



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 30, 2025 – 01:16 pm BST

PDB ID : 9IFP / pdb_00009ifp
Title : Unspecific peroxygenase from *Psathyrella aberdarensis* (PabUPO-II) in complex with 2,6-dimethoxyphenol
Authors : Fernandez-Garcia, A.; Sanz-Aparicio, J.
Deposited on : 2025-02-18
Resolution : 1.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

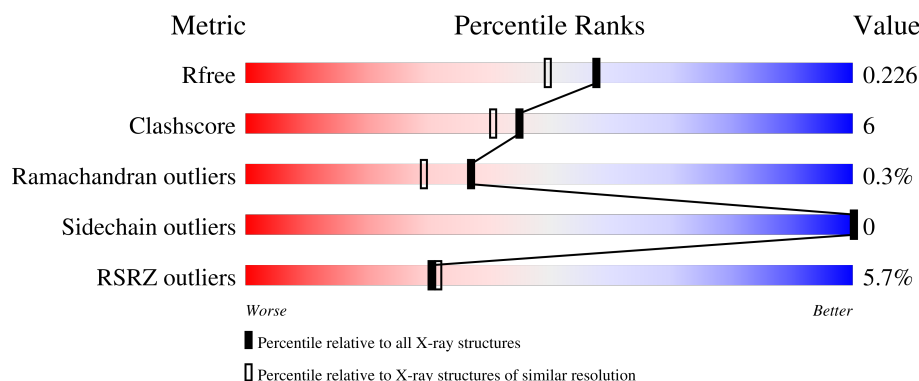
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	164625	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (1.90-1.90)

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

Mol	Chain	Length	Quality of chain
1	A	335	<div> <div>2%</div> <div> <div></div> <div>94%</div> <div>6%</div> </div> </div>
1	B	335	<div> <div>7%</div> <div> <div></div> <div>92%</div> <div>8%</div> </div> </div>
1	C	335	<div> <div>8%</div> <div> <div></div> <div>95%</div> <div>5%</div> </div> </div>
2	D	5	<div> <div>20%</div> <div>80%</div> </div>
3	E	7	<div> <div>29%</div> <div>71%</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
5	EPE	A	408	-	-	X	-
7	3DM	B	411	-	-	X	-
7	3DM	B	418	-	-	X	-

2 Entry composition [i](#)

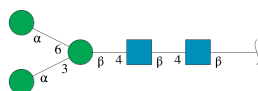
There are 13 unique types of molecules in this entry. The entry contains 9232 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Heme-thiolate peroxidase.

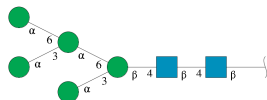
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	5	0
			2617	1662	452	497	6			
1	B	335	Total	C	N	O	S	0	3	0
			2609	1657	451	495	6			
1	C	335	Total	C	N	O	S	0	2	0
			2598	1650	448	494	6			

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



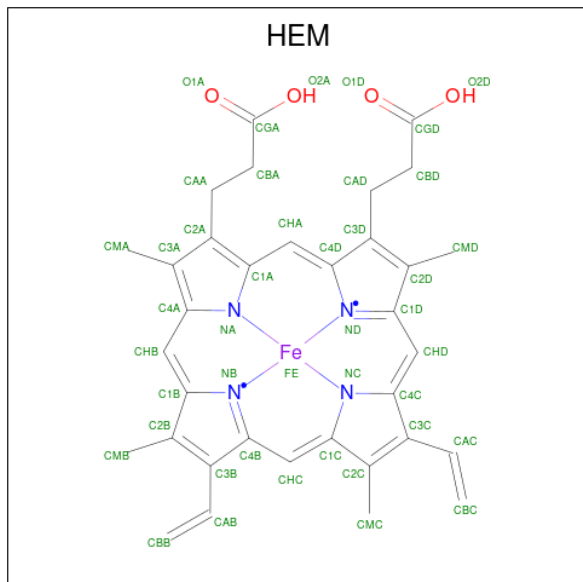
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	5	Total	C	N	O	0	0	0
			61	34	2	25			

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



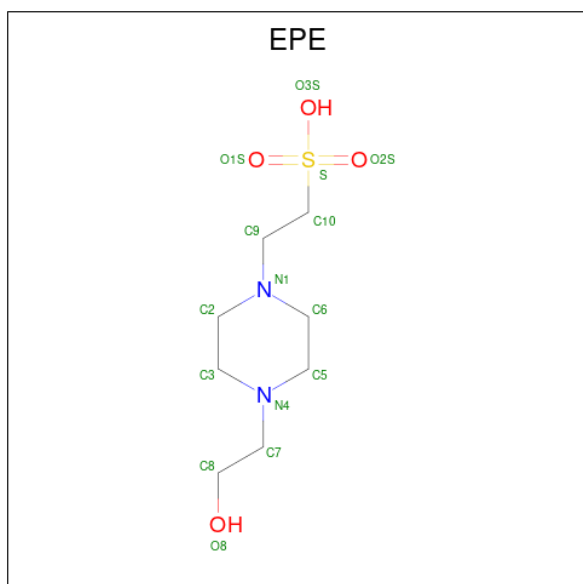
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



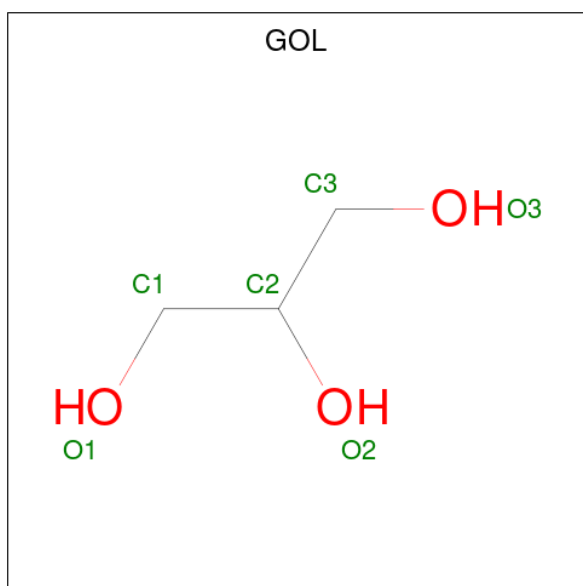
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



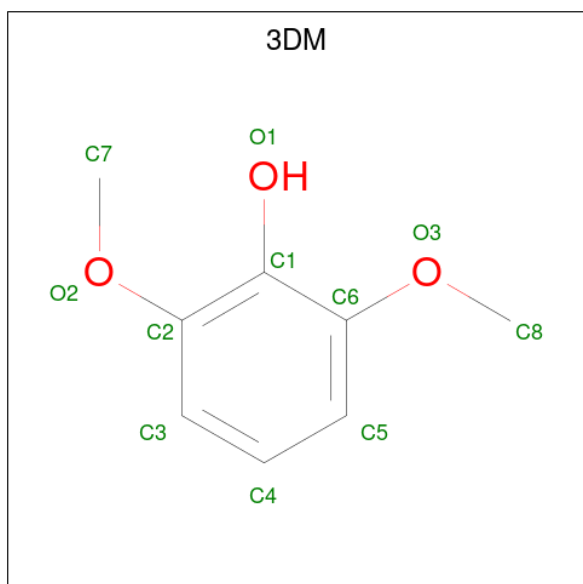
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is 2,6-dimethoxyphenol (CCD ID: 3DM) (formula: C₈H₁₀O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			11	8	3		
7	A	1	Total	C	O	0	0
			11	8	3		
7	A	1	Total	C	O	0	0
			11	8	3		
7	B	1	Total	C	O	0	0
			11	8	3		
7	B	1	Total	C	O	0	0
			11	8	3		
7	C	1	Total	C	O	0	0
			11	8	3		

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	B	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

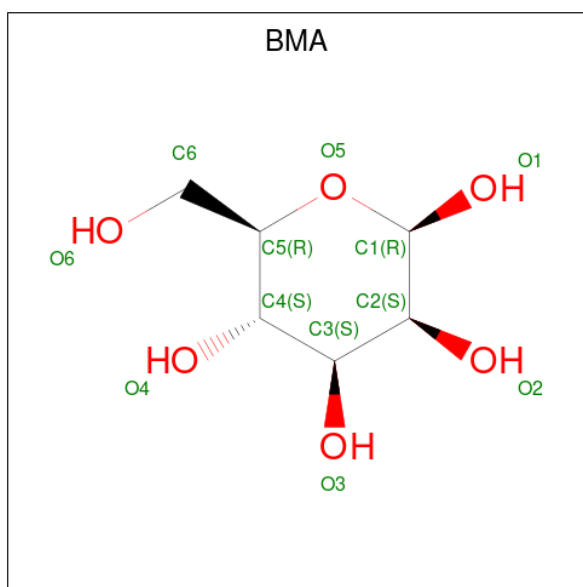
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Mg	0	0
			1	1		
9	B	1	Total	Mg	0	0
			1	1		
9	C	1	Total	Mg	0	0
			1	1		

- Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



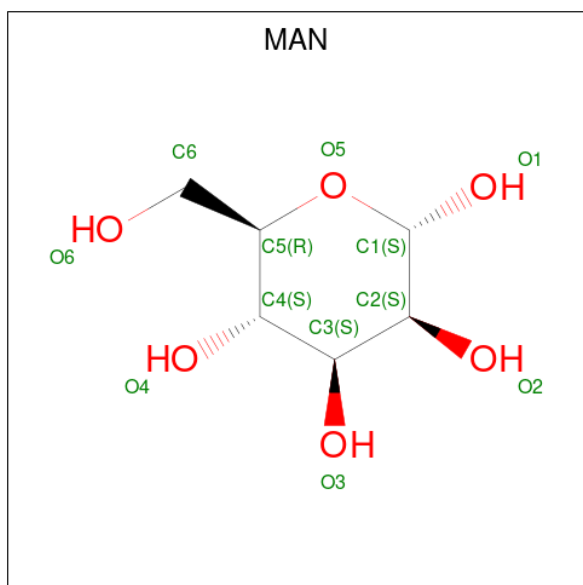
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	1	Total	C	N	O	0	0
			14	8	1	5		
10	B	1	Total	C	N	O	0	0
			14	8	1	5		
10	B	1	Total	C	N	O	0	0
			14	8	1	5		
10	B	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		
10	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 11 is beta-D-mannopyranose (CCD ID: BMA) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	C	O	0	0
			11	6	5		
11	B	1	Total	C	O	0	0
			11	6	5		
11	C	1	Total	C	O	0	0
			11	6	5		
11	C	1	Total	C	O	0	0
			11	6	5		

- Molecule 12 is alpha-D-mannopyranose (CCD ID: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	C	O	0	0
			11	6	5		
12	B	1	Total	C	O	0	0
			11	6	5		
12	B	1	Total	C	O	0	0
			11	6	5		
12	C	1	Total	C	O	0	0
			11	6	5		

- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	307	Total	O	0	0
			307	307		
13	B	212	Total	O	0	0
			212	212		
13	C	186	Total	O	0	0
			186	186		

3 Residue-property plots

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.

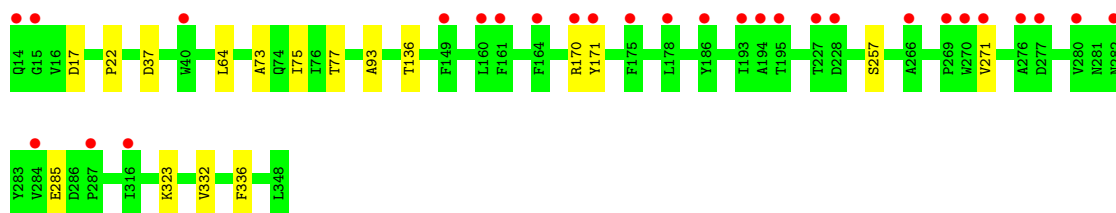
- Molecule 1: Heme-thiolate peroxidase



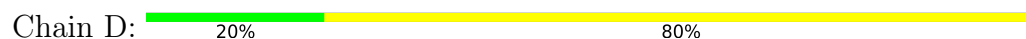
- Molecule 1: Heme-thiolate peroxidase



- Molecule 1: Heme-thiolate peroxidase



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



- Molecule 3: α -D-mannopyranose-(1-3)-[α -D-mannopyranose-(1-6)] α -D-mannopyranose-(1-6)-[α -D-mannopyranose-(1-3)] β -D-mannopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose-(1-4)-2-acetamido-2-deoxy- β -D-glucopyranose

Chain E:  29% 71%

MAG1
MAG2
EMA3
MAN4
MAN5
MAN6
MAN7

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	271.30Å 74.50Å 106.15Å 90.00° 111.80° 90.00°	Depositor
Resolution (Å)	45.93 – 1.90 45.93 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.93-1.90) 99.8 (45.93-1.90)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.200 , 0.219 0.208 , 0.226	Depositor DCC
R_{free} test set	7875 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtriage
Anisotropy	0.719	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.010 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9232	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: MAN, MG, GOL, HEM, BMA, NAG, SO4, 3DM, EPE

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	0/2713	0.92	1/3709 (0.0%)
1	B	0.55	0/2699	0.91	1/3690 (0.0%)
1	C	0.56	0/2685	0.92	1/3672 (0.0%)
All	All	0.57	0/8097	0.92	3/11071 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	37	ASP	CA-CB-CG	5.76	118.36	112.60
1	B	340	ASP	CA-CB-CG	5.30	117.90	112.60
1	A	67	ASP	CA-CB-CG	5.13	117.73	112.60

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	2617	0	2463	26	0
1	B	2609	0	2452	30	0
1	C	2598	0	2438	10	0
2	D	61	0	52	0	0
3	E	83	0	70	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	43	0	30	1	0
4	B	43	0	30	3	0
4	C	43	0	30	5	0
5	A	30	0	36	11	0
5	B	45	0	54	12	0
6	A	36	0	48	2	0
6	B	18	0	24	6	0
6	C	12	0	16	0	0
7	A	33	0	30	2	0
7	B	22	0	20	18	0
7	C	11	0	10	5	0
8	A	10	0	0	0	0
8	B	5	0	0	0	0
8	C	5	0	0	0	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	C	1	0	0	0	0
10	B	56	0	48	0	0
10	C	56	0	48	0	0
11	B	22	0	18	0	0
11	C	22	0	19	0	0
12	B	33	0	29	0	0
12	C	11	0	10	0	0
13	A	307	0	0	9	0
13	B	212	0	0	11	0
13	C	186	0	0	4	0
All	All	9232	0	7975	95	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 6.

