



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:00 AM UTC

PDB ID : 3MK7 / pdb\_00003mk7  
Title : The structure of CBB3 cytochrome oxidase  
Authors : Buschmann, S.; Warkentin, E.; Michel, H.; Ermler, U.  
Deposited on : 2010-04-14  
Resolution : 3.20 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](mailto:validation@mail.wwpdb.org)

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<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>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

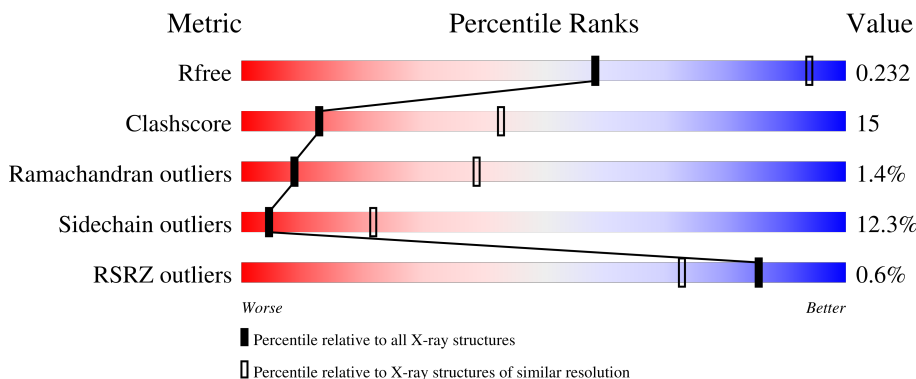
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


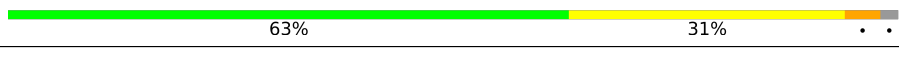



The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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  $\geq 3$ , 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	474	
1	D	474	
1	G	474	
1	K	474	
2	B	203	

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Mol	Chain	Length	Quality of chain
2	E	203	
2	H	203	
2	L	203	
3	C	311	
3	F	311	
3	I	311	
3	M	311	
4	U	30	
4	X	30	
4	Y	30	
4	Z	30	

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
11	FC6	C	323	-	-	X	-
11	FC6	F	323	-	-	X	-
11	FC6	I	323	-	-	X	-

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 31690 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 c oxidase, cbb3-type, subunit N.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	466	Total 3683	C 2461	N 593	O 607	S 22	0	0	0
1	D	463	Total 3663	C 2450	N 590	O 601	S 22	0	0	0
1	G	465	Total 3676	C 2457	N 592	O 605	S 22	0	0	0
1	K	465	Total 3676	C 2457	N 592	O 605	S 22	0	0	0

- Molecule 2 is a protein called Cytochrome c oxidase, cbb3-type, subunit O.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	197	Total 1548	C 981	N 268	O 289	S 10	0	0	0
2	E	197	Total 1548	C 981	N 268	O 289	S 10	0	0	0
2	H	197	Total 1548	C 981	N 268	O 289	S 10	0	0	0
2	L	197	Total 1548	C 981	N 268	O 289	S 10	0	0	0

- Molecule 3 is a protein called Cytochrome c oxidase, cbb3-type, subunit P.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	303	Total 2312	C 1483	N 391	O 427	S 11	0	0	0
3	F	303	Total 2312	C 1483	N 391	O 427	S 11	0	0	0
3	I	303	Total 2312	C 1483	N 391	O 427	S 11	0	0	0
3	M	303	Total 2312	C 1483	N 391	O 427	S 11	0	0	0



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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
5	K	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	K	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

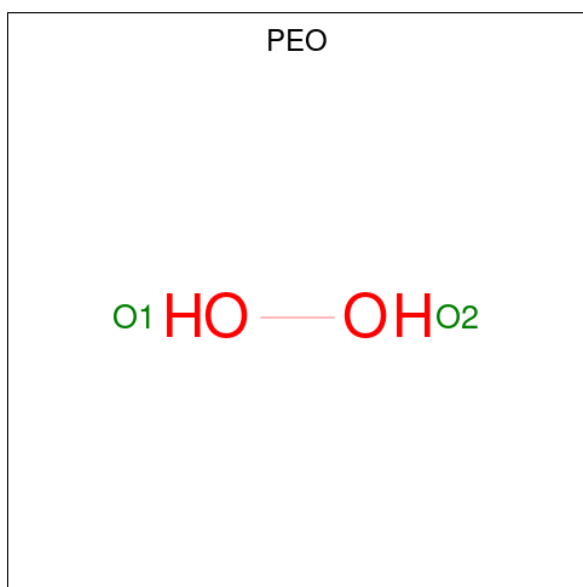
- Molecule 6 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cu	0	0
			1	1		
6	D	1	Total	Cu	0	0
			1	1		
6	G	1	Total	Cu	0	0
			1	1		
6	K	1	Total	Cu	0	0
			1	1		

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

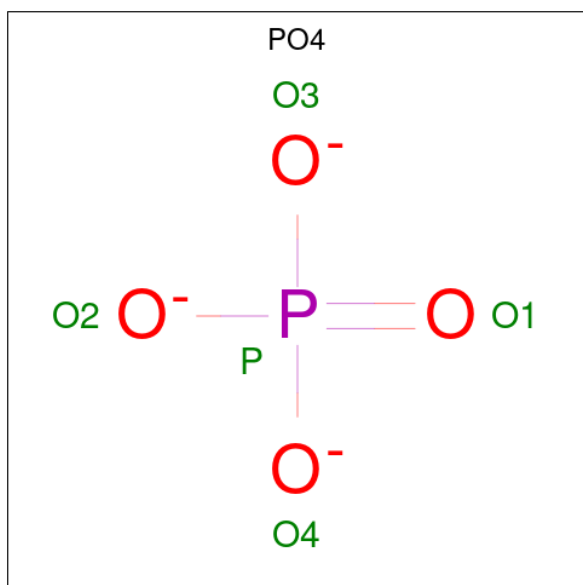
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Ca	0	0
			1	1		
7	B	1	Total	Ca	0	0
			1	1		
7	D	1	Total	Ca	0	0
			1	1		
7	E	1	Total	Ca	0	0
			1	1		
7	G	2	Total	Ca	0	0
			2	2		
7	K	2	Total	Ca	0	0
			2	2		

- Molecule 8 is HYDROGEN PEROXIDE (CCD ID: PEO) (formula: H<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total O 2 2	0	0
8	D	1	Total O 2 2	0	0
8	G	1	Total O 2 2	0	0
8	K	1	Total O 2 2	0	0

- Molecule 9 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).

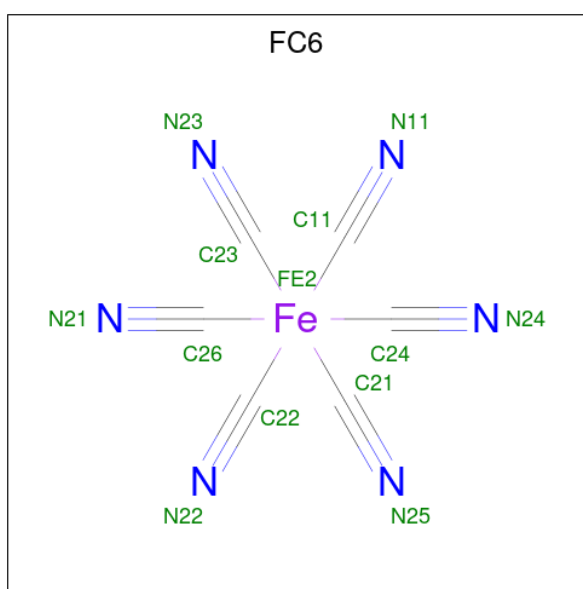




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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
10	I	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	L	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	M	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
10	M	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 11 is HEXACYANOFERRATE(3-) (CCD ID: FC6) (formula:  $C_6FeN_6$ ).

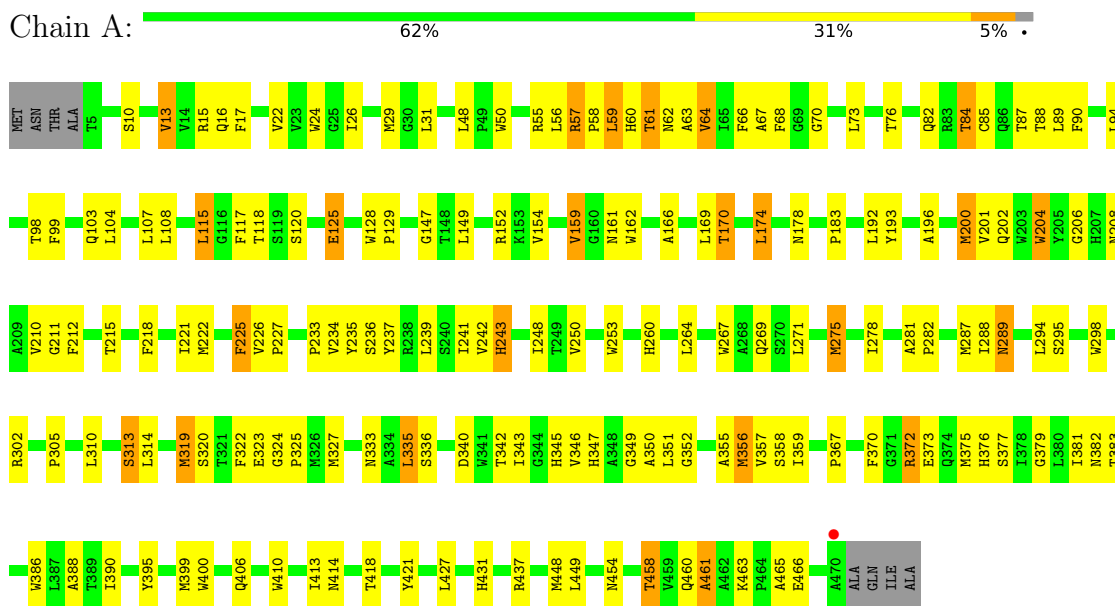


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
11	C	1	Total	C	Fe	N	0	0
			13	6	1	6		
11	F	1	Total	C	Fe	N	0	0
			13	6	1	6		
11	I	1	Total	C	Fe	N	0	0
			13	6	1	6		
11	M	1	Total	C	Fe	N	0	0
			13	6	1	6		

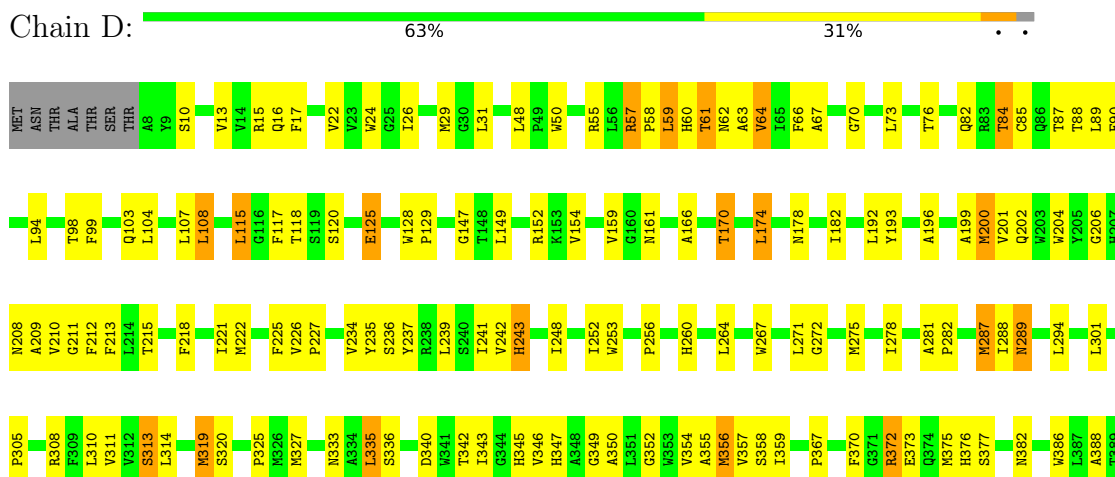
### 3 Residue-property plots [i](#)

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 c oxidase, cbb3-type, subunit N



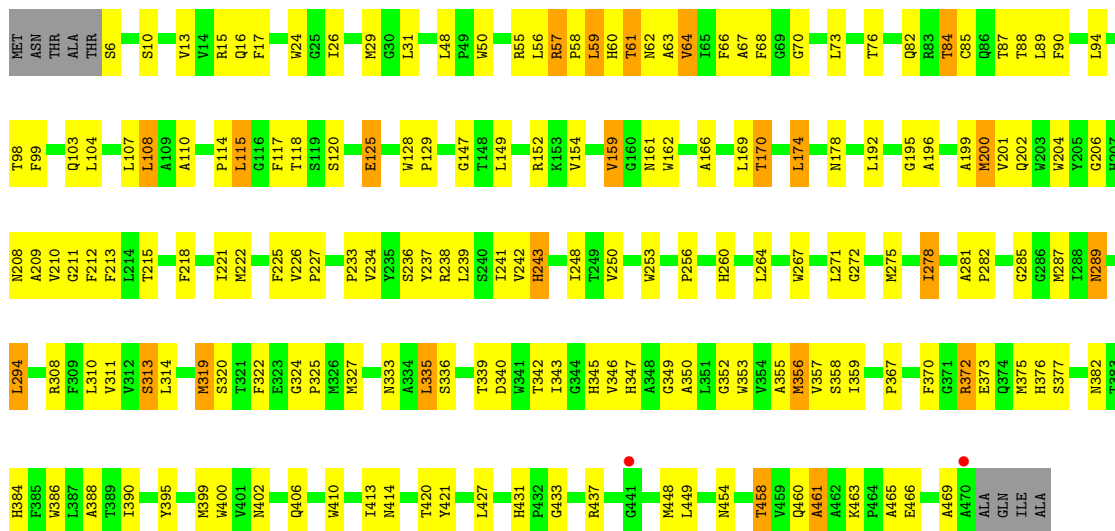
- Molecule 1: Cytochrome c oxidase, cbb3-type, subunit N





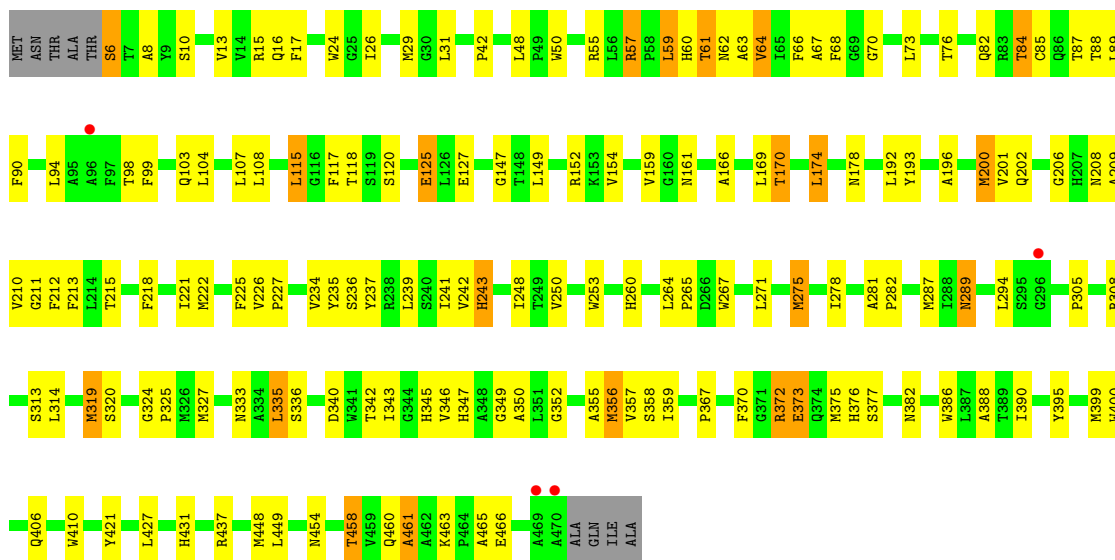
- Molecule 1: Cytochrome c oxidase, cbb3-type, subunit N

Chain G: 61% 32% 5%



- Molecule 1: Cytochrome c oxidase, cbb3-type, subunit N

Chain K: 65% 29%



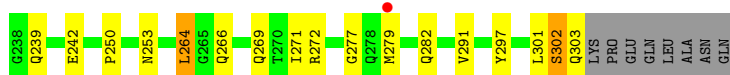
- Molecule 2: Cytochrome c oxidase, cbb3-type, subunit O

Chain B: 63% 30%

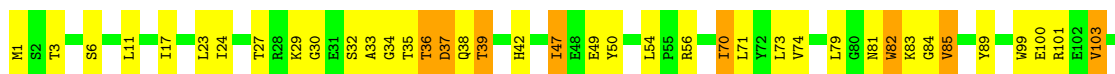




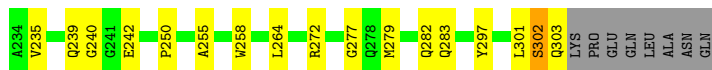
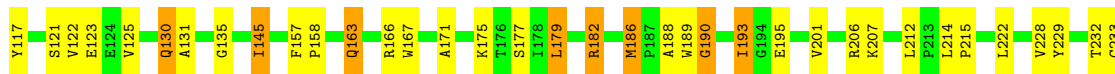
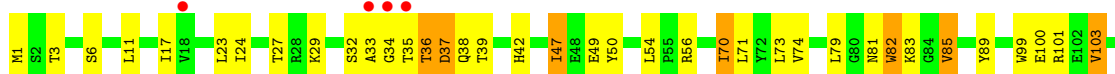
- Molecule 3: Cytochrome c oxidase, cbb3-type, subunit P



- Molecule 3: Cytochrome c oxidase, cbb3-type, subunit P



- Molecule 3: Cytochrome c oxidase, cbb3-type, subunit P

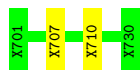


- Molecule 4: 30-mer peptide

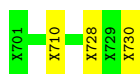




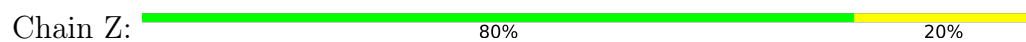
- Molecule 4: 30-mer peptide



- Molecule 4: 30-mer peptide



- Molecule 4: 30-mer peptide



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.47Å 279.93Å 175.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.20 15.00 – 3.20	Depositor EDS
% Data completeness (in resolution range)	98.5 (15.00-3.20) 97.4 (15.00-3.20)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.6.0046	Depositor
R, $R_{free}$	0.189 , 0.223 0.198 , 0.232	Depositor DCC
$R_{free}$ test set	6720 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	87.0	Xtrriage
Anisotropy	0.050	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 73.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	31690	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	117.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.95% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PO4, PEO, FC6, CA, HEC, CU, HEM

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.72	0/3811	0.93	4/5210 (0.1%)
1	D	0.49	0/3791	0.87	0/5182
1	G	0.64	1/3804 (0.0%)	0.91	2/5200 (0.0%)
1	K	0.57	2/3804 (0.1%)	0.88	1/5200 (0.0%)
2	B	0.83	0/1584	1.03	5/2146 (0.2%)
2	E	0.58	0/1584	0.93	1/2146 (0.0%)
2	H	0.77	1/1584 (0.1%)	1.03	3/2146 (0.1%)
2	L	0.65	0/1584	0.96	1/2146 (0.0%)
3	C	0.79	0/2374	1.03	7/3225 (0.2%)
3	F	0.55	0/2374	0.93	2/3225 (0.1%)
3	I	0.71	0/2374	0.98	1/3225 (0.0%)
3	M	0.81	1/2374 (0.0%)	1.04	0/3225
All	All	0.67	5/31042 (0.0%)	0.95	27/42276 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	101	GLY	C-O	6.58	1.29	1.23
1	K	6	SER	CB-OG	-6.16	1.29	1.42
3	M	188	ALA	CA-CB	-5.80	1.45	1.53
1	K	6	SER	CA-CB	5.64	1.64	1.53
1	G	469	ALA	CA-C	5.06	1.54	1.52

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	100	TRP	CA-C-N	-8.84	113.52	122.27
2	H	100	TRP	C-N-CA	-8.84	113.52	122.27
2	H	100	TRP	N-CA-C	-8.10	99.33	110.35
2	B	100	TRP	CA-C-N	-6.71	112.70	121.96
2	B	100	TRP	C-N-CA	-6.71	112.70	121.96

