



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 03:24 am BST

PDB ID : 5VVD
Title : Structure of human endothelial nitric oxide synthase heme domain in complex with 4-(2-(((2-Amino-4-methylquinolin-7-yl)methyl)amino)ethyl)benzonitrile
Authors : Li, H.; Poulos, T.L.
Deposited on : 2017-05-19
Resolution : 2.25 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 : 2.11
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) : 2.11

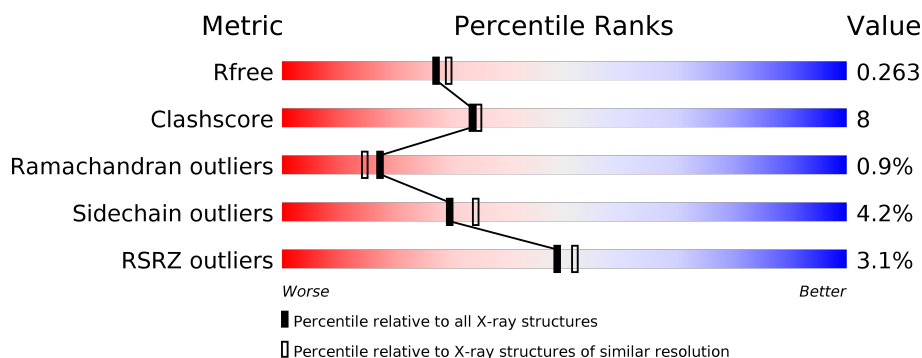
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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>5%</div> <div> <div></div> <div>67%</div> <div>21%</div> <div>• • 8%</div> </div> </div>
1	B	440	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>15%</div> <div>• 9%</div> </div> </div>
1	C	440	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>15%</div> <div>• 9%</div> </div> </div>
1	D	440	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>13%</div> <div>• 9%</div> </div> </div>

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 13501 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	404	Total	C	N	O	S	0	3	0
			3240	2064	570	590	16			
1	B	402	Total	C	N	O	S	0	4	0
			3224	2053	566	588	17			
1	C	401	Total	C	N	O	S	0	3	0
			3212	2046	563	587	16			
1	D	402	Total	C	N	O	S	0	4	0
			3224	2053	566	588	17			

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



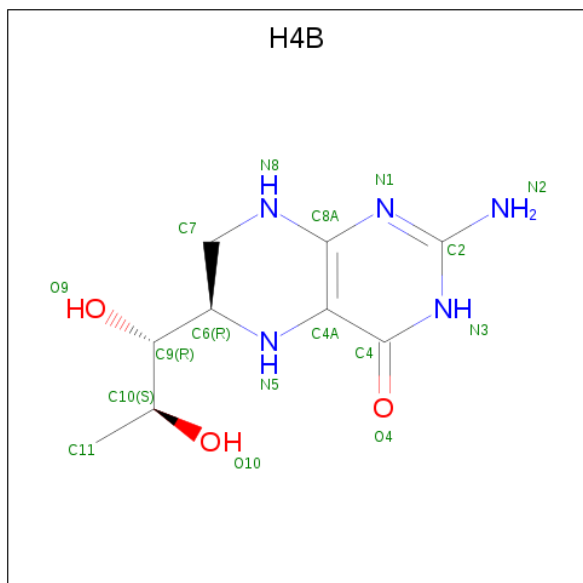
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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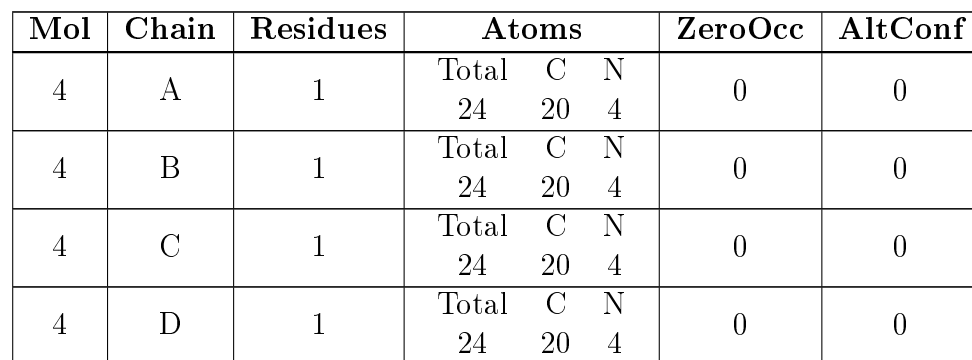
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).



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 4-(2-[(2-amino-4-methylquinolin-7-yl)methyl]amino)ethyl)benzonitrile (three-letter code: 9OG) (formula: $C_{20}H_{20}N_4$).



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- Chemical structure of BTB (2,2,3,3-tetrakis(benzotriazol-2-yl)propane) is shown. The structure features a central carbon atom (C2) bonded to two benzotriazole rings (C1, C3, C4, C5, C6, C7, C8) and two hydroxyl groups (O1, O2). The benzotriazole rings are labeled with carbon atoms (C1, C3, C4, C5, C6, C7, C8) and nitrogen atoms (N). The hydroxyl groups are labeled with oxygen atoms (O1, O2).

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

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Zn	0	0
			1	1		
6	D	1	Total	Zn	0	0
			1	1		

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



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

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Cl	0	0
			1	1		
8	A	1	Total	Cl	0	0
			1	1		
8	D	1	Total	Cl	0	0
			1	1		
8	C	1	Total	Cl	0	0
			1	1		

- Molecule 9 is GADOLINIUM ATOM (three-letter code: GD) (formula: Gd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	2	Total	Gd	0	0
			2	2		
9	A	1	Total	Gd	0	0
			1	1		
9	D	1	Total	Gd	0	0
			1	1		

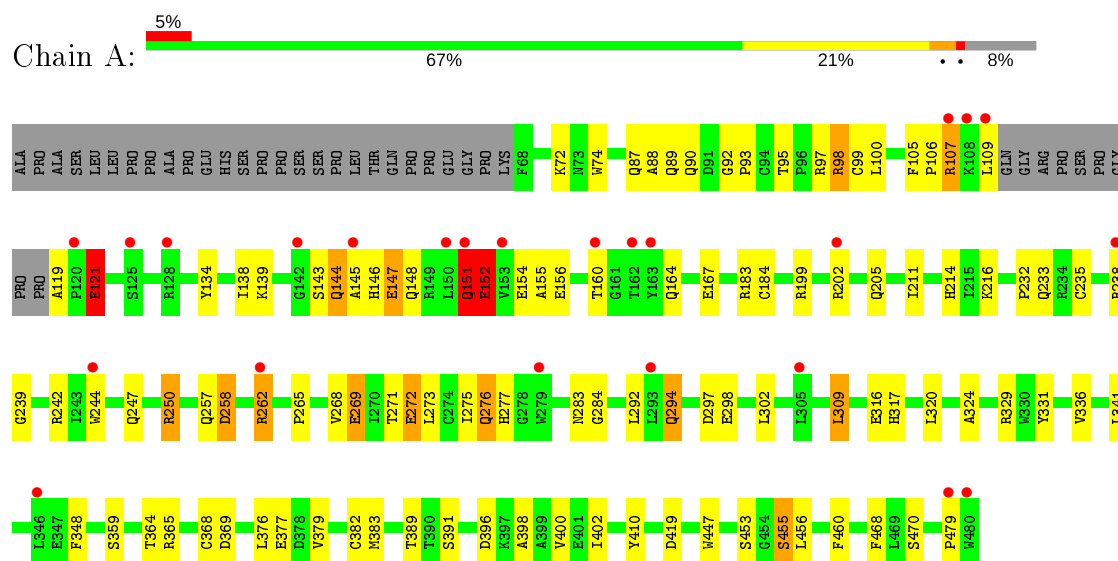
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	18	Total 18	O 18	0	0
10	B	35	Total 35	O 35	0	0
10	C	19	Total 19	O 19	0	0
10	D	17	Total 17	O 17	0	0

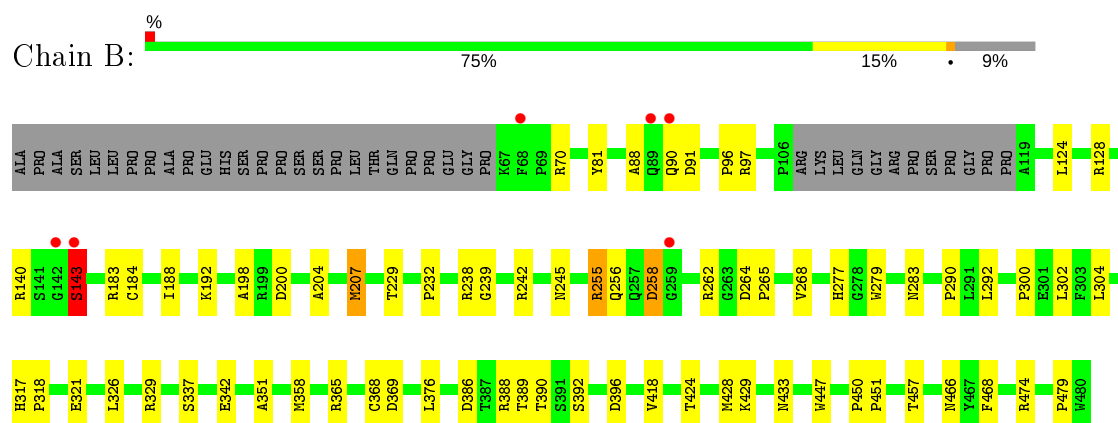
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

