



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 10, 2020 – 10:33 AM BST

PDB ID : 6V0A
Title : Crystal structure of cytochrome c nitrite reductase from the bacterium *Geobacter lovleyi* with bound sulfate
Authors : Satyanarayana, L.; Campecino, J.; Hegg, L.H.; Hu, J.
Deposited on : 2019-11-18
Resolution : 2.55 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 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 : 2.14.3.dev2
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) : 2.14.3.dev2

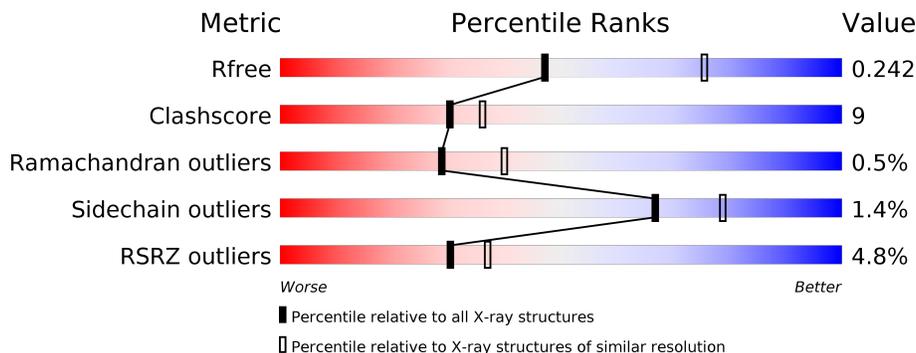
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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 on 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	482	
1	B	482	
1	C	482	
1	D	482	
1	E	482	
1	F	482	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	506	-	-	X	-
3	SO4	C	506	-	-	X	-

2 Entry composition [i](#)

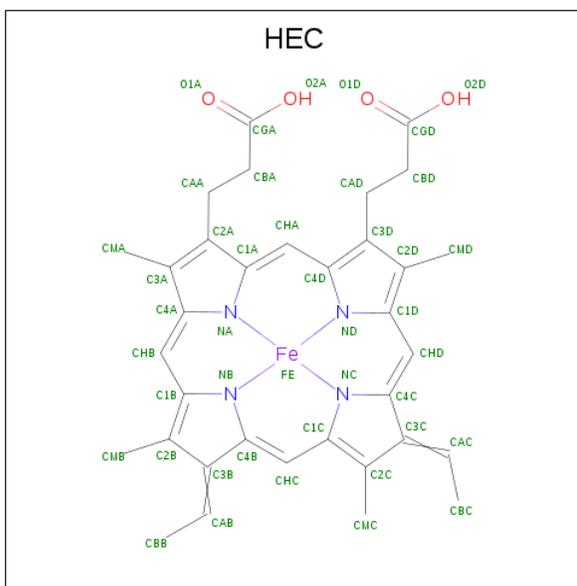
There are 4 unique types of molecules in this entry. The entry contains 23376 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Nitrite reductase (cytochrome; ammonia-forming).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	443	Total 3525	C 2237	N 600	O 661	S 27	0	0	0
1	B	444	Total 3538	C 2245	N 604	O 662	S 27	0	0	0
1	C	442	Total 3525	C 2237	N 601	O 660	S 27	0	0	0
1	D	444	Total 3534	C 2243	N 602	O 662	S 27	0	0	0
1	E	443	Total 3525	C 2237	N 600	O 661	S 27	0	0	0
1	F	441	Total 3514	C 2230	N 598	O 659	S 27	0	0	0

- Molecule 2 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$) (labeled as "Ligand of Interest" by author).



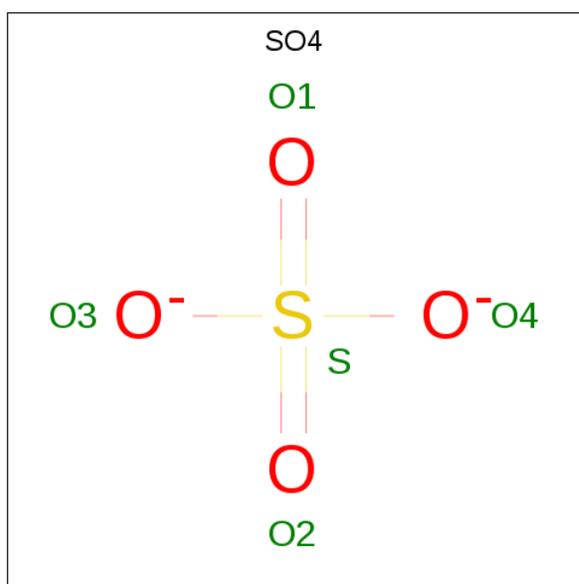
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0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

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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O S	0	0
			5	4 1		
3	B	1	Total	O S	0	0
			5	4 1		
3	C	1	Total	O S	0	0
			5	4 1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		

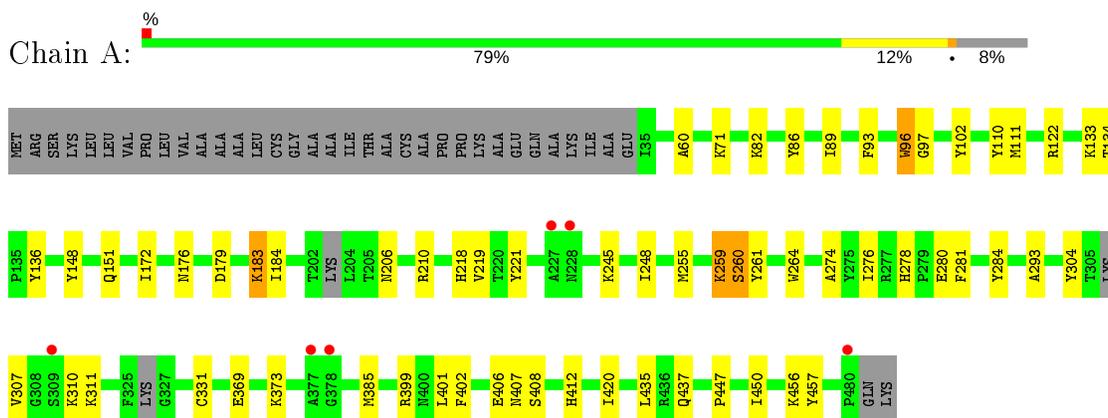
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	215	Total	O	0	0
			215	215		
4	B	236	Total	O	0	0
			236	236		
4	C	148	Total	O	0	0
			148	148		
4	D	134	Total	O	0	0
			134	134		
4	E	92	Total	O	0	0
			92	92		
4	F	70	Total	O	0	0
			70	70		

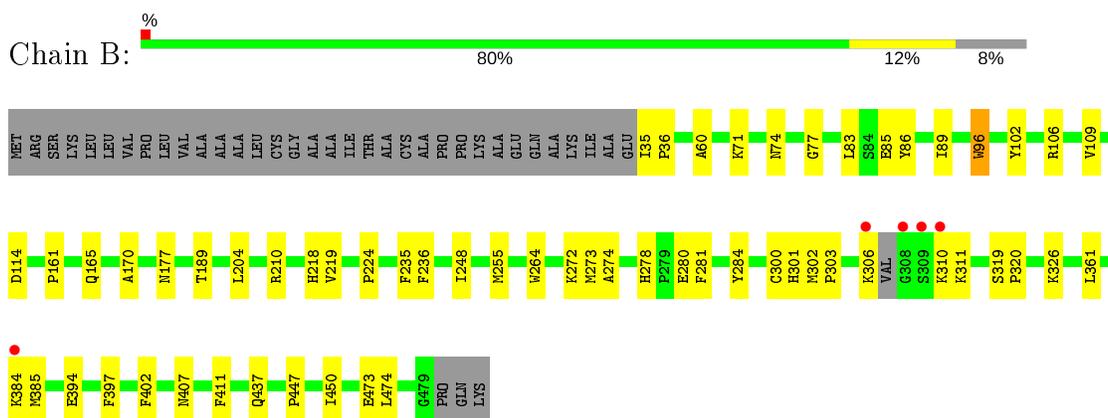
3 Residue-property plots

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.

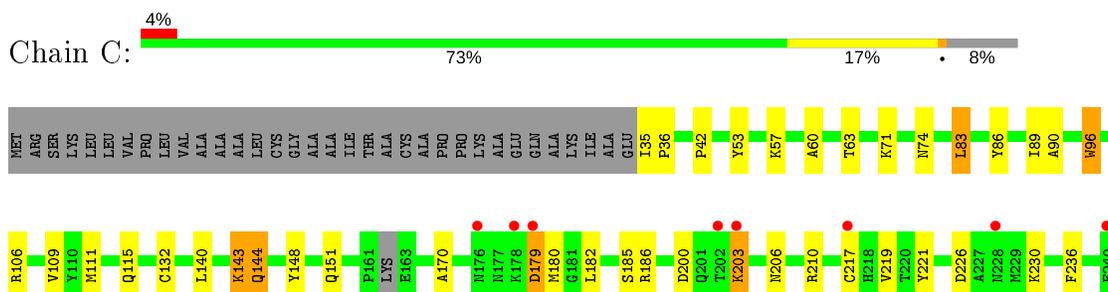
- Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)

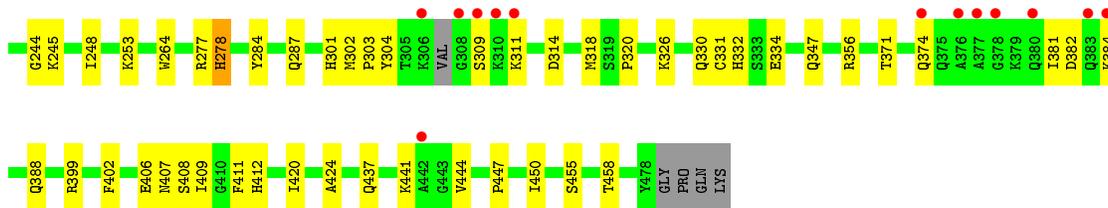


- Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)

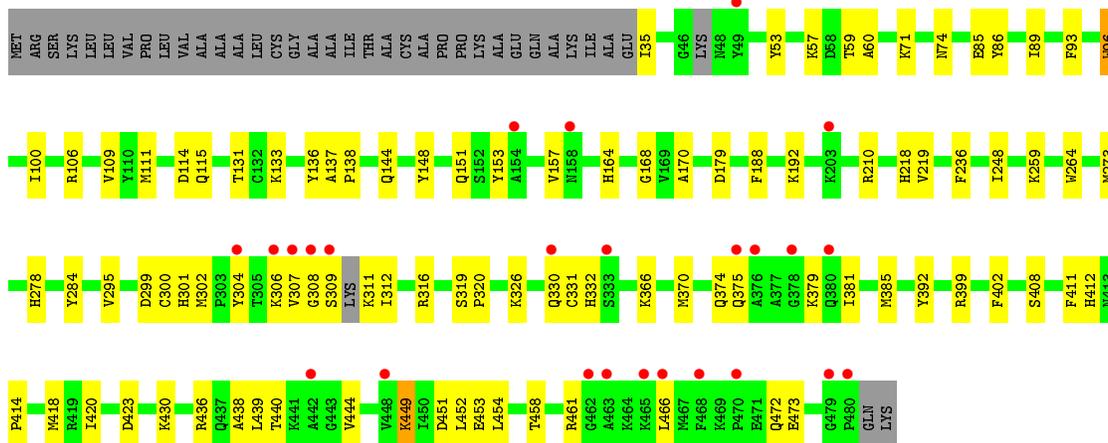


- Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)

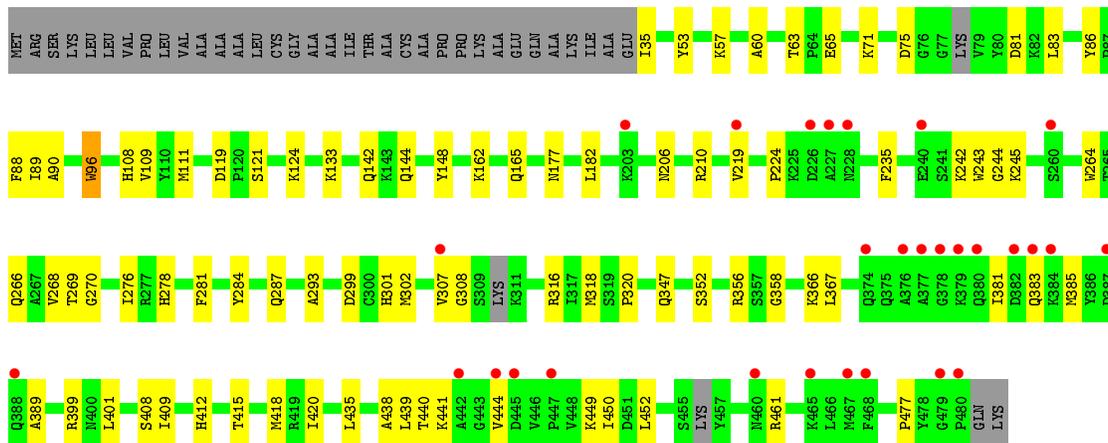




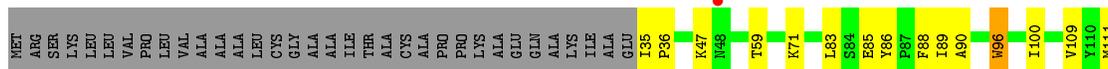
• Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)



• Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)



• Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	110.86Å 144.62Å 234.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.66 – 2.55 29.66 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.66-2.55) 99.0 (29.66-2.55)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 2.54Å)	Xtrriage
Refinement program	PHENIX 1.15.1_3469	Depositor
R, R_{free}	0.188 , 0.242 0.189 , 0.242	Depositor DCC
R_{free} test set	6076 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	33.7	Xtrriage
Anisotropy	0.322	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	23376	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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: SO4, HEC

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	0.49	0/3610	0.63	0/4861
1	B	0.49	0/3624	0.63	0/4878
1	C	0.48	0/3610	0.62	0/4859
1	D	0.46	0/3620	0.59	0/4875
1	E	0.44	0/3610	0.59	0/4861
1	F	0.42	0/3598	0.57	0/4844
All	All	0.46	0/21672	0.60	0/29178

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	3525	0	3433	44	0
1	B	3538	0	3457	38	0
1	C	3525	0	3440	55	0
1	D	3534	0	3448	73	0
1	E	3525	0	3432	65	0
1	F	3514	0	3422	71	0
2	A	215	0	151	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	215	0	150	23	0
2	C	215	0	150	16	0
2	D	215	0	151	24	0
2	E	215	0	150	19	0
2	F	215	0	150	20	0
3	A	5	0	0	2	0
3	B	5	0	0	0	0
3	C	5	0	0	2	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
4	A	215	0	0	2	0
4	B	236	0	0	0	0
4	C	148	0	0	1	0
4	D	134	0	0	4	0
4	E	92	0	0	4	0
4	F	70	0	0	3	0
All	All	23376	0	21534	409	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 409 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:A:331:CYS:SG	2:A:505:HEC:CAC	2.30	1.19
1:D:331:CYS:SG	2:D:505:HEC:CAC	2.41	1.07
1:A:331:CYS:SG	2:A:505:HEC:HAC	2.09	0.90
1:E:242:LYS:HD2	1:E:243:TRP:H	1.41	0.84
2:E:505:HEC:HBA2	2:F:505:HEC:HBA2	1.60	0.82

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	435/482 (90%)	419 (96%)	14 (3%)	2 (0%)	29	40
1	B	440/482 (91%)	426 (97%)	13 (3%)	1 (0%)	47	60
1	C	436/482 (90%)	419 (96%)	14 (3%)	3 (1%)	22	30
1	D	438/482 (91%)	421 (96%)	15 (3%)	2 (0%)	29	40
1	E	435/482 (90%)	415 (95%)	18 (4%)	2 (0%)	29	40
1	F	433/482 (90%)	410 (95%)	19 (4%)	4 (1%)	17	24
All	All	2617/2892 (90%)	2510 (96%)	93 (4%)	14 (0%)	29	40

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	143	LYS
1	F	220	THR
1	A	260	SER
1	D	308	GLY
1	F	308	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	376/404 (93%)	373 (99%)	3 (1%)	81	88
1	B	377/404 (93%)	373 (99%)	4 (1%)	73	83
1	C	376/404 (93%)	368 (98%)	8 (2%)	53	68
1	D	377/404 (93%)	370 (98%)	7 (2%)	57	72
1	E	376/404 (93%)	373 (99%)	3 (1%)	81	88
1	F	375/404 (93%)	369 (98%)	6 (2%)	62	77
All	All	2257/2424 (93%)	2226 (99%)	31 (1%)	67	79

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	309	SER
1	D	192	LYS
1	F	272	LYS
1	D	96	TRP
1	D	306	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	151	GLN
1	D	177	ASN
1	E	380	GLN
1	C	151	GLN
1	E	342	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](#)

36 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
2	HEC	B	505	1	26,50,50	2.09	6 (23%)	18,82,82	2.17	9 (50%)
2	HEC	D	505	1	26,50,50	2.35	5 (19%)	18,82,82	2.11	6 (33%)
2	HEC	C	501	1,3	26,50,50	2.25	5 (19%)	18,82,82	2.10	8 (44%)
2	HEC	F	502	1	26,50,50	1.93	5 (19%)	18,82,82	1.47	2 (11%)
2	HEC	E	502	1	26,50,50	2.19	4 (15%)	18,82,82	1.73	6 (33%)
2	HEC	C	502	1	26,50,50	2.27	4 (15%)	18,82,82	1.83	4 (22%)
2	HEC	A	505	1	26,50,50	2.19	6 (23%)	18,82,82	2.73	7 (38%)
2	HEC	F	503	1	26,50,50	2.28	5 (19%)	18,82,82	1.73	6 (33%)
2	HEC	B	503	1	26,50,50	2.34	6 (23%)	18,82,82	3.89	12 (66%)
3	SO4	B	506	2	4,4,4	0.13	0	6,6,6	0.56	0
3	SO4	A	506	2	4,4,4	0.16	0	6,6,6	0.60	0
3	SO4	C	506	2	4,4,4	0.14	0	6,6,6	0.55	0
2	HEC	F	501	1,3	26,50,50	1.86	6 (23%)	18,82,82	1.55	4 (22%)
2	HEC	F	504	1	26,50,50	2.31	4 (15%)	18,82,82	1.67	6 (33%)
2	HEC	E	501	1,3	26,50,50	2.31	5 (19%)	18,82,82	2.07	7 (38%)
2	HEC	E	503	1	26,50,50	2.25	5 (19%)	18,82,82	1.59	4 (22%)
3	SO4	E	506	2	4,4,4	0.23	0	6,6,6	0.40	0
2	HEC	A	501	1,3	26,50,50	2.37	4 (15%)	18,82,82	1.57	3 (16%)
2	HEC	B	501	1,3	26,50,50	2.18	5 (19%)	18,82,82	2.09	6 (33%)
3	SO4	F	506	2	4,4,4	0.22	0	6,6,6	0.27	0
2	HEC	A	503	1	26,50,50	2.22	5 (19%)	18,82,82	1.97	6 (33%)
2	HEC	A	504	1	26,50,50	2.20	6 (23%)	18,82,82	1.73	4 (22%)
2	HEC	D	502	1	26,50,50	2.08	4 (15%)	18,82,82	2.11	5 (27%)
2	HEC	C	504	1	26,50,50	2.32	5 (19%)	18,82,82	1.87	7 (38%)
2	HEC	D	501	1,3	26,50,50	2.22	7 (26%)	18,82,82	1.88	5 (27%)
2	HEC	E	505	1	26,50,50	2.10	5 (19%)	18,82,82	2.65	9 (50%)
2	HEC	F	505	1	26,50,50	2.26	5 (19%)	18,82,82	1.76	5 (27%)
2	HEC	B	504	1	26,50,50	2.30	4 (15%)	18,82,82	1.86	5 (27%)
2	HEC	D	504	1	26,50,50	2.14	4 (15%)	18,82,82	1.80	6 (33%)
2	HEC	A	502	1	26,50,50	2.14	4 (15%)	18,82,82	1.72	3 (16%)
3	SO4	D	506	2	4,4,4	0.23	0	6,6,6	0.49	0
2	HEC	D	503	1	26,50,50	2.20	4 (15%)	18,82,82	2.06	9 (50%)
2	HEC	C	503	1	26,50,50	2.08	5 (19%)	18,82,82	2.07	8 (44%)
2	HEC	B	502	1	26,50,50	2.19	4 (15%)	18,82,82	2.00	7 (38%)
2	HEC	E	504	1	26,50,50	2.13	5 (19%)	18,82,82	1.62	4 (22%)
2	HEC	C	505	1	26,50,50	2.02	5 (19%)	18,82,82	2.45	9 (50%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	B	505	1	-	1/6/54/54	-
2	HEC	D	505	1	-	1/6/54/54	-
2	HEC	C	501	1,3	-	0/6/54/54	-
2	HEC	F	502	1	-	0/6/54/54	-
2	HEC	E	502	1	-	0/6/54/54	-
2	HEC	C	502	1	-	0/6/54/54	-
2	HEC	A	505	1	-	1/6/54/54	-
2	HEC	F	503	1	-	0/6/54/54	-
2	HEC	B	503	1	-	1/6/54/54	-
2	HEC	F	501	1,3	-	0/6/54/54	-
2	HEC	F	504	1	-	0/6/54/54	-
2	HEC	E	501	1,3	-	0/6/54/54	-
2	HEC	E	503	1	-	0/6/54/54	-
2	HEC	A	501	1,3	-	0/6/54/54	-
2	HEC	B	501	1,3	-	0/6/54/54	-
2	HEC	A	503	1	-	0/6/54/54	-
2	HEC	A	504	1	-	0/6/54/54	-
2	HEC	D	502	1	-	0/6/54/54	-
2	HEC	C	504	1	-	0/6/54/54	-
2	HEC	D	501	1,3	-	0/6/54/54	-
2	HEC	E	505	1	-	0/6/54/54	-
2	HEC	F	505	1	-	0/6/54/54	-
2	HEC	B	504	1	-	0/6/54/54	-
2	HEC	D	504	1	-	0/6/54/54	-
2	HEC	A	502	1	-	0/6/54/54	-
2	HEC	D	503	1	-	0/6/54/54	-
2	HEC	C	503	1	-	0/6/54/54	-
2	HEC	B	502	1	-	0/6/54/54	-
2	HEC	E	504	1	-	0/6/54/54	-
2	HEC	C	505	1	-	3/6/54/54	-

The worst 5 of 147 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	505	HEC	C3B-C2B	-6.86	1.33	1.40
2	E	501	HEC	C3B-C2B	-6.61	1.33	1.40
2	A	504	HEC	C3B-C2B	-6.47	1.34	1.40
2	A	501	HEC	C3B-C2B	-6.44	1.34	1.40
2	B	503	HEC	C3B-C2B	-6.29	1.34	1.40

The worst 5 of 182 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	503	HEC	CBA-CAA-C2A	13.20	136.81	112.48
2	A	505	HEC	CBA-CAA-C2A	-5.97	101.47	112.48
2	A	505	HEC	CAD-CBD-CGD	-5.63	103.23	112.67
2	D	505	HEC	CBA-CAA-C2A	-4.94	103.37	112.48
2	E	505	HEC	CAD-CBD-CGD	-4.84	104.55	112.67

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	505	HEC	C2A-CAA-CBA-CGA
2	D	505	HEC	C2A-CAA-CBA-CGA
2	C	505	HEC	C2A-CAA-CBA-CGA
2	B	503	HEC	C2A-CAA-CBA-CGA
2	C	505	HEC	C1A-C2A-CAA-CBA

There are no ring outliers.

32 monomers are involved in 121 short contacts:

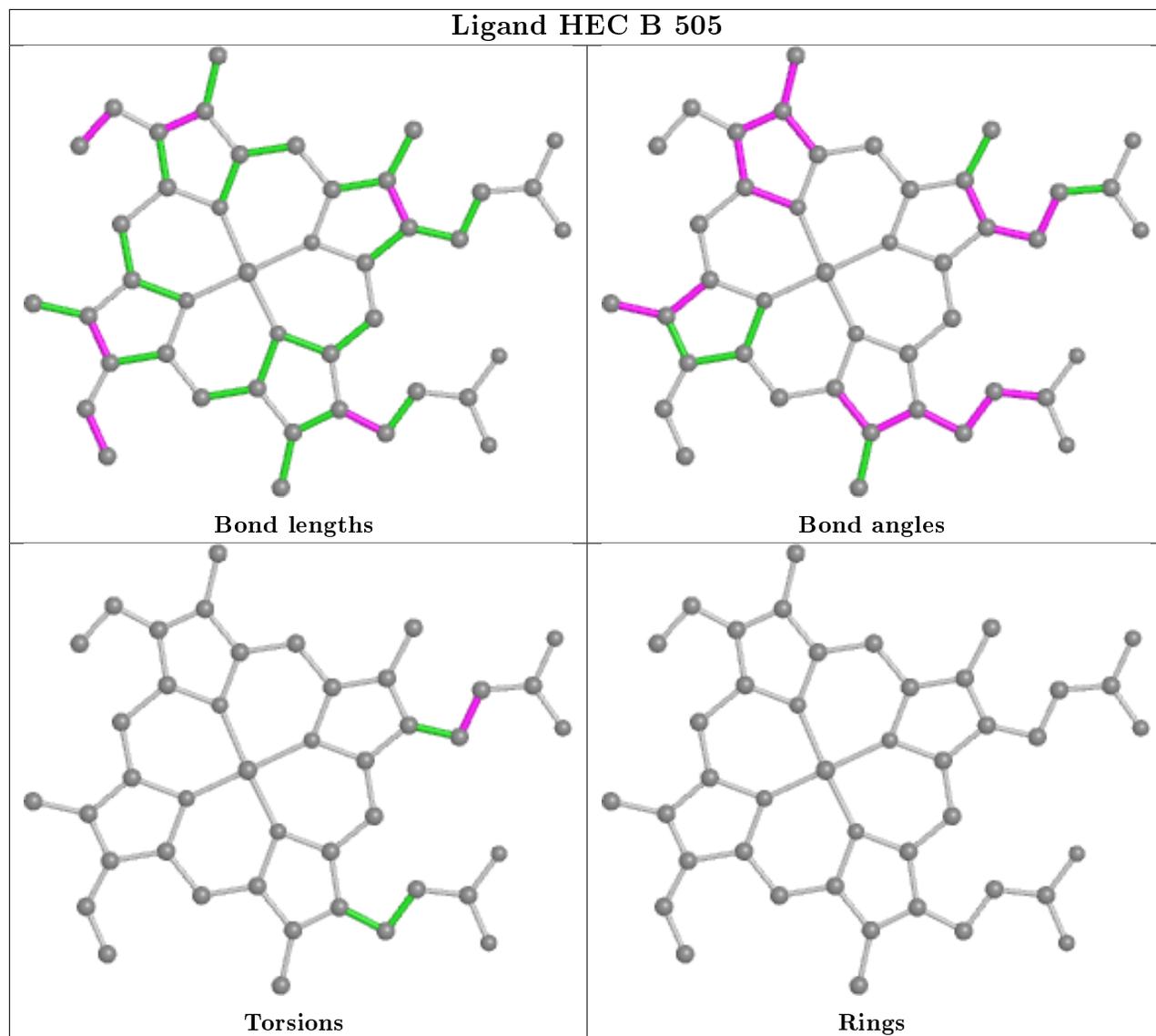
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	505	HEC	8	0
2	D	505	HEC	8	0
2	C	501	HEC	2	0
2	F	502	HEC	3	0
2	E	502	HEC	3	0
2	C	502	HEC	3	0
2	A	505	HEC	12	0
2	F	503	HEC	4	0
2	B	503	HEC	5	0
3	A	506	SO4	2	0
3	C	506	SO4	2	0
2	F	501	HEC	3	0
2	F	504	HEC	5	0
2	E	501	HEC	2	0
2	E	503	HEC	5	0
2	A	501	HEC	1	0
2	B	501	HEC	1	0
2	A	503	HEC	4	0
2	A	504	HEC	4	0
2	D	502	HEC	3	0
2	C	504	HEC	6	0

