



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 09:40 PM EDT

PDB ID : 1MHL / pdb_00001mhl
Title : CRYSTAL STRUCTURE OF HUMAN MYELOPEROXIDASE ISOFORM C
CRYSTALLIZED IN SPACE GROUP P2(1) AT PH 5.5 AND 20 DEG C
Authors : Fenna, R.E.; Zeng, J.; Davey, C.
Deposited on : 1995-06-09
Resolution : 2.25 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

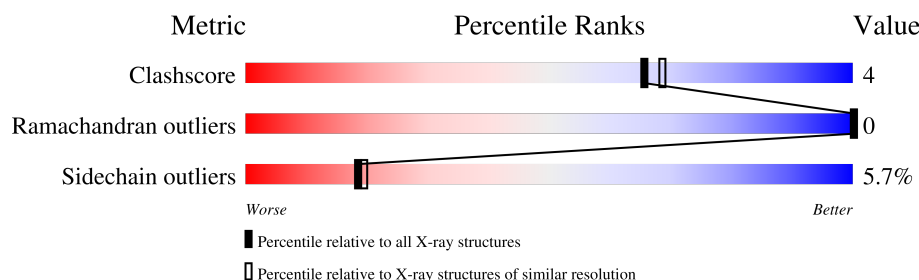
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)

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	108	69% 22% 5% . .
1	B	108	68% 25% . . .
2	C	466	73% 22% . .
2	D	466	75% 22% .
3	E	6	17% 67% 17%
3	F	6	50% 50%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 9847 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.

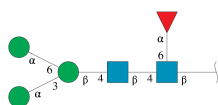
- Molecule 1 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	104	Total	C	N	O	S	12	0	0
			837	529	148	155	5			
1	B	104	Total	C	N	O	S	7	0	0
			837	529	148	155	5			

- Molecule 2 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	466	Total	C	N	O	S	82	0	0
			3732	2351	687	667	27			
2	D	466	Total	C	N	O	S	109	0	0
			3732	2351	687	667	27			

- Molecule 3 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)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	6	Total	C	N	O	0	0	0
			71	40	2	29			
3	F	6	Total	C	N	O	0	0	0
			71	40	2	29			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

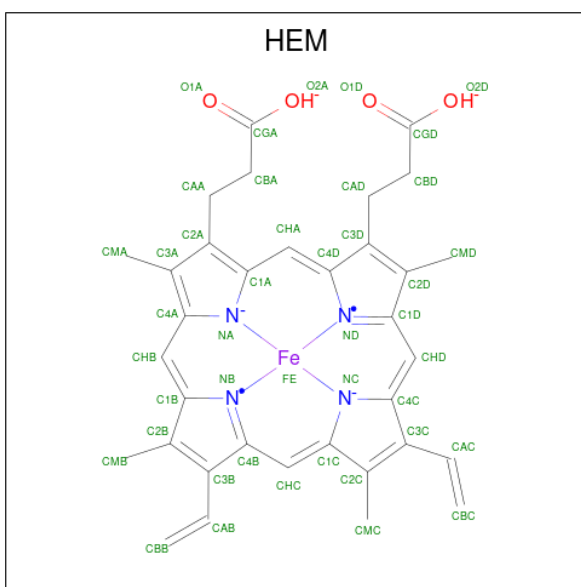
- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		
6	B	1	Total	Cl	0	0
			1	1		

- Molecule 7 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	55	Total O 55 55	0	0
8	C	158	Total O 158 158	0	0
8	B	58	Total O 58 58	0	0
8	D	150	Total O 150 150	0	0

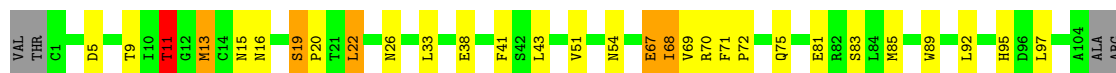
3 Residue-property plots

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. 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

Chain A: 