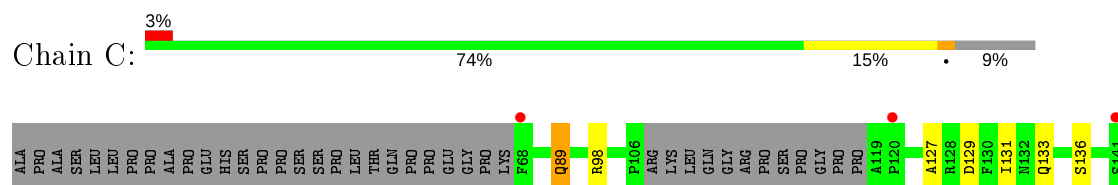
- Molecule 1: Nitric oxide synthase, endothelial

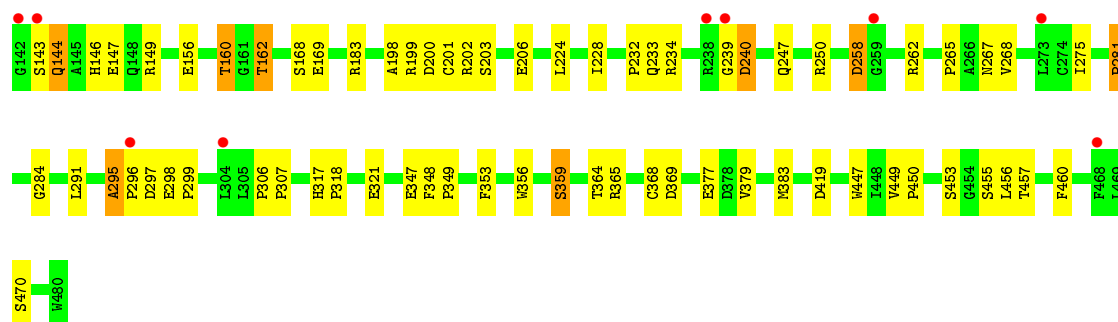


- Molecule 1: Nitric oxide synthase, endothelial

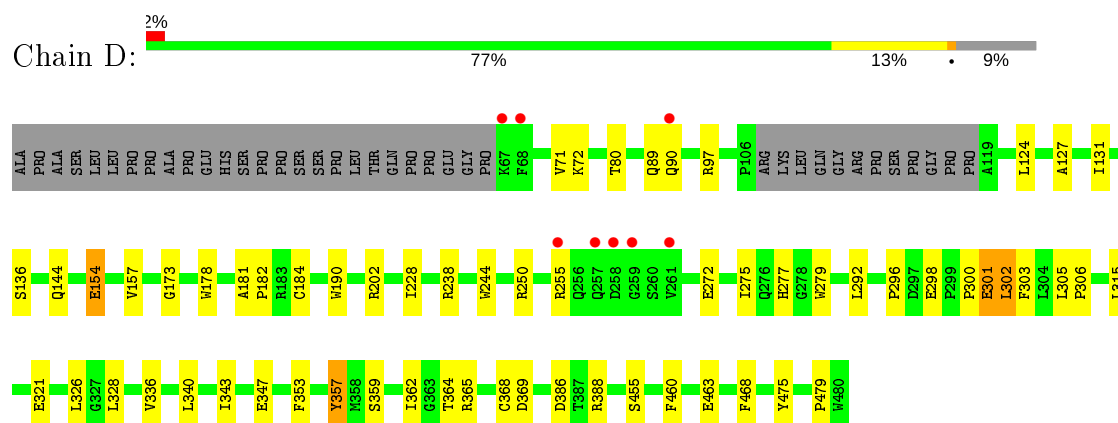


- Molecule 1: Nitric oxide synthase, endothelial





- Molecule 1: Nitric oxide synthase, endothelial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.34Å 153.13Å 109.24Å 90.00° 90.78° 90.00°	Depositor
Resolution (Å)	39.12 – 2.25 39.12 – 2.20	Depositor EDS
% Data completeness (in resolution range)	90.8 (39.12-2.25) 90.7 (39.12-2.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.27 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.206 , 0.269 0.203 , 0.263	Depositor DCC
R_{free} test set	4499 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	49.9	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.116 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13501	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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, H4B, CL, 9OG, GD, BTB, 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	0.38	0/3341	0.56	0/4551
1	B	0.43	0/3325	0.57	0/4531
1	C	0.42	0/3313	0.56	0/4515
1	D	0.45	0/3325	0.57	0/4531
All	All	0.42	0/13304	0.57	0/18128

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	4
1	B	0	1
1	C	0	2
1	D	0	1
All	All	0	8

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	107	ARG	Peptide
1	A	151	GLN	Peptide
1	A	152	GLU	Peptide
1	A	276	GLN	Peptide
1	B	143	SER	Peptide

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	3240	0	3151	73	0
1	B	3224	0	3131	46	0
1	C	3212	0	3114	43	0
1	D	3224	0	3131	37	0
2	A	43	0	30	5	0
2	B	43	0	30	5	0
2	C	43	0	30	1	0
2	D	43	0	30	7	0
3	A	17	0	15	1	0
3	B	17	0	15	2	0
3	C	17	0	15	1	0
3	D	17	0	15	1	0
4	A	24	0	0	1	0
4	B	24	0	0	1	0
4	C	24	0	0	0	0
4	D	24	0	0	2	0
5	A	42	0	56	12	0
5	B	56	0	72	11	0
5	C	28	0	38	5	0
5	D	28	0	36	9	0
6	A	1	0	0	0	0
6	D	1	0	0	0	0
7	A	6	0	8	1	0
7	C	6	0	8	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
9	A	1	0	0	0	0
9	B	2	0	0	0	0
9	D	1	0	0	0	0
10	A	18	0	0	2	0
10	B	35	0	0	1	0
10	C	19	0	0	0	0
10	D	17	0	0	1	0
All	All	13501	0	12925	223	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 223 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:PHE:HB3	1:A:107:ARG:HB3	1.55	0.88
1:D:321:GLU:OE2	5:D:505:BTB:O3	1.93	0.87
1:A:152:GLU:HG2	1:A:155:ALA:HB2	1.59	0.84
1:C:89:GLN:O	1:D:97:ARG:NH1	2.12	0.82
1:B:255:ARG:HH11	1:B:268:VAL:HG11	1.45	0.81

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	403/440 (92%)	380 (94%)	15 (4%)	8 (2%)	7	4
1	B	402/440 (91%)	388 (96%)	13 (3%)	1 (0%)	47	55
1	C	400/440 (91%)	384 (96%)	12 (3%)	4 (1%)	15	13
1	D	402/440 (91%)	384 (96%)	17 (4%)	1 (0%)	47	55
All	All	1607/1760 (91%)	1536 (96%)	57 (4%)	14 (1%)	17	14

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	GLU
1	A	139	LYS
1	A	145	ALA
1	A	147	GLU
1	A	152	GLU

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	346/373 (93%)	323 (93%)	23 (7%)	16	15
1	B	345/373 (92%)	336 (97%)	9 (3%)	46	55
1	C	343/373 (92%)	331 (96%)	12 (4%)	36	43
1	D	345/373 (92%)	330 (96%)	15 (4%)	29	33
All	All	1379/1492 (92%)	1320 (96%)	59 (4%)	30	33

5 of 59 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	255	ARG
1	C	160	THR
1	D	275	ILE
1	B	258	ASP
1	B	389	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	GLN
1	A	430	HIS
1	B	247	GLN
1	C	122	GLN
1	C	267	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