The worst 5 of 95 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)
7:B:411:3DM:H8A	7:B:418:3DM:C7	1.48	1.43
7:B:411:3DM:C8	7:B:418:3DM:O2	1.68	1.38
6:A:405:GOL:H12	13:A:643:HOH:O	1.48	1.12
5:B:410:EPE:H51	13:B:601:HOH:O	1.48	1.11
7:B:411:3DM:H8A	7:B:418:3DM:O2	0.90	1.07

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	338/335 (101%)	330 (98%)	7 (2%)	1 (0%)	37	29
1	B	336/335 (100%)	328 (98%)	7 (2%)	1 (0%)	37	29
1	C	335/335 (100%)	327 (98%)	7 (2%)	1 (0%)	37	29
All	All	1009/1005 (100%)	985 (98%)	21 (2%)	3 (0%)	37	29

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	SER
1	B	257	SER
1	C	257	SER

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	279/274 (102%)	279 (100%)	0	100	100
1	B	277/274 (101%)	277 (100%)	0	100	100
1	C	276/274 (101%)	276 (100%)	0	100	100
All	All	832/822 (101%)	832 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	B	200	GLN
1	B	324	ASN
1	C	200	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 ⓘ

12 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	D	1	2,1	14,14,15	0.50	0	17,19,21	1.64	3 (17%)
2	NAG	D	2	2	14,14,15	0.41	0	17,19,21	0.88	0
2	BMA	D	3	2	11,11,12	0.81	0	15,15,17	1.01	1 (6%)
2	MAN	D	4	2	11,11,12	1.07	2 (18%)	15,15,17	0.83	1 (6%)
2	MAN	D	5	2	11,11,12	1.32	1 (9%)	15,15,17	1.13	2 (13%)
3	NAG	E	1	3,1	14,14,15	0.39	0	17,19,21	0.60	0
3	NAG	E	2	3	14,14,15	0.36	0	17,19,21	1.29	2 (11%)
3	BMA	E	3	3	11,11,12	0.53	0	15,15,17	0.85	1 (6%)
3	MAN	E	4	3	11,11,12	0.64	0	15,15,17	1.10	1 (6%)
3	MAN	E	5	3	11,11,12	0.56	0	15,15,17	1.01	1 (6%)
3	MAN	E	6	3	11,11,12	0.59	0	15,15,17	1.00	1 (6%)
3	MAN	E	7	3	11,11,12	0.49	0	15,15,17	0.81	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	1	2,1	-	3/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1
2	MAN	D	5	2	-	1/2/19/22	0/1/1/1
3	NAG	E	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
3	MAN	E	5	3	-	0/2/19/22	0/1/1/1
3	MAN	E	6	3	-	2/2/19/22	0/1/1/1
3	MAN	E	7	3	-	2/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	5	MAN	O5-C5	3.03	1.49	1.43
2	D	4	MAN	O5-C5	2.29	1.48	1.43
2	D	4	MAN	C2-C3	2.13	1.55	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	C2-N2-C7	3.77	128.27	122.90
2	D	1	NAG	C1-C2-N2	3.76	116.91	110.49
3	E	2	NAG	C1-O5-C5	3.39	116.79	112.19
2	D	1	NAG	C1-O5-C5	3.06	116.34	112.19
3	E	6	MAN	C1-C2-C3	2.98	113.33	109.67

There are no chirality outliers.

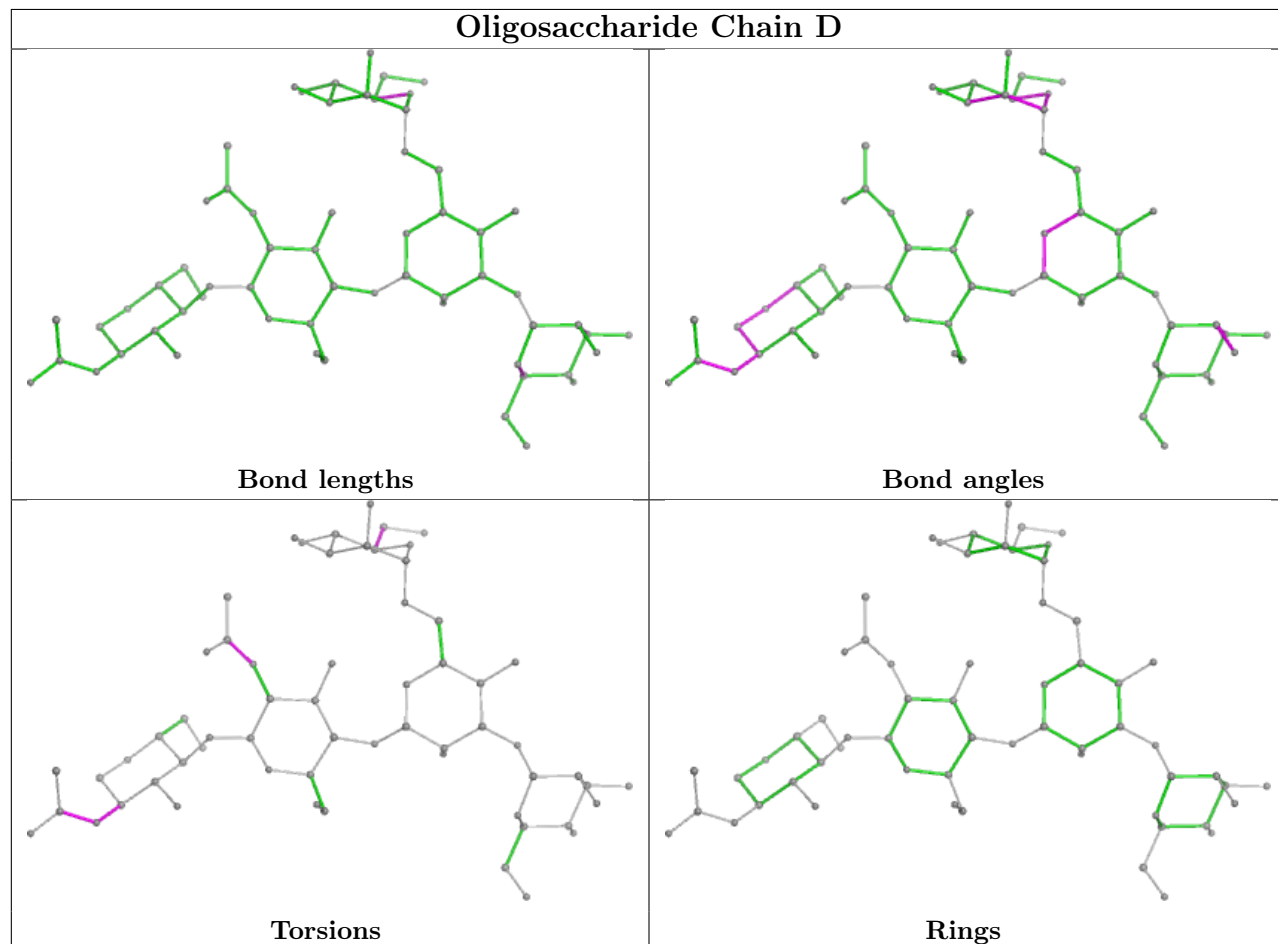
5 of 12 torsion outliers are listed below:

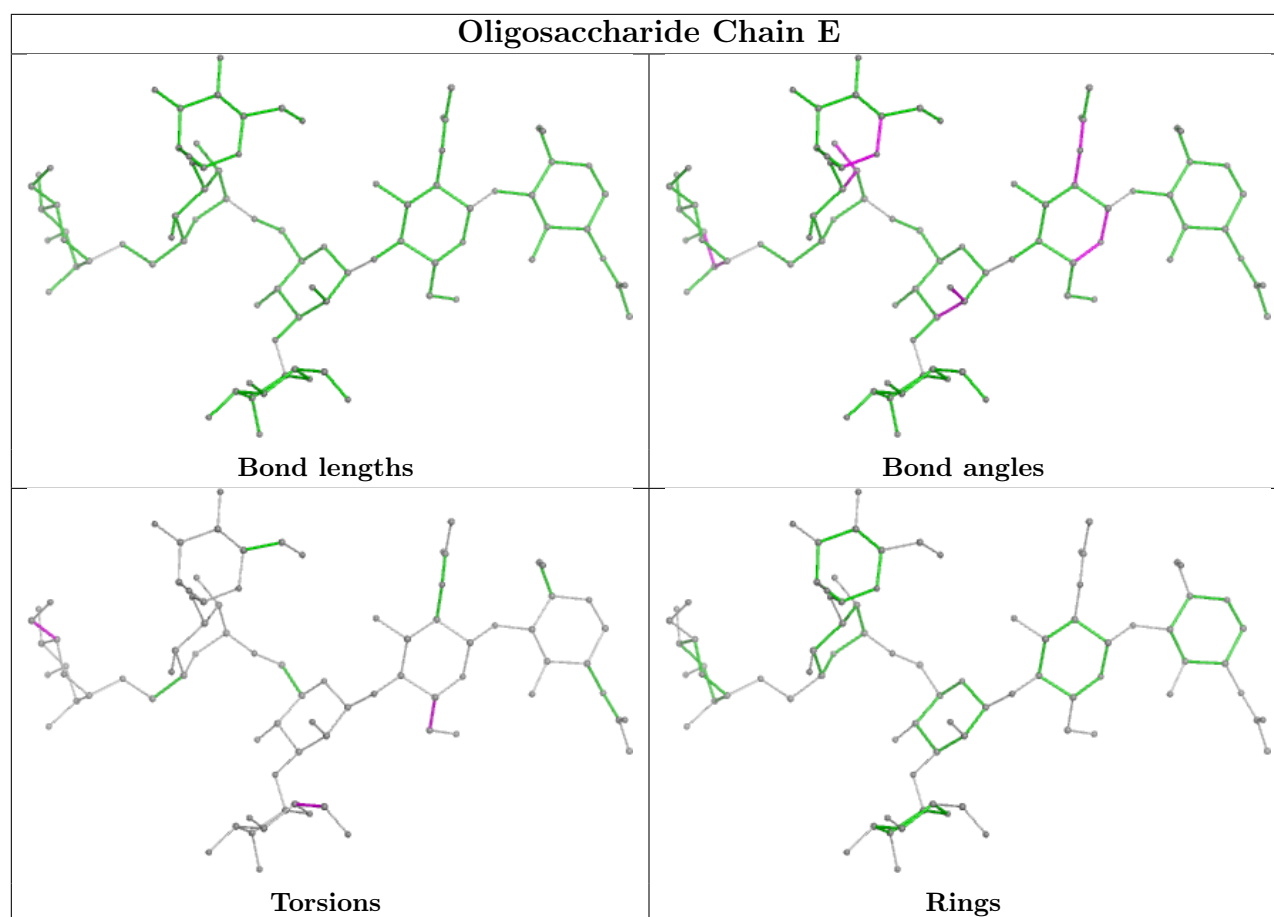
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C1-C2-N2-C7
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
3	E	2	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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





