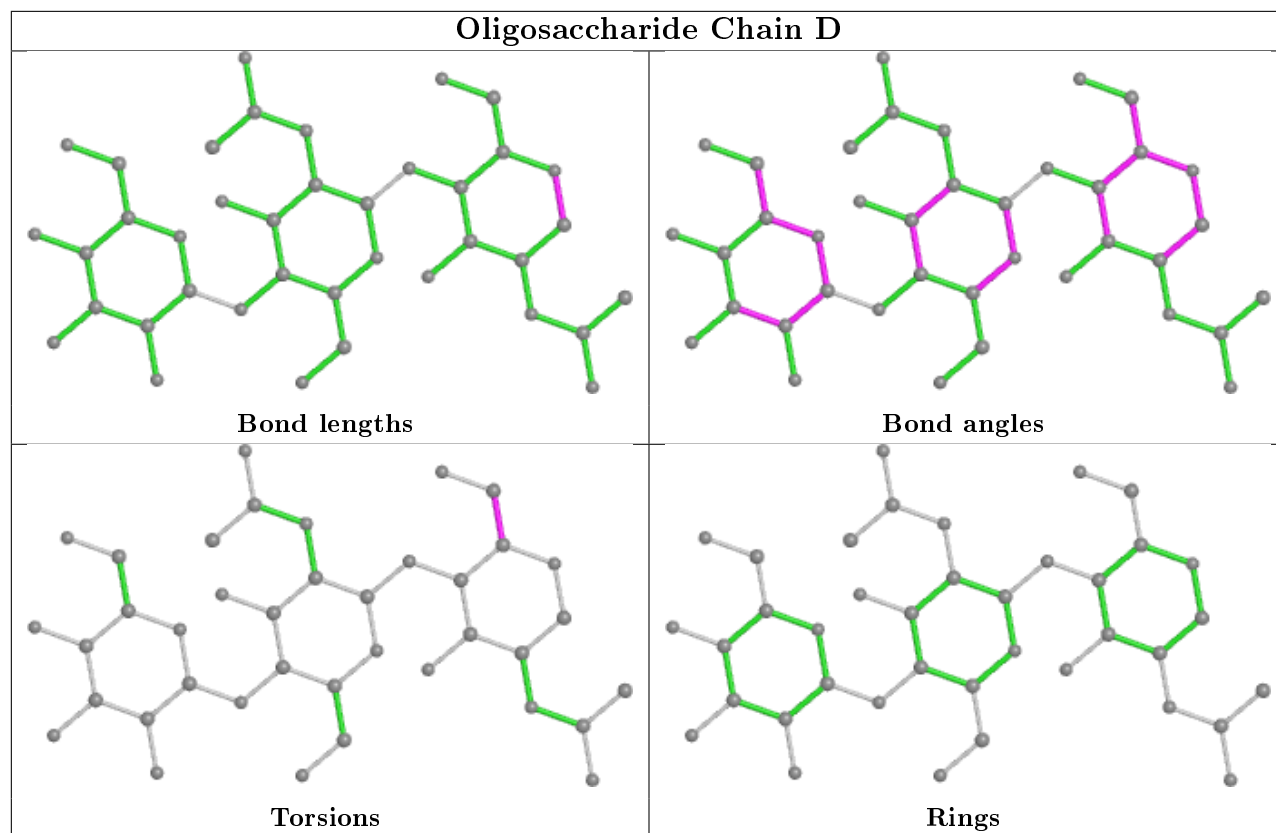
1 monomer is involved in 1 short contact:

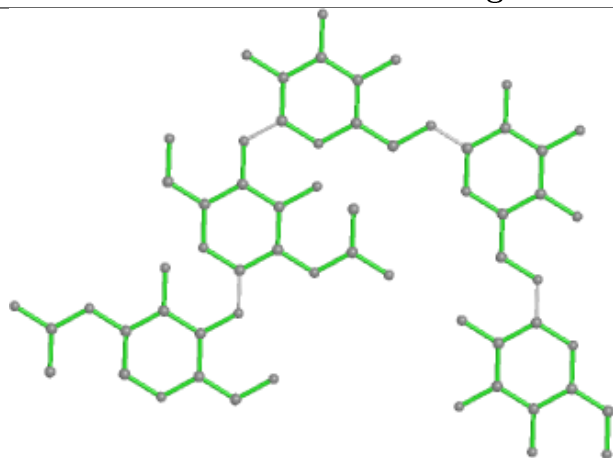
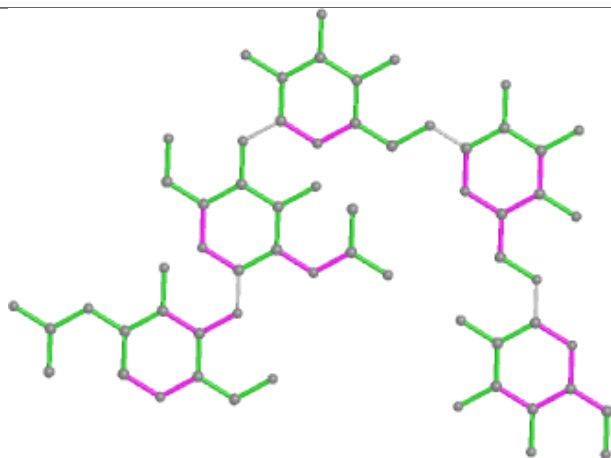
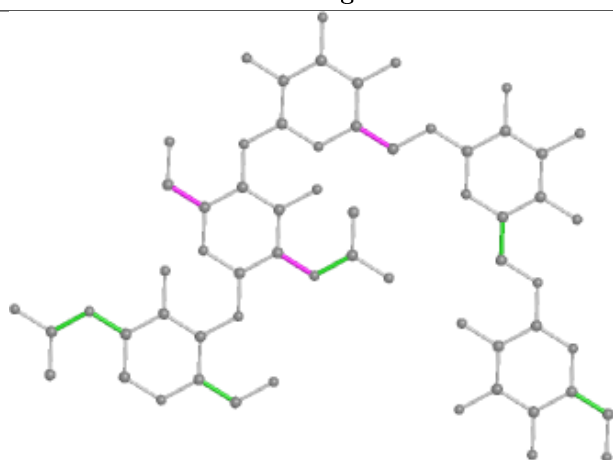
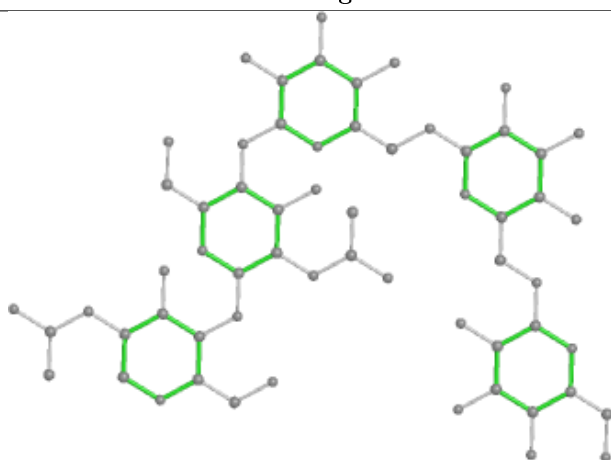
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	H	2	NDG	1	0

