



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2023 – 07:05 AM EDT

PDB ID : 2QJP
Title : Crystal structure of wild type rhodobacter sphaeroides with stigmatellin and antimycin inhibited
Authors : Esser, L.; Xia, D.
Deposited on : 2007-07-08
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

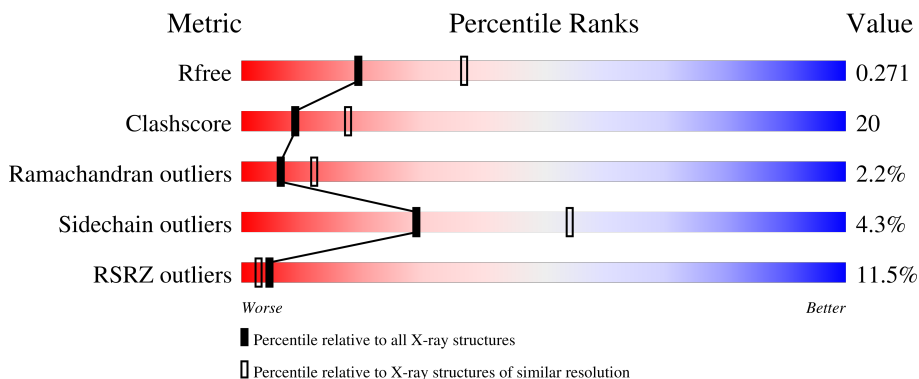
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	428	
1	D	428	
1	G	428	
1	J	428	
2	B	256	

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Mol	Chain	Length	Quality of chain
2	E	256	<p>22% 58% 38%</p>
2	H	256	<p>14% 54% 42%</p>
2	K	256	<p>19% 61% 35%</p>
3	C	179	<p>14% 60% 35% 5%</p>
3	F	179	<p>23% 54% 41% 5%</p>
3	I	179	<p>12% 58% 39%</p>
3	L	179	<p>23% 56% 37% 6%</p>

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 28227 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 Cytochrome b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	428	Total 3435	C 2319	N 545	O 556	S 15	0	0	0
1	D	428	Total 3435	C 2319	N 545	O 556	S 15	0	0	0
1	G	428	Total 3435	C 2319	N 545	O 556	S 15	0	0	0
1	J	428	Total 3435	C 2319	N 545	O 556	S 15	0	0	0

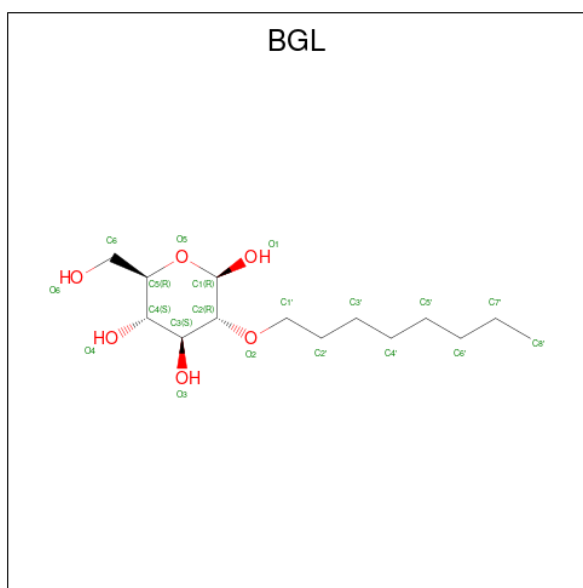
- Molecule 2 is a protein called Cytochrome c1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	256	Total 1953	C 1240	N 326	O 374	S 13	0	0	0
2	E	256	Total 1953	C 1240	N 326	O 374	S 13	0	0	0
2	H	256	Total 1953	C 1240	N 326	O 374	S 13	0	0	0
2	K	256	Total 1953	C 1240	N 326	O 374	S 13	0	0	0

- Molecule 3 is a protein called Ubiquinol-cytochrome c reductase iron-sulfur subunit.

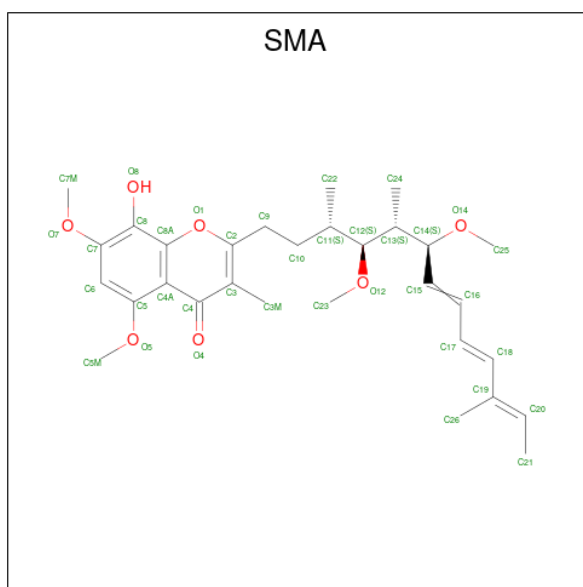
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	179	Total 1341	C 845	N 237	O 253	S 6	0	0	0
3	F	179	Total 1341	C 845	N 237	O 253	S 6	0	0	0
3	I	179	Total 1341	C 845	N 237	O 253	S 6	0	0	0
3	L	179	Total 1341	C 845	N 237	O 253	S 6	0	0	0

- Molecule 4 is 2-O-octyl-beta-D-glucopyranose (three-letter code: BGL) (formula: $C_{14}H_{28}O_6$).



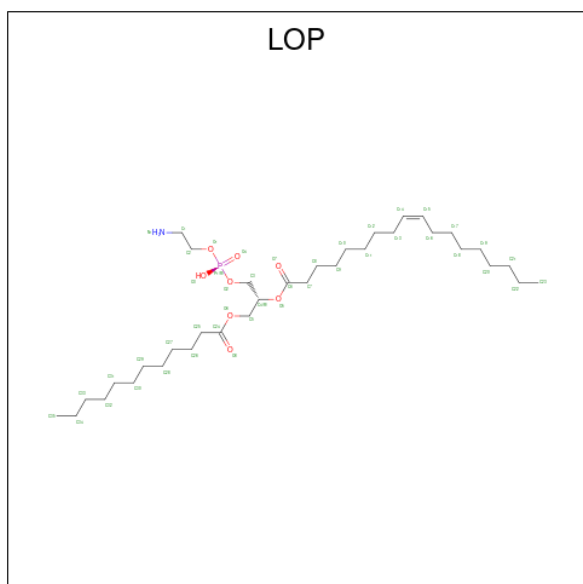
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	C O	0	0
			20	14 6		
4	E	1	Total	C O	0	0
			20	14 6		
4	G	1	Total	C O	0	0
			20	14 6		
4	J	1	Total	C O	0	0
			20	14 6		

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



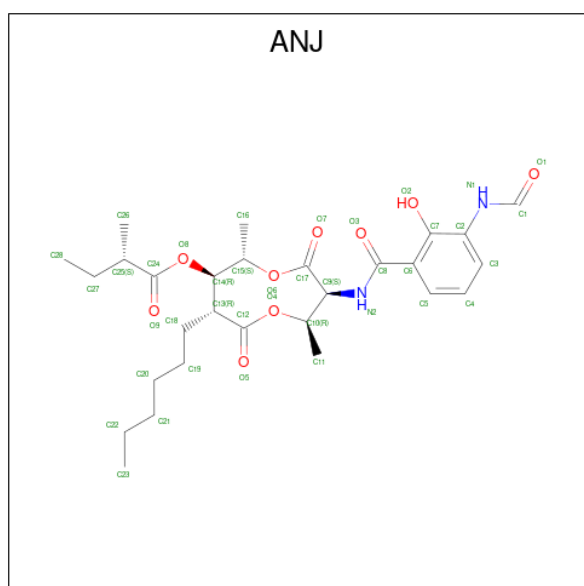
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	C O	0	0
			37	30 7		
6	D	1	Total	C O	0	0
			37	30 7		
6	G	1	Total	C O	0	0
			37	30 7		
6	J	1	Total	C O	0	0
			37	30 7		

- Molecule 7 is (1R)-2-{[(R)-(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(DODECANOYLOXY)METHYL]ETHYL (9Z)-OCTADEC-9-ENOATE (three-letter code: LOP) (formula: C₃₅H₆₈NO₈P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
7	A	1	Total	C	N	O	P	0	0
			45	35	1	8	1		
7	D	1	Total	C	N	O	P	0	0
			45	35	1	8	1		
7	G	1	Total	C	N	O	P	0	0
			45	35	1	8	1		
7	J	1	Total	C	N	O	P	0	0
			45	35	1	8	1		

- Molecule 8 is (2R,3S,6S,7R,8R)-3-[[3-(FORMYLAMINO)-2-HYDROXYBENZOYL]AMINO]-8-HEXYL-2,6-DIMETHYL-4,9-DIOXO-1,5-DIOXONAN-7-YL (2S)-2-METHYLBUTANOATE (three-letter code: ANJ) (formula: C₂₈H₄₀N₂O₉).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			39	28	2	9		
8	D	1	Total	C	N	O	0	0
			39	28	2	9		
8	G	1	Total	C	N	O	0	0
			39	28	2	9		
8	J	1	Total	C	N	O	0	0
			39	28	2	9		

- Molecule 9 is STRONTIUM ION (three-letter code: SR) (formula: Sr).

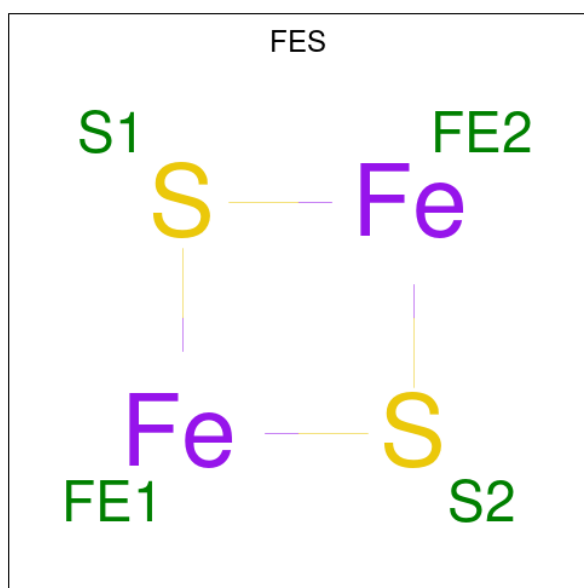
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Sr	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	E	1	Total 1	Sr 1	0	0
9	G	1	Total 1	Sr 1	0	0
9	H	1	Total 1	Sr 1	0	0
9	J	1	Total 1	Sr 1	0	0
9	K	1	Total 1	Sr 1	0	0

- Molecule 10 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	C	1	Total 4	Fe 2	S 2	0	0
10	F	1	Total 4	Fe 2	S 2	0	0
10	I	1	Total 4	Fe 2	S 2	0	0
10	L	1	Total 4	Fe 2	S 2	0	0

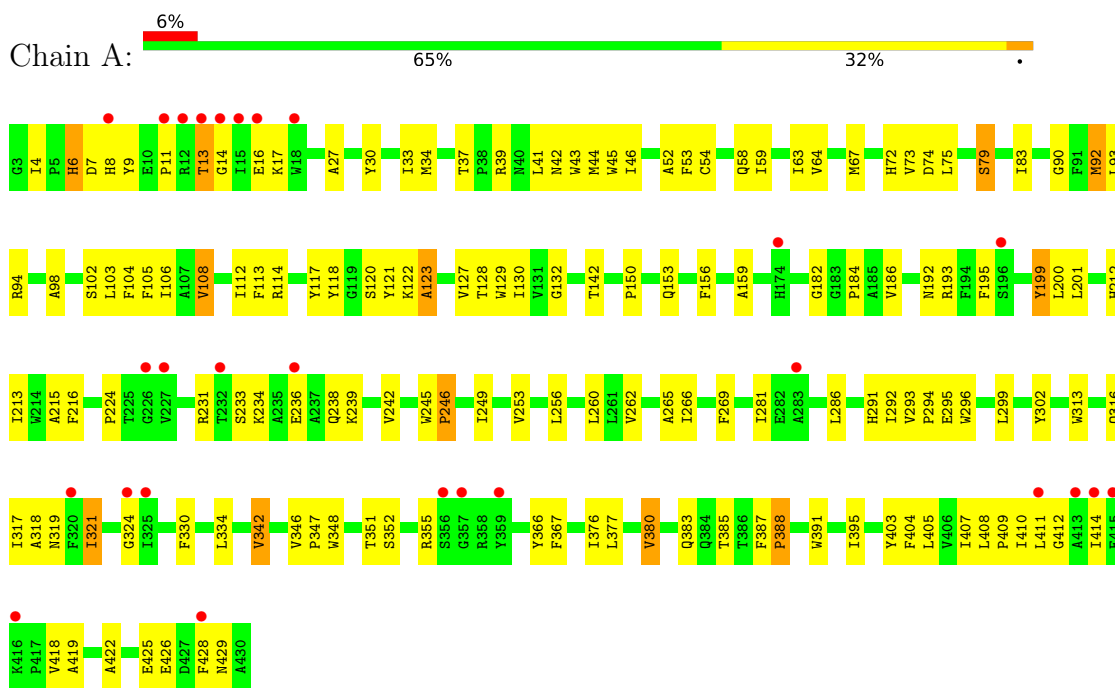
- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	36	Total O 36 36	0	0
11	B	7	Total O 7 7	0	0
11	C	13	Total O 13 13	0	0
11	D	41	Total O 41 41	0	0
11	E	3	Total O 3 3	0	0
11	F	13	Total O 13 13	0	0
11	G	41	Total O 41 41	0	0
11	H	4	Total O 4 4	0	0
11	I	14	Total O 14 14	0	0
11	J	23	Total O 23 23	0	0
11	K	3	Total O 3 3	0	0
11	L	11	Total O 11 11	0	0

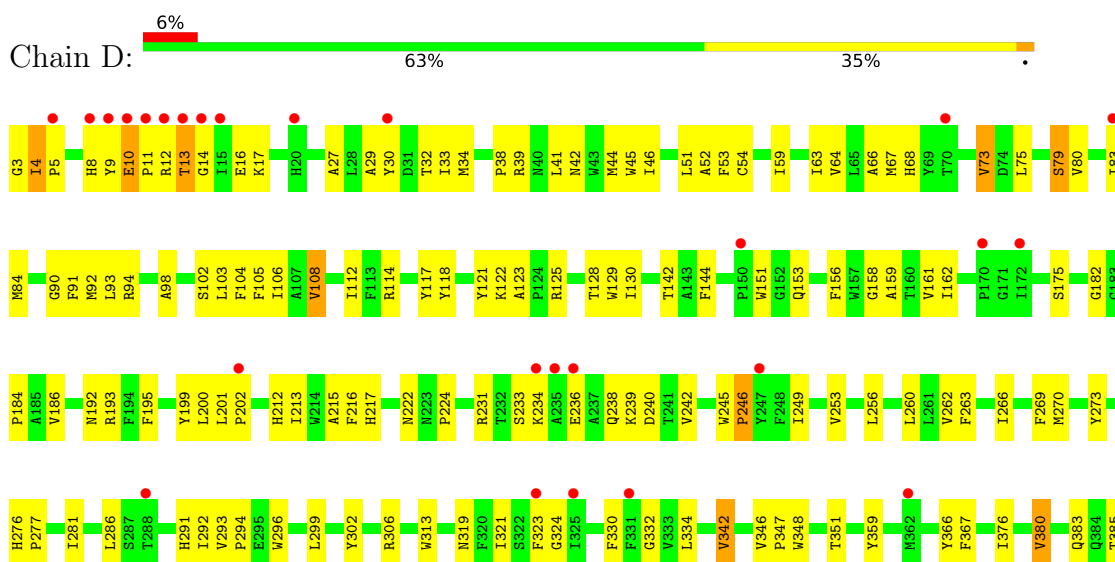
3 Residue-property plots [i](#)

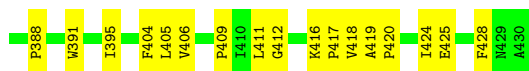
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

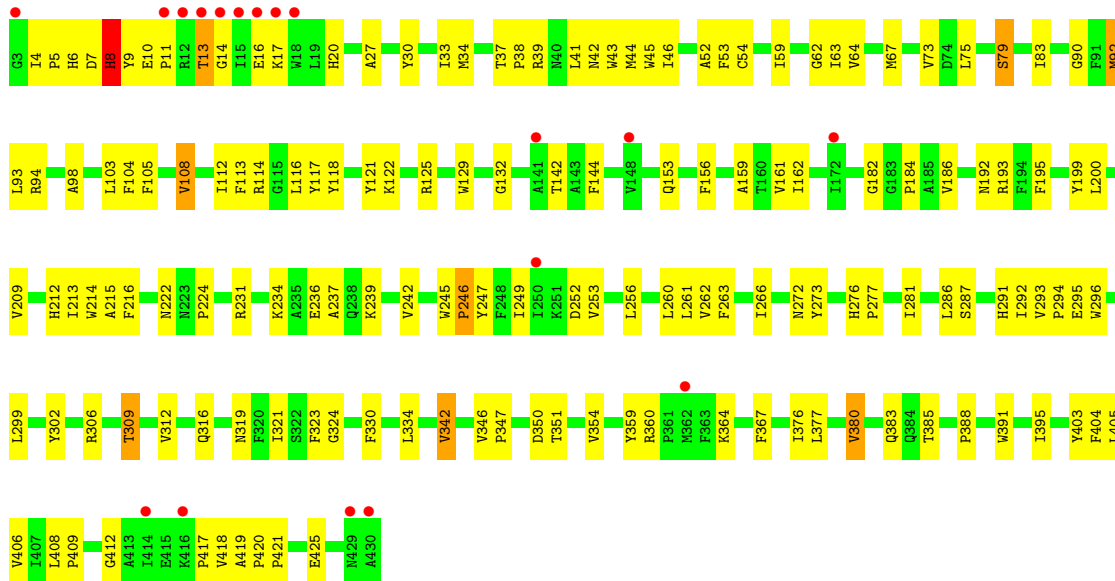


- Molecule 1: Cytochrome b

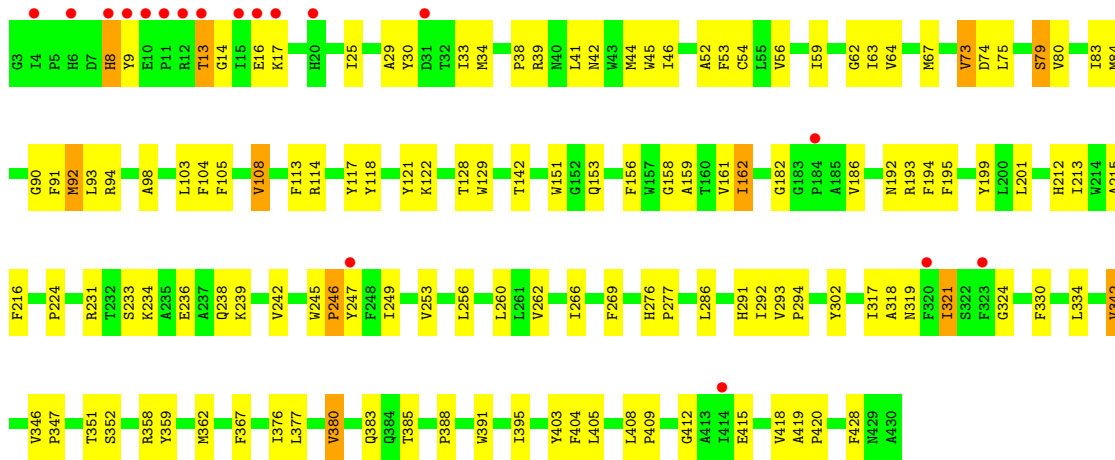




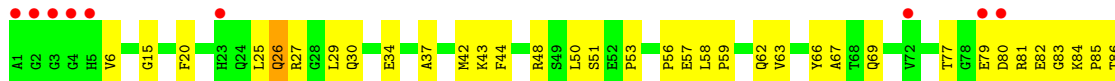
• Molecule 1: Cytochrome b

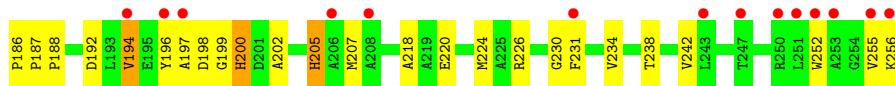
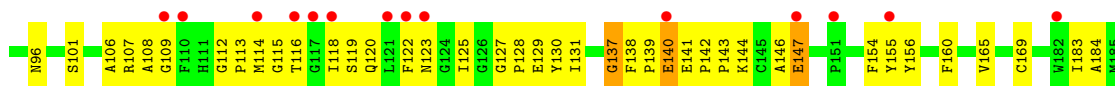


• Molecule 1: Cytochrome b

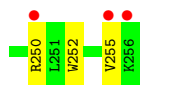
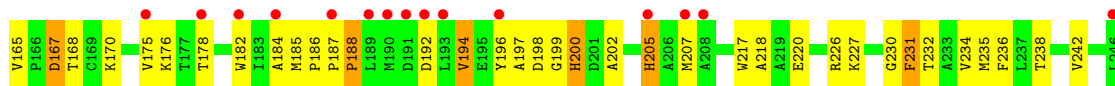
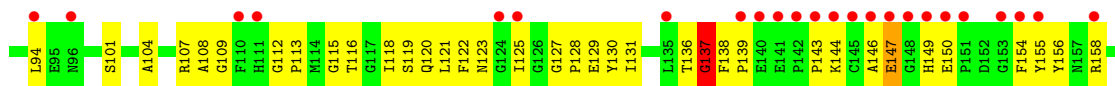
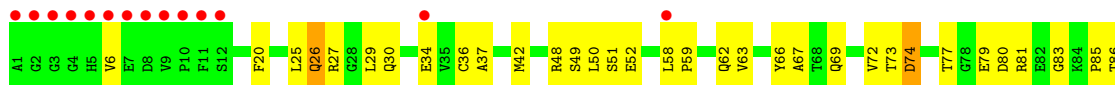


