



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:30 AM UTC

PDB ID : 3IS7 / pdb_00003is7
Title : Structure of mineralized Bfrb from Pseudomonas aeruginosa to 2.1A Resolution
Authors : Lovell, S.; Weeratunga, S.K.; Battaile, K.P.; Rivera, M.
Deposited on : 2009-08-25
Resolution : 2.10 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) : 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

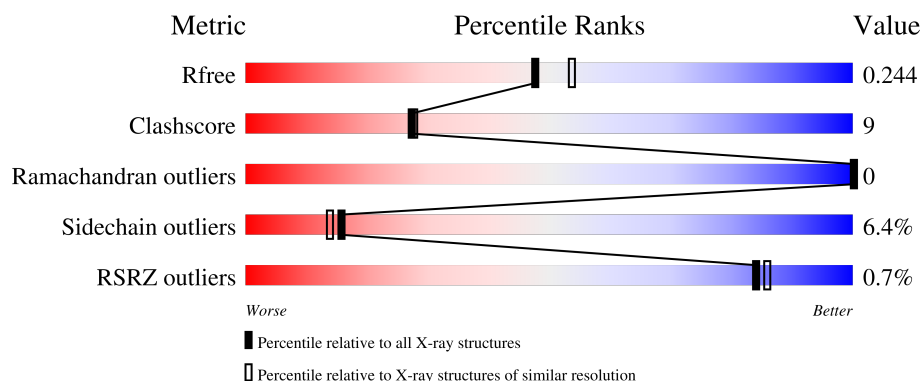
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	158	 80% 13% ...
1	B	158	 80% 15% ...
1	C	158	 82% 13% ...
1	D	158	 80% 13% ...
1	E	158	 82% 13% ...

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Mol	Chain	Length	Quality of chain
1	F	158	% 83% 13% ...
1	G	158	72% 23% ..
1	H	158	83% 14% ...
1	I	158	% 78% 15% ..
1	J	158	% 80% 16% ..
1	K	158	% 72% 19% 7% .
1	L	158	% 78% 16% ..
1	M	158	% 82% 13% ...
1	N	158	% 84% 11% ...
1	O	158	2% 77% 18% ..
1	P	158	% 80% 14% ..
1	Q	158	% 80% 15% ..
1	R	158	75% 22% ...
1	S	158	% 78% 15% 5% .
1	T	158	2% 75% 20% ..
1	U	158	% 80% 14% ...
1	V	158	% 75% 18% ...
1	W	158	75% 21% ..
1	X	158	% 80% 14% ...

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 32332 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 Bacterioferritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	0	0
			1251	791	213	241	6			
1	B	154	Total	C	N	O	S	0	0	0
			1262	798	216	242	6			
1	C	155	Total	C	N	O	S	0	0	0
			1261	797	215	243	6			
1	D	154	Total	C	N	O	S	0	0	0
			1266	801	217	242	6			
1	E	154	Total	C	N	O	S	0	0	0
			1259	797	214	242	6			
1	F	154	Total	C	N	O	S	0	0	0
			1260	797	215	242	6			
1	G	154	Total	C	N	O	S	0	0	0
			1266	801	217	242	6			
1	H	155	Total	C	N	O	S	0	0	0
			1270	804	217	243	6			
1	I	154	Total	C	N	O	S	0	0	0
			1262	798	216	242	6			
1	J	154	Total	C	N	O	S	0	0	0
			1259	796	215	242	6			
1	K	154	Total	C	N	O	S	0	0	0
			1267	801	218	242	6			
1	L	154	Total	C	N	O	S	0	0	0
			1263	799	216	242	6			
1	M	154	Total	C	N	O	S	0	0	0
			1260	798	216	240	6			
1	N	154	Total	C	N	O	S	0	0	0
			1260	798	214	242	6			
1	O	154	Total	C	N	O	S	0	0	0
			1259	796	215	242	6			
1	P	154	Total	C	N	O	S	0	0	0
			1262	798	216	242	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	154	Total 1260	C 798	N 214	O 242	S 6	0	0	0
1	R	155	Total 1272	C 805	N 218	O 243	S 6	0	0	0
1	S	154	Total 1259	C 796	N 215	O 242	S 6	0	0	0
1	T	154	Total 1259	C 796	N 215	O 242	S 6	0	0	0
1	U	154	Total 1264	C 799	N 217	O 242	S 6	0	0	0
1	V	154	Total 1260	C 797	N 215	O 242	S 6	0	0	0
1	W	155	Total 1274	C 806	N 219	O 243	S 6	0	0	0
1	X	154	Total 1263	C 799	N 216	O 242	S 6	0	0	0

- # HEM

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



WORLD WIDE
PDB
PROTEIN DATA BANK

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	J	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	N	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	P	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	Q	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	S	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	V	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	X	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	K 1	0	0
3	B	1	Total 1	K 1	0	0
3	C	1	Total 1	K 1	0	0
3	E	1	Total 1	K 1	0	0
3	G	1	Total 1	K 1	0	0
3	N	1	Total 1	K 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	68	Total 68	O 68	0	0
4	B	78	Total 78	O 78	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	72	Total 72	O 72	0	0
4	D	80	Total 80	O 80	0	0
4	E	53	Total 53	O 53	0	0
4	F	66	Total 66	O 66	0	0
4	G	74	Total 74	O 74	0	0
4	H	78	Total 78	O 78	0	0
4	I	61	Total 61	O 61	0	0
4	J	49	Total 49	O 49	0	0
4	K	67	Total 67	O 67	0	0
4	L	63	Total 63	O 63	0	0
4	M	60	Total 60	O 60	0	0
4	N	68	Total 68	O 68	0	0
4	O	59	Total 59	O 59	0	0
4	P	53	Total 53	O 53	0	0
4	Q	40	Total 40	O 40	0	0
4	R	43	Total 43	O 43	0	0
4	S	47	Total 47	O 47	0	0
4	T	46	Total 46	O 46	0	0
4	U	64	Total 64	O 64	0	0
4	V	52	Total 52	O 52	0	0
4	W	85	Total 85	O 85	0	0

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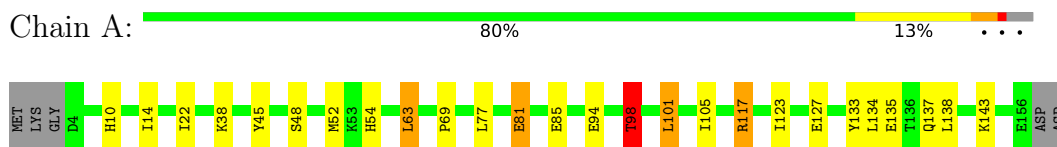
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	X	86	Total	O	0	0
			86	86		

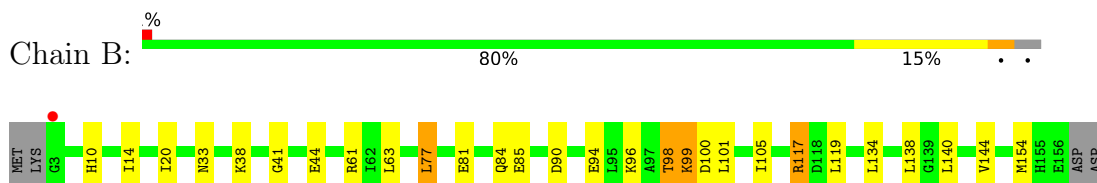
3 Residue-property plots [i](#)

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.

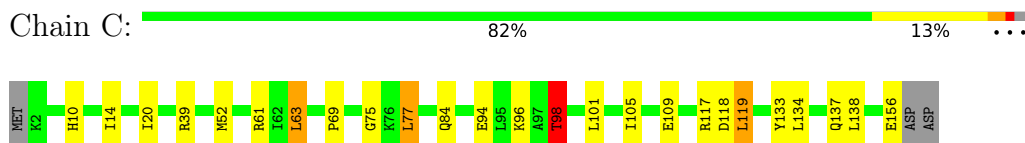
• Molecule 1: Bacterioferritin



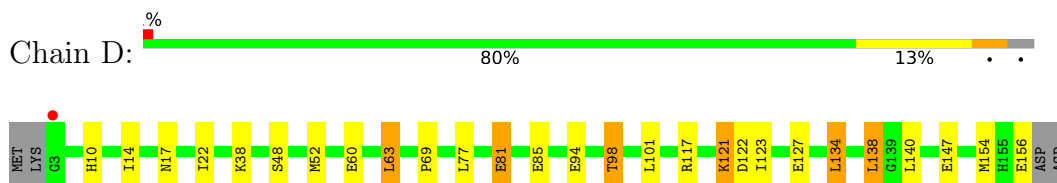
• Molecule 1: Bacterioferritin



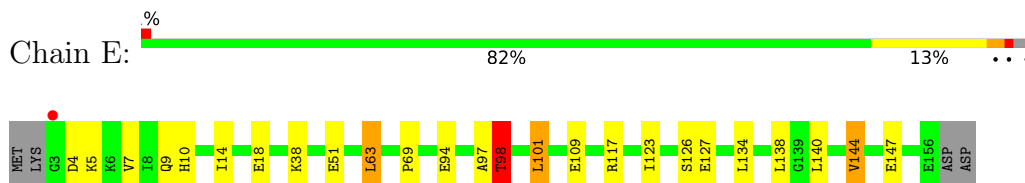
• Molecule 1: Bacterioferritin



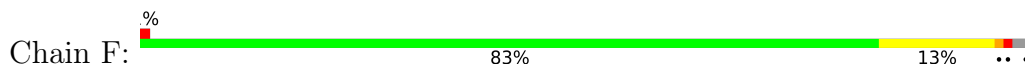
• Molecule 1: Bacterioferritin



• Molecule 1: Bacterioferritin

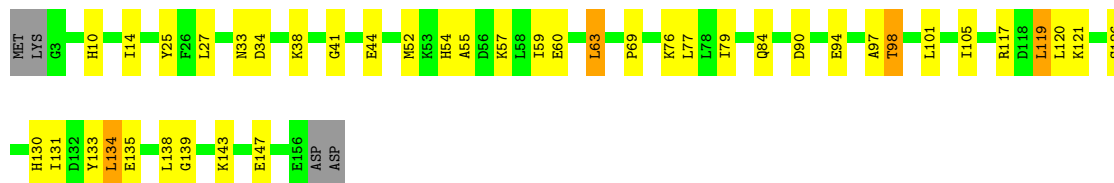


• Molecule 1: Bacterioferritin

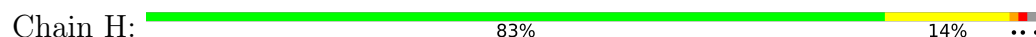




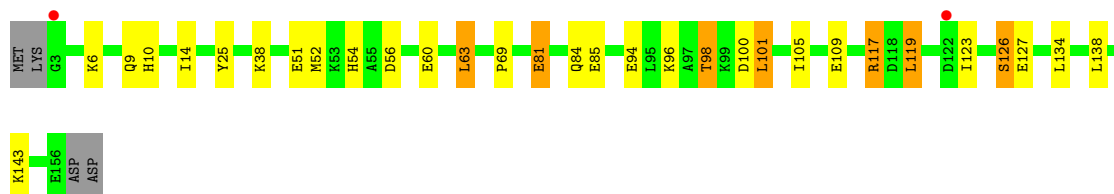
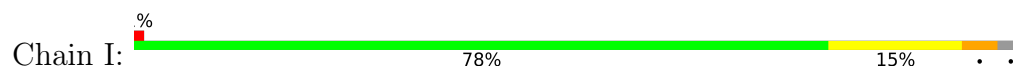
- Molecule 1: Bacterioferritin



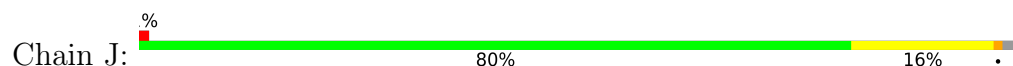
- Molecule 1: Bacterioferritin



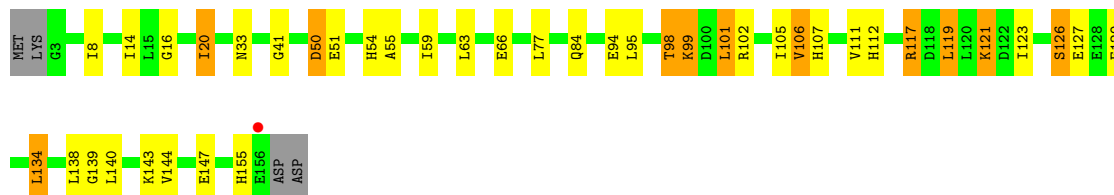
- Molecule 1: Bacterioferritin



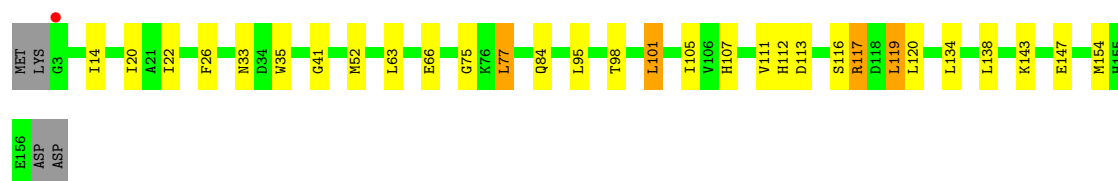
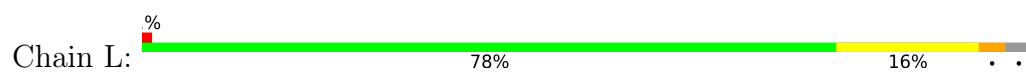
- Molecule 1: Bacterioferritin