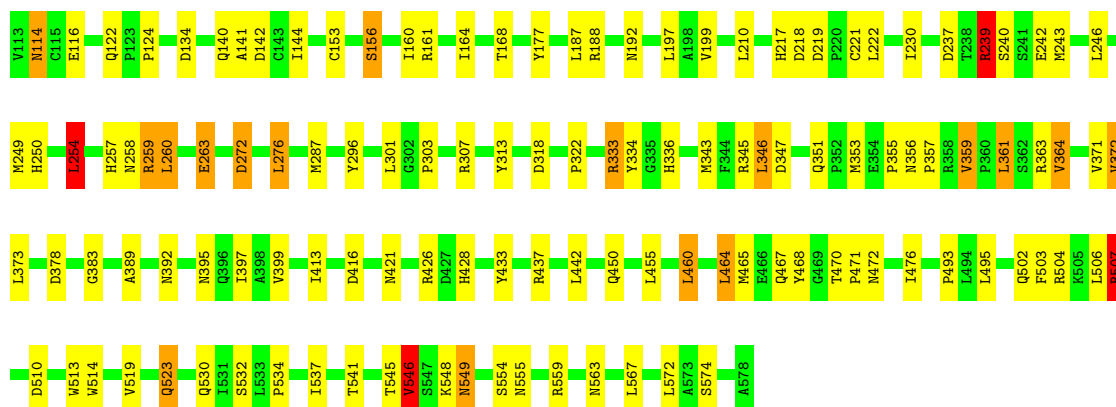
• Molecule 1: MYELOPEROXIDASE

Chain B: 



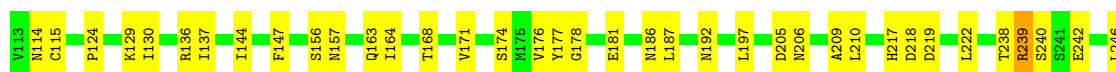
• Molecule 2: MYELOPEROXIDASE

Chain C: 



• Molecule 2: MYELOPEROXIDASE

Chain D: 





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

Chain E: 17% 67% 17%



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

Chain F: 50% 50%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	111.70Å 64.60Å 94.20Å 90.00° 97.90° 90.00°	Depositor
Resolution (Å)	8.00 – 2.25	Depositor
% Data completeness (in resolution range)	92.6 (8.00-2.25)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.0	Depositor
R, R_{free}	0.160 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9847	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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: FUC, BMA, HEM, NAG, CA, CL, 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	0.99	2/862 (0.2%)	1.93	23/1174 (2.0%)
1	B	0.93	1/862 (0.1%)	1.88	25/1174 (2.1%)
2	C	0.98	5/3818 (0.1%)	1.78	85/5180 (1.6%)
2	D	0.94	7/3818 (0.2%)	1.79	79/5180 (1.5%)
All	All	0.96	15/9360 (0.2%)	1.81	212/12708 (1.7%)

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
2	C	0	1
2	D	0	1
All	All	0	2

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	HIS	CD2-NE2	-7.50	1.29	1.37
1	B	95	HIS	CD2-NE2	-7.12	1.30	1.37
2	C	476	ILE	CA-CB	6.80	1.62	1.54
2	D	217	HIS	CD2-NE2	-6.42	1.30	1.37
2	D	359	VAL	CA-CB	6.42	1.62	1.54

The worst 5 of 212 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	546	VAL	N-CA-CB	-11.45	96.49	112.52
1	A	11	THR	N-CA-CB	-10.31	93.28	110.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	15	ASN	N-CA-C	-9.91	100.56	111.36
2	D	356	ASN	CA-CB-CG	9.71	122.31	112.60
2	D	177	TYR	N-CA-C	9.20	124.64	113.23

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	334	TYR	Sidechain
2	D	334	TYR	Sidechain

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	837	0	798	12	0
1	B	837	0	798	7	0
2	C	3732	0	3725	32	0
2	D	3732	0	3725	26	0
3	E	71	0	61	1	0
3	F	71	0	61	0	0
4	A	28	0	26	0	0
4	B	28	0	26	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	43	0	30	2	0
7	B	43	0	30	1	0
8	A	55	0	0	0	0
8	B	58	0	0	0	0
8	C	158	0	0	0	0
8	D	150	0	0	0	0
All	All	9847	0	9280	70	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 4.

