



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 15, 2026 – 12:17 PM JST

PDB ID : 9WTC / pdb_00009wtc
Title : Crystal structure of a selenate-soaked multiheme cytochrome c selenoprotein mutant (MccSep U325A)
Authors : Mihara, H.; Yoshizawa, T.; Izu, Y.; Inoue, M.; Aono, R.; Zhang, W.; Shibamoto, N.; Tobe, R.; Kurihara, T.; Matsumura, H.
Deposited on : 2025-09-16
Resolution : 2.20 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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

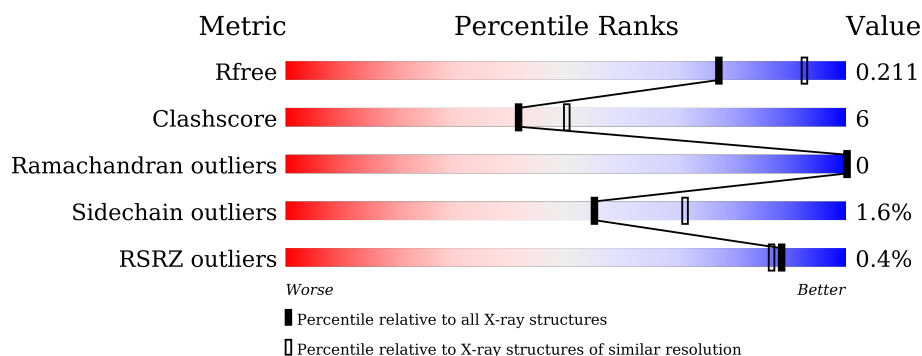
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	450	
1	B	450	
1	C	450	
1	D	450	

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
4	EDO	D	515	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15244 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Cytochrome c, Multiheme cytochrome c selenoprotein (MccSep).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	422	Total	C	N	O	S	0	9	0
			3322	2084	573	637	28			
1	B	422	Total	C	N	O	S	0	9	0
			3325	2091	572	634	28			
1	C	422	Total	C	N	O	S	0	6	0
			3318	2079	574	637	28			
1	D	422	Total	C	N	O	S	0	5	0
			3300	2070	571	631	28			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	325	ALA	-	linker	UNP Q748R4
A	326	PRO	-	linker	UNP Q748R4
A	327	THR	-	linker	UNP Q748R4
A	328	PRO	-	linker	UNP Q748R4
A	329	ASN	-	linker	UNP Q748R4
A	330	ARG	-	linker	UNP Q748R4
A	331	LEU	-	linker	UNP Q748R4
A	332	VAL	-	linker	UNP Q748R4
A	333	LEU	-	linker	UNP Q748R4
A	334	SER	-	linker	UNP Q748R4
A	335	VAL	-	linker	UNP Q748R4
A	336	ILE	-	linker	UNP Q748R4
A	337	ALA	-	linker	UNP Q748R4
A	338	LYS	-	linker	UNP Q748R4
A	339	THR	-	linker	UNP Q748R4
A	340	LYS	-	linker	UNP Q748R4
A	341	ASP	-	linker	UNP Q748R4
A	342	GLY	-	linker	UNP Q748R4
A	343	GLU	-	linker	UNP Q748R4
A	344	GLU	-	linker	UNP Q748R4
A	345	VAL	-	linker	UNP Q748R4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	346	PHE	-	linker	UNP Q748R4
A	347	ASN	-	linker	UNP Q748R4
A	348	GLN	-	linker	UNP Q748R4
A	349	GLU	-	linker	UNP Q748R4
A	350	LYS	-	linker	UNP Q748R4
A	351	ILE	-	linker	UNP Q748R4
A	352	TYR	-	linker	UNP Q748R4
B	325	ALA	-	linker	UNP Q748R4
B	326	PRO	-	linker	UNP Q748R4
B	327	THR	-	linker	UNP Q748R4
B	328	PRO	-	linker	UNP Q748R4
B	329	ASN	-	linker	UNP Q748R4
B	330	ARG	-	linker	UNP Q748R4
B	331	LEU	-	linker	UNP Q748R4
B	332	VAL	-	linker	UNP Q748R4
B	333	LEU	-	linker	UNP Q748R4
B	334	SER	-	linker	UNP Q748R4
B	335	VAL	-	linker	UNP Q748R4
B	336	ILE	-	linker	UNP Q748R4
B	337	ALA	-	linker	UNP Q748R4
B	338	LYS	-	linker	UNP Q748R4
B	339	THR	-	linker	UNP Q748R4
B	340	LYS	-	linker	UNP Q748R4
B	341	ASP	-	linker	UNP Q748R4
B	342	GLY	-	linker	UNP Q748R4
B	343	GLU	-	linker	UNP Q748R4
B	344	GLU	-	linker	UNP Q748R4
B	345	VAL	-	linker	UNP Q748R4
B	346	PHE	-	linker	UNP Q748R4
B	347	ASN	-	linker	UNP Q748R4
B	348	GLN	-	linker	UNP Q748R4
B	349	GLU	-	linker	UNP Q748R4
B	350	LYS	-	linker	UNP Q748R4
B	351	ILE	-	linker	UNP Q748R4
B	352	TYR	-	linker	UNP Q748R4
C	325	ALA	-	linker	UNP Q748R4
C	326	PRO	-	linker	UNP Q748R4
C	327	THR	-	linker	UNP Q748R4
C	328	PRO	-	linker	UNP Q748R4
C	329	ASN	-	linker	UNP Q748R4
C	330	ARG	-	linker	UNP Q748R4
C	331	LEU	-	linker	UNP Q748R4

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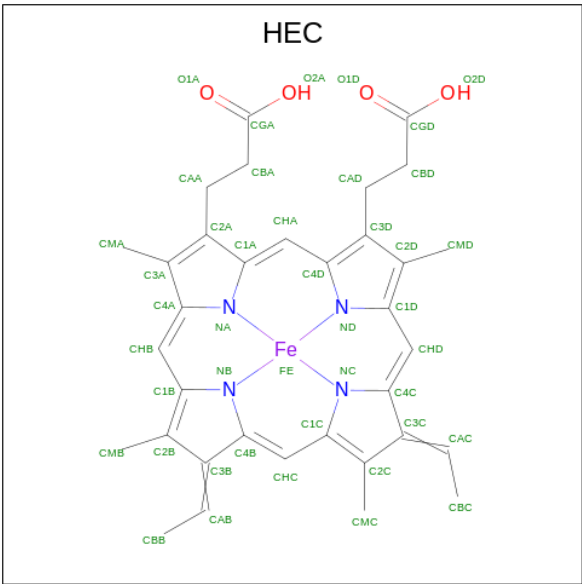
Chain	Residue	Modelled	Actual	Comment	Reference
C	332	VAL	-	linker	UNP Q748R4
C	333	LEU	-	linker	UNP Q748R4
C	334	SER	-	linker	UNP Q748R4
C	335	VAL	-	linker	UNP Q748R4
C	336	ILE	-	linker	UNP Q748R4
C	337	ALA	-	linker	UNP Q748R4
C	338	LYS	-	linker	UNP Q748R4
C	339	THR	-	linker	UNP Q748R4
C	340	LYS	-	linker	UNP Q748R4
C	341	ASP	-	linker	UNP Q748R4
C	342	GLY	-	linker	UNP Q748R4
C	343	GLU	-	linker	UNP Q748R4
C	344	GLU	-	linker	UNP Q748R4
C	345	VAL	-	linker	UNP Q748R4
C	346	PHE	-	linker	UNP Q748R4
C	347	ASN	-	linker	UNP Q748R4
C	348	GLN	-	linker	UNP Q748R4
C	349	GLU	-	linker	UNP Q748R4
C	350	LYS	-	linker	UNP Q748R4
C	351	ILE	-	linker	UNP Q748R4
C	352	TYR	-	linker	UNP Q748R4
D	325	ALA	-	linker	UNP Q748R4
D	326	PRO	-	linker	UNP Q748R4
D	327	THR	-	linker	UNP Q748R4
D	328	PRO	-	linker	UNP Q748R4
D	329	ASN	-	linker	UNP Q748R4
D	330	ARG	-	linker	UNP Q748R4
D	331	LEU	-	linker	UNP Q748R4
D	332	VAL	-	linker	UNP Q748R4
D	333	LEU	-	linker	UNP Q748R4
D	334	SER	-	linker	UNP Q748R4
D	335	VAL	-	linker	UNP Q748R4
D	336	ILE	-	linker	UNP Q748R4
D	337	ALA	-	linker	UNP Q748R4
D	338	LYS	-	linker	UNP Q748R4
D	339	THR	-	linker	UNP Q748R4
D	340	LYS	-	linker	UNP Q748R4
D	341	ASP	-	linker	UNP Q748R4
D	342	GLY	-	linker	UNP Q748R4
D	343	GLU	-	linker	UNP Q748R4
D	344	GLU	-	linker	UNP Q748R4
D	345	VAL	-	linker	UNP Q748R4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	346	PHE	-	linker	UNP Q748R4
D	347	ASN	-	linker	UNP Q748R4
D	348	GLN	-	linker	UNP Q748R4
D	349	GLU	-	linker	UNP Q748R4
D	350	LYS	-	linker	UNP Q748R4
D	351	ILE	-	linker	UNP Q748R4
D	352	TYR	-	linker	UNP Q748R4

- Molecule 2 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₄FeN₄O₄) (labeled as "Ligand of Interest" by depositor).



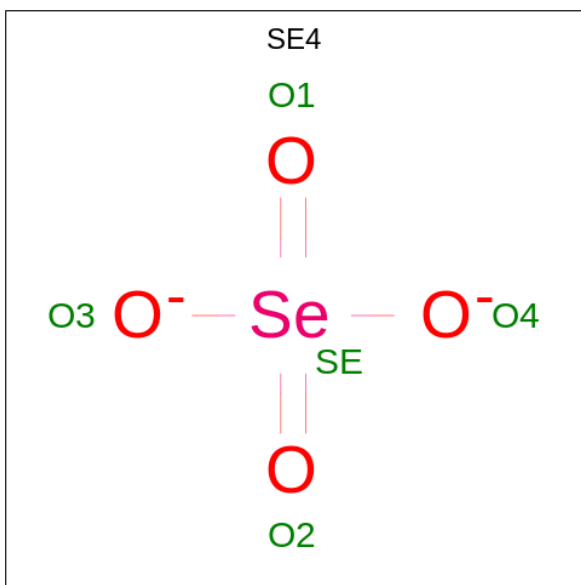
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0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

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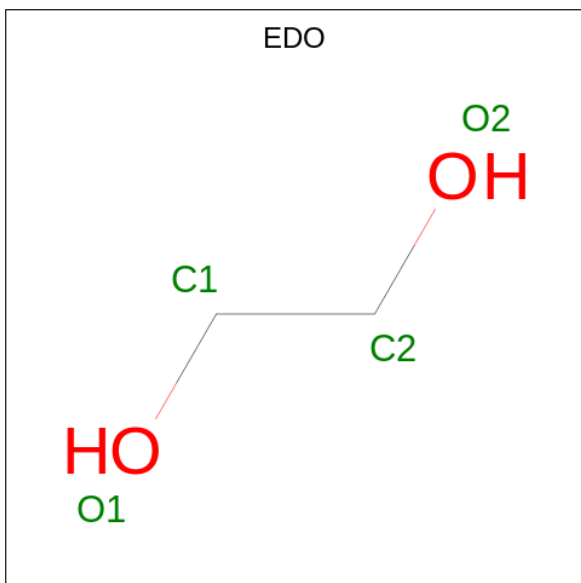
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0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

- Molecule 3 is SELENATE ION (CCD ID: SE4) (formula: O₄Se) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



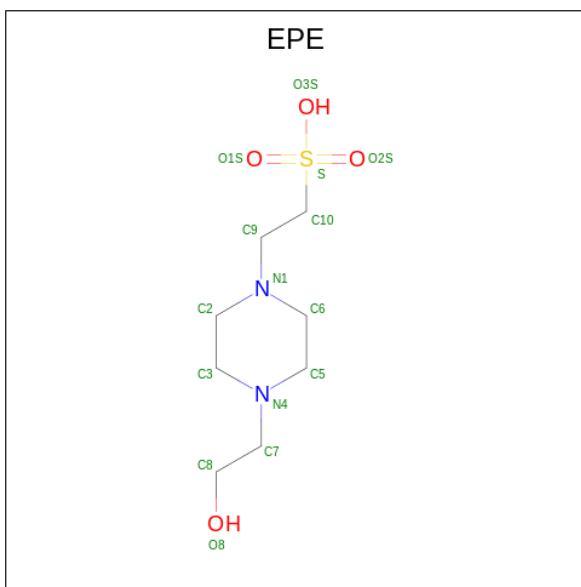
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0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

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

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

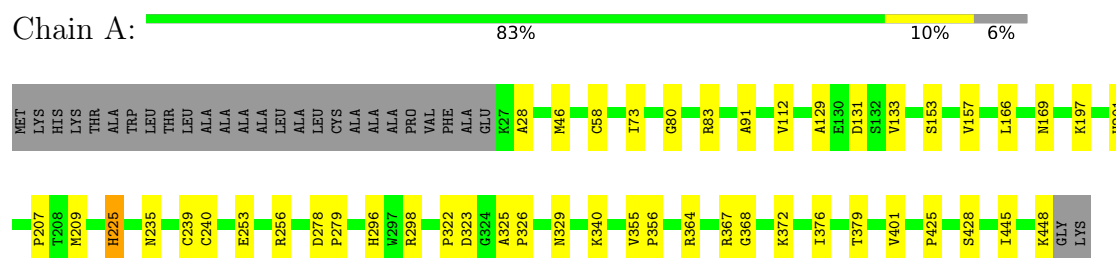
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	254	Total	O	0	0
			254	254		
6	B	253	Total	O	0	0
			253	253		
6	C	162	Total	O	0	0
			162	162		
6	D	247	Total	O	0	0
			247	247		

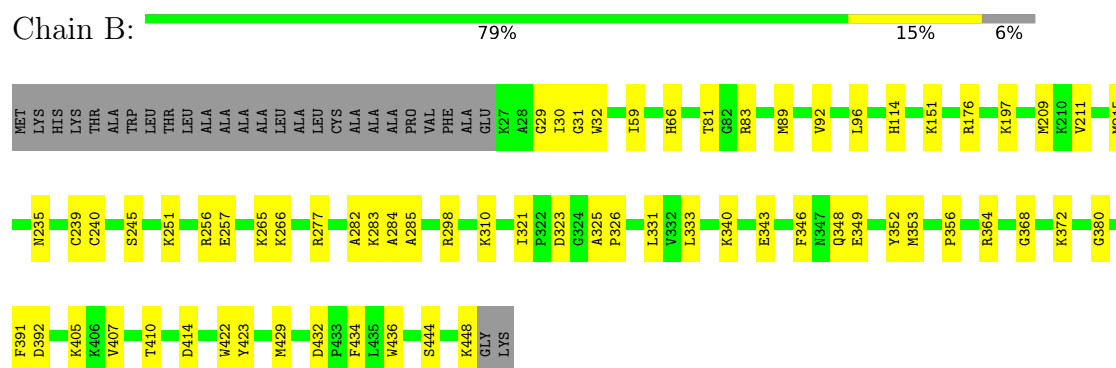
3 Residue-property plots

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

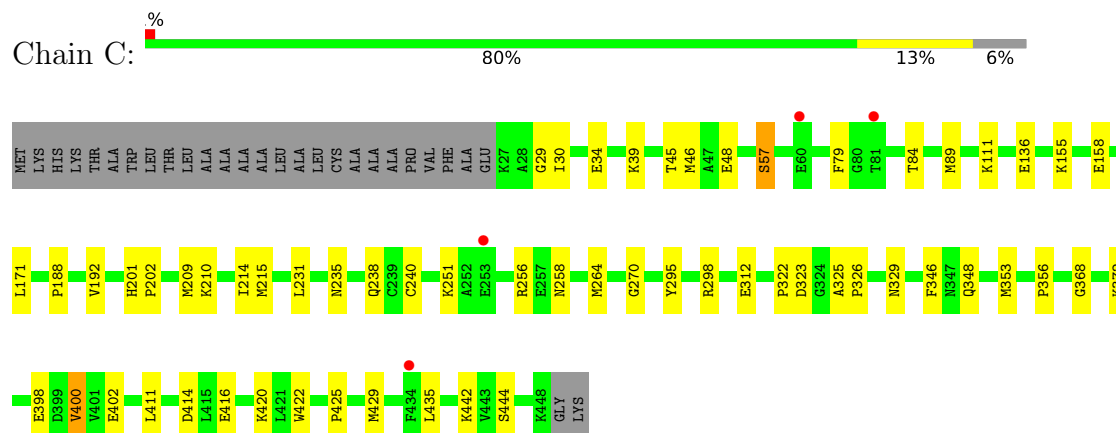
- Molecule 1: Cytochrome c, Multiheme cytochrome c selenoprotein (MccSep)



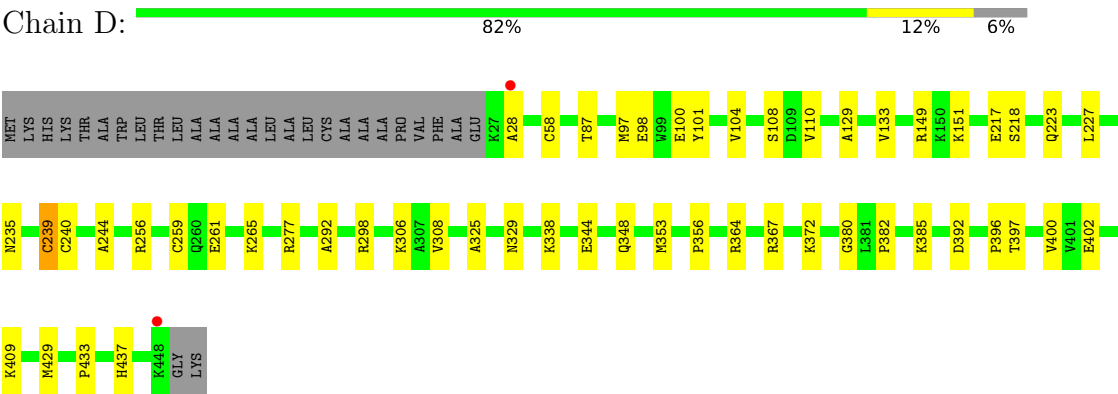
- Molecule 1: Cytochrome c, Multiheme cytochrome c selenoprotein (MccSep)



- Molecule 1: Cytochrome c, Multiheme cytochrome c selenoprotein (MccSep)



● Molecule 1: Cytochrome c,Multiheme cytochrome c selenoprotein (MccSep)



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.39Å 123.62Å 116.64Å 90.00° 91.60° 90.00°	Depositor
Resolution (Å)	44.06 – 2.20 44.06 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.06-2.20) 99.9 (44.06-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.168 , 0.214 0.166 , 0.211	Depositor DCC
R_{free} test set	5986 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.505	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.068 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	15244	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CSD, EDO, SE4, EPE, HEC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.32	0/3413	0.49	0/4611
1	B	0.32	0/3421	0.52	0/4623
1	C	0.30	0/3394	0.49	0/4585
1	D	0.33	0/3382	0.49	0/4569
All	All	0.32	0/13610	0.50	0/18388

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	225	HIS	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3322	0	3243	36	0
1	B	3325	0	3250	56	0
1	C	3318	0	3222	45	0
1	D	3300	0	3218	40	0
2	A	215	0	150	4	0
2	B	215	0	151	1	0
2	C	215	0	150	7	0
2	D	215	0	150	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	32	0	48	8	0
4	B	48	0	72	11	0
4	C	40	0	60	5	0
4	D	48	0	72	14	0
5	B	15	0	17	3	0
6	A	254	0	0	8	0
6	B	253	0	0	13	0
6	C	162	0	0	6	0
6	D	247	0	0	9	0
All	All	15244	0	13803	180	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.

All (180) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240[B]:CYS:SG	6:B:606:HOH:O	2.16	1.04
1:B:176:ARG:HH22	4:B:519:EDO:H11	1.28	0.99
1:C:240[B]:CYS:SG	6:C:606:HOH:O	2.21	0.98
1:D:240[B]:CYS:SG	6:D:605:HOH:O	2.21	0.98
1:D:397:THR:H	4:D:517:EDO:H22	1.40	0.85
1:B:284:ALA:HB1	4:B:518:EDO:H21	1.66	0.77
1:D:325:ALA:O	6:D:602:HOH:O	2.02	0.76
1:A:73:ILE:HD11	1:A:80:GLY:HA2	1.66	0.76
1:A:448:LYS:NZ	6:A:602:HOH:O	2.13	0.76
1:B:325:ALA:O	6:B:601:HOH:O	2.05	0.74
1:B:197:LYS:HB2	1:B:209:MET:HE3	1.71	0.73
1:B:245:SER:OG	6:B:602:HOH:O	2.09	0.70
1:B:392:ASP:H	4:B:515:EDO:H11	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:LEU:HD21	2:C:502:HEC:HBB3	1.72	0.70
1:A:253:GLU:HA	4:A:514:EDO:H12	1.73	0.69
4:D:515:EDO:O2	6:D:601:HOH:O	1.97	0.68
1:C:155:LYS:HA	1:C:158:GLU:HG3	1.73	0.68
1:D:298:ARG:HH12	4:D:501:EDO:H11	1.59	0.68
1:B:176:ARG:NH2	4:B:519:EDO:H11	2.07	0.67
1:B:298:ARG:HG2	6:B:603:HOH:O	1.95	0.67
1:B:31:GLY:HA3	4:B:508:EDO:H12	1.77	0.67
1:A:46:MET:HG2	1:A:166:LEU:HD11	1.77	0.66
1:A:325:ALA:O	6:A:603:HOH:O	2.14	0.65
4:A:512:EDO:H11	1:C:353:MET:HG2	1.78	0.65
1:B:346:PHE:CZ	1:B:348:GLN:HG3	2.32	0.65
1:B:323:ASP:OD1	6:B:601:HOH:O	2.14	0.65
1:C:312:GLU:HG3	4:C:512:EDO:H21	1.79	0.64
1:D:344:GLU:OE1	6:D:603:HOH:O	2.14	0.64
1:C:398:GLU:HG2	1:C:411:LEU:HD21	1.80	0.64
1:B:410:THR:HB	1:B:448:LYS:HE3	1.80	0.63
1:C:346:PHE:CZ	1:C:348:GLN:HG3	2.33	0.63
1:D:87:THR:HG22	2:D:504:HEC:HMB2	1.80	0.62
1:A:298:ARG:HH22	4:A:513:EDO:H21	1.65	0.60
1:C:188:PRO:HD2	4:C:508:EDO:H11	1.84	0.60
4:B:509:EDO:H22	1:D:353:MET:HG2	1.84	0.59
1:C:356:PRO:HB2	1:C:372:LYS:HG2	1.84	0.59
1:C:258:ASN:ND2	6:C:607:HOH:O	2.35	0.59
1:A:364:ARG:NH1	6:A:601:HOH:O	2.04	0.58
1:C:201:HIS:HB2	1:C:209:MET:HB3	1.84	0.58
1:A:298:ARG:HD3	6:A:801:HOH:O	2.02	0.58
1:D:364:ARG:NH1	6:D:607:HOH:O	2.34	0.57
1:C:326:PRO:HG2	1:C:425:PRO:O	2.05	0.57
1:B:298:ARG:NH1	6:B:603:HOH:O	2.31	0.57
1:B:285:ALA:HB3	1:B:436[B]:TRP:HZ2	1.70	0.56
1:D:100:GLU:HB2	4:D:516:EDO:H11	1.86	0.56
1:A:240[B]:CYS:SG	6:A:606:HOH:O	2.16	0.56
1:B:353:MET:HG2	4:D:502:EDO:H22	1.87	0.56
1:C:231:LEU:HD13	1:D:223:GLN:HA	1.89	0.55
1:C:416:GLU:HG3	6:C:663:HOH:O	2.05	0.54
1:B:81:THR:HB	5:B:507:EPE:H61	1.87	0.54
1:B:340:LYS:HE2	1:B:414:ASP:HB2	1.89	0.54
1:A:153:SER:O	1:A:157:VAL:HG23	2.08	0.54
1:B:265:LYS:NZ	6:B:611:HOH:O	2.40	0.54
1:A:326:PRO:HG2	1:A:425:PRO:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:PRO:HB2	1:A:372:LYS:HG2	1.90	0.53
1:A:367:ARG:HG2	1:C:298:ARG:CZ	2.39	0.53
2:C:506:HEC:HHA	2:C:506:HEC:CGD	2.38	0.53
1:C:46:MET:HG3	1:C:136:GLU:CD	2.33	0.53
1:D:239:CSD:OD2	1:D:325:ALA:HB2	2.08	0.52
2:B:505:HEC:HHA	2:B:505:HEC:CGD	2.39	0.52
1:A:112:VAL:HG23	1:A:131:ASP:HA	1.92	0.52
1:D:437:HIS:HA	4:D:511:EDO:H11	1.91	0.52
1:D:256:ARG:HD2	4:D:509:EDO:C1	2.40	0.51
2:C:503:HEC:HMC3	2:C:503:HEC:HBC3	1.93	0.51
1:B:423:TYR:HD2	1:B:436[B]:TRP:HZ3	1.58	0.50
1:C:256:ARG:HD2	4:C:509:EDO:C1	2.41	0.50
1:D:298:ARG:HH22	4:D:501:EDO:HO2	1.58	0.50
2:D:507:HEC:CGD	2:D:507:HEC:HHA	2.41	0.50
1:A:298:ARG:HH22	4:A:513:EDO:C2	2.25	0.50
1:B:282:ALA:C	1:B:436[B]:TRP:HE1	2.18	0.50
1:C:171:LEU:HD21	2:C:502:HEC:CBB	2.41	0.50
1:A:322:PRO:HB2	1:A:329[B]:ASN:ND2	2.26	0.50
1:D:98:GLU:HG3	6:D:757:HOH:O	2.11	0.50
1:D:217:GLU:OE1	4:D:515:EDO:H22	2.12	0.50
1:A:340:LYS:HE3	6:A:722:HOH:O	2.11	0.49
1:B:251:LYS:NZ	6:B:604:HOH:O	2.32	0.49
1:B:364:ARG:NH1	6:B:607:HOH:O	2.33	0.49
1:D:100:GLU:HG2	1:D:101:TYR:CZ	2.46	0.49
1:D:397:THR:N	4:D:517:EDO:H22	2.19	0.49
1:D:298:ARG:NH1	4:D:501:EDO:H11	2.27	0.49
1:B:256:ARG:HD2	4:B:510:EDO:C1	2.43	0.48
1:C:240[B]:CYS:SG	1:C:323:ASP:OD2	2.71	0.48
1:D:380:GLY:HA3	6:D:621:HOH:O	2.12	0.48
1:B:380:GLY:HA3	6:B:707:HOH:O	2.12	0.48
1:D:149:ARG:O	1:D:151:LYS:HE2	2.14	0.48
1:B:368:GLY:O	1:B:372:LYS:HG3	2.14	0.48
1:B:423:TYR:HD2	1:B:436[B]:TRP:CZ3	2.31	0.48
1:A:256:ARG:HD2	4:A:511:EDO:C1	2.43	0.48
1:A:129:ALA:HB1	1:A:133:VAL:HG21	1.96	0.48
1:B:240[B]:CYS:SG	1:B:323:ASP:OD2	2.72	0.48
1:B:310:LYS:HG2	4:B:513:EDO:H22	1.95	0.47
2:A:502:HEC:HBC3	2:A:502:HEC:HMC3	1.96	0.47
1:B:277:ARG:HG2	1:B:434:PHE:CZ	2.49	0.47
2:A:505:HEC:CGD	2:A:505:HEC:HHA	2.44	0.47
1:B:414:ASP:OD2	1:B:444:SER:HB3	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:400:VAL:HG23	1:C:402:GLU:HG3	1.95	0.47
1:A:225:HIS:ND1	6:A:606:HOH:O	2.29	0.47
1:B:257:GLU:OE2	1:B:266:LYS:HE2	2.14	0.47
1:B:298:ARG:CZ	1:D:367:ARG:HG2	2.44	0.47
1:A:197:LYS:HB2	1:A:209:MET:HE3	1.97	0.47
1:B:422:TRP:CD1	1:B:429:MET:HE1	2.50	0.47
1:D:97:MET:HG3	1:D:104:VAL:HG12	1.97	0.47
1:C:34[B]:GLU:HA	1:C:39:LYS:HE2	1.96	0.46
1:C:322:PRO:HB2	1:C:329[B]:ASN:ND2	2.30	0.46
1:D:356:PRO:HG3	1:D:372:LYS:HD3	1.97	0.46
1:C:442:LYS:HB3	1:C:442:LYS:HE3	1.83	0.46
1:C:45:THR:OG1	1:C:48:GLU:HG3	2.16	0.46
1:C:251:LYS:HA	1:C:251:LYS:HD2	1.69	0.46
1:B:432:ASP:OD2	5:B:507:EPE:H52	2.16	0.45
1:D:218:SER:H	4:D:515:EDO:H21	1.80	0.45
1:B:31:GLY:HA3	4:B:508:EDO:C1	2.45	0.45
1:C:57:SER:OG	6:C:601:HOH:O	2.21	0.45
1:C:89:MET:HE2	1:C:89:MET:HB2	1.81	0.45
1:B:298:ARG:HD3	6:B:668:HOH:O	2.17	0.45
1:C:215:MET:HE2	1:C:215:MET:HB2	1.78	0.45
1:B:239:CSD:HB2	1:B:240[B]:CYS:H	1.57	0.45
1:B:59:ILE:HG12	1:B:66:HIS:CG	2.52	0.44
1:D:306:LYS:NZ	1:D:392:ASP:OD2	2.50	0.44
1:C:414:ASP:OD1	1:C:444:SER:OG	2.26	0.44
2:C:502:HEC:HBA2	2:C:504:HEC:HMA2	1.99	0.44
1:D:129:ALA:HB1	1:D:133:VAL:HG21	1.99	0.44
1:D:338:LYS:NZ	6:D:626:HOH:O	2.51	0.44
1:B:391:PHE:HA	4:B:515:EDO:H11	1.99	0.44
1:A:376:ILE:O	4:B:510:EDO:O2	2.33	0.44
1:B:29:GLY:C	1:B:30:ILE:HD13	2.42	0.44
1:B:59:ILE:HG12	1:B:66:HIS:ND1	2.33	0.44
1:A:296:HIS:CE1	1:A:445:ILE:HD12	2.53	0.43
1:B:283:LYS:HA	1:B:283:LYS:HD3	1.68	0.43
1:B:356:PRO:HG3	6:B:744:HOH:O	2.18	0.43
1:C:240[A]:CYS:SG	2:C:503:HEC:HMD1	2.58	0.43
1:B:239:CSD:OD2	1:B:325:ALA:HB2	2.18	0.43
1:C:202:PRO:O	2:C:502:HEC:HBC2	2.19	0.43
1:A:83:ARG:HG2	2:A:502:HEC:HMA3	2.01	0.43
1:C:111:LYS:HD2	1:D:28:ALA:HB2	2.01	0.43
1:B:356:PRO:HG3	1:B:372:LYS:HD3	2.00	0.43
1:C:192:VAL:HG11	1:C:210:LYS:HD2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:429:MET:O	1:D:433:PRO:HG3	2.18	0.43
1:C:171:LEU:HD13	1:C:171:LEU:HA	1.91	0.43
2:A:502:HEC:HBC1	4:A:510:EDO:H22	2.01	0.42
1:B:89:MET:HE2	1:B:89:MET:HB2	1.76	0.42
1:D:218:SER:HB2	4:D:515:EDO:H21	2.01	0.42
1:A:28:ALA:HB1	1:B:114:HIS:NE2	2.35	0.42
1:B:32:TRP:CD1	1:B:32:TRP:H	2.36	0.42
1:B:326:PRO:HA	6:B:786:HOH:O	2.18	0.42
1:C:264:MET:HG2	1:C:270:GLY:O	2.19	0.42
1:D:402:GLU:OE2	1:D:409:LYS:NZ	2.31	0.42
1:A:256:ARG:HD2	4:A:511:EDO:O1	2.19	0.42
1:A:368:GLY:C	1:A:372:LYS:HD3	2.44	0.42
1:C:323:ASP:OD1	6:C:602:HOH:O	2.21	0.42
1:C:368:GLY:C	1:C:372:LYS:HD3	2.45	0.42
1:A:201:HIS:O	1:A:207:PRO:HA	2.20	0.42
1:C:29:GLY:C	1:C:30:ILE:HD13	2.45	0.42
1:C:422:TRP:CD1	1:C:429:MET:HE1	2.55	0.42
1:A:240[B]:CYS:SG	1:A:323:ASP:OD2	2.78	0.42
1:B:92:VAL:HG22	1:B:96:LEU:HD12	2.02	0.41
1:C:325:ALA:O	6:C:602:HOH:O	2.22	0.41
1:D:292:ALA:HA	1:D:308:VAL:O	2.19	0.41
1:B:333:LEU:O	1:B:349:GLU:HA	2.20	0.41
1:D:261[B]:GLU:OE1	1:D:265:LYS:HE2	2.19	0.41
1:D:227:LEU:HA	1:D:244:ALA:HB2	2.02	0.41
1:A:448:LYS:HB2	1:A:448:LYS:HE2	1.86	0.41
1:B:83:ARG:NH1	5:B:507:EPE:O1S	2.53	0.41
1:C:79:PHE:O	1:C:84:THR:HB	2.21	0.41
1:D:382:PRO:HG2	1:D:385:LYS:HB3	2.02	0.41
1:A:91:ALA:HB1	4:A:508:EDO:H22	2.03	0.41
1:A:169:ASN:HB2	6:A:799:HOH:O	2.20	0.41
1:A:278:ASP:HA	1:A:279:PRO:HD3	1.95	0.41
1:A:379:THR:OG1	4:C:501:EDO:H12	2.20	0.41
1:B:215:MET:HE2	1:B:215:MET:HB2	1.94	0.41
1:D:239:CSD:HD2	1:D:240[B]:CYS:HB2	1.86	0.41
1:D:396:PRO:HA	4:D:517:EDO:C2	2.51	0.41
1:A:239:CSD:HB2	1:A:240[B]:CYS:H	1.64	0.40
1:C:238:GLN:O	1:C:372:LYS:HE2	2.21	0.40
1:C:420:LYS:HG2	1:C:435:LEU:HD11	2.03	0.40
1:B:251:LYS:HA	1:B:251:LYS:HD2	1.78	0.40
1:D:277:ARG:HG3	6:D:680:HOH:O	2.21	0.40
1:C:258:ASN:ND2	4:C:511:EDO:H12	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:VAL:HG11	1:C:295:TYR:CE1	2.56	0.40
1:B:331:LEU:HB2	1:B:352:TYR:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	428/450 (95%)	407 (95%)	21 (5%)	0	100	100
1	B	428/450 (95%)	410 (96%)	18 (4%)	0	100	100
1	C	425/450 (94%)	407 (96%)	18 (4%)	0	100	100
1	D	424/450 (94%)	408 (96%)	16 (4%)	0	100	100
All	All	1705/1800 (95%)	1632 (96%)	73 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	360/368 (98%)	356 (99%)	4 (1%)	65	79
1	B	360/368 (98%)	353 (98%)	7 (2%)	50	66
1	C	357/368 (97%)	353 (99%)	4 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	356/368 (97%)	349 (98%)	7 (2%)	48 64
All	All	1433/1472 (97%)	1411 (98%)	22 (2%)	55 73

