



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 19, 2020 – 09:46 AM BST

PDB ID : 6POU
Title : Structure of human endothelial nitric oxide synthase heme domain in complex with 7-(4-(2-Aminoethyl)phenyl)-4-methylquinolin-2-amine
Authors : Li, H.; Poulos, T.L.
Deposited on : 2019-07-05
Resolution : 2.19 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.6
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.6

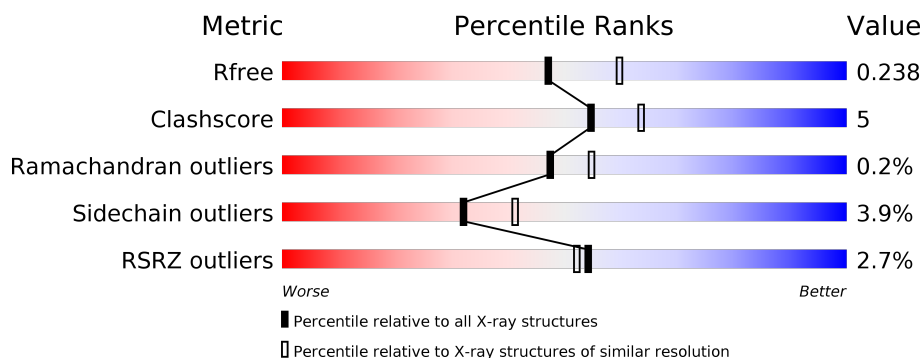
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	440	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>9%</div> </div> </div>
1	B	440	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>9%</div> </div> </div>
1	C	440	<div> <div>7%</div> <div> <div></div> <div>78%</div> <div>12%</div> <div>9%</div> </div> </div>
1	D	440	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>9%</div> <div>9%</div> </div> </div>
1	E	440	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>10%</div> <div>9%</div> </div> </div>
1	F	440	<div> <div>0%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>9%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	GD	B	509	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 20937 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.

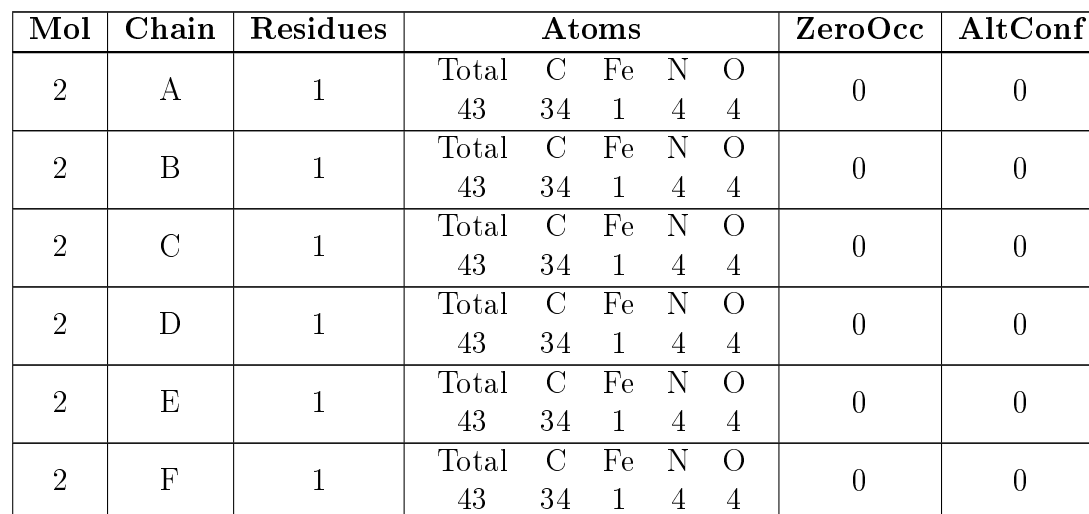
- Molecule 1 is a protein called Nitric oxide synthase, endothelial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	3	0
			3212	2046	563	587	16			
1	B	402	Total	C	N	O	S	0	4	0
			3225	2055	567	587	16			
1	C	401	Total	C	N	O	S	0	2	0
			3209	2044	563	586	16			
1	D	402	Total	C	N	O	S	0	3	0
			3218	2050	565	587	16			
1	E	401	Total	C	N	O	S	0	2	0
			3209	2044	563	586	16			
1	F	402	Total	C	N	O	S	0	2	0
			3215	2048	565	586	16			

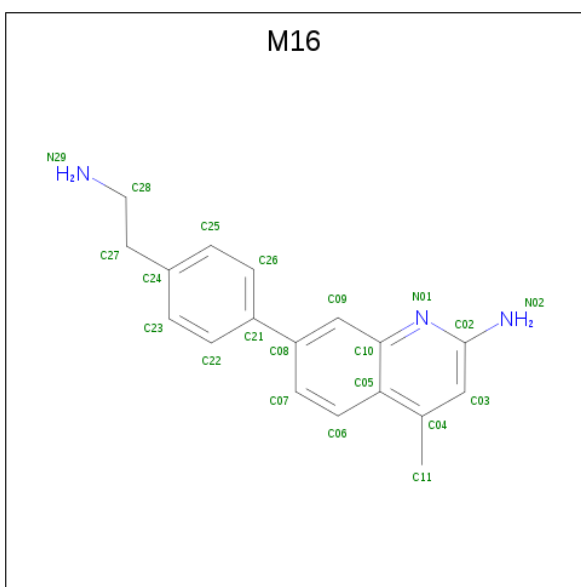
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	298	GLU	ASP	variant	UNP P29474
B	298	GLU	ASP	variant	UNP P29474
C	298	GLU	ASP	variant	UNP P29474
D	298	GLU	ASP	variant	UNP P29474
E	298	GLU	ASP	variant	UNP P29474
F	298	GLU	ASP	variant	UNP P29474

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

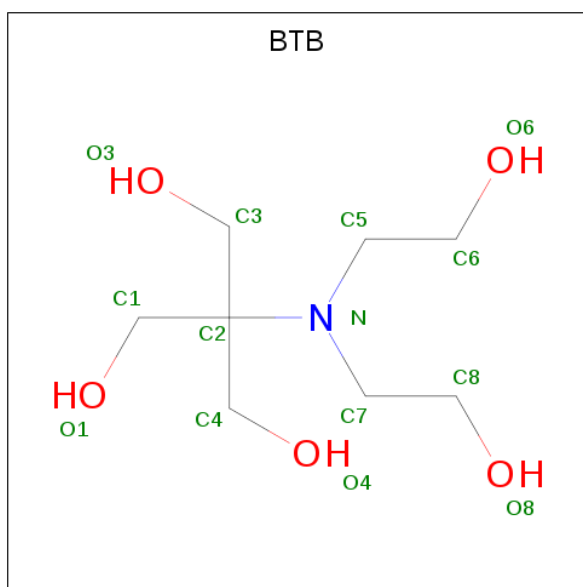


- Molecule 3 is 7-[4-(2-aminoethyl)phenyl]-4-methylquinolin-2-amine (three-letter code: M16) (formula: C₁₈H₁₉N₃) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			21	18	3		
3	A	1	Total	C	N	0	0
			21	18	3		
3	B	1	Total	C	N	0	0
			21	18	3		
3	B	1	Total	C	N	0	0
			21	18	3		
3	C	1	Total	C	N	0	0
			21	18	3		
3	C	1	Total	C	N	0	0
			21	18	3		
3	D	1	Total	C	N	0	0
			21	18	3		
3	D	1	Total	C	N	0	0
			21	18	3		
3	E	1	Total	C	N	0	0
			21	18	3		
3	F	1	Total	C	N	0	0
			21	18	3		
3	F	1	Total	C	N	0	0
			21	18	3		
3	F	1	Total	C	N	0	0
			21	18	3		

- Molecule 4 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		

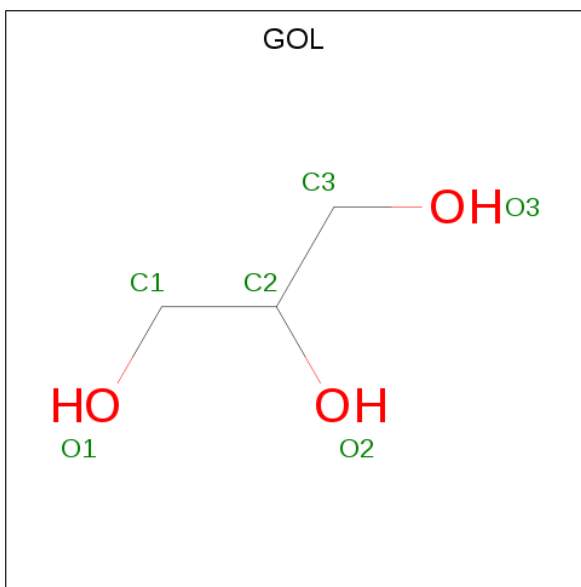
- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Zn	0	0
			1	1		
5	E	2	Total	Zn	0	0
			2	2		
5	B	1	Total	Zn	0	0
			1	1		
5	C	2	Total	Zn	0	0
			2	2		
5	A	2	Total	Zn	0	0
			2	2		
5	F	1	Total	Zn	0	0
			1	1		

- Molecule 6 is GADOLINIUM ATOM (three-letter code: GD) (formula: Gd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total	Gd	0	0
			2	2		
6	A	2	Total	Gd	0	0
			2	2		
6	D	2	Total	Gd	0	0
			2	2		
6	C	1	Total	Gd	0	0
			1	1		
6	F	1	Total	Gd	0	0
			1	1		

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

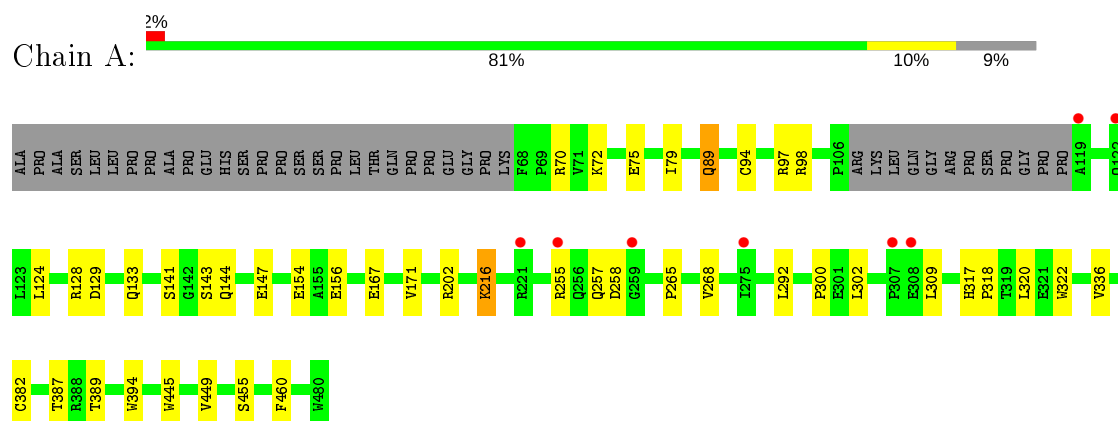
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	144	Total	O	0	0
			144	144		
8	B	155	Total	O	0	0
			155	155		
8	C	99	Total	O	0	0
			99	99		
8	D	150	Total	O	0	0
			150	150		
8	E	133	Total	O	0	0
			133	133		
8	F	177	Total	O	0	0
			177	177		

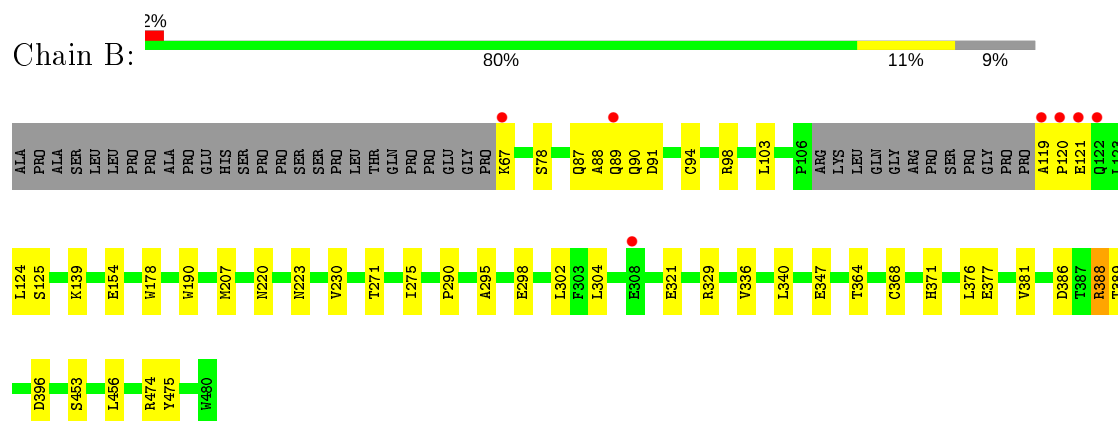
3 Residue-property plots [i](#)

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

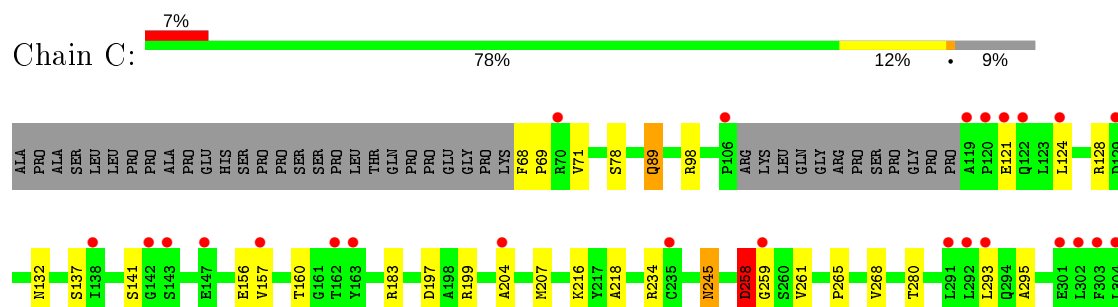
- Molecule 1: Nitric oxide synthase, endothelial



- Molecule 1: Nitric oxide synthase, endothelial

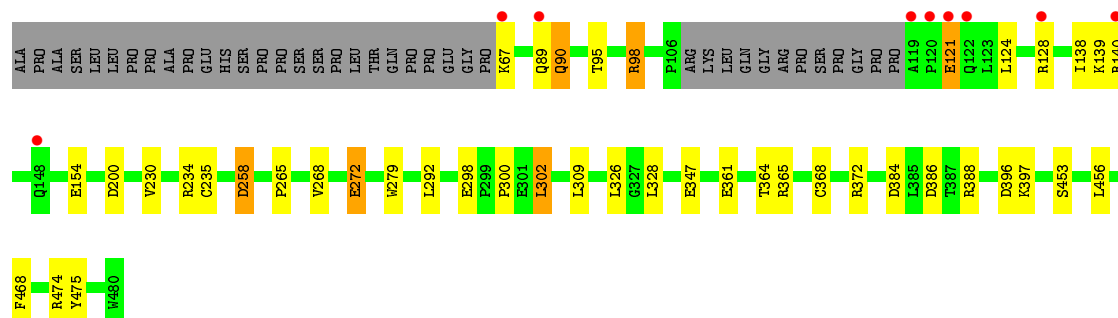
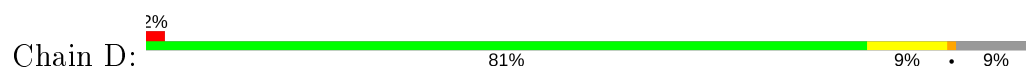


