



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 23, 2026 – 05:51 am BST

PDB ID : 2VR0 / pdb_00002vr0
Title : Crystal structure of cytochrome c nitrite reductase NrfHA complex bound to the HQNO inhibitor
Authors : Rodrigues, M.L.; Archer, M.
Deposited on : 2008-03-24
Resolution : 2.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

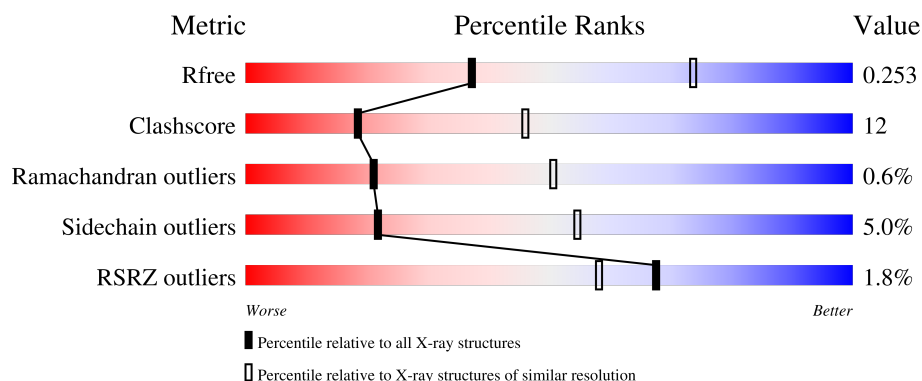
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	524	2% 77% 16% • 6%
1	B	524	2% 77% 15% • 5%
1	D	524	2% 78% 14% • 6%
1	E	524	2% 77% 15% • 6%
2	C	159	2% 75% 14% • 9%

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Mol	Chain	Length	Quality of chain
2	F	159	

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	HEC	A	1001	X	-	-	-
3	HEC	A	1002	X	-	-	-
3	HEC	A	1003	X	-	-	-
3	HEC	A	1004	X	-	-	-
3	HEC	A	1005	X	-	-	-
3	HEC	B	1001	X	-	-	-
3	HEC	B	1002	X	-	-	-
3	HEC	B	1003	X	-	-	-
3	HEC	B	1004	X	-	-	-
3	HEC	B	1005	X	-	-	-
3	HEC	C	1001	X	-	-	-
3	HEC	C	1004	X	-	-	-
3	HEC	D	1001	X	-	-	-
3	HEC	D	1002	X	-	-	-
3	HEC	D	1003	X	-	-	-
3	HEC	D	1004	X	-	-	-
3	HEC	D	1005	X	-	-	-
3	HEC	E	1001	X	-	-	-
3	HEC	E	1002	X	-	-	-
3	HEC	E	1003	X	-	-	-
3	HEC	E	1004	X	-	-	-
3	HEC	E	1005	X	-	-	-
3	HEC	F	1001	X	-	-	-
3	HEC	F	1003	X	-	-	-
3	HEC	F	1004	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19601 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.

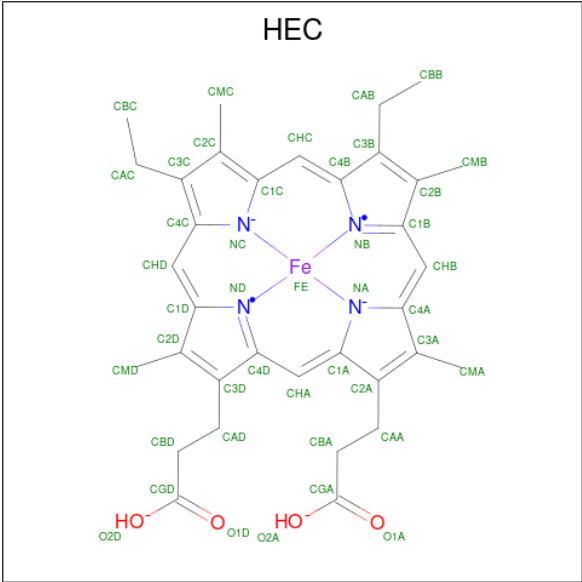
- Molecule 1 is a protein called CYTOCHROME C NITRITE REDUCTASE, CATALYTIC SUBUNIT NFRA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	495	Total	C	N	O	S	0	0	0
			4009	2546	692	742	29			
1	B	498	Total	C	N	O	S	0	1	0
			4035	2561	698	747	29			
1	D	494	Total	C	N	O	S	0	0	0
			4002	2541	691	741	29			
1	E	495	Total	C	N	O	S	0	0	0
			4007	2544	692	742	29			

- Molecule 2 is a protein called NAPC/NIRT CYTOCHROME C FAMILY PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	144	Total	C	N	O	S	0	1	0
			1088	675	200	197	16			
2	F	146	Total	C	N	O	S	0	0	0
			1096	680	200	200	16			

- Molecule 3 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{36}FeN_4O_4$).



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

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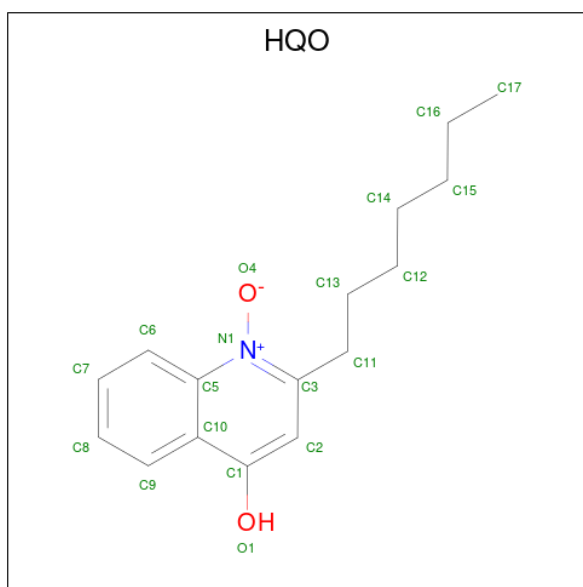
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	E	1	Total 43	C 34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

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Ca 2	0	0
4	B	2	Total 2	Ca 2	0	0
4	D	2	Total 2	Ca 2	0	0
4	E	2	Total 2	Ca 2	0	0

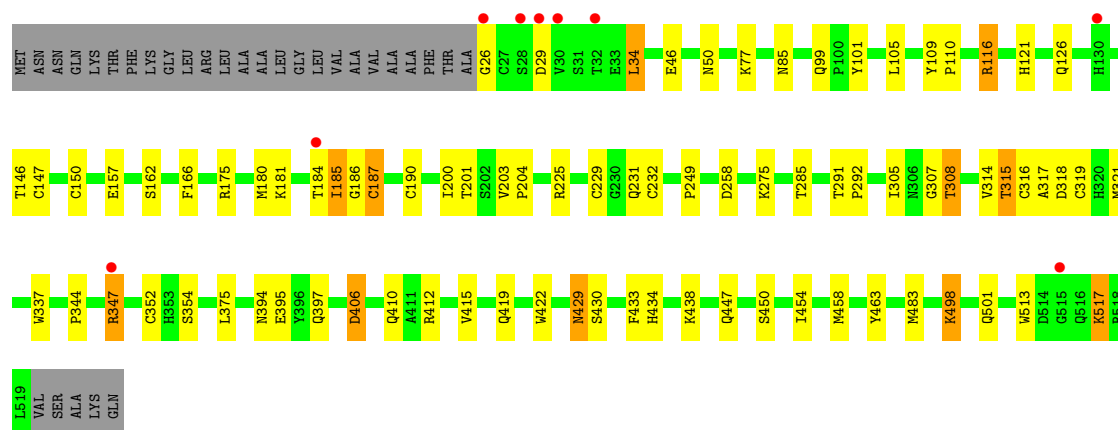
- Molecule 5 is 2-HEPTYL-4-HYDROXY QUINOLINE N-OXIDE (CCD ID: HQO) (formula: C₁₆H₂₁NO₂).



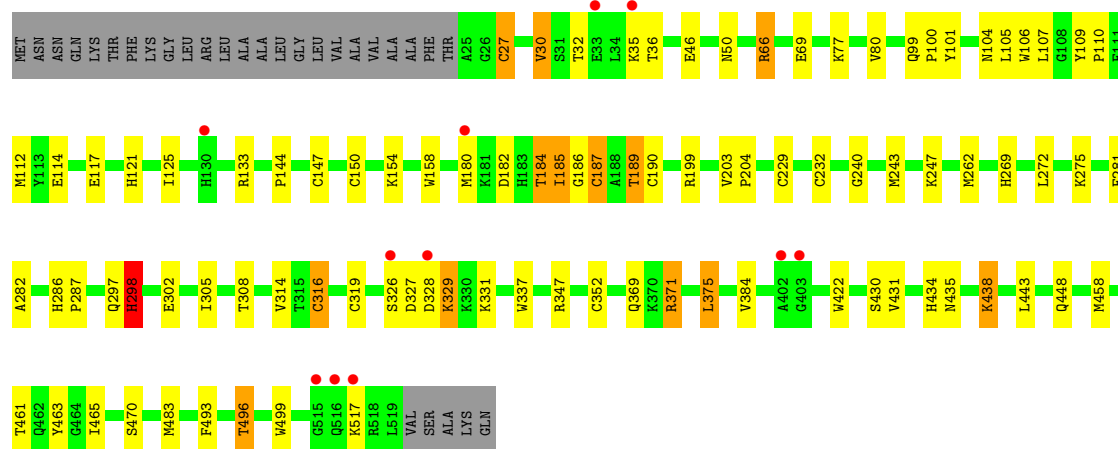
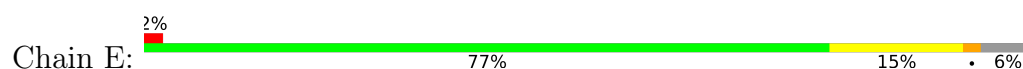
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			19	16	1	2		
5	F	1	Total	C	N	O	0	0
			19	16	1	2		

- Molecule 6 is water.

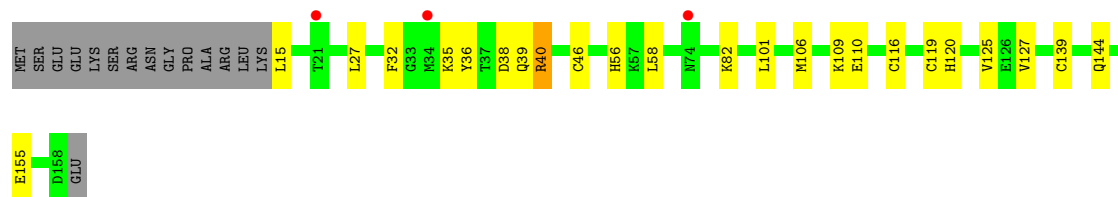
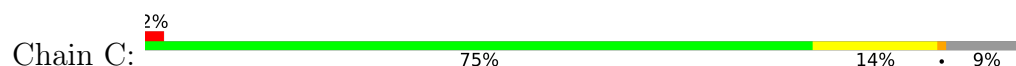
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	23	Total	O	0	0
			23	23		
6	B	41	Total	O	0	0
			41	41		
6	C	5	Total	O	0	0
			5	5		
6	D	21	Total	O	0	0
			21	21		
6	E	14	Total	O	0	0
			14	14		
6	F	10	Total	O	0	0
			10	10		



• Molecule 1: CYTOCHROME C NITRITE REDUCTASE, CATALYTIC SUBUNIT NFRA

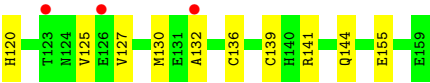


• Molecule 2: NAPC/NIRT CYTOCHROME C FAMILY PROTEIN



• Molecule 2: NAPC/NIRT CYTOCHROME C FAMILY PROTEIN





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.10Å 189.12Å 263.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	154.30 – 2.80 153.63 – 2.80	Depositor EDS
% Data completeness (in resolution range)	87.0 (154.30-2.80) 87.0 (153.63-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.3.0013	Depositor
R, R_{free}	0.220 , 0.261 0.215 , 0.253	Depositor DCC
R_{free} test set	2592 reflections (2.99%)	wwPDB-VP
Wilson B-factor (Å ²)	38.6	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 36.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	19601	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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: HEC, CA, HQO

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	0.71	0/4123	0.89	2/5579 (0.0%)
1	B	0.73	0/4150	0.93	3/5616 (0.1%)
1	D	0.67	0/4116	0.88	2/5569 (0.0%)
1	E	0.66	1/4121 (0.0%)	0.88	2/5576 (0.0%)
2	C	0.70	0/1109	0.98	2/1502 (0.1%)
2	F	0.66	0/1116	0.97	0/1509
All	All	0.69	1/18735 (0.0%)	0.90	11/25351 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	80	VAL	CA-CB	5.11	1.59	1.53

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	305	ILE	N-CA-C	7.21	117.98	110.62
1	E	27	CYS	N-CA-C	6.90	124.37	114.16
1	B	27	CYS	N-CA-C	5.77	123.10	110.80
1	B	154	LYS	N-CA-C	-5.71	105.81	112.89
2	C	40	ARG	CA-C-N	-5.61	113.25	119.19

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	4009	0	3876	90	0
1	B	4035	0	3898	86	0
1	D	4002	0	3869	86	0
1	E	4007	0	3875	93	0
2	C	1088	0	1084	37	0
2	F	1096	0	1099	51	0
3	A	215	0	156	38	0
3	B	215	0	157	43	0
3	C	172	0	124	32	0
3	D	215	0	158	43	0
3	E	215	0	159	44	0
3	F	172	0	127	44	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
5	C	19	0	21	1	0
5	F	19	0	21	2	0
6	A	23	0	0	0	0
6	B	41	0	0	2	0
6	C	5	0	0	0	0
6	D	21	0	0	2	0
6	E	14	0	0	0	0
6	F	10	0	0	1	0
All	All	19601	0	18624	456	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 12.

The worst 5 of 456 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:B:316:CYS:SG	3:B:1004:HEC:HAB	1.18	1.71
2:F:66:CYS:SG	3:F:1002:HEC:HAB	1.32	1.67
1:B:187:CYS:SG	3:B:1002:HEC:HAB	1.34	1.66
1:D:352:CYS:SG	3:D:1005:HEC:HAC	1.28	1.64
1:E:316:CYS:SG	3:E:1004:HEC:HAB	1.41	1.57

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	493/524 (94%)	473 (96%)	18 (4%)	2 (0%)	30	60
1	B	497/524 (95%)	474 (95%)	18 (4%)	5 (1%)	12	38
1	D	492/524 (94%)	469 (95%)	22 (4%)	1 (0%)	43	72
1	E	493/524 (94%)	470 (95%)	18 (4%)	5 (1%)	12	38
2	C	143/159 (90%)	138 (96%)	5 (4%)	0	100	100
2	F	144/159 (91%)	139 (96%)	4 (3%)	1 (1%)	18	47
All	All	2262/2414 (94%)	2163 (96%)	85 (4%)	14 (1%)	21	51

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	185	ILE
1	B	329	LYS
1	E	185	ILE
1	E	329	LYS
1	A	185	ILE

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	429/449 (96%)	412 (96%)	17 (4%)	28	63
1	B	431/449 (96%)	405 (94%)	26 (6%)	17	47
1	D	428/449 (95%)	410 (96%)	18 (4%)	26	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	428/449 (95%)	403 (94%)	25 (6%)	18	49
2	C	119/131 (91%)	114 (96%)	5 (4%)	26	61
2	F	120/131 (92%)	114 (95%)	6 (5%)	22	54
All	All	1955/2058 (95%)	1858 (95%)	97 (5%)	22	54

5 of 97 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	275	LYS
1	E	66	ARG
1	D	315	THR
1	D	517	LYS
1	E	187	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	462	GLN
2	F	56	HIS
2	C	56	HIS
1	D	97	HIS
1	D	269	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 38 ligands modelled in this entry, 8 are monoatomic - leaving 30 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	HEC	D	1003	1,4	50,50,50	1.75	8 (16%)	68,82,82	1.43	9 (13%)
5	HQO	F	1005	-	20,20,20	2.67	2 (10%)	18,26,26	1.24	2 (11%)
3	HEC	F	1004	2,1	50,50,50	1.89	8 (16%)	68,82,82	1.37	8 (11%)
3	HEC	F	1001	2	50,50,50	2.05	7 (14%)	68,82,82	1.53	10 (14%)
3	HEC	F	1003	2	50,50,50	1.87	8 (16%)	68,82,82	1.46	8 (11%)
3	HEC	B	1002	1	50,50,50	1.93	10 (20%)	68,82,82	1.55	13 (19%)
3	HEC	F	1002	2	50,50,50	1.95	7 (14%)	68,82,82	1.42	7 (10%)
3	HEC	C	1002	2	50,50,50	1.91	8 (16%)	68,82,82	1.71	12 (17%)
3	HEC	C	1004	2,1	50,50,50	1.92	6 (12%)	68,82,82	1.56	9 (13%)
3	HEC	C	1003	2	50,50,50	1.84	6 (12%)	68,82,82	1.54	12 (17%)
3	HEC	B	1003	1,4	50,50,50	1.81	7 (14%)	68,82,82	1.34	8 (11%)
3	HEC	E	1002	1	50,50,50	1.81	8 (16%)	68,82,82	1.31	8 (11%)
5	HQO	C	1005	-	20,20,20	2.65	2 (10%)	18,26,26	1.28	3 (16%)
3	HEC	D	1001	6,1	50,50,50	1.97	9 (18%)	68,82,82	1.54	8 (11%)
3	HEC	E	1003	1,4	50,50,50	1.81	7 (14%)	68,82,82	1.64	13 (19%)
3	HEC	C	1001	2	50,50,50	1.99	7 (14%)	68,82,82	1.33	7 (10%)
3	HEC	E	1004	1,4	50,50,50	1.92	8 (16%)	68,82,82	1.38	6 (8%)
3	HEC	A	1004	1,4	50,50,50	1.81	7 (14%)	68,82,82	1.26	7 (10%)
3	HEC	A	1005	1	50,50,50	1.87	7 (14%)	68,82,82	1.67	12 (17%)
3	HEC	A	1002	1	50,50,50	1.88	7 (14%)	68,82,82	1.31	7 (10%)
3	HEC	A	1001	1	50,50,50	1.93	7 (14%)	68,82,82	1.65	13 (19%)
3	HEC	E	1001	6,1	50,50,50	1.98	7 (14%)	68,82,82	1.43	8 (11%)
3	HEC	A	1003	1,4	50,50,50	1.88	9 (18%)	68,82,82	1.44	6 (8%)
3	HEC	B	1001	6,1	50,50,50	2.00	11 (22%)	68,82,82	1.70	15 (22%)
3	HEC	B	1004	1,4	50,50,50	2.00	12 (24%)	68,82,82	1.69	8 (11%)
3	HEC	D	1005	1	50,50,50	1.96	6 (12%)	68,82,82	1.38	8 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEC	B	1005	1	50,50,50	1.90	6 (12%)	68,82,82	1.52	16 (23%)
3	HEC	D	1002	1	50,50,50	1.94	7 (14%)	68,82,82	1.39	8 (11%)
3	HEC	E	1005	1	50,50,50	2.09	5 (10%)	68,82,82	1.77	18 (26%)
3	HEC	D	1004	1,4	50,50,50	1.97	7 (14%)	68,82,82	1.41	6 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	D	1003	1,4	1/1/3/7	4/14/54/54	-
5	HQO	F	1005	-	-	2/7/7/7	0/2/2/2
3	HEC	F	1004	2,1	1/1/3/7	9/14/54/54	-
3	HEC	F	1001	2	1/1/3/7	6/14/54/54	-
3	HEC	F	1003	2	1/1/3/7	5/14/54/54	-
3	HEC	B	1002	1	1/1/3/7	2/14/54/54	-
3	HEC	F	1002	2	-	4/14/54/54	-
3	HEC	C	1002	2	-	10/14/54/54	-
3	HEC	C	1004	2,1	1/1/3/7	8/14/54/54	-
3	HEC	C	1003	2	-	3/14/54/54	-
3	HEC	E	1002	1	1/1/3/7	6/14/54/54	-
3	HEC	B	1003	1,4	1/1/3/7	8/14/54/54	-
5	HQO	C	1005	-	-	4/7/7/7	0/2/2/2
3	HEC	D	1001	6,1	1/1/3/7	6/14/54/54	-
3	HEC	E	1003	1,4	1/1/3/7	6/14/54/54	-
3	HEC	C	1001	2	1/1/3/7	4/14/54/54	-
3	HEC	E	1004	1,4	1/1/3/7	6/14/54/54	-
3	HEC	A	1004	1,4	1/1/3/7	6/14/54/54	-
3	HEC	A	1005	1	1/1/3/7	9/14/54/54	-
3	HEC	A	1002	1	1/1/3/7	10/14/54/54	-
3	HEC	A	1001	1	1/1/3/7	7/14/54/54	-
3	HEC	E	1001	6,1	1/1/3/7	6/14/54/54	-
3	HEC	A	1003	1,4	1/1/3/7	8/14/54/54	-
3	HEC	B	1001	6,1	1/1/3/7	4/14/54/54	-
3	HEC	B	1004	1,4	1/1/3/7	9/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	D	1005	1	1/1/3/7	5/14/54/54	-
3	HEC	B	1005	1	1/1/3/7	9/14/54/54	-
3	HEC	D	1002	1	1/1/3/7	7/14/54/54	-
3	HEC	E	1005	1	1/1/3/7	9/14/54/54	-
3	HEC	D	1004	1,4	1/1/3/7	5/14/54/54	-

The worst 5 of 216 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	1005	HQO	O4-N1	-10.67	1.24	1.38
5	C	1005	HQO	O4-N1	-10.39	1.24	1.38
3	E	1001	HEC	C3D-C2D	8.79	1.55	1.36
3	A	1002	HEC	C3D-C2D	8.26	1.54	1.36
3	E	1005	HEC	C3D-C2D	8.16	1.54	1.36

The worst 5 of 275 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1001	HEC	C1D-ND-C4D	6.89	112.19	105.07
3	C	1002	HEC	C1D-ND-C4D	6.80	112.09	105.07
3	A	1001	HEC	C1D-ND-C4D	6.52	111.81	105.07
3	E	1001	HEC	C1D-ND-C4D	6.33	111.61	105.07
3	B	1001	HEC	C1D-ND-C4D	6.17	111.44	105.07

5 of 25 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1001	HEC	NA
3	A	1002	HEC	NA
3	A	1003	HEC	NA
3	A	1004	HEC	NA
3	A	1005	HEC	NA

5 of 187 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1002	HEC	C2D-C3D-CAD-CBD
3	A	1002	HEC	C4D-C3D-CAD-CBD
3	A	1003	HEC	C2D-C3D-CAD-CBD
3	B	1003	HEC	C2D-C3D-CAD-CBD
3	B	1003	HEC	C4D-C3D-CAD-CBD

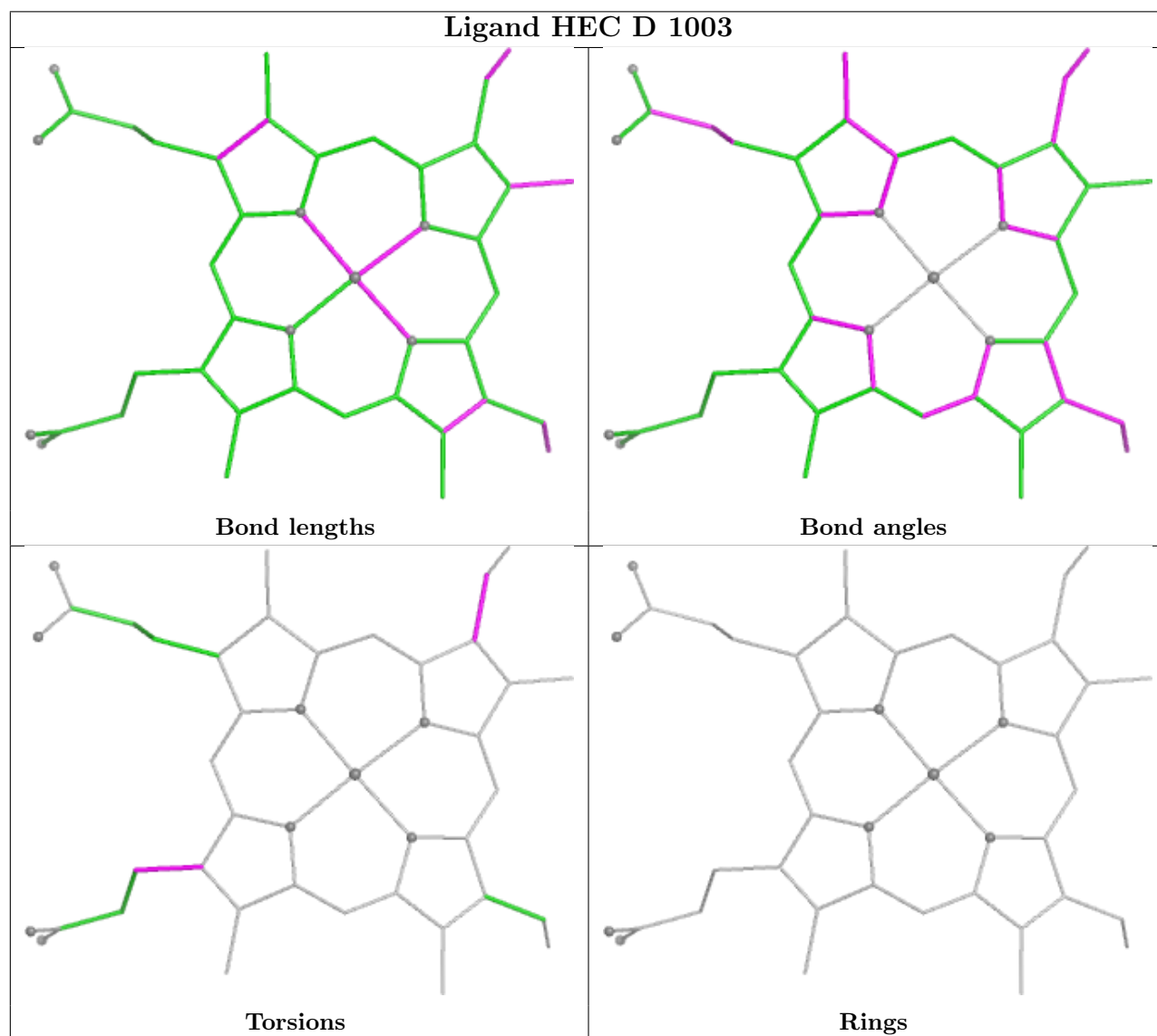
There are no ring outliers.