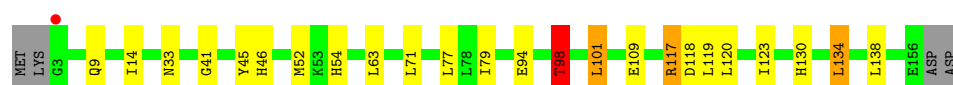
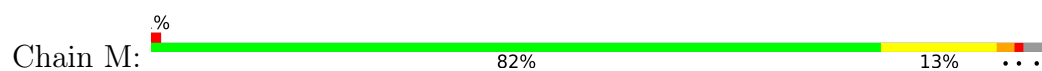
- Molecule 1: Bacterioferritin



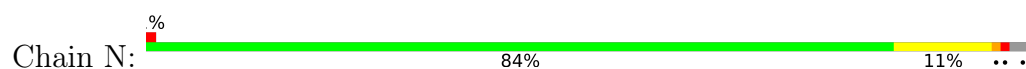
- Molecule 1: Bacterioferritin



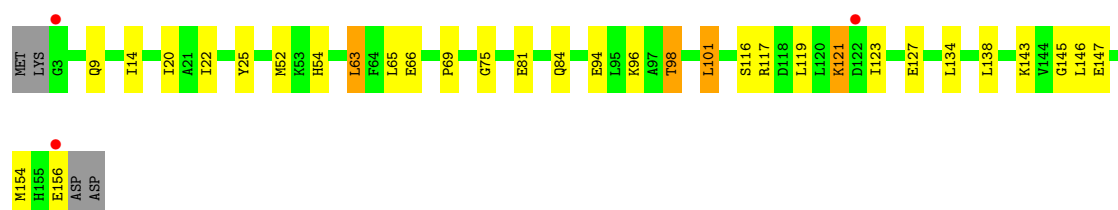
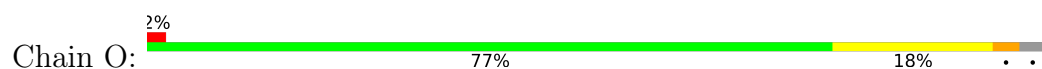
• Molecule 1: Bacterioferritin



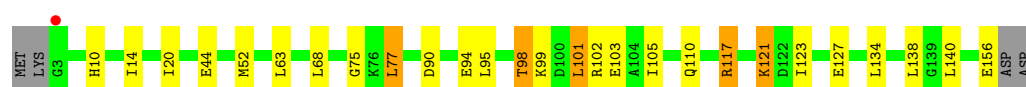
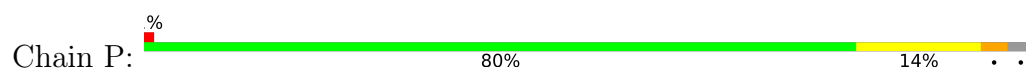
• Molecule 1: Bacterioferritin



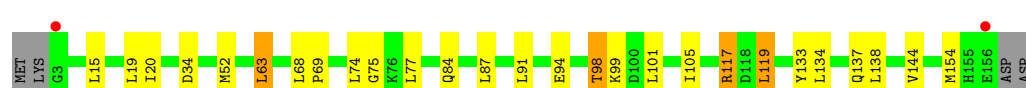
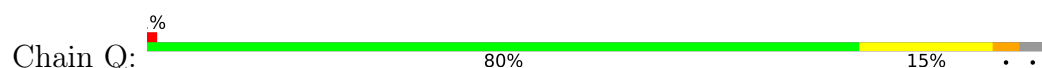
• Molecule 1: Bacterioferritin



• Molecule 1: Bacterioferritin



• Molecule 1: Bacterioferritin



• Molecule 1: Bacterioferritin

Chain R:  75% 22% ...



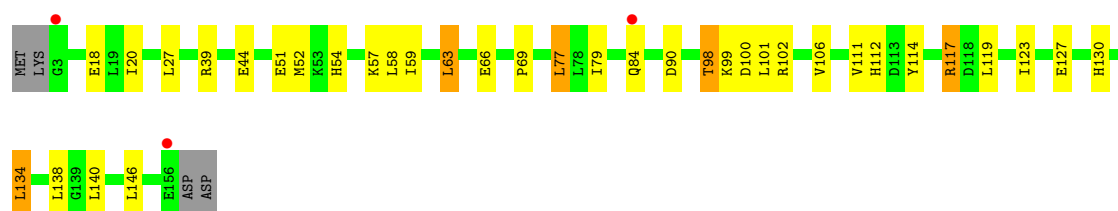
• Molecule 1: Bacterioferritin

Chain S:  78% 15% 5% .



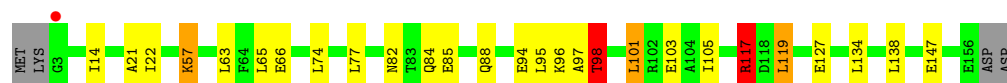
• Molecule 1: Bacterioferritin

Chain T:  75% 20% . .



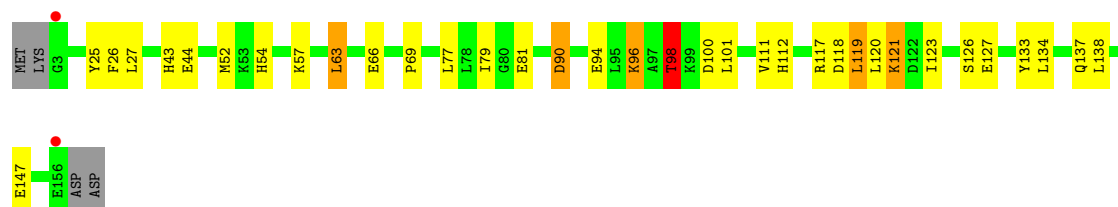
• Molecule 1: Bacterioferritin

Chain U:  80% 14% . . .



• Molecule 1: Bacterioferritin

Chain V:  75% 18% . . .



• Molecule 1: Bacterioferritin

Chain W:  75% 21% . .



Category	Number of Genes
MET	100
LYS	100
G3	100
I14	100
I20	100
L40	100
E44	100
D50	100
E51	100
M52	100
K53	100
K57	100
E60	100
L63	100
P69	100
L77	100
E81	100
E85	100
D90	100
E94	100
T98	100
L101	100
Q110	100
L119	100
L120	100
K121	100
S126	100
L134	100
L138	100
G139	100
K143	100
V144	100
M154	100
H155	100
E156	100
ASP	100

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	125.81Å 202.76Å 207.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.04 – 2.10 47.04 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.04-2.10) 99.8 (47.04-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.10Å)	Xtriage
Refinement program	REFMAC refmac _5.5.0066	Depositor
R, R_{free}	0.193 , 0.244 0.200 , 0.244	Depositor DCC
R_{free} test set	15512 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.002 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32332	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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: K, HEM

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	1.23	0/1272	1.11	2/1717 (0.1%)
1	B	1.29	1/1283 (0.1%)	1.07	0/1729
1	C	1.24	1/1282 (0.1%)	1.12	2/1730 (0.1%)
1	D	1.33	2/1287 (0.2%)	1.08	0/1733
1	E	1.30	2/1280 (0.2%)	1.08	1/1726 (0.1%)
1	F	1.33	0/1281	1.09	3/1727 (0.2%)
1	G	1.31	3/1287 (0.2%)	1.13	0/1733
1	H	1.26	1/1291 (0.1%)	1.17	2/1739 (0.1%)
1	I	1.24	0/1283	1.08	1/1729 (0.1%)
1	J	1.26	0/1280	1.07	1/1726 (0.1%)
1	K	1.28	3/1288 (0.2%)	1.08	3/1734 (0.2%)
1	L	1.23	1/1284 (0.1%)	1.07	0/1730
1	M	1.21	1/1281 (0.1%)	1.09	2/1726 (0.1%)
1	N	1.29	3/1281 (0.2%)	1.10	3/1727 (0.2%)
1	O	1.23	0/1280	1.07	1/1726 (0.1%)
1	P	1.24	1/1283 (0.1%)	1.08	0/1729
1	Q	1.23	3/1281 (0.2%)	1.10	2/1727 (0.1%)
1	R	1.17	0/1293	1.07	1/1741 (0.1%)
1	S	1.22	1/1280 (0.1%)	1.09	2/1726 (0.1%)
1	T	1.29	3/1280 (0.2%)	1.07	0/1726
1	U	1.23	1/1285 (0.1%)	1.12	2/1731 (0.1%)
1	V	1.22	1/1281 (0.1%)	1.10	3/1727 (0.2%)
1	W	1.24	0/1295	1.09	1/1743 (0.1%)
1	X	1.27	2/1284 (0.2%)	1.12	2/1730 (0.1%)
All	All	1.26	30/30802 (0.1%)	1.09	34/41512 (0.1%)

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	22	ILE	CA-CB	-8.00	1.45	1.54
1	T	59	ILE	CA-CB	-7.18	1.46	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	126	SER	N-CA	-6.46	1.38	1.46
1	Q	144	VAL	CA-CB	6.39	1.61	1.54
1	G	97	ALA	CA-CB	6.37	1.63	1.53

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	98	THR	N-CA-CB	-7.03	99.76	110.16
1	H	98	THR	N-CA-CB	-6.88	99.97	110.16
1	F	117	ARG	NE-CZ-NH1	6.67	128.17	121.50
1	V	90	ASP	N-CA-C	-6.64	104.04	111.28
1	C	98	THR	N-CA-CB	-6.45	100.61	110.16

There are no chirality outliers.

There are no planarity outliers.

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	1251	0	1211	20	0
1	B	1262	0	1234	21	0
1	C	1261	0	1218	16	0
1	D	1266	0	1245	21	0
1	E	1259	0	1222	13	0
1	F	1260	0	1227	11	0
1	G	1266	0	1245	21	0
1	H	1270	0	1242	15	0
1	I	1262	0	1234	27	0
1	J	1259	0	1225	20	0
1	K	1267	0	1250	34	0
1	L	1263	0	1236	20	0
1	M	1260	0	1234	17	0
1	N	1260	0	1224	14	0
1	O	1259	0	1225	21	0
1	P	1262	0	1234	15	0
1	Q	1260	0	1224	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	1272	0	1249	26	0
1	S	1259	0	1225	25	0
1	T	1259	0	1225	28	0
1	U	1264	0	1241	21	0
1	V	1260	0	1227	31	0
1	W	1274	0	1256	23	0
1	X	1263	0	1236	19	0
2	A	43	0	30	6	0
2	C	43	0	30	10	0
2	F	43	0	30	10	0
2	H	43	0	30	10	0
2	J	43	0	30	12	0
2	K	43	0	30	8	0
2	N	43	0	30	9	0
2	P	43	0	30	8	0
2	Q	43	0	30	7	0
2	S	43	0	30	6	0
2	V	43	0	30	5	0
2	X	43	0	30	9	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	N	1	0	0	0	0
4	A	68	0	0	6	0
4	B	78	0	0	5	0
4	C	72	0	0	3	0
4	D	80	0	0	4	0
4	E	53	0	0	3	0
4	F	66	0	0	5	0
4	G	74	0	0	7	0
4	H	78	0	0	5	0
4	I	61	0	0	6	0
4	J	49	0	0	5	0
4	K	67	0	0	8	0
4	L	63	0	0	4	0
4	M	60	0	0	6	0
4	N	68	0	0	2	0
4	O	59	0	0	8	0
4	P	53	0	0	1	0
4	Q	40	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	R	43	0	0	7	0
4	S	47	0	0	5	0
4	T	46	0	0	3	0
4	U	64	0	0	6	0
4	V	52	0	0	6	0
4	W	85	0	0	7	0
4	X	86	0	0	6	0
All	All	32332	0	29949	554	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 9.

The worst 5 of 554 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:J:98:THR:HG21	4:J:452:HOH:O	1.18	1.27
1:L:119:LEU:C	1:L:119:LEU:HD23	1.55	1.24
1:I:98:THR:HG21	4:I:1235:HOH:O	1.38	1.22
1:V:119:LEU:C	1:V:119:LEU:HD23	1.66	1.19
1:K:99:LYS:HB3	1:K:99:LYS:NZ	1.60	1.11

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	151/158 (96%)	150 (99%)	1 (1%)	0	100	100
1	B	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	C	153/158 (97%)	152 (99%)	1 (1%)	0	100	100
1	D	152/158 (96%)	150 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	152/158 (96%)	149 (98%)	3 (2%)	0	100	100
1	F	152/158 (96%)	152 (100%)	0	0	100	100
1	G	152/158 (96%)	152 (100%)	0	0	100	100
1	H	153/158 (97%)	153 (100%)	0	0	100	100
1	I	152/158 (96%)	150 (99%)	2 (1%)	0	100	100
1	J	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	K	152/158 (96%)	152 (100%)	0	0	100	100
1	L	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	M	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	N	152/158 (96%)	150 (99%)	2 (1%)	0	100	100
1	O	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	P	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	Q	152/158 (96%)	150 (99%)	2 (1%)	0	100	100
1	R	153/158 (97%)	152 (99%)	1 (1%)	0	100	100
1	S	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	T	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
1	U	152/158 (96%)	149 (98%)	3 (2%)	0	100	100
1	V	152/158 (96%)	150 (99%)	2 (1%)	0	100	100
1	W	153/158 (97%)	153 (100%)	0	0	100	100
1	X	152/158 (96%)	151 (99%)	1 (1%)	0	100	100
All	All	3651/3792 (96%)	3623 (99%)	28 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	135/144 (94%)	127 (94%)	8 (6%)	18	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	137/144 (95%)	129 (94%)	8 (6%)	18	16
1	C	135/144 (94%)	125 (93%)	10 (7%)	13	10
1	D	138/144 (96%)	130 (94%)	8 (6%)	18	16
1	E	135/144 (94%)	128 (95%)	7 (5%)	21	20
1	F	136/144 (94%)	127 (93%)	9 (7%)	15	13
1	G	138/144 (96%)	128 (93%)	10 (7%)	13	11
1	H	137/144 (95%)	131 (96%)	6 (4%)	25	26
1	I	137/144 (95%)	126 (92%)	11 (8%)	11	8
1	J	136/144 (94%)	130 (96%)	6 (4%)	25	26
1	K	139/144 (96%)	127 (91%)	12 (9%)	10	7
1	L	137/144 (95%)	129 (94%)	8 (6%)	18	16
1	M	136/144 (94%)	128 (94%)	8 (6%)	18	16
1	N	135/144 (94%)	128 (95%)	7 (5%)	21	20
1	O	136/144 (94%)	127 (93%)	9 (7%)	15	13
1	P	137/144 (95%)	128 (93%)	9 (7%)	15	13
1	Q	135/144 (94%)	125 (93%)	10 (7%)	13	10
1	R	138/144 (96%)	129 (94%)	9 (6%)	15	13
1	S	136/144 (94%)	127 (93%)	9 (7%)	15	13
1	T	136/144 (94%)	128 (94%)	8 (6%)	18	16
1	U	138/144 (96%)	129 (94%)	9 (6%)	15	13
1	V	136/144 (94%)	124 (91%)	12 (9%)	9	7
1	W	139/144 (96%)	131 (94%)	8 (6%)	18	16
1	X	137/144 (95%)	128 (93%)	9 (7%)	15	13
All	All	3279/3456 (95%)	3069 (94%)	210 (6%)	16	14

