



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 5, 2026 – 01:04 PM EDT

PDB ID : 3Q09 / pdb_00003q09
Title : Crystal Structure of Chlorite Dismutase from *D. Aromatica* at pH 9.0
Authors : Goblirsch, B.R.; Wilmot, C.M.
Deposited on : 2010-12-15
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

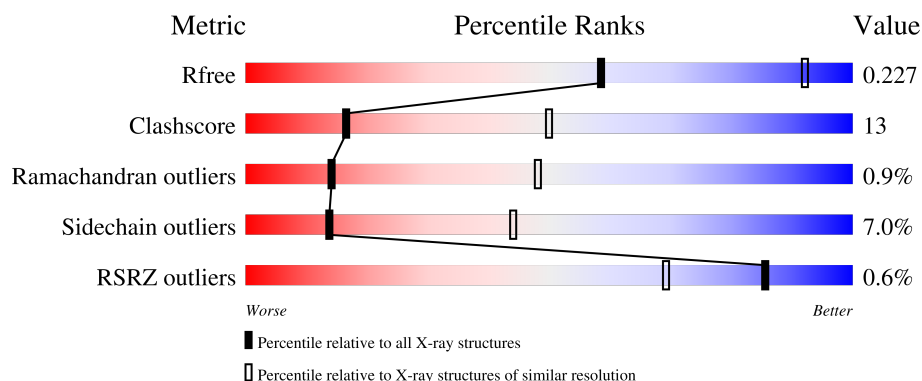
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



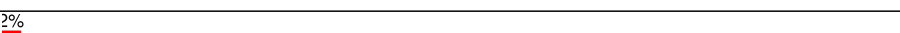
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	248	68% 26% • •
1	B	248	% 71% 23% • •
1	C	248	70% 23% • •
1	D	248	69% 27% • •
1	E	248	% 70% 23% • •

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Mol	Chain	Length	Quality of chain
1	F	248	 69% 27% . .
1	G	248	 68% 27% . .
1	H	248	 74% 20% . .
1	I	248	 73% 21% . .
1	J	248	 % 71% 23% . .
1	K	248	 73% 22% . .
1	L	248	 71% 23% . .
1	M	248	 % 72% 21% . .
1	N	248	 67% 27% . .
1	O	248	 75% 18% . .
1	P	248	 % 69% 25% . .
1	Q	248	 % 65% 28% . .
1	R	248	 % 67% 26% 5% .
1	S	248	 2% 67% 27% . .
1	T	248	 2% 60% 31% 5% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 39520 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 Chlorite dismutase.

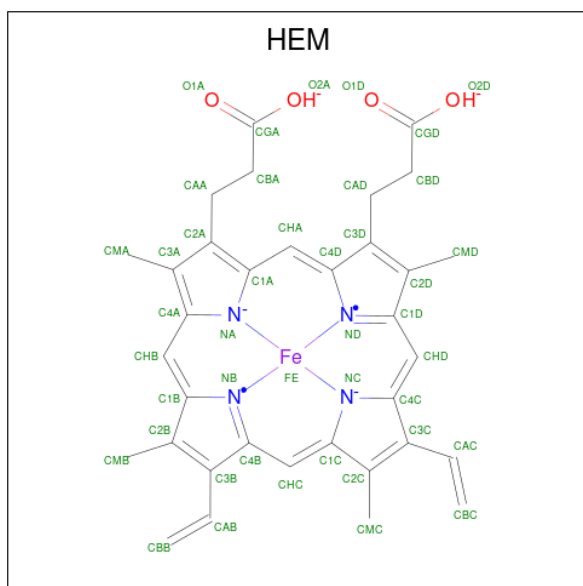
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	B	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	C	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	D	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	E	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	F	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	G	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	H	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	I	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	J	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	K	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	L	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	M	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	N	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	O	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	P	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	R	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	S	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			
1	T	241	Total	C	N	O	S	0	0	0
			1928	1239	325	359	5			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



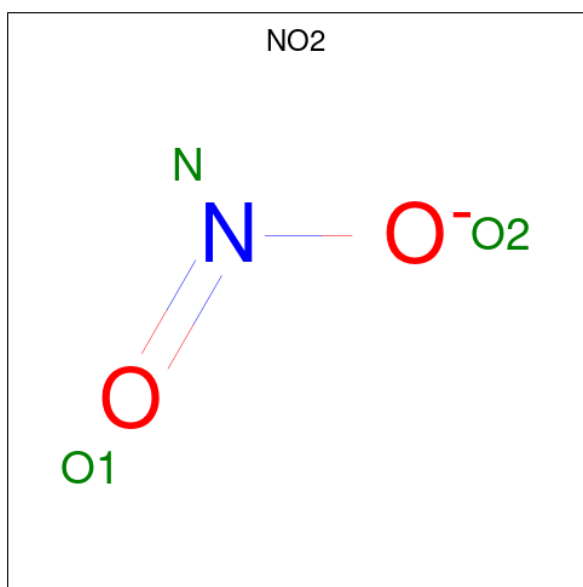
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	E	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	G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

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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	I	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	L	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	M	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	O	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	R	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	T	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is NITRITE ION (CCD ID: NO2) (formula: NO₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	N	O	0	0
			3	1	2		
3	B	1	Total	N	O	0	0
			3	1	2		
3	C	1	Total	N	O	0	0
			3	1	2		
3	D	1	Total	N	O	0	0
			3	1	2		
3	E	1	Total	N	O	0	0
			3	1	2		
3	F	1	Total	N	O	0	0
			3	1	2		
3	G	1	Total	N	O	0	0
			3	1	2		
3	H	1	Total	N	O	0	0
			3	1	2		
3	I	1	Total	N	O	0	0
			3	1	2		
3	J	1	Total	N	O	0	0
			3	1	2		
3	K	1	Total	N	O	0	0
			3	1	2		
3	L	1	Total	N	O	0	0
			3	1	2		
3	M	1	Total	N	O	0	0
			3	1	2		
3	N	1	Total	N	O	0	0
			3	1	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	O	1	Total	N	O	0	0
			3	1	2		
3	P	1	Total	N	O	0	0
			3	1	2		
3	Q	1	Total	N	O	0	0
			3	1	2		
3	R	1	Total	N	O	0	0
			3	1	2		
3	S	1	Total	N	O	0	0
			3	1	2		
3	T	1	Total	N	O	0	0
			3	1	2		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		
4	D	1	Total	Ca	0	0
			1	1		
4	E	1	Total	Ca	0	0
			1	1		
4	F	1	Total	Ca	0	0
			1	1		
4	G	1	Total	Ca	0	0
			1	1		
4	H	1	Total	Ca	0	0
			1	1		
4	I	1	Total	Ca	0	0
			1	1		
4	J	1	Total	Ca	0	0
			1	1		
4	K	1	Total	Ca	0	0
			1	1		
4	L	1	Total	Ca	0	0
			1	1		
4	M	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	N	1	Total 1	Ca 1	0	0
4	O	1	Total 1	Ca 1	0	0
4	P	1	Total 1	Ca 1	0	0
4	Q	1	Total 1	Ca 1	0	0
4	R	1	Total 1	Ca 1	0	0
4	S	1	Total 1	Ca 1	0	0
4	T	1	Total 1	Ca 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	O 1	0	0
5	B	1	Total 1	O 1	0	0
5	C	1	Total 1	O 1	0	0
5	D	1	Total 1	O 1	0	0
5	E	1	Total 1	O 1	0	0
5	F	1	Total 1	O 1	0	0
5	G	1	Total 1	O 1	0	0
5	H	1	Total 1	O 1	0	0
5	I	1	Total 1	O 1	0	0
5	J	1	Total 1	O 1	0	0
5	K	1	Total 1	O 1	0	0
5	L	1	Total 1	O 1	0	0

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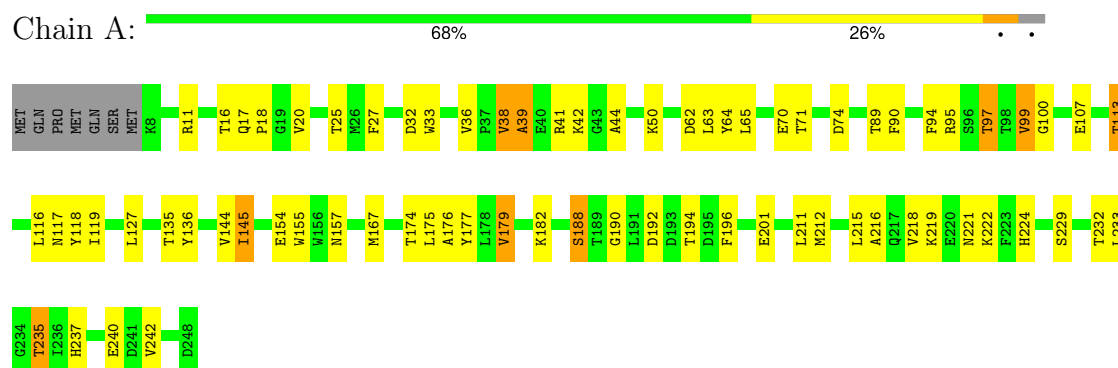
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	M	1	Total 1	O 1	0	0
5	N	1	Total 1	O 1	0	0
5	O	1	Total 1	O 1	0	0
5	P	1	Total 1	O 1	0	0
5	Q	1	Total 1	O 1	0	0
5	R	1	Total 1	O 1	0	0
5	S	1	Total 1	O 1	0	0
5	T	1	Total 1	O 1	0	0

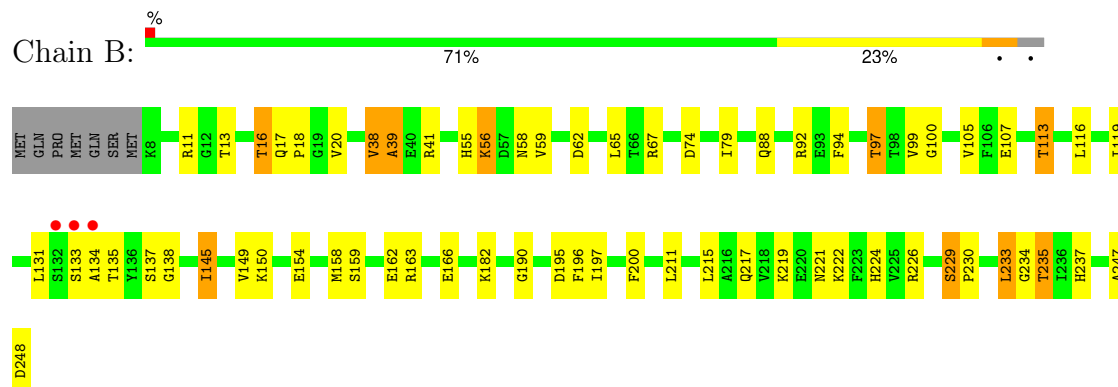
3 Residue-property plots [i](#)

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.

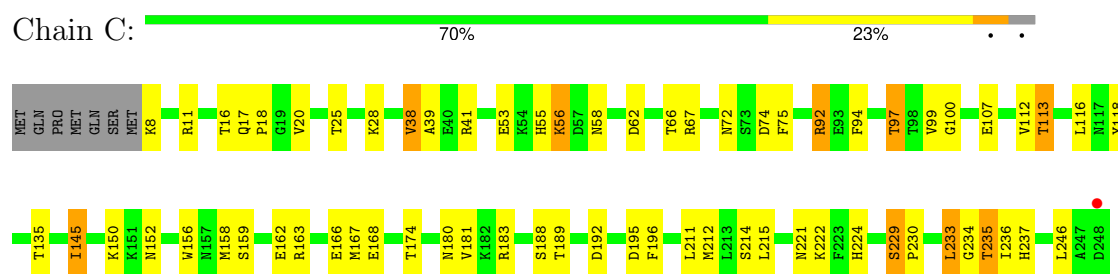
- Molecule 1: Chlorite dismutase



- Molecule 1: Chlorite dismutase

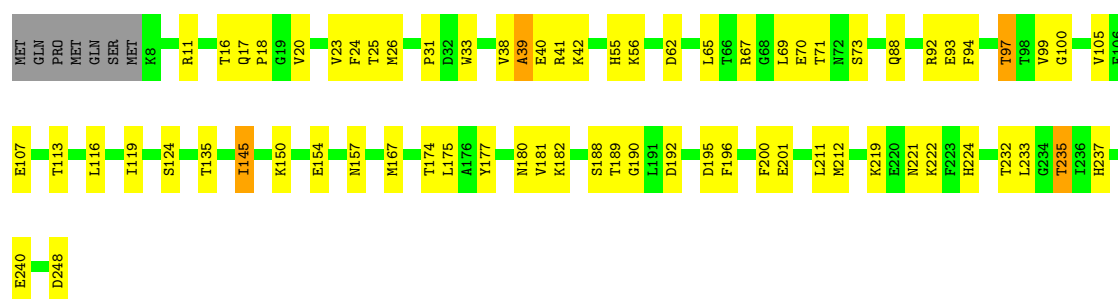


- Molecule 1: Chlorite dismutase



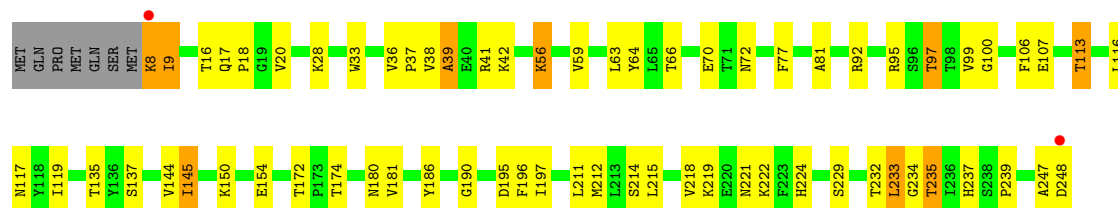
- Molecule 1: Chlorite dismutase

Chain D:  69% 27% . .



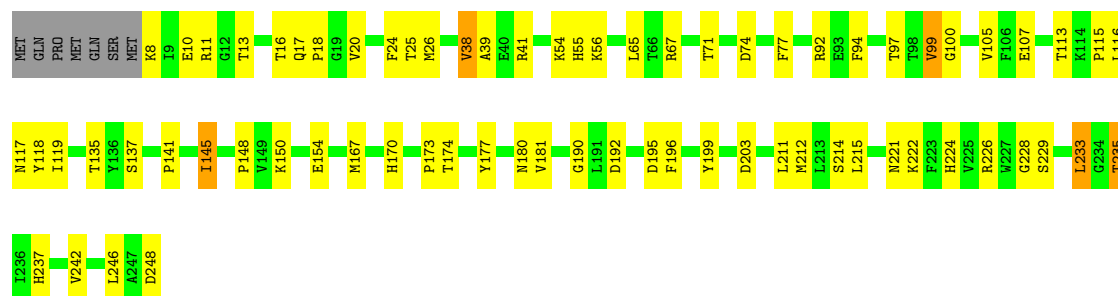
• Molecule 1: Chlorite dismutase

Chain E:  70% 23% . .



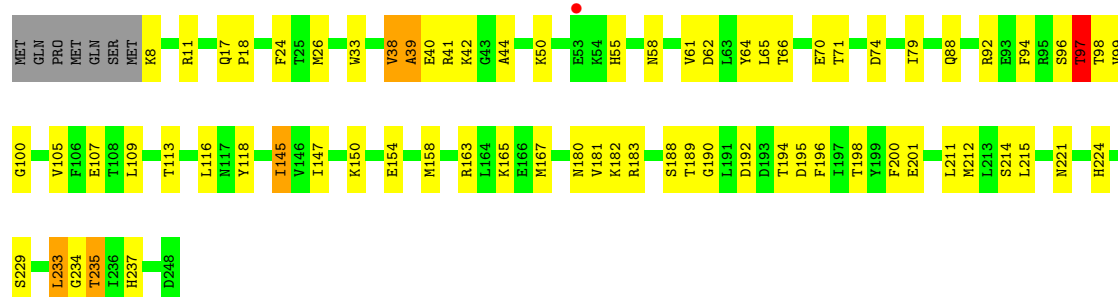
• Molecule 1: Chlorite dismutase

Chain F:  69% 27% . .



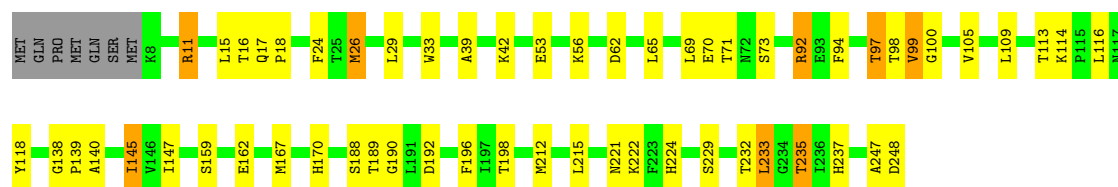
• Molecule 1: Chlorite dismutase

Chain G:  68% 27% . .