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	CYS
1	A	235	ASN
1	A	401	VAL
1	A	428	SER
1	B	151	LYS
1	B	211	VAL
1	B	235	ASN
1	B	321	ILE
1	B	343	GLU
1	B	405	LYS
1	B	407	VAL
1	C	57	SER
1	C	214	ILE
1	C	235	ASN
1	C	400	VAL
1	D	58	CYS
1	D	108	SER
1	D	110	VAL
1	D	235	ASN
1	D	259	CYS
1	D	348	GLN
1	D	400	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	388	HIS
1	A	441	GLN
1	B	358	GLN
1	C	189	GLN
1	C	258	ASN
1	C	348	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSD	A	239	2,1	3,7,8	0.99	0	1,8,10	0.82	0
1	CSD	C	239	2,1	3,7,8	1.04	0	1,8,10	0.34	0
1	CSD	D	239	2,1	3,7,8	1.09	0	1,8,10	3.06	1 (100%)
1	CSD	B	239	2,1	3,7,8	1.08	0	1,8,10	0.82	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
1	CSD	A	239	2,1	-	1/2/6/8	-
1	CSD	C	239	2,1	-	1/2/6/8	-
1	CSD	D	239	2,1	-	0/2/6/8	-
1	CSD	B	239	2,1	-	1/2/6/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	239	CSD	OD1-SG-CB	3.06	111.37	105.54

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	239	CSD	CA-CB-SG-OD1
1	B	239	CSD	CA-CB-SG-OD1
1	C	239	CSD	CA-CB-SG-OD1

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	239	CSD	1	0
1	D	239	CSD	2	0
1	B	239	CSD	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

67 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	HEC	C	503	1	46,50,50	3.53	5 (10%)	60,82,82	1.47	9 (15%)
2	HEC	D	507	1	46,50,50	3.59	7 (15%)	60,82,82	1.59	10 (16%)
4	EDO	A	513	-	3,3,3	0.54	0	2,2,2	0.14	0
2	HEC	B	505	1	46,50,50	3.54	7 (15%)	60,82,82	1.62	10 (16%)
2	HEC	C	504	1	46,50,50	3.53	7 (15%)	60,82,82	1.36	8 (13%)
4	EDO	A	514	-	3,3,3	0.52	0	2,2,2	0.09	0
4	EDO	B	518	-	3,3,3	0.45	0	2,2,2	0.14	0
4	EDO	C	512	-	3,3,3	0.45	0	2,2,2	0.39	0
2	HEC	C	505	1	46,50,50	3.65	6 (13%)	60,82,82	1.42	8 (13%)
4	EDO	D	513	-	3,3,3	0.54	0	2,2,2	0.20	0
5	EPE	B	507	-	15,15,15	0.79	1 (6%)	18,20,20	2.10	7 (38%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	509	-	3,3,3	0.49	0	2,2,2	0.36	0
4	EDO	D	514	-	3,3,3	0.53	0	2,2,2	0.19	0
4	EDO	D	502	-	3,3,3	0.43	0	2,2,2	0.58	0
4	EDO	C	514	-	3,3,3	0.48	0	2,2,2	0.34	0
2	HEC	B	502	1	46,50,50	3.59	7 (15%)	60,82,82	1.40	5 (8%)
4	EDO	B	516	-	3,3,3	0.48	0	2,2,2	0.38	0
2	HEC	B	503	1	46,50,50	3.55	6 (13%)	60,82,82	1.57	8 (13%)
2	HEC	A	503	1	46,50,50	3.49	9 (19%)	60,82,82	1.41	5 (8%)
2	HEC	B	504	1	46,50,50	3.60	5 (10%)	60,82,82	1.34	3 (5%)
4	EDO	B	511	-	3,3,3	0.45	0	2,2,2	0.41	0
4	EDO	D	512	-	3,3,3	0.50	0	2,2,2	0.25	0
4	EDO	B	515	-	3,3,3	0.46	0	2,2,2	0.48	0
3	SE4	C	507	-	4,4,4	0.57	0	1,6,6	2.68	1 (100%)
2	HEC	A	501	1	46,50,50	3.60	7 (15%)	60,82,82	1.34	7 (11%)
4	EDO	C	513	-	3,3,3	0.53	0	2,2,2	0.29	0
4	EDO	D	516	-	3,3,3	0.51	0	2,2,2	0.36	0
4	EDO	D	501	-	3,3,3	0.49	0	2,2,2	0.42	0
4	EDO	A	510	-	3,3,3	0.67	0	2,2,2	0.07	0
2	HEC	D	503	1	46,50,50	3.59	6 (13%)	60,82,82	1.65	12 (20%)
4	EDO	B	517	-	3,3,3	0.77	0	2,2,2	0.20	0
2	HEC	C	506	1	46,50,50	3.72	7 (15%)	60,82,82	1.60	10 (16%)
4	EDO	C	501	-	3,3,3	0.51	0	2,2,2	0.36	0
2	HEC	D	505	1	46,50,50	3.62	8 (17%)	60,82,82	1.38	7 (11%)
2	HEC	B	501	1	46,50,50	3.54	6 (13%)	60,82,82	1.52	8 (13%)
4	EDO	C	510	-	3,3,3	0.45	0	2,2,2	0.27	0
3	SE4	D	508	-	4,4,4	0.55	0	1,6,6	2.04	1 (100%)
4	EDO	B	513	-	3,3,3	0.59	0	2,2,2	0.21	0
4	EDO	D	517	-	3,3,3	0.53	0	2,2,2	0.37	0
4	EDO	A	511	-	3,3,3	0.60	0	2,2,2	0.38	0
4	EDO	A	508	-	3,3,3	0.51	0	2,2,2	0.51	0
4	EDO	B	512	-	3,3,3	0.49	0	2,2,2	0.60	0
4	EDO	B	514	-	3,3,3	0.48	0	2,2,2	0.34	0
3	SE4	A	506	-	4,4,4	0.59	0	1,6,6	2.84	1 (100%)
4	EDO	C	508	-	3,3,3	0.52	0	2,2,2	0.32	0
4	EDO	A	512	-	3,3,3	0.41	0	2,2,2	0.43	0
4	EDO	D	518	-	3,3,3	0.66	0	2,2,2	0.17	0
4	EDO	B	509	-	3,3,3	0.36	0	2,2,2	0.51	0
4	EDO	D	511	-	3,3,3	0.58	0	2,2,2	0.05	0
4	EDO	A	507	-	3,3,3	0.52	0	2,2,2	0.39	0
2	HEC	A	502	1	46,50,50	3.63	5 (10%)	60,82,82	1.41	7 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SE4	B	506	-	4,4,4	0.55	0	1,6,6	2.72	1 (100%)
4	EDO	D	515	-	3,3,3	0.46	0	2,2,2	0.19	0
4	EDO	D	509	-	3,3,3	0.56	0	2,2,2	0.18	0
2	HEC	D	506	1	46,50,50	3.61	7 (15%)	60,82,82	1.41	7 (11%)
2	HEC	A	504	1	46,50,50	3.67	7 (15%)	60,82,82	1.36	6 (10%)
4	EDO	B	510	-	3,3,3	0.52	0	2,2,2	0.37	0
4	EDO	C	516	-	3,3,3	0.57	0	2,2,2	0.41	0
2	HEC	A	505	1	46,50,50	3.54	6 (13%)	60,82,82	1.66	10 (16%)
2	HEC	D	504	1	46,50,50	3.59	6 (13%)	60,82,82	1.49	5 (8%)
4	EDO	B	519	-	3,3,3	0.78	0	2,2,2	0.45	0
4	EDO	C	515	-	3,3,3	0.60	0	2,2,2	0.15	0
2	HEC	C	502	1	46,50,50	3.60	6 (13%)	60,82,82	1.52	12 (20%)
4	EDO	C	509	-	3,3,3	0.56	0	2,2,2	0.22	0
4	EDO	B	508	-	3,3,3	0.46	0	2,2,2	0.50	0
4	EDO	D	510	-	3,3,3	0.54	0	2,2,2	0.47	0
4	EDO	C	511	-	3,3,3	0.36	0	2,2,2	0.35	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	C	503	1	-	7/14/54/54	-
2	HEC	D	507	1	-	9/14/54/54	-
4	EDO	A	513	-	-	0/1/1/1	-
2	HEC	B	505	1	-	9/14/54/54	-
2	HEC	C	504	1	-	6/14/54/54	-
4	EDO	A	514	-	-	0/1/1/1	-
4	EDO	B	518	-	-	0/1/1/1	-
4	EDO	C	512	-	-	1/1/1/1	-
2	HEC	C	505	1	-	4/14/54/54	-
4	EDO	D	513	-	-	0/1/1/1	-
5	EPE	B	507	-	-	4/9/19/19	0/1/1/1
4	EDO	A	509	-	-	0/1/1/1	-
4	EDO	D	514	-	-	1/1/1/1	-
4	EDO	D	502	-	-	0/1/1/1	-
4	EDO	C	514	-	-	0/1/1/1	-
2	HEC	B	502	1	-	8/14/54/54	-
4	EDO	B	516	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEC	B	503	1	-	6/14/54/54	-
2	HEC	A	503	1	-	8/14/54/54	-
2	HEC	B	504	1	-	4/14/54/54	-
4	EDO	B	511	-	-	0/1/1/1	-
4	EDO	D	512	-	-	0/1/1/1	-
4	EDO	B	515	-	-	0/1/1/1	-
2	HEC	A	501	1	-	6/14/54/54	-
4	EDO	C	513	-	-	0/1/1/1	-
4	EDO	D	516	-	-	0/1/1/1	-
4	EDO	D	501	-	-	1/1/1/1	-
4	EDO	A	510	-	-	0/1/1/1	-
2	HEC	D	503	1	-	8/14/54/54	-
4	EDO	B	517	-	-	0/1/1/1	-
2	HEC	C	506	1	-	7/14/54/54	-
4	EDO	C	501	-	-	0/1/1/1	-
2	HEC	D	505	1	-	6/14/54/54	-
2	HEC	B	501	1	-	6/14/54/54	-
4	EDO	C	510	-	-	0/1/1/1	-
4	EDO	B	513	-	-	0/1/1/1	-
4	EDO	D	517	-	-	1/1/1/1	-
4	EDO	A	511	-	-	0/1/1/1	-
4	EDO	A	508	-	-	0/1/1/1	-
4	EDO	B	512	-	-	1/1/1/1	-
4	EDO	B	514	-	-	1/1/1/1	-
4	EDO	C	508	-	-	1/1/1/1	-
4	EDO	D	518	-	-	1/1/1/1	-
4	EDO	A	512	-	-	0/1/1/1	-
4	EDO	B	509	-	-	0/1/1/1	-
4	EDO	D	511	-	-	1/1/1/1	-
4	EDO	A	507	-	-	0/1/1/1	-
2	HEC	A	502	1	-	7/14/54/54	-
4	EDO	D	515	-	-	0/1/1/1	-
4	EDO	D	509	-	-	0/1/1/1	-
2	HEC	D	506	1	-	4/14/54/54	-
2	HEC	A	504	1	-	6/14/54/54	-
4	EDO	B	510	-	-	0/1/1/1	-
4	EDO	C	516	-	-	0/1/1/1	-
2	HEC	A	505	1	-	9/14/54/54	-
2	HEC	D	504	1	-	8/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	519	-	-	1/1/1/1	-
4	EDO	C	515	-	-	0/1/1/1	-
2	HEC	C	502	1	-	6/14/54/54	-
4	EDO	C	509	-	-	0/1/1/1	-
4	EDO	B	508	-	-	0/1/1/1	-
4	EDO	D	510	-	-	1/1/1/1	-
4	EDO	C	511	-	-	1/1/1/1	-

All (131) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	506	HEC	CAC-C3C	16.90	1.56	1.34
2	B	504	HEC	CAC-C3C	16.87	1.56	1.34
2	D	505	HEC	CAC-C3C	16.78	1.56	1.34
2	A	502	HEC	CAC-C3C	16.72	1.56	1.34
2	C	505	HEC	CAB-C3B	16.60	1.56	1.34
2	A	501	HEC	CAC-C3C	16.51	1.56	1.34
2	C	504	HEC	CAC-C3C	16.51	1.56	1.34
2	D	507	HEC	CAC-C3C	16.49	1.56	1.34
2	A	504	HEC	CAB-C3B	16.43	1.55	1.34
2	C	506	HEC	CAB-C3B	16.43	1.55	1.34
2	A	504	HEC	CAC-C3C	16.34	1.55	1.34
2	D	503	HEC	CAC-C3C	16.30	1.55	1.34
2	B	505	HEC	CAC-C3C	16.24	1.55	1.34
2	B	502	HEC	CAC-C3C	16.20	1.55	1.34
2	D	506	HEC	CAC-C3C	16.19	1.55	1.34
2	B	503	HEC	CAC-C3C	16.19	1.55	1.34
2	A	505	HEC	CAC-C3C	16.07	1.55	1.34
2	C	502	HEC	CAC-C3C	16.06	1.55	1.34
2	D	504	HEC	CAB-C3B	16.05	1.55	1.34
2	D	506	HEC	CAB-C3B	16.04	1.55	1.34
2	C	502	HEC	CAB-C3B	16.02	1.55	1.34
2	A	503	HEC	CAC-C3C	16.00	1.55	1.34
2	C	505	HEC	CAC-C3C	15.90	1.55	1.34
2	B	501	HEC	CAC-C3C	15.89	1.55	1.34
2	D	503	HEC	CAB-C3B	15.86	1.55	1.34
2	C	503	HEC	CAC-C3C	15.85	1.55	1.34
2	D	504	HEC	CAC-C3C	15.85	1.55	1.34
2	B	502	HEC	CAB-C3B	15.80	1.55	1.34
2	C	503	HEC	CAB-C3B	15.69	1.55	1.34
2	B	501	HEC	CAB-C3B	15.66	1.54	1.34
2	A	501	HEC	CAB-C3B	15.65	1.54	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	502	HEC	CAB-C3B	15.60	1.54	1.34
2	A	505	HEC	CAB-C3B	15.60	1.54	1.34
2	D	507	HEC	CAB-C3B	15.54	1.54	1.34
2	D	505	HEC	CAB-C3B	15.51	1.54	1.34
2	B	503	HEC	CAB-C3B	15.48	1.54	1.34
2	B	505	HEC	CAB-C3B	15.22	1.54	1.34
2	B	504	HEC	CAB-C3B	15.21	1.54	1.34
2	C	504	HEC	CAB-C3B	14.74	1.53	1.34
2	A	503	HEC	CAB-C3B	14.67	1.53	1.34
2	C	502	HEC	CBB-CAB	-4.24	1.33	1.49
2	C	504	HEC	CBB-CAB	-4.13	1.34	1.49
2	A	504	HEC	CBB-CAB	-4.11	1.34	1.49
2	B	501	HEC	CBC-CAC	-4.08	1.34	1.49
2	C	503	HEC	CBB-CAB	-4.07	1.34	1.49
2	B	504	HEC	CBB-CAB	-4.03	1.34	1.49
2	A	503	HEC	CBC-CAC	-4.03	1.34	1.49
2	C	502	HEC	CBC-CAC	-4.01	1.34	1.49
2	C	505	HEC	CBC-CAC	-4.00	1.34	1.49
2	A	502	HEC	CBB-CAB	-3.97	1.34	1.49
2	A	502	HEC	CBC-CAC	-3.97	1.34	1.49
2	A	503	HEC	CBB-CAB	-3.97	1.34	1.49
2	D	503	HEC	CBB-CAB	-3.97	1.34	1.49
2	D	503	HEC	CBC-CAC	-3.96	1.34	1.49
2	C	503	HEC	CBC-CAC	-3.94	1.34	1.49
2	A	501	HEC	CBC-CAC	-3.94	1.34	1.49
2	D	507	HEC	CBB-CAB	-3.93	1.34	1.49
2	C	504	HEC	CBC-CAC	-3.91	1.34	1.49
2	D	505	HEC	CBB-CAB	-3.91	1.34	1.49
2	B	503	HEC	CBB-CAB	-3.90	1.34	1.49
2	C	506	HEC	CBB-CAB	-3.89	1.34	1.49
2	D	504	HEC	CBB-CAB	-3.88	1.35	1.49
2	B	505	HEC	CBB-CAB	-3.86	1.35	1.49
2	D	507	HEC	CBC-CAC	-3.85	1.35	1.49
2	B	503	HEC	CBC-CAC	-3.85	1.35	1.49
2	A	505	HEC	CBB-CAB	-3.84	1.35	1.49
2	B	502	HEC	CBC-CAC	-3.83	1.35	1.49
2	A	505	HEC	CBC-CAC	-3.82	1.35	1.49
2	B	501	HEC	CBB-CAB	-3.82	1.35	1.49
2	B	502	HEC	CBB-CAB	-3.82	1.35	1.49
2	C	506	HEC	CBC-CAC	-3.82	1.35	1.49
2	D	505	HEC	CBC-CAC	-3.82	1.35	1.49
2	D	506	HEC	CBB-CAB	-3.81	1.35	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	505	HEC	CBB-CAB	-3.80	1.35	1.49
2	D	504	HEC	CBC-CAC	-3.74	1.35	1.49
2	A	501	HEC	CBB-CAB	-3.71	1.35	1.49
2	A	504	HEC	CBC-CAC	-3.70	1.35	1.49
2	B	505	HEC	CBC-CAC	-3.65	1.35	1.49
2	D	506	HEC	CBC-CAC	-3.64	1.35	1.49
2	B	504	HEC	CBC-CAC	-3.49	1.36	1.49
2	B	504	HEC	CMB-C2B	2.59	1.56	1.50
5	B	507	EPE	C10-S	2.55	1.81	1.77
2	A	504	HEC	CMA-C3A	2.53	1.56	1.50
2	A	501	HEC	CMC-C2C	2.44	1.56	1.50
2	B	505	HEC	CMB-C2B	2.44	1.56	1.50
2	A	503	HEC	CMC-C2C	2.43	1.55	1.50
2	D	503	HEC	CMC-C2C	2.38	1.55	1.50
2	A	501	HEC	CMB-C2B	2.35	1.55	1.50
2	C	506	HEC	CMB-C2B	2.34	1.55	1.50
2	D	504	HEC	CMB-C2B	2.34	1.55	1.50
2	D	506	HEC	CMA-C3A	2.33	1.55	1.50
2	C	504	HEC	CMB-C2B	2.33	1.55	1.50
2	B	501	HEC	CMC-C2C	2.32	1.55	1.50
2	B	502	HEC	CMB-C2B	2.32	1.55	1.50
2	D	503	HEC	CMD-C2D	2.31	1.55	1.50
2	A	503	HEC	C3B-C2B	-2.31	1.33	1.41
2	A	504	HEC	CMB-C2B	2.29	1.55	1.50
2	C	506	HEC	CMC-C2C	2.28	1.55	1.50
2	C	505	HEC	CMA-C3A	2.27	1.55	1.50
2	A	502	HEC	CMC-C2C	2.23	1.55	1.50
2	D	505	HEC	CMC-C2C	2.22	1.55	1.50
2	D	507	HEC	CMB-C2B	2.17	1.55	1.50
2	C	503	HEC	CMC-C2C	2.16	1.55	1.50
2	D	505	HEC	C3B-C2B	-2.15	1.33	1.41
2	A	503	HEC	CMA-C3A	2.14	1.55	1.50
2	B	501	HEC	CMA-C3A	2.14	1.55	1.50
2	C	504	HEC	CMC-C2C	2.13	1.55	1.50
2	C	505	HEC	C3C-C2C	-2.13	1.33	1.41
2	D	506	HEC	CMC-C2C	2.12	1.55	1.50
2	B	505	HEC	C3B-C2B	-2.12	1.33	1.41
2	A	501	HEC	CMD-C2D	2.09	1.55	1.50
2	D	504	HEC	CMC-C2C	2.09	1.55	1.50
2	B	502	HEC	CMA-C3A	2.09	1.55	1.50
2	C	502	HEC	CMB-C2B	2.08	1.55	1.50
2	B	502	HEC	C3B-C2B	-2.07	1.34	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	503	HEC	CMB-C2B	2.07	1.55	1.50
2	A	504	HEC	C3C-C2C	-2.06	1.34	1.41
2	B	503	HEC	CMA-C3A	2.06	1.55	1.50
2	D	505	HEC	CAA-C2A	2.05	1.56	1.51
2	C	506	HEC	CMD-C2D	2.04	1.55	1.50
2	C	504	HEC	CMA-C3A	2.04	1.55	1.50
2	D	507	HEC	C3B-C2B	-2.03	1.34	1.41
2	A	505	HEC	CMC-C2C	2.03	1.55	1.50
2	D	505	HEC	CMB-C2B	2.03	1.55	1.50
2	D	506	HEC	CMD-C2D	2.02	1.55	1.50
2	A	503	HEC	CMD-C2D	2.02	1.55	1.50
2	D	507	HEC	CAA-C2A	2.02	1.56	1.51
2	B	505	HEC	CMA-C3A	2.01	1.55	1.50
2	C	502	HEC	CMD-C2D	2.01	1.55	1.50
2	A	505	HEC	CMB-C2B	2.00	1.55	1.50
2	A	503	HEC	CMB-C2B	2.00	1.55	1.50