5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 3 are monoatomic - leaving 45 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	$\# Z > 2$
7	3DM	A	411	-	11,11,11	0.53	0	14,14,14	0.79	0
10	NAG	B	414	10,11	14,14,15	0.37	0	17,19,21	0.75	0
5	EPE	B	412	-	15,15,15	0.94	2 (13%)	18,20,20	1.10	2 (11%)
6	GOL	A	404	-	5,5,5	0.34	0	5,5,5	0.46	0
5	EPE	B	410	-	15,15,15	0.64	1 (6%)	18,20,20	0.66	0
6	GOL	A	409	-	5,5,5	0.27	0	5,5,5	0.52	0
10	NAG	C	403	1,10	14,14,15	0.31	0	17,19,21	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	NAG	B	402	1,10	14,14,15	0.37	0	17,19,21	1.19	1 (5%)
6	GOL	A	405	-	5,5,5	0.26	0	5,5,5	0.46	0
11	BMA	B	415	10	11,11,12	1.12	1 (9%)	15,15,17	0.48	0
11	BMA	C	405	10	11,11,12	0.42	0	15,15,17	0.68	0
8	SO4	B	419	-	4,4,4	0.29	0	6,6,6	0.34	0
8	SO4	C	412	-	4,4,4	0.45	0	6,6,6	0.18	0
6	GOL	B	413	-	5,5,5	0.22	0	5,5,5	0.33	0
4	HEM	C	409	1,9	41,50,50	1.10	3 (7%)	45,82,82	2.03	15 (33%)
6	GOL	C	408	-	5,5,5	0.30	0	5,5,5	0.44	0
12	MAN	B	408	12	11,11,12	0.59	0	15,15,17	0.59	0
8	SO4	A	414	-	4,4,4	0.43	0	6,6,6	0.31	0
11	BMA	B	405	12,10	11,11,12	0.55	0	15,15,17	1.14	3 (20%)
8	SO4	A	413	-	4,4,4	0.62	0	6,6,6	0.50	0
5	EPE	B	409	-	15,15,15	0.60	1 (6%)	18,20,20	0.66	0
4	HEM	A	401	1,9	41,50,50	1.46	4 (9%)	45,82,82	1.90	12 (26%)
6	GOL	A	407	-	5,5,5	0.26	0	5,5,5	0.39	0
12	MAN	B	406	11	11,11,12	0.54	0	15,15,17	1.14	2 (13%)
4	HEM	B	401	1,9	41,50,50	1.40	6 (14%)	45,82,82	1.79	13 (28%)
10	NAG	C	404	10,11	14,14,15	0.33	0	17,19,21	0.83	0
7	3DM	B	418	-	11,11,11	0.77	0	14,14,14	1.36	2 (14%)
12	MAN	B	407	12,11	11,11,12	0.56	0	15,15,17	1.21	2 (13%)
7	3DM	A	412	-	11,11,11	0.57	0	14,14,14	0.99	0
7	3DM	C	411	-	11,11,11	0.44	0	14,14,14	0.51	0
6	GOL	C	410	-	5,5,5	0.45	0	5,5,5	0.31	0
10	NAG	C	401	1,10	14,14,15	0.36	0	17,19,21	0.92	1 (5%)
5	EPE	A	408	-	15,15,15	1.34	1 (6%)	18,20,20	1.39	3 (16%)
6	GOL	A	403	-	5,5,5	0.39	0	5,5,5	0.36	0
7	3DM	A	410	-	11,11,11	0.75	1 (9%)	14,14,14	1.07	1 (7%)
6	GOL	A	406	-	5,5,5	0.38	0	5,5,5	0.42	0
6	GOL	B	416	-	5,5,5	0.37	0	5,5,5	0.54	0
10	NAG	C	402	10,11	14,14,15	0.42	0	17,19,21	0.71	0
11	BMA	C	406	12,10	11,11,12	0.39	0	15,15,17	1.14	1 (6%)
12	MAN	C	407	11	11,11,12	0.76	0	15,15,17	0.88	1 (6%)
10	NAG	B	403	1,10	14,14,15	0.35	0	17,19,21	0.75	0
10	NAG	B	404	10,11	14,14,15	0.38	0	17,19,21	0.63	0
7	3DM	B	411	-	11,11,11	0.64	0	14,14,14	1.52	4 (28%)
5	EPE	A	402	-	15,15,15	0.63	1 (6%)	18,20,20	0.74	0
6	GOL	B	417	-	5,5,5	0.19	0	5,5,5	0.53	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	3DM	A	411	-	-	0/4/4/4	0/1/1/1
10	NAG	B	414	10,11	-	1/6/23/26	0/1/1/1
5	EPE	B	412	-	-	6/9/19/19	0/1/1/1
6	GOL	A	404	-	-	2/4/4/4	-
5	EPE	B	410	-	-	6/9/19/19	0/1/1/1
6	GOL	A	409	-	-	0/4/4/4	-
10	NAG	C	403	1,10	-	2/6/23/26	0/1/1/1
10	NAG	B	402	1,10	-	2/6/23/26	0/1/1/1
6	GOL	A	405	-	-	0/4/4/4	-
11	BMA	B	415	10	-	2/2/19/22	0/1/1/1
11	BMA	C	405	10	-	1/2/19/22	0/1/1/1
6	GOL	B	413	-	-	4/4/4/4	-
4	HEM	C	409	1,9	-	0/12/54/54	-
6	GOL	C	408	-	-	0/4/4/4	-
12	MAN	B	408	12	-	2/2/19/22	0/1/1/1
11	BMA	B	405	12,10	-	0/2/19/22	0/1/1/1
5	EPE	B	409	-	-	1/9/19/19	0/1/1/1
4	HEM	A	401	1,9	-	0/12/54/54	-
6	GOL	A	407	-	-	3/4/4/4	-
12	MAN	B	406	11	-	2/2/19/22	0/1/1/1
4	HEM	B	401	1,9	-	2/12/54/54	-
10	NAG	C	404	10,11	-	2/6/23/26	0/1/1/1
7	3DM	B	418	-	-	2/4/4/4	0/1/1/1
12	MAN	B	407	12,11	-	2/2/19/22	0/1/1/1
7	3DM	A	412	-	-	0/4/4/4	0/1/1/1
7	3DM	C	411	-	-	0/4/4/4	0/1/1/1
6	GOL	C	410	-	-	2/4/4/4	-
10	NAG	C	401	1,10	-	3/6/23/26	0/1/1/1
5	EPE	A	408	-	-	3/9/19/19	0/1/1/1
6	GOL	A	403	-	-	0/4/4/4	-
7	3DM	A	410	-	-	0/4/4/4	0/1/1/1
6	GOL	A	406	-	-	2/4/4/4	-
6	GOL	B	416	-	-	1/4/4/4	-
10	NAG	C	402	10,11	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	BMA	C	406	12,10	-	0/2/19/22	0/1/1/1
12	MAN	C	407	11	-	0/2/19/22	0/1/1/1
10	NAG	B	403	1,10	-	0/6/23/26	0/1/1/1
10	NAG	B	404	10,11	-	0/6/23/26	0/1/1/1
7	3DM	B	411	-	-	2/4/4/4	0/1/1/1
5	EPE	A	402	-	-	3/9/19/19	0/1/1/1
6	GOL	B	417	-	-	4/4/4/4	-

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	401	HEM	C1B-NB	-4.75	1.32	1.40
5	A	408	EPE	O3S-S	4.67	1.64	1.47
4	B	401	HEM	C4D-ND	-3.91	1.33	1.40
4	A	401	HEM	C4D-ND	-3.80	1.33	1.40
4	B	401	HEM	C1B-NB	-3.42	1.34	1.40

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	409	HEM	CHC-C4B-NB	4.92	129.78	124.43
4	A	401	HEM	C1B-NB-C4B	4.86	110.10	105.07
4	B	401	HEM	C1B-NB-C4B	4.42	109.64	105.07
5	A	408	EPE	O3S-S-C10	-4.32	98.78	105.77
4	A	401	HEM	CHC-C4B-NB	4.20	129.00	124.43

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

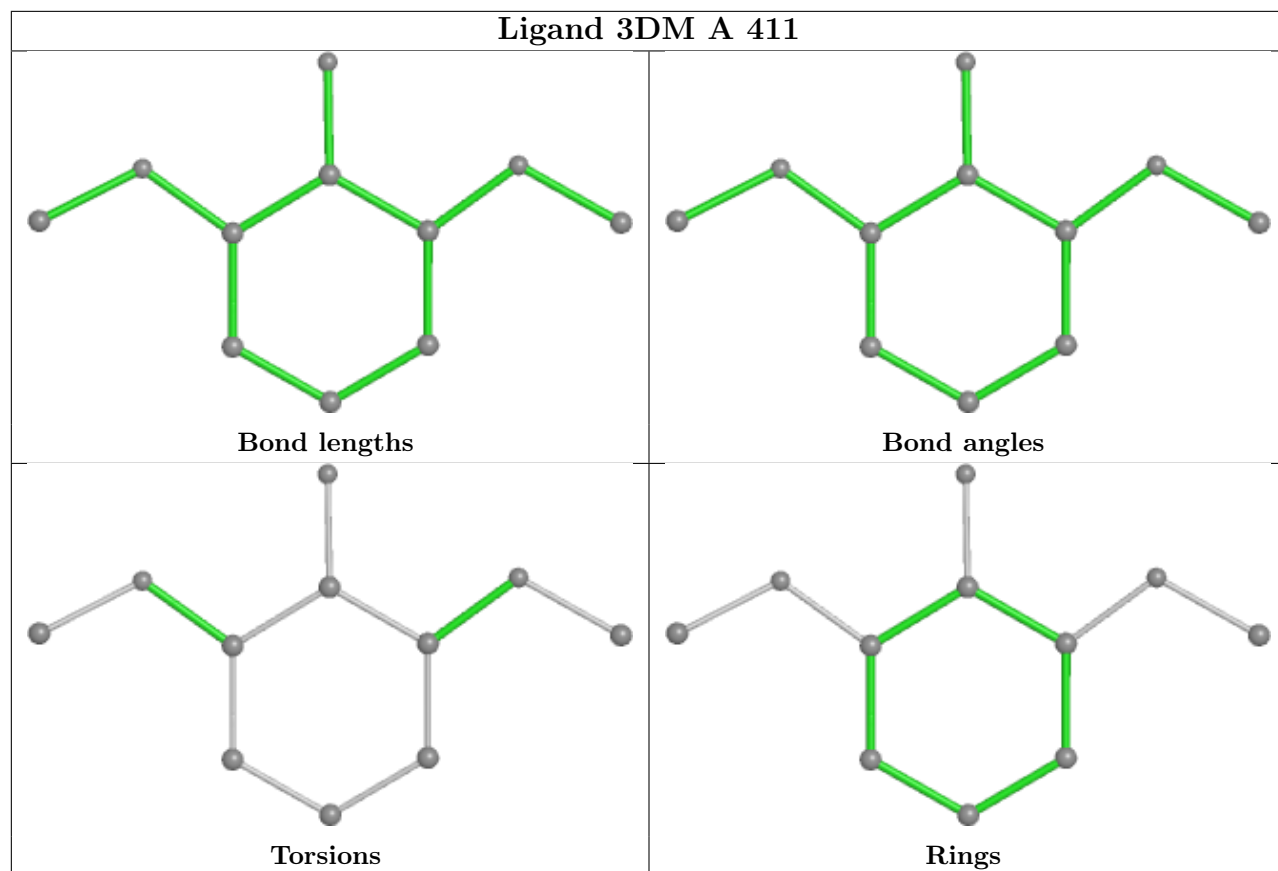
Mol	Chain	Res	Type	Atoms
5	A	402	EPE	C9-C10-S-O1S
5	A	402	EPE	C9-C10-S-O2S
5	A	402	EPE	C9-C10-S-O3S
5	A	408	EPE	S-C10-C9-N1
5	B	409	EPE	C10-C9-N1-C6