30 monomers are involved in 247 short contacts:

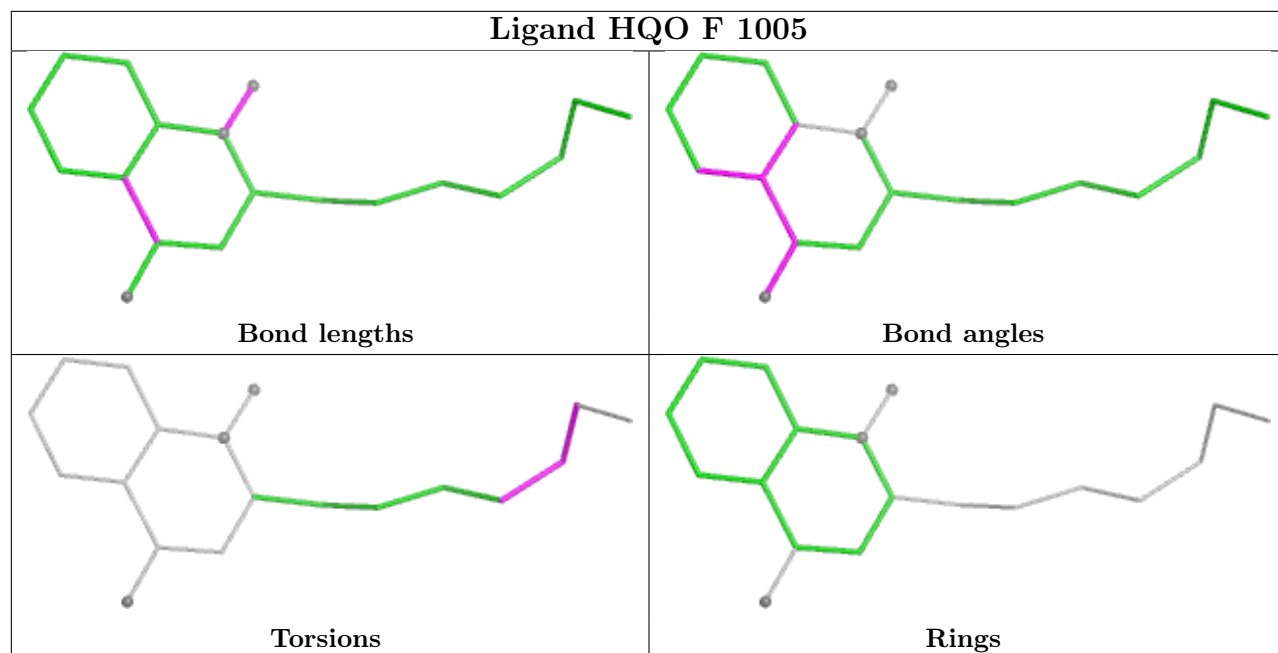
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1003	HEC	8	0
5	F	1005	HQO	2	0
3	F	1004	HEC	15	0
3	F	1001	HEC	4	0
3	F	1003	HEC	12	0
3	B	1002	HEC	6	0
3	F	1002	HEC	13	0
3	C	1002	HEC	9	0
3	C	1004	HEC	9	0
3	C	1003	HEC	10	0
3	B	1003	HEC	9	0
3	E	1002	HEC	10	0
5	C	1005	HQO	1	0
3	D	1001	HEC	12	0
3	E	1003	HEC	12	0
3	C	1001	HEC	4	0
3	E	1004	HEC	7	0
3	A	1004	HEC	8	0
3	A	1005	HEC	8	0
3	A	1002	HEC	7	0
3	A	1001	HEC	6	0
3	E	1001	HEC	11	0
3	A	1003	HEC	9	0
3	B	1001	HEC	5	0
3	B	1004	HEC	10	0
3	D	1005	HEC	5	0
3	B	1005	HEC	14	0
3	D	1002	HEC	11	0
3	E	1005	HEC	5	0
3	D	1004	HEC	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

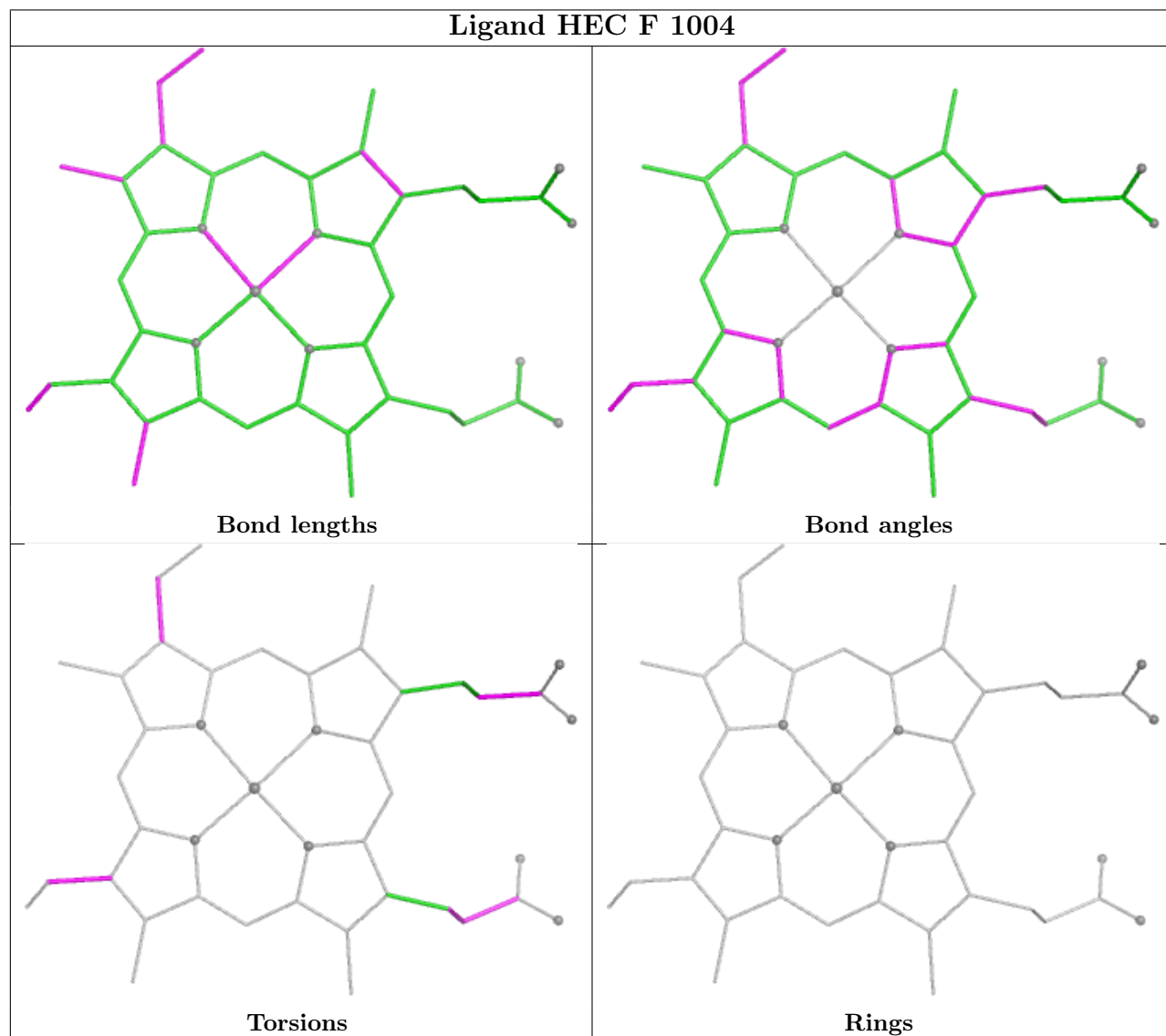
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

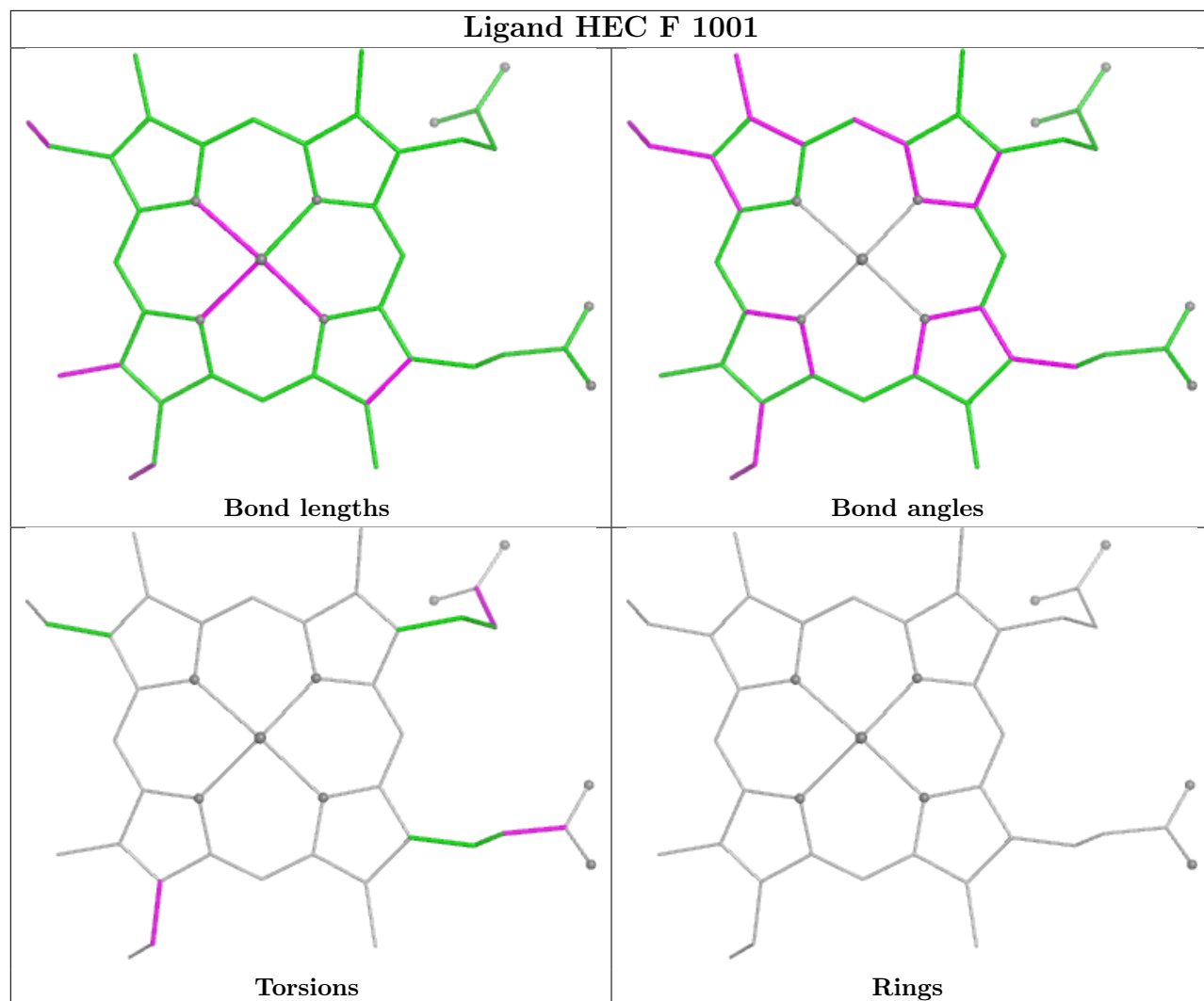


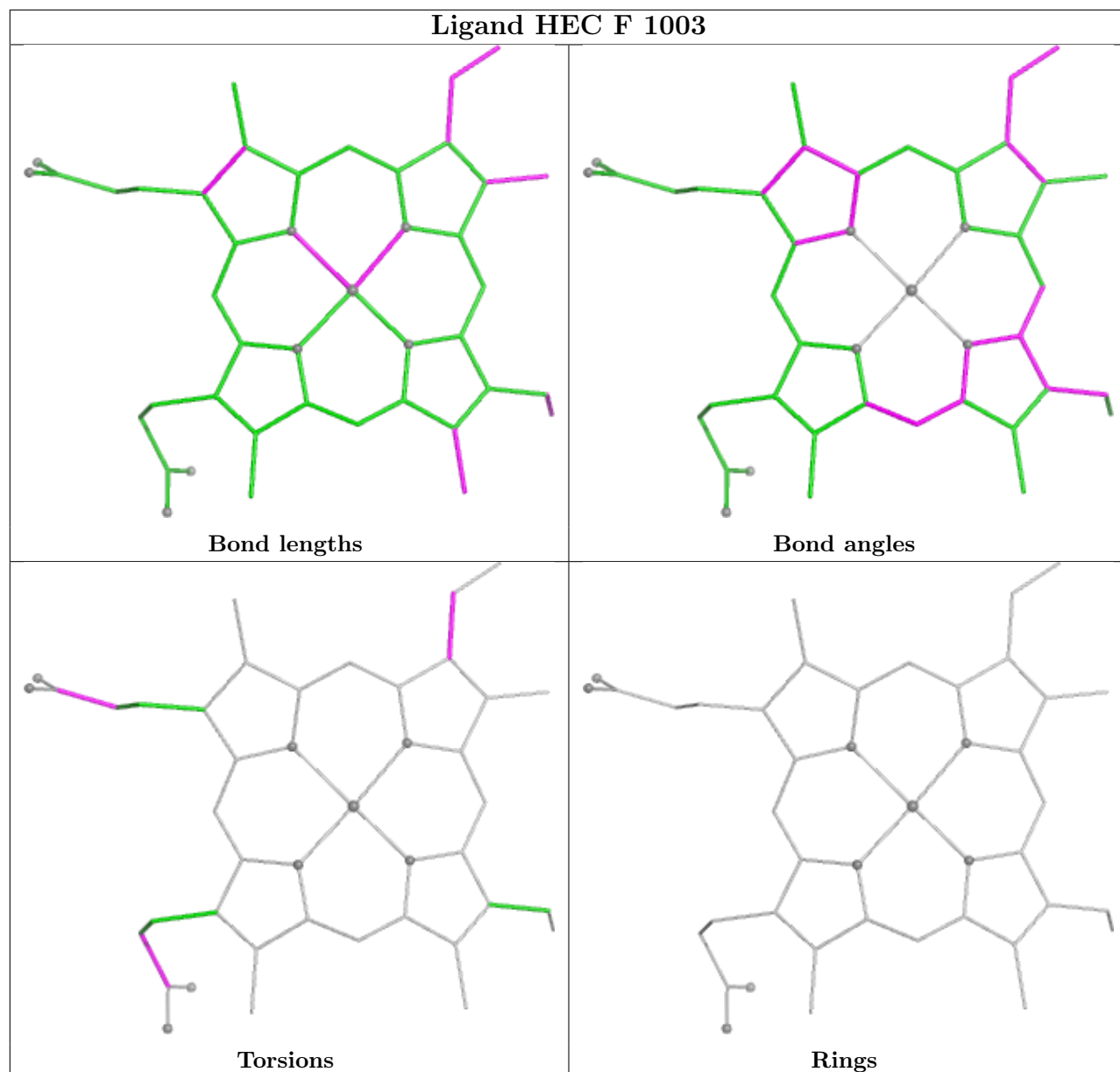
Ligand HQO F 1005

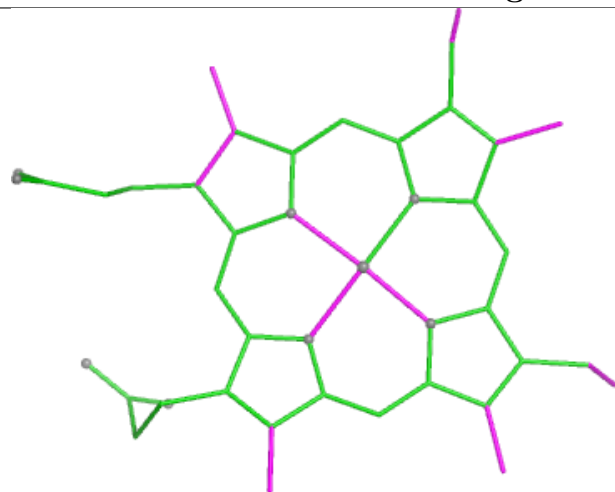
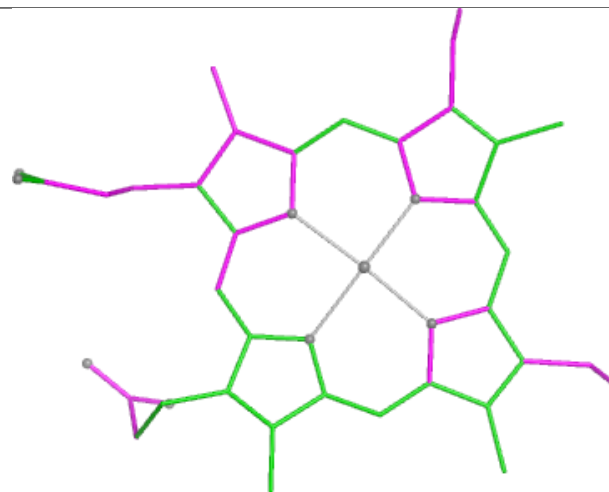
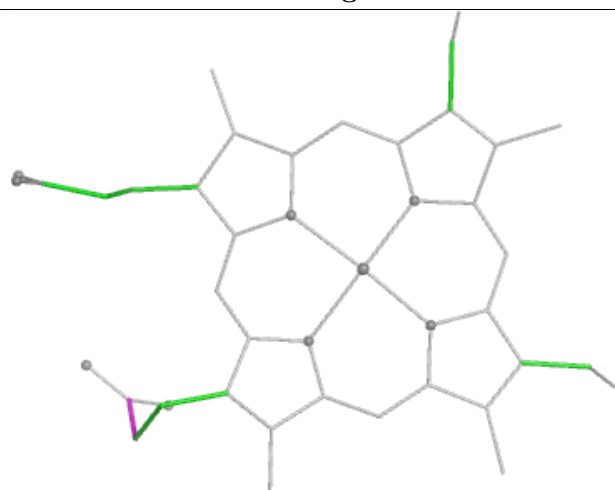
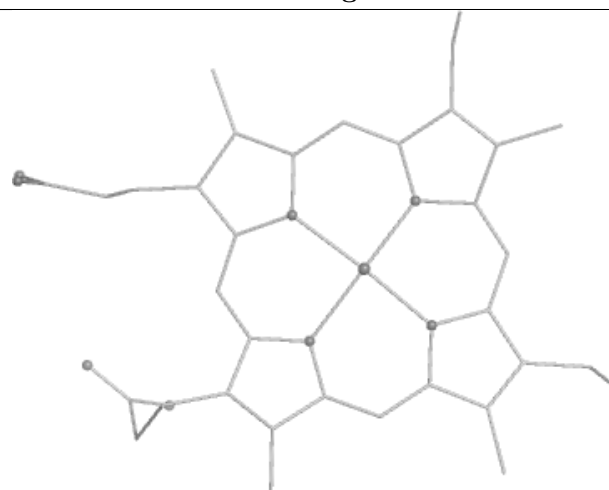


