



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 25, 2025 – 02:30 PM EST

PDB ID : 9MYV / pdb_00009myv
Title : Structure of human neuronal nitric oxide synthase R354A/G357D mutant heme domain bound with 2-(2-amino-6-fluoro-4-methylquinolin-7-yl)-5-(aminomethyl)phenol
Authors : Li, H.; Poulos, T.L.
Deposited on : 2025-01-22
Resolution : 2.15 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

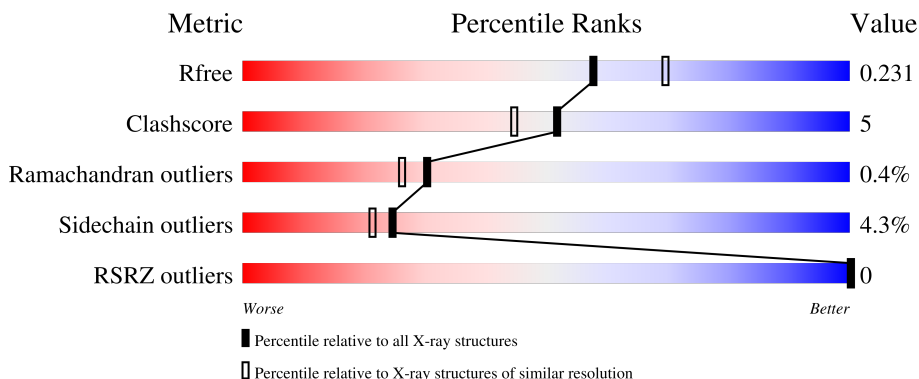
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.15 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}	164625	3336 (2.16-2.12)
Clashscore	180529	3585 (2.16-2.12)
Ramachandran outliers	177936	3554 (2.16-2.12)
Sidechain outliers	177891	3553 (2.16-2.12)
RSRZ outliers	164620	3337 (2.16-2.12)

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	423	
1	B	423	
1	C	423	
1	D	423	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14588 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, brain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	4	0
			3363	2157	572	613	21			
1	B	419	Total	C	N	O	S	0	3	0
			3431	2194	589	627	21			
1	C	420	Total	C	N	O	S	0	4	0
			3439	2200	590	627	22			
1	D	411	Total	C	N	O	S	0	2	0
			3355	2150	572	612	21			

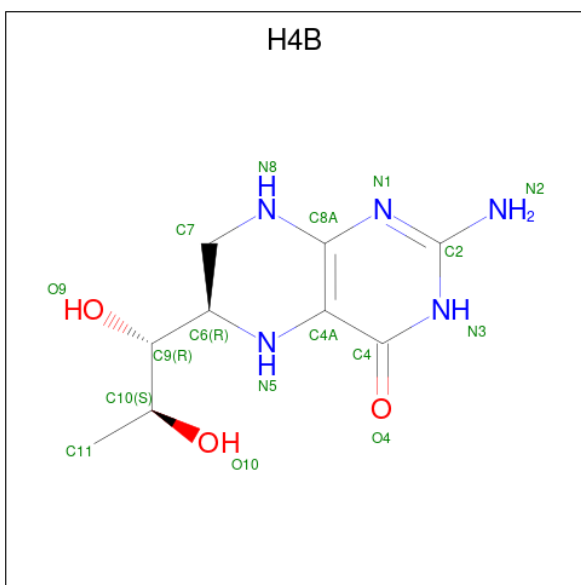
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	354	ALA	ARG	engineered mutation	UNP P29475
A	357	ASP	GLY	engineered mutation	UNP P29475
A	723	LEU	-	expression tag	UNP P29475
A	724	VAL	-	expression tag	UNP P29475
B	354	ALA	ARG	engineered mutation	UNP P29475
B	357	ASP	GLY	engineered mutation	UNP P29475
B	723	LEU	-	expression tag	UNP P29475
B	724	VAL	-	expression tag	UNP P29475
C	354	ALA	ARG	engineered mutation	UNP P29475
C	357	ASP	GLY	engineered mutation	UNP P29475
C	723	LEU	-	expression tag	UNP P29475
C	724	VAL	-	expression tag	UNP P29475
D	354	ALA	ARG	engineered mutation	UNP P29475
D	357	ASP	GLY	engineered mutation	UNP P29475
D	723	LEU	-	expression tag	UNP P29475
D	724	VAL	-	expression tag	UNP P29475

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

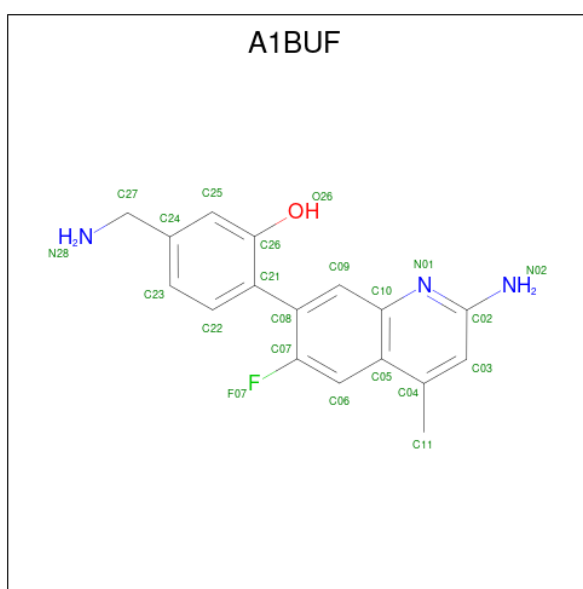


- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (CCD ID: H4B) (formula: $\text{C}_9\text{H}_{15}\text{N}_5\text{O}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		
3	C	1	Total	C	N	O	0	0
			17	9	5	3		
3	D	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is (2M)-2-(2-amino-6-fluoro-4-methylquinolin-7-yl)-5-(aminomethyl)phenol (CCD ID: A1BUF) (formula: C₁₇H₁₆FN₃O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	F	N	0	0
			21	17	1	3		
4	B	1	Total	C	F	N	O	0
			22	17	1	3	1	
4	C	1	Total	C	F	N	O	0
			22	17	1	3	1	
4	D	1	Total	C	F	N	O	0
			22	17	1	3	1	

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	Zn	0	0
			1	1		
6	C	1	Total	Zn	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	163	Total	O	0	0
			163	163		

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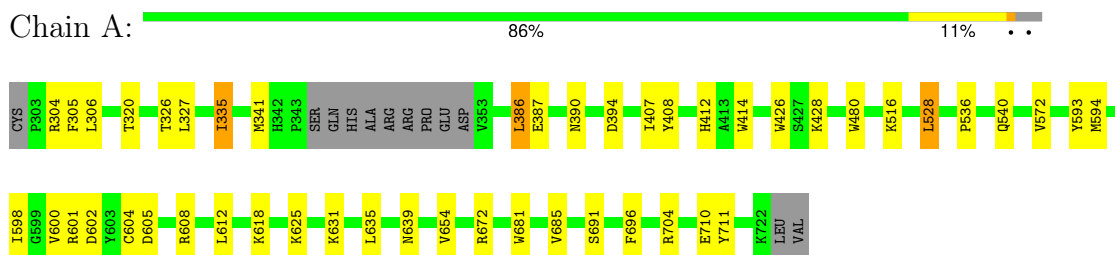
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	164	Total 164	O 164	0	0
7	C	145	Total 145	O 145	0	0
7	D	163	Total 163	O 163	0	0