- Molecule 1: Nitric oxide synthase, endothelial

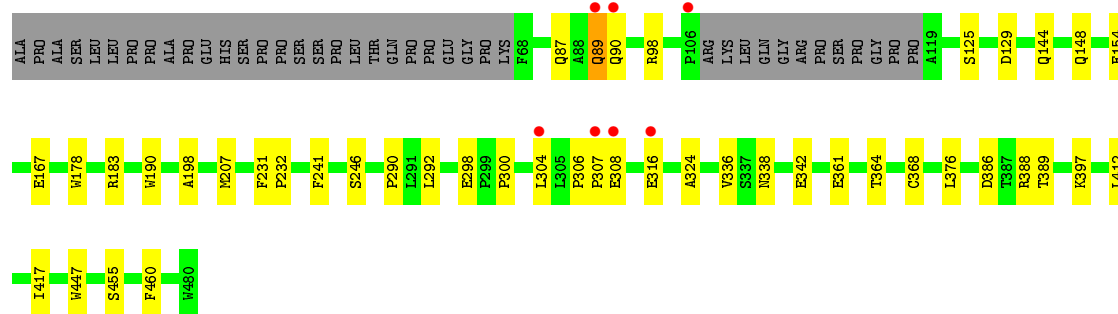
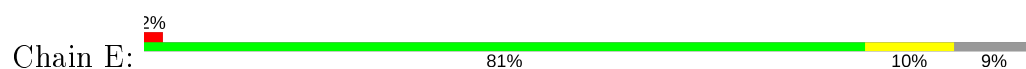




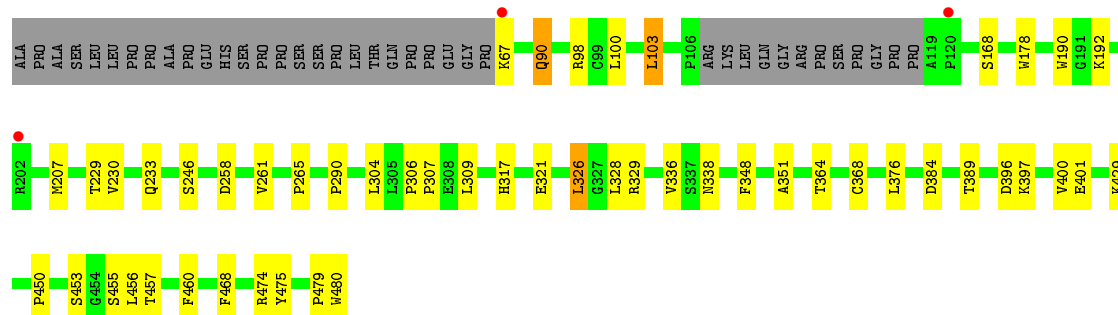
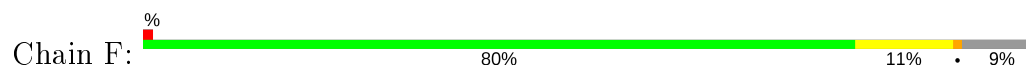
- Molecule 1: Nitric oxide synthase, endothelial



- Molecule 1: Nitric oxide synthase, endothelial



- Molecule 1: Nitric oxide synthase, endothelial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.92Å 153.55Å 175.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.61 – 2.19 79.61 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.3 (79.61-2.19) 99.4 (79.61-2.19)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	0.30	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.11.1-2575_1496: ???)	Depositor
R, R_{free}	0.189 , 0.243 0.183 , 0.238	Depositor DCC
R_{free} test set	7545 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.703	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20937	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.15% 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: GOL, ZN, BTB, GD, M16, HEM

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	0.39	0/3313	0.55	0/4515
1	B	0.41	0/3330	0.56	0/4537
1	C	0.36	0/3307	0.53	1/4507 (0.0%)
1	D	0.42	0/3319	0.56	0/4522
1	E	0.41	0/3307	0.55	0/4507
1	F	0.42	0/3313	0.56	0/4514
All	All	0.41	0/19889	0.55	1/27102 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	369	ASP	CB-CG-OD1	6.84	124.45	118.30

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	3212	0	3114	24	0
1	B	3225	0	3133	29	0
1	C	3209	0	3109	27	0
1	D	3218	0	3126	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	3209	0	3109	25	0
1	F	3215	0	3121	29	0
2	A	43	0	30	2	0
2	B	43	0	30	3	0
2	C	43	0	30	3	0
2	D	43	0	30	2	0
2	E	43	0	30	2	0
2	F	43	0	30	4	0
3	A	42	0	0	3	0
3	B	42	0	0	2	0
3	C	42	0	0	4	0
3	D	42	0	0	1	0
3	E	21	0	0	3	0
3	F	63	0	0	3	0
4	A	42	0	56	10	0
4	B	56	0	72	14	0
4	C	42	0	56	3	0
4	D	42	0	55	13	0
4	E	42	0	56	7	0
4	F	28	0	37	9	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
5	D	1	0	0	0	0
5	E	2	0	0	0	0
5	F	1	0	0	0	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
6	C	1	0	0	0	0
6	D	2	0	0	0	0
6	F	1	0	0	0	0
7	C	6	0	8	0	0
7	E	6	0	8	1	0
8	A	144	0	0	3	0
8	B	155	0	0	0	0
8	C	99	0	0	3	0
8	D	150	0	0	0	0
8	E	133	0	0	2	0
8	F	177	0	0	4	0
All	All	20937	0	19240	204	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 5.

The worst 5 of 204 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:D:505:BTB:HO6	4:D:505:BTB:HO8	0.90	0.90
4:F:806:BTB:HO6	4:F:806:BTB:HO4	1.25	0.82
1:A:75:GLU:O	1:B:371[B]:HIS:NE2	2.13	0.82
1:B:290:PRO:HB3	1:B:304:LEU:HD23	1.68	0.76
1:F:290:PRO:HB3	1:F:304:LEU:HD23	1.67	0.75

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	400/440 (91%)	391 (98%)	8 (2%)	1 (0%)	41	46
1	B	402/440 (91%)	395 (98%)	7 (2%)	0	100	100
1	C	399/440 (91%)	381 (96%)	15 (4%)	3 (1%)	19	19
1	D	401/440 (91%)	390 (97%)	11 (3%)	0	100	100
1	E	399/440 (91%)	390 (98%)	8 (2%)	1 (0%)	41	46
1	F	400/440 (91%)	391 (98%)	9 (2%)	0	100	100
All	All	2401/2640 (91%)	2338 (97%)	58 (2%)	5 (0%)	47	55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	258	ASP
1	A	89	GLN
1	C	259	GLY
1	E	89	GLN
1	C	89	GLN

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	343/373 (92%)	334 (97%)	9 (3%)	46	58
1	B	345/373 (92%)	331 (96%)	14 (4%)	30	39
1	C	342/373 (92%)	326 (95%)	16 (5%)	26	33
1	D	344/373 (92%)	329 (96%)	15 (4%)	28	35
1	E	342/373 (92%)	329 (96%)	13 (4%)	33	42
1	F	343/373 (92%)	329 (96%)	14 (4%)	30	39
All	All	2059/2238 (92%)	1978 (96%)	81 (4%)	32	41

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	388	ARG
1	D	200	ASP
1	F	230	VAL
1	C	389	THR
1	D	90	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 55 ligands modelled in this entry, 17 are monoatomic - leaving 38 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	BTB	B	505	6	13,13,13	0.66	0	7,16,16	0.85	0
4	BTB	C	504	6	13,13,13	0.45	0	7,16,16	0.56	0
3	M16	C	503	-	22,23,23	0.99	0	30,32,32	1.23	2 (6%)
3	M16	D	503	-	22,23,23	1.02	0	30,32,32	1.21	3 (10%)
4	BTB	B	507	-	13,13,13	0.41	0	7,16,16	0.71	0
2	HEM	E	501	1	27,50,50	1.88	5 (18%)	17,82,82	1.67	5 (29%)
4	BTB	C	506	-	13,13,13	0.42	0	7,16,16	0.74	0
2	HEM	C	501	1	27,50,50	1.81	5 (18%)	17,82,82	1.71	5 (29%)
4	BTB	D	505	-	13,13,13	0.88	1 (7%)	7,16,16	1.27	0
4	BTB	E	505	-	13,13,13	0.52	0	7,16,16	0.79	0
4	BTB	C	505	-	13,13,13	0.97	0	7,16,16	1.29	2 (28%)
3	M16	A	502	-	22,23,23	0.93	1 (4%)	30,32,32	1.18	2 (6%)
3	M16	D	502	-	22,23,23	0.87	0	30,32,32	1.01	3 (10%)
4	BTB	E	503	6	13,13,13	0.39	0	7,16,16	0.58	0
3	M16	F	801	-	22,23,23	0.95	0	30,32,32	1.09	2 (6%)
7	GOL	C	508	-	5,5,5	0.34	0	5,5,5	0.39	0
2	HEM	A	501	1	27,50,50	1.93	5 (18%)	17,82,82	1.44	2 (11%)
4	BTB	A	505	-	13,13,13	0.39	0	7,16,16	0.62	0
4	BTB	E	504	-	13,13,13	0.45	0	7,16,16	0.87	0
3	M16	F	803	-	22,23,23	0.83	1 (4%)	30,32,32	1.03	3 (10%)
4	BTB	A	504	6	13,13,13	0.46	0	7,16,16	0.80	0
3	M16	B	503	-	22,23,23	1.03	1 (4%)	30,32,32	1.36	4 (13%)
3	M16	E	502	-	22,23,23	1.05	2 (9%)	30,32,32	1.47	3 (10%)
4	BTB	B	504	6	13,13,13	0.59	0	7,16,16	0.63	0
4	BTB	F	805	6	13,13,13	0.57	0	7,16,16	0.61	0
3	M16	F	804	-	22,23,23	0.96	2 (9%)	30,32,32	1.53	5 (16%)
4	BTB	D	506	-	13,13,13	0.63	0	7,16,16	1.24	1 (14%)
3	M16	B	502	-	22,23,23	0.88	1 (4%)	30,32,32	1.25	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	D	501	1	27,50,50	1.85	5 (18%)	17,82,82	2.09	7 (41%)
4	BTB	B	506	-	13,13,13	0.39	0	7,16,16	0.54	0
3	M16	A	503	-	22,23,23	1.04	0	30,32,32	1.37	4 (13%)
4	BTB	A	509	6	13,13,13	0.35	0	7,16,16	0.46	0
4	BTB	F	806	-	13,13,13	0.52	0	7,16,16	1.09	0
7	GOL	E	507	-	5,5,5	0.73	0	5,5,5	2.28	2 (40%)
3	M16	C	502	-	22,23,23	1.00	1 (4%)	30,32,32	1.15	3 (10%)
4	BTB	D	504	6	13,13,13	0.62	0	7,16,16	1.00	0
2	HEM	F	802	1	27,50,50	1.94	4 (14%)	17,82,82	1.53	2 (11%)
2	HEM	B	501	1	27,50,50	1.91	4 (14%)	17,82,82	1.66	4 (23%)

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	BTB	B	505	6	-	10/21/21/21	-
4	BTB	C	504	6	-	3/21/21/21	-
3	M16	C	503	-	-	4/7/7/7	0/3/3/3
3	M16	D	503	-	-	0/7/7/7	0/3/3/3
4	BTB	B	507	-	-	4/21/21/21	-
2	HEM	E	501	1	-	0/6/54/54	-
4	BTB	C	506	-	-	11/21/21/21	-
2	HEM	C	501	1	-	0/6/54/54	-
4	BTB	D	505	-	-	7/21/21/21	-
4	BTB	E	505	-	-	4/21/21/21	-
4	BTB	C	505	-	-	11/21/21/21	-
3	M16	A	502	-	-	1/7/7/7	0/3/3/3
3	M16	D	502	-	-	2/7/7/7	0/3/3/3
4	BTB	E	503	6	-	7/21/21/21	-
3	M16	F	801	-	-	0/7/7/7	0/3/3/3
7	GOL	C	508	-	-	4/4/4/4	-
2	HEM	A	501	1	-	0/6/54/54	-
4	BTB	A	505	-	-	11/21/21/21	-
4	BTB	E	504	-	-	7/21/21/21	-
3	M16	F	803	-	-	4/7/7/7	0/3/3/3
4	BTB	A	504	6	-	5/21/21/21	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	M16	B	503	-	-	7/7/7/7	0/3/3/3
3	M16	E	502	-	-	5/7/7/7	0/3/3/3
4	BTB	B	504	6	-	3/21/21/21	-
4	BTB	F	805	6	-	14/21/21/21	-
3	M16	F	804	-	-	7/7/7/7	0/3/3/3
4	BTB	D	506	-	-	6/21/21/21	-
3	M16	B	502	-	-	3/7/7/7	0/3/3/3
2	HEM	D	501	1	-	0/6/54/54	-
4	BTB	B	506	-	-	11/21/21/21	-
3	M16	A	503	-	-	7/7/7/7	0/3/3/3
4	BTB	A	509	6	-	6/21/21/21	-
4	BTB	F	806	-	-	17/21/21/21	-
7	GOL	E	507	-	-	2/4/4/4	-
3	M16	C	502	-	-	3/7/7/7	0/3/3/3
4	BTB	D	504	6	-	7/21/21/21	-
2	HEM	F	802	1	-	0/6/54/54	-
2	HEM	B	501	1	-	0/6/54/54	-

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	802	HEM	C3B-C2B	-5.44	1.32	1.40
2	B	501	HEM	C3B-C2B	-5.21	1.33	1.40
2	A	501	HEM	C3B-C2B	-5.11	1.33	1.40
2	D	501	HEM	C3B-C2B	-4.34	1.34	1.40
2	B	501	HEM	C3C-C2C	-4.24	1.34	1.40

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	HEM	CMA-C3A-C4A	-5.03	120.73	128.46
2	B	501	HEM	CAD-CBD-CGD	-4.51	105.11	112.67
3	F	804	M16	C22-C21-C08	-3.96	114.49	121.36
7	E	507	GOL	O3-C3-C2	-3.88	91.61	110.20
2	F	802	HEM	CAD-CBD-CGD	-3.82	106.27	112.67

There are no chirality outliers.