All (168) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	505	HEC	CBB-CAB-C3B	-6.86	115.25	127.86
2	A	505	HEC	CBB-CAB-C3B	-6.43	116.05	127.86
2	A	503	HEC	CBB-CAB-C3B	-6.23	116.42	127.86
2	D	504	HEC	CBB-CAB-C3B	-6.00	116.84	127.86
2	B	503	HEC	CBB-CAB-C3B	-5.68	117.42	127.86
2	B	501	HEC	CBB-CAB-C3B	-5.61	117.55	127.86
2	D	505	HEC	CBB-CAB-C3B	-5.56	117.65	127.86
2	D	507	HEC	CBB-CAB-C3B	-5.51	117.72	127.86
2	B	504	HEC	CBB-CAB-C3B	-5.42	117.90	127.86
2	C	506	HEC	CBB-CAB-C3B	-5.40	117.94	127.86
2	D	506	HEC	CBB-CAB-C3B	-5.21	118.29	127.86
2	B	502	HEC	CBB-CAB-C3B	-5.16	118.37	127.86
2	C	504	HEC	CBB-CAB-C3B	-4.86	118.92	127.86
2	D	503	HEC	CBB-CAB-C3B	-4.82	119.00	127.86
2	A	504	HEC	CBB-CAB-C3B	-4.80	119.03	127.86
2	B	505	HEC	CBC-CAC-C3C	-4.75	119.13	127.86
2	C	506	HEC	CBC-CAC-C3C	-4.70	119.22	127.86
2	C	503	HEC	CBB-CAB-C3B	-4.65	119.31	127.86
2	D	504	HEC	CBC-CAC-C3C	-4.65	119.32	127.86
2	C	505	HEC	CBB-CAB-C3B	-4.57	119.45	127.86
2	B	502	HEC	CBC-CAC-C3C	-4.55	119.49	127.86
2	A	502	HEC	CBB-CAB-C3B	-4.43	119.72	127.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	506	HEC	CBC-CAC-C3C	-4.40	119.78	127.86
2	A	502	HEC	CBD-CAD-C3D	-4.33	100.58	112.63
2	A	501	HEC	CBB-CAB-C3B	-4.25	120.04	127.86
5	B	507	EPE	C5-N4-C3	4.21	118.31	108.83
2	D	507	HEC	CBC-CAC-C3C	-4.16	120.21	127.86
2	B	503	HEC	CBC-CAC-C3C	-4.02	120.47	127.86
2	A	504	HEC	CBC-CAC-C3C	-3.93	120.63	127.86
2	C	505	HEC	CBC-CAC-C3C	-3.76	120.95	127.86
2	A	503	HEC	CBC-CAC-C3C	-3.74	120.98	127.86
5	B	507	EPE	C7-N4-C3	3.66	120.60	111.23
5	B	507	EPE	C7-N4-C5	3.62	120.48	111.23
2	C	502	HEC	CBC-CAC-C3C	-3.60	121.24	127.86
2	C	503	HEC	CBC-CAC-C3C	-3.59	121.26	127.86
2	A	505	HEC	CBC-CAC-C3C	-3.58	121.29	127.86
2	D	503	HEC	CBC-CAC-C3C	-3.56	121.32	127.86
2	A	502	HEC	CBC-CAC-C3C	-3.55	121.33	127.86
2	B	504	HEC	CBC-CAC-C3C	-3.39	121.63	127.86
2	D	507	HEC	C4D-ND-C1D	3.37	108.65	105.35
2	C	505	HEC	C4A-NA-C1A	3.37	108.65	105.35
2	D	503	HEC	CAA-CBA-CGA	-3.36	106.37	113.60
2	B	503	HEC	C4D-ND-C1D	3.35	108.63	105.35
2	C	502	HEC	C4D-ND-C1D	3.28	108.56	105.35
2	C	502	HEC	C4A-NA-C1A	3.25	108.53	105.35
2	D	503	HEC	C4B-NB-C1B	3.22	108.51	105.35
2	B	503	HEC	C4C-NC-C1C	3.19	108.47	105.35
2	D	503	HEC	C4A-NA-C1A	3.18	108.46	105.35
2	B	502	HEC	CAA-CBA-CGA	-3.15	106.82	113.60
2	C	502	HEC	CBB-CAB-C3B	-3.15	122.07	127.86
2	A	502	HEC	C4B-NB-C1B	3.13	108.41	105.35
2	C	506	HEC	C4D-ND-C1D	3.12	108.40	105.35
2	C	506	HEC	CBA-CAA-C2A	-3.11	103.99	112.63
2	A	505	HEC	CBA-CAA-C2A	-3.08	104.07	112.63
2	B	503	HEC	C4A-NA-C1A	3.06	108.35	105.35
2	A	501	HEC	CBC-CAC-C3C	-3.06	122.24	127.86
2	D	507	HEC	C4A-NA-C1A	3.05	108.33	105.35
2	C	504	HEC	CBC-CAC-C3C	-3.03	122.28	127.86
2	B	501	HEC	CBC-CAC-C3C	-3.03	122.29	127.86
2	A	505	HEC	C4B-NB-C1B	3.02	108.30	105.35
2	C	506	HEC	C4C-NC-C1C	3.01	108.30	105.35
2	B	501	HEC	C4C-NC-C1C	2.98	108.27	105.35
2	A	505	HEC	C4A-NA-C1A	2.94	108.22	105.35
2	D	505	HEC	C4A-NA-C1A	2.94	108.22	105.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	503	HEC	C2A-C1A-NA	-2.93	107.47	110.32
2	B	505	HEC	C4B-NB-C1B	2.91	108.20	105.35
2	A	504	HEC	C4A-NA-C1A	2.91	108.20	105.35
2	C	505	HEC	C2A-C1A-NA	-2.91	107.49	110.32
2	A	505	HEC	C4D-ND-C1D	2.91	108.19	105.35
2	B	501	HEC	C4B-NB-C1B	2.90	108.19	105.35
2	D	507	HEC	C4C-NC-C1C	2.86	108.15	105.35
3	A	506	SE4	O2-SE-O1	-2.84	100.29	111.90
2	D	505	HEC	C4B-NB-C1B	2.84	108.12	105.35
2	A	504	HEC	C2A-C1A-NA	-2.83	107.57	110.32
2	D	505	HEC	CBC-CAC-C3C	-2.82	122.68	127.86
2	C	502	HEC	C2A-C1A-NA	-2.82	107.58	110.32
2	B	503	HEC	C4B-NB-C1B	2.82	108.11	105.35
2	C	503	HEC	CBD-CAD-C3D	-2.81	104.83	112.63
2	A	502	HEC	CBA-CAA-C2A	-2.81	104.83	112.63
2	C	503	HEC	C4B-NB-C1B	2.77	108.06	105.35
2	C	503	HEC	C4A-NA-C1A	2.75	108.04	105.35
2	C	506	HEC	C4B-NB-C1B	2.75	108.04	105.35
2	A	505	HEC	C4C-NC-C1C	2.73	108.03	105.35
3	B	506	SE4	O2-SE-O1	-2.72	100.77	111.90
2	C	504	HEC	C4D-ND-C1D	2.71	108.00	105.35
2	C	503	HEC	C4D-ND-C1D	2.71	108.00	105.35
2	B	503	HEC	C2A-C1A-NA	-2.69	107.70	110.32
2	D	505	HEC	C4D-ND-C1D	2.68	107.98	105.35
3	C	507	SE4	O2-SE-O1	-2.68	100.92	111.90
2	A	503	HEC	C4A-NA-C1A	2.68	107.97	105.35
2	A	505	HEC	O2A-CGA-CBA	2.68	122.64	114.03
2	D	506	HEC	C4A-NA-C1A	2.68	107.97	105.35
2	B	505	HEC	O2A-CGA-CBA	2.65	122.55	114.03
5	B	507	EPE	O3S-S-C10	2.65	110.05	105.77
2	D	504	HEC	CBD-CAD-C3D	-2.65	105.27	112.63
2	D	503	HEC	C4D-ND-C1D	2.63	107.92	105.35
2	D	503	HEC	C4C-NC-C1C	2.61	107.90	105.35
2	C	505	HEC	C4B-NB-C1B	2.59	107.89	105.35
2	A	503	HEC	CAA-CBA-CGA	-2.59	108.03	113.60
2	B	505	HEC	C4C-NC-C1C	2.59	107.88	105.35
2	C	502	HEC	C4C-NC-C1C	2.58	107.87	105.35
2	A	501	HEC	CAA-CBA-CGA	-2.56	108.08	113.60
5	B	507	EPE	C6-N1-C2	2.55	114.56	108.83
2	B	501	HEC	C4A-NA-C1A	2.54	107.84	105.35
2	D	507	HEC	C4B-NB-C1B	2.52	107.82	105.35
2	A	505	HEC	CAA-CBA-CGA	2.51	119.01	113.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	505	HEC	CHD-C1D-ND	2.51	128.47	123.85
2	B	505	HEC	CBA-CAA-C2A	-2.51	105.66	112.63
2	A	501	HEC	C4D-ND-C1D	2.49	107.79	105.35
2	B	505	HEC	C4D-ND-C1D	2.49	107.78	105.35
2	C	505	HEC	C3D-C4D-ND	-2.46	107.40	110.15
2	B	502	HEC	CAD-CBD-CGD	-2.45	108.33	113.60
2	A	501	HEC	CMC-C2C-C1C	-2.45	121.64	125.37
2	D	506	HEC	C4D-ND-C1D	2.45	107.75	105.35
2	C	502	HEC	C4B-NB-C1B	2.41	107.71	105.35
2	D	507	HEC	CBA-CAA-C2A	-2.41	105.93	112.63
2	C	506	HEC	O2D-CGD-CBD	2.40	121.75	114.03
2	D	505	HEC	C4C-NC-C1C	2.40	107.70	105.35
2	A	502	HEC	C4A-NA-C1A	2.40	107.70	105.35
2	B	503	HEC	C3D-C4D-ND	-2.40	107.47	110.15
2	C	506	HEC	C4A-NA-C1A	2.38	107.68	105.35
2	B	501	HEC	C4D-ND-C1D	2.37	107.67	105.35
2	D	506	HEC	C4B-NB-C1B	2.37	107.67	105.35
2	C	504	HEC	C4A-NA-C1A	2.35	107.65	105.35
2	D	503	HEC	C3D-C4D-ND	-2.35	107.52	110.15
2	C	502	HEC	CBD-CAD-C3D	-2.35	106.09	112.63
2	A	504	HEC	C4B-NB-C1B	2.35	107.64	105.35
2	C	504	HEC	CAA-CBA-CGA	-2.33	108.58	113.60
2	C	502	HEC	CAA-CBA-CGA	-2.33	108.59	113.60
2	C	504	HEC	C4B-NB-C1B	2.33	107.63	105.35
2	C	503	HEC	C4C-NC-C1C	2.31	107.61	105.35
2	A	501	HEC	C4A-NA-C1A	2.29	107.59	105.35
5	B	507	EPE	C9-N1-C2	-2.28	105.40	111.23
5	B	507	EPE	O2S-S-C10	2.28	109.66	106.92
2	C	506	HEC	O1D-CGD-CBD	-2.27	115.78	123.08
2	B	504	HEC	C4D-ND-C1D	2.26	107.56	105.35
2	D	507	HEC	O2A-CGA-CBA	2.25	121.25	114.03
2	D	503	HEC	CBD-CAD-C3D	-2.24	106.39	112.63
2	C	503	HEC	CAD-CBD-CGD	-2.24	108.78	113.60
2	C	505	HEC	C4D-ND-C1D	2.21	107.52	105.35
2	B	505	HEC	O2D-CGD-CBD	2.21	121.12	114.03
2	C	504	HEC	CHC-C4B-NB	2.20	126.82	124.44
2	B	505	HEC	C3B-C4B-NB	-2.20	107.51	110.58
2	B	505	HEC	C4A-NA-C1A	2.20	107.50	105.35
2	D	504	HEC	C4B-NB-C1B	2.19	107.49	105.35
2	A	501	HEC	C4C-NC-C1C	2.18	107.48	105.35
2	D	506	HEC	C4C-NC-C1C	2.13	107.43	105.35
2	A	504	HEC	C4C-NC-C1C	2.12	107.42	105.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	505	HEC	CBD-CAD-C3D	-2.12	106.74	112.63
2	C	502	HEC	C3C-C4C-NC	-2.11	107.64	110.58
2	C	506	HEC	C3D-C4D-ND	-2.10	107.80	110.15
2	D	503	HEC	CAA-C2A-C3A	-2.09	123.98	127.88
2	D	503	HEC	CHD-C4C-NC	2.09	126.70	124.44
2	A	505	HEC	C2A-C1A-NA	-2.08	108.30	110.32
2	B	502	HEC	CBD-CAD-C3D	-2.07	106.88	112.63
2	C	503	HEC	C2A-C1A-NA	-2.06	108.32	110.32
2	C	502	HEC	C3D-C4D-ND	-2.06	107.85	110.15
2	A	503	HEC	C4D-ND-C1D	2.04	107.35	105.35
3	D	508	SE4	O2-SE-O1	-2.04	103.56	111.90
2	D	506	HEC	C3D-C4D-ND	-2.04	107.87	110.15
2	D	507	HEC	C2D-C1D-ND	-2.03	107.00	110.08
2	C	504	HEC	C2A-C1A-NA	-2.02	108.36	110.32
2	A	502	HEC	C3B-C4B-NB	-2.02	107.77	110.58
2	D	507	HEC	O2D-CGD-CBD	2.02	120.50	114.03
2	D	504	HEC	C2A-C1A-NA	-2.01	108.37	110.32
2	C	502	HEC	C2D-C1D-ND	-2.00	107.03	110.08
2	B	501	HEC	CHB-C4A-NA	2.00	126.60	124.44
2	B	501	HEC	O2D-CGD-CBD	2.00	120.46	114.03

There are no chirality outliers.

All (150) 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
2	A	501	HEC	C4C-C3C-CAC-CBC
2	A	502	HEC	C2B-C3B-CAB-CBB
2	A	502	HEC	C4B-C3B-CAB-CBB
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

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Mol	Chain	Res	Type	Atoms
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	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	C4B-C3B-CAB-CBB
2	B	503	HEC	C2C-C3C-CAC-CBC
2	B	503	HEC	C4C-C3C-CAC-CBC
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	502	HEC	C2B-C3B-CAB-CBB
2	C	502	HEC	C4B-C3B-CAB-CBB
2	C	502	HEC	C2C-C3C-CAC-CBC
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	C	506	HEC	C2B-C3B-CAB-CBB
2	C	506	HEC	C4B-C3B-CAB-CBB
2	C	506	HEC	C2C-C3C-CAC-CBC

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Mol	Chain	Res	Type	Atoms
2	C	506	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	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	D	506	HEC	C2B-C3B-CAB-CBB
2	D	506	HEC	C4B-C3B-CAB-CBB
2	D	506	HEC	C2C-C3C-CAC-CBC
2	D	506	HEC	C4C-C3C-CAC-CBC
2	D	507	HEC	C2B-C3B-CAB-CBB
2	D	507	HEC	C4B-C3B-CAB-CBB
2	D	507	HEC	C2C-C3C-CAC-CBC
2	D	507	HEC	C4C-C3C-CAC-CBC
2	A	502	HEC	C2A-CAA-CBA-CGA
2	B	502	HEC	C3D-CAD-CBD-CGD
2	C	503	HEC	C2A-CAA-CBA-CGA
2	D	504	HEC	C2A-CAA-CBA-CGA
2	B	502	HEC	C2A-CAA-CBA-CGA
4	B	519	EDO	O1-C1-C2-O2
4	C	511	EDO	O1-C1-C2-O2
4	D	514	EDO	O1-C1-C2-O2
4	D	517	EDO	O1-C1-C2-O2
4	D	511	EDO	O1-C1-C2-O2
2	B	505	HEC	C3D-CAD-CBD-CGD
2	C	506	HEC	C3D-CAD-CBD-CGD
2	D	507	HEC	C3D-CAD-CBD-CGD
5	B	507	EPE	S-C10-C9-N1
5	B	507	EPE	C10-C9-N1-C2
5	B	507	EPE	C10-C9-N1-C6
2	A	505	HEC	C3D-CAD-CBD-CGD
5	B	507	EPE	C8-C7-N4-C5
4	C	508	EDO	O1-C1-C2-O2
2	D	504	HEC	C3D-CAD-CBD-CGD
2	A	501	HEC	CAA-CBA-CGA-O1A

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Mol	Chain	Res	Type	Atoms
2	B	501	HEC	CAA-CBA-CGA-O1A
2	C	506	HEC	CAA-CBA-CGA-O1A
2	A	501	HEC	CAA-CBA-CGA-O2A
2	D	504	HEC	CAA-CBA-CGA-O1A
2	A	505	HEC	CAA-CBA-CGA-O1A
2	B	502	HEC	CAA-CBA-CGA-O1A
2	C	503	HEC	CAA-CBA-CGA-O1A
2	C	503	HEC	CAA-CBA-CGA-O2A
2	D	503	HEC	CAA-CBA-CGA-O2A
2	B	505	HEC	CAA-CBA-CGA-O1A
2	D	503	HEC	CAA-CBA-CGA-O1A
2	C	506	HEC	CAA-CBA-CGA-O2A
2	D	507	HEC	CAA-CBA-CGA-O1A
2	A	505	HEC	CAA-CBA-CGA-O2A
2	D	504	HEC	CAA-CBA-CGA-O2A
2	B	501	HEC	CAA-CBA-CGA-O2A
2	A	504	HEC	C1A-C2A-CAA-CBA
2	D	507	HEC	CAA-CBA-CGA-O2A
2	B	502	HEC	CAA-CBA-CGA-O2A
2	A	502	HEC	CAA-CBA-CGA-O1A
4	C	512	EDO	O1-C1-C2-O2
4	D	518	EDO	O1-C1-C2-O2
2	D	505	HEC	CAA-CBA-CGA-O2A
2	A	503	HEC	CAD-CBD-CGD-O2D
2	D	505	HEC	CAA-CBA-CGA-O1A
2	A	503	HEC	CAA-CBA-CGA-O2A
2	C	502	HEC	CAA-CBA-CGA-O1A
2	B	505	HEC	CAA-CBA-CGA-O2A
2	A	505	HEC	CAD-CBD-CGD-O1D
2	C	504	HEC	CAA-CBA-CGA-O2A
2	B	505	HEC	CAD-CBD-CGD-O1D
2	A	503	HEC	CAA-CBA-CGA-O1A
2	B	503	HEC	CAA-CBA-CGA-O2A
4	D	501	EDO	O1-C1-C2-O2
2	A	505	HEC	CAD-CBD-CGD-O2D
2	A	503	HEC	CAD-CBD-CGD-O1D
2	C	504	HEC	CAA-CBA-CGA-O1A
2	A	504	HEC	C3A-C2A-CAA-CBA
2	B	503	HEC	CAA-CBA-CGA-O1A
2	D	507	HEC	CAD-CBD-CGD-O1D
2	B	505	HEC	CAD-CBD-CGD-O2D
2	D	503	HEC	CAD-CBD-CGD-O1D

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Mol	Chain	Res	Type	Atoms
2	C	502	HEC	CAA-CBA-CGA-O2A
2	A	502	HEC	CAA-CBA-CGA-O2A
4	B	512	EDO	O1-C1-C2-O2
4	B	514	EDO	O1-C1-C2-O2
4	D	510	EDO	O1-C1-C2-O2
2	D	503	HEC	CAD-CBD-CGD-O2D
2	D	507	HEC	CAD-CBD-CGD-O2D

There are no ring outliers.

35 monomers are involved in 54 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	503	HEC	2	0
2	D	507	HEC	1	0
4	A	513	EDO	2	0
2	B	505	HEC	1	0
2	C	504	HEC	1	0
4	A	514	EDO	1	0
4	B	518	EDO	1	0
4	C	512	EDO	1	0
5	B	507	EPE	3	0
4	D	502	EDO	1	0
4	B	515	EDO	2	0
4	D	516	EDO	1	0
4	D	501	EDO	3	0
4	A	510	EDO	1	0
2	C	506	HEC	1	0
4	C	501	EDO	1	0
4	B	513	EDO	1	0
4	D	517	EDO	3	0
4	A	511	EDO	2	0
4	A	508	EDO	1	0
4	C	508	EDO	1	0
4	A	512	EDO	1	0
4	B	509	EDO	1	0
4	D	511	EDO	1	0
2	A	502	HEC	3	0
4	D	515	EDO	4	0
4	D	509	EDO	1	0
4	B	510	EDO	2	0
2	A	505	HEC	1	0
2	D	504	HEC	1	0

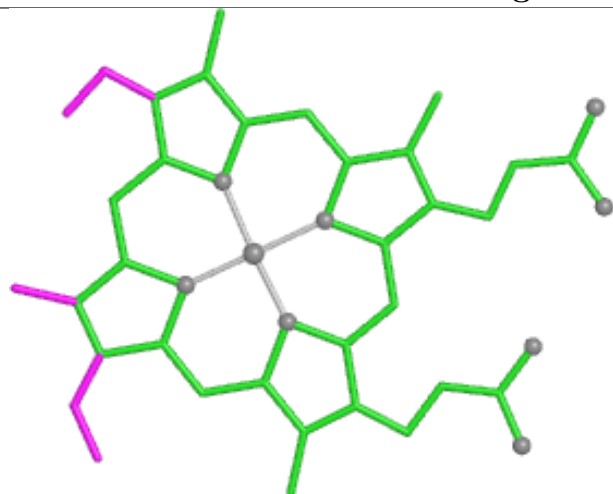
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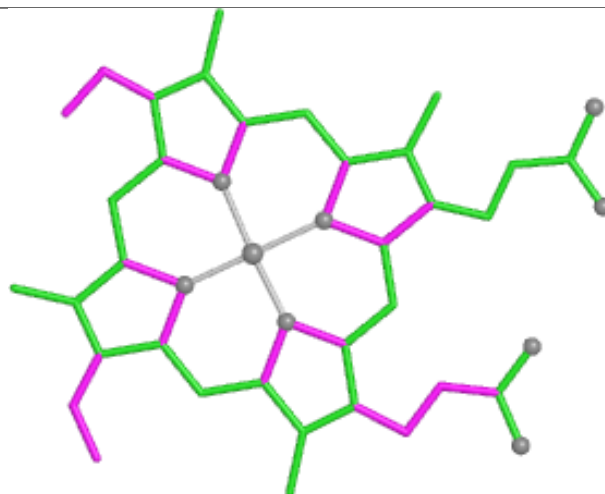
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	519	EDO	2	0
2	C	502	HEC	4	0
4	C	509	EDO	1	0
4	B	508	EDO	2	0
4	C	511	EDO	1	0

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.