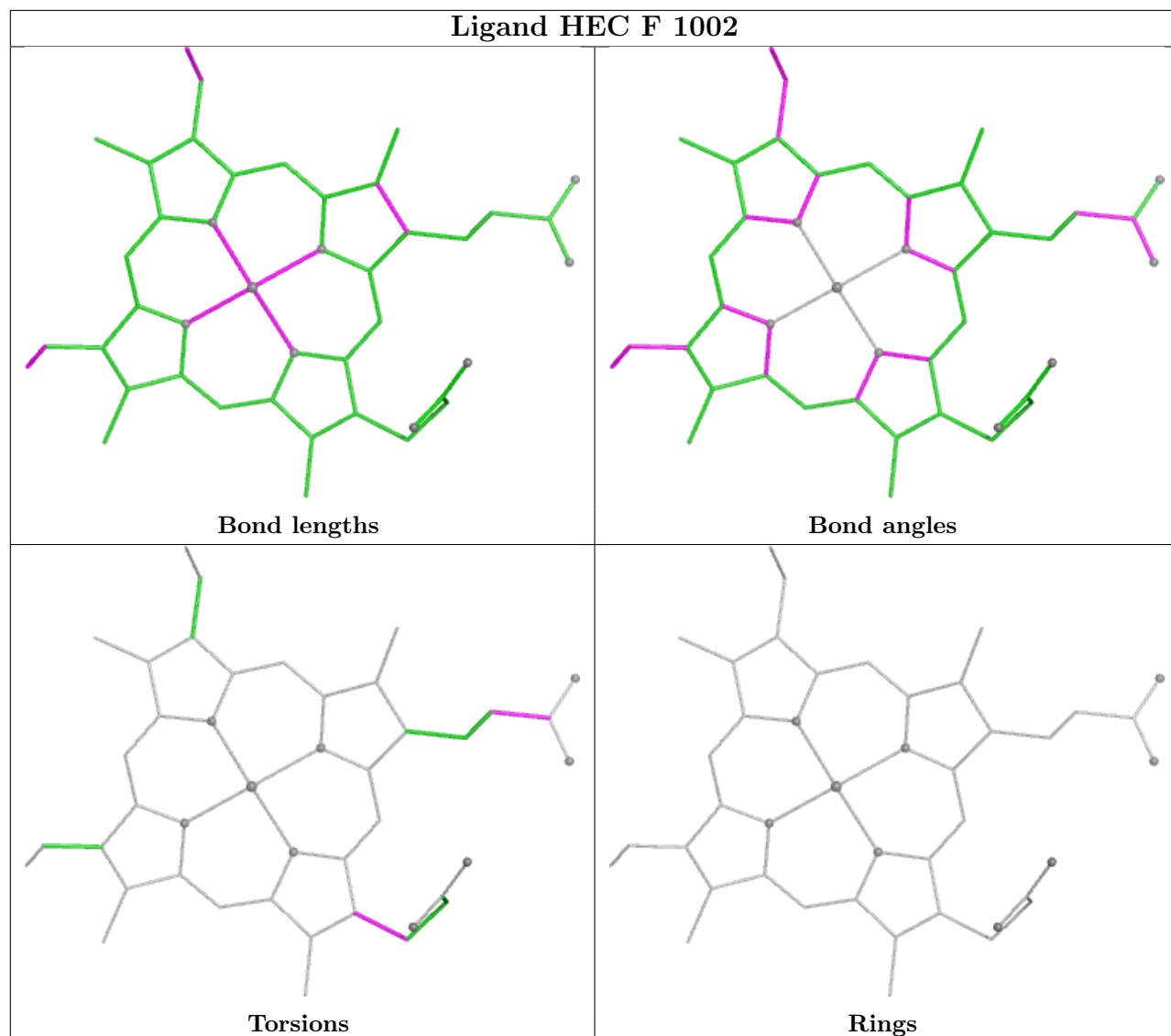
Ligand HEC F 1004

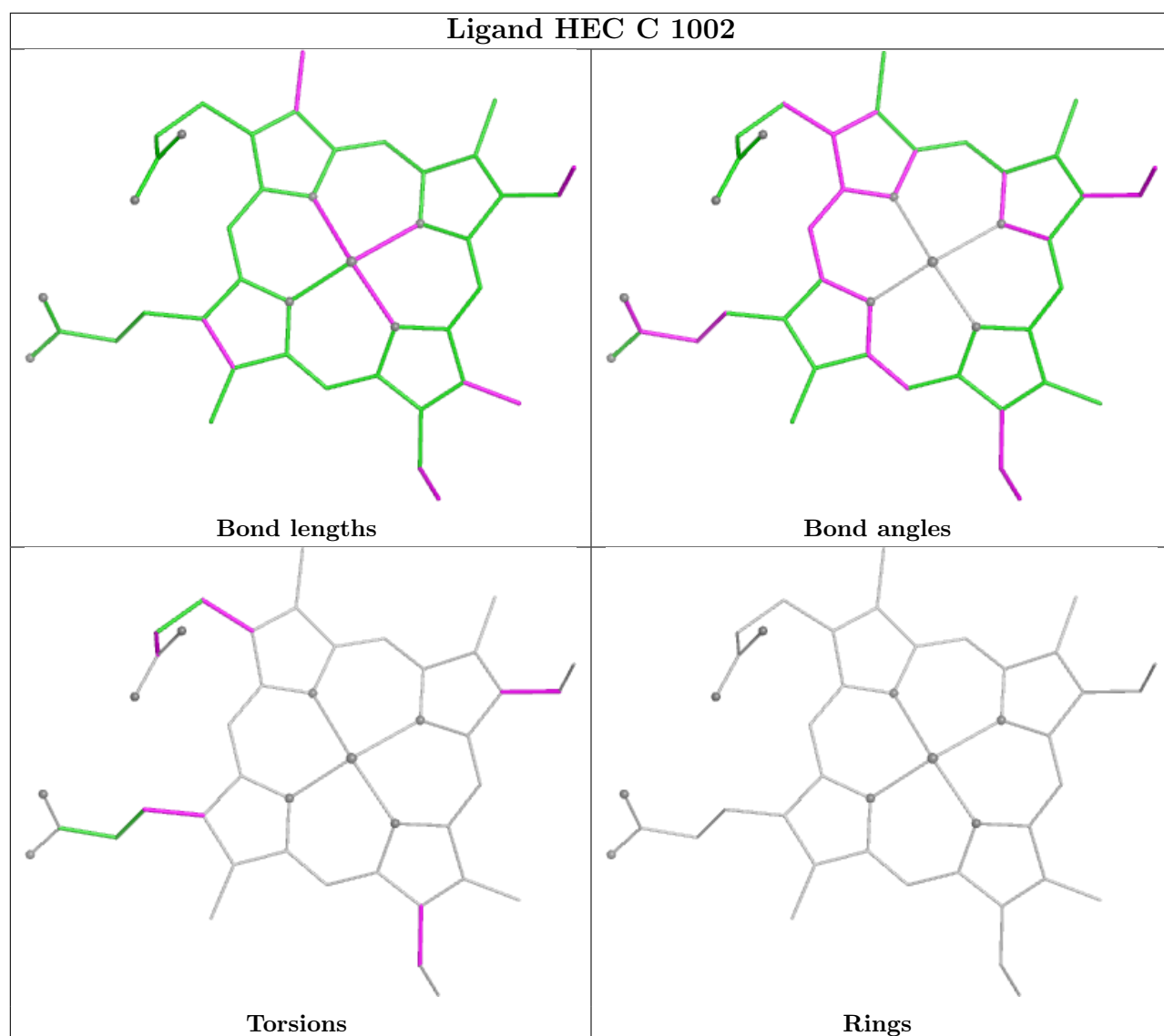




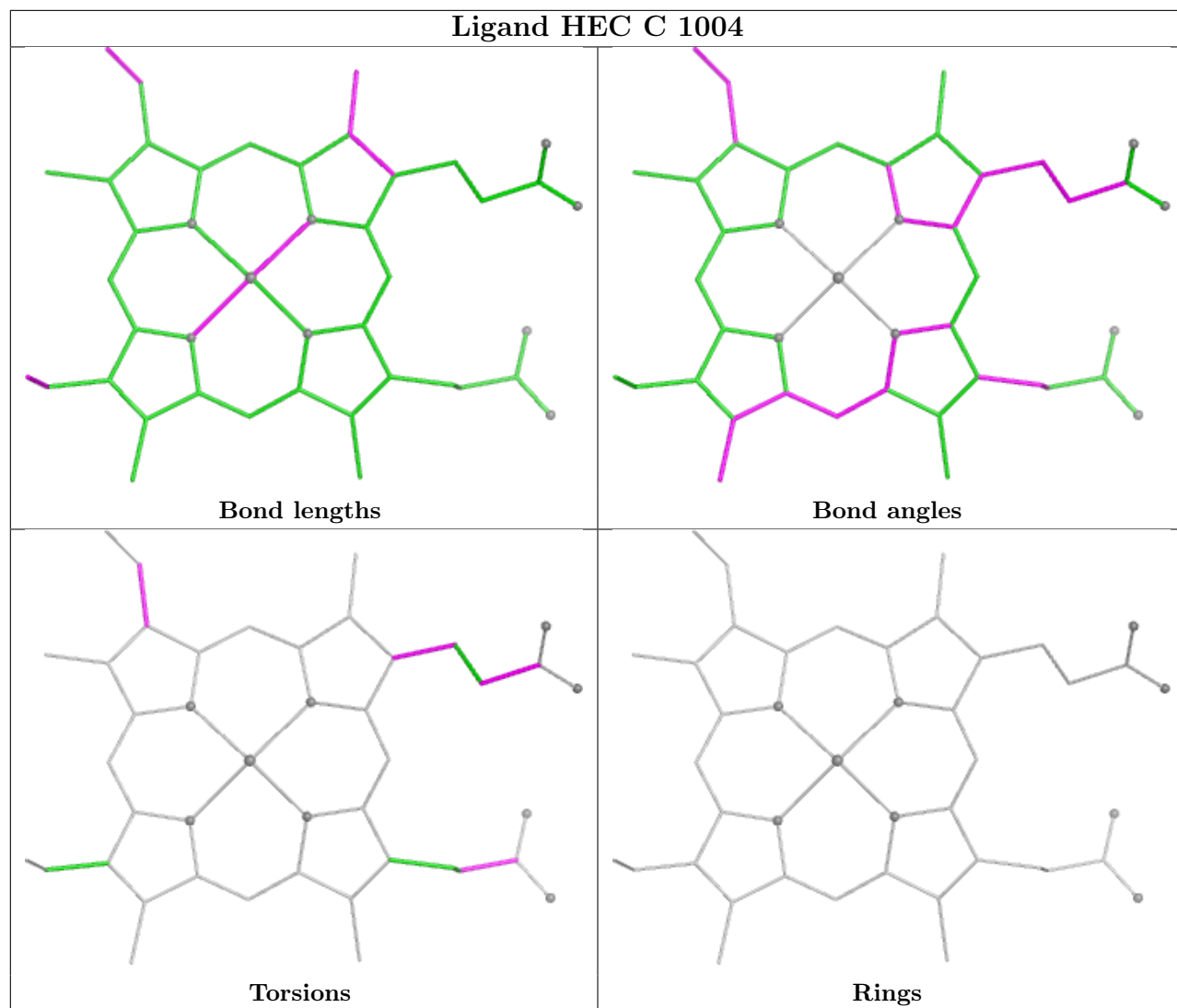


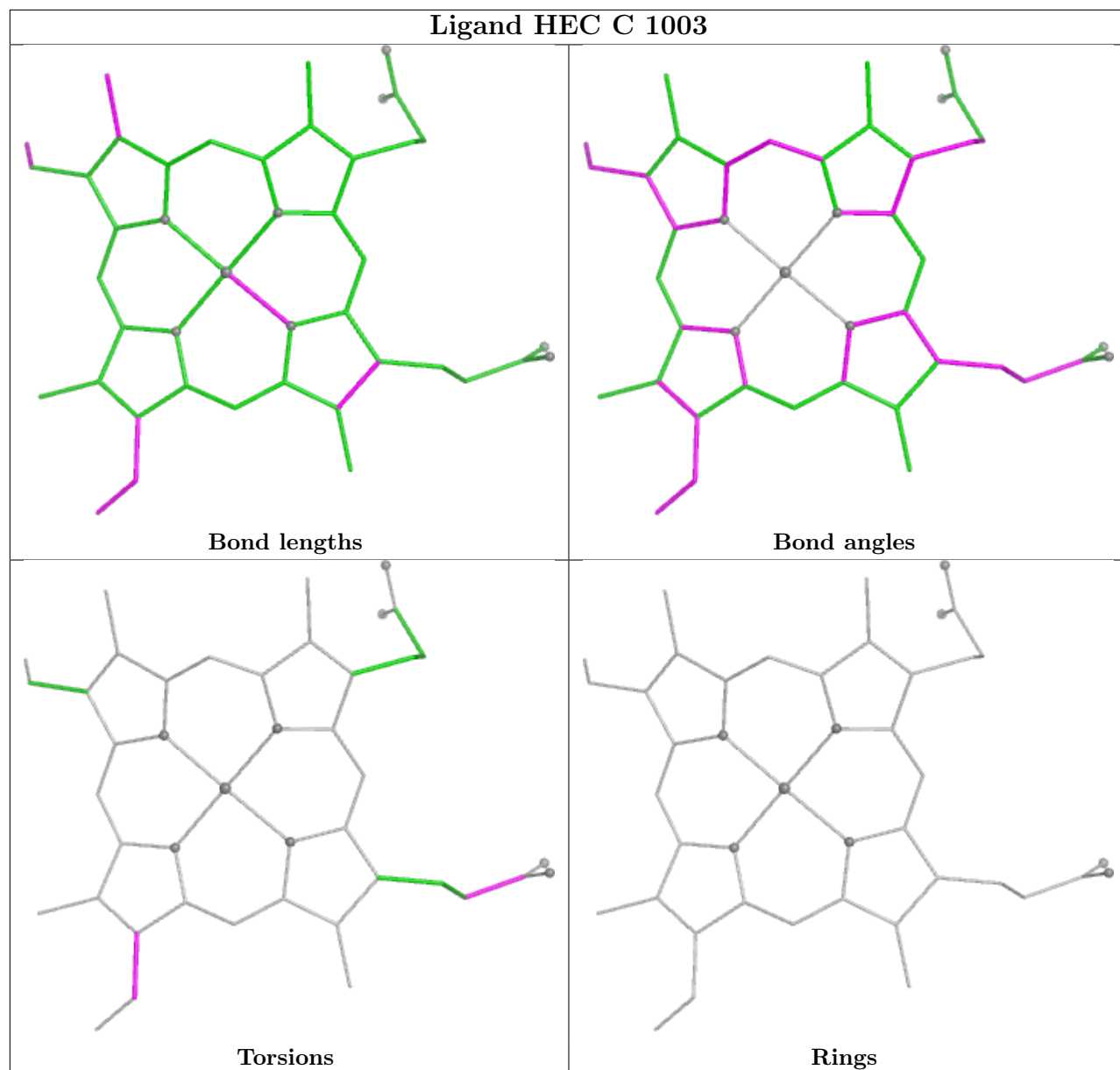
Ligand HEC B 1002**Bond lengths****Bond angles****Torsions****Rings**