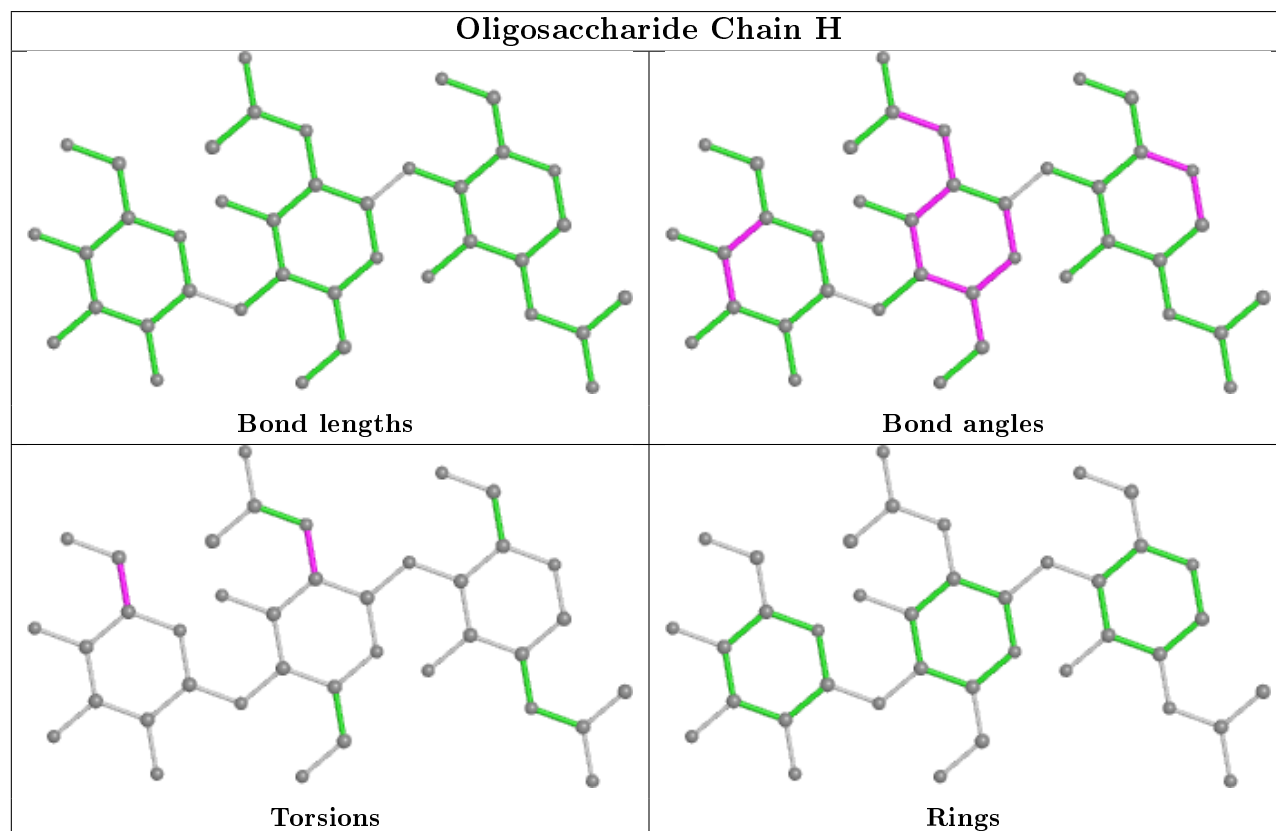
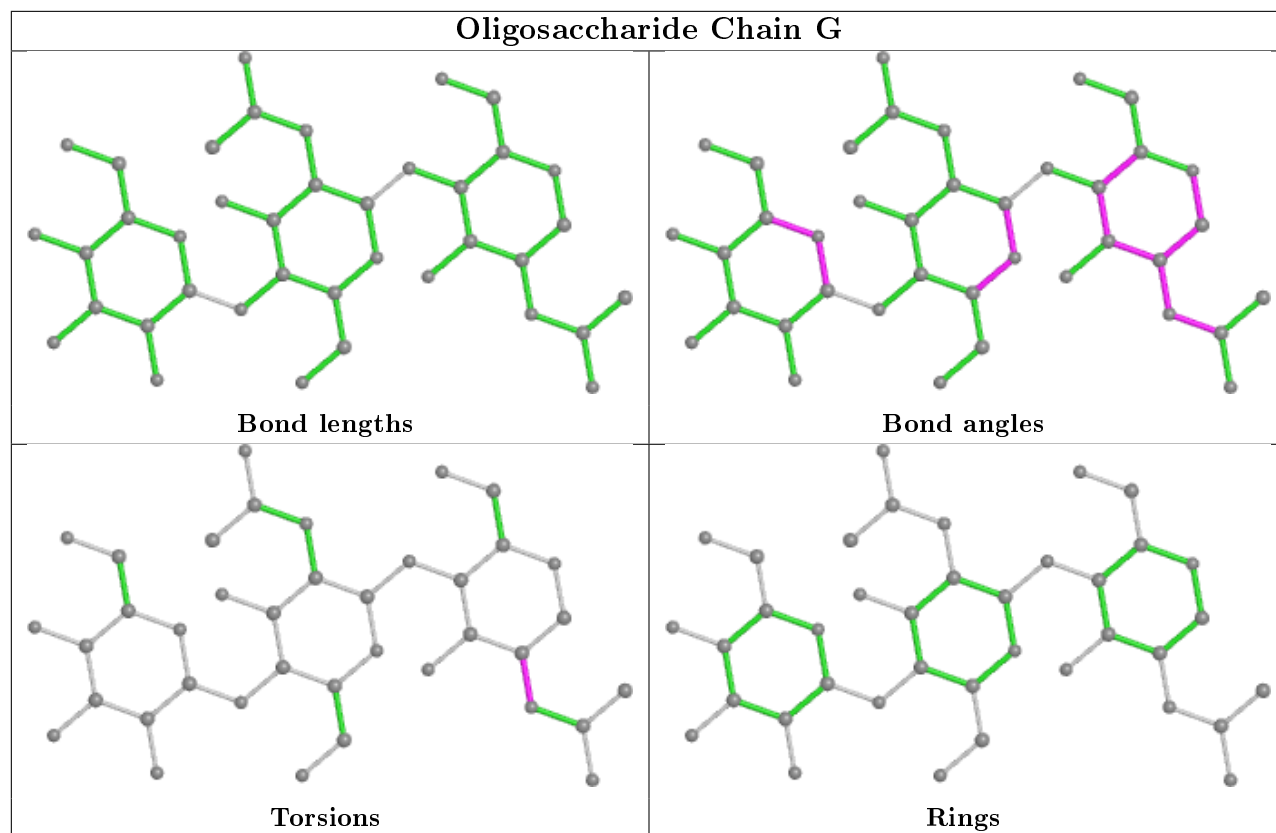
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.







**Oligosaccharide Chain E****Bond lengths****Bond angles****Torsions****Rings**



## 5.6 Ligand geometry

6 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	$\# Z  > 2$
9	FLP	A	701	-	16,19,19	1.44	1 (6%)	22,26,26	0.97	2 (9%)
8	HEM	B	601	11,2	27,50,50	2.17	6 (22%)	17,82,82	1.36	2 (11%)
10	BOG	B	1751	-	12,12,20	0.98	0	17,17,25	1.72	4 (23%)
10	BOG	A	751	-	20,20,20	0.76	0	25,25,25	1.85	4 (16%)
8	HEM	A	801	1,11	27,50,50	2.20	6 (22%)	17,82,82	1.26	1 (5%)
10	BOG	B	1750	-	13,13,20	0.87	0	18,18,25	1.69	3 (16%)

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	FLP	A	701	-	1/1/2/2	0/8/12/12	0/2/2/2
8	HEM	B	601	11,2	-	0/6/54/54	-
10	BOG	B	1751	-	-	2/2/22/31	0/1/1/1
10	BOG	A	751	-	-	7/11/31/31	0/1/1/1
8	HEM	A	801	1,11	-	1/6/54/54	-
10	BOG	B	1750	-	-	3/4/24/31	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)
8	A	801	HEM	C3D-C2D	5.60	1.54	1.37
8	B	601	HEM	C3D-C2D	5.53	1.54	1.37
9	A	701	FLP	C6-C2	-5.22	1.40	1.49
8	A	801	HEM	C3C-C2C	-4.57	1.34	1.40
8	B	601	HEM	C3C-C2C	-4.24	1.34	1.40

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	751	BOG	C1'-O1-C1	-5.74	104.32	113.84
10	B	1751	BOG	O5-C1-C2	-5.02	101.32	110.28
10	A	751	BOG	O5-C1-C2	-4.40	101.03	110.35
10	B	1750	BOG	C1'-O1-C1	-3.88	107.29	113.27
10	B	1750	BOG	O5-C1-C2	-3.88	102.14	110.35