5 of 193 torsion outliers are listed below:

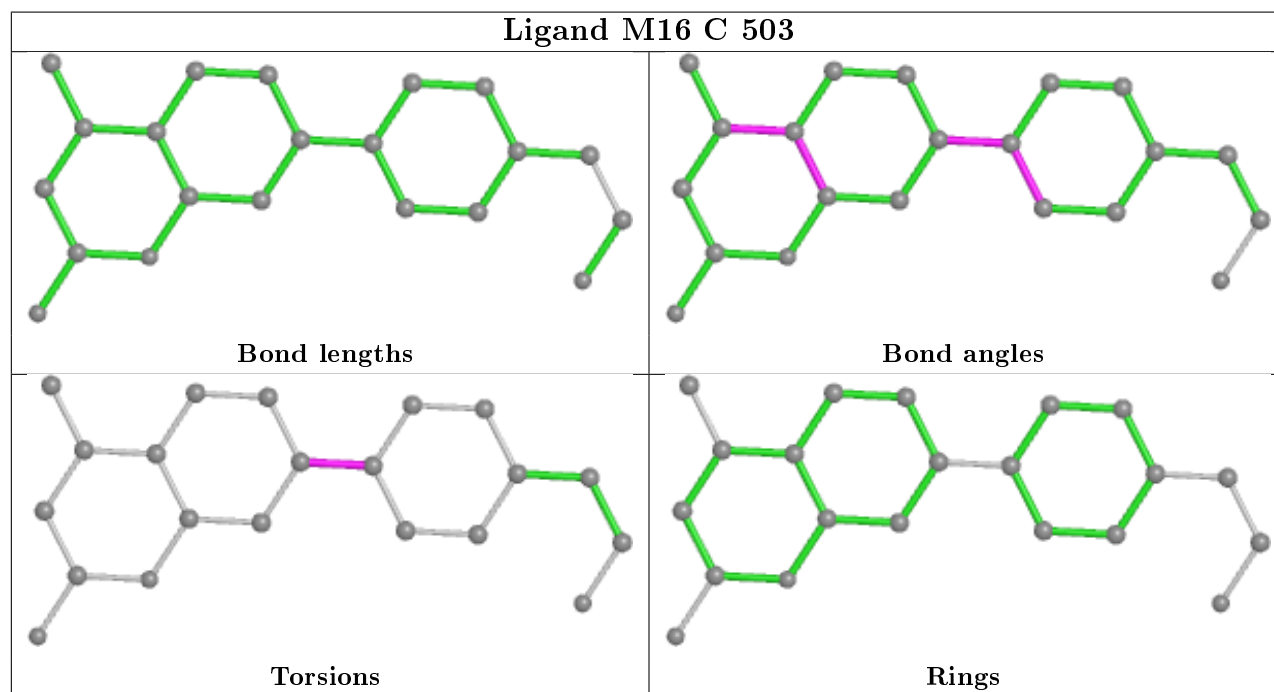
Mol	Chain	Res	Type	Atoms
4	B	505	BTB	C1-C2-C3-O3
4	B	505	BTB	C4-C2-C3-O3
4	B	505	BTB	N-C2-C3-O3
4	B	505	BTB	C1-C2-C4-O4
4	B	505	BTB	C3-C2-C4-O4

There are no ring outliers.

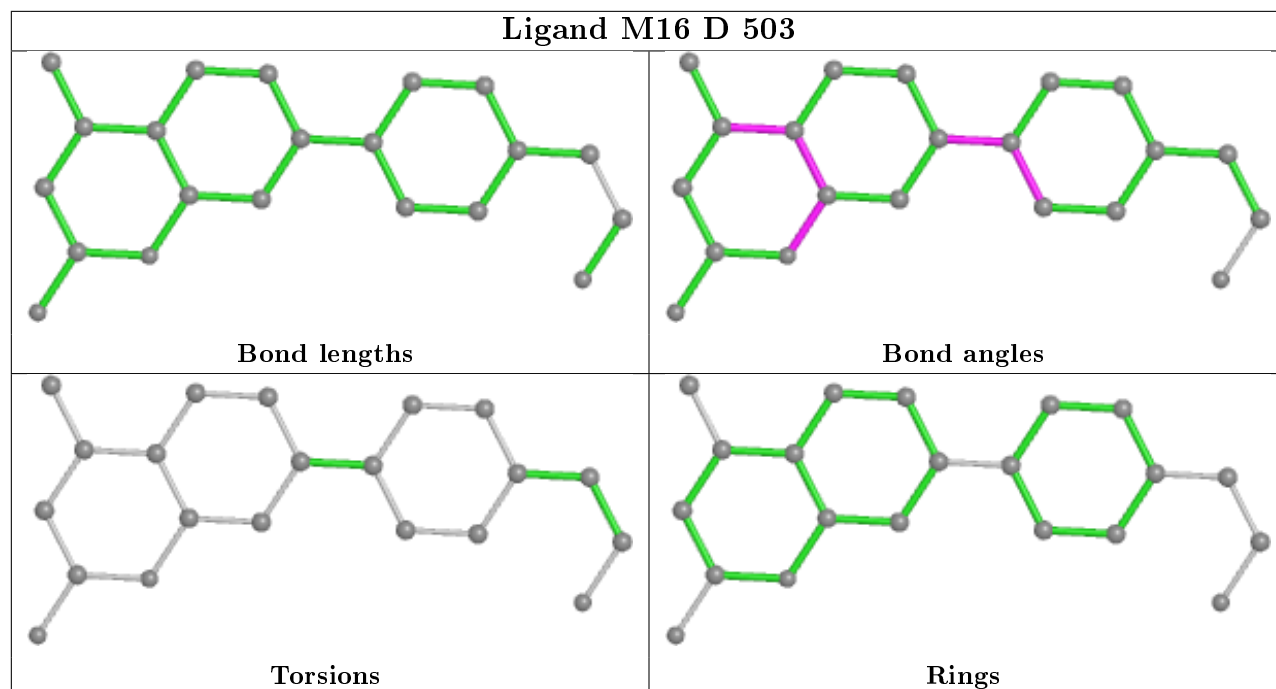
32 monomers are involved in 84 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	505	BTB	4	0
3	C	503	M16	1	0
4	B	507	BTB	3	0
2	E	501	HEM	2	0
4	C	506	BTB	1	0
2	C	501	HEM	3	0
4	D	505	BTB	6	0
4	E	505	BTB	1	0
4	C	505	BTB	2	0
3	A	502	M16	2	0
3	D	502	M16	1	0
3	F	801	M16	1	0
2	A	501	HEM	2	0
4	A	505	BTB	2	0
4	E	504	BTB	6	0
3	F	803	M16	2	0
4	A	504	BTB	4	0
3	E	502	M16	3	0
4	B	504	BTB	4	0
4	F	805	BTB	5	0
4	D	506	BTB	3	0
3	B	502	M16	2	0
2	D	501	HEM	2	0
4	B	506	BTB	3	0
3	A	503	M16	1	0
4	A	509	BTB	4	0
4	F	806	BTB	4	0
7	E	507	GOL	1	0
3	C	502	M16	3	0
4	D	504	BTB	4	0
2	F	802	HEM	4	0
2	B	501	HEM	3	0

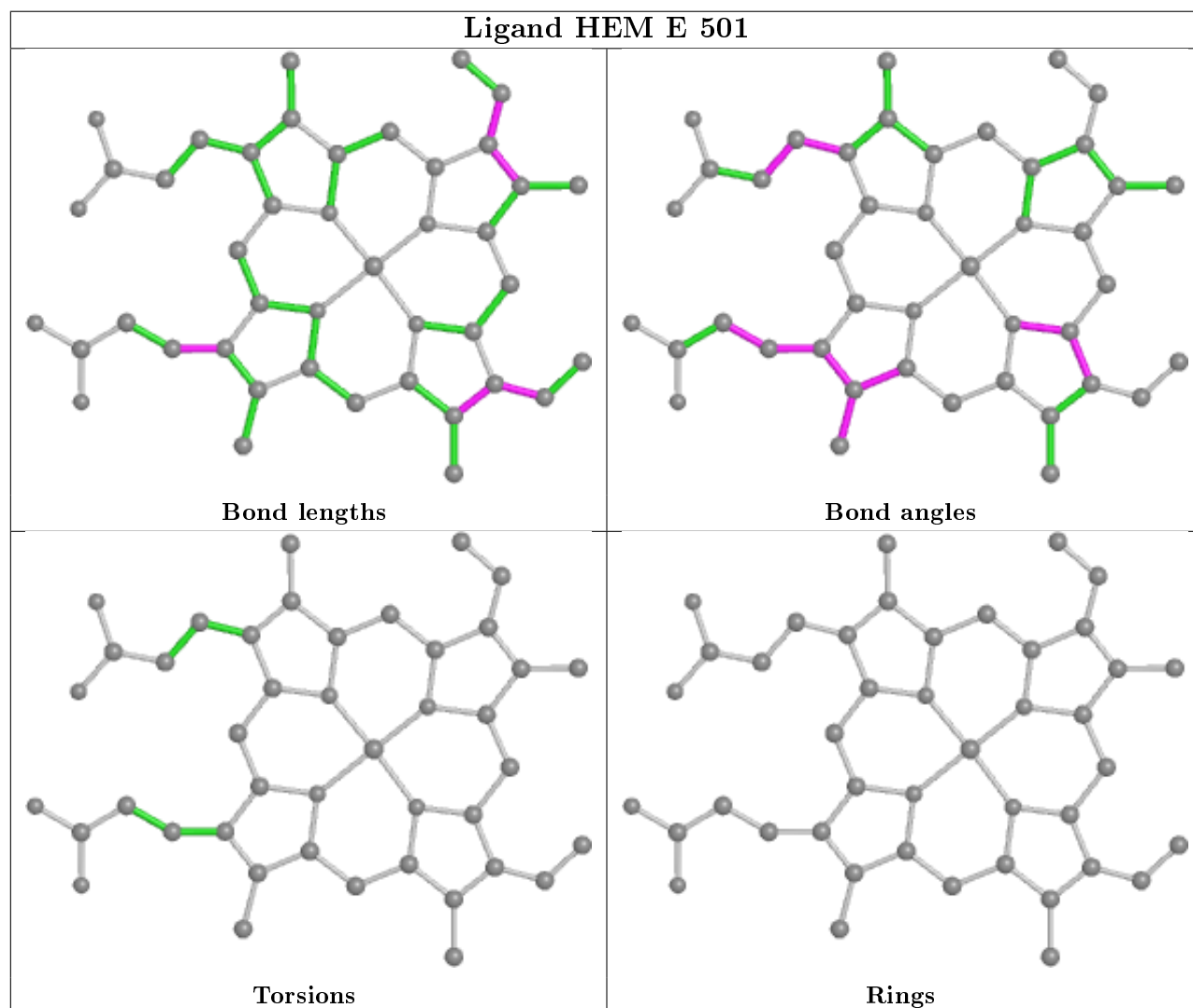
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

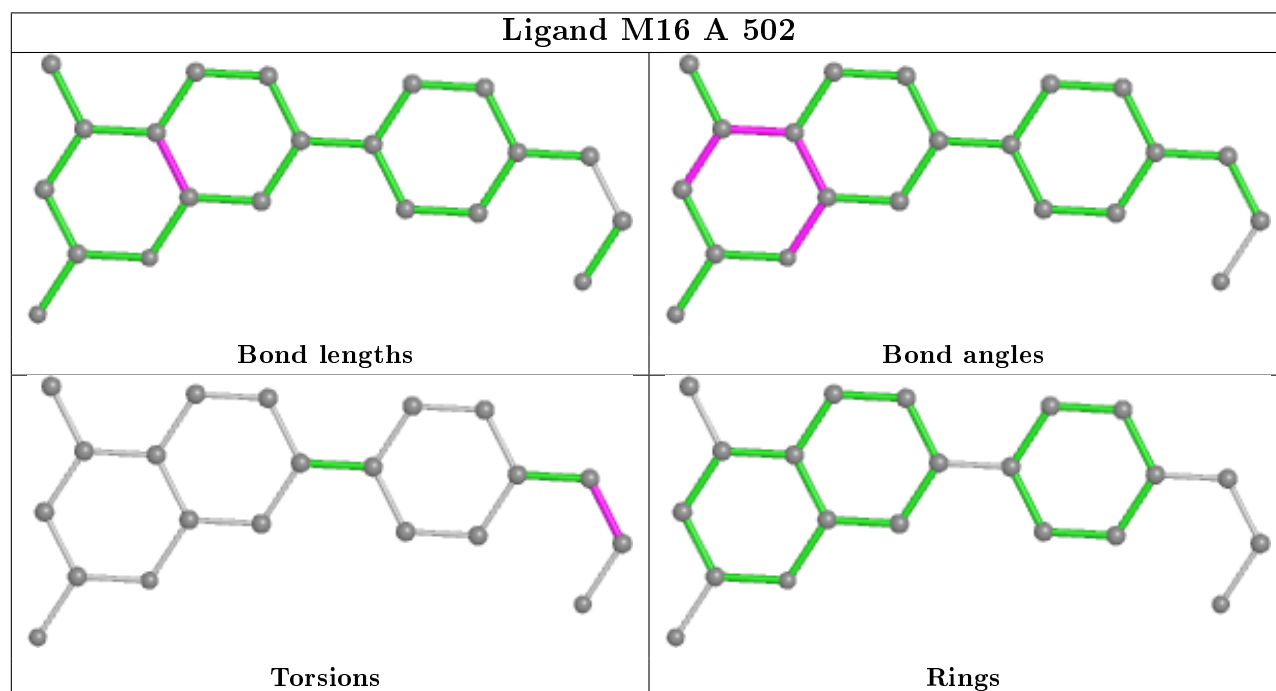
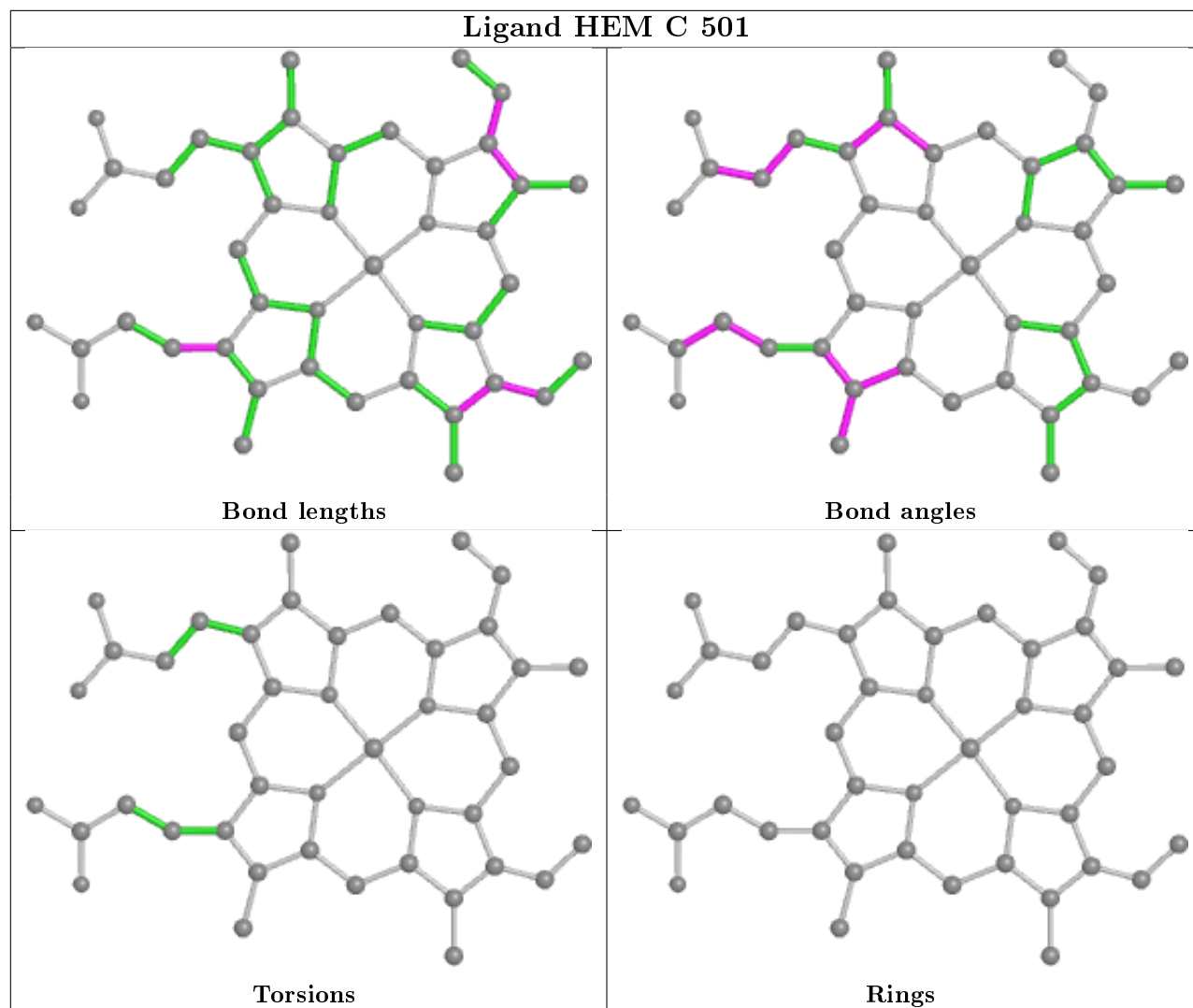