• Molecule 2: Cytochrome c1

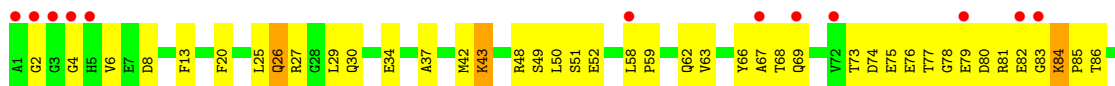




● Molecule 2: Cytochrome c1

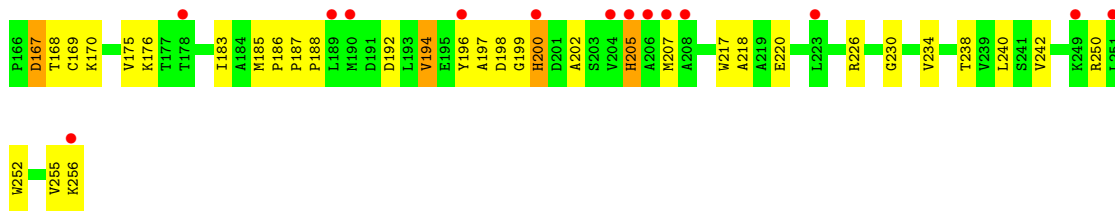


● Molecule 2: Cytochrome c1

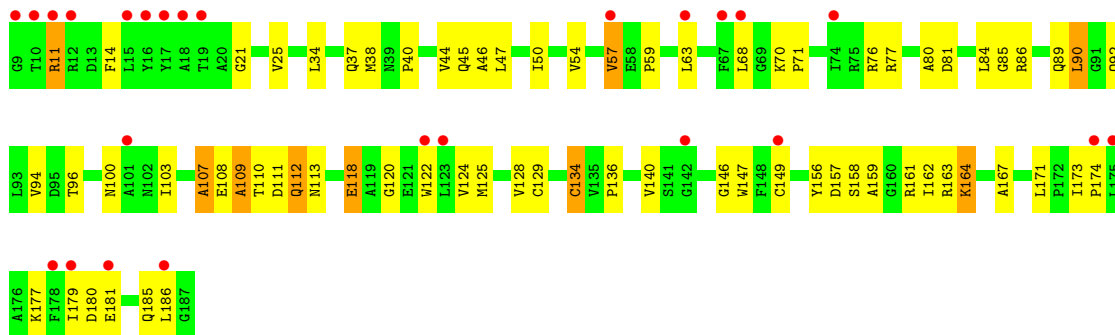


● Molecule 2: Cytochrome c1

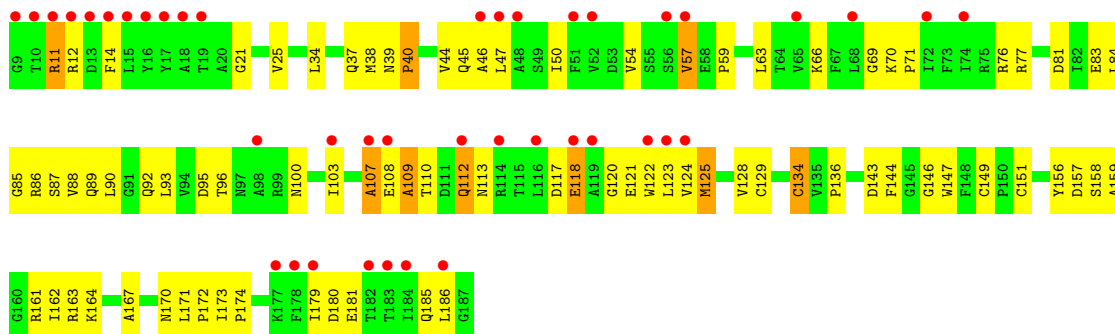




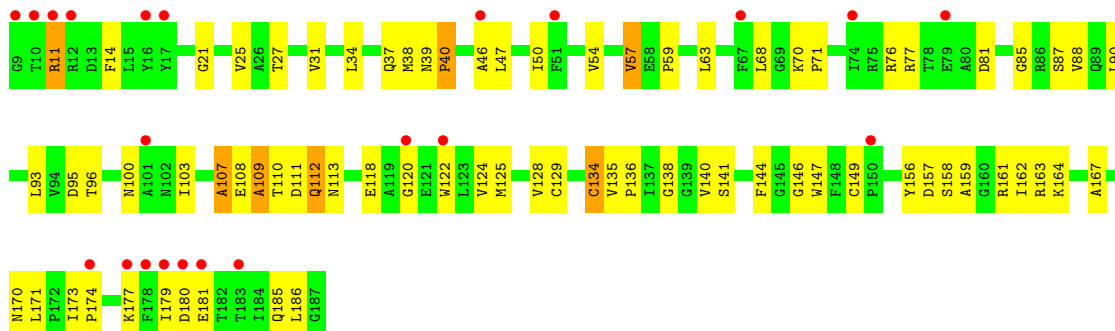
● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



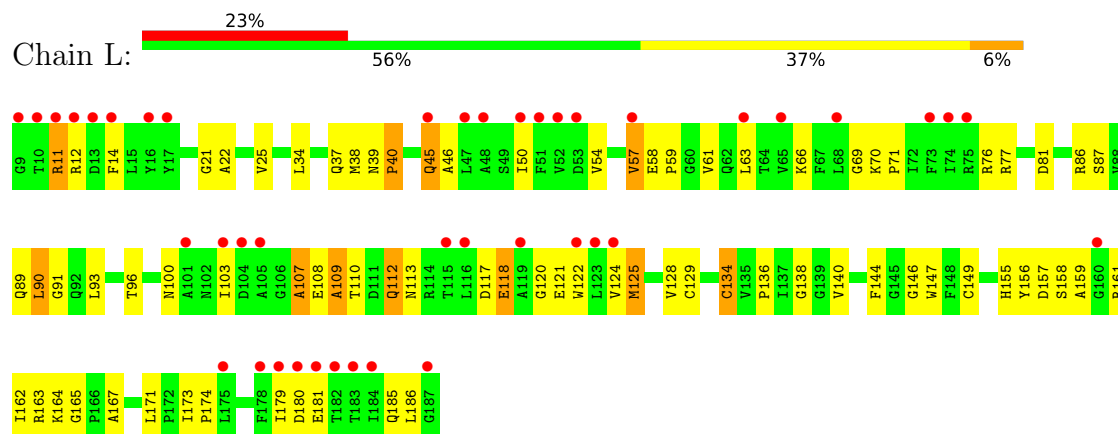
● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



● Molecule 3: Ubiquinol-cytochrome c reductase iron-sulfur subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.06Å 146.52Å 141.00Å 90.00° 110.21° 90.00°	Depositor
Resolution (Å)	17.98 – 2.60 47.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.0 (17.98-2.60) 97.7 (47.00-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.61Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.244 , 0.277 0.257 , 0.271	Depositor DCC
R_{free} test set	5654 reflections (2.05%)	wwPDB-VP
Wilson B-factor (Å ²)	61.8	Xtrriage
Anisotropy	0.271	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 64.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.000 for l,-k,h	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	28227	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.77 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.3332e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: BGL, SR, ANJ, HEM, LOP, FES, SMA

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	0.36	0/3565	0.64	0/4891
1	D	0.35	0/3565	0.63	0/4891
1	G	0.35	0/3565	0.64	0/4891
1	J	0.36	0/3565	0.65	0/4891
2	B	0.32	0/2010	0.64	1/2733 (0.0%)
2	E	0.31	0/2010	0.64	1/2733 (0.0%)
2	H	0.32	0/2010	0.65	1/2733 (0.0%)
2	K	0.31	0/2010	0.65	1/2733 (0.0%)
3	C	0.32	0/1371	0.69	0/1868
3	F	0.31	0/1371	0.68	1/1868 (0.1%)
3	I	0.32	0/1371	0.70	0/1868
3	L	0.31	0/1371	0.67	0/1868
All	All	0.34	0/27784	0.65	5/37968 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	137	GLY	N-CA-C	5.84	127.71	113.10
2	K	137	GLY	N-CA-C	5.55	126.98	113.10
2	E	137	GLY	N-CA-C	5.54	126.94	113.10
2	B	137	GLY	N-CA-C	5.51	126.87	113.10
3	F	47	LEU	CA-CB-CG	5.03	126.87	115.30

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	3435	0	3420	134	0
1	D	3435	0	3420	144	0
1	G	3435	0	3420	131	0
1	J	3435	0	3420	119	0
2	B	1953	0	1848	87	0
2	E	1953	0	1848	115	0
2	H	1953	0	1848	113	0
2	K	1953	0	1848	91	0
3	C	1341	0	1307	52	0
3	F	1341	0	1307	71	0
3	I	1341	0	1307	64	0
3	L	1341	0	1307	70	0
4	A	20	0	28	3	0
4	E	20	0	28	2	0
4	G	20	0	28	1	0
4	J	20	0	28	1	0
5	A	86	0	60	9	0
5	B	43	0	30	5	0
5	D	86	0	60	10	0
5	E	43	0	30	5	0
5	G	86	0	60	7	0
5	H	43	0	30	4	0
5	J	86	0	60	5	0
5	K	43	0	30	1	0
6	A	37	0	42	2	0
6	D	37	0	42	3	0
6	G	37	0	42	1	0
6	J	37	0	42	3	0
7	A	45	0	67	2	0
7	D	45	0	67	4	0
7	G	45	0	67	5	0
7	J	45	0	67	5	0
8	A	39	0	39	9	0
8	D	39	0	39	12	0
8	G	39	0	39	6	0
8	J	39	0	39	10	0
9	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	E	1	0	0	0	0
9	G	1	0	0	0	0
9	H	1	0	0	0	0
9	J	1	0	0	0	0
9	K	1	0	0	0	0
10	C	4	0	0	0	0
10	F	4	0	0	0	0
10	I	4	0	0	0	0
10	L	4	0	0	0	0
11	A	36	0	0	2	0
11	B	7	0	0	3	0
11	C	13	0	0	0	0
11	D	41	0	0	4	0
11	E	3	0	0	0	0
11	F	13	0	0	2	0
11	G	41	0	0	3	0
11	H	4	0	0	0	0
11	I	14	0	0	0	0
11	J	23	0	0	1	0
11	K	3	0	0	1	0
11	L	11	0	0	1	0
All	All	28227	0	27364	1123	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 20.

The worst 5 of 1123 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:D:213:ILE:HD11	8:D:504:ANJ:H14	1.39	1.05
1:J:213:ILE:HD11	8:J:505:ANJ:H14	1.40	1.04
1:A:317:ILE:O	1:A:321:ILE:HG22	1.60	1.02
1:A:213:ILE:HD11	8:A:504:ANJ:H14	1.39	1.01
1:J:317:ILE:O	1:J:321:ILE:HG22	1.62	1.00

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	426/428 (100%)	398 (93%)	24 (6%)	4 (1%)	17	35
1	D	426/428 (100%)	402 (94%)	21 (5%)	3 (1%)	22	43
1	G	426/428 (100%)	400 (94%)	22 (5%)	4 (1%)	17	35
1	J	426/428 (100%)	397 (93%)	26 (6%)	3 (1%)	22	43
2	B	254/256 (99%)	227 (89%)	21 (8%)	6 (2%)	6	10
2	E	254/256 (99%)	229 (90%)	18 (7%)	7 (3%)	5	7
2	H	254/256 (99%)	225 (89%)	21 (8%)	8 (3%)	4	6
2	K	254/256 (99%)	229 (90%)	18 (7%)	7 (3%)	5	7
3	C	177/179 (99%)	143 (81%)	23 (13%)	11 (6%)	1	1
3	F	177/179 (99%)	144 (81%)	25 (14%)	8 (4%)	2	3
3	I	177/179 (99%)	144 (81%)	26 (15%)	7 (4%)	3	3
3	L	177/179 (99%)	142 (80%)	26 (15%)	9 (5%)	2	2
All	All	3428/3452 (99%)	3080 (90%)	271 (8%)	77 (2%)	6	12

5 of 77 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	137	GLY
2	B	147	GLU
2	B	200	HIS
3	C	109	ALA
2	E	137	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	353/353 (100%)	336 (95%)	17 (5%)	25	49
1	D	353/353 (100%)	337 (96%)	16 (4%)	27	52
1	G	353/353 (100%)	334 (95%)	19 (5%)	22	44
1	J	353/353 (100%)	336 (95%)	17 (5%)	25	49
2	B	203/203 (100%)	198 (98%)	5 (2%)	47	73
2	E	203/203 (100%)	197 (97%)	6 (3%)	41	67
2	H	203/203 (100%)	195 (96%)	8 (4%)	32	58
2	K	203/203 (100%)	196 (97%)	7 (3%)	37	63
3	C	138/138 (100%)	133 (96%)	5 (4%)	35	61
3	F	138/138 (100%)	132 (96%)	6 (4%)	29	54
3	I	138/138 (100%)	132 (96%)	6 (4%)	29	54
3	L	138/138 (100%)	131 (95%)	7 (5%)	24	46
All	All	2776/2776 (100%)	2657 (96%)	119 (4%)	29	54

5 of 119 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	79	SER
2	K	194	VAL
1	G	385	THR
2	K	167	ASP
3	L	174	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	26	GLN
2	K	69	GLN
3	L	45	GLN
2	E	111	HIS
2	E	69	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 38 ligands modelled in this entry, 6 are monoatomic - leaving 32 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
5	HEM	A	502	1	41,50,50	1.33	4 (9%)	45,82,82	1.14	2 (4%)
4	BGL	G	431	-	20,20,20	0.86	1 (5%)	24,25,25	1.10	2 (8%)
4	BGL	A	431	-	20,20,20	1.06	1 (5%)	24,25,25	0.72	0
8	ANJ	D	504	-	40,40,40	1.81	11 (27%)	36,54,54	1.91	7 (19%)
5	HEM	D	502	1	41,50,50	1.44	5 (12%)	45,82,82	1.14	4 (8%)
6	SMA	A	1	-	38,38,38	2.28	9 (23%)	48,52,52	1.96	9 (18%)
7	LOP	G	504	-	44,44,44	0.60	0	47,49,49	1.30	6 (12%)
8	ANJ	J	505	-	40,40,40	1.82	11 (27%)	36,54,54	1.68	9 (25%)
5	HEM	J	502	1	41,50,50	1.42	5 (12%)	45,82,82	1.10	3 (6%)
7	LOP	D	503	-	44,44,44	0.56	0	47,49,49	1.28	8 (17%)
5	HEM	G	501	1	41,50,50	1.45	5 (12%)	45,82,82	1.05	2 (4%)
5	HEM	H	301	2	41,50,50	1.49	5 (12%)	45,82,82	1.09	2 (4%)
5	HEM	B	301	2	41,50,50	1.44	4 (9%)	45,82,82	1.09	2 (4%)
5	HEM	K	301	2	41,50,50	1.42	4 (9%)	45,82,82	1.08	2 (4%)
10	FES	I	200	3	0,4,4	-	-	-	-	-
10	FES	L	200	3	0,4,4	-	-	-	-	-
7	LOP	A	503	-	44,44,44	0.58	0	47,49,49	1.32	8 (17%)
10	FES	F	200	3	0,4,4	-	-	-	-	-
4	BGL	J	431	-	20,20,20	0.97	1 (5%)	24,25,25	0.79	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	HEM	G	502	1	41,50,50	1.43	5 (12%)	45,82,82	1.04	1 (2%)
6	SMA	D	2	-	38,38,38	2.26	8 (21%)	48,52,52	1.79	11 (22%)
6	SMA	J	503	-	38,38,38	2.16	7 (18%)	48,52,52	1.74	8 (16%)
6	SMA	G	503	-	38,38,38	2.34	8 (21%)	48,52,52	1.83	8 (16%)
5	HEM	J	501	1	41,50,50	1.40	4 (9%)	45,82,82	1.06	1 (2%)
5	HEM	A	501	1	41,50,50	1.49	4 (9%)	45,82,82	1.01	1 (2%)
10	FES	C	200	3	0,4,4	-	-	-	-	-
5	HEM	D	501	1	41,50,50	1.47	5 (12%)	45,82,82	1.06	2 (4%)
4	BGL	E	257	-	20,20,20	0.89	1 (5%)	24,25,25	1.14	2 (8%)
8	ANJ	G	505	-	40,40,40	1.79	9 (22%)	36,54,54	1.77	6 (16%)
7	LOP	J	504	-	44,44,44	0.56	0	47,49,49	1.39	9 (19%)
5	HEM	E	301	2	41,50,50	1.43	5 (12%)	45,82,82	1.06	1 (2%)
8	ANJ	A	504	-	40,40,40	1.79	9 (22%)	36,54,54	1.81	8 (22%)

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
5	HEM	A	502	1	-	6/12/54/54	-
4	BGL	G	431	-	-	0/11/31/31	0/1/1/1
4	BGL	A	431	-	-	0/11/31/31	0/1/1/1
8	ANJ	D	504	-	-	6/40/55/55	0/1/2/2
5	HEM	D	502	1	-	6/12/54/54	-
6	SMA	A	1	-	-	4/34/34/34	0/2/2/2
7	LOP	G	504	-	-	10/48/48/48	-
8	ANJ	J	505	-	-	6/40/55/55	0/1/2/2
5	HEM	J	502	1	-	6/12/54/54	-
7	LOP	D	503	-	-	13/48/48/48	-
5	HEM	G	501	1	-	4/12/54/54	-
5	HEM	H	301	2	-	7/12/54/54	-
5	HEM	B	301	2	-	5/12/54/54	-
5	HEM	K	301	2	-	6/12/54/54	-
10	FES	I	200	3	-	-	0/1/1/1
10	FES	L	200	3	-	-	0/1/1/1
7	LOP	A	503	-	-	12/48/48/48	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	FES	F	200	3	-	-	0/1/1/1
4	BGL	J	431	-	-	0/11/31/31	0/1/1/1
5	HEM	G	502	1	-	7/12/54/54	-
6	SMA	D	2	-	-	5/34/34/34	0/2/2/2
6	SMA	J	503	-	-	5/34/34/34	0/2/2/2
6	SMA	G	503	-	-	5/34/34/34	0/2/2/2
5	HEM	J	501	1	-	3/12/54/54	-
5	HEM	A	501	1	-	2/12/54/54	-
10	FES	C	200	3	-	-	0/1/1/1
5	HEM	D	501	1	-	4/12/54/54	-
4	BGL	E	257	-	-	0/11/31/31	0/1/1/1
8	ANJ	G	505	-	-	4/40/55/55	0/1/2/2
7	LOP	J	504	-	-	7/48/48/48	-
5	HEM	E	301	2	-	8/12/54/54	-
8	ANJ	A	504	-	-	2/40/55/55	0/1/2/2

The worst 5 of 131 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	G	503	SMA	O5-C5	7.56	1.49	1.37
6	A	1	SMA	O5-C5	7.52	1.49	1.37
6	G	503	SMA	O7-C7	7.42	1.49	1.37
6	D	2	SMA	O5-C5	7.40	1.48	1.37
6	A	1	SMA	O7-C7	7.18	1.48	1.37

The worst 5 of 124 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1	SMA	O7-C7-C8	7.45	122.06	114.54
8	G	505	ANJ	O6-C17-C9	-5.49	101.65	110.28
8	A	504	ANJ	O6-C17-C9	-5.45	101.70	110.28
8	D	504	ANJ	C19-C18-C13	-5.34	104.68	114.28
8	D	504	ANJ	O6-C17-C9	-5.09	102.27	110.28

There are no chirality outliers.

5 of 143 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	502	HEM	C2B-C3B-CAB-CBB

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Mol	Chain	Res	Type	Atoms
5	A	502	HEM	C4B-C3B-CAB-CBB
5	D	502	HEM	C2B-C3B-CAB-CBB
5	D	502	HEM	C4B-C3B-CAB-CBB
5	G	502	HEM	C2B-C3B-CAB-CBB

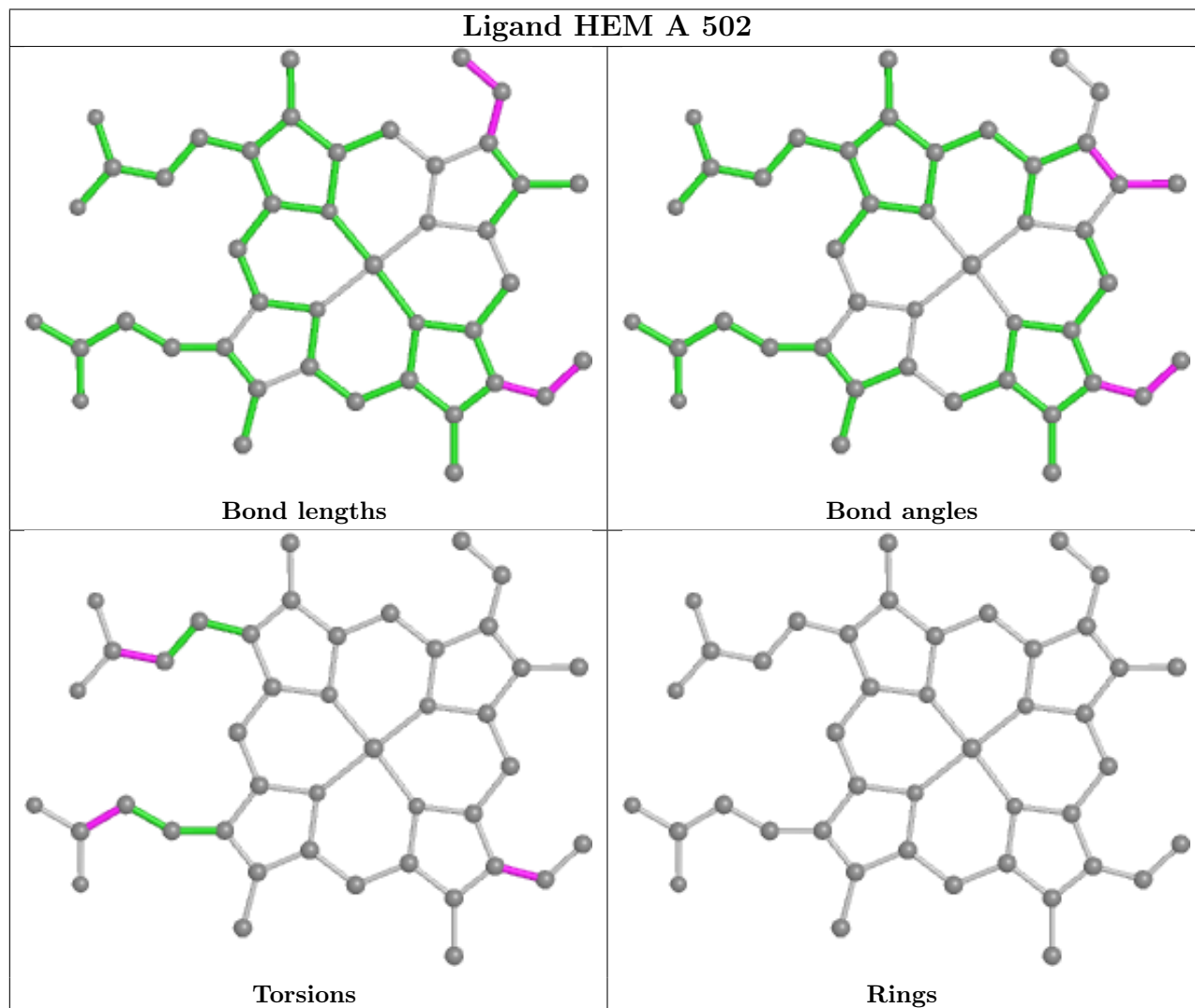
There are no ring outliers.