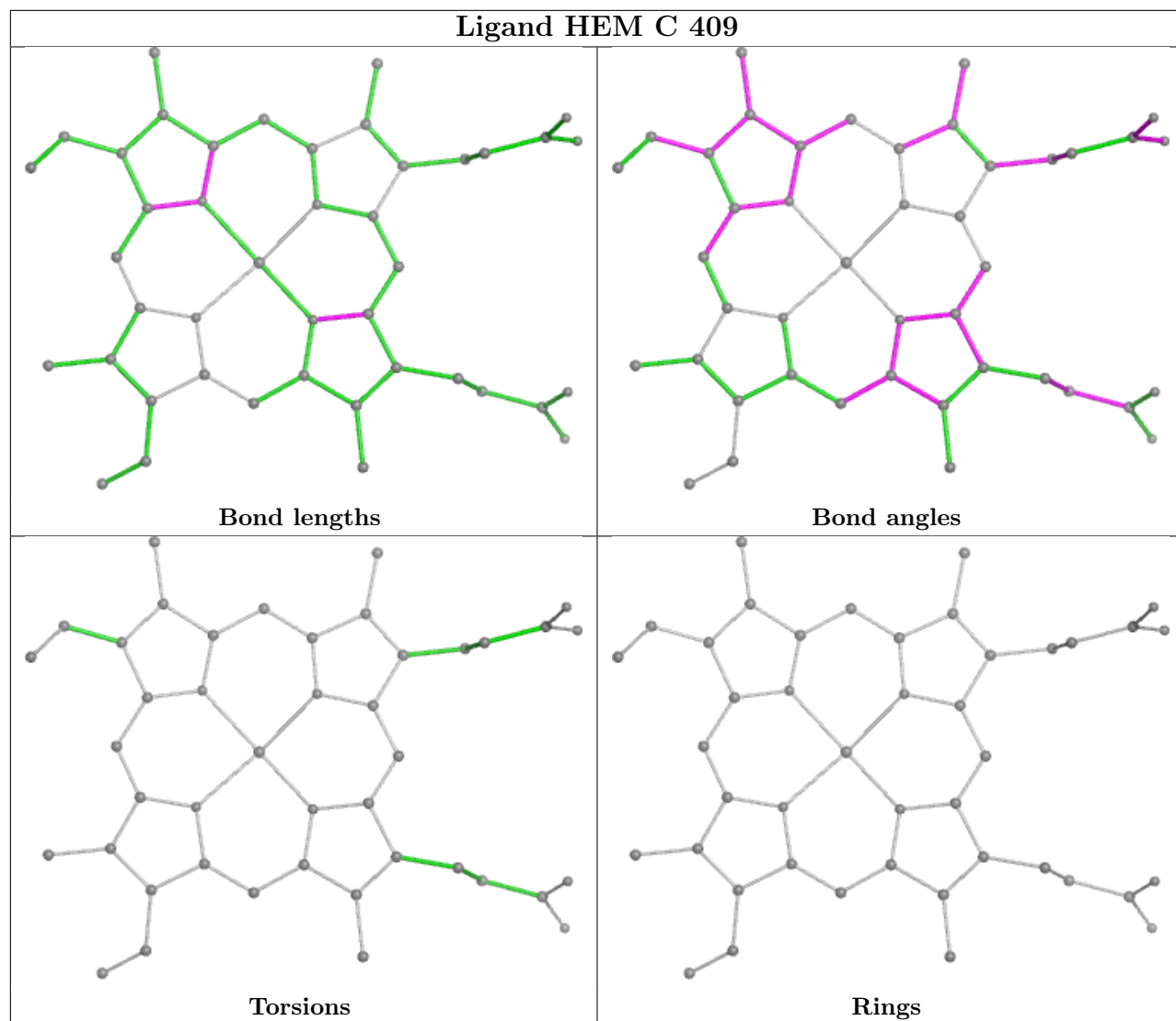
There are no ring outliers.

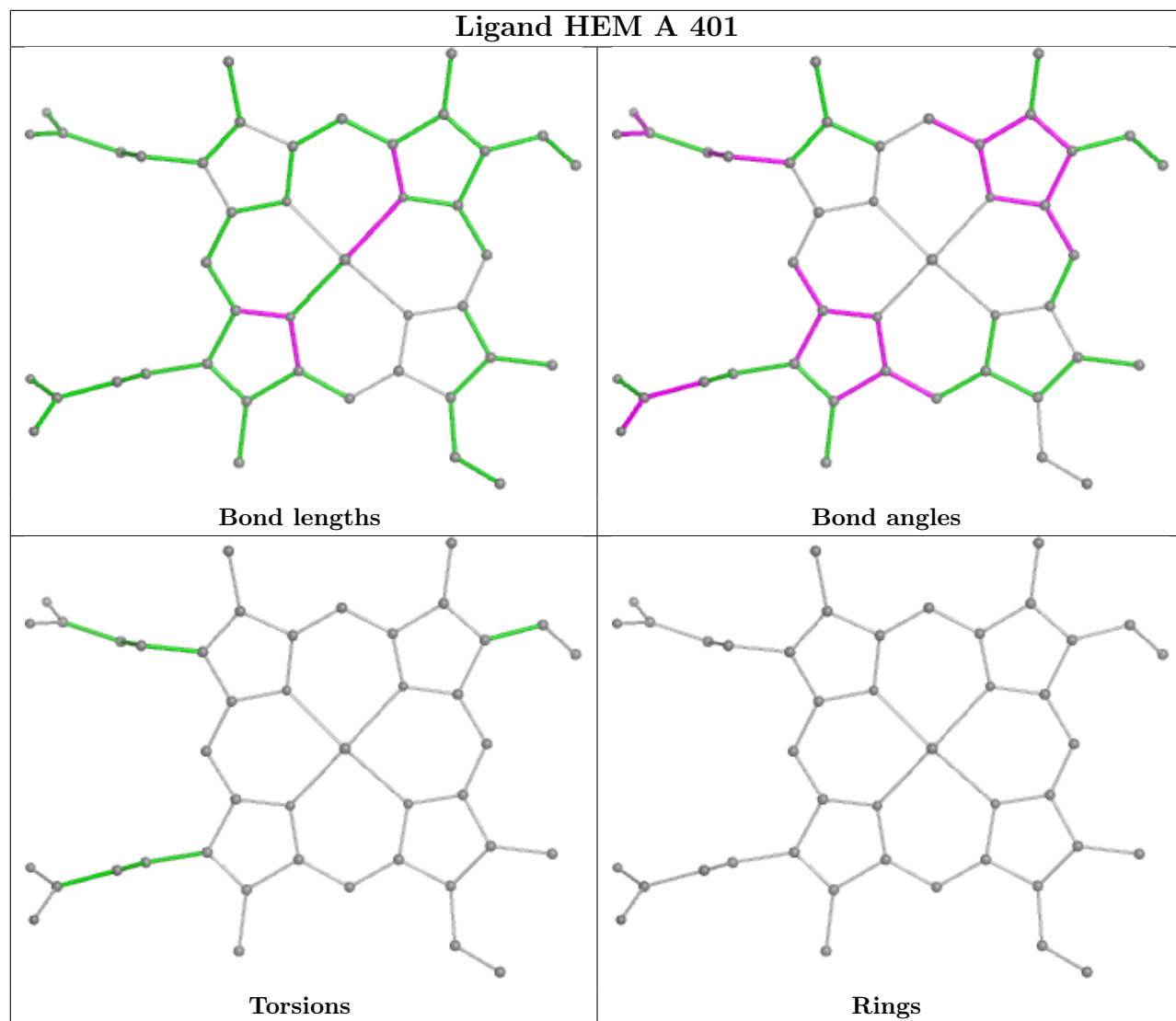
15 monomers are involved in 61 short contacts:

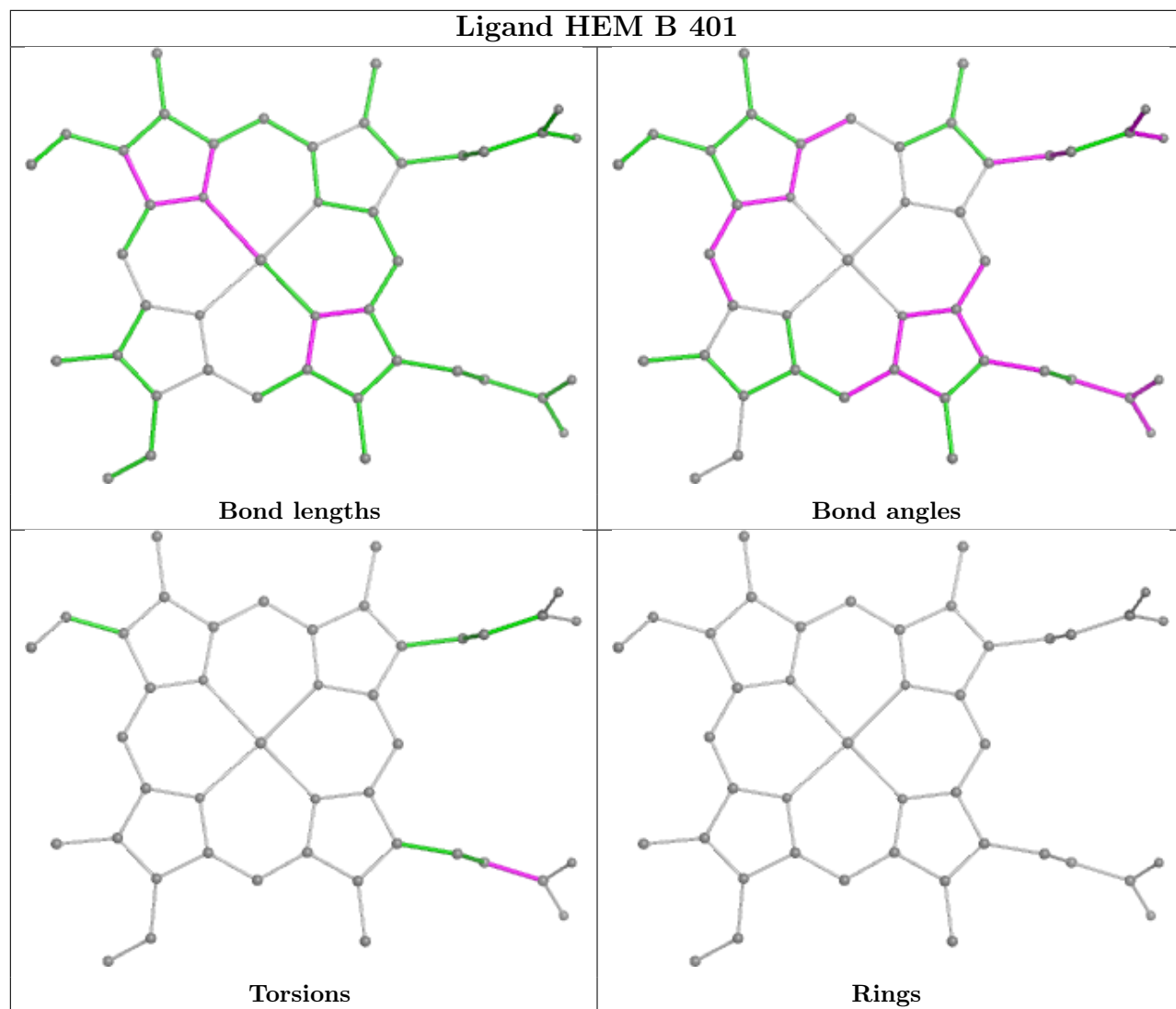
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	411	3DM	2	0
5	B	412	EPE	6	0
5	B	410	EPE	4	0
6	A	405	GOL	1	0
4	C	409	HEM	5	0
5	B	409	EPE	2	0
4	A	401	HEM	1	0
4	B	401	HEM	3	0
7	B	418	3DM	17	0
7	C	411	3DM	5	0
5	A	408	EPE	11	0
6	A	406	GOL	1	0
6	B	416	GOL	3	0
7	B	411	3DM	8	0
6	B	417	GOL	3	0