Ligand M16 D 503

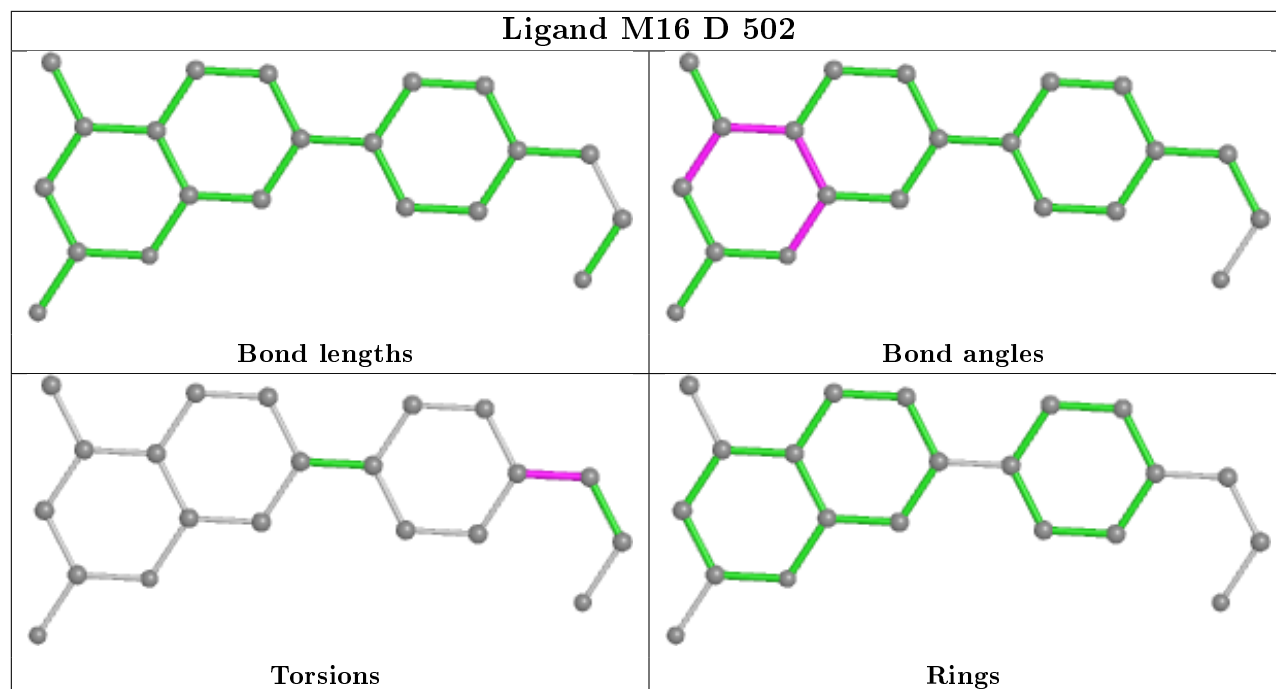


Ligand HEM E 501

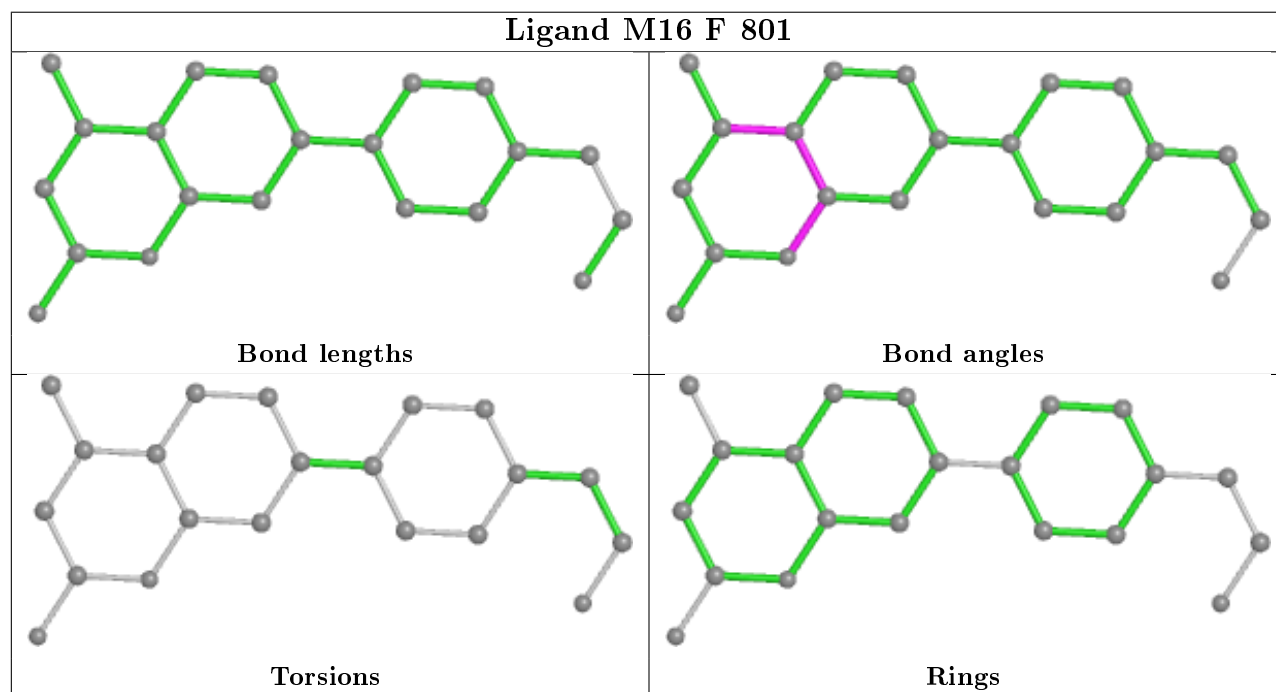


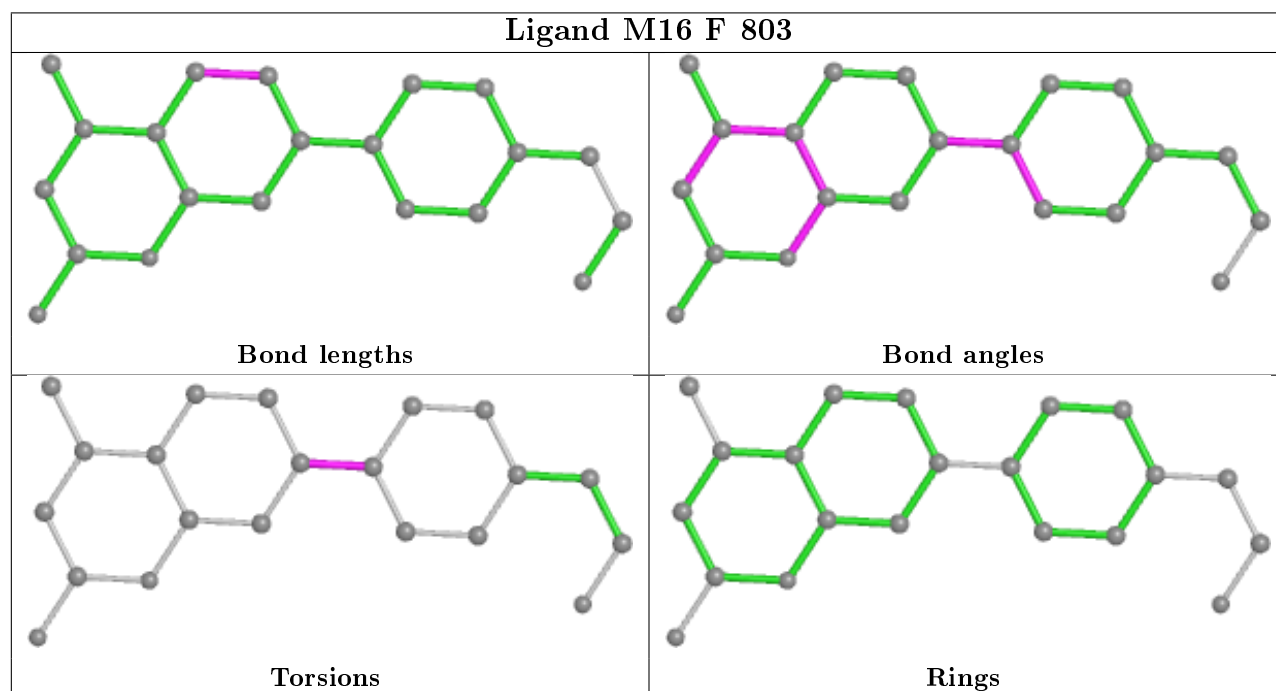
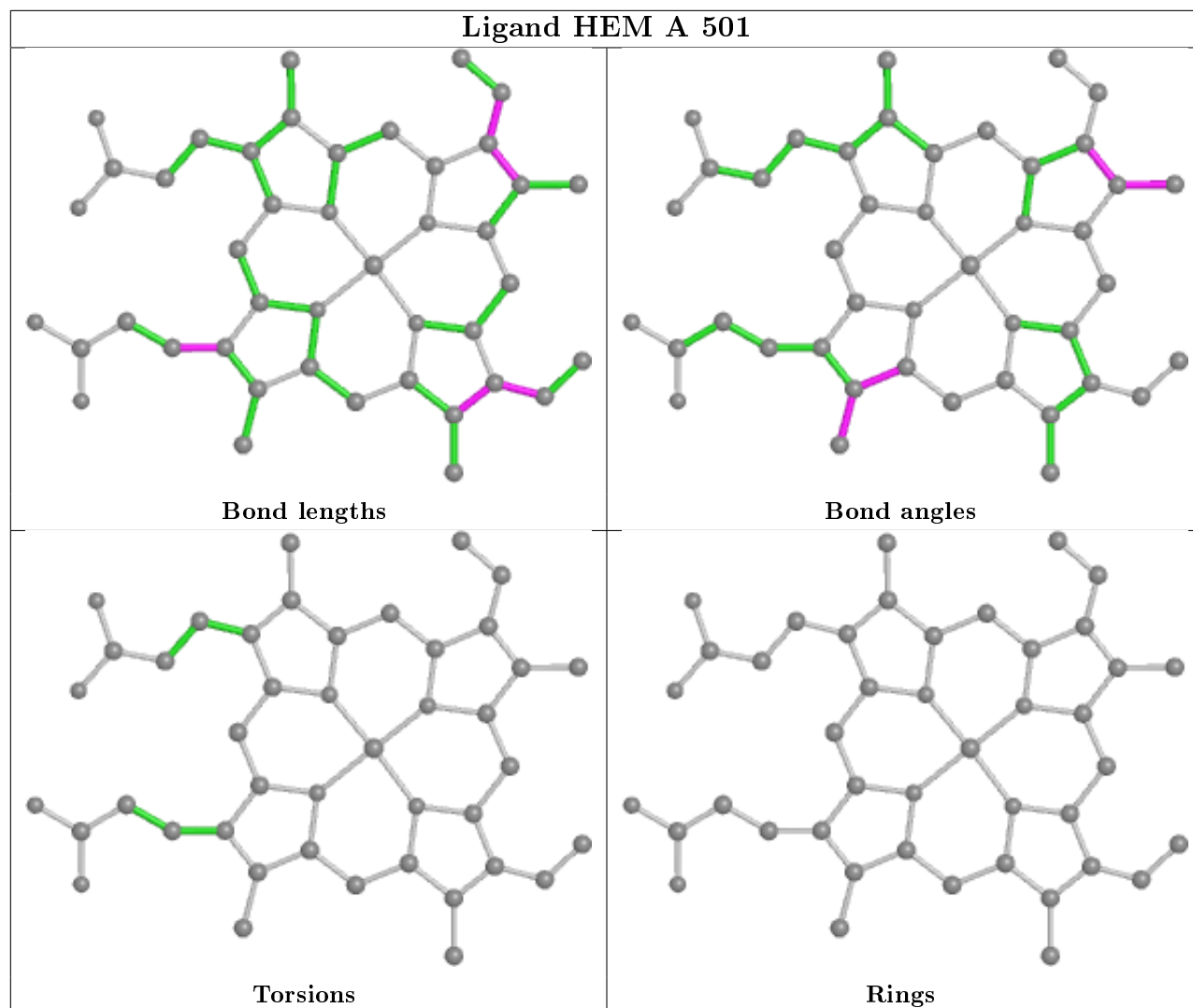


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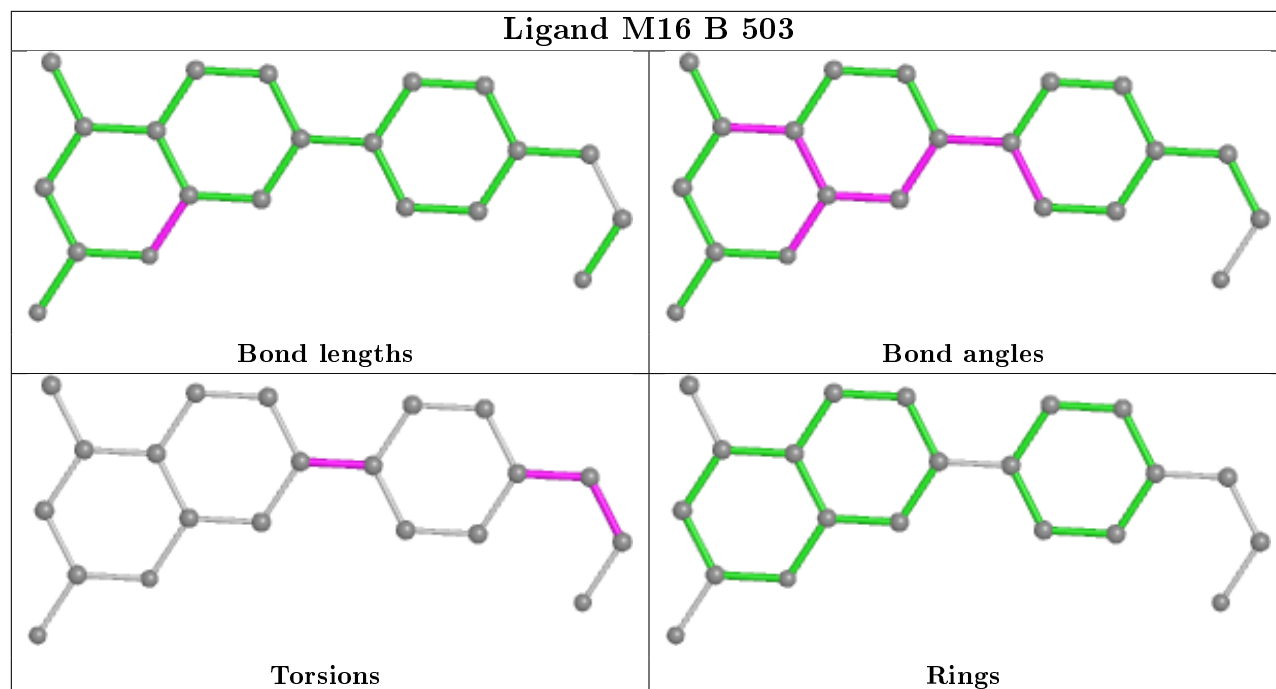