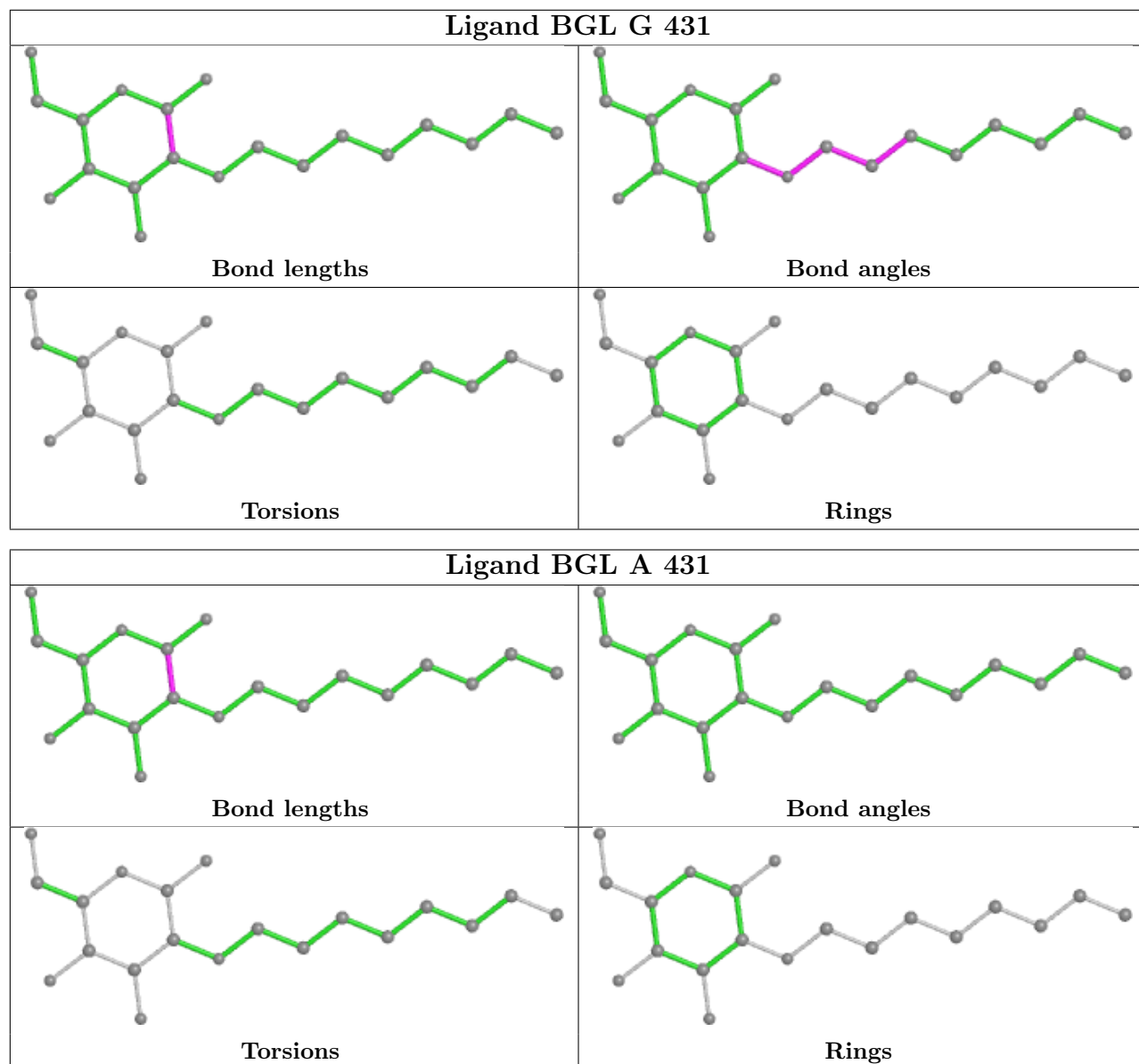
28 monomers are involved in 113 short contacts:

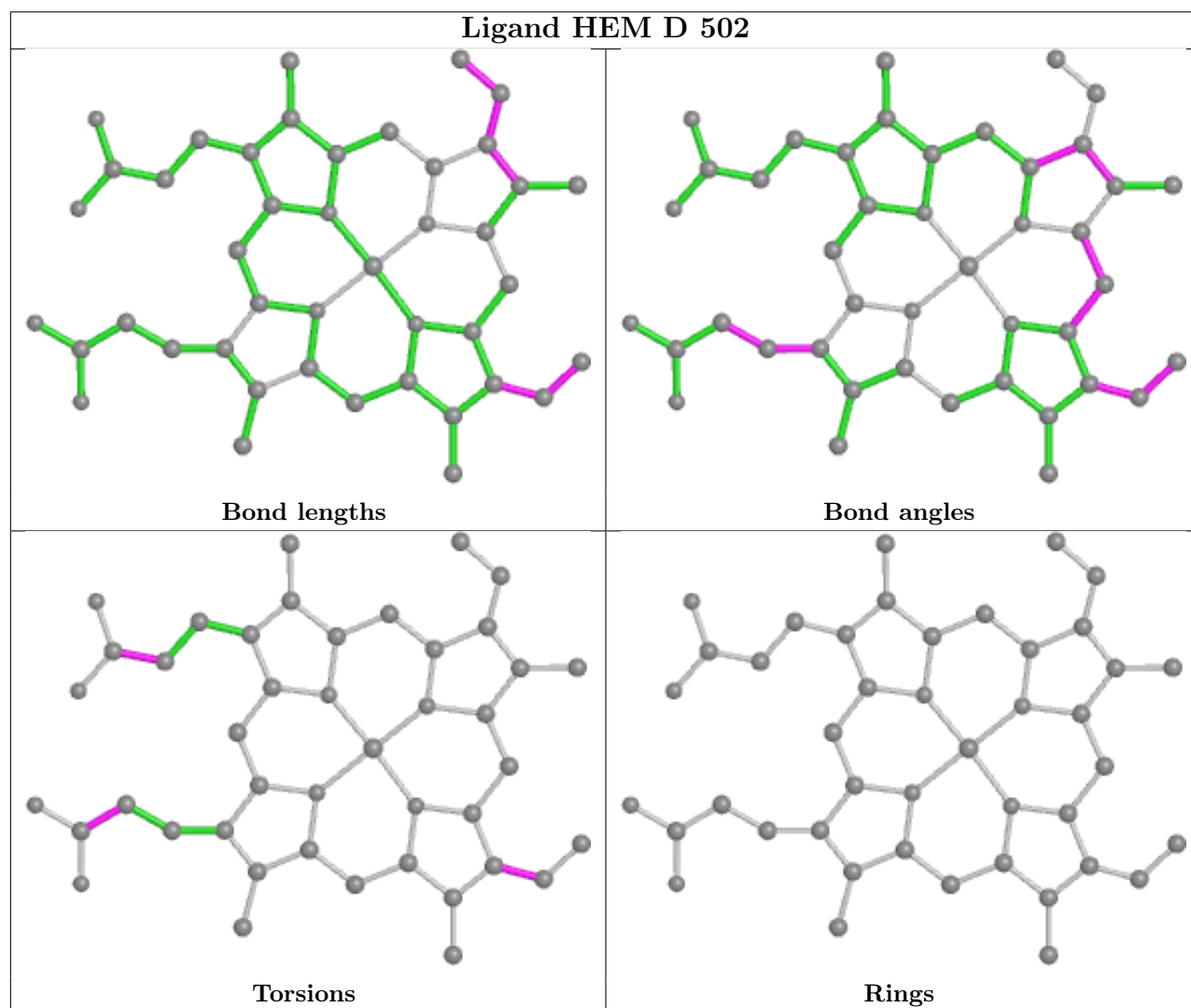
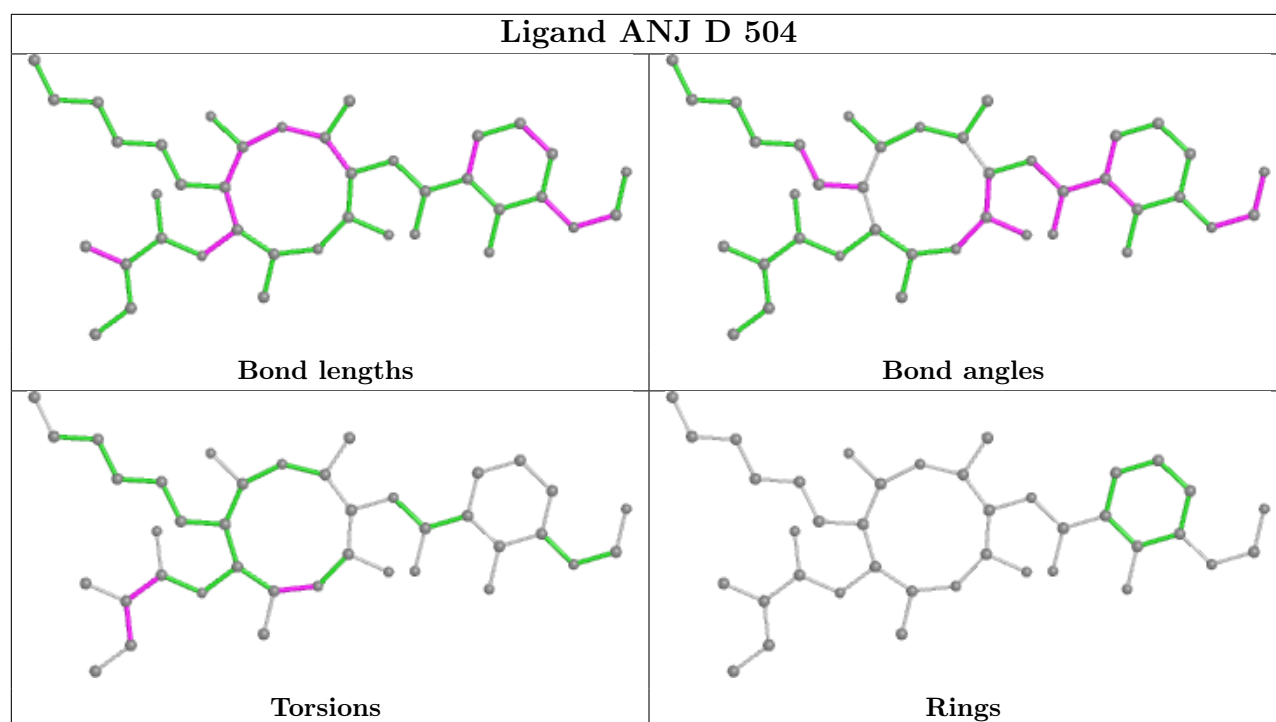
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	502	HEM	5	0
4	G	431	BGL	1	0
4	A	431	BGL	3	0
8	D	504	ANJ	12	0
5	D	502	HEM	5	0
6	A	1	SMA	2	0
7	G	504	LOP	5	0
8	J	505	ANJ	10	0
5	J	502	HEM	3	0
7	D	503	LOP	4	0
5	G	501	HEM	4	0
5	H	301	HEM	4	0
5	B	301	HEM	5	0
5	K	301	HEM	1	0
7	A	503	LOP	2	0
4	J	431	BGL	1	0
5	G	502	HEM	3	0
6	D	2	SMA	3	0
6	J	503	SMA	3	0
6	G	503	SMA	1	0
5	J	501	HEM	2	0
5	A	501	HEM	4	0
5	D	501	HEM	5	0
4	E	257	BGL	2	0
8	G	505	ANJ	6	0
7	J	504	LOP	5	0
5	E	301	HEM	5	0
8	A	504	ANJ	9	0

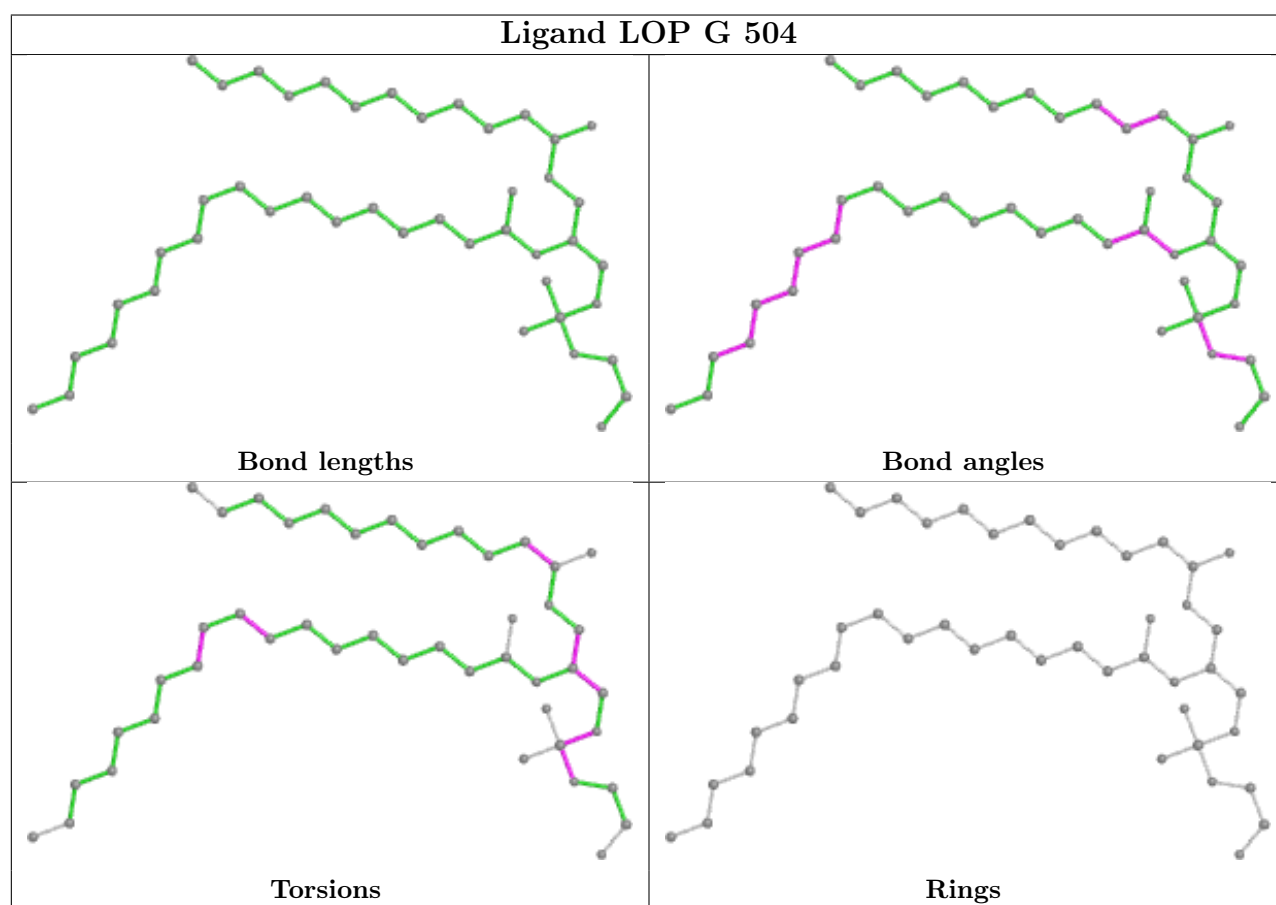
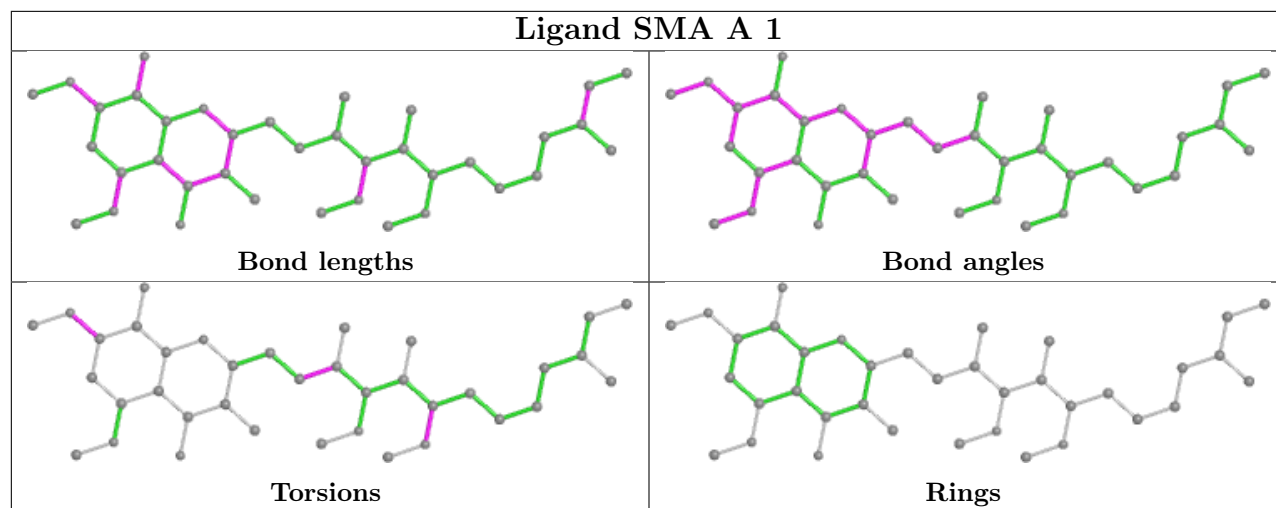
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

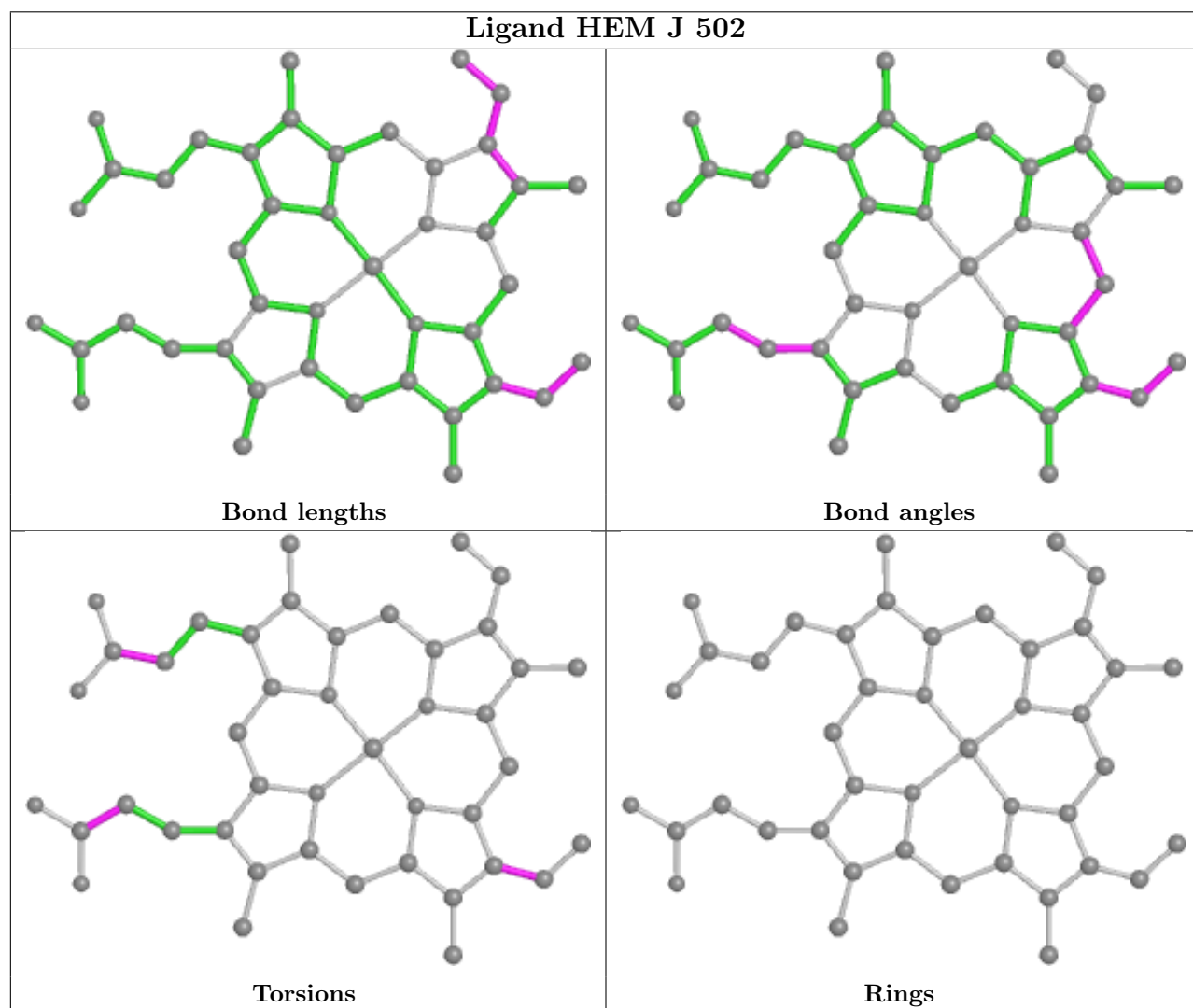
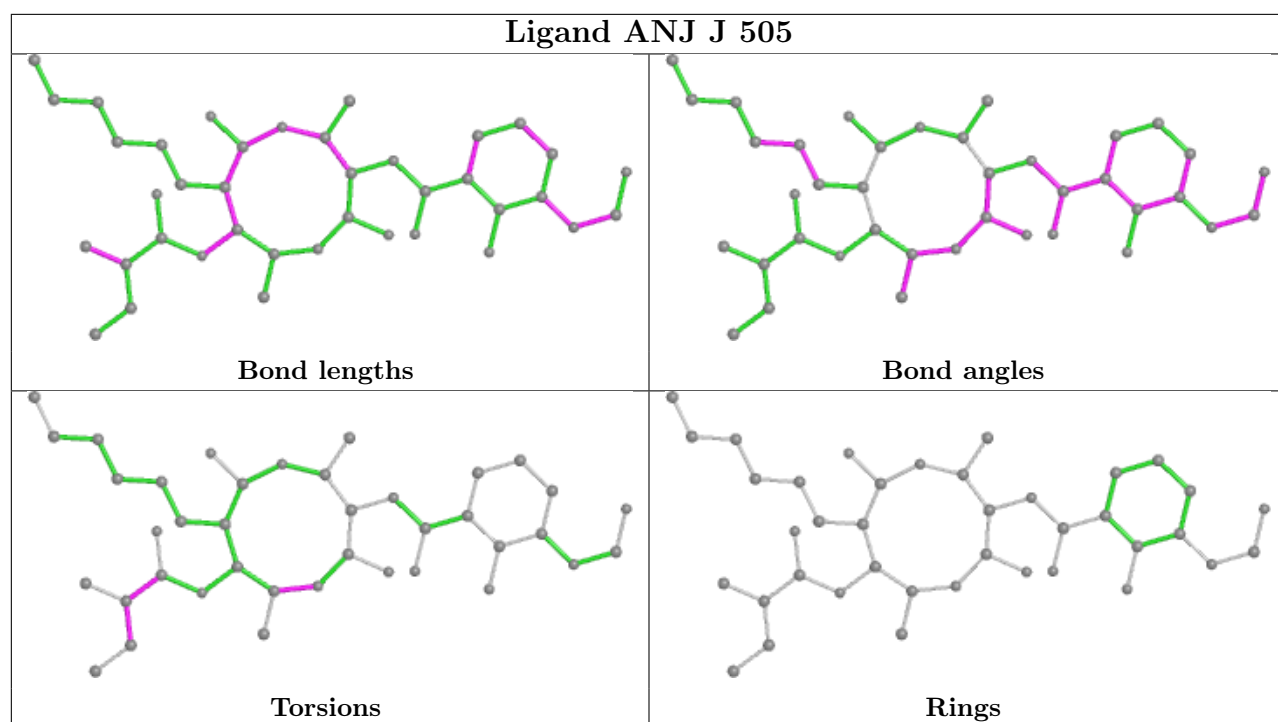
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