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	A	701	FLP	C12

5 of 13 torsion outliers are listed below:

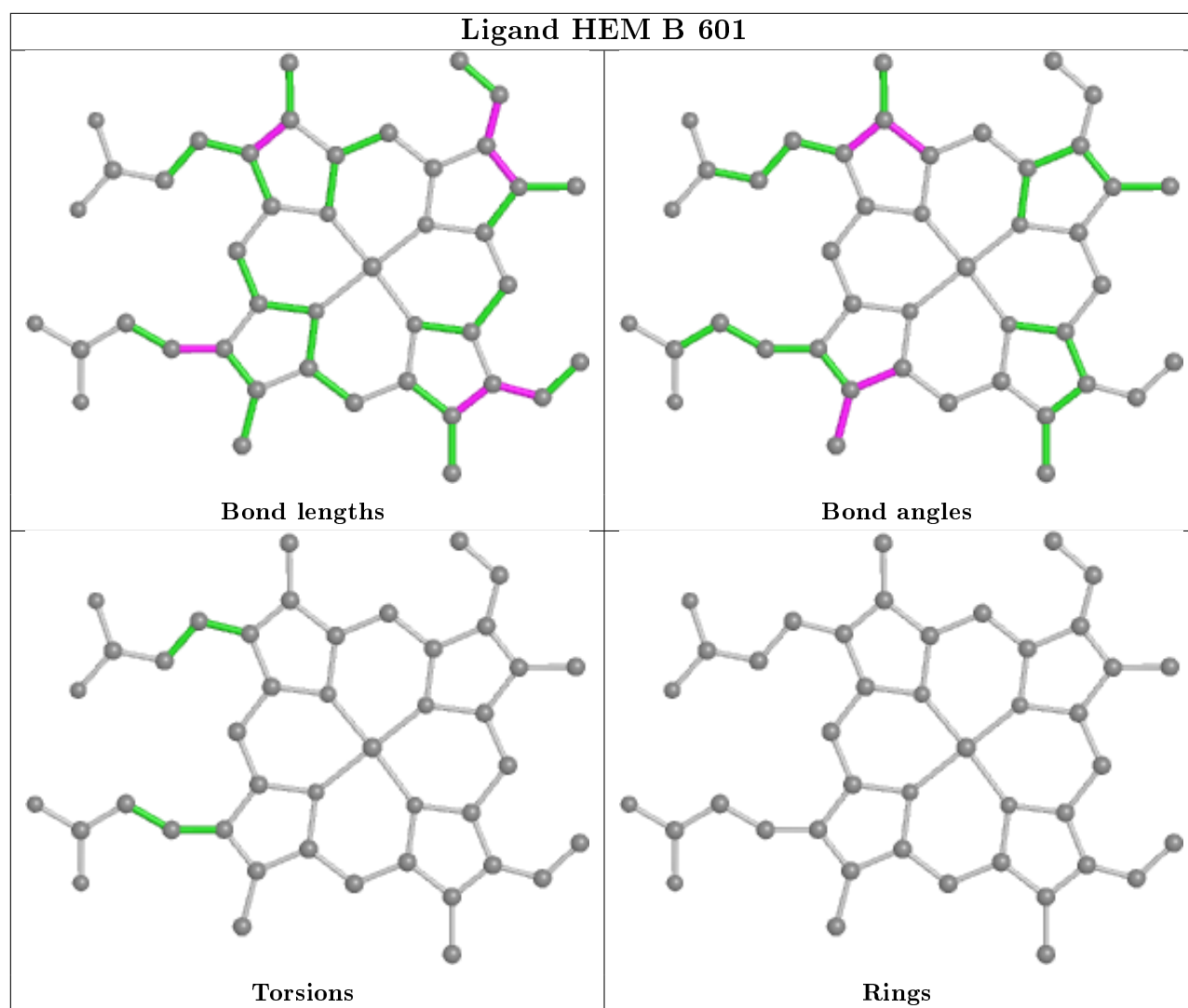
Mol	Chain	Res	Type	Atoms
8	A	801	HEM	C2A-CAA-CBA-CGA
10	B	1750	BOG	O5-C1-O1-C1'
10	B	1750	BOG	C2-C1-O1-C1'
10	B	1751	BOG	O5-C5-C6-O6
10	A	751	BOG	O5-C1-O1-C1'

There are no ring outliers.

3 monomers are involved in 3 short contacts:

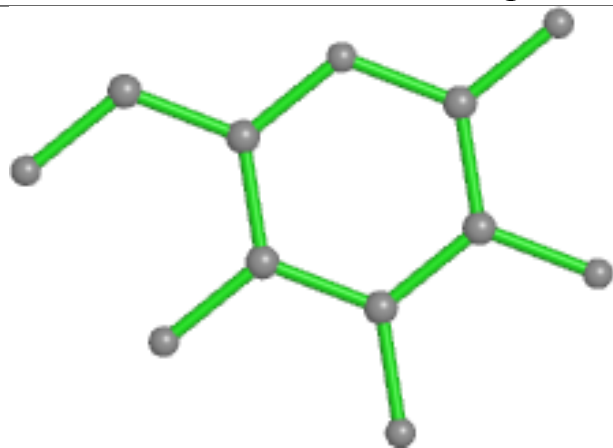
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	601	HEM	1	0
10	A	751	BOG	1	0
8	A	801	HEM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