The worst 5 of 70 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:19:SER:HB3	1:A:22:LEU:HD22	1.67	0.76
2:C:333:ARG:HH11	2:C:421:ASN:HD22	1.34	0.74
2:C:460:LEU:HD22	2:C:464:LEU:HD22	1.74	0.68
1:A:67:GLU:HG3	2:C:467:GLN:NE2	2.10	0.67
1:B:68:ILE:HD13	2:D:464:LEU:HD13	1.78	0.63

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%)	99 (97%)	3 (3%)	0	100	100
1	B	102/108 (94%)	98 (96%)	4 (4%)	0	100	100
2	C	464/466 (100%)	450 (97%)	14 (3%)	0	100	100
2	D	464/466 (100%)	455 (98%)	9 (2%)	0	100	100
All	All	1132/1148 (99%)	1102 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	90/93 (97%)	87 (97%)	3 (3%)	33	42
1	B	90/93 (97%)	86 (96%)	4 (4%)	25	29
2	C	411/411 (100%)	385 (94%)	26 (6%)	16	16
2	D	411/411 (100%)	387 (94%)	24 (6%)	18	19
All	All	1002/1008 (99%)	945 (94%)	57 (6%)	18	19

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	574	SER
2	D	567	LEU
2	D	210	LEU
2	D	547	SER
2	D	485	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	549	ASN
2	D	540	ASN
2	C	549	ASN
2	D	421	ASN
2	C	540	ASN

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
3	NAG	E	1	2,3	14,14,15	0.56	0	17,19,21	1.16	1 (5%)
3	NAG	E	2	3	14,14,15	0.91	0	17,19,21	1.04	2 (11%)
3	BMA	E	3	3	11,11,12	0.71	0	15,15,17	0.77	0
3	MAN	E	4	3	11,11,12	0.54	0	15,15,17	1.05	1 (6%)
3	MAN	E	5	3	11,11,12	0.61	0	15,15,17	0.99	1 (6%)
3	FUC	E	6	3	10,10,11	0.66	0	14,14,16	1.23	2 (14%)
3	NAG	F	1	2,3	14,14,15	0.70	0	17,19,21	1.54	2 (11%)
3	NAG	F	2	3	14,14,15	0.41	0	17,19,21	0.74	0
3	BMA	F	3	3	11,11,12	0.37	0	15,15,17	0.87	0
3	MAN	F	4	3	11,11,12	0.94	0	15,15,17	1.39	4 (26%)
3	MAN	F	5	3	11,11,12	0.75	0	15,15,17	1.50	2 (13%)
3	FUC	F	6	3	10,10,11	0.51	0	14,14,16	1.06	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
3	NAG	E	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	2/2/19/22	0/1/1/1
3	MAN	E	5	3	-	2/2/19/22	0/1/1/1
3	FUC	E	6	3	-	-	0/1/1/1
3	NAG	F	1	2,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	BMA	F	3	3	-	0/2/19/22	0/1/1/1
3	MAN	F	4	3	-	0/2/19/22	0/1/1/1
3	MAN	F	5	3	-	0/2/19/22	0/1/1/1
3	FUC	F	6	3	-	-	0/1/1/1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	F	5	MAN	C1-O5-C5	4.54	118.27	112.19
3	F	1	NAG	C1-C2-N2	4.43	117.41	110.43
3	F	4	MAN	O2-C2-C1	3.08	116.28	109.22
3	E	5	MAN	C1-O5-C5	2.84	115.99	112.19
3	E	4	MAN	O2-C2-C1	2.64	115.27	109.22

There are no chirality outliers.

All (4) torsion outliers are listed below:

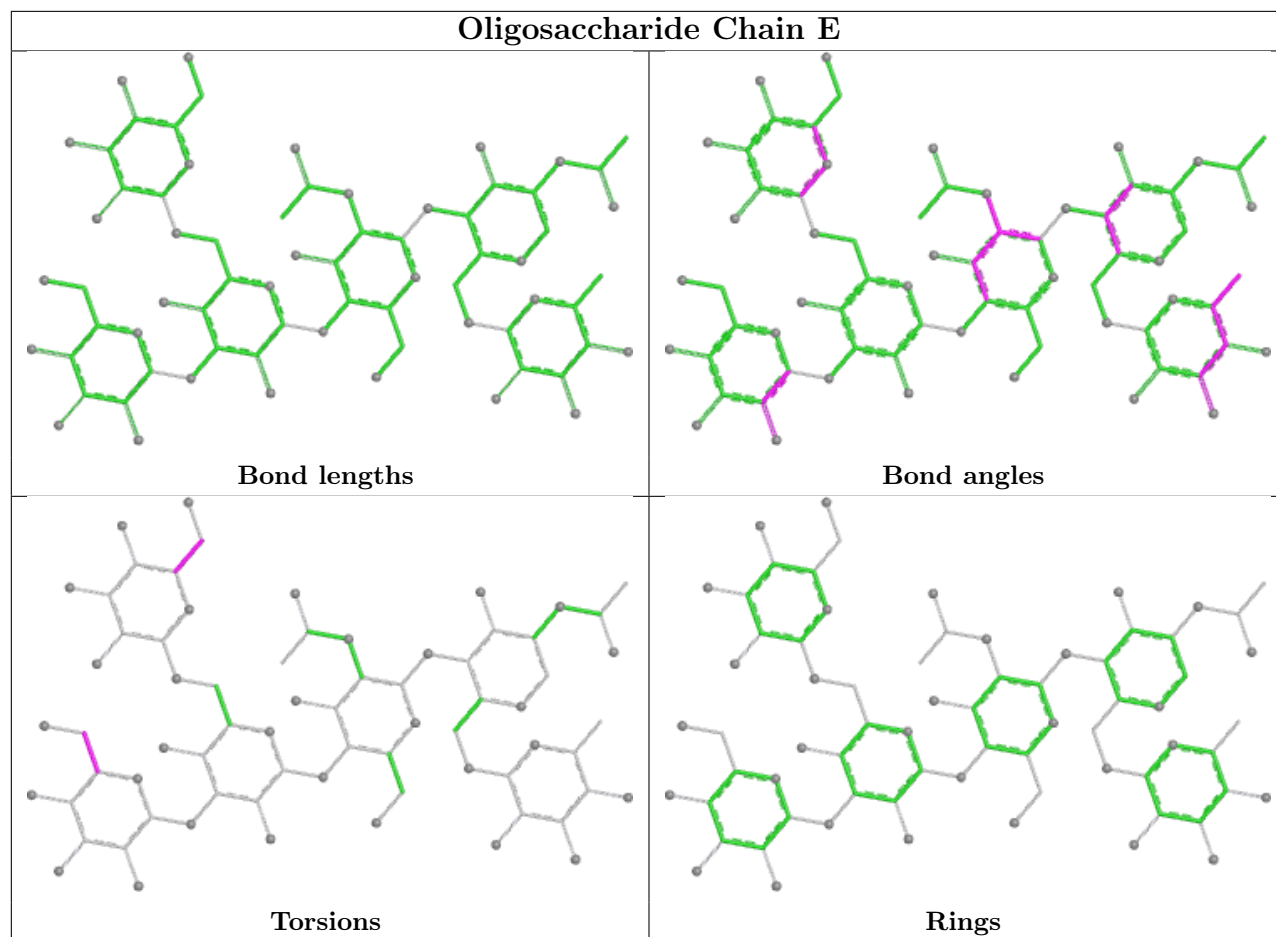
Mol	Chain	Res	Type	Atoms
3	E	4	MAN	O5-C5-C6-O6
3	E	5	MAN	O5-C5-C6-O6
3	E	5	MAN	C4-C5-C6-O6
3	E	4	MAN	C4-C5-C6-O6

