



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 12:09 PM UTC

PDB ID : 4FAS / pdb_00004fas
Title : Complex crystal structure of hydroxylamine oxidoreductase and NE1300 from Nitrosomonas europaea
Authors : Cedervall, P.E.; Wilmot, C.M.
Deposited on : 2012-05-22
Resolution : 2.10 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)
Xtrriage (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

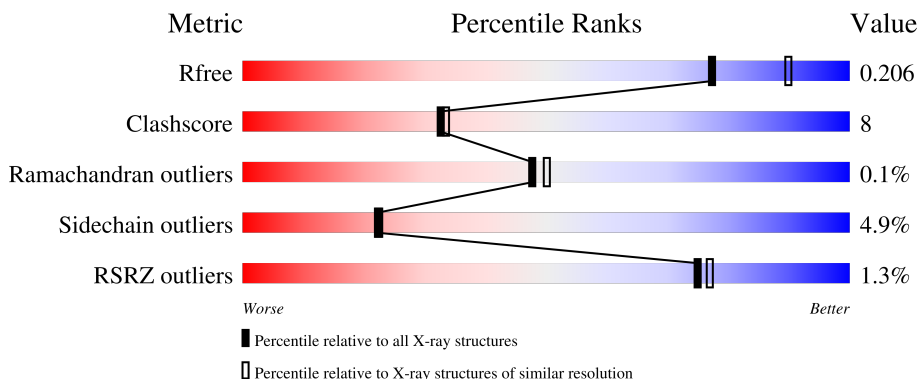
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	546	 75% 14% • 8%
1	B	546	 75% 14% • 8%
1	C	546	 76% 14% • 8%
2	D	69	 7% 62% 9% 29%
2	E	69	 13% 52% 14% • 29%

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Mol	Chain	Length	Quality of chain
2	F	69	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a small red segment (6%), a large green segment (54%), a yellow segment (16%), and a grey segment (29%). A small black dot is located on the yellow segment.</p>

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 15197 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 Hydroxylamine oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	502	4013	2495	711	775	32	0	1	0
1	B	502	4005	2491	710	772	32	0	1	0
1	C	502	4005	2491	710	772	32	0	0	0

- Molecule 2 is a protein called NE1300.

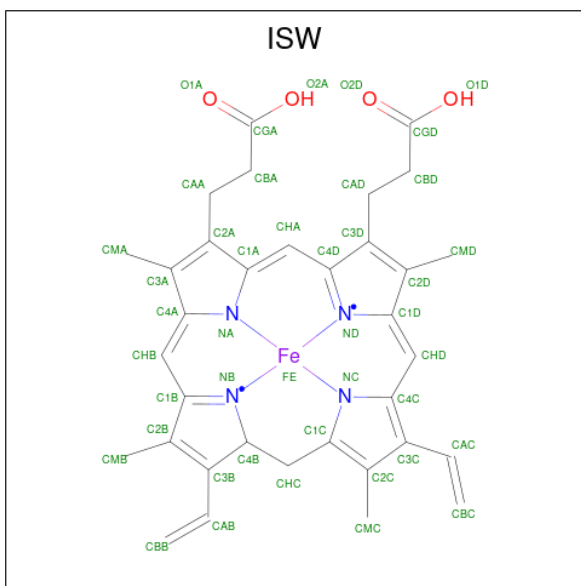
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	49	370	233	63	71	3	0	0	0
2	E	49	370	233	63	71	3	0	0	0
2	F	49	370	233	63	71	3	0	0	0

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

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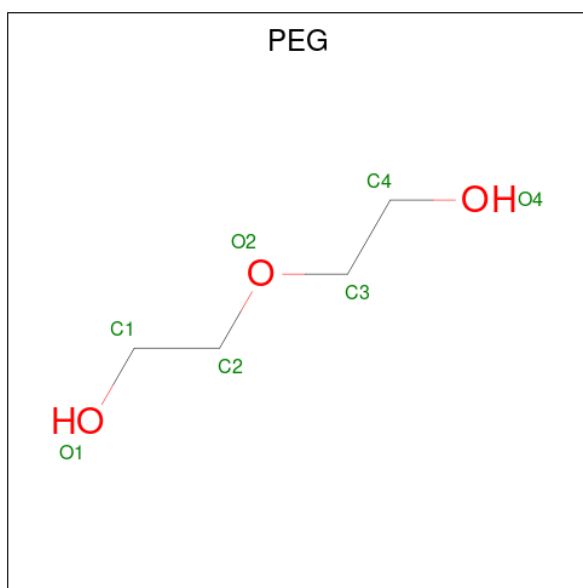
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
3	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- 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	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



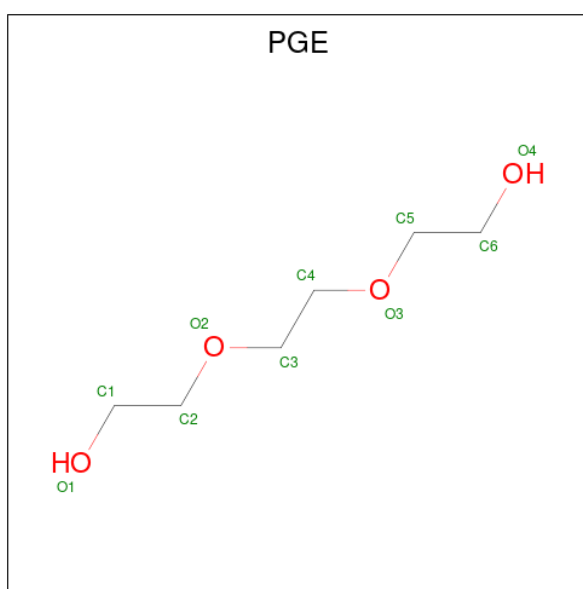
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	A	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0
5	B	1	Total C O 7 4 3	0	0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

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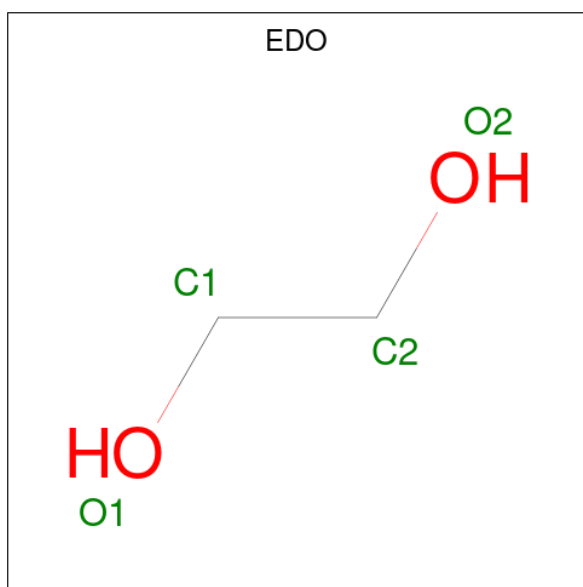
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		
6	C	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



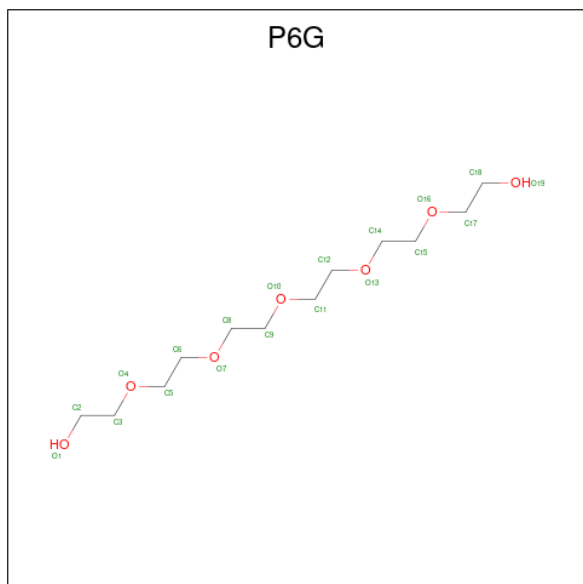
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0
7	C	1	Total C O 4 2 2	0	0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

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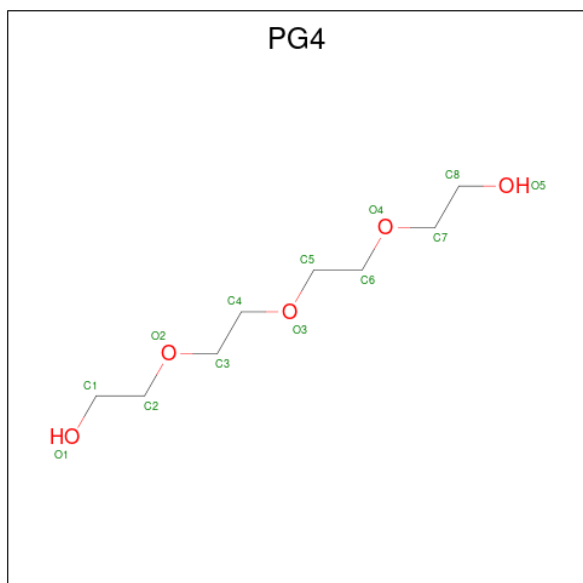
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



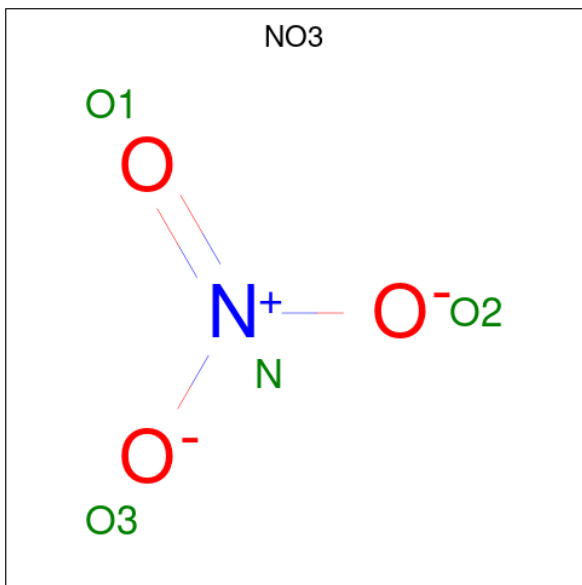
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			19	12	7		

- Molecule 9 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 10 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	N	O	0	0
			4	1	3		
10	B	1	Total	N	O	0	0
			4	1	3		
10	C	1	Total	N	O	0	0
			4	1	3		
10	F	1	Total	N	O	0	0
			4	1	3		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	237	Total	O	0	0
			237	237		
11	B	258	Total	O	0	0
			258	258		
11	C	244	Total	O	0	0
			244	244		
11	D	14	Total	O	0	0
			14	14		
11	E	10	Total	O	0	0
			10	10		

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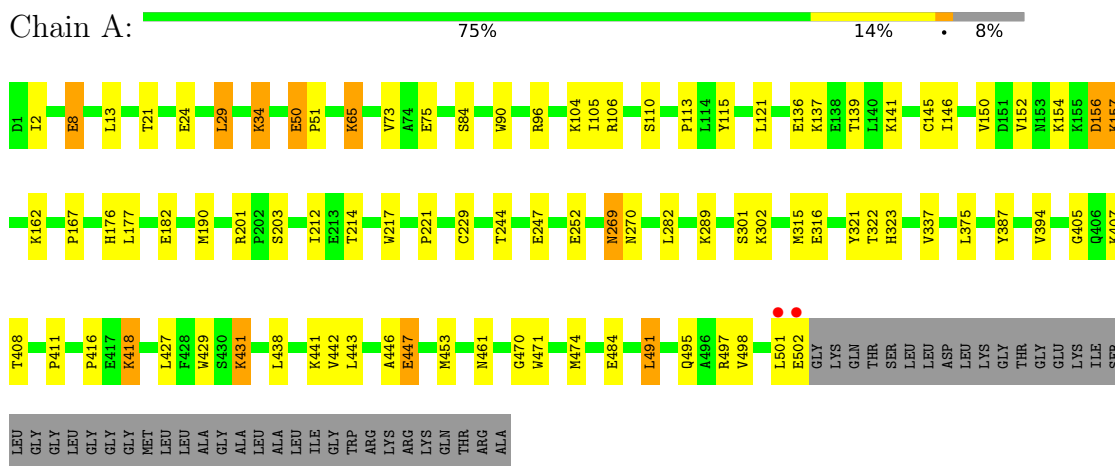
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	F	22	Total	O	0	0
			22	22		

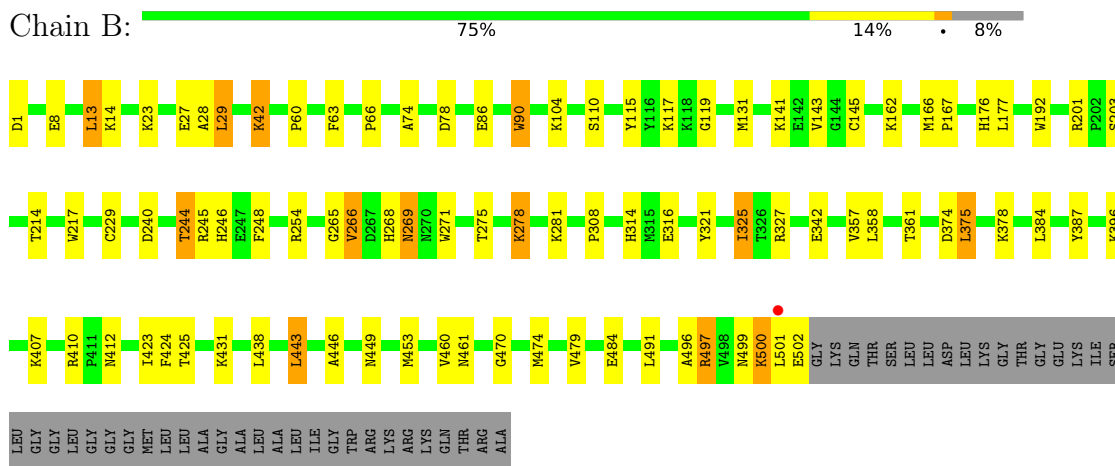
3 Residue-property plots

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.

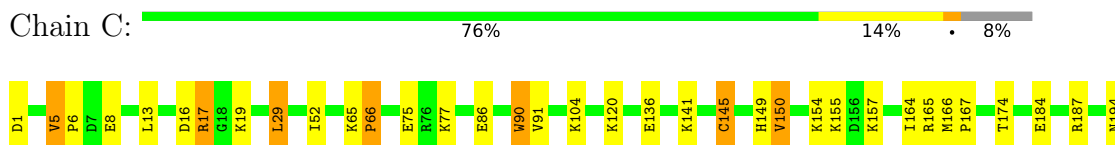
- Molecule 1: Hydroxylamine oxidoreductase

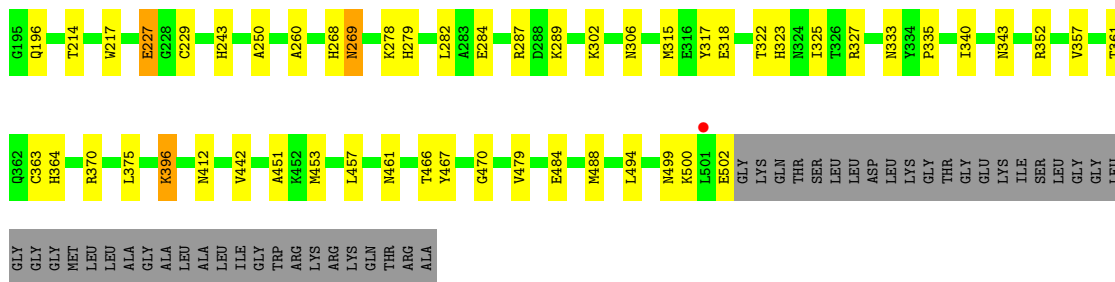


- Molecule 1: Hydroxylamine oxidoreductase

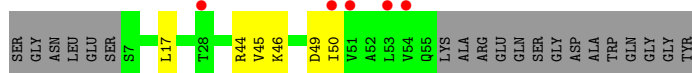


- Molecule 1: Hydroxylamine oxidoreductase





• Molecule 2: NE1300



• Molecule 2: NE1300



• Molecule 2: NE1300



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	140.73Å 142.62Å 107.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.89 – 2.10 42.89 – 2.10	Depositor EDS
% Data completeness (in resolution range)	79.9 (42.89-2.10) 79.9 (42.89-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.165 , 0.206 0.166 , 0.206	Depositor DCC
R_{free} test set	5071 reflections (4.03%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtrriage
Anisotropy	0.603	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.015 for k,h,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15197	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage'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: P6G, PG4, PEG, EDO, HEC, ISW, PGE, NO3

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	1.26	7/4116 (0.2%)	1.17	10/5578 (0.2%)
1	B	1.31	8/4108 (0.2%)	1.21	14/5567 (0.3%)
1	C	1.29	9/4108 (0.2%)	1.19	15/5567 (0.3%)
2	D	1.00	0/373	1.10	0/502
2	E	1.09	0/373	1.19	1/502 (0.2%)
2	F	1.16	0/373	1.18	0/502
All	All	1.27	24/13451 (0.2%)	1.19	40/18218 (0.2%)

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	466	THR	CA-C	8.99	1.56	1.52
1	C	91	VAL	CA-CB	6.34	1.62	1.54
1	C	363	CYS	C-O	-6.34	1.16	1.24
1	B	254	ARG	C-O	6.09	1.31	1.24
1	C	352	ARG	C-O	5.91	1.31	1.24

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	66	PRO	CA-C-N	-7.87	112.60	120.31
1	C	66	PRO	C-N-CA	-7.87	112.60	120.31
1	C	5	VAL	CA-C-N	6.34	126.31	119.78
1	C	5	VAL	C-N-CA	6.34	126.31	119.78
1	B	443	LEU	N-CA-C	-6.30	104.33	111.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4013	0	3811	62	0
1	B	4005	0	3807	64	0
1	C	4005	0	3808	61	0
2	D	370	0	391	1	0
2	E	370	0	391	9	0
2	F	370	0	391	8	0
3	A	301	0	210	8	0
3	B	301	0	210	10	0
3	C	301	0	210	13	0
4	A	43	0	28	10	0
4	B	43	0	28	10	0
4	C	43	0	28	11	0
5	A	42	0	60	6	0
5	B	28	0	40	4	0
5	C	42	0	60	4	0
5	F	7	0	10	1	0
6	A	10	0	14	1	0
6	C	10	0	14	4	0
7	A	16	0	24	3	0
7	B	20	0	30	0	0
7	C	24	0	36	3	0
8	B	19	0	26	1	0
9	B	13	0	18	1	0
10	B	8	0	0	0	0
10	C	4	0	0	0	0
10	F	4	0	0	0	0
11	A	237	0	0	4	0
11	B	258	0	0	1	0
11	C	244	0	0	3	0
11	D	14	0	0	0	0
11	E	10	0	0	0	0
11	F	22	0	0	1	0
All	All	15197	0	13645	221	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 221 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)
4:A:608:ISW:HBAA	3:B:605:HEC:O1D	1.65	0.96
4:B:608:ISW:HBAA	3:C:606:HEC:O1D	1.66	0.95
1:B:497:ARG:HB2	1:B:497:ARG:HH11	1.31	0.95
1:B:497:ARG:HH11	1:B:497:ARG:CB	1.80	0.94
1:B:13:LEU:HD21	1:B:29:LEU:HD13	1.49	0.92

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	501/546 (92%)	482 (96%)	19 (4%)	0	100	100
1	B	500/546 (92%)	483 (97%)	16 (3%)	1 (0%)	43	44
1	C	500/546 (92%)	478 (96%)	21 (4%)	1 (0%)	43	44
2	D	47/69 (68%)	45 (96%)	2 (4%)	0	100	100
2	E	47/69 (68%)	44 (94%)	3 (6%)	0	100	100
2	F	47/69 (68%)	45 (96%)	2 (4%)	0	100	100
All	All	1642/1845 (89%)	1577 (96%)	63 (4%)	2 (0%)	48	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	268	HIS
1	C	268	HIS

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	430/459 (94%)	407 (95%)	23 (5%)	20	19
1	B	429/459 (94%)	409 (95%)	20 (5%)	23	24
1	C	429/459 (94%)	413 (96%)	16 (4%)	30	33
2	D	43/57 (75%)	39 (91%)	4 (9%)	8	6
2	E	43/57 (75%)	39 (91%)	4 (9%)	8	6
2	F	43/57 (75%)	40 (93%)	3 (7%)	14	11
All	All	1417/1548 (92%)	1347 (95%)	70 (5%)	22	22

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	499	ASN
2	D	17	LEU
2	E	51	VAL
1	B	14	LYS
1	B	13	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	449	ASN
1	C	499	ASN
1	C	495	GLN
1	B	448	ASN
1	C	269	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](#)

