



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 11:52 PM BST

PDB ID : 1MYP
Title : X-RAY CRYSTAL STRUCTURE OF CANINE MYELOPEROXIDASE AT
3 ANGSTROMS RESOLUTION
Authors : Fenna, R.E.; Zeng, J.
Deposited on : 1992-04-15
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

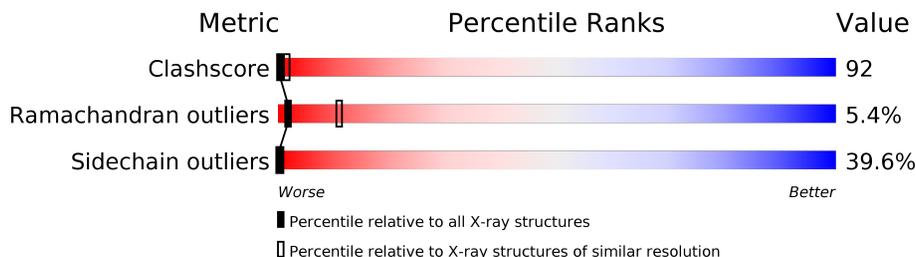
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	108	22% 32% 28% 14% .
1	B	108	19% 35% 27% 16% .
2	C	466	13% 40% 35% 12% .
2	D	466	16% 39% 33% 11% .
3	E	2	100%
3	F	2	100%
3	G	2	100%
3	H	2	50% 50%

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Mol	Chain	Length	Quality of chain
3	I	2	 100%
3	J	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	G	1	X	-	-	-
3	NAG	J	1	X	-	-	-
5	HEM	A	580	-	-	X	-
5	HEM	B	580	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9134 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 MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	104	Total 830	C 525	N 147	O 153	S 5	0	0	0
1	B	104	Total 830	C 525	N 147	O 153	S 5	0	0	0

- Molecule 2 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	462	Total 3609	C 2289	N 648	O 647	S 25	0	0	0
2	D	462	Total 3609	C 2289	N 648	O 647	S 25	0	0	0

- Molecule 3 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
			Total	C	N	O			
3	E	2	Total 28	C 16	N 2	O 10	0	0	0
3	F	2	Total 28	C 16	N 2	O 10	0	0	0
3	G	2	Total 28	C 16	N 2	O 10	0	0	0
3	H	2	Total 28	C 16	N 2	O 10	0	0	0
3	I	2	Total 28	C 16	N 2	O 10	0	0	0

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3 Residue-property plots [i](#)

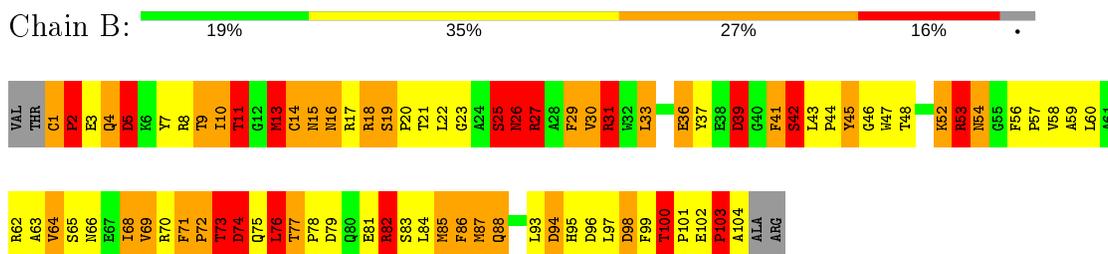
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

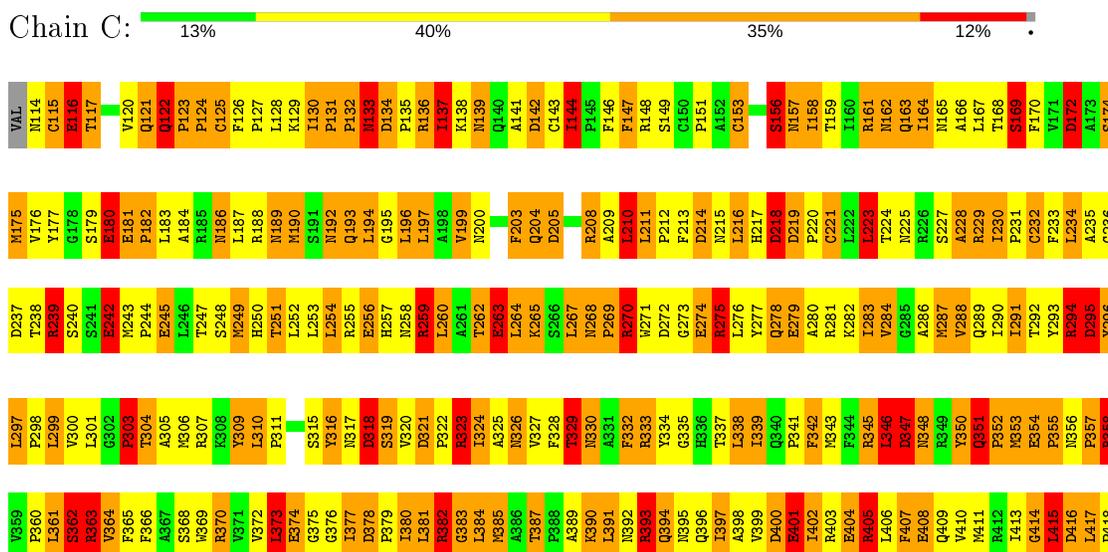
- Molecule 1: MYELOPEROXIDASE



- Molecule 1: MYELOPEROXIDASE



- Molecule 2: MYELOPEROXIDASE



MAG1
MAG2

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

Chain G:  100%MAG1
MAG2

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

Chain H:  50% 50%MAG1
MAG2

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

Chain I:  100%MAG1
MAG2

- Molecule 3: 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

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	133.00Å 133.00Å 203.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.257 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	9134	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

