



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 7, 2026 – 05:28 AM JST

PDB ID : 8HKJ / pdb_00008hkj
Title : Crystal structure of the CYP102A5 haem Domain isolated from *Bacillus cereus*
Authors : Stanfield, J.K.; Onoda, H.; Sugimoto, H.; Shoji, O.
Deposited on : 2022-11-27
Resolution : 2.80 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 : 1.8.5 (274361), CSD as541be (2020)
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

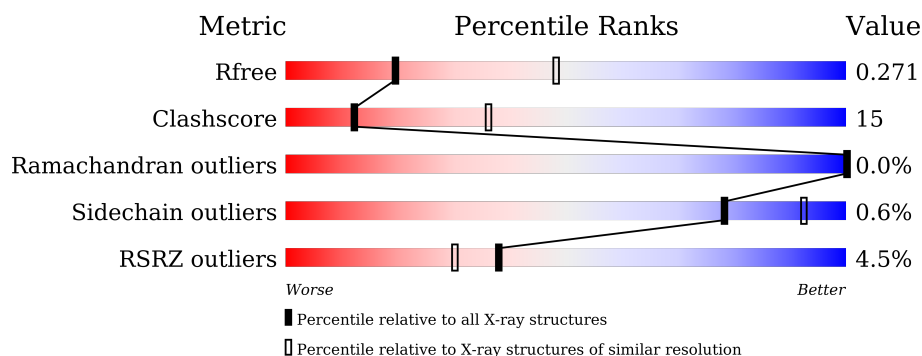
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	458	71% 22% 6%
1	B	458	66% 28% 6%
1	C	458	67% 24% 8%
1	D	458	67% 24% 9%
1	E	458	66% 26% 8%
1	F	458	66% 26% 9%

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Mol	Chain	Length	Quality of chain
1	G	458	
1	H	458	
1	I	458	
1	J	458	
1	K	458	
1	L	458	

2 Entry composition

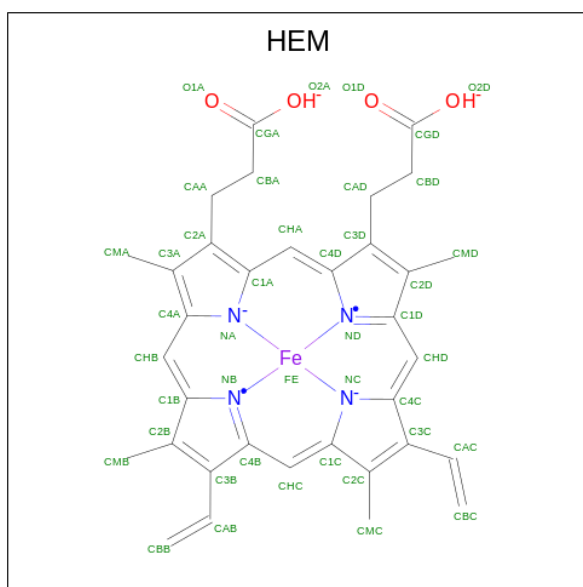
There are 3 unique types of molecules in this entry. The entry contains 41062 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional cytochrome P450/NADPH-P450 reductase.

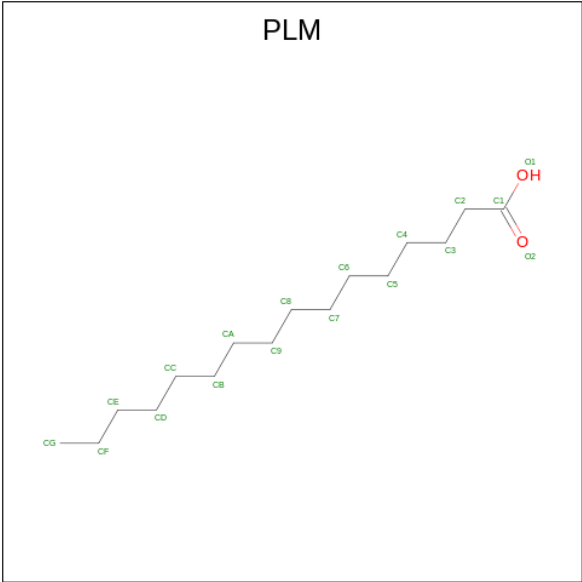
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	0	0	0
			3460	2213	582	648	17			
1	B	430	Total	C	N	O	S	0	0	0
			3473	2221	585	649	18			
1	C	421	Total	C	N	O	S	0	0	0
			3400	2180	569	634	17			
1	D	419	Total	C	N	O	S	0	0	0
			3380	2170	566	627	17			
1	E	422	Total	C	N	O	S	0	0	0
			3406	2183	574	632	17			
1	F	419	Total	C	N	O	S	0	0	0
			3382	2171	569	625	17			
1	G	401	Total	C	N	O	S	0	0	0
			3238	2084	542	595	17			
1	H	415	Total	C	N	O	S	0	0	0
			3354	2154	563	620	17			
1	I	399	Total	C	N	O	S	0	0	0
			3223	2075	538	594	16			
1	J	415	Total	C	N	O	S	0	0	0
			3351	2153	562	619	17			
1	K	416	Total	C	N	O	S	0	0	0
			3357	2154	564	622	17			
1	L	410	Total	C	N	O	S	0	0	0
			3306	2126	551	612	17			

- 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 43	C 34	Fe 1	N 4	O 4	0	0
2	B	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	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	E	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
2	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
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

- Molecule 3 is PALMITIC ACID (CCD ID: PLM) (formula: $C_{16}H_{32}O_2$).

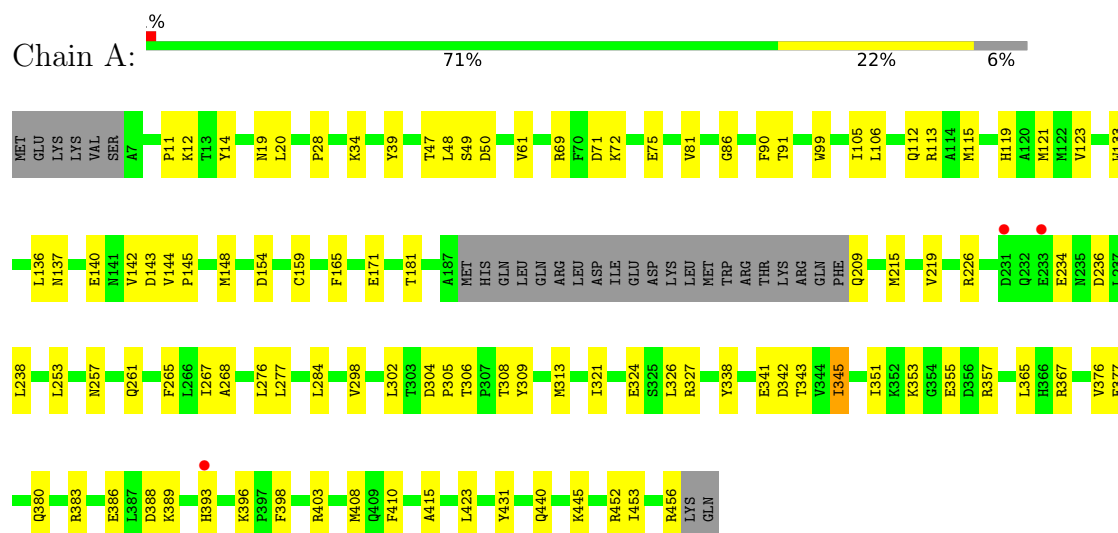


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			18	16	2		
3	B	1	Total	C	O	0	0
			18	16	2		
3	C	1	Total	C	O	0	0
			18	16	2		
3	D	1	Total	C	O	0	0
			18	16	2		
3	D	1	Total	C	O	0	0
			18	16	2		
3	E	1	Total	C	O	0	0
			18	16	2		
3	G	1	Total	C	O	0	0
			18	16	2		
3	H	1	Total	C	O	0	0
			18	16	2		
3	I	1	Total	C	O	0	0
			18	16	2		
3	J	1	Total	C	O	0	0
			18	16	2		
3	K	1	Total	C	O	0	0
			18	16	2		
3	L	1	Total	C	O	0	0
			18	16	2		

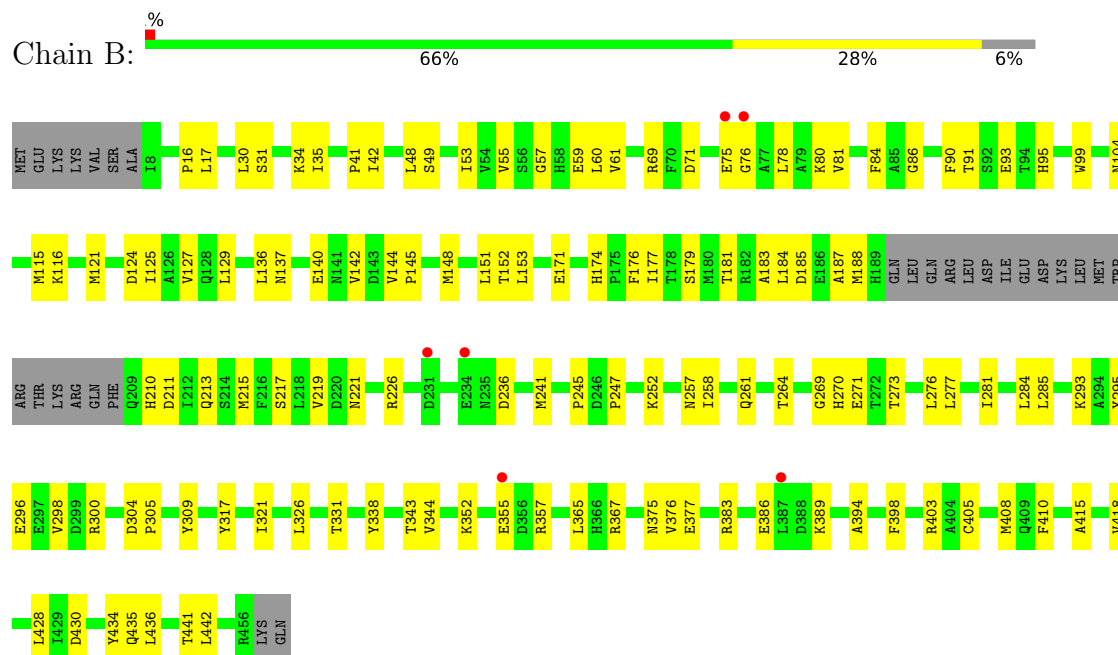
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

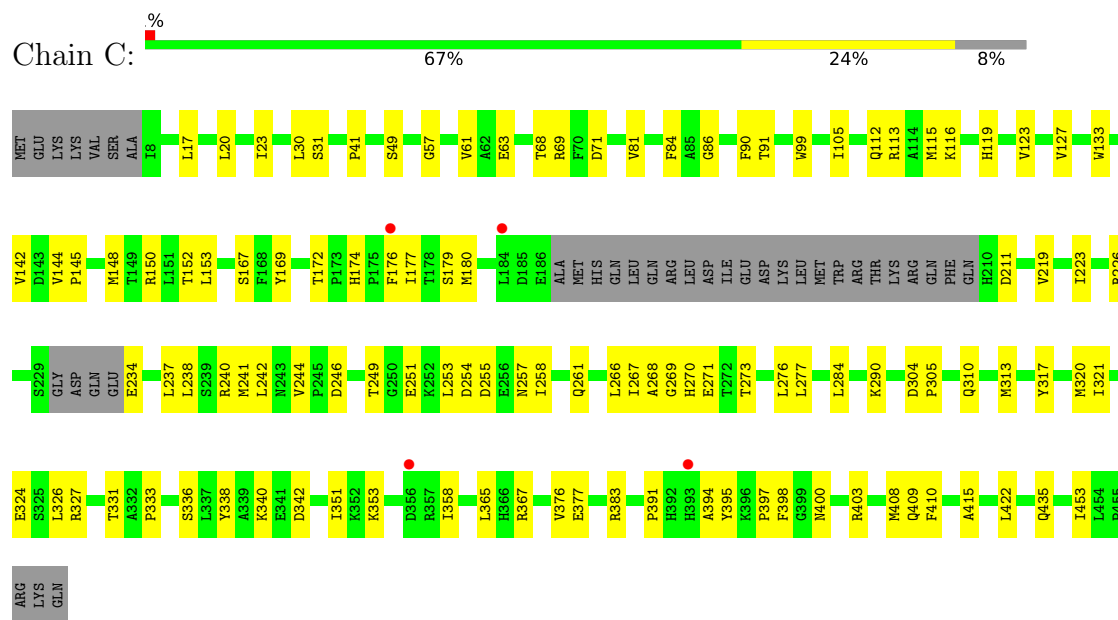
- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



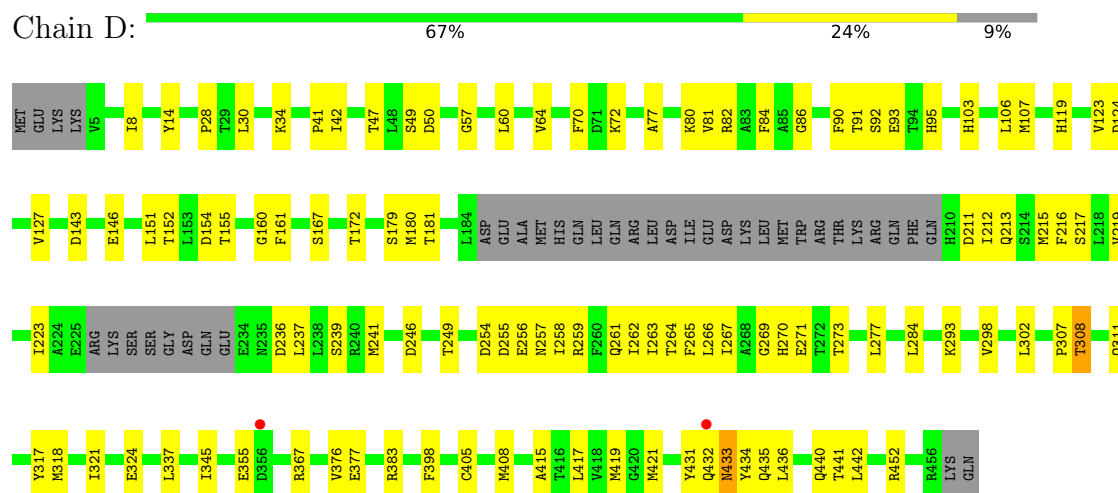
- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



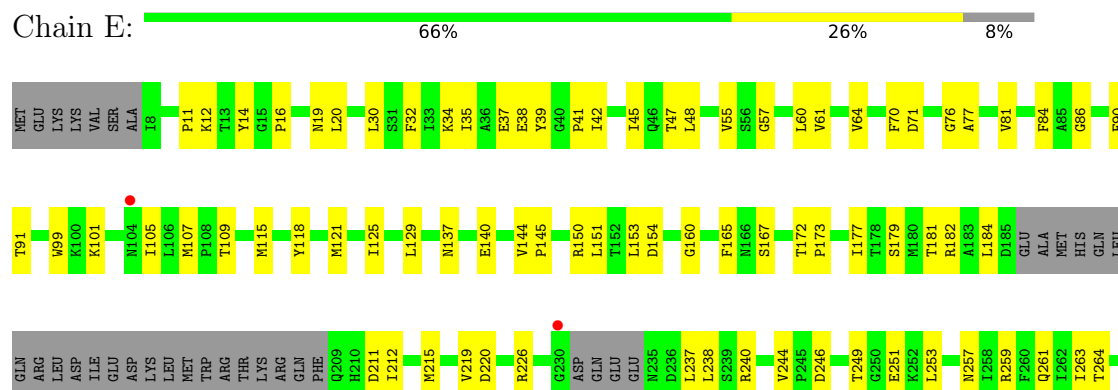
• Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase

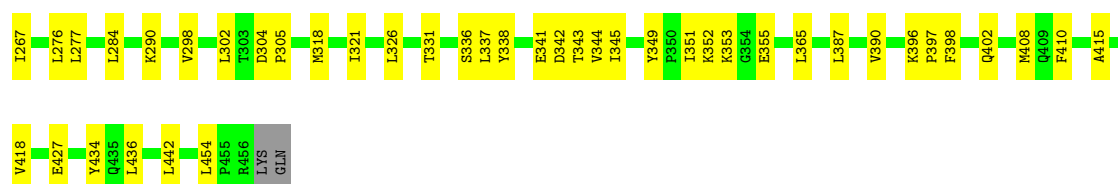


• Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase

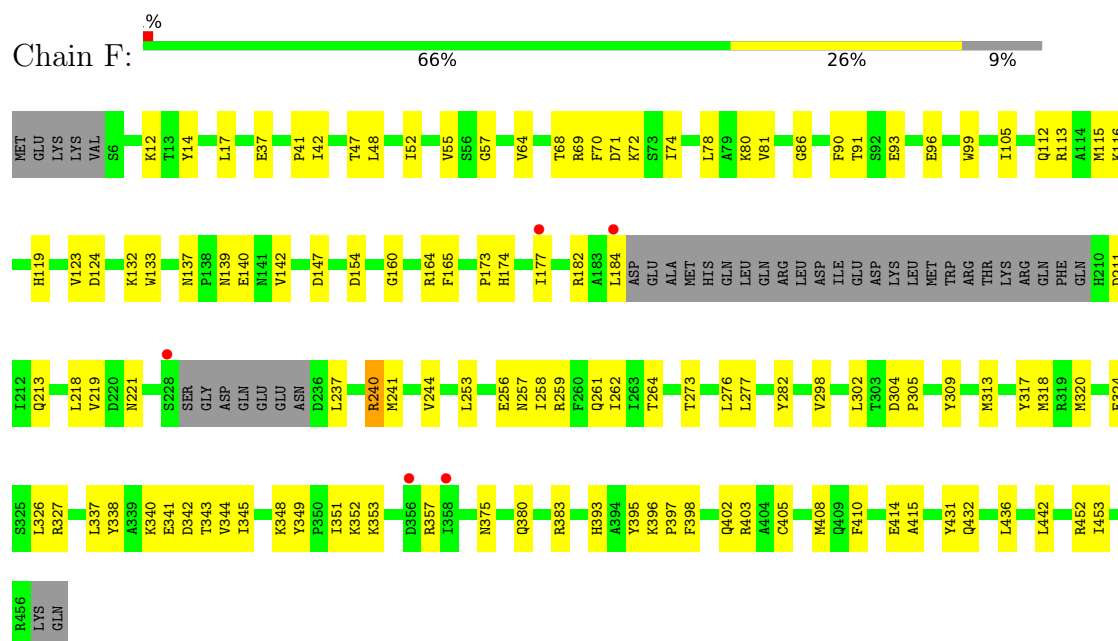


• Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase





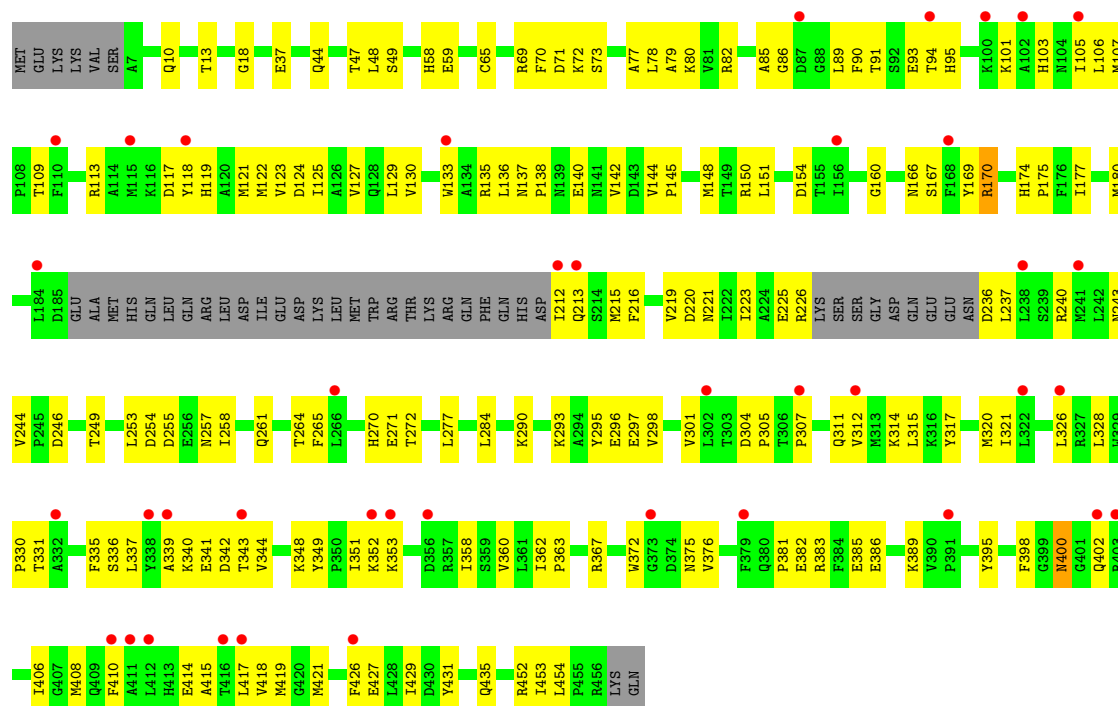
- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



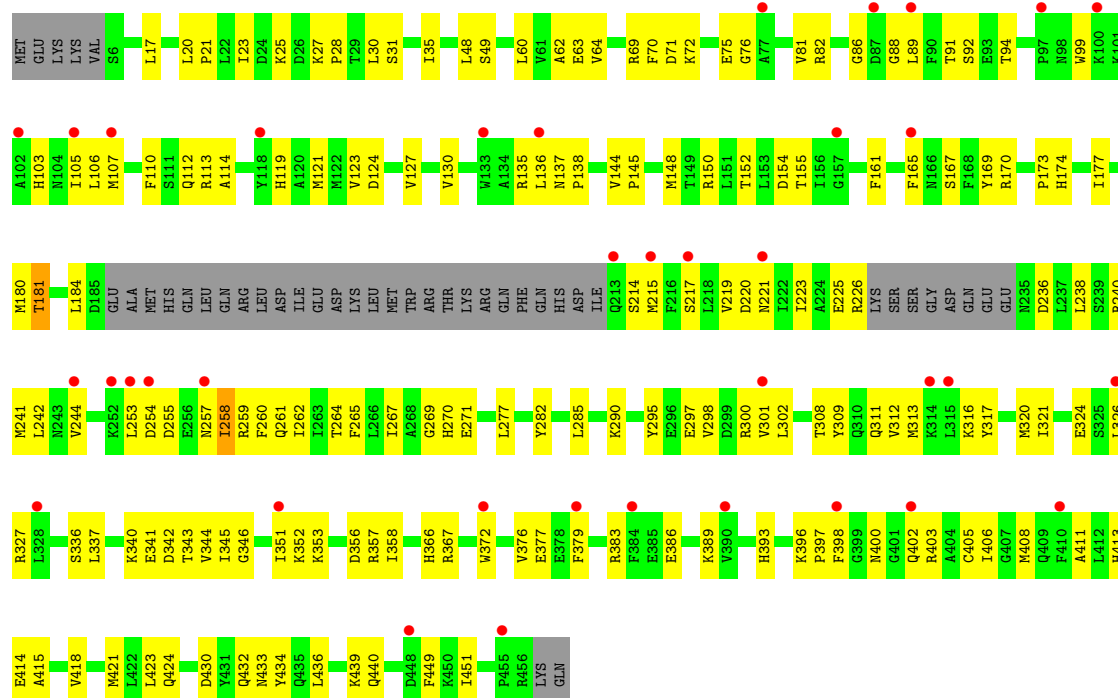
- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



- Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase

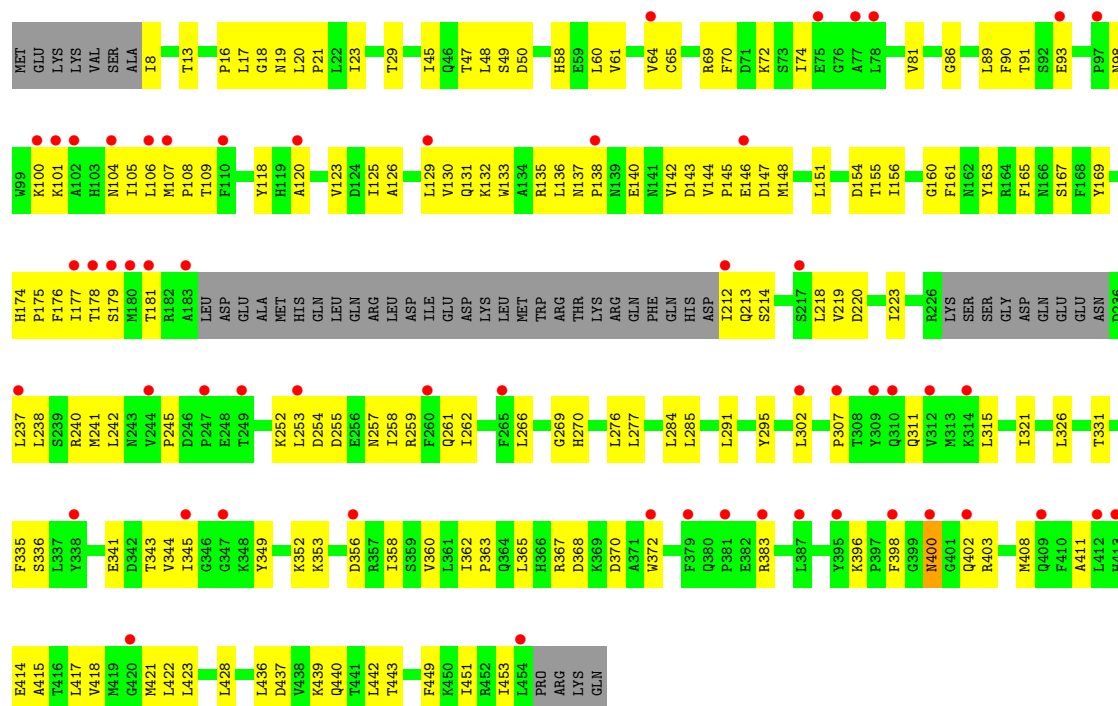


• Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase



• Molecule 1: Bifunctional cytochrome P450/NADPH-P450 reductase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	96.62Å 126.06Å 141.44Å 86.66° 79.47° 84.97°	Depositor
Resolution (Å)	19.96 – 2.80 19.96 – 2.80	Depositor EDS
% Data completeness (in resolution range)	91.5 (19.96-2.80) 97.8 (19.96-2.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 2.82Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.239 , 0.270 0.241 , 0.271	Depositor DCC
R_{free} test set	7977 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	65.7	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 62.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	41062	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.33% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, PLM

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	0.25	0/3540	0.50	0/4794
1	B	0.26	0/3554	0.51	0/4812
1	C	0.23	0/3479	0.49	0/4711
1	D	0.27	0/3459	0.54	0/4686
1	E	0.26	0/3485	0.52	0/4718
1	F	0.25	0/3461	0.50	0/4686
1	G	0.26	0/3313	0.55	0/4484
1	H	0.24	0/3432	0.51	0/4648
1	I	0.27	0/3300	0.57	0/4468
1	J	0.27	0/3429	0.56	0/4644
1	K	0.24	0/3435	0.52	0/4652
1	L	0.25	0/3383	0.57	0/4582
All	All	0.25	0/41270	0.53	0/55885

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3460	0	3435	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3473	0	3446	87	0
1	C	3400	0	3382	81	0
1	D	3380	0	3368	79	0
1	E	3406	0	3394	83	0
1	F	3382	0	3378	91	0
1	G	3238	0	3237	92	0
1	H	3354	0	3349	110	0
1	I	3223	0	3218	147	0
1	J	3351	0	3348	149	0
1	K	3357	0	3348	141	0
1	L	3306	0	3297	140	0
2	A	43	0	30	3	0
2	B	43	0	30	3	0
2	C	43	0	30	4	0
2	D	43	0	30	4	0
2	E	43	0	30	2	0
2	F	43	0	30	3	0
2	G	43	0	30	4	0
2	H	43	0	30	6	0
2	I	43	0	30	10	0
2	J	43	0	30	3	0
2	K	43	0	30	6	0
2	L	43	0	30	4	0
3	A	18	0	31	4	0
3	B	18	0	31	4	0
3	C	18	0	31	3	0
3	D	36	0	62	4	0
3	E	18	0	31	2	0
3	G	18	0	31	3	0
3	H	18	0	31	5	0
3	I	18	0	31	3	0
3	J	18	0	31	1	0
3	K	18	0	31	1	0
3	L	18	0	31	5	0
All	All	41062	0	40932	1270	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 15.

The worst 5 of 1270 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:K:302:LEU:HD11	1:K:424:GLN:HG3	1.25	1.15
1:H:65:CYS:HB3	1:H:400:ASN:ND2	1.71	1.06
1:I:65:CYS:HB2	1:I:400:ASN:ND2	1.77	1.00
1:J:10:GLN:HB3	1:J:44:GLN:HG3	1.48	0.94
1:K:302:LEU:HD11	1:K:424:GLN:CG	1.98	0.93

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	425/458 (93%)	411 (97%)	14 (3%)	0	100	100
1	B	426/458 (93%)	414 (97%)	12 (3%)	0	100	100
1	C	415/458 (91%)	401 (97%)	14 (3%)	0	100	100
1	D	413/458 (90%)	401 (97%)	11 (3%)	1 (0%)	43	72
1	E	416/458 (91%)	398 (96%)	18 (4%)	0	100	100
1	F	413/458 (90%)	399 (97%)	14 (3%)	0	100	100
1	G	393/458 (86%)	382 (97%)	11 (3%)	0	100	100
1	H	409/458 (89%)	394 (96%)	14 (3%)	1 (0%)	43	72
1	I	393/458 (86%)	381 (97%)	12 (3%)	0	100	100
1	J	409/458 (89%)	394 (96%)	15 (4%)	0	100	100
1	K	410/458 (90%)	397 (97%)	13 (3%)	0	100	100
1	L	404/458 (88%)	383 (95%)	21 (5%)	0	100	100
All	All	4926/5496 (90%)	4755 (96%)	169 (3%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	433	ASN
1	H	83	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	381/410 (93%)	377 (99%)	4 (1%)	68	88
1	B	383/410 (93%)	381 (100%)	2 (0%)	81	93
1	C	376/410 (92%)	374 (100%)	2 (0%)	81	93
1	D	373/410 (91%)	370 (99%)	3 (1%)	73	90
1	E	376/410 (92%)	375 (100%)	1 (0%)	86	95
1	F	373/410 (91%)	372 (100%)	1 (0%)	86	95
1	G	356/410 (87%)	353 (99%)	3 (1%)	73	90
1	H	370/410 (90%)	368 (100%)	2 (0%)	81	93
1	I	354/410 (86%)	353 (100%)	1 (0%)	86	95
1	J	369/410 (90%)	366 (99%)	3 (1%)	73	90
1	K	370/410 (90%)	367 (99%)	3 (1%)	73	90
1	L	364/410 (89%)	362 (100%)	2 (0%)	81	93
All	All	4445/4920 (90%)	4418 (99%)	27 (1%)	78	92

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	64	VAL
1	H	376	VAL
1	K	376	VAL
1	H	64	VAL
1	I	376	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	131	GLN
1	L	10	GLN
1	J	323	ASN
1	K	98	ASN
1	L	104	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](#)

24 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	PLM	E	502	-	17,17,17	0.82	1 (5%)	17,17,17	0.82	2 (11%)
3	PLM	K	502	-	17,17,17	1.14	1 (5%)	17,17,17	0.73	1 (5%)
3	PLM	H	502	-	17,17,17	0.61	0	17,17,17	0.85	2 (11%)
2	HEM	K	501	1	50,50,50	1.37	7 (14%)	66,82,82	1.23	9 (13%)
2	HEM	D	501	1	50,50,50	1.46	9 (18%)	66,82,82	1.28	7 (10%)
2	HEM	F	501	1	50,50,50	1.35	8 (16%)	66,82,82	1.24	6 (9%)
2	HEM	J	501	1	50,50,50	1.41	6 (12%)	66,82,82	1.34	11 (16%)
3	PLM	B	502	-	17,17,17	0.91	1 (5%)	17,17,17	0.77	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	G	501	1	50,50,50	1.42	7 (14%)	66,82,82	1.32	8 (12%)
3	PLM	I	502	-	17,17,17	1.12	1 (5%)	17,17,17	0.74	1 (5%)
3	PLM	D	503	-	17,17,17	0.71	0	17,17,17	0.86	2 (11%)
2	HEM	B	501	1	50,50,50	1.40	8 (16%)	66,82,82	1.19	7 (10%)
3	PLM	D	502	-	17,17,17	1.07	1 (5%)	17,17,17	0.81	2 (11%)
3	PLM	J	502	-	17,17,17	0.77	1 (5%)	17,17,17	0.84	2 (11%)
2	HEM	H	501	1	50,50,50	1.49	9 (18%)	66,82,82	1.29	7 (10%)
3	PLM	L	502	-	17,17,17	1.21	1 (5%)	17,17,17	0.70	0
2	HEM	L	501	1	50,50,50	1.40	9 (18%)	66,82,82	1.25	8 (12%)
2	HEM	I	501	1	50,50,50	1.47	7 (14%)	66,82,82	1.34	8 (12%)
2	HEM	C	501	1	50,50,50	1.38	6 (12%)	66,82,82	1.19	5 (7%)
3	PLM	C	502	-	17,17,17	0.98	1 (5%)	17,17,17	0.72	1 (5%)
3	PLM	G	502	-	17,17,17	1.14	1 (5%)	17,17,17	0.76	2 (11%)
3	PLM	A	502	-	17,17,17	0.91	1 (5%)	17,17,17	0.72	1 (5%)
2	HEM	A	501	1	50,50,50	1.43	6 (12%)	66,82,82	1.25	6 (9%)
2	HEM	E	501	1	50,50,50	1.48	7 (14%)	66,82,82	1.21	7 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLM	E	502	-	-	7/15/15/15	-
3	PLM	K	502	-	-	6/15/15/15	-
3	PLM	H	502	-	-	4/15/15/15	-
2	HEM	K	501	1	-	0/14/54/54	-
2	HEM	D	501	1	-	2/14/54/54	-
2	HEM	F	501	1	-	2/14/54/54	-
2	HEM	J	501	1	-	5/14/54/54	-
3	PLM	B	502	-	-	7/15/15/15	-
2	HEM	G	501	1	-	2/14/54/54	-
3	PLM	I	502	-	-	7/15/15/15	-
3	PLM	D	503	-	-	4/15/15/15	-
2	HEM	B	501	1	-	4/14/54/54	-
3	PLM	D	502	-	-	7/15/15/15	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLM	J	502	-	-	6/15/15/15	-
2	HEM	H	501	1	-	2/14/54/54	-
3	PLM	L	502	-	-	5/15/15/15	-
2	HEM	L	501	1	-	2/14/54/54	-
2	HEM	I	501	1	-	2/14/54/54	-
2	HEM	C	501	1	-	2/14/54/54	-
3	PLM	C	502	-	-	7/15/15/15	-
3	PLM	G	502	-	-	2/15/15/15	-
3	PLM	A	502	-	-	8/15/15/15	-
2	HEM	A	501	1	-	2/14/54/54	-
2	HEM	E	501	1	-	2/14/54/54	-

The worst 5 of 99 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	501	HEM	FE-NB	5.33	2.11	1.94
2	A	501	HEM	FE-NB	5.07	2.10	1.94
2	H	501	HEM	FE-NB	4.97	2.10	1.94
2	E	501	HEM	FE-NB	4.54	2.08	1.94
2	J	501	HEM	FE-NA	4.51	2.10	1.95

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	501	HEM	C4D-ND-C1D	3.58	108.77	105.07
2	D	501	HEM	C4D-ND-C1D	3.57	108.76	105.07
2	I	501	HEM	C4D-ND-C1D	3.51	108.70	105.07
2	I	501	HEM	C4A-NA-C1A	3.33	108.61	105.35
2	A	501	HEM	C4D-ND-C1D	3.26	108.44	105.07

There are no chirality outliers.

