



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 08:36 PM EDT

PDB ID : 2E9E / pdb_00002e9e
Title : Crystal structure of the complex of goat lactoperoxidase with Nitrate at 3.25 Å resolution
Authors : Singh, A.K.; Prem kumar, R.; Singh, N.; Sharma, S.; Singh, S.B.; Bhushan, A.; Kaur, P.; Singh, T.P.
Deposited on : 2007-01-25
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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

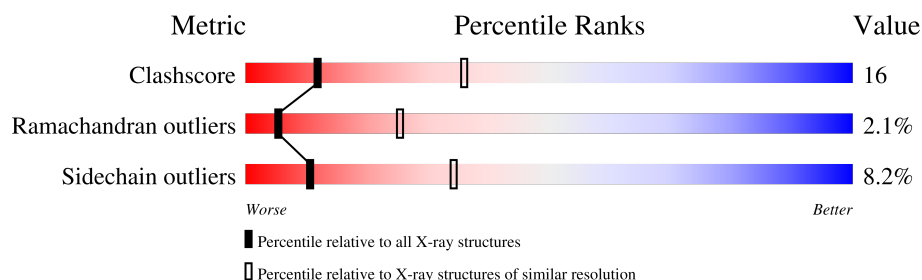
1 Overall quality at a glance

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))
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)

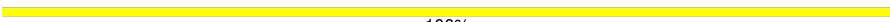
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	595	71% 24% 5% •
1	B	595	70% 23% 6% •
2	C	3	100%
2	D	3	67% 33%
2	G	3	67% 33%
3	E	3	100%
3	H	3	33% 67%
3	I	3	33% 67%

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Mol	Chain	Length	Quality of chain
4	F	2	 100%
4	J	2	 100%

2 Entry composition [i](#)

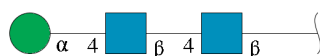
There are 12 unique types of molecules in this entry. The entry contains 10299 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

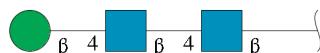
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	0	0
			4754	3021	844	863	26			
1	B	595	Total	C	N	O	S	0	0	0
			4754	3021	844	863	26			

- Molecule 2 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
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	D	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	G	3	Total	C	N	O	0	0	0
			39	22	2	15			

- 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	E	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			

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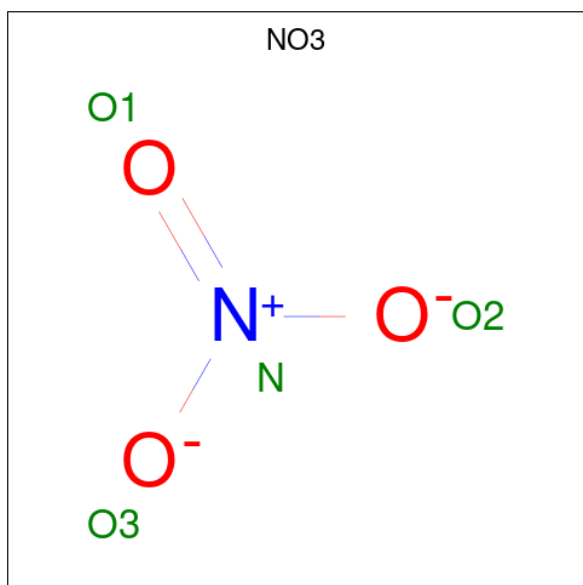
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 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
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



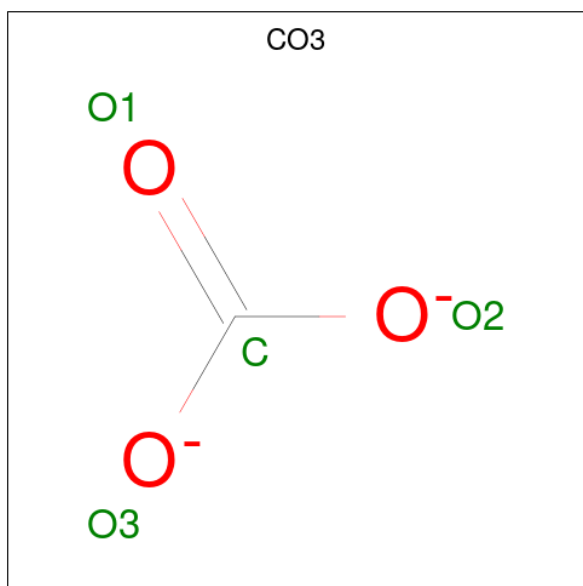
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	N	O	0	0
			4	1	3		
5	A	1	Total	N	O	0	0
			4	1	3		
5	B	1	Total	N	O	0	0
			4	1	3		

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

- Molecule 6 is CARBONATE ION (CCD ID: CO3) (formula: CO₃).

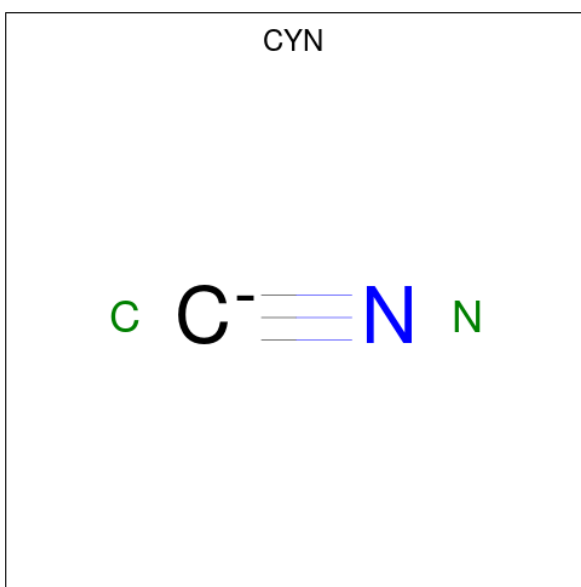


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	1	3		
6	B	1	Total	C	O	0	0
			4	1	3		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

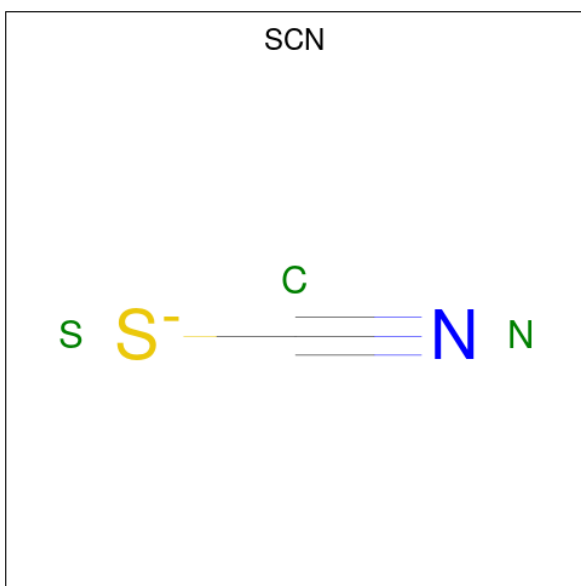
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	1	Total	Ca	0	0
			1	1		

- Molecule 8 is CYANIDE ION (CCD ID: CYN) (formula: CN).