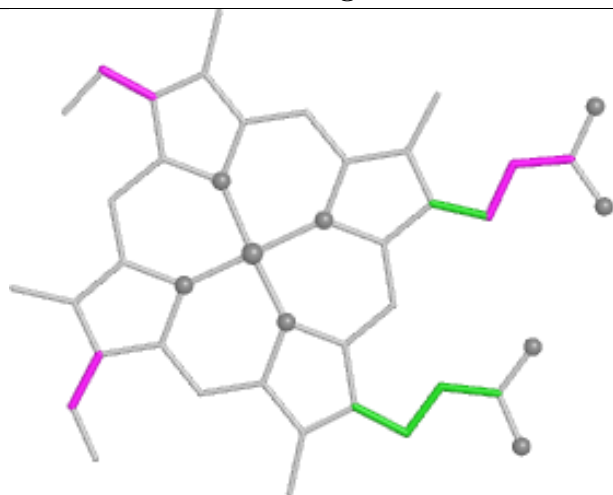
Ligand HEC C 503



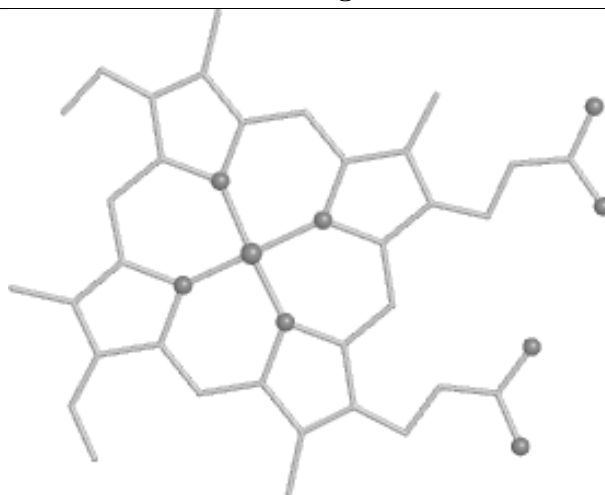
Bond lengths



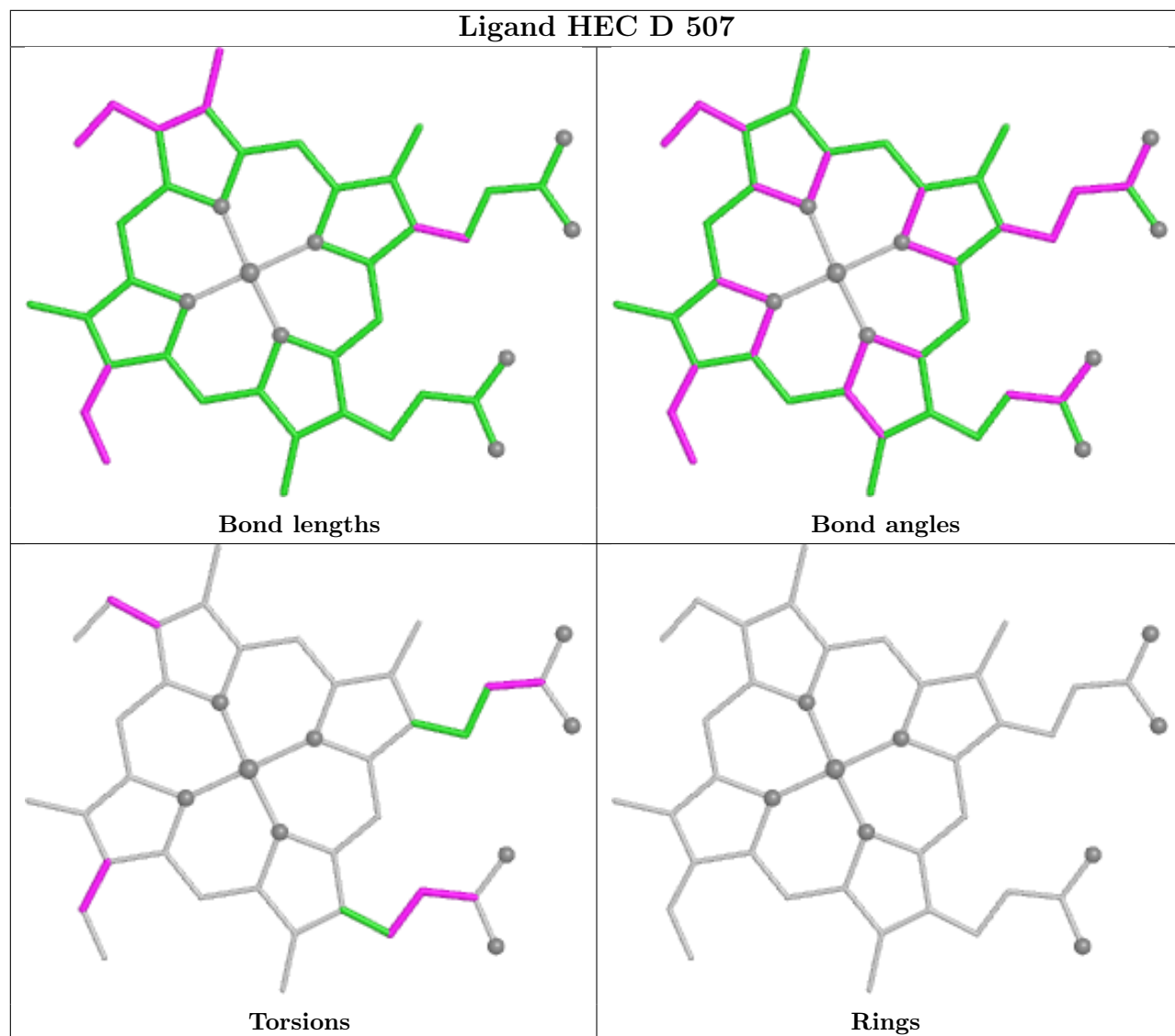
Bond angles



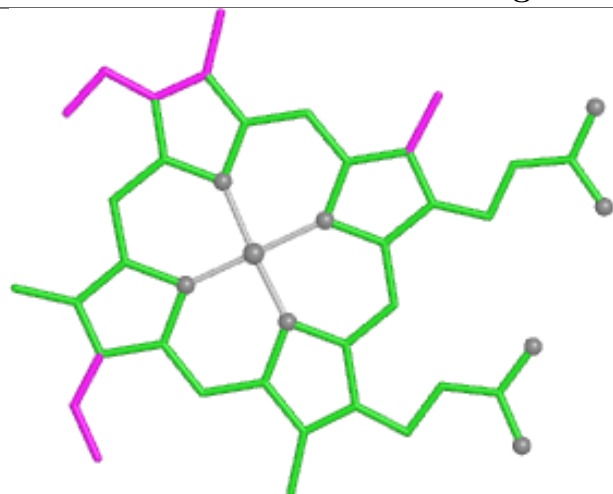
Torsions



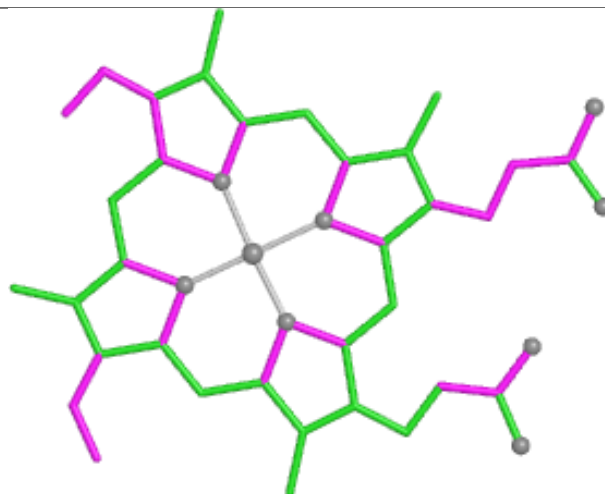
Rings



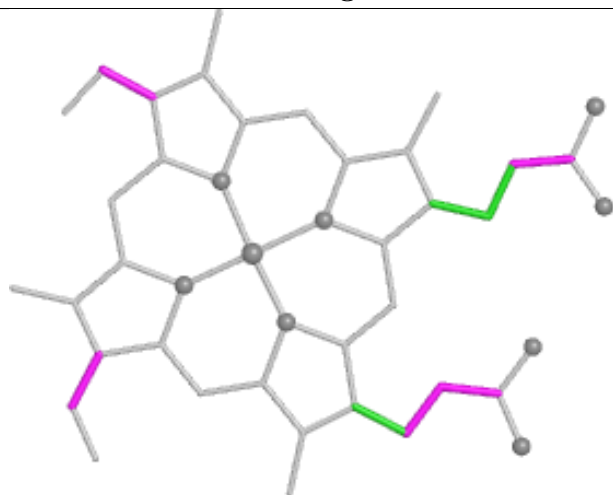
Ligand HEC B 505



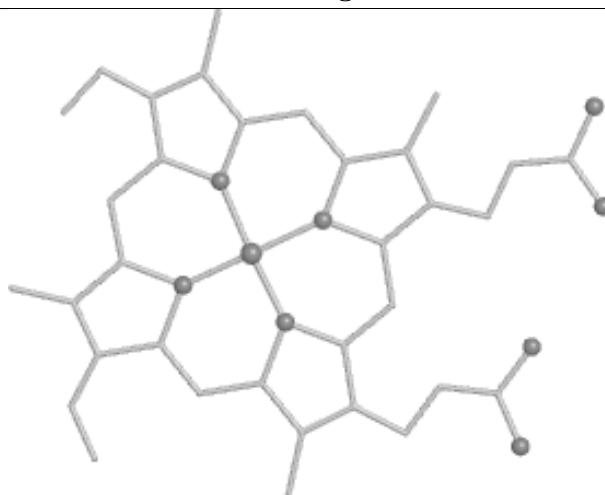
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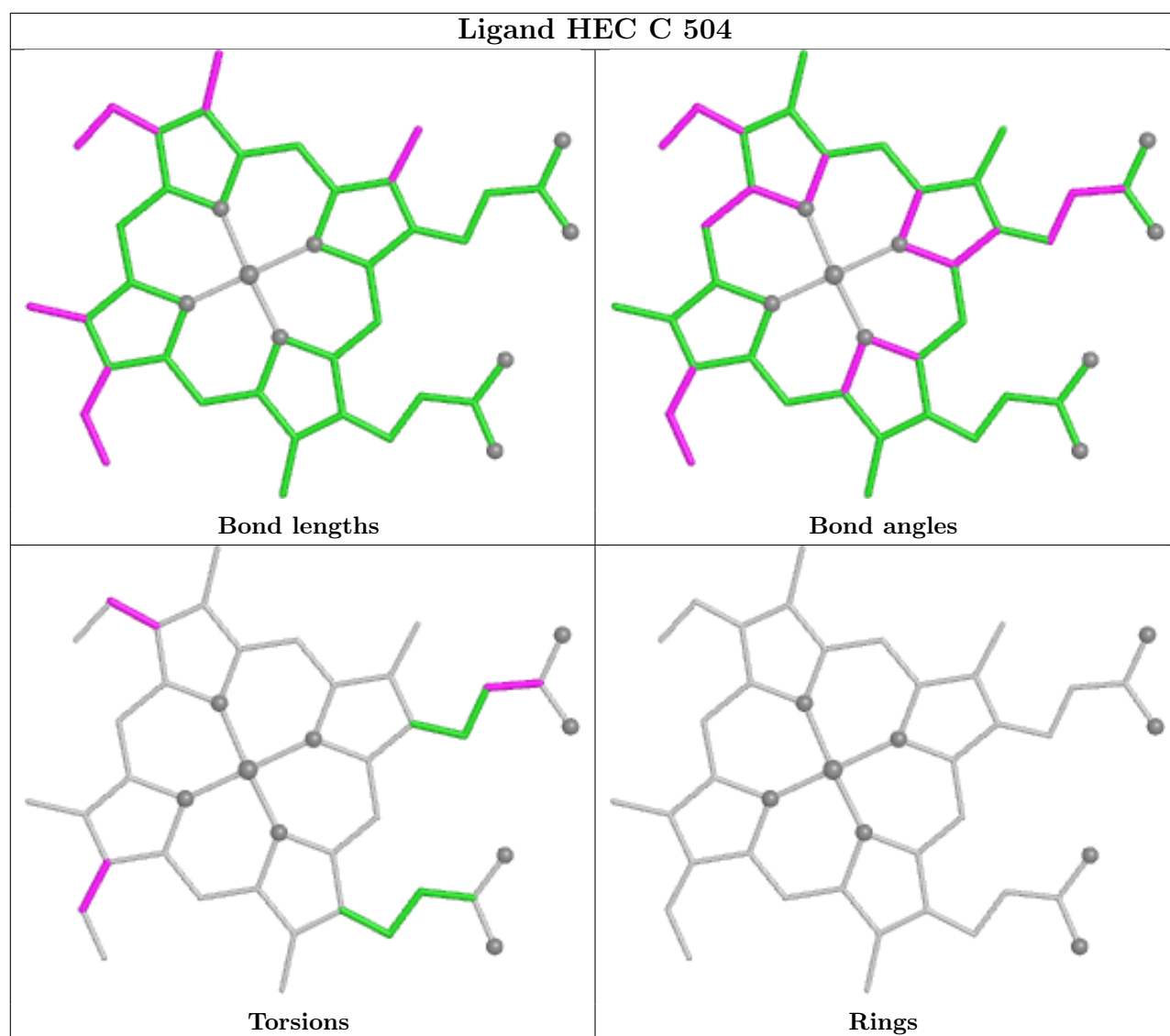
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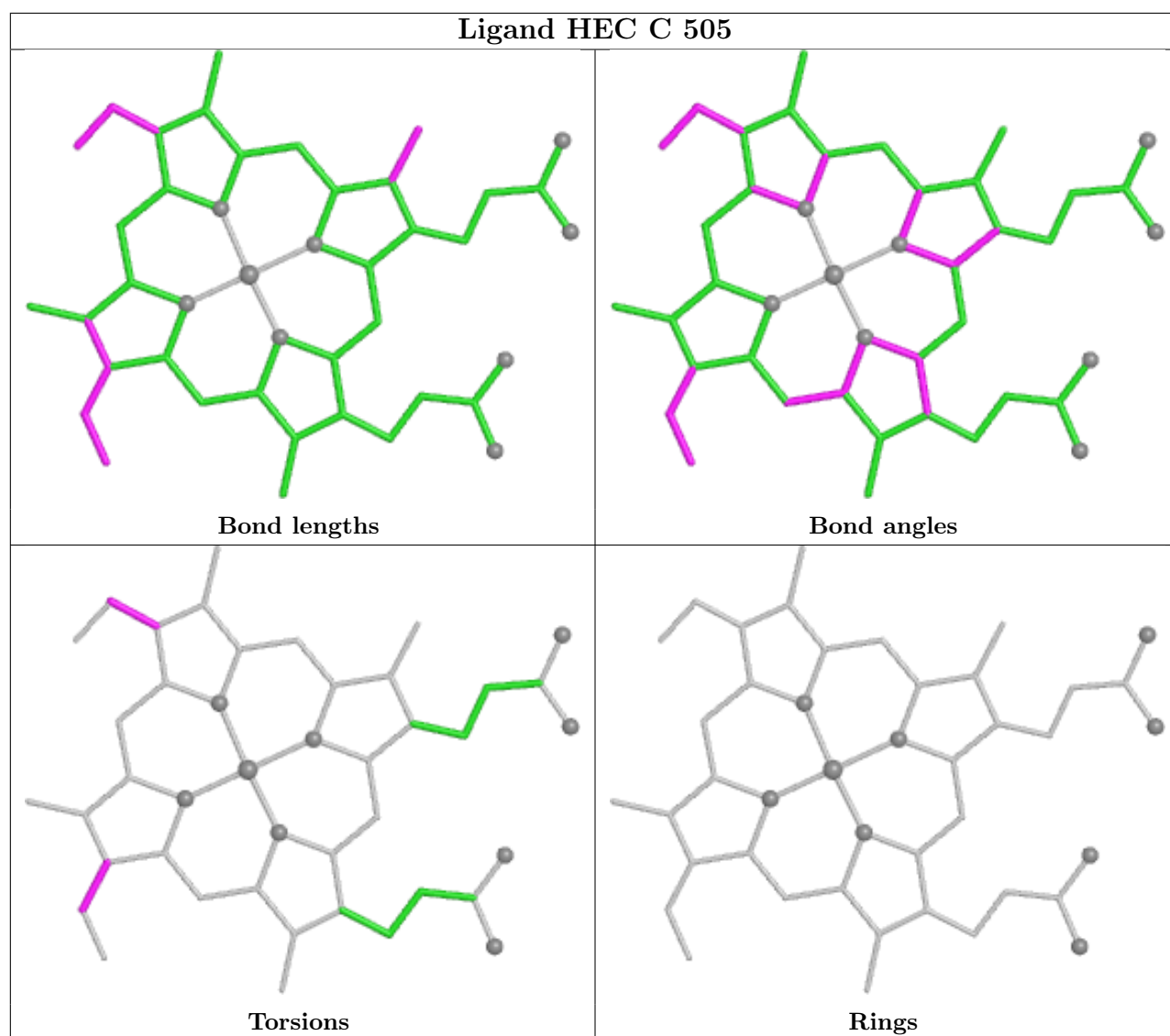


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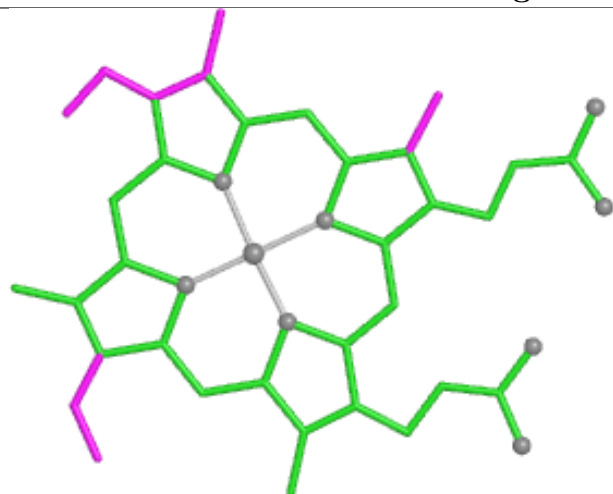


