



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 09:50 am BST

PDB ID : 3FO3  
Title : Structure of the Thioalkalivibrio nitratireducens cytochrome c nitrite reductase reduced by sodium dithionite (sulfite complex)  
Authors : Trofimov, A.A.; Polyakov, K.M.; Boyko, K.M.; Slutsky, A.; Tikhonova, T.V.; Antipov, A.N.; Zvyagilskaya, R.A.; Popov, A.N.; Lamzin, V.S.; Bourenkov, G.P.; Popov, V.O.  
Deposited on : 2008-12-27  
Resolution : 1.40 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)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

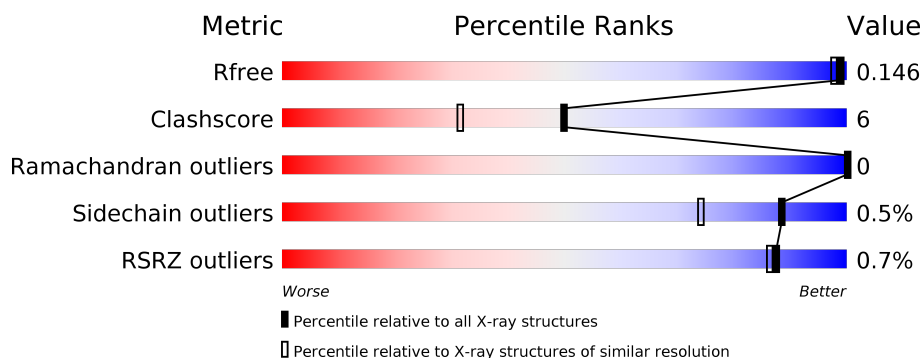
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	525	<div> <div style="width: 95%;"></div> <div>95%</div> </div>
1	B	525	<div> <div style="width: 93%;"></div> <div>93%</div> <div style="width: 5%;"></div> <div>5%</div> </div>

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
10	PG4	A	538[A]	-	X	-	-
10	PG4	B	547	-	-	X	-

## 2 Entry composition [i](#)

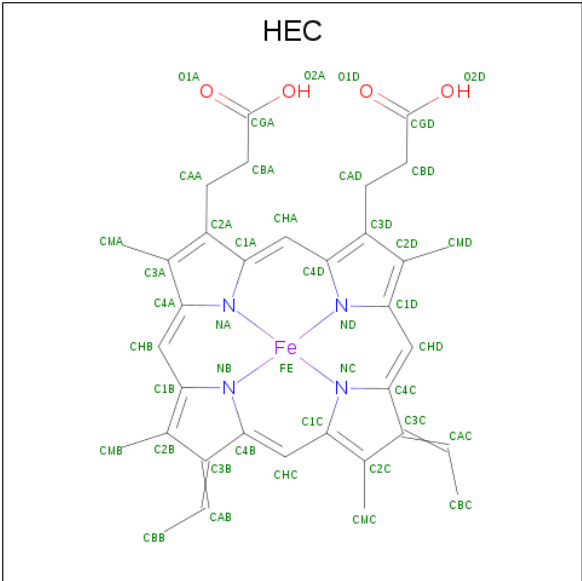
There are 12 unique types of molecules in this entry. The entry contains 16308 atoms, of which 5637 are hydrogens and 0 are deuteriums.

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 Eight-heme nitrite reductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	519	Total	C	H	N	O	S	0	19	1
			6892	2580	2734	754	786	38			
1	B	519	Total	C	H	N	O	S	0	21	1
			6913	2591	2727	762	796	37			

- Molecule 2 is HEME C (three-letter code: HEC) (formula: C<sub>34</sub>H<sub>34</sub>FeN<sub>4</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	A	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	A	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	A	1	Total	C	Fe	H	N	O	0	1
			55	36	1	8	4	6		

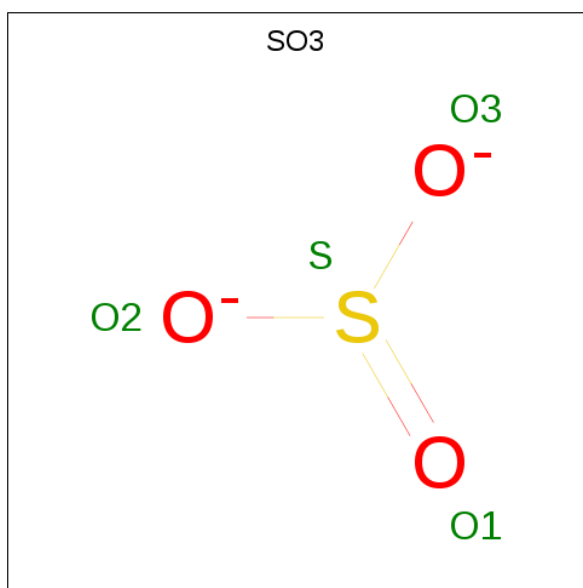
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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	A	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	A	1	Total	C	Fe	H	N	O	0	1
			55	36	1	8	4	6		
2	A	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	B	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	B	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	B	1	Total	C	Fe	H	N	O	0	1
			55	36	1	8	4	6		
2	B	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	B	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		
2	B	1	Total	C	Fe	H	N	O	0	1
			55	36	1	8	4	6		
2	B	1	Total	C	Fe	H	N	O	0	0
			55	34	1	12	4	4		

- Molecule 3 is SULFITE ION (three-letter code: SO3) (formula: O<sub>3</sub>S).

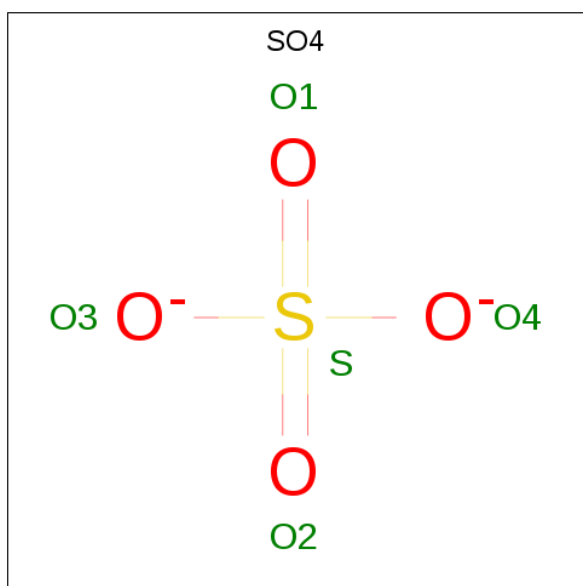


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O S 4 3 1	0	0
3	B	1	Total O S 4 3 1	0	0
3	B	1	Total O S 6 4 2	0	1

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

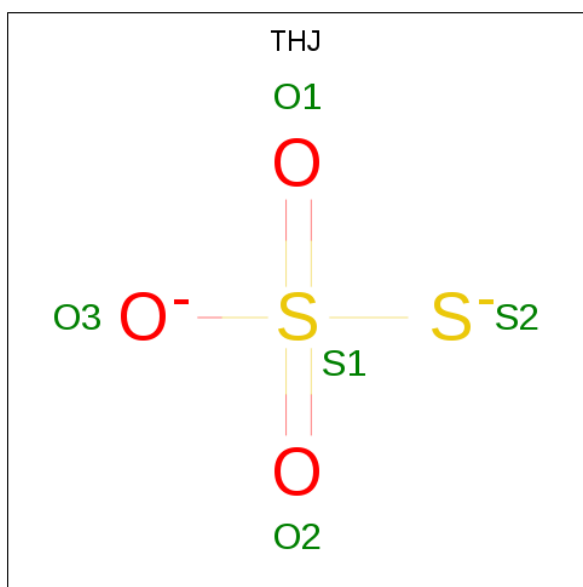
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Ca 2 2	0	0
4	A	2	Total Ca 2 2	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 6 is THIOSULFATE (three-letter code: THJ) (formula: O<sub>3</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	3	2		
6	B	1	Total	O	S	0	0
			5	3	2		

- Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	3	Total	Na	0	0
			3	3		
7	A	2	Total	Na	0	0
			2	2		

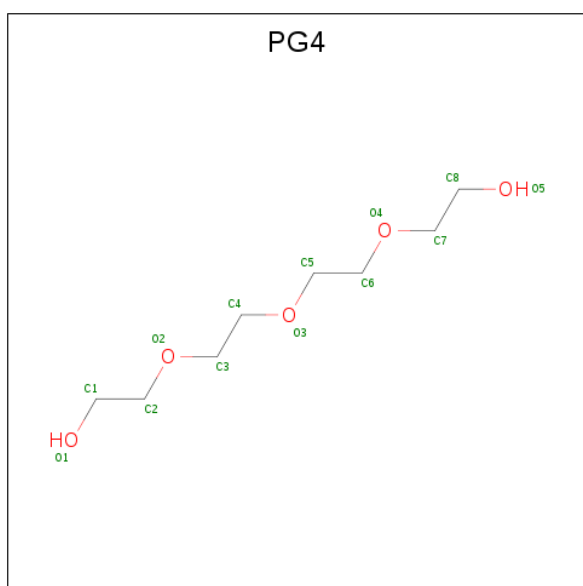
- Molecule 8 is 1-(2-METHOXY-ETHOXY)-2-{2-[2-(2-METHOXY-ETHOXY)-ETHOXY]-ETHANE (three-letter code: PG6) (formula: C<sub>12</sub>H<sub>26</sub>O<sub>6</sub>).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			8	4	1	3		
9	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 10 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			5	3	2		
10	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	1
			10	6	4		
10	A	1	Total	C	O	0	0
			6	4	2		
10	A	1	Total	C	O	0	0
			6	4	2		
10	A	1	Total	C	O	0	0
			6	4	2		
10	B	1	Total	C	O	0	0
			8	5	3		
10	B	1	Total	C	O	0	0
			10	6	4		
10	B	1	Total	C	O	0	0
			7	4	3		
10	B	1	Total	C	O	0	0
			5	3	2		
10	B	1	Total	C	O	0	0
			4	2	2		
10	B	1	Total	C	O	0	0
			5	3	2		
10	B	1	Total	C	O	0	0
			4	2	2		
10	B	1	Total	C	O	0	0
			5	3	2		
10	B	1	Total	C	O	0	0
			4	2	2		
10	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 11 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	701	Total	O	0	0
			701	701		
12	B	684	Total	O	0	0
			684	684		

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

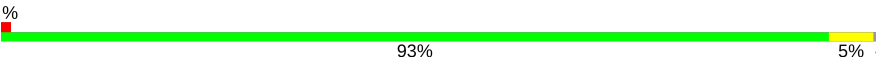
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

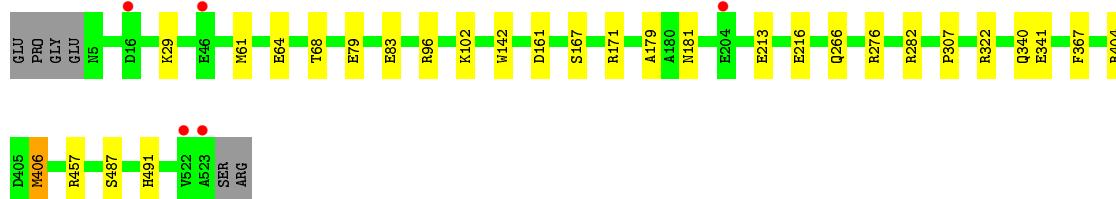
- Molecule 1: Eight-heme nitrite reductase

Chain A:  95%



- Molecule 1: Eight-heme nitrite reductase

Chain B:  93% 5%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	193.79 Å   193.79 Å   193.79 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	12.00 – 1.40 12.00 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (12.00-1.40) 99.6 (12.00-1.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.19 (at 1.40 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.126 , 0.139 0.135 , 0.146	Depositor DCC
$R_{free}$ test set	23479 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.45 , 57.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.024 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	16308	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.01% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, CA, HEC, SO3, PG6, PG4, SO4, ACT, TRS, THJ

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	0.60	1/4368 (0.0%)	0.76	3/5922 (0.1%)
1	B	0.62	2/4404 (0.0%)	0.78	8/5968 (0.1%)
All	All	0.61	3/8772 (0.0%)	0.77	11/11890 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	83	GLU	CD-OE1	5.98	1.32	1.25
1	A	83	GLU	CD-OE1	5.97	1.32	1.25
1	B	83	GLU	CG-CD	5.07	1.59	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	61[A]	MET	CA-CB-CG	-6.76	101.80	113.30
1	B	61[B]	MET	CA-CB-CG	-6.76	101.80	113.30
1	B	61[C]	MET	CA-CB-CG	-6.76	101.80	113.30
1	B	404	ARG	NE-CZ-NH2	-6.63	116.98	120.30
1	B	282	ARG	NE-CZ-NH1	6.27	123.44	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

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	4158	2734	3865	15	0
1	B	4186	2727	3886	39	0
2	A	352	88	196	11	0
2	B	352	88	196	7	0
3	A	4	0	0	0	0
3	B	10	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	A	5	0	0	1	0
6	B	5	0	0	0	0
7	A	2	0	0	0	0
7	B	3	0	0	0	0
8	A	49	0	61	13	0
8	B	30	0	38	3	0
9	A	8	0	12	1	0
9	B	8	0	12	3	0
10	A	37	0	43	3	0
10	B	59	0	69	22	0
11	B	4	0	3	0	0
12	A	701	0	0	25	0
12	B	684	0	0	32	0
All	All	10671	5637	8381	100	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 6.

The worst 5 of 100 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)
10:A:535:PG4:C3	12:A:624:HOH:O	1.69	1.29
10:B:540:PG4:C2	12:B:745:HOH:O	1.74	1.28
8:A:532:PG6:H121	12:A:990:HOH:O	0.94	1.11
10:B:547:PG4:H11	12:B:808:HOH:O	0.92	1.08
8:B:532:PG6:H121	12:B:996:HOH:O	0.88	1.05

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	537/525 (102%)	515 (96%)	22 (4%)	0	100	100
1	B	539/525 (103%)	517 (96%)	22 (4%)	0	100	100
All	All	1076/1050 (102%)	1032 (96%)	44 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	453/443 (102%)	447 (99%)	6 (1%)	69	42
1	B	458/443 (103%)	456 (100%)	2 (0%)	91	78
All	All	911/886 (103%)	903 (99%)	8 (1%)	88	58

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	278	ARG
1	B	406[B]	MET
1	A	406[B]	MET
1	A	61[C]	MET
1	A	406[A]	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	388	GLN
1	A	409	GLN
1	B	20	GLN
1	B	388	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 65 ligands modelled in this entry, 9 are monoatomic - leaving 56 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
2	HEC	B	1004	1,3	26,50,50	1.91	6 (23%)	18,82,82	1.21	2 (11%)
10	PG4	B	543	-	3,3,12	0.40	0	2,2,11	0.17	0
8	PG6	A	532	-	16,16,17	0.51	0	15,15,16	0.35	0
2	HEC	B	1001	1	26,50,50	2.14	5 (19%)	18,82,82	1.90	5 (27%)
2	HEC	A	1004	1,3	26,50,50	1.97	5 (19%)	18,82,82	1.72	4 (22%)
2	HEC	A	1006	1,4	26,50,50	2.02	5 (19%)	18,82,82	1.88	6 (33%)
10	PG4	B	544	-	4,4,12	0.47	0	3,3,11	0.21	0
2	HEC	B	1002	1	26,50,50	1.94	3 (11%)	18,82,82	1.88	5 (27%)
8	PG6	A	543	-	9,9,17	0.51	0	8,8,16	0.43	0
10	PG4	B	541	-	4,4,12	0.38	0	3,3,11	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	B	534	-	4,4,4	0.25	0	6,6,6	0.48	0
6	THJ	B	530	-	2,4,4	0.83	0	2,6,6	0.13	0
3	SO3	B	529[B]	-	1,3,3	0.59	0	0,3,3	0.00	-
9	TRS	B	533	-	7,7,7	0.28	0	9,9,9	0.36	0
6	THJ	A	530	-	2,4,4	0.92	0	2,6,6	0.08	0
3	SO3	B	526	2	1,3,3	2.21	1 (100%)	0,3,3	0.00	-
10	PG4	A	535	-	4,4,12	0.33	0	3,3,11	0.61	0
10	PG4	A	537	-	3,3,12	0.40	0	2,2,11	0.35	0
9	TRS	A	533	-	7,7,7	0.30	0	9,9,9	0.93	1 (11%)
3	SO3	A	526	2	1,3,3	1.98	0	0,3,3	0.00	-
8	PG6	B	535	-	7,7,17	0.44	0	6,6,16	0.58	0
2	HEC	A	1003[A]	-	26,50,50	2.12	5 (19%)	18,82,82	1.84	5 (27%)
10	PG4	A	539	-	5,5,12	0.45	0	4,4,11	0.51	0
2	HEC	A	1003[B]	-	26,50,50	2.12	5 (19%)	18,82,82	2.13	5 (27%)
11	ACT	B	546	-	1,3,3	0.16	0	0,3,3	0.00	-
10	PG4	B	536	-	7,7,12	0.42	0	6,6,11	0.73	0
2	HEC	B	1007[B]	4	26,50,50	2.02	4 (15%)	18,82,82	2.02	5 (27%)
10	PG4	A	538[B]	-	7,7,12	0.46	0	6,6,11	0.44	0
2	HEC	B	1003[B]	-	26,50,50	2.16	4 (15%)	18,82,82	2.34	6 (33%)
8	PG6	B	542	-	4,4,17	0.42	0	3,3,16	0.27	0
10	PG4	A	538[A]	-	7,4,12	21.44	1 (14%)	6,3,11	5.53	2 (33%)
2	HEC	B	1003[A]	-	26,50,50	2.16	4 (15%)	18,82,82	2.14	6 (33%)
2	HEC	A	1002	1	26,50,50	2.02	6 (23%)	18,82,82	1.72	5 (27%)
8	PG6	A	536	-	8,8,17	0.50	0	7,7,16	0.19	0
2	HEC	A	1005	1	26,50,50	2.00	4 (15%)	18,82,82	1.99	5 (27%)
2	HEC	B	1007[A]	-	26,50,50	2.02	4 (15%)	18,82,82	1.99	5 (27%)
2	HEC	A	1001	1	26,50,50	2.10	3 (11%)	18,82,82	1.61	4 (22%)
10	PG4	B	537	-	9,9,12	0.45	0	8,8,11	0.29	0
2	HEC	A	1007[A]	-	26,50,50	2.07	3 (11%)	18,82,82	1.98	7 (38%)
10	PG4	A	540	-	5,5,12	0.46	0	4,4,11	0.25	0
2	HEC	A	1007[B]	4	26,50,50	2.07	3 (11%)	18,82,82	2.00	7 (38%)
5	SO4	A	529	-	4,4,4	0.47	0	6,6,6	0.81	0
8	PG6	A	534	-	7,7,17	0.53	0	6,6,16	0.24	0
2	HEC	B	1005	1	26,50,50	1.99	5 (19%)	18,82,82	1.80	4 (22%)
10	PG4	B	538	-	6,6,12	0.42	0	5,5,11	0.41	0
10	PG4	B	545	-	3,3,12	0.33	0	2,2,11	0.35	0
2	HEC	B	1008	1	26,50,50	2.14	3 (11%)	18,82,82	1.77	4 (22%)
3	SO3	B	529[A]	-	1,3,3	0.88	0	0,3,3	0.00	-
2	HEC	B	1006	1,4	26,50,50	2.00	4 (15%)	18,82,82	1.84	6 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	PG6	B	532	-	16,16,17	0.56	0	15,15,16	0.45	0
10	PG4	A	541	-	5,5,12	0.52	0	4,4,11	0.40	0
2	HEC	A	1008	1	26,50,50	2.27	4 (15%)	18,82,82	1.92	5 (27%)
8	PG6	A	542	-	4,4,17	0.38	0	3,3,16	0.40	0
10	PG4	B	540	-	3,3,12	0.33	0	2,2,11	0.39	0
10	PG4	B	539	-	4,4,12	0.40	0	3,3,11	0.30	0
10	PG4	B	547	-	6,6,12	0.30	0	5,5,11	0.98	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
2	HEC	B	1004	1,3	-	0/6/54/54	-
10	PG4	B	543	-	-	1/1/1/10	-
8	PG6	A	532	-	-	0/14/14/15	-
2	HEC	B	1001	1	-	0/6/54/54	-
2	HEC	A	1004	1,3	-	0/6/54/54	-
2	HEC	A	1006	1,4	-	0/6/54/54	-
2	HEC	B	1002	1	-	0/6/54/54	-
8	PG6	A	543	-	-	6/7/7/15	-
10	PG4	B	541	-	-	0/2/2/10	-
9	TRS	B	533	-	-	9/9/9/9	-
10	PG4	B	545	-	-	1/1/1/10	-
10	PG4	B	540	-	-	0/1/1/10	-
10	PG4	A	537	-	-	0/1/1/10	-
9	TRS	A	533	-	-	6/9/9/9	-
10	PG4	A	540	-	-	2/3/3/10	-
8	PG6	B	535	-	-	1/5/5/15	-
2	HEC	A	1003[A]	-	-	0/6/54/54	-
10	PG4	A	539	-	-	1/3/3/10	-
2	HEC	A	1003[B]	-	-	2/6/54/54	-
10	PG4	B	536	-	-	4/5/5/10	-
2	HEC	A	1007[A]	-	-	0/6/54/54	-
10	PG4	A	538[B]	-	-	2/5/5/10	-
2	HEC	B	1003[B]	-	-	0/6/54/54	-
8	PG6	B	542	-	-	2/2/2/15	-
10	PG4	A	538[A]	-	-	4/5/2/10	-
2	HEC	B	1003[A]	-	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	A	1002	1	-	0/6/54/54	-
8	PG6	A	536	-	-	4/6/6/15	-
2	HEC	A	1005	1	-	0/6/54/54	-
2	HEC	B	1007[A]	-	-	0/6/54/54	-
2	HEC	A	1001	1	-	0/6/54/54	-
10	PG4	B	537	-	-	3/7/7/10	-
2	HEC	B	1007[B]	4	-	0/6/54/54	-
10	PG4	A	535	-	-	0/2/2/10	-
2	HEC	A	1007[B]	4	-	0/6/54/54	-
10	PG4	B	544	-	-	1/2/2/10	-
8	PG6	A	534	-	-	1/5/5/15	-
2	HEC	B	1005	1	-	0/6/54/54	-
10	PG4	B	538	-	-	4/4/4/10	-
2	HEC	B	1008	1	-	0/6/54/54	-
2	HEC	B	1006	1,4	-	0/6/54/54	-
8	PG6	B	532	-	-	0/14/14/15	-
10	PG4	A	541	-	-	1/3/3/10	-
2	HEC	A	1008	1	-	0/6/54/54	-
8	PG6	A	542	-	-	2/2/2/15	-
10	PG4	B	539	-	-	1/2/2/10	-
10	PG4	B	547	-	-	3/4/4/10	-

The worst 5 of 87 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	538[A]	PG4	O3-C5	56.71	3.88	1.42
2	A	1007[A]	HEC	C3B-C2B	-7.08	1.33	1.40
2	A	1007[B]	HEC	C3B-C2B	-7.08	1.33	1.40
2	A	1008	HEC	C3B-C2B	-6.79	1.33	1.40
2	A	1003[A]	HEC	C3C-C2C	-6.42	1.34	1.40

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	538[A]	PG4	C5-O3-C4	-13.08	56.63	113.29
2	B	1003[B]	HEC	CAA-CBA-CGA	-6.16	102.33	112.67
2	A	1003[B]	HEC	CBA-CAA-C2A	5.41	122.45	112.48
2	A	1007[A]	HEC	CMB-C2B-C1B	-5.32	120.29	128.46
2	A	1007[B]	HEC	CMB-C2B-C1B	-5.32	120.29	128.46

There are no chirality outliers.



