



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 03:37 AM UTC

PDB ID : 1DNU / pdb_00001dnu
Title : STRUCTURAL ANALYSES OF HUMAN MYELOPEROXIDASE-THIOCYANATE COMPLEX
Authors : Blair-Johnson, M.; Fiedler, T.J.; Fenna, R.E.
Deposited on : 1999-12-16
Resolution : 1.85 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)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

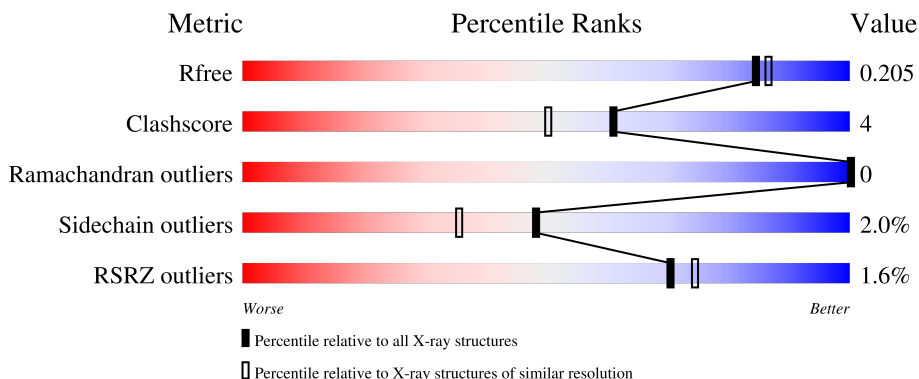
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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}	180053	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	104	 3% 92% 8%
1	B	104	 93% 7%
2	C	466	 2% 88% 12%
2	D	466	 2% 88% 12%
3	E	6	 83% 17%

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Mol	Chain	Length	Quality of chain
3	F	6	

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
9	ACY	C	606	-	-	X	-
9	ACY	D	607	-	-	X	-

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 10318 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 838	C 529	N 148	O 156	S 5	0	0	0
1	B	104	Total 838	C 529	N 148	O 156	S 5	0	0	0

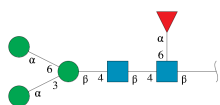
- Molecule 2 is a protein called MYELOPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	466	Total 3733	C 2351	N 687	O 668	S 27	0	0	0
2	D	466	Total 3733	C 2351	N 687	O 668	S 27	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

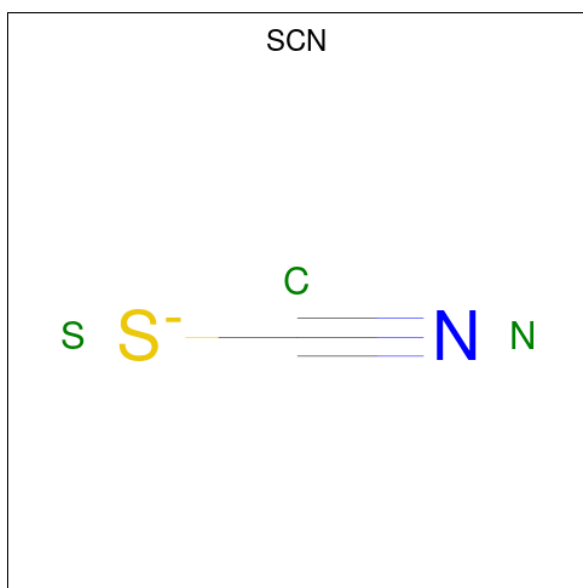
Chain	Residue	Modelled	Actual	Comment	Reference
C	150	CSO	CYS	modified residue	UNP P05164
D	150	CSO	CYS	modified residue	UNP P05164

- 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.



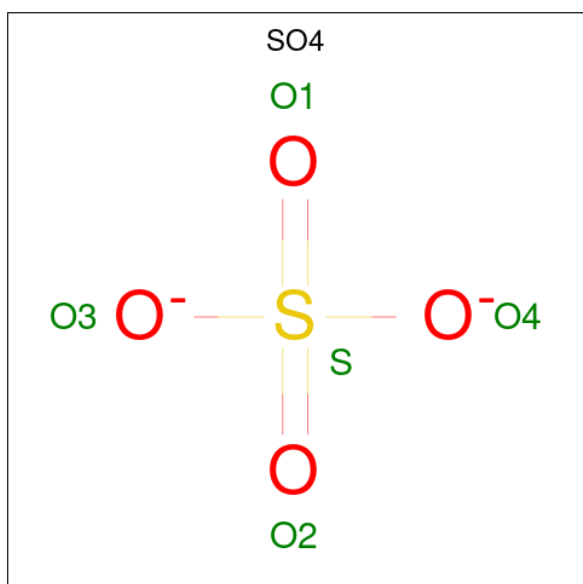
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	E	6	Total 71	C 40	N 2	O 29	0	0	0
3	F	6	Total 71	C 40	N 2	O 29	0	0	0

- Molecule 4 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



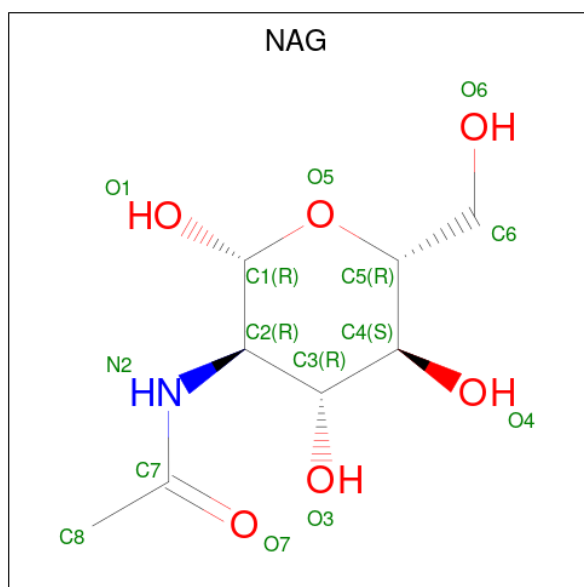
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	S		
4	A	1	Total 3	C 1	N 1	S 1	0	0
4	A	1	Total 3	C 1	N 1	S 1	0	0
4	B	1	Total 3	C 1	N 1	S 1	0	0
4	B	1	Total 3	C 1	N 1	S 1	0	0

