



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:24 AM UTC

PDB ID : 8BCX / pdb_00008bcx
Title : Crystal structure of NrfA-1 from *Geobacter metallireducens*
Authors : Denkhaus, L.; Siffert, F.; Einsle, O.
Deposited on : 2022-10-17
Resolution : 1.94 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 2022.3.0, CSD as543be (2022)
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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

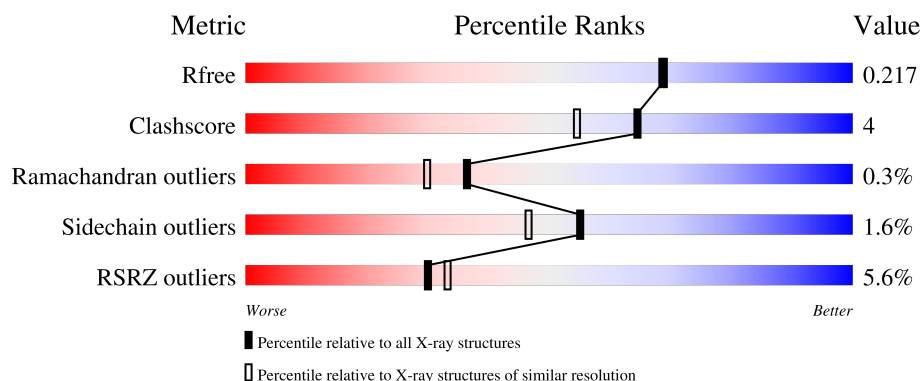
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	492	3% 81% 8% 11%
1	B	492	6% 79% 9% 12%
1	C	492	7% 80% 9% 10%
1	D	492	4% 80% 9% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15471 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Nitrite reductase (cytochrome; ammonia-forming).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3433	2185	594	631	23			
1	B	434	Total	C	N	O	S	0	0	0
			3398	2158	586	631	23			
1	C	443	Total	C	N	O	S	0	0	0
			3489	2217	608	641	23			
1	D	444	Total	C	N	O	S	0	0	0
			3493	2222	605	643	23			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	initiating methionine	UNP Q39YY5
A	-2	LYS	-	expression tag	UNP Q39YY5
A	-1	LYS	-	expression tag	UNP Q39YY5
A	0	THR	-	expression tag	UNP Q39YY5
A	1	ALA	-	expression tag	UNP Q39YY5
A	2	ILE	-	expression tag	UNP Q39YY5
A	3	ALA	-	expression tag	UNP Q39YY5
A	4	ILE	-	expression tag	UNP Q39YY5
A	5	ALA	-	expression tag	UNP Q39YY5
A	6	VAL	-	expression tag	UNP Q39YY5
A	7	ALA	-	expression tag	UNP Q39YY5
A	8	LEU	-	expression tag	UNP Q39YY5
A	9	ALA	-	expression tag	UNP Q39YY5
A	10	GLY	-	expression tag	UNP Q39YY5
A	11	PHE	-	expression tag	UNP Q39YY5
A	12	ALA	-	expression tag	UNP Q39YY5
A	13	THR	-	expression tag	UNP Q39YY5
A	14	VAL	-	expression tag	UNP Q39YY5
A	15	ALA	-	expression tag	UNP Q39YY5
A	16	GLN	-	expression tag	UNP Q39YY5
A	17	ALA	-	expression tag	UNP Q39YY5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	18	ALA	-	expression tag	UNP Q39YY5
A	19	SER	-	expression tag	UNP Q39YY5
A	20	TRP	-	expression tag	UNP Q39YY5
A	21	SER	-	expression tag	UNP Q39YY5
A	22	HIS	-	expression tag	UNP Q39YY5
A	23	PRO	-	expression tag	UNP Q39YY5
A	24	GLN	-	expression tag	UNP Q39YY5
A	25	PHE	-	expression tag	UNP Q39YY5
A	26	GLU	-	expression tag	UNP Q39YY5
A	27	LYS	-	expression tag	UNP Q39YY5
A	28	GLY	-	expression tag	UNP Q39YY5
A	29	ALA	-	expression tag	UNP Q39YY5
B	-3	MET	-	initiating methionine	UNP Q39YY5
B	-2	LYS	-	expression tag	UNP Q39YY5
B	-1	LYS	-	expression tag	UNP Q39YY5
B	0	THR	-	expression tag	UNP Q39YY5
B	1	ALA	-	expression tag	UNP Q39YY5
B	2	ILE	-	expression tag	UNP Q39YY5
B	3	ALA	-	expression tag	UNP Q39YY5
B	4	ILE	-	expression tag	UNP Q39YY5
B	5	ALA	-	expression tag	UNP Q39YY5
B	6	VAL	-	expression tag	UNP Q39YY5
B	7	ALA	-	expression tag	UNP Q39YY5
B	8	LEU	-	expression tag	UNP Q39YY5
B	9	ALA	-	expression tag	UNP Q39YY5
B	10	GLY	-	expression tag	UNP Q39YY5
B	11	PHE	-	expression tag	UNP Q39YY5
B	12	ALA	-	expression tag	UNP Q39YY5
B	13	THR	-	expression tag	UNP Q39YY5
B	14	VAL	-	expression tag	UNP Q39YY5
B	15	ALA	-	expression tag	UNP Q39YY5
B	16	GLN	-	expression tag	UNP Q39YY5
B	17	ALA	-	expression tag	UNP Q39YY5
B	18	ALA	-	expression tag	UNP Q39YY5
B	19	SER	-	expression tag	UNP Q39YY5
B	20	TRP	-	expression tag	UNP Q39YY5
B	21	SER	-	expression tag	UNP Q39YY5
B	22	HIS	-	expression tag	UNP Q39YY5
B	23	PRO	-	expression tag	UNP Q39YY5
B	24	GLN	-	expression tag	UNP Q39YY5
B	25	PHE	-	expression tag	UNP Q39YY5
B	26	GLU	-	expression tag	UNP Q39YY5

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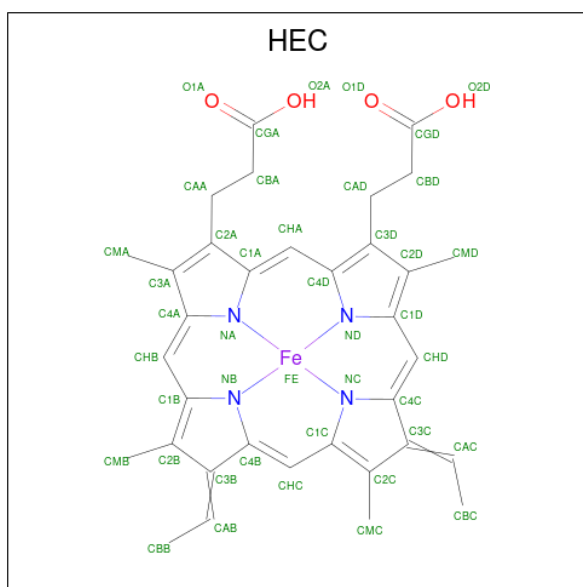
Chain	Residue	Modelled	Actual	Comment	Reference
B	27	LYS	-	expression tag	UNP Q39YY5
B	28	GLY	-	expression tag	UNP Q39YY5
B	29	ALA	-	expression tag	UNP Q39YY5
C	-3	MET	-	initiating methionine	UNP Q39YY5
C	-2	LYS	-	expression tag	UNP Q39YY5
C	-1	LYS	-	expression tag	UNP Q39YY5
C	0	THR	-	expression tag	UNP Q39YY5
C	1	ALA	-	expression tag	UNP Q39YY5
C	2	ILE	-	expression tag	UNP Q39YY5
C	3	ALA	-	expression tag	UNP Q39YY5
C	4	ILE	-	expression tag	UNP Q39YY5
C	5	ALA	-	expression tag	UNP Q39YY5
C	6	VAL	-	expression tag	UNP Q39YY5
C	7	ALA	-	expression tag	UNP Q39YY5
C	8	LEU	-	expression tag	UNP Q39YY5
C	9	ALA	-	expression tag	UNP Q39YY5
C	10	GLY	-	expression tag	UNP Q39YY5
C	11	PHE	-	expression tag	UNP Q39YY5
C	12	ALA	-	expression tag	UNP Q39YY5
C	13	THR	-	expression tag	UNP Q39YY5
C	14	VAL	-	expression tag	UNP Q39YY5
C	15	ALA	-	expression tag	UNP Q39YY5
C	16	GLN	-	expression tag	UNP Q39YY5
C	17	ALA	-	expression tag	UNP Q39YY5
C	18	ALA	-	expression tag	UNP Q39YY5
C	19	SER	-	expression tag	UNP Q39YY5
C	20	TRP	-	expression tag	UNP Q39YY5
C	21	SER	-	expression tag	UNP Q39YY5
C	22	HIS	-	expression tag	UNP Q39YY5
C	23	PRO	-	expression tag	UNP Q39YY5
C	24	GLN	-	expression tag	UNP Q39YY5
C	25	PHE	-	expression tag	UNP Q39YY5
C	26	GLU	-	expression tag	UNP Q39YY5
C	27	LYS	-	expression tag	UNP Q39YY5
C	28	GLY	-	expression tag	UNP Q39YY5
C	29	ALA	-	expression tag	UNP Q39YY5
D	-3	MET	-	initiating methionine	UNP Q39YY5
D	-2	LYS	-	expression tag	UNP Q39YY5
D	-1	LYS	-	expression tag	UNP Q39YY5
D	0	THR	-	expression tag	UNP Q39YY5
D	1	ALA	-	expression tag	UNP Q39YY5
D	2	ILE	-	expression tag	UNP Q39YY5

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Chain	Residue	Modelled	Actual	Comment	Reference
D	3	ALA	-	expression tag	UNP Q39YY5
D	4	ILE	-	expression tag	UNP Q39YY5
D	5	ALA	-	expression tag	UNP Q39YY5
D	6	VAL	-	expression tag	UNP Q39YY5
D	7	ALA	-	expression tag	UNP Q39YY5
D	8	LEU	-	expression tag	UNP Q39YY5
D	9	ALA	-	expression tag	UNP Q39YY5
D	10	GLY	-	expression tag	UNP Q39YY5
D	11	PHE	-	expression tag	UNP Q39YY5
D	12	ALA	-	expression tag	UNP Q39YY5
D	13	THR	-	expression tag	UNP Q39YY5
D	14	VAL	-	expression tag	UNP Q39YY5
D	15	ALA	-	expression tag	UNP Q39YY5
D	16	GLN	-	expression tag	UNP Q39YY5
D	17	ALA	-	expression tag	UNP Q39YY5
D	18	ALA	-	expression tag	UNP Q39YY5
D	19	SER	-	expression tag	UNP Q39YY5
D	20	TRP	-	expression tag	UNP Q39YY5
D	21	SER	-	expression tag	UNP Q39YY5
D	22	HIS	-	expression tag	UNP Q39YY5
D	23	PRO	-	expression tag	UNP Q39YY5
D	24	GLN	-	expression tag	UNP Q39YY5
D	25	PHE	-	expression tag	UNP Q39YY5
D	26	GLU	-	expression tag	UNP Q39YY5
D	27	LYS	-	expression tag	UNP Q39YY5
D	28	GLY	-	expression tag	UNP Q39YY5
D	29	ALA	-	expression tag	UNP Q39YY5

- Molecule 2 is HEME C (CCD ID: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



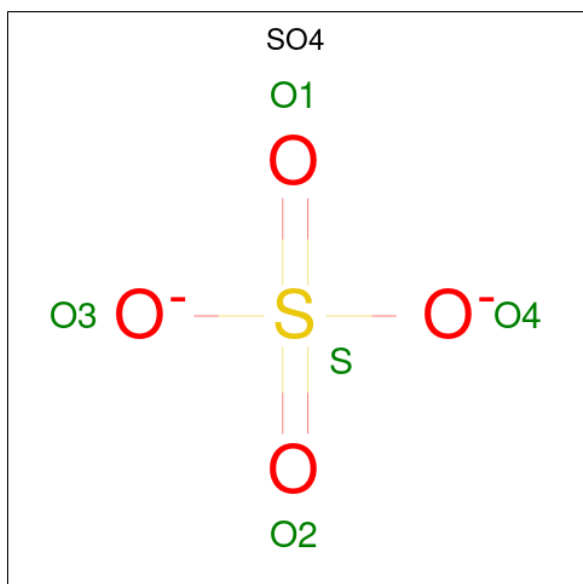
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0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

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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

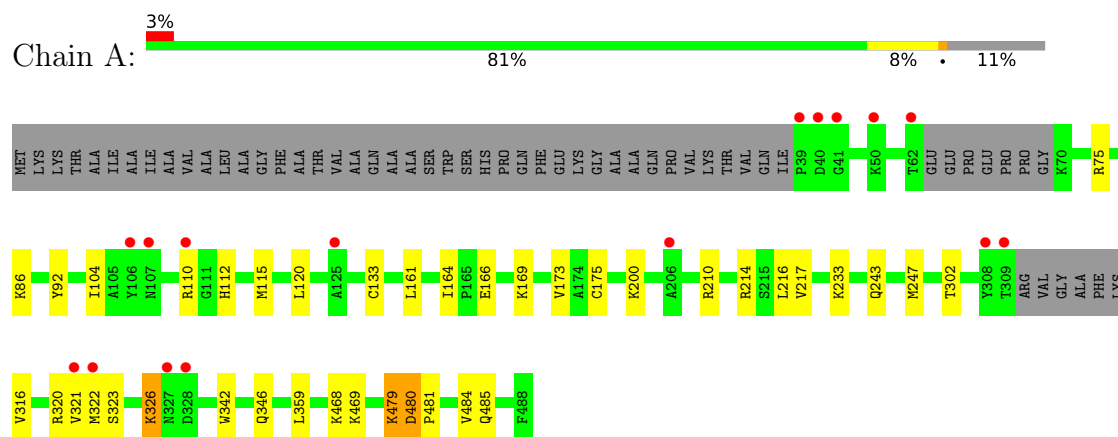
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	186	Total	O	0	1
			187	187		
4	B	154	Total	O	0	0
			154	154		
4	C	188	Total	O	0	1
			189	189		
4	D	197	Total	O	0	1
			198	198		

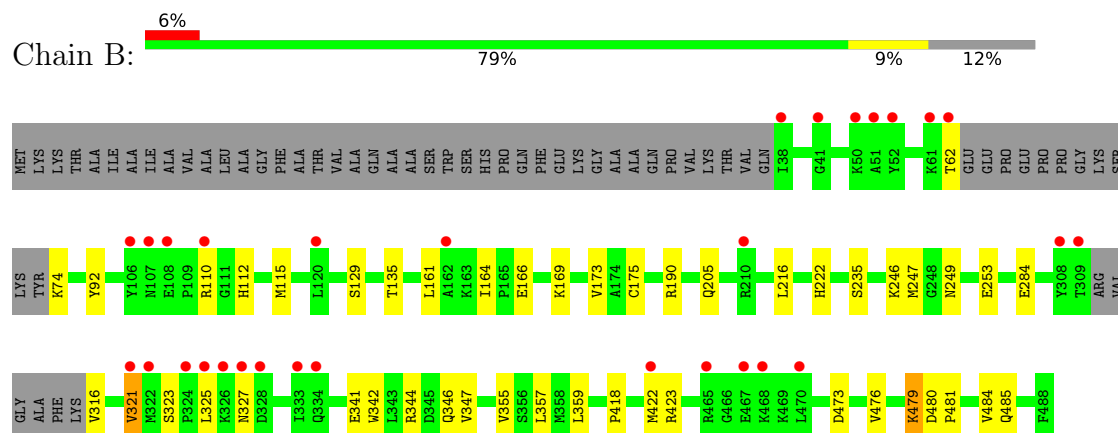
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

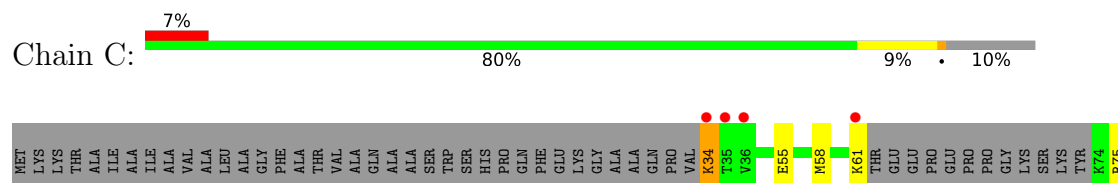
- Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)

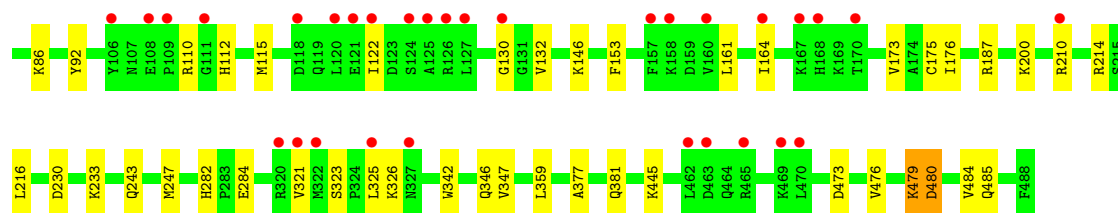


- Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)

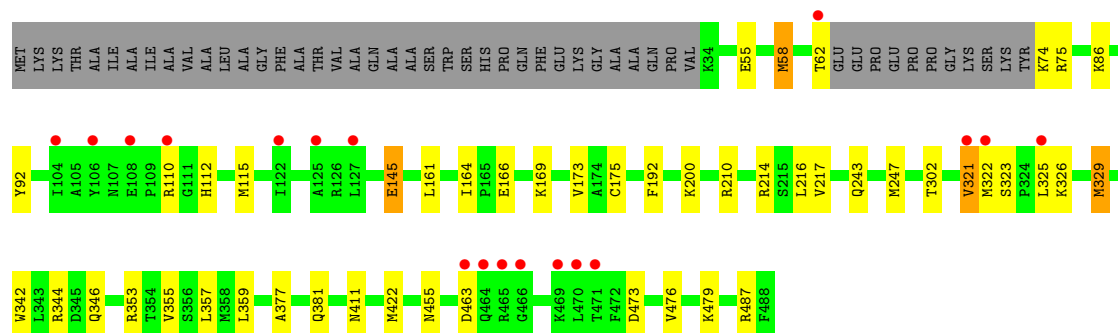
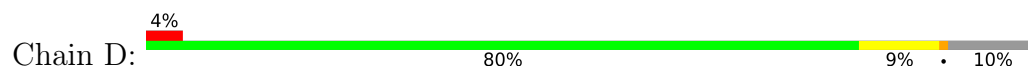


- Molecule 1: Nitrite reductase (cytochrome; ammonia-forming)





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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.08Å 91.97Å 123.94Å 90.00° 99.06° 90.00°	Depositor
Resolution (Å)	122.39 – 1.94 122.39 – 1.94	Depositor EDS
% Data completeness (in resolution range)	62.1 (122.39-1.94) 62.1 (122.39-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 1.94Å)	Xtriage
Refinement program	BUSTER 2.10.4 (8-JUN-2022)	Depositor
R, R_{free}	0.193 , 0.227 0.187 , 0.217	Depositor DCC
R_{free} test set	4540 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15471	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 45.55 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.2998e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEC, SO4

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.72	0/3510	1.02	3/4733 (0.1%)
1	B	0.72	0/3473	1.02	2/4690 (0.0%)
1	C	0.73	0/3567	1.03	4/4814 (0.1%)
1	D	0.77	2/3572 (0.1%)	1.03	3/4823 (0.1%)
All	All	0.74	2/14122 (0.0%)	1.03	12/19060 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	329	MET	SD-CE	-7.71	1.60	1.79
1	D	58	MET	SD-CE	-6.48	1.63	1.79

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	480	ASP	CA-CB-CG	6.94	119.54	112.60
1	D	479	LYS	CA-C-N	6.33	130.29	120.60
1	D	479	LYS	C-N-CA	6.33	130.29	120.60
1	A	479	LYS	CA-C-N	5.84	129.55	120.68
1	A	479	LYS	C-N-CA	5.84	129.55	120.68
1	B	479	LYS	CA-C-N	5.71	129.34	120.60
1	B	479	LYS	C-N-CA	5.71	129.34	120.60
1	A	480	ASP	CA-CB-CG	5.40	118.00	112.60
1	C	479	LYS	CA-C-N	5.22	128.59	120.60
1	C	479	LYS	C-N-CA	5.22	128.59	120.60
1	C	230	ASP	CA-CB-CG	5.17	117.77	112.60
1	D	411	ASN	CA-CB-CG	-5.07	107.53	112.60

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	3433	0	3390	25	0
1	B	3398	0	3339	25	0
1	C	3489	0	3453	27	0
1	D	3493	0	3450	31	0
2	A	215	0	150	6	0
2	B	215	0	150	6	0
2	C	215	0	150	2	0
2	D	215	0	150	6	0
3	A	15	0	0	0	0
3	B	20	0	0	0	0
3	C	15	0	0	0	0
3	D	20	0	0	0	0
4	A	187	0	0	0	0
4	B	154	0	0	0	0
4	C	189	0	0	1	0
4	D	198	0	0	1	0
All	All	15471	0	14232	114	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 4.