5 of 61 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	B	533	TRS	C2-C-C1-O1
9	B	533	TRS	C3-C-C1-O1
9	B	533	TRS	C1-C-C3-O3
9	A	533	TRS	C3-C-C2-O2
9	A	533	TRS	N-C-C2-O2

There are no ring outliers.

33 monomers are involved in 64 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1004	HEC	1	0
8	A	532	PG6	3	0
2	B	1001	HEC	1	0
2	A	1004	HEC	2	0
2	A	1006	HEC	1	0
2	B	1002	HEC	1	0
8	A	543	PG6	2	0
10	B	541	PG4	1	0
9	B	533	TRS	3	0
6	A	530	THJ	1	0
10	A	535	PG4	1	0
9	A	533	TRS	1	0
8	B	535	PG6	1	0
10	A	539	PG4	1	0
2	A	1003[B]	HEC	3	0
10	B	536	PG4	3	0
2	B	1007[B]	HEC	1	0
2	B	1003[B]	HEC	1	0
10	A	538[A]	PG4	1	0
2	A	1002	HEC	1	0
8	A	536	PG6	3	0
2	A	1001	HEC	2	0
10	B	537	PG4	1	0
2	A	1007[B]	HEC	1	0
10	B	538	PG4	2	0
2	B	1008	HEC	2	0
2	B	1006	HEC	1	0
8	B	532	PG6	2	0
2	A	1008	HEC	2	0
8	A	542	PG6	5	0
10	B	540	PG4	3	0

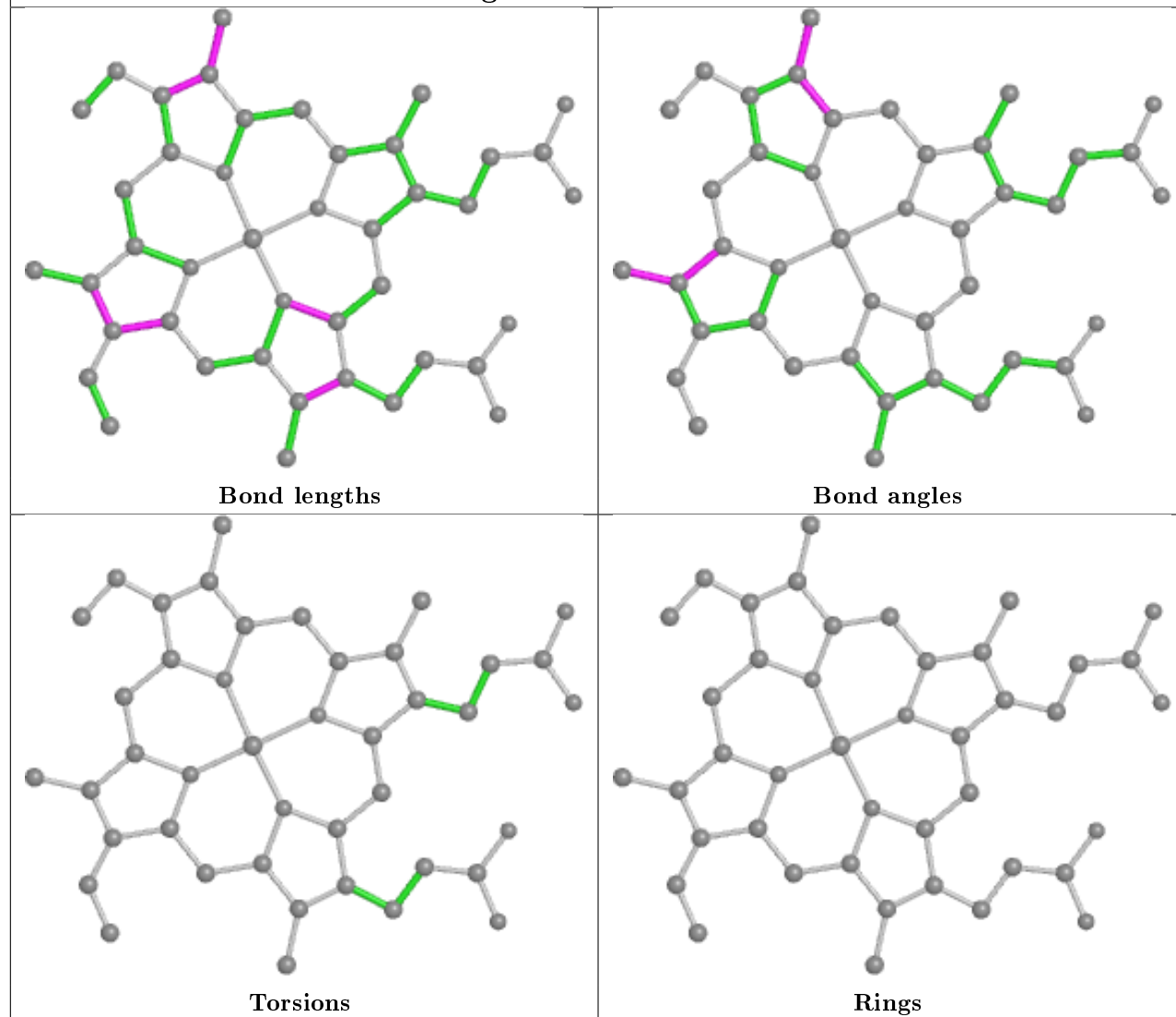
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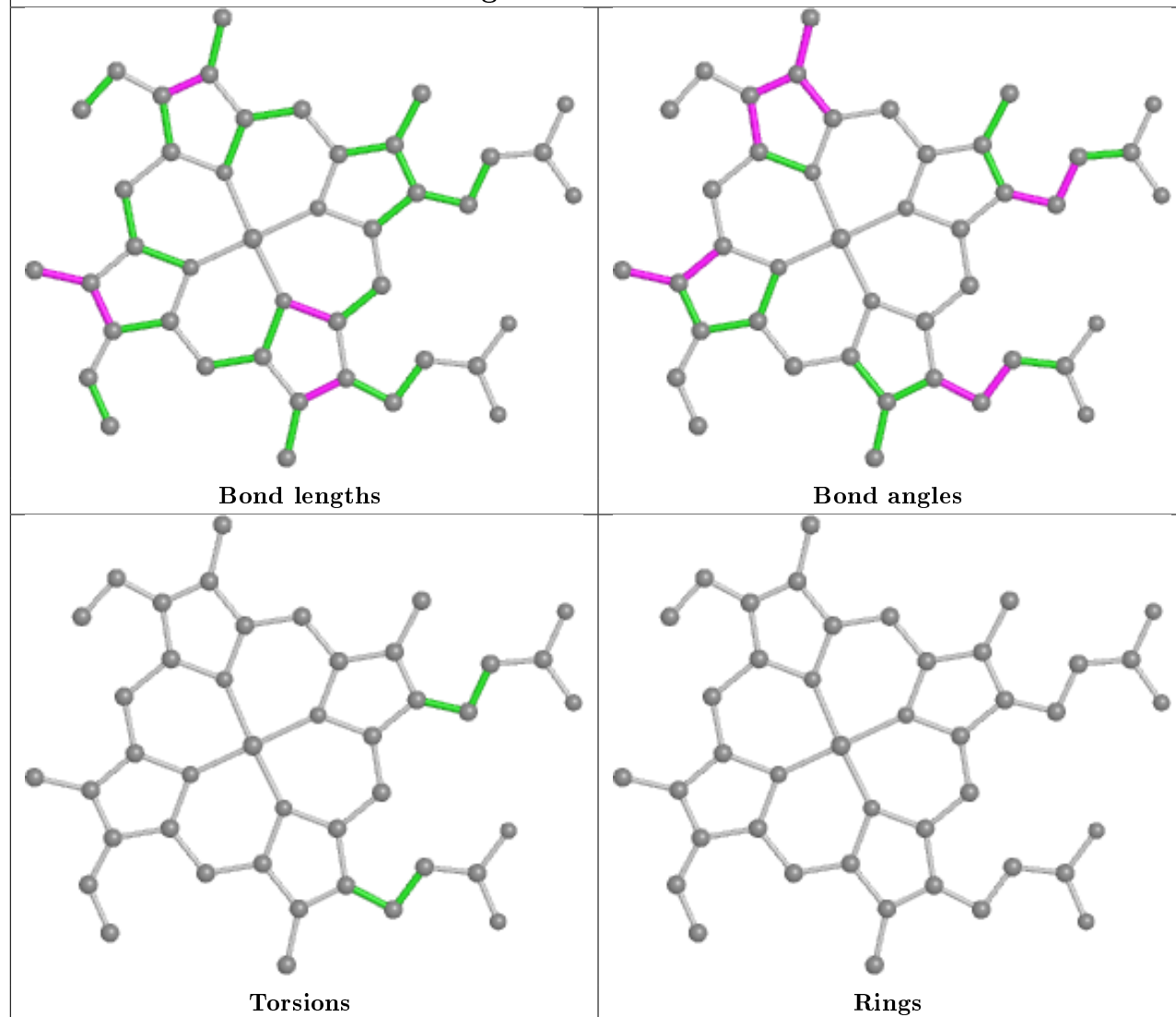
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	539	PG4	2	0
10	B	547	PG4	10	0

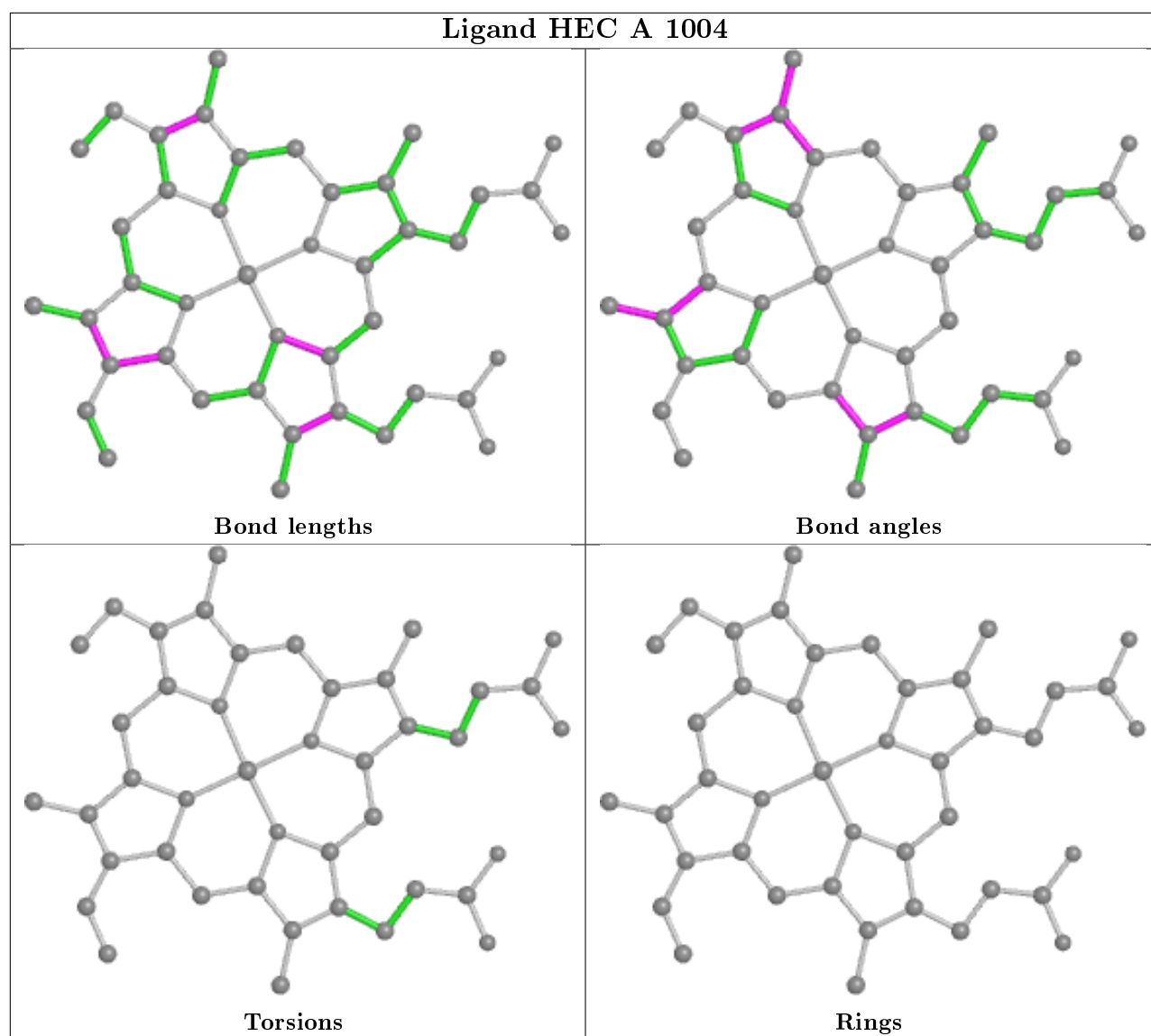
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 HEC B 1004

