



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 12, 2024 – 09:18 PM EDT

PDB ID : 7LAG
Title : CRYSTAL STRUCTURE OF MYELOPEROXIDASE SUBFORM C (MPO)
COMPLEX WITH Compound-14 AKA 7-({1-[(3-phenoxyphenyl)methyl]-1H
-pyrazol-4-yl}methyl)-3H-[1,2,3]triazolo[4,5-b]pyridin-5-amine
Authors : Khan, J.A.
Deposited on : 2021-01-06
Resolution : 2.85 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

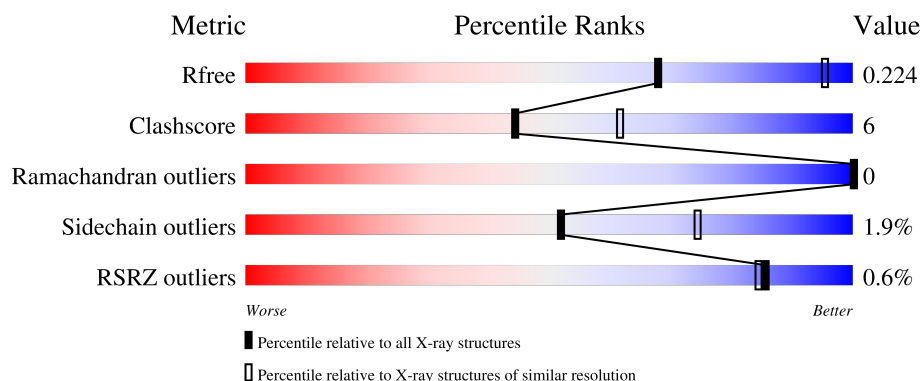
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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.







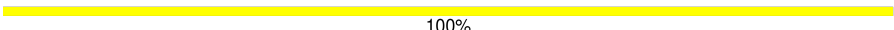


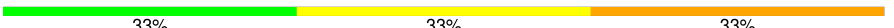


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	1268 (2.88-2.84)
Clashscore	180529	1351 (2.88-2.84)
Ramachandran outliers	177936	1318 (2.88-2.84)
Sidechain outliers	177891	1319 (2.88-2.84)
RSRZ outliers	164620	1269 (2.88-2.84)

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	105	<div> <div>3%</div> <div>89%</div> <div>10%</div> <div>.</div> </div>
1	D	105	<div> <div>%</div> <div>94%</div> <div>.</div> <div>.</div> </div>
1	F	105	<div> <div>4%</div> <div>90%</div> <div>7%</div> <div>..</div> </div>
1	H	105	<div> <div>90%</div> <div>8%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
2	B	466	 89% 11%
2	E	466	 88% 11%
2	G	466	 89% 11%
2	I	466	 89% 10%
3	C	2	 100%
3	L	2	 50% 50%
4	J	6	 83% 17%
4	K	6	 33% 33% 33%
4	M	6	 50% 33% 17%
4	N	6	 50% 50%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 18458 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 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	103	Total	C	N	O	S	3	0	0
			820	519	145	151	5			
1	D	103	Total	C	N	O	S	3	0	0
			814	517	145	147	5			
1	F	103	Total	C	N	O	S	3	0	0
			821	520	145	151	5			
1	H	103	Total	C	N	O	S	3	0	0
			820	519	145	151	5			

- Molecule 2 is a protein called Isoform H14 of Myeloperoxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	464	Total	C	N	O	S	23	0	0
			3602	2283	639	653	27			
2	E	465	Total	C	N	O	S	30	0	0
			3636	2303	655	651	27			
2	G	464	Total	C	N	O	S	26	0	0
			3620	2295	647	651	27			
2	I	464	Total	C	N	O	S	22	0	0
			3615	2295	641	652	27			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



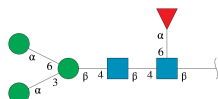
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	L	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 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.

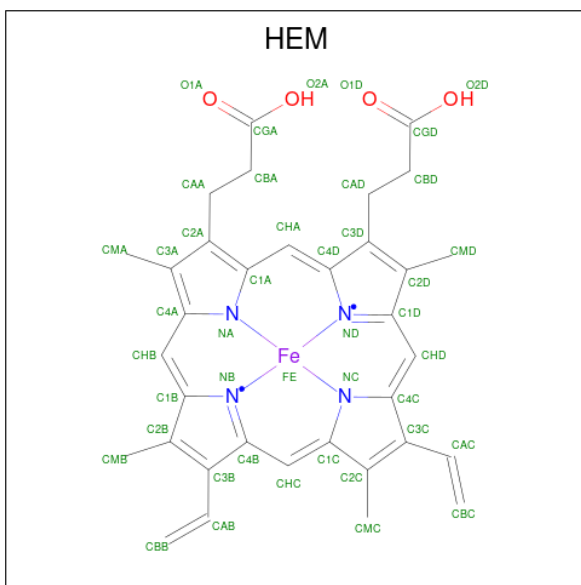


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	J	6	Total	C	N	O	0	0	0
			71	40	2	29			
4	K	6	Total	C	N	O	0	0	0
			71	40	2	29			
4	M	6	Total	C	N	O	0	0	0
			71	40	2	29			
4	N	6	Total	C	N	O	0	0	0
			71	40	2	29			

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

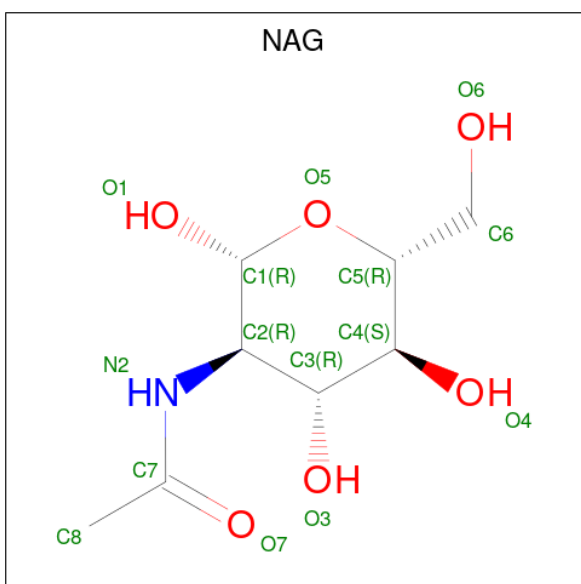
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		
5	B	1	Total	Cl	0	0
			1	1		
5	F	1	Total	Cl	0	0
			1	1		
5	G	1	Total	Cl	0	0
			1	1		

- Molecule 6 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	E	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
6	I	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

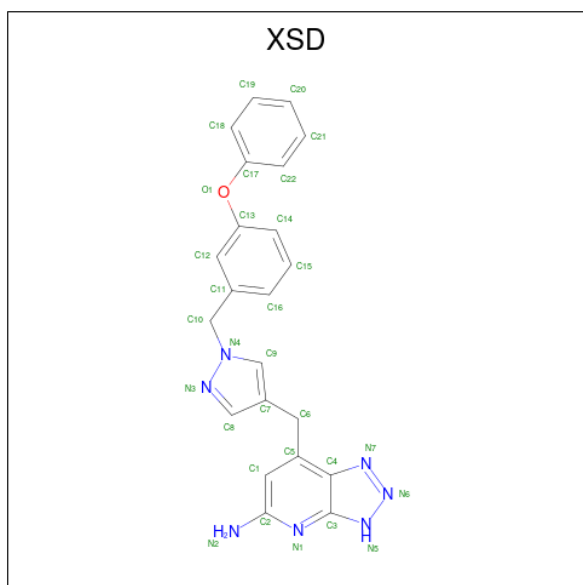


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		
7	G	1	Total	C	N	O	0	0
			14	8	1	5		
7	I	1	Total	C	N	O	0	0
			14	8	1	5		
7	I	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Ca	0	0
			1	1		
8	E	1	Total	Ca	0	0
			1	1		
8	G	1	Total	Ca	0	0
			1	1		
8	I	1	Total	Ca	0	0
			1	1		

- Molecule 9 is 7-({1-[(3-phenoxyphenyl)methyl]-1H-pyrazol-4-yl}methyl)-3H-[1,2,3]triazolo[4,5-b]pyridin-5-amine (three-letter code: XSD) (formula: C₂₂H₁₉N₇O) (labeled as "Ligand of Interest" by depositor).

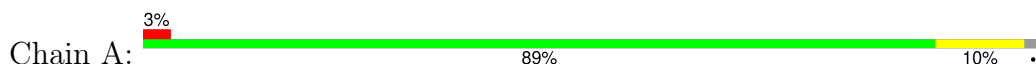


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			30	22	7	1		
9	E	1	Total	C	N	O	0	0
			30	22	7	1		
9	G	1	Total	C	N	O	0	0
			30	22	7	1		
9	I	1	Total	C	N	O	0	0
			30	22	7	1		

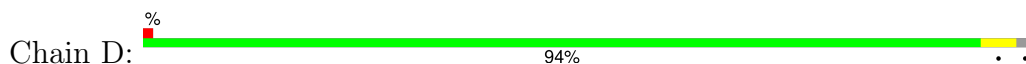
3 Residue-property plots [i](#)

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

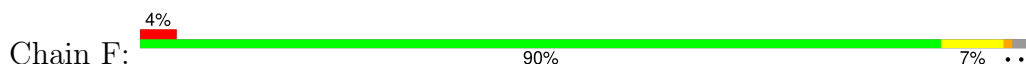
- Molecule 1: Myeloperoxidase light chain



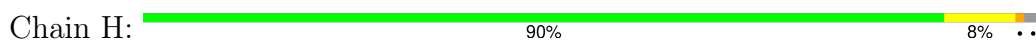
- Molecule 1: Myeloperoxidase light chain



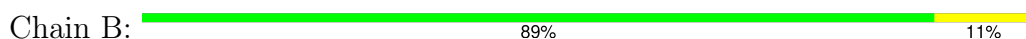
- Molecule 1: Myeloperoxidase light chain

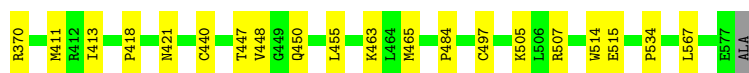


- Molecule 1: Myeloperoxidase light chain



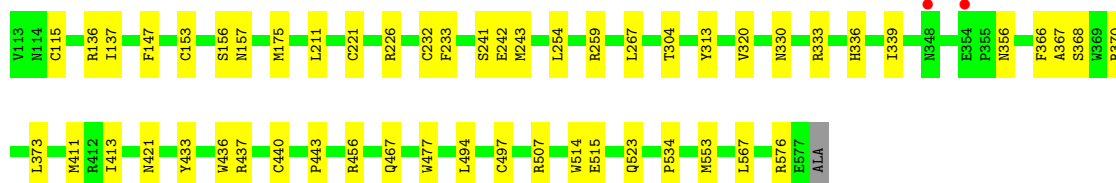
- Molecule 2: Isoform H14 of Myeloperoxidase





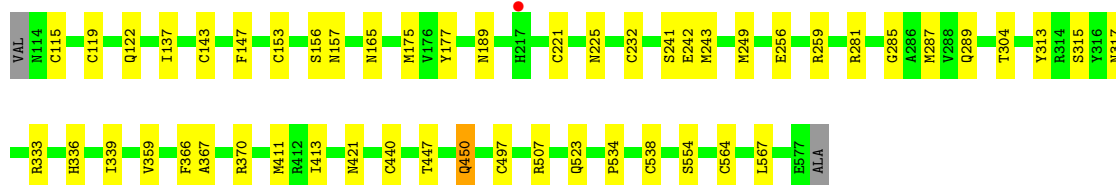
- Molecule 2: Isoform H14 of Myeloperoxidase

Chain E: 88% 11%



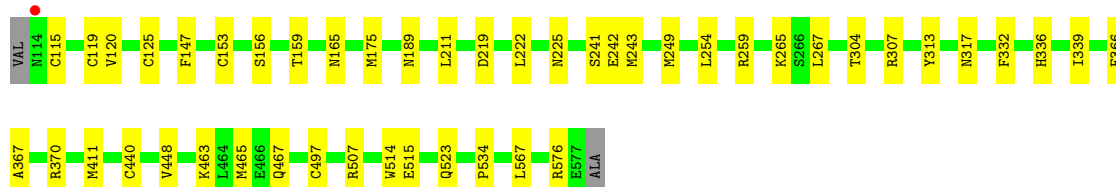
- Molecule 2: Isoform H14 of Myeloperoxidase

Chain G: 89% 11%



- Molecule 2: Isoform H14 of Myeloperoxidase

Chain I: 89% 10%



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

Chain C: 100%

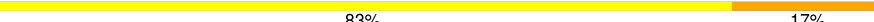


- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L: 50% 50%



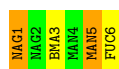
● Molecule 4: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  83% 17%



● Molecule 4: 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 K:  33% 33% 33%



● Molecule 4: 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 M:  50% 33% 17%



● Molecule 4: 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 N:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	143.46Å 149.89Å 228.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.20 – 2.85 47.20 – 2.85	Depositor EDS
% Data completeness (in resolution range)	98.8 (47.20-2.85) 99.9 (47.20-2.85)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 2.81Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.193 , 0.235 0.191 , 0.224	Depositor DCC
R_{free} test set	2898 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.020 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18458	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, CL, XSD, CA, NAG, HEM, BMA, FUC

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	0.48	0/845	0.66	0/1153
1	D	0.48	0/839	0.68	0/1145
1	F	0.48	0/846	0.66	0/1154
1	H	0.49	0/845	0.67	0/1153
2	B	0.49	0/3687	0.63	0/5021
2	E	0.50	0/3721	0.63	0/5064
2	G	0.51	0/3705	0.63	0/5044
2	I	0.49	0/3700	0.62	0/5037
All	All	0.49	0/18188	0.64	0/24771

There are no bond length outliers.