All (114) 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)
2:B:503:HEC:HHA	2:B:503:HEC:HBD1	1.60	0.83
1:D:455:ASN:HB2	1:D:487:ARG:HE	1.42	0.81
1:A:210:ARG:HE	1:A:214:ARG:HH22	1.33	0.74
1:A:480:ASP:OD1	1:A:481:PRO:HD2	1.91	0.70
1:A:210:ARG:HE	1:A:214:ARG:NH2	1.88	0.69
1:A:104:ILE:HD11	1:A:469:LYS:HE3	1.74	0.69
1:A:75:ARG:NH1	2:A:503:HEC:O2A	2.29	0.65
1:A:104:ILE:CD1	1:A:469:LYS:HE3	2.28	0.64
1:D:353:ARG:HG2	1:D:422:MET:CE	2.29	0.62
1:D:353:ARG:HG2	1:D:422:MET:HE1	1.81	0.61
1:B:112:HIS:HB3	1:B:173:VAL:HB	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:SER:HB3	1:A:326:LYS:HG3	1.83	0.60
1:C:210:ARG:NH1	1:C:214:ARG:HH22	2.00	0.60
1:D:55:GLU:HA	1:D:58:MET:HE2	1.85	0.58
1:C:480:ASP:HB3	1:C:484:VAL:HB	1.86	0.57
1:D:112:HIS:HB3	1:D:173:VAL:HB	1.86	0.56
1:D:74:LYS:HD2	1:D:355:VAL:HG21	1.86	0.56
1:B:62:THR:OG1	1:B:110:ARG:O	2.24	0.56
2:D:503:HEC:HBA1	4:D:746:HOH:O	2.06	0.55
1:D:357:LEU:CD1	1:D:422:MET:SD	2.95	0.55
1:D:455:ASN:HA	1:D:487:ARG:HG3	1.88	0.55
2:D:503:HEC:HBD1	2:D:503:HEC:HHA	1.89	0.55
1:C:342:TRP:O	1:C:346:GLN:HG2	2.07	0.54
1:A:173:VAL:HG22	2:A:504:HEC:HBC2	1.90	0.54
1:C:321:VAL:HG23	1:C:321:VAL:O	2.07	0.54
1:A:302:THR:HG21	2:A:505:HEC:HMD2	1.89	0.53
1:D:75:ARG:HH22	1:D:110:ARG:NH2	2.07	0.53
1:B:216:LEU:HD11	1:B:247:MET:HE1	1.90	0.53
1:B:418:PRO:O	1:B:422:MET:HG2	2.09	0.53
1:D:115:MET:HE2	2:D:504:HEC:HBD2	1.90	0.53
1:C:200:LYS:HD2	1:C:243:GLN:HG3	1.91	0.52
1:C:216:LEU:HD11	1:C:247:MET:HE1	1.90	0.52
1:D:357:LEU:HD12	1:D:422:MET:SD	2.49	0.52
1:D:216:LEU:HD11	1:D:247:MET:HE1	1.91	0.52
1:A:161:LEU:HD12	1:A:164:ILE:HD12	1.92	0.52
1:D:200:LYS:HD2	1:D:243:GLN:HG3	1.92	0.52
2:B:503:HEC:HBD1	2:B:503:HEC:CHA	2.32	0.52
1:C:115:MET:HE2	2:C:504:HEC:HBD2	1.91	0.51
1:C:75:ARG:HH22	1:C:110:ARG:NH2	2.08	0.51
1:A:216:LEU:HD11	1:A:247:MET:HE1	1.93	0.51
1:B:479:LYS:HG3	1:B:485:GLN:HG3	1.93	0.51
1:B:480:ASP:OD1	1:B:481:PRO:HD2	2.10	0.51
1:D:62:THR:OG1	1:D:110:ARG:O	2.29	0.51
1:B:115:MET:HE2	2:B:504:HEC:HBD2	1.92	0.51
1:D:210:ARG:HH21	1:D:214:ARG:HH22	1.59	0.50
1:D:323:SER:HB3	1:D:326:LYS:HB3	1.93	0.50
1:D:325:LEU:HD22	1:D:329:MET:HE1	1.94	0.50
1:A:112:HIS:HB3	1:A:173:VAL:HB	1.93	0.50
1:A:115:MET:HE2	2:A:504:HEC:HBD2	1.92	0.50
1:B:161:LEU:HD12	1:B:164:ILE:HD12	1.94	0.50
1:A:200:LYS:HD2	1:A:243:GLN:HG3	1.92	0.50
1:C:445:LYS:HD2	4:C:758:HOH:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:ASP:CB	1:A:484:VAL:HB	2.42	0.49
1:B:480:ASP:CB	1:B:484:VAL:HB	2.42	0.49
1:C:132:VAL:HG22	1:C:153:PHE:HD1	1.77	0.49
1:D:55:GLU:HA	1:D:58:MET:CE	2.43	0.49
1:D:342:TRP:O	1:D:346:GLN:HG2	2.12	0.49
1:B:325:LEU:HG	2:B:502:HEC:HBD2	1.95	0.49
1:C:161:LEU:HD12	1:C:164:ILE:HD12	1.94	0.49
1:D:455:ASN:CB	1:D:487:ARG:HE	2.21	0.48
2:B:501:HEC:O2A	2:B:504:HEC:O2D	2.31	0.48
1:C:323:SER:HB3	1:C:326:LYS:HB2	1.96	0.48
1:A:480:ASP:HB3	1:A:484:VAL:HB	1.96	0.48
1:B:135:THR:O	1:B:190:ARG:NH1	2.46	0.48
1:C:55:GLU:HA	1:C:58:MET:HE2	1.95	0.48
1:D:302:THR:HG21	2:D:501:HEC:HMD2	1.97	0.47
1:B:74:LYS:HD3	1:B:355:VAL:HG21	1.96	0.46
1:B:342:TRP:O	1:B:346:GLN:HG2	2.15	0.46
1:D:161:LEU:HD12	1:D:164:ILE:HD12	1.96	0.46
1:C:34:LYS:HA	1:C:34:LYS:HD2	1.73	0.46
1:B:323:SER:OG	2:B:502:HEC:O1D	2.30	0.46
1:C:480:ASP:CB	1:C:484:VAL:HB	2.46	0.45
1:C:173:VAL:HG22	2:C:504:HEC:HBC2	1.98	0.45
1:A:342:TRP:O	1:A:346:GLN:HG2	2.16	0.45
2:A:505:HEC:HHA	2:A:505:HEC:HBA1	1.99	0.45
1:B:129:SER:HA	1:B:235:SER:OG	2.17	0.44
1:C:377:ALA:O	1:C:381:GLN:HG3	2.18	0.44
1:B:325:LEU:HD11	1:B:347:VAL:HG11	1.99	0.44
1:D:377:ALA:O	1:D:381:GLN:HG3	2.18	0.44
1:C:473:ASP:HB3	1:C:476:VAL:HG23	2.00	0.44
1:B:92:TYR:HE2	1:B:359:LEU:HD23	1.83	0.44
1:D:473:ASP:HB3	1:D:476:VAL:HG23	2.00	0.43
1:C:176:ILE:O	1:C:187:ARG:NH1	2.51	0.43
1:B:357:LEU:CD1	1:B:422:MET:SD	3.06	0.43
1:C:112:HIS:HB3	1:C:173:VAL:HB	2.01	0.43
1:D:329:MET:HE3	1:D:344:ARG:HG3	2.00	0.43
1:A:110:ARG:HA	2:A:504:HEC:O1D	2.18	0.43
1:B:253:GLU:CD	1:B:423:ARG:HH22	2.27	0.42
1:B:473:ASP:HB3	1:B:476:VAL:HG23	2.01	0.42
1:C:86:LYS:HD3	1:C:86:LYS:HA	1.89	0.42
1:B:246:LYS:HE2	1:B:249:ASN:HD22	1.85	0.42
1:C:55:GLU:HA	1:C:58:MET:CE	2.49	0.42
1:A:320:ARG:NH1	1:A:322:MET:SD	2.93	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:92:TYR:HE2	1:D:359:LEU:HD23	1.84	0.42
1:A:92:TYR:HE2	1:A:359:LEU:HD23	1.85	0.41
1:C:325:LEU:HD11	1:C:347:VAL:HG11	2.02	0.41
1:D:166:GLU:HA	1:D:169:LYS:HG2	2.02	0.41
1:A:166:GLU:HA	1:A:169:LYS:HG2	2.02	0.41
1:D:86:LYS:HD3	1:D:86:LYS:HA	1.85	0.41
1:A:120:LEU:HD11	1:A:133:CYS:HB3	2.02	0.41
1:B:480:ASP:HB2	1:B:484:VAL:HB	2.01	0.41
1:A:86:LYS:HA	1:A:86:LYS:HD3	1.92	0.41
1:B:222:HIS:ND1	1:B:284:GLU:OE1	2.49	0.41
1:C:479:LYS:HG3	1:C:485:GLN:HG3	2.02	0.41
1:B:166:GLU:HA	1:B:169:LYS:HG2	2.02	0.41
1:C:210:ARG:HH12	1:C:214:ARG:HH22	1.67	0.41
1:B:341:GLU:OE1	1:B:344:ARG:NH1	2.49	0.40
1:D:110:ARG:CZ	2:D:505:HEC:HBA1	2.52	0.40
1:A:322:MET:HE3	1:A:326:LYS:HB2	2.04	0.40
1:D:145:GLU:HG2	1:D:192:PHE:CD2	2.57	0.40
1:A:479:LYS:HG3	1:A:485:GLN:HG3	2.04	0.40
1:C:92:TYR:HE2	1:C:359:LEU:HD23	1.85	0.40
1:C:233:LYS:HB3	1:C:233:LYS:HE3	1.84	0.40
1:D:323:SER:OG	2:D:503:HEC:O1D	2.38	0.40

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	431/492 (88%)	414 (96%)	16 (4%)	1 (0%)	43	37
1	B	428/492 (87%)	413 (96%)	14 (3%)	1 (0%)	43	37
1	C	439/492 (89%)	421 (96%)	16 (4%)	2 (0%)	24	15
1	D	440/492 (89%)	422 (96%)	17 (4%)	1 (0%)	43	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1738/1968 (88%)	1670 (96%)	63 (4%)	5 (0%)	36 30

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	130	GLY
1	A	321	VAL
1	B	321	VAL
1	D	321	VAL
1	C	282	HIS

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	360/407 (88%)	354 (98%)	6 (2%)	53 44
1	B	358/407 (88%)	353 (99%)	5 (1%)	59 52
1	C	368/407 (90%)	362 (98%)	6 (2%)	55 46
1	D	368/407 (90%)	362 (98%)	6 (2%)	55 46
All	All	1454/1628 (89%)	1431 (98%)	23 (2%)	55 46

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	175	CYS
1	A	217	VAL
1	A	233	LYS
1	A	316	VAL
1	A	326	LYS
1	A	468	LYS
1	B	175	CYS
1	B	205	GLN
1	B	316	VAL
1	B	321	VAL

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Mol	Chain	Res	Type
1	B	327	ASN
1	C	34	LYS
1	C	61	LYS
1	C	122	ILE
1	C	146	LYS
1	C	175	CYS
1	C	284	GLU
1	D	145	GLU
1	D	175	CYS
1	D	217	VAL
1	D	321	VAL
1	D	322	MET
1	D	463	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	384	GLN
1	B	249	ASN
1	B	270	GLN
1	B	327	ASN
1	C	258	GLN
1	C	270	GLN
1	D	119	GLN
1	D	270	GLN
1	D	346	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

34 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	SO4	D	508	-	4,4,4	0.37	0	6,6,6	0.22	0
3	SO4	D	509	-	4,4,4	0.32	0	6,6,6	0.59	0
2	HEC	D	504	1	46,50,50	1.40	7 (15%)	58,82,82	0.59	0
2	HEC	A	503	1	46,50,50	1.54	8 (17%)	58,82,82	0.91	2 (3%)
2	HEC	A	505	1	46,50,50	1.47	5 (10%)	58,82,82	0.62	0
2	HEC	B	503	1	46,50,50	1.48	5 (10%)	58,82,82	0.79	2 (3%)
3	SO4	B	508	-	4,4,4	0.35	0	6,6,6	0.19	0
2	HEC	A	501	1	46,50,50	1.38	5 (10%)	58,82,82	0.68	1 (1%)
2	HEC	C	501	1	46,50,50	1.48	6 (13%)	58,82,82	0.72	0
3	SO4	D	506	-	4,4,4	0.36	0	6,6,6	0.79	0
3	SO4	A	506	-	4,4,4	0.35	0	6,6,6	0.23	0
2	HEC	B	504	1	46,50,50	1.40	4 (8%)	58,82,82	0.58	0
3	SO4	C	506	-	4,4,4	0.33	0	6,6,6	1.09	1 (16%)
2	HEC	C	505	1	46,50,50	1.45	4 (8%)	58,82,82	0.61	0
2	HEC	C	502	1	46,50,50	1.48	6 (13%)	58,82,82	0.61	0
2	HEC	C	503	4,1	46,50,50	1.38	4 (8%)	58,82,82	0.67	0
3	SO4	A	507	-	4,4,4	0.32	0	6,6,6	0.19	0
3	SO4	A	508	-	4,4,4	0.30	0	6,6,6	0.15	0
2	HEC	D	503	1	46,50,50	1.53	6 (13%)	58,82,82	0.80	2 (3%)
2	HEC	D	505	4,1	46,50,50	1.39	5 (10%)	58,82,82	0.62	0
2	HEC	D	502	1	46,50,50	1.49	6 (13%)	58,82,82	0.83	1 (1%)
3	SO4	D	507	-	4,4,4	0.31	0	6,6,6	0.24	0
2	HEC	A	504	1	46,50,50	1.43	4 (8%)	58,82,82	0.58	0
3	SO4	B	507	-	4,4,4	0.31	0	6,6,6	0.44	0
2	HEC	B	501	4,1	46,50,50	1.48	4 (8%)	58,82,82	0.75	1 (1%)
3	SO4	C	507	-	4,4,4	0.36	0	6,6,6	0.75	0
3	SO4	C	508	-	4,4,4	0.33	0	6,6,6	0.36	0
2	HEC	D	501	1	46,50,50	1.44	5 (10%)	58,82,82	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEC	A	502	4,1	46,50,50	1.51	5 (10%)	58,82,82	0.58	0
3	SO4	B	506	-	4,4,4	0.41	0	6,6,6	0.49	0
2	HEC	B	502	1	46,50,50	1.56	5 (10%)	58,82,82	0.55	0
2	HEC	B	505	1	46,50,50	1.49	5 (10%)	58,82,82	0.60	0
3	SO4	B	509	-	4,4,4	0.36	0	6,6,6	0.19	0
2	HEC	C	504	1	46,50,50	1.43	6 (13%)	58,82,82	0.62	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	D	504	1	-	6/14/54/54	-
2	HEC	A	503	1	-	10/14/54/54	-
2	HEC	A	505	1	-	11/14/54/54	-
2	HEC	B	503	1	-	7/14/54/54	-
2	HEC	A	501	1	-	6/14/54/54	-
2	HEC	C	501	1	-	8/14/54/54	-
2	HEC	B	504	1	-	8/14/54/54	-
2	HEC	C	505	1	-	8/14/54/54	-
2	HEC	C	502	1	-	5/14/54/54	-
2	HEC	C	503	4,1	-	5/14/54/54	-
2	HEC	D	503	1	-	9/14/54/54	-
2	HEC	D	505	4,1	-	7/14/54/54	-
2	HEC	D	502	1	-	12/14/54/54	-
2	HEC	A	504	1	-	8/14/54/54	-
2	HEC	B	501	4,1	-	11/14/54/54	-
2	HEC	D	501	1	-	8/14/54/54	-
2	HEC	A	502	4,1	-	10/14/54/54	-
2	HEC	B	502	1	-	7/14/54/54	-
2	HEC	B	505	1	-	8/14/54/54	-
2	HEC	C	504	1	-	6/14/54/54	-

All (105) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEC	CBB-CAB	-4.87	1.31	1.49
2	C	501	HEC	CBC-CAC	-4.83	1.31	1.49
2	A	502	HEC	CBB-CAB	-4.81	1.31	1.49
2	B	502	HEC	CBC-CAC	-4.79	1.31	1.49
2	D	501	HEC	CBB-CAB	-4.76	1.31	1.49
2	D	502	HEC	CBC-CAC	-4.75	1.31	1.49
2	A	503	HEC	CBB-CAB	-4.68	1.32	1.49
2	B	503	HEC	CBC-CAC	-4.53	1.32	1.49
2	C	505	HEC	CBB-CAB	-4.42	1.33	1.49
2	B	505	HEC	CBB-CAB	-4.40	1.33	1.49
2	B	503	HEC	CBB-CAB	-4.39	1.33	1.49
2	A	505	HEC	CBB-CAB	-4.37	1.33	1.49
2	B	505	HEC	CBC-CAC	-4.37	1.33	1.49
2	C	505	HEC	CBC-CAC	-4.35	1.33	1.49
2	C	503	HEC	CBC-CAC	-4.31	1.33	1.49
2	A	504	HEC	CBC-CAC	-4.18	1.34	1.49
2	D	505	HEC	CBC-CAC	-4.16	1.34	1.49
2	C	502	HEC	CBC-CAC	-4.16	1.34	1.49
2	C	504	HEC	CBC-CAC	-4.16	1.34	1.49
2	A	505	HEC	CBC-CAC	-4.13	1.34	1.49
2	A	501	HEC	CBC-CAC	-4.11	1.34	1.49
2	D	503	HEC	CBC-CAC	-4.11	1.34	1.49
2	B	502	HEC	CBB-CAB	-4.10	1.34	1.49
2	A	503	HEC	CBC-CAC	-4.08	1.34	1.49
2	A	502	HEC	CBC-CAC	-4.00	1.34	1.49
2	D	502	HEC	CBB-CAB	-3.98	1.34	1.49
2	D	503	HEC	CBB-CAB	-3.96	1.34	1.49
2	D	503	HEC	CAC-C3C	3.92	1.47	1.35
2	A	503	HEC	CAC-C3C	3.92	1.47	1.35
2	C	502	HEC	CBB-CAB	-3.91	1.35	1.49
2	B	504	HEC	CAC-C3C	3.87	1.47	1.35
2	D	501	HEC	CAC-C3C	3.87	1.47	1.35
2	C	502	HEC	CAC-C3C	3.86	1.47	1.35
2	D	501	HEC	CBC-CAC	-3.86	1.35	1.49
2	A	501	HEC	CAC-C3C	3.85	1.47	1.35
2	C	504	HEC	CAC-C3C	3.84	1.47	1.35
2	D	503	HEC	CAB-C3B	3.84	1.47	1.35
2	B	501	HEC	CAC-C3C	3.84	1.47	1.35
2	D	504	HEC	CAC-C3C	3.84	1.47	1.35
2	A	505	HEC	CAC-C3C	3.84	1.47	1.35
2	C	505	HEC	CAB-C3B	3.82	1.47	1.35
2	B	505	HEC	CAB-C3B	3.82	1.47	1.35
2	A	505	HEC	CAB-C3B	3.82	1.47	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	503	HEC	CAC-C3C	3.82	1.47	1.35
2	B	505	HEC	CAC-C3C	3.81	1.47	1.35
2	C	501	HEC	CAC-C3C	3.81	1.47	1.35
2	D	505	HEC	CAC-C3C	3.80	1.47	1.35
2	B	504	HEC	CAB-C3B	3.80	1.47	1.35
2	C	504	HEC	CAB-C3B	3.79	1.47	1.35
2	A	504	HEC	CAB-C3B	3.79	1.47	1.35
2	D	501	HEC	CAB-C3B	3.77	1.47	1.35
2	D	505	HEC	CBB-CAB	-3.77	1.35	1.49
2	B	503	HEC	CAC-C3C	3.76	1.47	1.35
2	A	502	HEC	CAC-C3C	3.76	1.47	1.35
2	B	501	HEC	CBC-CAC	-3.76	1.35	1.49
2	B	504	HEC	CBC-CAC	-3.76	1.35	1.49
2	D	505	HEC	CAB-C3B	3.75	1.47	1.35
2	B	501	HEC	CAB-C3B	3.75	1.47	1.35
2	B	503	HEC	CAB-C3B	3.74	1.47	1.35
2	C	501	HEC	CAB-C3B	3.74	1.47	1.35
2	B	502	HEC	CAC-C3C	3.74	1.47	1.35
2	D	504	HEC	CBC-CAC	-3.73	1.35	1.49
2	D	502	HEC	CAB-C3B	3.73	1.47	1.35
2	C	505	HEC	CAC-C3C	3.73	1.47	1.35
2	B	502	HEC	CAB-C3B	3.72	1.47	1.35
2	D	504	HEC	CAB-C3B	3.72	1.47	1.35
2	A	504	HEC	CAC-C3C	3.71	1.47	1.35
2	A	501	HEC	CAB-C3B	3.70	1.47	1.35
2	C	503	HEC	CAB-C3B	3.70	1.47	1.35
2	A	501	HEC	CBB-CAB	-3.68	1.35	1.49
2	C	502	HEC	CAB-C3B	3.68	1.46	1.35
2	A	503	HEC	CAB-C3B	3.66	1.46	1.35
2	A	504	HEC	CBB-CAB	-3.65	1.36	1.49
2	D	502	HEC	CAC-C3C	3.64	1.46	1.35
2	B	504	HEC	CBB-CAB	-3.61	1.36	1.49
2	A	502	HEC	CAB-C3B	3.59	1.46	1.35
2	C	503	HEC	CBB-CAB	-3.57	1.36	1.49
2	C	501	HEC	CBB-CAB	-3.41	1.36	1.49
2	C	504	HEC	CBB-CAB	-3.26	1.37	1.49
2	D	503	HEC	CHA-C1A	3.13	1.44	1.38
2	D	504	HEC	CBB-CAB	-2.77	1.39	1.49
2	C	502	HEC	CHA-C1A	2.54	1.43	1.38
2	A	502	HEC	CHA-C1A	2.48	1.43	1.38
2	D	504	HEC	CHA-C1A	2.47	1.43	1.38
2	C	504	HEC	CHA-C1A	2.37	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	503	HEC	CHA-C1A	2.33	1.42	1.38
2	D	504	HEC	C1C-NC	-2.29	1.35	1.39
2	C	504	HEC	C1C-NC	-2.28	1.35	1.39
2	A	505	HEC	CHA-C1A	2.24	1.42	1.38
2	A	503	HEC	C1C-NC	-2.21	1.35	1.39
2	A	503	HEC	C1B-NB	-2.18	1.35	1.39
2	B	505	HEC	CHA-C1A	2.15	1.42	1.38
2	B	502	HEC	C1C-NC	-2.15	1.35	1.39
2	A	503	HEC	CHD-C1D	2.15	1.44	1.39
2	C	502	HEC	C1C-NC	-2.12	1.35	1.39
2	D	501	HEC	C1D-ND	-2.11	1.35	1.39
2	A	501	HEC	C1B-NB	-2.10	1.35	1.39
2	C	501	HEC	C1C-NC	-2.07	1.35	1.39
2	B	503	HEC	C1B-NB	-2.07	1.35	1.39
2	D	502	HEC	C1B-NB	-2.07	1.35	1.39
2	D	504	HEC	C1B-NB	-2.07	1.35	1.39
2	D	503	HEC	CHC-C1C	2.06	1.44	1.39
2	D	505	HEC	CHA-C1A	2.06	1.42	1.38
2	C	501	HEC	C1B-NB	-2.06	1.35	1.39
2	D	502	HEC	C1D-ND	-2.02	1.35	1.39

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	503	HEC	CAD-C3D-C4D	3.74	132.24	124.94
2	B	503	HEC	CAD-C3D-C4D	3.08	130.95	124.94
2	D	503	HEC	CAD-C3D-C4D	3.00	130.79	124.94
2	D	502	HEC	CAD-C3D-C4D	2.82	130.45	124.94
2	A	503	HEC	CAD-C3D-C2D	-2.71	120.98	127.07
3	C	506	SO4	O4-S-O2	-2.35	97.25	109.56
2	B	501	HEC	CAA-C2A-C3A	2.20	131.99	127.87
2	D	503	HEC	CAD-C3D-C2D	-2.07	122.44	127.07
2	B	503	HEC	CAD-C3D-C2D	-2.05	122.46	127.07
2	A	501	HEC	CAA-C2A-C1A	2.02	128.97	124.85

There are no chirality outliers.