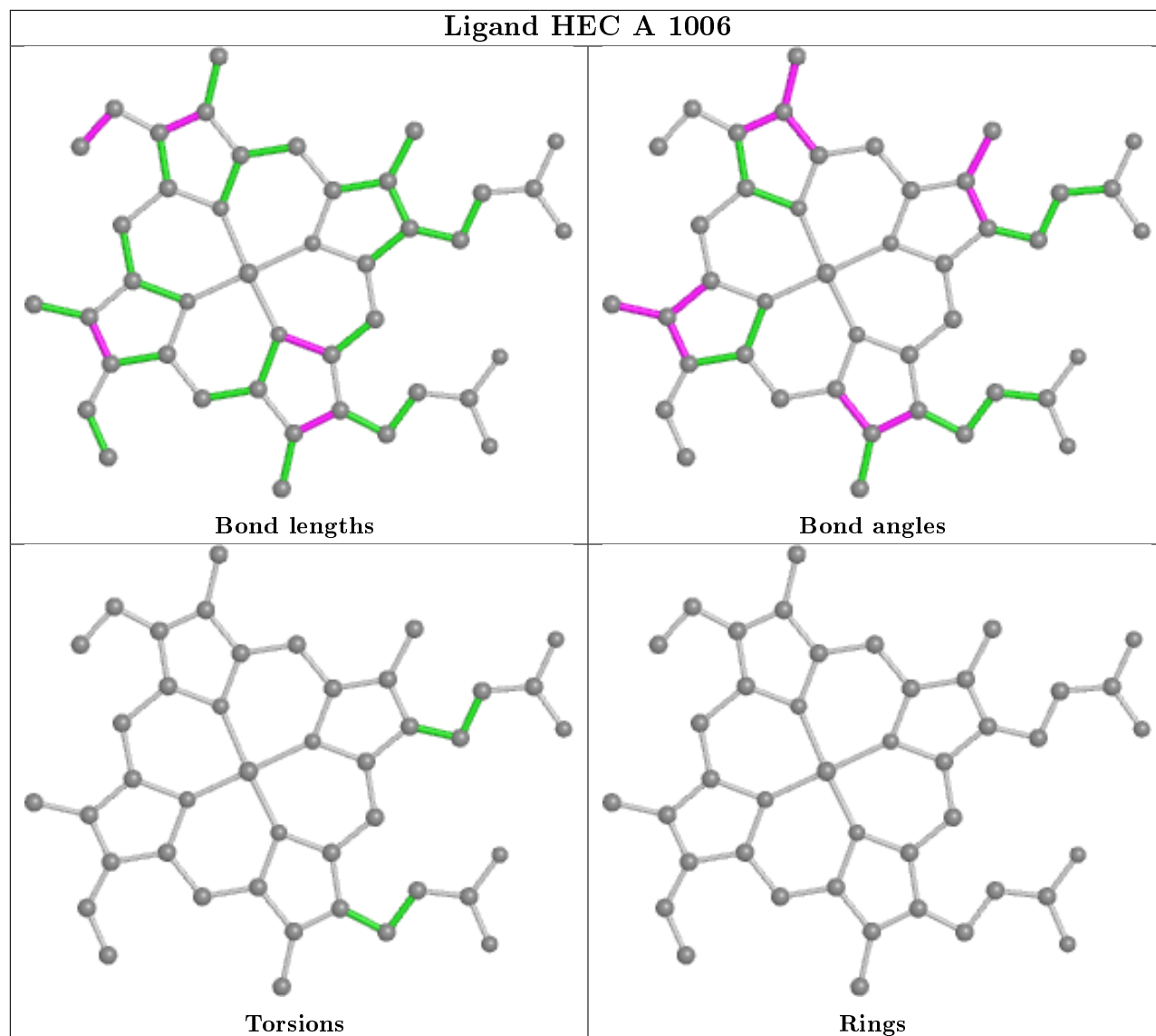


## Ligand HEC B 1001

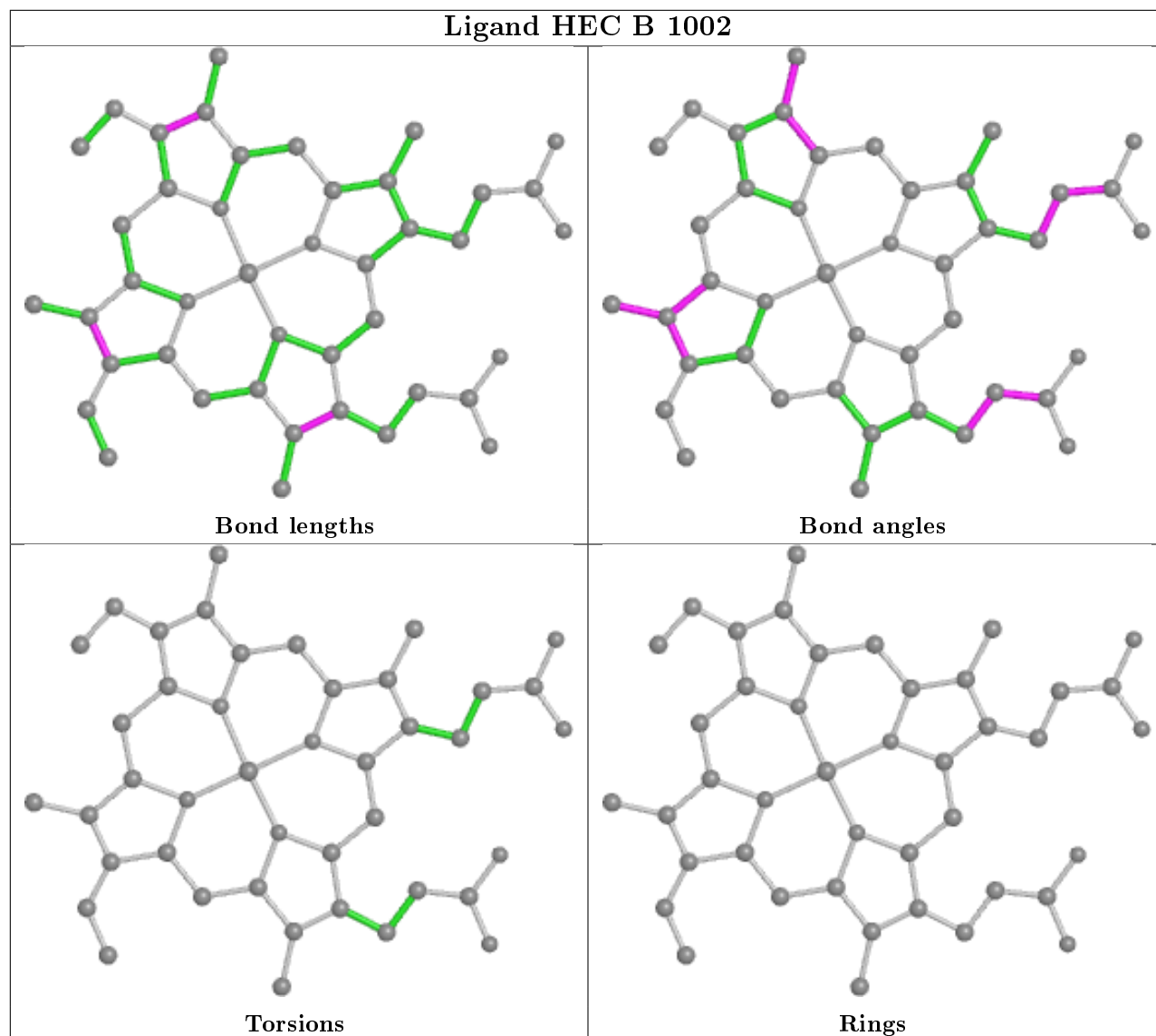




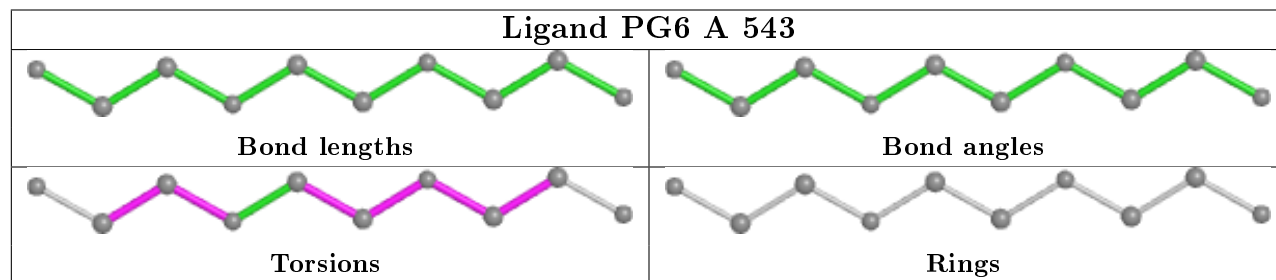
## Ligand HEC A 1006



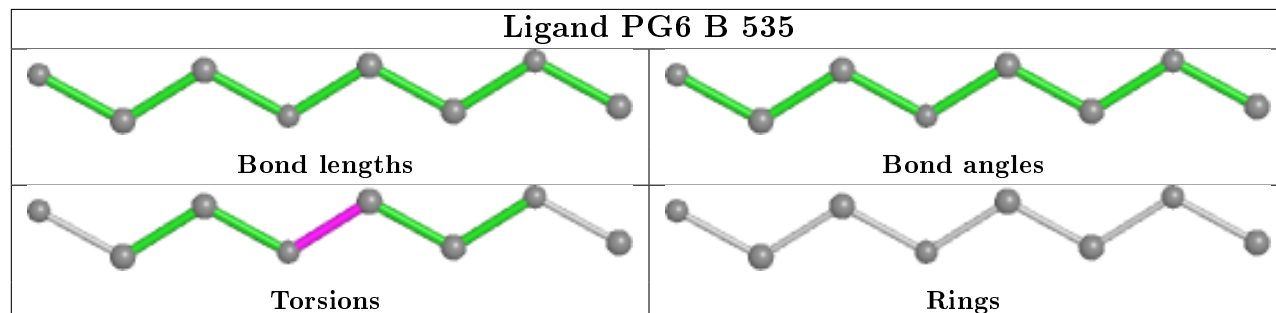
## Ligand HEC B 1002



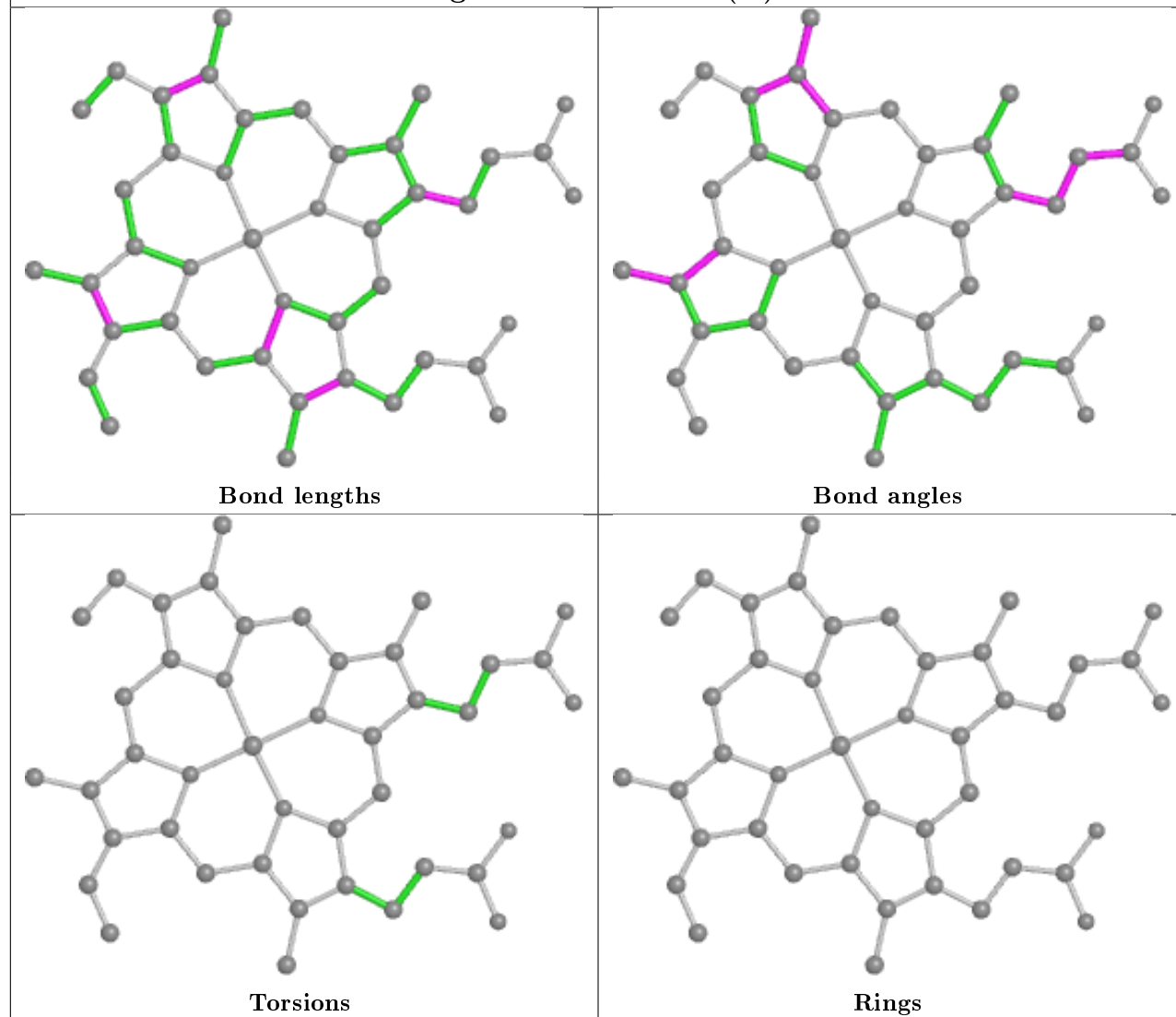
## Ligand PG6 A 543



## Ligand PG6 B 535

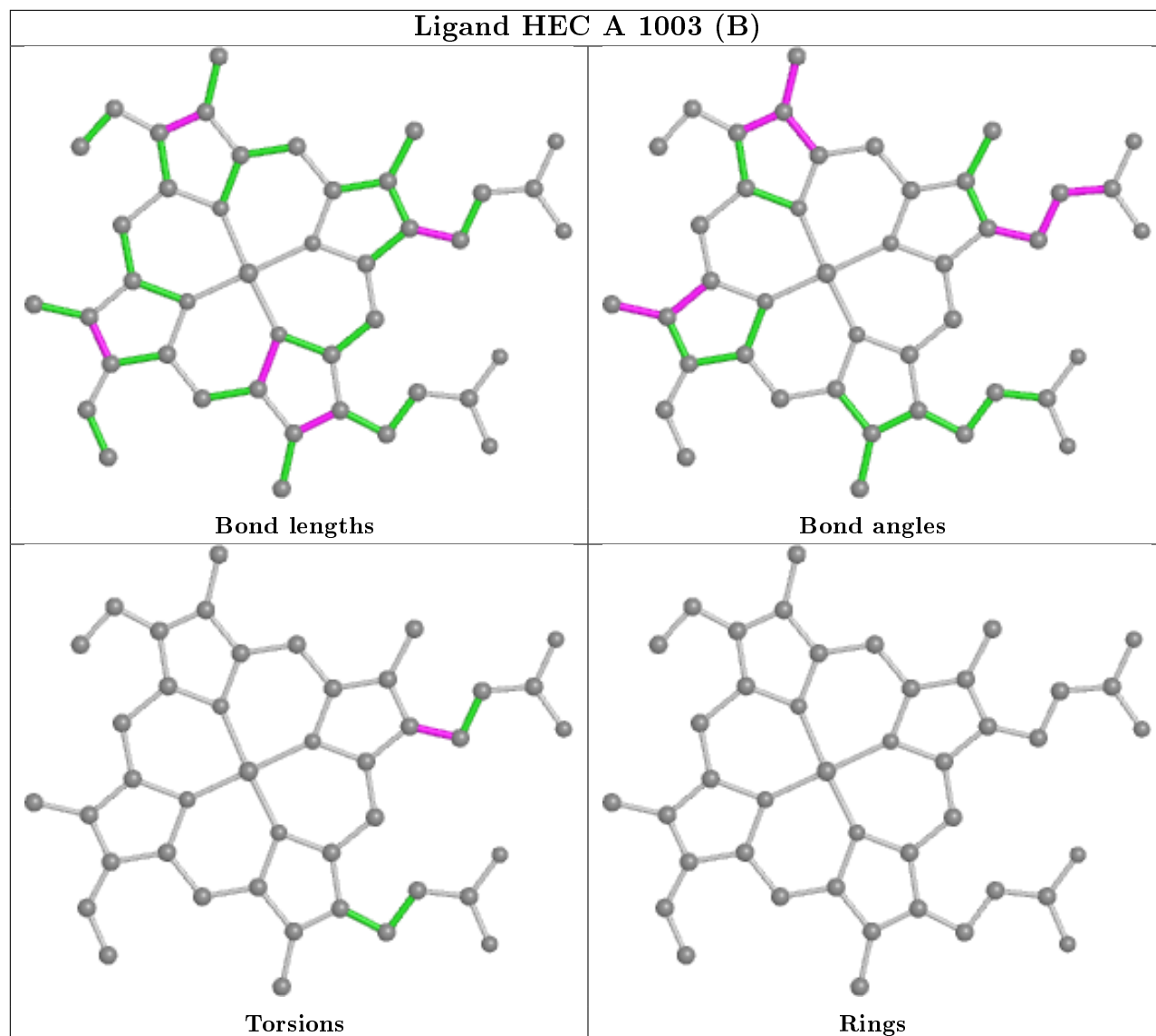


## Ligand HEC A 1003 (A)

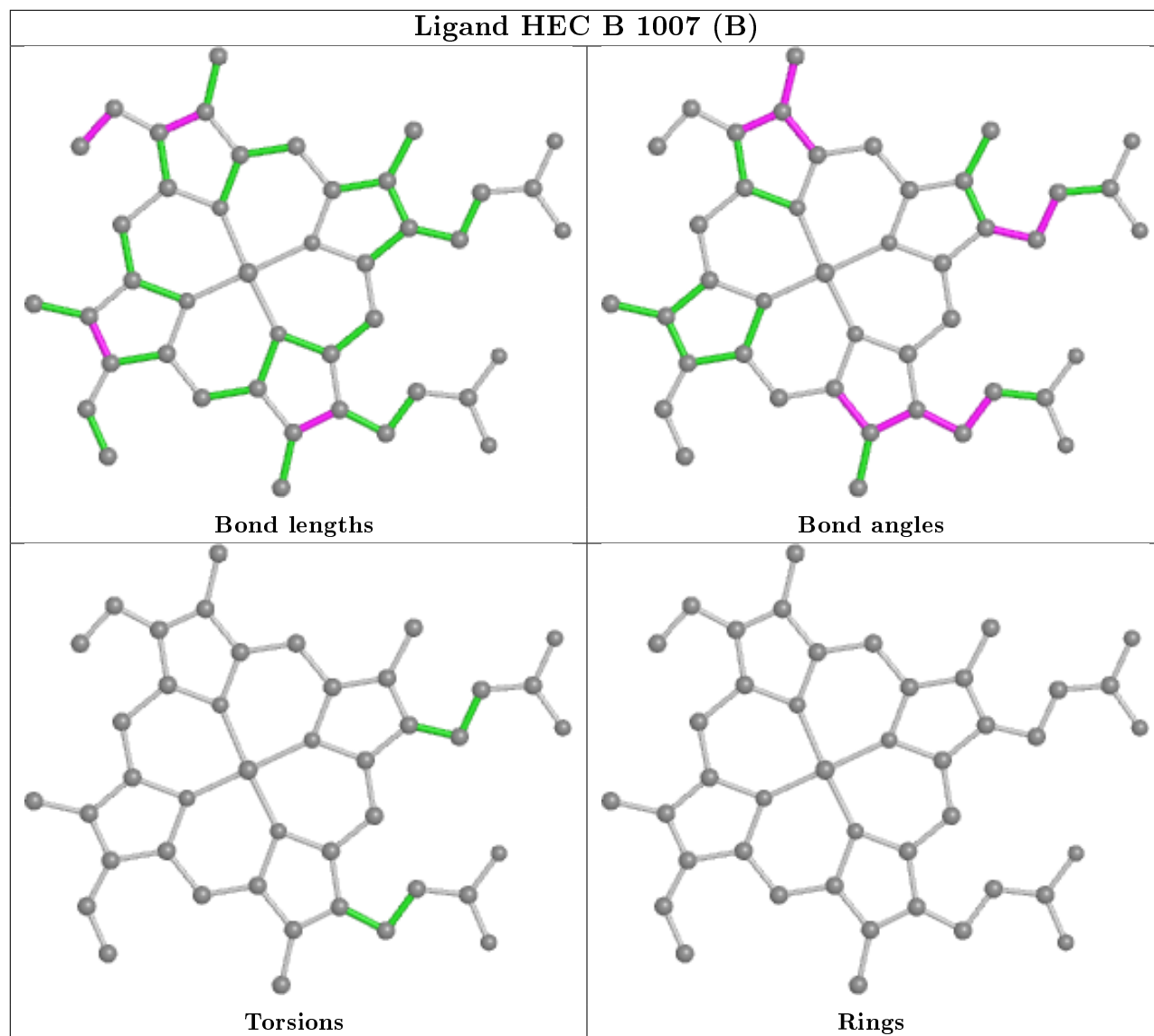




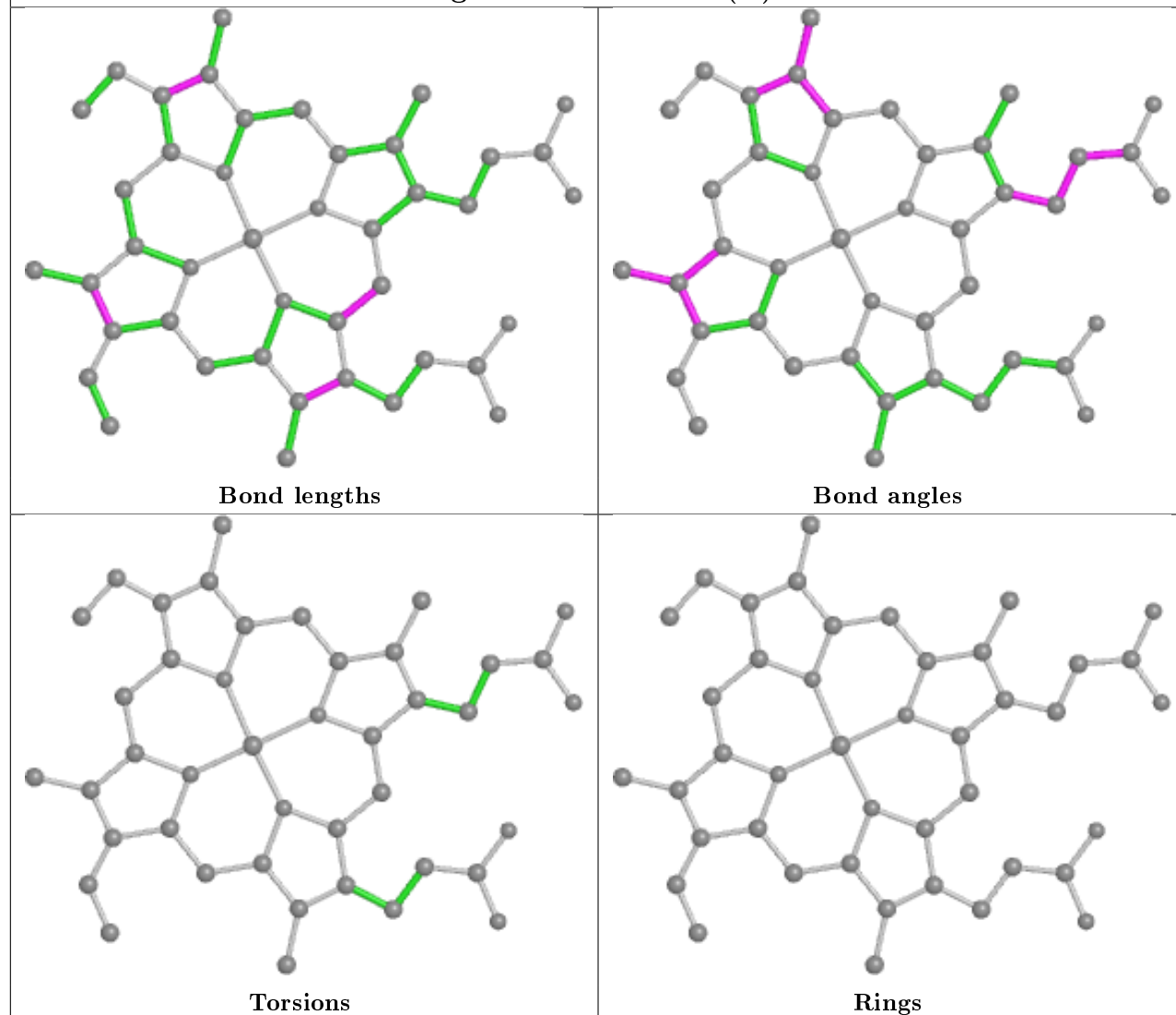
## Ligand HEC A 1003 (B)



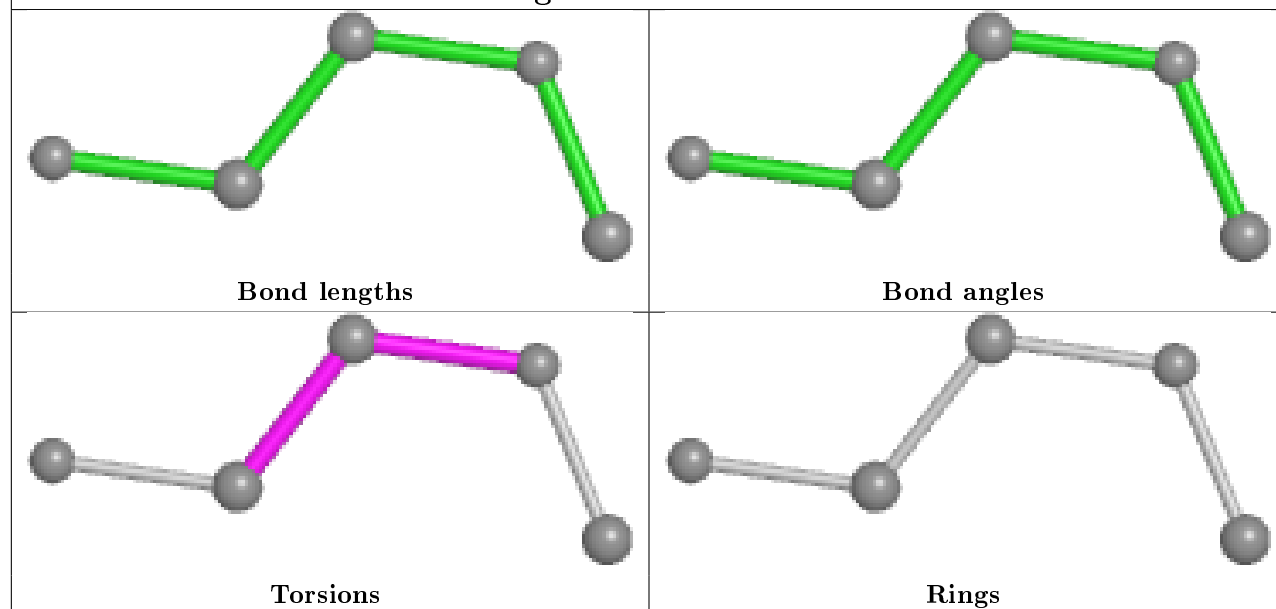
## Ligand HEC B 1007 (B)