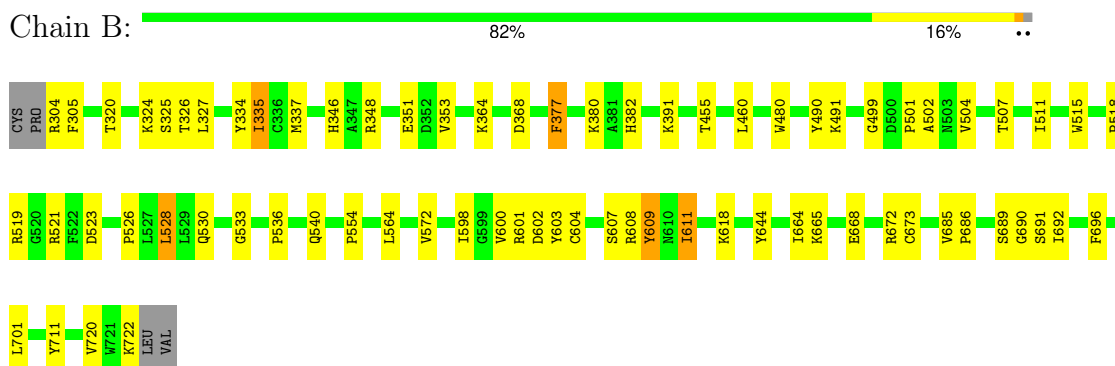
3 Residue-property plots

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.

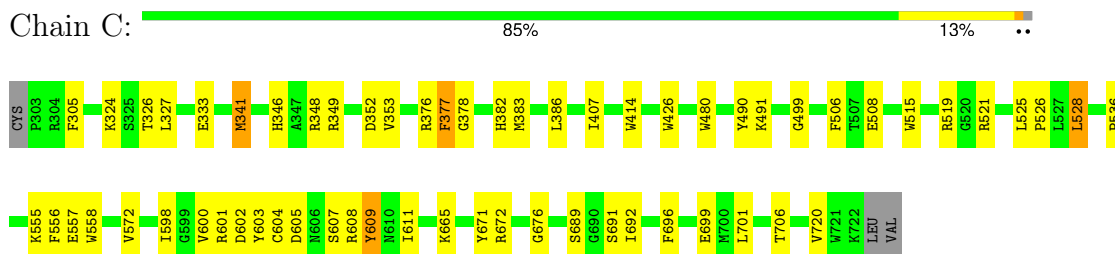
- Molecule 1: Nitric oxide synthase, brain



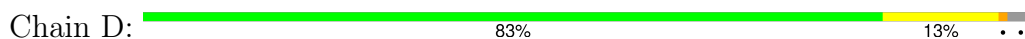
- Molecule 1: Nitric oxide synthase, brain

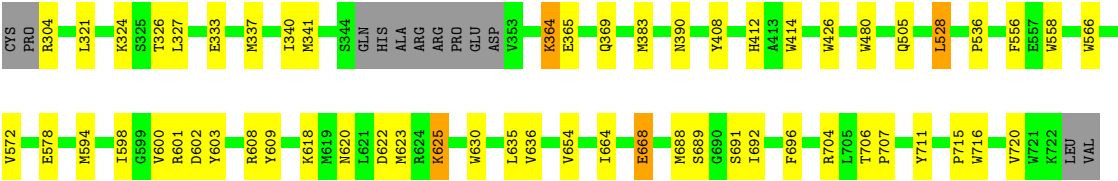


- Molecule 1: Nitric oxide synthase, brain



- Molecule 1: Nitric oxide synthase, brain





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	118.88Å 52.23Å 164.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.23 – 2.15 39.23 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.23-2.15) 99.8 (39.23-2.15)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.180 , 0.233 0.179 , 0.231	Depositor DCC
R_{free} test set	5562 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.632	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 29.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.479 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14588	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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: A1BUF, GOL, ZN, HEM, H4B

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.32	0/3471	0.51	0/4711
1	B	0.30	0/3538	0.49	0/4801
1	C	0.30	0/3550	0.51	0/4819
1	D	0.33	0/3456	0.51	0/4689
All	All	0.31	0/14015	0.50	0/19020

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

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	593	TYR	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3363	0	3286	36	0
1	B	3431	0	3341	38	0
1	C	3439	0	3355	27	0
1	D	3355	0	3271	33	0
2	A	43	0	30	3	0
2	B	43	0	30	3	0
2	C	43	0	30	2	0
2	D	43	0	30	3	0
3	A	17	0	15	2	0
3	B	17	0	15	1	0
3	C	17	0	15	1	0
3	D	17	0	15	2	0
4	A	21	0	0	1	0
4	B	22	0	0	1	0
4	C	22	0	0	1	0
4	D	22	0	0	1	0
5	A	12	0	16	1	0
5	B	6	0	8	0	0
5	C	12	0	16	1	0
5	D	6	0	8	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
7	A	163	0	0	3	0
7	B	164	0	0	2	0
7	C	145	0	0	1	0
7	D	163	0	0	1	0
All	All	14588	0	13481	138	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 138 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:LEU:HD22	1:A:536:PRO:HB2	1.55	0.86
1:D:528:LEU:HD22	1:D:536:PRO:HB2	1.65	0.77
1:C:528:LEU:HD22	1:C:536:PRO:HB2	1.67	0.76
1:D:337:MET:HE2	1:D:340:ILE:HG13	1.67	0.76
1:B:528:LEU:HD22	1:B:536:PRO:HB2	1.69	0.74

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	411/423 (97%)	406 (99%)	5 (1%)	0	100	100
1	B	420/423 (99%)	404 (96%)	13 (3%)	3 (1%)	19	13
1	C	422/423 (100%)	403 (96%)	16 (4%)	3 (1%)	19	13
1	D	409/423 (97%)	401 (98%)	8 (2%)	0	100	100
All	All	1662/1692 (98%)	1614 (97%)	42 (2%)	6 (0%)	30	26

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	351	GLU
1	C	305	PHE
1	B	346	HIS
1	C	377	PHE
1	B	377	PHE

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	371/378 (98%)	360 (97%)	11 (3%)	36	35
1	B	377/378 (100%)	360 (96%)	17 (4%)	23	19
1	C	379/378 (100%)	359 (95%)	20 (5%)	19	15
1	D	369/378 (98%)	353 (96%)	16 (4%)	25	21
All	All	1496/1512 (99%)	1432 (96%)	64 (4%)	25	21

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	528	LEU
1	D	618	LYS
1	B	618	LYS
1	B	611	ILE
1	D	620	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	430	GLN
1	C	441	HIS
1	D	669	ASN
1	C	445	ASN
1	B	441	HIS

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](#)