64 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
10	NO3	F	101	-	1,3,3	3.53	1 (100%)	0,3,3	-	-
3	HEC	B	601	1	46,50,50	2.52	17 (36%)	58,82,82	2.00	16 (27%)
5	PEG	C	611	-	6,6,6	0.56	0	5,5,5	0.61	0
4	ISW	C	601	1	47,50,50	3.23	27 (57%)	53,82,82	2.40	19 (35%)
3	HEC	B	606	1	46,50,50	2.41	20 (43%)	58,82,82	1.89	11 (18%)
5	PEG	C	622	-	6,6,6	0.97	0	5,5,5	1.20	0
7	EDO	A	619	-	3,3,3	0.54	0	2,2,2	0.36	0
5	PEG	B	609	-	6,6,6	0.47	0	5,5,5	0.93	0
5	PEG	A	612	-	6,6,6	0.53	0	5,5,5	0.35	0
3	HEC	A	604	1	46,50,50	2.31	19 (41%)	58,82,82	2.18	15 (25%)
3	HEC	C	607	1	46,50,50	2.33	21 (45%)	58,82,82	1.60	7 (12%)
5	PEG	B	612	-	6,6,6	0.69	0	5,5,5	0.70	0
3	HEC	B	604	1	46,50,50	2.29	19 (41%)	58,82,82	2.12	11 (18%)
3	HEC	A	607	1	46,50,50	2.55	24 (52%)	58,82,82	2.20	15 (25%)
6	PGE	A	615	-	9,9,9	0.68	0	8,8,8	0.79	0
7	EDO	B	620	-	3,3,3	0.70	0	2,2,2	0.42	0
8	P6G	B	613	-	18,18,18	0.49	0	17,17,17	0.74	0
10	NO3	B	617	-	1,3,3	2.76	1 (100%)	0,3,3	-	-
5	PEG	A	609	-	6,6,6	0.22	0	5,5,5	1.00	0
3	HEC	A	606	1	46,50,50	2.45	21 (45%)	58,82,82	2.10	10 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	EDO	B	621	-	3,3,3	0.46	0	2,2,2	0.20	0
5	PEG	A	610	-	6,6,6	0.28	0	5,5,5	1.04	0
5	PEG	C	612	-	6,6,6	0.47	0	5,5,5	0.83	0
3	HEC	A	602	1	46,50,50	2.47	20 (43%)	58,82,82	2.20	12 (20%)
5	PEG	B	610	-	6,6,6	0.50	0	5,5,5	0.48	0
10	NO3	C	619	-	1,3,3	3.37	1 (100%)	0,3,3	-	-
4	ISW	A	608	1	47,50,50	3.27	25 (53%)	53,82,82	2.76	24 (45%)
7	EDO	A	618	-	3,3,3	0.44	0	2,2,2	0.24	0
5	PEG	B	611	-	6,6,6	0.35	0	5,5,5	0.95	0
7	EDO	C	621	-	3,3,3	0.53	0	2,2,2	0.47	0
5	PEG	C	609	-	6,6,6	0.49	0	5,5,5	0.41	0
7	EDO	C	617	-	3,3,3	0.49	0	2,2,2	0.36	0
5	PEG	A	613	-	6,6,6	0.56	0	5,5,5	0.52	0
3	HEC	A	603	1	46,50,50	2.33	21 (45%)	58,82,82	1.93	11 (18%)
3	HEC	C	604	1	46,50,50	2.31	20 (43%)	58,82,82	2.26	12 (20%)
5	PEG	A	611	-	6,6,6	0.65	0	5,5,5	0.48	0
4	ISW	B	608	1	47,50,50	3.40	25 (53%)	53,82,82	2.49	21 (39%)
3	HEC	B	602	1	46,50,50	2.38	18 (39%)	58,82,82	1.72	7 (12%)
3	HEC	A	605	1	46,50,50	2.35	16 (34%)	58,82,82	1.88	16 (27%)
3	HEC	B	605	1	46,50,50	2.30	19 (41%)	58,82,82	1.64	12 (20%)
3	HEC	C	606	1	46,50,50	2.33	18 (39%)	58,82,82	1.88	9 (15%)
7	EDO	C	615	-	3,3,3	0.41	0	2,2,2	0.28	0
9	PG4	B	614	-	12,12,12	0.61	0	11,11,11	0.90	0
7	EDO	A	617	-	3,3,3	0.65	0	2,2,2	0.38	0
3	HEC	C	602	1	46,50,50	2.35	20 (43%)	58,82,82	2.00	10 (17%)
7	EDO	A	616	-	3,3,3	0.61	0	2,2,2	1.00	0
7	EDO	C	618	-	3,3,3	0.70	0	2,2,2	0.14	0
7	EDO	B	616	-	3,3,3	0.45	0	2,2,2	0.44	0
3	HEC	C	603	1	46,50,50	2.34	17 (36%)	58,82,82	1.88	12 (20%)
7	EDO	C	616	-	3,3,3	0.18	0	2,2,2	0.76	0
3	HEC	B	607	1	46,50,50	2.27	17 (36%)	58,82,82	1.95	12 (20%)
5	PEG	C	613	-	6,6,6	0.65	0	5,5,5	0.90	0
7	EDO	B	615	-	3,3,3	0.60	0	2,2,2	0.08	0
7	EDO	B	619	-	3,3,3	0.23	0	2,2,2	0.73	0
5	PEG	A	614	-	6,6,6	0.76	0	5,5,5	0.84	0
3	HEC	C	605	1	46,50,50	2.44	21 (45%)	58,82,82	2.22	15 (25%)
3	HEC	C	608	1	46,50,50	2.44	19 (41%)	58,82,82	2.18	16 (27%)
5	PEG	F	102	-	6,6,6	0.60	0	5,5,5	0.67	0
5	PEG	C	610	-	6,6,6	0.75	0	5,5,5	0.68	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	NO3	B	618	-	1,3,3	3.79	1 (100%)	0,3,3	-	-
6	PGE	C	614	-	9,9,9	0.36	0	8,8,8	1.00	0
7	EDO	C	620	-	3,3,3	0.81	0	2,2,2	0.38	0
3	HEC	B	603	1	46,50,50	2.43	16 (34%)	58,82,82	1.99	12 (20%)
3	HEC	A	601	1	46,50,50	2.46	19 (41%)	58,82,82	2.07	14 (24%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HEC	B	601	1	-	6/14/54/54	-
5	PEG	C	611	-	-	4/4/4/4	-
4	ISW	C	601	1	-	3/14/74/74	-
3	HEC	B	606	1	-	8/14/54/54	-
5	PEG	C	622	-	-	3/4/4/4	-
7	EDO	A	619	-	-	1/1/1/1	-
5	PEG	B	609	-	-	2/4/4/4	-
5	PEG	A	612	-	-	1/4/4/4	-
3	HEC	A	604	1	-	8/14/54/54	-
3	HEC	C	607	1	-	9/14/54/54	-
5	PEG	B	612	-	-	4/4/4/4	-
3	HEC	B	604	1	-	5/14/54/54	-
3	HEC	A	607	1	-	6/14/54/54	-
6	PGE	A	615	-	-	5/7/7/7	-
7	EDO	B	620	-	-	0/1/1/1	-
8	P6G	B	613	-	-	10/16/16/16	-
5	PEG	A	609	-	-	3/4/4/4	-
3	HEC	A	606	1	-	9/14/54/54	-
7	EDO	B	621	-	-	1/1/1/1	-
5	PEG	A	610	-	-	1/4/4/4	-
5	PEG	C	612	-	-	2/4/4/4	-
3	HEC	A	602	1	-	6/14/54/54	-
5	PEG	B	610	-	-	1/4/4/4	-
4	ISW	A	608	1	-	3/14/74/74	-
7	EDO	A	618	-	-	1/1/1/1	-
5	PEG	B	611	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	EDO	C	621	-	-	1/1/1/1	-
5	PEG	C	609	-	-	1/4/4/4	-
7	EDO	C	617	-	-	1/1/1/1	-
5	PEG	A	613	-	-	4/4/4/4	-
3	HEC	A	603	1	-	8/14/54/54	-
3	HEC	C	604	1	-	8/14/54/54	-
5	PEG	A	611	-	-	2/4/4/4	-
4	ISW	B	608	1	-	4/14/74/74	-
3	HEC	B	602	1	-	7/14/54/54	-
3	HEC	A	605	1	-	6/14/54/54	-
3	HEC	B	605	1	-	6/14/54/54	-
3	HEC	C	606	1	-	6/14/54/54	-
7	EDO	C	615	-	-	0/1/1/1	-
9	PG4	B	614	-	-	4/10/10/10	-
7	EDO	A	617	-	-	1/1/1/1	-
3	HEC	C	602	1	-	4/14/54/54	-
7	EDO	A	616	-	-	0/1/1/1	-
7	EDO	C	618	-	-	0/1/1/1	-
7	EDO	B	616	-	-	0/1/1/1	-
3	HEC	C	603	1	-	7/14/54/54	-
7	EDO	C	616	-	-	1/1/1/1	-
3	HEC	B	607	1	-	6/14/54/54	-
5	PEG	C	613	-	-	3/4/4/4	-
7	EDO	B	615	-	-	1/1/1/1	-
7	EDO	B	619	-	-	1/1/1/1	-
5	PEG	A	614	-	-	3/4/4/4	-
3	HEC	C	605	1	-	4/14/54/54	-
3	HEC	C	608	1	-	6/14/54/54	-
5	PEG	F	102	-	-	3/4/4/4	-
5	PEG	C	610	-	-	4/4/4/4	-
6	PGE	C	614	-	-	6/7/7/7	-
7	EDO	C	620	-	-	1/1/1/1	-
3	HEC	B	603	1	-	8/14/54/54	-
3	HEC	A	601	1	-	4/14/54/54	-

The worst 5 of 483 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	608	ISW	C2A-C3A	7.48	1.52	1.36
3	A	605	HEC	CAB-C3B	7.26	1.58	1.35
3	B	603	HEC	CAC-C3C	6.86	1.57	1.35
4	A	608	ISW	C3D-C2D	6.66	1.51	1.36
4	A	608	ISW	C2A-C3A	6.64	1.51	1.36

The worst 5 of 319 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	604	HEC	CBB-CAB-C3B	-10.13	107.19	127.43
3	B	604	HEC	CBB-CAB-C3B	-10.12	107.20	127.43
3	C	606	HEC	CBB-CAB-C3B	-9.90	107.64	127.43
3	A	602	HEC	CBB-CAB-C3B	-9.87	107.71	127.43
3	B	607	HEC	CBB-CAB-C3B	-9.33	108.79	127.43

There are no chirality outliers.

5 of 225 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	HEC	C2B-C3B-CAB-CBB
3	A	601	HEC	C4B-C3B-CAB-CBB
3	A	602	HEC	C2B-C3B-CAB-CBB
3	A	602	HEC	C4B-C3B-CAB-CBB
3	A	602	HEC	C2C-C3C-CAC-CBC

There are no ring outliers.

37 monomers are involved in 80 short contacts:

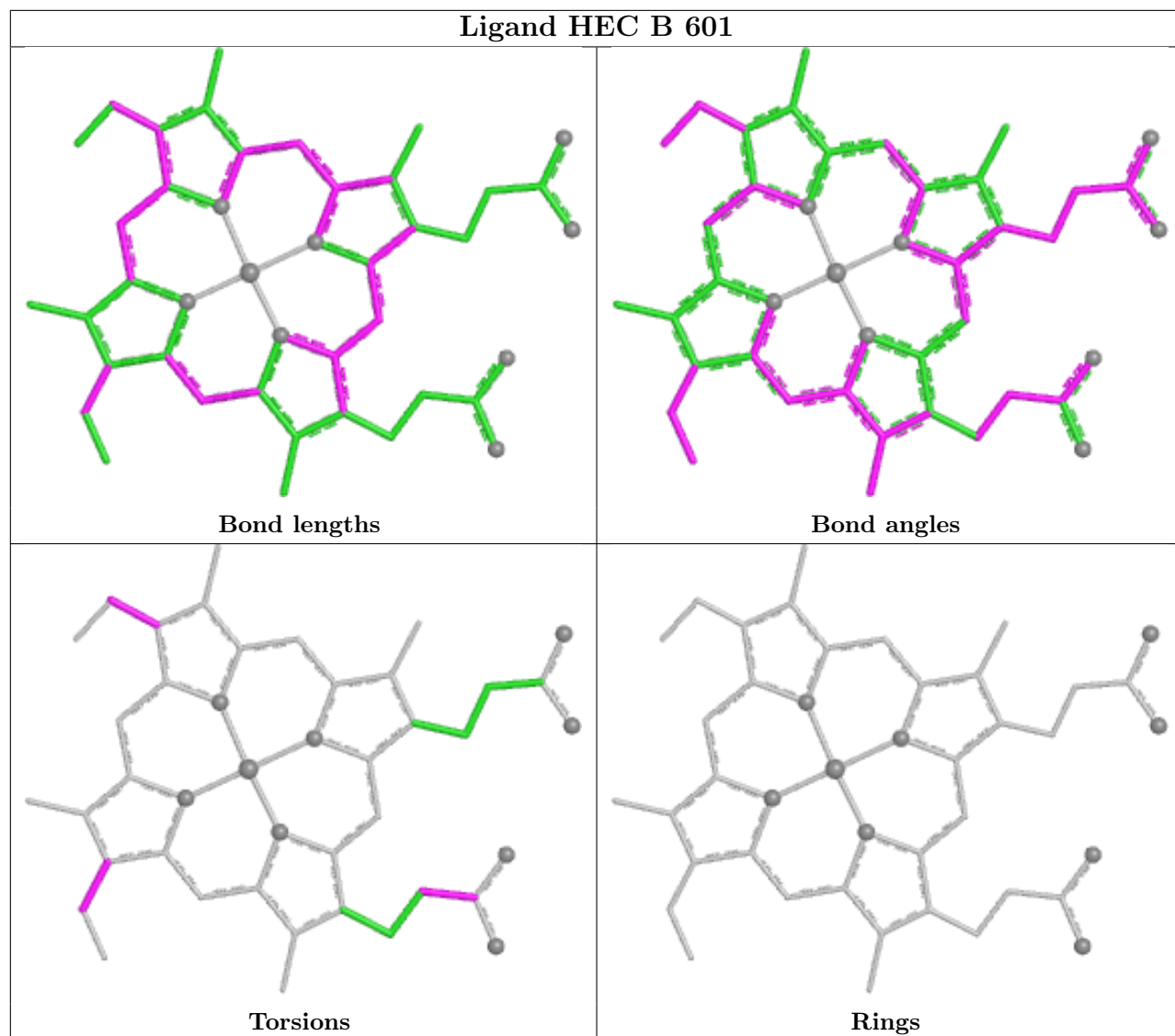
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	601	HEC	2	0
4	C	601	ISW	11	0
3	B	606	HEC	1	0
5	C	622	PEG	1	0
7	A	619	EDO	1	0
5	B	609	PEG	3	0
5	A	612	PEG	1	0
3	A	604	HEC	2	0
3	C	607	HEC	1	0
5	B	612	PEG	1	0
6	A	615	PGE	1	0
8	B	613	P6G	1	0
3	A	606	HEC	1	0

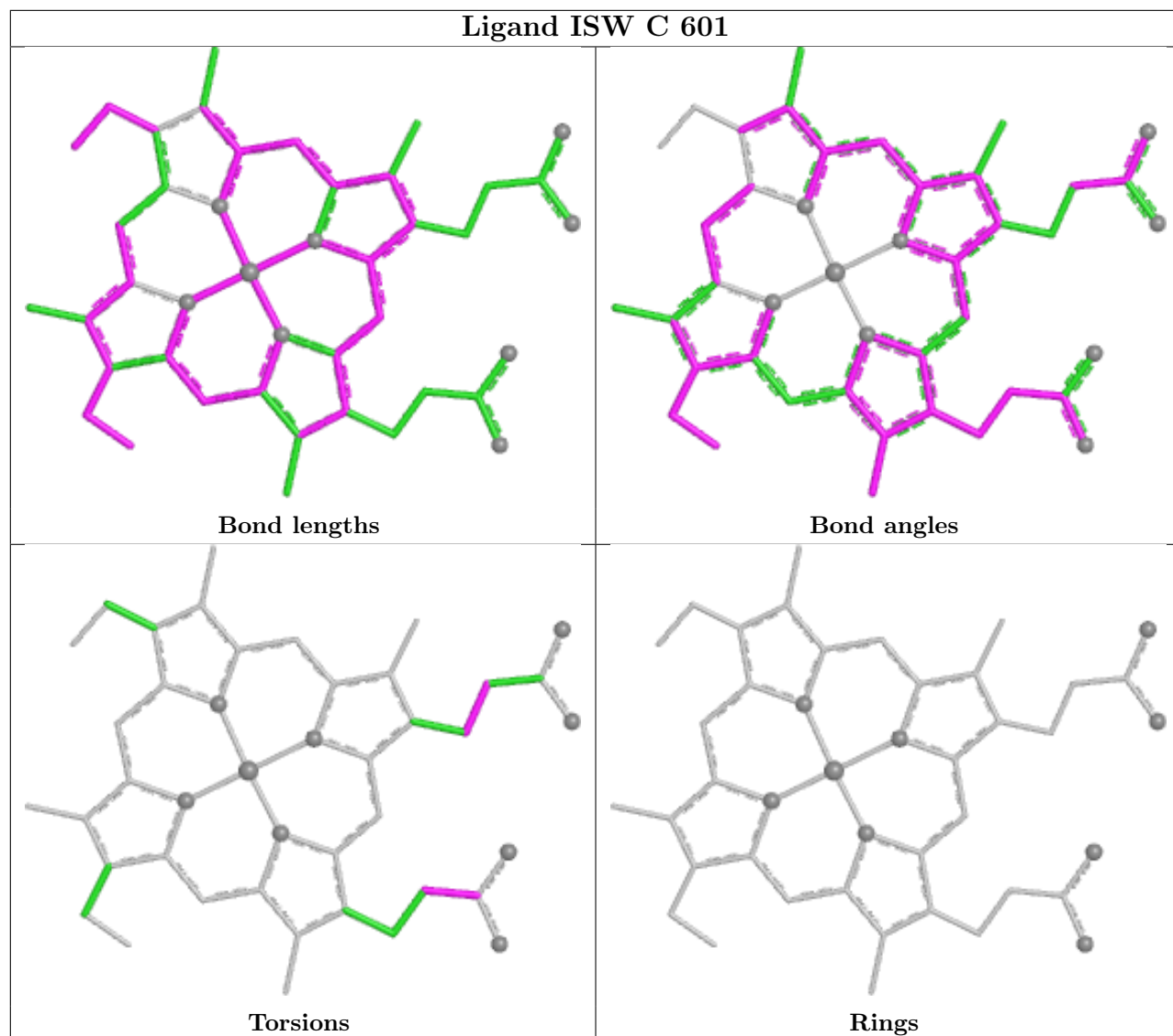
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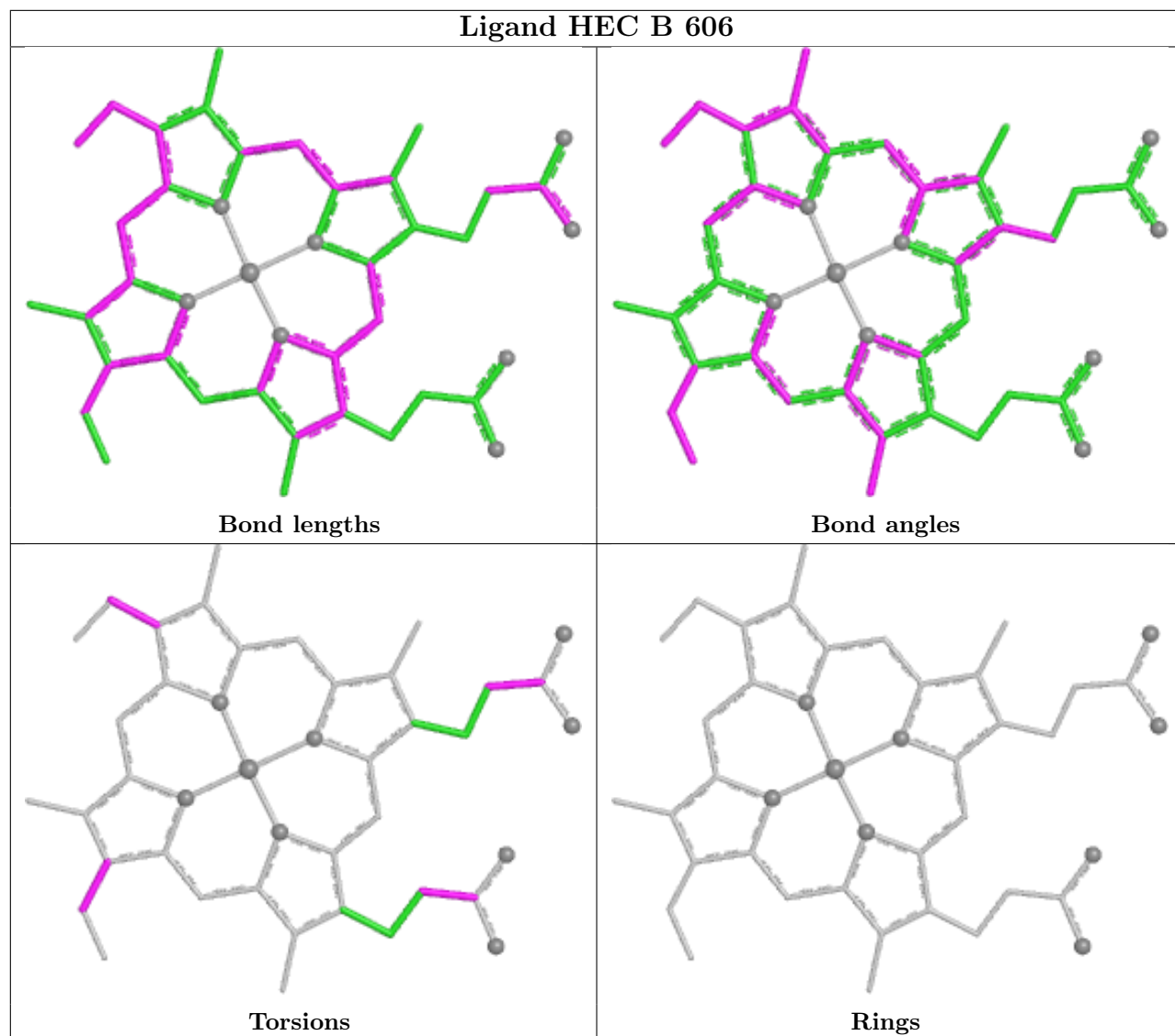
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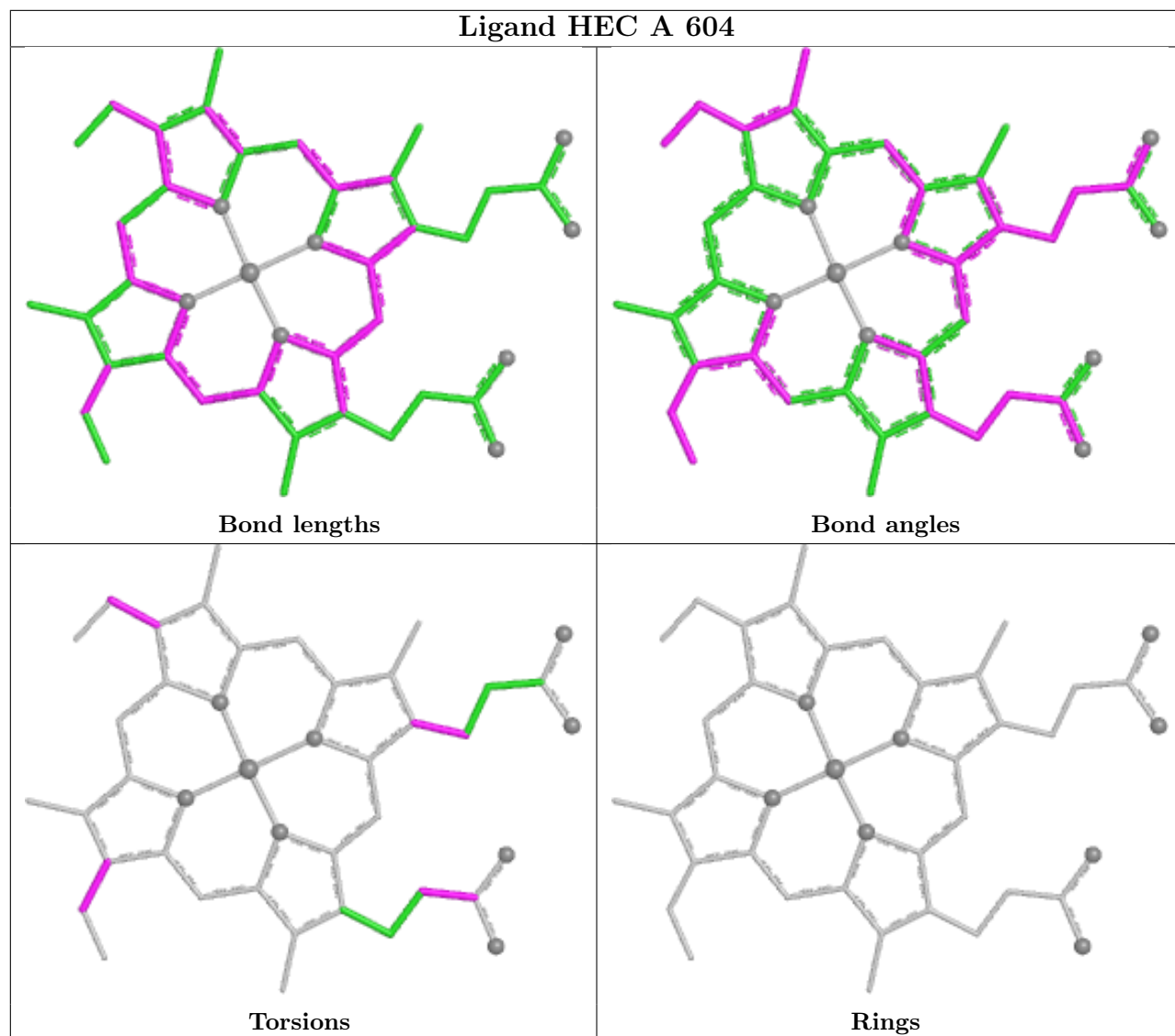
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	612	PEG	1	0
3	A	602	HEC	1	0
4	A	608	ISW	10	0
7	C	617	EDO	2	0
5	A	613	PEG	3	0
3	A	603	HEC	1	0
4	B	608	ISW	10	0
3	B	602	HEC	3	0
3	A	605	HEC	4	0
3	B	605	HEC	3	0
3	C	606	HEC	5	0
9	B	614	PG4	1	0
7	A	617	EDO	2	0
3	C	602	HEC	4	0
3	C	603	HEC	1	0
7	C	616	EDO	1	0
5	A	614	PEG	2	0
3	C	605	HEC	2	0
3	C	608	HEC	2	0
5	F	102	PEG	1	0
5	C	610	PEG	2	0
6	C	614	PGE	4	0
3	B	603	HEC	4	0
3	A	601	HEC	1	0

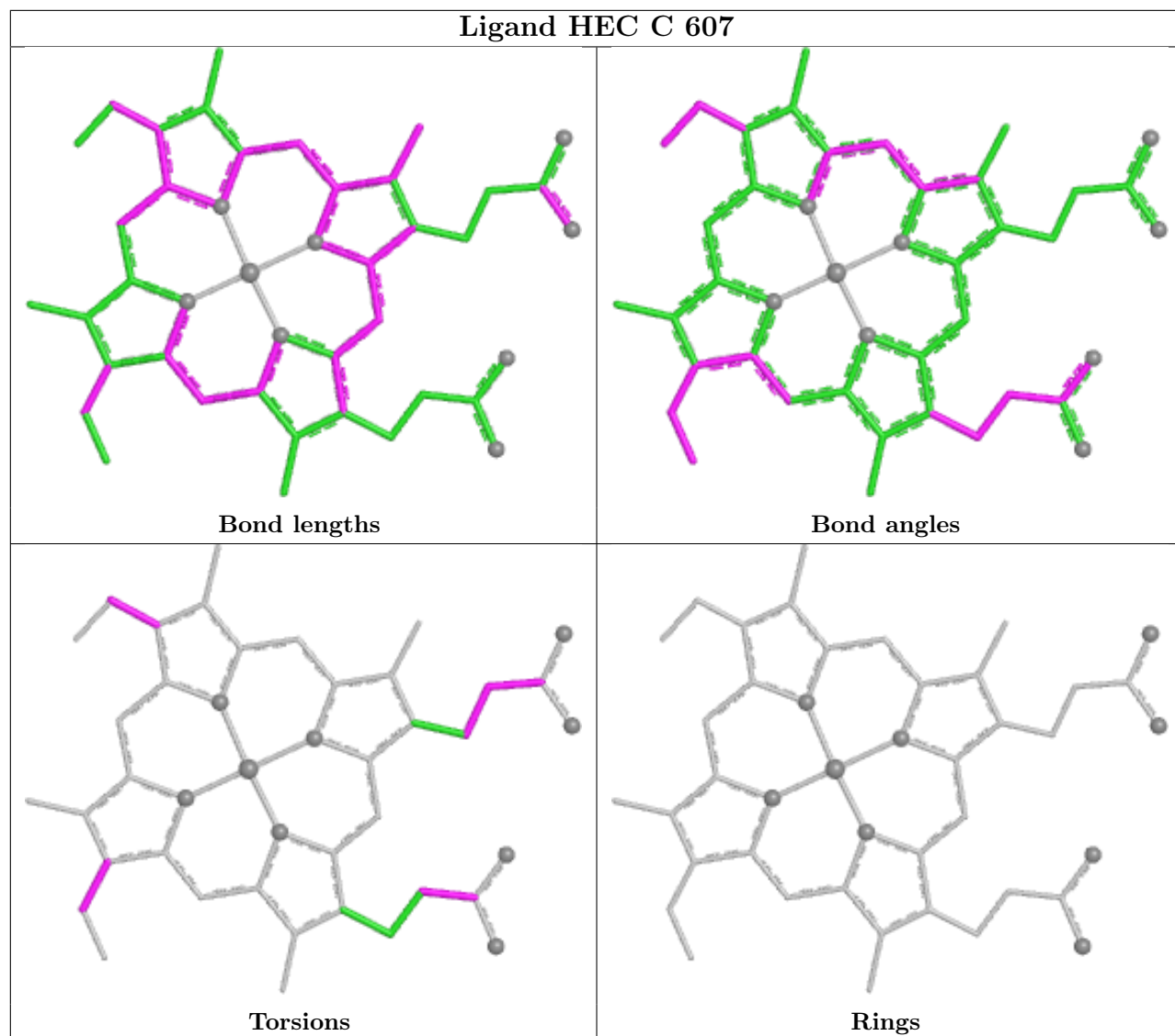
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