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 35 ligands modelled in this entry, 10 are monoatomic - leaving 25 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
5	BTB	C	505	-	13,13,13	0.40	0	7,16,16	0.79	0
5	BTB	A	505	-	13,13,13	0.49	0	7,16,16	1.15	1 (14%)
3	H4B	A	502	-	16,18,18	0.92	0	11,26,26	2.95	7 (63%)
5	BTB	B	504	9	13,13,13	0.49	0	7,16,16	0.78	0
5	BTB	A	506	9	13,13,13	0.36	0	7,16,16	0.86	0
2	HEM	D	502	1	27,50,50	2.13	6 (22%)	17,82,82	1.79	4 (23%)
3	H4B	B	502	-	16,18,18	0.87	0	11,26,26	2.89	7 (63%)
5	BTB	B	506	-	13,13,13	0.42	0	7,16,16	0.75	0
5	BTB	A	504	-	13,13,13	0.37	0	7,16,16	0.58	0
5	BTB	D	505	9	13,13,13	0.48	0	7,16,16	0.57	0
5	BTB	B	505	-	13,13,13	0.36	0	7,16,16	0.27	0
4	9OG	B	503	-	26,26,26	1.71	3 (11%)	33,35,35	1.03	1 (3%)
5	BTB	B	509	9	13,13,13	0.45	0	7,16,16	1.35	1 (14%)
2	HEM	B	501	1	27,50,50	2.08	5 (18%)	17,82,82	1.99	6 (35%)
4	9OG	D	504	-	26,26,26	1.61	1 (3%)	33,35,35	1.02	2 (6%)
3	H4B	D	503	-	16,18,18	0.83	0	11,26,26	2.82	7 (63%)
5	BTB	D	506	-	13,13,13	0.45	0	7,16,16	1.00	0
2	HEM	A	501	1	27,50,50	2.13	5 (18%)	17,82,82	1.46	3 (17%)
5	BTB	C	504	-	13,13,13	0.63	0	7,16,16	1.46	1 (14%)
4	9OG	C	503	-	26,26,26	1.61	2 (7%)	33,35,35	1.12	4 (12%)
7	GOL	C	506	-	5,5,5	0.45	0	5,5,5	0.58	0
3	H4B	C	502	-	16,18,18	1.03	1 (6%)	11,26,26	2.70	7 (63%)
7	GOL	A	508	-	5,5,5	0.36	0	5,5,5	0.34	0
4	9OG	A	503	-	26,26,26	1.67	2 (7%)	33,35,35	1.07	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	C	501	1	27,50,50	2.09	5 (18%)	17,82,82	2.23	5 (29%)

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
5	BTB	C	505	-	-	9/21/21/21	-
5	BTB	A	505	-	-	8/21/21/21	-
3	H4B	A	502	-	-	3/8/17/17	0/2/2/2
5	BTB	B	504	9	-	1/21/21/21	-
5	BTB	A	506	9	-	2/21/21/21	-
2	HEM	D	502	1	-	1/6/54/54	-
3	H4B	B	502	-	-	4/8/17/17	0/2/2/2
5	BTB	B	506	-	-	1/21/21/21	-
5	BTB	A	504	-	-	7/21/21/21	-
5	BTB	D	505	9	-	1/21/21/21	-
5	BTB	B	505	-	-	9/21/21/21	-
4	9OG	B	503	-	-	4/9/9/9	0/3/3/3
5	BTB	B	509	9	-	8/21/21/21	-
2	HEM	B	501	1	-	0/6/54/54	-
4	9OG	D	504	-	-	3/9/9/9	0/3/3/3
3	H4B	D	503	-	-	4/8/17/17	0/2/2/2
5	BTB	D	506	-	-	11/21/21/21	-
2	HEM	A	501	1	-	3/6/54/54	-
5	BTB	C	504	-	-	6/21/21/21	-
4	9OG	C	503	-	-	2/9/9/9	0/3/3/3
7	GOL	C	506	-	-	2/4/4/4	-
3	H4B	C	502	-	-	3/8/17/17	0/2/2/2
7	GOL	A	508	-	-	4/4/4/4	-
4	9OG	A	503	-	-	3/9/9/9	0/3/3/3
2	HEM	C	501	1	-	0/6/54/54	-

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	503	9OG	C24-C27	-7.13	1.28	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	9OG	C24-C27	-7.11	1.28	1.44
4	D	504	9OG	C24-C27	-6.79	1.29	1.44
4	C	503	9OG	C24-C27	-6.37	1.30	1.44
2	A	501	HEM	C3D-C2D	5.40	1.53	1.37

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	502	H4B	C4-C4A-C8A	5.68	119.62	114.57
2	C	501	HEM	CBD-CAD-C3D	-5.25	102.80	112.48
3	A	502	H4B	C4-C4A-C8A	5.06	119.06	114.57
3	A	502	H4B	C4-C4A-N5	4.66	123.03	119.12
2	C	501	HEM	CBA-CAA-C2A	-4.61	103.98	112.49

There are no chirality outliers.

5 of 99 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	505	BTB	O1-C1-C2-C3
5	C	505	BTB	O1-C1-C2-C4
5	C	505	BTB	O1-C1-C2-N
5	C	505	BTB	C1-C2-C4-O4
5	C	505	BTB	C3-C2-C4-O4

There are no ring outliers.

23 monomers are involved in 61 short contacts:

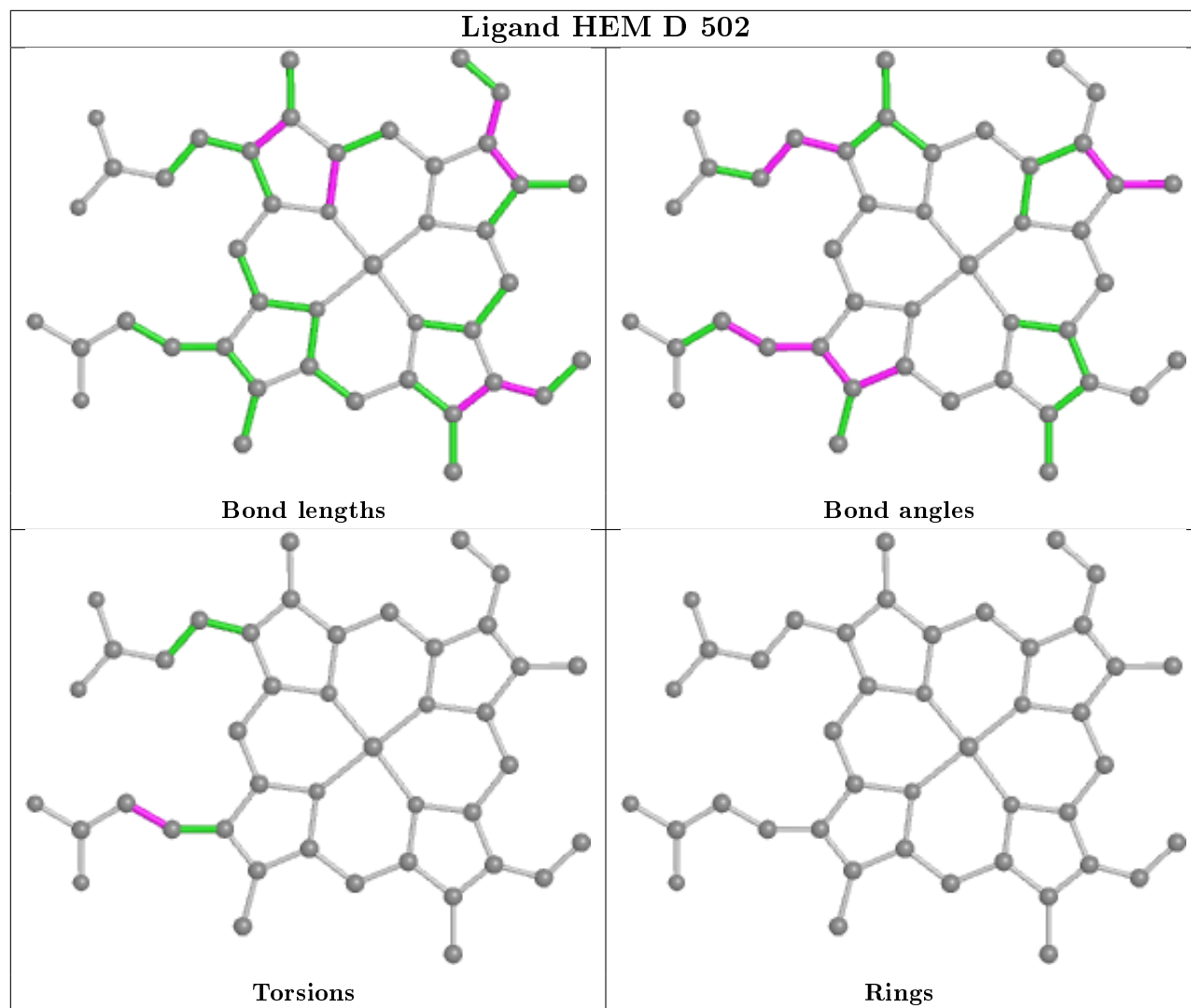
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	505	BTB	4	0
5	A	505	BTB	3	0
3	A	502	H4B	1	0
5	B	504	BTB	6	0
5	A	506	BTB	4	0
2	D	502	HEM	7	0
3	B	502	H4B	2	0
5	B	506	BTB	1	0
5	A	504	BTB	5	0
5	D	505	BTB	5	0
5	B	505	BTB	1	0
4	B	503	9OG	1	0
5	B	509	BTB	3	0