All (160) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	HEC	C2B-C3B-CAB-CBB
2	A	501	HEC	C4B-C3B-CAB-CBB
2	A	501	HEC	C2C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
2	A	501	HEC	C4C-C3C-CAC-CBC
2	A	502	HEC	C2C-C3C-CAC-CBC
2	A	502	HEC	C4C-C3C-CAC-CBC
2	A	503	HEC	C2B-C3B-CAB-CBB
2	A	503	HEC	C4B-C3B-CAB-CBB
2	A	503	HEC	C2C-C3C-CAC-CBC
2	A	503	HEC	C4C-C3C-CAC-CBC
2	A	504	HEC	C2B-C3B-CAB-CBB
2	A	504	HEC	C4B-C3B-CAB-CBB
2	A	504	HEC	C2C-C3C-CAC-CBC
2	A	504	HEC	C4C-C3C-CAC-CBC
2	A	505	HEC	C2B-C3B-CAB-CBB
2	A	505	HEC	C4B-C3B-CAB-CBB
2	A	505	HEC	C2C-C3C-CAC-CBC
2	A	505	HEC	C4C-C3C-CAC-CBC
2	B	501	HEC	C1A-C2A-CAA-CBA
2	B	501	HEC	C3A-C2A-CAA-CBA
2	B	501	HEC	C2B-C3B-CAB-CBB
2	B	501	HEC	C4B-C3B-CAB-CBB
2	B	501	HEC	C2C-C3C-CAC-CBC
2	B	501	HEC	C4C-C3C-CAC-CBC
2	B	502	HEC	C2B-C3B-CAB-CBB
2	B	502	HEC	C4B-C3B-CAB-CBB
2	B	502	HEC	C2C-C3C-CAC-CBC
2	B	502	HEC	C4C-C3C-CAC-CBC
2	B	503	HEC	C2B-C3B-CAB-CBB
2	B	503	HEC	C2C-C3C-CAC-CBC
2	B	503	HEC	C4C-C3C-CAC-CBC
2	B	503	HEC	C4D-C3D-CAD-CBD
2	B	504	HEC	C2B-C3B-CAB-CBB
2	B	504	HEC	C4B-C3B-CAB-CBB
2	B	504	HEC	C2C-C3C-CAC-CBC
2	B	504	HEC	C4C-C3C-CAC-CBC
2	B	505	HEC	C2B-C3B-CAB-CBB
2	B	505	HEC	C4B-C3B-CAB-CBB
2	B	505	HEC	C2C-C3C-CAC-CBC
2	B	505	HEC	C4C-C3C-CAC-CBC
2	C	501	HEC	C2B-C3B-CAB-CBB
2	C	501	HEC	C4B-C3B-CAB-CBB
2	C	502	HEC	C2B-C3B-CAB-CBB
2	C	502	HEC	C4B-C3B-CAB-CBB
2	C	502	HEC	C2C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
2	C	502	HEC	C4C-C3C-CAC-CBC
2	C	503	HEC	C2B-C3B-CAB-CBB
2	C	503	HEC	C4B-C3B-CAB-CBB
2	C	503	HEC	C2C-C3C-CAC-CBC
2	C	503	HEC	C4C-C3C-CAC-CBC
2	C	504	HEC	C2B-C3B-CAB-CBB
2	C	504	HEC	C4B-C3B-CAB-CBB
2	C	504	HEC	C2C-C3C-CAC-CBC
2	C	504	HEC	C4C-C3C-CAC-CBC
2	C	505	HEC	C2B-C3B-CAB-CBB
2	C	505	HEC	C4B-C3B-CAB-CBB
2	C	505	HEC	C2C-C3C-CAC-CBC
2	C	505	HEC	C4C-C3C-CAC-CBC
2	D	501	HEC	C2B-C3B-CAB-CBB
2	D	501	HEC	C4B-C3B-CAB-CBB
2	D	501	HEC	C2C-C3C-CAC-CBC
2	D	501	HEC	C4C-C3C-CAC-CBC
2	D	502	HEC	C2A-CAA-CBA-CGA
2	D	502	HEC	C2B-C3B-CAB-CBB
2	D	502	HEC	C4B-C3B-CAB-CBB
2	D	502	HEC	C2C-C3C-CAC-CBC
2	D	502	HEC	C4C-C3C-CAC-CBC
2	D	503	HEC	C2B-C3B-CAB-CBB
2	D	503	HEC	C4B-C3B-CAB-CBB
2	D	503	HEC	C2C-C3C-CAC-CBC
2	D	503	HEC	C4C-C3C-CAC-CBC
2	D	503	HEC	C4D-C3D-CAD-CBD
2	D	504	HEC	C2B-C3B-CAB-CBB
2	D	504	HEC	C4B-C3B-CAB-CBB
2	D	504	HEC	C2C-C3C-CAC-CBC
2	D	504	HEC	C4C-C3C-CAC-CBC
2	D	505	HEC	C2B-C3B-CAB-CBB
2	D	505	HEC	C4B-C3B-CAB-CBB
2	D	505	HEC	C2C-C3C-CAC-CBC
2	D	505	HEC	C4C-C3C-CAC-CBC
2	B	503	HEC	C2D-C3D-CAD-CBD
2	D	503	HEC	C2D-C3D-CAD-CBD
2	A	503	HEC	C2D-C3D-CAD-CBD
2	D	502	HEC	C2D-C3D-CAD-CBD
2	A	503	HEC	C4D-C3D-CAD-CBD
2	D	502	HEC	C4D-C3D-CAD-CBD
2	B	503	HEC	C3D-CAD-CBD-CGD

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Mol	Chain	Res	Type	Atoms
2	C	503	HEC	C2A-CAA-CBA-CGA
2	D	502	HEC	C3D-CAD-CBD-CGD
2	A	505	HEC	C3A-C2A-CAA-CBA
2	A	502	HEC	C3D-CAD-CBD-CGD
2	A	505	HEC	C2A-CAA-CBA-CGA
2	C	502	HEC	C3D-CAD-CBD-CGD
2	A	502	HEC	C2A-CAA-CBA-CGA
2	A	505	HEC	C1A-C2A-CAA-CBA
2	A	502	HEC	C4B-C3B-CAB-CBB
2	B	503	HEC	C4B-C3B-CAB-CBB
2	C	501	HEC	C4C-C3C-CAC-CBC
2	A	502	HEC	C2B-C3B-CAB-CBB
2	C	501	HEC	C2C-C3C-CAC-CBC
2	D	502	HEC	CAD-CBD-CGD-O2D
2	B	502	HEC	C2A-CAA-CBA-CGA
2	D	503	HEC	C3D-CAD-CBD-CGD
2	D	502	HEC	CAA-CBA-CGA-O2A
2	D	501	HEC	CAD-CBD-CGD-O2D
2	B	505	HEC	CAA-CBA-CGA-O2A
2	A	505	HEC	CAA-CBA-CGA-O1A
2	B	504	HEC	CAD-CBD-CGD-O1D
2	D	502	HEC	CAA-CBA-CGA-O1A
2	C	505	HEC	CAA-CBA-CGA-O2A
2	A	501	HEC	CAD-CBD-CGD-O2D
2	B	505	HEC	CAA-CBA-CGA-O1A
2	B	505	HEC	CAD-CBD-CGD-O1D
2	C	505	HEC	CAA-CBA-CGA-O1A
2	D	501	HEC	CAD-CBD-CGD-O1D
2	D	505	HEC	C2A-CAA-CBA-CGA
2	A	504	HEC	CAA-CBA-CGA-O1A
2	A	505	HEC	CAD-CBD-CGD-O1D
2	D	501	HEC	CAA-CBA-CGA-O2A
2	D	502	HEC	CAD-CBD-CGD-O1D
2	C	501	HEC	CAD-CBD-CGD-O1D
2	C	504	HEC	CAD-CBD-CGD-O1D
2	C	505	HEC	CAD-CBD-CGD-O1D
2	A	504	HEC	CAD-CBD-CGD-O1D
2	D	504	HEC	CAD-CBD-CGD-O1D
2	A	501	HEC	CAD-CBD-CGD-O1D
2	B	504	HEC	CAA-CBA-CGA-O1A
2	D	505	HEC	CAA-CBA-CGA-O1A
2	C	501	HEC	CAD-CBD-CGD-O2D

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Mol	Chain	Res	Type	Atoms
2	C	505	HEC	CAD-CBD-CGD-O2D
2	D	501	HEC	CAA-CBA-CGA-O1A
2	C	504	HEC	CAD-CBD-CGD-O2D
2	A	502	HEC	CAD-CBD-CGD-O2D
2	B	501	HEC	CAA-CBA-CGA-O1A
2	B	504	HEC	CAA-CBA-CGA-O2A
2	B	505	HEC	CAD-CBD-CGD-O2D
2	B	504	HEC	CAD-CBD-CGD-O2D
2	D	504	HEC	CAD-CBD-CGD-O2D
2	A	502	HEC	CAA-CBA-CGA-O2A
2	A	504	HEC	CAA-CBA-CGA-O2A
2	A	504	HEC	CAD-CBD-CGD-O2D
2	A	505	HEC	CAD-CBD-CGD-O2D
2	C	501	HEC	CAA-CBA-CGA-O2A
2	B	501	HEC	CAA-CBA-CGA-O2A
2	A	502	HEC	CAD-CBD-CGD-O1D
2	D	505	HEC	CAA-CBA-CGA-O2A
2	A	505	HEC	CAA-CBA-CGA-O2A
2	C	501	HEC	CAA-CBA-CGA-O1A
2	A	503	HEC	CAD-CBD-CGD-O2D
2	B	502	HEC	CAD-CBD-CGD-O1D
2	A	502	HEC	CAA-CBA-CGA-O1A
2	D	503	HEC	CAD-CBD-CGD-O2D
2	A	503	HEC	CAD-CBD-CGD-O1D
2	B	502	HEC	CAD-CBD-CGD-O2D
2	B	501	HEC	C2D-C3D-CAD-CBD
2	D	503	HEC	CAD-CBD-CGD-O1D
2	A	503	HEC	CAA-CBA-CGA-O2A
2	A	503	HEC	CAA-CBA-CGA-O1A
2	B	501	HEC	CAD-CBD-CGD-O1D
2	B	501	HEC	CAD-CBD-CGD-O2D

There are no ring outliers.

12 monomers are involved in 20 short contacts:

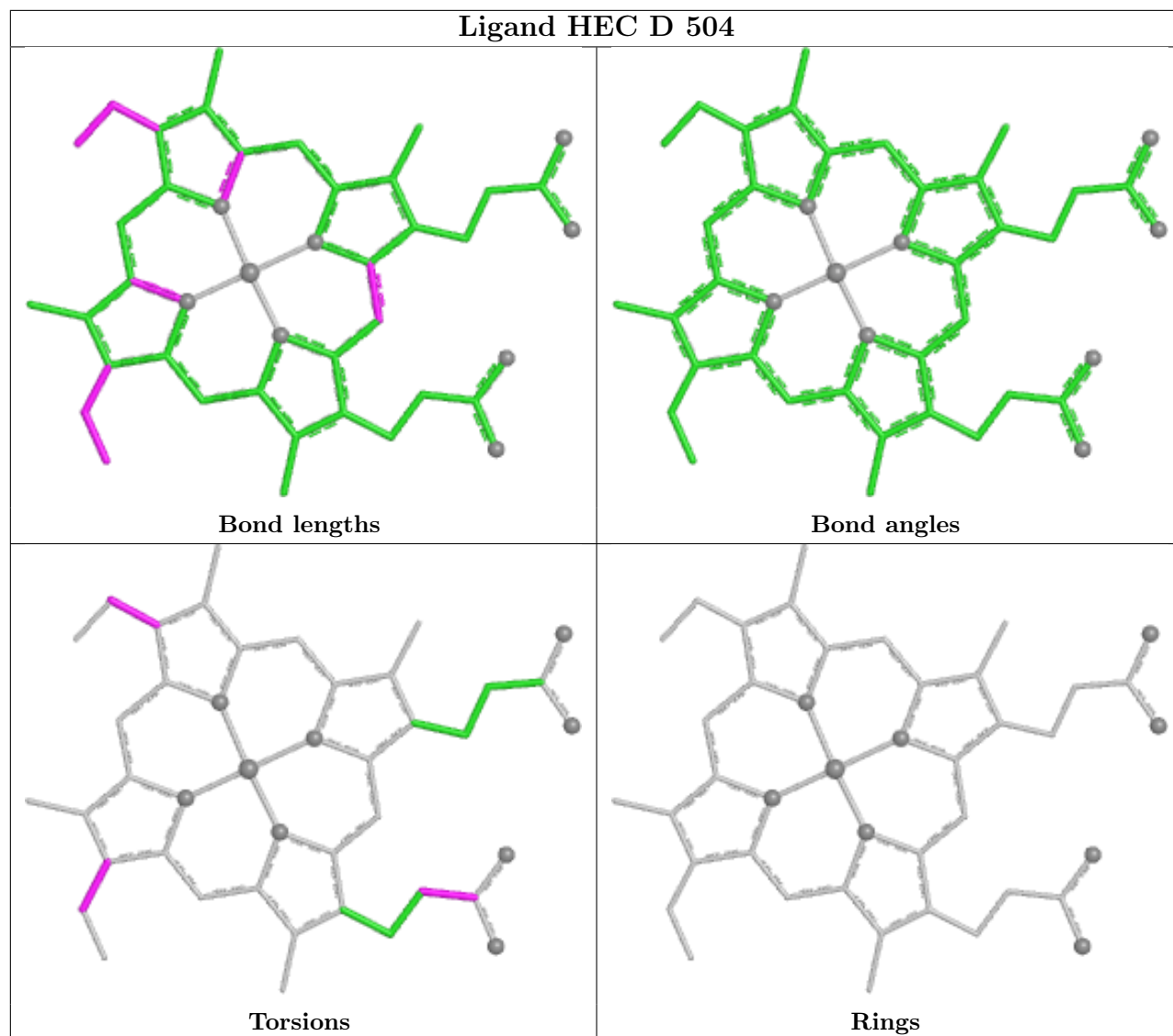
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	504	HEC	1	0
2	A	503	HEC	1	0
2	A	505	HEC	2	0
2	B	503	HEC	2	0
2	B	504	HEC	2	0
2	D	503	HEC	3	0

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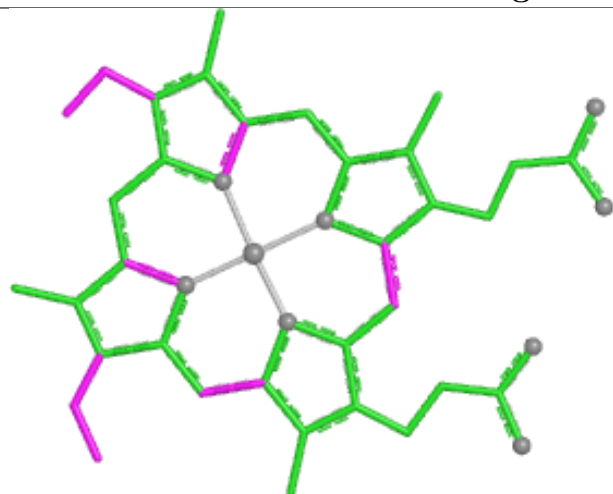
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	505	HEC	1	0
2	A	504	HEC	3	0
2	B	501	HEC	1	0
2	D	501	HEC	1	0
2	B	502	HEC	2	0
2	C	504	HEC	2	0

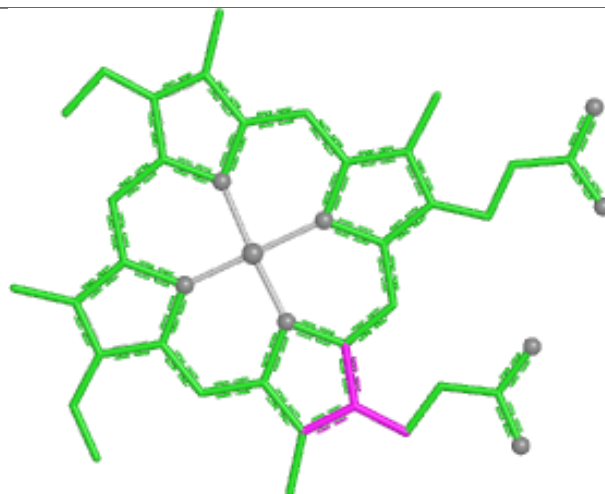
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