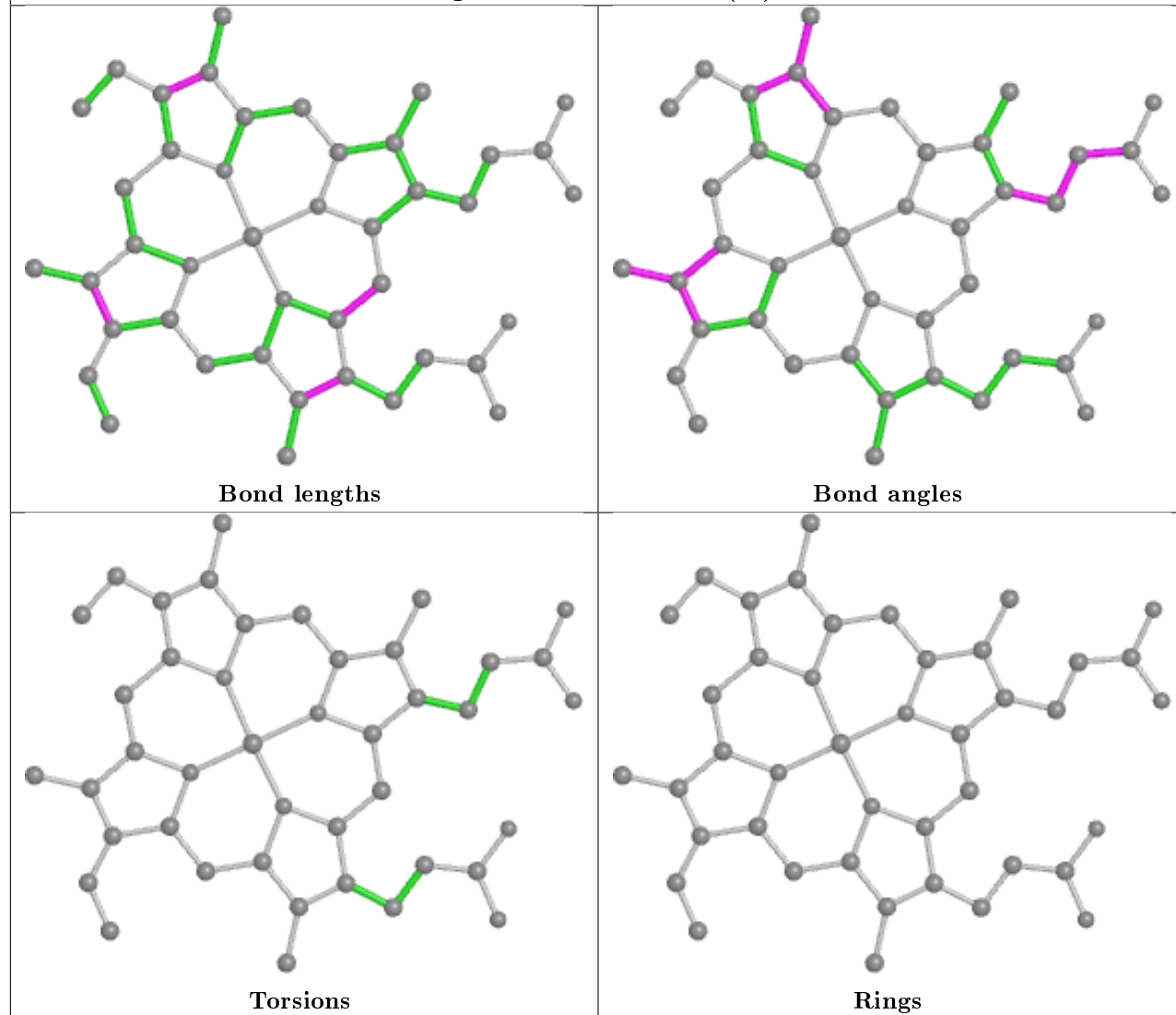
## Ligand HEC B 1003 (B)

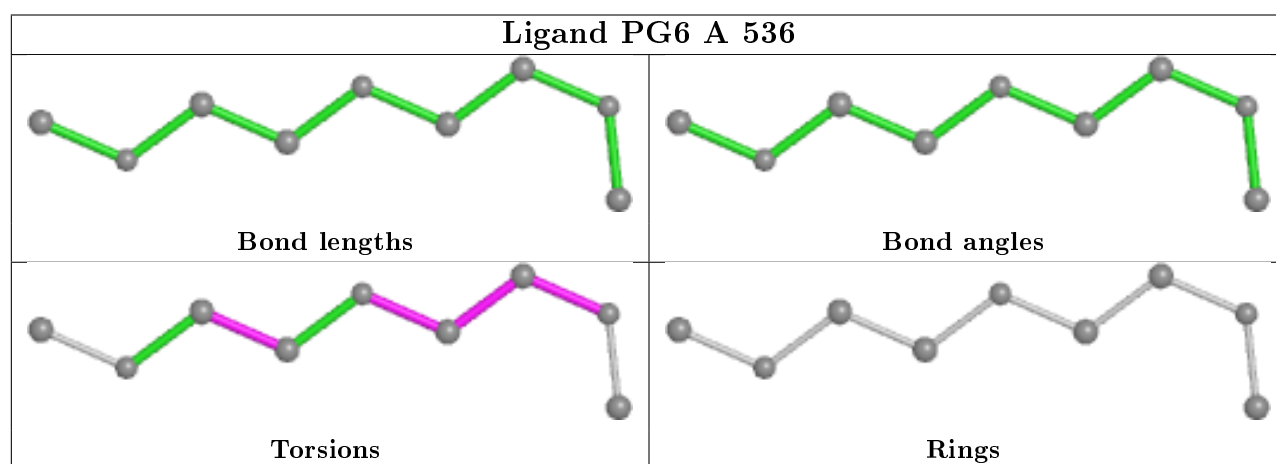
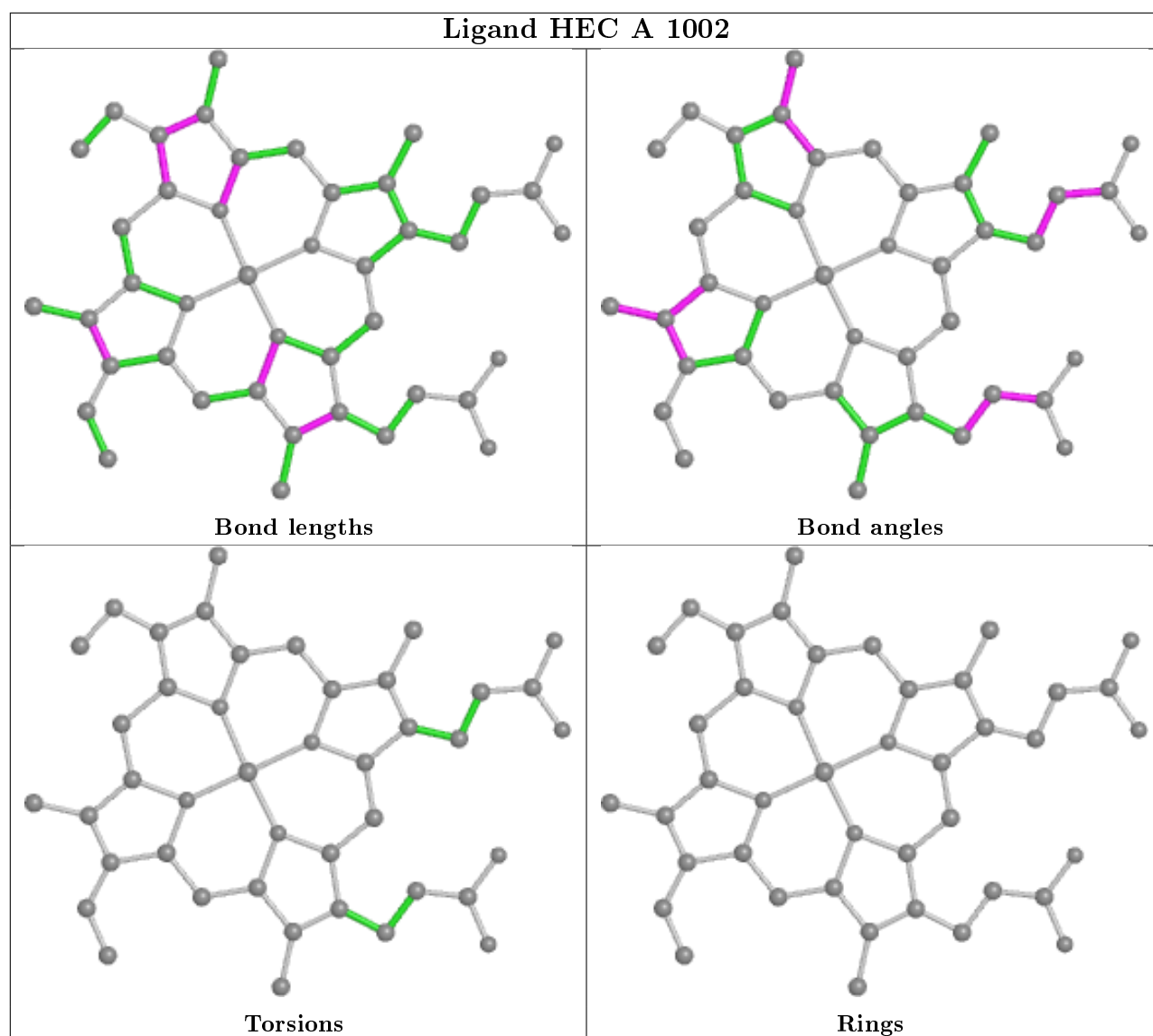


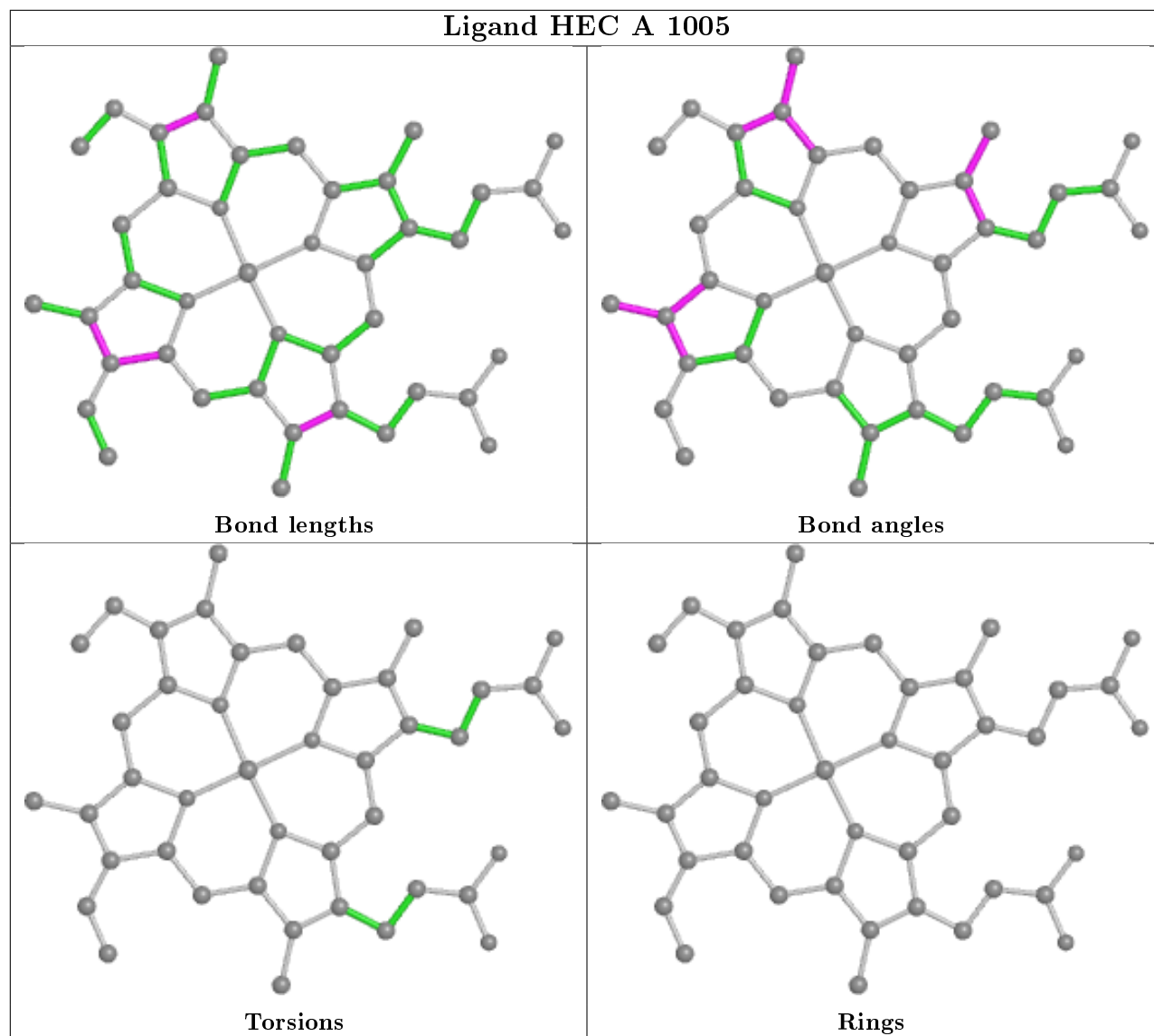
## Ligand PG6 B 542



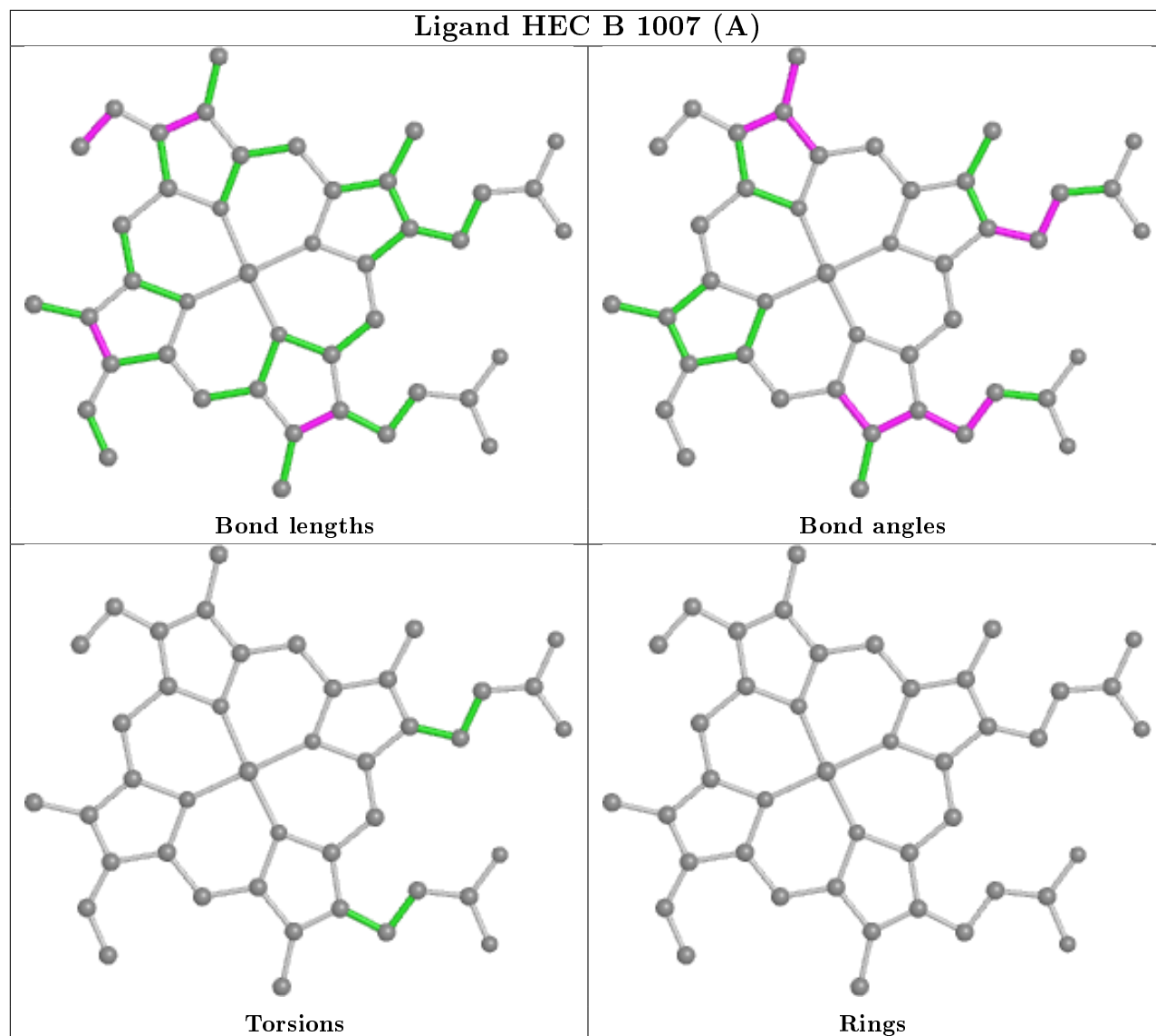
## Ligand HEC B 1003 (A)