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	112	VAL	Peptide

## 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	3683	0	3663	132	0
1	D	3663	0	3644	131	0
1	G	3676	0	3656	133	0
1	K	3676	0	3656	122	0
2	B	1548	0	1526	53	0
2	E	1548	0	1526	52	0
2	H	1548	0	1526	59	0
2	L	1548	0	1526	42	0
3	C	2312	0	2237	68	1
3	F	2312	0	2237	67	0
3	I	2312	0	2237	69	1
3	M	2312	0	2237	64	0
4	U	150	0	33	6	0
4	X	150	0	33	2	0
4	Y	150	0	33	4	0
4	Z	150	0	35	4	0
5	A	86	0	60	11	0
5	D	86	0	60	12	0
5	G	86	0	60	13	0
5	K	86	0	60	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1	0	0	0	0
6	D	1	0	0	0	0
6	G	1	0	0	0	0
6	K	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	D	1	0	0	0	0
7	E	1	0	0	0	0
7	G	2	0	0	0	0
7	K	2	0	0	0	0
8	A	2	0	0	0	0
8	D	2	0	0	0	0
8	G	2	0	0	0	0
8	K	2	0	0	0	0
9	A	5	0	0	0	0
9	D	5	0	0	0	0
9	G	5	0	0	0	0
9	K	5	0	0	0	0
10	B	43	0	30	3	0
10	C	86	0	60	8	0
10	E	43	0	30	2	0
10	F	86	0	60	15	0
10	H	43	0	30	4	0
10	I	86	0	60	5	0
10	L	43	0	30	2	0
10	M	86	0	60	8	0
11	C	13	0	0	4	0
11	F	13	0	0	10	0
11	I	13	0	0	6	0
11	M	13	0	0	3	0
All	All	31690	0	30405	939	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

The worst 5 of 939 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:359:ILE:HD11	1:A:448:MET:HE1	1.32	1.10
11:F:323:FC6:N24	3:I:215:PRO:HB3	1.66	1.10
1:K:359:ILE:HD11	1:K:448:MET:HE1	1.33	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:359:ILE:HD11	1:D:448:MET:HE1	1.28	1.10
1:G:359:ILE:HD11	1:G:448:MET:HE1	1.36	1.02

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:34:GLY:CA	3:I:39:THR:OG1[1_556]	2.10	0.10

## 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	464/474 (98%)	432 (93%)	27 (6%)	5 (1%)	11	43
1	D	461/474 (97%)	430 (93%)	26 (6%)	5 (1%)	11	43
1	G	463/474 (98%)	428 (92%)	30 (6%)	5 (1%)	11	43
1	K	463/474 (98%)	430 (93%)	28 (6%)	5 (1%)	11	43
2	B	195/203 (96%)	185 (95%)	8 (4%)	2 (1%)	12	45
2	E	195/203 (96%)	186 (95%)	7 (4%)	2 (1%)	12	45
2	H	195/203 (96%)	184 (94%)	9 (5%)	2 (1%)	12	45
2	L	195/203 (96%)	185 (95%)	8 (4%)	2 (1%)	12	45
3	C	301/311 (97%)	276 (92%)	17 (6%)	8 (3%)	4	25
3	F	301/311 (97%)	276 (92%)	19 (6%)	6 (2%)	6	31
3	I	301/311 (97%)	276 (92%)	19 (6%)	6 (2%)	6	31
3	M	301/311 (97%)	274 (91%)	20 (7%)	7 (2%)	5	29
All	All	3835/3952 (97%)	3562 (93%)	218 (6%)	55 (1%)	9	39

5 of 55 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	461	ALA
1	A	465	ALA
2	B	44	GLU
3	C	29	LYS
3	C	33	ALA

### 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	374/379 (99%)	331 (88%)	43 (12%)	5	24
1	D	371/379 (98%)	329 (89%)	42 (11%)	5	24
1	G	373/379 (98%)	330 (88%)	43 (12%)	5	24
1	K	373/379 (98%)	331 (89%)	42 (11%)	5	24
2	B	166/172 (96%)	145 (87%)	21 (13%)	4	20
2	E	166/172 (96%)	143 (86%)	23 (14%)	3	17
2	H	166/172 (96%)	144 (87%)	22 (13%)	4	19
2	L	166/172 (96%)	144 (87%)	22 (13%)	4	19
3	C	227/234 (97%)	196 (86%)	31 (14%)	3	18
3	F	227/234 (97%)	198 (87%)	29 (13%)	4	20
3	I	227/234 (97%)	197 (87%)	30 (13%)	4	19
3	M	227/234 (97%)	198 (87%)	29 (13%)	4	20
All	All	3063/3140 (98%)	2686 (88%)	377 (12%)	4	22

5 of 377 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	458	THR
1	K	57	ARG
2	H	36	GLN
3	I	39	THR
1	K	154	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 128 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	10	ASN
2	L	193	GLN
1	D	431	HIS
1	D	414	ASN
3	M	105	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 12 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	$\# Z  > 2$
10	HEC	E	211	2	46,50,50	1.94	7 (15%)	58,82,82	1.89	6 (10%)
8	PEO	D	508	6,5	1,1,1	0.30	0	-		
8	PEO	K	508	6,5	1,1,1	0.29	0	-		
9	PO4	G	506	-	4,4,4	0.61	0	6,6,6	1.01	0
11	FC6	I	323	-	12,12,12	1.02	0	-		
10	HEC	L	211	2	46,50,50	1.94	7 (15%)	58,82,82	1.96	8 (13%)
11	FC6	F	323	-	12,12,12	1.03	0	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	PEO	A	508	6,5	1,1,1	0.26	0	-		
10	HEC	C	322	3	46,50,50	1.90	8 (17%)	58,82,82	1.99	11 (18%)
11	FC6	M	323	-	12,12,12	1.24	2 (16%)	-		
5	HEM	K	502	7,1	50,50,50	1.83	10 (20%)	67,82,82	1.42	11 (16%)
5	HEM	D	502	7,1	50,50,50	1.80	8 (16%)	67,82,82	1.36	7 (10%)
10	HEC	B	211	2	46,50,50	1.94	7 (15%)	58,82,82	2.16	8 (13%)
10	HEC	I	322	3	46,50,50	1.90	6 (13%)	58,82,82	1.85	14 (24%)
5	HEM	K	501	7,1,8	50,50,50	1.86	10 (20%)	67,82,82	1.20	3 (4%)
10	HEC	F	321	3	46,50,50	1.85	6 (13%)	58,82,82	1.82	8 (13%)
11	FC6	C	323	-	12,12,12	1.27	1 (8%)	-		
5	HEM	A	501	8,1,7	50,50,50	1.79	11 (22%)	67,82,82	1.24	5 (7%)
10	HEC	C	321	3	46,50,50	1.95	7 (15%)	58,82,82	1.92	10 (17%)
9	PO4	K	506	-	4,4,4	0.75	0	6,6,6	0.85	0
10	HEC	I	321	3	46,50,50	1.95	7 (15%)	58,82,82	2.01	10 (17%)
5	HEM	G	502	7,1	50,50,50	1.74	9 (18%)	67,82,82	1.30	5 (7%)
10	HEC	M	322	3	46,50,50	1.97	8 (17%)	58,82,82	1.98	12 (20%)
5	HEM	G	501	7,1,8	50,50,50	1.82	9 (18%)	67,82,82	1.24	5 (7%)
9	PO4	D	506	-	4,4,4	0.77	0	6,6,6	0.70	0
10	HEC	F	322	3	46,50,50	1.90	9 (19%)	58,82,82	1.86	13 (22%)
10	HEC	H	211	2	46,50,50	1.99	10 (21%)	58,82,82	2.08	12 (20%)
9	PO4	A	506	-	4,4,4	0.85	0	6,6,6	1.20	1 (16%)
10	HEC	M	321	3	46,50,50	1.81	6 (13%)	58,82,82	2.29	9 (15%)
5	HEM	D	501	8,1,7	50,50,50	1.93	9 (18%)	67,82,82	1.21	4 (5%)
5	HEM	A	502	7,1	50,50,50	1.77	14 (28%)	67,82,82	1.47	11 (16%)
8	PEO	G	508	6,5	1,1,1	0.36	0	-		

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
10	HEC	E	211	2	-	8/14/54/54	-
10	HEC	L	211	2	-	8/14/54/54	-
10	HEC	C	322	3	-	6/14/54/54	-
5	HEM	K	502	7,1	-	3/14/54/54	-
5	HEM	D	502	7,1	-	4/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	HEC	B	211	2	-	8/14/54/54	-
10	HEC	I	322	3	-	6/14/54/54	-
5	HEM	K	501	7,1,8	-	8/14/54/54	-
10	HEC	F	321	3	-	6/14/54/54	-
5	HEM	A	501	8,1,7	-	8/14/54/54	-
10	HEC	C	321	3	-	6/14/54/54	-
10	HEC	I	321	3	-	6/14/54/54	-
5	HEM	G	502	7,1	-	2/14/54/54	-
10	HEC	M	322	3	-	6/14/54/54	-
5	HEM	G	501	7,1,8	-	8/14/54/54	-
10	HEC	F	322	3	-	6/14/54/54	-
10	HEC	H	211	2	-	8/14/54/54	-
10	HEC	M	321	3	-	6/14/54/54	-
5	HEM	D	501	8,1,7	-	8/14/54/54	-
5	HEM	A	502	7,1	-	4/14/54/54	-

The worst 5 of 171 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	501	HEM	C3D-C2D	7.93	1.53	1.36
5	D	502	HEM	C3D-C2D	7.67	1.53	1.36
5	K	501	HEM	C3D-C2D	7.61	1.53	1.36
5	G	502	HEM	C3D-C2D	7.60	1.53	1.36
5	K	502	HEM	C3D-C2D	7.55	1.53	1.36

The worst 5 of 173 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	211	HEC	CBB-CAB-C3B	-11.24	104.97	127.43
10	M	321	HEC	CBB-CAB-C3B	-10.34	106.78	127.43
10	H	211	HEC	CBB-CAB-C3B	-9.89	107.66	127.43
10	E	211	HEC	CBB-CAB-C3B	-9.37	108.70	127.43
10	L	211	HEC	CBB-CAB-C3B	-9.19	109.06	127.43

There are no chirality outliers.

5 of 125 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	HEM	C2C-C3C-CAC-CBC
5	D	501	HEM	C2C-C3C-CAC-CBC
5	G	501	HEM	C2C-C3C-CAC-CBC
5	K	501	HEM	C2C-C3C-CAC-CBC
10	B	211	HEC	C2B-C3B-CAB-CBB

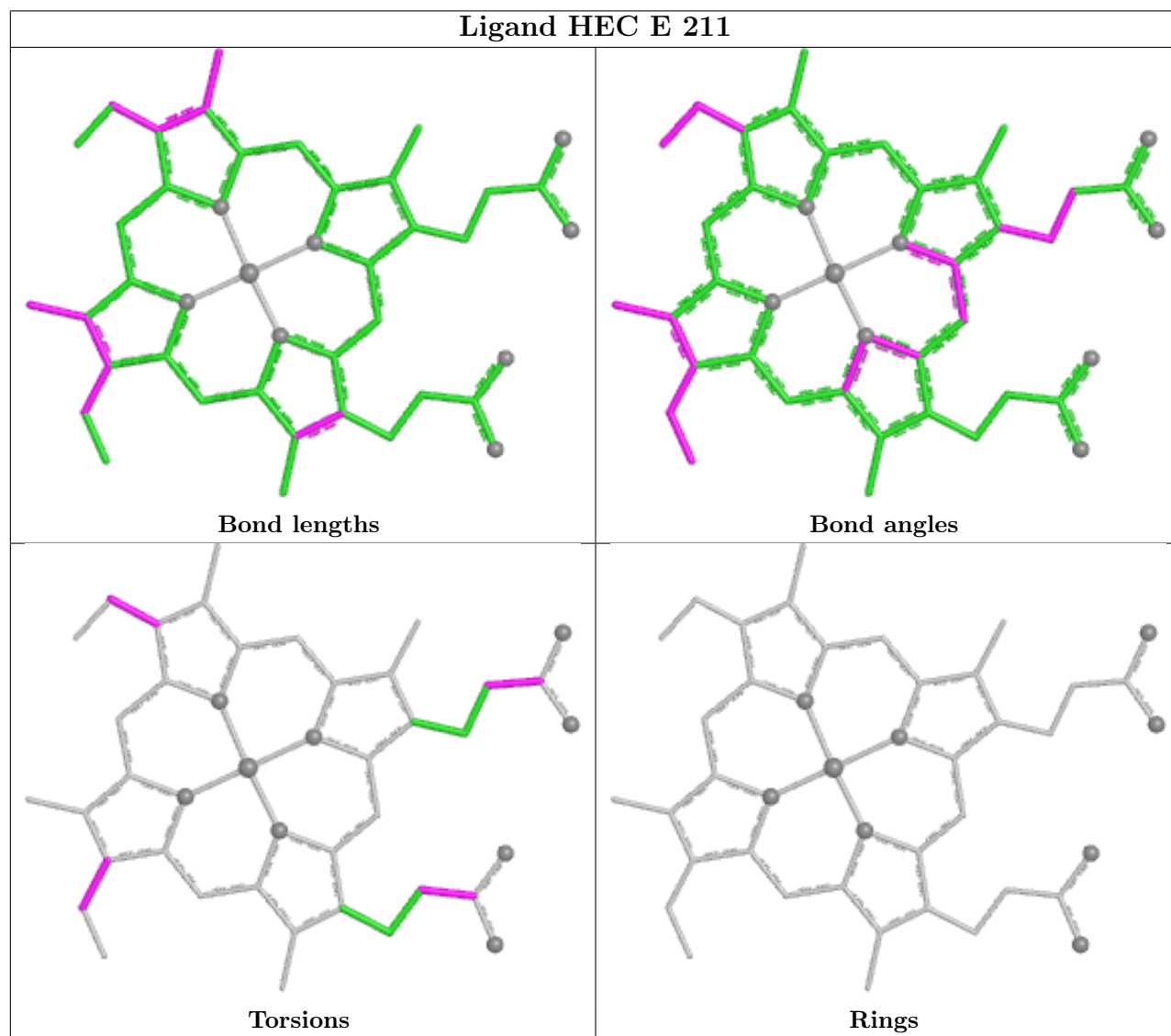
There are no ring outliers.

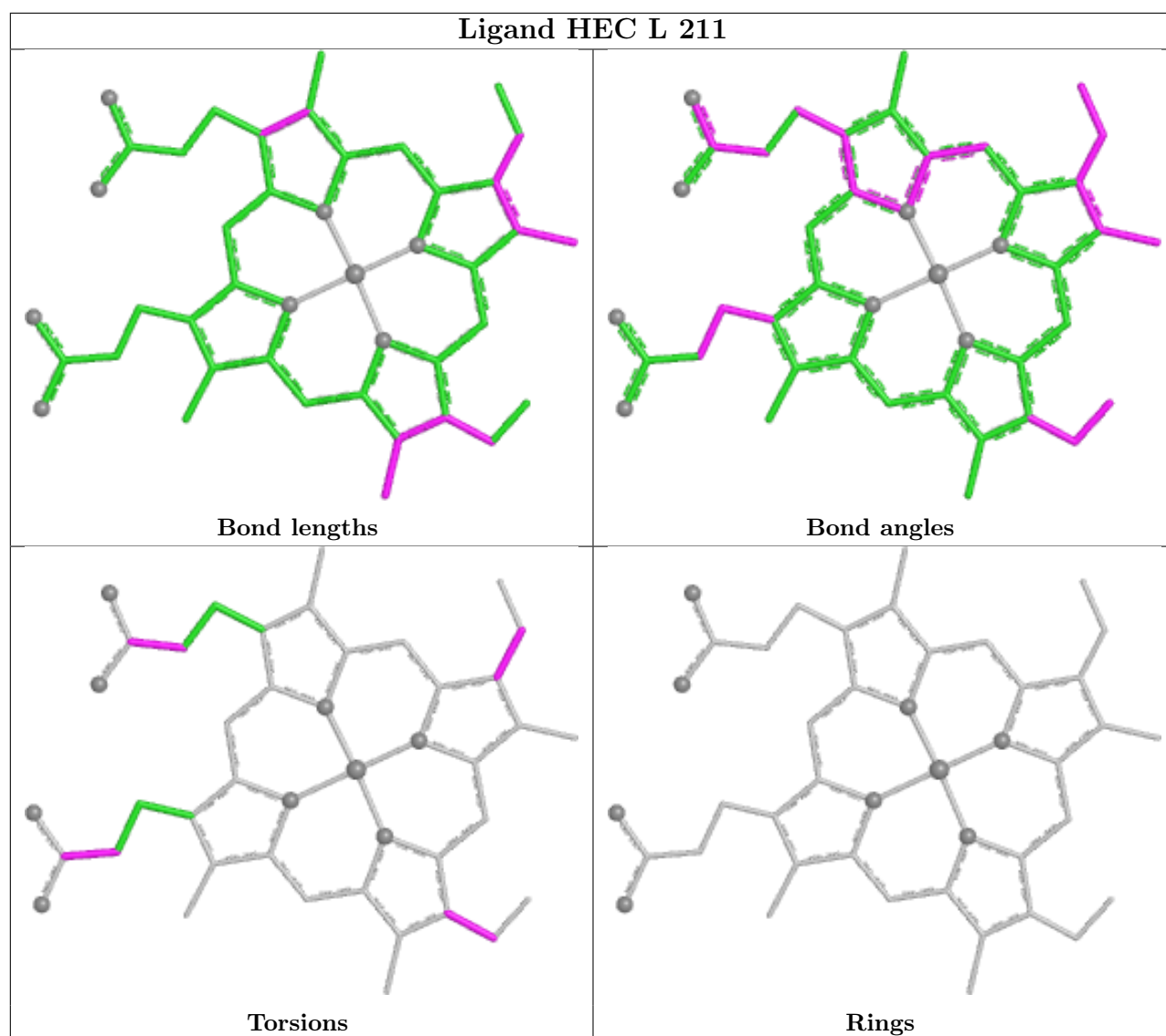
24 monomers are involved in 118 short contacts:

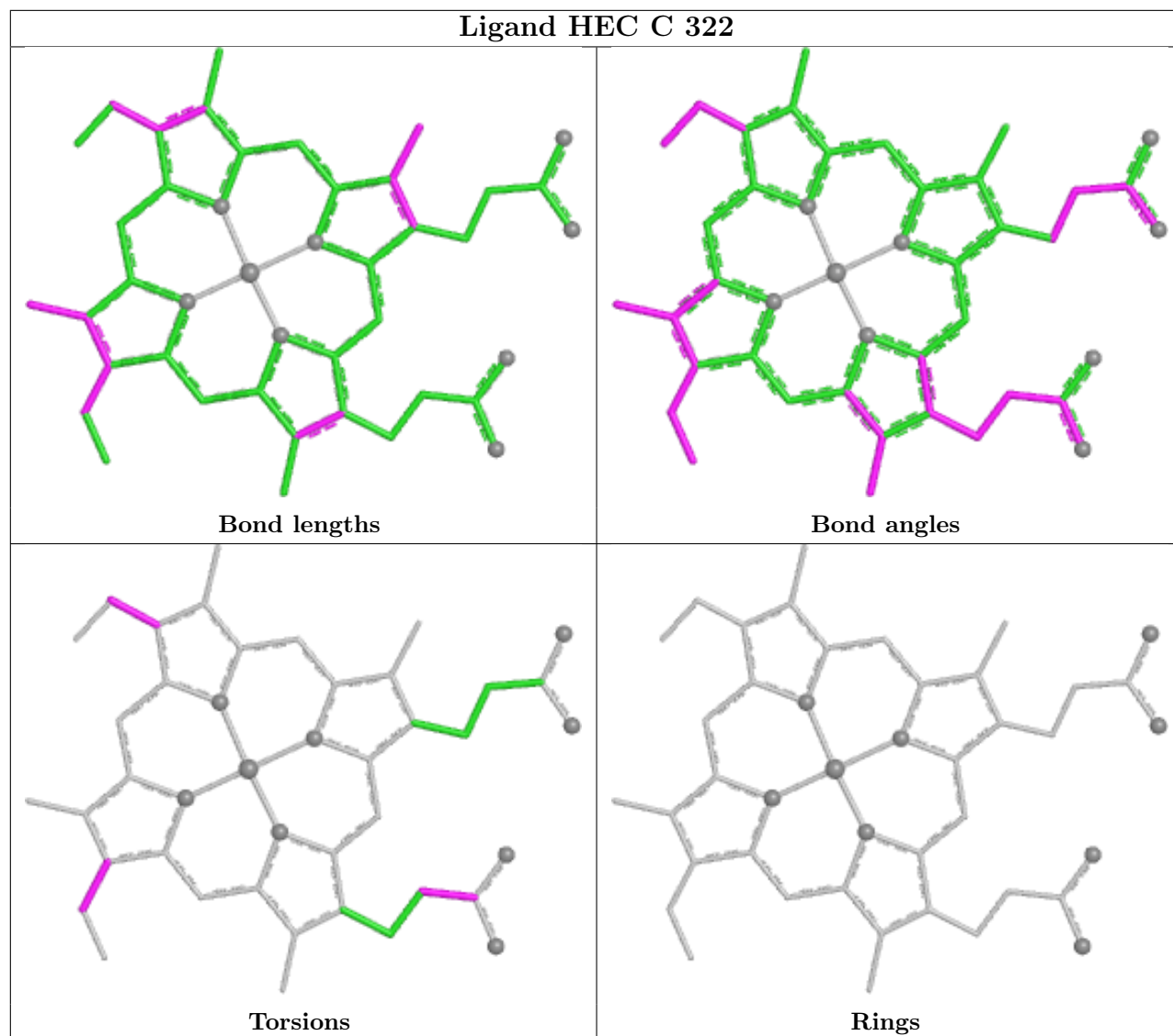
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	E	211	HEC	2	0
11	I	323	FC6	6	0
10	L	211	HEC	2	0
11	F	323	FC6	10	0
10	C	322	HEC	2	0
11	M	323	FC6	3	0
5	K	502	HEM	7	0
5	D	502	HEM	8	0
10	B	211	HEC	3	0
10	I	322	HEC	1	0
5	K	501	HEM	5	0
10	F	321	HEC	10	0
11	C	323	FC6	4	0
5	A	501	HEM	5	0
10	C	321	HEC	6	0
10	I	321	HEC	4	0
5	G	502	HEM	7	0
10	M	322	HEC	3	0
5	G	501	HEM	6	0
10	F	322	HEC	5	0
10	H	211	HEC	4	0
10	M	321	HEC	5	0
5	D	501	HEM	4	0
5	A	502	HEM	6	0