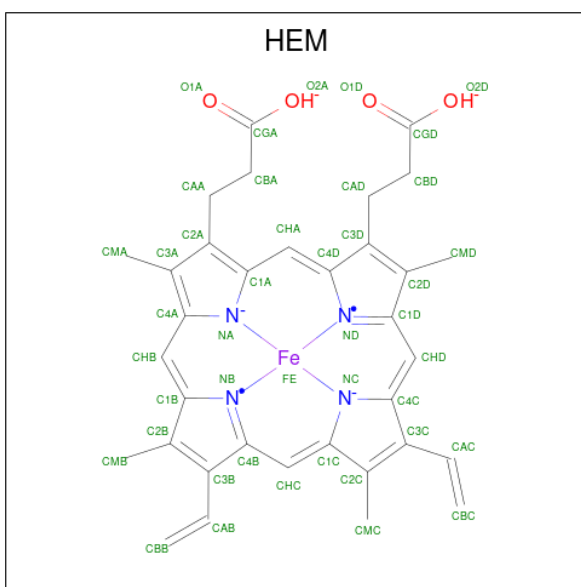
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	N	0	0
			2	1	1		

- Molecule 9 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



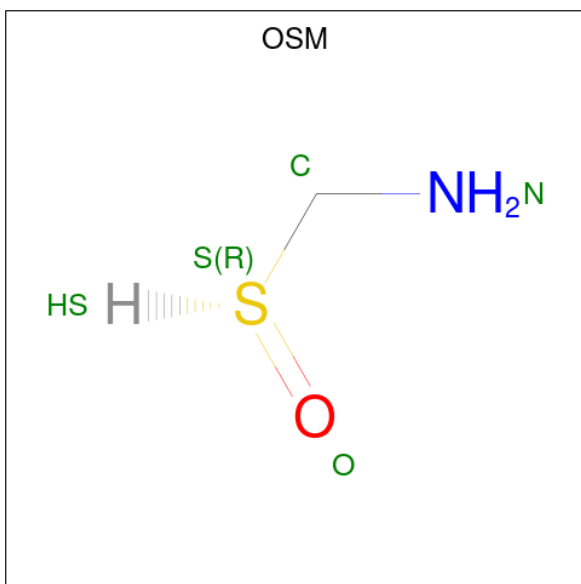
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 10 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

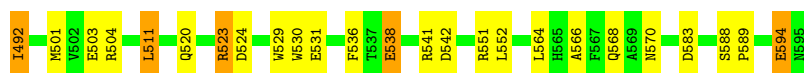
- Molecule 11 is 1-(OXIDOSULFANYL)METHANAMINE (CCD ID: OSM) (formula: CH₅NOS).



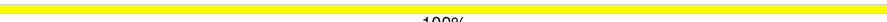
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	B	1	Total	C	N	O	S	0	0
			4	1	1	1	1		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	180	Total 180	O 180	0	0
12	B	200	Total 200	O 200	0	0

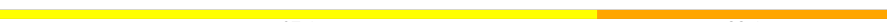


- Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  100%

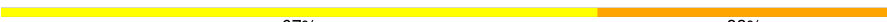


- Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  67% 33%

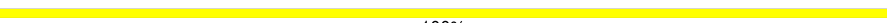


- Molecule 2: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  67% 33%



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

Chain E:  100%



- 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:  33% 67%



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

Chain I:  33% 67%



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

Chain F:  100%

MAG1
MAG2

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

Chain J:  100%

MAG1
MAG2

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.52Å 72.54Å 83.98Å 85.30° 84.06° 75.68°	Depositor
Resolution (Å)	20.00 – 3.25	Depositor
% Data completeness (in resolution range)	94.8 (20.00-3.25)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.169 , 0.203	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10299	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, CA, HEM, SCN, CYN, NO3, CO3, OSM, BMA, 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	0.68	0/4883	1.07	32/6632 (0.5%)
1	B	0.69	0/4883	1.07	28/6632 (0.4%)
All	All	0.69	0/9766	1.07	60/13264 (0.5%)

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

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

There are no bond length outliers.

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	13	VAL	N-CA-C	14.02	125.63	108.53
1	B	226	TYR	CA-C-N	-9.84	110.24	120.38
1	B	226	TYR	C-N-CA	-9.84	110.24	120.38
1	A	12	LEU	CA-C-N	-8.92	111.23	123.46
1	A	12	LEU	C-N-CA	-8.92	111.23	123.46

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	LEU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4754	0	4647	136	0
1	B	4754	0	4645	160	0
2	C	39	0	34	1	0
2	D	39	0	34	2	0
2	G	39	0	34	4	0
3	E	39	0	34	0	0
3	H	39	0	34	4	0
3	I	39	0	34	2	0
4	F	28	0	25	0	0
4	J	28	0	25	0	0
5	A	8	0	0	0	0
5	B	8	0	0	1	0
6	A	4	0	0	0	0
6	B	4	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	2	0	0	1	0
9	A	3	0	0	0	0
10	A	43	0	30	9	0
10	B	43	0	30	10	0
11	B	4	0	5	1	0
12	A	180	0	0	14	0
12	B	200	0	0	15	0
All	All	10299	0	9611	309	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 16.

The worst 5 of 309 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:LEU:HB2	1:A:13:VAL:HG23	1.21	1.19
1:A:8:ALA:HB1	1:A:9:PRO:HD2	1.36	1.08
1:B:12:LEU:HB2	1:B:13:VAL:HG23	1.13	1.08
1:B:258:GLU:OE2	10:B:821:HEM:HMB3	1.54	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:VAL:HG12	1:A:14:THR:H	1.16	1.05

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	593/595 (100%)	538 (91%)	40 (7%)	15 (2%)	4	22
1	B	593/595 (100%)	541 (91%)	42 (7%)	10 (2%)	7	29
All	All	1186/1190 (100%)	1079 (91%)	82 (7%)	25 (2%)	5	25

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	PRO
1	A	12	LEU
1	A	169	THR
1	A	171	PRO
1	B	9	PRO

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	517/517 (100%)	475 (92%)	42 (8%)	11	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	517/517 (100%)	474 (92%)	43 (8%)	10	34
All	All	1034/1034 (100%)	949 (92%)	85 (8%)	10	34

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	169	THR
1	B	360	ARG
1	B	187	LEU
1	B	268	LEU
1	B	464	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	571	ASN
1	B	63	GLN
1	B	497	ASN
1	A	595	ASN
1	B	68	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