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

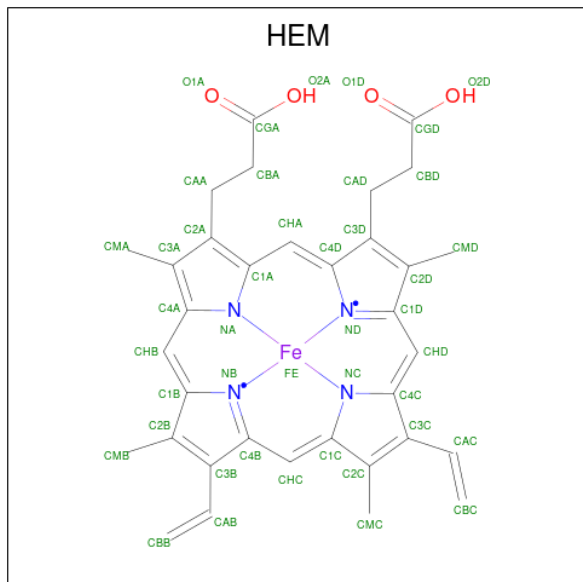


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	C	1	Total C N O 14 8 1 5	0	0
6	C	1	Total C N O 14 8 1 5	0	0
6	D	1	Total C N O 14 8 1 5	0	0
6	D	1	Total C N O 14 8 1 5	0	0

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

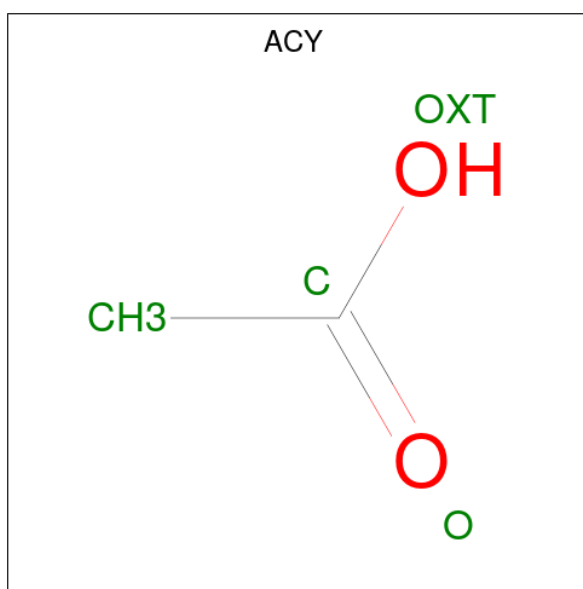
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total Ca 1 1	0	0
7	D	1	Total Ca 1 1	0	0

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



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


- Molecule 9 is ACETIC ACID (CCD ID: ACY) (formula: $C_2H_4O_2$).

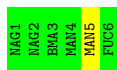


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	C	1	Total C O 4 2 2	0	0
9	C	1	Total C O 4 2 2	0	0
9	C	1	Total C O 4 2 2	0	0
9	D	1	Total C O 4 2 2	0	0
9	D	1	Total C O 4 2 2	0	0
9	D	1	Total C O 4 2 2	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	96	Total O 96 96	0	0
10	C	329	Total O 329 329	0	0
10	B	104	Total O 104 104	0	0
10	D	310	Total O 310 310	0	0

Chain E:  83% 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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	111.24Å 63.87Å 92.62Å 90.00° 97.54° 90.00°	Depositor
Resolution (Å)	10.00 – 1.85 10.00 – 1.86	Depositor EDS
% Data completeness (in resolution range)	98.7 (10.00-1.85) 97.5 (10.00-1.86)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.51 (at 1.86Å)	Xtrriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.178 , 0.210 0.172 , 0.205	Depositor DCC
R_{free} test set	5388 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	13.5	Xtrriage
Anisotropy	0.402	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 54.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10318	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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: SCN, SO4, MAN, CA, BMA, ACY, FUC, HEM, CSO, 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	0.85	0/863	0.99	1/1174 (0.1%)
1	B	0.79	0/863	0.97	1/1174 (0.1%)
2	C	0.83	0/3811	0.91	3/5168 (0.1%)
2	D	0.80	0/3811	0.91	5/5168 (0.1%)
All	All	0.82	0/9348	0.92	10/12684 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	336	HIS	ND1-CG-CD2	6.95	113.05	106.10
2	D	336	HIS	ND1-CG-CD2	6.34	112.44	106.10
2	D	336	HIS	CG-CD2-NE2	-6.07	101.13	107.20
2	D	397	ILE	N-CA-C	5.73	115.81	110.42
2	C	336	HIS	CG-CD2-NE2	-5.69	101.51	107.20

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	838	0	798	5	0
1	B	838	0	798	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	3733	0	3725	39	0
2	D	3733	0	3725	34	0
3	E	71	0	61	0	0
3	F	71	0	61	0	0
4	A	6	0	0	0	0
4	B	6	0	0	0	0
5	A	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
6	C	28	0	26	0	0
6	D	28	0	26	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	C	43	0	30	2	0
8	D	43	0	30	2	0
9	C	12	0	9	2	0
9	D	12	0	9	2	0
10	A	96	0	0	1	0
10	B	104	0	0	0	0
10	C	329	0	0	2	0
10	D	310	0	0	0	0
All	All	10318	0	9298	78	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 78 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:C:135:PRO:HG2	10:C:711:HOH:O	1.84	0.77
2:D:525:ARG:HH11	9:D:607:ACY:H2	1.48	0.75
2:C:348:ASN:H	2:C:348:ASN:HD22	1.37	0.71
2:C:465:MET:HE1	2:C:471:PRO:HD3	1.73	0.69
2:D:349:ARG:HG3	2:D:351:GLN:HG2	1.77	0.66

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	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
1	B	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
2	C	463/466 (99%)	450 (97%)	13 (3%)	0	100	100
2	D	463/466 (99%)	453 (98%)	10 (2%)	0	100	100
All	All	1130/1140 (99%)	1101 (97%)	29 (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	90/90 (100%)	88 (98%)	2 (2%)	45	32
1	B	90/90 (100%)	90 (100%)	0	100	100
2	C	410/410 (100%)	400 (98%)	10 (2%)	43	28
2	D	410/410 (100%)	402 (98%)	8 (2%)	48	36
All	All	1000/1000 (100%)	980 (98%)	20 (2%)	48	36

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	138	LYS
2	D	322	PRO
2	D	547	SER

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Mol	Chain	Res	Type
2	D	523	GLN
2	C	348	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	540	ASN
2	D	206	ASN
2	D	523	GLN
2	D	348	ASN
2	C	206	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](#)