5 of 210 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	119	LEU
1	Q	119	LEU
1	W	134	LEU
1	O	81	GLU
1	P	101	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	137	GLN
1	R	33	ASN
1	O	54	HIS
1	P	137	GLN
1	S	33	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	$\# Z > 2$
2	HEM	A	159	1	50,50,50	1.74	11 (22%)	67,82,82	1.73	14 (20%)
2	HEM	F	159	1	50,50,50	2.03	9 (18%)	67,82,82	2.12	23 (34%)
2	HEM	P	159	1	50,50,50	1.99	8 (16%)	67,82,82	2.10	25 (37%)
2	HEM	J	159	1	50,50,50	1.90	8 (16%)	67,82,82	2.22	23 (34%)
2	HEM	N	159	1	50,50,50	1.74	10 (20%)	67,82,82	1.61	14 (20%)
2	HEM	X	159	1	50,50,50	1.71	7 (14%)	67,82,82	1.60	12 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	V	159	1	50,50,50	1.95	11 (22%)	67,82,82	1.96	20 (29%)
2	HEM	C	159	1	50,50,50	1.86	8 (16%)	67,82,82	1.99	24 (35%)
2	HEM	H	159	1	50,50,50	1.70	8 (16%)	67,82,82	1.79	16 (23%)
2	HEM	Q	159	1	50,50,50	1.76	8 (16%)	67,82,82	1.80	18 (26%)
2	HEM	S	159	1	50,50,50	1.82	9 (18%)	67,82,82	1.78	16 (23%)
2	HEM	K	159	1	50,50,50	1.87	9 (18%)	67,82,82	1.76	19 (28%)

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	HEM	A	159	1	-	4/14/54/54	-
2	HEM	F	159	1	-	5/14/54/54	-
2	HEM	P	159	1	-	4/14/54/54	-
2	HEM	J	159	1	-	4/14/54/54	-
2	HEM	N	159	1	-	4/14/54/54	-
2	HEM	X	159	1	-	5/14/54/54	-
2	HEM	V	159	1	-	5/14/54/54	-
2	HEM	C	159	1	-	5/14/54/54	-
2	HEM	H	159	1	-	4/14/54/54	-
2	HEM	Q	159	1	-	4/14/54/54	-
2	HEM	S	159	1	-	4/14/54/54	-
2	HEM	K	159	1	-	4/14/54/54	-

The worst 5 of 106 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	159	HEM	FE-ND	8.06	2.19	1.94
2	P	159	HEM	C3D-C2D	7.68	1.53	1.36
2	K	159	HEM	C3D-C2D	7.34	1.52	1.36
2	V	159	HEM	C3D-C2D	7.34	1.52	1.36
2	S	159	HEM	C3D-C2D	7.16	1.52	1.36

The worst 5 of 224 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	159	HEM	CHC-C4B-NB	7.44	132.43	124.42
2	V	159	HEM	C4D-ND-C1D	7.04	113.54	105.21
2	F	159	HEM	C4D-ND-C1D	6.55	112.96	105.21
2	Q	159	HEM	C4D-ND-C1D	6.48	112.88	105.21
2	P	159	HEM	C4D-ND-C1D	5.88	112.17	105.21

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	159	HEM	C4C-C3C-CAC-CBC
2	V	159	HEM	C4C-C3C-CAC-CBC
2	P	159	HEM	CAD-CBD-CGD-O2D
2	V	159	HEM	CAD-CBD-CGD-O2D
2	H	159	HEM	CAD-CBD-CGD-O2D

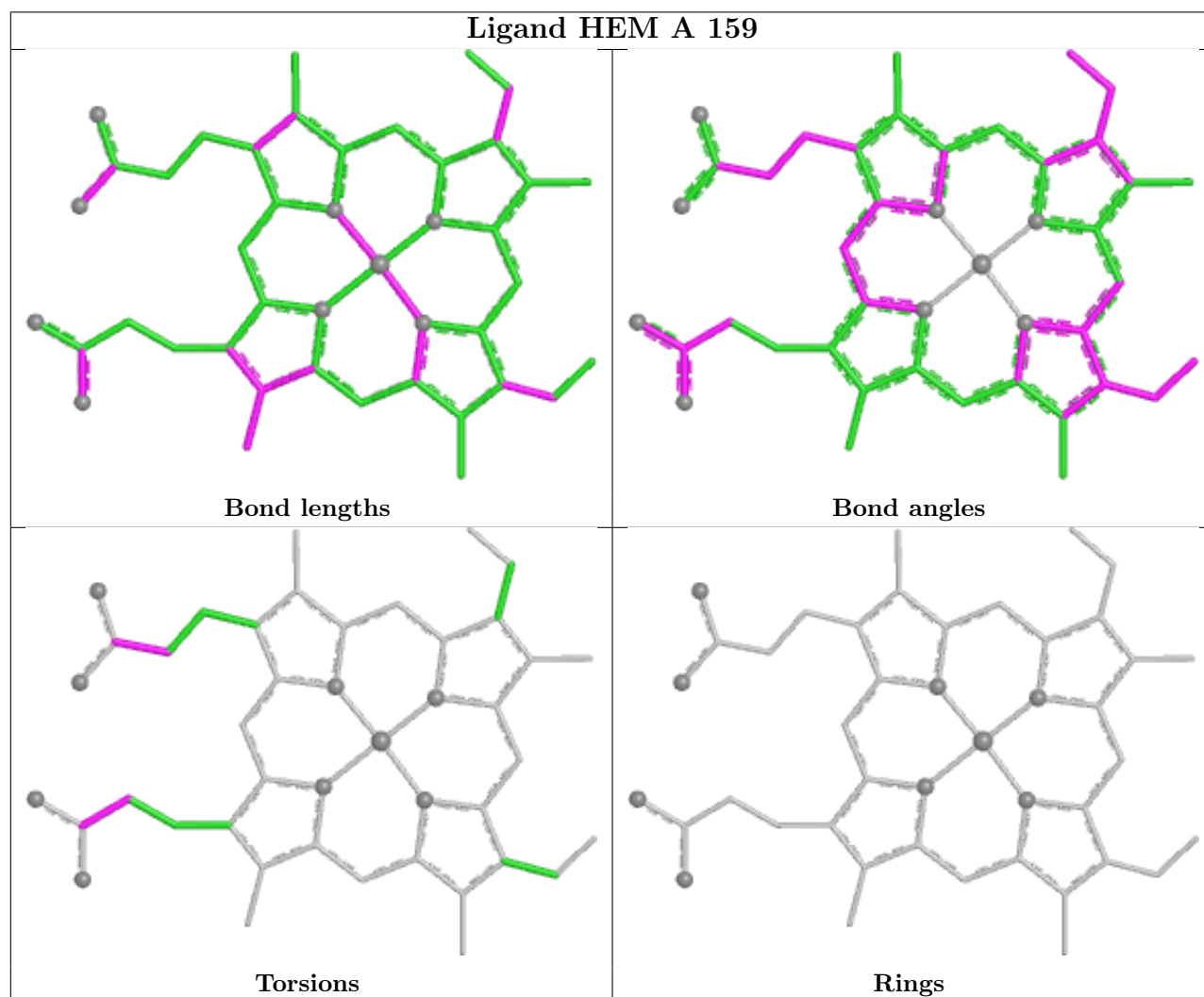
There are no ring outliers.

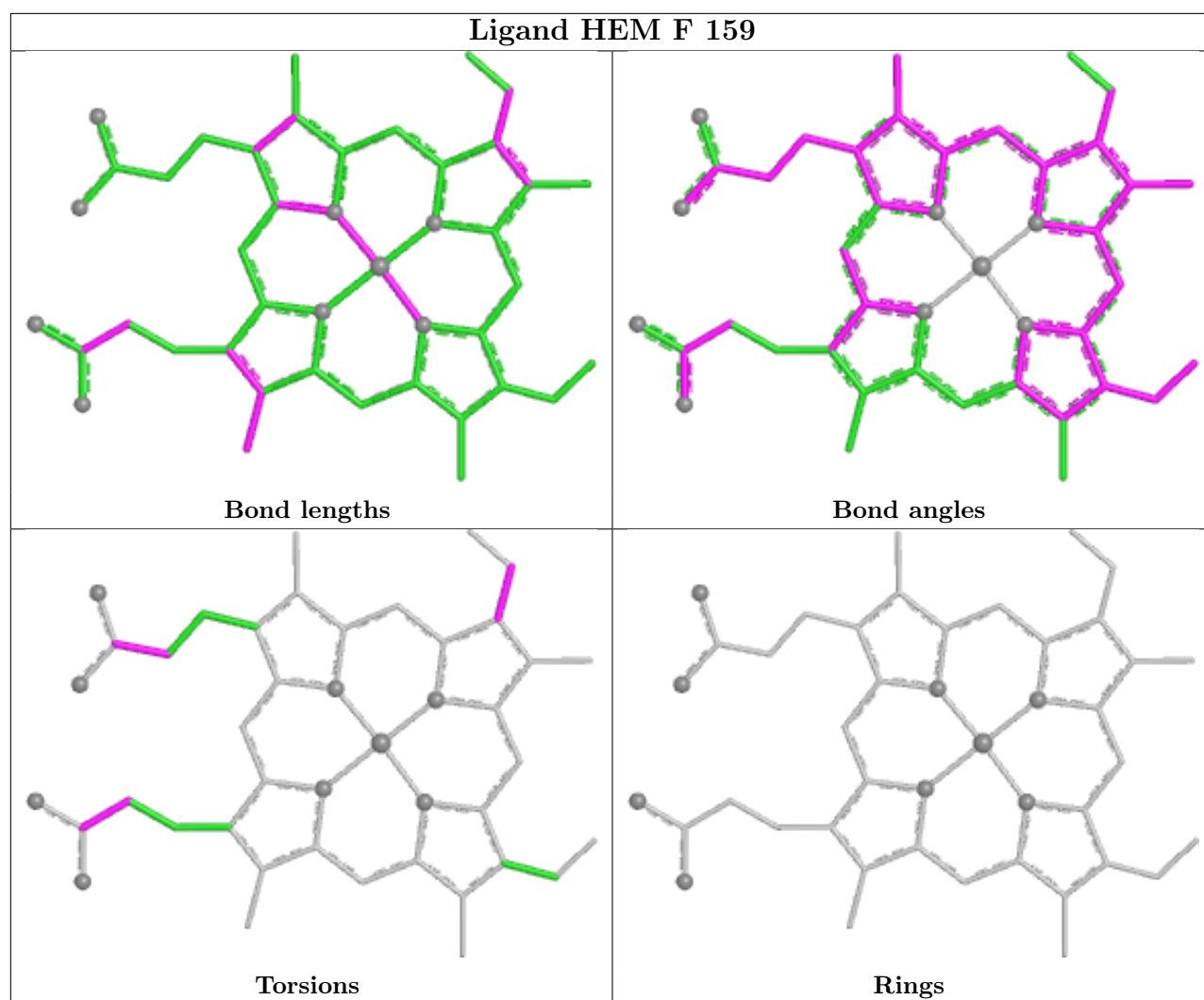
12 monomers are involved in 100 short contacts:

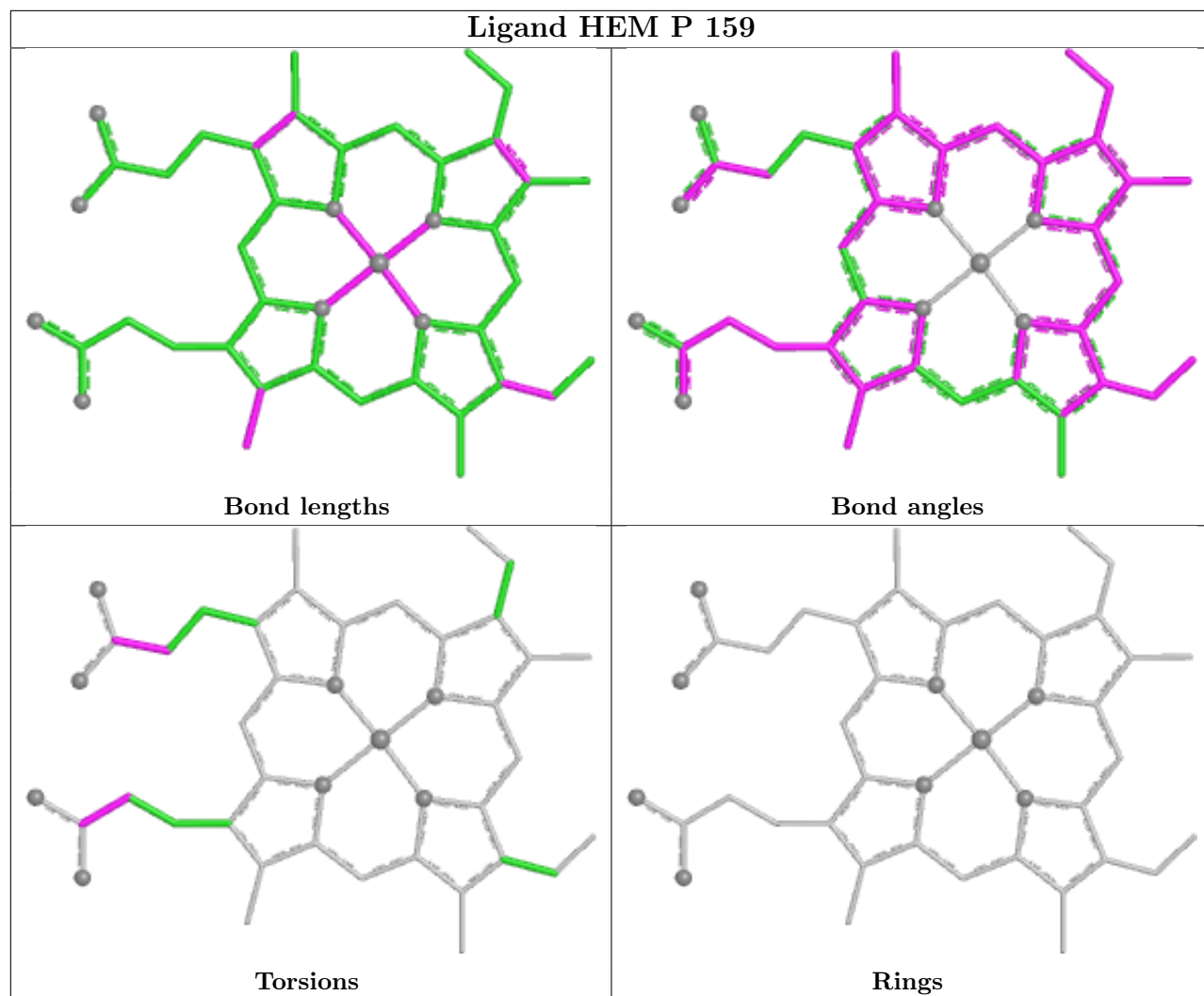
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	159	HEM	6	0
2	F	159	HEM	10	0
2	P	159	HEM	8	0
2	J	159	HEM	12	0
2	N	159	HEM	9	0
2	X	159	HEM	9	0
2	V	159	HEM	5	0
2	C	159	HEM	10	0
2	H	159	HEM	10	0
2	Q	159	HEM	7	0
2	S	159	HEM	6	0
2	K	159	HEM	8	0

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.

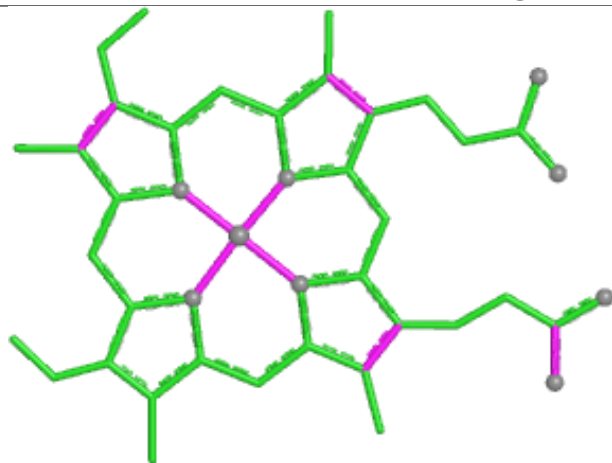
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