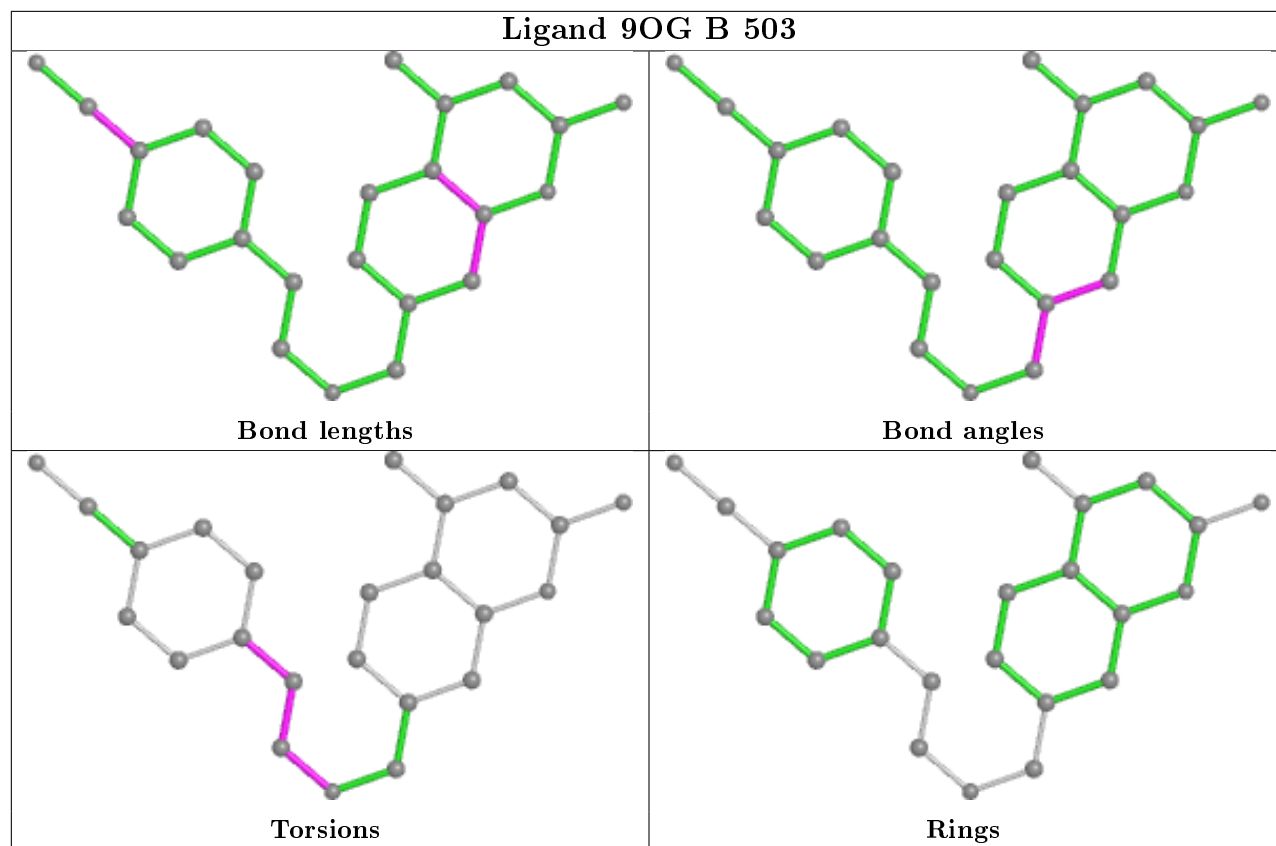
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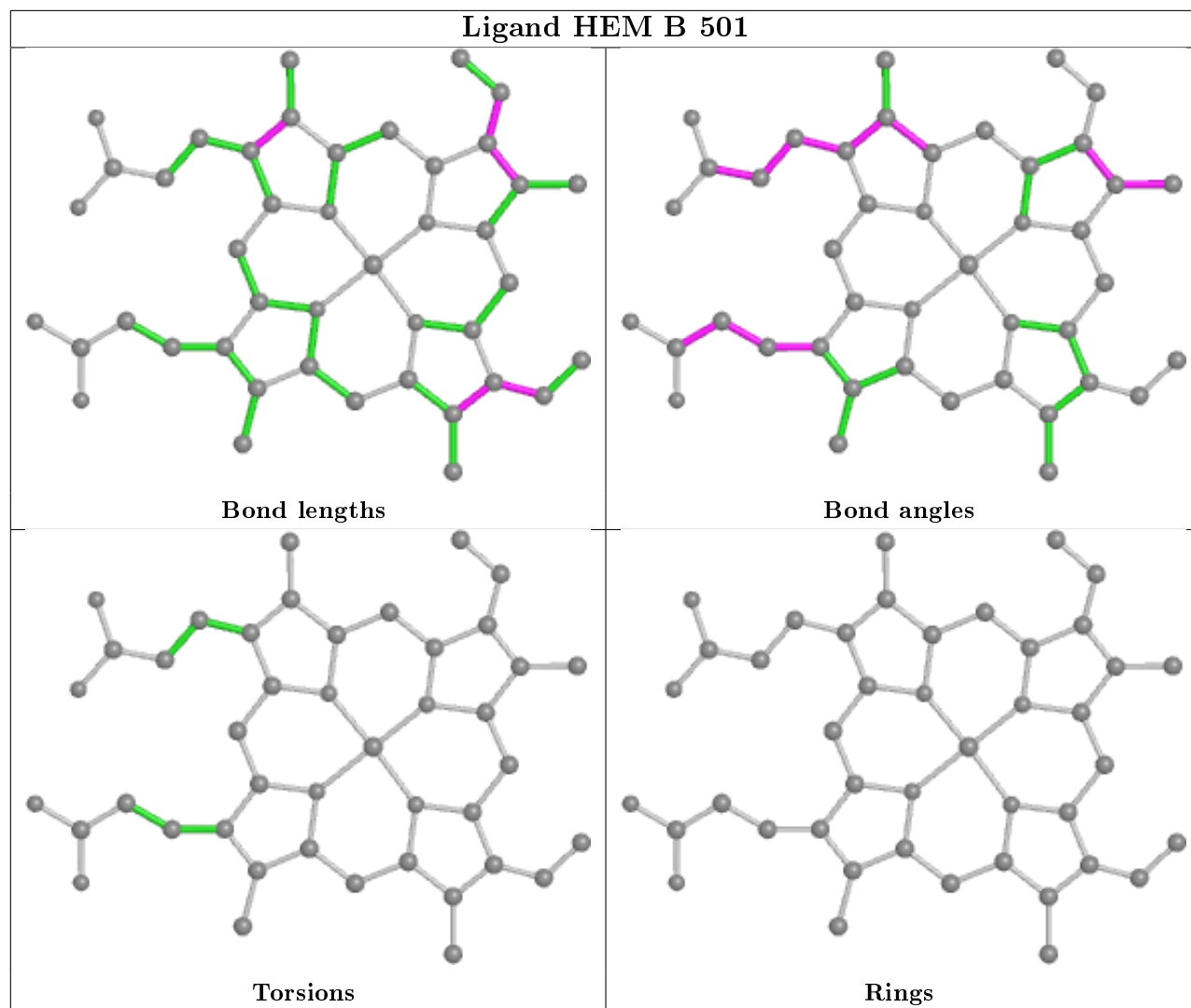
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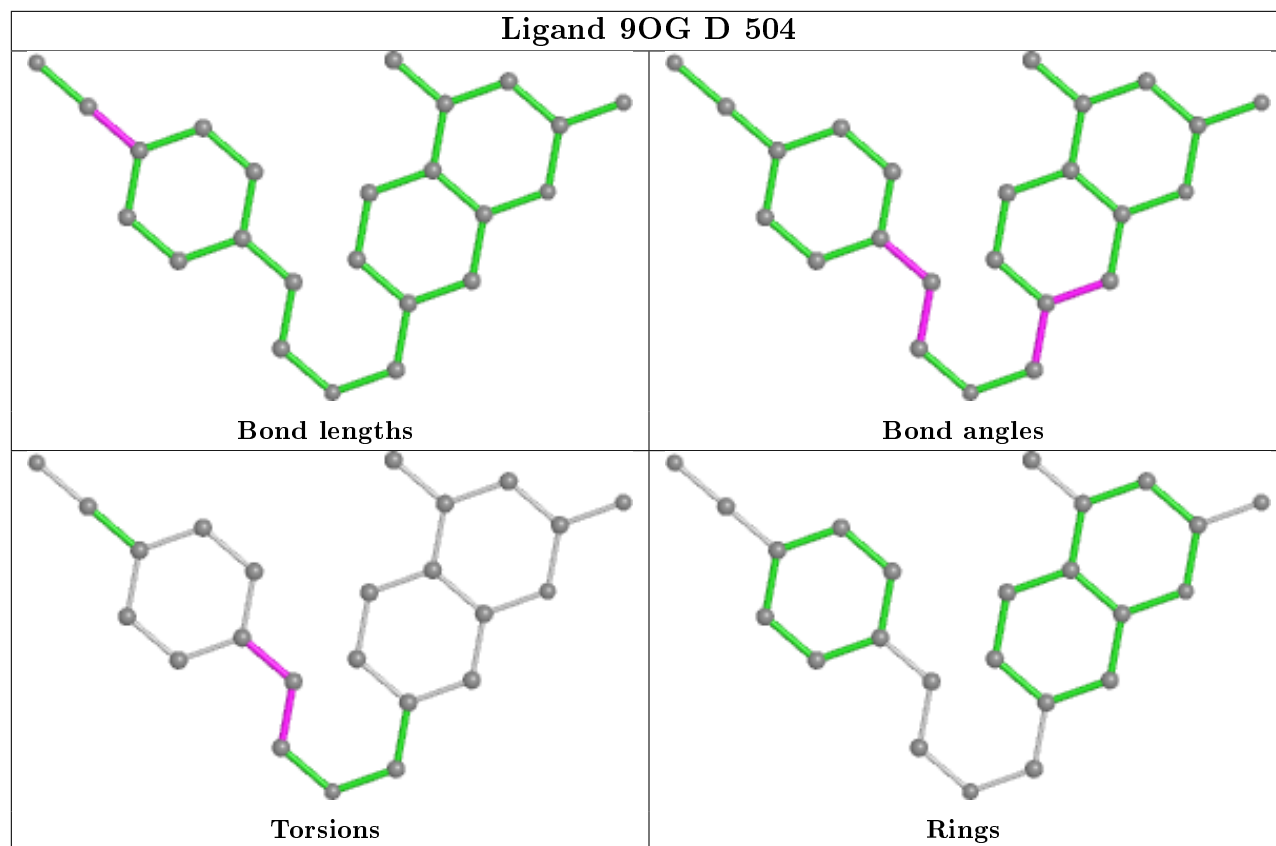
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	HEM	5	0
4	D	504	9OG	2	0
3	D	503	H4B	1	0
5	D	506	BTB	4	0
2	A	501	HEM	5	0
5	C	504	BTB	1	0
3	C	502	H4B	1	0
7	A	508	GOL	1	0
4	A	503	9OG	1	0
2	C	501	HEM	1	0