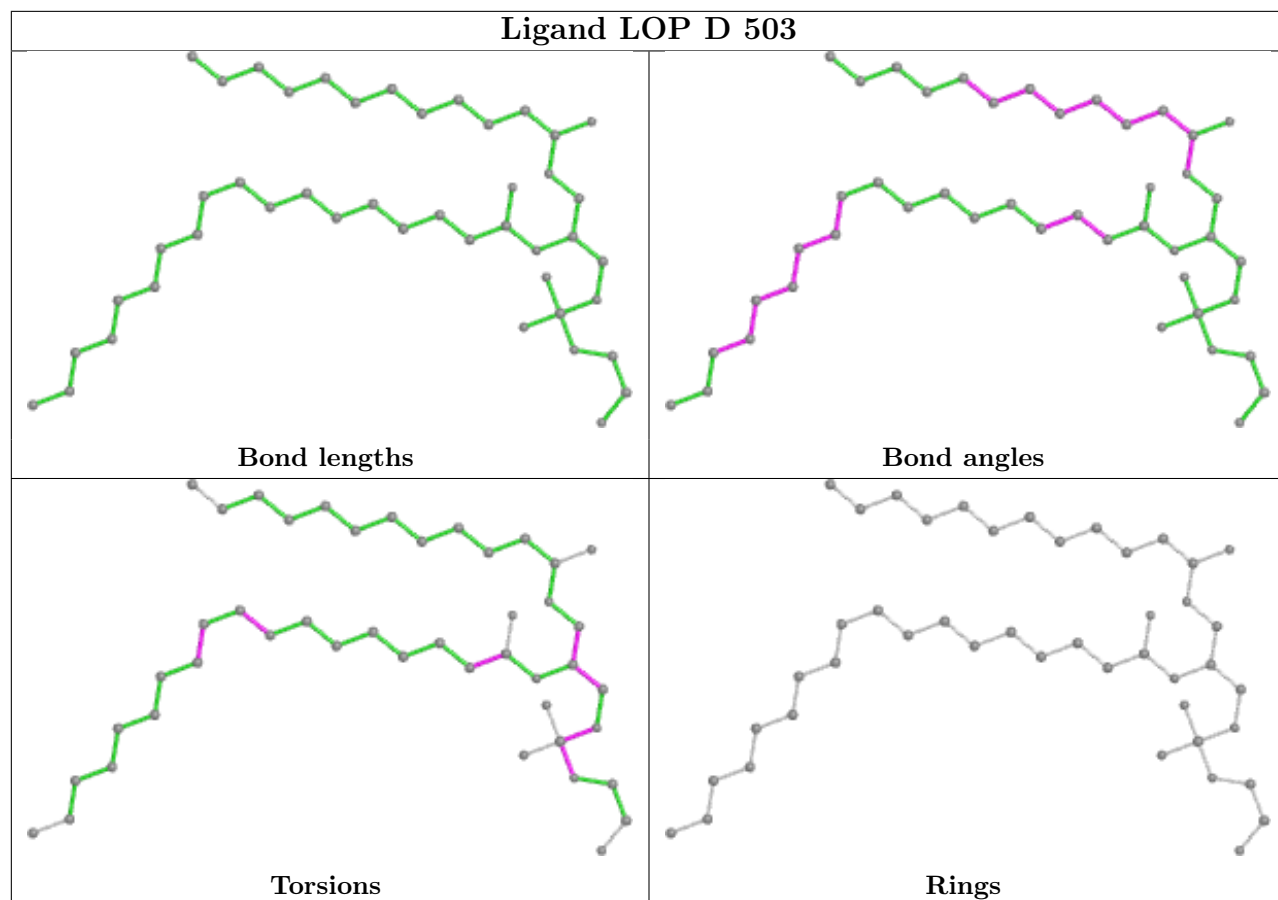


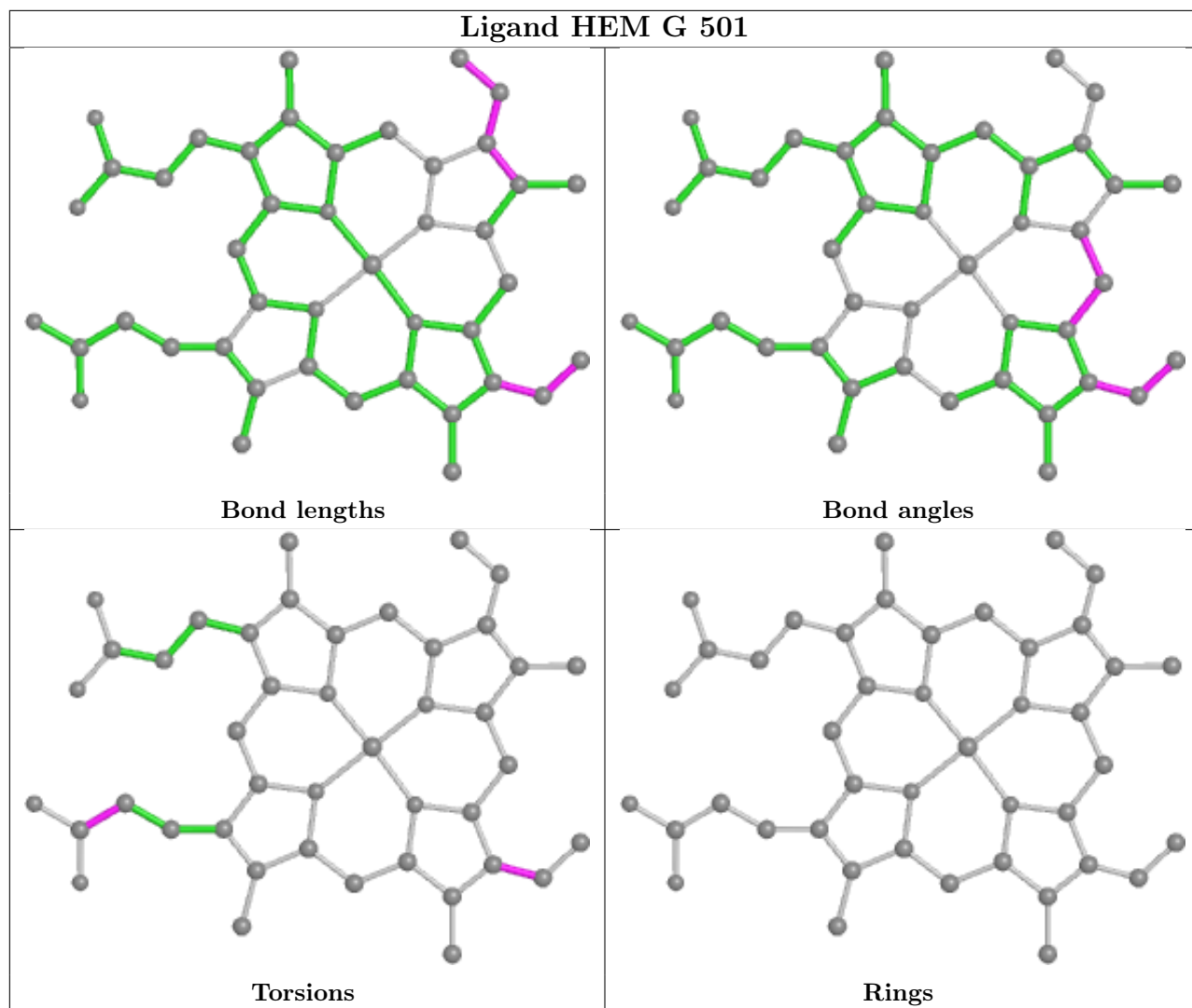


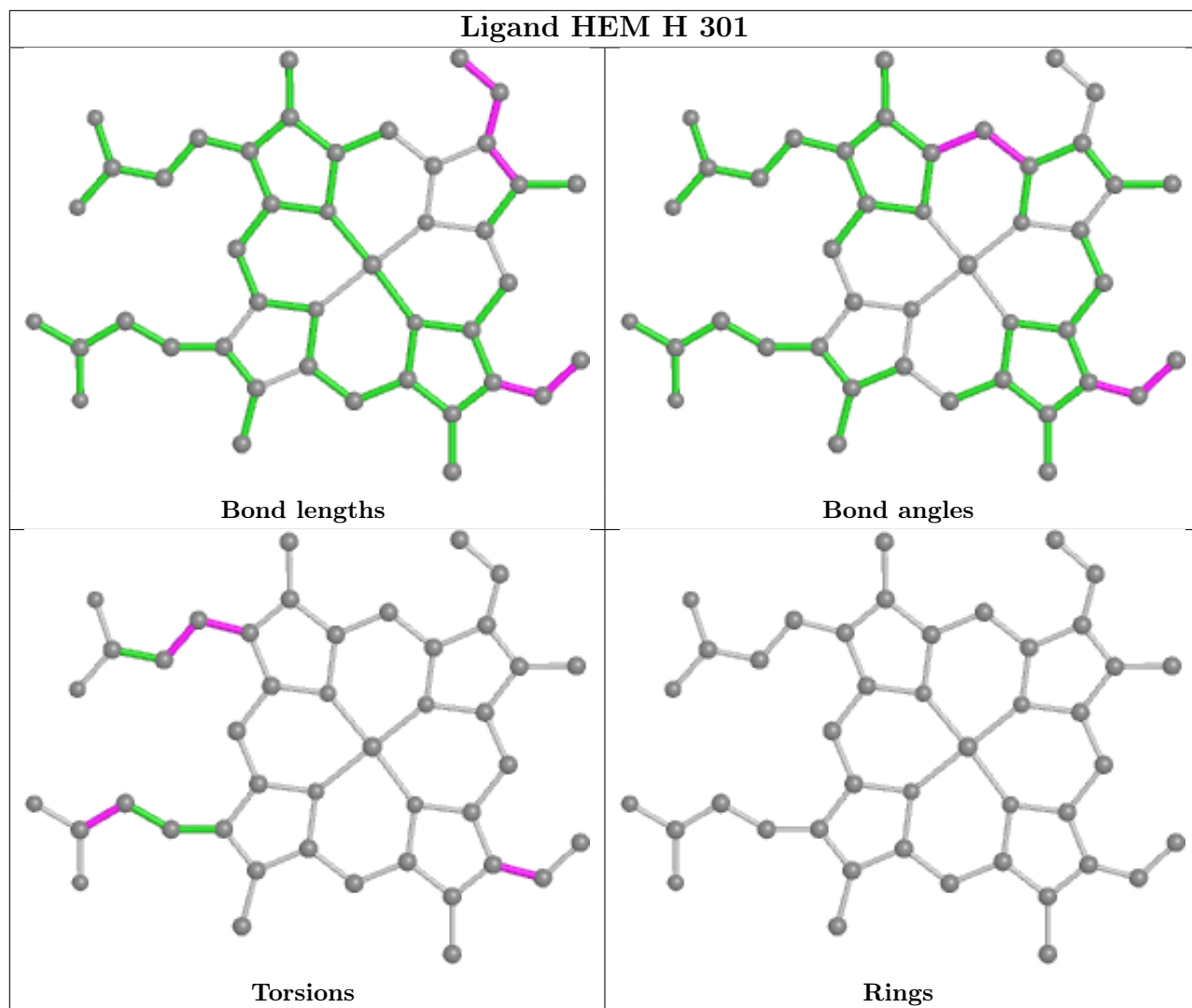


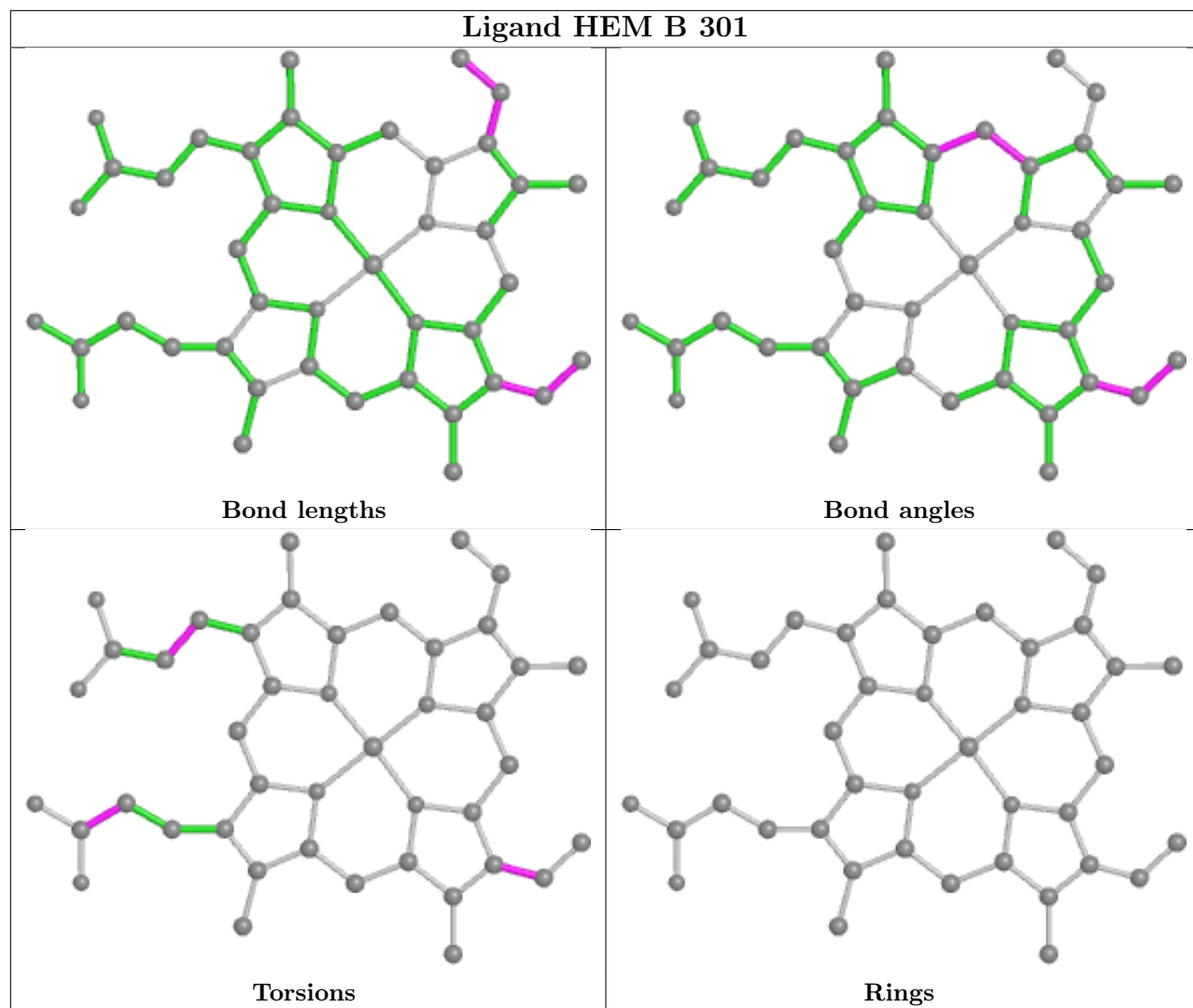


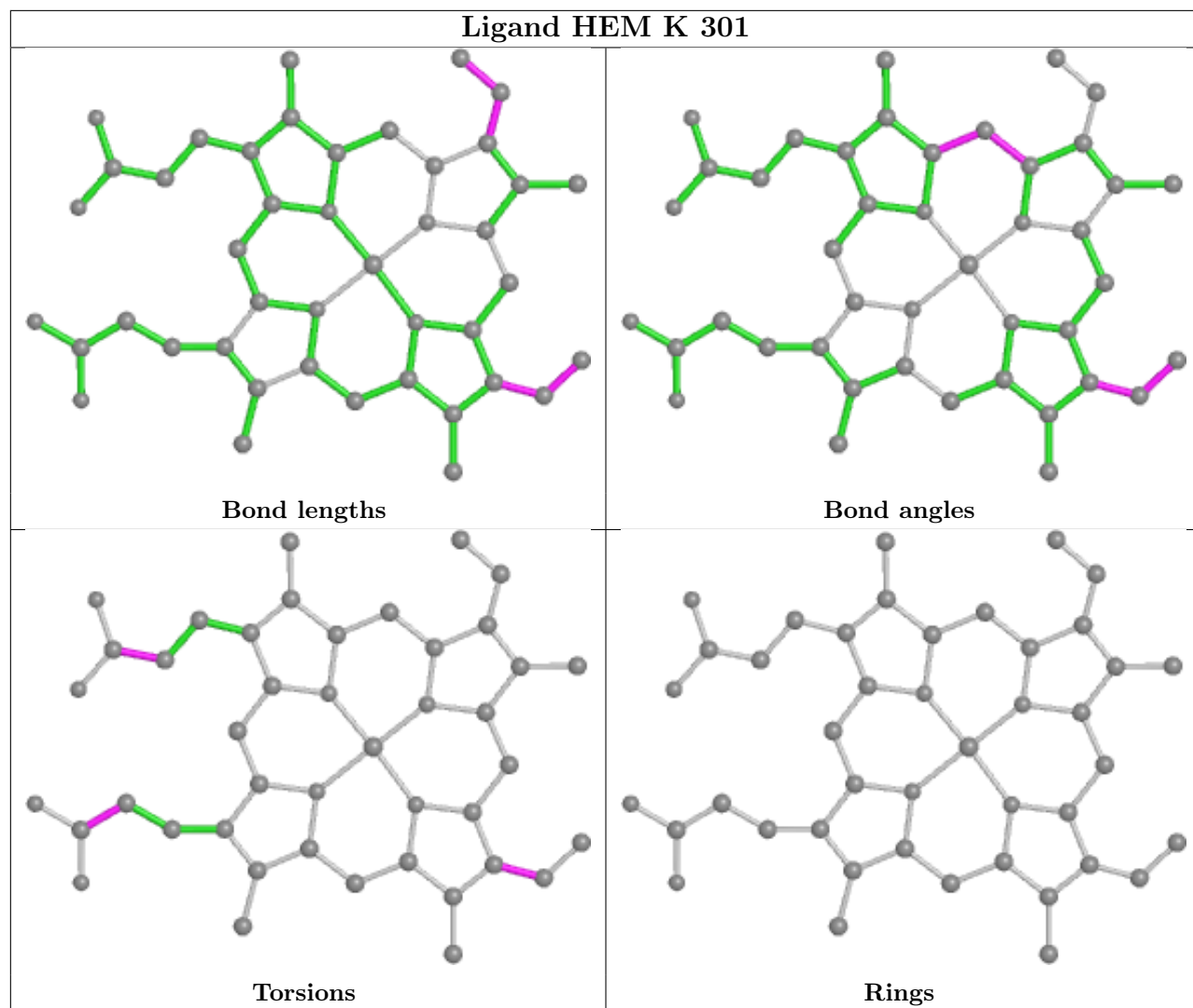


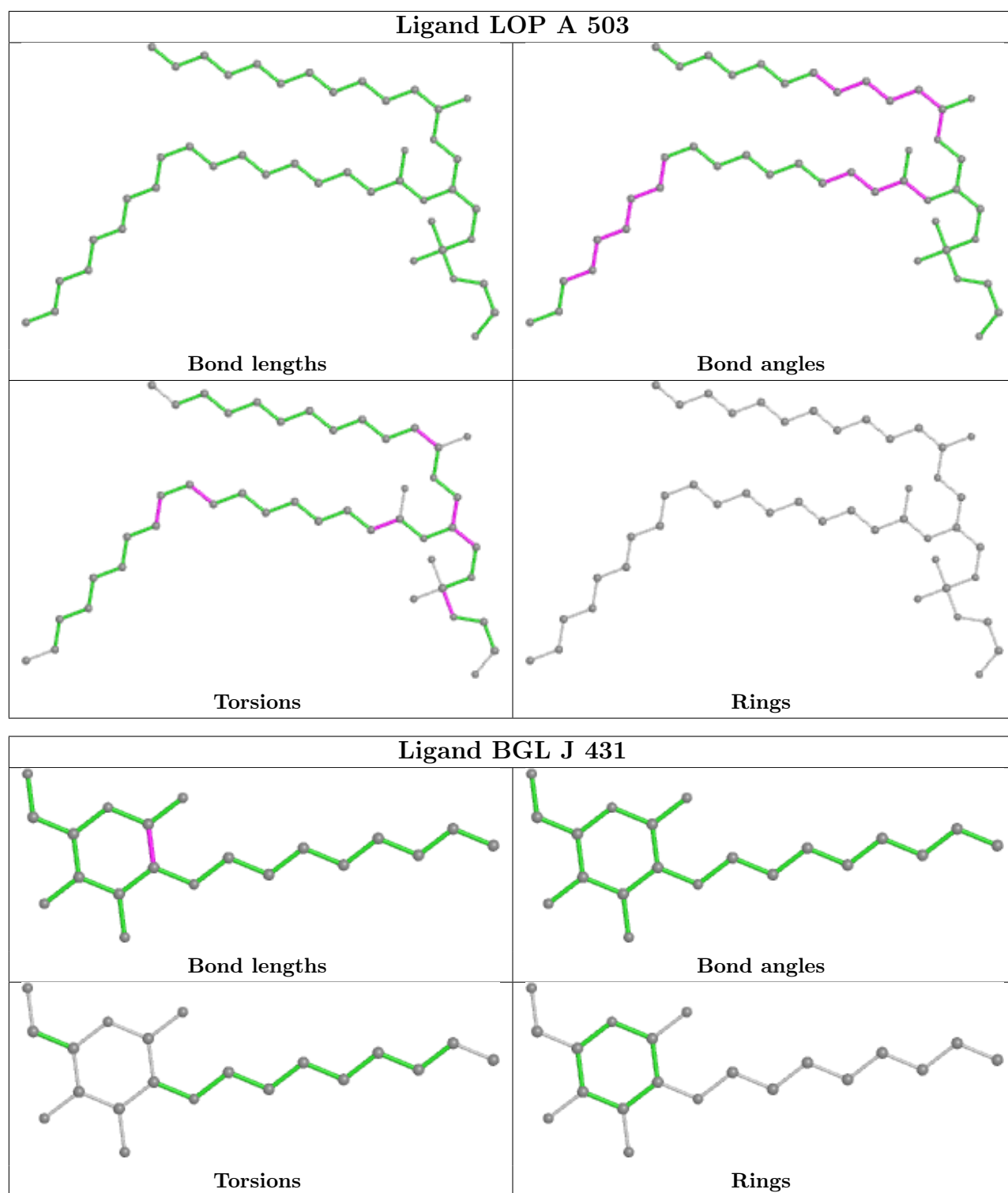


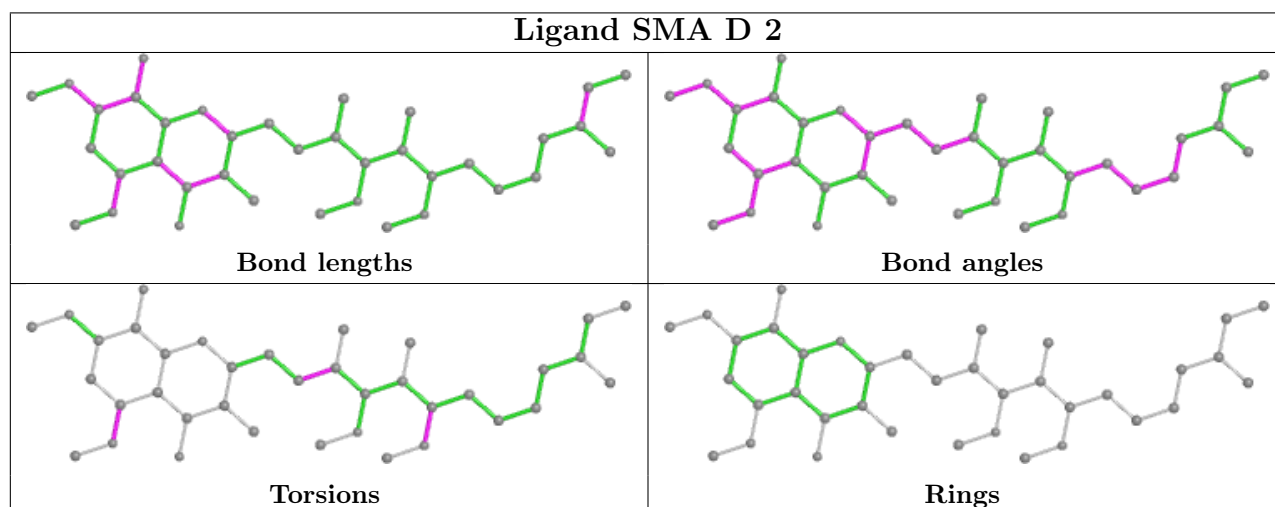
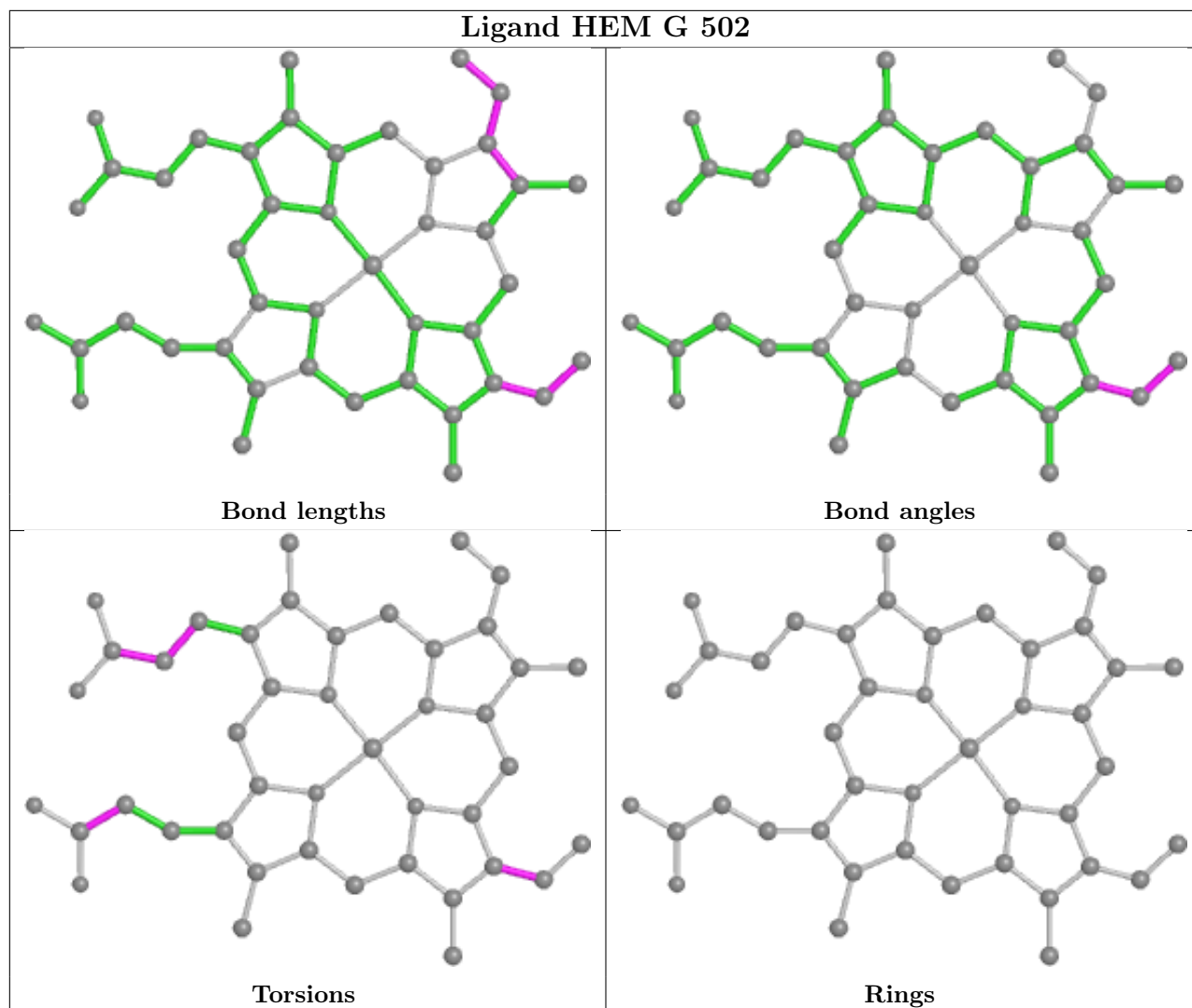