5 of 97 torsion outliers are listed below:

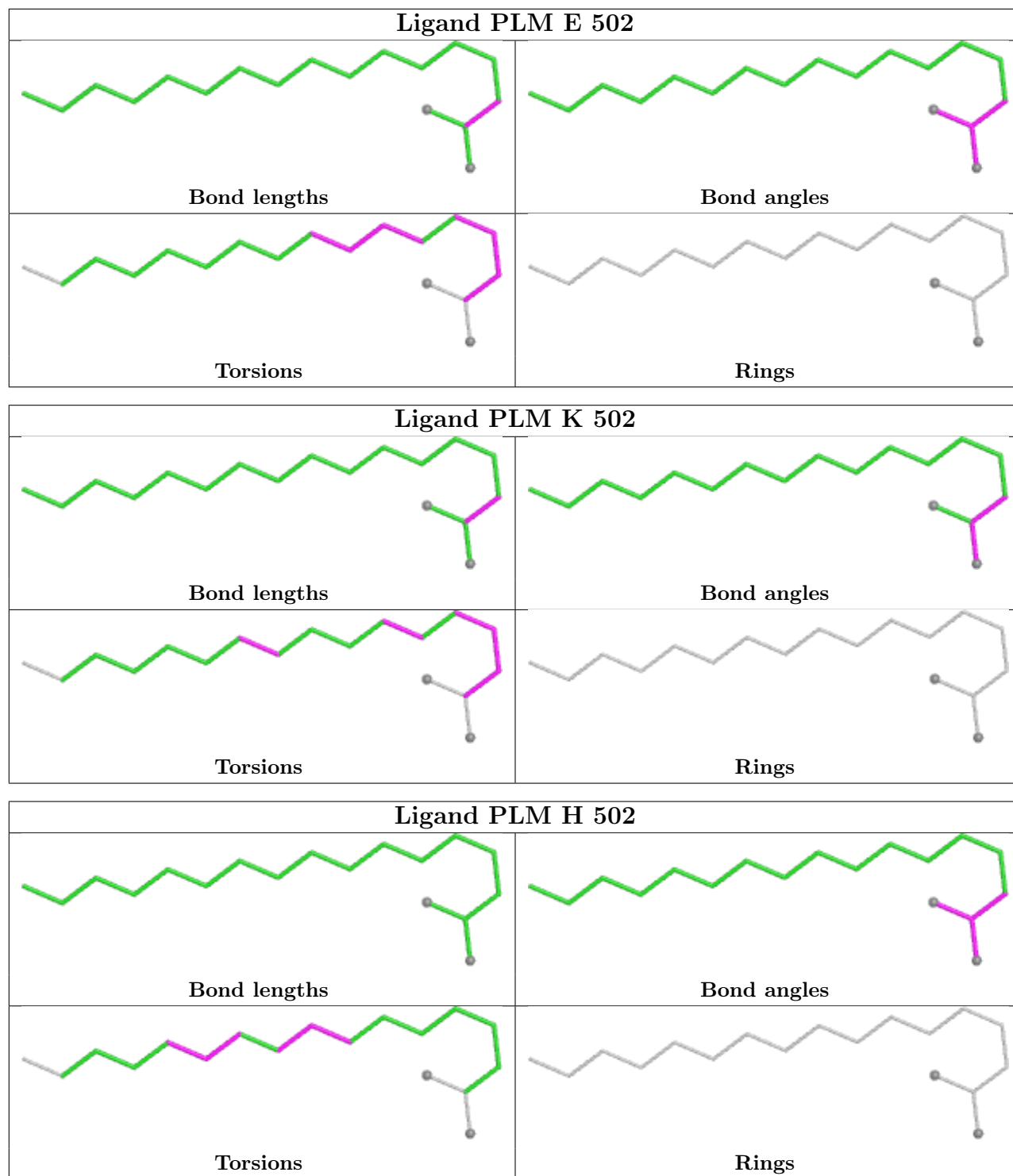
Mol	Chain	Res	Type	Atoms
3	A	502	PLM	C3-C4-C5-C6
3	K	502	PLM	C1-C2-C3-C4
3	C	502	PLM	C5-C6-C7-C8
3	D	503	PLM	C1-C2-C3-C4
3	H	502	PLM	C9-CA-CB-CC

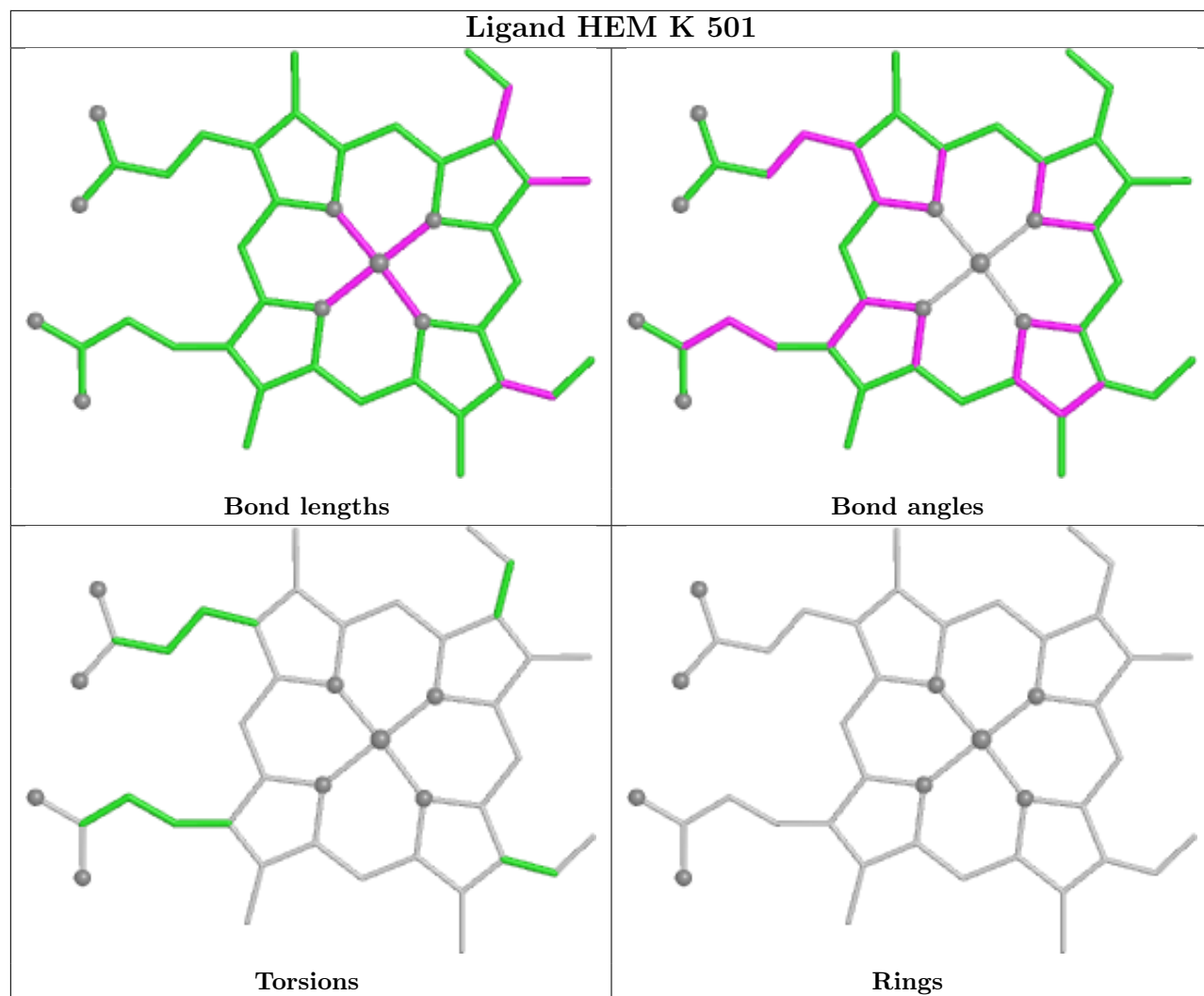
There are no ring outliers.

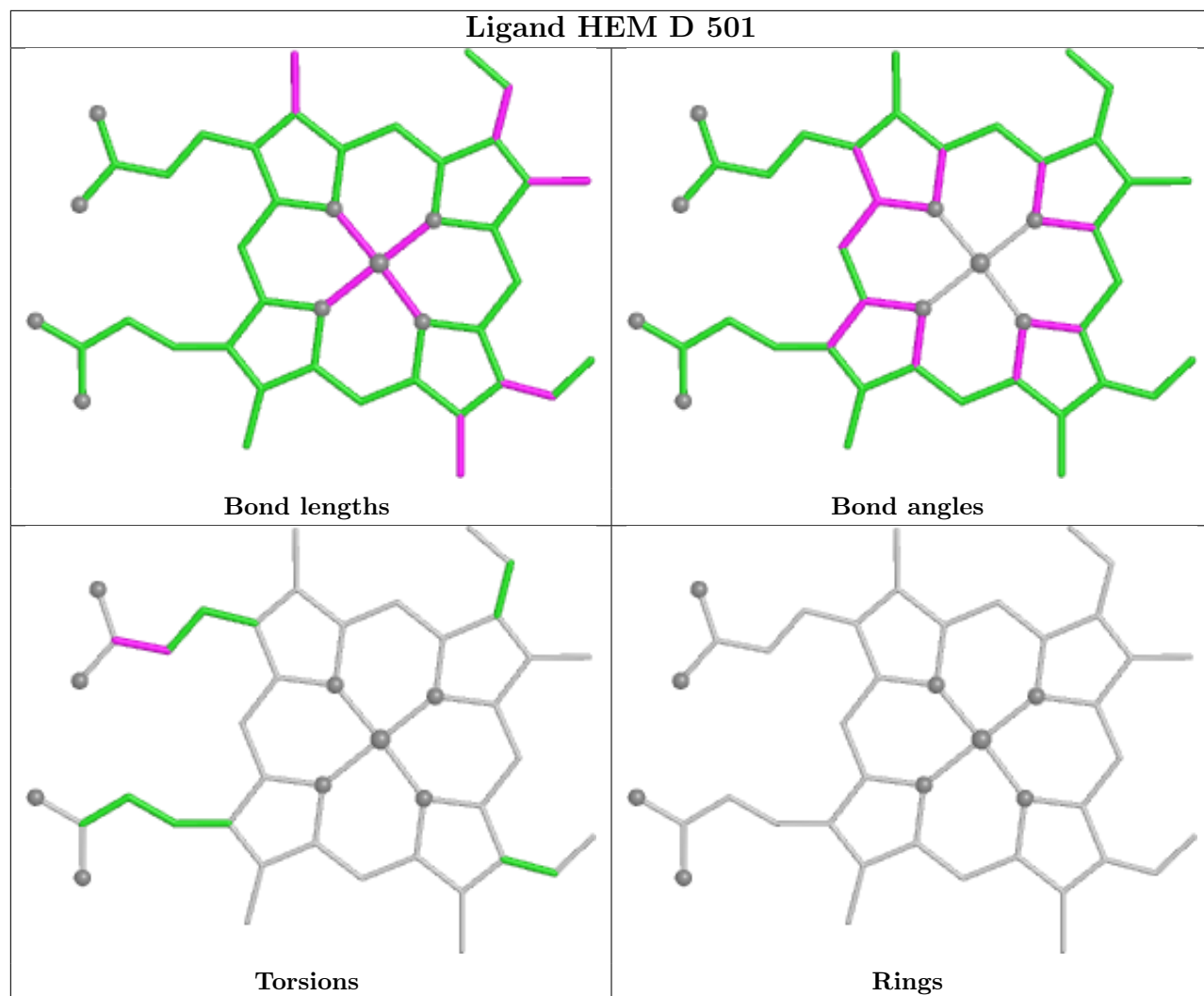
24 monomers are involved in 74 short contacts:

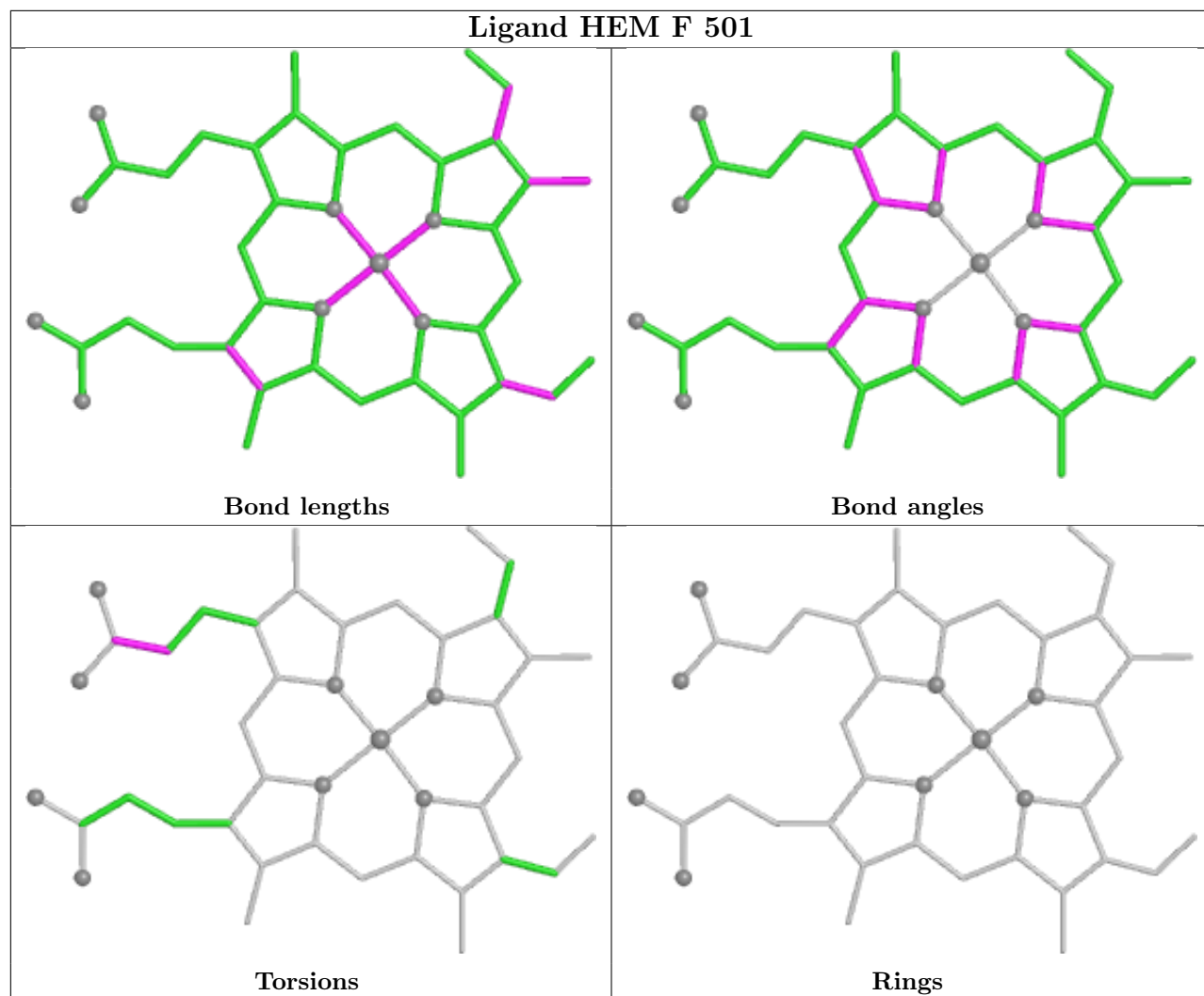
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	502	PLM	2	0
3	K	502	PLM	1	0
3	H	502	PLM	5	0
2	K	501	HEM	6	0
2	D	501	HEM	4	0
2	F	501	HEM	3	0
2	J	501	HEM	3	0
3	B	502	PLM	4	0
2	G	501	HEM	4	0
3	I	502	PLM	3	0
3	D	503	PLM	3	0
2	B	501	HEM	3	0
3	D	502	PLM	2	0
3	J	502	PLM	1	0
2	H	501	HEM	6	0
3	L	502	PLM	5	0
2	L	501	HEM	4	0
2	I	501	HEM	10	0
2	C	501	HEM	4	0
3	C	502	PLM	3	0
3	G	502	PLM	3	0
3	A	502	PLM	4	0
2	A	501	HEM	3	0
2	E	501	HEM	2	0