There are no bond angle outliers.

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	820	0	774	11	0
1	D	814	0	770	6	0
1	F	821	0	776	7	0
1	H	820	0	774	10	0
2	B	3602	0	3497	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	3636	0	3581	37	0
2	G	3620	0	3550	39	0
2	I	3615	0	3537	43	0
3	C	28	0	25	0	0
3	L	28	0	25	2	0
4	J	71	0	61	5	0
4	K	71	0	61	2	0
4	M	71	0	61	4	0
4	N	71	0	61	5	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
6	B	43	0	30	13	0
6	E	43	0	30	13	0
6	G	43	0	30	9	0
6	I	43	0	30	13	0
7	B	14	0	13	0	0
7	E	14	0	13	4	0
7	G	14	0	13	3	0
7	I	28	0	26	6	0
8	B	1	0	0	0	0
8	E	1	0	0	0	0
8	G	1	0	0	0	0
8	I	1	0	0	0	0
9	B	30	0	0	0	0
9	E	30	0	0	0	0
9	G	30	0	0	0	0
9	I	30	0	0	0	0
All	All	18458	0	17738	191	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 191 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:G:317:ASN:HD21	4:M:1:NAG:C1	1.30	1.45
2:I:189:ASN:HD21	7:I:602:NAG:C1	1.30	1.44
2:B:317:ASN:ND2	4:J:1:NAG:C1	1.85	1.39
2:I:317:ASN:HD21	4:N:1:NAG:C1	1.38	1.37

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:189:ASN:ND2	7:I:602:NAG:C1	2.03	1.20

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	101/105 (96%)	99 (98%)	2 (2%)	0	100	100
1	D	101/105 (96%)	100 (99%)	1 (1%)	0	100	100
1	F	101/105 (96%)	100 (99%)	1 (1%)	0	100	100
1	H	101/105 (96%)	99 (98%)	2 (2%)	0	100	100
2	B	462/466 (99%)	454 (98%)	8 (2%)	0	100	100
2	E	463/466 (99%)	453 (98%)	10 (2%)	0	100	100
2	G	462/466 (99%)	449 (97%)	13 (3%)	0	100	100
2	I	462/466 (99%)	452 (98%)	10 (2%)	0	100	100
All	All	2253/2284 (99%)	2206 (98%)	47 (2%)	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	87/90 (97%)	87 (100%)	0	100	100
1	D	85/90 (94%)	85 (100%)	0	100	100
1	F	87/90 (97%)	86 (99%)	1 (1%)	70	85
1	H	87/90 (97%)	86 (99%)	1 (1%)	70	85
2	B	380/411 (92%)	373 (98%)	7 (2%)	54	76
2	E	390/411 (95%)	381 (98%)	9 (2%)	45	70
2	G	386/411 (94%)	376 (97%)	10 (3%)	41	67
2	I	383/411 (93%)	376 (98%)	7 (2%)	54	76
All	All	1885/2004 (94%)	1850 (98%)	35 (2%)	52	74

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	175	MET
2	I	259	ARG
2	I	307	ARG
2	E	356	ASN
2	E	304	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	121	GLN
2	G	317	ASN
2	I	421	ASN
2	I	189	ASN
2	I	225	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 ⓘ

28 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	C	1	3,2	14,14,15	1.66	4 (28%)	17,19,21	2.36	6 (35%)
3	NAG	C	2	3	14,14,15	0.79	0	17,19,21	1.15	1 (5%)
4	NAG	J	1	4	14,14,15	0.33	0	17,19,21	0.75	1 (5%)
4	NAG	J	2	4	14,14,15	1.57	3 (21%)	17,19,21	2.15	4 (23%)
4	BMA	J	3	4	11,11,12	1.25	1 (9%)	15,15,17	1.55	5 (33%)
4	MAN	J	4	4	11,11,12	0.90	1 (9%)	15,15,17	1.73	3 (20%)
4	MAN	J	5	4	11,11,12	1.26	1 (9%)	15,15,17	1.50	2 (13%)
4	FUC	J	6	4	10,10,11	1.12	0	14,14,16	1.50	2 (14%)
4	NAG	K	1	4,2	14,14,15	1.24	1 (7%)	17,19,21	4.13	6 (35%)
4	NAG	K	2	4	14,14,15	0.28	0	17,19,21	0.53	0
4	BMA	K	3	4	11,11,12	0.59	0	15,15,17	1.23	3 (20%)
4	MAN	K	4	4	11,11,12	0.38	0	15,15,17	0.75	0
4	MAN	K	5	4	11,11,12	0.44	0	15,15,17	0.83	1 (6%)
4	FUC	K	6	4	10,10,11	0.41	0	14,14,16	0.74	1 (7%)
3	NAG	L	1	3	14,14,15	0.30	0	17,19,21	1.14	2 (11%)
3	NAG	L	2	3	14,14,15	0.28	0	17,19,21	0.62	0
4	NAG	M	1	4	14,14,15	0.40	0	17,19,21	1.08	1 (5%)
4	NAG	M	2	4	14,14,15	0.39	0	17,19,21	0.65	0
4	BMA	M	3	4	11,11,12	0.43	0	15,15,17	0.66	0
4	MAN	M	4	4	11,11,12	0.30	0	15,15,17	0.89	1 (6%)
4	MAN	M	5	4	11,11,12	0.30	0	15,15,17	0.98	1 (6%)
4	FUC	M	6	4	10,10,11	0.34	0	14,14,16	0.47	0
4	NAG	N	1	4	14,14,15	0.29	0	17,19,21	0.70	0
4	NAG	N	2	4	14,14,15	0.30	0	17,19,21	0.49	0
4	BMA	N	3	4	11,11,12	0.27	0	15,15,17	0.67	0
4	MAN	N	4	4	11,11,12	0.31	0	15,15,17	1.11	1 (6%)
4	MAN	N	5	4	11,11,12	0.37	0	15,15,17	0.78	1 (6%)
4	FUC	N	6	4	10,10,11	0.37	0	14,14,16	0.62	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	C	1	3,2	-	1/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
4	NAG	J	1	4	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
4	BMA	J	3	4	-	0/2/19/22	0/1/1/1
4	MAN	J	4	4	-	2/2/19/22	0/1/1/1
4	MAN	J	5	4	-	2/2/19/22	0/1/1/1
4	FUC	J	6	4	-	-	0/1/1/1
4	NAG	K	1	4,2	-	2/6/23/26	0/1/1/1
4	NAG	K	2	4	-	0/6/23/26	0/1/1/1
4	BMA	K	3	4	-	1/2/19/22	0/1/1/1
4	MAN	K	4	4	-	2/2/19/22	0/1/1/1
4	MAN	K	5	4	-	2/2/19/22	0/1/1/1
4	FUC	K	6	4	-	-	0/1/1/1
3	NAG	L	1	3	-	0/6/23/26	0/1/1/1
3	NAG	L	2	3	-	0/6/23/26	0/1/1/1
4	NAG	M	1	4	-	1/6/23/26	0/1/1/1
4	NAG	M	2	4	-	0/6/23/26	0/1/1/1
4	BMA	M	3	4	-	0/2/19/22	0/1/1/1
4	MAN	M	4	4	-	1/2/19/22	0/1/1/1
4	MAN	M	5	4	-	0/2/19/22	0/1/1/1
4	FUC	M	6	4	-	-	0/1/1/1
4	NAG	N	1	4	-	0/6/23/26	0/1/1/1
4	NAG	N	2	4	-	0/6/23/26	0/1/1/1
4	BMA	N	3	4	-	0/2/19/22	0/1/1/1
4	MAN	N	4	4	-	1/2/19/22	0/1/1/1
4	MAN	N	5	4	-	0/2/19/22	0/1/1/1
4	FUC	N	6	4	-	-	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	NAG	O5-C1	-3.51	1.37	1.43
4	J	2	NAG	O5-C1	-3.28	1.38	1.43
4	J	3	BMA	O5-C1	-2.94	1.38	1.43
4	J	5	MAN	O5-C1	-2.73	1.39	1.43
3	C	1	NAG	C1-C2	-2.61	1.48	1.52

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	K	1	NAG	O5-C1-C2	-10.65	94.81	111.29
4	K	1	NAG	C1-O5-C5	10.63	126.43	112.19
4	J	2	NAG	C1-O5-C5	5.82	119.99	112.19
3	C	1	NAG	C1-O5-C5	-5.78	104.44	112.19
4	K	1	NAG	C4-C3-C2	5.45	119.01	111.02

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

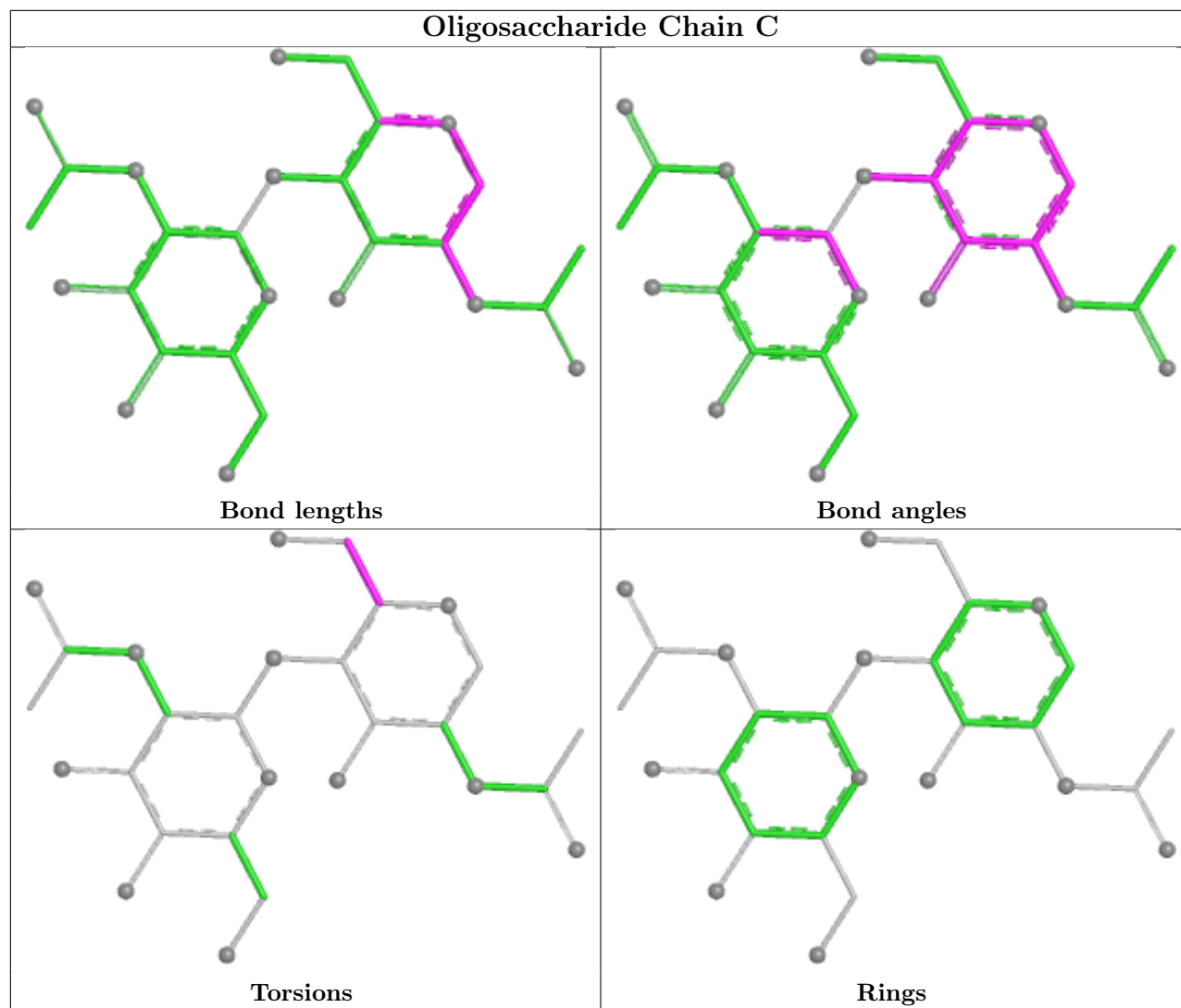
Mol	Chain	Res	Type	Atoms
4	K	1	NAG	O5-C5-C6-O6
4	K	1	NAG	C4-C5-C6-O6
4	J	4	MAN	C4-C5-C6-O6
4	J	4	MAN	O5-C5-C6-O6
4	K	5	MAN	C4-C5-C6-O6