22 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	C	1	1,2	14,14,15	0.62	0	17,19,21	0.77	0
2	NAG	C	2	2	14,14,15	0.68	0	17,19,21	1.40	3 (17%)
2	MAN	C	3	2	11,11,12	0.48	0	15,15,17	1.37	1 (6%)
2	NAG	D	1	1,2	14,14,15	0.74	1 (7%)	17,19,21	1.05	1 (5%)
2	NAG	D	2	2	14,14,15	0.80	0	17,19,21	1.29	2 (11%)
2	MAN	D	3	2	11,11,12	0.58	0	15,15,17	0.70	0
3	NAG	E	1	1,3	14,14,15	0.71	0	17,19,21	1.22	1 (5%)
3	NAG	E	2	3	14,14,15	0.56	0	17,19,21	1.58	2 (11%)
3	BMA	E	3	3	11,11,12	0.74	0	15,15,17	1.48	1 (6%)
4	NAG	F	1	1,4	14,14,15	0.63	0	17,19,21	1.55	2 (11%)
4	NAG	F	2	4	14,14,15	0.69	0	17,19,21	1.56	1 (5%)
2	NAG	G	1	1,2	14,14,15	0.77	0	17,19,21	1.69	5 (29%)
2	NAG	G	2	2	14,14,15	0.65	0	17,19,21	2.62	2 (11%)
2	MAN	G	3	2	11,11,12	0.87	0	15,15,17	1.79	3 (20%)
3	NAG	H	1	1,3	14,14,15	0.53	0	17,19,21	1.02	0
3	NAG	H	2	3	14,14,15	0.75	0	17,19,21	1.51	2 (11%)
3	BMA	H	3	3	11,11,12	0.72	0	15,15,17	2.18	4 (26%)
3	NAG	I	1	1,3	14,14,15	0.75	0	17,19,21	1.47	2 (11%)
3	NAG	I	2	3	14,14,15	0.72	0	17,19,21	1.39	2 (11%)
3	BMA	I	3	3	11,11,12	0.67	0	15,15,17	1.58	2 (13%)
4	NAG	J	1	1,4	14,14,15	0.65	0	17,19,21	1.61	3 (17%)
4	NAG	J	2	4	14,14,15	0.70	0	17,19,21	0.99	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	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	MAN	C	3	2	-	2/2/19/22	1/1/1/1
2	NAG	D	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	4/6/23/26	0/1/1/1
2	MAN	D	3	2	-	1/2/19/22	1/1/1/1
3	NAG	E	1	1,3	-	3/6/23/26	0/1/1/1
3	NAG	E	2	3	-	4/6/23/26	0/1/1/1

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	NAG	C1-C2	2.36	1.55	1.52

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	2	NAG	C1-O5-C5	8.51	123.60	112.19
3	H	3	BMA	C1-O5-C5	7.11	121.72	112.19
2	G	3	MAN	C1-O5-C5	5.33	119.33	112.19
3	I	3	BMA	C1-O5-C5	5.18	119.13	112.19
4	F	1	NAG	C4-C3-C2	4.85	118.13	111.02

There are no chirality outliers.

5 of 39 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2
4	F	2	NAG	C8-C7-N2-C2
4	F	2	NAG	O7-C7-N2-C2
4	J	2	NAG	C8-C7-N2-C2

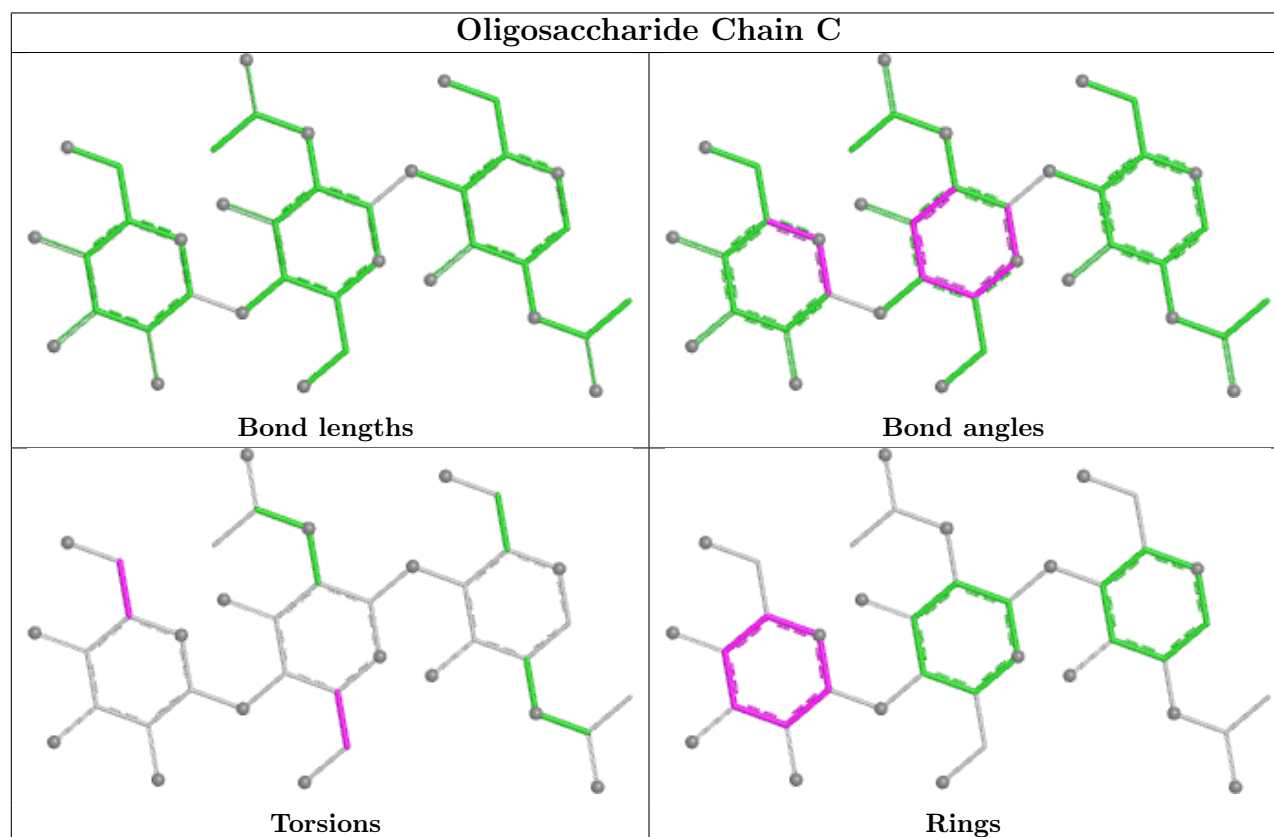
All (5) ring outliers are listed below:

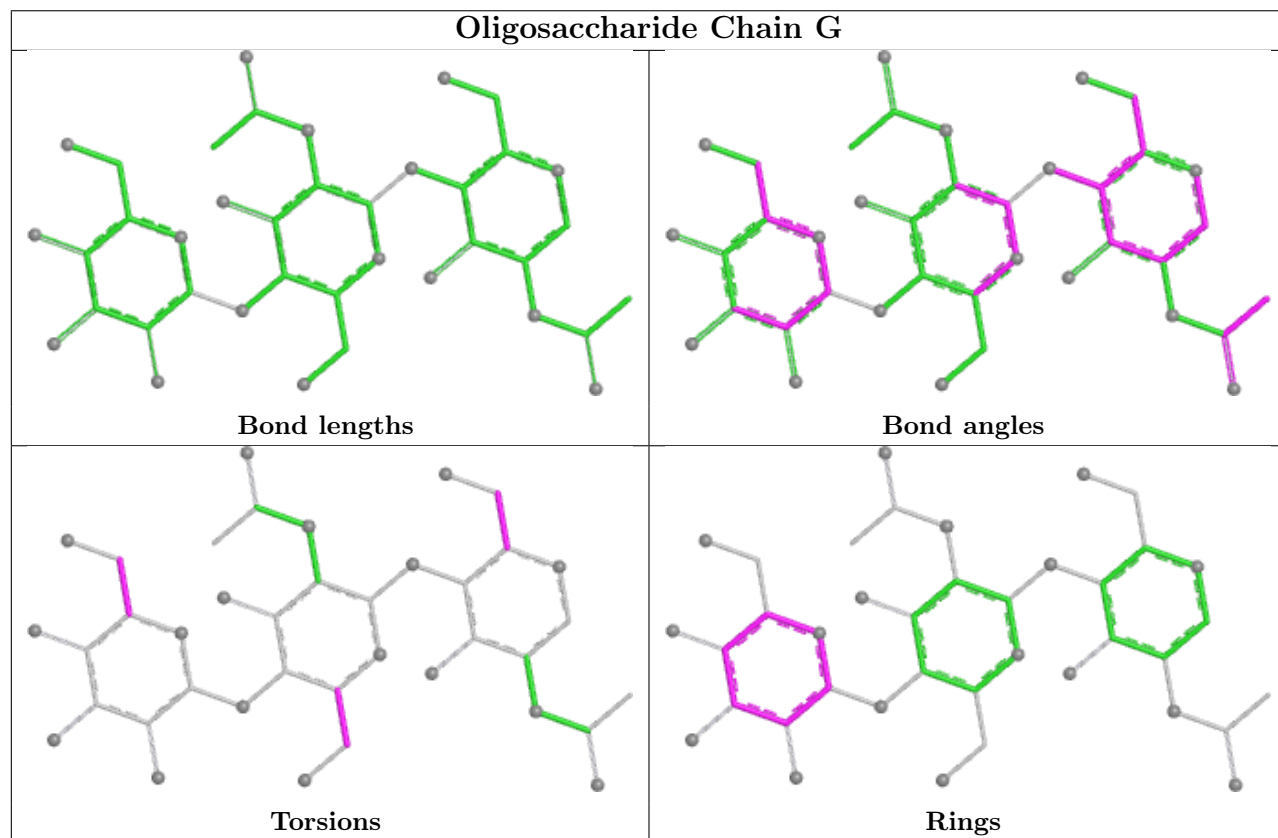
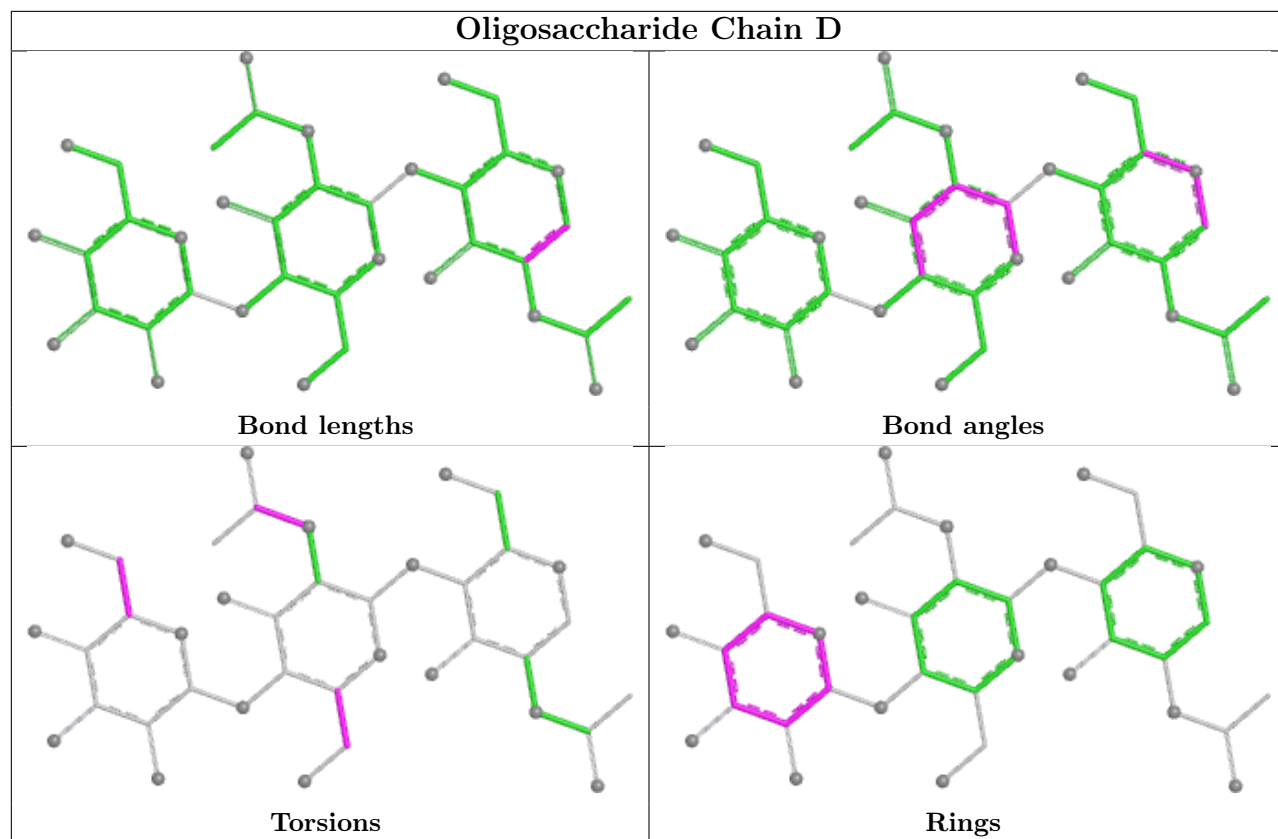
Mol	Chain	Res	Type	Atoms
2	G	3	MAN	C1-C2-C3-C4-C5-O5
2	D	3	MAN	C1-C2-C3-C4-C5-O5
3	I	3	BMA	C1-C2-C3-C4-C5-O5
3	E	3	BMA	C1-C2-C3-C4-C5-O5
2	C	3	MAN	C1-C2-C3-C4-C5-O5