Ligand M16 F 801

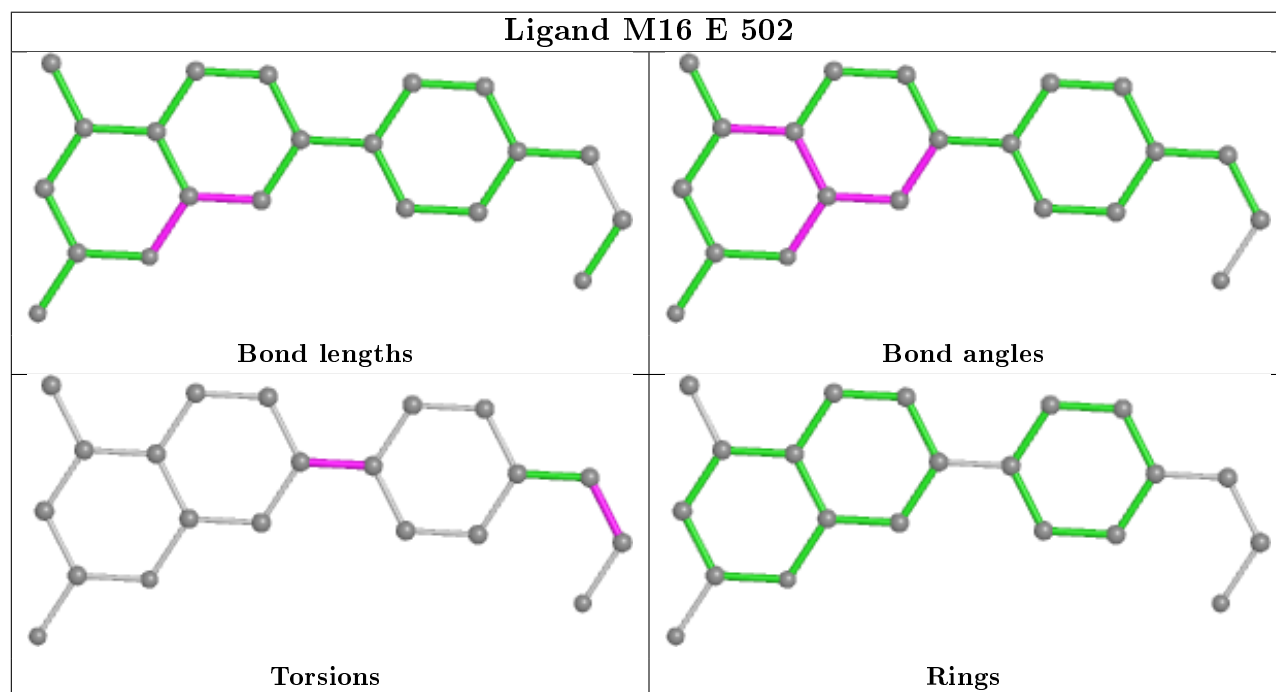




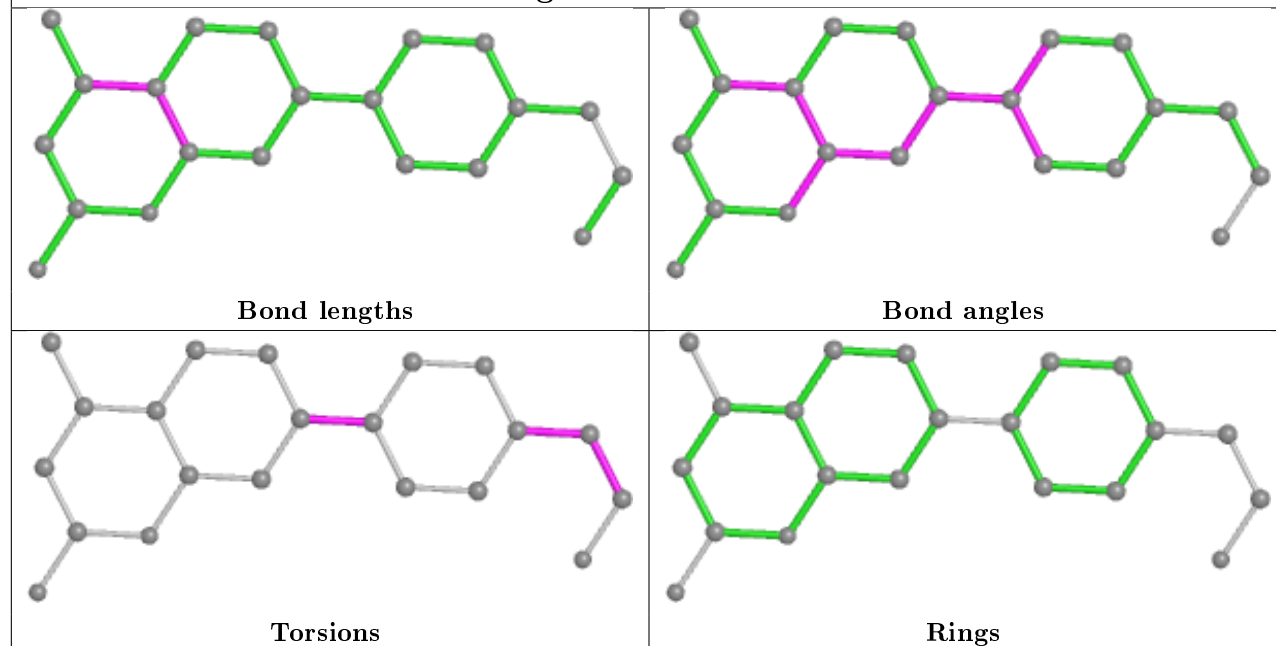
Ligand M16 B 503



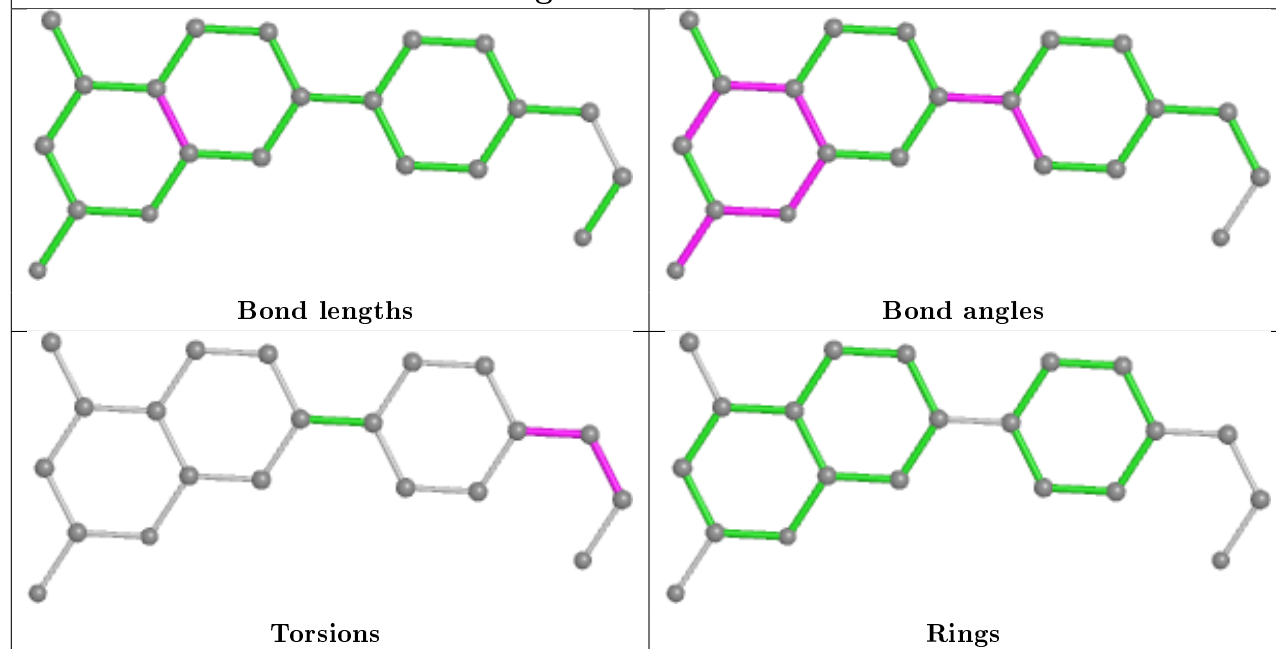
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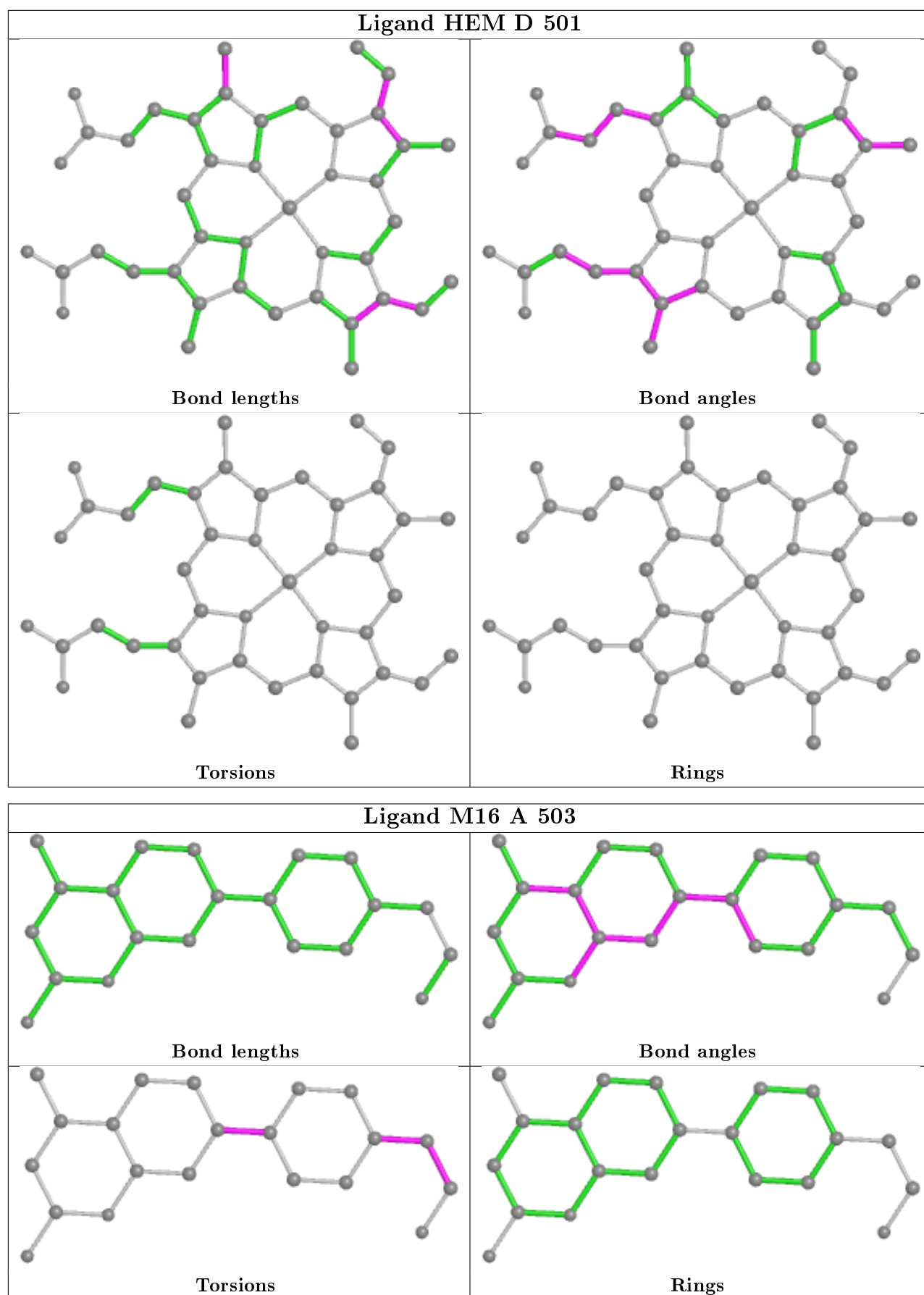