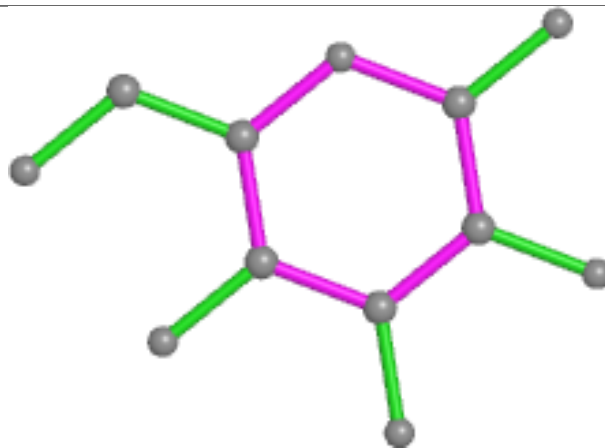




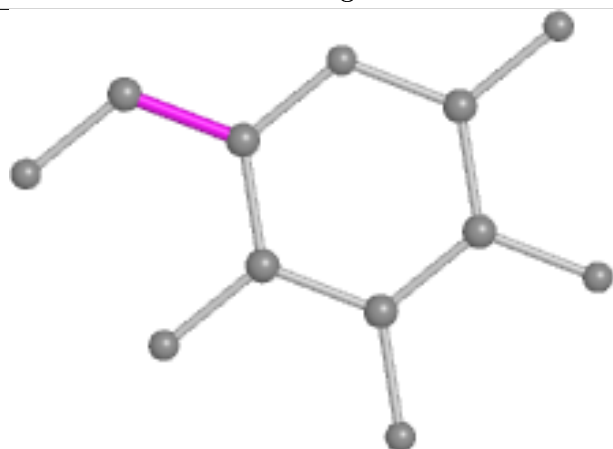
## Ligand BOG B 1751



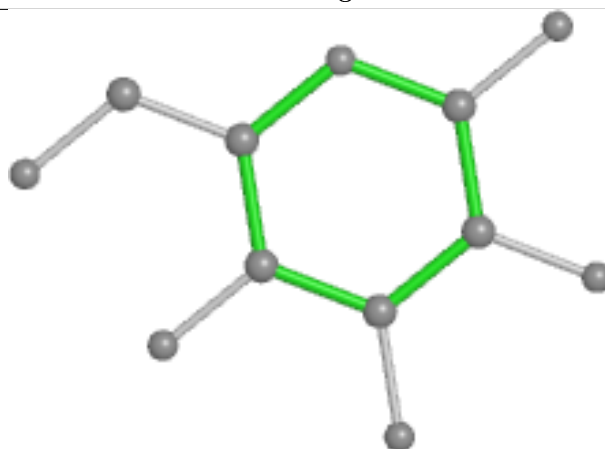
Bond lengths



Bond angles

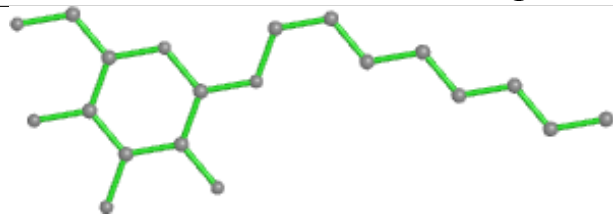


Torsions

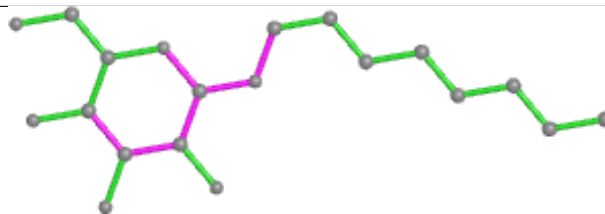


Rings

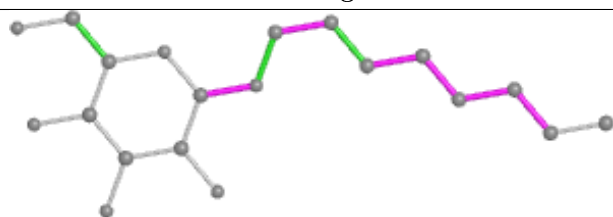
## Ligand BOG A 751



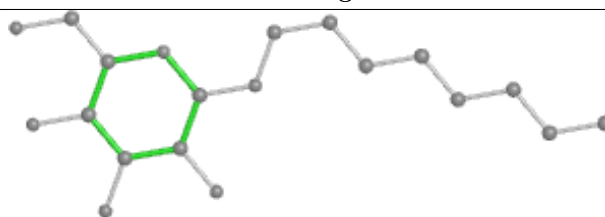
Bond lengths



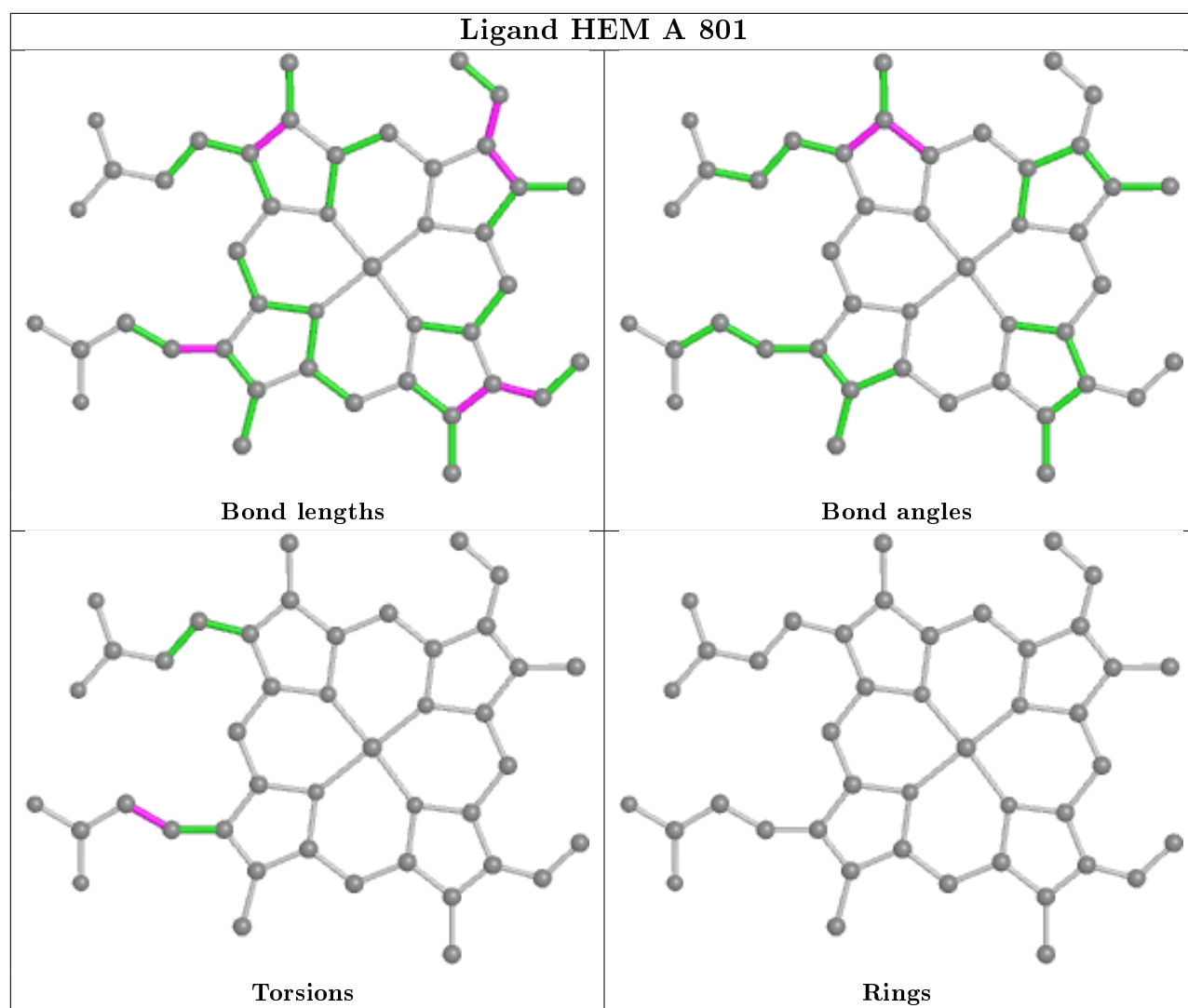
Bond angles

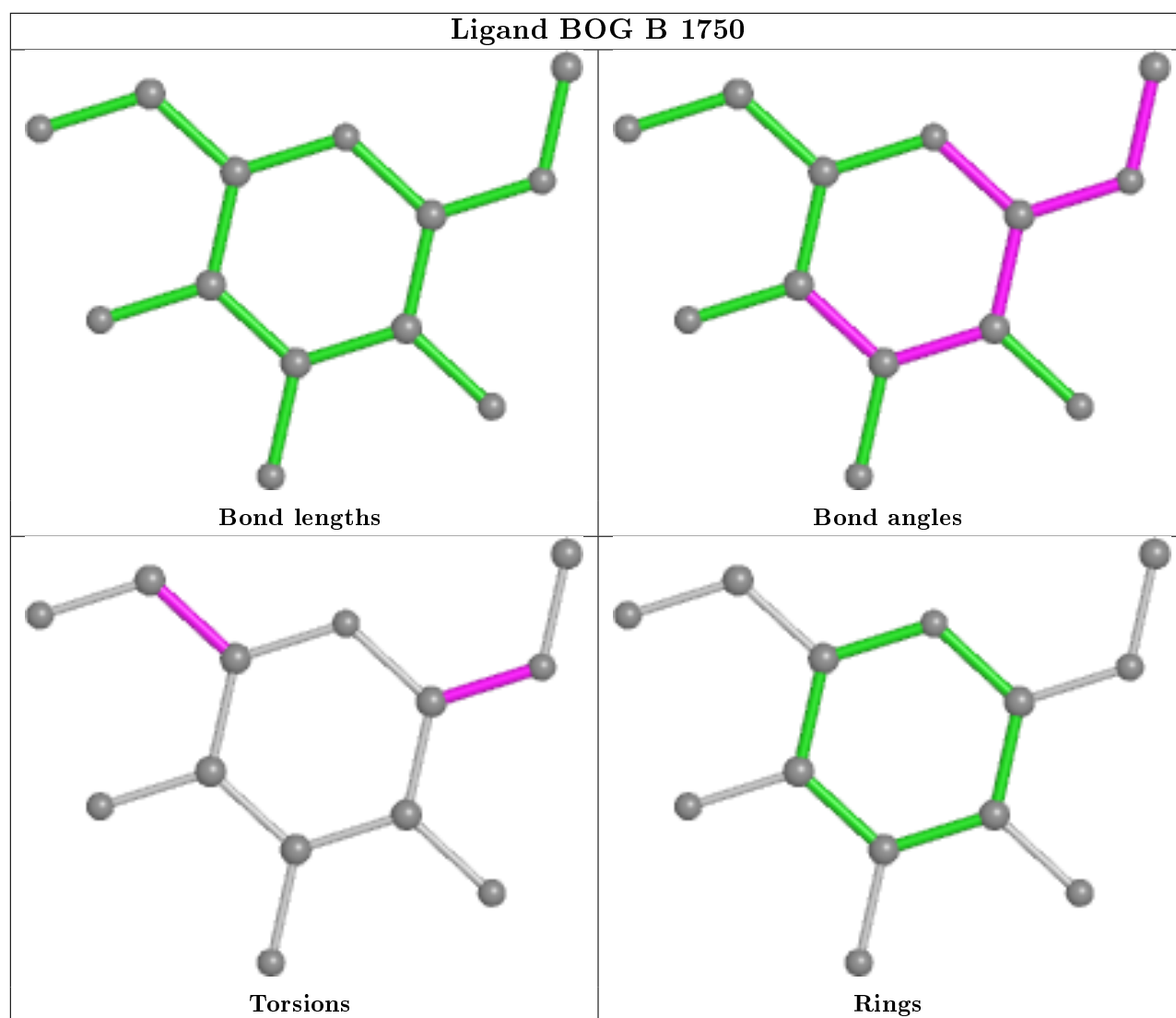


Torsions



Rings





## 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, 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	553/553 (100%)	0.07	15 (2%) 54 63	43, 56, 71, 79	0
2	B	553/553 (100%)	0.01	16 (2%) 51 61	44, 58, 74, 81	0