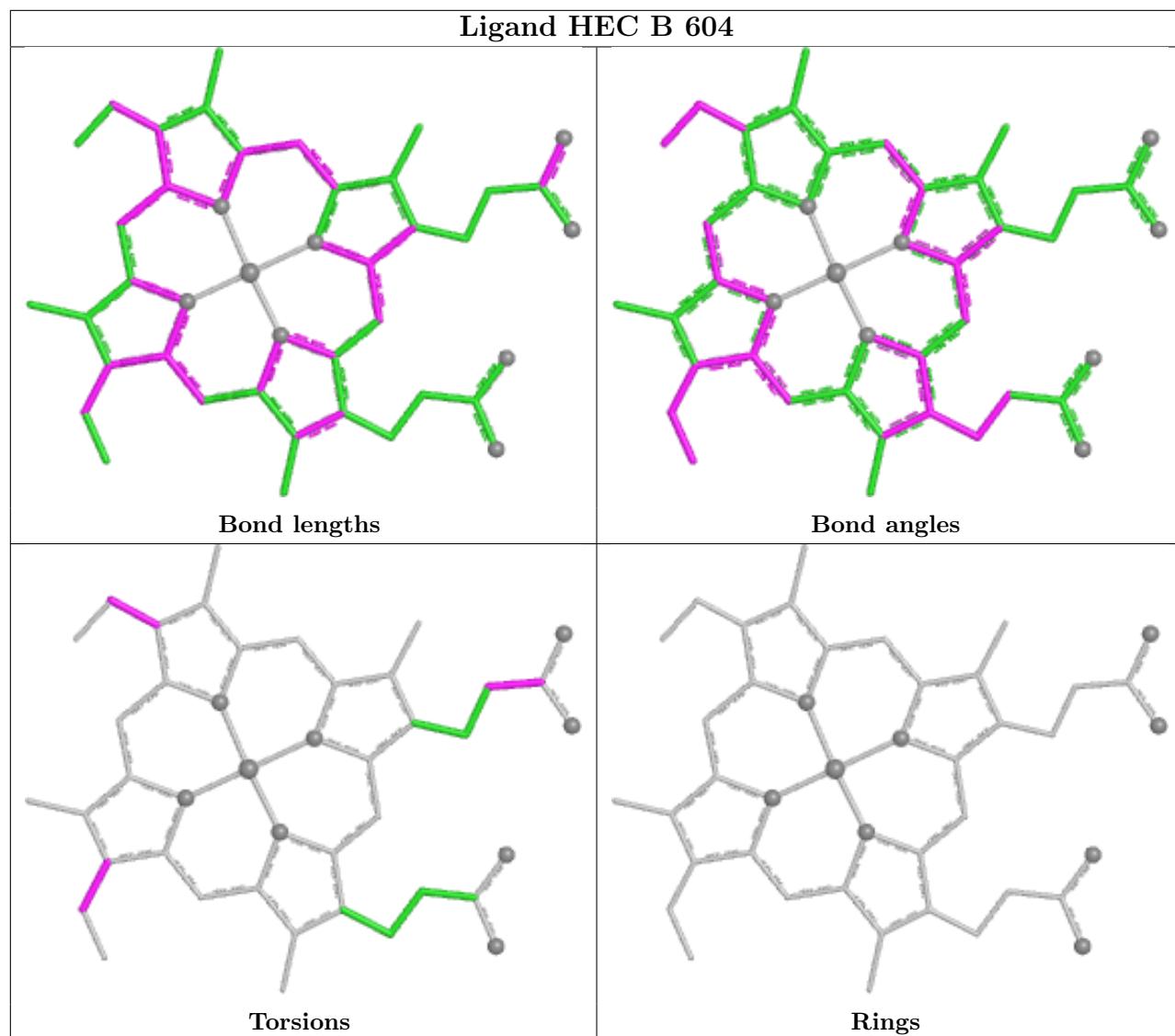


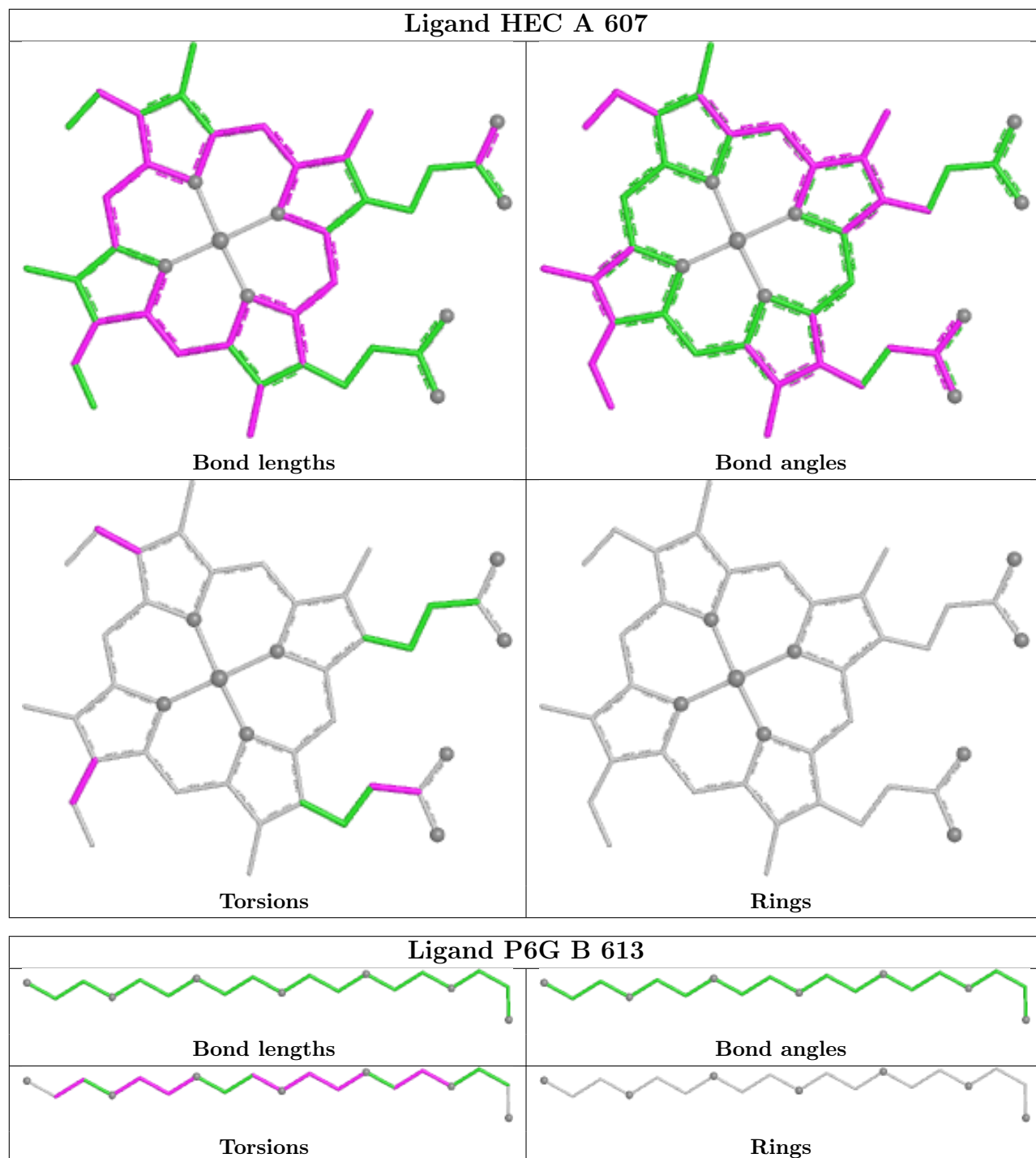


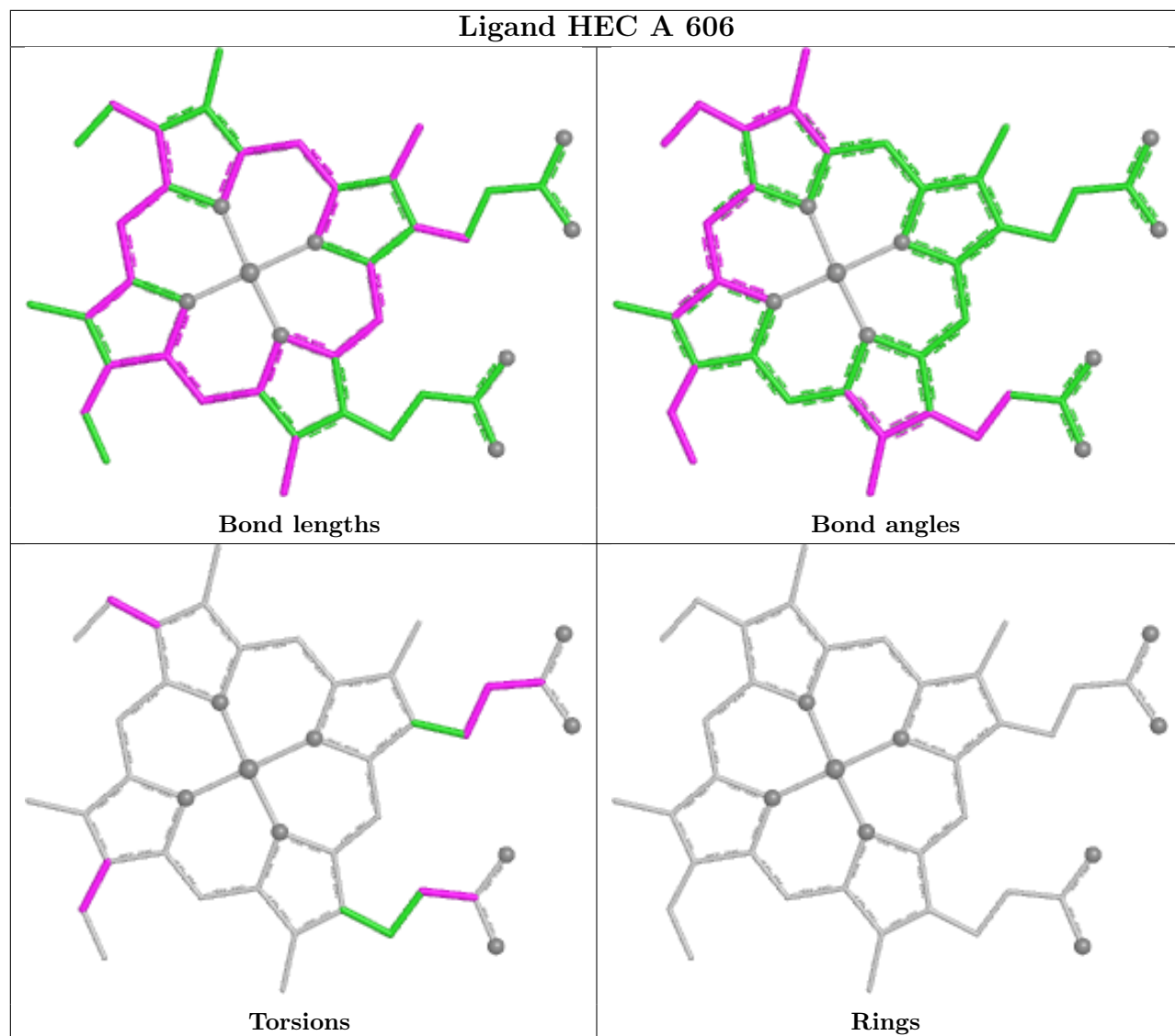


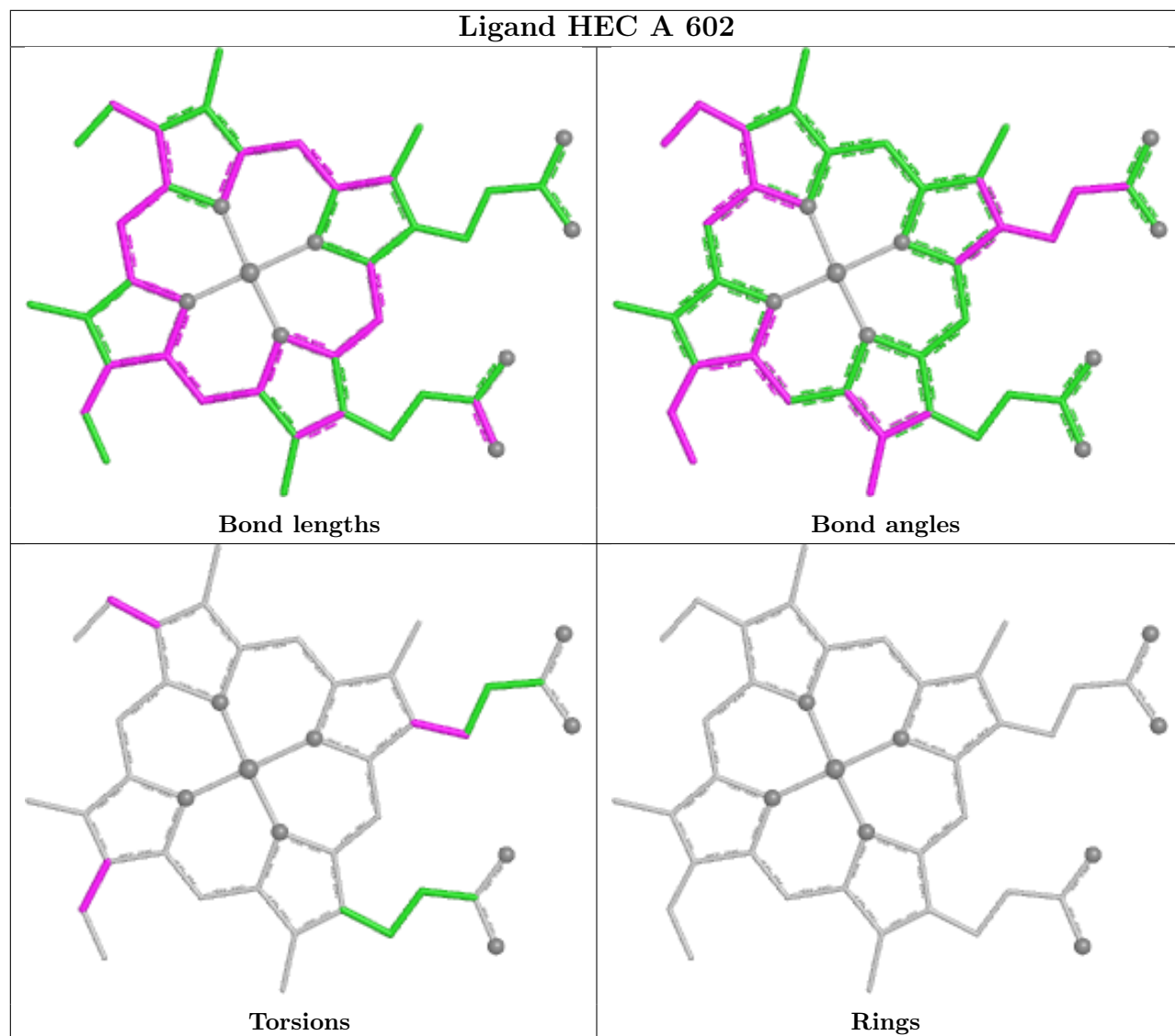


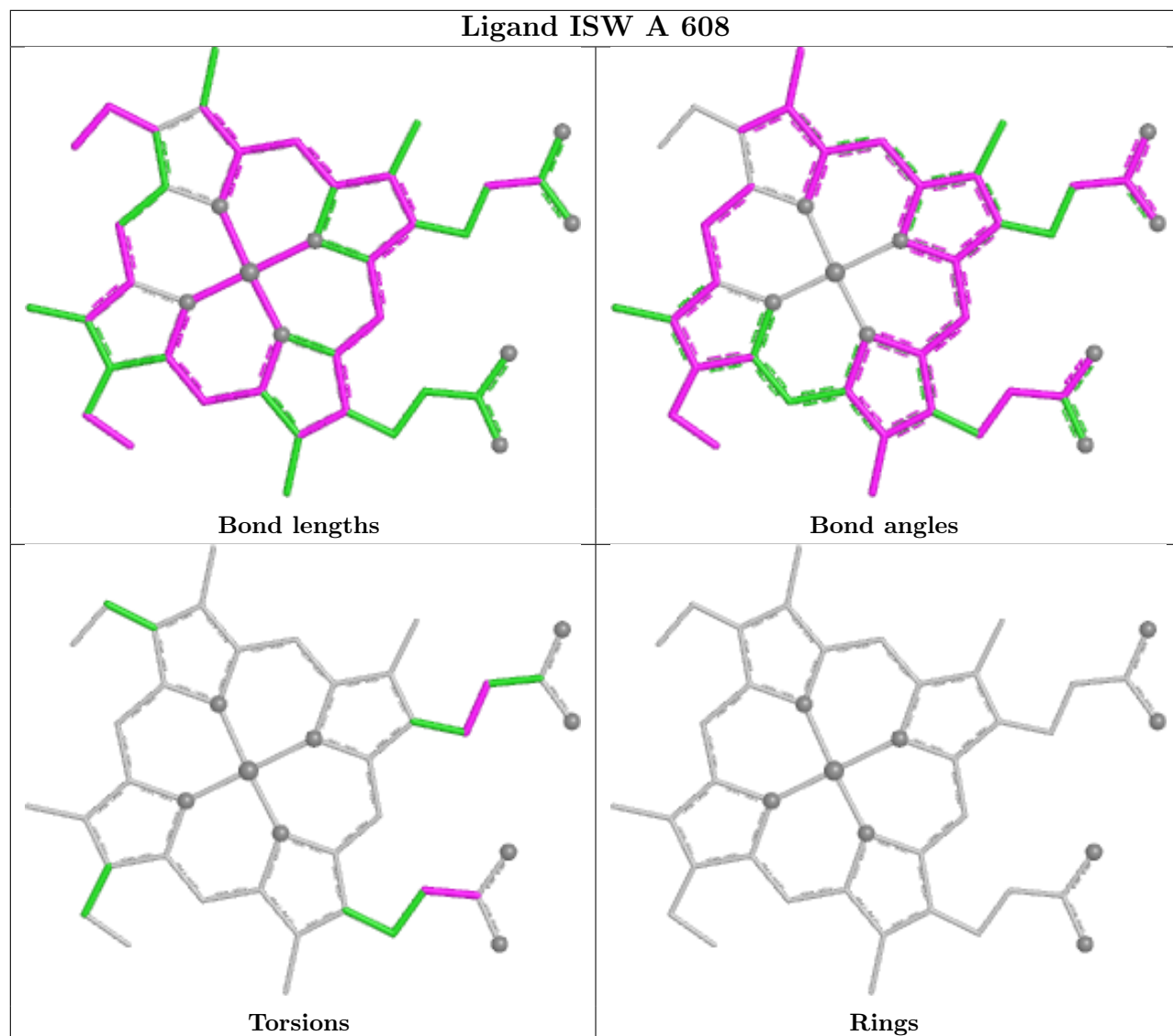


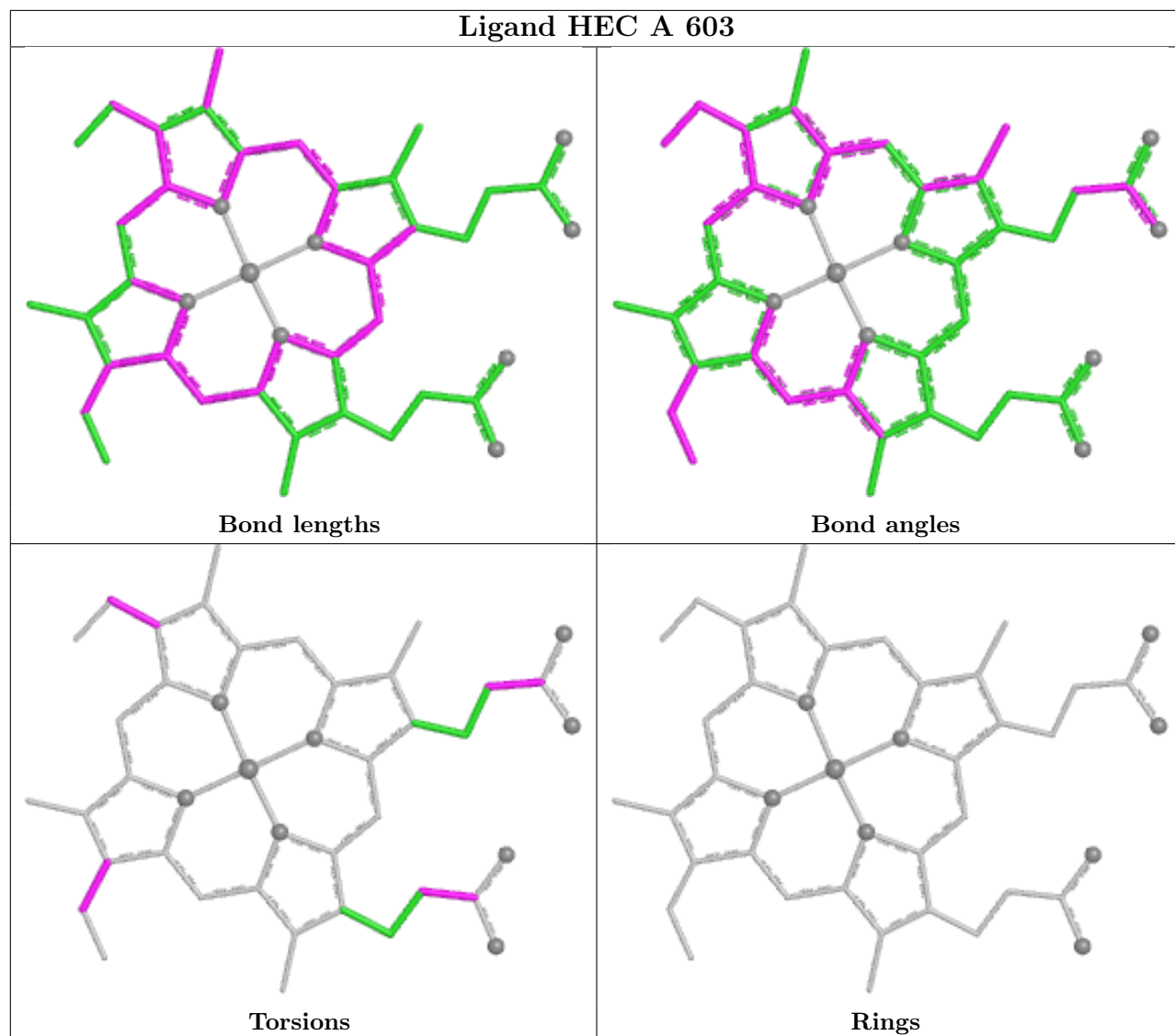


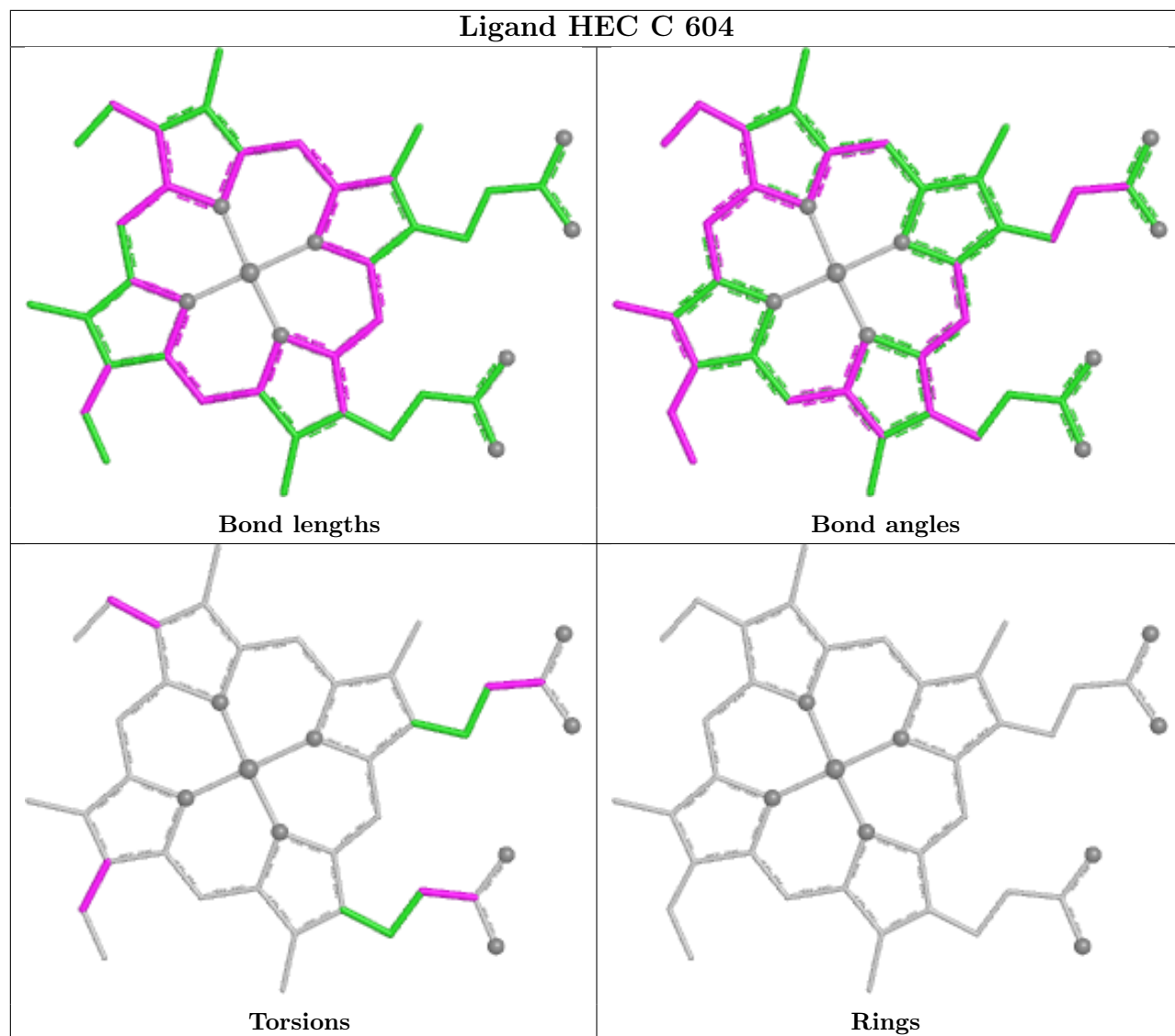


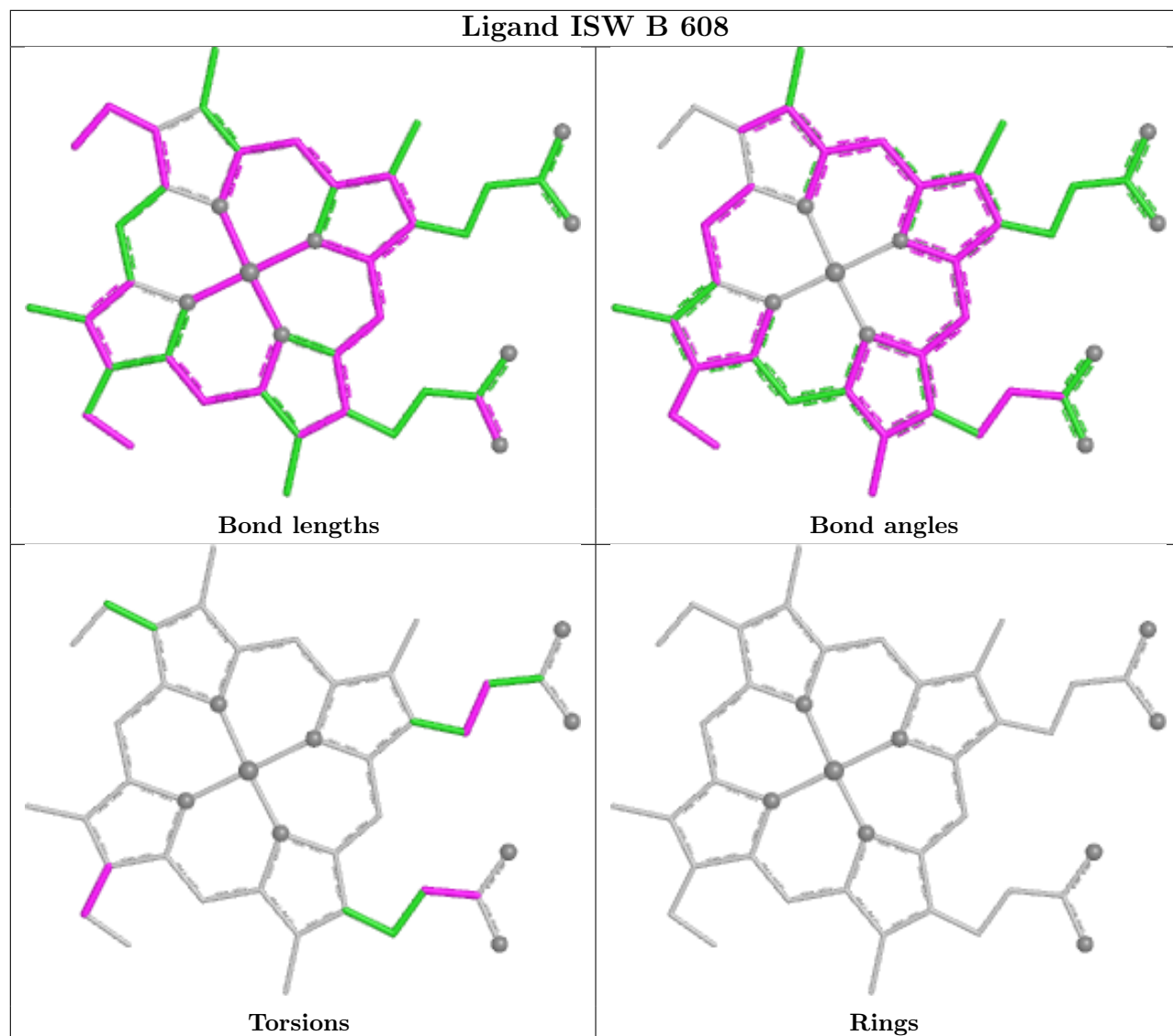


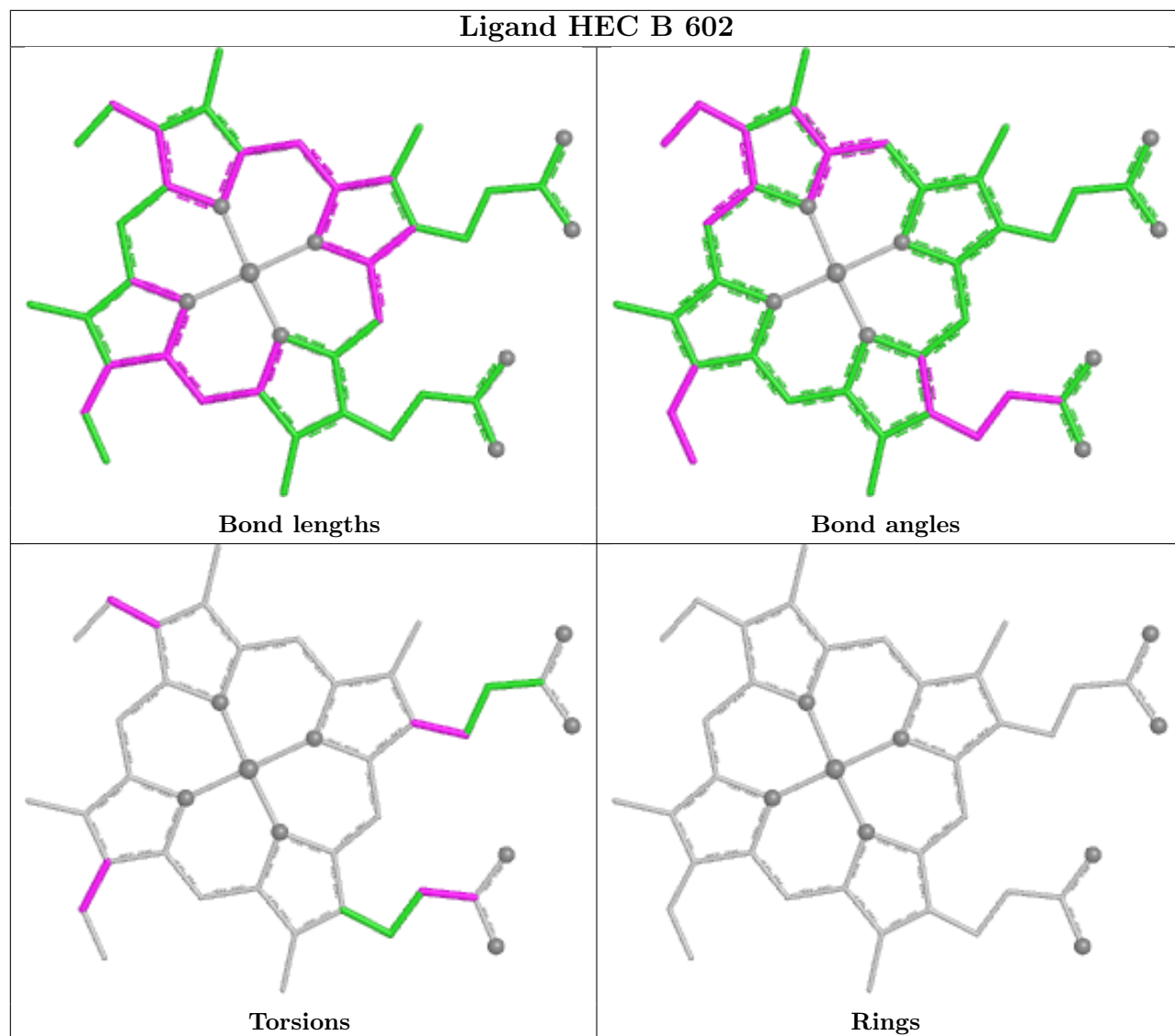


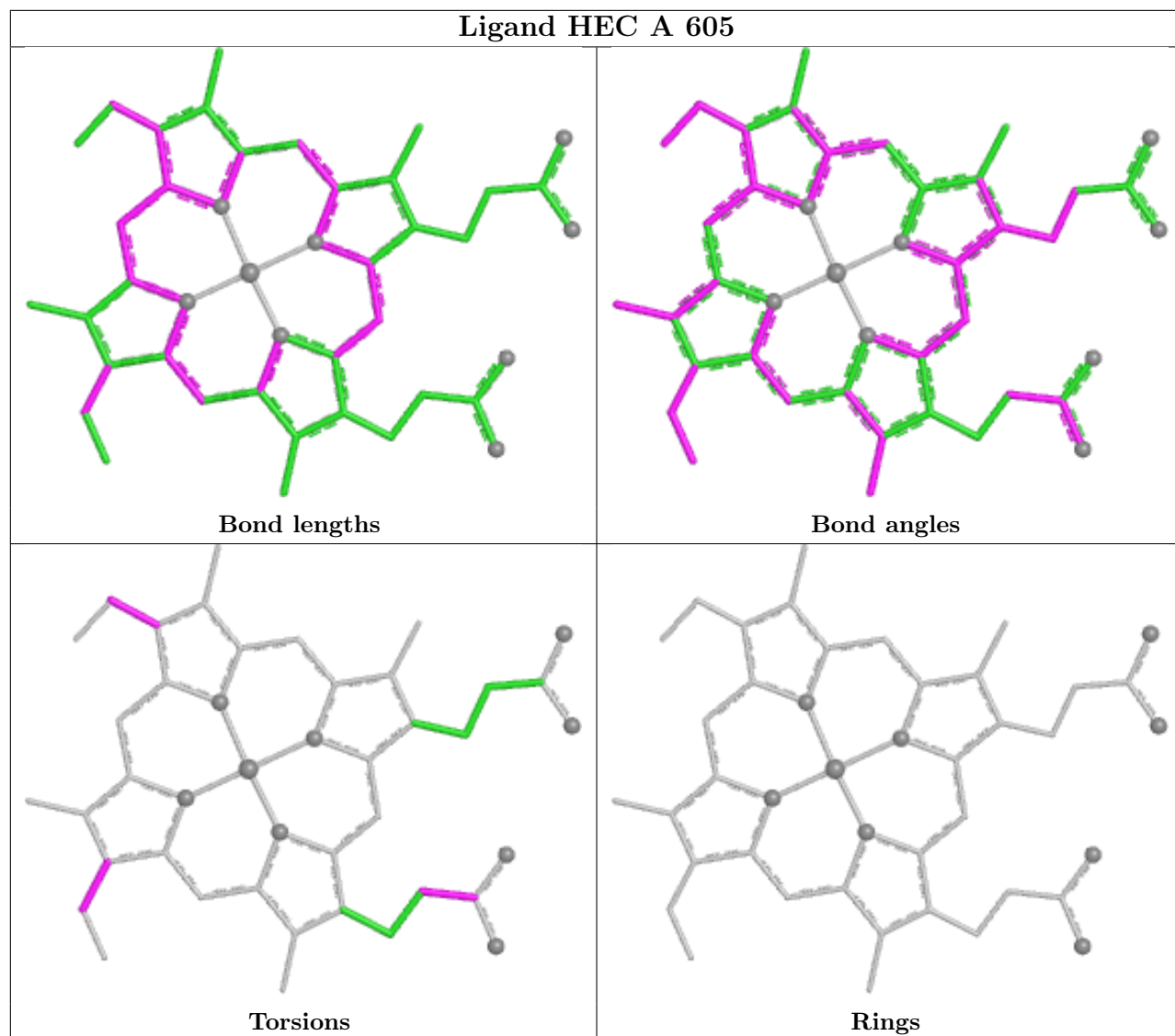


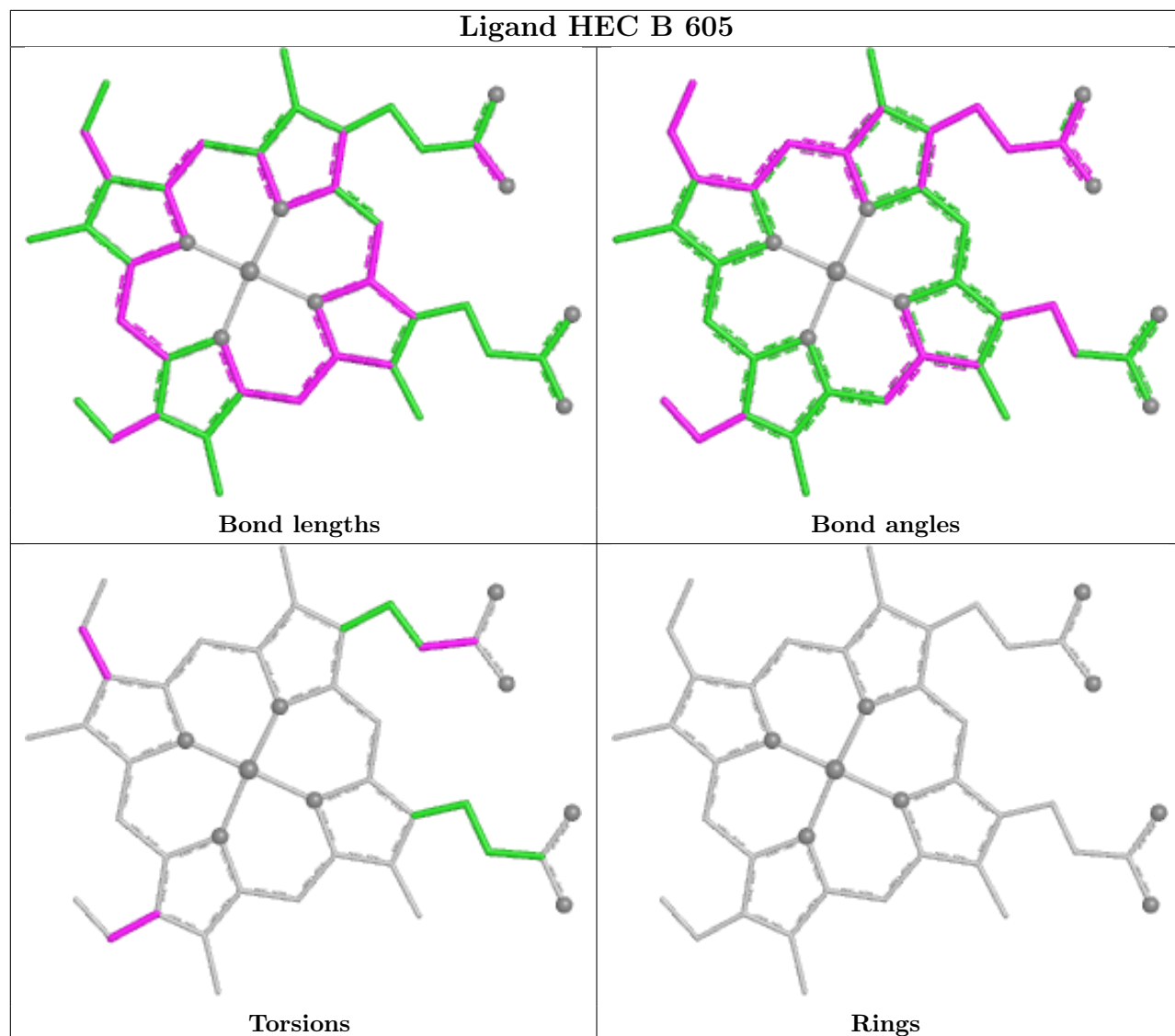


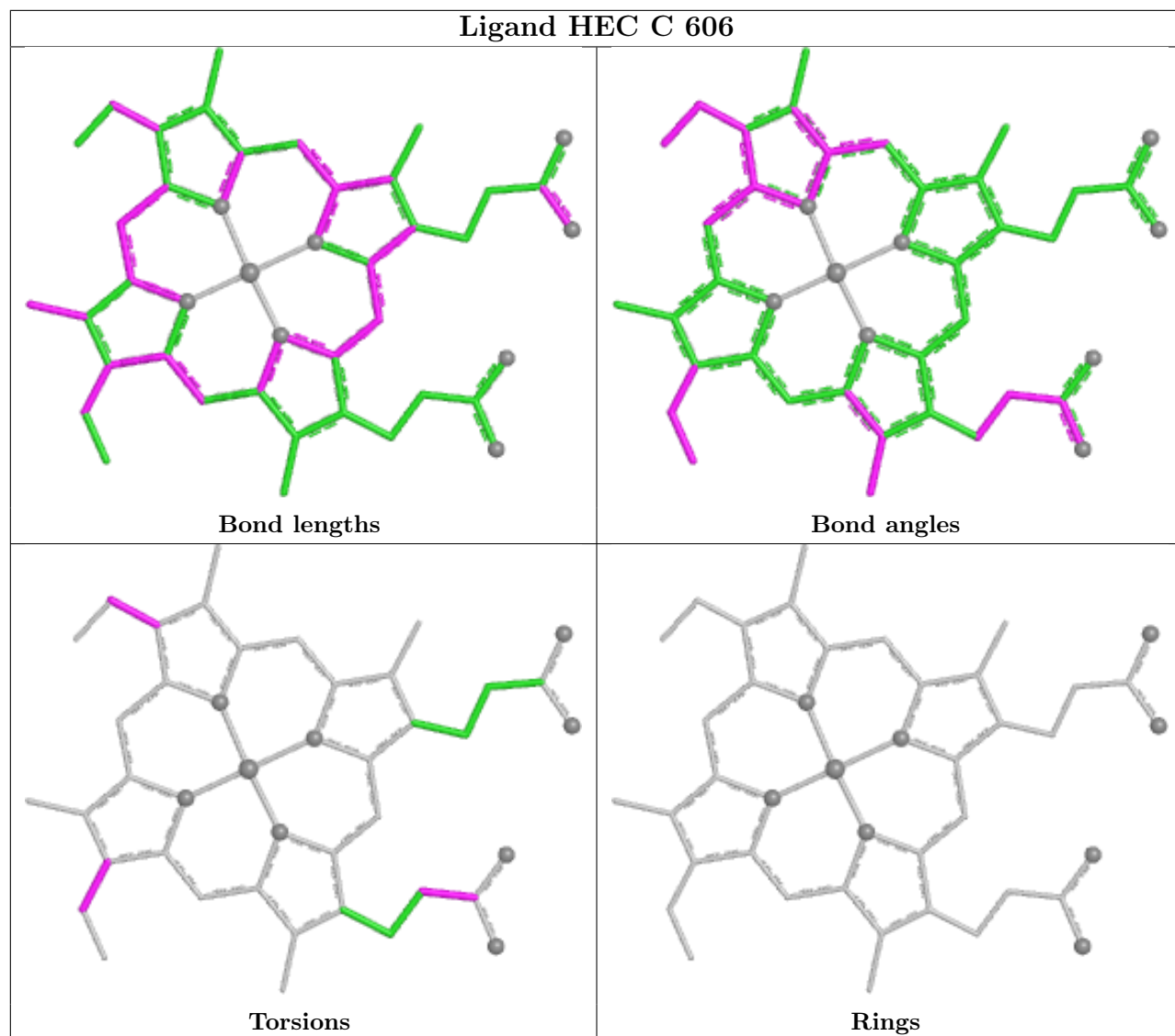


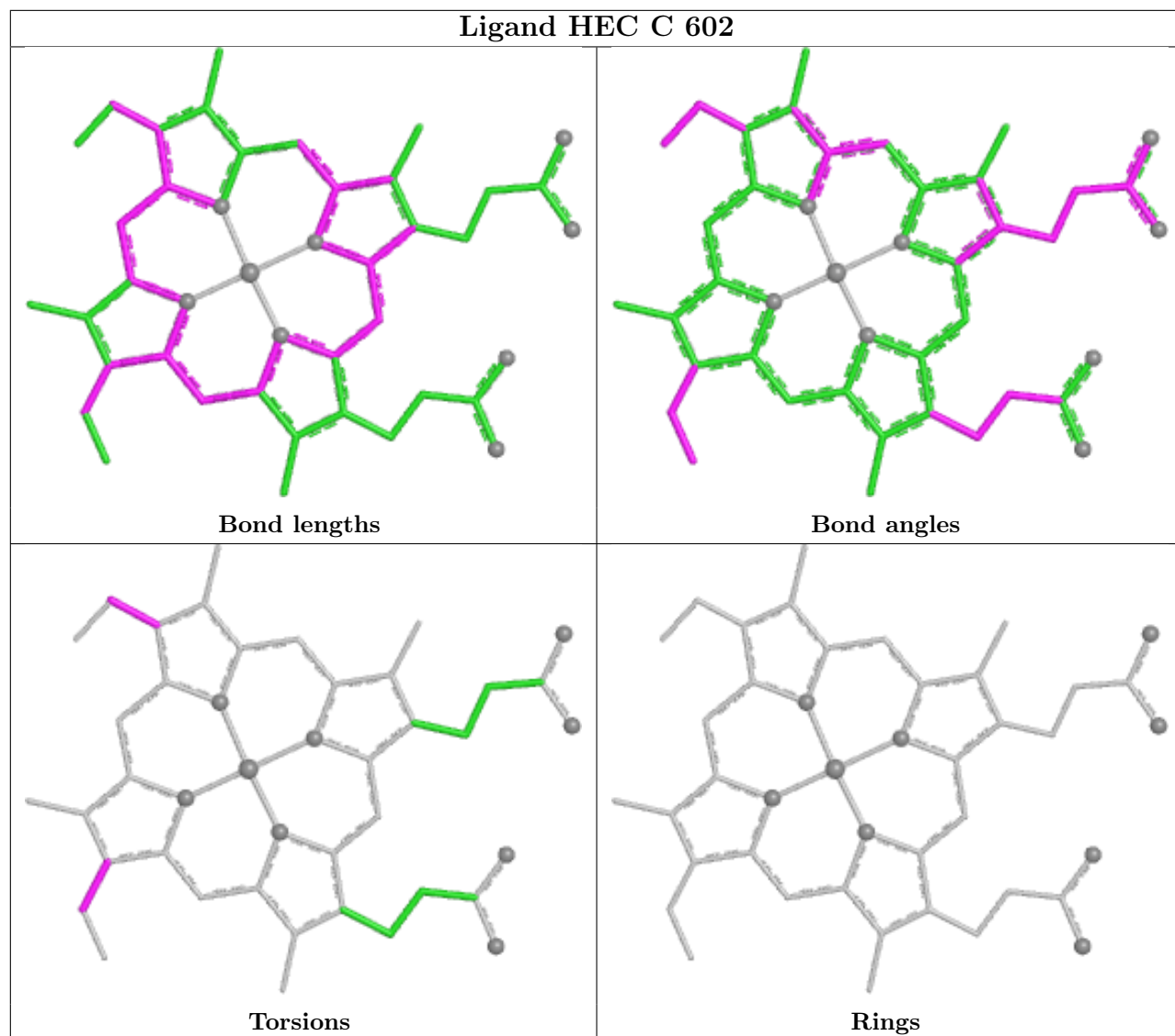


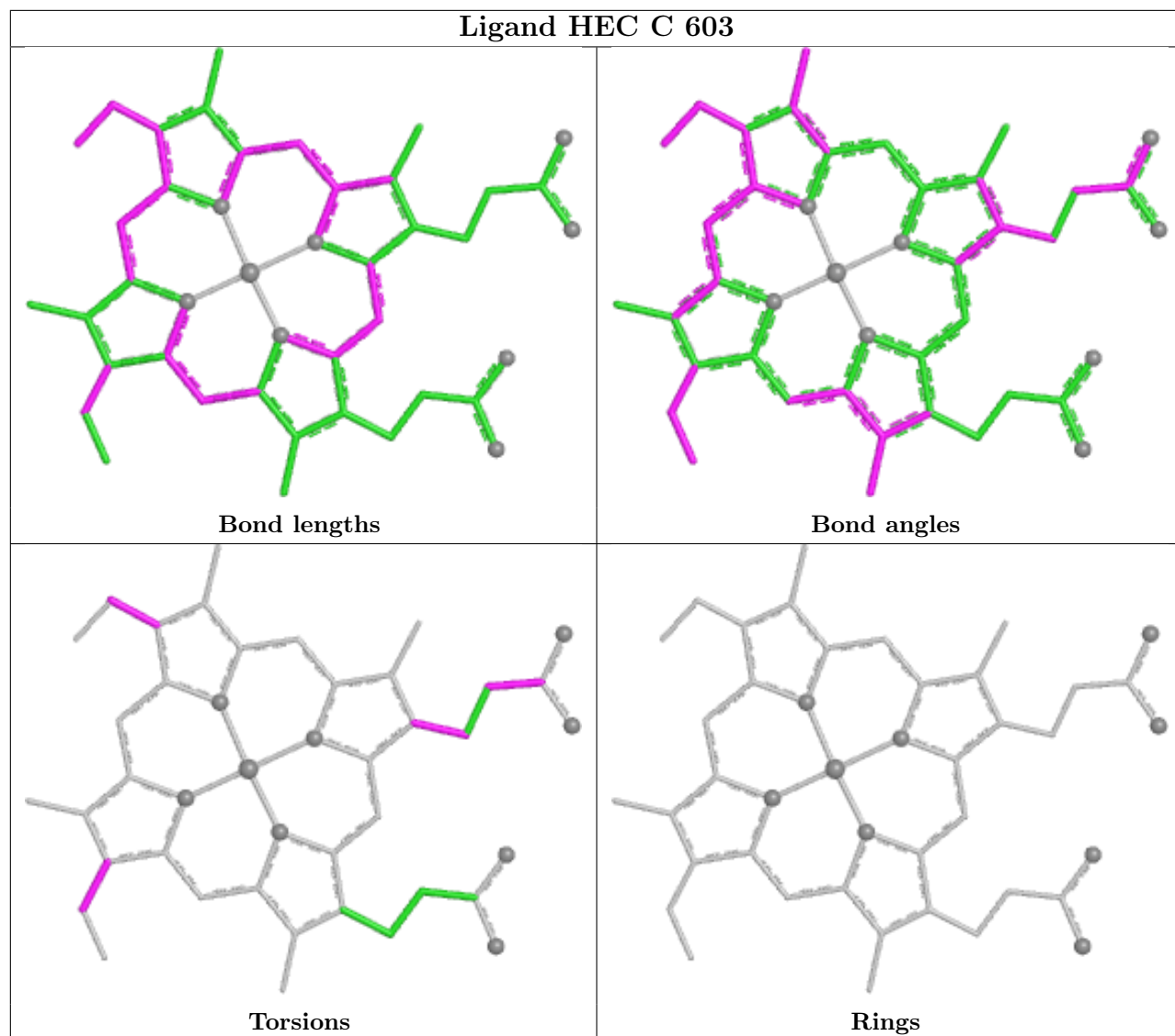


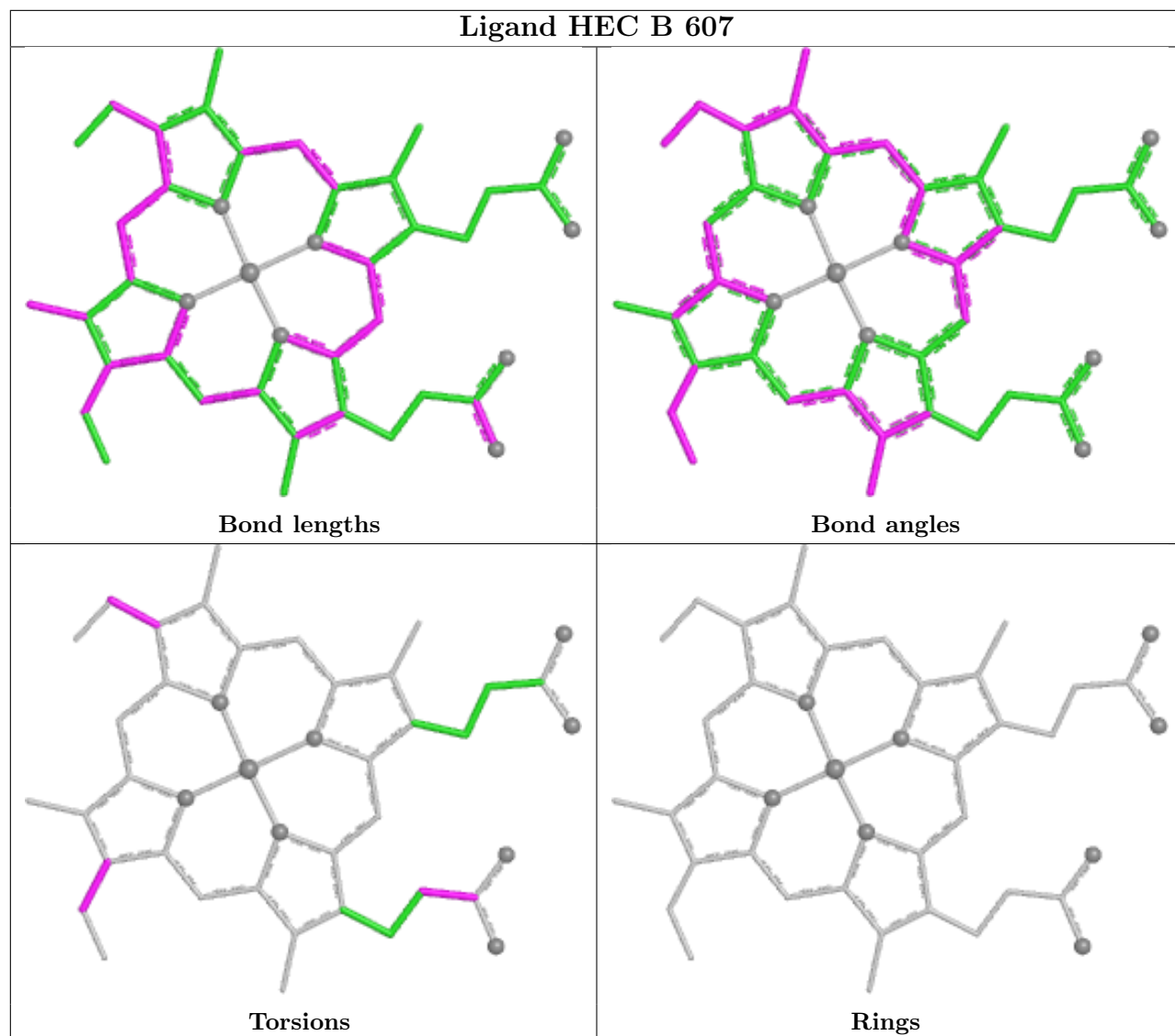


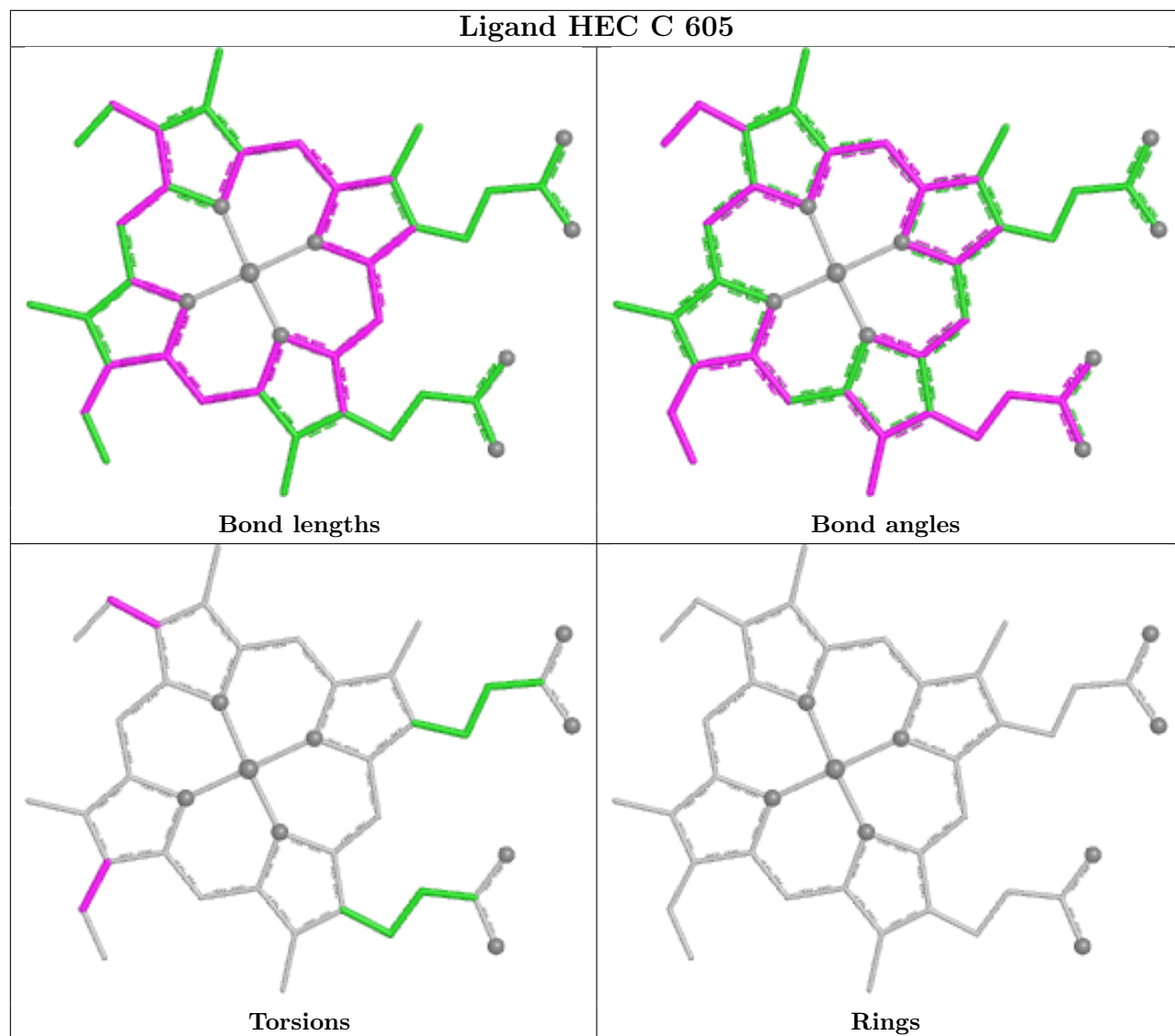


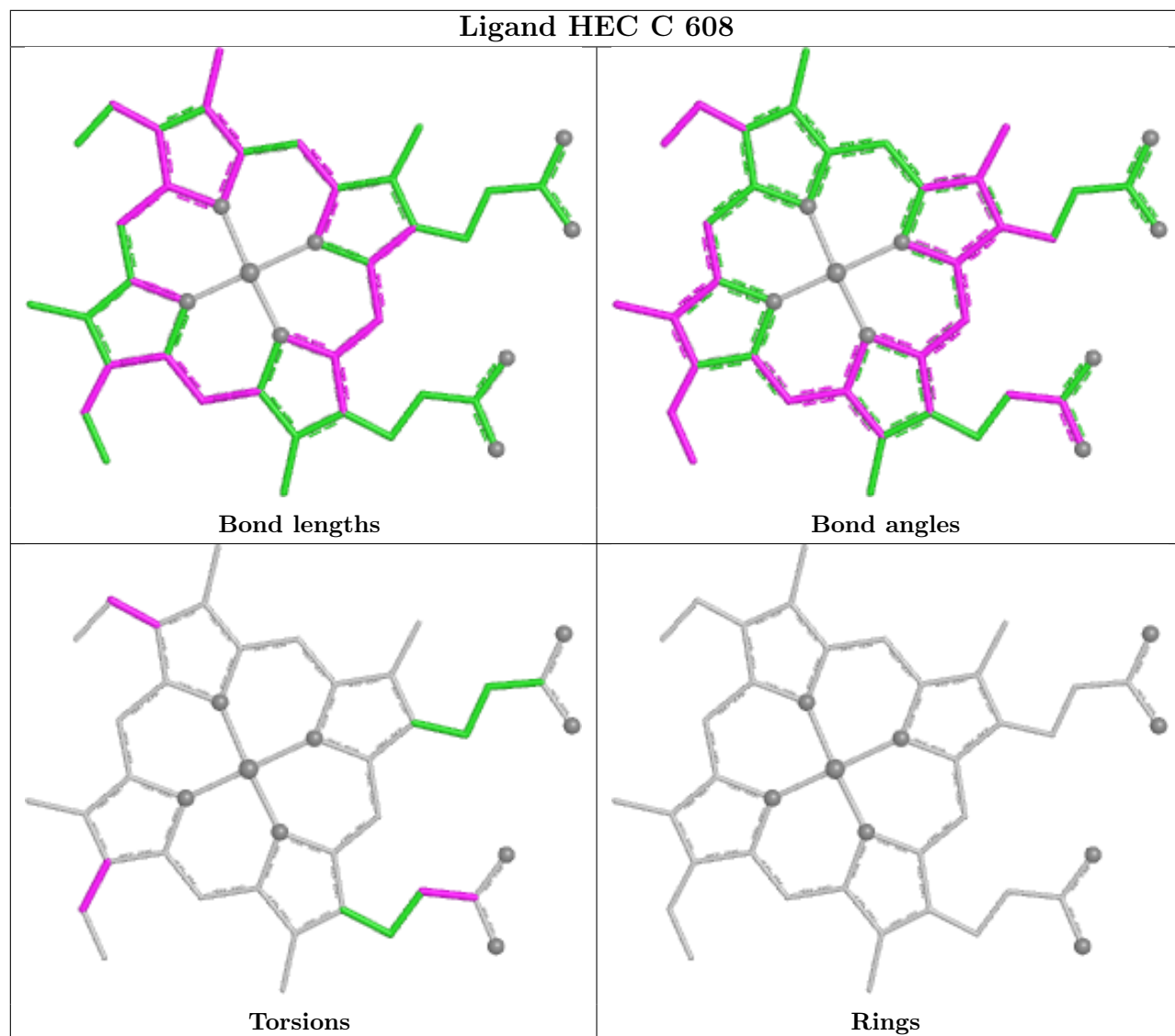


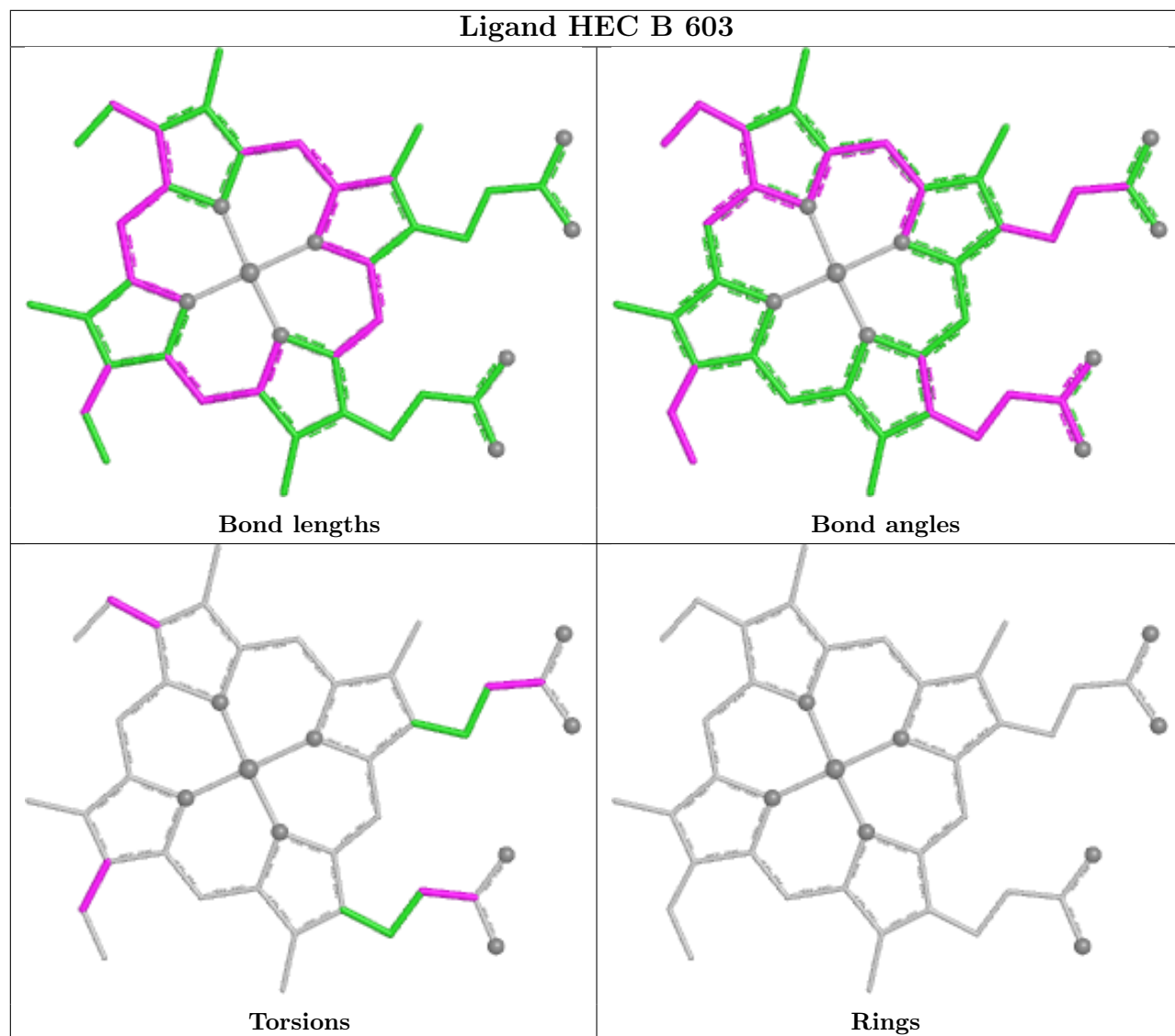


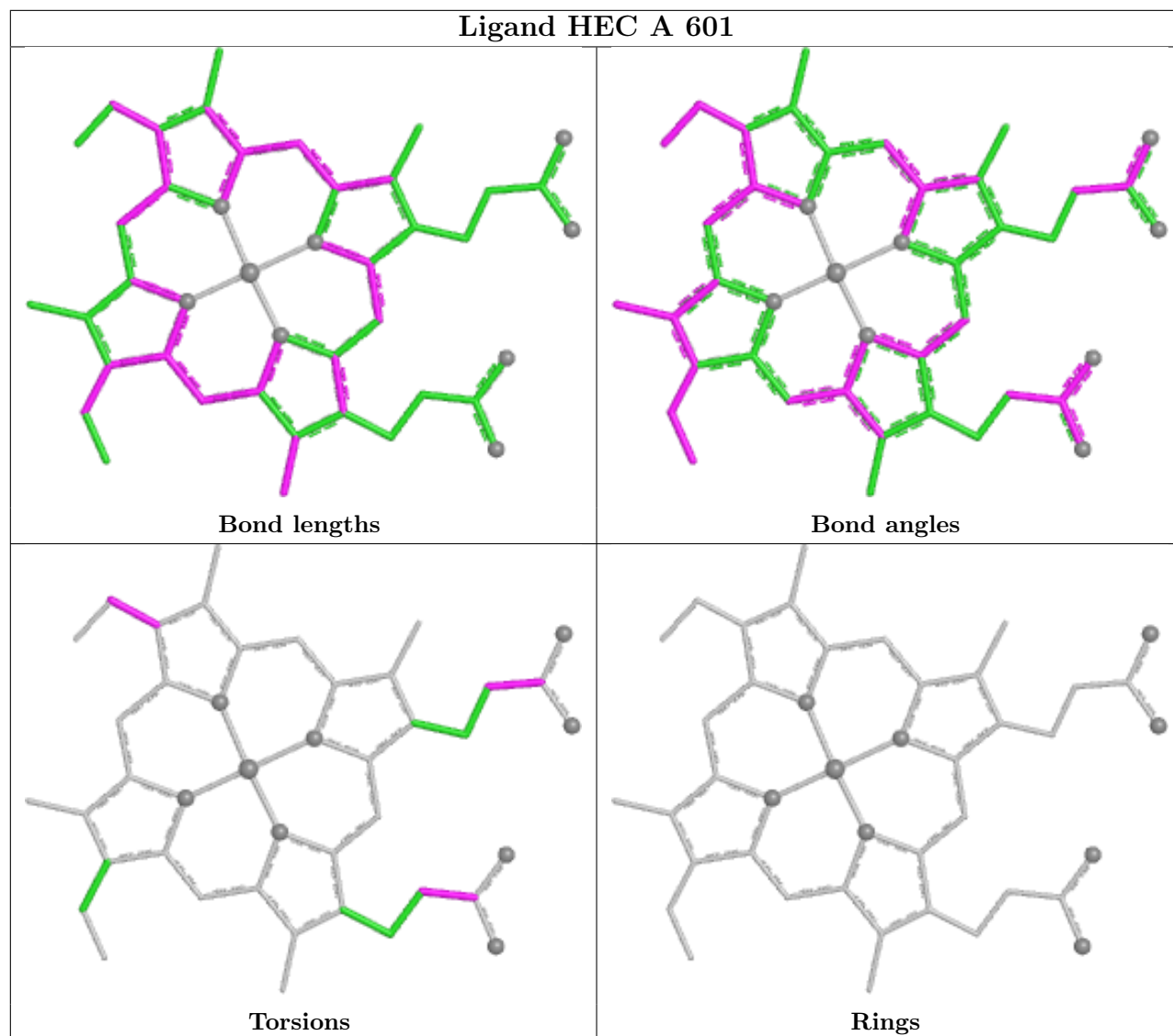












5.7 Other polymers [i](#)

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	502/546 (91%)	-0.36	2 (0%) 88 90	16, 33, 52, 88	1 (0%)
1	B	502/546 (91%)	-0.34	1 (0%) 91 92	18, 34, 53, 80	0