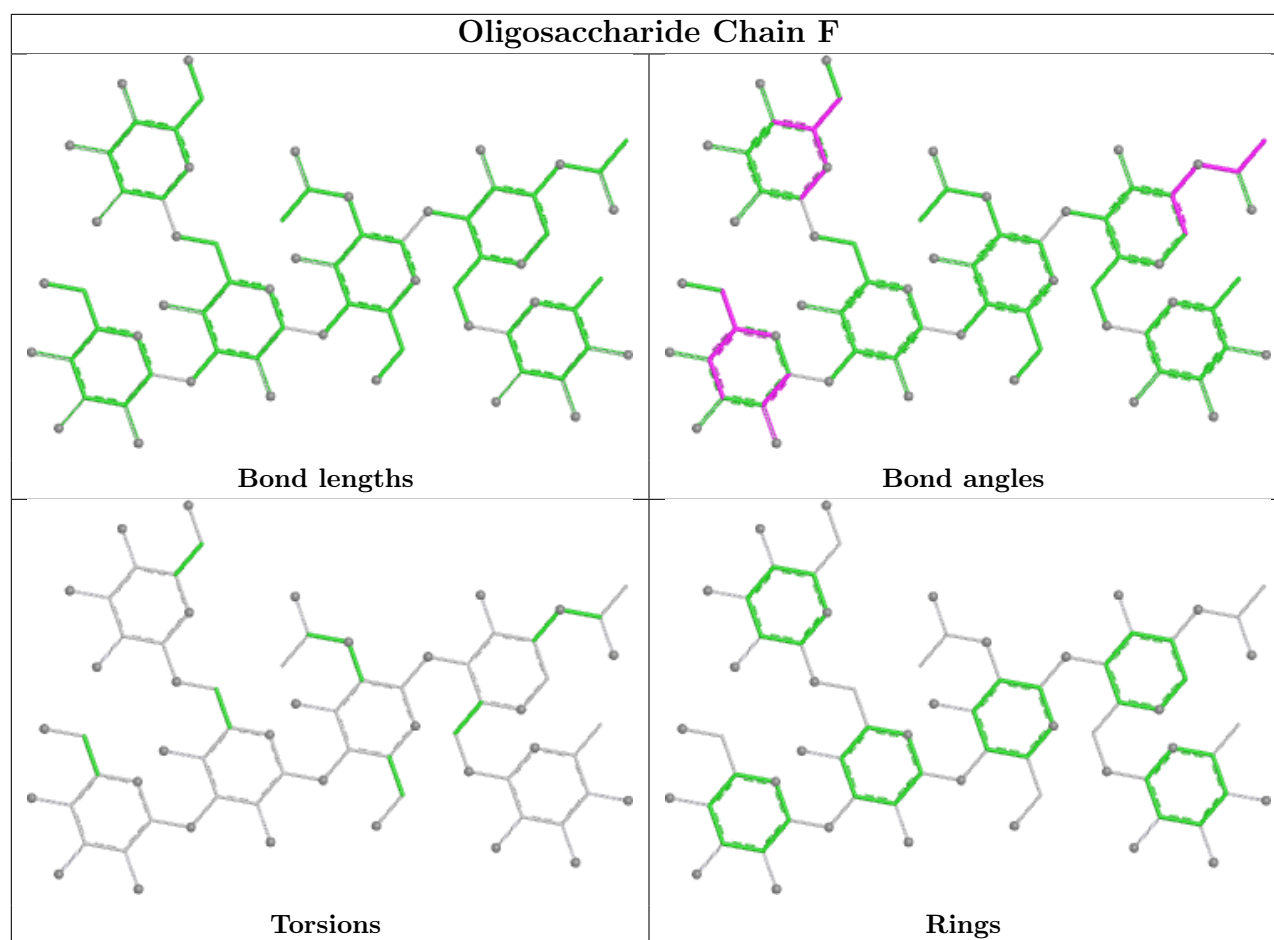
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	4	MAN	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 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	HEM	A	605	2	50,50,50	1.27	6 (12%)	67,82,82	0.95	1 (1%)
4	NAG	B	630	2	14,14,15	1.10	1 (7%)	17,19,21	1.41	3 (17%)
4	NAG	A	630	2	14,14,15	1.23	2 (14%)	17,19,21	2.01	5 (29%)
7	HEM	B	605	1,2	50,50,50	1.39	9 (18%)	67,82,82	0.97	1 (1%)
4	NAG	B	620	2	14,14,15	0.98	1 (7%)	17,19,21	1.45	2 (11%)
4	NAG	A	620	2	14,14,15	0.83	1 (7%)	17,19,21	0.86	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
7	HEM	A	605	2	-	6/14/54/54	-
4	NAG	B	630	2	-	0/6/23/26	0/1/1/1
4	NAG	A	630	2	-	0/6/23/26	0/1/1/1
7	HEM	B	605	1,2	-	5/14/54/54	-
4	NAG	B	620	2	-	1/6/23/26	0/1/1/1
4	NAG	A	620	2	-	2/6/23/26	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	605	HEM	FE-NB	3.72	2.06	1.94
4	A	630	NAG	C1-C2	-3.64	1.47	1.52
7	A	605	HEM	CBC-CAC	3.40	1.46	1.30
7	B	605	HEM	CBC-CAC	3.19	1.45	1.30
7	B	605	HEM	CBB-CAB	3.15	1.45	1.30

