



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:53 AM UTC

PDB ID : 6M0P / pdb_00006m0p
Title : Hydroxylamine oxidoreductase in complex with juglone
Authors : Fujiwara, T.; Fujimoto, Z.; Nishigaya, Y.; Yamazaki, T.
Deposited on : 2020-02-22
Resolution : 2.78 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	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

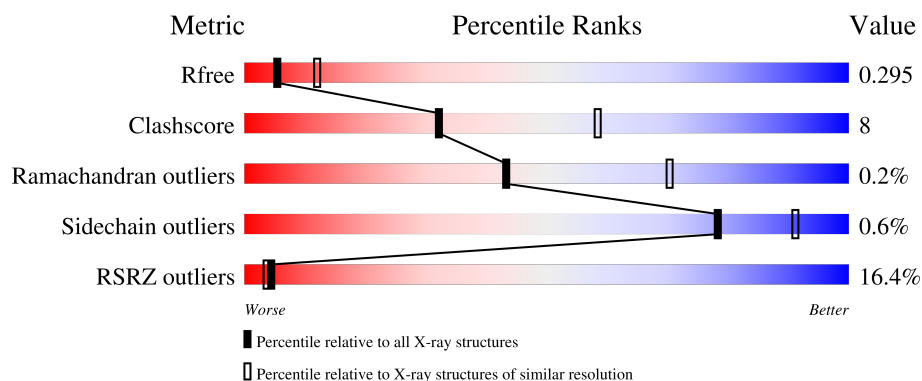
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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	570	13% 70%18%12%
1	C	570	16% 71%17%12%
1	E	570	15% 72%16%12%
2	B	91	9% 58%38%
2	D	91	8% 56%5%38%

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Mol	Chain	Length	Quality of chain
2	F	91	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: a red segment at the beginning labeled '12%', a green segment labeled '56%', a yellow segment labeled '5%', and a grey segment at the end labeled '38%'.

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14521 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.

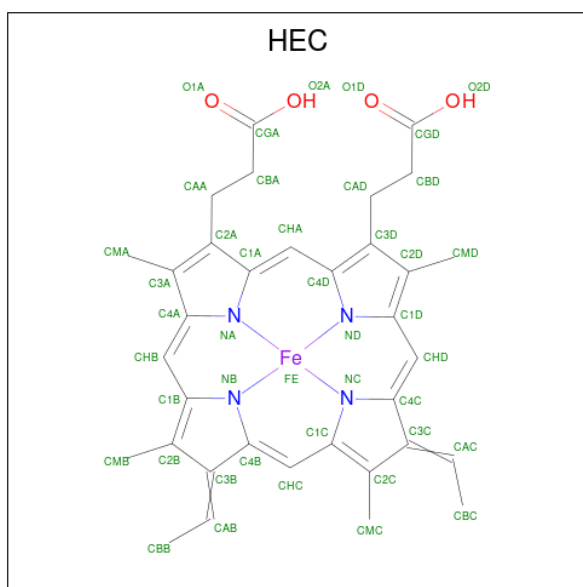
- Molecule 1 is a protein called Aerobic hydroxylamine oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	503	Total	C	N	O	S	0	0	0
			4009	2493	711	773	32			
1	C	503	Total	C	N	O	S	0	0	0
			4009	2493	711	773	32			
1	E	503	Total	C	N	O	S	0	0	0
			4009	2493	711	773	32			

- Molecule 2 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	56	Total	C	N	O	S	0	0	0
			423	263	75	82	3			
2	D	56	Total	C	N	O	S	0	0	0
			425	264	75	83	3			
2	F	56	Total	C	N	O	S	0	0	0
			425	264	75	83	3			

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

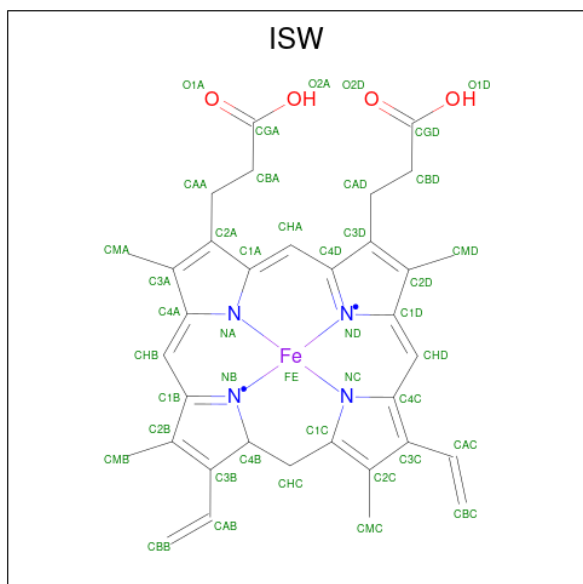
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	E	1	Total	C	Fe	N	O	
			43	34	1	4	4	
3	E	1	Total	C	Fe	N	O	
			43	34	1	4	4	
3	E	1	Total	C	Fe	N	O	
			43	34	1	4	4	
3	E	1	Total	C	Fe	N	O	
			43	34	1	4	4	
3	E	1	Total	C	Fe	N	O	
			43	34	1	4	4	
3	E	1	Total	C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

- Molecule 4 is {3,3'-[(9S)-8,13-diethenyl-3,7,12,17-tetramethyl-9,10-dihydroporphyrin-2,18-diyl-kappa 4 N 21 ,N 22 ,N 23 ,N 24]dipropanoato(2-)}iron (CCD ID: ISW) (formula: C₃₄H₃₄FeN₄O₄).



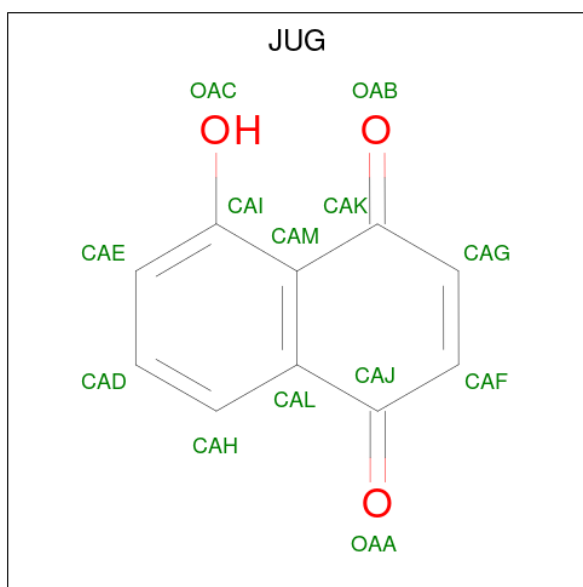
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
4	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
4	C	1	Total	C	Fe	N	O	
			43	34	1	4	4	

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



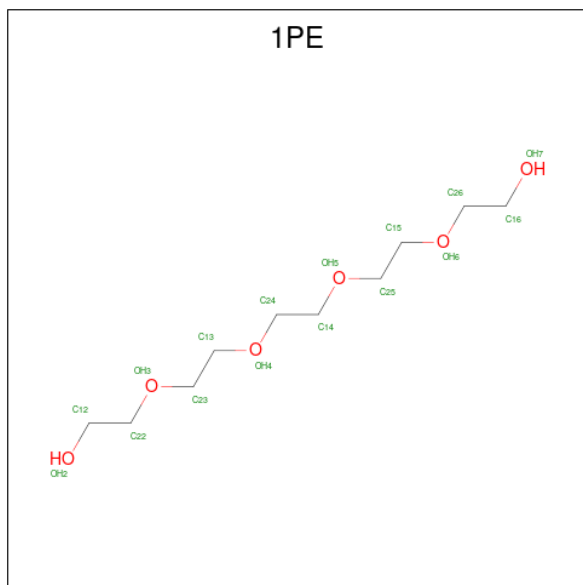
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is 5-hydroxynaphthalene-1,4-dione (CCD ID: JUG) (formula: $C_{10}H_6O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			13	10	3		
6	E	1	Total	C	O	0	0
			13	10	3		

- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



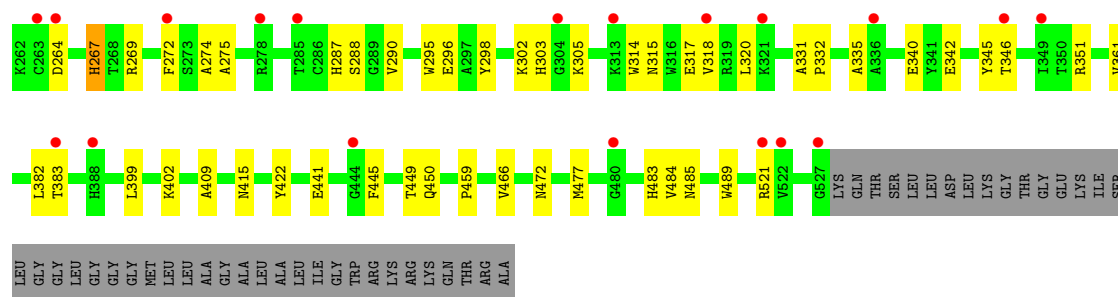
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			12	8	4		
7	C	1	Total	C	O	0	0
			16	10	6		

- Molecule 8 is water.

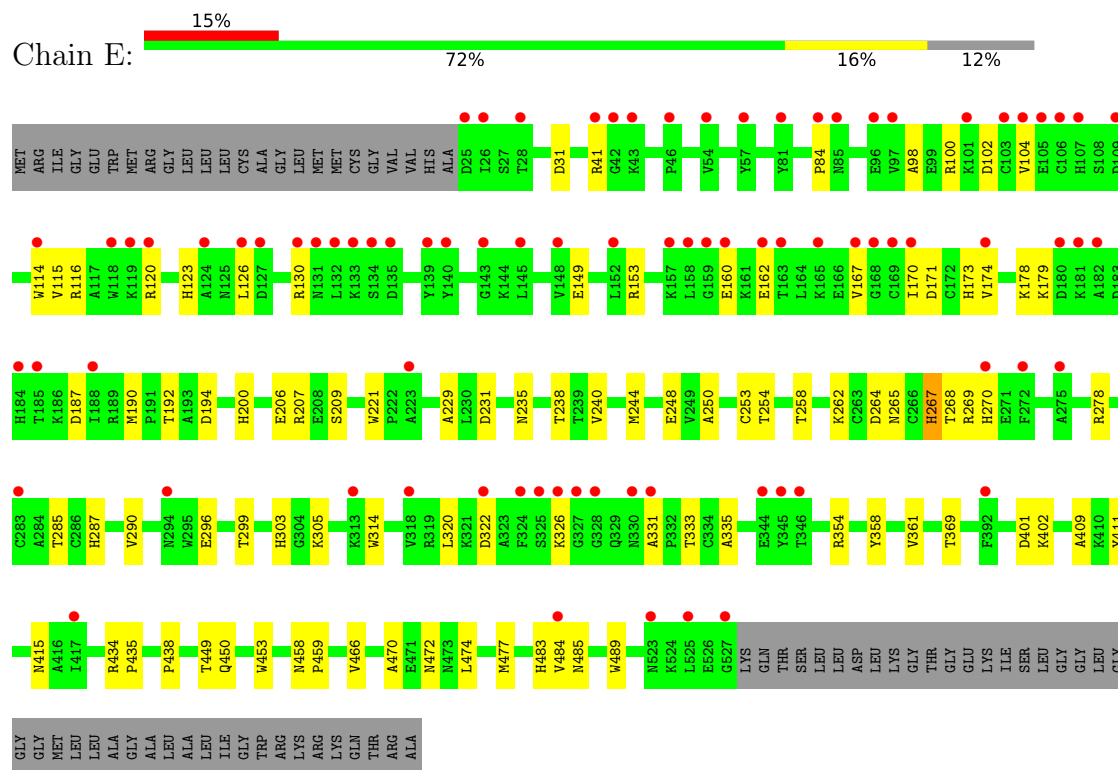
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	44	Total	O	0	0
			44	44		
8	B	5	Total	O	0	0
			5	5		
8	C	31	Total	O	0	0
			31	31		
8	D	7	Total	O	0	0
			7	7		
8	E	26	Total	O	0	0
			26	26		
8	F	1	Total	O	0	0
			1	1		

- Molecule 1: Aerobic hydroxylamine oxidoreductase

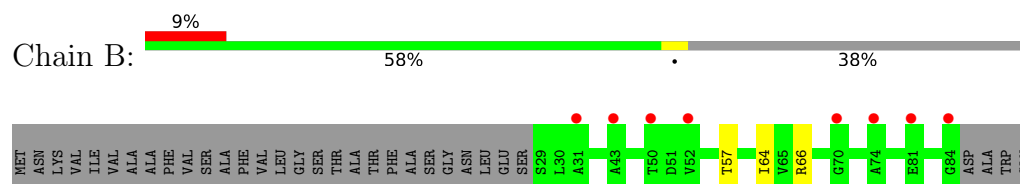




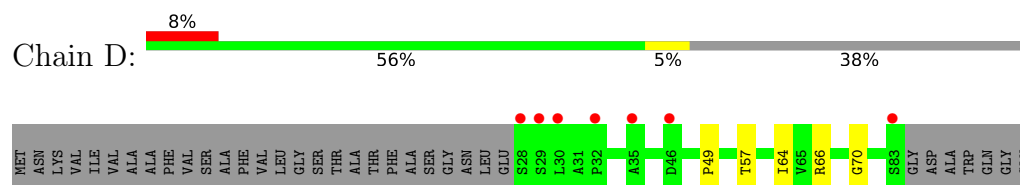
• Molecule 1: Aerobic hydroxylamine oxidoreductase



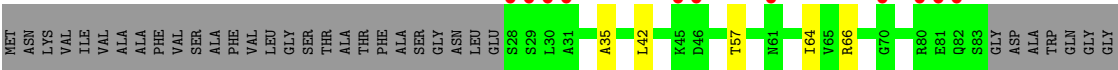
• Molecule 2: Uncharacterized protein



• Molecule 2: Uncharacterized protein



• Molecule 2: Uncharacterized protein



TYR

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	139.34Å 141.07Å 106.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.77 – 2.78 46.77 – 2.78	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.77-2.78) 99.9 (46.77-2.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.256 , 0.292 0.258 , 0.295	Depositor DCC
R_{free} test set	2661 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.729	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.010 for k,h,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	14521	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: JUG, 1PE, HEC, ISW, PEG

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	0.09	0/4112	0.26	0/5572
1	C	0.10	0/4112	0.27	0/5572
1	E	0.10	0/4112	0.27	0/5572
2	B	0.08	0/426	0.23	0/571
2	D	0.09	0/428	0.24	0/574
2	F	0.07	0/428	0.25	0/574
All	All	0.10	0/13618	0.26	0/18435

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4009	0	3808	79	0
1	C	4009	0	3808	69	0
1	E	4009	0	3808	71	0
2	B	423	0	444	2	0
2	D	425	0	446	3	0
2	F	425	0	446	4	0
3	A	301	0	210	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	301	0	209	16	0
3	E	301	0	210	14	0
4	A	86	0	56	8	0
4	C	43	0	28	4	0
5	A	14	0	20	1	0
5	E	7	0	10	0	0
6	C	13	0	6	1	0
6	E	13	0	6	2	0
7	C	28	0	37	1	0
8	A	44	0	0	2	0
8	B	5	0	0	0	0
8	C	31	0	0	1	0
8	D	7	0	0	0	0
8	E	26	0	0	1	0
8	F	1	0	0	0	0
All	All	14521	0	13552	223	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 8.

The worst 5 of 223 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:C:123:HIS:HB3	1:C:167:VAL:HB	1.69	0.75
1:A:100:ARG:HG2	1:A:170:ILE:HG21	1.70	0.72
1:C:264:ASP:OD2	1:C:269:ARG:NH1	2.23	0.71
1:A:123:HIS:CD2	3:A:602:HEC:ND	2.60	0.69
1:A:123:HIS:HB3	1:A:167:VAL:HB	1.75	0.68

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	501/570 (88%)	479 (96%)	21 (4%)	1 (0%)	43	70
1	C	501/570 (88%)	479 (96%)	21 (4%)	1 (0%)	43	70
1	E	501/570 (88%)	479 (96%)	21 (4%)	1 (0%)	43	70
2	B	54/91 (59%)	53 (98%)	1 (2%)	0	100	100
2	D	54/91 (59%)	53 (98%)	1 (2%)	0	100	100
2	F	54/91 (59%)	53 (98%)	1 (2%)	0	100	100
All	All	1665/1983 (84%)	1596 (96%)	66 (4%)	3 (0%)	43	70

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	484	VAL
1	C	484	VAL
1	E	484	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	429/477 (90%)	426 (99%)	3 (1%)	76	90
1	C	429/477 (90%)	426 (99%)	3 (1%)	76	90
1	E	429/477 (90%)	427 (100%)	2 (0%)	81	92
2	B	48/73 (66%)	48 (100%)	0	100	100
2	D	49/73 (67%)	49 (100%)	0	100	100
2	F	49/73 (67%)	49 (100%)	0	100	100
All	All	1433/1650 (87%)	1425 (99%)	8 (1%)	78	91

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

Mol	Chain	Res	Type
1	E	267	HIS
1	E	114	TRP

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Mol	Chain	Res	Type
1	C	185	THR
1	C	114	TRP
1	C	267	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	419	HIS
1	E	235	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

31 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$
4	ISW	A	611	8,1	47,50,50	6.18	24 (51%)	53,82,82	4.32	27 (50%)
3	HEC	C	606	1	46,50,50	1.83	7 (15%)	58,82,82	1.85	4 (6%)
3	HEC	C	601	1	46,50,50	1.83	7 (15%)	58,82,82	1.97	4 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEC	E	602	1	46,50,50	1.85	6 (13%)	58,82,82	1.85	4 (6%)
3	HEC	E	607	1	46,50,50	1.86	6 (13%)	58,82,82	1.77	4 (6%)
4	ISW	C	611	8,1	47,50,50	6.16	22 (46%)	53,82,82	4.36	26 (49%)
3	HEC	E	605	1	46,50,50	1.85	7 (15%)	58,82,82	1.89	4 (6%)
3	HEC	C	603	1	46,50,50	1.84	5 (10%)	58,82,82	1.98	4 (6%)
3	HEC	E	606	1	46,50,50	1.83	6 (13%)	58,82,82	1.87	4 (6%)
3	HEC	C	605	1	46,50,50	1.86	6 (13%)	58,82,82	1.88	4 (6%)
6	JUG	E	608	-	14,14,14	2.81	8 (57%)	20,20,20	1.07	1 (5%)
3	HEC	A	603	1	46,50,50	1.85	6 (13%)	58,82,82	1.90	4 (6%)
3	HEC	C	607	1	46,50,50	1.85	5 (10%)	58,82,82	1.67	4 (6%)
4	ISW	A	608	8,1	47,50,50	6.16	21 (44%)	53,82,82	4.33	27 (50%)
5	PEG	A	610	-	6,6,6	0.50	0	5,5,5	0.24	0
3	HEC	C	602	1	46,50,50	1.85	7 (15%)	58,82,82	1.85	3 (5%)
5	PEG	A	609	-	6,6,6	0.50	0	5,5,5	0.29	0
6	JUG	C	608	-	14,14,14	2.83	8 (57%)	20,20,20	1.04	1 (5%)
3	HEC	C	604	1	46,50,50	1.87	7 (15%)	58,82,82	1.83	5 (8%)
7	1PE	C	609	-	11,11,15	0.56	0	10,10,14	0.24	0
3	HEC	A	607	1	46,50,50	1.86	6 (13%)	58,82,82	1.78	4 (6%)
3	HEC	A	606	1	46,50,50	1.83	7 (15%)	58,82,82	1.84	4 (6%)
3	HEC	E	601	1	46,50,50	1.83	6 (13%)	58,82,82	1.94	4 (6%)
3	HEC	A	605	1	46,50,50	1.85	6 (13%)	58,82,82	1.87	4 (6%)
3	HEC	A	604	1	46,50,50	1.85	8 (17%)	58,82,82	1.88	5 (8%)
3	HEC	A	602	1	46,50,50	1.86	6 (13%)	58,82,82	1.94	5 (8%)
3	HEC	E	603	1	46,50,50	1.87	7 (15%)	58,82,82	1.95	4 (6%)
3	HEC	E	604	1	46,50,50	1.84	6 (13%)	58,82,82	1.88	4 (6%)
5	PEG	E	609	-	6,6,6	0.50	0	5,5,5	0.28	0
7	1PE	C	610	-	15,15,15	0.55	0	14,14,14	0.22	0
3	HEC	A	601	1	46,50,50	1.84	5 (10%)	58,82,82	1.96	4 (6%)

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
4	ISW	A	611	8,1	-	10/14/74/74	-
3	HEC	C	606	1	-	6/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	C	601	1	-	4/14/54/54	-
3	HEC	E	602	1	-	6/14/54/54	-
3	HEC	E	607	1	-	5/14/54/54	-
4	ISW	C	611	8,1	-	6/14/74/74	-
3	HEC	E	605	1	-	8/14/54/54	-
3	HEC	C	603	1	-	5/14/54/54	-
3	HEC	E	606	1	-	6/14/54/54	-
3	HEC	C	605	1	-	11/14/54/54	-
6	JUG	E	608	-	-	-	0/2/2/2
3	HEC	A	603	1	-	4/14/54/54	-
3	HEC	C	607	1	-	7/14/54/54	-
4	ISW	A	608	8,1	-	7/14/74/74	-
5	PEG	A	610	-	-	2/4/4/4	-
3	HEC	C	602	1	-	6/14/54/54	-
5	PEG	A	609	-	-	0/4/4/4	-
6	JUG	C	608	-	-	-	0/2/2/2
3	HEC	C	604	1	-	8/14/54/54	-
7	1PE	C	609	-	-	4/9/9/13	-
3	HEC	A	607	1	-	11/14/54/54	-
3	HEC	A	606	1	-	4/14/54/54	-
3	HEC	E	601	1	-	7/14/54/54	-
3	HEC	A	605	1	-	9/14/54/54	-
3	HEC	A	604	1	-	9/14/54/54	-
3	HEC	A	602	1	-	6/14/54/54	-
3	HEC	E	603	1	-	6/14/54/54	-
3	HEC	E	604	1	-	7/14/54/54	-
5	PEG	E	609	-	-	2/4/4/4	-
7	1PE	C	610	-	-	3/13/13/13	-
3	HEC	A	601	1	-	4/14/54/54	-

The worst 5 of 215 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	611	ISW	CHA-C1A	16.41	1.70	1.38
4	A	611	ISW	CHA-C1A	16.41	1.70	1.38
4	A	608	ISW	CHA-C1A	16.39	1.70	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	608	ISW	CHD-C4C	14.96	1.73	1.39
4	A	611	ISW	CHD-C4C	14.86	1.72	1.39

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	611	ISW	C1A-CHA-C4D	-13.50	97.33	126.02
4	A	608	ISW	C1A-CHA-C4D	-13.48	97.37	126.02
4	A	611	ISW	C1A-CHA-C4D	-13.45	97.42	126.02
4	A	611	ISW	C4C-CHD-C1D	-10.72	101.03	126.25
4	C	611	ISW	C4C-CHD-C1D	-10.63	101.25	126.25

There are no chirality outliers.