1	C	502/546 (91%)	-0.30	1 (0%) 91 92	18, 35, 55, 82	0
2	D	49/69 (71%)	0.90	5 (10%) 12 12	39, 58, 89, 96	0
2	E	49/69 (71%)	1.12	9 (18%) 3 3	36, 64, 94, 101	0
2	F	49/69 (71%)	0.42	4 (8%) 17 18	35, 48, 72, 84	0
All	All	1653/1845 (89%)	-0.23	22 (1%) 75 77	16, 35, 63, 101	1 (0%)

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	501	LEU	4.3
2	E	54	VAL	4.1
2	E	50	ILE	3.3
2	D	54	VAL	3.2
2	F	53	LEU	3.1

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 [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
10	NO3	F	101	4/4	0.78	0.13	70,71,71,71	0
10	NO3	B	618	4/4	0.81	0.16	67,68,68,69	0
7	EDO	B	616	4/4	0.83	0.16	60,61,62,63	0
5	PEG	A	614	7/7	0.83	0.19	54,61,63,64	0
7	EDO	A	617	4/4	0.83	0.17	63,63,63,65	0
6	PGE	A	615	10/10	0.84	0.14	52,55,62,62	0
7	EDO	A	616	4/4	0.84	0.15	44,46,46,50	0
10	NO3	C	619	4/4	0.84	0.10	72,72,72,72	0
5	PEG	B	612	7/7	0.84	0.18	63,68,69,71	0
7	EDO	C	618	4/4	0.86	0.14	51,52,53,55	0
8	P6G	B	613	19/19	0.87	0.14	54,60,64,65	0
5	PEG	C	611	7/7	0.87	0.14	54,60,63,64	0