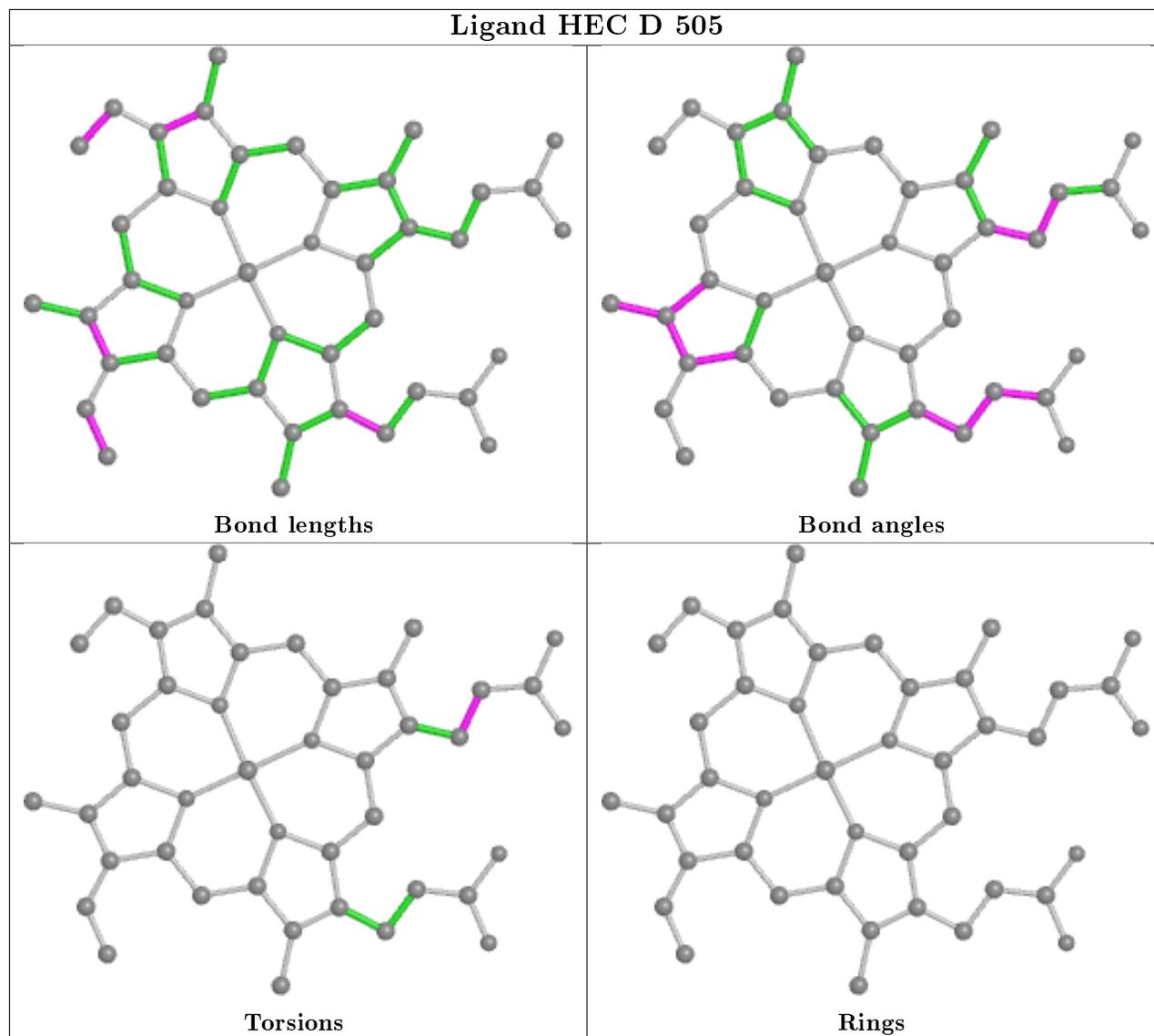
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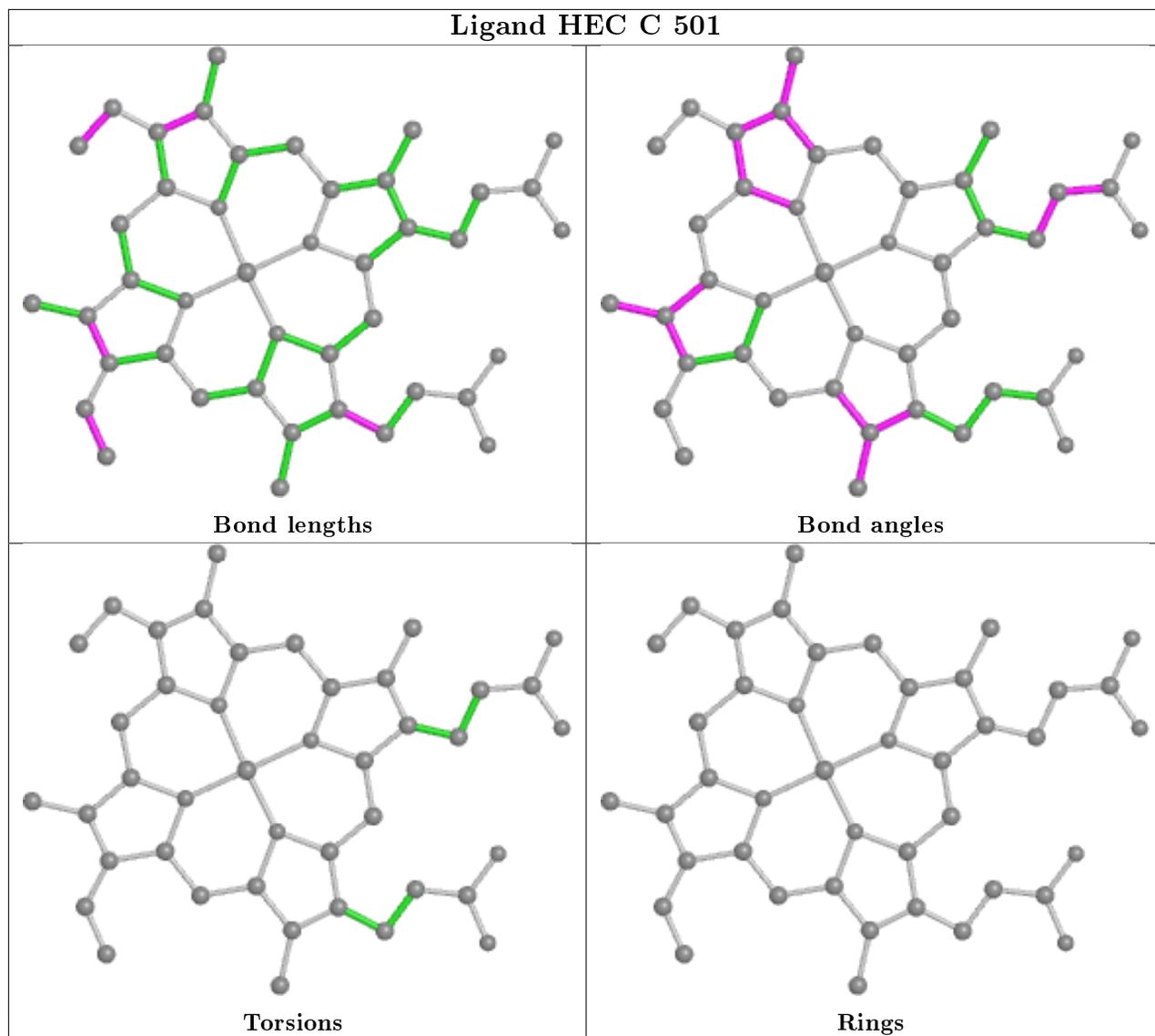
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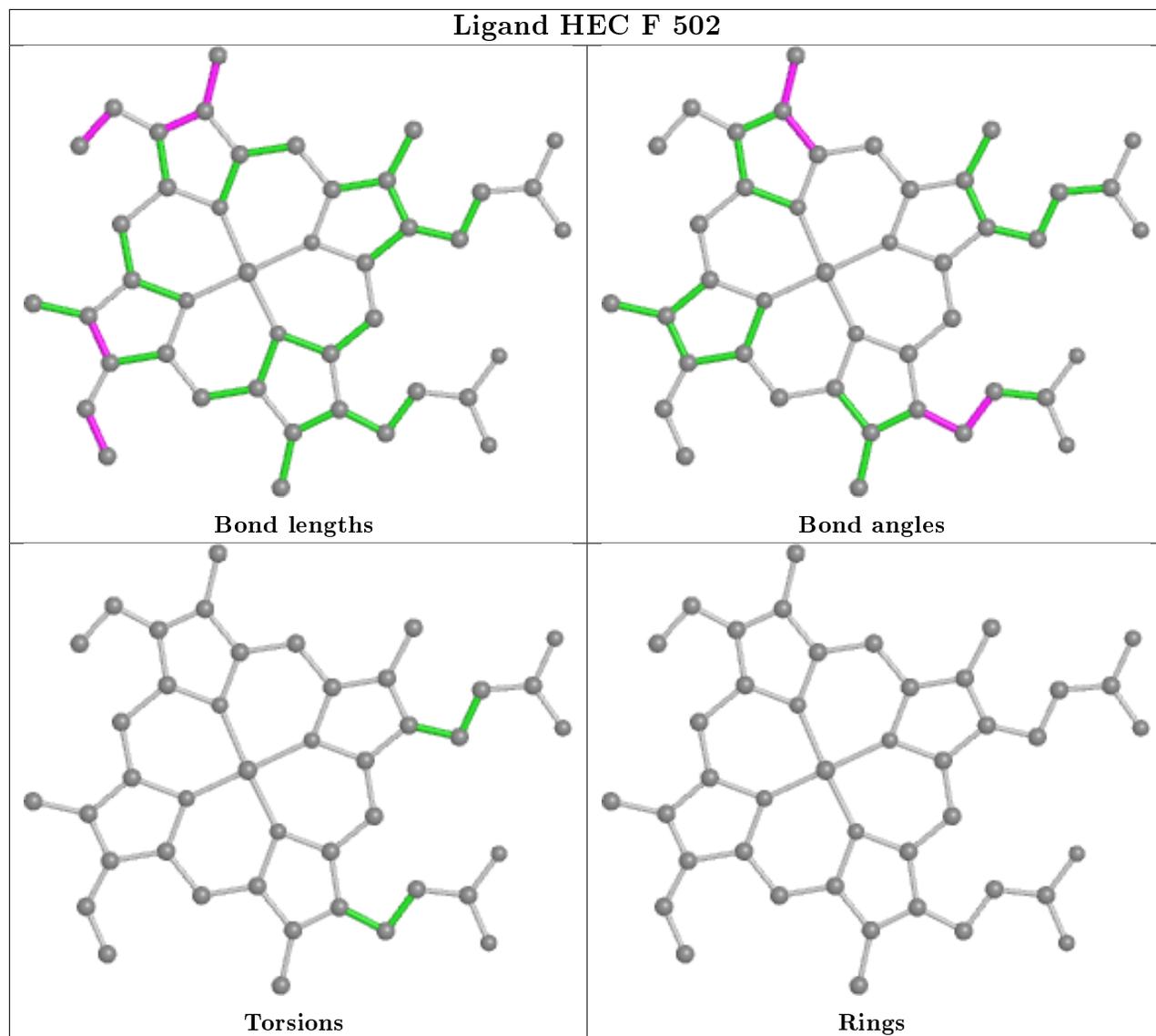
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	501	HEC	2	0
2	E	505	HEC	6	0
2	F	505	HEC	6	0
2	B	504	HEC	9	0
2	D	504	HEC	7	0
2	A	502	HEC	2	0
2	D	503	HEC	5	0
2	C	503	HEC	4	0
2	B	502	HEC	3	0
2	E	504	HEC	4	0
2	C	505	HEC	2	0

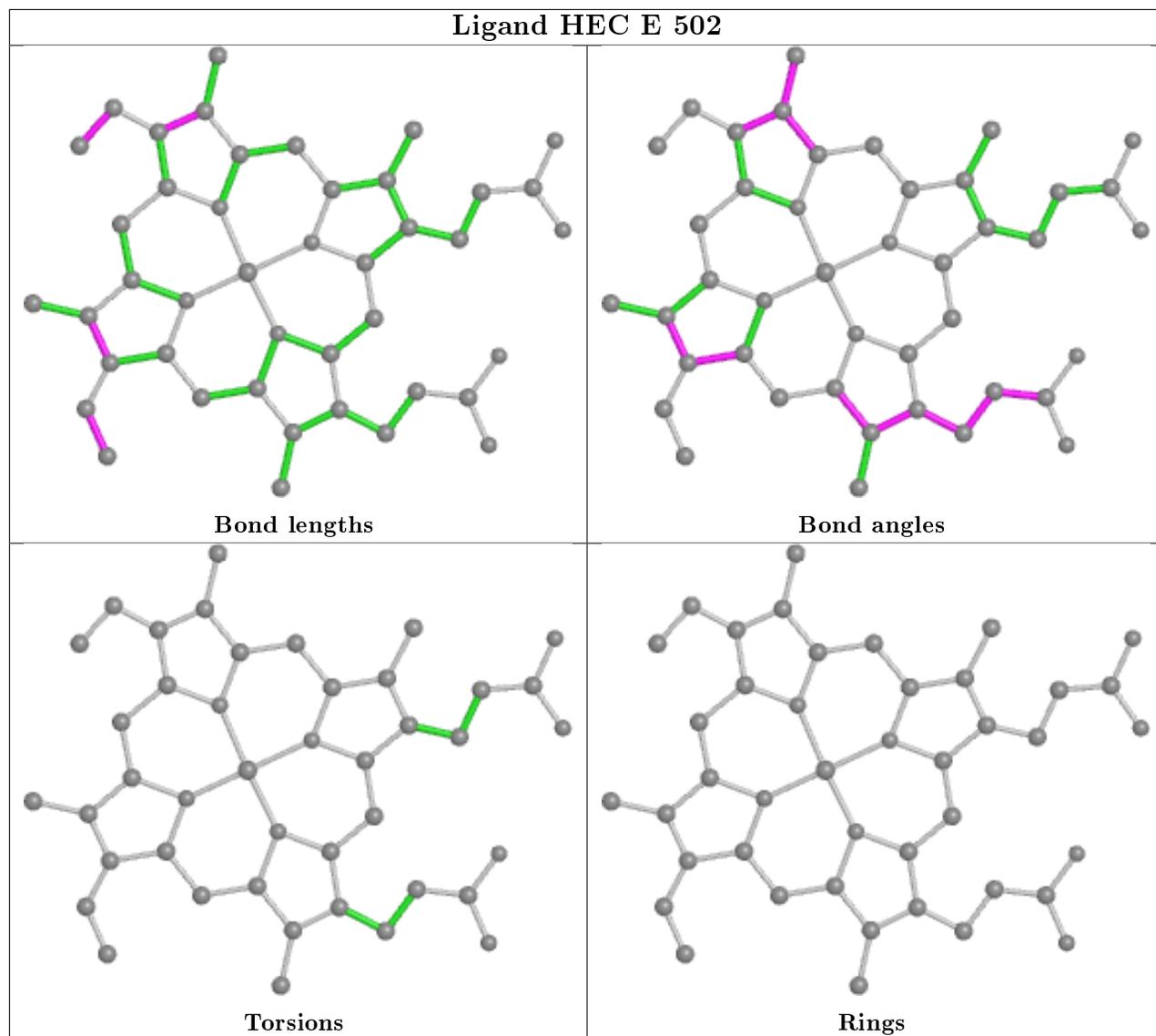
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