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

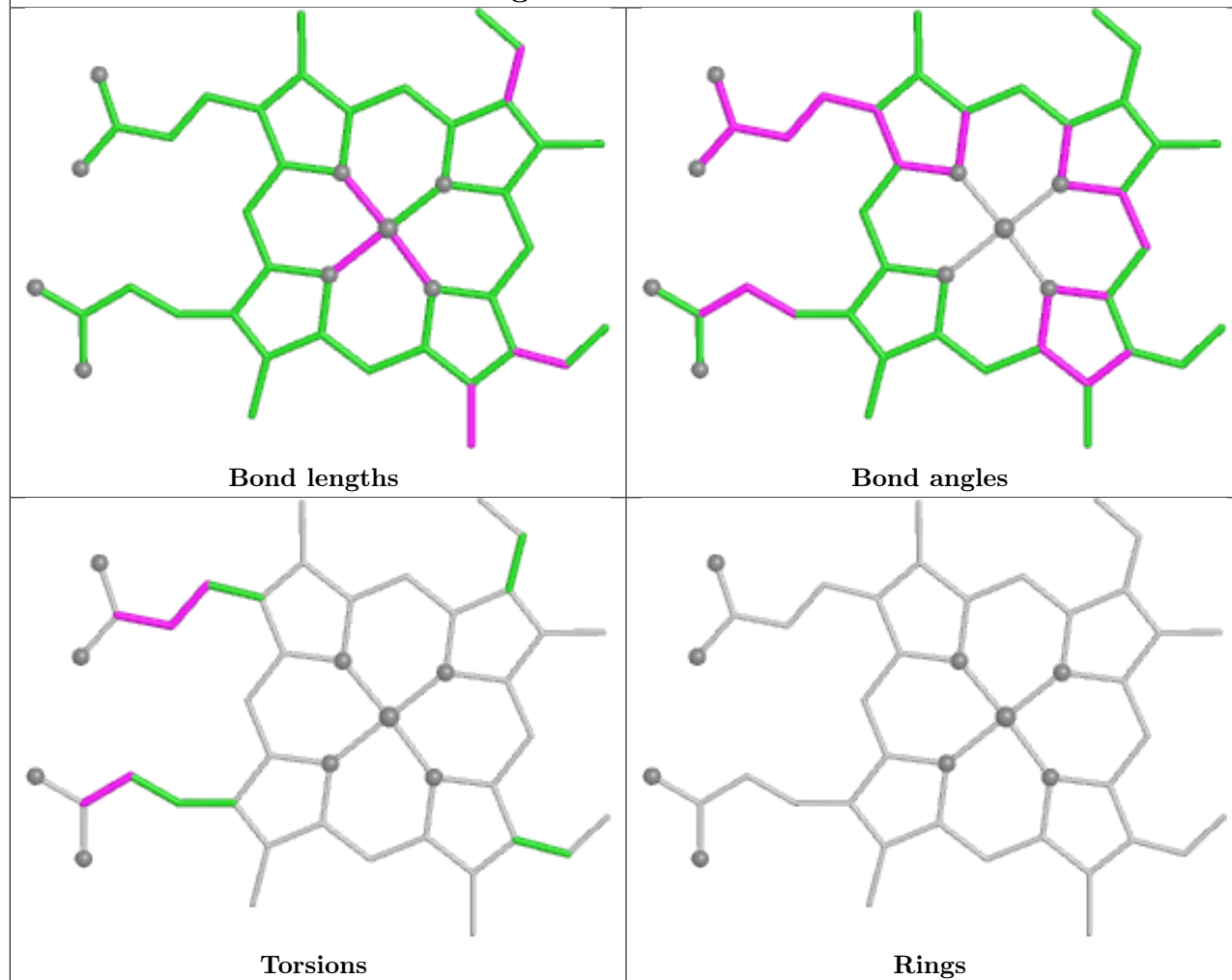




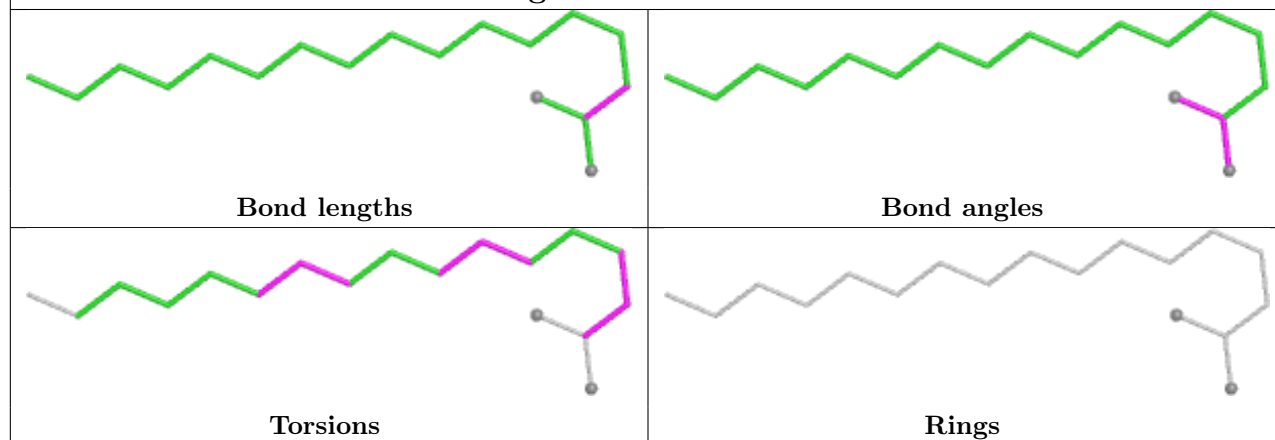


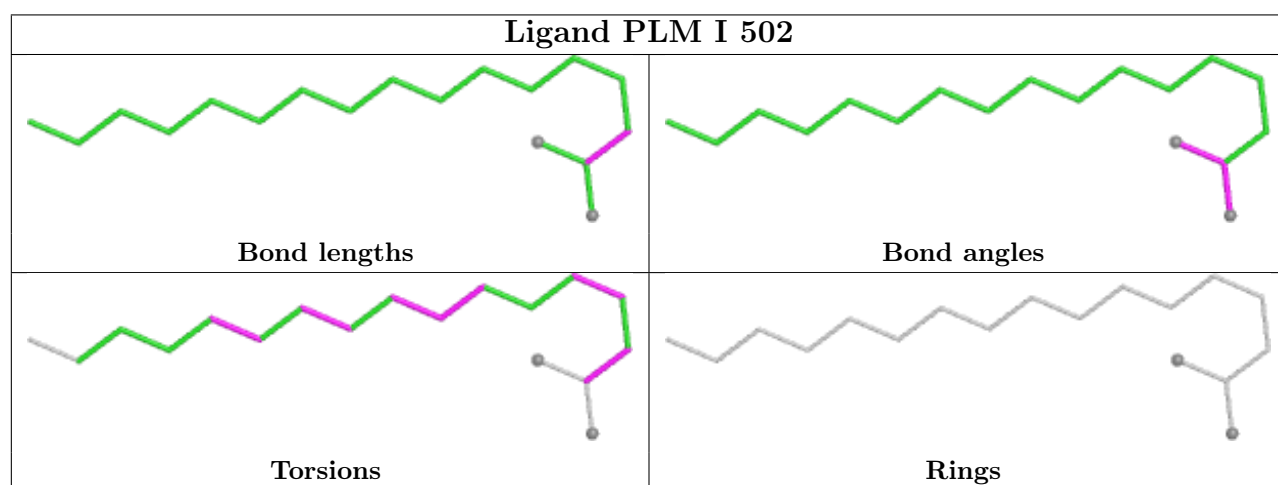
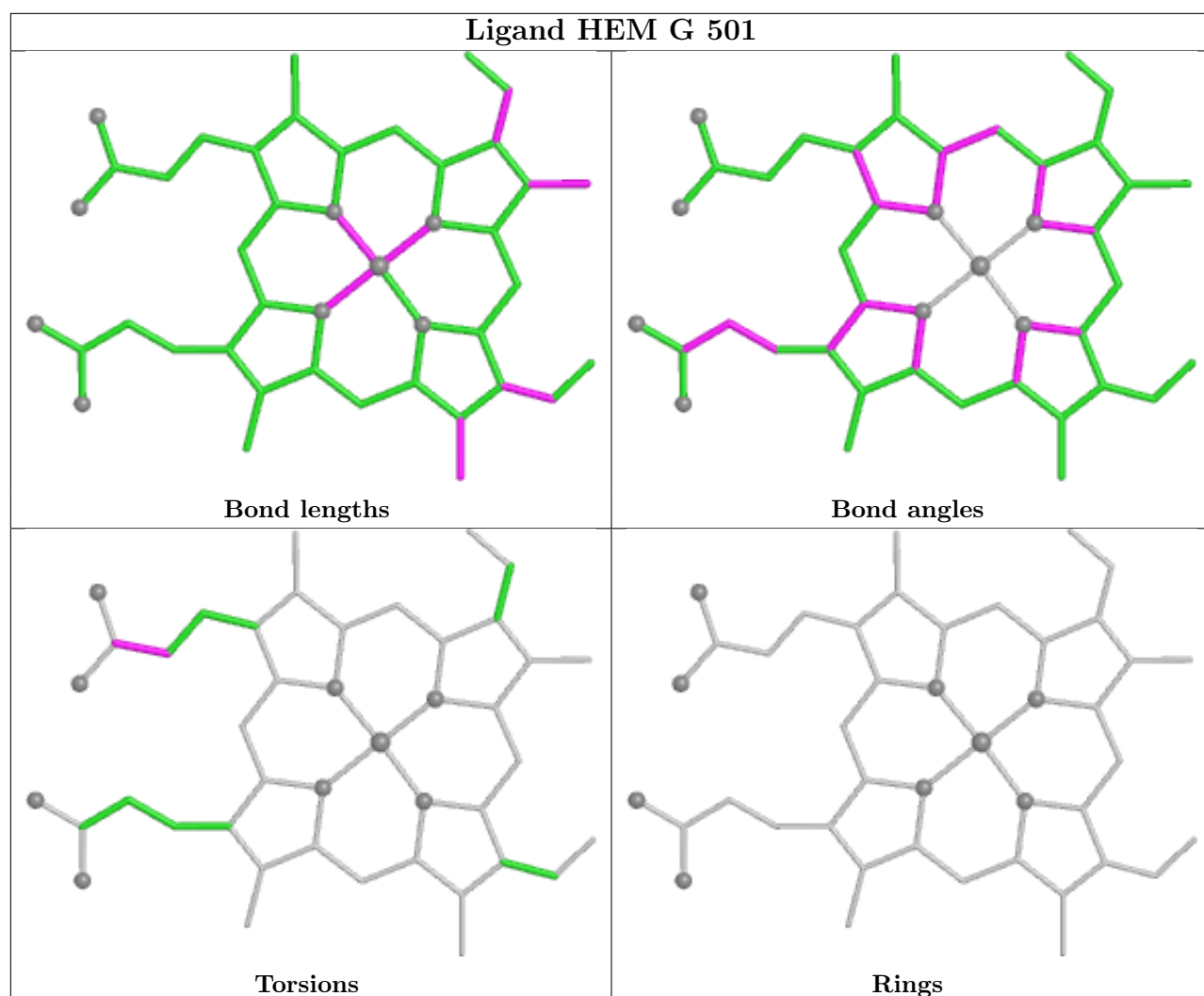


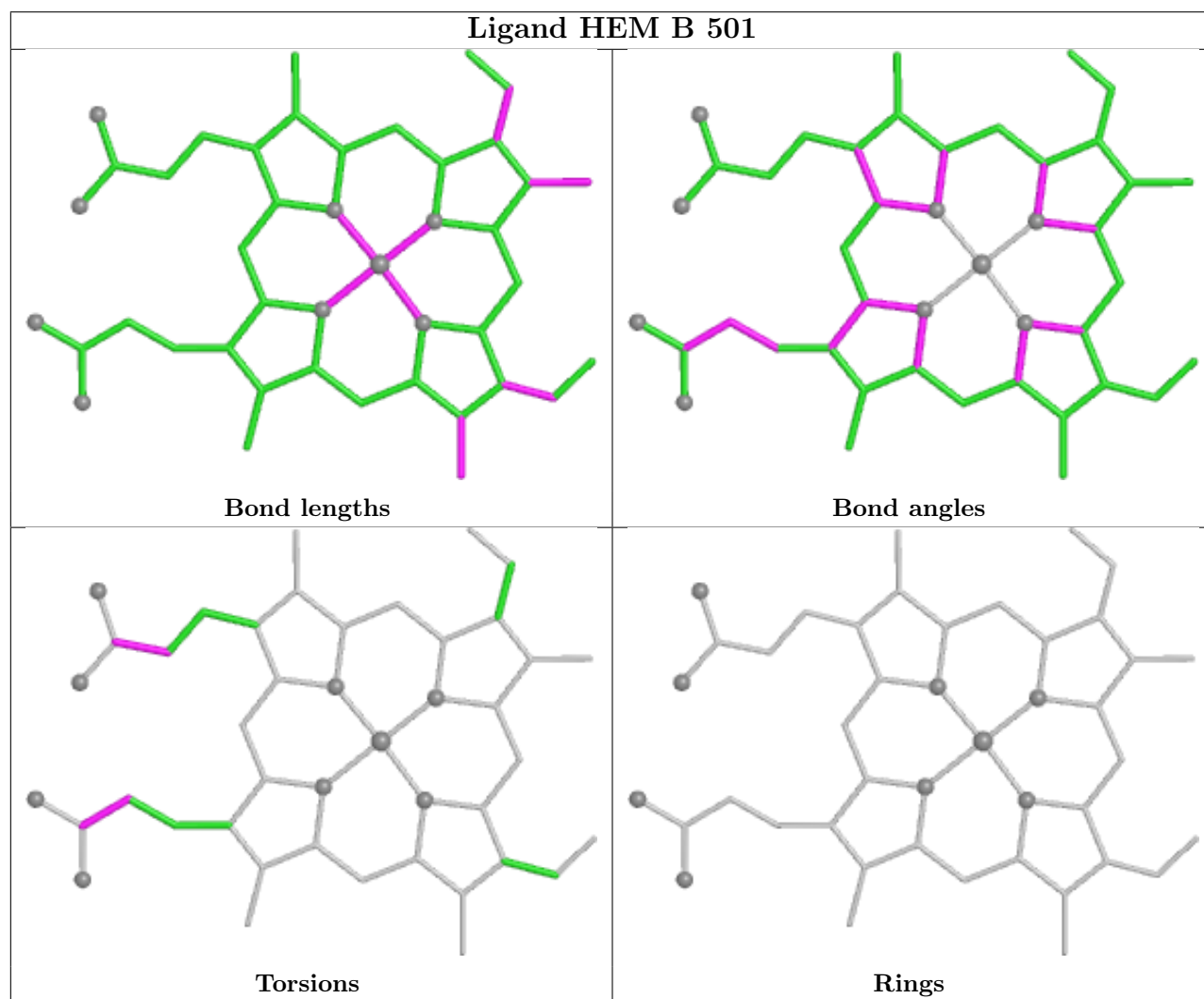
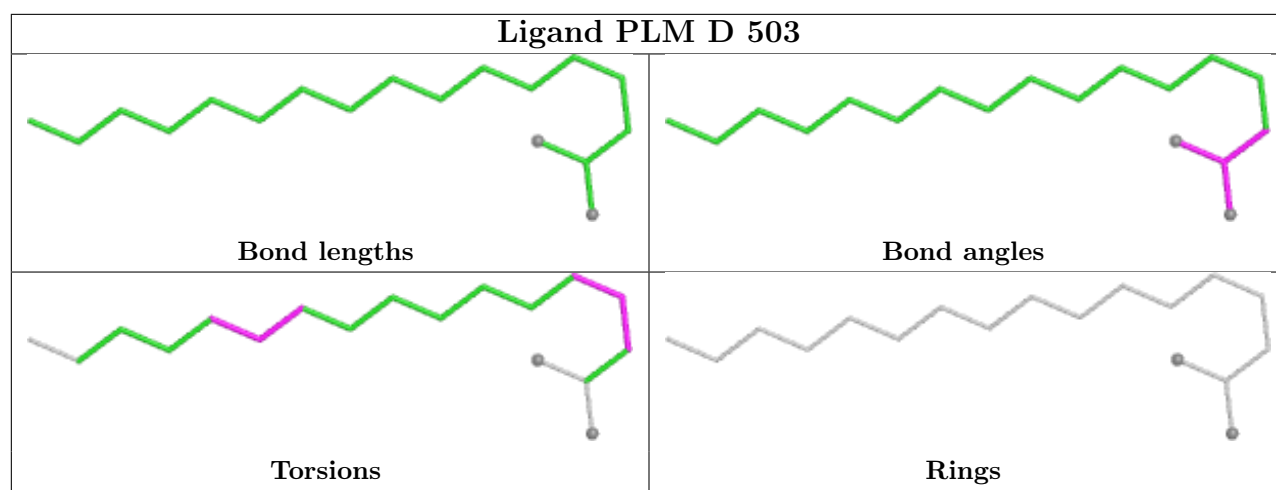
Ligand HEM J 501

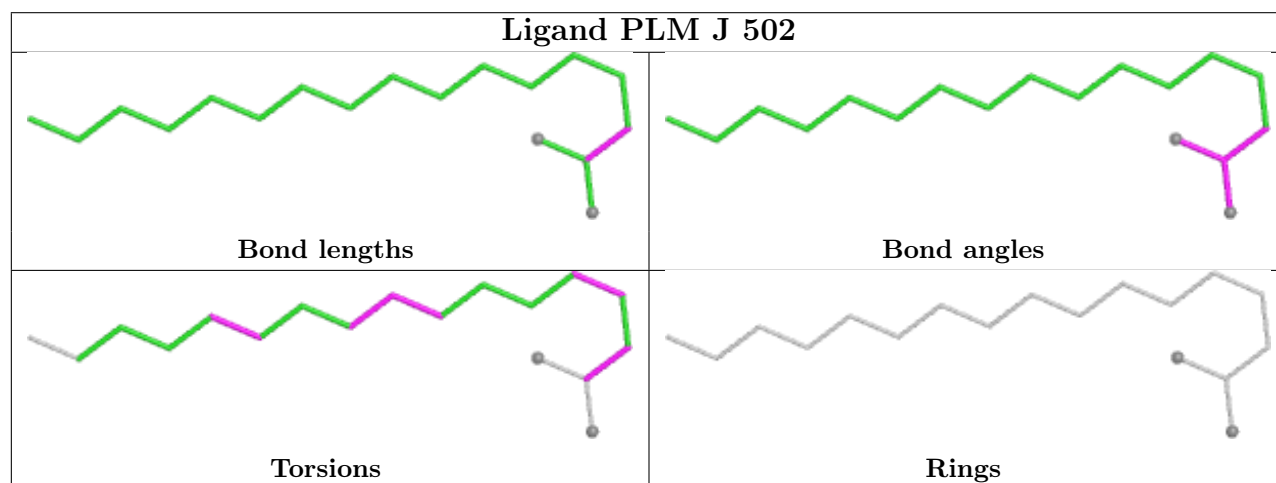
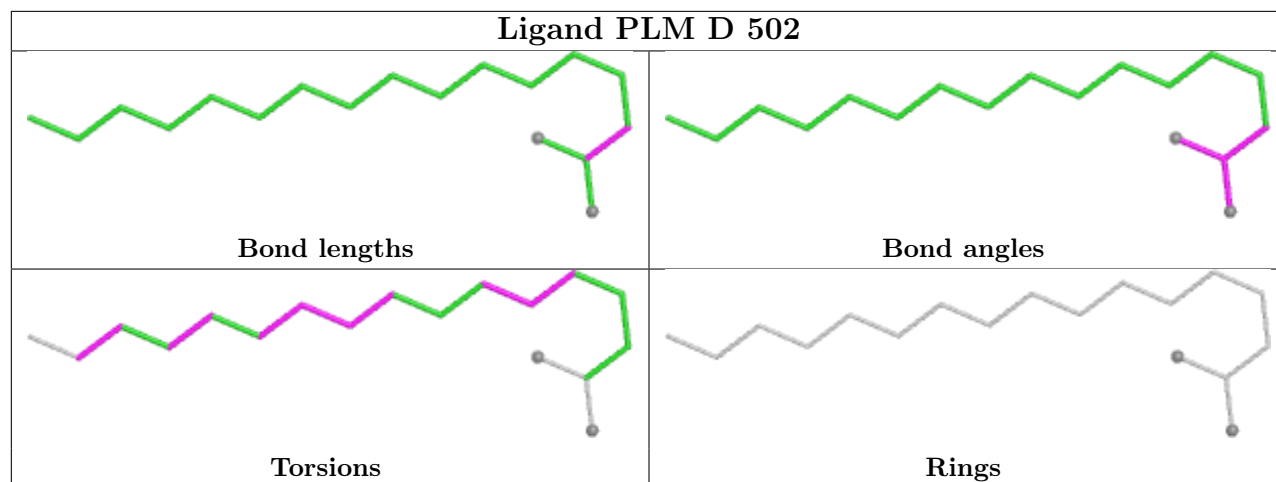