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: HEM, CA, NAG

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	0.86	5/855 (0.6%)	1.98	27/1166 (2.3%)
1	B	1.30	12/854 (1.4%)	2.10	44/1163 (3.8%)
2	C	1.03	28/3695 (0.8%)	2.16	158/5030 (3.1%)
2	D	1.13	26/3695 (0.7%)	2.15	163/5030 (3.2%)
All	All	1.08	71/9099 (0.8%)	2.13	392/12389 (3.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	3
1	B	0	4
2	C	6	12
2	D	5	13
All	All	13	32

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	560	ASP	C-N	26.88	1.95	1.34
2	D	179	SER	C-N	20.67	1.81	1.34
2	D	557	TYR	C-N	20.42	1.73	1.34
2	D	560	ASP	C-N	19.45	1.78	1.34
2	D	203	PHE	C-N	17.63	1.74	1.34

The worst 5 of 392 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	560	ASP	O-C-N	-21.52	88.26	122.70
2	C	560	ASP	O-C-N	-18.81	92.61	122.70
2	C	218	ASP	CB-CG-OD1	-18.33	101.80	118.30
2	D	202	ARG	O-C-N	-16.89	95.67	122.70
2	D	272	ASP	CB-CA-C	-16.82	76.77	110.40

5 of 13 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	14	CYS	CA
1	A	69	VAL	CA
2	C	137	ILE	CA
2	C	156	SER	CA
2	C	460	LEU	CA

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	GLU	Mainchain
1	A	6	LYS	Mainchain
1	A	79	ASP	Sidechain
2	C	122	GLN	Mainchain
2	C	133	ASN	Mainchain

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	830	0	785	198	0
1	B	830	0	784	186	0
2	C	3609	0	3529	859	0
2	D	3609	0	3529	605	0
3	E	28	0	25	2	0
3	F	28	0	25	1	0
3	G	28	0	25	5	0
3	H	28	0	25	1	0
3	I	28	0	25	6	0
3	J	28	0	25	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	43	0	30	35	0
5	B	43	0	30	32	0
All	All	9134	0	8837	1651	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 92.

The worst 5 of 1651 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:D:557:TYR:C	2:D:558:PRO:N	1.73	1.42
2:C:560:ASP:H	2:C:561:PHE:N	1.17	1.42
2:C:516:ASN:C	2:C:517:GLU:N	1.72	1.41
2:D:203:PHE:C	2:D:204:GLN:N	1.74	1.38
2:D:560:ASP:C	2:D:561:PHE:N	1.78	1.37

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	102/108 (94%)	75 (74%)	22 (22%)	5 (5%)	2 13
1	B	100/108 (93%)	80 (80%)	13 (13%)	7 (7%)	1 6
2	C	460/466 (99%)	349 (76%)	84 (18%)	27 (6%)	1 9
2	D	460/466 (99%)	356 (77%)	82 (18%)	22 (5%)	2 13
All	All	1122/1148 (98%)	860 (77%)	201 (18%)	61 (5%)	2 11

5 of 61 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	123	PRO
2	C	303	PRO
2	C	352	PRO
2	C	376	GLY
2	C	560	ASP

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	88/93 (95%)	52 (59%)	36 (41%)	0	0
1	B	88/93 (95%)	56 (64%)	32 (36%)	0	1
2	C	386/411 (94%)	228 (59%)	158 (41%)	0	0
2	D	386/411 (94%)	237 (61%)	149 (39%)	0	0
All	All	948/1008 (94%)	573 (60%)	375 (40%)	0	0

5 of 375 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	495	LEU
1	B	33	LEU
2	D	486	LYS
2	C	507	ARG
2	C	562	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	472	ASN
1	B	16	ASN
2	D	457	ASN
2	C	502	GLN
2	C	571	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](#)

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
3	NAG	E	1	3,2	14,14,15	1.09	1 (7%)	17,19,21	1.84	4 (23%)
3	NAG	E	2	3	14,14,15	1.82	2 (14%)	17,19,21	1.02	1 (5%)
3	NAG	F	1	3,2	14,14,15	1.04	1 (7%)	17,19,21	1.57	3 (17%)
3	NAG	F	2	3	14,14,15	1.08	1 (7%)	17,19,21	1.05	2 (11%)
3	NAG	G	1	3,2	14,14,15	1.00	1 (7%)	17,19,21	1.84	2 (11%)
3	NAG	G	2	3	14,14,15	1.10	1 (7%)	17,19,21	0.93	1 (5%)
3	NAG	H	1	3,2	14,14,15	1.16	1 (7%)	17,19,21	1.68	3 (17%)
3	NAG	H	2	3	14,14,15	1.09	1 (7%)	17,19,21	0.99	1 (5%)
3	NAG	I	1	3,2	14,14,15	0.98	1 (7%)	17,19,21	1.64	2 (11%)
3	NAG	I	2	3	14,14,15	0.93	1 (7%)	17,19,21	0.90	1 (5%)
3	NAG	J	1	3,2	14,14,15	1.07	1 (7%)	17,19,21	1.54	4 (23%)
3	NAG	J	2	3	14,14,15	0.97	1 (7%)	17,19,21	0.83	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	E	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	4/6/23/26	0/1/1/1
3	NAG	G	1	3,2	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	4/6/23/26	0/1/1/1
3	NAG	H	1	3,2	-	2/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	NAG	I	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	3/6/23/26	0/1/1/1
3	NAG	J	1	3,2	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	0/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	2	NAG	O4-C4	5.75	1.56	1.43
3	F	2	NAG	C8-C7	3.46	1.57	1.50
3	E	1	NAG	C8-C7	3.38	1.57	1.50
3	F	1	NAG	C8-C7	3.37	1.57	1.50
3	H	1	NAG	C8-C7	3.37	1.57	1.50