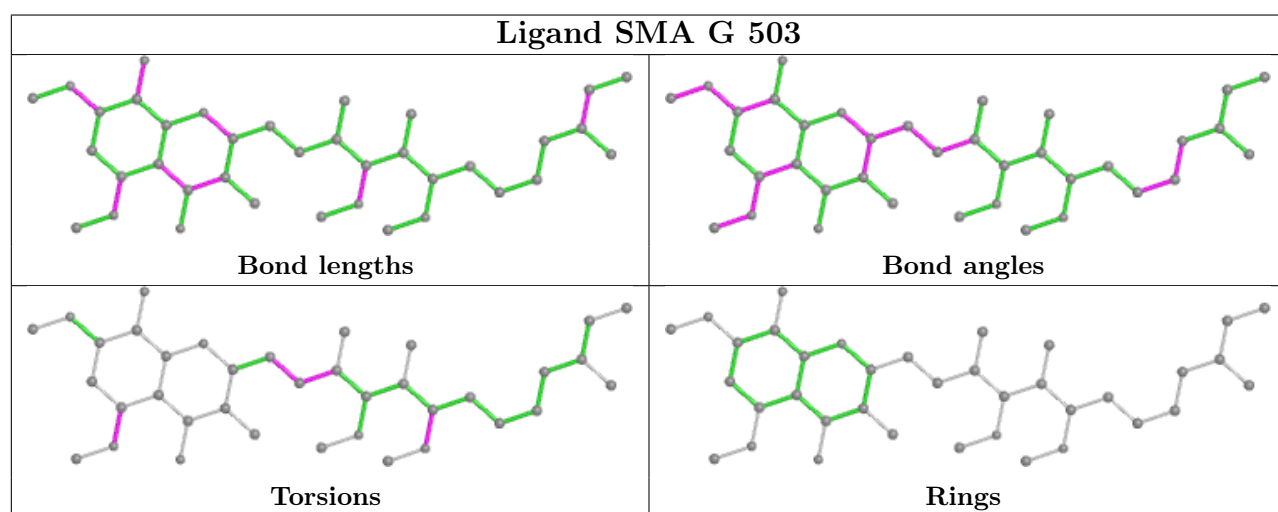
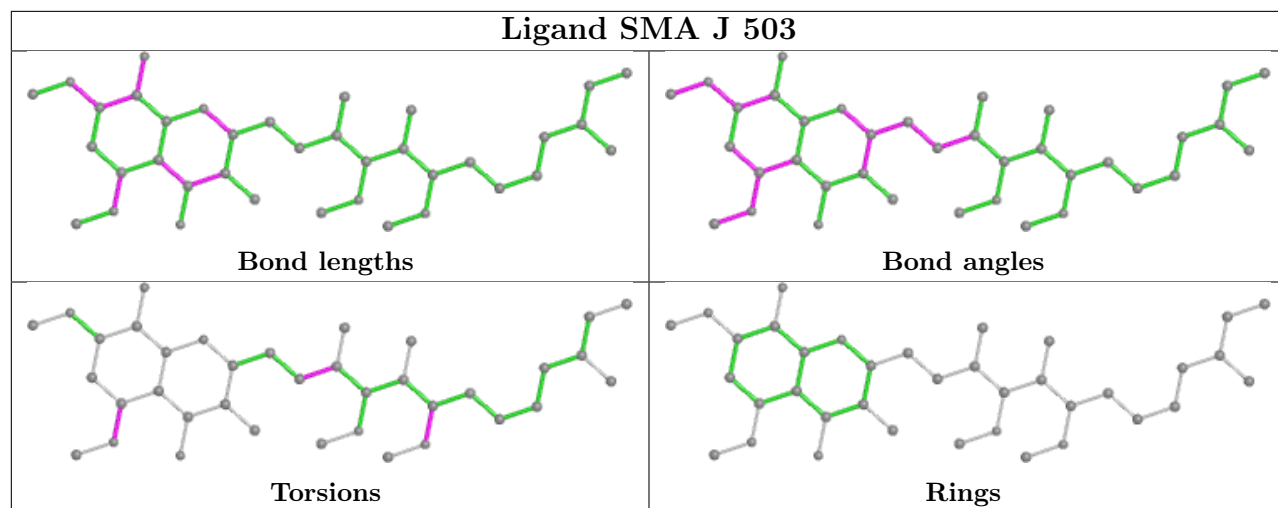


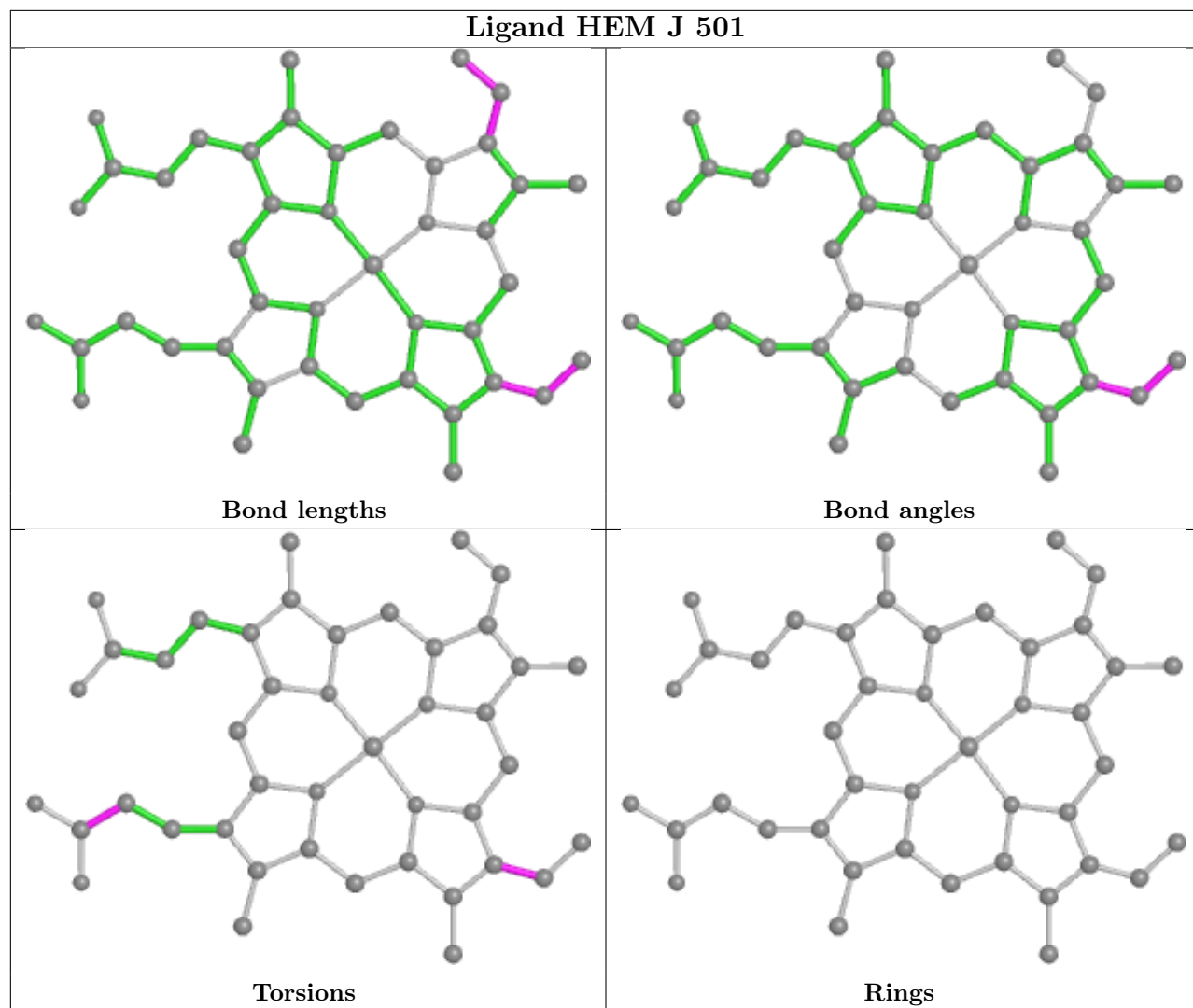


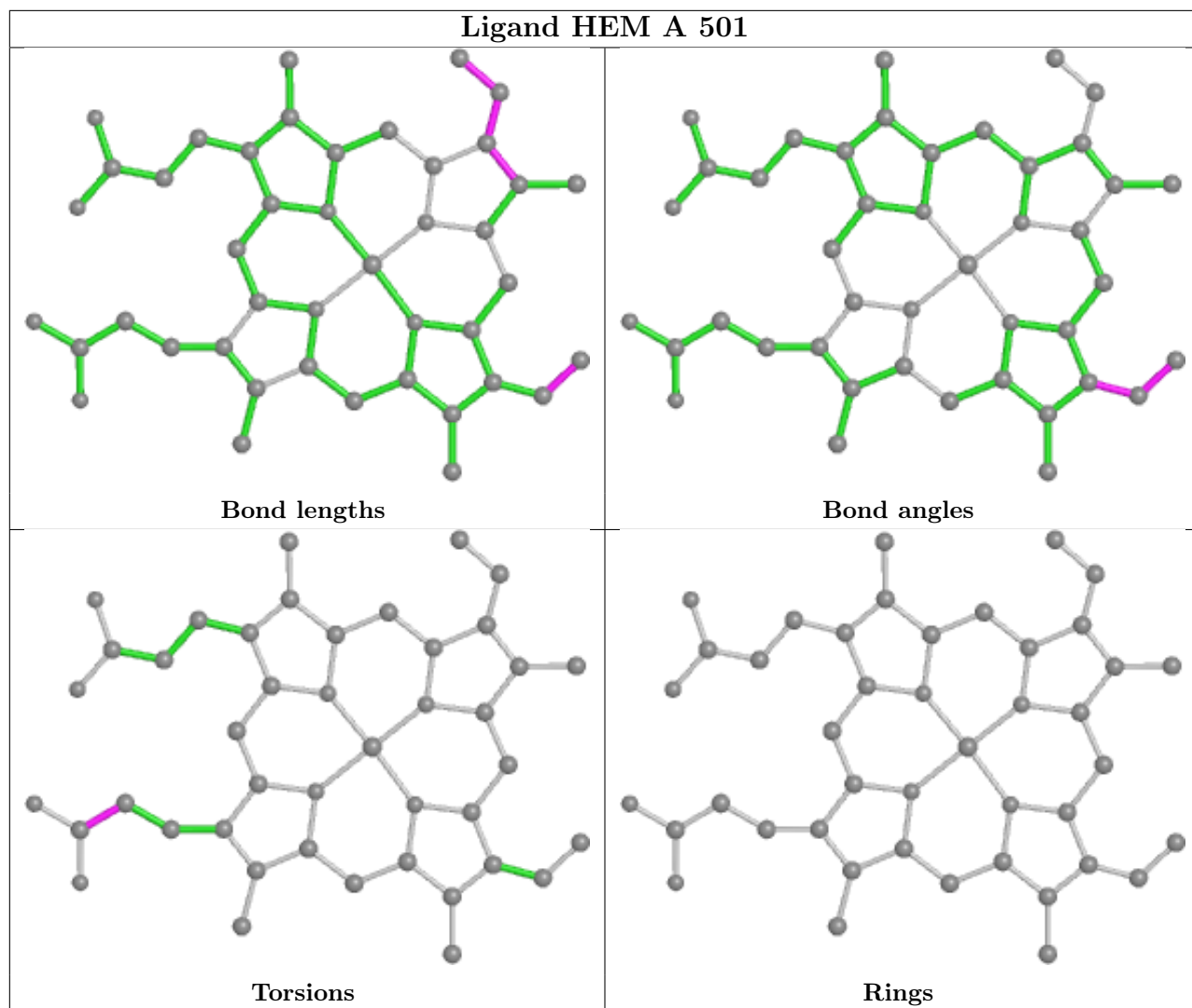


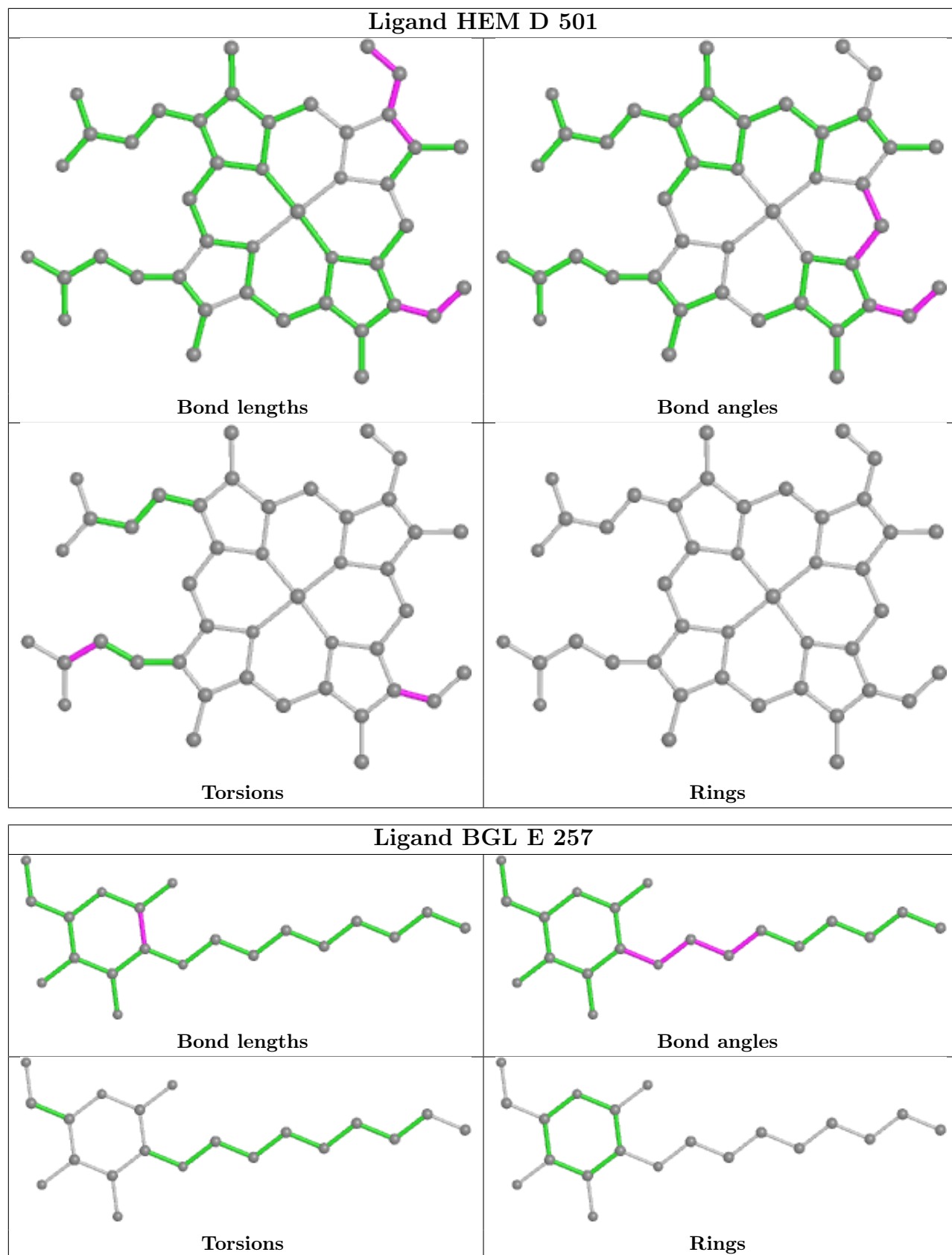


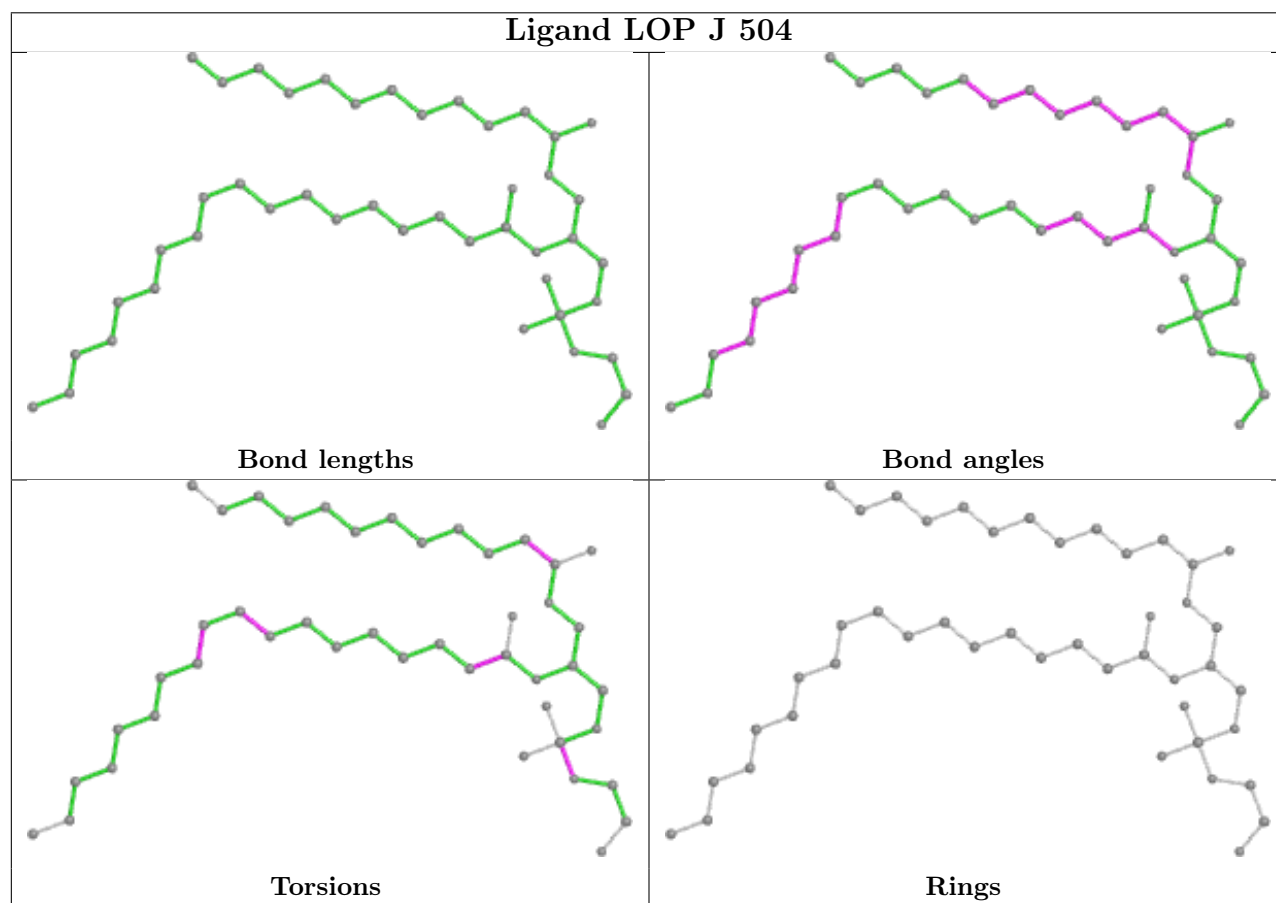
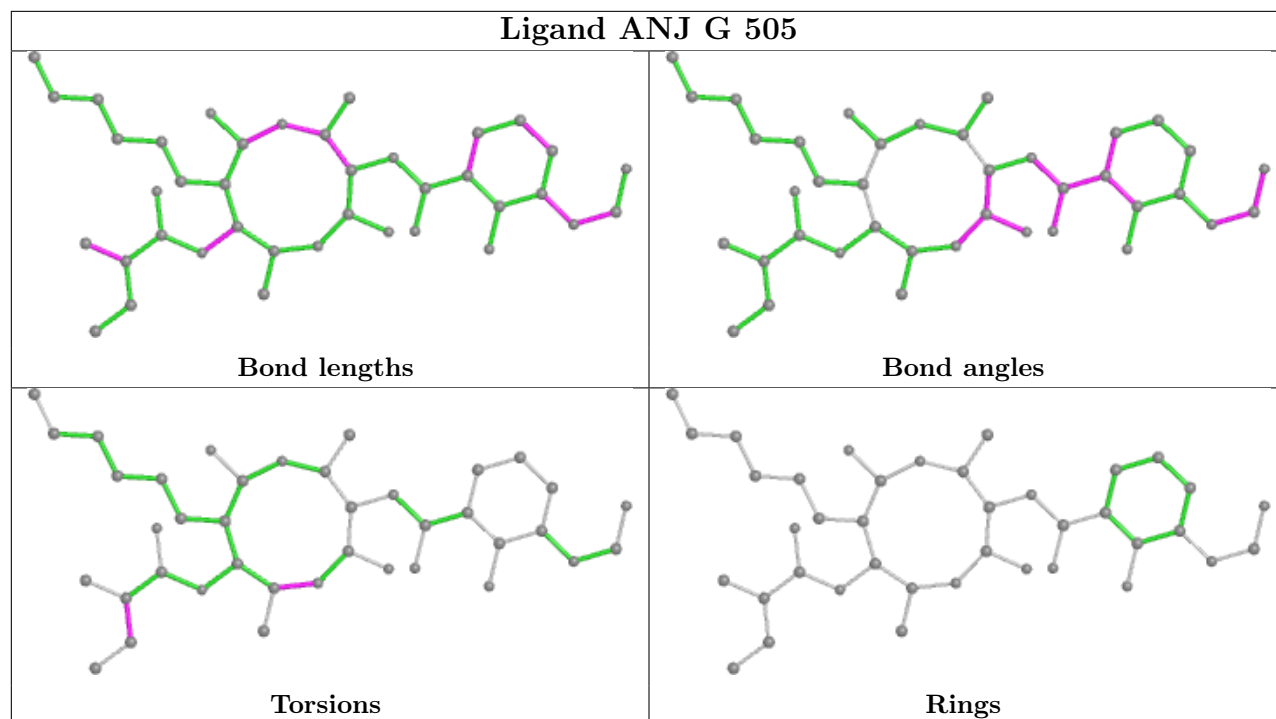