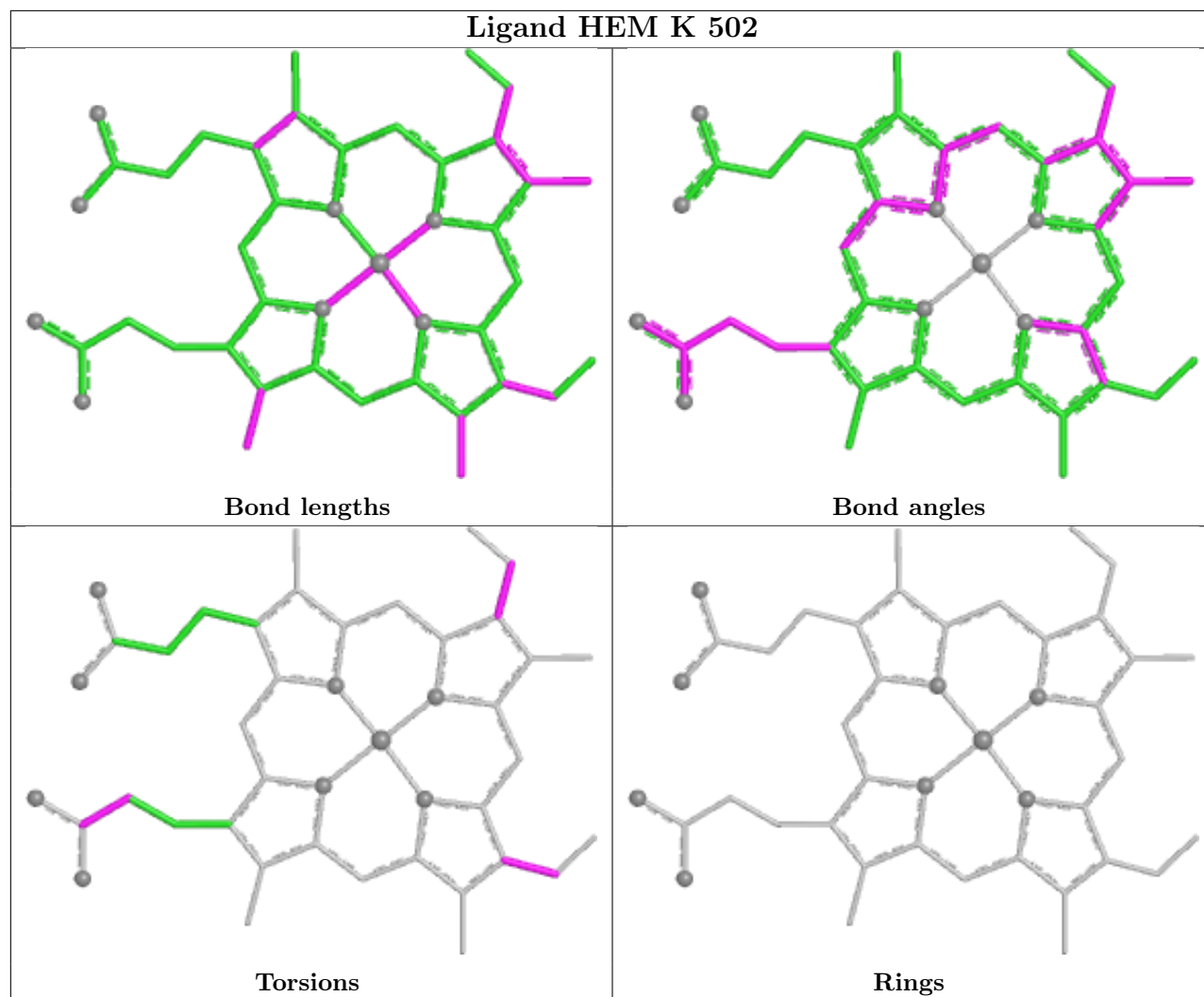
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

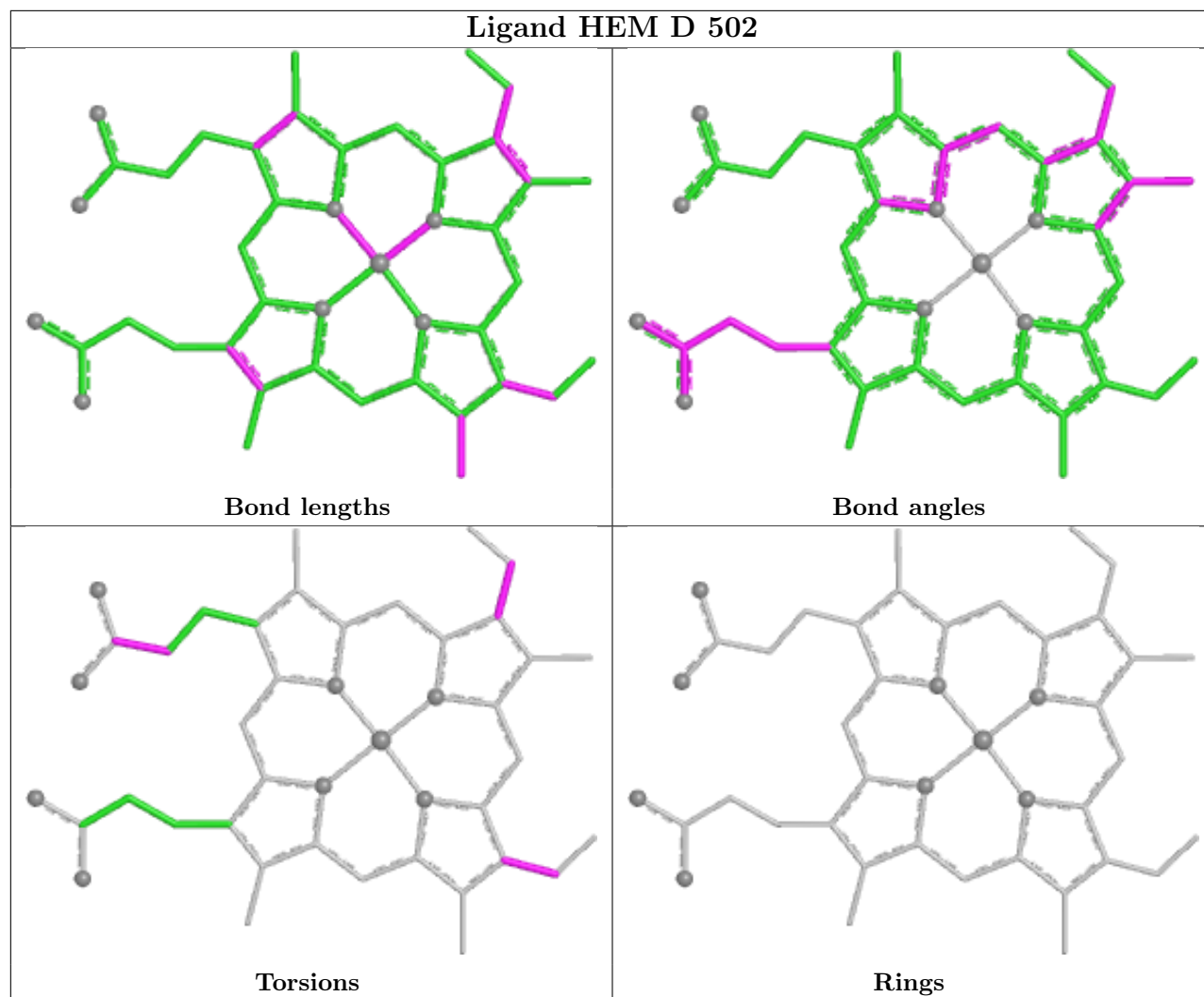
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