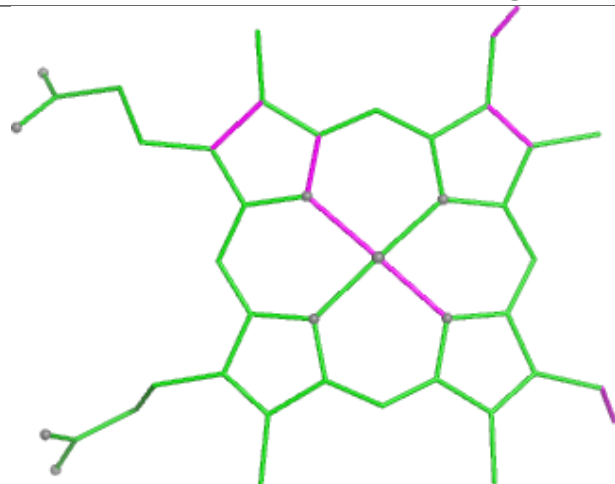


Ligand HEC C 1004

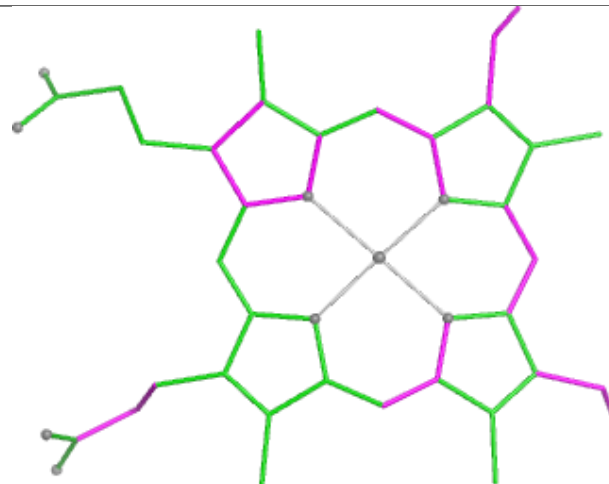




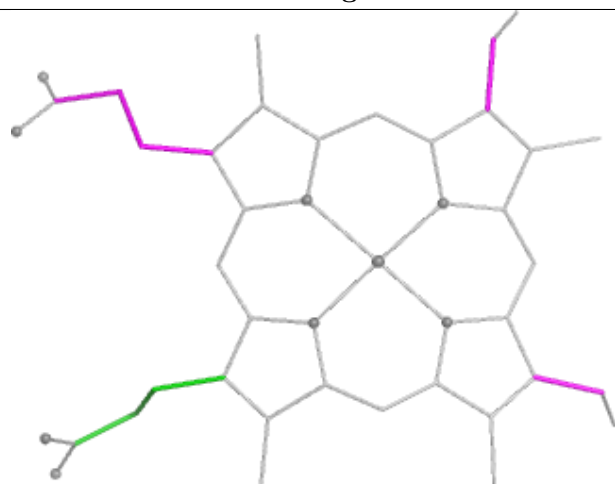
Ligand HEC B 1003



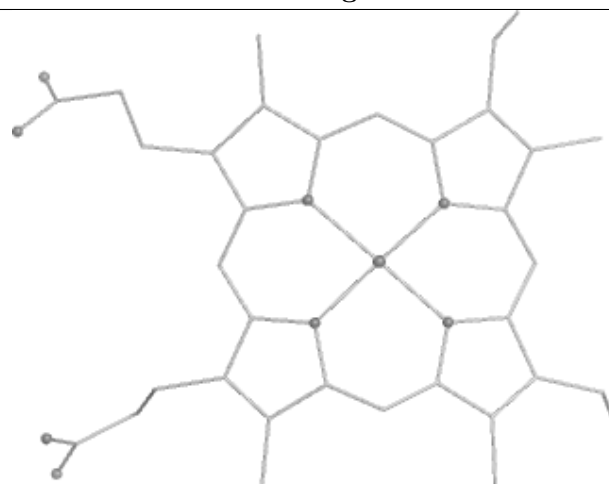
Bond lengths



Bond angles

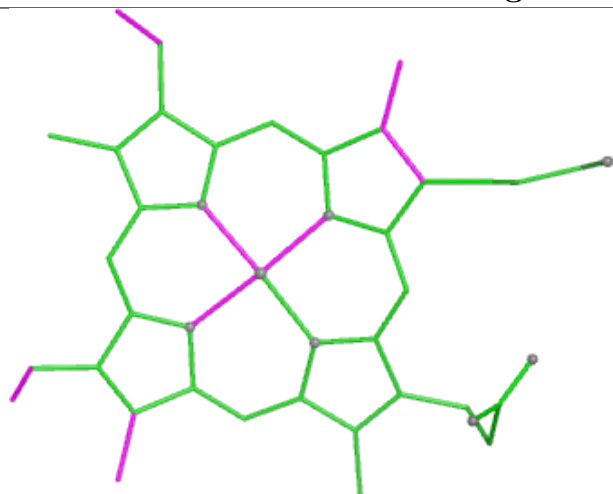


Torsions

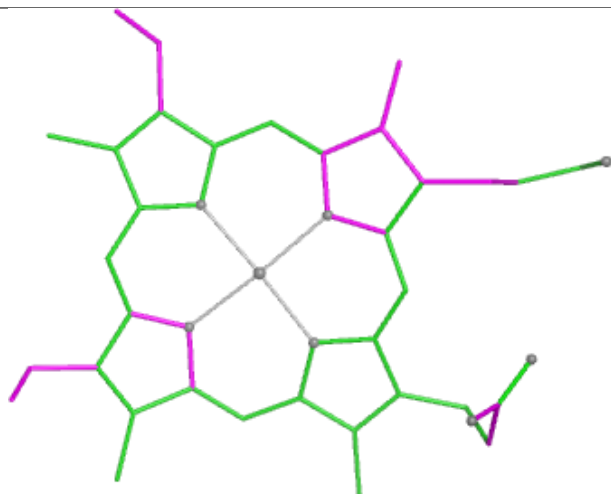


Rings

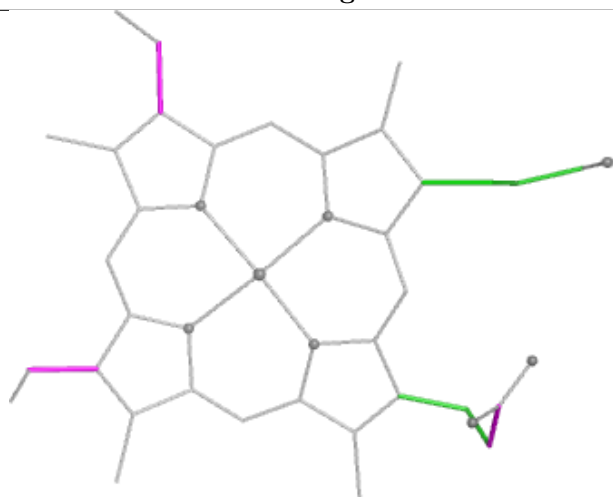
Ligand HEC E 1002



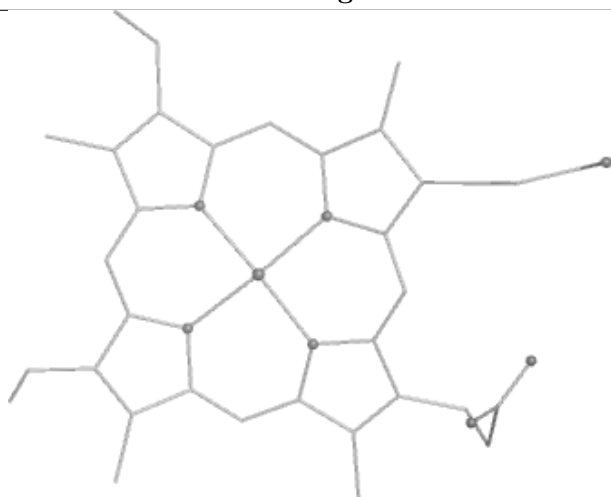
Bond lengths



Bond angles

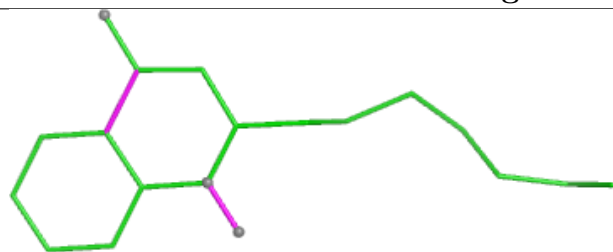


Torsions

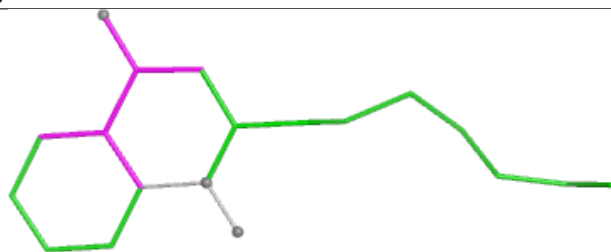


Rings

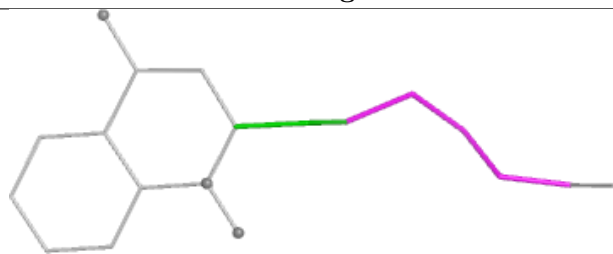
Ligand HQO C 1005



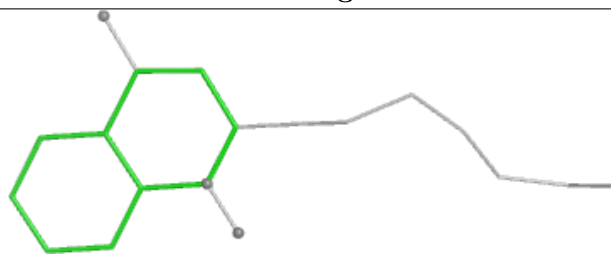
Bond lengths



Bond angles

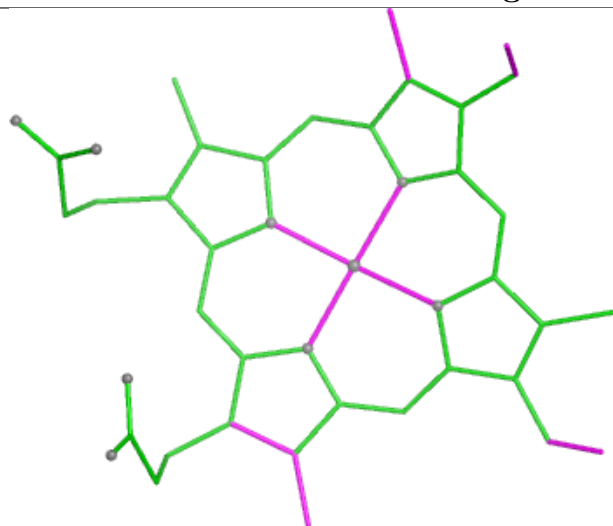


Torsions

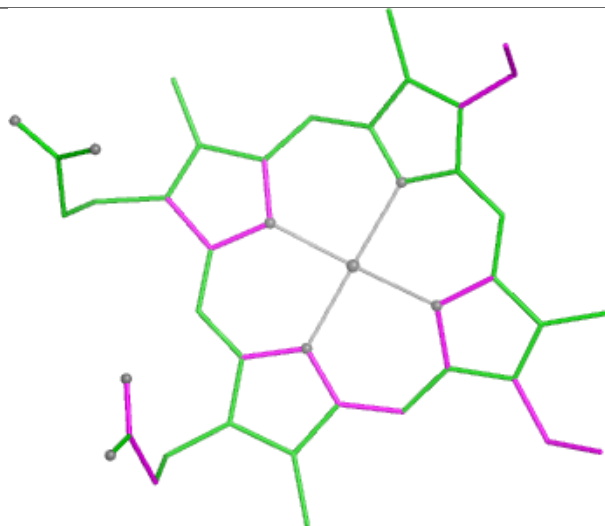


Rings

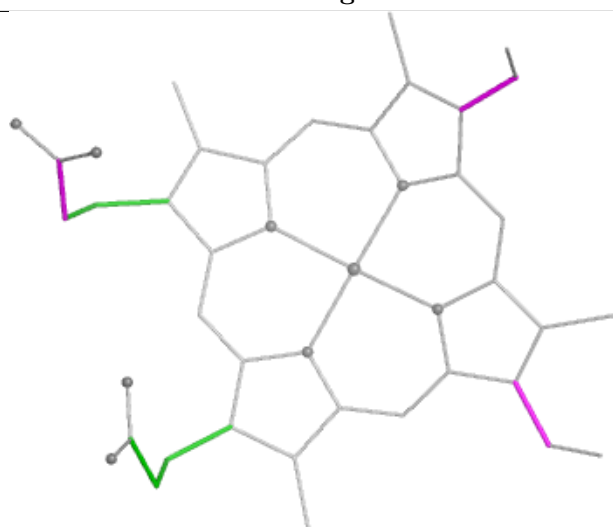
Ligand HEC D 1001



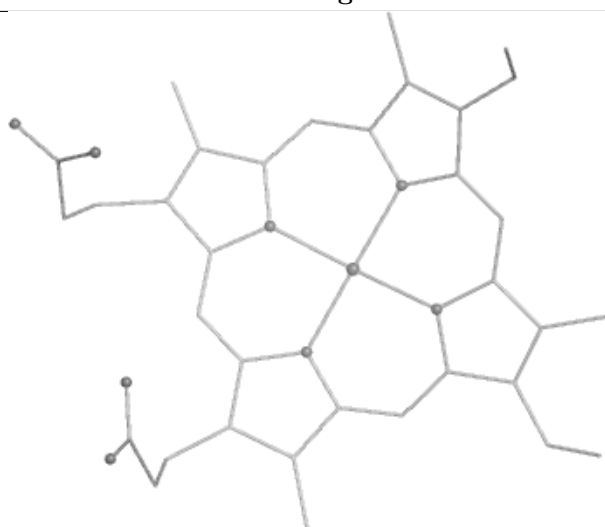