All	All	1106/1106 (100%)	0.04	31 (2%) 53 62	43, 56, 72, 81	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	280	PRO	4.2
2	B	123[A]	LEU	4.1
2	B	124[A]	ILE	3.3
2	B	488	ALA	3.2
1	A	107	PHE	3.2

### 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, 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.

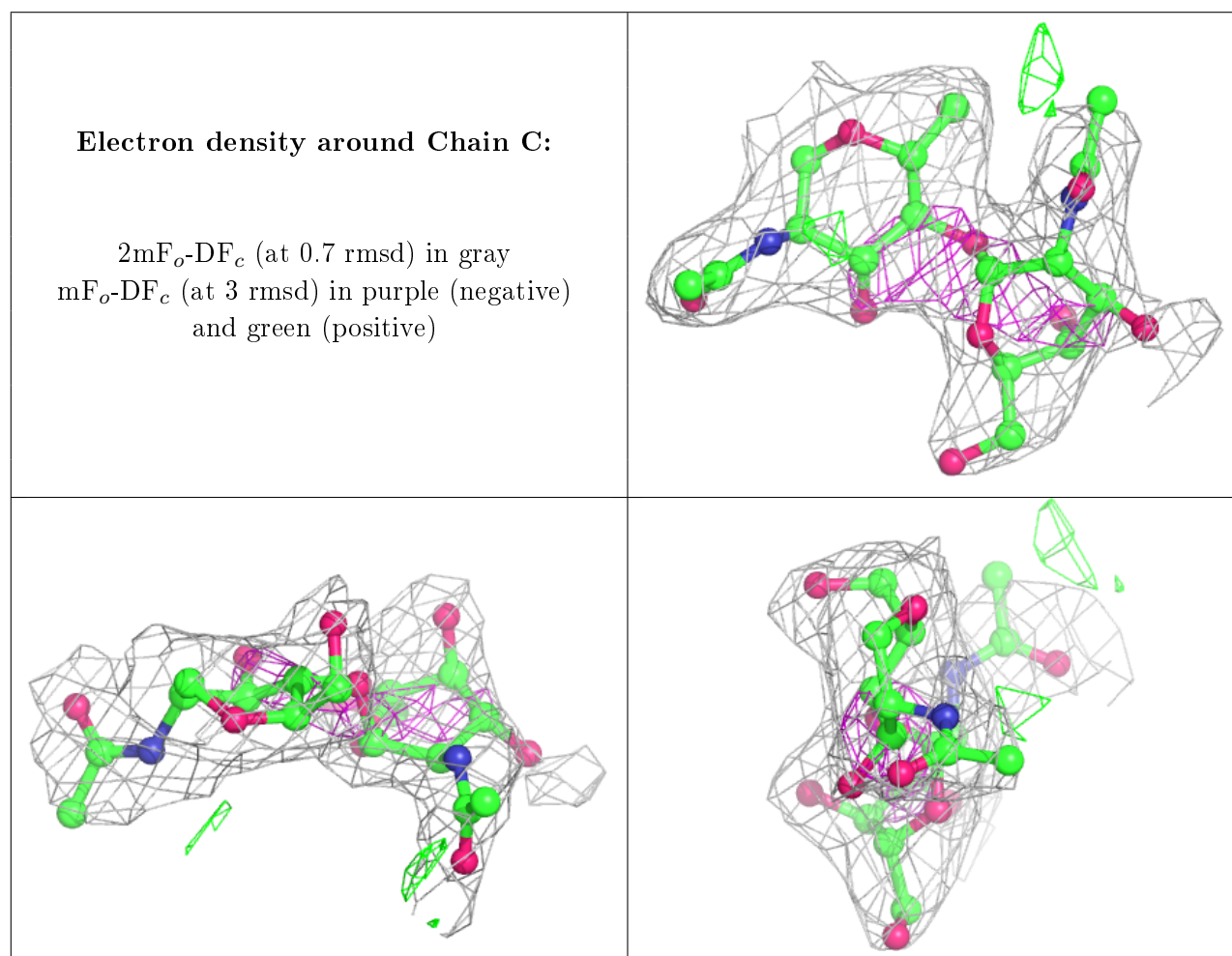
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	MAN	E	4	11/12	0.65	0.33	89,91,92,94	0
3	NDG	F	2	14/15	0.84	0.28	74,76,77,77	0
7	NDG	H	2	14/15	0.84	0.33	61,64,65,68	0
6	MAN	G	3	11/12	0.84	0.31	79,80,80,80	0
5	MAN	E	5	11/12	0.85	0.36	95,95,96,96	0