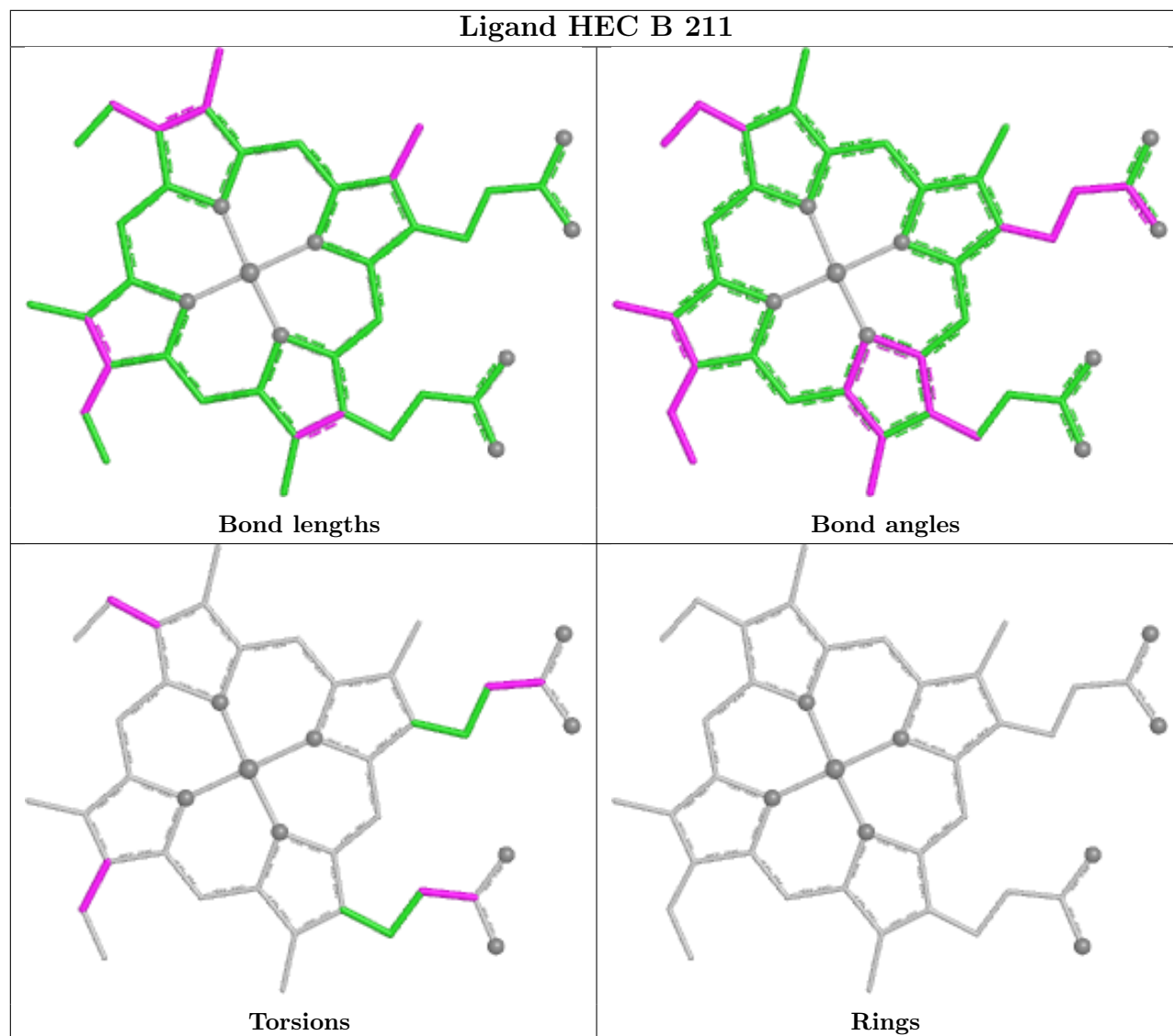


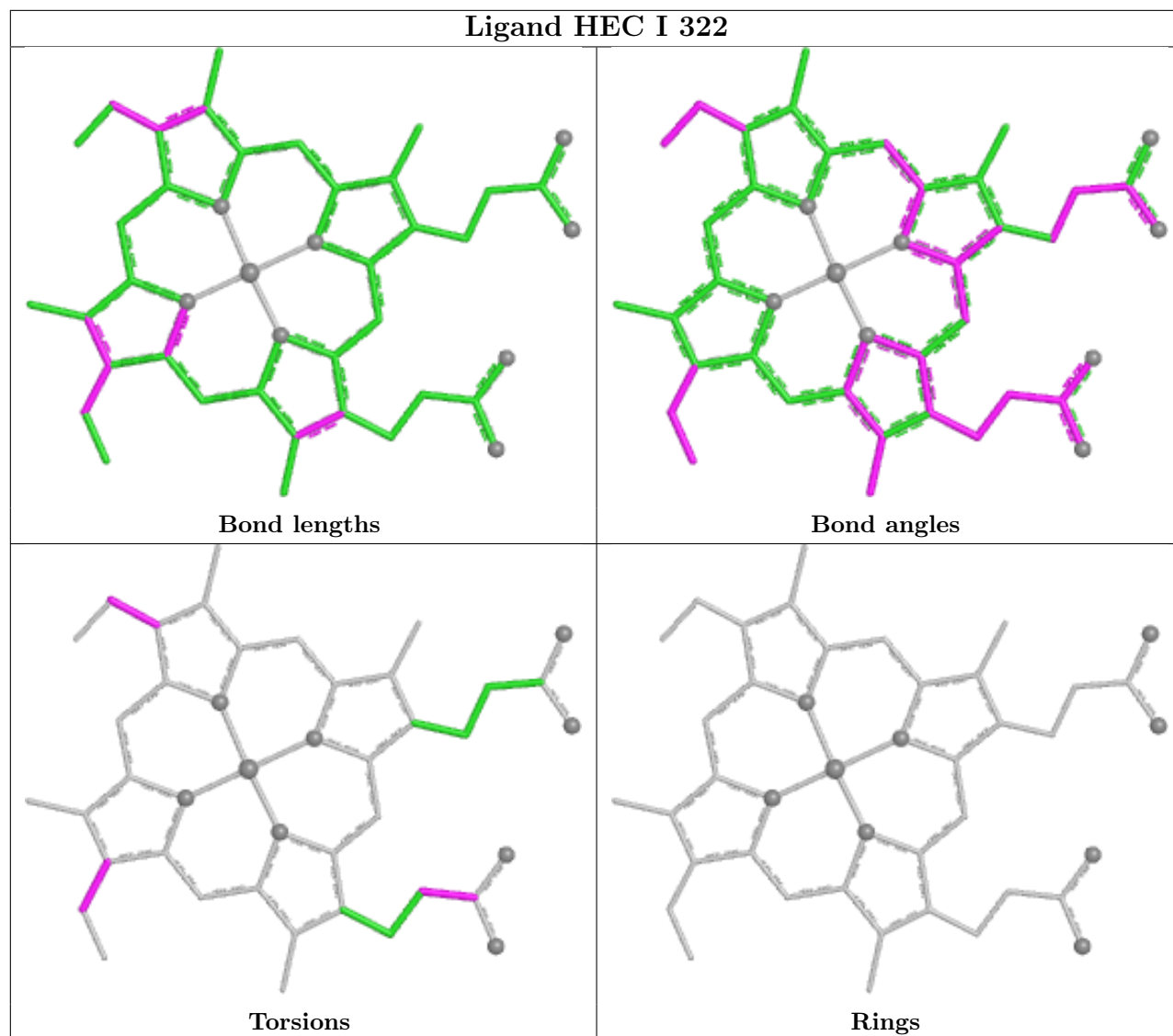


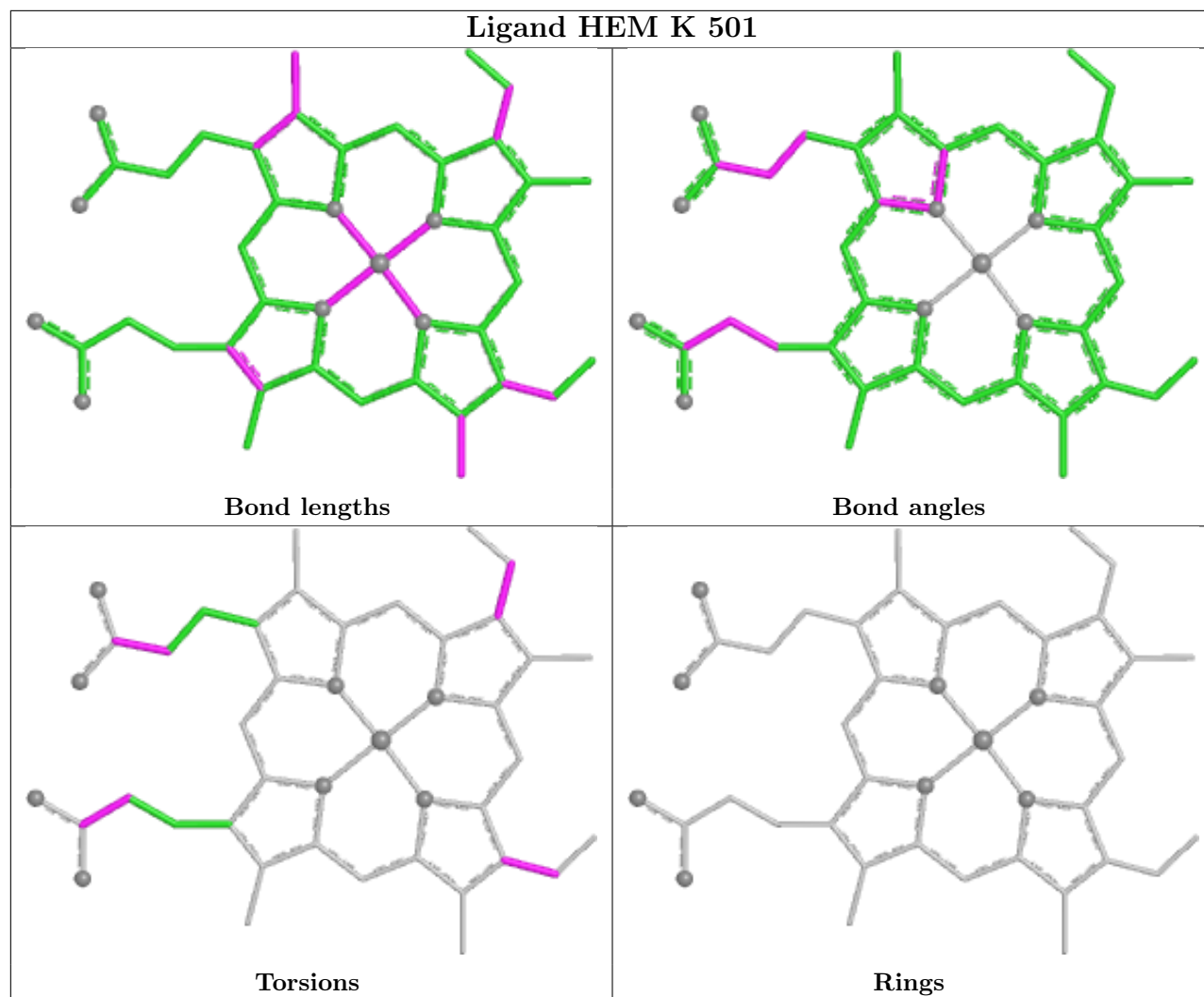


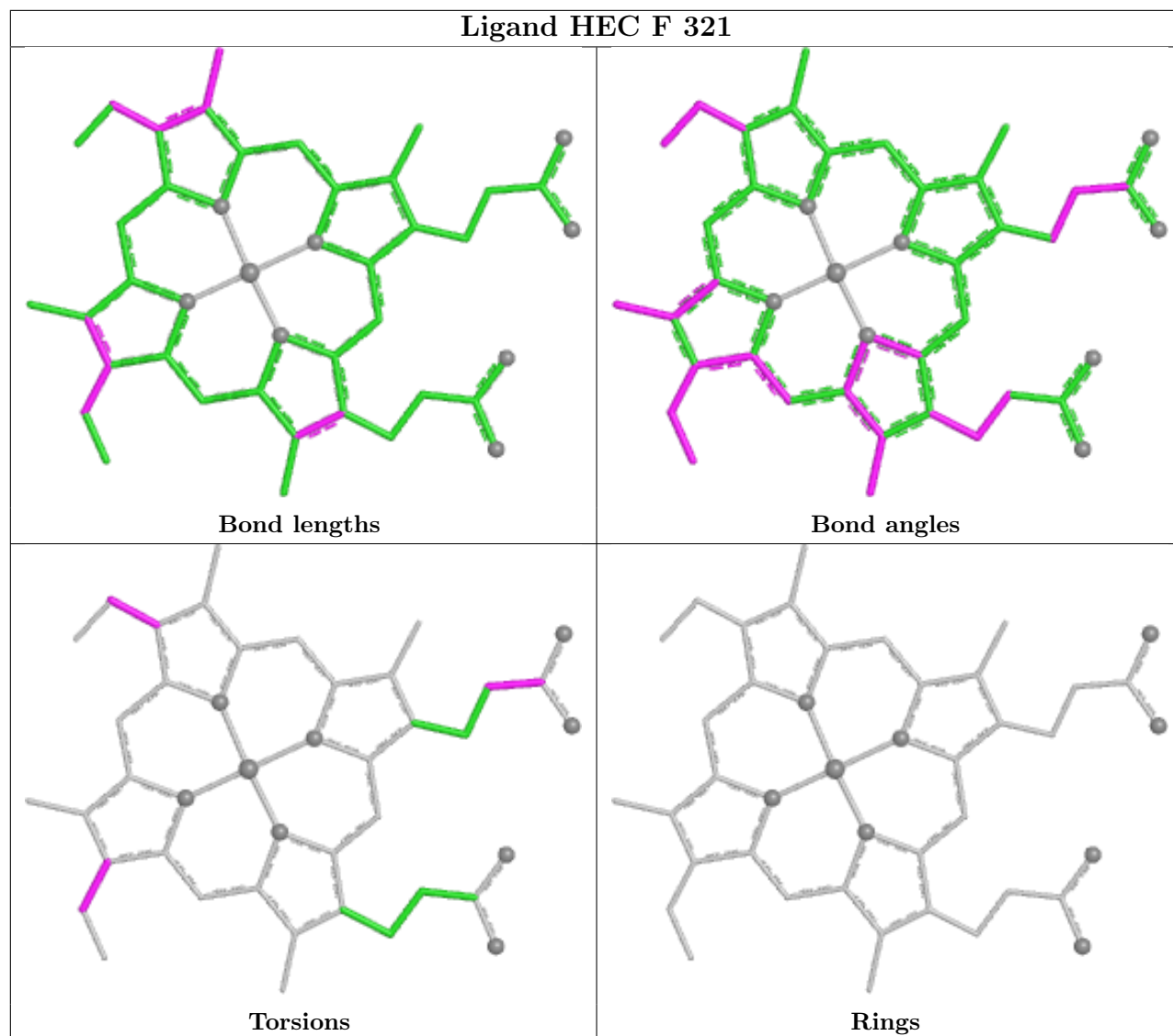


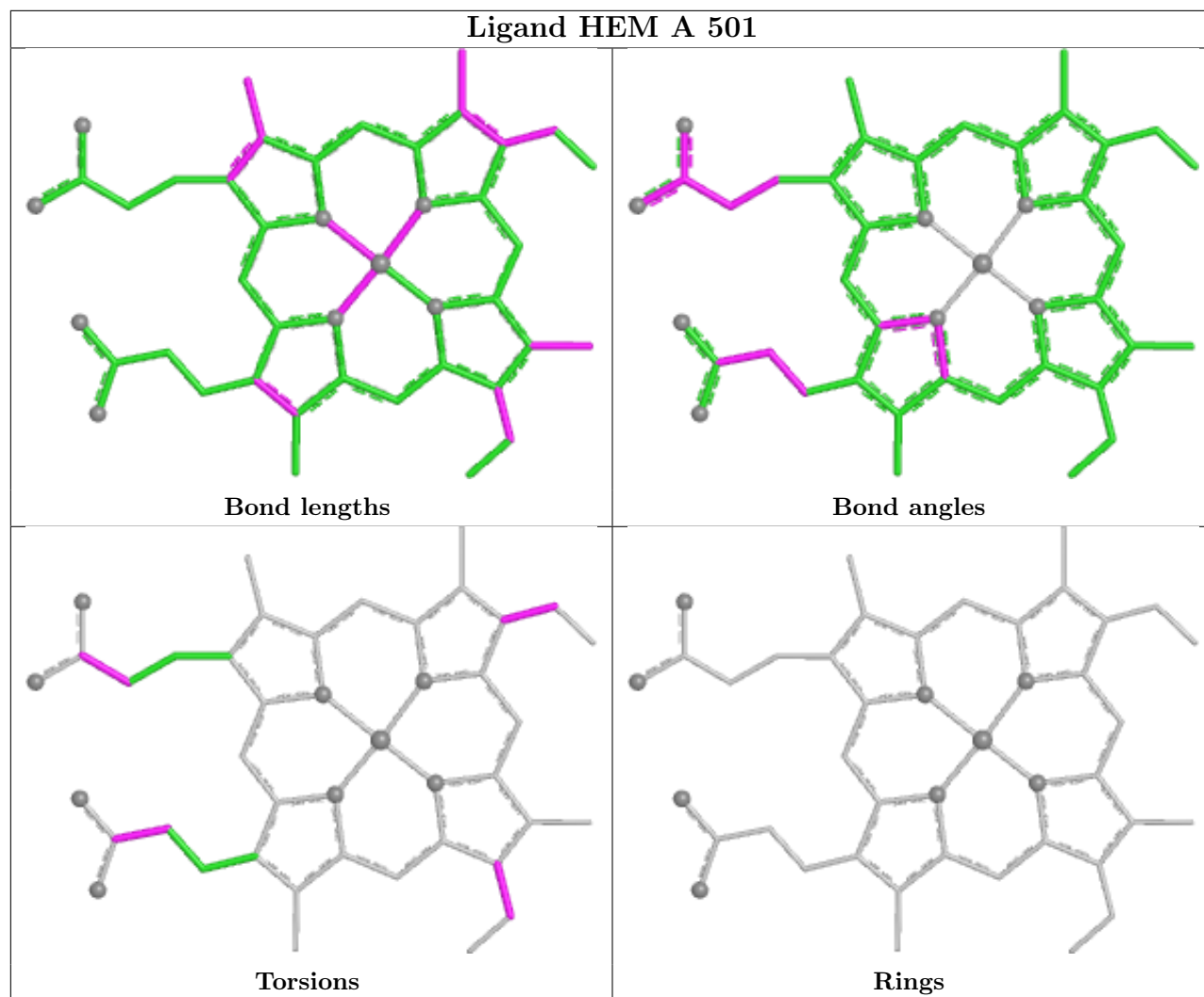


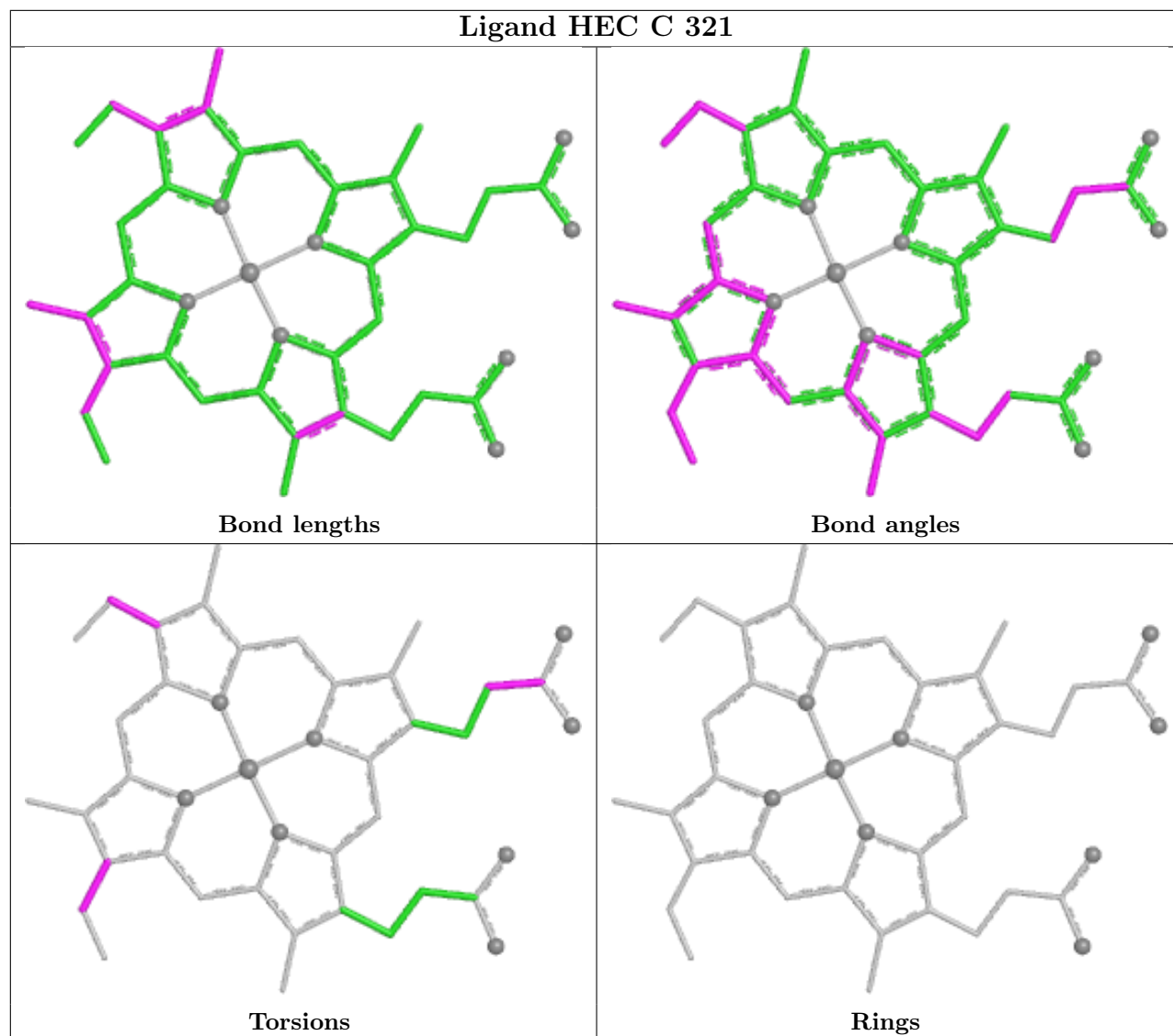


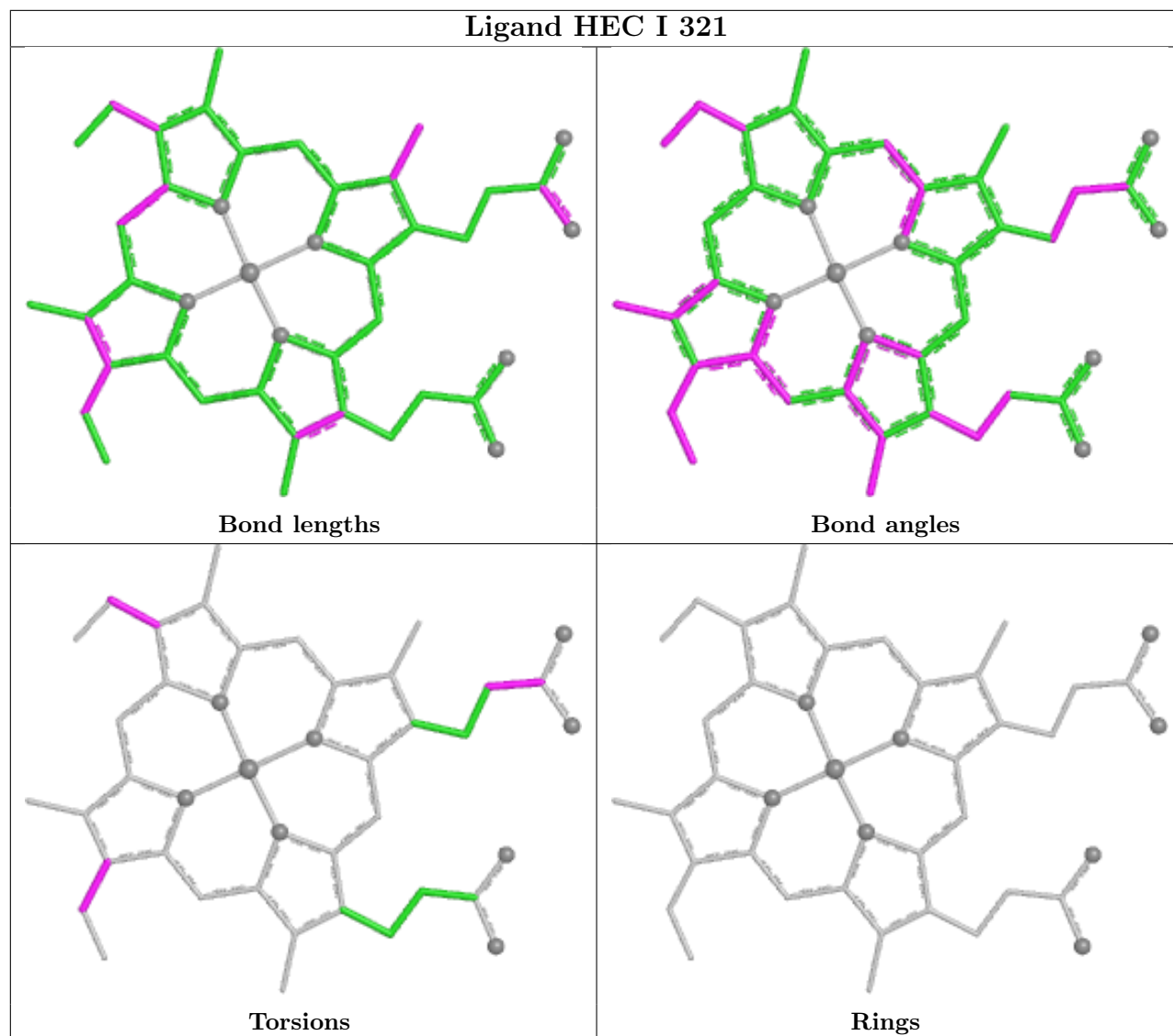


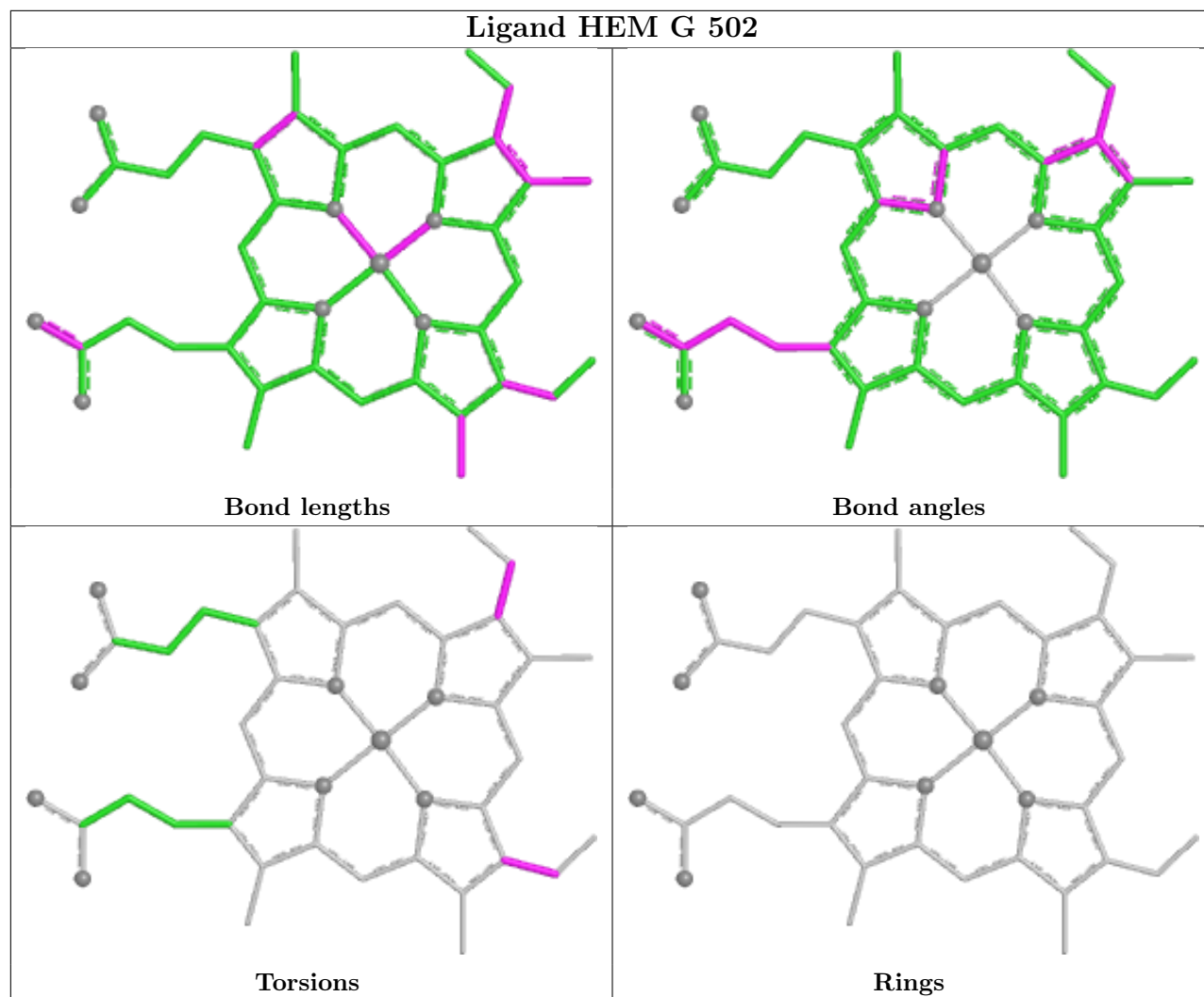


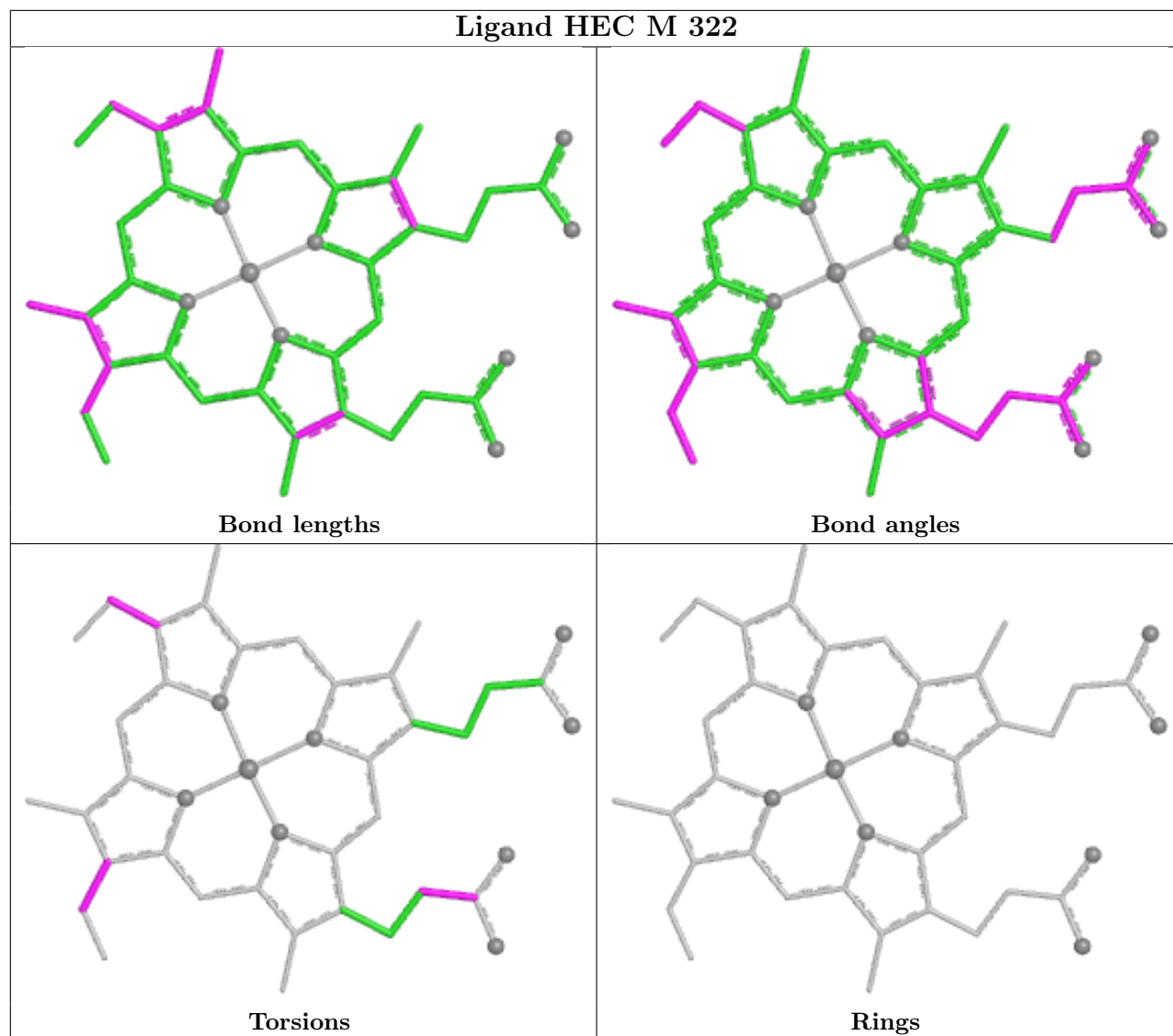


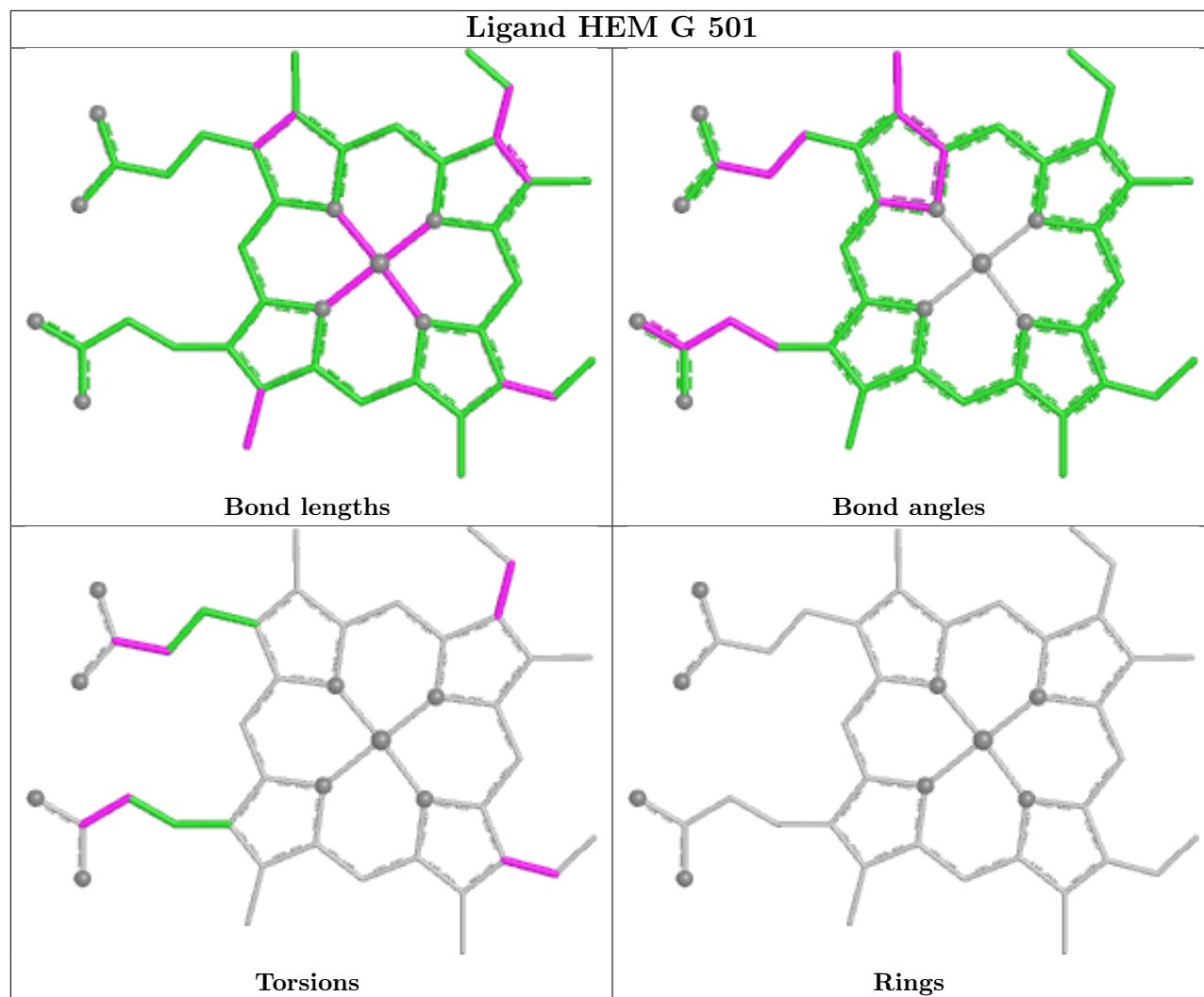


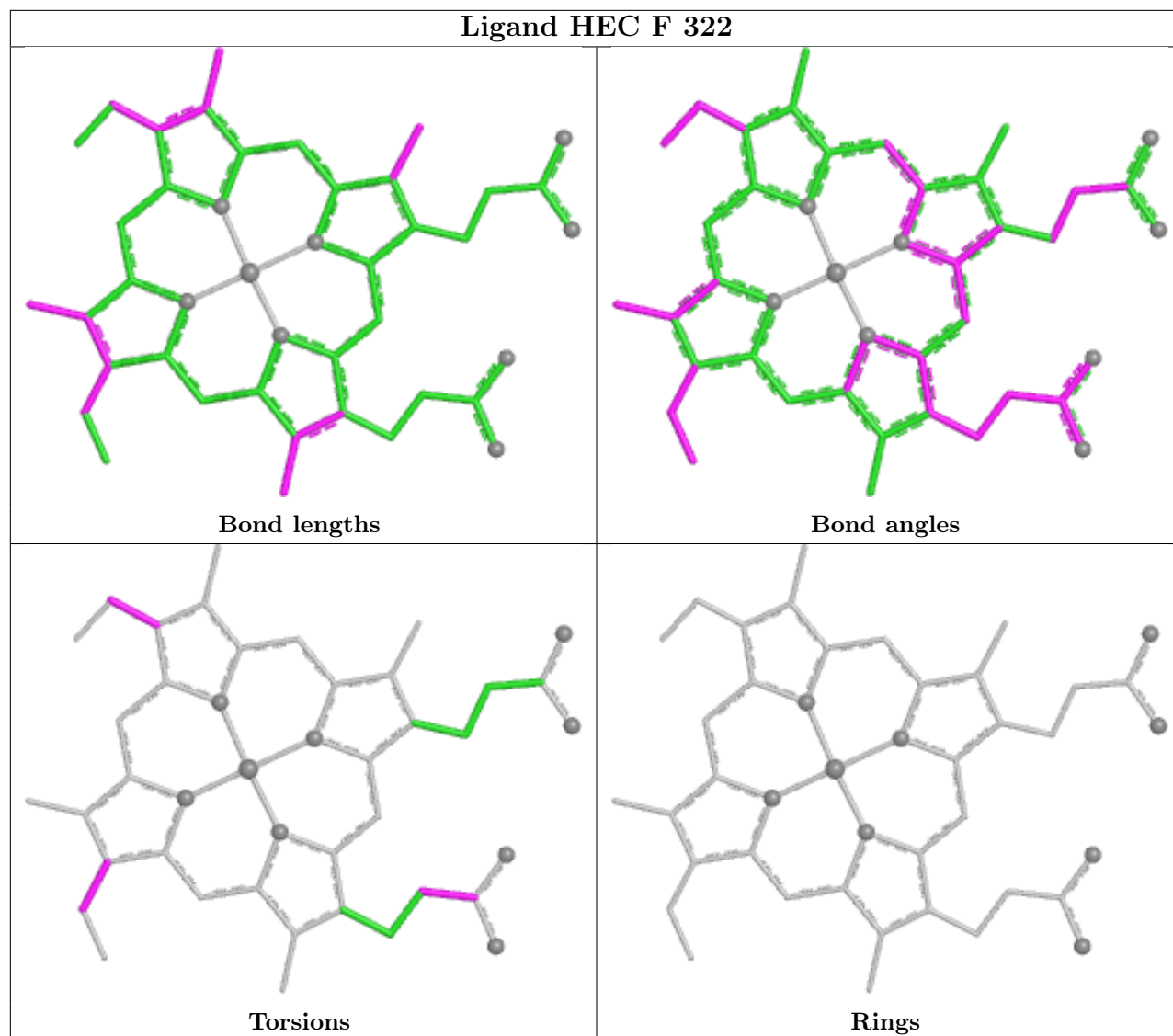


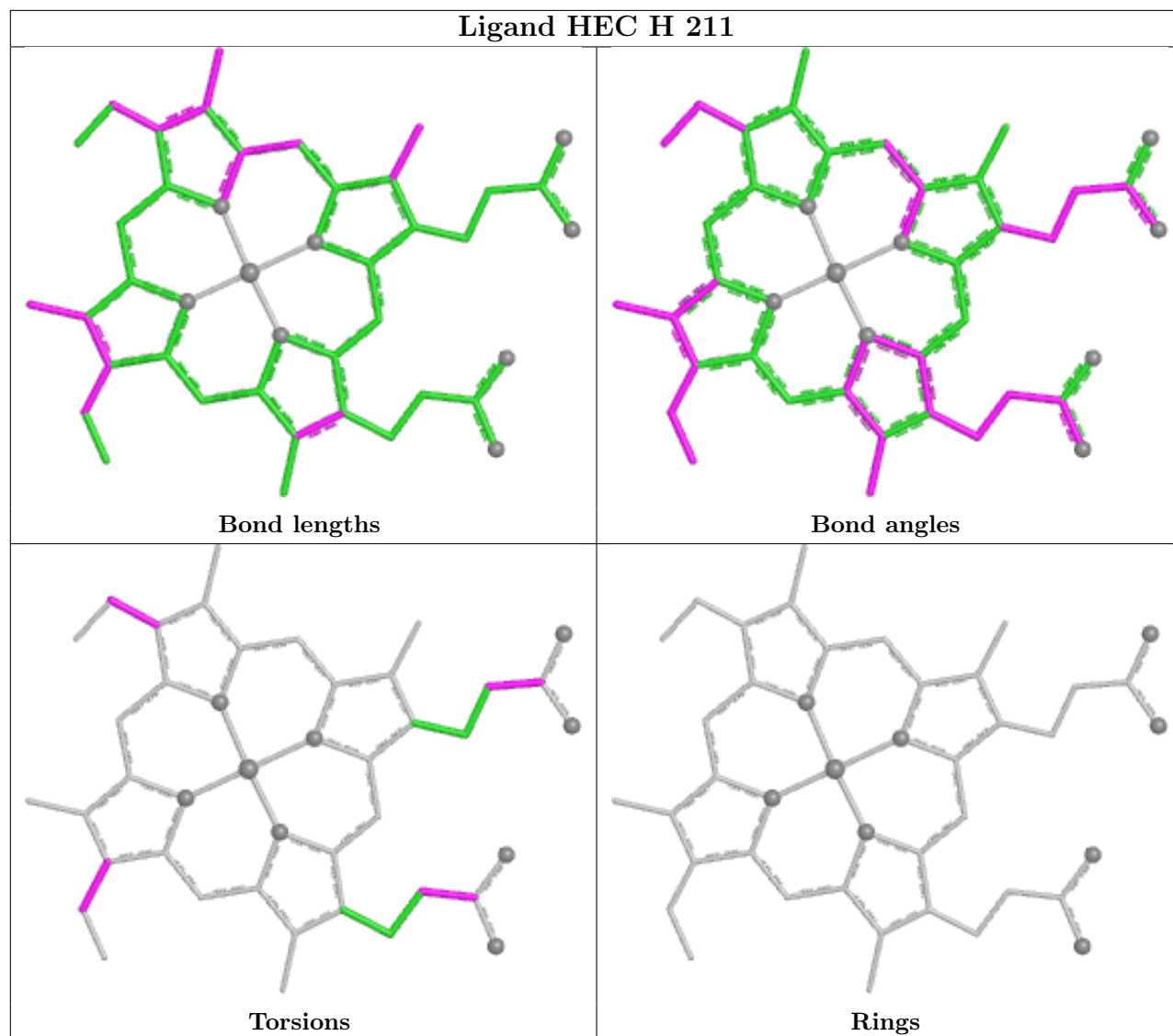


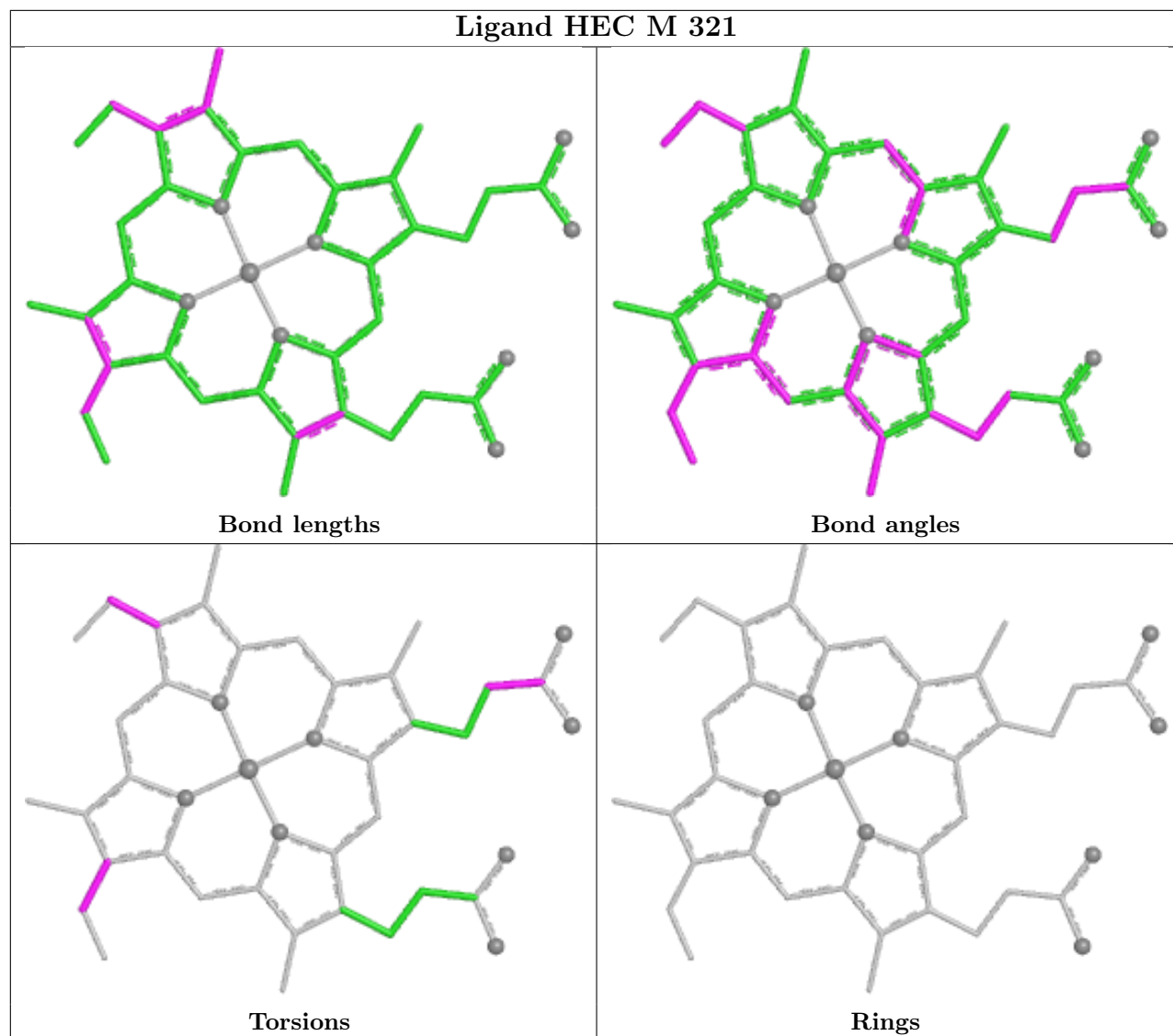


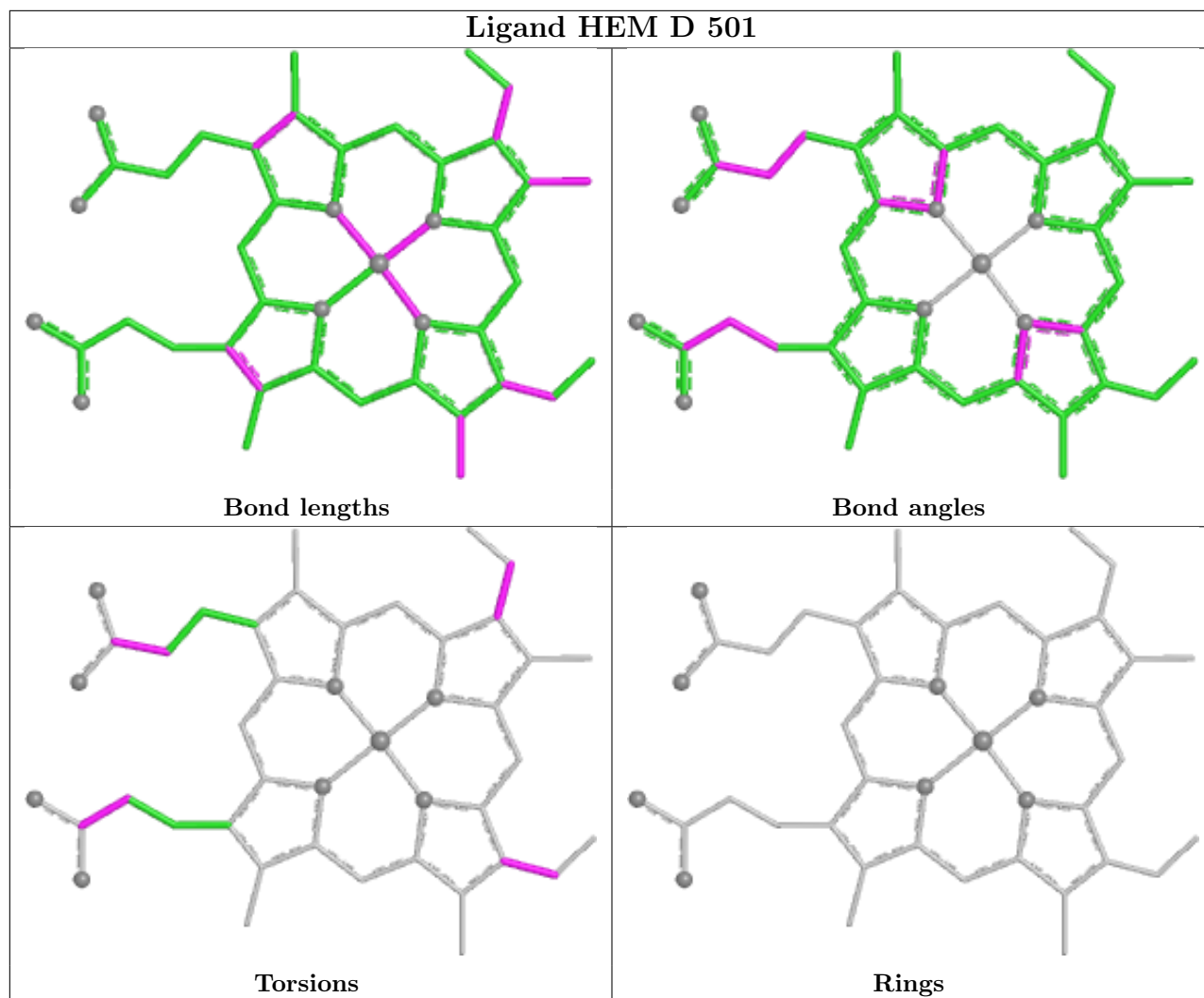


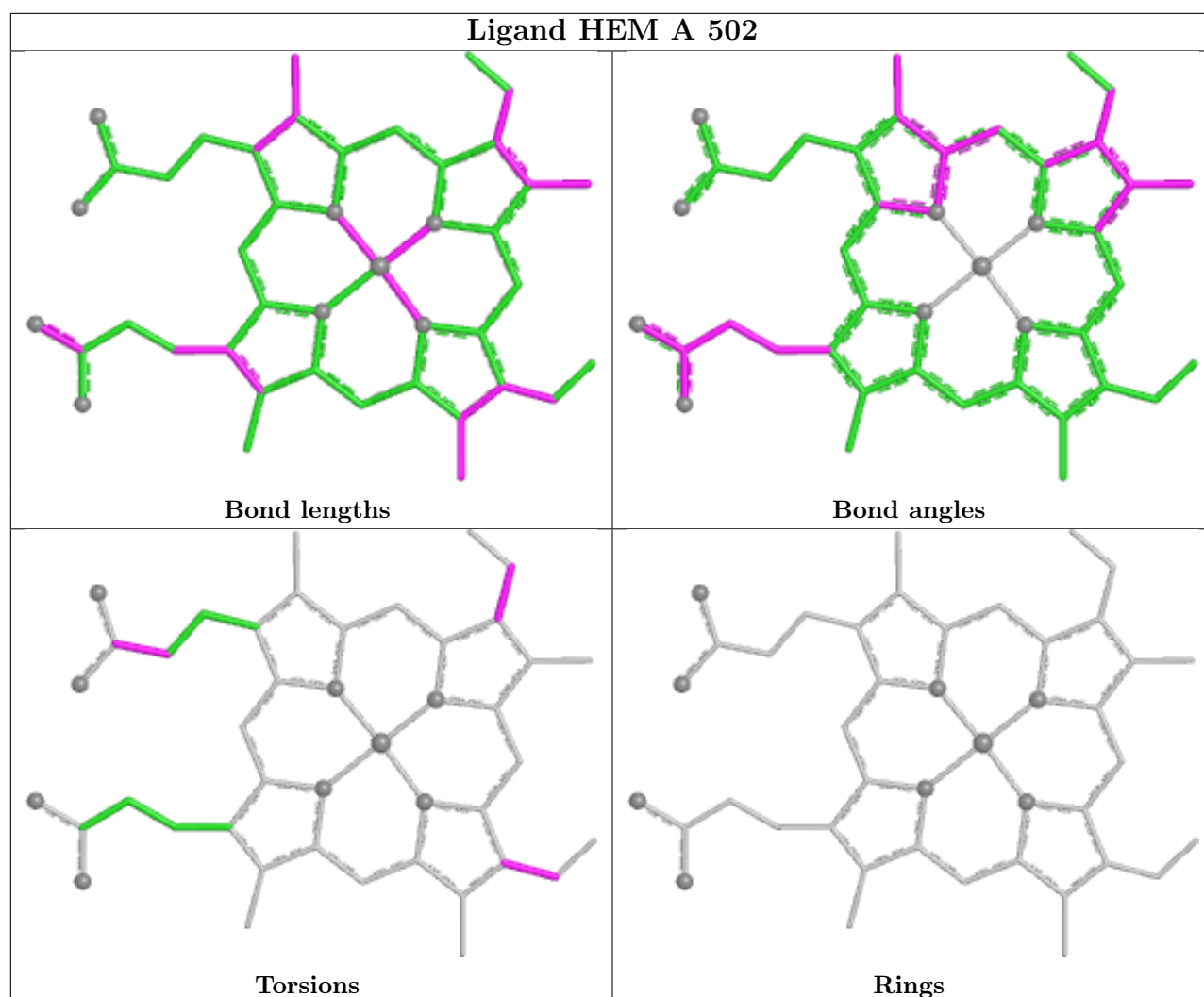












## 5.7 Other polymers [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	466/474 (98%)	-0.74	1 (0%) 91 85	44, 75, 127, 177	0
1	D	463/474 (97%)	-0.31	2 (0%) 88 79	73, 156, 249, 313	0
1	G	465/474 (98%)	-0.65	2 (0%) 88 79	54, 88, 133, 176	0
1	K	465/474 (98%)	-0.30	4 (0%) 81 64	64, 145, 232, 269	0
2	B	197/203 (97%)	-0.84	0 100 100	39, 64, 124, 172	0
2	E	197/203 (97%)	-0.29	1 (0%) 87 76	66, 140, 243, 290	0
2	H	197/203 (97%)	-0.70	1 (0%) 87 76	50, 78, 144, 200	0
2	L	197/203 (97%)	-0.43	0 100 100	51, 105, 244, 304	0
3	C	303/311 (97%)	-0.75	0 100 100	41, 77, 123, 179	0
3	F	303/311 (97%)	0.07	9 (2%) 52 33	71, 182, 279, 333	0
3	I	303/311 (97%)	-0.56	0 100 100	48, 100, 158, 209	0
3	M	303/311 (97%)	-0.45	4 (1%) 75 55	43, 81, 279, 345	0
4	U	0/30	-	-	-	-
4	X	0/30	-	-	-	-
4	Y	0/30	-	-	-	-
4	Z	0/30	-	-	-	-