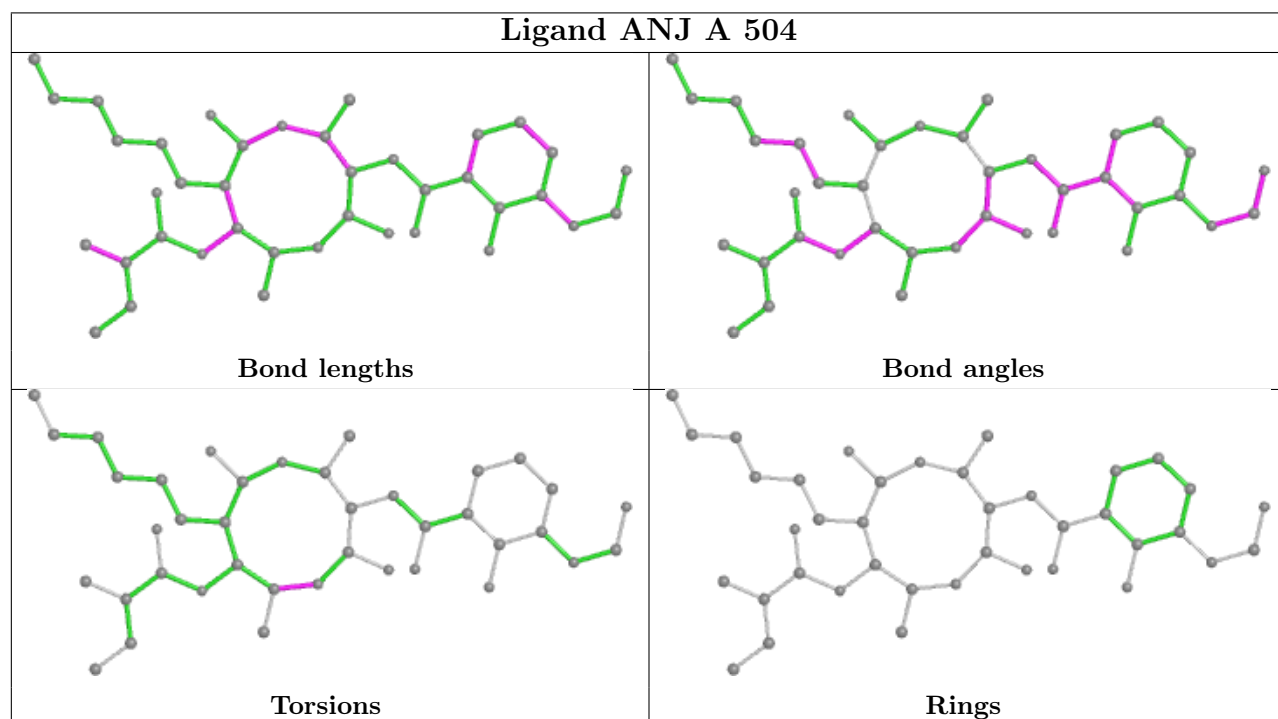
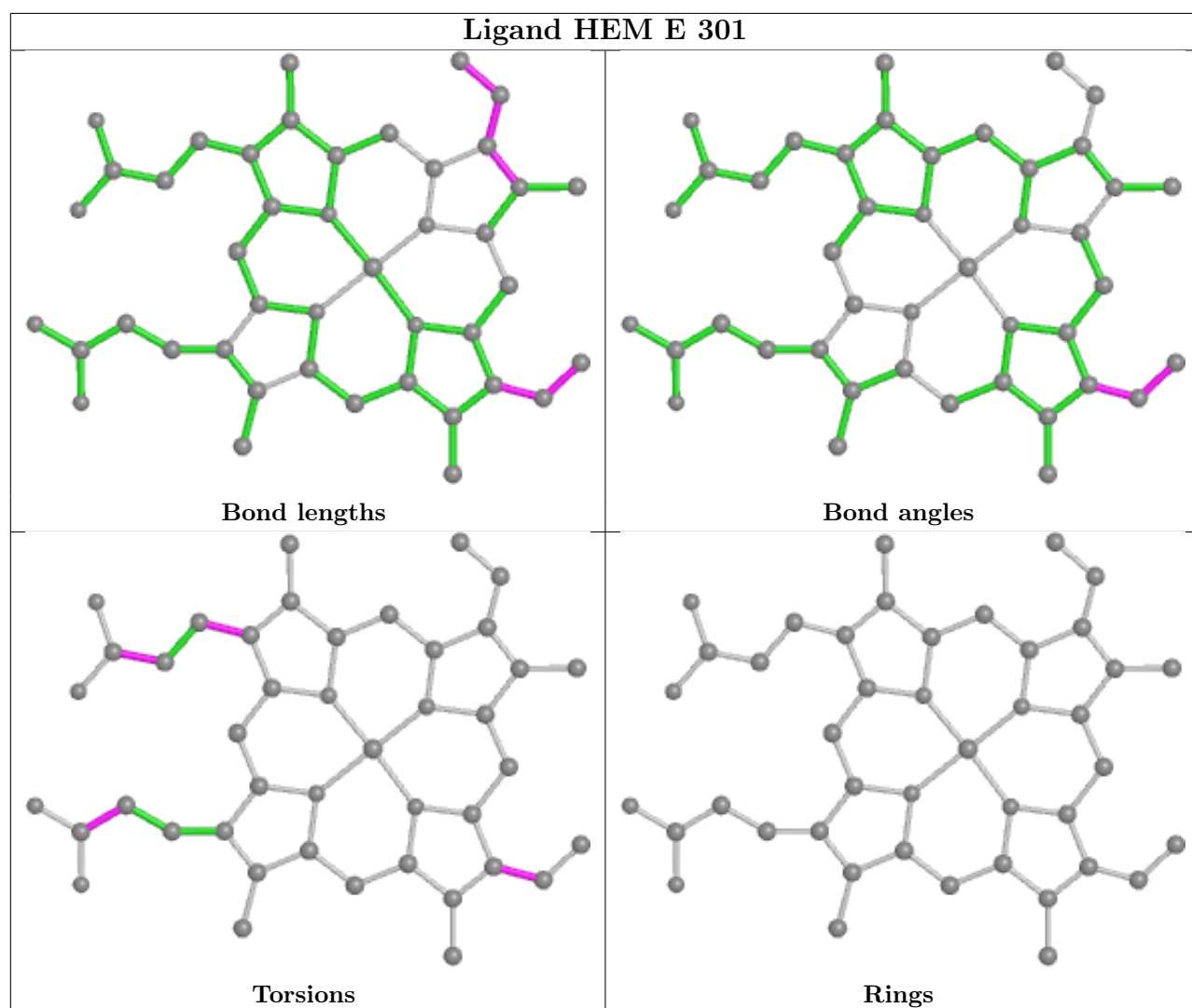












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	428/428 (100%)	0.66	27 (6%)	20 15	42, 63, 104, 129	0
1	D	428/428 (100%)	0.57	26 (6%)	21 16	43, 62, 100, 128	0
1	G	428/428 (100%)	0.57	18 (4%)	36 29	43, 64, 104, 128	0
1	J	428/428 (100%)	0.50	18 (4%)	36 29	43, 62, 100, 126	0
2	B	256/256 (100%)	0.92	37 (14%)	2 1	55, 89, 125, 149	0
2	E	256/256 (100%)	1.27	56 (21%)	0 0	65, 93, 128, 148	0
2	H	256/256 (100%)	0.88	35 (13%)	3 1	57, 90, 126, 151	0
2	K	256/256 (100%)	1.01	49 (19%)	1 0	62, 91, 127, 150	0
3	C	179/179 (100%)	0.99	25 (13%)	2 1	49, 82, 123, 155	0
3	F	179/179 (100%)	1.20	41 (22%)	0 0	49, 84, 124, 155	0
3	I	179/179 (100%)	0.93	22 (12%)	4 2	50, 83, 125, 156	0
3	L	179/179 (100%)	1.19	42 (23%)	0 0	52, 85, 124, 156	0
All	All	3452/3452 (100%)	0.81	396 (11%)	4 3	42, 75, 122, 156	0

The worst 5 of 396 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	2	GLY	12.6
2	K	4	GLY	12.5
2	B	2	GLY	11.5
2	K	3	GLY	11.3
3	I	9	GLY	11.3

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 monosaccharides 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.

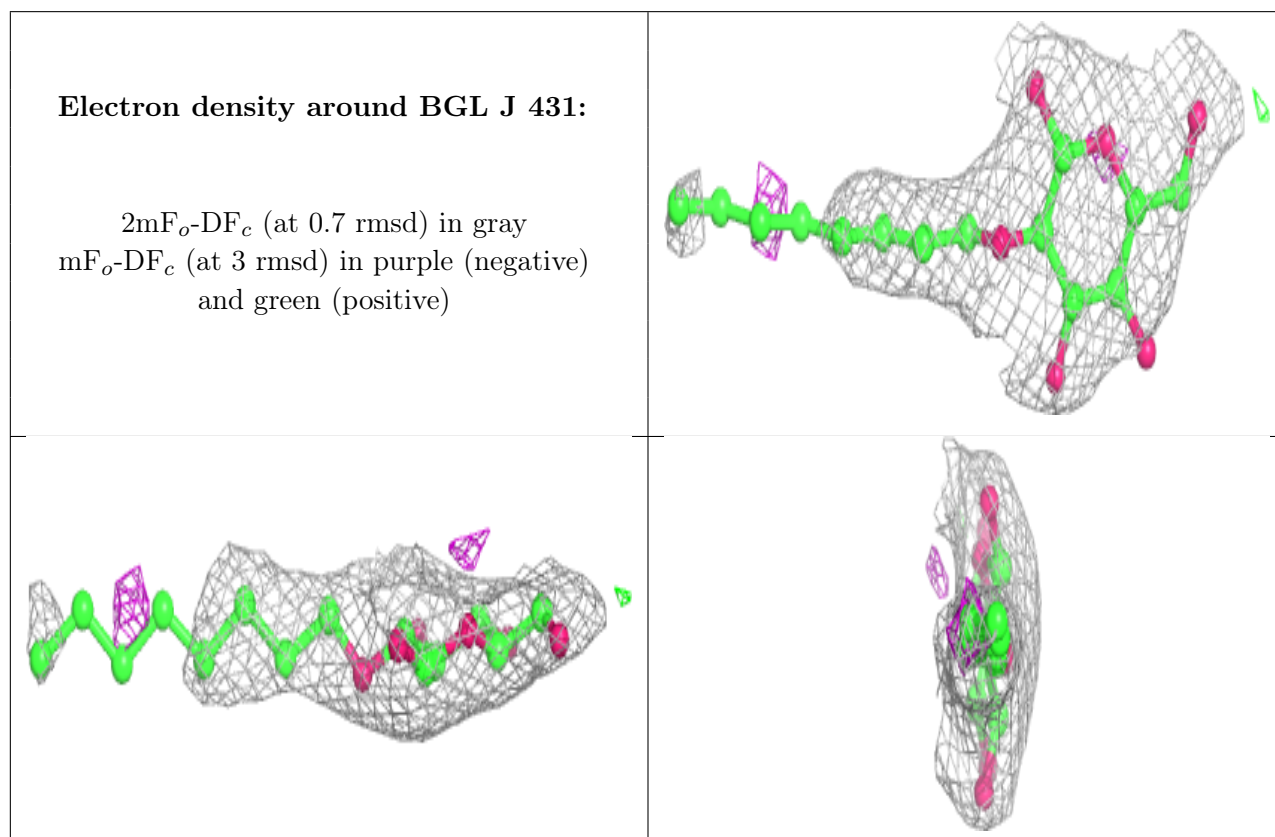
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	SR	E	258	1/1	0.75	0.08	126,126,126,126	0
9	SR	H	257	1/1	0.75	0.09	117,117,117,117	0
4	BGL	J	431	20/20	0.76	0.37	95,96,100,101	0
4	BGL	G	431	20/20	0.79	0.37	97,99,102,102	0
4	BGL	A	431	20/20	0.82	0.33	89,92,93,93	0
7	LOP	J	504	45/45	0.84	0.28	81,84,95,97	0
4	BGL	E	257	20/20	0.84	0.36	101,101,102,102	0
7	LOP	G	504	45/45	0.84	0.23	70,87,96,98	0
7	LOP	A	503	45/45	0.86	0.23	79,99,105,107	0
9	SR	J	432	1/1	0.86	0.30	114,114,114,114	0
9	SR	K	257	1/1	0.87	0.04	144,144,144,144	0
9	SR	G	432	1/1	0.88	0.26	135,135,135,135	0
7	LOP	D	503	45/45	0.88	0.24	75,88,94,94	0
8	ANJ	D	504	39/39	0.92	0.21	49,66,79,82	0
8	ANJ	G	505	39/39	0.92	0.25	69,72,79,81	0
8	ANJ	J	505	39/39	0.92	0.21	51,67,82,85	0
6	SMA	J	503	37/37	0.92	0.24	45,50,56,56	0
9	SR	B	257	1/1	0.93	0.07	126,126,126,126	0
8	ANJ	A	504	39/39	0.93	0.24	70,74,77,78	0
6	SMA	D	2	37/37	0.93	0.25	47,53,62,64	0
6	SMA	G	503	37/37	0.94	0.22	51,58,60,62	0
6	SMA	A	1	37/37	0.94	0.23	46,55,58,58	0
5	HEM	K	301	43/43	0.95	0.21	73,79,80,81	0
5	HEM	D	501	43/43	0.96	0.19	60,61,62,64	0
5	HEM	D	502	43/43	0.96	0.23	34,42,45,46	0
5	HEM	E	301	43/43	0.96	0.21	74,80,81,81	0
5	HEM	G	502	43/43	0.96	0.24	47,52,54,54	0
5	HEM	H	301	43/43	0.96	0.22	66,70,71,72	0
5	HEM	A	501	43/43	0.96	0.19	61,64,70,73	0
5	HEM	A	502	43/43	0.96	0.24	43,47,51,52	0
5	HEM	B	301	43/43	0.96	0.22	61,65,67,69	0
5	HEM	J	501	43/43	0.97	0.19	55,56,57,58	0

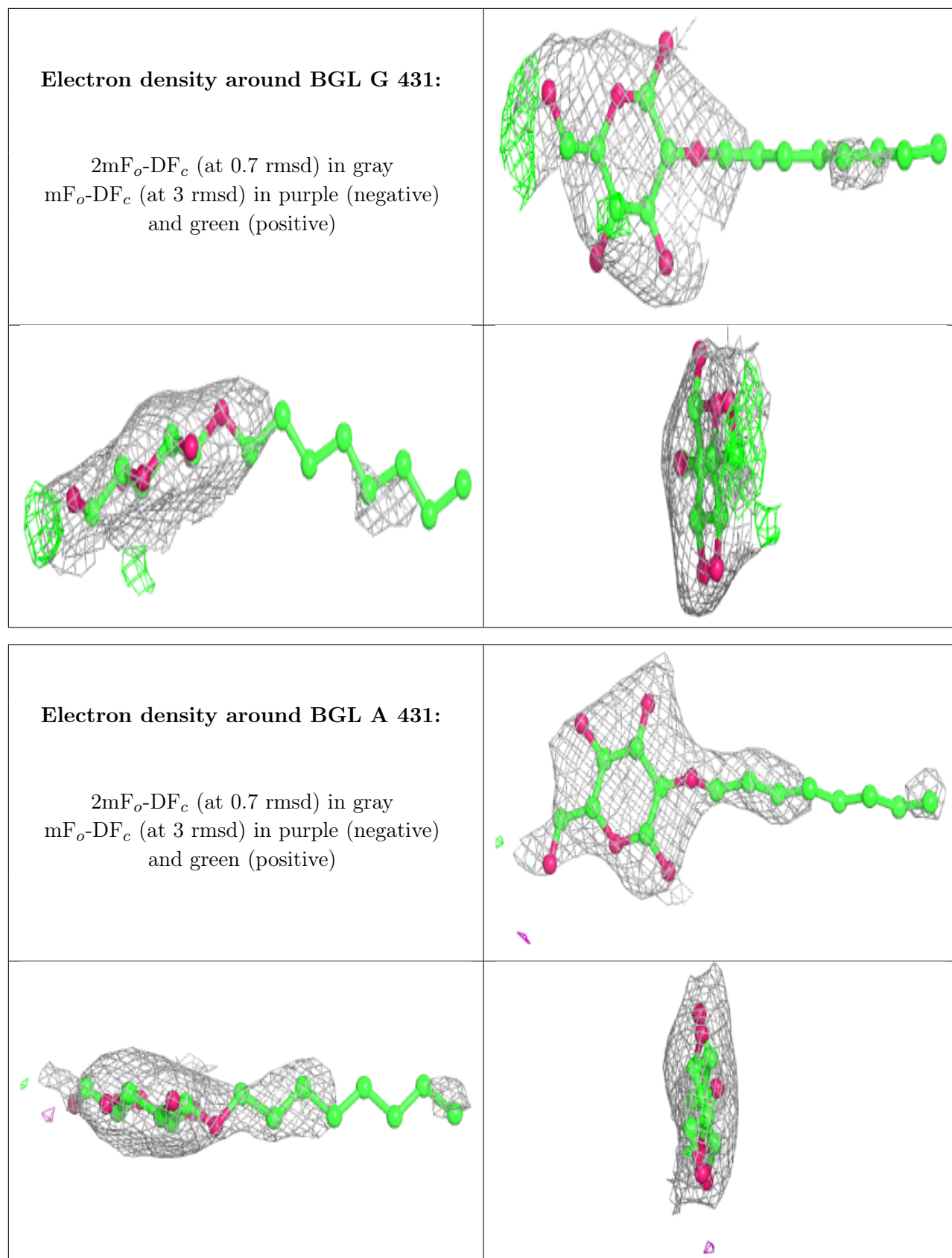
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	HEM	J	502	43/43	0.97	0.22	36,43,47,48	0
5	HEM	G	501	43/43	0.97	0.23	55,59,63,65	0
10	FES	C	200	4/4	0.97	0.19	54,54,54,54	0
10	FES	F	200	4/4	0.98	0.18	55,55,55,55	0
10	FES	I	200	4/4	0.98	0.21	53,53,54,54	0
10	FES	L	200	4/4	0.98	0.22	56,57,57,57	0

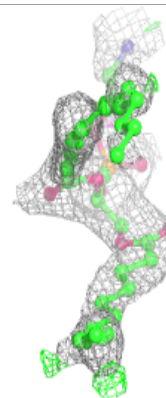
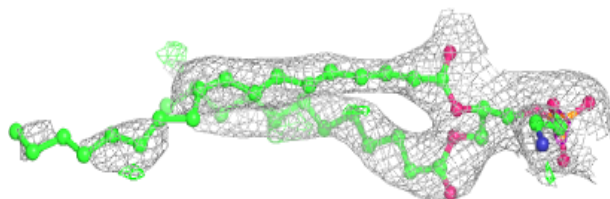
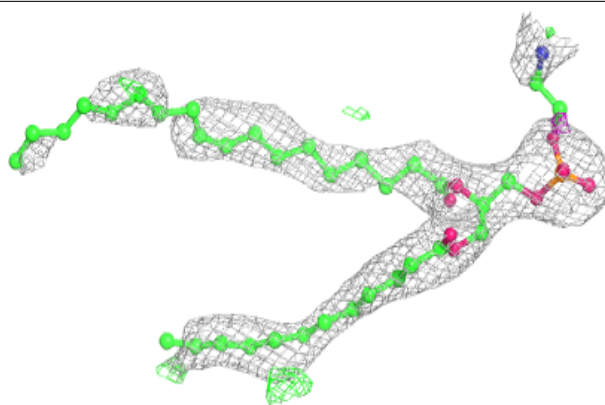
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



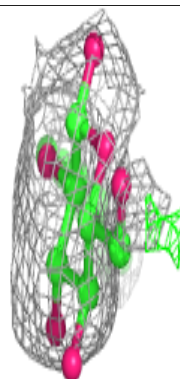
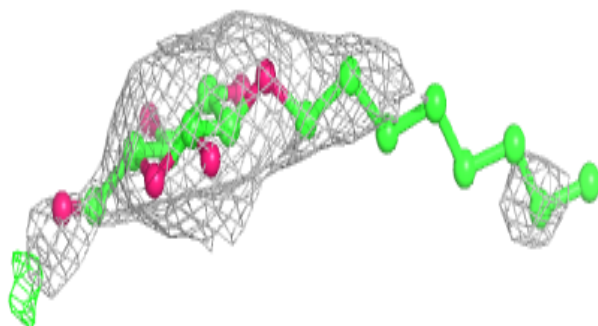
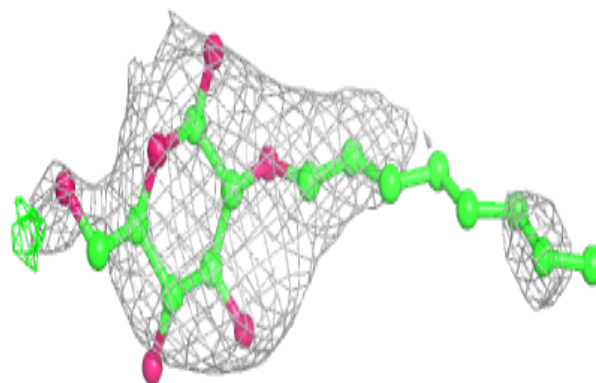


Electron density around LOP J 504:

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

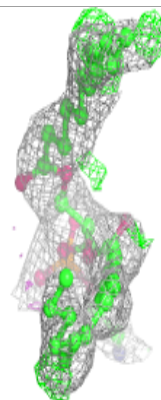
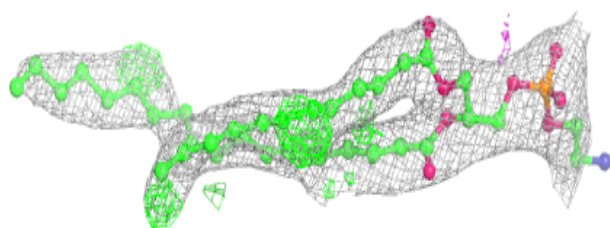
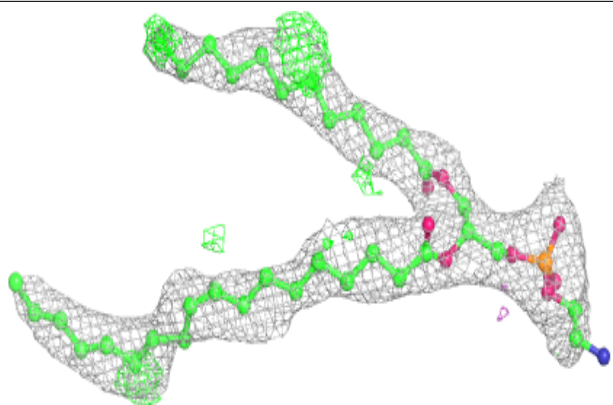
**Electron density around BGL E 257:**

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

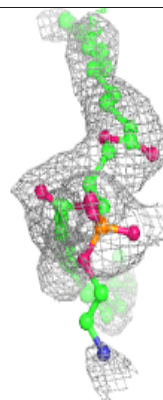
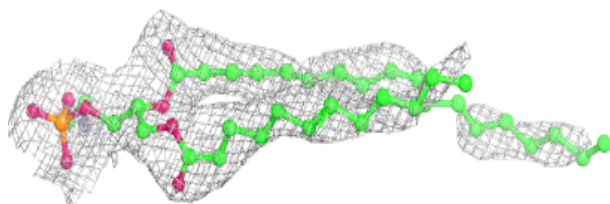
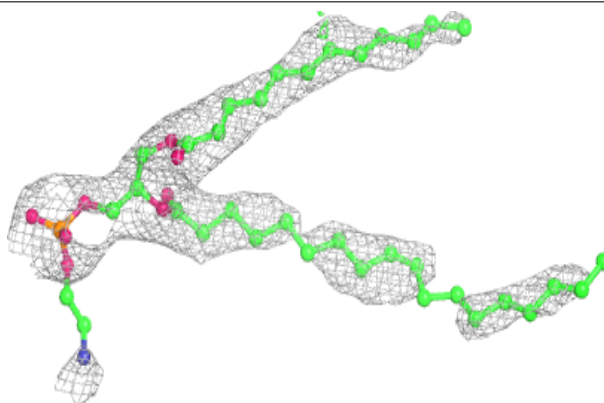