5 of 173 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	HEC	C2B-C3B-CAB-CBB
3	A	601	HEC	C2C-C3C-CAC-CBC
3	A	602	HEC	C2B-C3B-CAB-CBB
3	A	602	HEC	C2C-C3C-CAC-CBC
3	A	602	HEC	C4C-C3C-CAC-CBC

There are no ring outliers.

27 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	611	ISW	4	0
3	C	606	HEC	4	0
3	C	601	HEC	2	0
3	E	602	HEC	2	0
3	E	607	HEC	1	0
4	C	611	ISW	4	0
3	E	605	HEC	2	0
3	C	603	HEC	1	0
3	E	606	HEC	5	0
3	C	605	HEC	2	0
6	E	608	JUG	2	0
3	C	607	HEC	2	0
4	A	608	ISW	4	0
5	A	610	PEG	1	0
3	C	602	HEC	2	0

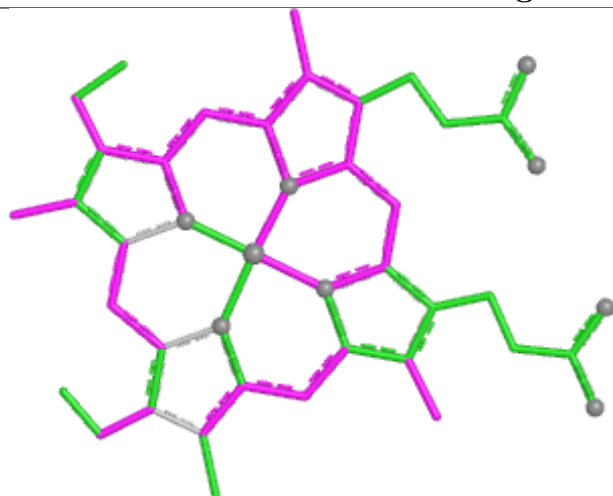
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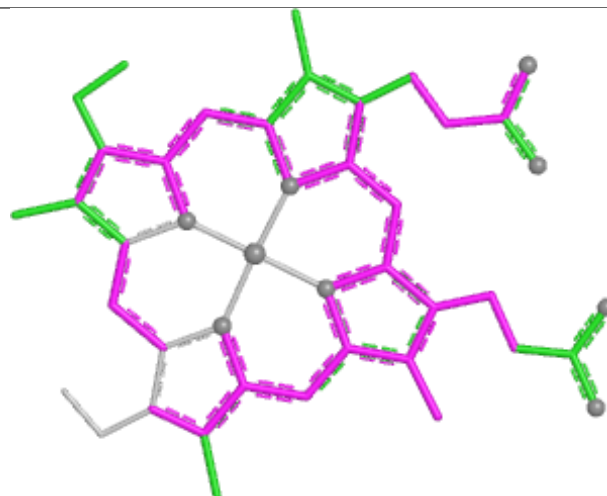
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	608	JUG	1	0
3	C	604	HEC	4	0
7	C	609	1PE	1	0
3	A	607	HEC	4	0
3	A	606	HEC	7	0
3	E	601	HEC	2	0
3	A	605	HEC	4	0
3	A	604	HEC	3	0
3	A	602	HEC	3	0
3	E	603	HEC	1	0
3	E	604	HEC	2	0
3	A	601	HEC	1	0

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.

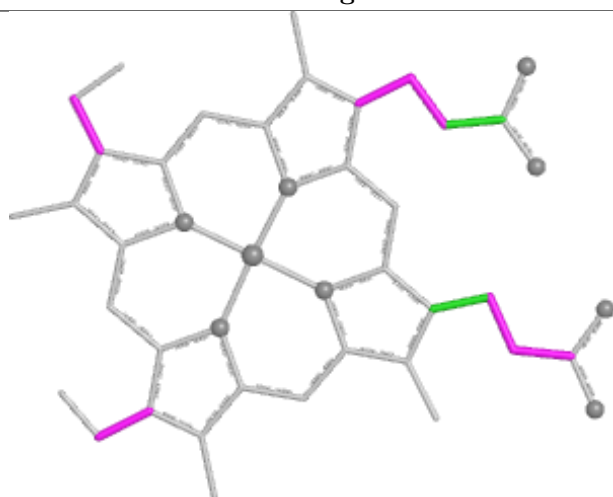
Ligand ISW A 611



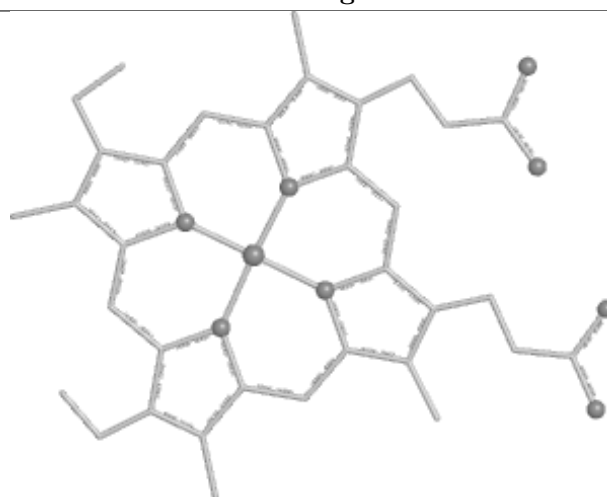
Bond lengths



Bond angles

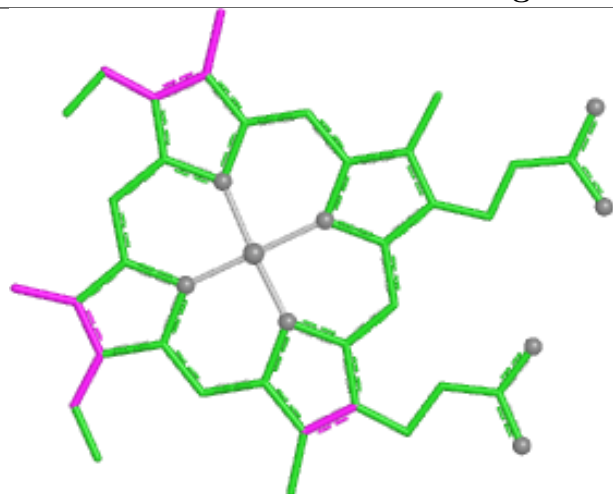


Torsions

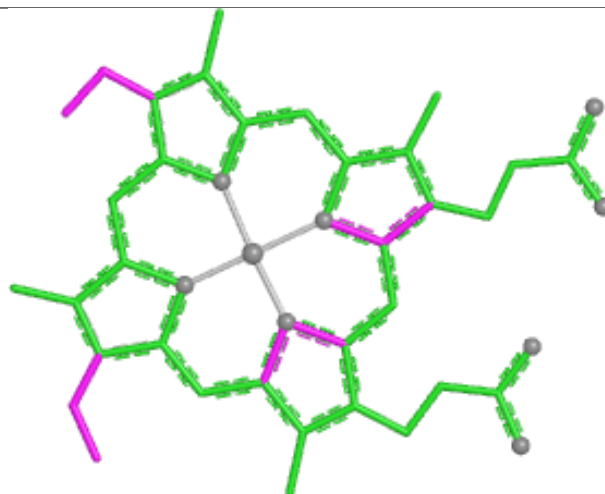


Rings

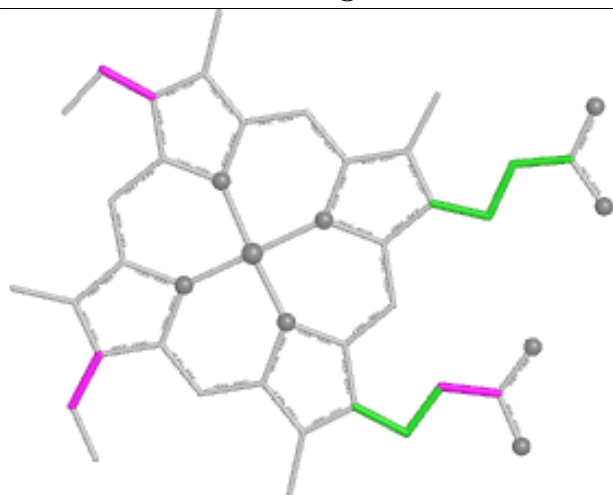
Ligand HEC C 606



Bond lengths



Bond angles

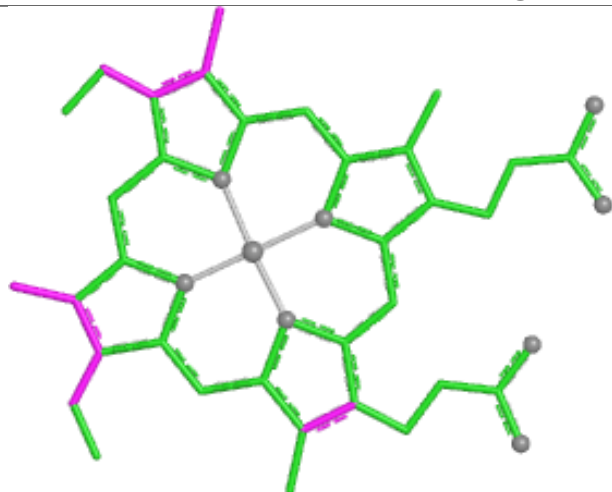


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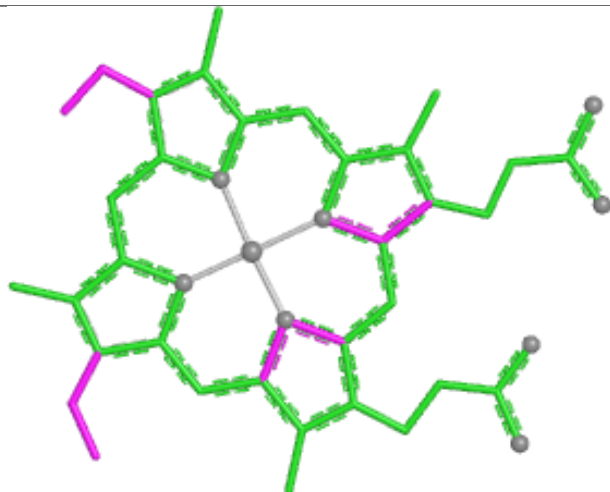


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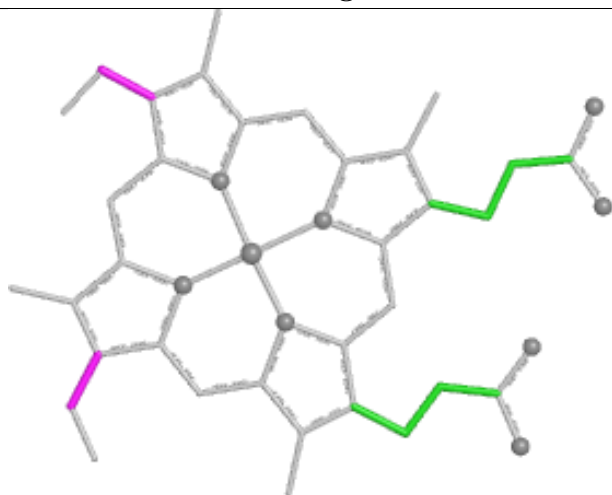
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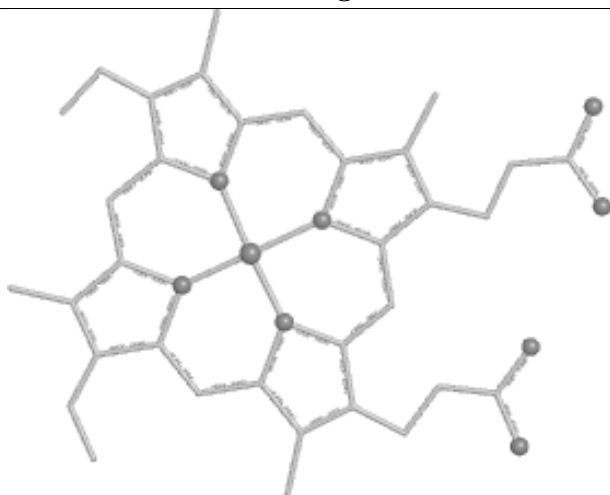
Bond lengths



Bond angles

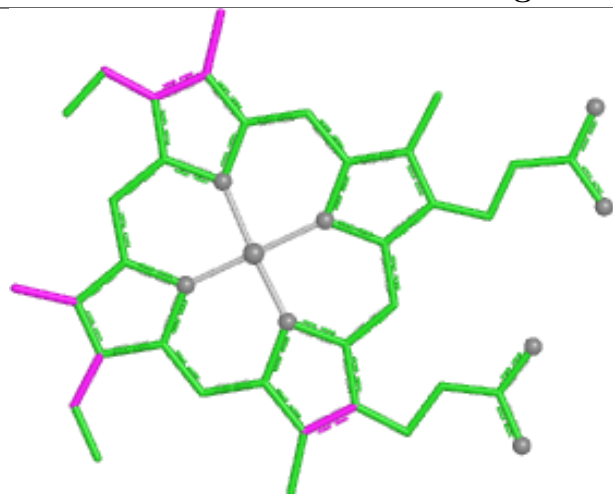


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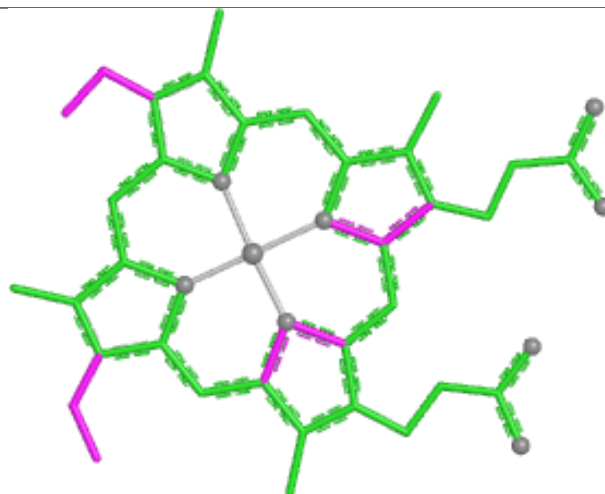


Rings

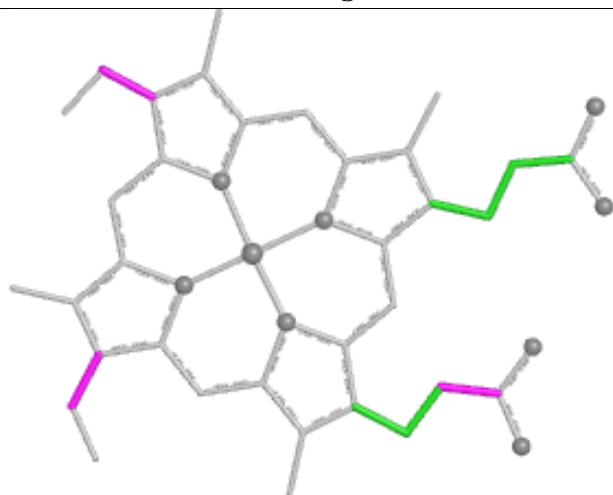
Ligand HEC E 602



Bond lengths



Bond angles

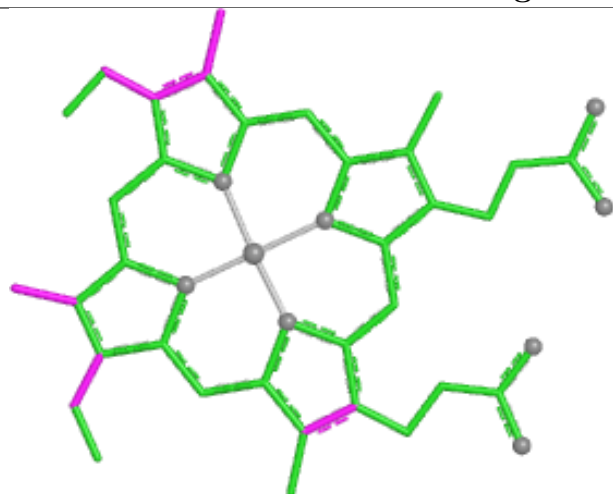


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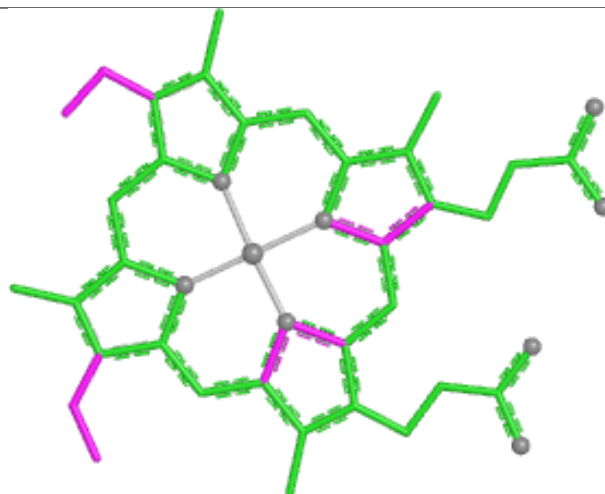


Rings

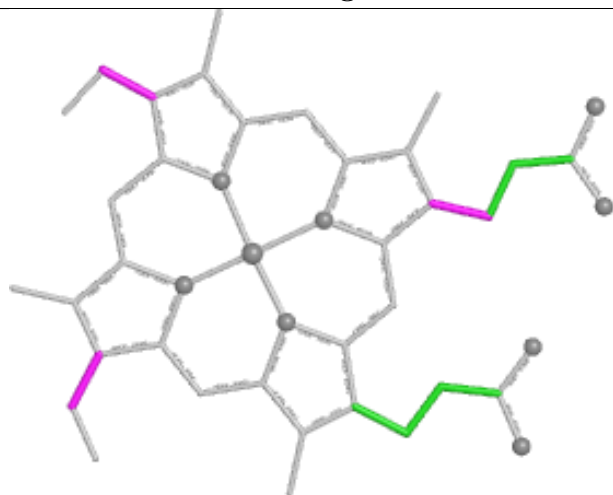
Ligand HEC E 607



Bond lengths



Bond angles

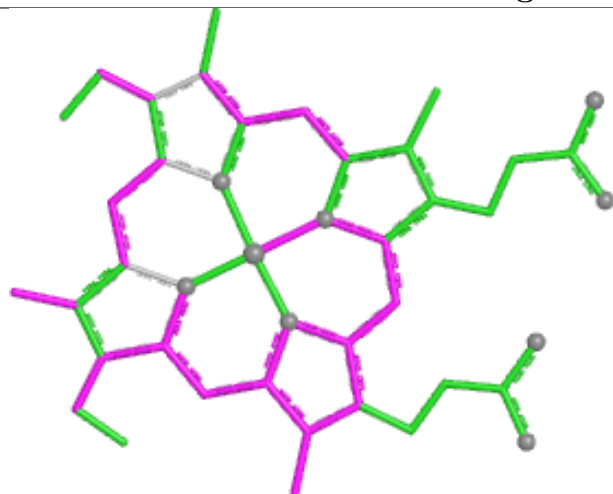


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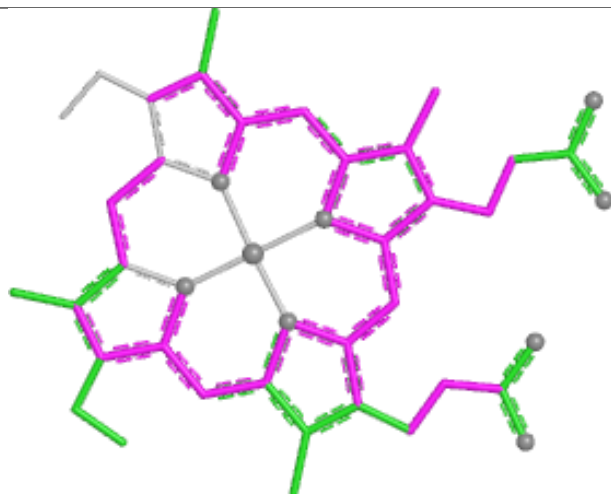