All	All	3859/4072 (94%)	-0.49	24 (0%) 85 73	39, 103, 235, 345	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	470	ALA	5.1
1	K	470	ALA	5.0
1	D	469	ALA	4.0
3	F	33	ALA	3.3
3	M	33	ALA	2.9

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

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

## 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
9	PO4	D	506	5/5	0.81	0.09	177,178,188,191	0
9	PO4	G	506	5/5	0.89	0.23	27,29,32,35	0
11	FC6	F	323	13/13	0.89	0.24	37,40,42,46	13
11	FC6	I	323	13/13	0.89	0.26	52,57,68,80	13
7	CA	G	505	1/1	0.90	0.06	91,91,91,91	0
9	PO4	K	506	5/5	0.91	0.06	140,144,146,153	0
10	HEC	F	322	43/43	0.91	0.14	34,43,47,50	0
10	HEC	F	321	43/43	0.93	0.14	20,24,28,35	0
9	PO4	A	506	5/5	0.94	0.15	21,22,23,24	0
7	CA	D	505	1/1	0.94	0.06	138,138,138,138	0
7	CA	A	505	1/1	0.94	0.05	88,88,88,88	0
7	CA	K	505	1/1	0.94	0.05	133,133,133,133	0
11	FC6	C	323	13/13	0.96	0.16	33,39,46,55	13
5	HEM	K	501	43/43	0.96	0.13	117,127,147,153	0
10	HEC	E	211	43/43	0.96	0.09	16,18,27,32	0
8	PEO	K	508	2/2	0.97	0.12	130,130,130,135	0
7	CA	G	504	1/1	0.97	0.05	74,74,74,74	0
10	HEC	L	211	43/43	0.97	0.08	18,21,26,30	0
10	HEC	C	322	43/43	0.98	0.06	22,28,34,36	0
5	HEM	K	502	43/43	0.98	0.10	85,102,115,125	0
5	HEM	D	501	43/43	0.98	0.09	96,121,137,149	0
5	HEM	D	502	43/43	0.98	0.08	83,96,110,112	0
10	HEC	H	211	43/43	0.98	0.06	24,27,32,38	0
10	HEC	I	321	43/43	0.98	0.07	20,24,34,39	0
10	HEC	I	322	43/43	0.98	0.06	24,28,31,36	0
7	CA	E	504	1/1	0.98	0.05	105,105,105,105	0