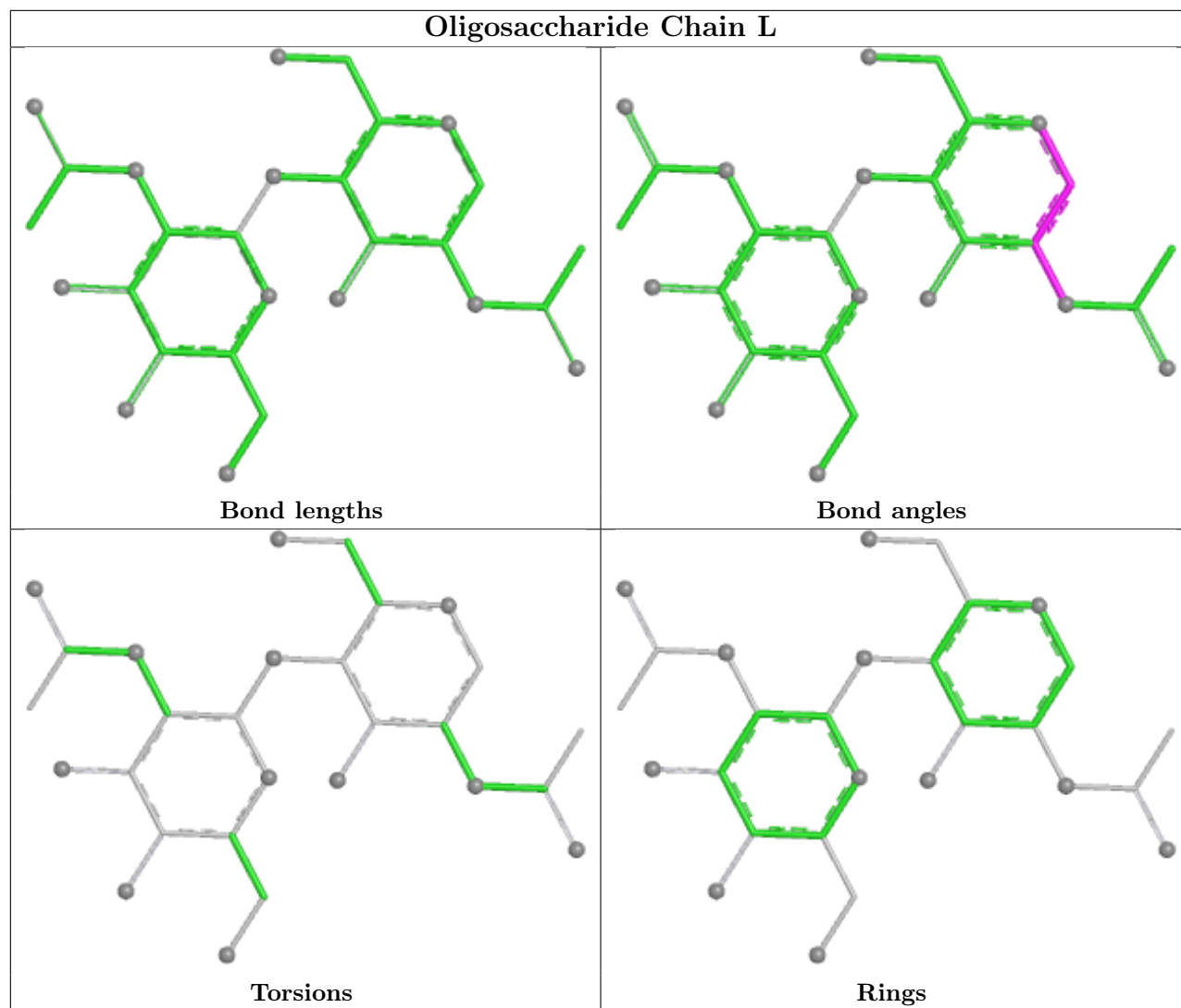
There are no ring outliers.

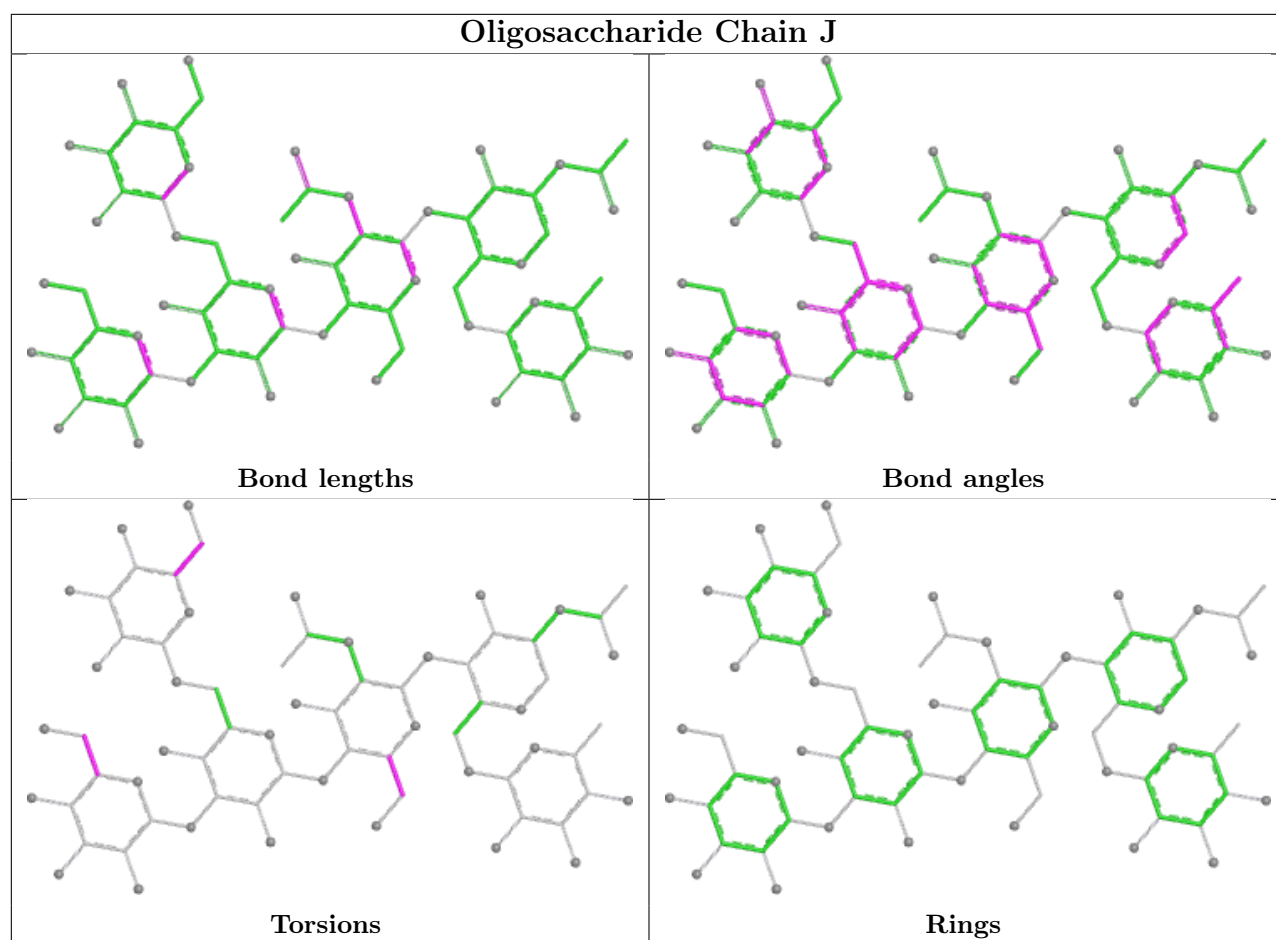
6 monomers are involved in 18 short contacts:

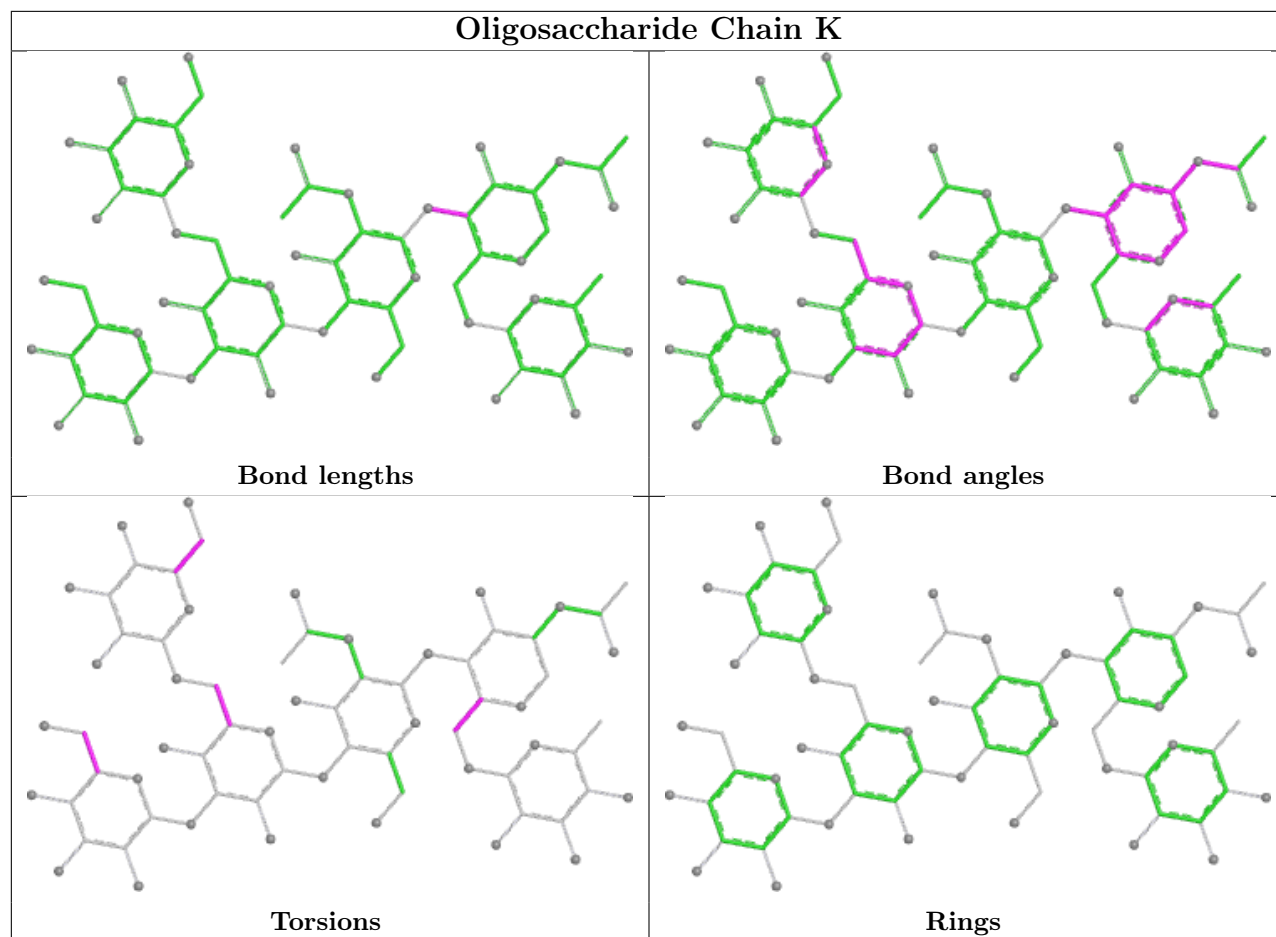
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	1	NAG	2	0
4	M	1	NAG	4	0
4	K	1	NAG	1	0
4	J	1	NAG	5	0
4	K	5	MAN	1	0
4	N	1	NAG	5	0