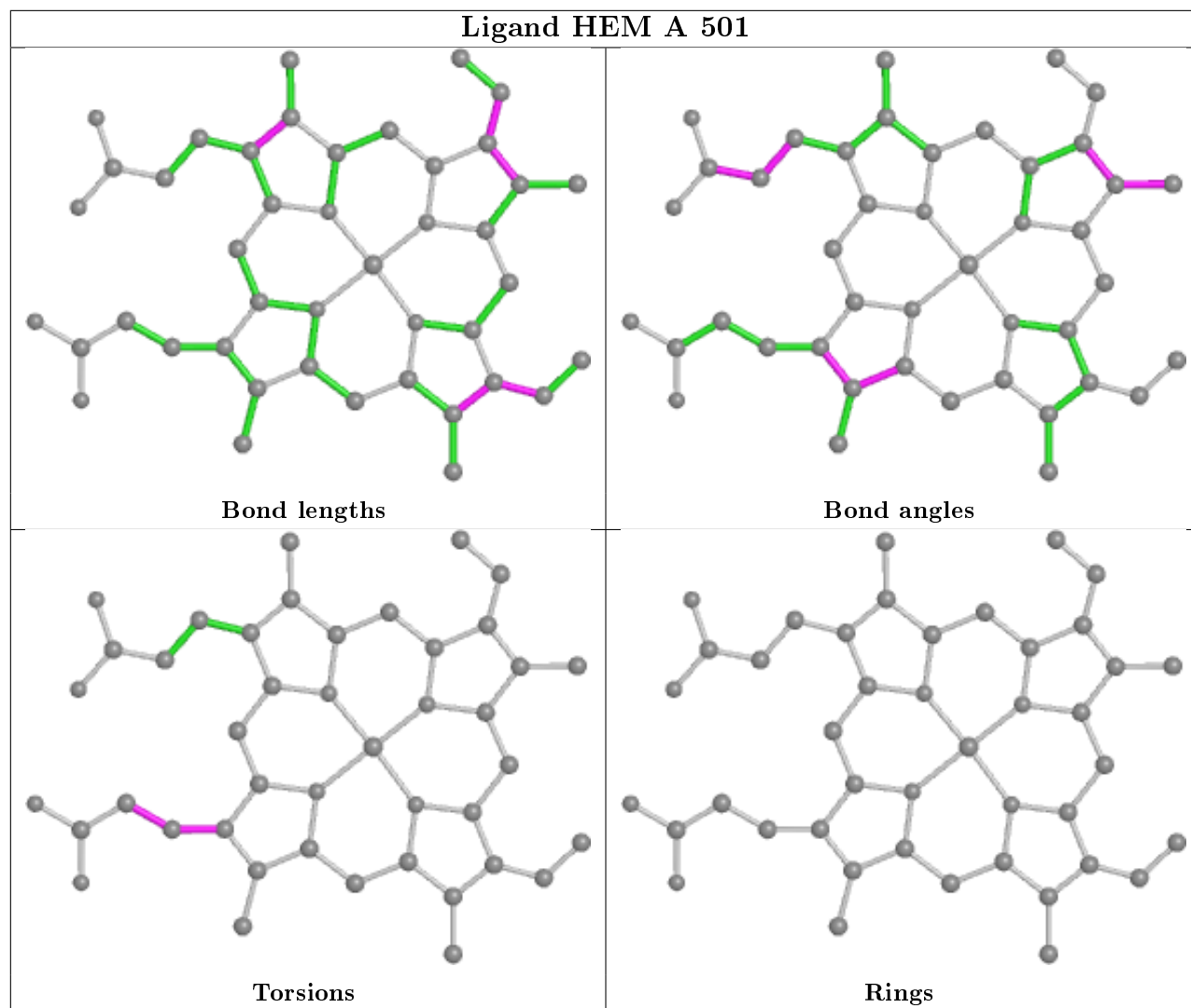
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