2 non-standard protein/DNA/RNA residues 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	CSO	C	150	2	3,6,7	0.76	0	1,6,8	1.12	0
2	CSO	D	150	2	3,6,7	0.72	0	1,6,8	1.26	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	CSO	C	150	2	-	0/1/5/7	-
2	CSO	D	150	2	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	0.76	0	17,19,21	0.85	0
3	NAG	E	2	3	14,14,15	0.59	0	17,19,21	0.83	0
3	BMA	E	3	3	11,11,12	0.70	0	15,15,17	0.53	0
3	MAN	E	4	3	11,11,12	1.02	0	15,15,17	0.53	0
3	MAN	E	5	3	11,11,12	0.61	0	15,15,17	0.67	1 (6%)
3	FUC	E	6	3	10,10,11	0.62	0	14,14,16	0.48	0
3	NAG	F	1	3,2	14,14,15	0.60	0	17,19,21	0.86	0
3	NAG	F	2	3	14,14,15	0.55	0	17,19,21	0.81	1 (5%)
3	BMA	F	3	3	11,11,12	0.57	0	15,15,17	0.58	0
3	MAN	F	4	3	11,11,12	0.88	0	15,15,17	0.66	1 (6%)
3	MAN	F	5	3	11,11,12	0.60	0	15,15,17	0.58	1 (6%)
3	FUC	F	6	3	10,10,11	0.55	0	14,14,16	0.38	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	3,2	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	-	0/2/19/22	0/1/1/1
3	MAN	E	5	3	-	0/2/19/22	0/1/1/1
3	FUC	E	6	3	-	-	0/1/1/1
3	NAG	F	1	3,2	-	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.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2	NAG	C4-C3-C2	-2.21	107.78	111.02
3	F	4	MAN	C1-O5-C5	2.11	115.01	112.19
3	F	5	MAN	C1-O5-C5	2.09	114.98	112.19
3	E	5	MAN	C1-O5-C5	2.02	114.89	112.19

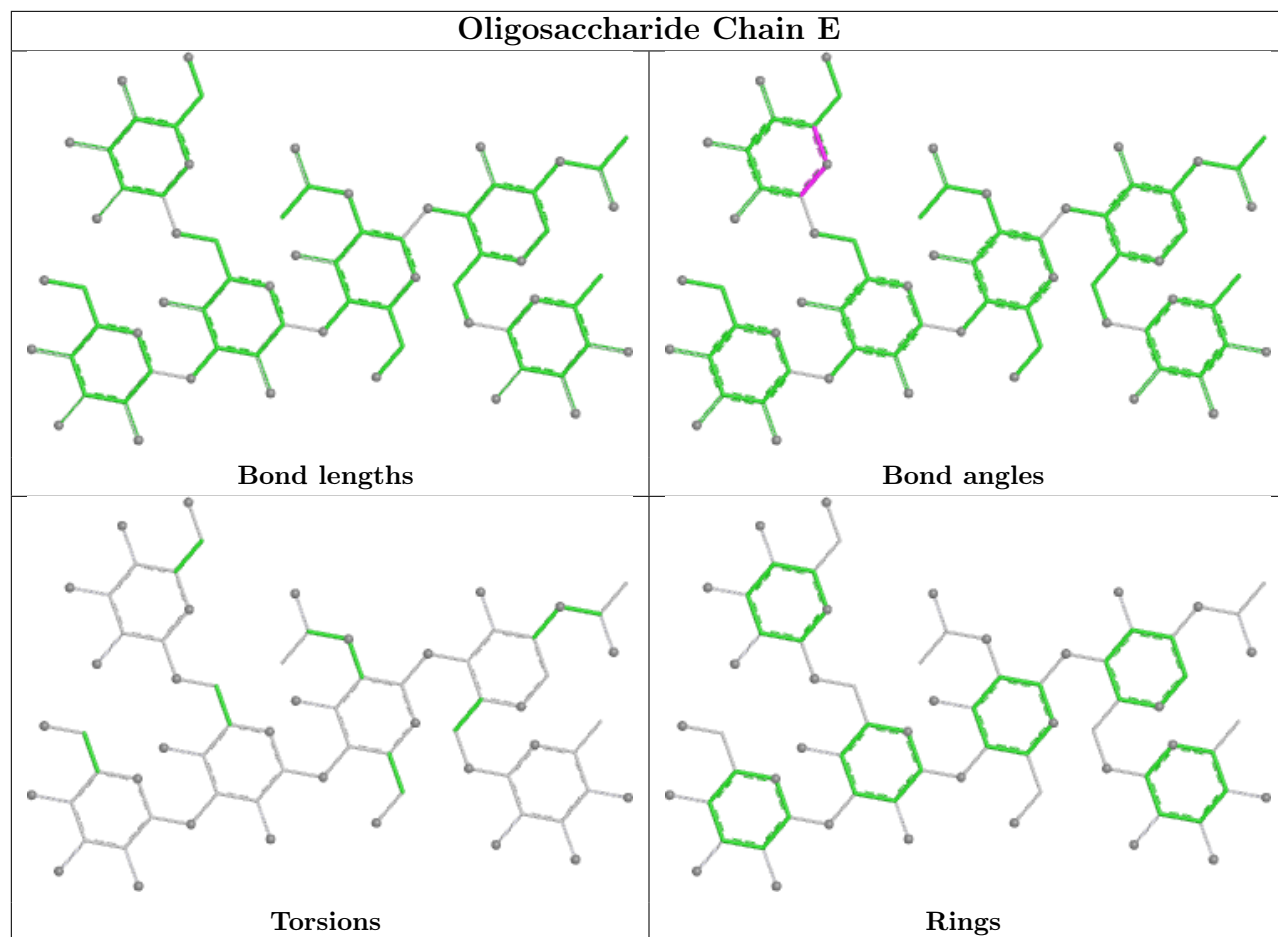
There are no chirality outliers.