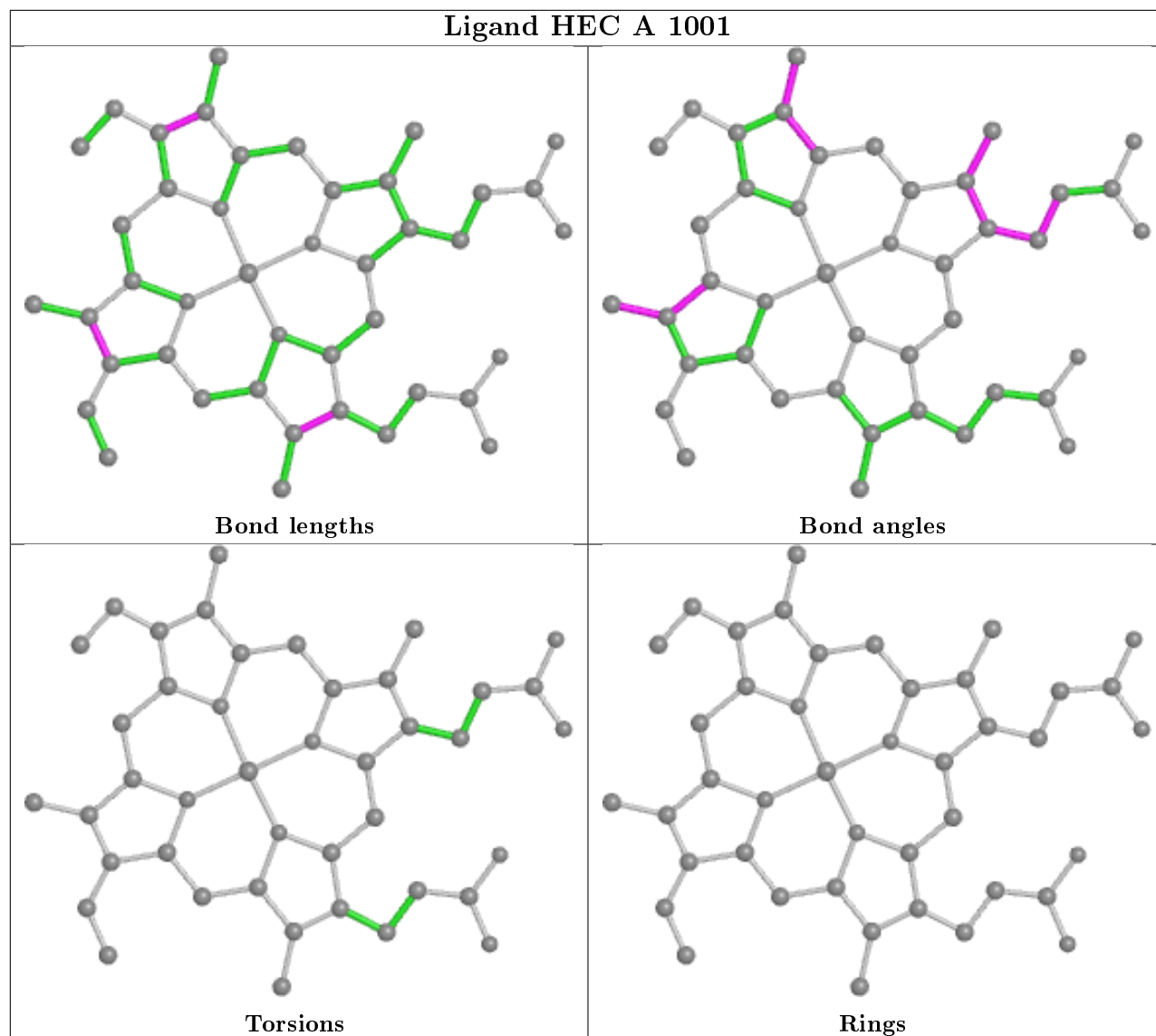




## Ligand HEC B 1007 (A)

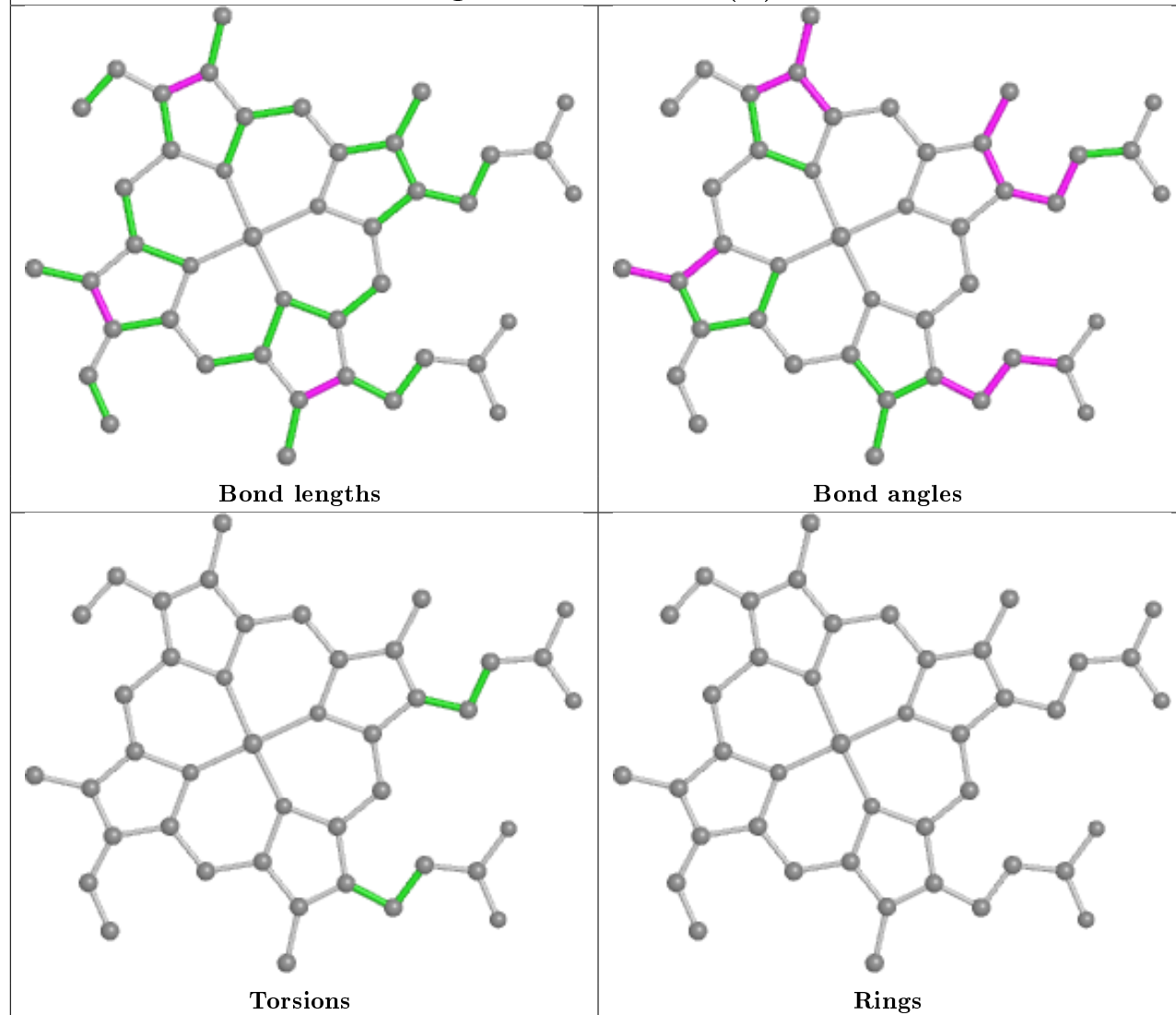


## Ligand HEC A 1001

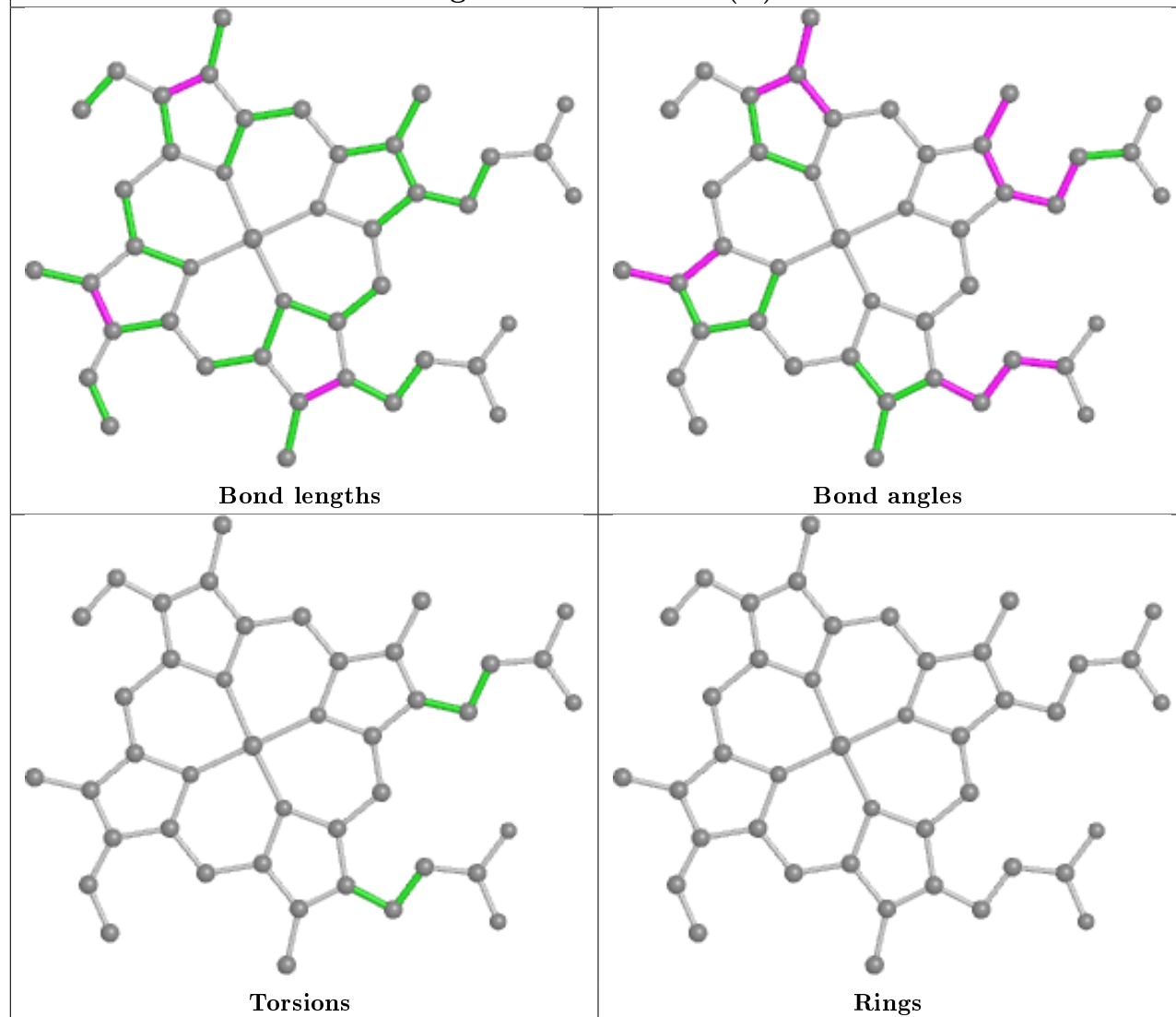




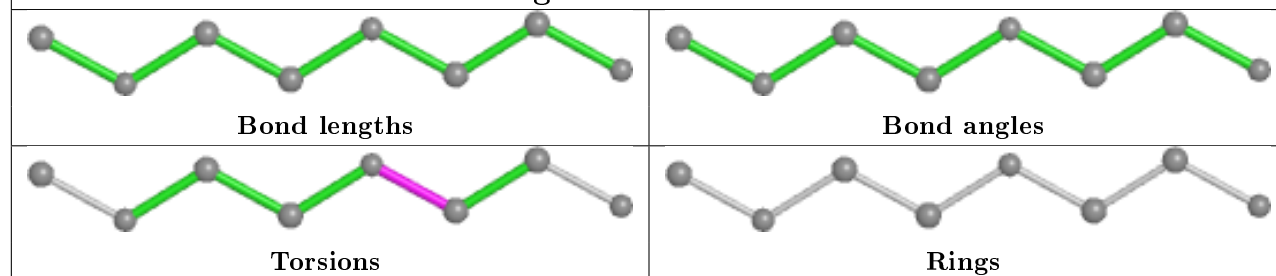
## Ligand HEC A 1007 (A)



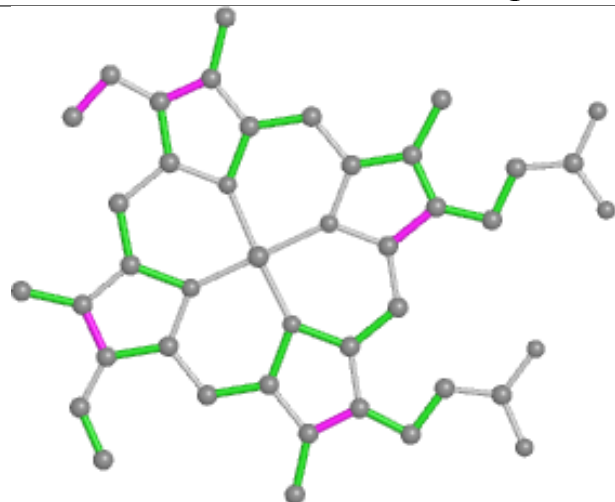
## Ligand HEC A 1007 (B)