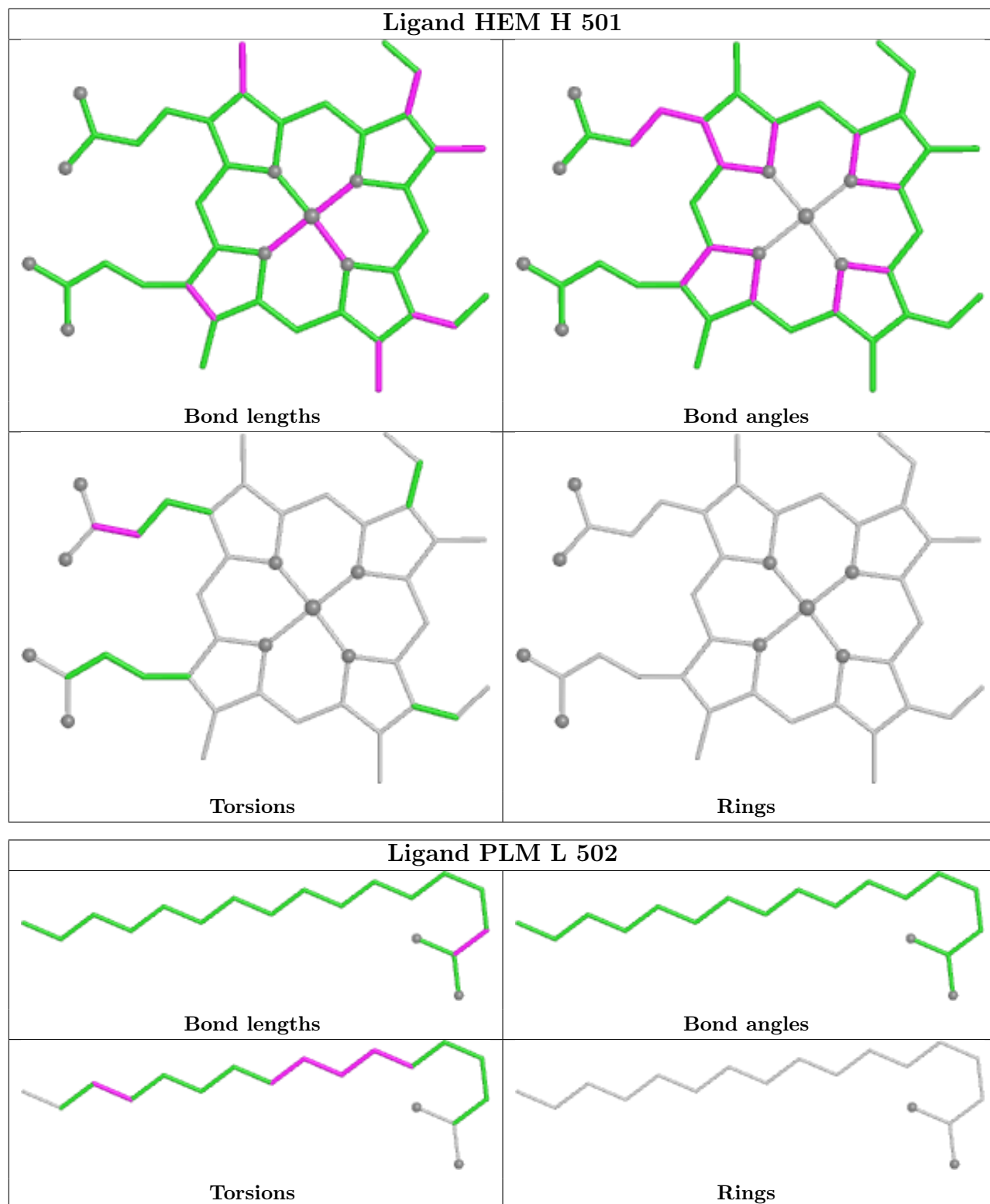
Ligand PLM B 502

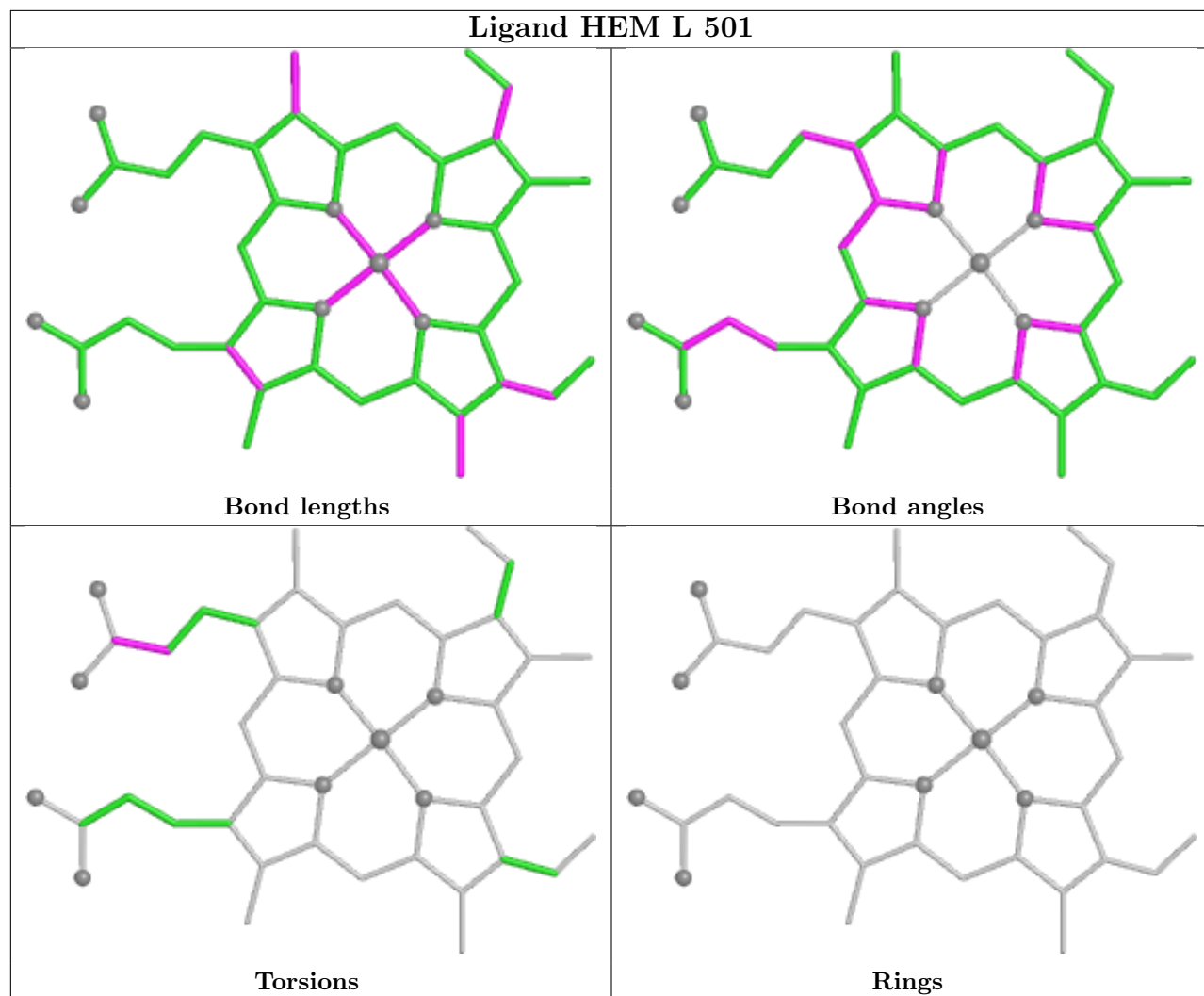




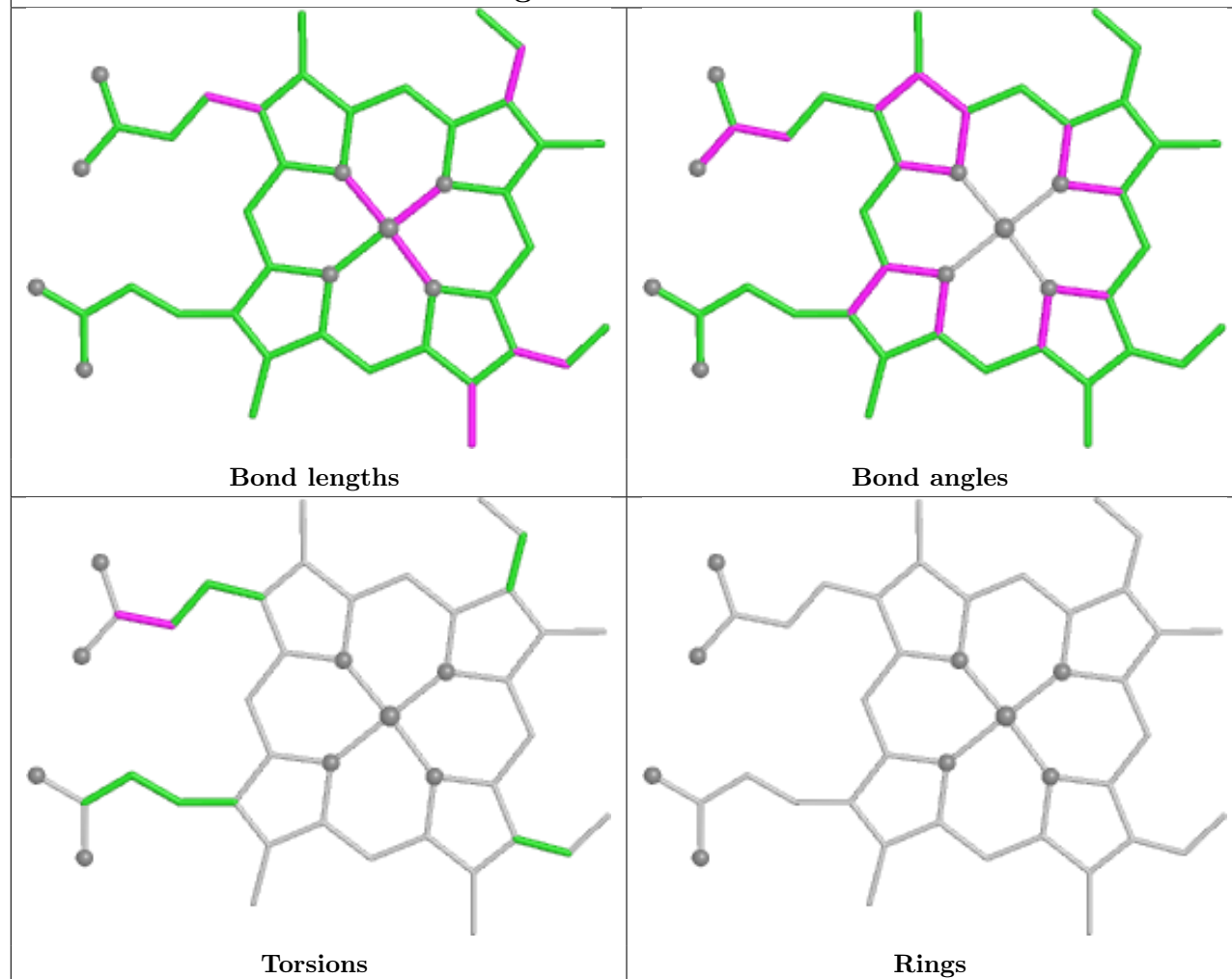


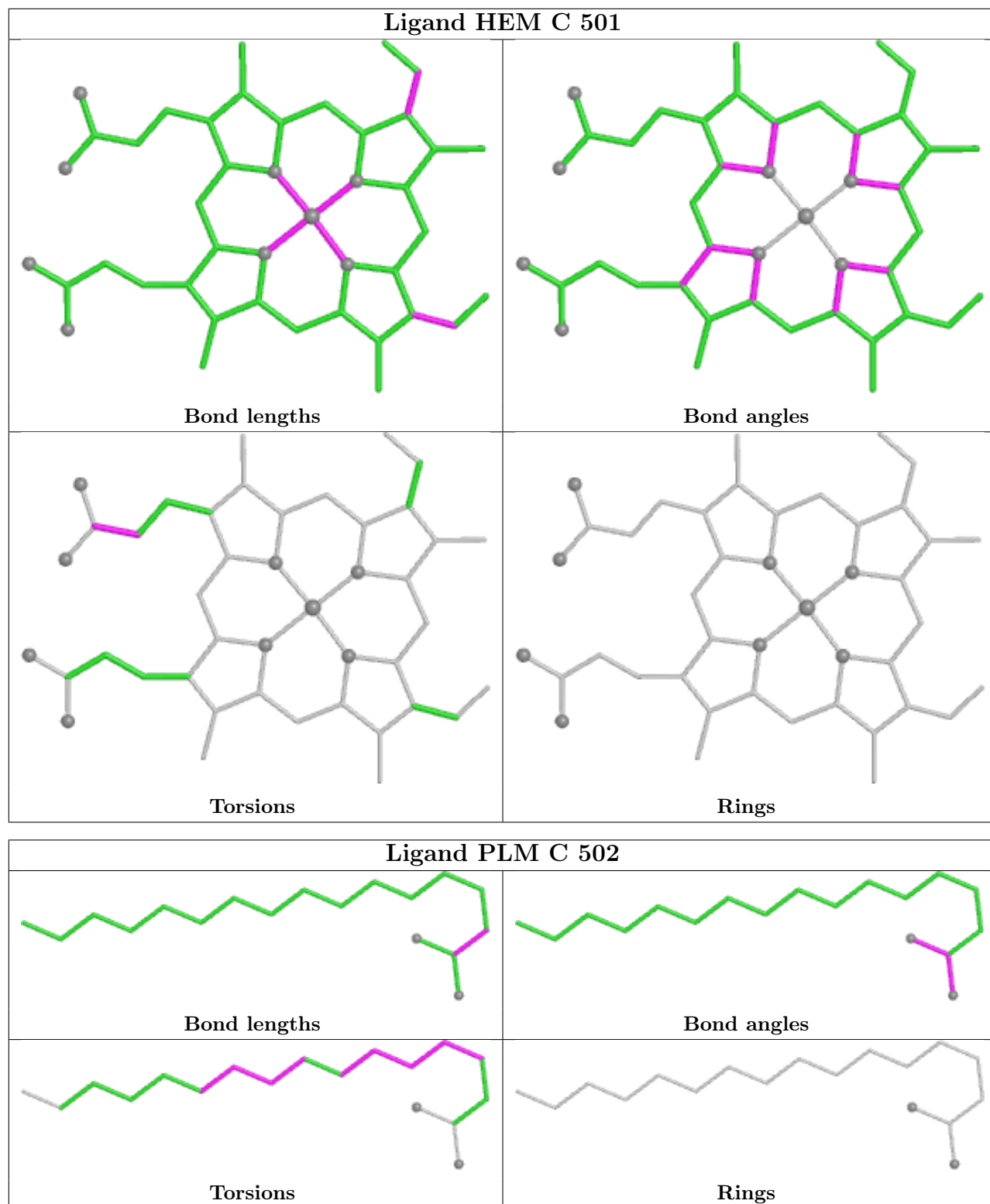


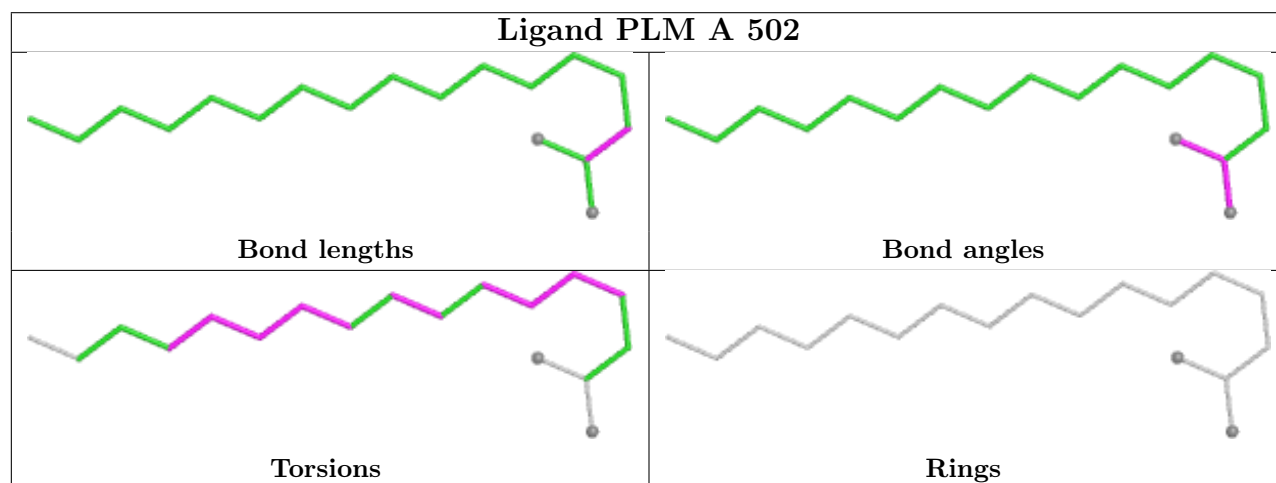
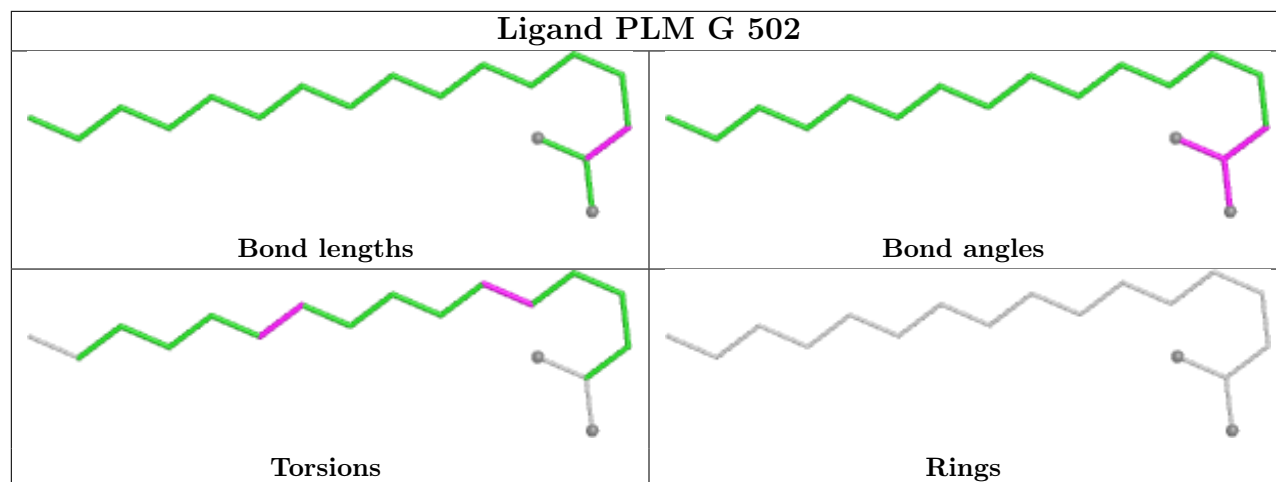


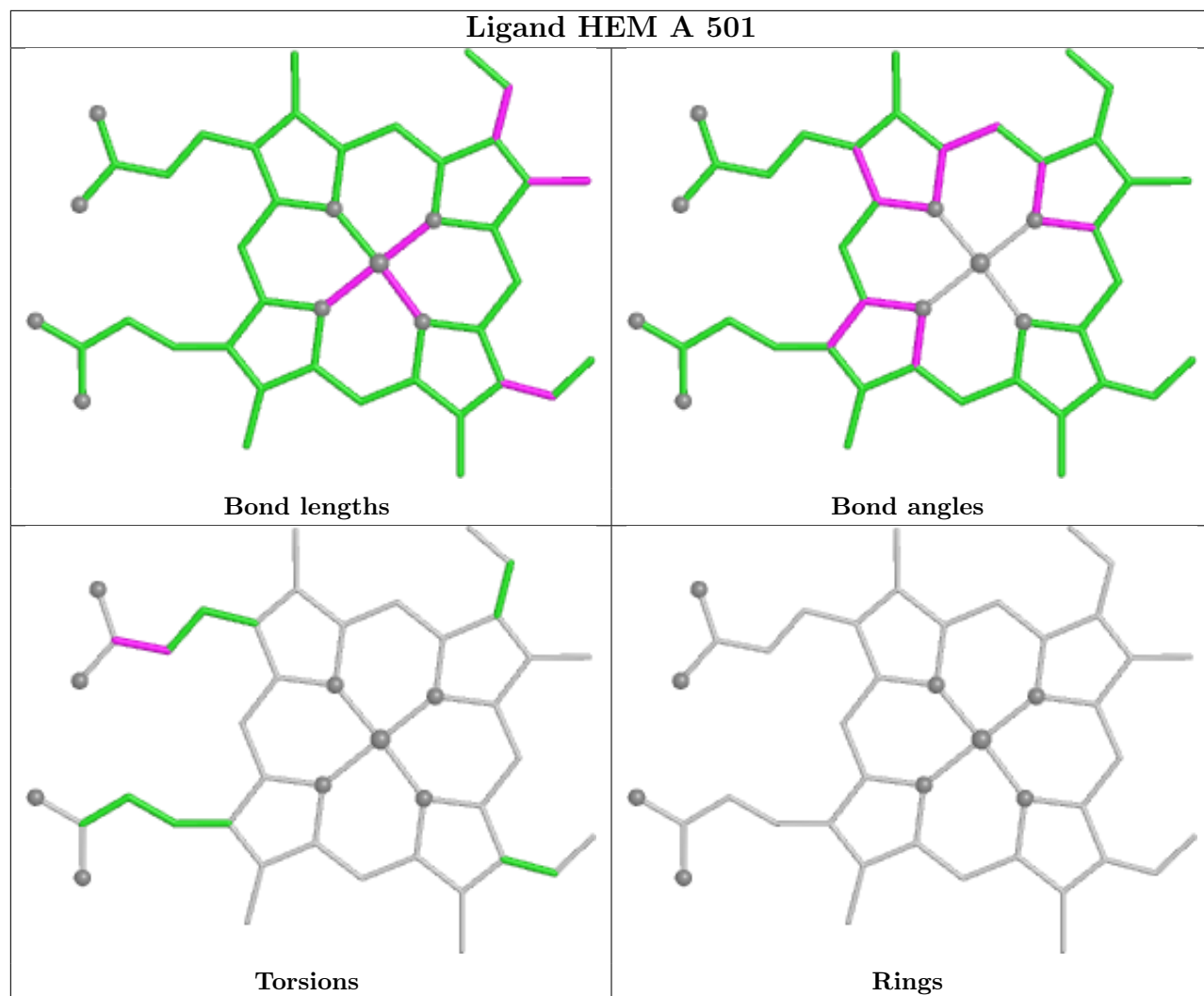


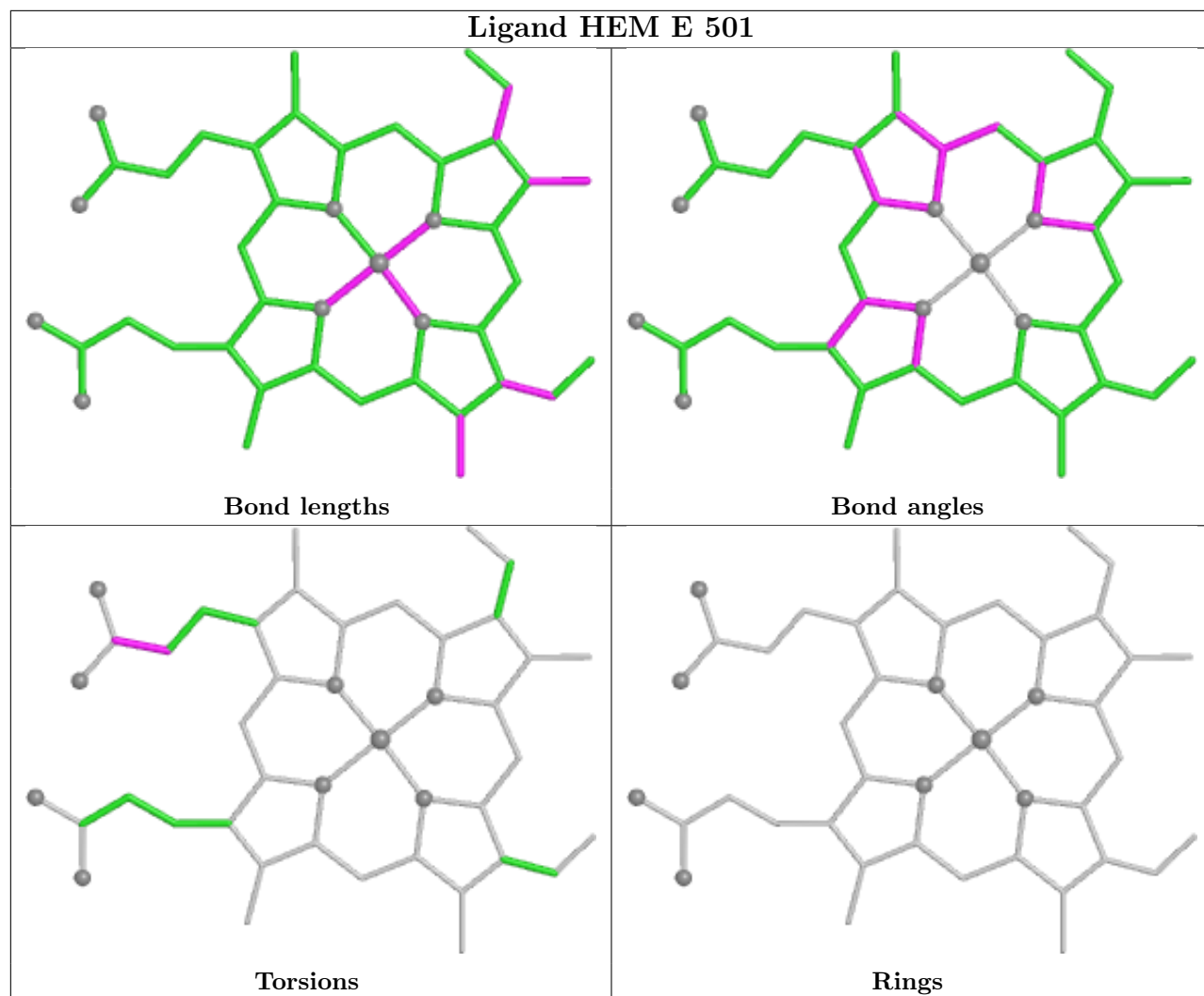
Ligand HEM I 501











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	429/458 (93%)	-0.05	3 (0%) 84 77	43, 64, 103, 154	0
1	B	430/458 (93%)	-0.12	6 (1%) 73 64	41, 61, 95, 136	0
1	C	421/458 (91%)	0.04	4 (0%) 79 72	43, 67, 100, 117	0
1	D	419/458 (91%)	-0.00	2 (0%) 87 82	38, 63, 107, 124	0
1	E	422/458 (92%)	0.06	2 (0%) 87 82	47, 69, 104, 126	0
1	F	419/458 (91%)	0.20	5 (1%) 76 68	47, 74, 106, 123	0
1	G	401/458 (87%)	0.42	16 (3%) 42 33	49, 83, 120, 136	0
1	H	415/458 (90%)	0.42	12 (2%) 53 43	58, 87, 122, 151	0
1	I	399/458 (87%)	0.95	40 (10%) 12 9	51, 113, 147, 168	0
1	J	415/458 (90%)	0.97	40 (9%) 13 10	55, 113, 150, 168	0
1	K	416/458 (90%)	0.95	37 (8%) 15 11	54, 112, 151, 174	0
1	L	410/458 (89%)	1.11	56 (13%) 6 5	65, 119, 156, 178	0
All	All	4996/5496 (90%)	0.41	223 (4%) 38 30	38, 81, 139, 178	0

The worst 5 of 223 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	356	ASP	4.0
1	G	375	ASN	3.8
1	I	255	ASP	3.7
1	L	180	MET	3.6
1	G	214	SER	3.6

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