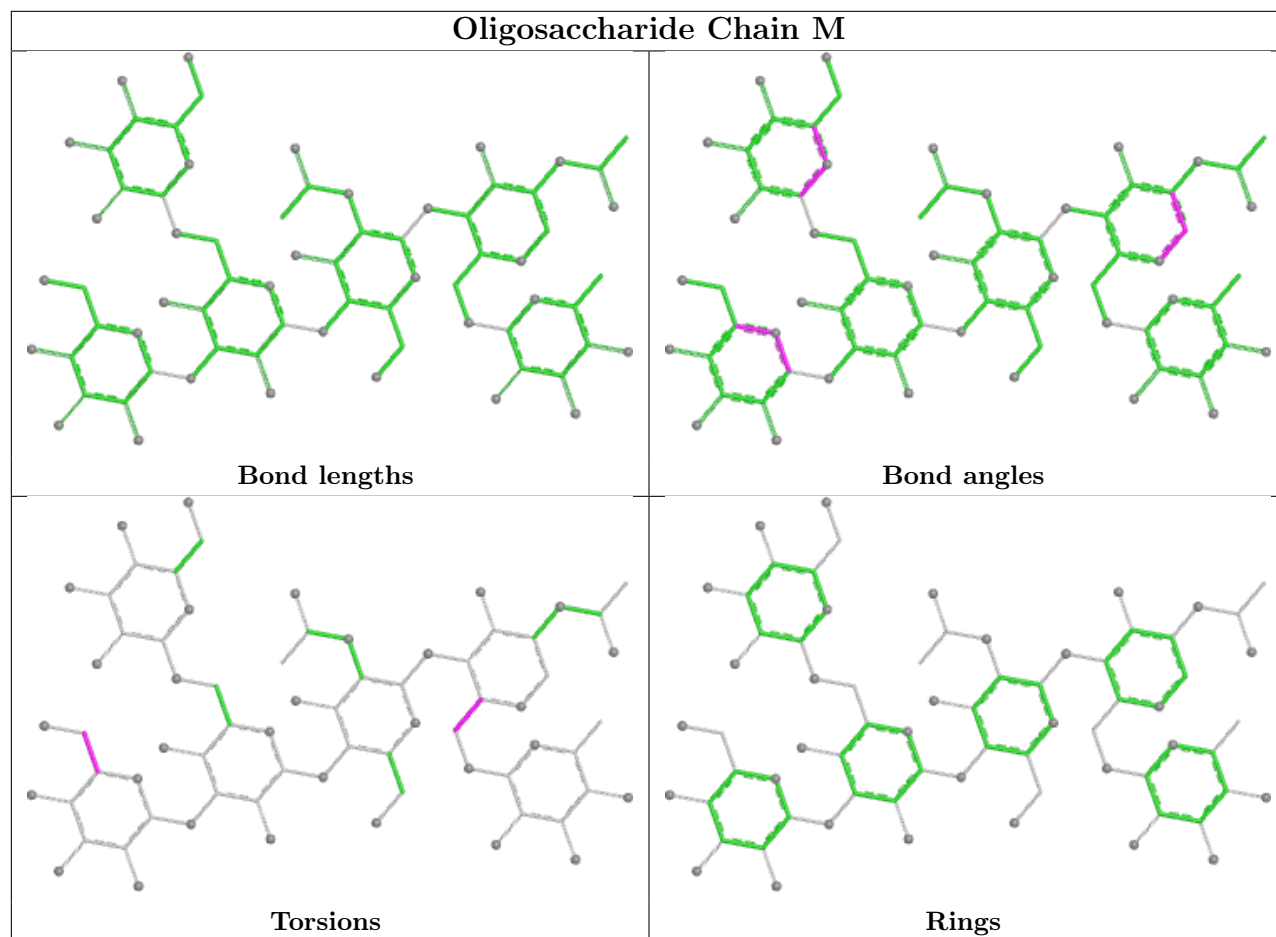
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

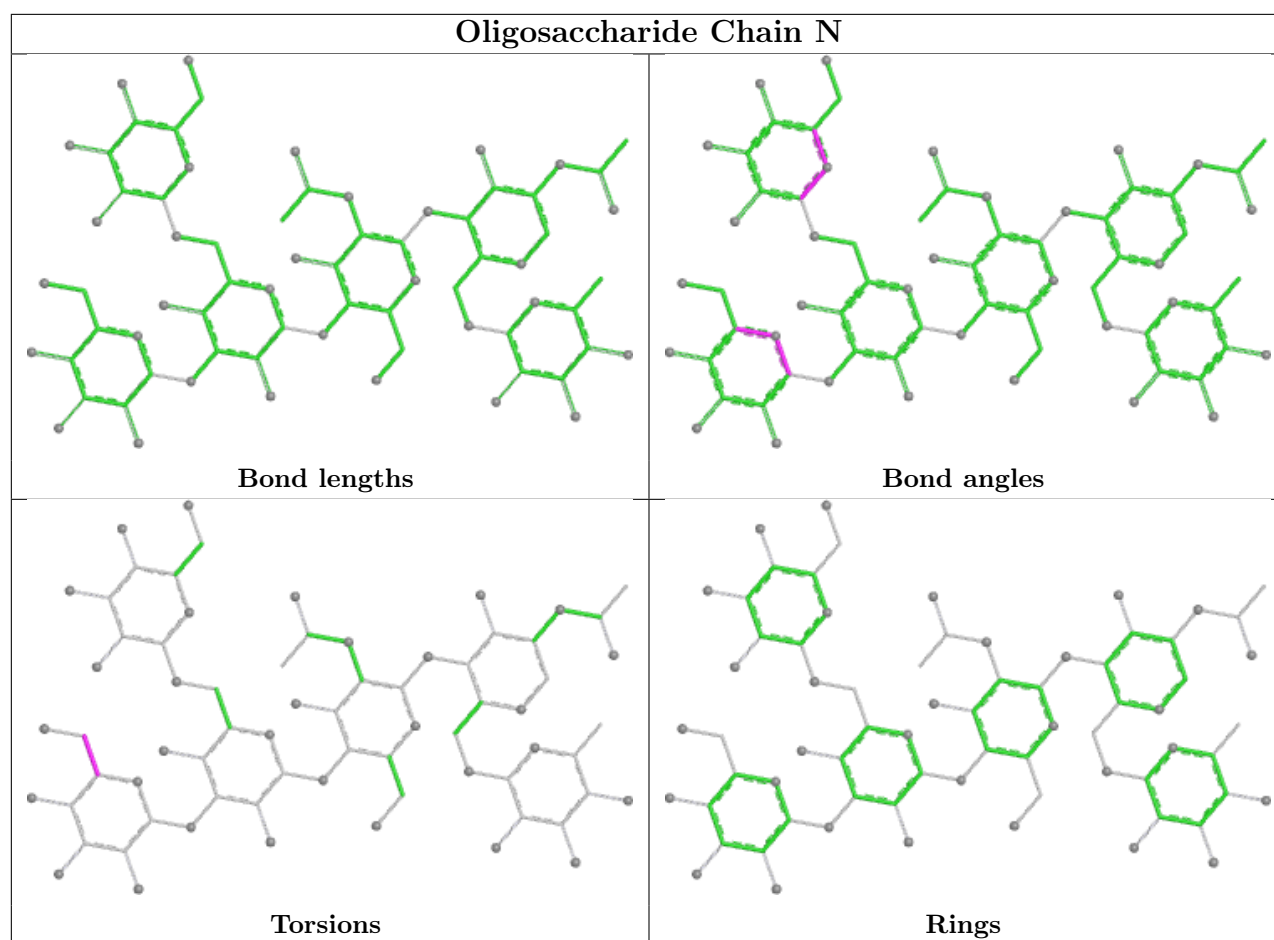












5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 8 are monoatomic - leaving 13 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	XSD	B	605	-	30,34,34	1.38	3 (10%)	35,47,47	0.65	0
6	HEM	E	601	2	42,50,50	1.44	9 (21%)	46,82,82	1.88	17 (36%)
7	NAG	I	603	-	14,14,15	0.26	0	17,19,21	0.76	1 (5%)
7	NAG	E	602	2	14,14,15	0.58	0	17,19,21	1.76	5 (29%)
6	HEM	B	601	2	42,50,50	1.43	8 (19%)	46,82,82	1.83	15 (32%)
7	NAG	G	602	-	14,14,15	0.30	0	17,19,21	0.83	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	XSD	G	605	-	30,34,34	1.04	2 (6%)	35,47,47	0.62	1 (2%)
7	NAG	B	602	2	14,14,15	1.00	1 (7%)	17,19,21	1.68	3 (17%)
6	HEM	G	601	2	42,50,50	1.43	6 (14%)	46,82,82	1.96	16 (34%)
7	NAG	I	602	-	14,14,15	0.29	0	17,19,21	0.84	1 (5%)
6	HEM	I	601	2	42,50,50	1.38	8 (19%)	46,82,82	1.82	13 (28%)
9	XSD	I	605	-	30,34,34	1.08	2 (6%)	35,47,47	0.73	2 (5%)
9	XSD	E	604	-	30,34,34	1.32	2 (6%)	35,47,47	0.78	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
9	XSD	B	605	-	-	0/12/12/12	0/5/5/5
6	HEM	E	601	2	-	5/12/54/54	-
7	NAG	I	603	-	-	0/6/23/26	0/1/1/1
7	NAG	E	602	2	-	3/6/23/26	0/1/1/1
6	HEM	B	601	2	-	5/12/54/54	-
7	NAG	G	602	-	-	0/6/23/26	0/1/1/1
9	XSD	G	605	-	-	0/12/12/12	0/5/5/5
7	NAG	B	602	2	-	2/6/23/26	0/1/1/1
6	HEM	G	601	2	-	5/12/54/54	-
7	NAG	I	602	-	-	0/6/23/26	0/1/1/1
6	HEM	I	601	2	-	5/12/54/54	-
9	XSD	I	605	-	-	0/12/12/12	0/5/5/5
9	XSD	E	604	-	-	1/12/12/12	0/5/5/5

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	605	XSD	C3-N5	6.01	1.44	1.34
9	E	604	XSD	C3-N5	5.11	1.42	1.34
9	I	605	XSD	C3-N5	4.12	1.41	1.34
9	G	605	XSD	C3-N5	3.90	1.40	1.34
6	B	601	HEM	C1B-NB	-3.76	1.33	1.40

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	601	HEM	CBA-CAA-C2A	-4.37	105.19	112.54
6	I	601	HEM	CBA-CAA-C2A	-4.37	105.19	112.54
6	E	601	HEM	CBA-CAA-C2A	-4.29	105.33	112.54
6	G	601	HEM	CHA-C4D-C3D	-4.14	117.60	125.23
6	B	601	HEM	CHA-C4D-ND	4.02	129.36	124.37

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	E	602	NAG	C8-C7-N2-C2
7	E	602	NAG	O7-C7-N2-C2
7	E	602	NAG	O5-C5-C6-O6
6	B	601	HEM	C4B-C3B-CAB-CBB
6	E	601	HEM	C4B-C3B-CAB-CBB

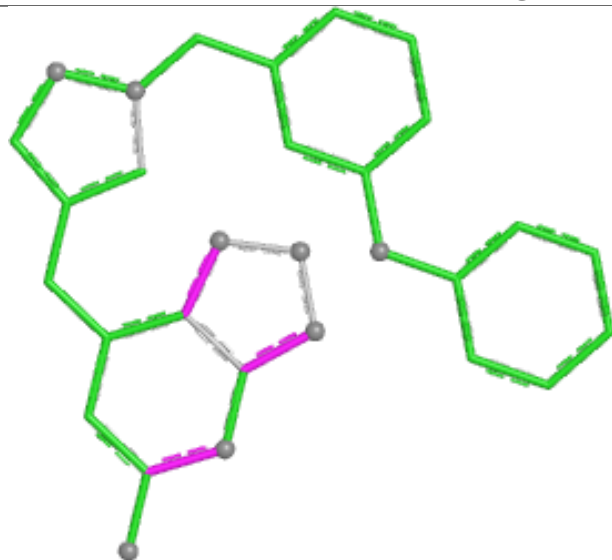
There are no ring outliers.