Of 20 ligands modelled in this entry, 2 are monoatomic - leaving 18 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
2	HEM	B	802	1	42,50,50	1.51	7 (16%)	46,82,82	1.74	10 (21%)
4	A1BUF	B	804	-	24,24,24	1.41	2 (8%)	34,35,35	1.80	9 (26%)
5	GOL	C	805	-	5,5,5	0.28	0	5,5,5	0.78	0
4	A1BUF	A	803	-	23,23,24	1.41	3 (13%)	32,33,35	1.79	9 (28%)
5	GOL	B	805	-	5,5,5	0.40	0	5,5,5	0.25	0
3	H4B	B	803	-	16,18,18	0.79	0	14,26,26	2.22	5 (35%)
3	H4B	D	802	-	16,18,18	0.68	0	14,26,26	2.27	6 (42%)
4	A1BUF	D	803	-	24,24,24	1.49	3 (12%)	34,35,35	1.32	5 (14%)
3	H4B	A	802	-	16,18,18	0.72	0	14,26,26	2.24	6 (42%)
3	H4B	C	802	-	16,18,18	0.81	0	14,26,26	2.33	6 (42%)
2	HEM	C	801	1	42,50,50	1.53	6 (14%)	46,82,82	1.69	11 (23%)
5	GOL	A	805	-	5,5,5	0.26	0	5,5,5	0.56	0
5	GOL	A	804	-	5,5,5	0.36	0	5,5,5	0.29	0
2	HEM	D	801	1	42,50,50	1.53	4 (9%)	46,82,82	1.70	8 (17%)
5	GOL	C	804	-	5,5,5	0.41	0	5,5,5	0.31	0
2	HEM	A	801	1	42,50,50	1.50	5 (11%)	46,82,82	1.69	12 (26%)
4	A1BUF	C	803	-	24,24,24	1.44	2 (8%)	34,35,35	1.44	6 (17%)
5	GOL	D	804	-	5,5,5	0.32	0	5,5,5	0.30	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	B	802	1	-	5/12/54/54	-
4	A1BUF	B	804	-	-	2/6/18/18	0/3/3/3
5	GOL	C	805	-	-	3/4/4/4	-
4	A1BUF	A	803	-	-	4/6/18/18	0/3/3/3
5	GOL	B	805	-	-	2/4/4/4	-
3	H4B	B	803	-	-	4/8/17/17	0/2/2/2
3	H4B	D	802	-	-	3/8/17/17	0/2/2/2
4	A1BUF	D	803	-	-	2/6/18/18	0/3/3/3
3	H4B	A	802	-	-	3/8/17/17	0/2/2/2
3	H4B	C	802	-	-	4/8/17/17	0/2/2/2
2	HEM	C	801	1	-	4/12/54/54	-
5	GOL	A	805	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	A	804	-	-	1/4/4/4	-
2	HEM	D	801	1	-	5/12/54/54	-
5	GOL	C	804	-	-	2/4/4/4	-
2	HEM	A	801	1	-	3/12/54/54	-
4	A1BUF	C	803	-	-	1/6/18/18	0/3/3/3
5	GOL	D	804	-	-	2/4/4/4	-

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	803	A1BUF	C08-C07	5.49	1.48	1.39
4	C	803	A1BUF	C08-C07	5.16	1.48	1.39
4	B	804	A1BUF	C08-C07	4.90	1.47	1.39
4	A	803	A1BUF	C08-C07	4.71	1.47	1.39
2	D	801	HEM	C3C-C2C	-4.49	1.34	1.40

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	804	A1BUF	C21-C08-C07	-5.30	117.66	122.45
3	C	802	H4B	C8A-C4A-C4	5.28	119.31	114.50
2	B	802	HEM	C4B-CHC-C1C	5.22	129.45	122.56
2	D	801	HEM	CBA-CAA-C2A	-5.09	103.98	112.54
3	B	803	H4B	C8A-C4A-C4	5.08	119.12	114.50

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	802	H4B	C7-C6-C9-O9
3	B	803	H4B	N5-C6-C9-O9
3	B	803	H4B	C7-C6-C9-O9
3	B	803	H4B	C7-C6-C9-C10
3	C	802	H4B	N5-C6-C9-O9

There are no ring outliers.

14 monomers are involved in 23 short contacts:

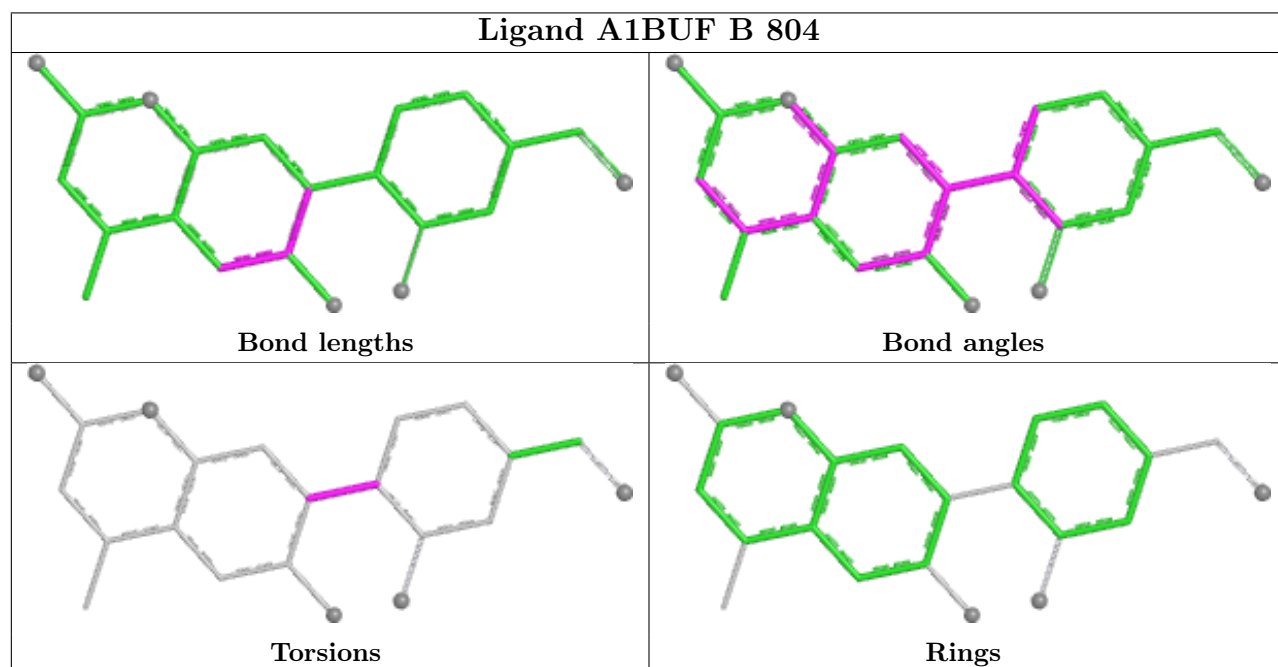
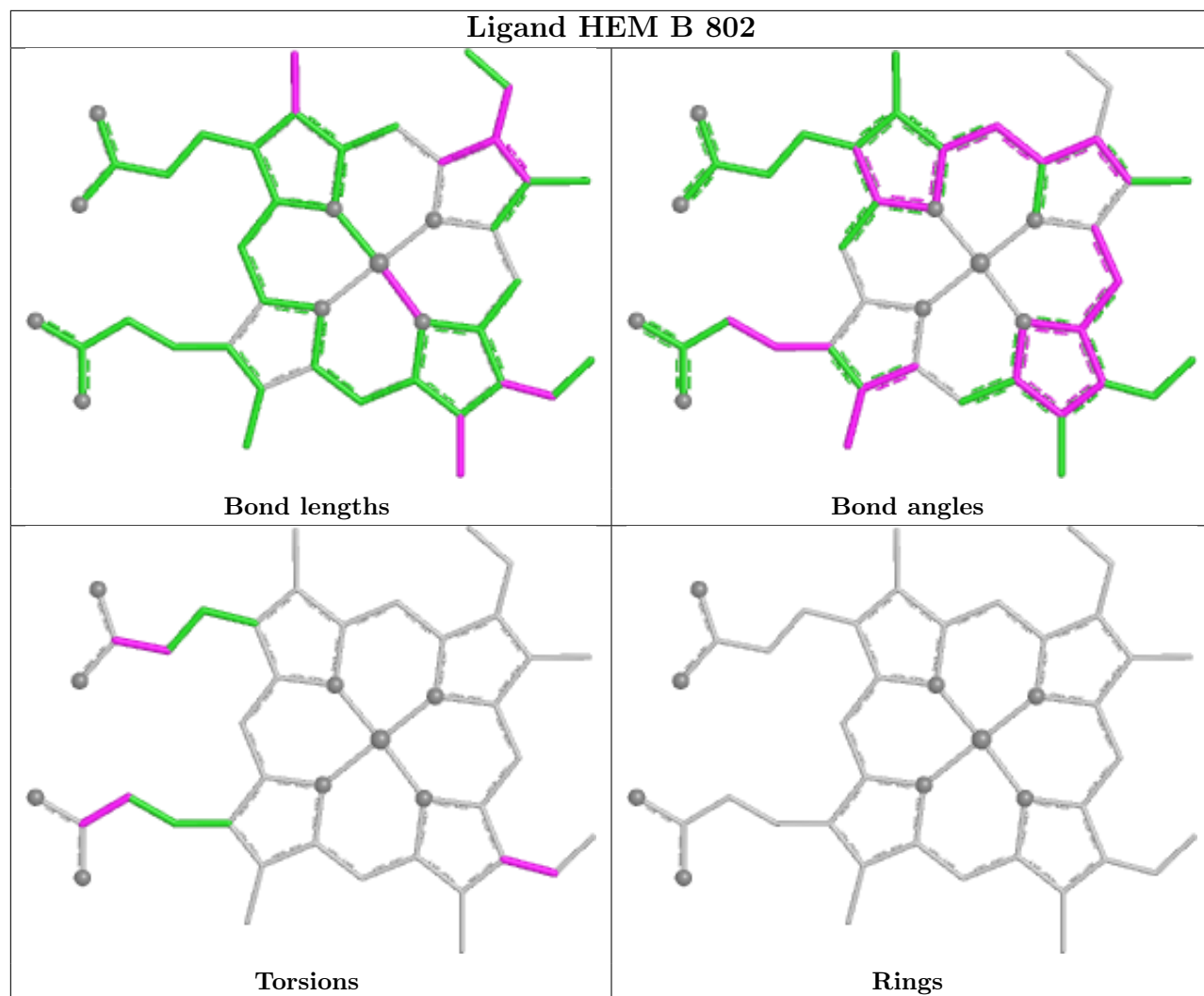
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	802	HEM	3	0