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	1	NAG	O4-C4-C5	-5.85	94.78	109.30
3	I	1	NAG	O4-C4-C5	5.77	123.63	109.30
3	H	1	NAG	O5-C5-C6	-5.16	99.11	107.20
3	F	1	NAG	O4-C4-C5	4.87	121.39	109.30
3	E	1	NAG	O4-C4-C5	-4.74	97.53	109.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	G	1	NAG	C1
3	J	1	NAG	C1

5 of 25 torsion outliers are listed below:

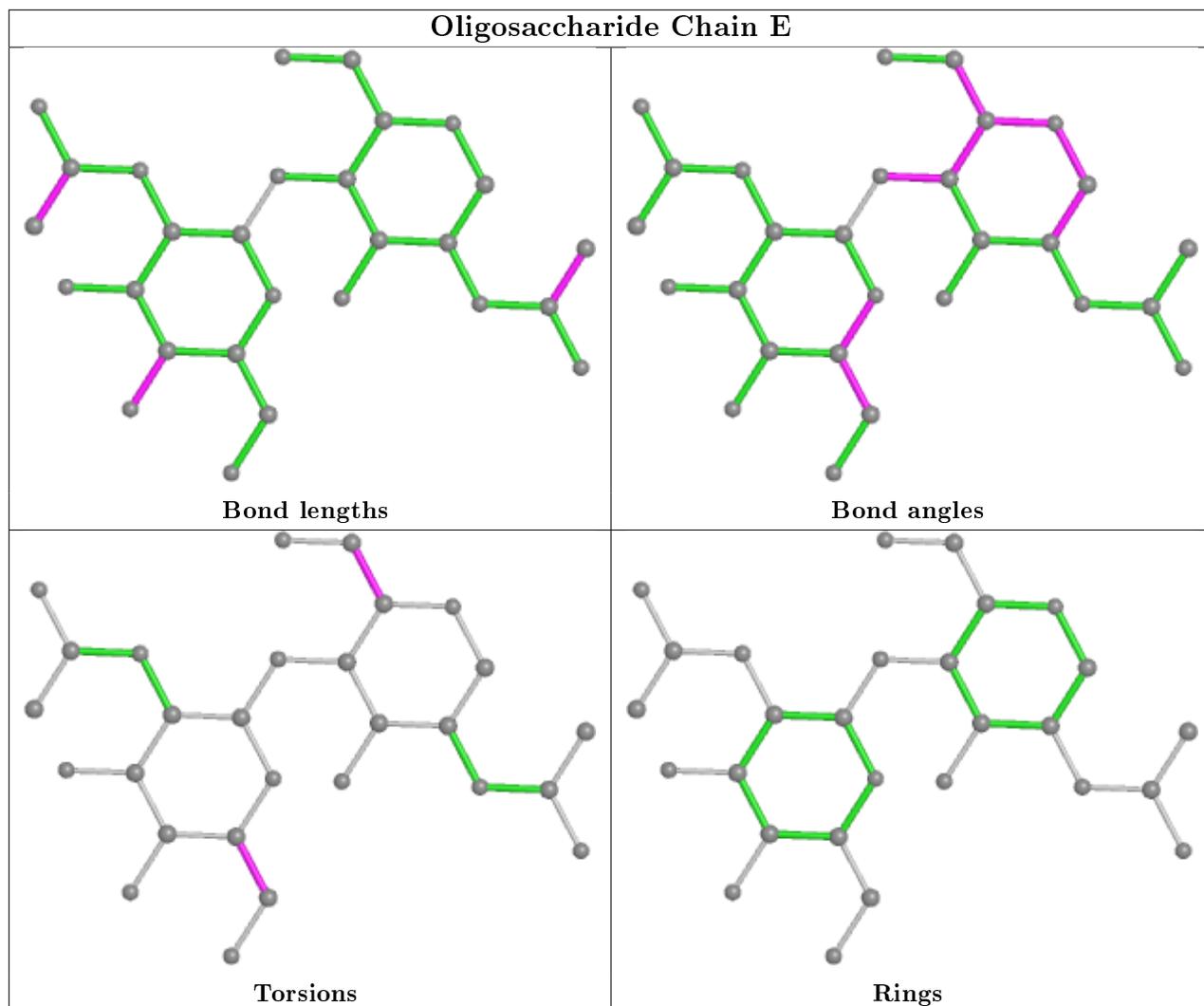
Mol	Chain	Res	Type	Atoms
3	I	2	NAG	C3-C2-N2-C7
3	J	1	NAG	C1-C2-N2-C7
3	G	2	NAG	C1-C2-N2-C7
3	H	2	NAG	C4-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6