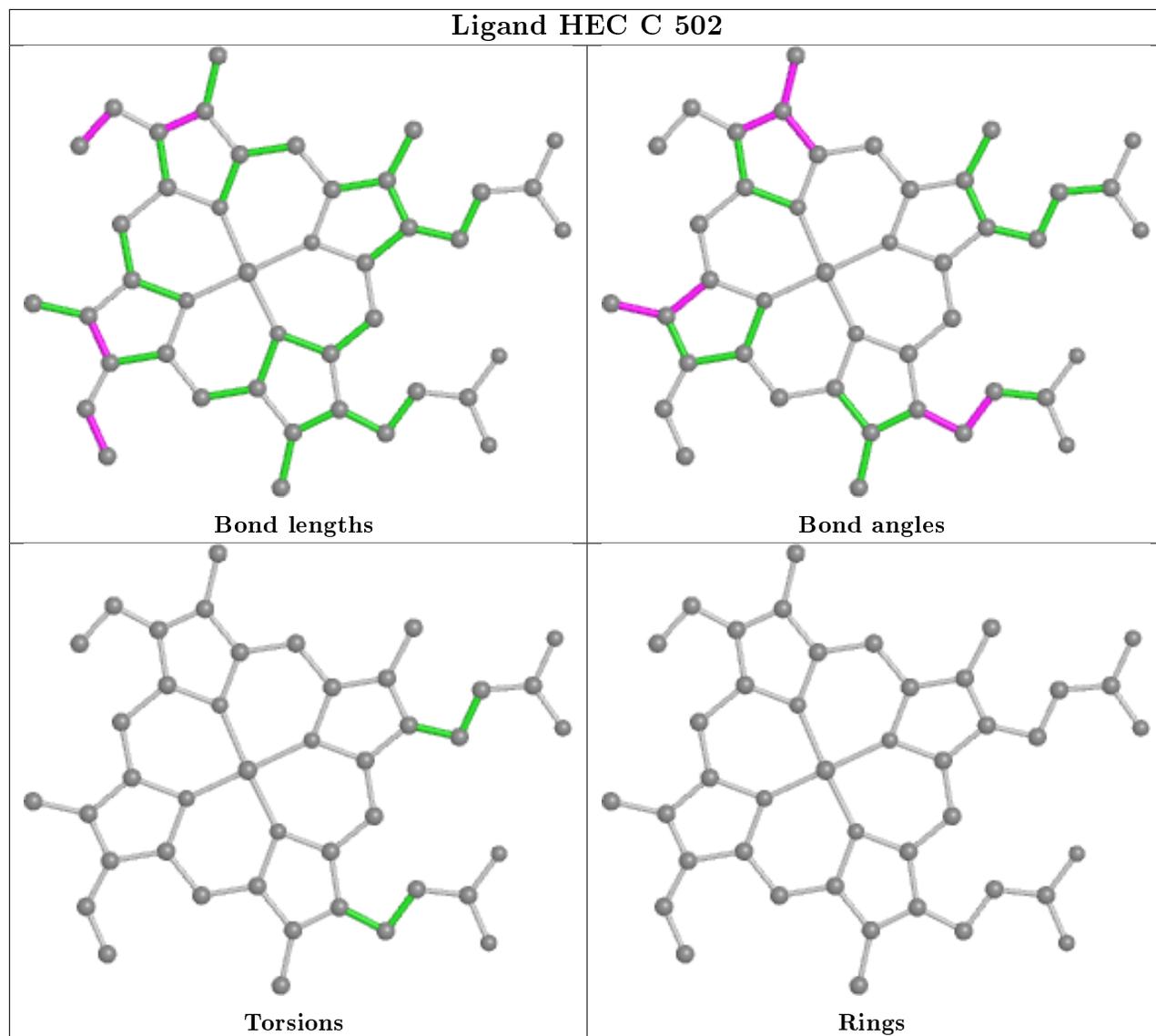


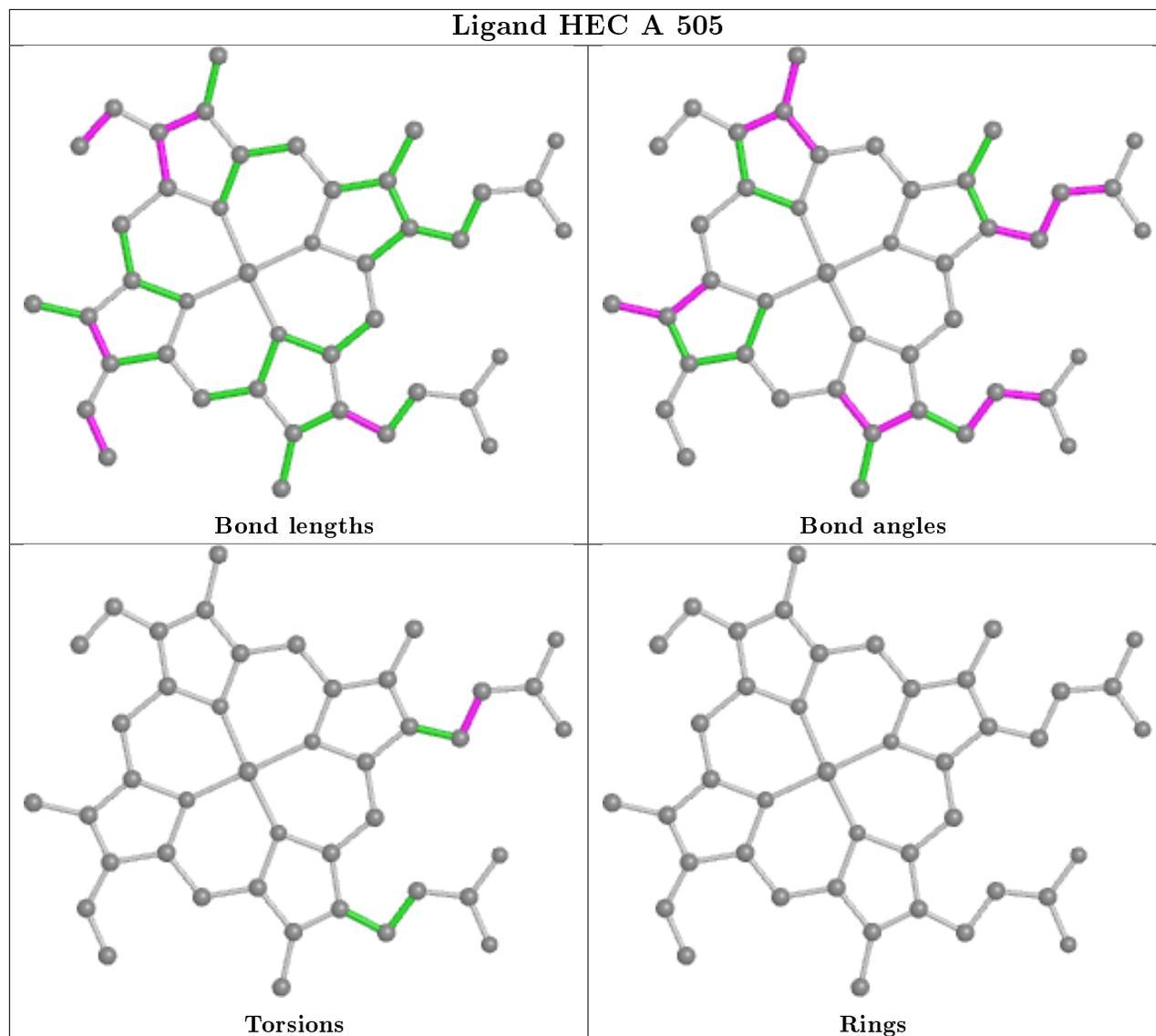


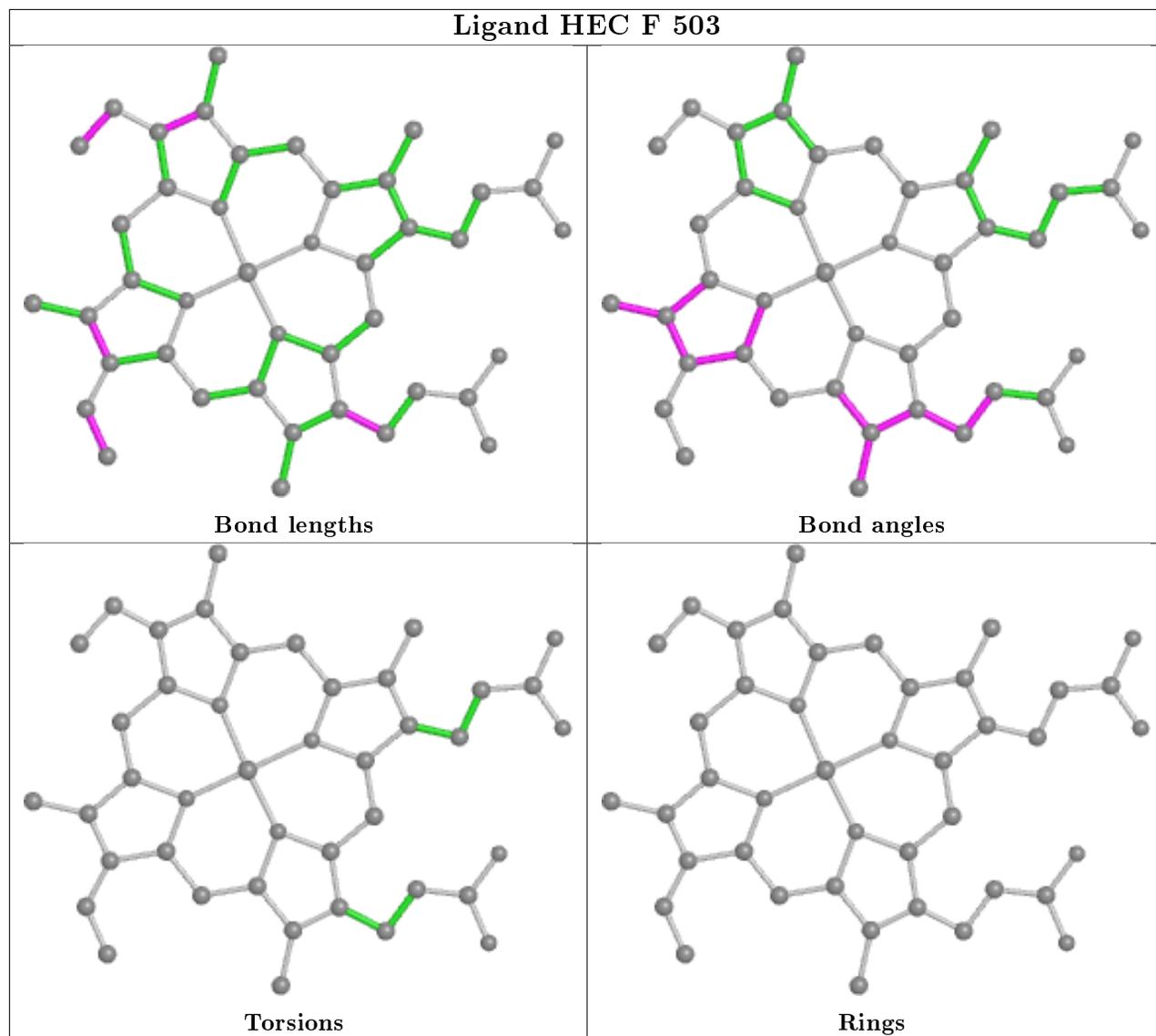


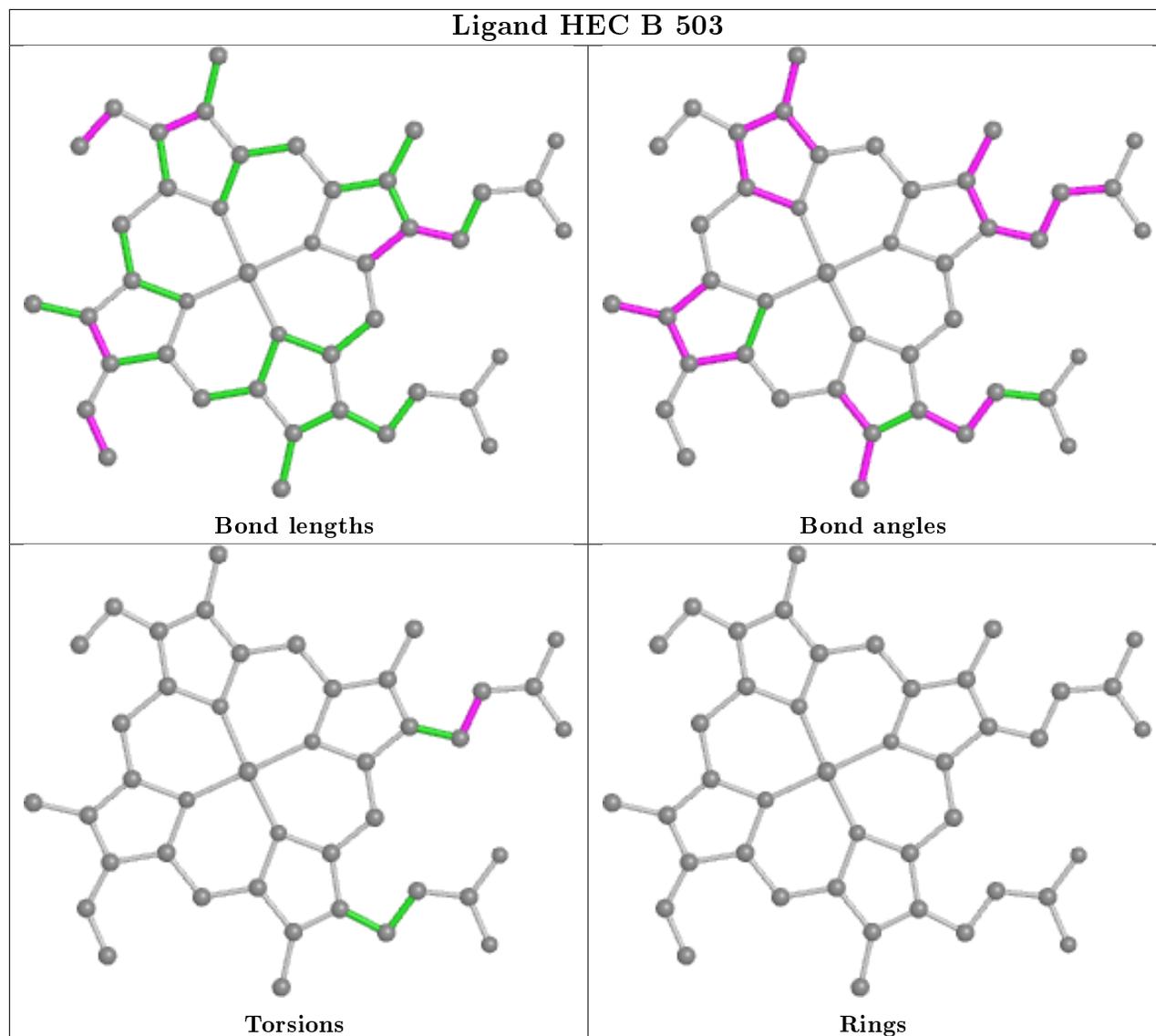


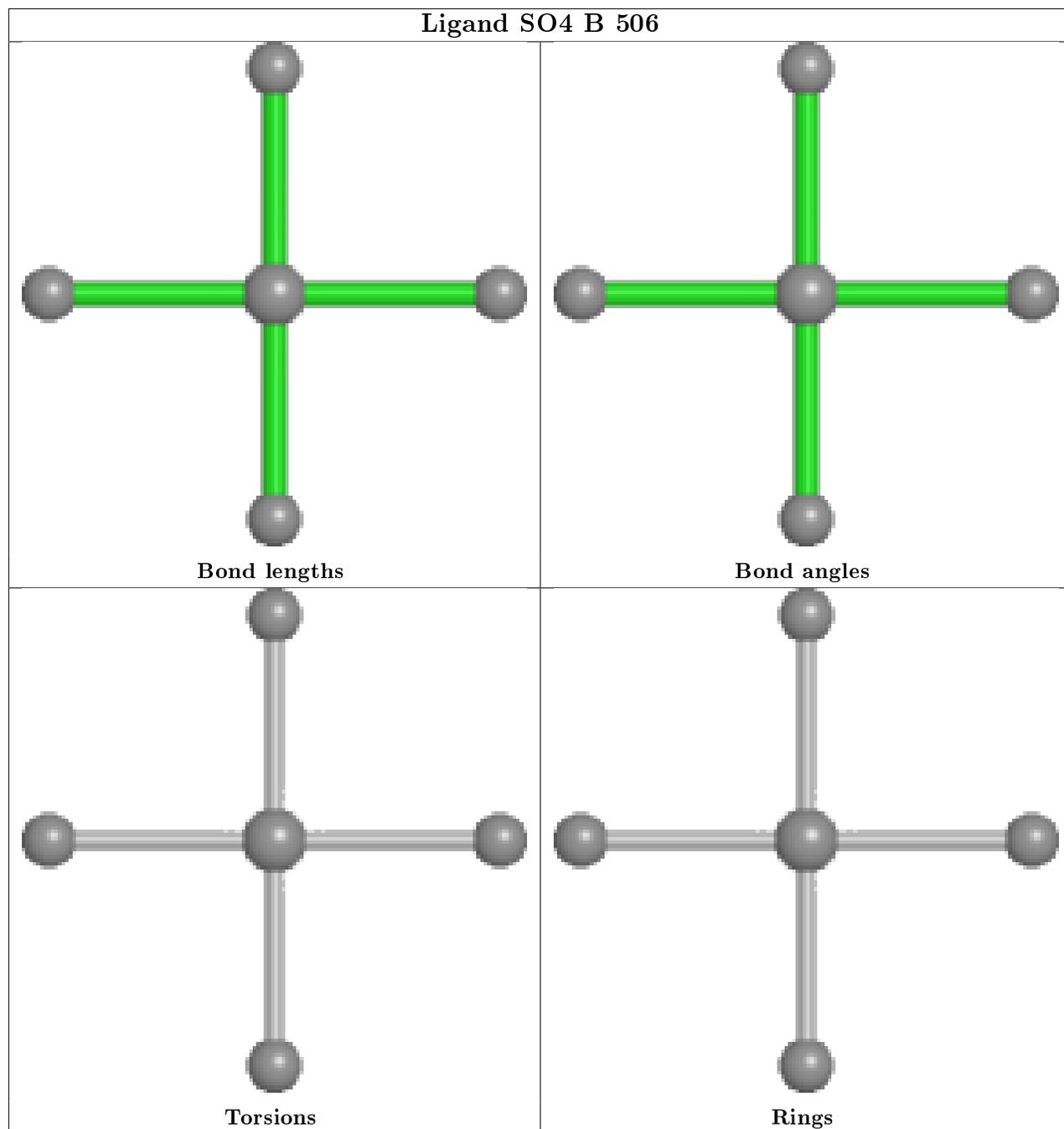


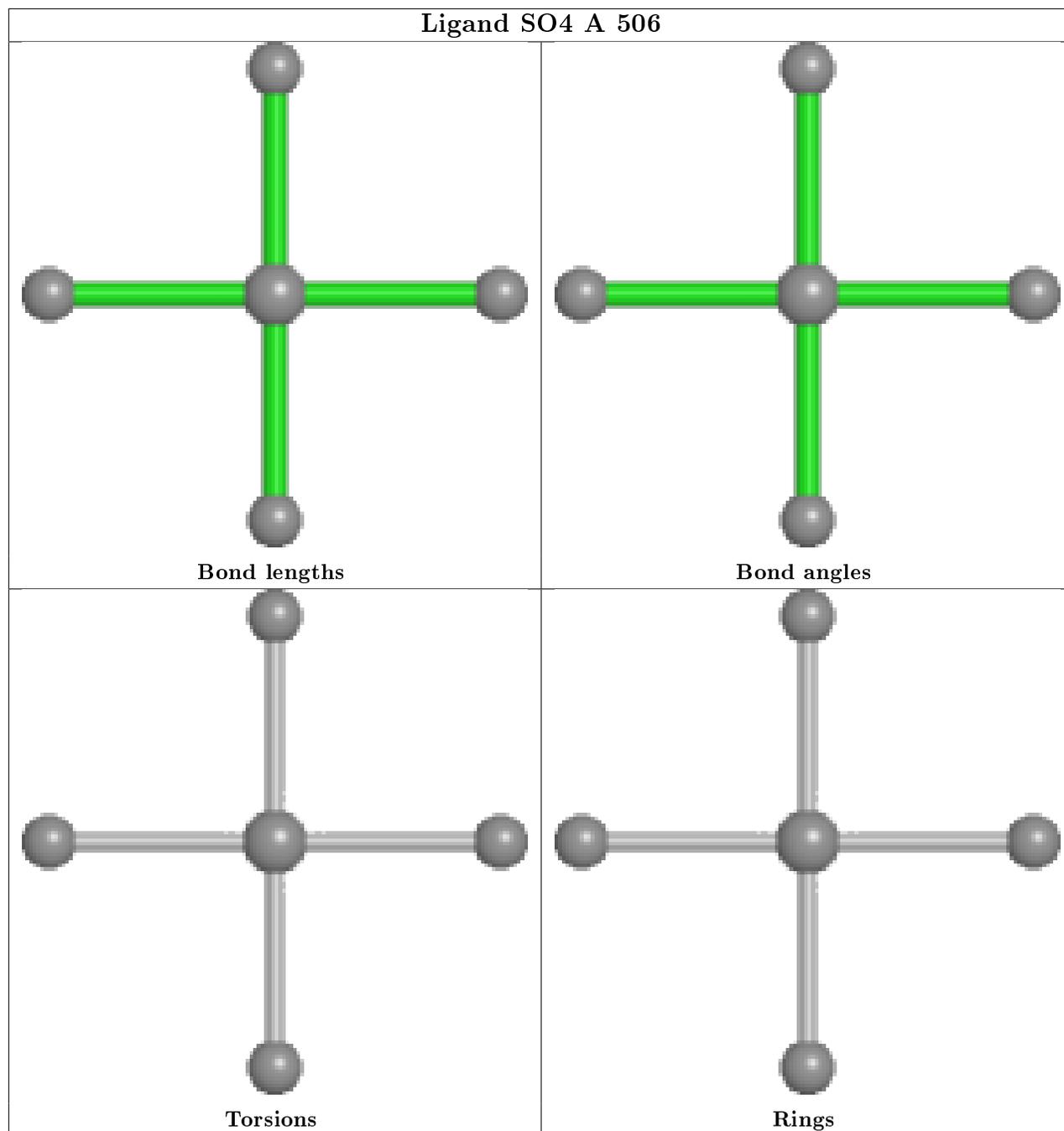


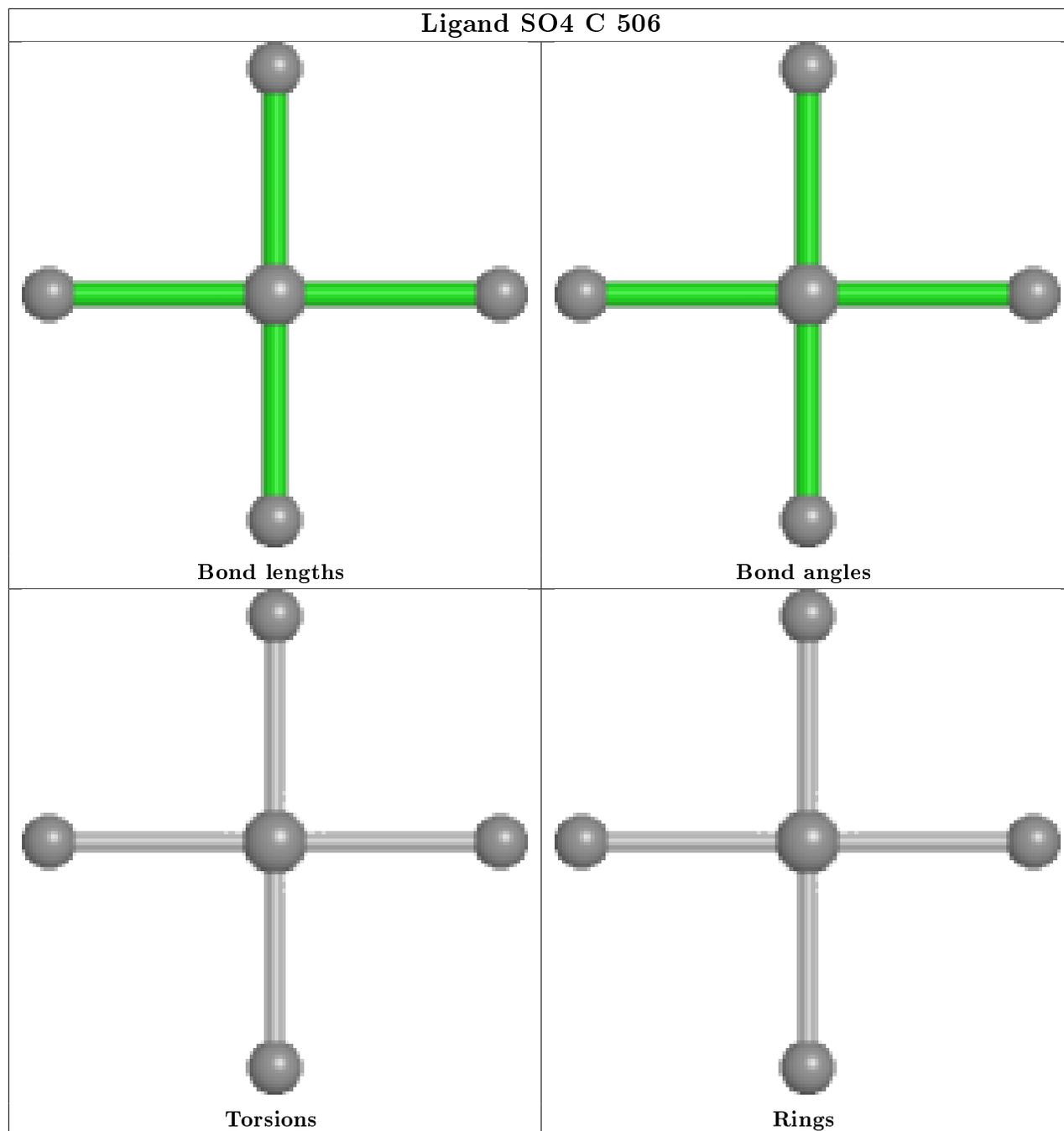


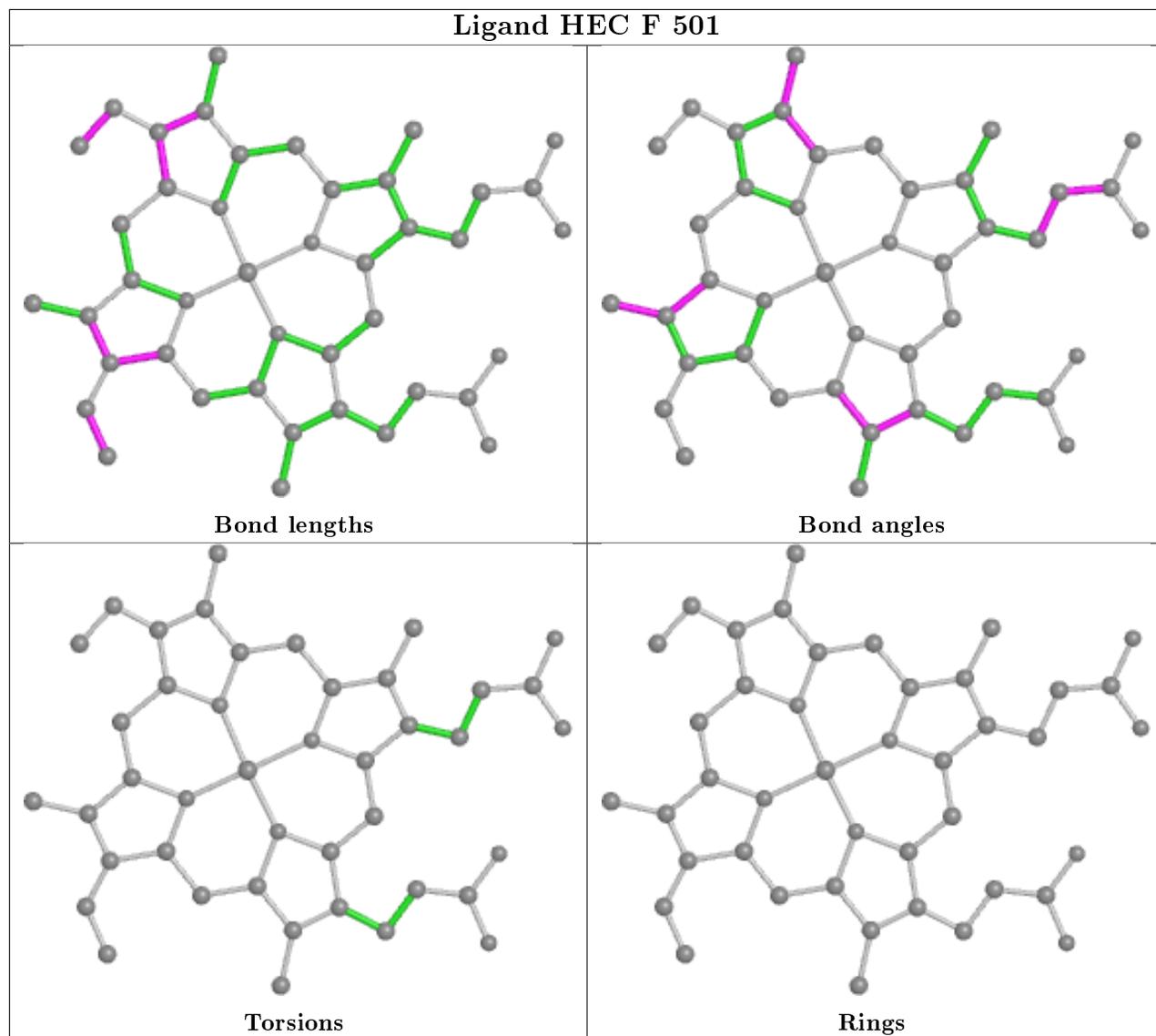


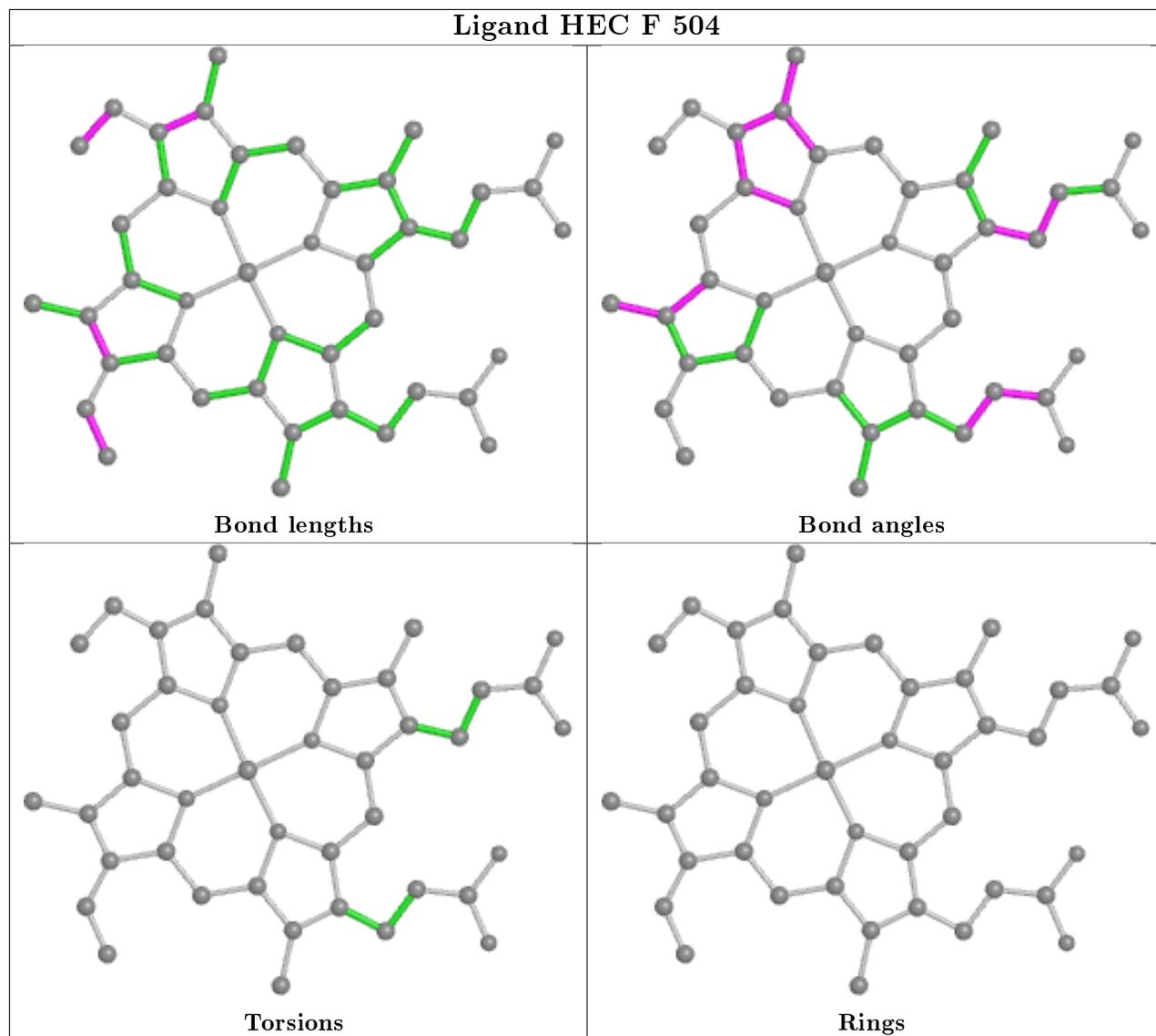


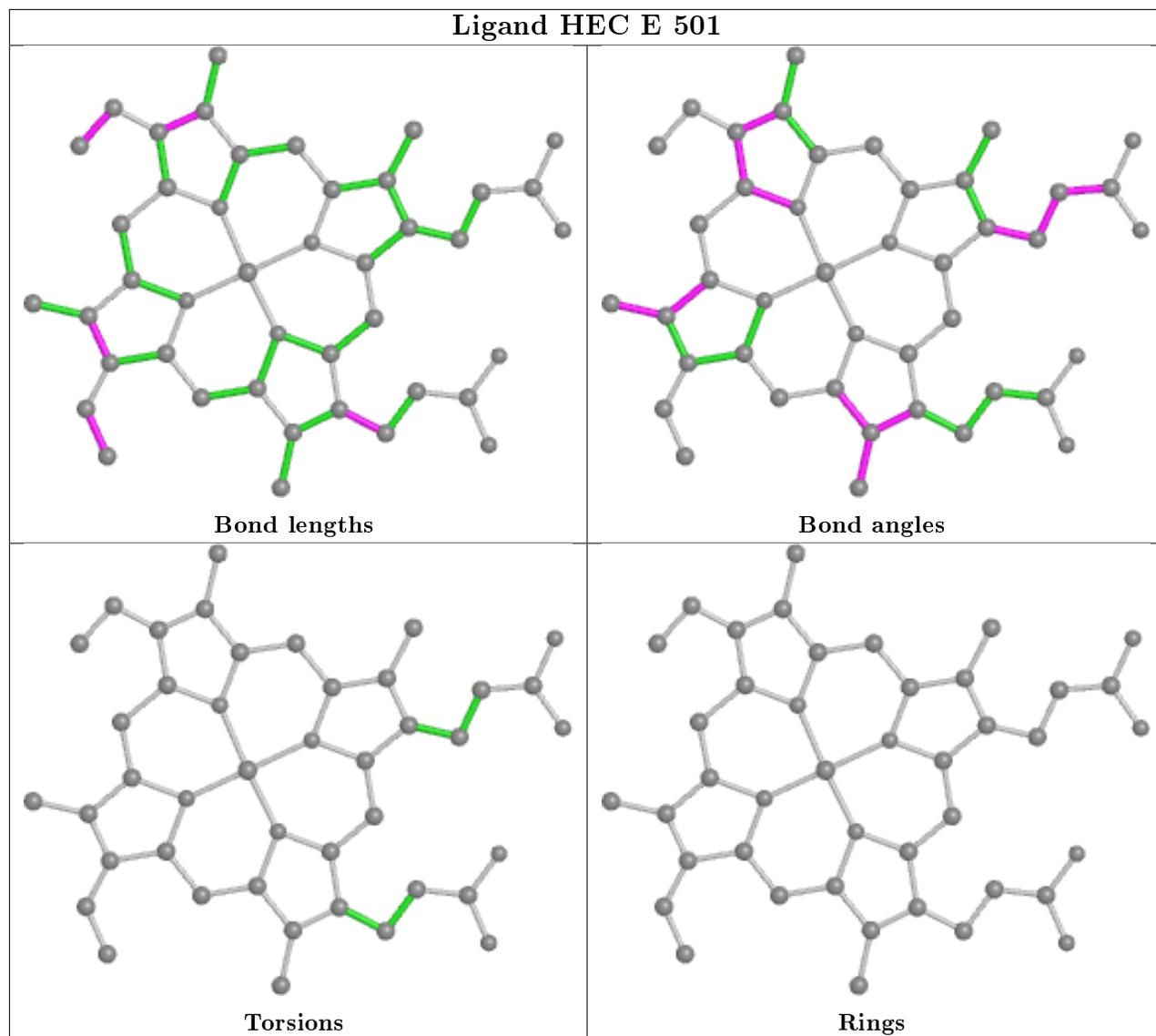


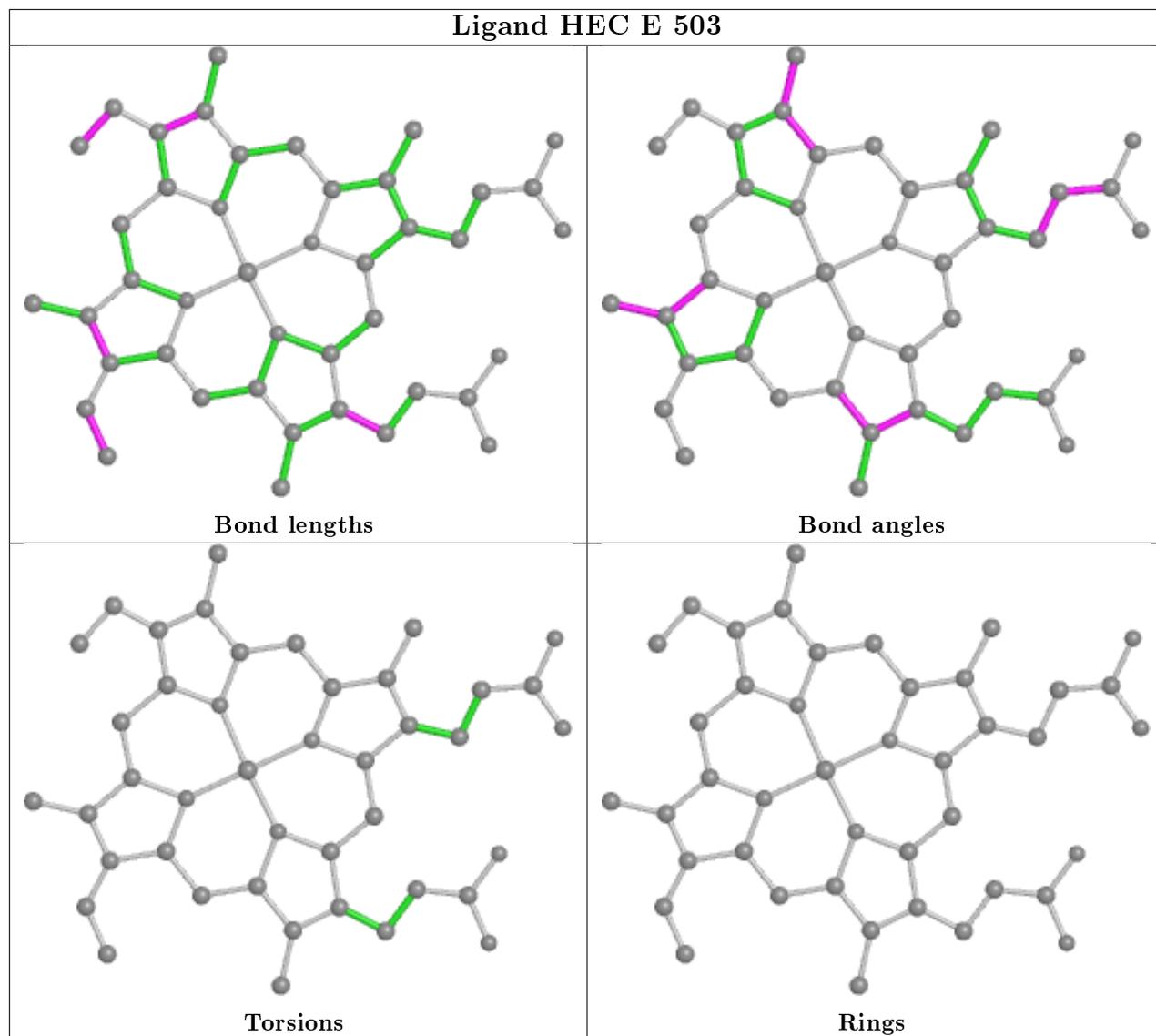


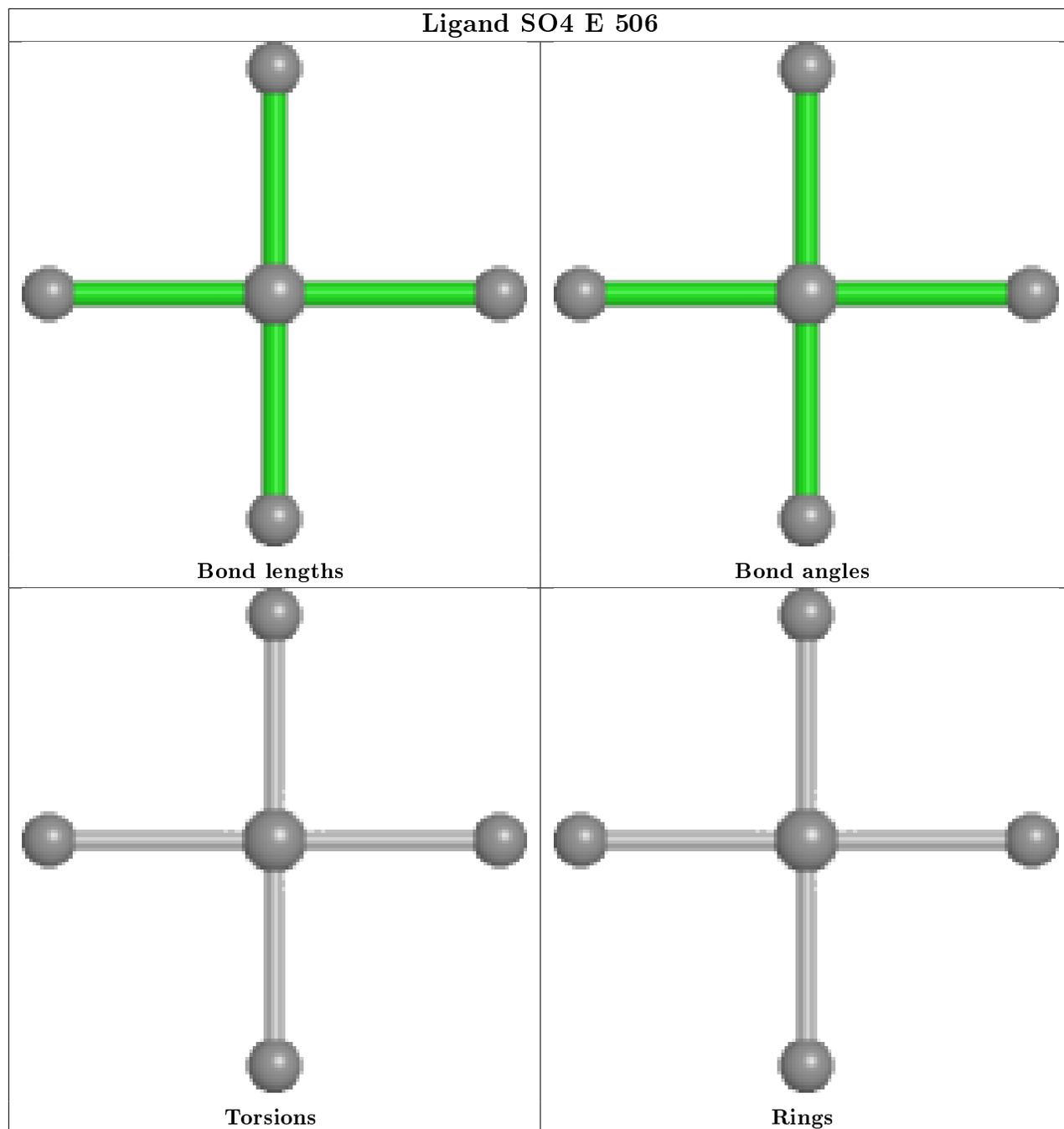


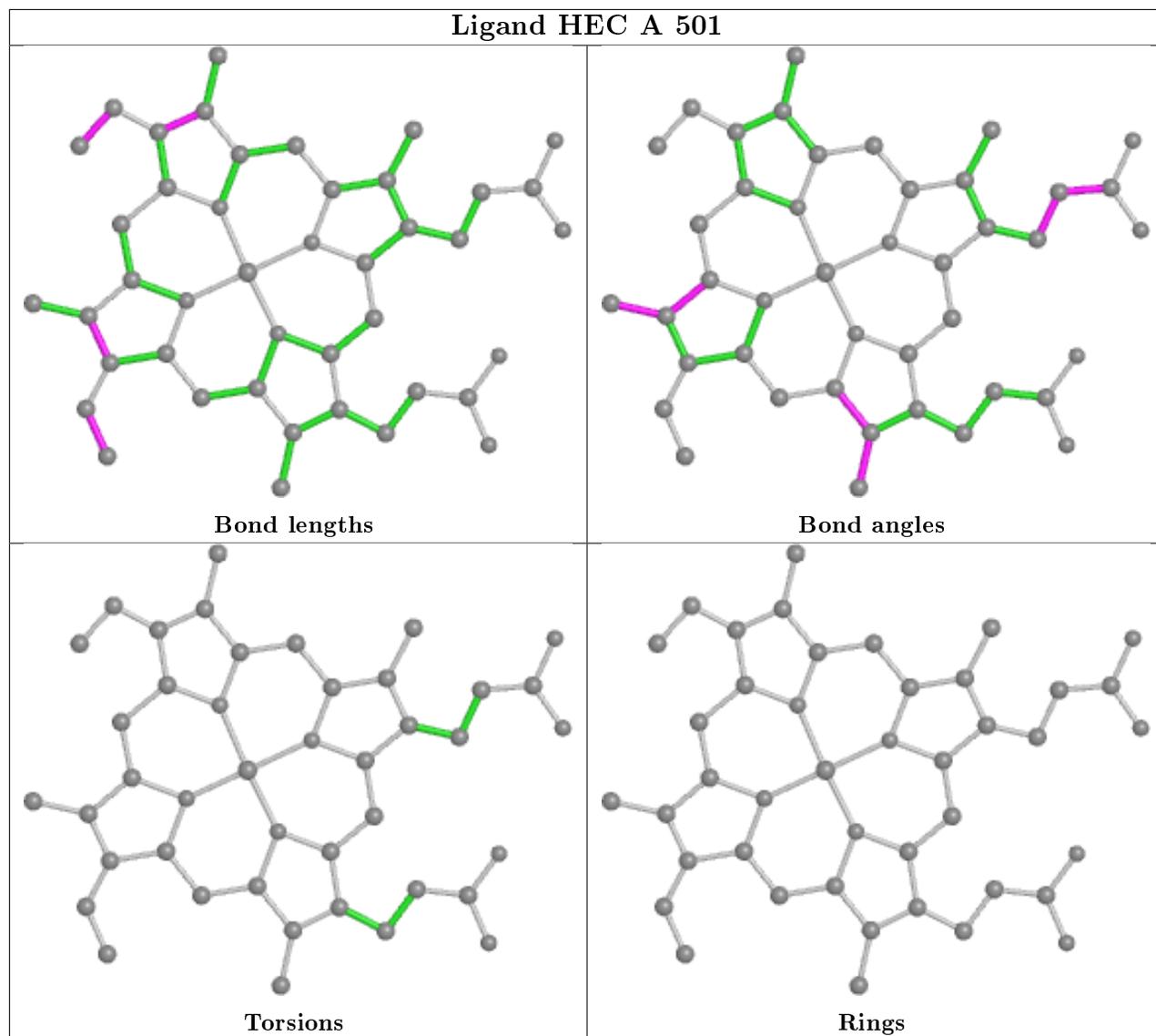


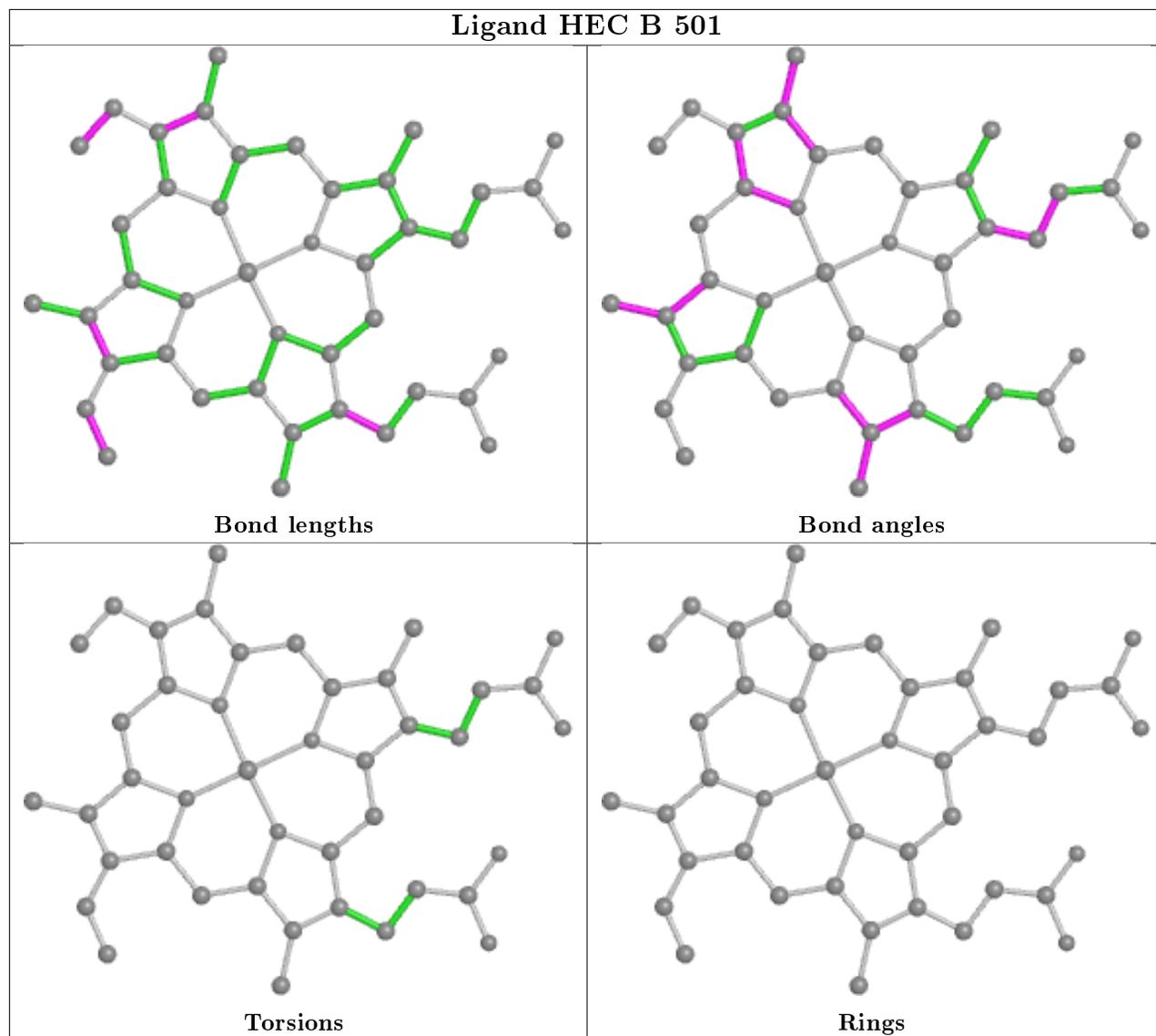


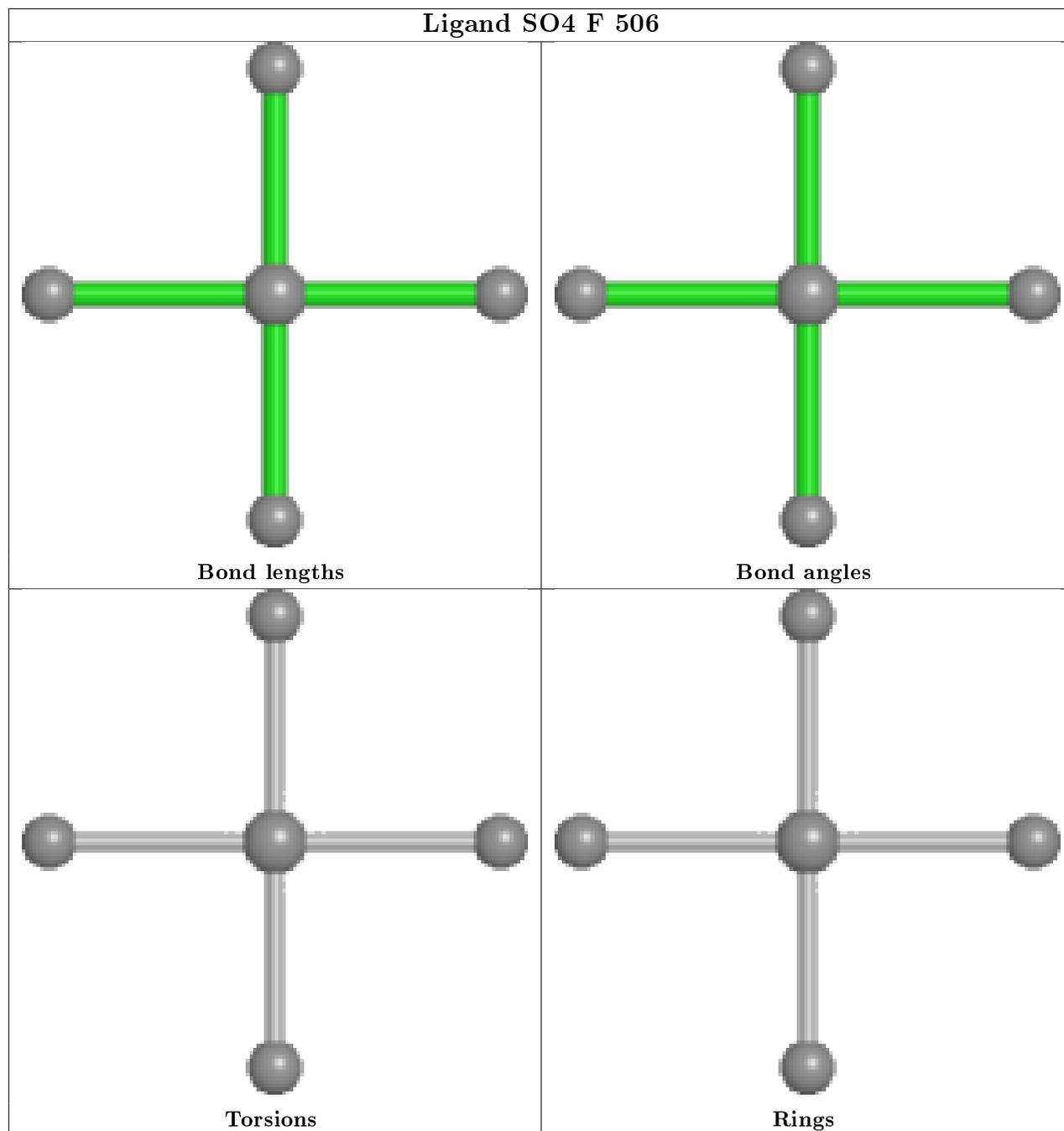


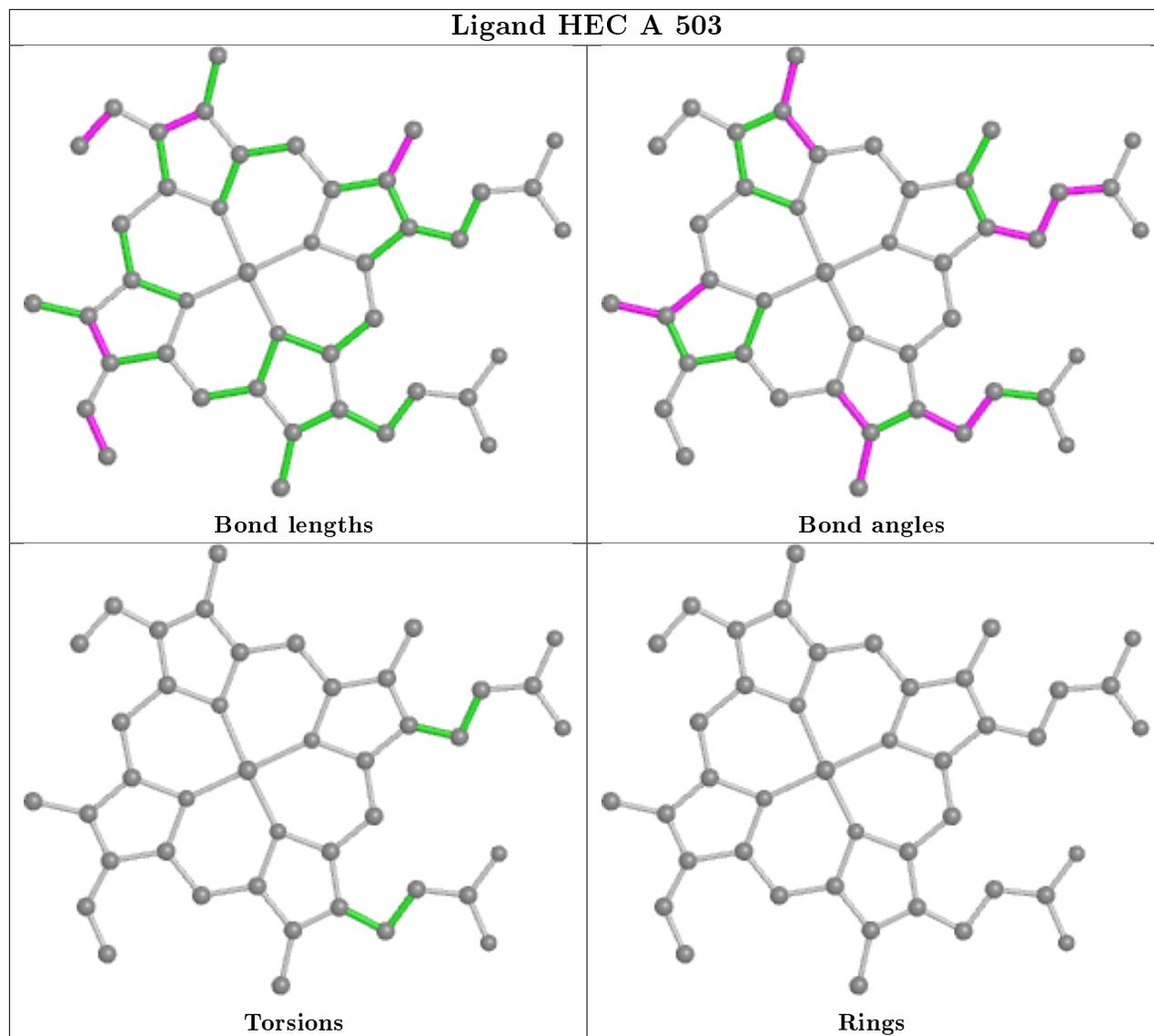


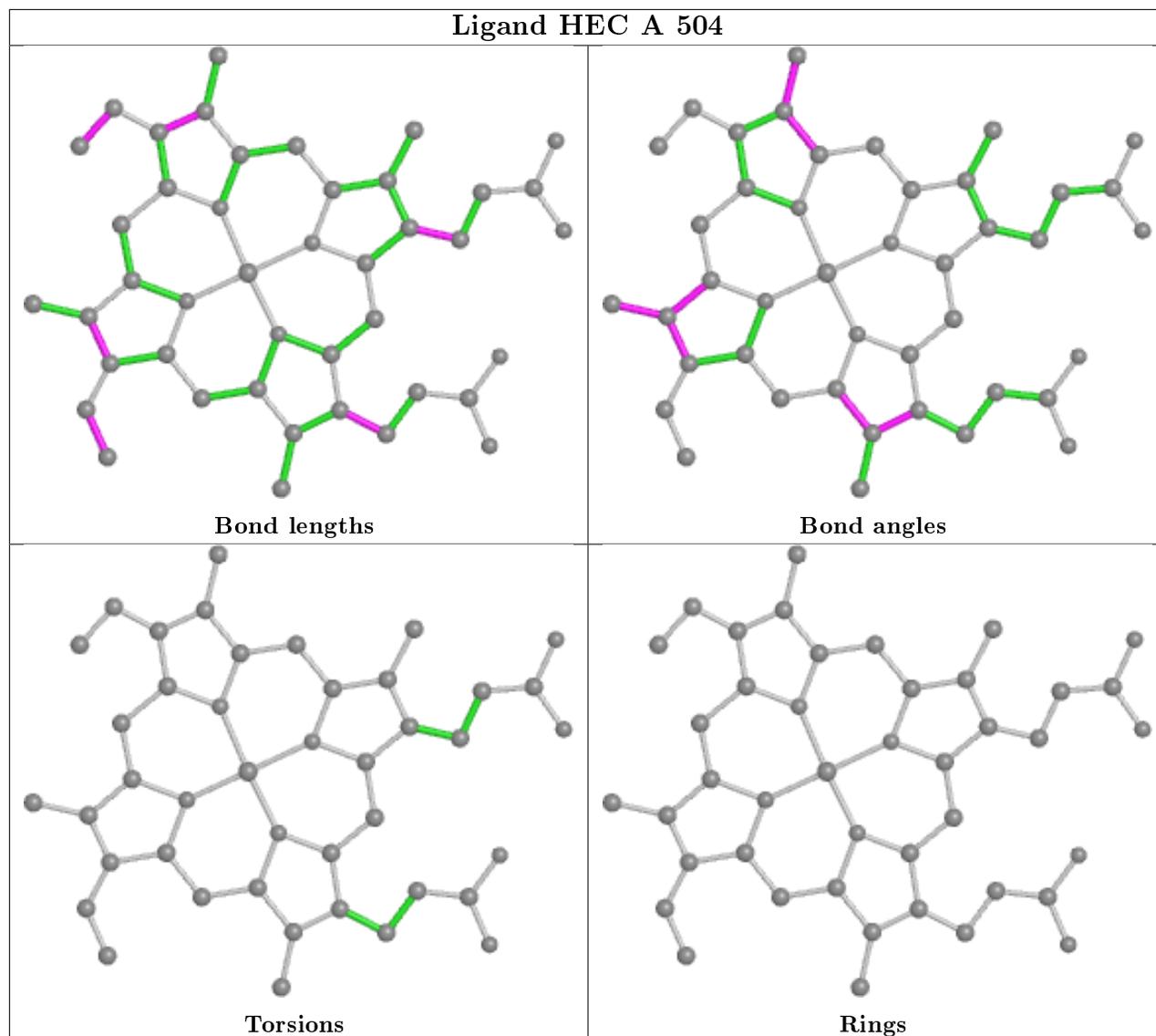


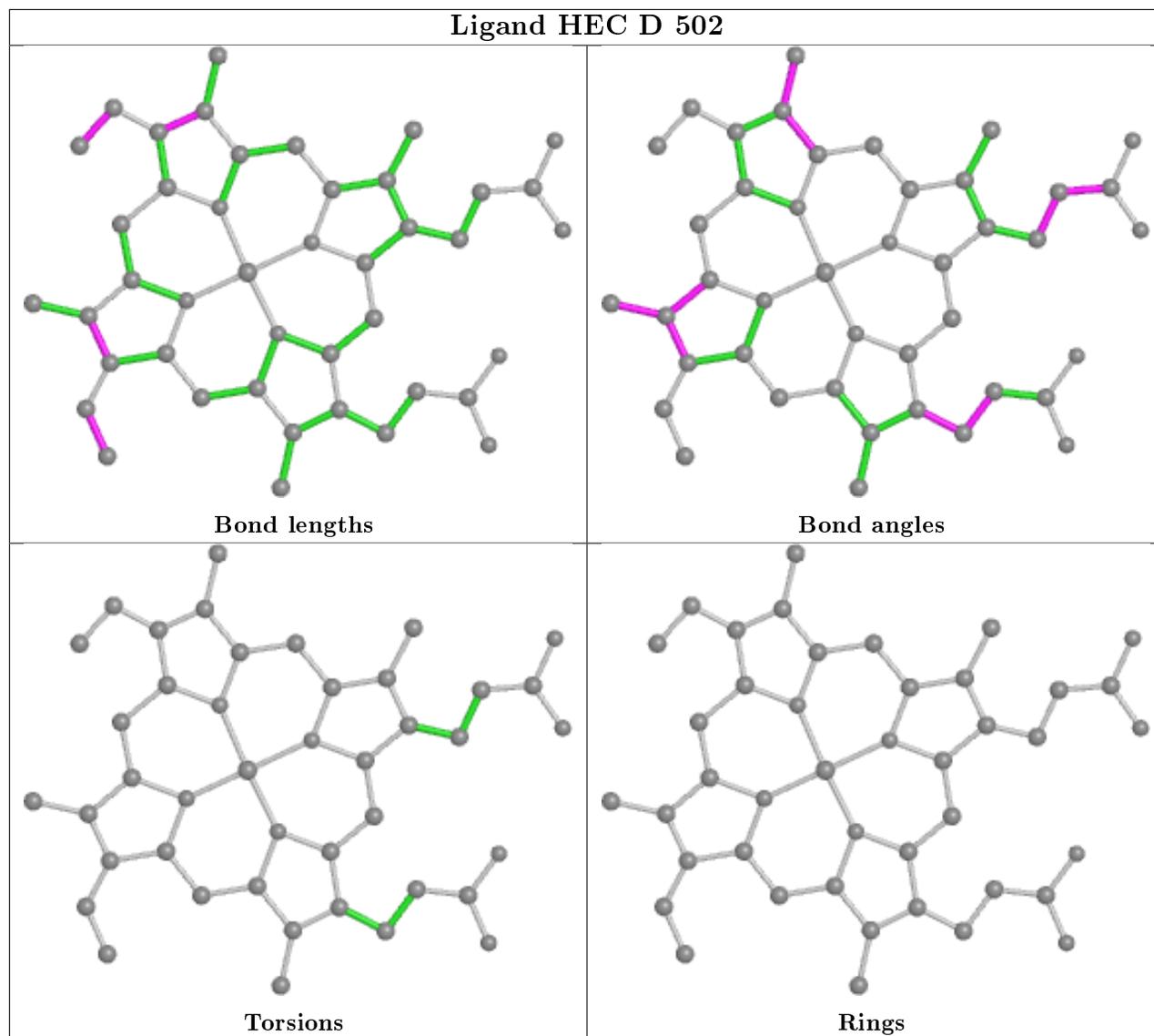


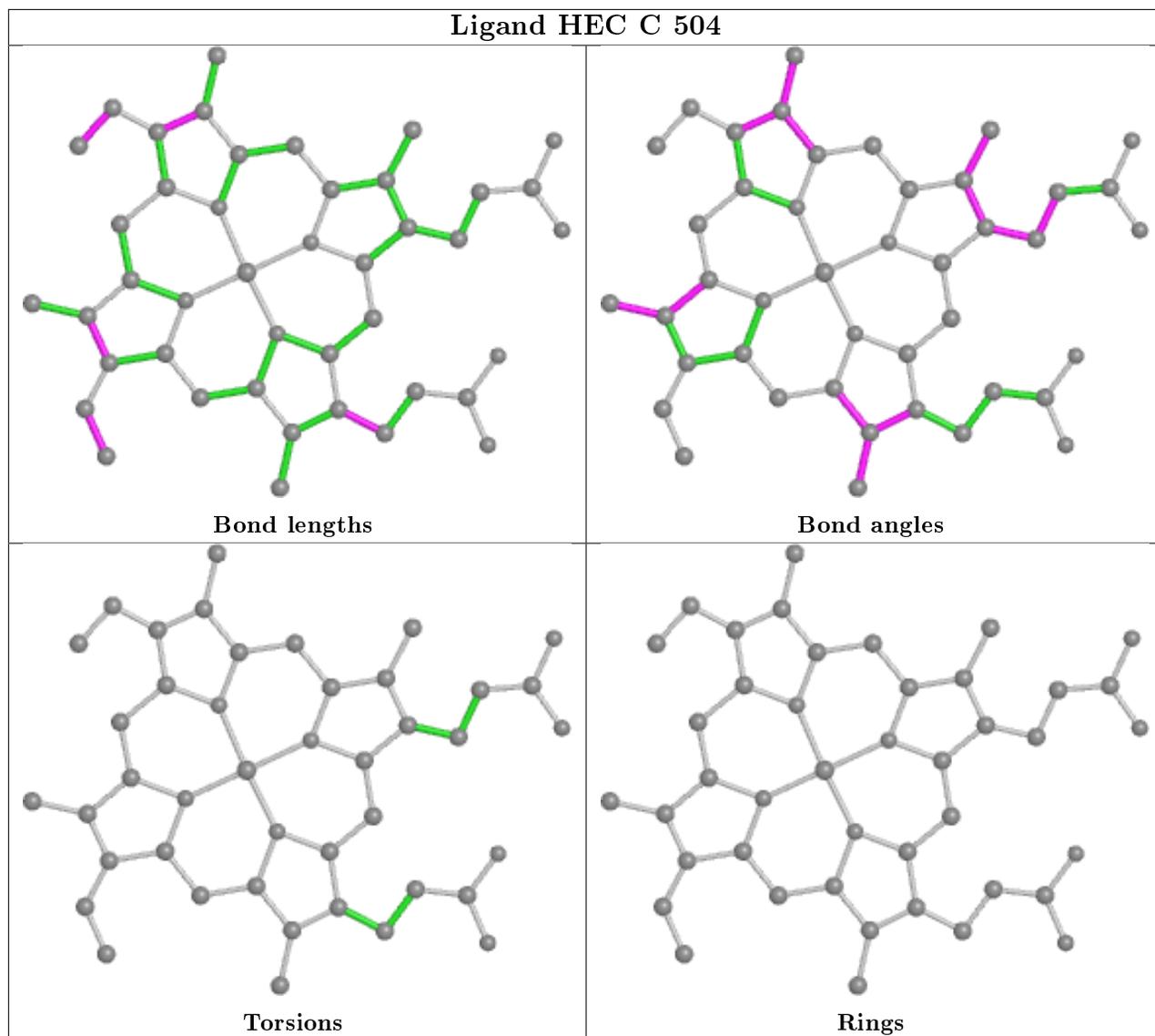


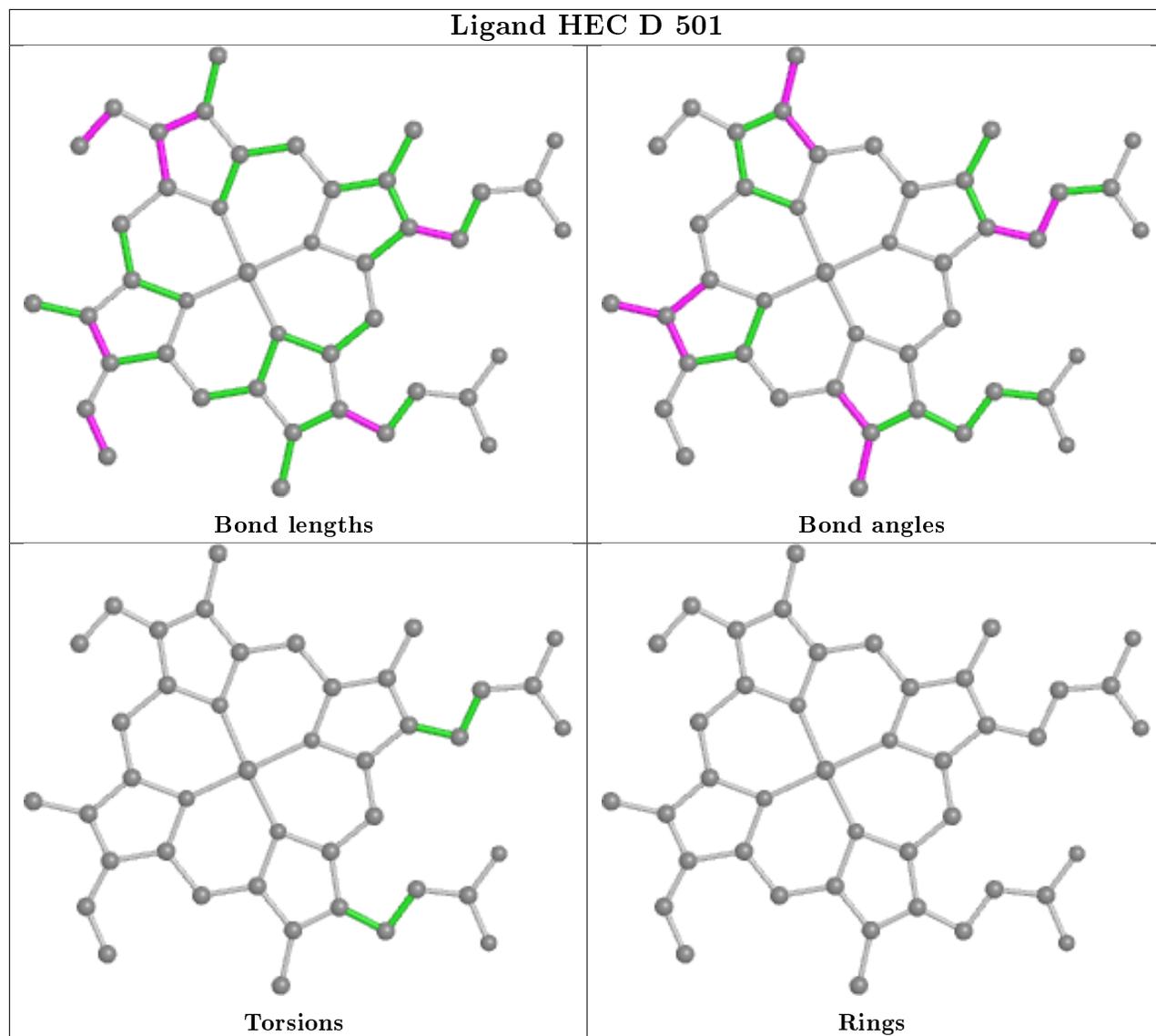


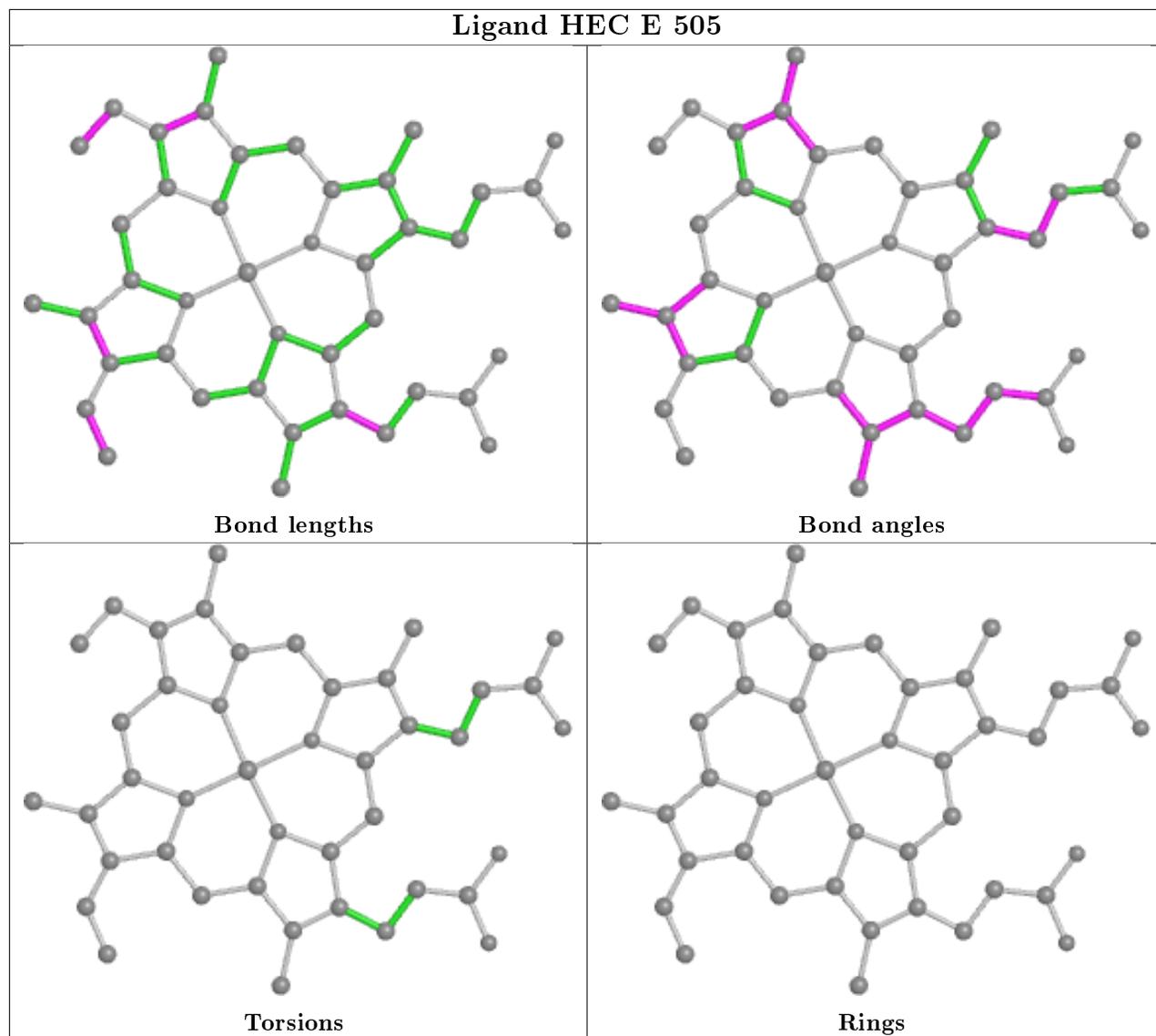


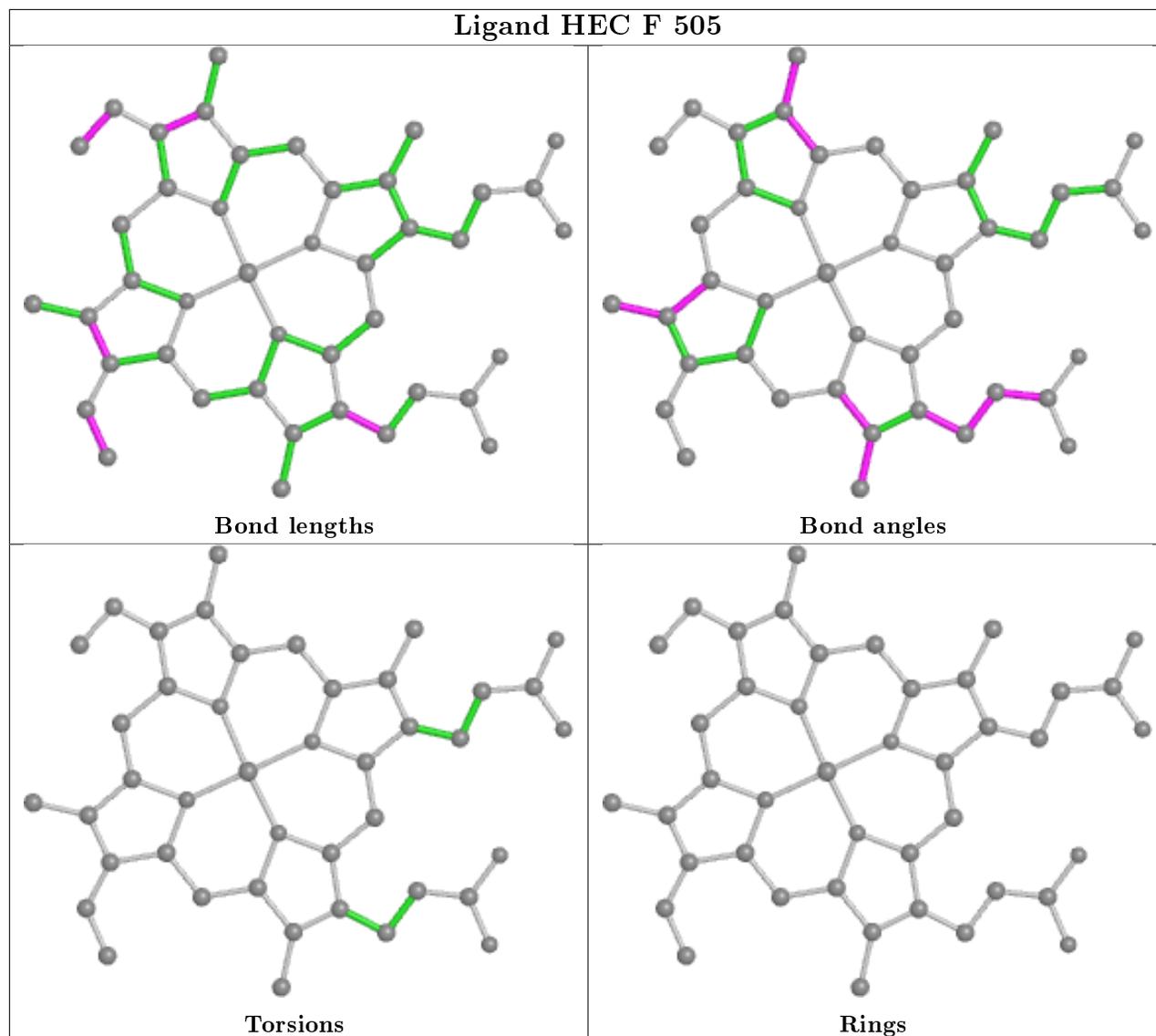


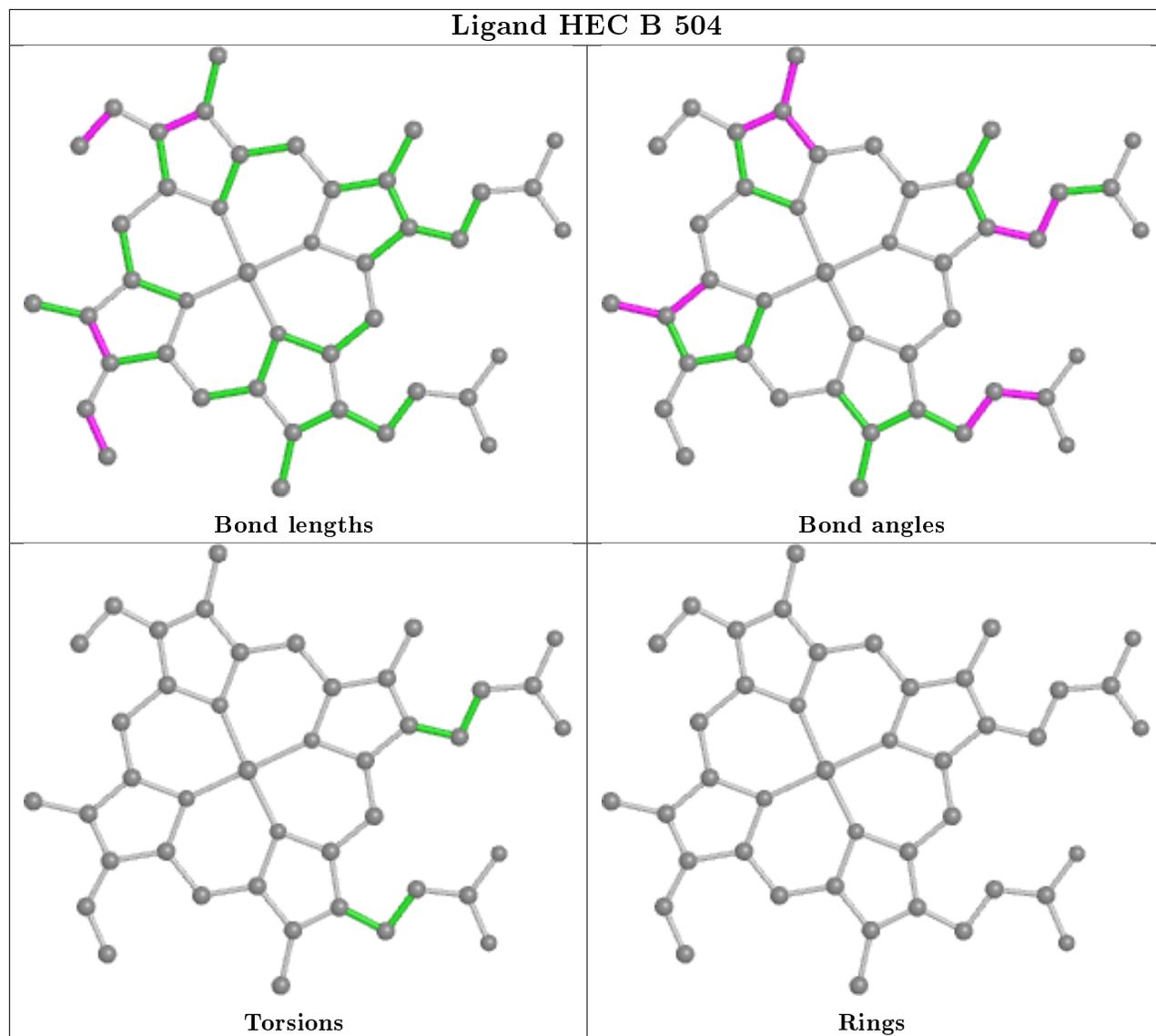


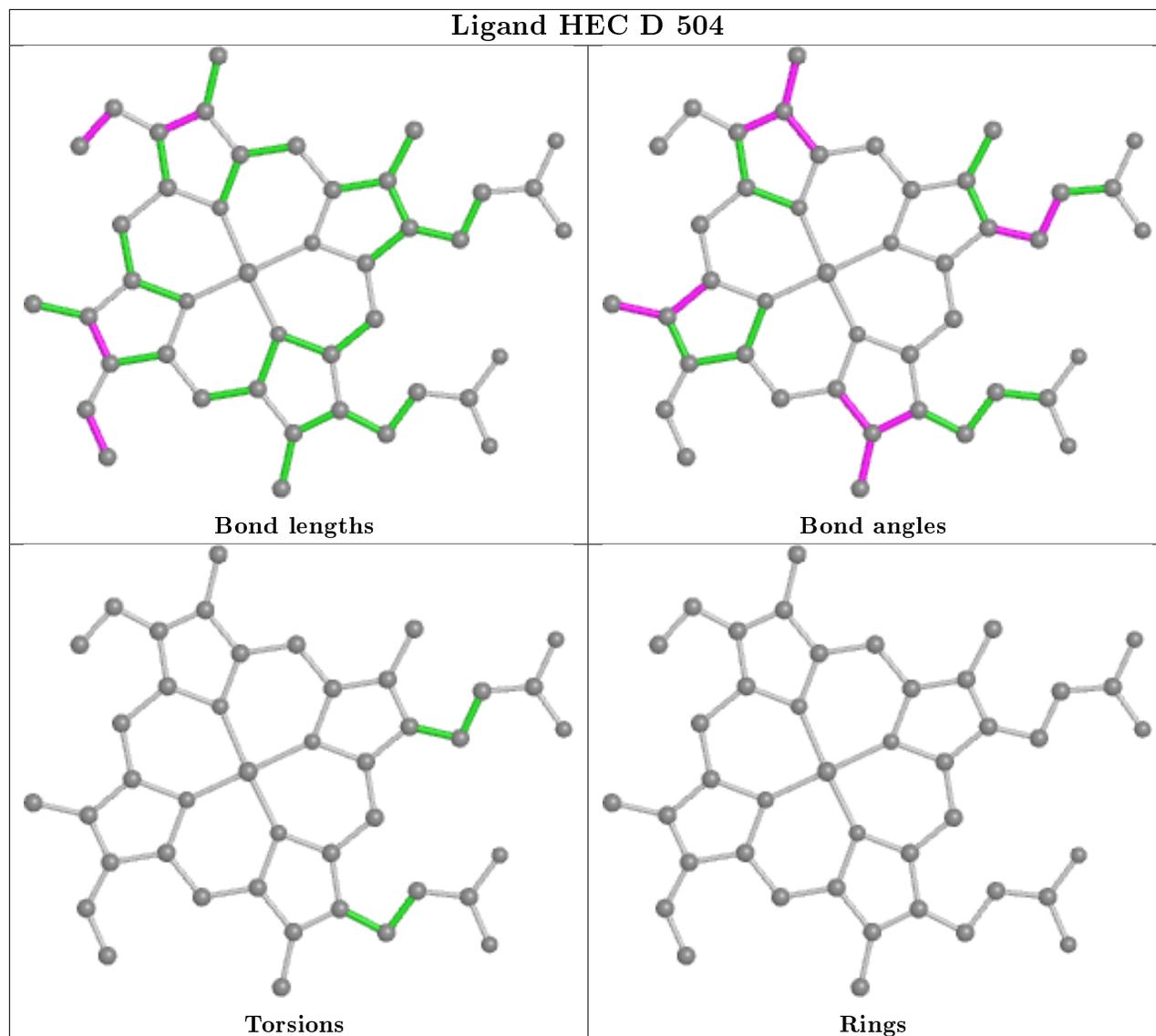


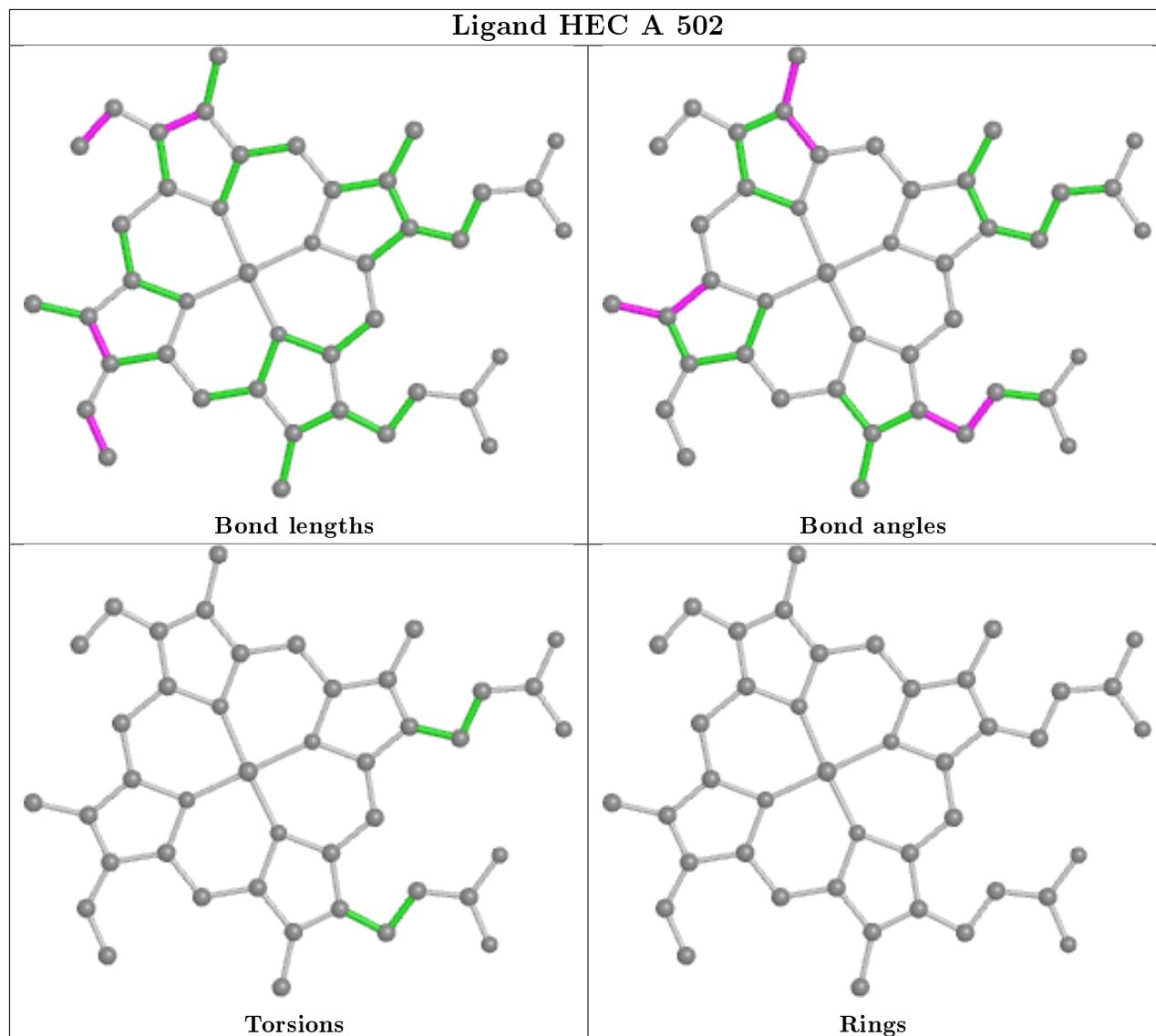


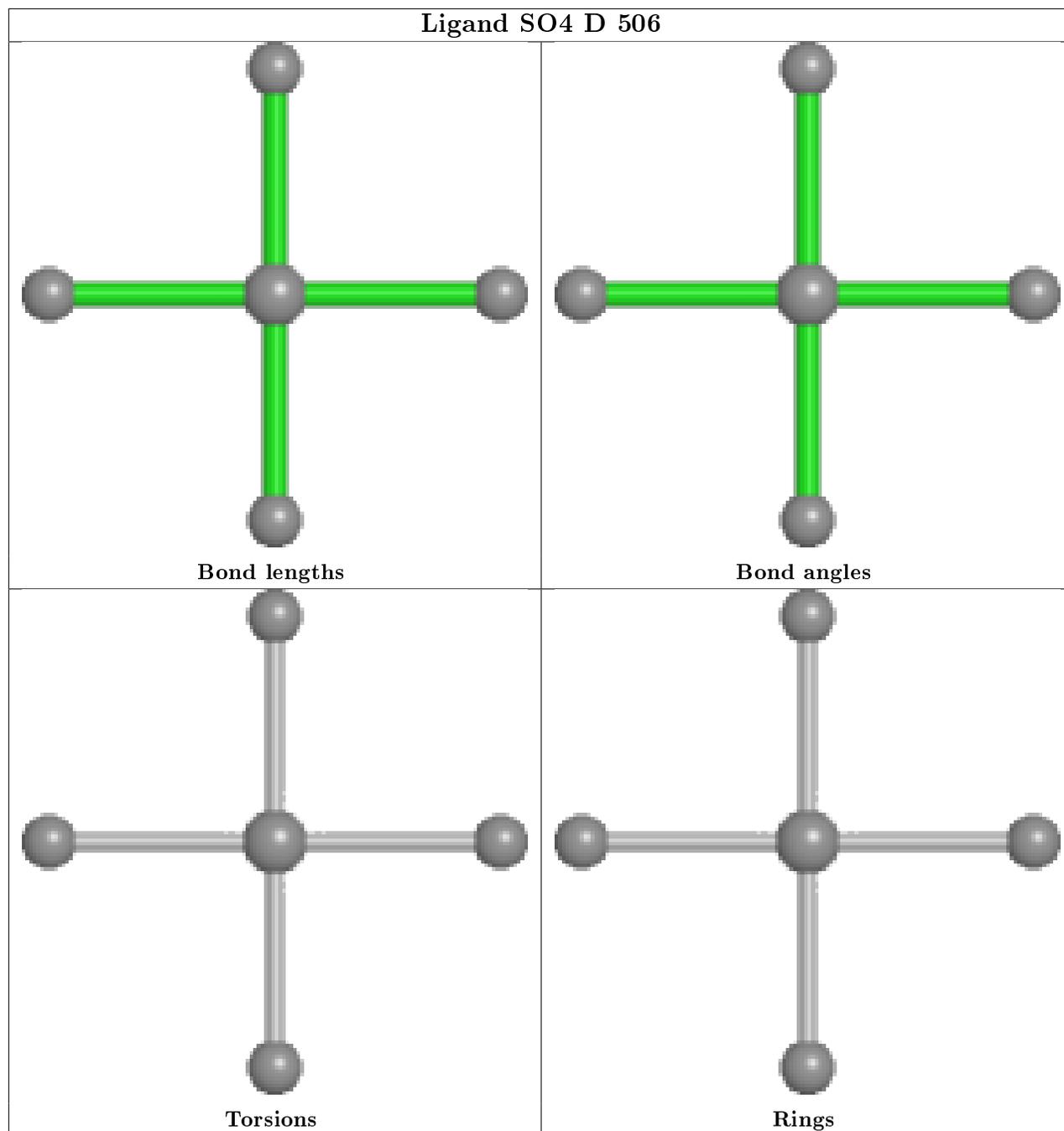


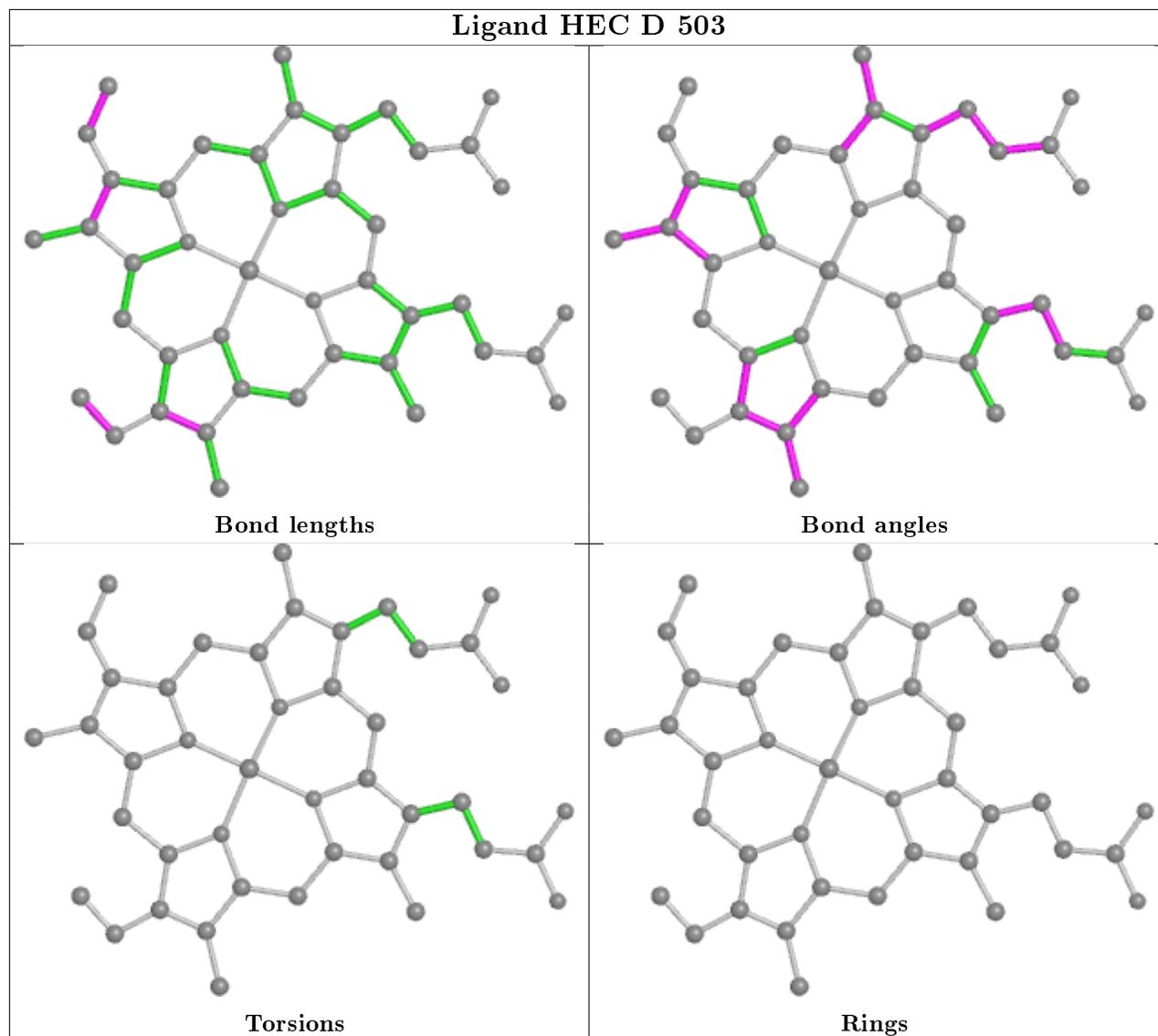


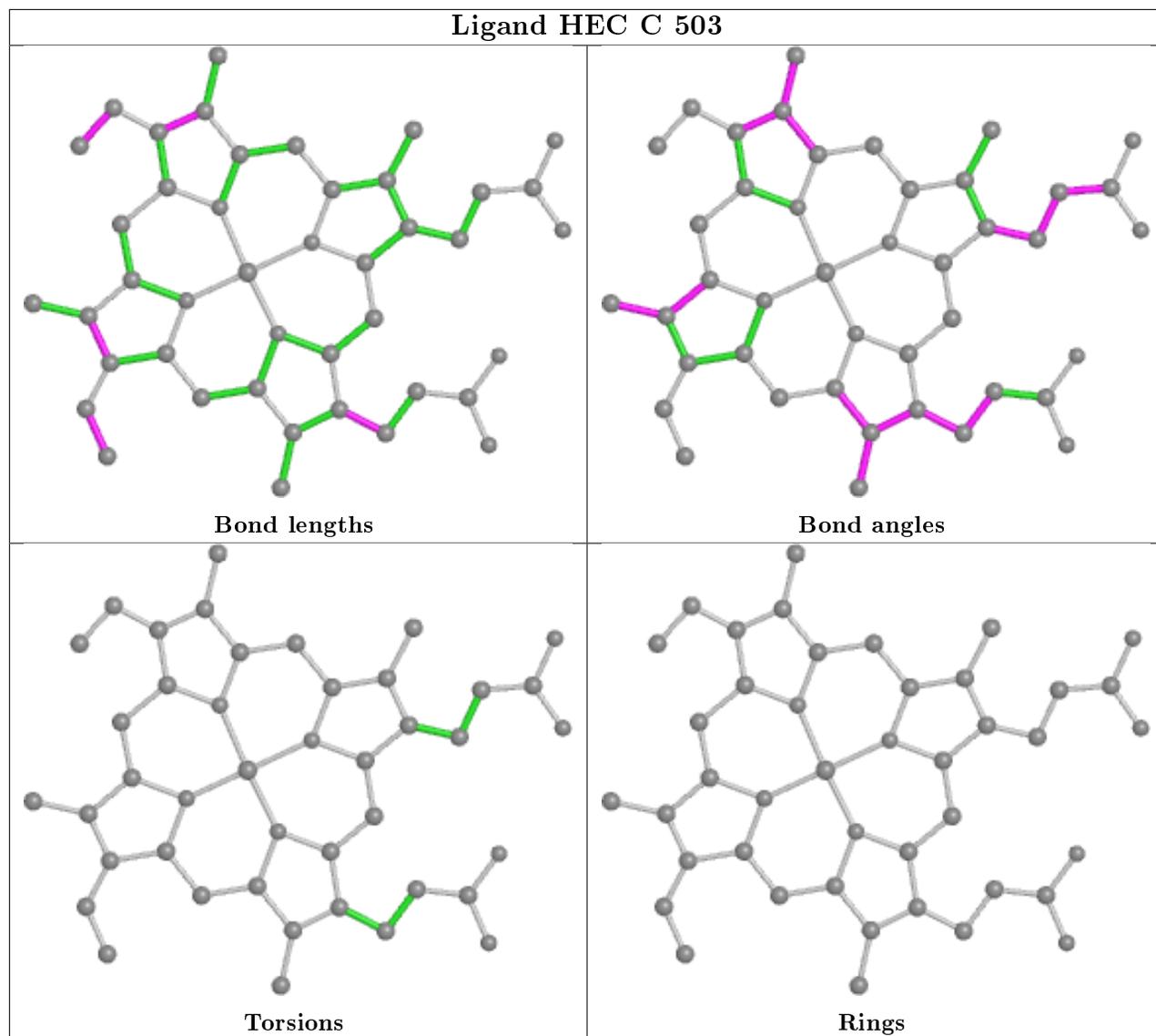


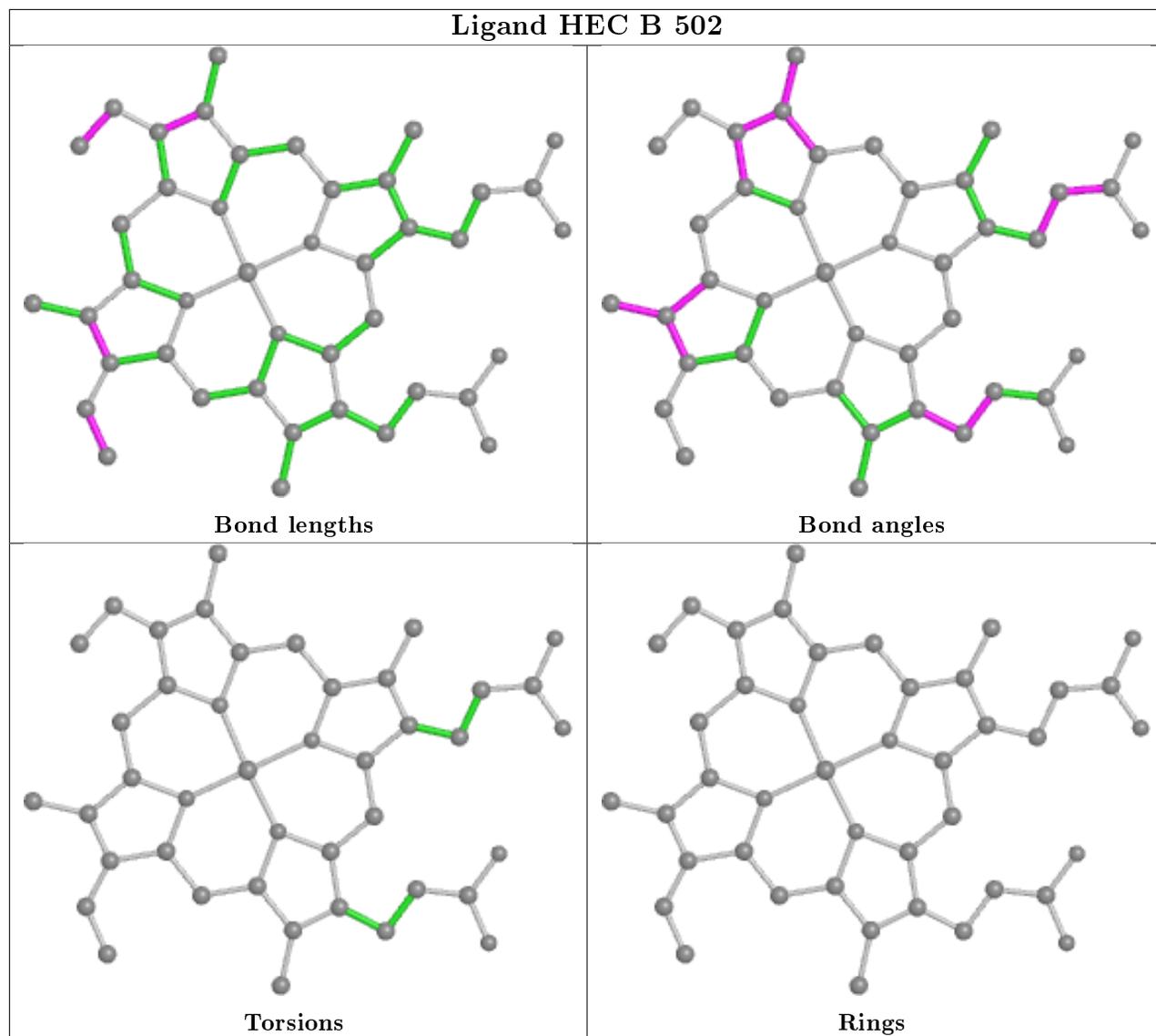