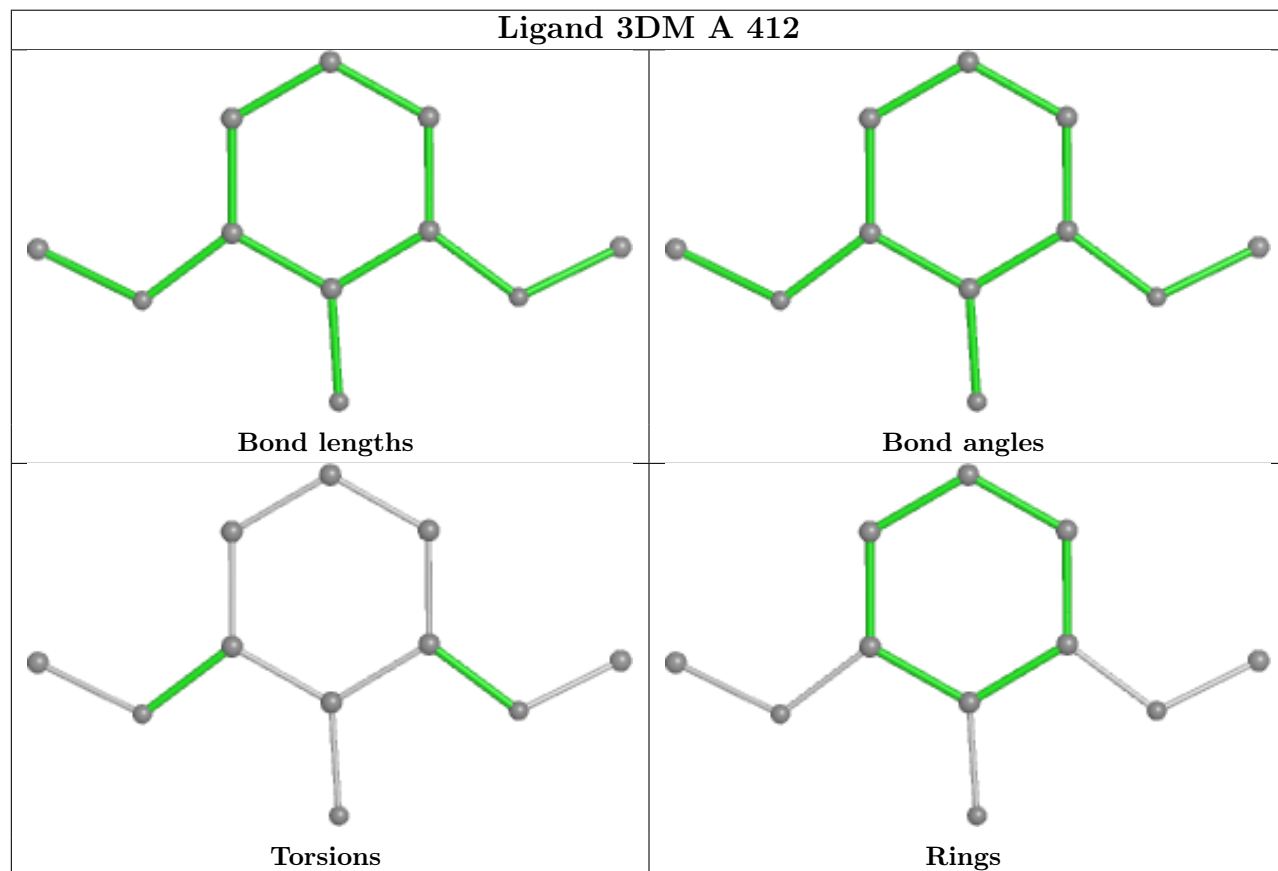
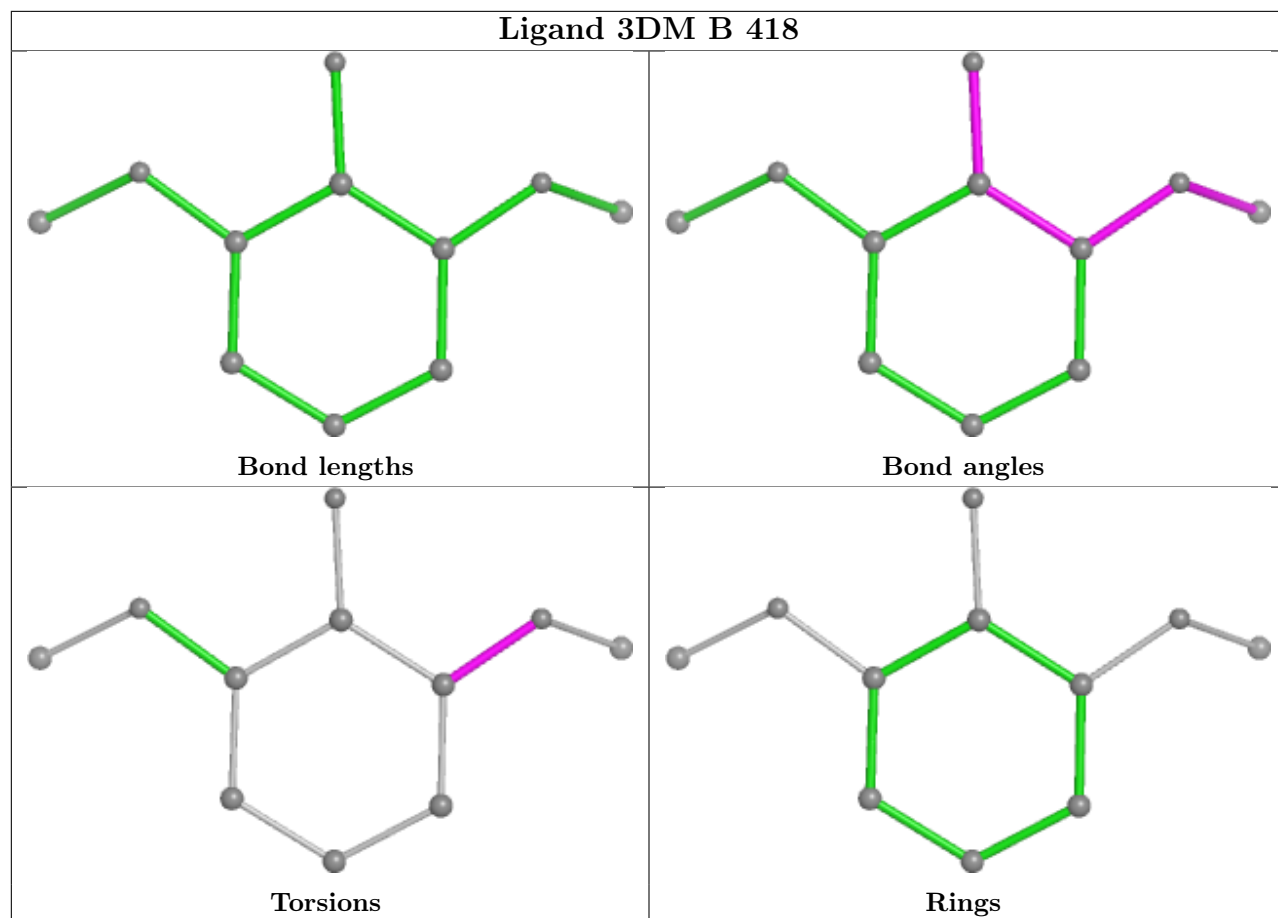
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