5	HEM	G	502	43/43	0.98	0.07	56,61,70,83	0

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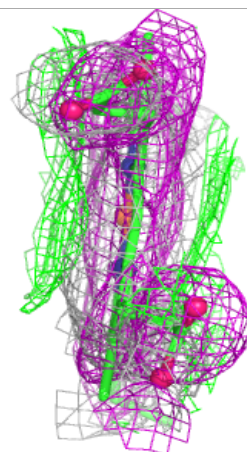
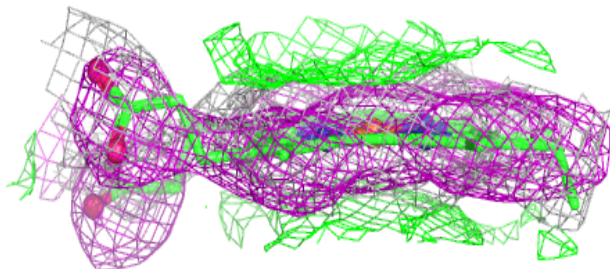
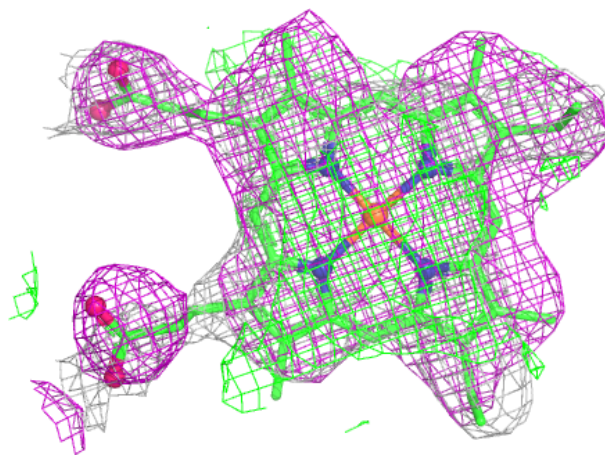
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	HEM	A	502	43/43	0.98	0.08	43,52,61,72	0
10	HEC	C	321	43/43	0.98	0.06	21,27,36,44	0
11	FC6	M	323	13/13	0.98	0.10	28,30,38,39	13
10	HEC	B	211	43/43	0.99	0.05	25,28,35,46	0
8	PEO	G	508	2/2	0.99	0.04	71,71,71,74	0
7	CA	B	504	1/1	0.99	0.06	51,51,51,51	0
10	HEC	M	321	43/43	0.99	0.06	18,25,35,43	0
10	HEC	M	322	43/43	0.99	0.06	19,23,27,34	0
5	HEM	A	501	43/43	0.99	0.06	47,57,64,71	0
7	CA	K	504	1/1	0.99	0.02	99,99,99,99	0
5	HEM	G	501	43/43	0.99	0.07	56,71,81,89	0
8	PEO	D	508	2/2	0.99	0.06	133,133,133,141	0
6	CU	K	503	1/1	1.00	0.07	135,135,135,135	0
8	PEO	A	508	2/2	1.00	0.04	57,57,57,63	0
6	CU	A	503	1/1	1.00	0.03	59,59,59,59	0
6	CU	D	503	1/1	1.00	0.01	115,115,115,115	0
6	CU	G	503	1/1	1.00	0.01	77,77,77,77	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.

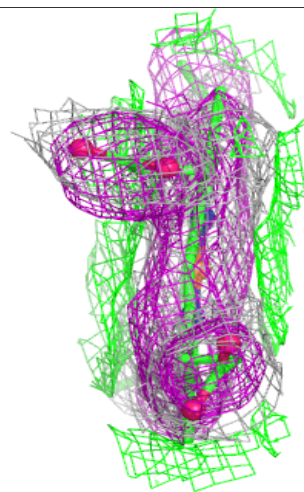
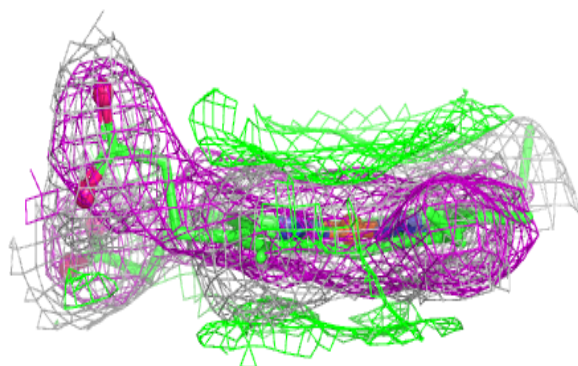
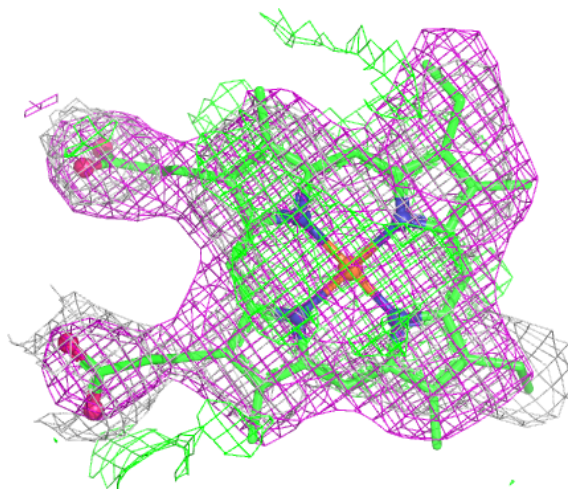
**Electron density around HEC F 322:**

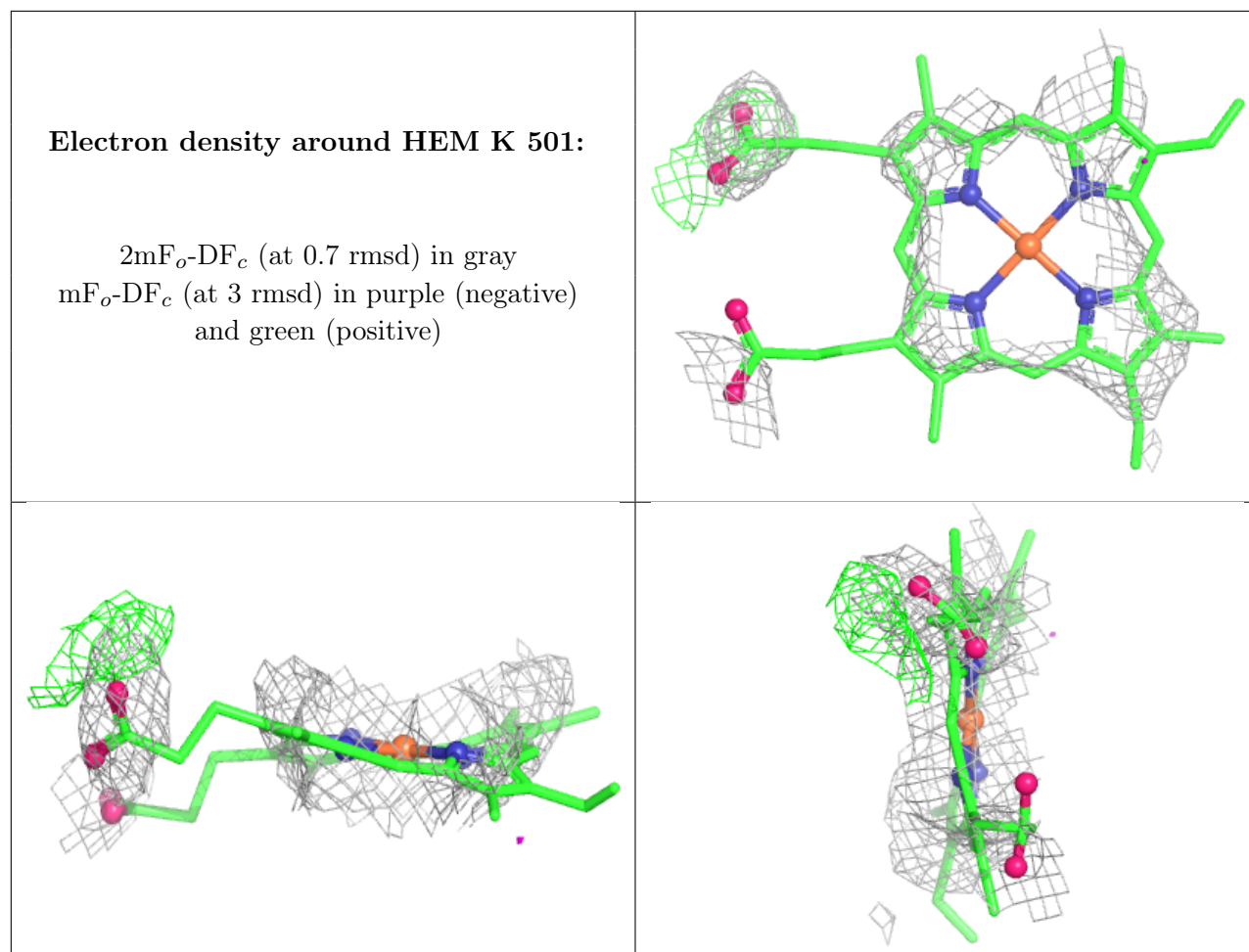
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEC F 321:**

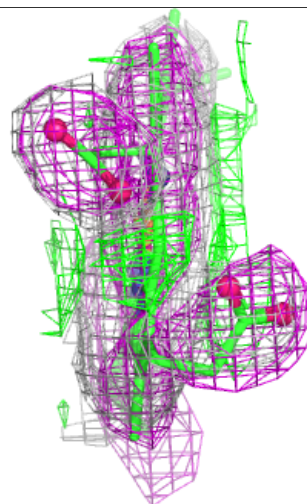
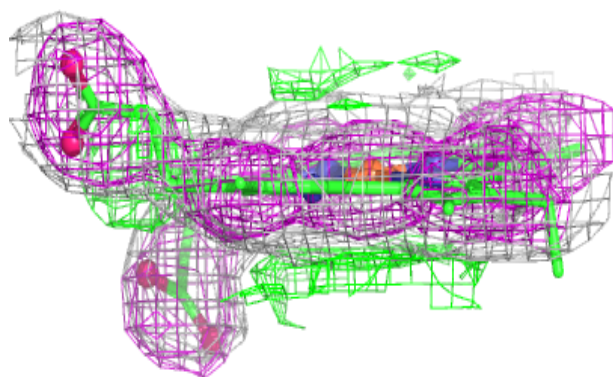
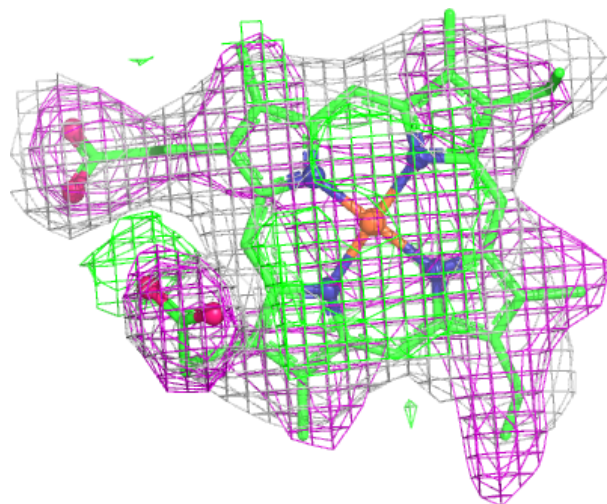
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