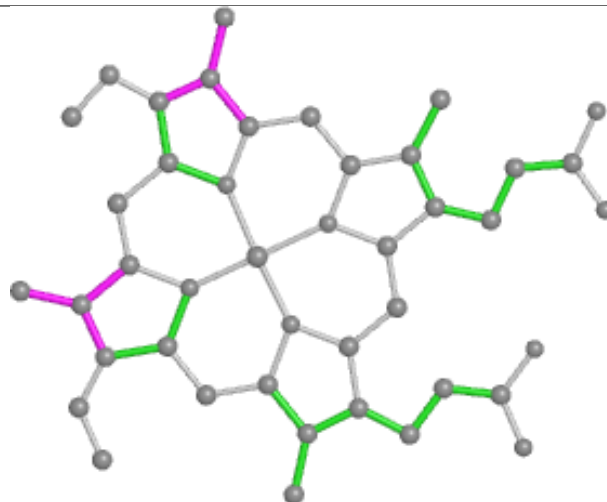
## Ligand PG6 A 534



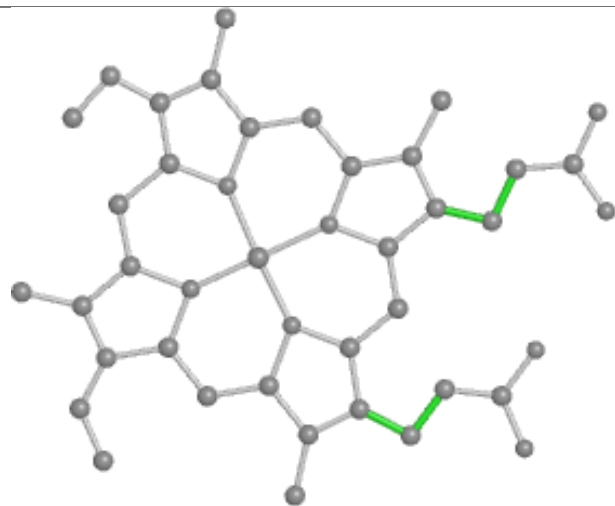
## Ligand HEC B 1005



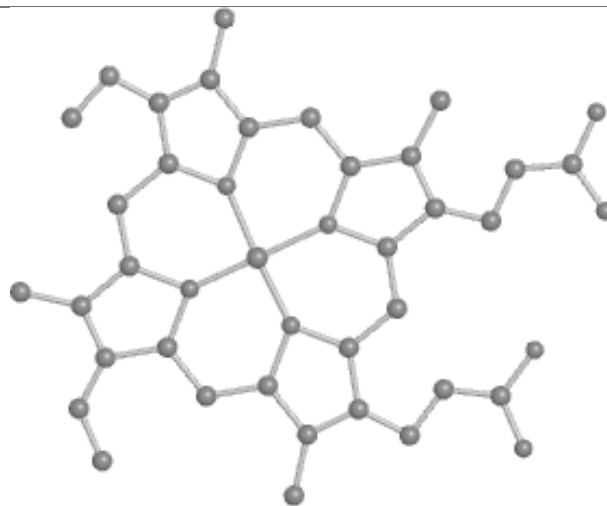
Bond lengths



Bond angles

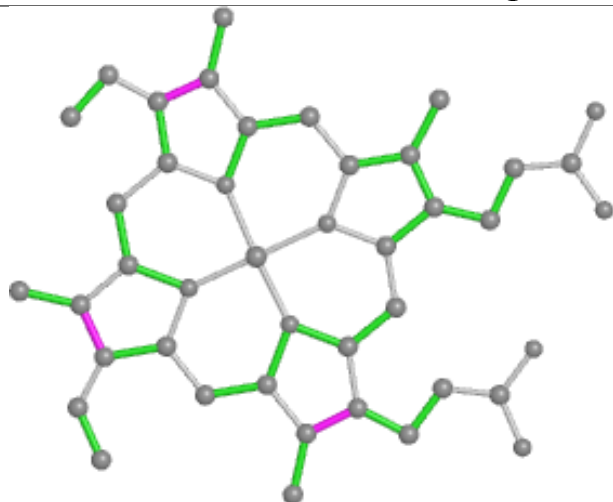


Torsions

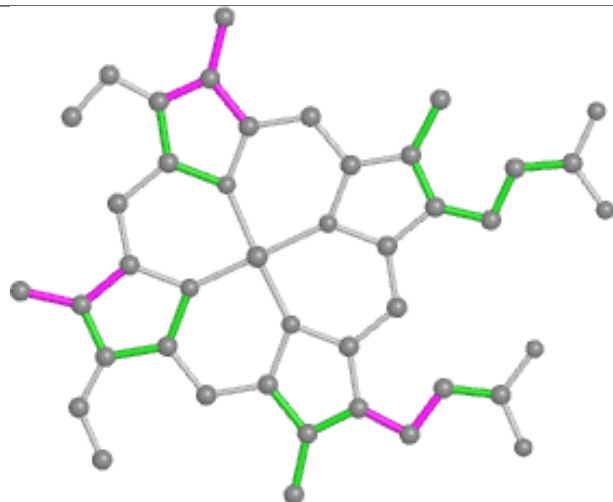


Rings

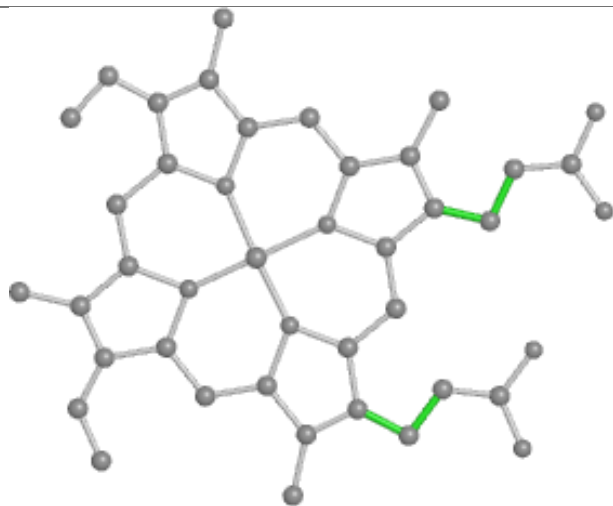
## Ligand HEC B 1008



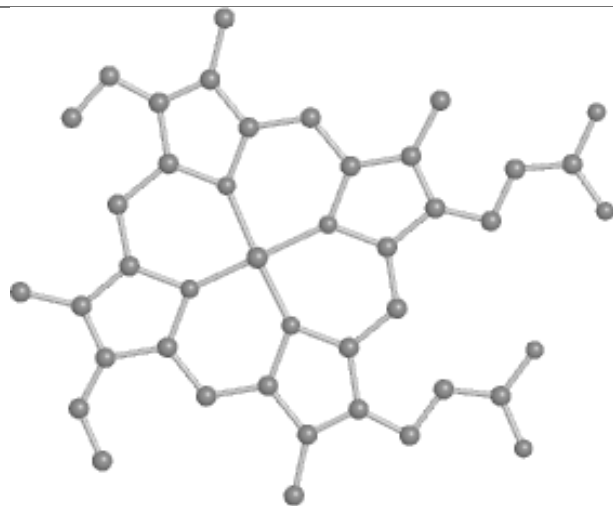
Bond lengths



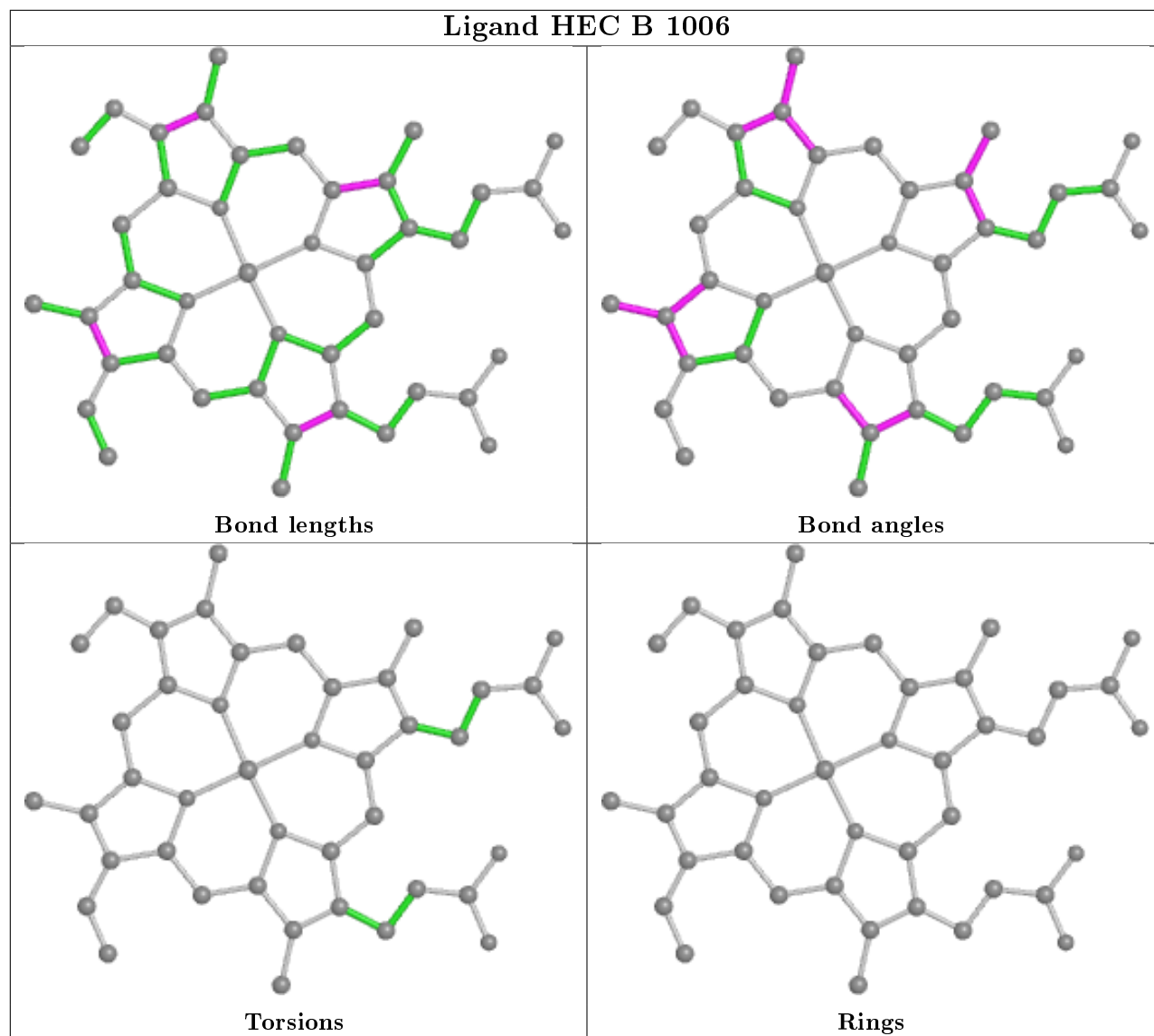
Bond angles



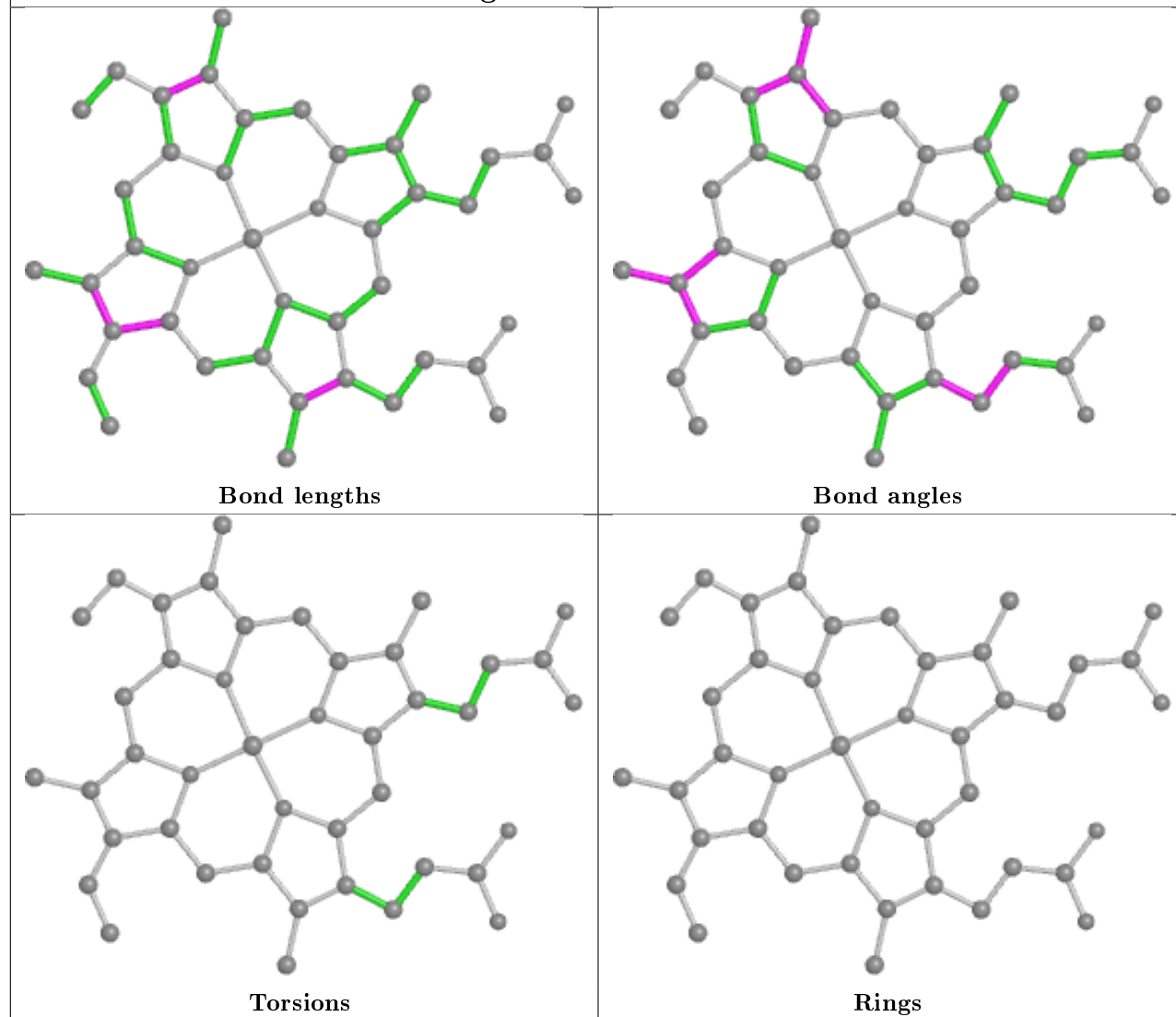
Torsions



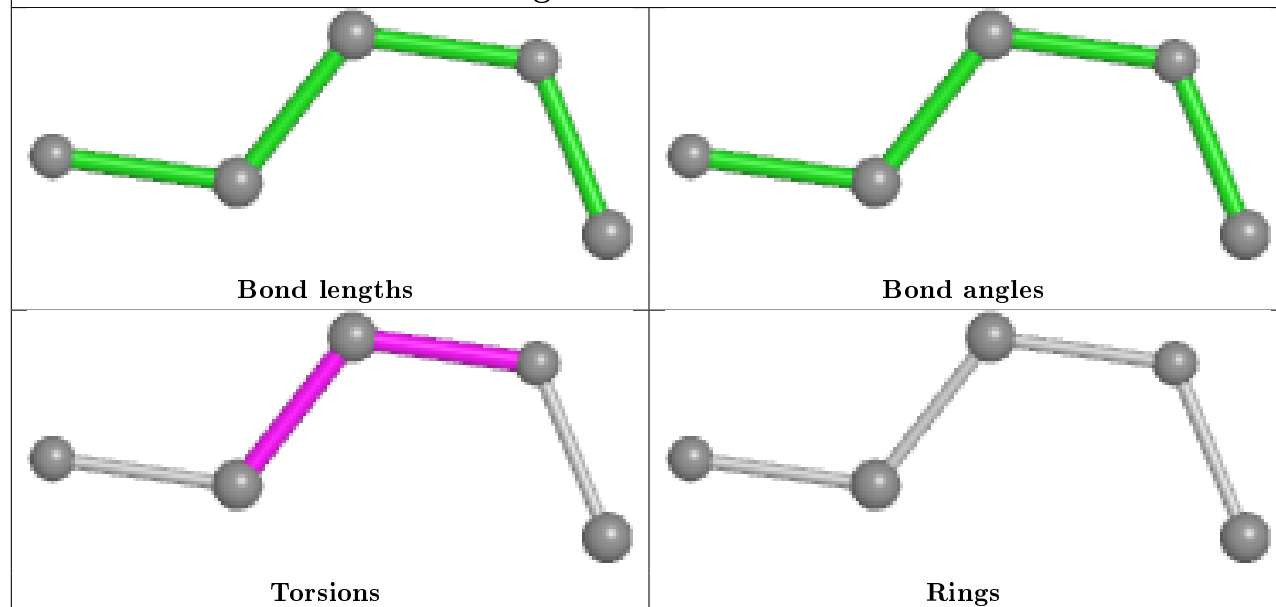
Rings



## Ligand HEC A 1008



## Ligand PG6 A 542



## 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	519/525 (98%)	-0.91	2 (0%) 92 91	11, 16, 25, 44	2 (0%)
1	B	519/525 (98%)	-0.85	5 (0%) 82 80	11, 15, 26, 44	3 (0%)
All	All	1038/1050 (98%)	-0.88	7 (0%) 87 86	11, 15, 26, 44	5 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	523	ALA	7.8
1	A	522	VAL	7.0
1	B	522	VAL	6.1
1	A	523	ALA	2.8
1	B	204	GLU	2.3

### 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 carbohydrates 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( $\text{\AA}^2$ )	Q<0.9
11	ACT	B	546	4/4	0.45	0.27	34,35,36,36	0
10	PG4	B	544	5/13	0.68	0.16	25,26,28,29	5
10	PG4	B	545	4/13	0.68	0.27	35,35,36,36	4
8	PG6	A	543	10/18	0.70	0.18	29,31,33,34	10
10	PG4	A	541	6/13	0.71	0.17	36,36,37,38	6
10	PG4	B	540	4/13	0.72	0.20	29,31,31,31	4
8	PG6	A	536	9/18	0.74	0.12	40,42,42,42	9
10	PG4	B	537	10/13	0.76	0.15	39,42,44,44	10
10	PG4	B	541	5/13	0.80	0.12	47,47,48,49	0
10	PG4	A	539	6/13	0.82	0.14	47,48,48,48	0
10	PG4	A	538[A]	5/13	0.83	0.14	36,38,40,41	2
9	TRS	B	533	8/8	0.83	0.22	15,15,16,16	8
10	PG4	A	538[B]	8/13	0.83	0.14	39,40,41,41	5
10	PG4	A	537	4/13	0.84	0.11	35,36,36,36	4
8	PG6	A	542	5/18	0.84	0.28	52,52,52,53	5
8	PG6	A	534	8/18	0.84	0.13	28,33,40,40	0
10	PG4	B	538	7/13	0.86	0.12	31,31,32,33	7
8	PG6	B	535	8/18	0.88	0.13	34,36,38,38	0
8	PG6	B	532	17/18	0.88	0.14	16,19,22,25	17
10	PG4	B	539	5/13	0.88	0.13	23,27,27,27	5
8	PG6	B	542	5/18	0.89	0.09	45,45,45,45	5
9	TRS	A	533	8/8	0.89	0.18	12,13,14,14	8
8	PG6	A	532	17/18	0.90	0.11	17,21,27,29	17
10	PG4	B	536	8/13	0.91	0.21	18,25,29,29	8
10	PG4	B	543	4/13	0.93	0.17	47,48,48,48	0
5	SO4	A	529	5/5	0.94	0.15	19,21,26,26	5
10	PG4	A	540	6/13	0.94	0.09	50,50,51,51	0
10	PG4	B	547	7/13	0.94	0.12	18,22,24,26	7
7	NA	B	548	1/1	0.95	0.06	24,24,24,24	1
6	THJ	A	530	5/5	0.96	0.07	24,24,24,28	5
7	NA	B	549	1/1	0.97	0.28	30,30,30,30	1
3	SO3	B	529[B]	4/4	0.97	0.24	17,18,22,22	4
3	SO3	B	529[A]	4/4	0.97	0.24	17,18,20,22	4
5	SO4	B	534	5/5	0.97	0.11	14,18,23,25	5
10	PG4	A	535	5/13	0.98	0.17	14,17,20,22	5
2	HEC	B	1003[A]	43/43	0.98	0.07	12,13,23,33	4
2	HEC	A	1008	43/43	0.98	0.06	12,14,22,34	0
2	HEC	A	1003[B]	43/43	0.98	0.07	11,13,23,29	4
2	HEC	B	1003[B]	43/43	0.98	0.07	12,13,23,33	4
2	HEC	A	1003[A]	43/43	0.98	0.07	11,13,21,29	4
7	NA	A	544	1/1	0.98	0.09	23,23,23,23	1
4	CA	B	528	1/1	0.99	0.04	18,18,18,18	1
2	HEC	A	1007[A]	43/43	0.99	0.04	10,11,13,14	4

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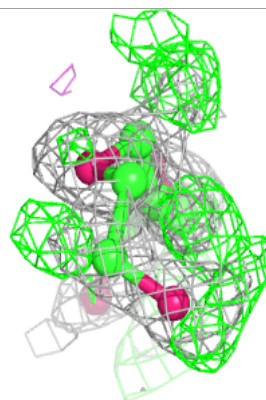
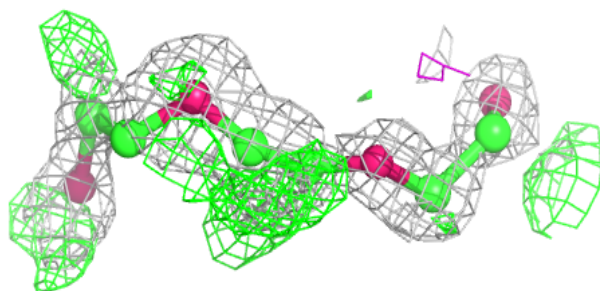
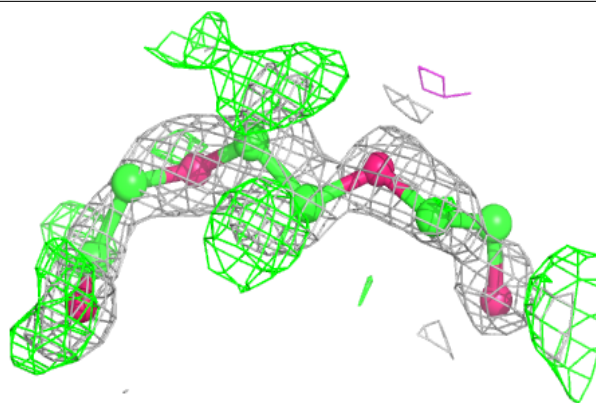
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	HEC	B	1007[B]	43/43	0.99	0.05	10,11,13,14	4
2	HEC	A	1007[B]	43/43	0.99	0.04	10,11,13,14	4
2	HEC	A	1004	43/43	0.99	0.04	11,12,14,17	0
4	CA	A	528	1/1	0.99	0.03	18,18,18,18	1
2	HEC	B	1005	43/43	0.99	0.05	10,12,15,19	0
3	SO3	A	526	4/4	0.99	0.04	14,15,17,18	0
6	THJ	B	530	5/5	0.99	0.05	23,23,23,25	5
2	HEC	A	1006	43/43	0.99	0.05	10,11,12,14	0
2	HEC	B	1008	43/43	0.99	0.05	11,14,21,32	0
2	HEC	B	1004	43/43	0.99	0.05	10,12,14,16	0
2	HEC	B	1006	43/43	0.99	0.05	9,11,12,13	0
2	HEC	A	1002	43/43	0.99	0.04	12,13,15,17	0
2	HEC	B	1002	43/43	0.99	0.04	13,15,17,19	0
2	HEC	B	1001	43/43	0.99	0.05	17,19,24,26	0
2	HEC	A	1005	43/43	0.99	0.05	11,12,16,19	0
2	HEC	B	1007[A]	43/43	0.99	0.05	10,11,13,14	4
2	HEC	A	1001	43/43	0.99	0.04	13,14,20,21	0
7	NA	B	531	1/1	1.00	0.12	23,23,23,23	1
4	CA	B	527	1/1	1.00	0.02	13,13,13,13	0
3	SO3	B	526	4/4	1.00	0.04	14,14,16,17	0
4	CA	A	527	1/1	1.00	0.02	13,13,13,13	0
7	NA	A	531	1/1	1.00	0.05	23,23,23,23	1

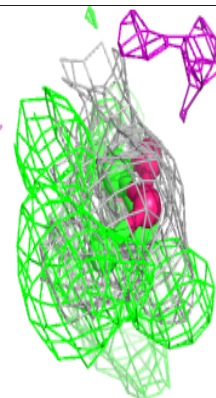
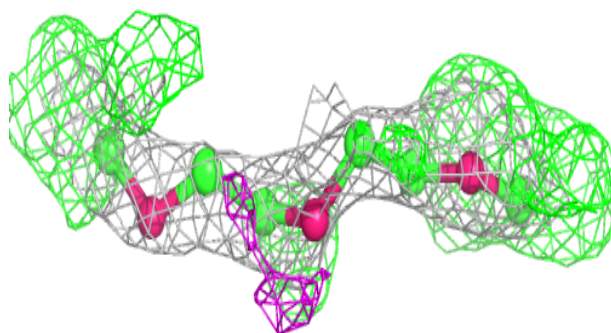
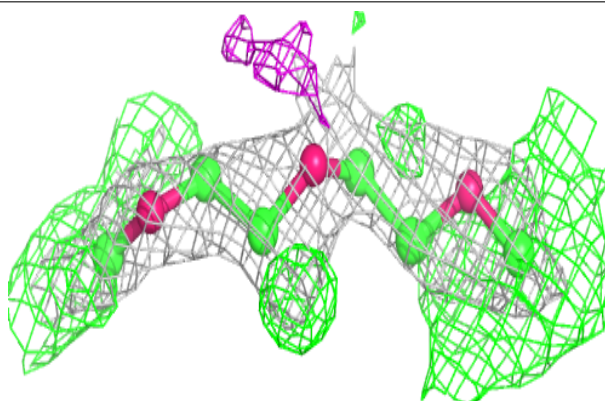
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around PG6 A 543:**

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

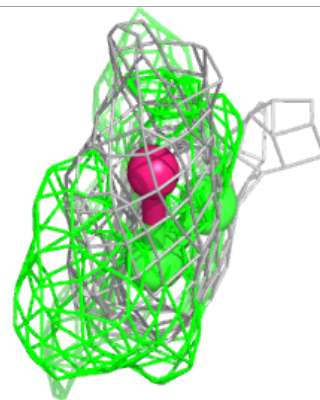
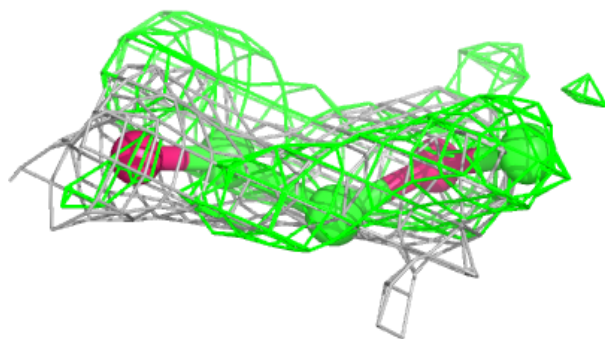
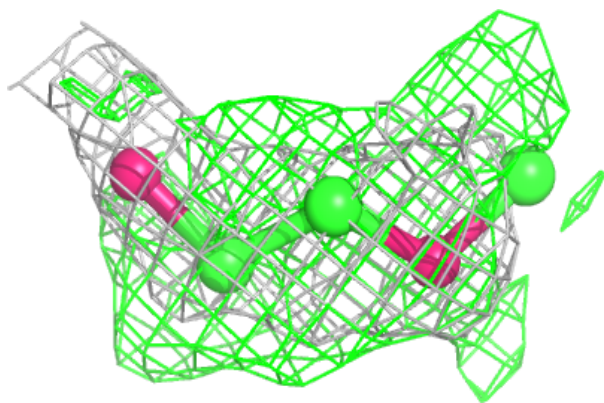
**Electron density around PG6 A 536:**

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

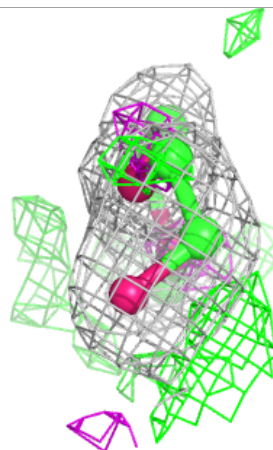
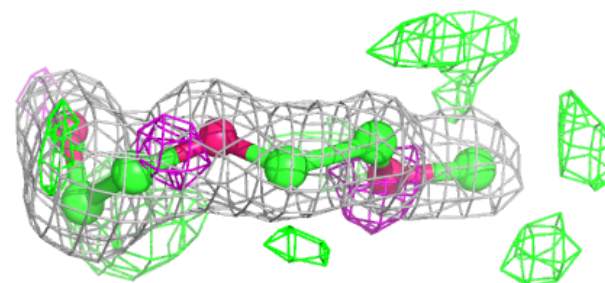
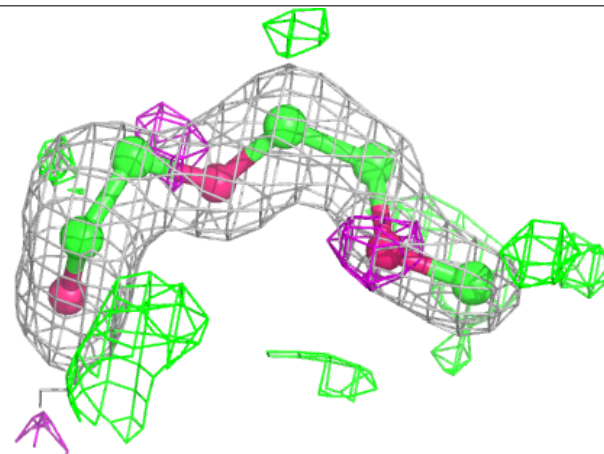


**Electron density around PG6 A 542:**

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

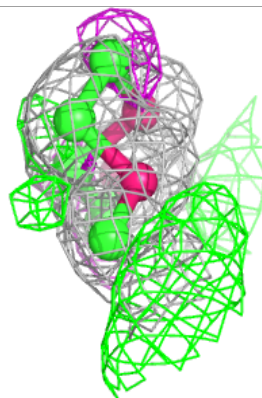
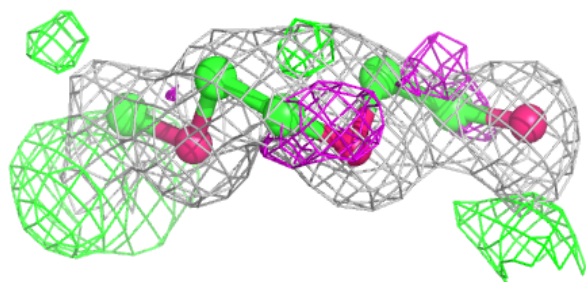
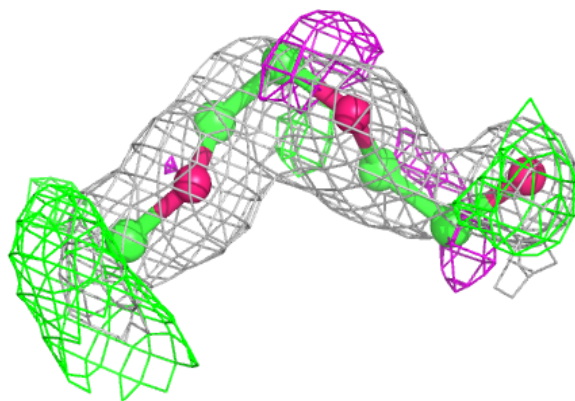
**Electron density around PG6 A 534:**