Rings

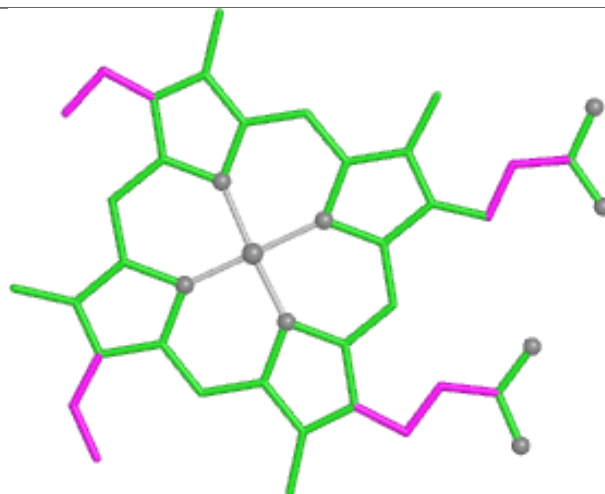




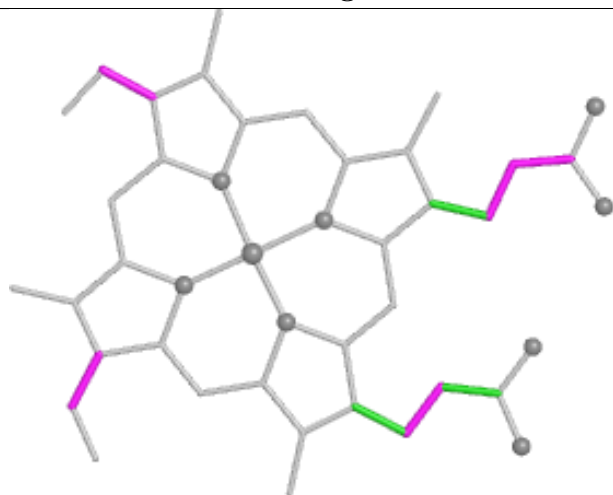
Ligand HEC B 502



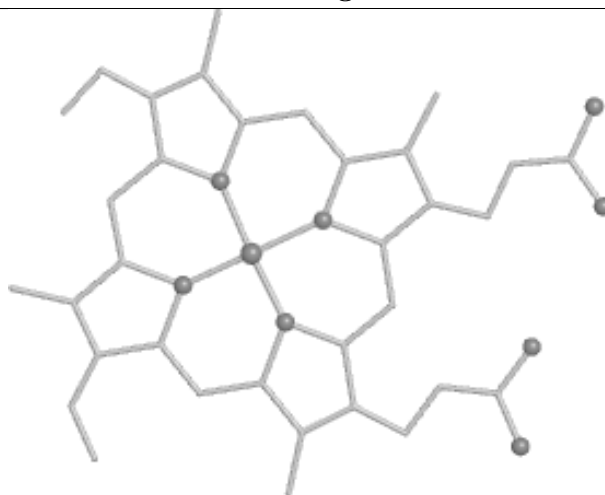
Bond lengths



Bond angles

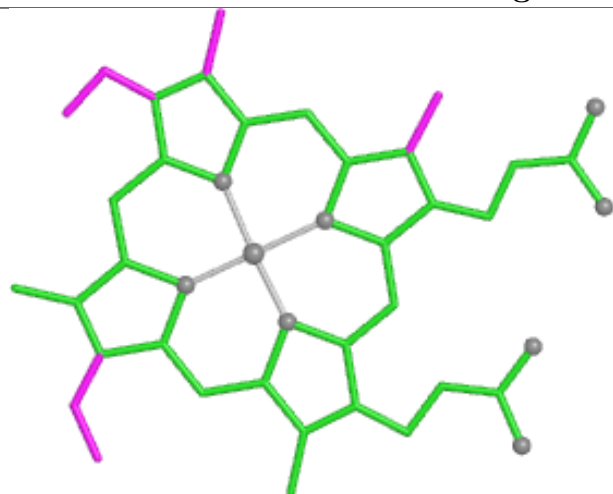


Torsions

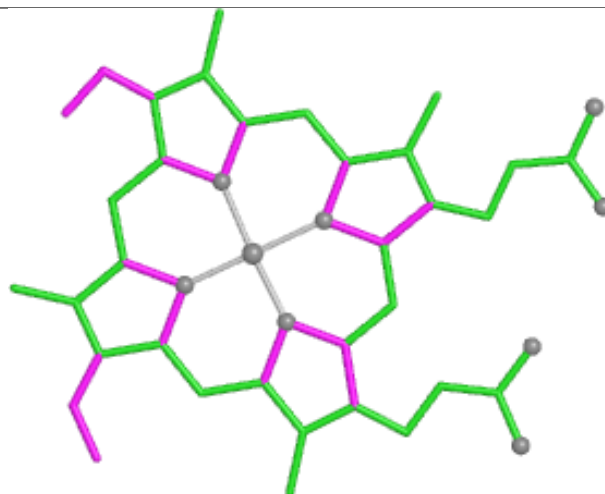


Rings

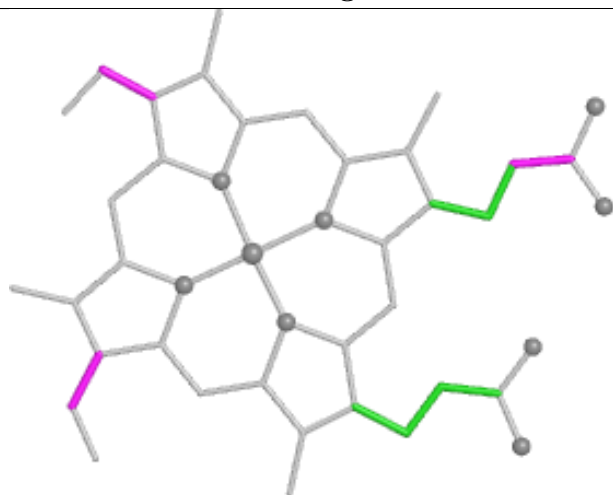
Ligand HEC B 503



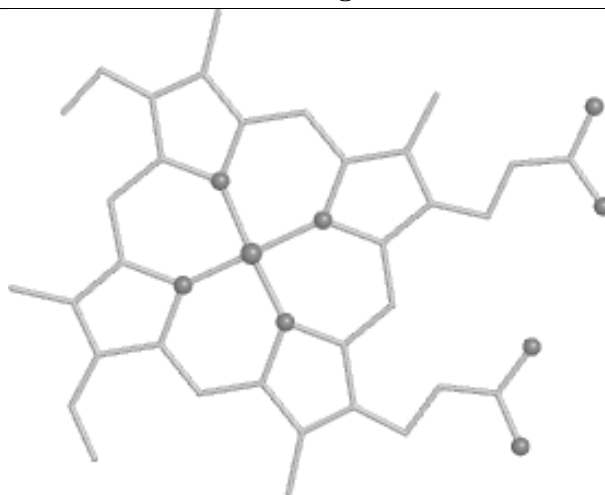
Bond lengths



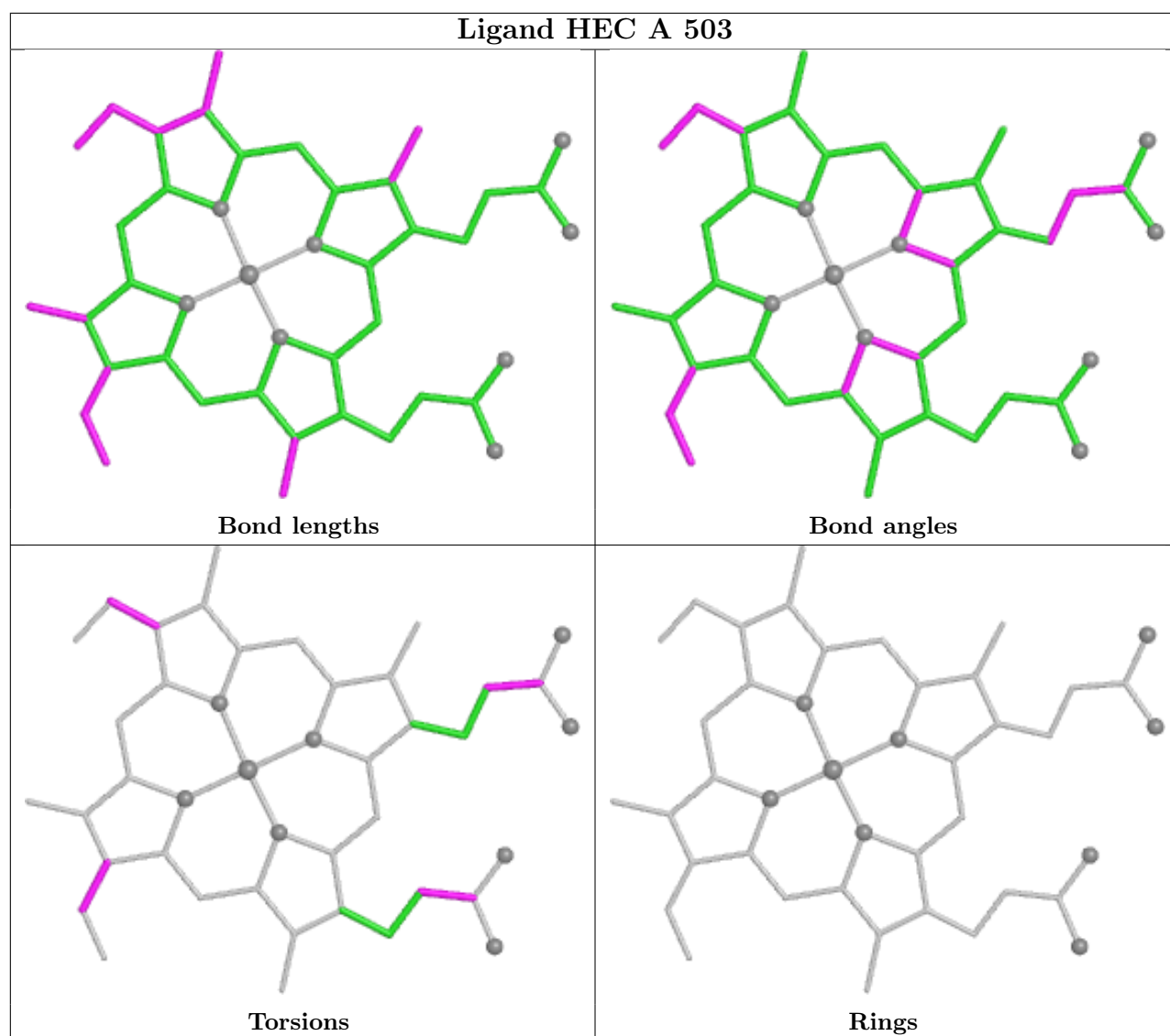
Bond angles

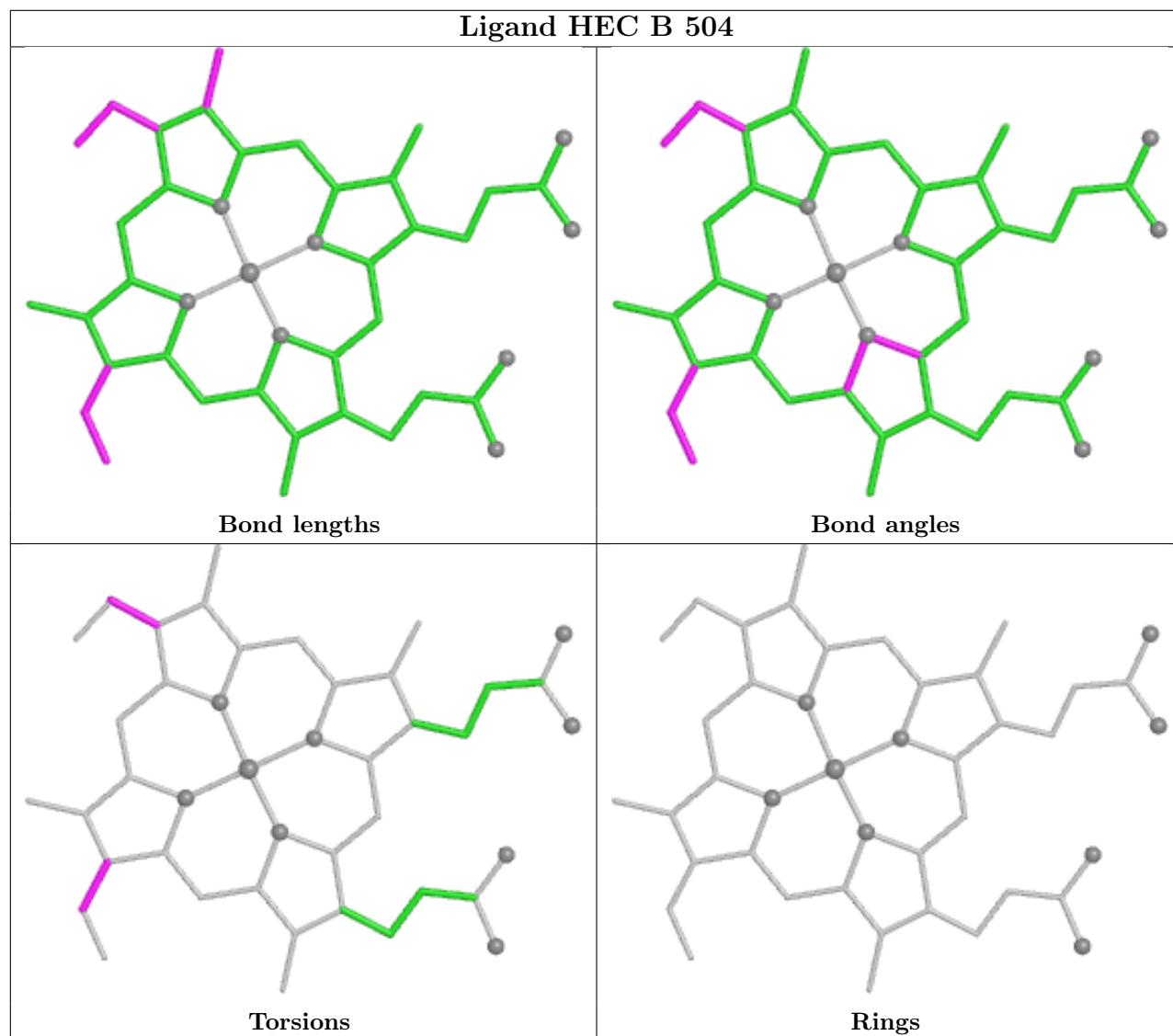


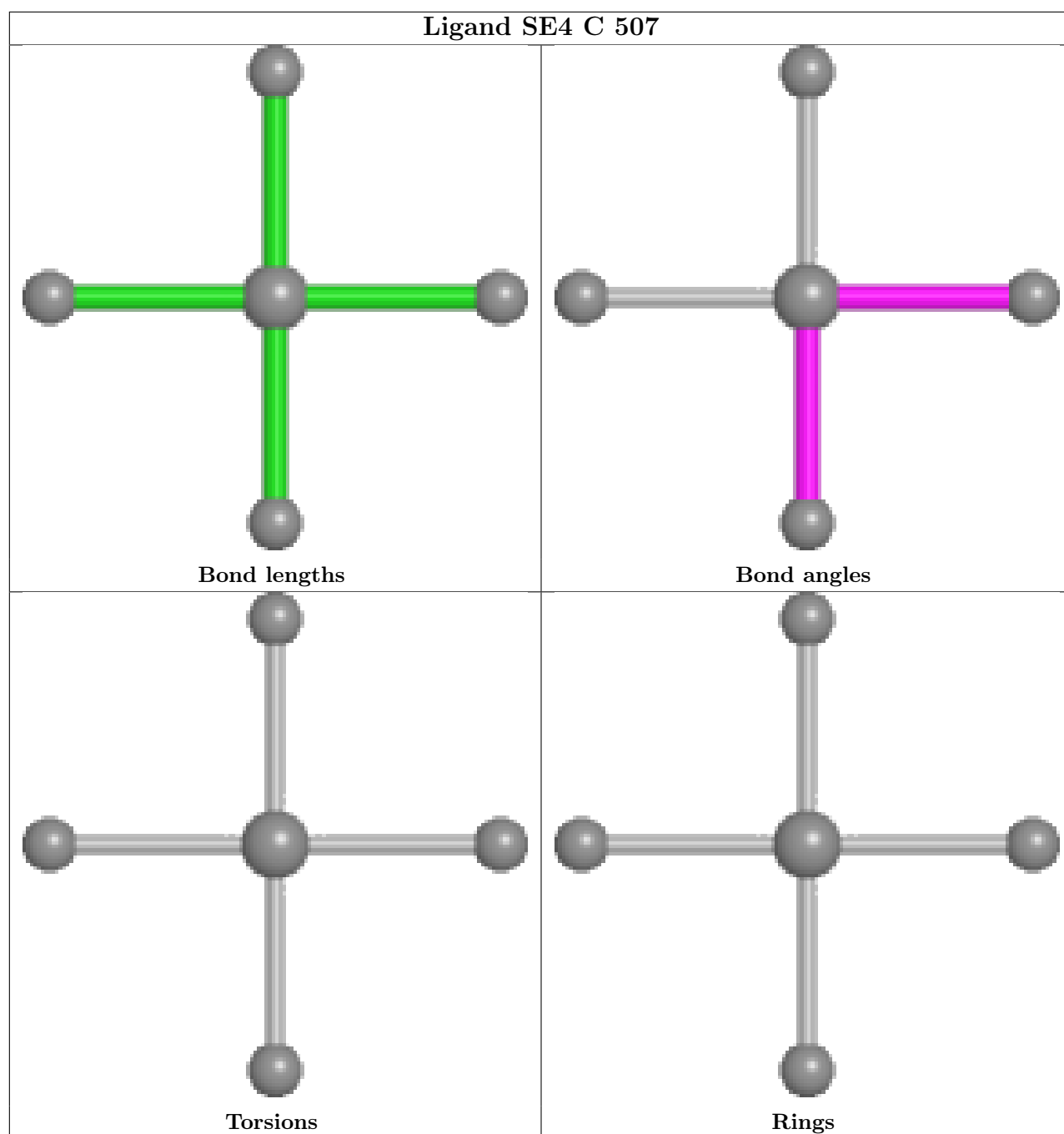
Torsions

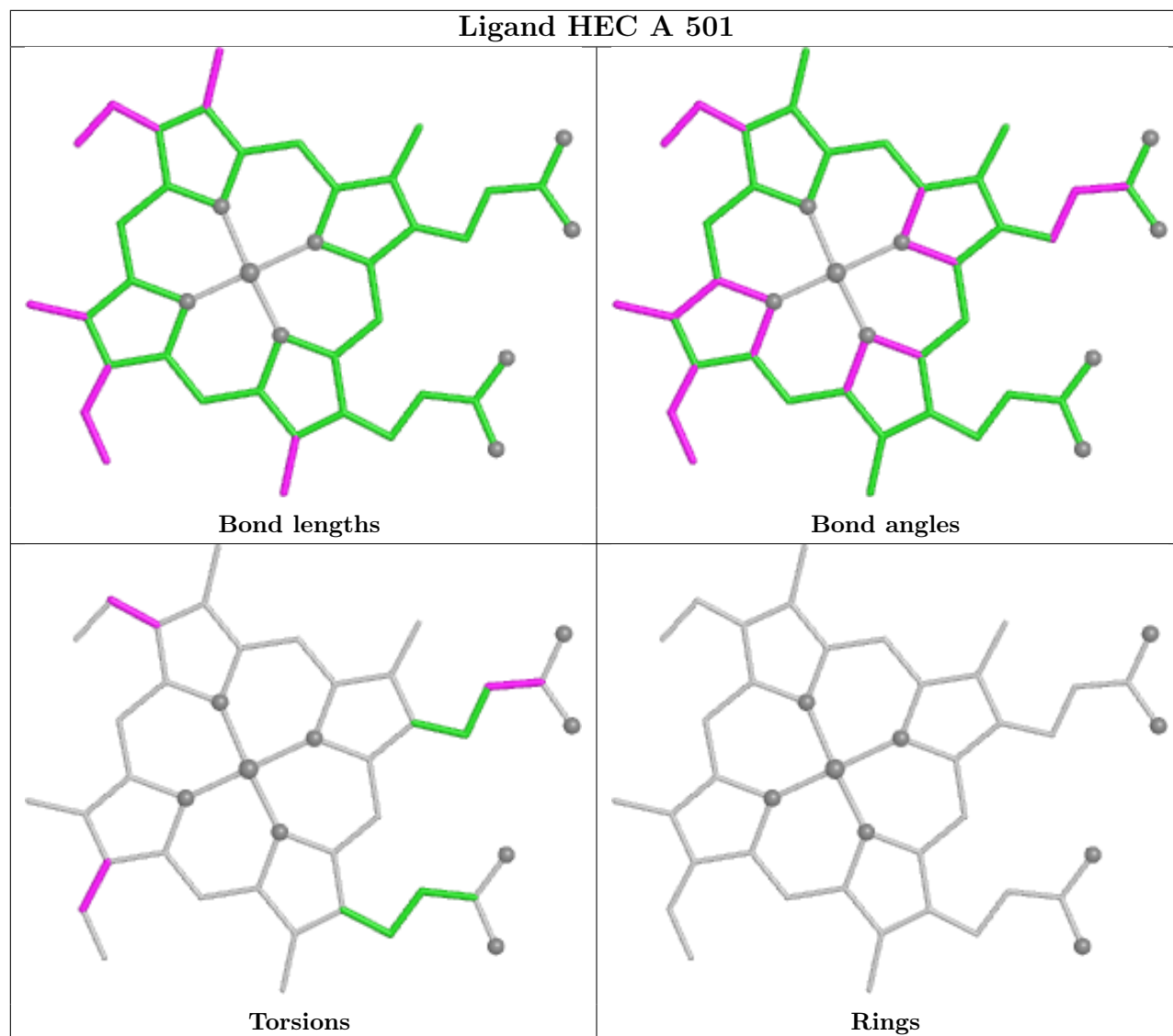


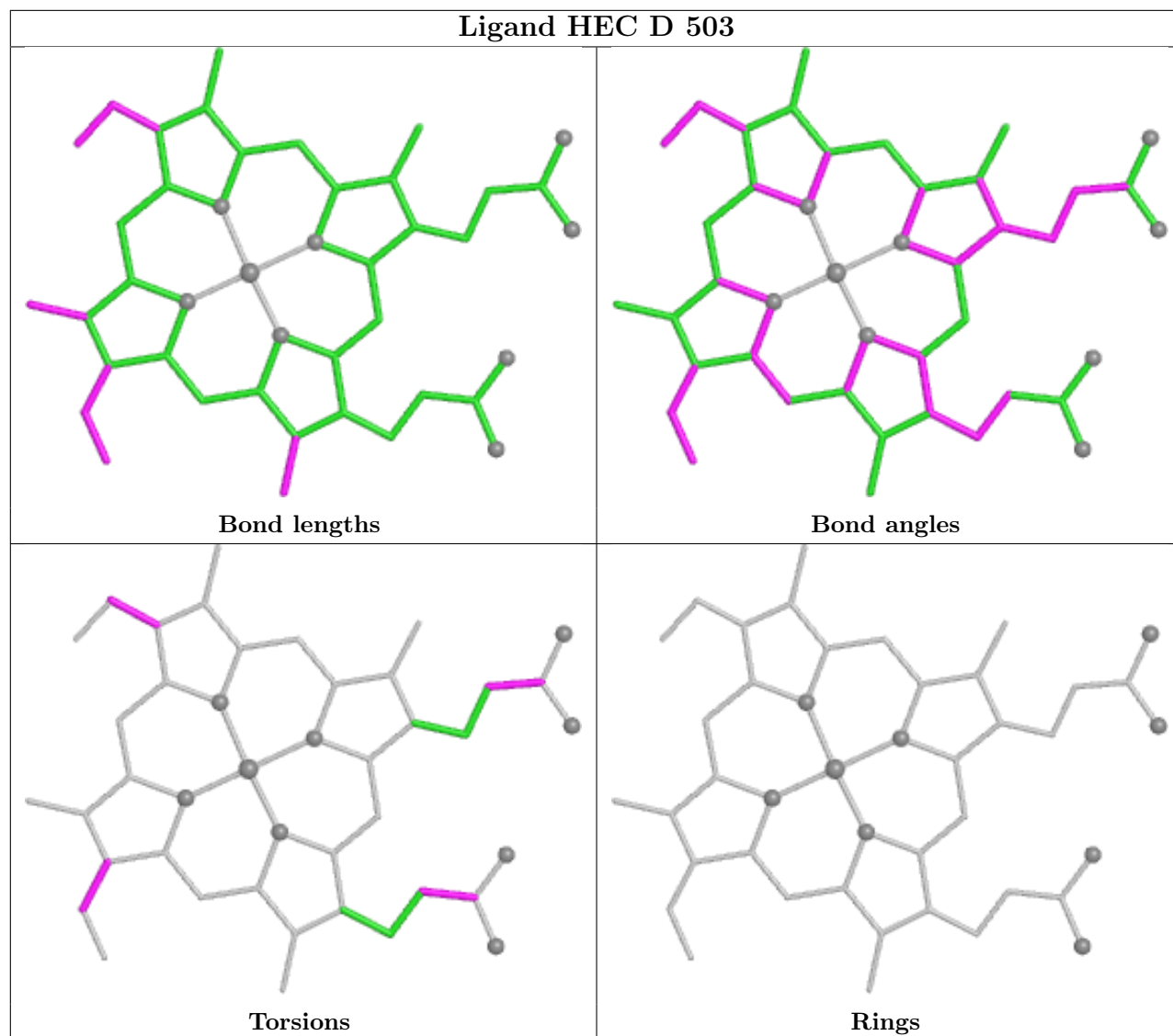
Rings

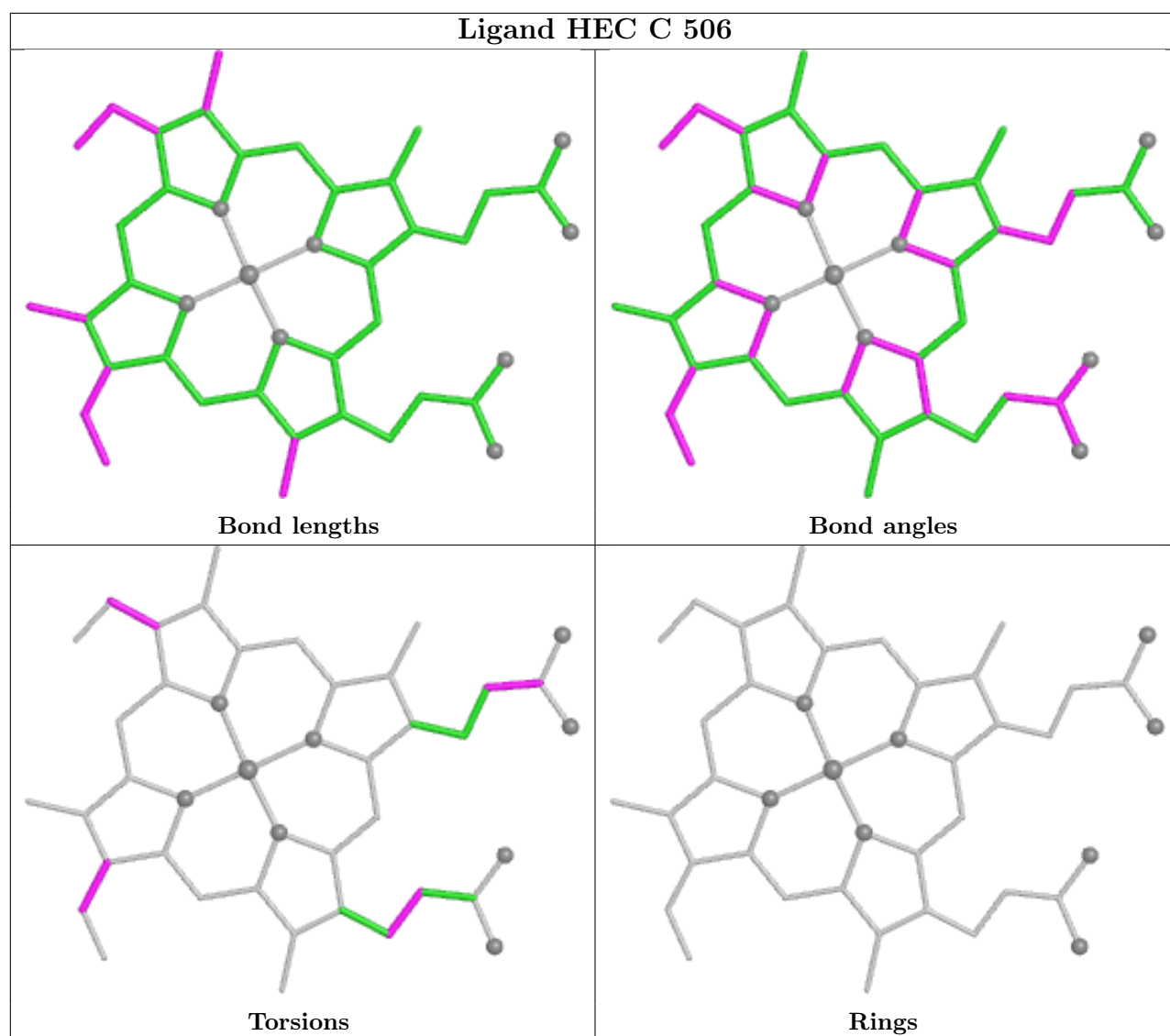


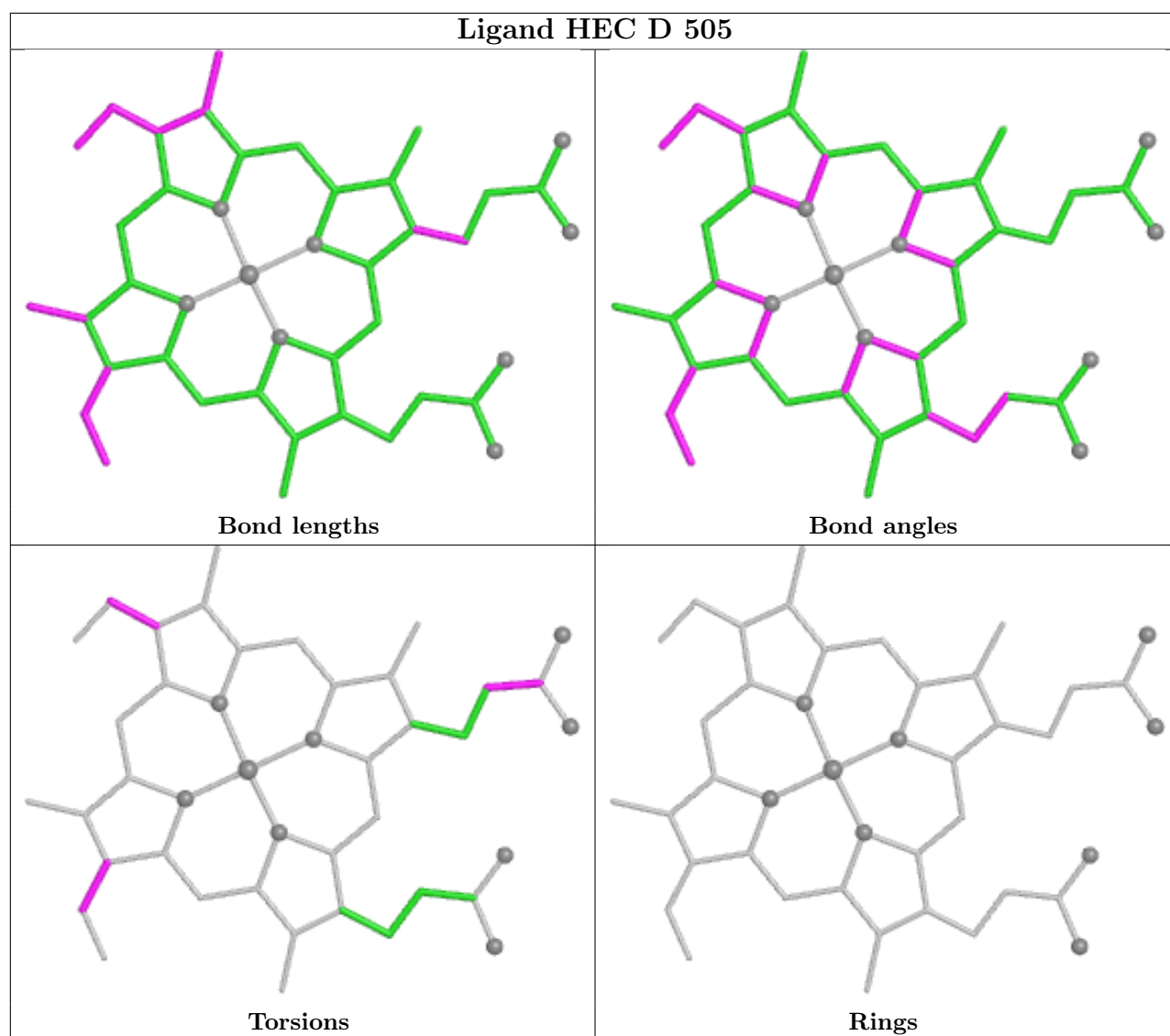




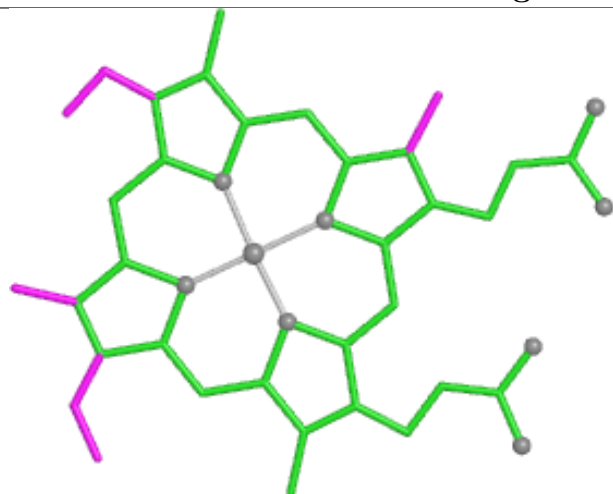




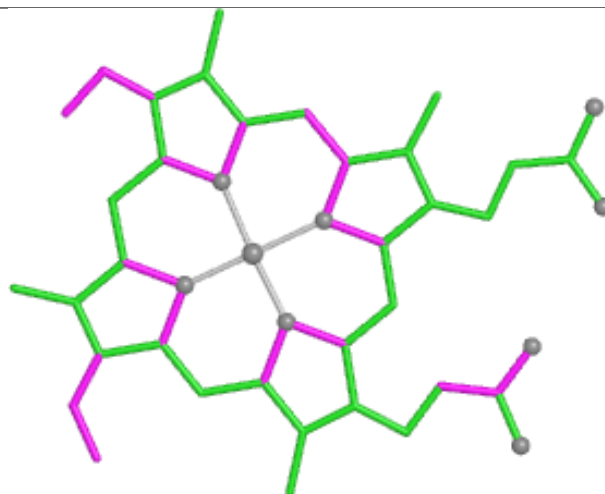




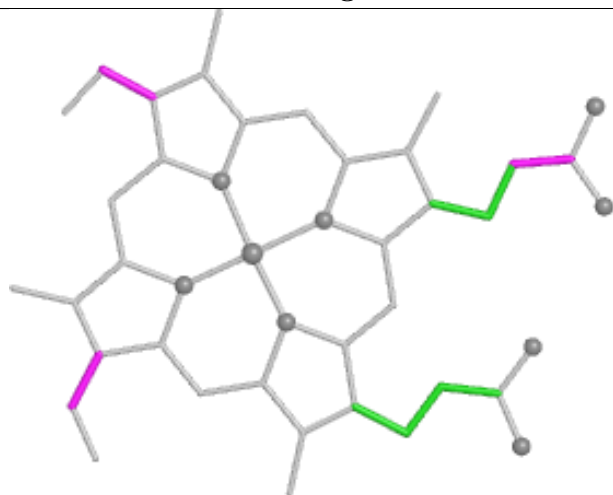
Ligand HEC B 501



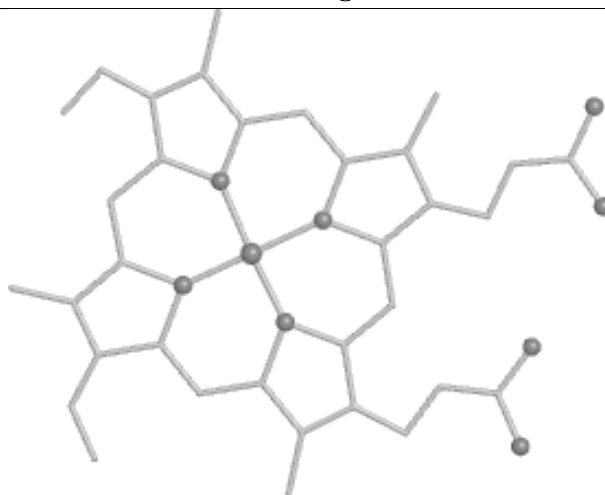
Bond lengths



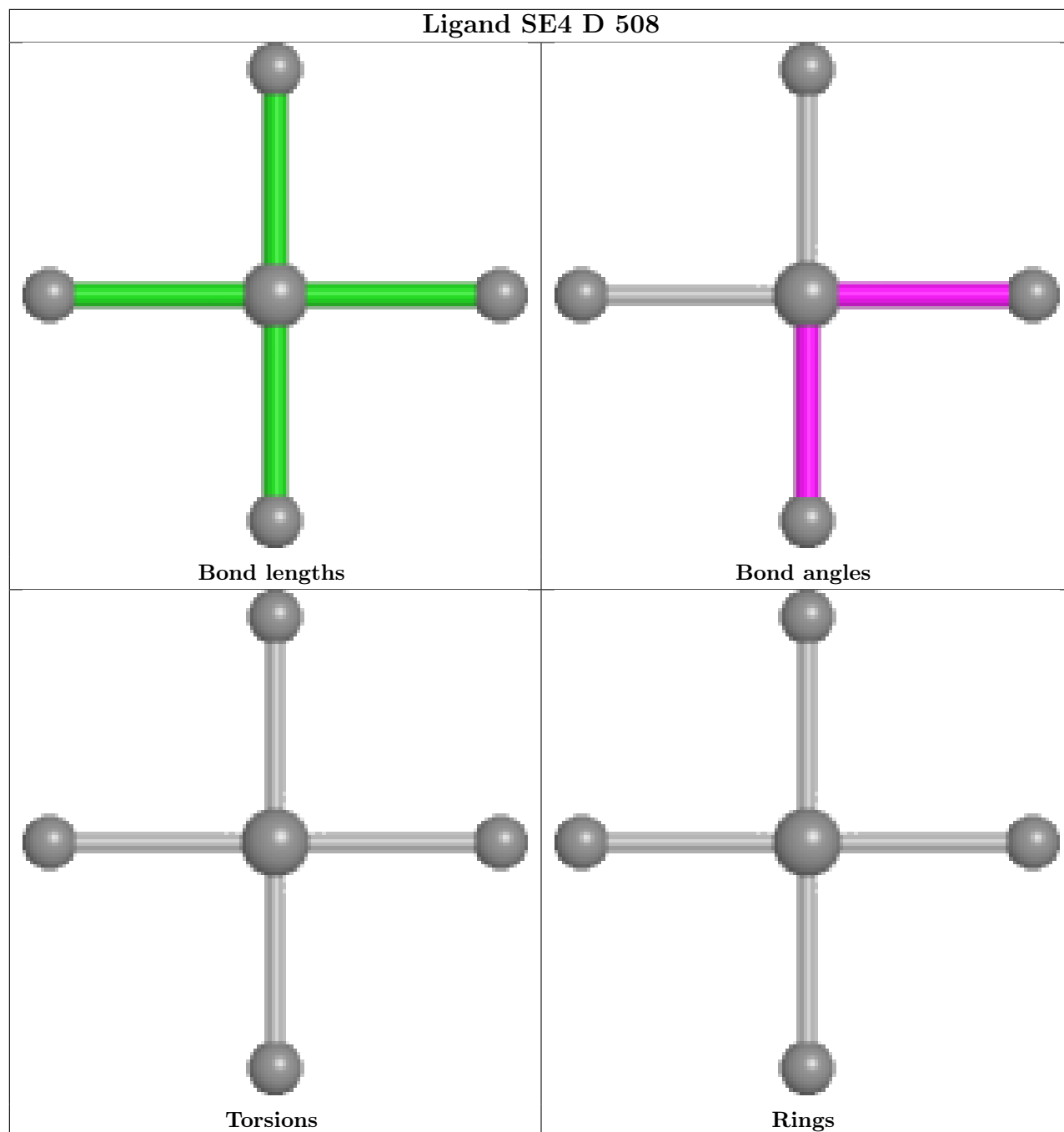
Bond angles

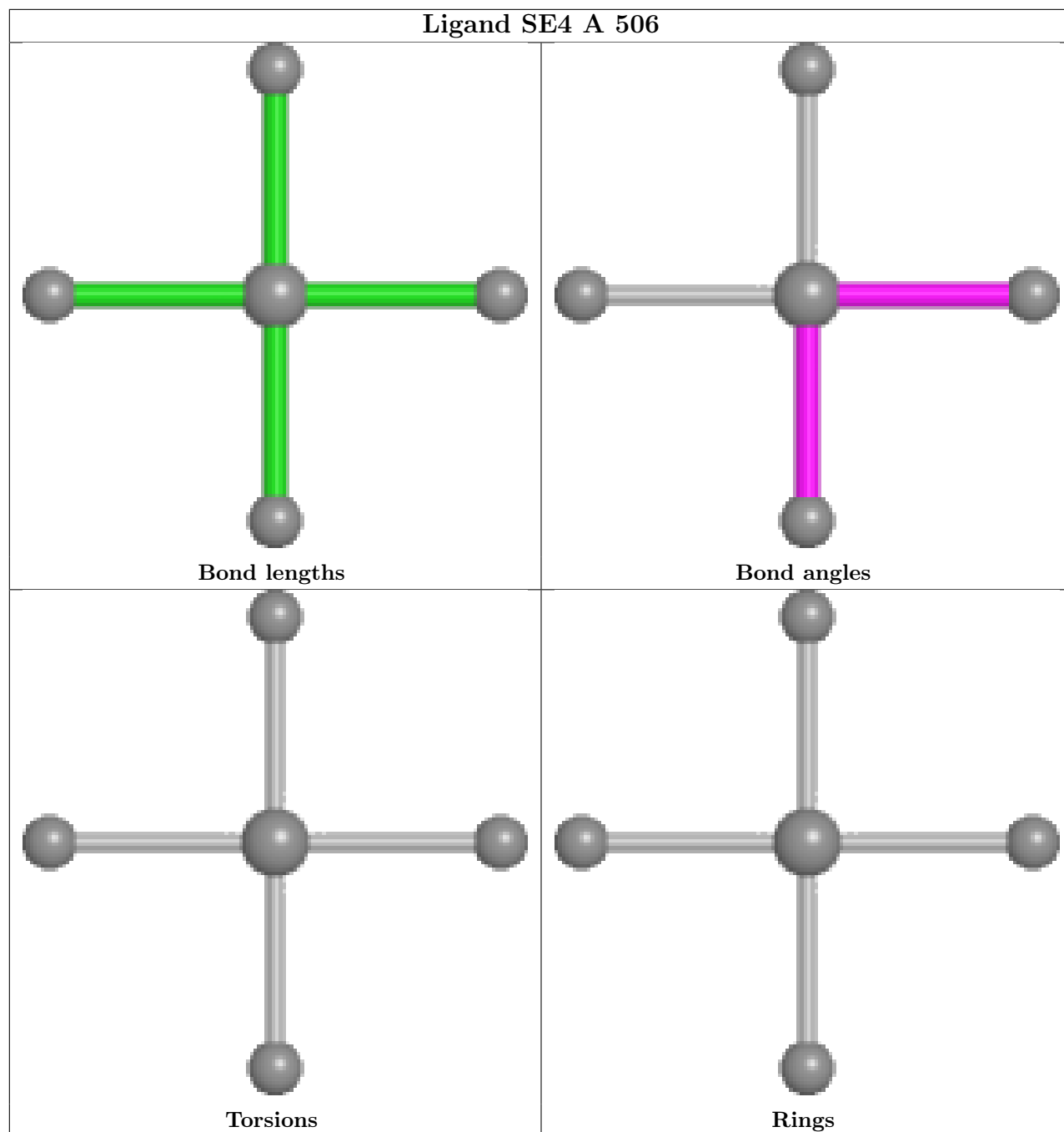


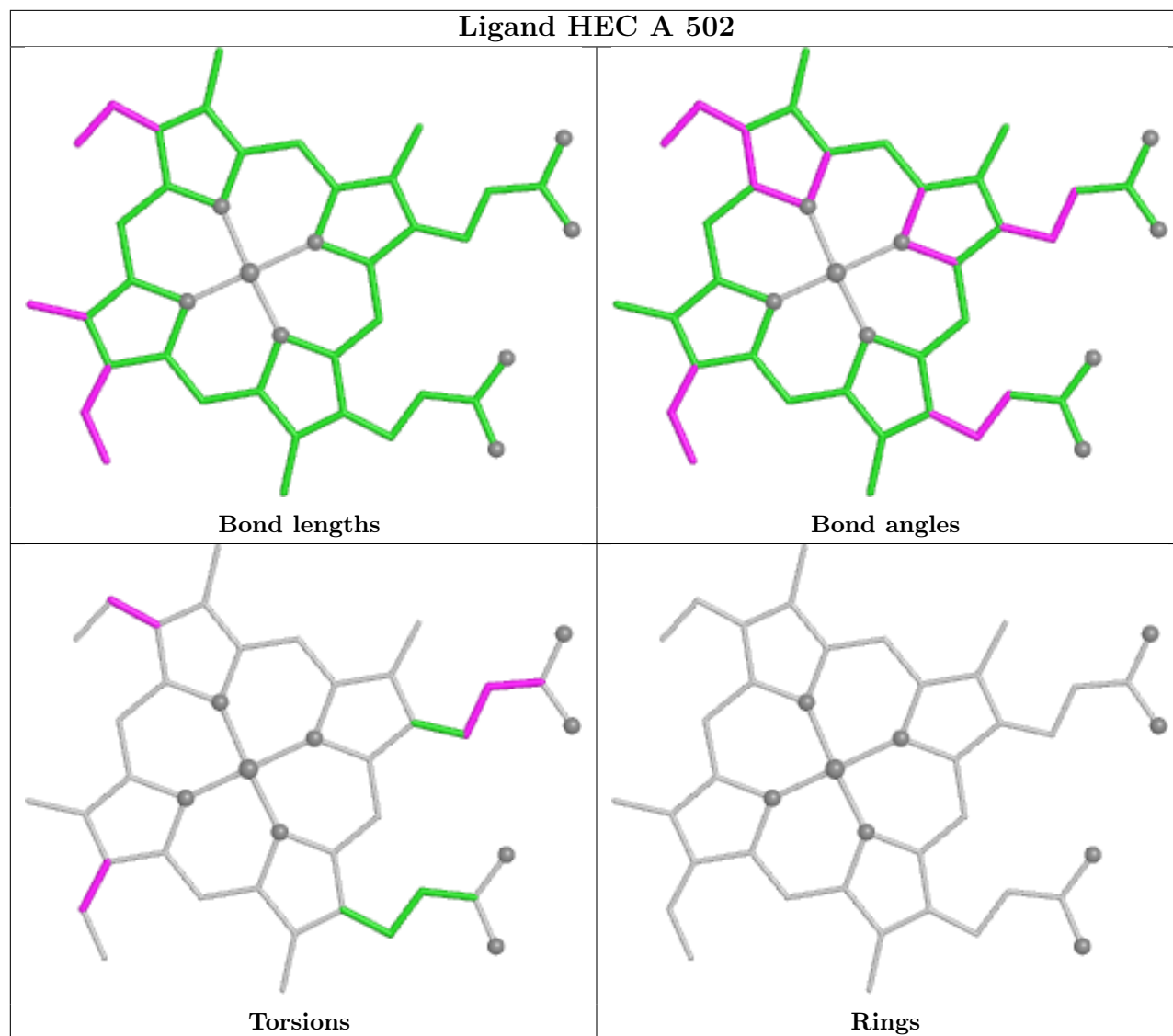
Torsions

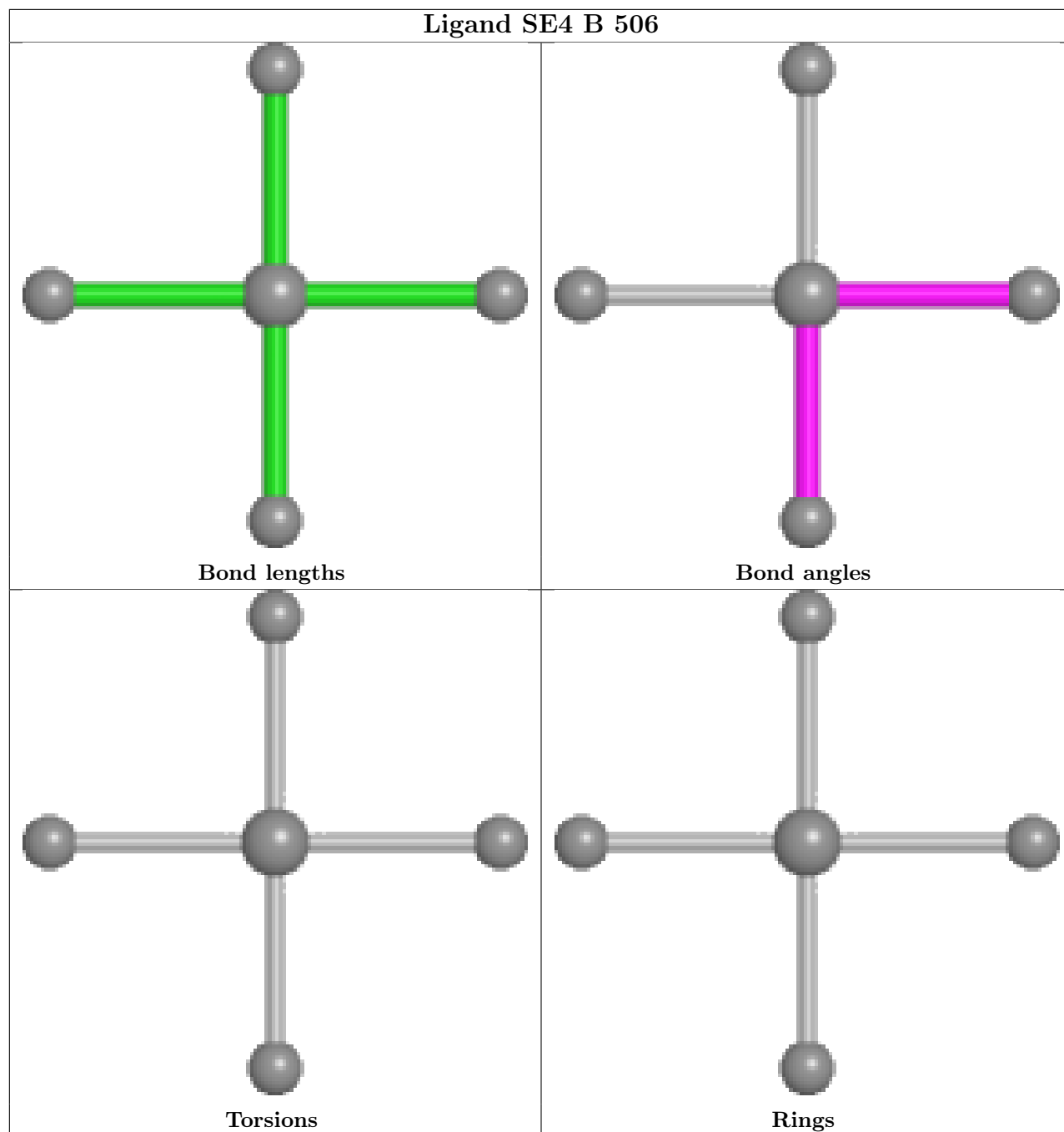


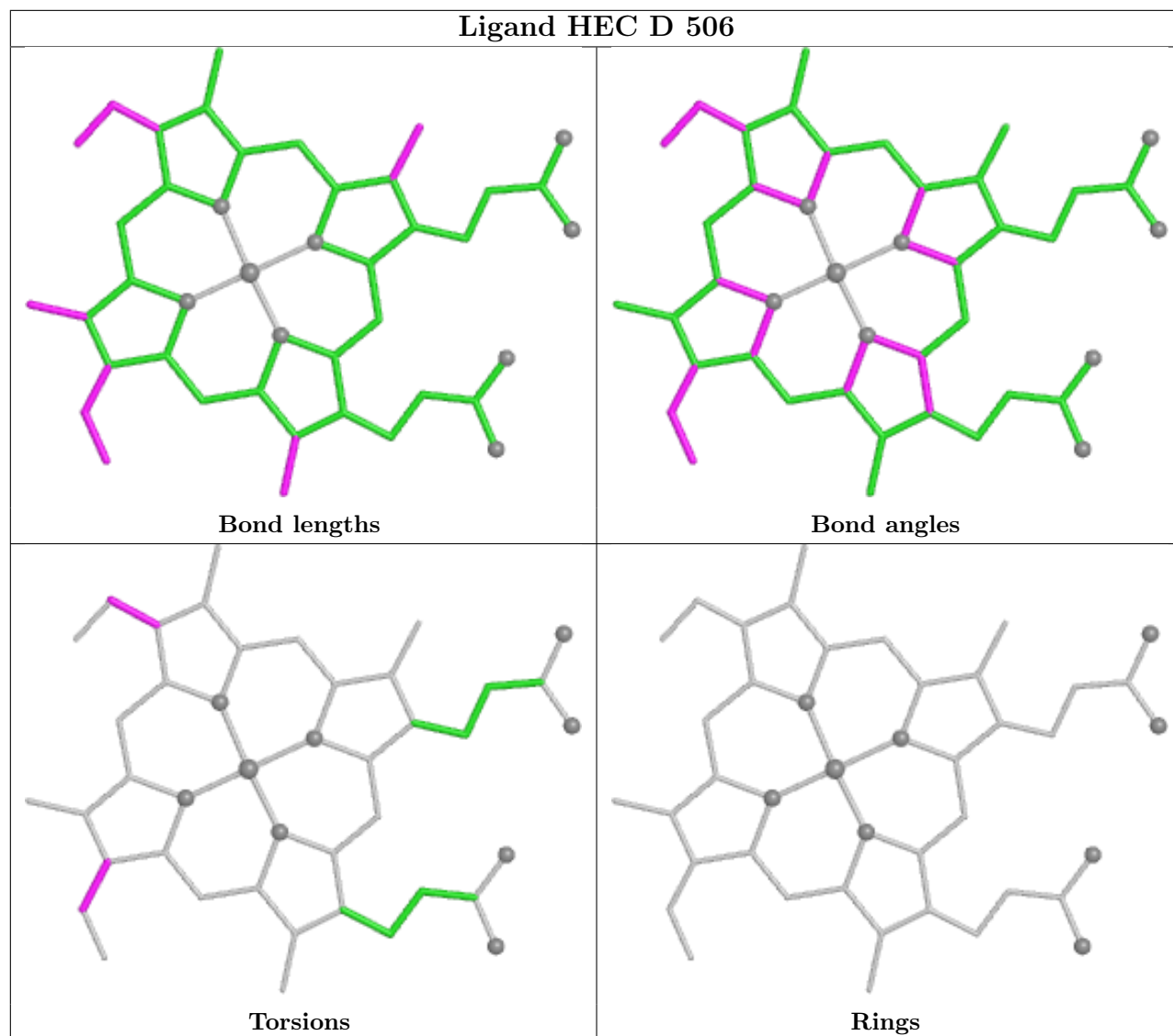
Rings

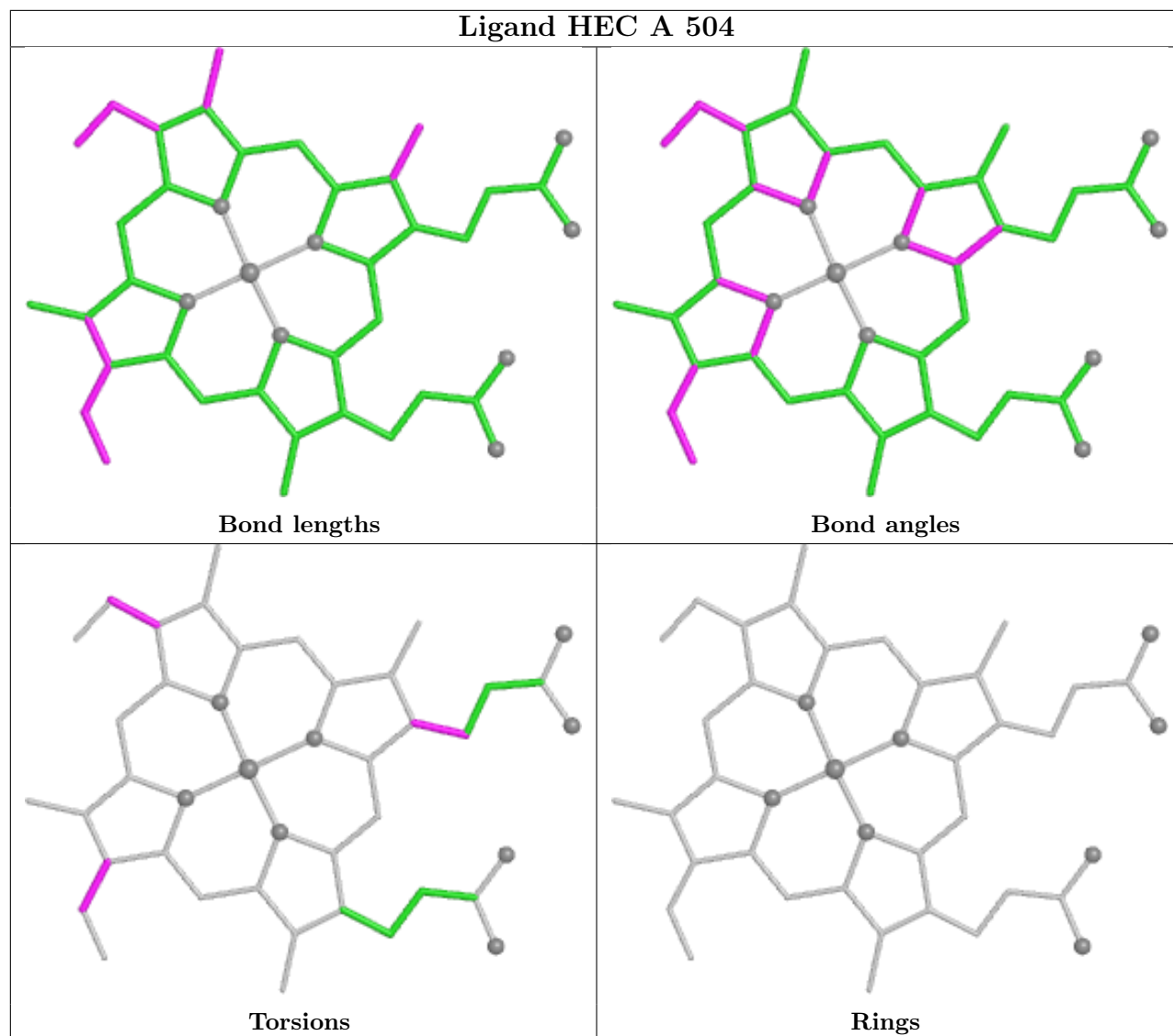


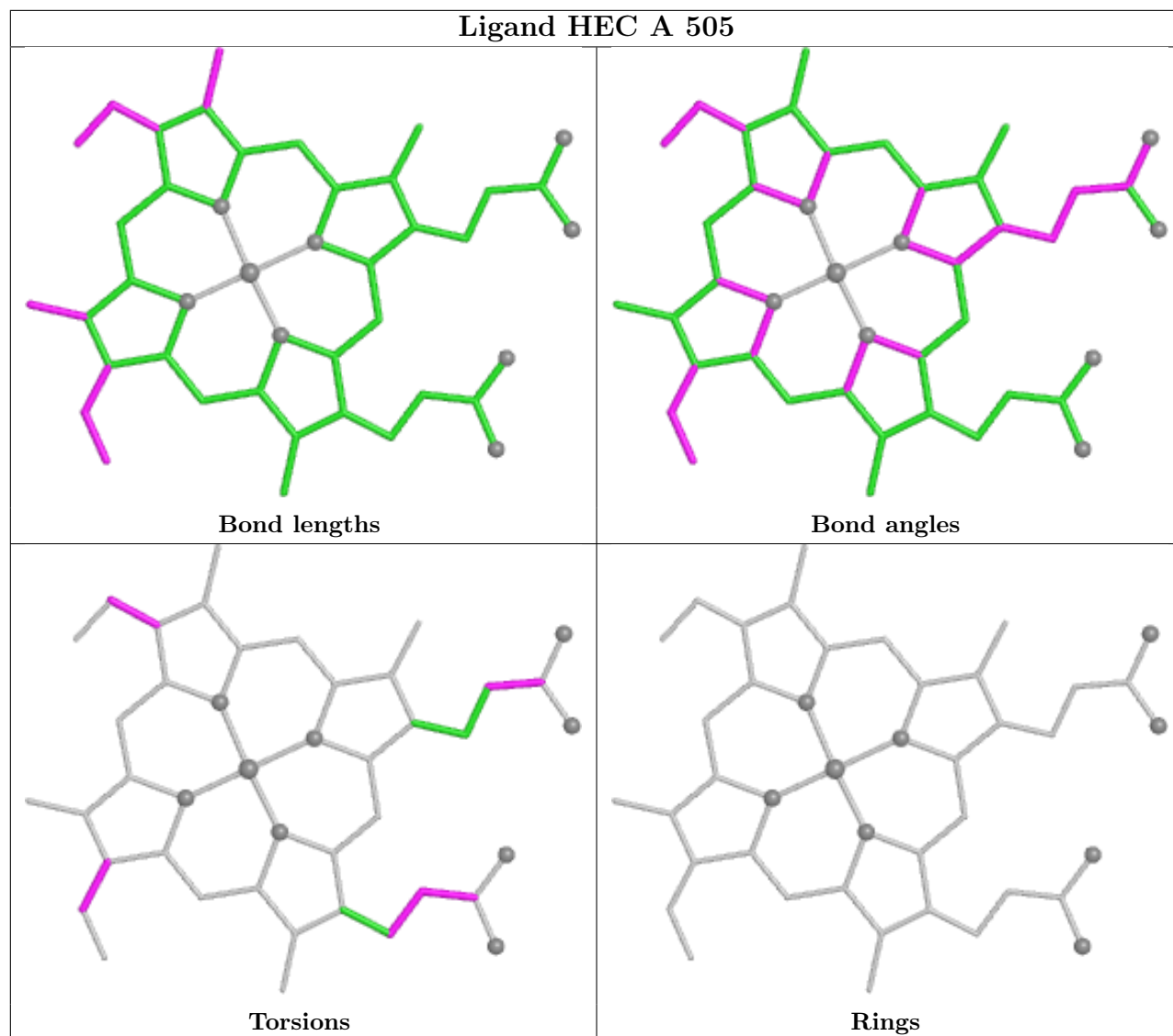


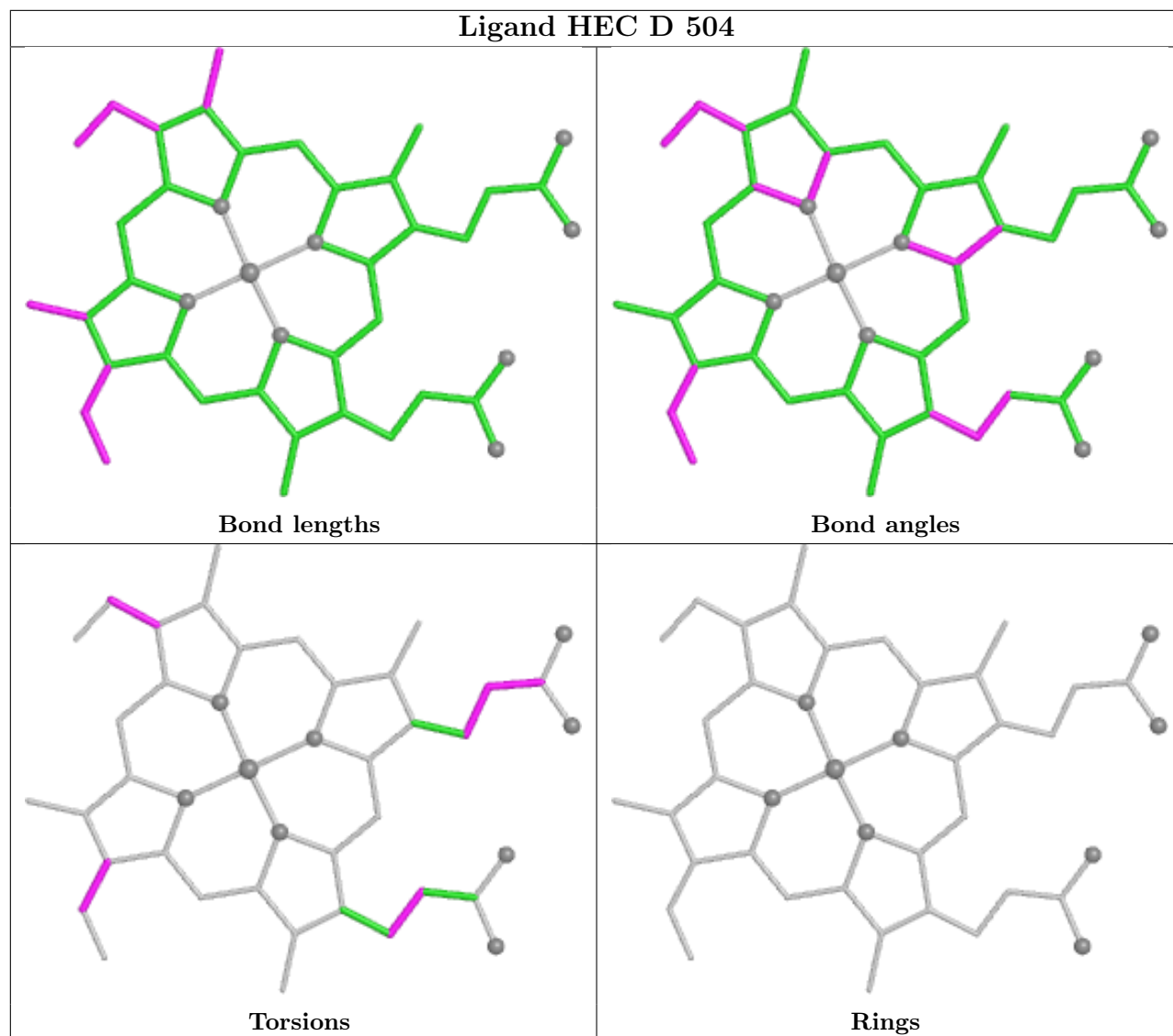


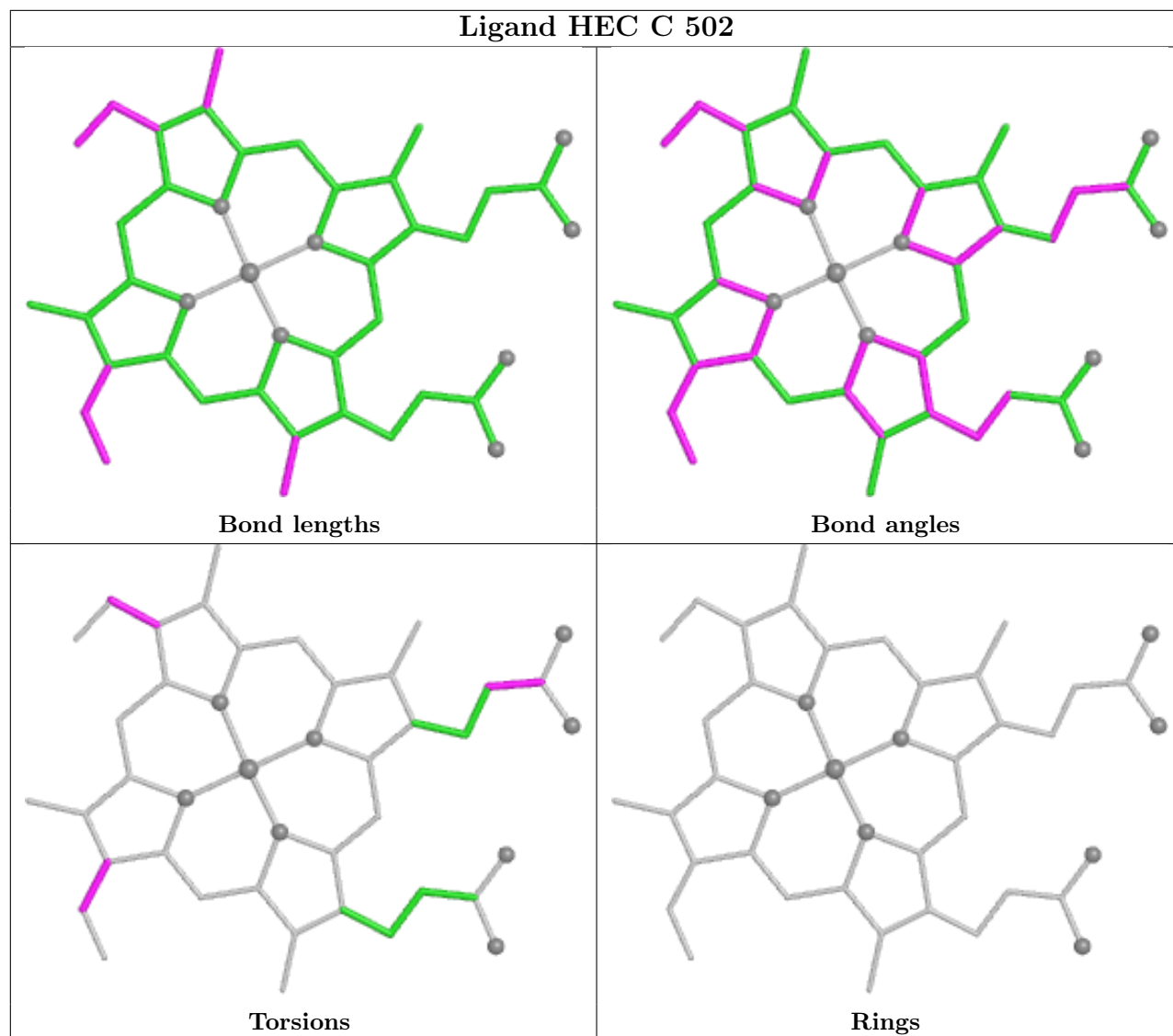












5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	421/450 (93%)	-0.32	0	100 100	17, 43, 66, 88	9 (2%)
1	B	421/450 (93%)	-0.38	0	100 100	20, 42, 62, 76	9 (2%)
1	C	421/450 (93%)	-0.15	4 (0%)	79 77	23, 48, 68, 100	6 (1%)
1	D	421/450 (93%)	-0.34	2 (0%)	87 85	21, 43, 62, 79	5 (1%)