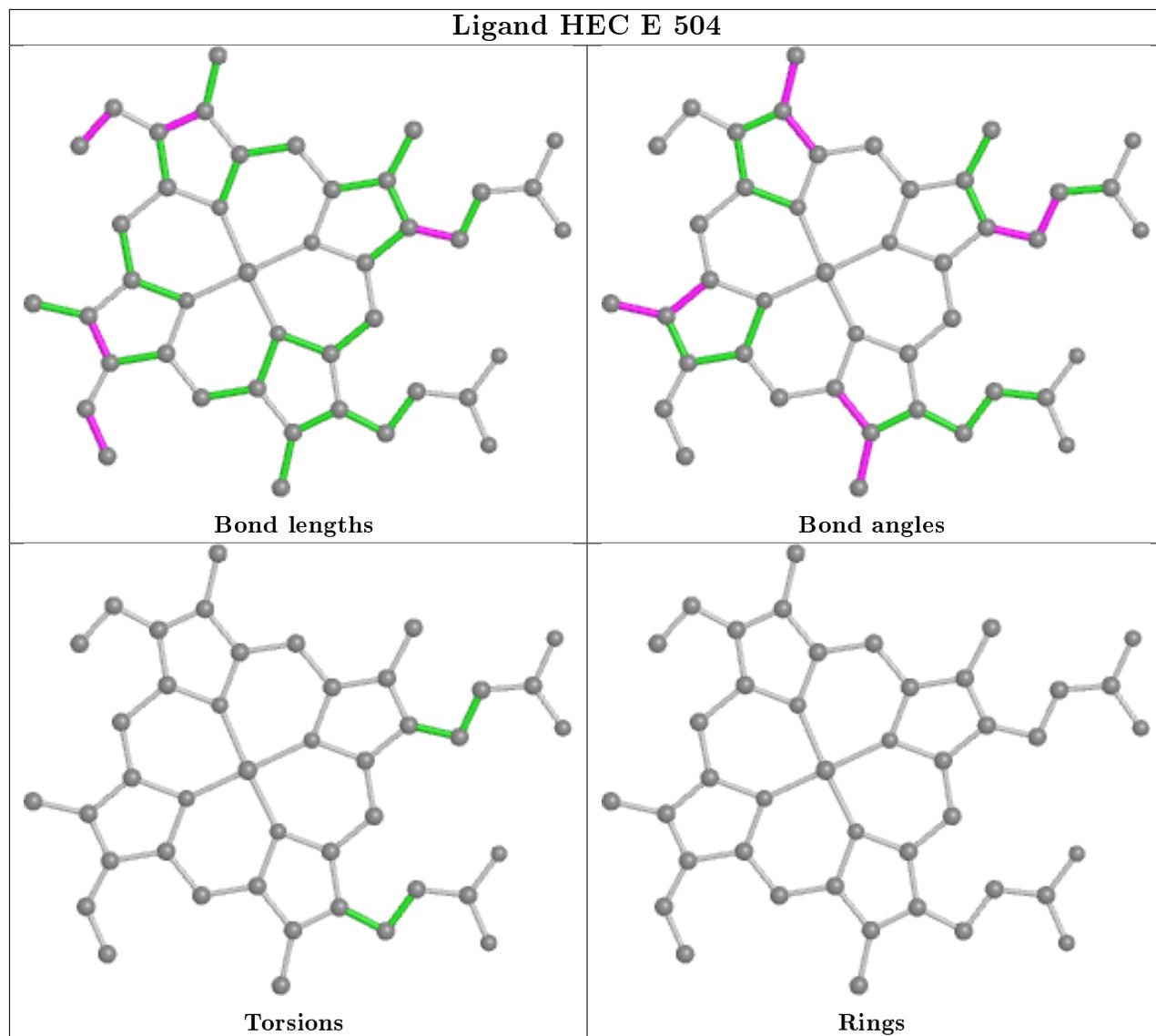


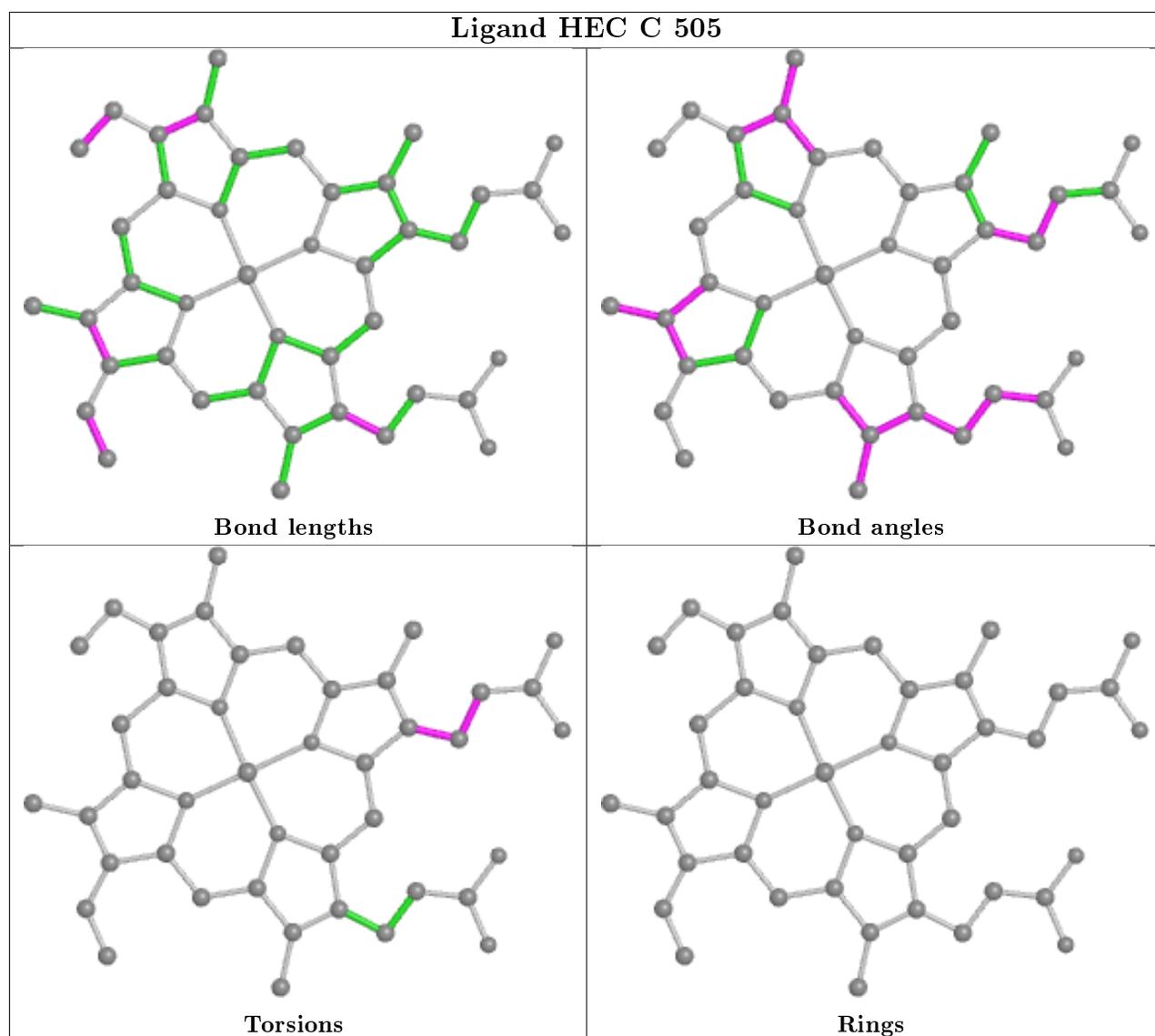












5.7 Other polymers [\(i\)](#)

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	443/482 (91%)	-0.19	6 (1%) 75 81	18, 28, 45, 64	0
1	B	444/482 (92%)	-0.22	5 (1%) 80 85	17, 28, 44, 91	0
1	C	442/482 (91%)	0.08	21 (4%) 30 37	21, 39, 60, 97	0
1	D	444/482 (92%)	0.17	25 (5%) 24 29	21, 40, 63, 99	0
1	E	443/482 (91%)	0.32	29 (6%) 18 22	28, 43, 71, 93	0
1	F	441/482 (91%)	0.41	41 (9%) 8 10	32, 48, 72, 91	0
All	All	2657/2892 (91%)	0.09	127 (4%) 30 37	17, 38, 64, 99	0

The worst 5 of 127 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	307	VAL	8.3
1	C	309	SER	6.3
1	C	310	LYS	6.0
1	F	376	ALA	5.7
1	B	310	LYS	5.3

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](#)

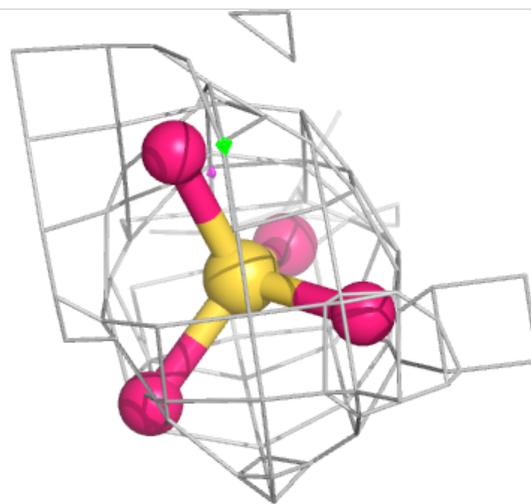
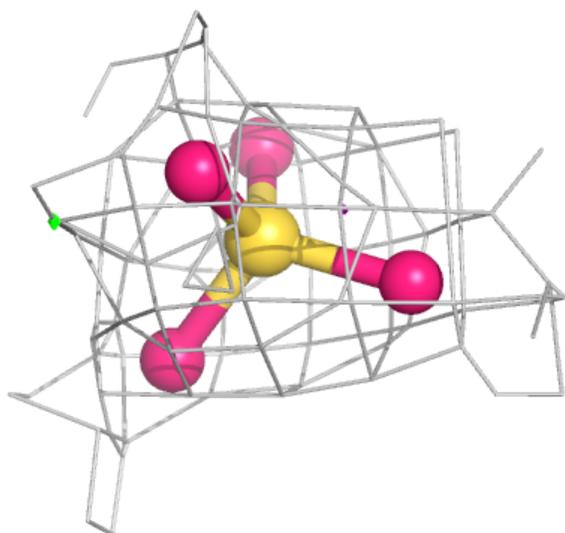
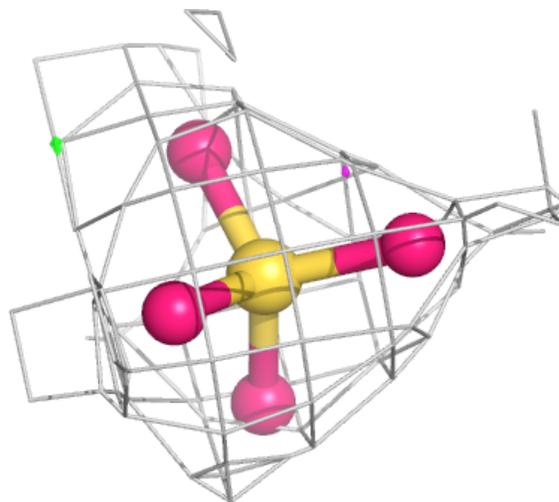
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	C	506	5/5	0.94	0.23	29,30,37,37	5
3	SO4	F	506	5/5	0.95	0.28	45,46,52,54	5
3	SO4	D	506	5/5	0.95	0.20	30,35,38,43	5
2	HEC	E	501	43/43	0.96	0.20	28,36,44,46	0
2	HEC	E	503	43/43	0.96	0.18	26,35,44,51	0
3	SO4	E	506	5/5	0.96	0.22	35,37,40,45	5
2	HEC	F	503	43/43	0.96	0.20	29,38,41,43	0