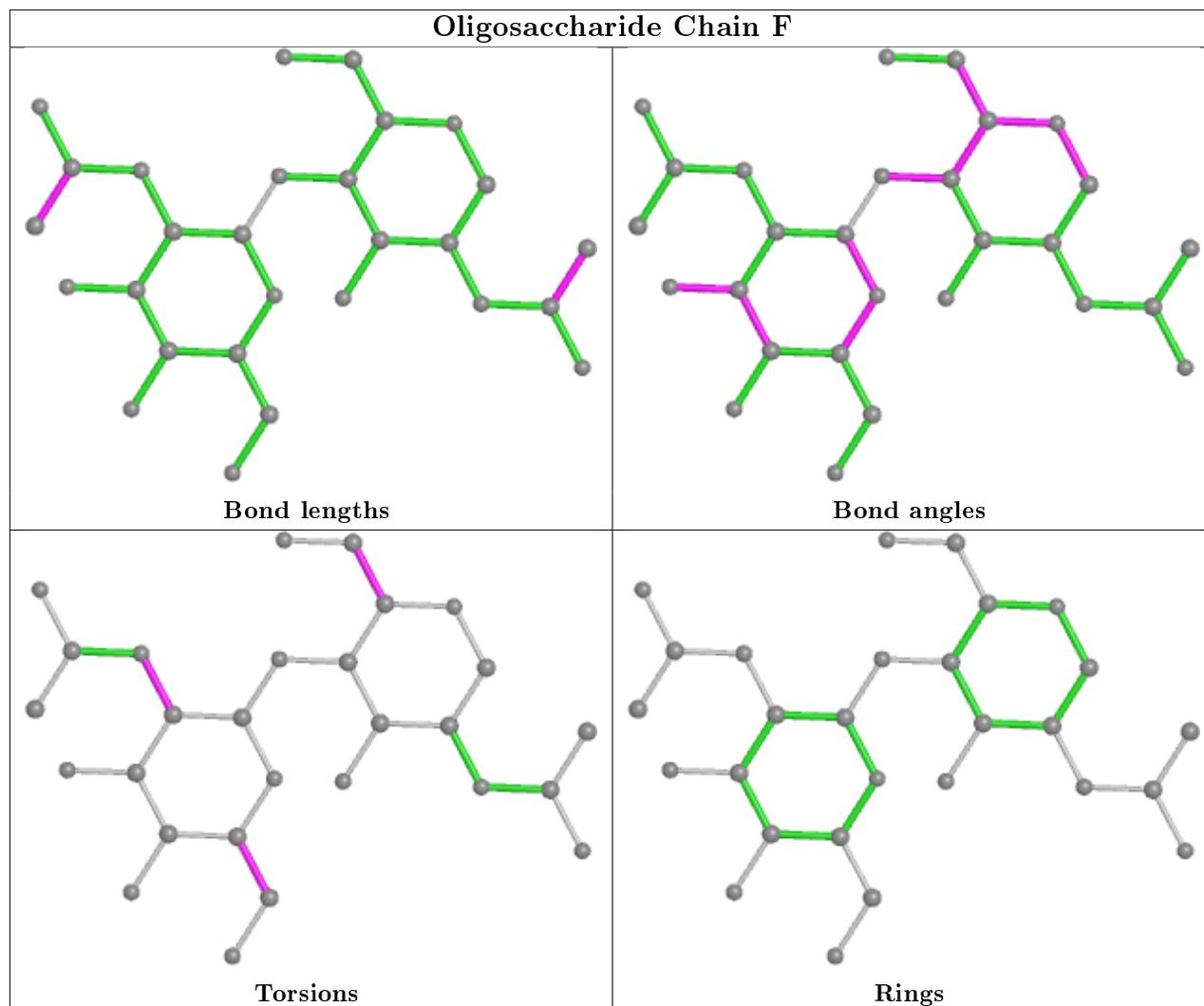
There are no ring outliers.

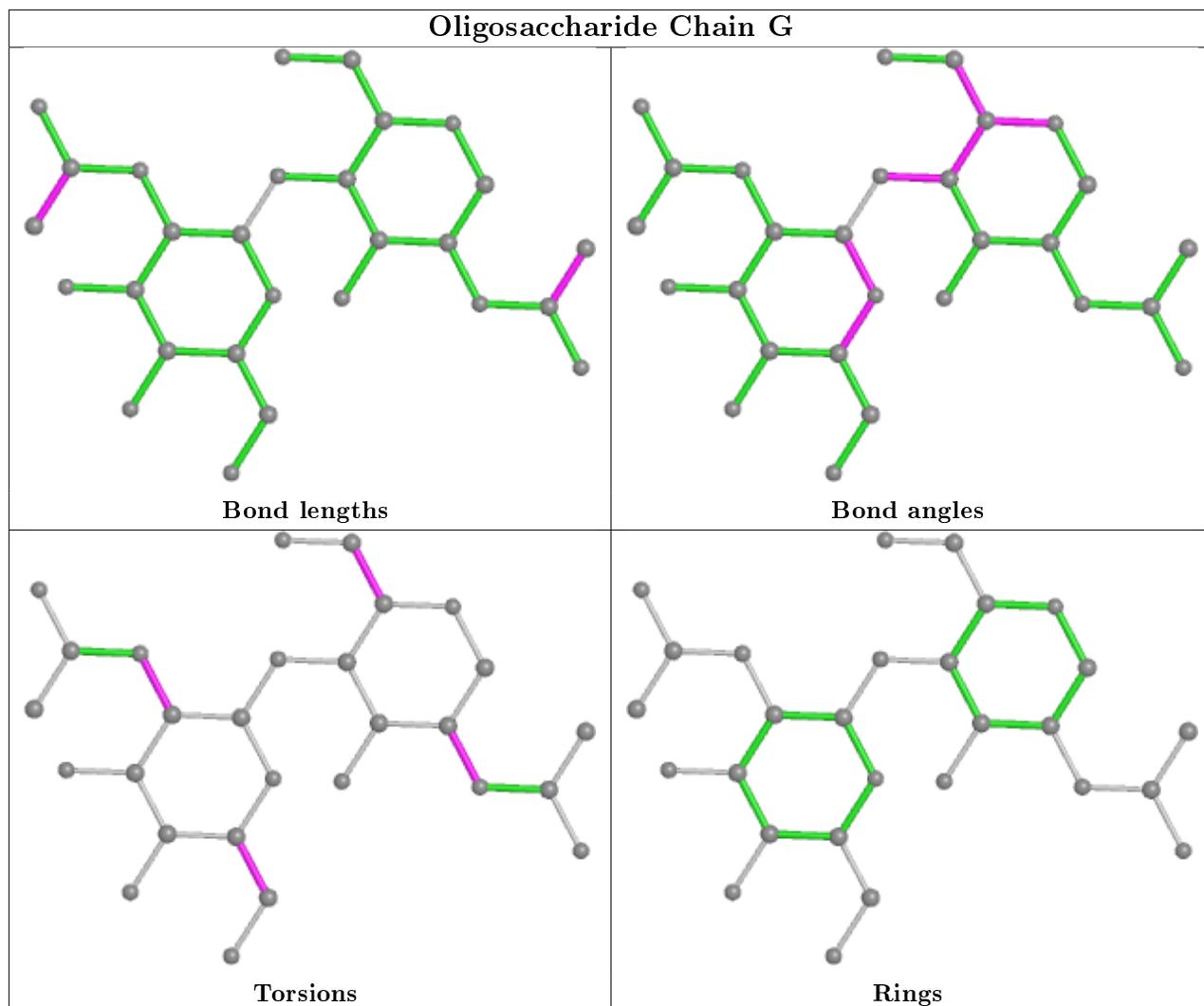
11 monomers are involved in 21 short contacts:

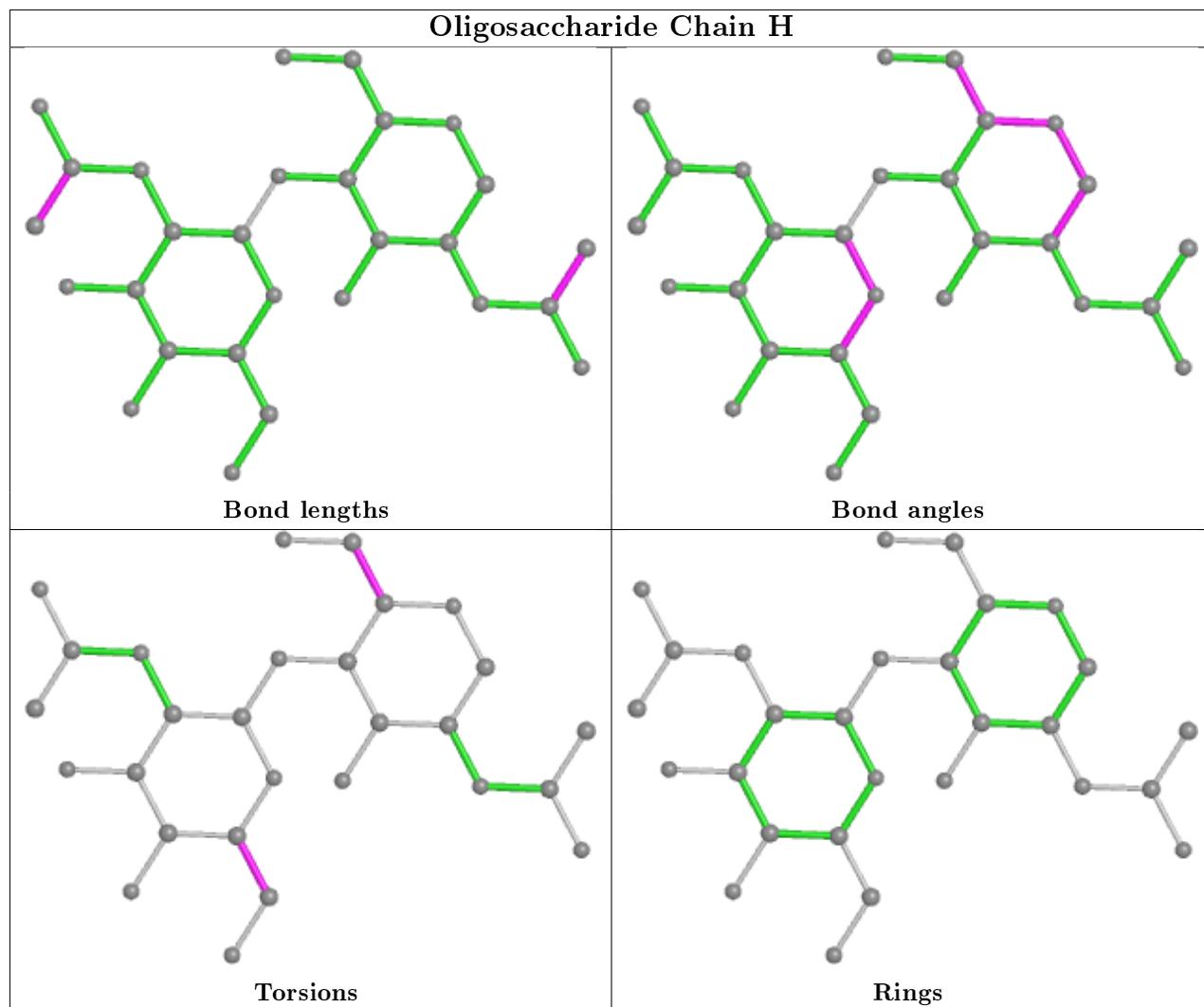
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	1	NAG	2	0
3	J	2	NAG	2	0
3	E	2	NAG	2	0
3	H	2	NAG	1	0
3	F	2	NAG	1	0
3	F	1	NAG	1	0
3	I	2	NAG	4	0
3	J	1	NAG	6	0
3	G	2	NAG	3	0
3	I	1	NAG	5	0
3	E	1	NAG	1	0