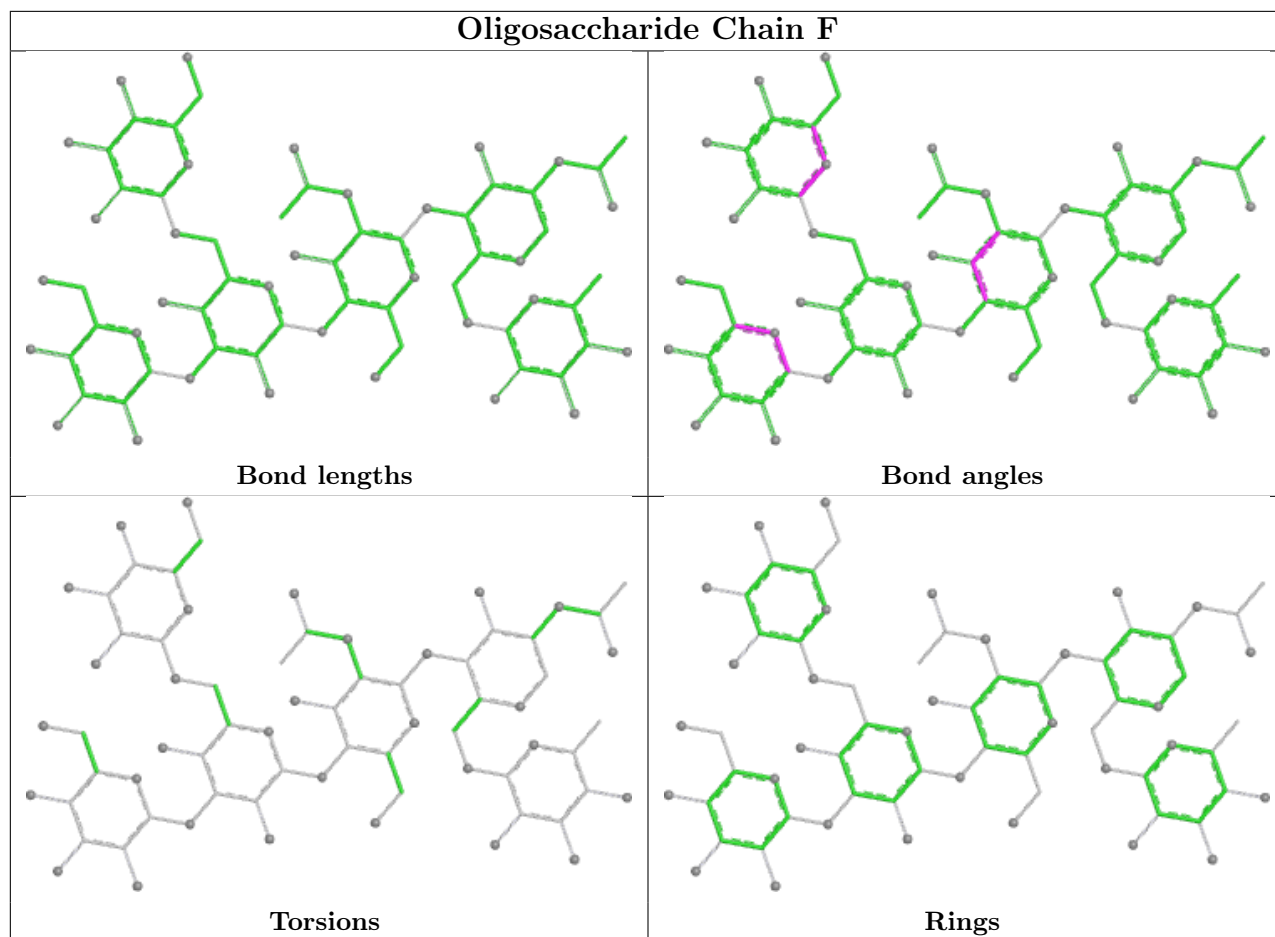
There are no torsion outliers.

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 21 ligands modelled in this entry, 2 are monoatomic - leaving 19 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
9	ACY	C	607	-	3,3,3	1.10	0	3,3,3	1.68	1 (33%)
9	ACY	D	606	-	3,3,3	1.31	0	3,3,3	1.62	1 (33%)
6	NAG	C	602	2	14,14,15	0.80	0	17,19,21	0.80	0
4	SCN	A	203	-	1,2,2	1.90	0	0,1,1	-	-
9	ACY	D	607	-	3,3,3	1.40	1 (33%)	3,3,3	1.69	1 (33%)
4	SCN	B	202	-	1,2,2	1.97	0	0,1,1	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	ACY	C	608	-	3,3,3	1.41	1 (33%)	3,3,3	1.61	1 (33%)
5	SO4	A	202	-	4,4,4	0.27	0	6,6,6	0.08	0
9	ACY	D	608	-	3,3,3	1.29	0	3,3,3	1.66	1 (33%)
4	SCN	A	201	-	1,2,2	1.55	0	0,1,1	-	-
8	HEM	D	601	10,2	50,50,50	1.12	6 (12%)	67,82,82	1.06	1 (1%)
8	HEM	C	605	2	50,50,50	1.15	3 (6%)	67,82,82	1.04	2 (2%)
5	SO4	D	605	-	4,4,4	0.45	0	6,6,6	0.12	0
6	NAG	C	601	2	14,14,15	0.82	1 (7%)	17,19,21	0.99	1 (5%)
5	SO4	C	604	-	4,4,4	0.46	0	6,6,6	0.17	0
6	NAG	D	602	2	14,14,15	0.68	0	17,19,21	0.68	0
4	SCN	B	201	-	1,2,2	1.69	0	0,1,1	-	-
9	ACY	C	606	-	3,3,3	1.16	0	3,3,3	1.59	1 (33%)
6	NAG	D	603	2	14,14,15	0.61	0	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
8	HEM	C	605	2	-	5/14/54/54	-
6	NAG	C	602	2	-	0/6/23/26	0/1/1/1
6	NAG	D	603	2	-	0/6/23/26	0/1/1/1
8	HEM	D	601	10,2	-	4/14/54/54	-
6	NAG	C	601	2	-	0/6/23/26	0/1/1/1
6	NAG	D	602	2	-	0/6/23/26	0/1/1/1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	D	601	HEM	CBB-CAB	3.32	1.46	1.30
8	C	605	HEM	CBB-CAB	3.25	1.46	1.30
8	C	605	HEM	CBC-CAC	2.98	1.44	1.30
8	D	601	HEM	CBC-CAC	2.81	1.43	1.30
8	C	605	HEM	CAC-C3C	-2.44	1.40	1.47

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	D	601	HEM	C3B-C4B-NB	4.14	112.44	109.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	605	HEM	C3B-C4B-NB	3.48	111.97	109.47
6	C	601	NAG	C1-O5-C5	2.86	116.02	112.19
6	D	603	NAG	C1-C2-N2	-2.37	106.69	110.43
9	D	607	ACY	O-C-CH3	-2.30	113.11	122.53