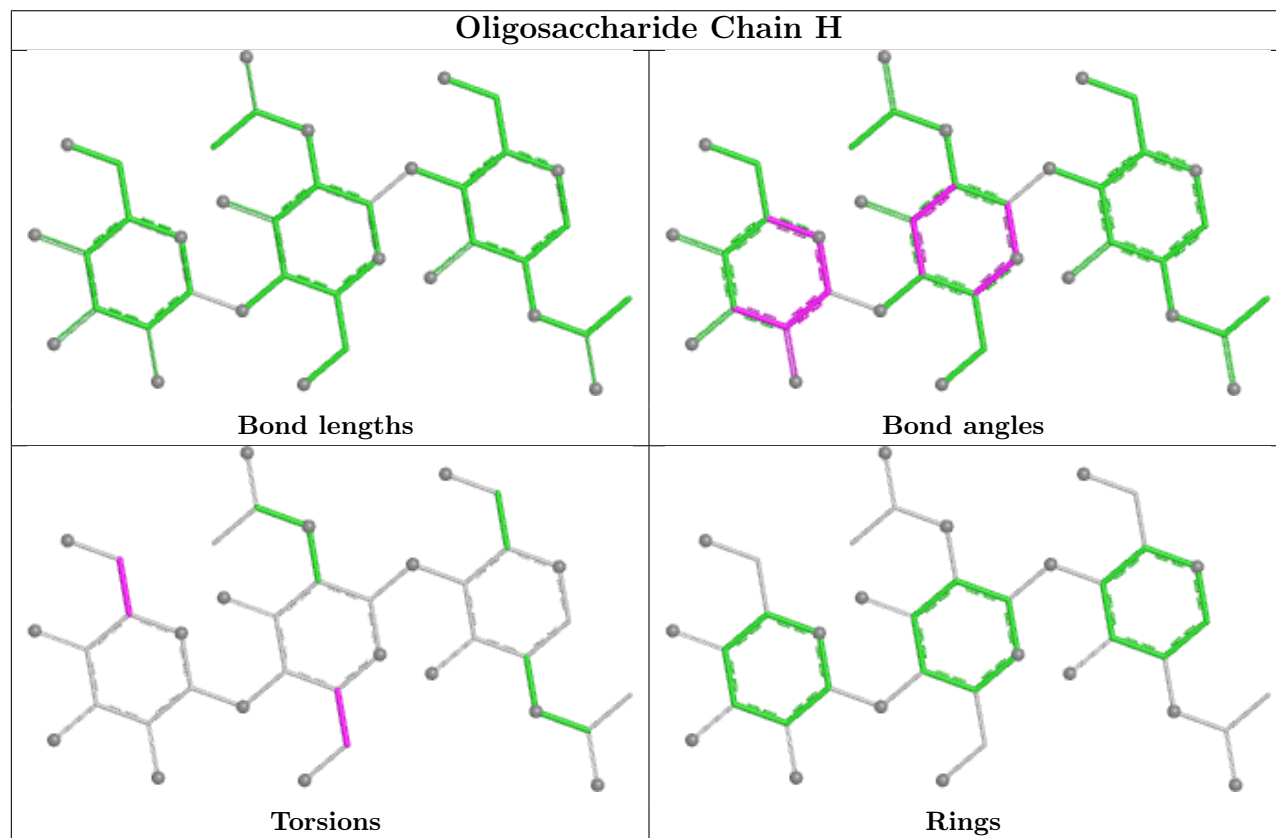
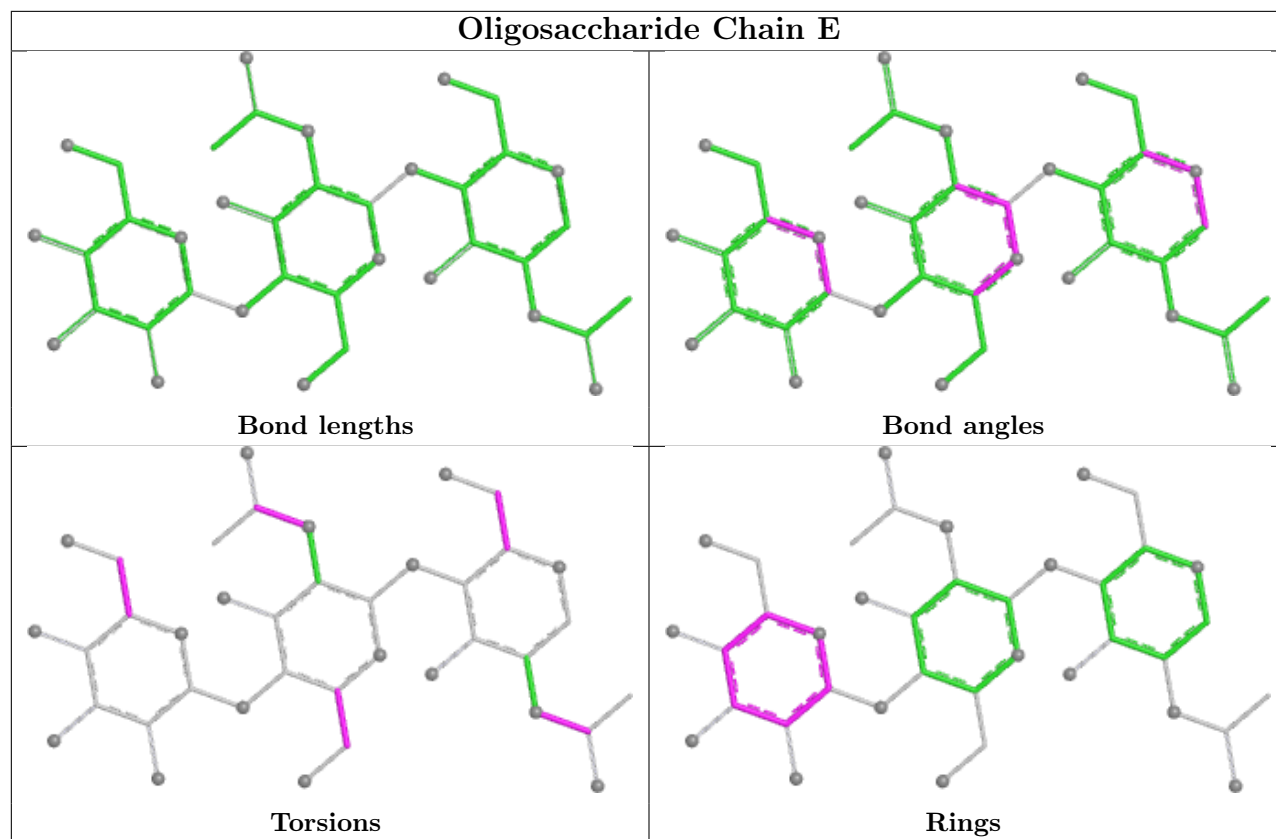
8 monomers are involved in 13 short contacts:

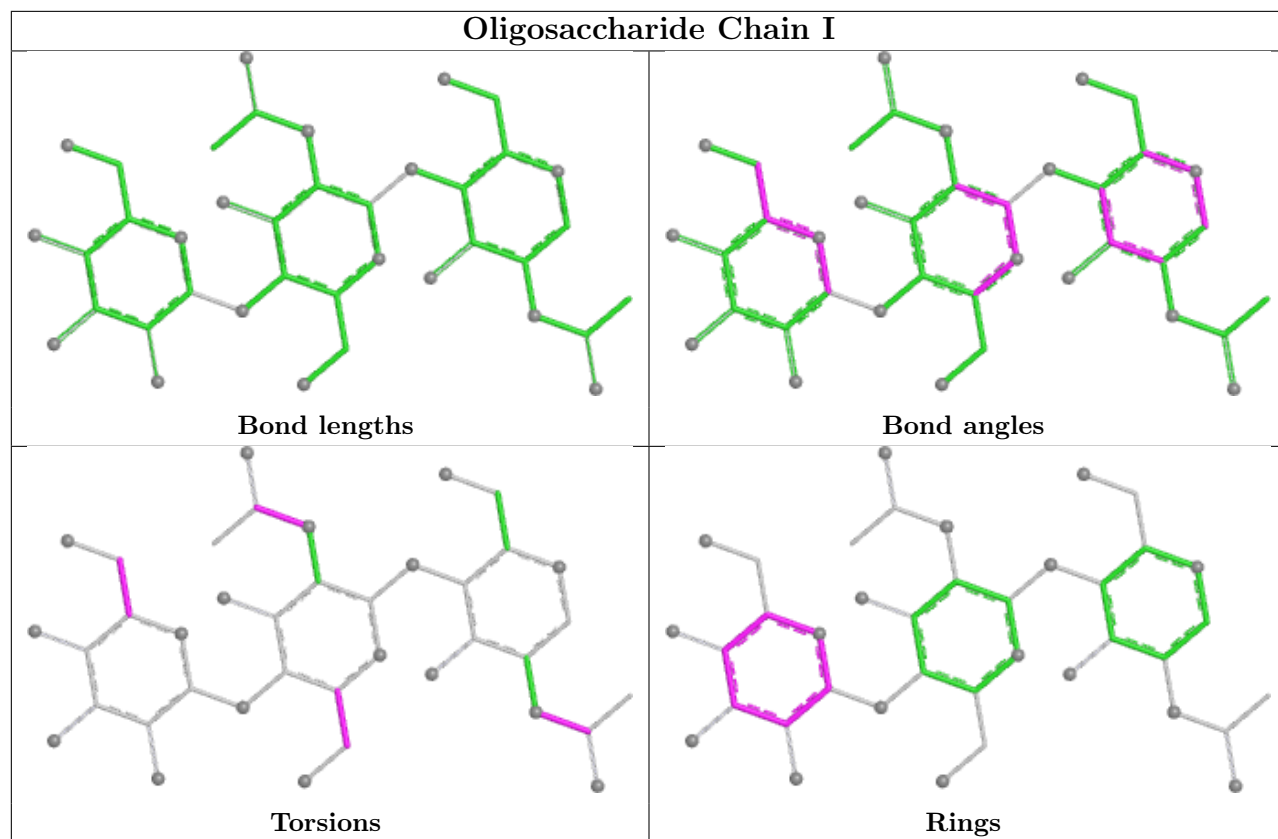
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	3	BMA	4	0
3	H	2	NAG	2	0
2	D	2	NAG	1	0
2	D	3	MAN	2	0
2	C	1	NAG	1	0
3	I	3	BMA	2	0
3	I	2	NAG	1	0
2	G	1	NAG	4	0

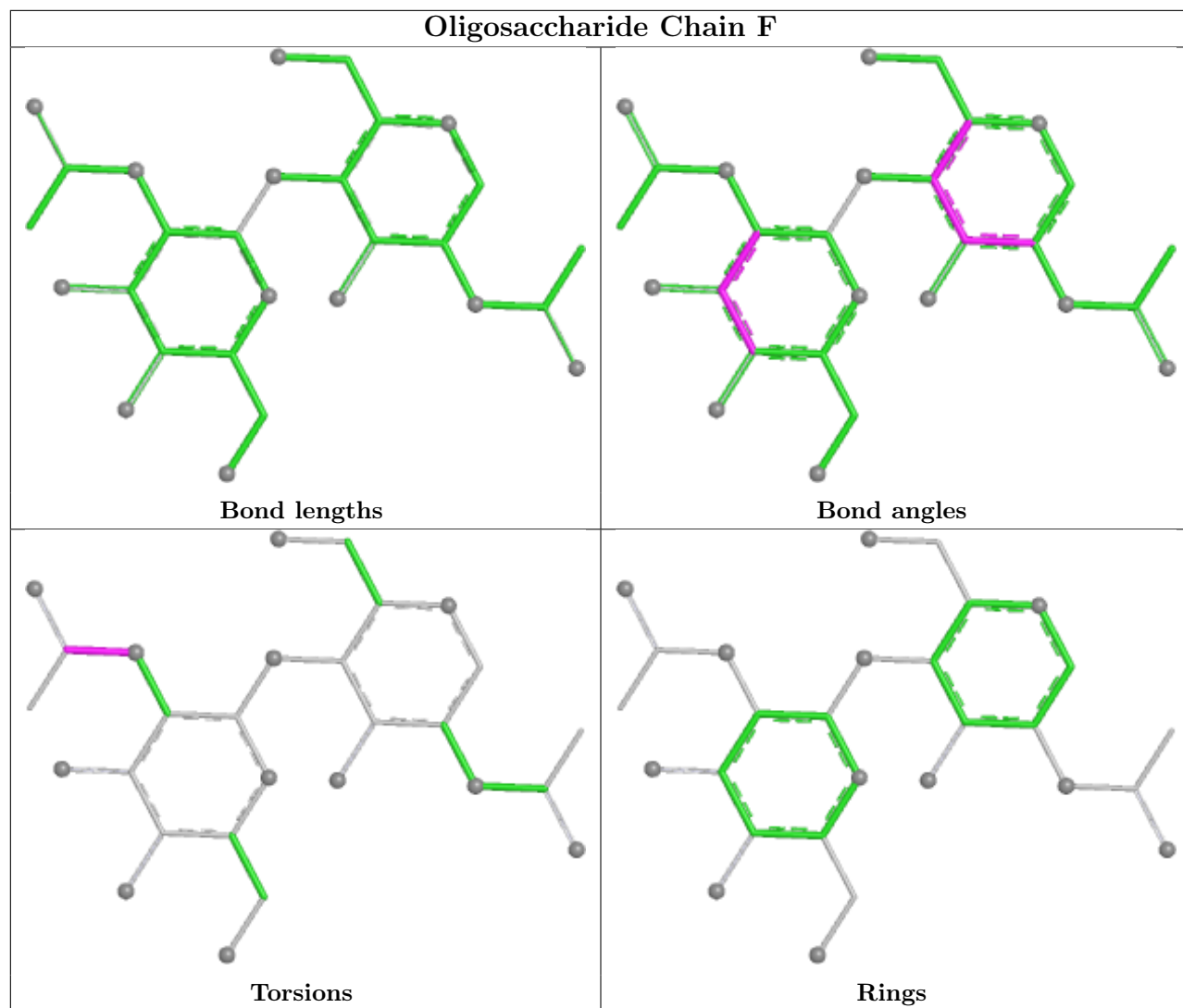
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