Bond lengths



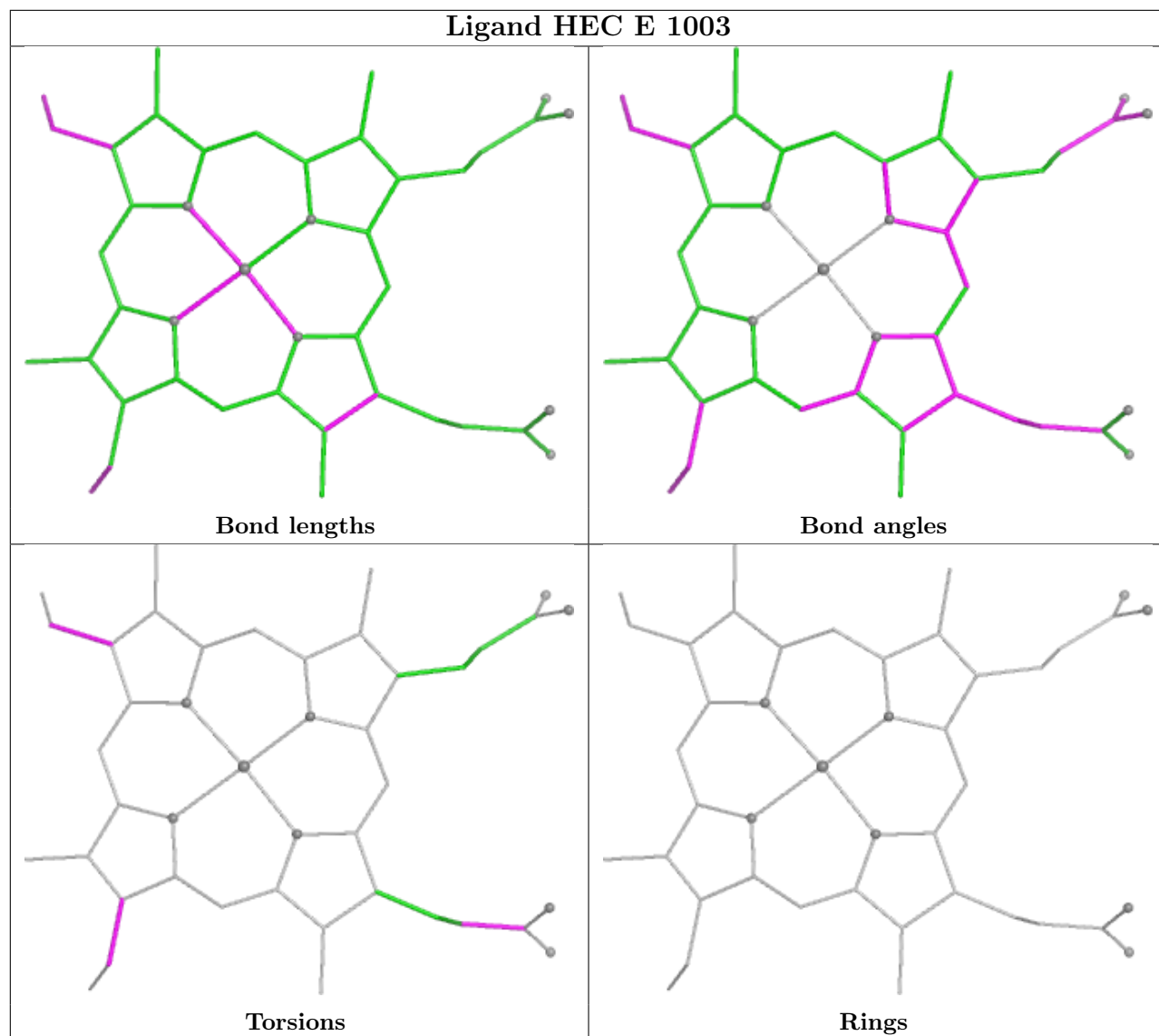
Bond angles

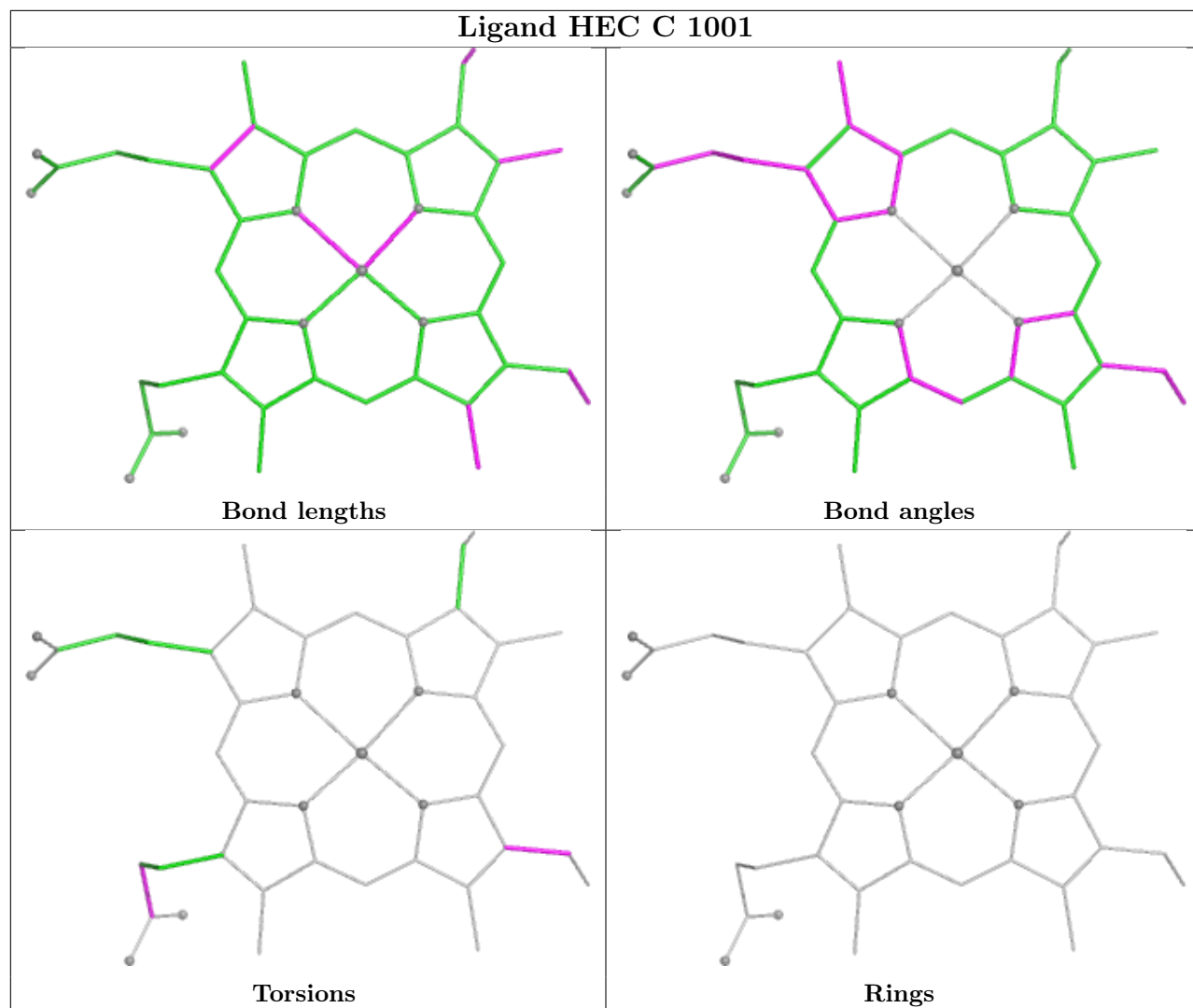


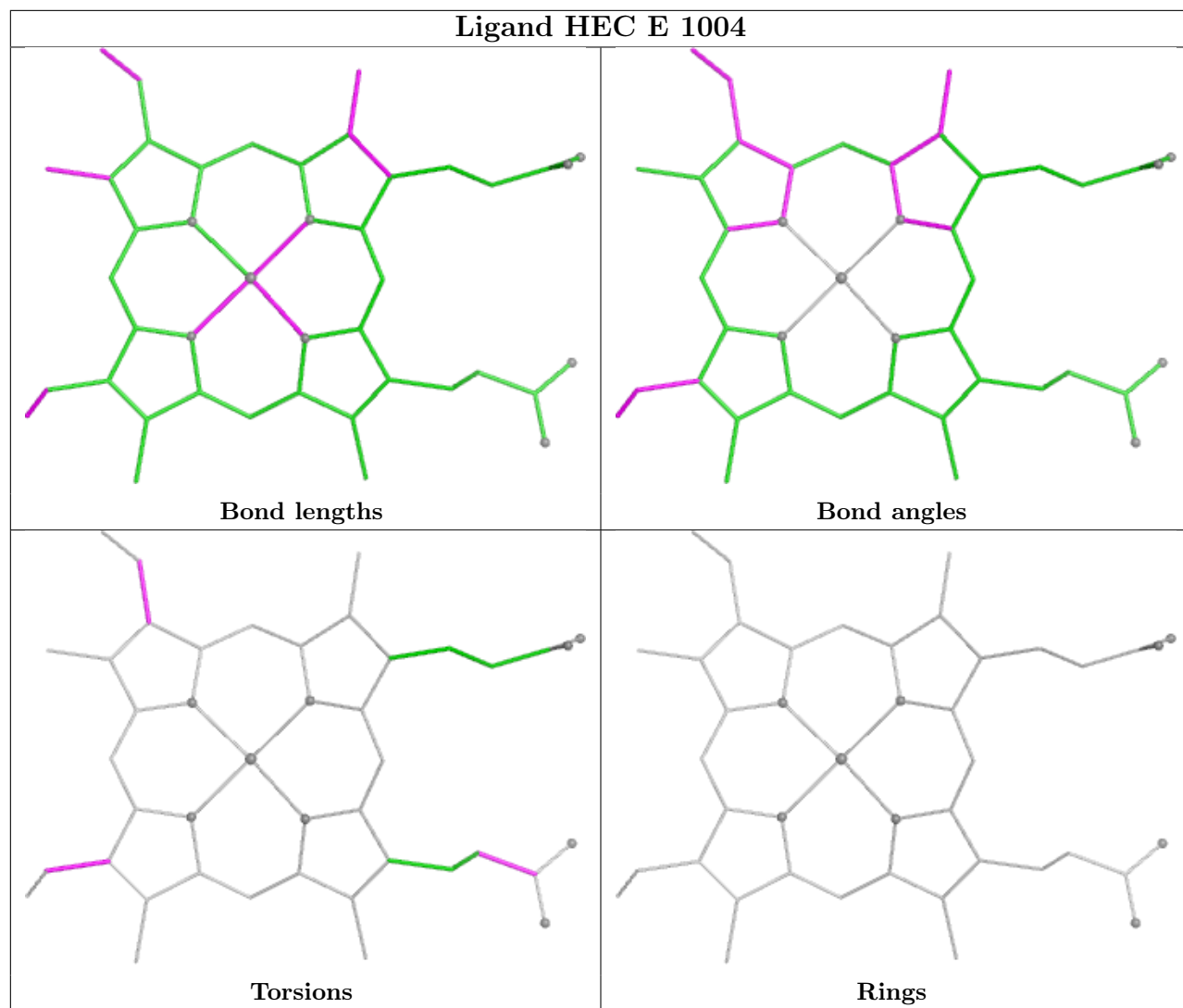
Torsions

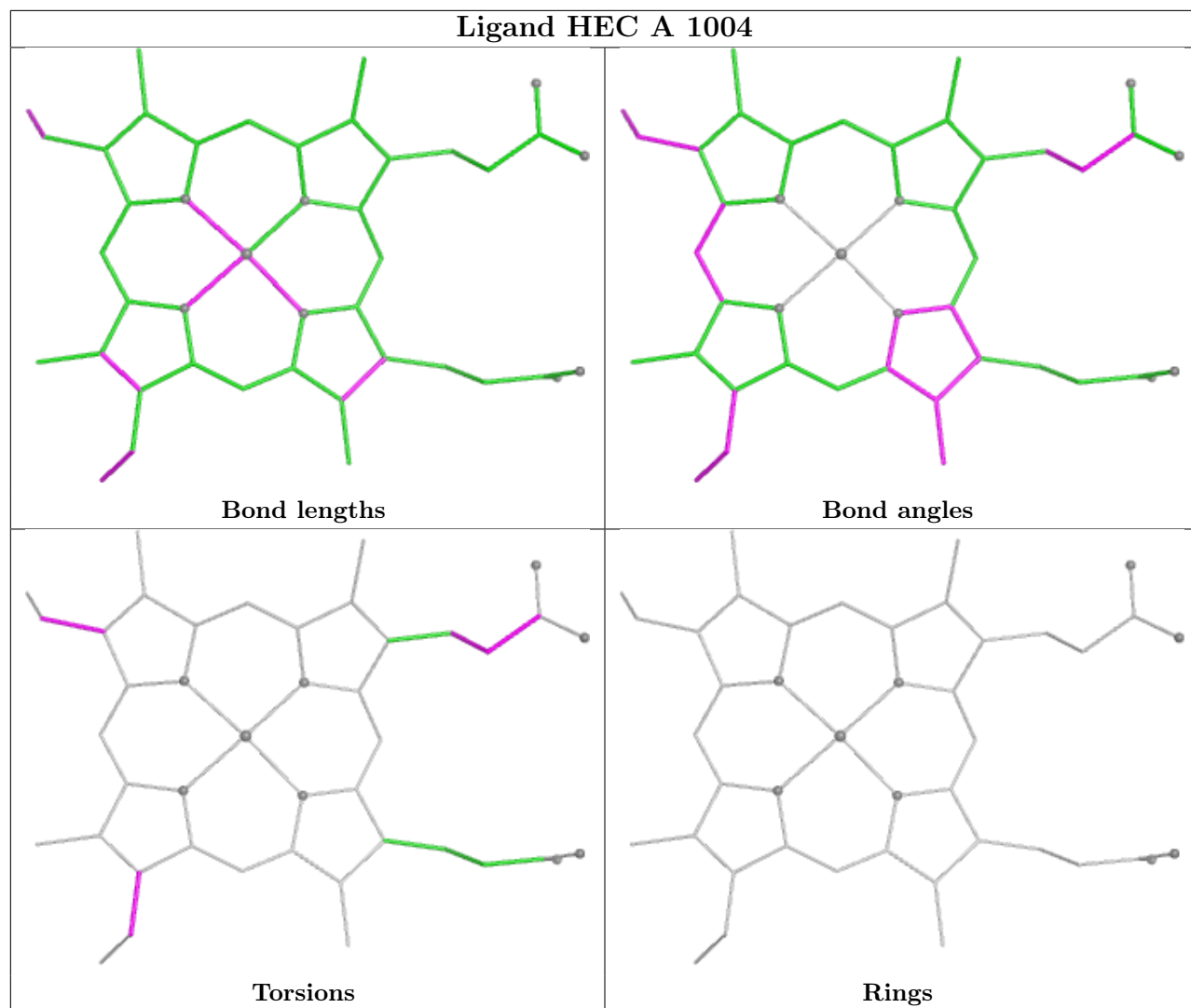


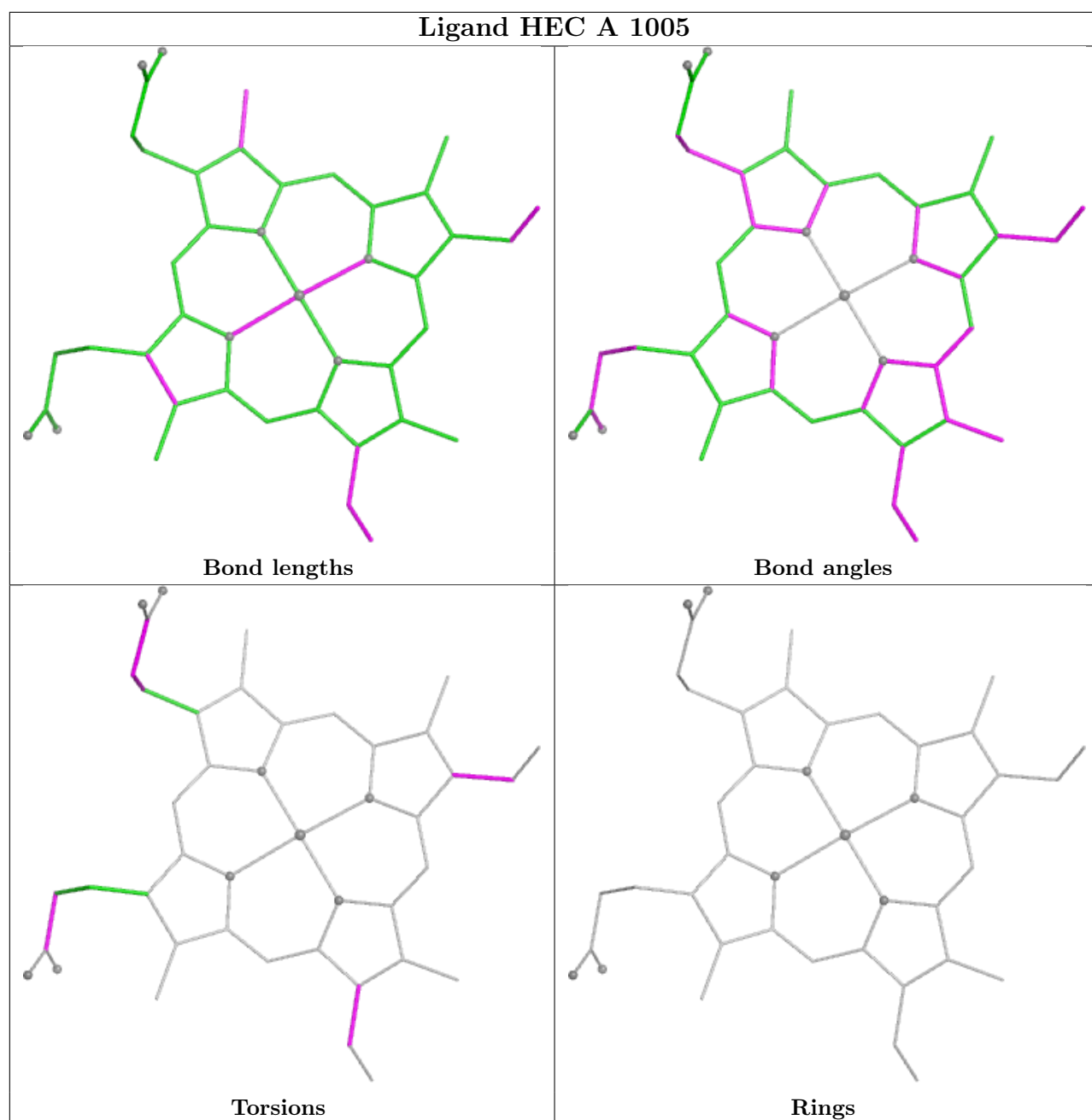
Rings



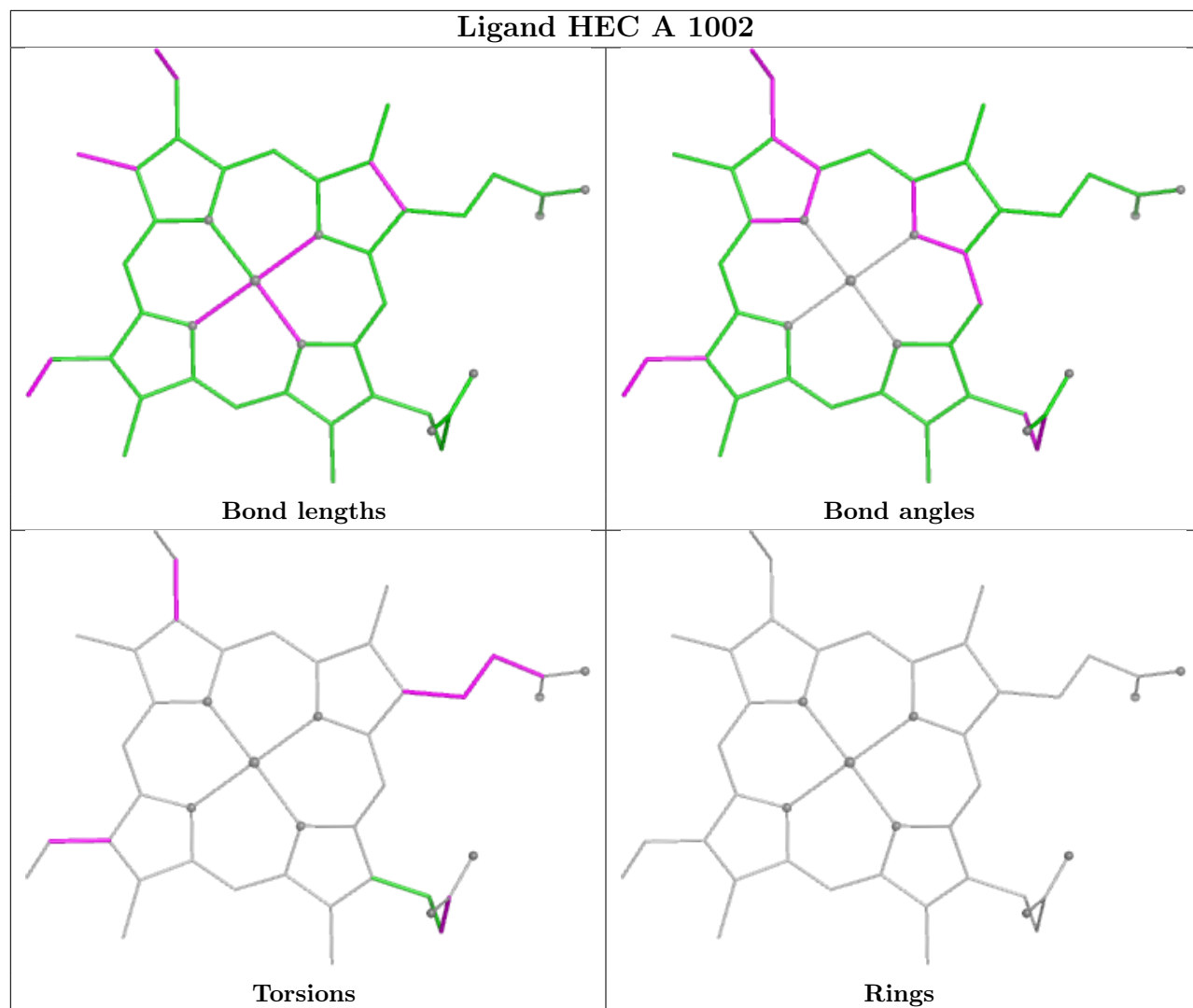




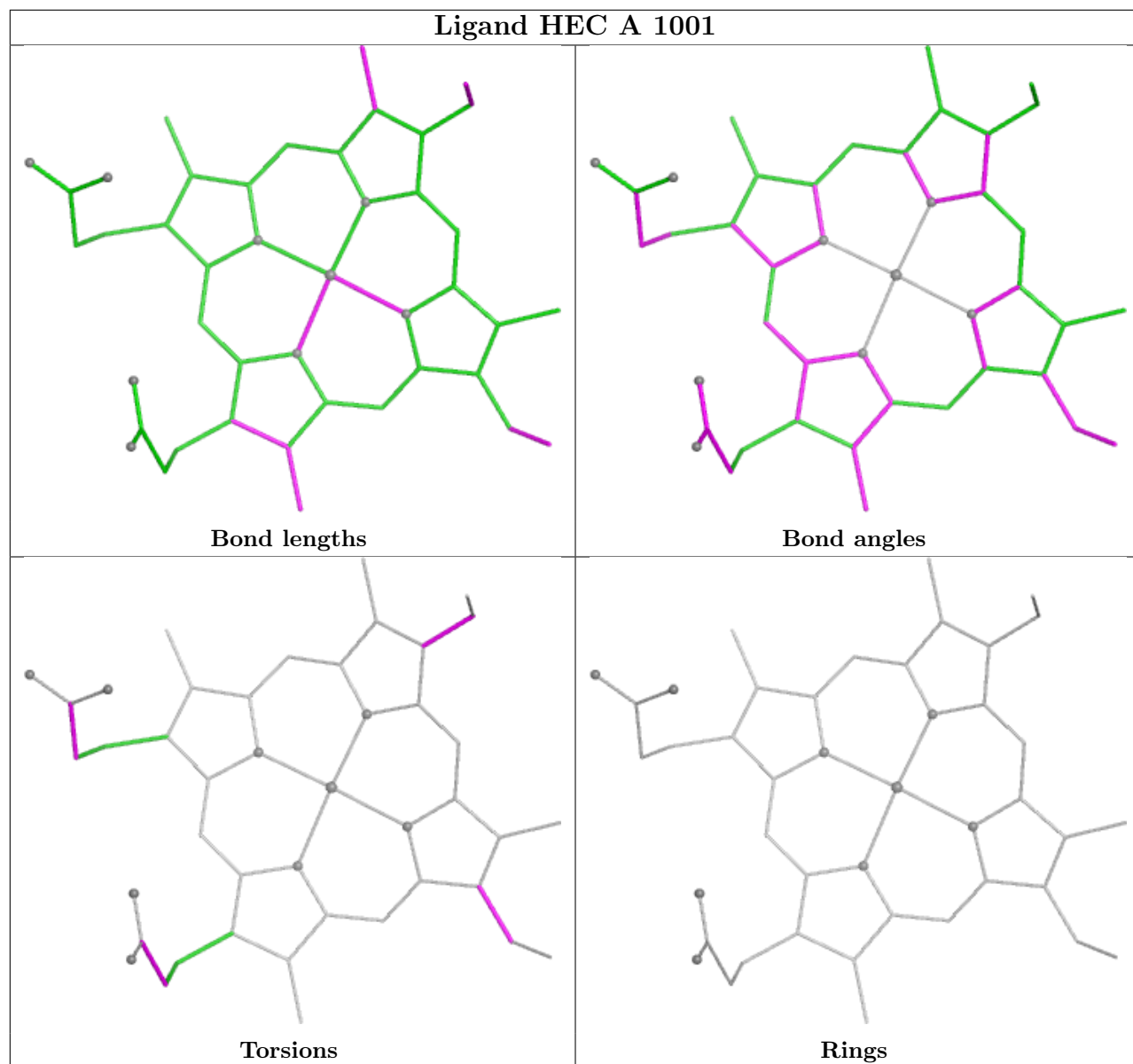




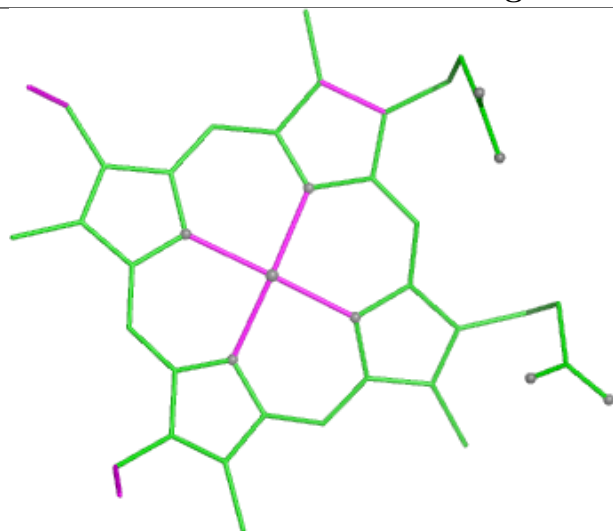
Ligand HEC A 1002



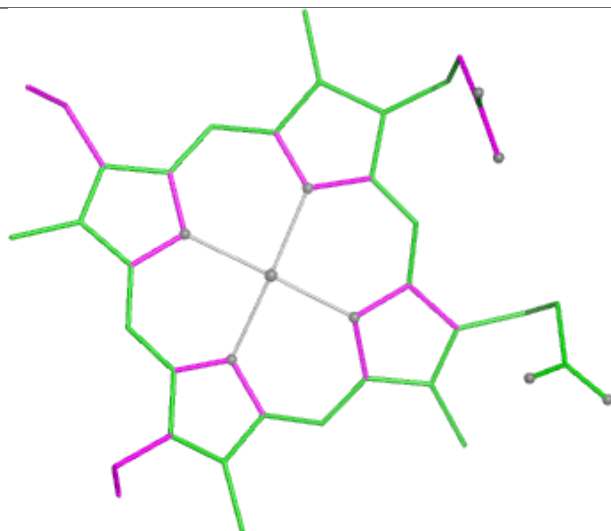
Ligand HEC A 1001



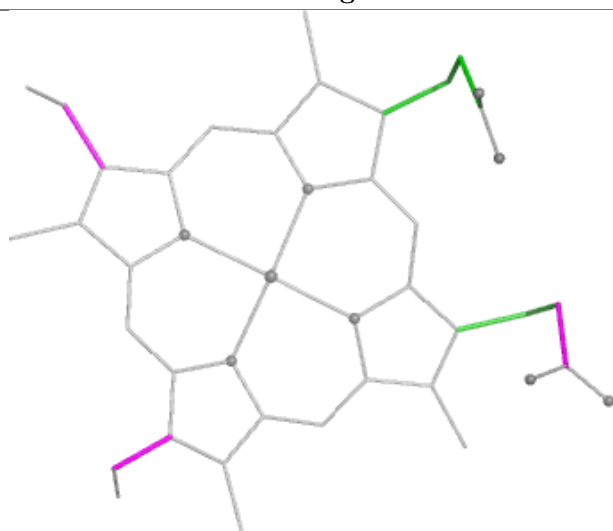
Ligand HEC E 1001



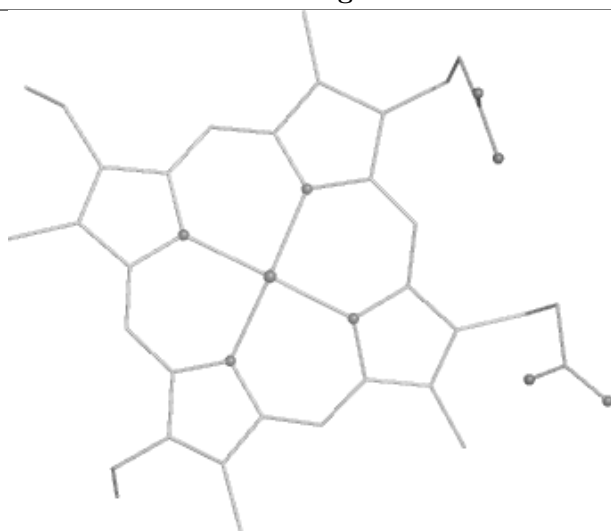
Bond lengths



Bond angles

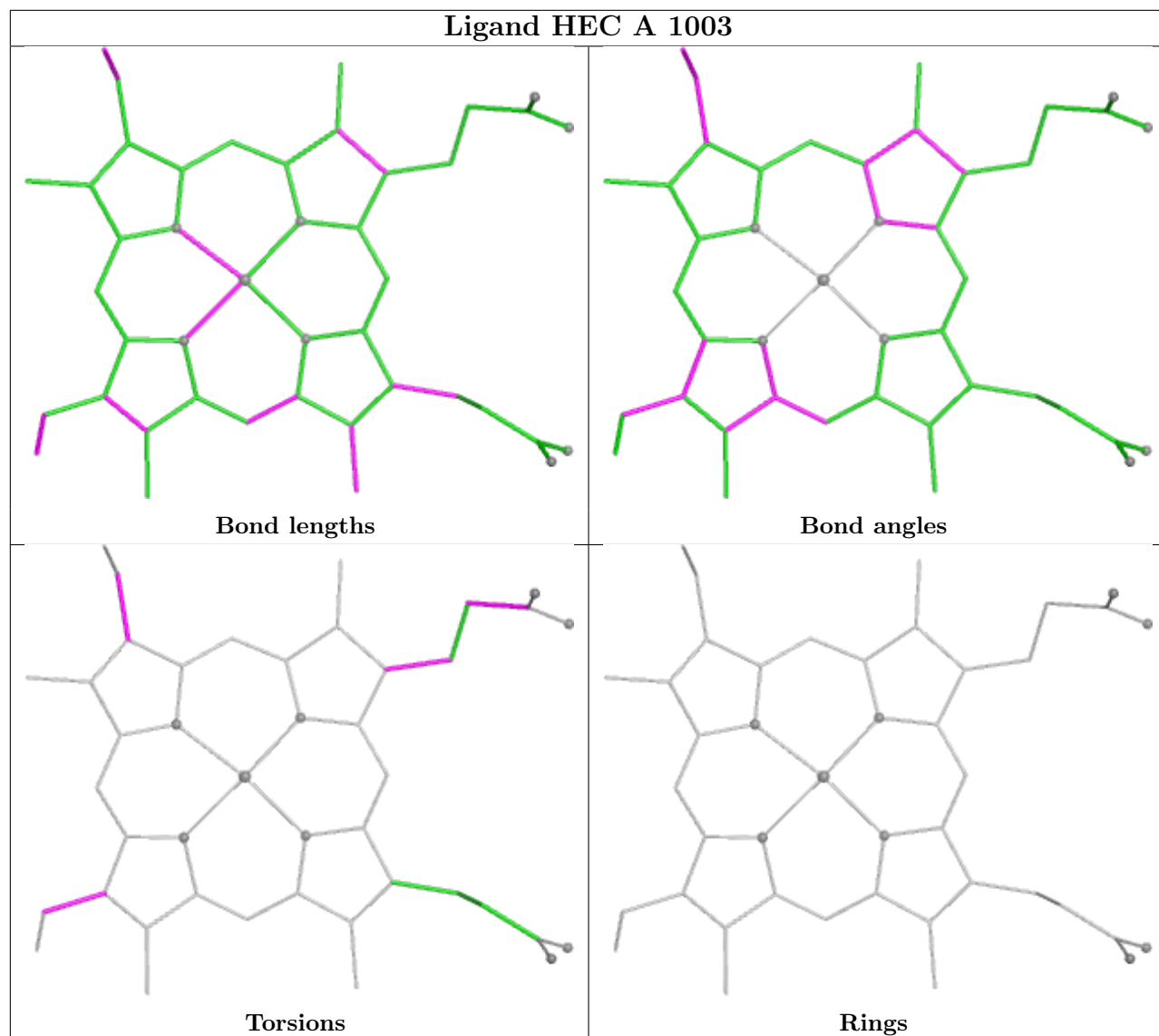


Torsions

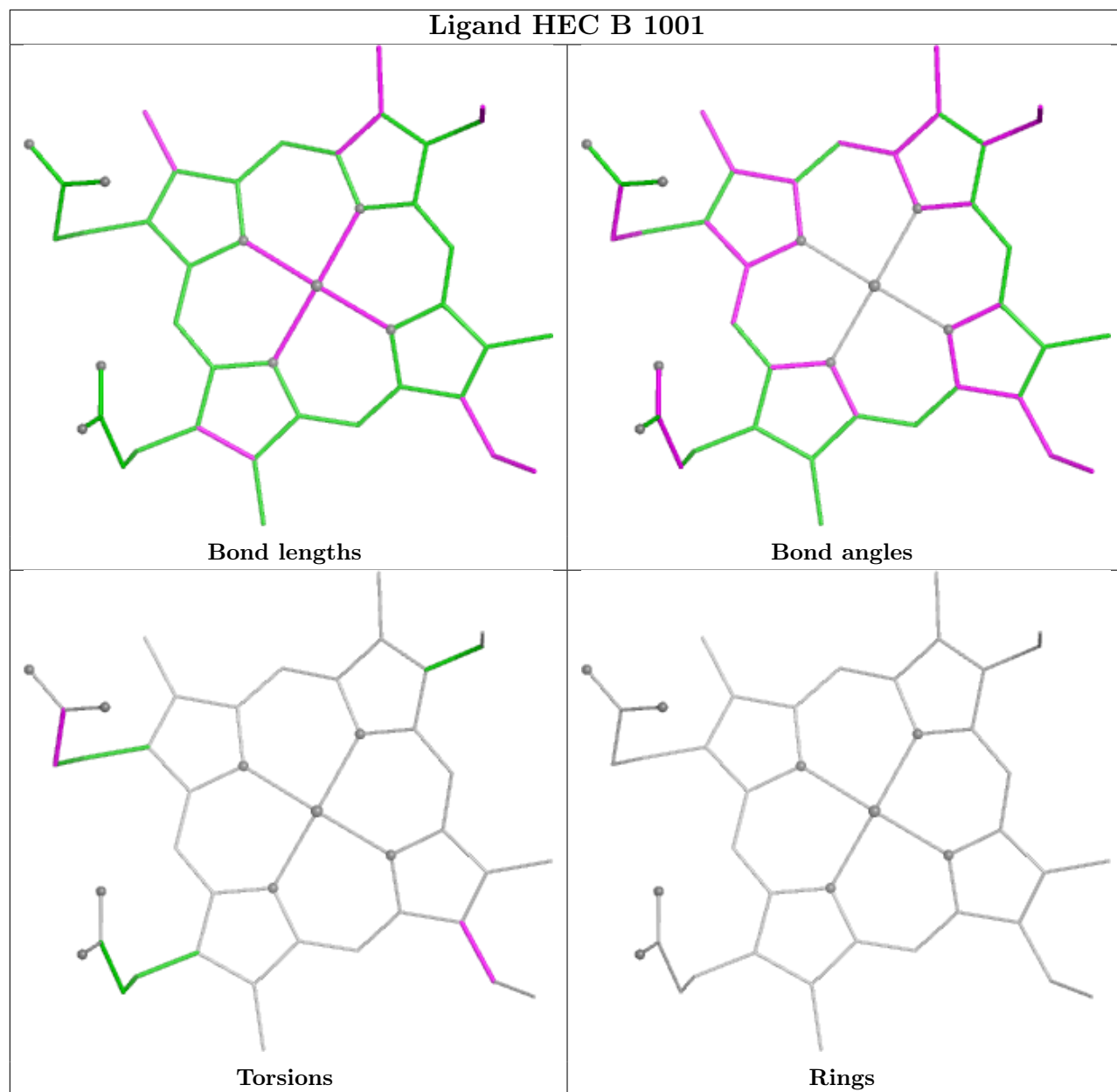


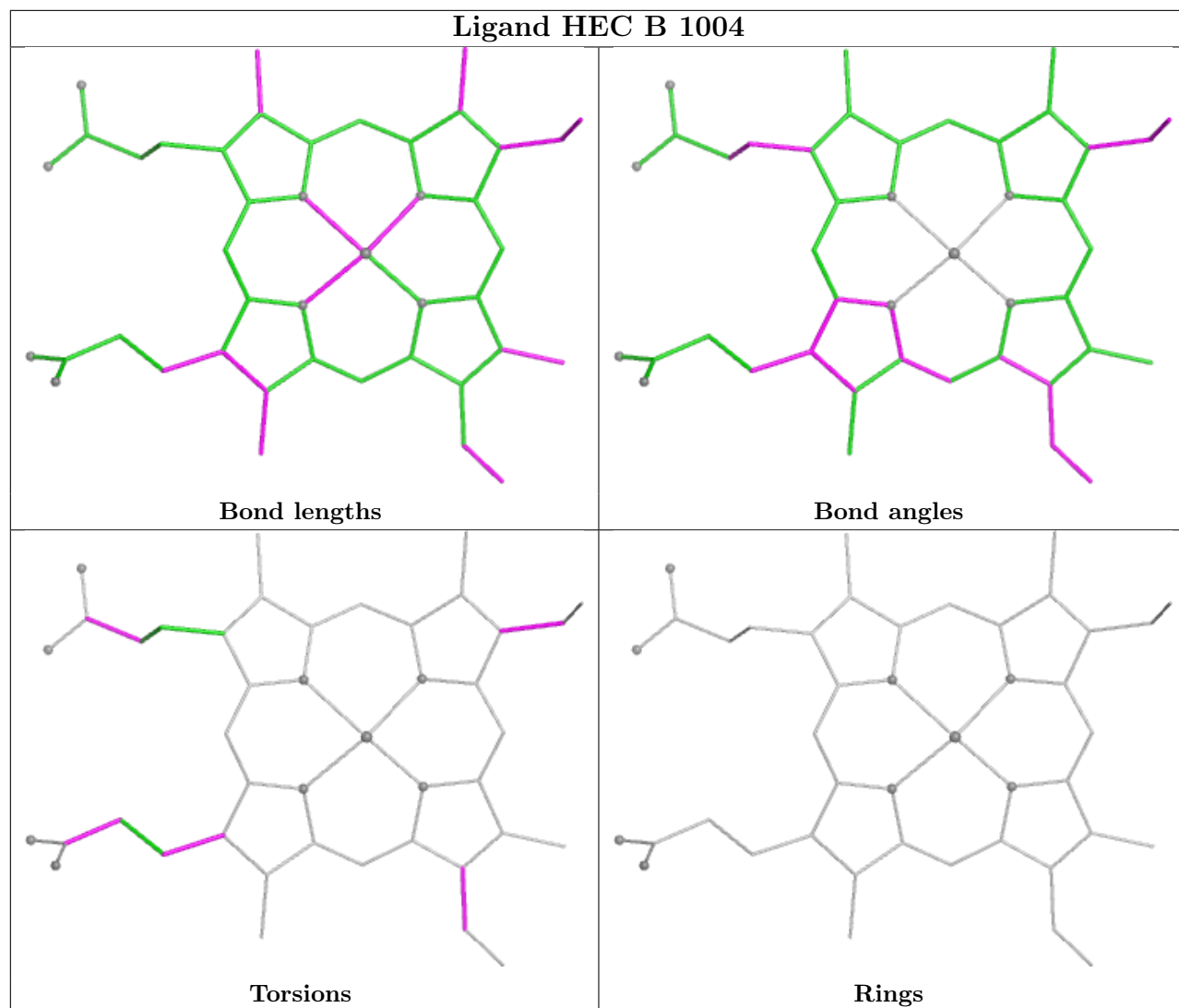
Rings

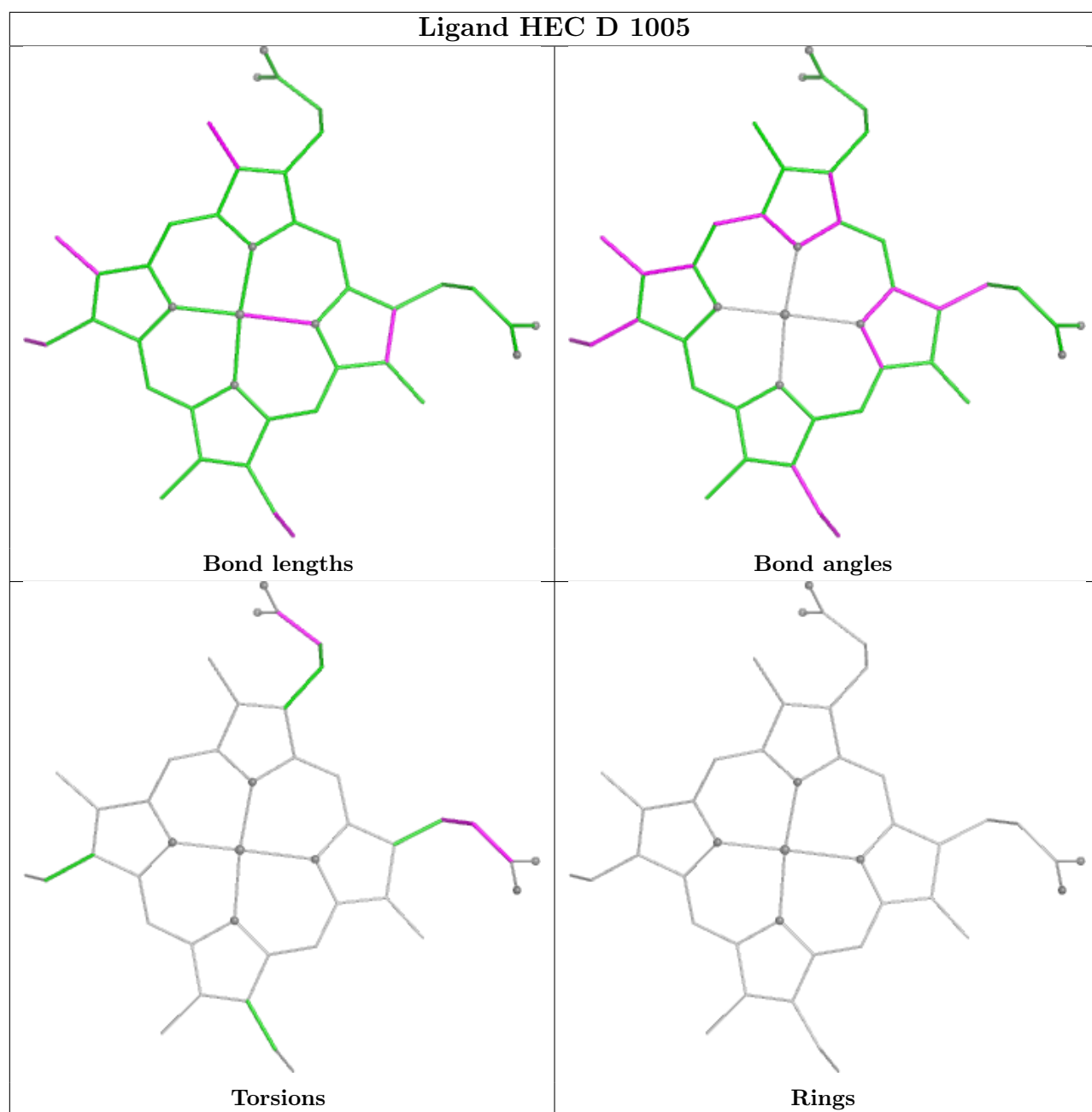
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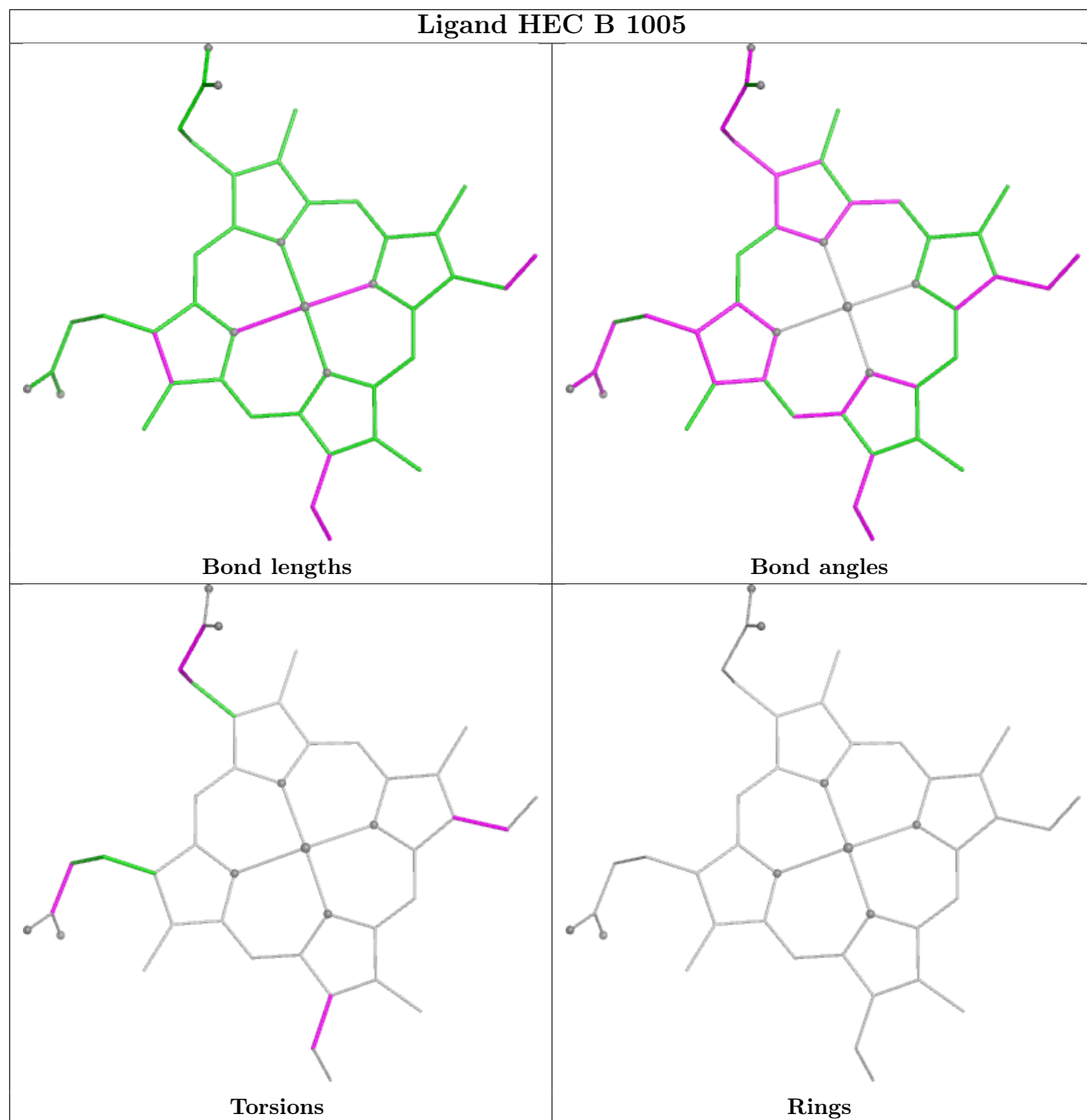