Ligand M16 F 804

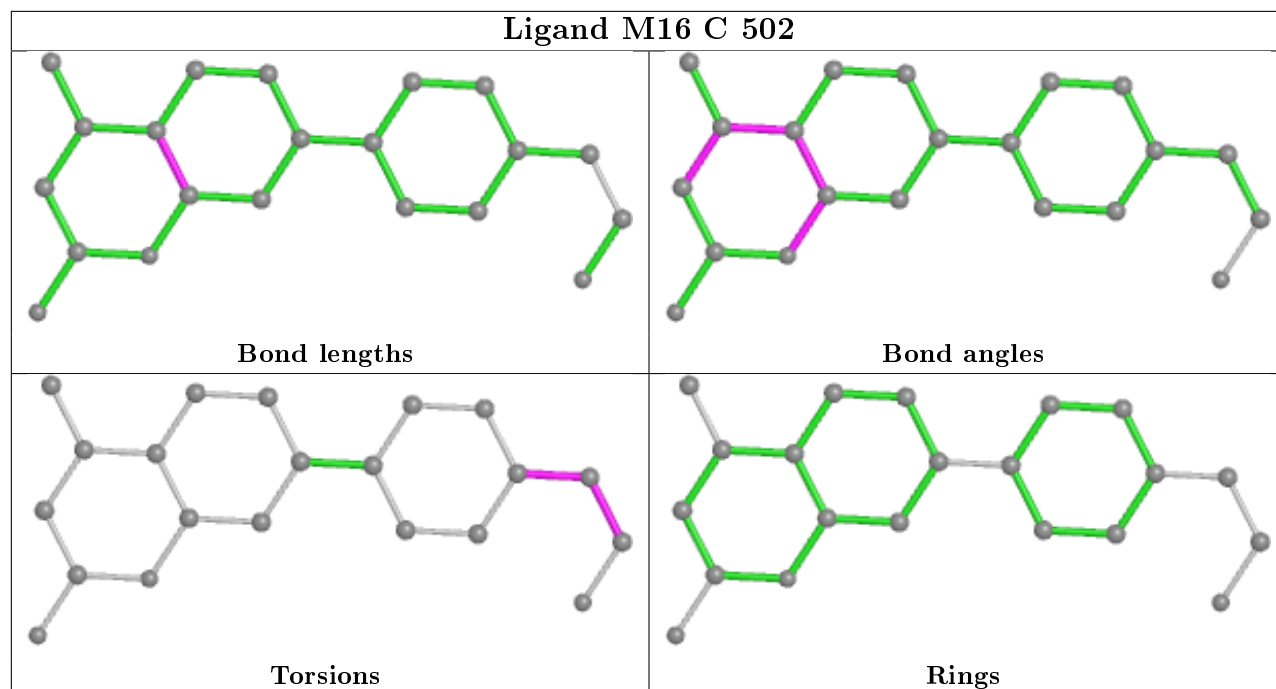


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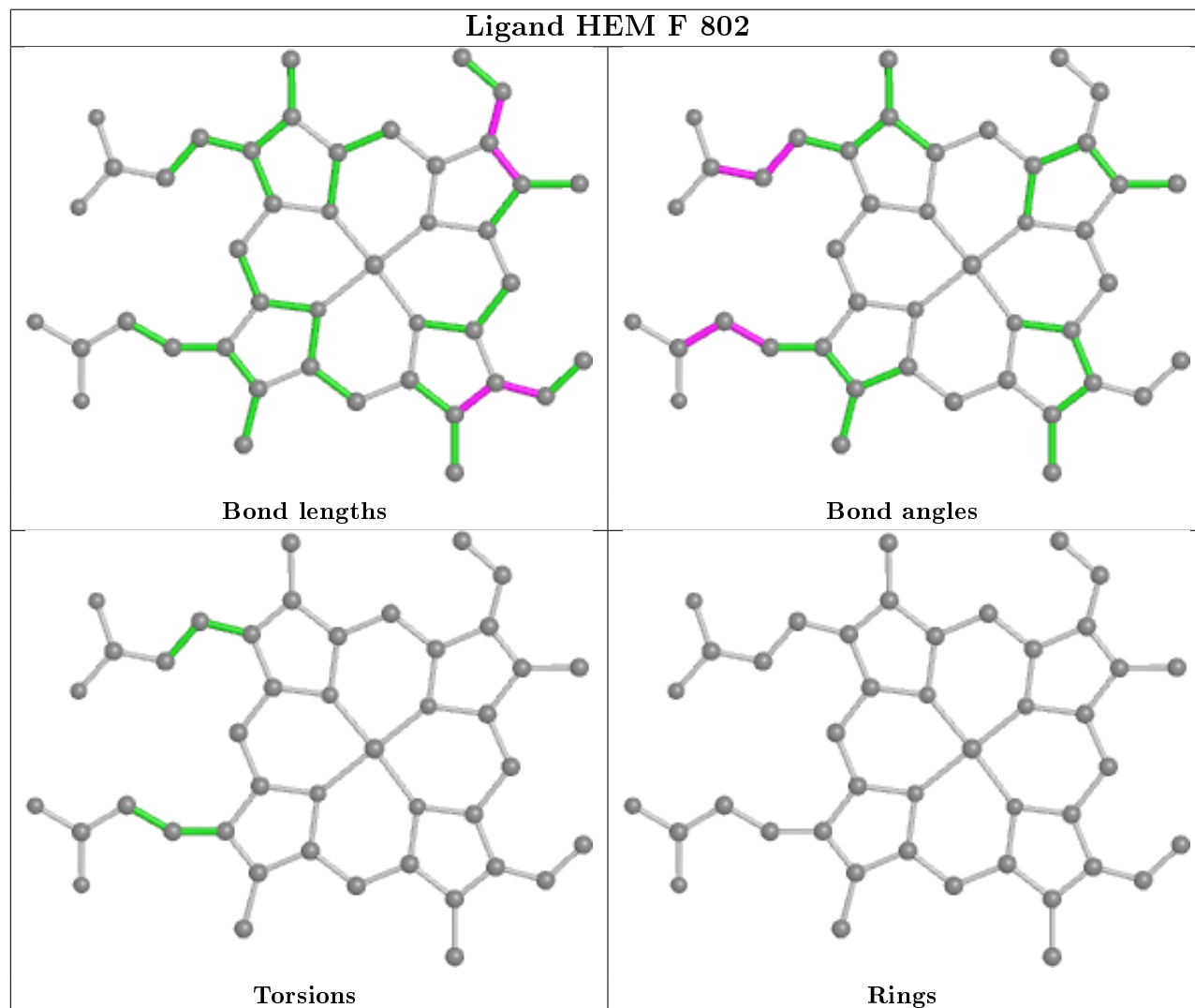


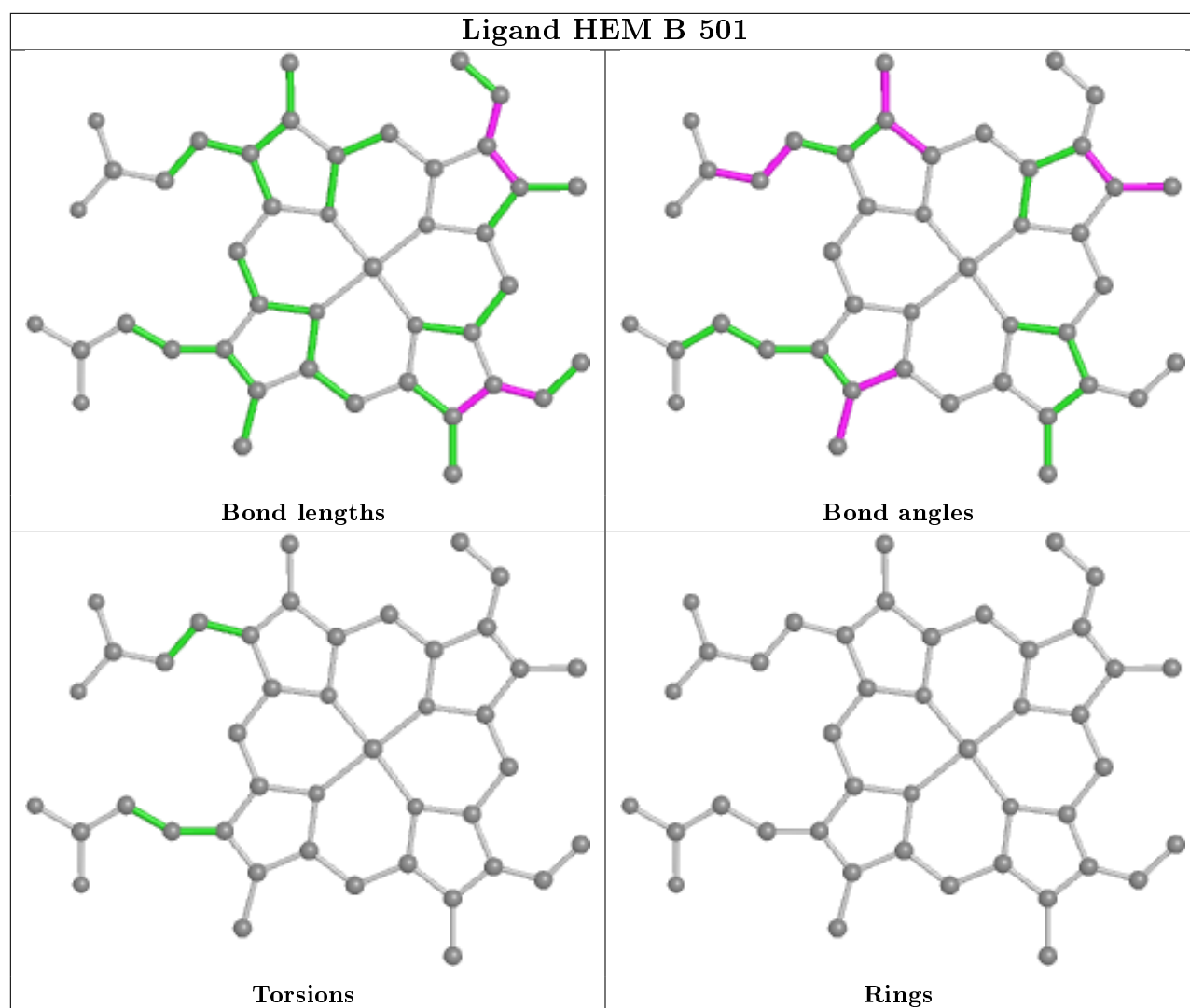


Ligand M16 C 502



Ligand HEM F 802





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	401/440 (91%)	-0.05	8 (1%) 65 63	18, 36, 78, 126	0
1	B	402/440 (91%)	-0.08	7 (1%) 70 68	18, 34, 63, 105	0
1	C	401/440 (91%)	0.29	31 (7%) 13 12	21, 48, 103, 129	0
1	D	402/440 (91%)	-0.03	9 (2%) 62 59	16, 34, 71, 111	0
1	E	401/440 (91%)	-0.06	7 (1%) 70 68	18, 34, 72, 101	0
1	F	402/440 (91%)	-0.13	3 (0%) 87 86	16, 33, 66, 104	0
All	All	2409/2640 (91%)	-0.01	65 (2%) 54 52	16, 36, 82, 129	0

The worst 5 of 65 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	119	ALA	10.5
1	D	67	LYS	6.4
1	C	308	GLU	5.7
1	B	119	ALA	5.2
1	A	259	GLY	4.8

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 monosaccharides 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	ZN	F	808	1/1	0.55	0.24	128,128,128,128	0
4	BTB	D	504	14/14	0.68	0.25	30,63,82,88	0
6	GD	B	509	1/1	0.69	0.43	195,195,195,195	0
4	BTB	A	504	14/14	0.72	0.21	46,68,77,80	0
4	BTB	C	505	14/14	0.72	0.16	67,78,84,85	0
4	BTB	B	506	14/14	0.74	0.15	74,79,83,85	0
6	GD	C	509	1/1	0.78	0.13	126,126,126,126	0
4	BTB	A	509	14/14	0.78	0.24	35,56,71,73	0
4	BTB	C	504	14/14	0.78	0.18	61,77,85,86	0
4	BTB	E	503	14/14	0.79	0.22	56,84,103,108	0
4	BTB	B	504	14/14	0.79	0.19	30,58,75,78	0
4	BTB	D	506	14/14	0.79	0.13	74,79,86,94	0
4	BTB	B	505	14/14	0.80	0.18	71,85,91,93	0
4	BTB	B	507	14/14	0.81	0.15	71,80,86,86	0
4	BTB	F	805	14/14	0.81	0.20	31,61,73,81	0
6	GD	D	507	1/1	0.81	0.30	132,132,132,132	0
4	BTB	A	505	14/14	0.82	0.18	76,85,92,93	0
4	BTB	E	505	14/14	0.82	0.19	60,72,85,87	0
4	BTB	F	806	14/14	0.85	0.21	54,70,78,81	0
4	BTB	E	504	14/14	0.85	0.18	63,70,92,100	0
5	ZN	B	510	1/1	0.85	0.17	104,104,104,104	0
4	BTB	C	506	14/14	0.88	0.16	59,66,86,94	0
5	ZN	D	509	1/1	0.88	0.20	122,122,122,122	0
3	M16	F	801	21/21	0.90	0.20	20,47,69,71	0
3	M16	C	503	21/21	0.90	0.18	31,53,80,81	0
7	GOL	C	508	6/6	0.92	0.18	35,50,61,64	0
3	M16	A	503	21/21	0.92	0.17	22,44,73,77	0
4	BTB	D	505	14/14	0.93	0.25	4,63,73,75	0
3	M16	C	502	21/21	0.93	0.12	25,53,69,75	0
3	M16	F	803	21/21	0.94	0.15	15,26,73,78	0
3	M16	B	503	21/21	0.94	0.15	18,37,74,74	0
3	M16	E	502	21/21	0.94	0.13	20,32,69,70	0
3	M16	B	502	21/21	0.94	0.13	15,34,65,70	0
2	HEM	D	501	43/43	0.94	0.14	7,21,44,49	0
3	M16	D	502	21/21	0.94	0.14	9,26,68,71	0
5	ZN	E	508	1/1	0.95	0.06	51,51,51,51	0
3	M16	F	804	21/21	0.95	0.14	19,28,80,81	0

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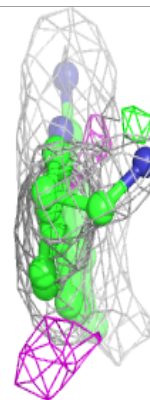
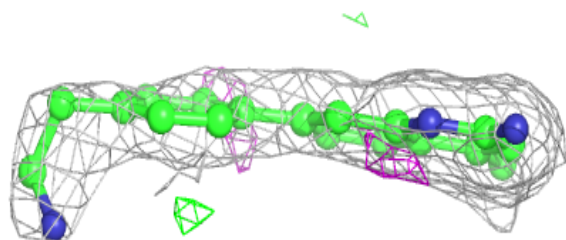
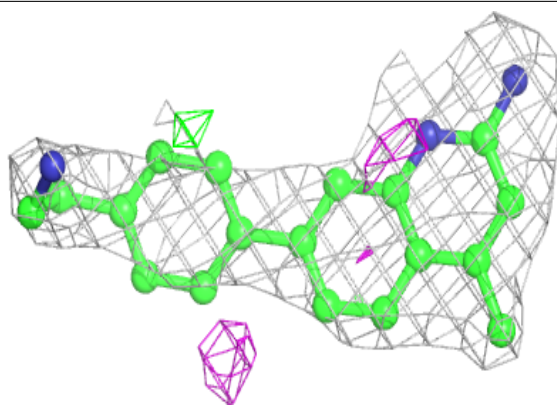
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	M16	A	502	21/21	0.95	0.14	23,30,73,76	0
3	M16	D	503	21/21	0.95	0.19	21,36,85,87	0
2	HEM	C	501	43/43	0.96	0.11	19,34,63,77	0
5	ZN	C	510	1/1	0.96	0.09	57,57,57,57	0
7	GOL	E	507	6/6	0.97	0.23	0,18,43,57	0
5	ZN	A	510	1/1	0.97	0.06	58,58,58,58	0
2	HEM	E	501	43/43	0.98	0.12	13,23,57,72	0
2	HEM	A	501	43/43	0.98	0.11	12,23,55,70	0
6	GD	A	507	1/1	0.98	0.07	81,81,81,81	0
2	HEM	F	802	43/43	0.98	0.13	8,20,56,67	0
2	HEM	B	501	43/43	0.98	0.12	11,22,49,53	0
5	ZN	E	506	1/1	0.99	0.11	32,32,32,32	0
6	GD	F	807	1/1	0.99	0.14	47,47,47,47	0
6	GD	B	508	1/1	0.99	0.10	38,38,38,38	0
6	GD	D	508	1/1	0.99	0.11	38,38,38,38	0
5	ZN	C	507	1/1	1.00	0.09	34,34,34,34	0
5	ZN	A	506	1/1	1.00	0.10	31,31,31,31	0
6	GD	A	508	1/1	1.00	0.08	36,36,36,36	0