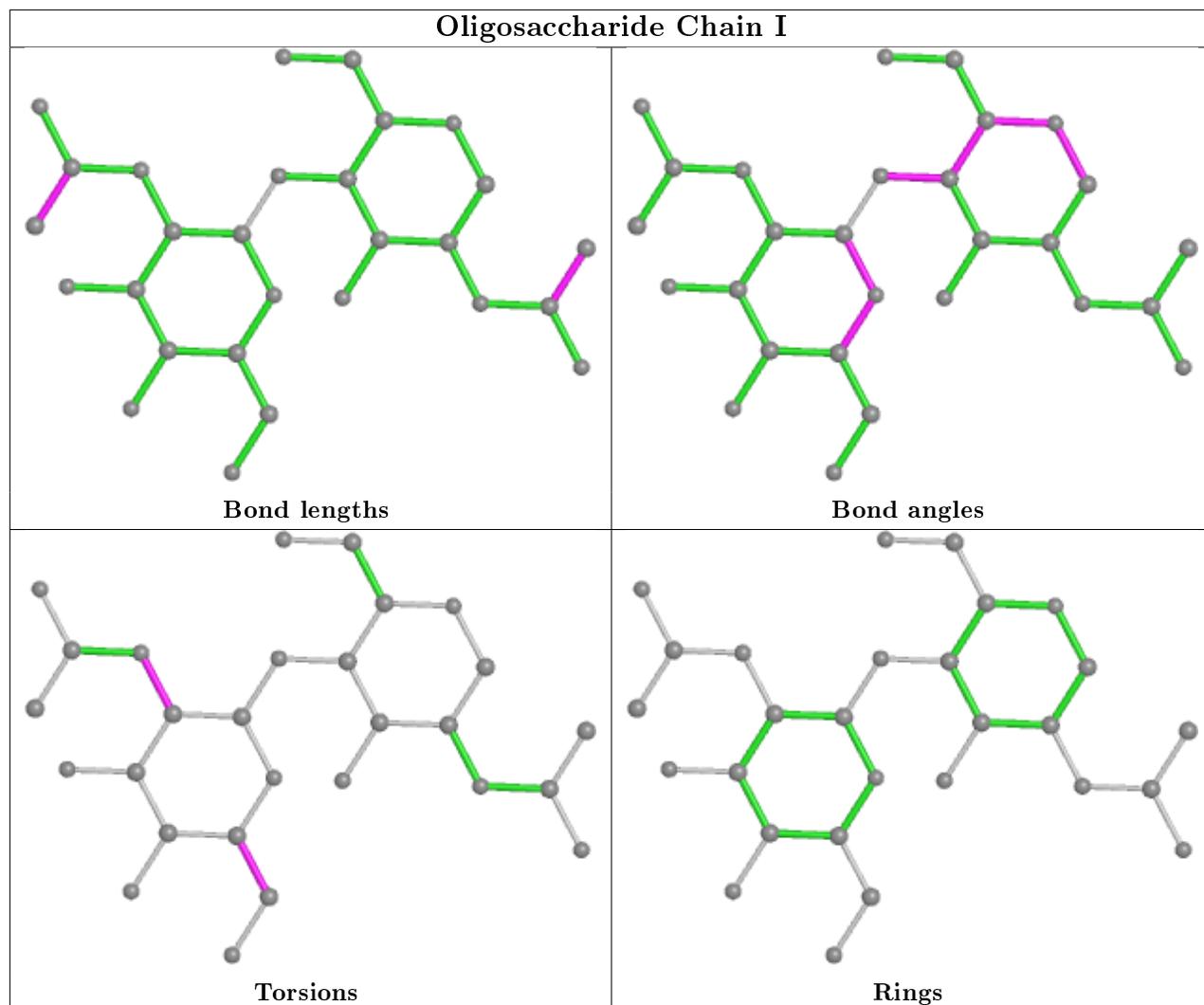
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