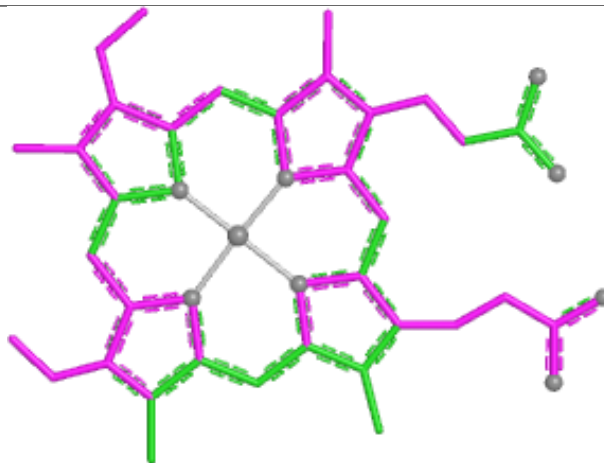




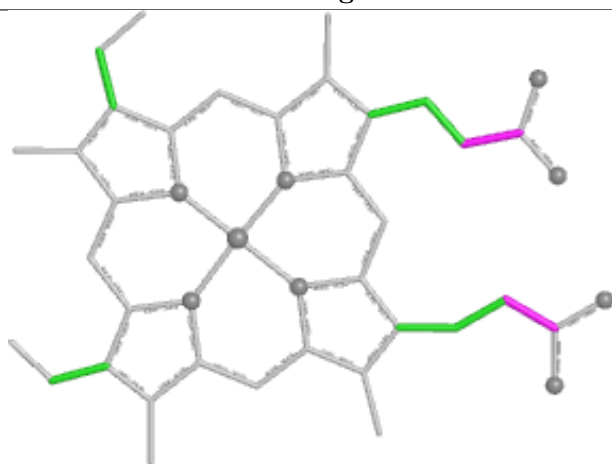
Ligand HEM J 159



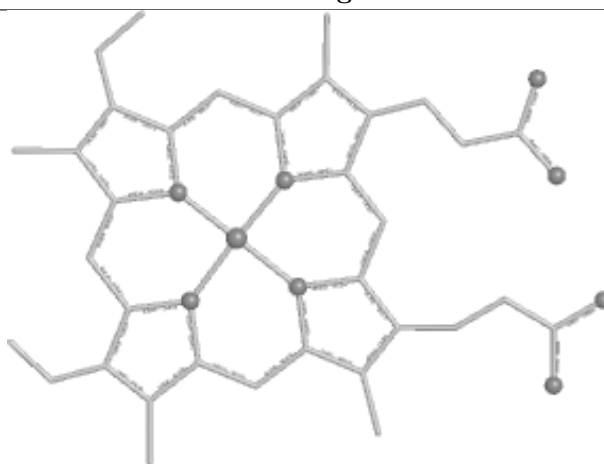
Bond lengths



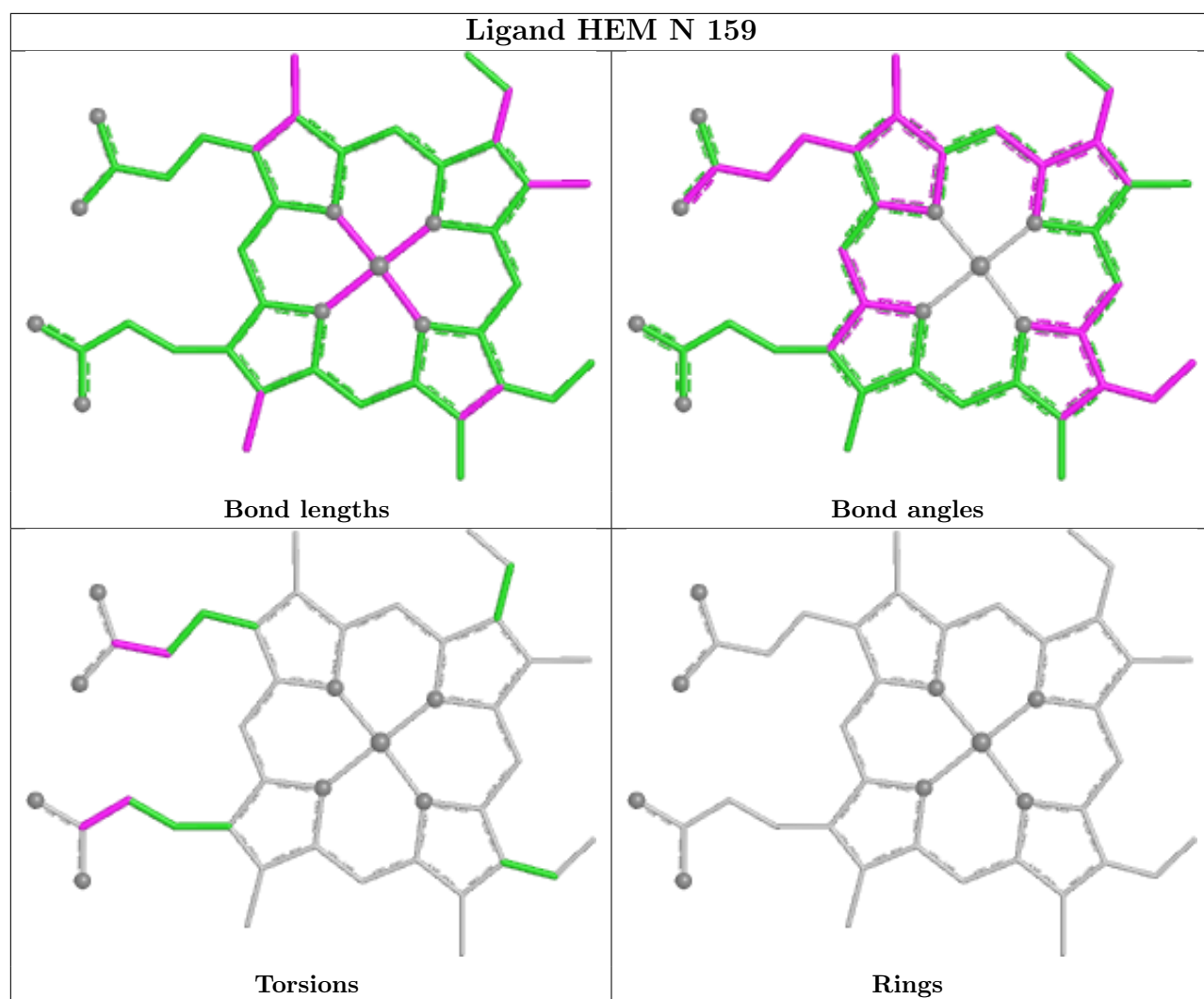
Bond angles

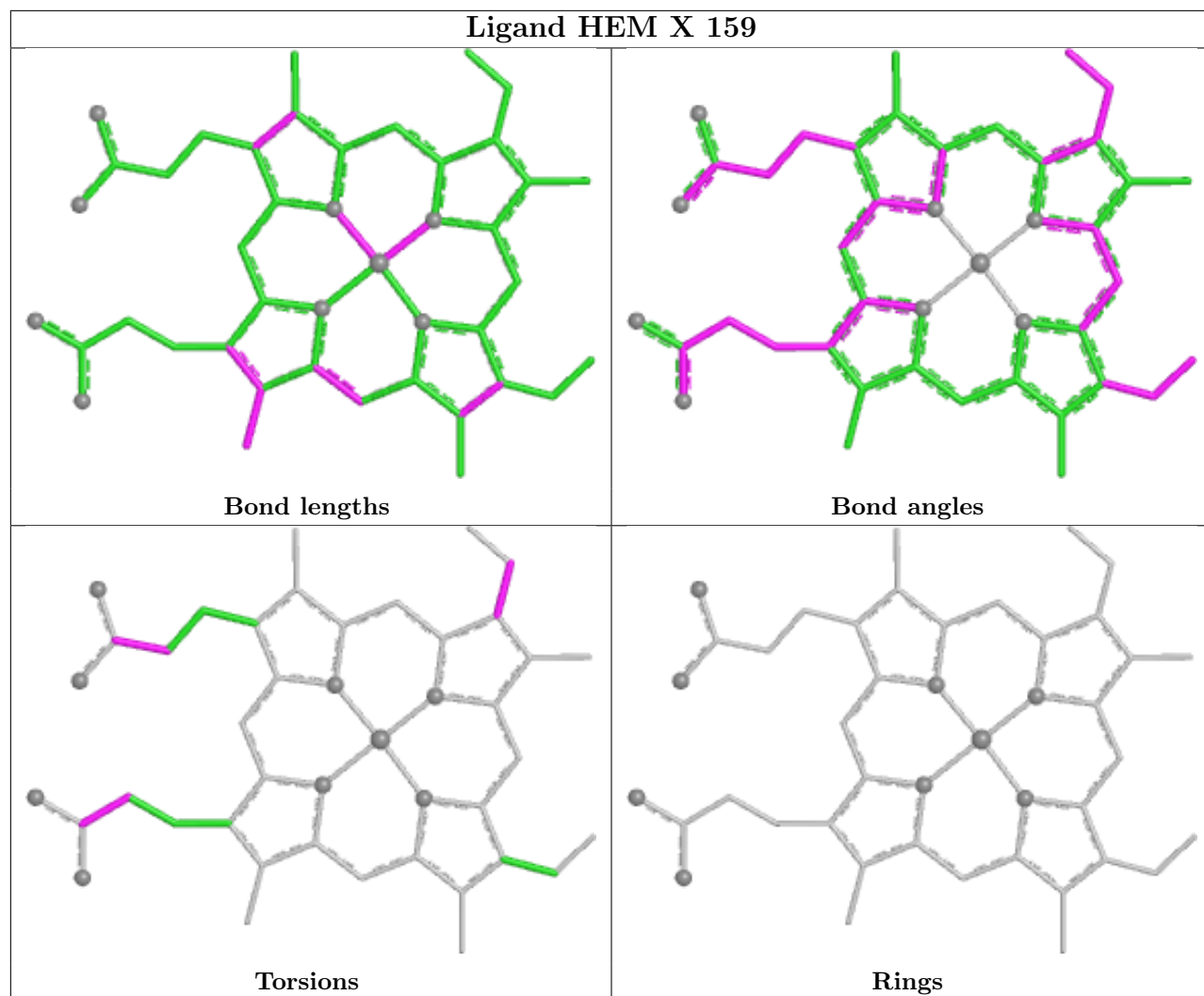


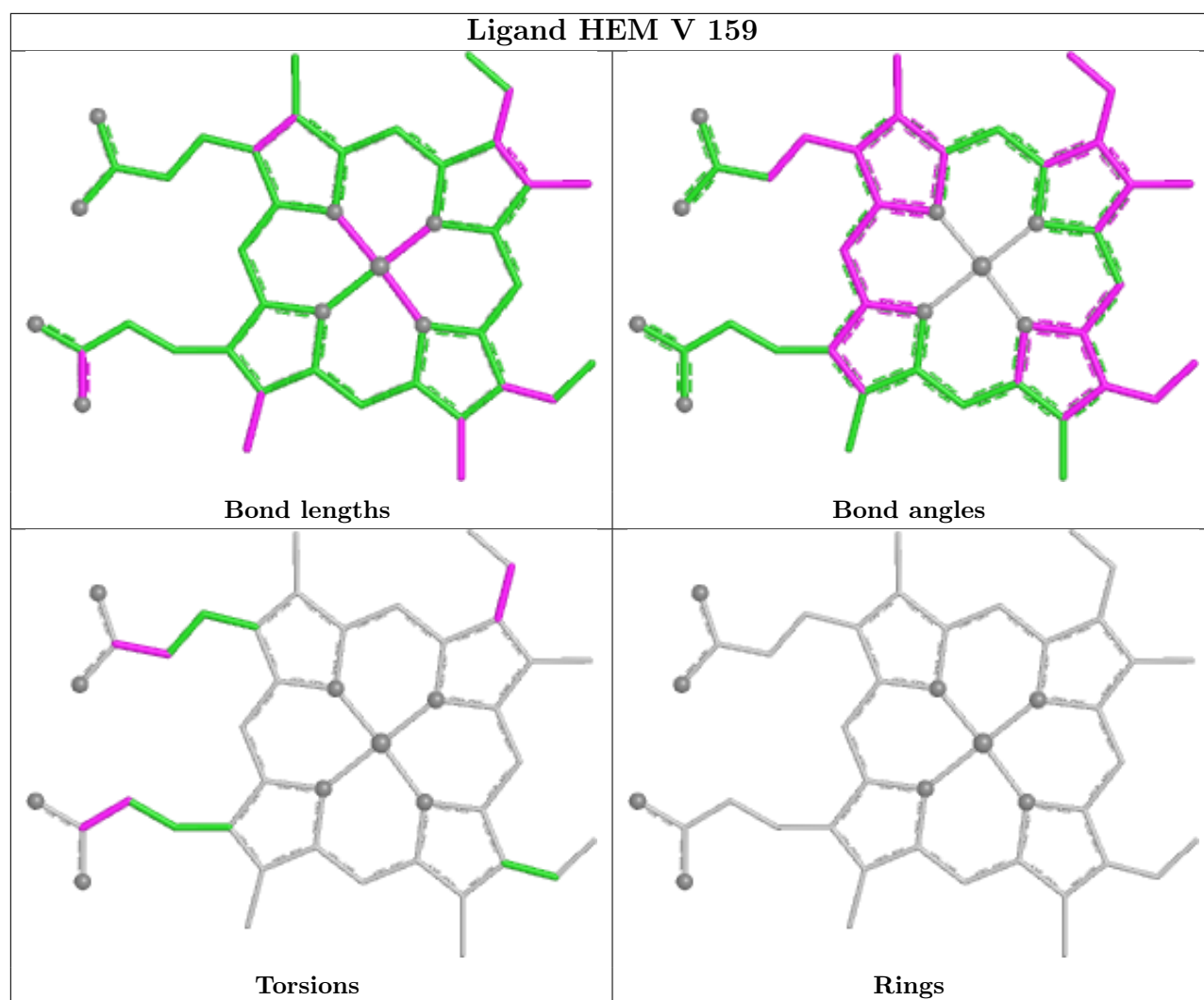
Torsions

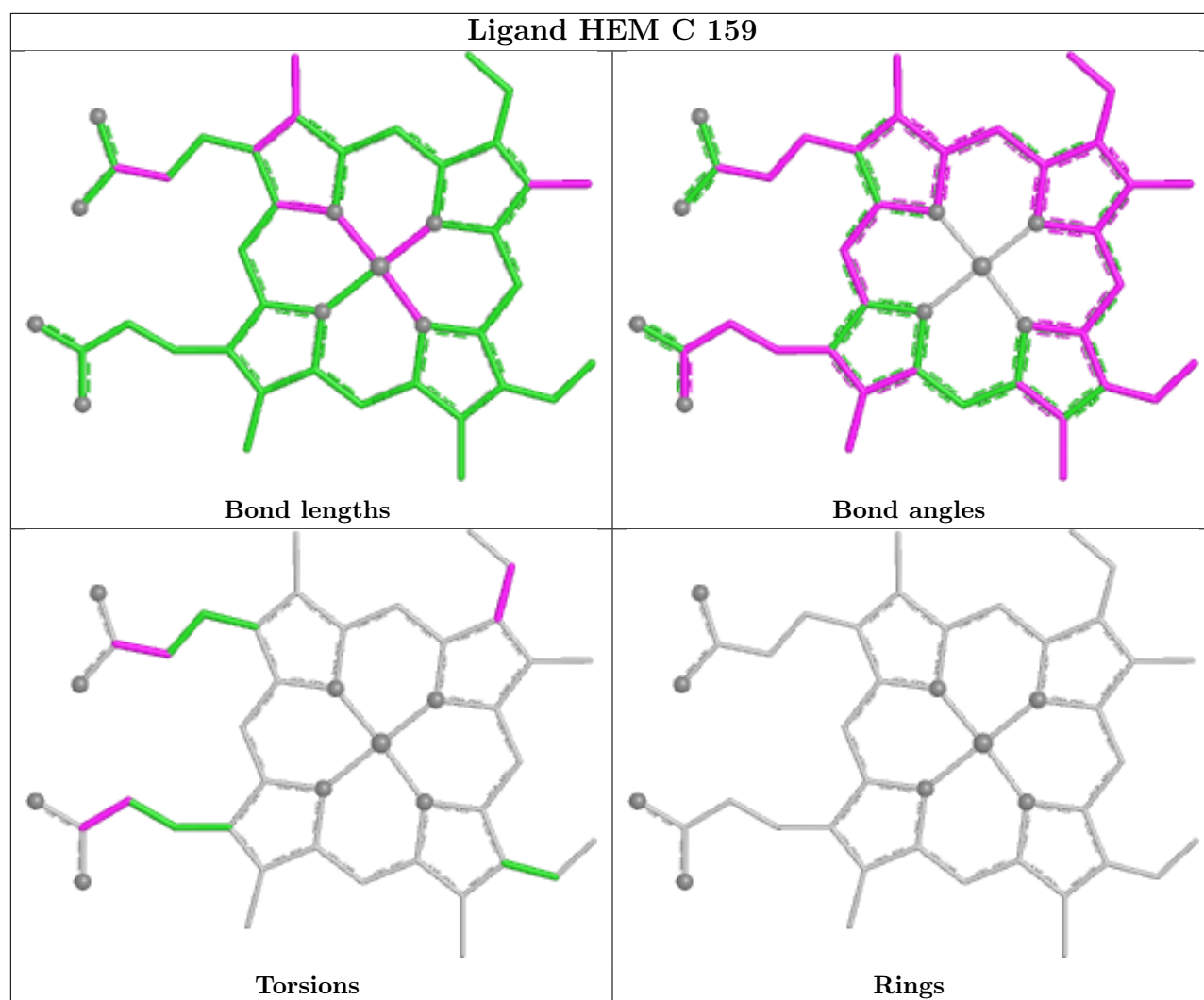


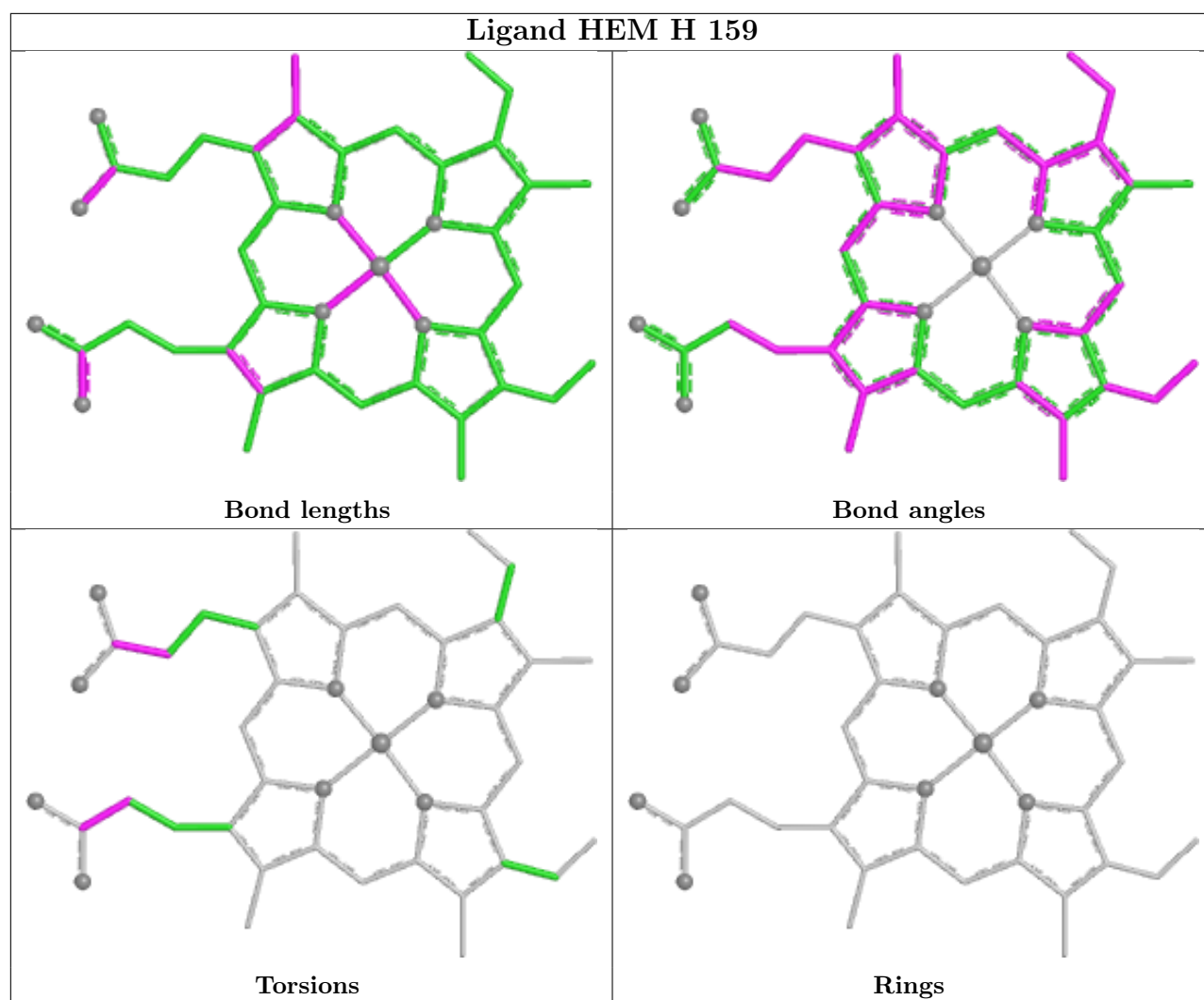
Rings

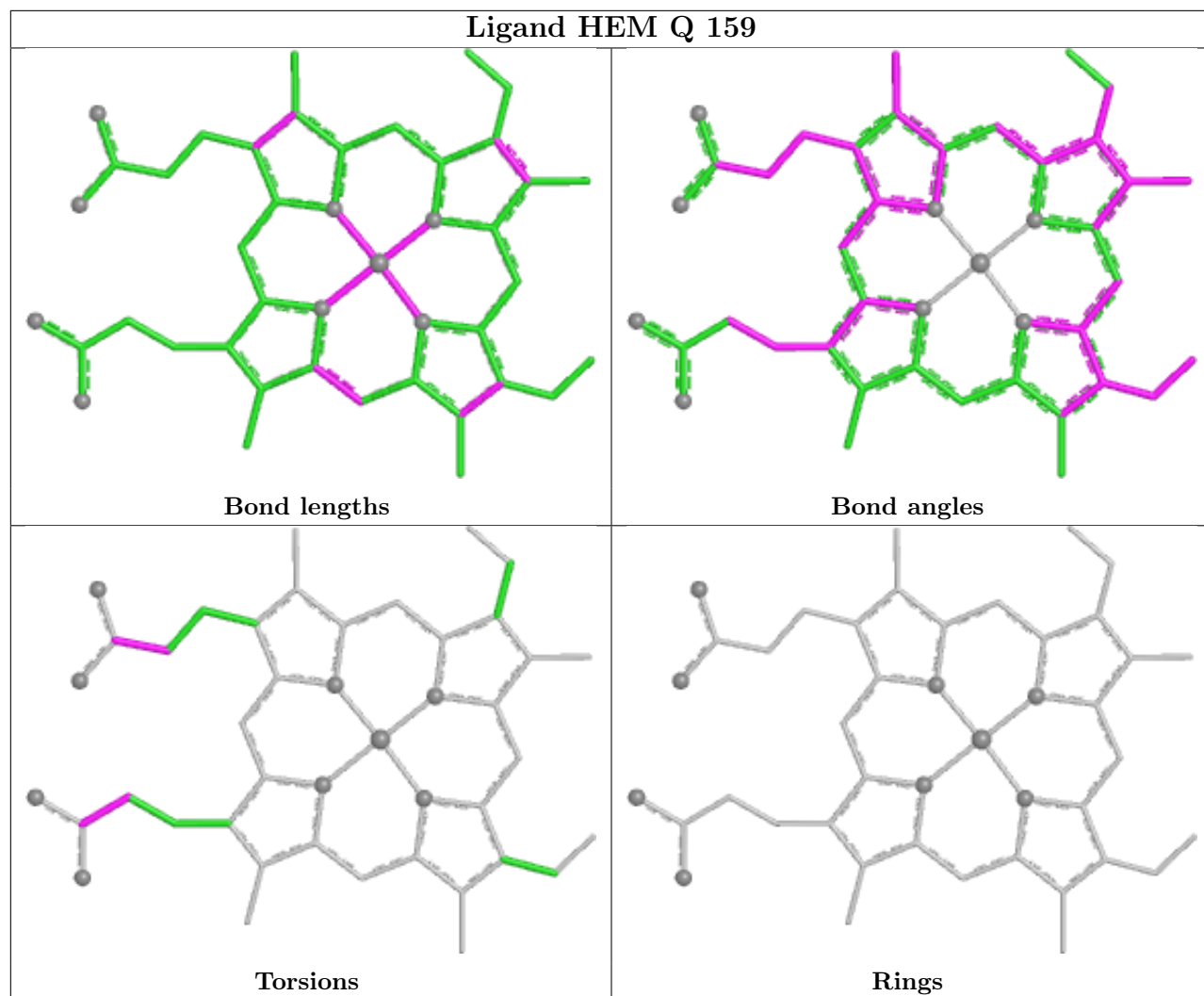


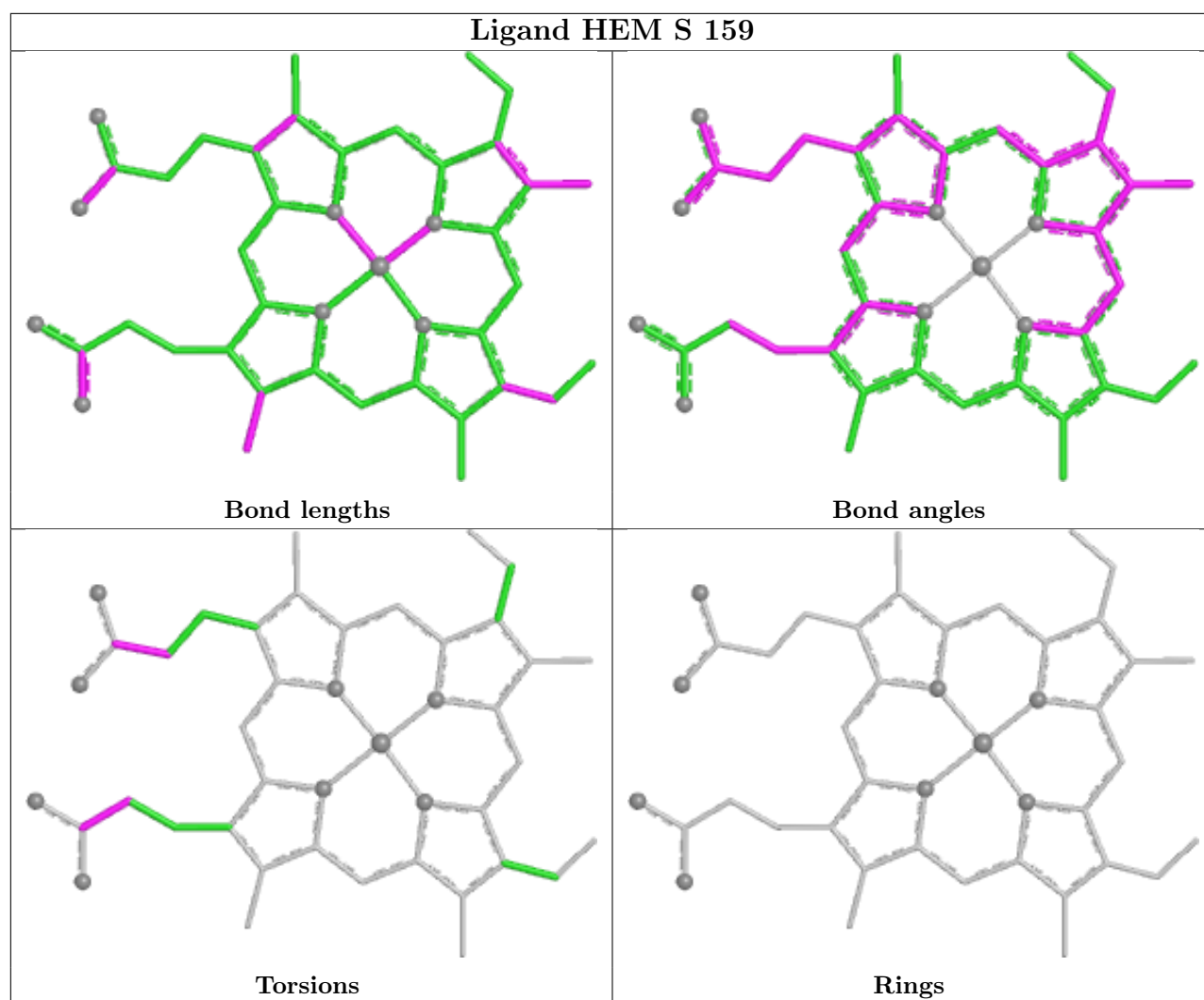


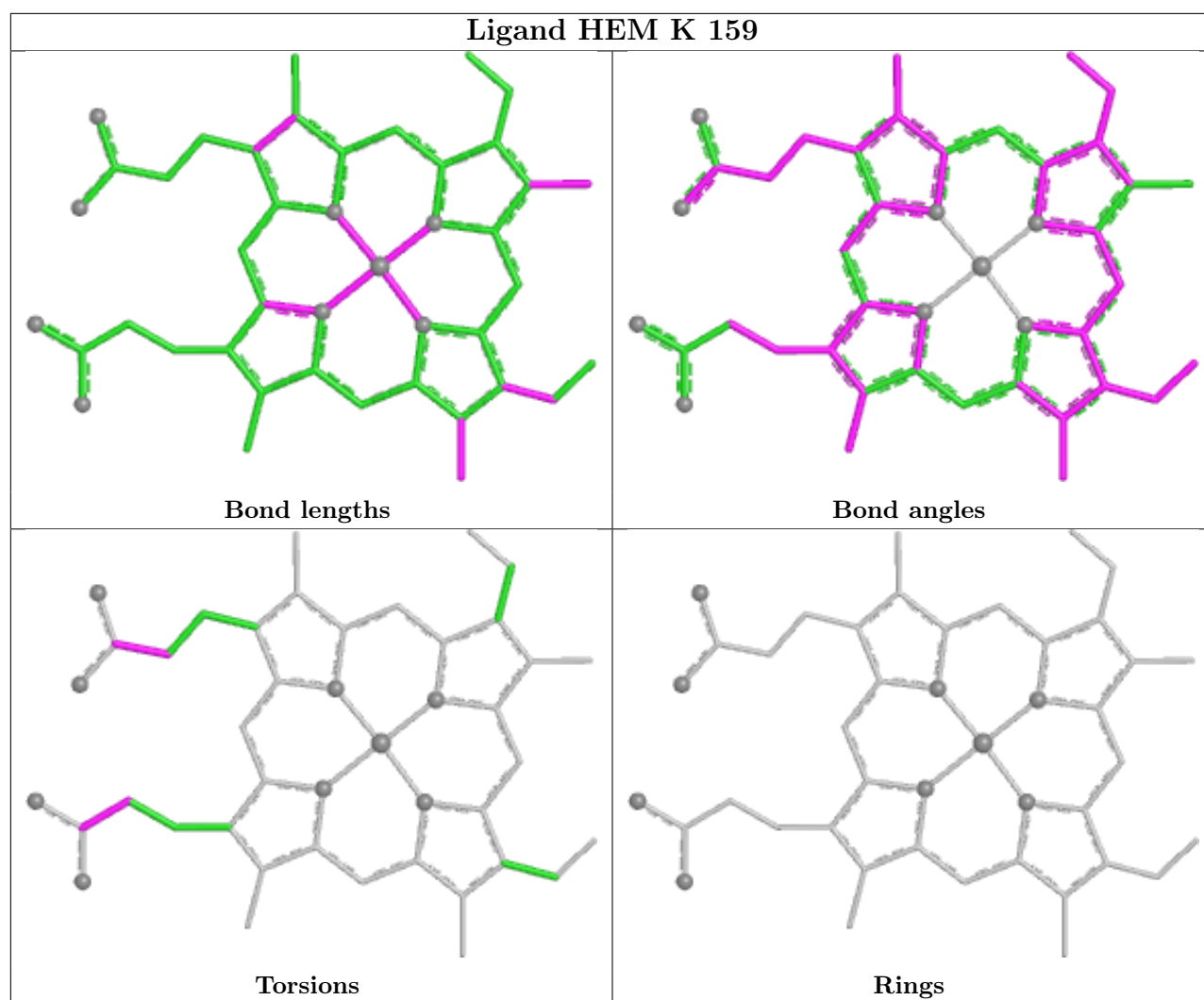












5.7 Other polymers [i](#)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	153/158 (96%)	-0.11	0 100 100	17, 24, 33, 42	0
1	B	154/158 (97%)	-0.16	1 (0%) 85 87	16, 24, 33, 39	0
1	C	155/158 (98%)	-0.06	0 100 100	18, 25, 34, 43	0
1	D	154/158 (97%)	-0.15	1 (0%) 85 87	17, 23, 32, 40	0
1	E	154/158 (97%)	-0.05	1 (0%) 85 87	18, 26, 34, 41	0
1	F	154/158 (97%)	-0.09	1 (0%) 85 87	17, 24, 33, 39	0
1	G	154/158 (97%)	-0.06	0 100 100	18, 26, 35, 41	0
1	H	155/158 (98%)	-0.14	0 100 100	15, 23, 33, 42	0
1	I	154/158 (97%)	0.14	2 (1%) 75 77	19, 29, 37, 42	0