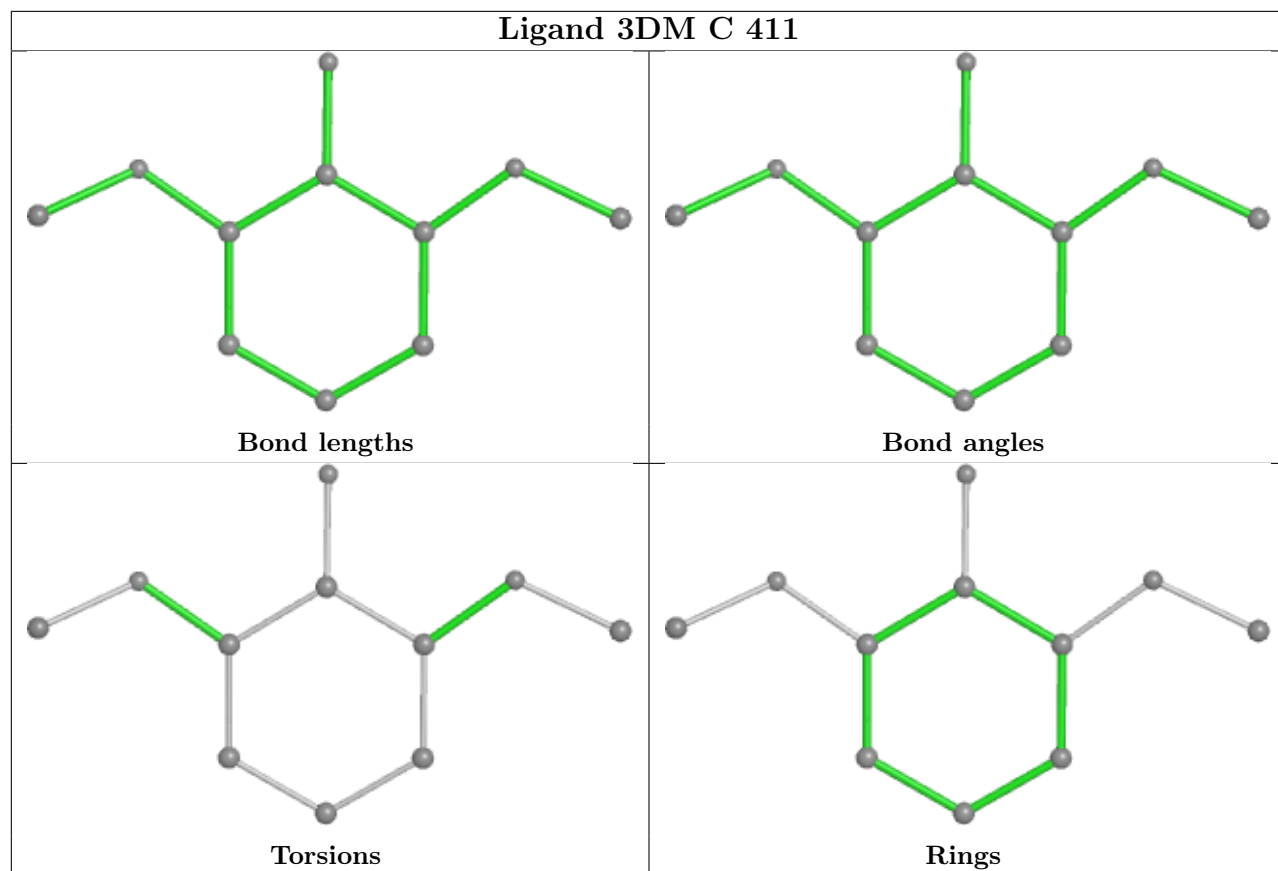




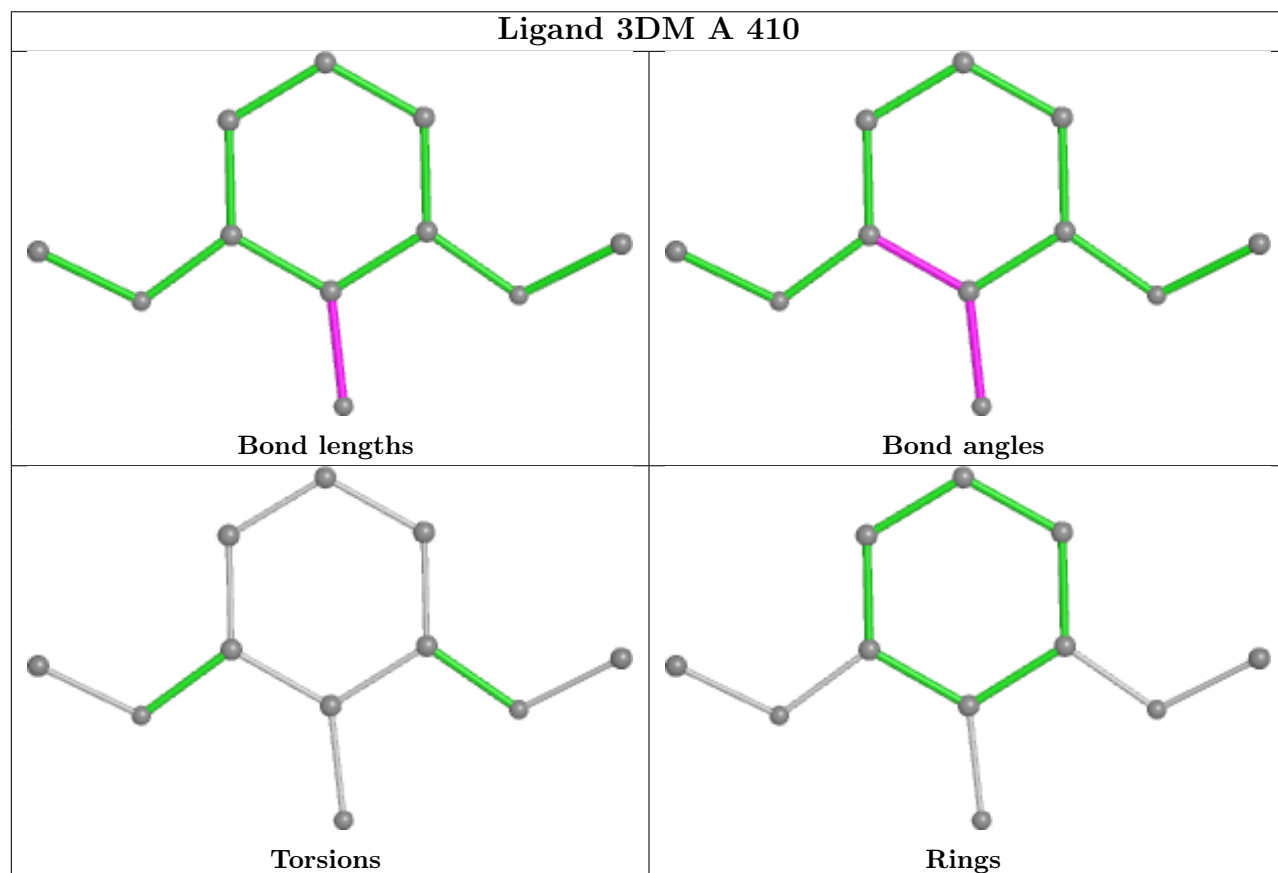


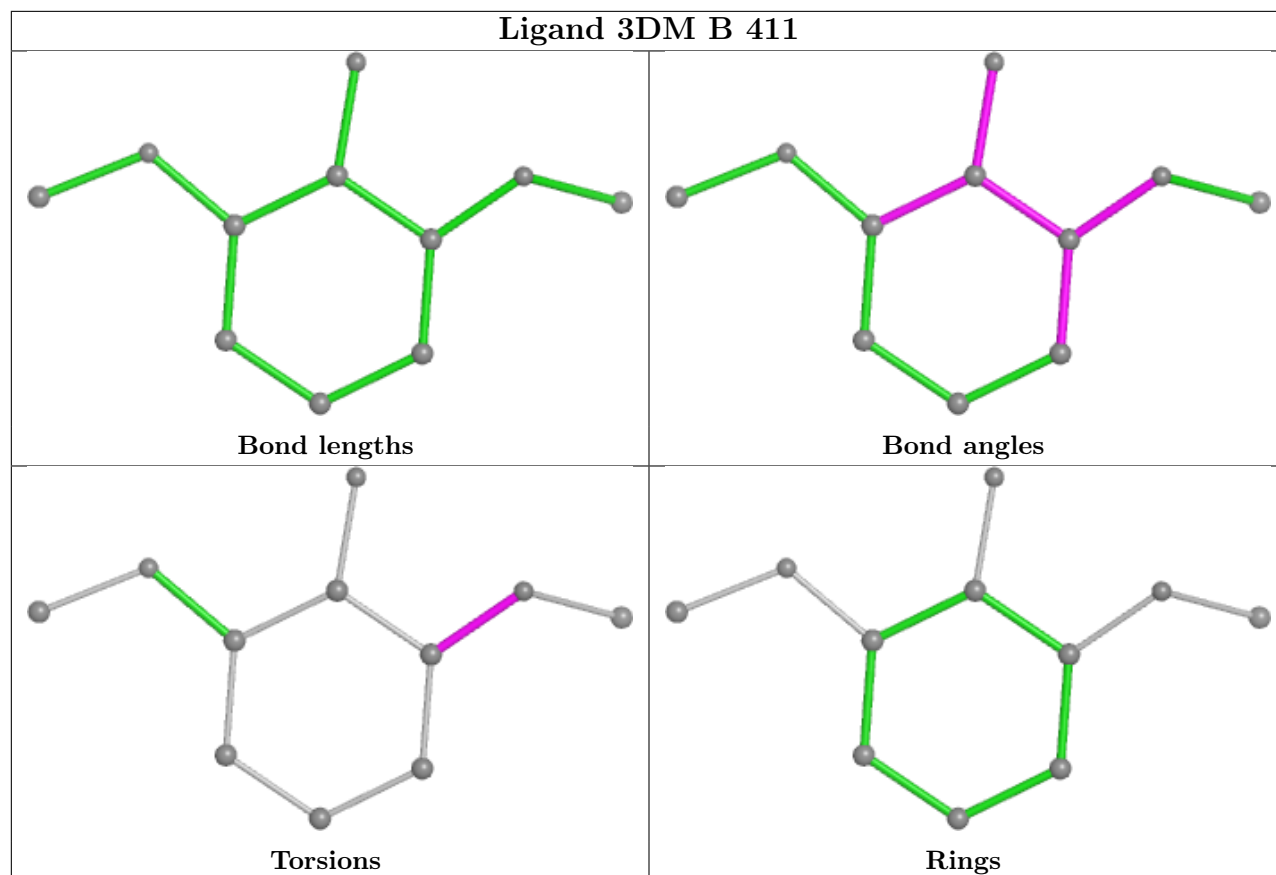


Ligand 3DM C 411



Ligand 3DM A 410





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	335/335 (100%)	0.01	7 (2%) 63 65	21, 38, 55, 115	5 (1%)
1	B	335/335 (100%)	0.47	22 (6%) 26 27	21, 46, 68, 135	3 (0%)
1	C	335/335 (100%)	0.66	28 (8%) 18 19	25, 48, 74, 112	2 (0%)
All	All	1005/1005 (100%)	0.38	57 (5%) 30 32	21, 44, 69, 135	10 (0%)

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	316	ILE	4.8
1	C	227	THR	4.3
1	A	316	ILE	3.6
1	A	14	GLN	3.5
1	B	227	THR	3.5

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

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

6.3 Carbohydrates [i](#)

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

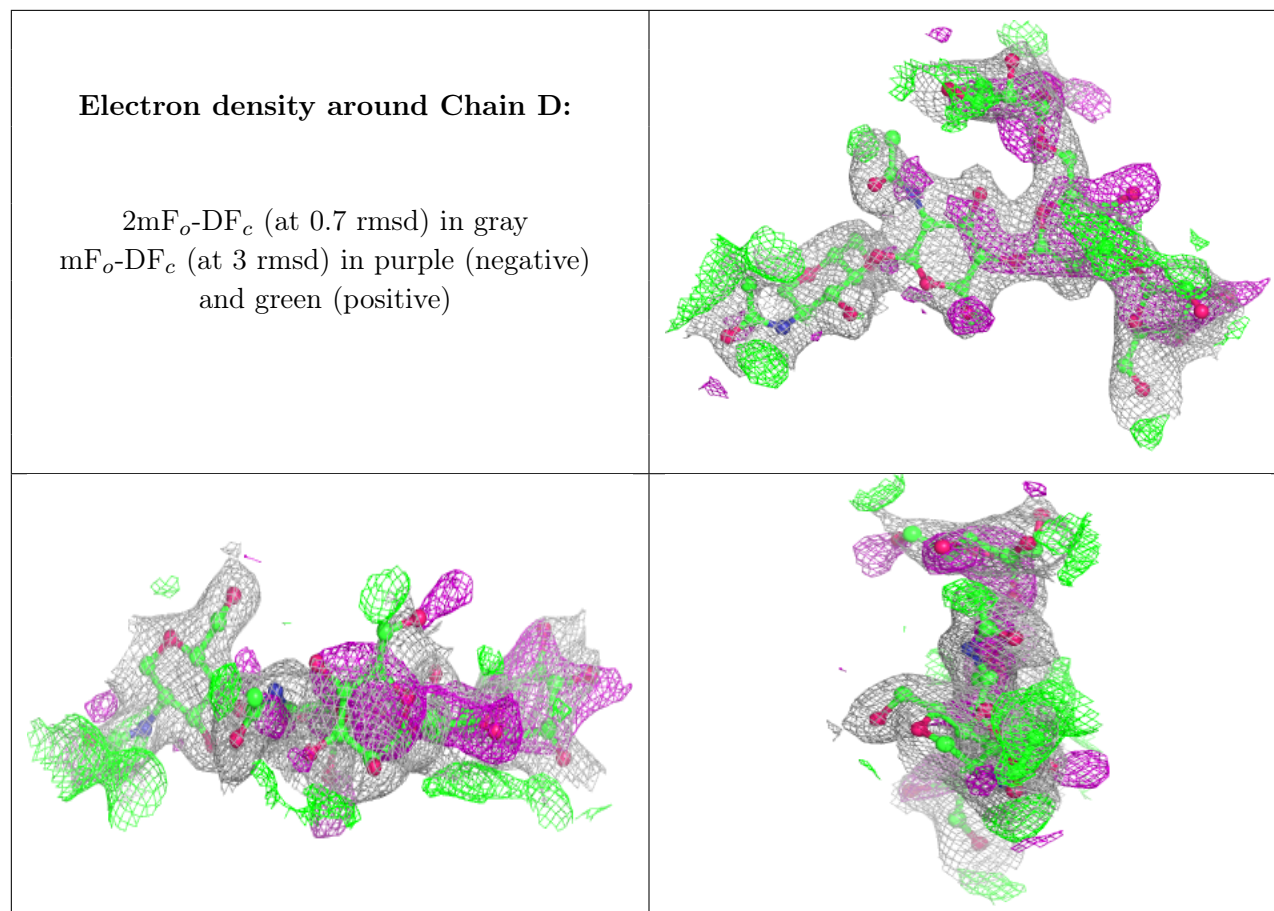
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	E	7	11/12	0.32	0.18	107,124,133,133	0
3	MAN	E	6	11/12	0.33	0.17	104,137,141,143	0
2	MAN	D	5	11/12	0.61	0.19	58,67,69,72	0

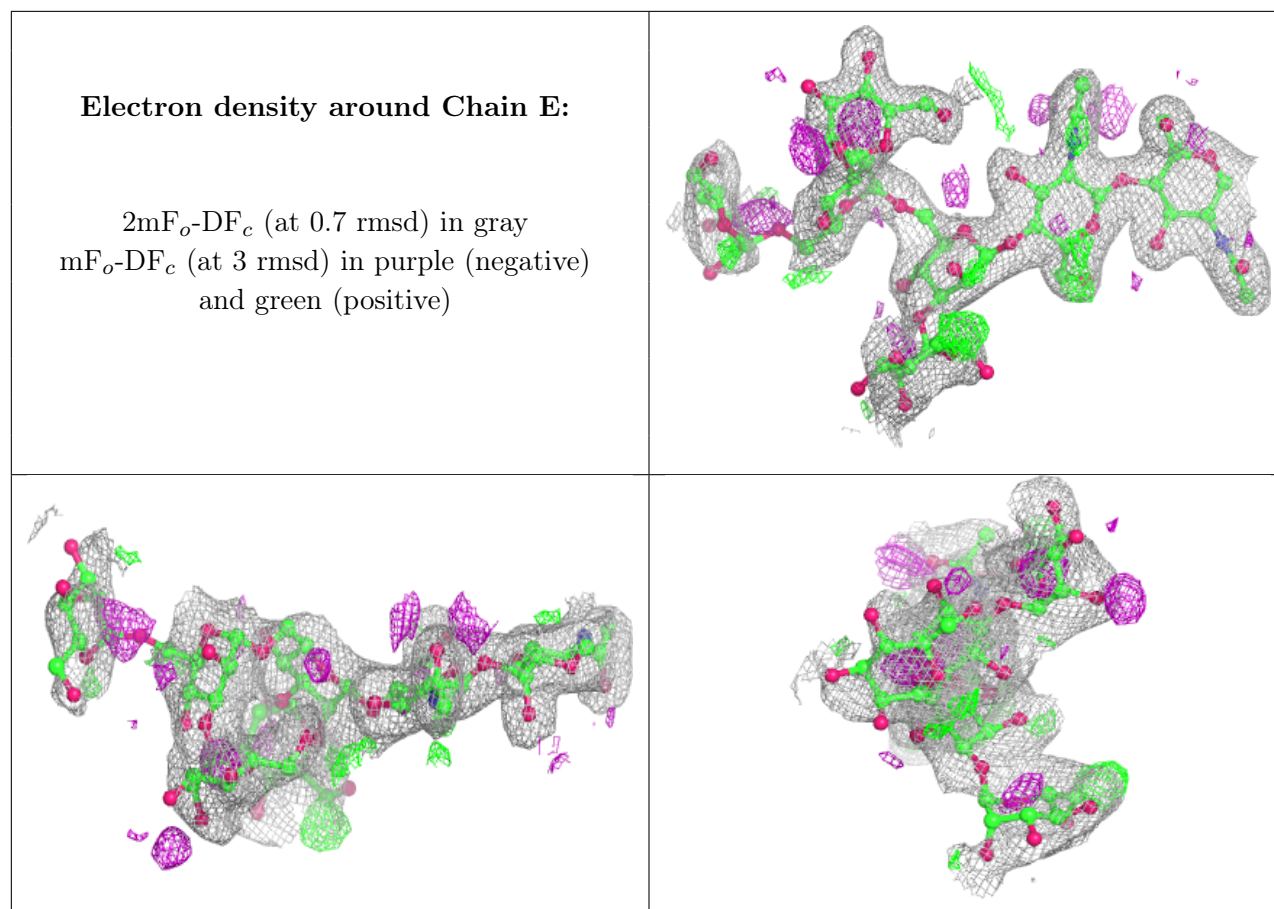
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BMA	D	3	11/12	0.62	0.20	59,68,72,74	0
3	MAN	E	4	11/12	0.65	0.16	91,100,119,143	0
2	NAG	D	1	14/15	0.68	0.20	47,59,78,90	0
2	MAN	D	4	11/12	0.70	0.18	58,62,66,66	0
3	MAN	E	5	11/12	0.76	0.16	64,86,94,95	0
3	BMA	E	3	11/12	0.80	0.14	67,87,96,111	0
3	NAG	E	2	14/15	0.87	0.12	43,53,67,68	0
2	NAG	D	2	14/15	0.88	0.12	49,55,62,63	0
3	NAG	E	1	14/15	0.95	0.08	39,42,46,48	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.