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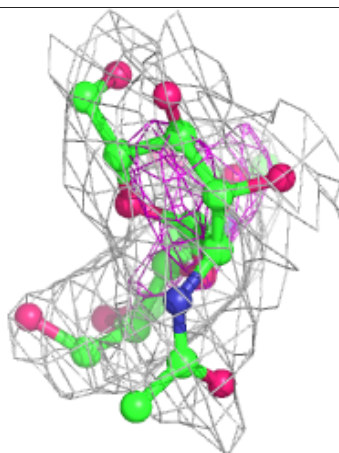
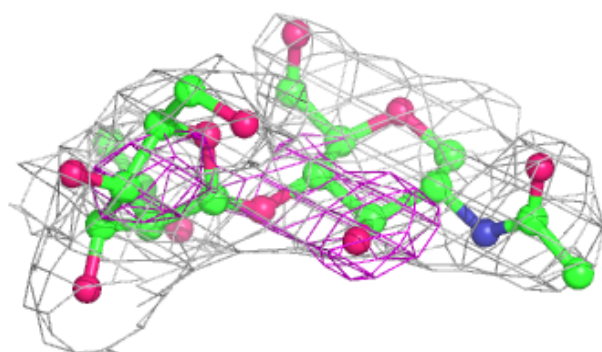
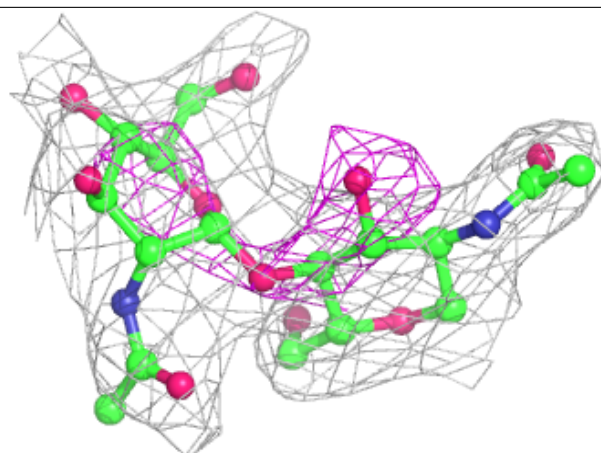
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NDG	C	2	14/15	0.86	0.32	75,77,79,79	0
7	BMA	H	3	11/12	0.86	0.39	69,70,70,70	0
5	NDG	E	2	14/15	0.88	0.34	64,67,69,73	0
6	NAG	G	1	14/15	0.90	0.27	56,59,63,67	0
4	BMA	D	3	11/12	0.90	0.33	77,78,79,79	0
6	NAG	G	2	14/15	0.91	0.28	71,73,75,77	0
5	BMA	E	3	11/12	0.91	0.38	77,80,84,87	0
3	NAG	F	1	14/15	0.92	0.29	59,65,67,71	0
3	NAG	C	1	14/15	0.92	0.20	60,66,68,72	0
4	NAG	D	1	14/15	0.93	0.19	56,60,62,66	0
4	NAG	D	2	14/15	0.93	0.17	69,71,73,75	0
5	NAG	E	1	14/15	0.94	0.14	46,49,53,58	0
7	NAG	H	1	14/15	0.95	0.13	45,48,51,56	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.

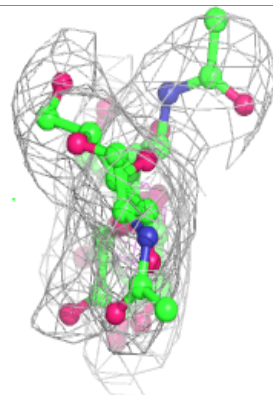
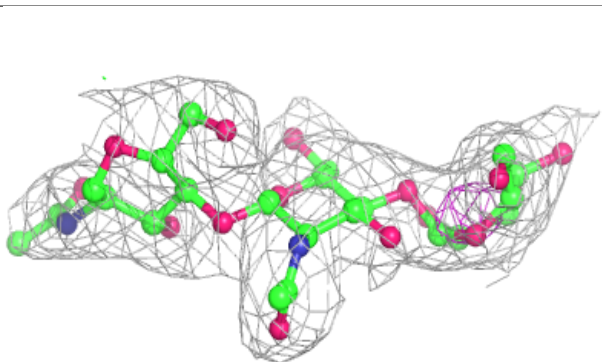
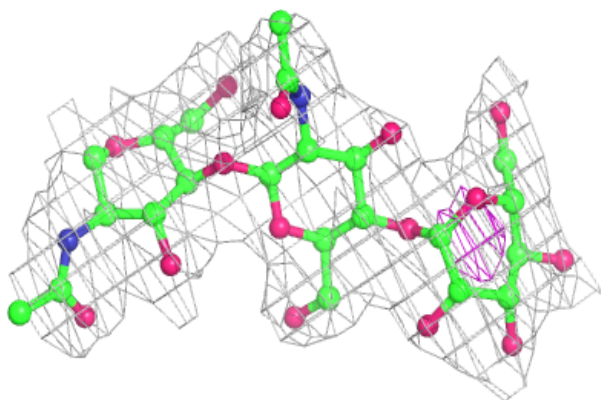


**Electron density around Chain F:**

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

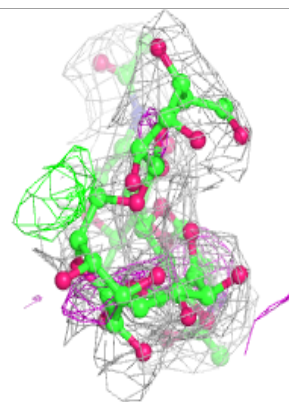
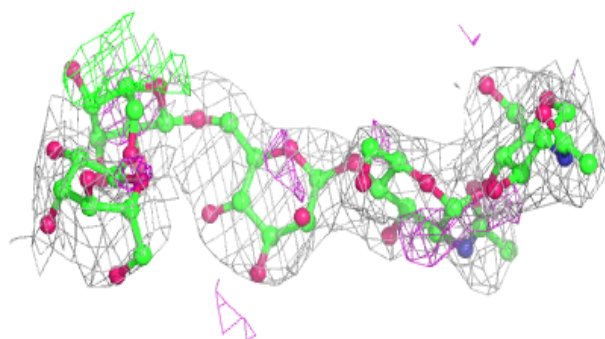
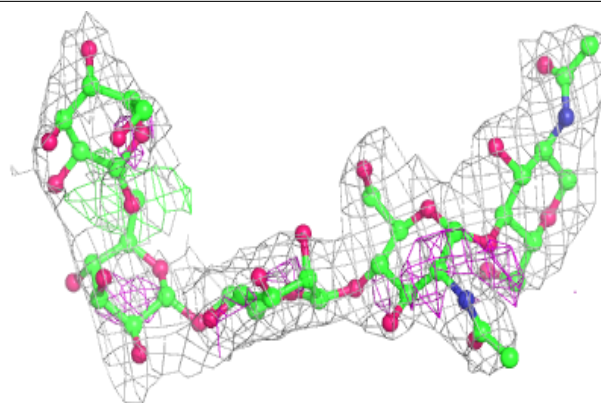
**Electron density around Chain D:**

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

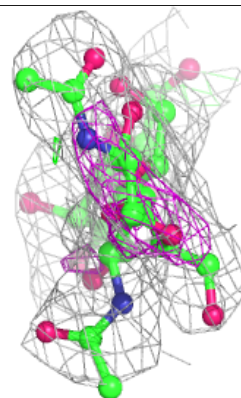
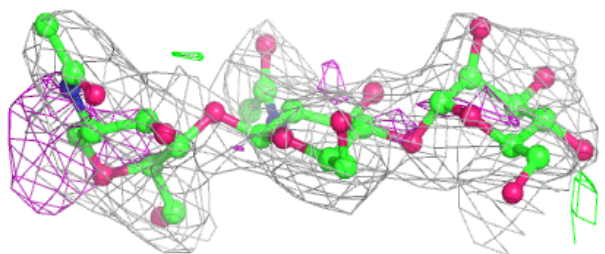
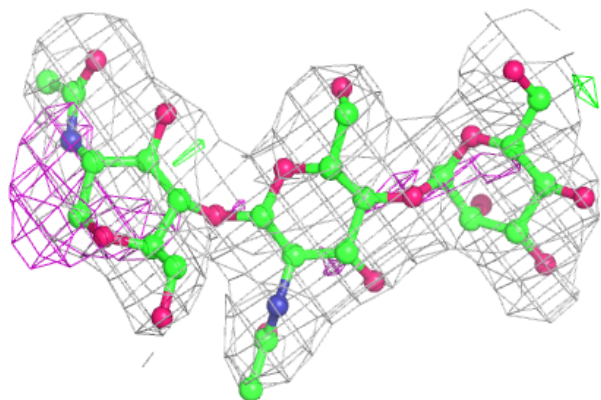