8 monomers are involved in 61 short contacts:

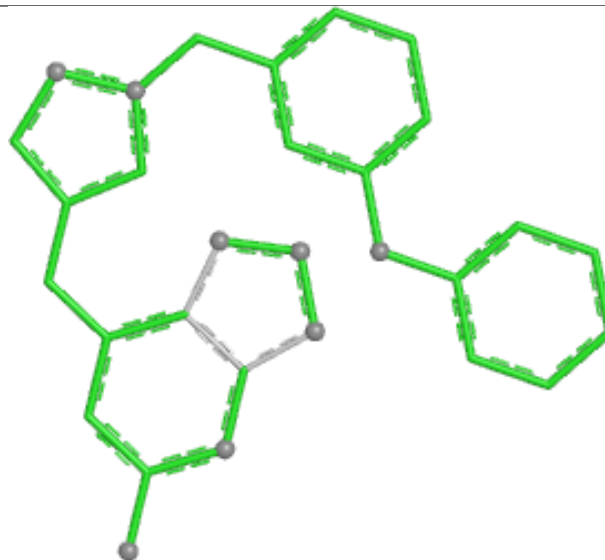
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	601	HEM	13	0
7	I	603	NAG	3	0
7	E	602	NAG	4	0
6	B	601	HEM	13	0
7	G	602	NAG	3	0
6	G	601	HEM	9	0
7	I	602	NAG	3	0
6	I	601	HEM	13	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