2	HEC	D	501	43/43	0.96	0.18	26,33,38,44	0
2	HEC	F	501	43/43	0.96	0.20	36,43,50,76	0
2	HEC	D	505	43/43	0.97	0.13	24,32,43,53	0
2	HEC	F	502	43/43	0.97	0.11	32,37,48,67	0
2	HEC	F	504	43/43	0.97	0.18	29,35,39,40	0
2	HEC	E	502	43/43	0.97	0.10	26,31,38,40	0
2	HEC	C	502	43/43	0.97	0.12	30,34,43,51	0
2	HEC	A	505	43/43	0.97	0.12	17,27,39,49	0
2	HEC	B	505	43/43	0.97	0.11	17,26,34,39	0
2	HEC	A	504	43/43	0.97	0.18	14,18,23,26	0
2	HEC	D	502	43/43	0.97	0.11	20,32,37,42	0
2	HEC	B	503	43/43	0.97	0.23	15,24,29,39	0
2	HEC	E	505	43/43	0.97	0.11	31,39,49,54	0
2	HEC	F	505	43/43	0.97	0.12	30,35,44,58	0
2	HEC	D	504	43/43	0.97	0.18	15,28,35,38	0
2	HEC	A	502	43/43	0.97	0.12	20,26,32,45	0
3	SO4	A	506	5/5	0.97	0.23	20,23,30,31	5
2	HEC	D	503	43/43	0.97	0.20	22,31,37,49	0
2	HEC	C	503	43/43	0.97	0.19	20,28,32,33	0
2	HEC	B	502	43/43	0.97	0.12	24,32,36,42	0
2	HEC	E	504	43/43	0.97	0.17	25,35,39,41	0
2	HEC	C	505	43/43	0.97	0.12	22,35,44,48	0
2	HEC	A	501	43/43	0.98	0.18	17,23,29,33	0
2	HEC	C	504	43/43	0.98	0.20	19,26,29,31	0
2	HEC	B	501	43/43	0.98	0.19	20,25,28,31	0
3	SO4	B	506	5/5	0.98	0.24	21,23,30,33	5
2	HEC	A	503	43/43	0.98	0.19	16,20,24,29	0
2	HEC	B	504	43/43	0.98	0.20	14,22,26,28	0
2	HEC	C	501	43/43	0.98	0.18	23,30,35,39	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.