**Electron density around Chain E:**

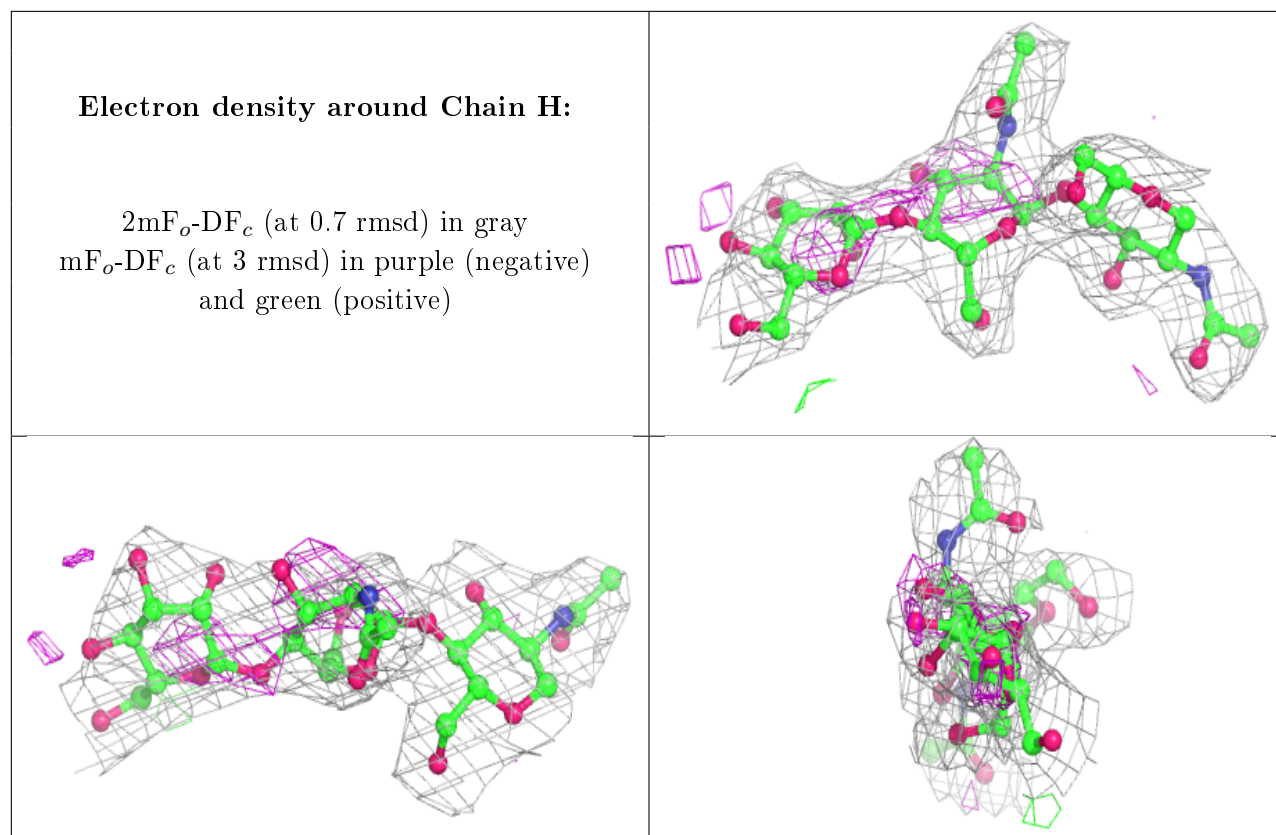
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**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 [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.

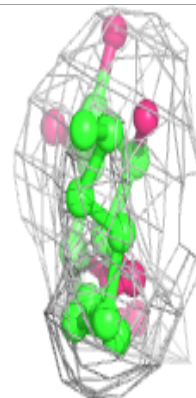
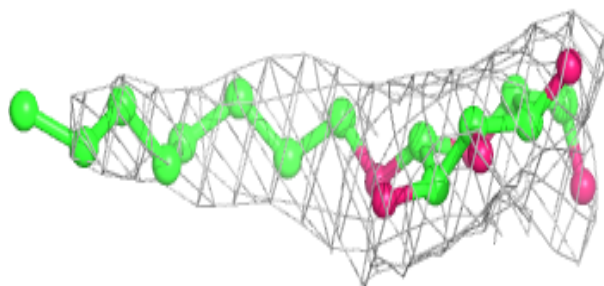
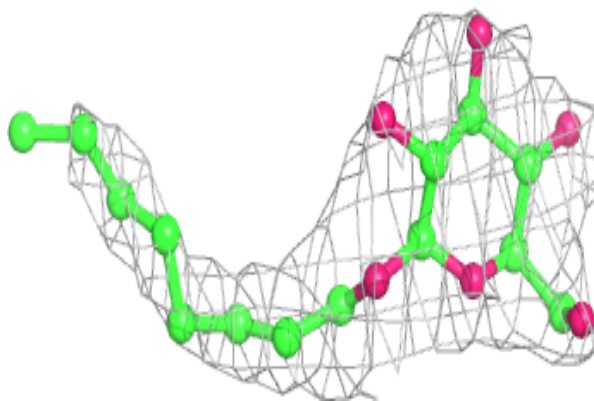
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
10	BOG	A	751	20/20	0.88	0.29	78,82,82,83	0
10	BOG	B	1750	13/20	0.90	0.27	94,94,94,95	0
10	BOG	B	1751	12/20	0.91	0.19	87,88,88,89	0
8	HEM	A	801	43/43	0.96	0.18	52,56,62,66	0
8	HEM	B	601	43/43	0.96	0.19	54,58,64,66	0
9	FLP	A	701	18/18	0.97	0.18	53,55,57,58	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.



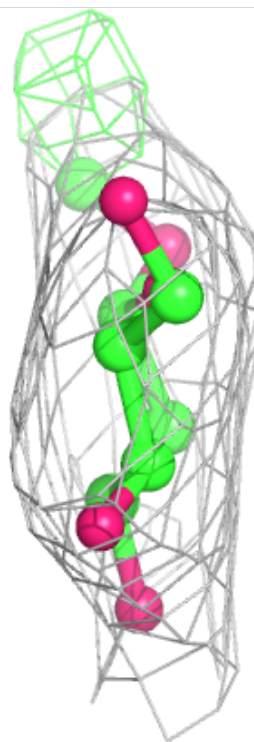
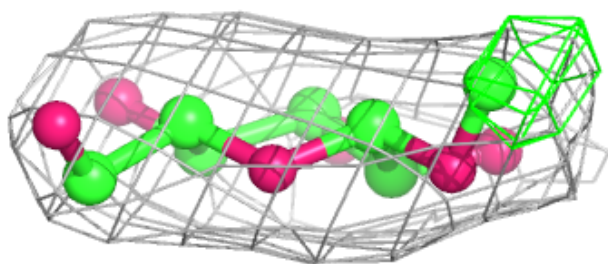
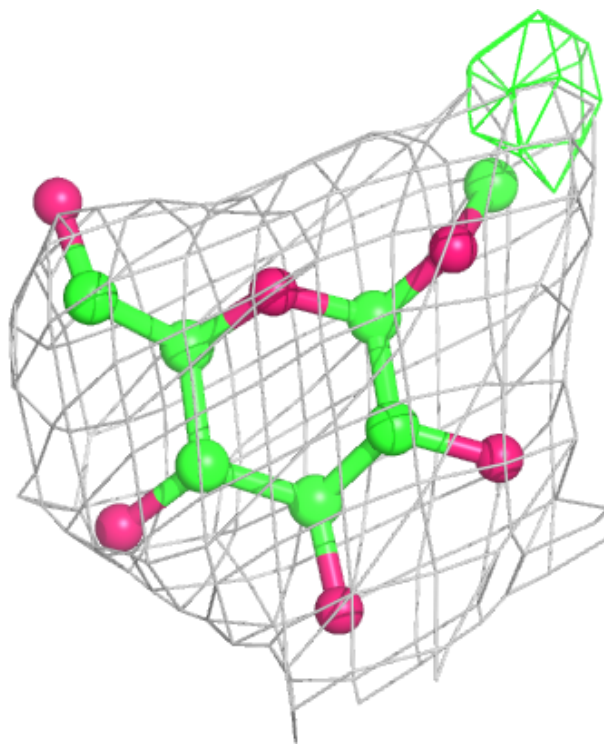
**Electron density around BOG A 751:**