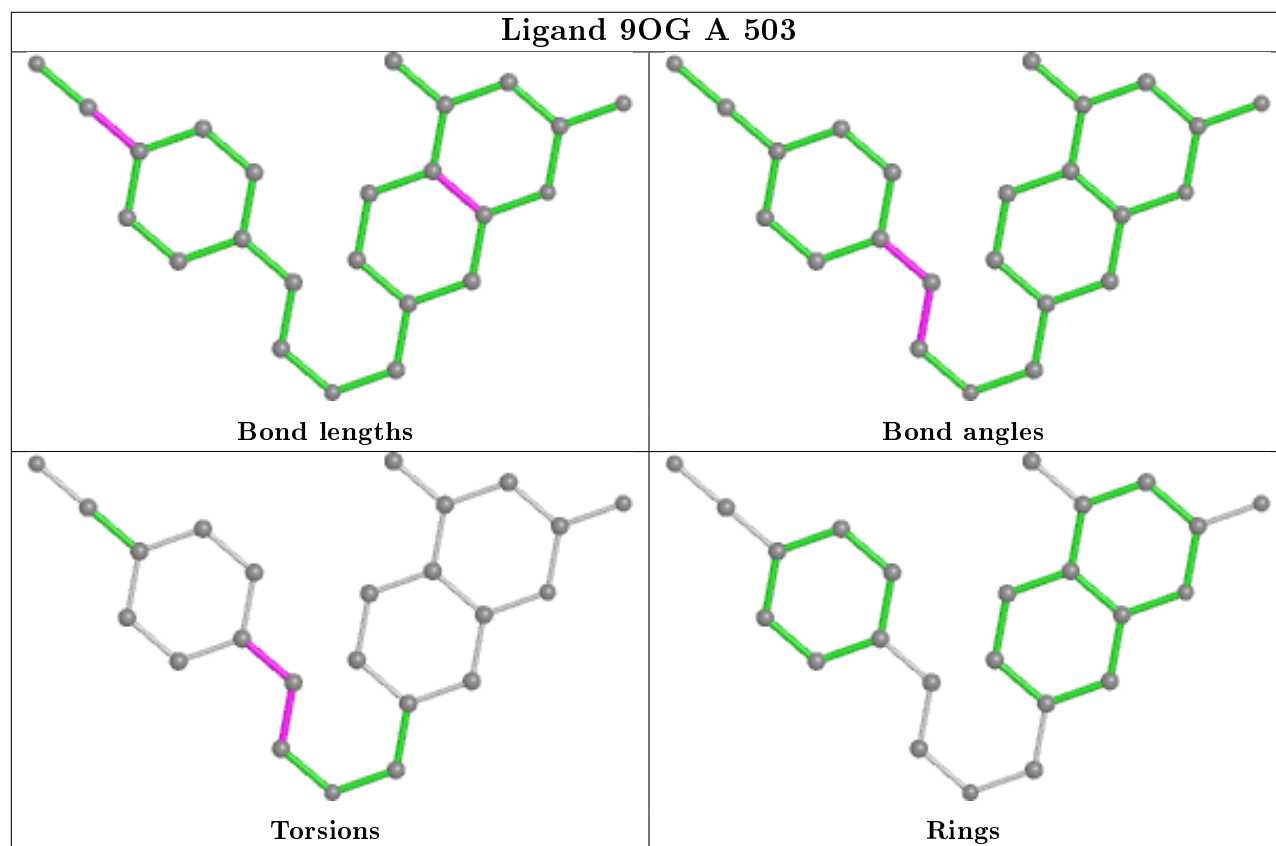
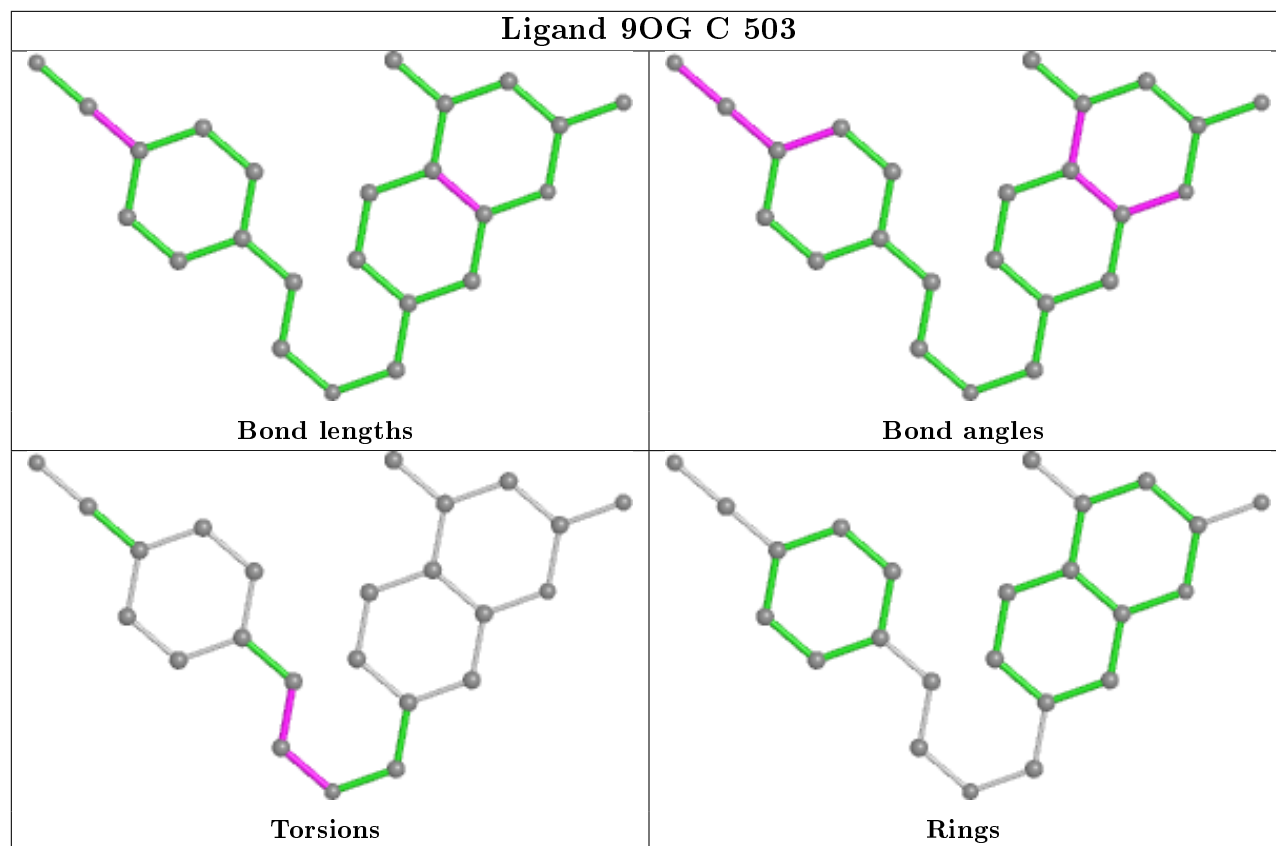


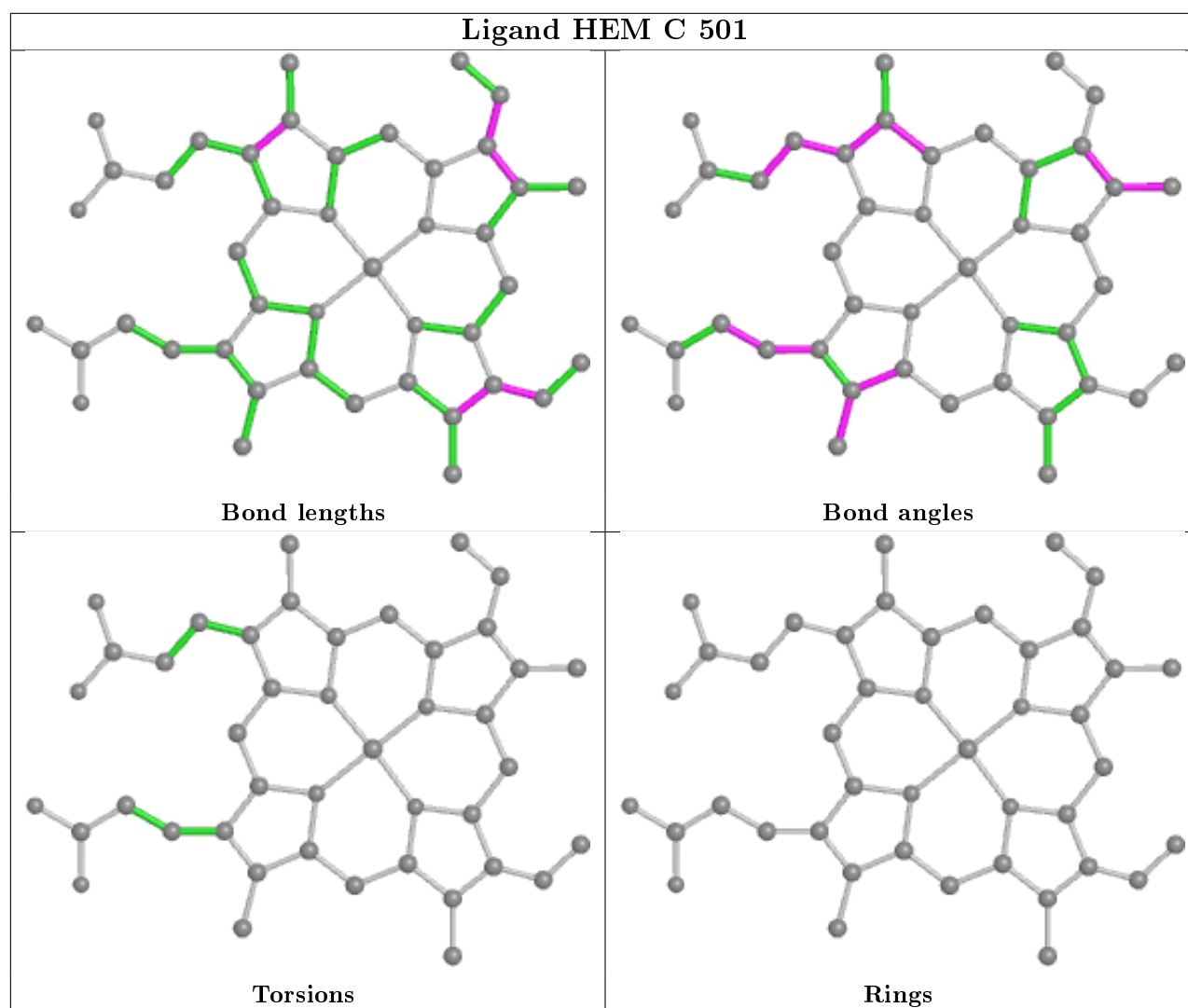












5.7 Other polymers [i](#)

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	404/440 (91%)	0.18	24 (5%)	22 24	42, 81, 143, 185	0
1	B	402/440 (91%)	-0.20	6 (1%)	73 75	39, 60, 103, 157	0
1	C	401/440 (91%)	-0.07	12 (2%)	50 53	41, 70, 114, 160	0
1	D	402/440 (91%)	-0.20	8 (1%)	65 68	38, 63, 103, 152	0
All	All	1609/1760 (91%)	-0.07	50 (3%)	49 52	38, 68, 125, 185	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	108	LYS	7.5
1	A	109	LEU	5.7
1	B	259	GLY	5.5
1	A	153	VAL	5.1
1	A	107	ARG	5.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