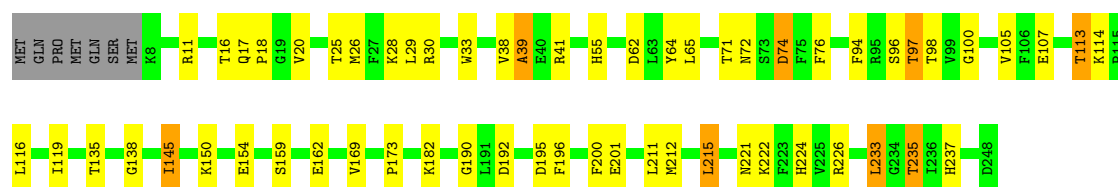
• Molecule 1: Chlorite dismutase

Chain H:  74% 20%



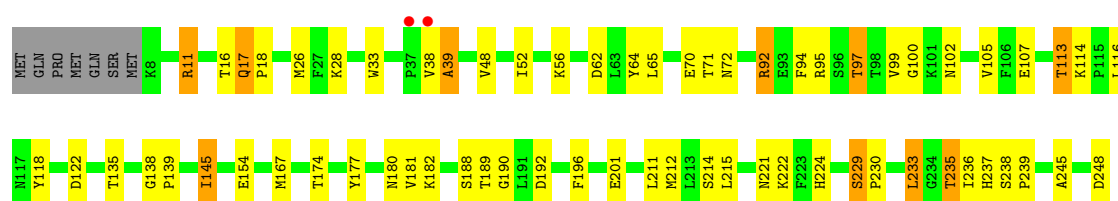
• Molecule 1: Chlorite dismutase

Chain I:  73% 21%



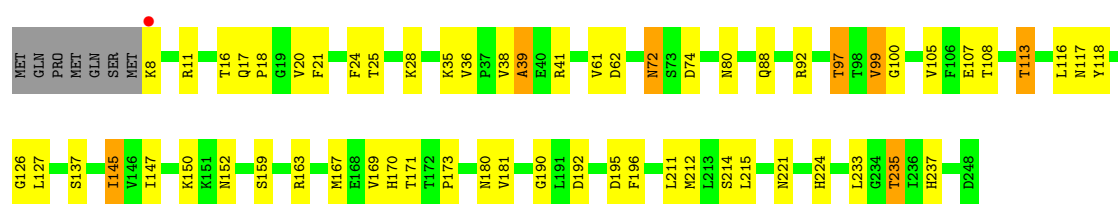
• Molecule 1: Chlorite dismutase

Chain J:  71% 23%



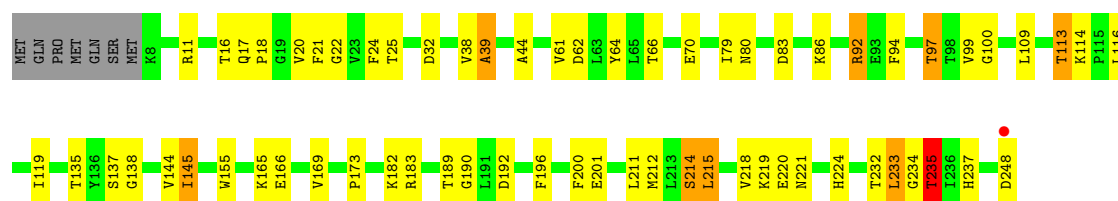
• Molecule 1: Chlorite dismutase

Chain K:  73% 22%

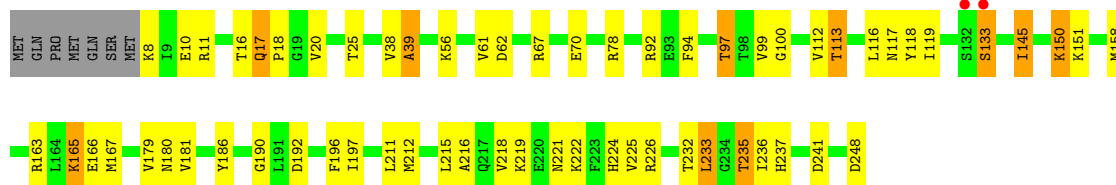


• Molecule 1: Chlorite dismutase

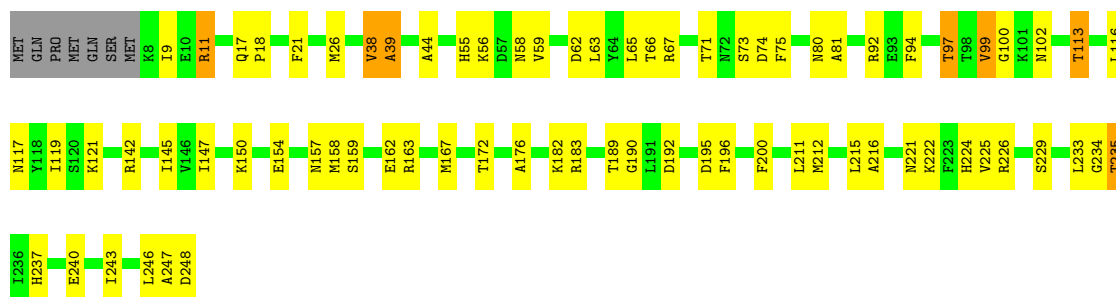
Chain L:  71% 23%



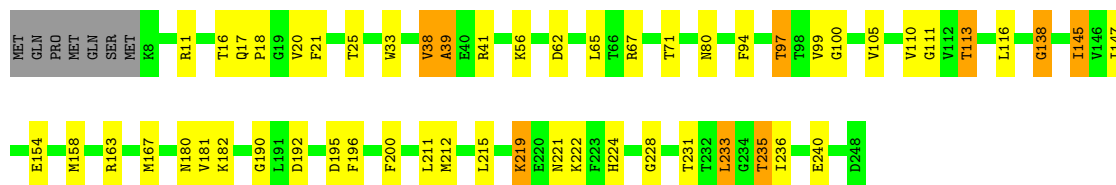
• Molecule 1: Chlorite dismutase



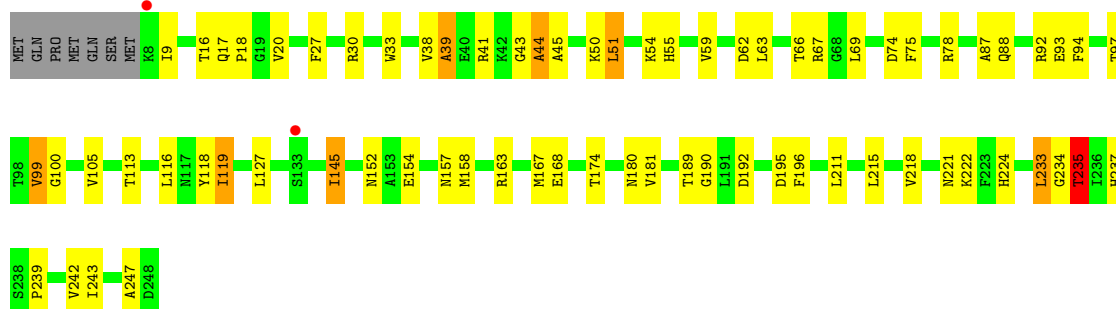
• Molecule 1: Chlorite dismutase



• Molecule 1: Chlorite dismutase



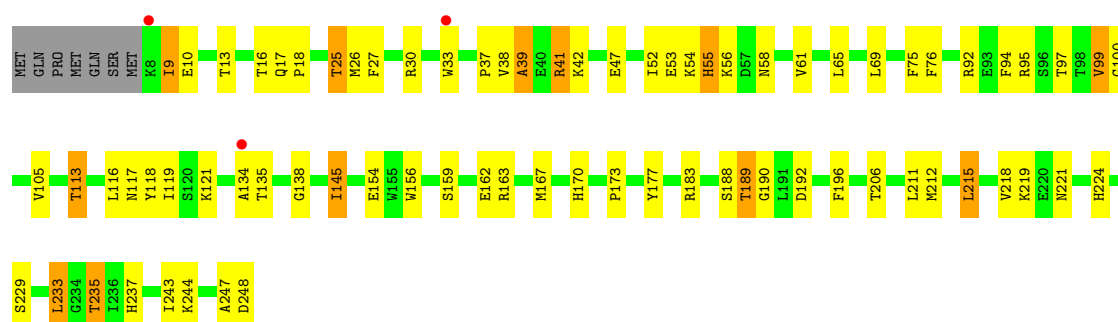
• Molecule 1: Chlorite dismutase



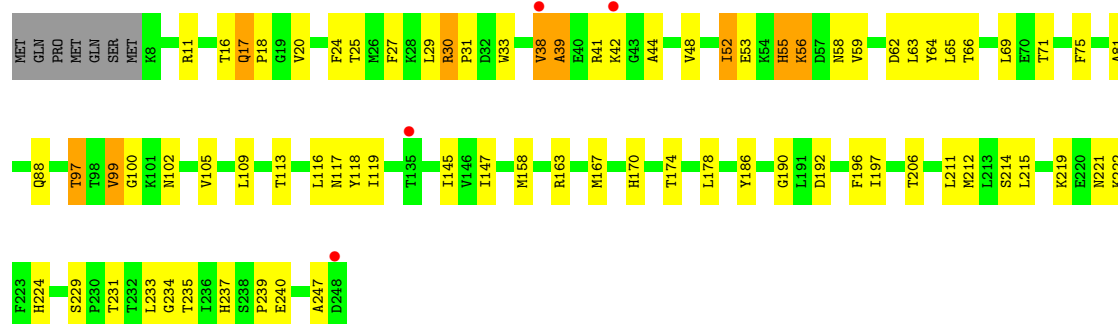
• Molecule 1: Chlorite dismutase



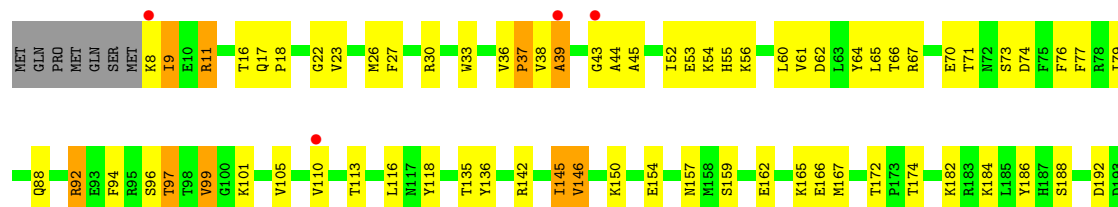
- Molecule 1: Chlorite dismutase



- Molecule 1: Chlorite dismutase



- Molecule 1: Chlorite dismutase



T194	D195	F196	D203	L211	W212	L215	V218	W221	H224	V225	R226	S229	T232	L233	G234	T235	I236	H237	E240	D241	V242	I243	K244	A245	L246	A247	D248
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	122.70Å 202.85Å 247.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.31 – 3.00 48.31 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.31-3.00) 99.6 (48.31-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.59 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.185 , 0.234 0.183 , 0.227	Depositor DCC
R_{free} test set	6174 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	39.8	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 21.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	39520	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NO2, CA, 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	0.95	0/1973	1.13	4/2676 (0.1%)
1	B	1.01	1/1973 (0.1%)	1.15	7/2676 (0.3%)
1	C	1.00	0/1973	1.14	5/2676 (0.2%)
1	D	0.95	1/1973 (0.1%)	1.10	4/2676 (0.1%)
1	E	1.01	0/1973	1.13	3/2676 (0.1%)
1	F	0.91	1/1973 (0.1%)	1.08	3/2676 (0.1%)
1	G	0.93	0/1973	1.08	2/2676 (0.1%)
1	H	0.93	0/1973	1.13	3/2676 (0.1%)
1	I	0.96	1/1973 (0.1%)	1.11	5/2676 (0.2%)
1	J	0.93	1/1973 (0.1%)	1.09	3/2676 (0.1%)
1	K	0.91	1/1973 (0.1%)	1.13	6/2676 (0.2%)
1	L	0.93	1/1973 (0.1%)	1.06	2/2676 (0.1%)
1	M	0.93	0/1973	1.15	10/2676 (0.4%)
1	N	0.89	2/1973 (0.1%)	1.05	5/2676 (0.2%)
1	O	0.88	1/1973 (0.1%)	1.07	4/2676 (0.1%)
1	P	1.08	10/1973 (0.5%)	1.11	9/2676 (0.3%)
1	Q	1.01	6/1973 (0.3%)	1.10	4/2676 (0.1%)
1	R	0.93	5/1973 (0.3%)	1.05	3/2676 (0.1%)
1	S	0.94	4/1973 (0.2%)	1.01	5/2676 (0.2%)
1	T	1.02	5/1973 (0.3%)	1.11	5/2676 (0.2%)
All	All	0.96	40/39460 (0.1%)	1.10	92/53520 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	1
1	L	0	1
1	M	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	O	0	1
All	All	0	5

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	55	HIS	CD2-NE2	13.46	1.52	1.37
1	P	44	ALA	C-N	10.21	1.47	1.33
1	Q	93	GLU	CD-OE1	9.61	1.43	1.25
1	S	55	HIS	ND1-CE1	-9.48	1.23	1.32
1	T	43	GLY	C-N	8.91	1.45	1.33

The worst 5 of 92 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	P	55	HIS	CA-CB-CG	-10.37	103.44	113.80
1	H	114	LYS	CA-C-N	-8.21	112.39	120.52
1	H	114	LYS	C-N-CA	-8.21	112.39	120.52
1	T	55	HIS	N-CA-C	7.62	121.99	111.55
1	Q	33	TRP	CE2-CD2-CE3	7.47	126.27	118.80

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	138	GLY	Peptide
1	L	138	GLY	Peptide
1	M	133	SER	Peptide
1	M	179	VAL	Peptide
1	O	138	GLY	Peptide

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	1928	0	1938	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1928	0	1938	51	0
1	C	1928	0	1938	52	0
1	D	1928	0	1938	59	0
1	E	1928	0	1938	55	0
1	F	1928	0	1938	55	0
1	G	1928	0	1938	66	0
1	H	1928	0	1938	47	0
1	I	1928	0	1938	49	0
1	J	1928	0	1938	58	0
1	K	1928	0	1938	42	0
1	L	1928	0	1938	49	0
1	M	1928	0	1938	42	0
1	N	1928	0	1938	60	0
1	O	1928	0	1938	42	0
1	P	1928	0	1938	60	0
1	Q	1928	0	1938	62	0
1	R	1928	0	1938	61	0
1	S	1928	0	1938	65	0
1	T	1928	0	1938	63	0
2	A	43	0	30	9	0
2	B	43	0	30	6	0
2	C	43	0	30	8	0
2	D	43	0	30	10	0
2	E	43	0	30	8	0
2	F	43	0	30	11	0
2	G	43	0	30	15	0
2	H	43	0	30	10	0
2	I	43	0	30	7	0
2	J	43	0	30	10	0
2	K	43	0	30	6	0
2	L	43	0	30	7	0
2	M	43	0	30	7	0
2	N	43	0	30	10	0
2	O	43	0	30	6	0
2	P	43	0	30	4	0
2	Q	43	0	30	9	0
2	R	43	0	30	14	0
2	S	43	0	30	11	0
2	T	43	0	30	7	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	1	0
3	H	3	0	0	0	0
3	I	3	0	0	0	0
3	J	3	0	0	0	0
3	K	3	0	0	0	0
3	L	3	0	0	1	0
3	M	3	0	0	0	0
3	N	3	0	0	0	0
3	O	3	0	0	0	0
3	P	3	0	0	0	0
3	Q	3	0	0	0	0
3	R	3	0	0	0	0
3	S	3	0	0	0	0
3	T	3	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
4	M	1	0	0	0	0
4	N	1	0	0	0	0
4	O	1	0	0	0	0
4	P	1	0	0	0	0
4	Q	1	0	0	0	0
4	R	1	0	0	0	0
4	S	1	0	0	0	0
4	T	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	2	0
5	C	1	0	0	1	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	1	0	0	1	0
5	G	1	0	0	0	0
5	H	1	0	0	2	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
5	K	1	0	0	0	0
5	L	1	0	0	2	0
5	M	1	0	0	0	0
5	N	1	0	0	0	0
5	O	1	0	0	0	0
5	P	1	0	0	0	0
5	Q	1	0	0	0	0
5	R	1	0	0	0	0
5	S	1	0	0	0	0
5	T	1	0	0	0	0
All	All	39520	0	39360	1018	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 13.

The worst 5 of 1018 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:O:97:THR:HG22	1:O:100:GLY:H	1.10	1.15
1:C:18:PRO:HA	1:C:113:THR:HG22	1.23	1.15
1:J:18:PRO:HA	1:J:113:THR:HG22	1.26	1.12
1:K:18:PRO:HA	1:K:113:THR:HG22	1.33	1.10
1:N:18:PRO:HA	1:N:113:THR:HG22	1.28	1.10

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	239/248 (96%)	230 (96%)	8 (3%)	1 (0%)	30	65
1	B	239/248 (96%)	228 (95%)	8 (3%)	3 (1%)	9	38
1	C	239/248 (96%)	231 (97%)	5 (2%)	3 (1%)	9	38
1	D	239/248 (96%)	232 (97%)	6 (2%)	1 (0%)	30	65
1	E	239/248 (96%)	228 (95%)	8 (3%)	3 (1%)	9	38
1	F	239/248 (96%)	226 (95%)	11 (5%)	2 (1%)	16	50
1	G	239/248 (96%)	228 (95%)	9 (4%)	2 (1%)	16	50
1	H	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	65
1	I	239/248 (96%)	226 (95%)	12 (5%)	1 (0%)	30	65
1	J	239/248 (96%)	229 (96%)	9 (4%)	1 (0%)	30	65
1	K	239/248 (96%)	228 (95%)	10 (4%)	1 (0%)	30	65
1	L	239/248 (96%)	231 (97%)	7 (3%)	1 (0%)	30	65
1	M	239/248 (96%)	228 (95%)	9 (4%)	2 (1%)	16	50
1	N	239/248 (96%)	225 (94%)	11 (5%)	3 (1%)	9	38
1	O	239/248 (96%)	227 (95%)	11 (5%)	1 (0%)	30	65
1	P	239/248 (96%)	223 (93%)	13 (5%)	3 (1%)	9	38
1	Q	239/248 (96%)	223 (93%)	12 (5%)	4 (2%)	7	32
1	R	239/248 (96%)	225 (94%)	11 (5%)	3 (1%)	9	38
1	S	239/248 (96%)	226 (95%)	9 (4%)	4 (2%)	7	32
1	T	239/248 (96%)	225 (94%)	12 (5%)	2 (1%)	16	50
All	All	4780/4960 (96%)	4546 (95%)	192 (4%)	42 (1%)	14	48

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	39	ALA
1	C	39	ALA
1	E	39	ALA
1	F	38	VAL
1	F	39	ALA

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	212/219 (97%)	194 (92%)	18 (8%)	10	36
1	B	212/219 (97%)	197 (93%)	15 (7%)	13	43
1	C	212/219 (97%)	196 (92%)	16 (8%)	12	41
1	D	212/219 (97%)	197 (93%)	15 (7%)	13	43
1	E	212/219 (97%)	195 (92%)	17 (8%)	11	38
1	F	212/219 (97%)	195 (92%)	17 (8%)	11	38
1	G	212/219 (97%)	198 (93%)	14 (7%)	15	46
1	H	212/219 (97%)	199 (94%)	13 (6%)	17	49
1	I	212/219 (97%)	200 (94%)	12 (6%)	18	52
1	J	212/219 (97%)	196 (92%)	16 (8%)	12	41
1	K	212/219 (97%)	199 (94%)	13 (6%)	17	49
1	L	212/219 (97%)	195 (92%)	17 (8%)	11	38
1	M	212/219 (97%)	198 (93%)	14 (7%)	15	46
1	N	212/219 (97%)	196 (92%)	16 (8%)	12	41
1	O	212/219 (97%)	199 (94%)	13 (6%)	17	49
1	P	212/219 (97%)	202 (95%)	10 (5%)	23	58
1	Q	212/219 (97%)	195 (92%)	17 (8%)	11	38
1	R	212/219 (97%)	195 (92%)	17 (8%)	11	38
1	S	212/219 (97%)	203 (96%)	9 (4%)	26	61
1	T	212/219 (97%)	193 (91%)	19 (9%)	9	34
All	All	4240/4380 (97%)	3942 (93%)	298 (7%)	14	44

5 of 298 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	192	ASP
1	T	135	THR
1	Q	25	THR
1	R	135	THR
1	F	248	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 120 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	72	ASN
1	S	157	ASN
1	L	157	ASN
1	S	58	ASN
1	T	221	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 60 ligands modelled in this entry, 20 are monoatomic - leaving 40 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	$\# Z > 2$
3	NO2	O	2000	2	1,2,2	4.48	1 (100%)	0,1,1	-	-
3	NO2	I	2000	2	1,2,2	3.88	1 (100%)	0,1,1	-	-
2	HEM	F	1000	1,3	50,50,50	1.91	8 (16%)	67,82,82	1.61	16 (23%)
3	NO2	D	2000	2	1,2,2	4.55	1 (100%)	0,1,1	-	-
2	HEM	H	1000	1,3	50,50,50	2.15	12 (24%)	67,82,82	1.68	15 (22%)
2	HEM	P	1000	1,3	50,50,50	2.06	14 (28%)	67,82,82	1.49	9 (13%)
2	HEM	Q	1000	1,3	50,50,50	2.46	14 (28%)	67,82,82	1.69	15 (22%)
3	NO2	A	2000	2	1,2,2	3.91	1 (100%)	0,1,1	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NO2	B	2000	2	1,2,2	4.37	1 (100%)	0,1,1	-	-
3	NO2	E	2000	2	1,2,2	3.96	1 (100%)	0,1,1	-	-
2	HEM	R	1000	1,3	50,50,50	1.99	10 (20%)	67,82,82	1.66	10 (14%)
3	NO2	N	2000	2	1,2,2	4.44	1 (100%)	0,1,1	-	-
2	HEM	A	1000	1,3	50,50,50	2.17	11 (22%)	67,82,82	1.58	14 (20%)
2	HEM	N	1000	1,3	50,50,50	2.13	11 (22%)	67,82,82	1.48	7 (10%)
3	NO2	S	2000	2	1,2,2	4.70	1 (100%)	0,1,1	-	-
2	HEM	B	1000	1,3	50,50,50	2.31	9 (18%)	67,82,82	1.80	16 (23%)
3	NO2	T	2000	2	1,2,2	4.34	1 (100%)	0,1,1	-	-
3	NO2	K	2000	2	1,2,2	4.79	1 (100%)	0,1,1	-	-
2	HEM	E	1000	1,3	50,50,50	1.84	9 (18%)	67,82,82	1.58	16 (23%)
2	HEM	O	1000	1,3	50,50,50	1.91	8 (16%)	67,82,82	1.35	8 (11%)
2	HEM	J	1000	1,3	50,50,50	2.23	9 (18%)	67,82,82	1.82	14 (20%)
3	NO2	G	2000	2	1,2,2	4.81	1 (100%)	0,1,1	-	-
3	NO2	C	2000	2	1,2,2	4.58	1 (100%)	0,1,1	-	-
2	HEM	G	1000	1,3	50,50,50	2.22	10 (20%)	67,82,82	1.93	18 (26%)
3	NO2	J	2000	2	1,2,2	4.54	1 (100%)	0,1,1	-	-
3	NO2	F	2000	2	1,2,2	4.56	1 (100%)	0,1,1	-	-
2	HEM	I	1000	1,3	50,50,50	2.23	8 (16%)	67,82,82	1.67	11 (16%)
3	NO2	H	2000	2	1,2,2	4.66	1 (100%)	0,1,1	-	-
2	HEM	D	1000	1,3	50,50,50	1.94	9 (18%)	67,82,82	1.46	9 (13%)
2	HEM	S	1000	1,3	50,50,50	2.23	10 (20%)	67,82,82	1.58	10 (14%)
3	NO2	Q	2000	2	1,2,2	4.79	1 (100%)	0,1,1	-	-
2	HEM	K	1000	1,3	50,50,50	1.94	13 (26%)	67,82,82	1.50	11 (16%)
2	HEM	T	1000	1,3	50,50,50	1.94	10 (20%)	67,82,82	1.49	10 (14%)
3	NO2	P	2000	2	1,2,2	4.78	1 (100%)	0,1,1	-	-
2	HEM	C	1000	1,3	50,50,50	2.13	11 (22%)	67,82,82	1.82	14 (20%)
2	HEM	L	1000	1,3	50,50,50	1.93	9 (18%)	67,82,82	1.61	13 (19%)
3	NO2	M	2000	2	1,2,2	6.31	1 (100%)	0,1,1	-	-
2	HEM	M	1000	1,3	50,50,50	2.04	8 (16%)	67,82,82	1.91	18 (26%)
3	NO2	R	2000	2	1,2,2	4.86	1 (100%)	0,1,1	-	-
3	NO2	L	2000	2	1,2,2	4.71	1 (100%)	0,1,1	-	-

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	F	1000	1,3	-	7/14/54/54	-
2	HEM	H	1000	1,3	-	4/14/54/54	-
2	HEM	P	1000	1,3	-	1/14/54/54	-
2	HEM	Q	1000	1,3	-	4/14/54/54	-
2	HEM	R	1000	1,3	-	6/14/54/54	-
2	HEM	A	1000	1,3	-	7/14/54/54	-
2	HEM	N	1000	1,3	-	6/14/54/54	-
2	HEM	B	1000	1,3	-	2/14/54/54	-
2	HEM	E	1000	1,3	-	6/14/54/54	-
2	HEM	O	1000	1,3	-	7/14/54/54	-
2	HEM	J	1000	1,3	-	7/14/54/54	-
2	HEM	G	1000	1,3	-	5/14/54/54	-
2	HEM	I	1000	1,3	-	3/14/54/54	-
2	HEM	D	1000	1,3	-	8/14/54/54	-
2	HEM	S	1000	1,3	-	5/14/54/54	-
2	HEM	K	1000	1,3	-	3/14/54/54	-
2	HEM	T	1000	1,3	-	7/14/54/54	-
2	HEM	C	1000	1,3	-	7/14/54/54	-
2	HEM	L	1000	1,3	-	5/14/54/54	-
2	HEM	M	1000	1,3	-	3/14/54/54	-

The worst 5 of 223 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	HEM	FE-ND	9.19	2.23	1.94
2	S	1000	HEM	C3D-C2D	9.10	1.56	1.36
2	Q	1000	HEM	C3D-C2D	9.05	1.56	1.36
2	B	1000	HEM	FE-ND	9.04	2.22	1.94
2	P	1000	HEM	C3D-C2D	8.97	1.56	1.36

The worst 5 of 254 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	1000	HEM	C4D-ND-C1D	7.38	113.94	105.21
2	G	1000	HEM	C4D-ND-C1D	7.00	113.50	105.21
2	I	1000	HEM	C4D-ND-C1D	6.78	113.24	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	R	1000	HEM	C4D-ND-C1D	6.56	112.97	105.21
2	B	1000	HEM	C4D-ND-C1D	6.46	112.85	105.21

There are no chirality outliers.