7	EDO	B	620	4/4	0.89	0.14	46,51,52,55	0
7	EDO	B	621	4/4	0.89	0.14	51,52,52,53	0
5	PEG	B	610	7/7	0.89	0.13	58,59,63,66	0
5	PEG	A	613	7/7	0.89	0.13	56,57,58,60	0
5	PEG	A	611	7/7	0.89	0.14	53,55,57,59	0
7	EDO	B	615	4/4	0.89	0.13	50,51,51,55	0
5	PEG	C	622	7/7	0.89	0.12	43,48,50,51	0
5	PEG	F	102	7/7	0.90	0.11	50,51,54,56	0
9	PG4	B	614	13/13	0.90	0.13	43,50,64,65	0
5	PEG	B	611	7/7	0.90	0.12	60,61,61,62	0
7	EDO	C	616	4/4	0.90	0.11	40,45,46,50	0
5	PEG	C	610	7/7	0.90	0.14	54,58,61,63	0
5	PEG	A	609	7/7	0.91	0.10	44,45,51,51	0
6	PGE	C	614	10/10	0.91	0.11	49,52,54,57	0
5	PEG	C	613	7/7	0.91	0.11	50,55,60,61	0
5	PEG	A	610	7/7	0.92	0.11	56,57,64,67	0
7	EDO	C	615	4/4	0.92	0.15	50,51,52,55	0
10	NO3	B	617	4/4	0.92	0.09	51,53,54,56	0
7	EDO	A	619	4/4	0.93	0.09	44,45,48,49	0
5	PEG	C	612	7/7	0.93	0.09	54,56,58,60	0
7	EDO	C	620	4/4	0.93	0.10	48,48,49,51	0
7	EDO	C	621	4/4	0.93	0.08	41,42,44,45	0
5	PEG	A	612	7/7	0.93	0.10	56,58,61,64	0
5	PEG	B	609	7/7	0.94	0.09	46,48,52,52	0
7	EDO	B	619	4/4	0.94	0.08	45,47,49,50	0