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

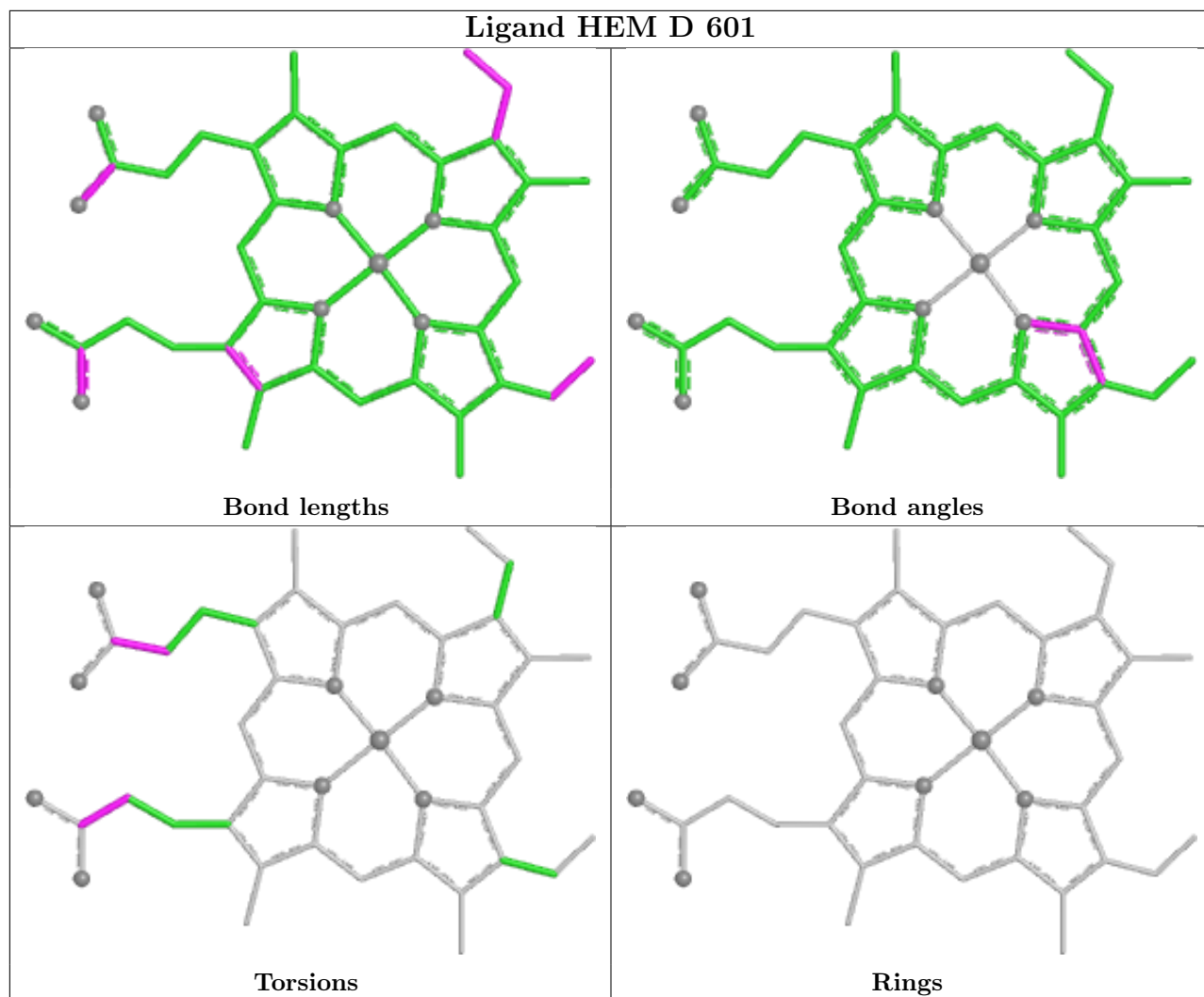
Mol	Chain	Res	Type	Atoms
8	C	605	HEM	CAD-CBD-CGD-O2D
8	C	605	HEM	CAA-CBA-CGA-O2A
8	D	601	HEM	CAD-CBD-CGD-O2D
8	C	605	HEM	CAD-CBD-CGD-O1D
8	D	601	HEM	CAD-CBD-CGD-O1D

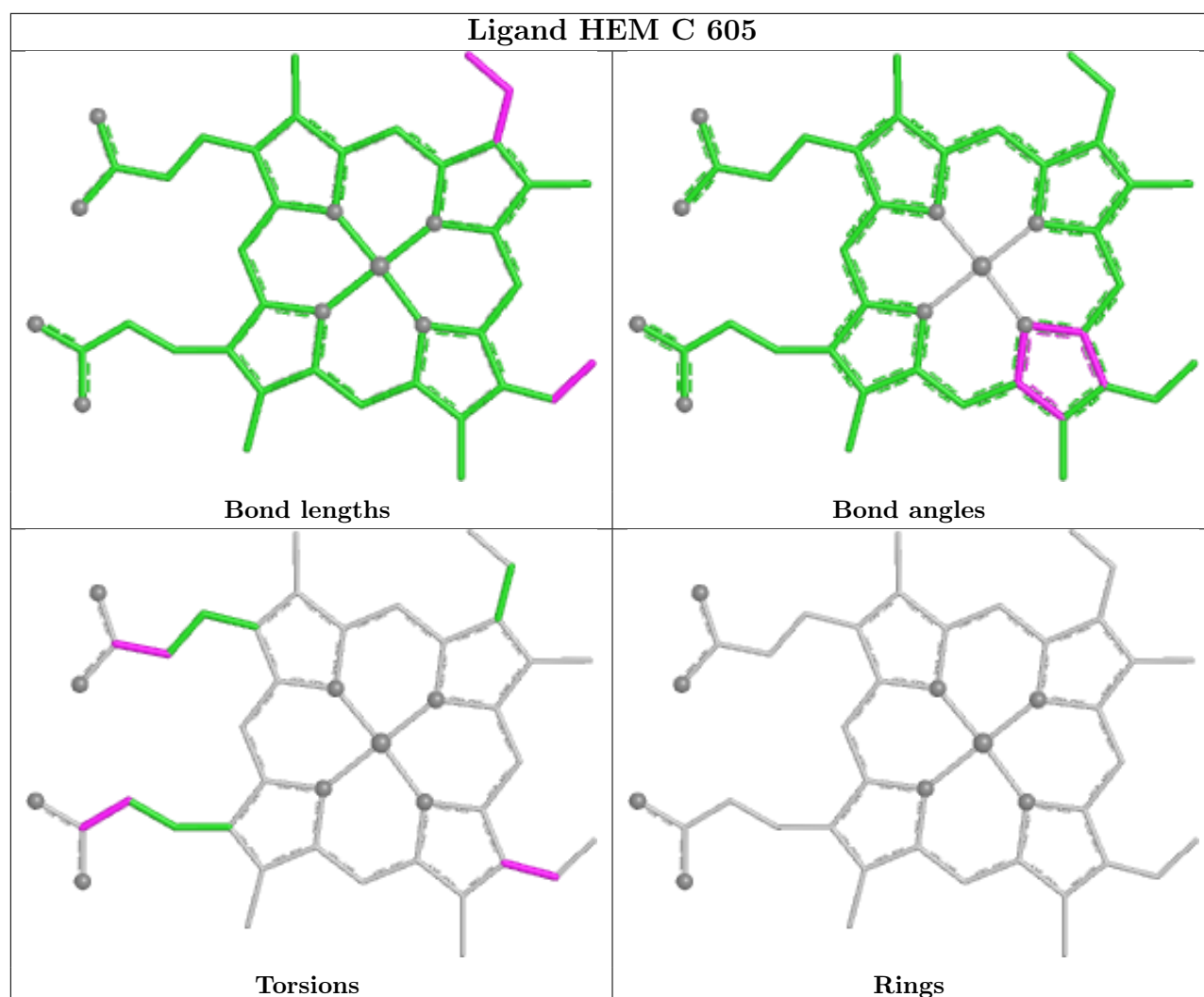
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	D	607	ACY	2	0
8	D	601	HEM	2	0
8	C	605	HEM	2	0
9	C	606	ACY	2	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](#)