5 of 103 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1000	HEM	C2B-C3B-CAB-CBB
2	A	1000	HEM	C4B-C3B-CAB-CBB
2	A	1000	HEM	C2C-C3C-CAC-CBC
2	B	1000	HEM	C2C-C3C-CAC-CBC
2	B	1000	HEM	C4C-C3C-CAC-CBC

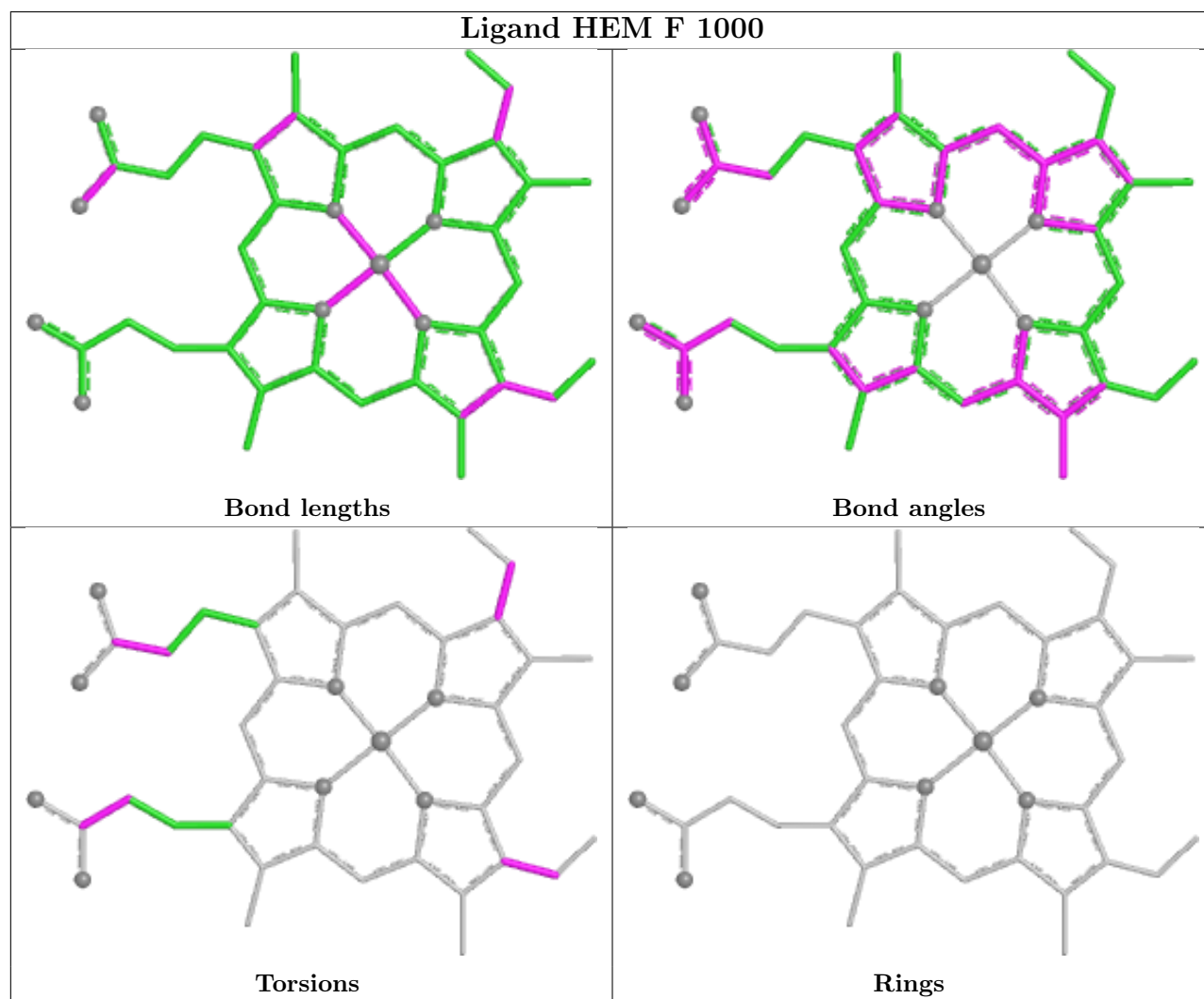
There are no ring outliers.

23 monomers are involved in 178 short contacts:

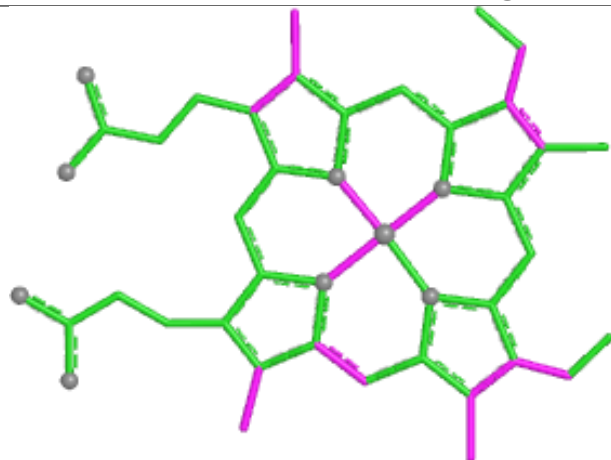
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1000	HEM	11	0
2	H	1000	HEM	10	0
2	P	1000	HEM	4	0
2	Q	1000	HEM	9	0
2	R	1000	HEM	14	0
2	A	1000	HEM	9	0
2	N	1000	HEM	10	0
2	B	1000	HEM	6	0
2	E	1000	HEM	8	0
2	O	1000	HEM	6	0
2	J	1000	HEM	10	0
3	G	2000	NO2	1	0
3	C	2000	NO2	1	0
2	G	1000	HEM	15	0
2	I	1000	HEM	7	0
2	D	1000	HEM	10	0
2	S	1000	HEM	11	0
2	K	1000	HEM	6	0
2	T	1000	HEM	7	0
2	C	1000	HEM	8	0
2	L	1000	HEM	7	0
2	M	1000	HEM	7	0
3	L	2000	NO2	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

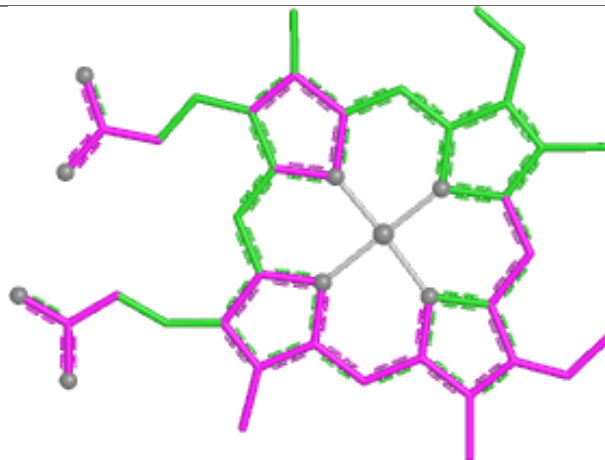
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within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