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, 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
10	NAG	C	404	14/15	0.15	0.22	97,125,135,150	0
11	BMA	C	405	11/12	0.29	0.18	130,153,164,164	0
12	MAN	B	406	11/12	0.42	0.16	119,134,141,144	0
11	BMA	B	415	11/12	0.51	0.20	60,65,69,69	0
11	BMA	C	406	11/12	0.63	0.16	115,125,136,143	0
7	3DM	B	418	11/11	0.63	0.29	44,51,54,57	11
8	SO4	C	412	5/5	0.64	0.16	59,60,63,68	0
7	3DM	B	411	11/11	0.65	0.26	46,49,53,54	11
5	EPE	B	410	15/15	0.67	0.28	92,125,165,182	0
6	GOL	A	407	6/6	0.67	0.19	48,51,52,55	0
8	SO4	A	414	5/5	0.67	0.18	59,60,63,64	0
11	BMA	B	405	11/12	0.68	0.15	87,101,113,126	0
12	MAN	B	407	11/12	0.68	0.14	91,100,107,109	0

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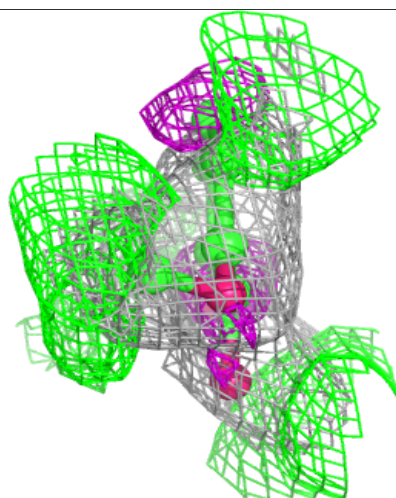
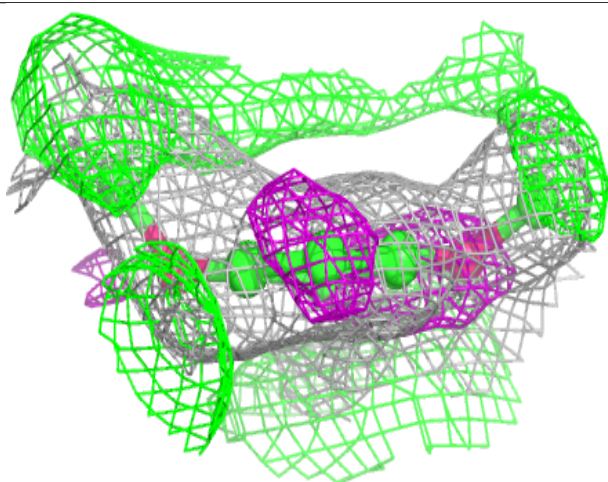
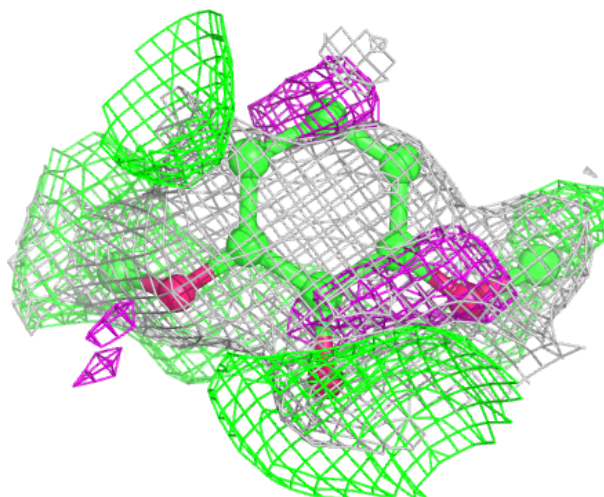
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	3DM	A	410	11/11	0.69	0.30	45,52,54,56	11
6	GOL	A	409	6/6	0.69	0.20	45,53,54,54	0
6	GOL	C	410	6/6	0.69	0.22	47,54,54,57	0
7	3DM	C	411	11/11	0.70	0.31	44,47,53,56	11
6	GOL	A	404	6/6	0.71	0.20	39,43,48,54	0
6	GOL	C	408	6/6	0.71	0.18	50,53,54,55	0
6	GOL	A	403	6/6	0.72	0.18	51,54,54,56	0
6	GOL	A	406	6/6	0.73	0.18	45,47,52,57	0
5	EPE	A	402	15/15	0.75	0.25	70,136,149,155	0
5	EPE	A	408	15/15	0.75	0.22	49,51,56,61	0
5	EPE	B	409	15/15	0.75	0.23	92,107,116,117	0
7	3DM	A	412	11/11	0.75	0.20	45,49,55,55	0
12	MAN	B	408	11/12	0.76	0.13	71,93,95,96	0
6	GOL	B	413	6/6	0.77	0.17	49,52,56,56	0
12	MAN	C	407	11/12	0.77	0.17	84,108,122,126	0
10	NAG	C	401	14/15	0.78	0.17	63,77,92,99	0
6	GOL	B	416	6/6	0.78	0.15	48,50,50,51	0
10	NAG	B	402	14/15	0.80	0.20	54,70,86,87	0
8	SO4	A	413	5/5	0.81	0.14	41,44,48,50	0
6	GOL	A	405	6/6	0.83	0.17	49,51,53,54	0
7	3DM	A	411	11/11	0.83	0.19	40,42,49,49	11
8	SO4	B	419	5/5	0.84	0.13	52,58,61,65	0
5	EPE	B	412	15/15	0.86	0.24	36,48,58,64	15
10	NAG	B	414	14/15	0.86	0.15	55,62,65,65	0
6	GOL	B	417	6/6	0.86	0.12	46,48,54,55	0
10	NAG	B	404	14/15	0.87	0.13	46,59,78,91	0
10	NAG	C	402	14/15	0.87	0.14	84,90,99,105	0
10	NAG	C	403	14/15	0.87	0.15	67,84,92,108	0
10	NAG	B	403	14/15	0.92	0.10	43,48,54,54	0
9	MG	A	415	1/1	0.93	0.07	46,46,46,46	0
4	HEM	C	409	43/43	0.97	0.08	33,37,42,43	0
4	HEM	B	401	43/43	0.98	0.07	34,38,44,51	0
9	MG	C	413	1/1	0.98	0.07	44,44,44,44	0
4	HEM	A	401	43/43	0.98	0.08	30,34,41,44	0
9	MG	B	420	1/1	1.00	0.04	39,39,39,39	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.

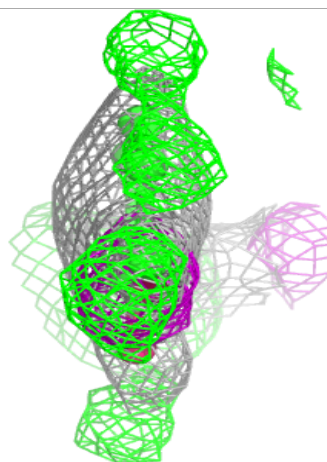
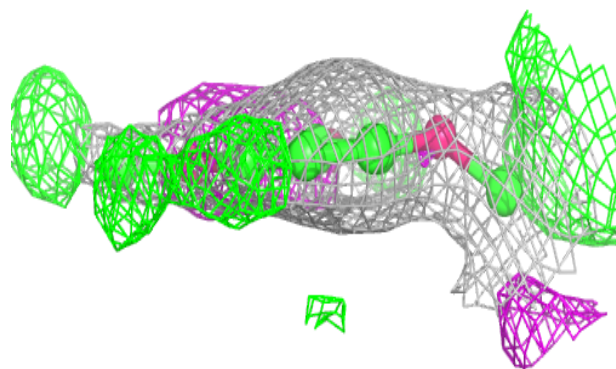
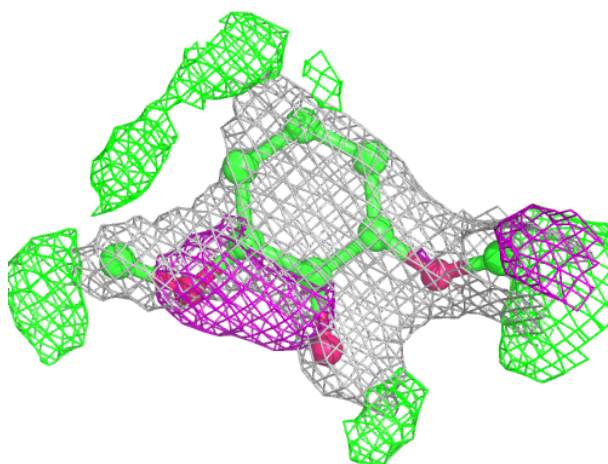
Electron density around 3DM B 418:

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



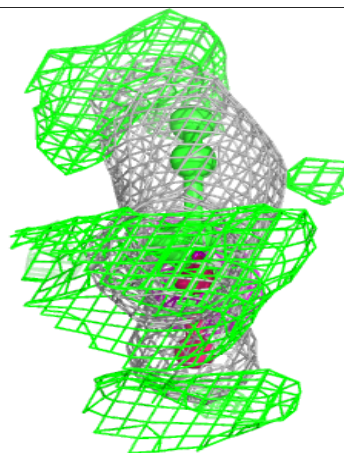
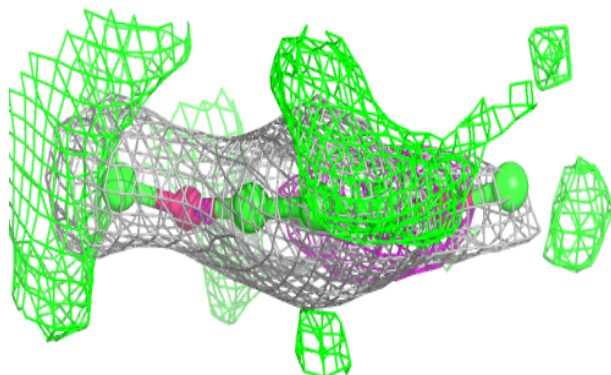
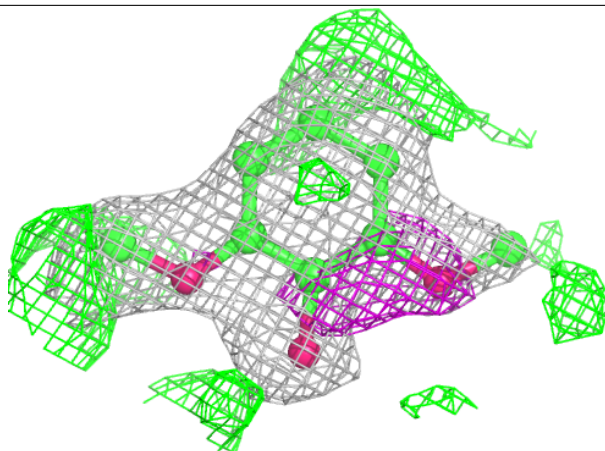
Electron density around 3DM B 411:

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



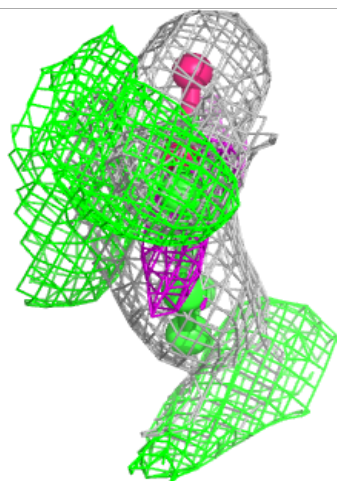
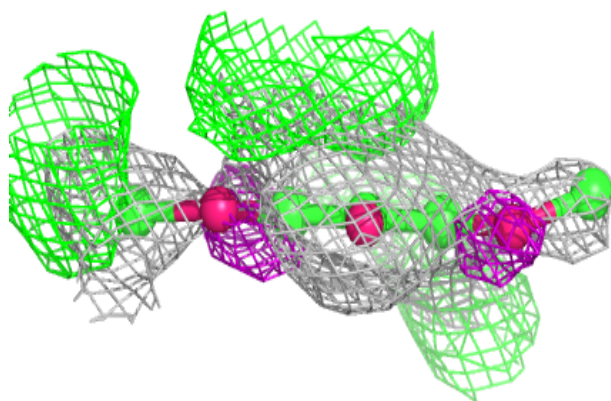
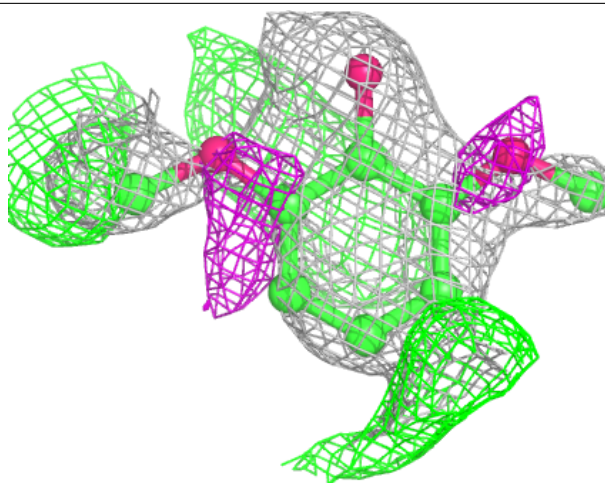
Electron density around 3DM A 410:

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



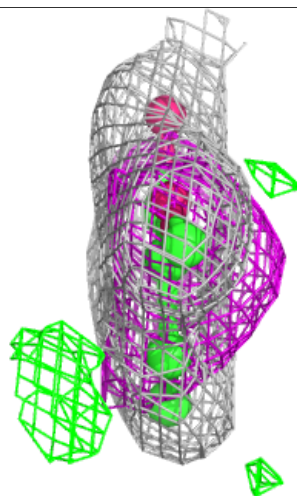
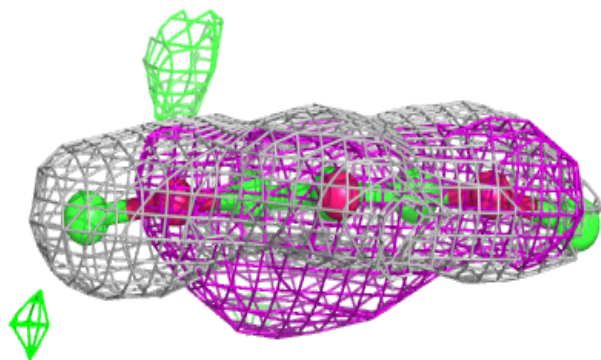
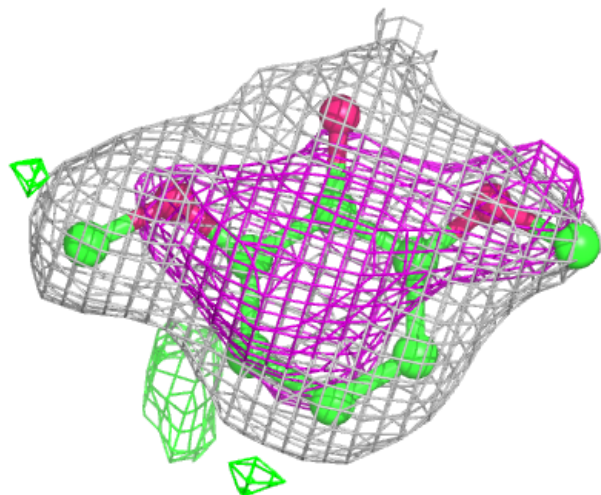
Electron density around 3DM C 411:

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



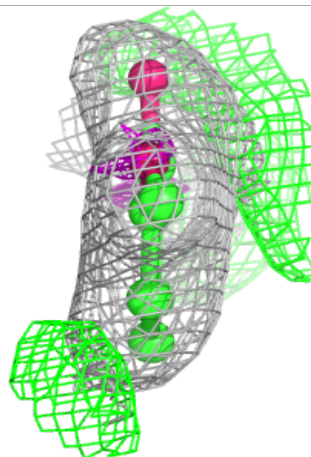
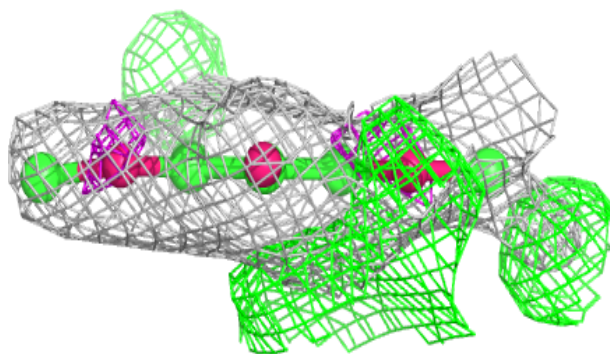
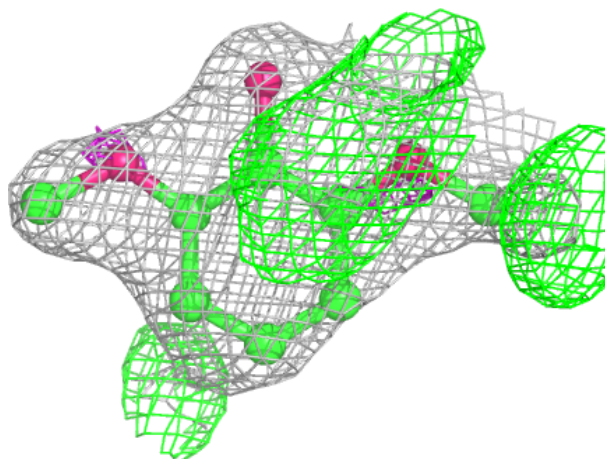
Electron density around 3DM A 412:

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



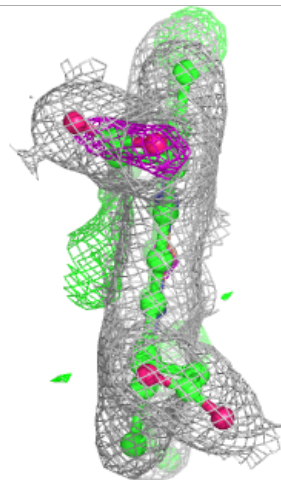
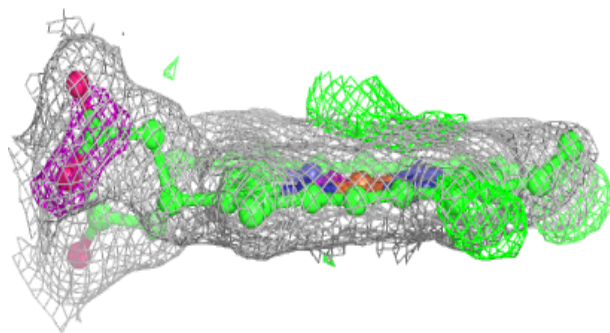
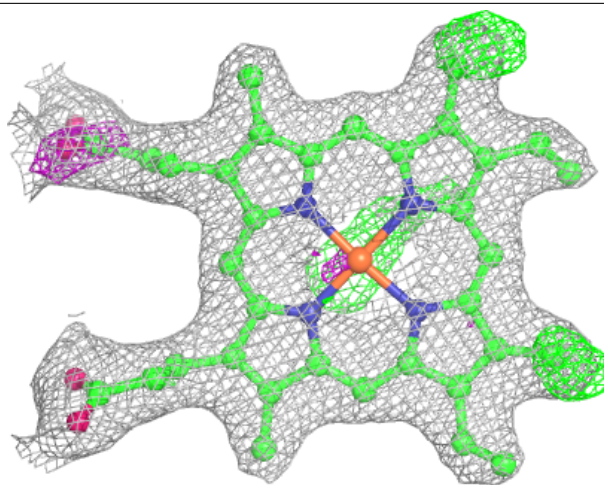
Electron density around 3DM A 411:

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



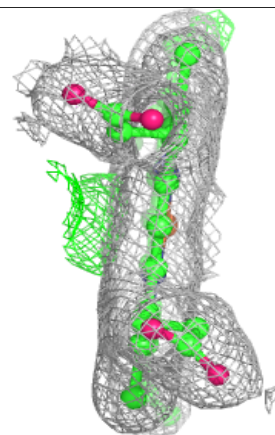
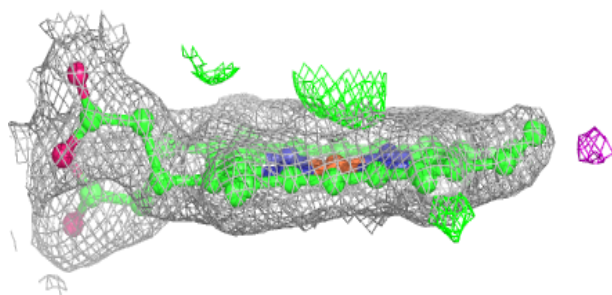
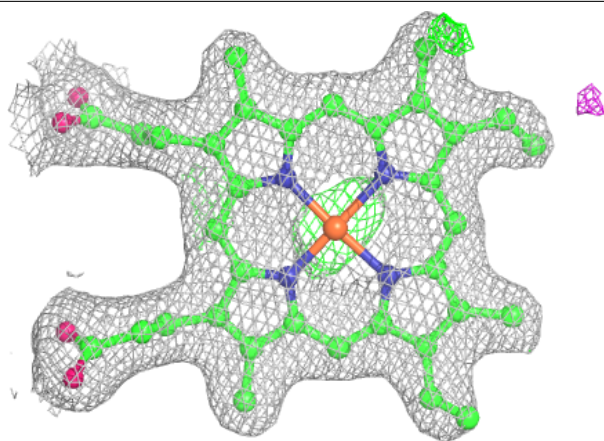
Electron density around HEM C 409:

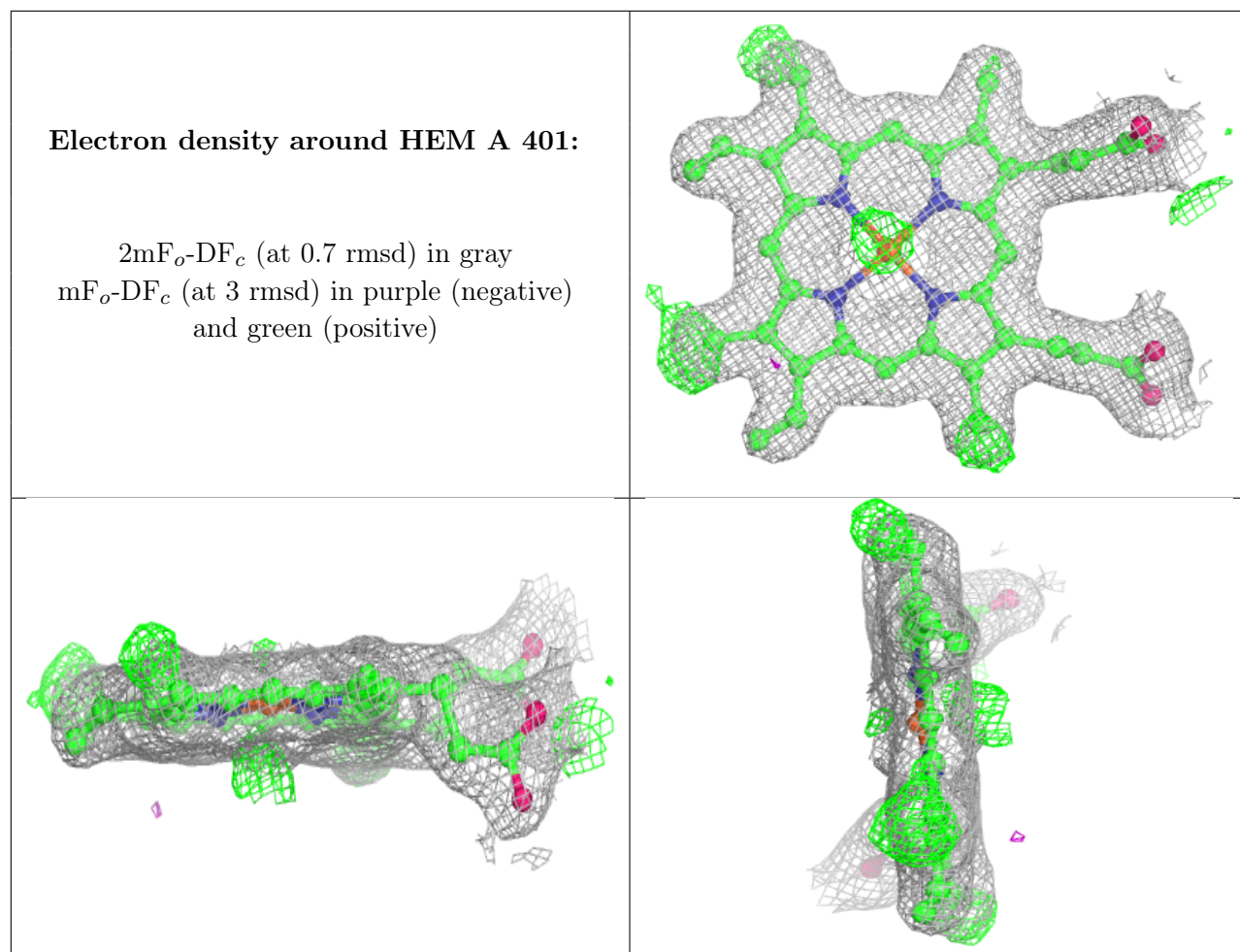
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 401:

$2mF_o - DF_c$ (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.