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	104/104 (100%)	-0.60	3 (2%) 53 57	6, 9, 23, 46	0
1	B	104/104 (100%)	-0.70	0 100 100	6, 10, 19, 24	0
2	C	465/466 (99%)	-0.56	8 (1%) 69 73	5, 10, 24, 39	0
2	D	465/466 (99%)	-0.45	7 (1%) 72 76	6, 12, 27, 43	0
All	All	1138/1140 (99%)	-0.53	18 (1%) 70 74	5, 11, 25, 46	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	113	VAL	10.0
2	D	217	HIS	5.2
2	C	355	PRO	5.1
2	C	217	HIS	3.9
2	D	355	PRO	3.8

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	CSO	C	150	7/8	0.93	0.06	8,10,11,15	0
2	CSO	D	150	7/8	0.95	0.05	6,8,10,14	0

6.3 Carbohydrates [i](#)

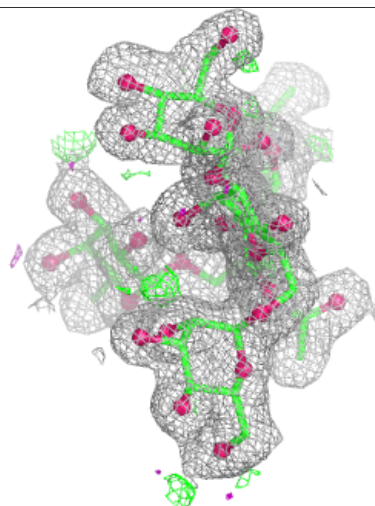
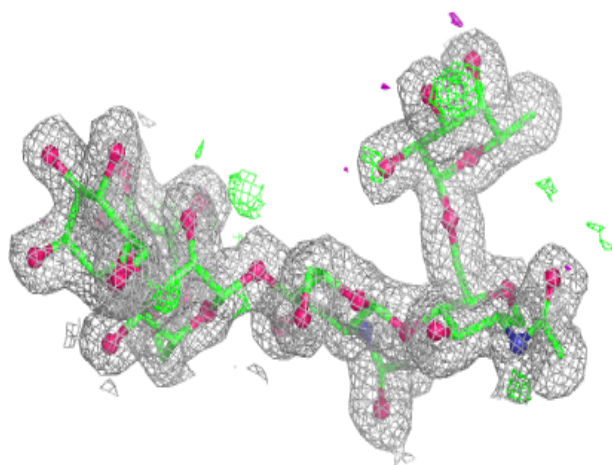
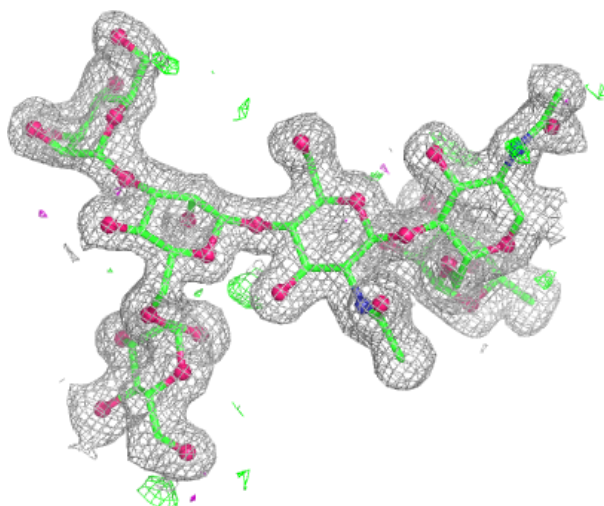
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