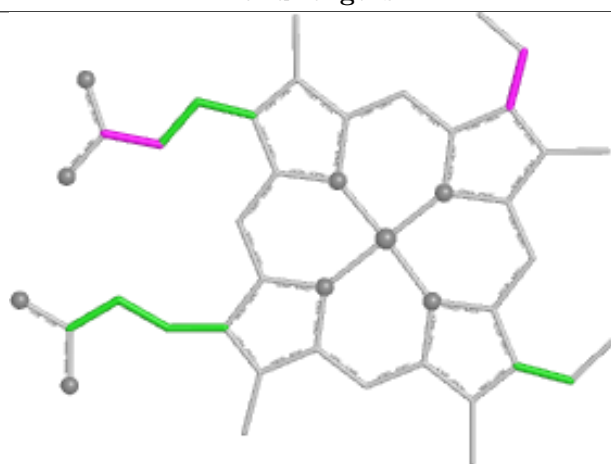
Ligand HEM H 1000



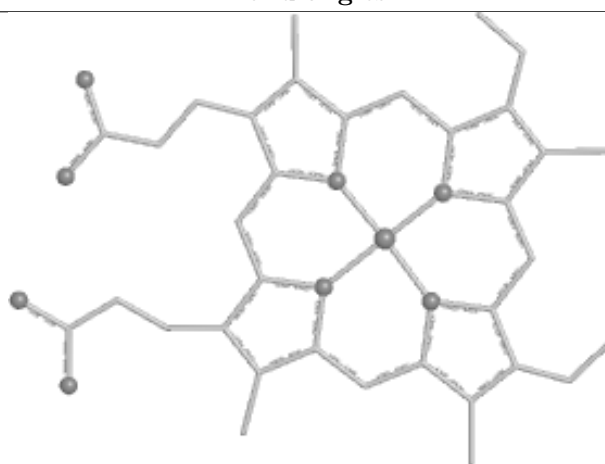
Bond lengths



Bond angles

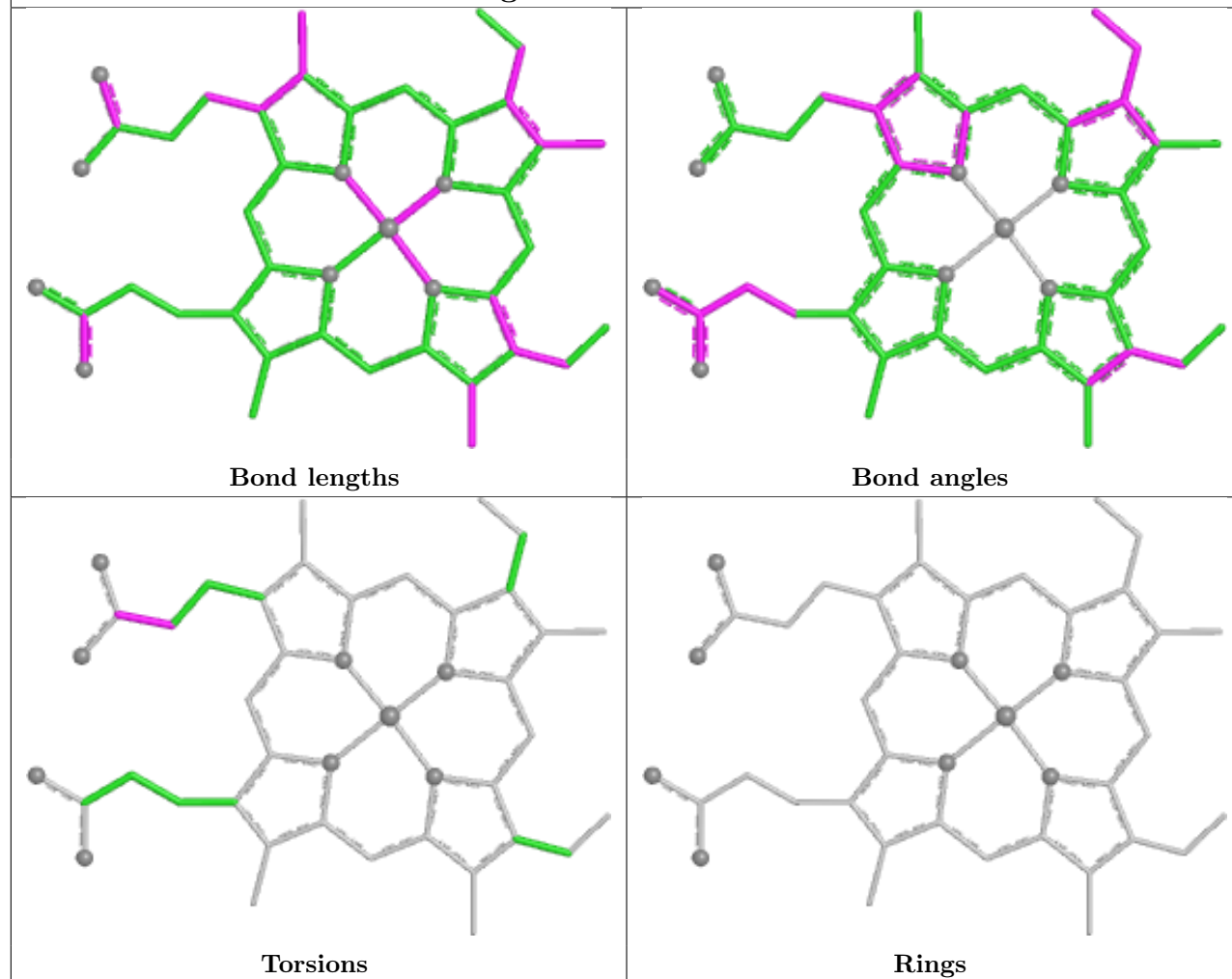


Torsions

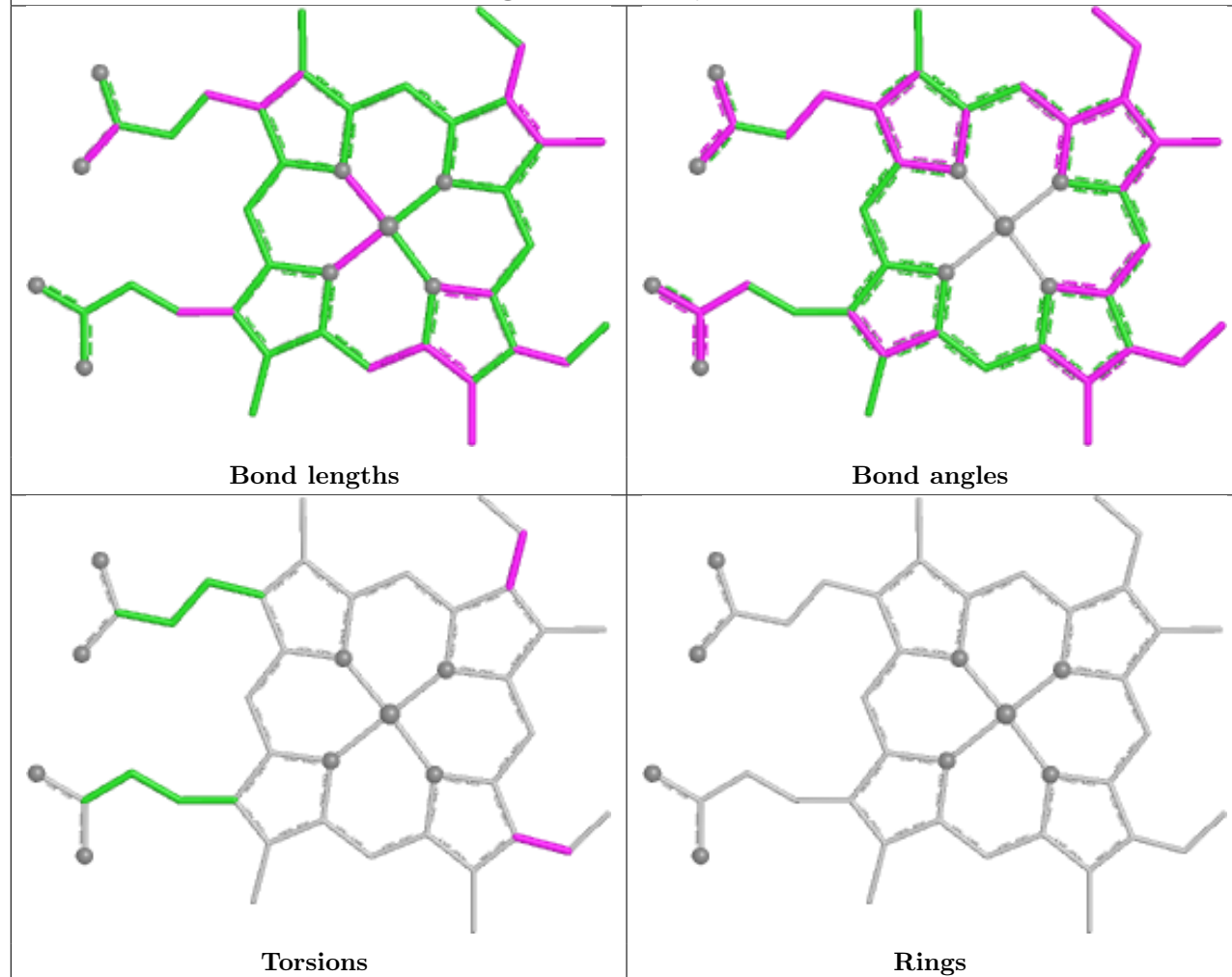


Rings

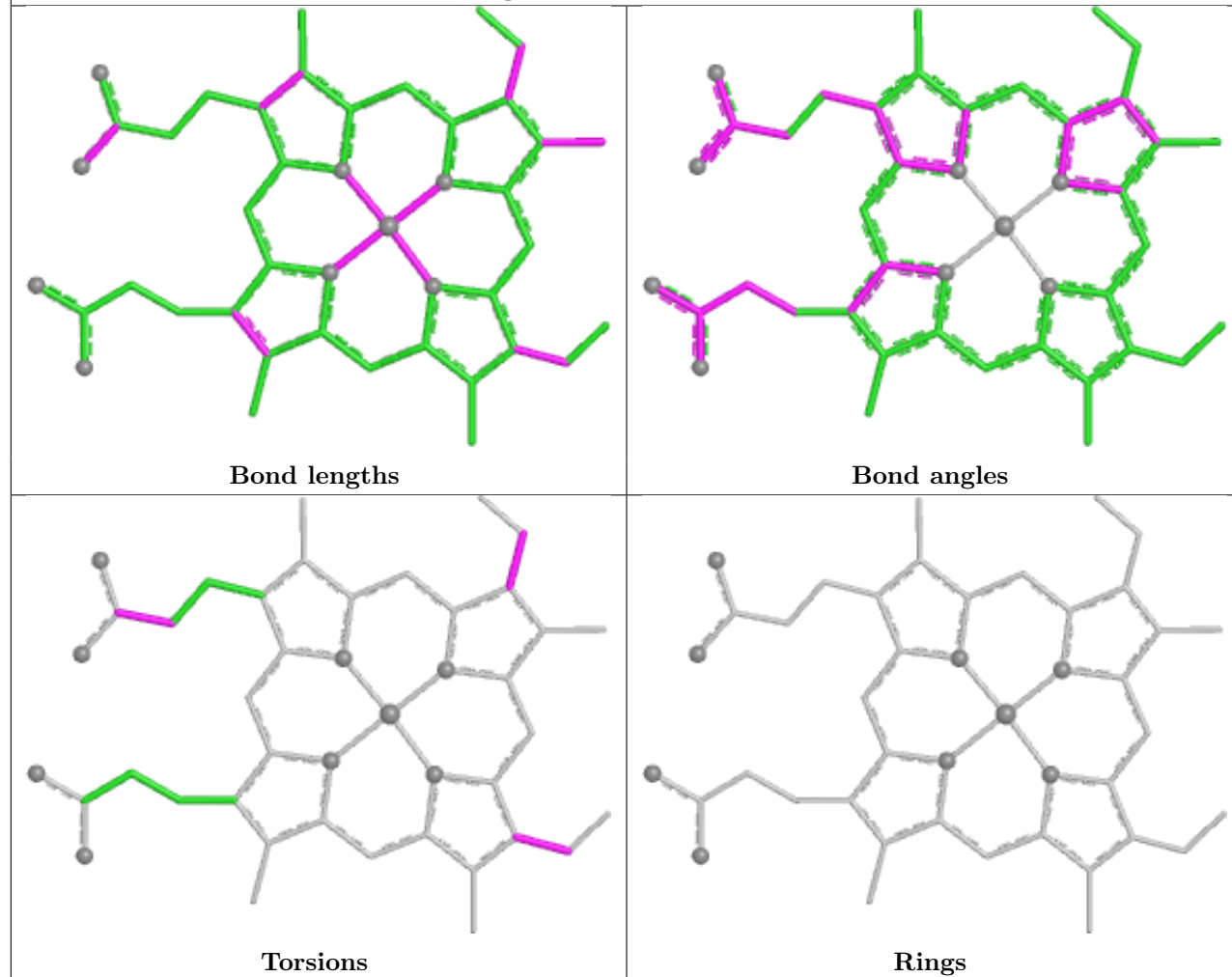
Ligand HEM P 1000



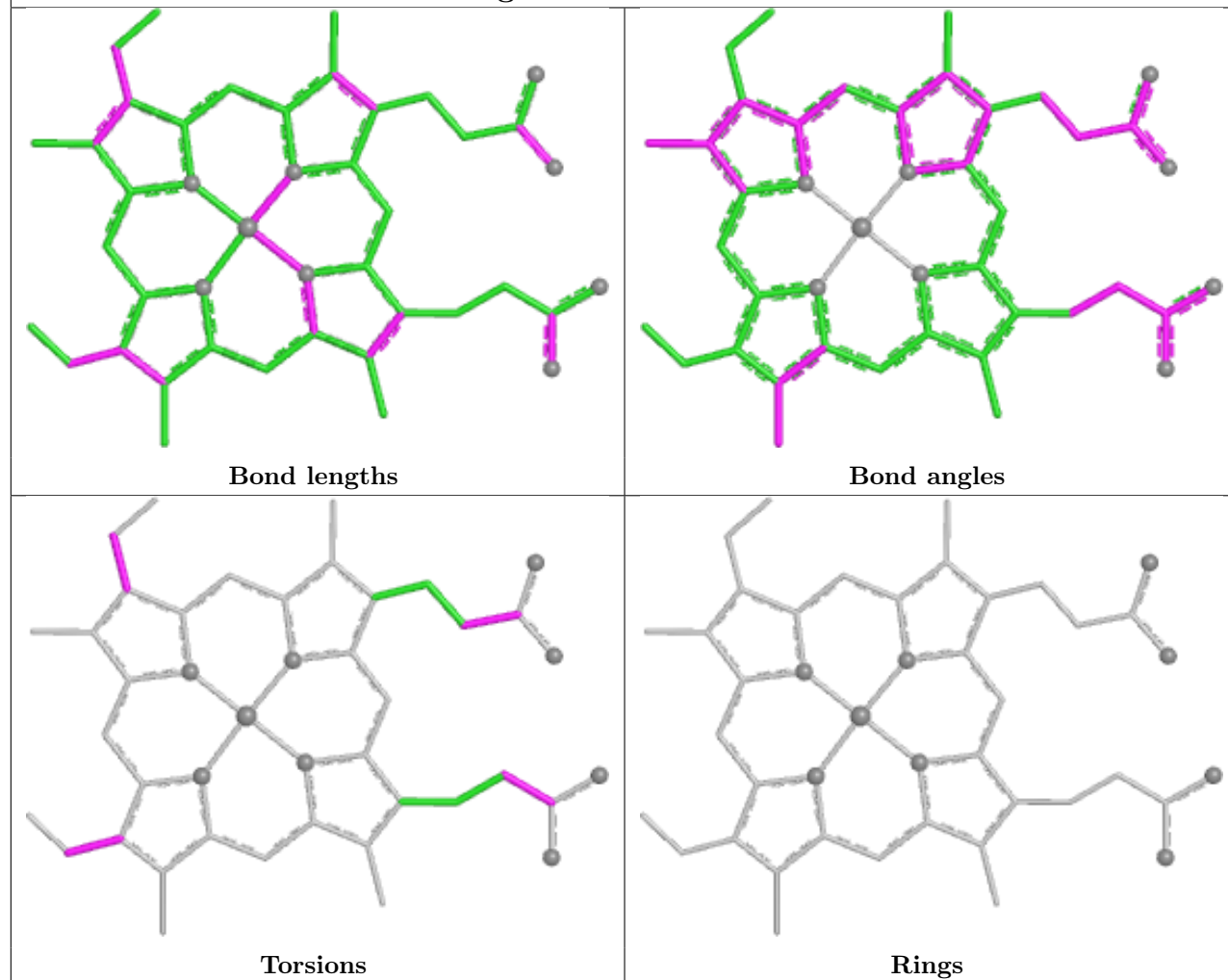
Ligand HEM Q 1000



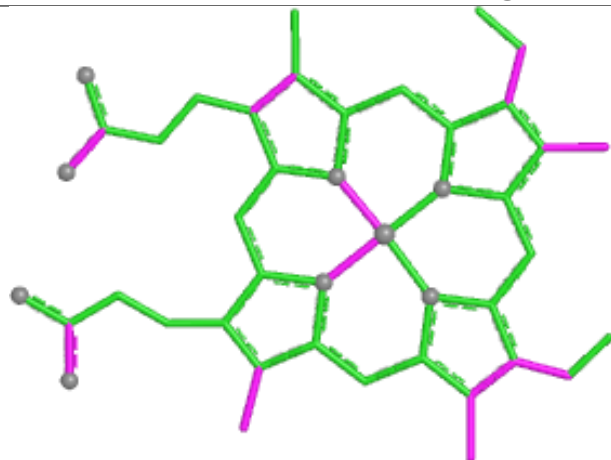
Ligand HEM R 1000



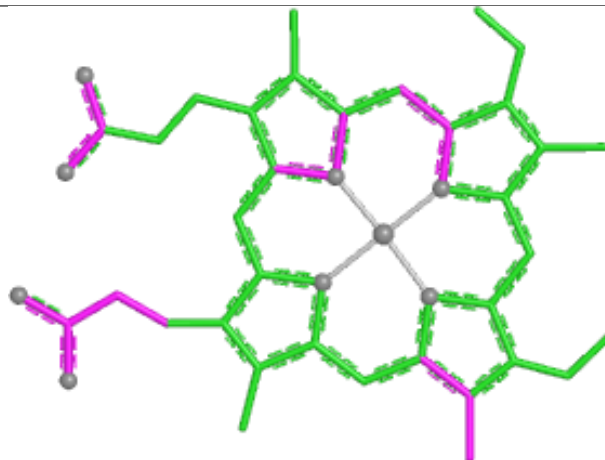
Ligand HEM A 1000



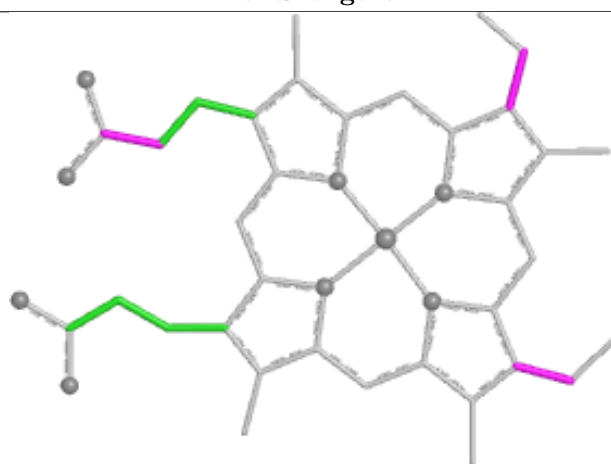
Ligand HEM N 1000



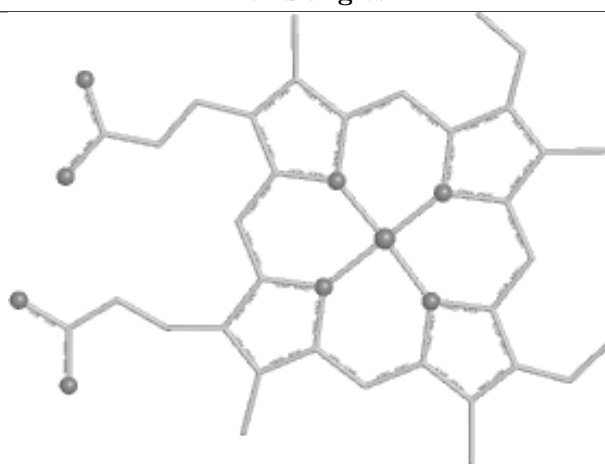
Bond lengths



Bond angles

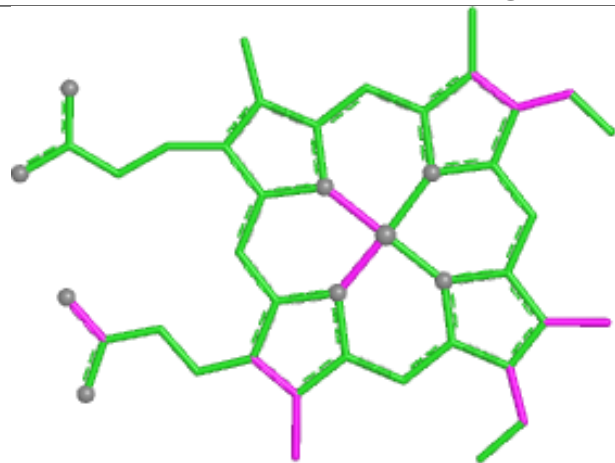


Torsions

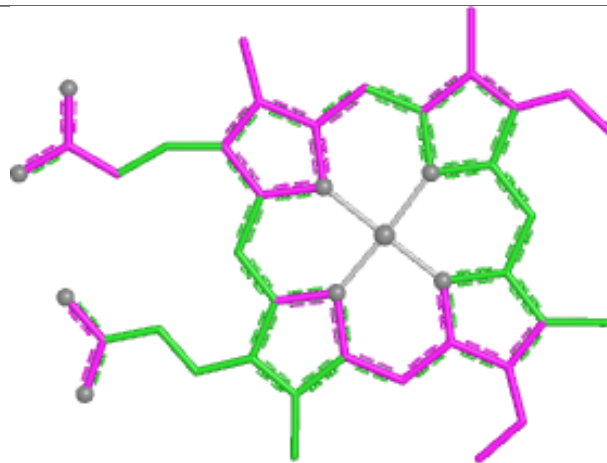


Rings

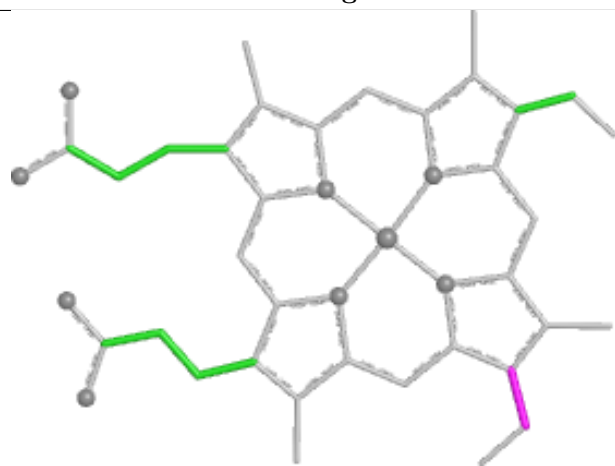
Ligand HEM B 1000



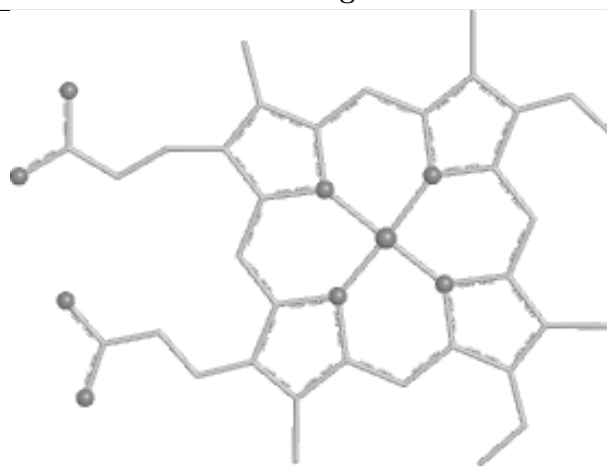
Bond lengths



Bond angles

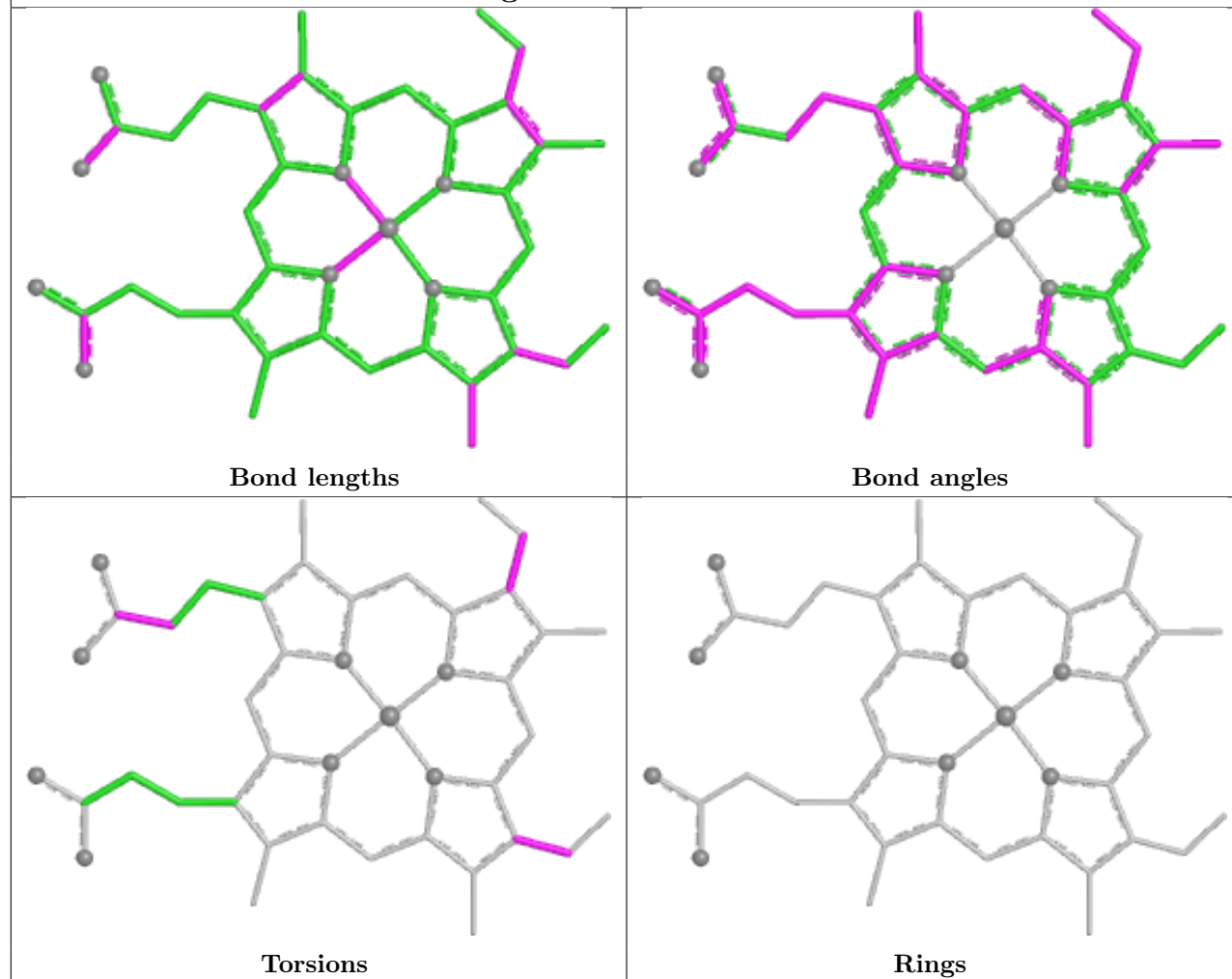


Torsions

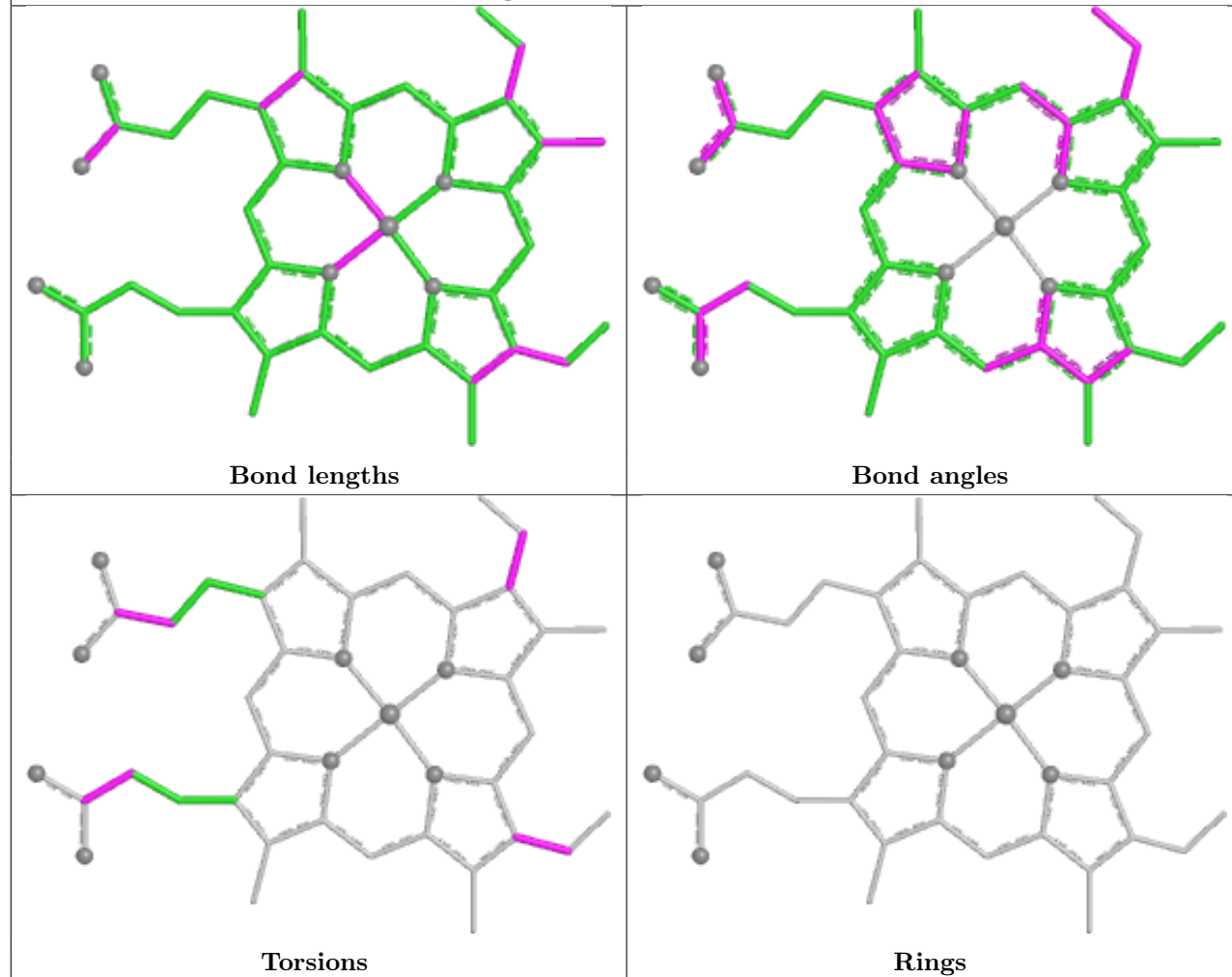


Rings

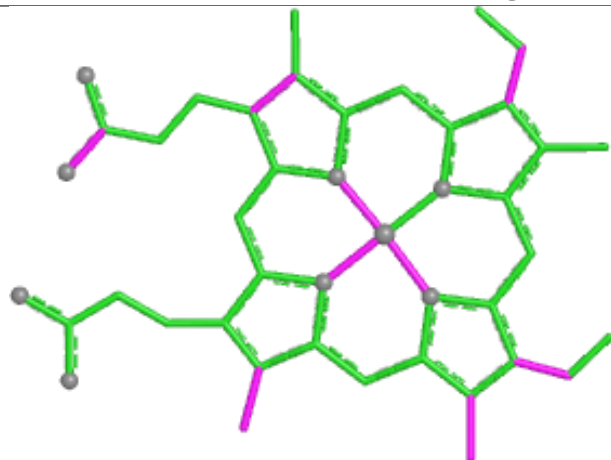
Ligand HEM E 1000