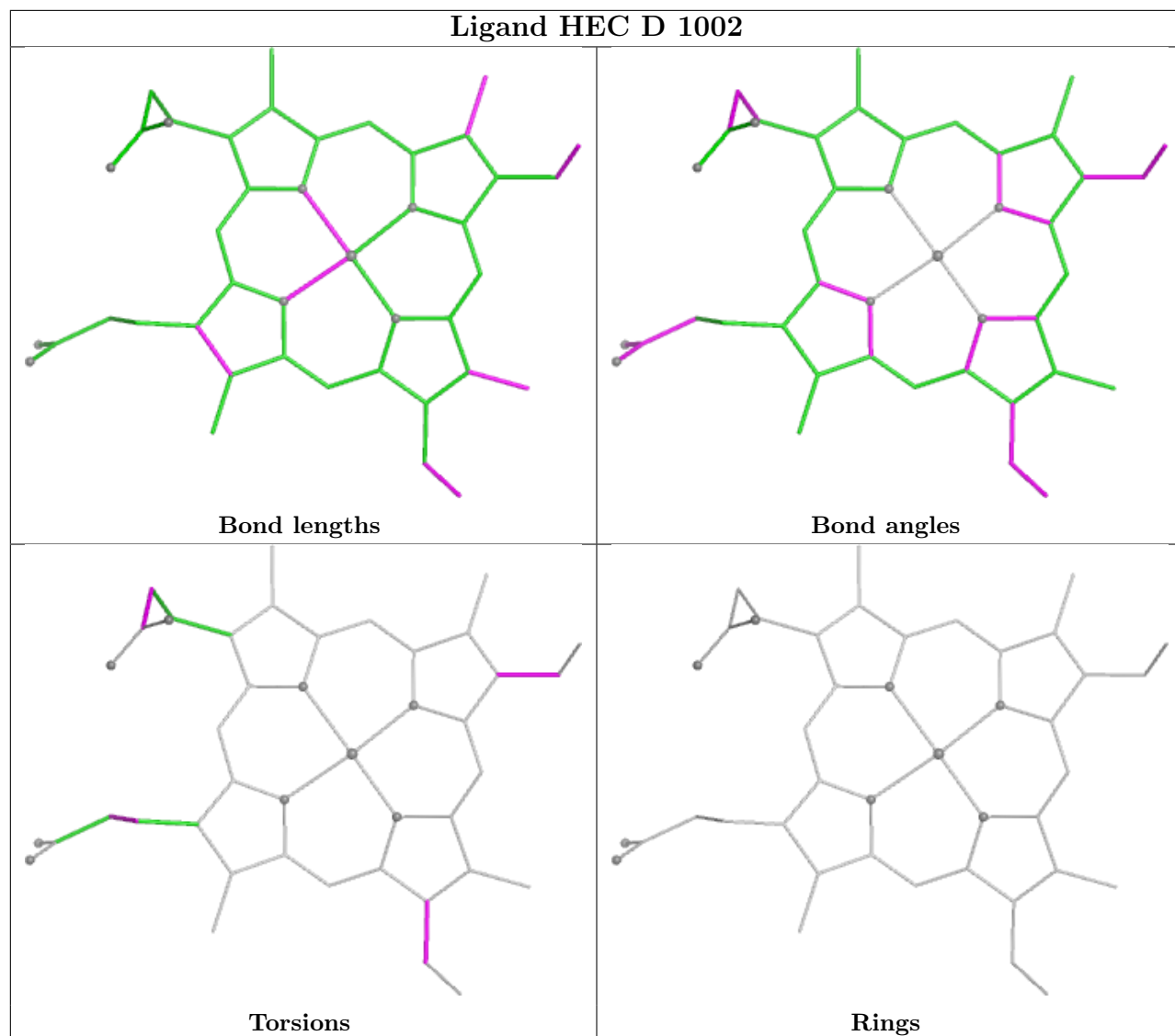
Ligand HEC B 1001

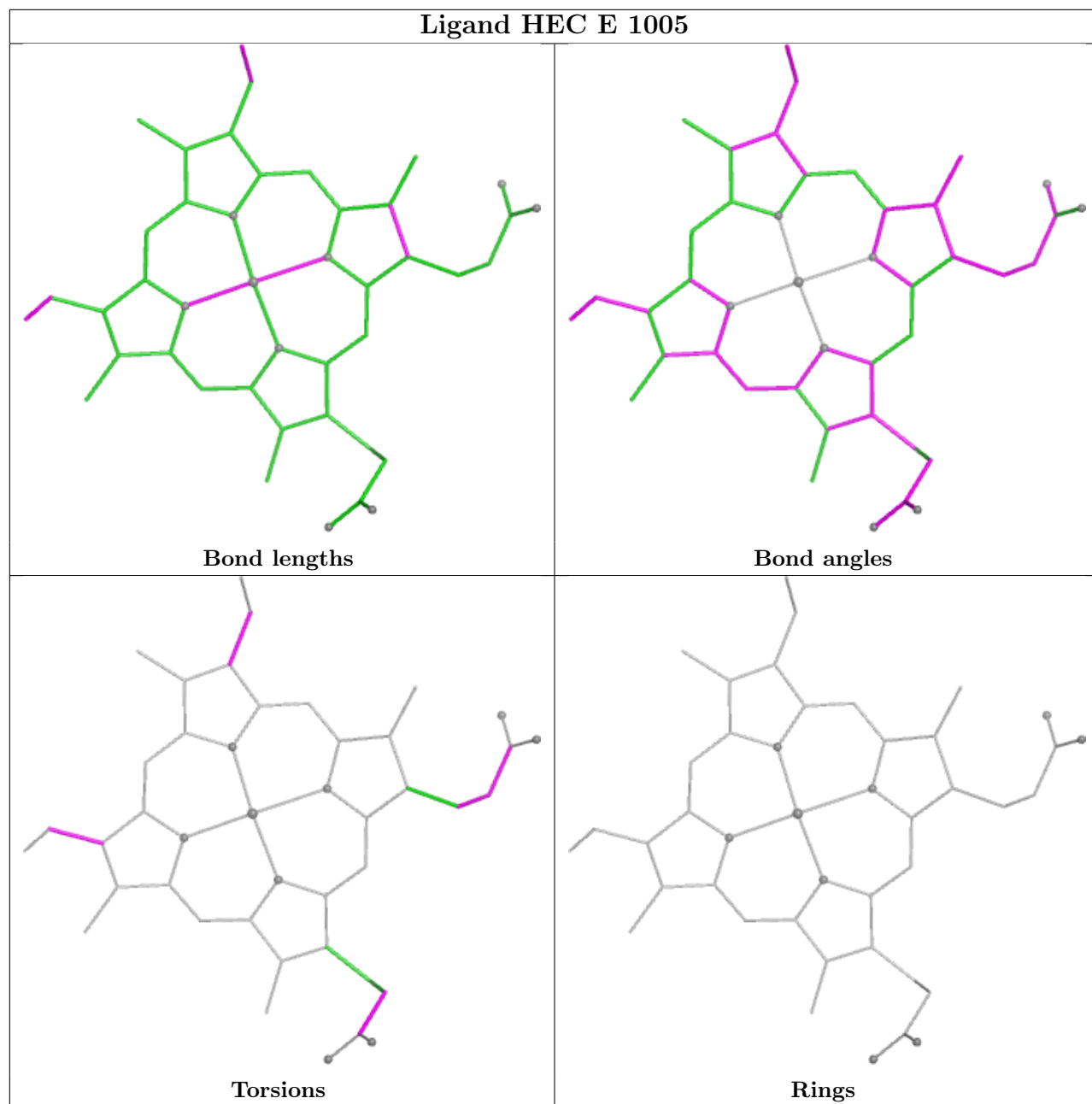


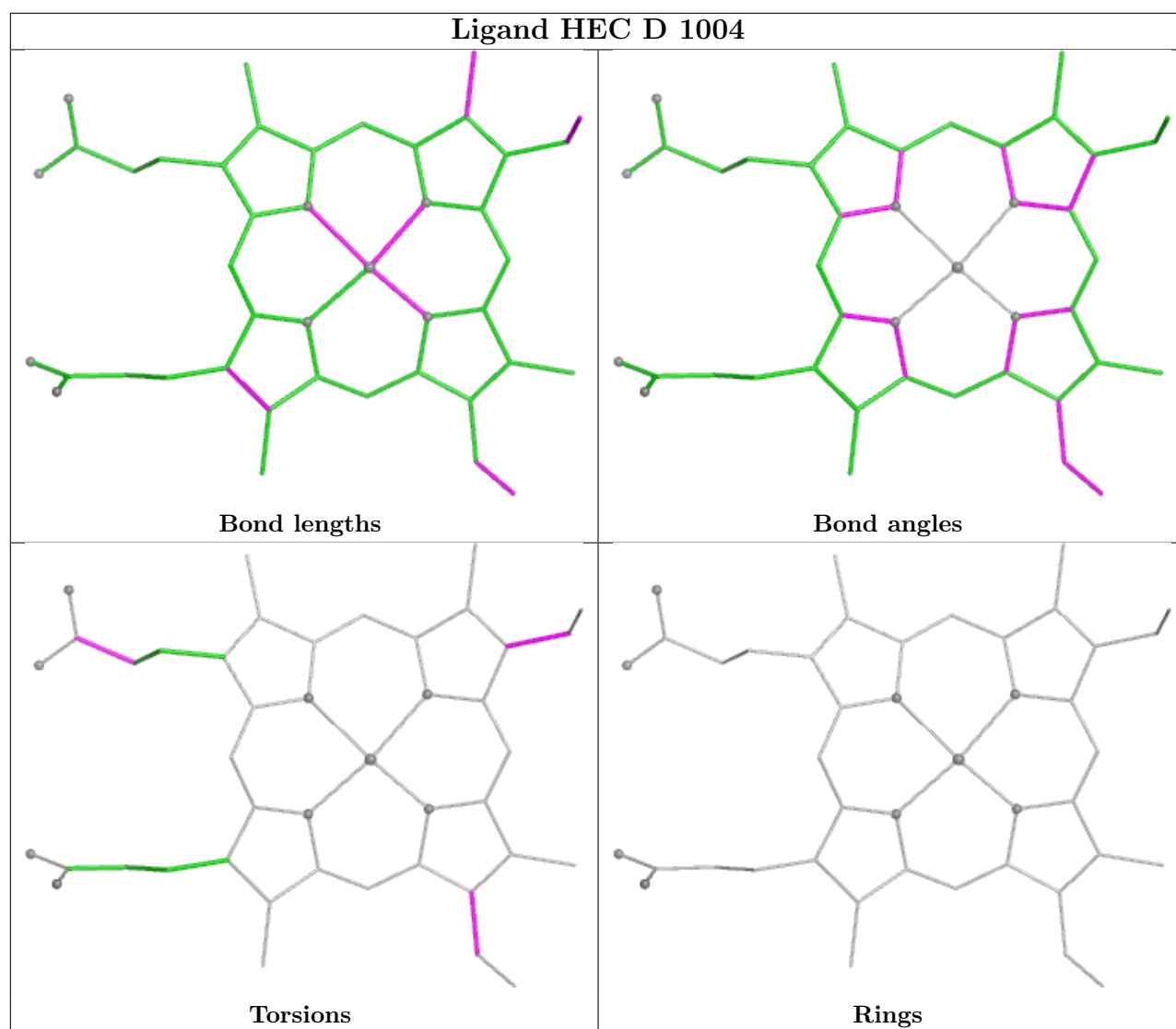












5.7 Other polymers [i](#)

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	495/524 (94%)	0.16	5 (1%) 79 72	22, 25, 27, 32	0
1	B	498/524 (95%)	-0.08	5 (1%) 79 72	13, 24, 27, 32	1 (0%)
1	D	494/524 (94%)	0.08	9 (1%) 67 58	22, 25, 27, 32	0
1	E	495/524 (94%)	0.33	11 (2%) 62 52	20, 24, 27, 32	0
2	C	144/159 (90%)	0.54	3 (2%) 63 54	13, 24, 27, 29	1 (0%)
2	F	146/159 (91%)	0.78	9 (6%) 26 20	21, 24, 27, 29	0
All	All	2272/2414 (94%)	0.19	42 (1%) 67 58	13, 25, 27, 32	2 (0%)

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	26	GLY	4.5
1	D	130	HIS	3.8
1	B	130[A]	HIS	3.7
1	A	347	ARG	3.6
1	E	326	SER	3.3

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	HQO	F	1005	19/19	0.82	0.22	66,67,68,68	0
5	HQO	C	1005	19/19	0.85	0.18	55,55,61,62	0
3	HEC	F	1001	43/43	0.95	0.11	38,41,48,52	0
3	HEC	A	1001	43/43	0.95	0.10	17,21,25,30	0
3	HEC	E	1001	43/43	0.95	0.11	29,31,33,36	0
3	HEC	A	1003	43/43	0.96	0.09	10,13,21,25	0
3	HEC	E	1002	43/43	0.96	0.10	27,30,33,37	0
3	HEC	E	1005	43/43	0.96	0.09	23,25,29,34	0
3	HEC	B	1001	43/43	0.96	0.10	9,13,17,21	0
4	CA	A	1007	1/1	0.96	0.07	36,36,36,36	0
4	CA	D	1006	1/1	0.96	0.04	30,30,30,30	0
3	HEC	C	1002	43/43	0.96	0.10	20,23,26,27	0
3	HEC	D	1003	43/43	0.96	0.09	14,19,26,27	0
3	HEC	D	1002	43/43	0.97	0.08	16,18,23,28	0
3	HEC	A	1004	43/43	0.97	0.09	3,7,17,21	0
3	HEC	B	1002	43/43	0.97	0.08	17,21,25,27	0
3	HEC	B	1003	43/43	0.97	0.08	4,7,18,18	0
3	HEC	E	1003	43/43	0.97	0.09	26,35,36,38	0
3	HEC	E	1004	43/43	0.97	0.09	25,29,31,32	0
3	HEC	B	1005	43/43	0.97	0.09	15,17,25,27	0
3	HEC	C	1001	43/43	0.97	0.09	22,25,33,37	0
3	HEC	F	1002	43/43	0.97	0.09	23,27,32,34	0
3	HEC	F	1003	43/43	0.97	0.09	13,18,25,28	0
3	HEC	F	1004	43/43	0.97	0.08	11,15,28,36	0
3	HEC	A	1005	43/43	0.97	0.08	9,15,18,24	0
3	HEC	C	1003	43/43	0.97	0.09	19,22,26,29	0
3	HEC	C	1004	43/43	0.97	0.08	16,20,28,32	0
3	HEC	D	1001	43/43	0.97	0.09	22,27,32,34	0
3	HEC	B	1004	43/43	0.98	0.07	2,3,11,15	0
3	HEC	D	1004	43/43	0.98	0.07	11,13,20,22	0
4	CA	D	1007	1/1	0.98	0.06	29,29,29,29	0
4	CA	E	1006	1/1	0.98	0.03	24,24,24,24	0
3	HEC	D	1005	43/43	0.98	0.07	15,17,24,26	0
3	HEC	A	1002	43/43	0.98	0.08	21,22,28,31	0
4	CA	B	1007	1/1	0.99	0.04	19,19,19,19	0
4	CA	E	1007	1/1	0.99	0.10	25,25,25,25	0
4	CA	A	1006	1/1	0.99	0.08	19,19,19,19	0

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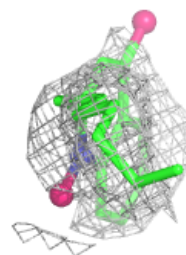
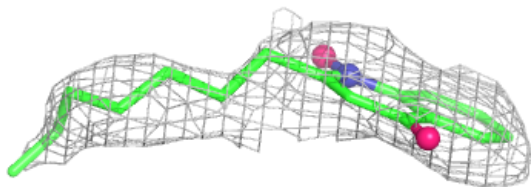
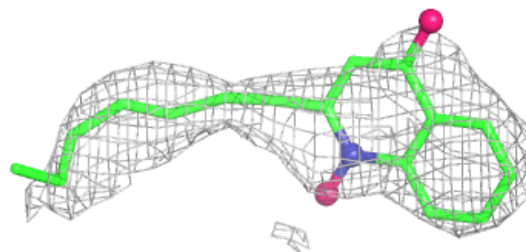
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	B	1006	1/1	0.99	0.07	20,20,20,20	0

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.

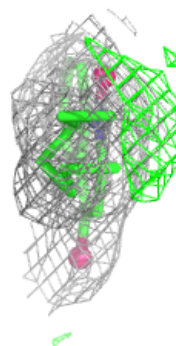
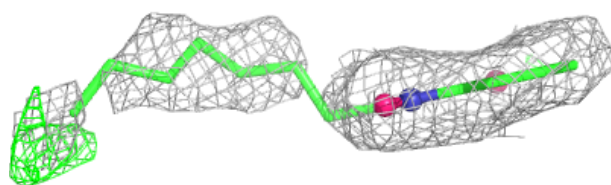
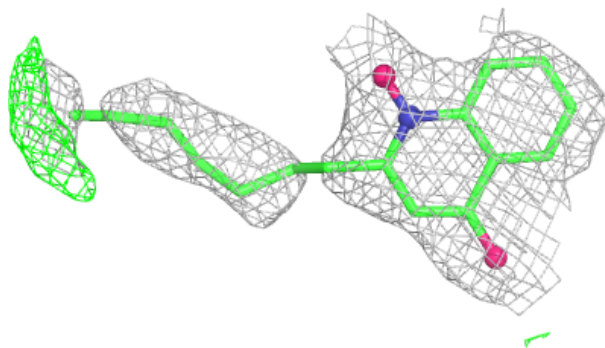
Electron density around HQO F 1005:

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



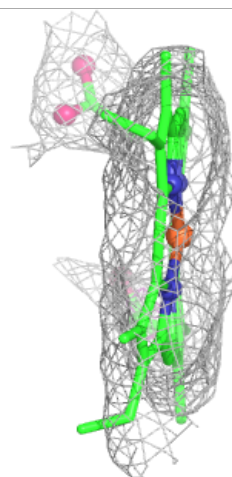
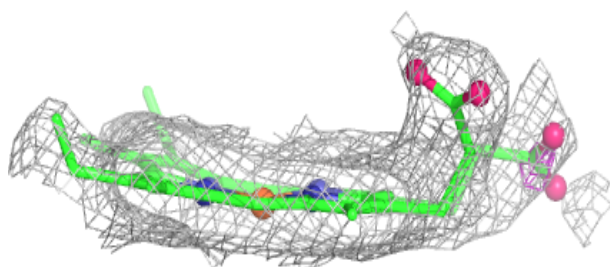
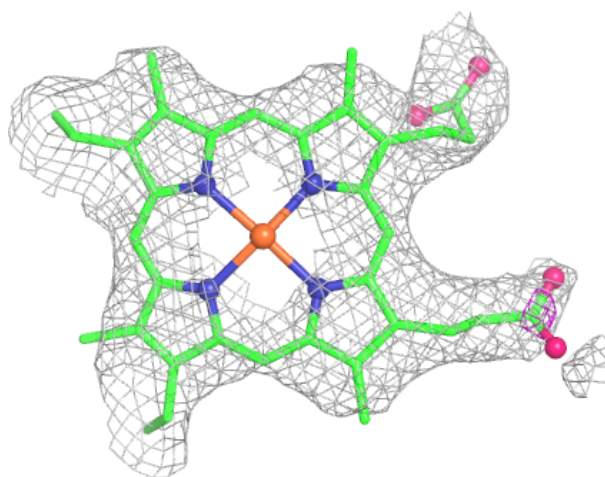
Electron density around HQO C 1005:

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and green (positive)



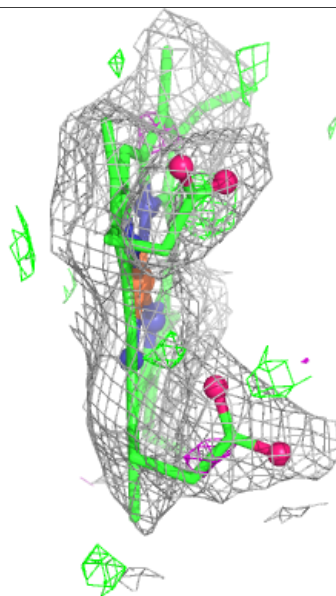
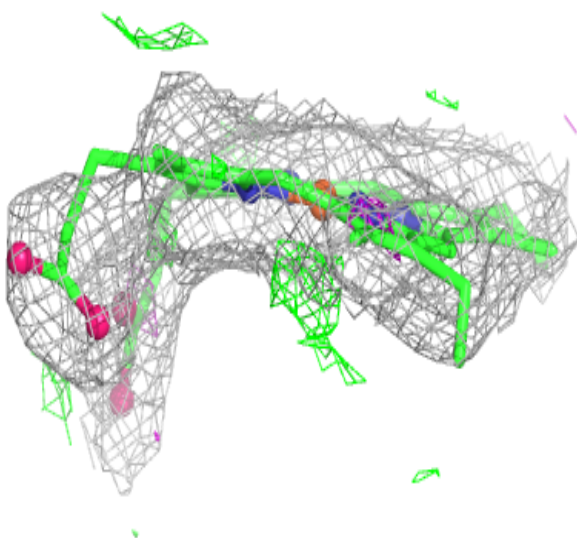
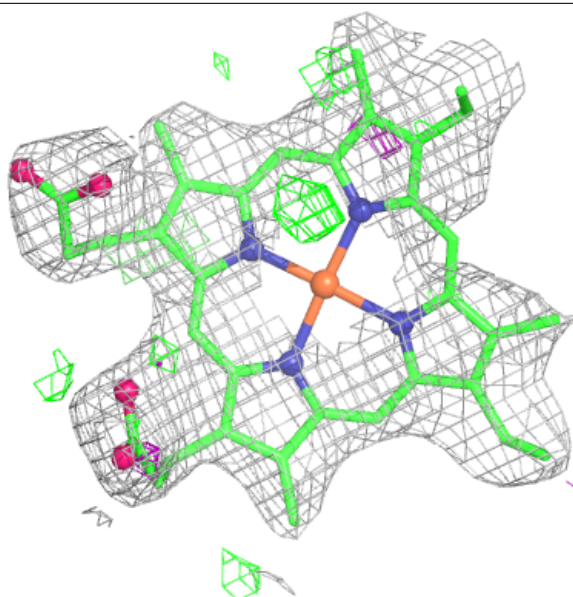
Electron density around HEC F 1001:

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and green (positive)



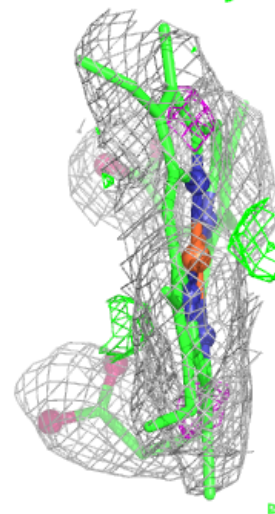
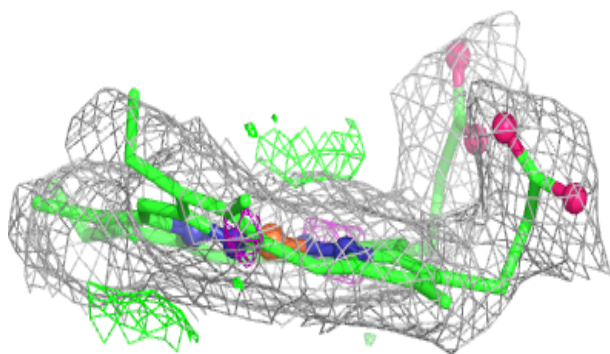
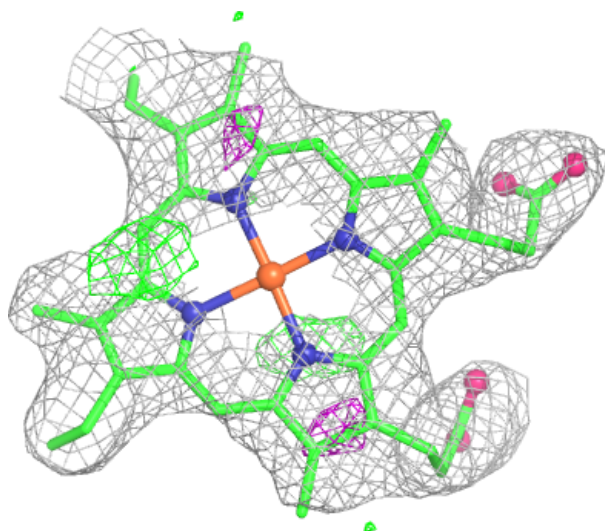
Electron density around HEC A 1001:

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and green (positive)



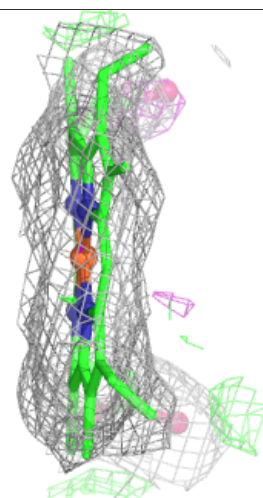
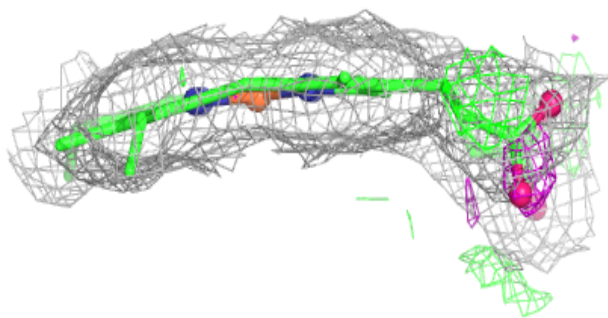
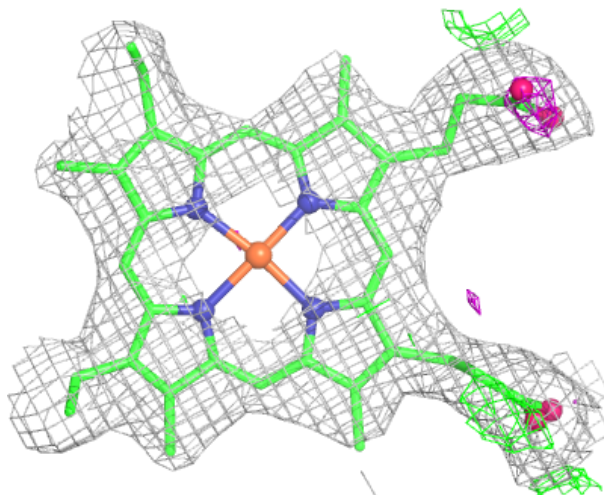
Electron density around HEC E 1001:

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



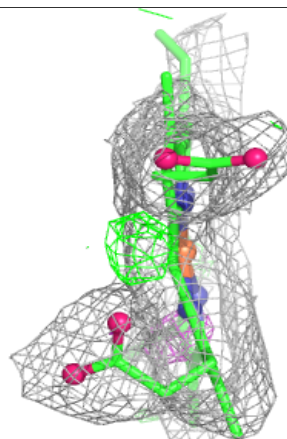
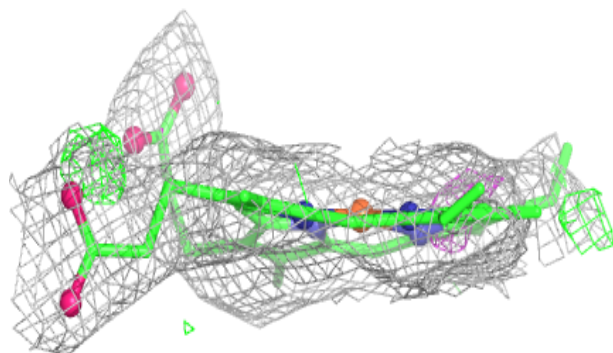
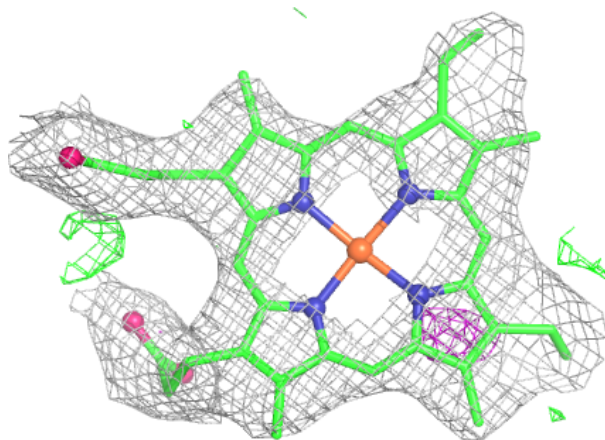
Electron density around HEC A 1003:

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



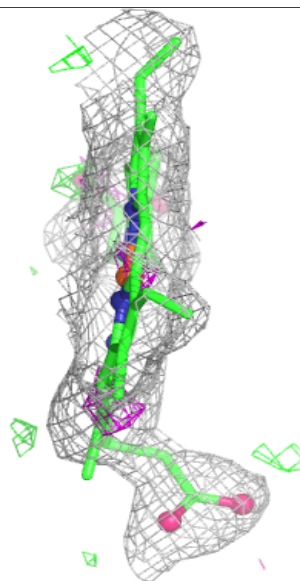
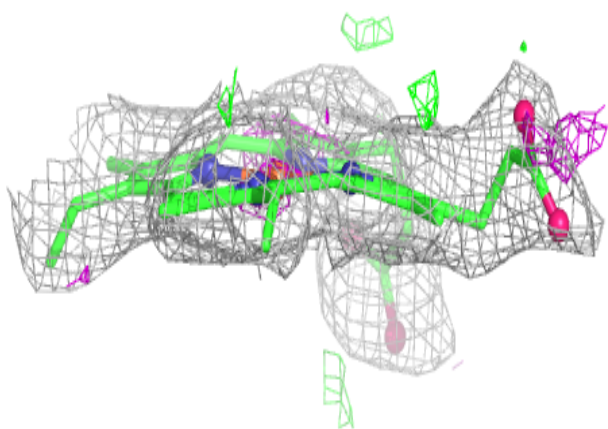
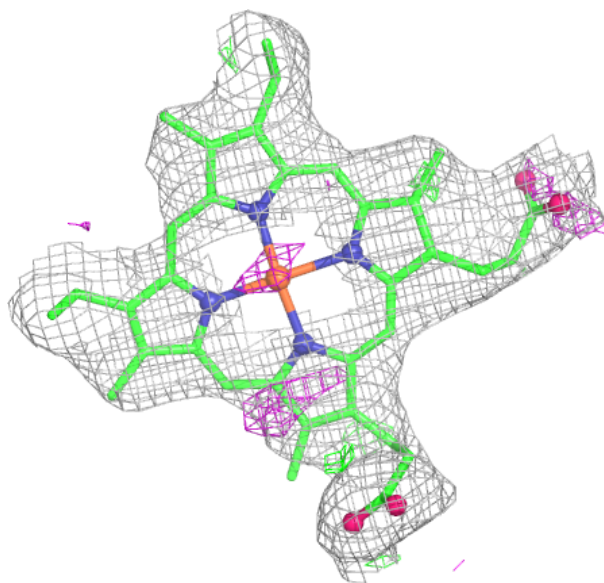
Electron density around HEC E 1002:

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and green (positive)



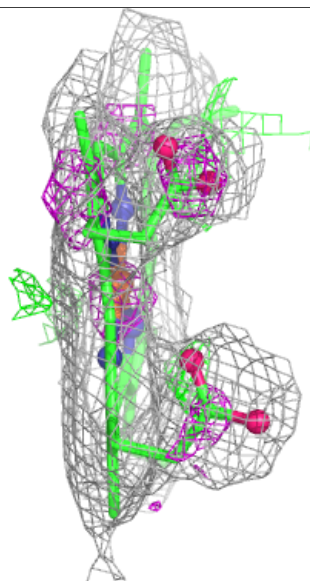
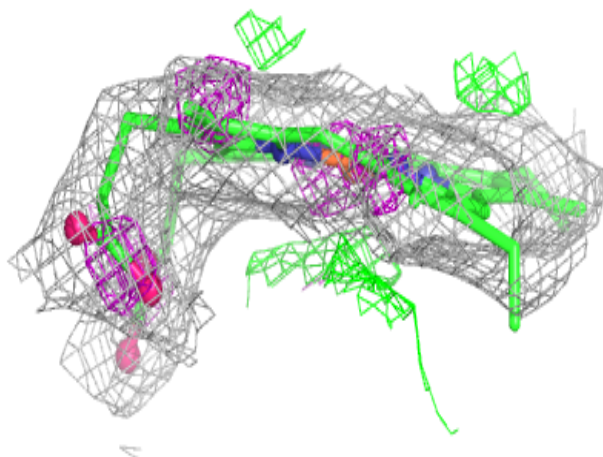
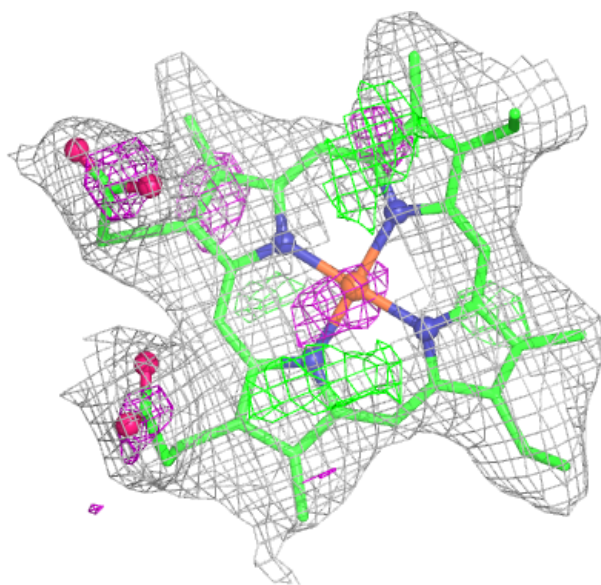
Electron density around HEC E 1005:

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and green (positive)



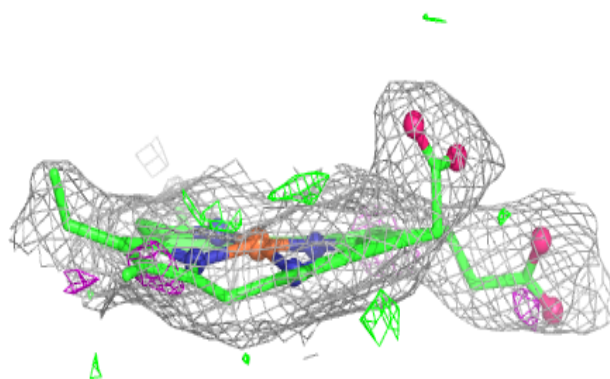
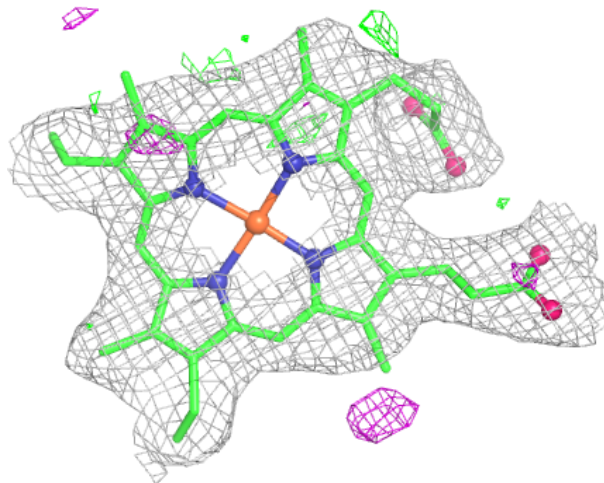
Electron density around HEC B 1001:

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and green (positive)



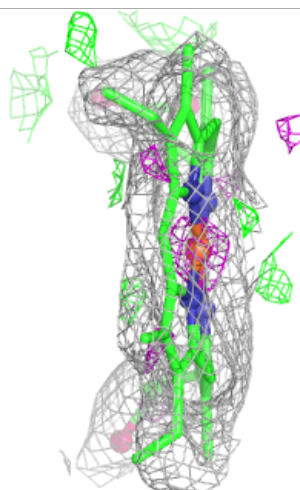
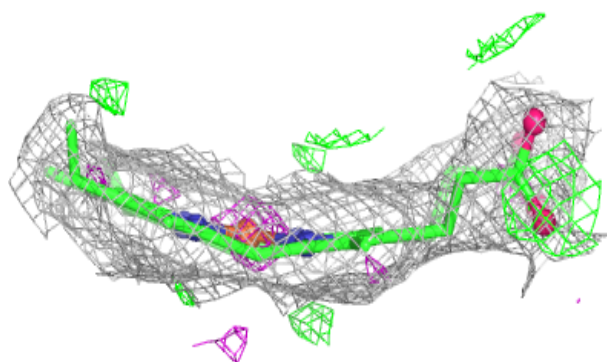
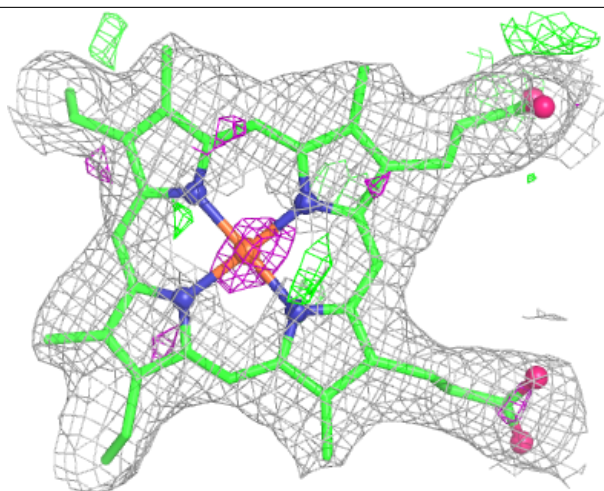
Electron density around HEC C 1002:

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and green (positive)



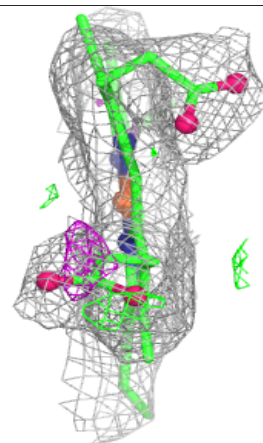
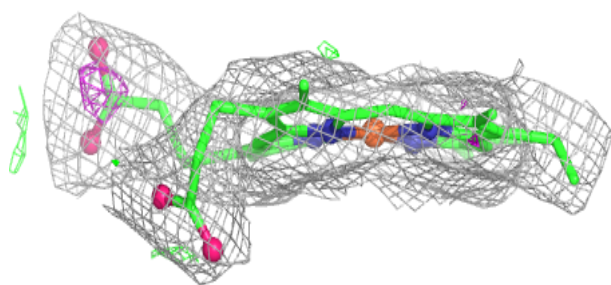
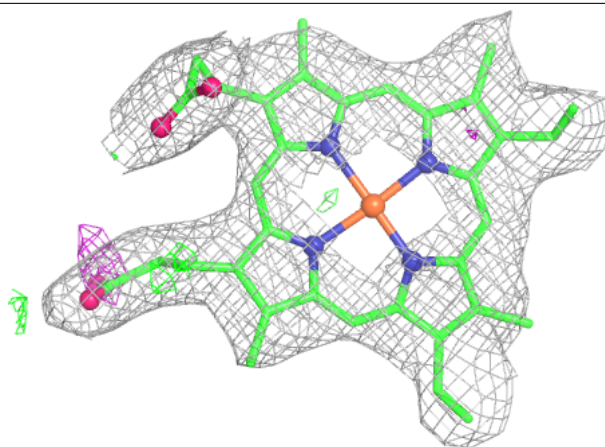
Electron density around HEC D 1003:

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



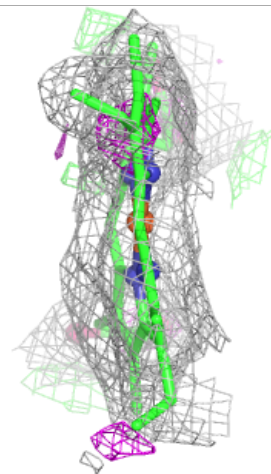
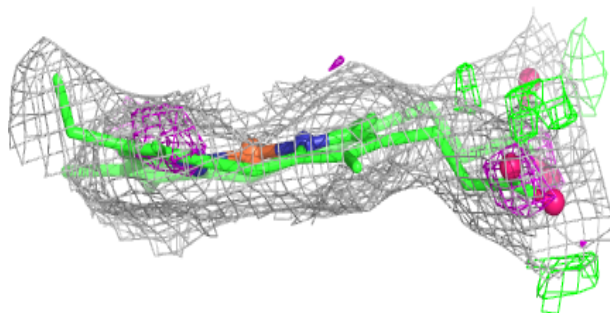
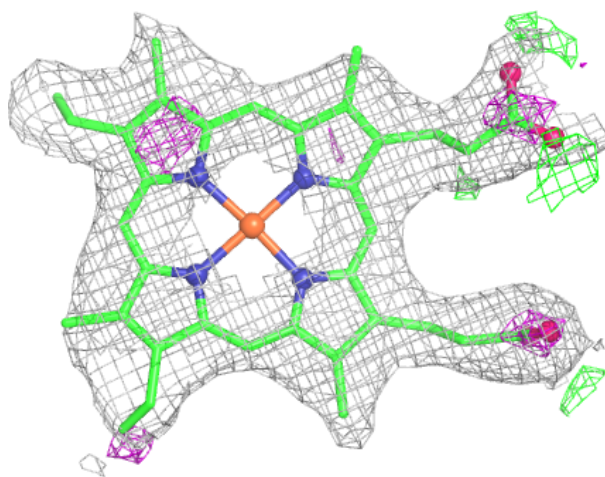
Electron density around HEC D 1002:

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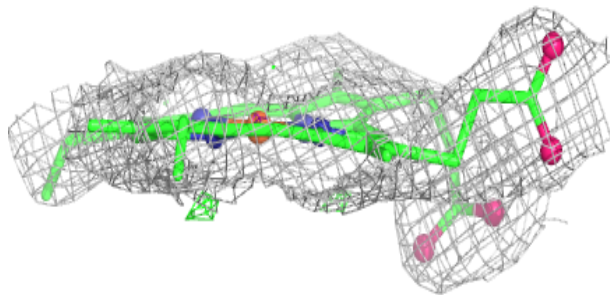
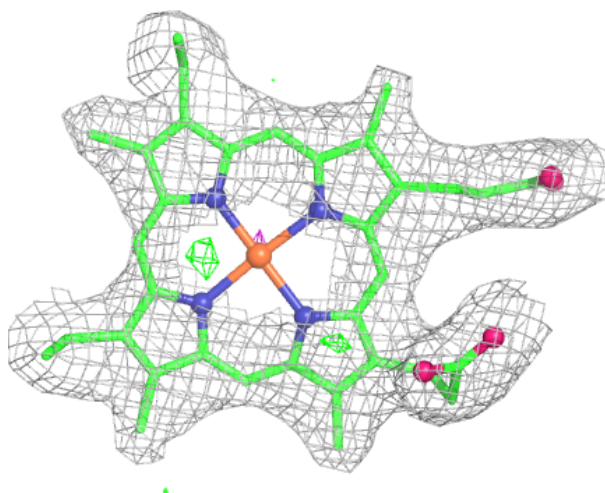
Electron density around HEC A 1004:

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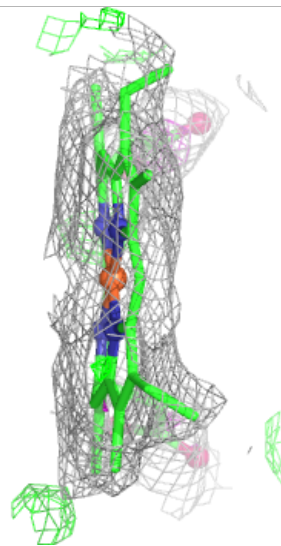
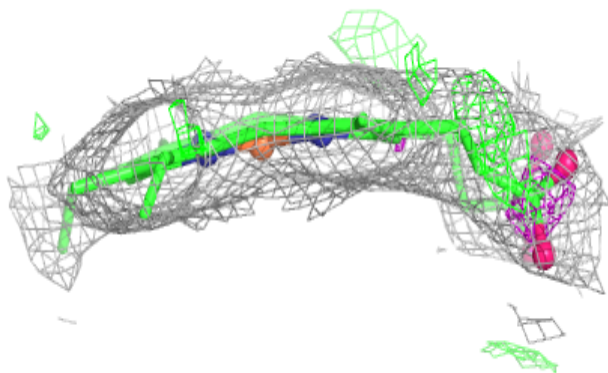
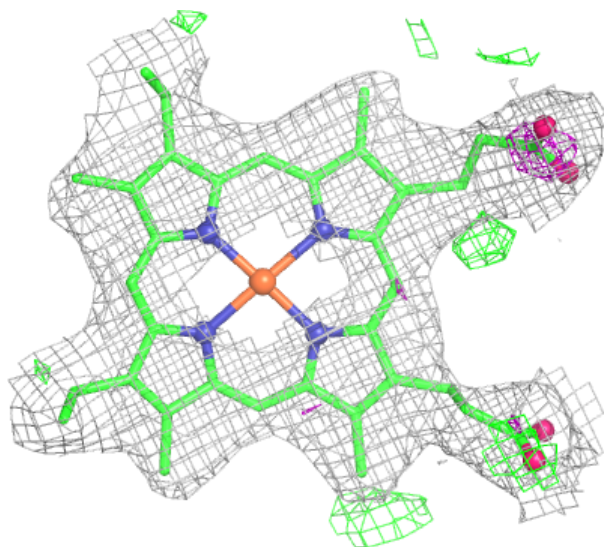
Electron density around HEC B 1002:

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and green (positive)



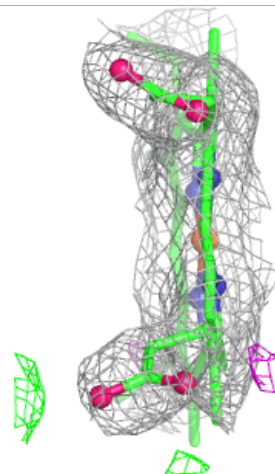
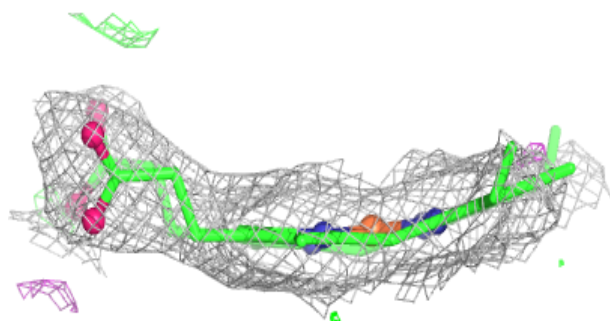
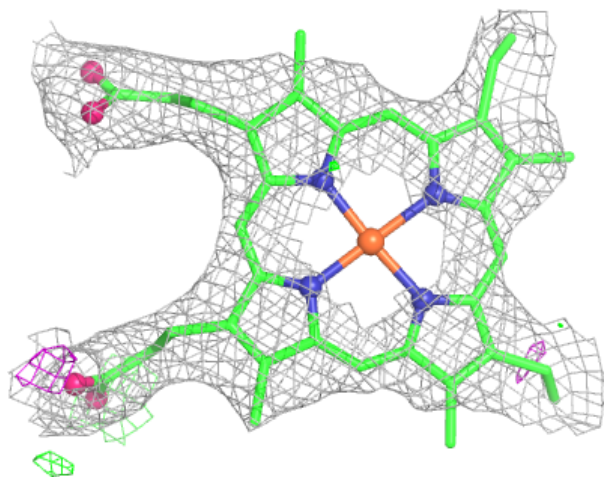
Electron density around HEC B 1003:

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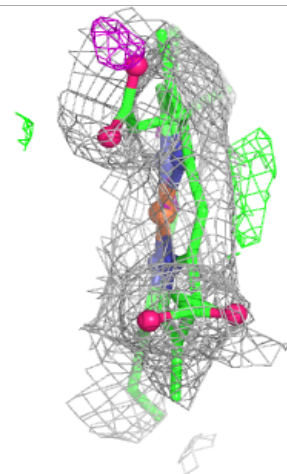
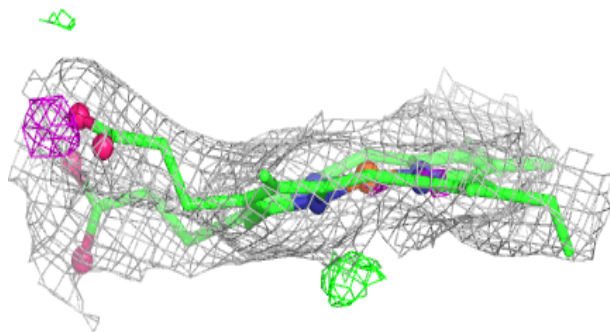
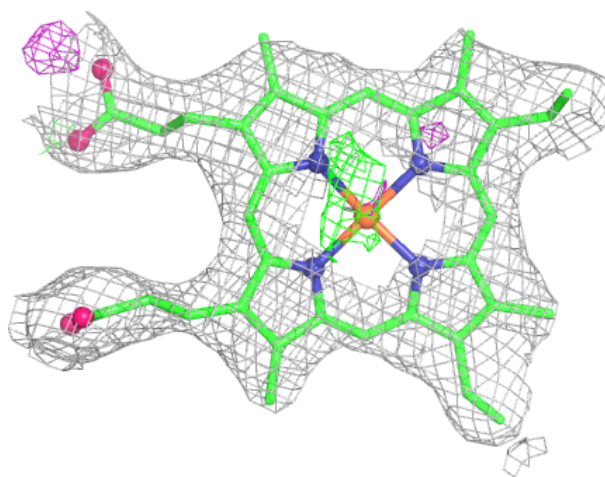
Electron density around HEC E 1003:

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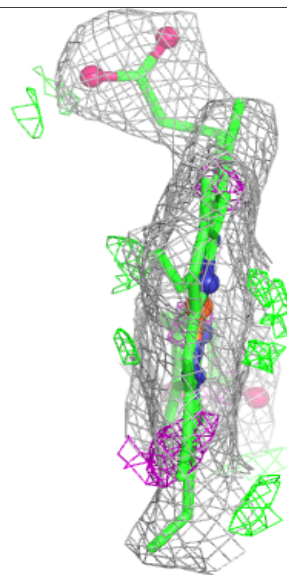
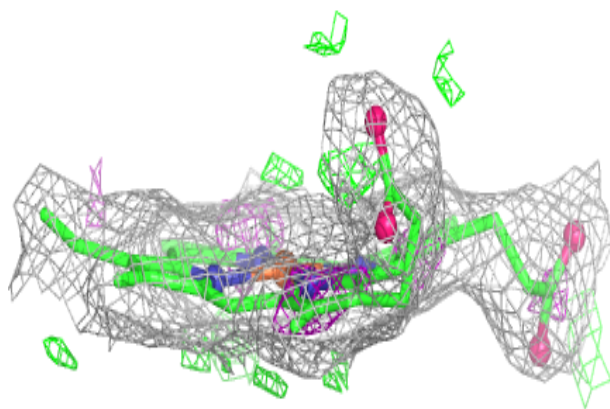
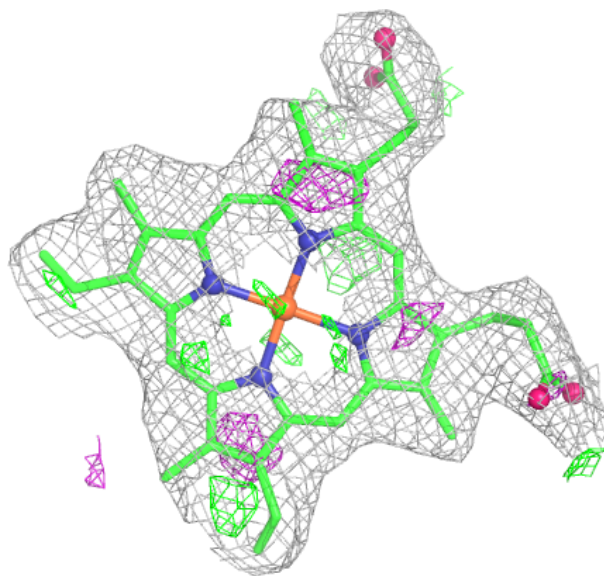
Electron density around HEC E 1004:

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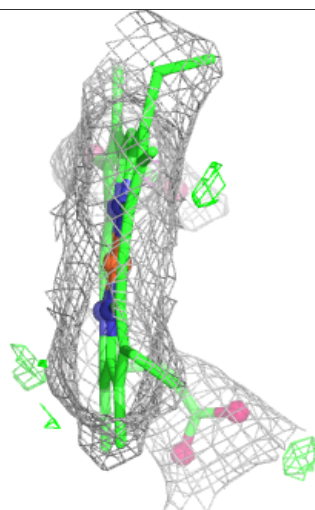
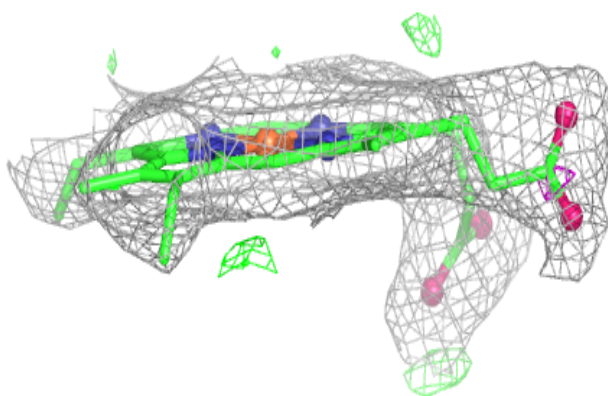
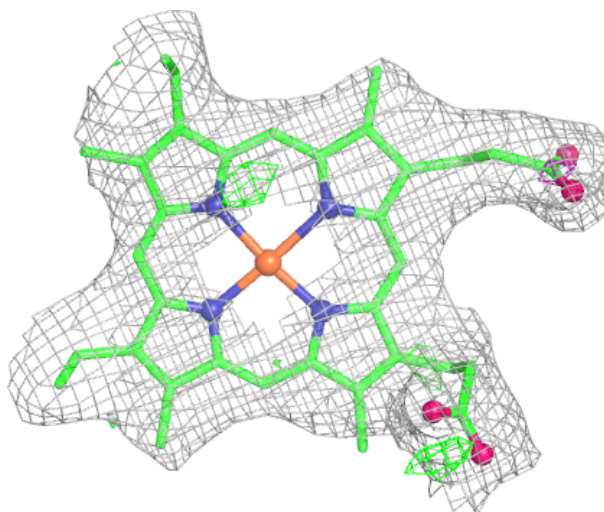
Electron density around HEC B 1005:

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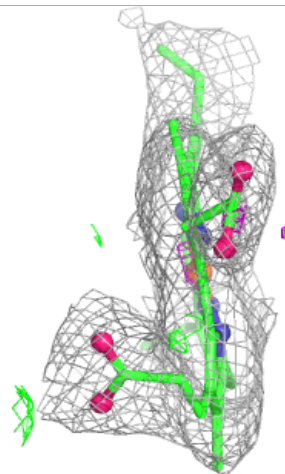
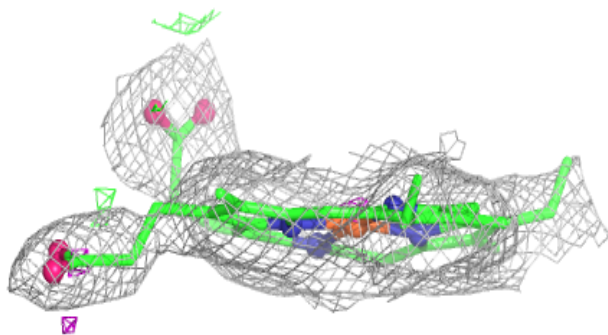
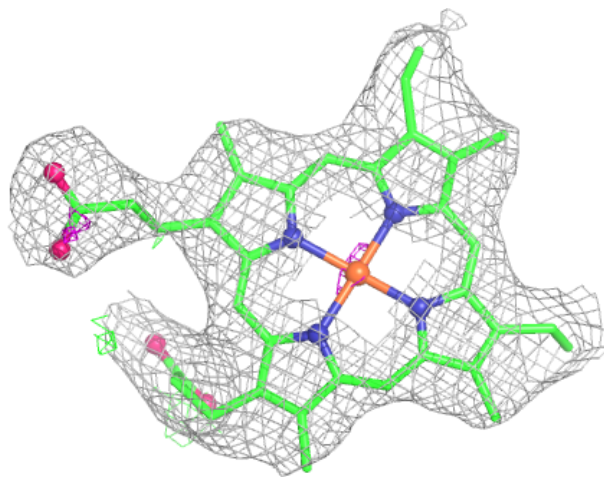
Electron density around HEC C 1001:

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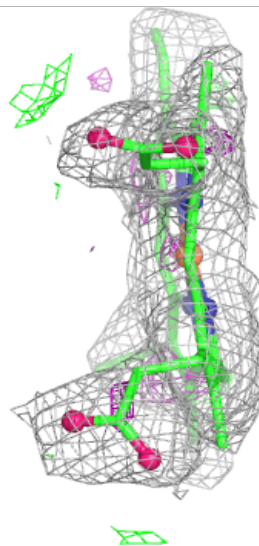
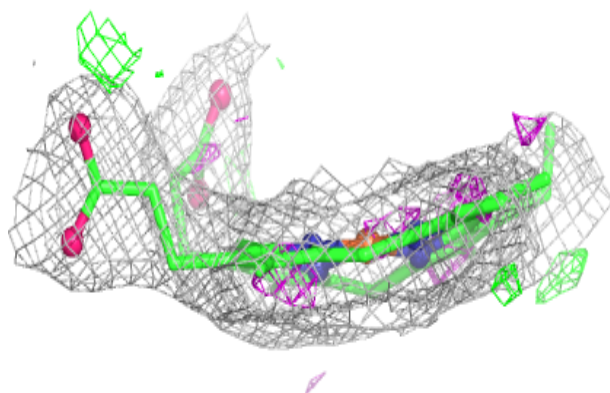
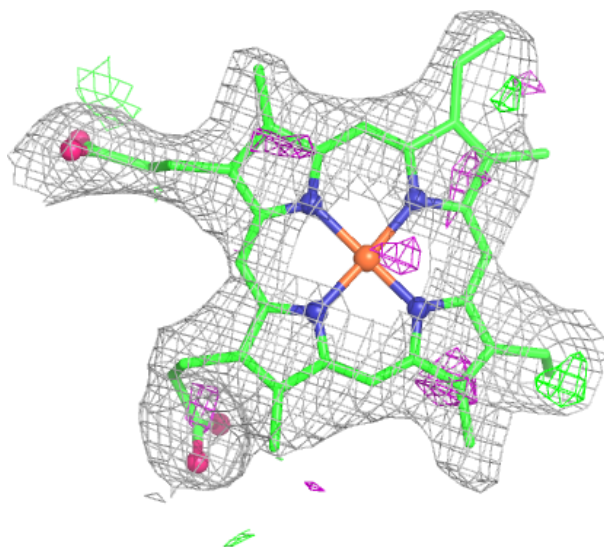
Electron density around HEC F 1002:

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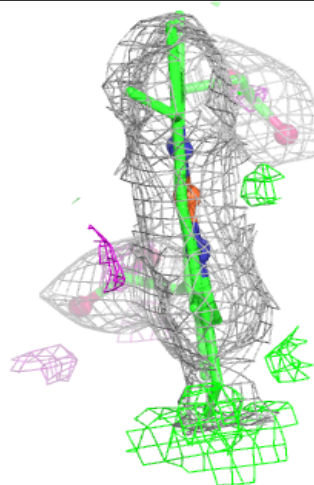
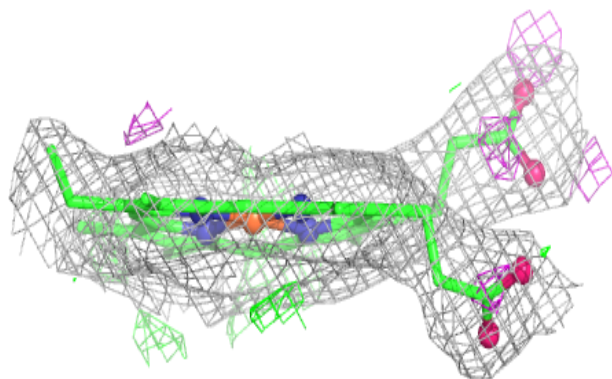
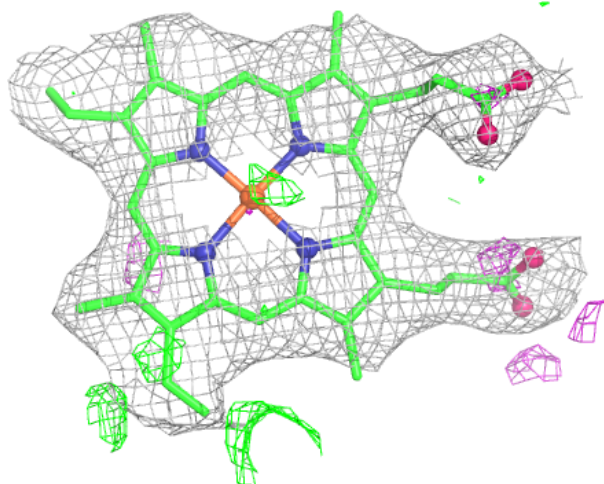
Electron density around HEC F 1003:

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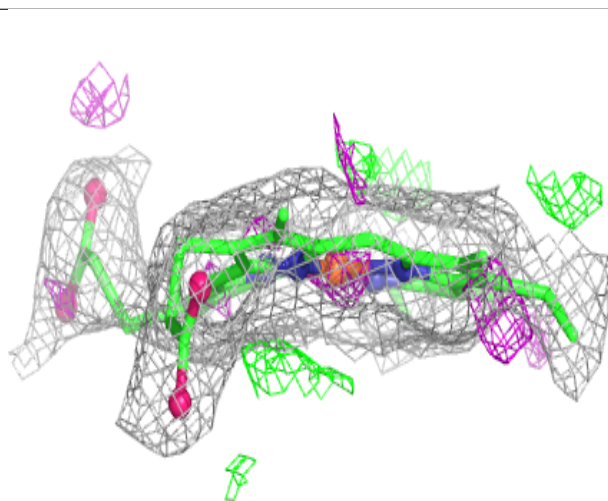
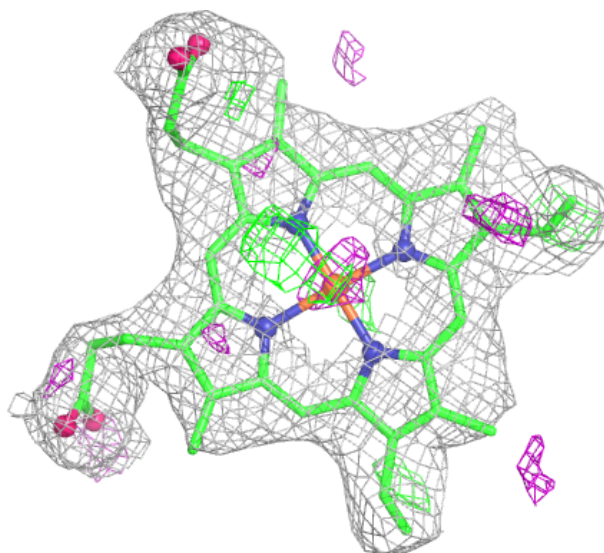
Electron density around HEC F 1004:

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and green (positive)



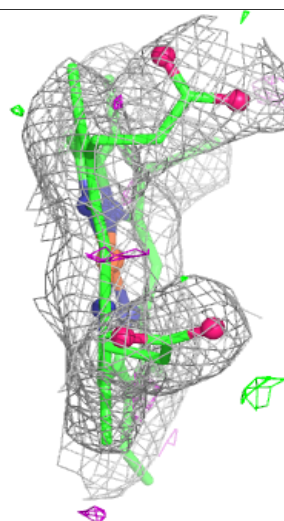
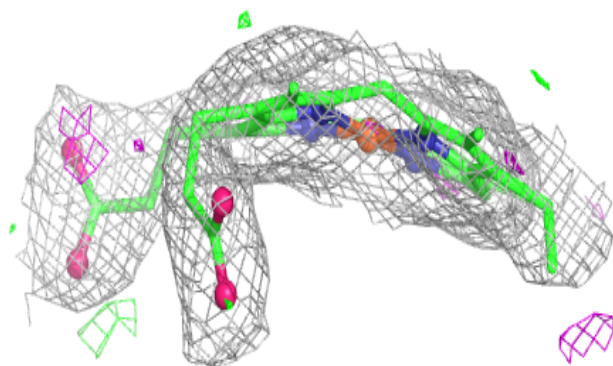
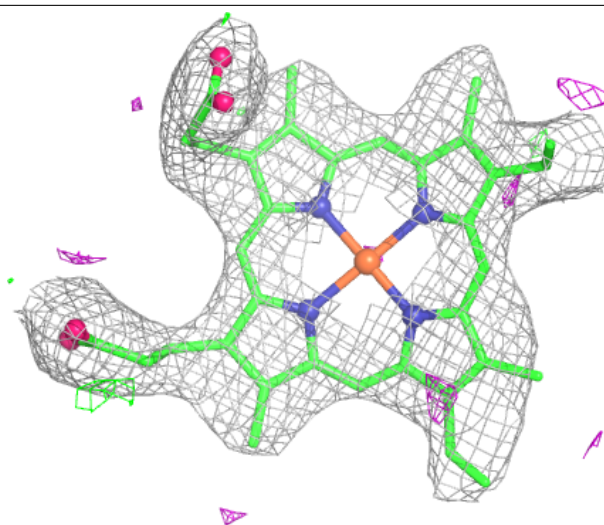
Electron density around HEC A 1005:

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and green (positive)



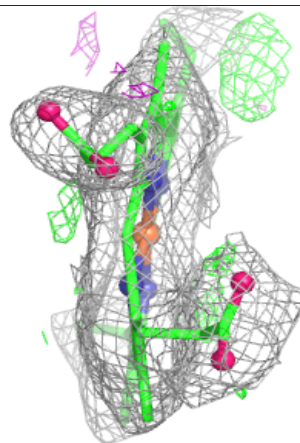
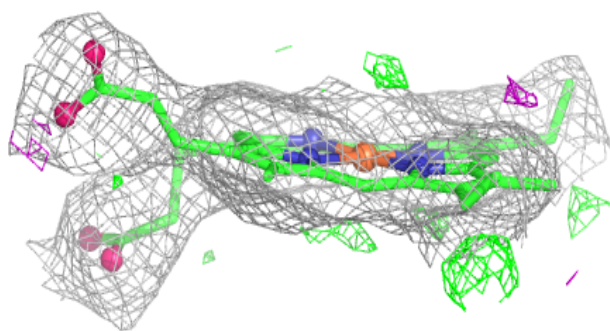
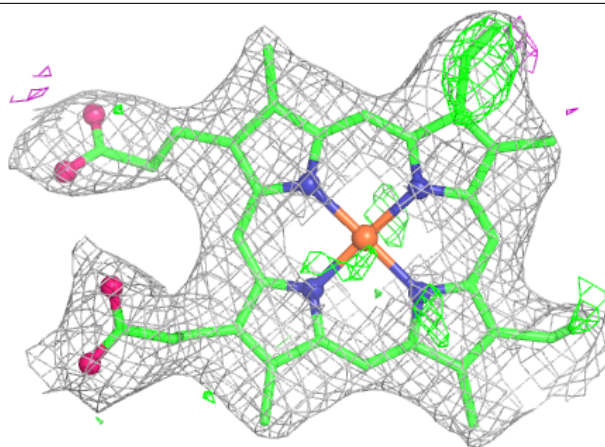
Electron density around HEC C 1003:

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



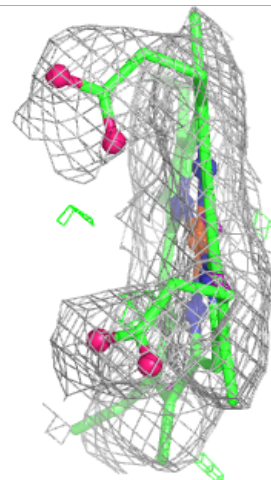
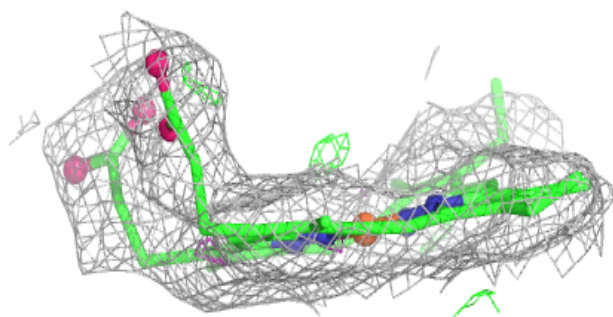
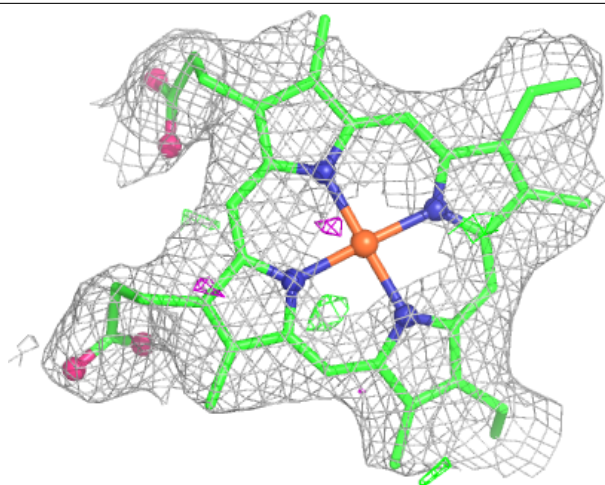
Electron density around HEC C 1004:

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



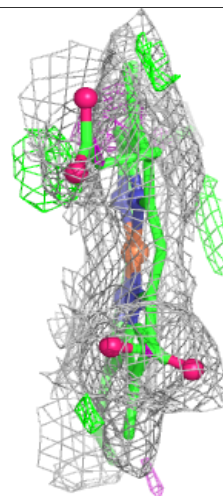
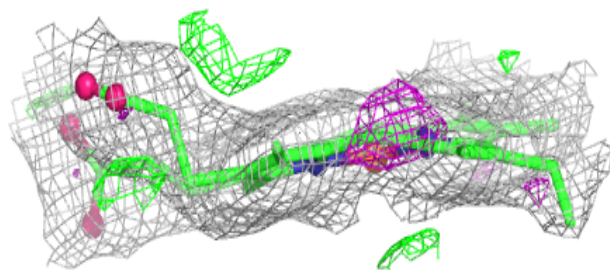
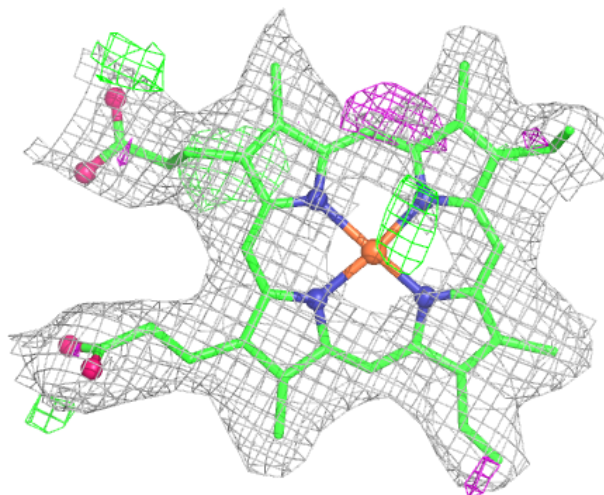
Electron density around HEC D 1001:

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



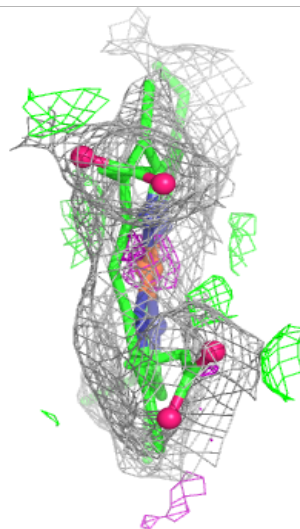
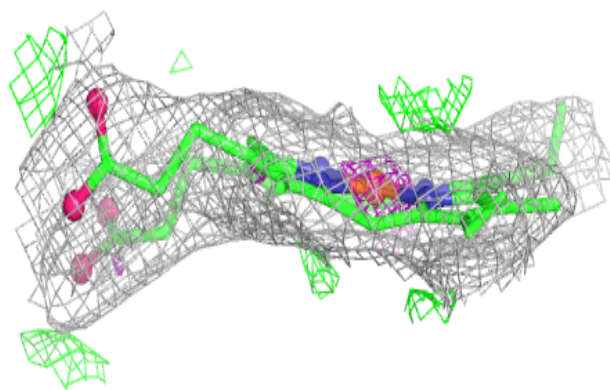
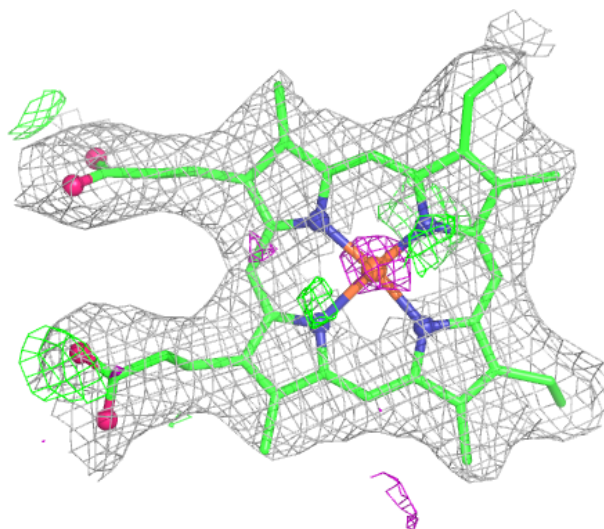
Electron density around HEC B 1004:

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



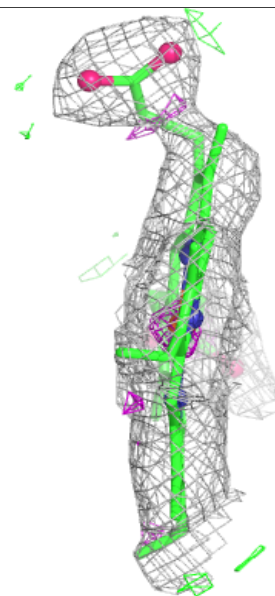
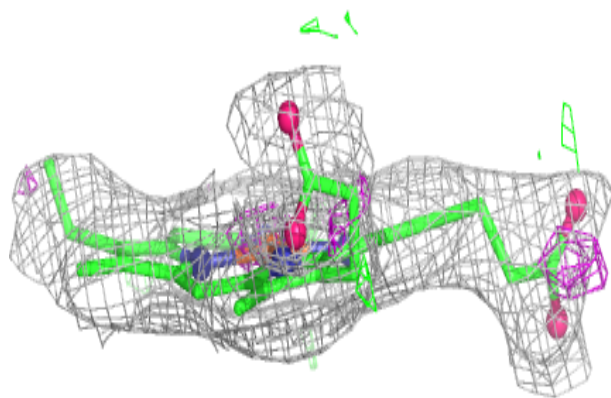
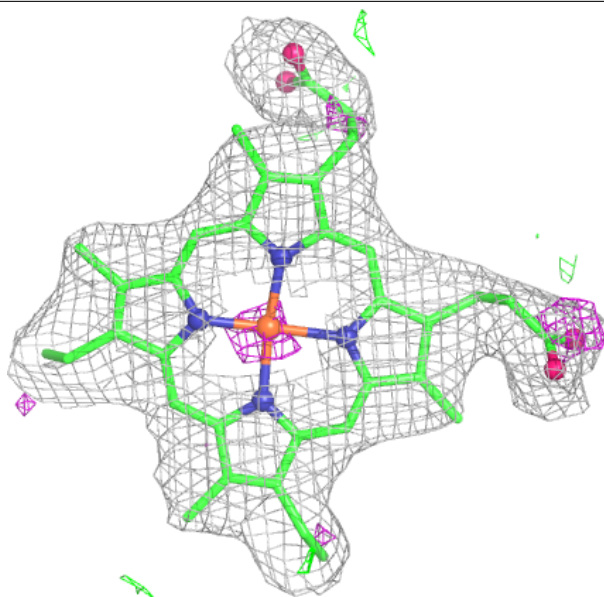
Electron density around HEC D 1004:

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



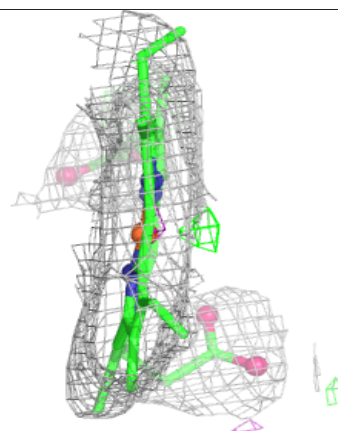
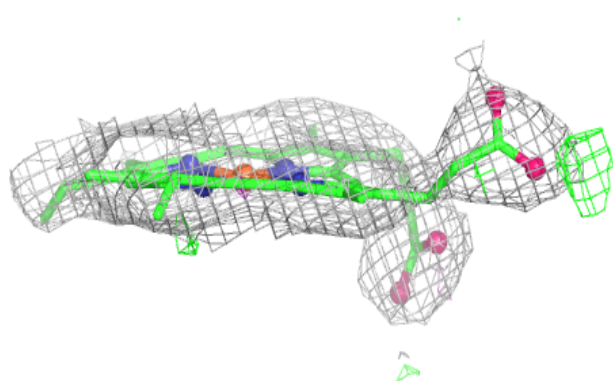
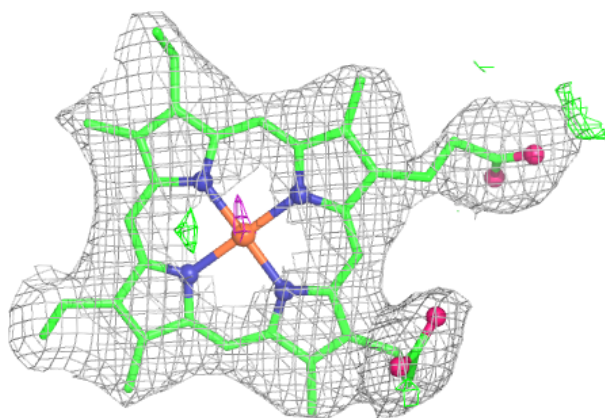
Electron density around HEC D 1005:

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



Electron density around HEC A 1002:

$2mF_o-DF_c$ (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.