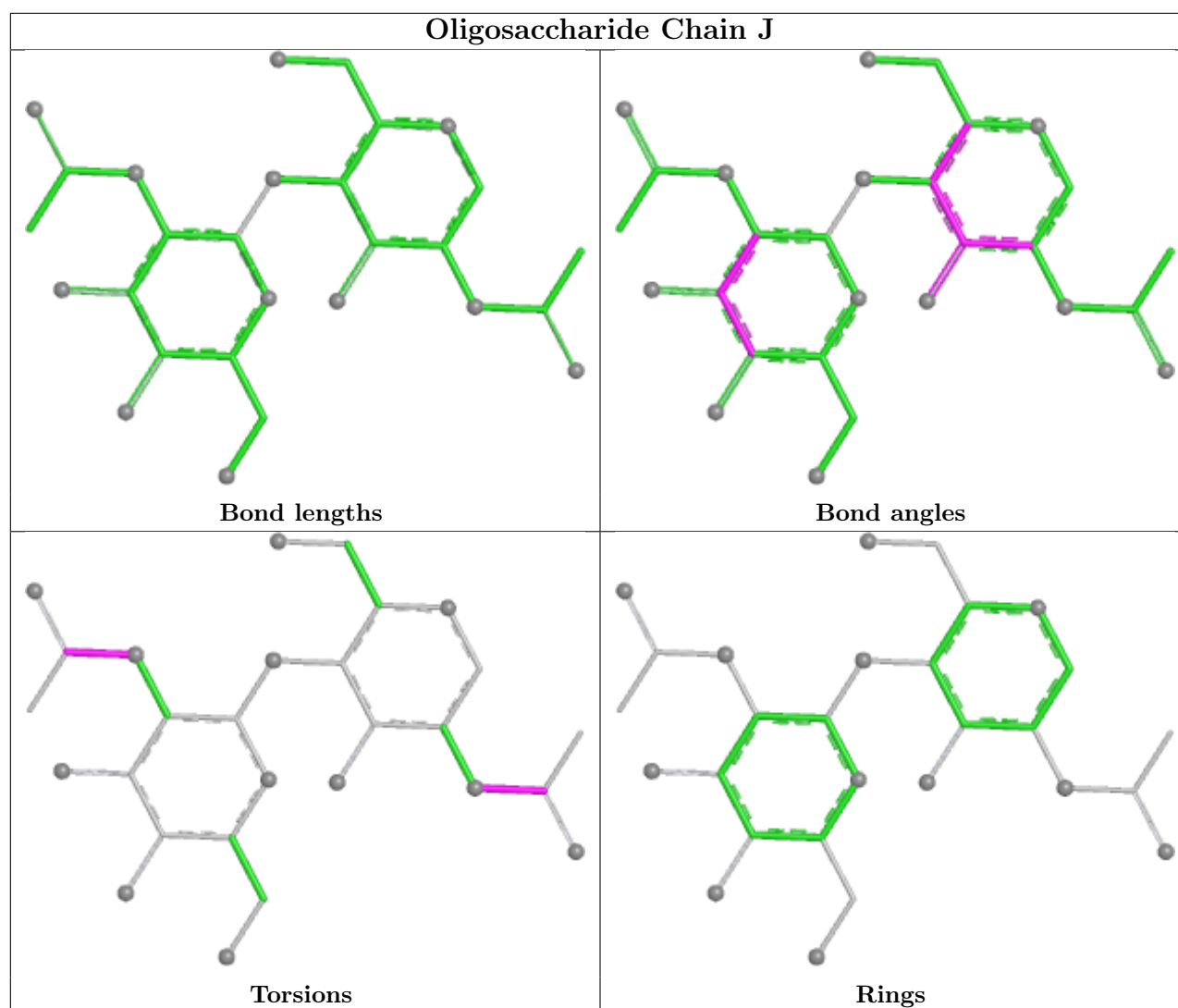












5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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	$\# Z > 2$
8	CYN	A	901	-	1,1,1	0.23	0	-	-	-
5	NO3	B	608	-	1,3,3	2.95	1 (100%)	0,3,3	-	-
5	NO3	A	607	-	1,3,3	3.56	1 (100%)	0,3,3	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	HEM	B	821	1	50,50,50	2.08	7 (14%)	67,82,82	1.53	10 (14%)
5	NO3	B	607	-	1,3,3	3.57	1 (100%)	0,3,3	-	-
5	NO3	A	608	-	1,3,3	3.11	1 (100%)	0,3,3	-	-
10	HEM	A	801	1	50,50,50	2.19	9 (18%)	67,82,82	1.51	12 (17%)
9	SCN	A	902	-	1,2,2	1.95	0	0,1,1	-	-
6	CO3	B	609	-	3,3,3	0.88	0	2,3,3	0.59	0
11	OSM	B	921	-	1,3,3	0.01	0	0,2,2	-	-
6	CO3	A	609	-	3,3,3	0.87	0	2,3,3	0.41	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
10	HEM	B	821	1	-	5/14/54/54	-
11	OSM	B	921	-	-	0/0/1/1	-
10	HEM	A	801	1	-	2/14/54/54	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	801	HEM	FE-NB	8.40	2.20	1.94
10	B	821	HEM	FE-NC	7.83	2.21	1.95
10	A	801	HEM	C3D-C2D	7.59	1.53	1.36
10	B	821	HEM	C3D-C2D	6.90	1.51	1.36
10	A	801	HEM	FE-NC	5.26	2.12	1.95

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	801	HEM	C4D-ND-C1D	6.07	112.40	105.21
10	B	821	HEM	C4D-ND-C1D	5.73	111.99	105.21
10	B	821	HEM	C3B-C2B-C1B	3.62	109.13	106.41
10	A	801	HEM	CMD-C2D-C1D	3.55	130.59	125.03
10	B	821	HEM	CMD-C2D-C1D	3.30	130.19	125.03