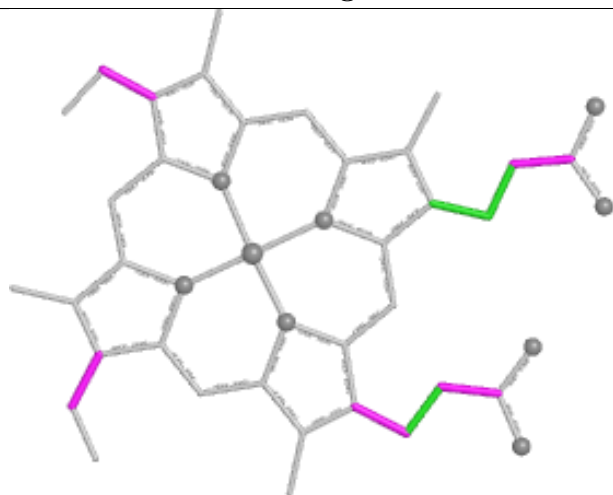
Ligand HEC A 503



Bond lengths



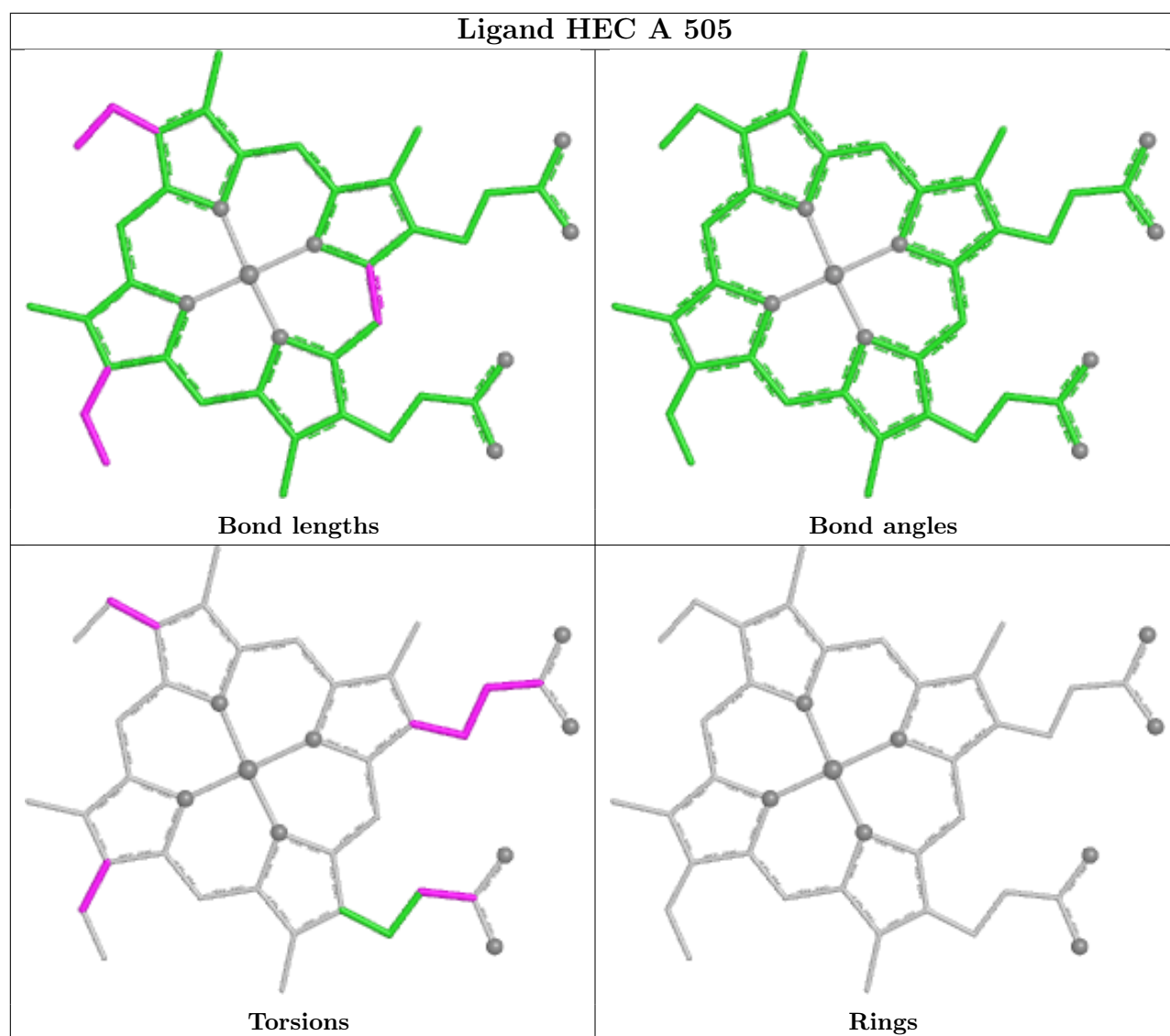
Bond angles



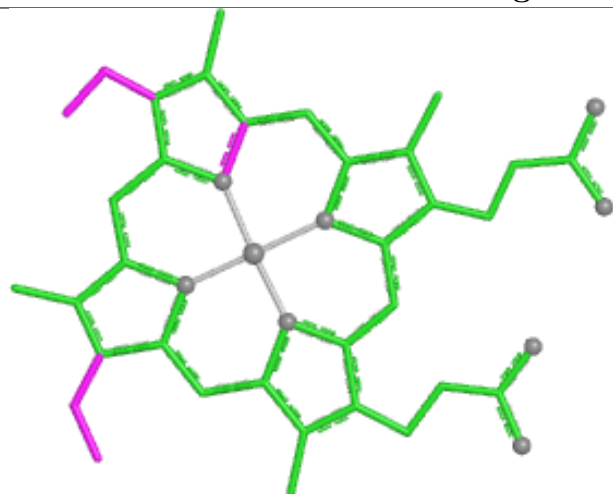
Torsions



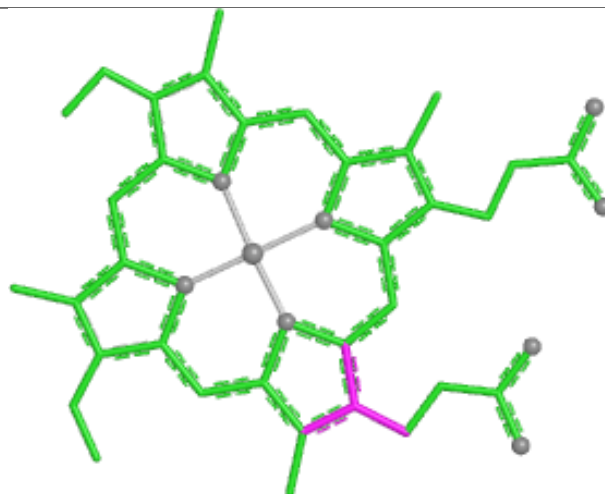
Rings



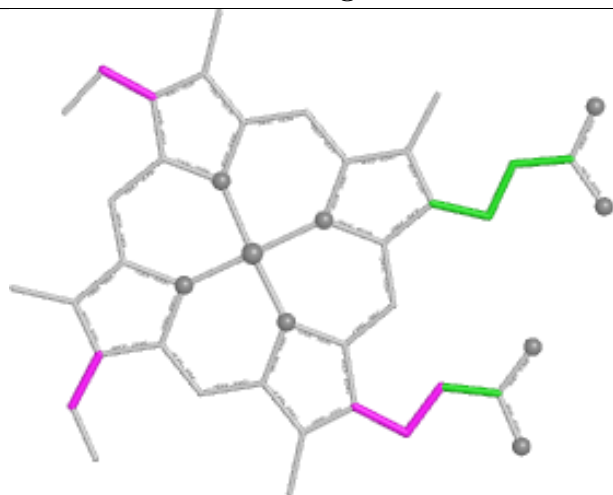
Ligand HEC B 503



Bond lengths



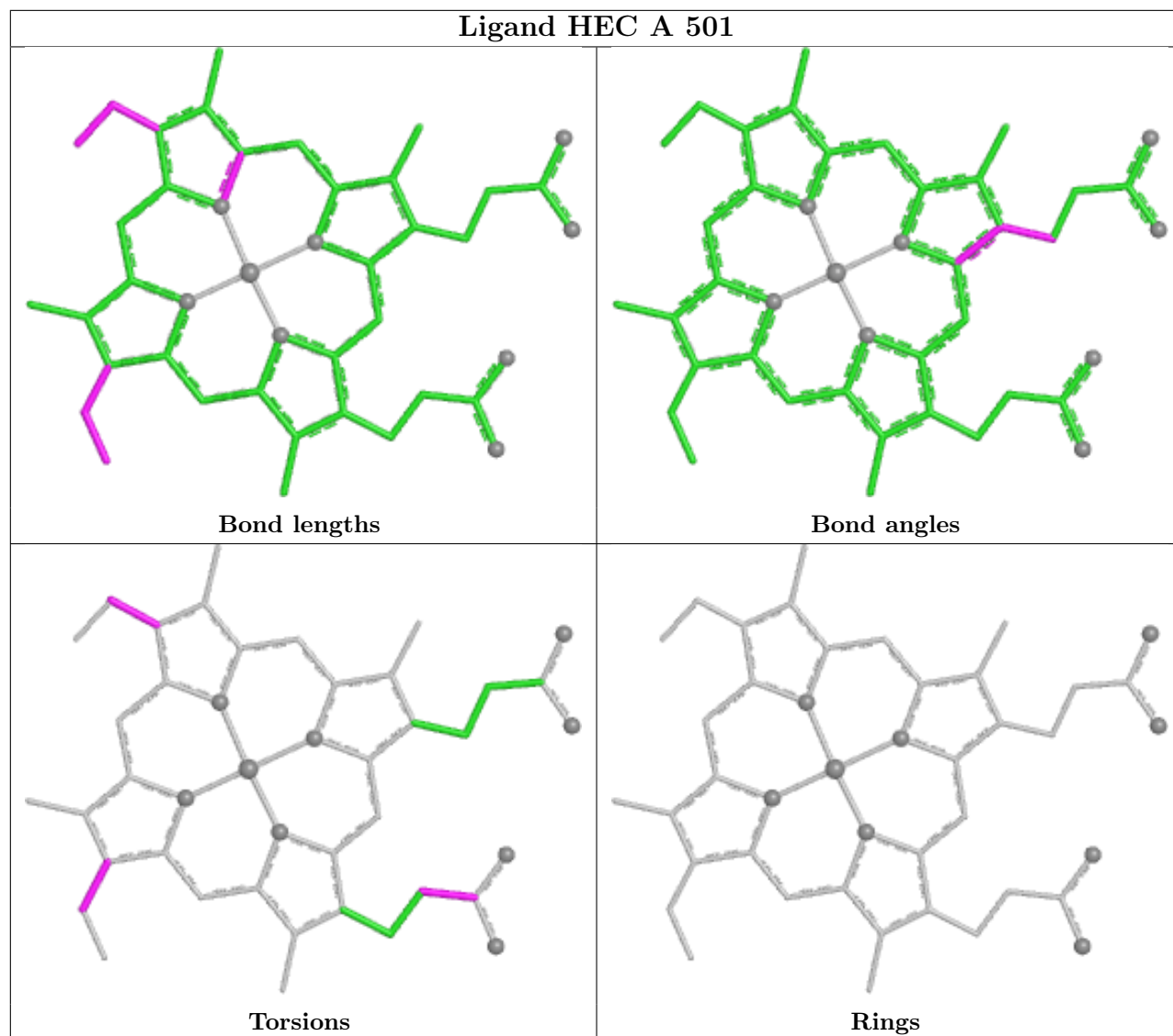
Bond angles



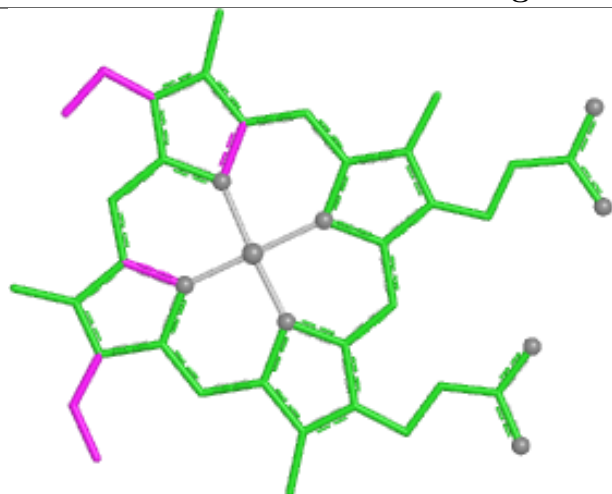
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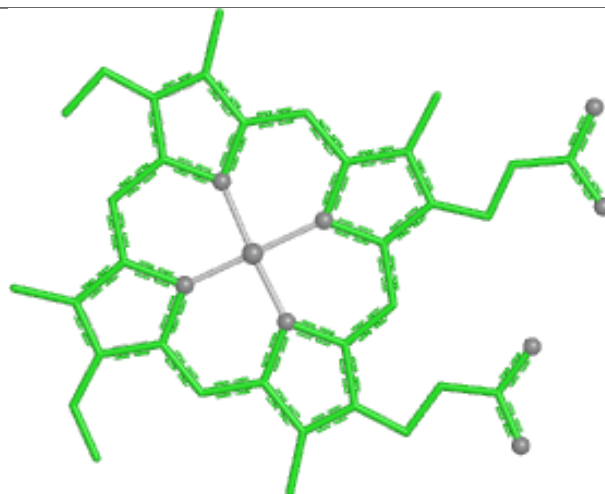
Rings