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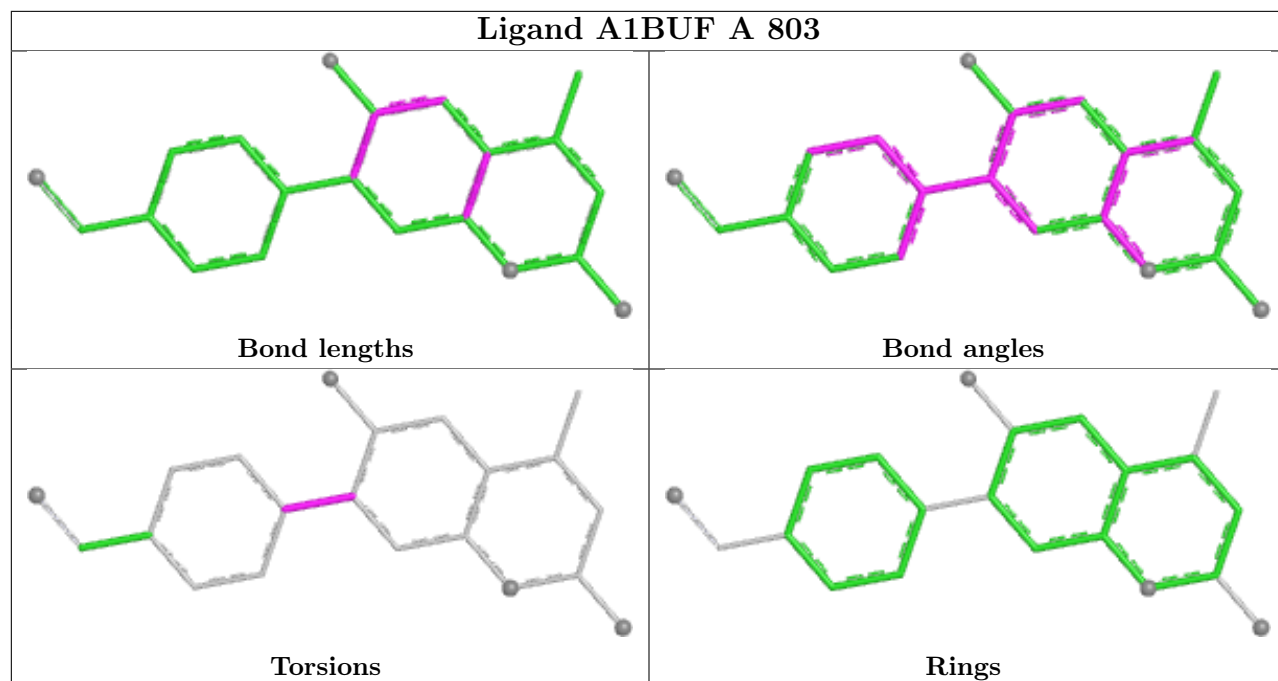
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	804	A1BUF	1	0
5	C	805	GOL	1	0
4	A	803	A1BUF	1	0
3	B	803	H4B	1	0
3	D	802	H4B	2	0
4	D	803	A1BUF	1	0
3	A	802	H4B	2	0
3	C	802	H4B	1	0
2	C	801	HEM	2	0
5	A	805	GOL	1	0
2	D	801	HEM	3	0
2	A	801	HEM	3	0
4	C	803	A1BUF	1	0

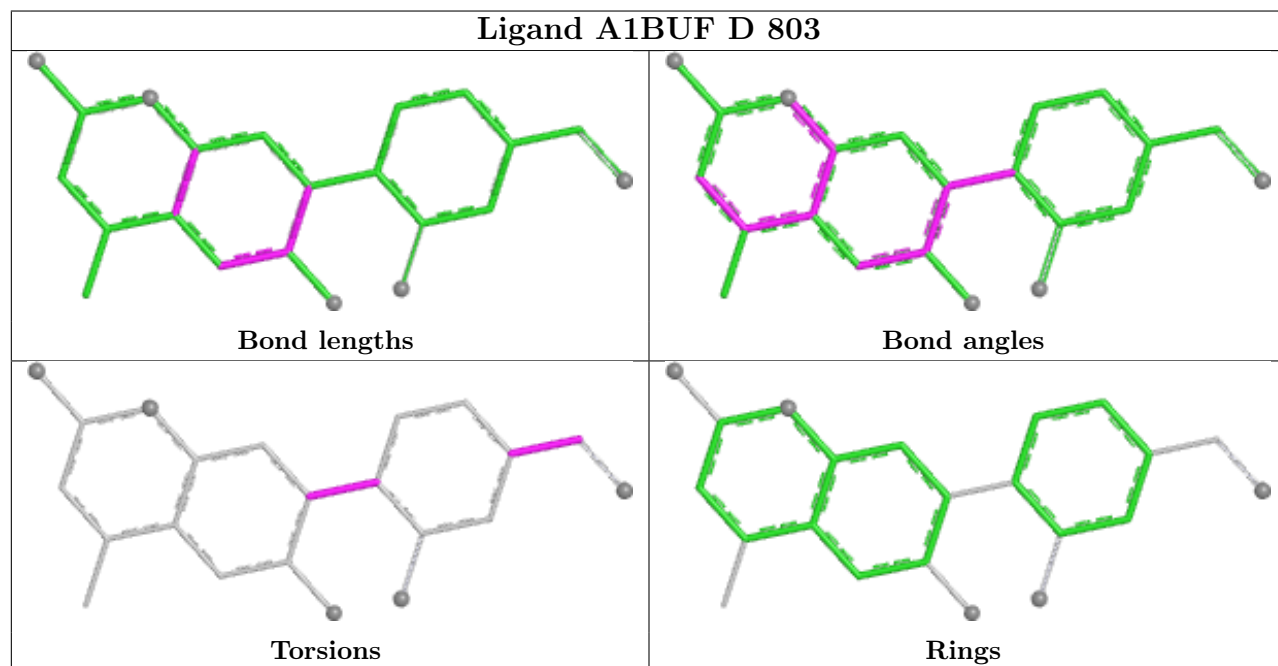
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