Electron density around LOP G 504:

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

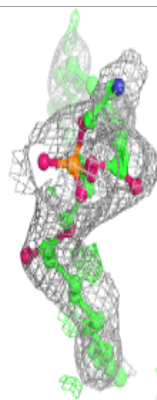
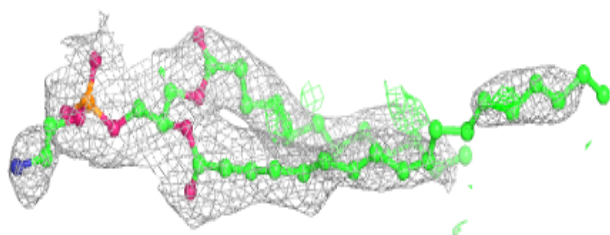
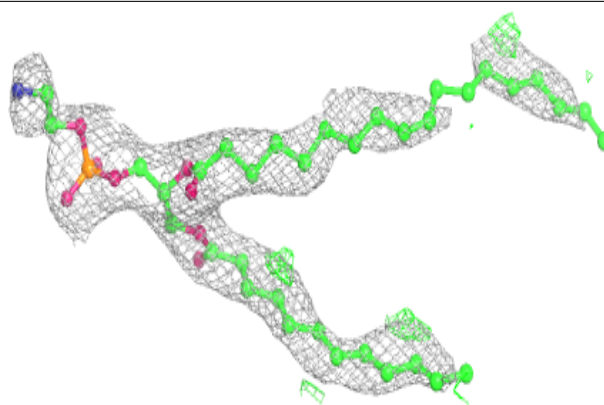
**Electron density around LOP A 503:**

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

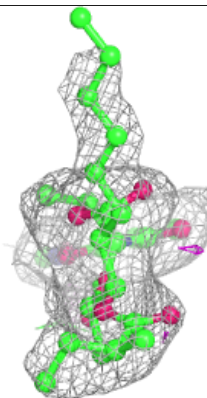
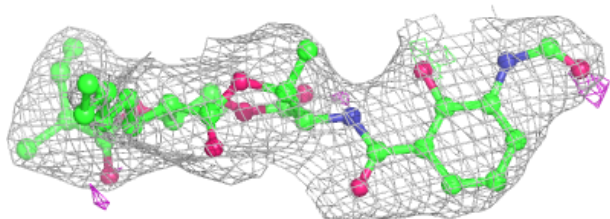
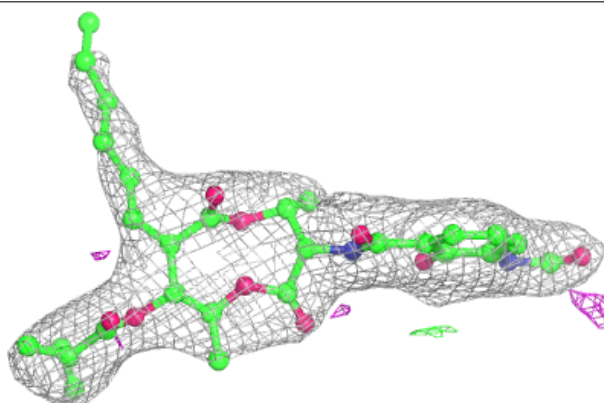


Electron density around LOP D 503:

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

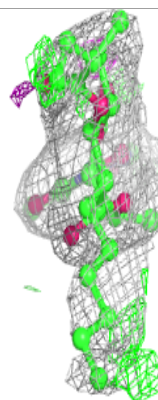
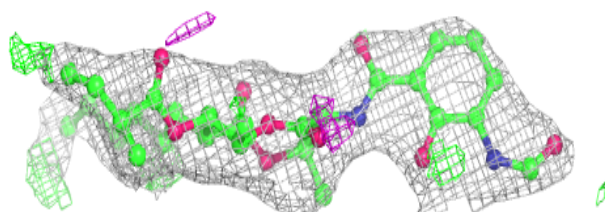
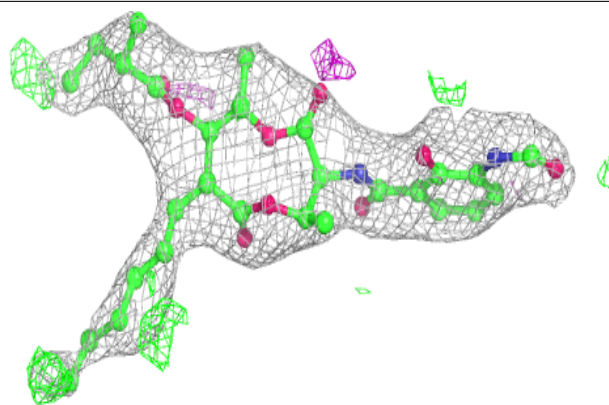
**Electron density around ANJ D 504:**

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

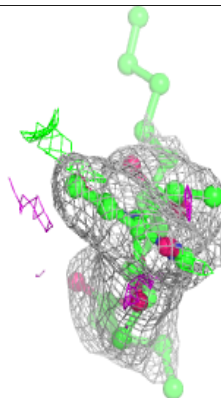
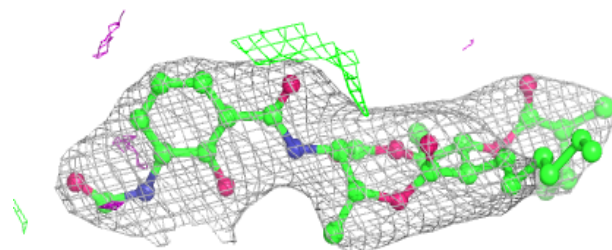
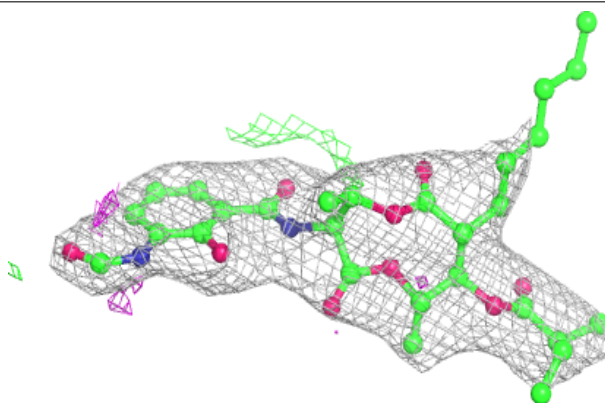


Electron density around ANJ G 505:

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

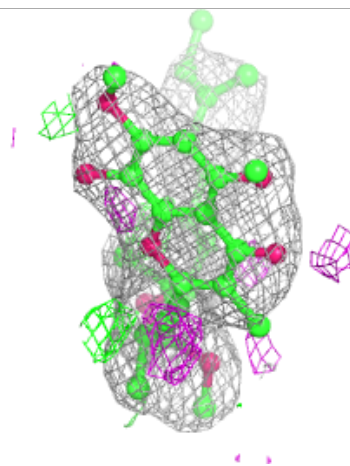
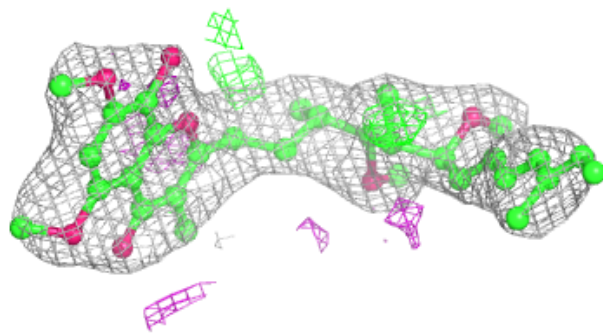
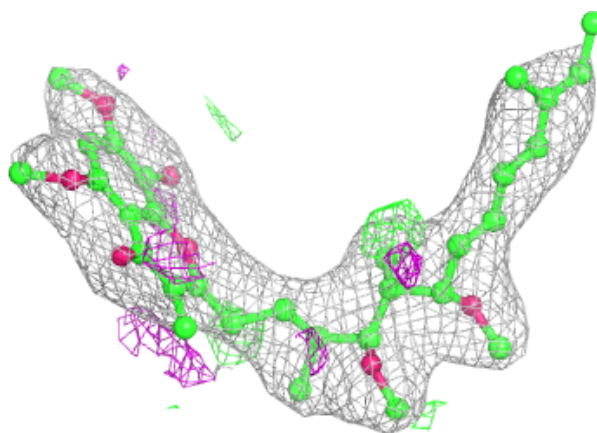
**Electron density around ANJ J 505:**

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



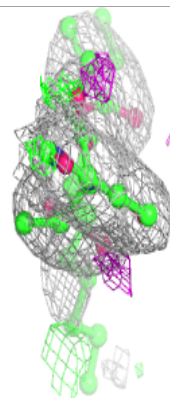
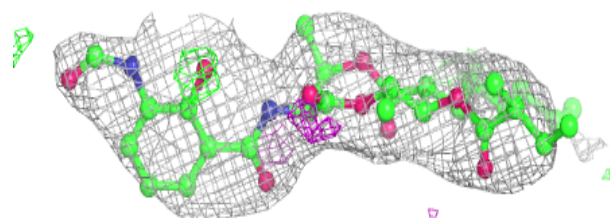
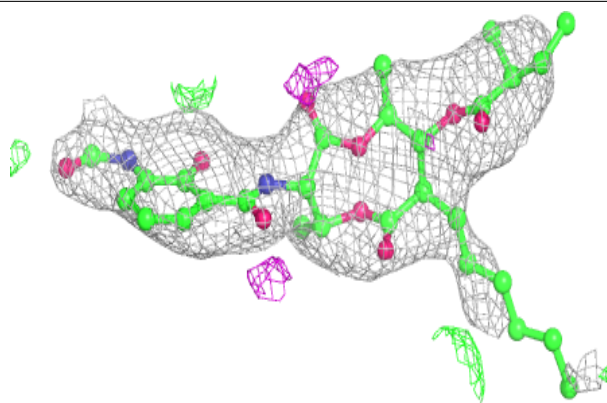
Electron density around SMA J 503:

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

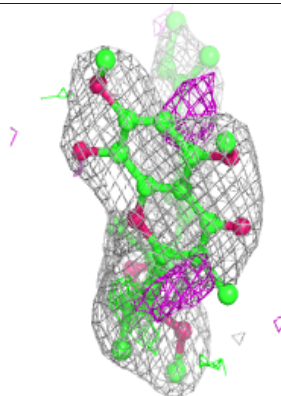
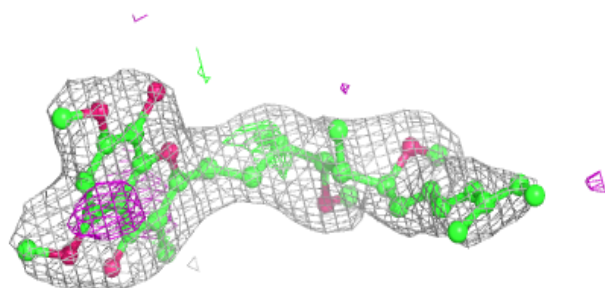
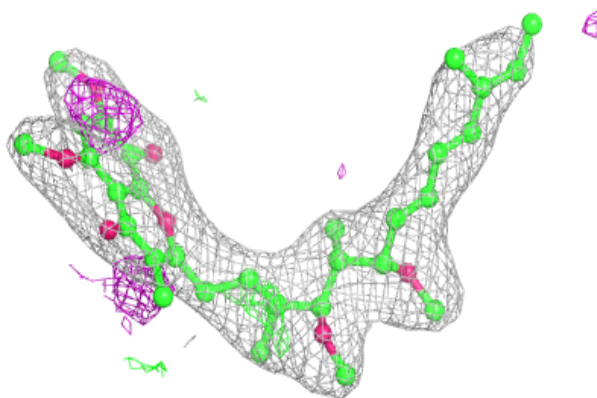


Electron density around ANJ A 504:

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

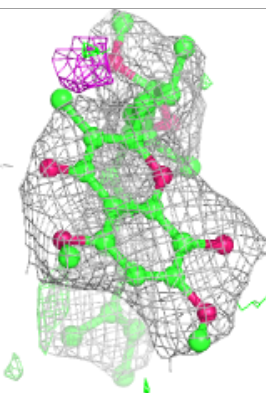
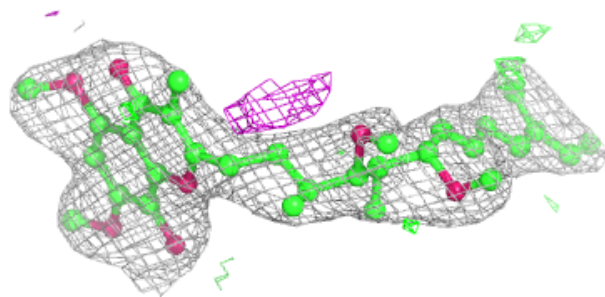
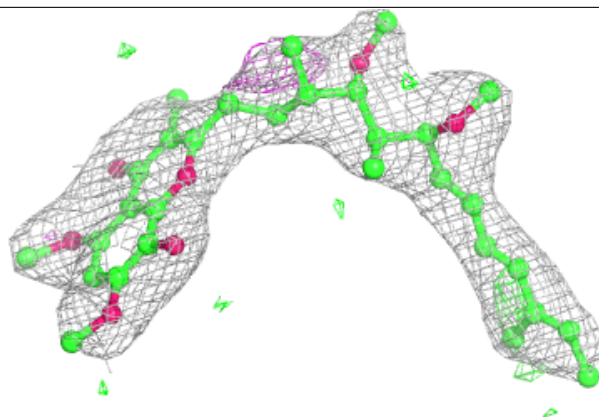
**Electron density around SMA D 2:**

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

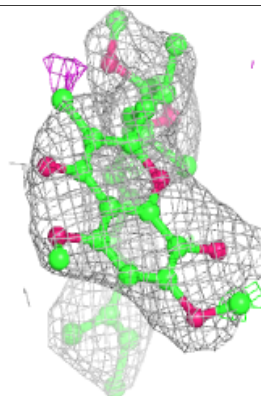
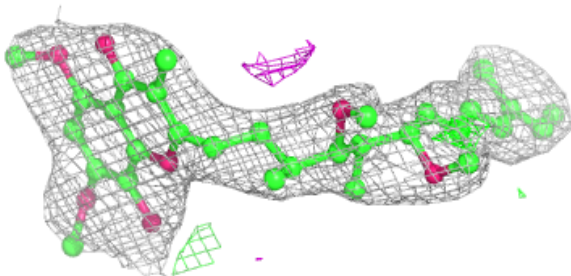
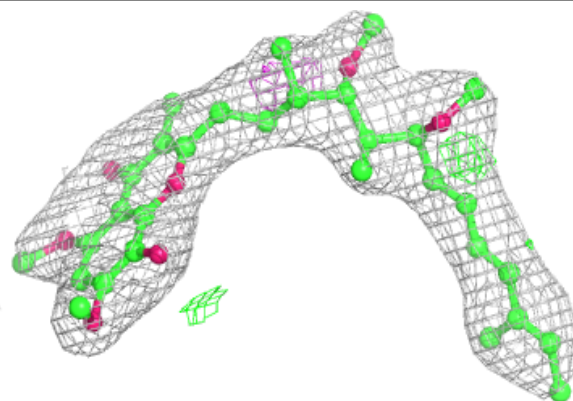


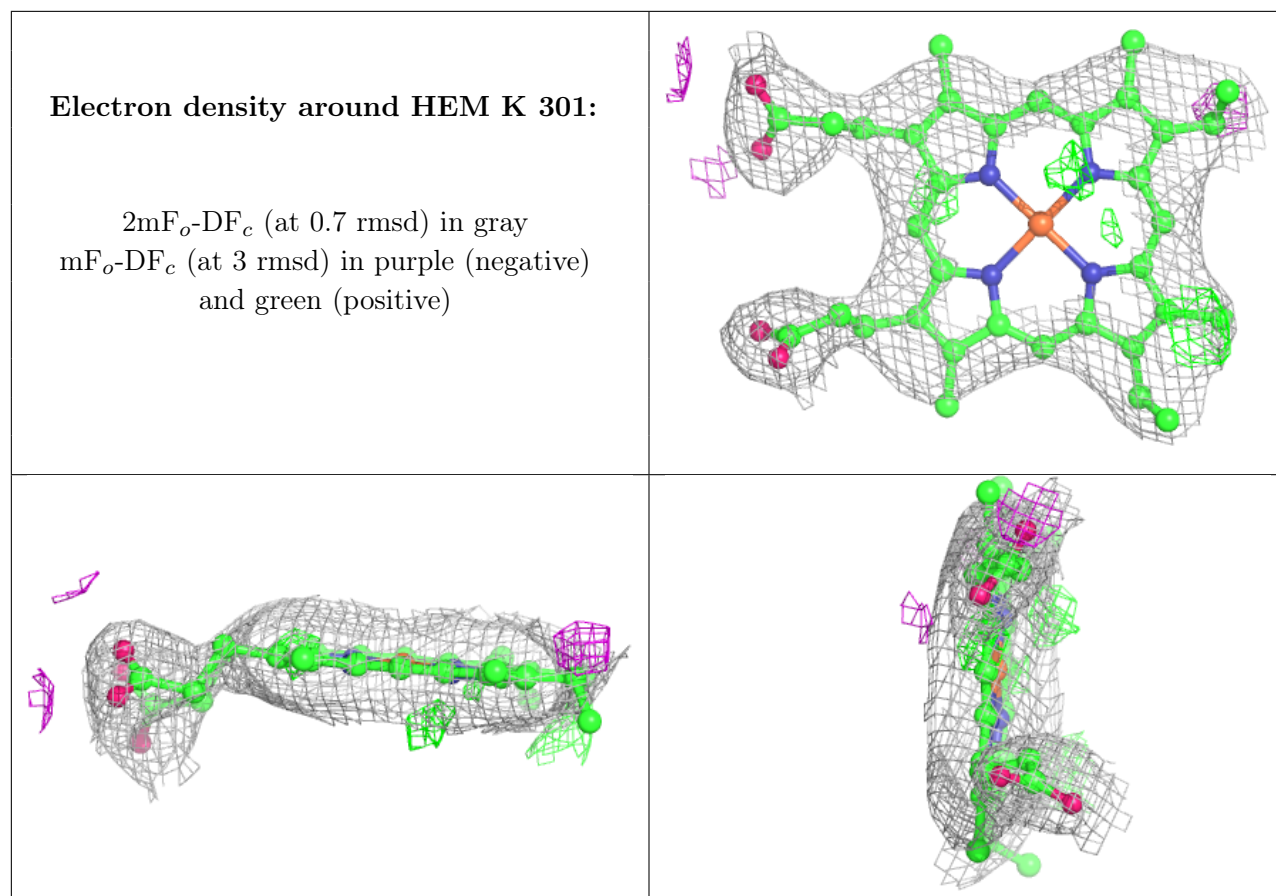
Electron density around SMA G 503:

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

**Electron density around SMA A 1:**

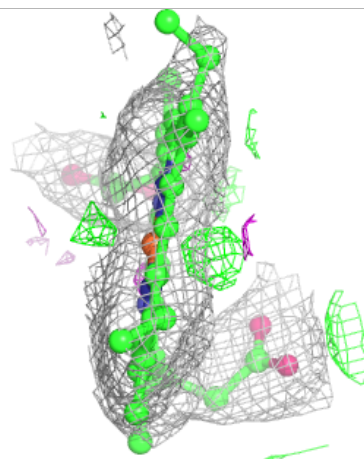
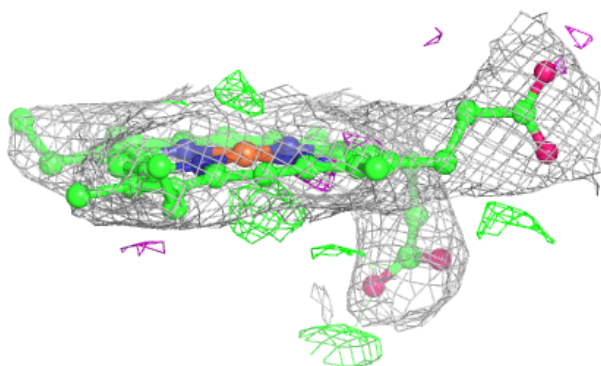
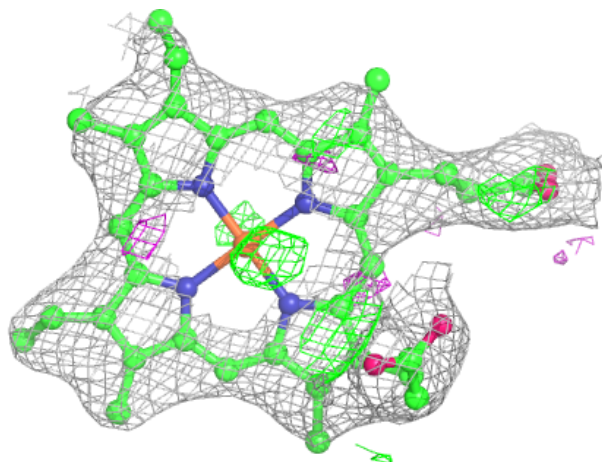
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





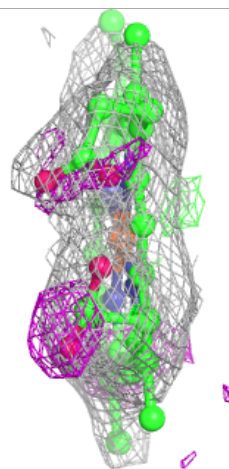
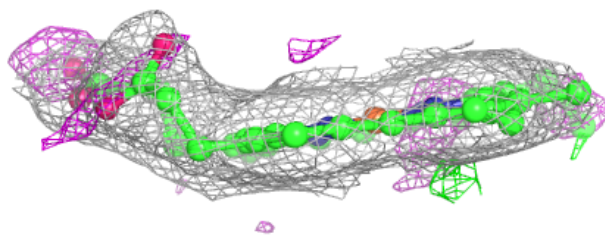
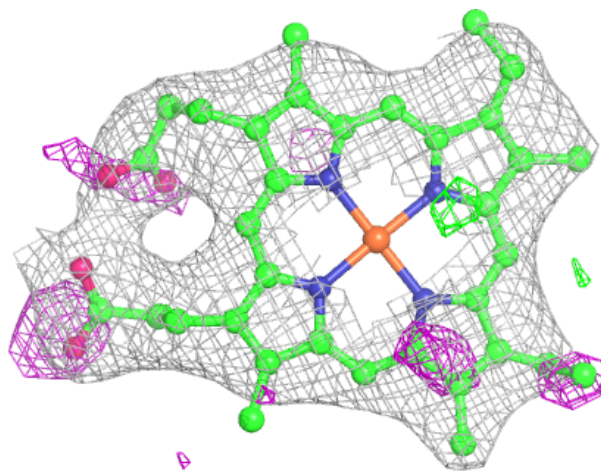
Electron density around HEM D 501:

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



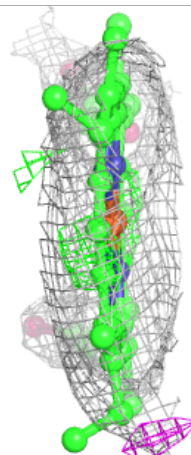
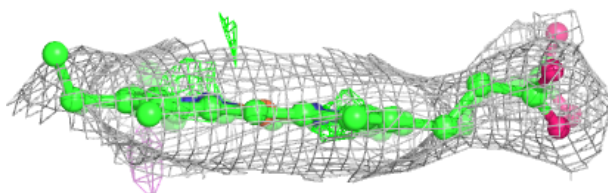
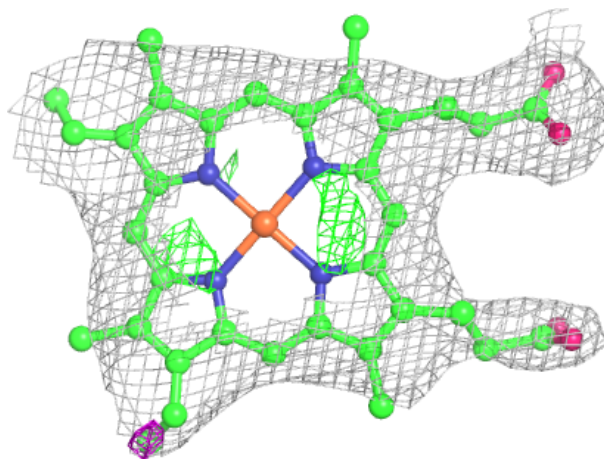
Electron density around HEM D 502:

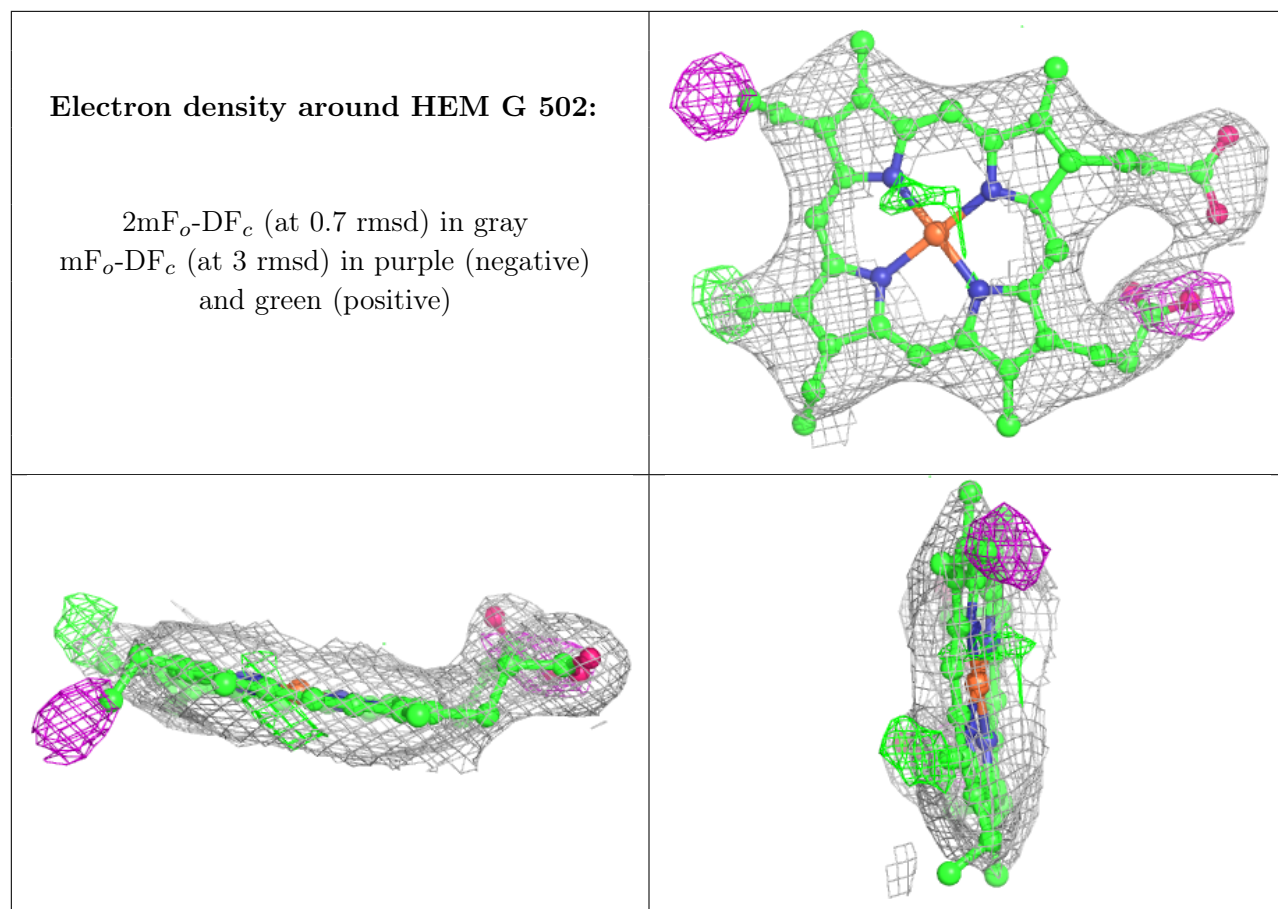
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM E 301:

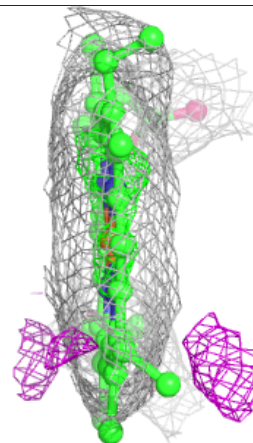
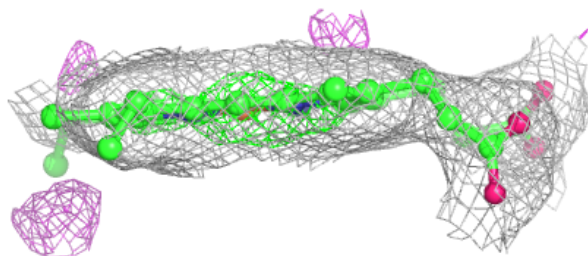
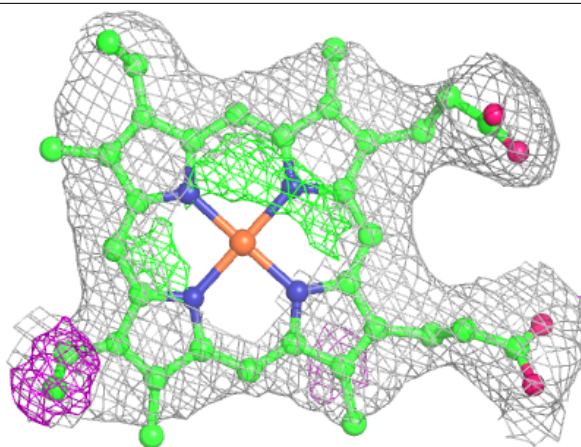
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





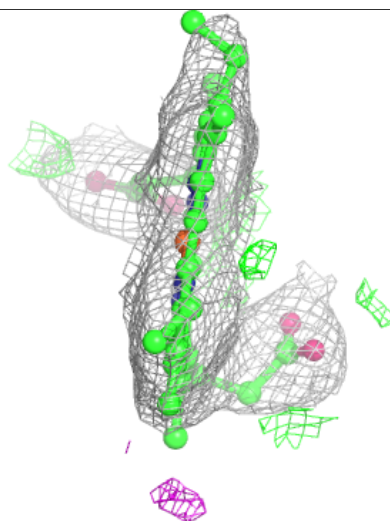
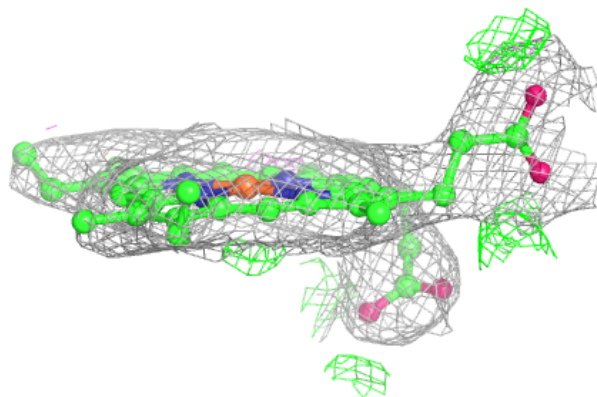
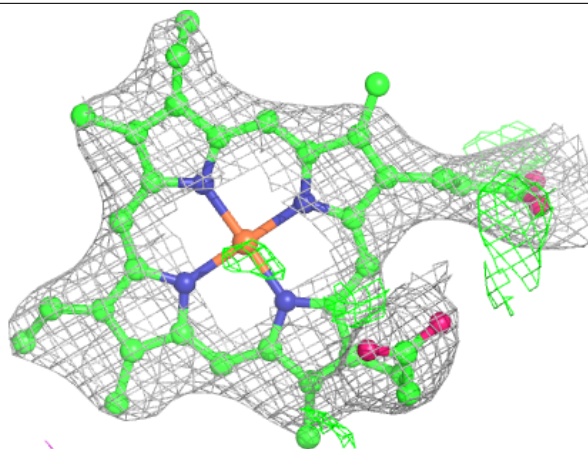
Electron density around HEM H 301:

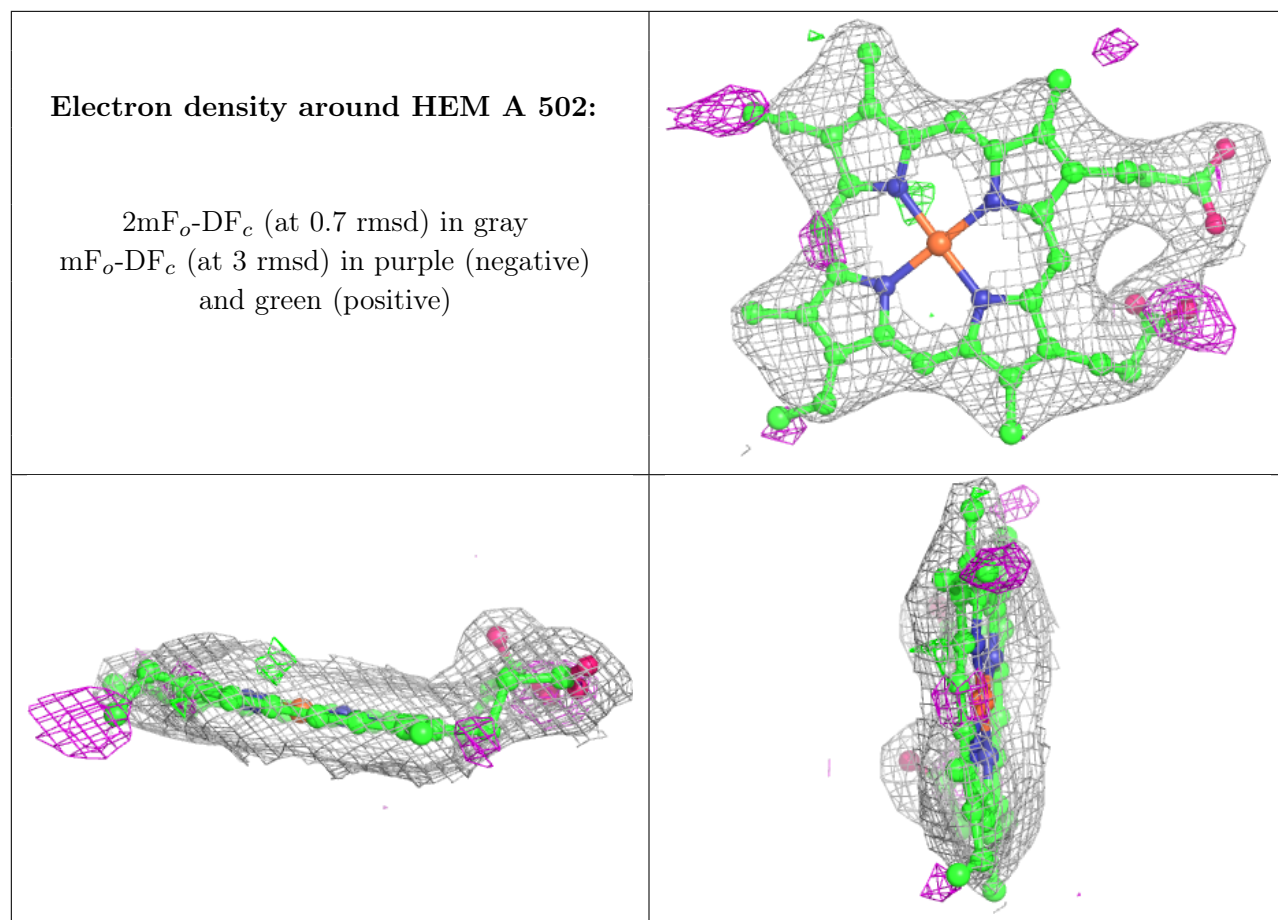
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 501:

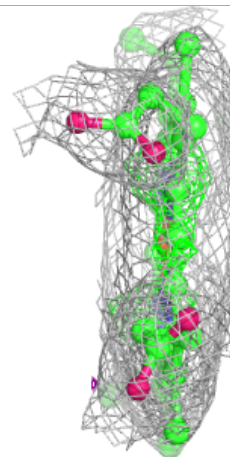
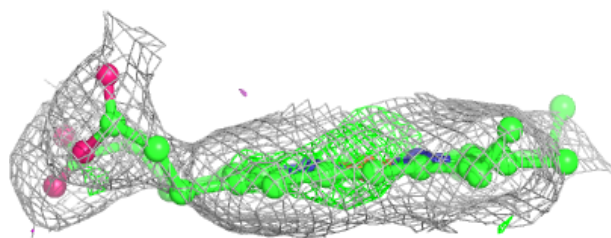
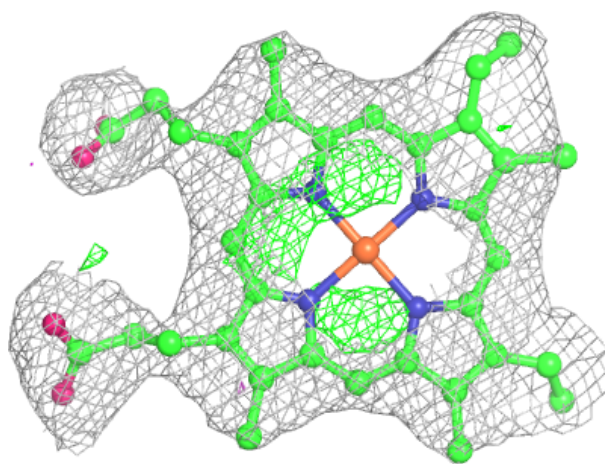
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





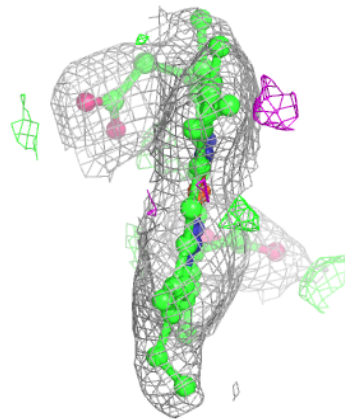
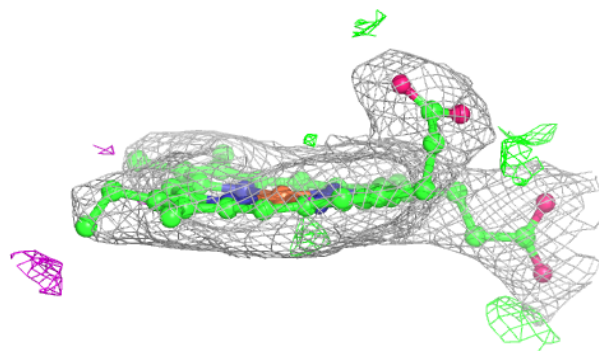
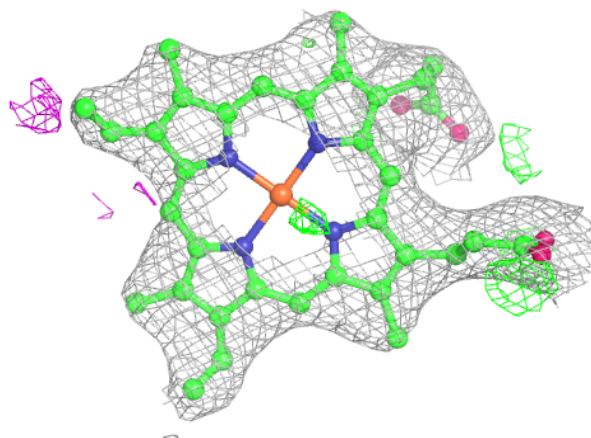
Electron density around HEM B 301:

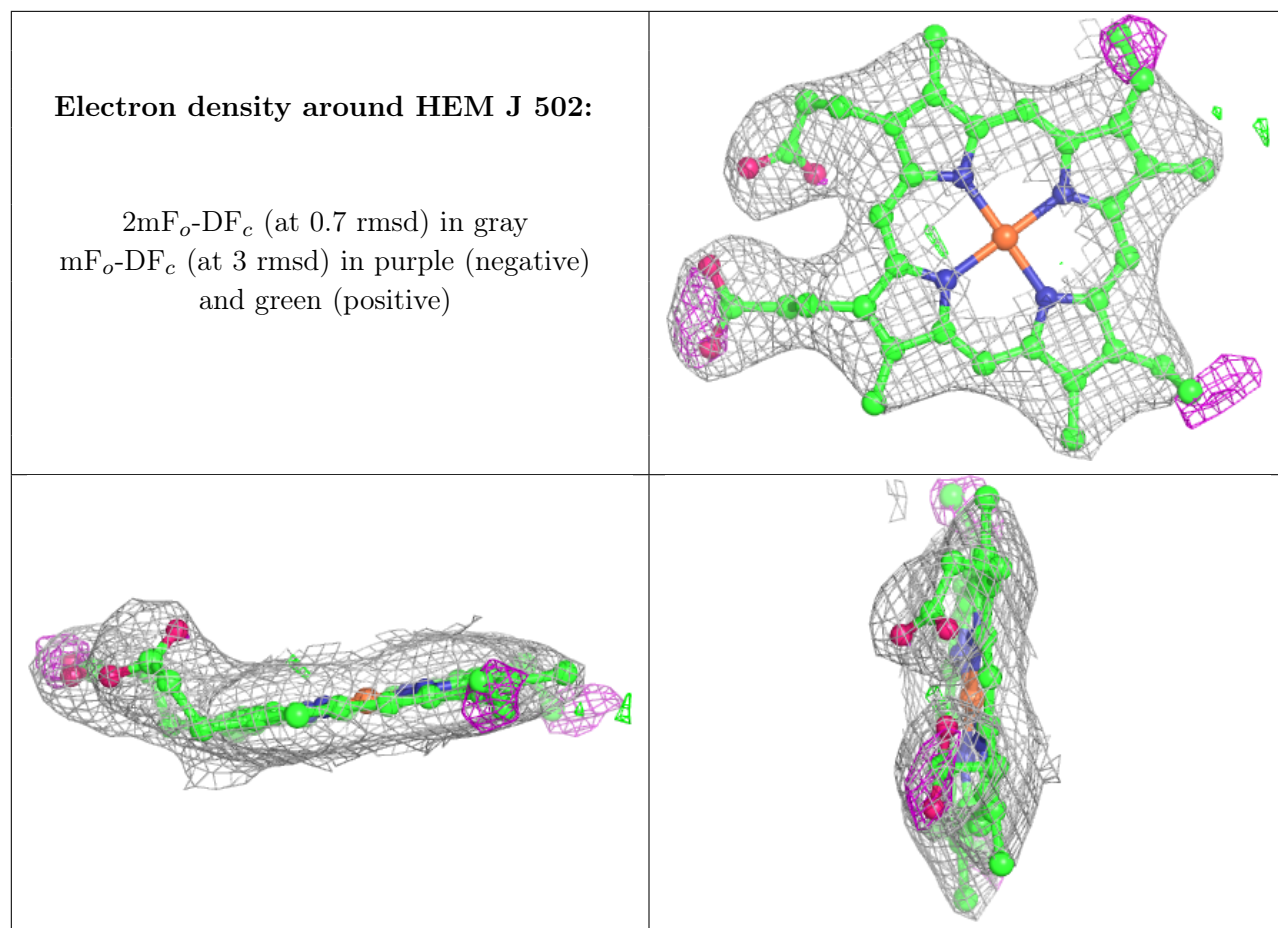
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

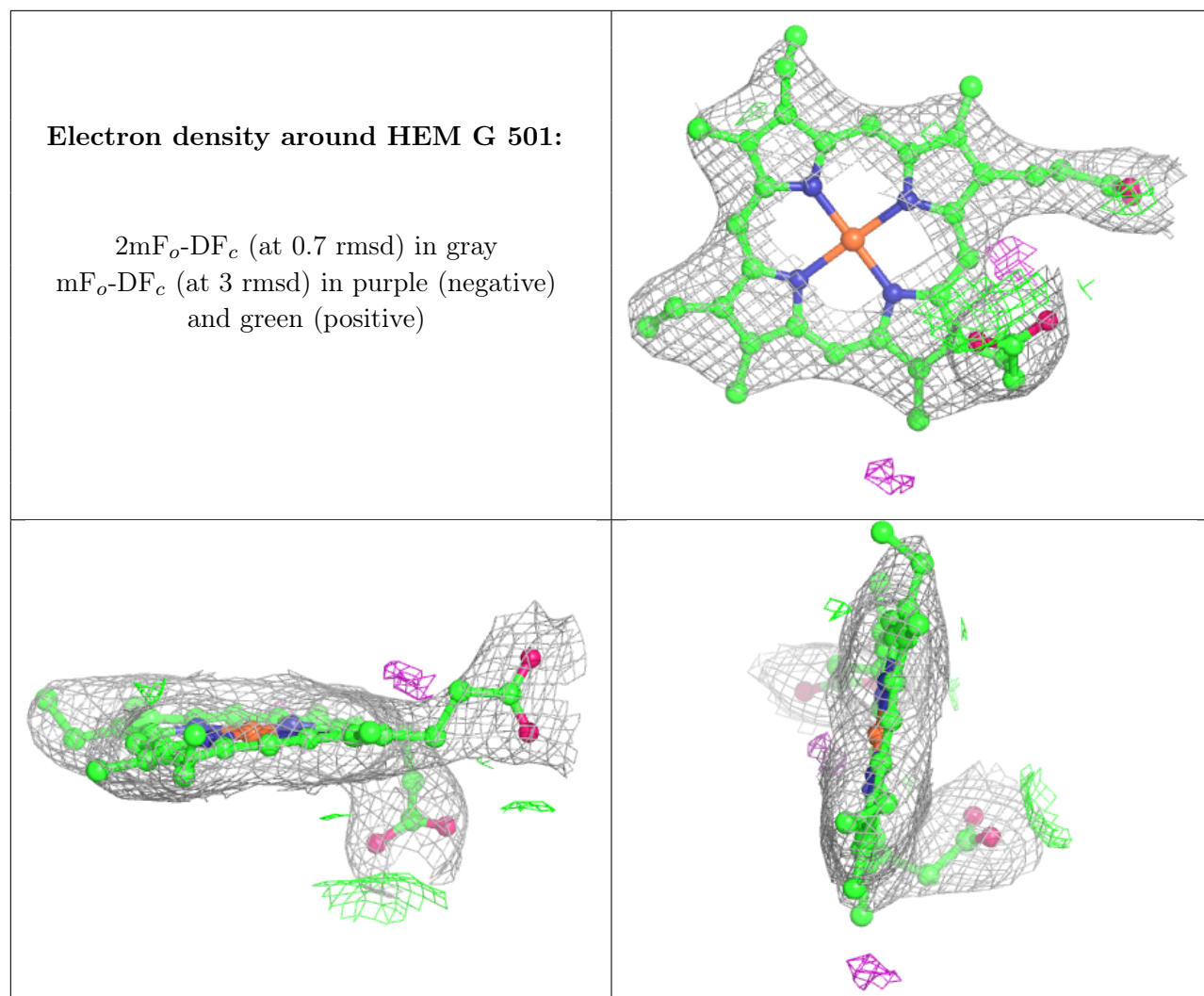


Electron density around HEM J 501:

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







6.5 Other polymers [i](#)

There are no such residues in this entry.