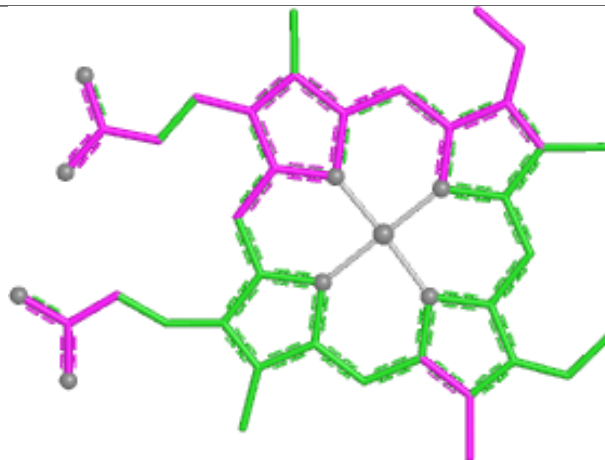
Ligand HEM O 1000



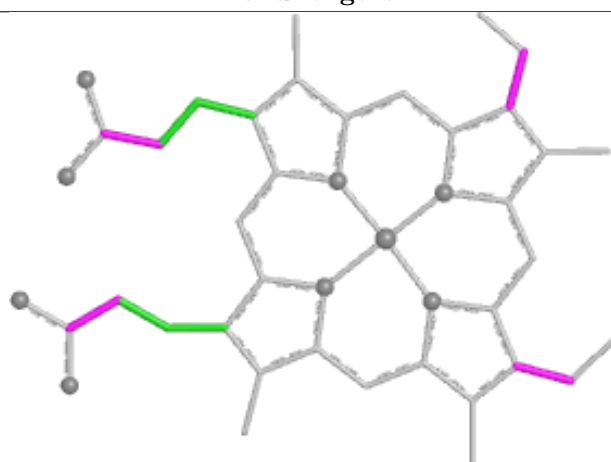
Ligand HEM J 1000



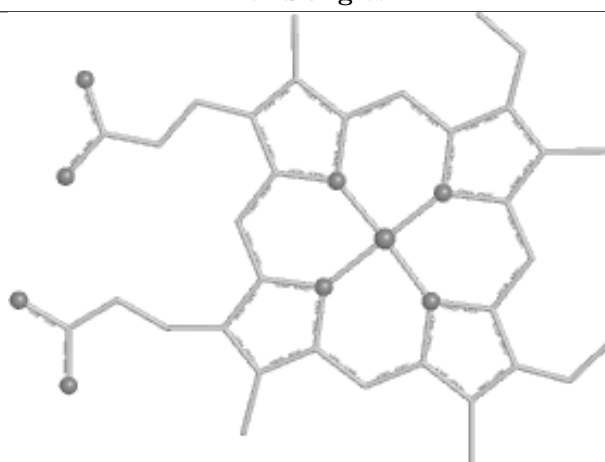
Bond lengths



Bond angles

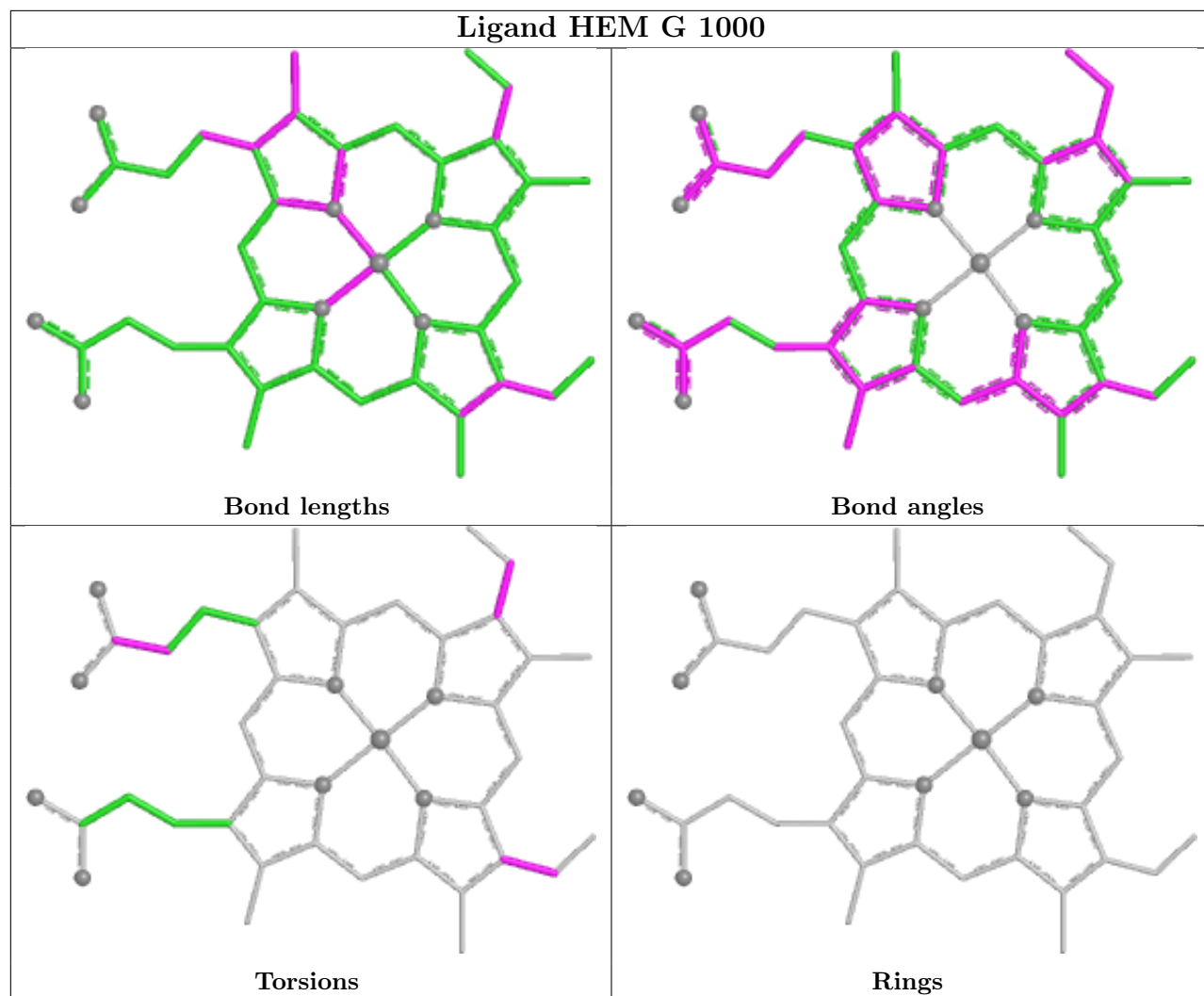


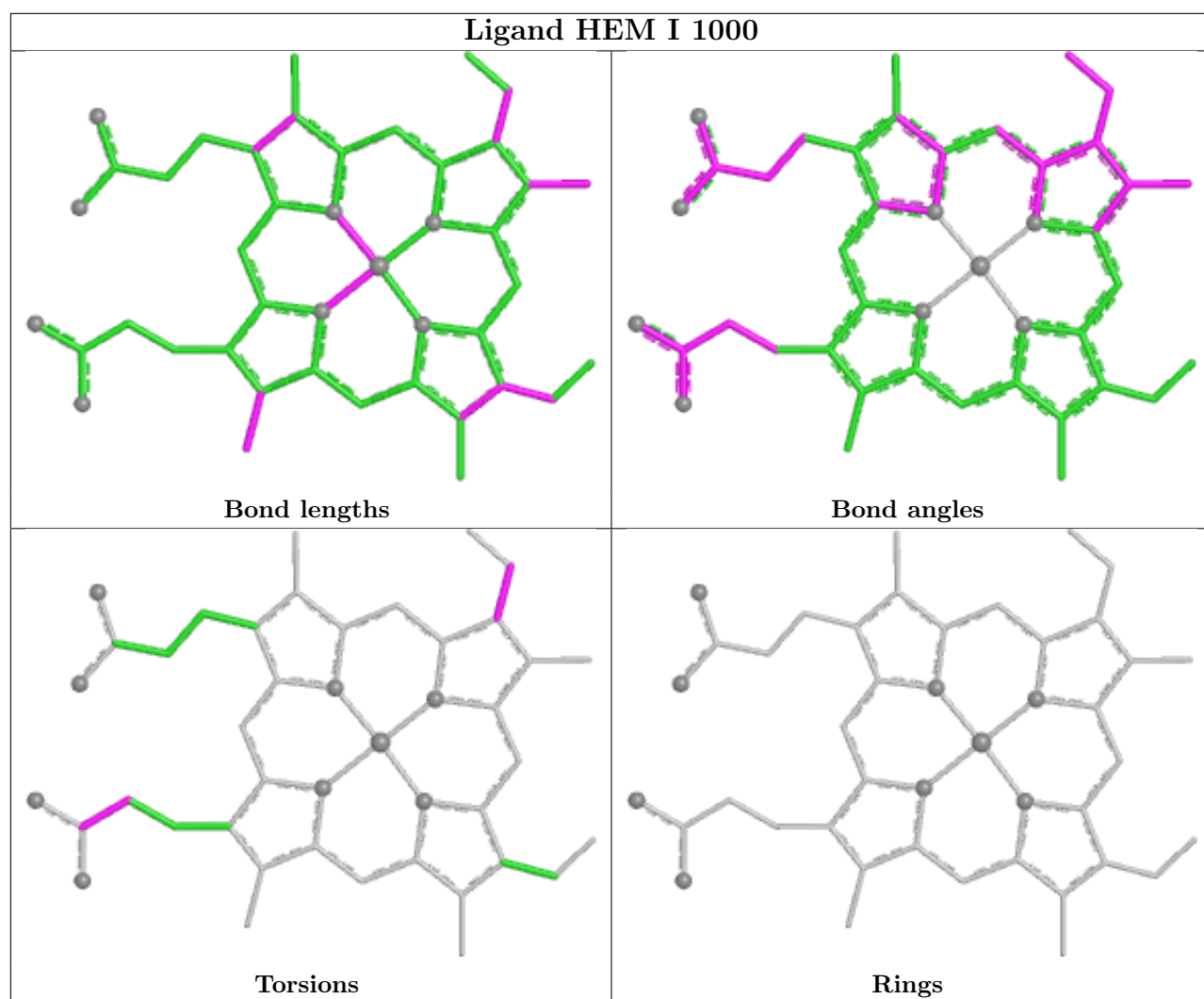
Torsions



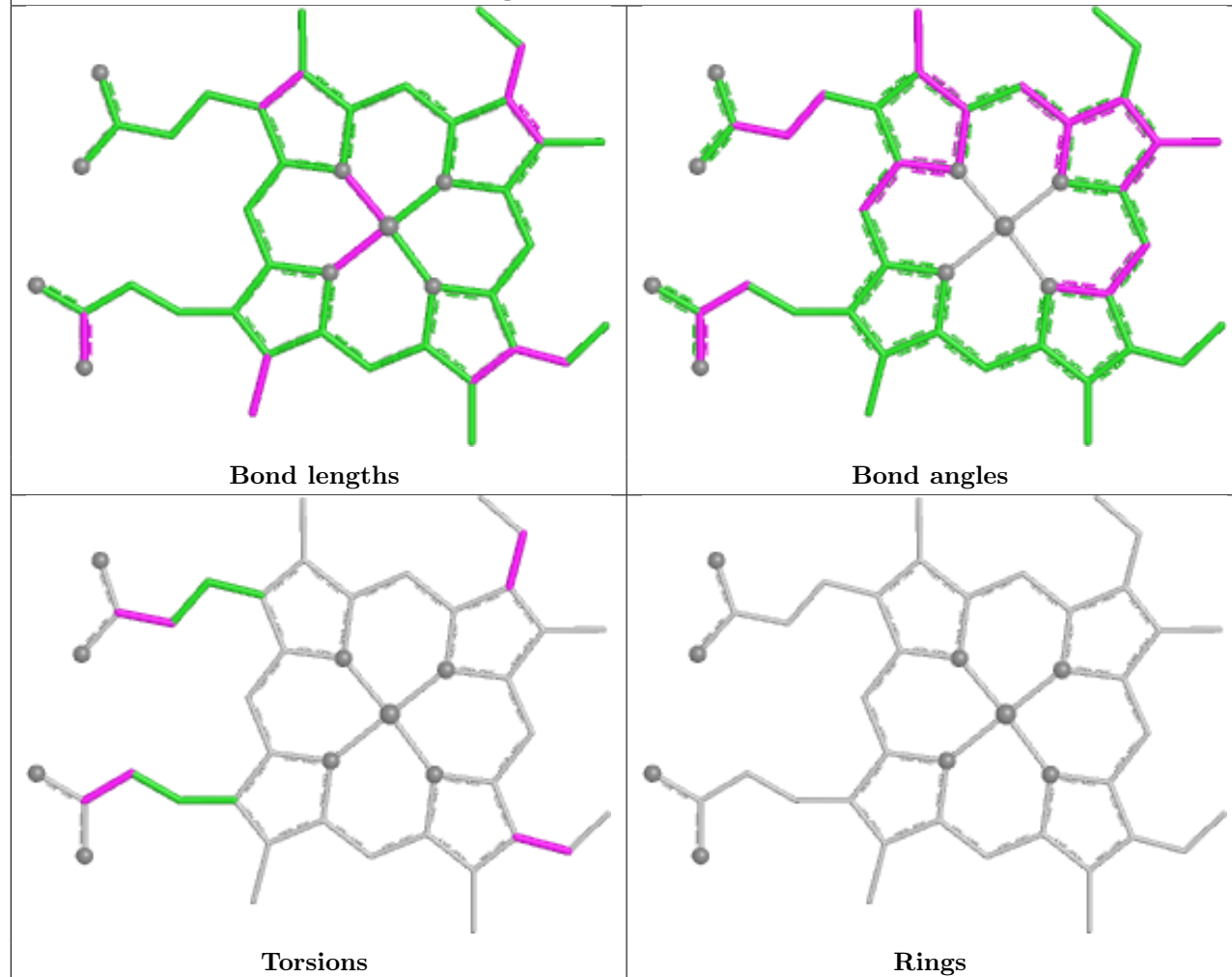
Rings

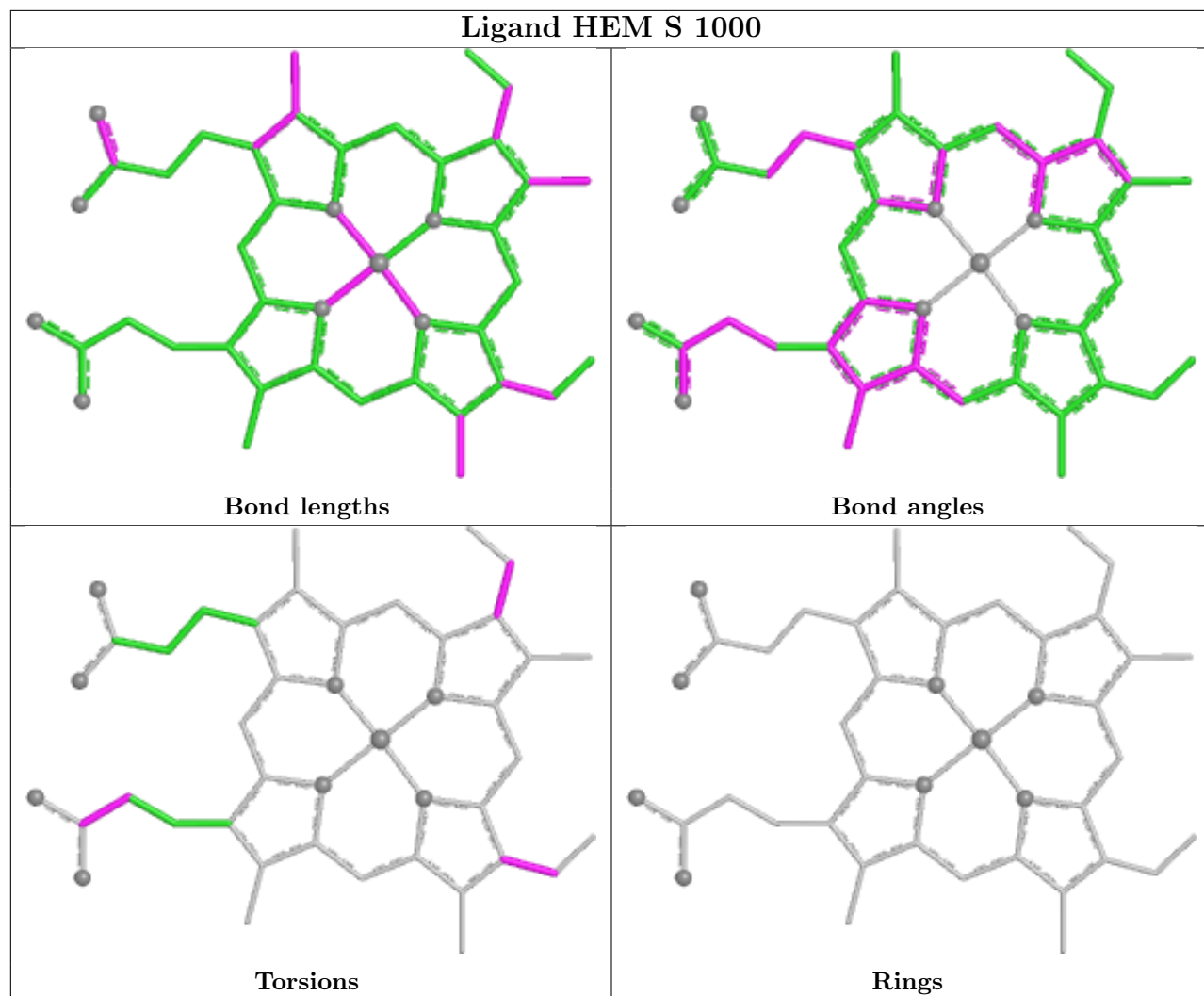
Ligand HEM G 1000



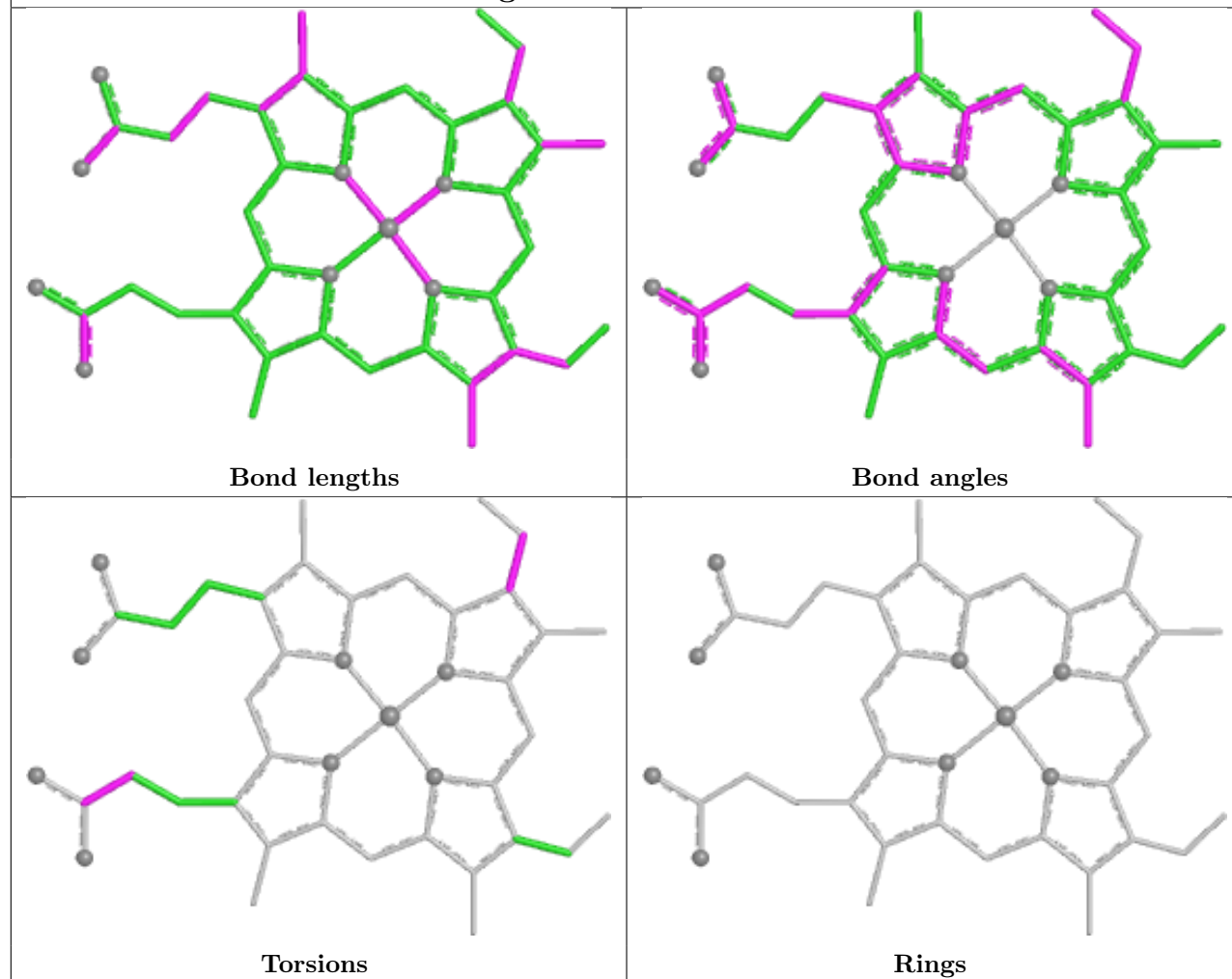


Ligand HEM D 1000

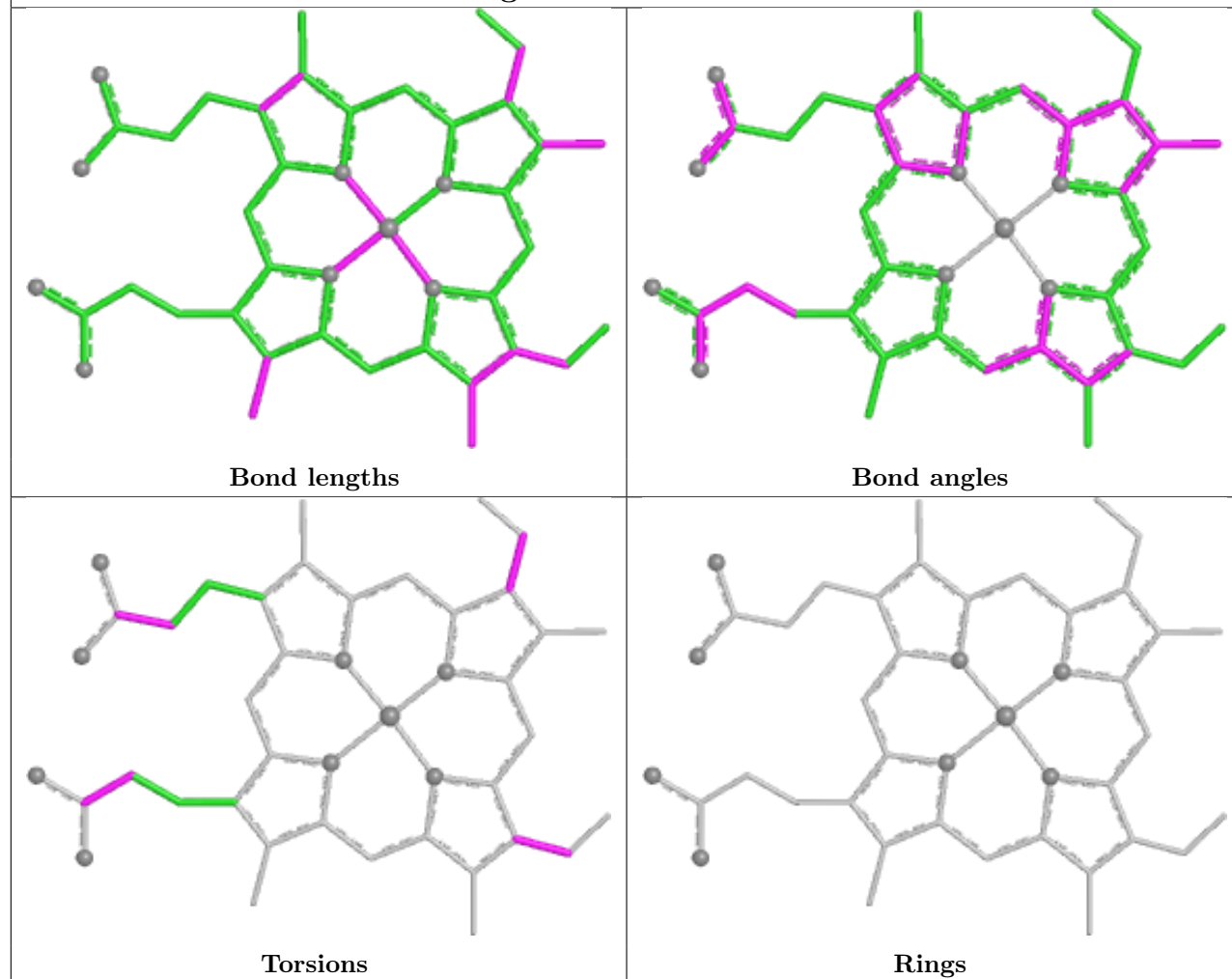




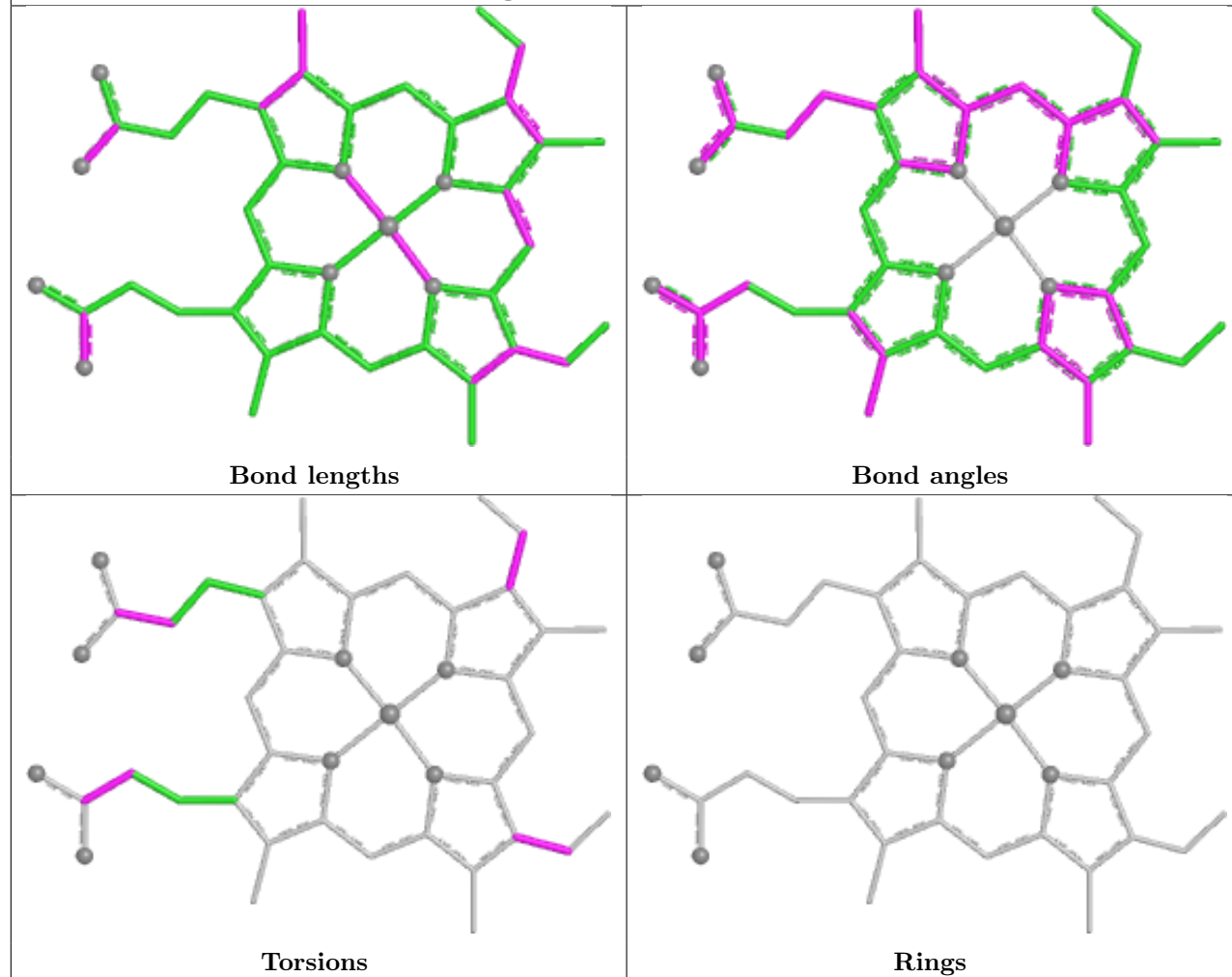
Ligand HEM K 1000

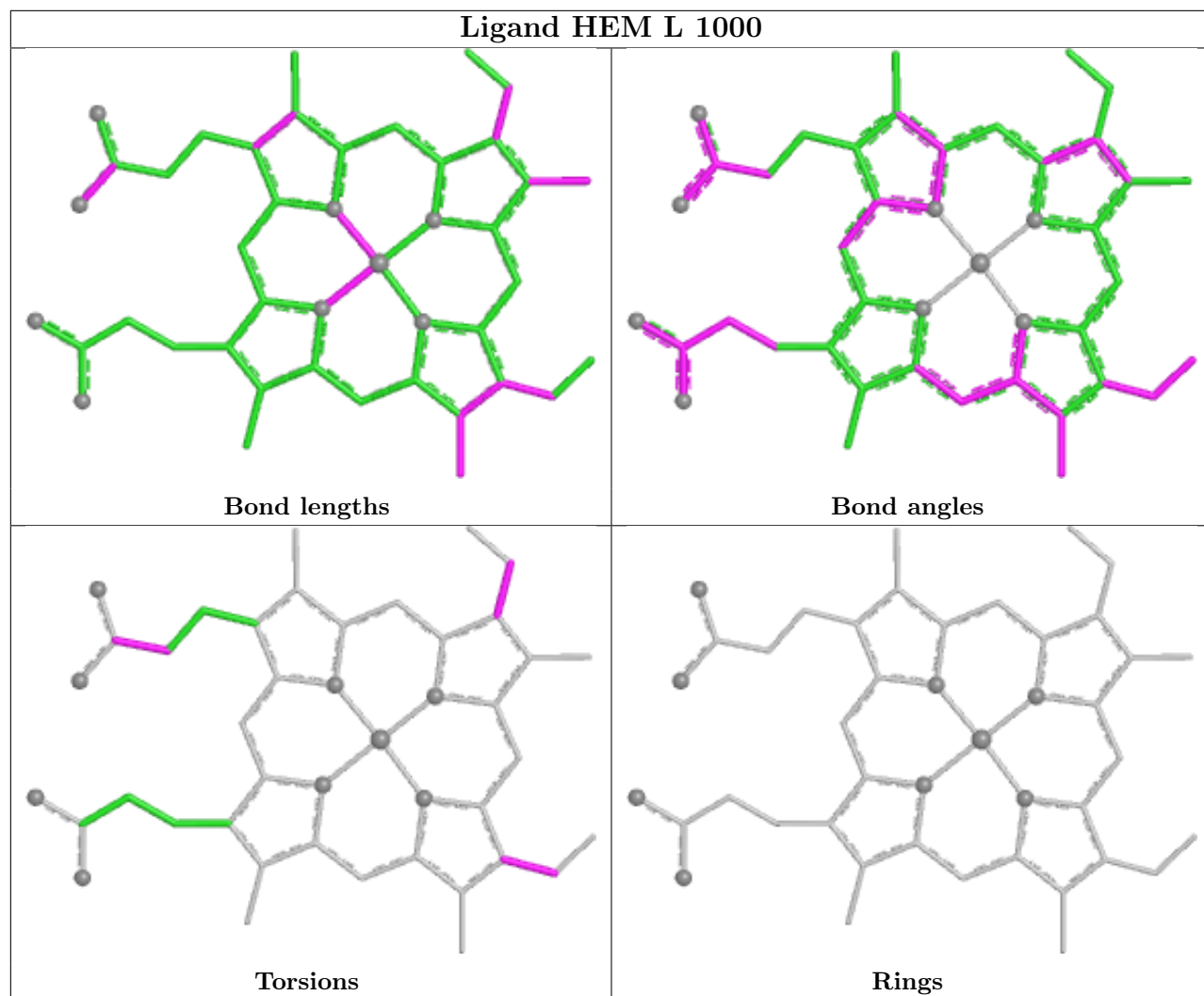


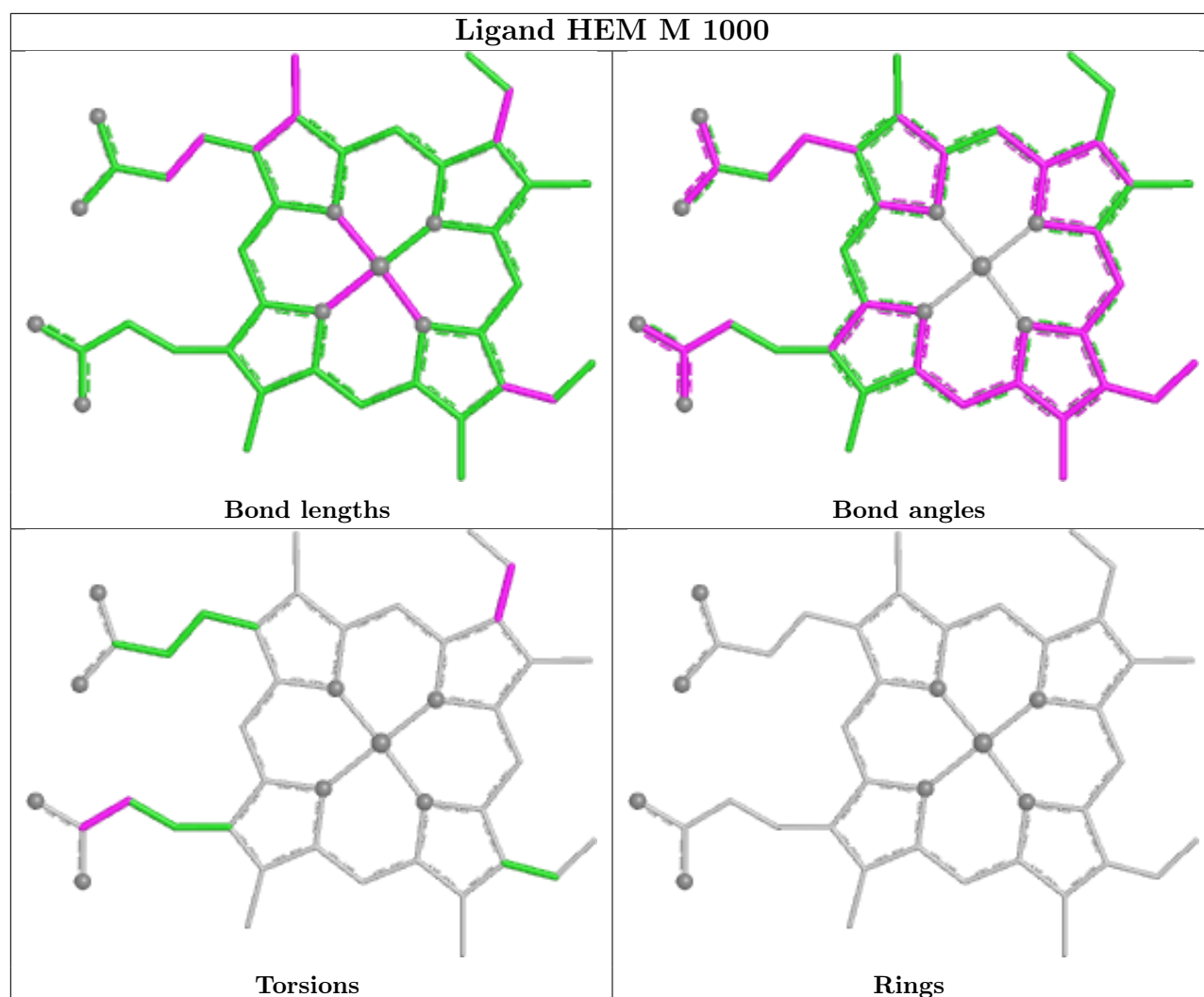
Ligand HEM T 1000



Ligand HEM C 1000







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	241/248 (97%)	-0.80	0 100 100	11, 24, 52, 62	0
1	B	241/248 (97%)	-0.68	3 (1%) 76 55	13, 24, 48, 70	0
1	C	241/248 (97%)	-0.78	1 (0%) 88 76	11, 23, 50, 68	0
1	D	241/248 (97%)	-0.70	0 100 100	14, 27, 54, 77	0
1	E	241/248 (97%)	-0.79	2 (0%) 82 64	9, 21, 47, 64	0