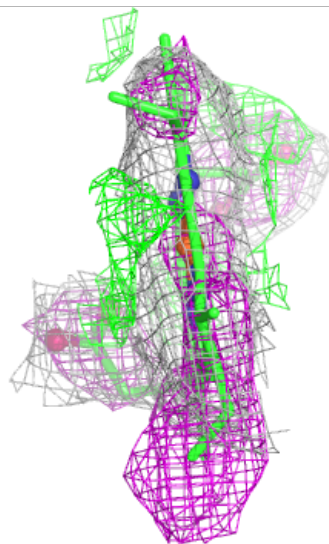
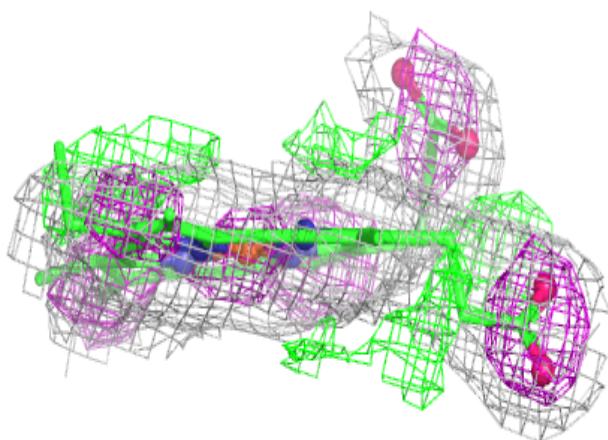
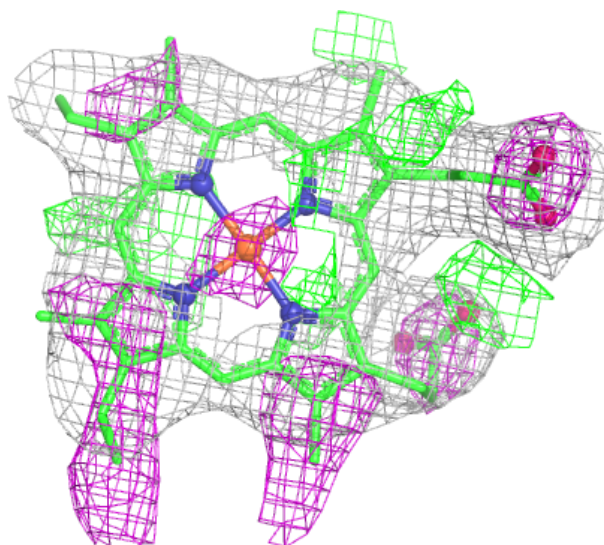
**Electron density around HEC E 211:**

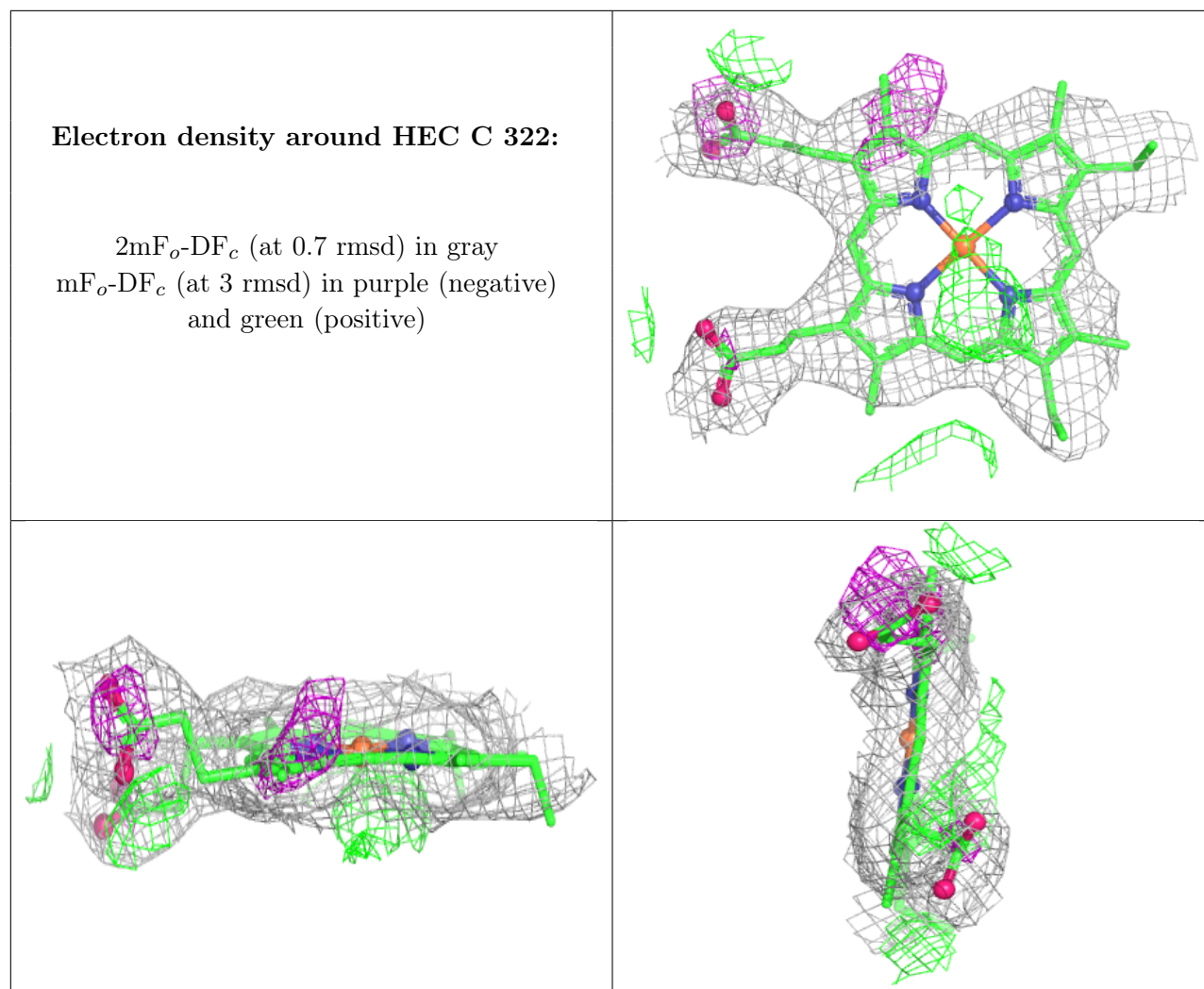
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEC L 211:**

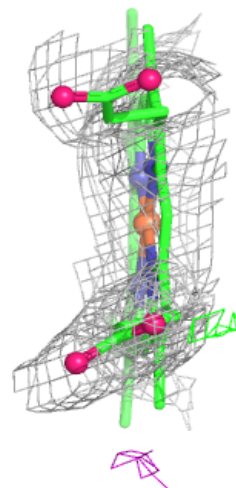
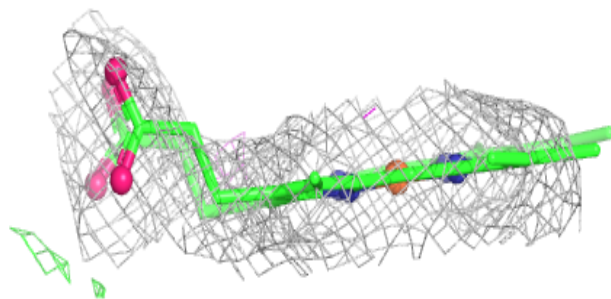
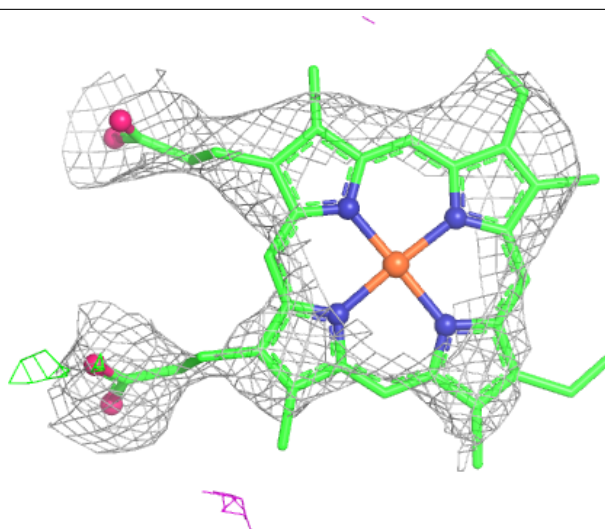
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

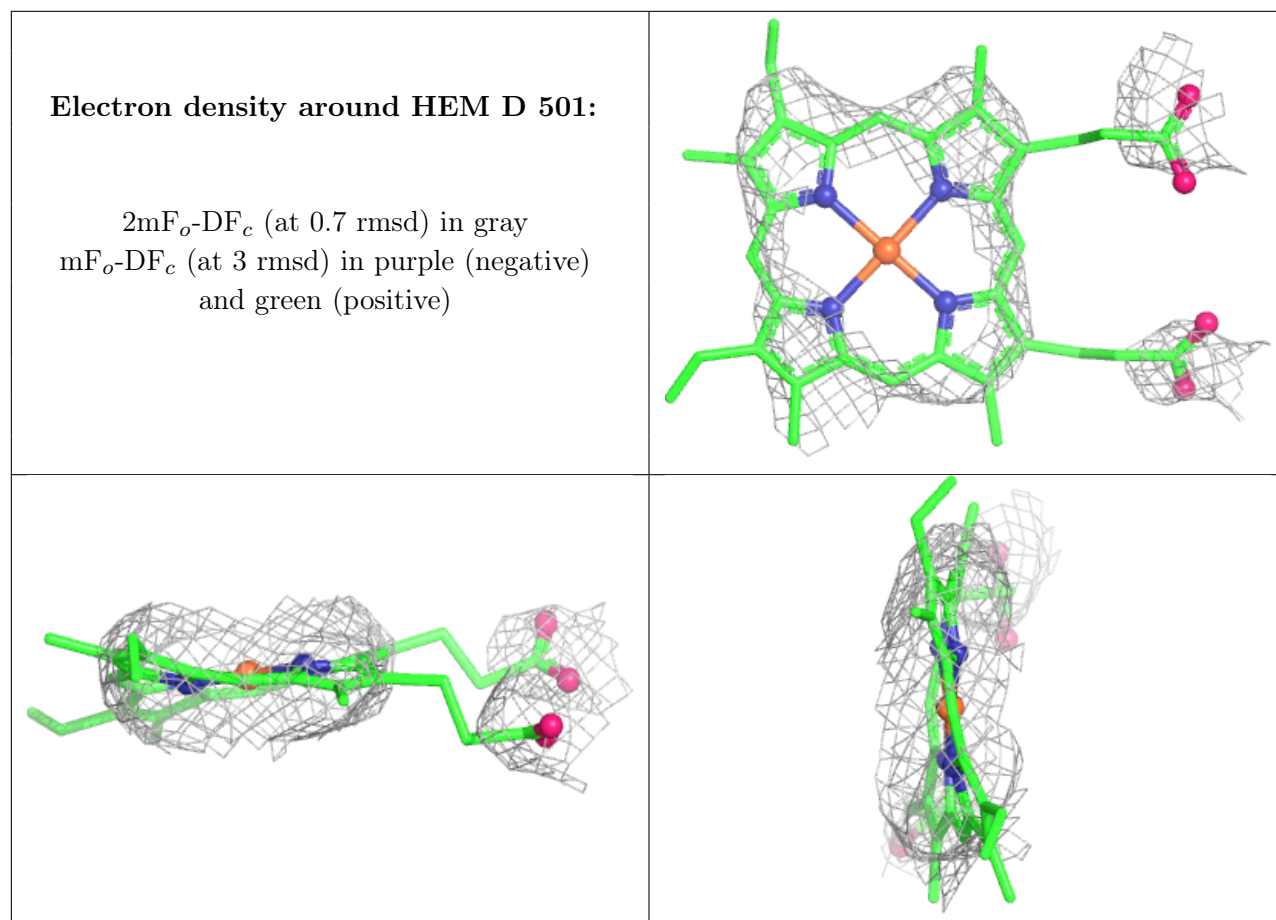


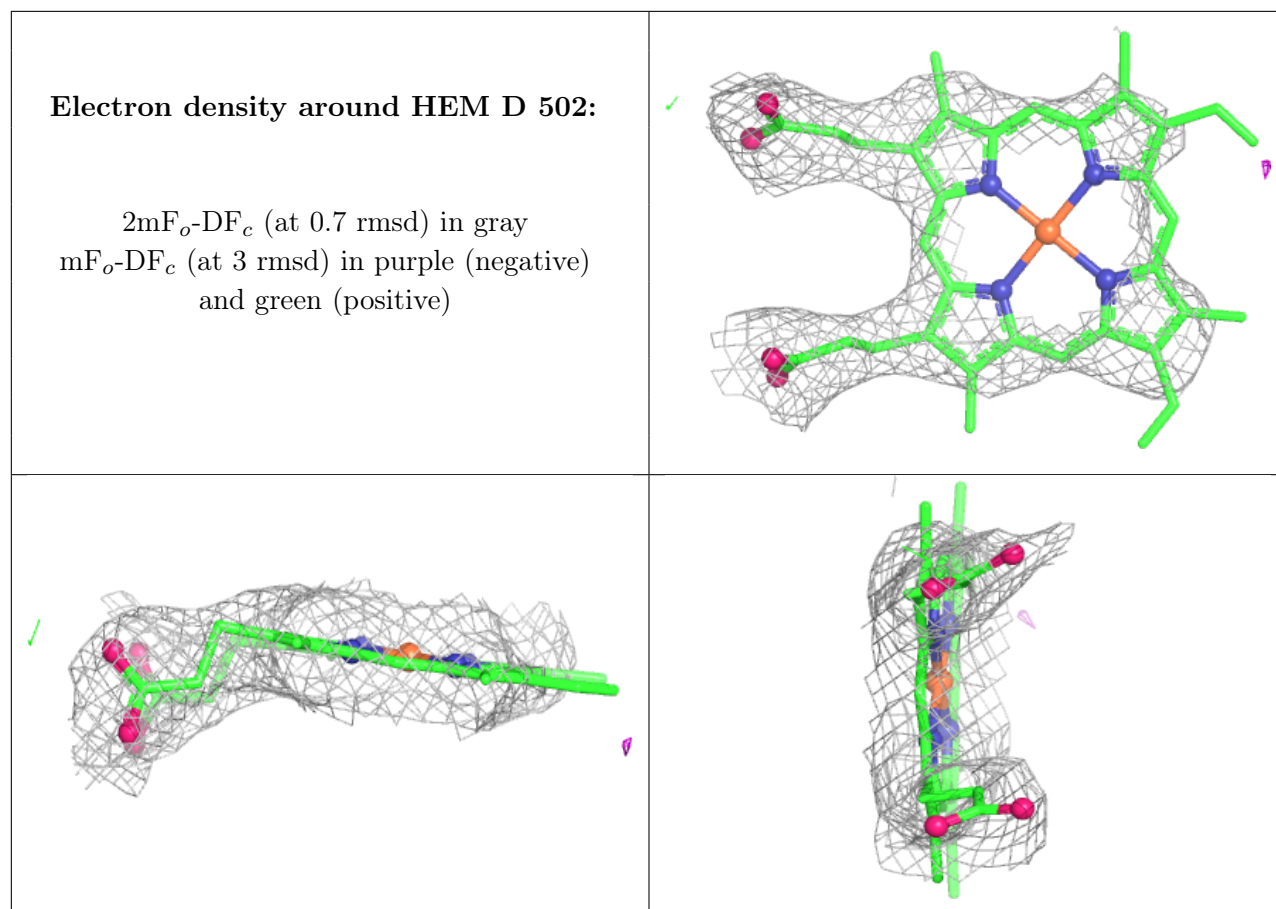


**Electron density around HEM K 502:**

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

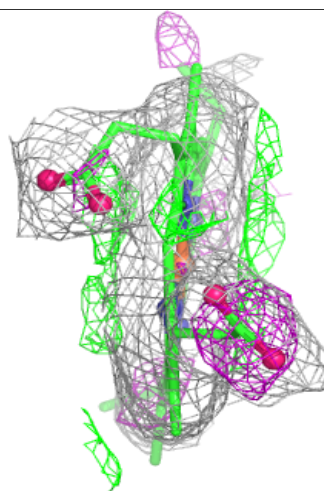
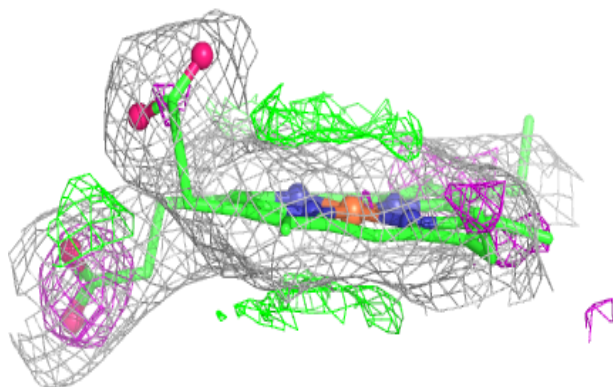
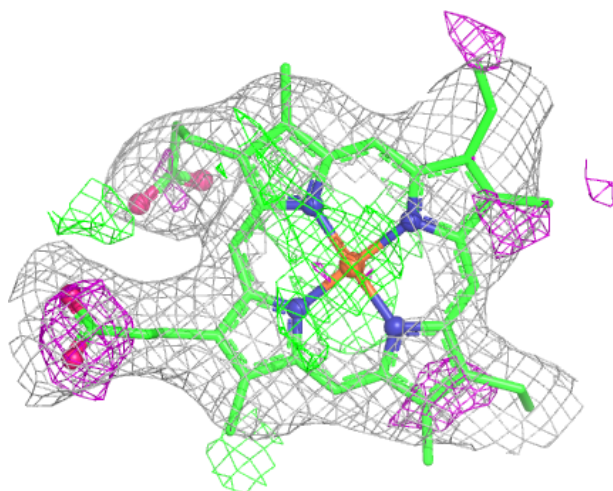






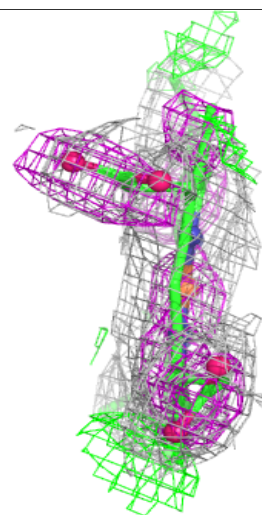
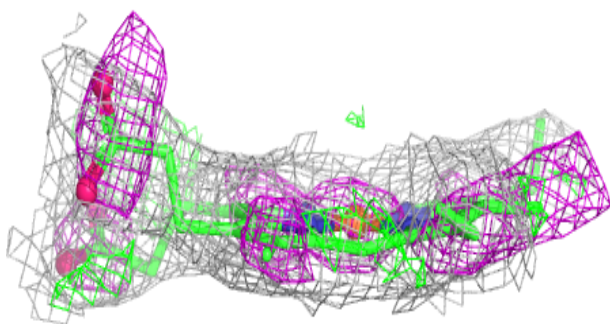
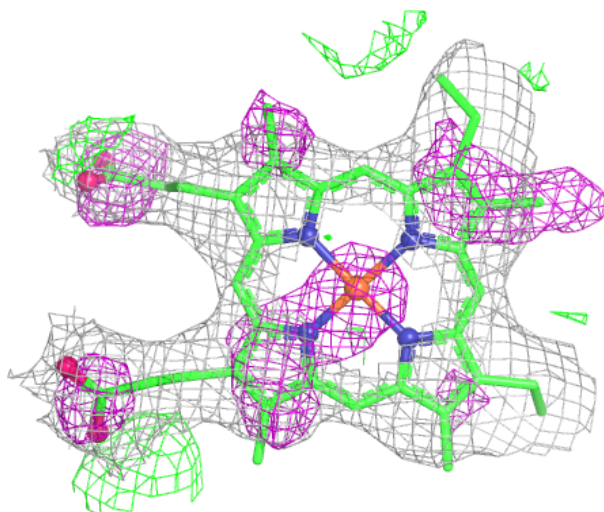
**Electron density around HEC H 211:**