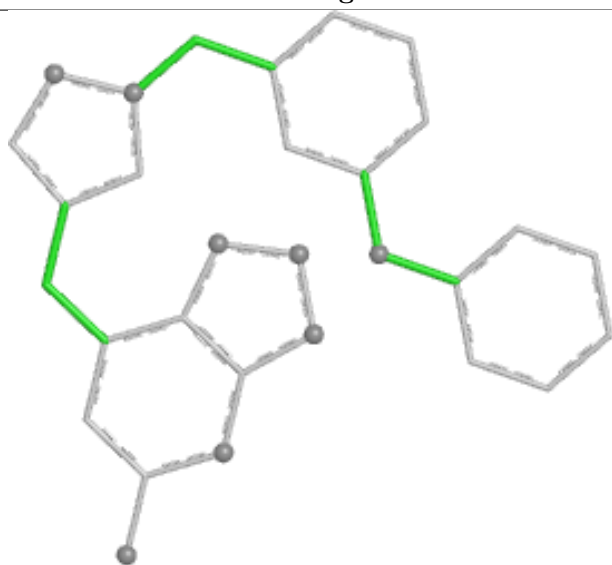
Ligand XSD B 605



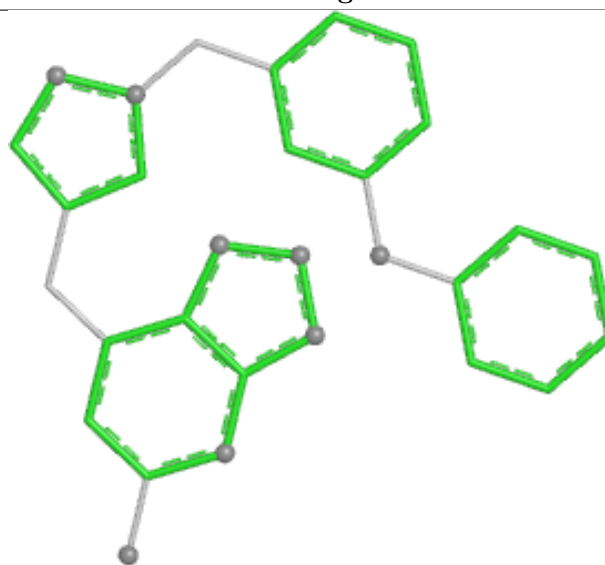
Bond lengths



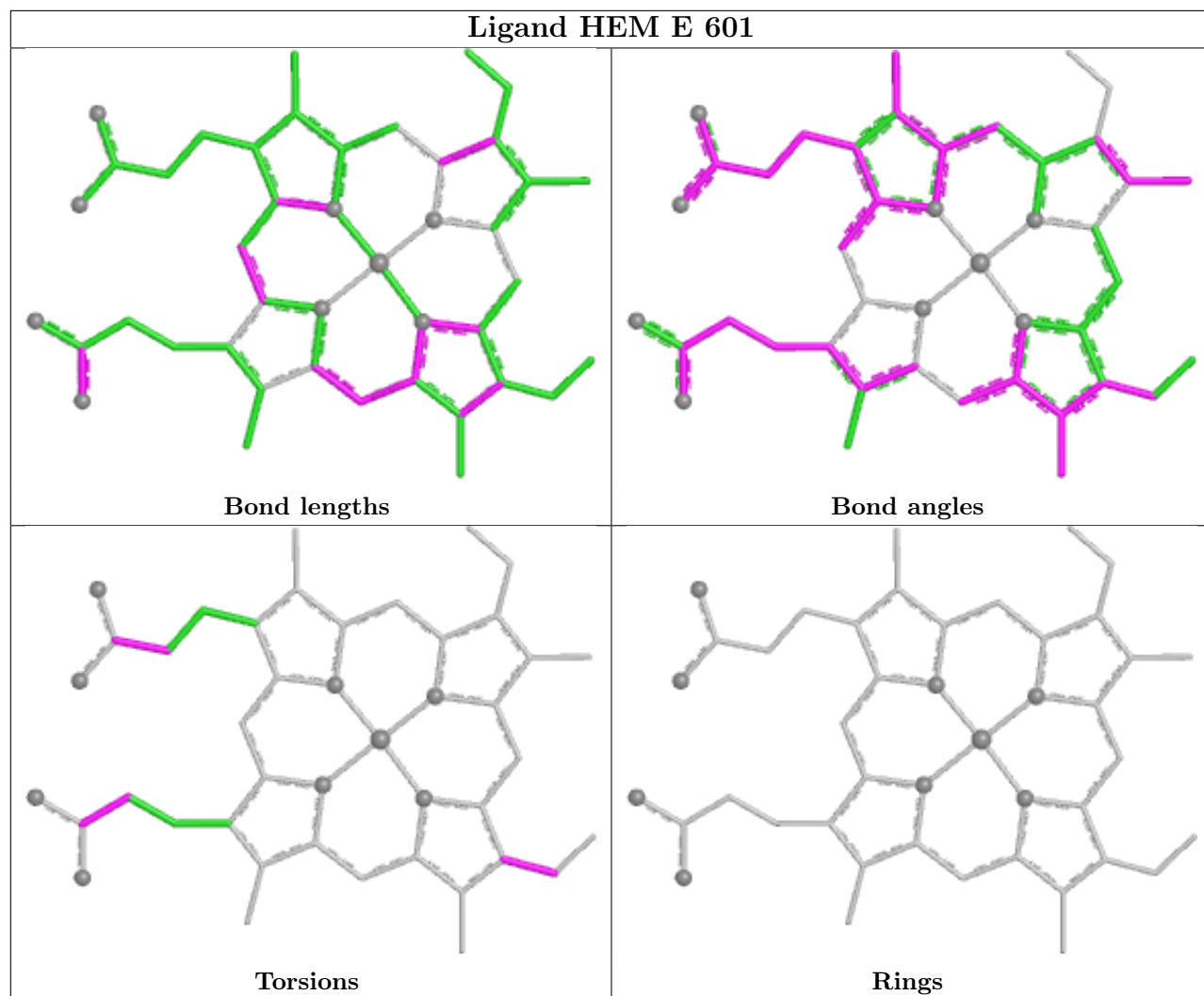
Bond angles

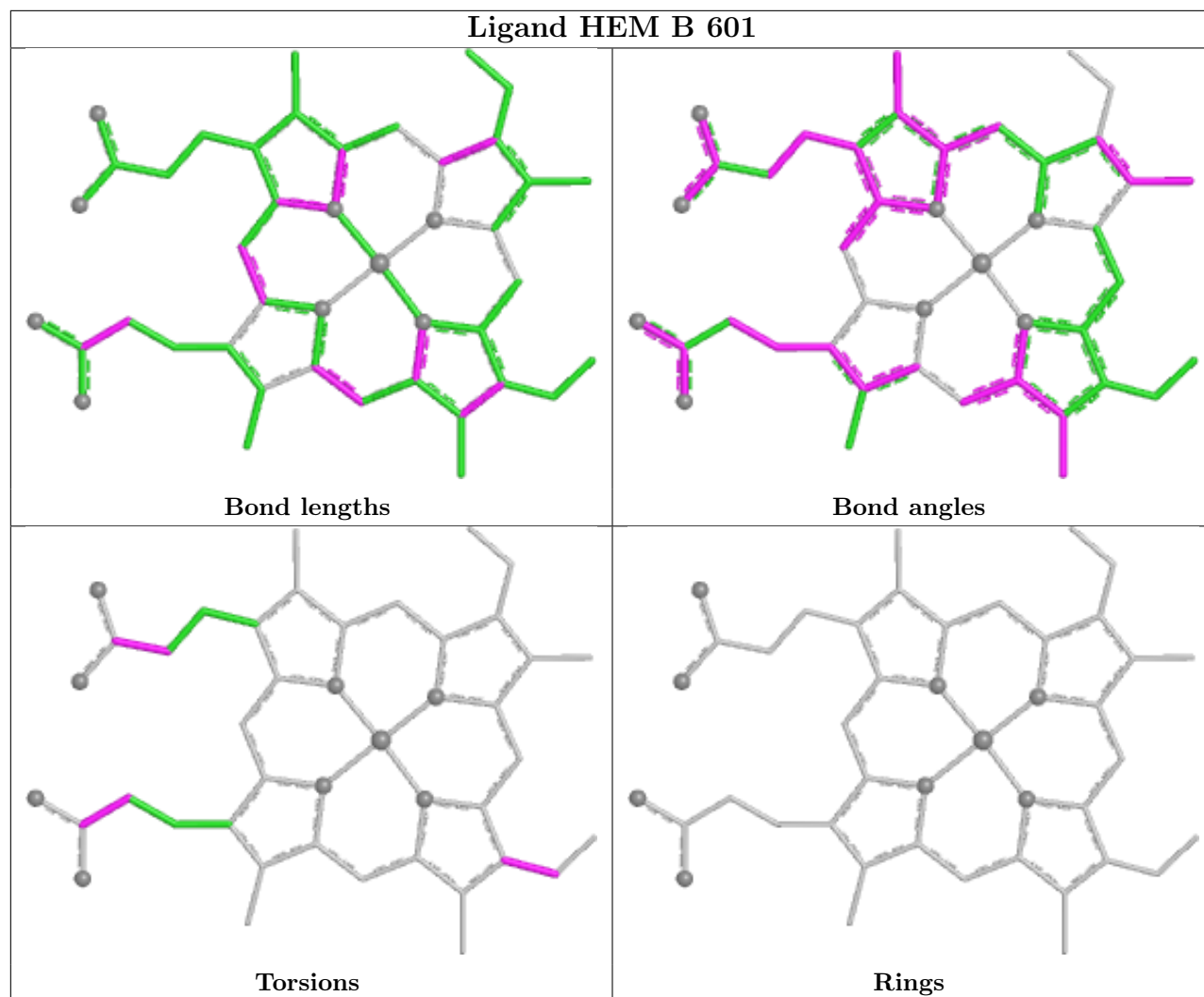


Torsions

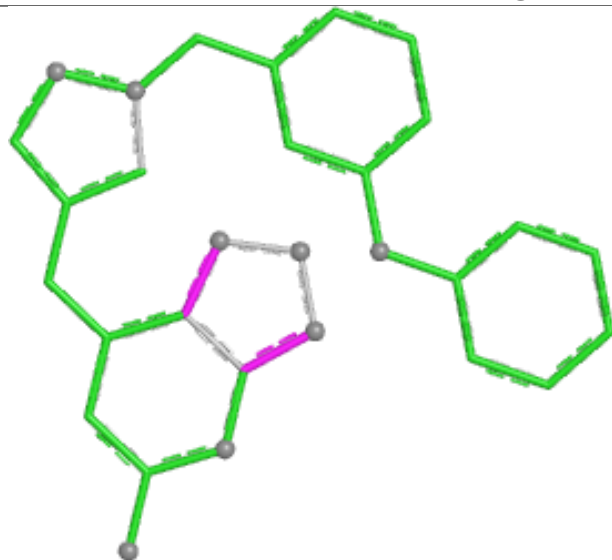


Rings

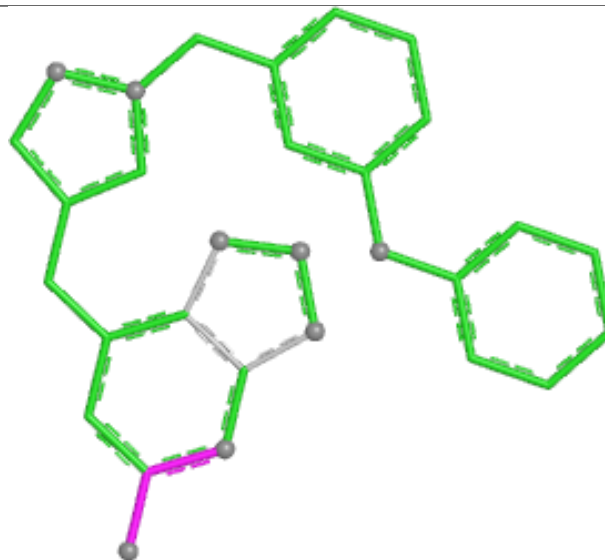




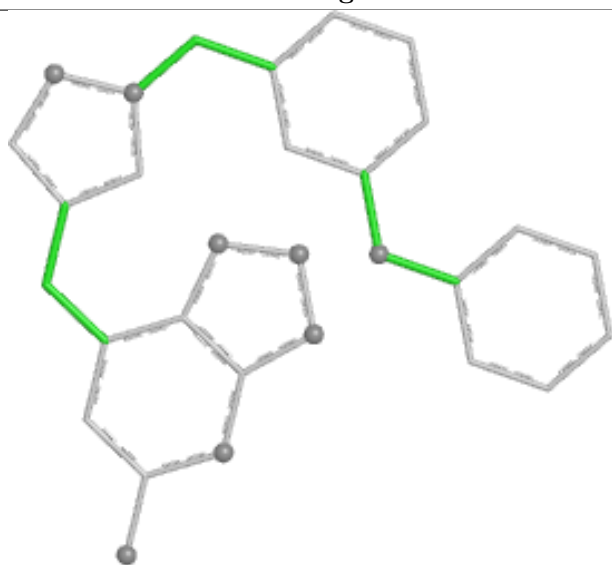
Ligand XSD G 605



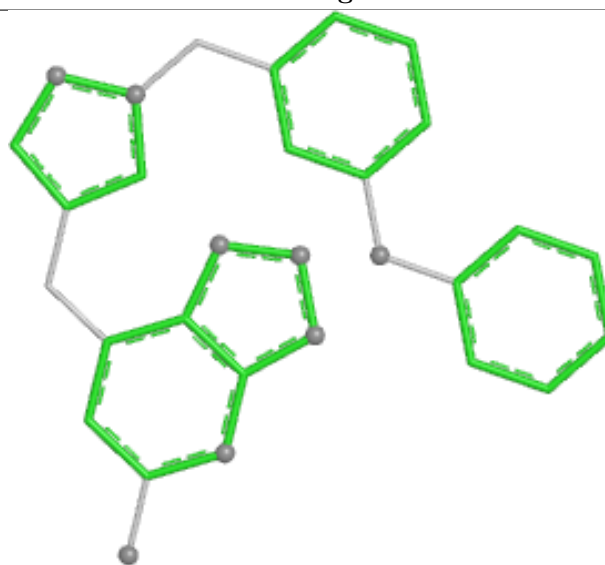
Bond lengths



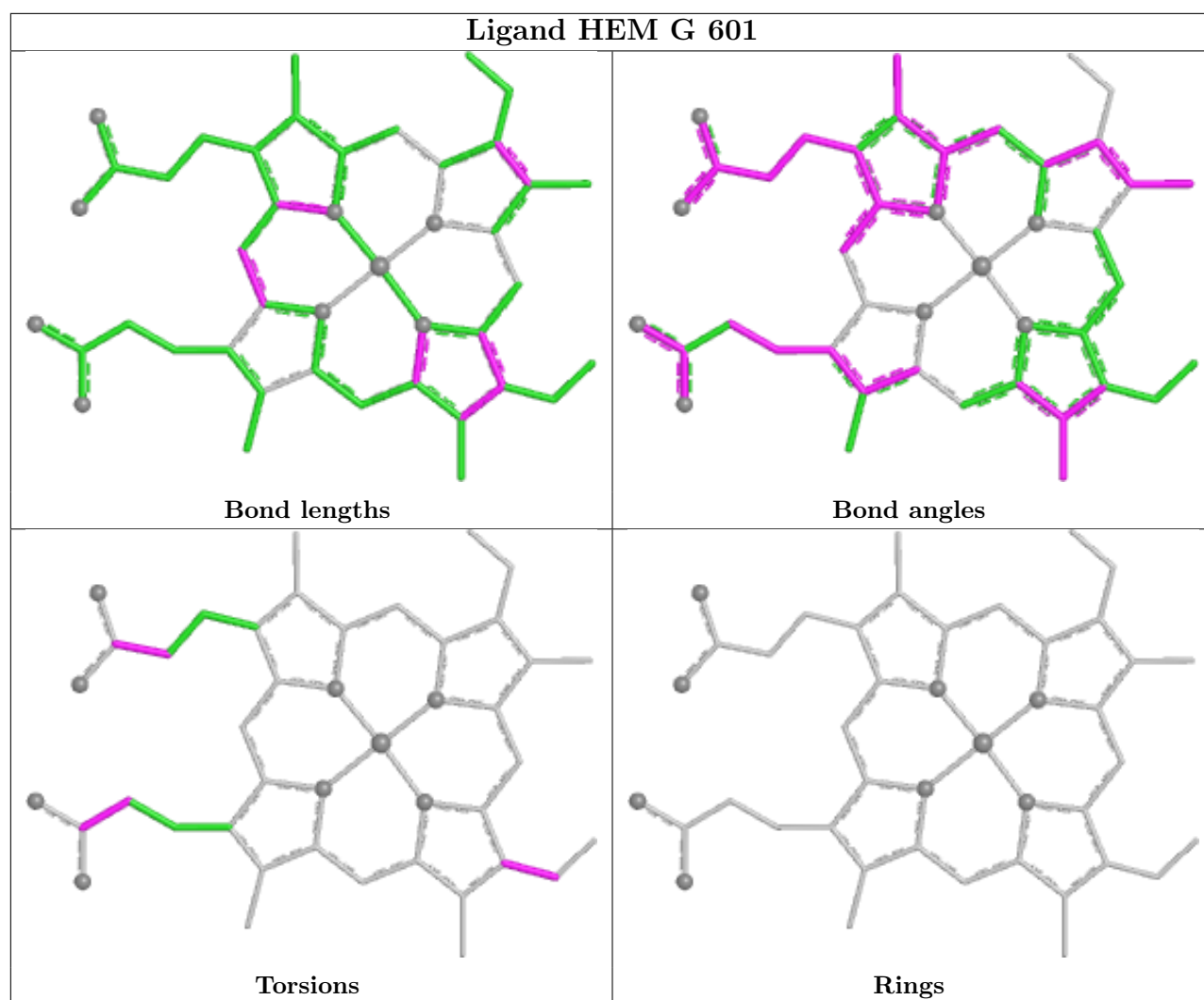
Bond angles



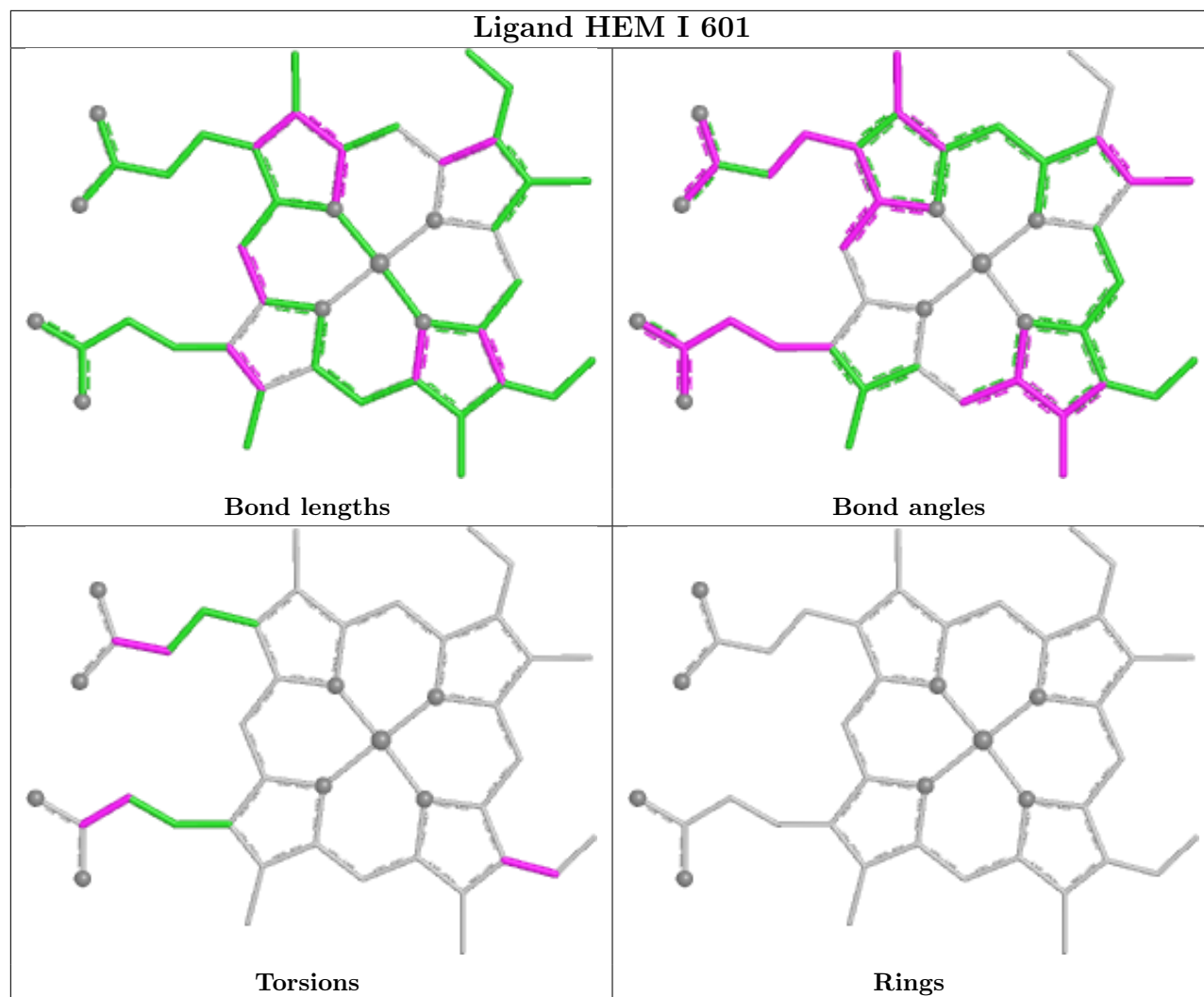
Torsions



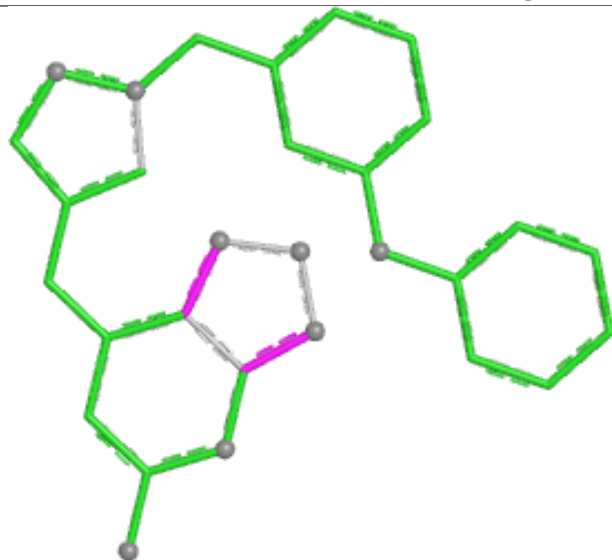
Rings



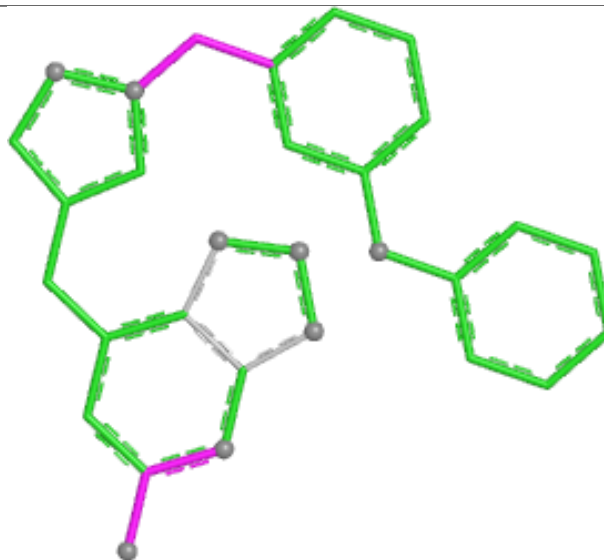
Ligand HEM I 601



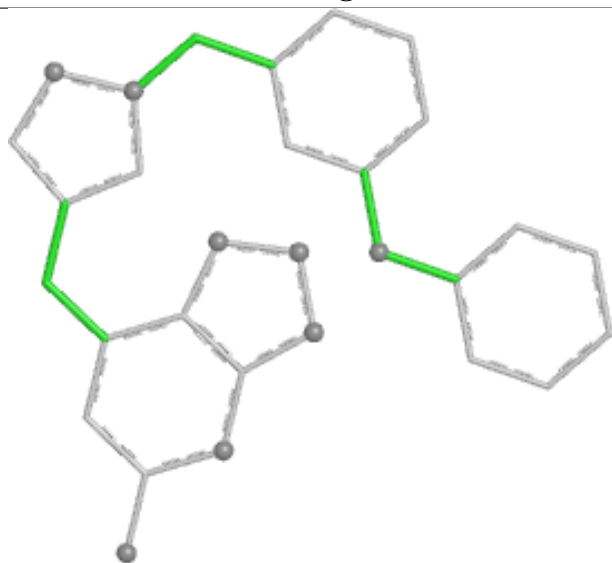
Ligand XSD I 605



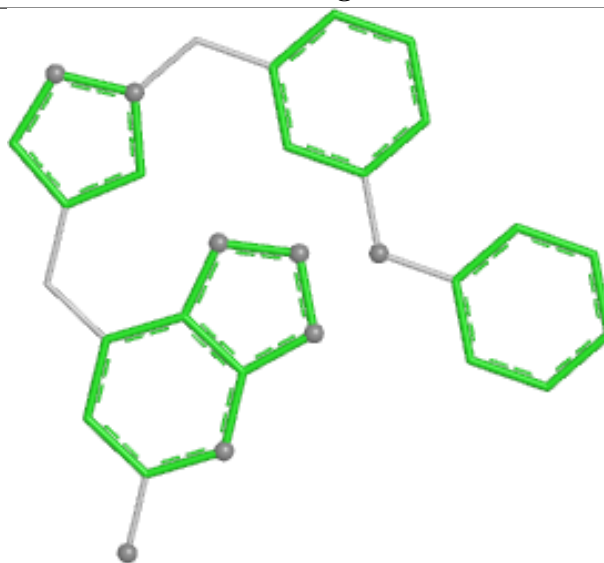
Bond lengths



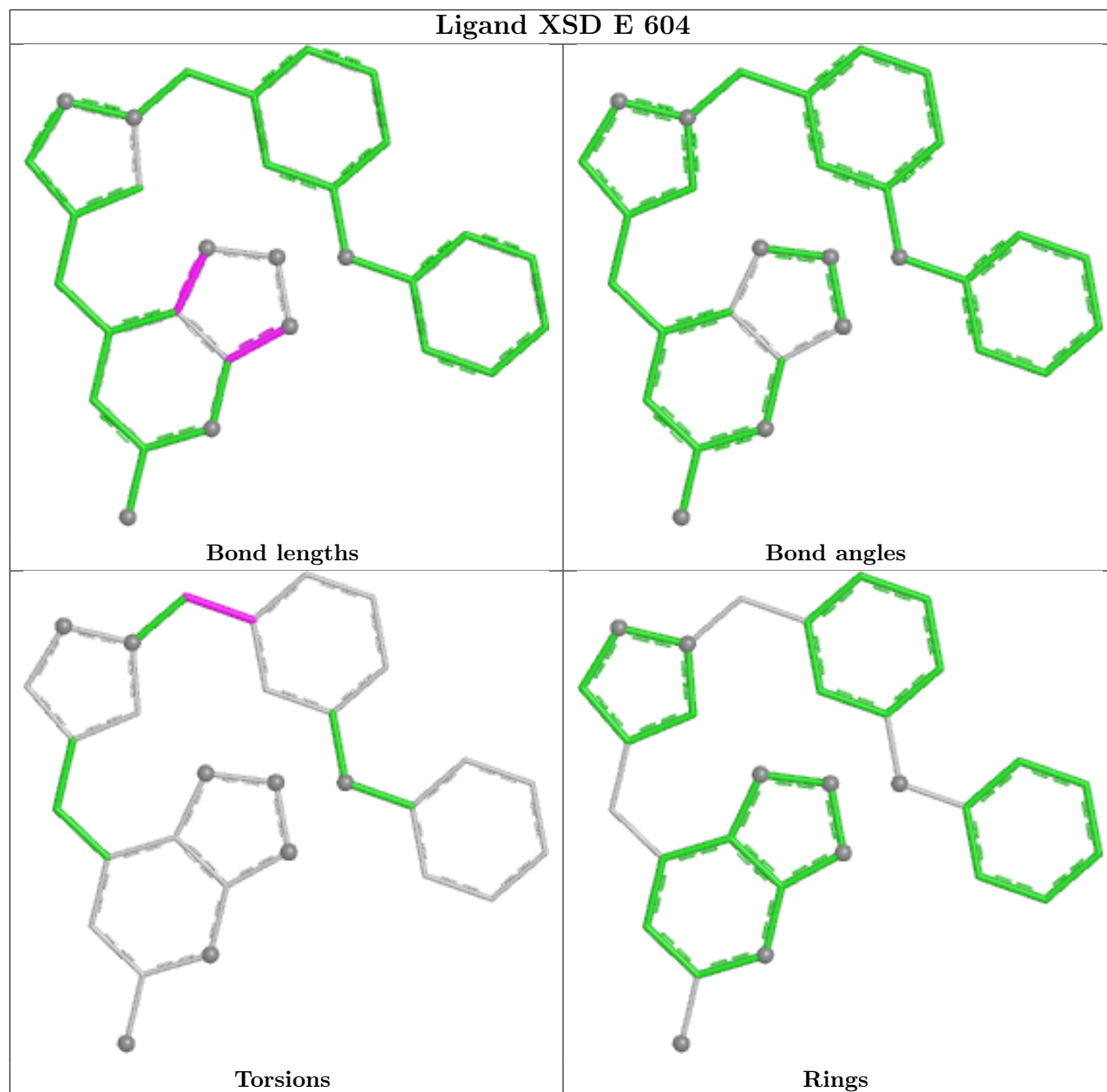
Bond angles



Torsions



Rings



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	103/105 (98%)	-0.35	3 (2%) 54 50	27, 40, 65, 90	1 (0%)
1	D	103/105 (98%)	-0.44	1 (0%) 79 78	26, 38, 62, 86	1 (0%)
1	F	103/105 (98%)	-0.46	4 (3%) 44 38	26, 39, 63, 94	1 (0%)
1	H	103/105 (98%)	-0.53	0 100 100	22, 37, 65, 69	1 (0%)
2	B	464/466 (99%)	-0.42	1 (0%) 92 93	23, 44, 64, 89	8 (1%)
2	E	465/466 (99%)	-0.46	2 (0%) 89 88	20, 41, 62, 76	11 (2%)
2	G	464/466 (99%)	-0.46	1 (0%) 92 93	23, 41, 62, 75	7 (1%)
2	I	464/466 (99%)	-0.43	1 (0%) 92 93	24, 41, 62, 78	9 (1%)
All	All	2269/2284 (99%)	-0.44	13 (0%) 85 84	20, 41, 63, 94	39 (1%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	114	ASN	4.6