All	All	1684/1800 (93%)	-0.30	6 (0%)	88 87	17, 44, 65, 100	29 (1%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	60[A]	GLU	3.0
1	D	28	ALA	2.6
1	D	448	LYS	2.2
1	C	434	PHE	2.1
1	C	253[A]	GLU	2.1
1	C	81	THR	2.1

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CSD	B	239	8/9	0.97	0.07	33,37,45,46	0
1	CSD	C	239	8/9	0.97	0.07	39,42,47,51	0
1	CSD	D	239	8/9	0.97	0.07	34,39,40,50	0
1	CSD	A	239	8/9	0.98	0.06	37,39,47,50	0

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EDO	D	501	4/4	0.65	0.19	61,63,64,70	0
4	EDO	C	515	4/4	0.67	0.23	64,67,71,72	0
4	EDO	A	513	4/4	0.67	0.25	67,67,71,73	0
4	EDO	D	516	4/4	0.73	0.16	55,59,71,81	0
4	EDO	D	518	4/4	0.78	0.21	42,58,73,75	0
4	EDO	D	513	4/4	0.80	0.23	64,65,65,65	0
4	EDO	C	514	4/4	0.81	0.15	58,64,66,70	0
4	EDO	B	519	4/4	0.81	0.22	40,41,54,59	0
4	EDO	D	517	4/4	0.82	0.14	50,51,52,62	4
4	EDO	A	511	4/4	0.83	0.19	50,56,58,59	0
4	EDO	C	513	4/4	0.84	0.19	51,54,55,56	4
4	EDO	B	517	4/4	0.85	0.17	51,54,60,64	0
4	EDO	B	513	4/4	0.86	0.16	40,40,43,44	4
4	EDO	B	516	4/4	0.86	0.14	50,55,56,59	4
4	EDO	D	511	4/4	0.86	0.13	47,53,59,65	0
4	EDO	D	512	4/4	0.86	0.15	45,49,59,60	0
5	EPE	B	507	15/15	0.86	0.16	56,60,68,70	15
4	EDO	A	509	4/4	0.87	0.12	48,59,60,66	0
4	EDO	D	509	4/4	0.88	0.14	49,52,52,60	0
4	EDO	A	514	4/4	0.88	0.27	42,51,54,62	0
4	EDO	B	510	4/4	0.89	0.15	50,52,56,59	0
4	EDO	C	512	4/4	0.89	0.16	43,43,46,51	4
4	EDO	C	508	4/4	0.90	0.17	49,59,59,61	0
4	EDO	D	510	4/4	0.90	0.18	50,52,53,65	0
4	EDO	C	510	4/4	0.90	0.12	43,46,48,52	4
4	EDO	B	514	4/4	0.90	0.12	46,49,56,56	4
4	EDO	B	509	4/4	0.90	0.13	44,44,56,56	0
4	EDO	D	514	4/4	0.90	0.14	42,42,43,48	4
4	EDO	A	508	4/4	0.90	0.17	44,45,53,53	4
4	EDO	B	508	4/4	0.90	0.15	42,63,66,71	0
4	EDO	C	501	4/4	0.90	0.10	41,42,47,61	0
4	EDO	D	502	4/4	0.90	0.12	40,41,44,45	4