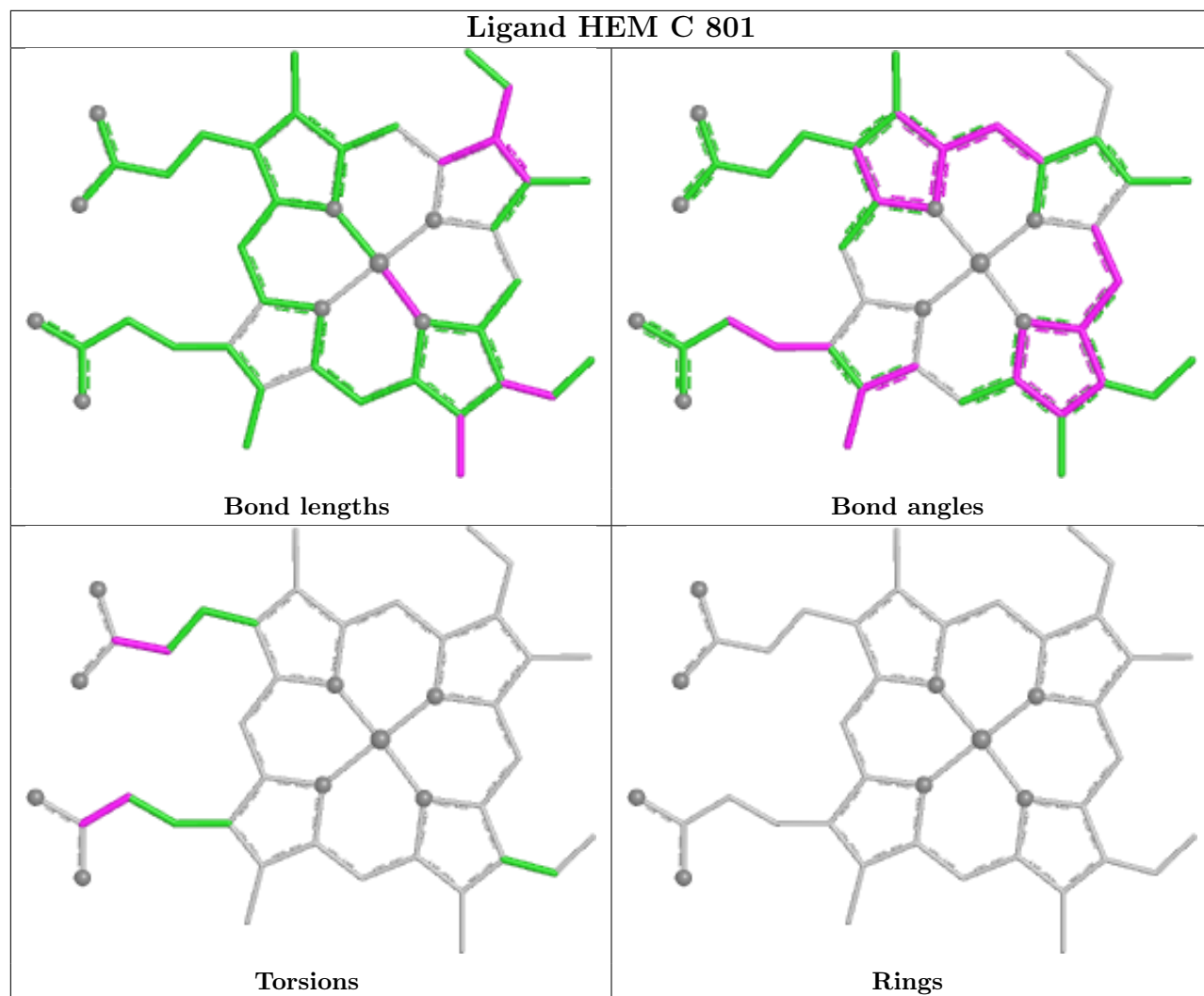


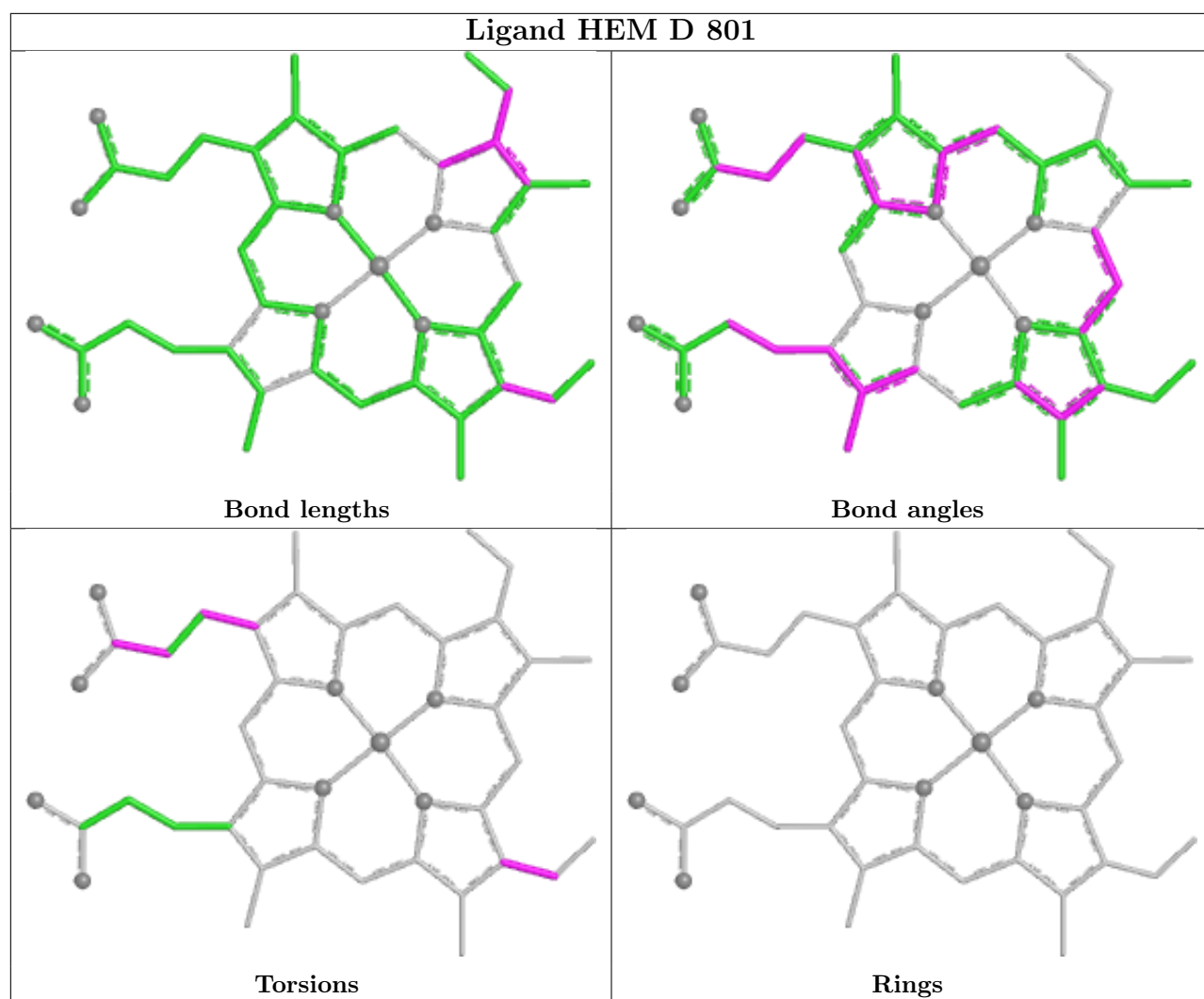
Ligand A1BUF A 803

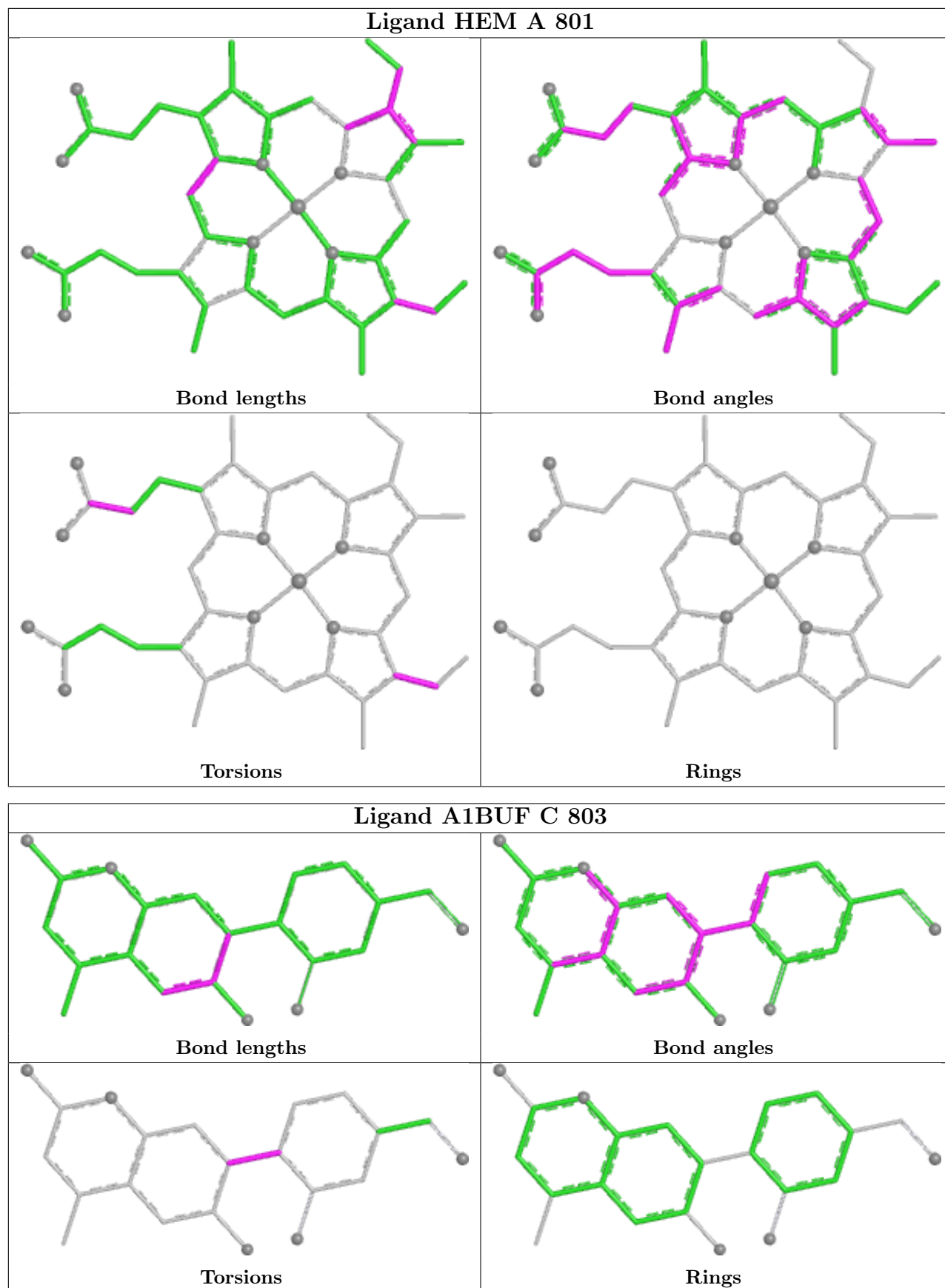


Ligand A1BUF D 803









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	411/423 (97%)	-1.45	0 100 100	25, 49, 87, 124	4 (0%)
1	B	419/423 (99%)	-1.41	0 100 100	27, 52, 99, 136	3 (0%)
1	C	420/423 (99%)	-1.40	0 100 100	26, 53, 96, 130	4 (0%)
1	D	411/423 (97%)	-1.45	0 100 100	24, 50, 86, 118	2 (0%)
All	All	1661/1692 (98%)	-1.43	0 100 100	24, 51, 94, 136	13 (0%)

There are no RSRZ outliers to report.

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
5	GOL	B	805	6/6	0.98	0.05	67,72,75,79	0
5	GOL	C	805	6/6	0.98	0.05	52,63,65,68	0
5	GOL	D	804	6/6	0.98	0.06	67,72,74,78	0
3	H4B	D	802	17/17	0.99	0.05	58,78,92,93	0

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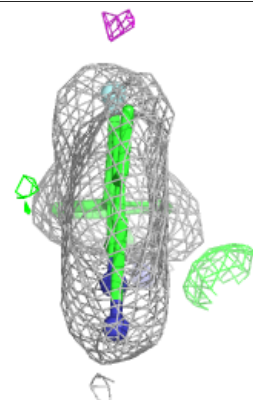