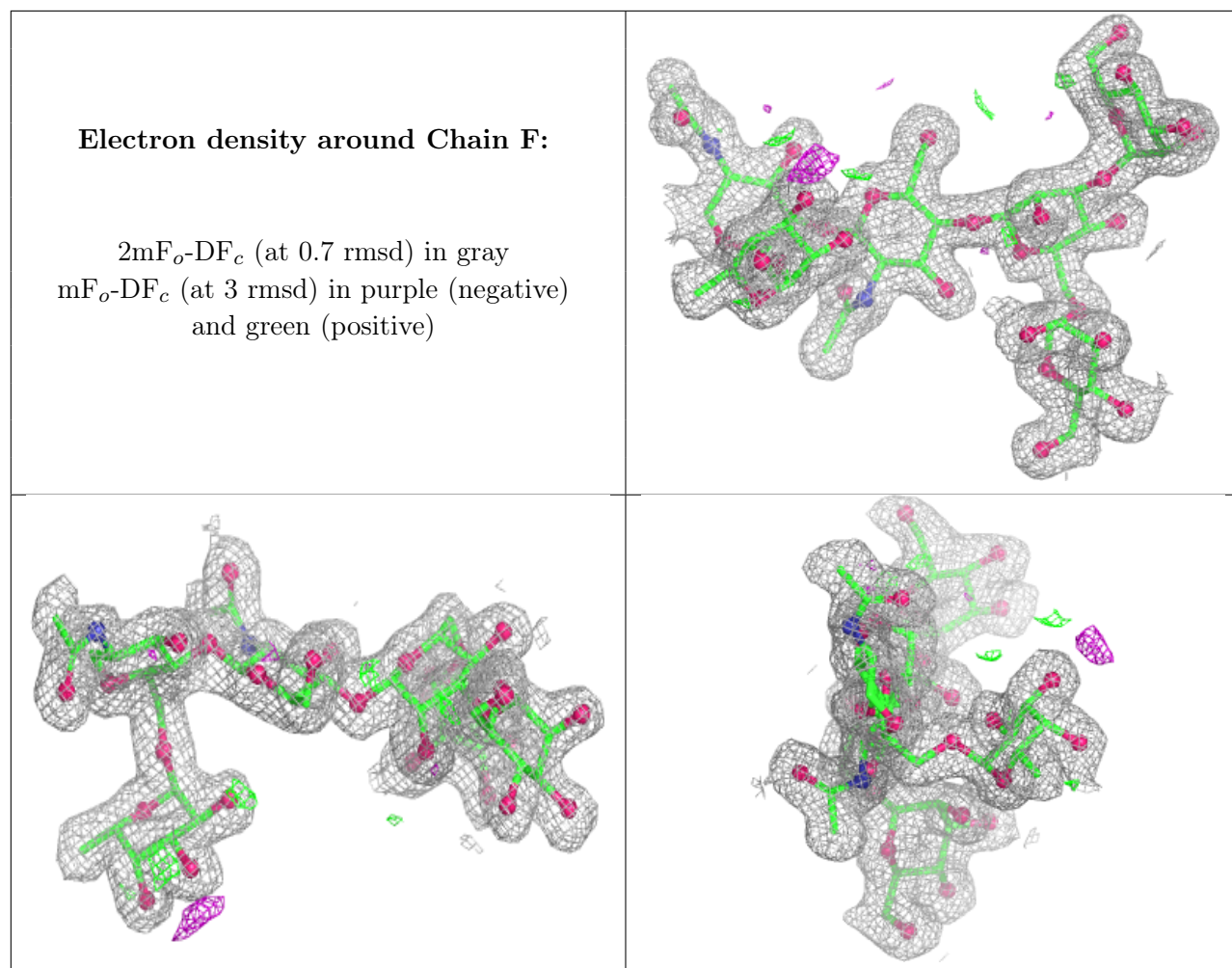
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MAN	F	4	11/12	0.86	0.09	22,24,28,30	0
3	MAN	E	4	11/12	0.90	0.07	24,26,27,27	0
3	NAG	E	1	14/15	0.94	0.06	8,12,16,17	0
3	FUC	E	6	10/11	0.94	0.05	15,16,18,19	0
3	NAG	F	1	14/15	0.94	0.06	10,12,17,20	0
3	BMA	E	3	11/12	0.94	0.07	11,13,16,21	0
3	MAN	E	5	11/12	0.95	0.05	13,15,17,18	0
3	FUC	F	6	10/11	0.95	0.05	14,15,17,18	0
3	NAG	E	2	14/15	0.96	0.05	8,10,11,11	0
3	MAN	F	5	11/12	0.96	0.05	13,14,16,17	0
3	BMA	F	3	11/12	0.96	0.05	10,12,15,19	0
3	NAG	F	2	14/15	0.97	0.04	8,11,12,13	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

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





6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

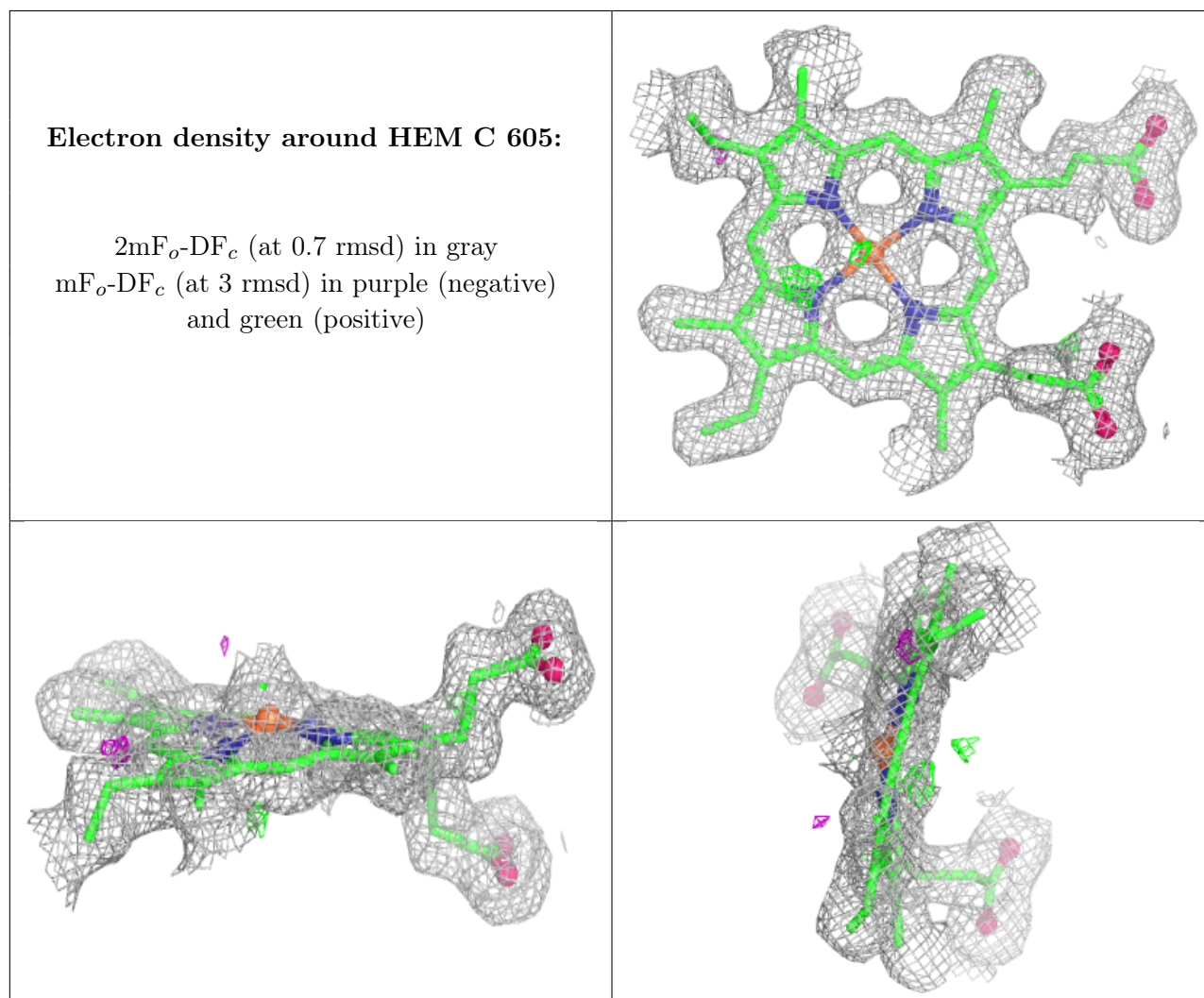
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	ACY	D	607	4/4	0.29	0.26	38,38,38,39	0
5	SO4	D	605	5/5	0.51	0.22	46,47,47,47	5
6	NAG	D	603	14/15	0.77	0.11	32,34,37,38	0
9	ACY	C	608	4/4	0.78	0.12	27,28,29,29	0
9	ACY	C	606	4/4	0.78	0.09	27,28,29,30	0
9	ACY	C	607	4/4	0.82	0.11	17,20,20,21	0
9	ACY	D	606	4/4	0.84	0.10	20,21,21,24	0
9	ACY	D	608	4/4	0.85	0.11	30,31,31,32	0
6	NAG	C	602	14/15	0.87	0.11	23,28,36,36	0
6	NAG	D	602	14/15	0.89	0.08	17,24,28,29	0