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	620	NAG	C1-O5-C5	4.49	118.20	112.19
4	A	630	NAG	C1-C2-N2	-3.73	104.55	110.43
4	A	630	NAG	C6-C5-C4	3.50	121.60	113.02
4	A	630	NAG	C3-C4-C5	-3.45	103.98	110.23
7	B	605	HEM	C3B-C4B-NB	3.34	111.87	109.47

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

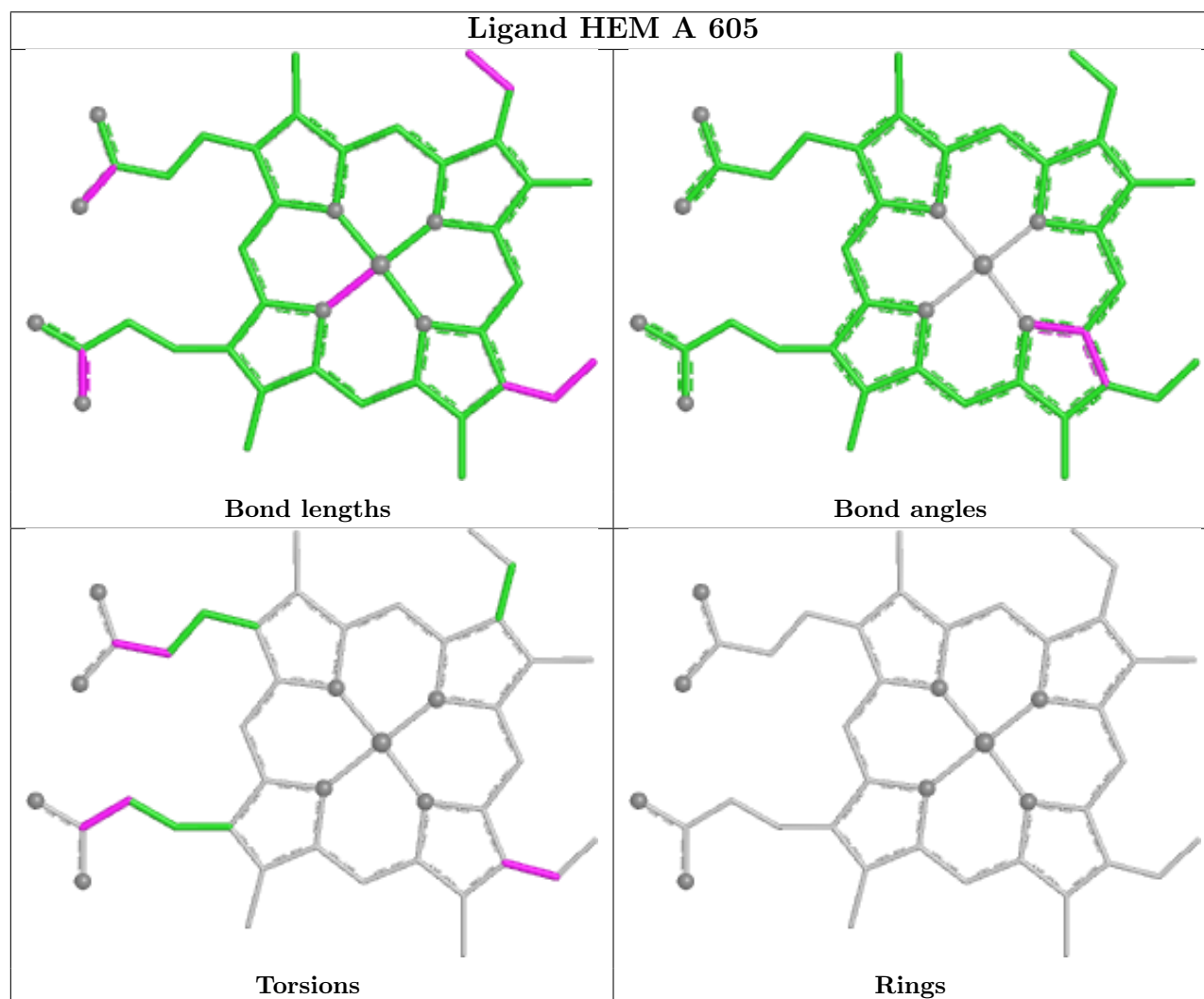
Mol	Chain	Res	Type	Atoms
7	A	605	HEM	C2B-C3B-CAB-CBB
4	A	620	NAG	C4-C5-C6-O6
4	A	620	NAG	O5-C5-C6-O6
4	B	620	NAG	O5-C5-C6-O6
7	B	605	HEM	CAD-CBD-CGD-O2D