2	I	114	ASN	3.4
1	F	3	GLU	2.7
1	A	4	GLN	2.6
1	D	3	GLU	2.5

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

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

6.3 Carbohydrates [i](#)

SUGAR-RSR INFOmissingINFO

6.4 Ligands ⓘ

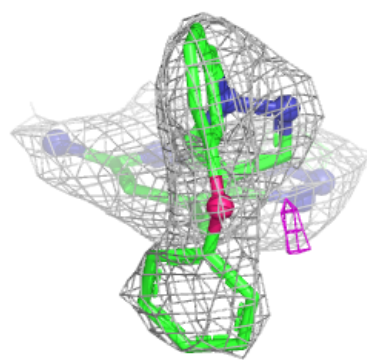
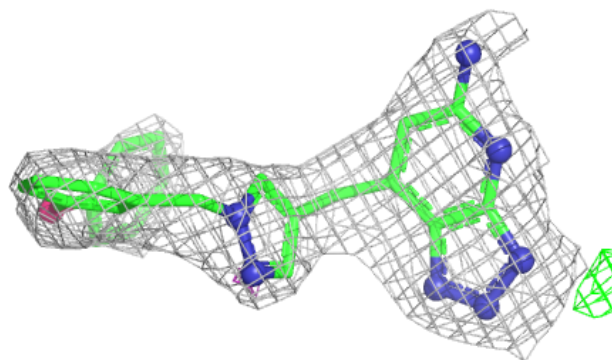
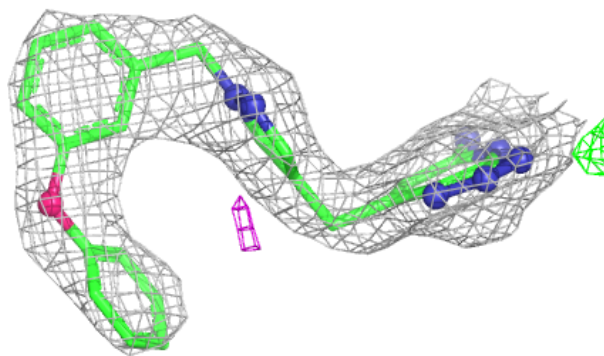
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	NAG	I	603	14/15	0.72	0.21	89,91,93,93	0
7	NAG	E	602	14/15	0.78	0.18	75,80,84,88	0
7	NAG	G	602	14/15	0.79	0.14	55,65,70,70	0
7	NAG	I	602	14/15	0.83	0.13	57,61,63,65	0
7	NAG	B	602	14/15	0.83	0.10	49,69,72,73	0
9	XSD	B	605	30/30	0.91	0.10	41,48,57,59	0
9	XSD	I	605	30/30	0.91	0.09	38,43,60,62	0
9	XSD	G	605	30/30	0.92	0.09	43,51,57,59	0
9	XSD	E	604	30/30	0.93	0.09	37,46,57,59	0
5	CL	G	604	1/1	0.95	0.18	43,43,43,43	0
5	CL	B	604	1/1	0.95	0.15	54,54,54,54	0
6	HEM	E	601	43/43	0.97	0.07	31,32,35,50	0
6	HEM	G	601	43/43	0.97	0.08	32,33,37,52	0
6	HEM	I	601	43/43	0.97	0.08	33,35,39,53	0
6	HEM	B	601	43/43	0.97	0.07	32,33,36,47	0
5	CL	A	201	1/1	0.98	0.06	31,31,31,31	0
5	CL	F	201	1/1	0.99	0.08	31,31,31,31	0
8	CA	G	603	1/1	0.99	0.03	34,34,34,34	0
8	CA	B	603	1/1	1.00	0.02	36,36,36,36	0
8	CA	I	604	1/1	1.00	0.05	32,32,32,32	0
8	CA	E	603	1/1	1.00	0.02	32,32,32,32	0

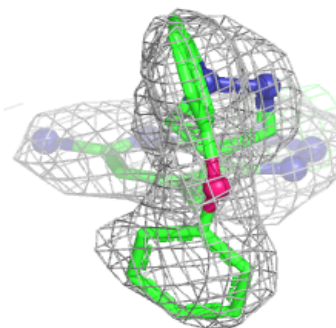
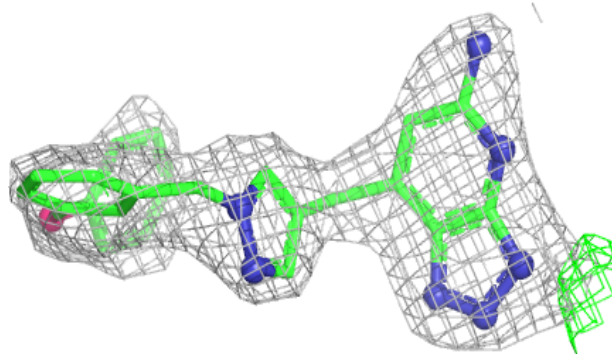
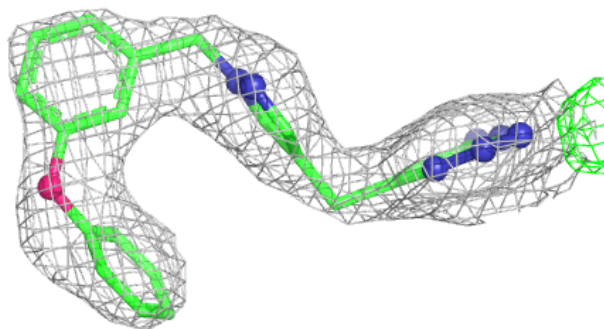
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around XSD B 605:

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

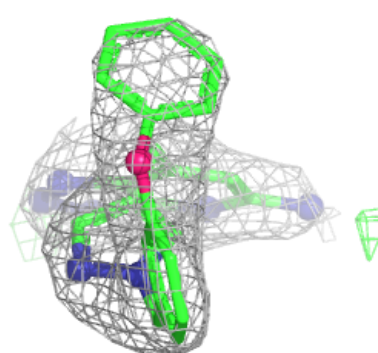
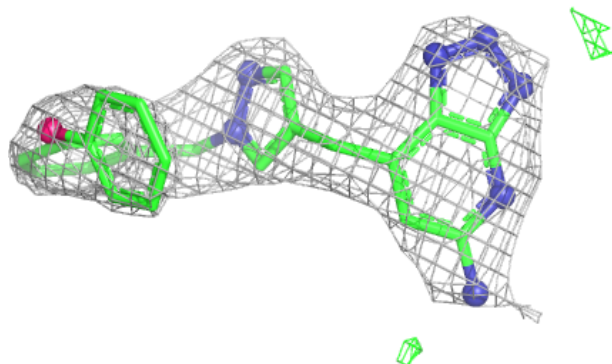
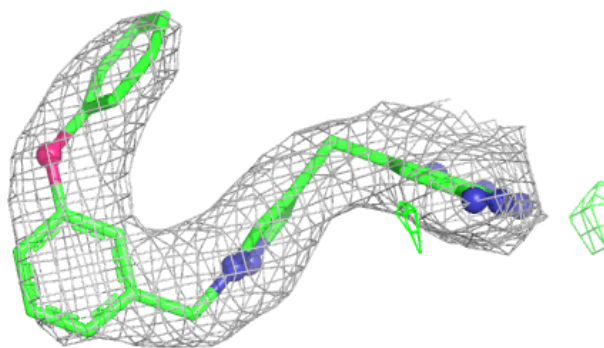
**Electron density around XSD I 605:**

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

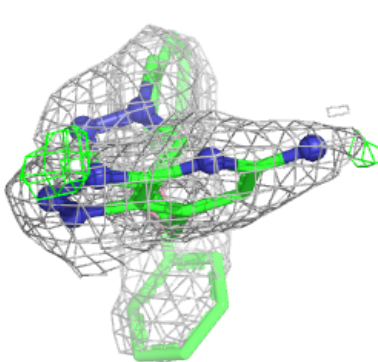
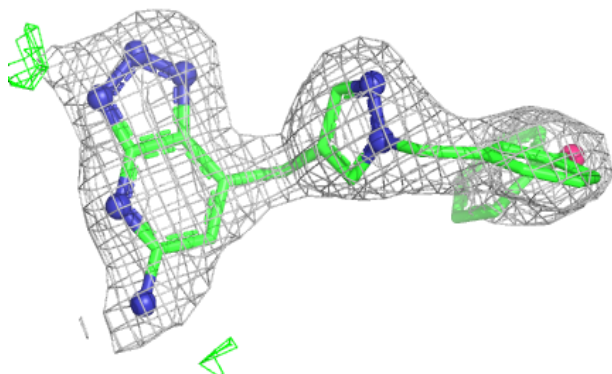
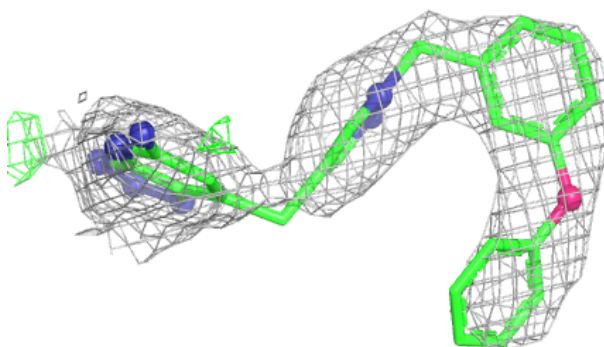


Electron density around XSD G 605:

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

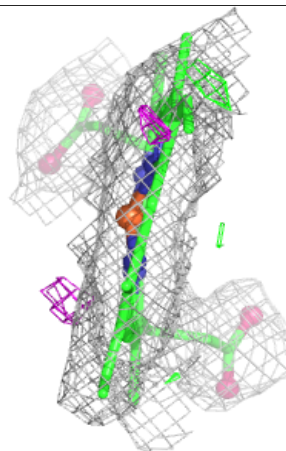
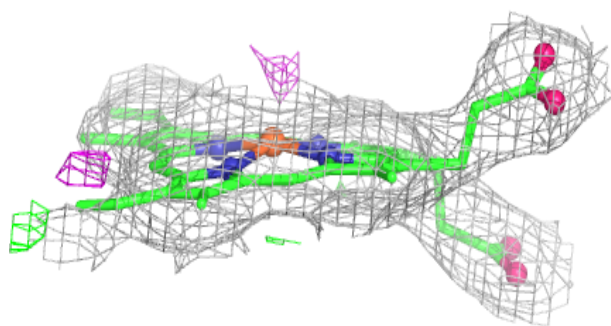
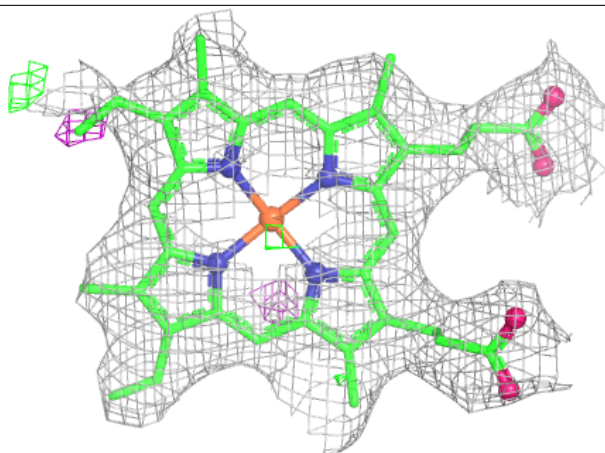
**Electron density around XSD E 604:**

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



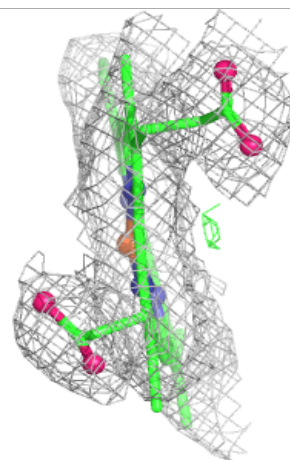
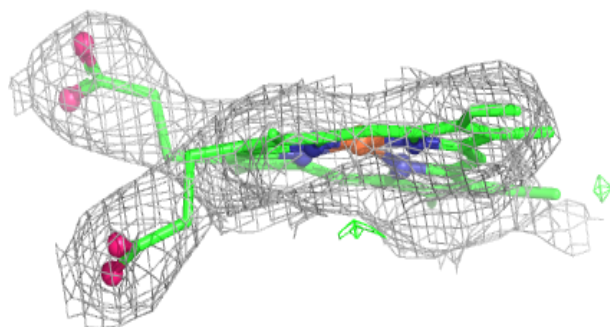
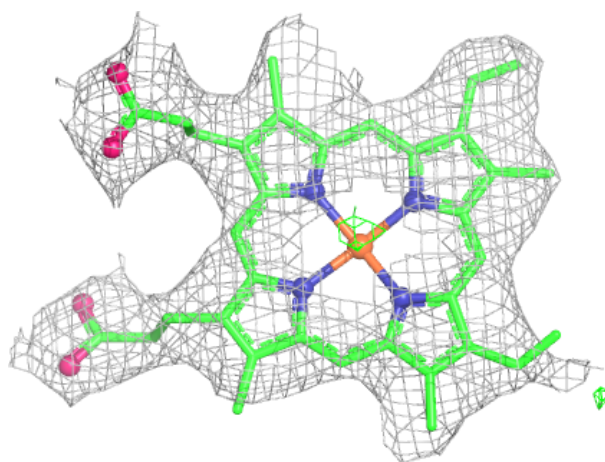
Electron density around HEM E 601:

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



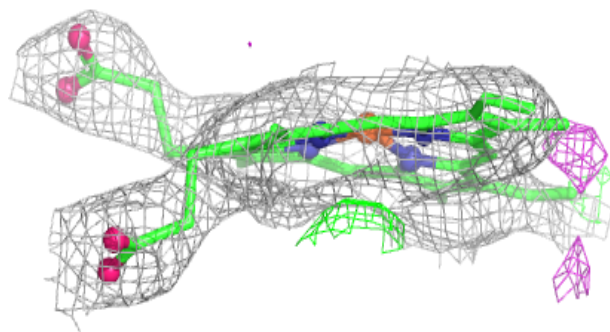
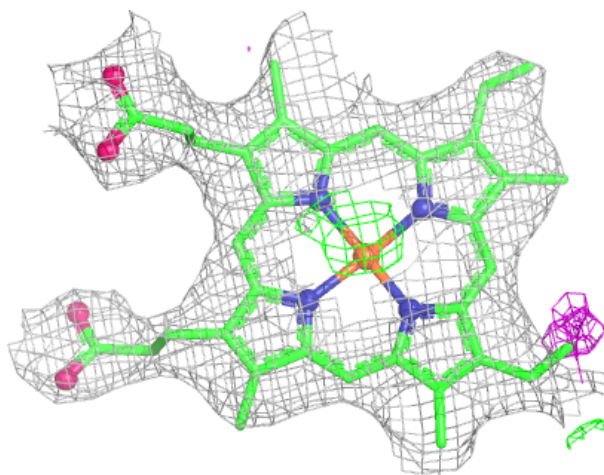
Electron density around HEM G 601:

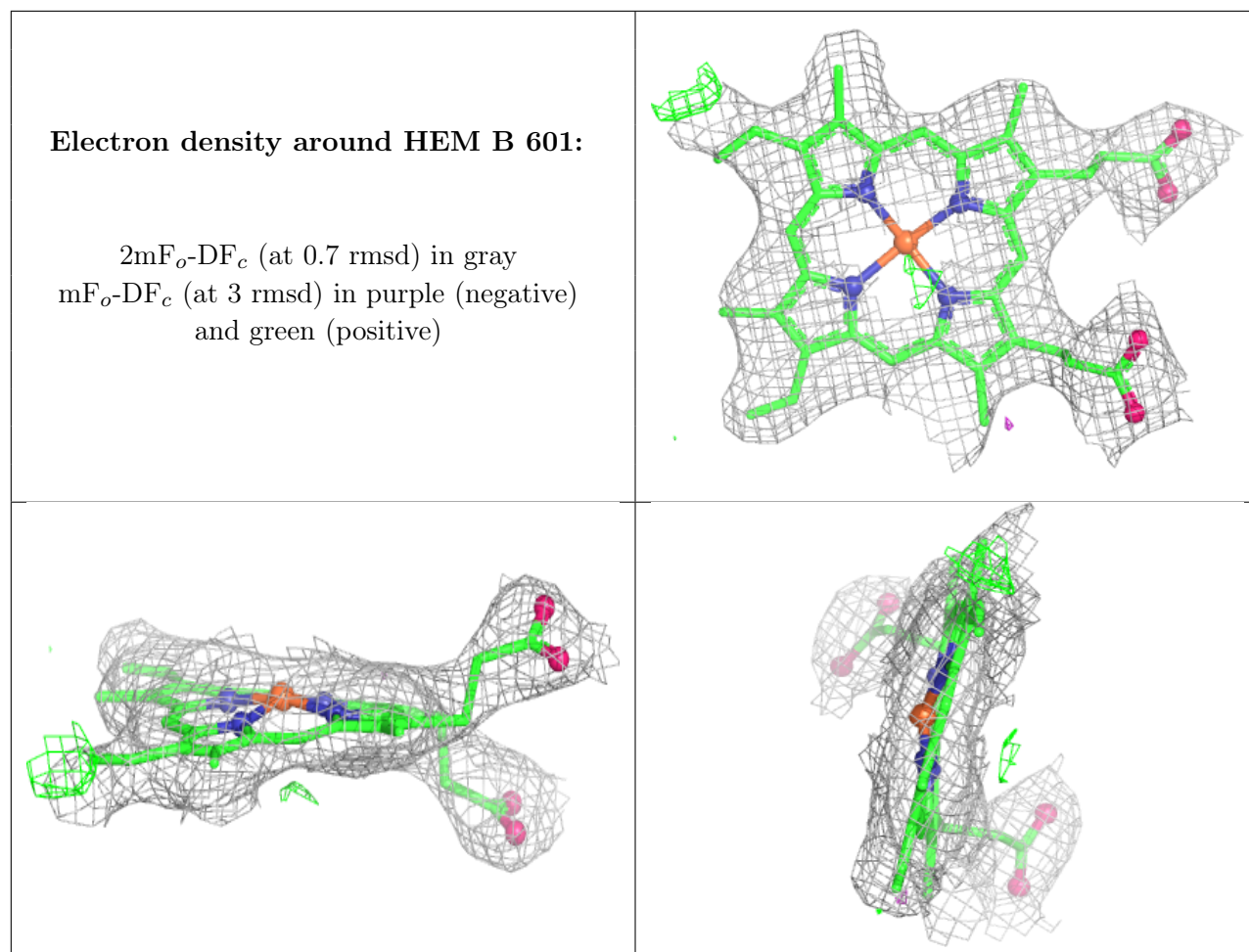
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM I 601:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.