1	J	154/158 (97%)	0.19	1 (0%) 85 87	21, 28, 37, 43	0
1	K	154/158 (97%)	0.12	1 (0%) 85 87	20, 28, 38, 42	0
1	L	154/158 (97%)	0.06	1 (0%) 85 87	20, 26, 35, 44	0
1	M	154/158 (97%)	0.07	1 (0%) 85 87	19, 27, 35, 45	0
1	N	154/158 (97%)	-0.06	1 (0%) 85 87	19, 25, 34, 43	0
1	O	154/158 (97%)	-0.03	3 (1%) 66 69	19, 24, 33, 42	0
1	P	154/158 (97%)	0.12	1 (0%) 85 87	21, 28, 37, 42	0
1	Q	154/158 (97%)	0.28	2 (1%) 75 77	22, 30, 38, 44	0
1	R	155/158 (98%)	0.29	0 100 100	23, 30, 39, 44	0
1	S	154/158 (97%)	0.20	2 (1%) 75 77	22, 28, 36, 41	0
1	T	154/158 (97%)	0.25	3 (1%) 66 69	22, 28, 38, 45	0
1	U	154/158 (97%)	0.01	1 (0%) 85 87	21, 26, 34, 42	0
1	V	154/158 (97%)	0.21	2 (1%) 75 77	21, 29, 38, 43	0
1	W	155/158 (98%)	-0.13	0 100 100	17, 24, 33, 41	0
1	X	154/158 (97%)	-0.18	2 (1%) 75 77	16, 23, 31, 39	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3699/3792 (97%)	0.03	27 (0%) 84 86	15, 26, 36, 45	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	3	GLY	3.8
1	T	3	GLY	3.7
1	U	3	GLY	3.5
1	V	3	GLY	3.2
1	L	3	GLY	3.2

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

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.