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



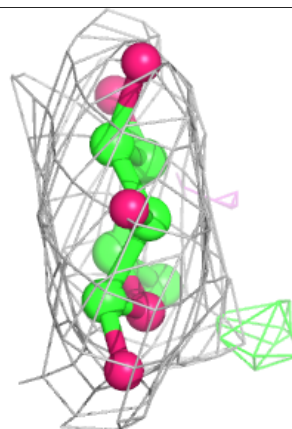
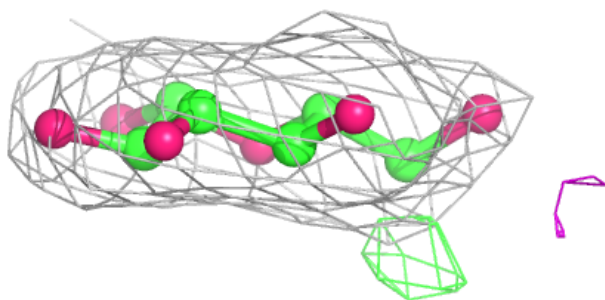
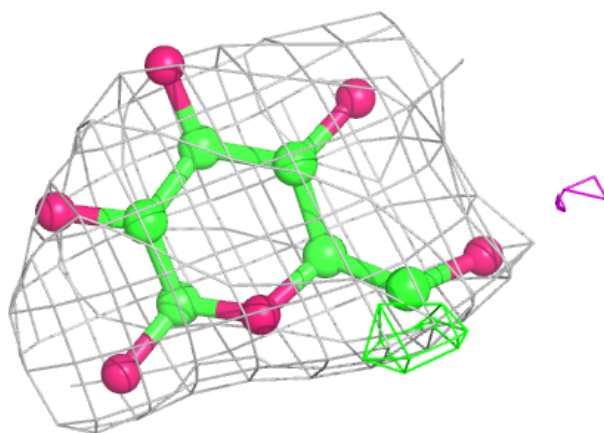
**Electron density around BOG B 1750:**

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



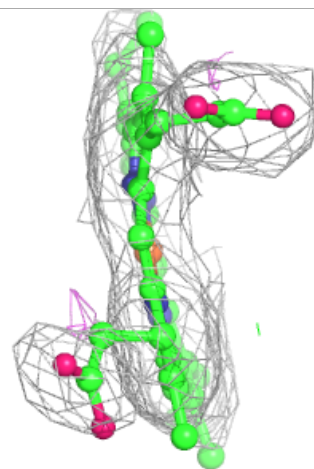
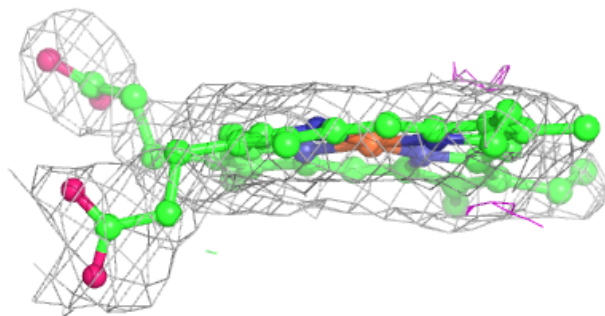
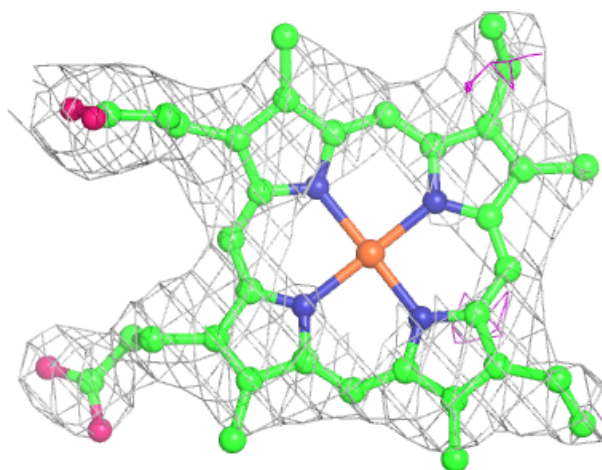
**Electron density around BOG B 1751:**

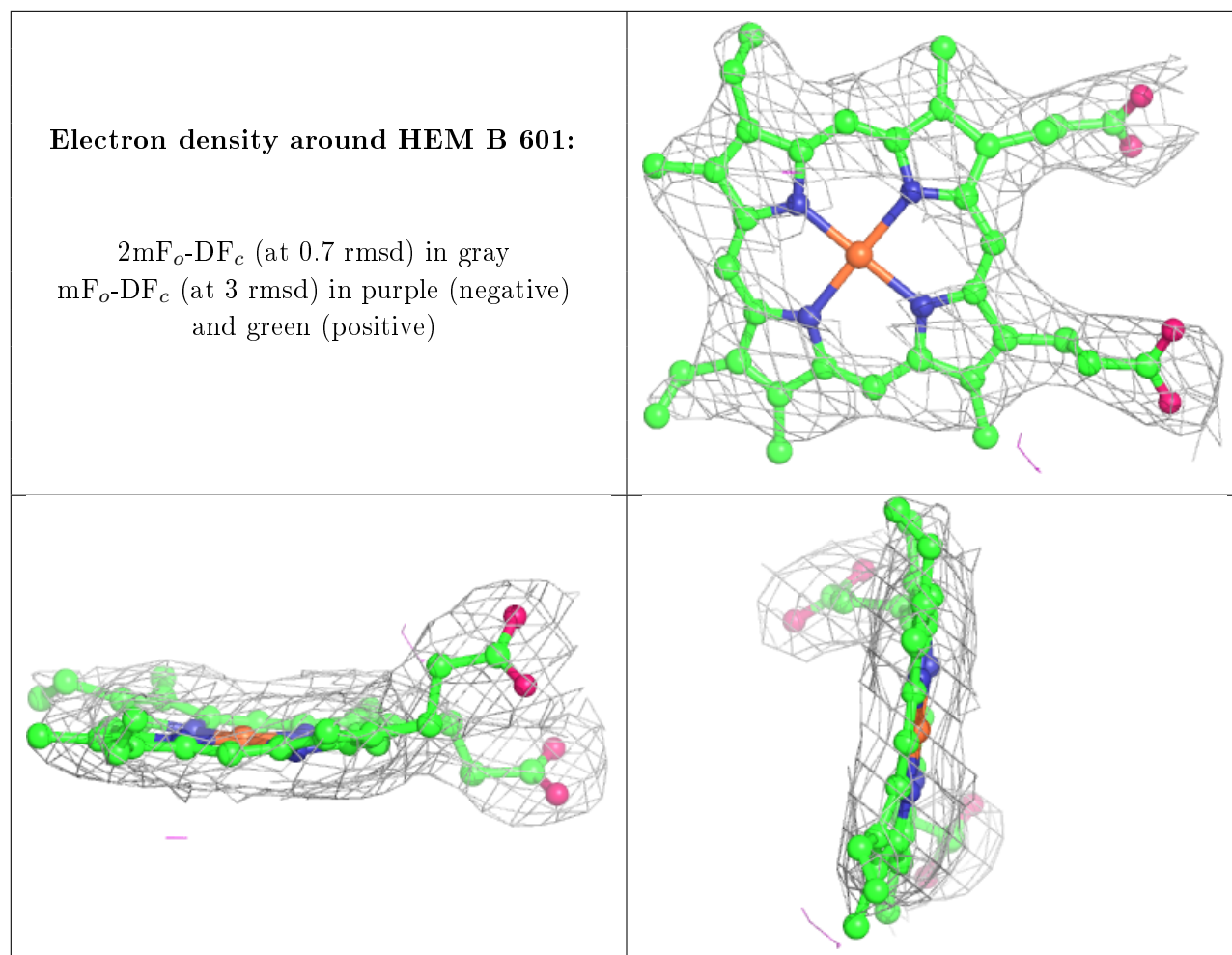
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEM 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)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.