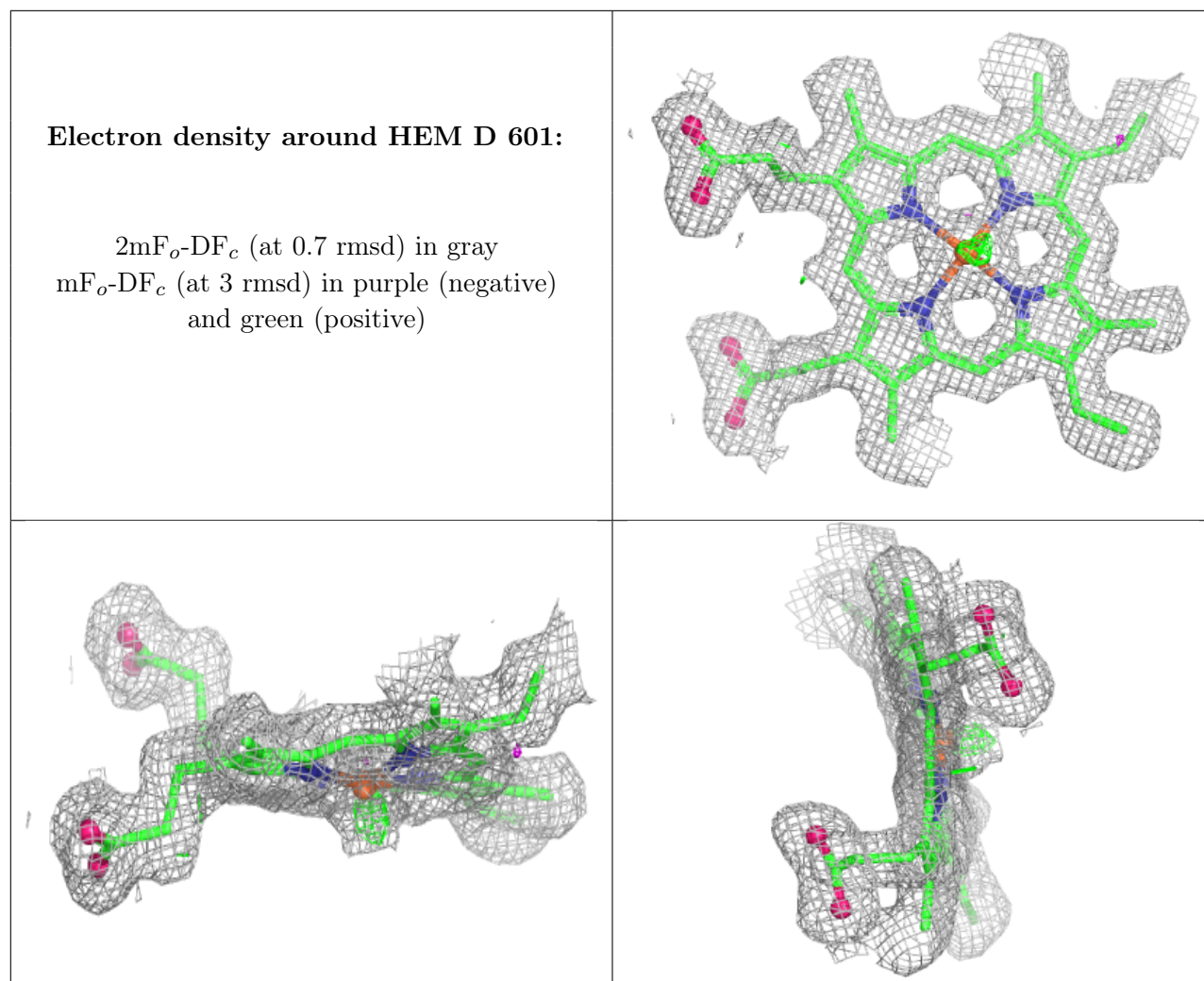
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	NAG	C	601	14/15	0.90	0.07	15,17,21,22	0
5	SO4	C	604	5/5	0.94	0.10	27,29,31,33	0
4	SCN	B	202	3/3	0.98	0.05	19,19,19,19	0
5	SO4	A	202	5/5	0.98	0.06	25,25,28,29	0
8	HEM	C	605	43/43	0.98	0.05	4,8,9,10	0
8	HEM	D	601	43/43	0.98	0.05	5,8,10,12	0
4	SCN	A	201	3/3	0.98	0.05	12,12,12,17	0
4	SCN	A	203	3/3	0.99	0.03	15,15,18,20	0
4	SCN	B	201	3/3	0.99	0.05	11,11,16,17	0
7	CA	C	603	1/1	1.00	0.02	10,10,10,10	0
7	CA	D	604	1/1	1.00	0.02	9,9,9,9	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.