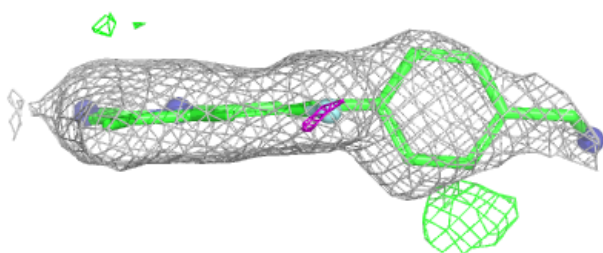
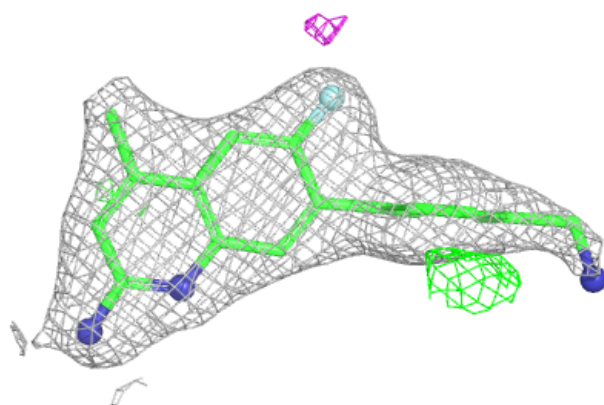
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	A1BUF	A	803	21/22	0.99	0.04	36,48,74,75	0
4	A1BUF	B	804	22/22	0.99	0.04	37,52,82,85	0
4	A1BUF	C	803	22/22	0.99	0.04	35,50,88,92	0
4	A1BUF	D	803	22/22	0.99	0.04	37,50,83,84	0
5	GOL	A	804	6/6	0.99	0.05	68,74,82,85	0
5	GOL	A	805	6/6	0.99	0.06	61,70,84,88	0
3	H4B	A	802	17/17	0.99	0.05	64,84,97,98	0
5	GOL	C	804	6/6	0.99	0.06	67,83,86,89	0
3	H4B	B	803	17/17	0.99	0.04	73,88,99,100	0
3	H4B	C	802	17/17	0.99	0.04	79,88,101,103	0
2	HEM	C	801	43/43	1.00	0.03	30,41,64,74	0
2	HEM	D	801	43/43	1.00	0.03	29,39,54,65	0
2	HEM	A	801	43/43	1.00	0.03	28,40,58,66	0
2	HEM	B	802	43/43	1.00	0.02	32,42,65,78	0
6	ZN	B	801	1/1	1.00	0.01	42,42,42,42	0
6	ZN	C	806	1/1	1.00	0.01	41,41,41,41	0