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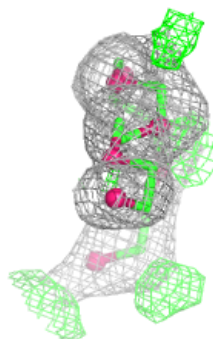
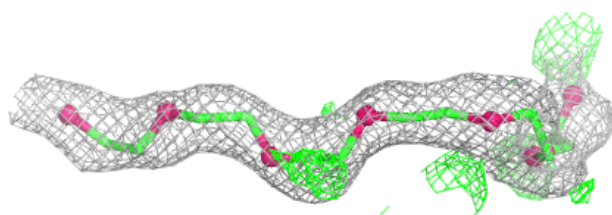
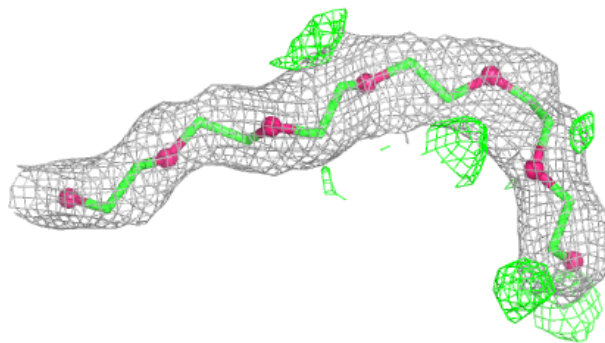
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	EDO	C	617	4/4	0.94	0.08	42,45,46,49	0
5	PEG	C	609	7/7	0.95	0.09	55,59,59,61	0
7	EDO	A	618	4/4	0.95	0.08	42,46,46,52	0
4	ISW	B	608	43/43	0.96	0.08	22,34,51,56	0
4	ISW	C	601	43/43	0.96	0.09	20,32,47,50	0
4	ISW	A	608	43/43	0.96	0.08	21,32,46,47	0
3	HEC	A	607	43/43	0.98	0.05	20,24,30,32	0
3	HEC	B	601	43/43	0.98	0.07	26,34,43,48	0
3	HEC	B	602	43/43	0.98	0.05	21,26,31,33	0
3	HEC	B	603	43/43	0.98	0.06	23,29,33,35	0
3	HEC	C	602	43/43	0.98	0.06	25,34,39,43	0
3	HEC	C	603	43/43	0.98	0.06	18,25,28,31	0
3	HEC	C	604	43/43	0.98	0.05	20,25,29,31	0
3	HEC	A	601	43/43	0.98	0.06	21,29,33,44	0
3	HEC	A	602	43/43	0.98	0.06	20,24,29,34	0
3	HEC	A	603	43/43	0.98	0.06	20,28,32,34	0
3	HEC	C	608	43/43	0.99	0.05	16,21,32,33	0
3	HEC	B	604	43/43	0.99	0.05	15,24,28,33	0
3	HEC	B	605	43/43	0.99	0.06	17,24,30,36	0
3	HEC	B	606	43/43	0.99	0.05	15,21,25,26	0
3	HEC	B	607	43/43	0.99	0.05	15,21,31,36	0
3	HEC	A	605	43/43	0.99	0.05	17,23,37,39	0
3	HEC	A	606	43/43	0.99	0.05	17,23,29,30	0
3	HEC	A	604	43/43	0.99	0.05	20,25,31,36	0
3	HEC	C	605	43/43	0.99	0.05	17,25,30,32	0
3	HEC	C	606	43/43	0.99	0.05	17,22,33,44	0
3	HEC	C	607	43/43	0.99	0.05	16,22,28,32	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.

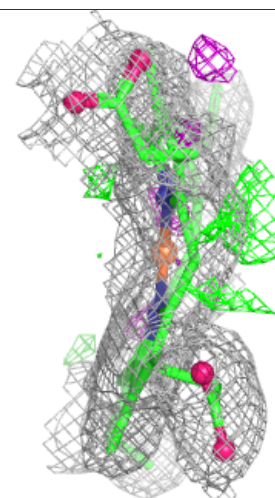
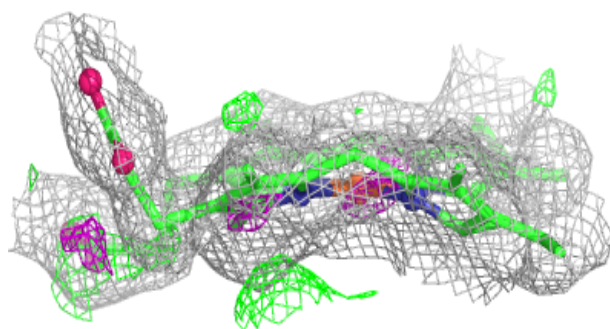
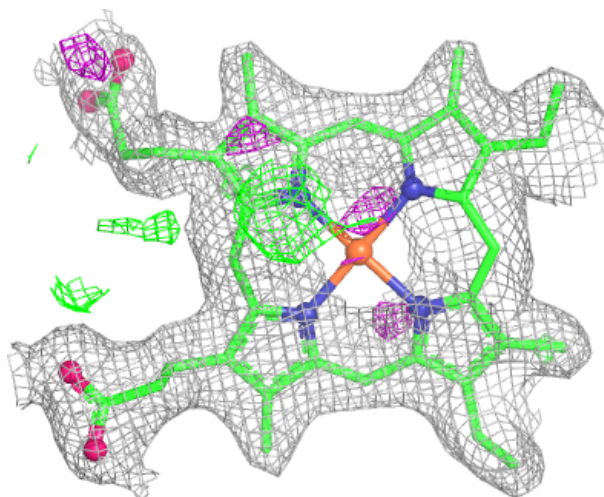
Electron density around P6G B 613:

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



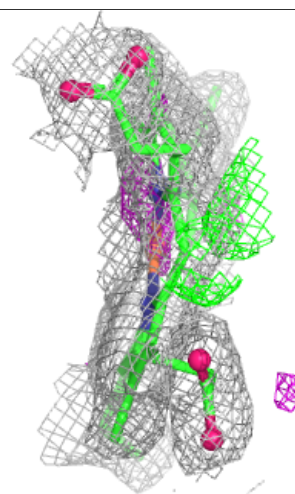
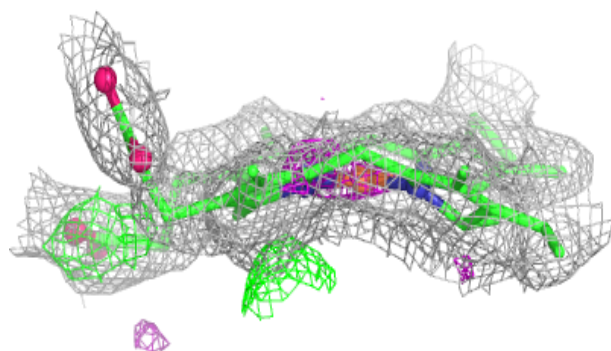
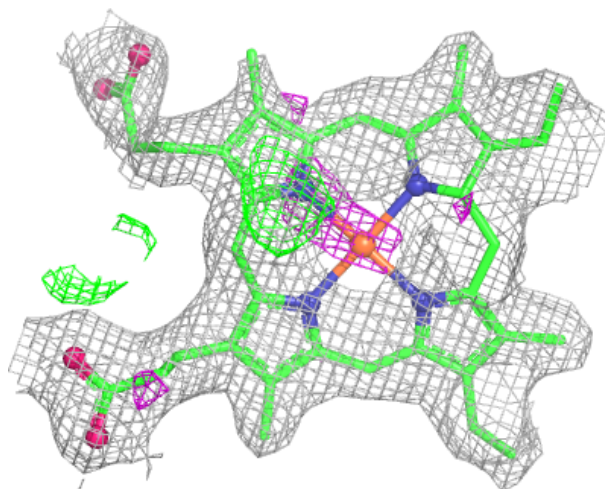
Electron density around ISW B 608:

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



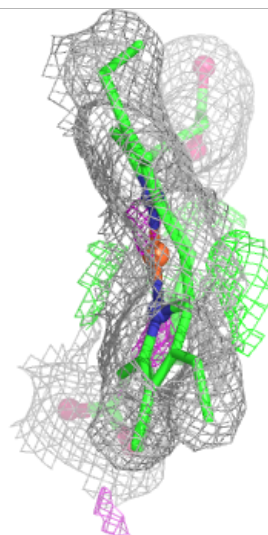
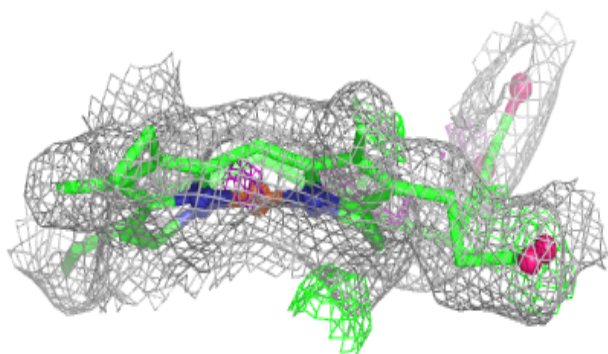
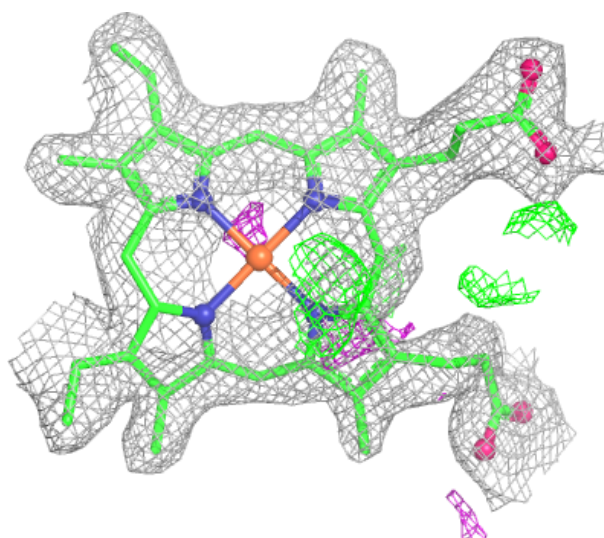
Electron density around ISW C 601:

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



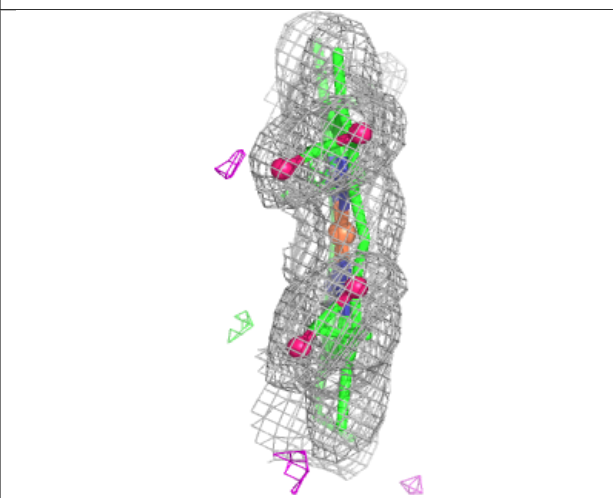
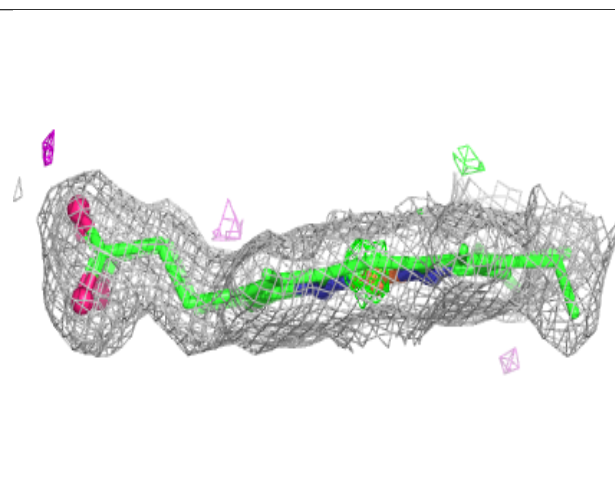
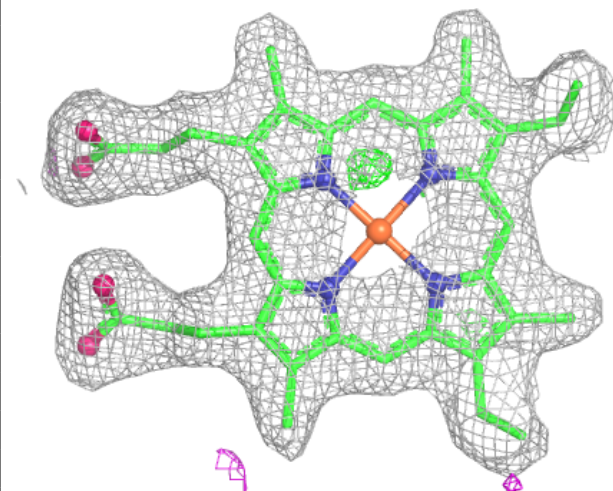
Electron density around ISW A 608:

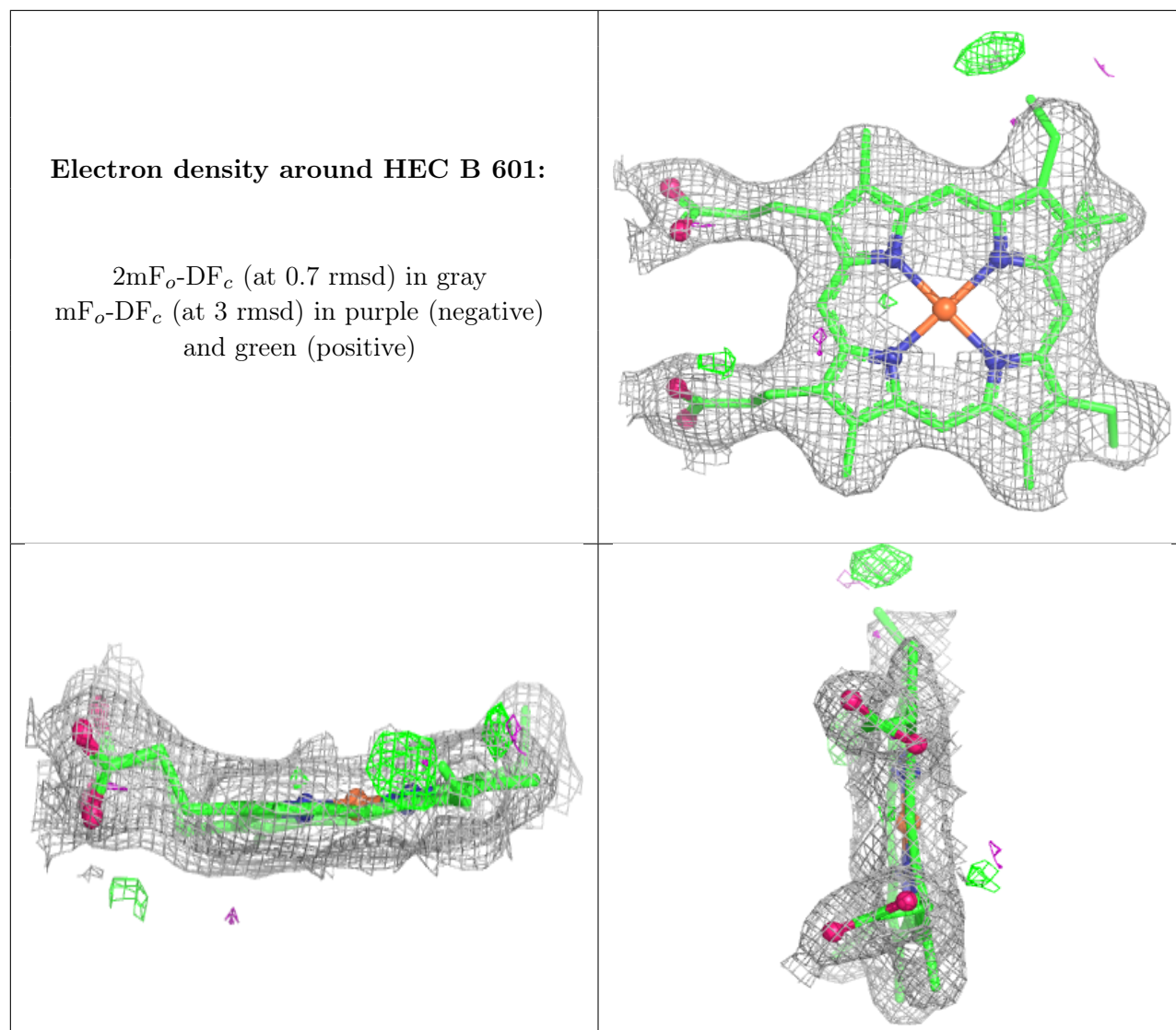
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
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and green (positive)



Electron density around HEC A 607:

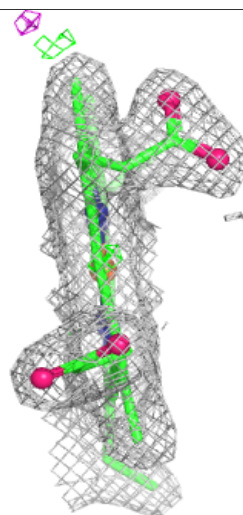
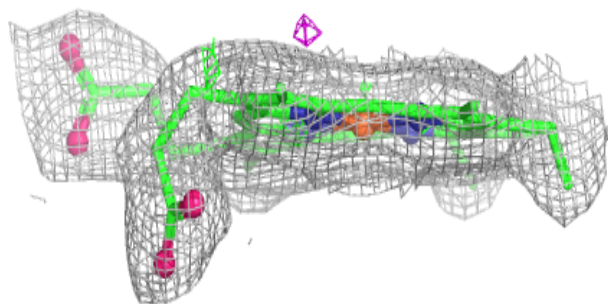
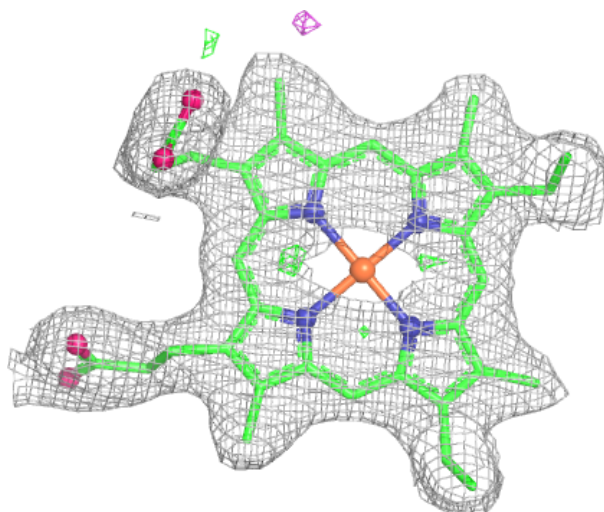
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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

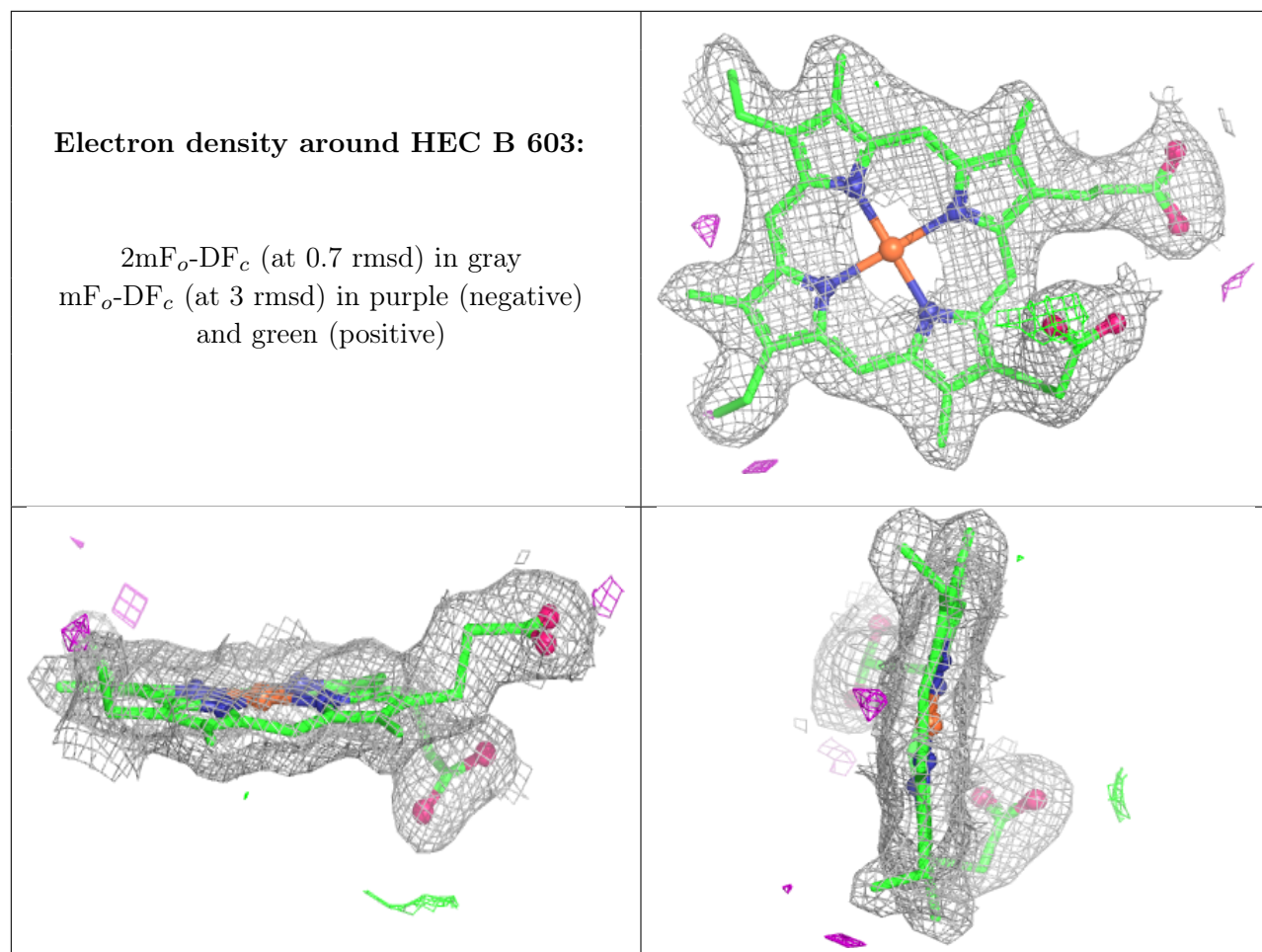




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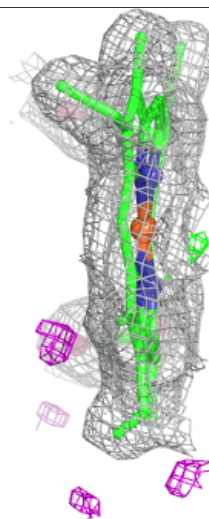
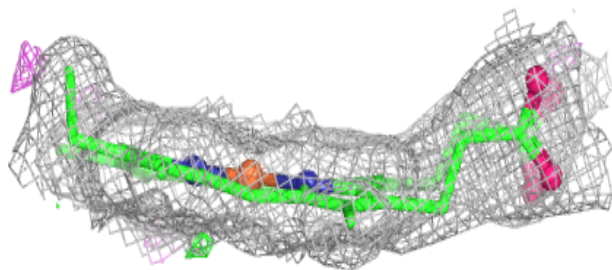
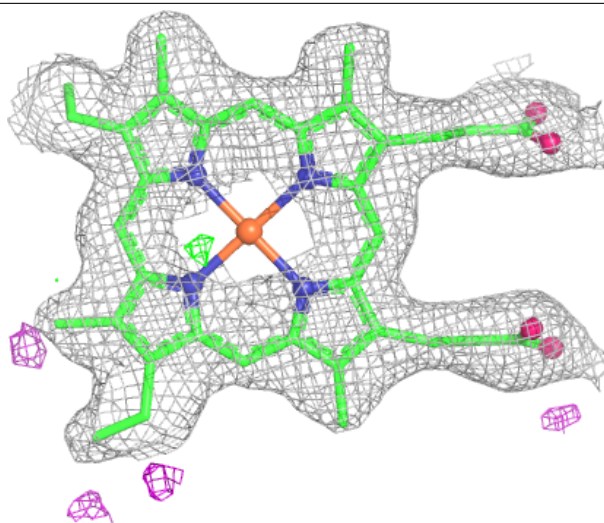
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