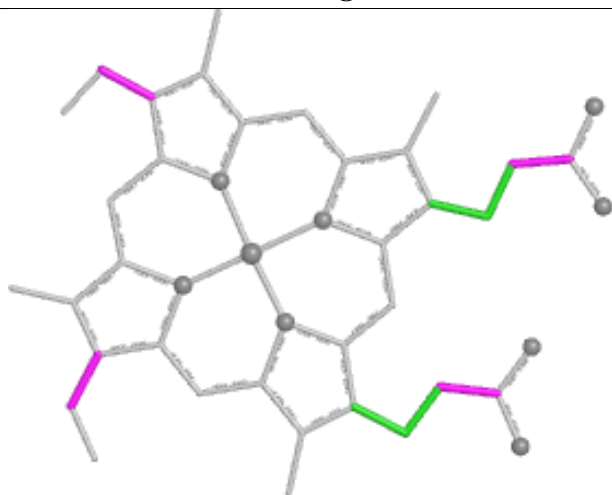
Ligand HEC C 501



Bond lengths



Bond angles

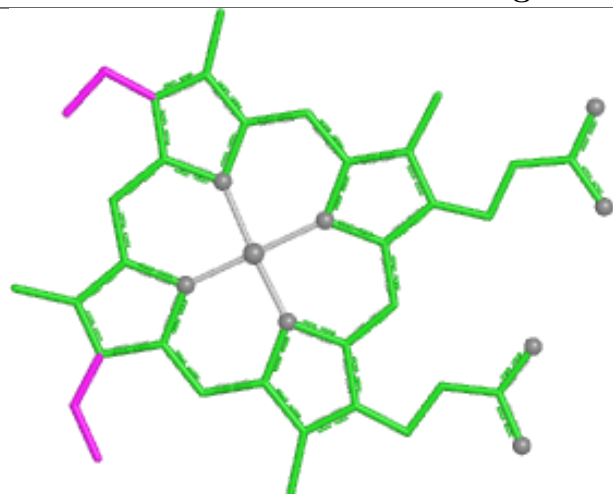


Torsions

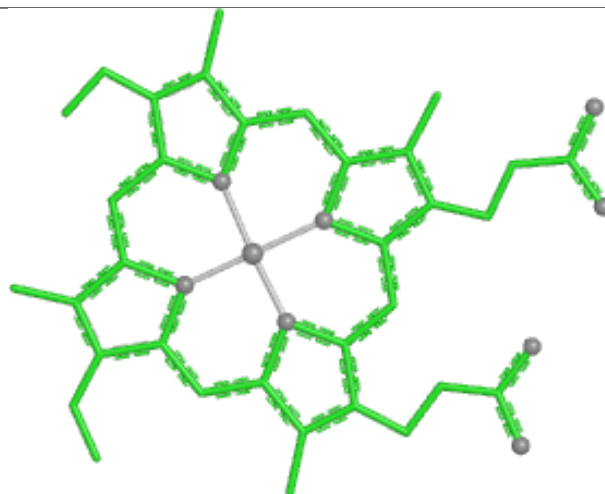


Rings

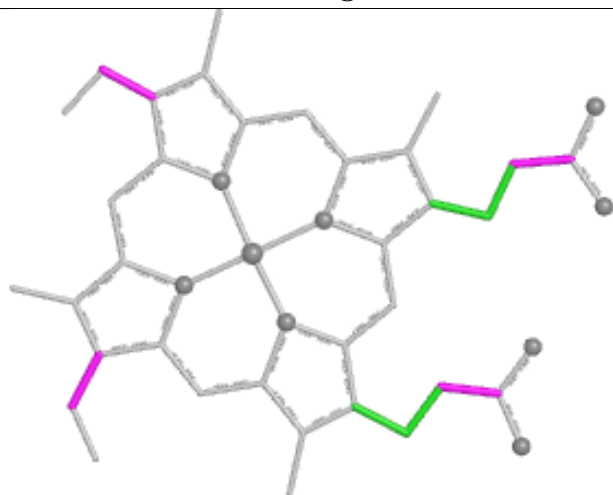
Ligand HEC B 504



Bond lengths



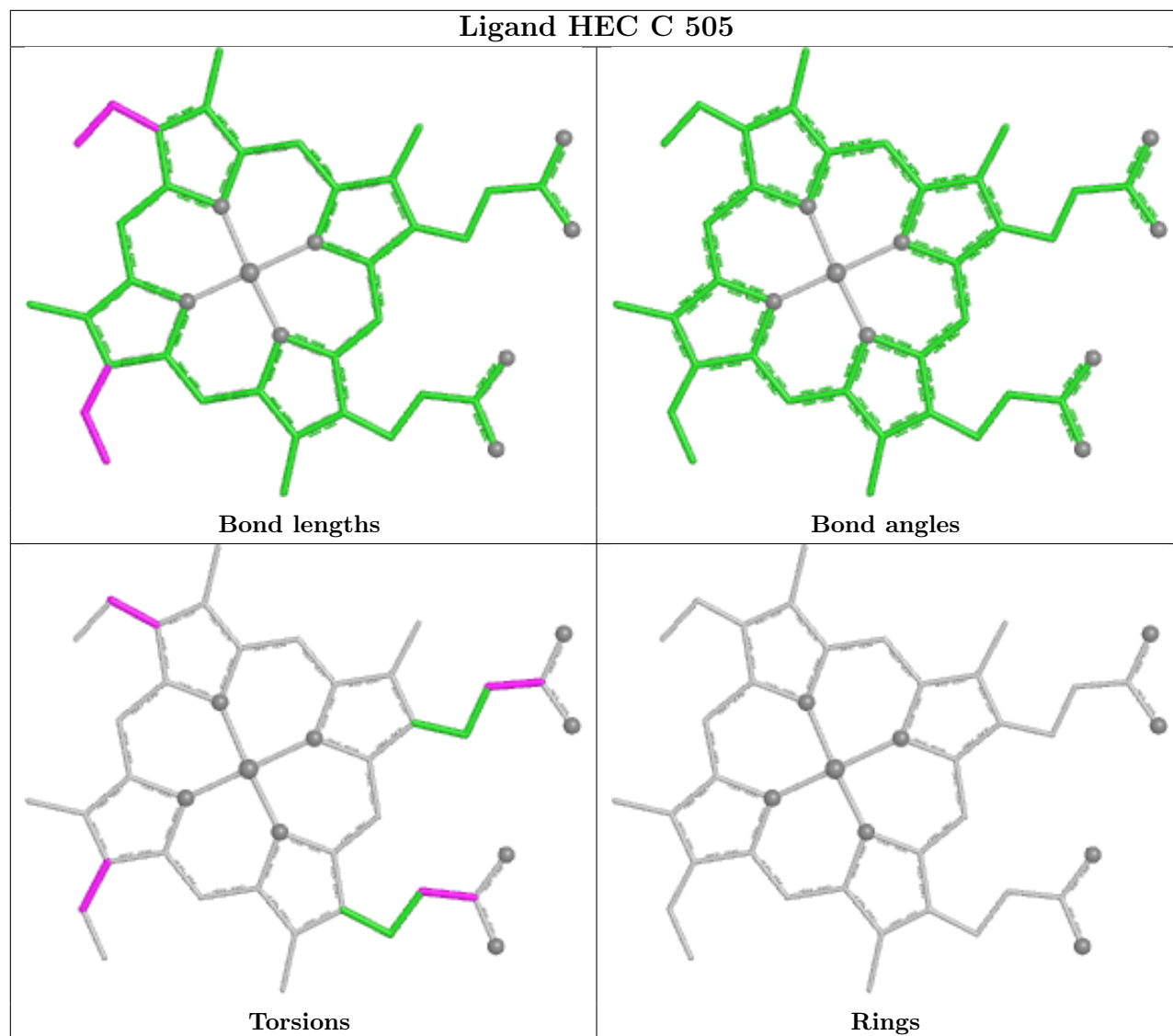
Bond angles

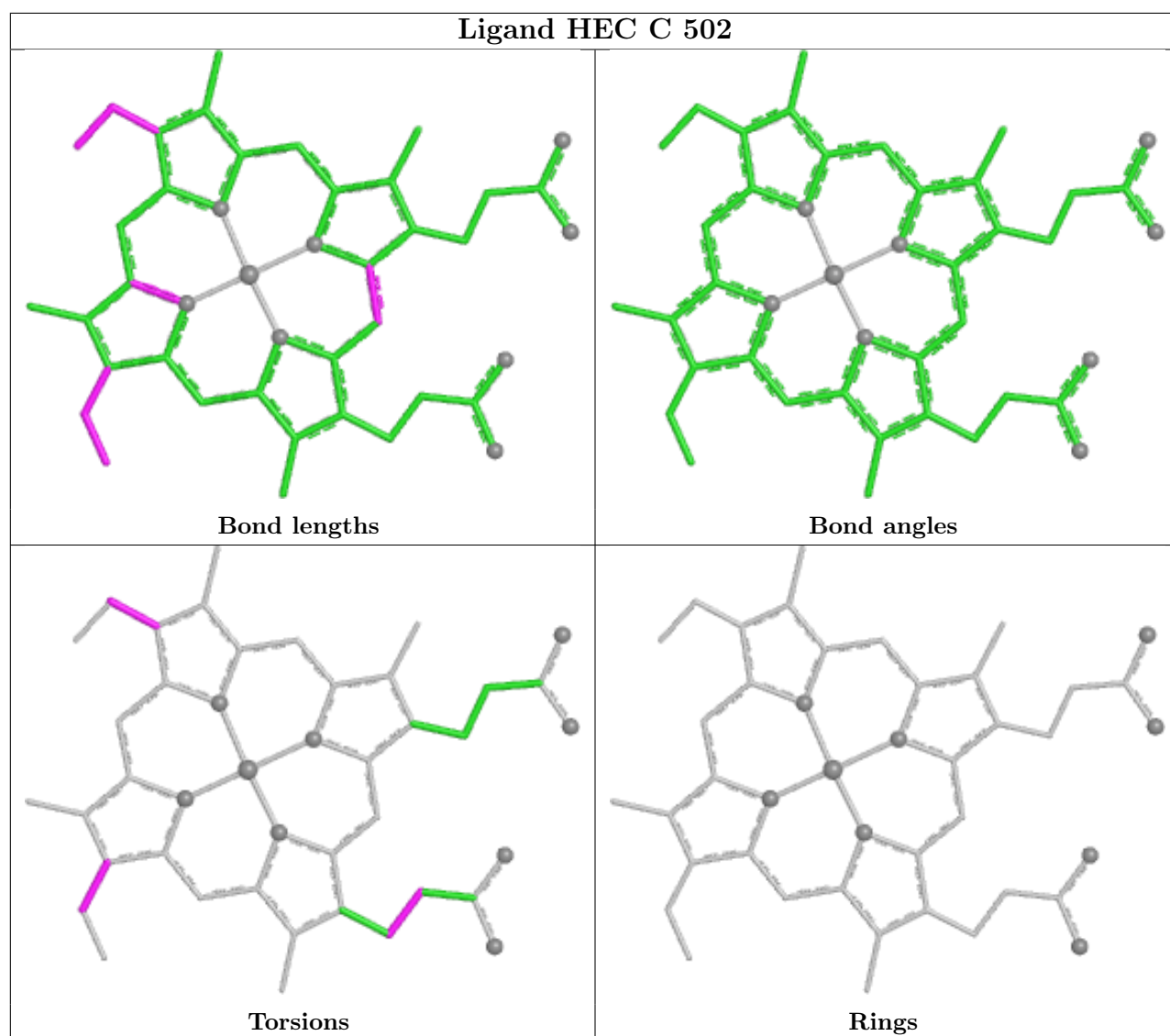


Torsions

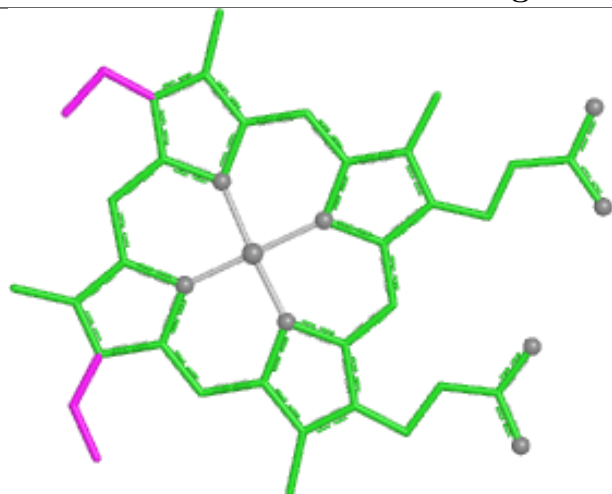


Rings

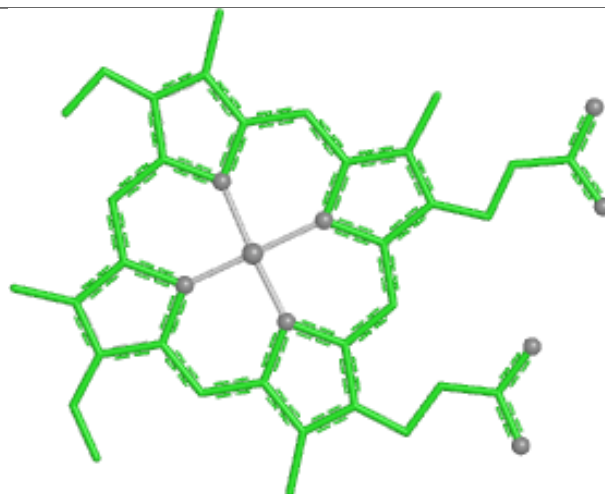




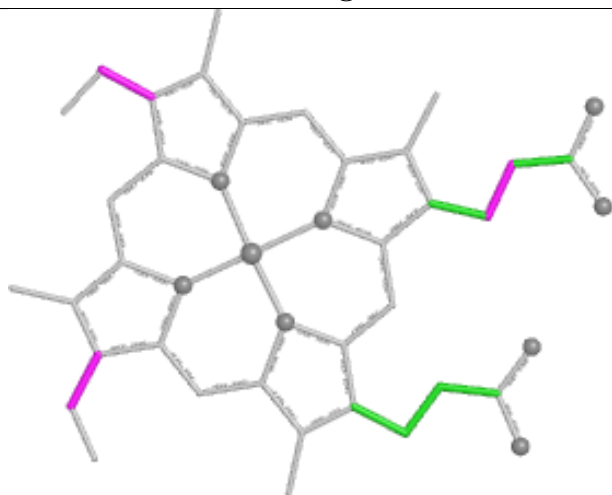
Ligand HEC C 503



Bond lengths



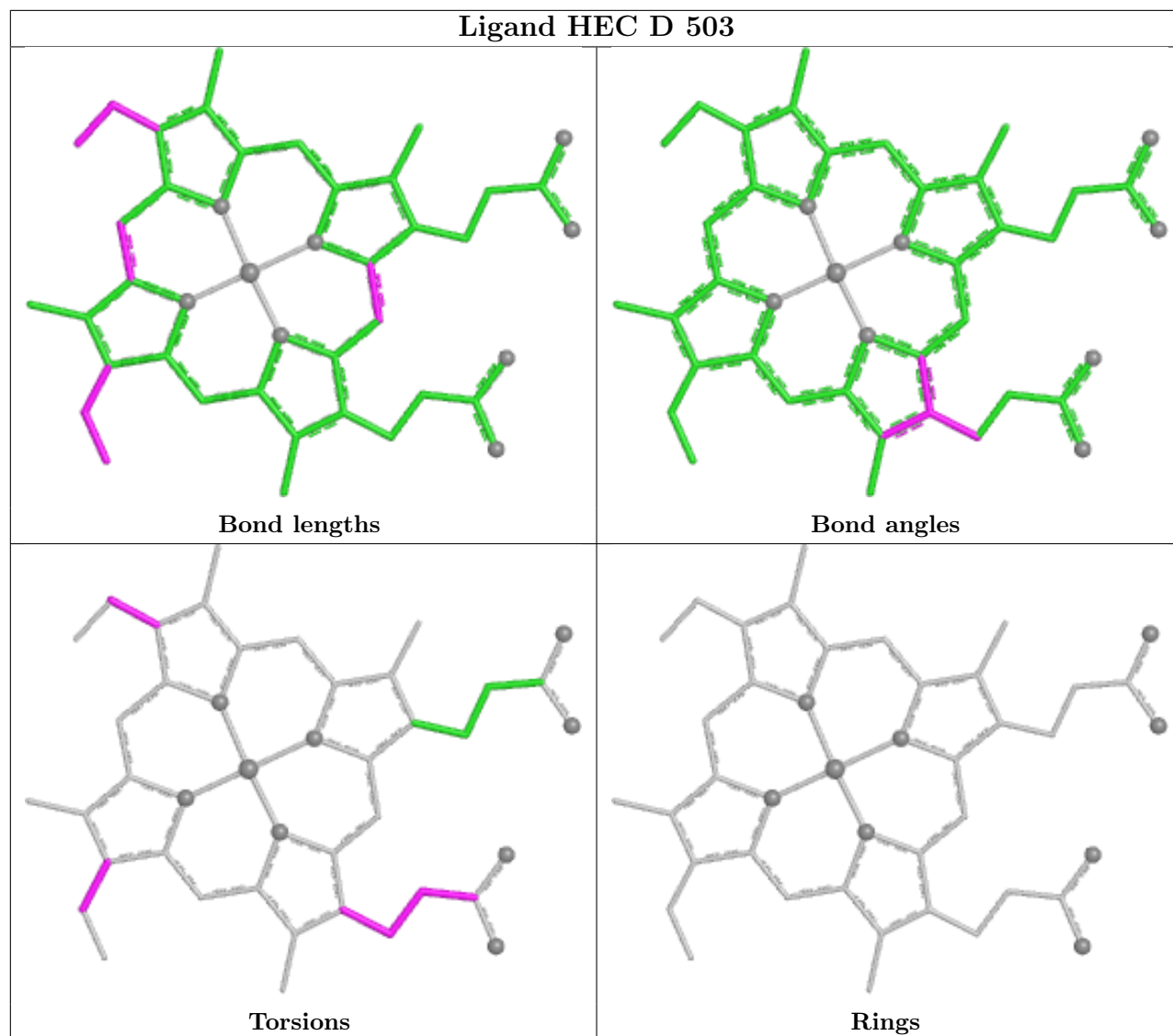
Bond angles

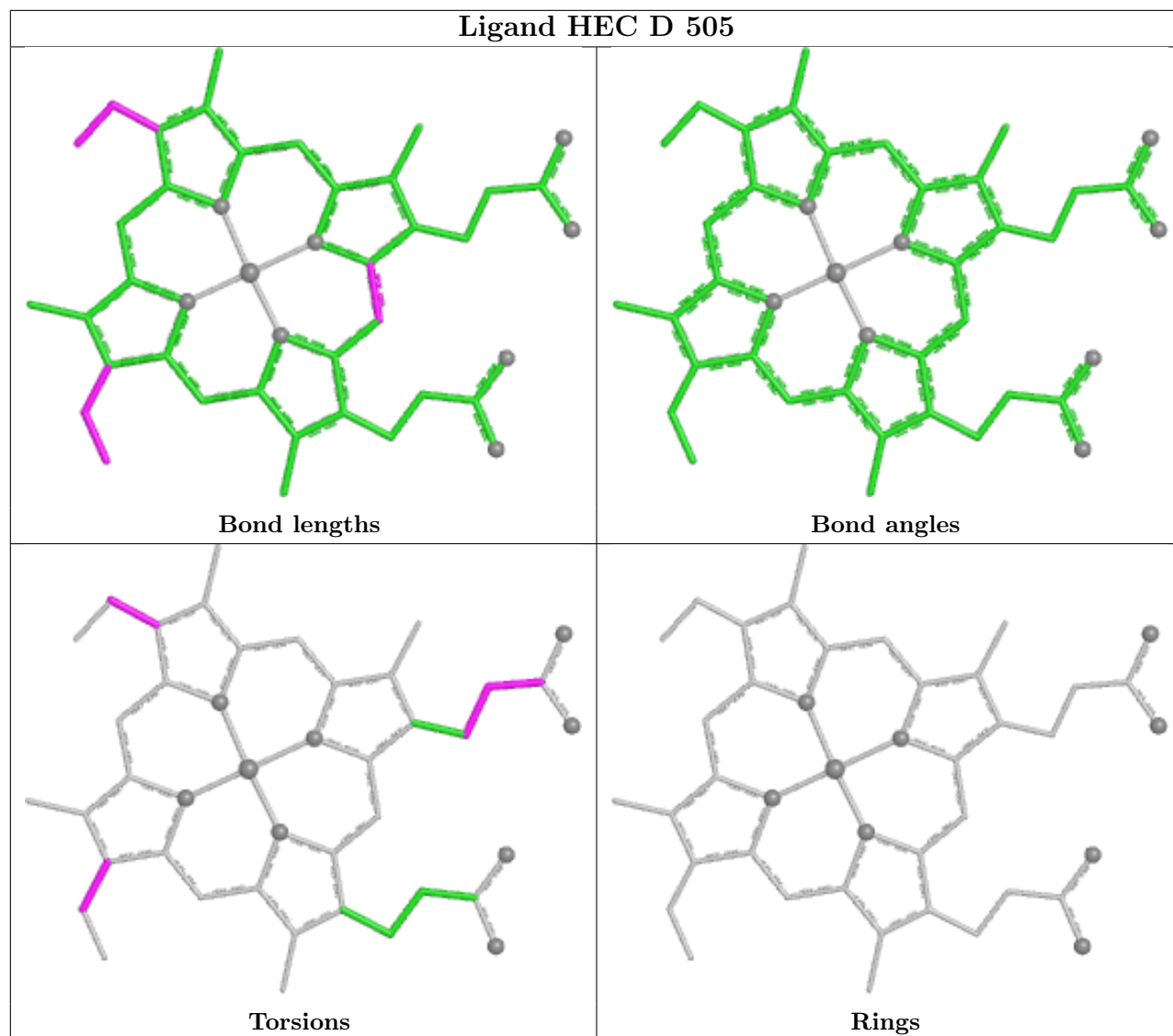


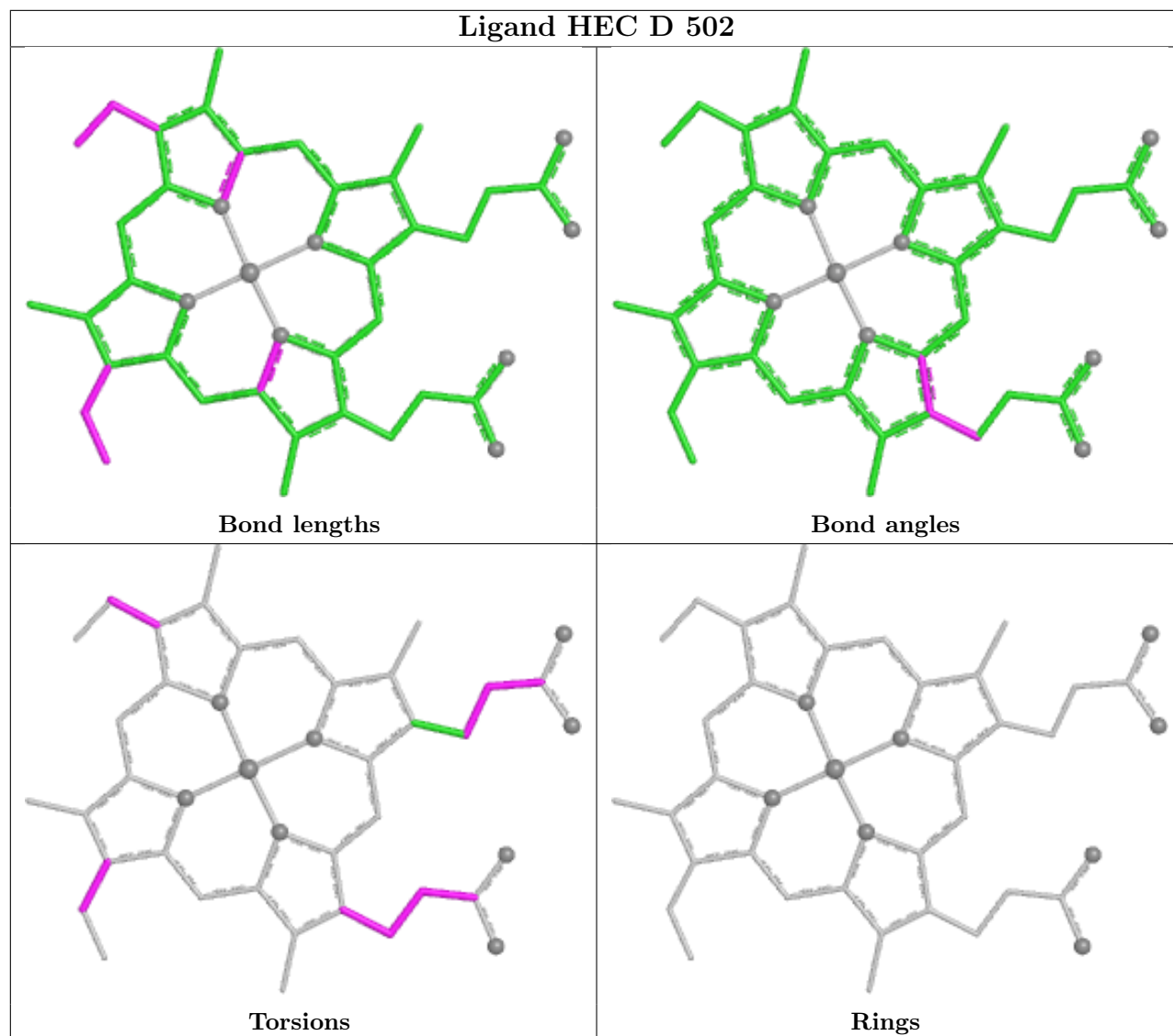
Torsions

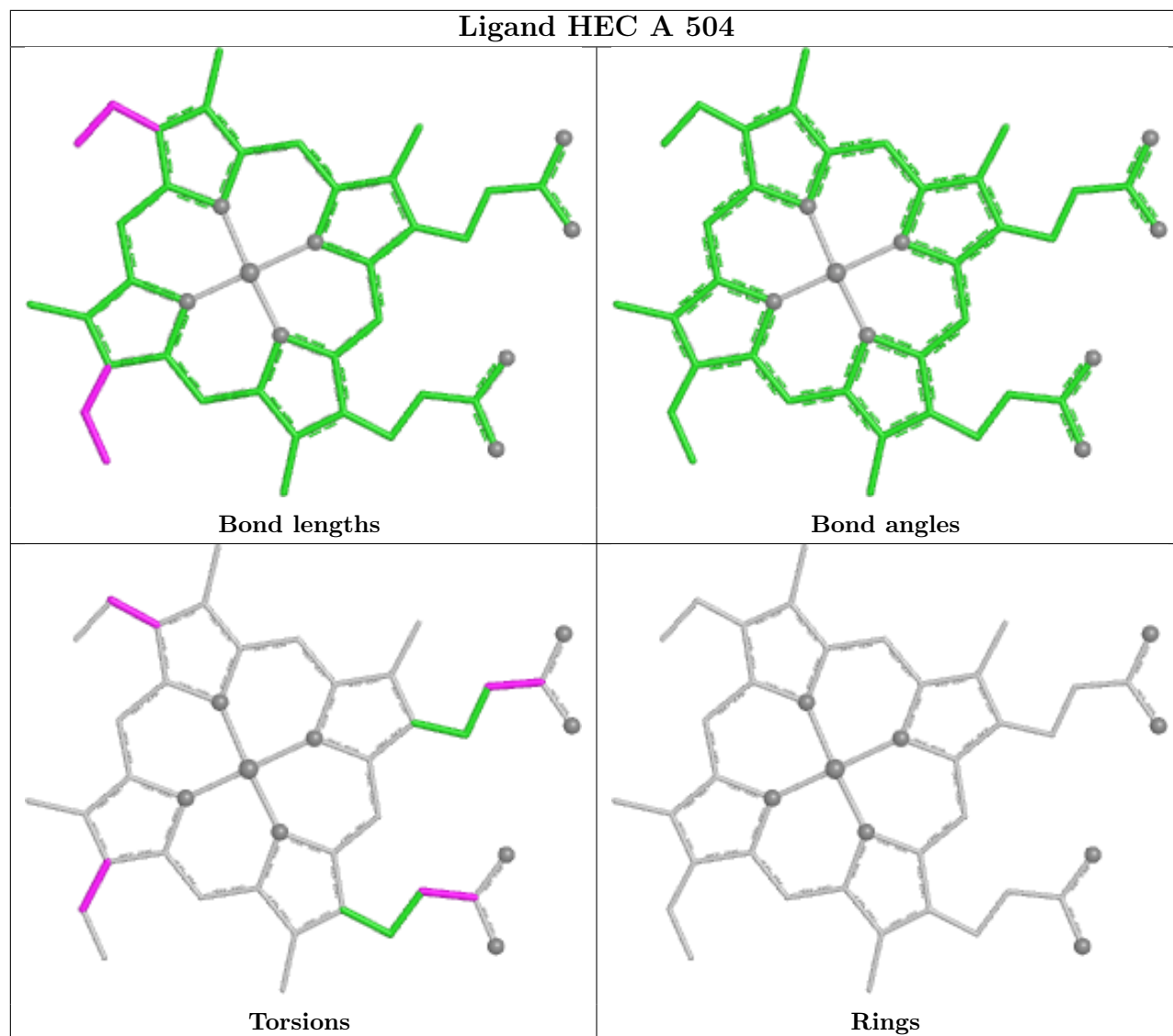


Rings

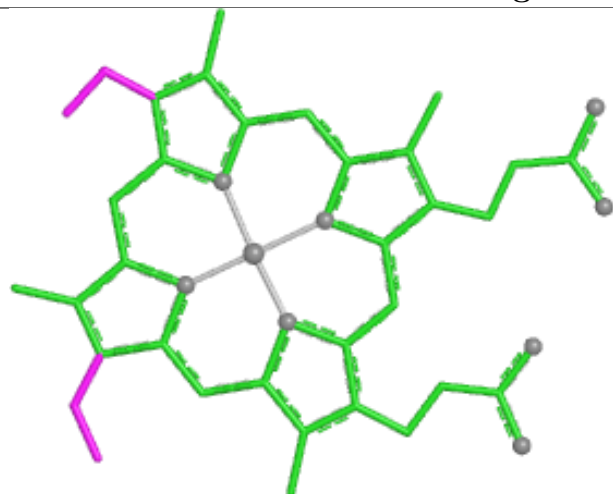




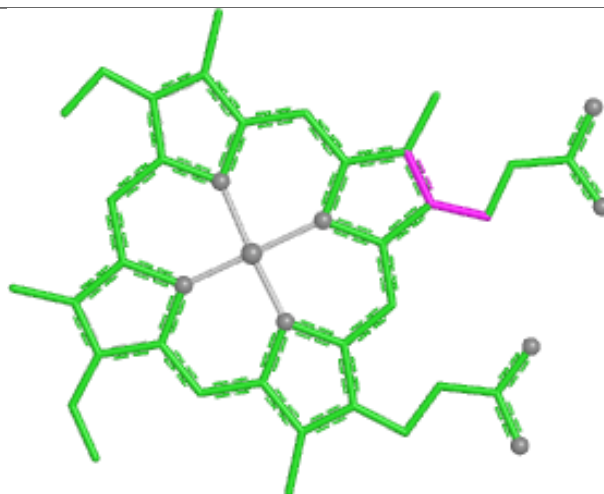




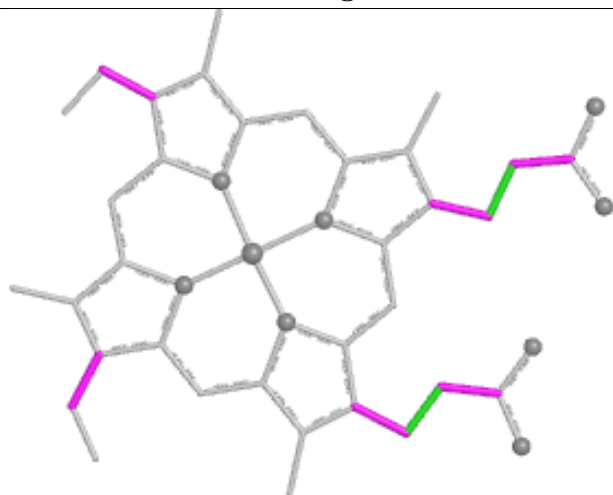
Ligand HEC B 501



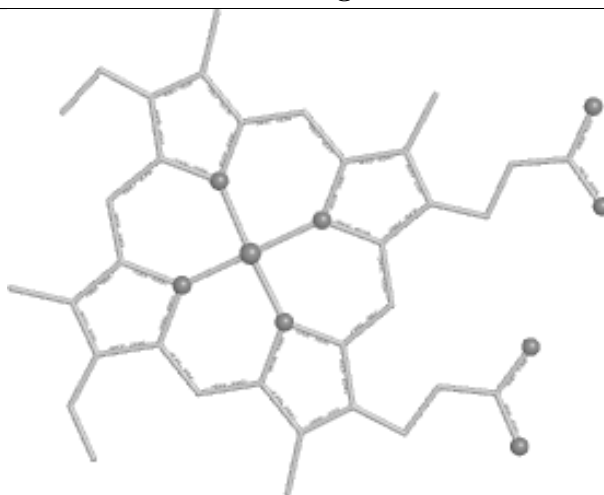
Bond lengths



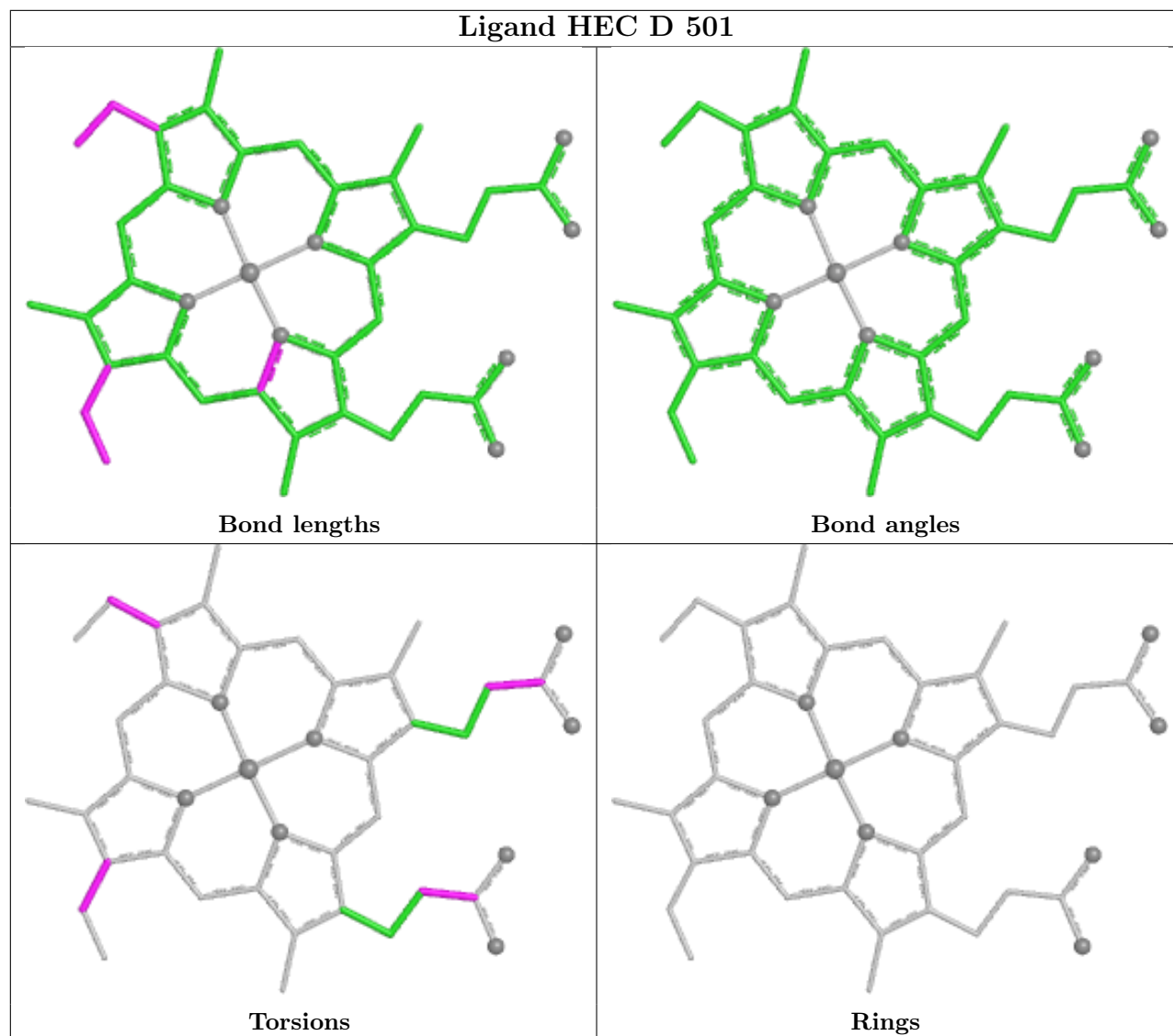
Bond angles

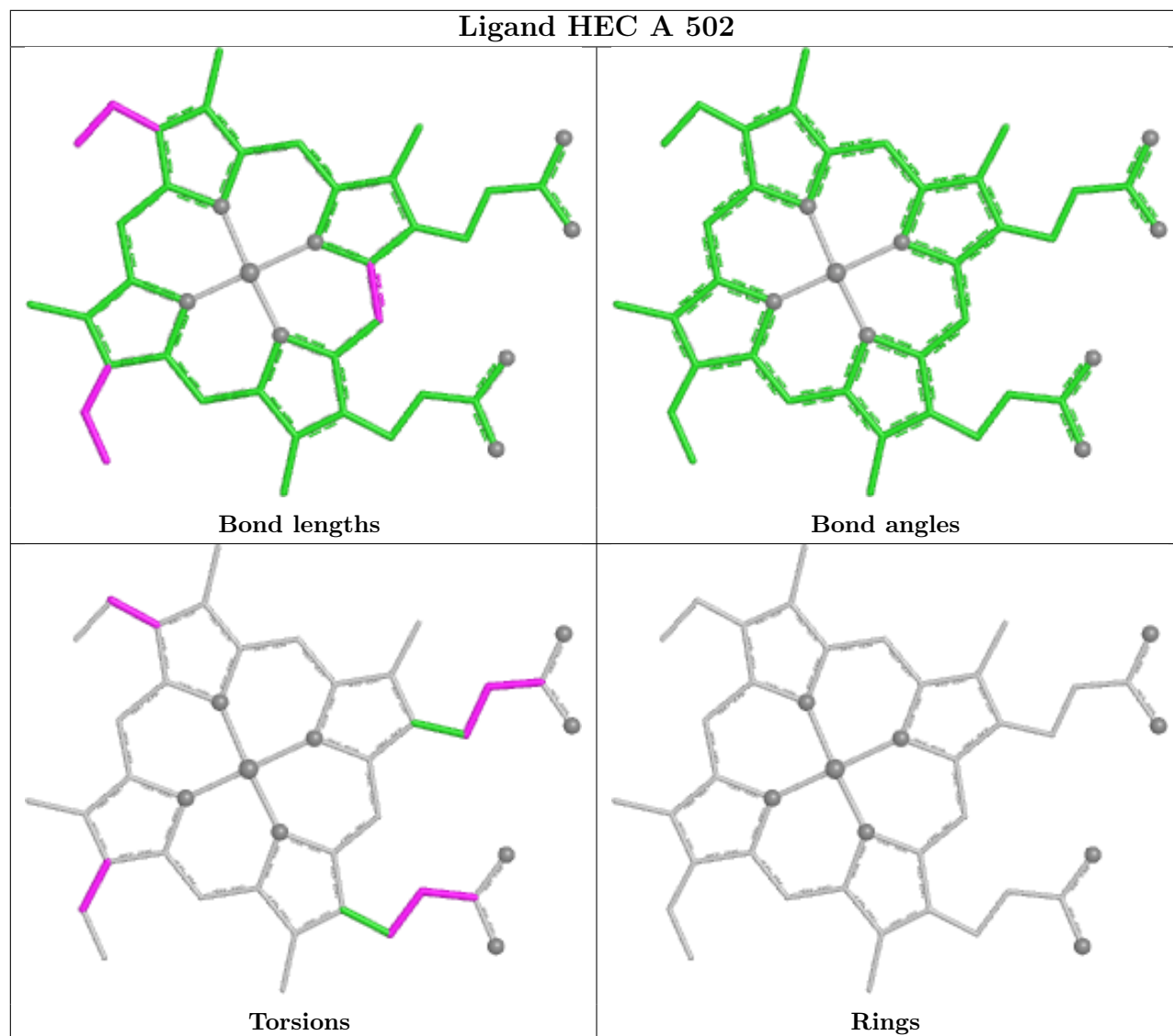


Torsions

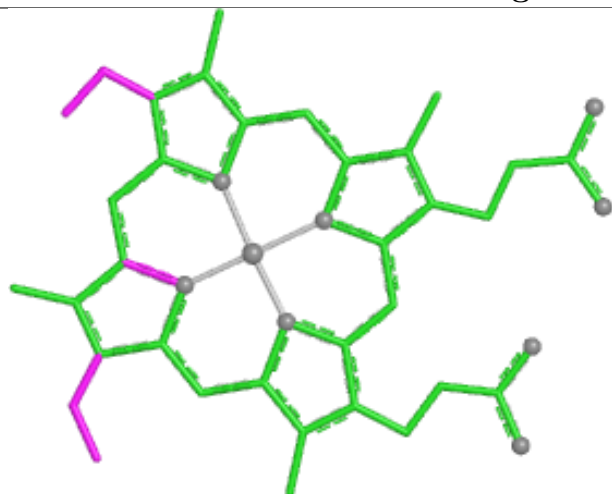


Rings

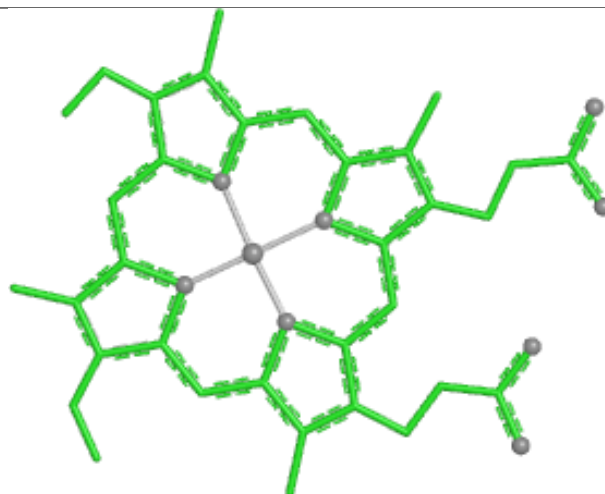




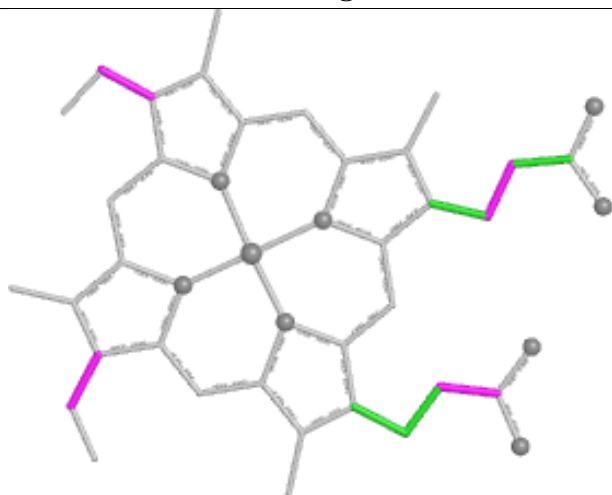
Ligand HEC B 502



Bond lengths



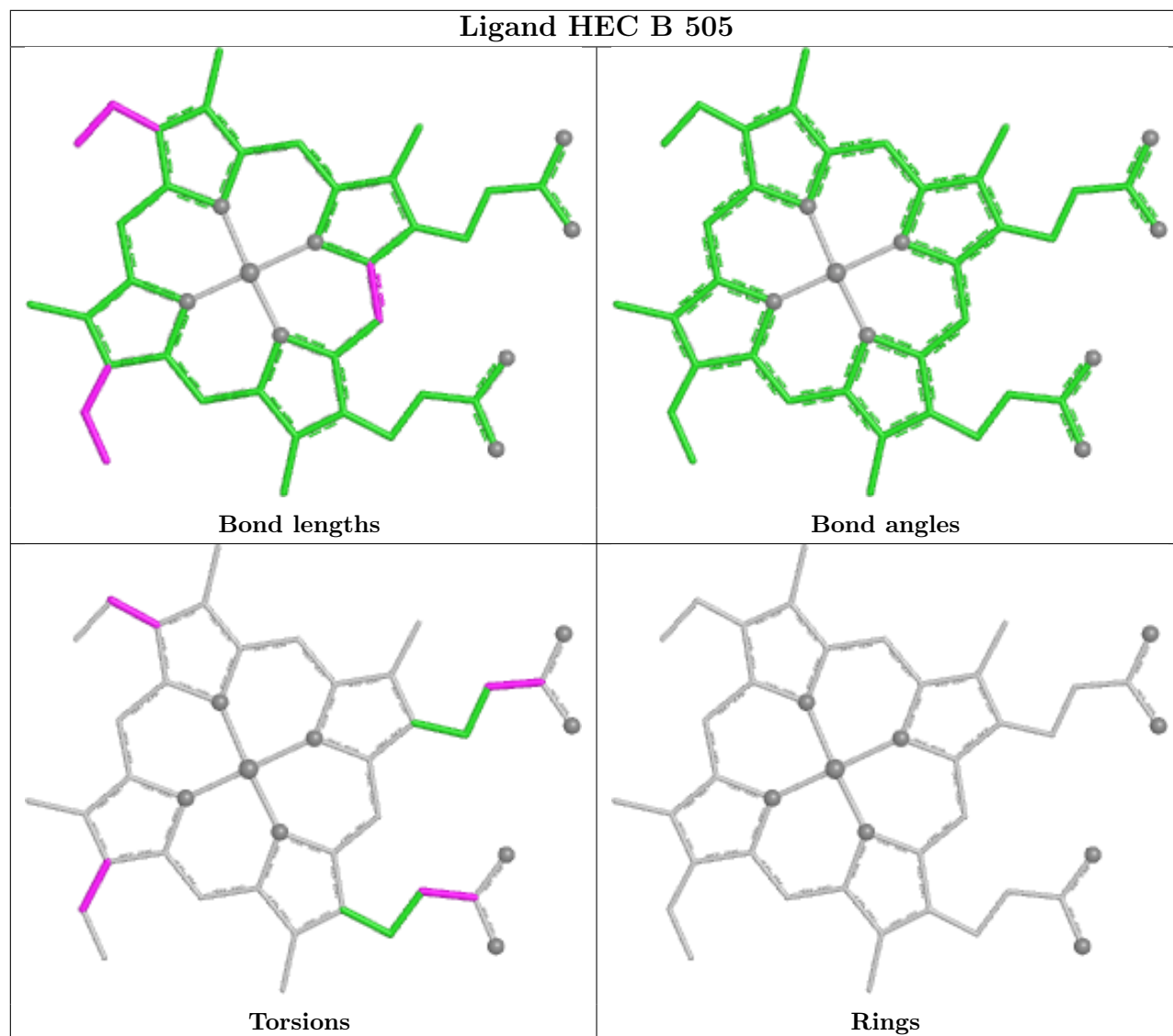
Bond angles

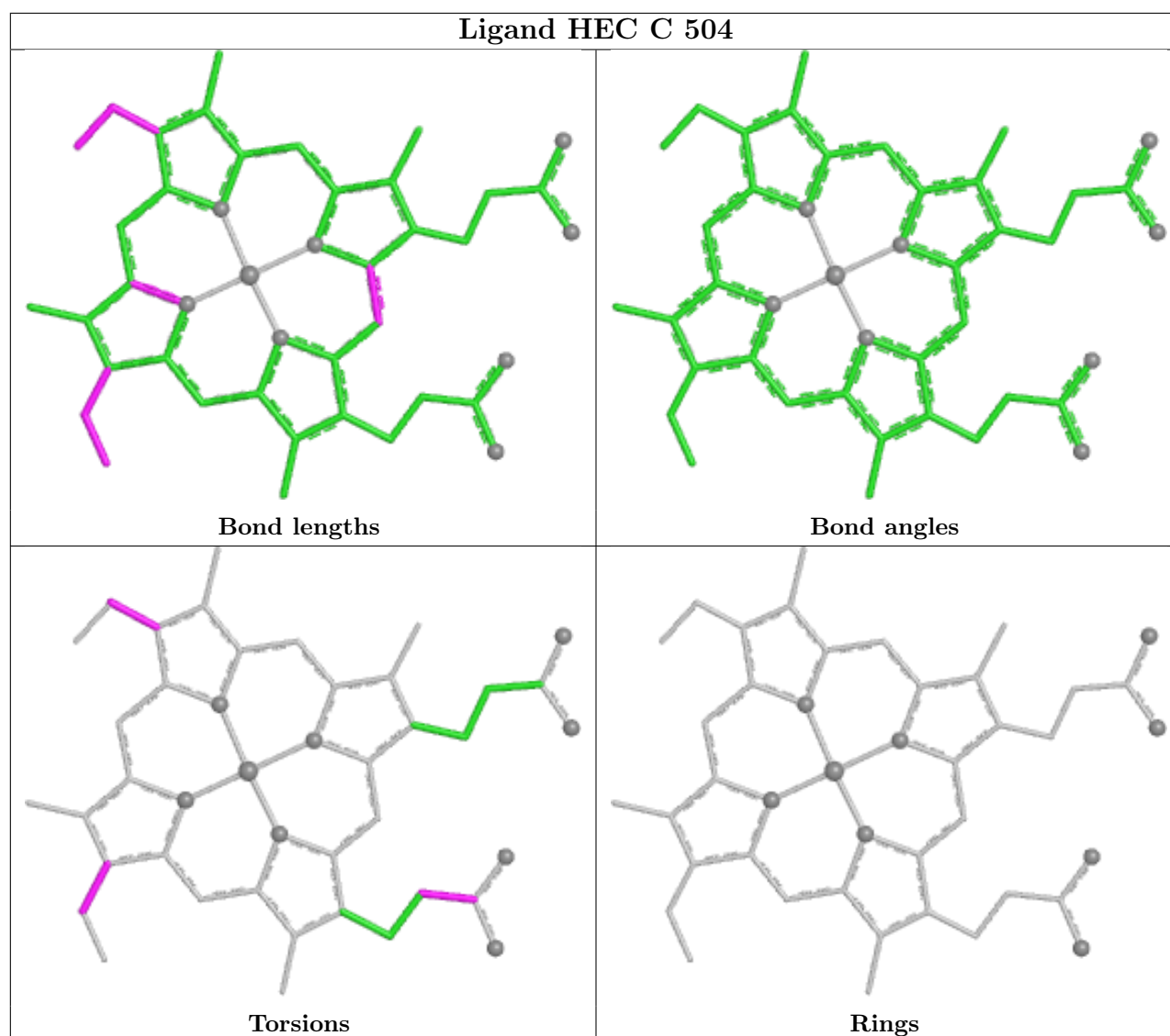


Torsions



Rings





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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	437/492 (88%)	0.19	16 (3%) 45 51	15, 33, 59, 77	0
1	B	434/492 (88%)	0.28	30 (6%) 23 26	13, 34, 69, 87	0
1	C	443/492 (90%)	0.21	35 (7%) 18 21	13, 33, 75, 86	0
1	D	444/492 (90%)	0.00	18 (4%) 41 46	11, 29, 61, 82	0
All	All	1758/1968 (89%)	0.17	99 (5%) 30 33	11, 32, 67, 87	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	106	TYR	5.6