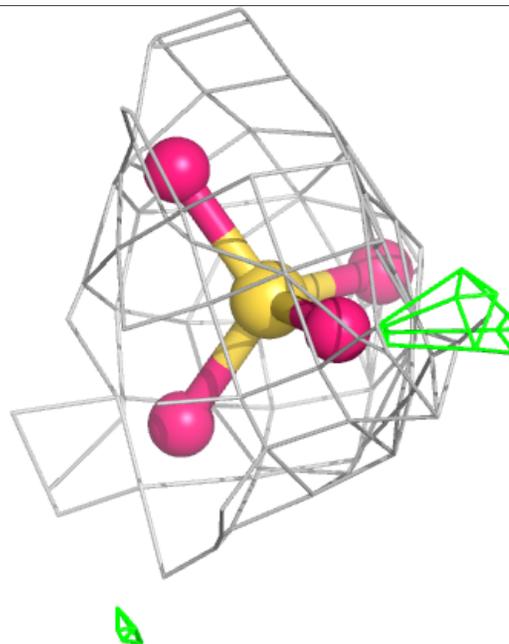
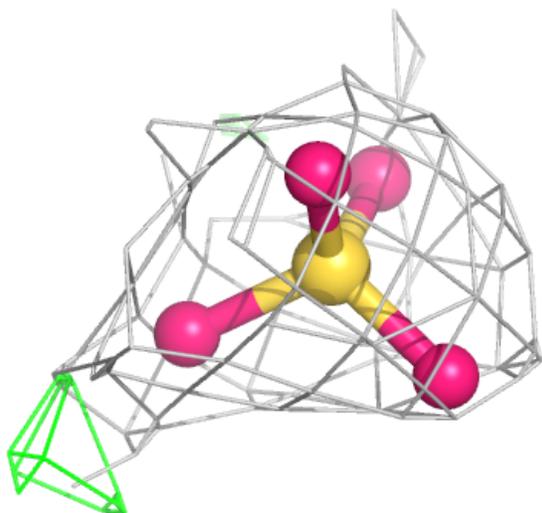
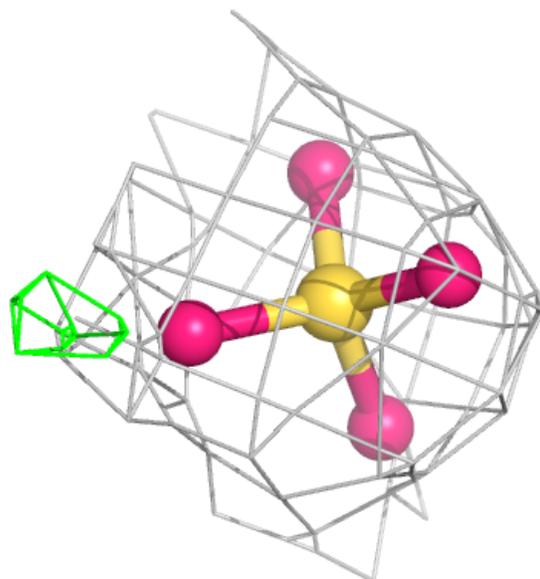
Electron density around SO4 C 506:

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



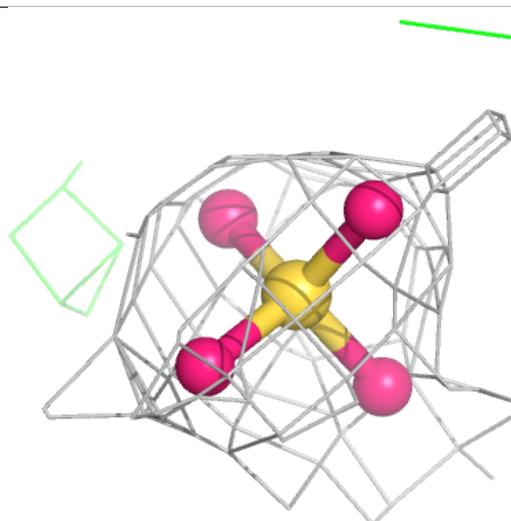
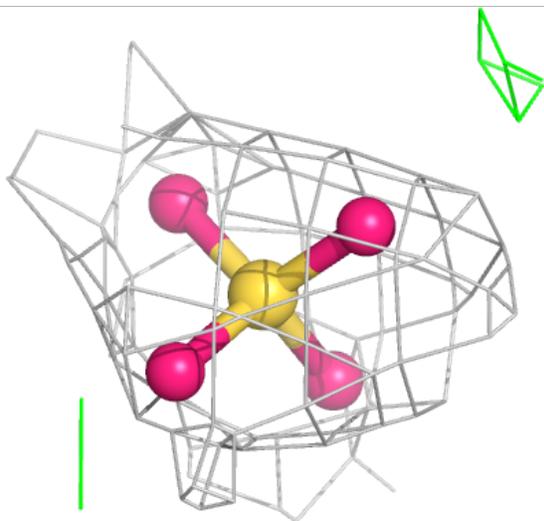
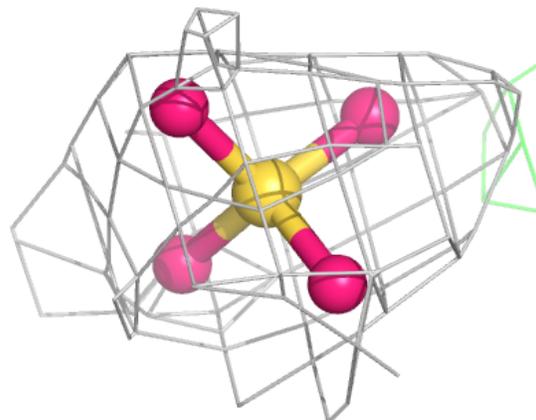
Electron density around SO4 F 506:

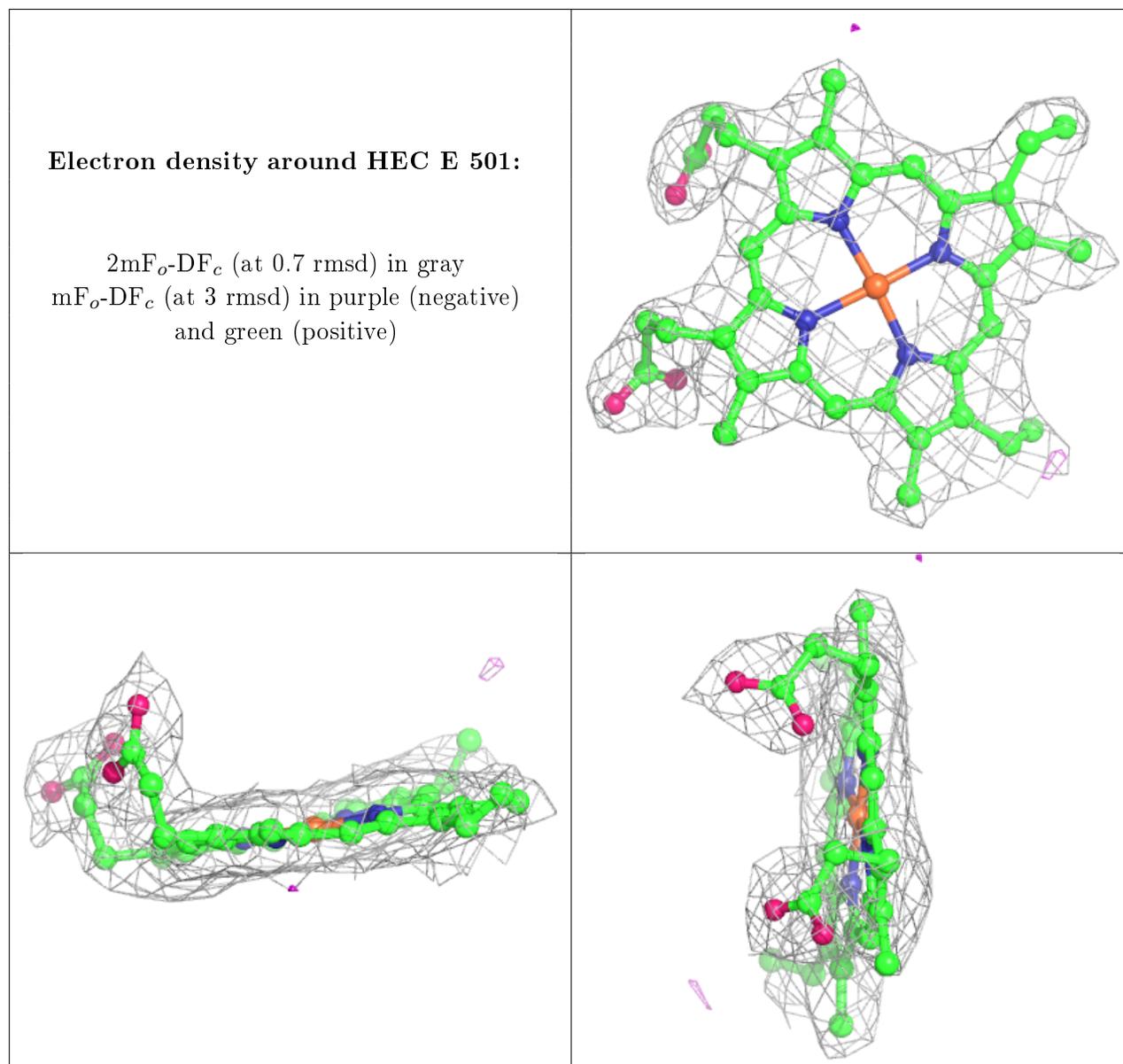
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around SO4 D 506:

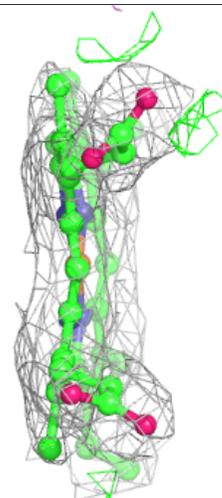
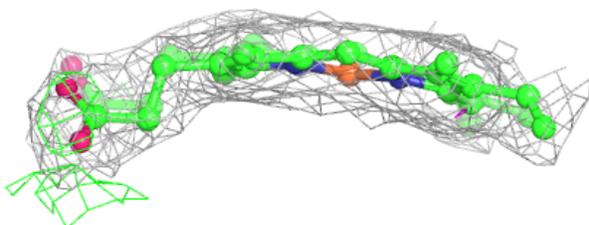
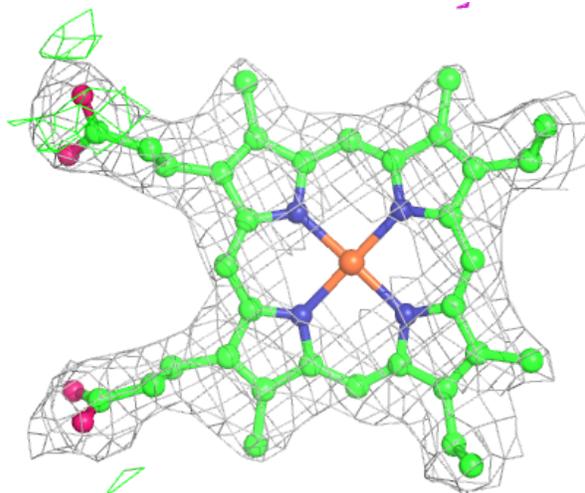
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





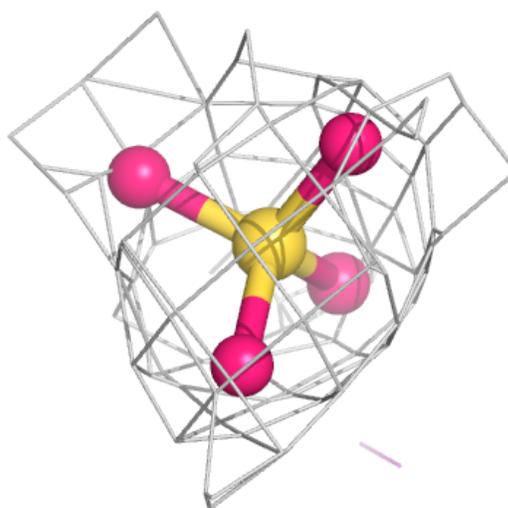
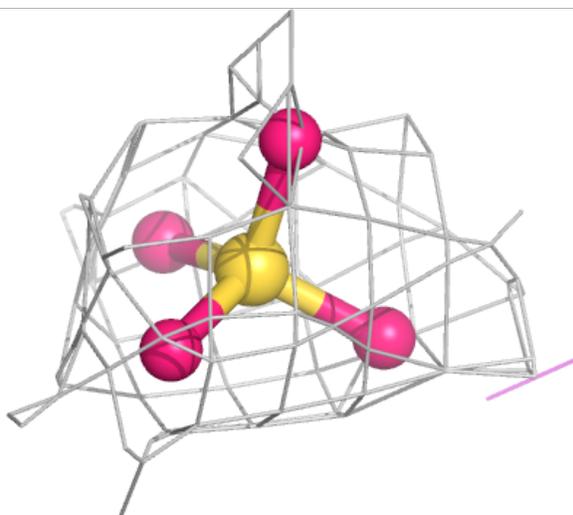
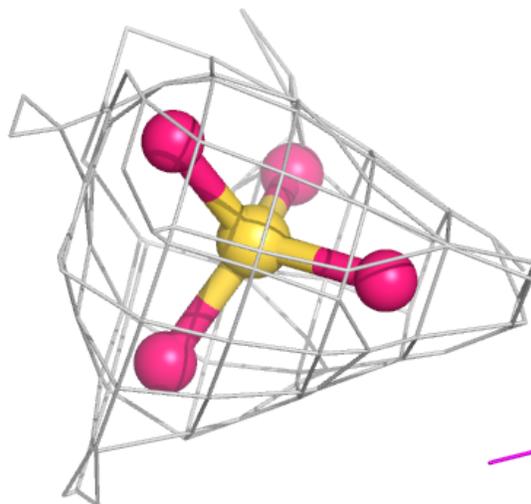
Electron density around HEC E 503:

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



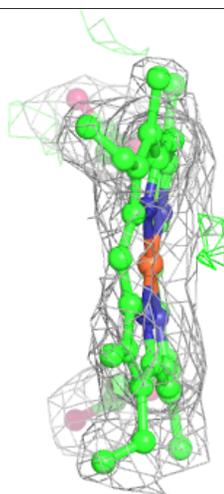
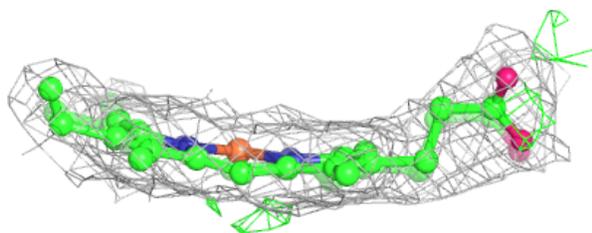
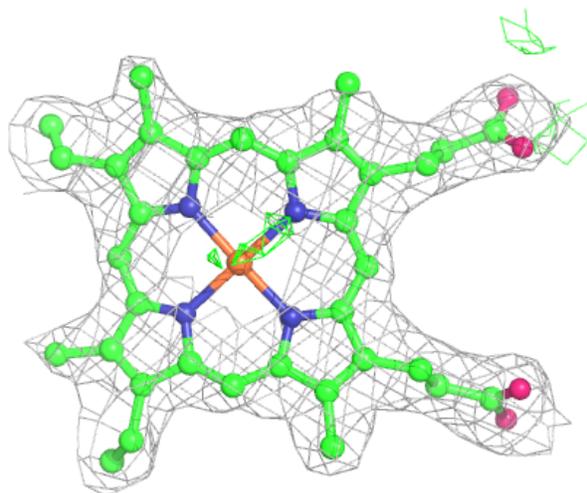
Electron density around SO4 E 506:

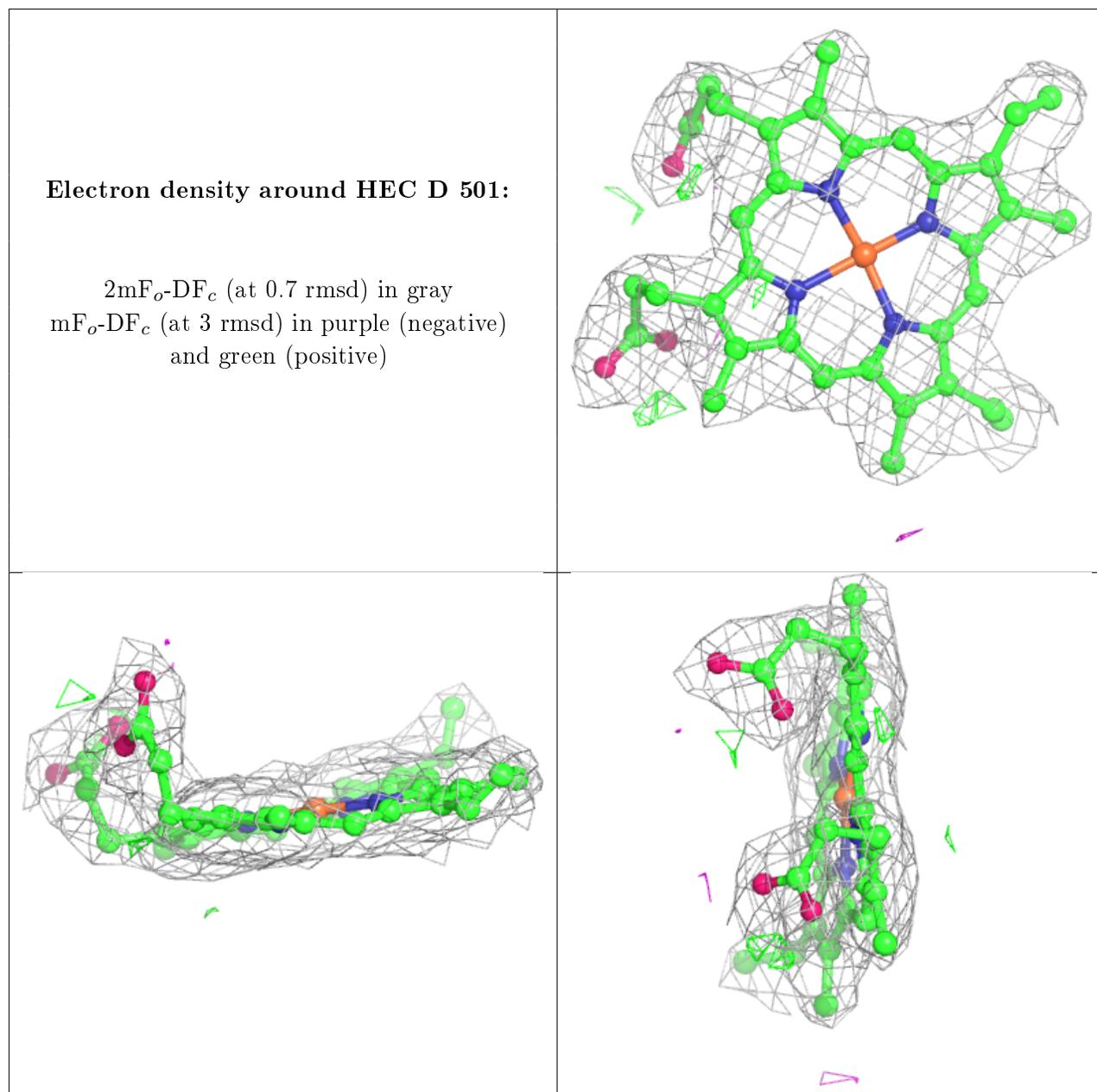
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC F 503:

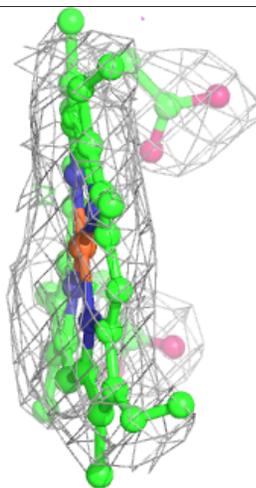
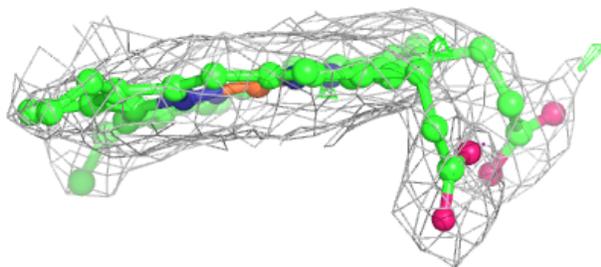
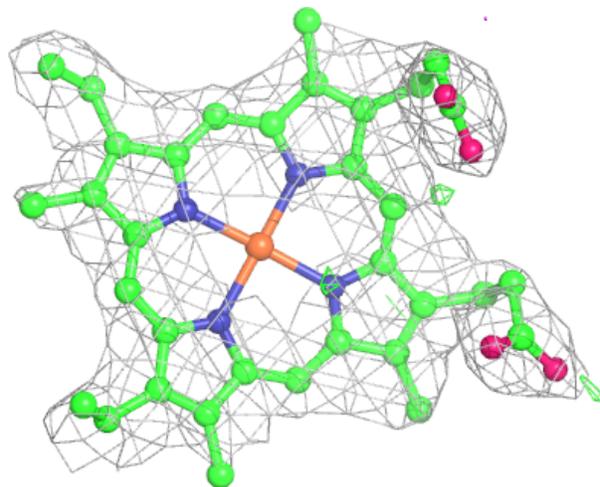
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





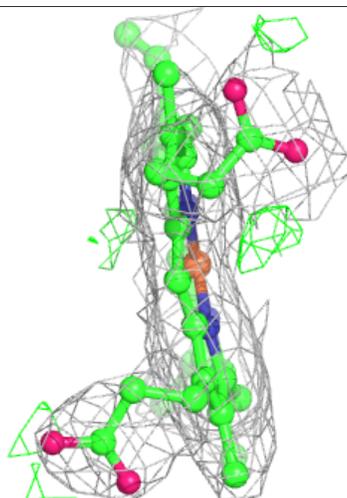
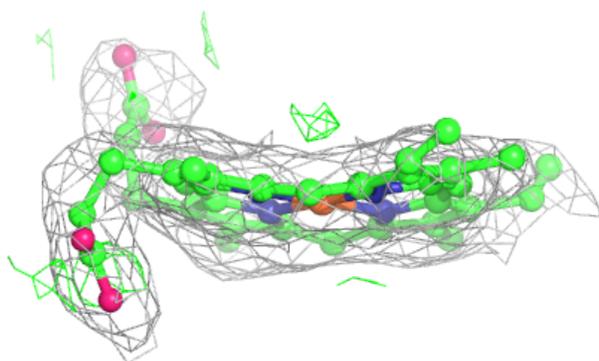
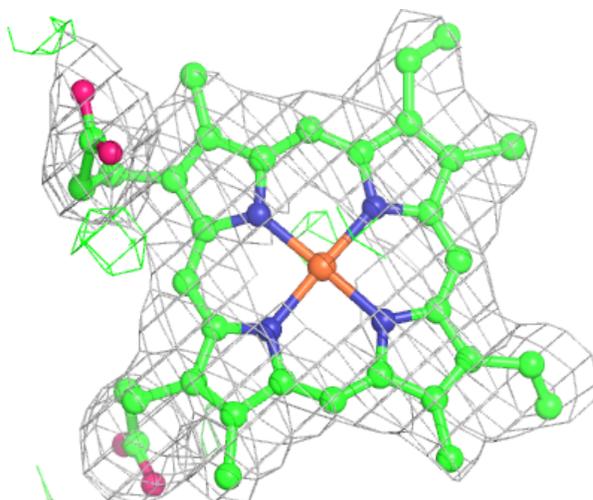
Electron density around HEC F 501:

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



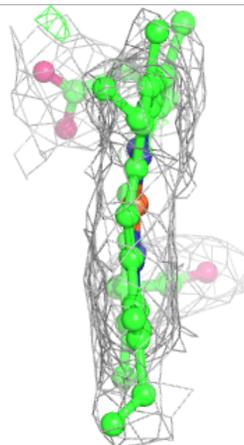
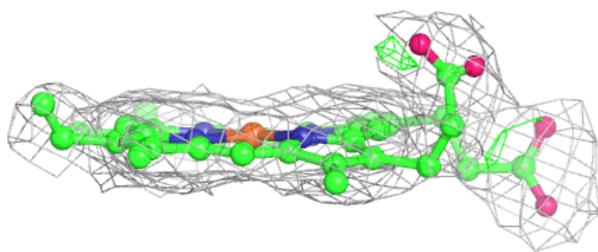
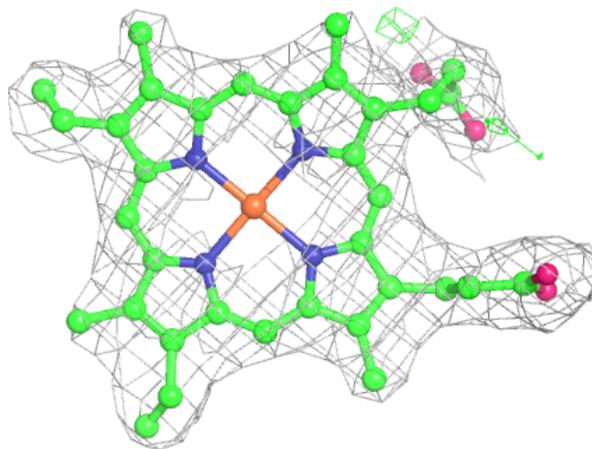
Electron density around HEC D 505:

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



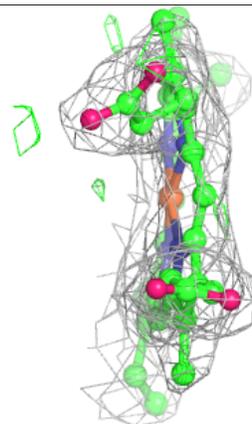
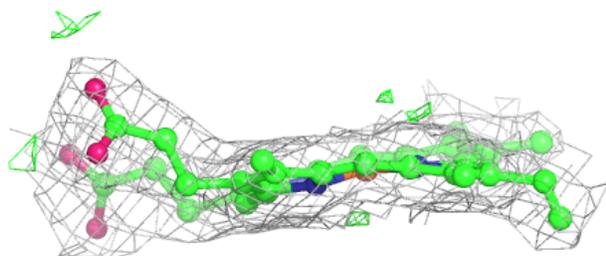
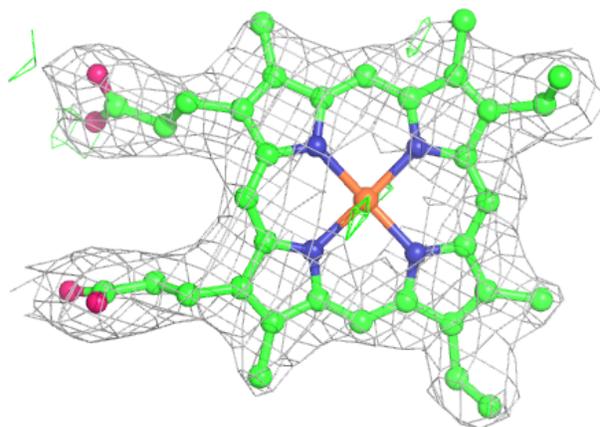
Electron density around HEC F 502:

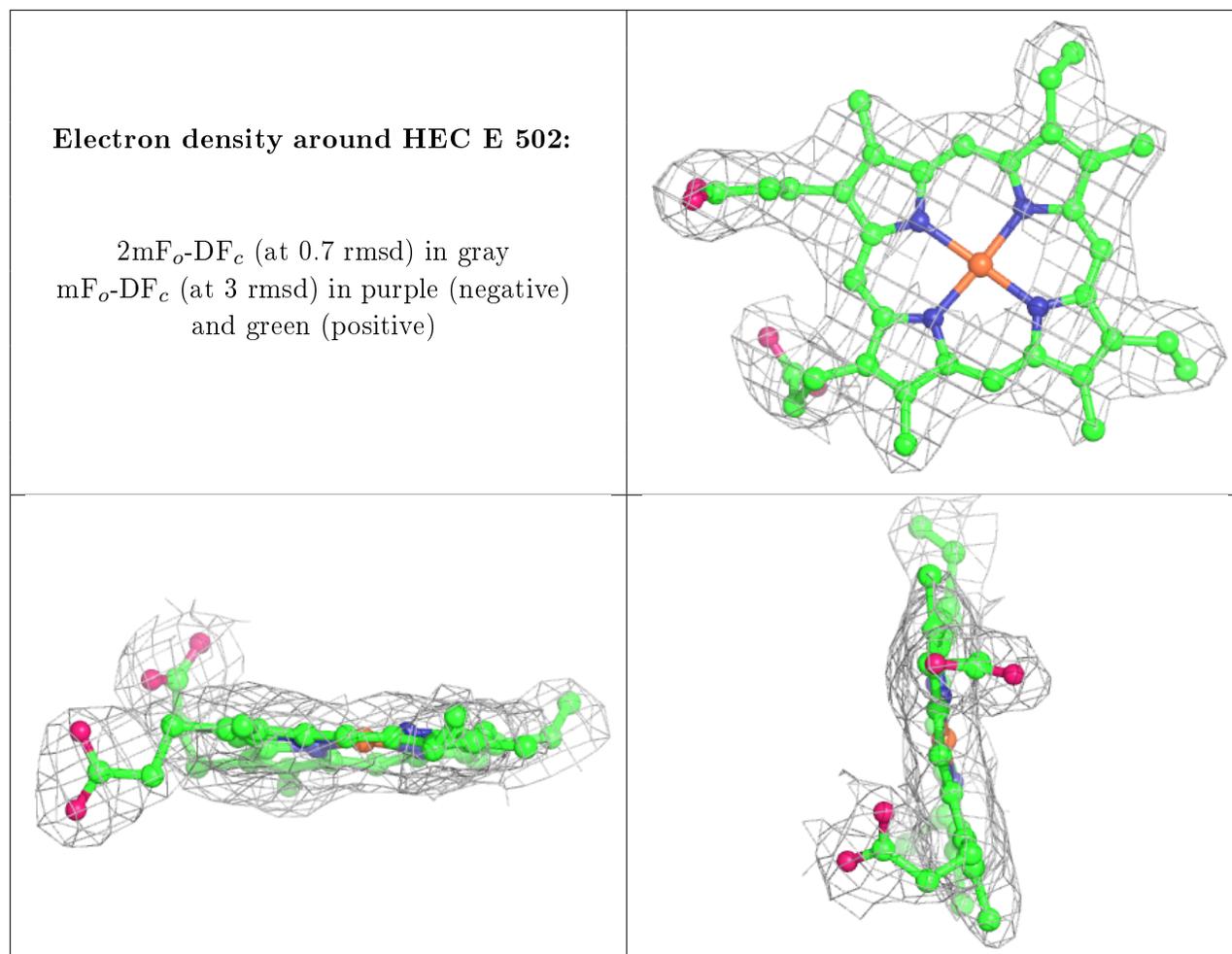
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