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

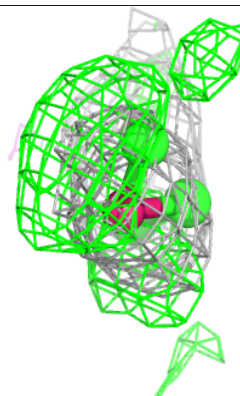
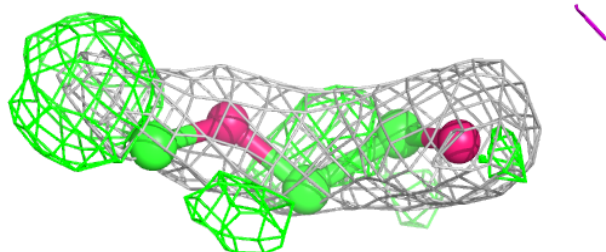
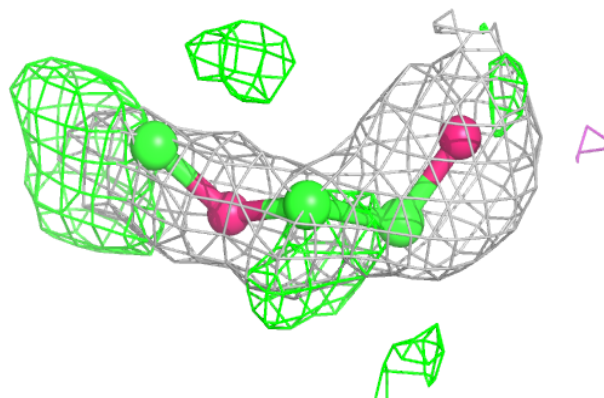


**Electron density around PG6 B 535:**

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

**Electron density around PG6 B 542:**

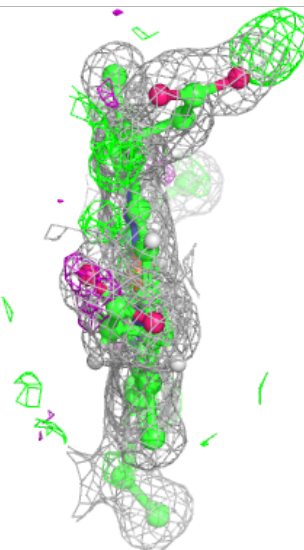
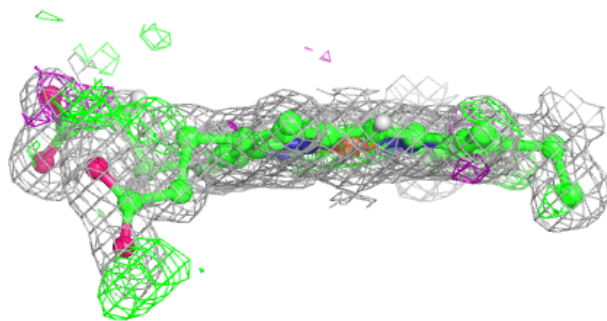
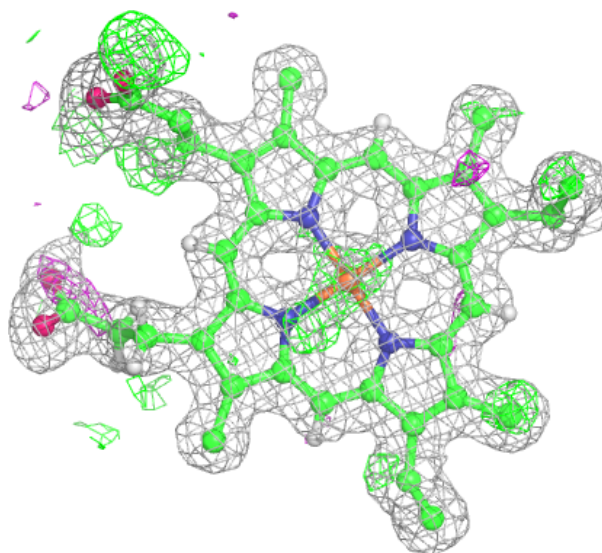
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





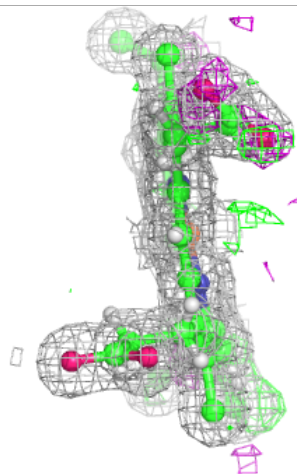
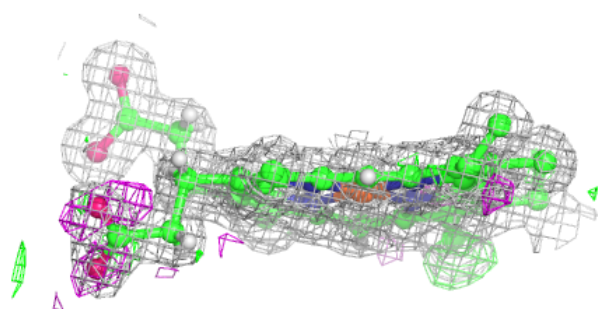
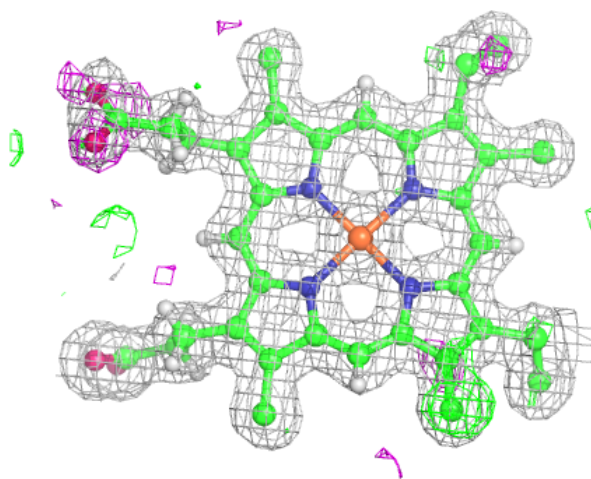
**Electron density around HEC B 1003 (A):**

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



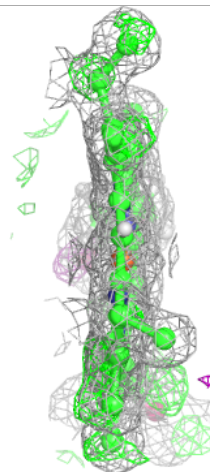
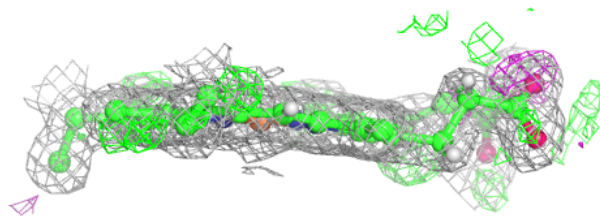
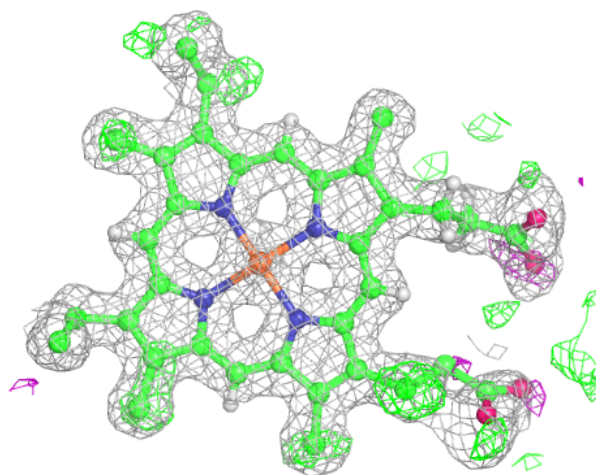
**Electron density around HEC A 1008:**

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



**Electron density around HEC A 1003 (B):**

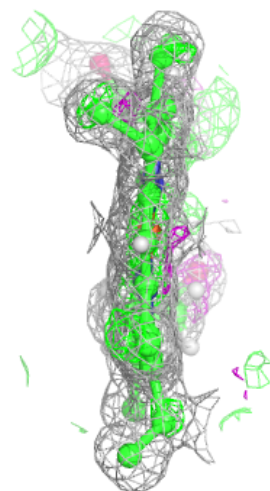
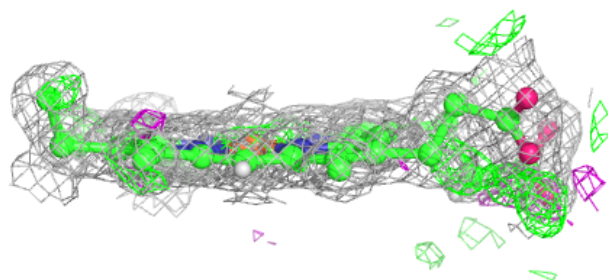
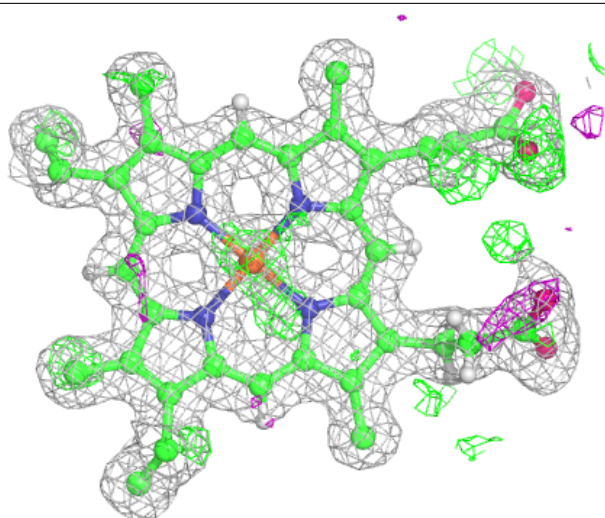
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





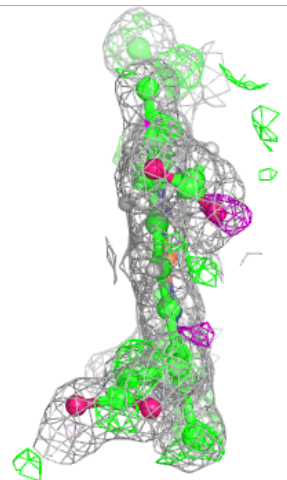
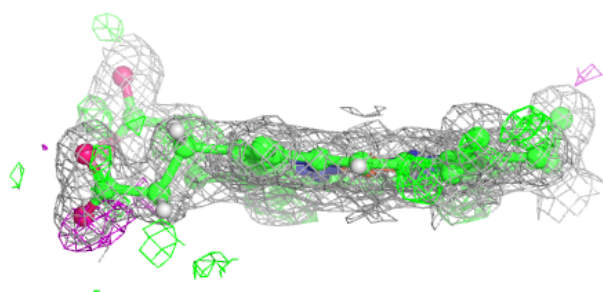
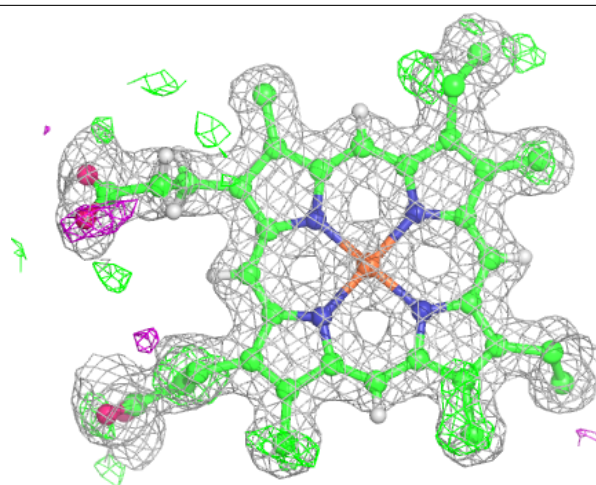
**Electron density around HEC B 1003 (B):**

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



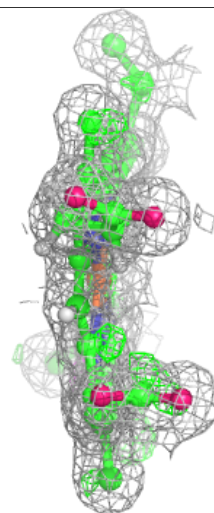
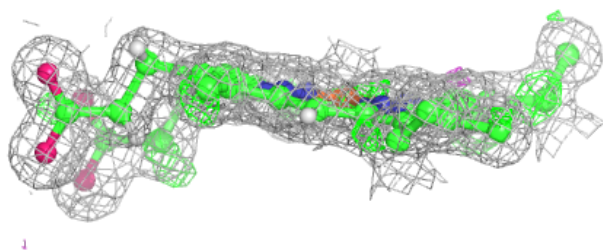
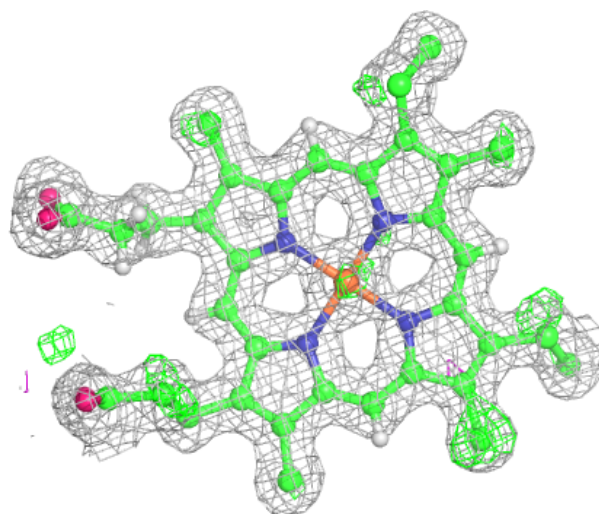
**Electron density around HEC A 1003 (A):**

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



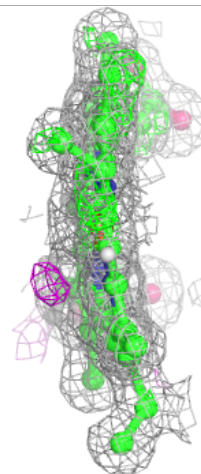
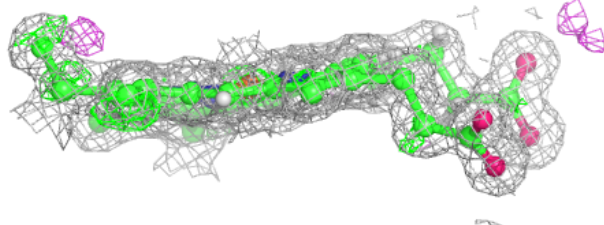
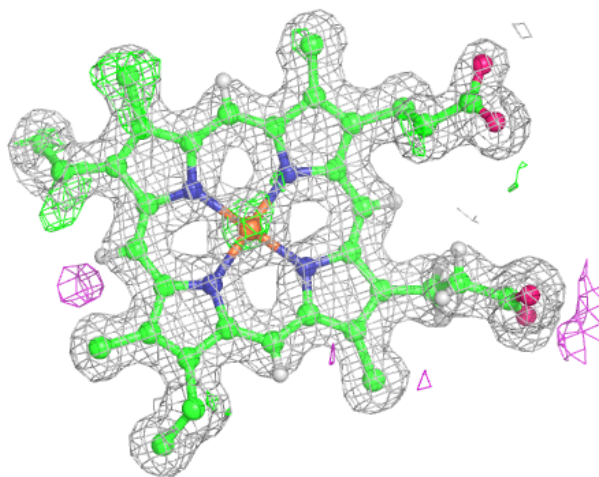
**Electron density around HEC A 1007 (A):**

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



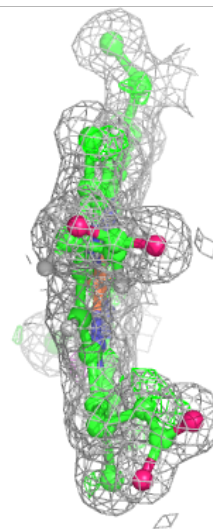
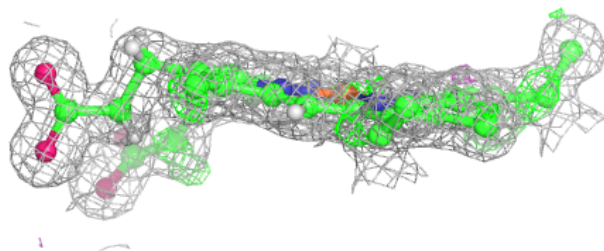
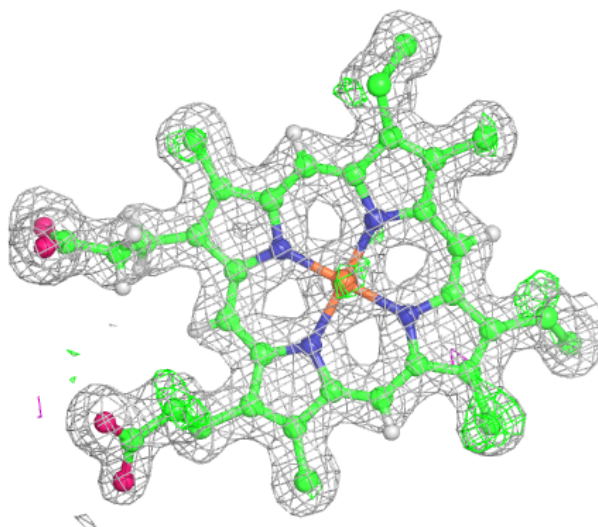
**Electron density around HEC B 1007 (B):**

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



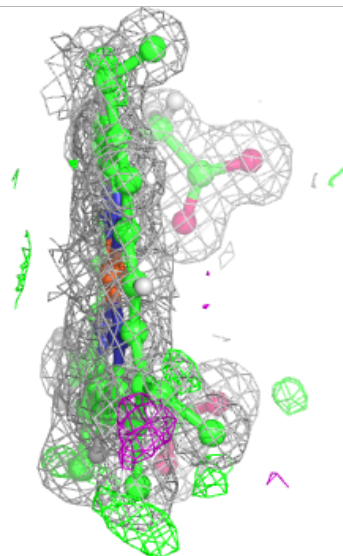
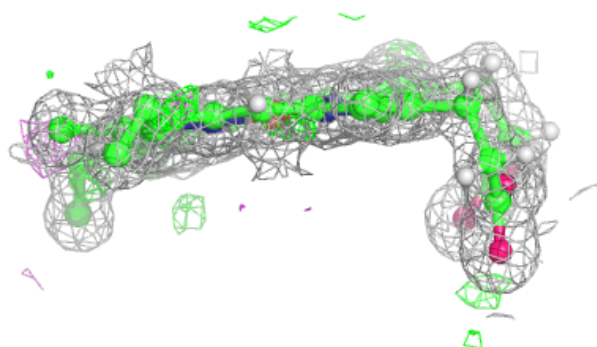
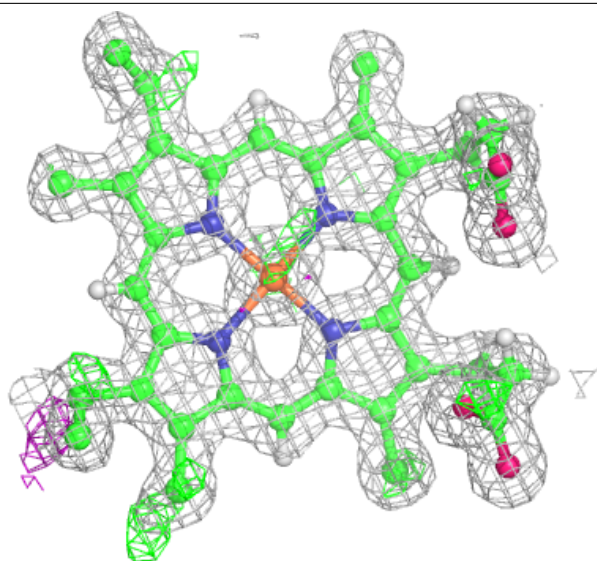
**Electron density around HEC A 1007 (B):**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEC A 1004:**

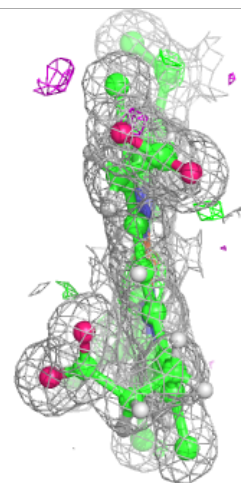
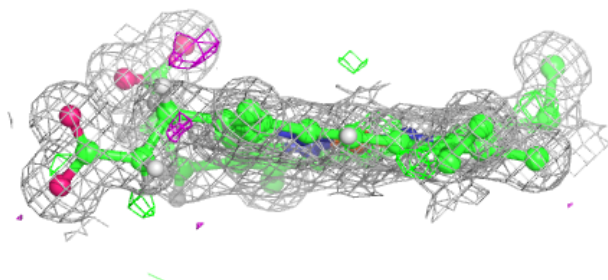
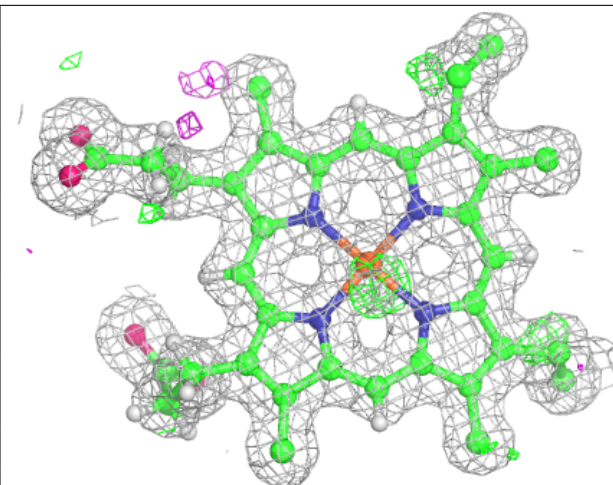
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