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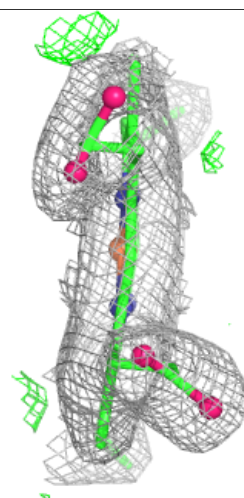
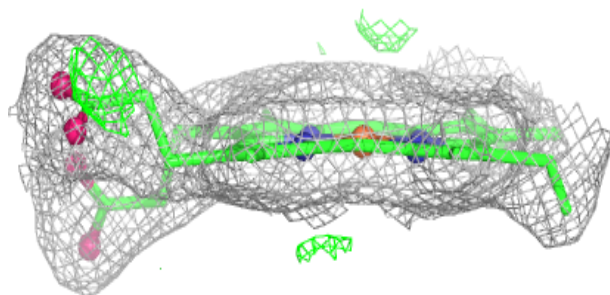
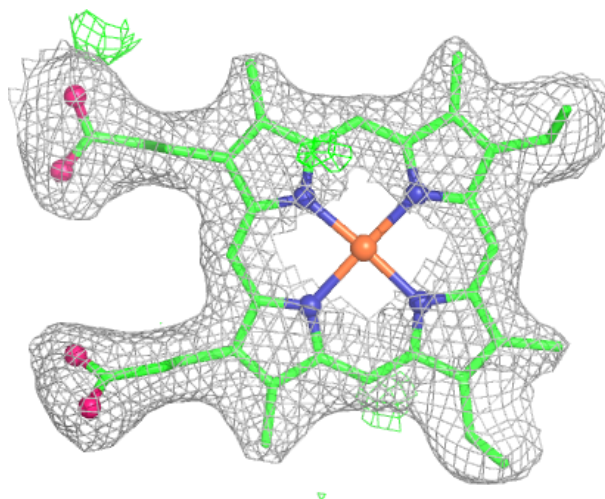
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	B	511	4/4	0.91	0.10	56,63,63,71	0
4	EDO	C	516	4/4	0.91	0.17	50,58,61,63	0
4	EDO	C	509	4/4	0.92	0.13	53,55,58,58	0
4	EDO	B	515	4/4	0.92	0.09	44,52,61,70	0
4	EDO	A	510	4/4	0.92	0.15	38,45,48,48	0
4	EDO	D	515	4/4	0.92	0.16	29,32,39,43	4
4	EDO	B	512	4/4	0.93	0.15	44,49,51,64	0
4	EDO	B	518	4/4	0.94	0.14	35,42,46,48	4
4	EDO	A	507	4/4	0.94	0.13	38,45,50,57	0
4	EDO	A	512	4/4	0.94	0.09	45,45,54,55	0
4	EDO	C	511	4/4	0.95	0.15	32,37,39,41	4
2	HEC	D	503	43/43	0.97	0.07	41,51,57,66	0
2	HEC	C	502	43/43	0.97	0.08	47,56,67,68	0
2	HEC	B	501	43/43	0.98	0.07	40,49,58,64	0
2	HEC	B	502	43/43	0.98	0.07	31,36,50,60	0
2	HEC	B	503	43/43	0.98	0.06	31,42,55,59	0
2	HEC	B	504	43/43	0.98	0.06	28,34,42,50	0
2	HEC	A	501	43/43	0.98	0.07	33,41,54,59	0
2	HEC	C	503	43/43	0.98	0.08	36,43,62,63	0
2	HEC	C	504	43/43	0.98	0.08	36,45,57,65	0
2	HEC	C	505	43/43	0.98	0.08	33,39,52,57	0
2	HEC	A	502	43/43	0.98	0.07	30,38,53,56	0
2	HEC	D	504	43/43	0.98	0.06	29,36,47,54	0
2	HEC	D	505	43/43	0.98	0.06	34,43,56,60	0
3	SE4	A	506	5/5	0.98	0.14	40,42,51,55	5
3	SE4	C	507	5/5	0.98	0.13	46,47,54,54	5
2	HEC	A	503	43/43	0.98	0.07	29,35,49,55	0
2	HEC	D	507	43/43	0.99	0.05	28,35,40,45	0
2	HEC	C	506	43/43	0.99	0.06	33,39,45,52	0
3	SE4	B	506	5/5	0.99	0.15	34,34,38,44	5
2	HEC	A	505	43/43	0.99	0.06	28,34,41,48	0
3	SE4	D	508	5/5	0.99	0.11	39,41,44,51	5
2	HEC	B	505	43/43	0.99	0.06	29,35,41,52	0
2	HEC	A	504	43/43	0.99	0.06	30,34,45,52	0
2	HEC	D	506	43/43	0.99	0.06	29,35,43,49	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.

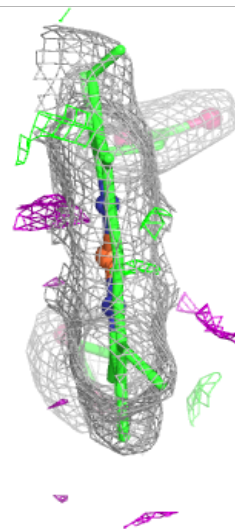
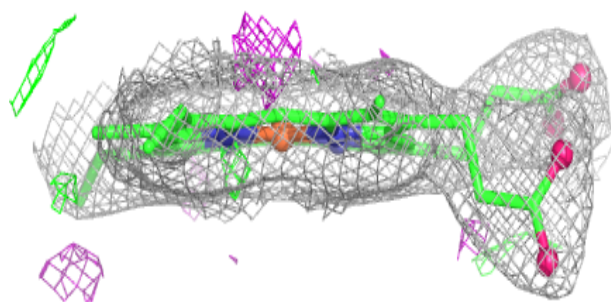
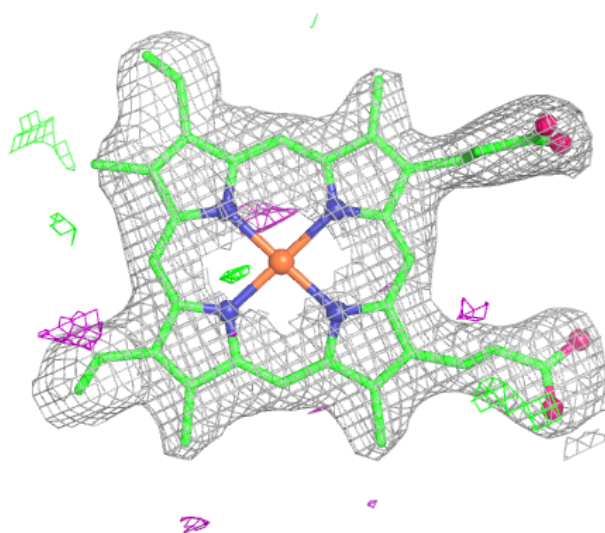
Electron density around HEC D 503:

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



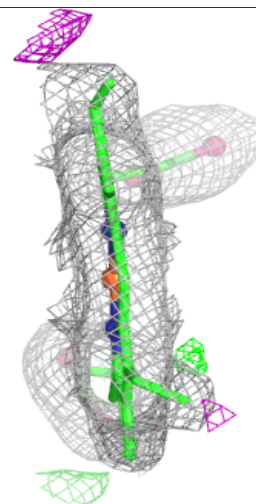
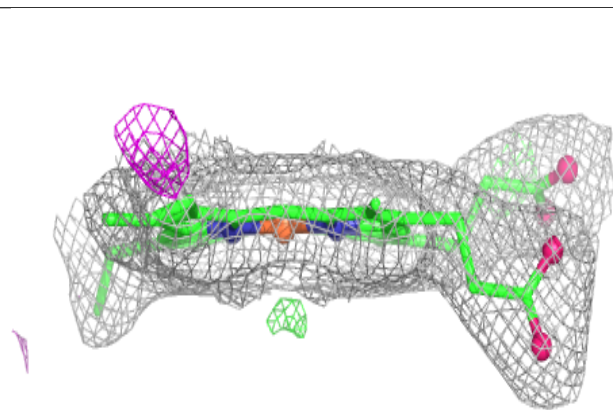
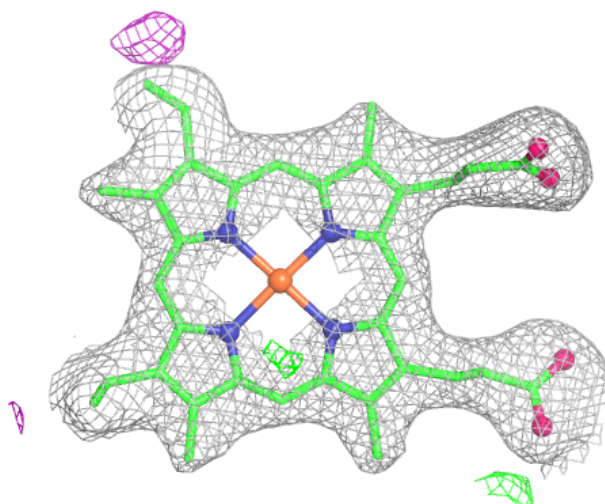
Electron density around HEC C 502:

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and green (positive)



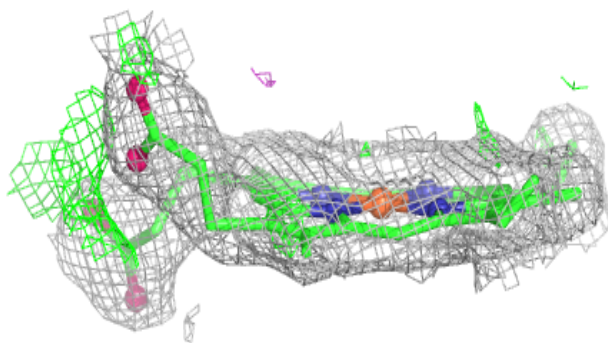
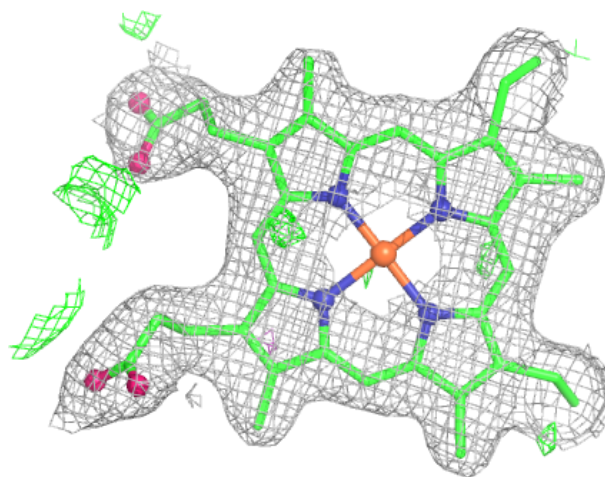
Electron density around HEC B 501:

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and green (positive)



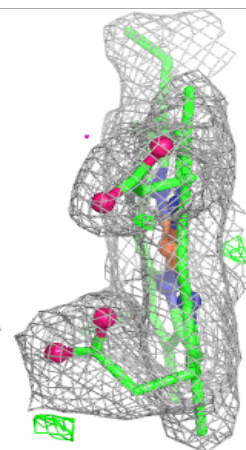
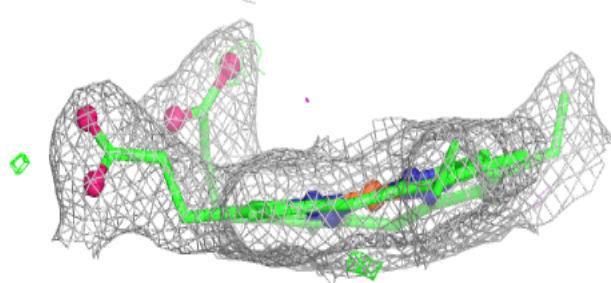
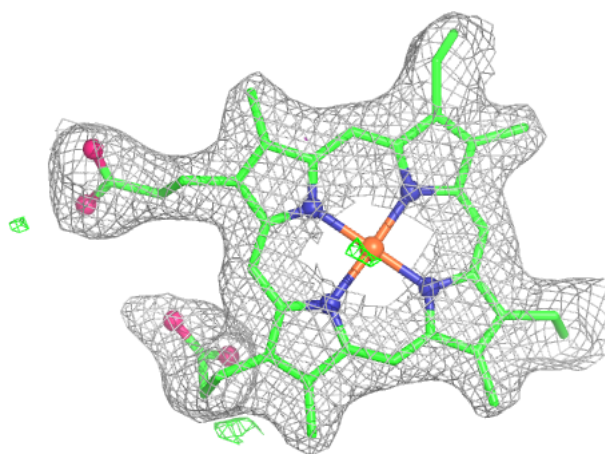
Electron density around HEC B 502:

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and green (positive)



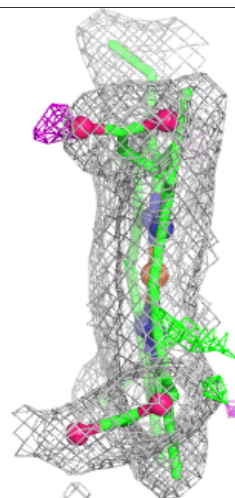
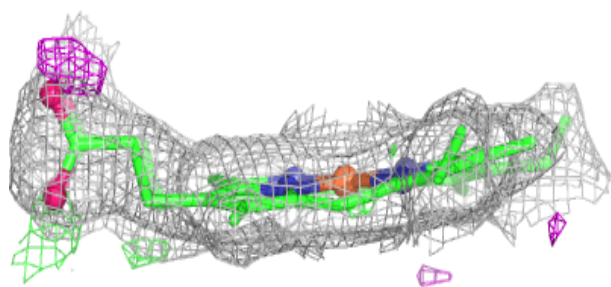
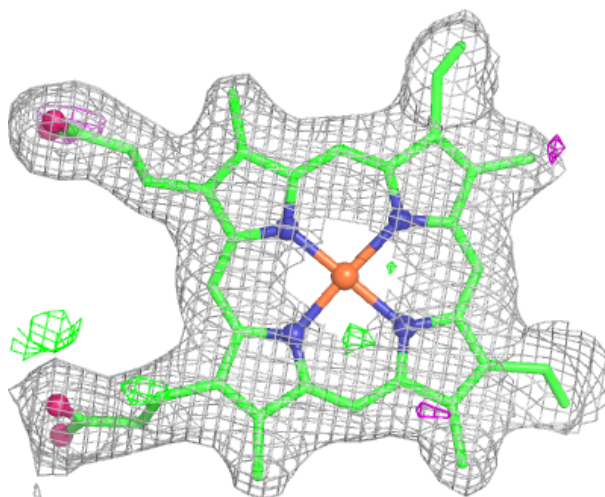
Electron density around HEC B 503:

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and green (positive)



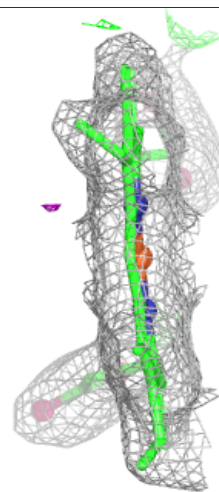
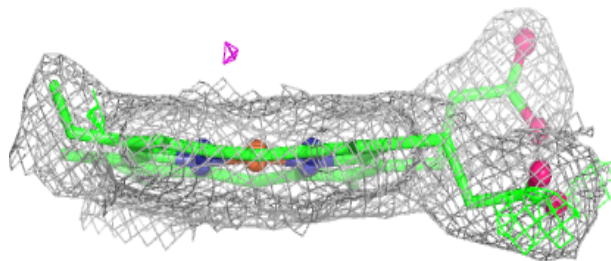
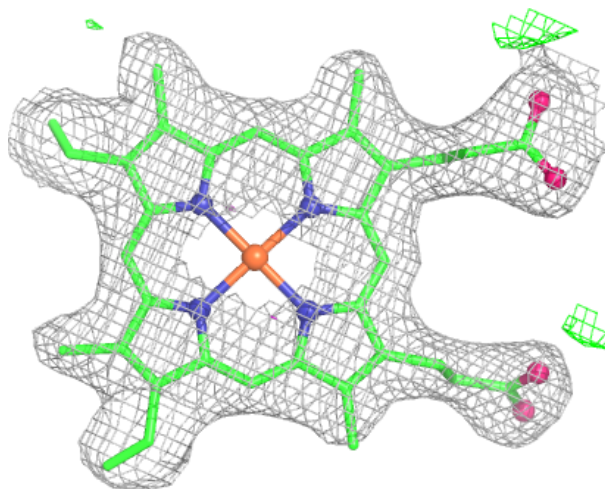
Electron density around HEC B 504:

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and green (positive)



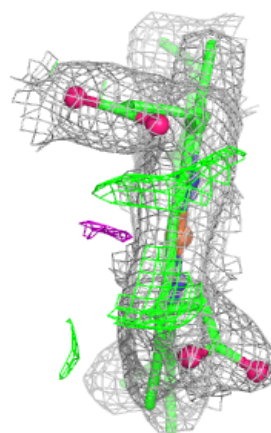
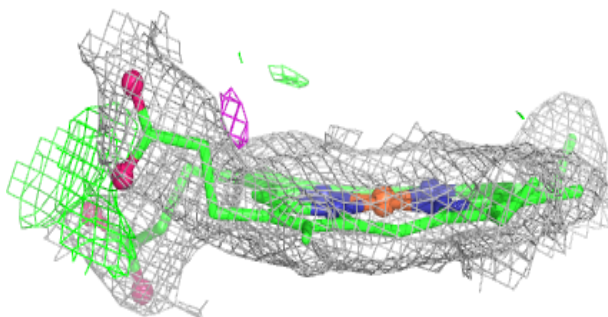
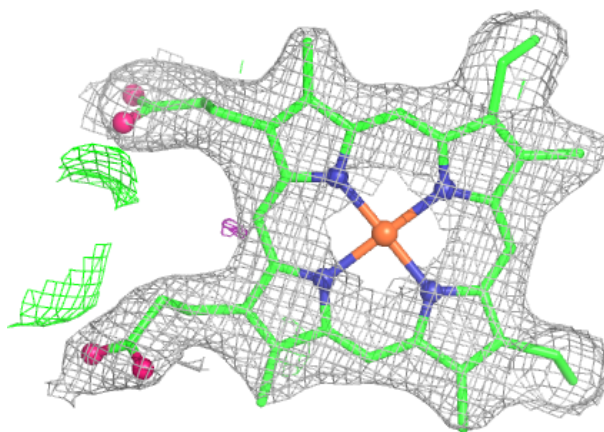
Electron density around HEC A 501:

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



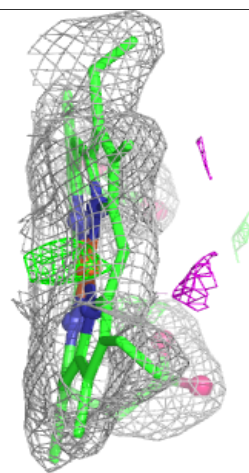
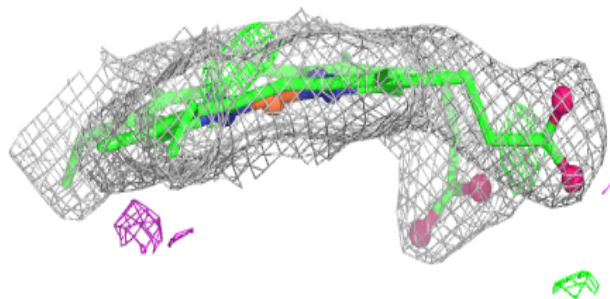
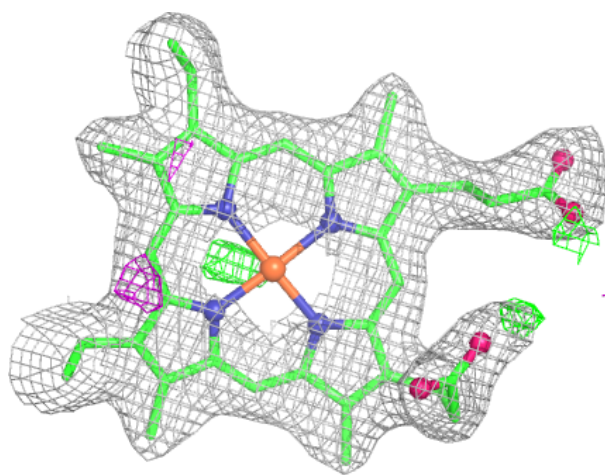
Electron density around HEC C 503:

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



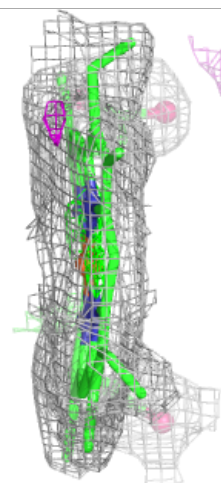
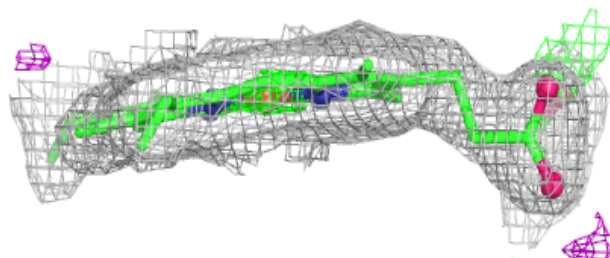
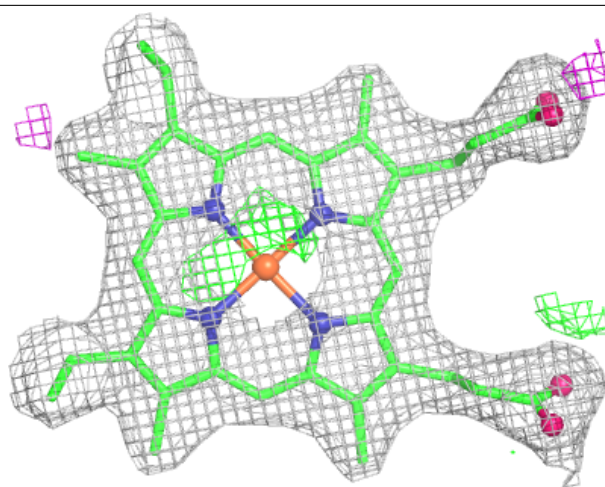
Electron density around HEC C 504:

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



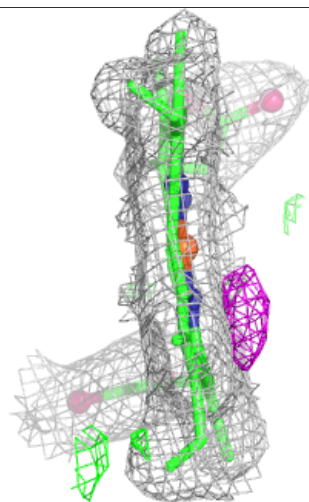
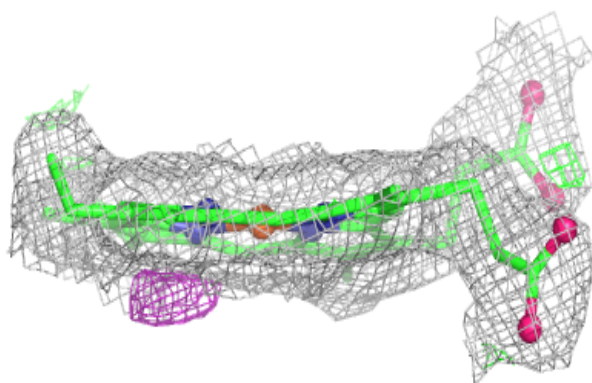
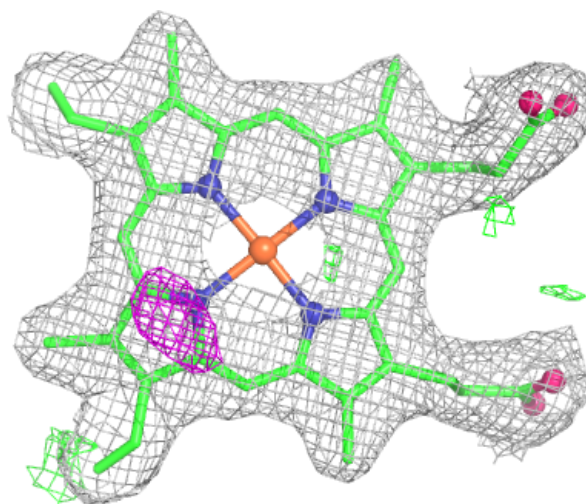
Electron density around HEC C 505:

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and green (positive)



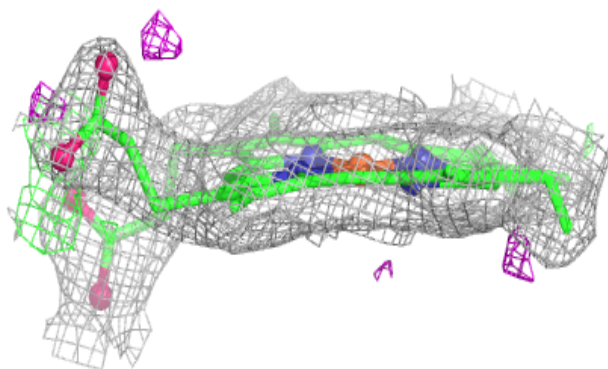
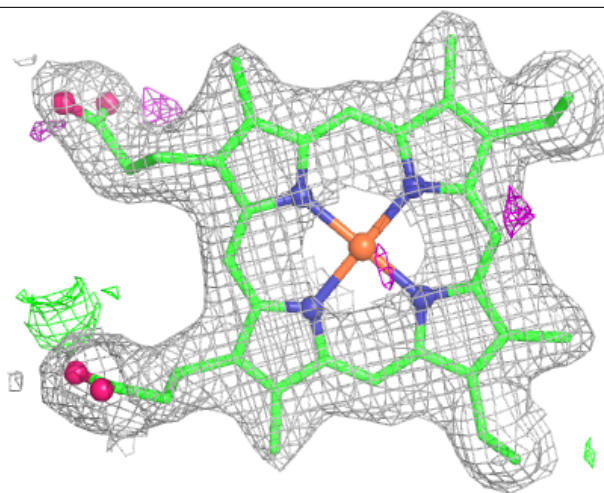
Electron density around HEC A 502:

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and green (positive)



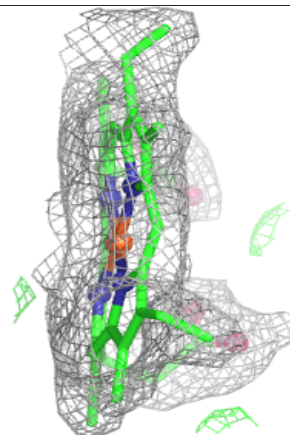
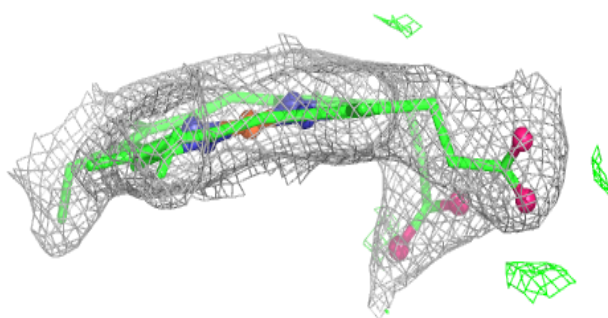
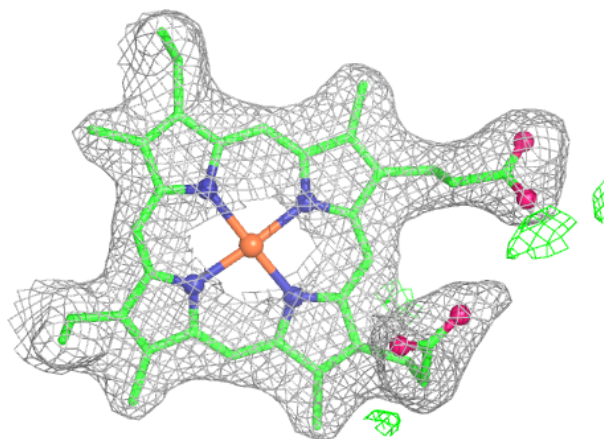
Electron density around HEC D 504:

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



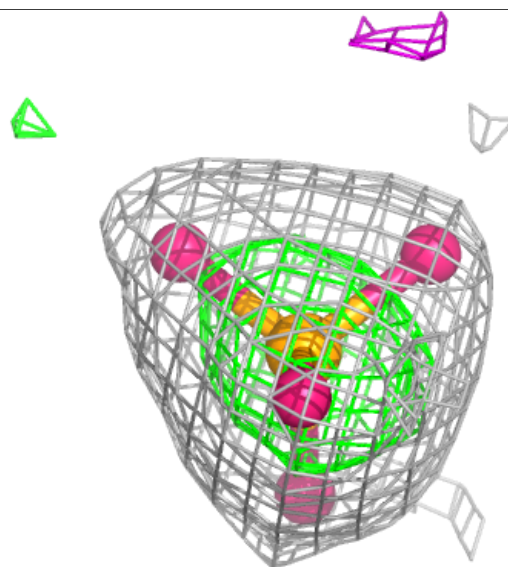
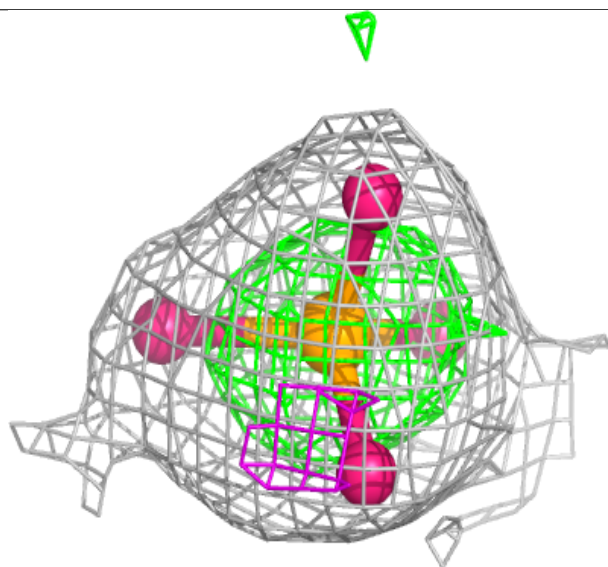
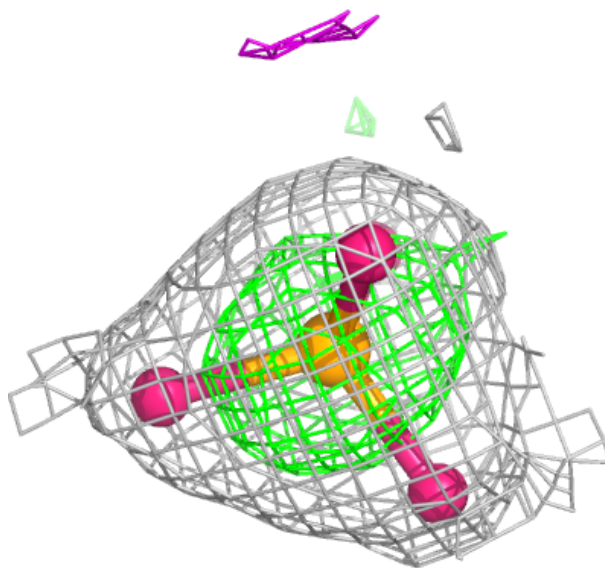
Electron density around HEC D 505:

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and green (positive)



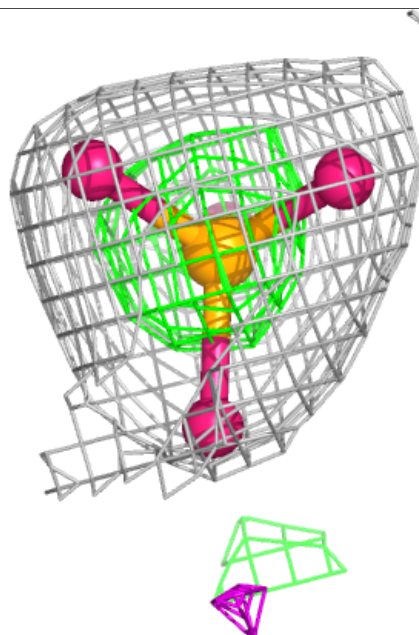
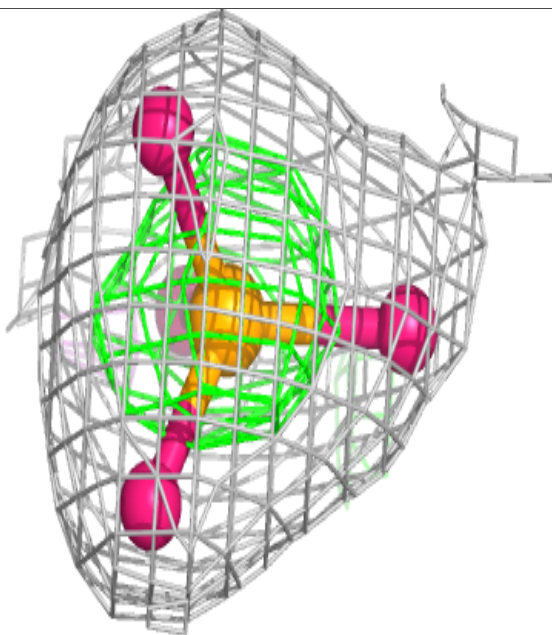
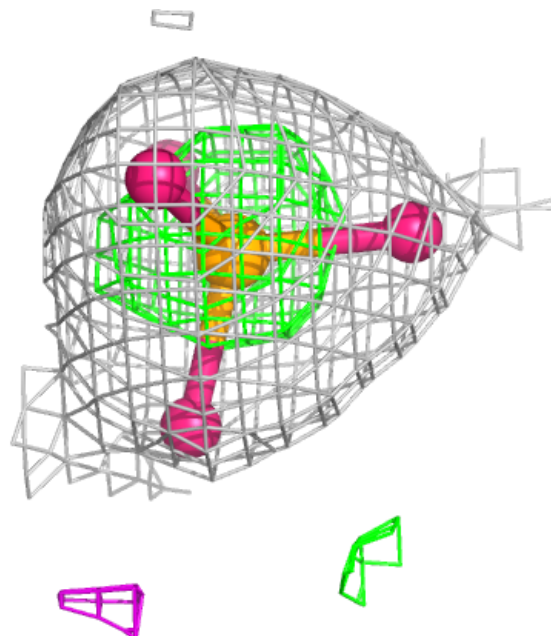
Electron density around SE4 A 506:

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and green (positive)



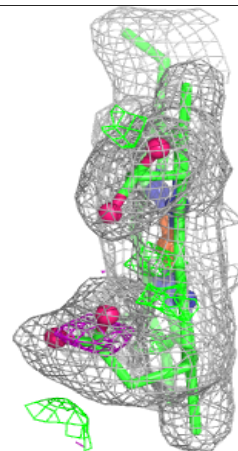
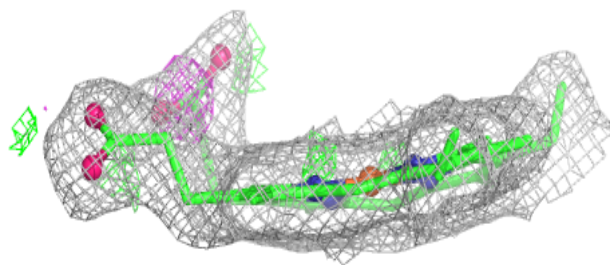
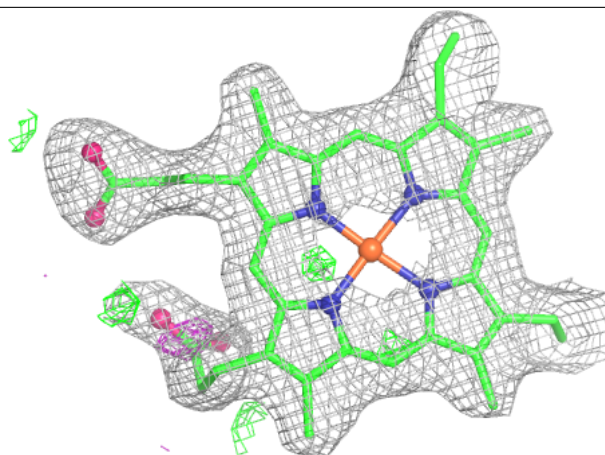
Electron density around SE4 C 507:

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and green (positive)



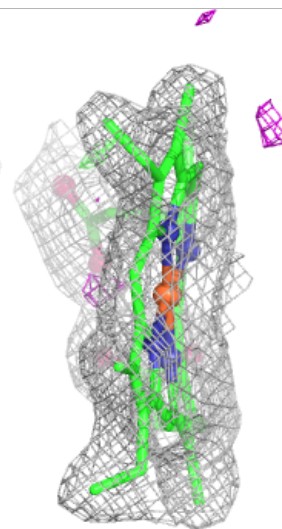
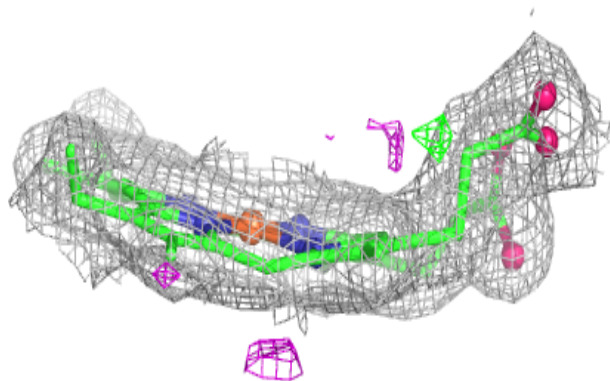
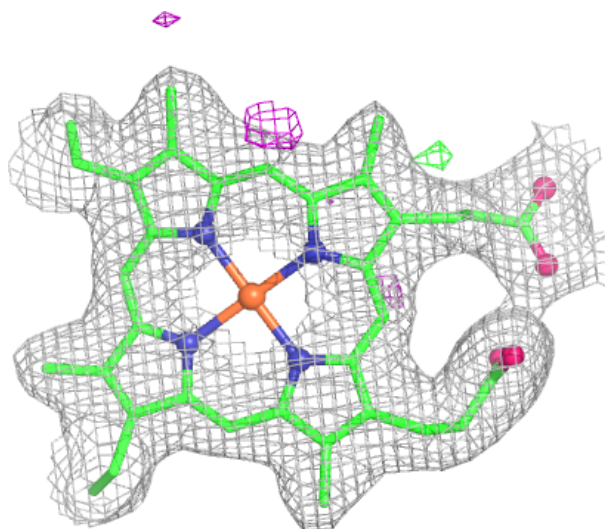
Electron density around HEC A 503:

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and green (positive)



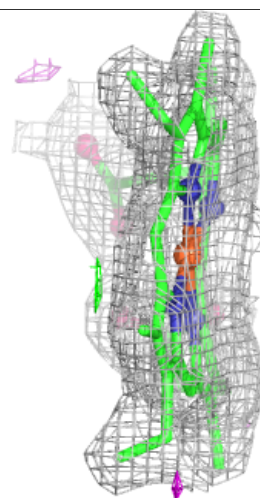
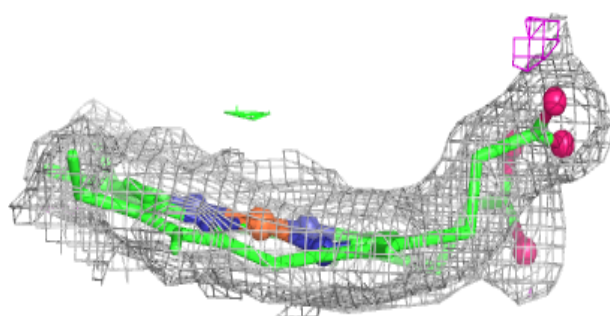
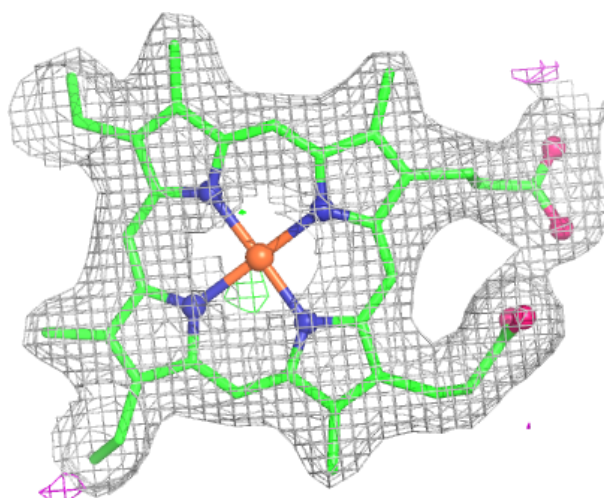
Electron density around HEC D 507:

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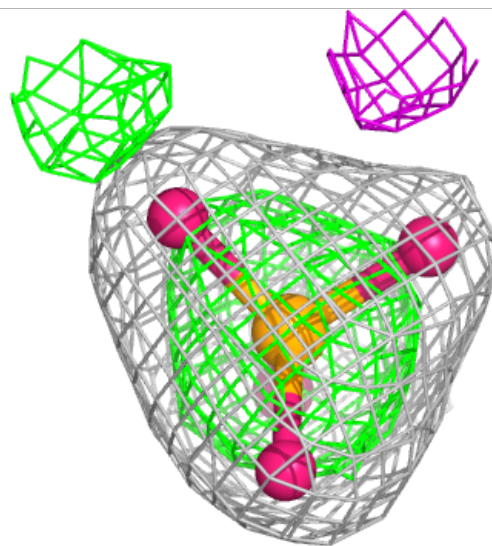
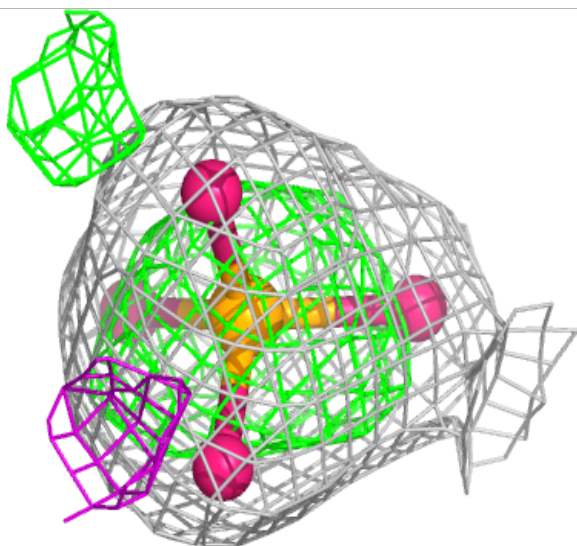
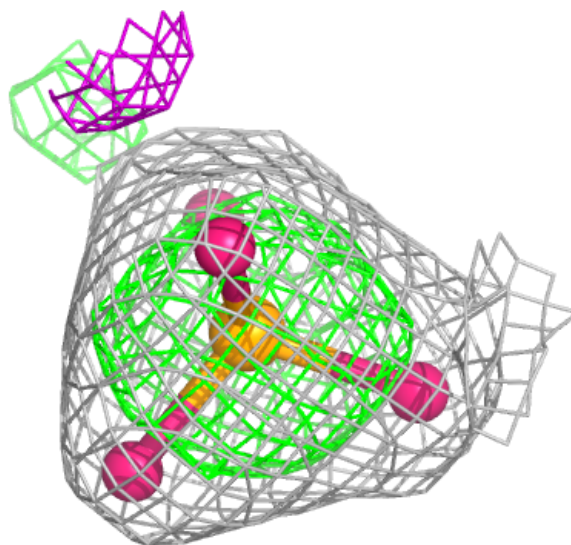
Electron density around HEC C 506:

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and green (positive)



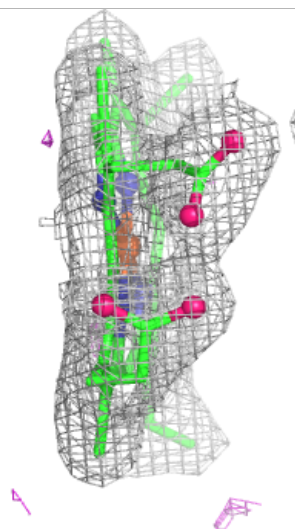
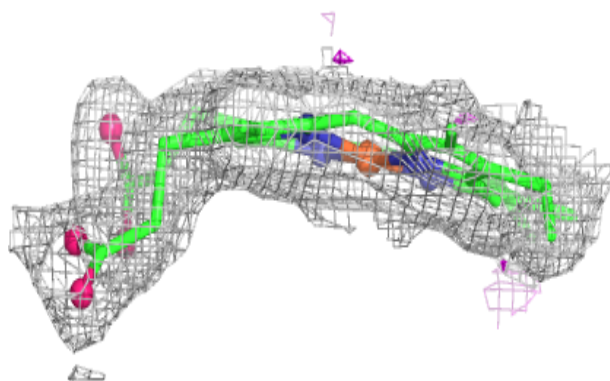
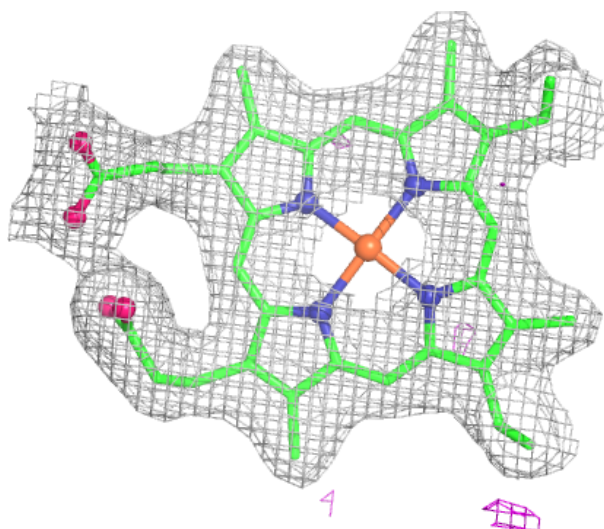
Electron density around SE4 B 506:

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and green (positive)



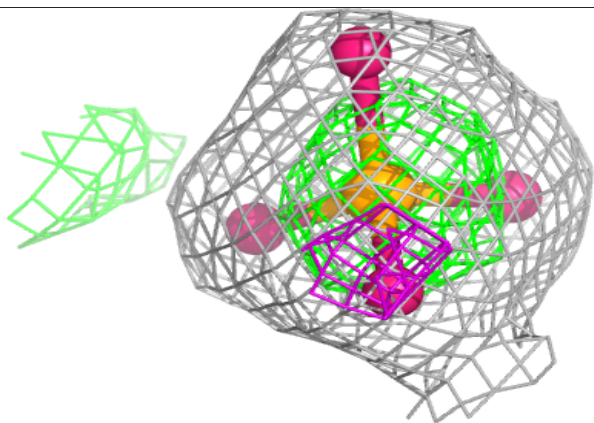
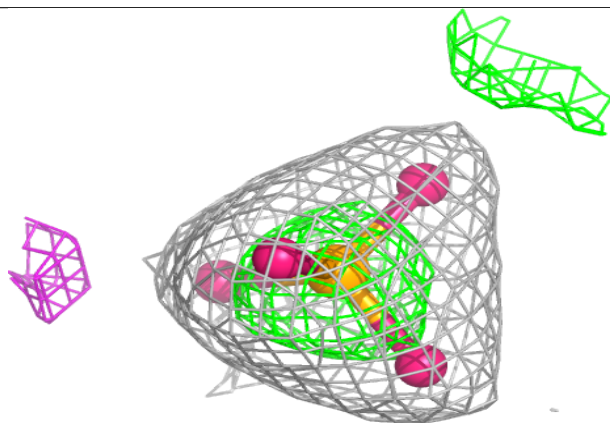
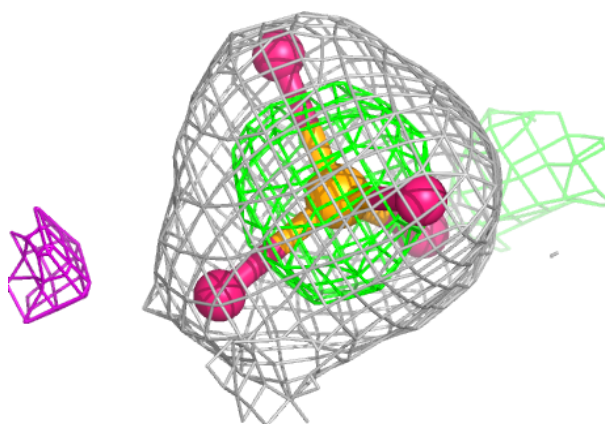
Electron density around HEC A 505:

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and green (positive)



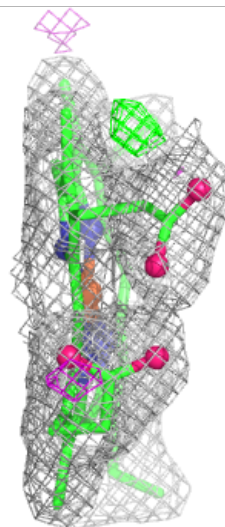
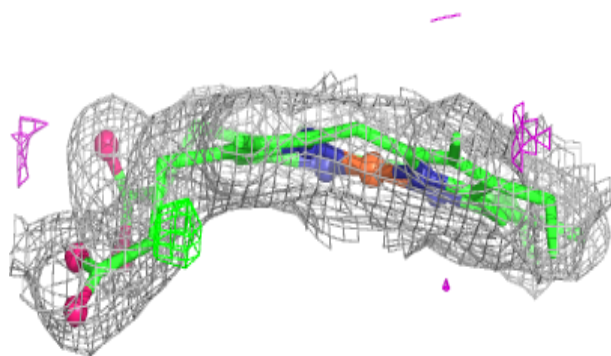
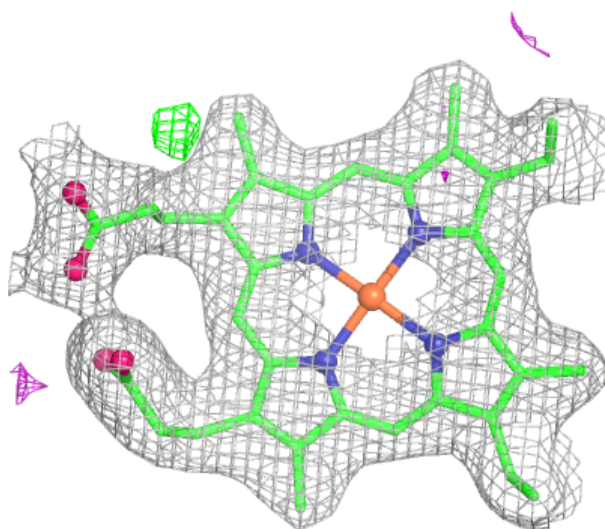
Electron density around SE4 D 508:

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and green (positive)



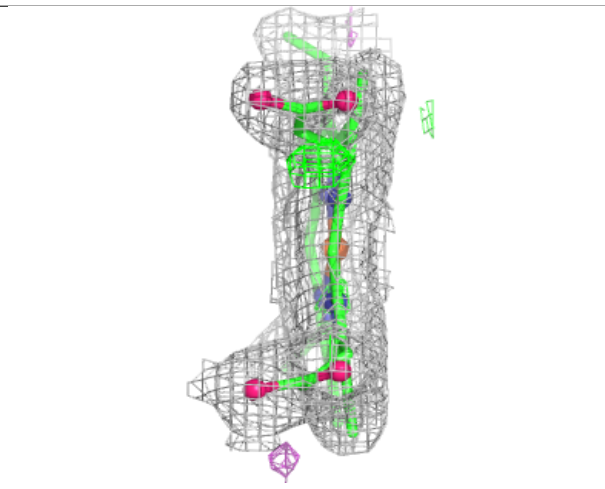
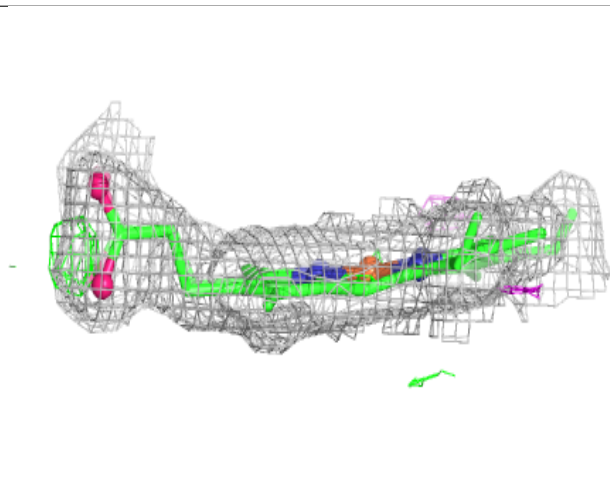
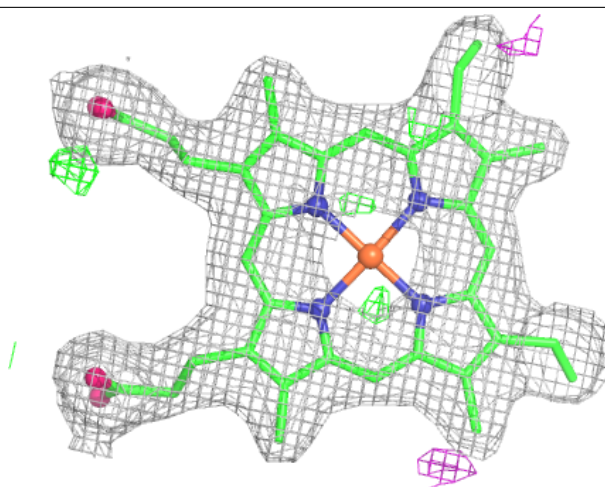
Electron density around HEC B 505:

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and green (positive)



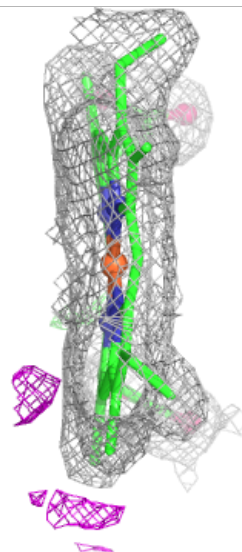
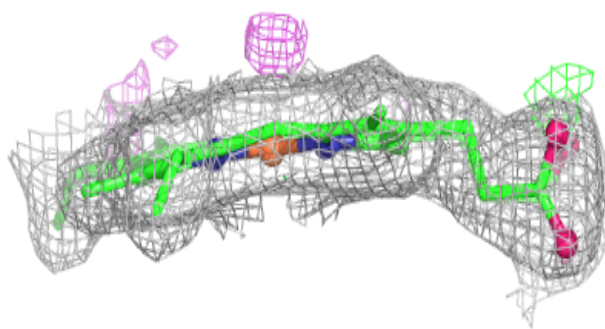
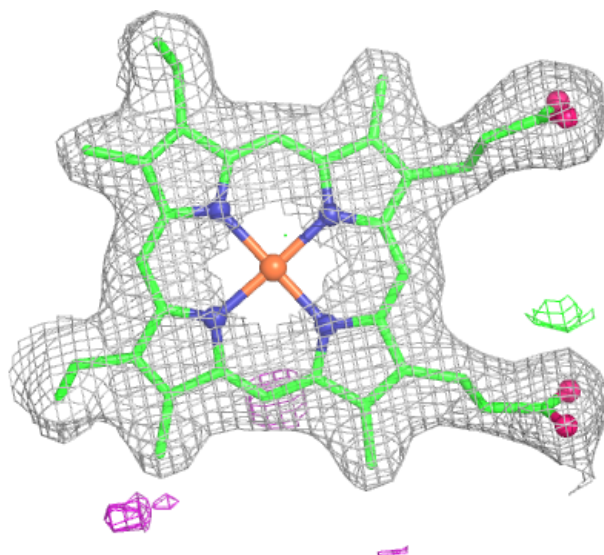
Electron density around HEC A 504:

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



Electron density around HEC D 506:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.