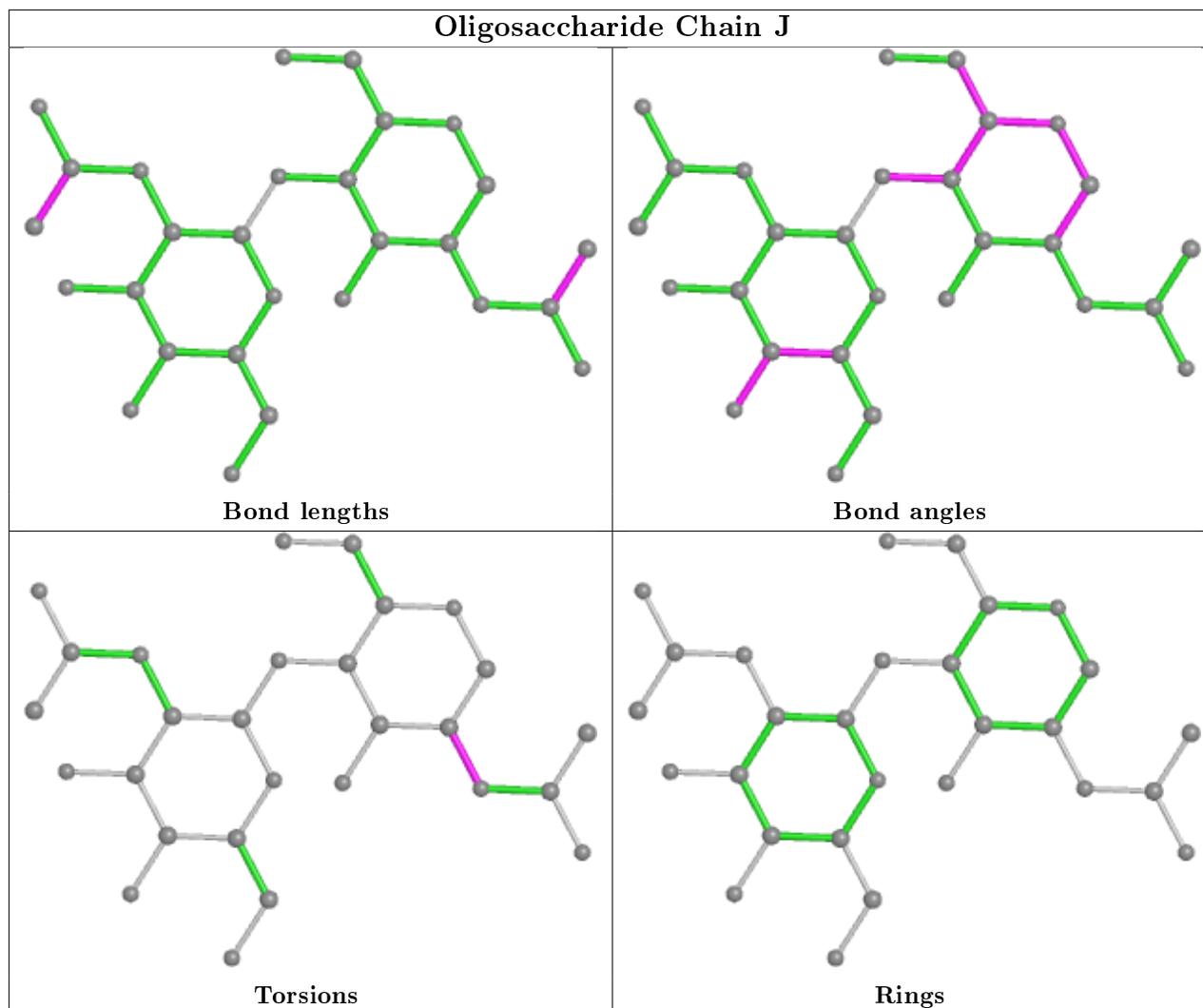












5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
5	HEM	A	580	2	27,50,50	1.53	3 (11%)	17,82,82	1.45	4 (23%)
5	HEM	B	580	2	27,50,50	1.60	4 (14%)	17,82,82	1.41	4 (23%)

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
5	HEM	A	580	2	-	2/6/54/54	-
5	HEM	B	580	2	-	0/6/54/54	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	580	HEM	C3C-C2C	-3.95	1.34	1.40
5	B	580	HEM	C3C-C2C	-3.85	1.35	1.40
5	A	580	HEM	C3B-C2B	-3.75	1.35	1.40
5	B	580	HEM	C3B-C2B	-3.68	1.35	1.40
5	B	580	HEM	C1D-CHD	-3.66	1.30	1.41

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	580	HEM	CAD-CBD-CGD	-2.81	107.96	112.67
5	A	580	HEM	CAD-CBD-CGD	-2.77	108.02	112.67
5	B	580	HEM	CAA-CBA-CGA	-2.72	108.10	112.67
5	A	580	HEM	CAA-CBA-CGA	-2.71	108.12	112.67
5	A	580	HEM	CBA-CAA-C2A	-2.56	107.77	112.49

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	580	HEM	C3A-C2A-CAA-CBA
5	A	580	HEM	C3D-CAD-CBD-CGD

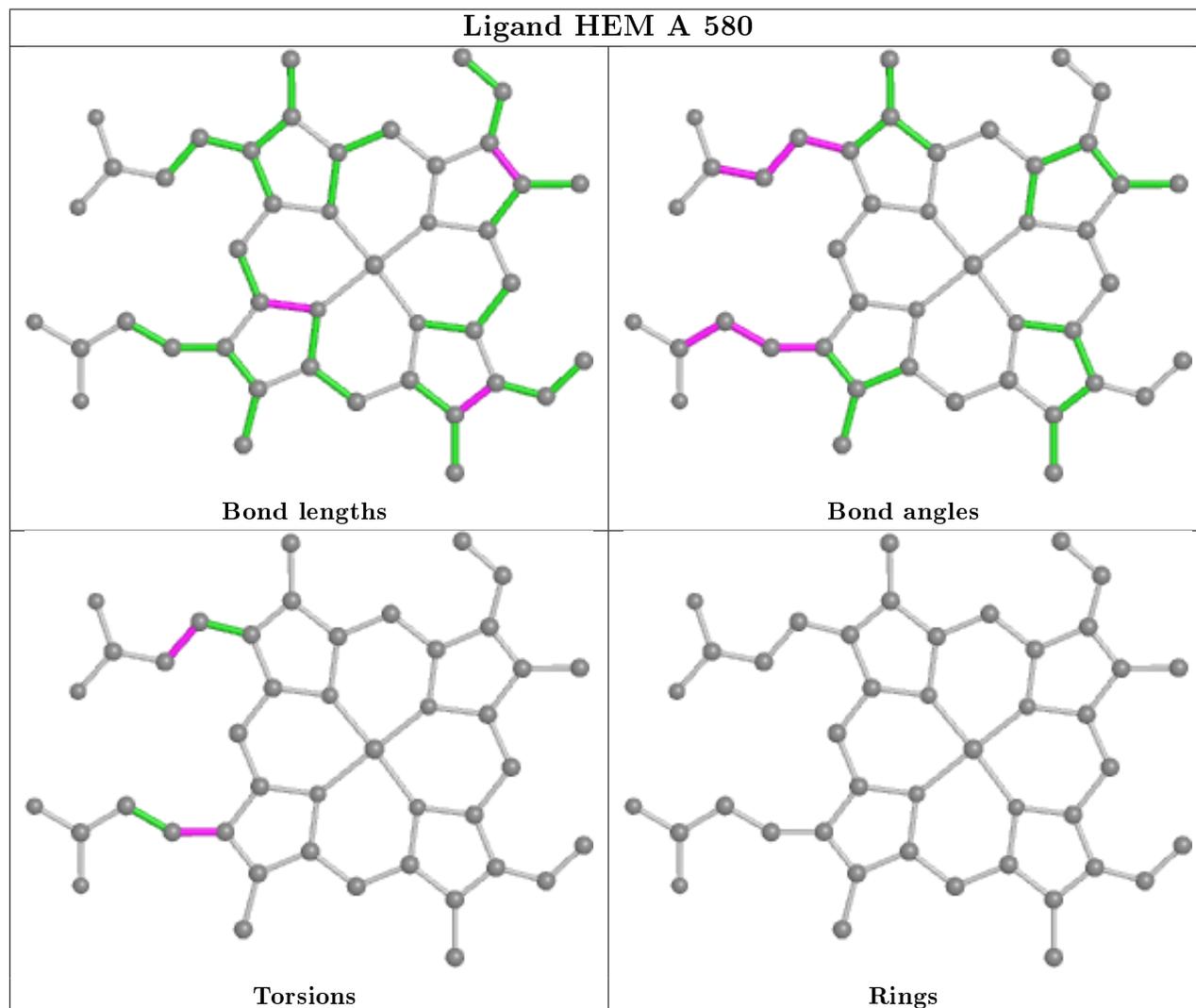
There are no ring outliers.