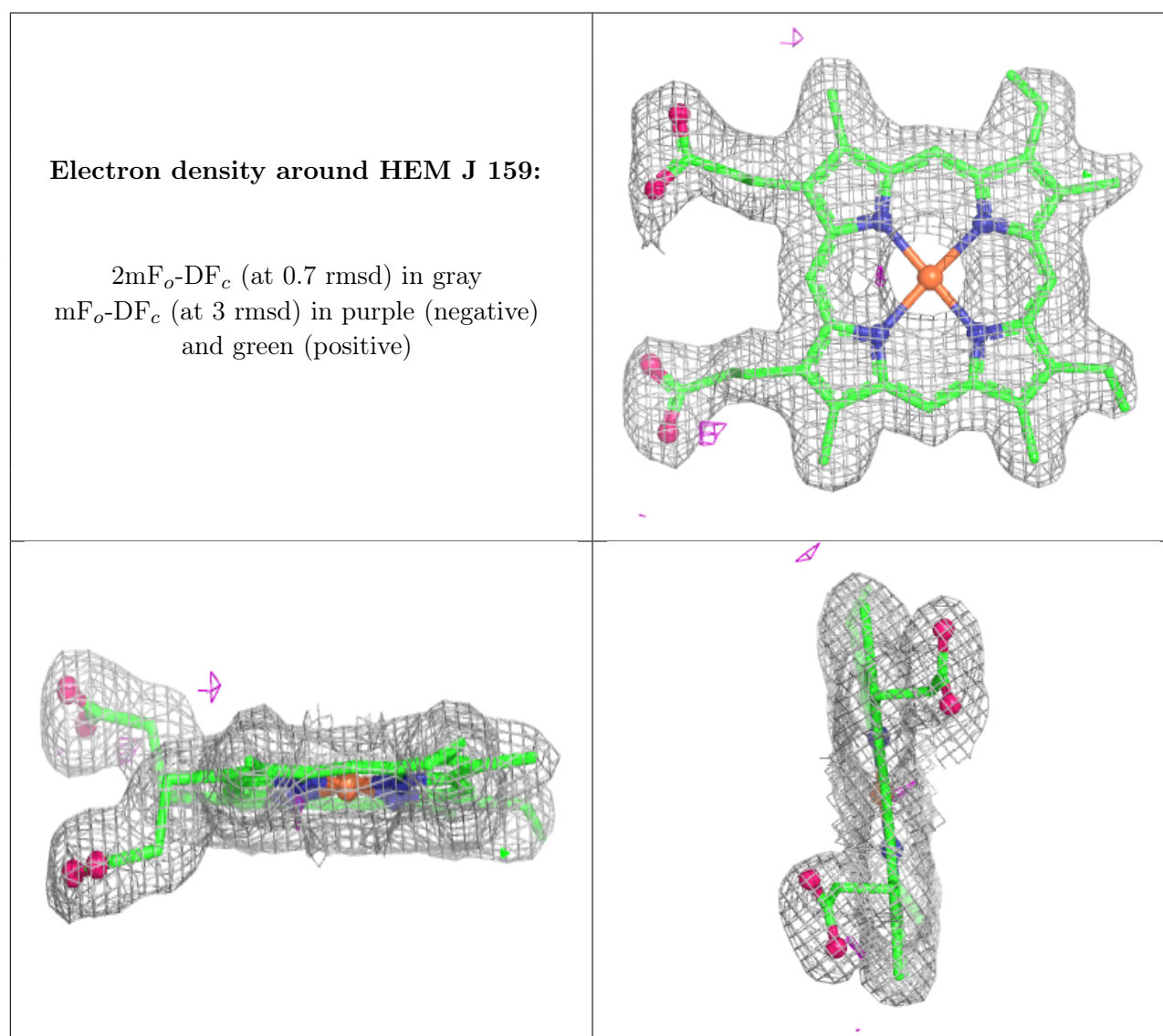
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	HEM	J	159	43/43	0.96	0.09	23,29,37,42	0
2	HEM	Q	159	43/43	0.96	0.09	25,31,36,40	0
2	HEM	V	159	43/43	0.96	0.08	24,28,35,38	0
2	HEM	H	159	43/43	0.97	0.08	16,22,36,38	0
2	HEM	A	159	43/43	0.97	0.08	18,22,31,37	0
2	HEM	K	159	43/43	0.97	0.09	21,27,34,40	0
2	HEM	N	159	43/43	0.97	0.08	20,26,35,39	0
2	HEM	P	159	43/43	0.97	0.09	24,29,36,38	0
2	HEM	C	159	43/43	0.97	0.08	18,23,31,35	0
2	HEM	S	159	43/43	0.97	0.09	23,28,38,43	0
2	HEM	F	159	43/43	0.97	0.08	19,25,35,38	0
2	HEM	X	159	43/43	0.97	0.07	18,23,34,37	0
3	K	C	160	1/1	0.98	0.04	23,23,23,23	0

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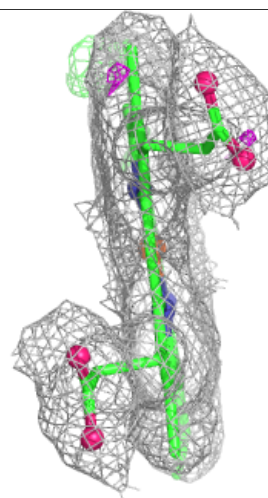
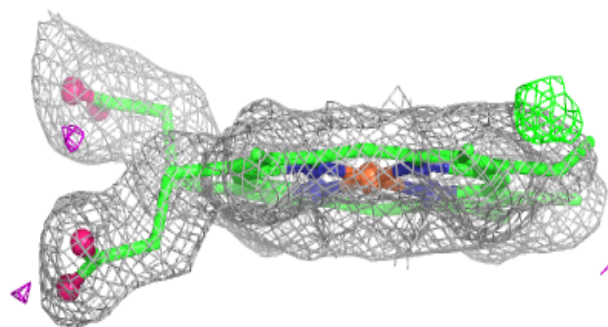
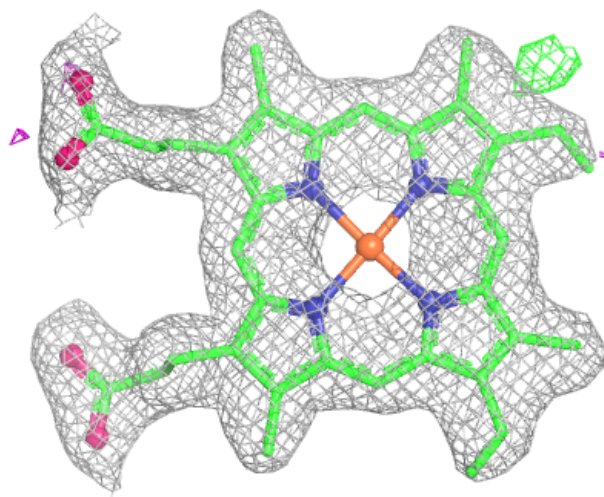
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	K	B	159	1/1	0.99	0.03	20,20,20,20	0
3	K	A	160	1/1	0.99	0.03	22,22,22,22	0
3	K	E	159	1/1	0.99	0.04	27,27,27,27	0
3	K	G	159	1/1	0.99	0.02	23,23,23,23	0
3	K	N	160	1/1	0.99	0.04	26,26,26,26	0

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.



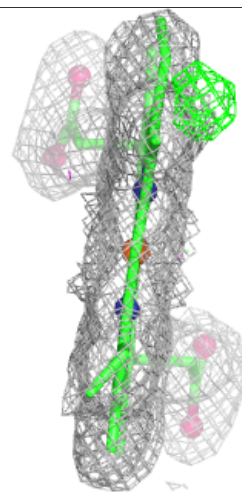
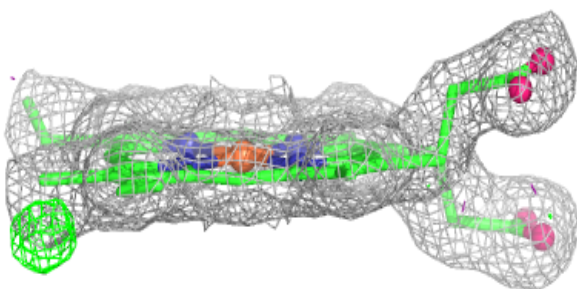
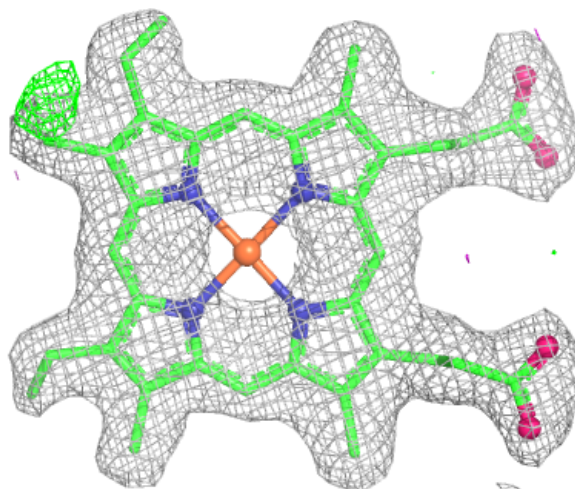
Electron density around HEM Q 159:

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



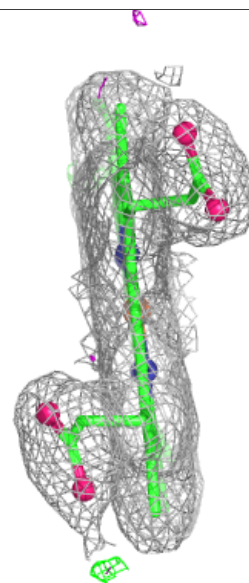
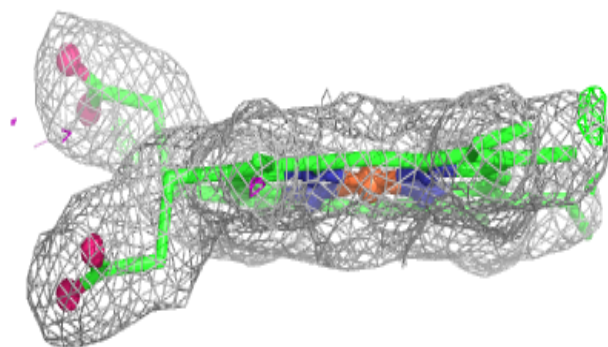
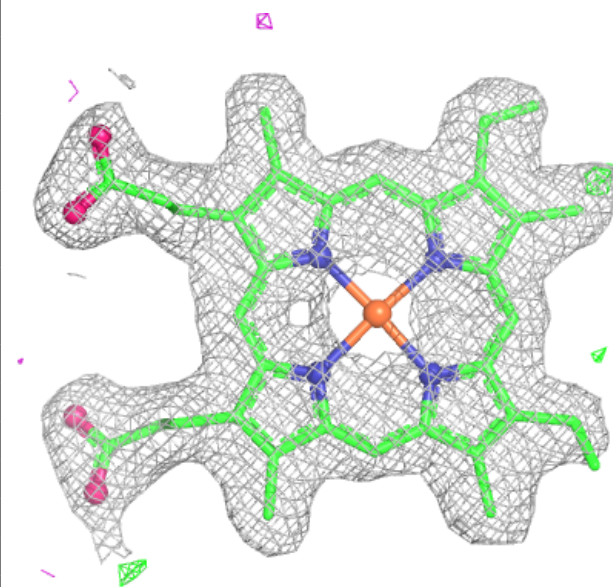
Electron density around HEM V 159:

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



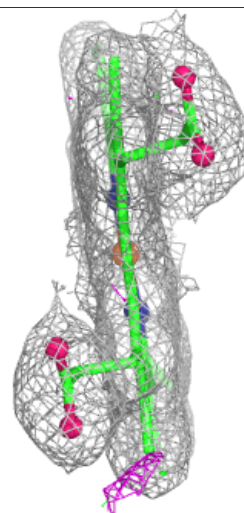
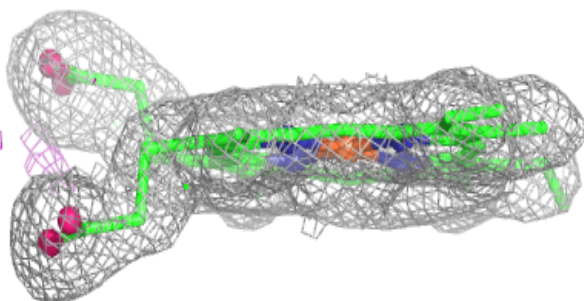
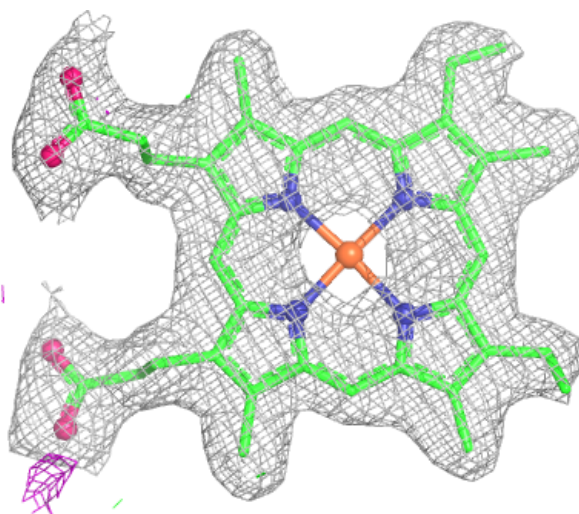
Electron density around HEM H 159:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



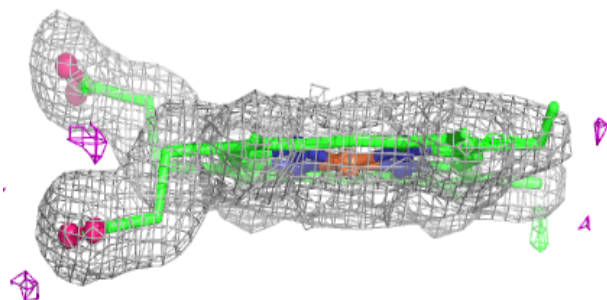
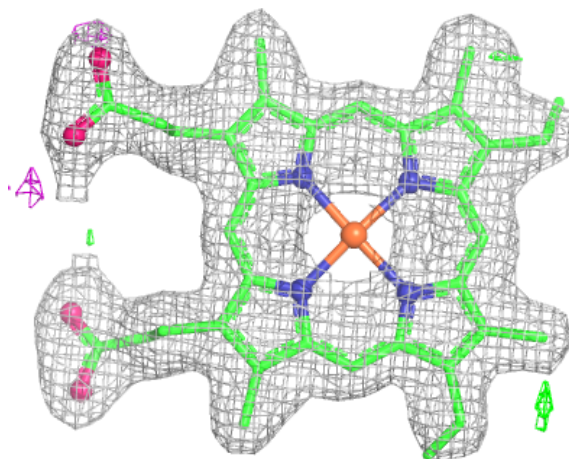
Electron density around HEM A 159:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