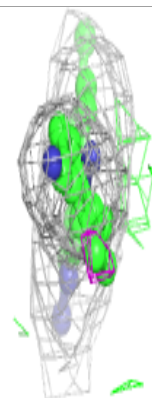
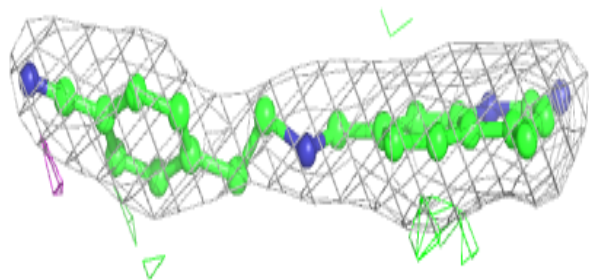
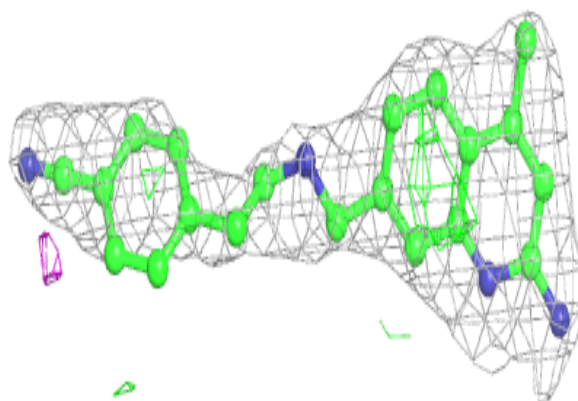
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	CL	A	509	1/1	0.61	0.12	91,91,91,91	0
5	BTB	C	505	14/14	0.79	0.13	74,96,107,109	0
8	CL	C	507	1/1	0.80	0.15	103,103,103,103	0
3	H4B	B	502	17/17	0.82	0.21	52,77,122,127	0
5	BTB	A	504	14/14	0.86	0.12	88,108,112,113	0
5	BTB	D	506	14/14	0.87	0.28	86,96,99,103	0
5	BTB	A	505	14/14	0.89	0.14	77,88,105,111	0
5	BTB	B	506	14/14	0.89	0.10	74,101,109,109	0
3	H4B	D	503	17/17	0.90	0.18	41,69,121,121	0
3	H4B	C	502	17/17	0.91	0.20	51,79,92,93	0
3	H4B	A	502	17/17	0.92	0.16	55,78,98,100	0
5	BTB	D	505	14/14	0.92	0.13	39,82,100,107	0
5	BTB	B	505	14/14	0.92	0.25	71,96,106,108	0
7	GOL	C	506	6/6	0.92	0.25	54,66,84,85	0
4	9OG	B	503	24/24	0.92	0.16	54,71,96,102	0
4	9OG	D	504	24/24	0.92	0.13	51,70,93,94	0
7	GOL	A	508	6/6	0.92	0.24	62,73,96,98	0
5	BTB	C	504	14/14	0.93	0.20	71,87,96,97	0
5	BTB	B	504	14/14	0.94	0.12	55,78,100,104	0
4	9OG	C	503	24/24	0.94	0.14	60,74,85,92	0
4	9OG	A	503	24/24	0.94	0.15	65,89,103,109	0
5	BTB	B	509	14/14	0.95	0.14	59,101,121,122	0
8	CL	D	507	1/1	0.95	0.10	69,69,69,69	0
5	BTB	A	506	14/14	0.95	0.13	73,93,98,98	0
8	CL	B	507	1/1	0.96	0.14	79,79,79,79	0
2	HEM	B	501	43/43	0.98	0.13	35,57,85,96	0
2	HEM	A	501	43/43	0.98	0.16	62,78,91,105	0
2	HEM	D	502	43/43	0.98	0.14	34,54,82,92	0
2	HEM	C	501	43/43	0.98	0.14	48,63,89,98	0
9	GD	A	510	1/1	0.99	0.18	105,105,105,105	0
9	GD	B	508	1/1	0.99	0.21	61,61,61,61	0
9	GD	B	510	1/1	0.99	0.14	102,102,102,102	0
6	ZN	D	501	1/1	1.00	0.14	60,60,60,60	0
6	ZN	A	507	1/1	1.00	0.15	73,73,73,73	0
9	GD	D	508	1/1	1.00	0.20	58,58,58,58	0

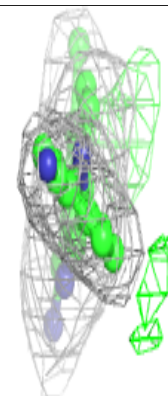
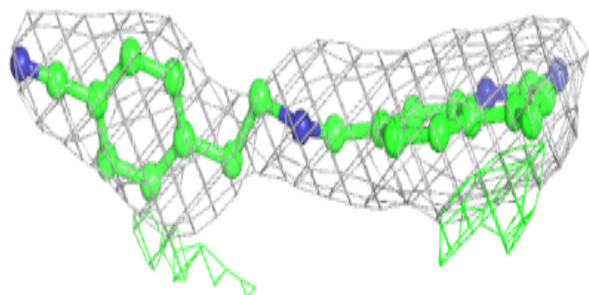
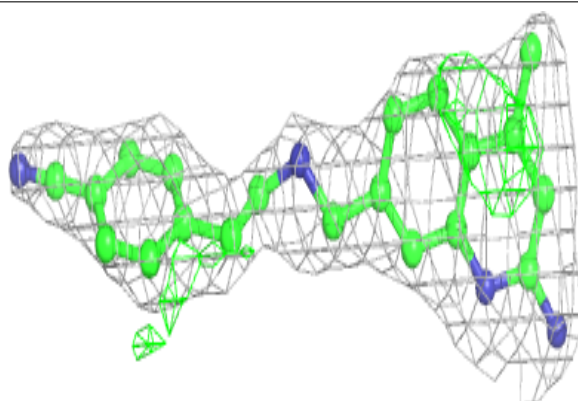
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 9OG 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)

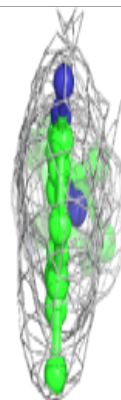
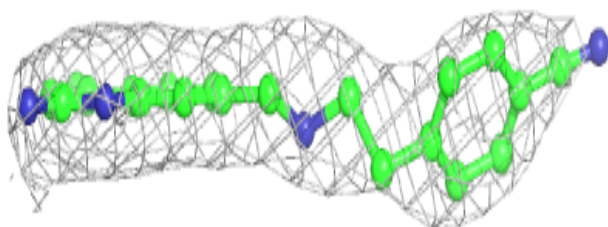
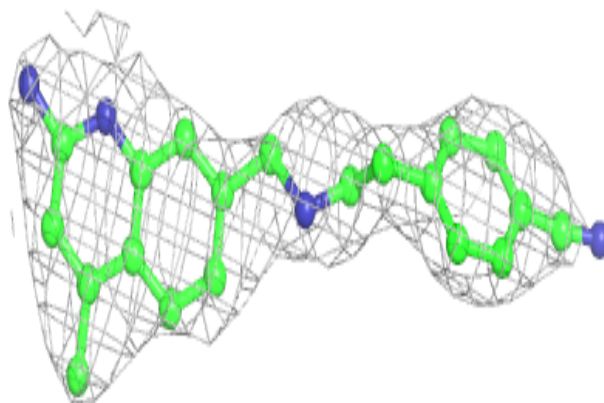
**Electron density around 9OG D 504:**