1	F	241/248 (97%)	-0.47	0 100 100	17, 40, 75, 96	0
1	G	241/248 (97%)	-0.60	1 (0%) 88 76	18, 34, 61, 90	0
1	H	241/248 (97%)	-0.74	0 100 100	14, 27, 55, 74	0
1	I	241/248 (97%)	-0.64	0 100 100	13, 28, 62, 80	0
1	J	241/248 (97%)	-0.59	2 (0%) 82 64	15, 32, 69, 88	0
1	K	241/248 (97%)	-0.55	1 (0%) 88 76	19, 34, 64, 87	0
1	L	241/248 (97%)	-0.60	1 (0%) 88 76	17, 31, 60, 81	0
1	M	241/248 (97%)	-0.63	2 (0%) 82 64	16, 29, 56, 79	0
1	N	241/248 (97%)	-0.54	0 100 100	19, 36, 71, 82	0
1	O	241/248 (97%)	-0.47	0 100 100	22, 41, 71, 96	0
1	P	241/248 (97%)	0.00	2 (0%) 82 64	38, 62, 108, 134	0
1	Q	241/248 (97%)	-0.19	3 (1%) 76 55	23, 52, 99, 120	0
1	R	241/248 (97%)	-0.11	3 (1%) 76 55	27, 56, 101, 124	0
1	S	241/248 (97%)	0.11	4 (1%) 69 45	39, 68, 110, 129	0
1	T	241/248 (97%)	0.11	4 (1%) 69 45	32, 63, 111, 135	0
All	All	4820/4960 (97%)	-0.48	29 (0%) 85 69	9, 36, 86, 135	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	132	SER	5.7
1	T	39	ALA	3.6
1	S	38	VAL	3.5
1	B	134	ALA	3.4
1	Q	132	SER	3.2

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](#)