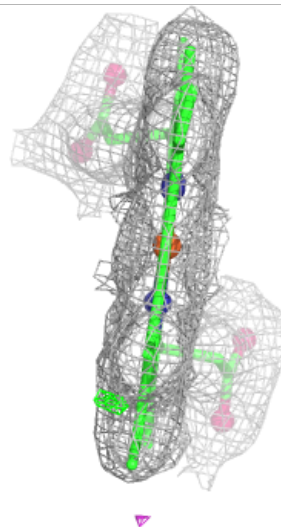
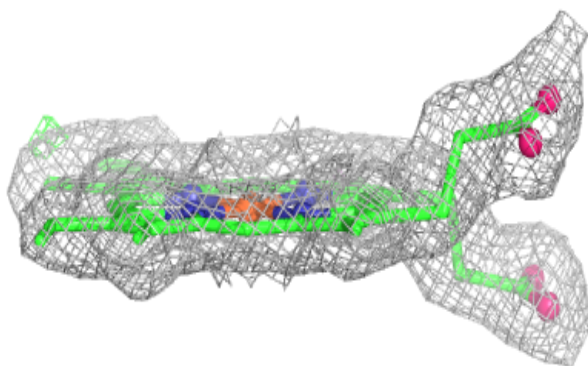
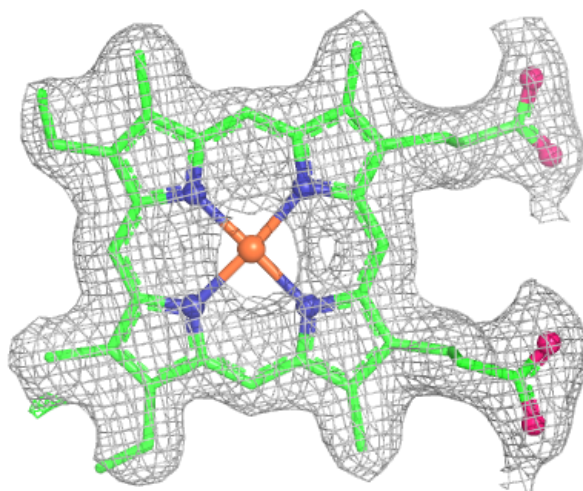
Electron density around HEM K 159:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



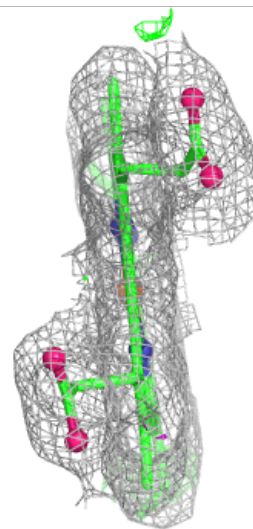
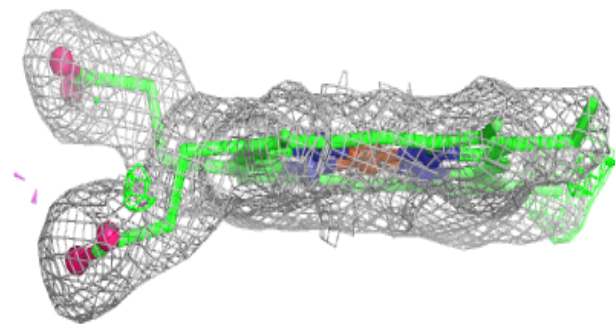
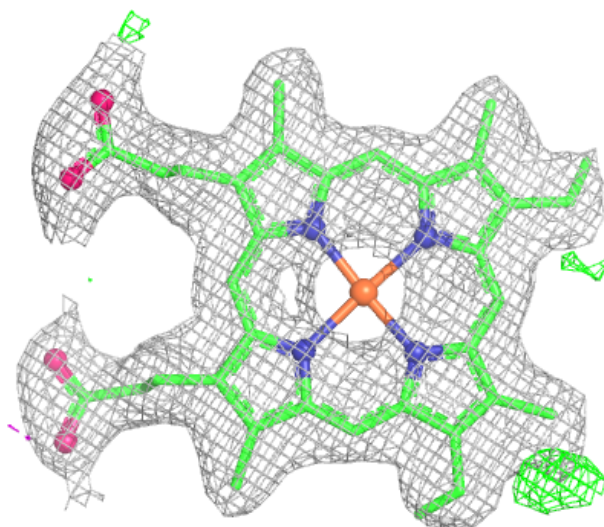
Electron density around HEM N 159:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



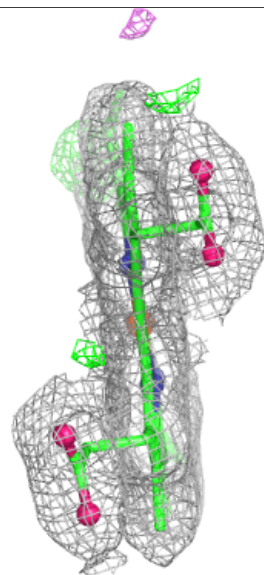
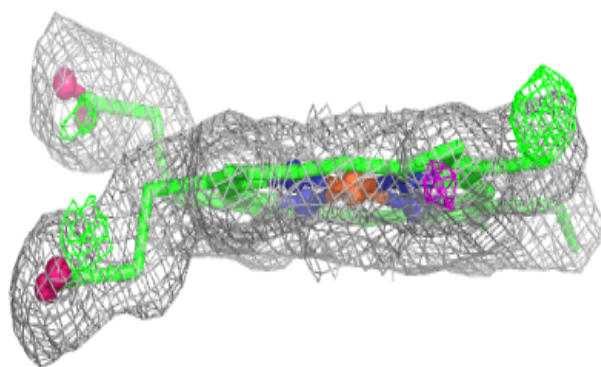
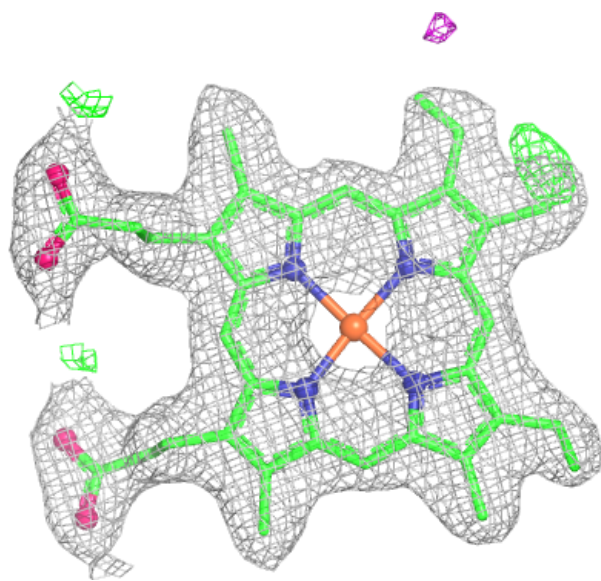
Electron density around HEM P 159:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



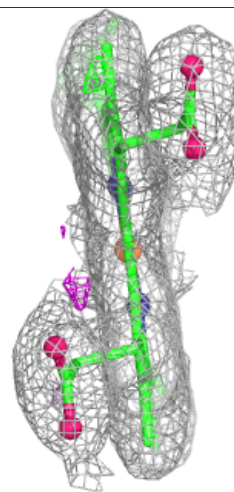
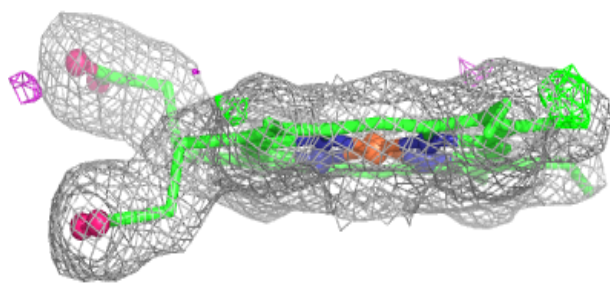
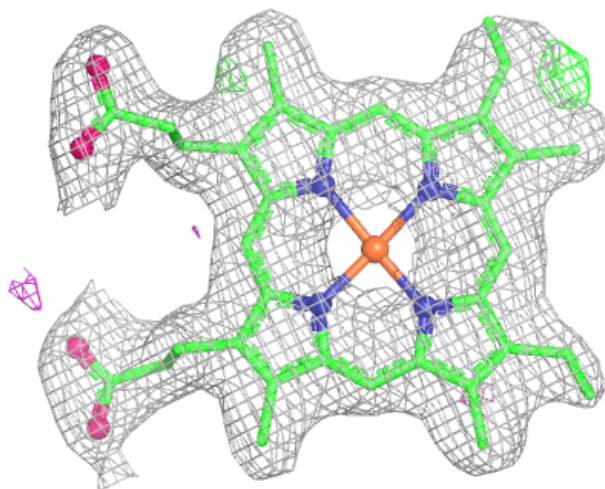
Electron density around HEM C 159:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



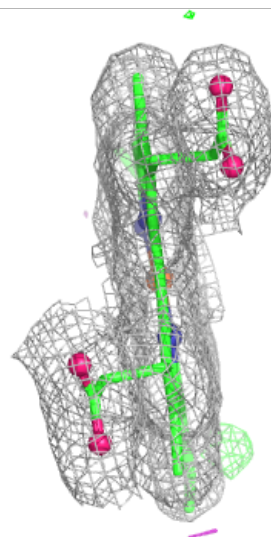
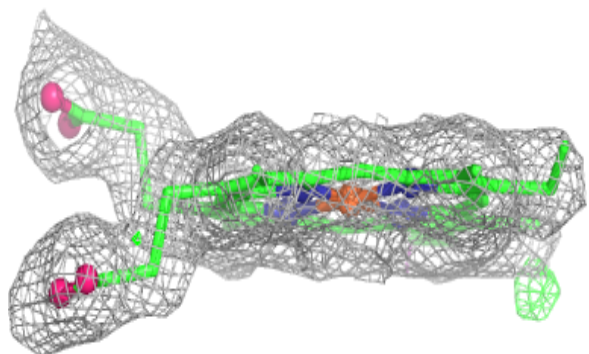
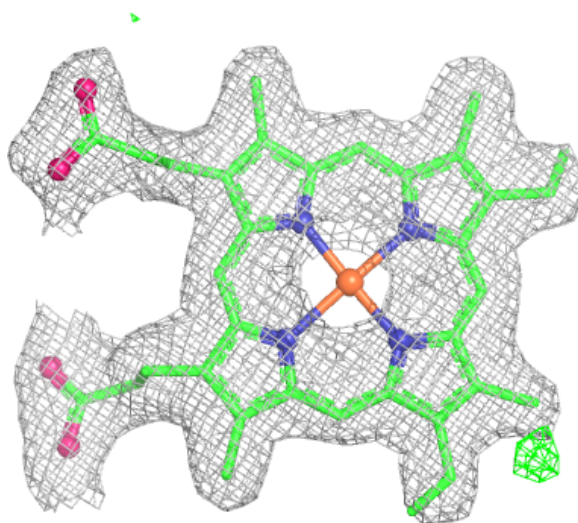
Electron density around HEM S 159:

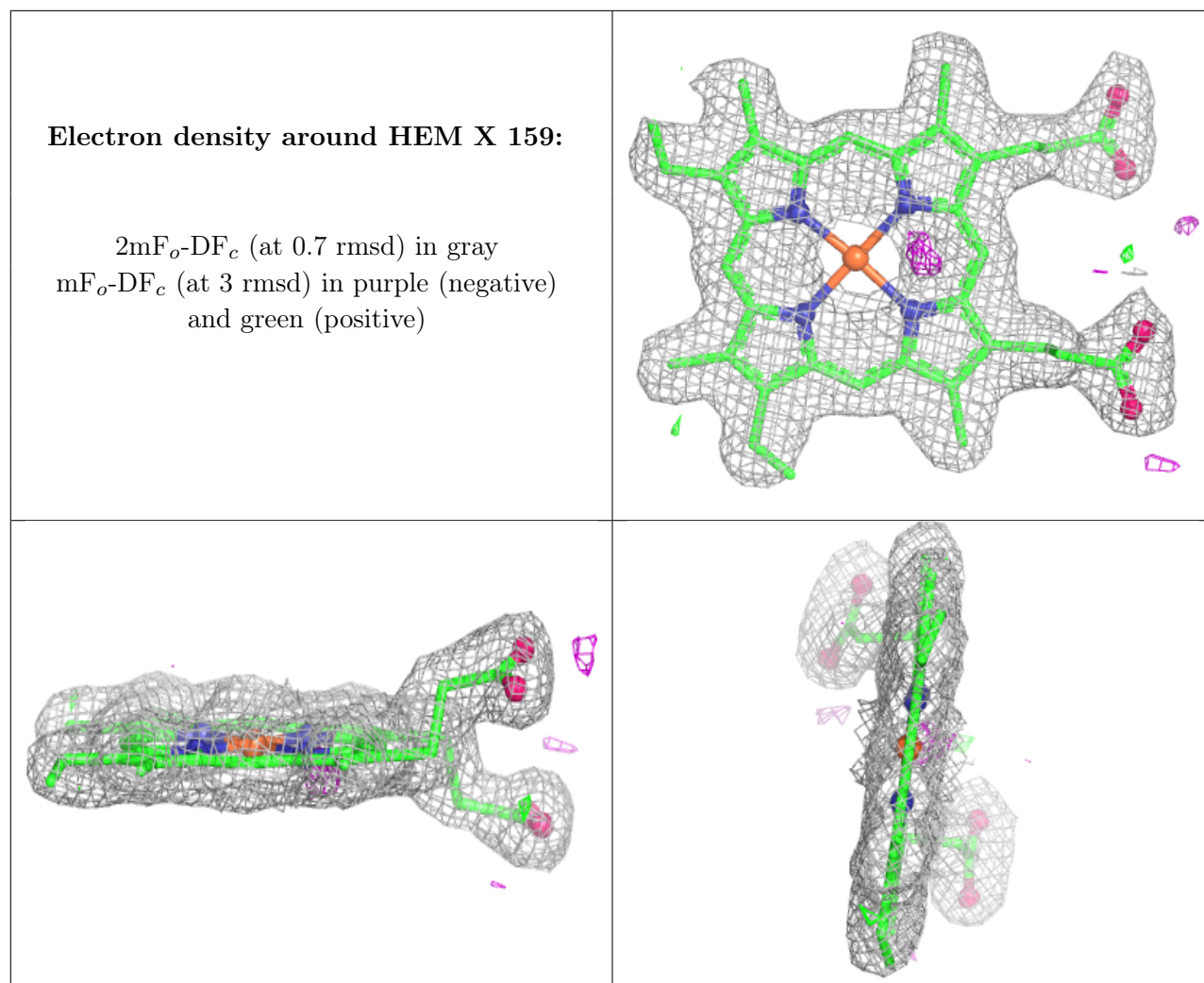
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM F 159:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.