1	A	106	TYR	5.5
1	C	321	VAL	5.0
1	C	127	LEU	4.6
1	B	106	TYR	4.4
1	B	62	THR	4.4
1	A	321	VAL	4.3
1	A	107	ASN	4.2
1	D	321	VAL	4.1
1	B	325	LEU	3.9
1	C	122	ILE	3.9
1	D	106	TYR	3.8
1	D	127	LEU	3.8
1	D	62	THR	3.8
1	D	464	GLN	3.8
1	A	40	ASP	3.7
1	A	39	PRO	3.7
1	B	50	LYS	3.7
1	A	308	TYR	3.6
1	B	38	ILE	3.6
1	B	321	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	308	TYR	3.5
1	B	309	THR	3.5
1	A	110	ARG	3.5
1	C	322	MET	3.4
1	D	322	MET	3.3
1	B	41	GLY	3.3
1	A	62	THR	3.2
1	B	328	ASP	3.1
1	A	322	MET	3.1
1	C	160	VAL	2.9
1	B	327	ASN	2.9
1	D	125	ALA	2.9
1	C	34	LYS	2.9
1	D	463	ASP	2.9
1	C	325	LEU	2.9
1	D	470	LEU	2.8
1	D	469	LYS	2.8
1	A	50	LYS	2.8
1	C	465	ARG	2.7
1	B	468	LYS	2.7
1	C	170	THR	2.7
1	D	325	LEU	2.7
1	C	61	LYS	2.7
1	C	36	VAL	2.7
1	C	126	ARG	2.6
1	B	324	PRO	2.6
1	A	125	ALA	2.6
1	C	125	ALA	2.6
1	A	41	GLY	2.6
1	B	108	GLU	2.6
1	A	309	THR	2.6
1	C	109	PRO	2.6
1	B	107	ASN	2.6
1	B	210	ARG	2.5
1	C	157	PHE	2.5
1	D	108	GLU	2.5
1	C	158	LYS	2.4
1	C	121	GLU	2.4
1	B	333	ILE	2.4
1	C	327	ASN	2.4
1	C	164	ILE	2.4
1	B	51	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	322	MET	2.4
1	C	210	ARG	2.3
1	C	320	ARG	2.3
1	D	104	ILE	2.3
1	B	334	GLN	2.3
1	B	467	GLU	2.2
1	C	108	GLU	2.2
1	C	124	SER	2.2
1	D	465	ARG	2.2
1	B	61	LYS	2.2
1	C	168	HIS	2.2
1	D	471	THR	2.2
1	C	130	GLY	2.2
1	A	206	ALA	2.2
1	B	110	ARG	2.2
1	B	465	ARG	2.2
1	B	470	LEU	2.1
1	C	120	LEU	2.1
1	A	327	ASN	2.1
1	A	328	ASP	2.1
1	C	118	ASP	2.1
1	C	463	ASP	2.1
1	B	326	LYS	2.1
1	C	470	LEU	2.1
1	C	35	THR	2.1
1	C	111	GLY	2.1
1	B	120	LEU	2.1
1	C	462	LEU	2.1
1	C	469	LYS	2.0
1	D	122	ILE	2.0
1	D	466	GLY	2.0
1	B	162	ALA	2.0
1	D	110	ARG	2.0
1	C	167	LYS	2.0
1	B	422	MET	2.0
1	B	52	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