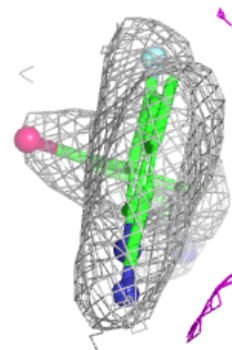
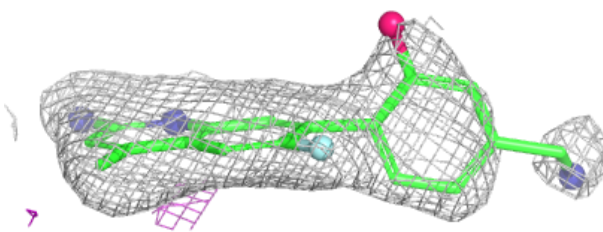
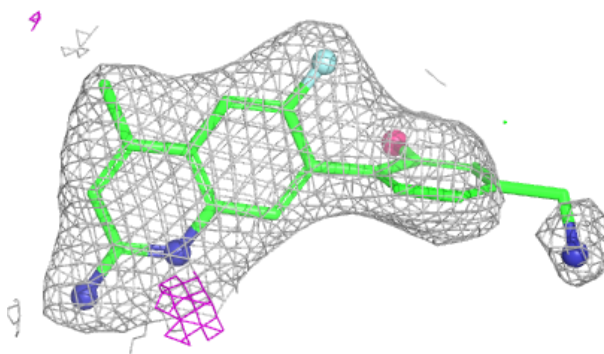
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1BUF A 803:

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

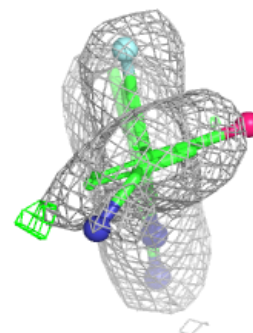
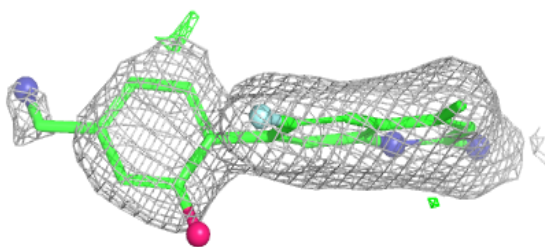
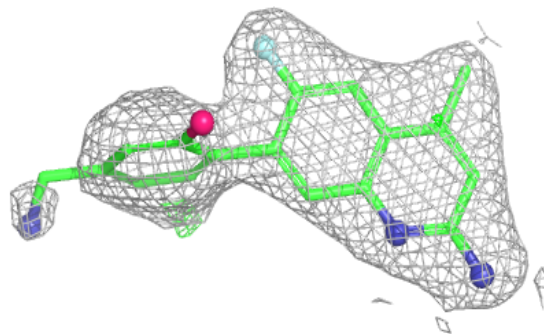
**Electron density around A1BUF B 804:**

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

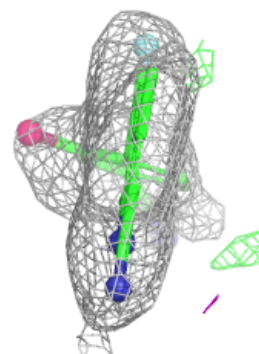
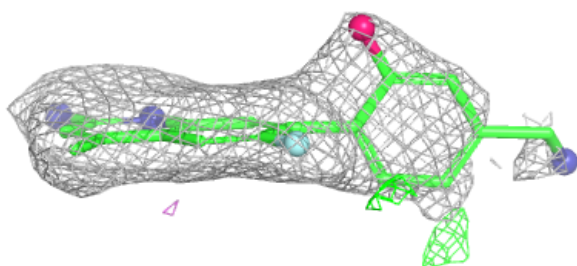
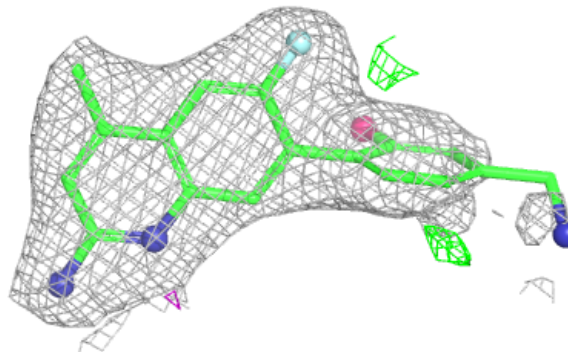


Electron density around A1BUF C 803:

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

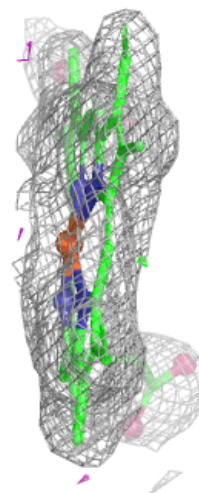
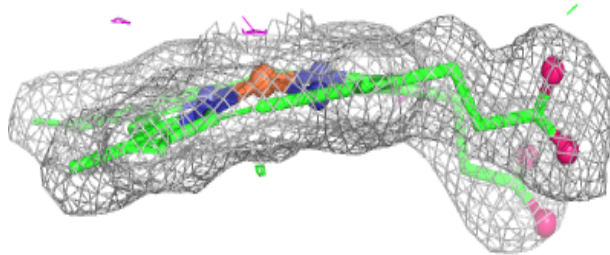
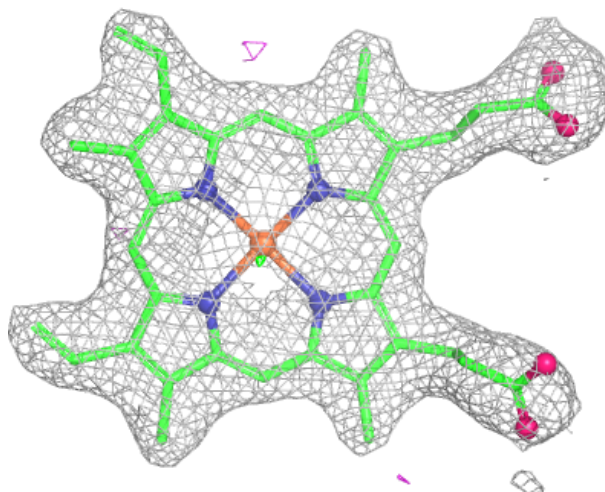
**Electron density around A1BUF D 803:**