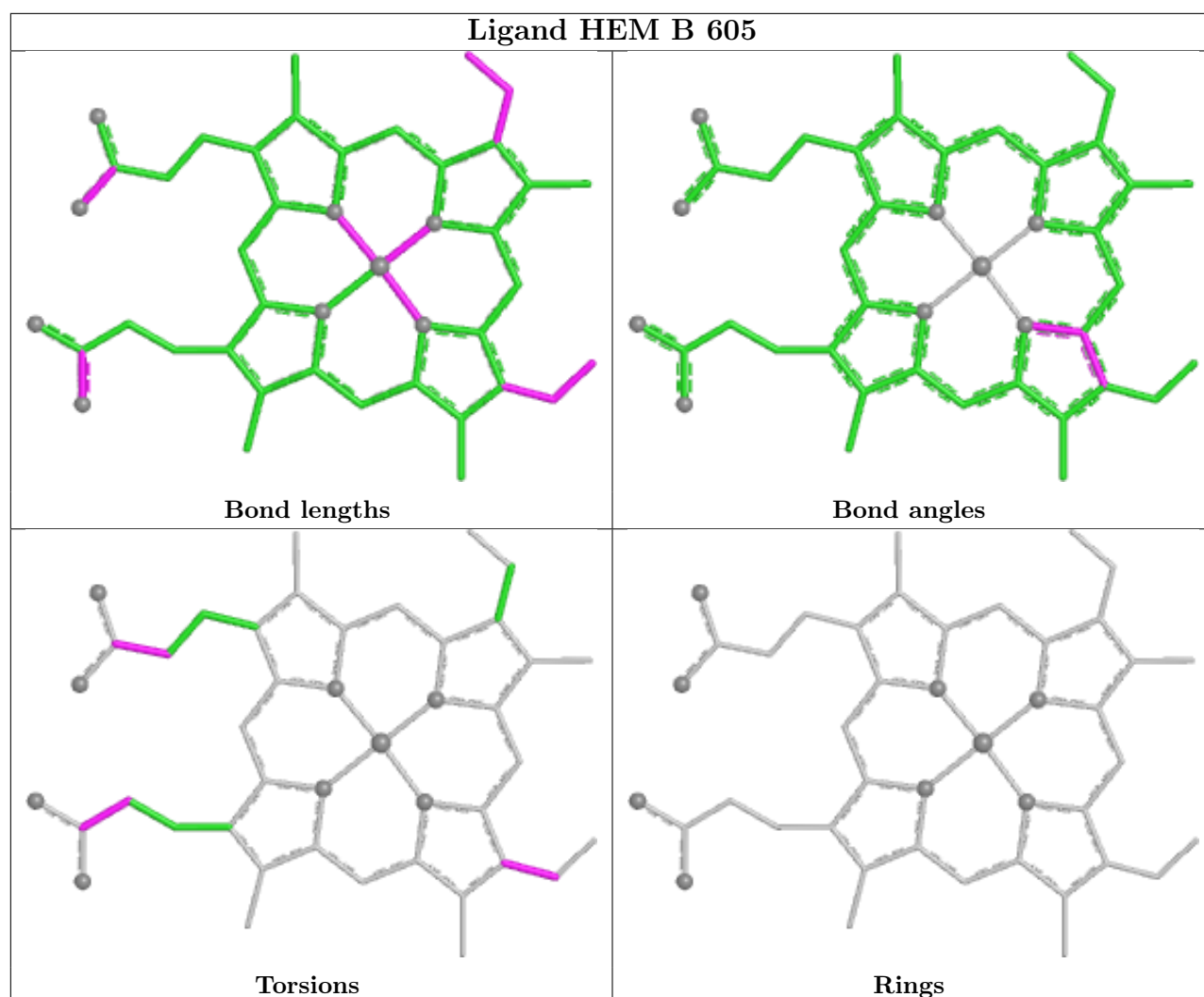
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	605	HEM	2	0
7	B	605	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.





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.