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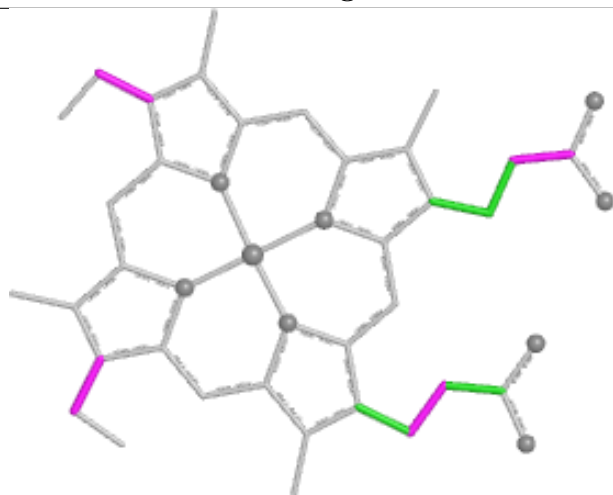
Ligand ISW C 611



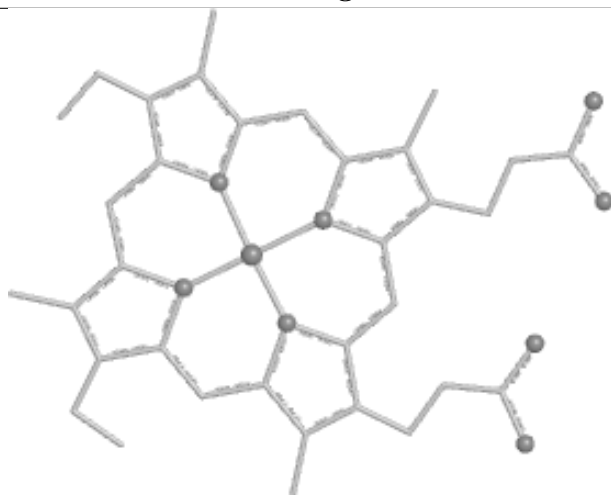
Bond lengths



Bond angles

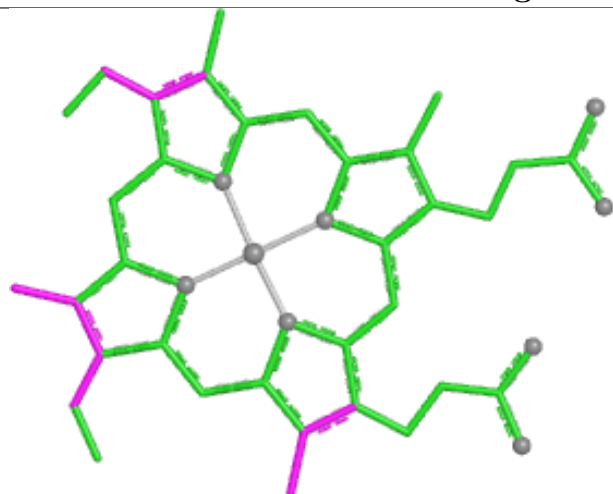


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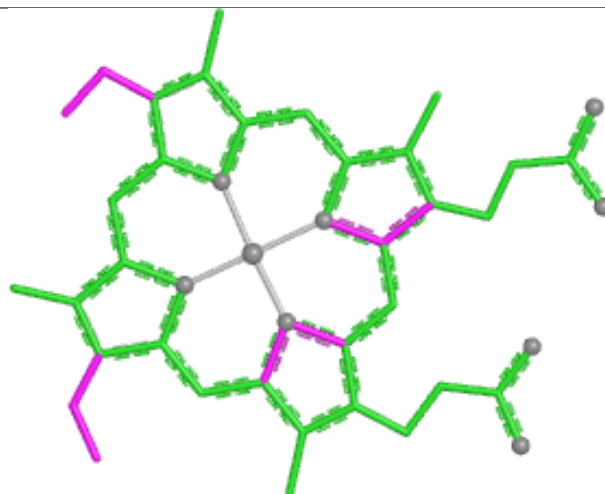


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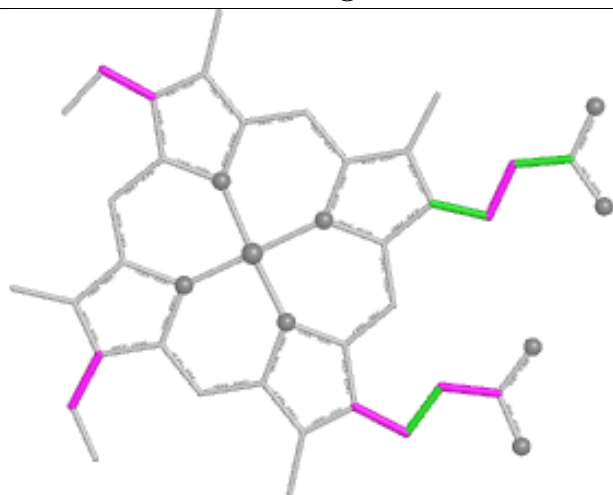
Ligand HEC E 605



Bond lengths



Bond angles

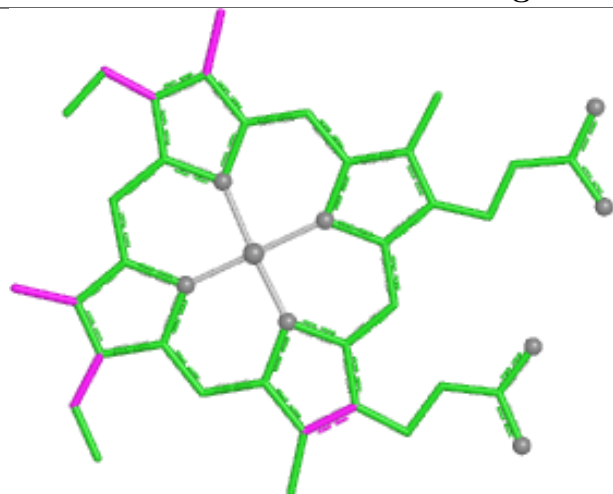


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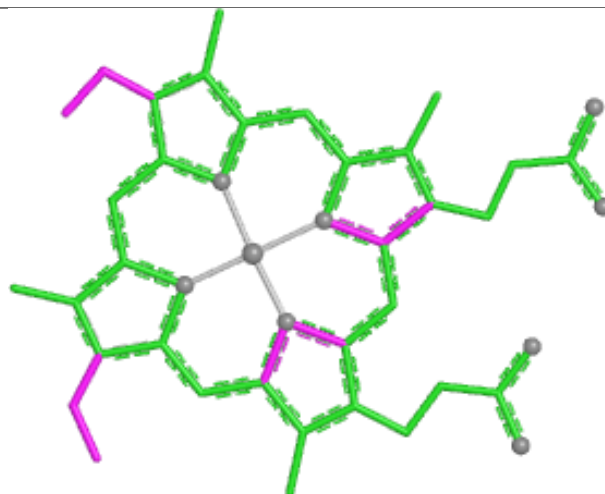


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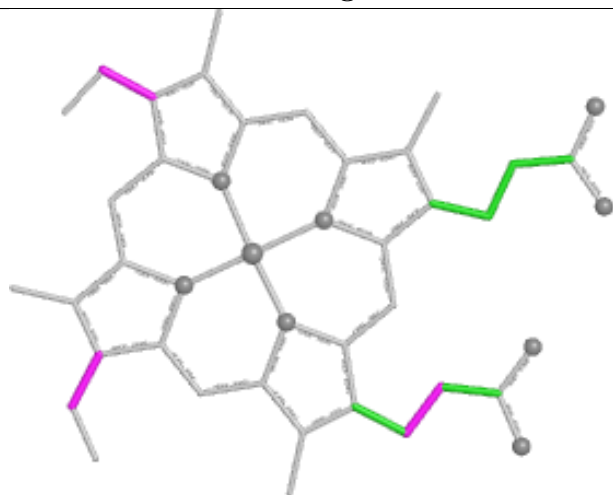
Ligand HEC C 603



Bond lengths



Bond angles

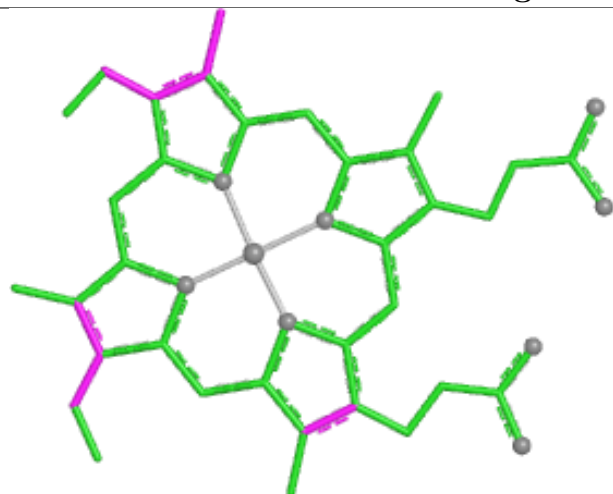


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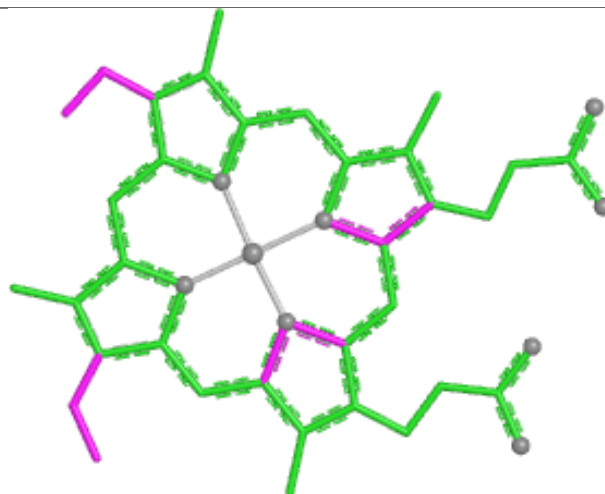


Rings

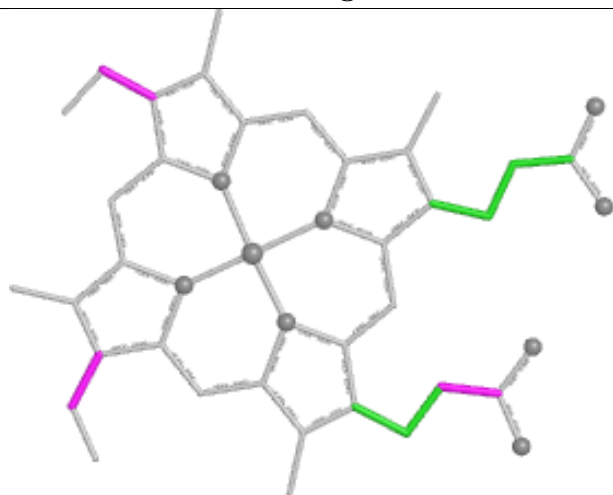
Ligand HEC E 606



Bond lengths



Bond angles

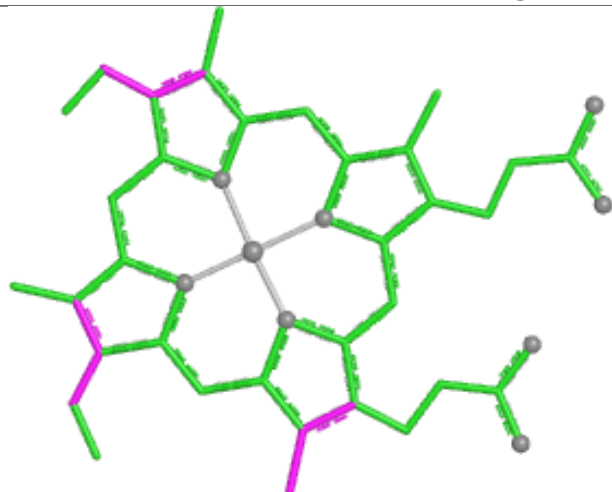


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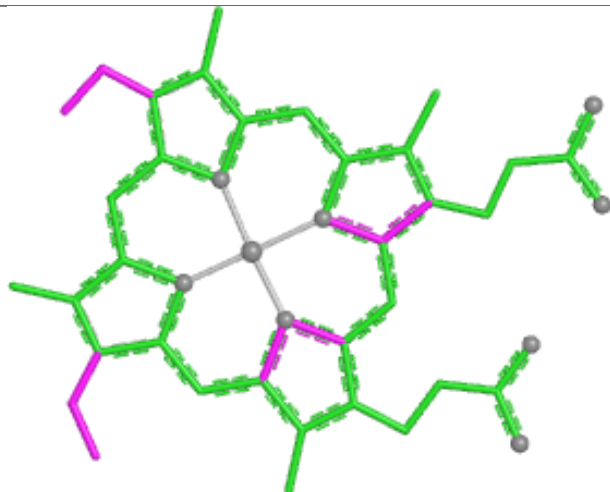


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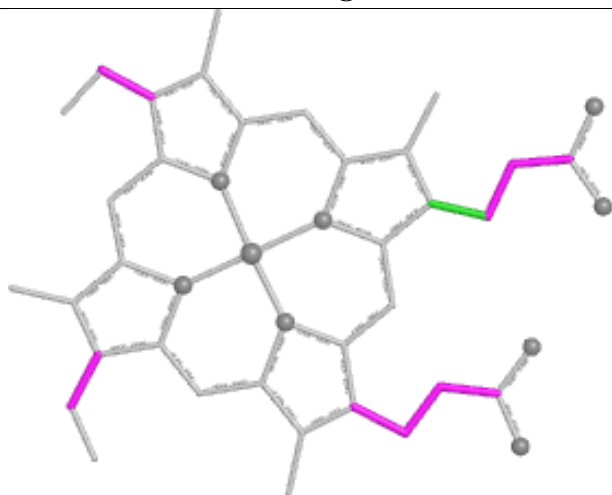
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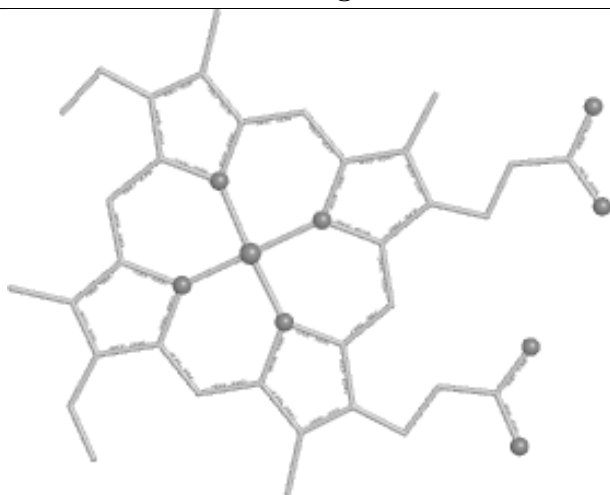
Bond lengths



Bond angles

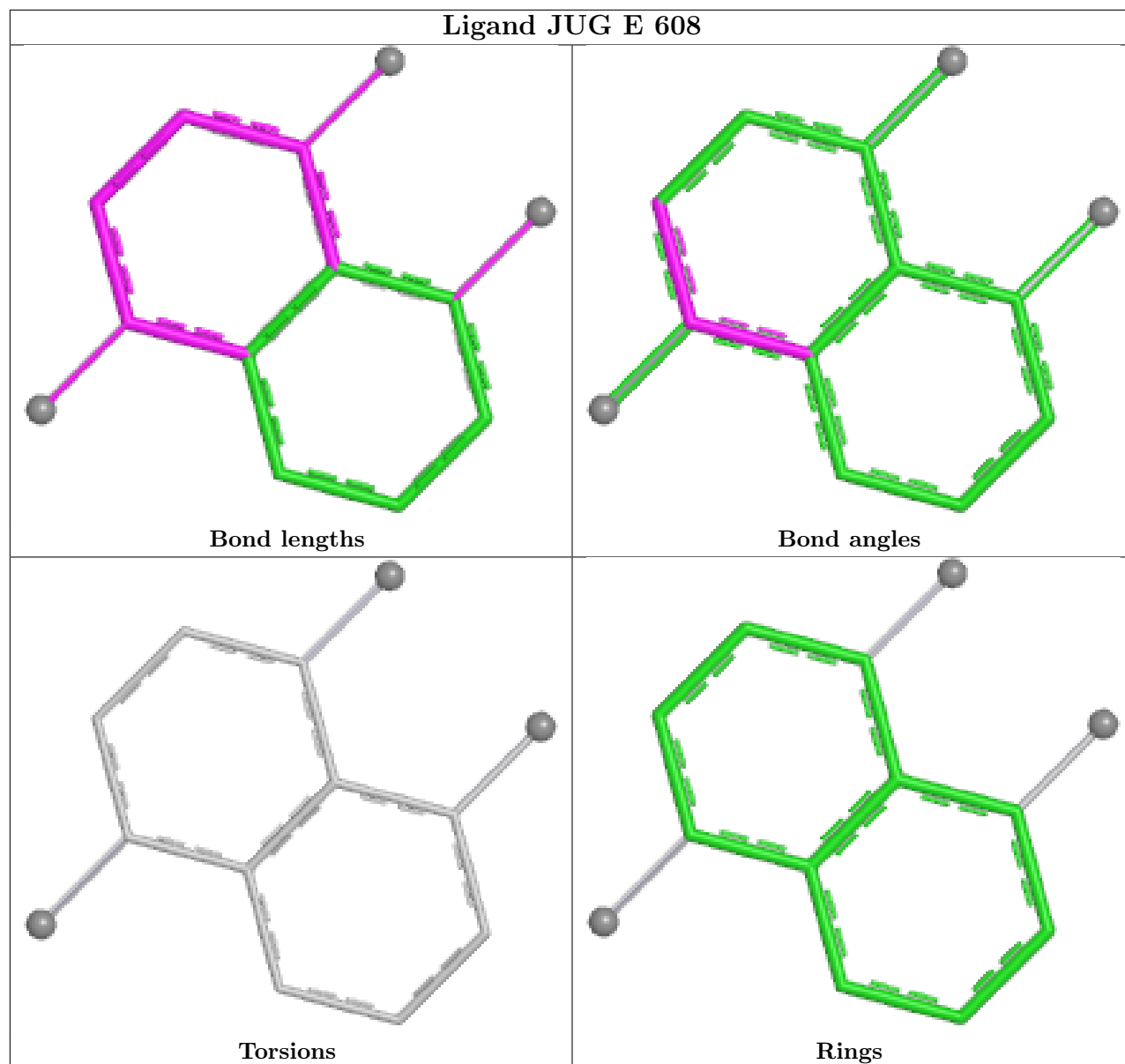


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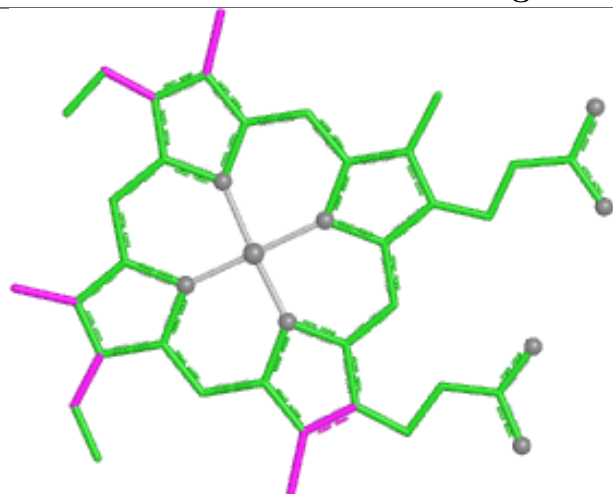


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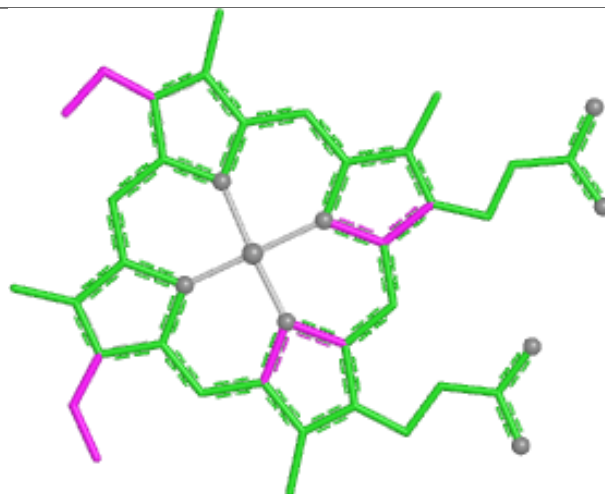
Ligand JUG E 608