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



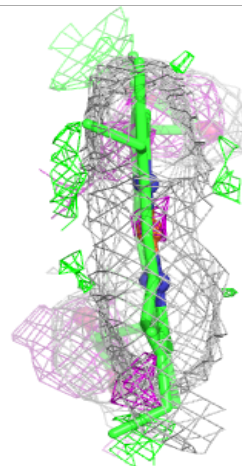
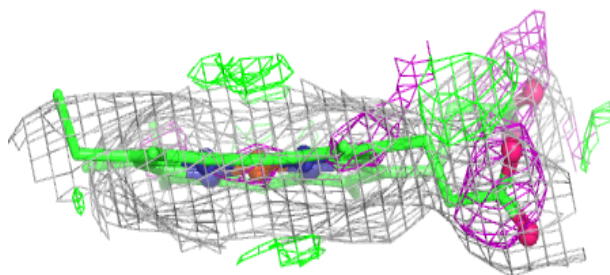
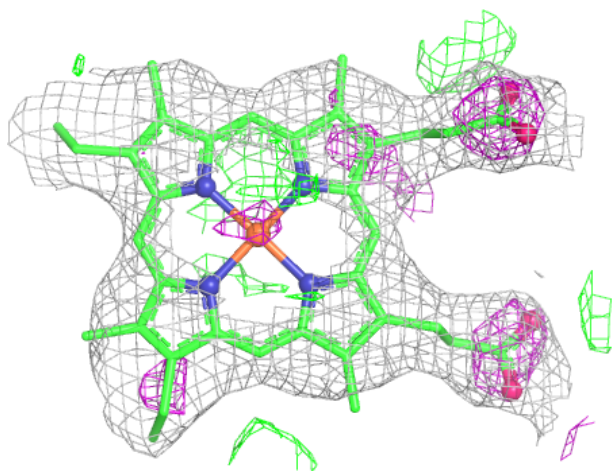
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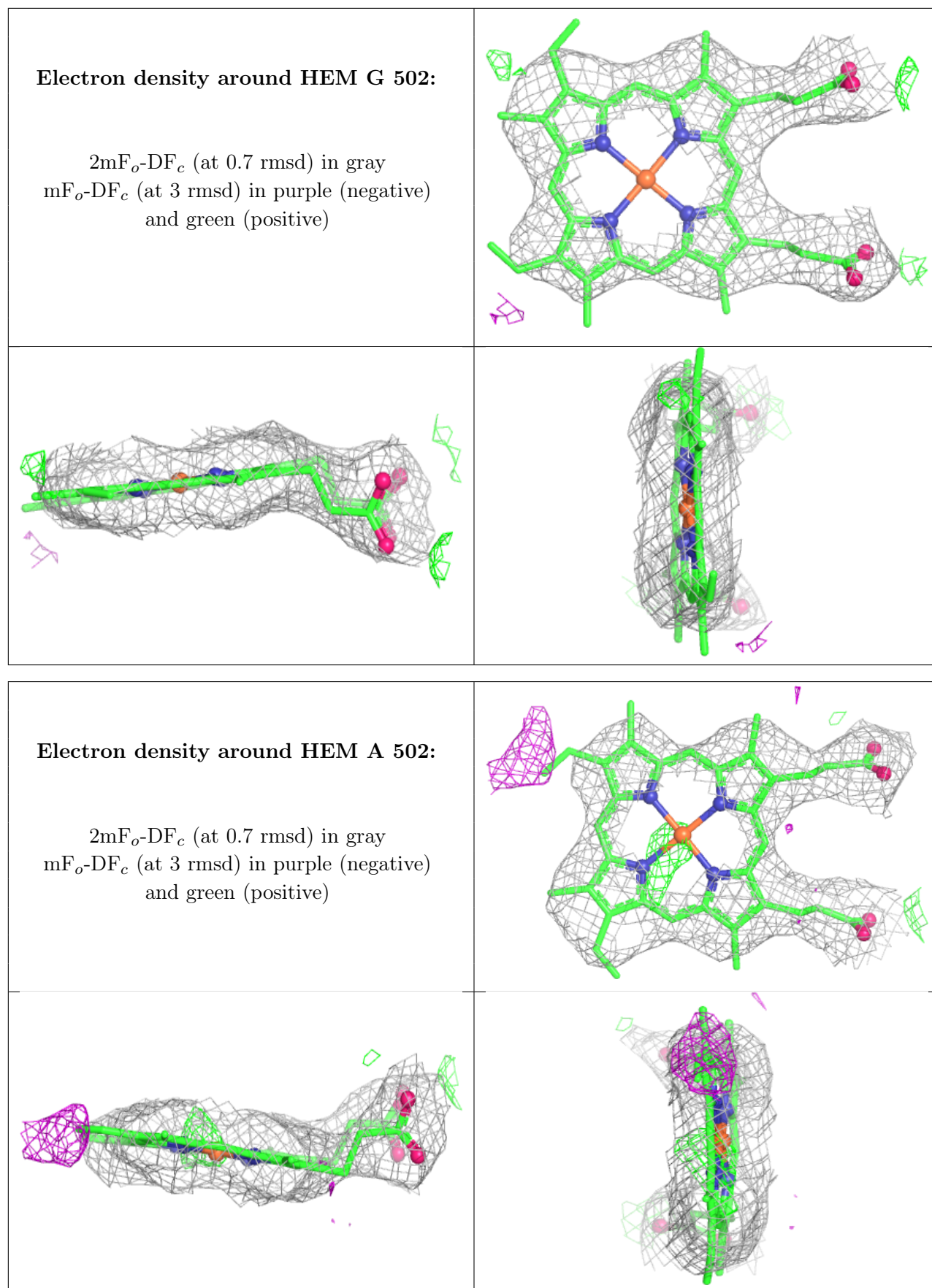
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

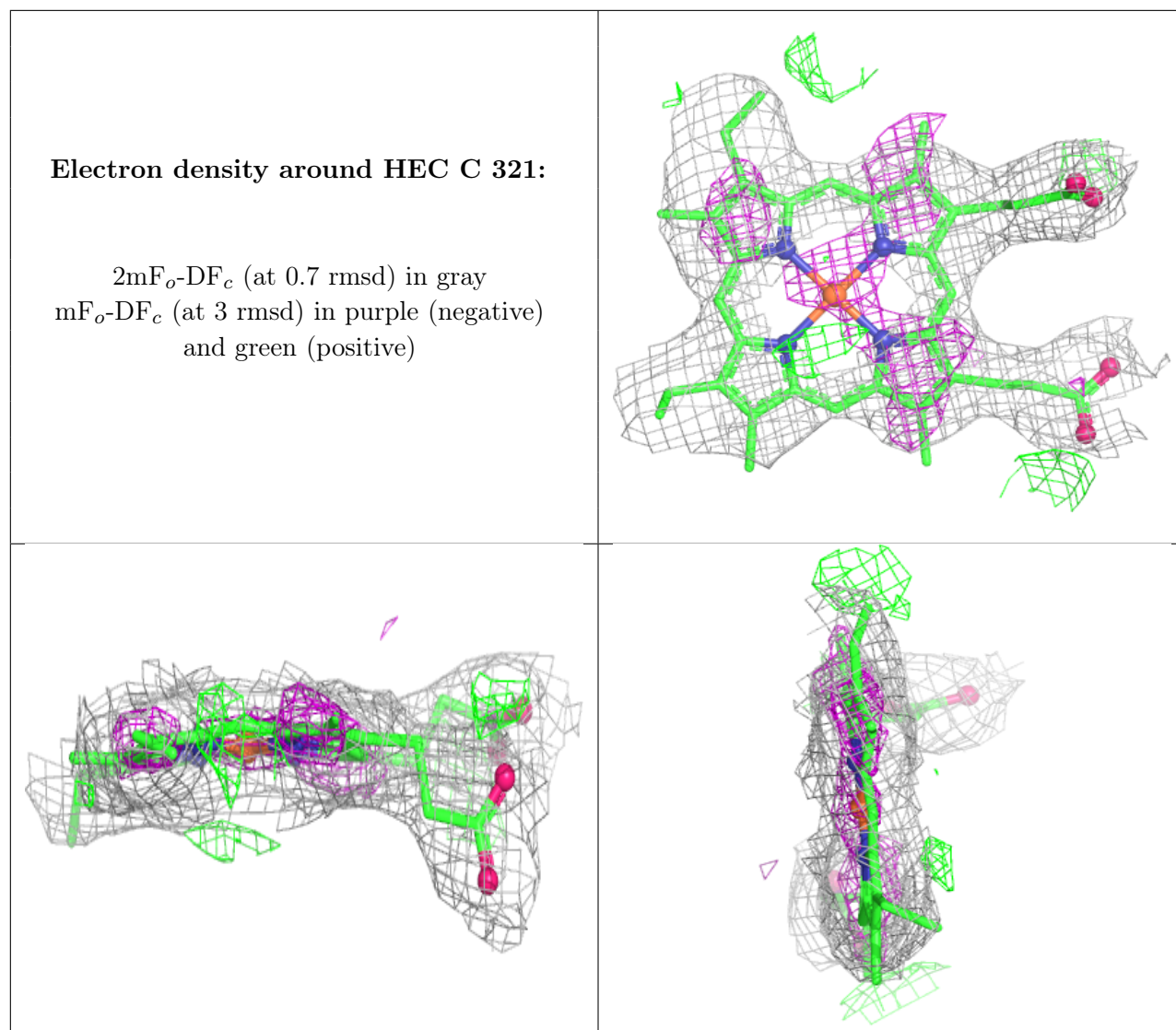


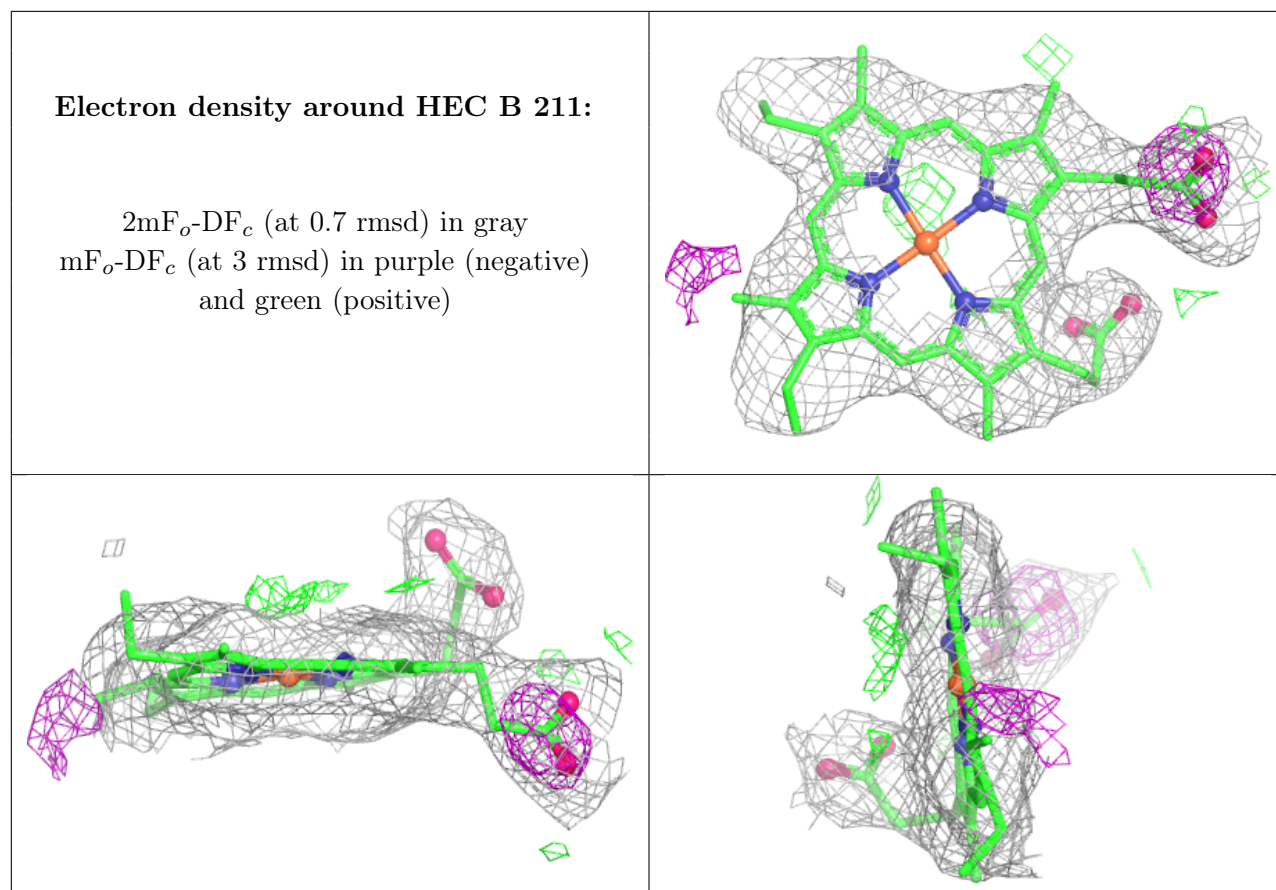
**Electron density around HEC I 322:**

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



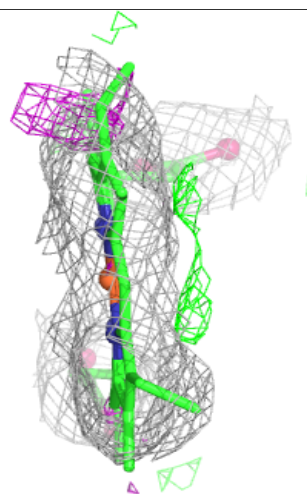
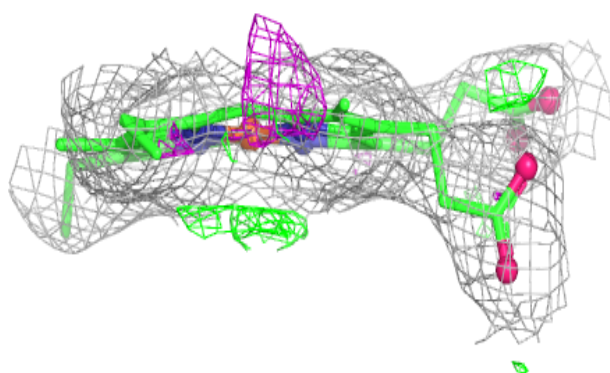
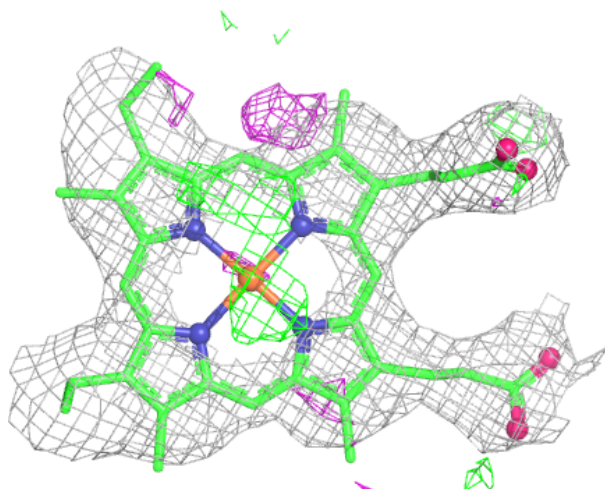






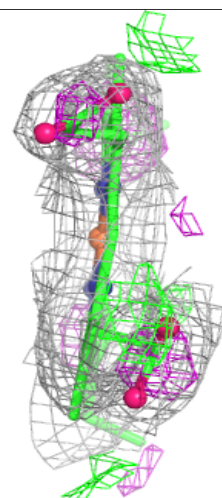
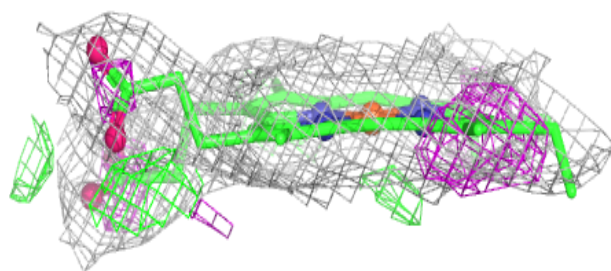
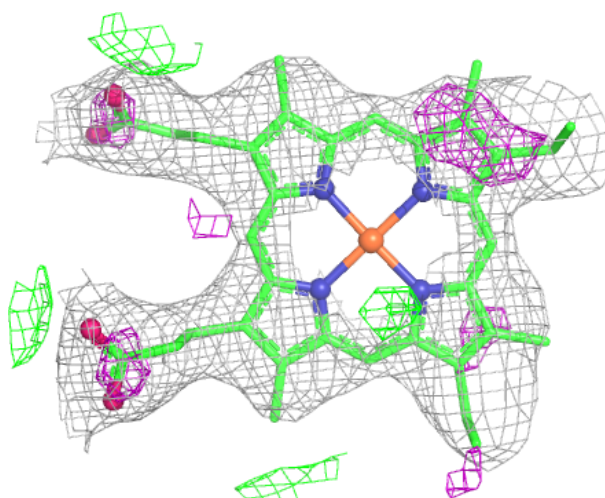
**Electron density around HEC M 321:**

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



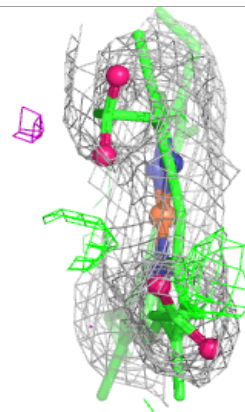
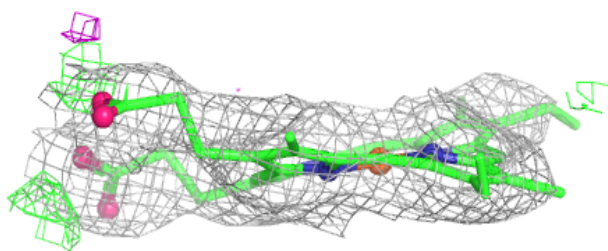
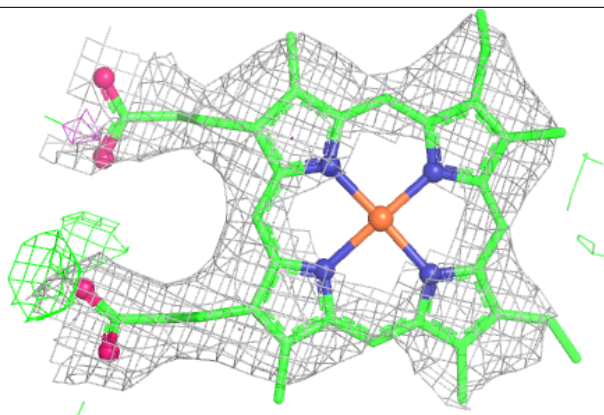
**Electron density around HEC M 322:**

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

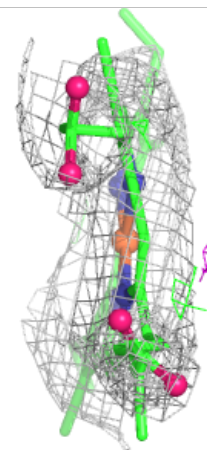
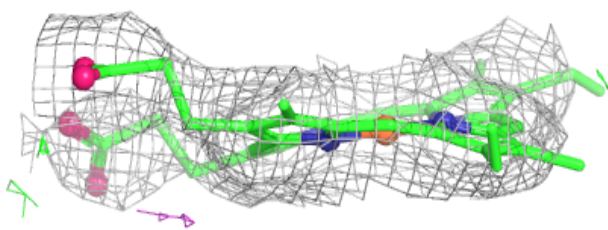
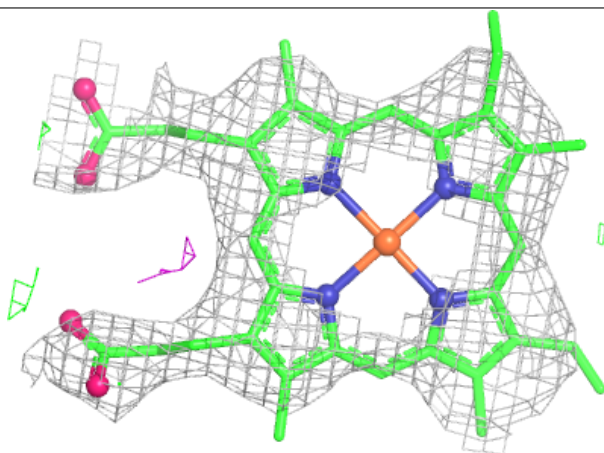


**Electron density around HEM A 501:**

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

**Electron density around HEM G 501:**

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.