There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
4	CA	S	1001	1/1	0.89	0.07	60,60,60,60	0
3	NO2	Q	2000	3/3	0.92	0.12	45,45,45,49	0
3	NO2	B	2000	3/3	0.92	0.19	32,32,36,43	0
3	NO2	N	2000	3/3	0.94	0.17	41,41,45,47	0
3	NO2	P	2000	3/3	0.94	0.10	55,55,55,55	0
3	NO2	I	2000	3/3	0.94	0.13	27,27,29,32	0
3	NO2	R	2000	3/3	0.94	0.17	48,48,50,52	0
3	NO2	M	2000	3/3	0.94	0.13	31,31,34,41	0
2	HEM	G	1000	43/43	0.95	0.11	21,26,36,39	0
3	NO2	G	2000	3/3	0.95	0.10	36,36,37,39	0
2	HEM	Q	1000	43/43	0.95	0.11	29,31,39,45	0
3	NO2	K	2000	3/3	0.95	0.11	34,34,36,39	0
3	NO2	T	2000	3/3	0.95	0.10	57,57,57,58	0
2	HEM	S	1000	43/43	0.95	0.11	45,55,64,71	0
2	HEM	B	1000	43/43	0.96	0.09	15,18,27,33	0
2	HEM	T	1000	43/43	0.96	0.09	39,46,52,59	0
3	NO2	A	2000	3/3	0.96	0.14	29,29,31,34	0
2	HEM	N	1000	43/43	0.96	0.09	22,31,40,48	0
3	NO2	C	2000	3/3	0.96	0.12	25,25,28,31	0

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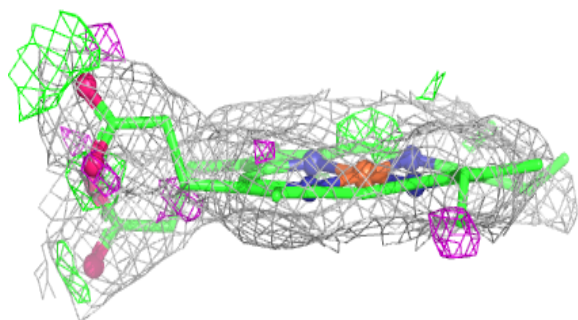
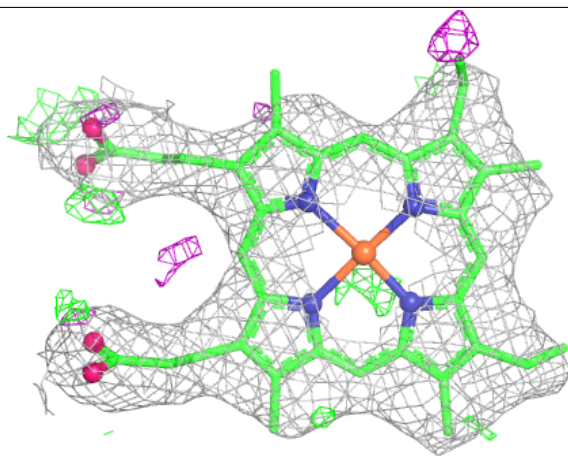
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	HEM	F	1000	43/43	0.96	0.10	24,33,42,47	0
3	NO2	S	2000	3/3	0.96	0.10	63,63,64,65	0
3	NO2	H	2000	3/3	0.96	0.11	28,28,30,33	0
4	CA	G	1001	1/1	0.96	0.07	24,24,24,24	0
2	HEM	R	1000	43/43	0.96	0.09	30,36,43,53	0
2	HEM	L	1000	43/43	0.97	0.08	18,22,30,35	0
2	HEM	M	1000	43/43	0.97	0.08	17,22,29,34	0
2	HEM	D	1000	43/43	0.97	0.08	15,22,31,35	0
3	NO2	J	2000	3/3	0.97	0.08	29,29,30,31	0
2	HEM	O	1000	43/43	0.97	0.09	27,34,42,46	0
3	NO2	L	2000	3/3	0.97	0.10	31,31,32,35	0
2	HEM	P	1000	43/43	0.97	0.09	41,45,52,55	0
2	HEM	E	1000	43/43	0.97	0.08	11,16,23,30	0
2	HEM	A	1000	43/43	0.97	0.07	13,19,28,36	0
2	HEM	C	1000	43/43	0.97	0.08	13,17,24,31	0
2	HEM	H	1000	43/43	0.97	0.08	12,19,29,33	0
2	HEM	I	1000	43/43	0.97	0.08	13,19,27,32	0
2	HEM	J	1000	43/43	0.97	0.08	15,20,28,35	0
2	HEM	K	1000	43/43	0.97	0.08	21,25,34,37	0
4	CA	I	1001	1/1	0.97	0.04	23,23,23,23	0
4	CA	K	1001	1/1	0.97	0.08	26,26,26,26	0
4	CA	M	1001	1/1	0.97	0.07	26,26,26,26	0
4	CA	N	1001	1/1	0.97	0.06	32,32,32,32	0
4	CA	R	1001	1/1	0.97	0.04	50,50,50,50	0
3	NO2	F	2000	3/3	0.97	0.11	40,40,42,44	0
4	CA	T	1001	1/1	0.97	0.07	52,52,52,52	0
3	NO2	D	2000	3/3	0.98	0.07	30,30,32,34	0
4	CA	J	1001	1/1	0.98	0.04	29,29,29,29	0
4	CA	A	1001	1/1	0.98	0.04	21,21,21,21	0
4	CA	L	1001	1/1	0.98	0.04	25,25,25,25	0
4	CA	B	1001	1/1	0.98	0.03	17,17,17,17	0
4	CA	C	1001	1/1	0.98	0.04	20,20,20,20	0
4	CA	O	1001	1/1	0.98	0.04	29,29,29,29	0
4	CA	P	1001	1/1	0.98	0.05	54,54,54,54	0
4	CA	Q	1001	1/1	0.98	0.03	48,48,48,48	0
4	CA	D	1001	1/1	0.98	0.04	24,24,24,24	0
3	NO2	O	2000	3/3	0.98	0.07	40,40,42,43	0
4	CA	H	1001	1/1	0.98	0.04	22,22,22,22	0
4	CA	F	1001	1/1	0.99	0.04	30,30,30,30	0
3	NO2	E	2000	3/3	0.99	0.06	22,22,24,28	0
4	CA	E	1001	1/1	0.99	0.02	13,13,13,13	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.

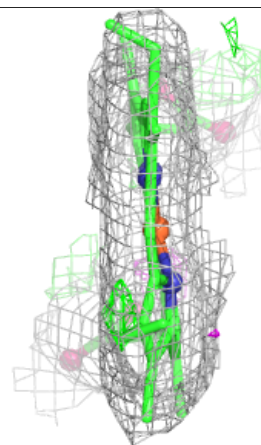
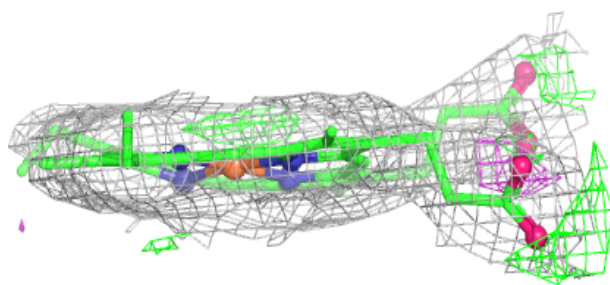
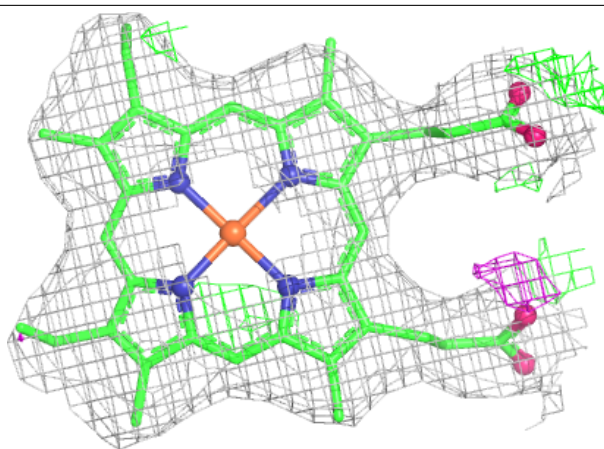
Electron density around HEM G 1000:

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



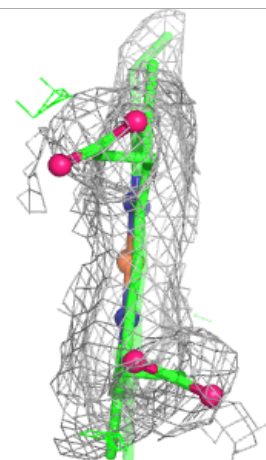
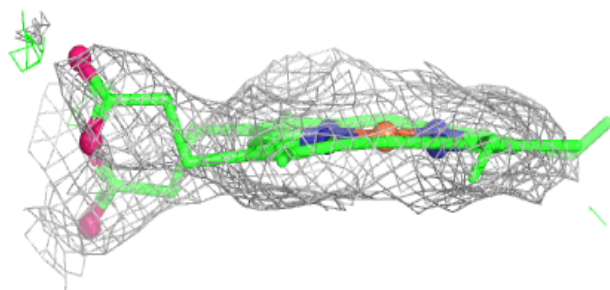
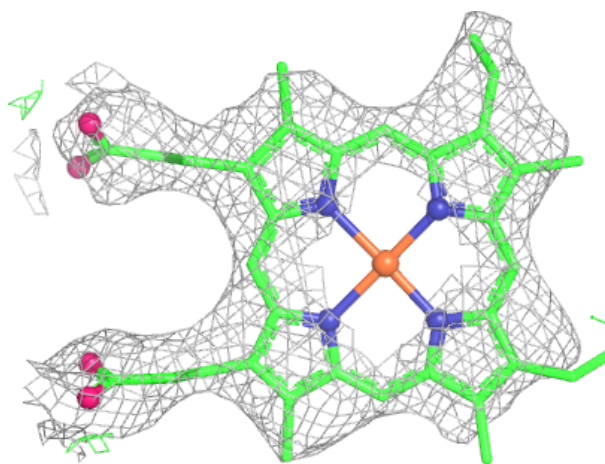
Electron density around HEM Q 1000:

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



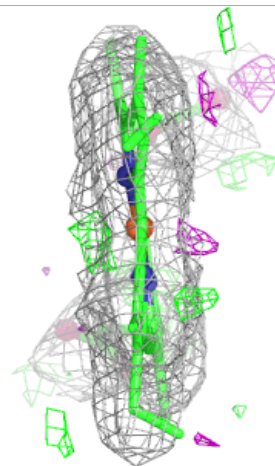
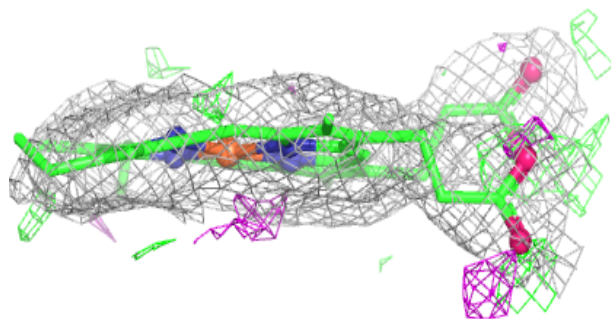
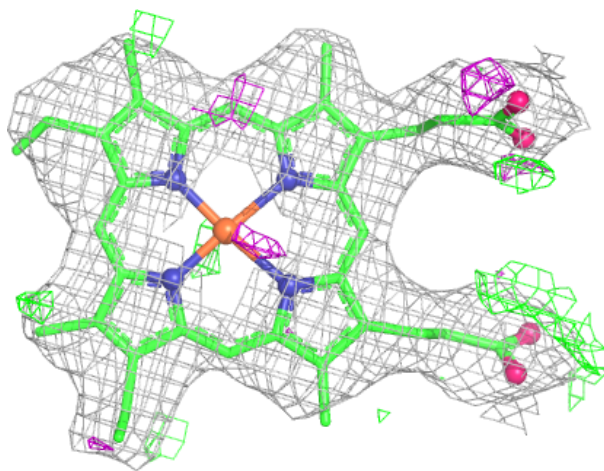
Electron density around HEM S 1000:

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and green (positive)



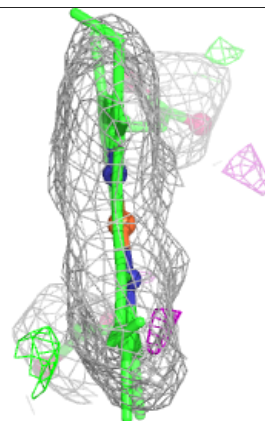
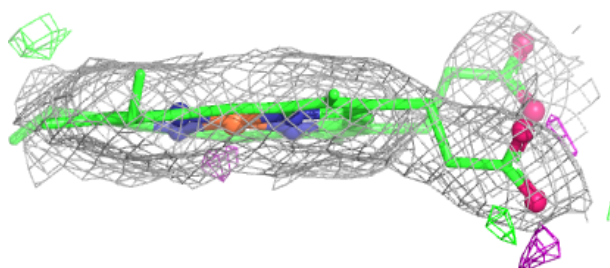
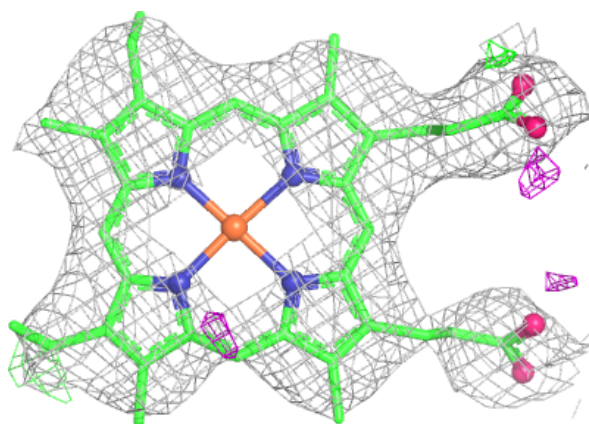
Electron density around HEM B 1000:

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



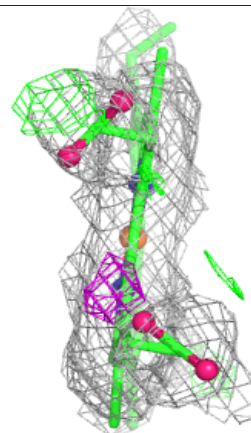
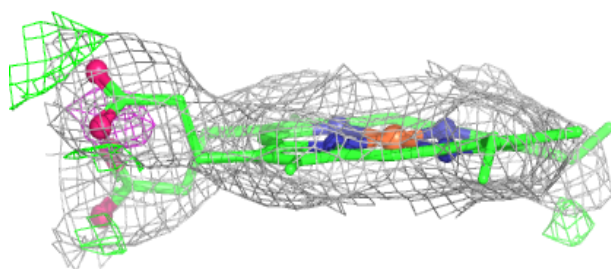
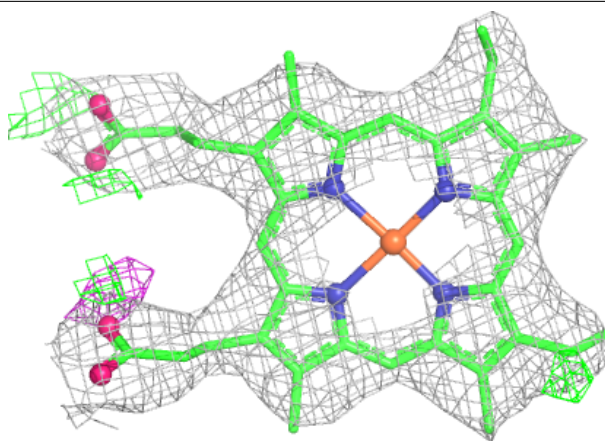
Electron density around HEM T 1000:

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



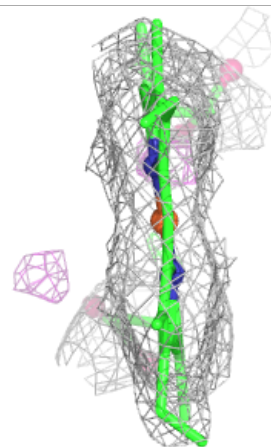
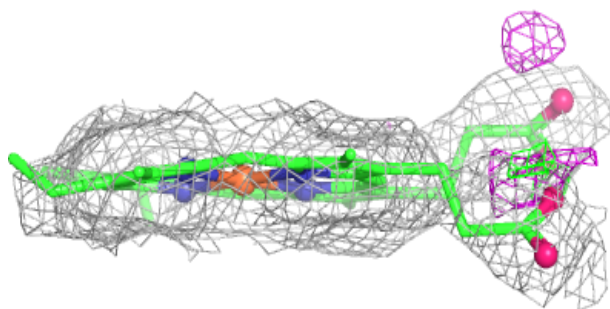
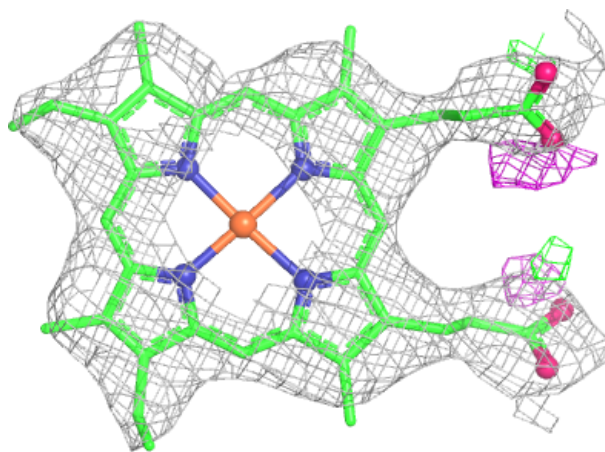
Electron density around HEM N 1000:

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



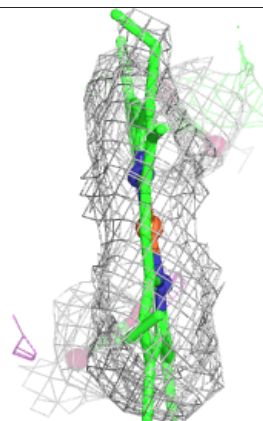
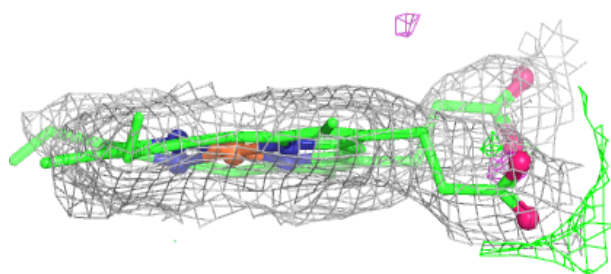
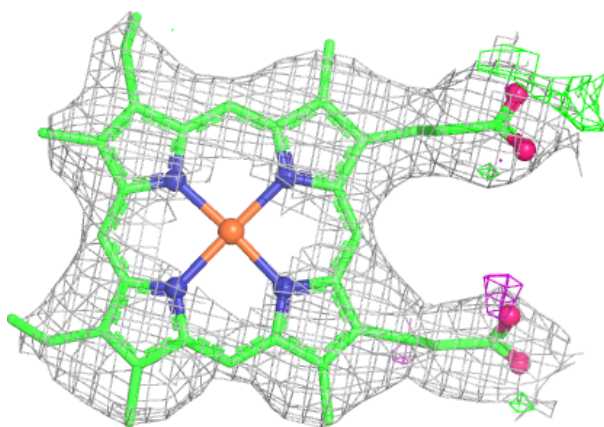
Electron density around HEM F 1000:

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



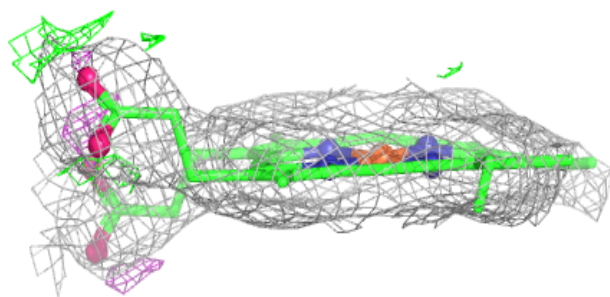
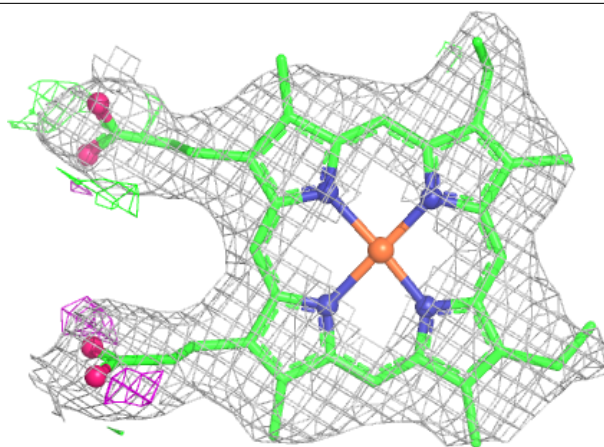
Electron density around HEM R 1000:

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



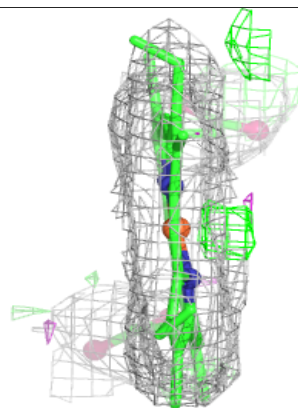
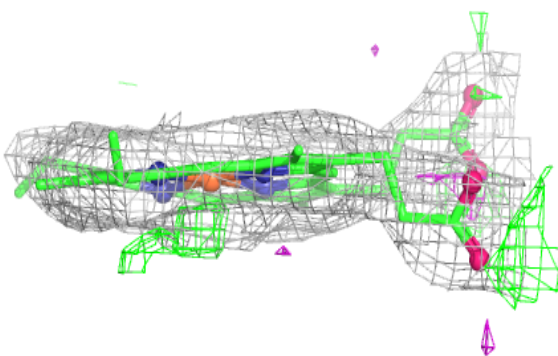
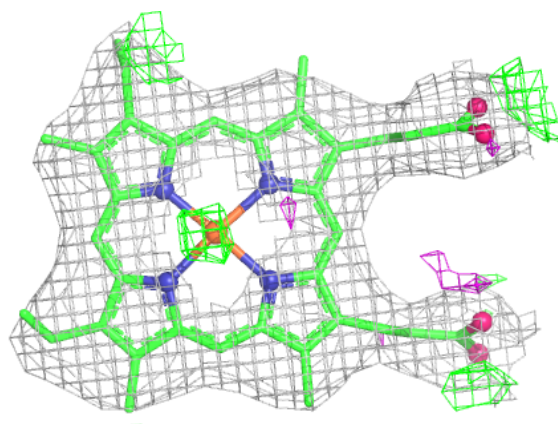
Electron density around HEM L 1000:

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

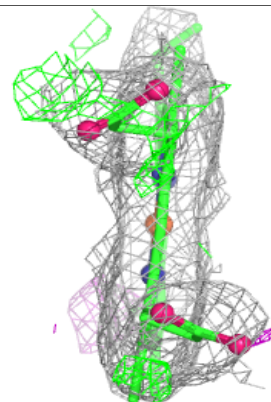
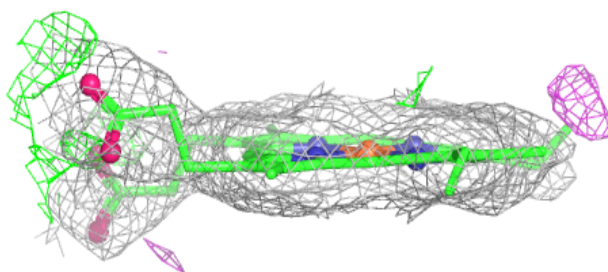
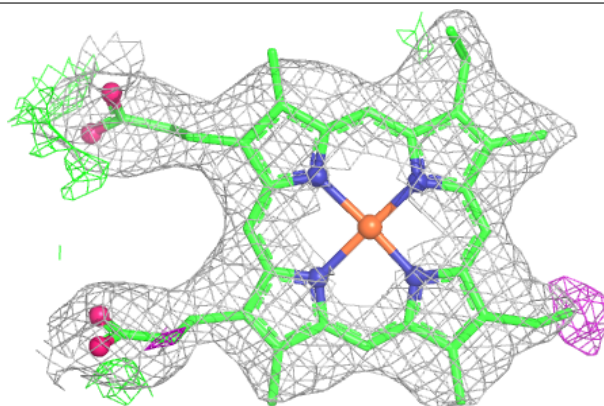


Electron density around HEM M 1000:

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

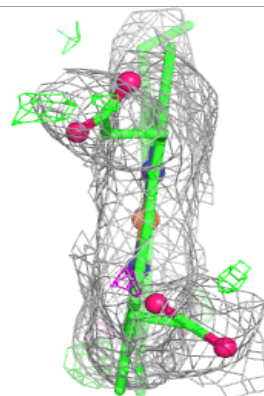
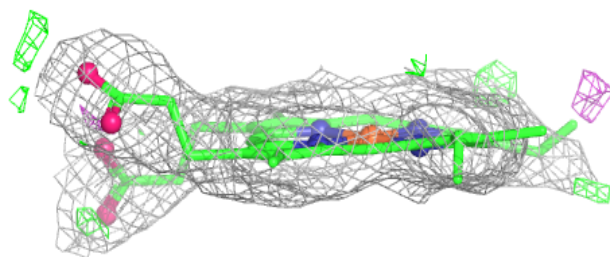
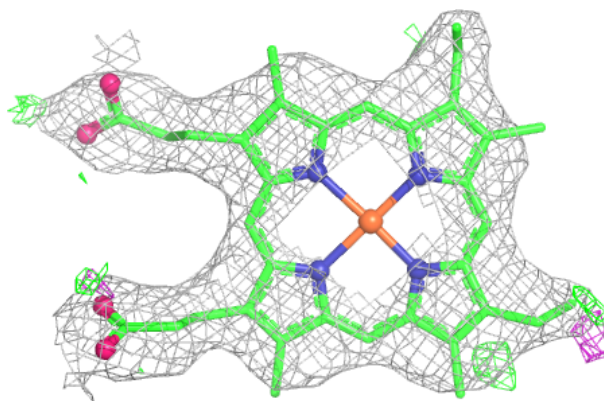
**Electron density around HEM D 1000:**

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

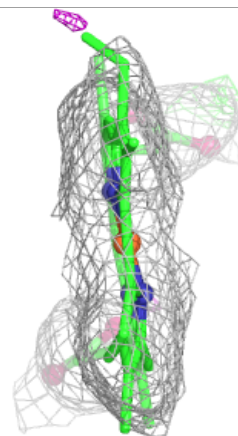
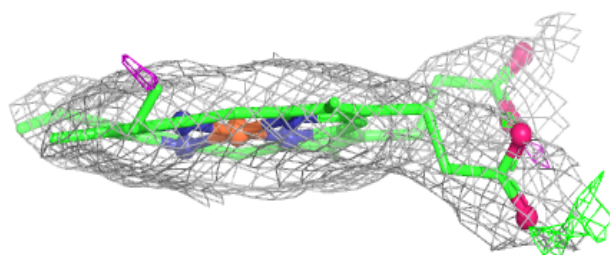
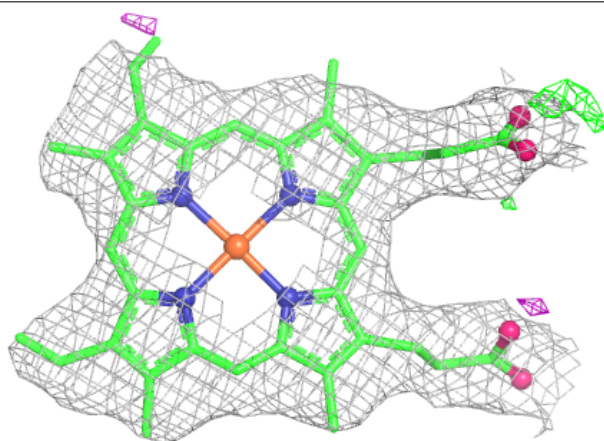


Electron density around HEM O 1000:

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

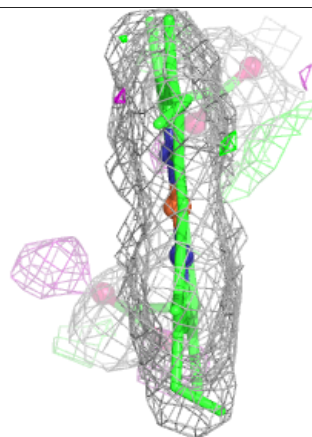
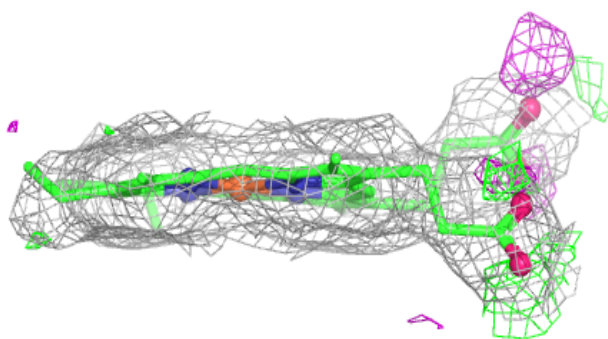
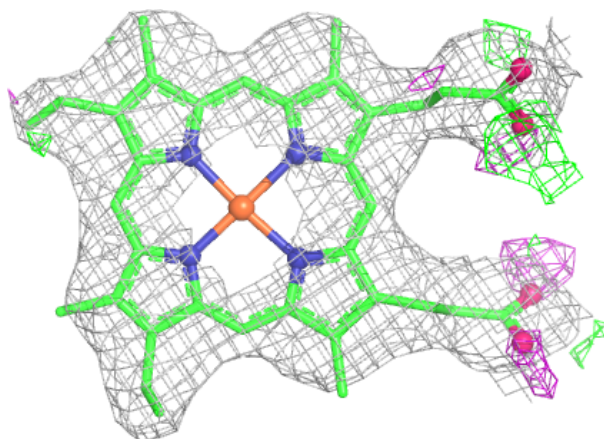
**Electron density around HEM P 1000:**

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



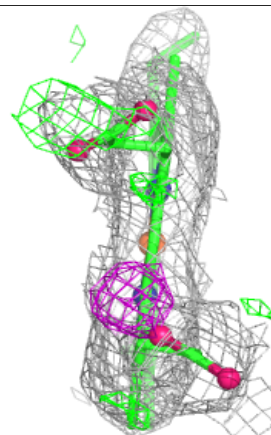
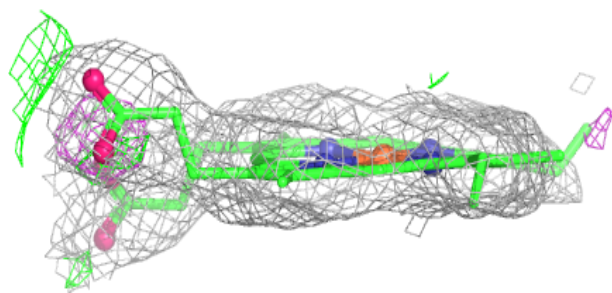
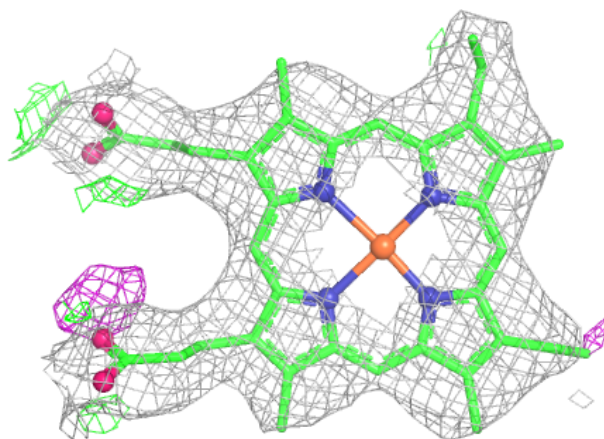
Electron density around HEM E 1000:

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



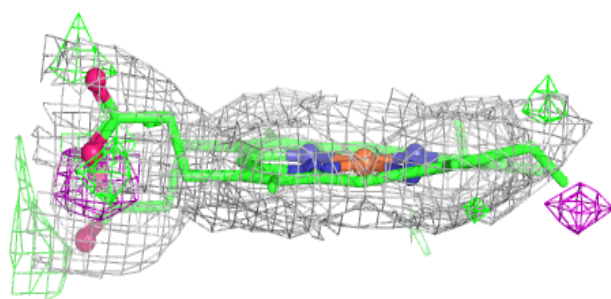
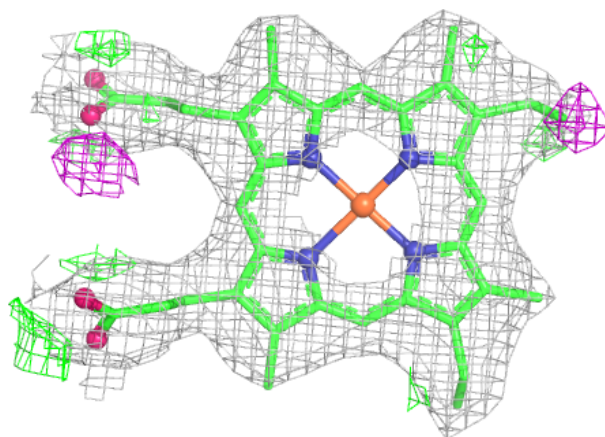
Electron density around HEM A 1000:

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



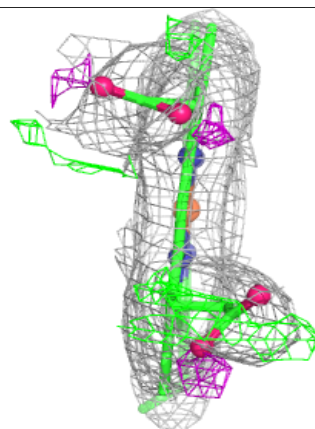
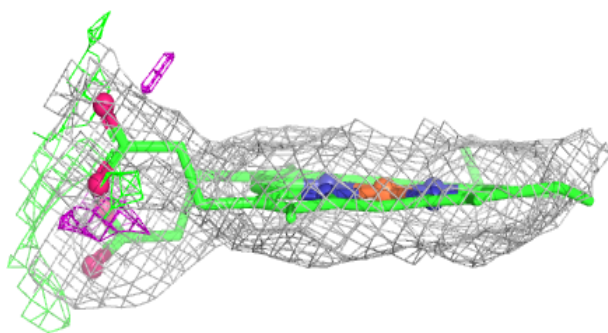
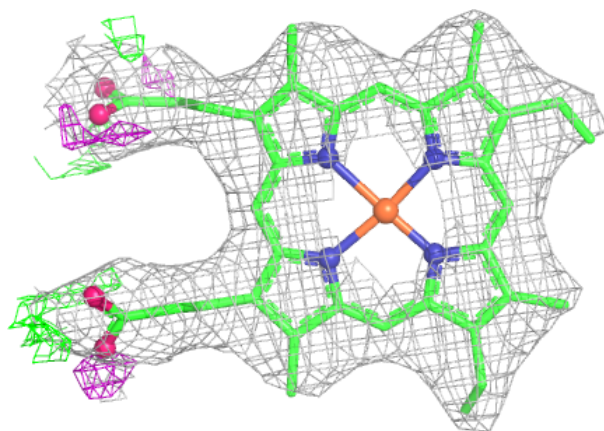
Electron density around HEM C 1000:

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



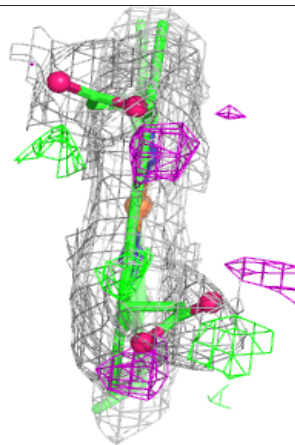
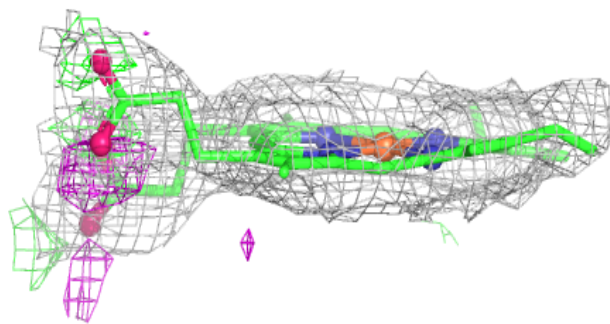
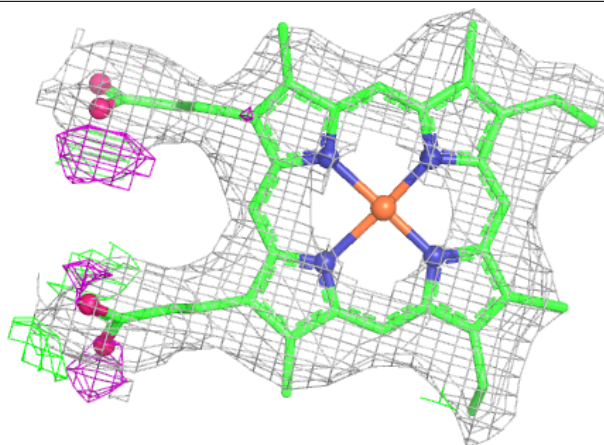
Electron density around HEM H 1000:

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



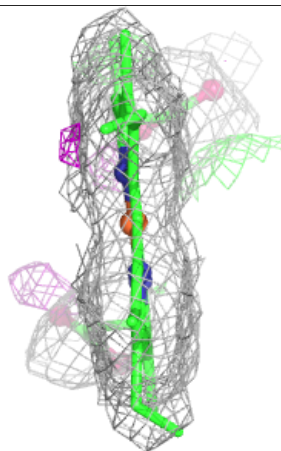
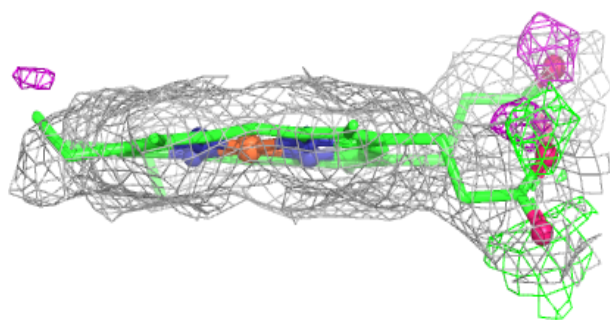
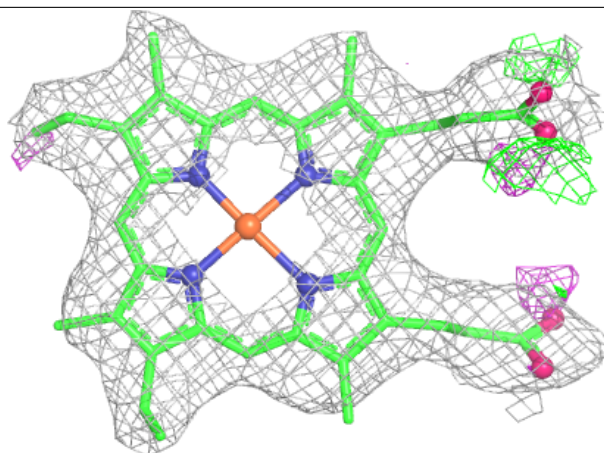
Electron density around HEM I 1000:

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



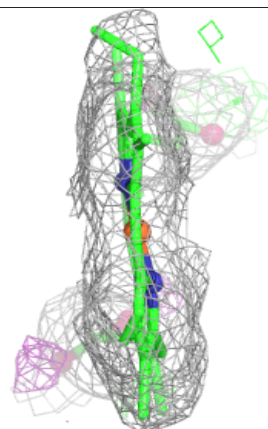
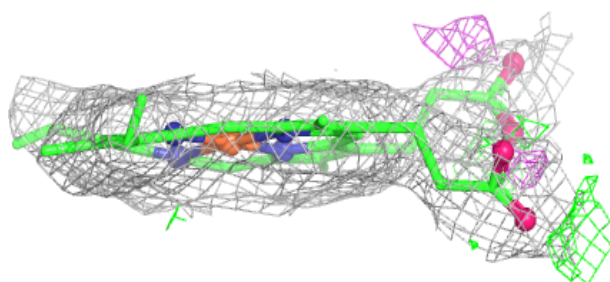
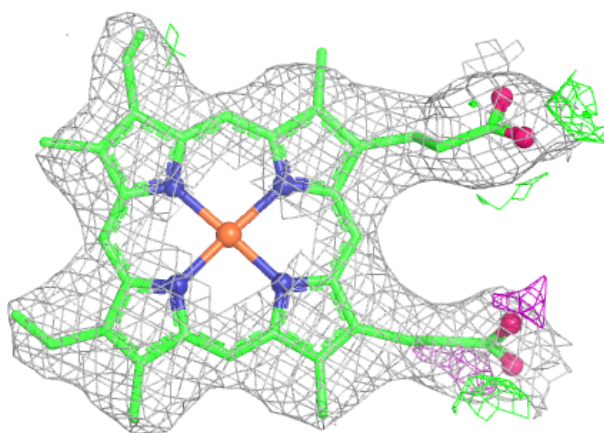
Electron density around HEM J 1000:

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



Electron density around HEM K 1000:

$2mF_o-DF_c$ (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.