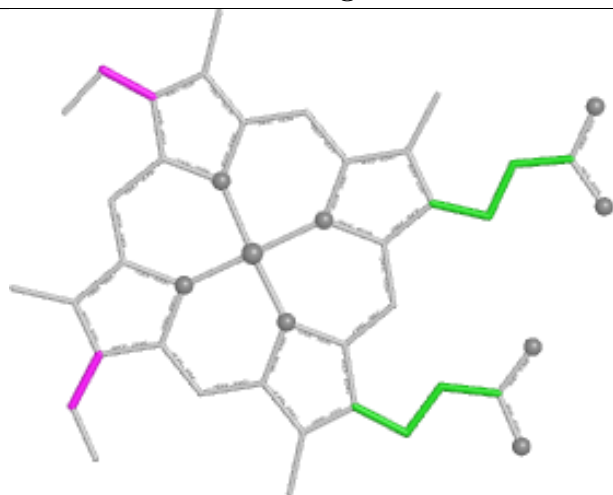
Ligand HEC A 603



Bond lengths



Bond angles

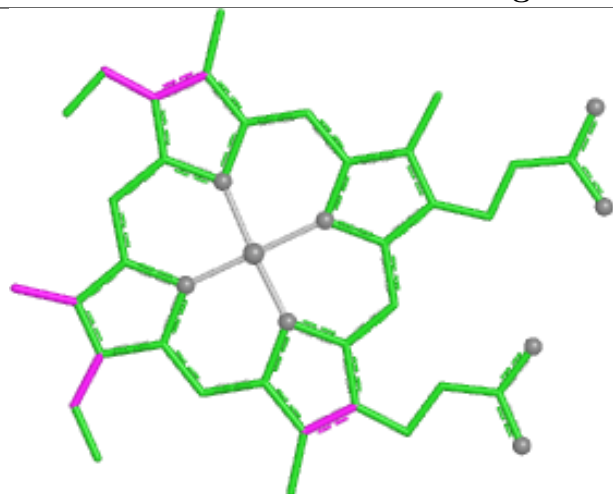


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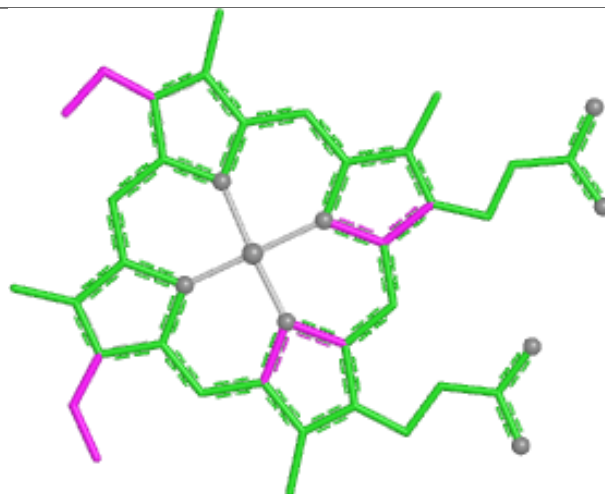


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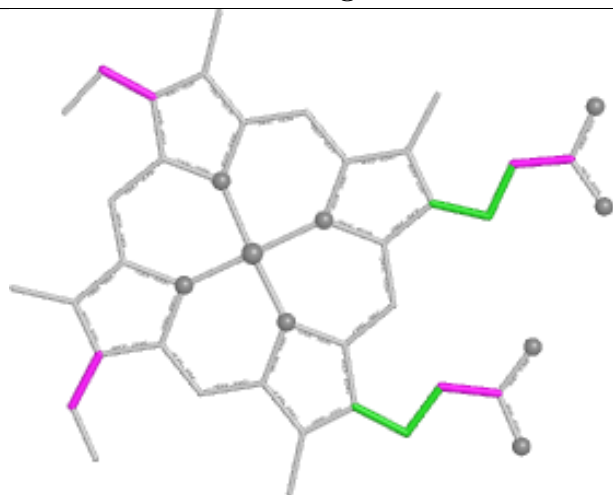
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Bond lengths



Bond angles

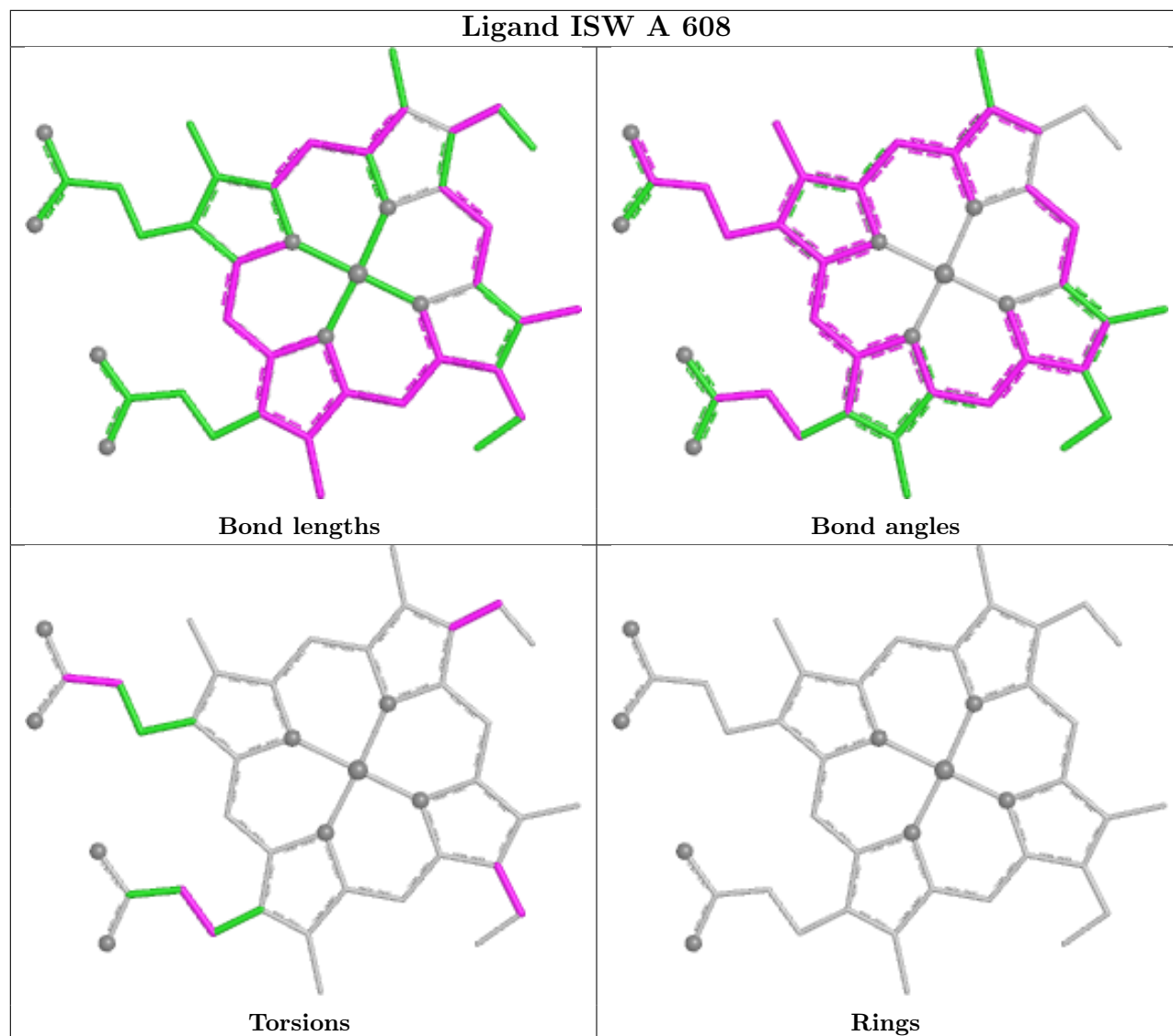


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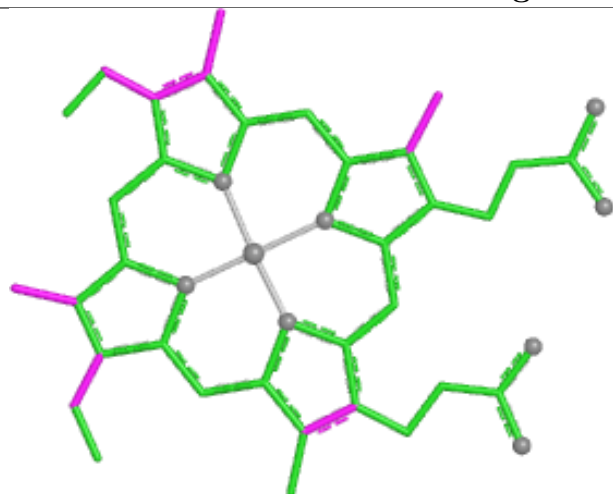


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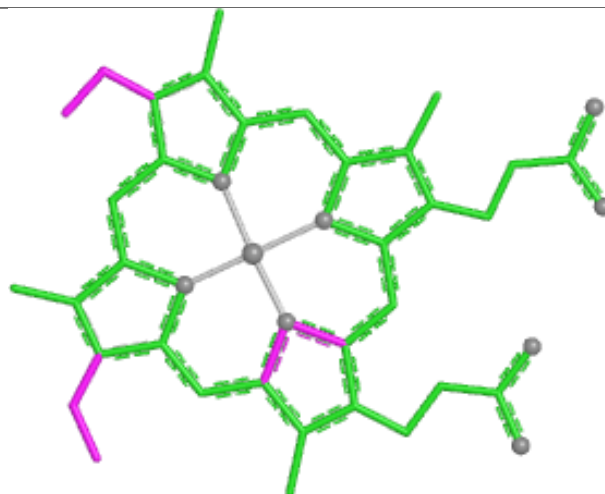
Ligand ISW A 608



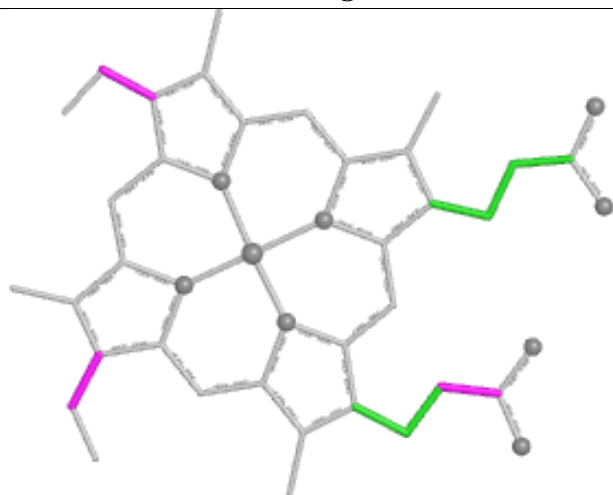
Ligand HEC C 602



Bond lengths



Bond angles

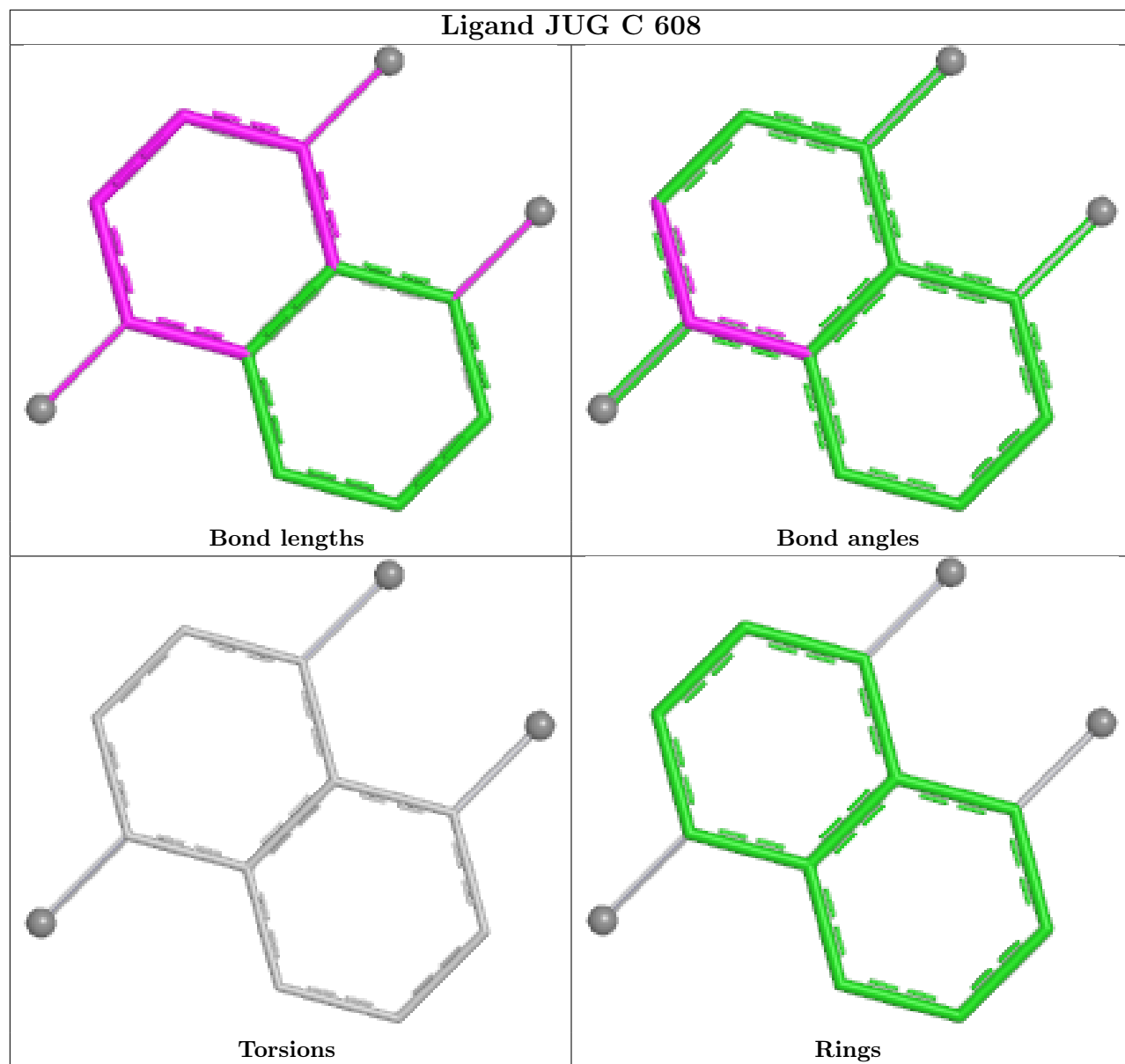


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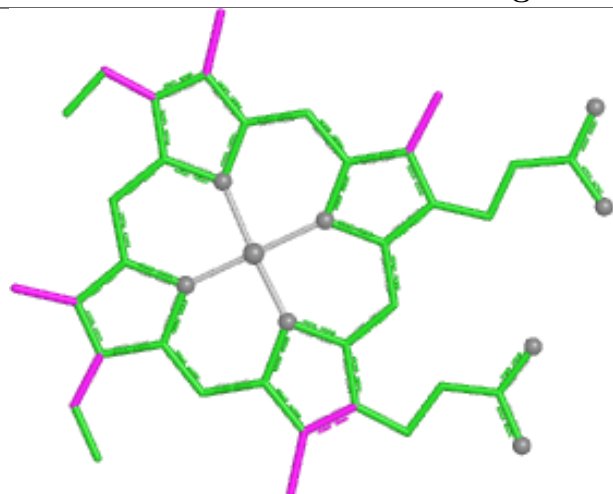


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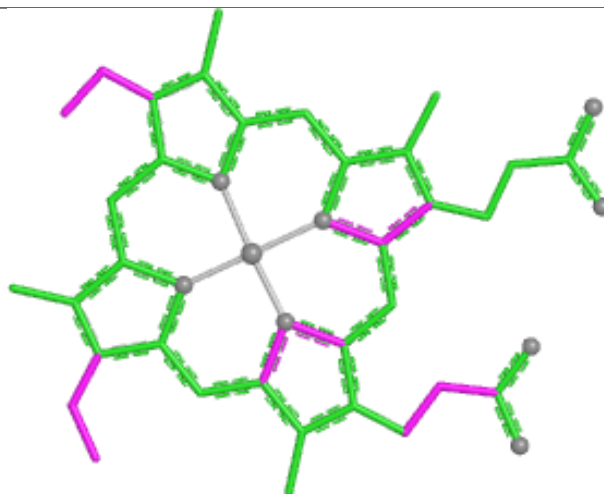
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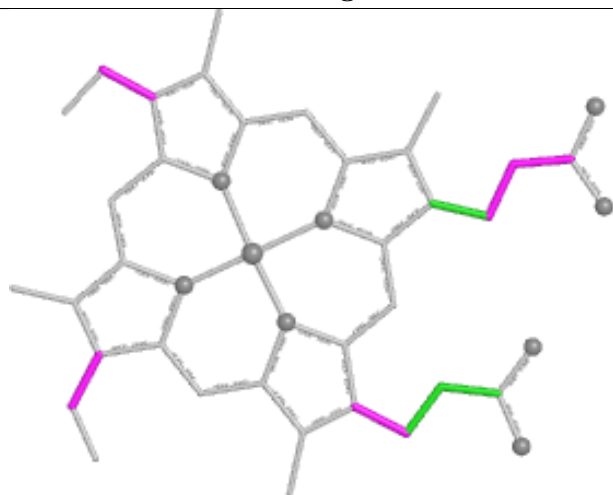
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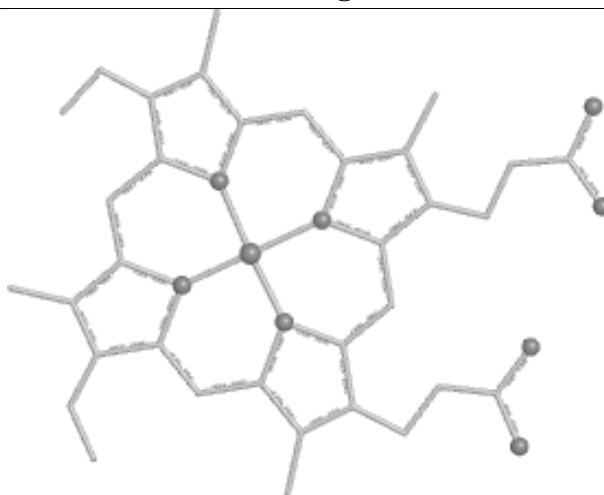
Bond lengths



Bond angles

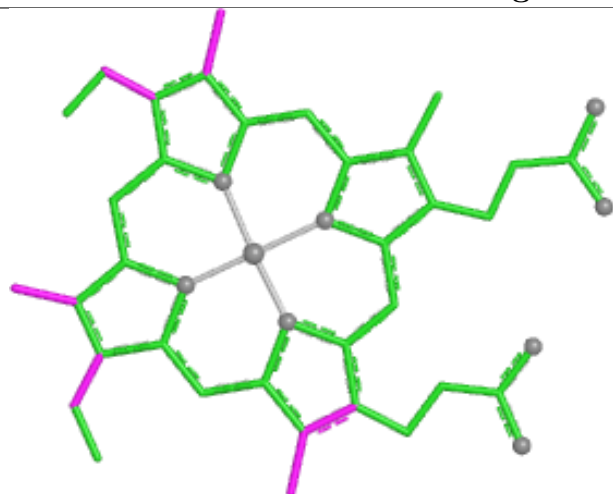


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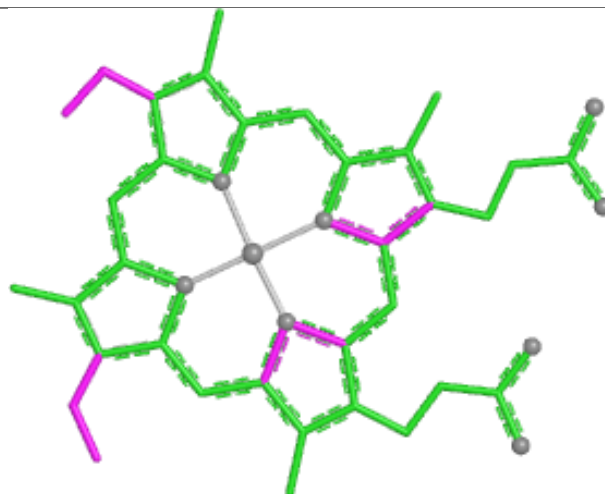