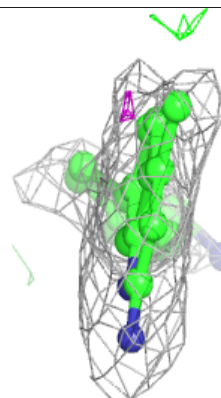
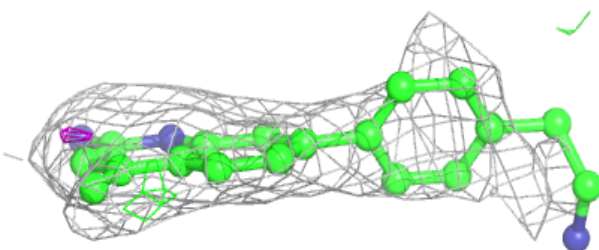
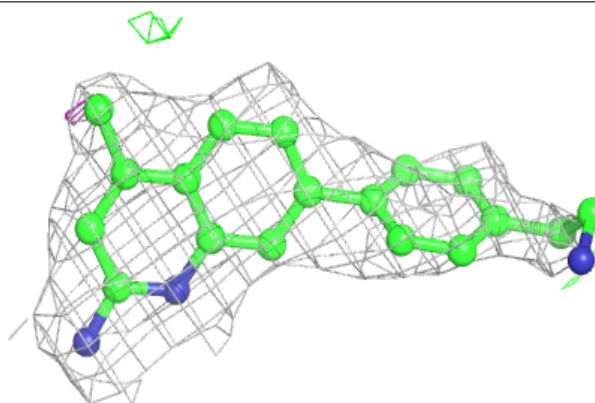
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around M16 F 801:

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

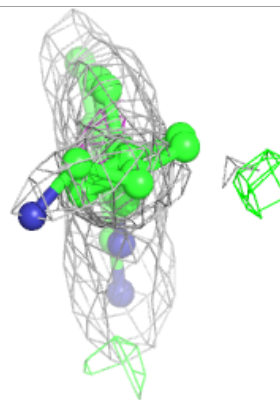
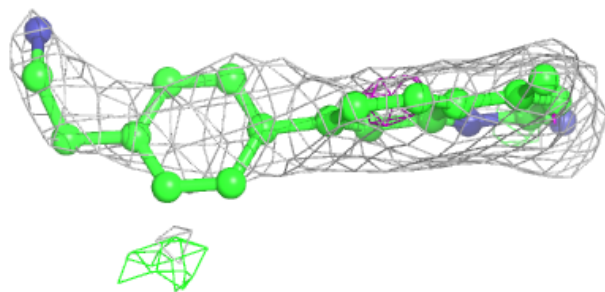
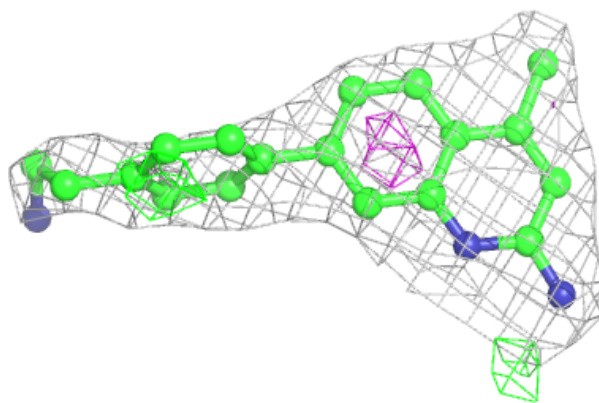
**Electron density around M16 C 503:**

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

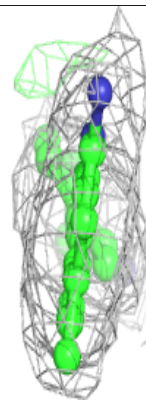
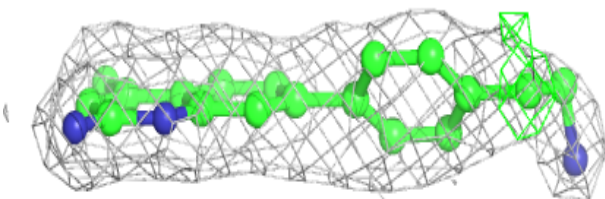
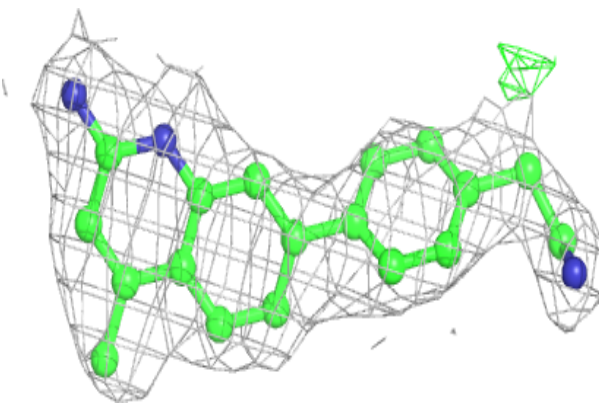


Electron density around M16 A 503:

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

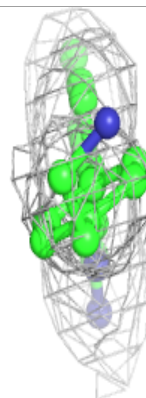
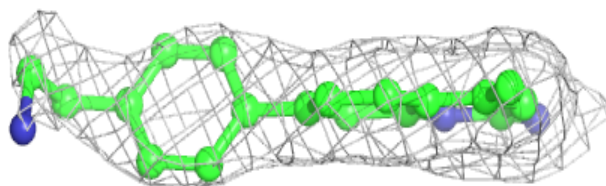
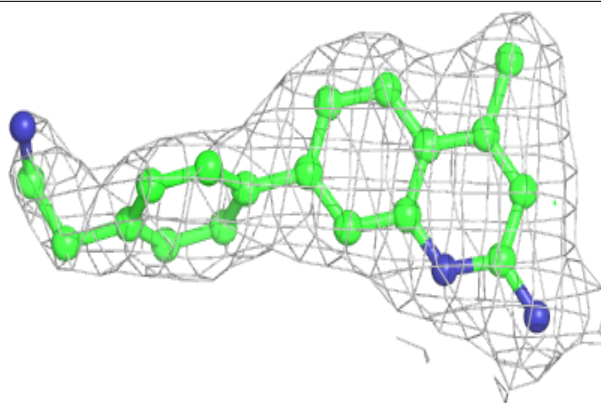
**Electron density around M16 C 502:**

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

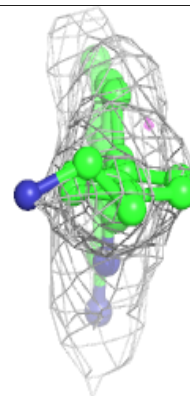
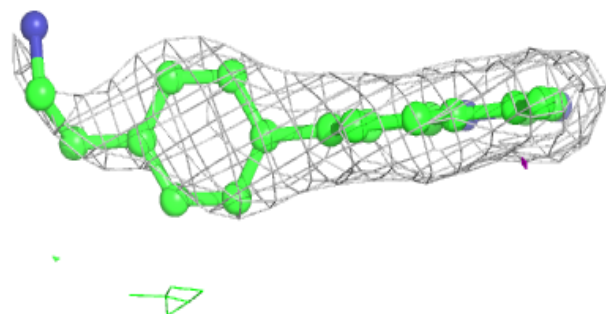
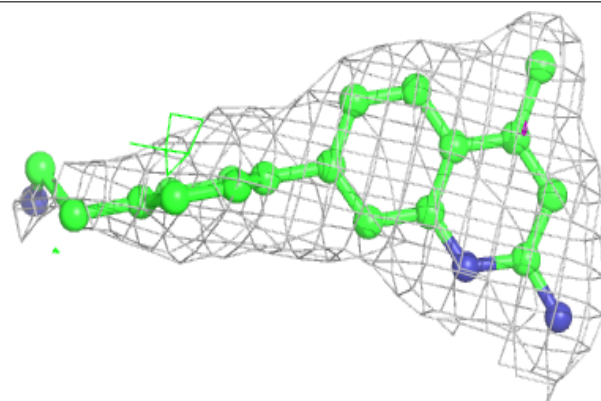


Electron density around M16 F 803:

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

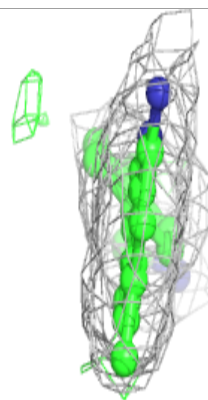
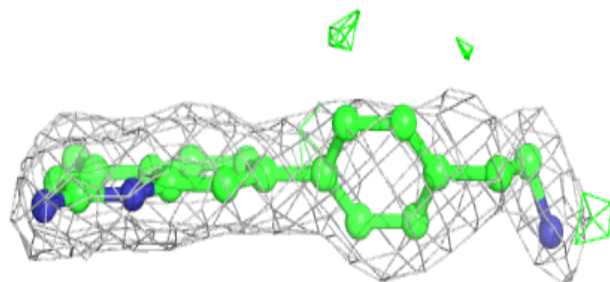
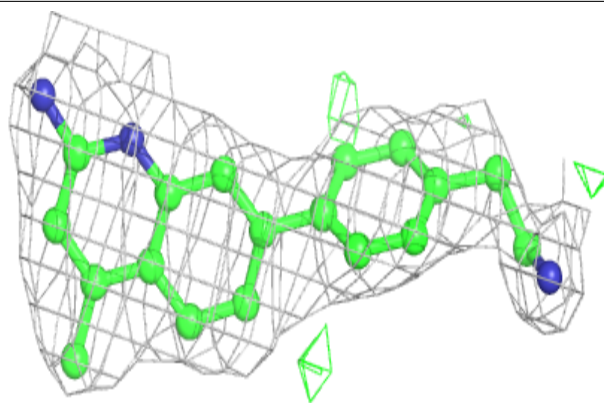
**Electron density around M16 B 503:**

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

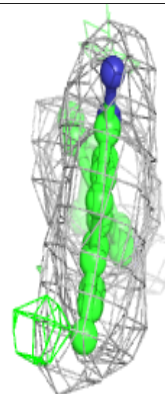
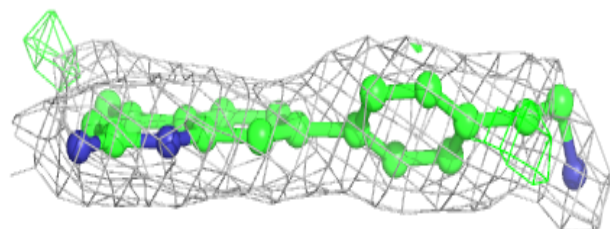
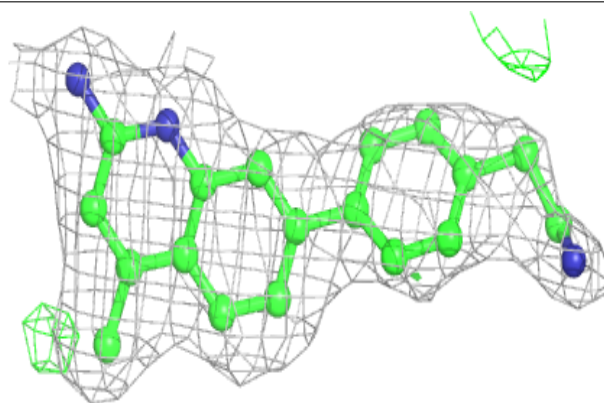


Electron density around M16 E 502:

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

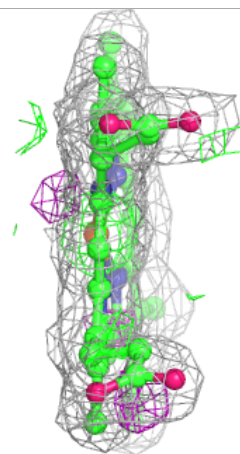
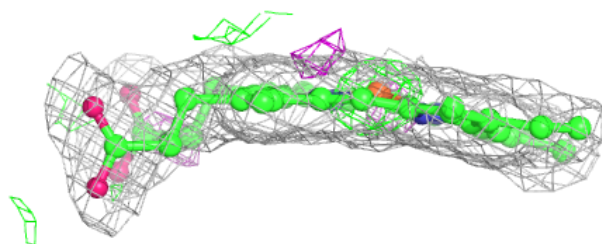
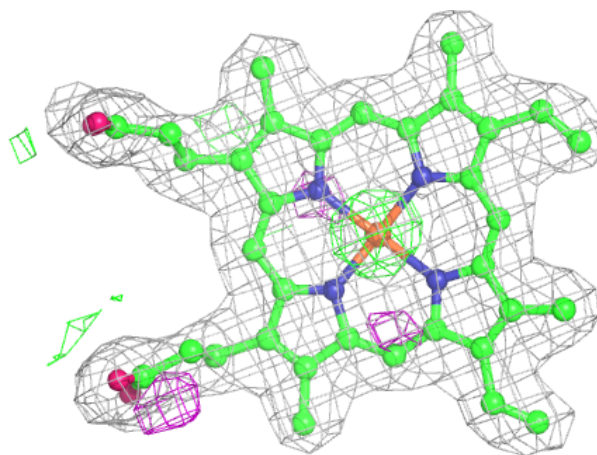
**Electron density around M16 B 502:**

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



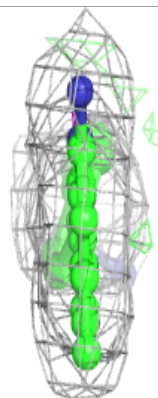
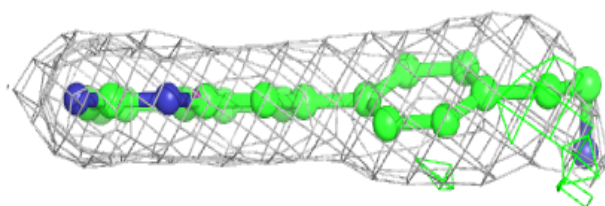
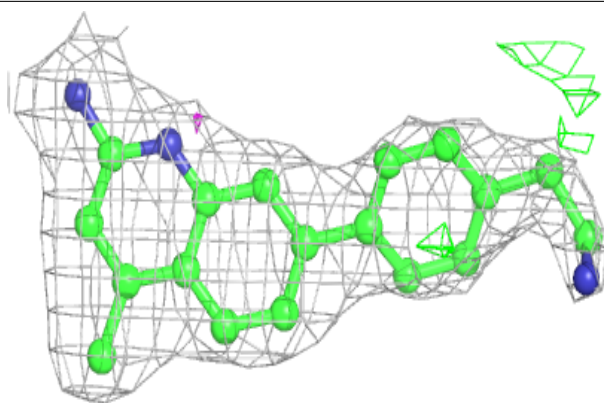
Electron density around HEM D 501:

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

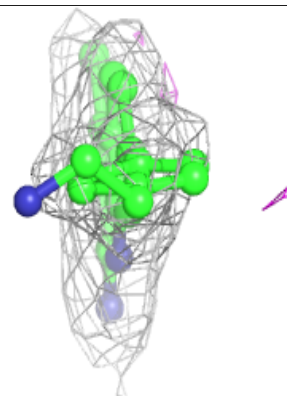
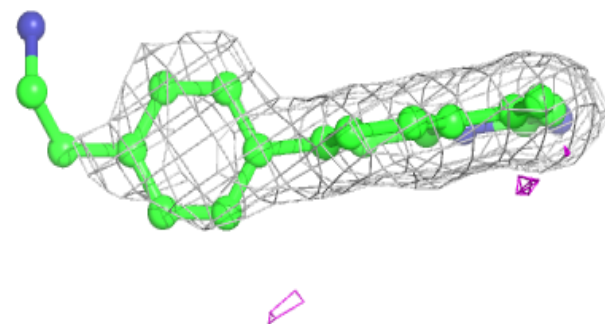
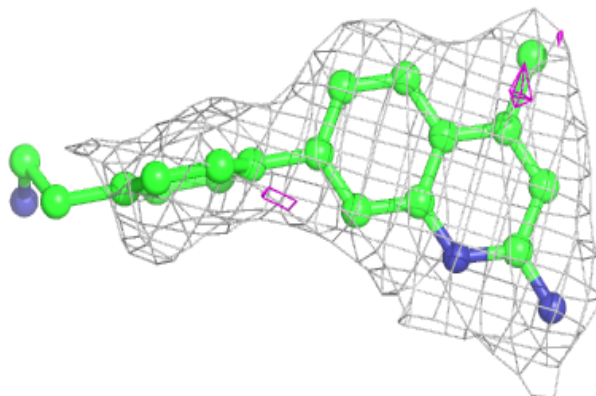


Electron density around M16 D 502:

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

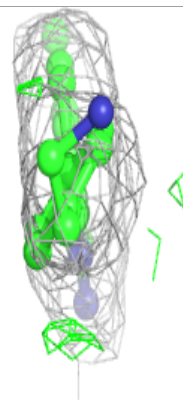
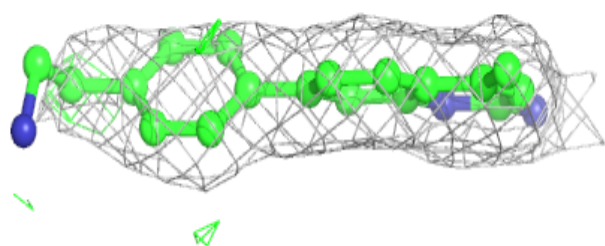
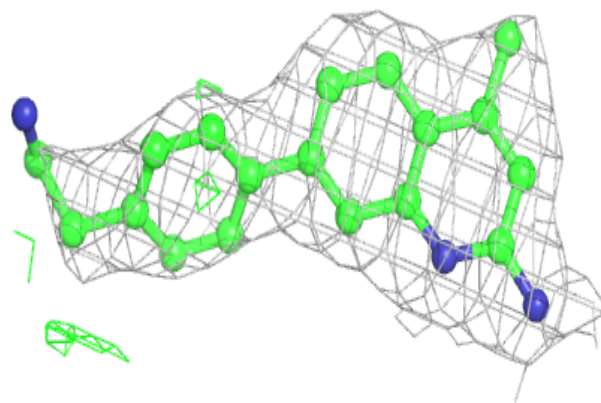
**Electron density around M16 F 804:**

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

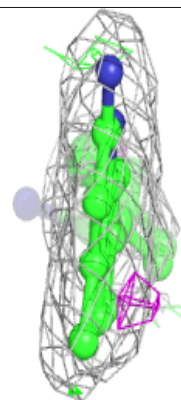
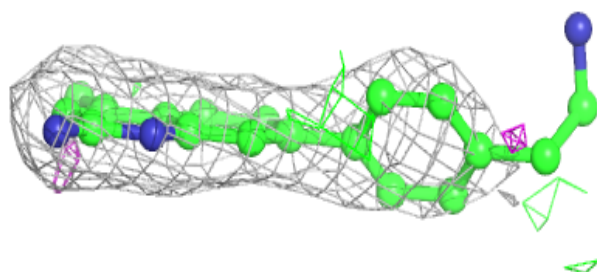
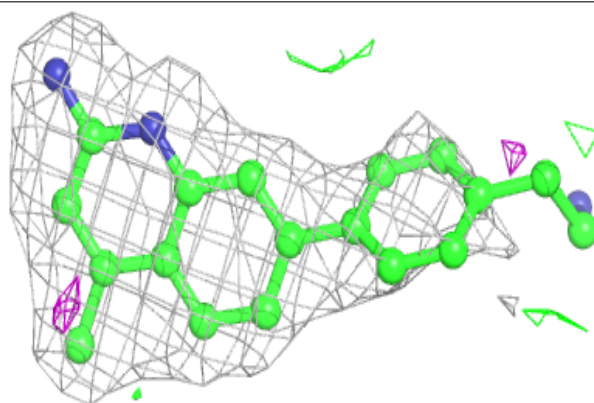


Electron density around M16 A 502:

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

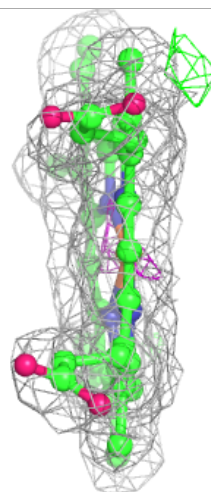
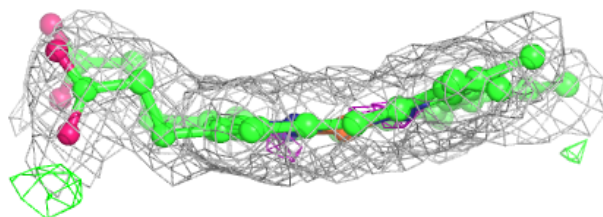
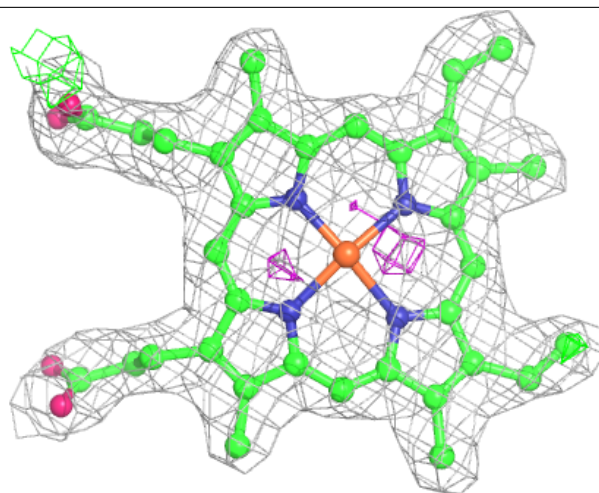
**Electron density around M16 D 503:**

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



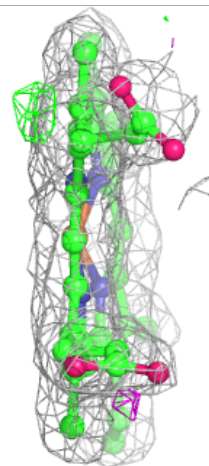
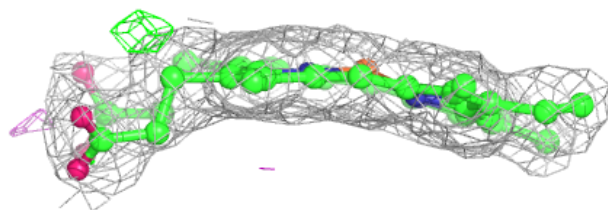
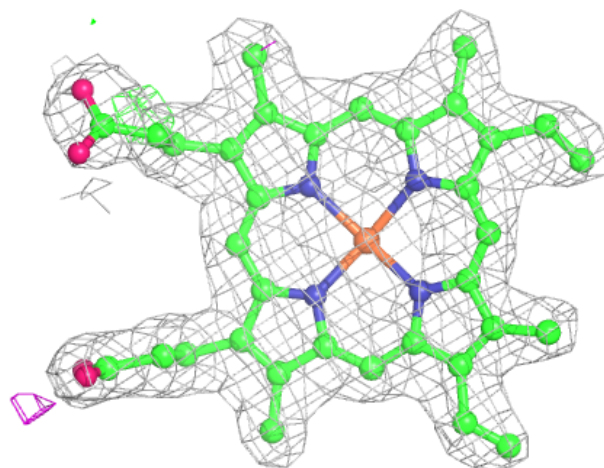
Electron density around HEM C 501:

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



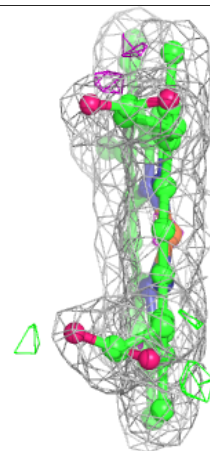
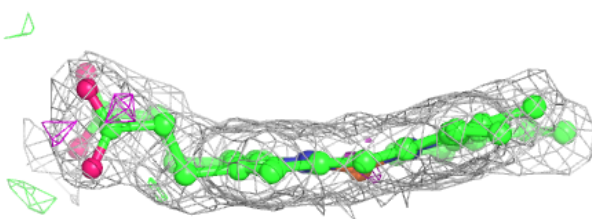
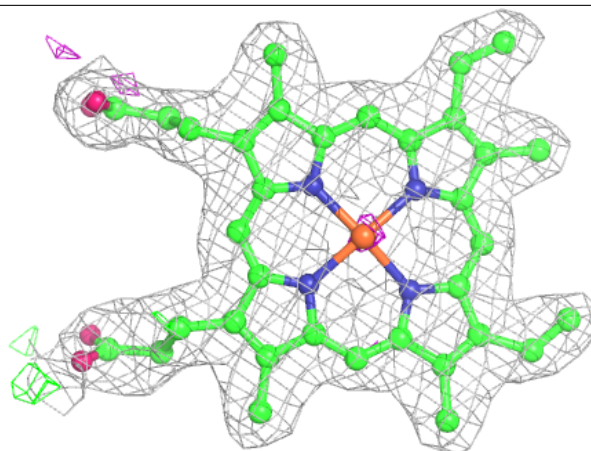
Electron density around HEM E 501:

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



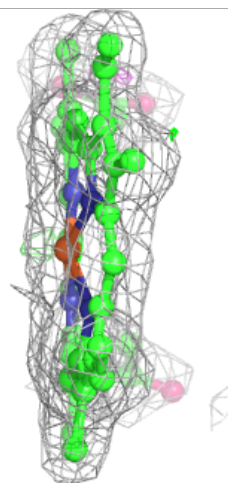
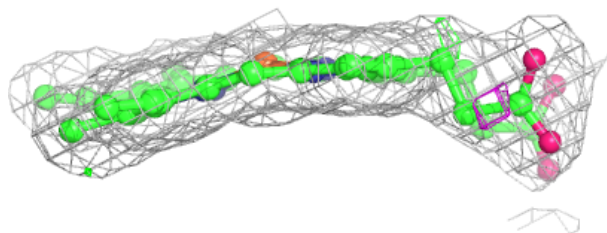
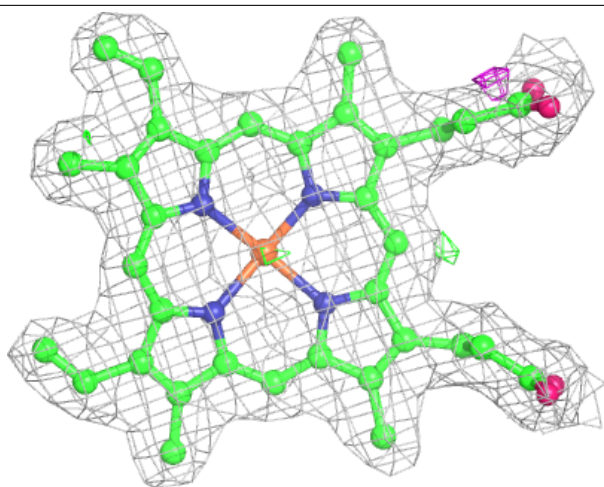
Electron density around HEM A 501:

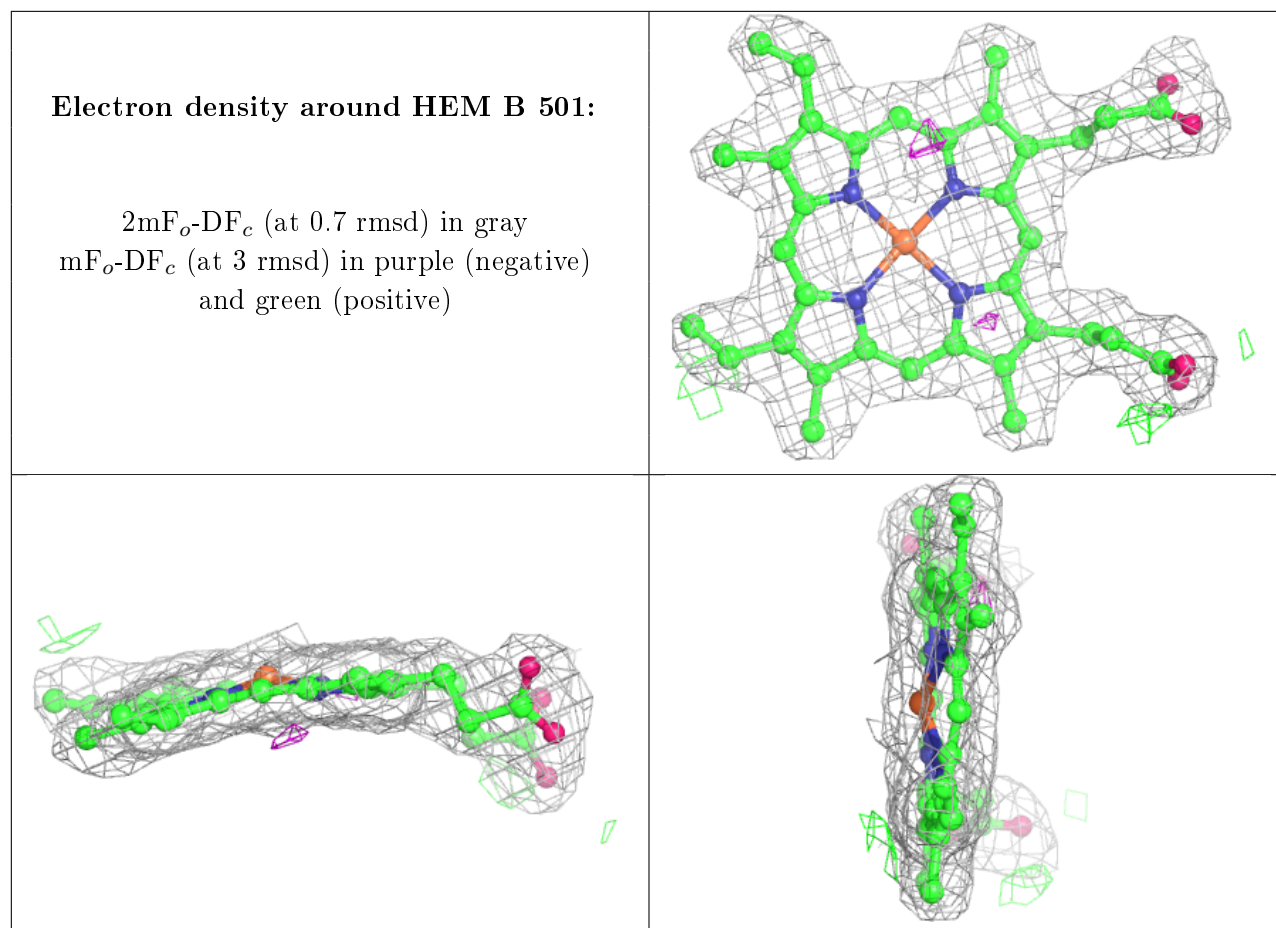
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM F 802:

$2mF_o-DF_c$ (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.