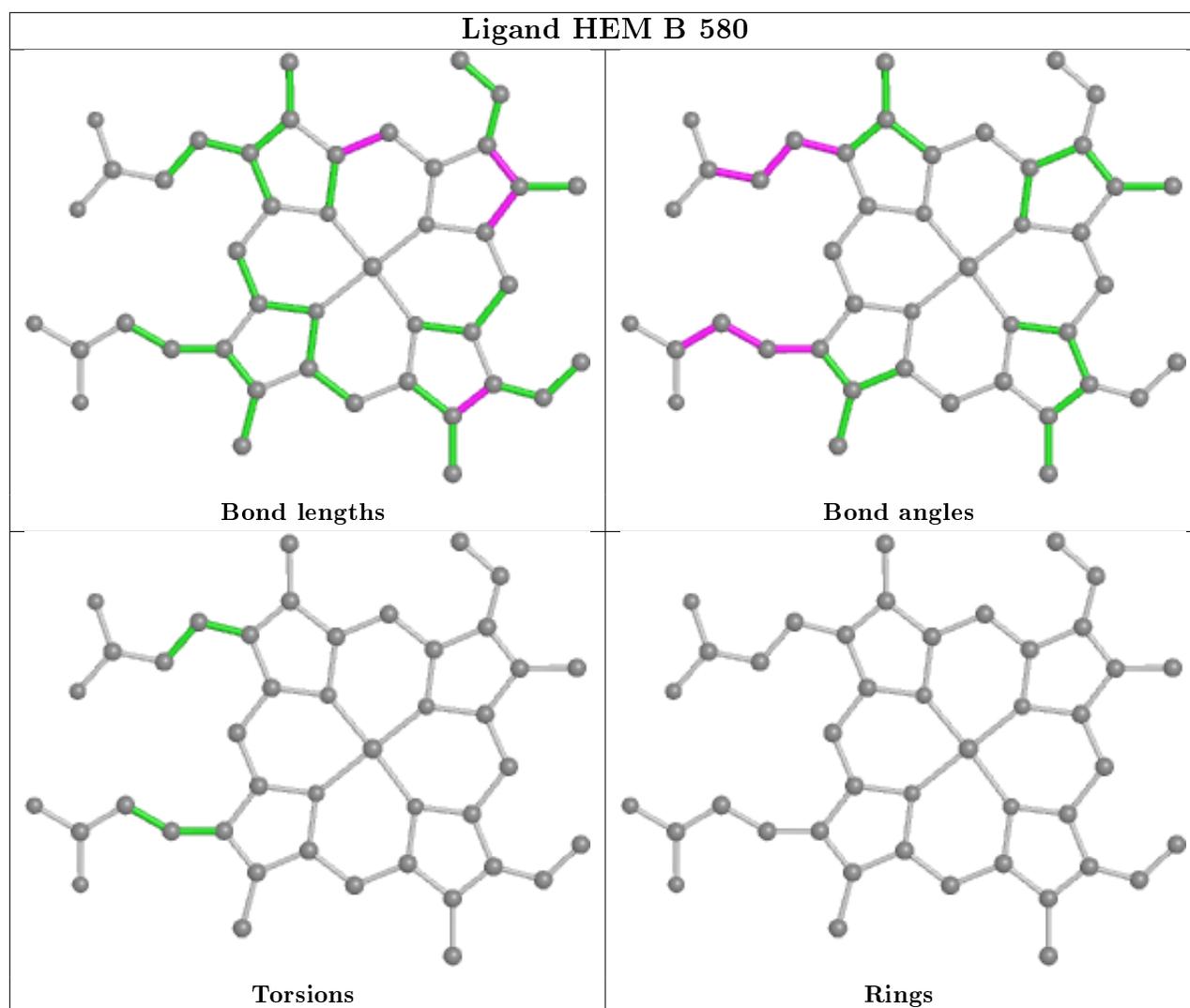
2 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	580	HEM	35	0
5	B	580	HEM	32	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	11
2	C	5
1	B	1

The worst 5 of 17 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3:GLU	C	4:GLN	N	2.32
1	C	560:ASP	C	561:PHE	N	1.95
1	D	179:SER	C	180:GLU	N	1.81
1	D	560:ASP	C	561:PHE	N	1.78
1	D	203:PHE	C	204:GLN	N	1.74

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.