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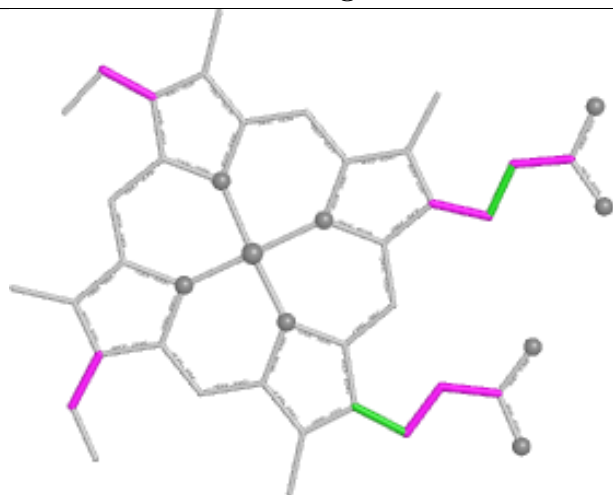
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Bond lengths



Bond angles

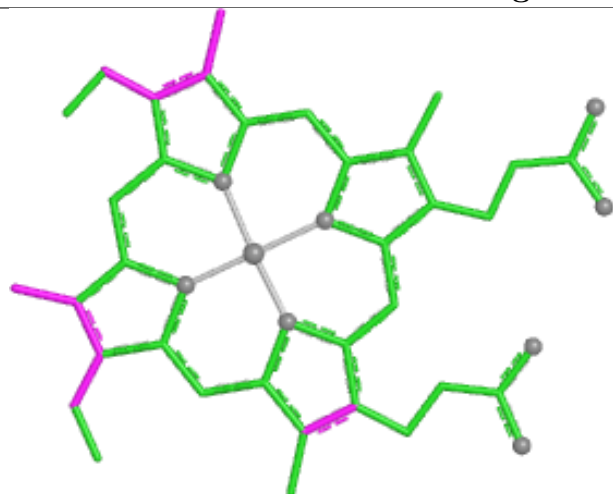


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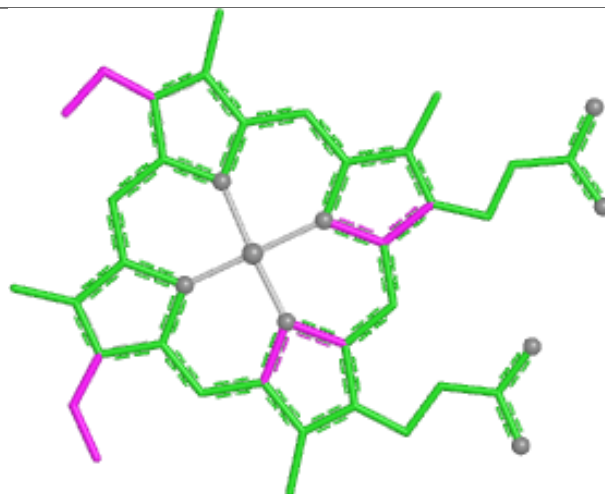


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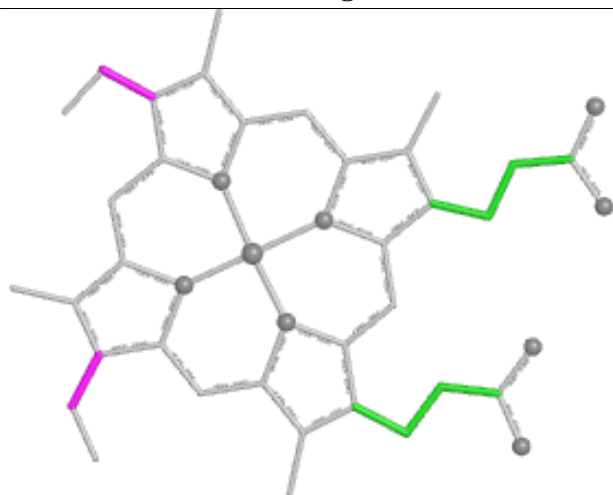
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Bond lengths



Bond angles

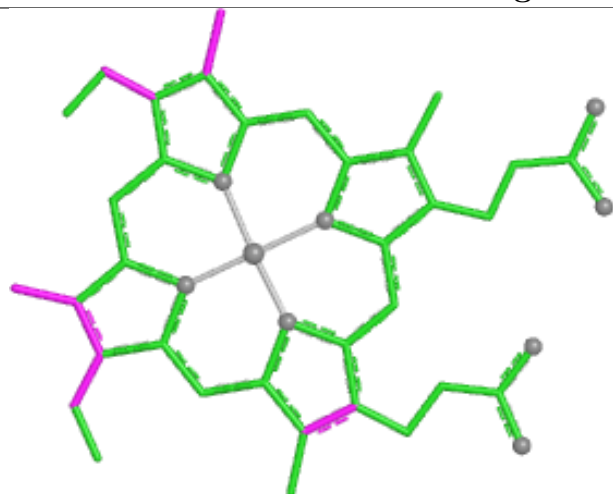


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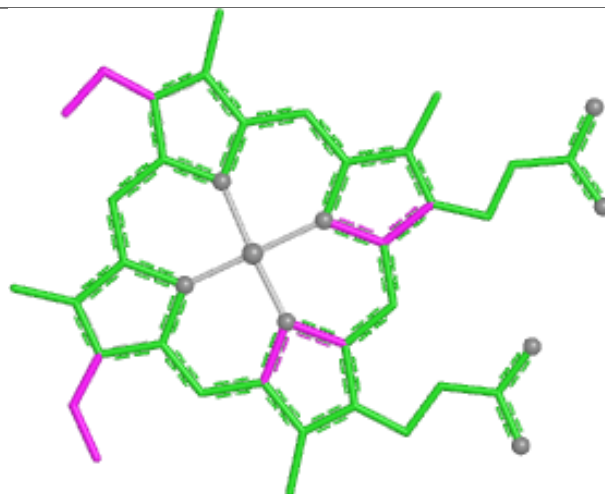


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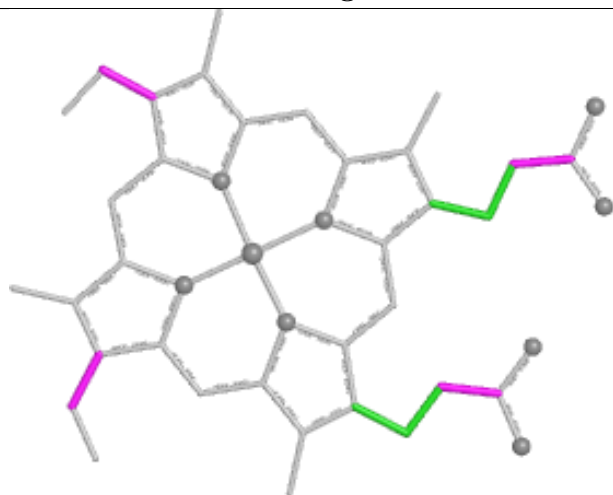
Ligand HEC E 601



Bond lengths



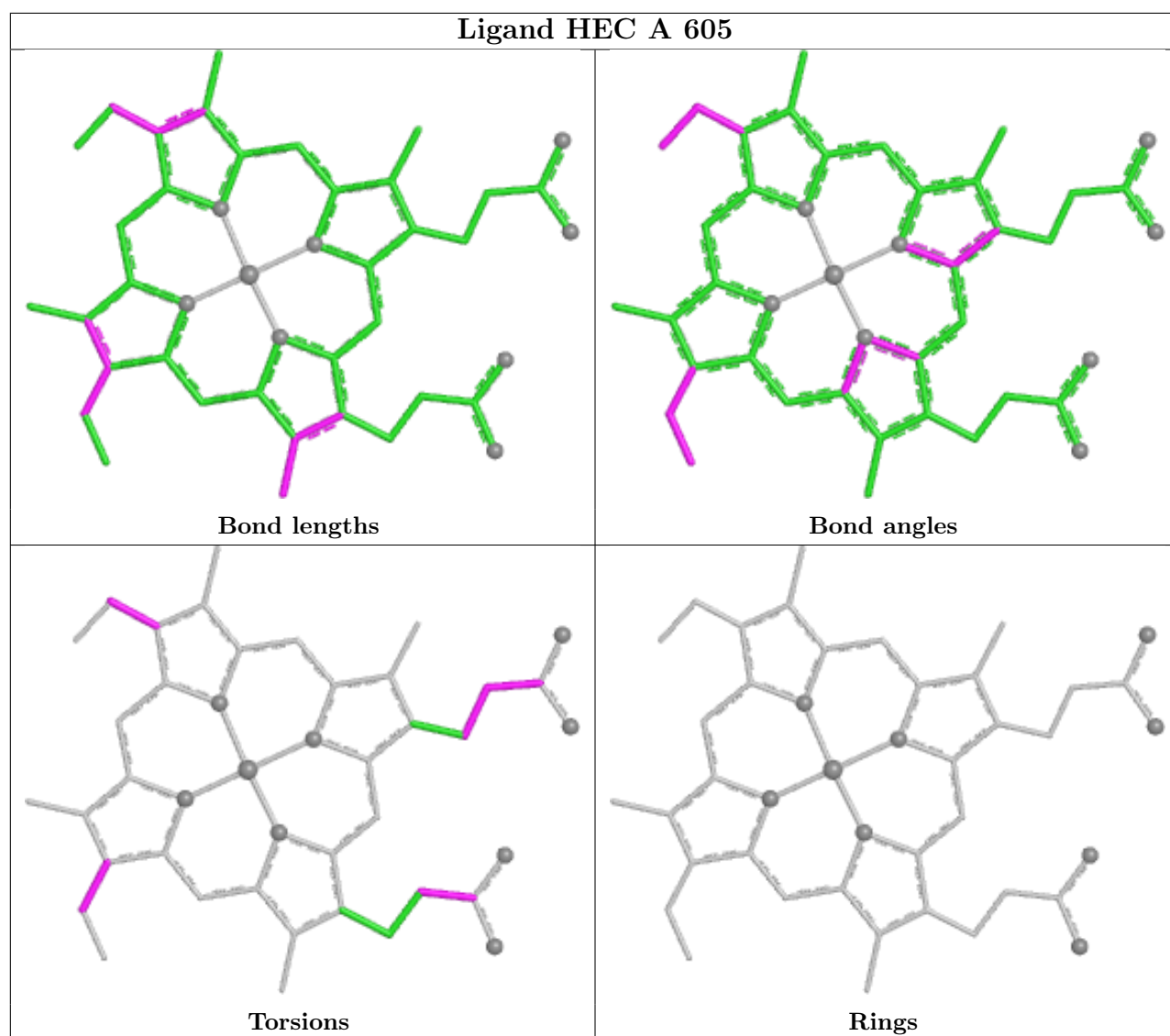
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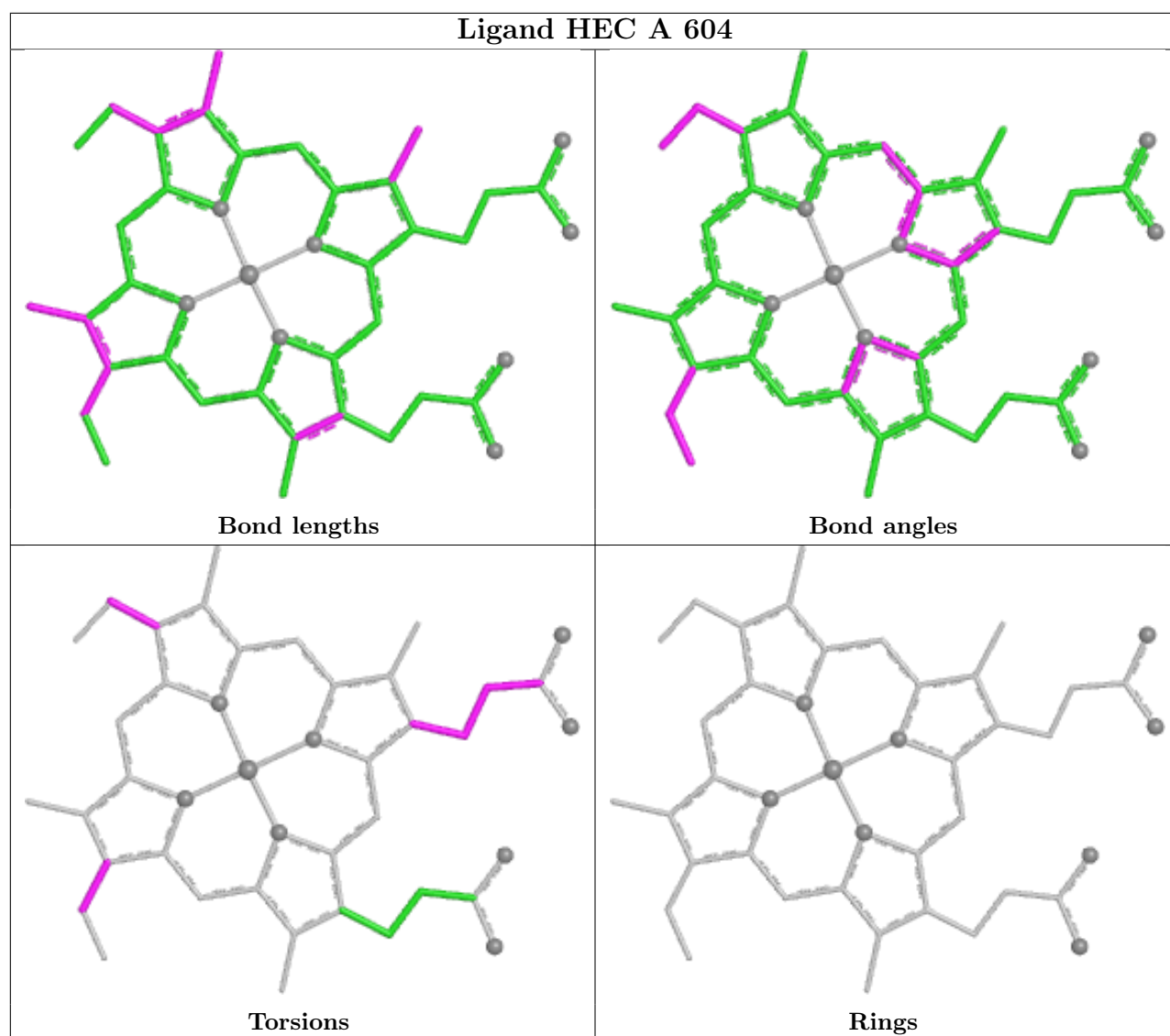


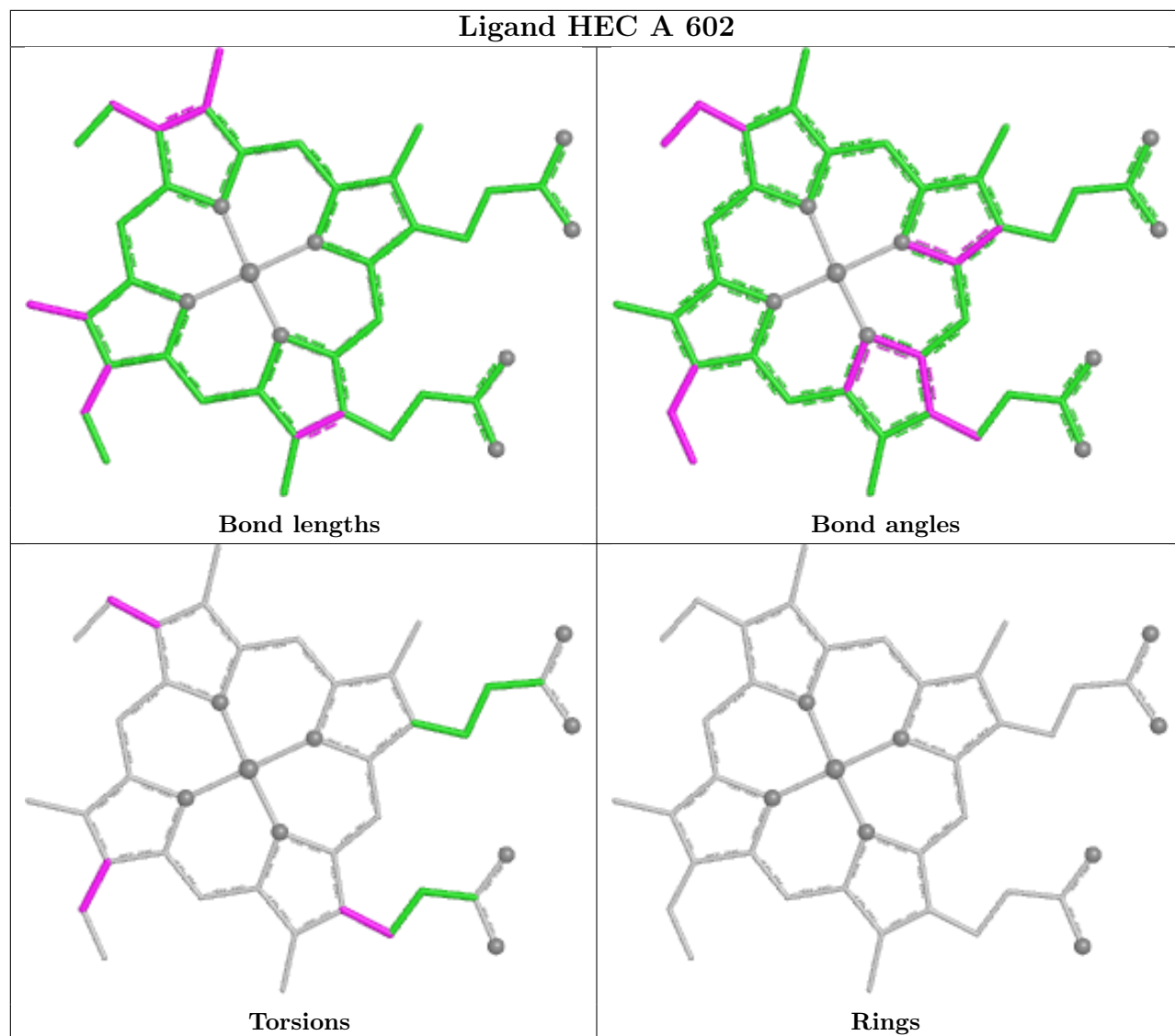
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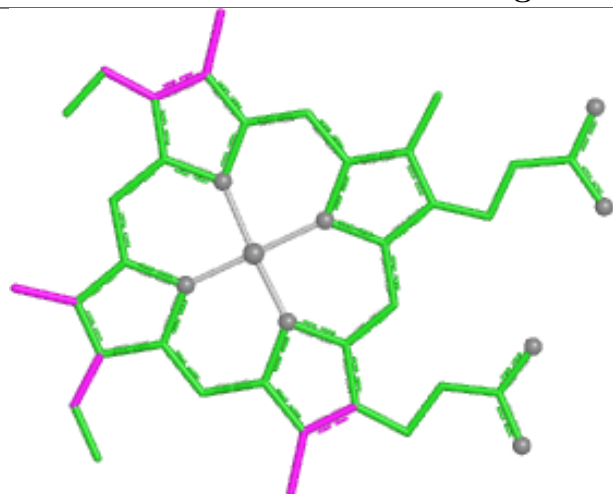
Rings



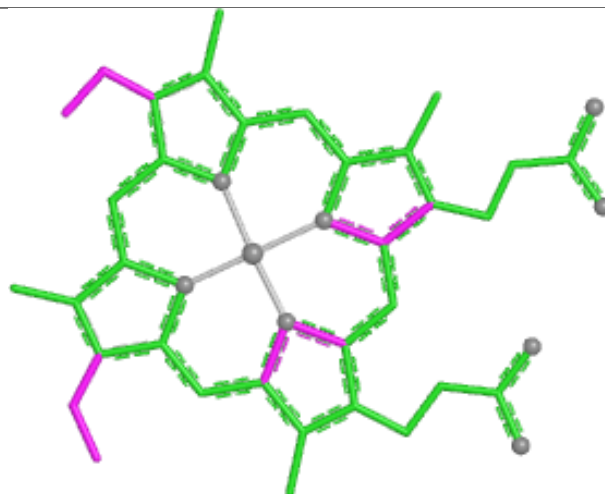




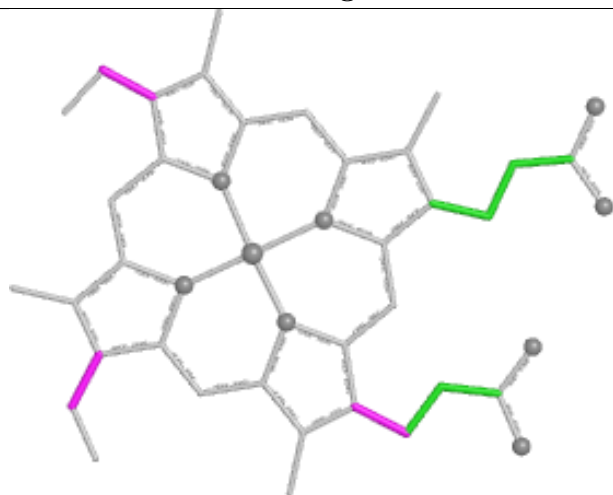
Ligand HEC E 603



Bond lengths



Bond angles

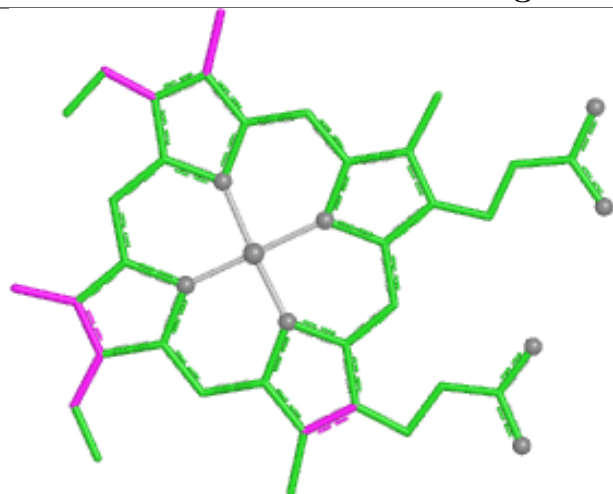


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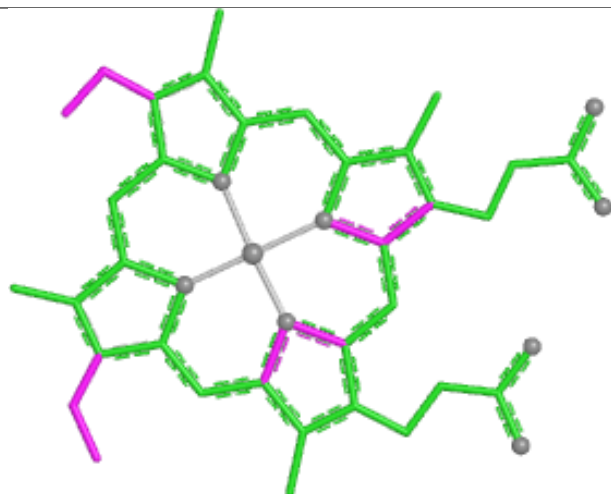