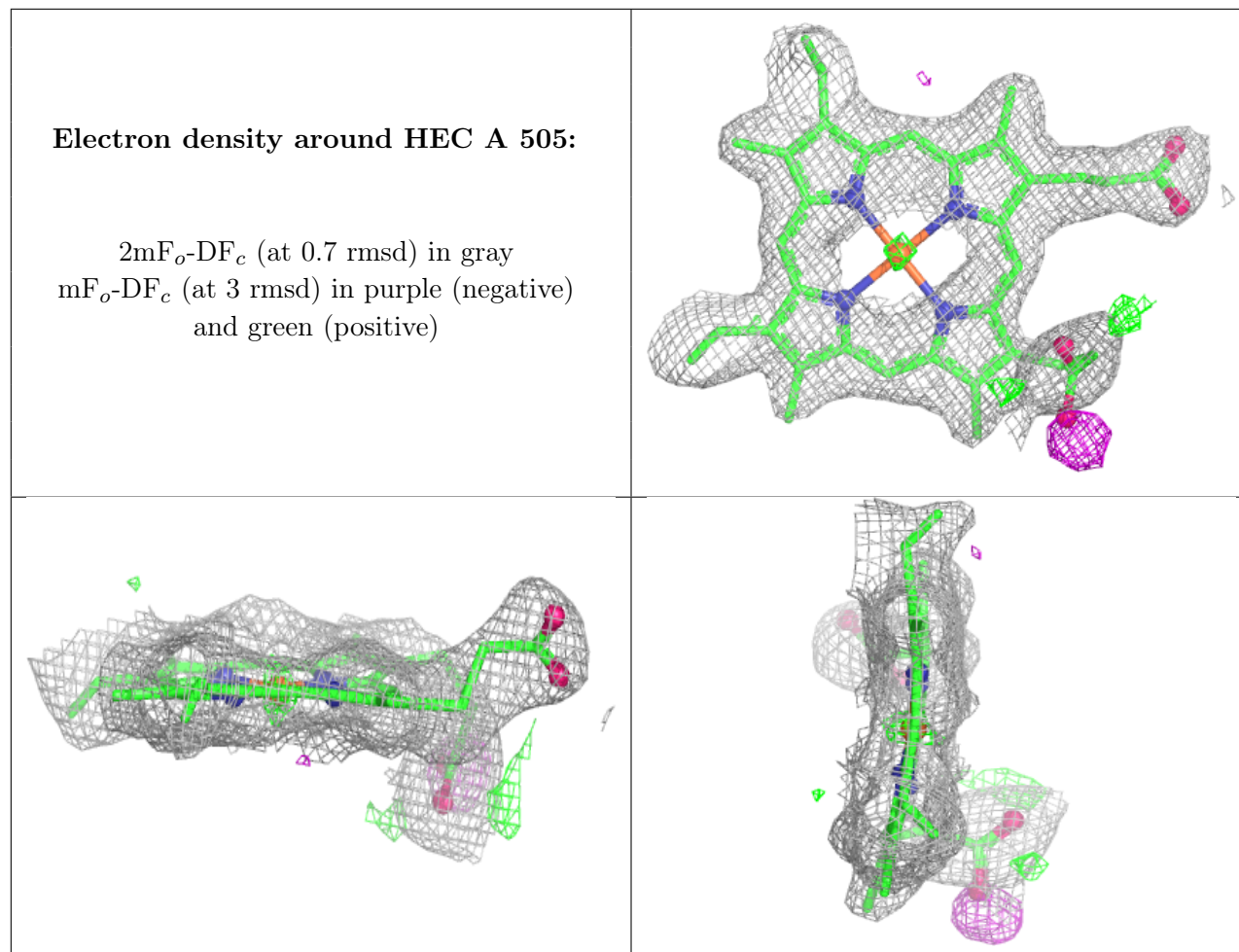
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	B	509	5/5	0.67	0.16	111,111,111,111	0
3	SO4	D	509	5/5	0.73	0.17	98,98,98,98	0
3	SO4	C	508	5/5	0.77	0.16	79,80,80,80	0
3	SO4	A	508	5/5	0.78	0.19	113,113,113,113	0
3	SO4	C	507	5/5	0.78	0.14	91,92,92,92	0
3	SO4	D	508	5/5	0.82	0.13	85,85,85,85	0
3	SO4	B	508	5/5	0.82	0.17	115,115,115,115	0
3	SO4	A	506	5/5	0.84	0.12	80,80,80,80	0
3	SO4	D	507	5/5	0.84	0.18	98,98,98,99	0
3	SO4	B	506	5/5	0.87	0.10	68,68,68,68	0
3	SO4	A	507	5/5	0.88	0.16	98,98,98,98	0
3	SO4	B	507	5/5	0.90	0.14	83,83,83,84	0
3	SO4	C	506	5/5	0.93	0.08	56,56,56,57	0
2	HEC	A	505	43/43	0.94	0.10	41,45,51,52	0
2	HEC	A	501	43/43	0.94	0.09	34,36,43,44	0
2	HEC	A	502	43/43	0.95	0.08	23,26,36,38	0
2	HEC	B	502	43/43	0.95	0.09	27,32,43,45	0
2	HEC	B	503	43/43	0.95	0.10	45,47,56,56	0
2	HEC	B	505	43/43	0.95	0.09	34,41,45,48	0
2	HEC	C	501	43/43	0.95	0.09	20,23,35,42	0
2	HEC	A	503	43/43	0.95	0.09	26,29,41,42	0
2	HEC	C	502	43/43	0.96	0.07	16,22,39,41	0
2	HEC	C	503	43/43	0.96	0.09	27,33,41,45	0
2	HEC	C	504	43/43	0.96	0.08	22,29,38,39	0
2	HEC	C	505	43/43	0.96	0.07	30,32,36,39	0
2	HEC	D	502	43/43	0.96	0.08	18,23,36,39	0
2	HEC	D	504	43/43	0.96	0.08	17,21,35,38	0
2	HEC	D	505	43/43	0.96	0.08	20,24,34,39	0
2	HEC	B	504	43/43	0.96	0.08	25,30,41,43	0
2	HEC	A	504	43/43	0.96	0.09	27,30,40,44	0
2	HEC	B	501	43/43	0.96	0.08	23,28,39,43	0
2	HEC	D	501	43/43	0.97	0.06	21,23,28,32	0

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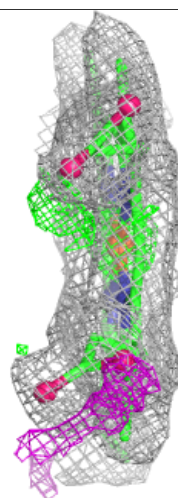
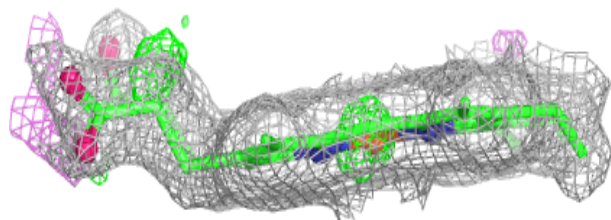
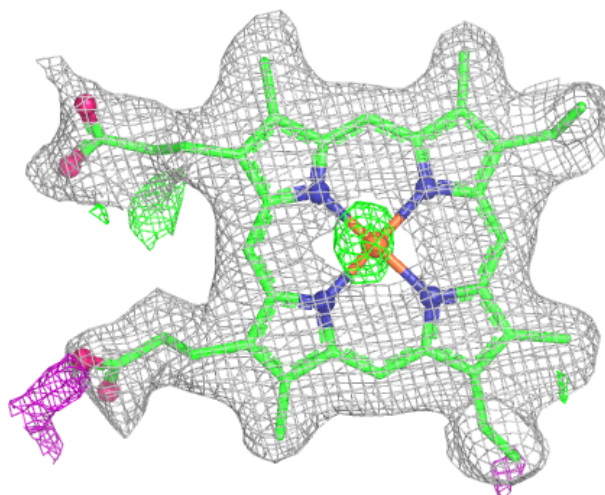
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	HEC	D	503	43/43	0.97	0.07	12,17,33,35	0
3	SO4	D	506	5/5	0.97	0.07	42,42,42,42	0

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



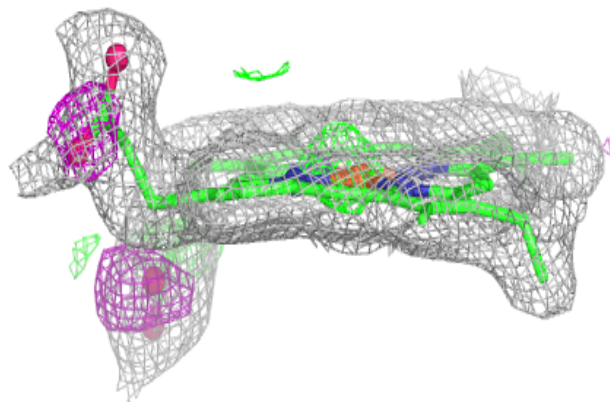
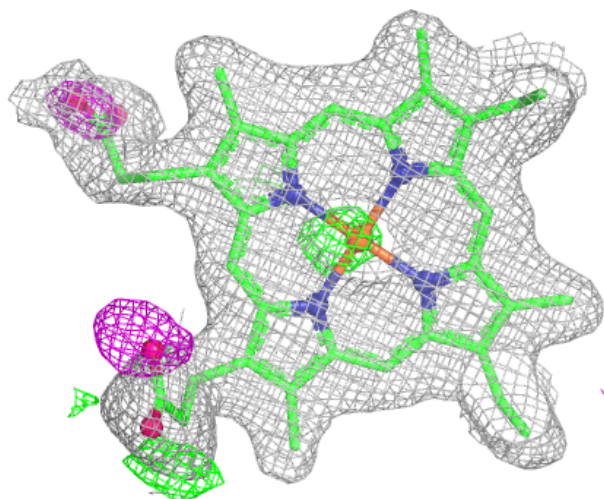
Electron density around HEC A 501:

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



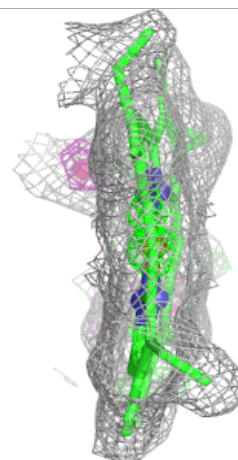
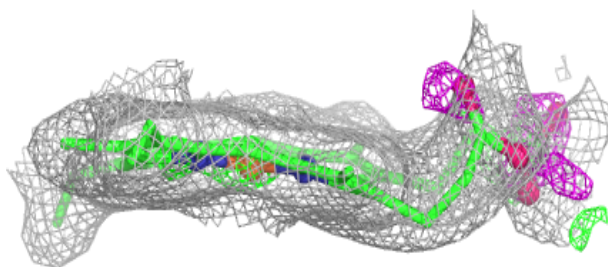
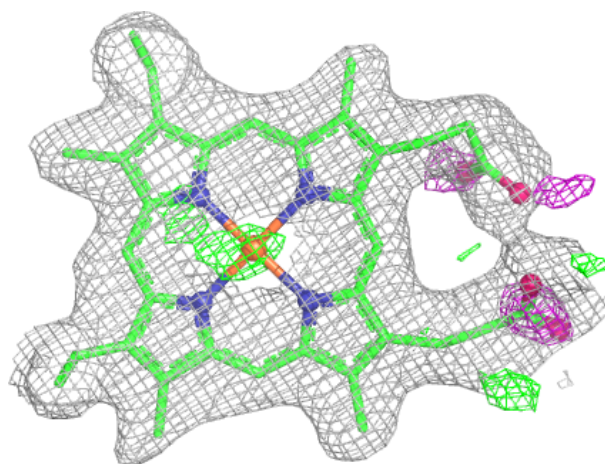
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and green (positive)



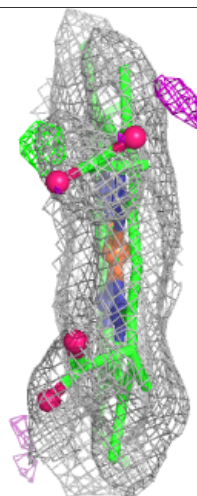
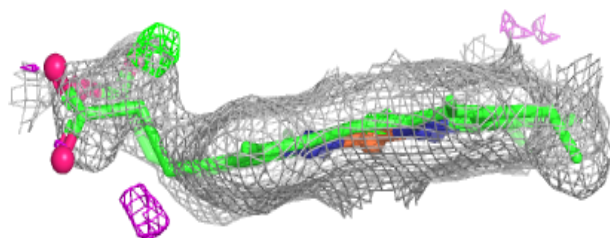
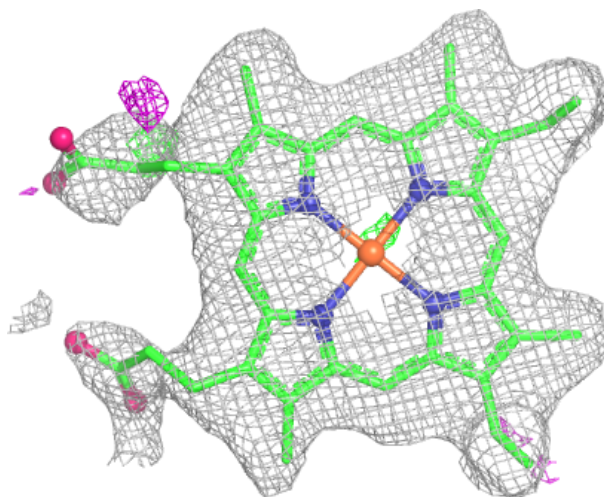
Electron density around HEC B 502:

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and green (positive)



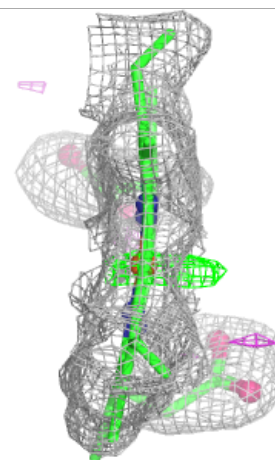
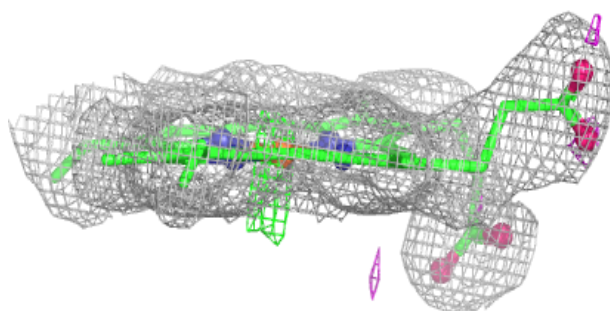
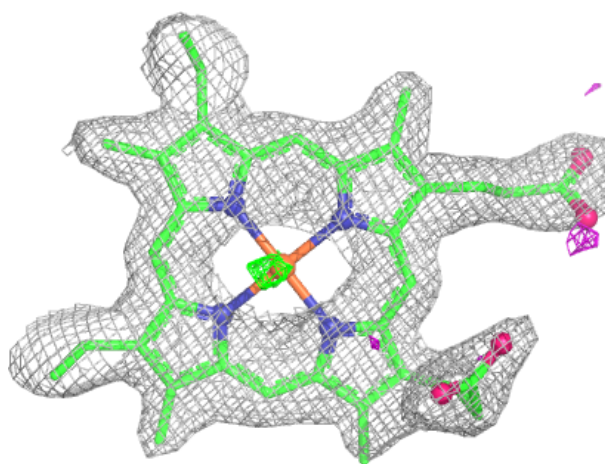
Electron density around HEC B 503:

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



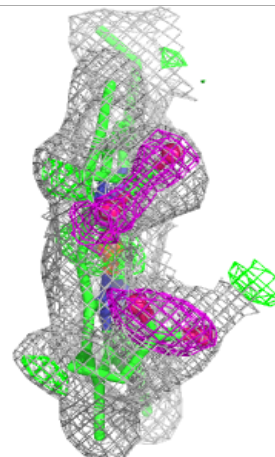
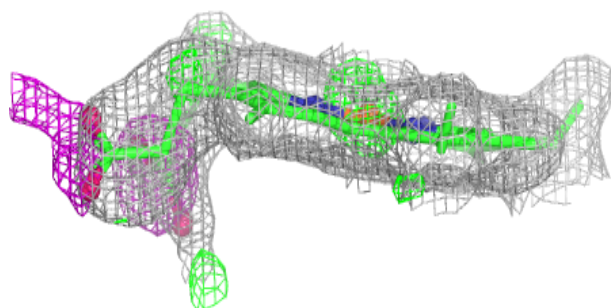
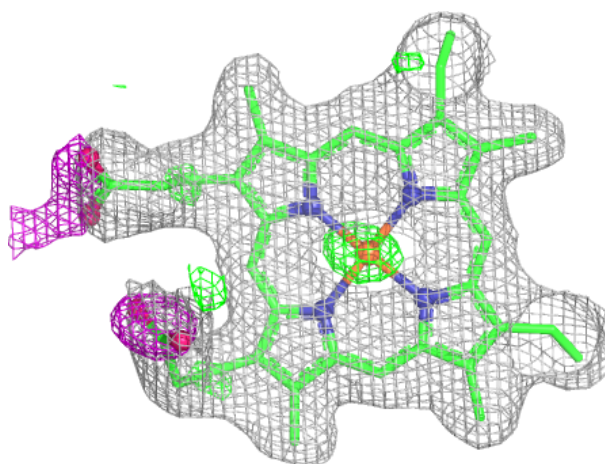
Electron density around HEC B 505:

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and green (positive)



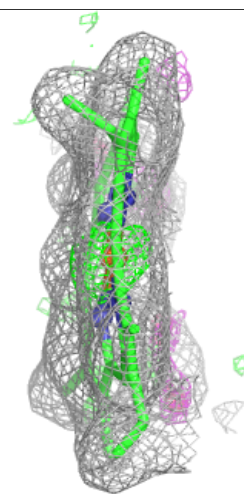
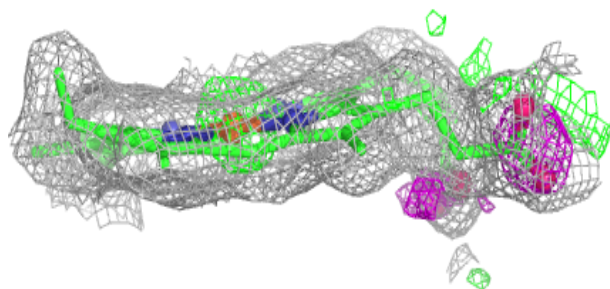
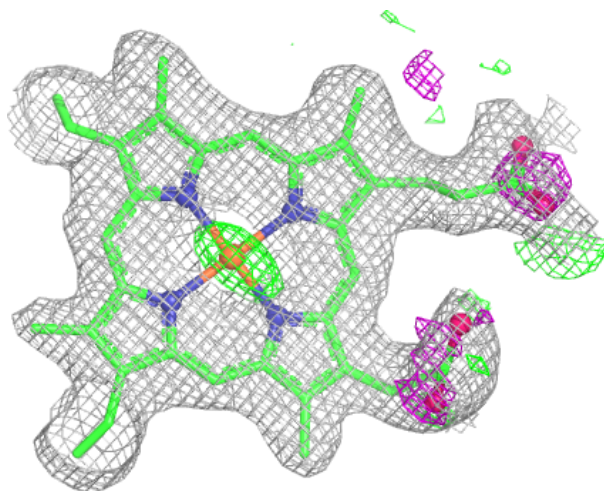
Electron density around HEC C 501:

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and green (positive)



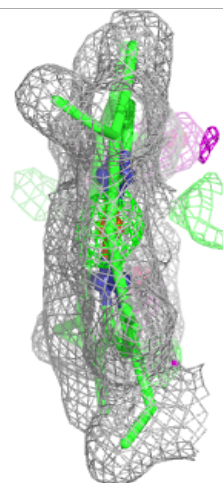
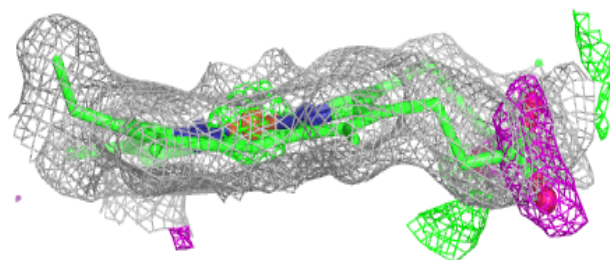
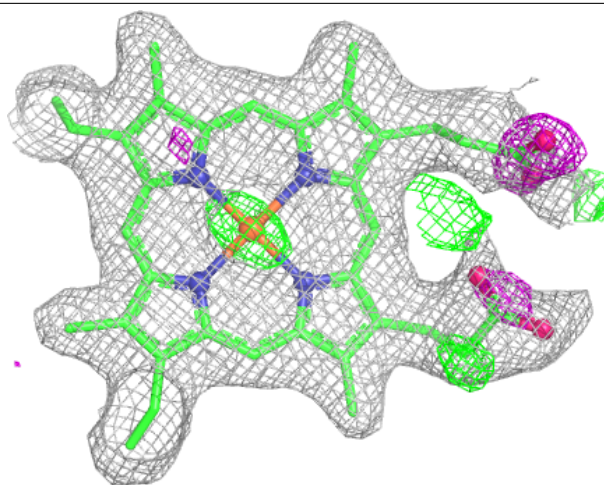
Electron density around HEC A 503:

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and green (positive)



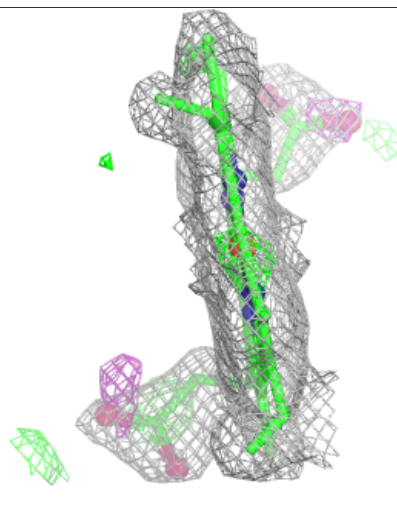
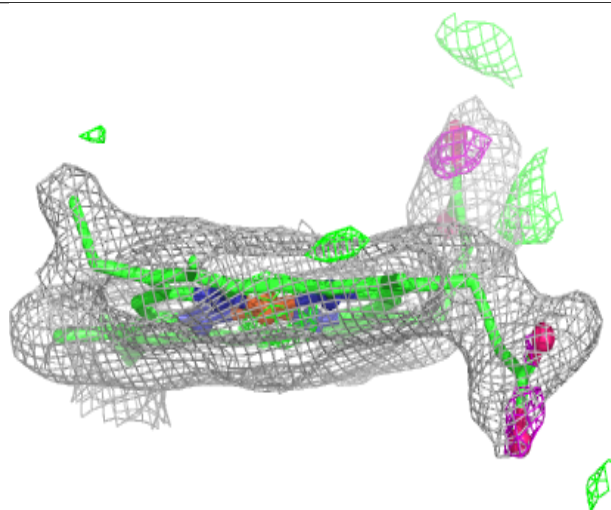
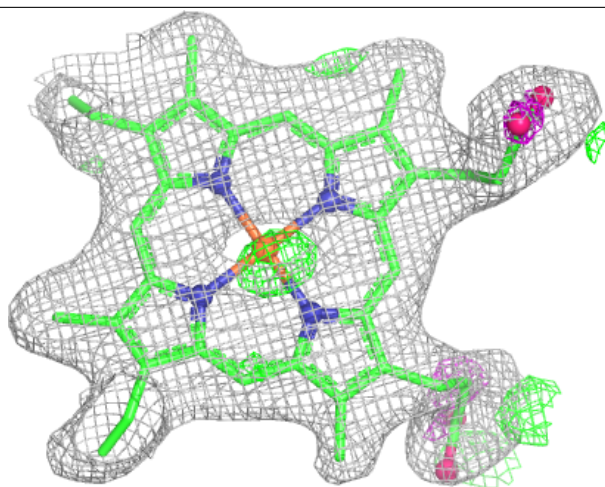
Electron density around HEC C 502:

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and green (positive)



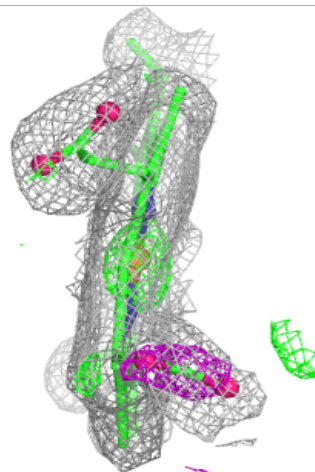
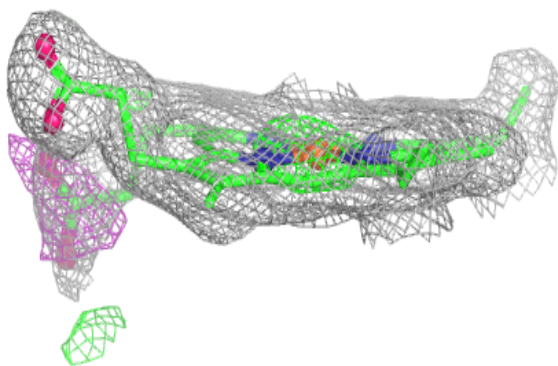
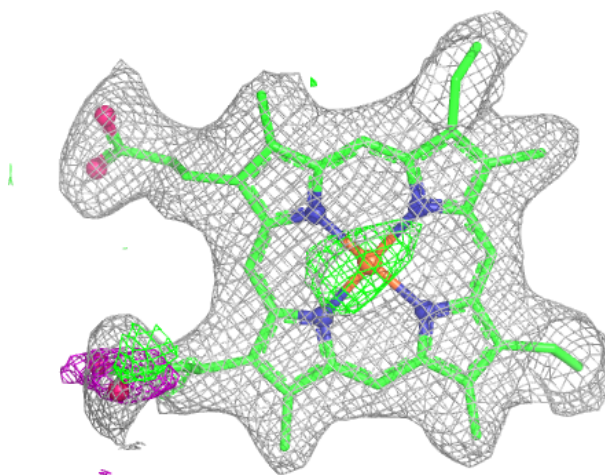
Electron density around HEC C 503:

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



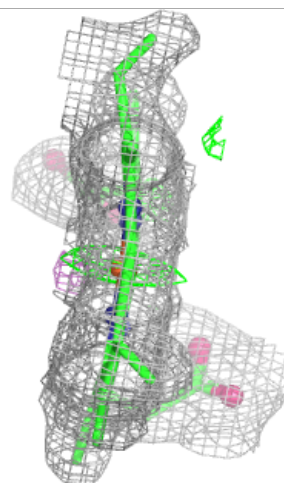
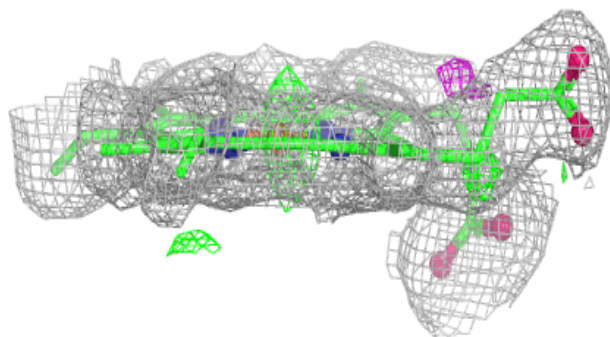
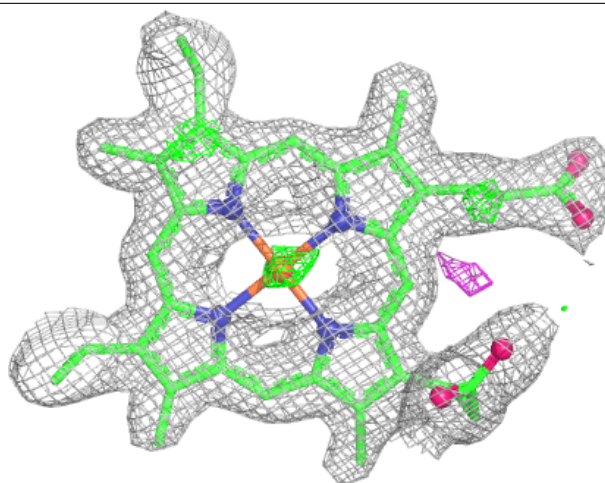
Electron density around HEC C 504:

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



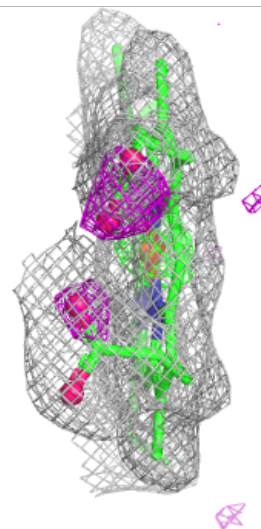
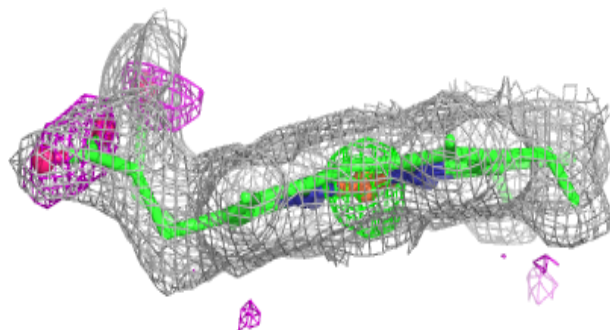
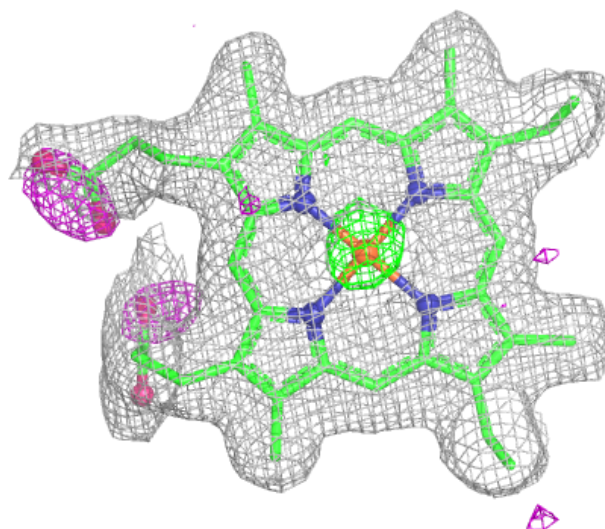
Electron density around HEC C 505:

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



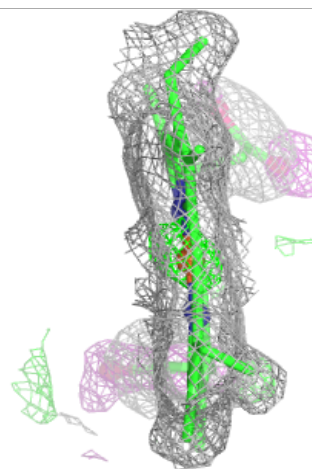
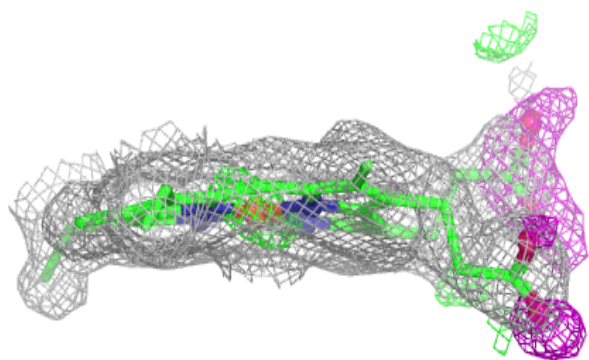
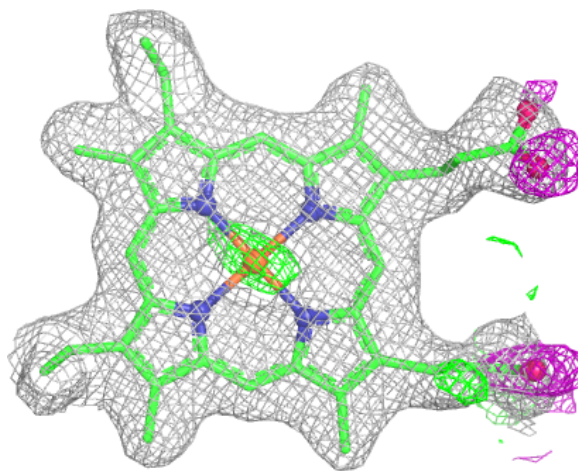
Electron density around HEC D 502:

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



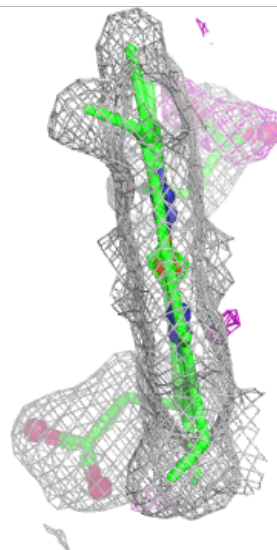
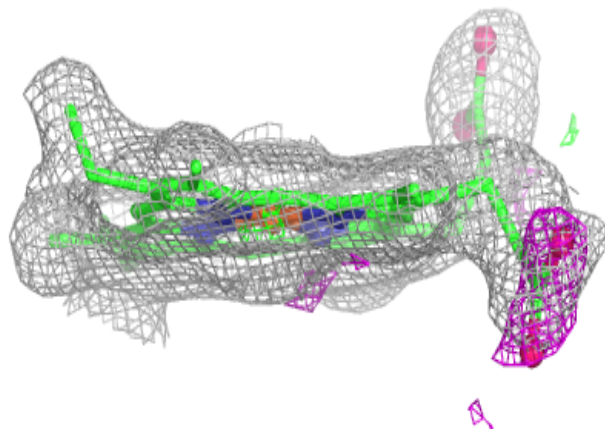
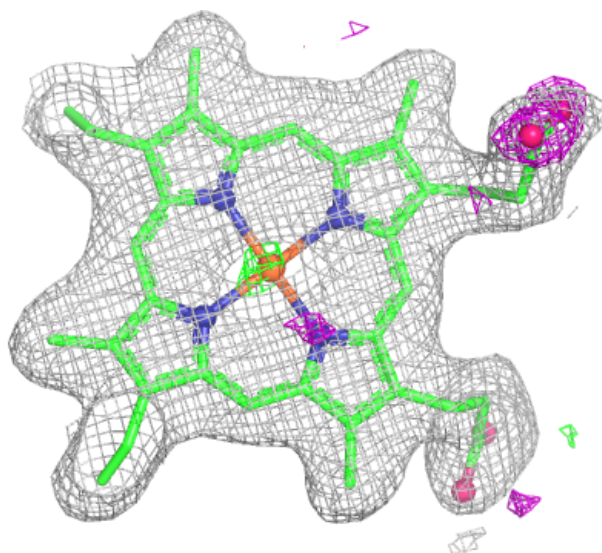
Electron density around HEC D 504:

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



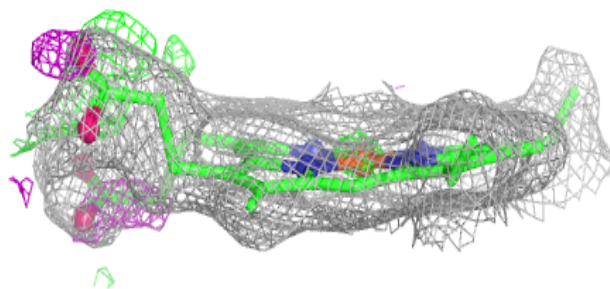
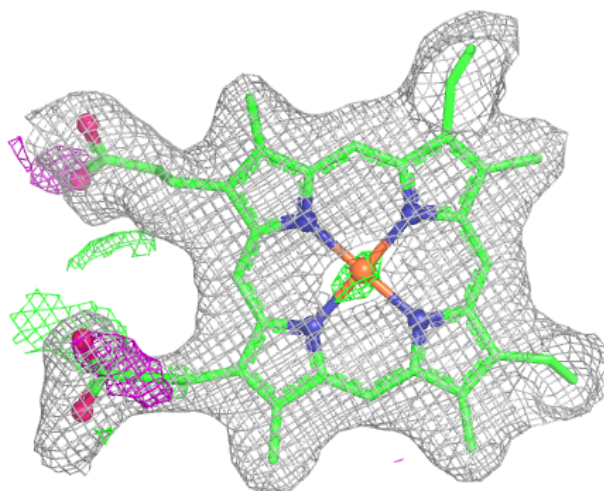
Electron density around HEC D 505:

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



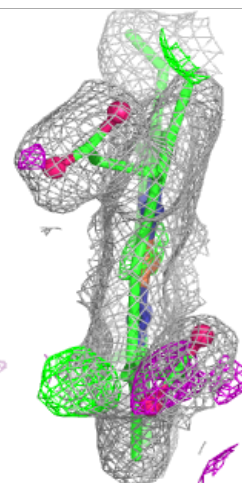
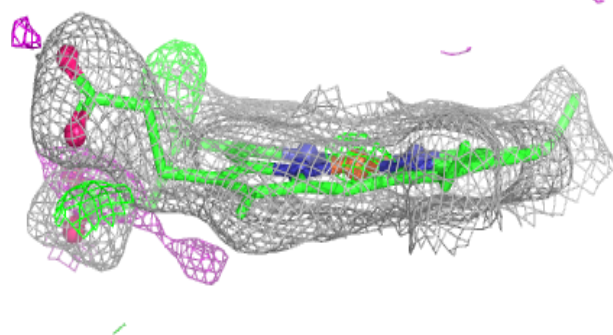
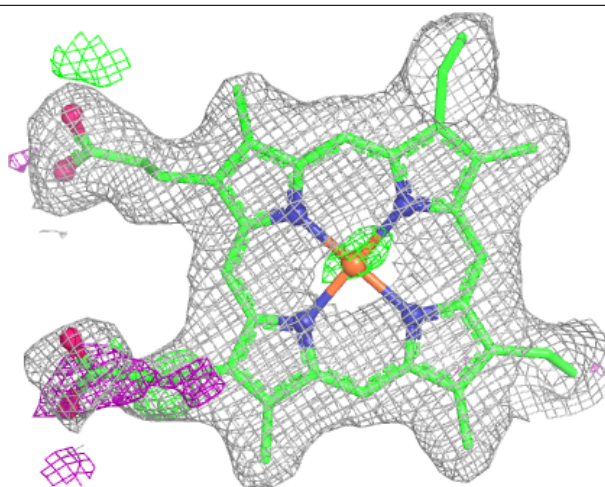
Electron density around HEC B 504:

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



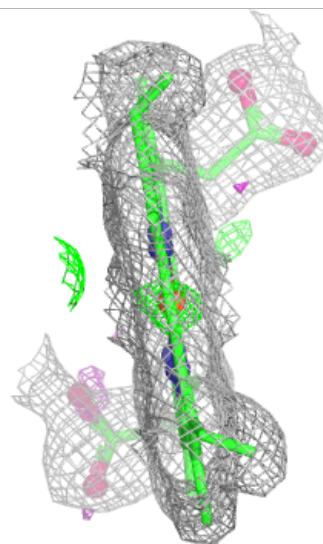
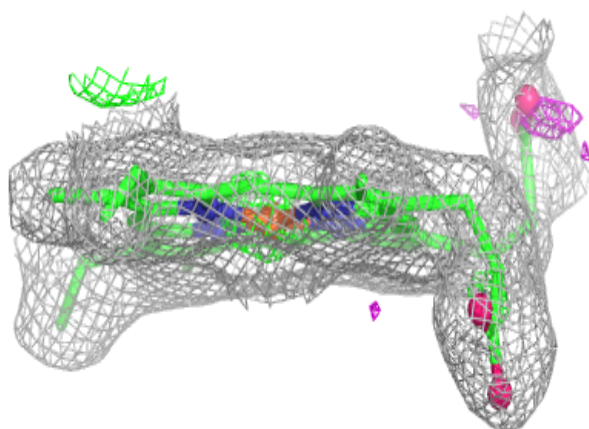
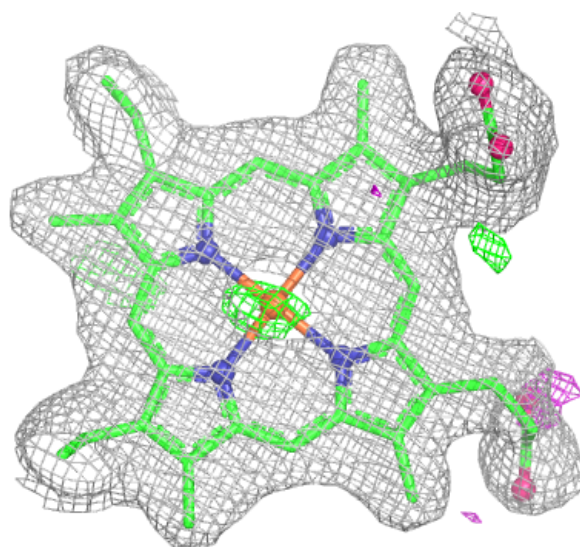
Electron density around HEC A 504:

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



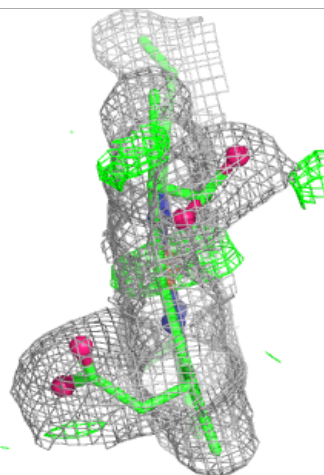
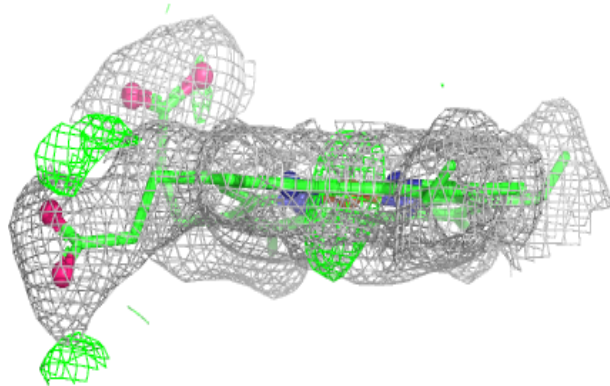
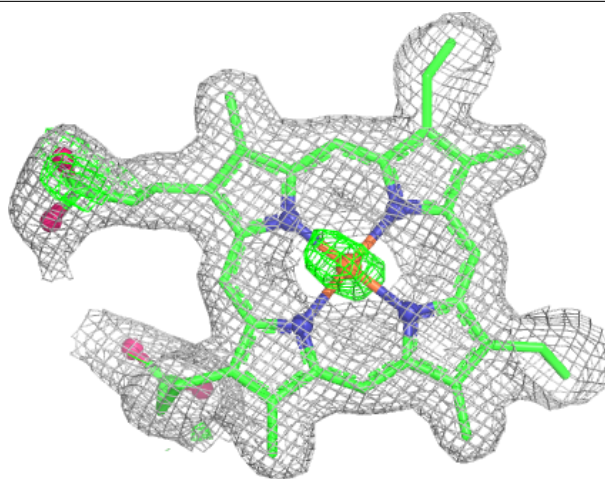
Electron density around HEC B 501:

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



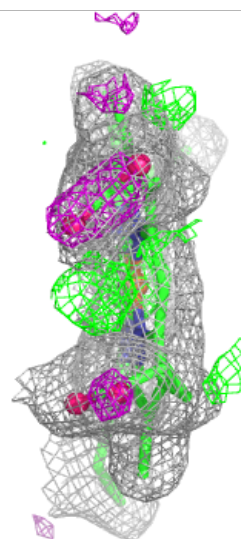
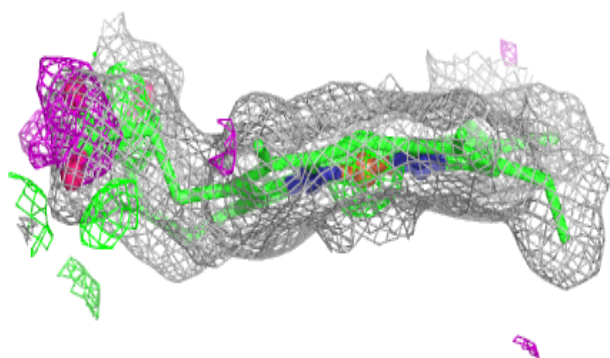
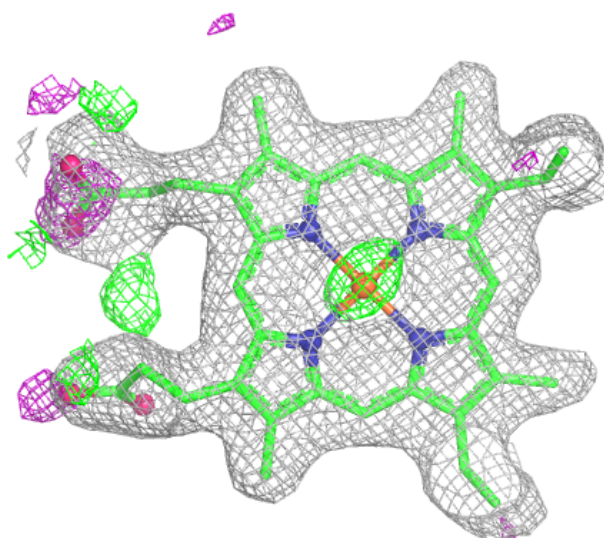
Electron density around HEC D 501:

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



Electron density around HEC D 503:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.