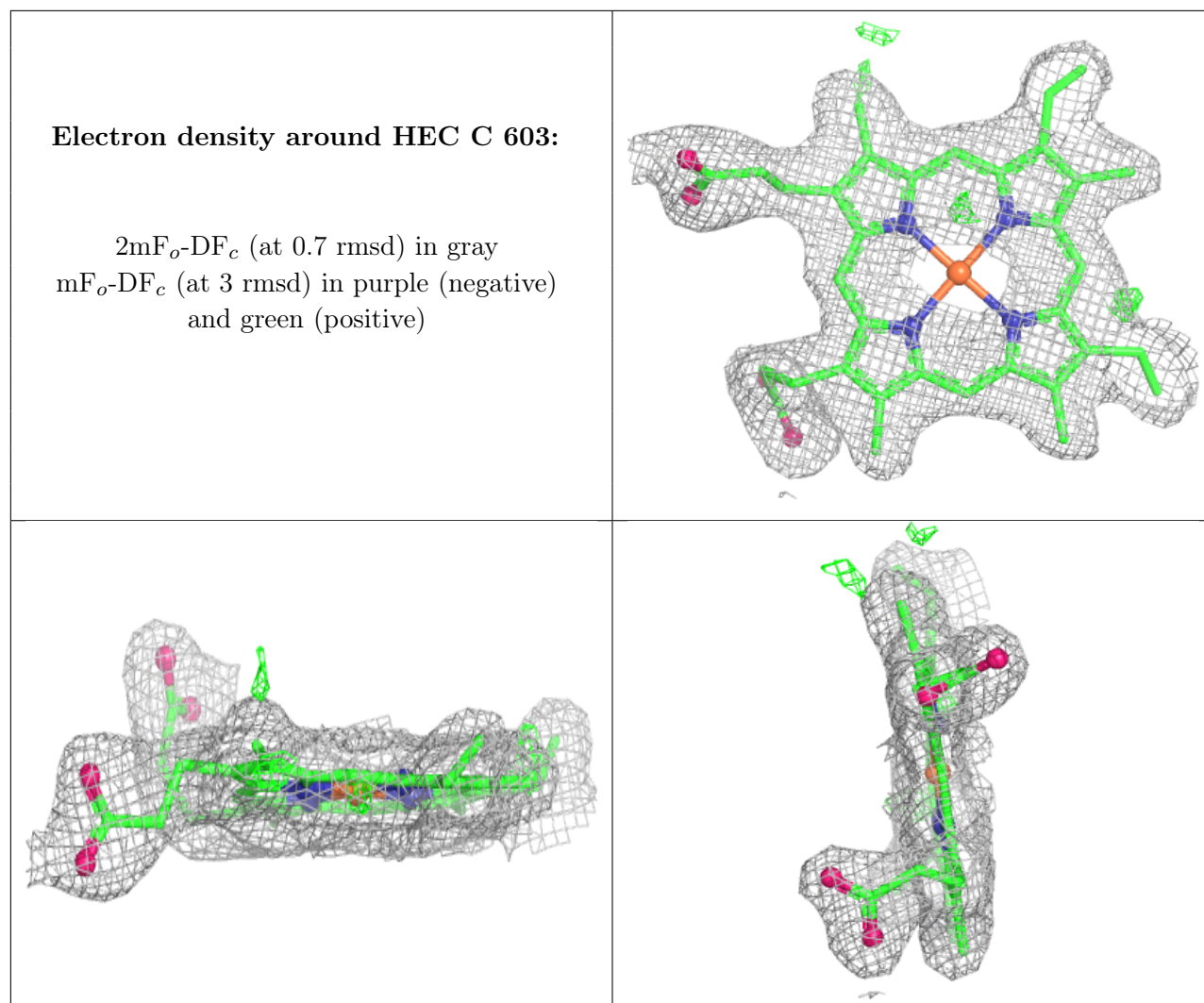


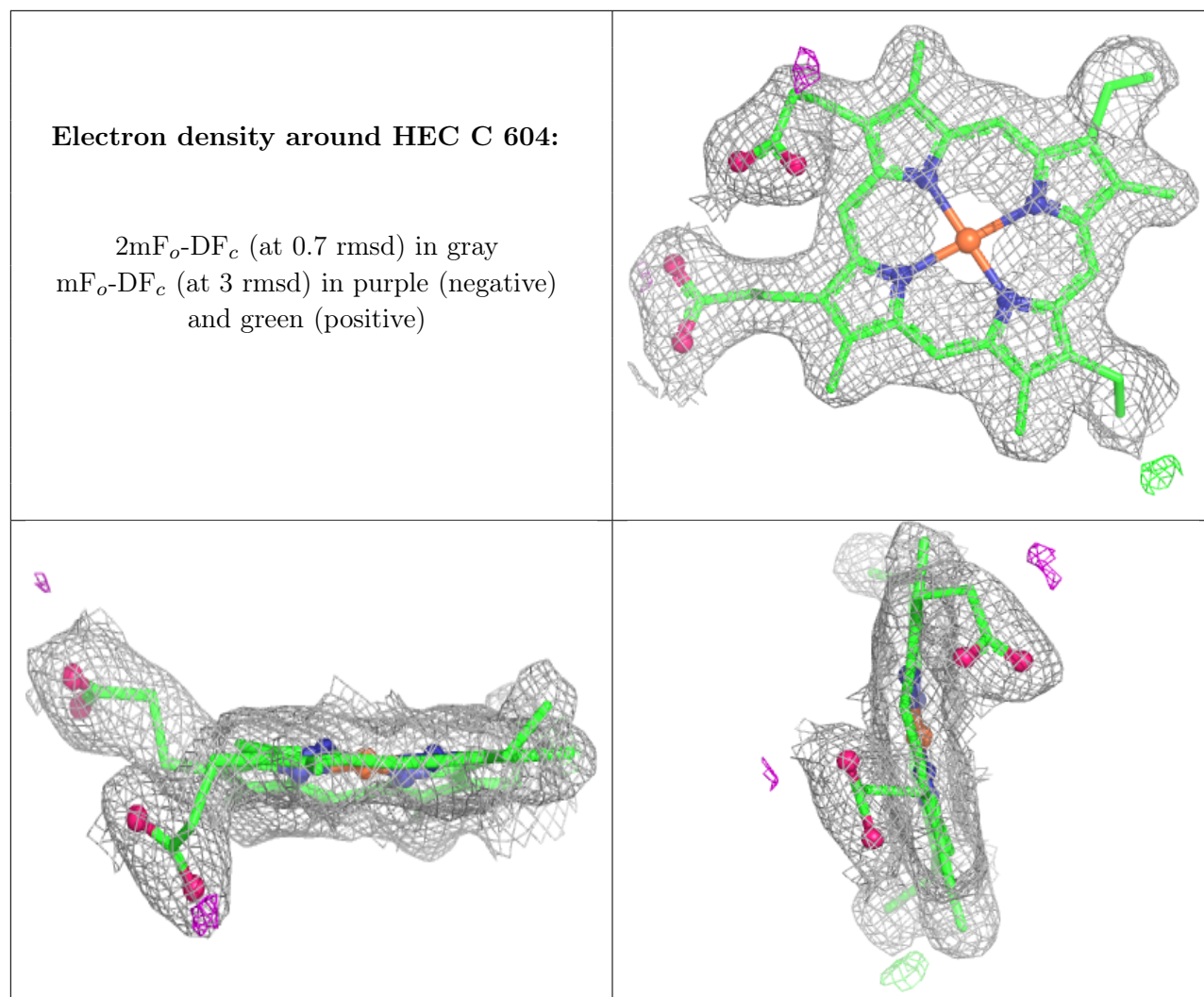


Electron density around HEC C 602:

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

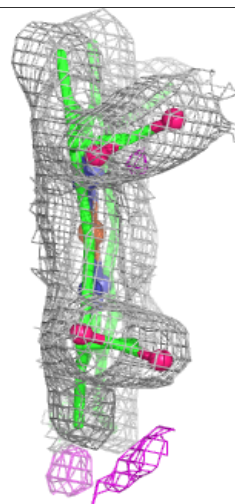
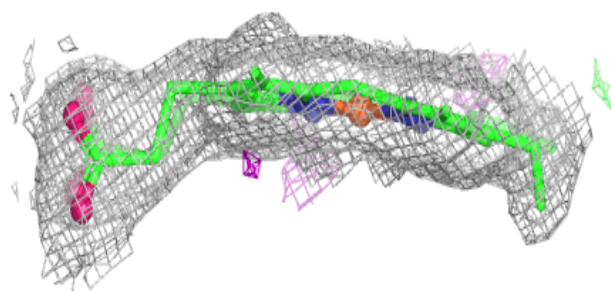
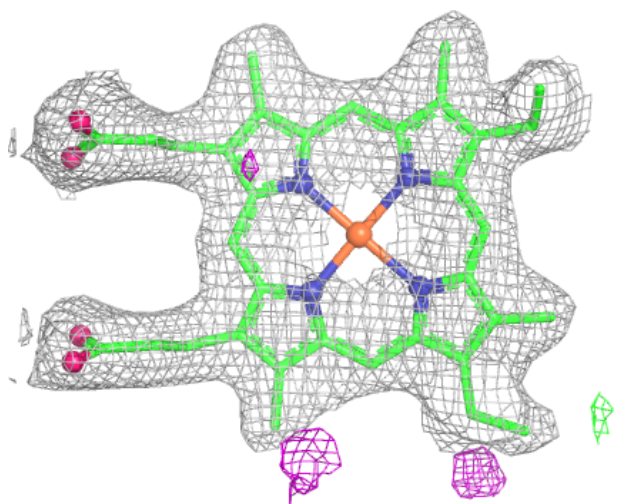






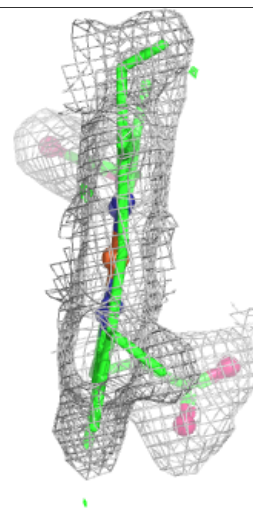
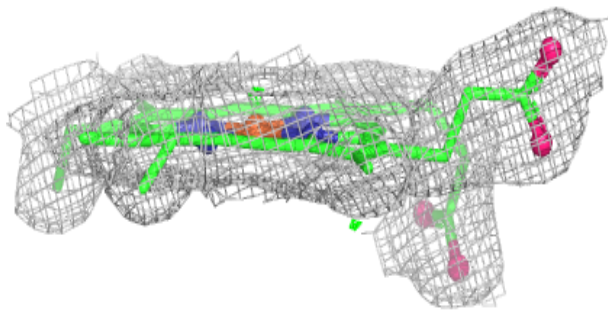
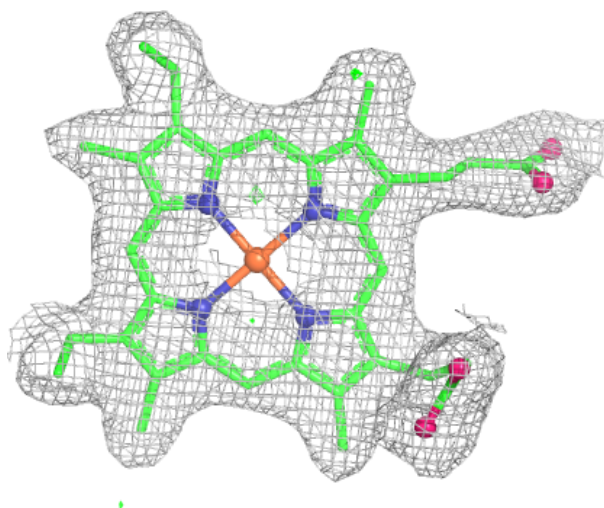
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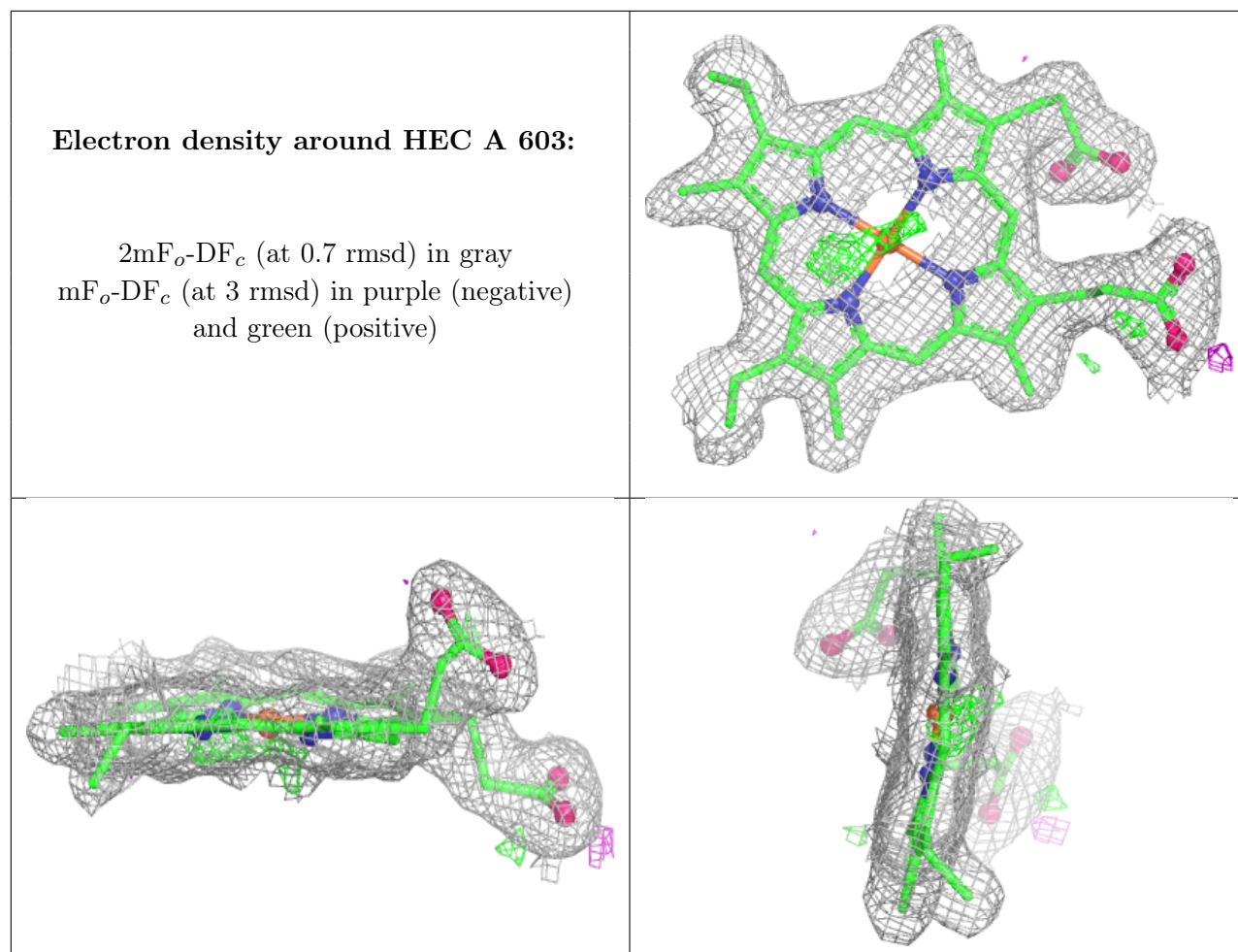
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEC A 602:

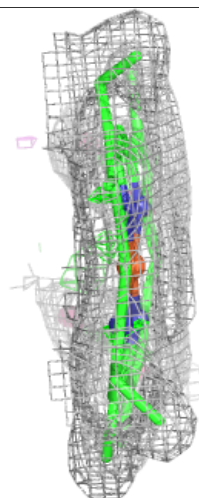
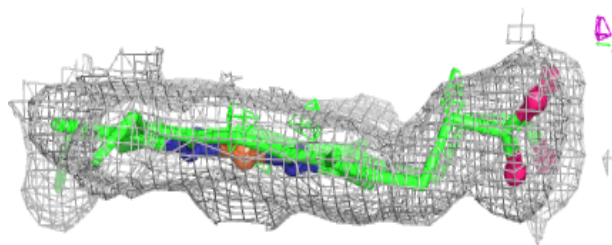
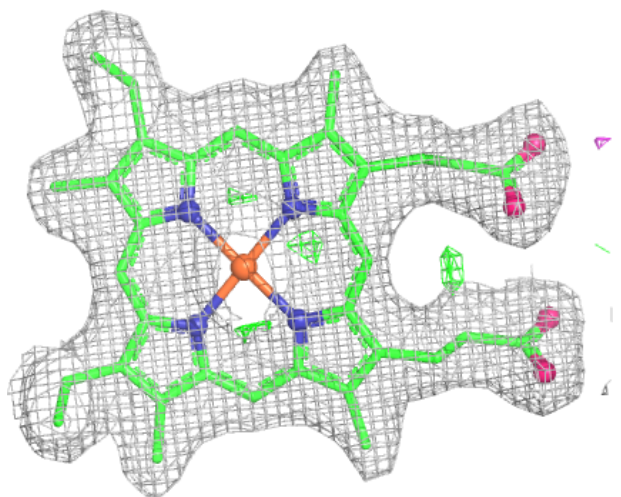
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

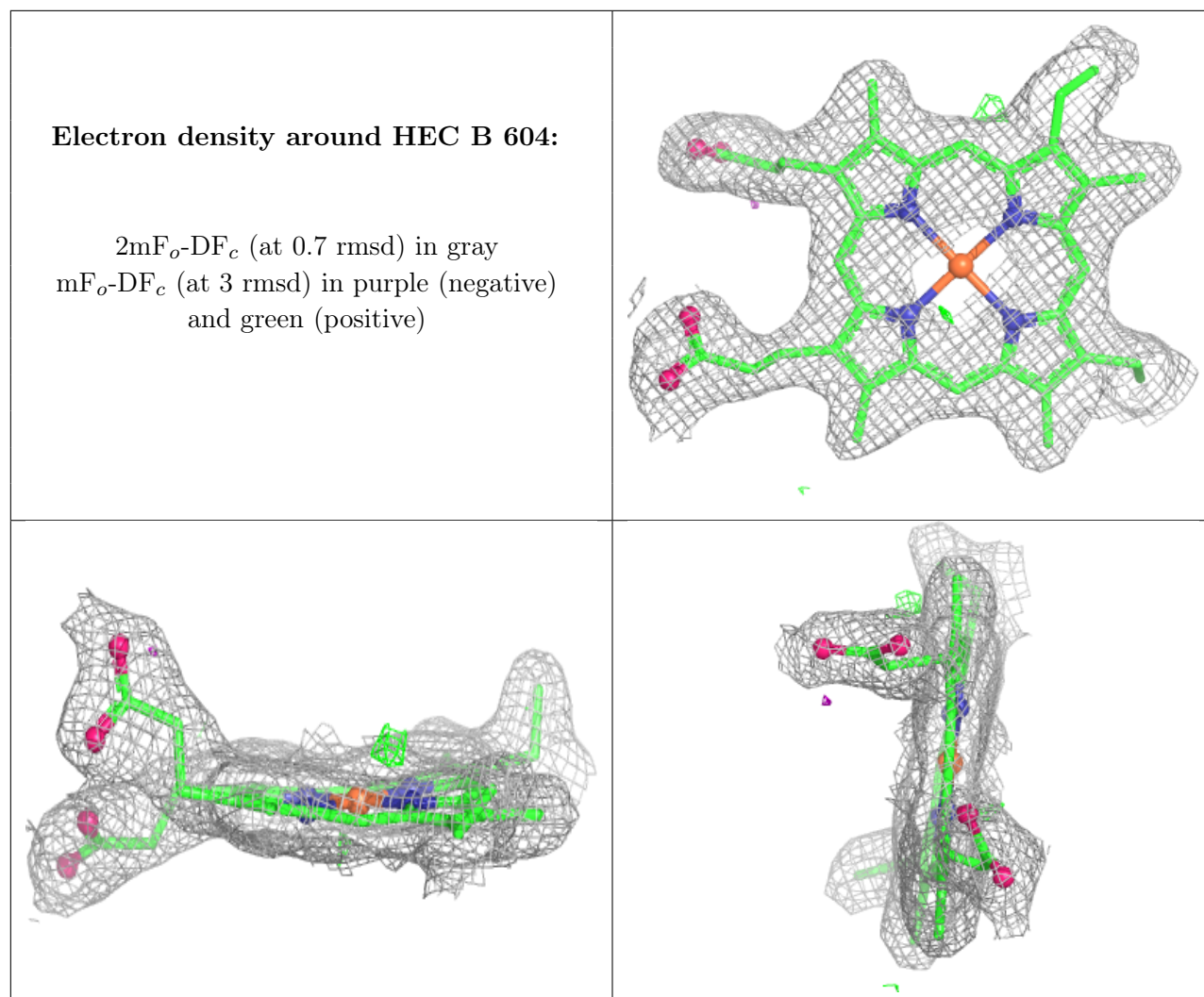


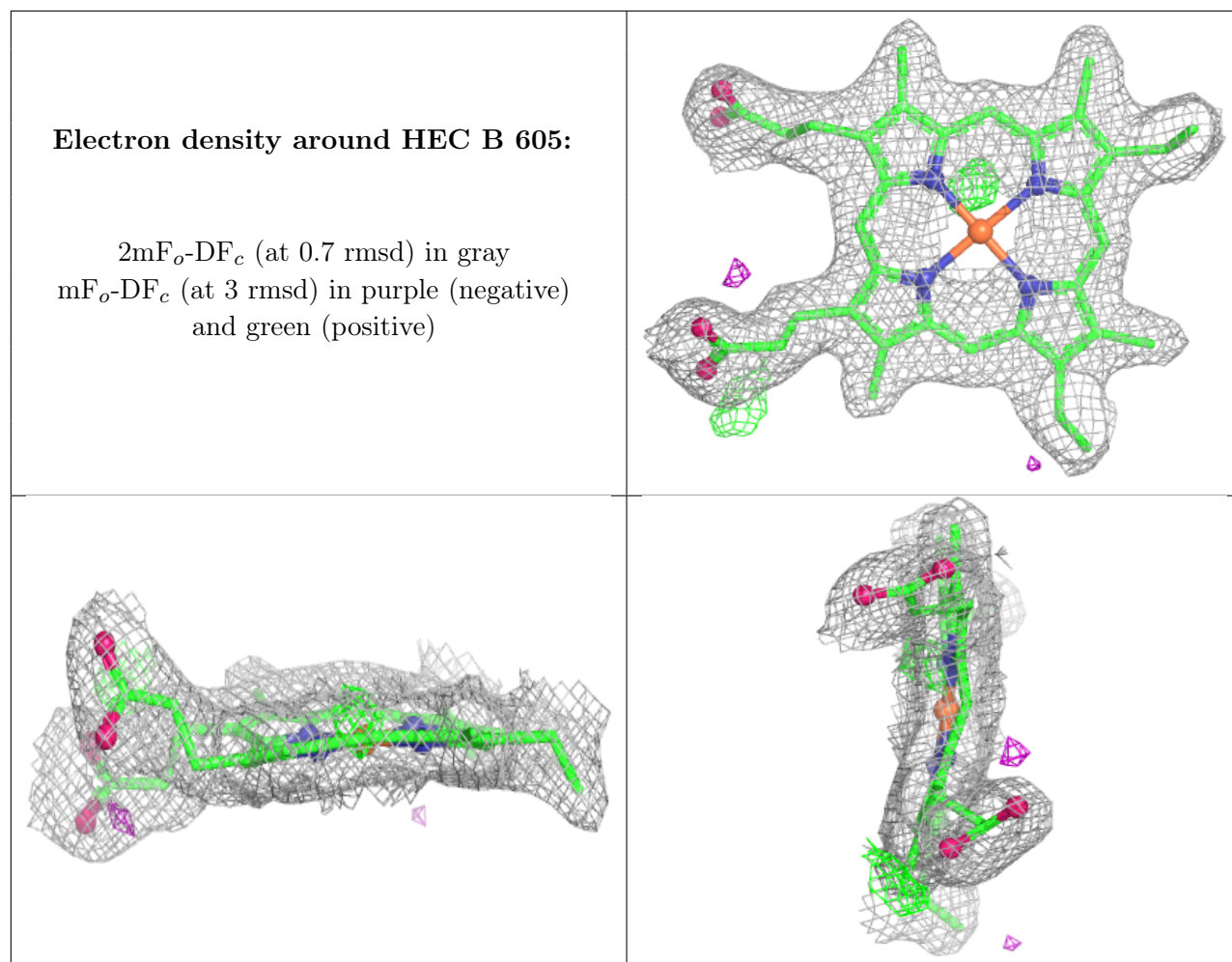


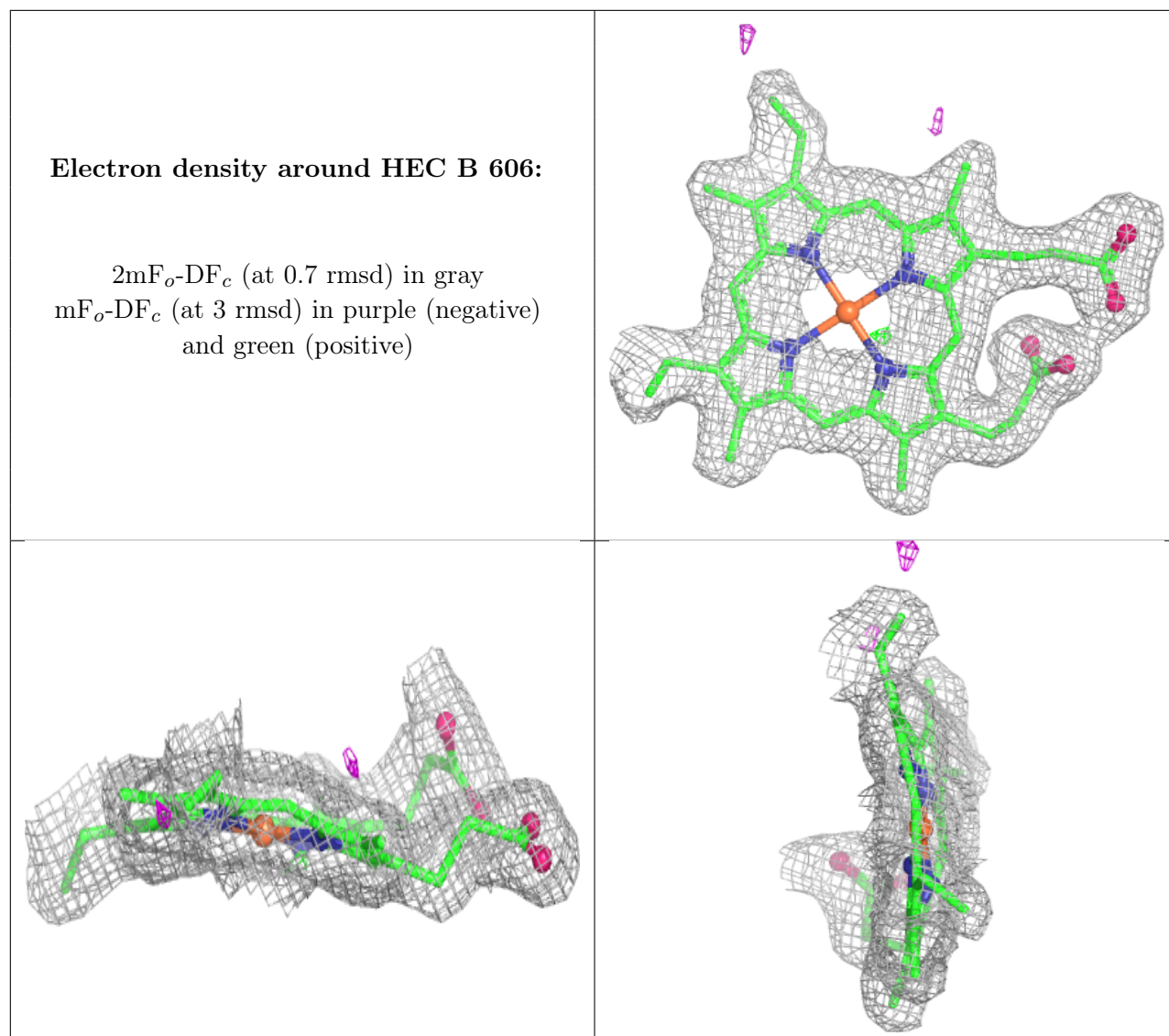
Electron density around HEC C 608:

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and green (positive)



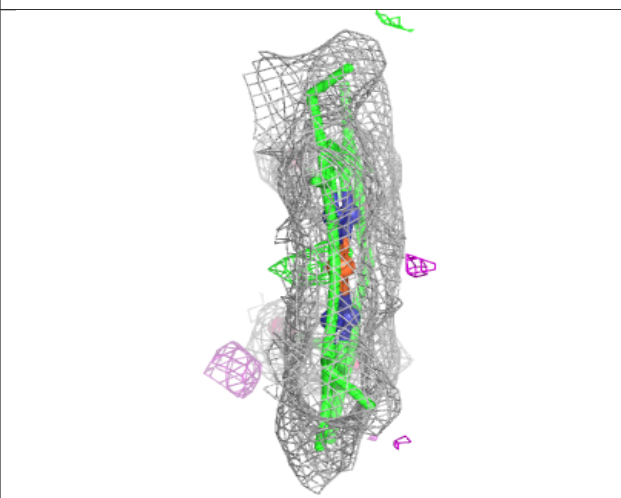
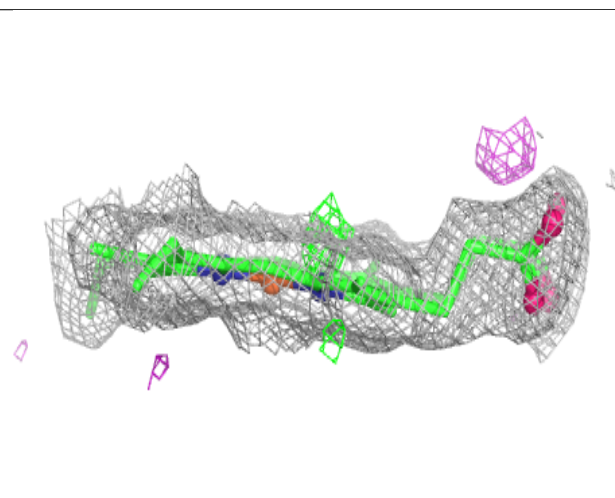
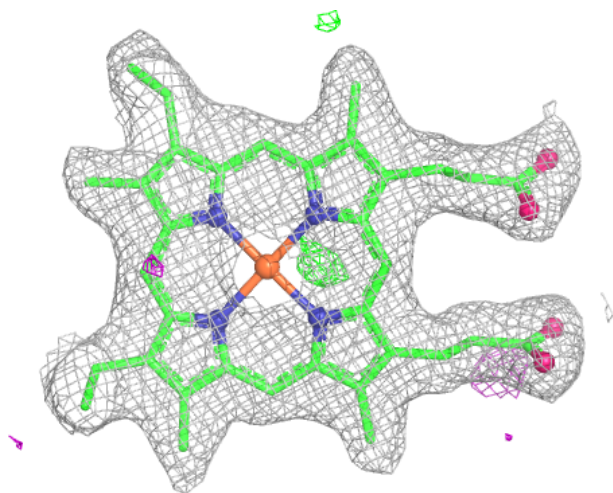


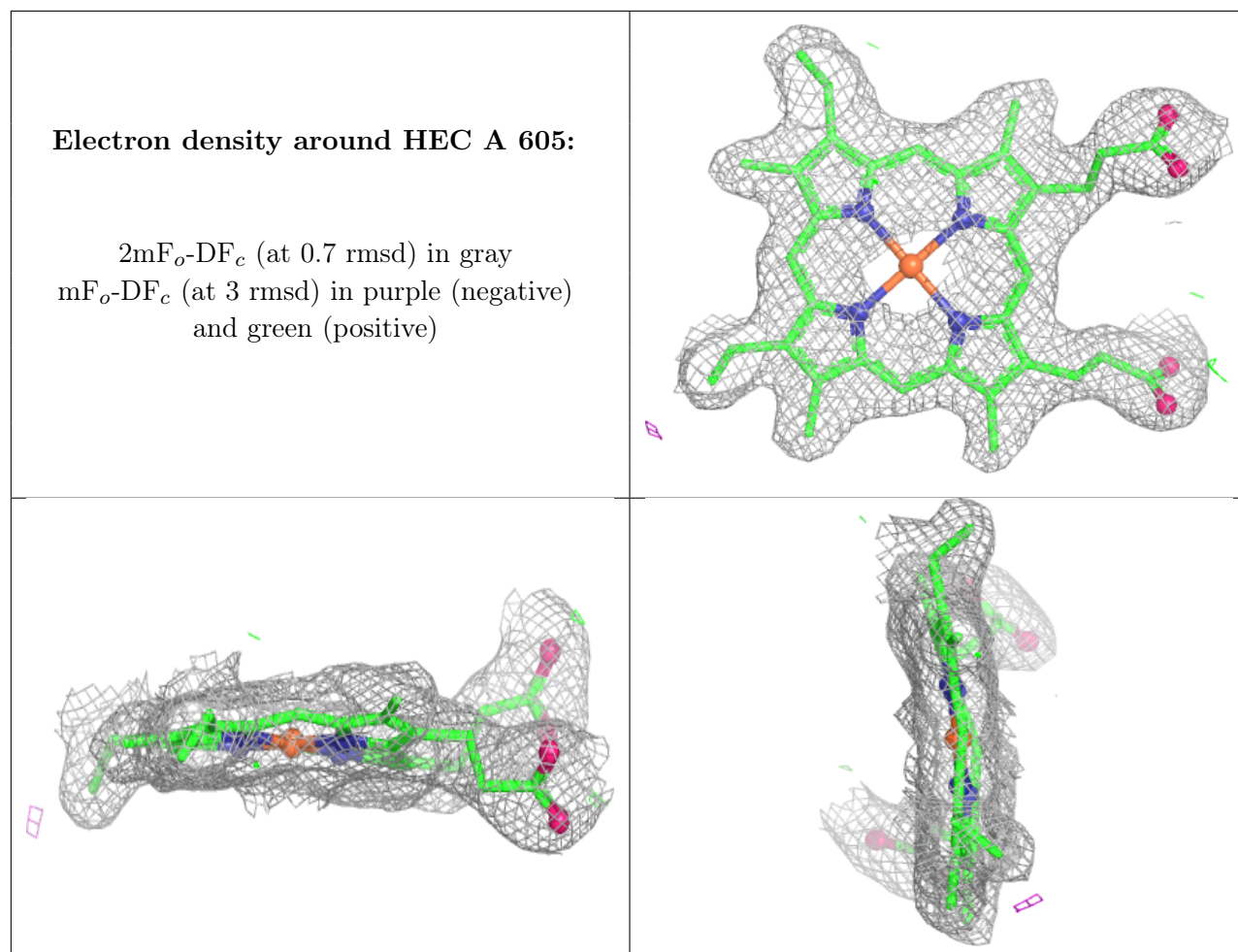


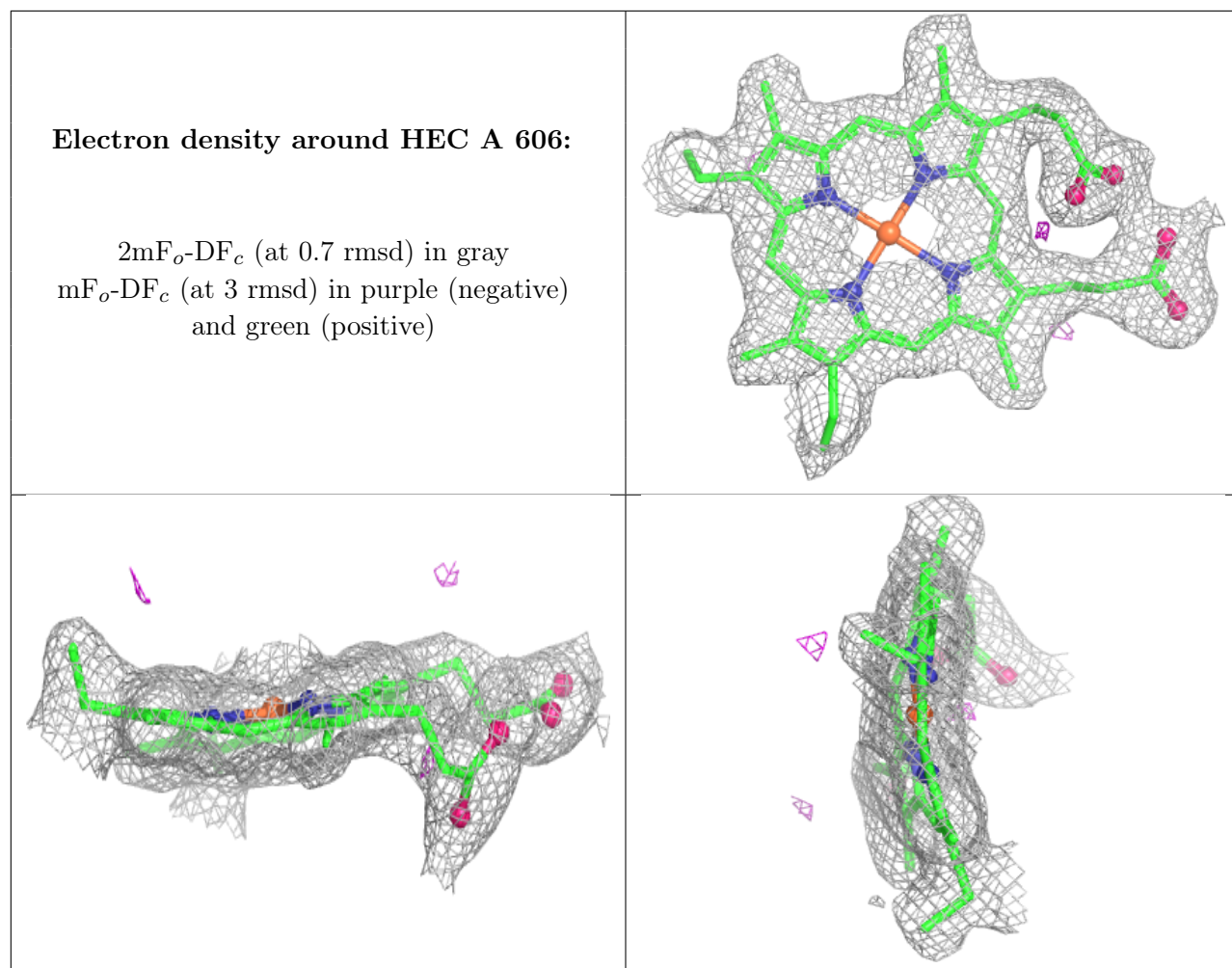


Electron density around HEC B 607:

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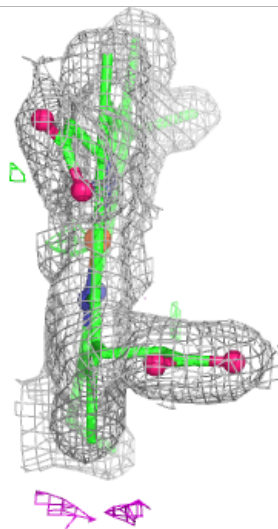
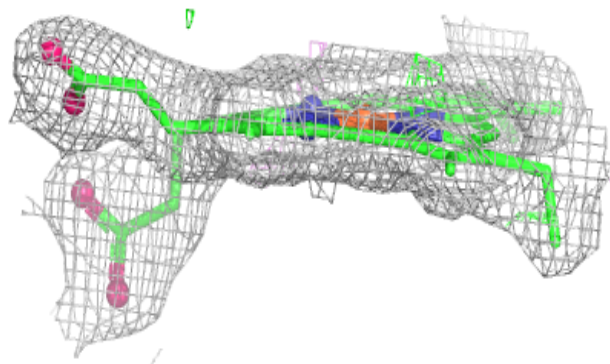
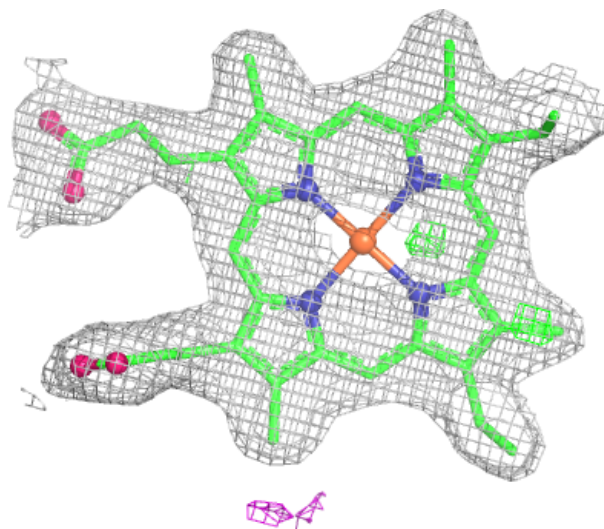






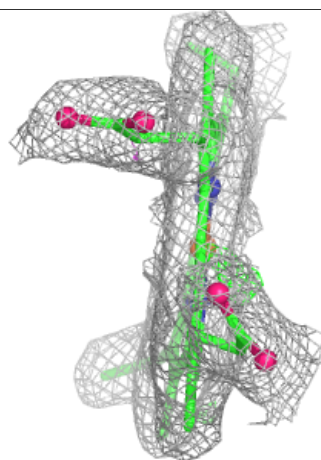
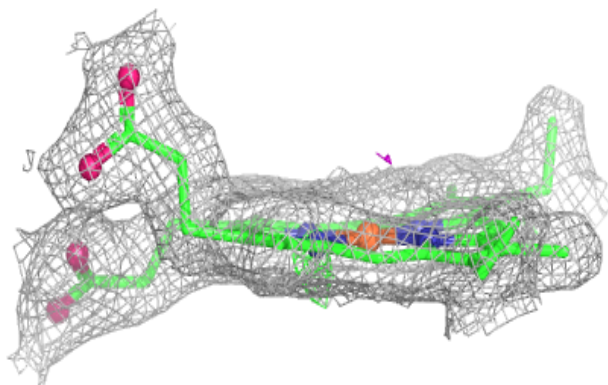
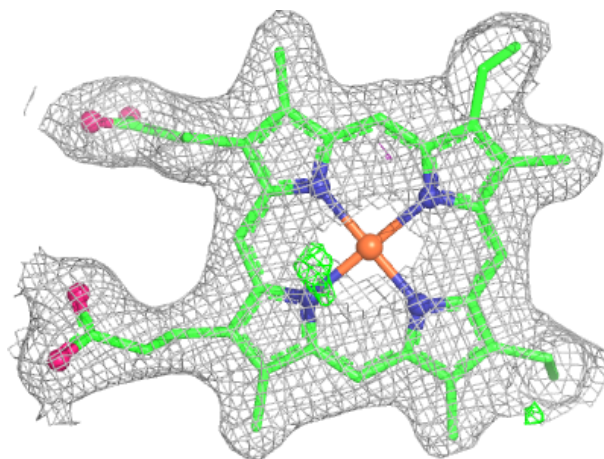
Electron density around HEC A 604:

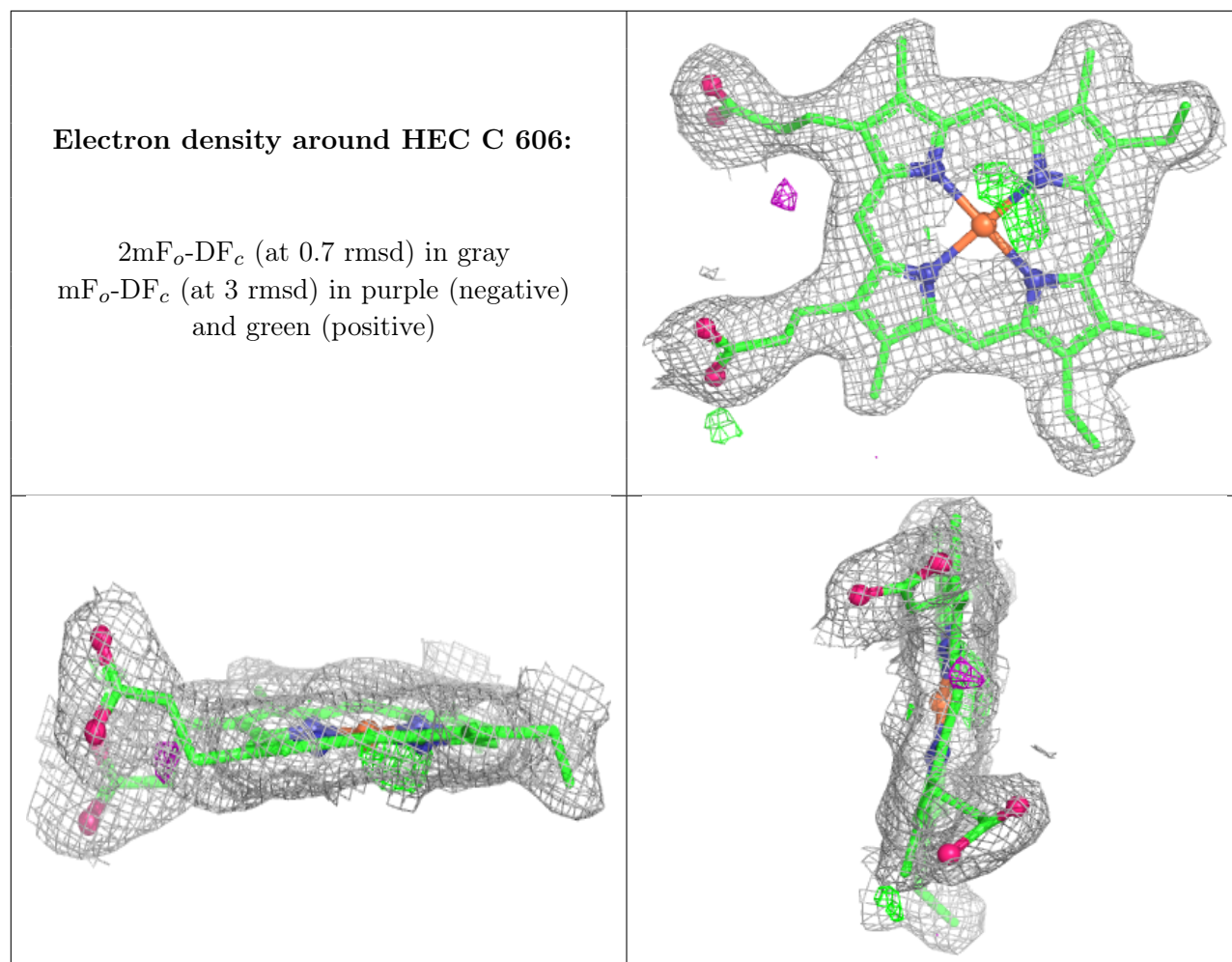
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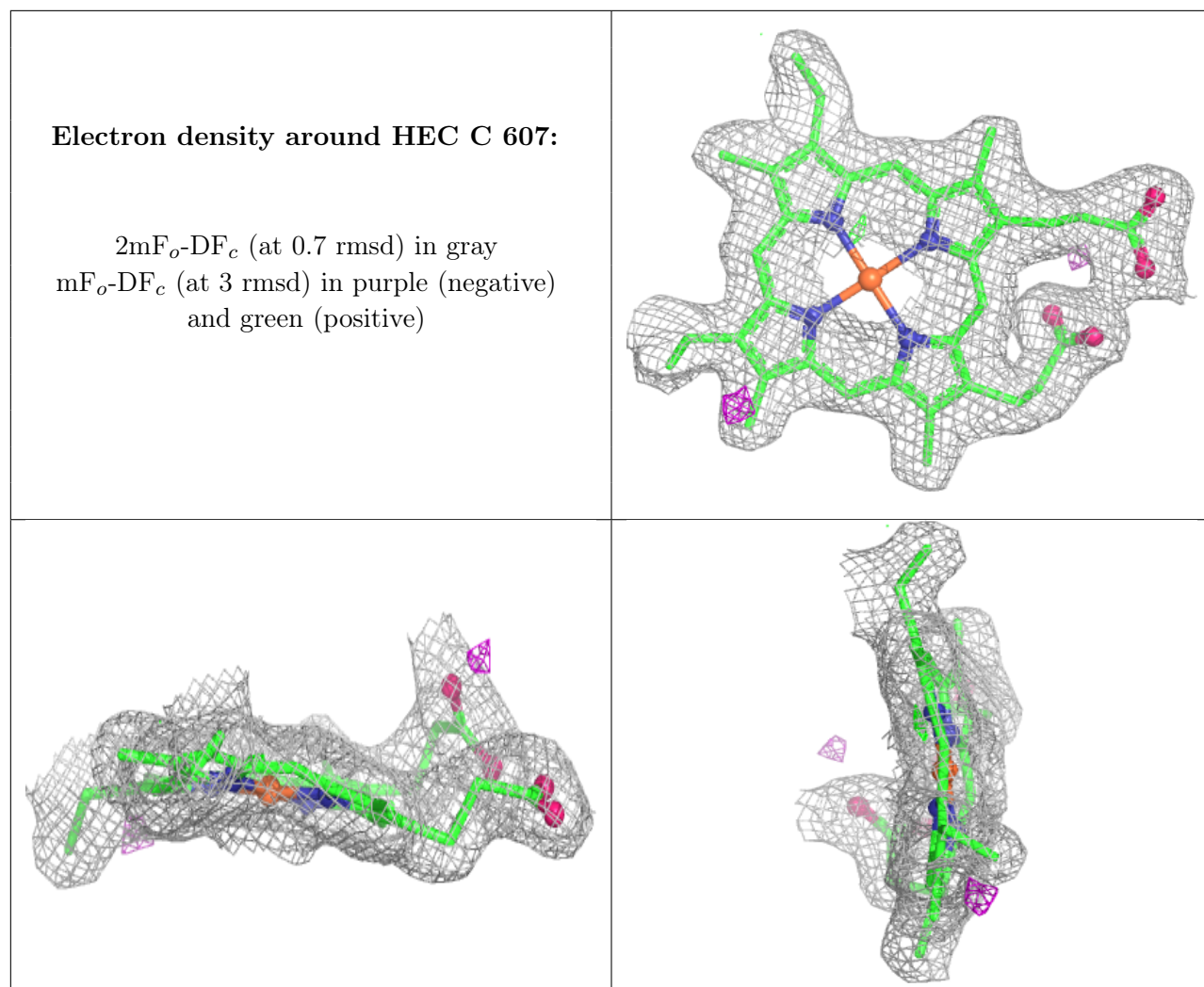


Electron density around HEC C 605:

$2mF_o-DF_c$ (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.