Rings

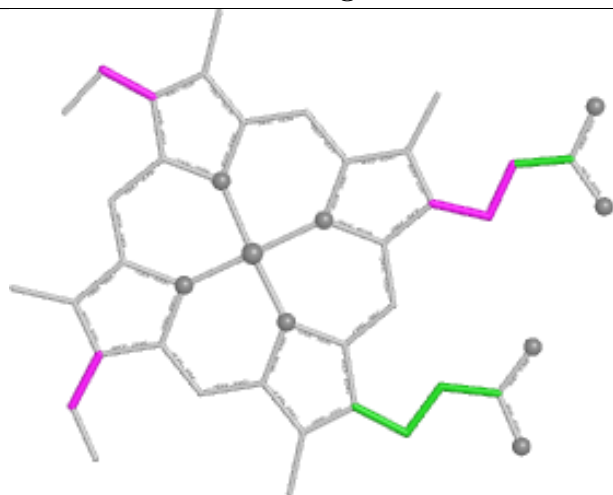
Ligand HEC E 604



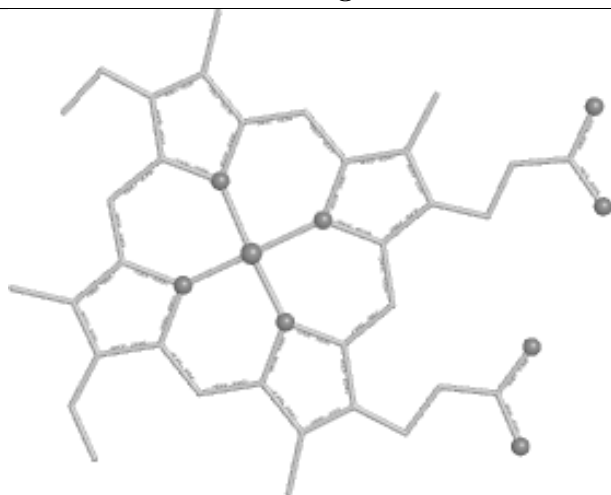
Bond lengths



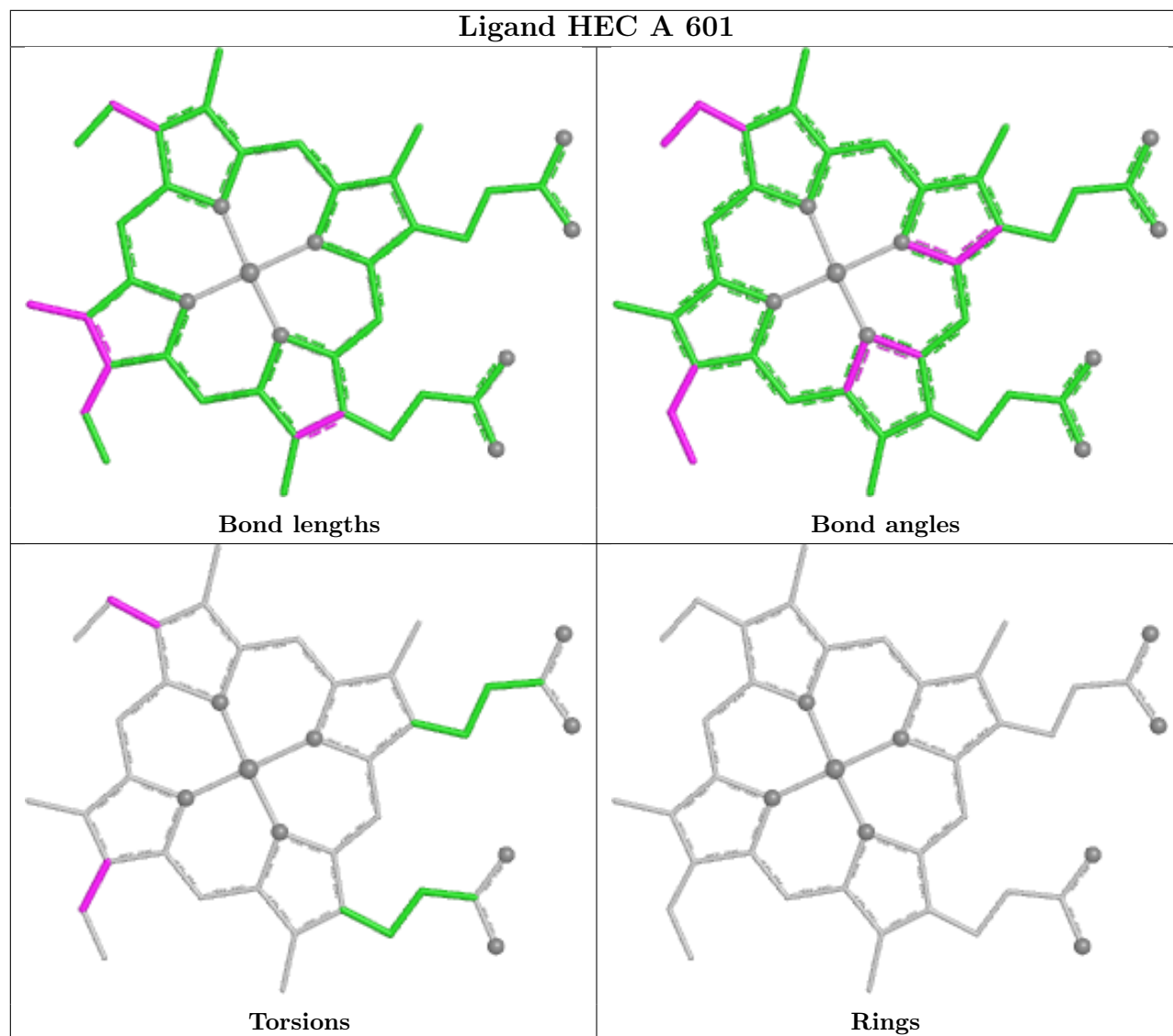
Bond angles



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	503/570 (88%)	1.19	76 (15%) 5 4	31, 60, 103, 142	0
1	C	503/570 (88%)	1.25	90 (17%) 3 3	22, 59, 103, 145	0
1	E	503/570 (88%)	1.15	83 (16%) 4 3	32, 61, 114, 171	0
2	B	56/91 (61%)	1.24	8 (14%) 6 5	48, 71, 121, 145	0
2	D	56/91 (61%)	0.87	7 (12%) 8 6	33, 48, 123, 156	0
2	F	56/91 (61%)	1.27	11 (19%) 3 2	53, 74, 133, 165	0
All	All	1677/1983 (84%)	1.19	275 (16%) 4 4	22, 61, 110, 171	0

The worst 5 of 275 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	159	GLY	5.7
1	C	159	GLY	5.0
1	C	158	LEU	4.9
1	A	36	ALA	4.6
1	E	170	ILE	4.5

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

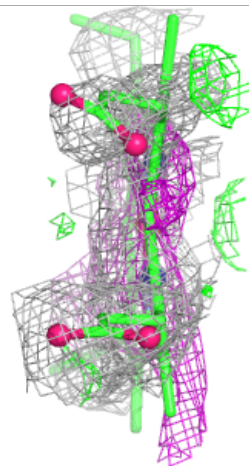
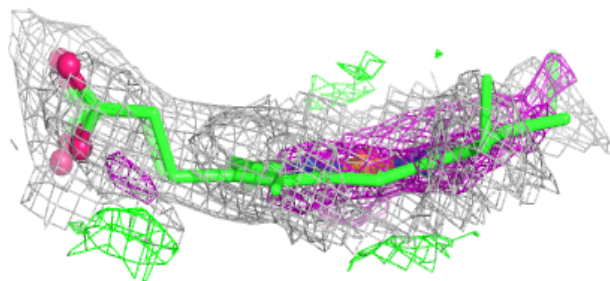
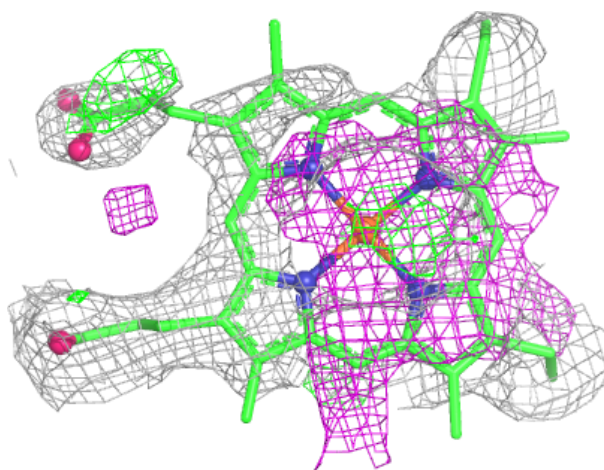
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	PEG	E	609	7/7	0.62	0.21	48,55,60,62	0
7	1PE	C	609	12/16	0.68	0.21	51,61,65,66	0
7	1PE	C	610	16/16	0.75	0.20	66,78,81,82	0
3	HEC	C	603	43/43	0.79	0.21	42,84,90,92	0
6	JUG	C	608	13/13	0.83	0.16	48,54,64,70	0
5	PEG	A	609	7/7	0.84	0.15	44,50,56,56	0
5	PEG	A	610	7/7	0.84	0.15	42,46,53,54	0
3	HEC	E	603	43/43	0.85	0.17	45,71,80,84	0
6	JUG	E	608	13/13	0.86	0.17	63,65,70,72	0
3	HEC	C	604	43/43	0.88	0.17	28,52,63,67	0
3	HEC	C	602	43/43	0.89	0.14	19,54,65,67	0
3	HEC	A	602	43/43	0.90	0.17	27,64,85,93	0
3	HEC	E	604	43/43	0.91	0.14	40,53,67,70	0
3	HEC	E	601	43/43	0.91	0.13	25,42,60,68	0
3	HEC	E	602	43/43	0.91	0.14	31,52,64,70	0
3	HEC	A	601	43/43	0.91	0.14	19,56,76,84	0
3	HEC	A	604	43/43	0.92	0.12	20,32,39,41	0
4	ISW	A	608	43/43	0.92	0.14	24,37,41,46	0
4	ISW	A	611	43/43	0.92	0.15	28,41,55,57	0
3	HEC	A	607	43/43	0.92	0.13	16,45,65,77	0
3	HEC	C	601	43/43	0.92	0.13	29,51,58,63	0
4	ISW	C	611	43/43	0.93	0.13	18,39,53,59	0
3	HEC	E	606	43/43	0.93	0.14	30,42,60,68	0
3	HEC	C	605	43/43	0.93	0.14	18,35,43,48	0
3	HEC	E	605	43/43	0.93	0.12	13,36,45,51	0
3	HEC	A	605	43/43	0.94	0.11	20,33,53,57	0
3	HEC	C	606	43/43	0.94	0.11	18,34,50,55	0
3	HEC	A	603	43/43	0.94	0.11	26,41,52,57	0
3	HEC	A	606	43/43	0.95	0.10	15,27,38,47	0
3	HEC	E	607	43/43	0.95	0.11	14,35,51,60	0
3	HEC	C	607	43/43	0.96	0.10	11,27,42,47	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.

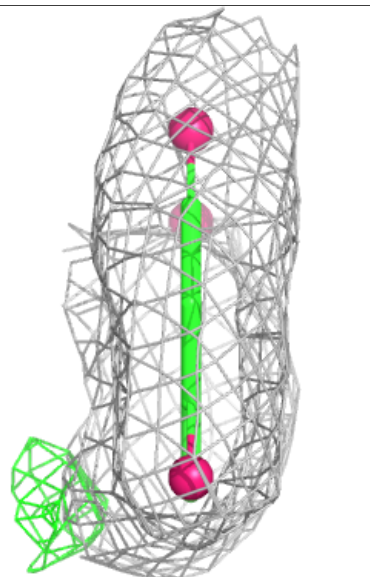
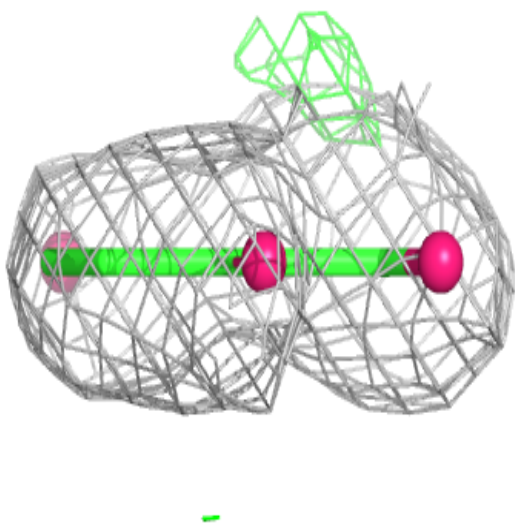
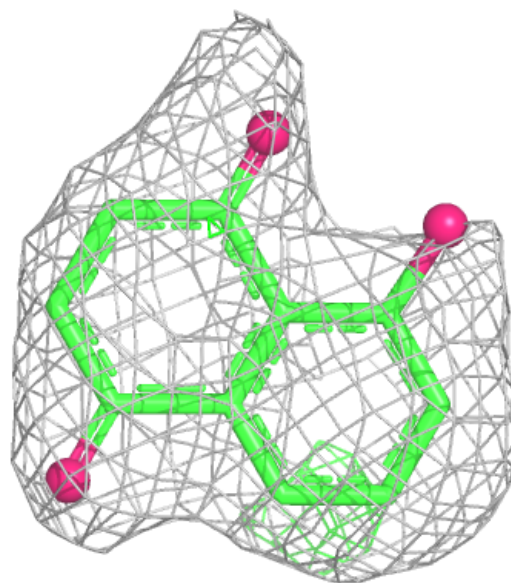
Electron density around HEC C 603:

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



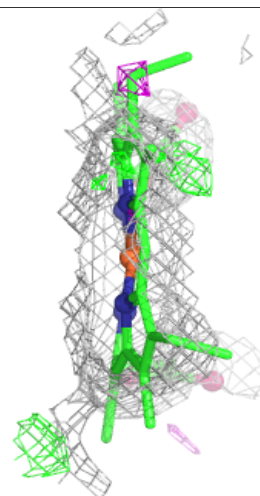
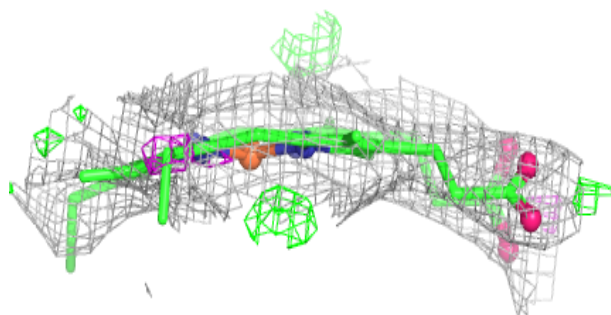
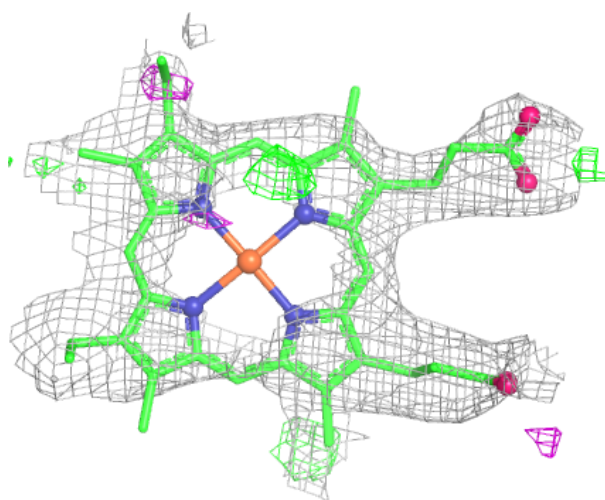
Electron density around JUG C 608:

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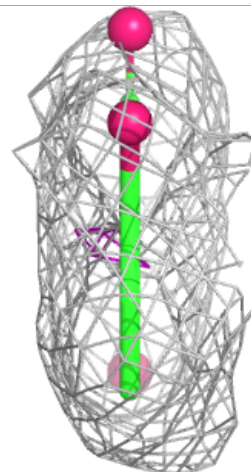
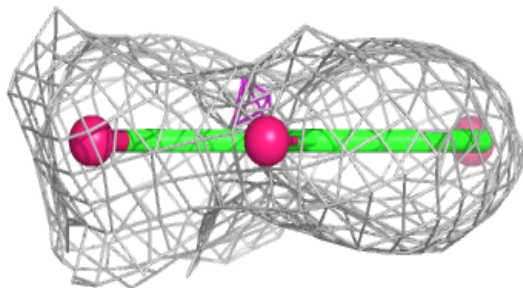
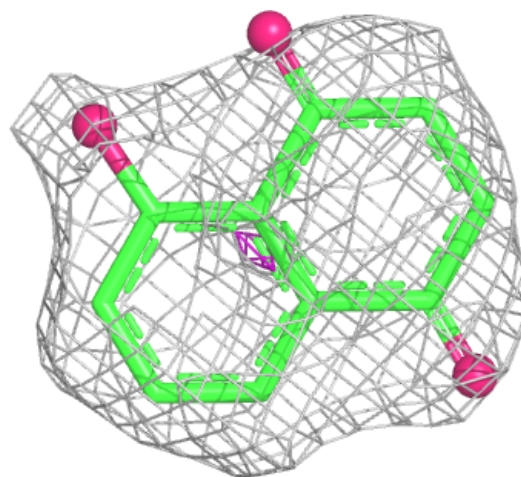
Electron density around HEC E 603:

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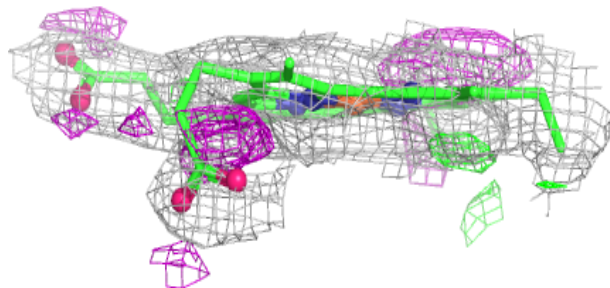
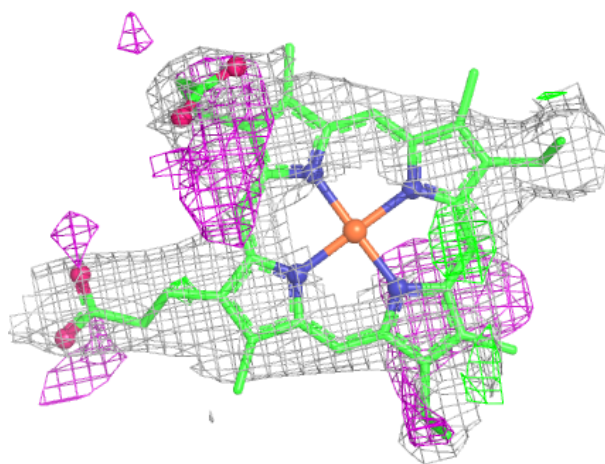
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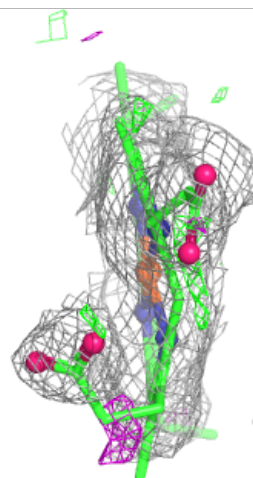
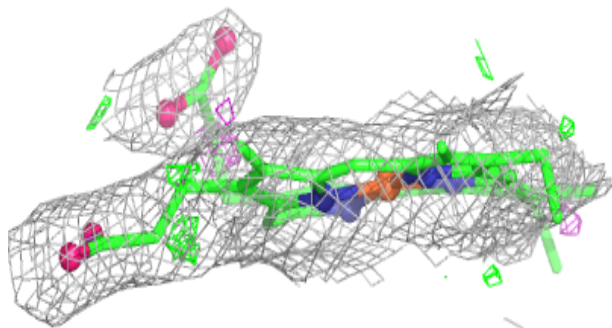
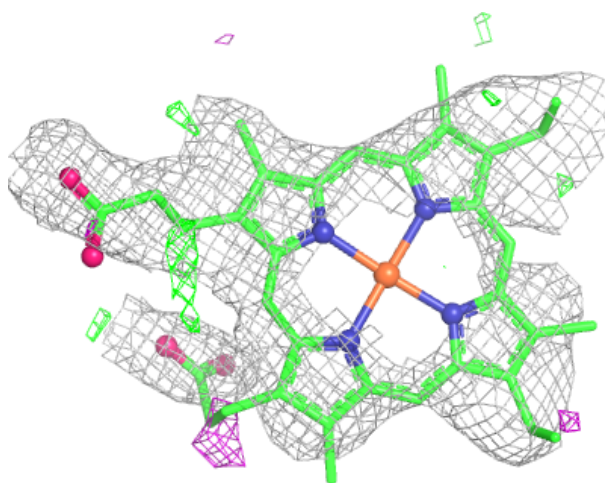
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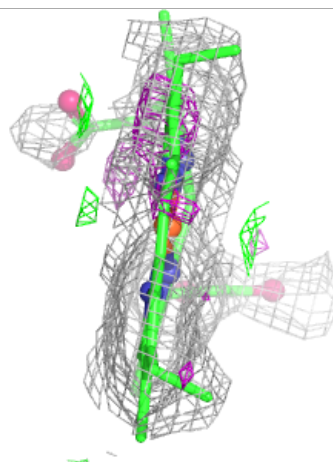
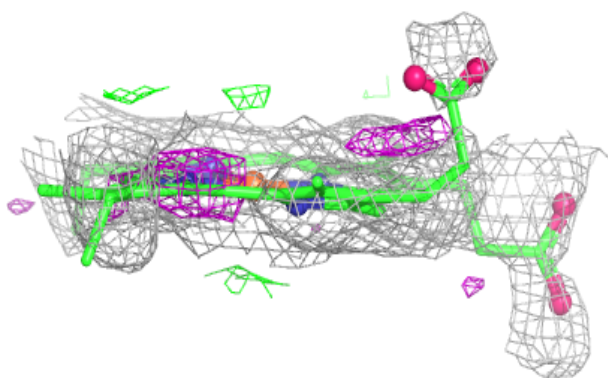
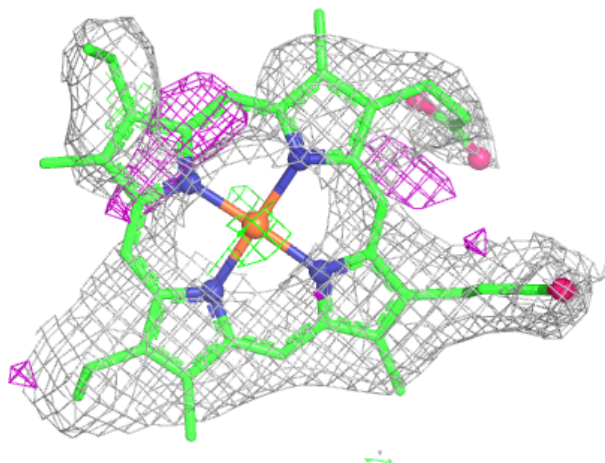
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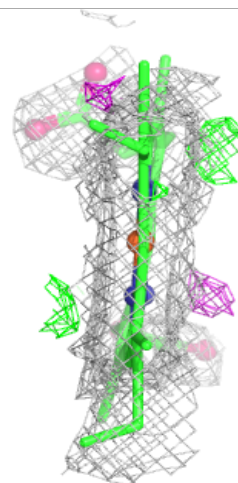
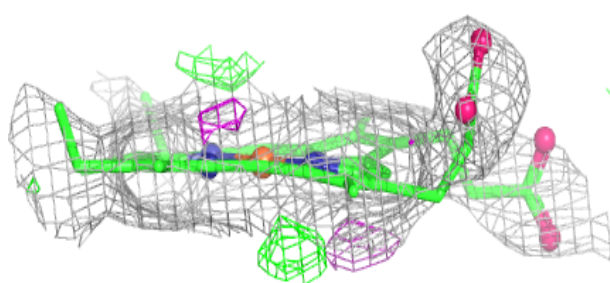
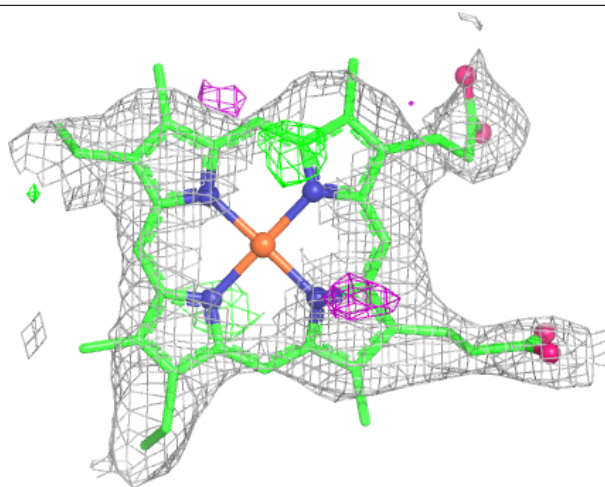
Electron density around HEC A 602:

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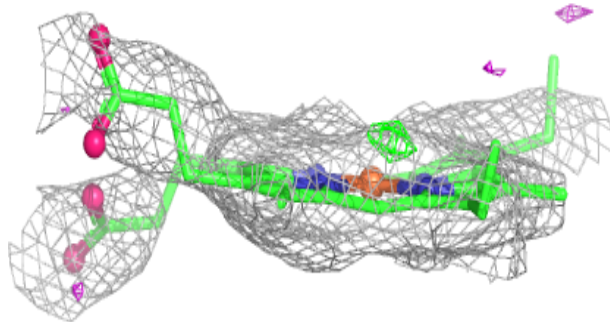
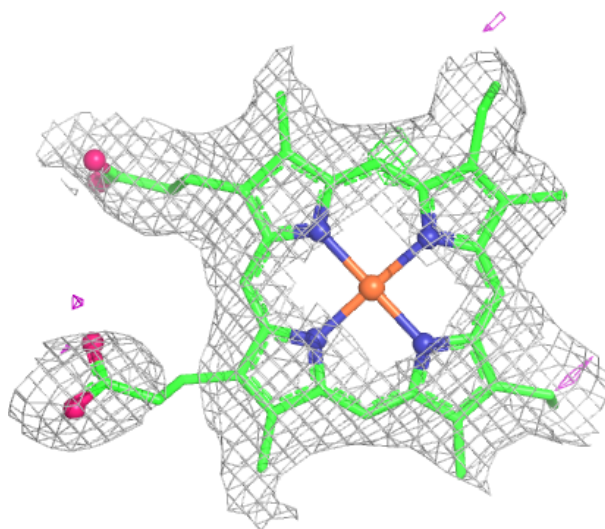
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and green (positive)



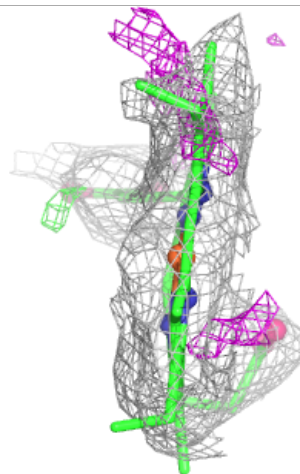
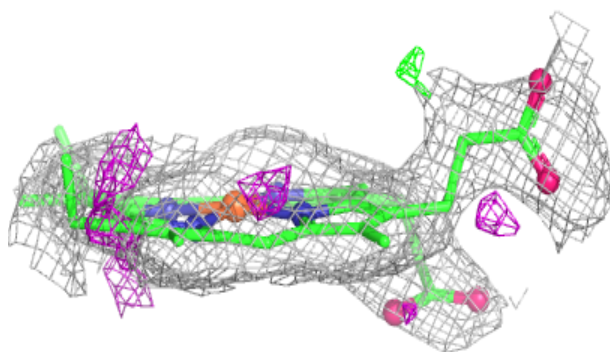
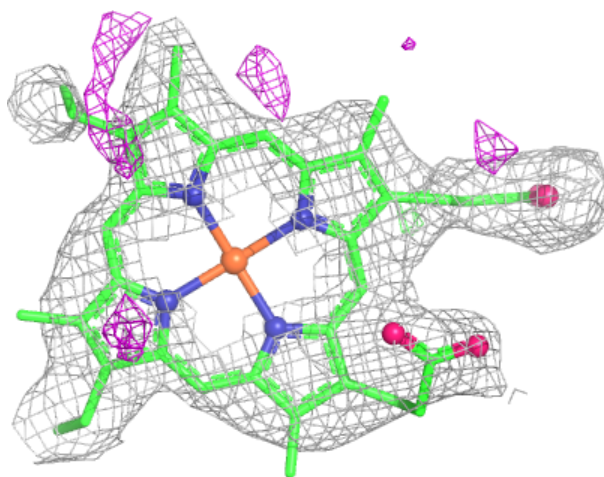
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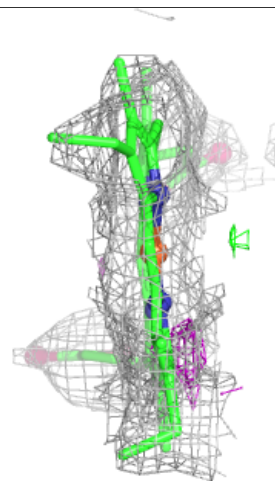
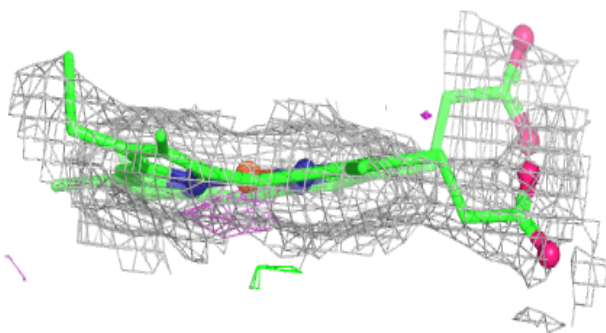
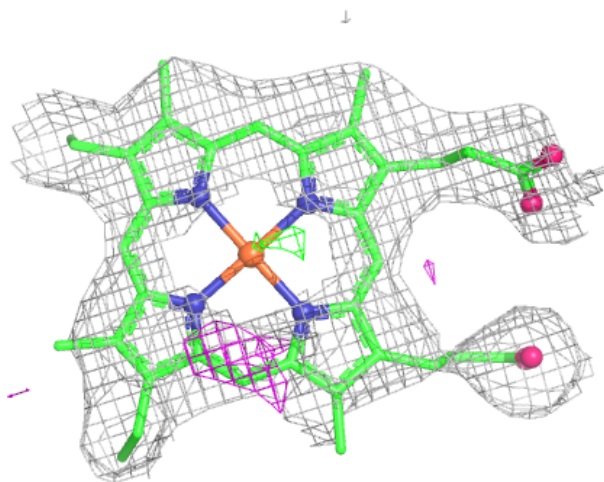
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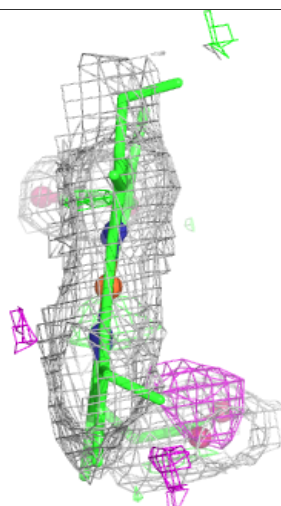
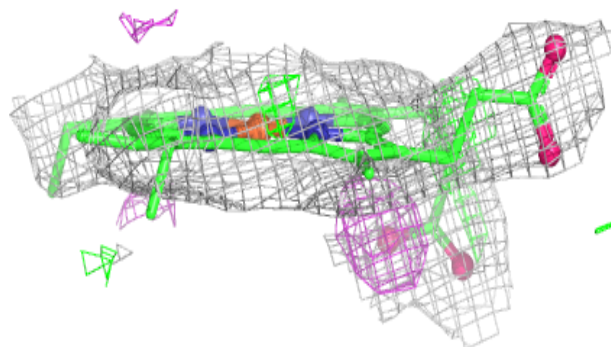
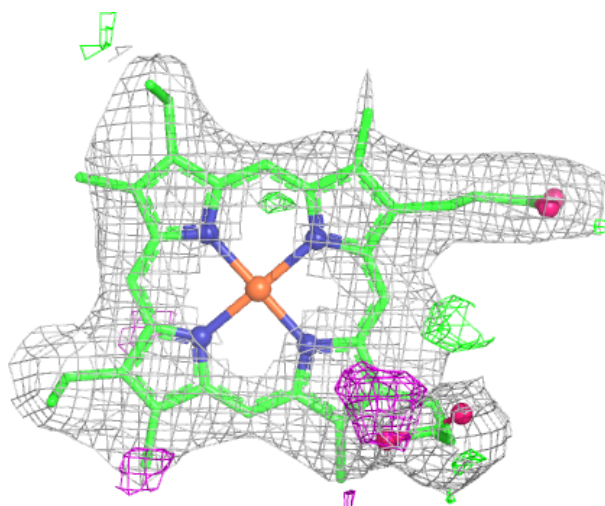
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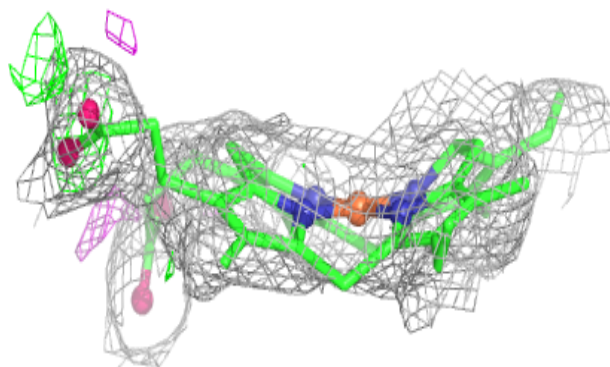
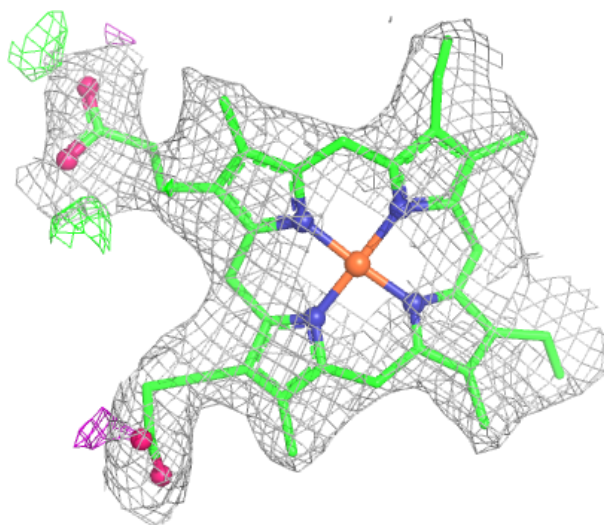
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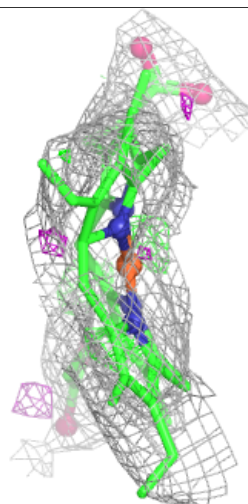
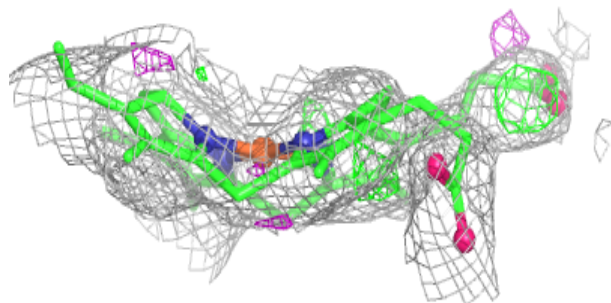
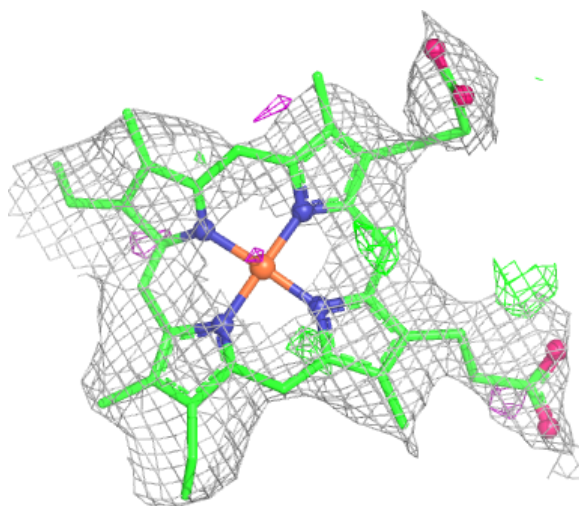
Electron density around ISW A 608:

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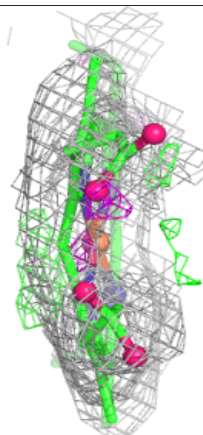
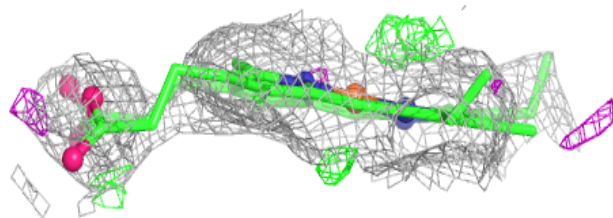
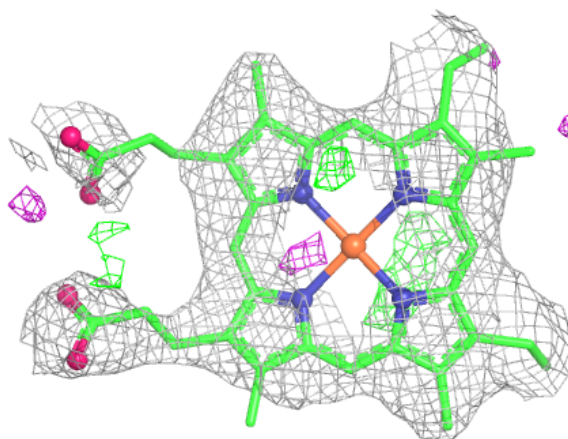
Electron density around ISW A 611:

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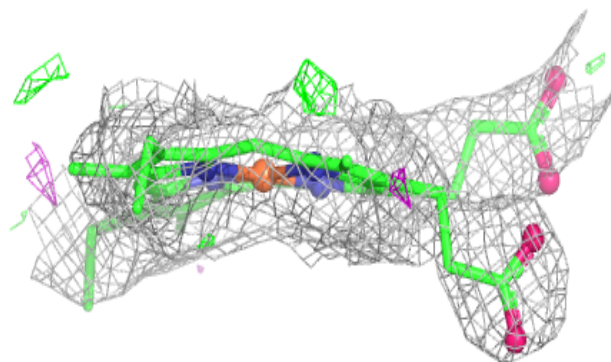
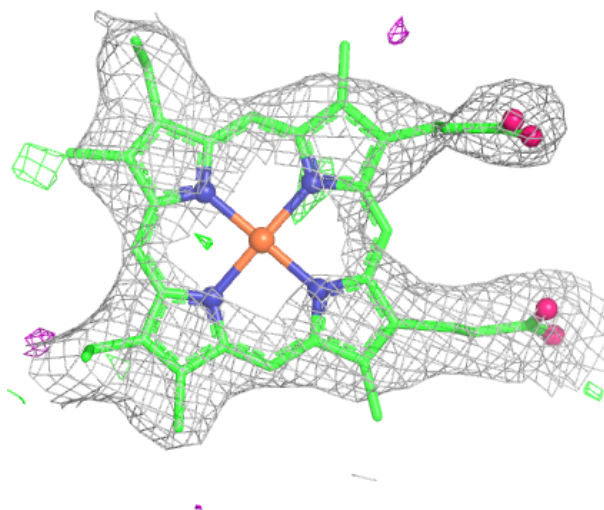
Electron density around HEC A 607:

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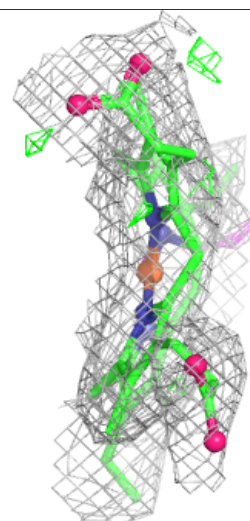
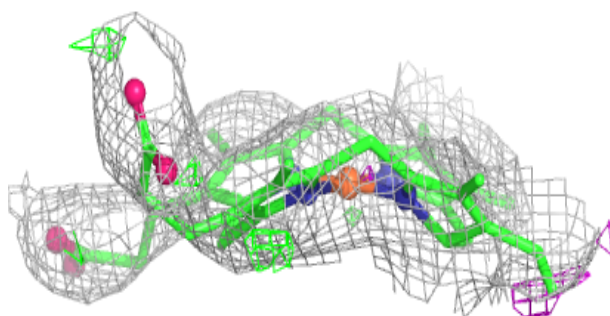
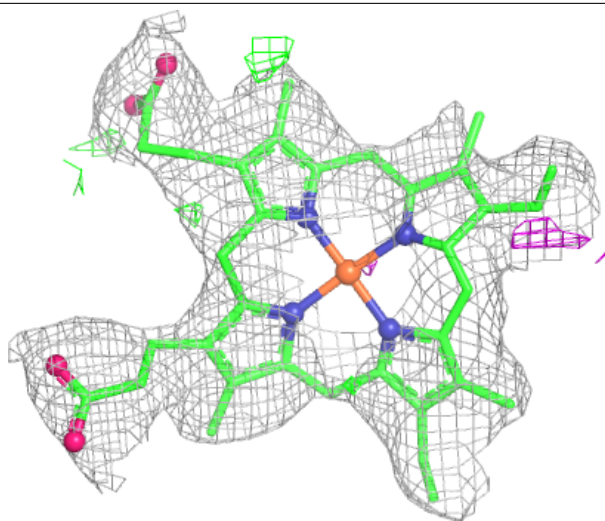
Electron density around HEC C 601:

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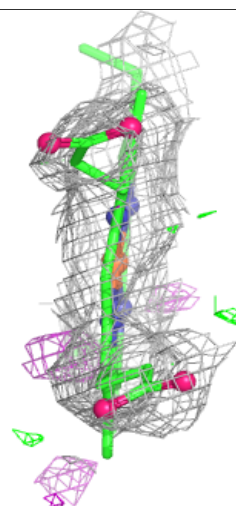
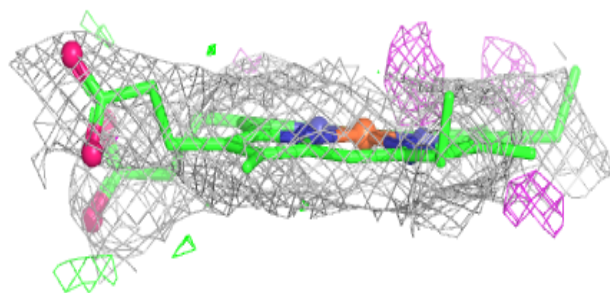
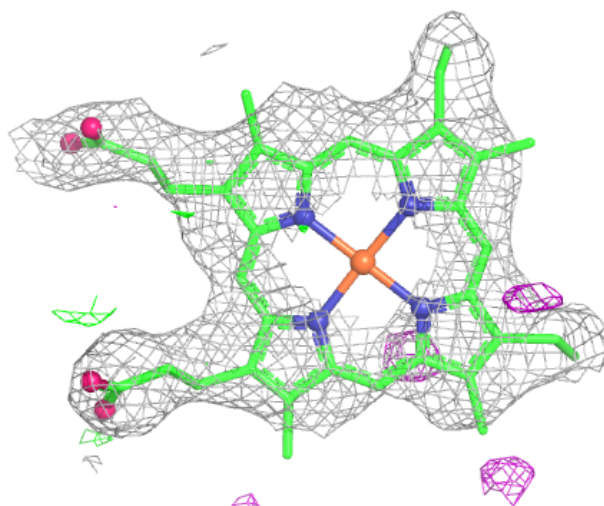
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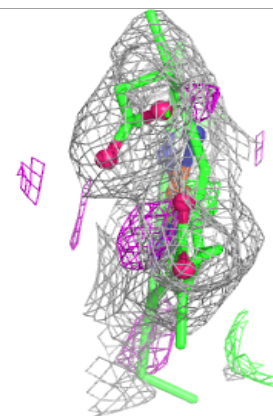
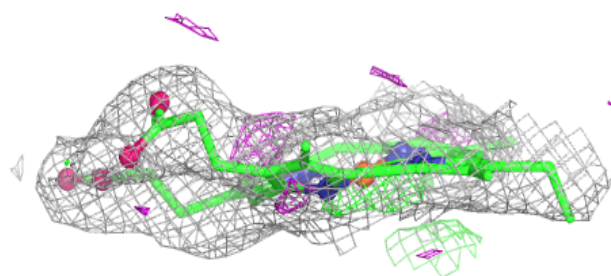
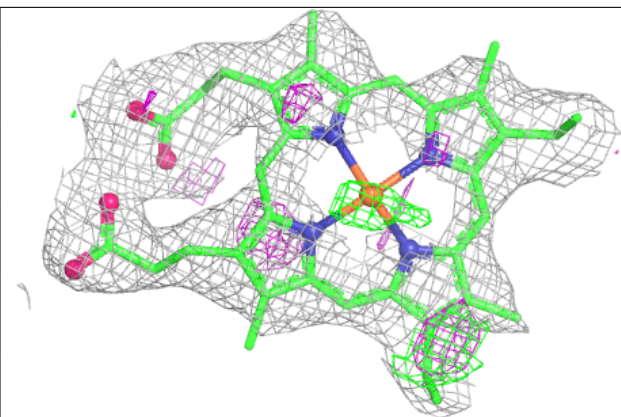
Electron density around HEC E 606:

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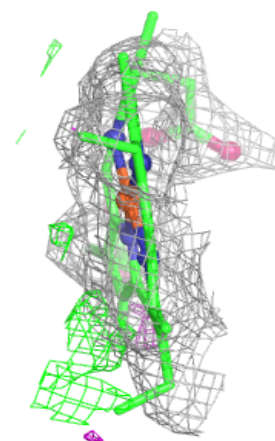
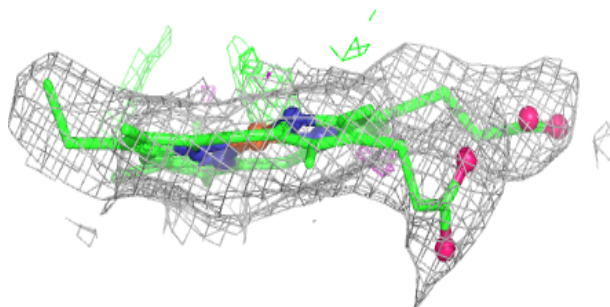
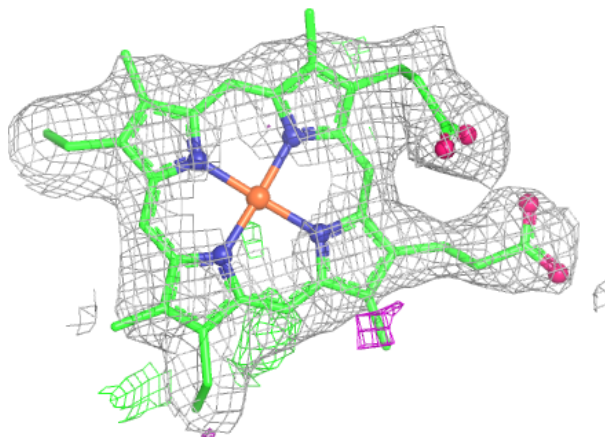
Electron density around HEC C 605:

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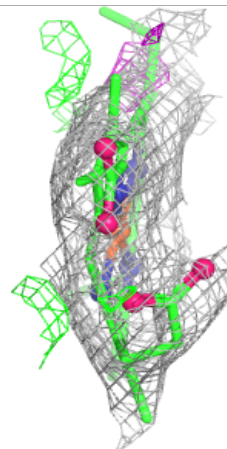
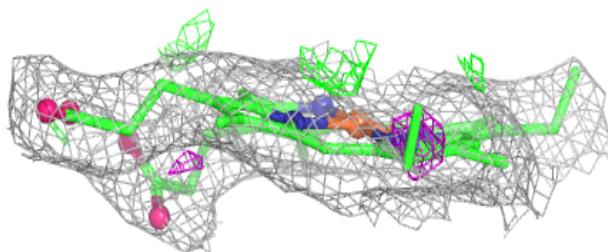
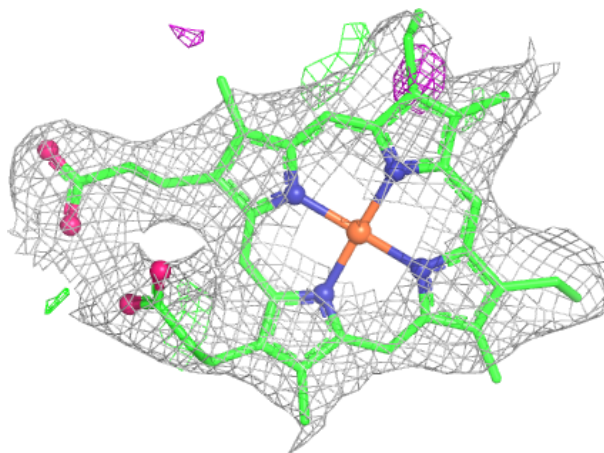
Electron density around HEC E 605:

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and green (positive)



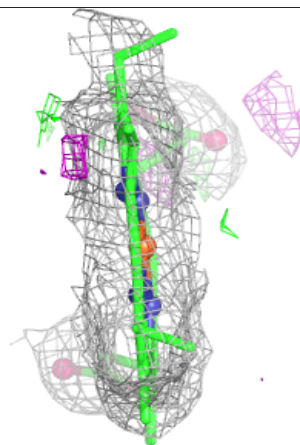
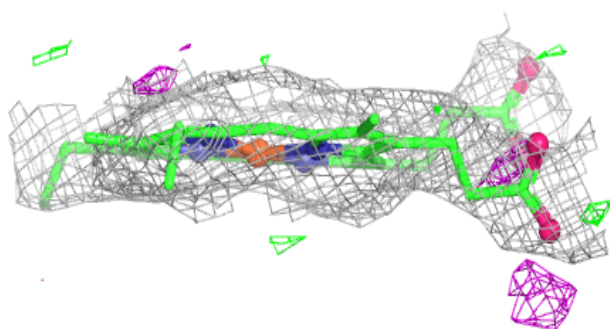
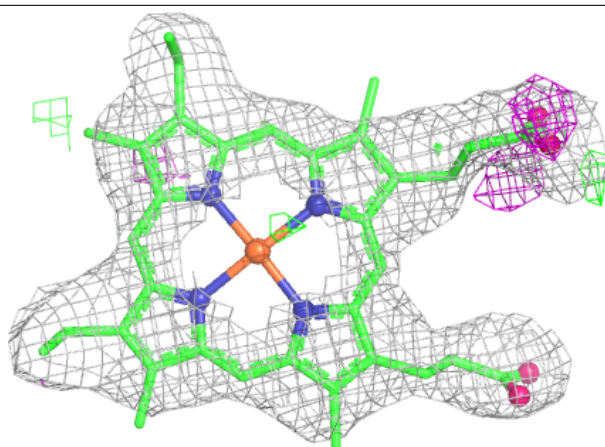
Electron density around HEC A 605:

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



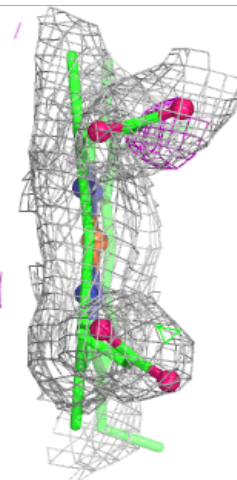
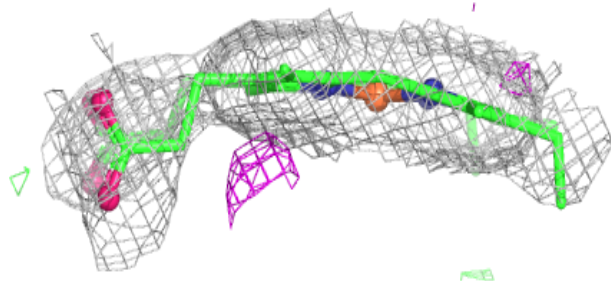
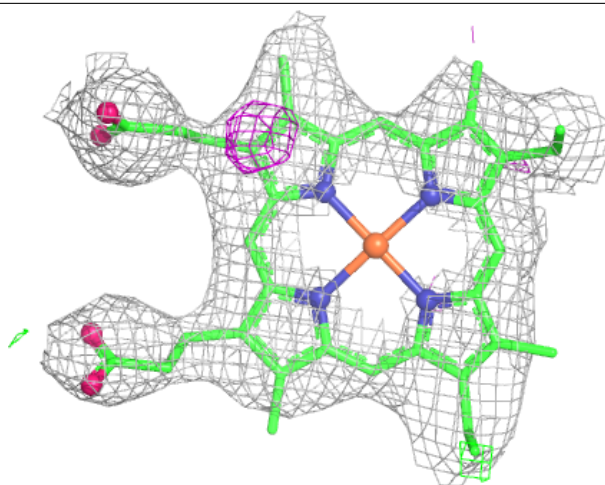
Electron density around HEC C 606:

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



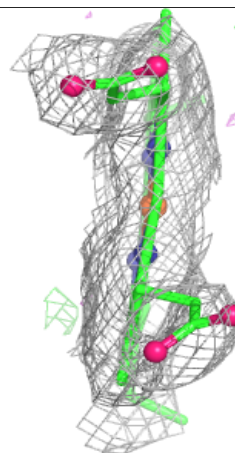
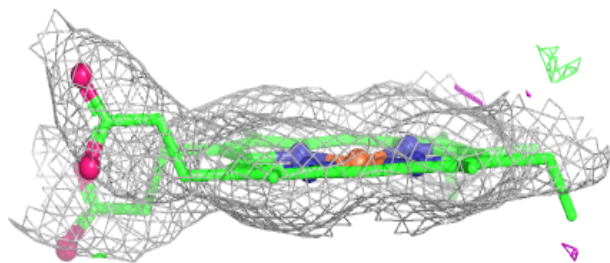
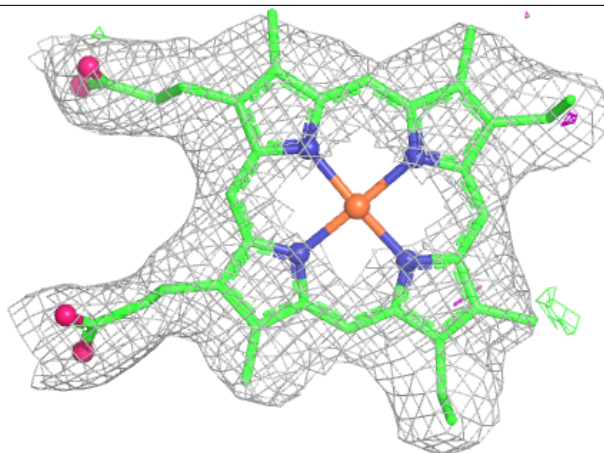
Electron density around HEC A 603:

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



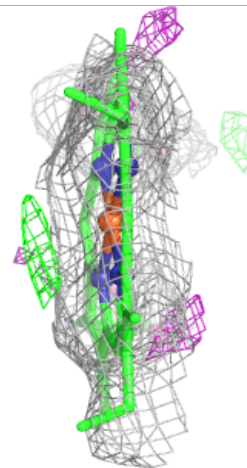
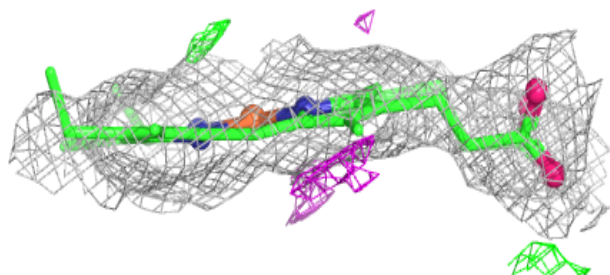
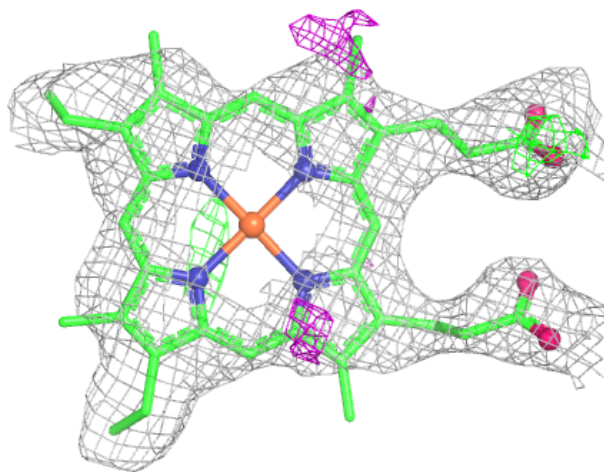
Electron density around HEC A 606:

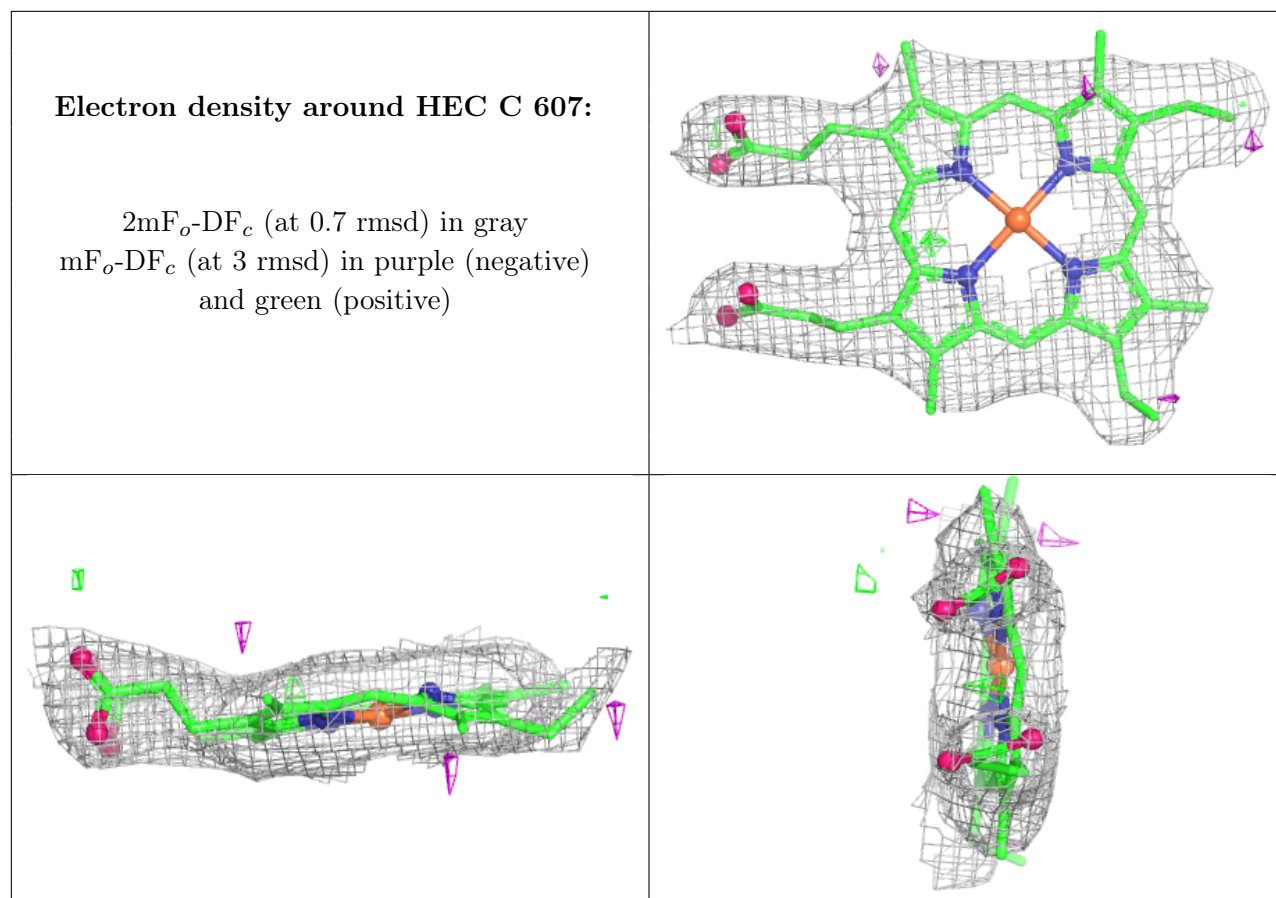
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC E 607:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.