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



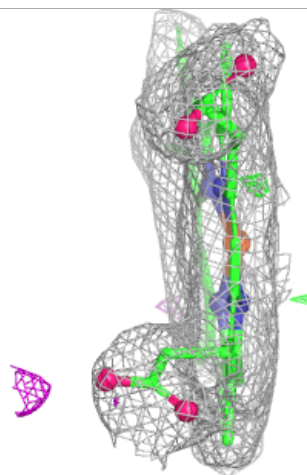
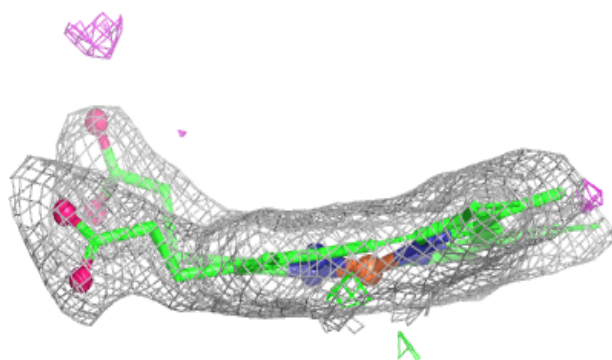
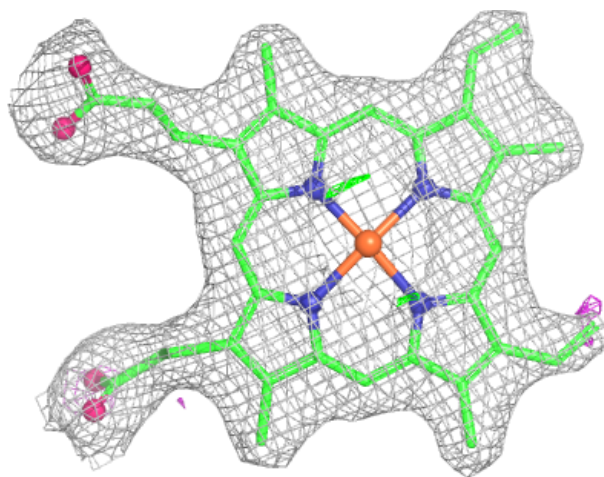
Electron density around HEM C 801:

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



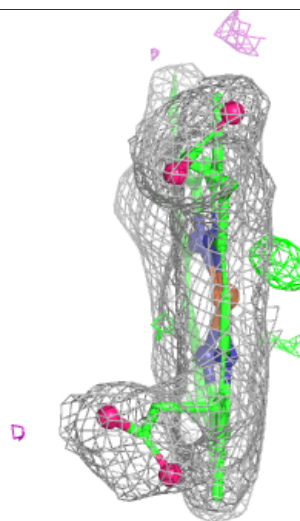
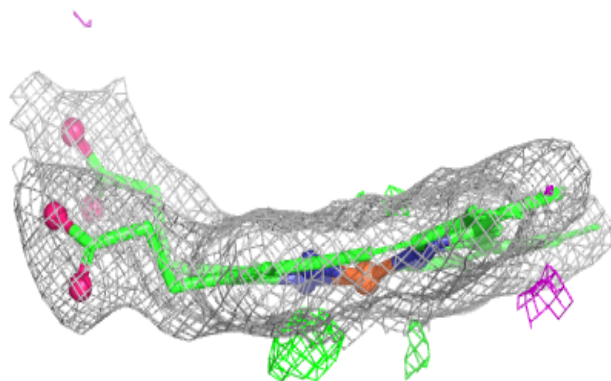
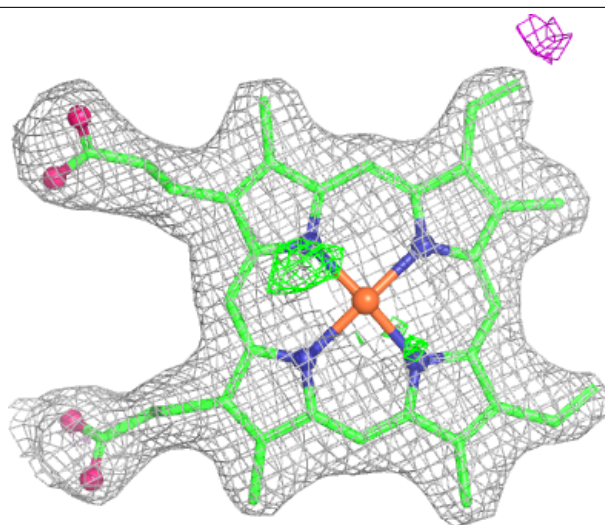
Electron density around HEM D 801:

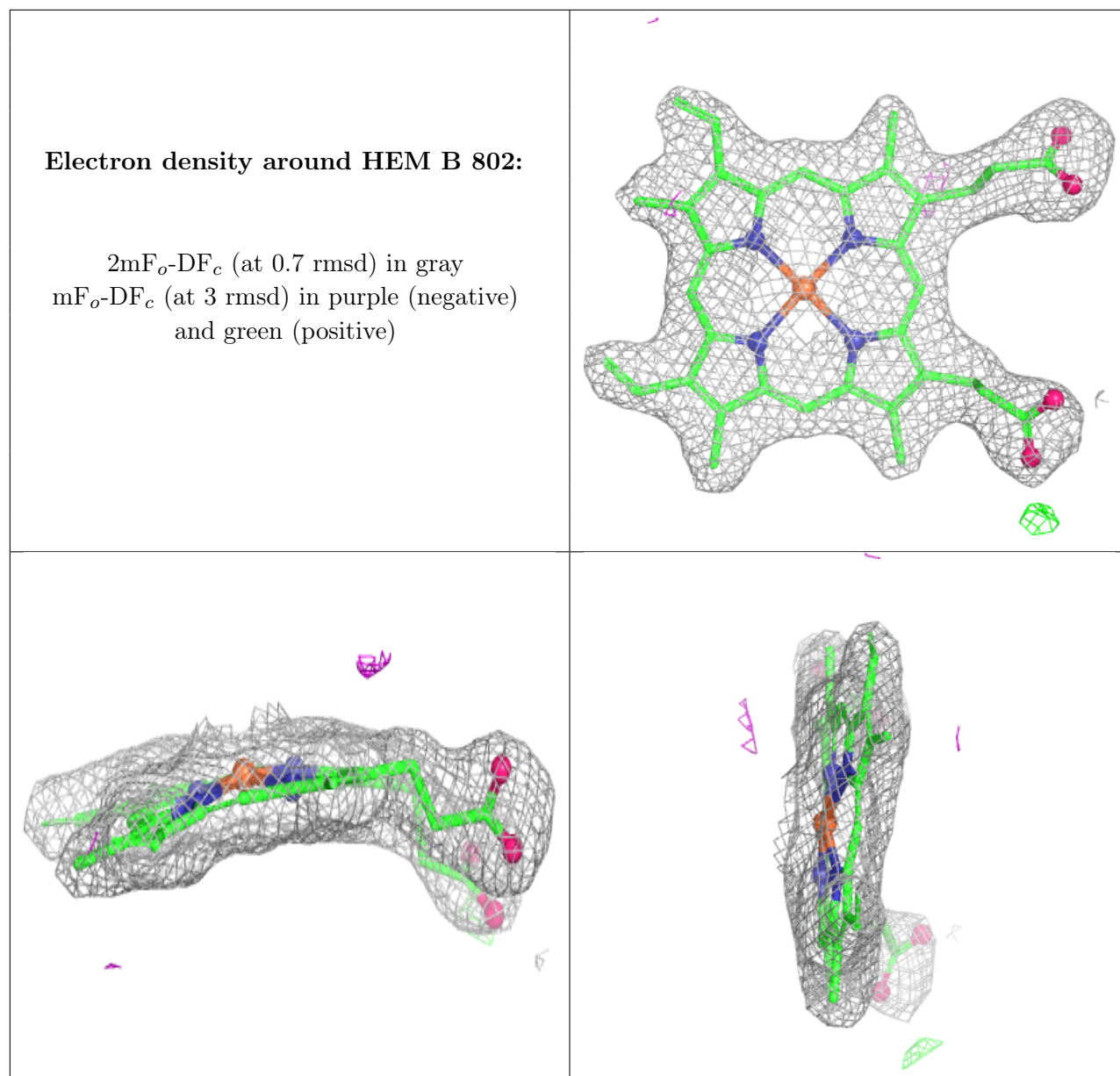
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 801:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.