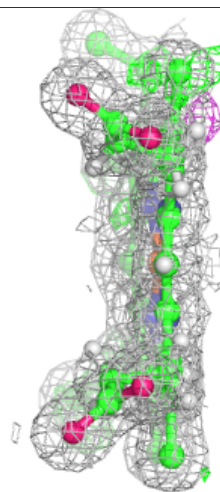
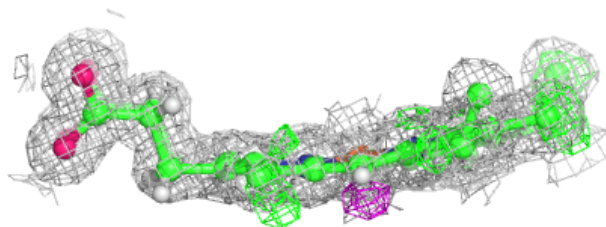
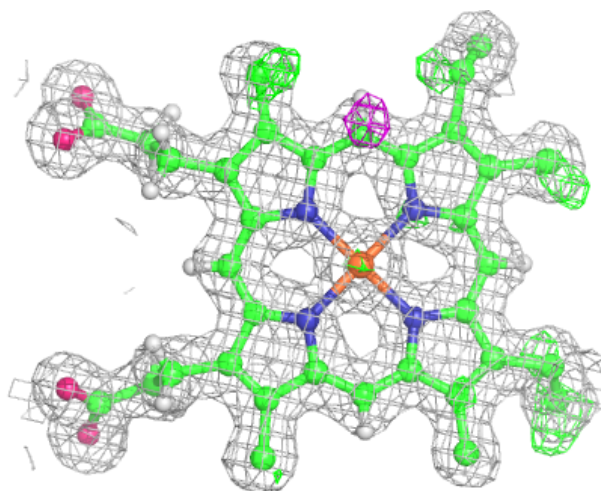
**Electron density around HEC B 1005:**

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



**Electron density around HEC A 1006:**

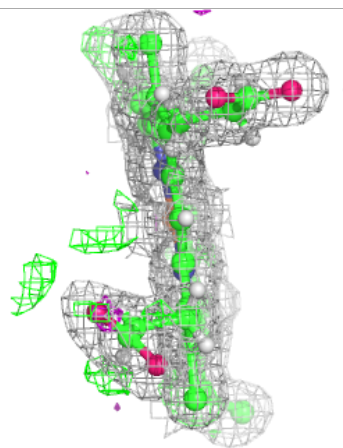
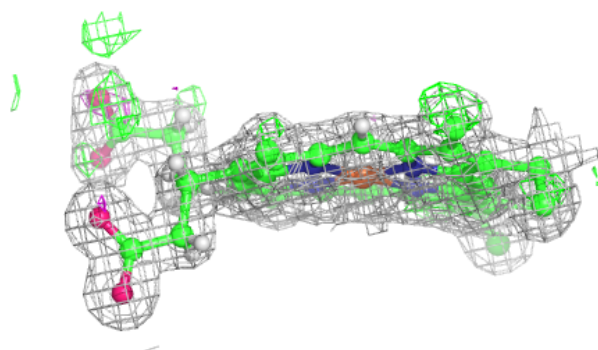
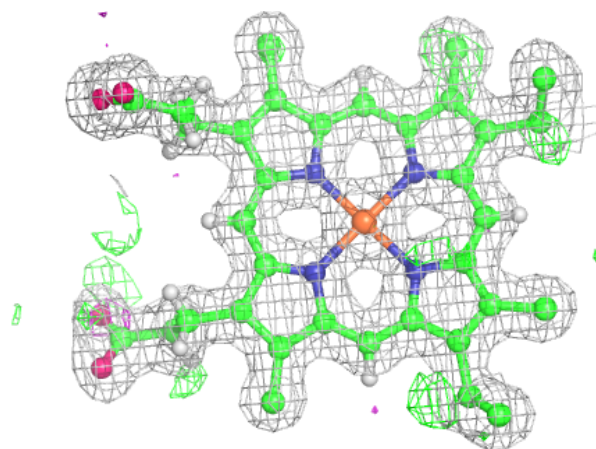
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





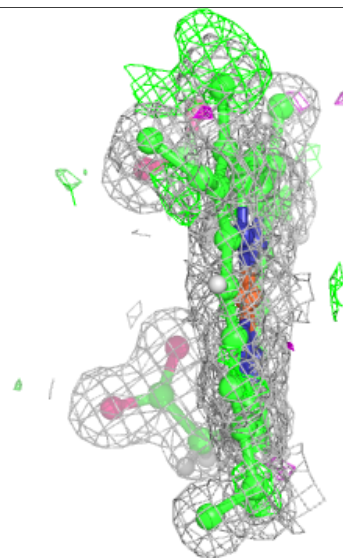
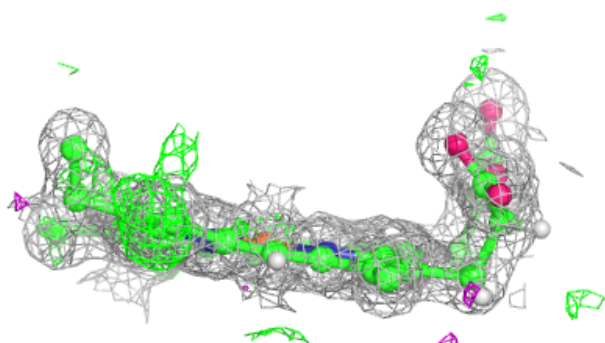
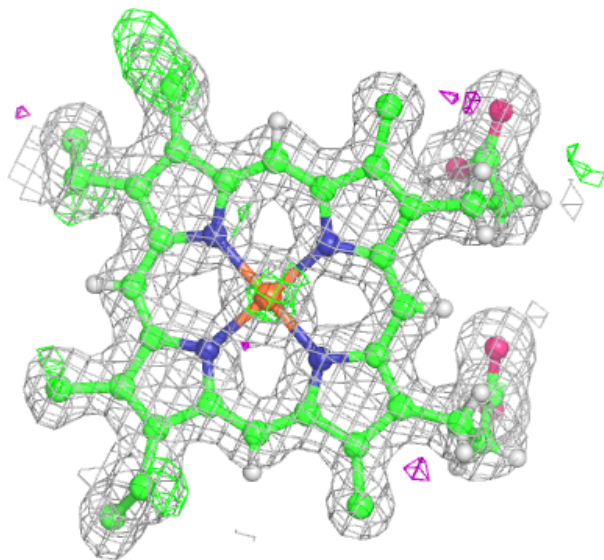
**Electron density around HEC B 1008:**

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



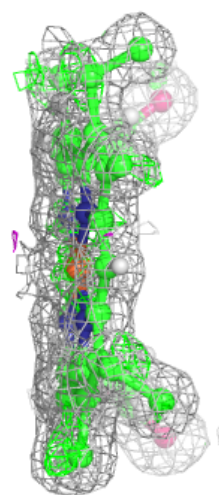
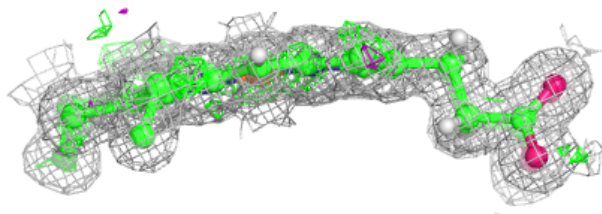
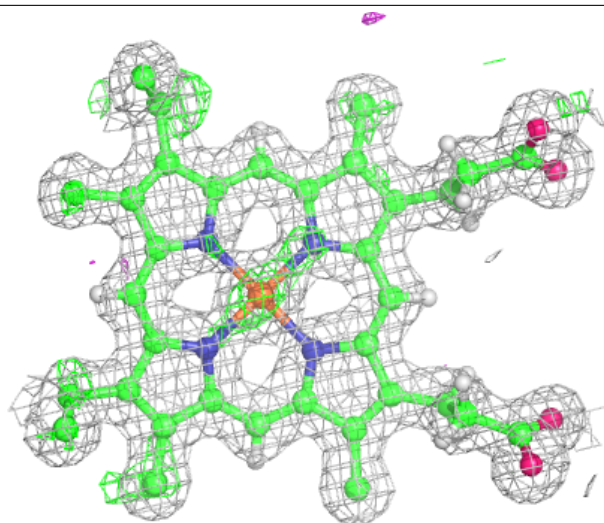
**Electron density around HEC B 1004:**

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



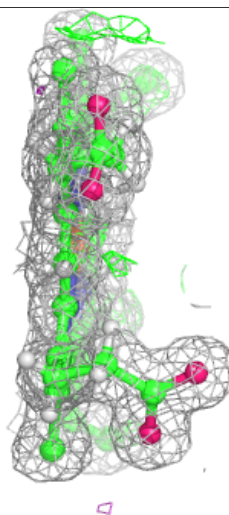
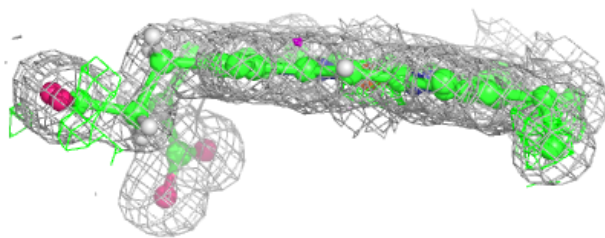
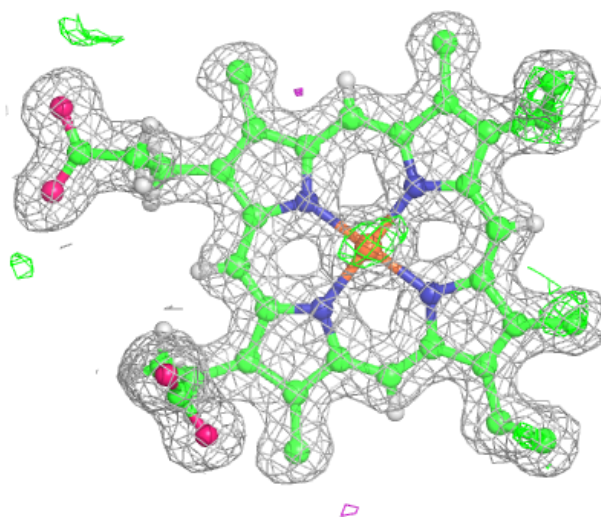
**Electron density around HEC B 1006:**

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



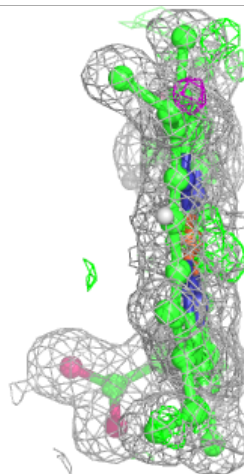
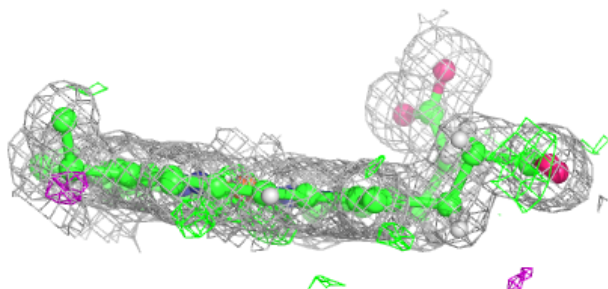
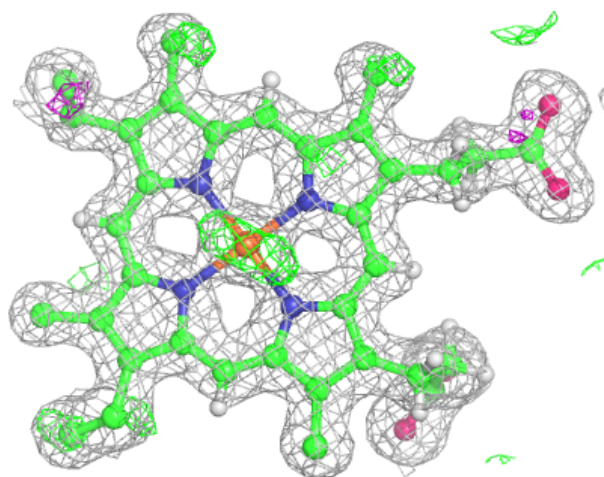
**Electron density around HEC A 1002:**

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



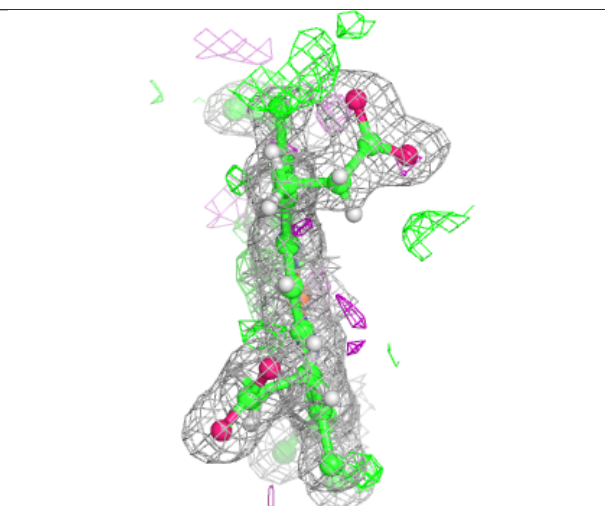
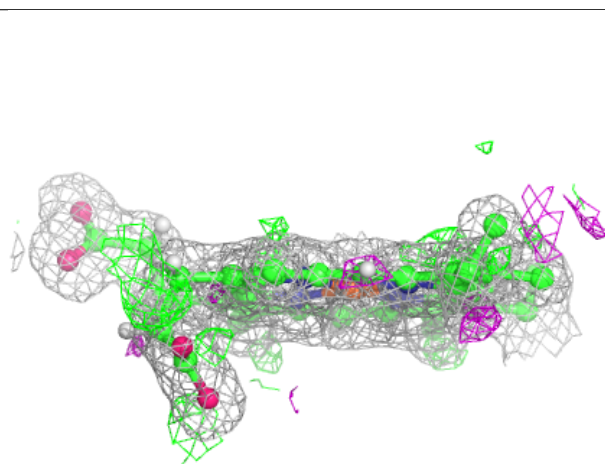
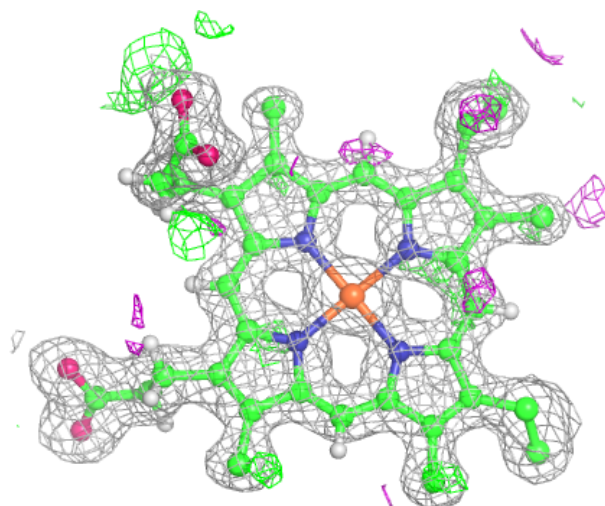
**Electron density around HEC B 1002:**

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



**Electron density around HEC B 1001:**

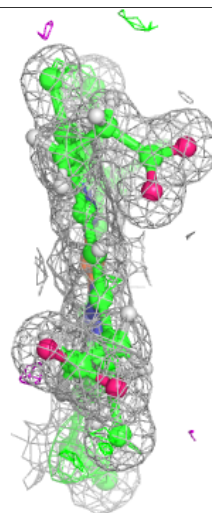
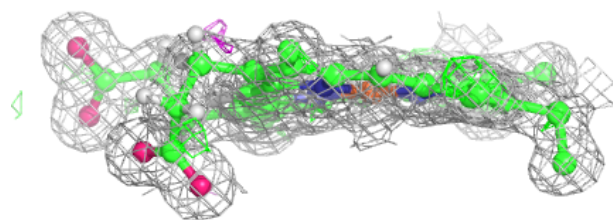
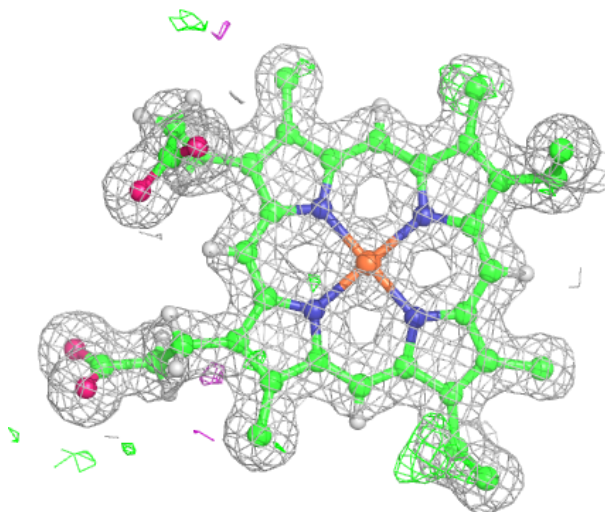
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





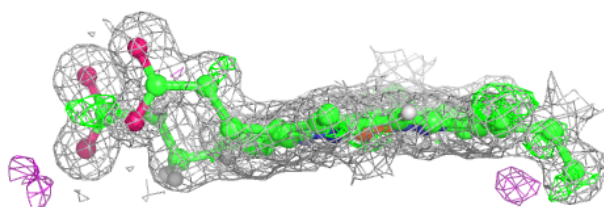
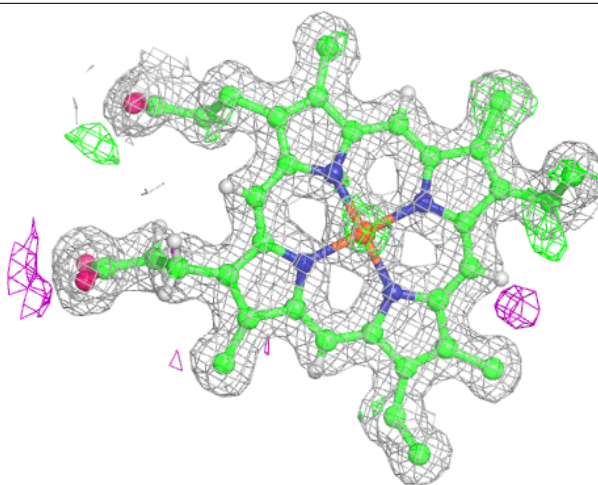
**Electron density around HEC A 1005:**

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



**Electron density around HEC B 1007 (A):**

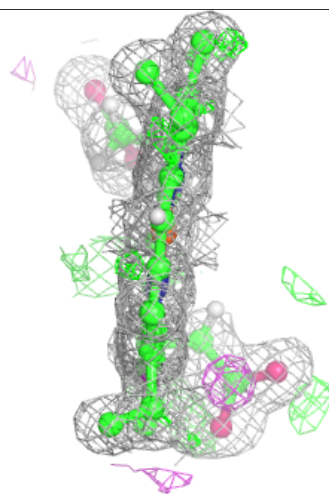
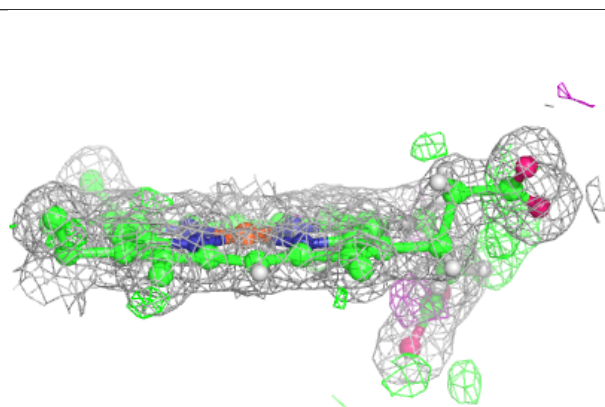
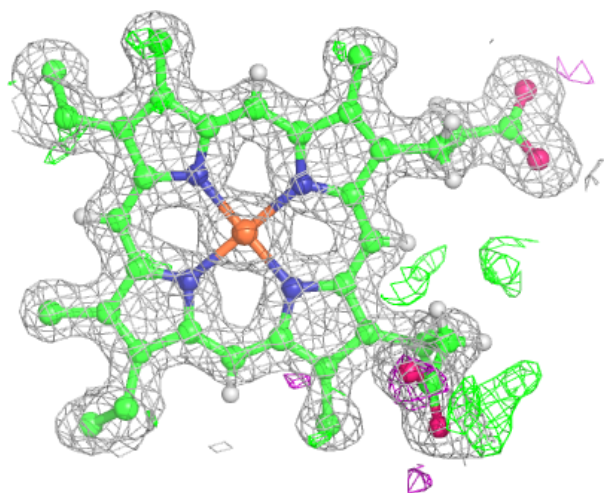
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around HEC A 1001:**

$2mF_o-DF_c$  (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.