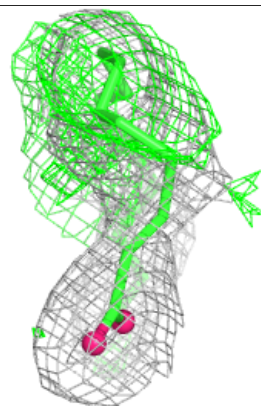
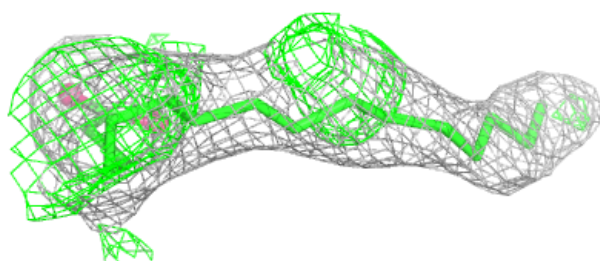
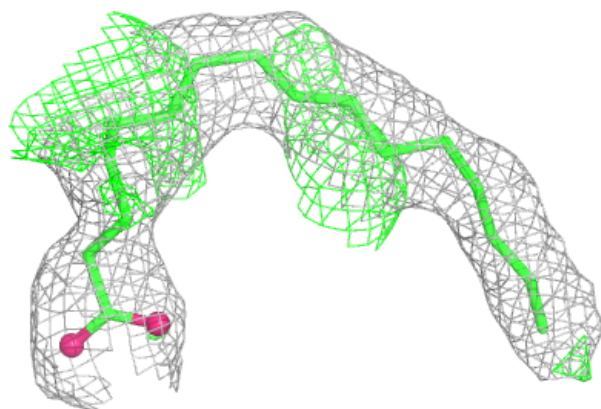
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PLM	G	502	18/18	0.75	0.19	46,61,69,72	0
3	PLM	L	502	18/18	0.77	0.20	50,67,75,75	0
3	PLM	D	502	18/18	0.79	0.21	36,56,81,87	0
3	PLM	K	502	18/18	0.79	0.17	35,51,77,79	0
3	PLM	D	503	18/18	0.79	0.19	44,58,62,62	0
3	PLM	H	502	18/18	0.81	0.18	59,66,73,76	0
3	PLM	E	502	18/18	0.81	0.17	45,61,71,71	0
3	PLM	B	502	18/18	0.81	0.19	41,57,61,65	0
3	PLM	A	502	18/18	0.84	0.16	40,53,62,64	0
3	PLM	C	502	18/18	0.85	0.16	38,49,55,57	0
3	PLM	I	502	18/18	0.85	0.15	32,57,72,75	0
3	PLM	J	502	18/18	0.87	0.14	37,60,74,77	0
2	HEM	J	501	43/43	0.93	0.15	86,95,113,117	0
2	HEM	L	501	43/43	0.93	0.15	94,101,119,123	0
2	HEM	K	501	43/43	0.94	0.13	83,97,113,124	0
2	HEM	I	501	43/43	0.95	0.13	93,107,118,120	0
2	HEM	F	501	43/43	0.96	0.09	43,52,65,70	0
2	HEM	G	501	43/43	0.96	0.10	63,74,88,89	0
2	HEM	E	501	43/43	0.96	0.08	33,38,63,69	0
2	HEM	B	501	43/43	0.97	0.07	36,46,56,68	0
2	HEM	H	501	43/43	0.97	0.09	57,76,99,102	0
2	HEM	C	501	43/43	0.97	0.08	26,37,59,61	0
2	HEM	A	501	43/43	0.98	0.06	34,42,52,58	0
2	HEM	D	501	43/43	0.98	0.07	40,51,60,62	0

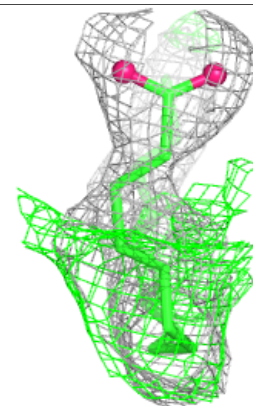
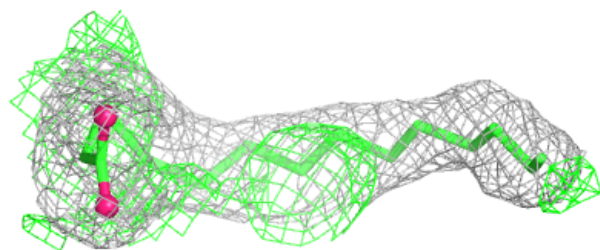
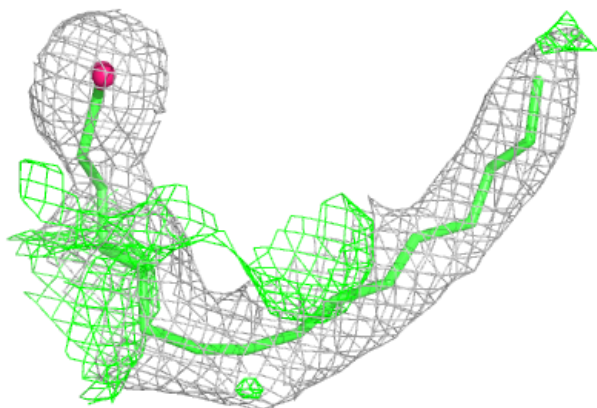
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PLM G 502:

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

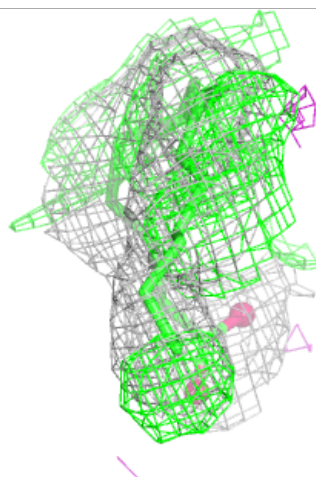
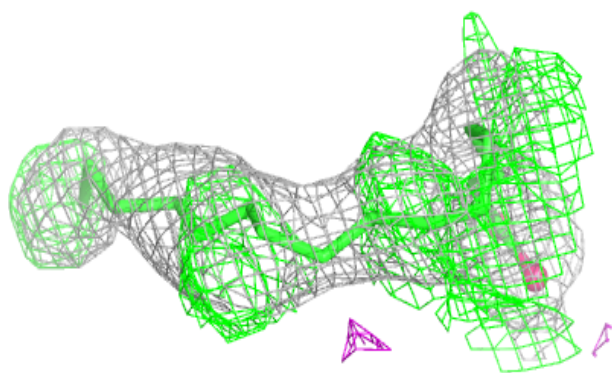
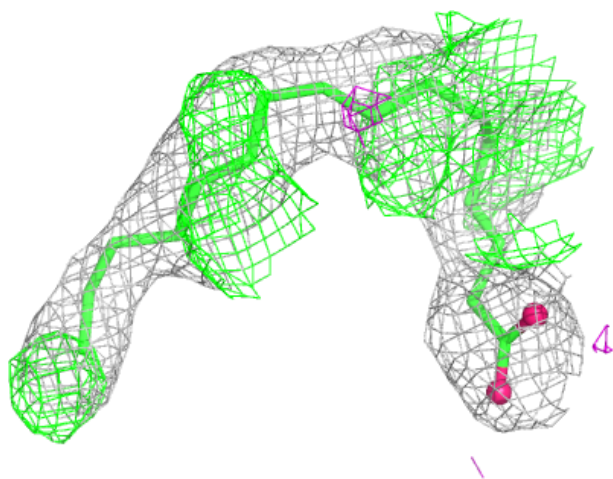
**Electron density around PLM L 502:**

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and green (positive)



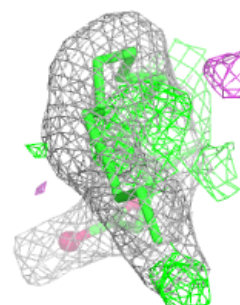
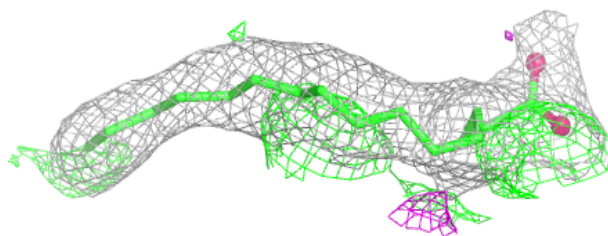
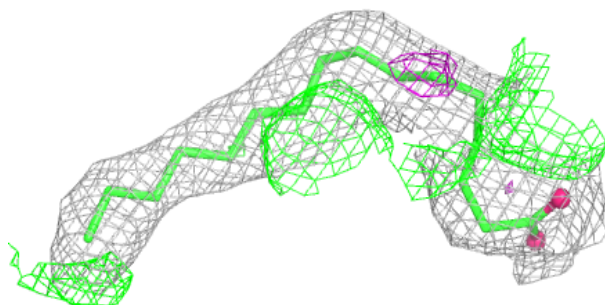
Electron density around PLM D 502:

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

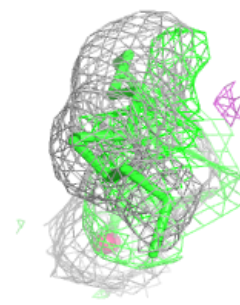
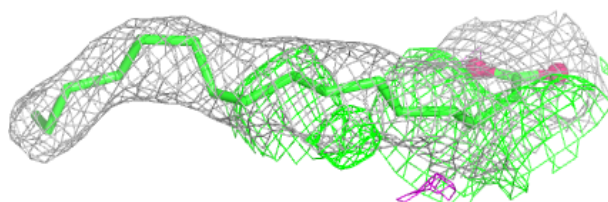
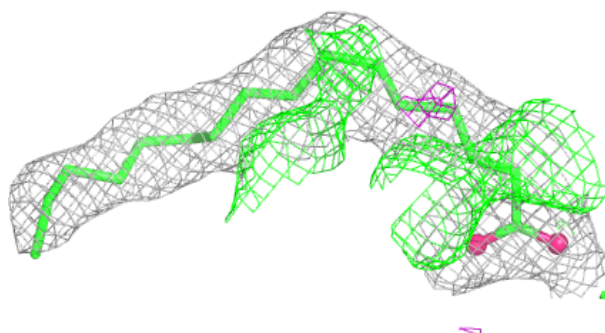


Electron density around PLM K 502:

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

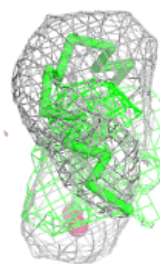
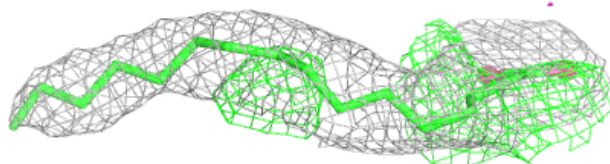
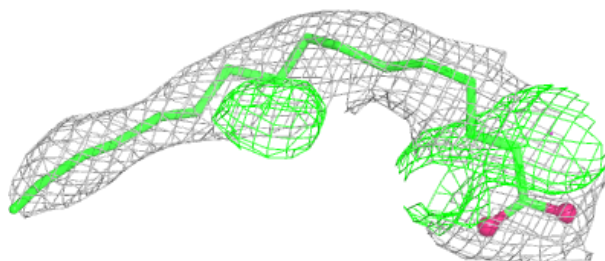
**Electron density around PLM D 503:**

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and green (positive)

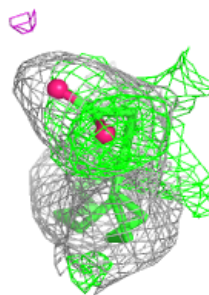
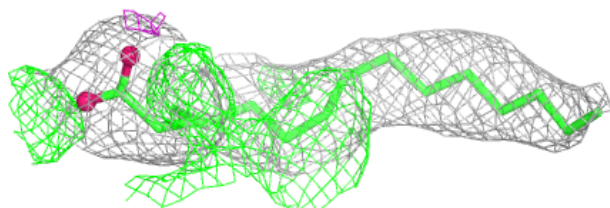
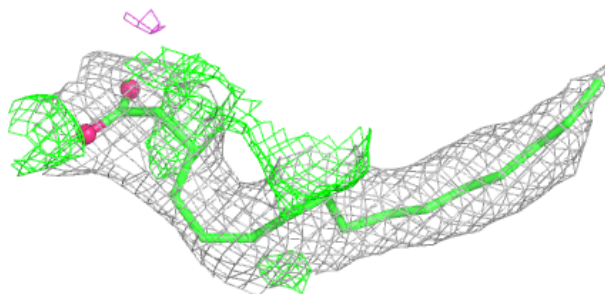


Electron density around PLM H 502:

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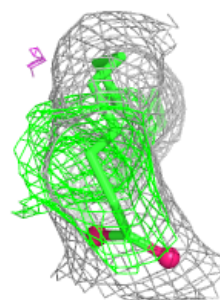
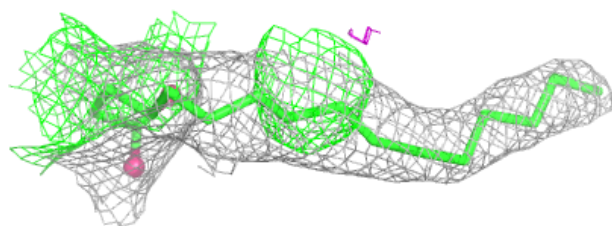
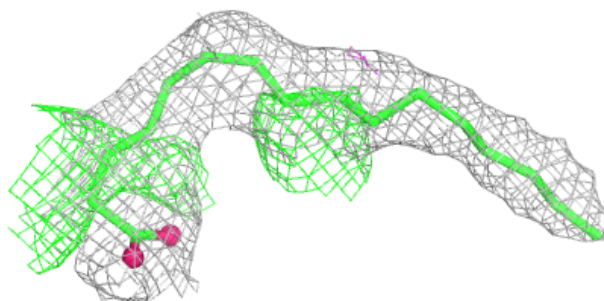
**Electron density around PLM E 502:**

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and green (positive)

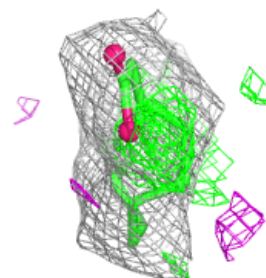
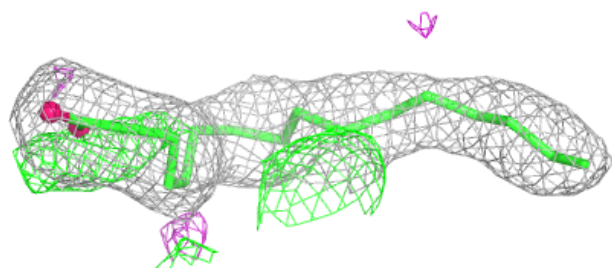
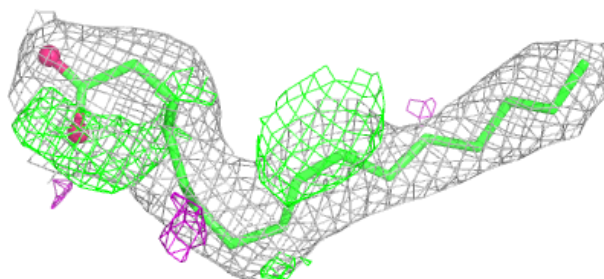


Electron density around PLM B 502:

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

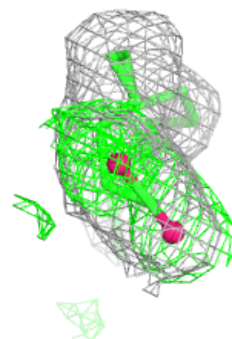
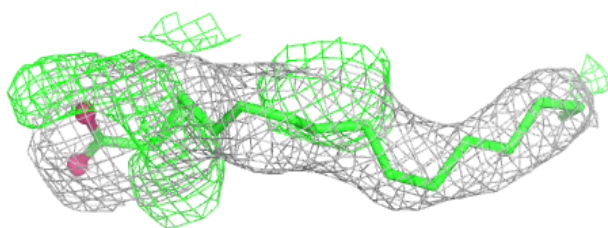
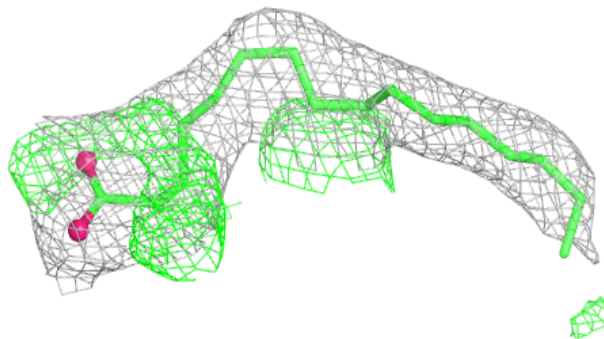
**Electron density around PLM A 502:**

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



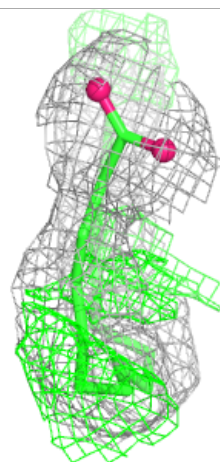
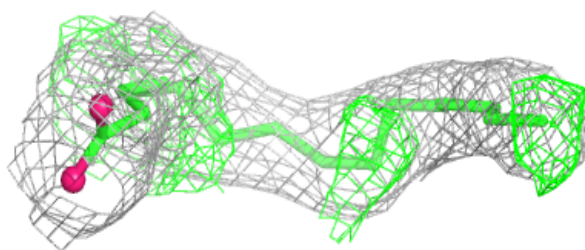
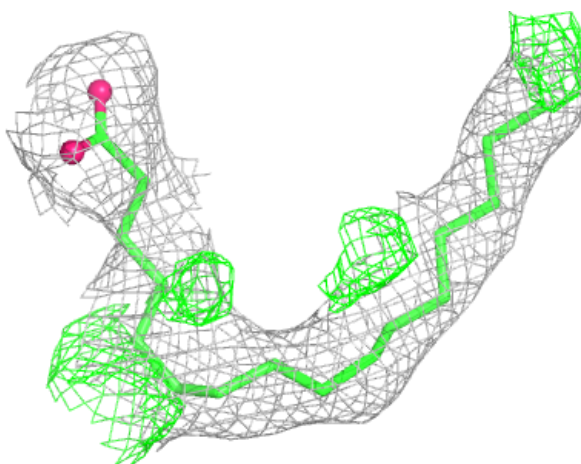
Electron density around PLM C 502:

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



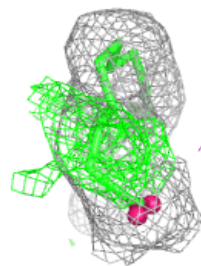
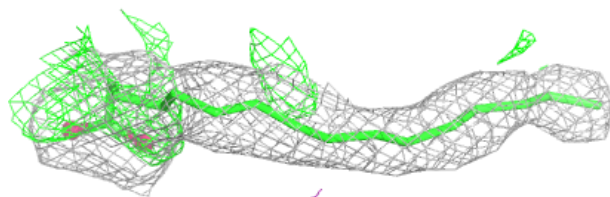
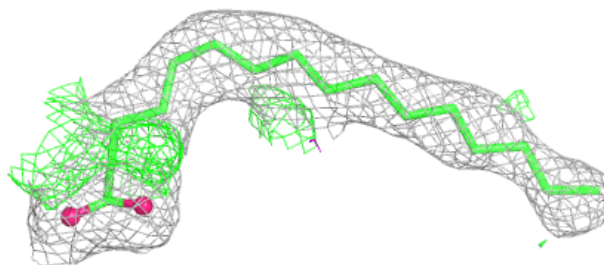
Electron density around PLM I 502:

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



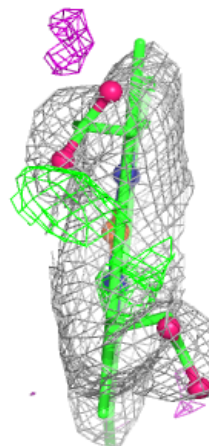
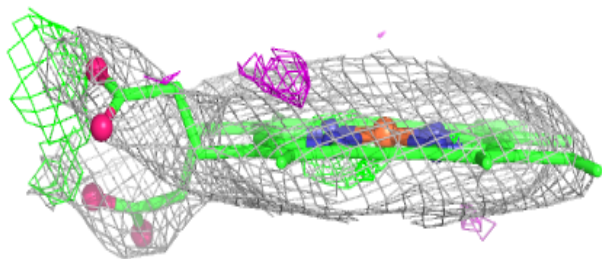
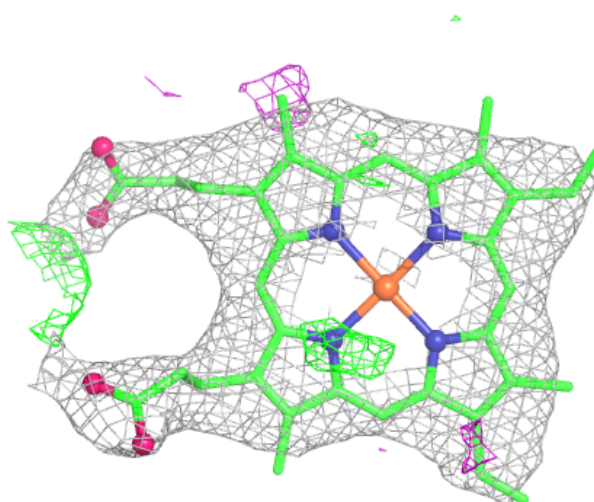
Electron density around PLM J 502:

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



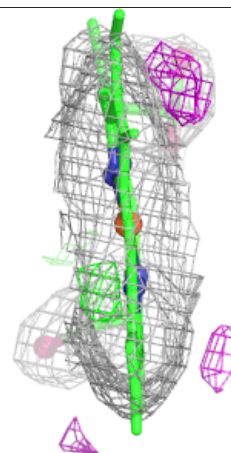
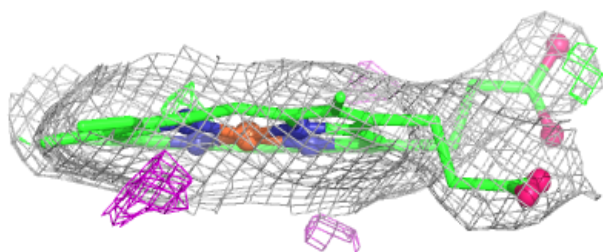
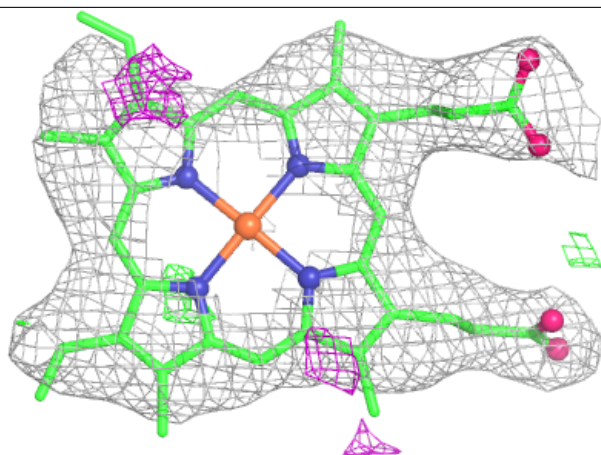
Electron density around HEM J 501:

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



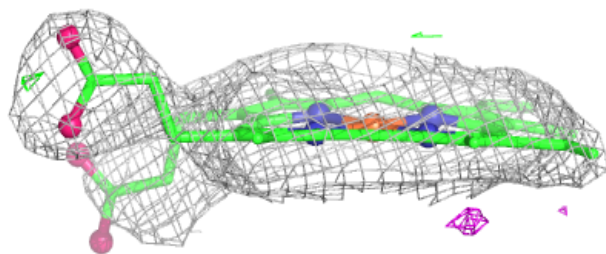
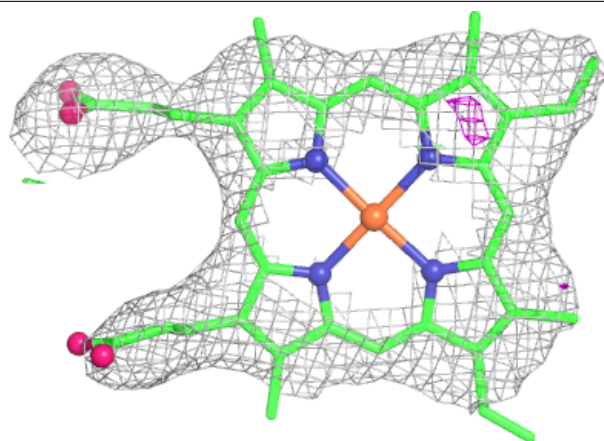
Electron density around HEM L 501:

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



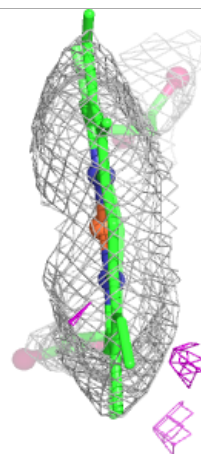
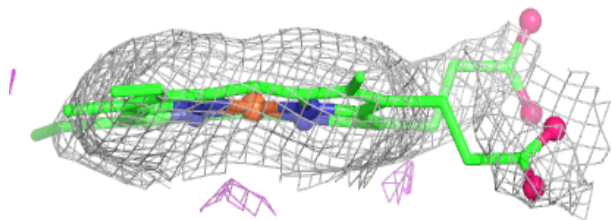
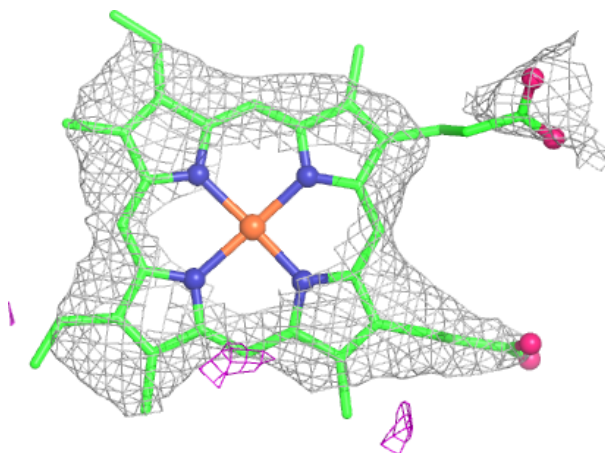
Electron density around HEM K 501:

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



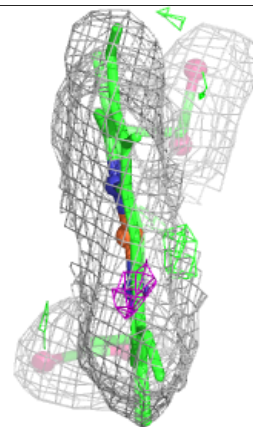
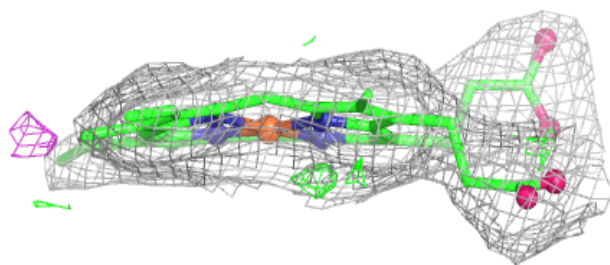
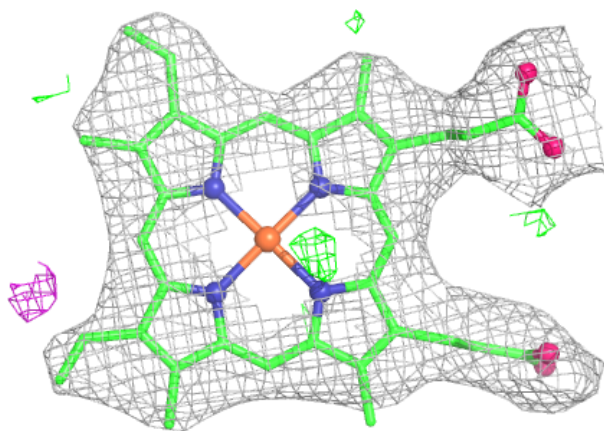
Electron density around HEM I 501:

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



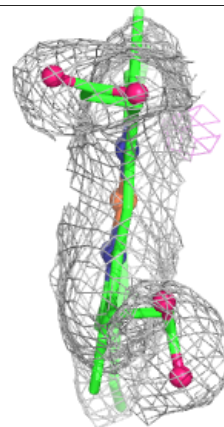
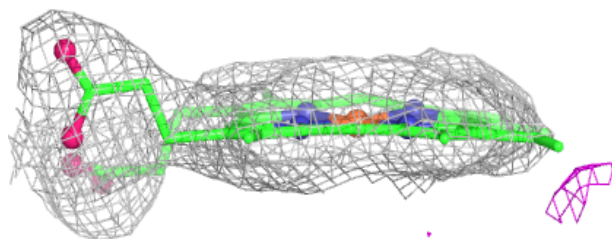
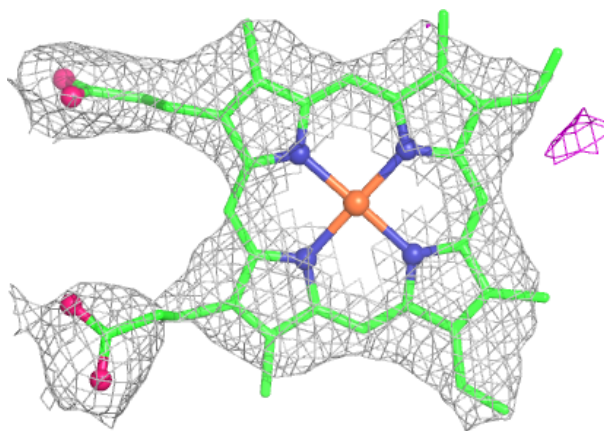
Electron density around HEM F 501:

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



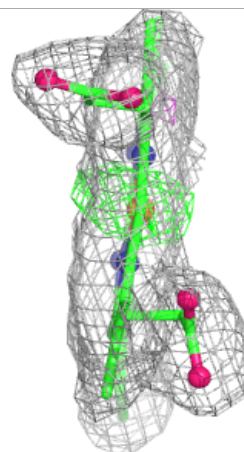
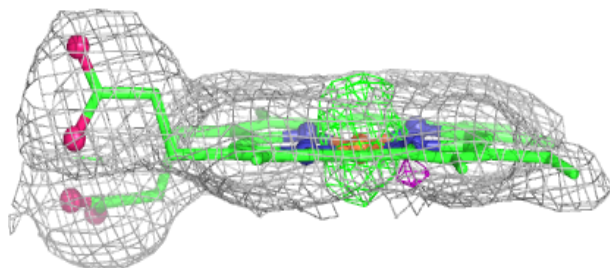
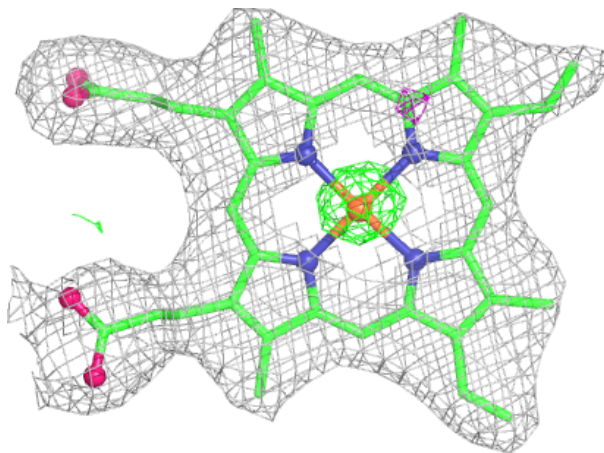
Electron density around HEM G 501:

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



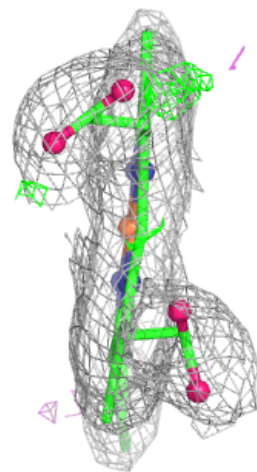
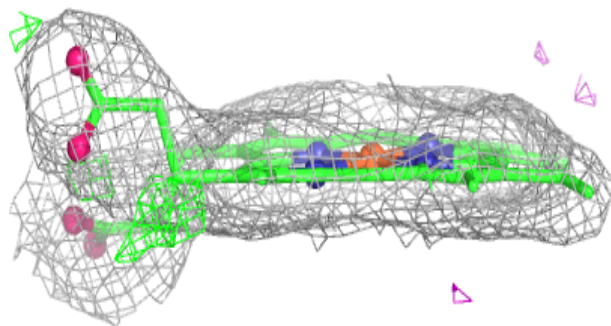
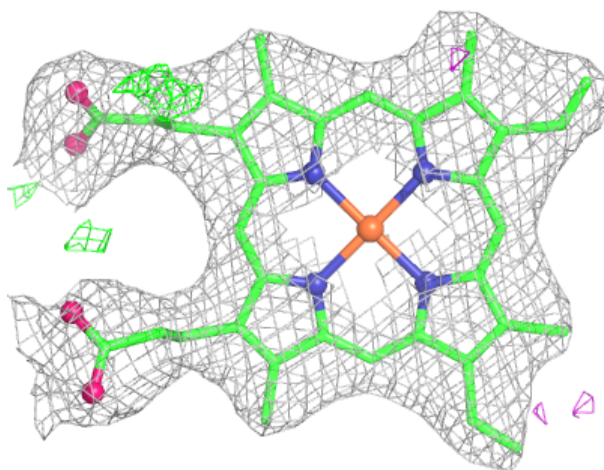
Electron density around HEM E 501:

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



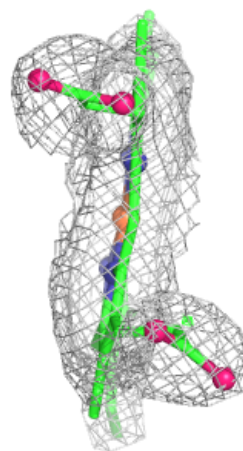
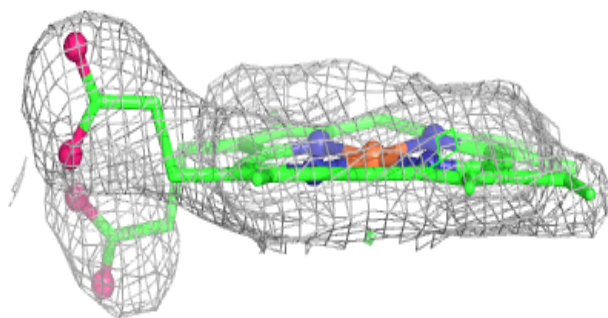
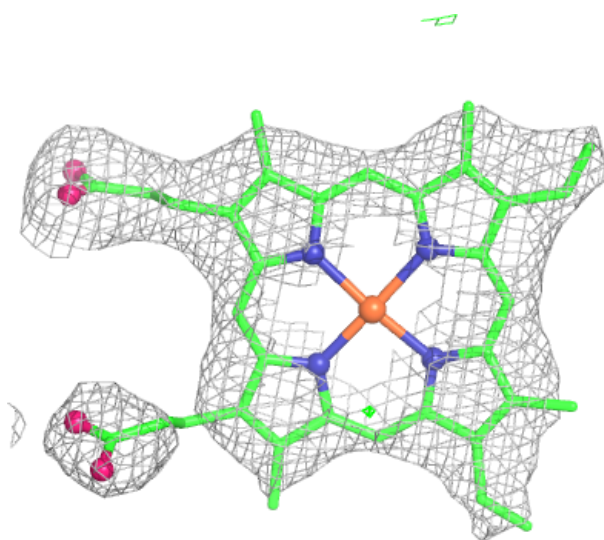
Electron density around HEM B 501:

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



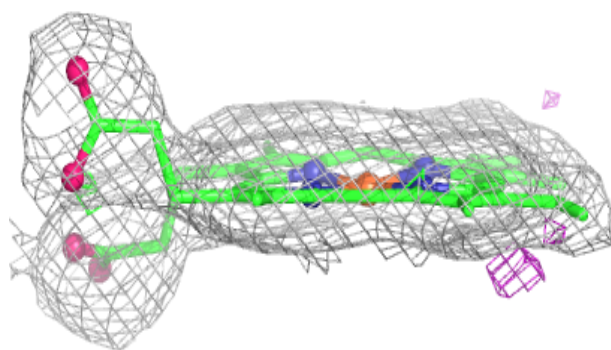
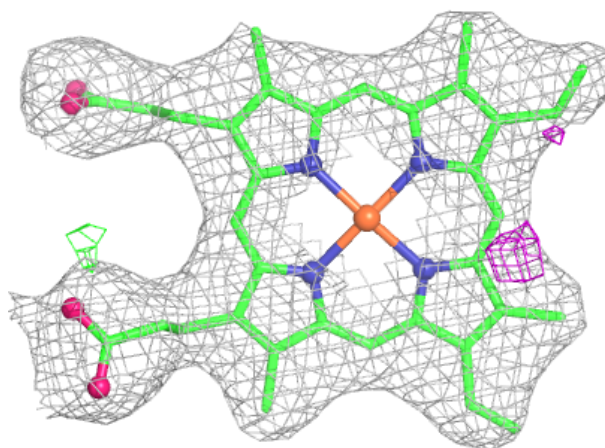
Electron density around HEM H 501:

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



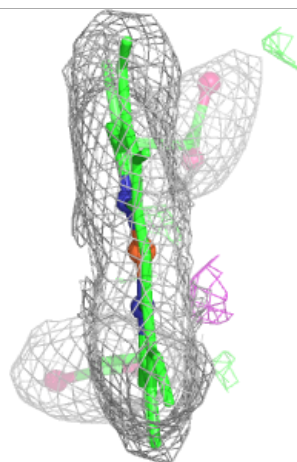
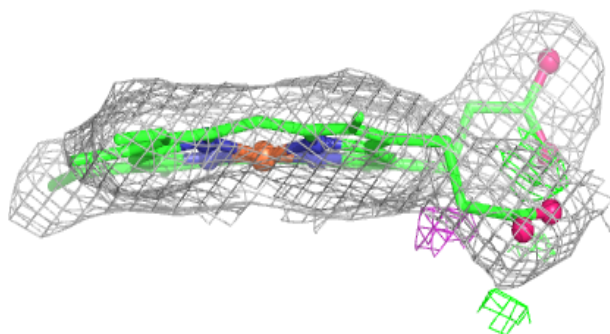
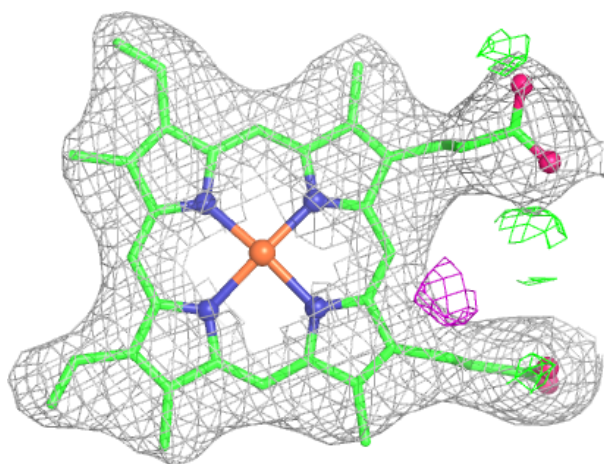
Electron density around HEM C 501:

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



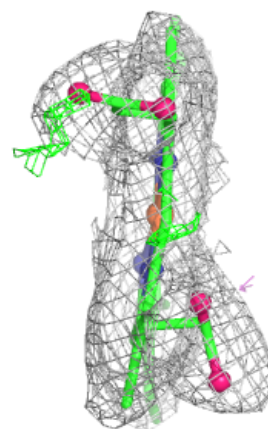
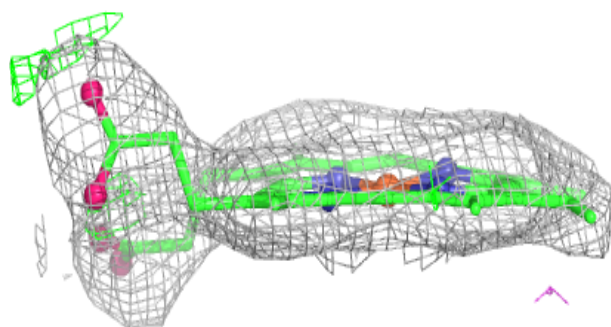
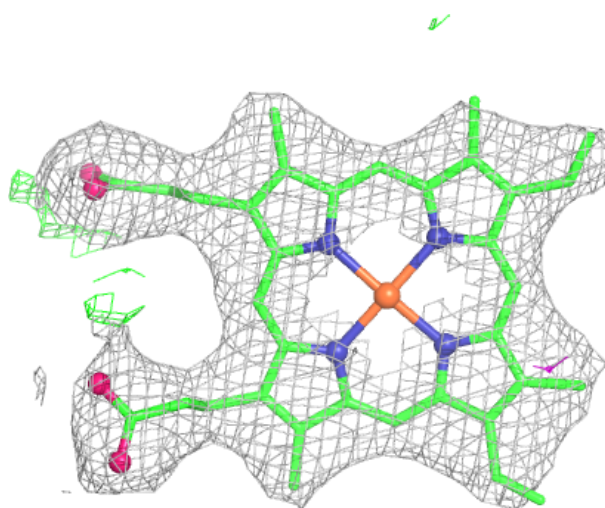
Electron density around HEM A 501:

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



Electron density around HEM D 501:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.