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

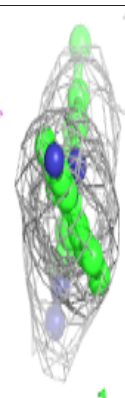
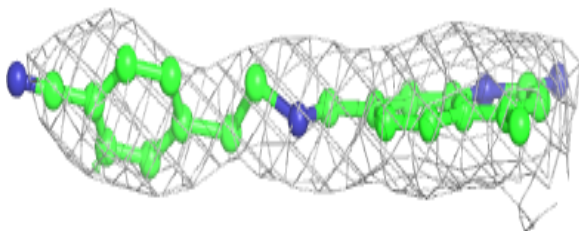
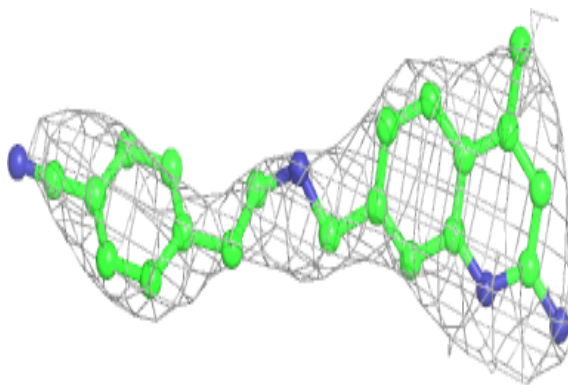


Electron density around 9OG C 503:

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

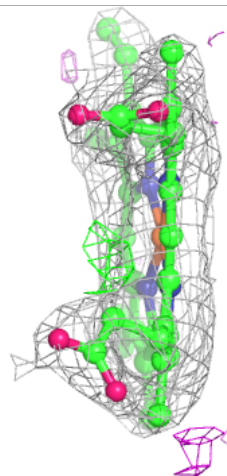
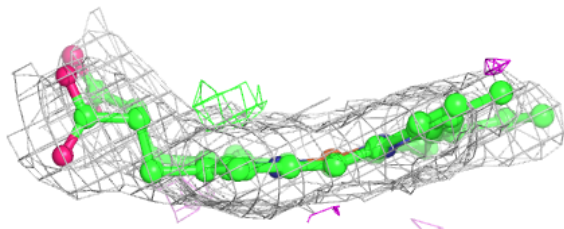
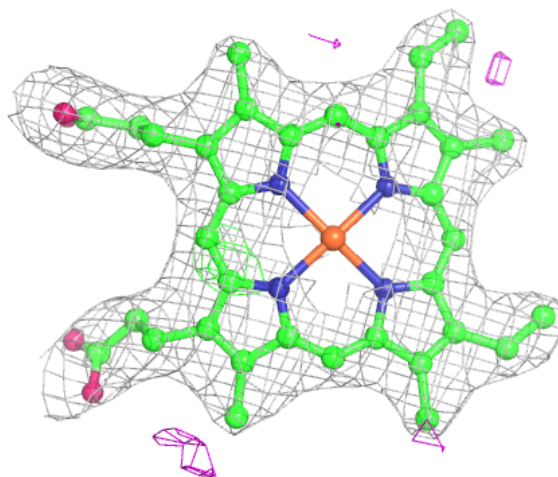
**Electron density around 9OG A 503:**

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and green (positive)



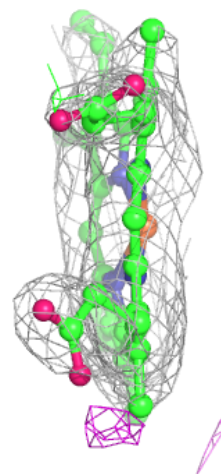
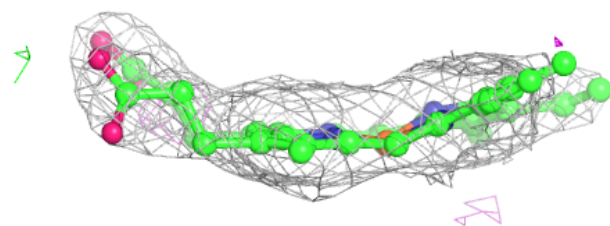
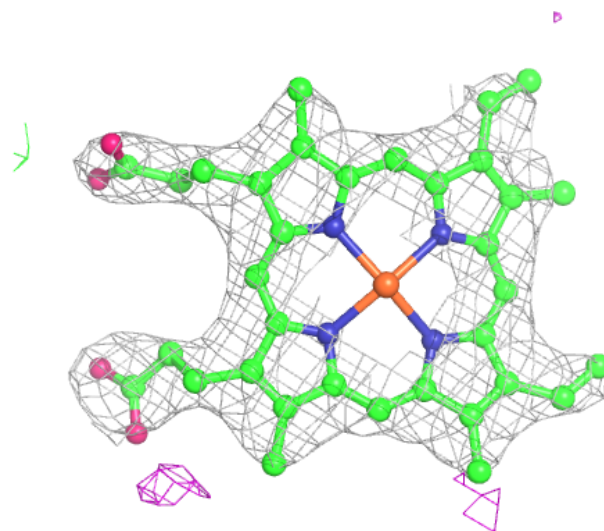
Electron density around HEM B 501:

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and green (positive)



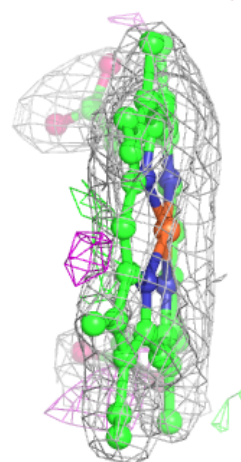
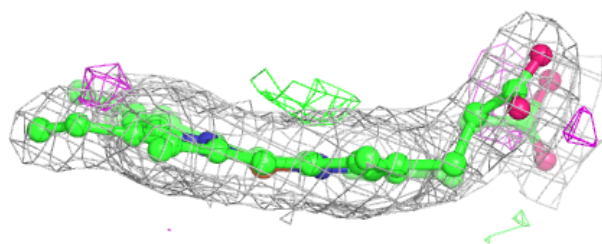
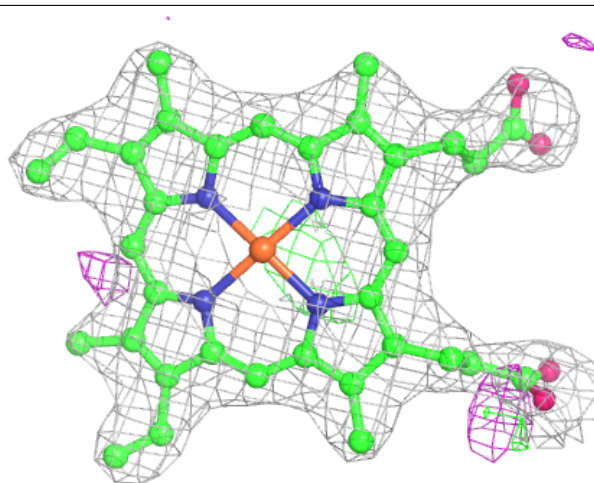
Electron density around HEM A 501:

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and green (positive)



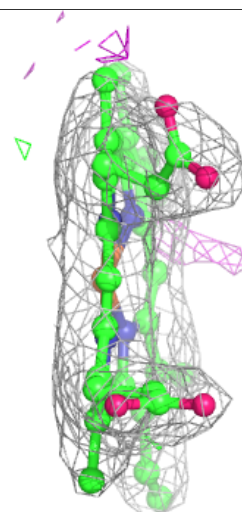
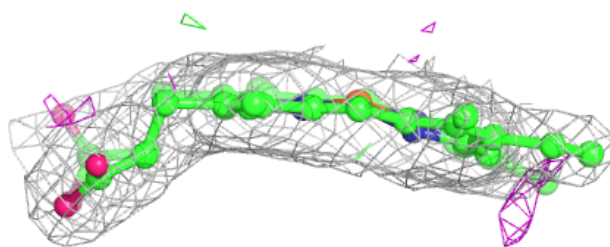
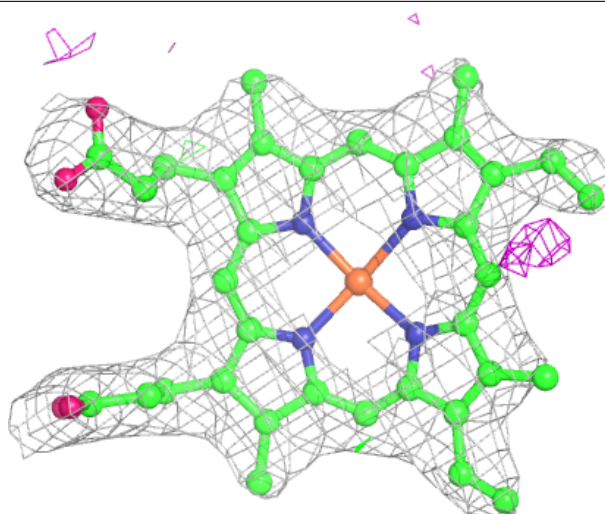
Electron density around HEM D 502:

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



Electron density around 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)



6.5 Other polymers ⓘ

There are no such residues in this entry.