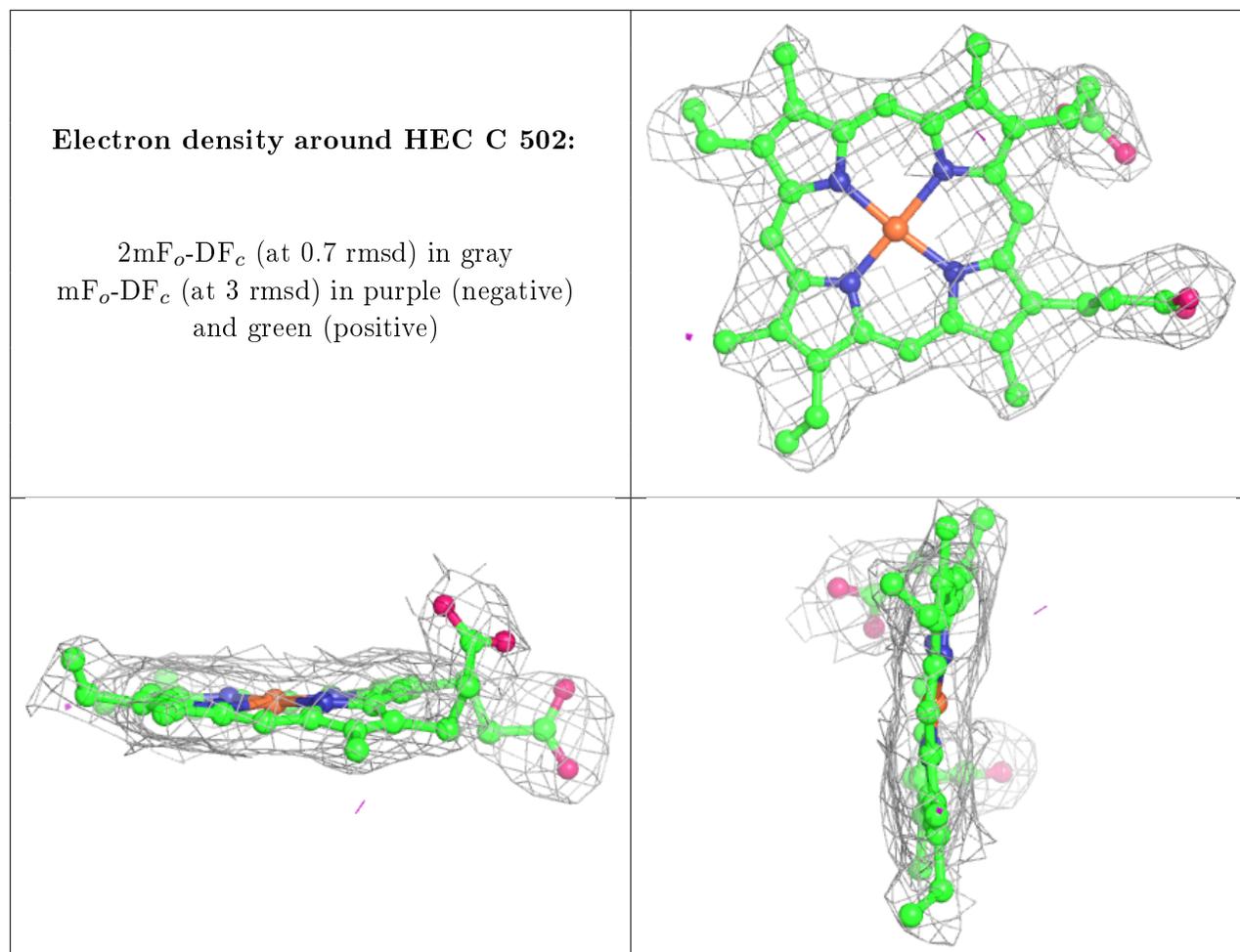


Electron density around HEC F 504:

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

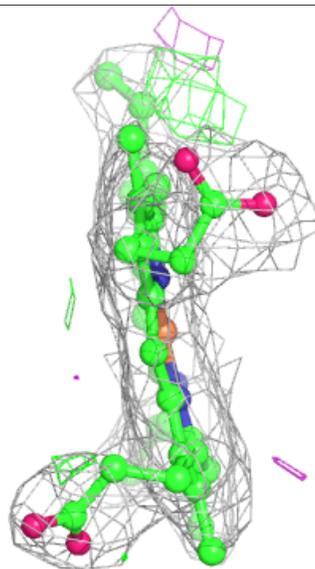
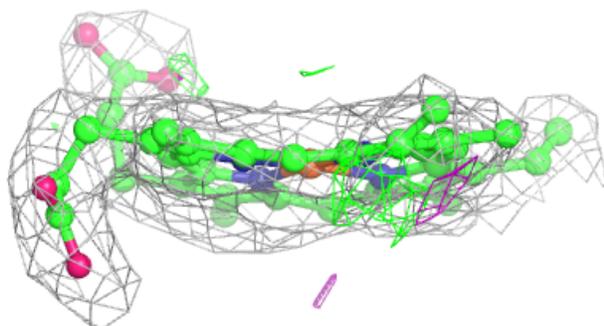
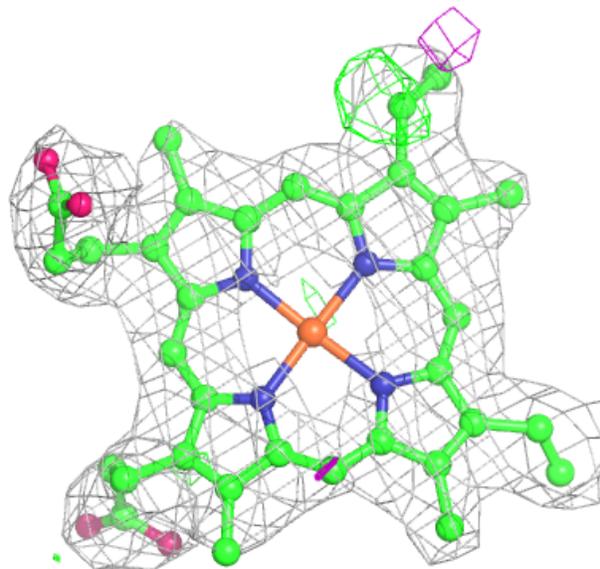






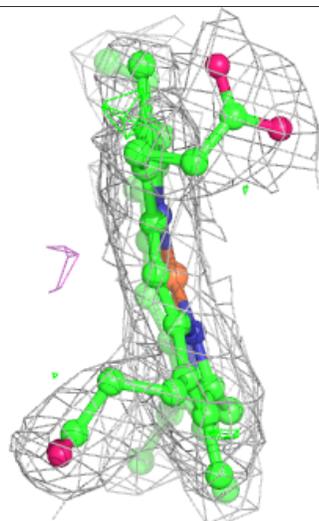
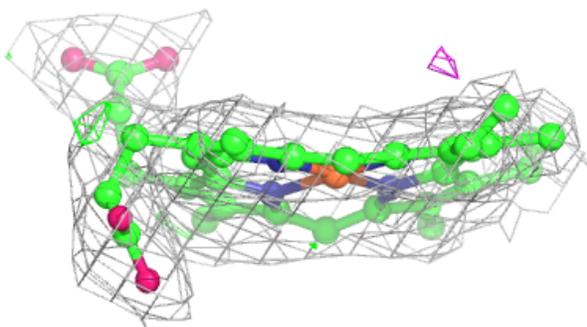
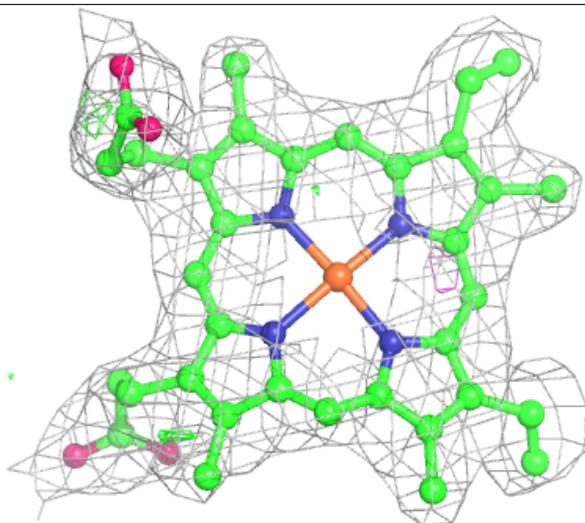
Electron density around HEC A 505:

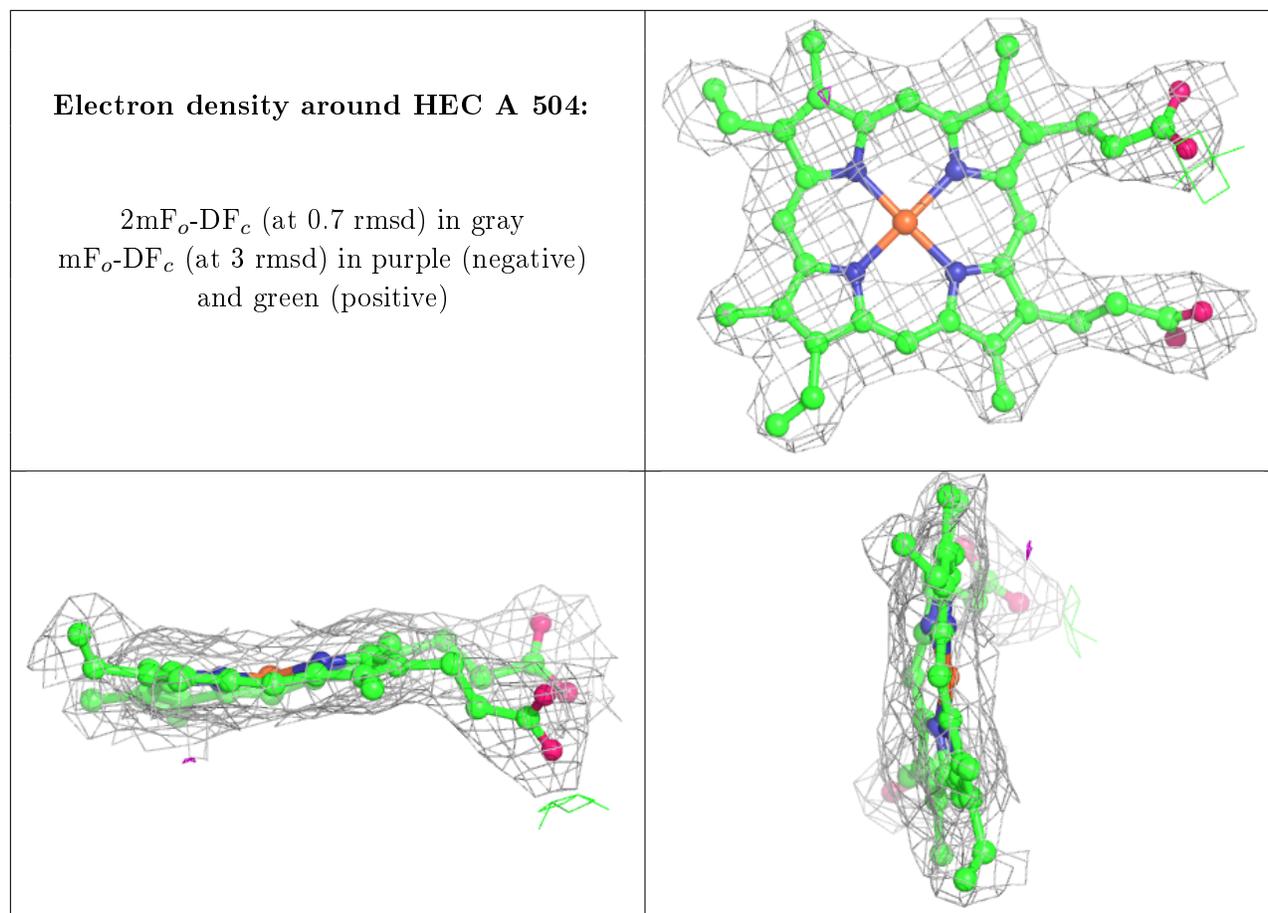
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

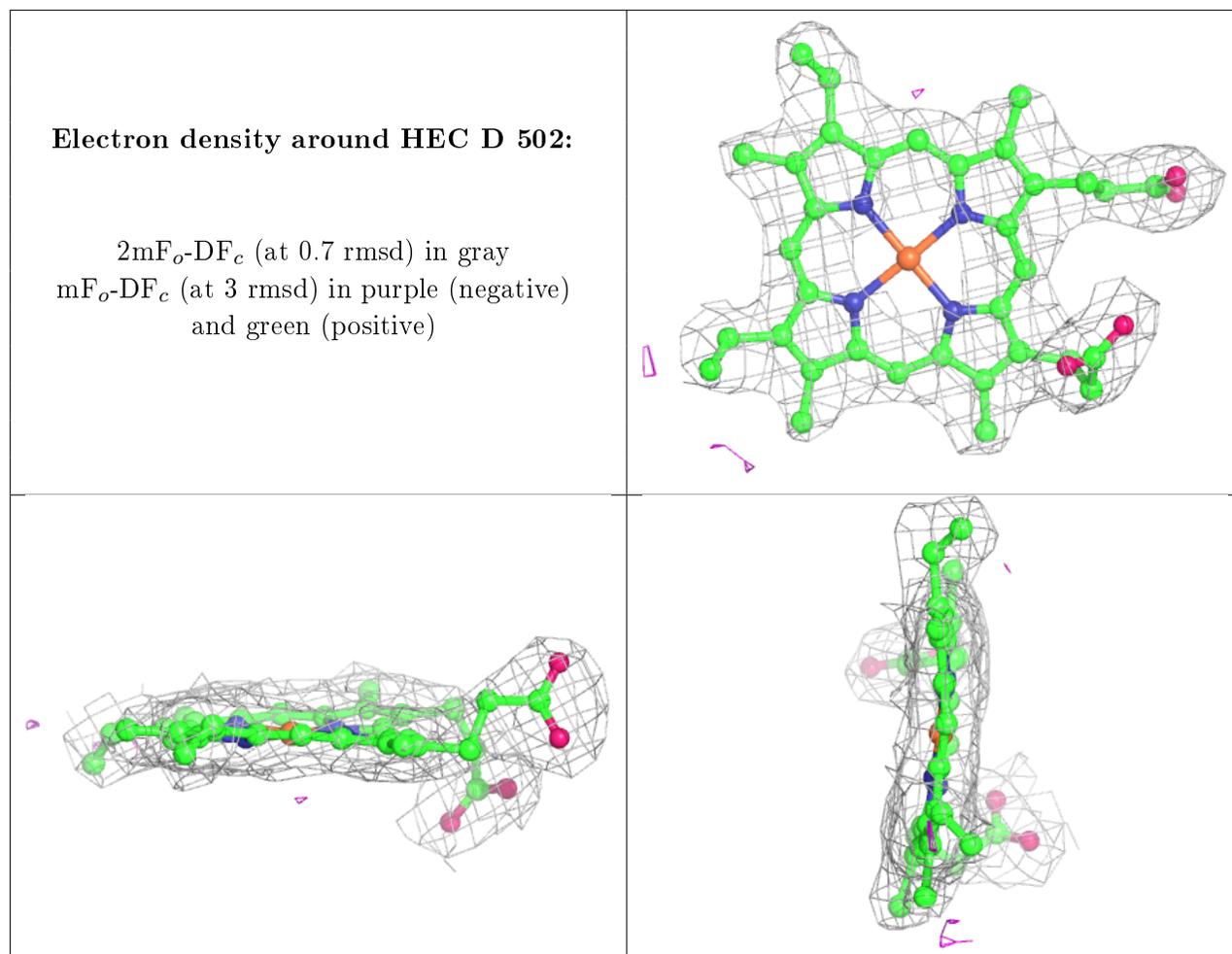


Electron density around HEC B 505:

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

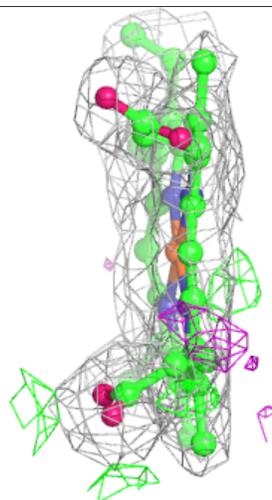
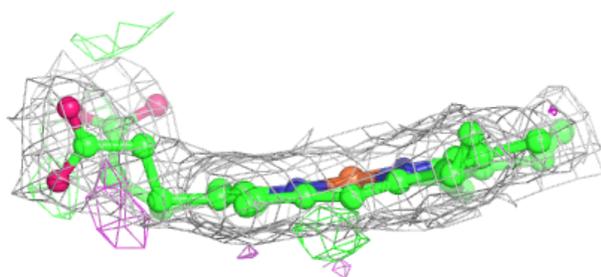
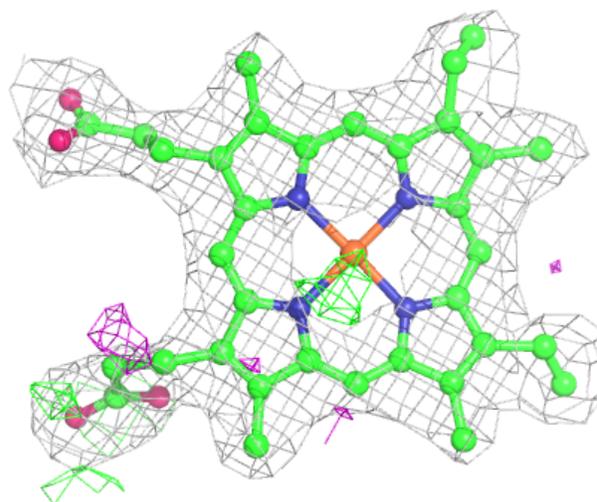






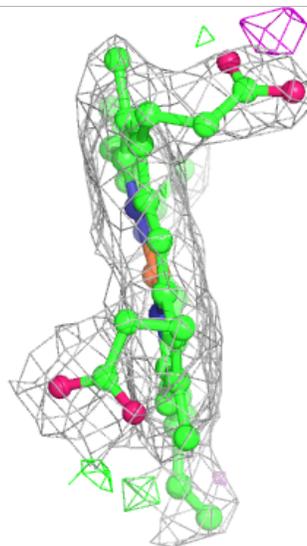
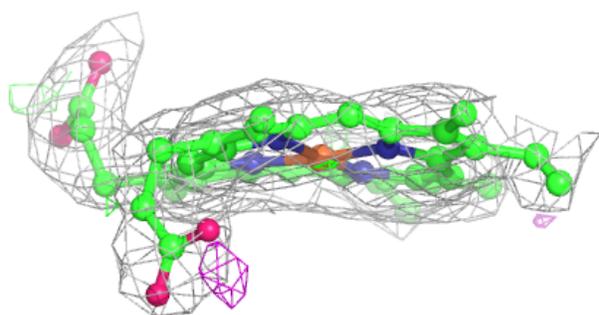
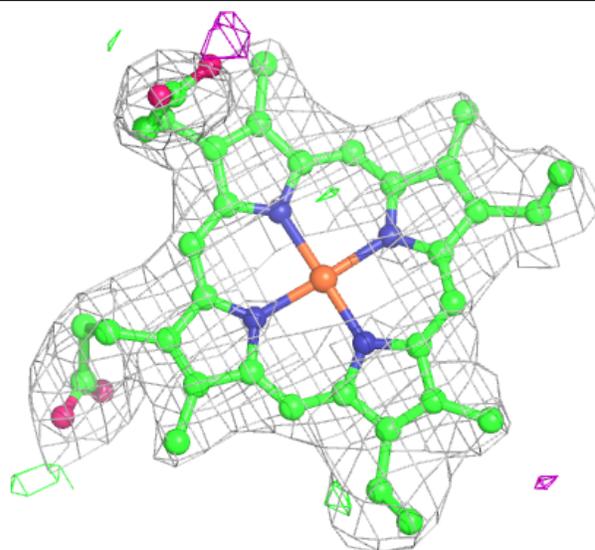
Electron density around HEC B 503:

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



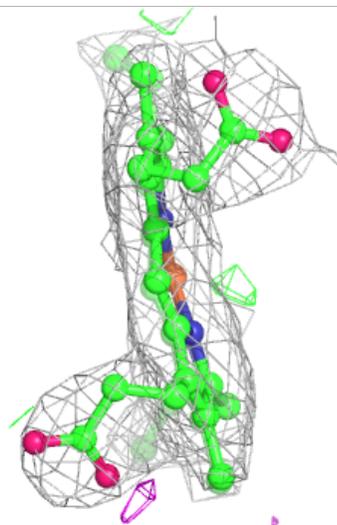
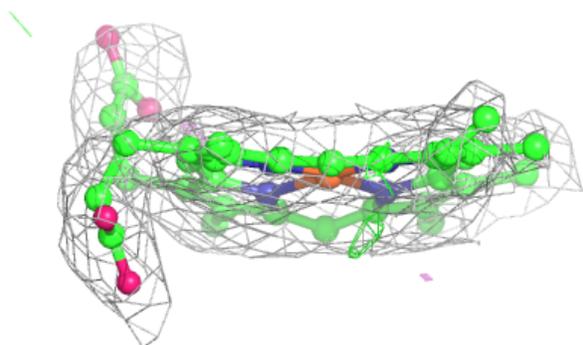
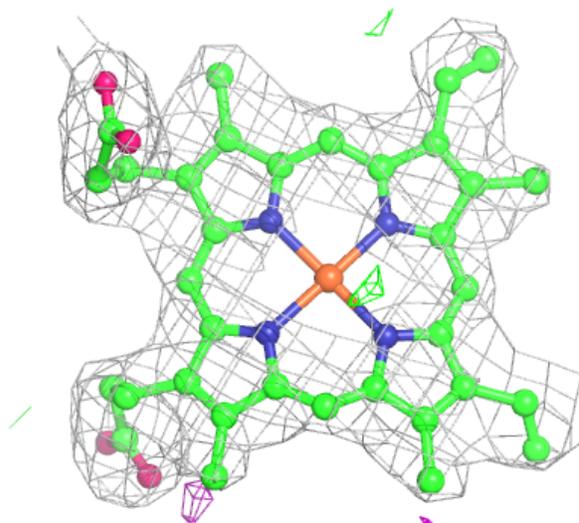
Electron density around HEC E 505:

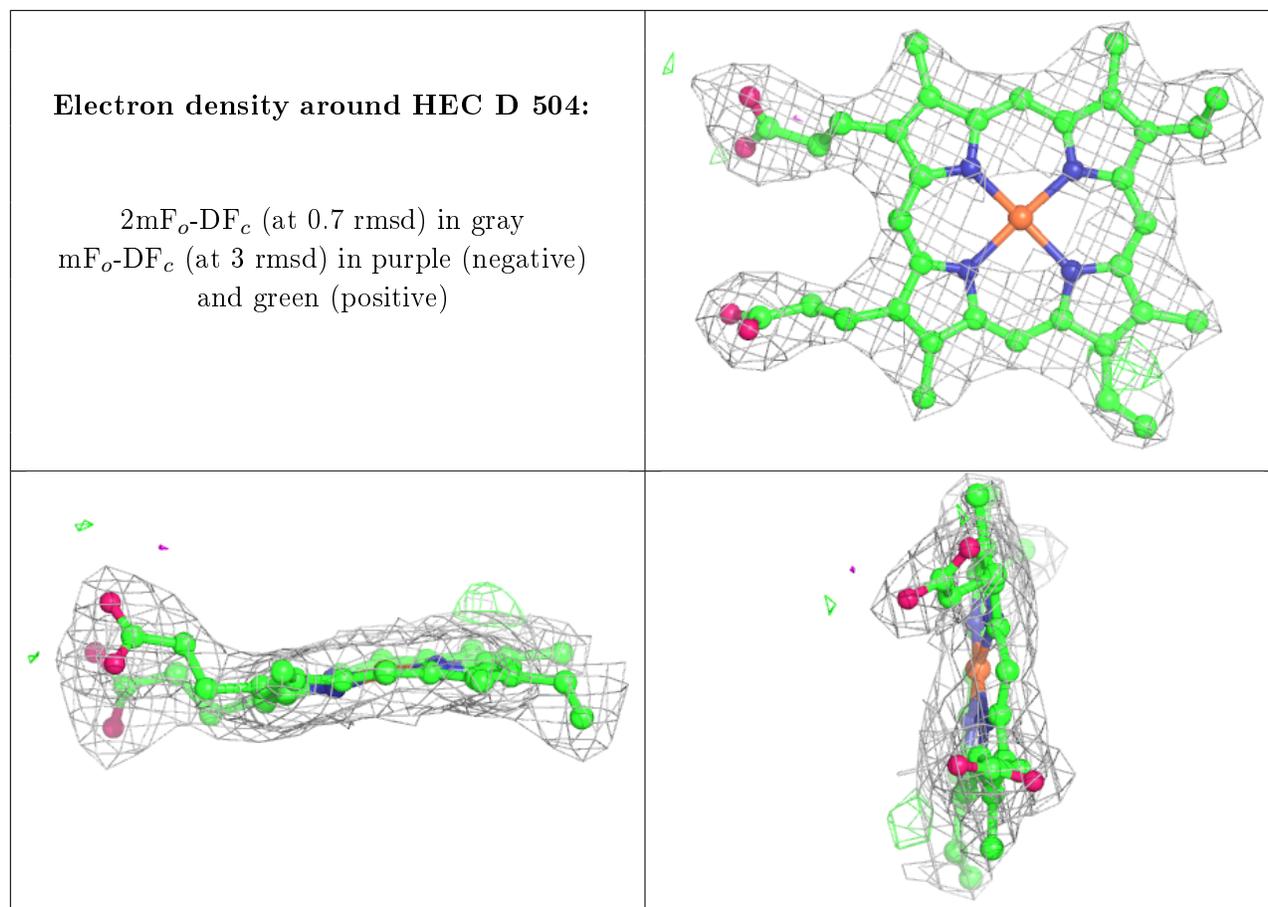
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC F 505:

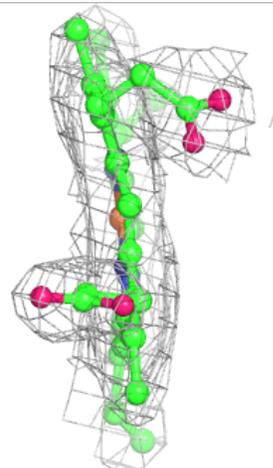
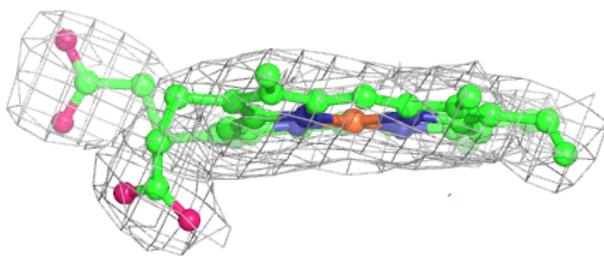
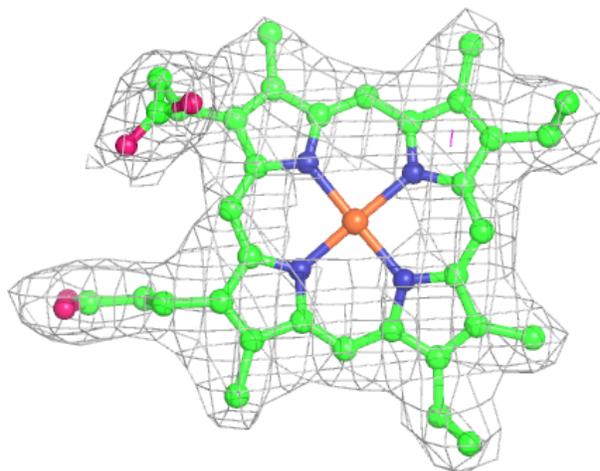
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





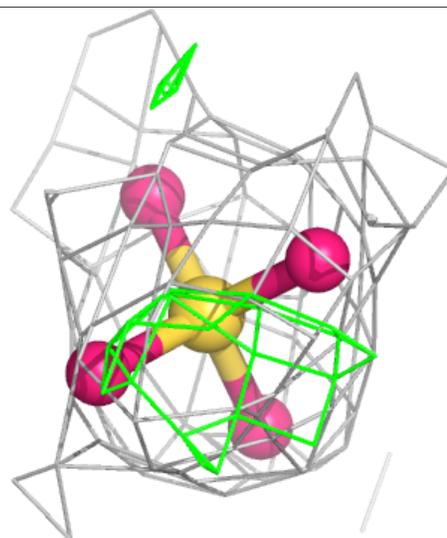
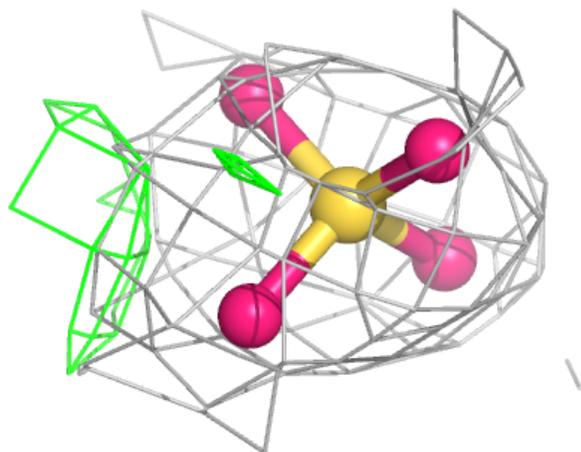
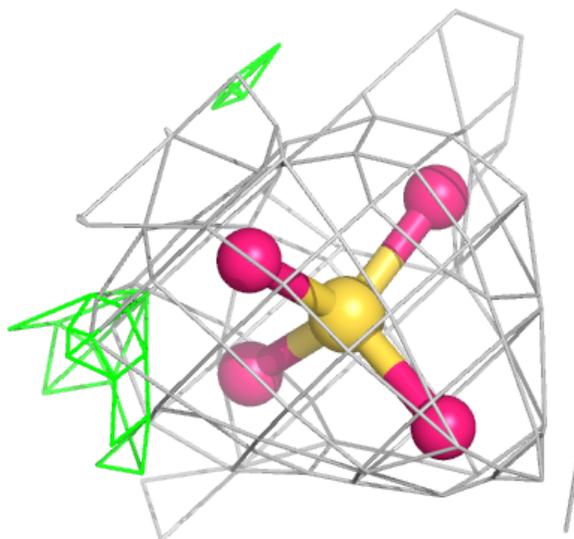
Electron density around HEC A 502:

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



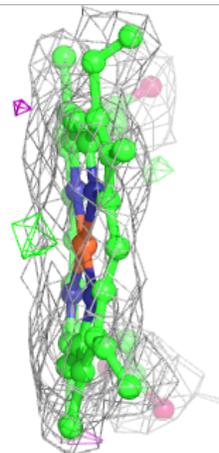
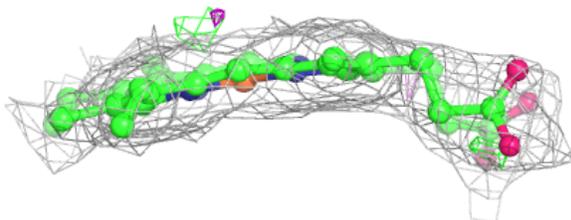
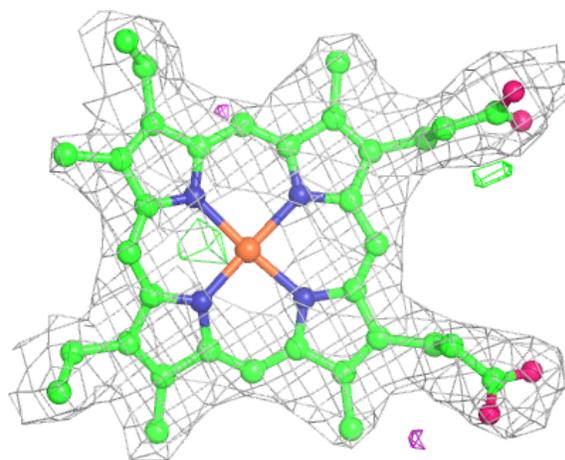
Electron density around SO4 A 506:

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



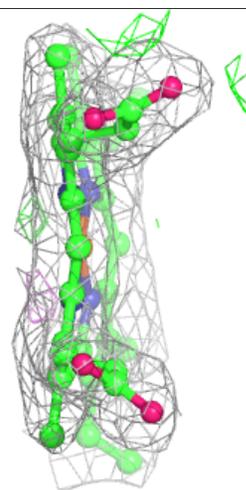
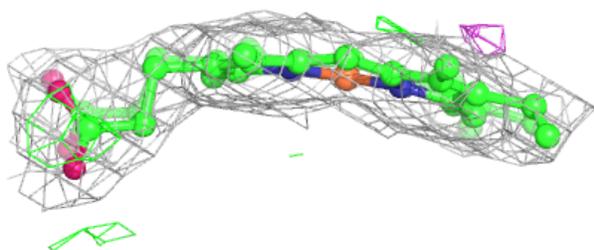
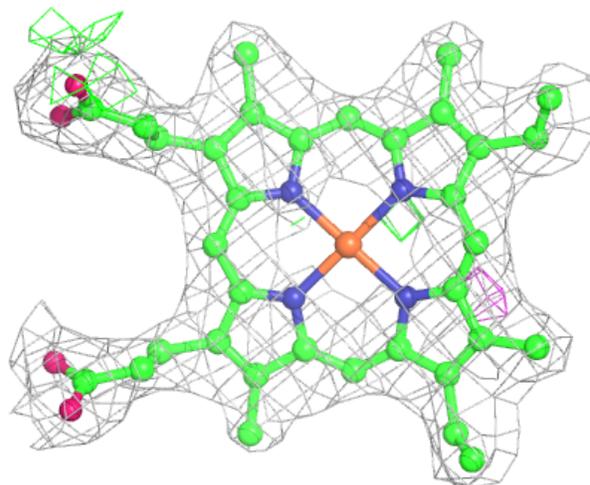
Electron density around HEC D 503:

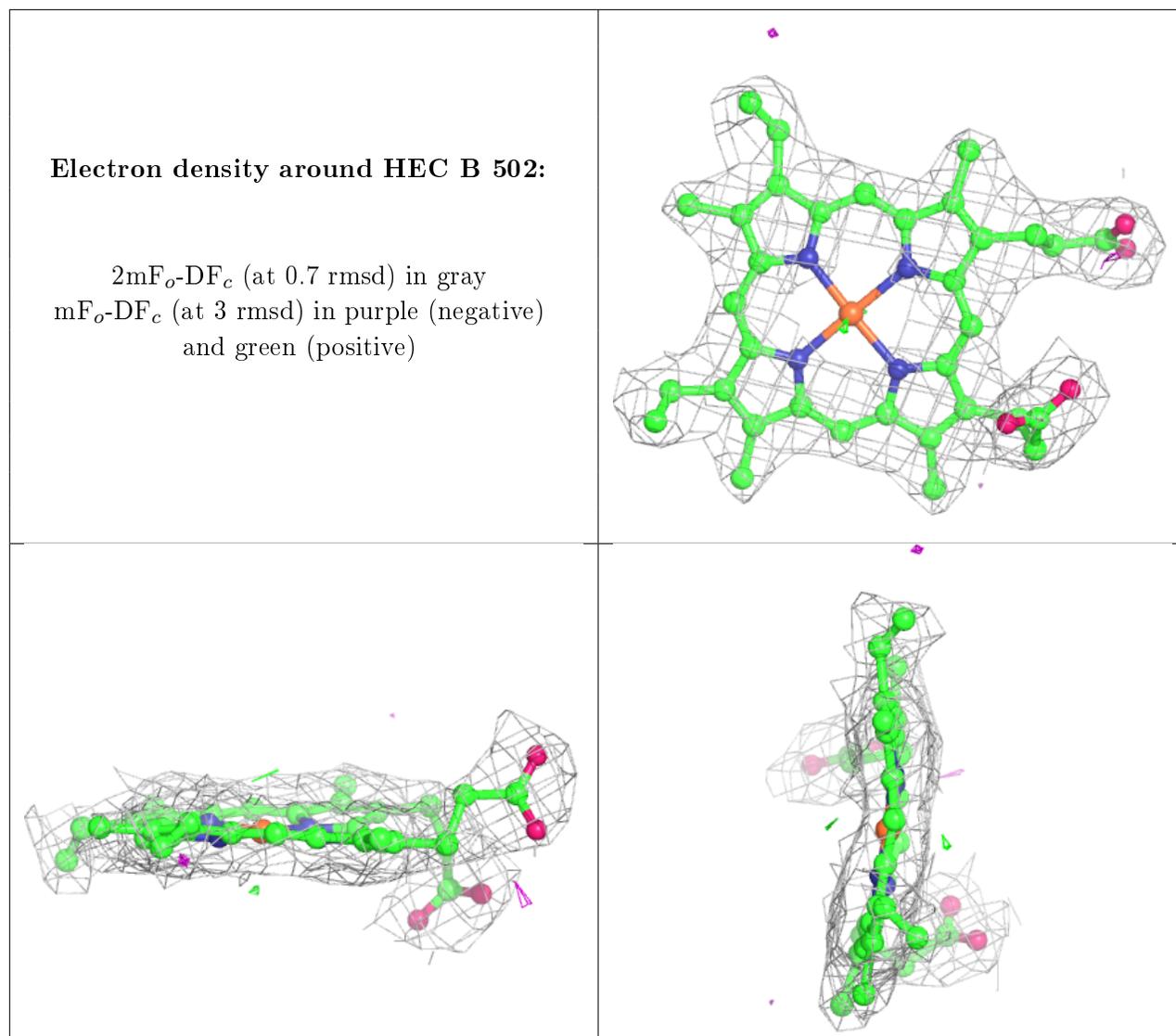
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

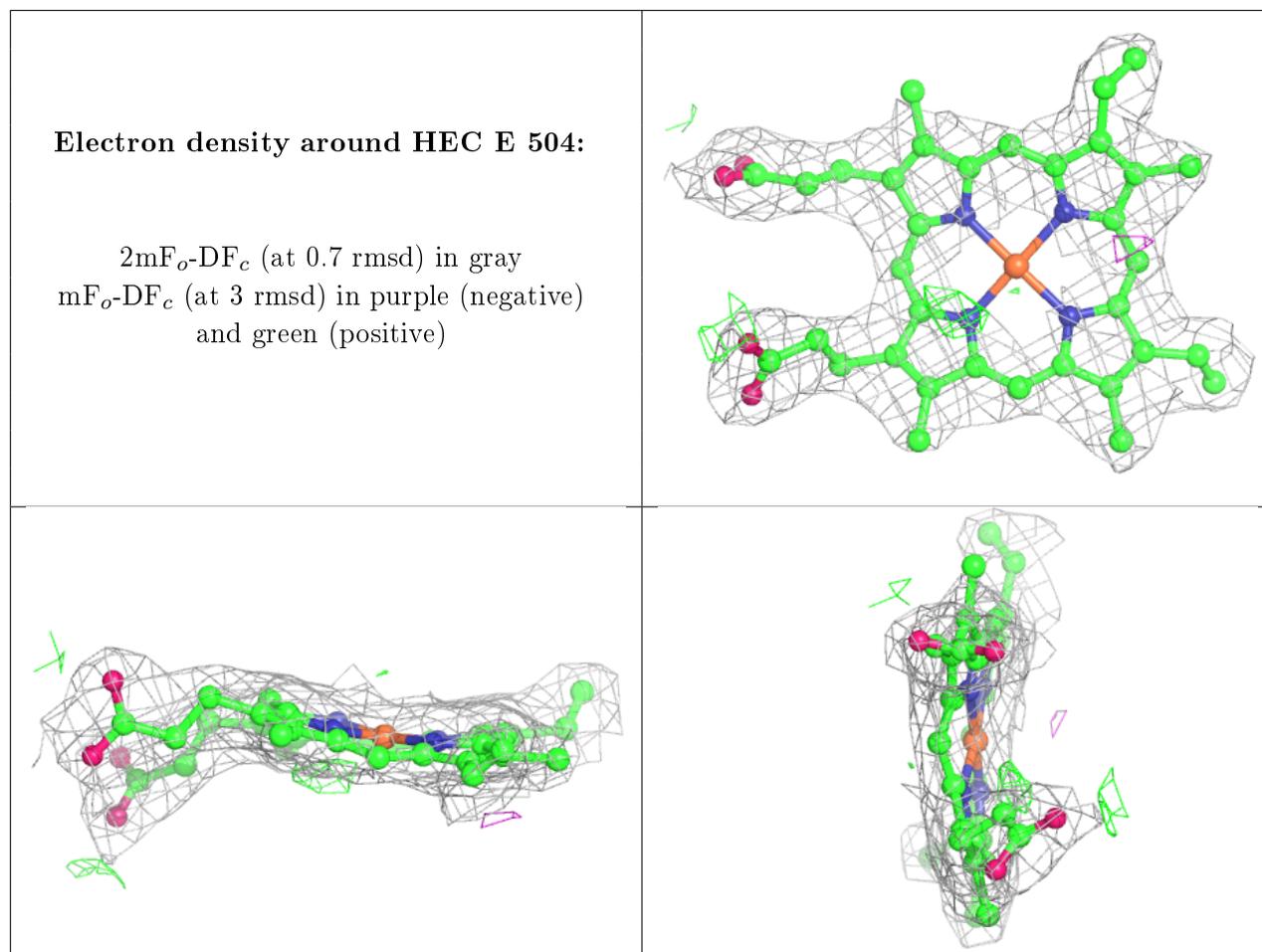


Electron density around HEC C 503:

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

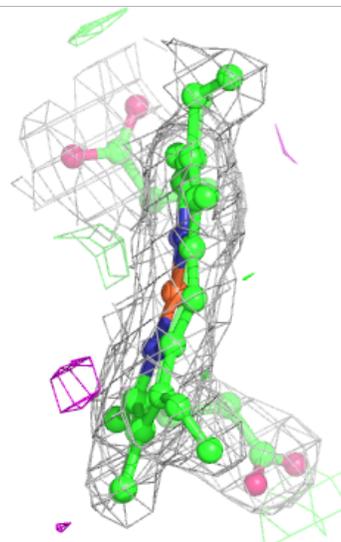
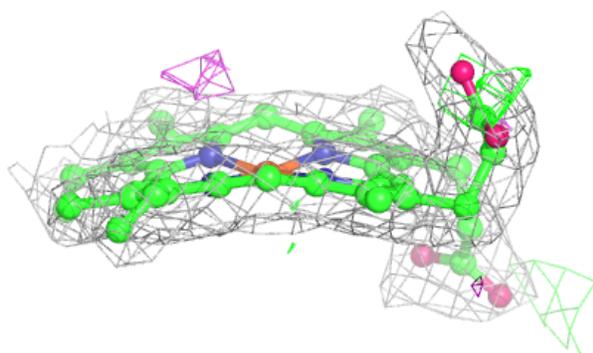
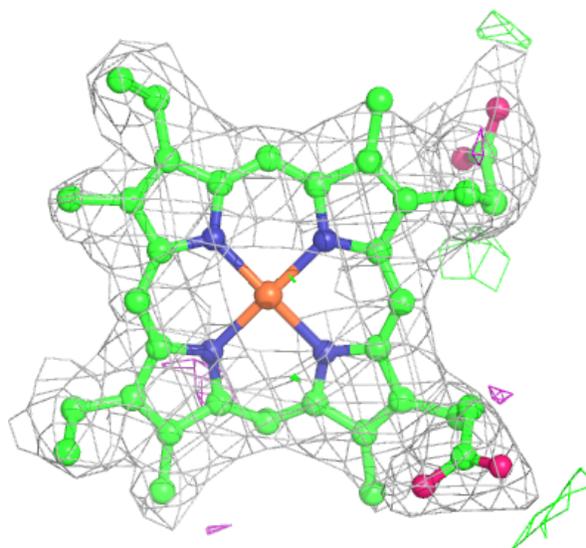






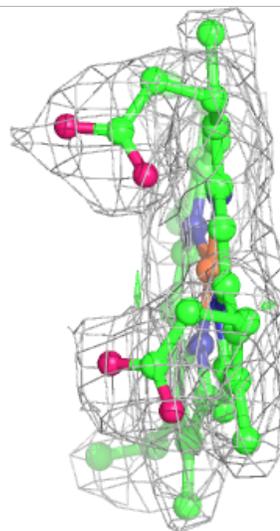
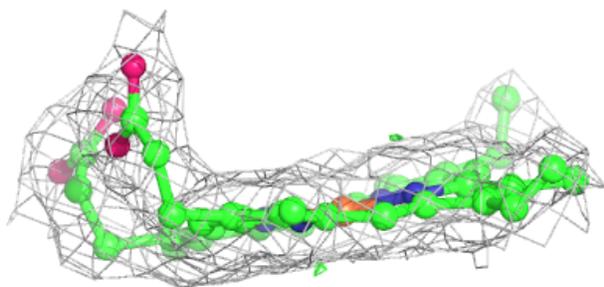
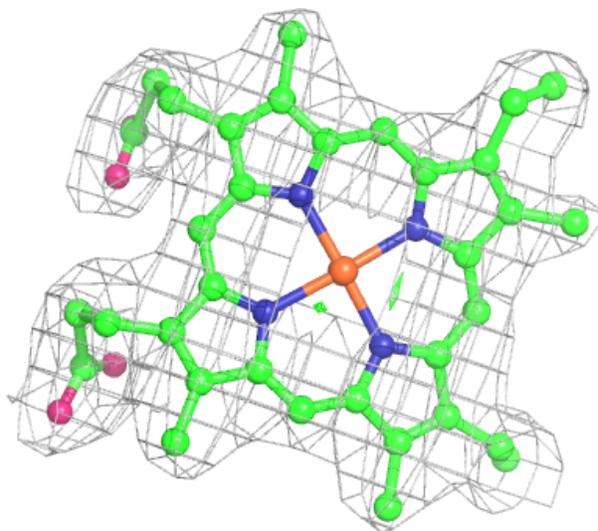
Electron density around HEC C 505:

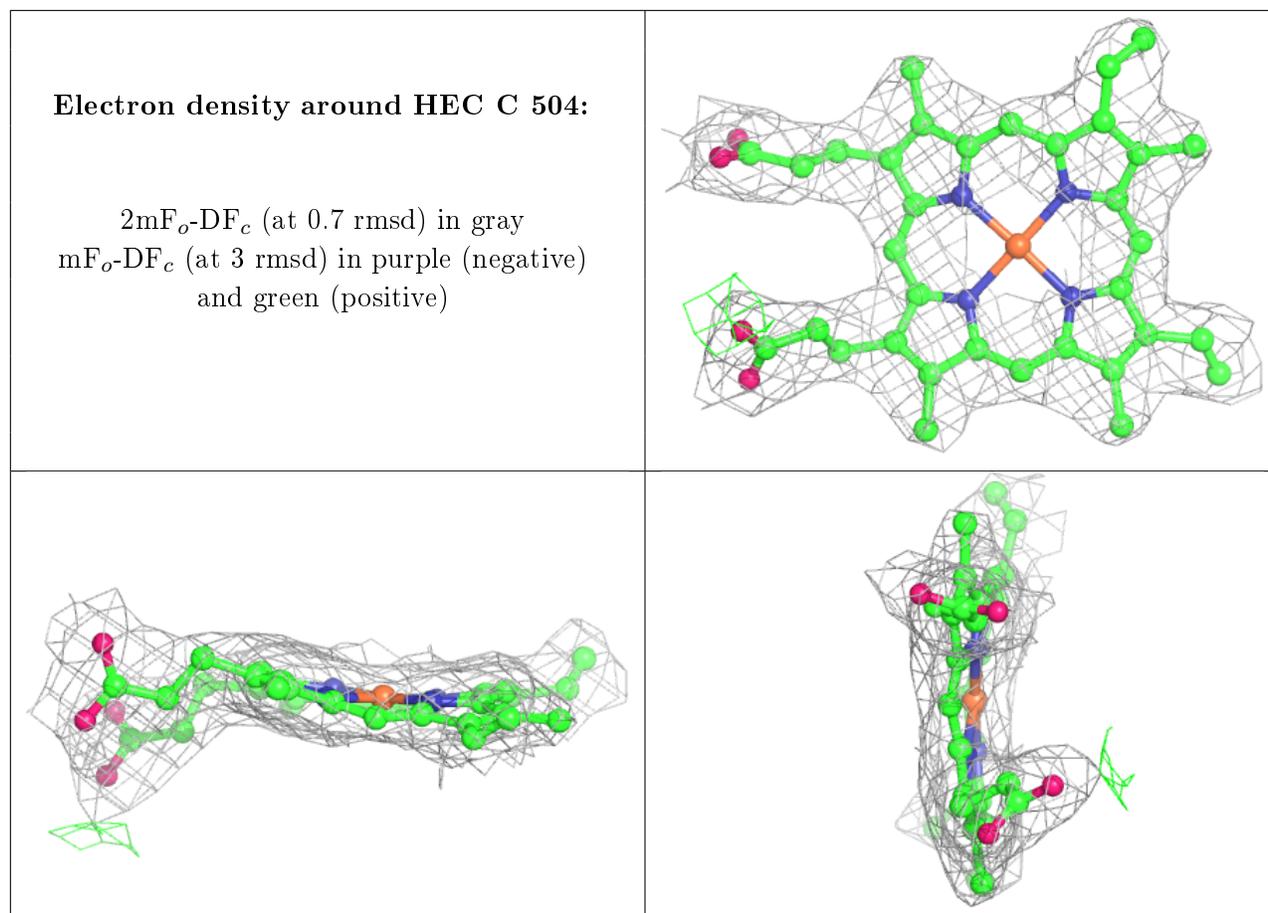
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC A 501:

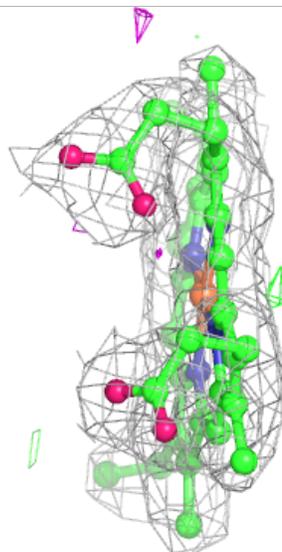
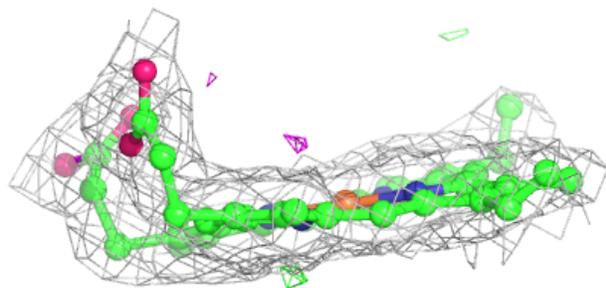
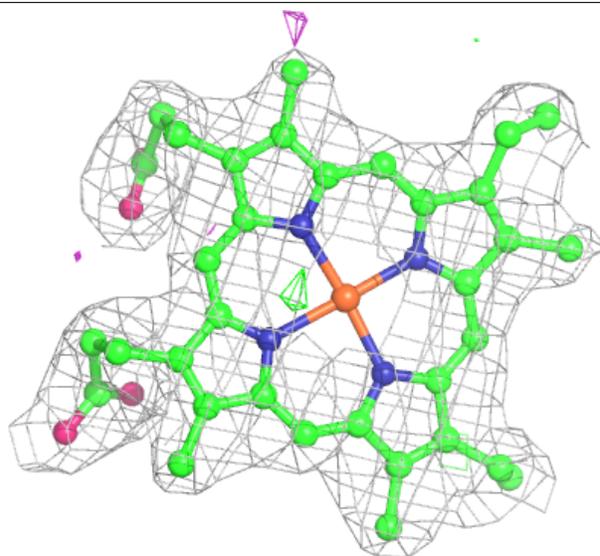
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





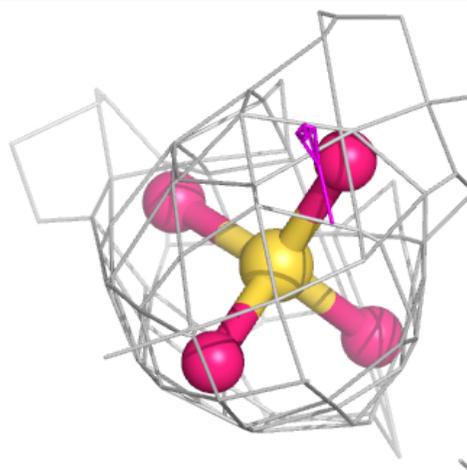
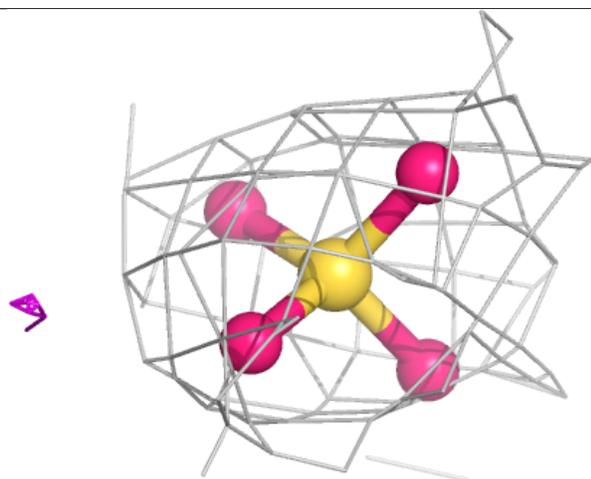
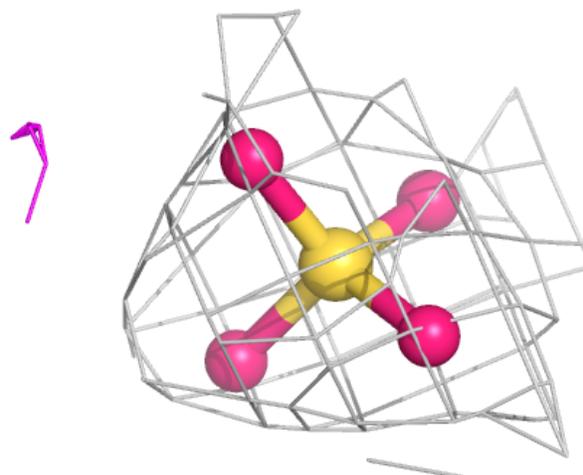
Electron density around HEC B 501:

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



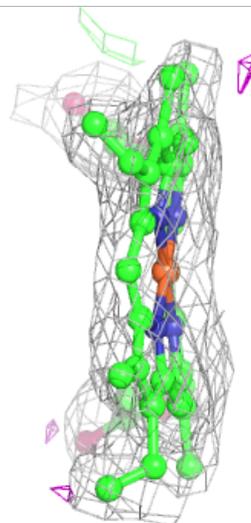
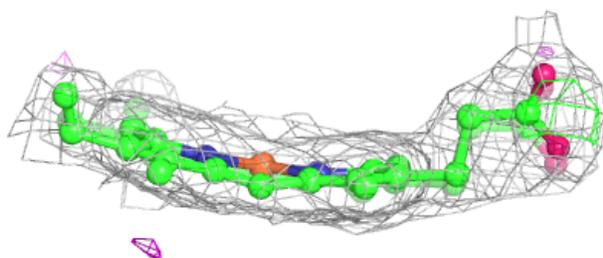
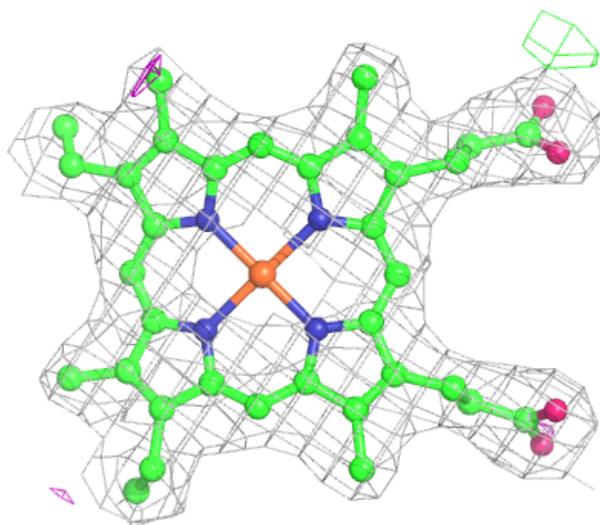
Electron density around SO4 B 506:

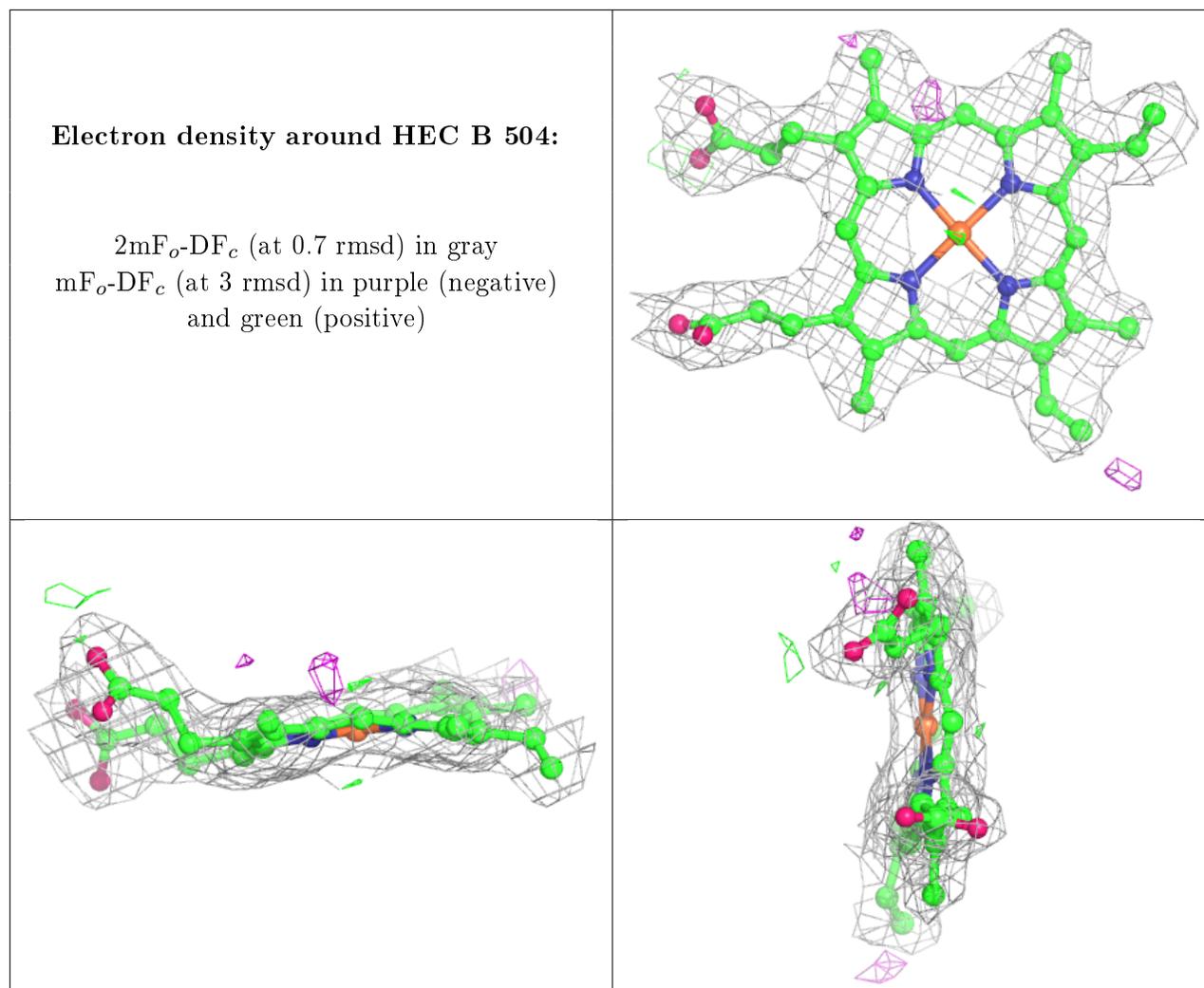
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

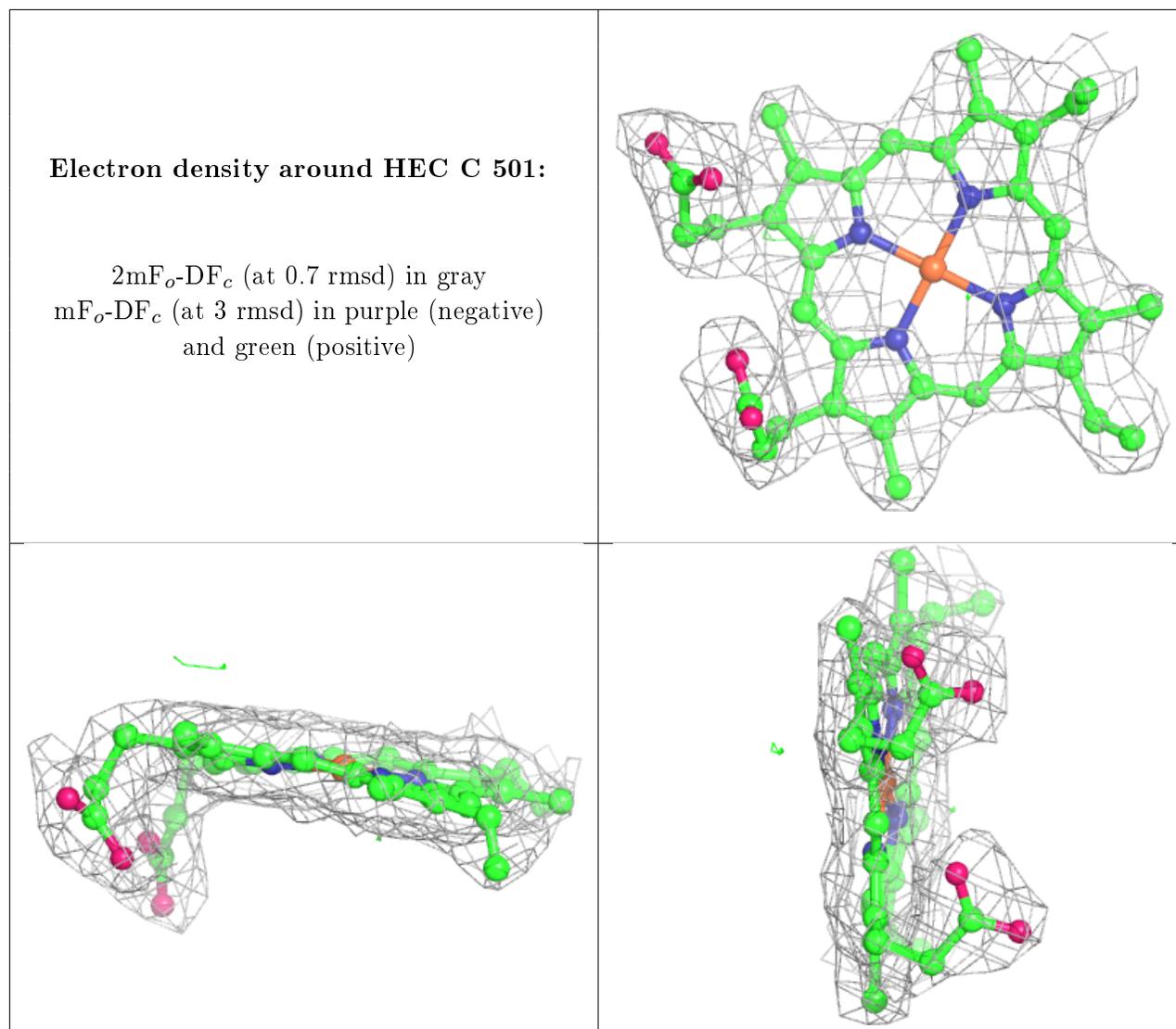


Electron density around HEC A 503:

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







6.5 Other polymers [i](#)

There are no such residues in this entry.