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

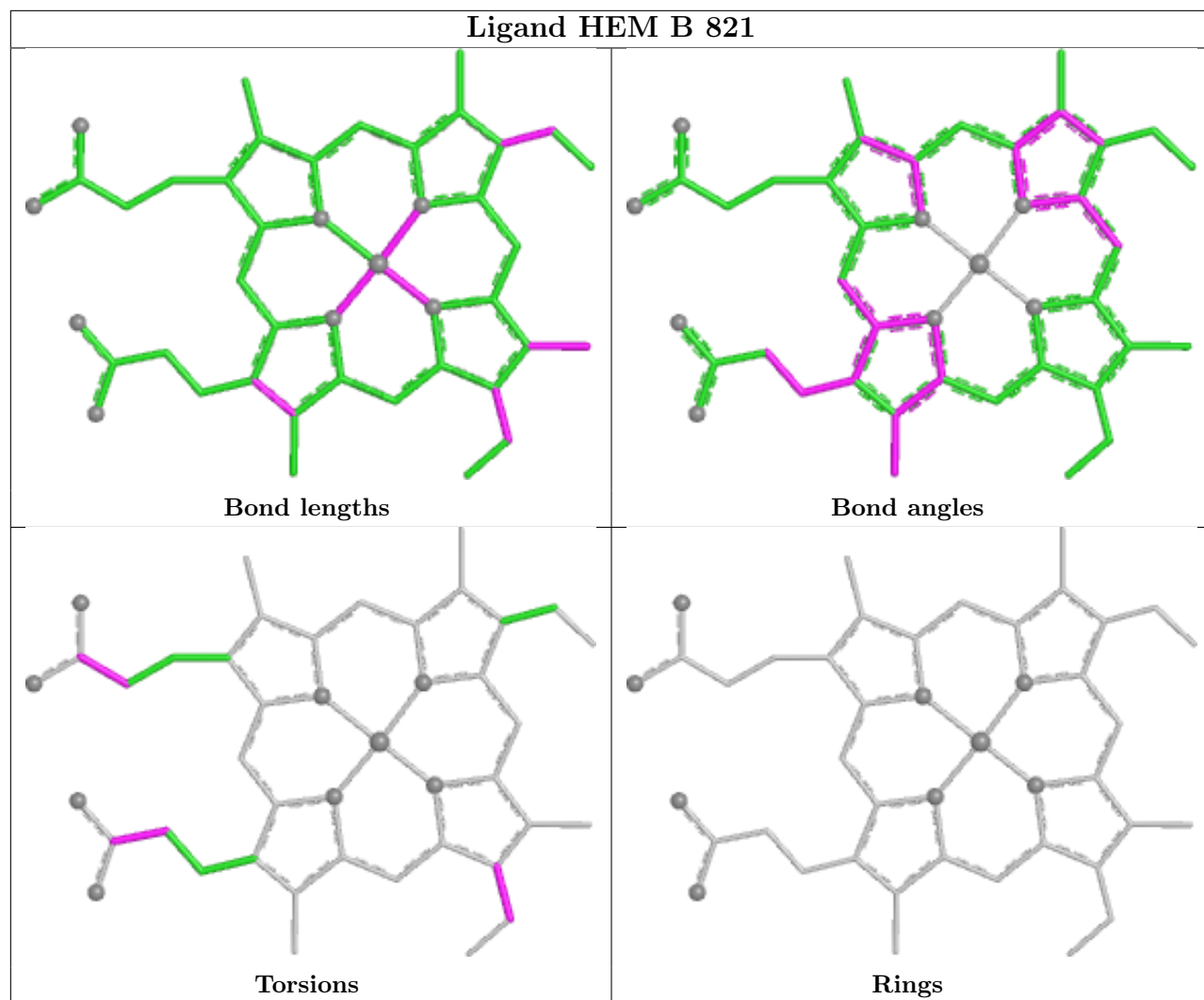
Mol	Chain	Res	Type	Atoms
10	B	821	HEM	CAD-CBD-CGD-O2D
10	B	821	HEM	CAD-CBD-CGD-O1D
10	B	821	HEM	CAA-CBA-CGA-O1A
10	B	821	HEM	CAA-CBA-CGA-O2A
10	A	801	HEM	CAD-CBD-CGD-O2D

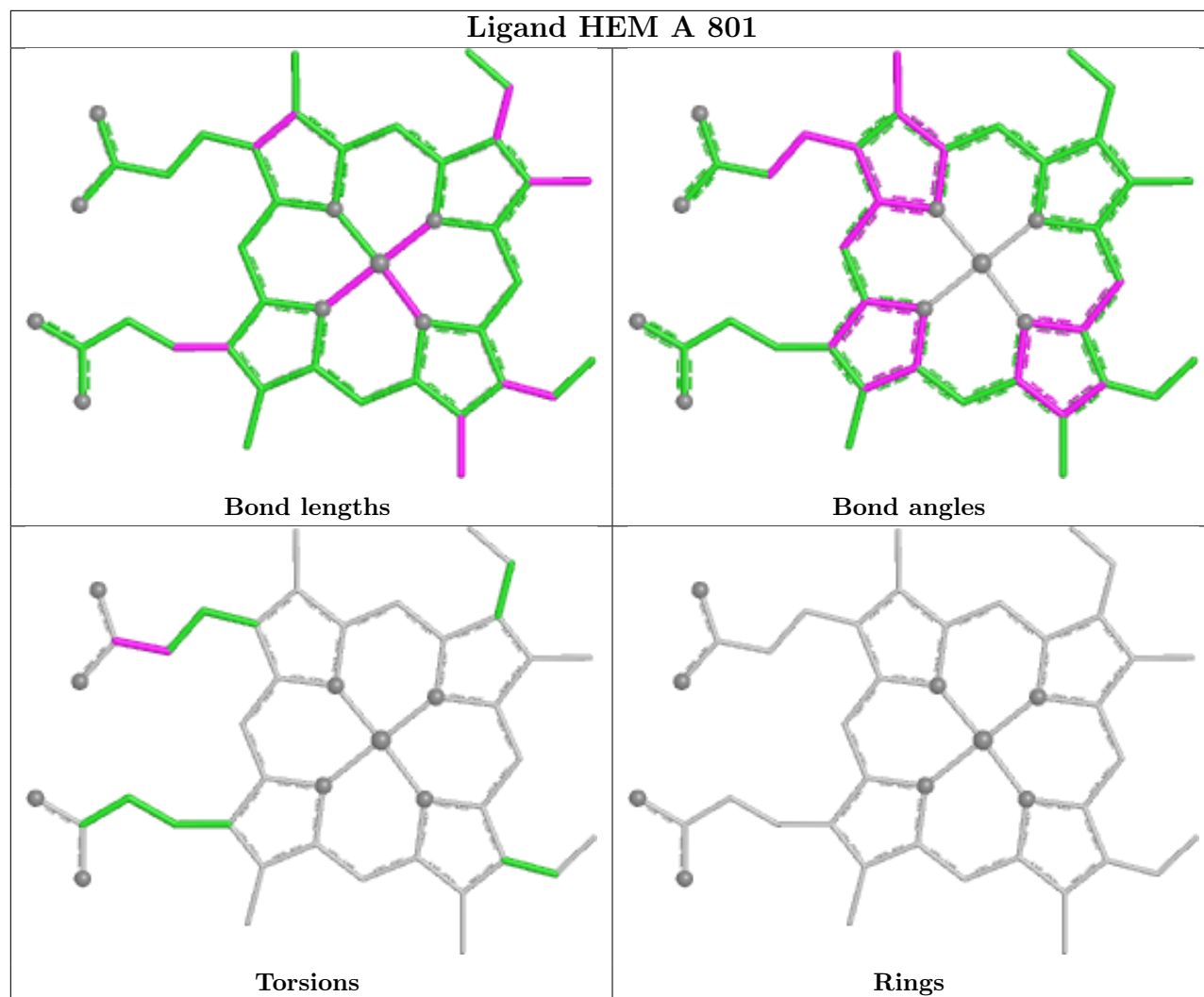
There are no ring outliers.

5 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	901	CYN	1	0
5	B	608	NO3	1	0
10	B	821	HEM	10	0
10	A	801	HEM	9	0
11	B	921	OSM	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.





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](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.